



Full wwPDB EM Validation Report ⓘ

Jun 21, 2026 – 07:51 am BST

PDB ID : 6ZTM / pdb_00006ztm
EMDB ID : EMD-11420
Title : E. coli 70S-RNAP expressome complex in collided state without NusG
Authors : Webster, M.W.; Takacs, M.; Weixlbaumer, A.
Deposited on : 2020-07-20
Resolution : 3.30 Å (reported)
Based on initial models : 6ALH, 4YBB

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

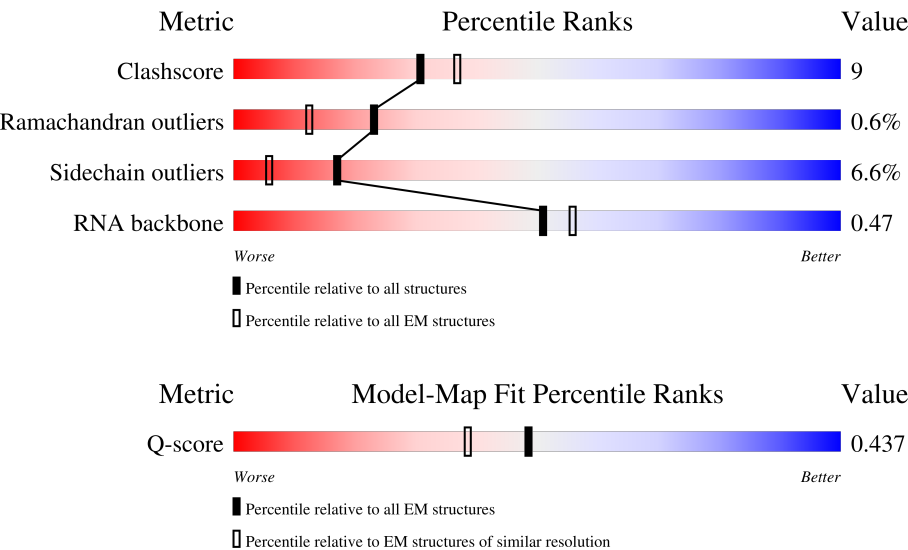
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal 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 i

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

The reported resolution of this entry is 3.30 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	15087 (2.80 - 3.80)

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	AA	1542	58% 33% 8% ..
2	AB	241	55% 72% 18% 6%
3	AC	233	18% 57% 27% 5% 10%

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Mol	Chain	Length	Quality of chain
4	AD	206	
5	AE	167	
6	AF	131	
7	AG	156	
8	AH	130	
9	AI	130	
10	AJ	103	
11	AK	129	
12	AL	124	
13	AM	118	
14	AN	101	
15	AO	89	
16	AP	82	
17	AQ	84	
18	AR	75	
19	AS	92	
20	AT	87	
21	AU	71	
22	AV	57	
23	AW	77	
24	AX	76	
25	BA	2904	
26	BB	120	
27	BC	273	
28	BD	209	

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Mol	Chain	Length	Quality of chain
29	BE	201	
30	BF	179	
31	BG	177	
32	BH	149	
33	BK	142	
34	BL	123	
35	BM	144	
36	BN	136	
37	BO	127	
38	BP	117	
39	BQ	115	
40	BR	118	
41	BS	103	
42	BT	110	
43	BU	100	
44	BV	104	
45	BW	94	
46	BX	85	
47	BY	78	
48	BZ	63	
49	B1	59	
50	B2	57	
51	B3	55	
52	B4	46	
53	B5	65	

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Mol	Chain	Length	Quality of chain
54	B6	50	
55	CN	39	
56	CT	39	
57	CA	329	
57	CB	329	
58	CC	1342	
59	CD	1407	

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 171689 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	AA	1533	Total	C	N	O	P	0	0
			32907	14682	6037	10655	1533		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	226	Total	C	N	O	S	0	0
			1765	1116	317	324	8		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	209	Total	C	N	O	S	0	0
			1640	1038	308	291	3		

- Molecule 4 is a protein called 30S ribosomal protein S4.

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

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	156	Total	C	N	O	S	0	0
			1148	715	217	210	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AE	9	CYS	GLY	conflict	UNP A0A090BZW5

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AF	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	153	Total	C	N	O	S	0	0
			1203	750	231	218	4		

- Molecule 8 is a protein called 30S ribosomal protein S8.

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

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AI	128	Total	C	N	O	S	0	0
			1031	639	207	182	3		

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	100	Total	C	N	O	S	0	0
			800	500	153	146	1		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AK	116	Total	C	N	O	S	0	0
			866	534	170	159	3		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL	122	Total	C	N	O	S	0	0
			949	587	195	163	4		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 14 is a protein called 30S ribosomal protein S14.

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

- Molecule 15 is a protein called 30S ribosomal protein S15.

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

- Molecule 16 is a protein called 30S ribosomal protein S16.

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

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	79	Total	C	N	O	S	0	0
			641	406	120	112	3		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	AR	54	Total	C	N	O	0	0
			443	281	81	81		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AS	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AT	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AU	70	Total	C	N	O	S	0	0
			590	366	125	98	1		

- Molecule 22 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	30	Total	C	N	O	P	0	0
			636	285	115	206	30		

- Molecule 23 is a RNA chain called tRNA(fmet) P-site.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	AW	77	Total	C	N	O	P	S	0	0
			1645	734	297	536	77	1		

- Molecule 24 is a RNA chain called Phe-NH-tRNA(Phe) A-site.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	AX	76	Total	C	N	O	P	S	0	0
			1624	724	290	533	76	1		

- Molecule 25 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BA	2901	Total	C	N	O	P	0	0
			62290	27795	11458	20136	2901		

- Molecule 26 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BB	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 27 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BC	272	Total	C	N	O	S	0	0
			2092	1294	425	366	7		

- Molecule 28 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BD	209	Total	C	N	O	S	0	0
			1566	980	288	294	4		

- Molecule 29 is a protein called 50S ribosomal protein L4.

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

- Molecule 30 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BF	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 31 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BG	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 32 is a protein called 50S ribosomal protein L9.

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

- Molecule 33 is a protein called 50S ribosomal protein L13.

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

- Molecule 34 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BL	123	Total	C	N	O	S	0	0
			947	593	181	167	6		

- Molecule 35 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BM	144	Total	C	N	O	S	0	0
			1052	653	207	190	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BM	77	VAL	ILE	conflict	UNP P02413

- Molecule 36 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BN	136	Total	C	N	O	S	0	0
			1075	686	205	178	6		

- Molecule 37 is a protein called 50S ribosomal protein L17.

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

- Molecule 38 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BP	117	Total	C	N	O	S	0	0
			900	557	179	163	1		

- Molecule 39 is a protein called 50S ribosomal protein L19.

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

- Molecule 40 is a protein called 50S ribosomal protein L20.

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

- Molecule 41 is a protein called 50S ribosomal protein L21.

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

- Molecule 42 is a protein called 50S ribosomal protein L22.

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

- Molecule 43 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BU	95	Total	C	N	O	S	0	0
			757	479	141	135	2		

- Molecule 44 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	BV	103	Total	C	N	O	0	0
			789	498	148	143		

- Molecule 45 is a protein called 50S ribosomal protein L25.

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

- Molecule 46 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BX	76	Total	C	N	O	S	0	0
			582	360	117	104	1		

- Molecule 47 is a protein called 50S ribosomal protein L28.

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

- Molecule 48 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BZ	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 49 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	B1	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	B2	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 51 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	B3	53	Total	C	N	O	0	0
			436	281	80	75		

- Molecule 52 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	B4	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 53 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	B5	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 54 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	B6	38	Total	C	N	O	S	0	0
			301	185	65	47	4		

- Molecule 55 is a DNA chain called Non-template DNA strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	CN	30	Total	C	N	O	P	0	0
			618	294	114	180	30		

- Molecule 56 is a DNA chain called Template DNA strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	CT	30	Total	C	N	O	P	0	0
			606	288	105	183	30		

- Molecule 57 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	CA	229	Total	C	N	O	S	0	0
			1775	1106	313	350	6		
57	CB	219	Total	C	N	O	S	0	0
			1684	1051	295	332	6		

- Molecule 58 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	CC	1320	Total	C	N	O	S	0	0
			10415	6535	1815	2021	44		

- Molecule 59 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	CD	1333	Total	C	N	O	S	0	0
			10375	6518	1851	1956	50		

- Molecule 60 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

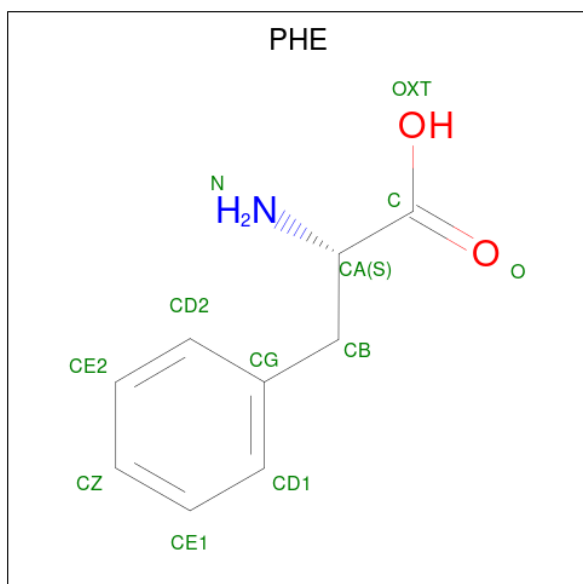
Mol	Chain	Residues	Atoms		AltConf
60	AA	119	Total	Mg	0
			119	119	
60	AW	2	Total	Mg	0
			2	2	

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Mol	Chain	Residues	Atoms		AltConf
60	BA	294	Total	Mg	0
			294	294	
60	BB	2	Total	Mg	0
			2	2	
60	BC	1	Total	Mg	0
			1	1	
60	BO	1	Total	Mg	0
			1	1	
60	B2	1	Total	Mg	0
			1	1	
60	CD	1	Total	Mg	0
			1	1	

- Molecule 61 is PHENYLALANINE (CCD ID: PHE) (formula: $C_9H_{11}NO_2$).



Mol	Chain	Residues	Atoms				AltConf
61	AX	1	Total	C	N	O	0
			11	9	1	1	

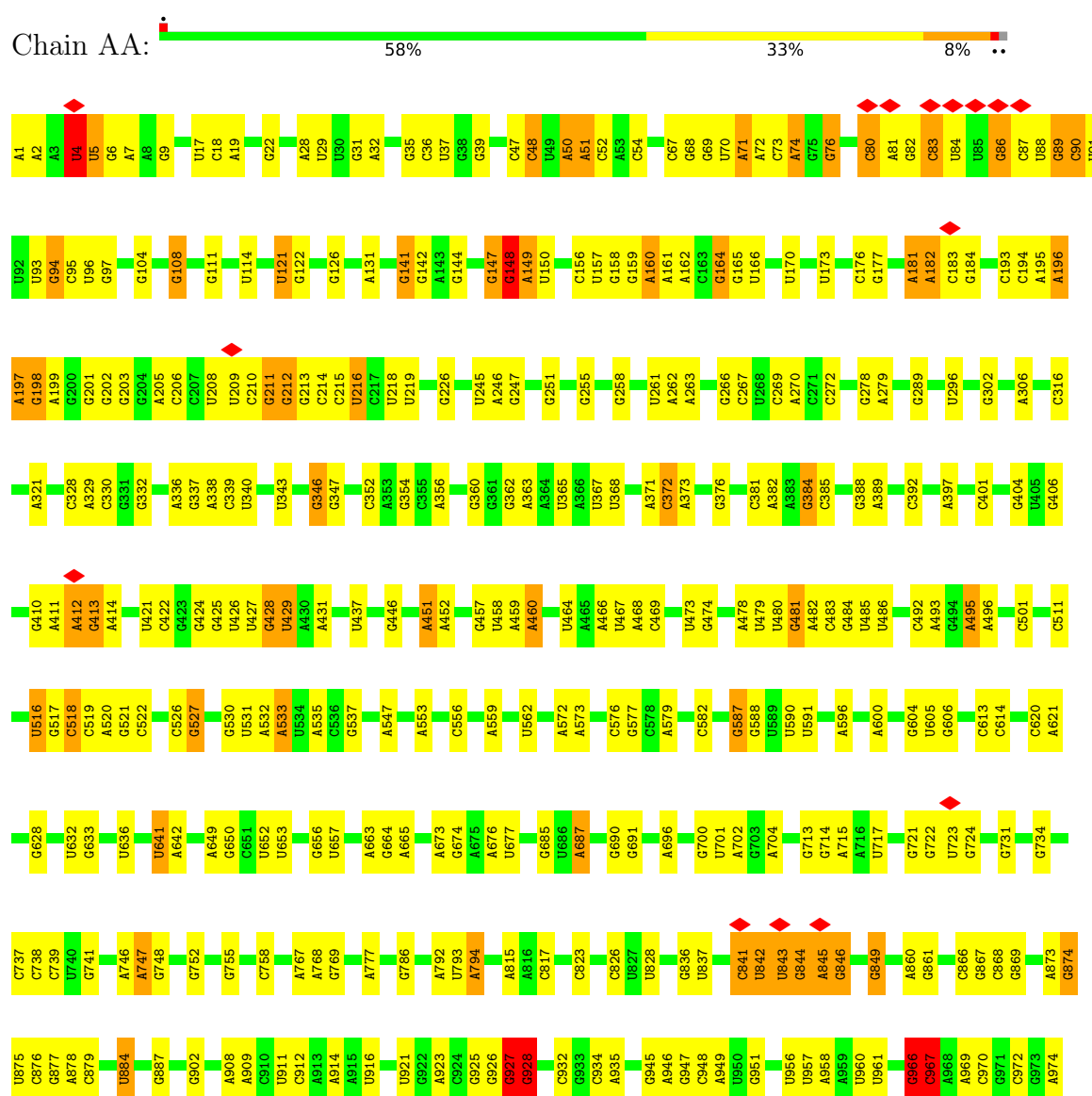
- Molecule 62 is ZINC ION (CCD ID: ZN) (formula: Zn).

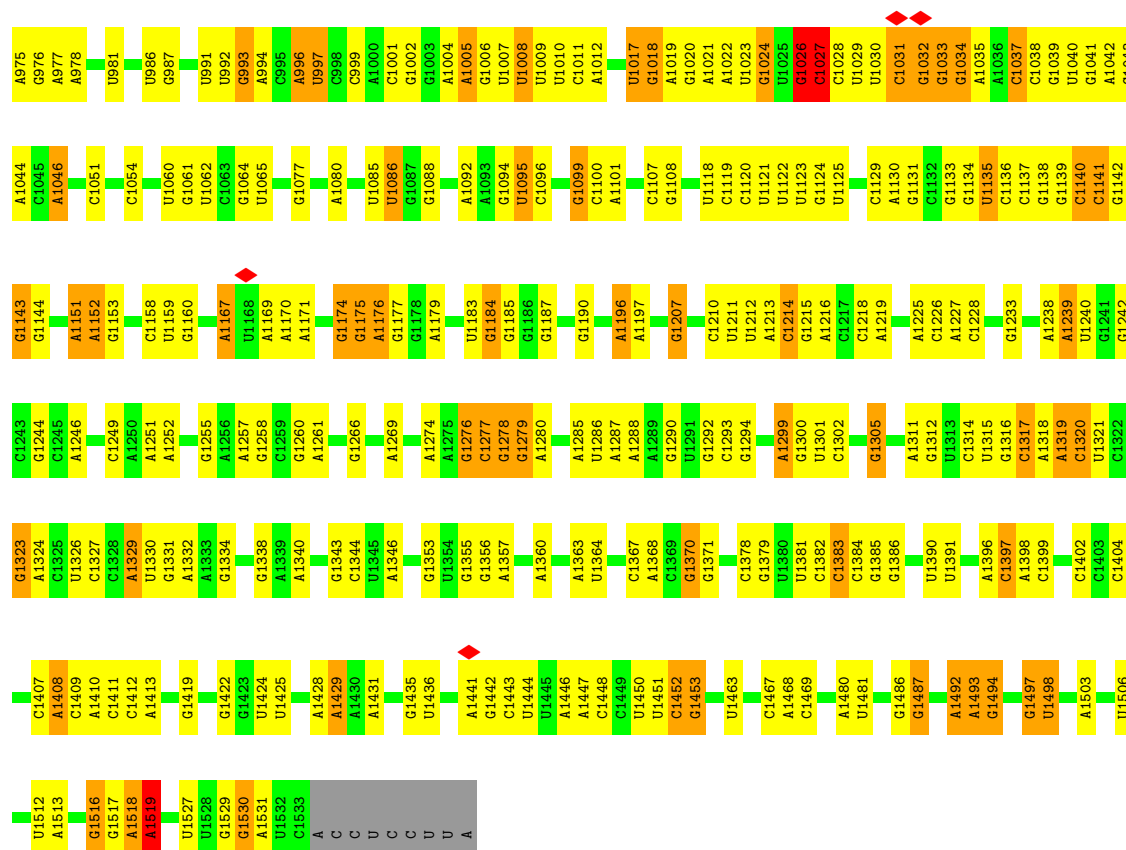
Mol	Chain	Residues	Atoms		AltConf
62	B6	1	Total	Zn	0
			1	1	
62	CD	2	Total	Zn	0
			2	2	

3 Residue-property plots

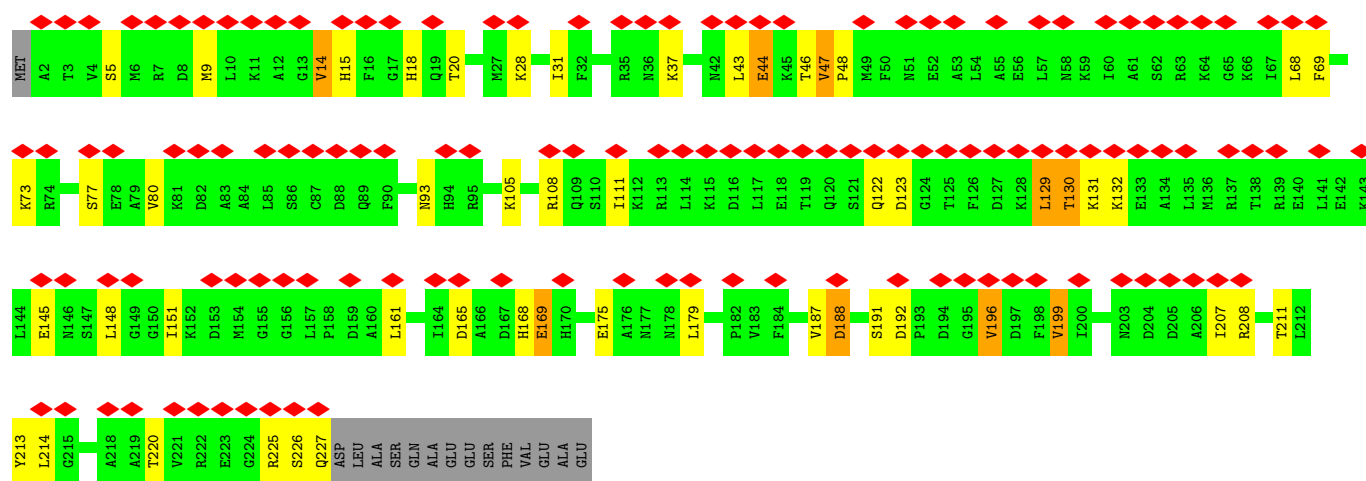
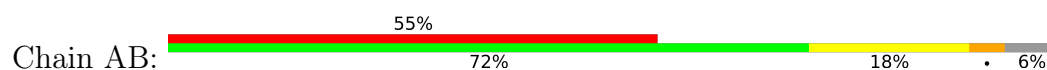
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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



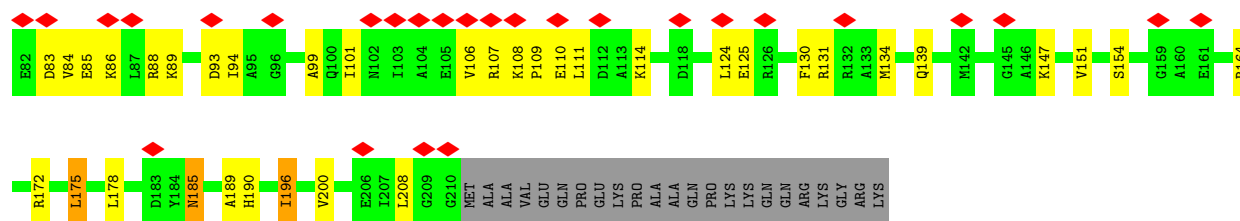


• Molecule 2: 30S ribosomal protein S2

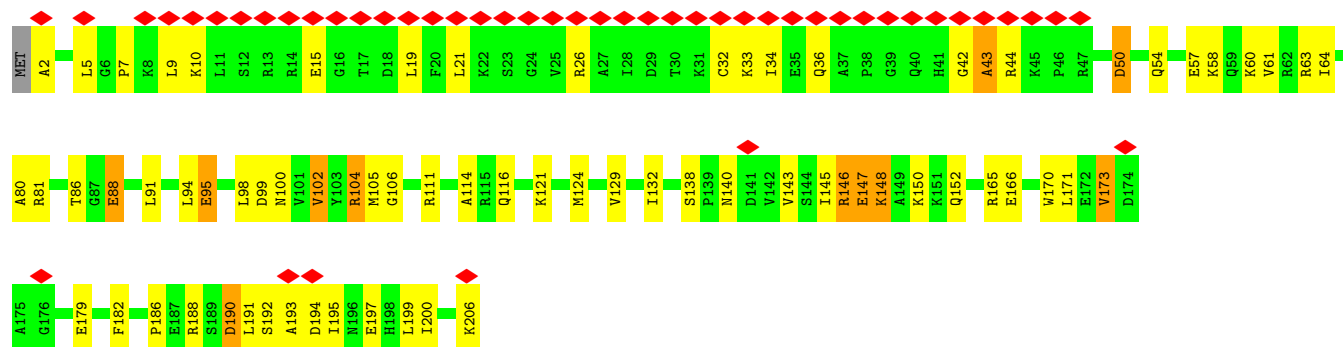


• Molecule 3: 30S ribosomal protein S3

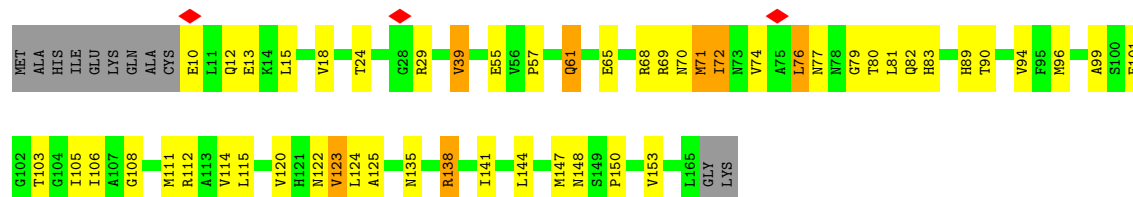




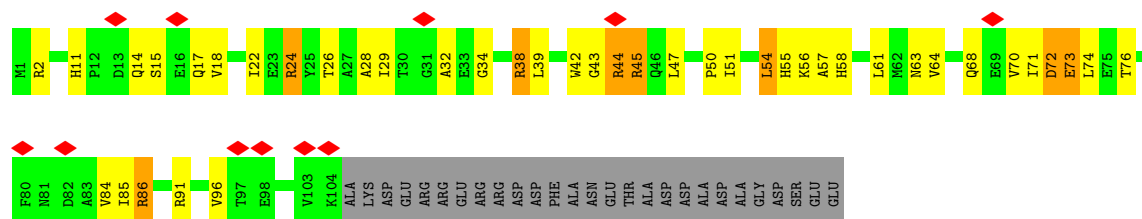
• Molecule 4: 30S ribosomal protein S4



• Molecule 5: 30S ribosomal protein S5

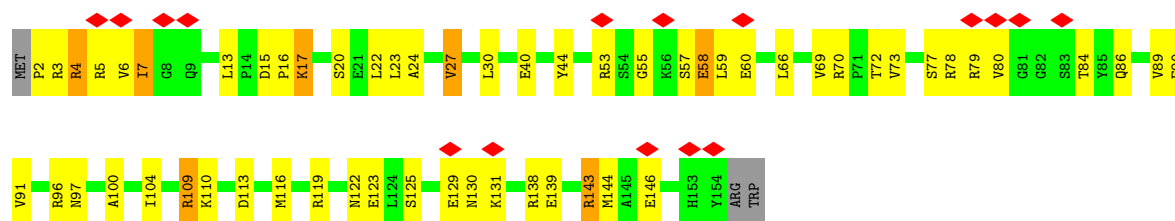


• Molecule 6: 30S ribosomal protein S6

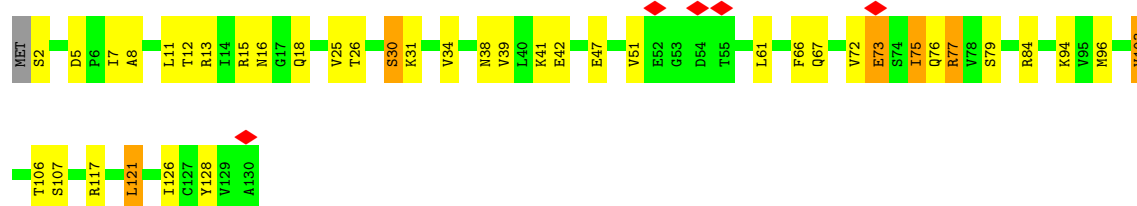


• Molecule 7: 30S ribosomal protein S7

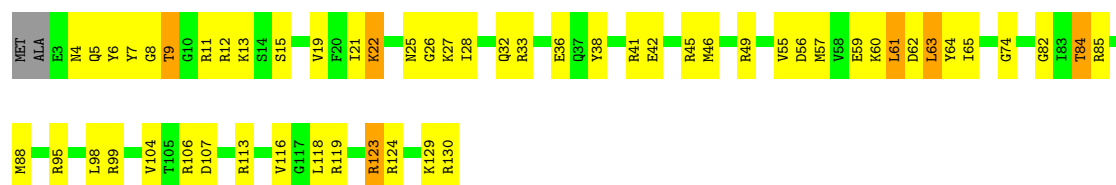




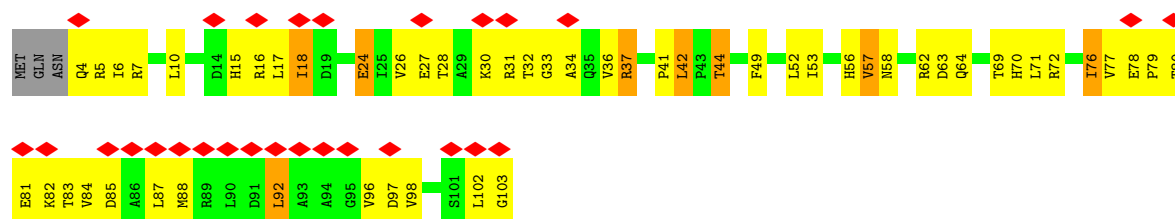
• Molecule 8: 30S ribosomal protein S8



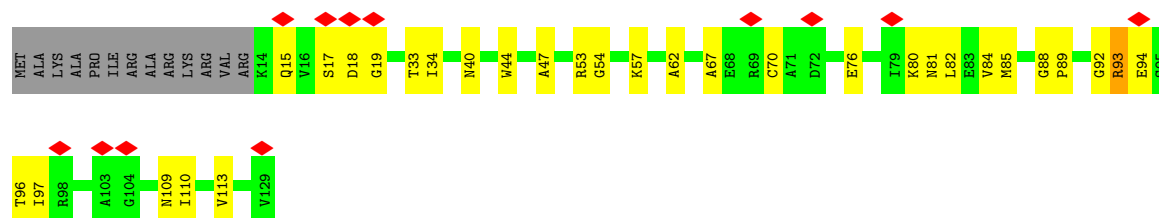
• Molecule 9: 30S ribosomal protein S9



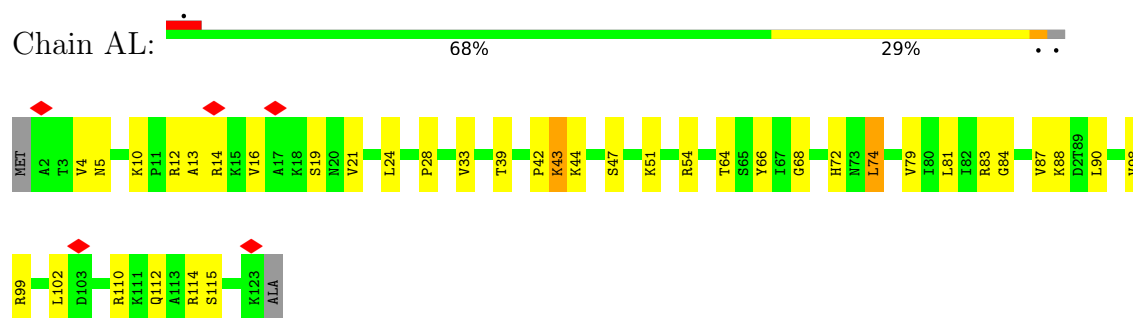
• Molecule 10: 30S ribosomal protein S10



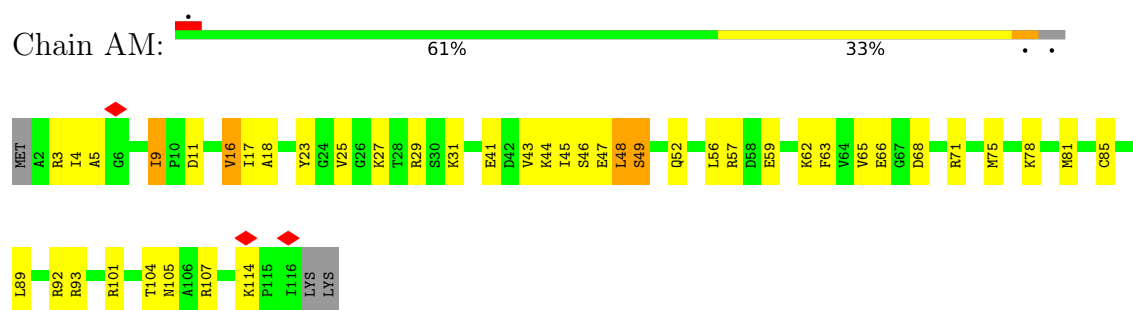
• Molecule 11: 30S ribosomal protein S11



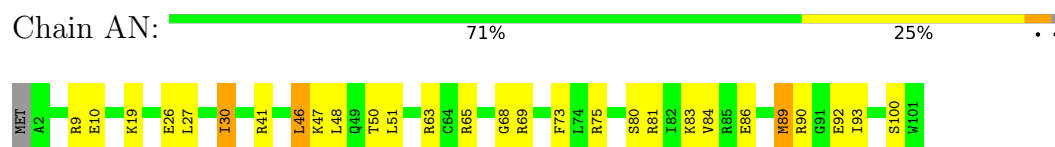
• Molecule 12: 30S ribosomal protein S12



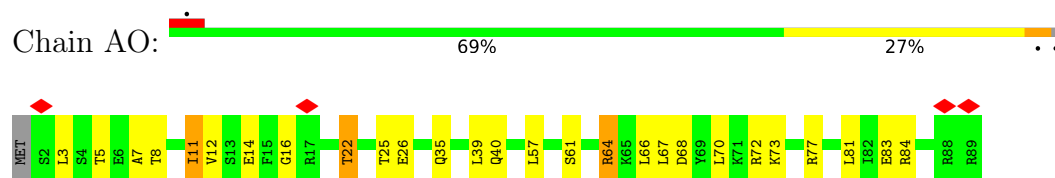
• Molecule 13: 30S ribosomal protein S13



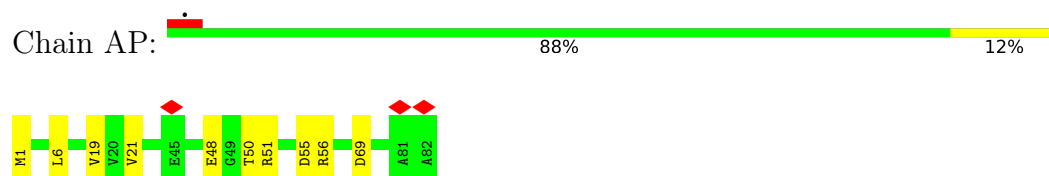
• Molecule 14: 30S ribosomal protein S14



• Molecule 15: 30S ribosomal protein S15



• Molecule 16: 30S ribosomal protein S16

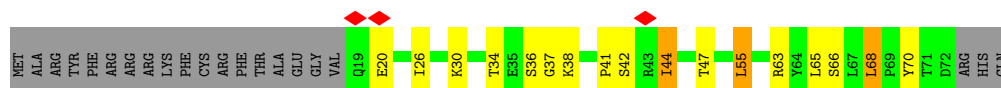


• Molecule 17: 30S ribosomal protein S17





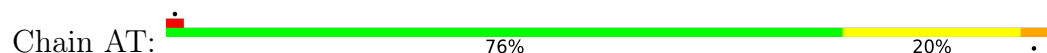
- Molecule 18: 30S ribosomal protein S18



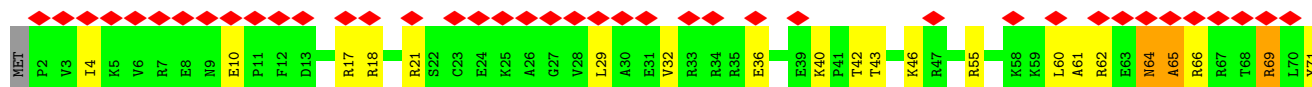
- Molecule 19: 30S ribosomal protein S19



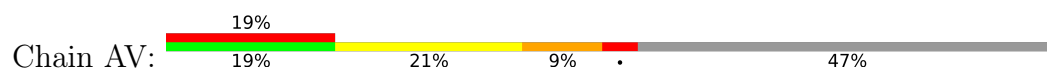
- Molecule 20: 30S ribosomal protein S20



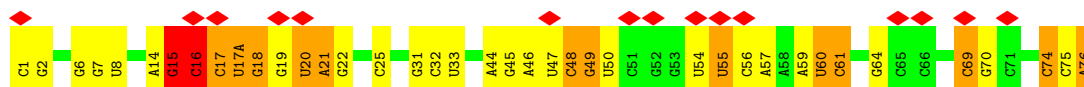
- Molecule 21: 30S ribosomal protein S21



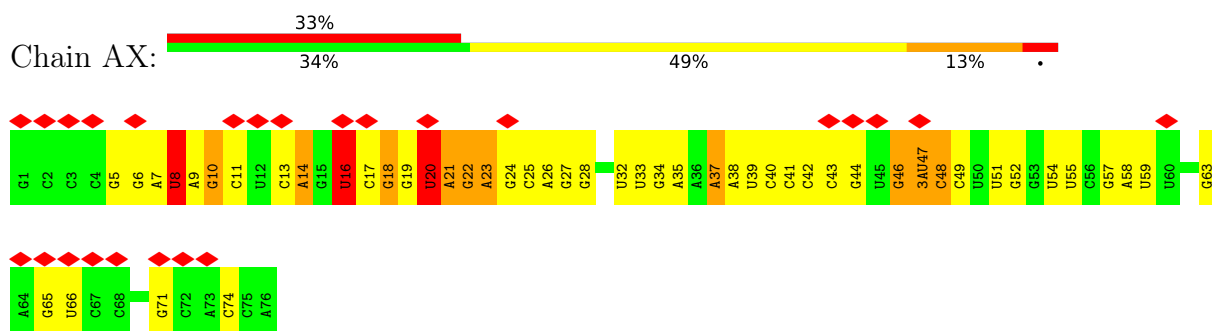
- Molecule 22: mRNA



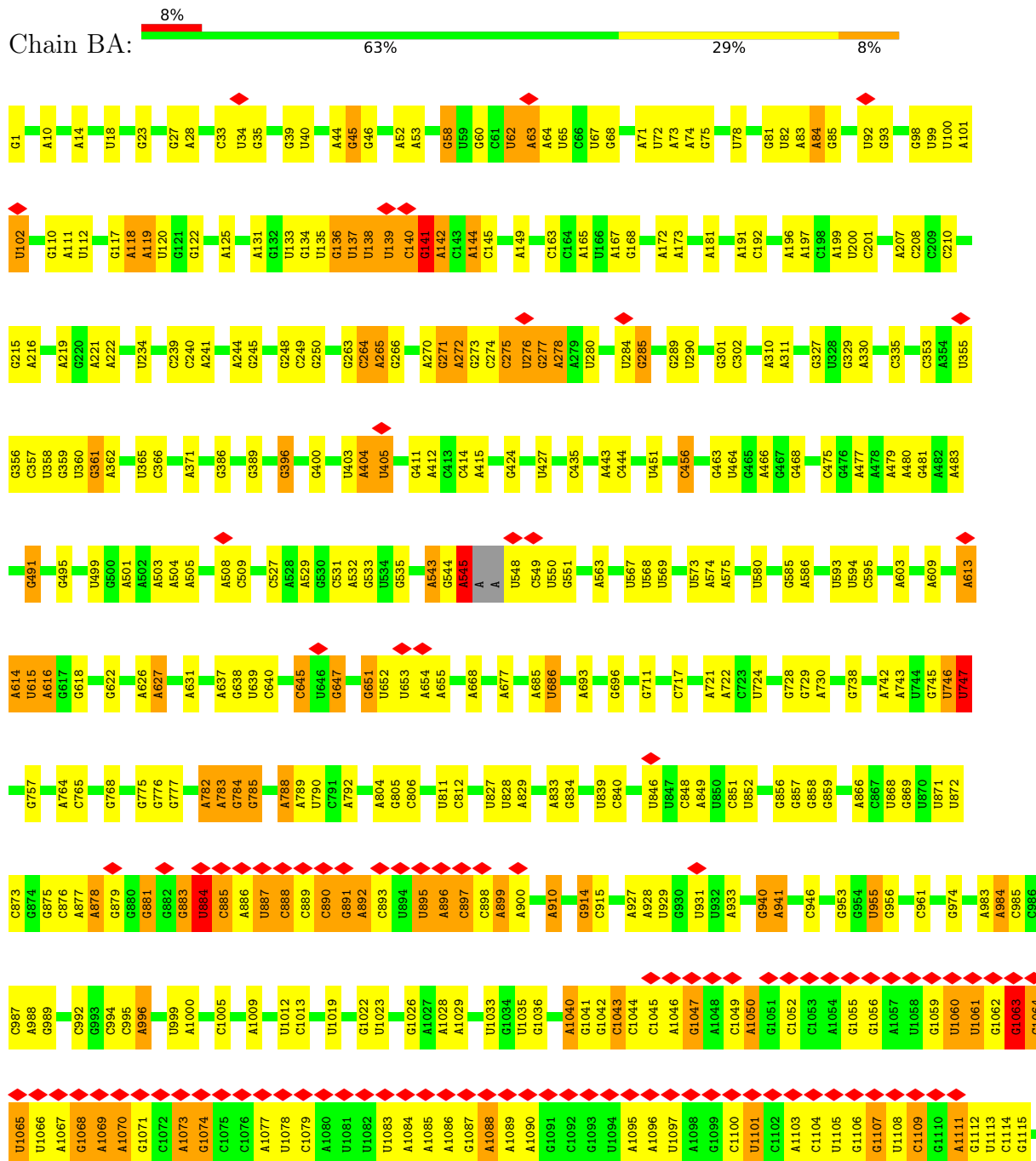
- Molecule 23: tRNA(fmet) P-site

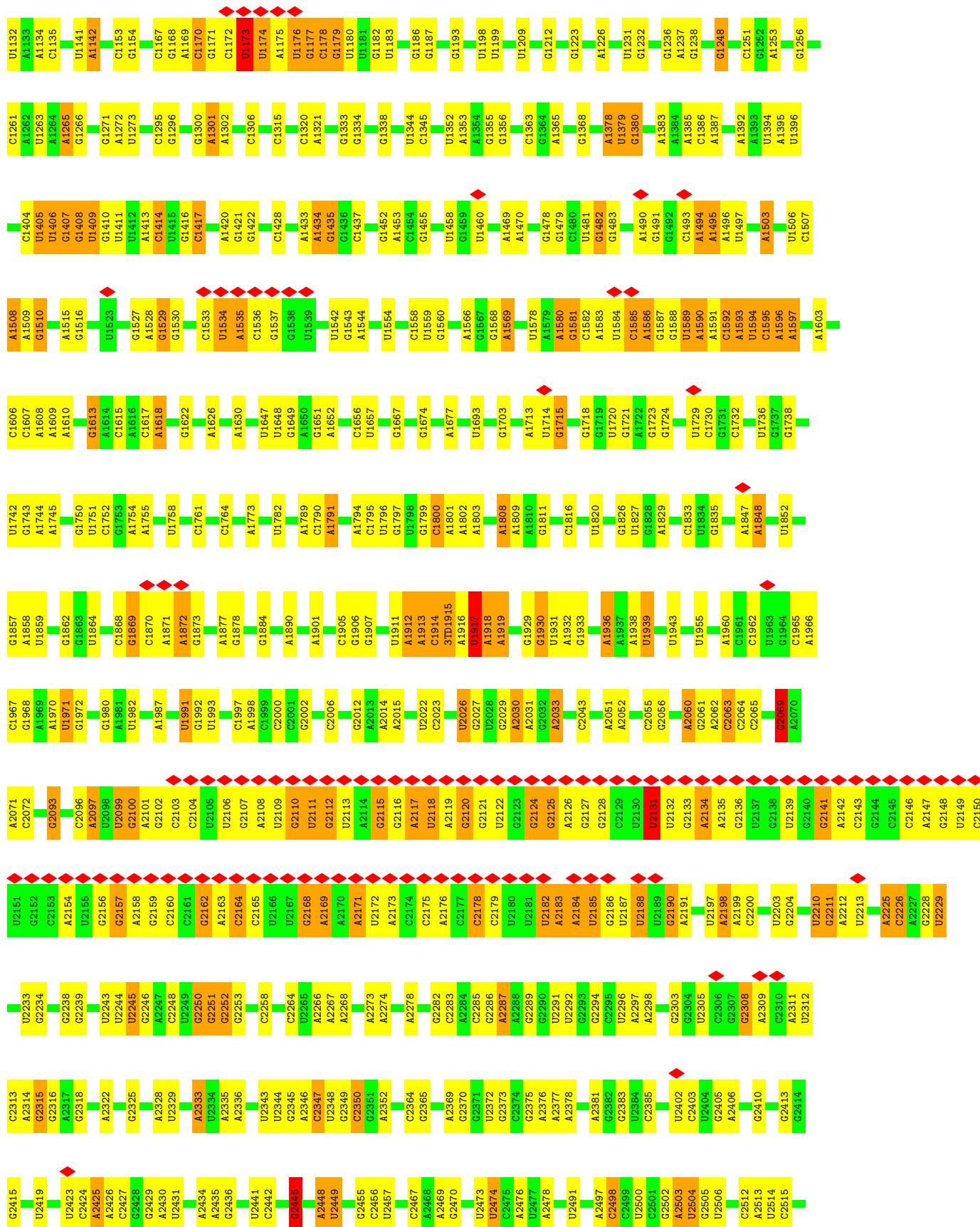


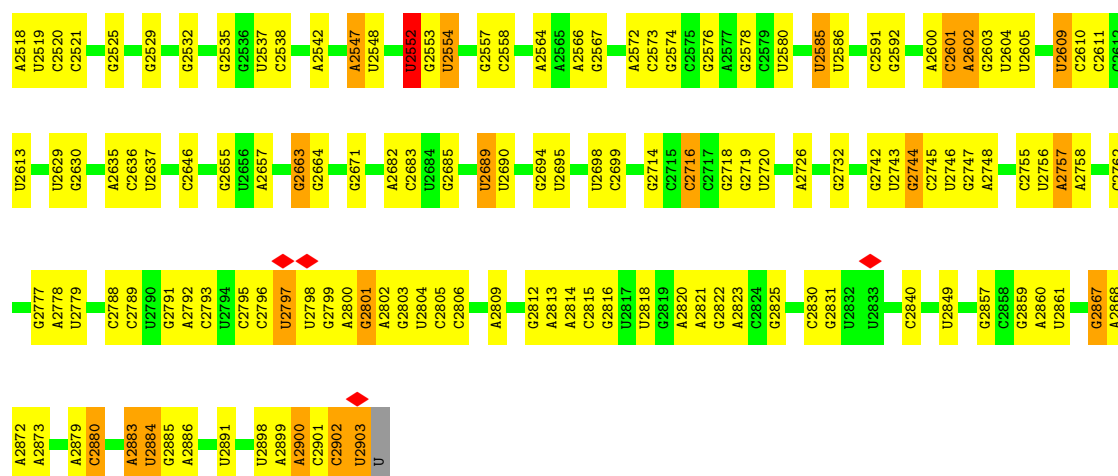
- Molecule 24: Phe-NH-tRNA(Phe) A-site



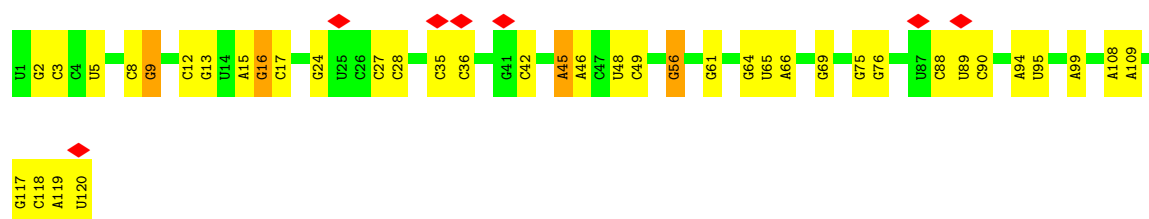
• Molecule 25: 23S ribosomal RNA



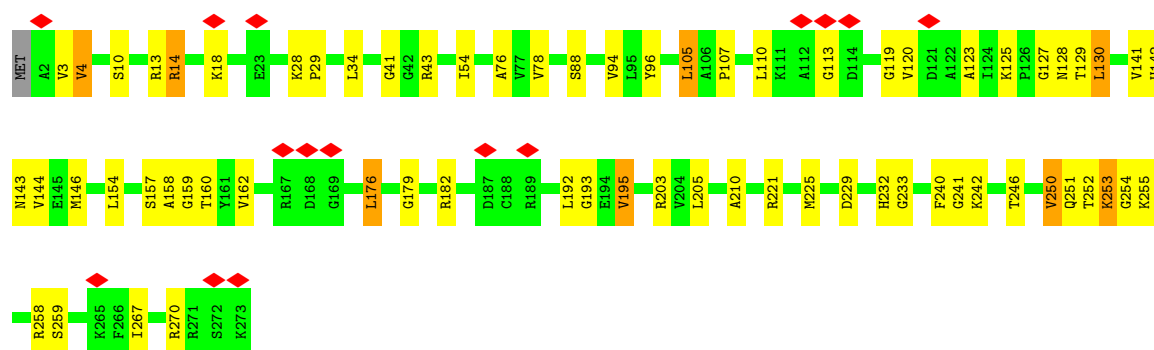
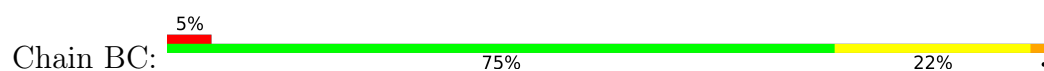




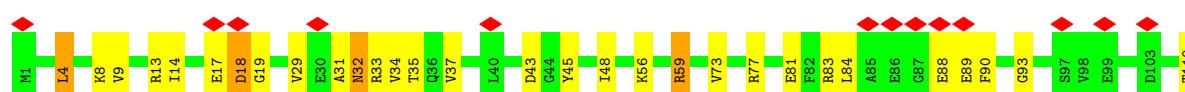
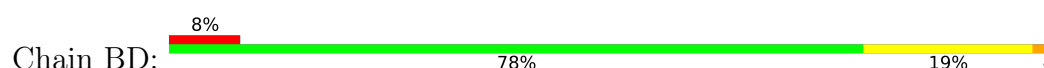
• Molecule 26: 5S ribosomal RNA

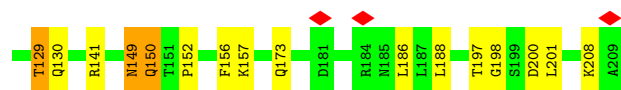


• Molecule 27: 50S ribosomal protein L2

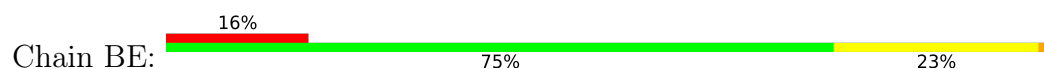


• Molecule 28: 50S ribosomal protein L3

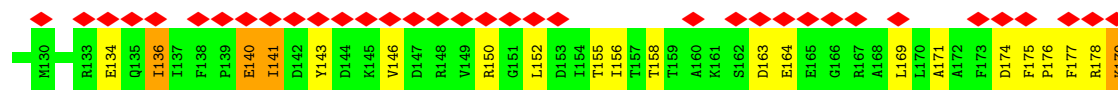
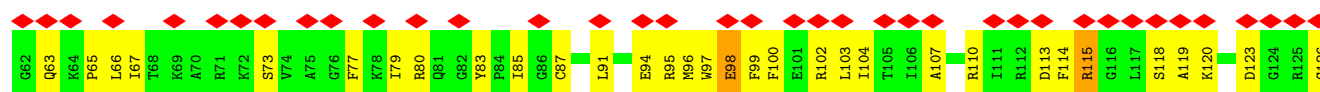
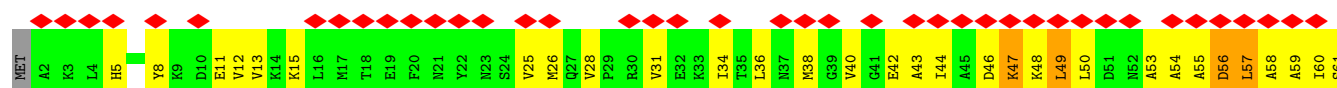




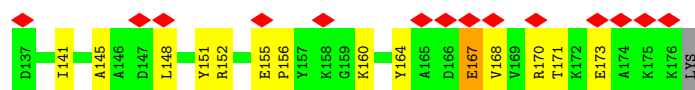
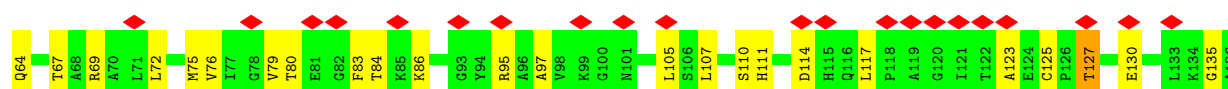
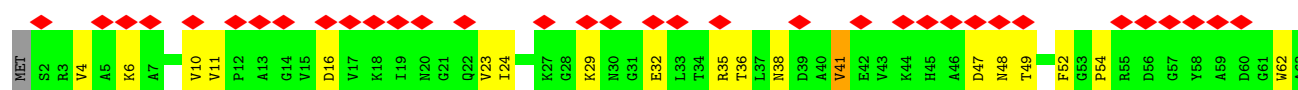
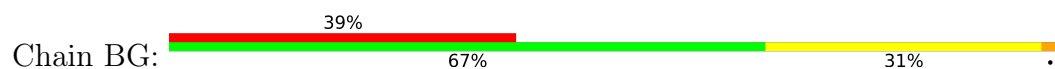
- Molecule 29: 50S ribosomal protein L4



- Molecule 30: 50S ribosomal protein L5

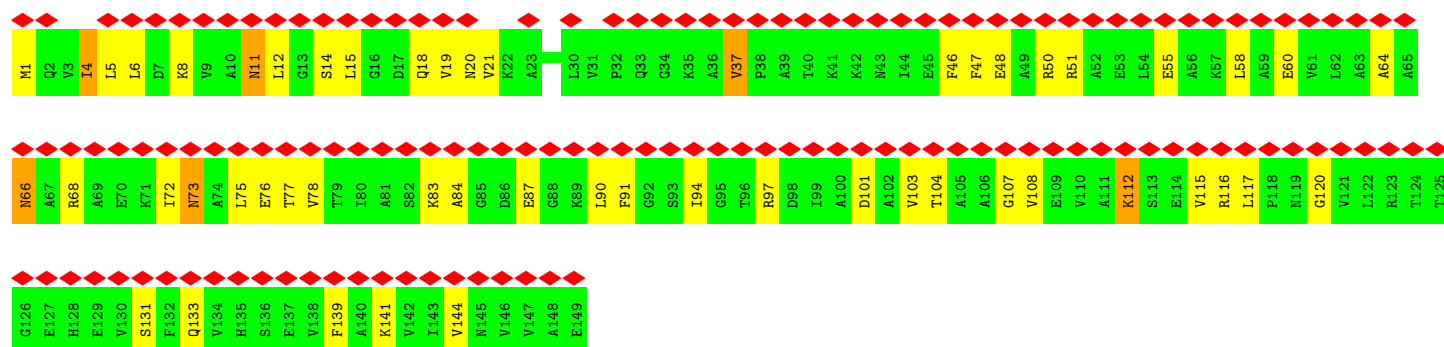


- Molecule 31: 50S ribosomal protein L6

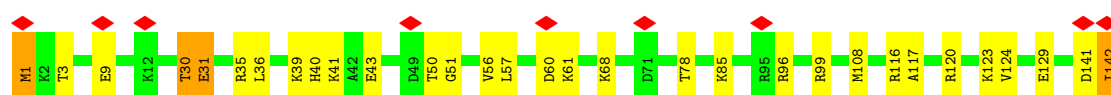
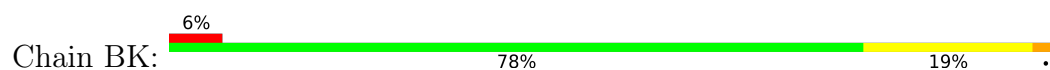


- Molecule 32: 50S ribosomal protein L9

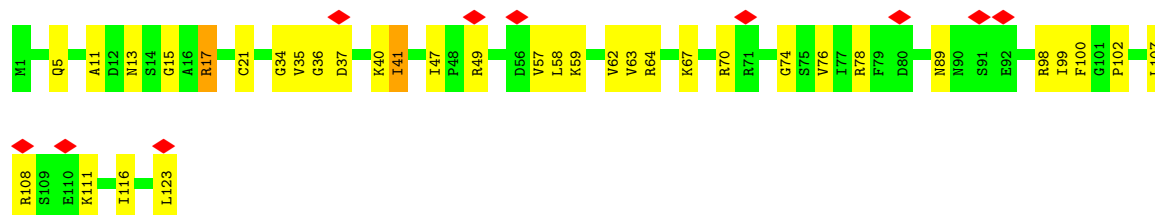
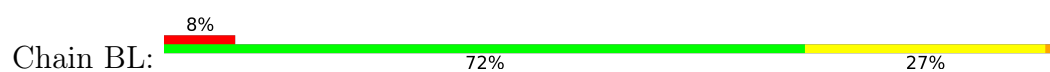




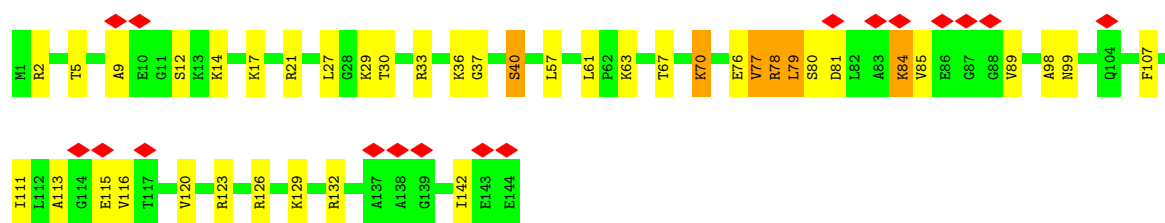
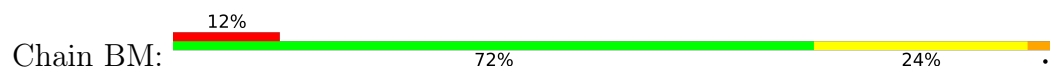
• Molecule 33: 50S ribosomal protein L13



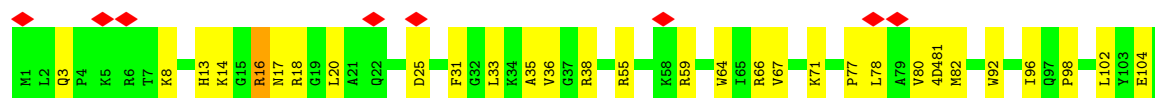
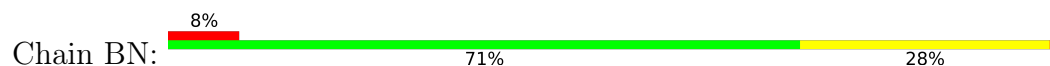
• Molecule 34: 50S ribosomal protein L14

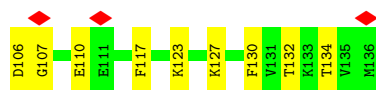


• Molecule 35: 50S ribosomal protein L15

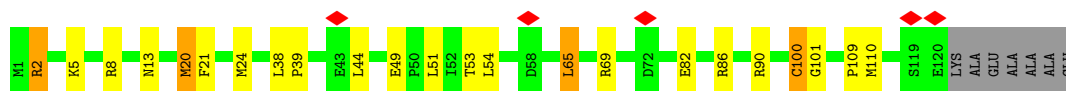
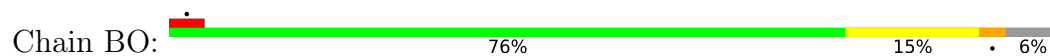


• Molecule 36: 50S ribosomal protein L16

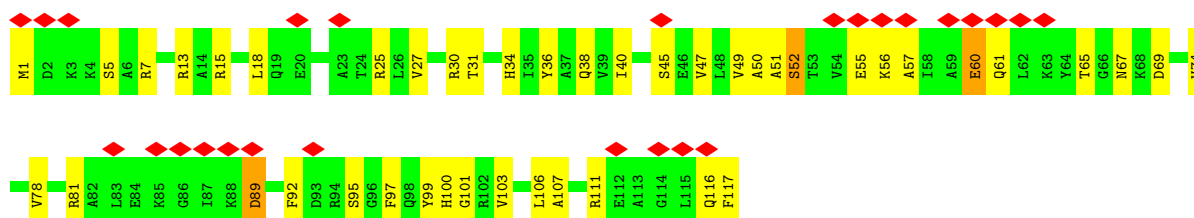




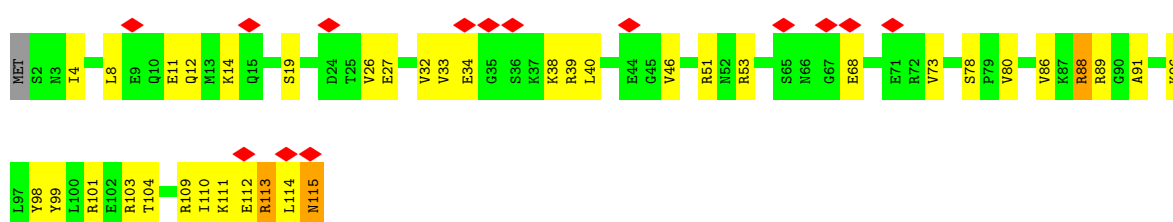
- Molecule 37: 50S ribosomal protein L17



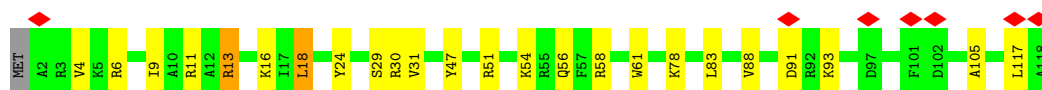
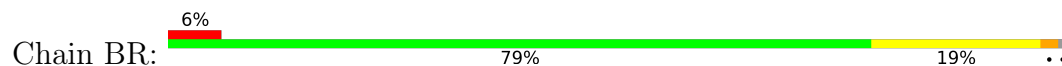
- Molecule 38: 50S ribosomal protein L18



- Molecule 39: 50S ribosomal protein L19



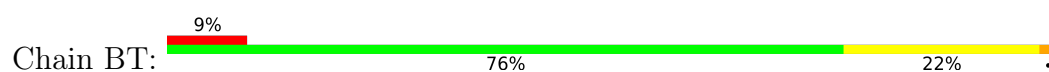
- Molecule 40: 50S ribosomal protein L20



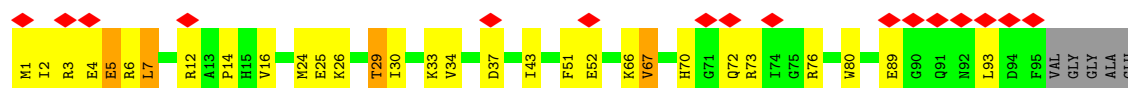
- Molecule 41: 50S ribosomal protein L21



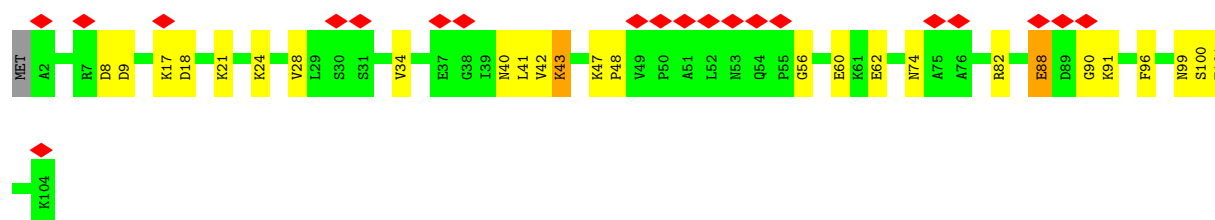
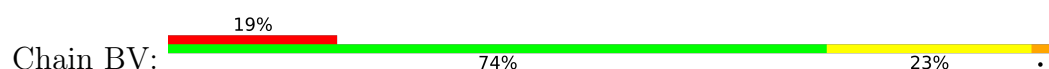
- Molecule 42: 50S ribosomal protein L22



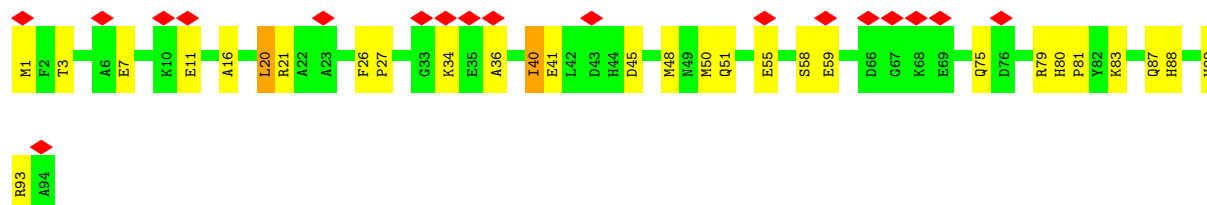
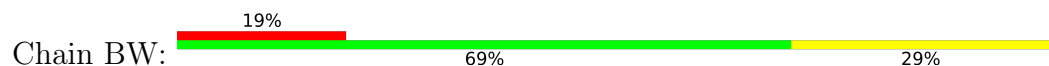
• Molecule 43: 50S ribosomal protein L23



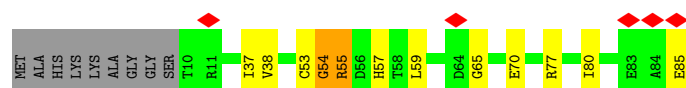
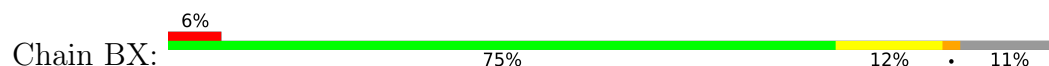
• Molecule 44: 50S ribosomal protein L24



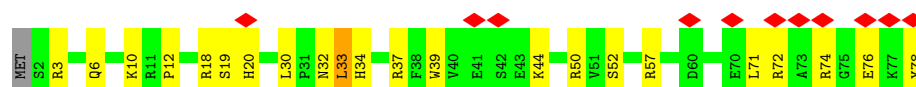
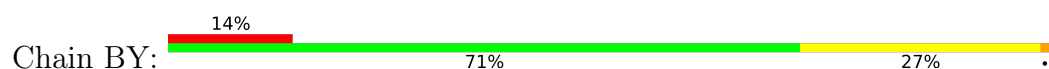
• Molecule 45: 50S ribosomal protein L25



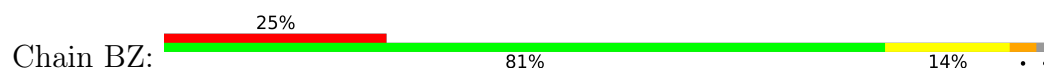
• Molecule 46: 50S ribosomal protein L27



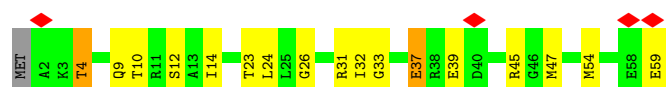
• Molecule 47: 50S ribosomal protein L28



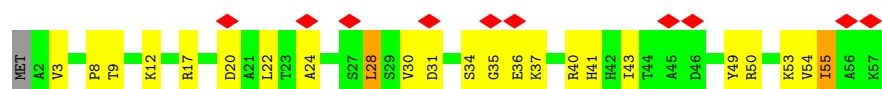
• Molecule 48: 50S ribosomal protein L29



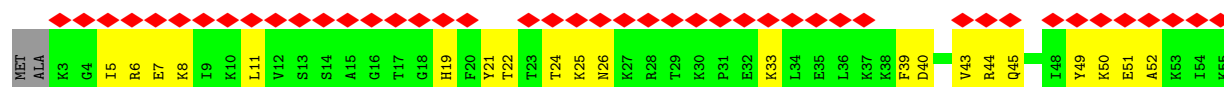
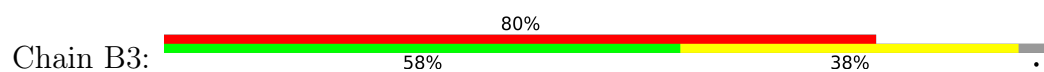
• Molecule 49: 50S ribosomal protein L30



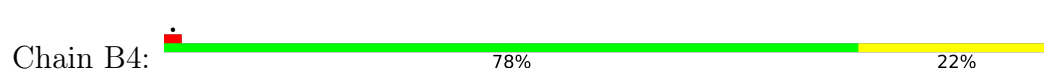
• Molecule 50: 50S ribosomal protein L32



• Molecule 51: 50S ribosomal protein L33



• Molecule 52: 50S ribosomal protein L34

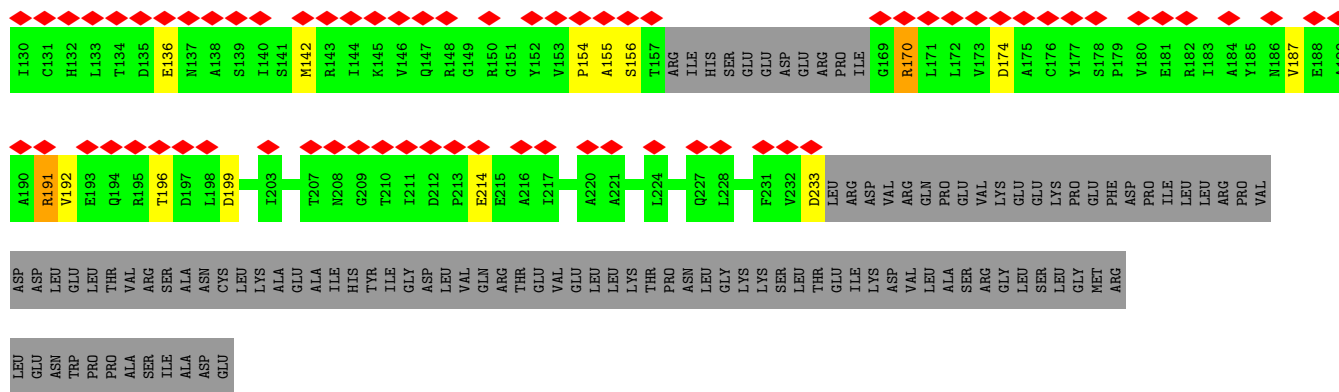


• Molecule 53: 50S ribosomal protein L35

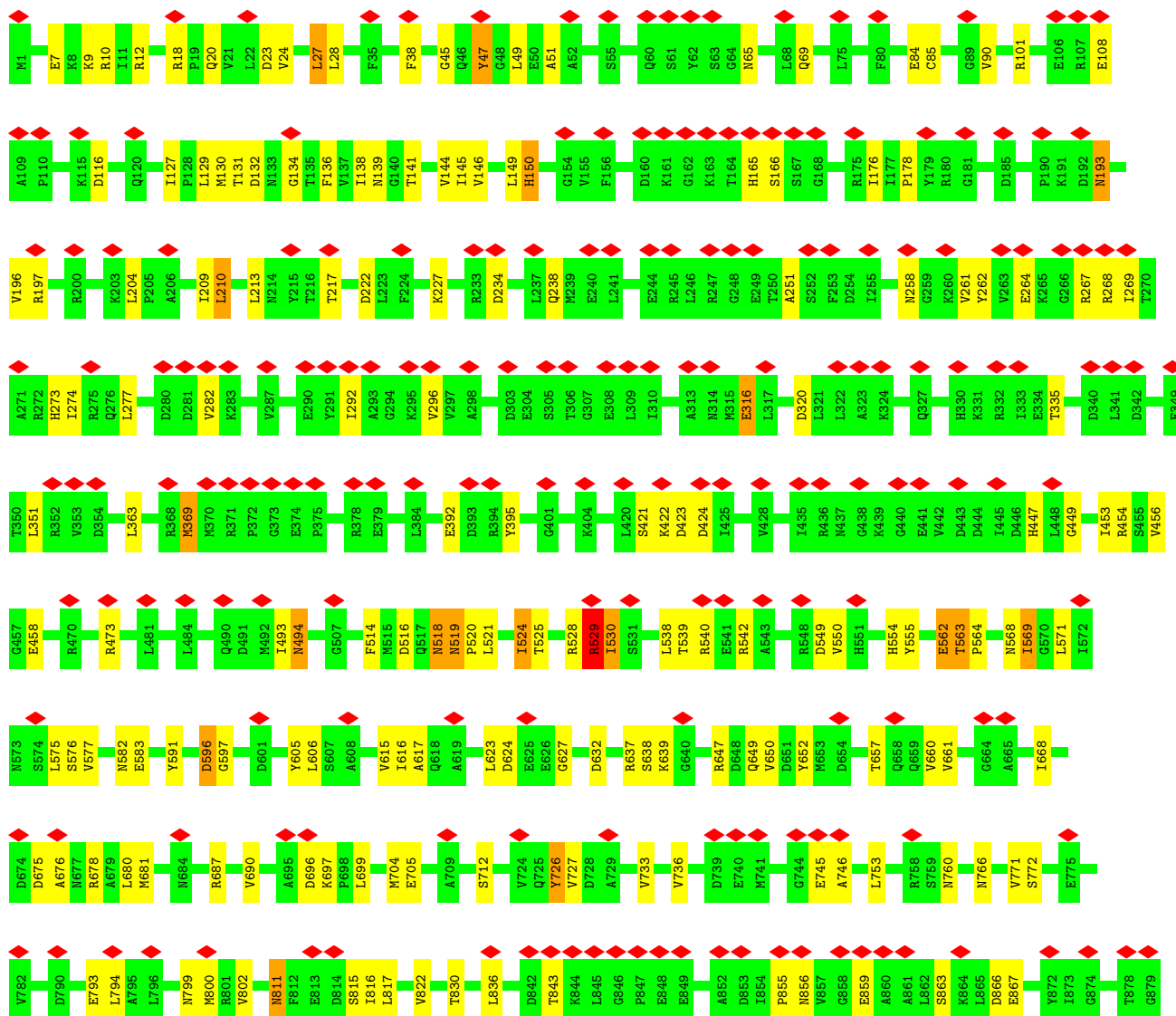
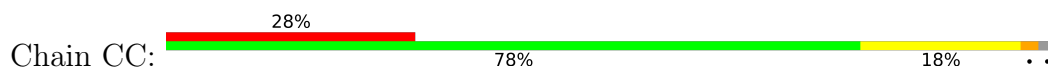


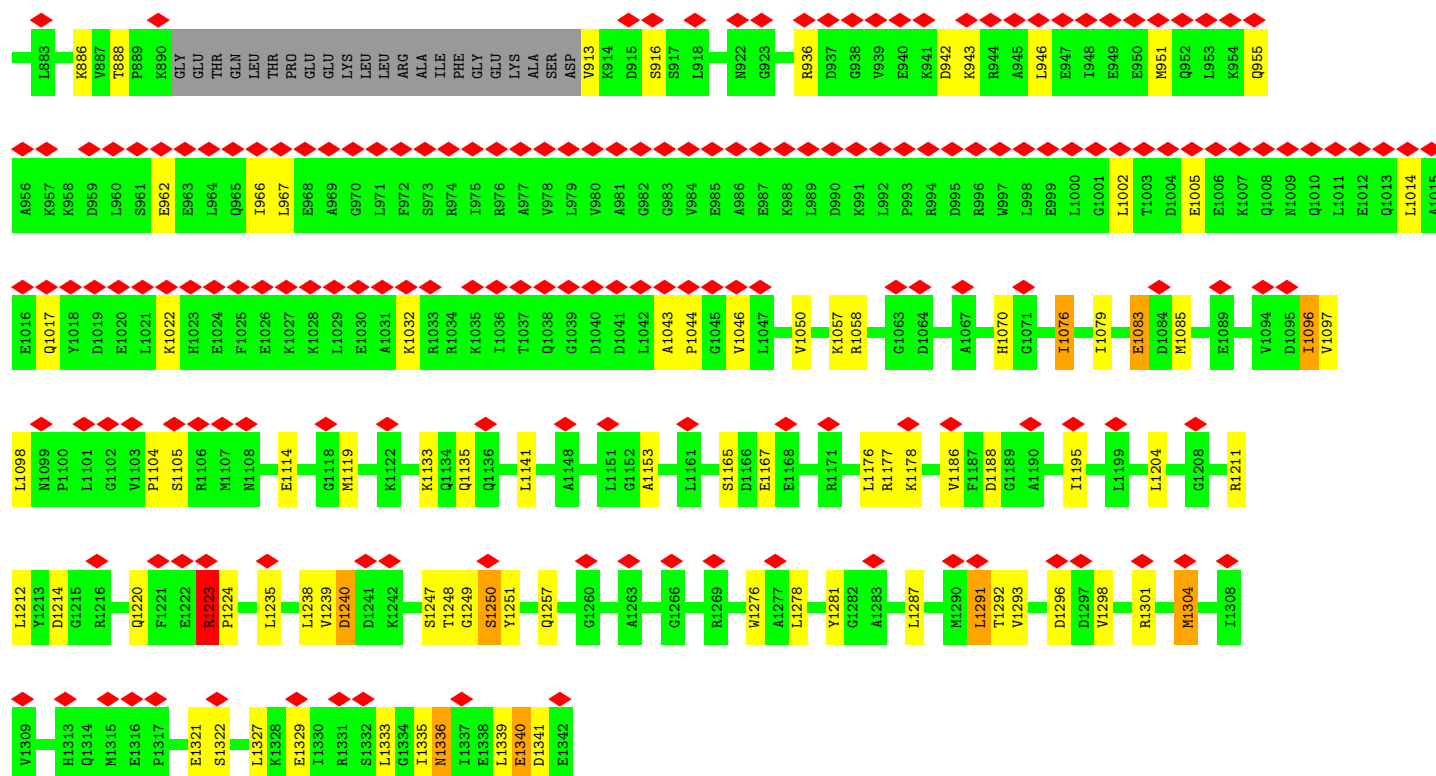
• Molecule 54: 50S ribosomal protein L36



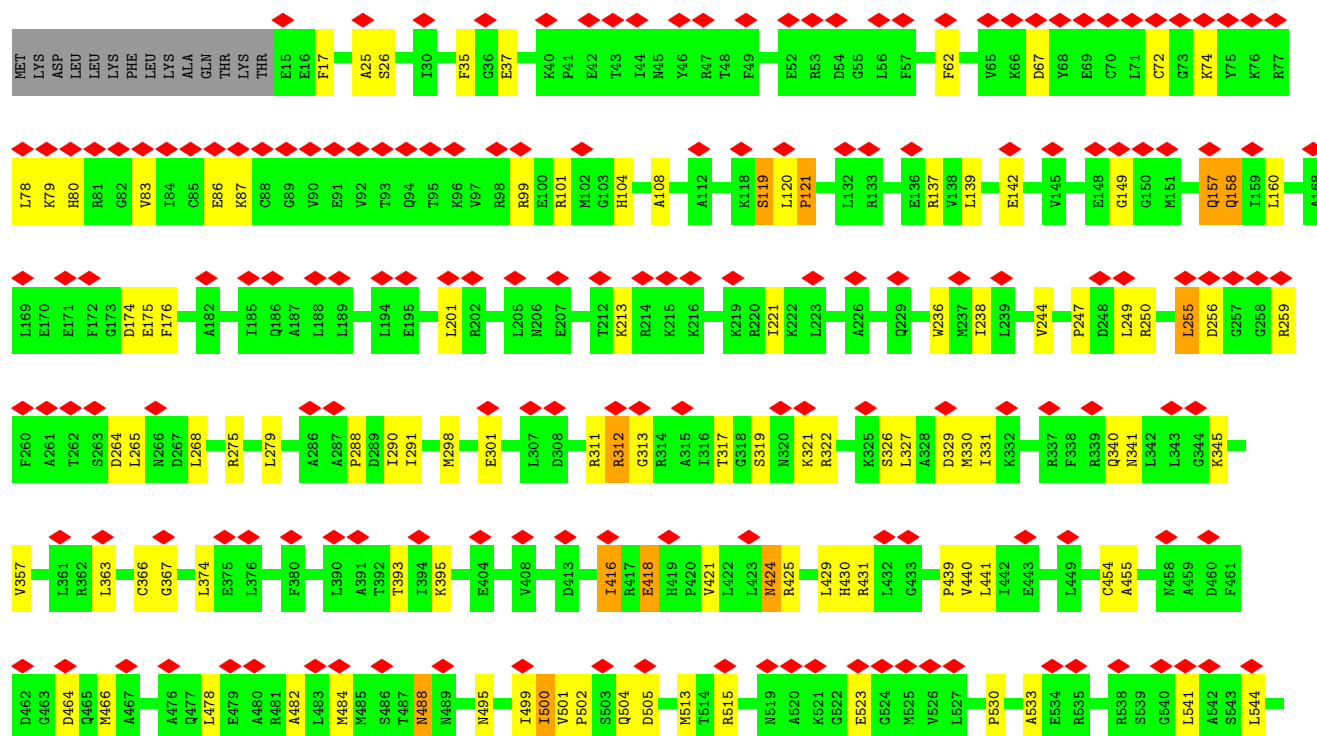
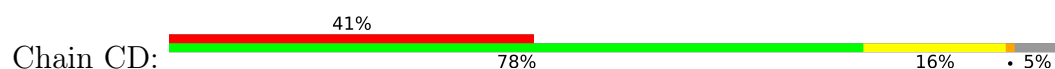


• Molecule 58: DNA-directed RNA polymerase subunit beta





• Molecule 59: DNA-directed RNA polymerase subunit beta'



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	18552	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	42	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.981	Depositor
Minimum map value	-0.434	Depositor
Average map value	0.021	Depositor
Map value standard deviation	0.068	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	688.0, 688.0, 688.0	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.075, 1.075, 1.075	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 3TD, 5MU, MIA, 4SU, 4D4, ZN, 5MC, OMU, 2MG, D2T, MEQ, 6MZ, G7M, 2MA, UR3, 1MG, 7MG, 3AU, PSU, H2U, 4OC, MG, OMG, OMC, MA6

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	AA	0.54	0/36569	0.60	14/57044 (0.0%)
2	AB	0.29	0/1796	0.65	2/2420 (0.1%)
3	AC	0.38	0/1667	0.63	0/2246
4	AD	0.44	0/1665	0.71	0/2227
5	AE	0.46	0/1161	0.70	0/1563
6	AF	0.36	0/867	0.69	0/1171
7	AG	0.30	0/1219	0.74	1/1635 (0.1%)
8	AH	0.48	0/989	0.65	0/1326
9	AI	0.39	0/1043	0.78	0/1387
10	AJ	0.37	0/810	0.82	0/1094
11	AK	0.35	0/882	0.62	0/1191
12	AL	0.52	0/954	0.79	2/1279 (0.2%)
13	AM	0.33	0/900	0.69	0/1204
14	AN	0.35	0/817	0.58	0/1088
15	AO	0.42	0/722	0.65	0/964
16	AP	0.57	0/659	0.69	0/884
17	AQ	0.46	0/650	0.73	0/871
18	AR	0.36	0/449	0.44	0/604
19	AS	0.37	0/680	0.68	0/915
20	AT	0.49	0/676	0.62	0/895
21	AU	0.33	0/598	0.75	1/792 (0.1%)
22	AV	0.92	0/709	0.85	1/1099 (0.1%)
23	AW	0.38	0/1725	0.62	2/2687 (0.1%)
24	AX	0.27	0/1584	0.31	0/2463
25	BA	0.49	3/69187 (0.0%)	0.59	15/107927 (0.0%)
26	BB	0.35	0/2872	0.49	0/4478
27	BC	0.45	0/2131	0.74	0/2863
28	BD	0.43	0/1576	0.65	0/2119
29	BE	0.39	0/1571	0.64	0/2113
30	BF	0.27	0/1444	0.75	0/1937
31	BG	0.30	0/1333	0.63	0/1805

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	BH	0.25	0/1122	0.85	1/1515 (0.1%)
33	BK	0.40	0/1152	0.57	0/1551
34	BL	0.42	0/956	0.67	0/1279
35	BM	0.40	0/1061	0.71	0/1412
36	BN	0.39	0/1081	0.61	0/1443
37	BO	0.45	0/973	0.67	0/1301
38	BP	0.30	0/910	0.69	0/1219
39	BQ	0.37	0/929	0.67	0/1242
40	BR	0.52	0/960	0.66	0/1278
41	BS	0.43	0/829	0.84	0/1107
42	BT	0.42	0/864	0.64	0/1156
43	BU	0.38	0/764	0.64	0/1021
44	BV	0.34	0/797	0.69	0/1062
45	BW	0.37	0/766	0.65	0/1025
46	BX	0.42	0/589	0.63	0/779
47	BY	0.40	0/635	0.55	0/848
48	BZ	0.32	0/502	0.59	0/667
49	B1	0.40	0/453	0.74	0/605
50	B2	0.46	0/450	0.88	0/599
51	B3	0.28	0/443	0.78	0/587
52	B4	0.47	0/380	0.63	0/498
53	B5	0.38	0/513	0.75	0/676
54	B6	0.46	0/302	0.76	0/397
55	CN	0.79	0/693	0.77	0/1068
56	CT	1.19	0/676	0.83	0/1039
57	CA	1.10	0/1797	0.96	0/2436
57	CB	0.81	0/1703	0.90	0/2308
58	CC	1.34	18/10581 (0.2%)	1.05	2/14275 (0.0%)
59	CD	1.10	6/10532 (0.1%)	0.97	3/14219 (0.0%)
All	All	0.63	27/183318 (0.0%)	0.68	44/270903 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	0	3
10	AJ	0	1
12	AL	0	1
13	AM	0	2
22	AV	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
25	BA	0	2
27	BC	0	1
37	BO	0	1
46	BX	0	1
53	B5	0	1
All	All	0	14

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	CD	424	ASN	CB-CG	-6.34	1.36	1.52
58	CC	799	ASN	CB-CG	-6.28	1.36	1.52
58	CC	519	ASN	CB-CG	-6.21	1.36	1.52
58	CC	530	ILE	CB-CG2	-6.14	1.32	1.52
59	CD	760	THR	CA-C	-6.12	1.42	1.52
58	CC	1076	ILE	CB-CG1	-6.09	1.41	1.53
58	CC	518	ASN	CB-CG	-5.94	1.37	1.52
25	BA	545	A	C1'-N9	-5.76	1.39	1.48
58	CC	146	VAL	CB-CG1	-5.61	1.34	1.52
58	CC	144	VAL	CB-CG1	-5.54	1.34	1.52
59	CD	424	ASN	CA-CB	-5.46	1.42	1.53
59	CD	1357	ILE	C-N	-5.45	1.15	1.34
58	CC	811	ASN	CB-CG	-5.43	1.38	1.52
59	CD	1333	THR	CB-CG2	-5.37	1.34	1.52
58	CC	136	PHE	CB-CG	-5.34	1.38	1.50
58	CC	146	VAL	CB-CG2	-5.33	1.34	1.52
58	CC	453	ILE	CB-CG2	-5.33	1.34	1.52
58	CC	816	ILE	CB-CG2	-5.30	1.35	1.52
59	CD	1145	PHE	CB-CG	-5.29	1.38	1.50
25	BA	548	U	C1'-N1	5.26	1.56	1.48
58	CC	802	VAL	CB-CG1	-5.24	1.35	1.52
58	CC	27	LEU	CG-CD2	-5.21	1.35	1.52
58	CC	712	SER	CA-C	-5.21	1.31	1.52
58	CC	520	PRO	CB-CG	-5.19	1.23	1.49
25	BA	543	A	C1'-N9	-5.19	1.40	1.48
58	CC	1096	ILE	CB-CG2	-5.17	1.35	1.52
58	CC	563	THR	CA-CB	-5.02	1.47	1.54

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	AU	64	ASN	N-CA-C	-9.44	95.23	109.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	1173	U	C5'-C4'-O4'	-8.39	97.22	109.80
22	AV	45	G	O3'-P-O5'	-8.36	91.46	104.00
25	BA	2131	U	O4'-C1'-N1	-7.74	96.89	108.50
1	AA	1027	C	C2-N1-C1'	6.92	139.57	118.80
1	AA	641	U	P-O3'-C3'	6.88	130.53	120.20
32	BH	107	GLY	N-CA-C	6.69	129.03	113.18
1	AA	641	U	C4'-C3'-O3'	6.57	119.25	109.40
25	BA	1173	U	C2'-C3'-O3'	-6.51	103.93	113.70
25	BA	884	U	N1-C1'-C2'	-6.49	102.26	112.00
25	BA	1172	C	C4'-C3'-O3'	6.40	119.00	109.40
25	BA	1063	G	O3'-P-O5'	6.35	113.53	104.00
58	CC	529	ARG	CA-CB-CG	6.29	126.68	114.10
1	AA	1027	C	C6-N1-C1'	-6.12	102.45	120.80
23	AW	16	C	O3'-P-O5'	5.95	112.92	104.00
1	AA	4	U	P-O3'-C3'	5.94	129.11	120.20
25	BA	1047	G	O4'-C1'-N9	5.88	117.02	108.20
25	BA	1077	A	N9-C1'-C2'	5.85	120.77	112.00
25	BA	2506	U	N1-C1'-C2'	-5.77	103.35	112.00
1	AA	1008	U	O3'-P-O5'	-5.72	95.41	104.00
25	BA	2900	A	O3'-P-O5'	5.50	112.26	104.00
12	AL	42	PRO	CA-C-N	5.50	133.22	121.45
12	AL	42	PRO	C-N-CA	5.50	133.22	121.45
25	BA	2131	U	N1-C1'-C2'	5.47	120.20	112.00
25	BA	1077	A	O4'-C1'-N9	5.44	116.65	108.50
1	AA	148	G	C1'-C2'-O2'	-5.41	100.29	108.40
25	BA	2184	A	N9-C1'-C2'	5.40	120.10	112.00
1	AA	121	U	C5'-C4'-O4'	-5.36	101.75	109.80
25	BA	1912	A	O3'-P-O5'	5.33	112.00	104.00
2	AB	130	THR	CA-C-N	5.32	131.70	121.54
2	AB	130	THR	C-N-CA	5.32	131.70	121.54
58	CC	210	LEU	CA-CB-CG	-5.31	97.70	116.30
1	AA	928	G	N9-C1'-C2'	-5.26	104.10	112.00
1	AA	1026	G	P-O3'-C3'	5.21	128.02	120.20
1	AA	1026	G	C4'-C3'-O3'	-5.21	105.19	113.00
59	CD	1329	THR	CA-C-N	-5.19	113.57	120.63
59	CD	1329	THR	C-N-CA	-5.19	113.57	120.63
1	AA	927	G	C4'-C3'-O3'	5.17	120.75	113.00
23	AW	15	G	C4'-C3'-O3'	5.14	117.10	109.40
7	AG	55	GLY	N-CA-C	5.12	125.33	113.18
1	AA	346	G	C4'-C3'-O3'	-5.07	105.39	113.00
25	BA	141	G	O3'-P-O5'	5.05	111.57	104.00
59	CD	502	PRO	N-CA-C	5.04	119.11	110.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	997	U	N1-C1'-C2'	5.03	119.54	112.00

There are no chirality outliers.

All (14) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	1027	C	Sidechain
1	AA	1034	G	Sidechain
1	AA	884	U	Sidechain
10	AJ	42	LEU	Mainchain
12	AL	43	LYS	Peptide
13	AM	48	LEU	Peptide
13	AM	49	SER	Peptide
22	AV	41	C	Sidechain
53	B5	31	HIS	Peptide
25	BA	1052	C	Sidechain
25	BA	1104	C	Sidechain
27	BC	176	LEU	Mainchain
37	BO	100	CYS	Mainchain
46	BX	54	GLY	Mainchain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	32907	0	16571	401	0
2	AB	1765	0	1792	36	0
3	AC	1640	0	1713	102	0
4	AD	1643	0	1706	63	0
5	AE	1148	0	1195	43	0
6	AF	848	0	846	30	0
7	AG	1203	0	1254	35	0
8	AH	979	0	1031	26	0
9	AI	1031	0	1076	49	0
10	AJ	800	0	839	39	0
11	AK	866	0	874	21	0
12	AL	949	0	1008	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	AM	891	0	952	37	0
14	AN	805	0	844	22	0
15	AO	714	0	734	13	0
16	AP	649	0	666	5	0
17	AQ	641	0	682	17	0
18	AR	443	0	466	13	0
19	AS	663	0	688	21	0
20	AT	670	0	719	14	0
21	AU	590	0	629	19	0
22	AV	636	0	327	20	0
23	AW	1645	0	842	25	0
24	AX	1624	0	823	35	0
25	BA	62290	0	31344	626	0
26	BB	2569	0	1301	25	0
27	BC	2092	0	2167	43	0
28	BD	1566	0	1618	31	0
29	BE	1552	0	1618	30	0
30	BF	1420	0	1457	66	0
31	BG	1313	0	1358	36	0
32	BH	1111	0	1148	35	0
33	BK	1129	0	1162	18	0
34	BL	947	0	1023	25	0
35	BM	1052	0	1127	26	0
36	BN	1075	0	1153	25	0
37	BO	960	0	999	15	0
38	BP	900	0	935	27	0
39	BQ	917	0	962	23	0
40	BR	947	0	1019	22	0
41	BS	816	0	839	17	0
42	BT	857	0	922	18	0
43	BU	757	0	820	21	0
44	BV	789	0	844	18	0
45	BW	753	0	780	18	0
46	BX	582	0	599	8	0
47	BY	625	0	652	13	0
48	BZ	501	0	531	7	0
49	B1	449	0	488	10	0
50	B2	444	0	458	18	0
51	B3	436	0	477	14	0
52	B4	377	0	418	9	0
53	B5	504	0	572	14	0
54	B6	301	0	341	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	CN	618	0	339	27	0
56	CT	606	0	338	36	0
57	CA	1775	0	1800	18	0
57	CB	1684	0	1713	20	0
58	CC	10415	0	10432	239	0
59	CD	10375	0	10597	187	0
60	AA	119	0	0	0	0
60	AW	2	0	0	0	0
60	B2	1	0	0	0	0
60	BA	294	0	0	0	0
60	BB	2	0	0	0	0
60	BC	1	0	0	0	0
60	BO	1	0	0	0	0
60	CD	1	0	0	0	0
61	AX	11	0	8	1	0
62	B6	1	0	0	0	0
62	CD	2	0	0	0	0
All	All	171689	0	122636	2541	0

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

All (2541) 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)
3:AC:109:PRO:HD2	58:CC:859:GLU:CG	1.58	1.34
4:AD:193:ALA:CA	59:CD:86:GLU:OE2	1.73	1.32
5:AE:10:GLU:HG3	59:CD:78:LEU:CD1	1.77	1.15
3:AC:109:PRO:HD2	58:CC:859:GLU:HG3	1.21	1.15
4:AD:191:LEU:O	59:CD:86:GLU:OE1	1.60	1.15
5:AE:10:GLU:HG3	59:CD:78:LEU:HD13	1.27	1.11
3:AC:78:GLY:O	58:CC:943:LYS:HD2	1.51	1.11
3:AC:80:LYS:NZ	58:CC:946:LEU:HD22	1.70	1.05
3:AC:77:ILE:CG2	58:CC:943:LYS:HE2	1.86	1.04
3:AC:108:LYS:HA	58:CC:859:GLU:HG3	1.40	1.03
1:AA:1175:G:HO2'	1:AA:1176:A:H8	1.10	0.99
4:AD:194:ASP:HB3	59:CD:74:LYS:NZ	1.79	0.97
30:BF:55:ALA:O	30:BF:59:ALA:N	1.97	0.97
3:AC:107:ARG:HH21	58:CC:863:SER:HB3	1.30	0.97
3:AC:109:PRO:CD	58:CC:859:GLU:HG3	1.93	0.97
24:AX:26:A:N6	24:AX:44:G:H1	1.62	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:77:ILE:HG21	58:CC:943:LYS:HE2	1.47	0.96
25:BA:284:U:H3	25:BA:356:G:H1	1.05	0.96
1:AA:181:A:HO2'	1:AA:182:A:H8	1.13	0.95
3:AC:107:ARG:O	58:CC:859:GLU:CG	2.15	0.95
24:AX:26:A:H61	24:AX:44:G:H1	0.98	0.95
25:BA:2141:G:H2'	25:BA:2142:A:H8	1.32	0.94
41:BS:73:LYS:HE3	41:BS:86:GLN:HG2	1.49	0.94
25:BA:2312:U:H5'	30:BF:85:ILE:HD11	1.50	0.93
21:AU:61:ALA:O	21:AU:65:ALA:HB3	1.68	0.93
46:BX:65:GLY:HA2	46:BX:85:GLU:HG2	1.49	0.93
25:BA:1040:A:N6	25:BA:1115:G:H1	1.65	0.93
3:AC:107:ARG:O	58:CC:859:GLU:CD	2.13	0.92
32:BH:47:PHE:HA	32:BH:51:ARG:HB2	1.49	0.92
25:BA:2135:A:N6	25:BA:2156:G:O2'	2.02	0.91
25:BA:2118:U:OP1	25:BA:2148:G:O2'	1.86	0.91
25:BA:2308:G:O6	25:BA:2311:A:N7	2.03	0.91
4:AD:194:ASP:HB3	59:CD:74:LYS:HZ3	1.32	0.91
30:BF:54:ALA:O	30:BF:58:ALA:N	2.02	0.91
3:AC:79:LYS:HE2	58:CC:942:ASP:HA	1.51	0.90
4:AD:193:ALA:HA	59:CD:86:GLU:OE2	0.98	0.90
13:AM:44:LYS:HB2	13:AM:47:GLU:HG2	1.53	0.90
1:AA:481:G:O2'	1:AA:483:C:N4	2.05	0.90
25:BA:1827:U:OP2	27:BC:221:ARG:NH1	2.05	0.89
13:AM:92:ARG:HD2	25:BA:888:C:H3'	1.55	0.89
25:BA:1040:A:H61	25:BA:1115:G:H1	1.10	0.89
3:AC:109:PRO:CD	58:CC:859:GLU:CG	2.48	0.88
21:AU:61:ALA:O	21:AU:64:ASN:O	1.90	0.88
25:BA:1936:A:H2	25:BA:1943:U:H3	1.17	0.88
3:AC:109:PRO:HD2	58:CC:859:GLU:CD	1.99	0.88
3:AC:107:ARG:HE	58:CC:863:SER:HB3	1.39	0.87
5:AE:10:GLU:CG	59:CD:78:LEU:CD1	2.51	0.87
25:BA:1724:G:H1	25:BA:1736:U:H3	1.19	0.87
44:BV:96:PHE:O	44:BV:100:SER:HA	1.73	0.87
25:BA:2141:G:H2'	25:BA:2142:A:C8	2.10	0.87
1:AA:537:G:OP1	12:AL:110:ARG:NH2	2.08	0.86
25:BA:1198:U:H4'	40:BR:9:ILE:HD11	1.56	0.86
25:BA:1998:A:OP2	28:BD:141:ARG:NH2	2.08	0.86
50:B2:30:VAL:HG22	50:B2:37:LYS:HG2	1.58	0.86
2:AB:187:VAL:HG11	2:AB:199:VAL:HG12	1.57	0.86
1:AA:1452:C:H4'	1:AA:1453:G:H5''	1.57	0.86
45:BW:20:LEU:HD21	45:BW:27:PRO:HD3	1.57	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2880:C:O2'	37:BO:90:ARG:NH1	2.09	0.85
3:AC:107:ARG:NH2	58:CC:863:SER:HB3	1.91	0.85
3:AC:80:LYS:HZ1	58:CC:946:LEU:HD22	1.36	0.85
3:AC:77:ILE:HG22	58:CC:943:LYS:HE2	1.57	0.84
22:AV:46:C:H2'	22:AV:47:G:H8	1.43	0.84
5:AE:10:GLU:CG	59:CD:78:LEU:HD13	2.06	0.83
1:AA:1261:A:N6	1:AA:1274:A:O2'	2.12	0.83
3:AC:107:ARG:O	58:CC:859:GLU:HB3	1.78	0.83
31:BG:170:ARG:NH2	54:B6:29:ALA:O	2.11	0.83
25:BA:1178:C:H2'	25:BA:1179:G:C8	2.15	0.82
25:BA:1534:U:H2'	25:BA:1535:A:H5''	1.60	0.82
25:BA:1481:U:H3	25:BA:1510:G:H1	1.25	0.82
25:BA:890:C:H3'	25:BA:891:G:H4'	1.62	0.82
25:BA:1590:A:H2'	25:BA:1591:A:C8	2.15	0.81
1:AA:73:C:N4	1:AA:94:G:O6	2.13	0.81
4:AD:147:GLU:HA	4:AD:150:LYS:HB2	1.62	0.81
29:BE:5:LEU:O	29:BE:9:GLN:HA	1.80	0.81
34:BL:36:GLY:N	34:BL:62:VAL:O	2.13	0.81
25:BA:276:U:O2'	25:BA:278:A:N7	2.12	0.81
1:AA:1051:C:O2	1:AA:1207:2MG:N2	2.13	0.81
1:AA:1006:G:H2'	1:AA:1007:U:H6	1.45	0.80
23:AW:15:G:H22	23:AW:48:C:H42	1.28	0.80
25:BA:2285:C:OP2	51:B3:6:ARG:NH1	2.13	0.80
29:BE:15:SER:HB3	29:BE:18:THR:HG22	1.63	0.80
22:AV:47:G:H2'	22:AV:48:C:H6	1.44	0.80
25:BA:883:G:N2	25:BA:884:U:O4	2.14	0.80
12:AL:83:ARG:NH1	12:AL:84:GLY:O	2.14	0.80
59:CD:429:LEU:H	59:CD:429:LEU:HD22	1.46	0.80
25:BA:1918:A:O2'	25:BA:1919:A:N7	2.15	0.80
25:BA:2110:G:OP1	25:BA:2143:C:O2'	1.99	0.80
4:AD:194:ASP:HA	59:CD:74:LYS:CE	2.11	0.80
57:CB:191:ARG:HB3	57:CB:196:THR:HG23	1.64	0.80
25:BA:881:G:H1	25:BA:895:U:H3	1.30	0.80
3:AC:107:ARG:CZ	58:CC:863:SER:O	2.29	0.79
12:AL:68:GLY:O	12:AL:99:ARG:NH1	2.15	0.79
30:BF:114:PHE:HE2	30:BF:176:PRO:HB2	1.46	0.79
3:AC:80:LYS:HZ2	58:CC:946:LEU:HD22	1.47	0.79
1:AA:522:C:O2	1:AA:527:G7M:N2	2.13	0.79
3:AC:107:ARG:O	58:CC:859:GLU:OE1	2.00	0.79
24:AX:16:H2U:N3	24:AX:59:U:O2	2.14	0.79
11:AK:88:GLY:O	11:AK:93:ARG:NH1	2.16	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:109:PRO:CD	58:CC:859:GLU:OE2	2.30	0.78
3:AC:107:ARG:HE	58:CC:863:SER:CB	1.94	0.78
6:AF:45:ARG:O	6:AF:56:LYS:HA	1.82	0.78
25:BA:1529:G:H1	25:BA:1542:U:H3	1.32	0.78
21:AU:10:GLU:OE2	21:AU:18:ARG:NH2	2.17	0.78
25:BA:550:U:H2'	25:BA:551:G:H8	1.47	0.78
1:AA:582:C:OP2	1:AA:758:C:N4	2.17	0.77
3:AC:107:ARG:O	58:CC:859:GLU:CB	2.33	0.77
25:BA:483:A:H5''	44:BV:47:LYS:HD2	1.67	0.77
25:BA:2107:G:H1	25:BA:2182:U:H3	0.81	0.77
25:BA:2162:G:OP2	25:BA:2164:C:N4	2.14	0.77
25:BA:2467:C:O2	36:BN:123:LYS:NZ	2.16	0.77
25:BA:2792:A:H2'	25:BA:2793:C:C6	2.20	0.77
20:AT:44:LYS:NZ	20:AT:83:ILE:O	2.18	0.77
3:AC:109:PRO:CD	58:CC:859:GLU:CD	2.57	0.77
12:AL:110:ARG:NH1	12:AL:112:GLN:O	2.18	0.77
59:CD:1186:TYR:OH	59:CD:1188:GLU:OE1	2.01	0.77
25:BA:475:C:O2	25:BA:479:A:N6	2.16	0.77
25:BA:2901:C:H2'	25:BA:2902:C:C6	2.20	0.77
56:CT:18:DC:H2'	56:CT:19:DG:C8	2.19	0.77
14:AN:46:LEU:HD12	19:AS:13:LEU:HD13	1.67	0.77
25:BA:284:U:O2	25:BA:356:G:N2	2.17	0.77
25:BA:1100:C:H2'	25:BA:1101:U:H6	1.49	0.76
19:AS:31:LEU:HB2	19:AS:49:ILE:HG22	1.66	0.76
1:AA:664:G:H22	1:AA:741:G:H1	1.31	0.76
32:BH:78:VAL:HG21	32:BH:103:VAL:HG22	1.67	0.76
25:BA:1040:A:N1	25:BA:1115:G:N2	2.33	0.76
31:BG:164:TYR:HB2	31:BG:167:GLU:HB3	1.66	0.76
1:AA:160:A:N6	1:AA:346:G:O6	2.18	0.76
1:AA:1382:C:O2'	7:AG:79:ARG:NH2	2.18	0.76
4:AD:194:ASP:CB	59:CD:74:LYS:NZ	2.48	0.76
57:CA:62:ASP:OD1	57:CA:63:GLY:N	2.19	0.76
1:AA:1160:G:OP2	2:AB:131:LYS:NZ	2.19	0.76
4:AD:192:SER:O	59:CD:86:GLU:OE2	2.04	0.76
3:AC:189:ALA:HB3	3:AC:196:ILE:HG23	1.67	0.76
9:AI:84:THR:HG23	9:AI:98:LEU:HD13	1.67	0.76
39:BQ:113:ARG:O	39:BQ:115:ASN:ND2	2.19	0.76
25:BA:1071:G:O6	25:BA:1100:C:N4	2.19	0.75
25:BA:2718:G:O4'	25:BA:2718:G:O2'	1.93	0.75
25:BA:444:C:OP1	29:BE:40:ARG:NH2	2.19	0.75
57:CB:74:VAL:HG21	57:CB:81:ILE:HD11	1.66	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:107:ARG:NE	58:CC:863:SER:HB3	2.00	0.75
30:BF:56:ASP:O	30:BF:60:ILE:HB	1.87	0.75
5:AE:101:GLU:OE2	5:AE:122:ASN:ND2	2.20	0.75
25:BA:783:A:H2'	25:BA:783:A:N3	2.00	0.75
25:BA:877:A:O2'	25:BA:900:A:N6	2.19	0.74
25:BA:878:A:N6	25:BA:899:A:O2'	2.21	0.74
25:BA:2831:G:OP2	28:BD:59:ARG:NH2	2.21	0.74
54:B6:23:ILE:HB	54:B6:37:GLN:HB3	1.68	0.74
59:CD:816:THR:OG1	59:CD:818:GLU:OE1	2.04	0.74
25:BA:1916:A:H2'	25:BA:1917:PSU:C6	2.23	0.74
17:AQ:79:VAL:HG22	17:AQ:80:GLU:HG3	1.70	0.74
22:AV:46:C:H2'	22:AV:47:G:C8	2.21	0.74
25:BA:1494:A:O2'	25:BA:1495:A:OP1	2.05	0.74
25:BA:1782:U:O2'	25:BA:2609:U:H5''	1.87	0.74
50:B2:54:VAL:HG23	50:B2:55:ILE:HD12	1.69	0.74
5:AE:111:MET:HE2	5:AE:125:ALA:HB1	1.68	0.74
1:AA:1463:U:H5''	39:BQ:109:ARG:HH11	1.53	0.73
5:AE:10:GLU:CB	59:CD:78:LEU:HD12	2.18	0.73
25:BA:443:A:C5	29:BE:40:ARG:HD2	2.23	0.73
1:AA:198:G:H2'	1:AA:199:A:H8	1.53	0.73
1:AA:263:A:OP2	20:AT:74:ARG:NH1	2.21	0.73
3:AC:108:LYS:CA	58:CC:859:GLU:HG3	2.17	0.73
38:BP:56:LYS:O	38:BP:60:GLU:HB2	1.89	0.73
44:BV:28:VAL:HG22	44:BV:34:VAL:HG12	1.69	0.73
1:AA:1006:G:O6	1:AA:1024:G:N2	2.20	0.73
44:BV:17:LYS:NZ	44:BV:40:ASN:OD1	2.20	0.73
37:BO:82:GLU:OE2	37:BO:86:ARG:NH2	2.20	0.73
1:AA:951:G:OP2	13:AM:101:ARG:NH2	2.21	0.73
8:AH:41:LYS:NZ	8:AH:47:GLU:O	2.21	0.73
59:CD:1179:PRO:HD2	59:CD:1184:ASP:HA	1.69	0.73
25:BA:1100:C:H2'	25:BA:1101:U:C6	2.23	0.73
1:AA:1086:U:O4	1:AA:1099:G:N1	2.18	0.72
13:AM:92:ARG:HB2	25:BA:888:C:H5'	1.71	0.72
35:BM:37:GLY:N	35:BM:40:SER:OG	2.22	0.72
58:CC:10:ARG:NH2	58:CC:793:GLU:OE1	2.21	0.72
25:BA:2069:G7M:N2	25:BA:2442:C:O2	2.16	0.72
25:BA:2099:U:H3	25:BA:2190:G:H1	1.34	0.72
36:BN:14:LYS:O	36:BN:71:LYS:NZ	2.22	0.72
2:AB:44:GLU:N	2:AB:44:GLU:OE2	2.21	0.72
3:AC:108:LYS:HA	58:CC:859:GLU:CG	2.18	0.72
30:BF:110:ARG:NH1	30:BF:136:ILE:O	2.20	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AE:10:GLU:CG	59:CD:78:LEU:HD12	2.20	0.72
30:BF:56:ASP:O	30:BF:60:ILE:N	2.21	0.72
44:BV:99:ASN:OD1	44:BV:101:GLU:HG2	1.89	0.72
25:BA:1592:C:H2'	25:BA:1593:A:H8	1.55	0.72
24:AX:26:A:N1	24:AX:44:G:N2	2.38	0.71
3:AC:79:LYS:CE	58:CC:942:ASP:HA	2.20	0.71
25:BA:729:G:OP1	27:BC:10:SER:OG	2.08	0.71
58:CC:27:LEU:O	58:CC:528:ARG:NH1	2.24	0.71
14:AN:47:LYS:O	14:AN:50:THR:OG1	2.06	0.71
14:AN:63:ARG:NH1	14:AN:68:GLY:O	2.24	0.71
25:BA:1406:U:C2'	25:BA:1407:G:H5''	2.20	0.71
25:BA:1592:C:H2'	25:BA:1593:A:C8	2.24	0.71
5:AE:10:GLU:CB	59:CD:78:LEU:CD1	2.69	0.71
17:AQ:76:VAL:HG23	17:AQ:77:ARG:HD2	1.73	0.71
25:BA:1693:U:O2	27:BC:14:ARG:NH1	2.24	0.71
24:AX:51:U:H2'	24:AX:52:G:H8	1.54	0.71
1:AA:974:A:OP1	14:AN:69:ARG:NH2	2.24	0.71
25:BA:881:G:O6	25:BA:895:U:O4	2.09	0.71
25:BA:1065:U:O2'	25:BA:1066:U:O4'	2.08	0.71
59:CD:454:CYS:SG	59:CD:455:ALA:N	2.64	0.71
25:BA:1529:G:O6	25:BA:1542:U:O4	2.08	0.70
25:BA:1481:U:O2	25:BA:1510:G:N2	2.24	0.70
1:AA:412:A:H62	1:AA:431:A:H61	1.39	0.70
1:AA:841:C:O2'	1:AA:843:U:OP2	2.05	0.70
19:AS:36:ARG:NH2	19:AS:75:ALA:O	2.24	0.70
25:BA:137:U:O2'	25:BA:138:U:OP1	2.08	0.70
1:AA:1277:C:O2'	1:AA:1278:G:H5''	1.91	0.70
4:AD:100:ASN:OD1	4:AD:111:ARG:NH1	2.25	0.70
27:BC:29:PRO:HG2	27:BC:34:LEU:HD11	1.74	0.70
59:CD:1157:ALA:HB2	59:CD:1210:ILE:HD11	1.74	0.70
22:AV:47:G:H2'	22:AV:48:C:C6	2.25	0.70
1:AA:181:A:O2'	1:AA:194:C:N4	2.24	0.70
23:AW:50:U:H3	23:AW:64:G:H1	1.38	0.70
44:BV:48:PRO:HG3	44:BV:56:GLY:HA3	1.74	0.70
1:AA:356:A:N3	1:AA:368:U:O2'	2.25	0.70
25:BA:2168:G:O2'	25:BA:2169:A:OP1	2.09	0.70
16:AP:55:ASP:OD1	16:AP:56:ARG:N	2.25	0.70
1:AA:83:C:O2	1:AA:86:G:N1	2.16	0.69
29:BE:1:MET:HB3	29:BE:14:VAL:HG23	1.72	0.69
47:BY:72:ARG:NH1	47:BY:78:TYR:OH	2.25	0.69
1:AA:437:U:H5''	4:AD:152:GLN:HE22	1.56	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1356:G:H2'	1:AA:1357:A:C8	2.27	0.69
4:AD:104:ARG:HA	4:AD:104:ARG:HH11	1.58	0.69
1:AA:1017:U:O2'	1:AA:1018:G:O4'	2.10	0.69
13:AM:81:MET:O	13:AM:92:ARG:NH1	2.25	0.69
1:AA:927:G:O2'	1:AA:928:G:H5'	1.93	0.69
25:BA:1223:G:OP1	41:BS:68:ARG:NH2	2.25	0.69
25:BA:2795:C:H2'	25:BA:2796:C:C6	2.28	0.69
58:CC:624:ASP:OD1	58:CC:627:GLY:N	2.25	0.69
8:AH:106:THR:HB	8:AH:121:LEU:HD12	1.72	0.69
38:BP:89:ASP:OD1	38:BP:89:ASP:N	2.26	0.69
1:AA:35:G:N3	12:AL:115:SER:OG	2.25	0.69
1:AA:1329:A:H5'	13:AM:29:ARG:HD2	1.74	0.69
25:BA:627:A:OP1	35:BM:78:ARG:NH2	2.19	0.69
25:BA:2106:U:H2'	25:BA:2107:G:H8	1.55	0.69
1:AA:86:G:H4'	1:AA:86:G:OP1	1.92	0.69
3:AC:107:ARG:HH21	58:CC:863:SER:CB	2.06	0.69
17:AQ:9:GLN:NE2	17:AQ:60:GLU:OE2	2.25	0.69
25:BA:1040:A:N6	25:BA:1115:G:N1	2.26	0.69
28:BD:35:THR:HG22	28:BD:73:VAL:HG21	1.73	0.69
36:BN:35:ALA:HB2	36:BN:102:LEU:HD11	1.75	0.69
7:AG:57:SER:OG	7:AG:58:GLU:OE2	2.08	0.69
59:CD:504:GLN:NE2	59:CD:505:ASP:OD1	2.18	0.69
8:AH:77:ARG:NH1	8:AH:79:SER:O	2.26	0.68
25:BA:550:U:H2'	25:BA:551:G:C8	2.27	0.68
25:BA:1901:A:OP2	27:BC:253:LYS:NZ	2.26	0.68
10:AJ:10:LEU:HB3	10:AJ:18:ILE:HD11	1.74	0.68
1:AA:4:U:O2'	1:AA:5:U:O5'	2.10	0.68
1:AA:195:A:O2'	1:AA:196:A:H5'	1.93	0.68
25:BA:1177:G:O2'	25:BA:1178:C:O5'	2.08	0.68
1:AA:1005:A:N6	1:AA:1024:G:O2'	2.27	0.68
25:BA:1607:C:N4	25:BA:1622:G:OP2	2.26	0.68
42:BT:82:MET:SD	42:BT:84:ARG:NH1	2.67	0.68
28:BD:8:LYS:O	28:BD:198:GLY:N	2.21	0.68
25:BA:1585:C:H2'	25:BA:1586:A:H8	1.59	0.68
27:BC:107:PRO:HD2	27:BC:110:LEU:HD22	1.75	0.68
25:BA:1044:C:O2'	25:BA:1111:A:N1	2.26	0.68
25:BA:2720:U:OP1	39:BQ:53:ARG:NH2	2.27	0.68
35:BM:107:PHE:HB3	35:BM:126:ARG:HH12	1.57	0.68
42:BT:22:ASP:OD1	42:BT:25:ARG:NH2	2.27	0.68
1:AA:464:U:O2'	1:AA:466:A:N7	2.23	0.67
4:AD:194:ASP:HA	59:CD:74:LYS:HE3	1.74	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:BG:145:ALA:HB1	31:BG:164:TYR:HE1	1.59	0.67
56:CT:19:DG:H2'	56:CT:20:DC:C6	2.29	0.67
1:AA:198:G:H2'	1:AA:199:A:C8	2.30	0.67
1:AA:1516:2MG:N2	1:AA:1519:MA6:OP2	2.27	0.67
13:AM:59:GLU:OE2	13:AM:62:LYS:NZ	2.27	0.67
25:BA:2683:C:OP1	39:BQ:51:ARG:NH1	2.27	0.67
25:BA:125:A:OP2	52:B4:19:ARG:NH2	2.24	0.67
25:BA:1226:A:OP1	40:BR:16:LYS:NZ	2.28	0.67
1:AA:1290:G:O2'	9:AI:41:ARG:NH2	2.27	0.67
3:AC:107:ARG:CZ	58:CC:863:SER:HB3	2.25	0.67
3:AC:80:LYS:NZ	58:CC:946:LEU:CD2	2.55	0.67
4:AD:43:ALA:O	4:AD:44:ARG:NH1	2.27	0.67
1:AA:1397:C:H5'	22:AV:23:C:H41	1.58	0.67
9:AI:25:ASN:HB3	9:AI:27:LYS:HE2	1.74	0.67
25:BA:1068:G:N2	25:BA:1095:A:O3'	2.27	0.67
4:AD:192:SER:C	59:CD:86:GLU:OE2	2.18	0.67
9:AI:42:GLU:OE2	9:AI:49:ARG:NH2	2.27	0.67
25:BA:1869:G:N2	25:BA:1871:A:O2'	2.27	0.67
25:BA:2857:G:N2	25:BA:2860:A:OP2	2.23	0.67
1:AA:1169:A:H2'	1:AA:1170:A:C8	2.29	0.66
1:AA:1249:C:H5	1:AA:1288:A:H62	1.43	0.66
23:AW:69:C:H2'	23:AW:70:G:H8	1.60	0.66
57:CB:27:THR:C	57:CB:28:LEU:HD22	2.19	0.66
1:AA:1422:G:O2'	34:BL:49:ARG:NH2	2.28	0.66
2:AB:43:LEU:O	2:AB:47:VAL:HG12	1.95	0.66
3:AC:93:ASP:OD1	3:AC:94:ILE:N	2.28	0.66
25:BA:2683:C:O2	34:BL:70:ARG:NH2	2.28	0.66
36:BN:106:ASP:OD1	36:BN:107:GLY:N	2.29	0.66
35:BM:78:ARG:HG2	35:BM:113:ALA:HB3	1.77	0.66
9:AI:116:VAL:HG13	10:AJ:62:ARG:HH21	1.61	0.66
17:AQ:40:ARG:HA	17:AQ:40:ARG:HE	1.59	0.66
25:BA:2175:C:H2'	25:BA:2176:A:C8	2.30	0.66
4:AD:170:TRP:CD2	4:AD:186:PRO:HB3	2.31	0.66
5:AE:115:LEU:HD13	5:AE:123:VAL:HG21	1.75	0.66
9:AI:21:ILE:HD13	9:AI:63:LEU:HB3	1.77	0.66
23:AW:21:A:N6	23:AW:46:A:O2'	2.29	0.66
25:BA:1857:G:O2'	25:BA:1884:G:N2	2.27	0.66
25:BA:1914:C:H2'	25:BA:1915:3TD:H6	1.77	0.66
25:BA:2364:C:OP1	46:BX:55:ARG:NH1	2.28	0.66
3:AC:58:GLU:OE1	3:AC:65:ARG:NH1	2.29	0.66
3:AC:79:LYS:HE2	58:CC:942:ASP:CA	2.23	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:639:U:H2'	25:BA:640:C:C6	2.30	0.66
36:BN:20:LEU:HD13	45:BW:81:PRO:HG2	1.78	0.66
12:AL:54:ARG:HB2	12:AL:54:ARG:HH11	1.59	0.66
31:BG:47:ASP:OD1	31:BG:48:ASN:N	2.24	0.66
32:BH:4:ILE:HG13	32:BH:18:GLN:HG3	1.78	0.66
4:AD:146:ARG:HH21	4:AD:148:LYS:HD3	1.61	0.65
14:AN:86:GLU:OE2	14:AN:90:ARG:NH2	2.29	0.65
25:BA:2328:A:H2'	25:BA:2329:U:C6	2.31	0.65
4:AD:194:ASP:CB	59:CD:74:LYS:HZ1	2.07	0.65
25:BA:491:G:O6	42:BT:49:LYS:NZ	2.27	0.65
25:BA:889:C:H2'	25:BA:890:C:H5'	1.79	0.65
45:BW:36:ALA:O	45:BW:93:ARG:NH2	2.25	0.65
4:AD:194:ASP:N	59:CD:74:LYS:HE2	2.11	0.65
27:BC:78:VAL:O	27:BC:113:GLY:N	2.29	0.65
1:AA:1239:A:H62	1:AA:1299:A:H62	1.44	0.65
23:AW:15:G:H22	23:AW:48:C:N4	1.94	0.65
25:BA:1154:G:OP2	40:BR:58:ARG:NH2	2.28	0.65
25:BA:2291:U:H2'	25:BA:2292:U:C6	2.32	0.65
1:AA:875:U:O2'	8:AH:15:ARG:NH1	2.29	0.65
45:BW:55:GLU:OE1	45:BW:55:GLU:N	2.29	0.65
55:CN:32:DA:H5'	55:CN:32:DA:C8	2.32	0.65
1:AA:411:A:OP1	4:AD:26:ARG:NH1	2.29	0.65
1:AA:1276:G:O2'	1:AA:1277:C:H5'	1.97	0.65
6:AF:43:GLY:HA2	6:AF:58:HIS:CE1	2.31	0.65
1:AA:1100:C:OP1	21:AU:69:ARG:NH2	2.30	0.65
1:AA:1317:C:O2	19:AS:37:ARG:NH2	2.29	0.65
24:AX:37:MIA:O2'	25:BA:1913:A:N1	2.28	0.65
25:BA:1064:C:O2'	25:BA:1065:U:O4'	2.15	0.65
47:BY:12:PRO:HB3	47:BY:30:LEU:HD23	1.78	0.65
22:AV:45:G:H5''	58:CC:540:ARG:NH2	2.11	0.65
28:BD:4:LEU:HD23	28:BD:29:VAL:HG11	1.79	0.65
56:CT:17:DG:C5	56:CT:18:DC:C5	2.84	0.65
8:AH:94:LYS:HD3	8:AH:117:ARG:HH12	1.62	0.65
57:CA:8:PHE:O	57:CA:10:LYS:NZ	2.26	0.64
6:AF:14:GLN:OE1	6:AF:14:GLN:N	2.31	0.64
24:AX:51:U:H2'	24:AX:52:G:C8	2.32	0.64
25:BA:1594:U:H2'	25:BA:1595:C:C6	2.31	0.64
1:AA:1051:C:N3	1:AA:1207:2MG:N1	2.35	0.64
46:BX:59:LEU:HD12	46:BX:80:ILE:HD12	1.78	0.64
1:AA:1006:G:H2'	1:AA:1007:U:C6	2.29	0.64
6:AF:29:ILE:HG23	6:AF:34:GLY:HA3	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:BG:52:PHE:CD1	31:BG:69:ARG:HB2	2.32	0.64
51:B3:6:ARG:HG2	51:B3:24:THR:HB	1.79	0.64
25:BA:613:A:N6	25:BA:616:A:N1	2.46	0.64
1:AA:1383:C:H2'	1:AA:1384:C:C6	2.33	0.64
25:BA:2102:G:N2	25:BA:2187:U:O2	2.31	0.64
56:CT:19:DG:C6	56:CT:20:DC:C4	2.86	0.64
58:CC:18:ARG:NH1	58:CC:1188:ASP:OD1	2.31	0.64
1:AA:1174:G:H2'	1:AA:1175:G:H5'	1.80	0.64
25:BA:994:C:OP2	40:BR:54:LYS:NZ	2.31	0.64
25:BA:2243:U:H2'	25:BA:2244:U:C6	2.32	0.64
16:AP:48:GLU:OE1	16:AP:51:ARG:NH2	2.30	0.64
1:AA:501:C:OP1	12:AL:114:ARG:NH2	2.31	0.64
25:BA:2795:C:H2'	25:BA:2796:C:H6	1.63	0.64
53:B5:42:ARG:HG3	53:B5:45:ARG:HH12	1.63	0.64
31:BG:35:ARG:NH1	31:BG:75:MET:SD	2.71	0.64
1:AA:1451:U:OP2	1:AA:1452:C:N4	2.31	0.63
3:AC:108:LYS:HD3	58:CC:859:GLU:HB2	1.80	0.63
4:AD:194:ASP:CA	59:CD:74:LYS:CE	2.76	0.63
56:CT:19:DG:C5	56:CT:20:DC:C5	2.86	0.63
24:AX:27:G:H2'	24:AX:28:G:H8	1.63	0.63
25:BA:1036:G:H1	25:BA:1119:U:H3	1.43	0.63
58:CC:251:ALA:HB2	58:CC:269:ILE:HD11	1.80	0.63
1:AA:246:A:N1	1:AA:278:G:O2'	2.29	0.63
21:AU:64:ASN:O	21:AU:66:ARG:N	2.30	0.63
25:BA:1009:A:OP2	33:BK:39:LYS:NZ	2.31	0.63
30:BF:118:SER:C	30:BF:120:LYS:H	2.07	0.63
37:BO:24:MET:HG2	37:BO:44:LEU:HD22	1.79	0.63
59:CD:429:LEU:HD22	59:CD:429:LEU:N	2.12	0.63
35:BM:80:SER:O	35:BM:84:LYS:HD3	1.98	0.63
23:AW:15:G:N2	23:AW:48:C:H42	1.96	0.63
25:BA:1261:C:OP2	42:BT:83:LYS:NZ	2.32	0.63
25:BA:2135:A:N6	25:BA:2156:G:HO2'	1.95	0.63
1:AA:1452:C:H4'	1:AA:1453:G:C5'	2.29	0.63
3:AC:25:ASN:OD1	3:AC:26:THR:N	2.32	0.63
12:AL:72:HIS:HB2	12:AL:74:LEU:HD23	1.79	0.63
25:BA:2282:G:O2'	25:BA:2425:A:N6	2.32	0.63
56:CT:9:DC:H2'	56:CT:10:DT:C6	2.34	0.63
58:CC:582:ASN:OD1	58:CC:583:GLU:N	2.31	0.63
3:AC:9:GLY:HA3	14:AN:89:MET:HE3	1.81	0.63
25:BA:1534:U:C2'	25:BA:1535:A:H5''	2.28	0.63
56:CT:19:DG:H2'	56:CT:20:DC:H6	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AG:79:ARG:HG3	7:AG:84:THR:HG22	1.80	0.62
25:BA:1108:U:H2'	25:BA:1109:C:C6	2.34	0.62
30:BF:58:ALA:HB2	30:BF:65:PRO:HD3	1.81	0.62
58:CC:696:ASP:CG	58:CC:697:LYS:H	2.06	0.62
1:AA:160:A:N6	1:AA:343:U:O2'	2.32	0.62
2:AB:47:VAL:HG13	2:AB:48:PRO:HD3	1.81	0.62
8:AH:76:GLN:HE21	8:AH:128:TYR:HD2	1.47	0.62
23:AW:15:G:O6	23:AW:48:C:O2	2.16	0.62
25:BA:1108:U:H2'	25:BA:1109:C:H6	1.63	0.62
1:AA:1233:G:OP1	9:AI:119:ARG:NH2	2.32	0.62
25:BA:1404:C:H2'	25:BA:1405:U:H5'	1.82	0.62
41:BS:1:MET:HG3	41:BS:43:ASN:HA	1.80	0.62
25:BA:2102:G:H2'	25:BA:2103:C:C6	2.34	0.62
27:BC:146:MET:HE3	27:BC:154:LEU:HD21	1.81	0.62
30:BF:98:GLU:OE1	30:BF:102:ARG:NH1	2.26	0.62
13:AM:52:GLN:OE1	13:AM:52:GLN:N	2.33	0.62
1:AA:201:G:H2'	1:AA:202:G:C8	2.34	0.62
25:BA:1019:U:OP1	25:BA:1035:U:O2'	2.13	0.62
25:BA:1406:U:H2'	25:BA:1407:G:H5''	1.80	0.62
25:BA:2333:A:OP2	46:BX:77:ARG:NH2	2.28	0.62
32:BH:97:ARG:HA	32:BH:112:LYS:HB3	1.81	0.62
34:BL:34:GLY:N	34:BL:37:ASP:OD2	2.31	0.62
59:CD:576:ARG:NH1	59:CD:593:ASN:O	2.32	0.62
1:AA:932:C:H3'	7:AG:3:ARG:HD2	1.82	0.62
1:AA:1343:G:H1'	9:AI:123:ARG:HH12	1.65	0.62
3:AC:62:LYS:N	3:AC:62:LYS:HE3	2.13	0.62
1:AA:986:U:H2'	1:AA:987:G:C8	2.34	0.62
2:AB:225:ARG:O	2:AB:227:GLN:NE2	2.33	0.62
13:AM:68:ASP:OD1	13:AM:71:ARG:NH2	2.33	0.62
25:BA:1527:G:N1	25:BA:1544:A:OP2	2.30	0.62
25:BA:2187:U:H2'	25:BA:2188:U:C6	2.34	0.62
25:BA:2245:U:O2'	25:BA:2436:G:OP2	2.16	0.62
32:BH:75:LEU:HD23	32:BH:75:LEU:H	1.64	0.62
9:AI:88:MET:HG3	9:AI:95:ARG:HG2	1.81	0.62
11:AK:89:PRO:HB3	21:AU:32:VAL:HG21	1.80	0.62
25:BA:1585:C:O2'	25:BA:1586:A:O4'	2.12	0.62
58:CC:12:ARG:HH21	58:CC:793:GLU:CD	2.07	0.62
7:AG:23:LEU:O	7:AG:27:VAL:HG13	2.00	0.61
23:AW:17:C:OP1	23:AW:60:U:O2'	2.18	0.61
24:AX:21:A:O2'	24:AX:46:7MG:O6	2.18	0.61
25:BA:265:A:N1	25:BA:427:U:O2'	2.29	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:B1:4:THR:OG1	49:B1:37:GLU:OE2	2.17	0.61
24:AX:6:G:H2'	24:AX:7:A:C8	2.35	0.61
25:BA:2071:A:H2'	25:BA:2072:C:C6	2.35	0.61
28:BD:48:ILE:HG23	28:BD:84:LEU:HD11	1.82	0.61
55:CN:38:DA:H2''	55:CN:39:DG:N7	2.14	0.61
57:CB:76:GLU:H	57:CB:76:GLU:CD	2.08	0.61
4:AD:166:GLU:OE2	4:AD:166:GLU:N	2.22	0.61
25:BA:2107:G:O6	25:BA:2182:U:O4	2.18	0.61
32:BH:116:ARG:HB2	32:BH:131:SER:HB2	1.82	0.61
1:AA:1135:U:O2'	1:AA:1138:G:N1	2.33	0.61
1:AA:1218:C:H2'	1:AA:1219:A:C8	2.36	0.61
3:AC:79:LYS:HE3	58:CC:943:LYS:N	2.16	0.61
13:AM:23:TYR:HB3	13:AM:66:GLU:HB3	1.82	0.61
1:AA:1383:C:H2'	1:AA:1384:C:H6	1.64	0.61
25:BA:792:A:N3	25:BA:2072:C:O2'	2.31	0.61
1:AA:302:G:OP1	12:AL:14:ARG:NH2	2.33	0.61
1:AA:1018:G:H2'	1:AA:1019:A:H8	1.66	0.61
2:AB:148:LEU:HD22	2:AB:151:ILE:HD11	1.82	0.61
10:AJ:92:LEU:HD23	10:AJ:98:VAL:HG11	1.83	0.61
25:BA:1404:C:C2'	25:BA:1405:U:H5'	2.31	0.61
45:BW:20:LEU:HD23	45:BW:21:ARG:N	2.16	0.61
5:AE:10:GLU:HB3	59:CD:78:LEU:HD12	1.81	0.61
7:AG:70:ARG:NH2	7:AG:97:ASN:OD1	2.33	0.61
59:CD:504:GLN:HG3	59:CD:505:ASP:H	1.65	0.61
27:BC:123:ALA:O	27:BC:128:ASN:ND2	2.34	0.61
29:BE:148:ILE:HB	29:BE:169:VAL:HG12	1.81	0.61
39:BQ:115:ASN:HD22	39:BQ:115:ASN:N	1.98	0.61
47:BY:3:ARG:HD2	47:BY:30:LEU:HD22	1.83	0.61
1:AA:1492:A:O2'	1:AA:1493:A:H5'	2.01	0.60
3:AC:109:PRO:HD2	58:CC:859:GLU:HG2	1.69	0.60
4:AD:194:ASP:HB3	59:CD:74:LYS:HZ1	1.62	0.60
20:AT:42:GLY:HA2	20:AT:86:LEU:HD11	1.83	0.60
29:BE:48:THR:HG23	29:BE:86:ALA:HB3	1.82	0.60
5:AE:150:PRO:HA	5:AE:153:VAL:HG22	1.83	0.60
1:AA:518:C:O2'	1:AA:530:G:N2	2.33	0.60
10:AJ:44:THR:HA	10:AJ:69:THR:O	2.01	0.60
25:BA:1056:G:O2'	25:BA:1086:A:O2'	2.15	0.60
1:AA:673:A:H2'	1:AA:674:G:C8	2.37	0.60
25:BA:1871:A:O2'	25:BA:1872:A:N7	2.35	0.60
25:BA:2252:G:H2'	25:BA:2253:G:H8	1.66	0.60
59:CD:523:GLU:CD	59:CD:709:ARG:HH22	2.07	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1179:A:OP2	9:AI:95:ARG:NH2	2.22	0.60
25:BA:2830:C:H3'	28:BD:59:ARG:HH22	1.65	0.60
3:AC:124:LEU:HD13	3:AC:196:ILE:HD13	1.84	0.60
3:AC:164:ARG:NH2	22:AV:25:U:O2'	2.35	0.60
1:AA:202:G:H21	1:AA:466:A:H61	1.48	0.60
24:AX:8:4SU:O2'	24:AX:21:A:N1	2.34	0.60
25:BA:645:C:H2'	25:BA:647:G:C8	2.36	0.60
25:BA:1469:A:H2'	25:BA:1470:A:C8	2.37	0.60
1:AA:1498:UR3:OP2	22:AV:16:A:O2'	2.20	0.60
17:AQ:25:ILE:HB	17:AQ:42:THR:HG23	1.81	0.60
25:BA:138:U:H6	25:BA:141:G:H1	1.49	0.60
36:BN:31:PHE:HD1	36:BN:132:THR:HG22	1.66	0.60
28:BD:45:TYR:HB2	28:BD:83:ARG:HH11	1.66	0.60
59:CD:441:LEU:HD22	59:CD:441:LEU:N	2.16	0.60
1:AA:844:G:H2'	1:AA:845:A:C2	2.35	0.59
10:AJ:53:ILE:HD11	10:AJ:63:ASP:HB2	1.84	0.59
25:BA:2883:A:OP2	50:B2:50:ARG:NH1	2.35	0.59
39:BQ:91:ALA:HB2	39:BQ:113:ARG:HB2	1.84	0.59
58:CC:525:THR:HG21	58:CC:687:ARG:HH11	1.67	0.59
59:CD:797:THR:HG22	59:CD:924:GLY:HA3	1.83	0.59
1:AA:1356:G:H2'	1:AA:1357:A:H8	1.65	0.59
25:BA:871:U:H2'	25:BA:872:U:C6	2.37	0.59
25:BA:1064:C:O2'	25:BA:1065:U:H5'	2.03	0.59
25:BA:2103:C:O2	25:BA:2186:G:N2	2.34	0.59
59:CD:1169:THR:OG1	59:CD:1173:ARG:HB3	2.02	0.59
25:BA:64:A:H2'	25:BA:65:U:C6	2.37	0.59
25:BA:210:C:OP1	52:B4:29:GLN:NE2	2.34	0.59
25:BA:1595:C:O2'	25:BA:1596:A:H5'	2.01	0.59
28:BD:34:VAL:O	28:BD:93:GLY:N	2.35	0.59
55:CN:27:DA:C4	55:CN:28:DA:C8	2.90	0.59
25:BA:335:C:OP2	44:BV:82:ARG:NH2	2.35	0.59
58:CC:705:GLU:HB3	58:CC:794:LEU:H	1.67	0.59
1:AA:1344:C:P	9:AI:124:ARG:HH11	2.25	0.59
1:AA:339:C:OP1	34:BL:13:ASN:ND2	2.35	0.59
1:AA:1152:A:OP1	10:AJ:70:HIS:ND1	2.35	0.59
5:AE:94:VAL:HB	5:AE:111:MET:HE1	1.83	0.59
25:BA:443:A:C6	29:BE:40:ARG:HD2	2.38	0.59
25:BA:896:A:O2'	25:BA:897:C:H6	1.85	0.59
25:BA:1169:A:H2'	25:BA:1170:C:H6	1.67	0.59
34:BL:59:LYS:NZ	34:BL:89:ASN:O	2.35	0.59
44:BV:96:PHE:O	44:BV:100:SER:CA	2.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:90:C:H2'	1:AA:91:U:H6	1.67	0.59
25:BA:2134:A:N7	25:BA:2157:G:O2'	2.36	0.59
30:BF:136:ILE:HG12	30:BF:143:TYR:HD1	1.68	0.59
32:BH:73:ASN:ND2	32:BH:76:GLU:HA	2.17	0.59
56:CT:20:DC:H2'	56:CT:21:DG:H8	1.68	0.59
59:CD:256:ASP:O	59:CD:259:ARG:NH2	2.22	0.59
1:AA:636:U:H5'	17:AQ:6:ARG:HE	1.66	0.59
1:AA:1390:U:H2'	1:AA:1391:U:C6	2.37	0.59
32:BH:8:LYS:NZ	32:BH:14:SER:OG	2.30	0.59
58:CC:23:ASP:OD1	58:CC:23:ASP:N	2.34	0.59
25:BA:1529:G:H2'	25:BA:1530:G:H8	1.68	0.59
38:BP:1:MET:O	38:BP:5:SER:CB	2.51	0.59
59:CD:429:LEU:H	59:CD:429:LEU:CD2	2.13	0.59
4:AD:7:PRO:HB2	4:AD:10:LYS:HB2	1.84	0.59
4:AD:50:ASP:OD1	4:AD:50:ASP:N	2.34	0.59
25:BA:140:C:H1'	25:BA:141:G:N2	2.17	0.59
29:BE:16:GLU:N	29:BE:16:GLU:OE2	2.32	0.59
32:BH:104:THR:HA	32:BH:108:VAL:O	2.03	0.59
55:CN:26:DG:OP2	58:CC:542:ARG:NH1	2.35	0.59
57:CA:67:GLU:OE1	58:CC:1057:LYS:NZ	2.33	0.59
1:AA:925:G:C6	1:AA:927:G:N7	2.71	0.58
3:AC:74:GLY:H	58:CC:867:GLU:CB	1.66	0.58
6:AF:26:THR:HG21	6:AF:39:LEU:HD22	1.85	0.58
16:AP:1:MET:SD	16:AP:1:MET:N	2.71	0.58
22:AV:40:A:O2'	22:AV:41:C:OP2	2.21	0.58
25:BA:1069:A:H4'	25:BA:1070:A:C8	2.38	0.58
59:CD:1069:ALA:HA	59:CD:1072:LYS:HB2	1.85	0.58
1:AA:82:G:O3'	1:AA:83:C:H4'	2.03	0.58
25:BA:987:C:O2'	25:BA:1000:A:N3	2.34	0.58
30:BF:56:ASP:N	30:BF:56:ASP:OD1	2.36	0.58
38:BP:38:GLN:HE21	38:BP:47:VAL:HG11	1.68	0.58
41:BS:14:VAL:HG21	41:BS:98:ILE:HG13	1.83	0.58
59:CD:317:THR:OG1	59:CD:322:ARG:O	2.20	0.58
25:BA:1494:A:H2'	25:BA:1495:A:C8	2.38	0.58
31:BG:83:PHE:HB2	31:BG:141:ILE:HD12	1.85	0.58
13:AM:16:VAL:HG13	13:AM:17:ILE:HD12	1.86	0.58
27:BC:41:GLY:O	27:BC:43:ARG:NH1	2.34	0.58
31:BG:41:VAL:HG12	31:BG:64:GLN:HB3	1.85	0.58
31:BG:127:THR:HG23	31:BG:130:GLU:H	1.67	0.58
1:AA:746:A:H2'	1:AA:747:A:C8	2.38	0.58
34:BL:17:ARG:HA	34:BL:17:ARG:HE	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BO:101:GLY:O	37:BO:110:MET:N	2.36	0.58
56:CT:17:DG:C6	56:CT:18:DC:C4	2.91	0.58
56:CT:18:DC:H2'	56:CT:19:DG:H8	1.65	0.58
3:AC:110:GLU:OE1	3:AC:110:GLU:N	2.36	0.58
7:AG:17:LYS:HG3	7:AG:44:TYR:CZ	2.38	0.58
38:BP:51:ALA:HB3	38:BP:78:VAL:HB	1.83	0.58
2:AB:68:LEU:HB3	2:AB:161:LEU:HD12	1.84	0.58
11:AK:92:GLY:C	11:AK:94:GLU:H	2.11	0.58
25:BA:535:G:N2	40:BR:56:GLN:OE1	2.35	0.58
31:BG:95:ARG:HH22	31:BG:97:ALA:HB2	1.69	0.58
35:BM:85:VAL:HG23	35:BM:98:ALA:HB2	1.84	0.58
59:CD:650:LYS:HE3	59:CD:742:GLY:O	2.02	0.58
1:AA:205:A:H2'	1:AA:206:C:C6	2.39	0.58
13:AM:92:ARG:NH1	25:BA:889:C:OP1	2.37	0.58
25:BA:172:A:H2'	25:BA:173:A:C8	2.39	0.58
25:BA:219:A:N3	25:BA:234:U:O2'	2.36	0.58
56:CT:26:DA:H2''	56:CT:27:DG:C8	2.39	0.58
9:AI:46:MET:N	9:AI:49:ARG:HH21	2.02	0.58
25:BA:141:G:H2'	25:BA:142:A:O4'	2.04	0.58
25:BA:895:U:O2'	25:BA:896:A:H2'	2.04	0.58
25:BA:927:A:H2'	25:BA:928:A:C8	2.39	0.58
25:BA:2448:A:O2'	25:BA:2449:H2U:H52	2.04	0.58
26:BB:8:C:O3'	38:BP:25:ARG:NH1	2.36	0.58
58:CC:525:THR:HG21	58:CC:687:ARG:NH1	2.18	0.58
59:CD:515:ARG:NH2	59:CD:718:SER:O	2.37	0.58
9:AI:12:ARG:HD2	9:AI:74:GLY:HA2	1.85	0.58
15:AO:14:GLU:OE1	15:AO:84:ARG:NH2	2.37	0.58
25:BA:614:A:O2'	25:BA:615:U:OP2	2.21	0.58
25:BA:135:U:H2'	25:BA:136:G:O4'	2.04	0.57
25:BA:2370:G:O2'	51:B3:44:ARG:NH1	2.37	0.57
1:AA:67:C:H2'	1:AA:68:G:C8	2.38	0.57
1:AA:80:C:N3	1:AA:81:A:N6	2.53	0.57
1:AA:713:G:H2'	1:AA:714:G:C8	2.40	0.57
38:BP:1:MET:O	38:BP:5:SER:HB3	2.04	0.57
58:CC:421:SER:H	58:CC:424:ASP:HB2	1.69	0.57
58:CC:591:TYR:OH	58:CC:637:ARG:NH2	2.36	0.57
1:AA:362:G:N2	1:AA:365:U:OP2	2.37	0.57
6:AF:63:ASN:ND2	6:AF:96:VAL:HG21	2.19	0.57
9:AI:62:ASP:OD1	9:AI:63:LEU:N	2.38	0.57
25:BA:1433:A:H2'	25:BA:1434:A:C8	2.39	0.57
11:AK:17:SER:O	11:AK:80:LYS:N	2.27	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:728:G:H4'	27:BC:13:ARG:HD3	1.85	0.57
37:BO:2:ARG:NE	37:BO:2:ARG:O	2.37	0.57
5:AE:12:GLN:OE1	59:CD:79:LYS:HD2	2.05	0.57
6:AF:17:GLN:HG2	32:BH:87:GLU:HG3	1.86	0.57
22:AV:44:C:H2'	22:AV:45:G:O4'	2.04	0.57
1:AA:51:A:N7	1:AA:114:U:O2'	2.36	0.57
25:BA:1105:U:H2'	25:BA:1106:G:H8	1.69	0.57
25:BA:1248:G:OP1	29:BE:44:ARG:NH1	2.38	0.57
56:CT:19:DG:C4	56:CT:20:DC:C5	2.93	0.57
10:AJ:81:GLU:N	10:AJ:81:GLU:OE2	2.38	0.57
13:AM:68:ASP:HA	13:AM:71:ARG:HH21	1.70	0.57
25:BA:1915:3TD:H2'	25:BA:1916:A:C8	2.40	0.57
58:CC:638:SER:OG	58:CC:639:LYS:N	2.32	0.57
58:CC:726:TYR:HB3	58:CC:733:VAL:CG1	2.34	0.57
4:AD:140:ASN:N	4:AD:182:PHE:O	2.38	0.57
7:AG:77:SER:OG	7:AG:86:GLN:OE1	2.17	0.57
45:BW:20:LEU:HD21	45:BW:26:PHE:HA	1.87	0.57
1:AA:966:2MG:H5''	1:AA:967:5MC:OP2	2.05	0.57
25:BA:1068:G:N2	25:BA:1095:A:O2'	2.31	0.57
34:BL:5:GLN:N	34:BL:21:CYS:O	2.37	0.57
1:AA:413:G:O2'	1:AA:428:G:N2	2.39	0.56
1:AA:1130:A:H2'	1:AA:1131:G:C8	2.40	0.56
1:AA:1130:A:H2'	1:AA:1131:G:H8	1.70	0.56
25:BA:277:G:H2'	25:BA:361:G:C6	2.40	0.56
25:BA:1056:G:H4'	25:BA:1086:A:H8	1.70	0.56
25:BA:1315:C:O2'	25:BA:1392:A:N3	2.34	0.56
25:BA:2333:A:P	46:BX:77:ARG:HH22	2.27	0.56
26:BB:28:C:H5''	38:BP:31:THR:HG21	1.87	0.56
1:AA:76:G:O6	1:AA:93:U:O4	2.22	0.56
1:AA:148:G:O2'	1:AA:149:A:O5'	2.23	0.56
1:AA:413:G:N2	1:AA:428:G:H1'	2.20	0.56
25:BA:2244:U:O2'	25:BA:2245:U:H5'	2.05	0.56
29:BE:145:ASP:HB3	29:BE:184:ASP:HB2	1.87	0.56
44:BV:74:ASN:HB3	44:BV:96:PHE:CE1	2.41	0.56
3:AC:107:ARG:O	58:CC:859:GLU:HG3	2.03	0.56
7:AG:113:ASP:O	7:AG:119:ARG:NE	2.37	0.56
13:AM:46:SER:OG	13:AM:47:GLU:OE2	2.20	0.56
23:AW:15:G:N1	23:AW:48:C:N3	2.49	0.56
24:AX:20:H2U:O2'	24:AX:21:A:H5''	2.06	0.56
25:BA:100:U:O2'	44:BV:91:LYS:NZ	2.39	0.56
29:BE:48:THR:OG1	29:BE:51:GLU:OE1	2.22	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:BH:84:ALA:HB2	32:BH:90:LEU:HD12	1.87	0.56
44:BV:62:GLU:OE1	44:BV:62:GLU:N	2.39	0.56
4:AD:95:GLU:HG2	4:AD:191:LEU:HD21	1.87	0.56
7:AG:138:ARG:HH21	7:AG:139:GLU:HG2	1.70	0.56
25:BA:653:U:O2	25:BA:653:U:H2'	2.06	0.56
25:BA:2519:U:O4'	25:BA:2542:A:N6	2.37	0.56
59:CD:160:LEU:HD23	59:CD:160:LEU:H	1.71	0.56
1:AA:1033:G:H2'	1:AA:1034:G:H8	1.70	0.56
29:BE:130:LYS:HB2	29:BE:133:LEU:HD12	1.87	0.56
58:CC:267:ARG:NE	58:CC:268:ARG:O	2.37	0.56
58:CC:519:ASN:C	58:CC:519:ASN:OD1	2.46	0.56
7:AG:7:ILE:HD13	7:AG:7:ILE:H	1.71	0.56
24:AX:34:G:H2'	24:AX:35:A:C8	2.41	0.56
25:BA:888:C:H1'	25:BA:889:C:H1'	1.86	0.56
25:BA:1914:C:H2'	25:BA:1915:3TD:C6	2.35	0.56
32:BH:50:ARG:NH1	32:BH:51:ARG:HE	2.04	0.56
1:AA:111:G:O6	1:AA:330:C:N4	2.27	0.56
1:AA:1266:G:N2	1:AA:1269:A:OP2	2.29	0.56
25:BA:172:A:H2'	25:BA:173:A:H8	1.71	0.56
30:BF:98:GLU:HG3	30:BF:99:PHE:N	2.21	0.56
55:CN:28:DA:H2''	55:CN:29:DG:H8	1.70	0.56
23:AW:69:C:H2'	23:AW:70:G:C8	2.40	0.56
43:BU:6:ARG:NH2	43:BU:37:ASP:OD2	2.36	0.56
58:CC:320:ASP:N	58:CC:320:ASP:OD1	2.37	0.56
5:AE:69:ARG:HG3	5:AE:70:ASN:ND2	2.21	0.56
25:BA:1591:A:H2'	25:BA:1592:C:H6	1.70	0.56
25:BA:2135:A:O2'	25:BA:2160:C:H5'	2.06	0.56
31:BG:148:LEU:HA	31:BG:151:TYR:HD2	1.70	0.56
46:BX:37:ILE:HG22	46:BX:38:VAL:HG23	1.88	0.56
58:CC:705:GLU:CD	58:CC:705:GLU:H	2.14	0.56
58:CC:1083:GLU:CD	58:CC:1083:GLU:H	2.13	0.56
1:AA:946:A:H2'	1:AA:947:G:C8	2.41	0.55
11:AK:92:GLY:O	11:AK:94:GLU:N	2.38	0.55
25:BA:1306:C:H41	25:BA:1606:C:H2'	1.72	0.55
30:BF:5:HIS:HB2	30:BF:97:TRP:CG	2.42	0.55
36:BN:77:PRO:HG2	36:BN:80:VAL:HG11	1.87	0.55
26:BB:119:A:H2'	26:BB:120:U:C6	2.40	0.55
29:BE:5:LEU:O	29:BE:9:GLN:CA	2.51	0.55
46:BX:53:CYS:SG	46:BX:57:HIS:HA	2.46	0.55
3:AC:80:LYS:HZ1	58:CC:946:LEU:CD2	2.14	0.55
4:AD:42:GLY:O	4:AD:44:ARG:N	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2119:A:H8	25:BA:2119:A:O5'	1.88	0.55
25:BA:2352:A:N6	25:BA:2365:G:O2'	2.39	0.55
25:BA:2840:C:H5''	37:BO:53:THR:HG21	1.88	0.55
1:AA:90:C:H2'	1:AA:91:U:C6	2.40	0.55
25:BA:856:G:H2'	25:BA:857:G:C8	2.41	0.55
32:BH:84:ALA:HA	32:BH:91:PHE:H	1.72	0.55
41:BS:30:GLY:N	41:BS:63:VAL:O	2.38	0.55
43:BU:34:VAL:HG21	43:BU:43:ILE:HD11	1.87	0.55
58:CC:392:GLU:H	58:CC:392:GLU:CD	2.12	0.55
58:CC:696:ASP:OD1	58:CC:697:LYS:N	2.39	0.55
58:CC:1176:LEU:O	58:CC:1178:LYS:N	2.40	0.55
59:CD:495:ASN:OD1	59:CD:495:ASN:N	2.37	0.55
5:AE:10:GLU:HB2	59:CD:78:LEU:HB2	1.89	0.55
25:BA:136:G:H4'	25:BA:136:G:OP1	2.05	0.55
25:BA:2111:U:O4'	25:BA:2118:U:O2'	2.24	0.55
29:BE:158:PHE:HA	29:BE:169:VAL:HG21	1.89	0.55
31:BG:156:PRO:O	31:BG:171:THR:OG1	2.21	0.55
19:AS:32:ARG:HG3	19:AS:57:HIS:CD2	2.41	0.55
25:BA:84:A:N1	25:BA:98:G:O2'	2.34	0.55
25:BA:1494:A:HO2'	25:BA:1495:A:P	2.29	0.55
25:BA:1594:U:H2'	25:BA:1595:C:H6	1.70	0.55
25:BA:2104:C:H5	25:BA:2186:G:N2	2.05	0.55
35:BM:2:ARG:N	35:BM:5:THR:OG1	2.27	0.55
57:CB:13:LEU:HA	57:CB:28:LEU:HD13	1.89	0.55
58:CC:726:TYR:C	58:CC:726:TYR:CD1	2.84	0.55
1:AA:339:C:OP2	34:BL:98:ARG:NH2	2.40	0.55
1:AA:1032:G:H21	1:AA:1033:G:H4'	1.72	0.55
15:AO:25:THR:HG23	15:AO:66:LEU:HD22	1.87	0.55
25:BA:1251:C:OP2	40:BR:6:ARG:NH2	2.39	0.55
1:AA:481:G:HO2'	1:AA:483:C:N4	2.05	0.55
4:AD:88:GLU:OE1	4:AD:88:GLU:N	2.39	0.55
10:AJ:41:PRO:HA	10:AJ:72:ARG:HD3	1.88	0.55
11:AK:67:ALA:HB2	11:AK:96:THR:HG23	1.87	0.55
25:BA:567:U:OP2	35:BM:29:LYS:NZ	2.39	0.55
25:BA:2115:G:H2'	25:BA:2117:A:OP2	2.07	0.55
25:BA:2788:C:O2'	25:BA:2809:A:N3	2.38	0.55
50:B2:31:ASP:O	50:B2:35:GLY:HA2	2.06	0.55
59:CD:175:GLU:CD	59:CD:175:GLU:H	2.15	0.55
1:AA:945:G:C2	1:AA:946:A:C8	2.95	0.55
1:AA:1119:C:OP1	9:AI:85:ARG:NH1	2.40	0.55
3:AC:109:PRO:HD2	58:CC:859:GLU:OE2	2.02	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1417:C:H1'	25:BA:1586:A:N1	2.22	0.55
30:BF:126:GLY:HA2	30:BF:163:ASP:HA	1.88	0.55
1:AA:993:G:O2'	1:AA:994:A:N7	2.39	0.55
9:AI:33:ARG:HH11	9:AI:38:TYR:HA	1.71	0.55
12:AL:54:ARG:HB2	12:AL:54:ARG:NH1	2.21	0.55
33:BK:60:ASP:OD2	33:BK:61:LYS:NZ	2.38	0.55
51:B3:22:THR:HG23	53:B5:34:THR:HG23	1.89	0.55
1:AA:147:G:O2'	1:AA:148:G:O4'	2.25	0.54
1:AA:205:A:H2'	1:AA:206:C:H6	1.71	0.54
1:AA:215:C:H2'	1:AA:216:U:O4'	2.06	0.54
6:AF:24:ARG:HH12	6:AF:28:ALA:HB2	1.71	0.54
10:AJ:42:LEU:HB2	10:AJ:71:LEU:HB3	1.89	0.54
25:BA:2698:U:H2'	25:BA:2699:C:C6	2.42	0.54
55:CN:34:DT:H6	55:CN:34:DT:H5'	1.70	0.54
58:CC:1165:SER:O	58:CC:1167:GLU:N	2.37	0.54
1:AA:1124:G:N2	1:AA:1125:U:O4	2.26	0.54
3:AC:107:ARG:NE	58:CC:863:SER:O	2.40	0.54
5:AE:148:ASN:ND2	8:AH:73:GLU:OE1	2.40	0.54
8:AH:31:LYS:O	8:AH:34:VAL:HG22	2.07	0.54
15:AO:3:LEU:HB2	15:AO:35:GLN:OE1	2.06	0.54
24:AX:43:C:H2'	24:AX:44:G:C8	2.41	0.54
25:BA:1193:G:OP1	35:BM:14:LYS:NZ	2.29	0.54
35:BM:9:ALA:O	35:BM:12:SER:OG	2.19	0.54
1:AA:1018:G:H2'	1:AA:1019:A:C8	2.42	0.54
1:AA:1318:A:H5''	19:AS:3:ARG:HH22	1.72	0.54
3:AC:77:ILE:HA	3:AC:84:VAL:HG23	1.89	0.54
23:AW:1:C:H2'	23:AW:2:G:C8	2.43	0.54
25:BA:244:A:OP2	53:B5:8:ARG:NH2	2.40	0.54
31:BG:86:LYS:HZ2	31:BG:86:LYS:HB3	1.73	0.54
34:BL:17:ARG:HA	34:BL:17:ARG:NE	2.23	0.54
58:CC:423:ASP:N	58:CC:423:ASP:OD1	2.33	0.54
58:CC:494:ASN:C	58:CC:494:ASN:HD22	2.08	0.54
58:CC:1070:HIS:NE2	58:CC:1114:GLU:OE1	2.41	0.54
58:CC:1321:GLU:OE2	59:CD:99:ARG:NH1	2.41	0.54
59:CD:37:GLU:HB2	59:CD:104:HIS:CE1	2.41	0.54
1:AA:714:G:H2'	1:AA:715:A:C8	2.42	0.54
3:AC:79:LYS:CE	58:CC:943:LYS:N	2.70	0.54
7:AG:143:ARG:HG3	7:AG:144:MET:N	2.22	0.54
9:AI:116:VAL:HG13	10:AJ:62:ARG:NH2	2.21	0.54
29:BE:1:MET:HE2	29:BE:113:VAL:HG11	1.88	0.54
1:AA:1007:U:H2'	1:AA:1008:U:C6	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1808:A:H3'	25:BA:1809:A:C8	2.43	0.54
25:BA:2190:G:H2'	25:BA:2191:A:O4'	2.07	0.54
26:BB:24:G:N7	26:BB:56:G:H2'	2.22	0.54
31:BG:95:ARG:HH12	31:BG:97:ALA:HB2	1.71	0.54
58:CC:7:GLU:O	58:CC:9:LYS:N	2.35	0.54
1:AA:837:U:O2	1:AA:849:G:O6	2.25	0.54
13:AM:4:ILE:HG23	13:AM:57:ARG:HG2	1.88	0.54
19:AS:20:GLU:OE1	19:AS:21:LYS:N	2.40	0.54
25:BA:2314:A:H2'	25:BA:2315:G:C8	2.42	0.54
32:BH:73:ASN:HD22	32:BH:76:GLU:HA	1.72	0.54
2:AB:208:ARG:O	2:AB:211:THR:OG1	2.22	0.54
24:AX:37:MIA:H2'	24:AX:38:A:O4'	2.07	0.54
41:BS:27:ILE:HG21	41:BS:63:VAL:HG21	1.89	0.54
1:AA:1240:U:O4	7:AG:109:ARG:NH1	2.41	0.54
1:AA:1315:U:O2'	1:AA:1360:A:N3	2.41	0.54
3:AC:125:GLU:OE2	3:AC:190:HIS:N	2.38	0.54
5:AE:76:LEU:HD13	5:AE:79:GLY:H	1.73	0.54
8:AH:8:ALA:O	8:AH:12:THR:HG23	2.07	0.54
15:AO:25:THR:HG21	15:AO:70:LEU:HD13	1.89	0.54
25:BA:1724:G:N2	25:BA:1736:U:O2	2.37	0.54
25:BA:2178:C:H2'	25:BA:2179:C:C5	2.43	0.54
25:BA:2258:C:O2'	25:BA:2427:C:OP2	2.19	0.54
33:BK:56:VAL:HB	33:BK:124:VAL:HG13	1.89	0.54
51:B3:33:LYS:HG2	51:B3:52:ALA:HB2	1.90	0.54
4:AD:98:LEU:O	4:AD:102:VAL:HG12	2.08	0.54
7:AG:129:GLU:CD	7:AG:131:LYS:H	2.15	0.54
25:BA:956:G:N7	36:BN:14:LYS:NZ	2.47	0.54
25:BA:1405:U:O2'	25:BA:1406:U:O4'	2.26	0.54
25:BA:2547:A:H2'	25:BA:2548:U:C6	2.43	0.54
55:CN:31:DG:H2''	55:CN:32:DA:C8	2.42	0.54
58:CC:524:ILE:HG22	58:CC:525:THR:N	2.22	0.54
1:AA:31:G:O2'	1:AA:48:C:N4	2.41	0.54
1:AA:1318:A:H5''	19:AS:3:ARG:NH2	2.23	0.54
8:AH:5:ASP:OD1	8:AH:77:ARG:NH2	2.39	0.54
25:BA:1434:A:HO2'	25:BA:1435:G:H8	1.56	0.54
25:BA:1826:G:O2'	25:BA:1971:U:OP2	2.26	0.54
43:BU:33:LYS:HG2	43:BU:80:TRP:CZ3	2.43	0.54
55:CN:26:DG:C6	55:CN:27:DA:N6	2.76	0.54
58:CC:1079:ILE:HG23	58:CC:1079:ILE:O	2.08	0.54
1:AA:1184:G:C2	1:AA:1185:G:C8	2.96	0.53
6:AF:44:ARG:HB2	6:AF:44:ARG:HH11	1.71	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1301:A:H2	25:BA:1626:A:H2	1.55	0.53
25:BA:1506:U:H2'	25:BA:1507:C:C6	2.43	0.53
25:BA:1595:C:H2'	25:BA:1596:A:C8	2.43	0.53
30:BF:60:ILE:HD13	30:BF:140:GLU:HB2	1.90	0.53
31:BG:24:ILE:HG21	31:BG:72:LEU:HD21	1.90	0.53
32:BH:66:ASN:C	32:BH:66:ASN:HD22	2.15	0.53
6:AF:32:ALA:CB	6:AF:70:VAL:HG11	2.39	0.53
10:AJ:56:HIS:ND1	10:AJ:57:VAL:HG22	2.23	0.53
14:AN:81:ARG:O	14:AN:84:VAL:HG22	2.08	0.53
25:BA:285:G:O6	25:BA:355:U:O2	2.26	0.53
36:BN:66:ARG:NH1	36:BN:104:GLU:OE1	2.33	0.53
38:BP:57:ALA:O	38:BP:61:GLN:HG2	2.08	0.53
59:CD:367:GLY:HA2	59:CD:440:VAL:O	2.08	0.53
1:AA:337:G:H2'	1:AA:338:A:C8	2.42	0.53
3:AC:21:THR:HG23	3:AC:58:GLU:HB3	1.90	0.53
25:BA:1095:A:H2'	25:BA:1096:A:C8	2.43	0.53
25:BA:1421:G:C2	25:BA:1422:G:C8	2.96	0.53
25:BA:1869:G:N2	25:BA:1872:A:OP2	2.40	0.53
58:CC:12:ARG:NE	58:CC:793:GLU:OE2	2.36	0.53
58:CC:178:PRO:HB3	58:CC:395:TYR:CZ	2.44	0.53
1:AA:73:C:C2'	1:AA:74:A:H5'	2.38	0.53
1:AA:1210:C:O4'	1:AA:1214:C:N4	2.41	0.53
1:AA:1323:G:H2'	1:AA:1324:A:C8	2.44	0.53
2:AB:15:HIS:HB3	2:AB:43:LEU:HD21	1.89	0.53
2:AB:168:HIS:ND1	2:AB:169:GLU:OE1	2.42	0.53
25:BA:995:C:OP2	40:BR:54:LYS:HE3	2.08	0.53
25:BA:1529:G:O6	25:BA:1542:U:C4	2.61	0.53
25:BA:1789:A:OP1	27:BC:221:ARG:HG3	2.08	0.53
30:BF:40:VAL:C	30:BF:42:GLU:H	2.17	0.53
50:B2:28:LEU:HD12	50:B2:37:LYS:HB3	1.90	0.53
57:CB:191:ARG:NH2	57:CB:192:VAL:O	2.42	0.53
1:AA:197:A:H4'	1:AA:198:G:O5'	2.06	0.53
1:AA:826:C:O2	8:AH:16:ASN:ND2	2.42	0.53
5:AE:89:HIS:NE2	5:AE:138:ARG:HG3	2.24	0.53
10:AJ:6:ILE:HB	10:AJ:76:ILE:HG23	1.90	0.53
25:BA:645:C:H2'	25:BA:647:G:N7	2.23	0.53
25:BA:898:C:C4	25:BA:899:A:C8	2.96	0.53
25:BA:2405:G:OP1	35:BM:70:LYS:NZ	2.40	0.53
25:BA:2636:C:H2'	25:BA:2637:U:C6	2.43	0.53
56:CT:21:DG:C6	56:CT:22:DC:N4	2.77	0.53
58:CC:538:LEU:HD12	58:CC:539:THR:N	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:492:C:H2'	1:AA:493:A:C8	2.44	0.53
1:AA:496:A:H2'	1:AA:496:A:N3	2.24	0.53
24:AX:27:G:H2'	24:AX:28:G:C8	2.42	0.53
32:BH:115:VAL:O	32:BH:116:ARG:NH1	2.41	0.53
1:AA:108:G:C6	20:AT:10:ARG:HG3	2.43	0.53
7:AG:53:ARG:HH12	7:AG:122:ASN:HA	1.74	0.53
30:BF:25:VAL:O	30:BF:28:VAL:HG12	2.08	0.53
38:BP:7:ARG:NH1	38:BP:95:SER:O	2.41	0.53
1:AA:412:A:H62	1:AA:431:A:N6	2.05	0.53
2:AB:77:SER:HB2	2:AB:93:ASN:HB2	1.90	0.53
2:AB:188:ASP:OD1	2:AB:188:ASP:N	2.31	0.53
10:AJ:87:LEU:HD12	10:AJ:88:MET:N	2.23	0.53
25:BA:273:G:H2'	25:BA:274:C:O4'	2.09	0.53
25:BA:1084:A:H2'	25:BA:1085:A:C8	2.44	0.53
58:CC:150:HIS:CE1	58:CC:454:ARG:HG3	2.43	0.53
59:CD:825:VAL:HG13	59:CD:825:VAL:O	2.08	0.53
1:AA:1382:C:C2'	1:AA:1383:C:H5'	2.39	0.53
1:AA:1397:C:OP2	5:AE:29:ARG:NH2	2.29	0.53
57:CA:218:ARG:NH1	57:CB:233:ASP:OD1	2.42	0.53
59:CD:312:ARG:HG2	59:CD:313:GLY:N	2.24	0.53
1:AA:1001:C:H2'	1:AA:1002:G:H8	1.74	0.53
6:AF:44:ARG:HB2	6:AF:44:ARG:NH1	2.24	0.53
6:AF:47:LEU:HD21	6:AF:57:ALA:HB3	1.90	0.53
14:AN:26:GLU:O	14:AN:30:ILE:HG22	2.08	0.53
25:BA:144:A:H2'	25:BA:145:C:C6	2.44	0.53
25:BA:886:A:N6	25:BA:892:A:H1'	2.24	0.53
25:BA:1980:G:O2'	25:BA:1982:U:OP2	2.26	0.53
30:BF:34:ILE:HG12	30:BF:156:ILE:HG12	1.91	0.53
32:BH:46:PHE:O	32:BH:51:ARG:HD2	2.09	0.53
59:CD:441:LEU:HD22	59:CD:441:LEU:H	1.73	0.53
1:AA:522:C:N3	1:AA:527:G7M:N1	2.41	0.52
1:AA:932:C:O3'	7:AG:4:ARG:NH2	2.42	0.52
4:AD:15:GLU:HG3	4:AD:60:LYS:HA	1.91	0.52
18:AR:37:GLY:O	18:AR:63:ARG:NH2	2.42	0.52
25:BA:631:A:N3	25:BA:2415:G:O2'	2.43	0.52
25:BA:2636:C:H2'	25:BA:2637:U:H6	1.73	0.52
2:AB:108:ARG:O	2:AB:111:ILE:HG12	2.09	0.52
4:AD:80:ALA:HA	4:AD:86:THR:HG22	1.91	0.52
6:AF:47:LEU:HD13	6:AF:51:ILE:HG13	1.92	0.52
25:BA:1042:G:O2'	25:BA:1043:C:H6	1.92	0.52
25:BA:2900:A:C6	25:BA:2901:C:N4	2.77	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:BC:259:SER:O	27:BC:259:SER:OG	2.26	0.52
38:BP:99:TYR:OH	38:BP:111:ARG:NH1	2.41	0.52
59:CD:35:PHE:CD1	59:CD:101:ARG:HB3	2.44	0.52
1:AA:921:U:O2	5:AE:24:THR:OG1	2.28	0.52
13:AM:29:ARG:HH12	13:AM:63:PHE:HB3	1.75	0.52
25:BA:2285:C:P	51:B3:6:ARG:HH12	2.32	0.52
30:BF:94:GLU:HG3	30:BF:95:ARG:N	2.25	0.52
32:BH:83:LYS:O	32:BH:91:PHE:HB3	2.09	0.52
39:BQ:32:VAL:HG12	39:BQ:34:GLU:HG2	1.92	0.52
39:BQ:88:ARG:HH21	39:BQ:112:GLU:HG3	1.73	0.52
44:BV:18:ASP:HA	44:BV:21:LYS:HZ3	1.72	0.52
2:AB:129:LEU:HD12	2:AB:130:THR:H	1.73	0.52
9:AI:22:LYS:HG2	9:AI:62:ASP:HB3	1.90	0.52
10:AJ:76:ILE:HG12	10:AJ:79:PRO:HG3	1.91	0.52
13:AM:11:ASP:HA	13:AM:45:ILE:HB	1.91	0.52
14:AN:48:LEU:HD12	14:AN:51:LEU:HD12	1.90	0.52
25:BA:1028:A:H2'	25:BA:1029:A:C8	2.45	0.52
25:BA:1169:A:H2'	25:BA:1170:C:C6	2.43	0.52
25:BA:1568:G:N7	27:BC:28:LYS:NZ	2.57	0.52
25:BA:1596:A:O2'	25:BA:1597:A:H5'	2.09	0.52
25:BA:1615:C:OP2	25:BA:1617:C:N4	2.24	0.52
28:BD:37:VAL:HG21	28:BD:90:PHE:O	2.09	0.52
31:BG:145:ALA:HB1	31:BG:164:TYR:CE1	2.41	0.52
58:CC:1340:GLU:OE1	58:CC:1341:ASP:N	2.34	0.52
9:AI:26:GLY:HA2	9:AI:61:LEU:O	2.10	0.52
58:CC:1333:LEU:C	58:CC:1335:ILE:H	2.18	0.52
59:CD:978:ARG:HD3	59:CD:1197:ASN:O	2.09	0.52
1:AA:866:C:C4	1:AA:867:G:H1'	2.44	0.52
1:AA:1497:G:H1'	1:AA:1518:MA6:H2	1.91	0.52
9:AI:36:GLU:OE1	9:AI:36:GLU:N	2.38	0.52
25:BA:240:C:OP2	25:BA:241:A:O2'	2.23	0.52
31:BG:10:VAL:HA	31:BG:49:THR:HG22	1.90	0.52
31:BG:86:LYS:HB3	31:BG:86:LYS:NZ	2.24	0.52
1:AA:613:C:OP1	4:AD:81:ARG:NH1	2.37	0.52
1:AA:823:C:HO2'	8:AH:2:SER:N	2.07	0.52
1:AA:1135:U:HO2'	1:AA:1138:G:H1	1.57	0.52
25:BA:639:U:H2'	25:BA:640:C:H6	1.72	0.52
25:BA:1479:G:HO2'	25:BA:1560:G:HO2'	1.52	0.52
25:BA:1930:G:O2'	25:BA:1968:G:O6	2.26	0.52
30:BF:31:VAL:HG23	30:BF:169:LEU:HD21	1.92	0.52
34:BL:63:VAL:HA	34:BL:107:LEU:HD21	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:BP:55:GLU:CD	38:BP:81:ARG:HH22	2.18	0.52
1:AA:437:U:H5''	4:AD:152:GLN:NE2	2.23	0.52
2:AB:187:VAL:HG23	2:AB:191:SER:HB2	1.91	0.52
25:BA:887:U:O2'	25:BA:888:C:H5''	2.10	0.52
30:BF:11:GLU:HB3	30:BF:15:LYS:HE3	1.92	0.52
31:BG:107:LEU:HD13	31:BG:152:ARG:HB2	1.91	0.52
31:BG:148:LEU:HA	31:BG:151:TYR:CD2	2.45	0.52
34:BL:102:PRO:HB2	34:BL:123:LEU:HD23	1.92	0.52
13:AM:65:VAL:HG22	13:AM:66:GLU:HG2	1.92	0.52
24:AX:6:G:H2'	24:AX:7:A:H8	1.75	0.52
25:BA:1113:U:H2'	25:BA:1114:C:C6	2.45	0.52
25:BA:1168:G:H2'	25:BA:1169:A:C8	2.45	0.52
25:BA:1266:G:OP2	50:B2:17:ARG:NE	2.41	0.52
25:BA:2252:G:H2'	25:BA:2253:G:C8	2.45	0.52
30:BF:11:GLU:O	30:BF:15:LYS:HG3	2.10	0.52
41:BS:61:ALA:HB2	41:BS:98:ILE:HD13	1.92	0.52
58:CC:193:ASN:HD22	58:CC:193:ASN:N	2.08	0.52
1:AA:1034:G:H2'	1:AA:1035:A:C8	2.45	0.52
3:AC:58:GLU:HG3	3:AC:65:ARG:HB3	1.92	0.52
5:AE:10:GLU:HB2	59:CD:78:LEU:CB	2.40	0.52
8:AH:66:PHE:CD2	8:AH:67:GLN:HG3	2.45	0.52
10:AJ:34:ALA:HB2	10:AJ:83:THR:HG21	1.92	0.52
30:BF:100:PHE:O	30:BF:104:ILE:HG22	2.09	0.52
35:BM:61:LEU:O	53:B5:13:ARG:NE	2.37	0.52
58:CC:726:TYR:CD1	58:CC:727:VAL:N	2.78	0.52
1:AA:159:G:N2	1:AA:162:A:OP2	2.43	0.51
1:AA:1530:G:H2'	1:AA:1531:A:C8	2.45	0.51
9:AI:57:MET:HG2	9:AI:60:LYS:HD2	1.92	0.51
15:AO:5:THR:O	15:AO:8:THR:OG1	2.26	0.51
25:BA:357:C:H2'	25:BA:358:U:H6	1.74	0.51
25:BA:1173:U:C2	25:BA:1176:U:O2	2.63	0.51
25:BA:1667:G:O2'	25:BA:1991:U:O4	2.24	0.51
28:BD:77:ARG:NH1	28:BD:200:ASP:OD1	2.44	0.51
29:BE:170:ARG:NH2	29:BE:176:ASP:OD1	2.42	0.51
58:CC:85:CYS:SG	58:CC:90:VAL:HG23	2.50	0.51
58:CC:296:VAL:O	58:CC:335:THR:HB	2.10	0.51
59:CD:801:VAL:HG12	59:CD:920:ALA:HB3	1.91	0.51
1:AA:89:G:H2'	1:AA:90:C:C6	2.44	0.51
1:AA:363:A:C6	12:AL:28:PRO:HD2	2.45	0.51
1:AA:687:A:N1	1:AA:700:G:O2'	2.33	0.51
3:AC:80:LYS:HZ2	58:CC:946:LEU:CD2	2.19	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:AU:62:ARG:O	21:AU:66:ARG:HB3	2.11	0.51
25:BA:2102:G:N1	25:BA:2187:U:C2	2.79	0.51
42:BT:1:MET:N	42:BT:110:ARG:HH11	2.07	0.51
43:BU:4:GLU:HA	43:BU:7:LEU:HD22	1.92	0.51
1:AA:925:G:C2	1:AA:927:G:C8	2.99	0.51
8:AH:7:ILE:HB	8:AH:77:ARG:NH2	2.25	0.51
24:AX:41:C:H2'	24:AX:42:C:C6	2.46	0.51
25:BA:134:G:H2'	25:BA:135:U:C6	2.46	0.51
25:BA:1174:U:H2'	25:BA:1175:A:C8	2.45	0.51
1:AA:218:U:H2'	1:AA:219:U:O4'	2.11	0.51
3:AC:77:ILE:HG22	58:CC:943:LYS:CE	2.34	0.51
5:AE:80:THR:HA	5:AE:120:VAL:HG13	1.93	0.51
13:AM:52:GLN:O	13:AM:56:LEU:HG	2.10	0.51
25:BA:1754:A:N1	25:BA:2716:C:O2'	2.40	0.51
30:BF:55:ALA:O	30:BF:59:ALA:HB3	2.11	0.51
42:BT:4:ILE:HG12	42:BT:106:VAL:HG22	1.92	0.51
59:CD:301:GLU:OE1	59:CD:312:ARG:NH1	2.37	0.51
11:AK:47:ALA:HB1	11:AK:62:ALA:HB1	1.90	0.51
25:BA:2124:G:N1	25:BA:2175:C:N3	2.59	0.51
49:B1:9:GLN:O	49:B1:33:GLY:N	2.44	0.51
59:CD:288:PRO:HD2	59:CD:291:ILE:HD12	1.93	0.51
1:AA:1010:U:H2'	1:AA:1011:C:C6	2.45	0.51
10:AJ:5:ARG:HB2	10:AJ:77:VAL:HA	1.92	0.51
13:AM:41:GLU:H	13:AM:41:GLU:CD	2.16	0.51
14:AN:83:LYS:HA	14:AN:86:GLU:HG3	1.92	0.51
25:BA:1820:U:O2'	27:BC:158:ALA:HB3	2.11	0.51
30:BF:83:TYR:O	30:BF:85:ILE:HG23	2.11	0.51
58:CC:766:ASN:CG	58:CC:766:ASN:O	2.53	0.51
59:CD:275:ARG:HH11	59:CD:298:MET:HB3	1.76	0.51
1:AA:1:A:H2'	1:AA:2:A:C8	2.45	0.51
1:AA:1062:U:O4	3:AC:3:GLN:NE2	2.43	0.51
9:AI:119:ARG:NH1	9:AI:123:ARG:HE	2.08	0.51
23:AW:76:A:HO3'	25:BA:2063:C:HO2'	1.58	0.51
25:BA:1059:G:N7	25:BA:1060:U:H2'	2.25	0.51
25:BA:2315:G:HO2'	25:BA:2316:G:H8	1.58	0.51
25:BA:2886:A:C5	50:B2:40:ARG:NH2	2.79	0.51
31:BG:135:GLY:N	31:BG:141:ILE:HD11	2.26	0.51
1:AA:1039:G:H2'	1:AA:1040:U:C6	2.46	0.51
3:AC:86:LYS:O	3:AC:89:LYS:HG3	2.11	0.51
25:BA:1585:C:H2'	25:BA:1586:A:C8	2.42	0.51
25:BA:2120:G:O2'	25:BA:2121:G:H5'	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:BC:252:THR:HG23	27:BC:253:LYS:HG3	1.93	0.51
29:BE:195:GLN:O	29:BE:198:GLU:HG2	2.11	0.51
58:CC:811:ASN:ND2	58:CC:1097:VAL:O	2.43	0.51
59:CD:1075:ARG:HH21	59:CD:1102:PRO:HA	1.75	0.51
25:BA:2287:A:C8	25:BA:2289:G:C8	2.99	0.51
58:CC:632:ASP:N	58:CC:632:ASP:OD1	2.39	0.51
1:AA:1029:U:N3	1:AA:1033:G:C2	2.79	0.51
12:AL:81:LEU:HB3	12:AL:98:VAL:CG1	2.41	0.51
25:BA:1593:A:H2'	25:BA:1594:U:C6	2.45	0.51
45:BW:21:ARG:NH2	45:BW:87:GLN:O	2.37	0.51
58:CC:274:ILE:HA	58:CC:277:LEU:HD12	1.93	0.51
59:CD:366:CYS:O	59:CD:439:PRO:HA	2.11	0.51
1:AA:958:A:OP1	19:AS:55:ARG:NH1	2.43	0.50
24:AX:51:U:H3	24:AX:63:G:H1	1.59	0.50
25:BA:1528:A:N6	25:BA:1543:G:O2'	2.44	0.50
25:BA:2689:U:OP2	25:BA:2719:G:N2	2.39	0.50
27:BC:251:GLN:OE1	27:BC:255:LYS:HB2	2.11	0.50
30:BF:143:TYR:O	30:BF:146:VAL:HG12	2.11	0.50
58:CC:855:PRO:HG3	58:CC:913:VAL:HG23	1.93	0.50
1:AA:690:G:O6	11:AK:53:ARG:NH1	2.43	0.50
3:AC:78:GLY:C	58:CC:943:LYS:HD2	2.32	0.50
14:AN:46:LEU:O	14:AN:50:THR:HG23	2.10	0.50
25:BA:357:C:H2'	25:BA:358:U:C6	2.46	0.50
25:BA:568:U:H1'	25:BA:2030:6MZ:H9C1	1.94	0.50
25:BA:686:U:O4	52:B4:12:ARG:HB2	2.12	0.50
25:BA:910:A:C6	36:BN:13:HIS:CE1	2.99	0.50
30:BF:43:ALA:HA	30:BF:46:ASP:O	2.11	0.50
49:B1:12:SER:HB3	49:B1:32:ILE:HD11	1.93	0.50
59:CD:326:SER:O	59:CD:329:ASP:N	2.43	0.50
1:AA:4:U:O2'	1:AA:5:U:P	2.69	0.50
8:AH:30:SER:O	8:AH:34:VAL:HG13	2.10	0.50
19:AS:32:ARG:HH11	19:AS:34:TRP:HH2	1.59	0.50
25:BA:400:G:N7	47:BY:57:ARG:NH1	2.56	0.50
25:BA:1141:U:H4'	25:BA:1142:A:O4'	2.11	0.50
26:BB:5:U:OP1	26:BB:61:G:O2'	2.26	0.50
26:BB:49:C:OP1	38:BP:101:GLY:HA3	2.10	0.50
29:BE:108:ILE:O	29:BE:112:LEU:HD13	2.11	0.50
41:BS:77:PHE:HD1	41:BS:84:ARG:HB3	1.76	0.50
55:CN:27:DA:C6	55:CN:28:DA:C6	3.00	0.50
57:CA:68:TYR:CD1	57:CA:68:TYR:N	2.79	0.50
1:AA:71:A:H2'	1:AA:72:A:C8	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1006:G:N2	1:AA:1023:U:O2	2.44	0.50
1:AA:1225:A:H2'	1:AA:1226:C:C5	2.47	0.50
20:AT:8:LYS:O	20:AT:12:ILE:HG13	2.11	0.50
25:BA:543:A:C6	25:BA:551:G:C6	2.99	0.50
25:BA:585:G:N7	40:BR:6:ARG:NH1	2.59	0.50
25:BA:1591:A:H2'	25:BA:1592:C:C6	2.46	0.50
25:BA:1871:A:O2'	25:BA:1872:A:C8	2.65	0.50
25:BA:2136:G:C6	25:BA:2156:G:H1'	2.46	0.50
25:BA:2291:U:H2'	25:BA:2292:U:H6	1.75	0.50
27:BC:4:VAL:HG13	27:BC:18:LYS:HB2	1.94	0.50
42:BT:25:ARG:HG3	42:BT:74:ILE:HG22	1.93	0.50
59:CD:137:ARG:HG3	59:CD:142:GLU:HB2	1.94	0.50
1:AA:604:G:H2'	1:AA:605:U:O4'	2.12	0.50
3:AC:71:ALA:HA	3:AC:106:VAL:HB	1.93	0.50
3:AC:79:LYS:H	3:AC:79:LYS:HD2	1.75	0.50
7:AG:22:LEU:HD21	7:AG:66:LEU:HD12	1.94	0.50
18:AR:34:THR:HG22	18:AR:38:LYS:H	1.76	0.50
25:BA:677:A:O2'	25:BA:2071:A:H5'	2.12	0.50
45:BW:7:GLU:HB2	45:BW:41:GLU:HG2	1.94	0.50
56:CT:18:DC:O2	56:CT:19:DG:C8	2.64	0.50
59:CD:504:GLN:HG3	59:CD:505:ASP:N	2.25	0.50
1:AA:72:A:C6	1:AA:73:C:C5	2.99	0.50
1:AA:1120:C:H2'	1:AA:1121:U:H6	1.76	0.50
1:AA:1530:G:N7	21:AU:46:LYS:HE2	2.27	0.50
10:AJ:26:VAL:O	10:AJ:30:LYS:HG2	2.11	0.50
25:BA:1378:A:O2'	25:BA:1380:G:N7	2.45	0.50
25:BA:1529:G:H2'	25:BA:1530:G:C8	2.46	0.50
25:BA:2106:U:H2'	25:BA:2107:G:C8	2.42	0.50
25:BA:2187:U:O2'	25:BA:2188:U:O4'	2.29	0.50
33:BK:96:ARG:HE	33:BK:99:ARG:HG2	1.76	0.50
53:B5:62:LEU:HB3	53:B5:65:ALA:HB3	1.93	0.50
59:CD:961:SER:HB2	59:CD:981:GLU:HB2	1.94	0.50
1:AA:50:A:O2'	1:AA:360:G:N2	2.45	0.50
2:AB:14:VAL:HB	2:AB:213:TYR:OH	2.12	0.50
22:AV:40:A:O2'	22:AV:40:A:N3	2.33	0.50
23:AW:17:C:C2	23:AW:17(A):U:H5	2.29	0.50
25:BA:1590:A:H2'	25:BA:1591:A:H8	1.73	0.50
50:B2:31:ASP:O	50:B2:35:GLY:CA	2.60	0.50
1:AA:88:U:H3'	1:AA:89:G:C8	2.47	0.50
26:BB:16:G:N2	26:BB:69:G:H1'	2.27	0.50
27:BC:205:LEU:HB3	27:BC:210:ALA:HB3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:949:A:N7	13:AM:105:ASN:ND2	2.60	0.50
6:AF:44:ARG:O	6:AF:45:ARG:NH2	2.45	0.50
14:AN:80:SER:O	14:AN:84:VAL:HG13	2.11	0.50
25:BA:686:U:H6	25:BA:788:A:N1	2.09	0.50
25:BA:868:U:O2	36:BN:8:LYS:NZ	2.42	0.50
30:BF:42:GLU:HB3	30:BF:49:LEU:HD23	1.94	0.50
33:BK:36:LEU:O	33:BK:51:GLY:HA3	2.12	0.50
35:BM:57:LEU:HD22	53:B5:54:ASP:HB3	1.93	0.50
59:CD:530:PRO:O	59:CD:533:ALA:HB3	2.12	0.50
1:AA:296:U:O2'	1:AA:556:C:O2	2.30	0.49
22:AV:48:C:H2'	22:AV:49:G:C1'	2.41	0.49
25:BA:1042:G:HO2'	25:BA:1043:C:H6	1.59	0.49
25:BA:1068:G:C2	25:BA:1096:A:H5'	2.47	0.49
55:CN:28:DA:H2''	55:CN:29:DG:C8	2.46	0.49
57:CA:102:LEU:HD23	57:CA:103:ASN:N	2.27	0.49
58:CC:696:ASP:CG	58:CC:697:LYS:N	2.67	0.49
7:AG:15:ASP:OD1	7:AG:20:SER:N	2.31	0.49
16:AP:6:LEU:CD2	16:AP:19:VAL:HG22	2.42	0.49
22:AV:47:G:C4	22:AV:48:C:C5	3.00	0.49
25:BA:396:G:OP2	47:BY:10:LYS:NZ	2.45	0.49
25:BA:647:G:N2	25:BA:2350:C:O2'	2.43	0.49
25:BA:768:G:N2	25:BA:1379:U:O2'	2.46	0.49
42:BT:17:VAL:HG12	42:BT:76:VAL:HG21	1.93	0.49
9:AI:106:ARG:NH1	9:AI:107:ASP:O	2.39	0.49
25:BA:64:A:H2'	25:BA:65:U:H6	1.76	0.49
25:BA:851:C:H2'	25:BA:852:U:C6	2.47	0.49
35:BM:81:ASP:OD1	35:BM:84:LYS:HE2	2.11	0.49
38:BP:36:TYR:HA	38:BP:52:SER:HB3	1.94	0.49
56:CT:9:DC:H2'	56:CT:10:DT:H71	1.93	0.49
56:CT:17:DG:C6	56:CT:18:DC:C5	3.00	0.49
1:AA:339:C:P	34:BL:13:ASN:HD22	2.35	0.49
1:AA:371:A:H2'	1:AA:372:C:O4'	2.13	0.49
1:AA:978:A:C5	1:AA:1319:A:C2	3.00	0.49
9:AI:55:VAL:O	9:AI:57:MET:N	2.45	0.49
10:AJ:28:THR:O	10:AJ:32:THR:HG22	2.12	0.49
25:BA:1069:A:N1	25:BA:1096:A:H5''	2.27	0.49
50:B2:43:ILE:HG22	50:B2:49:TYR:HB2	1.94	0.49
1:AA:451:A:H1'	1:AA:452:A:C2	2.47	0.49
1:AA:1176:A:H2'	1:AA:1177:G:C8	2.48	0.49
1:AA:1183:U:H3'	1:AA:1184:G:C5'	2.42	0.49
1:AA:1246:A:C6	1:AA:1292:G:C6	3.00	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:28:LYS:HA	2:AB:31:ILE:HD12	1.94	0.49
24:AX:18:G:O2'	24:AX:57:G:N2	2.28	0.49
25:BA:1178:C:H2'	25:BA:1179:G:H8	1.71	0.49
25:BA:1199:U:H1'	40:BR:4:VAL:HG22	1.93	0.49
30:BF:31:VAL:HA	30:BF:158:THR:HG22	1.93	0.49
34:BL:70:ARG:HH12	34:BL:74:GLY:HA2	1.78	0.49
38:BP:40:ILE:HG12	38:BP:47:VAL:HG22	1.94	0.49
57:CB:34:GLY:N	57:CB:199:ASP:OD2	2.46	0.49
59:CD:813:ASP:OD1	59:CD:883:ARG:NH2	2.35	0.49
17:AQ:25:ILE:O	17:AQ:25:ILE:HG22	2.13	0.49
22:AV:47:G:C2	22:AV:48:C:C4	3.00	0.49
43:BU:6:ARG:HH22	43:BU:37:ASP:CG	2.20	0.49
51:B3:11:LEU:HD23	51:B3:51:GLU:HB2	1.95	0.49
57:CB:28:LEU:HD22	57:CB:28:LEU:N	2.27	0.49
58:CC:516:ASP:O	58:CC:518:ASN:N	2.41	0.49
1:AA:1022:A:C6	1:AA:1023:U:C4	3.01	0.49
1:AA:1244:G:C6	1:AA:1294:G:C6	3.01	0.49
3:AC:32:ASN:HB3	3:AC:59:ARG:NH2	2.28	0.49
3:AC:64:ILE:HG13	3:AC:99:ALA:HA	1.94	0.49
4:AD:193:ALA:C	59:CD:74:LYS:HE2	2.38	0.49
8:AH:18:GLN:HG3	8:AH:72:VAL:CG1	2.42	0.49
24:AX:20:H2U:O2	24:AX:20:H2U:H2'	2.12	0.49
30:BF:47:LYS:HA	30:BF:47:LYS:HE3	1.95	0.49
30:BF:57:LEU:HD12	30:BF:87:CYS:SG	2.52	0.49
39:BQ:33:VAL:O	39:BQ:33:VAL:HG12	2.13	0.49
40:BR:13:ARG:HH21	40:BR:13:ARG:HB3	1.78	0.49
58:CC:261:VAL:HG21	58:CC:264:GLU:HG2	1.94	0.49
59:CD:67:ASP:N	59:CD:67:ASP:OD1	2.43	0.49
1:AA:76:G:H1	1:AA:93:U:H3	1.60	0.49
1:AA:201:G:H2'	1:AA:202:G:H8	1.76	0.49
1:AA:1360:A:OP2	14:AN:75:ARG:NH2	2.46	0.49
1:AA:1435:G:H2'	1:AA:1436:U:C6	2.47	0.49
4:AD:121:LYS:HB3	4:AD:129:VAL:HG21	1.95	0.49
13:AM:65:VAL:HG22	13:AM:66:GLU:H	1.77	0.49
17:AQ:77:ARG:HD2	17:AQ:77:ARG:N	2.28	0.49
25:BA:58:G:O2'	25:BA:73:A:N1	2.41	0.49
25:BA:1263:U:O2'	50:B2:8:PRO:HD2	2.12	0.49
25:BA:2162:G:H3'	25:BA:2164:C:H5	1.78	0.49
25:BA:2743:U:H2'	25:BA:2744:G:O4'	2.13	0.49
32:BH:6:LEU:HD13	32:BH:37:VAL:HB	1.95	0.49
58:CC:617:ALA:HB2	58:CC:650:VAL:HG21	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:CD:425:ARG:HE	59:CD:464:ASP:CG	2.21	0.49
1:AA:269:C:H2'	1:AA:270:A:C8	2.48	0.49
1:AA:1277:C:HO2'	1:AA:1279:G:H8	1.60	0.49
3:AC:109:PRO:CG	58:CC:859:GLU:OE2	2.59	0.49
4:AD:19:LEU:HD22	4:AD:64:ILE:HG13	1.95	0.49
4:AD:54:GLN:HG2	4:AD:199:LEU:HD22	1.95	0.49
7:AG:69:VAL:HG13	7:AG:100:ALA:HB1	1.95	0.49
10:AJ:56:HIS:CE1	10:AJ:57:VAL:HG13	2.48	0.49
23:AW:16:C:C2'	23:AW:17:C:H5'	2.42	0.49
25:BA:652:U:O2	25:BA:652:U:H3'	2.13	0.49
25:BA:992:C:OP1	40:BR:47:TYR:OH	2.25	0.49
25:BA:1056:G:H4'	25:BA:1086:A:C8	2.47	0.49
25:BA:2125:G:OP2	25:BA:2125:G:H8	1.96	0.49
25:BA:2286:G:H22	51:B3:25:LYS:HA	1.77	0.49
27:BC:142:HIS:HD2	27:BC:193:GLY:O	1.95	0.49
55:CN:23:DT:H1'	55:CN:24:DC:C4	2.47	0.49
58:CC:1239:VAL:HG13	58:CC:1240:ASP:N	2.27	0.49
1:AA:35:G:H2'	1:AA:36:C:C6	2.48	0.49
1:AA:927:G:C2'	1:AA:928:G:H5'	2.42	0.49
1:AA:1140:C:HO2'	1:AA:1141:C:C5'	2.26	0.49
3:AC:62:LYS:HE3	3:AC:62:LYS:H	1.77	0.49
13:AM:41:GLU:OE1	13:AM:41:GLU:N	2.34	0.49
24:AX:65:G:H2'	24:AX:66:U:C6	2.48	0.49
25:BA:1068:G:N2	25:BA:1096:A:H5'	2.28	0.49
25:BA:2315:G:O2'	25:BA:2316:G:O4'	2.31	0.49
25:BA:2646:C:OP2	25:BA:2732:G:O2'	2.24	0.49
25:BA:2805:C:H2'	25:BA:2806:C:O4'	2.13	0.49
28:BD:9:VAL:O	28:BD:197:THR:HG23	2.12	0.49
28:BD:129:THR:HG23	28:BD:130:GLN:O	2.13	0.49
33:BK:1:MET:HE1	41:BS:13:ARG:NH2	2.28	0.49
55:CN:32:DA:H5'	55:CN:32:DA:H8	1.76	0.49
59:CD:767:LEU:HD12	59:CD:767:LEU:N	2.28	0.49
1:AA:1431:A:H2	1:AA:1469:C:H41	1.58	0.48
8:AH:11:LEU:HD22	8:AH:75:ILE:HD11	1.95	0.48
9:AI:63:LEU:HD12	9:AI:65:ILE:HD11	1.94	0.48
15:AO:26:GLU:OE2	15:AO:77:ARG:NE	2.35	0.48
25:BA:2346:A:H4'	25:BA:2347:C:OP2	2.13	0.48
29:BE:144:GLU:HG2	29:BE:145:ASP:H	1.78	0.48
30:BF:36:LEU:HD22	30:BF:152:LEU:HD12	1.95	0.48
58:CC:1119:MET:HA	58:CC:1119:MET:HE3	1.95	0.48
1:AA:1383:C:O2'	1:AA:1384:C:H5'	2.11	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:7:PRO:HA	3:AC:10:ILE:HG22	1.94	0.48
25:BA:137:U:HO2'	25:BA:138:U:P	2.34	0.48
25:BA:1063:G:O2'	25:BA:1064:C:H5'	2.13	0.48
25:BA:1408:G:H2'	25:BA:1409:U:C6	2.48	0.48
27:BC:141:VAL:HG12	27:BC:192:LEU:HD13	1.95	0.48
28:BD:149:ASN:OD1	28:BD:150:MEQ:N	2.45	0.48
29:BE:16:GLU:H	29:BE:16:GLU:CD	2.22	0.48
30:BF:55:ALA:O	30:BF:59:ALA:CA	2.60	0.48
50:B2:40:ARG:HG3	50:B2:41:HIS:ND1	2.28	0.48
56:CT:9:DC:H2'	56:CT:10:DT:C5	2.48	0.48
56:CT:20:DC:H2'	56:CT:21:DG:C8	2.47	0.48
59:CD:805:GLN:OE1	59:CD:1348:LYS:HB2	2.13	0.48
59:CD:907:HIS:ND1	59:CD:908:ILE:O	2.36	0.48
1:AA:1314:C:H2'	1:AA:1315:U:H6	1.78	0.48
7:AG:72:THR:HA	7:AG:96:ARG:HH11	1.78	0.48
9:AI:19:VAL:HG11	9:AI:82:GLY:C	2.38	0.48
20:AT:71:LYS:HG3	20:AT:74:ARG:HH21	1.79	0.48
24:AX:10:G:H2'	24:AX:11:C:C6	2.47	0.48
25:BA:63:A:H2	43:BU:70:HIS:CD2	2.32	0.48
25:BA:495:G:N3	42:BT:61:ASN:ND2	2.58	0.48
25:BA:1063:G:O2'	25:BA:1064:C:O4'	2.31	0.48
28:BD:32:ASN:HD22	28:BD:32:ASN:N	2.10	0.48
31:BG:105:LEU:HD11	31:BG:148:LEU:HD22	1.94	0.48
35:BM:79:LEU:HB3	35:BM:116:VAL:HB	1.94	0.48
42:BT:41:LYS:HE3	50:B2:22:LEU:HD11	1.95	0.48
58:CC:680:LEU:HD23	58:CC:680:LEU:C	2.38	0.48
1:AA:1251:A:H2'	1:AA:1252:A:C8	2.48	0.48
3:AC:78:GLY:O	58:CC:943:LYS:CD	2.41	0.48
18:AR:34:THR:HG23	18:AR:36:SER:H	1.78	0.48
25:BA:1063:G:HO2'	25:BA:1064:C:H6	1.60	0.48
25:BA:1386:C:H2'	25:BA:1387:A:C8	2.48	0.48
25:BA:2185:U:C4	25:BA:2186:G:N7	2.81	0.48
35:BM:132:ARG:HG3	35:BM:142:ILE:HD12	1.94	0.48
39:BQ:8:LEU:O	39:BQ:11:GLU:HG2	2.14	0.48
57:CB:11:PRO:O	57:CB:12:ARG:HD2	2.12	0.48
57:CB:61:ILE:HD12	57:CB:142:MET:HB3	1.96	0.48
12:AL:81:LEU:HB3	12:AL:98:VAL:HG12	1.94	0.48
13:AM:71:ARG:HD3	30:BF:113:ASP:OD2	2.14	0.48
25:BA:545:A:C2	25:BA:549:C:N3	2.82	0.48
25:BA:940:G:H5''	25:BA:941:A:OP2	2.13	0.48
25:BA:2557:G:H2'	25:BA:2558:C:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BD:34:VAL:O	28:BD:93:GLY:CA	2.61	0.48
28:BD:186:LEU:HD21	39:BQ:4:ILE:HG12	1.94	0.48
47:BY:74:ARG:HD2	47:BY:76:GLU:HG2	1.94	0.48
55:CN:28:DA:C6	55:CN:29:DG:C6	3.01	0.48
56:CT:19:DG:C4	56:CT:20:DC:C6	3.01	0.48
56:CT:22:DC:C2	56:CT:23:DC:C5	3.01	0.48
58:CC:493:ILE:C	58:CC:493:ILE:HD12	2.39	0.48
58:CC:576:SER:OG	58:CC:577:VAL:N	2.47	0.48
1:AA:160:A:H2'	1:AA:161:A:O4'	2.13	0.48
4:AD:194:ASP:CA	59:CD:74:LYS:NZ	2.76	0.48
10:AJ:31:ARG:C	10:AJ:33:GLY:H	2.22	0.48
25:BA:742:A:H2'	25:BA:743:A:C8	2.49	0.48
25:BA:2099:U:O4	25:BA:2190:G:O6	2.31	0.48
25:BA:2314:A:H2'	25:BA:2315:G:H8	1.79	0.48
28:BD:37:VAL:HG22	28:BD:48:ILE:HG22	1.96	0.48
32:BH:133:GLN:HG3	32:BH:139:PHE:HE1	1.79	0.48
39:BQ:99:TYR:O	39:BQ:103:ARG:HG2	2.14	0.48
56:CT:19:DG:C5	56:CT:20:DC:C4	3.02	0.48
1:AA:126:G:OP1	1:AA:605:U:O2'	2.20	0.48
1:AA:769:G:H4'	1:AA:1513:A:H4'	1.95	0.48
1:AA:1314:C:H2'	1:AA:1315:U:C6	2.48	0.48
9:AI:26:GLY:N	9:AI:59:GLU:O	2.47	0.48
18:AR:41:PRO:HG2	18:AR:44:ILE:HB	1.95	0.48
25:BA:1394:U:H4'	25:BA:1603:A:H4'	1.95	0.48
25:BA:2118:U:OP1	25:BA:2149:U:H5'	2.13	0.48
30:BF:40:VAL:O	30:BF:42:GLU:N	2.38	0.48
30:BF:55:ALA:O	30:BF:59:ALA:CB	2.61	0.48
42:BT:41:LYS:O	42:BT:44:ALA:HB3	2.13	0.48
55:CN:32:DA:H1'	55:CN:33:DT:O4'	2.14	0.48
58:CC:1058:ARG:HH21	58:CC:1240:ASP:CG	2.20	0.48
59:CD:1159:ILE:O	59:CD:1206:ARG:N	2.43	0.48
1:AA:652:U:O4	1:AA:752:G:O2'	2.23	0.48
1:AA:923:A:O2'	1:AA:1399:C:OP2	2.29	0.48
1:AA:1228:C:H5'	13:AM:114:LYS:O	2.13	0.48
2:AB:47:VAL:HG13	2:AB:48:PRO:CD	2.42	0.48
5:AE:106:ILE:HB	5:AE:124:LEU:HD23	1.95	0.48
8:AH:13:ARG:NH1	8:AH:26:THR:O	2.46	0.48
22:AV:45:G:H5''	58:CC:540:ARG:HH22	1.79	0.48
25:BA:191:A:H2'	25:BA:192:C:C6	2.49	0.48
25:BA:1063:G:C4	25:BA:1064:C:C6	3.01	0.48
25:BA:2111:U:H5'	25:BA:2112:G:OP2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2233:U:H2'	25:BA:2234:G:C8	2.49	0.48
1:AA:768:A:N3	1:AA:1512:U:O2'	2.47	0.48
3:AC:109:PRO:HD3	58:CC:859:GLU:CD	2.36	0.48
25:BA:875:G:C6	25:BA:876:C:C4	3.01	0.48
25:BA:1932:A:H2'	25:BA:1933:G:O4'	2.14	0.48
25:BA:2812:G:H2'	25:BA:2813:A:O4'	2.13	0.48
26:BB:48:U:H2'	26:BB:49:C:C6	2.49	0.48
32:BH:50:ARG:HH12	32:BH:51:ARG:HE	1.62	0.48
58:CC:529:ARG:NH2	58:CC:562:GLU:OE2	2.46	0.48
58:CC:1238:LEU:N	58:CC:1238:LEU:HD23	2.29	0.48
1:AA:996:A:C4	1:AA:997:U:C5	3.02	0.48
1:AA:1320:C:N3	19:AS:36:ARG:NH1	2.62	0.48
4:AD:7:PRO:HB2	4:AD:10:LYS:CB	2.43	0.48
4:AD:188:ARG:NH2	4:AD:195:ILE:O	2.47	0.48
7:AG:69:VAL:HG11	7:AG:104:ILE:HD11	1.95	0.48
25:BA:910:A:N3	25:BA:2264:C:O2'	2.35	0.48
33:BK:9:GLU:OE1	33:BK:9:GLU:N	2.45	0.48
58:CC:1085:MET:HE2	58:CC:1085:MET:HA	1.95	0.48
1:AA:17:U:H2'	1:AA:18:C:C6	2.49	0.47
1:AA:996:A:C6	1:AA:997:U:C4	3.02	0.47
1:AA:1367:C:OP1	10:AJ:62:ARG:NH2	2.47	0.47
2:AB:20:THR:HG22	2:AB:37:LYS:HG2	1.95	0.47
2:AB:196:VAL:HG21	2:AB:199:VAL:HG13	1.96	0.47
10:AJ:53:ILE:HD11	10:AJ:63:ASP:N	2.29	0.47
25:BA:1581:G:C6	25:BA:1582:C:C4	3.02	0.47
25:BA:1595:C:H2'	25:BA:1596:A:H8	1.77	0.47
25:BA:2244:U:H2'	25:BA:2245:U:C6	2.49	0.47
30:BF:8:TYR:HA	30:BF:12:VAL:HB	1.95	0.47
37:BO:20:MET:HG3	37:BO:21:PHE:N	2.28	0.47
41:BS:28:ALA:HB3	41:BS:31:GLU:OE1	2.14	0.47
55:CN:27:DA:C2	55:CN:28:DA:C4	3.02	0.47
58:CC:596:ASP:OD1	58:CC:597:GLY:N	2.38	0.47
59:CD:175:GLU:CD	59:CD:175:GLU:N	2.72	0.47
33:BK:3:THR:HG21	40:BR:61:TRP:HE1	1.78	0.47
58:CC:234:ASP:HB3	58:CC:238:GLN:NE2	2.29	0.47
59:CD:301:GLU:OE1	59:CD:312:ARG:NE	2.46	0.47
59:CD:746:LEU:HD23	59:CD:758:PRO:HB3	1.96	0.47
1:AA:837:U:C2	1:AA:849:G:O6	2.67	0.47
1:AA:1261:A:N6	1:AA:1274:A:HO2'	2.10	0.47
27:BC:119:GLY:O	27:BC:130:LEU:HB3	2.14	0.47
31:BG:38:ASN:HB3	31:BG:41:VAL:HG13	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:BQ:34:GLU:CD	39:BQ:39:ARG:HD3	2.40	0.47
58:CC:138:ILE:HA	58:CC:138:ILE:HD13	1.53	0.47
58:CC:267:ARG:HH22	58:CC:273:HIS:CE1	2.31	0.47
59:CD:1292:LEU:HD11	59:CD:1297:LYS:HB2	1.95	0.47
7:AG:72:THR:HA	7:AG:96:ARG:NH1	2.28	0.47
25:BA:463:G:N2	25:BA:466:A:OP2	2.40	0.47
25:BA:1040:A:N6	25:BA:1115:G:C6	2.80	0.47
25:BA:1503:A:OP1	25:BA:1503:A:H4'	2.15	0.47
25:BA:2448:A:H3'	25:BA:2449:H2U:H61	1.96	0.47
30:BF:60:ILE:HG12	30:BF:141:ILE:HG12	1.95	0.47
51:B3:19:HIS:ND1	51:B3:49:TYR:OH	2.46	0.47
57:CA:79:LEU:HD23	57:CA:79:LEU:O	2.15	0.47
58:CC:530:ILE:HD13	58:CC:530:ILE:HA	1.65	0.47
58:CC:699:LEU:HA	58:CC:699:LEU:HD23	1.61	0.47
59:CD:849:LEU:HA	59:CD:856:ILE:HA	1.96	0.47
4:AD:166:GLU:H	4:AD:166:GLU:CD	2.16	0.47
5:AE:83:HIS:NE2	5:AE:147:MET:HG3	2.29	0.47
10:AJ:42:LEU:HB2	10:AJ:71:LEU:CB	2.43	0.47
25:BA:1580:A:H5''	25:BA:1580:A:H8	1.78	0.47
25:BA:2273:A:H2'	25:BA:2274:A:C8	2.49	0.47
40:BR:88:VAL:HG22	41:BS:51:VAL:HG12	1.96	0.47
56:CT:21:DG:H2'	56:CT:22:DC:C6	2.50	0.47
58:CC:1292:THR:OG1	58:CC:1293:VAL:N	2.47	0.47
59:CD:26:SER:HB3	59:CD:236:TRP:CZ2	2.49	0.47
1:AA:88:U:H3'	1:AA:89:G:H8	1.79	0.47
1:AA:657:U:O2	15:AO:22:THR:OG1	2.32	0.47
1:AA:685:G:N2	1:AA:704:A:OP2	2.40	0.47
20:AT:39:ILE:HD11	20:AT:83:ILE:HD12	1.96	0.47
21:AU:17:ARG:O	21:AU:21:ARG:HG3	2.15	0.47
24:AX:23:A:H2'	24:AX:24:G:C8	2.50	0.47
24:AX:57:G:OP2	36:BN:59:ARG:NH1	2.48	0.47
25:BA:1613:G:H1	25:BA:1617:C:HO2'	1.62	0.47
25:BA:2164:C:O2	25:BA:2164:C:H2'	2.14	0.47
25:BA:2521:C:O2'	25:BA:2564:A:N3	2.41	0.47
29:BE:109:LEU:HA	29:BE:109:LEU:HD23	1.71	0.47
59:CD:393:THR:HG23	59:CD:395:LYS:H	1.80	0.47
1:AA:159:G:H1'	1:AA:162:A:N6	2.29	0.47
1:AA:1040:U:H2'	1:AA:1041:G:C8	2.50	0.47
1:AA:1255:G:O2'	1:AA:1258:G:N3	2.35	0.47
1:AA:1316:G:N1	1:AA:1319:A:OP2	2.47	0.47
3:AC:124:LEU:HA	3:AC:124:LEU:HD23	1.74	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AF:45:ARG:HD3	6:AF:45:ARG:HA	1.71	0.47
19:AS:48:THR:HG22	19:AS:61:PHE:HB2	1.96	0.47
25:BA:62:U:O2'	25:BA:63:A:N7	2.26	0.47
25:BA:839:U:H2'	25:BA:840:C:C6	2.50	0.47
25:BA:1916:A:H2'	25:BA:1917:PSU:H6	1.75	0.47
25:BA:2104:C:H5	25:BA:2186:G:H21	1.61	0.47
25:BA:2635:A:O2'	28:BD:81:GLU:HG3	2.15	0.47
25:BA:2803:G:H2'	25:BA:2804:U:C6	2.49	0.47
25:BA:2830:C:H3'	28:BD:59:ARG:NH2	2.30	0.47
26:BB:42:C:C5	30:BF:66:LEU:HD22	2.49	0.47
35:BM:33:ARG:NH2	35:BM:40:SER:O	2.48	0.47
40:BR:78:LYS:HE2	40:BR:117:LEU:HD13	1.97	0.47
45:BW:7:GLU:O	45:BW:40:ILE:HA	2.15	0.47
49:B1:24:LEU:HD11	49:B1:54:MET:HE2	1.96	0.47
58:CC:1333:LEU:O	58:CC:1335:ILE:N	2.48	0.47
59:CD:158:GLN:NE2	59:CD:158:GLN:O	2.46	0.47
59:CD:1143:ASP:C	59:CD:1143:ASP:OD1	2.57	0.47
1:AA:104:G:OP1	20:AT:16:LYS:NZ	2.31	0.47
1:AA:195:A:C2'	1:AA:196:A:H5'	2.44	0.47
1:AA:966:2MG:O2'	9:AI:129:LYS:O	2.33	0.47
1:AA:1408:A:H2'	1:AA:1409:C:H6	1.79	0.47
10:AJ:18:ILE:HD12	10:AJ:18:ILE:HA	1.66	0.47
14:AN:27:LEU:O	14:AN:30:ILE:HG23	2.15	0.47
25:BA:1796:U:O2'	27:BC:254:GLY:N	2.34	0.47
25:BA:2029:G:N1	25:BA:2033:A:OP2	2.35	0.47
58:CC:129:LEU:HD23	58:CC:129:LEU:HA	1.68	0.47
1:AA:860:A:H2'	1:AA:861:G:O4'	2.14	0.47
1:AA:1167:A:C5	1:AA:1169:A:C6	3.03	0.47
1:AA:1527:U:H5	21:AU:42:THR:HG21	1.80	0.47
13:AM:75:MET:SD	13:AM:78:LYS:HE2	2.55	0.47
25:BA:877:A:C6	25:BA:899:A:C6	3.03	0.47
26:BB:2:G:C6	26:BB:119:A:C6	3.02	0.47
26:BB:118:C:C2	26:BB:119:A:C8	3.02	0.47
30:BF:54:ALA:O	30:BF:55:ALA:C	2.57	0.47
31:BG:52:PHE:CZ	31:BG:72:LEU:HD22	2.50	0.47
42:BT:36:LEU:HD13	42:BT:48:LYS:HA	1.96	0.47
10:AJ:52:LEU:HB2	14:AN:81:ARG:HD2	1.95	0.47
25:BA:1062:G:C8	25:BA:1088:A:C8	3.03	0.47
25:BA:1177:G:O2'	25:BA:1178:C:O4'	2.32	0.47
25:BA:2006:C:O2'	25:BA:2823:A:N3	2.47	0.47
25:BA:2901:C:N3	25:BA:2902:C:N4	2.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:BF:91:LEU:C	30:BF:96:MET:HB2	2.40	0.47
32:BH:97:ARG:HB3	32:BH:112:LYS:HD3	1.95	0.47
34:BL:13:ASN:HB3	34:BL:100:PHE:HE1	1.80	0.47
39:BQ:89:ARG:HB2	39:BQ:113:ARG:NH1	2.30	0.47
58:CC:269:ILE:HD12	58:CC:269:ILE:N	2.29	0.47
59:CD:664:ILE:HG22	59:CD:678:ARG:HG2	1.97	0.47
59:CD:1249:ASN:OD1	59:CD:1250:ASP:N	2.48	0.47
1:AA:464:U:O2	1:AA:466:A:H3'	2.16	0.46
1:AA:1033:G:C2	1:AA:1034:G:C4	3.03	0.46
1:AA:1088:G:H1'	21:AU:71:TYR:HB3	1.97	0.46
1:AA:1424:U:H2'	1:AA:1425:U:O4'	2.15	0.46
8:AH:18:GLN:OE1	8:AH:18:GLN:HA	2.14	0.46
20:AT:55:GLN:O	20:AT:58:VAL:HG23	2.15	0.46
25:BA:721:A:H2'	25:BA:722:A:C8	2.50	0.46
25:BA:866:A:C8	25:BA:914:G:C6	3.04	0.46
25:BA:1056:G:C2'	25:BA:1103:A:H61	2.28	0.46
25:BA:1065:U:O2'	25:BA:1066:U:O5'	2.31	0.46
25:BA:2186:G:H2'	25:BA:2187:U:C6	2.50	0.46
25:BA:2469:A:H4'	36:BN:55:ARG:HD2	1.98	0.46
33:BK:30:THR:HG22	33:BK:31:GLU:N	2.31	0.46
1:AA:1486:G:H2'	1:AA:1487:G:O4'	2.16	0.46
3:AC:73:PRO:O	3:AC:76:VAL:N	2.48	0.46
10:AJ:24:GLU:OE1	10:AJ:92:LEU:HD12	2.15	0.46
15:AO:70:LEU:HD12	15:AO:70:LEU:HA	1.68	0.46
21:AU:60:LEU:O	21:AU:64:ASN:HB2	2.15	0.46
25:BA:929:U:H1'	49:B1:26:GLY:O	2.14	0.46
25:BA:989:G:OP2	49:B1:12:SER:HB2	2.15	0.46
25:BA:2149:U:H2'	25:BA:2150:C:C6	2.50	0.46
34:BL:64:ARG:NH1	34:BL:102:PRO:O	2.43	0.46
38:BP:27:VAL:HG21	38:BP:40:ILE:HD12	1.98	0.46
1:AA:212:G:C2	1:AA:213:G:C8	3.03	0.46
3:AC:20:SER:OG	3:AC:40:ARG:NH2	2.48	0.46
3:AC:77:ILE:HA	3:AC:84:VAL:CG2	2.44	0.46
8:AH:103:VAL:HG22	8:AH:126:ILE:HB	1.96	0.46
9:AI:32:GLN:OE1	9:AI:64:TYR:OH	2.32	0.46
11:AK:109:ASN:OD1	11:AK:110:ILE:N	2.48	0.46
25:BA:806:C:HO2'	25:BA:2445:2MG:HO2'	1.54	0.46
25:BA:1723:G:H3'	25:BA:1724:G:H8	1.81	0.46
25:BA:1852:U:O2	25:BA:1890:A:N6	2.48	0.46
27:BC:13:ARG:HH22	27:BC:18:LYS:HE3	1.80	0.46
45:BW:3:THR:O	45:BW:50:MET:HE1	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:CB:154:PRO:C	57:CB:156:SER:H	2.24	0.46
59:CD:255:LEU:HG	59:CD:256:ASP:H	1.80	0.46
59:CD:466:MET:HB2	59:CD:466:MET:HE3	1.70	0.46
9:AI:9:THR:HG23	9:AI:85:ARG:HH11	1.81	0.46
19:AS:50:ALA:HB1	19:AS:57:HIS:HB3	1.97	0.46
24:AX:25:C:C2	24:AX:26:A:C8	3.03	0.46
25:BA:274:C:H3'	25:BA:275:C:H6	1.80	0.46
25:BA:2124:G:H2'	25:BA:2125:G:O4'	2.14	0.46
45:BW:80:HIS:ND1	45:BW:83:LYS:HB2	2.31	0.46
54:B6:23:ILE:HB	54:B6:37:GLN:CB	2.40	0.46
57:CA:179:PRO:HA	57:CA:208:ASN:ND2	2.30	0.46
59:CD:416:ILE:O	59:CD:416:ILE:HG23	2.15	0.46
1:AA:148:G:O2'	1:AA:149:A:C5'	2.64	0.46
1:AA:956:U:H2'	1:AA:957:U:O4'	2.16	0.46
7:AG:4:ARG:HH11	7:AG:5:ARG:NH2	2.13	0.46
9:AI:12:ARG:O	9:AI:15:SER:N	2.48	0.46
28:BD:188:LEU:HD21	39:BQ:8:LEU:HD21	1.98	0.46
30:BF:58:ALA:HA	30:BF:63:GLN:O	2.16	0.46
59:CD:265:LEU:O	59:CD:268:LEU:N	2.45	0.46
3:AC:124:LEU:HD13	3:AC:196:ILE:CD1	2.46	0.46
20:AT:35:VAL:HG21	20:AT:54:MET:HG2	1.97	0.46
25:BA:550:U:C2	25:BA:551:G:N7	2.83	0.46
25:BA:1009:A:N3	25:BA:1153:C:O2'	2.44	0.46
25:BA:1064:C:HO2'	25:BA:1065:U:C1'	2.29	0.46
25:BA:1413:A:H2'	25:BA:1414:C:O4'	2.14	0.46
25:BA:1693:U:O2'	27:BC:14:ARG:NH2	2.43	0.46
25:BA:2315:G:O2'	25:BA:2316:G:H8	1.98	0.46
25:BA:2514:U:H2'	25:BA:2515:C:C6	2.51	0.46
25:BA:2747:G:O6	25:BA:2755:C:H5''	2.15	0.46
26:BB:27:C:OP1	38:BP:34:HIS:NE2	2.40	0.46
32:BH:72:ILE:HG22	32:BH:108:VAL:HG22	1.97	0.46
33:BK:60:ASP:CG	33:BK:61:LYS:HZ3	2.24	0.46
49:B1:23:THR:HG23	49:B1:47:MET:HG2	1.98	0.46
59:CD:62:PHE:O	59:CD:101:ARG:NH2	2.46	0.46
59:CD:247:PRO:HA	59:CD:250:ARG:CZ	2.45	0.46
1:AA:1320:C:C2	19:AS:72:GLY:HA3	2.50	0.46
3:AC:79:LYS:HE3	3:AC:79:LYS:HB3	1.56	0.46
6:AF:85:ILE:HG13	6:AF:86:ARG:H	1.81	0.46
10:AJ:56:HIS:CG	10:AJ:57:VAL:H	2.34	0.46
11:AK:34:ILE:HG12	11:AK:70:CYS:SG	2.56	0.46
12:AL:39:THR:HG22	12:AL:51:LYS:HD3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:AV:48:C:H2'	22:AV:49:G:O4'	2.16	0.46
24:AX:24:G:H2'	24:AX:25:C:C6	2.51	0.46
25:BA:1363:C:O2'	25:BA:1809:A:N3	2.45	0.46
25:BA:1847:A:H1'	25:BA:1848:A:N7	2.31	0.46
44:BV:88:GLU:C	44:BV:90:GLY:H	2.23	0.46
58:CC:705:GLU:OE1	58:CC:705:GLU:N	2.41	0.46
1:AA:158:G:C6	1:AA:159:G:C5	3.03	0.46
1:AA:1412:C:H2'	1:AA:1413:A:C8	2.51	0.46
5:AE:57:PRO:O	5:AE:61:GLN:NE2	2.48	0.46
6:AF:73:GLU:HG3	6:AF:74:LEU:N	2.31	0.46
7:AG:17:LYS:HE2	7:AG:17:LYS:HB3	1.61	0.46
7:AG:109:ARG:CG	7:AG:109:ARG:HH11	2.29	0.46
11:AK:33:THR:HG22	11:AK:44:TRP:CB	2.46	0.46
25:BA:280:U:O4	25:BA:361:G:N2	2.49	0.46
25:BA:1744:A:H3'	25:BA:1745:A:H8	1.81	0.46
25:BA:2314:A:H1'	30:BF:155:THR:HG21	1.97	0.46
31:BG:29:LYS:NZ	31:BG:80:THR:O	2.44	0.46
41:BS:1:MET:HA	41:BS:42:ALA:O	2.15	0.46
41:BS:34:GLU:HG2	41:BS:60:LYS:HG2	1.97	0.46
54:B6:2:LYS:HE2	54:B6:32:LYS:O	2.15	0.46
1:AA:203:G:N2	1:AA:215:C:C2	2.84	0.46
1:AA:1023:U:H2'	1:AA:1024:G:O4'	2.16	0.46
25:BA:102:U:O4	48:BZ:2:LYS:N	2.49	0.46
25:BA:2572:A:N6	28:BD:150:MEQ:HE1	2.30	0.46
25:BA:2884:U:C5	50:B2:40:ARG:HD2	2.51	0.46
29:BE:37:ALA:HA	29:BE:40:ARG:HG3	1.98	0.46
33:BK:117:ALA:HA	33:BK:120:ARG:NH2	2.31	0.46
39:BQ:40:LEU:HD12	39:BQ:40:LEU:HA	1.80	0.46
58:CC:696:ASP:OD1	58:CC:696:ASP:N	2.45	0.46
58:CC:1336:ASN:HD22	58:CC:1336:ASN:C	2.22	0.46
59:CD:424:ASN:ND2	59:CD:424:ASN:C	2.73	0.46
59:CD:513:MET:HG3	59:CD:544:LEU:HD21	1.98	0.46
1:AA:6:G:N2	5:AE:103:THR:OG1	2.49	0.46
1:AA:1088:G:H21	1:AA:1167:A:N6	2.14	0.46
1:AA:1408:A:H2'	1:AA:1409:C:C6	2.51	0.46
21:AU:55:ARG:HD3	21:AU:55:ARG:HA	1.74	0.46
25:BA:1073:A:H2'	25:BA:1074:G:O4'	2.16	0.46
25:BA:1078:U:H5''	25:BA:1079:C:OP1	2.16	0.46
25:BA:2314:A:O2'	25:BA:2315:G:H5'	2.16	0.46
28:BD:150:MEQ:HE21	28:BD:150:MEQ:HB3	1.45	0.46
29:BE:4:VAL:HA	29:BE:11:ALA:HA	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:BF:103:LEU:HA	30:BF:107:ALA:HB3	1.97	0.46
39:BQ:99:TYR:HD1	39:BQ:103:ARG:HD2	1.81	0.46
42:BT:17:VAL:HG11	42:BT:103:ILE:HG12	1.98	0.46
59:CD:891:ASP:OD1	59:CD:1286:LYS:NZ	2.49	0.46
59:CD:1309:ILE:HG13	59:CD:1310:THR:N	2.31	0.46
1:AA:1032:G:N2	1:AA:1033:G:H4'	2.31	0.45
3:AC:40:ARG:NH1	3:AC:55:ILE:O	2.48	0.45
25:BA:804:A:H2'	25:BA:806:C:C4	2.51	0.45
25:BA:833:A:H2'	25:BA:834:G:C8	2.52	0.45
27:BC:159:GLY:HA2	27:BC:195:VAL:O	2.16	0.45
33:BK:40:HIS:CE1	33:BK:41:LYS:HG2	2.51	0.45
35:BM:77:VAL:O	35:BM:111:ILE:HG12	2.16	0.45
1:AA:401:C:O2'	1:AA:621:A:N3	2.44	0.45
1:AA:473:U:C2	1:AA:474:G:C8	3.04	0.45
3:AC:107:ARG:HE	58:CC:863:SER:CA	2.29	0.45
5:AE:12:GLN:CD	59:CD:79:LYS:HD2	2.41	0.45
22:AV:47:G:C2	22:AV:48:C:C5	3.04	0.45
24:AX:21:A:N6	24:AX:48:C:O4'	2.48	0.45
25:BA:747:5MU:O2	25:BA:2014:A:H1'	2.17	0.45
27:BC:251:GLN:NE2	27:BC:252:THR:O	2.49	0.45
28:BD:14:ILE:HD13	39:BQ:12:GLN:HE22	1.82	0.45
28:BD:152:PRO:HG3	28:BD:156:PHE:CZ	2.52	0.45
32:BH:131:SER:OG	32:BH:141:LYS:NZ	2.50	0.45
57:CB:66:HIS:O	57:CB:66:HIS:ND1	2.44	0.45
13:AM:5:ALA:HB1	13:AM:65:VAL:HG21	1.98	0.45
25:BA:1385:A:O2'	25:BA:1396:U:O2	2.31	0.45
32:BH:75:LEU:HD12	32:BH:77:THR:O	2.16	0.45
37:BO:100:CYS:O	37:BO:110:MET:HB2	2.16	0.45
43:BU:14:PRO:HD3	48:BZ:30:MET:SD	2.56	0.45
45:BW:27:PRO:O	45:BW:88:HIS:HA	2.16	0.45
55:CN:10:DG:H2''	55:CN:11:DT:H72	1.97	0.45
58:CC:514:PHE:CE1	58:CC:760:ASN:HB3	2.51	0.45
58:CC:1291:LEU:HD21	59:CD:1351:VAL:HG13	1.97	0.45
58:CC:1340:GLU:CD	58:CC:1341:ASP:H	2.21	0.45
59:CD:1050:THR:C	59:CD:1057:SER:HB3	2.41	0.45
2:AB:122:GLN:HG3	2:AB:123:ASP:N	2.32	0.45
3:AC:31:ASP:OD1	14:AN:65:ARG:NH1	2.42	0.45
10:AJ:80:THR:O	10:AJ:84:VAL:HG12	2.17	0.45
11:AK:92:GLY:C	11:AK:94:GLU:N	2.75	0.45
18:AR:42:SER:OG	18:AR:47:THR:O	2.34	0.45
25:BA:67:U:C2	25:BA:68:G:C8	3.04	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:475:C:N3	25:BA:479:A:N7	2.64	0.45
25:BA:2532:G:O2'	25:BA:2657:A:N1	2.50	0.45
25:BA:2742:G:OP2	54:B6:24:ARG:NH1	2.43	0.45
25:BA:2745:C:C4	25:BA:2746:U:C4	3.04	0.45
31:BG:4:VAL:HG12	31:BG:69:ARG:HD3	1.97	0.45
35:BM:70:LYS:NZ	35:BM:70:LYS:HB2	2.31	0.45
43:BU:5:GLU:H	43:BU:5:GLU:HG3	1.43	0.45
57:CA:102:LEU:HD23	57:CA:102:LEU:C	2.41	0.45
58:CC:38:PHE:CZ	58:CC:49:LEU:HD21	2.51	0.45
58:CC:563:THR:OG1	58:CC:564:PRO:HD2	2.16	0.45
58:CC:866:ASP:C	58:CC:866:ASP:OD1	2.60	0.45
59:CD:363:LEU:HA	59:CD:363:LEU:HD12	1.73	0.45
59:CD:1075:ARG:NH2	59:CD:1102:PRO:HA	2.31	0.45
1:AA:739:C:OP1	6:AF:2:ARG:NH1	2.50	0.45
1:AA:1122:U:H2'	1:AA:1123:U:C6	2.52	0.45
6:AF:38:ARG:NH2	6:AF:63:ASN:OD1	2.50	0.45
13:AM:9:ILE:HG23	13:AM:18:ALA:HB1	1.98	0.45
25:BA:111:A:C6	25:BA:112:U:C4	3.04	0.45
25:BA:133:U:H2'	25:BA:134:G:O4'	2.17	0.45
25:BA:1306:C:N4	25:BA:1606:C:H2'	2.31	0.45
25:BA:2000:C:OP1	37:BO:5:LYS:NZ	2.47	0.45
25:BA:2178:C:H2'	25:BA:2179:C:H5	1.80	0.45
27:BC:176:LEU:O	27:BC:179:GLY:N	2.40	0.45
33:BK:141:ASP:O	33:BK:142:ILE:HD13	2.16	0.45
34:BL:76:VAL:HG12	39:BQ:73:VAL:HB	1.98	0.45
1:AA:911:U:H2'	1:AA:912:C:C6	2.52	0.45
1:AA:1130:A:O2'	9:AI:5:GLN:OE1	2.34	0.45
3:AC:70:THR:HG21	3:AC:76:VAL:HG21	1.99	0.45
6:AF:15:SER:HA	6:AF:18:VAL:HG23	1.99	0.45
9:AI:12:ARG:CD	9:AI:74:GLY:HA2	2.46	0.45
9:AI:41:ARG:NH1	9:AI:41:ARG:HB2	2.32	0.45
25:BA:1751:U:H2'	25:BA:1752:C:C6	2.52	0.45
26:BB:48:U:P	38:BP:30:ARG:HH22	2.39	0.45
30:BF:175:PHE:HB3	30:BF:177:PHE:CE2	2.51	0.45
32:BH:11:ASN:O	32:BH:11:ASN:ND2	2.47	0.45
33:BK:99:ARG:HD2	33:BK:99:ARG:HA	1.81	0.45
35:BM:63:LYS:HG2	53:B5:13:ARG:HD3	1.98	0.45
35:BM:89:VAL:HG11	35:BM:123:ARG:HH21	1.81	0.45
47:BY:33:LEU:HD13	47:BY:50:ARG:HG2	1.98	0.45
47:BY:39:TRP:HZ2	47:BY:44:LYS:HD3	1.81	0.45
56:CT:4:DT:H2''	56:CT:5:DG:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:CB:66:HIS:CG	57:CB:68:TYR:HB3	2.52	0.45
58:CC:28:LEU:HD23	58:CC:28:LEU:HA	1.54	0.45
59:CD:119:SER:OG	59:CD:120:LEU:N	2.50	0.45
59:CD:120:LEU:HB3	59:CD:121:PRO:CD	2.47	0.45
59:CD:478:LEU:HD23	59:CD:478:LEU:HA	1.63	0.45
59:CD:1332:LEU:HA	59:CD:1332:LEU:HD12	1.73	0.45
1:AA:211:G:C5	1:AA:212:G:H1'	2.52	0.45
1:AA:278:G:OP2	17:AQ:43:LYS:NZ	2.35	0.45
3:AC:59:ARG:HB3	3:AC:64:ILE:HG22	1.98	0.45
11:AK:84:VAL:HG11	11:AK:97:ILE:HG22	1.99	0.45
22:AV:39:A:OP2	58:CC:1250:SER:OG	2.22	0.45
25:BA:2131:U:O2	25:BA:2131:U:H3'	2.17	0.45
30:BF:136:ILE:HG12	30:BF:143:TYR:CD1	2.50	0.45
34:BL:40:LYS:HE3	34:BL:57:VAL:HG12	1.99	0.45
58:CC:1043:ALA:O	58:CC:1046:VAL:HG22	2.17	0.45
58:CC:1204:LEU:HD23	58:CC:1204:LEU:HA	1.69	0.45
59:CD:850:LYS:N	59:CD:855:ASP:O	2.33	0.45
59:CD:1325:PHE:CD1	59:CD:1325:PHE:C	2.94	0.45
1:AA:1037:C:H2'	1:AA:1038:C:C6	2.52	0.45
1:AA:1299:A:O2'	1:AA:1301:U:O4'	2.29	0.45
5:AE:90:THR:OG1	5:AE:135:ASN:OD1	2.25	0.45
7:AG:122:ASN:O	7:AG:125:SER:OG	2.31	0.45
18:AR:26:ILE:O	18:AR:30:LYS:N	2.37	0.45
24:AX:14:A:N1	24:AX:22:G:H1'	2.32	0.45
59:CD:213:LYS:O	59:CD:213:LYS:HD3	2.17	0.45
59:CD:952:VAL:HG13	59:CD:1014:GLY:H	1.81	0.45
1:AA:970:C:N4	9:AI:130:ARG:OXT	2.41	0.45
1:AA:1305:G:N2	1:AA:1331:G:O2'	2.44	0.45
3:AC:85:GLU:OE2	3:AC:88:ARG:NH2	2.38	0.45
9:AI:130:ARG:NH2	23:AW:33:U:OP2	2.48	0.45
12:AL:87:VAL:O	12:AL:87:VAL:HG12	2.17	0.45
25:BA:1869:G:C2	25:BA:1873:G:C6	3.04	0.45
27:BC:76:ALA:HB2	27:BC:96:TYR:CD2	2.52	0.45
36:BN:3:GLN:HE21	36:BN:92:TRP:HE1	1.65	0.45
42:BT:1:MET:H1	42:BT:110:ARG:HH11	1.64	0.45
54:B6:14:CYS:O	54:B6:15:LYS:HD3	2.17	0.45
55:CN:26:DG:C4	55:CN:27:DA:N7	2.85	0.45
57:CB:34:GLY:H	57:CB:199:ASP:CG	2.25	0.45
1:AA:36:C:H2'	1:AA:37:U:O4'	2.17	0.45
1:AA:590:U:H2'	1:AA:591:U:C6	2.52	0.45
1:AA:1029:U:O4	1:AA:1031:C:H1'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1118:U:H2'	1:AA:1119:C:H6	1.81	0.45
5:AE:13:GLU:CB	5:AE:39:VAL:HG12	2.46	0.45
13:AM:92:ARG:CB	25:BA:888:C:H5'	2.45	0.45
15:AO:7:ALA:O	15:AO:11:ILE:HD13	2.17	0.45
25:BA:39:G:H2'	25:BA:40:U:C6	2.52	0.45
25:BA:614:A:C8	25:BA:614:A:OP2	2.70	0.45
25:BA:626:A:H2'	35:BM:78:ARG:NH2	2.32	0.45
25:BA:2537:U:H2'	25:BA:2538:C:C6	2.51	0.45
48:BZ:10:SER:OG	48:BZ:11:VAL:N	2.50	0.45
53:B5:55:LEU:O	53:B5:58:VAL:HG12	2.17	0.45
58:CC:176:ILE:HG21	58:CC:176:ILE:HD13	1.67	0.45
58:CC:392:GLU:CD	58:CC:392:GLU:N	2.75	0.45
58:CC:616:ILE:HA	58:CC:652:TYR:O	2.17	0.45
58:CC:836:LEU:HA	58:CC:836:LEU:HD23	1.83	0.45
59:CD:317:THR:HG21	59:CD:321:LYS:HA	1.99	0.45
59:CD:1349:GLU:CD	59:CD:1349:GLU:H	2.24	0.45
1:AA:1152:A:H2'	1:AA:1153:G:O4'	2.17	0.44
6:AF:22:ILE:CG2	6:AF:39:LEU:HD21	2.47	0.44
10:AJ:76:ILE:CG1	10:AJ:79:PRO:HG3	2.48	0.44
25:BA:289:G:H2'	25:BA:290:U:C6	2.53	0.44
25:BA:1656:C:H2'	25:BA:1657:U:H6	1.82	0.44
25:BA:2225:A:O2'	25:BA:2226:C:OP2	2.31	0.44
31:BG:76:VAL:O	31:BG:79:VAL:HG12	2.16	0.44
42:BT:58:ALA:O	42:BT:62:ASP:HB3	2.17	0.44
57:CB:107:ILE:HD11	57:CB:136:GLU:HA	2.00	0.44
58:CC:145:ILE:CG2	58:CC:456:VAL:HG22	2.47	0.44
58:CC:316:GLU:CD	58:CC:316:GLU:H	2.22	0.44
58:CC:605:TYR:C	58:CC:606:LEU:HD12	2.42	0.44
59:CD:903:LEU:HA	59:CD:903:LEU:HD13	1.68	0.44
59:CD:1342:ASP:C	59:CD:1342:ASP:OD1	2.58	0.44
1:AA:587:G:OP1	8:AH:84:ARG:NH2	2.50	0.44
1:AA:590:U:H2'	1:AA:591:U:H6	1.83	0.44
1:AA:677:U:H3	1:AA:713:G:H22	1.65	0.44
1:AA:1007:U:OP1	14:AN:19:LYS:HE3	2.17	0.44
2:AB:226:SER:O	2:AB:227:GLN:HB2	2.17	0.44
25:BA:44:A:H2'	25:BA:45:G:O4'	2.17	0.44
25:BA:271:G:C4	25:BA:272:A:C8	3.06	0.44
25:BA:359:G:C5	25:BA:360:U:C5	3.06	0.44
25:BA:593:U:H2'	25:BA:594:U:C6	2.52	0.44
25:BA:888:C:H1'	25:BA:889:C:C1'	2.46	0.44
25:BA:1063:G:C5	25:BA:1064:C:C5	3.05	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1071:G:H1'	25:BA:1089:A:H2'	1.99	0.44
25:BA:2109:U:N3	25:BA:2110:G:O6	2.50	0.44
43:BU:3:ARG:HD3	43:BU:3:ARG:HA	1.76	0.44
58:CC:936:ARG:HH22	58:CC:1044:PRO:HA	1.82	0.44
58:CC:1257:GLN:NE2	59:CD:345:LYS:HD3	2.32	0.44
1:AA:147:G:H2'	1:AA:148:G:C8	2.52	0.44
1:AA:1088:G:H21	1:AA:1167:A:H62	1.65	0.44
3:AC:72:ARG:O	3:AC:75:ILE:HG22	2.16	0.44
7:AG:24:ALA:O	7:AG:27:VAL:HG22	2.17	0.44
23:AW:17(A):U:OP2	23:AW:61:C:H5'	2.17	0.44
25:BA:2012:G:OP1	42:BT:98:LYS:NZ	2.50	0.44
25:BA:2100:G:C5	25:BA:2190:G:C2	3.06	0.44
25:BA:2349:G:C6	25:BA:2369:A:C6	3.05	0.44
32:BH:115:VAL:HG12	32:BH:117:LEU:HD12	1.99	0.44
36:BN:67:VAL:HG21	36:BN:96:ILE:HD11	1.99	0.44
43:BU:25:GLU:HG3	43:BU:26:LYS:N	2.31	0.44
58:CC:363:LEU:HA	58:CC:363:LEU:HD23	1.73	0.44
58:CC:571:LEU:HD23	58:CC:571:LEU:HA	1.47	0.44
1:AA:261:U:C5	20:AT:74:ARG:NH1	2.86	0.44
1:AA:1384:C:H2'	1:AA:1385:G:C8	2.53	0.44
23:AW:74:C:H5'	25:BA:2602:A:C5'	2.47	0.44
25:BA:78:U:OP1	48:BZ:7:ARG:NH2	2.51	0.44
25:BA:301:G:OP2	44:BV:82:ARG:NH1	2.51	0.44
25:BA:1408:G:H2'	25:BA:1409:U:H6	1.83	0.44
27:BC:246:THR:OG1	27:BC:250:VAL:HG13	2.17	0.44
28:BD:8:LYS:HB2	28:BD:201:LEU:HD11	1.99	0.44
32:BH:5:LEU:O	32:BH:6:LEU:HD12	2.16	0.44
35:BM:17:LYS:HE2	35:BM:27:LEU:HD11	1.99	0.44
36:BN:3:GLN:HE21	36:BN:92:TRP:NE1	2.14	0.44
52:B4:41:ARG:HB2	52:B4:41:ARG:CZ	2.47	0.44
59:CD:424:ASN:ND2	59:CD:424:ASN:O	2.50	0.44
1:AA:427:U:OP2	1:AA:428:G:O2'	2.29	0.44
4:AD:188:ARG:NH1	59:CD:86:GLU:OE2	2.41	0.44
11:AK:40:ASN:OD1	11:AK:40:ASN:N	2.51	0.44
14:AN:41:ARG:NH2	19:AS:6:LYS:O	2.50	0.44
17:AQ:8:LEU:HD23	17:AQ:25:ILE:HG21	1.99	0.44
25:BA:1069:A:C2	25:BA:1096:A:H5''	2.52	0.44
25:BA:1796:U:H2'	25:BA:1797:G:H8	1.83	0.44
29:BE:18:THR:HG21	29:BE:197:GLU:HG3	1.99	0.44
31:BG:69:ARG:HG2	31:BG:69:ARG:HH11	1.82	0.44
37:BO:54:LEU:HD21	37:BO:65:LEU:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:BR:105:ALA:HB1	41:BS:40:MET:HE1	1.98	0.44
41:BS:36:ALA:HA	41:BS:58:VAL:HG23	2.00	0.44
41:BS:37:GLU:HA	41:BS:37:GLU:OE1	2.17	0.44
58:CC:1327:LEU:HD23	58:CC:1327:LEU:HA	1.70	0.44
1:AA:28:A:O2'	1:AA:296:U:OP1	2.32	0.44
1:AA:71:A:H2'	1:AA:72:A:H8	1.83	0.44
1:AA:946:A:H2'	1:AA:947:G:H8	1.81	0.44
1:AA:1026:G:H1	1:AA:1035:A:H61	1.65	0.44
2:AB:43:LEU:HA	2:AB:46:THR:HB	1.99	0.44
3:AC:66:VAL:HG13	3:AC:101:ILE:HA	1.98	0.44
3:AC:108:LYS:HA	58:CC:859:GLU:CB	2.48	0.44
9:AI:8:GLY:O	9:AI:19:VAL:HG12	2.18	0.44
20:AT:10:ARG:HD3	20:AT:10:ARG:HA	1.82	0.44
21:AU:29:LEU:O	21:AU:32:VAL:HG22	2.18	0.44
25:BA:1794:A:H2'	25:BA:1795:C:C6	2.52	0.44
25:BA:2102:G:N1	25:BA:2187:U:N3	2.65	0.44
25:BA:2308:G:N2	25:BA:2311:A:OP2	2.50	0.44
26:BB:2:G:H2'	26:BB:3:C:C6	2.53	0.44
38:BP:92:PHE:CZ	38:BP:107:ALA:HB2	2.52	0.44
56:CT:4:DT:C2	56:CT:5:DG:N7	2.86	0.44
1:AA:562:U:C2	12:AL:13:ALA:O	2.71	0.44
1:AA:620:C:C2	4:AD:132:ILE:HG13	2.53	0.44
1:AA:1176:A:H2'	1:AA:1177:G:O4'	2.17	0.44
5:AE:71:MET:C	5:AE:72:ILE:HD12	2.42	0.44
5:AE:77:ASN:HB2	5:AE:82:GLN:NE2	2.33	0.44
10:AJ:49:PHE:O	10:AJ:64:GLN:HA	2.18	0.44
19:AS:12:ASP:OD1	19:AS:35:SER:OG	2.32	0.44
25:BA:65:U:O2'	25:BA:456:C:N3	2.49	0.44
25:BA:927:A:O2'	49:B1:39:GLU:OE2	2.32	0.44
25:BA:1060:U:H4'	25:BA:1061:U:O5'	2.15	0.44
25:BA:2867:G:O2'	25:BA:2868:A:OP2	2.35	0.44
34:BL:21:CYS:HA	34:BL:41:ILE:HG22	1.99	0.44
52:B4:24:THR:HG23	52:B4:27:GLY:H	1.83	0.44
55:CN:28:DA:C4	55:CN:29:DG:C5	3.06	0.44
58:CC:569:ILE:O	58:CC:571:LEU:N	2.51	0.44
58:CC:1212:LEU:HA	58:CC:1212:LEU:HD23	1.66	0.44
58:CC:1278:LEU:HD23	58:CC:1278:LEU:HA	1.49	0.44
59:CD:789:LYS:HE2	59:CD:789:LYS:HB3	1.62	0.44
1:AA:1134:G:N1	1:AA:1141:C:C4	2.86	0.44
1:AA:1140:C:O2'	1:AA:1141:C:O5'	2.32	0.44
2:AB:18:HIS:NE2	2:AB:188:ASP:OD2	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AD:15:GLU:OE2	4:AD:63:ARG:NH1	2.50	0.44
6:AF:2:ARG:NH2	6:AF:68:GLN:OE1	2.50	0.44
11:AK:85:MET:HE3	11:AK:85:MET:HB3	1.87	0.44
25:BA:996:A:OP2	40:BR:93:LYS:NZ	2.43	0.44
25:BA:1049:C:C2'	25:BA:1050:A:H5'	2.47	0.44
25:BA:2183:A:H2'	25:BA:2184:A:H8	1.83	0.44
25:BA:2591:C:H2'	25:BA:2592:G:C8	2.53	0.44
33:BK:41:LYS:NZ	33:BK:50:THR:O	2.51	0.44
54:B6:7:VAL:HG11	54:B6:36:ARG:C	2.43	0.44
58:CC:261:VAL:HG21	58:CC:264:GLU:CD	2.42	0.44
58:CC:1238:LEU:N	58:CC:1238:LEU:CD2	2.81	0.44
59:CD:238:ILE:HD12	59:CD:238:ILE:HG23	1.71	0.44
1:AA:562:U:O2	12:AL:13:ALA:N	2.51	0.44
1:AA:1026:G:H1	1:AA:1035:A:N6	2.16	0.44
6:AF:73:GLU:O	6:AF:76:THR:OG1	2.31	0.44
7:AG:2:PRO:HG2	7:AG:5:ARG:HB2	2.00	0.44
7:AG:58:GLU:OE2	7:AG:59:LEU:N	2.46	0.44
23:AW:18:G:H8	23:AW:18:G:OP1	2.01	0.44
58:CC:196:VAL:HG21	58:CC:209:ILE:HD11	2.00	0.44
58:CC:794:LEU:HA	58:CC:794:LEU:HD12	1.71	0.44
58:CC:1276:TRP:CE2	59:CD:801:VAL:HG21	2.52	0.44
59:CD:770:LEU:HD13	59:CD:770:LEU:HA	1.69	0.44
1:AA:193:C:H2'	1:AA:194:C:C6	2.53	0.43
1:AA:384:G:H2'	1:AA:385:C:C6	2.53	0.43
1:AA:721:G:H4'	1:AA:722:G:O4'	2.18	0.43
1:AA:1321:U:O2'	19:AS:78:ARG:NH2	2.51	0.43
2:AB:69:PHE:HB3	2:AB:80:VAL:HG13	2.00	0.43
5:AE:10:GLU:CB	59:CD:78:LEU:HB2	2.47	0.43
14:AN:83:LYS:HA	14:AN:83:LYS:HD3	1.83	0.43
23:AW:74:C:H5'	25:BA:2602:A:H5'	2.00	0.43
25:BA:277:G:H8	25:BA:361:G:C5	2.35	0.43
25:BA:464:U:O3'	52:B4:12:ARG:NH1	2.51	0.43
25:BA:651:G:C6	25:BA:652:U:H5	2.36	0.43
25:BA:2060:A:OP2	29:BE:66:GLY:HA2	2.18	0.43
44:BV:18:ASP:HA	44:BV:21:LYS:NZ	2.33	0.43
56:CT:5:DG:H2'	56:CT:6:DA:C8	2.53	0.43
58:CC:528:ARG:HH11	58:CC:528:ARG:HD2	1.63	0.43
58:CC:1096:ILE:HD13	58:CC:1096:ILE:HG21	1.65	0.43
59:CD:430:HIS:O	59:CD:431:ARG:C	2.61	0.43
1:AA:1033:G:H2'	1:AA:1034:G:C8	2.53	0.43
1:AA:1135:U:H2'	1:AA:1137:C:C4	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AD:91:LEU:HD23	4:AD:91:LEU:HA	1.73	0.43
23:AW:15:G:C6	23:AW:48:C:O2	2.71	0.43
24:AX:5:G:H2'	24:AX:6:G:H8	1.83	0.43
25:BA:245:G:O6	53:B5:8:ARG:NH1	2.51	0.43
25:BA:594:U:H2'	25:BA:595:C:C6	2.54	0.43
25:BA:784:G:H5'	25:BA:785:G:OP1	2.18	0.43
25:BA:1301:A:C2	25:BA:1626:A:H2	2.35	0.43
25:BA:1542:U:H2'	25:BA:1543:G:O4'	2.18	0.43
36:BN:36:VAL:O	36:BN:98:PRO:HB3	2.18	0.43
55:CN:30:DA:C6	55:CN:31:DG:C6	3.07	0.43
58:CC:1296:ASP:OD2	58:CC:1322:SER:OG	2.33	0.43
59:CD:108:ALA:HB3	59:CD:279:LEU:HD23	2.00	0.43
59:CD:340:GLN:HG3	59:CD:341:ASN:OD1	2.18	0.43
59:CD:500:ILE:O	59:CD:500:ILE:HG22	2.18	0.43
1:AA:1006:G:C5	1:AA:1007:U:C5	3.06	0.43
25:BA:2788:C:H2'	25:BA:2789:C:C6	2.53	0.43
26:BB:8:C:H5''	38:BP:15:ARG:NH2	2.33	0.43
27:BC:78:VAL:HG21	27:BC:110:LEU:HD21	2.01	0.43
30:BF:73:SER:OG	30:BF:80:ARG:HA	2.18	0.43
56:CT:10:DT:H2''	56:CT:11:DC:C6	2.53	0.43
56:CT:19:DG:C6	56:CT:20:DC:N4	2.87	0.43
57:CA:213:PRO:HA	57:CA:216:ALA:HB3	2.00	0.43
58:CC:69:GLN:OE1	58:CC:101:ARG:NE	2.44	0.43
58:CC:131:THR:HG22	58:CC:132:ASP:N	2.34	0.43
58:CC:1336:ASN:C	58:CC:1336:ASN:ND2	2.77	0.43
59:CD:424:ASN:O	59:CD:424:ASN:CG	2.61	0.43
59:CD:747:MET:HE2	59:CD:775:SER:HA	1.99	0.43
1:AA:73:C:O2'	1:AA:74:A:H5'	2.19	0.43
1:AA:519:C:H2'	1:AA:520:A:O4'	2.18	0.43
2:AB:175:GLU:O	2:AB:179:LEU:HD22	2.19	0.43
4:AD:94:LEU:HD23	4:AD:94:LEU:HA	1.85	0.43
4:AD:102:VAL:HG13	4:AD:114:ALA:HB1	1.99	0.43
6:AF:85:ILE:HG13	6:AF:86:ARG:N	2.33	0.43
9:AI:7:TYR:CG	9:AI:8:GLY:N	2.87	0.43
25:BA:499:U:H5''	44:BV:43:LYS:HE2	1.99	0.43
25:BA:651:G:C6	25:BA:652:U:C5	3.07	0.43
25:BA:1070:A:C8	25:BA:1097:U:H4'	2.52	0.43
25:BA:1494:A:H2'	25:BA:1495:A:H8	1.83	0.43
25:BA:1868:C:H2'	25:BA:1869:G:H8	1.83	0.43
25:BA:2266:A:H4'	25:BA:2267:A:N3	2.33	0.43
31:BG:16:ASP:N	31:BG:16:ASP:OD1	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:BG:23:VAL:HA	31:BG:36:THR:HA	1.99	0.43
36:BN:117:PHE:HD2	36:BN:130:PHE:CD1	2.37	0.43
37:BO:2:ARG:HG2	37:BO:5:LYS:HB2	2.00	0.43
37:BO:101:GLY:O	37:BO:109:PRO:HA	2.18	0.43
58:CC:127:ILE:O	58:CC:127:ILE:HG13	2.18	0.43
58:CC:1281:TYR:CE2	59:CD:484:MET:HE3	2.53	0.43
59:CD:149:GLY:HA2	59:CD:176:PHE:HB2	1.98	0.43
1:AA:908:A:H2'	1:AA:909:A:C8	2.52	0.43
1:AA:947:G:H5''	13:AM:107:ARG:HB2	2.01	0.43
1:AA:996:A:N7	1:AA:1046:A:O2'	2.51	0.43
1:AA:1026:G:H2'	1:AA:1027:C:C5	2.54	0.43
3:AC:11:ARG:NH2	3:AC:175:LEU:O	2.44	0.43
11:AK:33:THR:HG22	11:AK:44:TRP:HB3	2.00	0.43
25:BA:1187:G:H8	25:BA:1187:G:O5'	2.01	0.43
30:BF:44:ILE:HG21	30:BF:79:ILE:HG22	2.01	0.43
45:BW:11:GLU:HG3	45:BW:16:ALA:HB1	2.00	0.43
53:B5:27:ALA:O	53:B5:28:ASN:HB2	2.18	0.43
55:CN:29:DG:H2''	55:CN:30:DA:O5'	2.18	0.43
56:CT:6:DA:C2	56:CT:7:DA:C5	3.07	0.43
58:CC:771:VAL:H	58:CC:771:VAL:HG22	1.61	0.43
58:CC:1214:ASP:C	58:CC:1214:ASP:OD1	2.61	0.43
58:CC:1329:GLU:OE1	59:CD:330:MET:HE2	2.17	0.43
1:AA:473:U:N3	1:AA:474:G:N7	2.66	0.43
1:AA:874:G:C6	1:AA:875:U:C4	3.07	0.43
3:AC:58:GLU:OE1	3:AC:65:ARG:HD2	2.19	0.43
16:AP:69:ASP:N	16:AP:69:ASP:OD1	2.50	0.43
25:BA:1177:G:O2'	25:BA:1178:C:H6	2.01	0.43
25:BA:1295:C:C2	25:BA:1296:G:C8	3.06	0.43
25:BA:2064:C:H2'	25:BA:2065:C:C6	2.53	0.43
25:BA:2747:G:O2'	31:BG:67:THR:HG23	2.18	0.43
28:BD:84:LEU:HD22	28:BD:88:GLU:O	2.19	0.43
33:BK:78:THR:HG21	33:BK:85:LYS:HE2	2.01	0.43
51:B3:40:ASP:HB3	51:B3:43:VAL:HG12	2.00	0.43
59:CD:1248:ILE:HD13	59:CD:1248:ILE:HG21	1.82	0.43
1:AA:1039:G:H2'	1:AA:1040:U:H6	1.84	0.43
1:AA:1041:G:H2'	1:AA:1042:A:C8	2.54	0.43
1:AA:1382:C:C2	1:AA:1383:C:C5	3.07	0.43
18:AR:65:LEU:O	18:AR:66:SER:OG	2.31	0.43
22:AV:41:C:H6	22:AV:41:C:H2'	1.45	0.43
25:BA:139:U:C4	43:BU:1:MET:HG2	2.54	0.43
25:BA:277:G:H8	25:BA:361:G:C6	2.36	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:848:C:H2'	25:BA:849:A:H8	1.83	0.43
25:BA:1799:G:OP1	27:BC:258:ARG:HD2	2.18	0.43
25:BA:2120:G:N1	25:BA:2179:C:N4	2.66	0.43
25:BA:2552:OMU:HM22	25:BA:2553:G:N7	2.34	0.43
36:BN:17:ASN:O	36:BN:38:ARG:NH1	2.52	0.43
58:CC:668:ILE:HD13	58:CC:668:ILE:HG21	1.69	0.43
59:CD:319:SER:O	59:CD:321:LYS:N	2.46	0.43
1:AA:1382:C:H2'	1:AA:1383:C:H5'	2.00	0.43
4:AD:99:ASP:O	4:AD:102:VAL:HG13	2.18	0.43
15:AO:26:GLU:HG3	15:AO:81:LEU:HD22	2.01	0.43
25:BA:527:C:O2'	25:BA:2779:U:O2'	2.37	0.43
25:BA:1533:C:H2'	25:BA:1534:U:C6	2.54	0.43
25:BA:1720:U:H2'	25:BA:1721:G:O4'	2.19	0.43
25:BA:2104:C:C5	25:BA:2186:G:N2	2.85	0.43
25:BA:2655:G:O2'	25:BA:2664:G:O6	2.31	0.43
26:BB:9:G:O2'	38:BP:45:SER:OG	2.18	0.43
29:BE:145:ASP:HA	29:BE:166:LYS:HB3	2.01	0.43
32:BH:1:MET:O	32:BH:20:ASN:HA	2.19	0.43
43:BU:51:PHE:HD1	43:BU:93:LEU:HD11	1.84	0.43
43:BU:67:VAL:HA	43:BU:76:ARG:HA	2.00	0.43
45:BW:59:GLU:OE1	45:BW:59:GLU:N	2.51	0.43
58:CC:1133:LYS:O	58:CC:1135:GLN:NE2	2.47	0.43
59:CD:576:ARG:HD3	59:CD:593:ASN:HA	2.00	0.43
1:AA:158:G:C5	1:AA:164:G:C6	3.07	0.43
1:AA:1064:G:H1'	1:AA:1190:G:N2	2.34	0.43
1:AA:1450:U:O2'	1:AA:1453:G:O6	2.31	0.43
3:AC:6:HIS:CE1	3:AC:8:ASN:HB3	2.54	0.43
5:AE:13:GLU:HB2	5:AE:39:VAL:HG12	2.00	0.43
25:BA:885:C:O2'	25:BA:886:A:N7	2.51	0.43
25:BA:1059:G:C8	25:BA:1060:U:H2'	2.54	0.43
25:BA:1060:U:H1'	25:BA:1062:G:H5'	2.01	0.43
32:BH:50:ARG:CZ	32:BH:51:ARG:HE	2.31	0.43
55:CN:36:DA:H2''	55:CN:37:DG:C8	2.54	0.43
58:CC:1105:SER:HB2	59:CD:731:ARG:HB3	2.00	0.43
1:AA:1006:G:C4	1:AA:1007:U:C5	3.07	0.43
2:AB:9:MET:O	2:AB:14:VAL:HG13	2.19	0.43
6:AF:42:TRP:HZ2	6:AF:61:LEU:HD22	1.84	0.43
24:AX:27:G:C2	24:AX:44:G:C2	3.07	0.43
25:BA:1265:A:H4'	25:BA:1266:G:H4'	2.00	0.43
30:BF:38:MET:HE1	30:BF:56:ASP:HB2	2.00	0.43
30:BF:50:LEU:HD21	30:BF:67:ILE:HG23	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:BR:24:TYR:O	40:BR:29:SER:HB3	2.17	0.43
41:BS:41:ILE:HG13	41:BS:54:VAL:HG11	2.00	0.43
47:BY:32:ASN:OD1	47:BY:34:HIS:NE2	2.51	0.43
58:CC:473:ARG:HH11	58:CC:473:ARG:HG3	1.83	0.43
58:CC:1098:LEU:N	58:CC:1098:LEU:HD12	2.29	0.43
59:CD:482:ALA:O	59:CD:488:ASN:ND2	2.50	0.43
59:CD:1256:ILE:HD12	59:CD:1256:ILE:HG23	1.60	0.43
1:AA:381:C:H2'	1:AA:382:A:O4'	2.19	0.42
1:AA:1492:A:OP1	12:AL:44:LYS:HA	2.19	0.42
9:AI:27:LYS:HE3	9:AI:27:LYS:HB2	1.89	0.42
25:BA:201:C:OP1	47:BY:18:ARG:NH1	2.46	0.42
25:BA:207:A:H2'	25:BA:208:C:O4'	2.18	0.42
25:BA:1437:C:O2'	25:BA:1516:G:O2'	2.29	0.42
25:BA:1868:C:H2'	25:BA:1869:G:C8	2.54	0.42
31:BG:117:LEU:HD11	31:BG:123:ALA:HB2	2.00	0.42
32:BH:19:VAL:HG13	32:BH:21:VAL:HG13	2.01	0.42
56:CT:12:DT:H6	56:CT:12:DT:H2'	1.66	0.42
58:CC:623:LEU:C	58:CC:623:LEU:HD12	2.44	0.42
59:CD:357:VAL:O	59:CD:357:VAL:HG13	2.18	0.42
59:CD:1172:LYS:HE3	59:CD:1191:PRO:HA	2.01	0.42
1:AA:676:A:H2'	1:AA:677:U:H6	1.84	0.42
1:AA:837:U:O2	1:AA:849:G:C6	2.72	0.42
1:AA:1107:C:C4	1:AA:1108:G:C8	3.07	0.42
1:AA:1239:A:H62	1:AA:1299:A:N6	2.15	0.42
11:AK:18:ASP:CG	11:AK:81:ASN:HB2	2.44	0.42
21:AU:40:LYS:O	21:AU:43:THR:OG1	2.28	0.42
23:AW:44:A:H2'	23:AW:45:G:O4'	2.18	0.42
23:AW:56:C:O5'	23:AW:56:C:H6	2.03	0.42
61:AX:101:PHE:HA	25:BA:2585:U:O4	2.19	0.42
25:BA:811:U:H2'	35:BM:21:ARG:HA	2.01	0.42
25:BA:988:A:C5	49:B1:14:ILE:HG21	2.55	0.42
25:BA:2455:G:H2'	25:BA:2456:C:C6	2.54	0.42
27:BC:142:HIS:HD1	27:BC:143:ASN:HB2	1.84	0.42
30:BF:56:ASP:O	30:BF:60:ILE:CB	2.62	0.42
36:BN:16:ARG:HA	36:BN:16:ARG:HD3	1.67	0.42
43:BU:2:ILE:HG23	43:BU:7:LEU:HD21	2.00	0.42
51:B3:21:TYR:OH	51:B3:39:PHE:O	2.23	0.42
56:CT:10:DT:H2'	56:CT:11:DC:C5	2.54	0.42
58:CC:549:ASP:OD1	58:CC:550:VAL:N	2.52	0.42
1:AA:674:G:N2	1:AA:717:U:O2	2.50	0.42
1:AA:690:G:H2'	1:AA:691:G:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1329:A:C5	1:AA:1330:U:C5	3.07	0.42
1:AA:1410:A:H2'	1:AA:1411:C:C6	2.54	0.42
10:AJ:53:ILE:HG12	10:AJ:62:ARG:HA	1.99	0.42
20:AT:44:LYS:NZ	20:AT:86:LEU:HB3	2.34	0.42
25:BA:1410:G:C6	25:BA:1411:U:C4	3.07	0.42
25:BA:2228:G:H2'	25:BA:2229:U:C6	2.55	0.42
25:BA:2600:A:H2'	25:BA:2601:C:C6	2.54	0.42
31:BG:54:PRO:HG2	31:BG:62:TRP:CE2	2.55	0.42
40:BR:9:ILE:H	40:BR:9:ILE:HD12	1.83	0.42
56:CT:17:DG:C4	56:CT:18:DC:C6	3.07	0.42
58:CC:962:GLU:O	58:CC:966:ILE:HD13	2.20	0.42
58:CC:1195:ILE:HG21	58:CC:1195:ILE:HD13	1.77	0.42
59:CD:826:ILE:HG23	59:CD:831:VAL:HG12	2.01	0.42
1:AA:150:U:C4	1:AA:170:U:C4	3.08	0.42
1:AA:410:G:H2'	1:AA:429:U:C5	2.54	0.42
3:AC:79:LYS:HZ3	58:CC:942:ASP:HA	1.84	0.42
3:AC:151:VAL:HG23	3:AC:200:VAL:HG22	2.01	0.42
4:AD:33:LYS:HD3	4:AD:36:GLN:HG3	2.00	0.42
10:AJ:4:GLN:N	10:AJ:103:GLY:OXT	2.52	0.42
22:AV:43:G:C6	22:AV:44:C:C4	3.07	0.42
24:AX:18:G:H21	24:AX:57:G:H2'	1.84	0.42
25:BA:693:A:O2'	25:BA:1353:A:N3	2.46	0.42
25:BA:886:A:H1'	25:BA:887:U:H5''	2.02	0.42
25:BA:1022:G:O6	33:BK:68:LYS:NZ	2.34	0.42
25:BA:1917:PSU:H2'	25:BA:1918:A:O4'	2.20	0.42
25:BA:2093:G:H21	25:BA:2198:A:N6	2.16	0.42
25:BA:2285:C:P	51:B3:26:ASN:HD22	2.42	0.42
25:BA:2902:C:C2'	25:BA:2903:U:H5'	2.50	0.42
53:B5:26:HIS:NE2	53:B5:48:ALA:HB2	2.34	0.42
55:CN:26:DG:C4	55:CN:27:DA:C5	3.07	0.42
57:CA:39:LEU:O	57:CA:40:GLY:C	2.62	0.42
58:CC:204:LEU:HD21	58:CC:369:MET:SD	2.59	0.42
58:CC:1014:LEU:HD12	58:CC:1017:GLN:HB3	2.00	0.42
58:CC:1257:GLN:CD	59:CD:345:LYS:HB2	2.45	0.42
58:CC:1339:LEU:HD22	59:CD:17:PHE:CG	2.55	0.42
59:CD:548:VAL:HG22	59:CD:549:LYS:N	2.35	0.42
59:CD:1302:TYR:CD1	59:CD:1302:TYR:C	2.98	0.42
1:AA:1151:A:O2'	1:AA:1152:A:O4'	2.38	0.42
1:AA:1315:U:H2'	1:AA:1316:G:O4'	2.19	0.42
3:AC:2:GLY:O	3:AC:4:LYS:NZ	2.41	0.42
3:AC:73:PRO:O	3:AC:74:GLY:C	2.63	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AF:72:ASP:O	6:AF:76:THR:HG23	2.19	0.42
7:AG:129:GLU:OE1	7:AG:131:LYS:N	2.53	0.42
9:AI:130:ARG:HH22	23:AW:33:U:P	2.41	0.42
19:AS:41:PHE:N	19:AS:44:MET:SD	2.89	0.42
25:BA:414:C:H2'	25:BA:415:A:C8	2.54	0.42
25:BA:1469:A:H2'	25:BA:1470:A:H8	1.81	0.42
30:BF:44:ILE:HG22	30:BF:83:TYR:HD2	1.84	0.42
38:BP:67:ASN:ND2	38:BP:69:ASP:OD1	2.52	0.42
48:BZ:6:LEU:HD23	48:BZ:9:LYS:HD2	2.00	0.42
52:B4:21:ARG:O	52:B4:27:GLY:HA3	2.19	0.42
55:CN:27:DA:C5	55:CN:28:DA:N7	2.88	0.42
58:CC:196:VAL:HG22	58:CC:197:ARG:N	2.34	0.42
58:CC:1304:MET:HA	58:CC:1304:MET:HE3	2.02	0.42
1:AA:426:U:OP1	4:AD:33:LYS:HD2	2.20	0.42
1:AA:478:A:P	1:AA:478:A:H8	2.43	0.42
1:AA:533:A:O2'	1:AA:535:A:OP2	2.35	0.42
1:AA:792:A:H1'	1:AA:794:A:N7	2.35	0.42
3:AC:23:PHE:CD2	10:AJ:97:ASP:HB2	2.55	0.42
5:AE:10:GLU:CB	59:CD:78:LEU:HD13	2.43	0.42
25:BA:274:C:H2'	25:BA:275:C:O4'	2.20	0.42
25:BA:580:U:O3'	40:BR:31:VAL:HG13	2.20	0.42
25:BA:2183:A:C2	25:BA:2184:A:C5	3.07	0.42
25:BA:2200:C:OP1	47:BY:37:ARG:HG3	2.19	0.42
25:BA:2225:A:H4'	25:BA:2226:C:O5'	2.20	0.42
25:BA:2646:C:O5'	25:BA:2646:C:H6	2.01	0.42
25:BA:2801:G:C2	25:BA:2802:A:C8	3.07	0.42
26:BB:117:G:C6	26:BB:118:C:N4	2.87	0.42
28:BD:18:ASP:OD1	28:BD:19:GLY:N	2.53	0.42
29:BE:40:ARG:HH12	29:BE:92:HIS:CE1	2.37	0.42
30:BF:115:ARG:HB2	30:BF:178:ARG:HH21	1.84	0.42
37:BO:38:LEU:HB3	37:BO:39:PRO:HD3	2.00	0.42
39:BQ:19:SER:O	39:BQ:19:SER:OG	2.30	0.42
43:BU:3:ARG:NH1	43:BU:5:GLU:OE2	2.47	0.42
50:B2:17:ARG:C	50:B2:20:ASP:H	2.27	0.42
53:B5:28:ASN:HD22	53:B5:40:ARG:HH11	1.67	0.42
58:CC:521:LEU:HA	58:CC:521:LEU:HD12	1.74	0.42
58:CC:1336:ASN:HB2	59:CD:25:ALA:HB2	2.01	0.42
59:CD:416:ILE:HD13	59:CD:416:ILE:HG21	1.58	0.42
59:CD:499:ILE:C	59:CD:501:VAL:H	2.27	0.42
1:AA:165:G:H2'	1:AA:166:U:H6	1.84	0.42
1:AA:613:C:H2'	1:AA:614:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:130:PHE:CG	3:AC:131:ARG:N	2.88	0.42
3:AC:147:LYS:HB3	3:AC:147:LYS:HE3	1.59	0.42
7:AG:30:LEU:HD11	7:AG:116:MET:HE2	2.00	0.42
10:AJ:34:ALA:HB1	10:AJ:76:ILE:CD1	2.50	0.42
11:AK:19:GLY:C	11:AK:82:LEU:HD12	2.45	0.42
11:AK:54:GLY:N	11:AK:57:LYS:HG2	2.35	0.42
21:AU:69:ARG:H	21:AU:69:ARG:HG3	1.55	0.42
24:AX:40:C:H2'	24:AX:41:C:C6	2.55	0.42
25:BA:358:U:H2'	25:BA:359:G:C8	2.53	0.42
25:BA:365:U:H2'	25:BA:366:C:O4'	2.20	0.42
25:BA:1168:G:C6	25:BA:1169:A:C6	3.08	0.42
25:BA:2015:A:C6	50:B2:3:VAL:HG23	2.54	0.42
25:BA:2162:G:P	25:BA:2164:C:H41	2.36	0.42
25:BA:2473:U:C4	25:BA:2474:U:C5	3.07	0.42
29:BE:58:LYS:NZ	29:BE:70:SER:O	2.52	0.42
30:BF:179:LYS:HE2	30:BF:179:LYS:HB2	1.92	0.42
43:BU:12:ARG:HD3	43:BU:12:ARG:HA	1.74	0.42
57:CA:180:VAL:HG12	57:CA:207:THR:HG22	2.02	0.42
57:CB:43:LEU:HD23	57:CB:43:LEU:HA	1.85	0.42
58:CC:210:LEU:HD23	58:CC:210:LEU:HA	1.60	0.42
58:CC:675:ASP:OD1	58:CC:675:ASP:C	2.63	0.42
59:CD:35:PHE:CZ	59:CD:101:ARG:HD2	2.55	0.42
59:CD:488:ASN:N	59:CD:488:ASN:OD1	2.48	0.42
59:CD:636:GLY:O	59:CD:638:SER:N	2.49	0.42
1:AA:562:U:H1'	12:AL:12:ARG:HB3	2.02	0.42
1:AA:876:C:H1'	8:AH:12:THR:HG21	2.00	0.42
1:AA:1012:A:C6	1:AA:1018:G:C6	3.08	0.42
1:AA:1140:C:O2'	1:AA:1141:C:H6	2.02	0.42
1:AA:1143:G:N3	1:AA:1144:G:C8	2.88	0.42
2:AB:105:LYS:H	2:AB:105:LYS:HG3	1.67	0.42
13:AM:43:VAL:HG21	13:AM:48:LEU:HD21	2.02	0.42
15:AO:12:VAL:O	15:AO:16:GLY:HA3	2.20	0.42
17:AQ:81:LYS:H	17:AQ:81:LYS:HG3	1.59	0.42
25:BA:27:G:O2'	25:BA:28:A:OP2	2.35	0.42
25:BA:468:G:N7	52:B4:39:ARG:NH2	2.60	0.42
25:BA:848:C:H2'	25:BA:849:A:C8	2.54	0.42
25:BA:1715:G:O2'	25:BA:1743:G:O6	2.34	0.42
26:BB:2:G:C6	26:BB:3:C:C4	3.08	0.42
30:BF:118:SER:OG	30:BF:119:ALA:N	2.50	0.42
31:BG:52:PHE:CE2	31:BG:72:LEU:HD22	2.55	0.42
31:BG:69:ARG:HG2	31:BG:69:ARG:NH1	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:CT:2:DT:H2''	56:CT:3:DC:H5	1.85	0.42
58:CC:217:THR:HG23	58:CC:351:LEU:HD21	2.02	0.42
58:CC:1211:ARG:NH1	58:CC:1220:GLN:OE1	2.52	0.42
58:CC:1333:LEU:C	58:CC:1335:ILE:N	2.78	0.42
59:CD:264:ASP:OD1	59:CD:264:ASP:N	2.51	0.42
59:CD:700:ASN:C	59:CD:700:ASN:HD22	2.27	0.42
1:AA:141:G:N2	1:AA:142:G:H1'	2.35	0.42
1:AA:696:A:H1'	1:AA:786:G:O2'	2.20	0.42
1:AA:1120:C:H2'	1:AA:1121:U:C6	2.54	0.42
6:AF:11:HIS:CE1	6:AF:54:LEU:HD22	2.55	0.42
18:AR:63:ARG:HD3	18:AR:70:TYR:CD1	2.55	0.42
25:BA:829:A:N7	25:BA:2248:C:H5'	2.34	0.42
25:BA:879:G:N1	25:BA:899:A:H1'	2.34	0.42
25:BA:1106:G:C4	25:BA:1107:G:C8	3.07	0.42
25:BA:2096:C:C2	25:BA:2097:A:C8	3.07	0.42
25:BA:2419:U:OP2	53:B5:33:LEU:HD13	2.20	0.42
25:BA:2757:A:C2	25:BA:2758:A:C8	3.07	0.42
29:BE:176:ASP:O	29:BE:179:SER:OG	2.30	0.42
34:BL:11:ALA:O	34:BL:100:PHE:HD1	2.02	0.42
42:BT:23:LEU:HD11	50:B2:24:ALA:N	2.34	0.42
43:BU:51:PHE:CD1	43:BU:93:LEU:HD21	2.55	0.42
48:BZ:5:GLU:O	48:BZ:8:GLU:HG2	2.19	0.42
58:CC:456:VAL:H	58:CC:456:VAL:HG23	1.53	0.42
58:CC:538:LEU:HD12	58:CC:538:LEU:C	2.44	0.42
58:CC:1176:LEU:HA	58:CC:1176:LEU:HD23	1.79	0.42
1:AA:884:U:H6	1:AA:884:U:H2'	1.50	0.42
1:AA:1125:U:OP1	10:AJ:37:ARG:NE	2.53	0.42
1:AA:1174:G:C2'	1:AA:1175:G:H5'	2.47	0.42
1:AA:1385:G:H2'	1:AA:1386:G:O4'	2.20	0.42
1:AA:1428:A:H2'	1:AA:1429:A:O4'	2.19	0.42
4:AD:105:MET:HG2	4:AD:173:VAL:HG13	2.01	0.42
9:AI:41:ARG:HB2	9:AI:41:ARG:HH11	1.84	0.42
10:AJ:53:ILE:HD11	10:AJ:63:ASP:CB	2.49	0.42
13:AM:23:TYR:HD1	13:AM:66:GLU:HA	1.84	0.42
25:BA:1167:C:C2	25:BA:1168:G:C8	3.08	0.42
25:BA:1333:G:C2	25:BA:1334:G:C8	3.08	0.42
25:BA:1596:A:O2'	25:BA:1597:A:C5'	2.68	0.42
25:BA:2026:U:H2'	25:BA:2027:G:O4'	2.20	0.42
25:BA:2815:C:C2	25:BA:2816:G:C8	3.07	0.42
28:BD:173:GLN:OE1	28:BD:208:LYS:HE3	2.19	0.42
30:BF:26:MET:HE2	30:BF:26:MET:HA	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:BF:53:ALA:HB2	30:BF:150:ARG:NH1	2.34	0.42
55:CN:27:DA:H1'	55:CN:28:DA:H5'	2.01	0.42
58:CC:84:GLU:OE2	58:CC:1032:LYS:NZ	2.48	0.42
58:CC:530:ILE:HG23	58:CC:530:ILE:HD12	1.63	0.42
58:CC:746:ALA:HB2	58:CC:967:LEU:HD21	2.02	0.42
59:CD:72:CYS:HB2	59:CD:87:LYS:HD3	2.01	0.42
1:AA:6:G:O2'	1:AA:7:A:H8	2.03	0.41
1:AA:844:G:H3'	1:AA:844:G:N3	2.35	0.41
1:AA:1121:U:C2	1:AA:1122:U:C5	3.08	0.41
2:AB:111:ILE:HG22	2:AB:148:LEU:HD13	2.02	0.41
18:AR:20:GLU:OE1	18:AR:20:GLU:N	2.53	0.41
19:AS:70:LYS:O	19:AS:73:GLU:N	2.53	0.41
25:BA:1338:G:O6	43:BU:66:LYS:NZ	2.50	0.41
25:BA:1588:G:C2	25:BA:1589:U:C4	3.08	0.41
25:BA:1652:A:OP1	37:BO:8:ARG:HD3	2.20	0.41
25:BA:2111:U:O2	25:BA:2111:U:H2'	2.19	0.41
25:BA:2364:C:H2'	25:BA:2365:G:O4'	2.20	0.41
30:BF:57:LEU:O	30:BF:61:SER:OG	2.20	0.41
32:BH:15:LEU:HD13	32:BH:15:LEU:O	2.20	0.41
38:BP:74:VAL:HG13	38:BP:106:LEU:HD12	2.01	0.41
49:B1:45:ARG:NH1	49:B1:59:GLU:OE2	2.53	0.41
57:CA:205:MET:SD	57:CA:213:PRO:HG3	2.60	0.41
58:CC:139:ASN:C	58:CC:141:THR:H	2.27	0.41
58:CC:524:ILE:HG21	58:CC:524:ILE:HD13	1.76	0.41
58:CC:817:LEU:HA	58:CC:817:LEU:HD12	1.70	0.41
59:CD:174:ASP:C	59:CD:176:PHE:H	2.28	0.41
59:CD:1175:LEU:HB2	59:CD:1190:ILE:HD12	2.01	0.41
1:AA:606:G:N2	1:AA:632:U:OP1	2.44	0.41
1:AA:738:C:OP1	6:AF:91:ARG:HD2	2.20	0.41
1:AA:877:G:H2'	1:AA:878:A:H8	1.85	0.41
1:AA:878:A:C2	1:AA:879:C:C2	3.08	0.41
1:AA:1134:G:C8	1:AA:1135:U:C5	3.08	0.41
1:AA:1368:A:OP1	9:AI:113:ARG:NH2	2.53	0.41
4:AD:57:GLU:CD	4:AD:58:LYS:N	2.78	0.41
7:AG:5:ARG:HB3	7:AG:7:ILE:HG23	2.03	0.41
13:AM:25:VAL:HG13	13:AM:29:ARG:HB3	2.01	0.41
14:AN:73:PHE:HE1	14:AN:75:ARG:HA	1.85	0.41
17:AQ:7:THR:C	17:AQ:8:LEU:HD12	2.45	0.41
17:AQ:20:SER:OG	17:AQ:71:LYS:NZ	2.35	0.41
25:BA:529:A:OP2	33:BK:116:ARG:NH2	2.45	0.41
25:BA:851:C:H2'	25:BA:852:U:H6	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1482:G:C6	25:BA:1508:A:N6	2.88	0.41
25:BA:1800:C:OP2	27:BC:182:ARG:NH1	2.53	0.41
25:BA:2344:U:H6	25:BA:2344:U:H2'	1.71	0.41
26:BB:75:G:H2'	26:BB:76:G:O4'	2.20	0.41
34:BL:108:ARG:HA	34:BL:116:ILE:HG13	2.02	0.41
48:BZ:14:LEU:HD22	48:BZ:53:VAL:HG13	2.02	0.41
58:CC:213:LEU:HA	58:CC:213:LEU:HD23	1.73	0.41
58:CC:569:ILE:HD13	58:CC:569:ILE:HG21	1.60	0.41
58:CC:1014:LEU:HD12	58:CC:1014:LEU:HA	1.87	0.41
58:CC:1251:TYR:CE1	58:CC:1301:ARG:CZ	3.03	0.41
59:CD:139:LEU:HD23	59:CD:139:LEU:HA	1.68	0.41
1:AA:553:A:H5''	12:AL:21:VAL:HG21	2.02	0.41
1:AA:600:A:H5'	8:AH:121:LEU:HA	2.02	0.41
1:AA:841:C:O2'	1:AA:842:U:O5'	2.39	0.41
1:AA:1022:A:C2	1:AA:1023:U:C2	3.08	0.41
1:AA:1034:G:H2'	1:AA:1035:A:H8	1.84	0.41
3:AC:51:SER:O	3:AC:51:SER:OG	2.34	0.41
5:AE:81:LEU:HD23	5:AE:81:LEU:HA	1.82	0.41
8:AH:39:VAL:O	8:AH:42:GLU:HG2	2.20	0.41
9:AI:36:GLU:HA	9:AI:45:ARG:HE	1.84	0.41
10:AJ:15:HIS:O	10:AJ:18:ILE:HG22	2.20	0.41
10:AJ:52:LEU:HD23	10:AJ:62:ARG:HD3	2.02	0.41
15:AO:64:ARG:NH1	15:AO:68:ASP:OD1	2.53	0.41
25:BA:18:U:OP1	40:BR:30:ARG:NH2	2.40	0.41
25:BA:1209:U:O2'	25:BA:1237:A:N1	2.43	0.41
25:BA:1587:G:H2'	25:BA:1588:G:H8	1.85	0.41
31:BG:160:LYS:HB3	31:BG:160:LYS:HE2	1.73	0.41
32:BH:50:ARG:NH2	32:BH:51:ARG:HE	2.17	0.41
34:BL:123:LEU:HD13	34:BL:123:LEU:HA	1.94	0.41
56:CT:20:DC:C2	56:CT:21:DG:N7	2.88	0.41
57:CA:85:LEU:HD23	57:CA:85:LEU:HA	1.84	0.41
57:CB:66:HIS:CE1	57:CB:68:TYR:HD1	2.39	0.41
58:CC:1141:LEU:HD12	58:CC:1141:LEU:HA	1.84	0.41
59:CD:541:LEU:HD23	59:CD:541:LEU:HA	1.84	0.41
1:AA:156:C:H2'	1:AA:157:U:O4'	2.19	0.41
1:AA:996:A:N6	1:AA:1046:A:O4'	2.53	0.41
1:AA:1060:U:H2'	1:AA:1061:G:H8	1.85	0.41
2:AB:187:VAL:CG1	2:AB:199:VAL:HG12	2.41	0.41
3:AC:108:LYS:HB3	3:AC:111:LEU:HD13	2.02	0.41
7:AG:58:GLU:OE2	7:AG:58:GLU:N	2.53	0.41
9:AI:28:ILE:HG13	9:AI:63:LEU:HD21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:AR:65:LEU:HD23	18:AR:65:LEU:HA	1.85	0.41
25:BA:1173:U:O2'	25:BA:1175:A:N7	2.49	0.41
25:BA:1355:G:C2	25:BA:1356:G:C8	3.08	0.41
25:BA:1380:G:O2'	25:BA:1569:A:N6	2.54	0.41
25:BA:1877:A:H2'	25:BA:1878:G:O4'	2.21	0.41
25:BA:2125:G:H2'	25:BA:2173:A:H61	1.84	0.41
25:BA:2822:G:O5'	25:BA:2822:G:H8	2.03	0.41
27:BC:107:PRO:HG2	27:BC:127:GLY:HA2	2.02	0.41
27:BC:144:VAL:HG21	27:BC:162:VAL:HG21	2.02	0.41
32:BH:55:GLU:HA	32:BH:58:LEU:HD12	2.02	0.41
55:CN:28:DA:C4	55:CN:29:DG:N7	2.89	0.41
56:CT:20:DC:O2	56:CT:21:DG:C8	2.73	0.41
58:CC:45:GLY:O	58:CC:51:ALA:HB2	2.19	0.41
58:CC:1251:TYR:CE1	58:CC:1301:ARG:NH1	2.88	0.41
59:CD:311:ARG:HH11	59:CD:311:ARG:HD3	1.72	0.41
59:CD:1350:ASN:ND2	59:CD:1358:PRO:HD3	2.34	0.41
1:AA:767:A:H2'	1:AA:768:A:O4'	2.21	0.41
1:AA:844:G:N2	1:AA:846:G:C4	2.88	0.41
1:AA:1251:A:H2'	1:AA:1252:A:O4'	2.21	0.41
3:AC:33:LEU:HD21	14:AN:93:ILE:HG12	2.03	0.41
4:AD:57:GLU:OE1	4:AD:200:ILE:HG13	2.19	0.41
5:AE:10:GLU:HB2	59:CD:78:LEU:CD1	2.49	0.41
8:AH:18:GLN:HE21	8:AH:72:VAL:HG12	1.85	0.41
10:AJ:32:THR:CG2	10:AJ:83:THR:HG23	2.50	0.41
19:AS:48:THR:HA	19:AS:61:PHE:HA	2.03	0.41
20:AT:5:LYS:HB2	20:AT:5:LYS:HE3	1.53	0.41
21:AU:36:GLU:OE1	21:AU:36:GLU:HA	2.20	0.41
25:BA:52:A:H2'	25:BA:53:A:C8	2.55	0.41
25:BA:550:U:O2	25:BA:551:G:C8	2.73	0.41
25:BA:782:A:C6	27:BC:225:MET:HE2	2.55	0.41
25:BA:984:A:H2'	25:BA:984:A:N3	2.36	0.41
25:BA:1405:U:H2'	25:BA:1406:U:C5	2.56	0.41
25:BA:2071:A:H2'	25:BA:2072:C:H6	1.83	0.41
25:BA:2343:U:HO2'	25:BA:2373:G:HO2'	1.66	0.41
25:BA:2901:C:C2	25:BA:2902:C:C4	3.08	0.41
35:BM:27:LEU:HD23	35:BM:27:LEU:HA	1.89	0.41
58:CC:1223:ARG:HA	58:CC:1224:PRO:HD3	1.92	0.41
59:CD:554:GLU:OE1	59:CD:588:PRO:HA	2.20	0.41
2:AB:214:LEU:HD23	2:AB:214:LEU:HA	1.97	0.41
4:AD:105:MET:HE3	4:AD:171:LEU:HD13	2.01	0.41
5:AE:81:LEU:HD11	5:AE:96:MET:HG3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:263:G:H2'	25:BA:264:C:O4'	2.21	0.41
25:BA:638:G:H2'	25:BA:639:U:O4'	2.21	0.41
25:BA:1056:G:H1'	25:BA:1103:A:H61	1.85	0.41
25:BA:1528:A:H2'	25:BA:1529:G:O4'	2.20	0.41
25:BA:2303:G:O6	25:BA:2314:A:N6	2.54	0.41
25:BA:2576:G:H5'	25:BA:2578:G:N7	2.35	0.41
25:BA:2901:C:C4	25:BA:2902:C:N4	2.89	0.41
27:BC:232:HIS:HA	27:BC:242:LYS:HE3	2.03	0.41
30:BF:178:ARG:O	30:BF:179:LYS:HD3	2.21	0.41
38:BP:55:GLU:OE1	38:BP:81:ARG:NH2	2.47	0.41
43:BU:29:THR:OG1	43:BU:30:ILE:N	2.52	0.41
51:B3:43:VAL:HG21	51:B3:45:GLN:HE21	1.85	0.41
56:CT:4:DT:H2''	56:CT:5:DG:C8	2.55	0.41
58:CC:1248:THR:HG22	58:CC:1249:GLY:N	2.36	0.41
59:CD:331:ILE:HD13	59:CD:331:ILE:HG21	1.89	0.41
59:CD:872:LEU:HD22	59:CD:877:VAL:HG21	2.02	0.41
1:AA:495:A:C2	1:AA:496:A:C6	3.08	0.41
4:AD:9:LEU:HD13	4:AD:32:CYS:SG	2.61	0.41
5:AE:55:GLU:N	5:AE:55:GLU:OE2	2.53	0.41
25:BA:1:G:N2	25:BA:2903:U:O2	2.54	0.41
25:BA:117:G:OP2	25:BA:119:A:O2'	2.35	0.41
25:BA:167:A:C2	25:BA:168:G:H1'	2.55	0.41
25:BA:613:A:H8	25:BA:613:A:O5'	2.03	0.41
25:BA:896:A:O2'	25:BA:897:C:O4'	2.32	0.41
25:BA:1231:U:H2'	25:BA:1232:G:H8	1.85	0.41
25:BA:2187:U:O5'	25:BA:2187:U:H6	2.03	0.41
25:BA:2210:U:H4'	25:BA:2211:G:C5'	2.51	0.41
25:BA:2298:A:H61	25:BA:2318:G:H1'	1.85	0.41
30:BF:57:LEU:HA	30:BF:57:LEU:HD23	1.83	0.41
43:BU:6:ARG:HA	43:BU:6:ARG:HD2	1.85	0.41
45:BW:48:MET:O	45:BW:51:GLN:HG3	2.21	0.41
58:CC:1105:SER:OG	59:CD:731:ARG:NE	2.51	0.41
58:CC:1235:LEU:HA	58:CC:1235:LEU:HD23	1.75	0.41
59:CD:157:GLN:CG	59:CD:158:GLN:H	2.34	0.41
59:CD:290:ILE:H	59:CD:290:ILE:HD12	1.85	0.41
1:AA:94:G:N2	1:AA:97:G:O6	2.53	0.41
1:AA:1183:U:H3'	1:AA:1184:G:H5''	2.02	0.41
1:AA:1326:U:H2'	1:AA:1327:C:H6	1.86	0.41
1:AA:1467:C:H2'	1:AA:1468:A:C8	2.56	0.41
1:AA:1492:A:N6	12:AL:47:SER:OG	2.54	0.41
1:AA:1527:U:C5	21:AU:42:THR:HG21	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AE:144:LEU:HD23	5:AE:144:LEU:HA	1.79	0.41
13:AM:92:ARG:HH11	25:BA:888:C:H3'	1.85	0.41
15:AO:67:LEU:HD23	15:AO:67:LEU:HA	1.69	0.41
17:AQ:17:MET:HE3	17:AQ:20:SER:HB3	2.03	0.41
18:AR:34:THR:N	18:AR:38:LYS:O	2.51	0.41
25:BA:118:A:C8	25:BA:119:A:C8	3.08	0.41
25:BA:543:A:N1	25:BA:551:G:C6	2.89	0.41
25:BA:1802:A:H2'	25:BA:1803:A:C8	2.56	0.41
25:BA:2532:G:N2	25:BA:2663:G:O2'	2.54	0.41
27:BC:105:LEU:O	27:BC:107:PRO:HD3	2.20	0.41
36:BN:134:THR:HG21	45:BW:79:ARG:CZ	2.51	0.41
37:BO:49:GLU:O	37:BO:53:THR:HG23	2.20	0.41
42:BT:36:LEU:HD23	42:BT:36:LEU:HA	1.93	0.41
57:CA:58:GLU:OE1	57:CA:170:ARG:HD3	2.21	0.41
57:CA:185:TYR:CD1	57:CA:185:TYR:C	2.99	0.41
58:CC:447:HIS:C	58:CC:449:GLY:N	2.77	0.41
59:CD:80:HIS:O	59:CD:83:VAL:HG22	2.21	0.41
59:CD:160:LEU:HD23	59:CD:160:LEU:N	2.34	0.41
59:CD:374:LEU:HD23	59:CD:374:LEU:C	2.45	0.41
59:CD:416:ILE:O	59:CD:418:GLU:N	2.53	0.41
1:AA:413:G:H21	1:AA:428:G:H1'	1.86	0.41
1:AA:868:C:H2'	1:AA:869:G:O4'	2.21	0.41
1:AA:1095:U:H2'	1:AA:1096:C:C6	2.56	0.41
1:AA:1443:C:H2'	1:AA:1444:U:O4'	2.20	0.41
2:AB:129:LEU:C	2:AB:131:LYS:N	2.79	0.41
3:AC:114:LYS:HE2	3:AC:185:ASN:OD1	2.21	0.41
4:AD:5:LEU:HD23	4:AD:5:LEU:HA	1.78	0.41
4:AD:190:ASP:OD1	4:AD:190:ASP:C	2.64	0.41
5:AE:105:ILE:O	5:AE:112:ARG:NH2	2.54	0.41
9:AI:4:ASN:HB3	9:AI:6:TYR:CE1	2.56	0.41
17:AQ:54:GLY:N	17:AQ:57:ASP:OD2	2.47	0.41
25:BA:274:C:H3'	25:BA:275:C:C6	2.55	0.41
25:BA:404:A:H5''	25:BA:405:U:OP1	2.21	0.41
25:BA:631:A:OP2	53:B5:23:LYS:NZ	2.37	0.41
25:BA:1078:U:O2	25:BA:1088:A:H2'	2.20	0.41
25:BA:1182:G:H2'	25:BA:1183:U:O4'	2.20	0.41
25:BA:1794:A:H2'	25:BA:1795:C:H6	1.86	0.41
25:BA:2125:G:H1	25:BA:2171:A:P	2.44	0.41
25:BA:2313:C:N3	25:BA:2314:A:N7	2.69	0.41
25:BA:2314:A:C2	25:BA:2315:G:C5	3.09	0.41
25:BA:2345:G:N3	25:BA:2381:A:H2'	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2500:U:O2'	25:BA:2504:PSU:OP1	2.37	0.41
25:BA:2685:G:OP1	34:BL:78:ARG:NH2	2.53	0.41
25:BA:2898:U:C2	25:BA:2899:A:N7	2.89	0.41
27:BC:225:MET:HB3	27:BC:229:ASP:HB2	2.02	0.41
30:BF:171:ALA:O	30:BF:174:ASP:N	2.43	0.41
36:BN:82:MET:HE3	36:BN:82:MET:HB3	1.88	0.41
40:BR:83:LEU:HD22	40:BR:88:VAL:HB	2.02	0.41
45:BW:75:GLN:HB2	45:BW:92:VAL:HG13	2.03	0.41
45:BW:80:HIS:CE1	45:BW:83:LYS:HD2	2.54	0.41
46:BX:54:GLY:O	46:BX:57:HIS:N	2.53	0.41
50:B2:34:SER:OG	50:B2:36:GLU:HG2	2.21	0.41
55:CN:26:DG:C8	55:CN:26:DG:H5''	2.56	0.41
55:CN:27:DA:C4	55:CN:28:DA:N7	2.89	0.41
56:CT:5:DG:H2'	56:CT:6:DA:O4'	2.21	0.41
57:CB:66:HIS:ND1	57:CB:68:TYR:HB3	2.36	0.41
58:CC:24:VAL:HG21	58:CC:704:MET:HE1	2.02	0.41
58:CC:145:ILE:N	58:CC:145:ILE:HD12	2.36	0.41
58:CC:222:ASP:OD1	58:CC:227:LYS:NZ	2.45	0.41
58:CC:421:SER:O	58:CC:422:LYS:C	2.62	0.41
58:CC:447:HIS:C	58:CC:449:GLY:H	2.28	0.41
58:CC:554:HIS:O	58:CC:555:TYR:C	2.61	0.41
58:CC:615:VAL:O	58:CC:615:VAL:HG13	2.20	0.41
58:CC:660:VAL:HG13	58:CC:661:VAL:HG13	2.02	0.41
58:CC:753:LEU:HD23	58:CC:753:LEU:HA	1.75	0.41
58:CC:1104:PRO:HA	59:CD:740:LEU:HD11	2.03	0.41
59:CD:201:LEU:HD23	59:CD:221:ILE:HG22	2.03	0.41
59:CD:327:LEU:O	59:CD:330:MET:N	2.51	0.41
59:CD:572:THR:HG23	59:CD:573:THR:N	2.35	0.41
59:CD:619:ILE:HD12	59:CD:619:ILE:HA	1.86	0.41
1:AA:81:A:H2'	1:AA:82:G:O4'	2.21	0.41
1:AA:336:A:C6	1:AA:337:G:C5	3.09	0.41
1:AA:404:G:N7	4:AD:2:ALA:HB3	2.35	0.41
1:AA:1038:C:C2	1:AA:1039:G:C8	3.09	0.41
1:AA:1077:G:N2	1:AA:1080:A:OP2	2.44	0.41
1:AA:1277:C:C2'	1:AA:1278:G:H5''	2.51	0.41
1:AA:1370:G:C2	1:AA:1371:G:C8	3.09	0.41
4:AD:145:ILE:HD13	4:AD:145:ILE:HA	1.94	0.41
9:AI:99:ARG:HD2	9:AI:104:VAL:HG21	2.02	0.41
11:AK:85:MET:HE3	11:AK:113:VAL:HG11	2.02	0.41
12:AL:81:LEU:O	12:AL:98:VAL:HG12	2.21	0.41
13:AM:3:ARG:O	13:AM:57:ARG:NH2	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1060:U:C1'	25:BA:1062:G:H5'	2.51	0.41
25:BA:1105:U:H2'	25:BA:1106:G:C8	2.53	0.41
25:BA:1495:A:H2'	25:BA:1496:A:C8	2.56	0.41
25:BA:1790:C:H2'	25:BA:1791:A:C5	2.56	0.41
25:BA:2250:G:O2'	25:BA:2497:A:OP2	2.33	0.41
25:BA:2308:G:C6	30:BF:77:PHE:CZ	3.09	0.41
25:BA:2899:A:H2'	25:BA:2900:A:H8	1.86	0.41
26:BB:2:G:O6	26:BB:119:A:N6	2.54	0.41
27:BC:157:SER:O	27:BC:160:THR:OG1	2.17	0.41
32:BH:64:ALA:O	32:BH:68:ARG:HG2	2.20	0.41
38:BP:49:VAL:HG12	38:BP:50:ALA:N	2.36	0.41
44:BV:42:VAL:O	44:BV:60:GLU:HA	2.21	0.41
58:CC:138:ILE:HD12	58:CC:138:ILE:HG23	1.78	0.41
58:CC:149:LEU:HA	58:CC:149:LEU:HD12	1.87	0.41
58:CC:166:SER:HB2	59:CD:1151:LYS:HE3	2.03	0.41
59:CD:249:LEU:HA	59:CD:249:LEU:HD23	1.85	0.41
59:CD:830:ASP:OD1	59:CD:832:LYS:NZ	2.43	0.41
1:AA:1215:G:C2	1:AA:1216:A:C8	3.09	0.40
3:AC:74:GLY:N	58:CC:867:GLU:CB	2.48	0.40
3:AC:79:LYS:H	3:AC:79:LYS:CD	2.34	0.40
7:AG:110:LYS:HA	7:AG:110:LYS:HD2	1.67	0.40
13:AM:65:VAL:HG22	13:AM:66:GLU:N	2.36	0.40
25:BA:239:C:O2'	25:BA:622:G:O2'	2.21	0.40
25:BA:389:G:C8	25:BA:2413:G:H4'	2.57	0.40
25:BA:456:C:H2'	43:BU:73:ARG:HH11	1.86	0.40
25:BA:955:PSU:H6	25:BA:955:PSU:O5'	2.04	0.40
25:BA:1040:A:H2'	25:BA:1041:G:O4'	2.20	0.40
25:BA:2377:A:O2'	38:BP:117:PHE:O	2.39	0.40
25:BA:2694:G:H2'	25:BA:2695:U:O4'	2.22	0.40
36:BN:25:ASP:OD1	36:BN:25:ASP:N	2.46	0.40
39:BQ:14:LYS:NZ	39:BQ:78:SER:O	2.37	0.40
47:BY:6:GLN:O	47:BY:74:ARG:NH2	2.53	0.40
57:CA:27:THR:C	57:CA:28:LEU:HD12	2.46	0.40
58:CC:456:VAL:C	58:CC:458:GLU:H	2.29	0.40
58:CC:678:ARG:NH1	58:CC:681:MET:SD	2.94	0.40
58:CC:690:VAL:H	58:CC:690:VAL:HG12	1.73	0.40
58:CC:886:LYS:HB3	58:CC:916:SER:O	2.22	0.40
59:CD:755:ILE:HG22	59:CD:757:THR:H	1.85	0.40
59:CD:871:LEU:O	59:CD:874:GLU:HB3	2.21	0.40
1:AA:1160:G:H5'	2:AB:131:LYS:NZ	2.36	0.40
1:AA:1292:G:C6	1:AA:1293:C:C4	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1408:A:C6	1:AA:1494:G:C6	3.09	0.40
1:AA:1518:MA6:O5'	1:AA:1518:MA6:H8	2.21	0.40
4:AD:106:GLY:HA2	4:AD:165:ARG:HH22	1.87	0.40
4:AD:194:ASP:CA	59:CD:74:LYS:HE2	2.47	0.40
5:AE:13:GLU:OE2	5:AE:68:ARG:NH2	2.53	0.40
5:AE:99:ALA:HB3	5:AE:103:THR:HG21	2.04	0.40
7:AG:16:PRO:HB2	9:AI:42:GLU:HG3	2.04	0.40
9:AI:32:GLN:HE21	9:AI:32:GLN:HB2	1.75	0.40
11:AK:18:ASP:HA	11:AK:81:ASN:O	2.21	0.40
12:AL:66:TYR:HB2	12:AL:87:VAL:HG21	2.03	0.40
17:AQ:38:ILE:HD12	17:AQ:40:ARG:HD2	2.03	0.40
18:AR:68:LEU:HD13	18:AR:68:LEU:HA	1.88	0.40
21:AU:29:LEU:HA	21:AU:32:VAL:HG22	2.04	0.40
23:AW:55:PSU:O5'	23:AW:55:PSU:H6	2.04	0.40
25:BA:81:G:H2'	25:BA:82:U:O4'	2.21	0.40
25:BA:638:G:C5	25:BA:651:G:C2	3.09	0.40
25:BA:711:G:C6	25:BA:721:A:C6	3.09	0.40
25:BA:1872:A:H8	25:BA:1872:A:O5'	2.04	0.40
25:BA:2175:C:H2'	25:BA:2176:A:N7	2.36	0.40
25:BA:2287:A:N7	25:BA:2289:G:C8	2.90	0.40
26:BB:12:C:H5'	26:BB:15:A:H61	1.86	0.40
27:BC:267:ILE:HG21	27:BC:270:ARG:HD2	2.03	0.40
30:BF:114:PHE:CE2	30:BF:176:PRO:HB2	2.37	0.40
47:BY:19:SER:OG	47:BY:20:HIS:N	2.54	0.40
52:B4:41:ARG:HB2	52:B4:41:ARG:NH2	2.36	0.40
59:CD:1356:LEU:HD23	59:CD:1356:LEU:HA	1.85	0.40
1:AA:211:G:C6	1:AA:212:G:H1'	2.56	0.40
1:AA:425:G:C6	1:AA:426:U:C4	3.10	0.40
1:AA:676:A:H2'	1:AA:677:U:C6	2.56	0.40
1:AA:947:G:C6	1:AA:948:C:C4	3.09	0.40
1:AA:981:U:OP1	14:AN:9:ARG:NH1	2.55	0.40
1:AA:1246:A:N1	1:AA:1292:G:C6	2.89	0.40
1:AA:1319:A:C8	1:AA:1323:G:C5	3.09	0.40
1:AA:1355:G:H2'	1:AA:1356:G:H8	1.86	0.40
1:AA:1480:A:H2'	1:AA:1481:U:O4'	2.21	0.40
6:AF:50:PRO:HB3	6:AF:55:HIS:CD2	2.55	0.40
23:AW:7:G:O2'	23:AW:49:G:O5'	2.27	0.40
25:BA:404:A:H4'	25:BA:405:U:H5''	2.02	0.40
25:BA:1063:G:O2'	25:BA:1064:C:H6	2.04	0.40
25:BA:2347:C:C2	25:BA:2348:U:C5	3.10	0.40
25:BA:2375:G:N2	25:BA:2378:A:OP2	2.38	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2552:OMU:C2	25:BA:2554:U:H5''	2.51	0.40
25:BA:2797:U:H6	25:BA:2797:U:H2'	1.78	0.40
26:BB:65:U:C4	26:BB:108:A:C4	3.08	0.40
28:BD:31:ALA:O	28:BD:33:ARG:HD3	2.21	0.40
28:BD:48:ILE:O	28:BD:48:ILE:HG13	2.21	0.40
30:BF:55:ALA:O	30:BF:56:ASP:C	2.61	0.40
36:BN:33:LEU:HD13	36:BN:117:PHE:HB3	2.03	0.40
39:BQ:98:TYR:O	39:BQ:101:ARG:HB3	2.21	0.40
51:B3:7:GLU:HG2	51:B3:8:LYS:N	2.36	0.40
57:CB:58:GLU:OE2	57:CB:170:ARG:NE	2.44	0.40
58:CC:951:MET:O	58:CC:955:GLN:HG2	2.21	0.40
59:CD:884:SER:OG	59:CD:885:VAL:N	2.55	0.40
1:AA:176:C:C2	1:AA:177:G:C2	3.10	0.40
1:AA:213:G:C8	1:AA:214:C:C5	3.10	0.40
1:AA:663:A:H2'	1:AA:664:G:O4'	2.22	0.40
1:AA:737:C:H5''	6:AF:91:ARG:HG3	2.03	0.40
1:AA:1119:C:OP2	9:AI:11:ARG:NH2	2.54	0.40
2:AB:73:LYS:HE2	2:AB:73:LYS:HB2	1.71	0.40
4:AD:124:MET:HE2	4:AD:146:ARG:HA	2.02	0.40
8:AH:34:VAL:O	8:AH:38:ASN:ND2	2.52	0.40
12:AL:43:LYS:HG2	12:AL:44:LYS:H	1.86	0.40
25:BA:197:A:H2	25:BA:2434:A:H62	1.70	0.40
25:BA:289:G:H2'	25:BA:290:U:O4'	2.21	0.40
25:BA:2104:C:H41	25:BA:2186:G:N2	2.19	0.40
25:BA:2182:U:O2'	25:BA:2183:A:C8	2.68	0.40
26:BB:42:C:C6	30:BF:66:LEU:HB2	2.56	0.40
26:BB:45:A:C4	26:BB:46:A:C8	3.10	0.40
26:BB:94:A:H2'	26:BB:95:U:O4'	2.21	0.40
27:BC:240:PHE:O	27:BC:242:LYS:NZ	2.31	0.40
34:BL:15:GLY:O	34:BL:47:ILE:HG23	2.22	0.40
34:BL:59:LYS:HG3	34:BL:89:ASN:HA	2.04	0.40
40:BR:18:LEU:HA	40:BR:18:LEU:HD13	1.80	0.40
44:BV:41:LEU:HB3	44:BV:60:GLU:HG2	2.03	0.40
57:CA:11:PRO:HB3	57:CA:31:LEU:HD21	2.02	0.40
58:CC:267:ARG:NH2	58:CC:268:ARG:O	2.54	0.40
58:CC:675:ASP:OD1	58:CC:676:ALA:N	2.54	0.40
58:CC:1333:LEU:HA	58:CC:1333:LEU:HD23	1.84	0.40
58:CC:1339:LEU:HA	58:CC:1339:LEU:HD23	1.88	0.40
59:CD:441:LEU:N	59:CD:441:LEU:CD2	2.84	0.40
59:CD:1310:THR:O	59:CD:1310:THR:HG22	2.20	0.40
1:AA:148:G:O2'	1:AA:149:A:P	2.79	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:255:G:C2	1:AA:272:C:C2	3.10	0.40
1:AA:346:G:H4'	39:BQ:39:ARG:HH12	1.87	0.40
1:AA:459:A:H2'	1:AA:460:A:C8	2.56	0.40
1:AA:495:A:C6	1:AA:496:A:N6	2.89	0.40
1:AA:1012:A:N6	1:AA:1018:G:O6	2.54	0.40
1:AA:1054:C:C5	1:AA:1196:A:C8	3.10	0.40
1:AA:1134:G:H3'	1:AA:1135:U:C5	2.57	0.40
2:AB:207:ILE:O	2:AB:211:THR:HG23	2.21	0.40
3:AC:93:ASP:OD1	3:AC:94:ILE:HG13	2.22	0.40
13:AM:85:CYS:HB3	19:AS:74:PHE:CE1	2.56	0.40
17:AQ:25:ILE:O	17:AQ:26:GLU:C	2.64	0.40
18:AR:55:LEU:HA	18:AR:55:LEU:HD12	1.84	0.40
24:AX:8:4SU:H2'	24:AX:13:C:N4	2.36	0.40
24:AX:23:A:C2	24:AX:24:G:C5	3.10	0.40
25:BA:92:U:H2'	25:BA:93:G:O4'	2.22	0.40
25:BA:873:C:H4'	36:BN:64:TRP:CD1	2.57	0.40
25:BA:2552:OMU:H6	25:BA:2552:OMU:O5'	2.22	0.40
25:BA:2813:A:C4	25:BA:2814:A:C8	3.10	0.40
35:BM:77:VAL:HG12	35:BM:78:ARG:H	1.86	0.40
38:BP:7:ARG:HD2	38:BP:97:PHE:CZ	2.57	0.40
50:B2:53:LYS:HE3	50:B2:55:ILE:O	2.22	0.40
58:CC:130:MET:SD	58:CC:134:GLY:HA2	2.61	0.40
58:CC:647:ARG:C	58:CC:649:GLN:H	2.30	0.40
59:CD:421:VAL:O	59:CD:421:VAL:HG23	2.21	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
2	AB	224/241 (93%)	208 (93%)	15 (7%)	1 (0%)	30 60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	AC	207/233 (89%)	194 (94%)	10 (5%)	3 (1%)	9	33
4	AD	203/206 (98%)	193 (95%)	9 (4%)	1 (0%)	24	55
5	AE	154/167 (92%)	143 (93%)	10 (6%)	1 (1%)	21	52
6	AF	102/131 (78%)	95 (93%)	7 (7%)	0	100	100
7	AG	151/156 (97%)	142 (94%)	8 (5%)	1 (1%)	18	49
8	AH	127/130 (98%)	117 (92%)	9 (7%)	1 (1%)	16	45
9	AI	126/130 (97%)	115 (91%)	9 (7%)	2 (2%)	7	31
10	AJ	98/103 (95%)	88 (90%)	7 (7%)	3 (3%)	3	20
11	AK	114/129 (88%)	99 (87%)	14 (12%)	1 (1%)	14	43
12	AL	119/124 (96%)	109 (92%)	8 (7%)	2 (2%)	7	30
13	AM	113/118 (96%)	106 (94%)	6 (5%)	1 (1%)	14	43
14	AN	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
15	AO	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
16	AP	80/82 (98%)	79 (99%)	1 (1%)	0	100	100
17	AQ	77/84 (92%)	70 (91%)	7 (9%)	0	100	100
18	AR	52/75 (69%)	50 (96%)	2 (4%)	0	100	100
19	AS	81/92 (88%)	80 (99%)	1 (1%)	0	100	100
20	AT	84/87 (97%)	84 (100%)	0	0	100	100
21	AU	68/71 (96%)	66 (97%)	1 (2%)	1 (2%)	8	32
27	BC	270/273 (99%)	249 (92%)	18 (7%)	3 (1%)	11	39
28	BD	206/209 (99%)	195 (95%)	10 (5%)	1 (0%)	24	55
29	BE	199/201 (99%)	190 (96%)	9 (4%)	0	100	100
30	BF	176/179 (98%)	162 (92%)	14 (8%)	0	100	100
31	BG	173/177 (98%)	158 (91%)	15 (9%)	0	100	100
32	BH	147/149 (99%)	132 (90%)	14 (10%)	1 (1%)	18	49
33	BK	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
34	BL	121/123 (98%)	115 (95%)	6 (5%)	0	100	100
35	BM	142/144 (99%)	132 (93%)	8 (6%)	2 (1%)	9	33
36	BN	133/136 (98%)	128 (96%)	5 (4%)	0	100	100
37	BO	118/127 (93%)	105 (89%)	13 (11%)	0	100	100
38	BP	115/117 (98%)	104 (90%)	10 (9%)	1 (1%)	14	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	BQ	112/115 (97%)	101 (90%)	11 (10%)	0	100	100
40	BR	115/118 (98%)	111 (96%)	4 (4%)	0	100	100
41	BS	101/103 (98%)	98 (97%)	2 (2%)	1 (1%)	12	40
42	BT	108/110 (98%)	103 (95%)	5 (5%)	0	100	100
43	BU	93/100 (93%)	88 (95%)	5 (5%)	0	100	100
44	BV	101/104 (97%)	96 (95%)	4 (4%)	1 (1%)	12	40
45	BW	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
46	BX	74/85 (87%)	70 (95%)	4 (5%)	0	100	100
47	BY	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
48	BZ	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
49	B1	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
50	B2	54/57 (95%)	48 (89%)	6 (11%)	0	100	100
51	B3	51/55 (93%)	49 (96%)	2 (4%)	0	100	100
52	B4	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
53	B5	62/65 (95%)	57 (92%)	4 (6%)	1 (2%)	7	31
54	B6	36/50 (72%)	35 (97%)	1 (3%)	0	100	100
57	CA	227/329 (69%)	217 (96%)	10 (4%)	0	100	100
57	CB	215/329 (65%)	204 (95%)	10 (5%)	1 (0%)	24	55
58	CC	1316/1342 (98%)	1197 (91%)	110 (8%)	9 (1%)	18	49
59	CD	1327/1407 (94%)	1222 (92%)	95 (7%)	10 (1%)	16	45
All	All	8623/9235 (93%)	8034 (93%)	540 (6%)	49 (1%)	23	52

All (49) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	AI	13	LYS
9	AI	56	ASP
11	AK	93	ARG
12	AL	88	LYS
27	BC	241	GLY
58	CC	165	HIS
59	CD	1159	ILE
2	AB	165	ASP
3	AC	51	SER
10	AJ	57	VAL

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Mol	Chain	Res	Type
21	AU	65	ALA
28	BD	149	ASN
35	BM	36	LYS
38	BP	100	HIS
53	B5	32	ILE
57	CB	155	ALA
58	CC	47	TYR
59	CD	1051	ASP
4	AD	43	ALA
7	AG	130	ASN
32	BH	120	GLY
41	BS	53	PHE
58	CC	258	ASN
58	CC	1177	ARG
59	CD	119	SER
59	CD	121	PRO
59	CD	712	GLN
59	CD	854	ALA
59	CD	1200	GLU
3	AC	14	ILE
12	AL	102	LEU
27	BC	233	GLY
27	BC	253	LYS
35	BM	99	ASN
44	BV	8	ASP
58	CC	282	VAL
58	CC	596	ASP
58	CC	1153	ALA
59	CD	586	GLY
10	AJ	78	GLU
13	AM	49	SER
59	CD	312	ARG
3	AC	60	PRO
10	AJ	58	ASN
58	CC	1223	ARG
5	AE	108	GLY
8	AH	75	ILE
58	CC	1186	VAL
59	CD	500	ILE

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	
2	AB	187/199 (94%)	174 (93%)	13 (7%)	14	41
3	AC	171/190 (90%)	152 (89%)	19 (11%)	6	22
4	AD	172/173 (99%)	153 (89%)	19 (11%)	6	23
5	AE	118/126 (94%)	105 (89%)	13 (11%)	6	23
6	AF	91/112 (81%)	80 (88%)	11 (12%)	5	20
7	AG	126/129 (98%)	107 (85%)	19 (15%)	3	13
8	AH	104/105 (99%)	94 (90%)	10 (10%)	8	29
9	AI	106/107 (99%)	99 (93%)	7 (7%)	15	43
10	AJ	87/90 (97%)	72 (83%)	15 (17%)	2	10
11	AK	89/99 (90%)	87 (98%)	2 (2%)	45	66
12	AL	102/103 (99%)	91 (89%)	11 (11%)	6	23
13	AM	93/96 (97%)	86 (92%)	7 (8%)	12	38
14	AN	83/84 (99%)	77 (93%)	6 (7%)	13	40
15	AO	76/77 (99%)	66 (87%)	10 (13%)	4	17
16	AP	65/65 (100%)	63 (97%)	2 (3%)	35	60
17	AQ	73/78 (94%)	62 (85%)	11 (15%)	3	13
18	AR	47/65 (72%)	44 (94%)	3 (6%)	16	44
19	AS	72/79 (91%)	67 (93%)	5 (7%)	14	41
20	AT	65/66 (98%)	58 (89%)	7 (11%)	6	23
21	AU	60/61 (98%)	58 (97%)	2 (3%)	33	59
27	BC	217/218 (100%)	203 (94%)	14 (6%)	15	43
28	BD	163/163 (100%)	151 (93%)	12 (7%)	13	38
29	BE	165/165 (100%)	149 (90%)	16 (10%)	8	28
30	BF	149/150 (99%)	134 (90%)	15 (10%)	7	26
31	BG	136/138 (99%)	122 (90%)	14 (10%)	7	25
32	BH	114/114 (100%)	102 (90%)	12 (10%)	6	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	BK	116/116 (100%)	106 (91%)	10 (9%)	10	33
34	BL	104/104 (100%)	97 (93%)	7 (7%)	15	42
35	BM	103/103 (100%)	91 (88%)	12 (12%)	5	20
36	BN	108/108 (100%)	103 (95%)	5 (5%)	24	53
37	BO	100/103 (97%)	94 (94%)	6 (6%)	17	46
38	BP	87/87 (100%)	79 (91%)	8 (9%)	8	30
39	BQ	99/100 (99%)	84 (85%)	15 (15%)	3	13
40	BR	89/90 (99%)	84 (94%)	5 (6%)	19	47
41	BS	84/84 (100%)	77 (92%)	7 (8%)	10	34
42	BT	93/93 (100%)	88 (95%)	5 (5%)	20	49
43	BU	82/84 (98%)	73 (89%)	9 (11%)	6	23
44	BV	84/85 (99%)	80 (95%)	4 (5%)	23	52
45	BW	78/78 (100%)	72 (92%)	6 (8%)	12	37
46	BX	58/63 (92%)	56 (97%)	2 (3%)	32	59
47	BY	67/68 (98%)	64 (96%)	3 (4%)	24	53
48	BZ	54/55 (98%)	52 (96%)	2 (4%)	30	58
49	B1	48/49 (98%)	44 (92%)	4 (8%)	10	34
50	B2	47/48 (98%)	43 (92%)	4 (8%)	10	33
51	B3	48/49 (98%)	46 (96%)	2 (4%)	26	55
52	B4	38/38 (100%)	36 (95%)	2 (5%)	20	49
53	B5	51/52 (98%)	51 (100%)	0	100	100
54	B6	34/44 (77%)	34 (100%)	0	100	100
57	CA	197/286 (69%)	193 (98%)	4 (2%)	48	68
57	CB	187/286 (65%)	177 (95%)	10 (5%)	20	49
58	CC	1139/1157 (98%)	1093 (96%)	46 (4%)	28	56
59	CD	1118/1168 (96%)	1094 (98%)	24 (2%)	47	67
All	All	7244/7650 (95%)	6767 (93%)	477 (7%)	17	43

All (477) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AB	5	SER
2	AB	14	VAL

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Mol	Chain	Res	Type
2	AB	44	GLU
2	AB	47	VAL
2	AB	129	LEU
2	AB	132	LYS
2	AB	145	GLU
2	AB	169	GLU
2	AB	188	ASP
2	AB	192	ASP
2	AB	196	VAL
2	AB	199	VAL
2	AB	220	THR
3	AC	3	GLN
3	AC	14	ILE
3	AC	21	THR
3	AC	33	LEU
3	AC	35	SER
3	AC	59	ARG
3	AC	62	LYS
3	AC	66	VAL
3	AC	79	LYS
3	AC	83	ASP
3	AC	134	MET
3	AC	139	GLN
3	AC	154	SER
3	AC	172	ARG
3	AC	175	LEU
3	AC	178	LEU
3	AC	185	ASN
3	AC	196	ILE
3	AC	208	LEU
4	AD	21	LEU
4	AD	34	ILE
4	AD	50	ASP
4	AD	61	VAL
4	AD	88	GLU
4	AD	95	GLU
4	AD	102	VAL
4	AD	104	ARG
4	AD	116	GLN
4	AD	138	SER
4	AD	143	VAL
4	AD	146	ARG

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Mol	Chain	Res	Type
4	AD	147	GLU
4	AD	148	LYS
4	AD	173	VAL
4	AD	179	GLU
4	AD	190	ASP
4	AD	197	GLU
4	AD	206	LYS
5	AE	15	LEU
5	AE	18	VAL
5	AE	39	VAL
5	AE	61	GLN
5	AE	65	GLU
5	AE	71	MET
5	AE	72	ILE
5	AE	74	VAL
5	AE	76	LEU
5	AE	114	VAL
5	AE	123	VAL
5	AE	138	ARG
5	AE	141	ILE
6	AF	24	ARG
6	AF	38	ARG
6	AF	44	ARG
6	AF	45	ARG
6	AF	54	LEU
6	AF	64	VAL
6	AF	71	ILE
6	AF	72	ASP
6	AF	73	GLU
6	AF	84	VAL
6	AF	86	ARG
7	AG	4	ARG
7	AG	6	VAL
7	AG	7	ILE
7	AG	13	LEU
7	AG	17	LYS
7	AG	27	VAL
7	AG	40	GLU
7	AG	58	GLU
7	AG	60	GLU
7	AG	73	VAL
7	AG	78	ARG

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Mol	Chain	Res	Type
7	AG	80	VAL
7	AG	89	VAL
7	AG	90	GLU
7	AG	91	VAL
7	AG	109	ARG
7	AG	123	GLU
7	AG	143	ARG
7	AG	146	GLU
8	AH	25	VAL
8	AH	30	SER
8	AH	51	VAL
8	AH	61	LEU
8	AH	73	GLU
8	AH	77	ARG
8	AH	96	MET
8	AH	103	VAL
8	AH	107	SER
8	AH	121	LEU
9	AI	9	THR
9	AI	22	LYS
9	AI	61	LEU
9	AI	63	LEU
9	AI	84	THR
9	AI	118	LEU
9	AI	123	ARG
10	AJ	7	ARG
10	AJ	16	ARG
10	AJ	17	LEU
10	AJ	18	ILE
10	AJ	24	GLU
10	AJ	27	GLU
10	AJ	36	VAL
10	AJ	37	ARG
10	AJ	44	THR
10	AJ	76	ILE
10	AJ	82	LYS
10	AJ	85	ASP
10	AJ	92	LEU
10	AJ	96	VAL
10	AJ	102	LEU
11	AK	15	GLN
11	AK	76	GLU

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Mol	Chain	Res	Type
12	AL	4	VAL
12	AL	5	ASN
12	AL	10	LYS
12	AL	16	VAL
12	AL	19	SER
12	AL	24	LEU
12	AL	33	VAL
12	AL	64	THR
12	AL	74	LEU
12	AL	79	VAL
12	AL	90	LEU
13	AM	9	ILE
13	AM	16	VAL
13	AM	27	LYS
13	AM	31	LYS
13	AM	89	LEU
13	AM	93	ARG
13	AM	104	THR
14	AN	10	GLU
14	AN	30	ILE
14	AN	46	LEU
14	AN	89	MET
14	AN	92	GLU
14	AN	100	SER
15	AO	11	ILE
15	AO	22	THR
15	AO	39	LEU
15	AO	40	GLN
15	AO	57	LEU
15	AO	61	SER
15	AO	64	ARG
15	AO	72	ARG
15	AO	73	LYS
15	AO	83	GLU
16	AP	21	VAL
16	AP	50	THR
17	AQ	5	ILE
17	AQ	26	GLU
17	AQ	27	ARG
17	AQ	33	ILE
17	AQ	40	ARG
17	AQ	41	THR

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Mol	Chain	Res	Type
17	AQ	42	THR
17	AQ	53	CYS
17	AQ	57	ASP
17	AQ	75	LEU
17	AQ	79	VAL
18	AR	44	ILE
18	AR	55	LEU
18	AR	68	LEU
19	AS	20	GLU
19	AS	31	LEU
19	AS	49	ILE
19	AS	51	VAL
19	AS	58	VAL
20	AT	6	SER
20	AT	25	ARG
20	AT	48	GLN
20	AT	54	MET
20	AT	57	ILE
20	AT	58	VAL
20	AT	83	ILE
21	AU	4	ILE
21	AU	69	ARG
27	BC	3	VAL
27	BC	4	VAL
27	BC	14	ARG
27	BC	54	ILE
27	BC	88	SER
27	BC	94	VAL
27	BC	105	LEU
27	BC	120	VAL
27	BC	125	LYS
27	BC	129	THR
27	BC	130	LEU
27	BC	195	VAL
27	BC	203	ARG
27	BC	250	VAL
28	BD	4	LEU
28	BD	13	ARG
28	BD	17	GLU
28	BD	18	ASP
28	BD	32	ASN
28	BD	43	ASP

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Mol	Chain	Res	Type
28	BD	56	LYS
28	BD	59	ARG
28	BD	89	GLU
28	BD	110	THR
28	BD	129	THR
28	BD	157	LYS
29	BE	2	GLU
29	BE	3	LEU
29	BE	21	ARG
29	BE	40	ARG
29	BE	57	LYS
29	BE	65	THR
29	BE	73	ILE
29	BE	77	ILE
29	BE	88	ARG
29	BE	111	GLU
29	BE	113	VAL
29	BE	119	ILE
29	BE	123	LYS
29	BE	130	LYS
29	BE	152	GLU
29	BE	184	ASP
30	BF	13	VAL
30	BF	47	LYS
30	BF	48	LYS
30	BF	49	LEU
30	BF	56	ASP
30	BF	57	LEU
30	BF	98	GLU
30	BF	115	ARG
30	BF	123	ASP
30	BF	134	GLU
30	BF	136	ILE
30	BF	140	GLU
30	BF	141	ILE
30	BF	164	GLU
30	BF	179	LYS
31	BG	6	LYS
31	BG	11	VAL
31	BG	32	GLU
31	BG	41	VAL
31	BG	84	THR

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Mol	Chain	Res	Type
31	BG	110	SER
31	BG	111	HIS
31	BG	114	ASP
31	BG	125	CYS
31	BG	127	THR
31	BG	155	GLU
31	BG	167	GLU
31	BG	168	VAL
31	BG	173	GLU
32	BH	4	ILE
32	BH	11	ASN
32	BH	12	LEU
32	BH	37	VAL
32	BH	48	GLU
32	BH	60	GLU
32	BH	66	ASN
32	BH	73	ASN
32	BH	94	ILE
32	BH	101	ASP
32	BH	112	LYS
32	BH	144	VAL
33	BK	1	MET
33	BK	30	THR
33	BK	31	GLU
33	BK	35	ARG
33	BK	43	GLU
33	BK	57	LEU
33	BK	108	MET
33	BK	123	LYS
33	BK	129	GLU
33	BK	142	ILE
34	BL	17	ARG
34	BL	35	VAL
34	BL	41	ILE
34	BL	58	LEU
34	BL	67	LYS
34	BL	99	ILE
34	BL	111	LYS
35	BM	30	THR
35	BM	40	SER
35	BM	67	THR
35	BM	70	LYS

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Mol	Chain	Res	Type
35	BM	76	GLU
35	BM	77	VAL
35	BM	78	ARG
35	BM	79	LEU
35	BM	84	LYS
35	BM	115	GLU
35	BM	120	VAL
35	BM	129	LYS
36	BN	16	ARG
36	BN	18	ARG
36	BN	78	LEU
36	BN	110	GLU
36	BN	127	LYS
37	BO	2	ARG
37	BO	13	ASN
37	BO	20	MET
37	BO	51	LEU
37	BO	65	LEU
37	BO	69	ARG
38	BP	13	ARG
38	BP	18	LEU
38	BP	52	SER
38	BP	60	GLU
38	BP	65	THR
38	BP	89	ASP
38	BP	103	VAL
38	BP	116	GLN
39	BQ	26	VAL
39	BQ	27	GLU
39	BQ	38	LYS
39	BQ	46	VAL
39	BQ	68	GLU
39	BQ	80	VAL
39	BQ	86	VAL
39	BQ	88	ARG
39	BQ	96	LYS
39	BQ	104	THR
39	BQ	110	ILE
39	BQ	111	LYS
39	BQ	113	ARG
39	BQ	114	LEU
39	BQ	115	ASN

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Mol	Chain	Res	Type
40	BR	11	ARG
40	BR	13	ARG
40	BR	18	LEU
40	BR	51	ARG
40	BR	91	ASP
41	BS	10	LYS
41	BS	20	VAL
41	BS	39	LEU
41	BS	46	GLU
41	BS	48	LYS
41	BS	54	VAL
41	BS	86	GLN
42	BT	29	VAL
42	BT	41	LYS
42	BT	59	GLU
42	BT	65	ASP
42	BT	110	ARG
43	BU	5	GLU
43	BU	7	LEU
43	BU	16	VAL
43	BU	24	MET
43	BU	29	THR
43	BU	52	GLU
43	BU	67	VAL
43	BU	72	GLN
43	BU	89	GLU
44	BV	9	ASP
44	BV	24	LYS
44	BV	43	LYS
44	BV	88	GLU
45	BW	1	MET
45	BW	20	LEU
45	BW	34	LYS
45	BW	40	ILE
45	BW	45	ASP
45	BW	58	SER
46	BX	55	ARG
46	BX	70	GLU
47	BY	33	LEU
47	BY	52	SER
47	BY	71	LEU
48	BZ	5	GLU

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Mol	Chain	Res	Type
48	BZ	11	VAL
49	B1	4	THR
49	B1	10	THR
49	B1	31	ARG
49	B1	37	GLU
50	B2	9	THR
50	B2	12	LYS
50	B2	28	LEU
50	B2	55	ILE
51	B3	5	ILE
51	B3	50	LYS
52	B4	22	MET
52	B4	44	VAL
57	CA	7	GLU
57	CA	13	LEU
57	CA	74	VAL
57	CA	101	THR
57	CB	41	ASN
57	CB	48	LEU
57	CB	66	HIS
57	CB	76	GLU
57	CB	83	LEU
57	CB	170	ARG
57	CB	174	ASP
57	CB	187	VAL
57	CB	191	ARG
57	CB	214	GLU
58	CC	20	GLN
58	CC	47	TYR
58	CC	65	ASN
58	CC	108	GLU
58	CC	116	ASP
58	CC	150	HIS
58	CC	193	ASN
58	CC	262	TYR
58	CC	292	ILE
58	CC	316	GLU
58	CC	369	MET
58	CC	494	ASN
58	CC	524	ILE
58	CC	529	ARG
58	CC	562	GLU

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Mol	Chain	Res	Type
58	CC	568	ASN
58	CC	569	ILE
58	CC	575	LEU
58	CC	657	THR
58	CC	726	TYR
58	CC	736	VAL
58	CC	745	GLU
58	CC	772	SER
58	CC	800	MET
58	CC	815	SER
58	CC	822	VAL
58	CC	830	THR
58	CC	843	THR
58	CC	856	ASN
58	CC	888	THR
58	CC	1002	LEU
58	CC	1005	GLU
58	CC	1022	LYS
58	CC	1050	VAL
58	CC	1076	ILE
58	CC	1083	GLU
58	CC	1223	ARG
58	CC	1240	ASP
58	CC	1247	SER
58	CC	1250	SER
58	CC	1287	LEU
58	CC	1291	LEU
58	CC	1298	VAL
58	CC	1304	MET
58	CC	1336	ASN
58	CC	1340	GLU
59	CD	157	GLN
59	CD	158	GLN
59	CD	244	VAL
59	CD	255	LEU
59	CD	416	ILE
59	CD	418	GLU
59	CD	488	ASN
59	CD	592	VAL
59	CD	709	ARG
59	CD	802	ASP
59	CD	826	ILE

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Mol	Chain	Res	Type
59	CD	839	VAL
59	CD	856	ILE
59	CD	1041	ILE
59	CD	1046	ILE
59	CD	1141	VAL
59	CD	1144	LEU
59	CD	1163	VAL
59	CD	1165	PHE
59	CD	1167	LYS
59	CD	1195	GLN
59	CD	1237	VAL
59	CD	1261	LEU
59	CD	1334	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (60) such sidechains are listed below:

Mol	Chain	Res	Type
2	AB	120	GLN
2	AB	178	ASN
3	AC	123	GLN
4	AD	74	ASN
4	AD	116	GLN
5	AE	61	GLN
5	AE	82	GLN
5	AE	132	ASN
6	AF	11	HIS
6	AF	17	GLN
7	AG	148	ASN
8	AH	4	GLN
8	AH	76	GLN
9	AI	31	ASN
9	AI	75	GLN
9	AI	110	GLN
10	AJ	58	ASN
10	AJ	99	GLN
11	AK	15	GLN
11	AK	118	HIS
15	AO	38	HIS
15	AO	46	HIS
16	AP	18	GLN
16	AP	59	HIS
18	AR	54	GLN

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Mol	Chain	Res	Type
27	BC	143	ASN
27	BC	197	ASN
29	BE	115	GLN
29	BE	136	GLN
31	BG	20	ASN
31	BG	45	HIS
31	BG	73	ASN
32	BH	2	GLN
32	BH	33	GLN
33	BK	130	HIS
36	BN	3	GLN
37	BO	9	GLN
37	BO	13	ASN
37	BO	31	HIS
38	BP	29	HIS
39	BQ	12	GLN
39	BQ	75	GLN
39	BQ	115	ASN
43	BU	28	ASN
43	BU	70	HIS
45	BW	75	GLN
46	BX	76	ASN
50	B2	6	ASN
52	B4	6	GLN
57	CA	194	GLN
58	CC	60	GLN
58	CC	518	ASN
58	CC	573	ASN
58	CC	686	GLN
58	CC	1008	GLN
58	CC	1111	GLN
59	CD	469	HIS
59	CD	861	ASN
59	CD	929	GLN
59	CD	1227	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1532/1542 (99%)	294 (19%)	32 (2%)
22	AV	28/57 (49%)	12 (42%)	1 (3%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
23	AW	76/77 (98%)	24 (31%)	6 (7%)
24	AX	75/76 (98%)	19 (25%)	0
25	BA	2899/2904 (99%)	565 (19%)	66 (2%)
26	BB	119/120 (99%)	15 (12%)	0
All	All	4729/4776 (99%)	929 (19%)	105 (2%)

All (929) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	4	U
1	AA	5	U
1	AA	9	G
1	AA	19	A
1	AA	22	G
1	AA	29	U
1	AA	32	A
1	AA	39	G
1	AA	47	C
1	AA	48	C
1	AA	50	A
1	AA	51	A
1	AA	52	C
1	AA	54	C
1	AA	69	G
1	AA	70	U
1	AA	71	A
1	AA	74	A
1	AA	76	G
1	AA	80	C
1	AA	83	C
1	AA	84	U
1	AA	86	G
1	AA	87	C
1	AA	89	G
1	AA	90	C
1	AA	94	G
1	AA	95	C
1	AA	96	U
1	AA	108	G
1	AA	121	U
1	AA	122	G
1	AA	131	A

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Mol	Chain	Res	Type
1	AA	141	G
1	AA	144	G
1	AA	148	G
1	AA	149	A
1	AA	160	A
1	AA	164	G
1	AA	173	U
1	AA	181	A
1	AA	182	A
1	AA	183	C
1	AA	184	G
1	AA	196	A
1	AA	197	A
1	AA	198	G
1	AA	208	U
1	AA	209	U
1	AA	210	C
1	AA	211	G
1	AA	212	G
1	AA	216	U
1	AA	226	G
1	AA	245	U
1	AA	247	G
1	AA	251	G
1	AA	258	G
1	AA	262	A
1	AA	266	G
1	AA	267	C
1	AA	279	A
1	AA	289	G
1	AA	306	A
1	AA	316	C
1	AA	321	A
1	AA	328	C
1	AA	329	A
1	AA	332	G
1	AA	340	U
1	AA	347	G
1	AA	352	C
1	AA	354	G
1	AA	367	U
1	AA	372	C

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Mol	Chain	Res	Type
1	AA	373	A
1	AA	376	G
1	AA	384	G
1	AA	388	G
1	AA	389	A
1	AA	392	C
1	AA	397	A
1	AA	406	G
1	AA	412	A
1	AA	413	G
1	AA	414	A
1	AA	421	U
1	AA	422	C
1	AA	424	G
1	AA	429	U
1	AA	446	G
1	AA	451	A
1	AA	457	G
1	AA	458	U
1	AA	460	A
1	AA	467	U
1	AA	468	A
1	AA	469	C
1	AA	479	U
1	AA	480	U
1	AA	481	G
1	AA	482	A
1	AA	484	G
1	AA	485	U
1	AA	486	U
1	AA	495	A
1	AA	511	C
1	AA	516	PSU
1	AA	517	G
1	AA	518	C
1	AA	521	G
1	AA	526	C
1	AA	531	U
1	AA	532	A
1	AA	533	A
1	AA	547	A
1	AA	559	A

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Mol	Chain	Res	Type
1	AA	572	A
1	AA	573	A
1	AA	576	C
1	AA	577	G
1	AA	579	A
1	AA	587	G
1	AA	588	G
1	AA	596	A
1	AA	628	G
1	AA	633	G
1	AA	641	U
1	AA	642	A
1	AA	649	A
1	AA	650	G
1	AA	653	U
1	AA	656	G
1	AA	665	A
1	AA	687	A
1	AA	702	A
1	AA	723	U
1	AA	724	G
1	AA	731	G
1	AA	734	G
1	AA	747	A
1	AA	748	G
1	AA	755	G
1	AA	777	A
1	AA	793	U
1	AA	794	A
1	AA	815	A
1	AA	817	C
1	AA	828	U
1	AA	836	G
1	AA	841	C
1	AA	842	U
1	AA	843	U
1	AA	844	G
1	AA	845	A
1	AA	846	G
1	AA	849	G
1	AA	874	G
1	AA	887	G

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Mol	Chain	Res	Type
1	AA	902	G
1	AA	914	A
1	AA	916	U
1	AA	926	G
1	AA	927	G
1	AA	928	G
1	AA	934	C
1	AA	935	A
1	AA	960	U
1	AA	961	U
1	AA	966	2MG
1	AA	967	5MC
1	AA	969	A
1	AA	972	C
1	AA	975	A
1	AA	976	G
1	AA	977	A
1	AA	991	U
1	AA	992	U
1	AA	993	G
1	AA	996	A
1	AA	999	C
1	AA	1004	A
1	AA	1005	A
1	AA	1009	U
1	AA	1017	U
1	AA	1018	G
1	AA	1020	G
1	AA	1021	A
1	AA	1024	G
1	AA	1026	G
1	AA	1028	C
1	AA	1030	U
1	AA	1031	C
1	AA	1032	G
1	AA	1033	G
1	AA	1037	C
1	AA	1043	G
1	AA	1044	A
1	AA	1046	A
1	AA	1065	U
1	AA	1085	U

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Mol	Chain	Res	Type
1	AA	1086	U
1	AA	1092	A
1	AA	1094	G
1	AA	1095	U
1	AA	1099	G
1	AA	1101	A
1	AA	1133	G
1	AA	1135	U
1	AA	1136	C
1	AA	1139	G
1	AA	1140	C
1	AA	1141	C
1	AA	1142	G
1	AA	1143	G
1	AA	1151	A
1	AA	1152	A
1	AA	1158	C
1	AA	1159	U
1	AA	1167	A
1	AA	1171	A
1	AA	1174	G
1	AA	1175	G
1	AA	1176	A
1	AA	1184	G
1	AA	1187	G
1	AA	1196	A
1	AA	1197	A
1	AA	1211	U
1	AA	1212	U
1	AA	1213	A
1	AA	1214	C
1	AA	1227	A
1	AA	1238	A
1	AA	1239	A
1	AA	1242	G
1	AA	1257	A
1	AA	1260	G
1	AA	1276	G
1	AA	1277	C
1	AA	1278	G
1	AA	1279	G
1	AA	1280	A

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Mol	Chain	Res	Type
1	AA	1285	A
1	AA	1286	U
1	AA	1287	A
1	AA	1299	A
1	AA	1300	G
1	AA	1302	C
1	AA	1305	G
1	AA	1311	A
1	AA	1312	G
1	AA	1317	C
1	AA	1320	C
1	AA	1323	G
1	AA	1329	A
1	AA	1332	A
1	AA	1334	G
1	AA	1338	G
1	AA	1340	A
1	AA	1346	A
1	AA	1353	G
1	AA	1363	A
1	AA	1364	U
1	AA	1370	G
1	AA	1378	C
1	AA	1379	G
1	AA	1381	U
1	AA	1383	C
1	AA	1396	A
1	AA	1397	C
1	AA	1398	A
1	AA	1404	C
1	AA	1408	A
1	AA	1419	G
1	AA	1429	A
1	AA	1441	A
1	AA	1442	G
1	AA	1446	A
1	AA	1447	A
1	AA	1448	C
1	AA	1452	C
1	AA	1453	G
1	AA	1487	G
1	AA	1492	A

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Mol	Chain	Res	Type
1	AA	1493	A
1	AA	1494	G
1	AA	1497	G
1	AA	1503	A
1	AA	1506	U
1	AA	1517	G
1	AA	1519	MA6
1	AA	1529	G
1	AA	1530	G
22	AV	15	C
22	AV	16	A
22	AV	19	U
22	AV	24	A
22	AV	25	U
22	AV	26	A
22	AV	27	C
22	AV	40	A
22	AV	41	C
22	AV	42	G
22	AV	45	G
22	AV	49	G
23	AW	6	G
23	AW	14	A
23	AW	15	G
23	AW	16	C
23	AW	17	C
23	AW	17(A)	U
23	AW	18	G
23	AW	19	G
23	AW	20	H2U
23	AW	21	A
23	AW	22	G
23	AW	25	C
23	AW	31	G
23	AW	47	U
23	AW	48	C
23	AW	49	G
23	AW	57	A
23	AW	59	A
23	AW	60	U
23	AW	61	C
23	AW	69	C

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Mol	Chain	Res	Type
23	AW	74	C
23	AW	75	C
23	AW	76	A
24	AX	8	4SU
24	AX	9	A
24	AX	10	G
24	AX	14	A
24	AX	16	H2U
24	AX	17	C
24	AX	18	G
24	AX	19	G
24	AX	20	H2U
24	AX	21	A
24	AX	22	G
24	AX	23	A
24	AX	33	U
24	AX	47	3AU
24	AX	48	C
24	AX	49	C
24	AX	58	A
24	AX	71	G
24	AX	74	C
25	BA	10	A
25	BA	14	A
25	BA	23	G
25	BA	34	U
25	BA	35	G
25	BA	45	G
25	BA	46	G
25	BA	58	G
25	BA	60	G
25	BA	62	U
25	BA	63	A
25	BA	71	A
25	BA	72	U
25	BA	74	A
25	BA	75	G
25	BA	83	A
25	BA	84	A
25	BA	85	G
25	BA	99	U
25	BA	101	A

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Mol	Chain	Res	Type
25	BA	102	U
25	BA	110	G
25	BA	118	A
25	BA	119	A
25	BA	120	U
25	BA	122	G
25	BA	131	A
25	BA	136	G
25	BA	138	U
25	BA	139	U
25	BA	140	C
25	BA	141	G
25	BA	142	A
25	BA	144	A
25	BA	149	A
25	BA	163	C
25	BA	165	A
25	BA	181	A
25	BA	196	A
25	BA	199	A
25	BA	200	U
25	BA	215	G
25	BA	216	A
25	BA	221	A
25	BA	222	A
25	BA	248	G
25	BA	249	C
25	BA	250	G
25	BA	264	C
25	BA	265	A
25	BA	266	G
25	BA	270	A
25	BA	271	G
25	BA	272	A
25	BA	275	C
25	BA	276	U
25	BA	277	G
25	BA	278	A
25	BA	285	G
25	BA	302	C
25	BA	310	A
25	BA	311	A

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Mol	Chain	Res	Type
25	BA	327	G
25	BA	329	G
25	BA	330	A
25	BA	353	C
25	BA	361	G
25	BA	362	A
25	BA	371	A
25	BA	386	G
25	BA	396	G
25	BA	403	U
25	BA	405	U
25	BA	411	G
25	BA	412	A
25	BA	424	G
25	BA	435	C
25	BA	451	U
25	BA	456	C
25	BA	477	A
25	BA	480	A
25	BA	481	G
25	BA	491	G
25	BA	501	A
25	BA	503	A
25	BA	504	A
25	BA	505	A
25	BA	508	A
25	BA	509	C
25	BA	531	C
25	BA	532	A
25	BA	533	G
25	BA	544	G
25	BA	545	A
25	BA	563	A
25	BA	569	U
25	BA	573	U
25	BA	574	A
25	BA	575	A
25	BA	586	A
25	BA	603	A
25	BA	609	A
25	BA	613	A
25	BA	614	A

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Mol	Chain	Res	Type
25	BA	615	U
25	BA	616	A
25	BA	618	G
25	BA	627	A
25	BA	637	A
25	BA	645	C
25	BA	647	G
25	BA	651	G
25	BA	654	A
25	BA	655	A
25	BA	668	A
25	BA	685	A
25	BA	686	U
25	BA	696	G
25	BA	717	C
25	BA	724	U
25	BA	730	A
25	BA	738	G
25	BA	746	PSU
25	BA	747	5MU
25	BA	757	G
25	BA	764	A
25	BA	765	C
25	BA	775	G
25	BA	776	G
25	BA	777	G
25	BA	782	A
25	BA	783	A
25	BA	784	G
25	BA	785	G
25	BA	788	A
25	BA	789	A
25	BA	790	U
25	BA	805	G
25	BA	812	C
25	BA	827	U
25	BA	828	U
25	BA	846	U
25	BA	858	G
25	BA	859	G
25	BA	869	G
25	BA	878	A

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Mol	Chain	Res	Type
25	BA	881	G
25	BA	883	G
25	BA	884	U
25	BA	885	C
25	BA	887	U
25	BA	888	C
25	BA	890	C
25	BA	891	G
25	BA	892	A
25	BA	893	C
25	BA	895	U
25	BA	896	A
25	BA	897	C
25	BA	899	A
25	BA	910	A
25	BA	914	G
25	BA	915	C
25	BA	931	U
25	BA	933	A
25	BA	940	G
25	BA	941	A
25	BA	946	C
25	BA	953	G
25	BA	961	C
25	BA	974	G
25	BA	983	A
25	BA	984	A
25	BA	985	C
25	BA	996	A
25	BA	999	U
25	BA	1005	C
25	BA	1012	U
25	BA	1013	C
25	BA	1023	U
25	BA	1026	G
25	BA	1033	U
25	BA	1040	A
25	BA	1043	C
25	BA	1045	C
25	BA	1046	A
25	BA	1047	G
25	BA	1050	A

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Mol	Chain	Res	Type
25	BA	1055	G
25	BA	1060	U
25	BA	1061	U
25	BA	1063	G
25	BA	1064	C
25	BA	1065	U
25	BA	1067	A
25	BA	1068	G
25	BA	1069	A
25	BA	1070	A
25	BA	1073	A
25	BA	1074	G
25	BA	1083	U
25	BA	1087	G
25	BA	1088	A
25	BA	1090	A
25	BA	1101	U
25	BA	1107	G
25	BA	1111	A
25	BA	1112	G
25	BA	1119	U
25	BA	1122	G
25	BA	1128	G
25	BA	1129	A
25	BA	1130	U
25	BA	1132	U
25	BA	1134	A
25	BA	1135	C
25	BA	1142	A
25	BA	1170	C
25	BA	1171	G
25	BA	1173	U
25	BA	1174	U
25	BA	1176	U
25	BA	1177	G
25	BA	1178	C
25	BA	1179	G
25	BA	1180	U
25	BA	1186	G
25	BA	1212	G
25	BA	1236	G
25	BA	1238	G

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Mol	Chain	Res	Type
25	BA	1248	G
25	BA	1253	A
25	BA	1256	G
25	BA	1265	A
25	BA	1271	G
25	BA	1272	A
25	BA	1273	U
25	BA	1301	A
25	BA	1302	A
25	BA	1320	C
25	BA	1321	A
25	BA	1345	C
25	BA	1352	U
25	BA	1365	A
25	BA	1368	G
25	BA	1378	A
25	BA	1379	U
25	BA	1380	G
25	BA	1383	A
25	BA	1395	A
25	BA	1405	U
25	BA	1406	U
25	BA	1407	G
25	BA	1408	G
25	BA	1409	U
25	BA	1414	C
25	BA	1416	G
25	BA	1417	C
25	BA	1420	A
25	BA	1428	C
25	BA	1434	A
25	BA	1435	G
25	BA	1452	G
25	BA	1453	A
25	BA	1455	G
25	BA	1458	U
25	BA	1460	U
25	BA	1478	G
25	BA	1482	G
25	BA	1483	G
25	BA	1490	A
25	BA	1491	G

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Mol	Chain	Res	Type
25	BA	1493	C
25	BA	1495	A
25	BA	1497	U
25	BA	1503	A
25	BA	1508	A
25	BA	1509	A
25	BA	1510	G
25	BA	1515	A
25	BA	1529	G
25	BA	1534	U
25	BA	1535	A
25	BA	1536	C
25	BA	1537	G
25	BA	1554	U
25	BA	1558	C
25	BA	1559	U
25	BA	1566	A
25	BA	1569	A
25	BA	1578	U
25	BA	1580	A
25	BA	1581	G
25	BA	1583	A
25	BA	1584	U
25	BA	1585	C
25	BA	1586	A
25	BA	1589	U
25	BA	1590	A
25	BA	1592	C
25	BA	1593	A
25	BA	1594	U
25	BA	1595	C
25	BA	1596	A
25	BA	1597	A
25	BA	1608	A
25	BA	1609	A
25	BA	1610	A
25	BA	1613	G
25	BA	1618	6MZ
25	BA	1630	A
25	BA	1647	U
25	BA	1648	U
25	BA	1649	G

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Mol	Chain	Res	Type
25	BA	1651	G
25	BA	1674	G
25	BA	1677	A
25	BA	1703	G
25	BA	1713	A
25	BA	1714	U
25	BA	1715	G
25	BA	1718	G
25	BA	1729	U
25	BA	1730	C
25	BA	1732	C
25	BA	1738	G
25	BA	1742	U
25	BA	1750	G
25	BA	1755	A
25	BA	1758	U
25	BA	1761	C
25	BA	1764	C
25	BA	1773	A
25	BA	1791	A
25	BA	1800	C
25	BA	1801	A
25	BA	1808	A
25	BA	1811	G
25	BA	1816	C
25	BA	1829	A
25	BA	1833	C
25	BA	1848	A
25	BA	1858	A
25	BA	1859	U
25	BA	1862	G
25	BA	1864	U
25	BA	1869	G
25	BA	1870	C
25	BA	1872	A
25	BA	1905	C
25	BA	1906	G
25	BA	1907	G
25	BA	1912	A
25	BA	1913	A
25	BA	1914	C
25	BA	1917	PSU

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Mol	Chain	Res	Type
25	BA	1918	A
25	BA	1919	A
25	BA	1929	G
25	BA	1930	G
25	BA	1931	U
25	BA	1936	A
25	BA	1938	A
25	BA	1939	5MU
25	BA	1955	U
25	BA	1960	A
25	BA	1965	C
25	BA	1966	A
25	BA	1967	C
25	BA	1970	A
25	BA	1971	U
25	BA	1972	G
25	BA	1987	A
25	BA	1991	U
25	BA	1992	G
25	BA	1993	U
25	BA	1997	C
25	BA	2002	G
25	BA	2022	U
25	BA	2023	C
25	BA	2026	U
25	BA	2031	A
25	BA	2033	A
25	BA	2043	C
25	BA	2051	A
25	BA	2052	A
25	BA	2055	C
25	BA	2056	G
25	BA	2060	A
25	BA	2061	G
25	BA	2062	A
25	BA	2063	C
25	BA	2069	G7M
25	BA	2093	G
25	BA	2097	A
25	BA	2099	U
25	BA	2100	G
25	BA	2101	A

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Mol	Chain	Res	Type
25	BA	2108	A
25	BA	2110	G
25	BA	2111	U
25	BA	2112	G
25	BA	2113	U
25	BA	2115	G
25	BA	2116	G
25	BA	2117	A
25	BA	2118	U
25	BA	2120	G
25	BA	2122	U
25	BA	2124	G
25	BA	2125	G
25	BA	2126	A
25	BA	2127	G
25	BA	2128	G
25	BA	2131	U
25	BA	2132	U
25	BA	2133	G
25	BA	2134	A
25	BA	2139	U
25	BA	2141	G
25	BA	2146	C
25	BA	2147	A
25	BA	2154	A
25	BA	2157	G
25	BA	2158	A
25	BA	2159	G
25	BA	2162	G
25	BA	2163	A
25	BA	2164	C
25	BA	2165	C
25	BA	2169	A
25	BA	2171	A
25	BA	2172	U
25	BA	2178	C
25	BA	2182	U
25	BA	2183	A
25	BA	2185	U
25	BA	2188	U
25	BA	2190	G
25	BA	2197	U

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Mol	Chain	Res	Type
25	BA	2198	A
25	BA	2199	A
25	BA	2203	U
25	BA	2204	G
25	BA	2210	U
25	BA	2211	G
25	BA	2212	A
25	BA	2213	U
25	BA	2225	A
25	BA	2226	C
25	BA	2229	U
25	BA	2238	G
25	BA	2239	G
25	BA	2245	U
25	BA	2246	G
25	BA	2250	G
25	BA	2251	OMG
25	BA	2252	G
25	BA	2268	A
25	BA	2278	A
25	BA	2283	C
25	BA	2287	A
25	BA	2294	G
25	BA	2297	A
25	BA	2305	U
25	BA	2308	G
25	BA	2309	A
25	BA	2315	G
25	BA	2322	A
25	BA	2325	G
25	BA	2333	A
25	BA	2335	A
25	BA	2336	A
25	BA	2347	C
25	BA	2350	C
25	BA	2372	U
25	BA	2376	A
25	BA	2383	G
25	BA	2385	C
25	BA	2402	U
25	BA	2403	C
25	BA	2406	A

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Mol	Chain	Res	Type
25	BA	2410	G
25	BA	2423	U
25	BA	2424	C
25	BA	2425	A
25	BA	2426	A
25	BA	2429	G
25	BA	2430	A
25	BA	2431	U
25	BA	2435	A
25	BA	2441	U
25	BA	2445	2MG
25	BA	2448	A
25	BA	2470	G
25	BA	2474	U
25	BA	2476	A
25	BA	2478	A
25	BA	2491	U
25	BA	2498	OMC
25	BA	2502	G
25	BA	2503	2MA
25	BA	2505	G
25	BA	2512	C
25	BA	2513	A
25	BA	2518	A
25	BA	2520	C
25	BA	2525	G
25	BA	2529	G
25	BA	2535	G
25	BA	2547	A
25	BA	2552	OMU
25	BA	2554	U
25	BA	2566	A
25	BA	2567	G
25	BA	2573	C
25	BA	2574	G
25	BA	2585	U
25	BA	2586	U
25	BA	2601	C
25	BA	2602	A
25	BA	2603	G
25	BA	2609	U
25	BA	2610	C

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Mol	Chain	Res	Type
25	BA	2611	C
25	BA	2613	U
25	BA	2629	U
25	BA	2630	G
25	BA	2663	G
25	BA	2671	G
25	BA	2682	A
25	BA	2689	U
25	BA	2690	U
25	BA	2714	G
25	BA	2716	C
25	BA	2726	A
25	BA	2744	G
25	BA	2748	A
25	BA	2757	A
25	BA	2762	C
25	BA	2777	G
25	BA	2778	A
25	BA	2791	G
25	BA	2797	U
25	BA	2798	U
25	BA	2799	G
25	BA	2800	A
25	BA	2801	G
25	BA	2818	U
25	BA	2820	A
25	BA	2821	A
25	BA	2825	G
25	BA	2849	U
25	BA	2859	G
25	BA	2861	U
25	BA	2867	G
25	BA	2872	A
25	BA	2879	A
25	BA	2880	C
25	BA	2883	A
25	BA	2884	U
25	BA	2885	G
25	BA	2891	U
25	BA	2902	C
25	BA	2903	U
26	BB	9	G

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Mol	Chain	Res	Type
26	BB	13	G
26	BB	16	G
26	BB	17	C
26	BB	35	C
26	BB	36	C
26	BB	45	A
26	BB	56	G
26	BB	64	G
26	BB	66	A
26	BB	88	C
26	BB	89	U
26	BB	90	C
26	BB	99	A
26	BB	109	A

All (105) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	4	U
1	AA	5	U
1	AA	70	U
1	AA	147	G
1	AA	148	G
1	AA	181	A
1	AA	182	A
1	AA	183	C
1	AA	197	A
1	AA	209	U
1	AA	421	U
1	AA	428	G
1	AA	481	G
1	AA	587	G
1	AA	641	U
1	AA	701	U
1	AA	793	U
1	AA	873	A
1	AA	961	U
1	AA	991	U
1	AA	992	U
1	AA	1129	C
1	AA	1196	A
1	AA	1211	U

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Mol	Chain	Res	Type
1	AA	1213	A
1	AA	1214	C
1	AA	1277	C
1	AA	1299	A
1	AA	1319	A
1	AA	1363	A
1	AA	1396	A
1	AA	1447	A
22	AV	39	A
23	AW	15	G
23	AW	16	C
23	AW	18	G
23	AW	19	G
23	AW	47	U
23	AW	60	U
25	BA	33	C
25	BA	62	U
25	BA	71	A
25	BA	101	A
25	BA	137	U
25	BA	138	U
25	BA	140	C
25	BA	196	A
25	BA	199	A
25	BA	271	G
25	BA	310	A
25	BA	404	A
25	BA	503	A
25	BA	685	A
25	BA	764	A
25	BA	776	G
25	BA	784	G
25	BA	883	G
25	BA	884	U
25	BA	892	A
25	BA	984	A
25	BA	1045	C
25	BA	1060	U
25	BA	1064	C
25	BA	1067	A
25	BA	1069	A
25	BA	1109	C

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Mol	Chain	Res	Type
25	BA	1111	A
25	BA	1128	G
25	BA	1173	U
25	BA	1300	G
25	BA	1320	C
25	BA	1344	U
25	BA	1395	A
25	BA	1405	U
25	BA	1407	G
25	BA	1408	G
25	BA	1434	A
25	BA	1490	A
25	BA	1494	A
25	BA	1509	A
25	BA	1596	A
25	BA	1608	A
25	BA	1913	A
25	BA	1918	A
25	BA	2062	A
25	BA	2146	C
25	BA	2162	G
25	BA	2168	G
25	BA	2197	U
25	BA	2198	A
25	BA	2210	U
25	BA	2212	A
25	BA	2225	A
25	BA	2250	G
25	BA	2296	U
25	BA	2308	G
25	BA	2425	A
25	BA	2573	C
25	BA	2585	U
25	BA	2601	C
25	BA	2610	C
25	BA	2756	U
25	BA	2797	U
25	BA	2798	U
25	BA	2873	A

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
1	MA6	AA	1519	1	23,26,27	1.61	6 (26%)	34,38,41	4.10	11 (32%)
24	5MU	AX	54	24	19,22,23	1.37	4 (21%)	28,32,35	2.11	6 (21%)
36	4D4	BN	81	36	9,11,12	2.47	3 (33%)	8,13,15	0.84	0
28	MEQ	BD	150	28	8,9,10	0.94	0	5,10,12	0.97	1 (20%)
25	OMU	BA	2552	25	19,22,23	2.80	6 (31%)	26,31,34	1.85	5 (19%)
25	PSU	BA	2605	25	18,21,22	1.08	2 (11%)	22,30,33	1.88	3 (13%)
25	5MU	BA	747	25	19,22,23	1.41	4 (21%)	28,32,35	2.25	6 (21%)
24	7MG	AX	46	24	20,25,27	3.16	10 (50%)	27,37,42	2.05	7 (25%)
24	H2U	AX	20	24	18,21,22	3.21	5 (27%)	21,30,33	1.90	5 (23%)
24	3AU	AX	47	24	18,21,29	3.41	8 (44%)	26,30,43	1.66	4 (15%)
25	PSU	BA	2457	25	18,21,22	1.06	2 (11%)	22,30,33	2.09	6 (27%)
1	5MC	AA	967	1	18,22,23	3.85	7 (38%)	26,32,35	1.11	2 (7%)
25	5MC	BA	1962	25	18,22,23	3.70	7 (38%)	26,32,35	1.11	1 (3%)
25	6MZ	BA	2030	25	22,25,26	2.65	6 (27%)	30,36,39	2.64	12 (40%)
25	PSU	BA	955	25	18,21,22	1.17	3 (16%)	22,30,33	1.94	5 (22%)
1	MA6	AA	1518	1	23,26,27	1.62	5 (21%)	34,38,41	3.74	11 (32%)
23	PSU	AW	55	23	18,21,22	1.03	1 (5%)	22,30,33	1.96	5 (22%)
25	PSU	BA	2580	25	18,21,22	1.09	2 (11%)	22,30,33	2.27	8 (36%)
25	PSU	BA	2604	25	18,21,22	1.04	2 (11%)	22,30,33	1.90	5 (22%)
25	3TD	BA	1915	25	18,22,23	4.39	10 (55%)	22,32,35	2.04	4 (18%)
1	2MG	AA	966	1	22,25,27	2.48	9 (40%)	33,37,41	2.66	11 (33%)
25	PSU	BA	1917	25	18,21,22	1.00	3 (16%)	22,30,33	1.90	5 (22%)
25	H2U	BA	2449	25	18,21,22	2.74	5 (27%)	21,30,33	2.10	5 (23%)
24	PSU	AX	55	24	18,21,22	1.01	1 (5%)	22,30,33	1.94	5 (22%)
25	2MG	BA	1835	25	23,26,27	2.70	9 (39%)	32,38,41	2.78	10 (31%)
23	H2U	AW	20	23	18,21,22	3.05	5 (27%)	21,30,33	2.03	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
23	OMC	AW	32	23,60	19,22,23	2.90	8 (42%)	26,31,34	0.82	0
23	5MU	AW	54	23	19,22,23	1.38	5 (26%)	28,32,35	2.20	8 (28%)
25	PSU	BA	2504	25,60	18,21,22	1.12	3 (16%)	22,30,33	2.11	6 (27%)
25	PSU	BA	1911	25	18,21,22	1.11	2 (11%)	22,30,33	1.87	4 (18%)
1	PSU	AA	516	1,60	18,21,22	1.03	2 (11%)	22,30,33	2.04	7 (31%)
24	PSU	AX	39	24	18,21,22	1.11	2 (11%)	22,30,33	1.86	4 (18%)
25	1MG	BA	745	25	22,26,27	2.66	6 (27%)	33,39,42	1.87	7 (21%)
25	2MG	BA	2445	25	23,26,27	2.70	8 (34%)	32,38,41	2.83	9 (28%)
1	UR3	AA	1498	1	19,22,23	2.40	6 (31%)	26,32,35	1.29	1 (3%)
25	PSU	BA	746	25,60	18,21,22	1.12	3 (16%)	22,30,33	2.04	6 (27%)
24	4SU	AX	8	24	18,21,22	4.03	8 (44%)	26,30,33	2.20	4 (15%)
25	OMG	BA	2251	23,25	23,26,27	2.45	9 (39%)	33,38,41	1.98	11 (33%)
1	G7M	AA	527	1	23,26,27	2.59	9 (39%)	35,39,42	2.59	12 (34%)
12	D2T	AL	89	12	6,7,10	1.02	0	5,8,13	1.07	0
24	MIA	AX	37	24	21,24,32	1.76	4 (19%)	31,35,47	2.10	9 (29%)
23	4SU	AW	8	23	18,21,22	4.08	8 (44%)	26,30,33	2.21	5 (19%)
25	5MU	BA	1939	25,60	19,22,23	1.45	3 (15%)	28,32,35	2.36	6 (21%)
25	2MA	BA	2503	25,60	22,25,26	3.93	11 (50%)	33,37,40	2.60	10 (30%)
1	5MC	AA	1407	1	18,22,23	3.75	7 (38%)	26,32,35	1.03	1 (3%)
1	2MG	AA	1207	1	22,25,27	2.43	9 (40%)	33,37,41	2.50	11 (33%)
25	G7M	BA	2069	25	23,26,27	2.58	9 (39%)	35,39,42	2.43	11 (31%)
25	OMC	BA	2498	25,60	19,22,23	2.69	7 (36%)	26,31,34	0.84	1 (3%)
1	4OC	AA	1402	1,60	20,23,24	3.29	9 (45%)	26,32,35	1.05	3 (11%)
25	6MZ	BA	1618	25	22,25,26	2.64	5 (22%)	30,36,39	2.43	12 (40%)
24	PSU	AX	32	24	18,21,22	1.03	1 (5%)	22,30,33	1.73	4 (18%)
24	H2U	AX	16	24	18,21,22	2.99	5 (27%)	21,30,33	1.94	5 (23%)
1	2MG	AA	1516	1	23,26,27	2.66	9 (39%)	32,38,41	2.75	11 (34%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MA6	AA	1519	1	-	6/11/29/30	0/3/3/3
24	5MU	AX	54	24	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
36	4D4	BN	81	36	-	7/11/12/14	-
28	MEQ	BD	150	28	-	3/8/9/11	-
25	OMU	BA	2552	25	-	2/9/27/28	0/2/2/2
25	PSU	BA	2605	25	-	0/7/25/26	0/2/2/2
25	5MU	BA	747	25	-	0/7/25/26	0/2/2/2
24	7MG	AX	46	24	-	4/7/34/38	0/3/3/3
24	H2U	AX	20	24	-	5/7/38/39	0/2/2/2
24	3AU	AX	47	24	-	0/7/25/35	0/2/2/2
25	PSU	BA	2457	25	-	0/7/25/26	0/2/2/2
1	5MC	AA	967	1	-	3/7/25/26	0/2/2/2
25	5MC	BA	1962	25	-	0/7/25/26	0/2/2/2
25	6MZ	BA	2030	25	-	2/9/27/28	0/3/3/3
25	PSU	BA	955	25	-	0/7/25/26	0/2/2/2
1	MA6	AA	1518	1	-	3/11/29/30	0/3/3/3
23	PSU	AW	55	23	-	1/7/25/26	0/2/2/2
25	PSU	BA	2580	25	-	0/7/25/26	0/2/2/2
25	PSU	BA	2604	25	-	0/7/25/26	0/2/2/2
25	3TD	BA	1915	25	-	0/7/25/26	0/2/2/2
1	2MG	AA	966	1	-	2/7/25/28	0/3/3/3
25	PSU	BA	1917	25	-	2/7/25/26	0/2/2/2
25	H2U	BA	2449	25	-	0/7/38/39	0/2/2/2
24	PSU	AX	55	24	-	2/7/25/26	0/2/2/2
25	2MG	BA	1835	25	-	0/9/27/28	0/3/3/3
23	H2U	AW	20	23	-	7/7/38/39	0/2/2/2
23	OMC	AW	32	23,60	-	0/9/27/28	0/2/2/2
23	5MU	AW	54	23	-	0/7/25/26	0/2/2/2
25	PSU	BA	2504	25,60	-	0/7/25/26	0/2/2/2
25	PSU	BA	1911	25	-	1/7/25/26	0/2/2/2
1	PSU	AA	516	1,60	-	2/7/25/26	0/2/2/2
24	PSU	AX	39	24	-	0/7/25/26	0/2/2/2
25	1MG	BA	745	25	-	0/7/25/26	0/3/3/3
25	2MG	BA	2445	25	-	2/9/27/28	0/3/3/3
1	UR3	AA	1498	1	-	0/7/25/26	0/2/2/2
25	PSU	BA	746	25,60	-	1/7/25/26	0/2/2/2
24	4SU	AX	8	24	-	0/7/25/26	0/2/2/2
25	OMG	BA	2251	23,25	-	0/9/27/28	0/3/3/3
1	G7M	AA	527	1	-	1/7/25/26	0/3/3/3
12	D2T	AL	89	12	-	1/5/6/14	-
24	MIA	AX	37	24	-	0/7/25/34	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	4SU	AW	8	23	-	0/7/25/26	0/2/2/2
25	5MU	BA	1939	25,60	-	2/7/25/26	0/2/2/2
25	2MA	BA	2503	25,60	-	2/7/25/26	0/3/3/3
1	5MC	AA	1407	1	-	0/7/25/26	0/2/2/2
1	2MG	AA	1207	1	-	2/7/25/28	0/3/3/3
25	G7M	BA	2069	25	-	2/7/25/26	0/3/3/3
25	OMC	BA	2498	25,60	-	2/9/27/28	0/2/2/2
1	4OC	AA	1402	1,60	-	0/9/29/30	0/2/2/2
25	6MZ	BA	1618	25	-	2/9/27/28	0/3/3/3
24	PSU	AX	32	24	-	0/7/25/26	0/2/2/2
24	H2U	AX	16	24	-	1/7/38/39	0/2/2/2
1	2MG	AA	1516	1	-	0/9/27/28	0/3/3/3

All (283) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	BA	2503	2MA	C4-N3	12.22	1.49	1.34
25	BA	1915	3TD	C6-C5	11.44	1.48	1.35
25	BA	1618	6MZ	C6-N6	10.48	1.45	1.34
24	AX	20	H2U	C2-N1	10.34	1.50	1.35
25	BA	2030	6MZ	C6-N6	10.34	1.45	1.34
25	BA	1915	3TD	C2-N1	9.65	1.49	1.37
23	AW	20	H2U	C2-N1	9.55	1.49	1.35
1	AA	967	5MC	C6-C5	9.49	1.50	1.34
1	AA	1407	5MC	C6-C5	9.43	1.50	1.34
24	AX	8	4SU	C4-N3	9.20	1.47	1.37
23	AW	8	4SU	C4-N3	9.20	1.47	1.37
24	AX	16	H2U	C2-N1	9.13	1.48	1.35
25	BA	1962	5MC	C6-C5	9.08	1.49	1.34
25	BA	2449	H2U	C2-N1	7.99	1.47	1.35
25	BA	1835	2MG	C2-N3	7.59	1.46	1.31
25	BA	2445	2MG	C2-N3	7.55	1.46	1.31
24	AX	8	4SU	C2-N1	7.51	1.50	1.38
24	AX	47	3AU	C2-N1	7.51	1.50	1.38
23	AW	8	4SU	C2-N1	7.48	1.50	1.38
25	BA	745	1MG	C2-N3	7.45	1.48	1.34
1	AA	1516	2MG	C2-N3	7.37	1.46	1.31
1	AA	967	5MC	C4-N3	7.15	1.46	1.34
25	BA	1962	5MC	C4-N3	7.10	1.46	1.34
24	AX	47	3AU	C6-C5	7.01	1.51	1.35
25	BA	2503	2MA	C2-N3	6.87	1.46	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	1407	5MC	C4-N3	6.76	1.45	1.34
25	BA	2503	2MA	C6-N1	6.70	1.44	1.35
1	AA	967	5MC	C2-N3	6.56	1.49	1.36
1	AA	1402	4OC	C4-N3	6.55	1.44	1.32
24	AX	47	3AU	C2-N3	6.46	1.49	1.38
25	BA	2552	OMU	C2-N3	6.43	1.49	1.38
1	AA	1407	5MC	C2-N3	6.38	1.49	1.36
24	AX	20	H2U	C2-N3	6.36	1.49	1.38
23	AW	8	4SU	C2-N3	6.34	1.49	1.38
25	BA	2251	OMG	C4-N3	6.32	1.49	1.34
1	AA	1402	4OC	C6-C5	6.31	1.49	1.35
24	AX	16	H2U	C2-N3	6.31	1.49	1.38
25	BA	1962	5MC	C2-N3	6.30	1.49	1.36
23	AW	20	H2U	C2-N3	6.27	1.49	1.38
24	AX	8	4SU	C2-N3	6.25	1.49	1.38
23	AW	32	OMC	C2-N3	6.20	1.48	1.36
25	BA	2069	G7M	C5-N7	-6.08	1.32	1.39
23	AW	8	4SU	C6-C5	6.02	1.49	1.35
1	AA	966	2MG	C2-N3	5.99	1.47	1.33
1	AA	527	G7M	C5-N7	-5.96	1.32	1.39
25	BA	1915	3TD	C6-N1	5.92	1.46	1.36
24	AX	8	4SU	C6-C5	5.90	1.48	1.35
24	AX	37	MIA	C6-N6	5.86	1.48	1.34
23	AW	32	OMC	C6-C5	5.82	1.48	1.35
25	BA	745	1MG	C4-N3	5.80	1.48	1.34
1	AA	1498	UR3	C6-C5	5.77	1.48	1.35
24	AX	46	7MG	C4-N3	5.75	1.47	1.34
25	BA	2552	OMU	C6-C5	5.74	1.48	1.35
24	AX	46	7MG	C2-N3	5.73	1.47	1.33
25	BA	2069	G7M	C4-N3	5.71	1.47	1.34
24	AX	8	4SU	C4-S4	-5.71	1.57	1.68
25	BA	2449	H2U	C2-N3	5.68	1.48	1.38
36	BN	81	4D4	CZ-NE	5.66	1.44	1.33
1	AA	1207	2MG	C2-N3	5.65	1.46	1.33
1	AA	527	G7M	C4-N3	5.57	1.47	1.34
25	BA	2498	OMC	C2-N3	5.56	1.47	1.36
23	AW	8	4SU	C4-S4	-5.50	1.58	1.68
23	AW	8	4SU	C5-C4	5.49	1.49	1.42
25	BA	2498	OMC	C6-C5	5.49	1.47	1.35
1	AA	1498	UR3	C2-N1	5.48	1.46	1.38
1	AA	1402	4OC	C2-N3	5.46	1.47	1.36
25	BA	1915	3TD	C1'-C5	-5.42	1.37	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	BA	2503	2MA	C2-N1	5.42	1.43	1.34
1	AA	966	2MG	C4-N3	5.36	1.47	1.34
1	AA	967	5MC	C4-N4	5.31	1.47	1.34
25	BA	1962	5MC	C4-N4	5.31	1.47	1.34
1	AA	1402	4OC	O2-C2	-5.22	1.14	1.23
24	AX	46	7MG	C4-N9	5.21	1.43	1.37
1	AA	1407	5MC	C4-N4	5.16	1.47	1.34
24	AX	47	3AU	C4-N3	5.09	1.47	1.38
25	BA	2251	OMG	C2-N2	5.07	1.46	1.34
1	AA	1207	2MG	C4-N3	5.07	1.46	1.34
25	BA	1835	2MG	C4-N3	5.06	1.46	1.34
25	BA	745	1MG	C2-N2	4.96	1.43	1.34
25	BA	2251	OMG	C2-N3	4.91	1.45	1.33
24	AX	8	4SU	C5-C4	4.90	1.48	1.42
24	AX	16	H2U	C4-N3	4.89	1.45	1.37
25	BA	2552	OMU	C2-N1	4.88	1.46	1.38
23	AW	32	OMC	C4-N3	4.87	1.44	1.34
1	AA	967	5MC	C6-N1	4.86	1.46	1.38
25	BA	2445	2MG	C4-N3	4.82	1.45	1.34
24	AX	20	H2U	C4-N3	4.82	1.45	1.37
1	AA	1402	4OC	C4-N4	4.80	1.45	1.35
1	AA	527	G7M	C2-N3	4.77	1.44	1.33
1	AA	1516	2MG	C4-N3	4.76	1.45	1.34
1	AA	1407	5MC	C6-N1	4.73	1.46	1.38
23	AW	32	OMC	C4-N4	4.72	1.45	1.33
23	AW	20	H2U	C4-N3	4.72	1.45	1.37
24	AX	46	7MG	C2-N2	4.66	1.45	1.34
25	BA	2069	G7M	C2-N3	4.61	1.44	1.33
25	BA	1915	3TD	C2-N3	4.61	1.48	1.38
1	AA	967	5MC	C2-N1	4.58	1.49	1.40
1	AA	527	G7M	C2-N2	4.52	1.44	1.34
25	BA	2498	OMC	C4-N4	4.51	1.44	1.33
25	BA	1962	5MC	C6-N1	4.51	1.45	1.38
25	BA	2498	OMC	C4-N3	4.40	1.43	1.34
25	BA	2069	G7M	C2-N2	4.33	1.44	1.34
25	BA	1835	2MG	C2-N2	4.28	1.42	1.33
25	BA	2503	2MA	C5-C6	4.26	1.52	1.41
1	AA	1407	5MC	C2-N1	4.25	1.49	1.40
1	AA	1402	4OC	C5-C4	4.17	1.49	1.40
25	BA	2449	H2U	C4-N3	4.17	1.44	1.37
1	AA	1516	2MG	C2-N2	4.15	1.42	1.33
24	AX	46	7MG	C5-C4	4.15	1.43	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AW	32	OMC	C2-N1	4.13	1.49	1.40
1	AA	966	2MG	C2-N2	4.09	1.43	1.34
24	AX	46	7MG	C2-N1	4.09	1.47	1.37
25	BA	2445	2MG	C2-N2	4.07	1.42	1.33
24	AX	46	7MG	C5-C6	4.05	1.52	1.42
25	BA	2552	OMU	O4-C4	-4.05	1.16	1.24
1	AA	1498	UR3	C2-N3	4.02	1.46	1.39
25	BA	2445	2MG	C5-N7	-4.00	1.31	1.39
25	BA	2445	2MG	O6-C6	-3.99	1.16	1.23
1	AA	1207	2MG	C2-N2	3.93	1.43	1.34
25	BA	745	1MG	C5-N7	-3.92	1.31	1.39
1	AA	1207	2MG	O6-C6	-3.92	1.16	1.23
25	BA	1835	2MG	O6-C6	-3.91	1.16	1.23
25	BA	1962	5MC	C2-N1	3.86	1.48	1.40
1	AA	966	2MG	O6-C6	-3.79	1.16	1.23
1	AA	1516	2MG	O6-C6	-3.77	1.16	1.23
1	AA	1402	4OC	C2-N1	3.75	1.48	1.40
1	AA	1516	2MG	C5-N7	-3.72	1.31	1.39
1	AA	1516	2MG	C2-N1	3.70	1.42	1.36
25	BA	2445	2MG	C2-N1	3.65	1.42	1.36
25	BA	2552	OMU	C4-N3	3.63	1.45	1.38
1	AA	1518	MA6	C6-N6	3.54	1.47	1.36
24	AX	46	7MG	O6-C6	-3.52	1.16	1.23
25	BA	2498	OMC	C2-N1	3.52	1.47	1.40
25	BA	2503	2MA	C8-N7	3.50	1.38	1.31
25	BA	1835	2MG	C2-N1	3.49	1.42	1.36
25	BA	1835	2MG	C5-N7	-3.48	1.32	1.39
1	AA	1402	4OC	CM4-N4	3.48	1.51	1.45
25	BA	2030	6MZ	C5-C4	-3.46	1.32	1.39
1	AA	1519	MA6	C5-C4	-3.44	1.32	1.39
25	BA	1939	5MU	C4-N3	-3.42	1.32	1.38
25	BA	2251	OMG	C5-N7	-3.40	1.32	1.39
25	BA	2552	OMU	O2-C2	-3.39	1.16	1.23
1	AA	1518	MA6	C5-C4	-3.38	1.32	1.39
24	AX	46	7MG	C6-N1	3.37	1.45	1.38
24	AX	39	PSU	C6-C5	3.33	1.39	1.35
1	AA	966	2MG	C5-N7	-3.33	1.32	1.39
1	AA	1519	MA6	C6-N6	3.32	1.46	1.36
25	BA	747	5MU	C4-N3	-3.32	1.32	1.38
24	AX	47	3AU	C6-N1	3.32	1.46	1.38
25	BA	1939	5MU	C6-N1	-3.29	1.32	1.38
23	AW	8	4SU	O2-C2	-3.29	1.17	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	1207	2MG	C5-N7	-3.29	1.32	1.39
25	BA	1618	6MZ	C5-C4	-3.24	1.33	1.39
36	BN	81	4D4	CZ-NH2	3.23	1.45	1.32
25	BA	2498	OMC	O2-C2	-3.23	1.17	1.23
1	AA	527	G7M	C5-C6	3.21	1.52	1.43
25	BA	2503	2MA	C6-N6	-3.19	1.26	1.34
24	AX	8	4SU	O2-C2	-3.16	1.17	1.23
23	AW	8	4SU	C6-N1	3.13	1.45	1.38
25	BA	2069	G7M	C5-C6	3.07	1.51	1.43
25	BA	1911	PSU	C6-C5	3.03	1.38	1.35
24	AX	46	7MG	C5-N7	3.02	1.44	1.35
24	AX	32	PSU	C6-C5	3.00	1.38	1.35
25	BA	1939	5MU	C2-N3	-2.99	1.32	1.38
24	AX	8	4SU	C6-N1	2.98	1.45	1.38
25	BA	745	1MG	C5-C6	2.98	1.53	1.45
25	BA	2503	2MA	C5-N7	-2.97	1.33	1.39
24	AX	47	3AU	O4-C4	-2.96	1.18	1.24
25	BA	747	5MU	C6-N1	-2.95	1.33	1.38
23	AW	32	OMC	O2-C2	-2.94	1.18	1.23
1	AA	1518	MA6	C8-N9	-2.94	1.32	1.37
25	BA	1618	6MZ	C5-N7	-2.93	1.33	1.39
1	AA	1519	MA6	C8-N9	-2.92	1.32	1.37
25	BA	1915	3TD	O2-C2	-2.91	1.17	1.23
1	AA	527	G7M	O6-C6	-2.90	1.18	1.23
23	AW	55	PSU	C6-C5	2.90	1.38	1.35
1	AA	1516	2MG	C4-N9	-2.89	1.30	1.38
24	AX	47	3AU	C5-C4	2.89	1.50	1.43
25	BA	2030	6MZ	C5-N7	-2.88	1.33	1.39
23	AW	32	OMC	C6-N1	2.87	1.44	1.38
25	BA	2069	G7M	O6-C6	-2.86	1.18	1.23
25	BA	2445	2MG	C4-N9	-2.85	1.30	1.38
1	AA	527	G7M	C4-N9	-2.84	1.30	1.38
25	BA	2069	G7M	C4-N9	-2.84	1.30	1.38
25	BA	1915	3TD	C4-N3	2.82	1.46	1.40
24	AX	37	MIA	C4-N9	-2.80	1.31	1.37
25	BA	2498	OMC	C6-N1	2.80	1.44	1.38
1	AA	1498	UR3	O2-C2	-2.78	1.17	1.22
24	AX	54	5MU	C4-N3	-2.77	1.33	1.38
25	BA	1962	5MC	O2-C2	-2.77	1.18	1.23
25	BA	1835	2MG	C4-N9	-2.75	1.30	1.38
25	BA	1915	3TD	O4-C4	-2.75	1.17	1.23
24	AX	55	PSU	C6-C5	2.74	1.38	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	BA	2030	6MZ	C8-N9	-2.73	1.32	1.37
25	BA	2449	H2U	O2-C2	-2.73	1.18	1.23
1	AA	1518	MA6	C10-N6	2.71	1.51	1.45
25	BA	746	PSU	O4'-C1'	-2.71	1.40	1.43
25	BA	747	5MU	C2-N3	-2.68	1.33	1.38
24	AX	37	MIA	C5-N7	-2.67	1.34	1.39
1	AA	1402	4OC	C6-N1	2.66	1.44	1.38
1	AA	1207	2MG	C4-N9	-2.66	1.31	1.38
24	AX	37	MIA	C5-C4	-2.66	1.34	1.39
25	BA	1915	3TD	C10-N3	2.65	1.51	1.47
25	BA	2251	OMG	O6-C6	-2.61	1.18	1.23
1	AA	966	2MG	C4-N9	-2.59	1.31	1.38
23	AW	54	5MU	C4-N3	-2.59	1.34	1.38
25	BA	2503	2MA	C8-N9	-2.57	1.32	1.37
1	AA	1519	MA6	C10-N6	2.56	1.51	1.45
25	BA	1618	6MZ	C8-N9	-2.56	1.32	1.37
1	AA	1207	2MG	C6-N1	2.53	1.43	1.38
25	BA	2030	6MZ	C6-N1	-2.53	1.31	1.35
1	AA	1407	5MC	O2-C2	-2.53	1.19	1.23
23	AW	20	H2U	O2-C2	-2.53	1.18	1.23
1	AA	967	5MC	O2-C2	-2.51	1.19	1.23
24	AX	54	5MU	C6-N1	-2.51	1.33	1.38
1	AA	1519	MA6	C5-N7	-2.50	1.34	1.39
24	AX	47	3AU	O2-C2	-2.50	1.18	1.23
25	BA	1835	2MG	C6-N1	2.50	1.43	1.38
1	AA	1518	MA6	C5-N7	-2.50	1.34	1.39
25	BA	2504	PSU	C6-C5	2.49	1.38	1.35
1	AA	966	2MG	C6-N1	2.49	1.43	1.38
1	AA	516	PSU	C6-C5	2.48	1.38	1.35
23	AW	54	5MU	C6-N1	-2.48	1.33	1.38
1	AA	1498	UR3	O4-C4	-2.48	1.18	1.23
1	AA	1516	2MG	C6-N1	2.47	1.43	1.38
1	AA	1498	UR3	C6-N1	2.46	1.43	1.38
23	AW	54	5MU	C4-C5	2.46	1.48	1.44
24	AX	54	5MU	C6-C5	2.45	1.38	1.34
25	BA	1618	6MZ	C6-N1	-2.42	1.31	1.35
25	BA	2449	H2U	O4-C4	-2.42	1.18	1.23
25	BA	2251	OMG	C6-N1	2.40	1.43	1.38
25	BA	955	PSU	C4-C5	-2.39	1.37	1.44
25	BA	2251	OMG	C4-N9	-2.37	1.31	1.38
36	BN	81	4D4	CZ-NH1	-2.36	1.25	1.34
1	AA	527	G7M	C2-N1	2.35	1.43	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	BA	2251	OMG	C2-N1	2.35	1.43	1.37
25	BA	2503	2MA	CM2-C2	2.34	1.56	1.49
24	AX	20	H2U	O2-C2	-2.34	1.18	1.23
25	BA	955	PSU	C6-C5	2.32	1.38	1.35
25	BA	2445	2MG	C6-N1	2.31	1.43	1.38
25	BA	2504	PSU	O4'-C1'	-2.29	1.40	1.43
25	BA	2580	PSU	C4-C5	-2.28	1.37	1.44
25	BA	2605	PSU	C6-C5	2.28	1.38	1.35
23	AW	54	5MU	C6-C5	2.28	1.38	1.34
24	AX	16	H2U	O2-C2	-2.27	1.18	1.23
1	AA	966	2MG	C5-C6	2.27	1.52	1.44
24	AX	20	H2U	O4-C4	-2.27	1.18	1.23
25	BA	2604	PSU	C4-C5	-2.27	1.37	1.44
25	BA	2069	G7M	C2-N1	2.26	1.43	1.37
1	AA	1207	2MG	C5-C6	2.24	1.52	1.44
24	AX	54	5MU	C2-N3	-2.24	1.34	1.38
25	BA	745	1MG	C4-N9	-2.23	1.32	1.38
25	BA	1915	3TD	O4'-C1'	-2.22	1.40	1.43
23	AW	32	OMC	C5-C4	2.22	1.48	1.42
1	AA	1516	2MG	C5-C6	2.22	1.52	1.44
25	BA	746	PSU	C4-C5	-2.22	1.37	1.44
25	BA	2580	PSU	C6-C5	2.22	1.37	1.35
23	AW	54	5MU	C2-N3	-2.21	1.34	1.38
25	BA	2604	PSU	C6-C5	2.20	1.37	1.35
24	AX	16	H2U	O4-C4	-2.20	1.18	1.23
25	BA	1917	PSU	O4'-C1'	-2.18	1.40	1.43
1	AA	1519	MA6	C8-N7	2.17	1.35	1.31
25	BA	1917	PSU	C4-C5	-2.17	1.38	1.44
25	BA	2251	OMG	C5-C6	2.15	1.52	1.44
23	AW	20	H2U	O4-C4	-2.15	1.18	1.23
25	BA	2504	PSU	C4-C5	-2.14	1.38	1.44
25	BA	2457	PSU	C6-C5	2.14	1.37	1.35
25	BA	2457	PSU	C4-C5	-2.13	1.38	1.44
25	BA	1911	PSU	O4'-C1'	-2.11	1.40	1.43
25	BA	1917	PSU	C6-C5	2.10	1.37	1.35
1	AA	516	PSU	C4-C5	-2.10	1.38	1.44
25	BA	746	PSU	C6-C5	2.09	1.37	1.35
1	AA	1207	2MG	C2-N1	2.07	1.42	1.37
25	BA	2605	PSU	C4-C5	-2.07	1.38	1.44
25	BA	1835	2MG	C5-C6	2.07	1.52	1.44
1	AA	966	2MG	C2-N1	2.05	1.42	1.37
25	BA	2069	G7M	C6-N1	2.03	1.42	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	BA	955	PSU	C2'-C1'	-2.02	1.51	1.53
1	AA	527	G7M	C6-N1	2.02	1.42	1.38
24	AX	39	PSU	C4-C5	-2.02	1.38	1.44
25	BA	747	5MU	C6-C5	2.02	1.37	1.34
25	BA	2503	2MA	C5-C4	-2.01	1.35	1.39
25	BA	2030	6MZ	C4-N9	-2.00	1.33	1.37

All (315) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1519	MA6	N1-C6-N6	-17.90	97.51	117.08
1	AA	1518	MA6	N1-C6-N6	-15.65	99.97	117.08
1	AA	1519	MA6	C5-C6-N6	9.62	142.06	125.30
1	AA	966	2MG	C1'-N9-C8	-8.39	102.82	126.70
1	AA	1518	MA6	C5-C6-N6	8.34	139.82	125.30
25	BA	2445	2MG	C1'-N9-C8	-8.10	103.63	126.70
25	BA	1835	2MG	C1'-N9-C8	-7.92	104.15	126.70
23	AW	8	4SU	C4-N3-C2	-7.77	119.79	127.34
24	AX	8	4SU	C4-N3-C2	-7.50	120.05	127.34
25	BA	2503	2MA	C1'-N9-C8	-7.47	110.27	127.14
25	BA	2445	2MG	C1'-N9-C4	7.43	148.56	126.50
1	AA	1207	2MG	C1'-N9-C8	-7.37	105.71	126.70
1	AA	1516	2MG	C1'-N9-C8	-7.37	105.71	126.70
25	BA	2030	6MZ	C9-N6-C6	-7.37	116.52	122.87
1	AA	966	2MG	C1'-N9-C4	7.26	148.07	126.50
25	BA	2449	H2U	C4-N3-C2	-7.12	119.89	125.79
25	BA	1835	2MG	C1'-N9-C4	7.01	147.33	126.50
23	AW	20	H2U	C4-N3-C2	-7.00	119.98	125.79
1	AA	1516	2MG	C1'-N9-C4	6.90	146.99	126.50
24	AX	46	7MG	C5-C4-N3	-6.80	120.78	127.80
24	AX	16	H2U	C4-N3-C2	-6.74	120.20	125.79
24	AX	20	H2U	C4-N3-C2	-6.50	120.40	125.79
1	AA	1207	2MG	C1'-N9-C4	6.47	145.73	126.50
1	AA	527	G7M	C1'-N9-C8	-6.29	105.49	126.74
25	BA	1915	3TD	N1-C2-N3	6.22	121.05	116.14
1	AA	527	G7M	C1'-N9-C4	6.12	144.69	126.50
25	BA	2069	G7M	C1'-N9-C8	-6.01	106.46	126.74
25	BA	1835	2MG	C2-N3-C4	5.96	119.43	112.04
25	BA	1939	5MU	C4-N3-C2	-5.94	119.66	127.35
24	AX	8	4SU	C5-C4-N3	5.81	120.08	114.69
25	BA	2552	OMU	C4-N3-C2	-5.80	118.92	126.58
25	BA	747	5MU	C4-N3-C2	-5.80	119.84	127.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1516	2MG	C2-N3-C4	5.78	119.21	112.04
25	BA	2069	G7M	C1'-N9-C4	5.73	143.52	126.50
1	AA	1519	MA6	N1-C2-N3	-5.68	119.72	128.60
1	AA	527	G7M	CN7-N7-C5	5.66	133.80	126.77
25	BA	2030	6MZ	N1-C2-N3	-5.65	119.76	128.60
25	BA	2503	2MA	N9-C8-N7	-5.63	106.21	113.91
25	BA	2445	2MG	C2-N3-C4	5.59	118.97	112.04
25	BA	2503	2MA	C4-N9-C1'	5.57	139.85	126.59
25	BA	745	1MG	C5-C4-N3	-5.52	119.50	128.46
23	AW	8	4SU	C5-C4-N3	5.48	119.77	114.69
1	AA	1518	MA6	C5-C4-N3	-5.48	119.61	126.75
25	BA	1618	6MZ	N1-C2-N3	-5.44	120.09	128.60
24	AX	37	MIA	N3-C2-N1	-5.43	120.11	128.60
25	BA	1939	5MU	N3-C2-N1	5.42	122.09	114.89
1	AA	1519	MA6	C5-C4-N3	-5.38	119.73	126.75
25	BA	1618	6MZ	C9-N6-C6	-5.34	118.27	122.87
24	AX	54	5MU	C4-N3-C2	-5.31	120.47	127.35
25	BA	2503	2MA	C5-C4-N3	-5.30	121.23	127.19
25	BA	747	5MU	N3-C2-N1	5.29	121.92	114.89
23	AW	54	5MU	C4-N3-C2	-5.28	120.51	127.35
25	BA	1618	6MZ	C5-C4-N3	-5.27	119.88	126.75
25	BA	2457	PSU	C4-N3-C2	-5.23	118.81	126.34
25	BA	2504	PSU	N1-C2-N3	5.23	121.05	115.13
25	BA	2580	PSU	N1-C2-N3	5.17	120.99	115.13
1	AA	1518	MA6	N1-C2-N3	-5.15	120.54	128.60
25	BA	2580	PSU	C4-N3-C2	-5.14	118.94	126.34
24	AX	54	5MU	N3-C2-N1	5.09	121.65	114.89
25	BA	2605	PSU	C4-N3-C2	-5.06	119.06	126.34
25	BA	2069	G7M	CN7-N7-C5	5.05	133.05	126.77
24	AX	55	PSU	C4-N3-C2	-5.02	119.10	126.34
25	BA	955	PSU	C4-N3-C2	-4.99	119.14	126.34
25	BA	2504	PSU	C4-N3-C2	-4.99	119.15	126.34
25	BA	2030	6MZ	N9-C8-N7	-4.99	107.09	113.91
1	AA	1516	2MG	C2-N1-C6	-4.98	118.75	124.48
24	AX	47	3AU	C4-N3-C2	-4.97	120.02	126.58
23	AW	54	5MU	C5-C4-N3	4.94	119.53	115.31
24	AX	37	MIA	C5-C4-N3	-4.94	120.30	126.75
25	BA	2030	6MZ	C5-C4-N3	-4.94	120.31	126.75
25	BA	2445	2MG	C2-N1-C6	-4.93	118.81	124.48
25	BA	2604	PSU	C4-N3-C2	-4.93	119.24	126.34
25	BA	747	5MU	C5-C4-N3	4.89	119.49	115.31
25	BA	1939	5MU	C5-C4-N3	4.88	119.47	115.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	527	G7M	CN7-N7-C8	-4.87	117.32	124.84
25	BA	955	PSU	N1-C2-N3	4.85	120.62	115.13
1	AA	1498	UR3	C4-N3-C2	-4.84	120.01	124.56
25	BA	2457	PSU	N1-C2-N3	4.82	120.59	115.13
24	AX	55	PSU	N1-C2-N3	4.78	120.54	115.13
1	AA	516	PSU	C4-N3-C2	-4.72	119.54	126.34
25	BA	1911	PSU	N1-C2-N3	4.72	120.47	115.13
24	AX	39	PSU	N1-C2-N3	4.71	120.47	115.13
24	AX	37	MIA	N9-C8-N7	-4.71	107.47	113.91
25	BA	1939	5MU	C5-C6-N1	-4.70	118.50	123.34
23	AW	55	PSU	C4-N3-C2	-4.68	119.60	126.34
25	BA	2604	PSU	N1-C2-N3	4.65	120.40	115.13
25	BA	1911	PSU	C4-N3-C2	-4.65	119.64	126.34
25	BA	1917	PSU	N1-C2-N3	4.63	120.37	115.13
25	BA	1917	PSU	C4-N3-C2	-4.62	119.68	126.34
24	AX	39	PSU	C4-N3-C2	-4.61	119.70	126.34
25	BA	746	PSU	C4-N3-C2	-4.60	119.71	126.34
1	AA	1518	MA6	N9-C8-N7	-4.53	107.71	113.91
25	BA	1618	6MZ	N9-C8-N7	-4.53	107.71	113.91
25	BA	2605	PSU	N1-C2-N3	4.52	120.25	115.13
24	AX	32	PSU	C4-N3-C2	-4.50	119.85	126.34
23	AW	54	5MU	N3-C2-N1	4.48	120.84	114.89
25	BA	746	PSU	N1-C2-N3	4.46	120.19	115.13
24	AX	54	5MU	C5-C4-N3	4.42	119.08	115.31
25	BA	747	5MU	C5-C6-N1	-4.38	118.83	123.34
1	AA	1519	MA6	N9-C8-N7	-4.37	107.94	113.91
1	AA	1518	MA6	C4-C5-C6	4.34	120.74	115.88
25	BA	2069	G7M	CN7-N7-C8	-4.33	118.15	124.84
23	AW	55	PSU	N1-C2-N3	4.32	120.03	115.13
25	BA	2251	OMG	C1'-N9-C8	-4.30	114.44	126.70
1	AA	966	2MG	C5-C4-N3	-4.29	121.51	128.46
25	BA	1835	2MG	C2-N1-C6	-4.29	119.55	124.48
25	BA	1939	5MU	O4-C4-C5	-4.26	119.96	124.90
24	AX	54	5MU	O4-C4-C5	-4.26	119.96	124.90
25	BA	1915	3TD	C4-N3-C2	-4.25	120.00	124.61
25	BA	2251	OMG	C5-C4-N3	-4.23	121.59	128.46
1	AA	527	G7M	C2-N3-C4	4.23	119.84	112.30
1	AA	1207	2MG	C2-N3-C4	4.23	119.83	112.30
25	BA	2445	2MG	C5-C4-N3	-4.22	121.62	128.46
24	AX	32	PSU	N1-C2-N3	4.20	119.89	115.13
24	AX	46	7MG	C2-N3-C4	4.20	119.78	112.30
1	AA	1516	2MG	C5-C4-N3	-4.11	121.80	128.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	1962	5MC	C5-C6-N1	-4.11	119.11	123.34
1	AA	1207	2MG	C5-C4-N3	-4.09	121.83	128.46
1	AA	966	2MG	C2-N3-C4	4.08	119.56	112.30
1	AA	516	PSU	N1-C2-N3	4.08	119.75	115.13
1	AA	527	G7M	C5-C6-N1	4.07	120.29	111.79
25	BA	1835	2MG	C5-C4-N3	-4.04	121.90	128.46
25	BA	1939	5MU	O2-C2-N1	-4.01	117.46	122.79
25	BA	2552	OMU	N3-C2-N1	3.99	120.19	114.89
23	AW	8	4SU	N3-C2-N1	3.91	120.08	114.89
25	BA	2069	G7M	C2-N3-C4	3.89	119.23	112.30
25	BA	2251	OMG	N9-C8-N7	-3.88	106.08	113.39
24	AX	47	3AU	N3-C2-N1	3.87	120.03	114.89
25	BA	745	1MG	N9-C4-N3	3.87	133.71	125.94
24	AX	8	4SU	C5-C4-S4	-3.87	119.48	124.47
25	BA	2069	G7M	C5-C6-N1	3.87	119.86	111.79
25	BA	2251	OMG	C2-N3-C4	3.84	119.14	112.30
1	AA	1516	2MG	CM2-N2-C2	-3.83	115.39	123.86
23	AW	54	5MU	O4-C4-C5	-3.83	120.46	124.90
25	BA	2503	2MA	C4-N9-C8	3.82	109.86	105.73
23	AW	54	5MU	C5-C6-N1	-3.81	119.42	123.34
25	BA	1915	3TD	C6-C5-C4	3.80	120.85	118.22
25	BA	1618	6MZ	C4-C5-C6	3.76	119.72	116.81
1	AA	1518	MA6	N3-C4-N9	3.70	133.18	127.08
24	AX	54	5MU	C5-C6-N1	-3.70	119.54	123.34
1	AA	1519	MA6	C4-C5-C6	3.68	120.00	115.88
25	BA	747	5MU	O4-C4-C5	-3.68	120.64	124.90
25	BA	2552	OMU	C5-C4-N3	3.65	120.30	114.84
25	BA	2069	G7M	O6-C6-C5	-3.65	119.83	128.06
1	AA	1519	MA6	C2-N3-C4	3.65	120.37	111.75
25	BA	2030	6MZ	C2-N3-C4	3.64	120.34	111.75
1	AA	527	G7M	O6-C6-C5	-3.63	119.86	128.06
25	BA	1618	6MZ	C2-N3-C4	3.58	120.20	111.75
25	BA	747	5MU	O2-C2-N1	-3.56	118.05	122.79
25	BA	745	1MG	C2-N3-C4	3.54	119.93	111.98
25	BA	2030	6MZ	C5-N7-C8	3.53	108.53	103.51
23	AW	20	H2U	N3-C2-N1	3.53	120.38	116.65
1	AA	1407	5MC	C5-C6-N1	-3.52	119.71	123.34
1	AA	1207	2MG	N9-C8-N7	-3.50	106.81	113.39
25	BA	2503	2MA	C5-N7-C8	3.47	108.44	103.51
25	BA	2449	H2U	N3-C2-N1	3.45	120.30	116.65
25	BA	2445	2MG	CM2-N2-C2	-3.43	116.29	123.86
1	AA	966	2MG	N9-C8-N7	-3.43	106.94	113.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	AX	37	MIA	C2-N3-C4	3.42	119.84	111.75
1	AA	527	G7M	C5-C4-N3	-3.42	121.59	128.15
25	BA	745	1MG	N9-C8-N7	-3.40	106.98	113.39
1	AA	1519	MA6	C2-N1-C6	3.39	119.77	111.75
1	AA	967	5MC	C5-C6-N1	-3.39	119.85	123.34
24	AX	47	3AU	C5-C4-N3	3.38	119.90	114.84
1	AA	1518	MA6	C2-N3-C4	3.37	119.71	111.75
25	BA	2503	2MA	N3-C2-N1	-3.37	119.53	125.72
24	AX	8	4SU	N3-C2-N1	3.26	119.22	114.89
25	BA	2069	G7M	C5-C4-N3	-3.26	121.90	128.15
25	BA	1917	PSU	O2-C2-N1	-3.25	119.21	122.79
25	BA	1911	PSU	O2-C2-N1	-3.22	119.24	122.79
23	AW	8	4SU	C5-C4-S4	-3.22	120.32	124.47
24	AX	37	MIA	C5-N7-C8	3.22	108.08	103.51
25	BA	1835	2MG	N9-C8-N7	-3.21	107.34	113.39
1	AA	1207	2MG	C2-N1-C6	-3.17	119.31	125.10
1	AA	1518	MA6	C2-N1-C6	3.15	119.20	111.75
25	BA	2552	OMU	O4-C4-C5	-3.15	119.62	125.16
24	AX	46	7MG	O6-C6-C5	-3.15	120.02	127.24
25	BA	1618	6MZ	C5-N7-C8	3.13	107.95	103.51
1	AA	1519	MA6	N3-C4-N9	3.10	132.19	127.08
1	AA	527	G7M	C2-N1-C6	-3.07	119.50	125.10
1	AA	966	2MG	C2-N1-C6	-3.06	119.52	125.10
25	BA	2449	H2U	O2-C2-N1	-3.04	119.29	123.11
25	BA	2503	2MA	N3-C4-N9	3.02	131.19	126.99
1	AA	516	PSU	O2-C2-N1	-3.00	119.49	122.79
23	AW	54	5MU	C5M-C5-C4	2.98	122.05	118.77
25	BA	1618	6MZ	N3-C4-N9	2.98	131.99	127.08
24	AX	20	H2U	C5-C4-N3	2.97	119.99	116.65
25	BA	955	PSU	O2-C2-N1	-2.96	119.53	122.79
24	AX	37	MIA	N3-C4-N9	2.95	131.94	127.08
25	BA	2504	PSU	O2-C2-N1	-2.95	119.54	122.79
25	BA	2604	PSU	O2-C2-N1	-2.95	119.55	122.79
1	AA	1519	MA6	C5-N7-C8	2.94	107.69	103.51
25	BA	745	1MG	C1'-N9-C4	-2.90	117.87	126.50
1	AA	1518	MA6	C5-N7-C8	2.90	107.63	103.51
25	BA	1917	PSU	C6-N1-C2	-2.90	119.72	122.68
25	BA	1835	2MG	CM2-N2-C2	-2.90	117.45	123.86
24	AX	46	7MG	C2-N1-C6	-2.90	119.81	125.10
24	AX	47	3AU	O4-C4-C5	-2.90	120.06	125.16
25	BA	2251	OMG	C1'-N9-C4	2.90	135.11	126.50
1	AA	516	PSU	O4'-C1'-C2'	2.90	109.23	105.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	2251	OMG	N9-C4-N3	2.90	131.75	125.94
25	BA	746	PSU	O2-C2-N1	-2.89	119.61	122.79
25	BA	2580	PSU	O2-C2-N1	-2.89	119.61	122.79
25	BA	2251	OMG	C2-N1-C6	-2.89	119.83	125.10
25	BA	2445	2MG	N9-C8-N7	-2.88	107.96	113.39
25	BA	2069	G7M	C2-N1-C6	-2.87	119.86	125.10
1	AA	1516	2MG	N9-C8-N7	-2.87	107.99	113.39
1	AA	1207	2MG	C5-C6-N1	2.86	120.45	113.19
24	AX	20	H2U	C5-C6-N1	2.85	121.01	111.61
24	AX	16	H2U	C5-C4-N3	2.82	119.82	116.65
1	AA	966	2MG	C5-C6-N1	2.81	120.31	113.19
25	BA	2580	PSU	O4'-C1'-C2'	2.79	109.08	105.14
24	AX	55	PSU	O2-C2-N1	-2.79	119.72	122.79
24	AX	16	H2U	N3-C2-N1	2.77	119.59	116.65
25	BA	2030	6MZ	C4-C5-C6	2.77	118.96	116.81
1	AA	1518	MA6	C4-N9-C8	2.77	108.73	105.73
23	AW	20	H2U	C5-C4-N3	2.77	119.76	116.65
23	AW	20	H2U	C5-C6-N1	2.76	120.72	111.61
25	BA	2580	PSU	C3'-C2'-C1'	2.75	104.84	101.64
25	BA	2445	2MG	O6-C6-C5	-2.75	119.31	126.60
25	BA	2449	H2U	C5-C4-N3	2.74	119.73	116.65
24	AX	39	PSU	O2-C2-N1	-2.74	119.78	122.79
25	BA	2030	6MZ	C4-C5-N7	-2.73	107.29	110.62
25	BA	1835	2MG	C5-C6-N1	2.72	120.10	113.19
25	BA	2580	PSU	C6-N1-C2	-2.71	119.92	122.68
25	BA	1835	2MG	O6-C6-C5	-2.70	119.43	126.60
25	BA	2445	2MG	C5-C6-N1	2.69	120.03	113.19
1	AA	1516	2MG	C5-C6-N1	2.68	119.99	113.19
25	BA	745	1MG	C5-C6-N1	2.67	120.07	114.91
1	AA	516	PSU	C3'-C2'-C1'	2.66	104.74	101.64
24	AX	20	H2U	N3-C2-N1	2.66	119.47	116.65
25	BA	746	PSU	C6-C5-C4	2.65	120.05	118.20
24	AX	32	PSU	O2-C2-N1	-2.65	119.88	122.79
24	AX	16	H2U	C5-C6-N1	2.65	120.33	111.61
25	BA	1911	PSU	C6-N1-C2	-2.65	119.98	122.68
25	BA	2251	OMG	C5-C6-N1	2.65	119.91	113.19
24	AX	37	MIA	C4-N9-C8	2.64	108.59	105.73
25	BA	2449	H2U	C5-C6-N1	2.64	120.30	111.61
24	AX	39	PSU	C6-N1-C2	-2.63	120.00	122.68
25	BA	746	PSU	O2'-C2'-C3'	2.62	120.28	111.82
25	BA	2457	PSU	O2-C2-N1	-2.61	119.91	122.79
25	BA	2069	G7M	N9-C8-N7	-2.61	105.76	112.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	2504	PSU	C6-N1-C2	-2.59	120.03	122.68
1	AA	1516	2MG	O6-C6-C5	-2.57	119.79	126.60
25	BA	2030	6MZ	C5-C6-N1	2.56	120.93	118.20
25	BA	2251	OMG	O6-C6-C5	-2.54	119.86	126.60
25	BA	2030	6MZ	C4-N9-C8	2.52	108.46	105.73
1	AA	1402	4OC	C6-C5-C4	2.52	120.04	116.96
25	BA	1835	2MG	N1-C2-N3	-2.52	120.06	123.95
23	AW	54	5MU	O2-C2-N1	-2.51	119.44	122.79
1	AA	527	G7M	N9-C8-N7	-2.50	106.02	112.21
24	AX	55	PSU	C6-C5-C4	2.49	119.94	118.20
23	AW	55	PSU	C3'-C2'-C1'	2.49	104.53	101.64
24	AX	46	7MG	C5-C6-N1	2.48	119.71	112.31
23	AW	55	PSU	O2'-C2'-C3'	2.48	119.86	111.82
24	AX	46	7MG	N9-C4-N3	2.48	129.18	125.47
24	AX	54	5MU	O2-C2-N1	-2.48	119.49	122.79
1	AA	1207	2MG	N2-C2-N1	2.48	121.99	116.71
1	AA	966	2MG	O6-C6-C5	-2.47	120.05	126.60
25	BA	2504	PSU	C6-C5-C4	2.46	119.92	118.20
25	BA	955	PSU	C6-N1-C2	-2.45	120.18	122.68
1	AA	527	G7M	N2-C2-N1	2.43	121.90	116.71
25	BA	2503	2MA	CM2-C2-N1	2.43	120.95	117.15
25	BA	2030	6MZ	C5-C4-N9	2.43	108.61	105.78
25	BA	2030	6MZ	N3-C4-N9	2.42	131.07	127.08
24	AX	46	7MG	C5-C4-N9	2.41	110.04	106.68
25	BA	1915	3TD	O4'-C1'-C2'	2.41	108.54	105.14
1	AA	1402	4OC	CM4-N4-C4	-2.40	117.76	122.45
1	AA	1207	2MG	O6-C6-C5	-2.40	120.24	126.60
1	AA	527	G7M	N9-C4-N3	2.35	130.66	125.94
25	BA	2604	PSU	C6-C5-C4	2.35	119.84	118.20
25	BA	1618	6MZ	C4-N9-C8	2.34	108.27	105.73
25	BA	2498	OMC	O3'-C3'-C2'	2.33	117.79	111.17
24	AX	37	MIA	C1'-N9-C8	-2.32	121.91	127.14
25	BA	2251	OMG	C8-N9-C4	2.31	110.44	106.05
25	BA	2457	PSU	C6-C5-C4	2.31	119.81	118.20
1	AA	516	PSU	O2'-C2'-C3'	2.30	119.25	111.82
1	AA	966	2MG	N9-C4-N3	2.29	130.54	125.94
25	BA	2457	PSU	O4'-C1'-C2'	2.28	108.36	105.14
25	BA	746	PSU	C6-N1-C2	-2.27	120.36	122.68
25	BA	2251	OMG	C8-N7-C5	2.27	108.34	104.24
25	BA	2069	G7M	N9-C4-N3	2.26	130.47	125.94
24	AX	16	H2U	O2-C2-N1	-2.25	120.28	123.11
1	AA	1207	2MG	C8-N7-C5	2.25	108.31	104.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	1618	6MZ	C5-C6-N1	2.23	120.58	118.20
25	BA	2503	2MA	C4-C5-N7	-2.23	107.90	110.62
1	AA	1516	2MG	C5-C4-N9	2.22	109.66	105.63
23	AW	54	5MU	C5M-C5-C6	-2.21	119.89	122.85
25	BA	2552	OMU	O2-C2-N1	-2.21	119.84	122.79
25	BA	2580	PSU	C6-C5-C4	2.21	119.74	118.20
25	BA	1917	PSU	O4'-C1'-C2'	2.21	108.26	105.14
25	BA	1618	6MZ	C4-C5-N7	-2.21	107.93	110.62
1	AA	1207	2MG	C4-C5-N7	-2.17	107.28	110.72
24	AX	55	PSU	C6-N1-C2	-2.16	120.47	122.68
25	BA	2504	PSU	O2'-C2'-C3'	2.16	118.81	111.82
1	AA	1519	MA6	C4-N9-C8	2.15	108.06	105.73
24	AX	20	H2U	O2-C2-N3	-2.15	117.50	121.50
25	BA	2604	PSU	C6-N1-C2	-2.15	120.49	122.68
28	BD	150	MEQ	CB-CG-CD	-2.14	108.25	113.04
1	AA	516	PSU	C6-N1-C2	-2.14	120.50	122.68
1	AA	966	2MG	C8-N7-C5	2.13	108.10	104.24
23	AW	55	PSU	C6-N1-C2	-2.13	120.51	122.68
25	BA	2605	PSU	O2-C2-N1	-2.12	120.46	122.79
1	AA	967	5MC	CM5-C5-C6	-2.12	120.02	122.85
25	BA	955	PSU	O2'-C2'-C3'	2.12	118.67	111.82
1	AA	966	2MG	O3'-C3'-C4'	2.11	117.16	111.05
25	BA	745	1MG	C8-N7-C5	2.11	108.06	104.24
23	AW	8	4SU	O2-C2-N1	-2.11	119.98	122.79
1	AA	1516	2MG	C4-C5-N7	-2.08	107.43	110.72
25	BA	2457	PSU	O2'-C2'-C3'	2.08	118.54	111.82
25	BA	2580	PSU	O2'-C2'-C3'	2.07	118.52	111.82
1	AA	1402	4OC	O2-C2-N3	-2.06	118.98	122.33
24	AX	37	MIA	C4-C5-N7	-2.06	108.11	110.62
24	AX	32	PSU	C6-N1-C2	-2.06	120.58	122.68
25	BA	1618	6MZ	C5-C4-N9	2.02	108.13	105.78

There are no chirality outliers.

All (70) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	AA	966	2MG	O4'-C4'-C5'-O5'
1	AA	966	2MG	C3'-C4'-C5'-O5'
1	AA	1518	MA6	C5-C6-N6-C9
1	AA	1518	MA6	C5-C6-N6-C10
1	AA	1519	MA6	O4'-C4'-C5'-O5'
1	AA	1519	MA6	C5-C6-N6-C9

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Mol	Chain	Res	Type	Atoms
1	AA	1519	MA6	C5-C6-N6-C10
24	AX	20	H2U	O4'-C4'-C5'-O5'
24	AX	20	H2U	C3'-C4'-C5'-O5'
36	BN	81	4D4	C-CA-CB-OB
36	BN	81	4D4	C-CA-CB-CG
36	BN	81	4D4	N-CA-CB-OB
36	BN	81	4D4	N-CA-CB-CG
36	BN	81	4D4	OB-CB-CG-CD
23	AW	20	H2U	O4'-C4'-C5'-O5'
23	AW	20	H2U	C3'-C4'-C5'-O5'
23	AW	20	H2U	O4'-C1'-N1-C2
23	AW	20	H2U	O4'-C1'-N1-C6
25	BA	1618	6MZ	O4'-C4'-C5'-O5'
25	BA	1618	6MZ	C3'-C4'-C5'-O5'
25	BA	2552	OMU	O4'-C4'-C5'-O5'
24	AX	20	H2U	C2'-C1'-N1-C2
1	AA	967	5MC	O4'-C4'-C5'-O5'
1	AA	1519	MA6	C3'-C4'-C5'-O5'
25	BA	1917	PSU	C3'-C4'-C5'-O5'
25	BA	1917	PSU	O4'-C4'-C5'-O5'
25	BA	2503	2MA	O4'-C4'-C5'-O5'
25	BA	2552	OMU	C3'-C4'-C5'-O5'
1	AA	516	PSU	C3'-C4'-C5'-O5'
1	AA	967	5MC	C3'-C4'-C5'-O5'
1	AA	1207	2MG	O4'-C4'-C5'-O5'
25	BA	2498	OMC	C3'-C4'-C5'-O5'
25	BA	2503	2MA	C3'-C4'-C5'-O5'
1	AA	1518	MA6	N1-C6-N6-C10
1	AA	1519	MA6	N1-C6-N6-C10
24	AX	20	H2U	C2'-C1'-N1-C6
23	AW	20	H2U	C2'-C1'-N1-C6
28	BD	150	MEQ	NE2-CD-CG-CB
28	BD	150	MEQ	OE1-CD-CG-CB
25	BA	2445	2MG	C3'-C4'-C5'-O5'
25	BA	2498	OMC	O4'-C4'-C5'-O5'
24	AX	16	H2U	C4'-C5'-O5'-P
23	AW	20	H2U	C4'-C5'-O5'-P
36	BN	81	4D4	CA-CB-CG-CD
24	AX	46	7MG	O4'-C1'-N9-C4
23	AW	20	H2U	C2'-C1'-N1-C2
25	BA	2445	2MG	O4'-C4'-C5'-O5'
24	AX	20	H2U	C4'-C5'-O5'-P

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Mol	Chain	Res	Type	Atoms
24	AX	46	7MG	C4'-C5'-O5'-P
25	BA	1911	PSU	O4'-C4'-C5'-O5'
25	BA	2030	6MZ	O4'-C4'-C5'-O5'
24	AX	46	7MG	C2'-C1'-N9-C8
25	BA	1939	5MU	O4'-C4'-C5'-O5'
28	BD	150	MEQ	CA-CB-CG-CD
1	AA	527	G7M	C4'-C5'-O5'-P
25	BA	2069	G7M	C4'-C5'-O5'-P
24	AX	46	7MG	O4'-C1'-N9-C8
24	AX	55	PSU	O4'-C1'-C5-C4
1	AA	516	PSU	O4'-C4'-C5'-O5'
1	AA	1519	MA6	C4'-C5'-O5'-P
1	AA	1207	2MG	C3'-C4'-C5'-O5'
23	AW	55	PSU	C3'-C4'-C5'-O5'
25	BA	1939	5MU	C3'-C4'-C5'-O5'
24	AX	55	PSU	O4'-C1'-C5-C6
25	BA	746	PSU	O4'-C1'-C5-C6
25	BA	2069	G7M	O4'-C4'-C5'-O5'
25	BA	2030	6MZ	C3'-C4'-C5'-O5'
36	BN	81	4D4	O-C-CA-CB
12	AL	89	D2T	CA-CB-CG-OD2
1	AA	967	5MC	C4'-C5'-O5'-P

There are no ring outliers.

25 monomers are involved in 39 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	AA	1519	MA6	1	0
28	BD	150	MEQ	3	0
25	BA	2552	OMU	3	0
25	BA	747	5MU	1	0
24	AX	46	7MG	1	0
24	AX	20	H2U	2	0
1	AA	967	5MC	1	0
25	BA	2030	6MZ	1	0
25	BA	955	PSU	1	0
1	AA	1518	MA6	2	0
23	AW	55	PSU	1	0
25	BA	1915	3TD	3	0
1	AA	966	2MG	2	0
25	BA	1917	PSU	3	0
25	BA	2449	H2U	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	BA	2504	PSU	1	0
25	BA	2445	2MG	1	0
1	AA	1498	UR3	1	0
24	AX	8	4SU	2	0
1	AA	527	G7M	2	0
24	AX	37	MIA	2	0
1	AA	1207	2MG	2	0
25	BA	2069	G7M	1	0
24	AX	16	H2U	1	0
1	AA	1516	2MG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 425 ligands modelled in this entry, 424 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
61	PHE	AX	101	24	10,11,12	0.49	0	10,13,15	0.24	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
61	PHE	AX	101	24	-	2/5/6/8	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
61	AX	101	PHE	CA-CB-CG-CD1
61	AX	101	PHE	CA-CB-CG-CD2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
61	AX	101	PHE	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
59	CD	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	CD	1357:ILE	C	1358:PRO	N	1.15

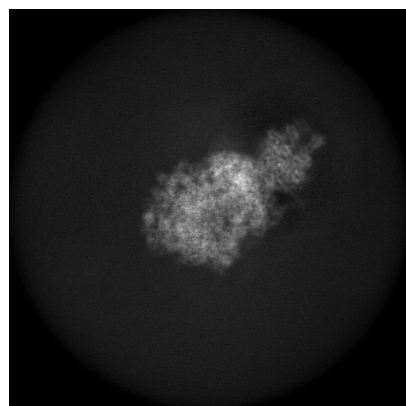
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11420. These allow visual inspection of the internal detail of the map and identification of artifacts.

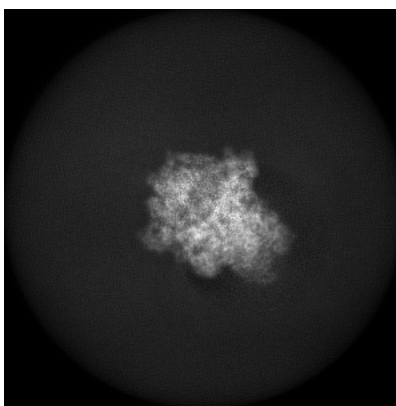
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

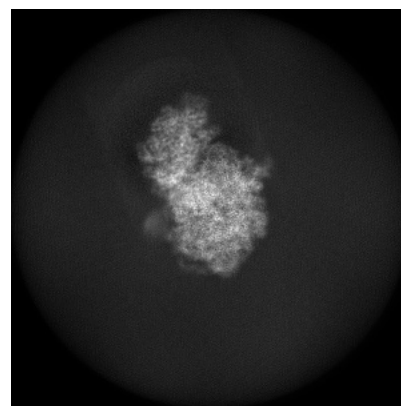
6.1.1 Primary map



X

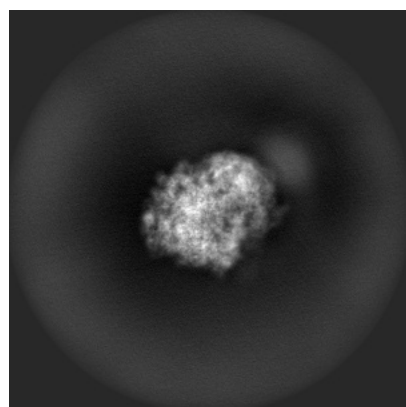


Y

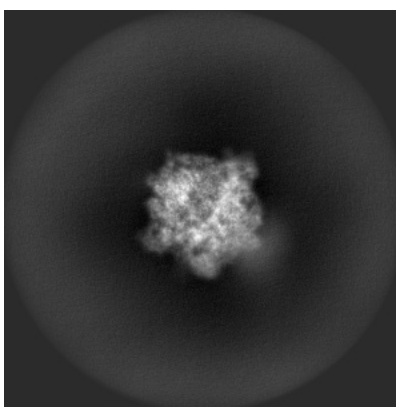


Z

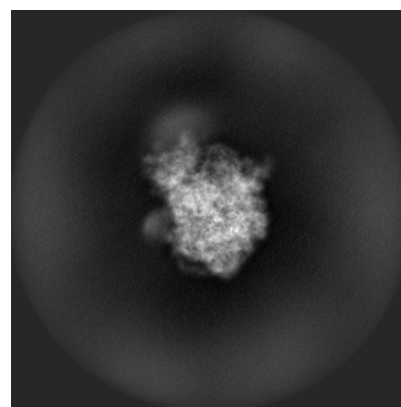
6.1.2 Raw map



X



Y

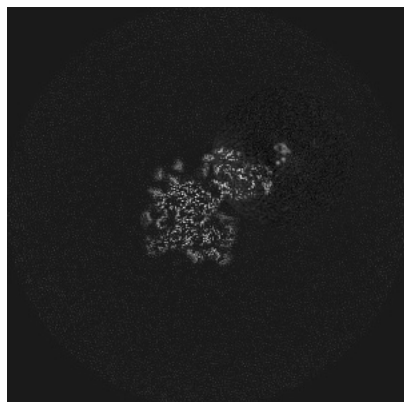


Z

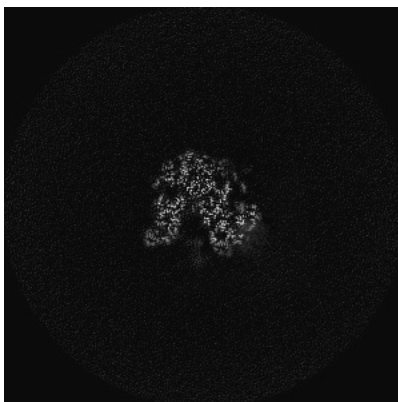
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

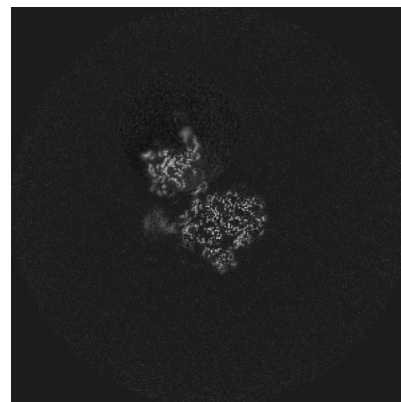
6.2.1 Primary map



X Index: 320

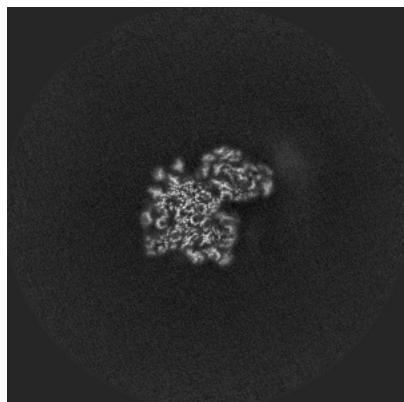


Y Index: 320

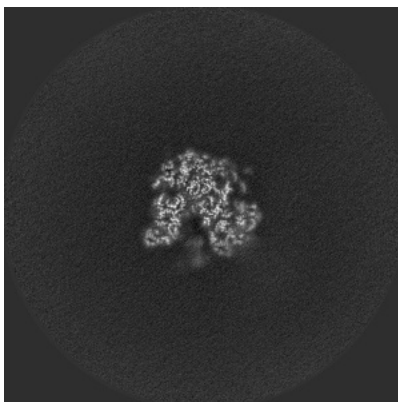


Z Index: 320

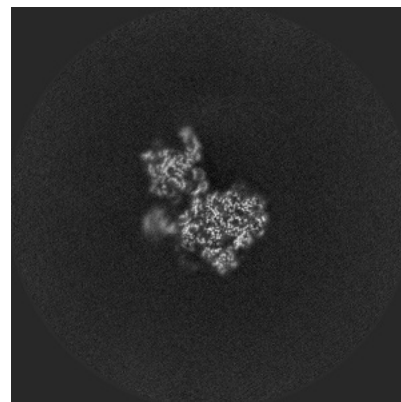
6.2.2 Raw map



X Index: 320



Y Index: 320

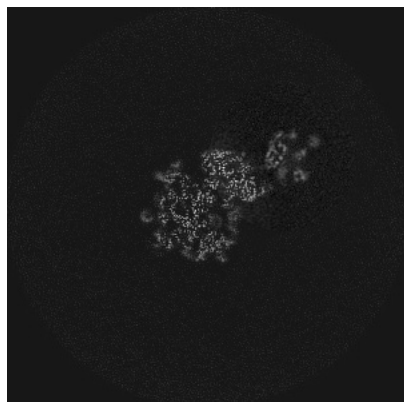


Z Index: 320

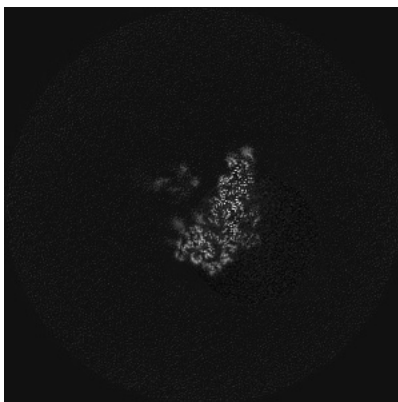
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

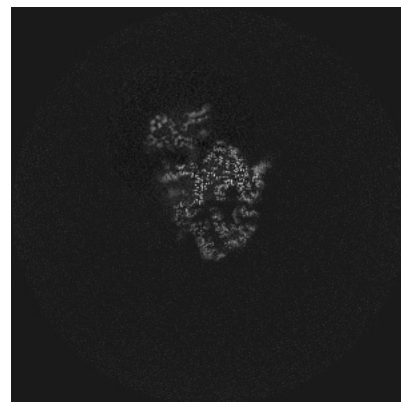
6.3.1 Primary map



X Index: 309

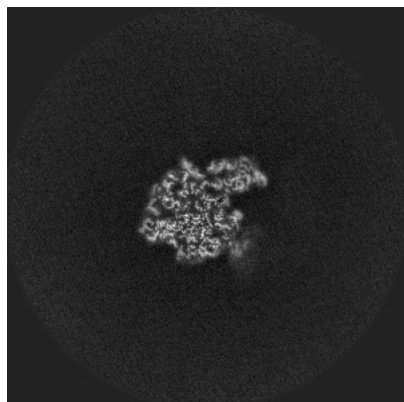


Y Index: 373

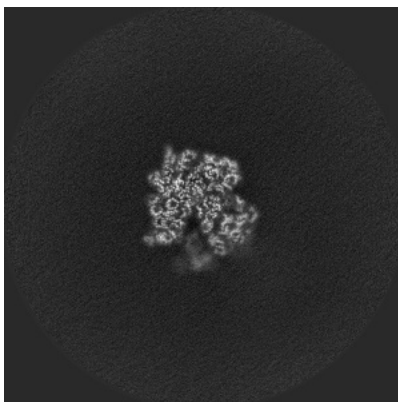


Z Index: 368

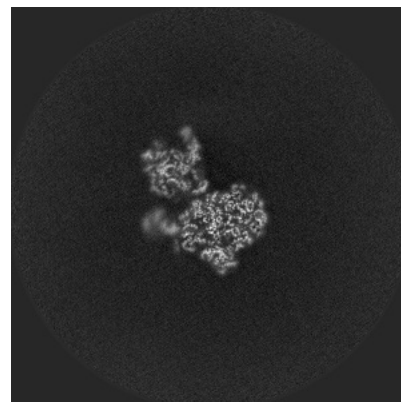
6.3.2 Raw map



X Index: 358



Y Index: 312

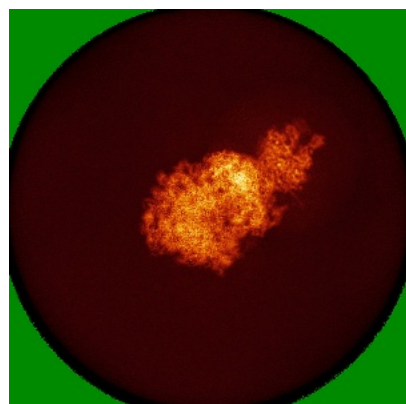


Z Index: 323

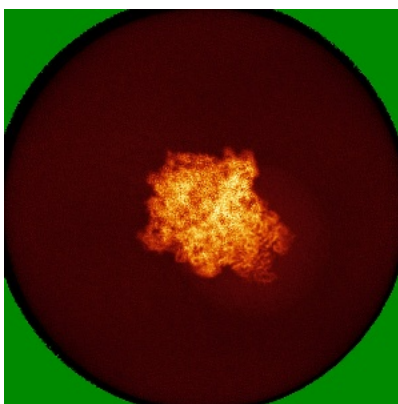
The images above show the largest variance slices of the map in three orthogonal directions.

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

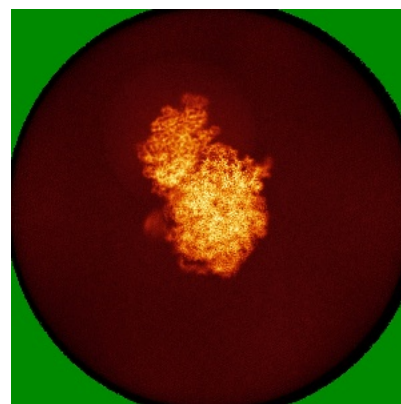
6.4.1 Primary map



X

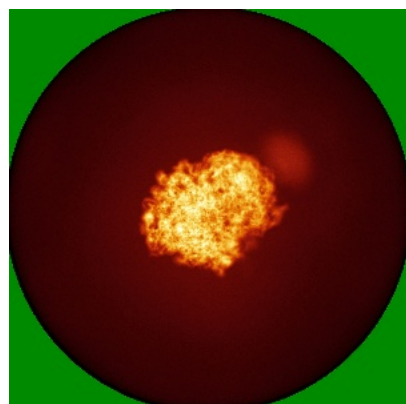


Y

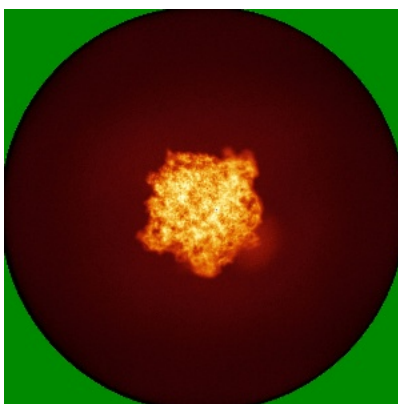


Z

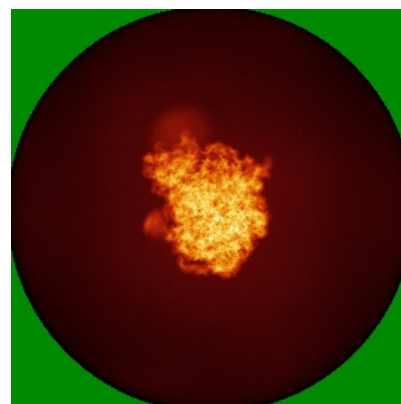
6.4.2 Raw map



X



Y

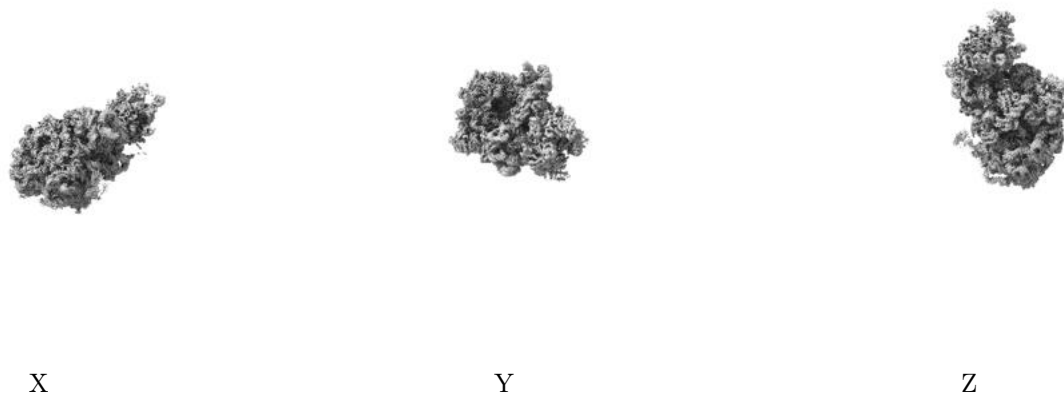


Z

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

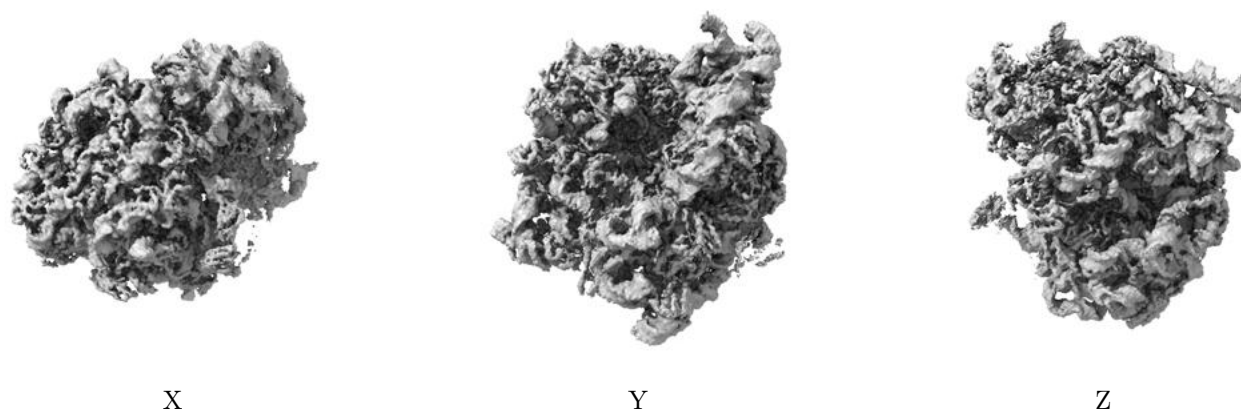
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

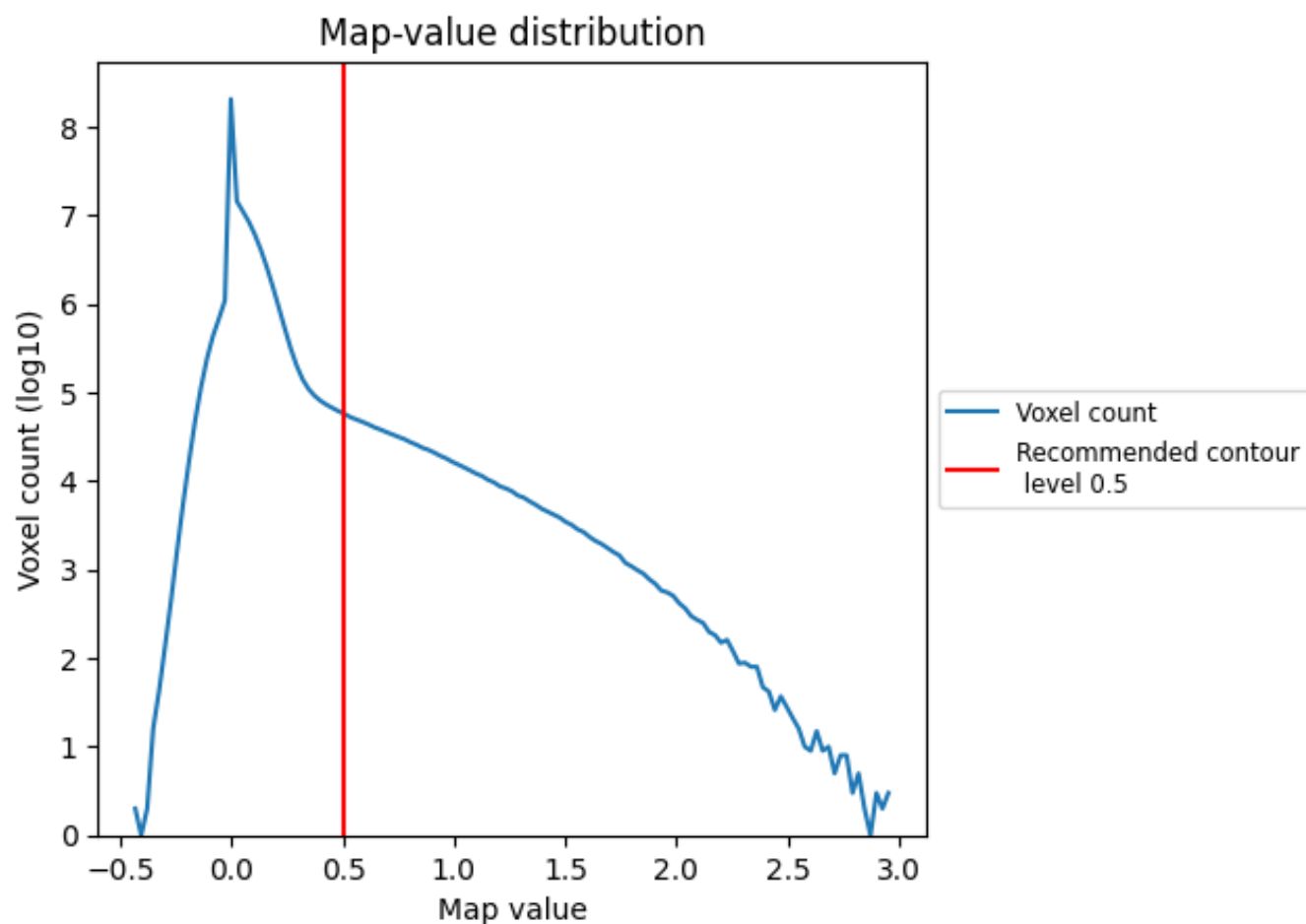
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

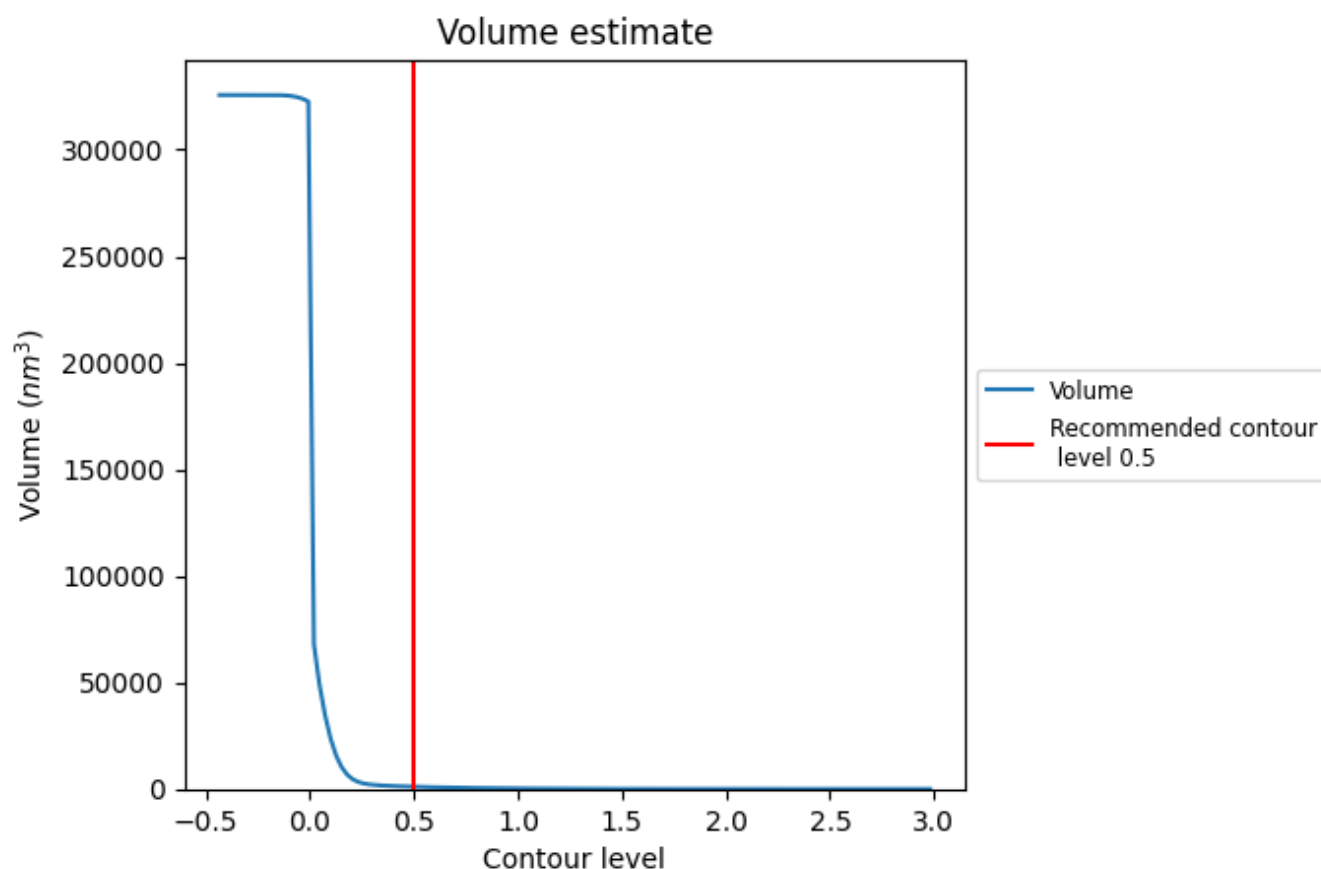
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

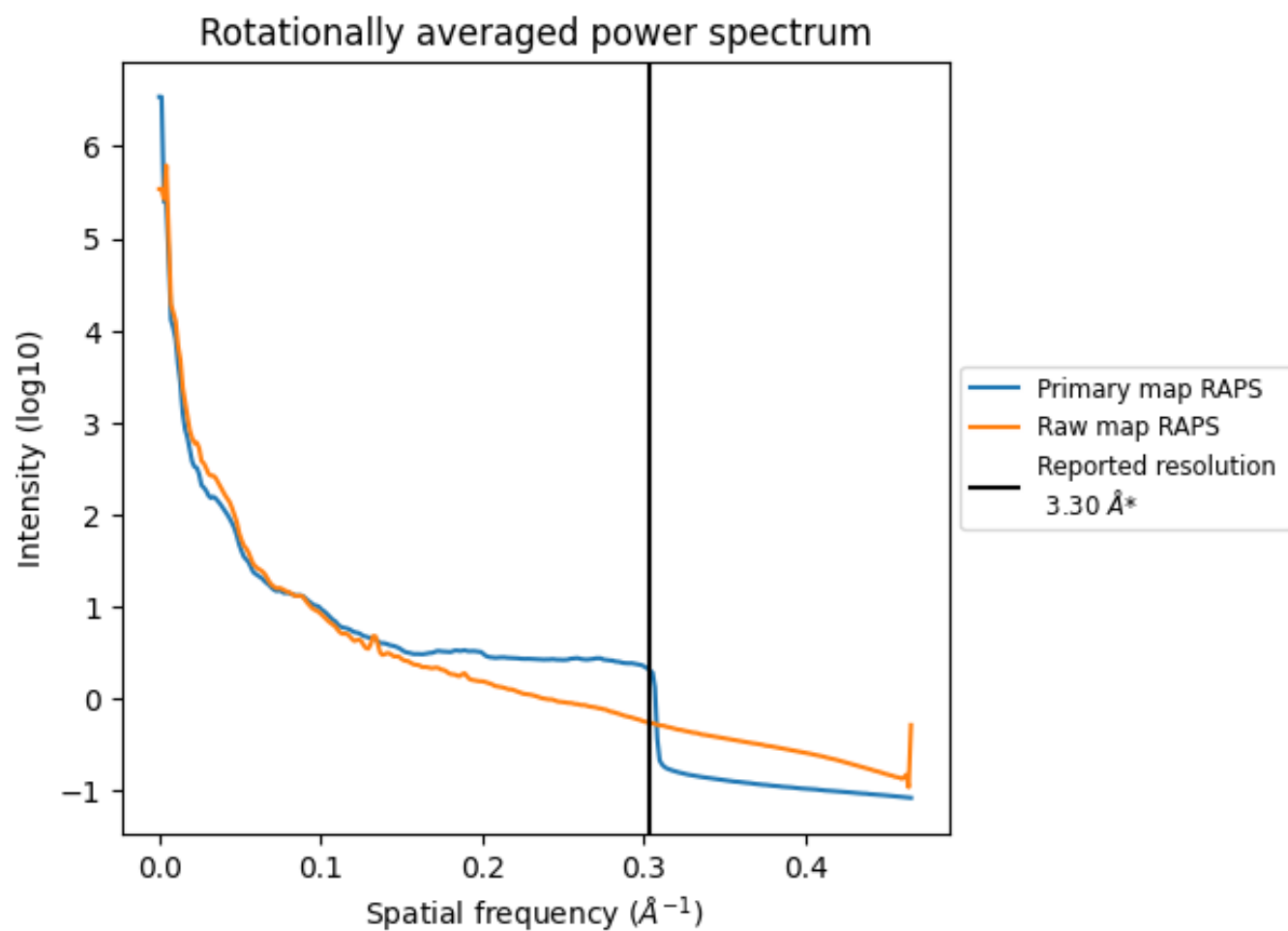
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1043 nm^3 ; this corresponds to an approximate mass of 942 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 ⓘ

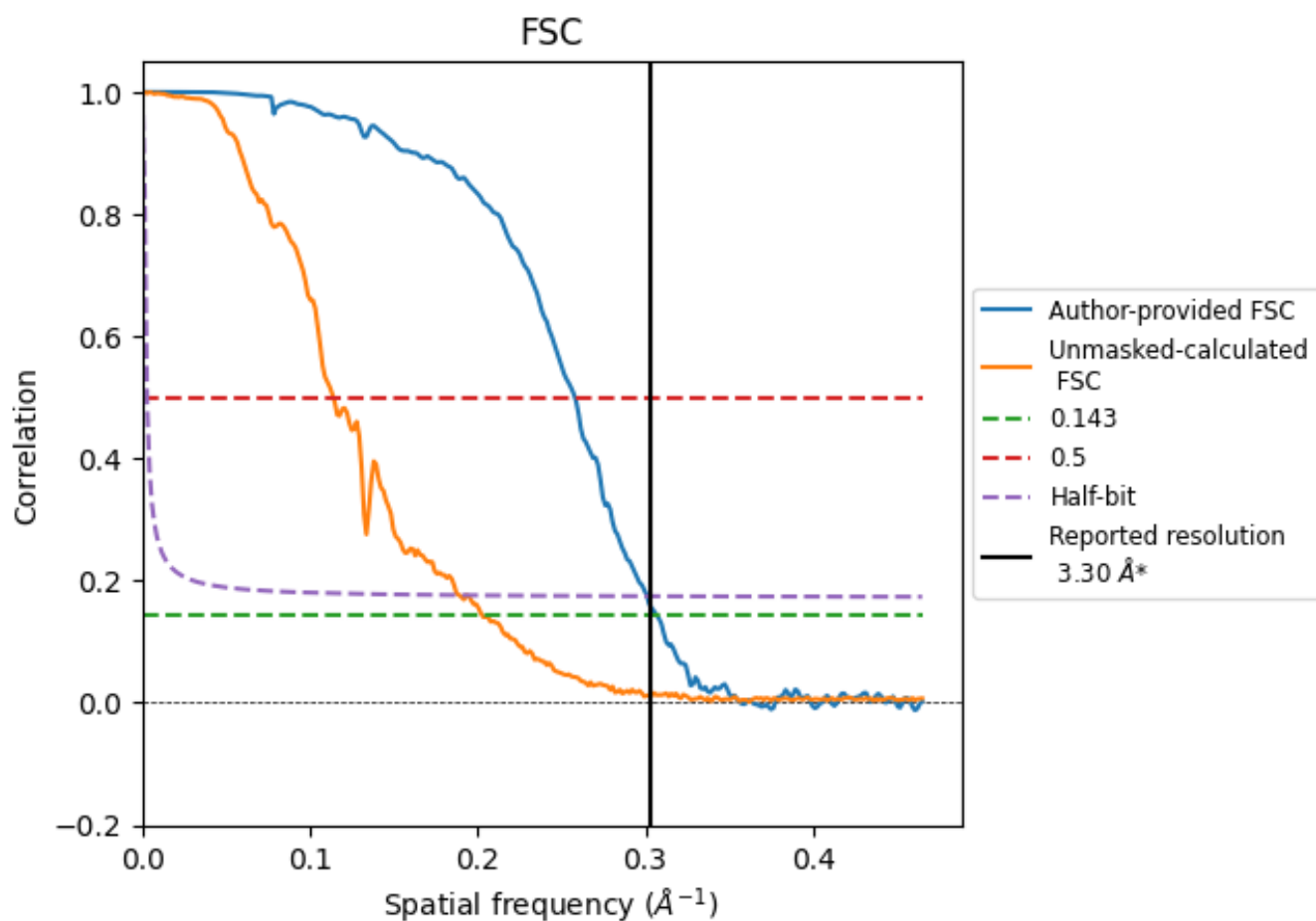


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.303 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

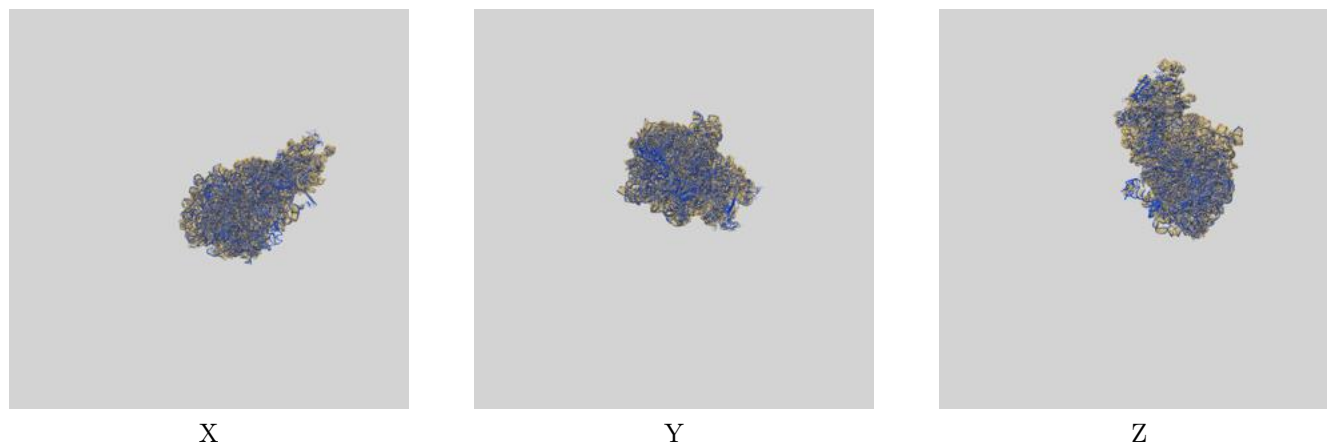
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.26	3.88	3.32
Unmasked-calculated*	4.93	8.78	5.29

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.93 differs from the reported value 3.3 by more than 10 %

9 Map-model fit [i](#)

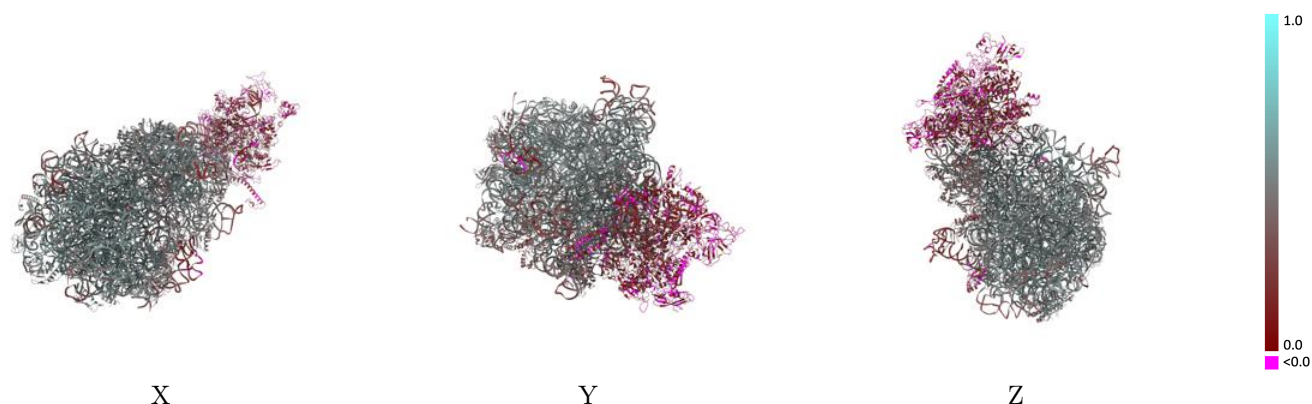
This section contains information regarding the fit between EMDB map EMD-11420 and PDB model 6ZTM. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

9.1 Map-model overlay [i](#)



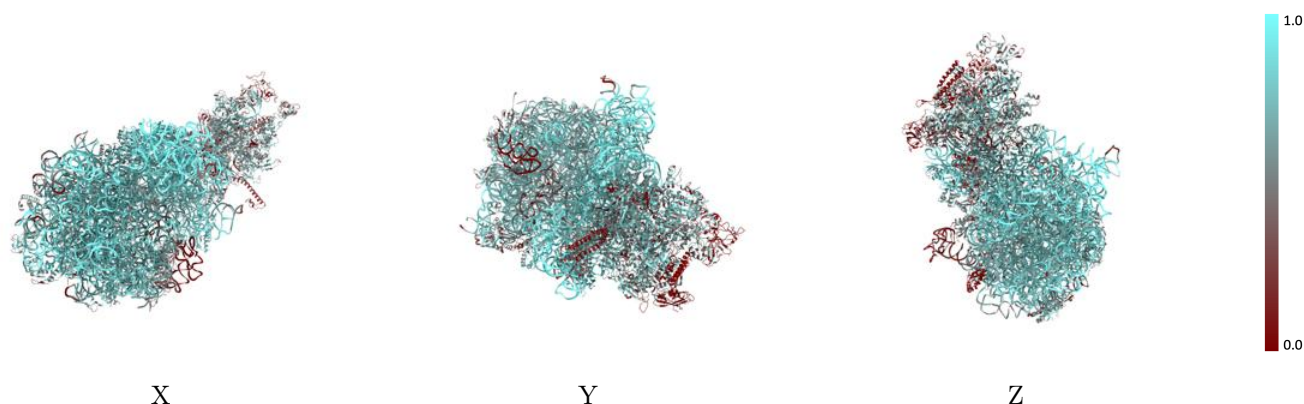
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



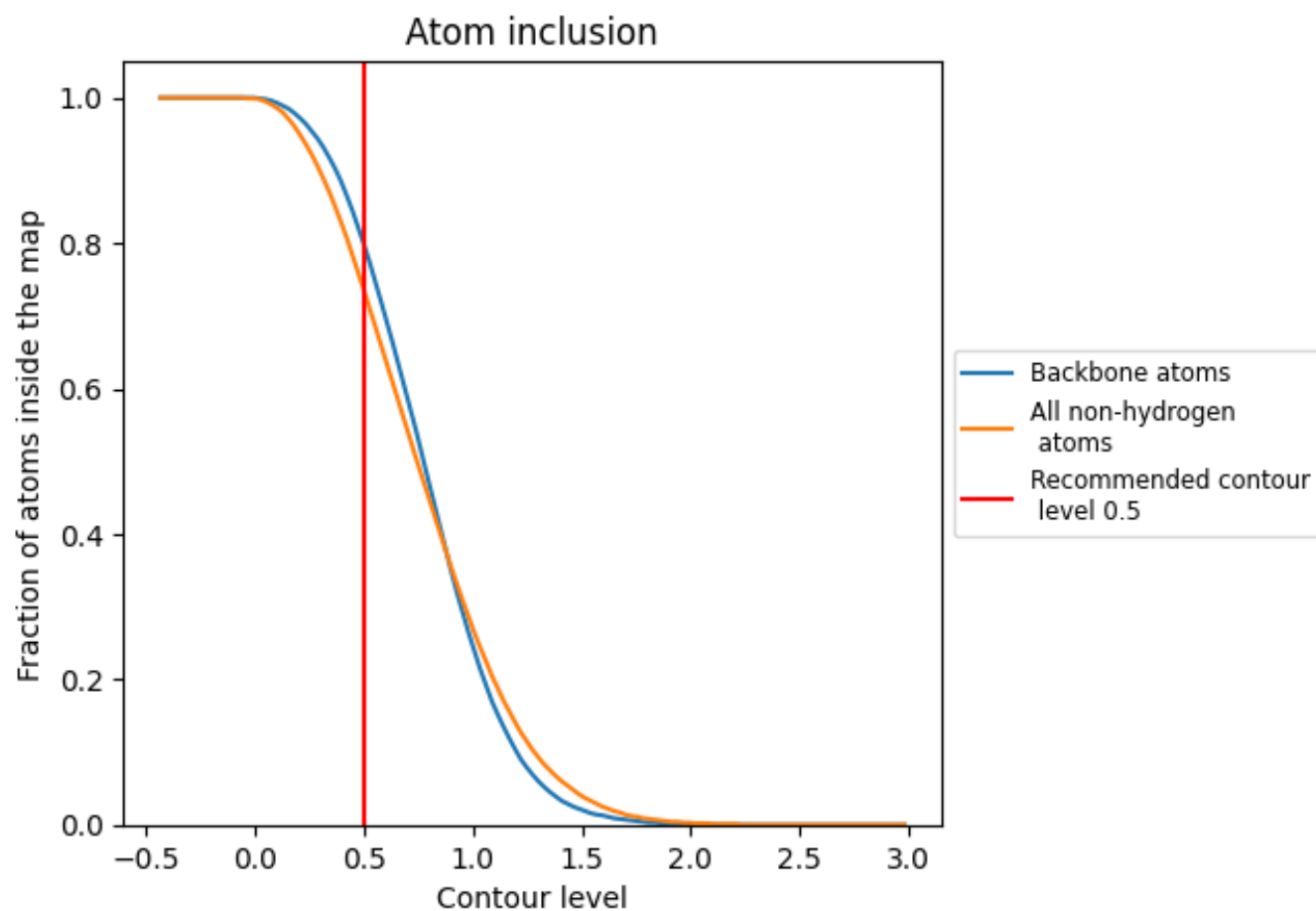
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.5).

9.4 Atom inclusion ⓘ



At the recommended contour level, 80% of all backbone atoms, 74% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7350	 0.4370
AA	 0.9360	 0.4900
AB	 0.3530	 0.3850
AC	 0.5940	 0.4560
AD	 0.5870	 0.4460
AE	 0.7400	 0.4930
AF	 0.6190	 0.4420
AG	 0.6490	 0.4010
AH	 0.7760	 0.5070
AI	 0.8010	 0.4310
AJ	 0.5810	 0.4130
AK	 0.6530	 0.4640
AL	 0.7840	 0.5210
AM	 0.7400	 0.3980
AN	 0.7620	 0.4590
AO	 0.7560	 0.4820
AP	 0.8520	 0.5230
AQ	 0.8030	 0.5060
AR	 0.7630	 0.5250
AS	 0.8330	 0.4470
AT	 0.8000	 0.4960
AU	 0.3410	 0.3650
AV	 0.5500	 0.3260
AW	 0.6000	 0.4060
AX	 0.4960	 0.4260
B1	 0.6610	 0.5180
B2	 0.6710	 0.5100
B3	 0.2080	 0.4270
B4	 0.7630	 0.5640
B5	 0.6680	 0.5390
B6	 0.6680	 0.5250
BA	 0.8220	 0.5010
BB	 0.7950	 0.4490
BC	 0.7060	 0.5340
BD	 0.6770	 0.5240



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Chain	Atom inclusion	Q-score
BE	 0.6310	 0.5020
BF	 0.3360	 0.3560
BG	 0.4480	 0.4220
BH	 0.0600	 0.2330
BK	 0.6860	 0.5180
BL	 0.6530	 0.5190
BM	 0.6580	 0.5060
BN	 0.6660	 0.5230
BO	 0.7260	 0.5270
BP	 0.5660	 0.4390
BQ	 0.6280	 0.4950
BR	 0.7460	 0.5320
BS	 0.6860	 0.5130
BT	 0.6630	 0.5180
BU	 0.5790	 0.4790
BV	 0.5770	 0.4730
BW	 0.6020	 0.4740
BX	 0.6870	 0.5390
BY	 0.6560	 0.5230
BZ	 0.5810	 0.4550
CA	 0.4570	 0.1670
CB	 0.2220	 0.1040
CC	 0.5240	 0.1740
CD	 0.4280	 0.1480
CN	 0.5050	 0.1520
CT	 0.7590	 0.2430