



Full wwPDB EM Validation Report ⓘ

Jun 21, 2026 – 12:14 am BST

PDB ID : 6ZU1 / pdb_00006zu1
EMDB ID : EMD-11426
Title : E. coli 70S-RNAP expressome complex in uncoupled state 2
Authors : Webster, M.W.; Takacs, M.; Weixlbaumer, A.
Deposited on : 2020-07-21
Resolution : 3.00 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:

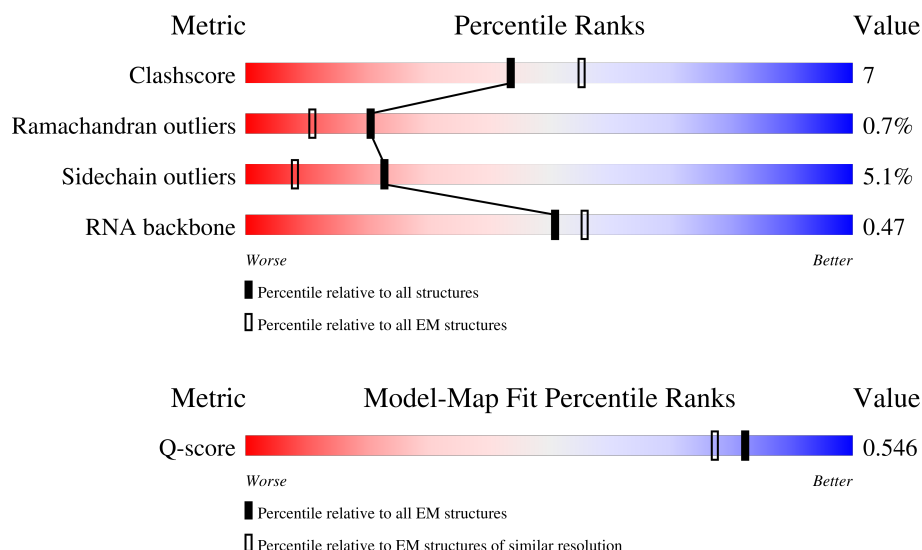
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal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

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

The reported resolution of this entry is 3.00 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.



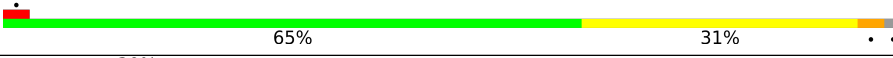
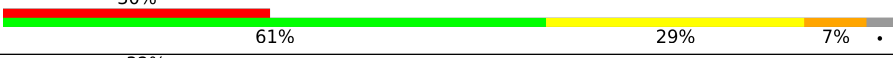
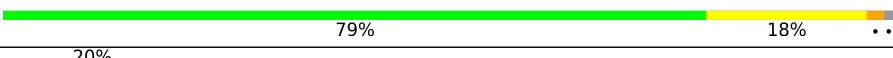
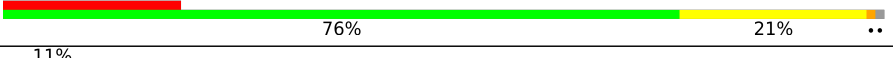
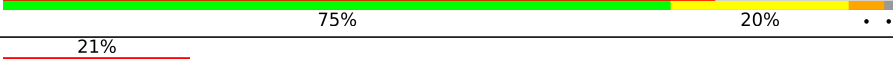
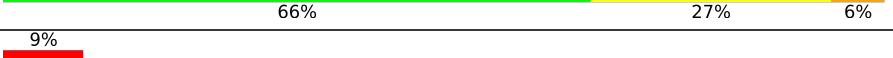
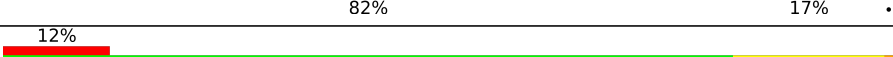
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	
2	AB	241	
3	AC	233	

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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	53	
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	B7	70	
56	CN	39	
57	CT	39	
58	CA	329	
58	CB	329	
59	CC	1342	
60	CD	1407	
61	CE	91	

2 Entry composition

There are 64 unique types of molecules in this entry. The entry contains 172846 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
			32909	14684	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	154	Total	C	N	O	S	0	0
			1214	756	235	219	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	117	Total	C	N	O	S	0	0
			877	540	174	160	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
			951	588	195	163	5		

- 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	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AR	66	Total	C	N	O	S	0	0
			545	344	102	98	1		

- 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	27	Total	C	N	O	P	0	0
			572	256	102	187	27		

- 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
			1630	730	290	533	76	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BA	2900	Total	C	N	O	P	0	0
			62270	27786	11456	20128	2900		

- 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	96	Total	C	N	O	S	0	0
			764	484	142	136	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
			376	228	89	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 protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	B7	70	Total	C	N	O	S	0	0
			549	339	104	100	6		

- Molecule 56 is a DNA chain called Non-template DNA strand.

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

- Molecule 57 is a DNA chain called Template DNA strand.

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

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

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

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

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

- Molecule 60 is a protein called DNA-directed RNA polymerase subunit beta'.

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

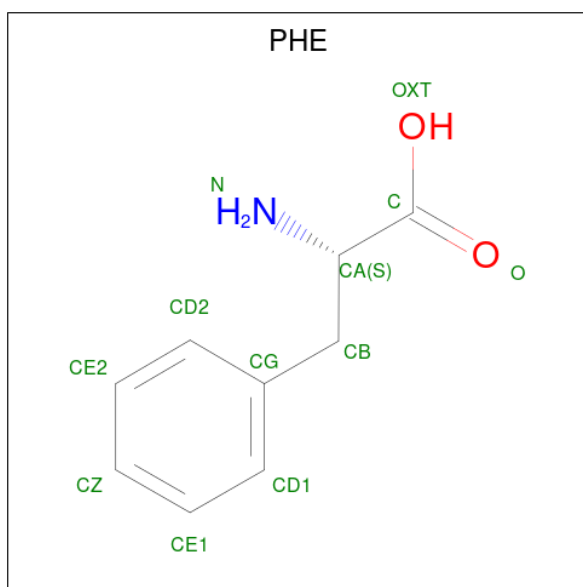
- Molecule 61 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	CE	61	Total	C	N	O	S	0	0
			478	295	90	92	1		

- Molecule 62 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
62	AA	143	Total	Mg	0
			143	143	
62	AI	1	Total	Mg	0
			1	1	
62	AL	1	Total	Mg	0
			1	1	
62	AM	1	Total	Mg	0
			1	1	
62	AW	5	Total	Mg	0
			5	5	
62	AX	1	Total	Mg	0
			1	1	
62	BA	317	Total	Mg	0
			317	317	
62	BB	9	Total	Mg	0
			9	9	
62	BC	3	Total	Mg	0
			3	3	
62	BN	1	Total	Mg	0
			1	1	
62	BO	1	Total	Mg	0
			1	1	
62	BQ	1	Total	Mg	0
			1	1	
62	BV	1	Total	Mg	0
			1	1	
62	BX	1	Total	Mg	0
			1	1	
62	CD	1	Total	Mg	0
			1	1	

- Molecule 63 is PHENYLALANINE (CCD ID: PHE) (formula: C₉H₁₁NO₂).



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

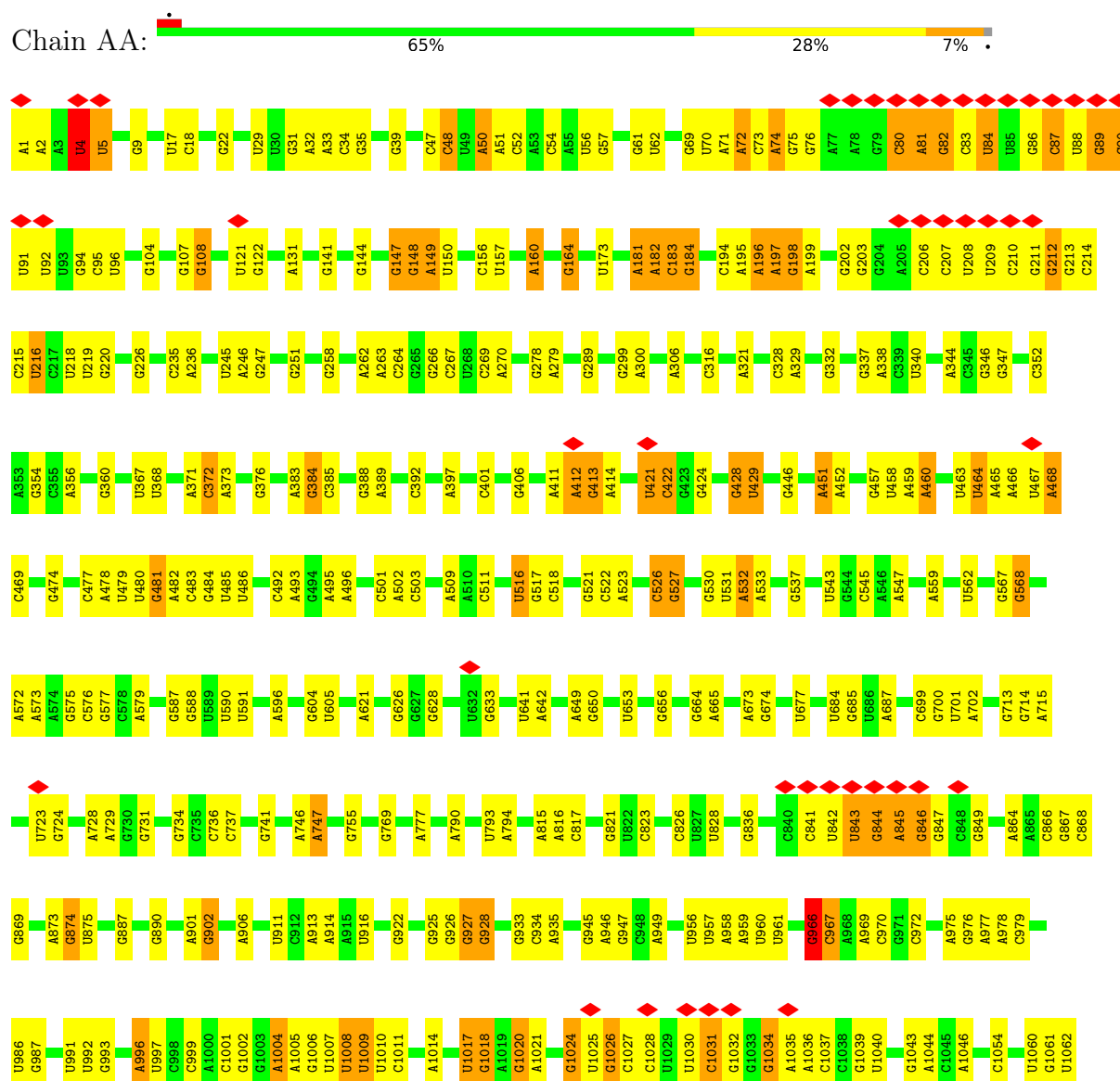
- Molecule 64 is ZINC ION (CCD ID: ZN) (formula: Zn).

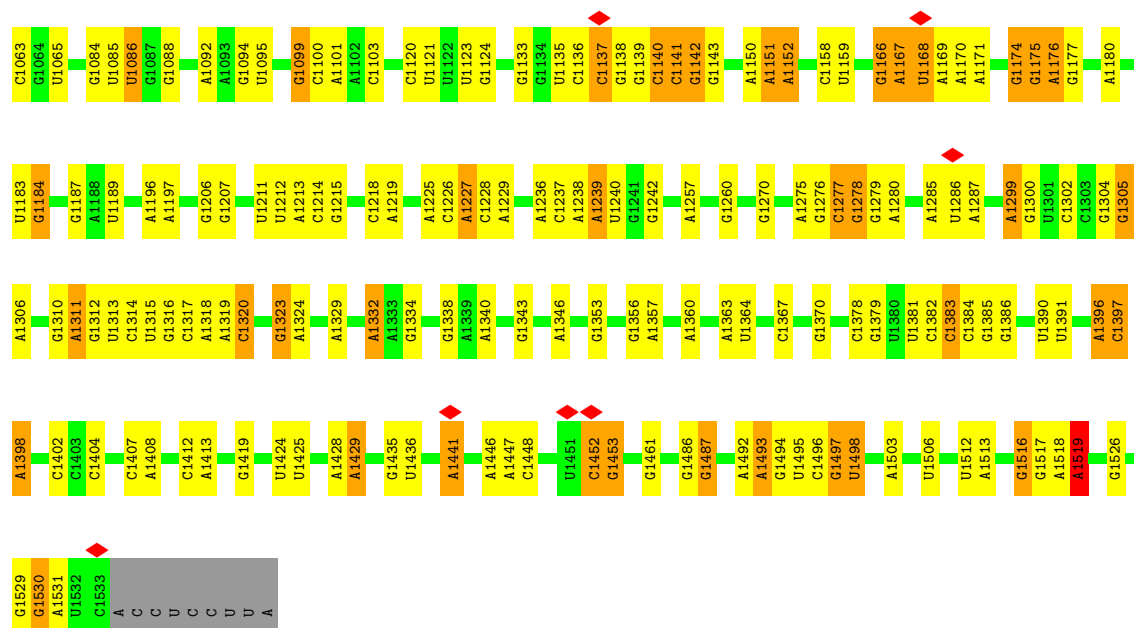
Mol	Chain	Residues	Atoms		AltConf
64	B6	1	Total	Zn	0
			1	1	
64	B7	1	Total	Zn	0
			1	1	
64	CD	2	Total	Zn	0
			2	2	

3 Residue-property plots

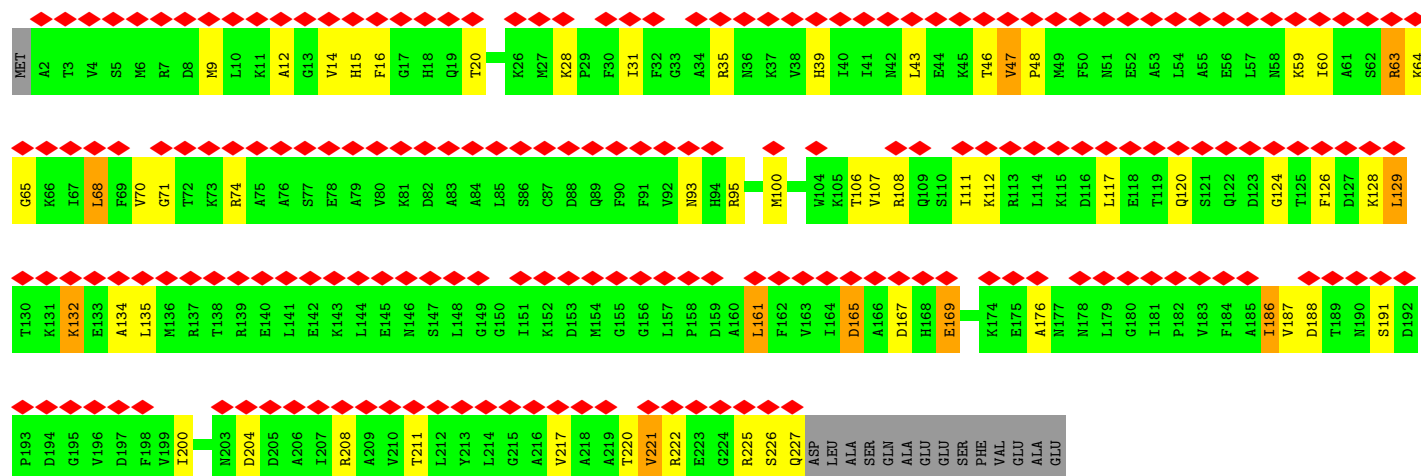
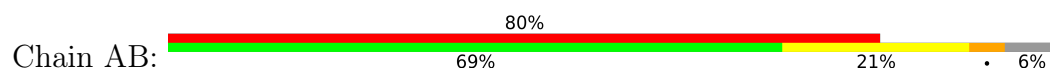
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

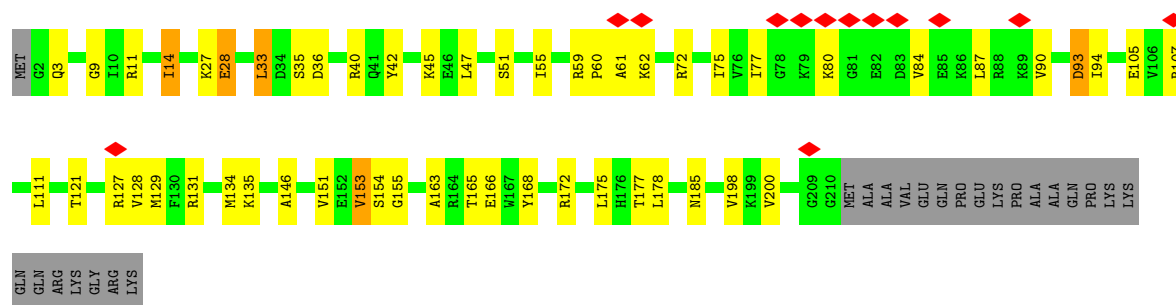




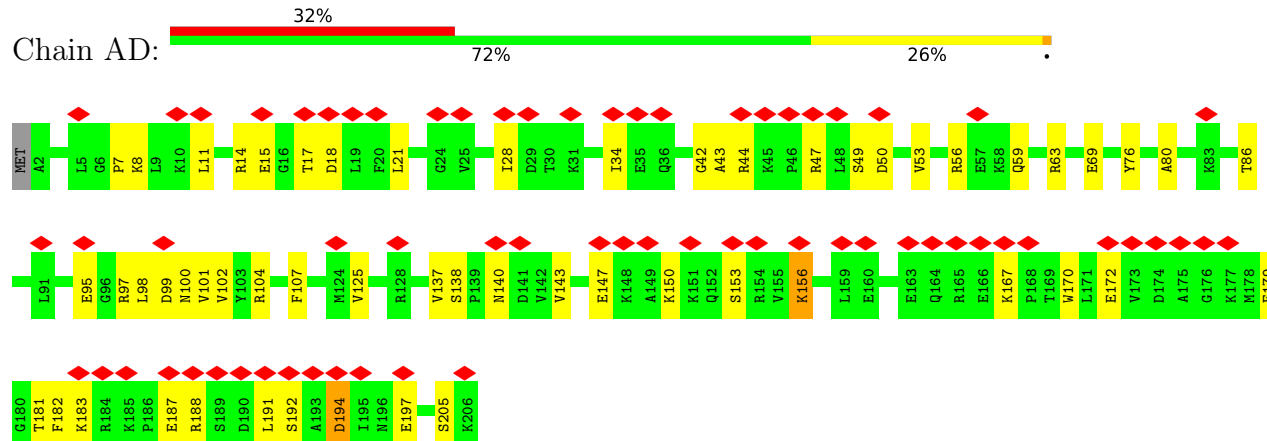
• Molecule 2: 30S ribosomal protein S2



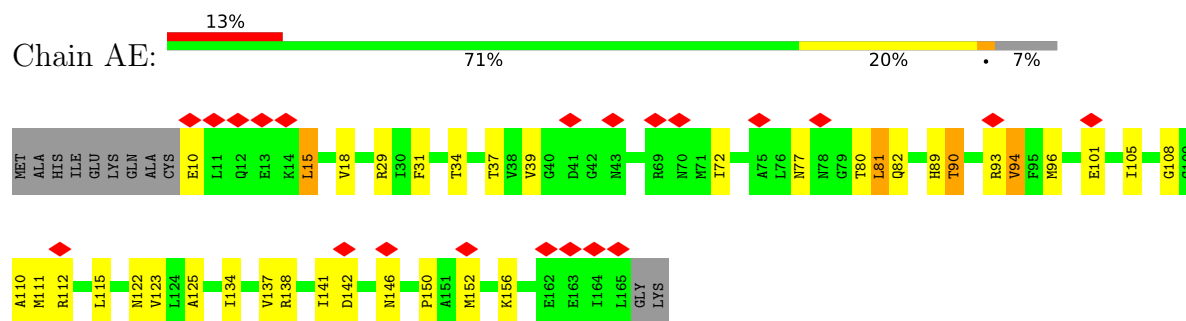
• Molecule 3: 30S ribosomal protein S3



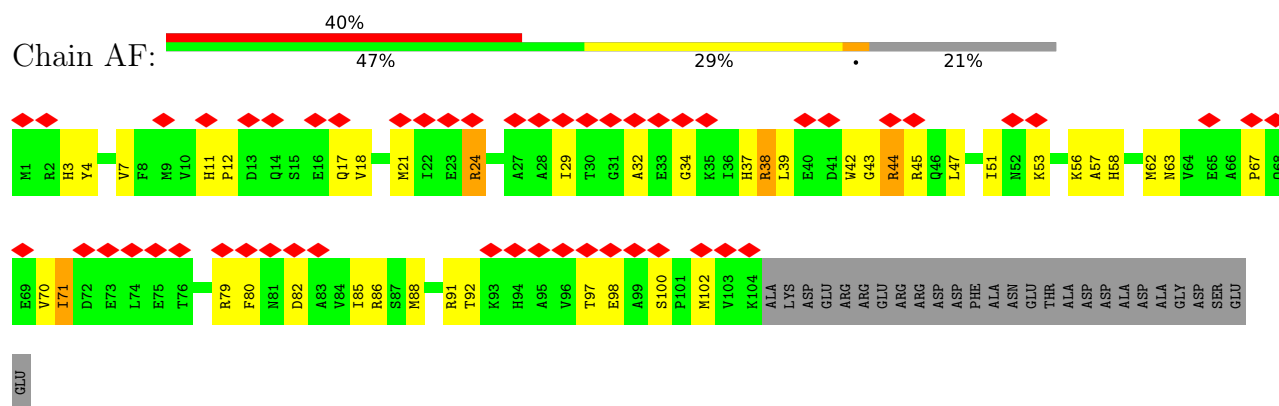
- Molecule 4: 30S ribosomal protein S4



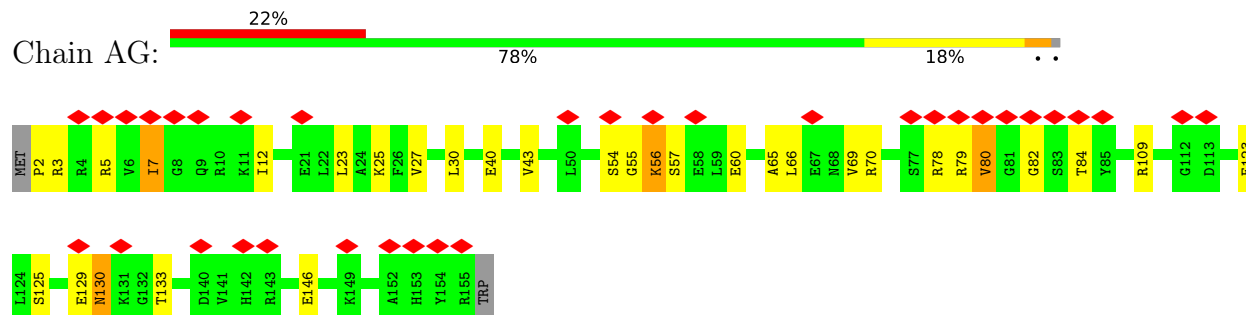
- Molecule 5: 30S ribosomal protein S5



- Molecule 6: 30S ribosomal protein S6

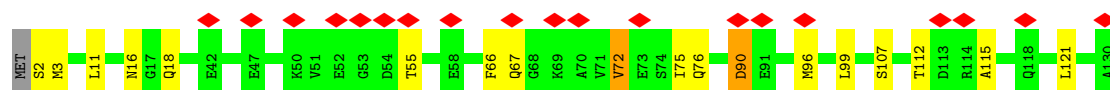


- Molecule 7: 30S ribosomal protein S7



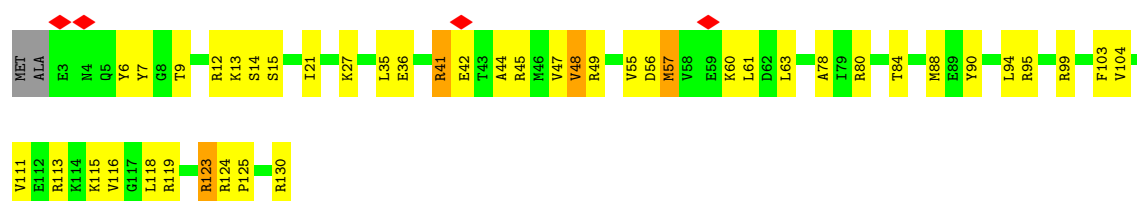
- Molecule 8: 30S ribosomal protein S8

Chain AH: 



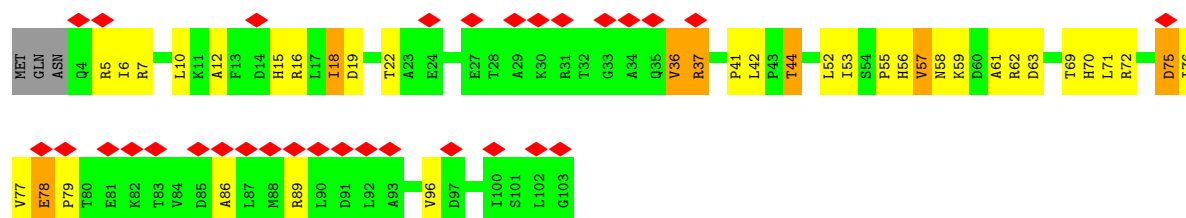
- Molecule 9: 30S ribosomal protein S9

Chain AI: 



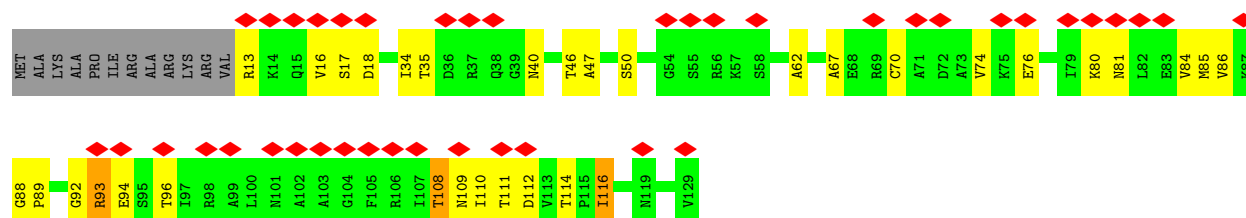
- Molecule 10: 30S ribosomal protein S10

Chain AJ: 



- Molecule 11: 30S ribosomal protein S11

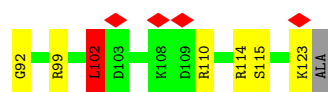
Chain AK: 



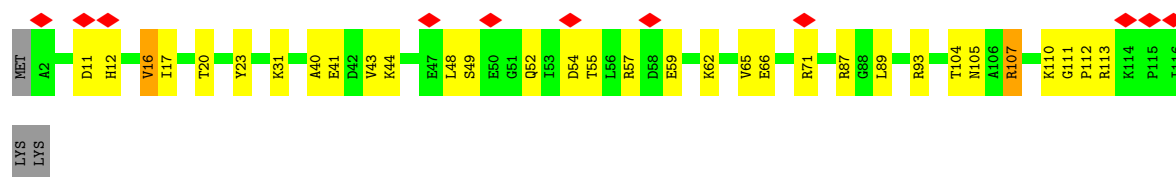
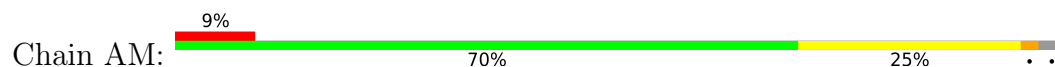
- Molecule 12: 30S ribosomal protein S12

Chain AL: 

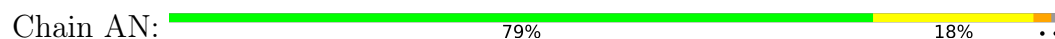




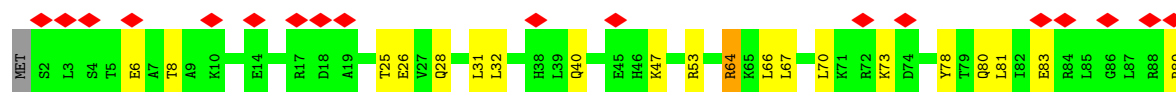
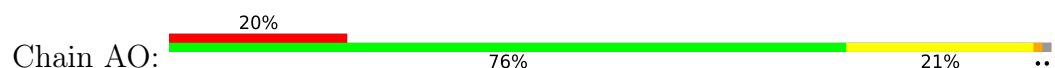
- Molecule 13: 30S ribosomal protein S13



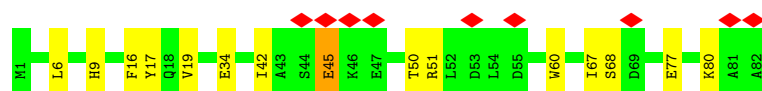
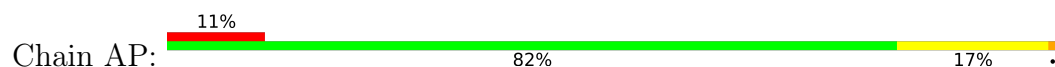
- Molecule 14: 30S ribosomal protein S14



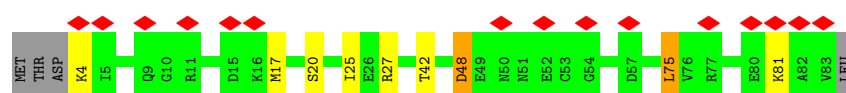
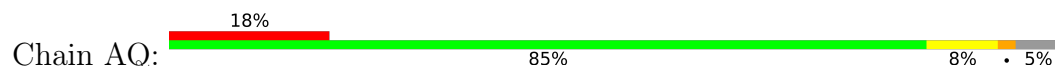
- Molecule 15: 30S ribosomal protein S15



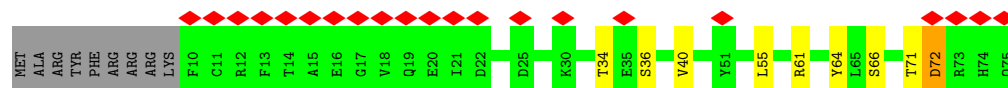
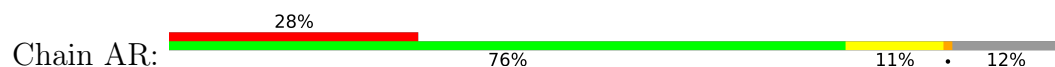
- Molecule 16: 30S ribosomal protein S16



- Molecule 17: 30S ribosomal protein S17



- Molecule 18: 30S ribosomal protein S18



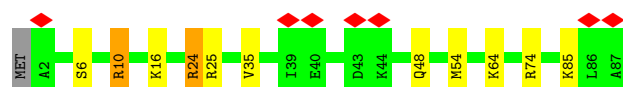
- Molecule 19: 30S ribosomal protein S19

Chain AS: 



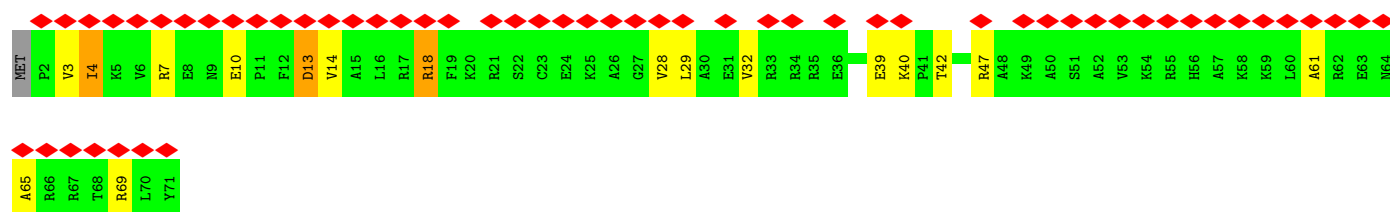
- Molecule 20: 30S ribosomal protein S20

Chain AT: 



- Molecule 21: 30S ribosomal protein S21

Chain AU: 



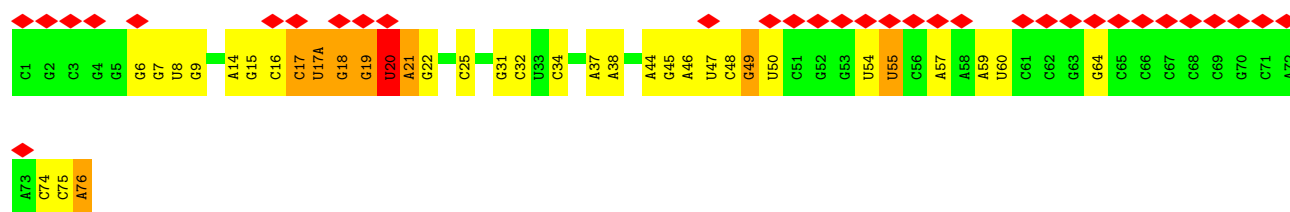
- Molecule 22: mRNA

Chain AV: 



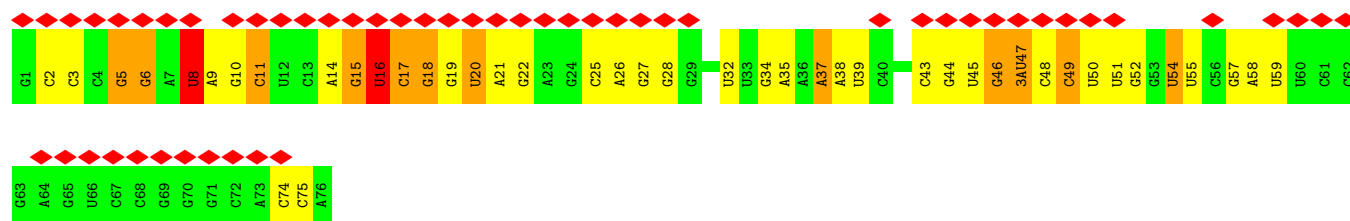
- Molecule 23: tRNA(fmet) P-site

Chain AW: 

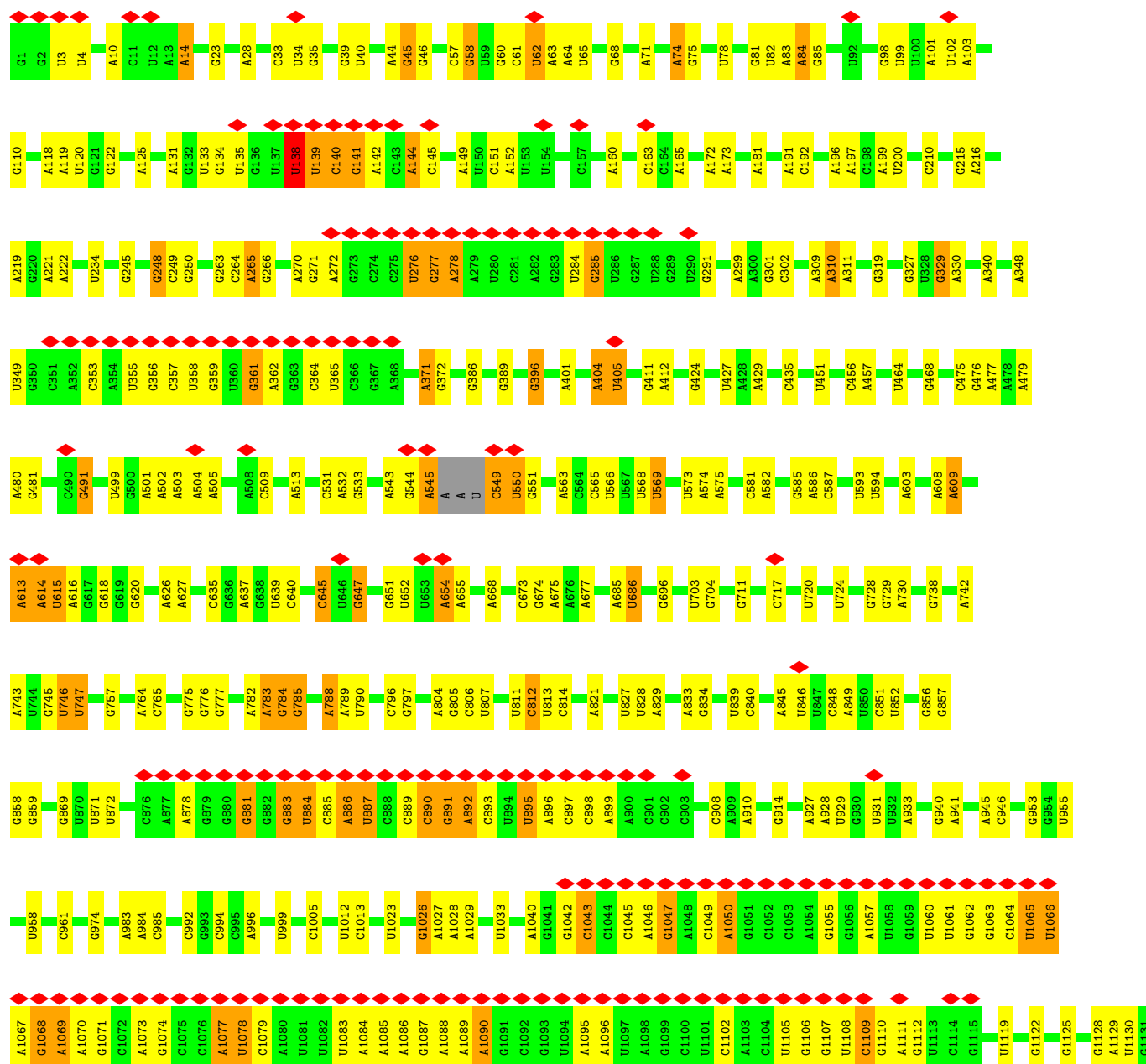


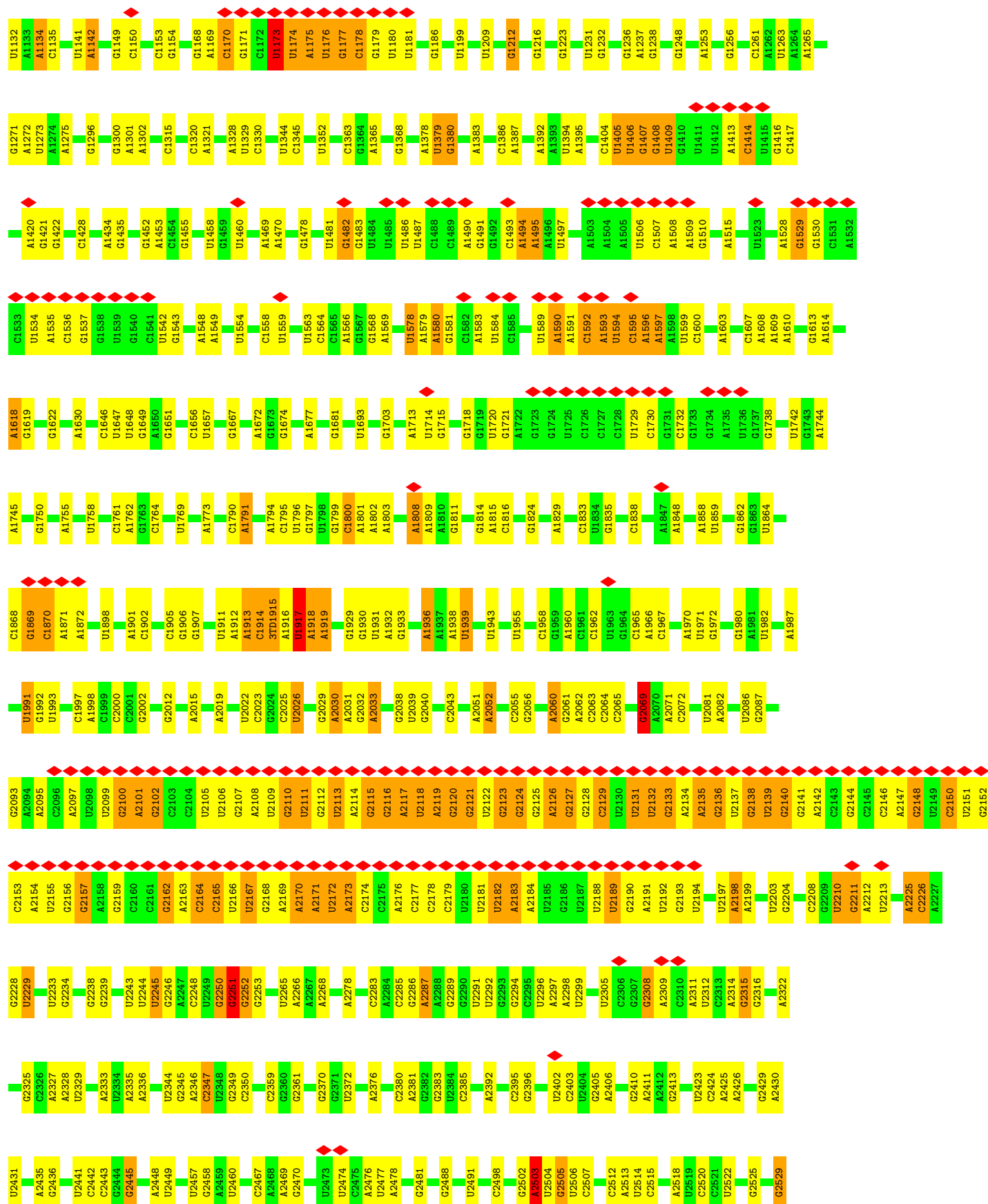
- Molecule 24: Phe-NH-tRNA(Phe) A-site

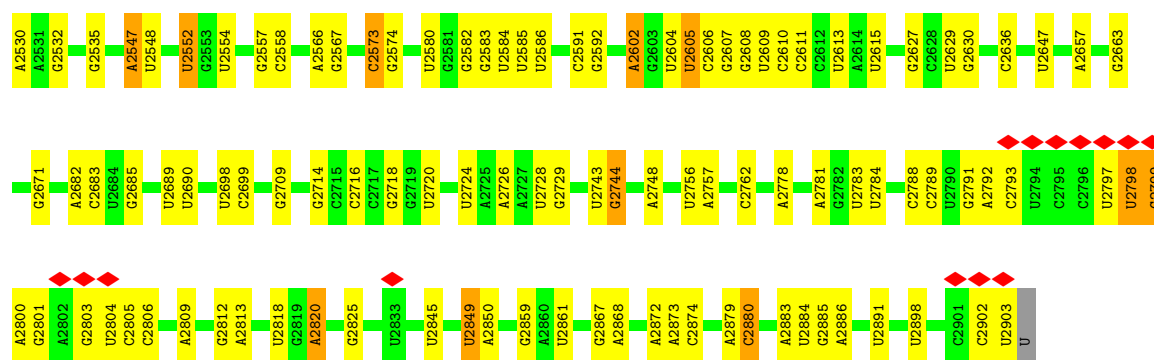
Chain AX: 



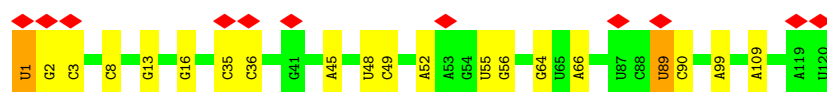
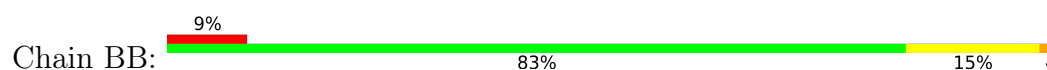
• Molecule 25: 23S ribosomal RNA



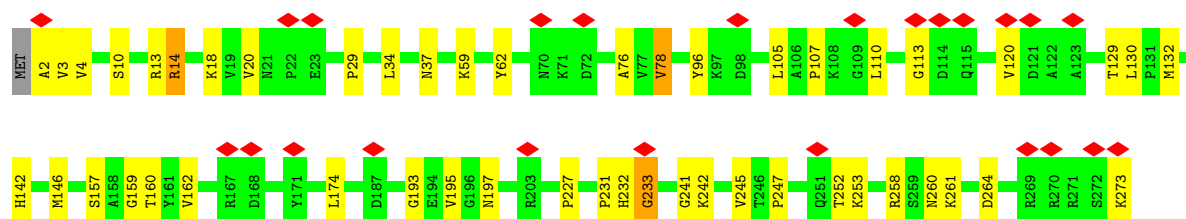
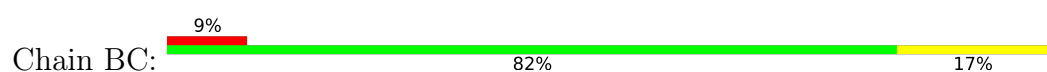




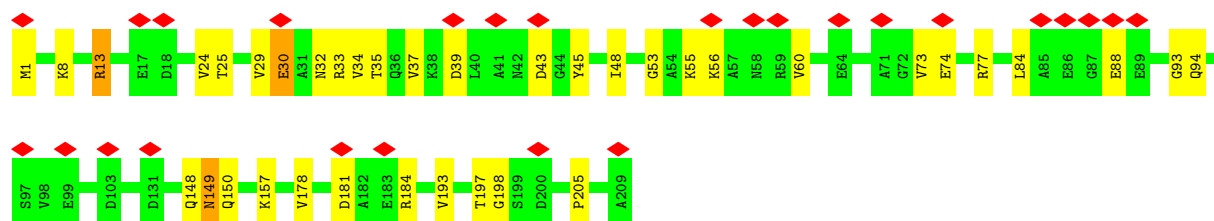
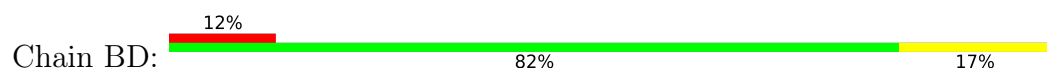
• Molecule 26: 5S ribosomal RNA



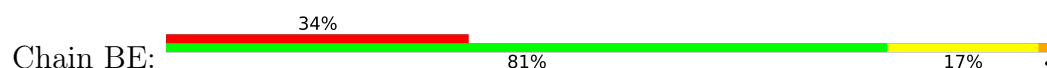
• Molecule 27: 50S ribosomal protein L2

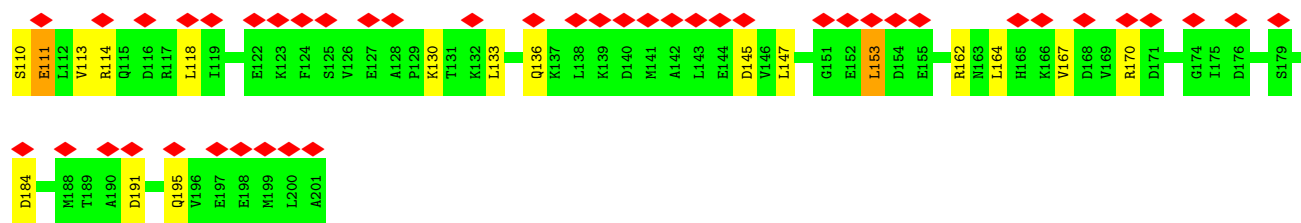


• Molecule 28: 50S ribosomal protein L3

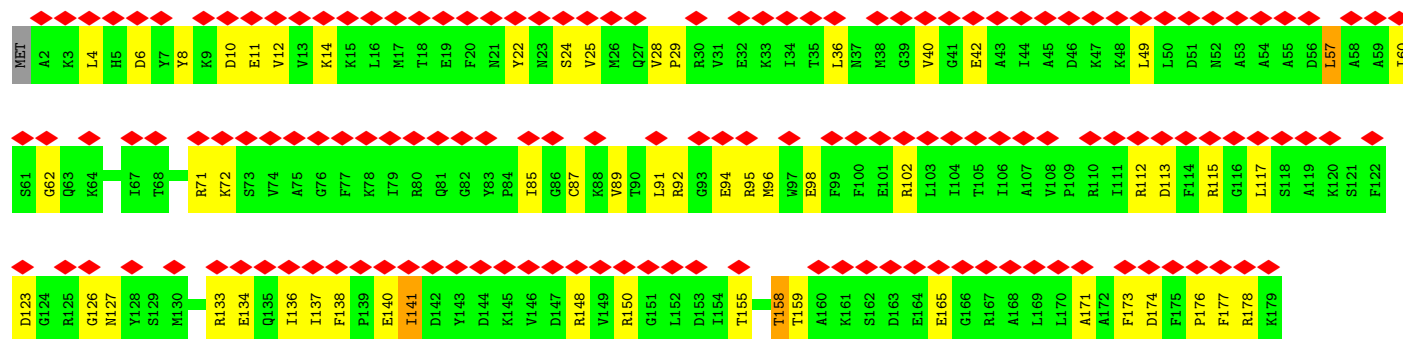
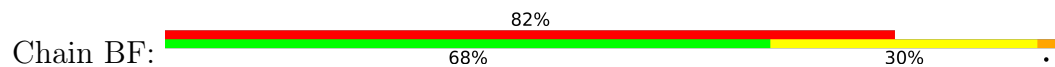


• Molecule 29: 50S ribosomal protein L4

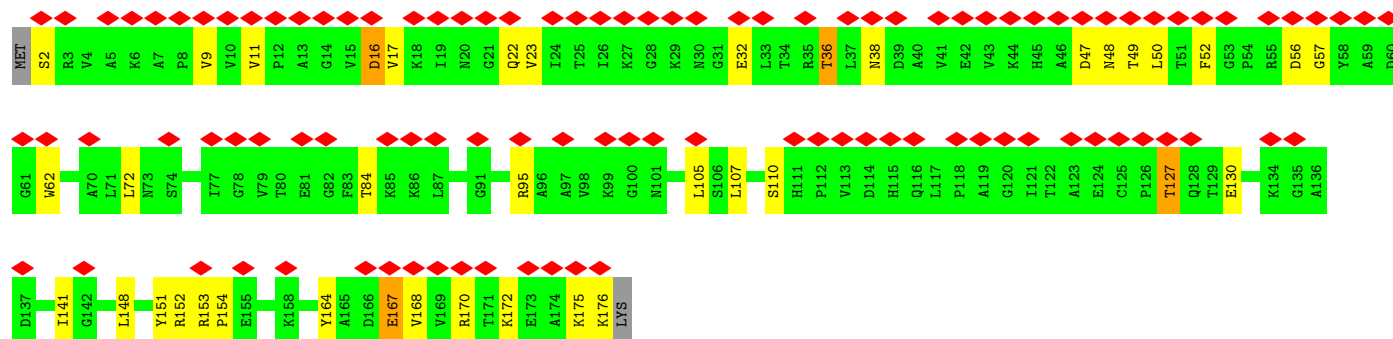
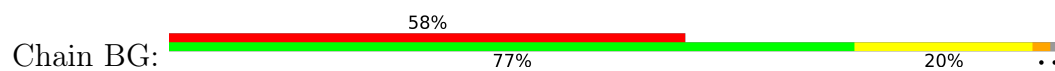




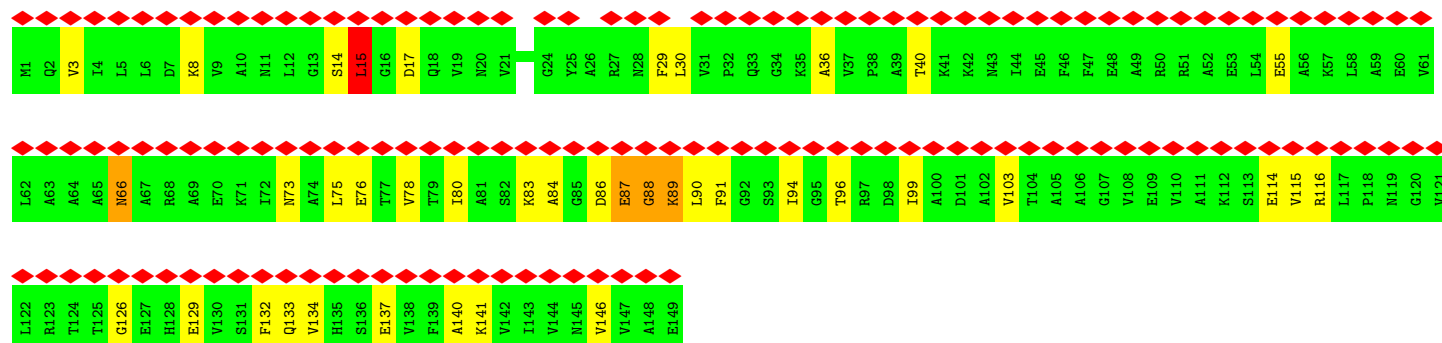
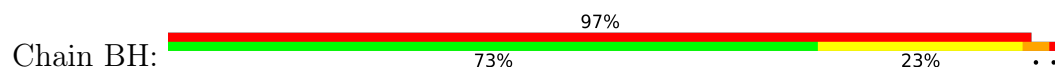
• Molecule 30: 50S ribosomal protein L5



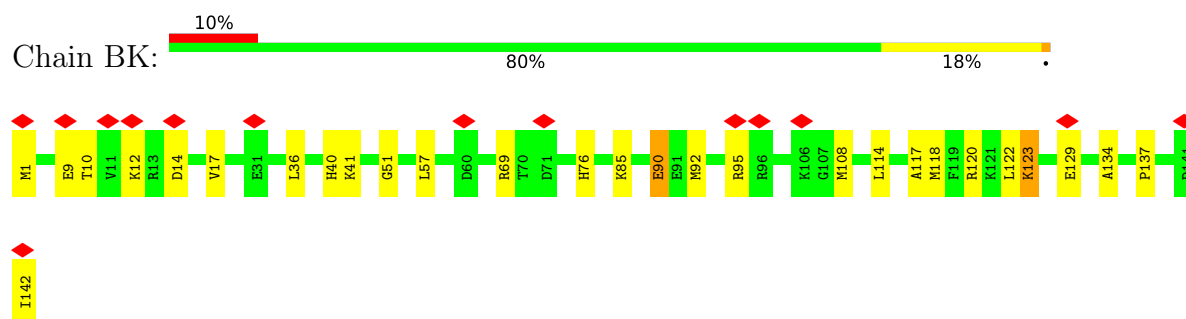
• Molecule 31: 50S ribosomal protein L6



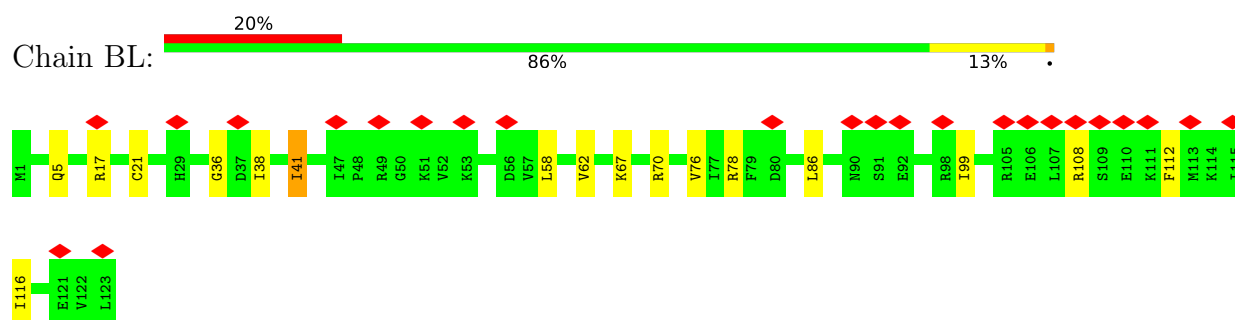
• Molecule 32: 50S ribosomal protein L9



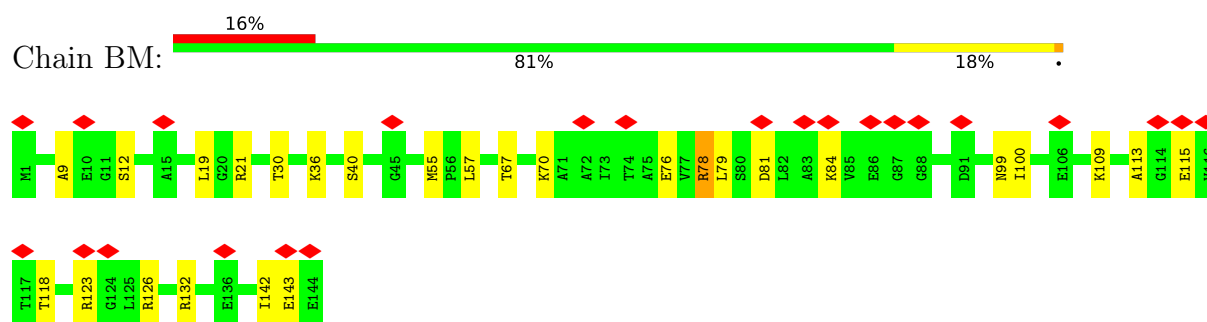
- Molecule 33: 50S ribosomal protein L13



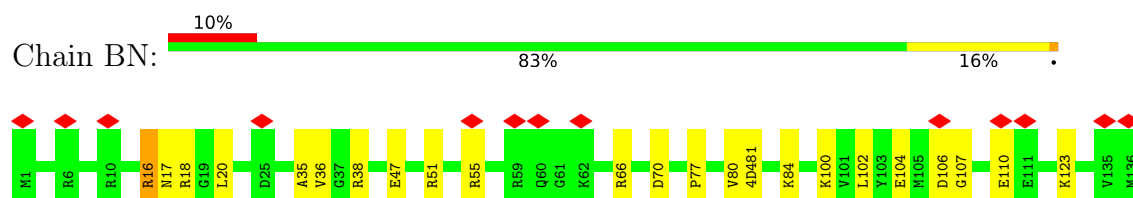
- Molecule 34: 50S ribosomal protein L14



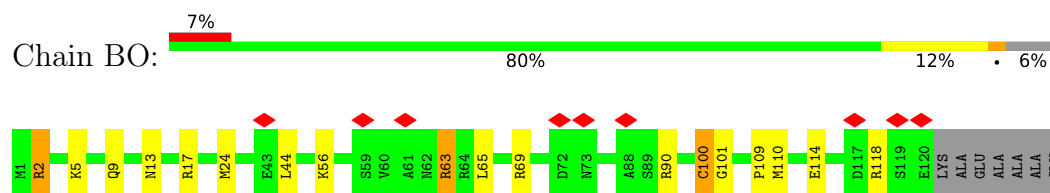
- Molecule 35: 50S ribosomal protein L15



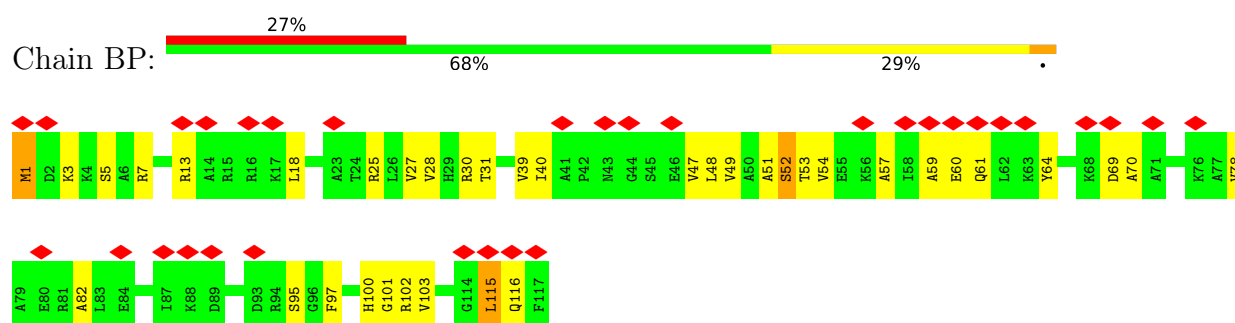
- Molecule 36: 50S ribosomal protein L16



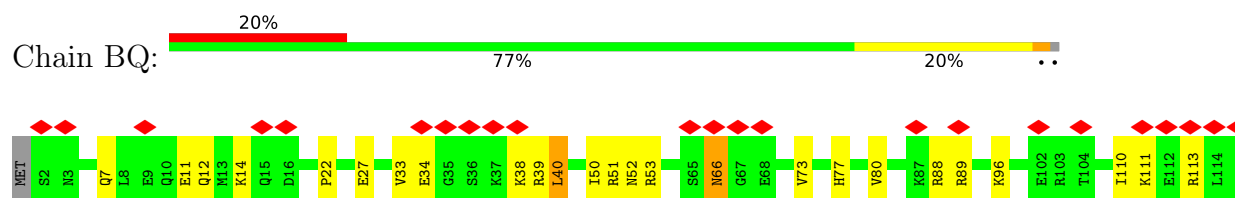
- Molecule 37: 50S ribosomal protein L17



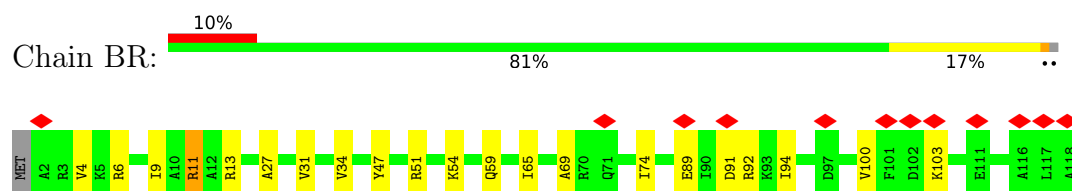
- Molecule 38: 50S ribosomal protein L18



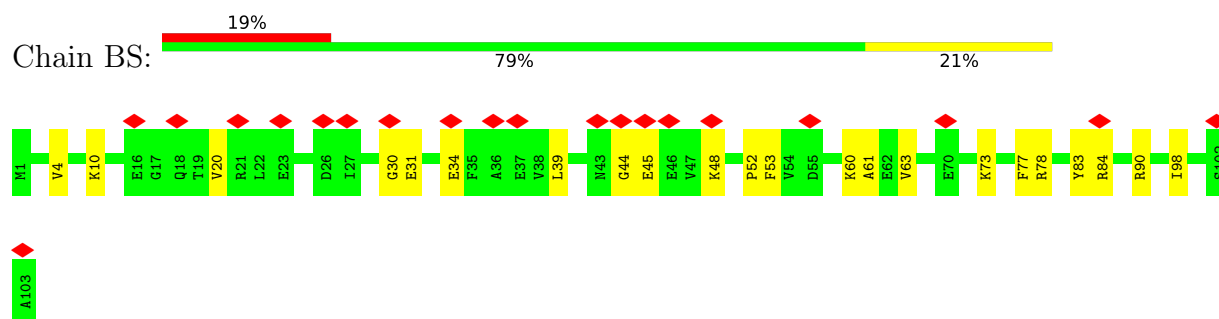
- Molecule 39: 50S ribosomal protein L19



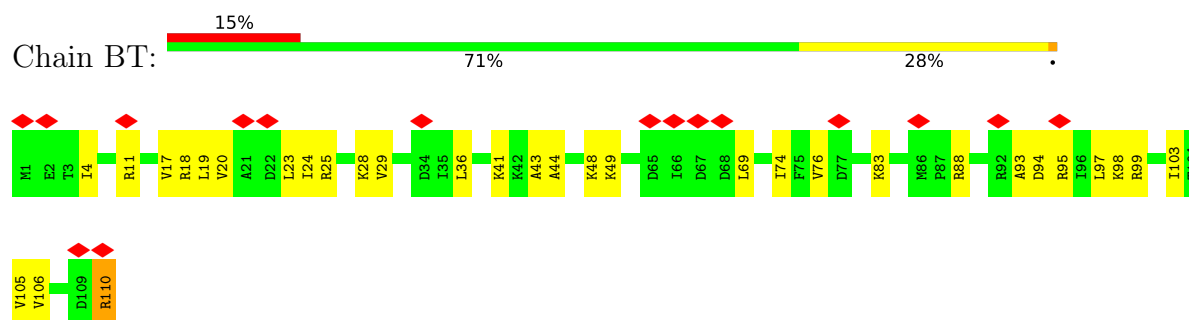
- Molecule 40: 50S ribosomal protein L20



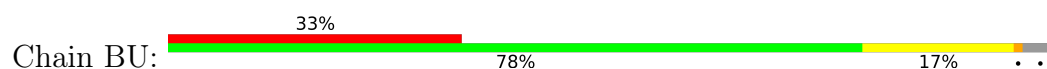
- Molecule 41: 50S ribosomal protein L21

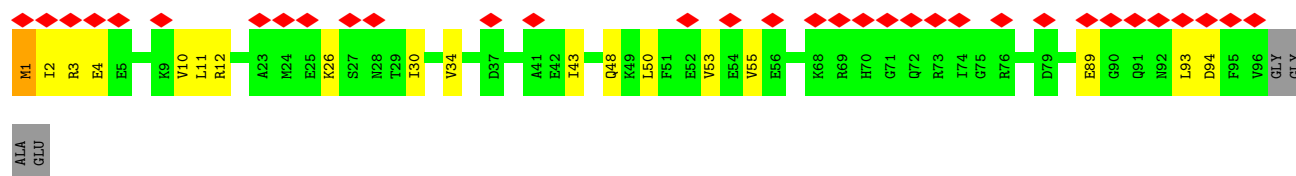


- Molecule 42: 50S ribosomal protein L22



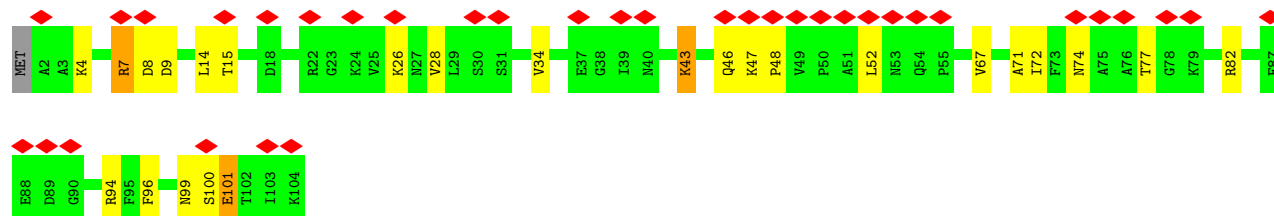
- Molecule 43: 50S ribosomal protein L23





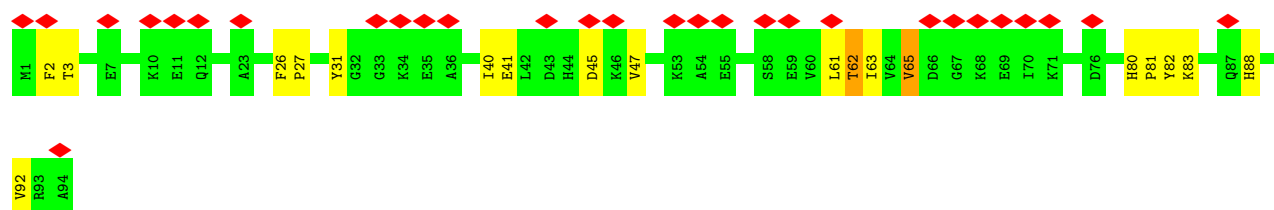
- Molecule 44: 50S ribosomal protein L24

Chain BV: 34% 75% 21% . .



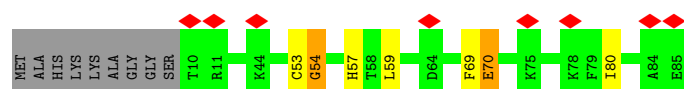
- Molecule 45: 50S ribosomal protein L25

Chain BW: 31% 80% 18% .



- Molecule 46: 50S ribosomal protein L27

Chain BX: 9% 81% 6% 11%



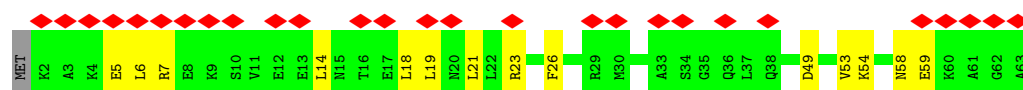
- Molecule 47: 50S ribosomal protein L28

Chain BY: 17% 79% 19%

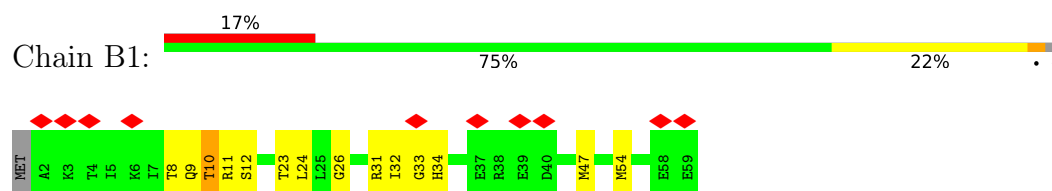


- Molecule 48: 50S ribosomal protein L29

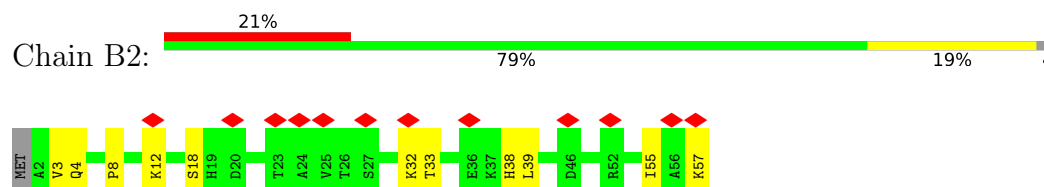
Chain BZ: 43% 76% 22%



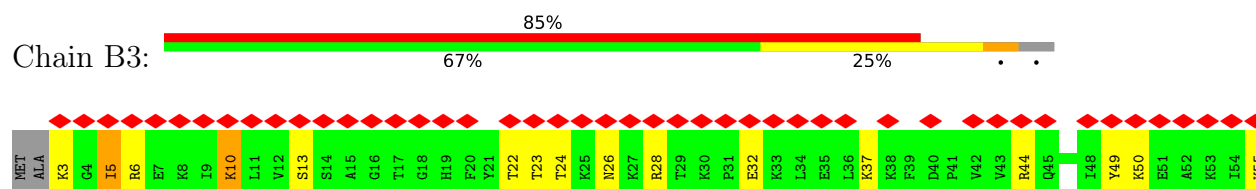
• Molecule 49: 50S ribosomal protein L30



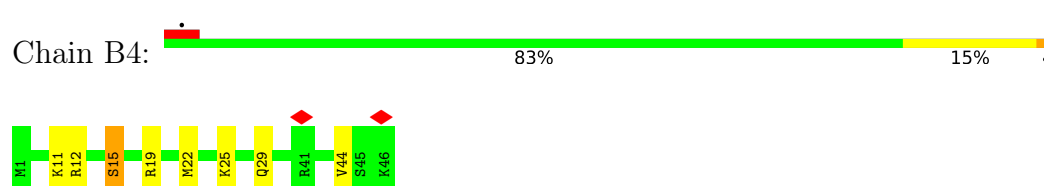
• Molecule 50: 50S ribosomal protein L32



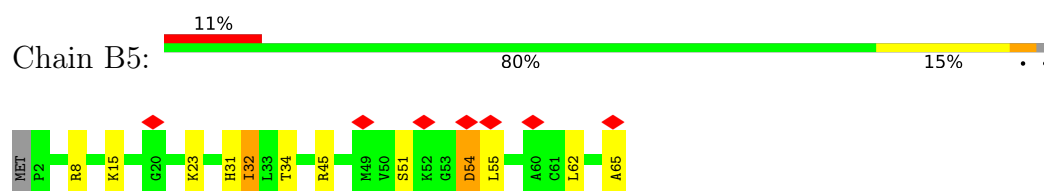
• Molecule 51: 50S ribosomal protein L33



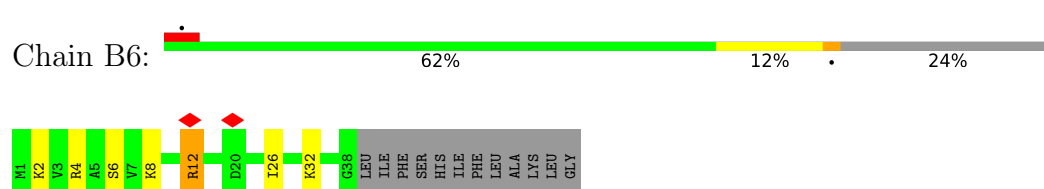
• Molecule 52: 50S ribosomal protein L34



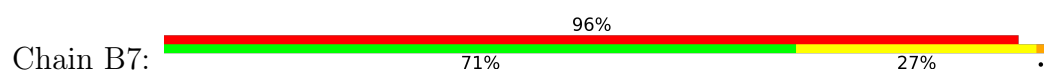
• Molecule 53: 50S ribosomal protein L35

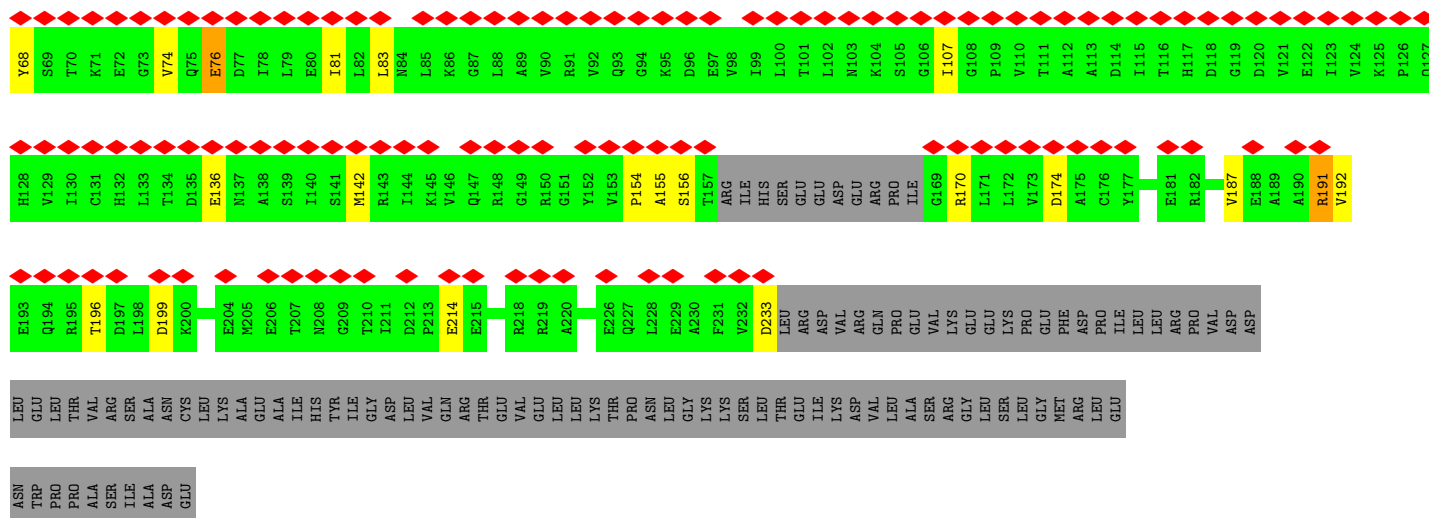


• Molecule 54: 50S ribosomal protein L36

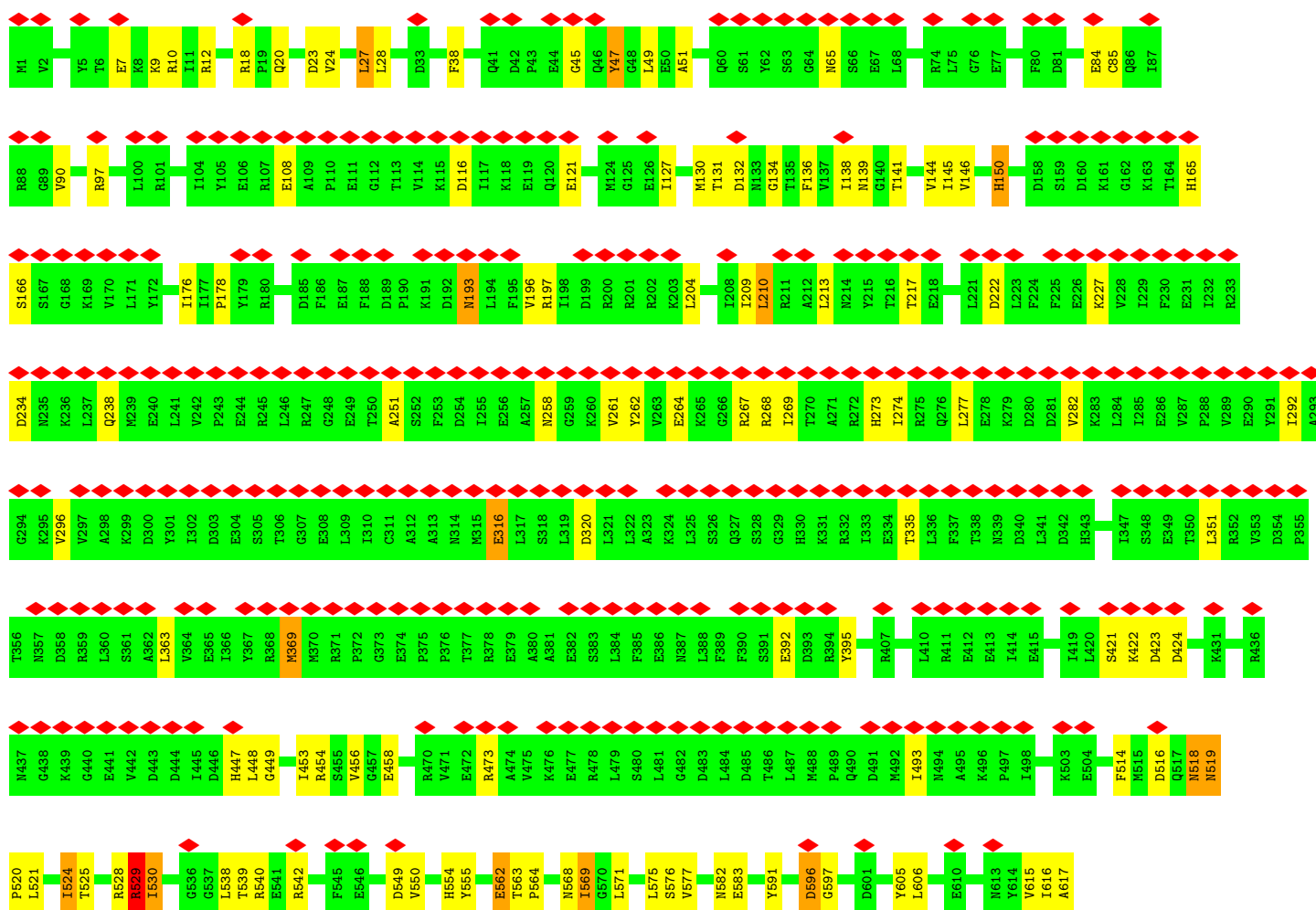
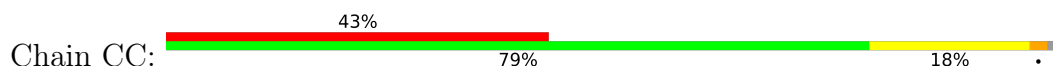


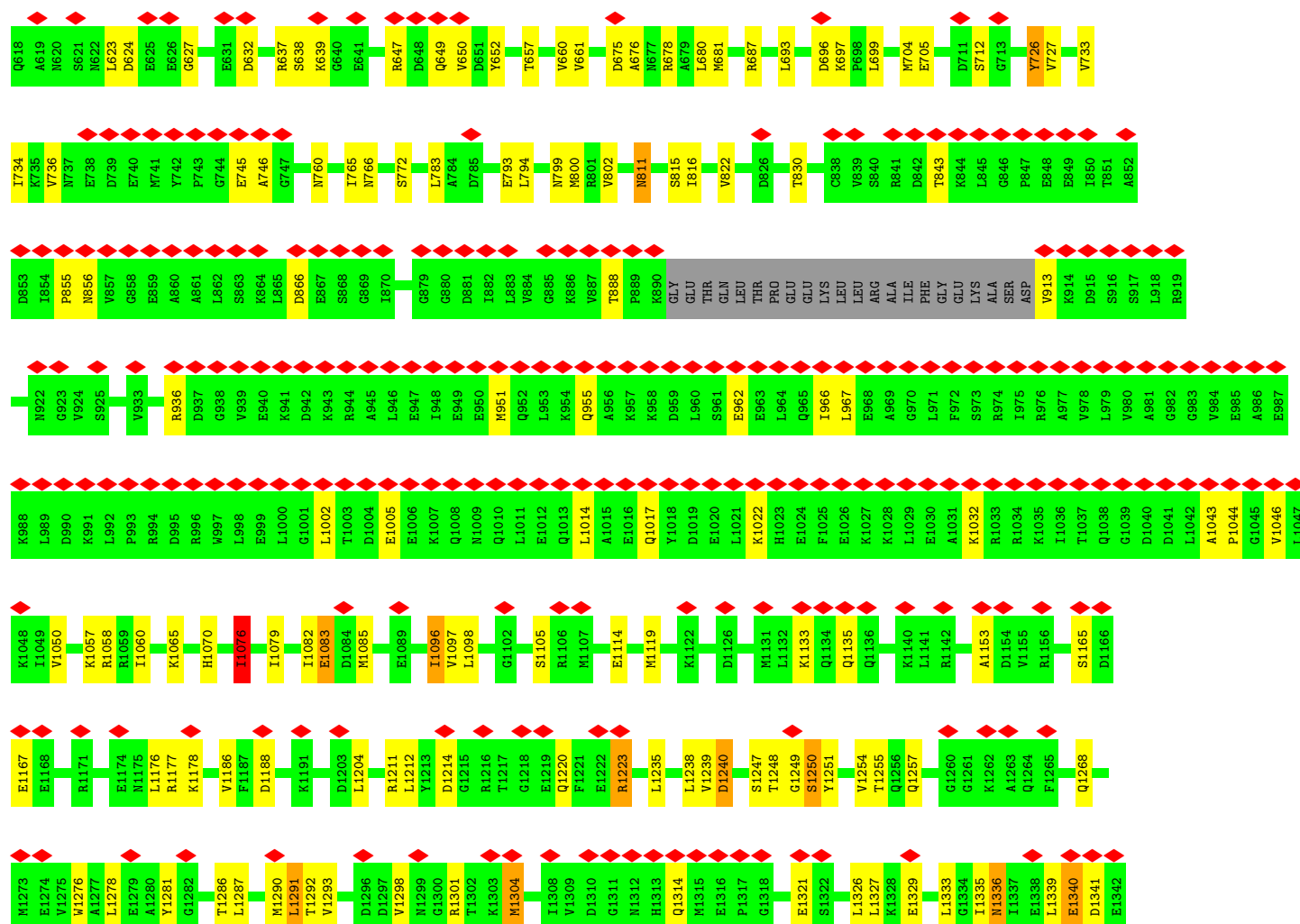
• Molecule 55: 50S ribosomal protein L31



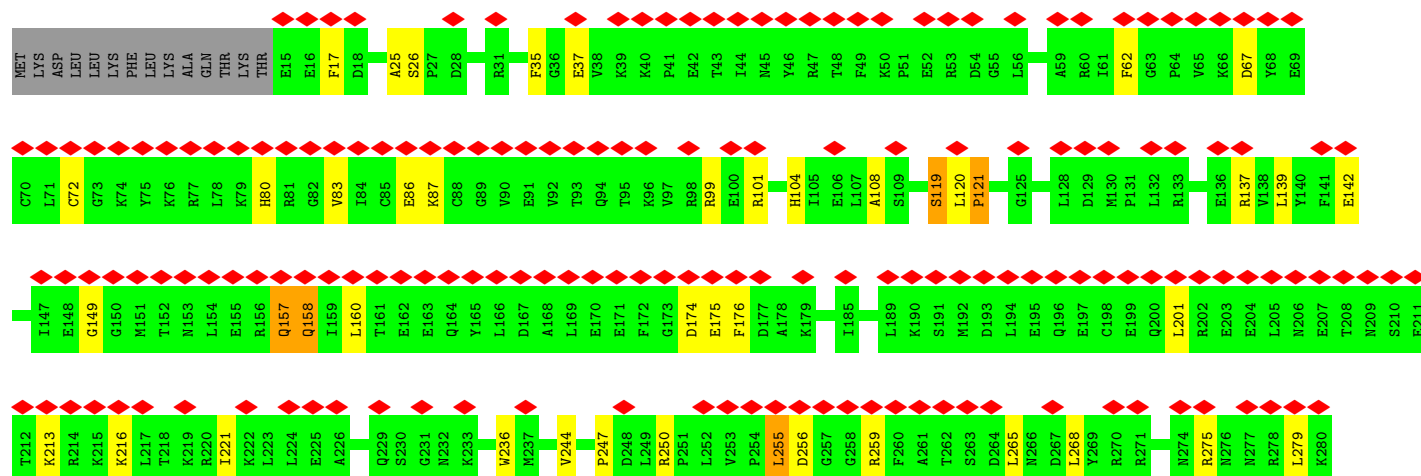
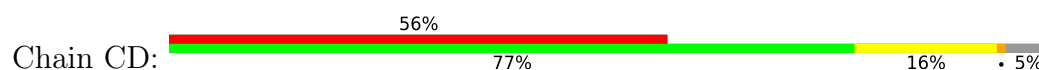


• Molecule 59: DNA-directed RNA polymerase subunit beta

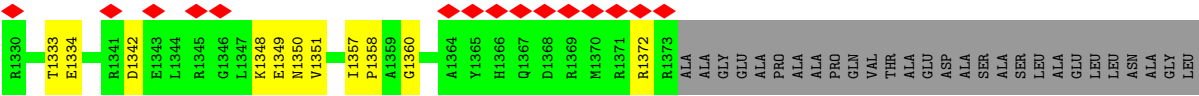
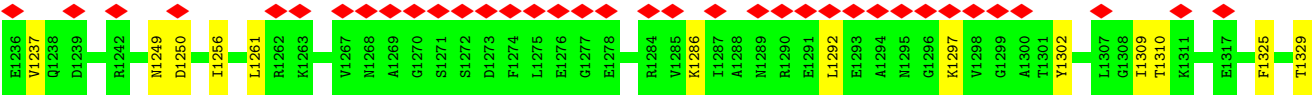




• Molecule 60: DNA-directed RNA polymerase subunit beta'

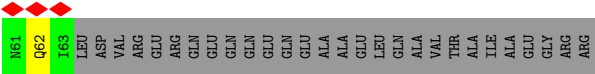
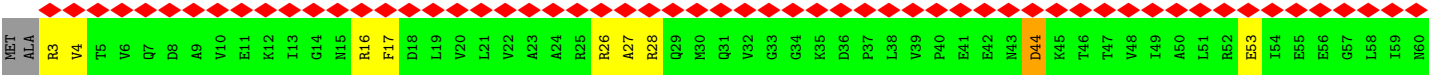






GLY
GLY
SER
ASP
ASN
GLU

● Molecule 61: DNA-directed RNA polymerase subunit omega



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	32195	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	2.947	Depositor
Minimum map value	-0.370	Depositor
Average map value	0.029	Depositor
Map value standard deviation	0.076	Depositor
Recommended contour level	0.5	Depositor
Map size ($\text{\AA}$)	547.04004, 547.04004, 547.04004	wwPDB
Map dimensions	520, 520, 520	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.052, 1.052, 1.052	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.51	0/36569	0.54	2/57044 (0.0%)
2	AB	0.28	0/1796	0.57	0/2420
3	AC	0.47	0/1667	0.62	0/2246
4	AD	0.35	0/1665	0.60	0/2227
5	AE	0.39	0/1161	0.63	0/1563
6	AF	0.35	0/867	0.70	0/1171
7	AG	0.35	0/1230	0.71	4/1649 (0.2%)
8	AH	0.36	0/989	0.54	0/1326
9	AI	0.51	0/1043	0.75	2/1387 (0.1%)
10	AJ	0.47	0/810	0.76	0/1094
11	AK	0.34	0/893	0.60	0/1205
12	AL	0.41	0/954	0.75	1/1279 (0.1%)
13	AM	0.41	0/900	0.65	0/1204
14	AN	0.49	0/817	0.57	0/1088
15	AO	0.34	0/722	0.61	0/964
16	AP	0.41	0/659	0.59	0/884
17	AQ	0.38	0/657	0.57	0/881
18	AR	0.33	0/554	0.67	0/743
19	AS	0.47	0/680	0.67	0/915
20	AT	0.41	0/676	0.57	0/895
21	AU	0.27	0/598	0.59	0/792
22	AV	0.97	0/637	0.86	1/987 (0.1%)
23	AW	0.38	0/1725	0.55	0/2687
24	AX	0.26	0/1584	0.31	0/2463
25	BA	0.43	2/69165 (0.0%)	0.52	4/107893 (0.0%)
26	BB	0.36	0/2872	0.45	0/4478
27	BC	0.40	0/2131	0.64	2/2863 (0.1%)
28	BD	0.41	0/1576	0.61	0/2119
29	BE	0.34	0/1571	0.59	0/2113
30	BF	0.27	0/1444	0.58	0/1937
31	BG	0.28	0/1333	0.58	0/1805

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	BH	0.23	0/1122	0.68	2/1515 (0.1%)
33	BK	0.37	0/1152	0.55	0/1551
34	BL	0.39	0/956	0.62	0/1279
35	BM	0.38	0/1061	0.67	0/1412
36	BN	0.36	0/1081	0.56	0/1443
37	BO	0.42	0/973	0.66	0/1301
38	BP	0.32	0/910	0.64	0/1219
39	BQ	0.38	0/929	0.61	0/1242
40	BR	0.45	0/960	0.64	0/1278
41	BS	0.38	0/829	0.74	0/1107
42	BT	0.39	0/864	0.63	0/1156
43	BU	0.32	0/771	0.56	0/1031
44	BV	0.30	0/797	0.58	0/1062
45	BW	0.34	0/766	0.59	0/1025
46	BX	0.37	0/589	0.54	0/779
47	BY	0.37	0/635	0.54	0/848
48	BZ	0.29	0/502	0.57	0/667
49	B1	0.36	0/453	0.64	0/605
50	B2	0.38	0/450	0.61	0/599
51	B3	0.26	0/443	0.71	0/587
52	B4	0.43	0/379	0.62	0/496
53	B5	0.37	0/513	0.70	0/676
54	B6	0.42	0/302	0.65	0/397
55	B7	0.25	0/559	0.72	0/745
56	CN	0.79	0/693	0.77	0/1068
57	CT	1.18	0/676	0.83	0/1039
58	CA	1.10	0/1797	0.96	0/2436
58	CB	0.81	0/1703	0.90	0/2308
59	CC	1.34	17/10581 (0.2%)	1.05	2/14275 (0.0%)
60	CD	1.10	6/10532 (0.1%)	0.97	3/14219 (0.0%)
61	CE	0.49	0/480	0.83	0/647
All	All	0.60	25/184403 (0.0%)	0.63	23/272334 (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	1
5	AE	0	1
13	AM	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
22	AV	0	1
25	BA	0	1
37	BO	0	1
46	BX	0	1
53	B5	0	1
All	All	0	8

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	CC	799	ASN	CB-CG	-6.30	1.36	1.52
60	CD	424	ASN	CB-CG	-6.30	1.36	1.52
59	CC	519	ASN	CB-CG	-6.21	1.36	1.52
59	CC	530	ILE	CB-CG2	-6.16	1.32	1.52
60	CD	760	THR	CA-C	-6.09	1.42	1.52
59	CC	1076	ILE	CB-CG1	-6.07	1.41	1.53
59	CC	518	ASN	CB-CG	-5.97	1.37	1.52
59	CC	146	VAL	CB-CG1	-5.59	1.34	1.52
59	CC	144	VAL	CB-CG1	-5.53	1.34	1.52
25	BA	543	A	C1'-N9	-5.50	1.39	1.48
25	BA	545	A	C1'-N9	-5.46	1.39	1.48
60	CD	1357	ILE	C-N	-5.46	1.15	1.34
60	CD	424	ASN	CA-CB	-5.45	1.43	1.53
59	CC	811	ASN	CB-CG	-5.43	1.38	1.52
60	CD	1333	THR	CB-CG2	-5.36	1.34	1.52
59	CC	146	VAL	CB-CG2	-5.35	1.34	1.52
60	CD	1145	PHE	CB-CG	-5.31	1.38	1.50
59	CC	136	PHE	CB-CG	-5.31	1.38	1.50
59	CC	453	ILE	CB-CG2	-5.31	1.35	1.52
59	CC	816	ILE	CB-CG2	-5.31	1.35	1.52
59	CC	712	SER	CA-C	-5.23	1.31	1.52
59	CC	27	LEU	CG-CD2	-5.21	1.35	1.52
59	CC	802	VAL	CB-CG1	-5.20	1.35	1.52
59	CC	520	PRO	CB-CG	-5.18	1.23	1.49
59	CC	1096	ILE	CB-CG2	-5.17	1.35	1.52

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	AV	49	G	O3'-P-O5'	-8.34	91.50	104.00
59	CC	529	ARG	CA-CB-CG	6.25	126.60	114.10
25	BA	1173	U	C5'-C4'-O4'	-6.00	100.81	109.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	BH	88	GLY	CA-C-N	5.65	132.32	121.54
32	BH	88	GLY	C-N-CA	5.65	132.32	121.54
7	AG	55	GLY	N-CA-C	5.61	126.48	113.18
12	AL	44	LYS	N-CA-C	5.54	122.07	109.81
7	AG	54	SER	CA-C-N	-5.43	110.76	121.41
7	AG	54	SER	C-N-CA	-5.43	110.76	121.41
59	CC	210	LEU	CA-CB-CG	-5.33	97.64	116.30
25	BA	2573	C	N1-C1'-C2'	-5.26	104.11	112.00
1	AA	4	U	P-O3'-C3'	5.22	128.03	120.20
60	CD	1329	THR	CA-C-N	-5.20	113.55	120.63
60	CD	1329	THR	C-N-CA	-5.20	113.55	120.63
7	AG	56	LYS	N-CA-C	5.16	121.79	110.80
25	BA	138	U	N1-C1'-C2'	-5.15	104.28	112.00
9	AI	12	ARG	CA-C-N	5.15	131.37	121.54
9	AI	12	ARG	C-N-CA	5.15	131.37	121.54
27	BC	78	VAL	CA-C-N	5.06	129.08	120.88
27	BC	78	VAL	C-N-CA	5.06	129.08	120.88
60	CD	502	PRO	N-CA-C	5.04	119.12	110.95
1	AA	4	U	C2'-C3'-O3'	5.03	117.05	109.50
25	BA	1173	U	C2'-C3'-O3'	-5.02	106.18	113.70

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	1034	G	Sidechain
5	AE	89	HIS	Peptide
13	AM	65	VAL	Peptide
22	AV	45	C	Sidechain
53	B5	31	HIS	Peptide
25	BA	138	U	Sidechain
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	32909	0	16580	277	0
2	AB	1765	0	1792	65	0
3	AC	1640	0	1713	31	0
4	AD	1643	0	1707	33	0
5	AE	1148	0	1195	20	0
6	AF	848	0	846	31	0
7	AG	1214	0	1267	18	0
8	AH	979	0	1031	10	0
9	AI	1031	0	1076	33	0
10	AJ	800	0	839	28	0
11	AK	877	0	887	26	0
12	AL	951	0	1012	26	0
13	AM	891	0	952	23	0
14	AN	805	0	844	14	0
15	AO	714	0	734	12	0
16	AP	649	0	666	8	0
17	AQ	648	0	691	6	0
18	AR	545	0	560	6	0
19	AS	663	0	688	11	0
20	AT	670	0	719	11	0
21	AU	590	0	629	13	0
22	AV	572	0	294	21	0
23	AW	1645	0	842	14	0
24	AX	1630	0	837	30	0
25	BA	62270	0	31335	453	0
26	BB	2569	0	1301	11	0
27	BC	2092	0	2167	33	0
28	BD	1566	0	1618	27	0
29	BE	1552	0	1618	23	0
30	BF	1420	0	1457	35	0
31	BG	1313	0	1358	20	0
32	BH	1111	0	1148	31	0
33	BK	1129	0	1162	13	0
34	BL	947	0	1023	10	0
35	BM	1052	0	1127	12	0
36	BN	1075	0	1155	13	0
37	BO	960	0	1000	12	0
38	BP	900	0	935	22	0
39	BQ	917	0	962	13	0
40	BR	947	0	1019	16	0
41	BS	816	0	839	10	0
42	BT	857	0	922	26	0
43	BU	764	0	829	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	BV	789	0	843	14	0
45	BW	753	0	780	11	0
46	BX	582	0	598	4	0
47	BY	625	0	652	6	0
48	BZ	501	0	531	8	0
49	B1	449	0	488	7	0
50	B2	444	0	458	7	0
51	B3	436	0	477	13	0
52	B4	376	0	414	7	0
53	B5	504	0	572	9	0
54	B6	301	0	340	4	0
55	B7	549	0	551	15	0
56	CN	618	0	339	27	0
57	CT	606	0	338	37	0
58	CA	1775	0	1800	19	0
58	CB	1684	0	1713	18	0
59	CC	10415	0	10432	186	0
60	CD	10375	0	10597	172	0
61	CE	478	0	496	26	0
62	AA	143	0	0	0	0
62	AI	1	0	0	0	0
62	AL	1	0	0	0	0
62	AM	1	0	0	0	0
62	AW	5	0	0	0	0
62	AX	1	0	0	0	0
62	BA	317	0	0	0	0
62	BB	9	0	0	0	0
62	BC	3	0	0	0	0
62	BN	1	0	0	0	0
62	BO	1	0	0	0	0
62	BQ	1	0	0	0	0
62	BV	1	0	0	0	0
62	BX	1	0	0	0	0
62	CD	1	0	0	0	0
63	AX	11	0	8	1	0
64	B6	1	0	0	0	0
64	B7	1	0	0	0	0
64	CD	2	0	0	0	0
All	All	172846	0	123803	1897	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (1897) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:226:SER:N	61:CE:62:GLN:HE22	1.17	1.42
2:AB:226:SER:N	61:CE:62:GLN:NE2	1.66	1.41
2:AB:227:GLN:CB	60:CD:1372:ARG:NH2	1.84	1.41
2:AB:227:GLN:HB2	60:CD:1372:ARG:NH2	1.10	1.37
2:AB:226:SER:CA	61:CE:62:GLN:NE2	2.21	1.04
2:AB:227:GLN:CB	60:CD:1372:ARG:HH21	1.71	0.94
25:BA:2285:C:OP2	51:B3:6:ARG:NH1	1.99	0.94
1:AA:481:G:O2'	1:AA:483:C:N4	2.01	0.93
25:BA:1936:A:H2	25:BA:1943:U:H3	1.16	0.92
1:AA:411:A:H4'	1:AA:412:A:H5'	1.53	0.90
2:AB:226:SER:CA	61:CE:62:GLN:HE21	1.81	0.90
18:AR:36:SER:HA	18:AR:72:ASP:HB2	1.52	0.90
24:AX:18:G:O2'	24:AX:57:G:N2	2.07	0.88
2:AB:227:GLN:CB	60:CD:1372:ARG:HH22	1.71	0.88
13:AM:107:ARG:NH1	13:AM:111:GLY:O	2.07	0.88
6:AF:86:ARG:NH1	18:AR:64:TYR:O	2.08	0.87
25:BA:1216:G:OP1	40:BR:11:ARG:NH1	2.09	0.86
2:AB:227:GLN:HB2	60:CD:1372:ARG:CZ	2.04	0.86
17:AQ:48:ASP:HB2	17:AQ:75:LEU:HD23	1.59	0.84
17:AQ:27:ARG:NH1	17:AQ:42:THR:OG1	2.10	0.84
6:AF:42:TRP:HB3	6:AF:45:ARG:HH11	1.40	0.84
1:AA:522:C:O2	1:AA:527:G7M:N2	2.10	0.83
9:AI:119:ARG:HH11	9:AI:125:PRO:HB3	1.44	0.82
22:AV:51:G:H2'	22:AV:52:C:H6	1.44	0.82
2:AB:227:GLN:HB3	60:CD:1372:ARG:NH2	1.91	0.82
5:AE:115:LEU:HD13	5:AE:123:VAL:HG11	1.58	0.82
2:AB:222:ARG:O	61:CE:62:GLN:OE1	1.98	0.81
48:BZ:14:LEU:HD22	48:BZ:53:VAL:HG23	1.62	0.81
1:AA:864:A:H5''	5:AE:90:THR:HB	1.63	0.81
25:BA:2880:C:O2'	37:BO:90:ARG:NH1	2.14	0.81
22:AV:50:C:H2'	22:AV:51:G:H8	1.43	0.81
3:AC:77:ILE:HA	3:AC:84:VAL:HG23	1.63	0.80
25:BA:1590:A:H2'	25:BA:1591:A:C8	2.16	0.80
25:BA:2164:C:OP2	25:BA:2170:A:N6	2.15	0.80
1:AA:1025:U:H5''	1:AA:1026:G:H5'	1.64	0.79
25:BA:475:C:O2	25:BA:479:A:N6	2.15	0.79
60:CD:429:LEU:H	60:CD:429:LEU:HD22	1.47	0.79
12:AL:83:ARG:NH1	12:AL:84:GLY:O	2.16	0.79
1:AA:537:G:OP1	12:AL:110:ARG:NH2	2.15	0.78
25:BA:783:A:H2'	25:BA:783:A:N3	1.99	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:CD:1186:TYR:OH	60:CD:1188:GLU:OE1	2.01	0.78
2:AB:227:GLN:HB2	60:CD:1372:ARG:HH21	1.27	0.78
25:BA:2718:G:O4'	25:BA:2718:G:O2'	1.90	0.78
29:BE:111:GLU:OE1	29:BE:114:ARG:NH1	2.16	0.78
57:CT:18:DC:H2'	57:CT:19:DG:C8	2.19	0.78
1:AA:1239:A:H62	1:AA:1299:A:H62	1.30	0.78
5:AE:111:MET:HE2	5:AE:125:ALA:HB1	1.66	0.78
25:BA:2685:G:OP1	34:BL:78:ARG:NH2	2.17	0.77
58:CB:191:ARG:HB3	58:CB:196:THR:HG23	1.64	0.77
24:AX:26:A:H61	24:AX:44:G:H1	1.29	0.77
25:BA:284:U:H3	25:BA:356:G:H1	1.32	0.77
58:CB:74:VAL:HG21	58:CB:81:ILE:HD11	1.66	0.77
11:AK:88:GLY:O	11:AK:93:ARG:NH1	2.18	0.77
25:BA:2069:G7M:N2	25:BA:2442:C:O2	2.12	0.76
27:BC:78:VAL:O	27:BC:113:GLY:N	2.15	0.76
25:BA:1528:A:H2'	25:BA:1529:G:O4'	1.84	0.76
2:AB:226:SER:HA	61:CE:62:GLN:HE21	1.50	0.76
9:AI:84:THR:HG21	9:AI:103:PHE:HB3	1.67	0.76
12:AL:68:GLY:O	12:AL:99:ARG:NH1	2.19	0.76
28:BD:8:LYS:O	28:BD:198:GLY:N	2.18	0.76
25:BA:2135:A:H3'	25:BA:2136:G:H8	1.51	0.76
2:AB:227:GLN:HB2	60:CD:1372:ARG:HH22	1.22	0.75
24:AX:26:A:N6	24:AX:44:G:H1	1.83	0.75
25:BA:2116:G:H1	25:BA:2164:C:H42	1.32	0.75
38:BP:7:ARG:NH1	38:BP:95:SER:O	2.19	0.75
22:AV:50:C:H2'	22:AV:51:G:C8	2.21	0.75
25:BA:1918:A:O2'	25:BA:1919:A:N7	2.19	0.75
58:CA:62:ASP:OD1	58:CA:63:GLY:N	2.19	0.75
25:BA:2467:C:O2	36:BN:123:LYS:NZ	2.20	0.75
43:BU:30:ILE:HG21	43:BU:93:LEU:HD13	1.69	0.75
4:AD:147:GLU:HA	4:AD:150:LYS:HB2	1.67	0.75
33:BK:12:LYS:NZ	33:BK:14:ASP:OD1	2.20	0.74
2:AB:226:SER:H	61:CE:62:GLN:NE2	1.54	0.74
47:BY:41:GLU:OE2	47:BY:44:LYS:NZ	2.19	0.74
1:AA:1305:G:H21	1:AA:1332:A:H2	1.33	0.74
25:BA:2308:G:O6	25:BA:2311:A:N7	2.21	0.74
1:AA:664:G:H22	1:AA:741:G:H1	1.36	0.74
2:AB:225:ARG:HB2	61:CE:62:GLN:CD	2.13	0.74
60:CD:816:THR:OG1	60:CD:818:GLU:OE1	2.04	0.74
25:BA:2312:U:H5'	30:BF:85:ILE:HD11	1.68	0.74
6:AF:21:MET:HG2	6:AF:24:ARG:HH21	1.53	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AM:54:ASP:OD1	13:AM:55:THR:N	2.21	0.74
51:B3:6:ARG:HG2	51:B3:24:THR:HB	1.70	0.73
2:AB:129:LEU:HB2	2:AB:134:ALA:HB2	1.68	0.73
2:AB:225:ARG:HD3	61:CE:62:GLN:O	1.87	0.73
25:BA:2012:G:OP1	42:BT:11:ARG:NH2	2.21	0.73
25:BA:2243:U:H2'	25:BA:2244:U:C6	2.24	0.73
1:AA:4:U:O2'	1:AA:5:U:O5'	2.07	0.73
25:BA:276:U:O2'	25:BA:278:A:N7	2.22	0.73
60:CD:1179:PRO:HD2	60:CD:1184:ASP:HA	1.69	0.73
4:AD:188:ARG:NH2	4:AD:192:SER:O	2.19	0.73
25:BA:881:G:H1	25:BA:895:U:H3	1.37	0.73
25:BA:1808:A:O2'	47:BY:3:ARG:NH1	2.21	0.73
1:AA:263:A:OP1	20:AT:74:ARG:NH1	2.22	0.72
6:AF:17:GLN:HG2	32:BH:87:GLU:HB3	1.71	0.72
25:BA:2298:A:OP1	30:BF:71:ARG:NH2	2.22	0.72
1:AA:1311:A:OP1	55:B7:59:ARG:NH2	2.19	0.72
6:AF:24:ARG:NH1	32:BH:86:ASP:OD2	2.22	0.72
10:AJ:53:ILE:HD11	10:AJ:63:ASP:HB2	1.72	0.72
25:BA:807:U:O2	29:BE:69:ARG:NH2	2.23	0.72
25:BA:1607:C:N4	25:BA:1622:G:OP2	2.23	0.72
10:AJ:10:LEU:HB3	10:AJ:18:ILE:HD11	1.72	0.72
59:CC:10:ARG:NH2	59:CC:793:GLU:OE1	2.21	0.72
19:AS:36:ARG:NH2	19:AS:75:ALA:O	2.22	0.72
29:BE:1:MET:HB3	29:BE:14:VAL:HG23	1.72	0.72
2:AB:226:SER:H	61:CE:62:GLN:HE22	0.72	0.71
3:AC:33:LEU:HD21	14:AN:93:ILE:HG12	1.71	0.71
1:AA:1086:U:O4	1:AA:1099:G:N1	2.15	0.71
37:BO:63:ARG:HG2	37:BO:63:ARG:HH21	1.56	0.71
25:BA:1406:U:C2'	25:BA:1407:G:H5''	2.20	0.71
25:BA:1407:G:H2'	25:BA:1408:G:H8	1.54	0.71
25:BA:2683:C:OP1	39:BQ:51:ARG:NH1	2.24	0.71
34:BL:36:GLY:N	34:BL:62:VAL:O	2.22	0.71
22:AV:51:G:H2'	22:AV:52:C:C6	2.25	0.71
2:AB:225:ARG:C	61:CE:62:GLN:NE2	2.48	0.71
23:AW:21:A:O2'	23:AW:46:A:N6	2.23	0.71
44:BV:28:VAL:HG22	44:BV:34:VAL:HG12	1.73	0.71
25:BA:2162:G:OP2	25:BA:2164:C:N4	2.23	0.70
60:CD:454:CYS:SG	60:CD:455:ALA:N	2.64	0.70
1:AA:90:C:H2'	1:AA:91:U:H6	1.55	0.70
42:BT:4:ILE:HG12	42:BT:106:VAL:HG22	1.72	0.70
1:AA:736:C:OP1	18:AR:61:ARG:NH1	2.25	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:545:A:C2	25:BA:549:C:C2	2.80	0.70
59:CC:27:LEU:O	59:CC:528:ARG:NH1	2.24	0.70
25:BA:550:U:H2'	25:BA:551:G:H8	1.56	0.70
37:BO:9:GLN:O	37:BO:17:ARG:NH2	2.24	0.70
25:BA:568:U:H1'	25:BA:2030:6MZ:H9C1	1.74	0.70
1:AA:1452:C:H4'	1:AA:1453:G:H5''	1.74	0.70
4:AD:95:GLU:OE1	4:AD:100:ASN:ND2	2.25	0.70
60:CD:1157:ALA:HB2	60:CD:1210:ILE:HD11	1.74	0.69
3:AC:93:ASP:OD1	3:AC:94:ILE:N	2.25	0.69
25:BA:2172:U:O2'	25:BA:2174:C:OP2	2.10	0.69
37:BO:24:MET:HG2	37:BO:44:LEU:HD22	1.75	0.69
25:BA:1108:U:H2'	25:BA:1109:C:C6	2.27	0.69
25:BA:2139:U:O2	25:BA:2152:G:O6	2.09	0.69
25:BA:2182:U:O2	25:BA:2183:A:N6	2.22	0.69
37:BO:101:GLY:O	37:BO:110:MET:N	2.23	0.69
38:BP:31:THR:O	38:BP:102:ARG:NH1	2.25	0.69
25:BA:2370:G:O2'	51:B3:44:ARG:NH1	2.25	0.68
57:CT:19:DG:H2'	57:CT:20:DC:C6	2.29	0.68
25:BA:78:U:OP1	48:BZ:7:ARG:NH2	2.27	0.68
43:BU:1:MET:HE2	43:BU:2:ILE:HB	1.74	0.68
25:BA:1494:A:O2'	25:BA:1495:A:OP1	2.10	0.68
6:AF:38:ARG:NH1	6:AF:98:GLU:O	2.24	0.68
25:BA:2118:U:O4	25:BA:2148:G:N2	2.27	0.68
25:BA:1177:G:O2'	25:BA:1178:C:O5'	2.11	0.68
51:B3:6:ARG:NH1	51:B3:26:ASN:HB2	2.09	0.68
19:AS:27:ASP:OD1	19:AS:29:LYS:N	2.27	0.67
12:AL:87:VAL:HG11	12:AL:90:LEU:HD22	1.76	0.67
27:BC:107:PRO:HD2	27:BC:110:LEU:HD22	1.75	0.67
25:BA:673:C:OP1	29:BE:49:ARG:NH2	2.27	0.67
25:BA:871:U:H2'	25:BA:872:U:C6	2.30	0.67
4:AD:28:ILE:HD12	4:AD:34:ILE:HG12	1.76	0.67
25:BA:389:G:C8	25:BA:2413:G:H4'	2.29	0.67
25:BA:1916:A:H2'	25:BA:1917:PSU:C6	2.30	0.67
25:BA:1800:C:H5'	27:BC:146:MET:HE1	1.77	0.67
59:CC:624:ASP:OD1	59:CC:627:GLY:N	2.25	0.67
1:AA:1017:U:O2'	1:AA:1018:G:O4'	2.13	0.67
1:AA:1343:G:H1'	9:AI:123:ARG:HH12	1.58	0.67
1:AA:1397:C:OP2	5:AE:29:ARG:NH2	2.27	0.66
11:AK:109:ASN:ND2	21:AU:4:ILE:O	2.28	0.66
58:CB:27:THR:C	58:CB:28:LEU:HD22	2.19	0.66
1:AA:769:G:H4'	1:AA:1513:A:H4'	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:186:ILE:HA	2:AB:200:ILE:HG13	1.75	0.66
24:AX:37:MIA:O2'	25:BA:1913:A:N1	2.26	0.66
25:BA:2245:U:O2'	25:BA:2436:G:OP2	2.12	0.66
25:BA:2530:A:N7	31:BG:172:LYS:NZ	2.43	0.66
1:AA:1239:A:H62	1:AA:1299:A:N6	1.94	0.66
2:AB:226:SER:N	61:CE:62:GLN:HE21	1.78	0.66
4:AD:172:GLU:HG3	4:AD:183:LYS:HE3	1.76	0.66
22:AV:49:G:H5''	59:CC:540:ARG:NH2	2.11	0.66
1:AA:523:A:N6	12:AL:89:D2T:OD2	2.24	0.66
19:AS:50:ALA:HB1	19:AS:57:HIS:HB3	1.76	0.66
25:BA:2720:U:OP1	39:BQ:53:ARG:NH2	2.28	0.66
25:BA:711:G:H1	25:BA:720:U:H3	1.44	0.66
25:BA:2162:G:O2'	25:BA:2163:A:N7	2.28	0.66
30:BF:112:ARG:NH1	30:BF:134:GLU:OE2	2.29	0.66
21:AU:13:ASP:OD1	21:AU:13:ASP:N	2.19	0.66
28:BD:33:ARG:HA	28:BD:94:GLN:O	1.96	0.66
11:AK:92:GLY:C	11:AK:94:GLU:H	2.04	0.66
25:BA:812:C:OP1	40:BR:13:ARG:NH1	2.29	0.66
2:AB:226:SER:CB	61:CE:62:GLN:NE2	2.59	0.66
25:BA:1592:C:H2'	25:BA:1593:A:H8	1.60	0.66
36:BN:66:ARG:NH1	36:BN:104:GLU:OE2	2.29	0.66
25:BA:550:U:H2'	25:BA:551:G:C8	2.31	0.66
25:BA:1084:A:H2'	25:BA:1085:A:C8	2.31	0.66
25:BA:2252:G:H2'	25:BA:2253:G:H8	1.60	0.66
28:BD:30:GLU:OE2	28:BD:30:GLU:N	2.29	0.66
31:BG:16:ASP:OD1	31:BG:16:ASP:N	2.27	0.65
1:AA:501:C:OP1	12:AL:114:ARG:NH2	2.29	0.65
25:BA:284:U:O2	25:BA:356:G:N2	2.26	0.65
25:BA:652:U:OP2	25:BA:654:A:N6	2.30	0.65
25:BA:2134:A:N6	25:BA:2157:G:O2'	2.30	0.65
4:AD:18:ASP:HB2	4:AD:28:ILE:HD13	1.79	0.65
6:AF:45:ARG:O	6:AF:56:LYS:HA	1.95	0.65
10:AJ:42:LEU:HB2	10:AJ:71:LEU:HB3	1.78	0.65
57:CT:17:DG:C5	57:CT:18:DC:C5	2.84	0.65
1:AA:481:G:HO2'	1:AA:483:C:N4	1.92	0.65
1:AA:1010:U:H2'	1:AA:1011:C:C6	2.31	0.65
25:BA:2153:C:H2'	25:BA:2154:A:C8	2.31	0.65
25:BA:2683:C:O2	34:BL:70:ARG:NH2	2.30	0.65
1:AA:195:A:O2'	1:AA:196:A:H5'	1.97	0.65
11:AK:92:GLY:O	11:AK:94:GLU:N	2.28	0.65
3:AC:40:ARG:NH1	3:AC:55:ILE:O	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:15:HIS:HB3	2:AB:43:LEU:HD11	1.79	0.64
10:AJ:36:VAL:HA	10:AJ:76:ILE:HA	1.78	0.64
26:BB:55:U:HO2'	30:BF:24:SER:HG	1.44	0.64
1:AA:1061:G:OP2	3:AC:3:GLN:NE2	2.29	0.64
60:CD:429:LEU:HD22	60:CD:429:LEU:N	2.12	0.64
2:AB:186:ILE:HD11	2:AB:204:ASP:HA	1.79	0.64
26:BB:8:C:O3'	38:BP:25:ARG:NH1	2.30	0.64
59:CC:18:ARG:NH1	59:CC:1188:ASP:OD1	2.31	0.64
28:BD:48:ILE:HG23	28:BD:84:LEU:HD11	1.80	0.64
56:CN:32:DA:H5'	56:CN:32:DA:C8	2.32	0.64
57:CT:19:DG:C6	57:CT:20:DC:C4	2.86	0.64
59:CC:696:ASP:CG	59:CC:697:LYS:H	2.06	0.64
2:AB:226:SER:HB3	61:CE:62:GLN:NE2	2.13	0.64
59:CC:582:ASN:OD1	59:CC:583:GLU:N	2.31	0.64
5:AE:80:THR:HG23	5:AE:122:ASN:O	1.98	0.63
12:AL:79:VAL:HG12	12:AL:102:LEU:HD23	1.80	0.63
13:AM:23:TYR:HB3	13:AM:66:GLU:HG2	1.80	0.63
30:BF:102:ARG:NH1	55:B7:9:TYR:OH	2.32	0.63
10:AJ:75:ASP:OD1	10:AJ:75:ASP:N	2.32	0.63
25:BA:2140:G:H2'	25:BA:2141:G:C8	2.33	0.63
25:BA:1592:C:H2'	25:BA:1593:A:C8	2.33	0.63
25:BA:2120:G:H5''	25:BA:2172:U:H5''	1.79	0.63
25:BA:210:C:OP1	52:B4:29:GLN:NE2	2.29	0.63
6:AF:45:ARG:HD3	6:AF:102:MET:HE2	1.79	0.63
25:BA:2071:A:H2'	25:BA:2072:C:C6	2.34	0.63
32:BH:126:GLY:H	32:BH:146:VAL:HB	1.63	0.63
57:CT:19:DG:H2'	57:CT:20:DC:H6	1.63	0.63
57:CT:19:DG:C5	57:CT:20:DC:C5	2.87	0.63
60:CD:504:GLN:NE2	60:CD:505:ASP:OD1	2.18	0.63
1:AA:337:G:H2'	1:AA:338:A:C8	2.34	0.62
25:BA:2349:G:OP1	53:B5:45:ARG:NH2	2.32	0.62
27:BC:157:SER:O	27:BC:160:THR:OG1	2.14	0.62
31:BG:17:VAL:HG11	31:BG:50:LEU:HD21	1.80	0.62
56:CN:38:DA:H2''	56:CN:39:DG:N7	2.14	0.62
1:AA:823:C:HO2'	8:AH:2:SER:N	1.97	0.62
2:AB:225:ARG:HB2	61:CE:62:GLN:OE1	1.99	0.62
15:AO:64:ARG:NH1	15:AO:89:ARG:O	2.26	0.62
31:BG:164:TYR:HB2	31:BG:167:GLU:HB3	1.80	0.62
36:BN:106:ASP:OD1	36:BN:107:GLY:N	2.32	0.62
60:CD:576:ARG:NH1	60:CD:593:ASN:O	2.32	0.62
2:AB:225:ARG:HB3	61:CE:62:GLN:O	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AW:76:A:HO2'	63:AX:101:PHE:N	1.97	0.62
24:AX:17:C:H1'	24:AX:18:G:H5''	1.82	0.62
25:BA:1870:C:H4'	25:BA:1870:C:OP2	1.98	0.62
44:BV:7:ARG:NH1	44:BV:26:LYS:O	2.32	0.62
49:B1:9:GLN:O	49:B1:33:GLY:N	2.31	0.62
14:AN:33:ASP:O	14:AN:41:ARG:NH2	2.33	0.62
42:BT:110:ARG:OXT	42:BT:110:ARG:NE	2.29	0.62
2:AB:16:PHE:HE1	2:AB:35:ARG:HH21	1.48	0.62
15:AO:80:GLN:O	15:AO:83:GLU:HG2	2.00	0.62
25:BA:1407:G:H2'	25:BA:1408:G:C8	2.34	0.62
29:BE:153:LEU:HD12	29:BE:153:LEU:H	1.64	0.62
59:CC:12:ARG:HH21	59:CC:793:GLU:CD	2.07	0.62
1:AA:90:C:H2'	1:AA:91:U:C6	2.33	0.62
1:AA:197:A:O2'	1:AA:220:G:N2	2.32	0.62
2:AB:227:GLN:HB3	60:CD:1372:ARG:HH21	1.54	0.62
25:BA:1178:C:H2'	25:BA:1179:G:C8	2.35	0.62
6:AF:29:ILE:HG23	6:AF:34:GLY:HA3	1.82	0.62
25:BA:545:A:N1	25:BA:549:C:C4	2.67	0.62
25:BA:1871:A:O2'	25:BA:1872:A:O4'	2.16	0.62
1:AA:746:A:H2'	1:AA:747:A:C8	2.34	0.62
1:AA:1174:G:H2'	1:AA:1175:G:H5'	1.82	0.62
5:AE:31:PHE:HE1	22:AV:24:A:H62	1.48	0.62
21:AU:40:LYS:HE2	21:AU:42:THR:HG22	1.82	0.62
27:BC:252:THR:HG23	27:BC:253:LYS:HG3	1.81	0.62
35:BM:123:ARG:NH1	35:BM:143:GLU:OE2	2.34	0.61
38:BP:39:VAL:HB	38:BP:49:VAL:HG22	1.82	0.61
1:AA:35:G:N3	12:AL:115:SER:OG	2.34	0.61
11:AK:67:ALA:HB2	11:AK:96:THR:HG23	1.82	0.61
25:BA:340:A:O2'	29:BE:162:ARG:NH1	2.33	0.61
60:CD:523:GLU:CD	60:CD:709:ARG:HH22	2.08	0.61
1:AA:421:U:O2	3:AC:127:ARG:NH2	2.33	0.61
25:BA:2126:A:O2'	25:BA:2162:G:N2	2.34	0.61
25:BA:2792:A:H2'	25:BA:2793:C:C6	2.35	0.61
52:B4:11:LYS:O	52:B4:15:SER:OG	2.16	0.61
57:CT:9:DC:H2'	57:CT:10:DT:C6	2.34	0.61
58:CB:76:GLU:H	58:CB:76:GLU:CD	2.08	0.61
59:CC:251:ALA:HB2	59:CC:269:ILE:HD11	1.80	0.61
3:AC:134:MET:HG2	3:AC:168:TYR:HD2	1.66	0.61
25:BA:491:G:O6	42:BT:49:LYS:NZ	2.32	0.61
25:BA:620:G:O6	29:BE:98:LYS:NZ	2.33	0.61
2:AB:28:LYS:HA	2:AB:31:ILE:HD12	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:CA:67:GLU:OE1	59:CC:1057:LYS:NZ	2.33	0.61
25:BA:2110:G:H5'	25:BA:2118:U:O2'	2.01	0.61
25:BA:2127:G:H2'	25:BA:2128:G:C8	2.36	0.61
1:AA:844:G:C2	1:AA:846:G:H1'	2.36	0.61
49:B1:12:SER:HB2	49:B1:32:ILE:HD11	1.82	0.61
3:AC:36:ASP:OD1	3:AC:59:ARG:NH1	2.33	0.61
9:AI:21:ILE:HD12	9:AI:61:LEU:HD23	1.83	0.61
9:AI:57:MET:HB3	9:AI:61:LEU:HD13	1.83	0.61
24:AX:26:A:N1	24:AX:44:G:N2	2.48	0.61
25:BA:1095:A:H2'	25:BA:1096:A:C8	2.36	0.61
25:BA:1386:C:H2'	25:BA:1387:A:C8	2.36	0.61
25:BA:1404:C:C2'	25:BA:1405:U:H5'	2.31	0.61
25:BA:1494:A:H2'	25:BA:1495:A:C8	2.36	0.61
25:BA:1579:A:H2'	25:BA:1580:A:C8	2.36	0.60
25:BA:2189:U:H2'	25:BA:2190:G:C8	2.35	0.60
25:BA:2250:G:OP1	36:BN:84:LYS:NZ	2.24	0.60
25:BA:2128:G:H3'	25:BA:2129:C:C5'	2.31	0.60
35:BM:78:ARG:HG2	35:BM:113:ALA:HB3	1.84	0.60
1:AA:1004:A:C6	1:AA:1026:G:H1'	2.36	0.60
15:AO:47:LYS:O	15:AO:53:ARG:NH2	2.27	0.60
25:BA:1404:C:H2'	25:BA:1405:U:H5'	1.84	0.60
27:BC:232:HIS:HA	27:BC:242:LYS:HD3	1.83	0.60
60:CD:441:LEU:HD22	60:CD:441:LEU:N	2.16	0.60
1:AA:890:G:O2'	1:AA:906:A:N6	2.34	0.60
42:BT:17:VAL:HG11	42:BT:103:ILE:HG12	1.83	0.60
60:CD:504:GLN:HG3	60:CD:505:ASP:H	1.65	0.60
59:CC:525:THR:HG21	59:CC:687:ARG:HH11	1.67	0.60
13:AM:71:ARG:NH1	55:B7:50:ASP:OD2	2.33	0.60
42:BT:25:ARG:HG3	42:BT:74:ILE:HG22	1.84	0.60
2:AB:43:LEU:O	2:AB:47:VAL:HG22	2.01	0.60
7:AG:57:SER:HB3	7:AG:60:GLU:HG2	1.84	0.60
25:BA:1169:A:H2'	25:BA:1170:C:C6	2.35	0.60
25:BA:2286:G:OP2	51:B3:6:ARG:NH2	2.34	0.60
32:BH:115:VAL:O	32:BH:116:ARG:NH1	2.33	0.60
1:AA:1356:G:H2'	1:AA:1357:A:C8	2.36	0.60
57:CT:18:DC:H2'	57:CT:19:DG:H8	1.65	0.60
59:CC:423:ASP:N	59:CC:423:ASP:OD1	2.33	0.60
60:CD:429:LEU:H	60:CD:429:LEU:CD2	2.13	0.60
1:AA:4:U:HO2'	1:AA:5:U:C5'	2.14	0.60
1:AA:927:G:O2'	1:AA:928:G:H5'	2.02	0.60
8:AH:18:GLN:HE21	8:AH:72:VAL:HG12	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:BP:69:ASP:OD1	38:BP:70:ALA:N	2.34	0.60
60:CD:650:LYS:HE3	60:CD:742:GLY:O	2.02	0.60
1:AA:73:C:C2'	1:AA:74:A:H5'	2.32	0.60
1:AA:81:A:N6	1:AA:89:G:O6	2.35	0.60
1:AA:108:G:C6	20:AT:10:ARG:HG2	2.37	0.60
4:AD:15:GLU:OE2	4:AD:56:ARG:NH2	2.35	0.59
20:AT:35:VAL:HG21	20:AT:54:MET:HG2	1.84	0.59
25:BA:245:G:O6	53:B5:8:ARG:NH1	2.35	0.59
36:BN:77:PRO:HG2	36:BN:80:VAL:HG11	1.84	0.59
56:CN:27:DA:C4	56:CN:28:DA:C8	2.90	0.59
61:CE:44:ASP:OD1	61:CE:44:ASP:N	2.29	0.59
59:CC:705:GLU:HB3	59:CC:794:LEU:H	1.67	0.59
25:BA:2000:C:OP1	37:BO:5:LYS:NZ	2.35	0.59
1:AA:933:G:O6	7:AG:3:ARG:NH2	2.35	0.59
2:AB:108:ARG:O	2:AB:111:ILE:HG12	2.02	0.59
4:AD:194:ASP:OD1	60:CD:86:GLU:OE1	2.20	0.59
29:BE:191:ASP:OD2	29:BE:195:GLN:NE2	2.36	0.59
1:AA:1008:U:H2'	1:AA:1009:U:C6	2.37	0.59
22:AV:44:A:O2'	22:AV:45:C:OP2	2.21	0.59
39:BQ:7:GLN:O	39:BQ:11:GLU:HG3	2.03	0.59
1:AA:1035:A:H2'	1:AA:1036:A:H8	1.67	0.59
1:AA:1276:G:O2'	1:AA:1277:C:H5'	2.02	0.59
4:AD:11:LEU:HD13	4:AD:63:ARG:HG2	1.83	0.59
25:BA:1406:U:H2'	25:BA:1407:G:H5''	1.84	0.59
60:CD:797:THR:HG22	60:CD:924:GLY:HA3	1.83	0.59
60:CD:1069:ALA:HA	60:CD:1072:LYS:HB2	1.85	0.59
28:BD:35:THR:HG22	28:BD:73:VAL:HG21	1.84	0.59
1:AA:1137:C:O2	1:AA:1138:G:N1	2.36	0.59
47:BY:6:GLN:O	47:BY:74:ARG:NH2	2.35	0.59
60:CD:1169:THR:OG1	60:CD:1173:ARG:HB3	2.02	0.59
1:AA:198:G:H2'	1:AA:199:A:H8	1.67	0.58
10:AJ:86:ALA:N	10:AJ:89:ARG:HH11	2.00	0.58
56:CN:26:DG:OP2	59:CC:542:ARG:NH1	2.35	0.58
1:AA:148:G:O2'	1:AA:149:A:O5'	2.21	0.58
23:AW:19:G:H5''	23:AW:20:H2U:H52	1.85	0.58
25:BA:1169:A:H2'	25:BA:1170:C:H6	1.67	0.58
25:BA:1868:C:H2'	25:BA:1869:G:H8	1.67	0.58
33:BK:9:GLU:HG2	33:BK:10:THR:N	2.18	0.58
1:AA:1390:U:H2'	1:AA:1391:U:C6	2.38	0.58
15:AO:6:GLU:CD	15:AO:6:GLU:H	2.11	0.58
36:BN:20:LEU:HD13	45:BW:81:PRO:HG2	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:CC:525:THR:HG21	59:CC:687:ARG:NH1	2.18	0.58
4:AD:63:ARG:HH11	4:AD:63:ARG:HG3	1.68	0.58
9:AI:57:MET:HG3	9:AI:60:LYS:HD2	1.85	0.58
25:BA:2469:A:N6	25:BA:2481:G:O2'	2.36	0.58
43:BU:34:VAL:HG21	43:BU:43:ILE:HD11	1.85	0.58
12:AL:57:LEU:HD11	12:AL:82:ILE:HD11	1.86	0.58
1:AA:1343:G:OP1	9:AI:124:ARG:NH1	2.36	0.58
25:BA:2129:C:OP1	25:BA:2129:C:H4'	2.04	0.58
45:BW:3:THR:HA	45:BW:62:THR:HG23	1.85	0.58
60:CD:515:ARG:NH2	60:CD:718:SER:O	2.37	0.58
4:AD:125:VAL:HG22	4:AD:143:VAL:HG22	1.86	0.58
6:AF:67:PRO:HG2	6:AF:70:VAL:HG23	1.86	0.58
33:BK:9:GLU:HG2	33:BK:10:THR:HG23	1.85	0.58
59:CC:519:ASN:C	59:CC:519:ASN:OD1	2.46	0.58
1:AA:1169:A:H2'	1:AA:1170:A:C8	2.39	0.58
3:AC:134:MET:HE3	3:AC:168:TYR:CE2	2.39	0.58
21:AU:10:GLU:OE1	21:AU:18:ARG:NH1	2.36	0.58
25:BA:1177:G:O2'	25:BA:1178:C:H6	1.87	0.58
25:BA:2189:U:H2'	25:BA:2190:G:H8	1.69	0.58
33:BK:92:MET:SD	33:BK:95:ARG:NH2	2.77	0.58
54:B6:12:ARG:HB3	54:B6:12:ARG:HH11	1.69	0.58
57:CT:17:DG:C6	57:CT:18:DC:C4	2.91	0.58
1:AA:182:A:O2'	1:AA:183:C:H3'	2.03	0.58
1:AA:198:G:H2'	1:AA:199:A:C8	2.39	0.58
8:AH:11:LEU:HD22	8:AH:75:ILE:HD11	1.85	0.58
25:BA:1028:A:H2'	25:BA:1029:A:C8	2.39	0.58
25:BA:1174:U:O2'	25:BA:1175:A:O4'	2.22	0.58
25:BA:1494:A:HO2'	25:BA:1495:A:P	2.27	0.58
3:AC:9:GLY:HA3	14:AN:89:MET:HE3	1.86	0.57
22:AV:48:C:H2'	22:AV:49:G:O4'	2.04	0.57
24:AX:18:G:HO2'	24:AX:57:G:H22	1.45	0.57
53:B5:51:SER:OG	53:B5:54:ASP:OD1	2.20	0.57
57:CT:20:DC:H2'	57:CT:21:DG:H8	1.68	0.57
1:AA:1323:G:H2'	1:AA:1324:A:C8	2.40	0.57
6:AF:38:ARG:HG2	6:AF:63:ASN:HB2	1.86	0.57
25:BA:265:A:N1	25:BA:427:U:O2'	2.25	0.57
1:AA:481:G:HO2'	1:AA:483:C:H41	1.49	0.57
2:AB:217:VAL:O	2:AB:221:VAL:HG12	2.04	0.57
3:AC:105:GLU:OE1	3:AC:107:ARG:HD3	2.05	0.57
6:AF:12:PRO:O	6:AF:44:ARG:NH2	2.38	0.57
14:AN:47:LYS:O	14:AN:50:THR:OG1	2.12	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1105:U:H2'	25:BA:1106:G:H8	1.68	0.57
41:BS:30:GLY:N	41:BS:63:VAL:O	2.36	0.57
44:BV:4:LYS:O	44:BV:94:ARG:NH2	2.35	0.57
57:CT:19:DG:C4	57:CT:20:DC:C5	2.93	0.57
59:CC:638:SER:OG	59:CC:639:LYS:N	2.32	0.57
7:AG:27:VAL:HG11	7:AG:40:GLU:HG2	1.86	0.57
25:BA:1591:A:H2'	25:BA:1592:C:H6	1.69	0.57
25:BA:1808:A:H3'	25:BA:1809:A:C8	2.39	0.57
29:BE:145:ASP:HB3	29:BE:184:ASP:HB2	1.86	0.57
37:BO:100:CYS:O	37:BO:110:MET:HB2	2.05	0.57
60:CD:317:THR:OG1	60:CD:322:ARG:O	2.20	0.57
1:AA:496:A:H2'	1:AA:496:A:N3	2.20	0.57
25:BA:2122:U:H3'	25:BA:2123:G:H8	1.68	0.57
25:BA:2315:G:O2'	25:BA:2316:G:O4'	2.23	0.57
57:CT:26:DA:H2''	57:CT:27:DG:C8	2.39	0.57
59:CC:392:GLU:CD	59:CC:392:GLU:H	2.12	0.57
59:CC:726:TYR:HB3	59:CC:733:VAL:CG1	2.34	0.57
60:CD:256:ASP:O	60:CD:259:ARG:NH2	2.22	0.57
42:BT:20:VAL:HG11	42:BT:44:ALA:HA	1.85	0.57
8:AH:66:PHE:CD2	8:AH:67:GLN:HG3	2.40	0.57
25:BA:1168:G:H1	25:BA:1181:U:H3	1.53	0.57
37:BO:2:ARG:NE	37:BO:2:ARG:O	2.38	0.57
2:AB:12:ALA:O	2:AB:208:ARG:NH1	2.36	0.57
25:BA:1408:G:H2'	25:BA:1409:U:C6	2.40	0.57
59:CC:421:SER:H	59:CC:424:ASP:HB2	1.69	0.57
2:AB:47:VAL:HG23	2:AB:48:PRO:HD3	1.87	0.56
25:BA:2392:A:H2	35:BM:55:MET:HE2	1.69	0.56
27:BC:29:PRO:HG2	27:BC:34:LEU:HD11	1.86	0.56
56:CN:34:DT:H6	56:CN:34:DT:H5'	1.70	0.56
1:AA:1001:C:H2'	1:AA:1002:G:H8	1.70	0.56
9:AI:44:ALA:O	9:AI:48:VAL:HG12	2.05	0.56
24:AX:37:MIA:H152	24:AX:38:A:N1	2.21	0.56
25:BA:994:C:OP2	40:BR:54:LYS:NZ	2.36	0.56
25:BA:2119:A:H2'	25:BA:2168:G:H22	1.69	0.56
25:BA:2328:A:H2'	25:BA:2329:U:C6	2.39	0.56
42:BT:11:ARG:NH1	42:BT:99:ARG:O	2.38	0.56
59:CC:591:TYR:OH	59:CC:637:ARG:NH2	2.36	0.56
59:CC:705:GLU:CD	59:CC:705:GLU:H	2.13	0.56
59:CC:1083:GLU:CD	59:CC:1083:GLU:H	2.13	0.56
1:AA:202:G:HO2'	1:AA:468:A:H8	1.54	0.56
25:BA:160:A:N3	25:BA:2208:C:O2'	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:CC:267:ARG:NE	59:CC:268:ARG:O	2.37	0.56
4:AD:187:GLU:O	4:AD:191:LEU:HD22	2.06	0.56
25:BA:2591:C:H2'	25:BA:2592:G:C8	2.41	0.56
28:BD:33:ARG:NH1	28:BD:53:GLY:O	2.37	0.56
59:CC:7:GLU:O	59:CC:9:LYS:N	2.35	0.56
59:CC:12:ARG:NE	59:CC:793:GLU:OE2	2.36	0.56
1:AA:157:U:O2	1:AA:164:G:O6	2.24	0.56
25:BA:639:U:H2'	25:BA:640:C:C6	2.40	0.56
25:BA:2116:G:O4'	25:BA:2165:C:N4	2.39	0.56
36:BN:35:ALA:HB2	36:BN:102:LEU:HD11	1.88	0.56
60:CD:495:ASN:OD1	60:CD:495:ASN:N	2.37	0.56
1:AA:1277:C:O2'	1:AA:1278:G:O5'	2.24	0.56
2:AB:108:ARG:O	2:AB:112:LYS:HG3	2.05	0.56
12:AL:35:THR:OG1	12:AL:54:ARG:O	2.21	0.56
25:BA:2506:U:O2	25:BA:2506:U:H2'	2.05	0.56
1:AA:842:U:H4'	1:AA:846:G:C6	2.41	0.56
20:AT:24:ARG:HH11	20:AT:24:ARG:HA	1.71	0.56
25:BA:1153:C:OP1	40:BR:92:ARG:NH1	2.39	0.56
59:CC:696:ASP:OD1	59:CC:697:LYS:N	2.39	0.56
25:BA:2547:A:H2'	25:BA:2548:U:C6	2.41	0.56
32:BH:89:LYS:HG3	32:BH:90:LEU:H	1.71	0.56
1:AA:844:G:N7	1:AA:845:A:N6	2.53	0.56
7:AG:7:ILE:HD13	7:AG:7:ILE:H	1.71	0.56
32:BH:73:ASN:HD21	32:BH:141:LYS:H	1.54	0.56
10:AJ:42:LEU:HB2	10:AJ:71:LEU:CB	2.35	0.55
25:BA:1667:G:O2'	25:BA:1991:U:O4	2.22	0.55
56:CN:28:DA:H2''	56:CN:29:DG:H8	1.70	0.55
1:AA:575:G:O2'	1:AA:821:G:OP2	2.23	0.55
9:AI:47:VAL:HG13	9:AI:80:ARG:HD3	1.87	0.55
25:BA:1794:A:H2'	25:BA:1795:C:C6	2.41	0.55
29:BE:21:ARG:NH2	29:BE:106:LYS:HD3	2.22	0.55
50:B2:32:LYS:HG3	50:B2:33:THR:HG23	1.86	0.55
1:AA:1311:A:H5''	55:B7:59:ARG:NH1	2.21	0.55
21:AU:14:VAL:O	21:AU:18:ARG:HG2	2.05	0.55
51:B3:6:ARG:HH12	51:B3:26:ASN:HB2	1.69	0.55
55:B7:30:HIS:CG	55:B7:31:ASP:H	2.24	0.55
25:BA:2252:G:H2'	25:BA:2253:G:C8	2.40	0.55
59:CC:1165:SER:O	59:CC:1167:GLU:N	2.37	0.55
25:BA:645:C:H2'	25:BA:647:G:C8	2.41	0.55
32:BH:83:LYS:O	32:BH:90:LEU:HD12	2.06	0.55
1:AA:1383:C:H2'	1:AA:1384:C:C6	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:927:A:H2'	25:BA:928:A:C8	2.42	0.55
58:CA:8:PHE:O	58:CA:10:LYS:NZ	2.26	0.55
21:AU:61:ALA:O	21:AU:65:ALA:HB3	2.07	0.55
25:BA:141:G:N7	43:BU:1:MET:HE3	2.22	0.55
25:BA:686:U:H6	25:BA:788:A:N1	2.05	0.55
30:BF:57:LEU:HD12	30:BF:87:CYS:SG	2.47	0.55
42:BT:17:VAL:HG12	42:BT:76:VAL:HG21	1.88	0.55
46:BX:59:LEU:HD12	46:BX:80:ILE:HD12	1.88	0.55
48:BZ:5:GLU:HG2	48:BZ:6:LEU:HD12	1.89	0.55
54:B6:6:SER:OG	54:B6:8:LYS:NZ	2.34	0.55
59:CC:726:TYR:C	59:CC:726:TYR:CD1	2.84	0.55
60:CD:175:GLU:CD	60:CD:175:GLU:H	2.15	0.55
1:AA:202:G:H21	1:AA:466:A:H61	1.53	0.55
25:BA:464:U:O3'	52:B4:12:ARG:NH1	2.40	0.55
25:BA:2144:G:O2'	25:BA:2147:A:N6	2.40	0.55
60:CD:37:GLU:HB2	60:CD:104:HIS:CE1	2.41	0.55
11:AK:93:ARG:NH2	11:AK:112:ASP:OD2	2.39	0.55
25:BA:833:A:H2'	25:BA:834:G:C8	2.41	0.55
29:BE:113:VAL:HG12	29:BE:118:LEU:HD23	1.89	0.55
59:CC:1176:LEU:O	59:CC:1178:LYS:N	2.39	0.55
13:AM:16:VAL:HG13	13:AM:17:ILE:HD12	1.89	0.55
25:BA:1141:U:H4'	25:BA:1142:A:O4'	2.06	0.55
38:BP:1:MET:O	38:BP:5:SER:OG	2.25	0.55
44:BV:34:VAL:HG13	44:BV:67:VAL:HG22	1.88	0.55
28:BD:149:ASN:OD1	28:BD:150:MEQ:N	2.40	0.54
30:BF:141:ILE:C	30:BF:141:ILE:HD12	2.32	0.54
31:BG:52:PHE:CE1	31:BG:72:LEU:HD22	2.42	0.54
1:AA:842:U:O2'	1:AA:845:A:OP2	2.18	0.54
3:AC:11:ARG:NH2	3:AC:177:THR:O	2.38	0.54
56:CN:31:DG:H2''	56:CN:32:DA:C8	2.42	0.54
2:AB:14:VAL:HG23	2:AB:43:LEU:HD21	1.90	0.54
25:BA:881:G:O6	25:BA:895:U:O4	2.26	0.54
25:BA:1108:U:H2'	25:BA:1109:C:H6	1.68	0.54
25:BA:1261:C:OP2	42:BT:83:LYS:NZ	2.40	0.54
25:BA:1405:U:O2'	25:BA:1406:U:O4'	2.25	0.54
1:AA:1020:G:OP1	1:AA:1020:G:H4'	2.06	0.54
4:AD:80:ALA:HA	4:AD:86:THR:HG22	1.89	0.54
4:AD:102:VAL:HG13	4:AD:107:PHE:HB2	1.90	0.54
25:BA:139:U:O4	43:BU:1:MET:N	2.39	0.54
25:BA:1595:C:O2'	25:BA:1596:A:H5'	2.08	0.54
25:BA:2153:C:H2'	25:BA:2154:A:H8	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2291:U:H2'	25:BA:2292:U:C6	2.42	0.54
59:CC:538:LEU:HD12	59:CC:539:THR:N	2.23	0.54
1:AA:104:G:OP1	20:AT:16:LYS:NZ	2.33	0.54
11:AK:86:VAL:HG11	11:AK:93:ARG:HG3	1.89	0.54
25:BA:1047:G:N2	25:BA:1110:G:O2'	2.40	0.54
25:BA:1594:U:H2'	25:BA:1595:C:C6	2.43	0.54
25:BA:2064:C:H2'	25:BA:2065:C:C6	2.42	0.54
25:BA:2136:G:O6	25:BA:2155:U:O2	2.26	0.54
25:BA:2636:C:O2'	28:BD:45:TYR:OH	2.26	0.54
58:CB:13:LEU:HA	58:CB:28:LEU:HD13	1.89	0.54
1:AA:966:2MG:HM22	23:AW:34:C:H5'	1.90	0.54
9:AI:88:MET:SD	9:AI:95:ARG:HG2	2.47	0.54
25:BA:1796:U:H2'	25:BA:1797:G:H8	1.72	0.54
59:CC:23:ASP:OD1	59:CC:23:ASP:N	2.34	0.54
59:CC:524:ILE:HG22	59:CC:525:THR:N	2.22	0.54
60:CD:301:GLU:OE1	60:CD:312:ARG:NH1	2.37	0.54
1:AA:107:G:N7	20:AT:10:ARG:NH2	2.55	0.54
25:BA:2627:G:O2'	25:BA:2781:A:N1	2.36	0.54
56:CN:26:DG:C6	56:CN:27:DA:N6	2.76	0.54
60:CD:367:GLY:HA2	60:CD:440:VAL:O	2.08	0.54
9:AI:21:ILE:HG23	9:AI:61:LEU:HD23	1.88	0.54
19:AS:3:ARG:HE	19:AS:7:LYS:HB3	1.72	0.54
25:BA:1057:A:N7	25:BA:1086:A:H2'	2.21	0.54
48:BZ:18:LEU:HD21	48:BZ:54:LYS:HE3	1.90	0.54
1:AA:986:U:H2'	1:AA:987:G:C8	2.43	0.54
1:AA:1277:C:HO2'	1:AA:1278:G:P	2.30	0.54
2:AB:167:ASP:OD2	2:AB:191:SER:OG	2.26	0.54
11:AK:34:ILE:HB	11:AK:74:VAL:HG11	1.89	0.54
30:BF:8:TYR:HA	30:BF:12:VAL:HB	1.90	0.54
11:AK:89:PRO:HG3	21:AU:32:VAL:HG11	1.90	0.53
11:AK:47:ALA:HB1	11:AK:62:ALA:HB1	1.90	0.53
25:BA:1591:A:H2'	25:BA:1592:C:C6	2.43	0.53
31:BG:52:PHE:CZ	31:BG:72:LEU:HD22	2.43	0.53
59:CC:1079:ILE:HG23	59:CC:1079:ILE:O	2.07	0.53
60:CD:160:LEU:HD23	60:CD:160:LEU:H	1.71	0.53
1:AA:196:A:OP1	20:AT:64:LYS:NZ	2.42	0.53
1:AA:864:A:C5'	5:AE:90:THR:HB	2.36	0.53
5:AE:94:VAL:HG13	5:AE:111:MET:HE1	1.90	0.53
1:AA:181:A:O2'	1:AA:194:C:N4	2.42	0.53
3:AC:134:MET:HE3	3:AC:168:TYR:CD2	2.44	0.53
60:CD:441:LEU:HD22	60:CD:441:LEU:H	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:CD:825:VAL:HG13	60:CD:825:VAL:O	2.08	0.53
4:AD:8:LYS:HB3	4:AD:21:LEU:HB3	1.90	0.53
25:BA:84:A:N1	25:BA:98:G:O2'	2.37	0.53
25:BA:1090:A:C2	25:BA:1102:C:H1'	2.44	0.53
29:BE:21:ARG:O	29:BE:114:ARG:NH2	2.41	0.53
46:BX:69:PHE:C	46:BX:70:GLU:HG3	2.33	0.53
59:CC:150:HIS:CE1	59:CC:454:ARG:HG3	2.43	0.53
60:CD:907:HIS:ND1	60:CD:908:ILE:O	2.36	0.53
9:AI:7:TYR:HH	9:AI:9:THR:HG1	1.55	0.53
25:BA:2244:U:H2'	25:BA:2245:U:C6	2.44	0.53
41:BS:34:GLU:HG2	41:BS:60:LYS:HG2	1.89	0.53
28:BD:30:GLU:CD	28:BD:30:GLU:H	2.15	0.53
39:BQ:14:LYS:HE3	39:BQ:77:HIS:HA	1.89	0.53
48:BZ:19:LEU:HD23	48:BZ:23:ARG:HH22	1.73	0.53
59:CC:632:ASP:N	59:CC:632:ASP:OD1	2.39	0.53
4:AD:49:SER:O	4:AD:53:VAL:HG13	2.09	0.53
25:BA:585:G:N7	40:BR:6:ARG:NH1	2.57	0.53
25:BA:1394:U:H4'	25:BA:1603:A:H4'	1.91	0.53
59:CC:1070:HIS:NE2	59:CC:1114:GLU:OE1	2.41	0.53
60:CD:35:PHE:CD1	60:CD:101:ARG:HB3	2.44	0.53
1:AA:1310:G:OP2	13:AM:87:ARG:NH2	2.41	0.53
25:BA:674:G:H5''	29:BE:71:GLY:N	2.24	0.53
25:BA:1590:A:H2'	25:BA:1591:A:H8	1.72	0.53
25:BA:2127:G:H2'	25:BA:2128:G:H8	1.72	0.53
29:BE:48:THR:HG23	29:BE:86:ALA:HB3	1.91	0.53
57:CT:21:DG:C6	57:CT:22:DC:N4	2.77	0.53
24:AX:75:C:O2	25:BA:2507:C:O2'	2.26	0.53
1:AA:356:A:N3	1:AA:368:U:O2'	2.34	0.52
25:BA:992:C:OP1	40:BR:47:TYR:OH	2.23	0.52
25:BA:1047:G:O2'	25:BA:1110:G:N1	2.40	0.52
32:BH:78:VAL:HG21	32:BH:103:VAL:HG22	1.91	0.52
59:CC:516:ASP:O	59:CC:518:ASN:N	2.41	0.52
1:AA:299:G:H2'	1:AA:300:A:C8	2.44	0.52
25:BA:285:G:O6	25:BA:355:U:O2	2.27	0.52
25:BA:301:G:OP2	44:BV:82:ARG:NH1	2.42	0.52
25:BA:2144:G:H1'	25:BA:2147:A:H61	1.73	0.52
30:BF:36:LEU:HB2	30:BF:89:VAL:CG1	2.39	0.52
49:B1:23:THR:HG23	49:B1:47:MET:HG2	1.90	0.52
58:CB:191:ARG:NH2	58:CB:192:VAL:O	2.42	0.52
1:AA:206:C:H2'	1:AA:207:C:O4'	2.09	0.52
1:AA:945:G:C2	1:AA:946:A:C8	2.98	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:946:A:H2'	1:AA:947:G:C8	2.45	0.52
1:AA:966:2MG:H5''	1:AA:967:5MC:OP2	2.08	0.52
25:BA:2178:C:H2'	25:BA:2179:C:C6	2.44	0.52
25:BA:2244:U:O2'	25:BA:2245:U:H5'	2.09	0.52
25:BA:2685:G:P	34:BL:78:ARG:HH22	2.33	0.52
30:BF:22:TYR:OH	30:BF:165:GLU:OE2	2.14	0.52
38:BP:82:ALA:HB3	38:BP:115:LEU:HD11	1.91	0.52
58:CA:218:ARG:NH1	58:CB:233:ASP:OD1	2.42	0.52
59:CC:726:TYR:CD1	59:CC:727:VAL:N	2.78	0.52
1:AA:913:A:OP1	12:AL:88:LYS:NZ	2.42	0.52
1:AA:1383:C:O2'	1:AA:1384:C:H5'	2.09	0.52
3:AC:131:ARG:NH2	3:AC:166:GLU:OE1	2.42	0.52
25:BA:1379:U:O3'	25:BA:1380:G:H8	1.93	0.52
30:BF:8:TYR:OH	30:BF:29:PRO:O	2.25	0.52
51:B3:3:LYS:HG2	51:B3:5:ILE:HG12	1.91	0.52
25:BA:1084:A:O2'	25:BA:1105:U:O2'	2.27	0.52
25:BA:1469:A:H2'	25:BA:1470:A:C8	2.45	0.52
29:BE:130:LYS:HB2	29:BE:133:LEU:HD12	1.89	0.52
6:AF:11:HIS:ND1	6:AF:12:PRO:HD2	2.24	0.52
6:AF:43:GLY:HA2	6:AF:58:HIS:CE1	2.45	0.52
14:AN:48:LEU:HD12	14:AN:51:LEU:HD12	1.91	0.52
59:CC:296:VAL:O	59:CC:335:THR:HB	2.10	0.52
18:AR:34:THR:HG22	18:AR:40:VAL:HG22	1.92	0.52
27:BC:159:GLY:HA2	27:BC:195:VAL:O	2.10	0.52
60:CD:801:VAL:HG12	60:CD:920:ALA:HB3	1.91	0.52
1:AA:1495:U:O2'	25:BA:1919:A:N1	2.34	0.52
25:BA:645:C:H2'	25:BA:647:G:N7	2.25	0.52
25:BA:2128:G:H3'	25:BA:2129:C:H5''	1.92	0.52
45:BW:2:PHE:HB2	45:BW:61:LEU:HD23	1.92	0.52
60:CD:312:ARG:HG2	60:CD:313:GLY:N	2.24	0.52
25:BA:2150:C:H2'	25:BA:2151:U:C6	2.45	0.52
59:CC:85:CYS:SG	59:CC:90:VAL:HG23	2.50	0.52
59:CC:178:PRO:HB3	59:CC:395:TYR:CZ	2.44	0.52
59:CC:766:ASN:CG	59:CC:766:ASN:O	2.53	0.52
8:AH:18:GLN:HG3	8:AH:72:VAL:HG13	1.92	0.52
9:AI:113:ARG:HG3	9:AI:115:LYS:HZ3	1.75	0.52
59:CC:193:ASN:HD22	59:CC:193:ASN:N	2.08	0.52
1:AA:1167:A:H1'	1:AA:1168:U:OP1	2.10	0.51
3:AC:155:GLY:HA2	3:AC:163:ALA:HB1	1.91	0.51
39:BQ:33:VAL:O	39:BQ:33:VAL:HG12	2.10	0.51
59:CC:1340:GLU:OE1	59:CC:1341:ASP:N	2.34	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:401:C:O2'	1:AA:621:A:N3	2.36	0.51
1:AA:1311:A:H5''	55:B7:59:ARG:HH12	1.76	0.51
59:CC:1321:GLU:OE2	60:CD:99:ARG:NH1	2.41	0.51
59:CC:1333:LEU:C	59:CC:1335:ILE:H	2.18	0.51
60:CD:504:GLN:HG3	60:CD:505:ASP:N	2.25	0.51
10:AJ:53:ILE:HD11	10:AJ:63:ASP:CB	2.39	0.51
25:BA:1529:G:H2'	25:BA:1530:G:H8	1.74	0.51
25:BA:2171:A:O2'	25:BA:2173:A:OP1	2.29	0.51
25:BA:2728:U:HO2'	25:BA:2729:G:H8	1.57	0.51
26:BB:1:U:HO2'	26:BB:2:G:H8	1.57	0.51
28:BD:13:ARG:O	39:BQ:12:GLN:NE2	2.41	0.51
56:CN:28:DA:H2''	56:CN:29:DG:C8	2.46	0.51
60:CD:1075:ARG:HH21	60:CD:1102:PRO:HA	1.75	0.51
1:AA:1166:G:O2'	1:AA:1167:A:OP1	2.24	0.51
1:AA:1183:U:H3'	1:AA:1184:G:C5'	2.41	0.51
9:AI:84:THR:HG21	9:AI:103:PHE:CB	2.39	0.51
25:BA:856:G:H2'	25:BA:857:G:C8	2.46	0.51
25:BA:1296:G:OP1	25:BA:2709:G:O2'	2.21	0.51
25:BA:1596:A:O2'	25:BA:1597:A:H5'	2.10	0.51
41:BS:61:ALA:HB2	41:BS:98:ILE:HD13	1.92	0.51
47:BY:12:PRO:HB3	47:BY:30:LEU:HD23	1.91	0.51
57:CT:18:DC:O2	57:CT:19:DG:C8	2.64	0.51
1:AA:673:A:H2'	1:AA:674:G:C8	2.45	0.51
1:AA:1218:C:H2'	1:AA:1219:A:C8	2.46	0.51
25:BA:614:A:O2'	25:BA:615:U:OP2	2.25	0.51
25:BA:2503:2MA:O2'	25:BA:2505:G:OP2	2.29	0.51
60:CD:275:ARG:HH11	60:CD:298:MET:HB3	1.76	0.51
60:CD:366:CYS:O	60:CD:439:PRO:HA	2.11	0.51
1:AA:714:G:H2'	1:AA:715:A:C8	2.46	0.51
10:AJ:55:PRO:HA	14:AN:82:ILE:HD11	1.91	0.51
23:AW:50:U:H3	23:AW:64:G:H1	1.57	0.51
25:BA:2788:C:O2'	25:BA:2809:A:N3	2.41	0.51
1:AA:56:U:H2'	1:AA:57:G:C8	2.46	0.51
1:AA:1175:G:O2'	1:AA:1176:A:H8	1.92	0.51
1:AA:1270:G:HO2'	1:AA:1313:U:HO2'	1.57	0.51
1:AA:1383:C:H2'	1:AA:1384:C:H6	1.75	0.51
3:AC:61:ALA:O	3:AC:62:LYS:HD3	2.10	0.51
4:AD:140:ASN:N	4:AD:182:PHE:O	2.44	0.51
29:BE:110:SER:O	29:BE:113:VAL:HG22	2.10	0.51
1:AA:31:G:O2'	1:AA:48:C:N4	2.43	0.51
24:AX:15:G:H3'	24:AX:16:H2U:H62	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:BV:74:ASN:HB3	44:BV:96:PHE:CE1	2.46	0.51
59:CC:320:ASP:N	59:CC:320:ASP:OD1	2.37	0.51
1:AA:413:G:N2	1:AA:428:G:H1'	2.25	0.51
3:AC:47:LEU:HD21	3:AC:87:LEU:HD11	1.92	0.51
11:AK:109:ASN:HD21	11:AK:111:THR:HG23	1.76	0.51
25:BA:172:A:H2'	25:BA:173:A:C8	2.46	0.51
25:BA:396:G:OP2	47:BY:10:LYS:NZ	2.44	0.51
25:BA:2119:A:C8	25:BA:2168:G:N1	2.79	0.51
25:BA:2165:C:H2'	25:BA:2166:U:O4'	2.10	0.51
25:BA:2788:C:H2'	25:BA:2789:C:C6	2.46	0.51
30:BF:171:ALA:O	30:BF:174:ASP:N	2.42	0.51
44:BV:99:ASN:OD1	44:BV:101:GLU:HB2	2.11	0.51
1:AA:91:U:H2'	1:AA:92:U:C6	2.46	0.51
3:AC:61:ALA:C	3:AC:62:LYS:HD3	2.36	0.51
7:AG:79:ARG:NH1	7:AG:82:GLY:O	2.44	0.51
24:AX:14:A:H2'	24:AX:15:G:O4'	2.10	0.51
31:BG:56:ASP:OD1	31:BG:57:GLY:N	2.44	0.51
45:BW:27:PRO:O	45:BW:88:HIS:HA	2.10	0.51
1:AA:371:A:H2'	1:AA:372:C:O4'	2.11	0.50
17:AQ:17:MET:HE3	17:AQ:20:SER:HB3	1.92	0.50
25:BA:889:C:H2'	25:BA:890:C:C6	2.46	0.50
25:BA:1049:C:C2'	25:BA:1050:A:H5'	2.41	0.50
25:BA:1796:U:H2'	25:BA:1797:G:C8	2.46	0.50
32:BH:73:ASN:ND2	32:BH:141:LYS:H	2.09	0.50
38:BP:51:ALA:HB3	38:BP:78:VAL:HB	1.92	0.50
57:CT:9:DC:H2'	57:CT:10:DT:H71	1.93	0.50
60:CD:1159:ILE:O	60:CD:1206:ARG:N	2.43	0.50
22:AV:51:G:C2	22:AV:52:C:C4	3.00	0.50
24:AX:54:5MU:H4'	36:BN:51:ARG:HE	1.76	0.50
25:BA:2025:C:H2'	25:BA:2026:U:C6	2.46	0.50
25:BA:2615:U:C2	50:B2:4:GLN:HA	2.46	0.50
1:AA:147:G:O2'	1:AA:148:G:O4'	2.29	0.50
25:BA:929:U:H1'	49:B1:26:GLY:O	2.10	0.50
25:BA:2133:G:H2'	25:BA:2157:G:H22	1.75	0.50
25:BA:2799:G:O2'	25:BA:2800:A:H5''	2.11	0.50
6:AF:3:HIS:HB2	6:AF:92:THR:O	2.12	0.50
10:AJ:56:HIS:ND1	10:AJ:57:VAL:HG22	2.27	0.50
25:BA:2127:G:H21	25:BA:2173:A:C4'	2.25	0.50
25:BA:2155:U:H2'	25:BA:2156:G:C8	2.47	0.50
32:BH:86:ASP:O	32:BH:88:GLY:N	2.42	0.50
56:CN:27:DA:C6	56:CN:28:DA:C6	3.00	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1229:A:OP2	13:AM:113:ARG:NH1	2.40	0.50
22:AV:52:C:H2'	22:AV:53:G:C1'	2.41	0.50
25:BA:2154:A:H2'	25:BA:2155:U:O4'	2.12	0.50
56:CN:23:DT:H1'	56:CN:24:DC:C4	2.47	0.50
59:CC:855:PRO:HG3	59:CC:913:VAL:HG23	1.93	0.50
60:CD:326:SER:O	60:CD:329:ASP:N	2.43	0.50
2:AB:100:MET:HA	2:AB:107:VAL:HG21	1.94	0.50
13:AM:52:GLN:OE1	13:AM:52:GLN:N	2.45	0.50
25:BA:499:U:H5''	44:BV:43:LYS:HE2	1.93	0.50
25:BA:784:G:H5'	25:BA:785:G:OP1	2.12	0.50
25:BA:1814:G:OP2	25:BA:1815:A:O2'	2.24	0.50
31:BG:105:LEU:HD11	31:BG:148:LEU:HD22	1.94	0.50
58:CA:68:TYR:N	58:CA:68:TYR:CD1	2.79	0.50
60:CD:1360:GLY:HA2	61:CE:17:PHE:CZ	2.47	0.50
42:BT:24:ILE:HD13	42:BT:36:LEU:HD11	1.94	0.50
44:BV:14:LEU:HD11	44:BV:71:ALA:HB2	1.93	0.50
10:AJ:5:ARG:HH21	10:AJ:7:ARG:CZ	2.24	0.50
12:AL:5:ASN:O	12:AL:9:ARG:HG3	2.12	0.50
25:BA:1916:A:H2'	25:BA:1917:PSU:H6	1.77	0.50
30:BF:95:ARG:HG3	55:B7:1:MET:HE3	1.93	0.50
31:BG:22:GLN:NE2	31:BG:38:ASN:O	2.45	0.50
40:BR:27:ALA:HB1	40:BR:31:VAL:HB	1.93	0.50
59:CC:617:ALA:HB2	59:CC:650:VAL:HG21	1.93	0.50
59:CC:811:ASN:ND2	59:CC:1097:VAL:O	2.43	0.50
2:AB:222:ARG:O	61:CE:62:GLN:CD	2.53	0.50
25:BA:1506:U:H2'	25:BA:1507:C:C6	2.47	0.50
25:BA:1744:A:H3'	25:BA:1745:A:H8	1.76	0.50
25:BA:1901:A:OP2	27:BC:253:LYS:NZ	2.29	0.50
58:CA:102:LEU:HD23	58:CA:103:ASN:N	2.27	0.50
5:AE:80:THR:HG22	5:AE:81:LEU:H	1.77	0.49
25:BA:890:C:OP2	25:BA:890:C:H6	1.95	0.49
25:BA:1868:C:H2'	25:BA:1869:G:C8	2.45	0.49
27:BC:4:VAL:HG23	27:BC:18:LYS:HB2	1.94	0.49
38:BP:52:SER:HB2	38:BP:54:VAL:HG22	1.94	0.49
60:CD:288:PRO:HD2	60:CD:291:ILE:HD12	1.93	0.49
1:AA:684:U:H2'	1:AA:685:G:O4'	2.12	0.49
1:AA:1530:G:H2'	1:AA:1531:A:C8	2.47	0.49
3:AC:105:GLU:OE1	3:AC:107:ARG:NH1	2.33	0.49
28:BD:30:GLU:OE1	28:BD:77:ARG:NH1	2.45	0.49
60:CD:67:ASP:N	60:CD:67:ASP:OD1	2.43	0.49
60:CD:813:ASP:OD1	60:CD:883:ARG:NH2	2.35	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:477:C:H2'	1:AA:478:A:C8	2.47	0.49
1:AA:713:G:H2'	1:AA:714:G:C8	2.47	0.49
25:BA:1579:A:H2'	25:BA:1580:A:H8	1.76	0.49
25:BA:2345:G:N3	25:BA:2381:A:H2'	2.28	0.49
25:BA:2477:U:O2	54:B6:4:ARG:NH2	2.46	0.49
42:BT:36:LEU:HD13	42:BT:48:LYS:HA	1.93	0.49
57:CT:17:DG:C6	57:CT:18:DC:C5	3.00	0.49
60:CD:961:SER:HB2	60:CD:981:GLU:HB2	1.94	0.49
1:AA:677:U:H3	1:AA:713:G:H22	1.58	0.49
1:AA:1240:U:O4	7:AG:109:ARG:NH1	2.45	0.49
9:AI:55:VAL:HG11	9:AI:94:LEU:HD13	1.94	0.49
30:BF:40:VAL:C	30:BF:42:GLU:H	2.19	0.49
41:BS:78:ARG:HB3	41:BS:83:TYR:HB3	1.94	0.49
58:CB:28:LEU:HD22	58:CB:28:LEU:N	2.27	0.49
59:CC:274:ILE:HA	59:CC:277:LEU:HD12	1.93	0.49
60:CD:530:PRO:O	60:CD:533:ALA:HB3	2.12	0.49
1:AA:346:G:OP1	39:BQ:39:ARG:NH2	2.45	0.49
1:AA:1001:C:H2'	1:AA:1002:G:C8	2.47	0.49
2:AB:227:GLN:CA	60:CD:1372:ARG:HH22	2.23	0.49
7:AG:65:ALA:O	7:AG:69:VAL:HG23	2.13	0.49
25:BA:2265:U:OP2	25:BA:2266:A:O2'	2.28	0.49
42:BT:74:ILE:HD12	42:BT:105:VAL:HG22	1.94	0.49
56:CN:28:DA:C6	56:CN:29:DG:C6	3.01	0.49
57:CT:19:DG:C4	57:CT:20:DC:C6	3.01	0.49
59:CC:261:VAL:HG21	59:CC:264:GLU:HG2	1.94	0.49
24:AX:5:G:O2'	24:AX:6:G:H5'	2.12	0.49
25:BA:1794:A:H2'	25:BA:1795:C:H6	1.77	0.49
30:BF:127:ASN:HD22	30:BF:158:THR:H	1.60	0.49
31:BG:127:THR:HG23	31:BG:130:GLU:HB2	1.93	0.49
42:BT:11:ARG:HH21	42:BT:98:LYS:HE3	1.77	0.49
59:CC:1119:MET:HA	59:CC:1119:MET:HE3	1.95	0.49
2:AB:68:LEU:HD22	2:AB:70:VAL:HG22	1.94	0.49
4:AD:76:TYR:HH	4:AD:205:SER:HG	1.60	0.49
16:AP:6:LEU:HD22	16:AP:17:TYR:HB3	1.95	0.49
22:AV:51:G:C4	22:AV:52:C:C5	3.00	0.49
25:BA:1363:C:O2'	25:BA:1809:A:N3	2.44	0.49
25:BA:2147:A:C4	25:BA:2148:G:H1'	2.48	0.49
34:BL:76:VAL:HG12	39:BQ:73:VAL:HB	1.95	0.49
1:AA:949:A:N7	13:AM:105:ASN:ND2	2.61	0.49
7:AG:125:SER:O	7:AG:129:GLU:HG2	2.13	0.49
9:AI:119:ARG:HB3	9:AI:123:ARG:HG2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AM:71:ARG:NH2	30:BF:113:ASP:OD1	2.45	0.49
25:BA:2060:A:OP2	29:BE:66:GLY:HA2	2.13	0.49
28:BD:25:THR:HG21	28:BD:193:VAL:HG22	1.95	0.49
30:BF:117:LEU:O	30:BF:178:ARG:HB2	2.13	0.49
31:BG:23:VAL:HG22	31:BG:36:THR:HB	1.95	0.49
57:CT:22:DC:C2	57:CT:23:DC:C5	3.01	0.49
58:CB:11:PRO:O	58:CB:12:ARG:HD2	2.12	0.49
59:CC:680:LEU:HD23	59:CC:680:LEU:C	2.38	0.49
60:CD:158:GLN:O	60:CD:158:GLN:NE2	2.46	0.49
1:AA:1006:G:C6	1:AA:1024:G:C2	3.00	0.49
1:AA:1305:G:HO2'	1:AA:1306:A:H8	1.60	0.49
1:AA:1382:C:C2'	1:AA:1383:C:H5'	2.42	0.49
11:AK:114:THR:HG21	21:AU:32:VAL:HG21	1.94	0.49
25:BA:1672:A:C2	25:BA:2582:G:H5'	2.48	0.49
32:BH:8:LYS:NZ	32:BH:137:GLU:OE2	2.46	0.49
1:AA:72:A:H2'	1:AA:73:C:O4'	2.13	0.49
1:AA:1025:U:H5''	1:AA:1026:G:C5'	2.40	0.49
2:AB:107:VAL:O	2:AB:111:ILE:HG23	2.12	0.49
24:AX:49:C:H2'	24:AX:50:U:C6	2.48	0.49
25:BA:886:A:N6	25:BA:887:U:O2	2.45	0.49
51:B3:5:ILE:HG21	51:B3:28:ARG:HD2	1.94	0.49
13:AM:57:ARG:NE	55:B7:35:ASP:OD2	2.46	0.48
19:AS:27:ASP:OD1	19:AS:28:LYS:N	2.46	0.48
25:BA:219:A:N3	25:BA:234:U:O2'	2.37	0.48
25:BA:1175:A:H62	25:BA:1177:G:H1'	1.78	0.48
25:BA:2112:G:H3'	25:BA:2113:U:C6	2.48	0.48
1:AA:87:C:H2'	1:AA:88:U:C6	2.48	0.48
1:AA:474:G:OP1	16:AP:80:LYS:NZ	2.30	0.48
1:AA:841:C:H2'	1:AA:843:U:H5'	1.95	0.48
1:AA:874:G:C6	1:AA:875:U:C4	3.01	0.48
1:AA:1516:2MG:N2	1:AA:1519:MA6:OP2	2.46	0.48
25:BA:728:G:H4'	27:BC:13:ARG:HD3	1.96	0.48
25:BA:1231:U:H2'	25:BA:1232:G:H8	1.78	0.48
25:BA:1998:A:O2'	25:BA:2724:U:O2'	2.28	0.48
25:BA:2166:U:H5	25:BA:2170:A:H61	1.60	0.48
25:BA:2210:U:H4'	25:BA:2211:G:H5'	1.95	0.48
26:BB:1:U:O2'	26:BB:2:G:H8	1.96	0.48
32:BH:115:VAL:HG22	32:BH:132:PHE:CZ	2.48	0.48
45:BW:31:TYR:O	45:BW:92:VAL:HA	2.12	0.48
59:CC:493:ILE:C	59:CC:493:ILE:HD12	2.39	0.48
59:CC:1238:LEU:N	59:CC:1238:LEU:HD23	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AH:90:ASP:OD1	8:AH:90:ASP:N	2.43	0.48
10:AJ:77:VAL:HG12	10:AJ:78:GLU:OE1	2.14	0.48
25:BA:1914:C:H2'	25:BA:1915:3TD:O4	2.14	0.48
45:BW:63:ILE:HG22	45:BW:65:VAL:HG22	1.95	0.48
57:CT:20:DC:H2'	57:CT:21:DG:C8	2.47	0.48
2:AB:47:VAL:HG23	2:AB:48:PRO:CD	2.43	0.48
15:AO:25:THR:HG21	15:AO:70:LEU:HD13	1.95	0.48
23:AW:44:A:H2'	23:AW:45:G:O4'	2.14	0.48
25:BA:1175:A:H8	25:BA:1176:U:H4'	1.78	0.48
59:CC:1058:ARG:HH21	59:CC:1240:ASP:CG	2.20	0.48
60:CD:137:ARG:HG3	60:CD:142:GLU:HB2	1.94	0.48
1:AA:4:U:HO2'	1:AA:5:U:P	2.35	0.48
1:AA:1493:A:H2'	25:BA:1913:A:N1	2.28	0.48
25:BA:581:C:H2'	25:BA:582:A:C8	2.49	0.48
25:BA:2182:U:H1'	25:BA:2183:A:N7	2.28	0.48
25:BA:2344:U:H3'	51:B3:37:LYS:O	2.13	0.48
1:AA:1062:U:H2'	1:AA:1063:C:C6	2.49	0.48
1:AA:1498:UR3:OP2	22:AV:16:A:O2'	2.31	0.48
22:AV:44:A:O2'	22:AV:44:A:N3	2.33	0.48
38:BP:1:MET:O	38:BP:5:SER:CB	2.62	0.48
55:B7:30:HIS:CG	55:B7:31:ASP:N	2.81	0.48
57:CT:9:DC:H2'	57:CT:10:DT:C5	2.48	0.48
1:AA:246:A:N1	1:AA:278:G:O2'	2.40	0.48
1:AA:1014:A:C2	1:AA:1219:A:H1'	2.49	0.48
8:AH:18:GLN:HG3	8:AH:72:VAL:CG1	2.42	0.48
25:BA:1568:G:H4'	27:BC:59:LYS:HG2	1.95	0.48
25:BA:2038:G:H2'	25:BA:2039:U:O4'	2.14	0.48
42:BT:17:VAL:HA	42:BT:43:ALA:HB1	1.95	0.48
42:BT:88:ARG:NH2	42:BT:94:ASP:OD2	2.46	0.48
59:CC:234:ASP:HB3	59:CC:238:GLN:NE2	2.29	0.48
60:CD:1292:LEU:HD11	60:CD:1297:LYS:HB2	1.95	0.48
1:AA:866:C:C4	1:AA:867:G:H1'	2.49	0.48
25:BA:1057:A:C8	25:BA:1086:A:H2'	2.49	0.48
25:BA:1068:G:O6	25:BA:1069:A:N6	2.47	0.48
25:BA:2698:U:H2'	25:BA:2699:C:C6	2.49	0.48
27:BC:142:HIS:HD2	27:BC:193:GLY:O	1.96	0.48
29:BE:147:LEU:HD11	29:BE:170:ARG:HD2	1.95	0.48
56:CN:27:DA:C2	56:CN:28:DA:C4	3.02	0.48
56:CN:32:DA:H1'	56:CN:33:DT:O4'	2.14	0.48
57:CT:19:DG:C5	57:CT:20:DC:C4	3.02	0.48
59:CC:1278:LEU:HA	59:CC:1278:LEU:HD23	1.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:50:A:O2'	1:AA:360:G:N2	2.47	0.48
1:AA:1318:A:H5''	19:AS:3:ARG:NH2	2.29	0.48
6:AF:85:ILE:HG13	6:AF:86:ARG:N	2.29	0.48
9:AI:88:MET:HE1	9:AI:104:VAL:HG13	1.96	0.48
11:AK:34:ILE:HG12	11:AK:70:CYS:SG	2.54	0.48
25:BA:2114:A:N6	25:BA:2168:G:O6	2.47	0.48
26:BB:2:G:H2'	26:BB:3:C:C6	2.49	0.48
32:BH:86:ASP:C	32:BH:88:GLY:H	2.21	0.48
43:BU:48:GLN:HE21	43:BU:55:VAL:H	1.62	0.48
56:CN:32:DA:H5'	56:CN:32:DA:H8	1.76	0.48
59:CC:1085:MET:HE2	59:CC:1085:MET:HA	1.95	0.48
1:AA:218:U:H2'	1:AA:219:U:O4'	2.14	0.48
1:AA:1316:G:N1	1:AA:1319:A:OP2	2.42	0.48
25:BA:1042:G:O2'	25:BA:1043:C:H6	1.97	0.48
25:BA:2532:G:O2'	25:BA:2657:A:N1	2.43	0.48
59:CC:529:ARG:NH2	59:CC:562:GLU:OE2	2.46	0.48
1:AA:269:C:H2'	1:AA:270:A:C8	2.48	0.47
1:AA:562:U:H1'	12:AL:12:ARG:HB3	1.95	0.47
4:AD:101:VAL:HG21	4:AD:137:VAL:HG21	1.96	0.47
6:AF:88:MET:HE1	18:AR:61:ARG:HG2	1.96	0.47
15:AO:78:TYR:OH	15:AO:89:ARG:OXT	2.28	0.47
27:BC:132:MET:HE1	27:BC:174:LEU:HD21	1.95	0.47
30:BF:4:LEU:HD23	30:BF:4:LEU:HA	1.73	0.47
33:BK:114:LEU:HG	33:BK:118:MET:HE3	1.96	0.47
59:CC:267:ARG:HH22	59:CC:273:HIS:CE1	2.31	0.47
60:CD:805:GLN:OE1	60:CD:1348:LYS:HB2	2.13	0.47
1:AA:56:U:H2'	1:AA:57:G:H8	1.79	0.47
1:AA:844:G:H2'	1:AA:845:A:C8	2.49	0.47
1:AA:1039:G:H2'	1:AA:1040:U:C6	2.49	0.47
1:AA:1152:A:OP1	10:AJ:70:HIS:ND1	2.47	0.47
7:AG:79:ARG:HG3	7:AG:84:THR:HG22	1.95	0.47
13:AM:16:VAL:O	13:AM:20:THR:HG23	2.14	0.47
25:BA:581:C:H2'	25:BA:582:A:H8	1.79	0.47
55:B7:12:ILE:HD12	55:B7:32:LEU:HB2	1.96	0.47
60:CD:849:LEU:HA	60:CD:856:ILE:HA	1.96	0.47
1:AA:1034:G:H2'	1:AA:1035:A:C8	2.50	0.47
6:AF:79:ARG:HG3	6:AF:80:PHE:N	2.28	0.47
13:AM:59:GLU:OE2	13:AM:62:LYS:NZ	2.42	0.47
28:BD:55:LYS:HD3	28:BD:60:VAL:HG22	1.95	0.47
47:BY:13:VAL:HG22	47:BY:29:PHE:HB2	1.95	0.47
60:CD:1143:ASP:C	60:CD:1143:ASP:OD1	2.57	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:73:C:O2'	1:AA:74:A:H5'	2.15	0.47
6:AF:67:PRO:HG2	6:AF:70:VAL:CG2	2.43	0.47
9:AI:41:ARG:HH21	9:AI:41:ARG:HG3	1.79	0.47
25:BA:1407:G:O2'	25:BA:1408:G:H5'	2.15	0.47
25:BA:2131:U:H5'	25:BA:2132:U:OP1	2.15	0.47
25:BA:2135:A:H3'	25:BA:2136:G:C8	2.41	0.47
25:BA:2138:G:H2'	25:BA:2139:U:O4'	2.14	0.47
25:BA:2141:G:H2'	25:BA:2142:A:O4'	2.15	0.47
25:BA:2233:U:H2'	25:BA:2234:G:C8	2.50	0.47
25:BA:2522:U:O2'	25:BA:2647:U:OP1	2.29	0.47
59:CC:696:ASP:OD1	59:CC:696:ASP:N	2.45	0.47
59:CC:699:LEU:HD23	59:CC:699:LEU:HA	1.61	0.47
60:CD:26:SER:HB3	60:CD:236:TRP:CZ2	2.49	0.47
60:CD:62:PHE:O	60:CD:101:ARG:NH2	2.46	0.47
1:AA:1228:C:OP2	13:AM:110:LYS:NZ	2.44	0.47
2:AB:120:GLN:OE1	2:AB:124:GLY:HA3	2.14	0.47
3:AC:72:ARG:HD3	3:AC:75:ILE:HD12	1.97	0.47
3:AC:153:VAL:HG13	3:AC:198:VAL:HG22	1.96	0.47
25:BA:134:G:H2'	25:BA:135:U:C6	2.50	0.47
59:CC:269:ILE:HD12	59:CC:269:ILE:N	2.29	0.47
60:CD:425:ARG:HE	60:CD:464:ASP:CG	2.21	0.47
1:AA:1277:C:O2'	1:AA:1278:G:P	2.72	0.47
7:AG:66:LEU:O	7:AG:70:ARG:HG3	2.15	0.47
9:AI:55:VAL:HG12	9:AI:57:MET:SD	2.55	0.47
25:BA:2243:U:H2'	25:BA:2244:U:H6	1.77	0.47
25:BA:2327:A:H2'	25:BA:2328:A:C8	2.49	0.47
32:BH:66:ASN:C	32:BH:66:ASN:HD22	2.21	0.47
46:BX:53:CYS:SG	46:BX:57:HIS:HA	2.54	0.47
57:CT:21:DG:H2'	57:CT:22:DC:C6	2.49	0.47
58:CA:79:LEU:HD23	58:CA:79:LEU:O	2.15	0.47
59:CC:1239:VAL:HG13	59:CC:1240:ASP:N	2.27	0.47
60:CD:767:LEU:HD12	60:CD:767:LEU:N	2.28	0.47
1:AA:160:A:H1'	1:AA:344:A:C5	2.49	0.47
1:AA:1054:C:N4	24:AX:34:G:C8	2.83	0.47
1:AA:1088:G:H21	1:AA:1167:A:N6	2.13	0.47
3:AC:135:LYS:NZ	3:AC:168:TYR:OH	2.47	0.47
8:AH:112:THR:HG23	8:AH:115:ALA:H	1.78	0.47
15:AO:8:THR:HG23	15:AO:31:LEU:HD21	1.95	0.47
24:AX:27:G:H2'	24:AX:28:G:C8	2.49	0.47
25:BA:141:G:H4'	25:BA:1596:A:H5''	1.95	0.47
25:BA:613:A:H5''	25:BA:613:A:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:811:U:H2'	35:BM:21:ARG:HA	1.96	0.47
25:BA:1614:A:C2	42:BT:93:ALA:HB2	2.50	0.47
25:BA:2743:U:H2'	25:BA:2744:G:O4'	2.15	0.47
28:BD:32:ASN:HD22	28:BD:32:ASN:N	2.11	0.47
29:BE:51:GLU:OE1	29:BE:88:ARG:NH1	2.48	0.47
45:BW:80:HIS:CE1	45:BW:83:LYS:HD2	2.50	0.47
59:CC:576:SER:OG	59:CC:577:VAL:N	2.47	0.47
59:CC:1292:THR:OG1	59:CC:1293:VAL:N	2.47	0.47
59:CC:1336:ASN:HD22	59:CC:1336:ASN:C	2.23	0.47
60:CD:175:GLU:CD	60:CD:175:GLU:N	2.72	0.47
60:CD:746:LEU:HD23	60:CD:758:PRO:HB3	1.96	0.47
1:AA:451:A:H1'	1:AA:452:A:C2	2.49	0.47
1:AA:901:A:C5	1:AA:902:G:H1'	2.50	0.47
10:AJ:52:LEU:HD21	10:AJ:59:LYS:HD2	1.96	0.47
25:BA:626:A:H2'	35:BM:78:ARG:NH2	2.30	0.47
25:BA:1315:C:O2'	25:BA:1392:A:N3	2.41	0.47
25:BA:2119:A:H62	25:BA:2167:U:H1'	1.80	0.47
27:BC:227:PRO:HA	27:BC:233:GLY:HA2	1.95	0.47
33:BK:69:ARG:HG2	33:BK:90:GLU:HG3	1.95	0.47
56:CN:10:DG:H2''	56:CN:11:DT:H72	1.97	0.47
60:CD:664:ILE:HG22	60:CD:678:ARG:HG2	1.97	0.47
60:CD:850:LYS:N	60:CD:855:ASP:O	2.33	0.47
1:AA:91:U:H2'	1:AA:92:U:H6	1.80	0.47
1:AA:1026:G:C4	1:AA:1027:C:C5	3.02	0.47
4:AD:59:GLN:OE1	4:AD:63:ARG:NH1	2.42	0.47
6:AF:85:ILE:HG13	6:AF:86:ARG:H	1.80	0.47
32:BH:17:ASP:OD1	32:BH:17:ASP:N	2.46	0.47
58:CA:179:PRO:HA	58:CA:208:ASN:ND2	2.30	0.47
60:CD:255:LEU:HG	60:CD:256:ASP:H	1.79	0.47
2:AB:187:VAL:HG13	2:AB:191:SER:HB2	1.97	0.47
24:AX:15:G:C3'	24:AX:16:H2U:H62	2.45	0.47
25:BA:1386:C:H2'	25:BA:1387:A:H8	1.79	0.47
25:BA:1405:U:H2'	25:BA:1406:U:C6	2.50	0.47
25:BA:2124:G:O2'	25:BA:2174:C:N3	2.33	0.47
34:BL:38:ILE:HD11	34:BL:112:PHE:CZ	2.50	0.47
51:B3:13:SER:HB3	51:B3:49:TYR:CZ	2.49	0.47
60:CD:247:PRO:HA	60:CD:250:ARG:CZ	2.45	0.47
60:CD:1249:ASN:OD1	60:CD:1250:ASP:N	2.48	0.47
1:AA:842:U:H4'	1:AA:846:G:N1	2.29	0.46
25:BA:813:U:H2'	25:BA:814:C:C6	2.51	0.46
25:BA:2114:A:H2'	25:BA:2114:A:N3	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:BC:105:LEU:O	27:BC:107:PRO:HD3	2.16	0.46
32:BH:8:LYS:HA	32:BH:14:SER:HA	1.97	0.46
43:BU:4:GLU:CD	48:BZ:19:LEU:HD11	2.40	0.46
1:AA:81:A:N6	1:AA:89:G:C6	2.84	0.46
1:AA:203:G:O2'	1:AA:465:A:N1	2.47	0.46
1:AA:464:U:O2'	1:AA:466:A:N7	2.31	0.46
1:AA:790:A:OP1	23:AW:38:A:O2'	2.32	0.46
1:AA:922:G:N3	1:AA:1398:A:H2	2.13	0.46
7:AG:2:PRO:HG2	7:AG:5:ARG:HB2	1.98	0.46
25:BA:1178:C:H2'	25:BA:1179:G:H8	1.77	0.46
53:B5:62:LEU:HB3	53:B5:65:ALA:HB2	1.98	0.46
60:CD:393:THR:HG23	60:CD:395:LYS:H	1.80	0.46
1:AA:459:A:H2'	1:AA:460:A:C8	2.50	0.46
1:AA:1189:U:OP1	14:AN:98:LYS:NZ	2.48	0.46
2:AB:71:GLY:O	2:AB:93:ASN:HA	2.15	0.46
6:AF:39:LEU:HD13	6:AF:62:MET:HG2	1.97	0.46
40:BR:89:GLU:HG3	41:BS:52:PRO:HB3	1.98	0.46
60:CD:424:ASN:ND2	60:CD:424:ASN:C	2.73	0.46
1:AA:567:G:H2'	1:AA:568:G:O4'	2.16	0.46
1:AA:826:C:O2	8:AH:16:ASN:ND2	2.49	0.46
5:AE:80:THR:HG22	5:AE:81:LEU:N	2.30	0.46
13:AM:49:SER:HB2	13:AM:52:GLN:OE1	2.15	0.46
22:AV:52:C:H2'	22:AV:53:G:O4'	2.16	0.46
25:BA:1932:A:H2'	25:BA:1933:G:O4'	2.15	0.46
25:BA:2812:G:H2'	25:BA:2813:A:O4'	2.16	0.46
50:B2:38:HIS:ND1	50:B2:39:LEU:O	2.48	0.46
51:B3:22:THR:HG23	53:B5:34:THR:HG23	1.98	0.46
59:CC:316:GLU:CD	59:CC:316:GLU:H	2.22	0.46
60:CD:139:LEU:HD23	60:CD:139:LEU:HA	1.68	0.46
1:AA:195:A:C2'	1:AA:196:A:H5'	2.45	0.46
4:AD:98:LEU:O	4:AD:101:VAL:HG22	2.15	0.46
13:AM:17:ILE:O	13:AM:20:THR:OG1	2.32	0.46
13:AM:40:ALA:O	13:AM:43:VAL:HG22	2.14	0.46
16:AP:9:HIS:O	16:AP:16:PHE:N	2.44	0.46
25:BA:686:U:O4	52:B4:12:ARG:HB2	2.16	0.46
25:BA:851:C:H2'	25:BA:852:U:C6	2.50	0.46
58:CB:154:PRO:C	58:CB:156:SER:H	2.24	0.46
1:AA:1006:G:C5	1:AA:1007:U:C5	3.04	0.46
2:AB:188:ASP:HB2	2:AB:204:ASP:OD2	2.16	0.46
4:AD:95:GLU:HG3	4:AD:191:LEU:HD11	1.98	0.46
25:BA:1790:C:H2'	25:BA:1791:A:C5	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:CD:466:MET:HB2	60:CD:466:MET:HE3	1.70	0.46
3:AC:27:LYS:HB3	3:AC:28:GLU:OE1	2.16	0.46
5:AE:101:GLU:OE1	5:AE:122:ASN:ND2	2.49	0.46
13:AM:107:ARG:HH12	13:AM:112:PRO:C	2.23	0.46
24:AX:2:C:H2'	24:AX:3:C:H6	1.80	0.46
25:BA:829:A:N7	25:BA:2248:C:H5'	2.31	0.46
30:BF:25:VAL:O	30:BF:28:VAL:HG22	2.16	0.46
59:CC:1333:LEU:O	59:CC:1335:ILE:N	2.48	0.46
14:AN:7:LYS:O	14:AN:11:VAL:HG13	2.15	0.46
25:BA:248:G:H5'	25:BA:250:G:N7	2.30	0.46
25:BA:348:A:H2'	25:BA:349:U:O4'	2.16	0.46
42:BT:69:LEU:HD23	42:BT:69:LEU:HA	1.77	0.46
58:CB:34:GLY:N	58:CB:199:ASP:OD2	2.46	0.46
59:CC:514:PHE:CE1	59:CC:760:ASN:HB3	2.51	0.46
59:CC:1204:LEU:HD23	59:CC:1204:LEU:HA	1.69	0.46
1:AA:1175:G:N3	1:AA:1176:A:C8	2.84	0.46
24:AX:27:G:H2'	24:AX:28:G:H8	1.81	0.46
24:AX:51:U:H2'	24:AX:52:G:H8	1.80	0.46
42:BT:95:ARG:NH1	42:BT:95:ARG:HG2	2.30	0.46
58:CB:61:ILE:HD12	58:CB:142:MET:HB3	1.96	0.46
59:CC:1291:LEU:HD21	60:CD:1351:VAL:HG13	1.97	0.46
1:AA:183:C:H4'	1:AA:184:G:OP2	2.15	0.46
11:AK:116:ILE:HD13	11:AK:116:ILE:H	1.80	0.46
17:AQ:25:ILE:O	17:AQ:25:ILE:HG22	2.16	0.46
25:BA:133:U:H2'	25:BA:134:G:O4'	2.16	0.46
25:BA:144:A:H2'	25:BA:145:C:C6	2.51	0.46
25:BA:191:A:H2'	25:BA:192:C:C6	2.51	0.46
25:BA:355:U:H2'	25:BA:356:G:H8	1.81	0.46
25:BA:2086:U:H2'	25:BA:2087:G:C8	2.50	0.46
25:BA:2114:A:C6	25:BA:2115:G:H1'	2.50	0.46
30:BF:137:ILE:HG13	30:BF:138:PHE:N	2.31	0.46
39:BQ:66:ASN:OD1	39:BQ:66:ASN:N	2.49	0.46
40:BR:100:VAL:O	40:BR:103:LYS:NZ	2.48	0.46
60:CD:1050:THR:C	60:CD:1057:SER:HB3	2.41	0.46
1:AA:337:G:H2'	1:AA:338:A:H8	1.78	0.45
1:AA:1176:A:H2'	1:AA:1177:G:C8	2.51	0.45
2:AB:129:LEU:CB	2:AB:134:ALA:HB2	2.41	0.45
22:AV:49:G:H5''	59:CC:540:ARG:HH22	1.79	0.45
24:AX:8:4SU:O2'	24:AX:21:A:N1	2.37	0.45
25:BA:1028:A:N6	25:BA:1125:G:H2'	2.31	0.45
25:BA:1065:U:O2'	25:BA:1066:U:O5'	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1838:C:N4	25:BA:1898:U:H2'	2.30	0.45
25:BA:2128:G:H4'	25:BA:2174:C:H4'	1.98	0.45
59:CC:794:LEU:HA	59:CC:794:LEU:HD12	1.71	0.45
1:AA:4:U:O2'	1:AA:5:U:P	2.75	0.45
1:AA:17:U:H2'	1:AA:18:C:C6	2.50	0.45
1:AA:1180:A:P	9:AI:99:ARG:HH22	2.39	0.45
1:AA:1305:G:O2'	1:AA:1306:A:H8	1.99	0.45
11:AK:110:ILE:HB	21:AU:4:ILE:HD13	1.98	0.45
25:BA:1799:G:OP1	27:BC:258:ARG:HD2	2.16	0.45
25:BA:2114:A:N1	25:BA:2115:G:O2'	2.43	0.45
25:BA:2123:G:H2'	25:BA:2123:G:N3	2.31	0.45
30:BF:91:LEU:C	30:BF:96:MET:HB2	2.40	0.45
41:BS:60:LYS:HE2	41:BS:60:LYS:HB3	1.68	0.45
60:CD:149:GLY:HA2	60:CD:176:PHE:HB2	1.98	0.45
60:CD:474:LEU:HD21	61:CE:27:ALA:HB3	1.97	0.45
1:AA:1356:G:H2'	1:AA:1357:A:H8	1.78	0.45
14:AN:8:ALA:O	14:AN:11:VAL:HG22	2.16	0.45
24:AX:43:C:H2'	24:AX:44:G:H8	1.80	0.45
25:BA:639:U:H2'	25:BA:640:C:H6	1.81	0.45
25:BA:1328:A:HO2'	25:BA:1329:U:H6	1.62	0.45
25:BA:1486:U:H2'	25:BA:1487:U:C6	2.52	0.45
42:BT:18:ARG:HG3	42:BT:76:VAL:HB	1.98	0.45
54:B6:2:LYS:HE3	54:B6:32:LYS:O	2.15	0.45
58:CA:102:LEU:HD23	58:CA:102:LEU:C	2.41	0.45
59:CC:563:THR:OG1	59:CC:564:PRO:HD2	2.16	0.45
60:CD:265:LEU:O	60:CD:268:LEU:N	2.45	0.45
60:CD:636:GLY:O	60:CD:638:SER:N	2.49	0.45
25:BA:2015:A:C6	50:B2:3:VAL:HG23	2.52	0.45
29:BE:109:LEU:O	29:BE:113:VAL:HG13	2.16	0.45
30:BF:8:TYR:HB2	30:BF:173:PHE:CZ	2.52	0.45
49:B1:24:LEU:HD11	49:B1:54:MET:HE2	1.98	0.45
51:B3:10:LYS:HD2	51:B3:55:LYS:HG2	1.98	0.45
60:CD:952:VAL:HG13	60:CD:1014:GLY:H	1.81	0.45
25:BA:310:A:H5''	44:BV:15:THR:HG23	1.98	0.45
25:BA:545:A:C2	25:BA:549:C:N3	2.84	0.45
25:BA:1209:U:O2'	25:BA:1237:A:N1	2.46	0.45
25:BA:2039:U:H2'	25:BA:2040:G:C8	2.52	0.45
32:BH:88:GLY:O	32:BH:89:LYS:O	2.35	0.45
53:B5:15:LYS:HB2	53:B5:23:LYS:HZ3	1.81	0.45
1:AA:1060:U:H2'	1:AA:1061:G:H8	1.81	0.45
4:AD:104:ARG:HG2	4:AD:170:TRP:CZ2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AG:78:ARG:HG3	7:AG:80:VAL:HG22	1.99	0.45
9:AI:6:TYR:CE2	9:AI:90:TYR:HD1	2.34	0.45
23:AW:18:G:H8	23:AW:18:G:OP1	2.00	0.45
25:BA:2172:U:OP2	25:BA:2172:U:H4'	2.16	0.45
56:CN:26:DG:C4	56:CN:27:DA:N7	2.85	0.45
57:CT:4:DT:H2''	57:CT:5:DG:H8	1.82	0.45
58:CB:34:GLY:H	58:CB:199:ASP:CG	2.25	0.45
59:CC:1076:ILE:O	59:CC:1076:ILE:HG13	2.15	0.45
60:CD:213:LYS:O	60:CD:213:LYS:HD3	2.17	0.45
60:CD:891:ASP:OD1	60:CD:1286:LYS:NZ	2.49	0.45
60:CD:1075:ARG:NH2	60:CD:1102:PRO:HA	2.31	0.45
1:AA:925:G:C6	1:AA:927:G:N7	2.84	0.45
1:AA:958:A:OP1	19:AS:55:ARG:NH1	2.41	0.45
1:AA:1061:G:H5'	10:AJ:61:ALA:HB2	1.98	0.45
1:AA:1435:G:H2'	1:AA:1436:U:C6	2.52	0.45
2:AB:222:ARG:O	61:CE:62:GLN:NE2	2.50	0.45
5:AE:111:MET:HE2	5:AE:125:ALA:CB	2.42	0.45
25:BA:1149:G:H2'	25:BA:1150:C:C6	2.51	0.45
25:BA:2228:G:H2'	25:BA:2229:U:H6	1.82	0.45
25:BA:2605:PSU:H2'	25:BA:2606:C:C6	2.52	0.45
35:BM:109:LYS:HG2	35:BM:126:ARG:HB2	1.98	0.45
36:BN:17:ASN:O	36:BN:38:ARG:NH1	2.49	0.45
59:CC:38:PHE:CZ	59:CC:49:LEU:HD21	2.51	0.45
59:CC:261:VAL:HG21	59:CC:264:GLU:CD	2.42	0.45
59:CC:1043:ALA:O	59:CC:1046:VAL:HG22	2.17	0.45
1:AA:927:G:C2'	1:AA:928:G:H5'	2.47	0.45
1:AA:1151:A:OP1	10:AJ:44:THR:HG22	2.16	0.45
1:AA:1367:C:H5''	9:AI:116:VAL:HG22	1.98	0.45
10:AJ:37:ARG:HH11	10:AJ:37:ARG:CA	2.29	0.45
22:AV:24:A:H2'	22:AV:25:U:O4'	2.16	0.45
25:BA:404:A:H4'	25:BA:405:U:H5''	1.99	0.45
25:BA:677:A:O2'	25:BA:2071:A:H5'	2.17	0.45
26:BB:2:G:H2'	26:BB:3:C:H6	1.80	0.45
34:BL:5:GLN:N	34:BL:21:CYS:O	2.46	0.45
34:BL:38:ILE:HD11	34:BL:112:PHE:HZ	1.81	0.45
42:BT:20:VAL:O	42:BT:23:LEU:HB2	2.17	0.45
59:CC:1314:GLN:HG3	61:CE:28:ARG:HH22	1.81	0.45
60:CD:301:GLU:OE1	60:CD:312:ARG:NE	2.46	0.45
60:CD:601:ILE:HG21	60:CD:601:ILE:HD13	1.72	0.45
9:AI:36:GLU:HA	9:AI:45:ARG:HE	1.82	0.45
25:BA:125:A:OP2	52:B4:19:ARG:NH2	2.41	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:357:C:H2'	25:BA:358:U:H6	1.82	0.45
25:BA:1406:U:O2'	25:BA:1407:G:H5''	2.17	0.45
25:BA:2052:A:O2'	28:BD:148:GLN:O	2.29	0.45
25:BA:2299:U:OP1	30:BF:72:LYS:NZ	2.50	0.45
27:BC:76:ALA:HB2	27:BC:96:TYR:CD2	2.51	0.45
35:BM:57:LEU:HD22	53:B5:54:ASP:HB2	1.99	0.45
59:CC:1314:GLN:CG	61:CE:28:ARG:HH22	2.30	0.45
1:AA:35:G:N2	12:AL:115:SER:OG	2.49	0.45
1:AA:522:C:N3	1:AA:527:G7M:N1	2.53	0.45
2:AB:60:ILE:CG2	2:AB:65:GLY:HA3	2.46	0.45
21:AU:39:GLU:OE2	21:AU:47:ARG:NE	2.33	0.45
25:BA:1681:G:O2'	25:BA:1762:A:N3	2.45	0.45
27:BC:2:ALA:N	27:BC:20:VAL:O	2.50	0.45
27:BC:120:VAL:HG21	32:BH:91:PHE:CD2	2.52	0.45
30:BF:40:VAL:O	30:BF:42:GLU:N	2.43	0.45
32:BH:132:PHE:HB2	32:BH:140:ALA:HB3	1.99	0.45
42:BT:95:ARG:HH12	42:BT:97:LEU:HD21	1.81	0.45
43:BU:93:LEU:HD23	43:BU:94:ASP:O	2.15	0.45
44:BV:74:ASN:HB3	44:BV:96:PHE:CD1	2.52	0.45
58:CB:66:HIS:CG	58:CB:68:TYR:HB3	2.52	0.45
59:CC:571:LEU:HA	59:CC:571:LEU:HD23	1.47	0.45
59:CC:605:TYR:C	59:CC:606:LEU:HD12	2.42	0.45
60:CD:424:ASN:ND2	60:CD:424:ASN:O	2.50	0.45
60:CD:1342:ASP:C	60:CD:1342:ASP:OD1	2.58	0.45
11:AK:110:ILE:O	21:AU:4:ILE:HG23	2.17	0.44
12:AL:54:ARG:NH1	12:AL:64:THR:OG1	2.50	0.44
22:AV:51:G:C2	22:AV:52:C:C5	3.04	0.44
23:AW:17:C:H2'	23:AW:17(A):U:C6	2.52	0.44
25:BA:151:C:H2'	25:BA:152:A:H8	1.82	0.44
25:BA:1593:A:H2'	25:BA:1594:U:C6	2.52	0.44
26:BB:55:U:O2'	30:BF:24:SER:OG	2.26	0.44
35:BM:132:ARG:HG3	35:BM:142:ILE:HD12	1.99	0.44
59:CC:616:ILE:HA	59:CC:652:TYR:O	2.17	0.44
59:CC:705:GLU:OE1	59:CC:705:GLU:N	2.41	0.44
59:CC:1257:GLN:NE2	60:CD:345:LYS:HD3	2.32	0.44
59:CC:1276:TRP:CE2	60:CD:801:VAL:HG21	2.52	0.44
5:AE:105:ILE:O	5:AE:112:ARG:NH2	2.50	0.44
5:AE:110:ALA:HB1	5:AE:137:VAL:HG23	1.98	0.44
10:AJ:6:ILE:HG12	10:AJ:79:PRO:HG3	2.00	0.44
25:BA:197:A:H4'	25:BA:2069:G7M:OP2	2.17	0.44
25:BA:2081:U:H2'	25:BA:2082:A:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2529:G:H4'	31:BG:175:LYS:HE2	1.99	0.44
28:BD:34:VAL:O	28:BD:93:GLY:HA2	2.17	0.44
52:B4:12:ARG:NH2	52:B4:44:VAL:HG21	2.31	0.44
56:CN:28:DA:C4	56:CN:29:DG:C5	3.06	0.44
57:CT:4:DT:C2	57:CT:5:DG:N7	2.86	0.44
59:CC:145:ILE:CG2	59:CC:456:VAL:HG22	2.47	0.44
59:CC:936:ARG:HH22	59:CC:1044:PRO:HA	1.82	0.44
60:CD:340:GLN:HG3	60:CD:341:ASN:OD1	2.18	0.44
60:CD:1159:ILE:HB	60:CD:1160:SER:H	1.59	0.44
60:CD:1256:ILE:HG23	60:CD:1256:ILE:HD12	1.60	0.44
1:AA:459:A:H2'	1:AA:460:A:H8	1.82	0.44
1:AA:1496:C:H2'	1:AA:1497:G:O4'	2.17	0.44
4:AD:42:GLY:O	4:AD:44:ARG:N	2.45	0.44
14:AN:46:LEU:O	14:AN:50:THR:HG23	2.17	0.44
23:AW:7:G:O2'	23:AW:49:G:O5'	2.30	0.44
25:BA:1495:A:N3	25:BA:1578:U:O2'	2.48	0.44
25:BA:2122:U:H5'	25:BA:2123:G:OP2	2.17	0.44
28:BD:84:LEU:HD22	28:BD:88:GLU:O	2.16	0.44
30:BF:10:ASP:HB2	30:BF:11:GLU:OE1	2.18	0.44
34:BL:108:ARG:HA	34:BL:116:ILE:HG13	1.98	0.44
60:CD:674:THR:HG1	60:CD:677:GLU:CD	2.24	0.44
1:AA:81:A:H2'	1:AA:82:G:H5'	2.00	0.44
25:BA:371:A:H61	25:BA:401:A:H3'	1.82	0.44
25:BA:587:C:C2	35:BM:19:LEU:HD12	2.52	0.44
25:BA:593:U:H2'	25:BA:594:U:C6	2.52	0.44
25:BA:908:C:O2'	36:BN:70:ASP:OD2	2.31	0.44
30:BF:136:ILE:HA	30:BF:141:ILE:HD11	1.99	0.44
36:BN:36:VAL:HG22	45:BW:82:TYR:HB2	1.98	0.44
44:BV:47:LYS:HD2	44:BV:48:PRO:HD2	2.00	0.44
57:CT:12:DT:H6	57:CT:12:DT:H2'	1.66	0.44
60:CD:120:LEU:HB3	60:CD:121:PRO:CD	2.47	0.44
60:CD:513:MET:HG3	60:CD:544:LEU:HD21	1.98	0.44
60:CD:789:LYS:HB3	60:CD:789:LYS:HE2	1.62	0.44
1:AA:1137:C:H1'	1:AA:1138:G:N2	2.33	0.44
10:AJ:44:THR:HA	10:AJ:69:THR:O	2.17	0.44
14:AN:46:LEU:HD22	19:AS:13:LEU:HB2	1.98	0.44
15:AO:26:GLU:HG2	15:AO:81:LEU:HD22	1.98	0.44
25:BA:57:C:H2'	25:BA:58:G:O4'	2.18	0.44
25:BA:711:G:N2	25:BA:720:U:O2	2.38	0.44
25:BA:839:U:H2'	25:BA:840:C:C6	2.53	0.44
25:BA:1027:A:C2	25:BA:2488:G:H5'	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2314:A:H1'	30:BF:155:THR:HG21	1.98	0.44
48:BZ:21:LEU:HD11	48:BZ:49:ASP:HB3	1.99	0.44
59:CC:392:GLU:CD	59:CC:392:GLU:N	2.75	0.44
1:AA:90:C:C2	1:AA:91:U:C5	3.06	0.44
1:AA:413:G:H21	1:AA:428:G:H1'	1.81	0.44
9:AI:27:LYS:HB2	9:AI:27:LYS:HE3	1.60	0.44
17:AQ:17:MET:HG3	17:AQ:20:SER:HB2	2.00	0.44
25:BA:68:G:N2	25:BA:74:A:OP2	2.51	0.44
25:BA:615:U:H6	25:BA:615:U:H5'	1.82	0.44
25:BA:635:C:OP2	35:BM:126:ARG:NH2	2.50	0.44
25:BA:1596:A:O2'	25:BA:1597:A:C5'	2.65	0.44
25:BA:2121:G:H8	25:BA:2121:G:O5'	2.00	0.44
31:BG:2:SER:HA	31:BG:62:TRP:CE3	2.53	0.44
31:BG:148:LEU:HA	31:BG:151:TYR:HD2	1.82	0.44
39:BQ:34:GLU:OE2	39:BQ:39:ARG:NE	2.36	0.44
59:CC:28:LEU:HD23	59:CC:28:LEU:HA	1.54	0.44
9:AI:21:ILE:HD13	9:AI:63:LEU:HG	1.99	0.44
12:AL:42:PRO:HB2	12:AL:46:ASN:HB2	1.99	0.44
25:BA:2052:A:H4'	28:BD:148:GLN:O	2.18	0.44
25:BA:2228:G:H2'	25:BA:2229:U:C6	2.52	0.44
37:BO:56:LYS:NZ	37:BO:90:ARG:O	2.46	0.44
58:CA:213:PRO:HA	58:CA:216:ALA:HB3	2.00	0.44
60:CD:830:ASP:OD1	60:CD:832:LYS:NZ	2.43	0.44
1:AA:383:A:C5	1:AA:384:G:H1'	2.53	0.44
5:AE:72:ILE:HD12	5:AE:72:ILE:O	2.18	0.44
25:BA:1744:A:H3'	25:BA:1745:A:C8	2.53	0.44
27:BC:231:PRO:HB2	27:BC:245:VAL:HG21	1.99	0.44
55:B7:11:GLU:HA	55:B7:25:ARG:HA	2.00	0.44
59:CC:363:LEU:HD23	59:CC:363:LEU:HA	1.74	0.44
59:CC:596:ASP:CG	59:CC:597:GLY:H	2.21	0.44
59:CC:1238:LEU:N	59:CC:1238:LEU:CD2	2.81	0.44
60:CD:317:THR:HG21	60:CD:321:LYS:HA	1.99	0.44
60:CD:1309:ILE:HG13	60:CD:1310:THR:N	2.31	0.44
1:AA:212:G:C2	1:AA:213:G:C8	3.05	0.44
3:AC:45:LYS:HB2	3:AC:45:LYS:HE3	1.75	0.44
25:BA:796:C:H2'	25:BA:797:G:C8	2.53	0.44
25:BA:2314:A:O2'	25:BA:2315:G:H5'	2.18	0.44
28:BD:33:ARG:NH2	28:BD:74:GLU:O	2.51	0.44
37:BO:63:ARG:HH21	37:BO:63:ARG:CG	2.27	0.44
59:CC:1014:LEU:HD12	59:CC:1017:GLN:HB3	2.00	0.44
60:CD:488:ASN:N	60:CD:488:ASN:OD1	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:CD:1349:GLU:H	60:CD:1349:GLU:CD	2.24	0.44
1:AA:684:U:O2'	11:AK:40:ASN:HB3	2.16	0.43
11:AK:46:THR:O	11:AK:50:SER:OG	2.32	0.43
14:AN:24:ARG:NH1	14:AN:55:SER:OG	2.51	0.43
25:BA:1212:G:H1'	25:BA:1237:A:N6	2.32	0.43
25:BA:1542:U:H2'	25:BA:1543:G:O4'	2.18	0.43
25:BA:2146:C:H4'	25:BA:2147:A:C8	2.53	0.43
25:BA:2820:A:N1	28:BD:197:THR:OG1	2.50	0.43
31:BG:9:VAL:O	31:BG:49:THR:HA	2.18	0.43
55:B7:69:SER:O	55:B7:70:LYS:O	2.35	0.43
58:CB:107:ILE:HD11	58:CB:136:GLU:HA	1.99	0.43
59:CC:866:ASP:C	59:CC:866:ASP:OD1	2.60	0.43
59:CC:1314:GLN:CB	61:CE:28:ARG:HH22	2.31	0.43
59:CC:1329:GLU:OE1	60:CD:330:MET:HE2	2.17	0.43
60:CD:430:HIS:O	60:CD:431:ARG:C	2.61	0.43
60:CD:641:ILE:HD12	60:CD:641:ILE:HA	1.70	0.43
1:AA:428:G:OP2	4:AD:7:PRO:HG2	2.17	0.43
1:AA:1031:C:H4'	1:AA:1032:G:C2	2.53	0.43
5:AE:15:LEU:HB2	5:AE:37:THR:HG22	1.99	0.43
6:AF:4:TYR:CE1	6:AF:91:ARG:HG2	2.54	0.43
9:AI:55:VAL:O	9:AI:57:MET:N	2.52	0.43
25:BA:138:U:H6	25:BA:140:C:N3	2.16	0.43
25:BA:1328:A:H2'	25:BA:1330:C:C5	2.53	0.43
27:BC:273:LYS:HB3	27:BC:273:LYS:HE2	1.89	0.43
31:BG:107:LEU:HD13	31:BG:152:ARG:HB2	2.00	0.43
44:BV:74:ASN:OD1	44:BV:77:THR:OG1	2.35	0.43
45:BW:26:PHE:HZ	45:BW:47:VAL:HG11	1.83	0.43
59:CC:448:LEU:HD23	59:CC:448:LEU:HA	1.82	0.43
59:CC:554:HIS:O	59:CC:555:TYR:C	2.61	0.43
59:CC:696:ASP:CG	59:CC:697:LYS:N	2.67	0.43
59:CC:1340:GLU:CD	59:CC:1341:ASP:H	2.21	0.43
1:AA:699:C:C2'	1:AA:700:G:H5'	2.48	0.43
4:AD:50:ASP:O	4:AD:53:VAL:HG22	2.18	0.43
7:AG:30:LEU:HD22	7:AG:43:VAL:HG23	1.99	0.43
25:BA:2120:G:O2'	25:BA:2121:G:O5'	2.27	0.43
33:BK:40:HIS:CE1	33:BK:41:LYS:HG2	2.53	0.43
38:BP:53:THR:O	38:BP:59:ALA:HB2	2.18	0.43
58:CA:82:LEU:HA	58:CA:82:LEU:HD23	1.65	0.43
60:CD:424:ASN:O	60:CD:424:ASN:CG	2.61	0.43
60:CD:500:ILE:O	60:CD:500:ILE:HG22	2.18	0.43
60:CD:747:MET:HE2	60:CD:775:SER:HA	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:CD:903:LEU:HA	60:CD:903:LEU:HD13	1.68	0.43
1:AA:604:G:H2'	1:AA:605:U:O4'	2.19	0.43
1:AA:978:A:C5	1:AA:1319:A:C2	3.06	0.43
11:AK:85:MET:HG2	11:AK:111:THR:OG1	2.18	0.43
25:BA:892:A:H2'	25:BA:893:C:C6	2.53	0.43
25:BA:1413:A:H2'	25:BA:1414:C:O4'	2.17	0.43
25:BA:1802:A:H2'	25:BA:1803:A:C8	2.53	0.43
25:BA:2783:U:H2'	25:BA:2784:U:C6	2.54	0.43
25:BA:2803:G:H2'	25:BA:2804:U:C6	2.52	0.43
25:BA:2845:U:H5''	39:BQ:52:ASN:O	2.18	0.43
60:CD:265:LEU:HA	60:CD:265:LEU:HD23	1.67	0.43
1:AA:197:A:H4'	1:AA:198:G:O5'	2.17	0.43
6:AF:4:TYR:CD2	6:AF:71:ILE:HG12	2.54	0.43
10:AJ:41:PRO:HA	10:AJ:72:ARG:HD3	2.01	0.43
22:AV:43:A:OP2	59:CC:1250:SER:OG	2.22	0.43
23:AW:76:A:H2'	25:BA:2602:A:N6	2.33	0.43
25:BA:1077:A:H2'	25:BA:1078:U:O4'	2.19	0.43
33:BK:36:LEU:O	33:BK:51:GLY:HA3	2.18	0.43
37:BO:114:GLU:OE2	37:BO:118:ARG:NH2	2.51	0.43
59:CC:127:ILE:O	59:CC:127:ILE:HG13	2.18	0.43
59:CC:549:ASP:OD1	59:CC:550:VAL:N	2.52	0.43
60:CD:307:LEU:HD23	60:CD:307:LEU:HA	1.77	0.43
1:AA:213:G:C8	1:AA:214:C:C5	3.06	0.43
1:AA:562:U:O2	12:AL:13:ALA:N	2.51	0.43
1:AA:957:U:O2	1:AA:959:A:H8	2.02	0.43
1:AA:1226:C:H4'	1:AA:1227:A:OP1	2.18	0.43
1:AA:1396:A:H4'	1:AA:1397:C:H5''	1.99	0.43
1:AA:1486:G:H2'	1:AA:1487:G:O4'	2.19	0.43
4:AD:95:GLU:CD	4:AD:100:ASN:HD21	2.23	0.43
5:AE:152:MET:O	5:AE:156:LYS:HG3	2.19	0.43
6:AF:53:LYS:HB3	6:AF:53:LYS:HE2	1.71	0.43
9:AI:118:LEU:CD2	9:AI:124:ARG:HG2	2.49	0.43
11:AK:111:THR:HG22	21:AU:3:VAL:HG13	2.00	0.43
23:AW:55:PSU:O5'	23:AW:55:PSU:H6	2.00	0.43
24:AX:25:C:H2'	24:AX:26:A:O4'	2.18	0.43
25:BA:742:A:H2'	25:BA:743:A:C8	2.53	0.43
25:BA:1078:U:H5''	25:BA:1079:C:OP1	2.18	0.43
25:BA:1824:G:O3'	27:BC:247:PRO:HD3	2.19	0.43
25:BA:2108:A:H8	25:BA:2108:A:O5'	2.01	0.43
25:BA:2591:C:H2'	25:BA:2592:G:H8	1.83	0.43
39:BQ:22:PRO:HD3	39:BQ:50:ILE:HD12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:BT:95:ARG:HG2	42:BT:95:ARG:HH11	1.84	0.43
45:BW:80:HIS:ND1	45:BW:83:LYS:HB2	2.33	0.43
57:CT:10:DT:H2'	57:CT:11:DC:C6	2.53	0.43
59:CC:521:LEU:HA	59:CC:521:LEU:HD12	1.74	0.43
59:CC:1212:LEU:HA	59:CC:1212:LEU:HD23	1.67	0.43
60:CD:482:ALA:O	60:CD:488:ASN:ND2	2.50	0.43
60:CD:576:ARG:HD3	60:CD:593:ASN:HA	2.00	0.43
1:AA:1236:A:H2'	1:AA:1237:C:C6	2.54	0.43
6:AF:32:ALA:HB1	6:AF:70:VAL:HG21	2.00	0.43
15:AO:70:LEU:HD12	15:AO:70:LEU:HA	1.71	0.43
25:BA:299:A:N3	25:BA:319:G:O2'	2.43	0.43
25:BA:813:U:H2'	25:BA:814:C:H6	1.82	0.43
25:BA:1177:G:O2'	25:BA:1178:C:C6	2.71	0.43
25:BA:2798:U:H1'	25:BA:2799:G:C6	2.54	0.43
25:BA:2849:U:H4'	25:BA:2868:A:C2	2.54	0.43
27:BC:261:LYS:HA	27:BC:264:ASP:OD2	2.19	0.43
28:BD:149:ASN:CG	28:BD:150:MEQ:H	2.25	0.43
40:BR:9:ILE:HD13	40:BR:9:ILE:HA	1.87	0.43
58:CB:28:LEU:HD13	58:CB:28:LEU:HA	1.75	0.43
59:CC:131:THR:HG22	59:CC:132:ASP:N	2.34	0.43
59:CC:1105:SER:HB2	60:CD:731:ARG:HB3	2.00	0.43
59:CC:1235:LEU:HA	59:CC:1235:LEU:HD23	1.75	0.43
1:AA:843:U:O4	1:AA:844:G:N1	2.51	0.43
1:AA:970:C:N4	9:AI:130:ARG:O	2.51	0.43
1:AA:1225:A:H2'	1:AA:1226:C:C5	2.54	0.43
1:AA:1385:G:H2'	1:AA:1386:G:O4'	2.19	0.43
3:AC:111:LEU:HD22	3:AC:146:ALA:HB2	2.00	0.43
6:AF:18:VAL:HG21	6:AF:58:HIS:CD2	2.54	0.43
9:AI:41:ARG:HH21	9:AI:41:ARG:CG	2.31	0.43
25:BA:729:G:OP1	27:BC:10:SER:OG	2.25	0.43
33:BK:17:VAL:HG23	33:BK:137:PRO:HB2	2.00	0.43
33:BK:76:HIS:CE1	33:BK:85:LYS:HB2	2.53	0.43
35:BM:9:ALA:O	35:BM:12:SER:OG	2.29	0.43
36:BN:16:ARG:HD3	36:BN:16:ARG:HA	1.74	0.43
59:CC:569:ILE:O	59:CC:571:LEU:N	2.51	0.43
59:CC:623:LEU:C	59:CC:623:LEU:HD12	2.44	0.43
60:CD:357:VAL:O	60:CD:357:VAL:HG13	2.18	0.43
1:AA:80:C:N4	1:AA:81:A:H62	2.16	0.43
1:AA:728:A:H2'	1:AA:729:A:C8	2.54	0.43
1:AA:1035:A:N3	1:AA:1036:A:C8	2.87	0.43
4:AD:8:LYS:HB3	4:AD:21:LEU:CB	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AG:78:ARG:HE	7:AG:78:ARG:HB2	1.59	0.43
13:AM:44:LYS:O	13:AM:48:LEU:HG	2.19	0.43
25:BA:468:G:H5''	29:BE:55:SER:HB3	2.01	0.43
25:BA:1105:U:H2'	25:BA:1106:G:C8	2.52	0.43
25:BA:1263:U:O2'	50:B2:8:PRO:HD2	2.18	0.43
25:BA:1917:PSU:H2'	25:BA:1918:A:O4'	2.19	0.43
25:BA:2117:A:O2'	25:BA:2118:U:H4'	2.19	0.43
25:BA:2346:A:H4'	25:BA:2347:C:OP2	2.18	0.43
27:BC:105:LEU:HD23	27:BC:105:LEU:HA	1.89	0.43
30:BF:72:LYS:HE2	30:BF:72:LYS:HB3	1.75	0.43
38:BP:57:ALA:O	38:BP:61:GLN:HG2	2.19	0.43
43:BU:26:LYS:HB3	43:BU:26:LYS:HE2	1.73	0.43
59:CC:1214:ASP:C	59:CC:1214:ASP:OD1	2.61	0.43
1:AA:156:C:H2'	1:AA:157:U:O4'	2.19	0.43
1:AA:590:U:H2'	1:AA:591:U:C6	2.53	0.43
1:AA:1314:C:H2'	1:AA:1315:U:C6	2.54	0.43
1:AA:1424:U:H2'	1:AA:1425:U:O4'	2.19	0.43
2:AB:126:PHE:HE2	2:AB:129:LEU:HB3	1.84	0.43
5:AE:81:LEU:HD11	5:AE:96:MET:HG3	2.01	0.43
6:AF:37:HIS:O	6:AF:97:THR:HG23	2.19	0.43
10:AJ:56:HIS:O	10:AJ:57:VAL:O	2.37	0.43
25:BA:675:A:N3	25:BA:2443:C:O2'	2.41	0.43
25:BA:2081:U:H2'	25:BA:2082:A:H8	1.84	0.43
28:BD:37:VAL:HG22	28:BD:48:ILE:HG22	2.00	0.43
38:BP:3:LYS:HB3	38:BP:3:LYS:HE3	1.78	0.43
56:CN:27:DA:H1'	56:CN:28:DA:H5'	2.01	0.43
59:CC:196:VAL:HG22	59:CC:197:ARG:N	2.34	0.43
59:CC:473:ARG:HH11	59:CC:473:ARG:HG3	1.83	0.43
59:CC:1098:LEU:N	59:CC:1098:LEU:HD12	2.30	0.43
60:CD:1325:PHE:CD1	60:CD:1325:PHE:C	2.94	0.43
1:AA:84:U:H2'	1:AA:86:G:N2	2.34	0.42
1:AA:147:G:H2'	1:AA:148:G:C8	2.54	0.42
2:AB:60:ILE:O	2:AB:63:ARG:HG3	2.19	0.42
22:AV:47:G:C6	22:AV:48:C:C4	3.07	0.42
25:BA:2019:A:H4'	40:BR:34:VAL:HG21	2.00	0.42
28:BD:1:MET:SD	28:BD:205:PRO:HG2	2.59	0.42
32:BH:114:GLU:HG2	32:BH:134:VAL:HG12	2.00	0.42
52:B4:25:LYS:HE3	52:B4:25:LYS:HB3	1.85	0.42
56:CN:26:DG:C4	56:CN:27:DA:C5	3.07	0.42
56:CN:29:DG:H2''	56:CN:30:DA:O5'	2.19	0.42
57:CT:5:DG:H2'	57:CT:6:DA:C8	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:CT:10:DT:H2''	57:CT:11:DC:C5	2.54	0.42
57:CT:19:DG:C6	57:CT:20:DC:N4	2.87	0.42
59:CC:84:GLU:OE2	59:CC:1032:LYS:NZ	2.48	0.42
1:AA:202:G:O2'	1:AA:468:A:H8	2.01	0.42
1:AA:1492:A:OP1	12:AL:44:LYS:HB2	2.19	0.42
14:AN:27:LEU:HD23	14:AN:27:LEU:HA	1.91	0.42
25:BA:1026:G:OP1	25:BA:1134:A:O2'	2.28	0.42
25:BA:2312:U:H5'	30:BF:85:ILE:CD1	2.44	0.42
31:BG:11:VAL:N	31:BG:48:ASN:O	2.45	0.42
40:BR:69:ALA:HB1	40:BR:74:ILE:HG23	2.02	0.42
42:BT:28:LYS:HB3	42:BT:28:LYS:HE3	1.81	0.42
43:BU:10:VAL:HG12	43:BU:11:LEU:HD23	2.01	0.42
58:CA:183:ILE:HG23	58:CA:183:ILE:HD12	1.69	0.42
59:CC:210:LEU:HA	59:CC:210:LEU:HD23	1.60	0.42
59:CC:392:GLU:N	59:CC:392:GLU:OE2	2.38	0.42
59:CC:765:ILE:HD13	59:CC:765:ILE:HG21	1.86	0.42
59:CC:1336:ASN:C	59:CC:1336:ASN:ND2	2.77	0.42
60:CD:108:ALA:HB3	60:CD:279:LEU:HD23	2.00	0.42
60:CD:770:LEU:HA	60:CD:770:LEU:HD13	1.70	0.42
1:AA:384:G:H2'	1:AA:385:C:C6	2.54	0.42
10:AJ:5:ARG:HB2	10:AJ:77:VAL:HA	2.01	0.42
13:AM:40:ALA:HB3	13:AM:43:VAL:HG13	2.01	0.42
15:AO:67:LEU:HD22	15:AO:78:TYR:CE1	2.55	0.42
24:AX:34:G:H2'	24:AX:35:A:C8	2.54	0.42
26:BB:48:U:P	38:BP:30:ARG:HH22	2.42	0.42
38:BP:57:ALA:O	38:BP:60:GLU:HG2	2.19	0.42
60:CD:499:ILE:C	60:CD:501:VAL:H	2.27	0.42
6:AF:47:LEU:HD21	6:AF:57:ALA:HB3	2.00	0.42
9:AI:60:LYS:C	9:AI:61:LEU:HD12	2.44	0.42
25:BA:1494:A:H2'	25:BA:1495:A:H8	1.81	0.42
25:BA:2315:G:HO2'	25:BA:2316:G:H8	1.64	0.42
30:BF:148:ARG:HD2	30:BF:150:ARG:NH1	2.34	0.42
32:BH:84:ALA:HB2	32:BH:90:LEU:CD1	2.49	0.42
35:BM:81:ASP:HB3	35:BM:100:ILE:HD13	2.00	0.42
38:BP:18:LEU:HD23	38:BP:18:LEU:HA	1.70	0.42
59:CC:196:VAL:HG21	59:CC:209:ILE:HD11	2.00	0.42
59:CC:1286:THR:HG22	59:CC:1290:MET:HE2	2.02	0.42
1:AA:868:C:H2'	1:AA:869:G:O4'	2.19	0.42
1:AA:1320:C:O2	19:AS:36:ARG:NH1	2.51	0.42
3:AC:93:ASP:OD1	3:AC:93:ASP:C	2.62	0.42
23:AW:20:H2U:H61	23:AW:20:H2U:H5'	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:565:C:H2'	25:BA:566:U:O4'	2.20	0.42
25:BA:703:U:H2'	25:BA:704:G:O4'	2.20	0.42
56:CN:30:DA:C6	56:CN:31:DG:C6	3.07	0.42
59:CC:1176:LEU:HA	59:CC:1176:LEU:HD23	1.79	0.42
1:AA:979:C:O2	14:AN:59:ARG:HD3	2.19	0.42
1:AA:1006:G:H2'	1:AA:1007:U:H6	1.85	0.42
9:AI:80:ARG:O	9:AI:84:THR:HG23	2.20	0.42
10:AJ:19:ASP:O	10:AJ:22:THR:HG22	2.19	0.42
24:AX:49:C:H2'	24:AX:50:U:H6	1.84	0.42
25:BA:848:C:H2'	25:BA:849:A:H8	1.85	0.42
27:BC:142:HIS:CG	27:BC:195:VAL:HG23	2.55	0.42
28:BD:24:VAL:HG12	28:BD:178:VAL:HG21	2.02	0.42
30:BF:141:ILE:HD12	30:BF:141:ILE:O	2.20	0.42
31:BG:23:VAL:HA	31:BG:36:THR:HA	2.02	0.42
40:BR:11:ARG:HG2	40:BR:11:ARG:HH11	1.84	0.42
57:CT:6:DA:C2	57:CT:7:DA:C5	3.07	0.42
59:CC:176:ILE:HD13	59:CC:176:ILE:HG21	1.67	0.42
59:CC:217:THR:HG23	59:CC:351:LEU:HD21	2.02	0.42
59:CC:1304:MET:HA	59:CC:1304:MET:HE3	2.02	0.42
60:CD:1302:TYR:CD1	60:CD:1302:TYR:C	2.98	0.42
60:CD:1350:ASN:ND2	60:CD:1358:PRO:HD3	2.34	0.42
1:AA:526:C:P	12:AL:88:LYS:HE2	2.60	0.42
1:AA:1123:U:C2'	1:AA:1124:G:H5'	2.49	0.42
2:AB:9:MET:O	2:AB:14:VAL:HG22	2.20	0.42
2:AB:161:LEU:HD22	2:AB:176:ALA:HB2	2.02	0.42
11:AK:18:ASP:HA	11:AK:81:ASN:O	2.19	0.42
25:BA:476:G:H4'	25:BA:502:A:N1	2.34	0.42
25:BA:1199:U:H1'	40:BR:4:VAL:HG22	2.02	0.42
25:BA:1548:A:H2'	25:BA:1549:A:C8	2.54	0.42
25:BA:1769:U:O2'	25:BA:1958:C:OP1	2.37	0.42
25:BA:2123:G:N1	25:BA:2176:A:N6	2.68	0.42
25:BA:2225:A:H4'	25:BA:2226:C:O5'	2.19	0.42
25:BA:2359:C:O2'	53:B5:54:ASP:OD2	2.34	0.42
37:BO:101:GLY:O	37:BO:109:PRO:HA	2.20	0.42
56:CN:36:DA:H2''	56:CN:37:DG:C8	2.54	0.42
57:CT:4:DT:H2''	57:CT:5:DG:C8	2.55	0.42
57:CT:20:DC:O2	57:CT:21:DG:C8	2.73	0.42
58:CA:39:LEU:O	58:CA:40:GLY:C	2.62	0.42
59:CC:24:VAL:HG21	59:CC:704:MET:HE1	2.02	0.42
59:CC:45:GLY:O	59:CC:51:ALA:HB2	2.19	0.42
59:CC:139:ASN:C	59:CC:141:THR:H	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:CC:447:HIS:C	59:CC:449:GLY:N	2.77	0.42
59:CC:1133:LYS:O	59:CC:1135:GLN:NE2	2.47	0.42
59:CC:1281:TYR:CE2	60:CD:484:MET:HE3	2.54	0.42
60:CD:174:ASP:C	60:CD:176:PHE:H	2.28	0.42
60:CD:336:GLY:O	60:CD:337:ARG:C	2.63	0.42
60:CD:962:ASN:ND2	60:CD:979:ASN:O	2.51	0.42
1:AA:263:A:P	20:AT:74:ARG:HH12	2.43	0.42
1:AA:1441:A:H62	1:AA:1461:G:H21	1.68	0.42
7:AG:2:PRO:CG	7:AG:5:ARG:HB2	2.50	0.42
7:AG:12:ILE:O	7:AG:12:ILE:HG13	2.20	0.42
19:AS:51:VAL:HG21	19:AS:71:LEU:HB3	2.01	0.42
25:BA:64:A:H2'	25:BA:65:U:C6	2.55	0.42
25:BA:1563:U:H2'	25:BA:1564:C:C6	2.55	0.42
25:BA:1599:U:H2'	25:BA:1600:C:C6	2.55	0.42
30:BF:148:ARG:HD2	30:BF:150:ARG:HH12	1.85	0.42
41:BS:44:GLY:O	41:BS:45:GLU:HG3	2.20	0.42
41:BS:77:PHE:HD1	41:BS:84:ARG:HB3	1.83	0.42
42:BT:36:LEU:HB3	42:BT:48:LYS:HB2	2.02	0.42
43:BU:50:LEU:HD23	48:BZ:26:PHE:CZ	2.55	0.42
58:CA:205:MET:SD	58:CA:213:PRO:HG3	2.60	0.42
59:CC:530:ILE:HA	59:CC:530:ILE:HD13	1.64	0.42
59:CC:962:GLU:O	59:CC:966:ILE:HD13	2.20	0.42
59:CC:1336:ASN:HB2	60:CD:25:ALA:HB2	2.01	0.42
61:CE:26:ARG:HE	61:CE:53:GLU:CD	2.25	0.42
1:AA:235:C:H2'	1:AA:236:A:C8	2.55	0.42
1:AA:502:A:H2'	1:AA:503:C:O4'	2.20	0.42
1:AA:532:A:N6	1:AA:1206:G:O2'	2.51	0.42
2:AB:43:LEU:HA	2:AB:46:THR:HB	2.02	0.42
7:AG:23:LEU:O	7:AG:27:VAL:HG23	2.20	0.42
25:BA:277:G:H2'	25:BA:277:G:N3	2.35	0.42
25:BA:608:A:H2'	25:BA:609:A:C8	2.55	0.42
25:BA:1693:U:O2'	27:BC:14:ARG:NH2	2.53	0.42
25:BA:2805:C:H2'	25:BA:2806:C:O4'	2.20	0.42
59:CC:421:SER:O	59:CC:422:LYS:C	2.62	0.42
59:CC:538:LEU:HD12	59:CC:538:LEU:C	2.44	0.42
60:CD:554:GLU:OE1	60:CD:588:PRO:HA	2.20	0.42
60:CD:618:VAL:H	60:CD:618:VAL:HG22	1.68	0.42
1:AA:1103:C:O2	2:AB:106:THR:HG21	2.20	0.42
1:AA:1151:A:HO2'	1:AA:1152:A:H8	1.60	0.42
3:AC:42:TYR:CZ	3:AC:90:VAL:HG11	2.54	0.42
6:AF:51:ILE:HD11	18:AR:66:SER:OG	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AG:12:ILE:HD13	7:AG:25:LYS:HE3	2.02	0.42
12:AL:87:VAL:HG12	12:AL:89:D2T:OD2	2.20	0.42
13:AM:31:LYS:NZ	13:AM:41:GLU:OE1	2.53	0.42
15:AO:28:GLN:OE1	15:AO:66:LEU:HD11	2.20	0.42
16:AP:67:ILE:HG22	16:AP:68:SER:O	2.20	0.42
24:AX:37:MIA:H163	24:AX:37:MIA:H122	1.72	0.42
25:BA:3:U:H2'	25:BA:4:U:C6	2.54	0.42
25:BA:39:G:H2'	25:BA:40:U:C6	2.55	0.42
25:BA:1529:G:H2'	25:BA:1530:G:C8	2.55	0.42
25:BA:2458:G:O2'	25:BA:2460:U:O4	2.33	0.42
26:BB:49:C:OP1	38:BP:101:GLY:HA3	2.19	0.42
31:BG:105:LEU:HD13	31:BG:107:LEU:HD11	2.01	0.42
32:BH:73:ASN:ND2	32:BH:141:LYS:O	2.47	0.42
36:BN:36:VAL:HG13	45:BW:82:TYR:CD2	2.55	0.42
40:BR:65:ILE:CD1	40:BR:92:ARG:HB2	2.49	0.42
59:CC:1333:LEU:C	59:CC:1335:ILE:N	2.78	0.42
60:CD:544:LEU:HD12	60:CD:544:LEU:HA	1.74	0.42
60:CD:548:VAL:HG22	60:CD:549:LYS:N	2.35	0.42
60:CD:700:ASN:C	60:CD:700:ASN:HD22	2.27	0.42
60:CD:826:ILE:HG23	60:CD:831:VAL:HG12	2.02	0.42
1:AA:1:A:H2'	1:AA:2:A:C8	2.55	0.41
1:AA:522:C:OP2	12:AL:66:TYR:OH	2.31	0.41
1:AA:911:U:OP1	12:AL:92:GLY:HA2	2.20	0.41
3:AC:178:LEU:HD23	3:AC:178:LEU:HA	1.73	0.41
12:AL:25:GLU:CD	12:AL:59:ASN:HD22	2.27	0.41
20:AT:10:ARG:HD3	20:AT:10:ARG:HA	1.86	0.41
25:BA:1175:A:N7	25:BA:1176:U:O2'	2.47	0.41
25:BA:2012:G:P	42:BT:11:ARG:HH22	2.40	0.41
25:BA:2151:U:H2'	25:BA:2152:G:H8	1.85	0.41
57:CT:17:DG:C4	57:CT:18:DC:C6	3.07	0.41
57:CT:20:DC:C2	57:CT:21:DG:N7	2.88	0.41
58:CA:11:PRO:HB3	58:CA:31:LEU:HD21	2.02	0.41
59:CC:204:LEU:HD21	59:CC:369:MET:SD	2.59	0.41
59:CC:222:ASP:OD1	59:CC:227:LYS:NZ	2.45	0.41
59:CC:524:ILE:HG21	59:CC:524:ILE:HD13	1.76	0.41
59:CC:569:ILE:HG21	59:CC:569:ILE:HD13	1.60	0.41
59:CC:1257:GLN:CD	60:CD:345:LYS:HB2	2.45	0.41
59:CC:1339:LEU:HA	59:CC:1339:LEU:HD23	1.88	0.41
60:CD:361:LEU:HA	60:CD:361:LEU:HD23	1.79	0.41
60:CD:374:LEU:HD23	60:CD:374:LEU:C	2.45	0.41
1:AA:33:A:H2'	1:AA:34:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1100:C:OP2	2:AB:95:ARG:HD3	2.21	0.41
3:AC:175:LEU:HA	3:AC:175:LEU:HD23	1.61	0.41
9:AI:15:SER:HB2	9:AI:78:ALA:HB2	2.02	0.41
21:AU:7:ARG:HB2	21:AU:10:GLU:CD	2.45	0.41
22:AV:51:G:N2	57:CT:18:DC:O2	2.51	0.41
25:BA:14:A:H2'	50:B2:18:SER:OG	2.20	0.41
25:BA:891:G:C2	25:BA:892:A:C8	3.08	0.41
25:BA:1656:C:H2'	25:BA:1657:U:H6	1.86	0.41
25:BA:1980:G:O2'	25:BA:1982:U:OP2	2.32	0.41
25:BA:2395:C:H2'	25:BA:2396:G:O4'	2.20	0.41
32:BH:30:LEU:HB3	32:BH:36:ALA:HB3	2.02	0.41
59:CC:7:GLU:C	59:CC:9:LYS:H	2.26	0.41
59:CC:213:LEU:HD23	59:CC:213:LEU:HA	1.73	0.41
59:CC:1096:ILE:HD13	59:CC:1096:ILE:HG21	1.65	0.41
59:CC:1248:THR:HG22	59:CC:1249:GLY:N	2.35	0.41
60:CD:72:CYS:HB2	60:CD:87:LYS:HD3	2.02	0.41
60:CD:160:LEU:HD23	60:CD:160:LEU:N	2.34	0.41
60:CD:416:ILE:O	60:CD:418:GLU:N	2.53	0.41
60:CD:871:LEU:O	60:CD:874:GLU:HB3	2.21	0.41
1:AA:845:A:H5''	1:AA:846:G:H8	1.85	0.41
1:AA:956:U:H2'	1:AA:957:U:O4'	2.20	0.41
3:AC:151:VAL:HG22	3:AC:200:VAL:HG22	2.02	0.41
4:AD:99:ASP:OD1	4:AD:100:ASN:N	2.53	0.41
15:AO:32:LEU:HD23	15:AO:32:LEU:HA	1.93	0.41
16:AP:34:GLU:OE1	16:AP:60:TRP:NE1	2.29	0.41
25:BA:263:G:O2'	25:BA:429:A:N3	2.47	0.41
29:BE:147:LEU:HD11	29:BE:170:ARG:HG3	2.01	0.41
53:B5:15:LYS:HB2	53:B5:23:LYS:NZ	2.36	0.41
55:B7:37:CYS:O	55:B7:41:HIS:HB2	2.20	0.41
56:CN:37:DG:H2''	56:CN:38:DA:OP2	2.19	0.41
60:CD:612:LEU:HA	60:CD:612:LEU:HD13	1.86	0.41
60:CD:755:ILE:HG22	60:CD:757:THR:H	1.85	0.41
1:AA:61:G:H2'	1:AA:62:U:O4'	2.21	0.41
1:AA:1384:C:H2'	1:AA:1385:G:C8	2.56	0.41
12:AL:102:LEU:HD13	12:AL:102:LEU:H	1.86	0.41
25:BA:61:C:C4	25:BA:62:U:H5	2.38	0.41
25:BA:364:C:H2'	25:BA:365:U:C6	2.56	0.41
25:BA:1223:G:OP2	41:BS:90:ARG:NH1	2.45	0.41
25:BA:2032:G:C8	28:BD:150:MEQ:HE3	2.56	0.41
25:BA:2171:A:H4'	25:BA:2172:U:OP1	2.20	0.41
25:BA:2183:A:H2'	25:BA:2184:A:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:BC:260:ASN:HD22	27:BC:260:ASN:HA	1.73	0.41
33:BK:117:ALA:O	33:BK:120:ARG:HB2	2.21	0.41
38:BP:27:VAL:HG21	38:BP:40:ILE:HD12	2.03	0.41
40:BR:94:ILE:HG21	41:BS:4:VAL:HG11	2.01	0.41
51:B3:6:ARG:CG	51:B3:24:THR:HB	2.47	0.41
59:CC:1060:ILE:HD13	59:CC:1060:ILE:HG21	1.89	0.41
59:CC:1251:TYR:CE1	59:CC:1301:ARG:NH1	2.88	0.41
60:CD:213:LYS:HZ3	60:CD:216:LYS:HG3	1.85	0.41
60:CD:472:LEU:HA	60:CD:472:LEU:HD23	1.80	0.41
60:CD:872:LEU:HD22	60:CD:877:VAL:HG21	2.02	0.41
1:AA:492:C:H2'	1:AA:493:A:C8	2.56	0.41
1:AA:816:A:OP1	1:AA:1526:G:O2'	2.32	0.41
1:AA:1086:U:H5	1:AA:1099:G:H22	1.67	0.41
1:AA:1141:C:HO2'	1:AA:1142:G:P	2.44	0.41
9:AI:35:LEU:HD11	9:AI:48:VAL:HG11	2.02	0.41
12:AL:123:LYS:HB2	12:AL:123:LYS:HE2	1.76	0.41
20:AT:85:LYS:HE3	20:AT:85:LYS:HB2	1.88	0.41
25:BA:358:U:H2'	25:BA:359:G:C8	2.55	0.41
25:BA:2251:OMG:HM23	25:BA:2251:OMG:H1'	1.69	0.41
25:BA:2405:G:O2'	25:BA:2411:A:N6	2.54	0.41
25:BA:2850:A:N7	25:BA:2868:A:O2'	2.43	0.41
30:BF:94:GLU:HG3	30:BF:95:ARG:N	2.36	0.41
32:BH:115:VAL:HG22	32:BH:132:PHE:CE2	2.55	0.41
55:B7:44:PHE:CD1	55:B7:45:THR:HG23	2.55	0.41
59:CC:166:SER:HB2	60:CD:1151:LYS:HE3	2.03	0.41
59:CC:1268:GLN:OE1	60:CD:352:ARG:NH1	2.53	0.41
60:CD:35:PHE:CZ	60:CD:101:ARG:HD2	2.55	0.41
60:CD:290:ILE:HD12	60:CD:290:ILE:H	1.85	0.41
1:AA:90:C:O2'	1:AA:91:U:H5'	2.20	0.41
1:AA:626:G:O3'	16:AP:51:ARG:NH2	2.53	0.41
1:AA:1006:G:C4	1:AA:1007:U:C6	3.09	0.41
1:AA:1140:C:O2'	1:AA:1141:C:O5'	2.36	0.41
1:AA:1512:U:H2'	1:AA:1513:A:C8	2.56	0.41
4:AD:14:ARG:HG3	4:AD:56:ARG:NH2	2.36	0.41
4:AD:97:ARG:O	4:AD:101:VAL:HG13	2.20	0.41
4:AD:153:SER:HA	4:AD:156:LYS:HG2	2.02	0.41
10:AJ:53:ILE:HG12	10:AJ:62:ARG:HA	2.02	0.41
23:AW:17:C:H2'	23:AW:17(A):U:H6	1.85	0.41
25:BA:2557:G:H2'	25:BA:2558:C:C6	2.56	0.41
25:BA:2607:G:H2'	25:BA:2608:G:O4'	2.21	0.41
29:BE:164:LEU:HB2	29:BE:167:VAL:HB	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:B1:31:ARG:HG2	49:B1:34:HIS:HB2	2.02	0.41
56:CN:27:DA:C5	56:CN:28:DA:N7	2.88	0.41
59:CC:530:ILE:HG23	59:CC:530:ILE:HD12	1.63	0.41
59:CC:1326:LEU:O	59:CC:1327:LEU:C	2.63	0.41
60:CD:1310:THR:O	60:CD:1310:THR:HG22	2.20	0.41
1:AA:421:U:H5'	1:AA:422:C:C6	2.55	0.41
1:AA:1140:C:HO2'	1:AA:1141:C:C5'	2.33	0.41
1:AA:1315:U:O2'	1:AA:1360:A:N3	2.52	0.41
5:AE:77:ASN:HB2	5:AE:82:GLN:NE2	2.36	0.41
11:AK:109:ASN:OD1	11:AK:111:THR:HG23	2.21	0.41
25:BA:833:A:H2'	25:BA:834:G:H8	1.84	0.41
25:BA:1902:C:H4'	27:BC:242:LYS:O	2.20	0.41
25:BA:2287:A:C8	25:BA:2289:G:C8	3.08	0.41
27:BC:162:VAL:HG11	27:BC:174:LEU:HD13	2.02	0.41
32:BH:80:ILE:HG12	32:BH:94:ILE:HG21	2.02	0.41
38:BP:7:ARG:HD2	38:BP:97:PHE:CZ	2.56	0.41
59:CC:549:ASP:OD2	60:CD:750:PRO:HB3	2.21	0.41
59:CC:660:VAL:HG13	59:CC:661:VAL:HG13	2.02	0.41
59:CC:1333:LEU:HA	59:CC:1333:LEU:HD23	1.84	0.41
59:CC:1339:LEU:HD22	60:CD:17:PHE:CG	2.55	0.41
60:CD:416:ILE:HG21	60:CD:416:ILE:HD13	1.58	0.41
1:AA:149:A:H2'	1:AA:150:U:O4'	2.20	0.41
1:AA:545:C:H5'	4:AD:69:GLU:HB2	2.03	0.41
1:AA:1120:C:H2'	1:AA:1121:U:H6	1.85	0.41
1:AA:1175:G:O2'	1:AA:1176:A:P	2.78	0.41
10:AJ:10:LEU:HD23	10:AJ:10:LEU:HA	1.95	0.41
24:AX:5:G:C2	24:AX:6:G:C5	3.08	0.41
25:BA:569:U:H5''	25:BA:821:A:C2	2.55	0.41
25:BA:1153:C:H2'	25:BA:1154:G:O4'	2.20	0.41
28:BD:39:ASP:N	28:BD:39:ASP:OD1	2.54	0.41
57:CT:2:DT:H2''	57:CT:3:DC:H5	1.85	0.41
59:CC:130:MET:SD	59:CC:134:GLY:HA2	2.61	0.41
59:CC:606:LEU:HD12	59:CC:606:LEU:N	2.36	0.41
59:CC:615:VAL:O	59:CC:615:VAL:HG13	2.20	0.41
59:CC:1251:TYR:CE1	59:CC:1301:ARG:CZ	3.03	0.41
60:CD:201:LEU:HD23	60:CD:221:ILE:HG22	2.03	0.41
60:CD:355:ILE:HD13	60:CD:355:ILE:HG21	1.78	0.41
60:CD:1172:LYS:HE3	60:CD:1191:PRO:HA	2.01	0.41
1:AA:81:A:C6	1:AA:89:G:C6	3.08	0.41
1:AA:215:C:H2'	1:AA:216:U:O4'	2.19	0.41
1:AA:263:A:H2'	1:AA:264:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:428:G:H4'	1:AA:429:U:O5'	2.21	0.41
1:AA:509:A:N3	1:AA:543:U:O2'	2.42	0.41
1:AA:1367:C:H5'	10:AJ:62:ARG:NH1	2.36	0.41
2:AB:20:THR:HA	2:AB:39:HIS:CE1	2.55	0.41
2:AB:60:ILE:HG23	2:AB:65:GLY:HA3	2.03	0.41
2:AB:208:ARG:O	2:AB:211:THR:OG1	2.30	0.41
5:AE:150:PRO:HG3	8:AH:99:LEU:HD21	2.03	0.41
10:AJ:15:HIS:O	10:AJ:18:ILE:HG22	2.21	0.41
11:AK:116:ILE:H	11:AK:116:ILE:CD1	2.34	0.41
16:AP:45:GLU:N	16:AP:45:GLU:OE1	2.54	0.41
24:AX:10:G:H2'	24:AX:11:C:C6	2.55	0.41
25:BA:28:A:H1'	25:BA:513:A:C2	2.56	0.41
25:BA:804:A:H2'	25:BA:806:C:C4	2.56	0.41
25:BA:1062:G:C2	25:BA:1077:A:N6	2.83	0.41
25:BA:1481:U:H2'	25:BA:1482:G:H4'	2.03	0.41
25:BA:2100:G:H1	25:BA:2189:U:H3	1.69	0.41
25:BA:2105:U:H2'	25:BA:2106:U:C6	2.56	0.41
25:BA:2210:U:H4'	25:BA:2211:G:C5'	2.51	0.41
25:BA:2291:U:H2'	25:BA:2292:U:H6	1.86	0.41
25:BA:2291:U:OP1	25:BA:2380:C:O2'	2.33	0.41
25:BA:2583:G:H2'	25:BA:2584:U:O4'	2.21	0.41
28:BD:181:ASP:OD2	28:BD:184:ARG:NH1	2.52	0.41
31:BG:153:ARG:HG3	31:BG:154:PRO:HD2	2.03	0.41
32:BH:80:ILE:HG12	32:BH:94:ILE:CG2	2.50	0.41
32:BH:84:ALA:HB2	32:BH:90:LEU:HD12	2.02	0.41
32:BH:94:ILE:HG22	32:BH:99:ILE:HG13	2.02	0.41
32:BH:96:THR:HG22	32:BH:115:VAL:HB	2.02	0.41
46:BX:54:GLY:O	46:BX:57:HIS:N	2.54	0.41
50:B2:55:ILE:HG13	50:B2:57:LYS:H	1.85	0.41
56:CN:28:DA:C4	56:CN:29:DG:N7	2.89	0.41
58:CA:27:THR:C	58:CA:28:LEU:HD12	2.46	0.41
58:CB:66:HIS:ND1	58:CB:68:TYR:HB3	2.36	0.41
59:CC:97:ARG:HB3	59:CC:121:GLU:HB2	2.03	0.41
59:CC:138:ILE:HD12	59:CC:138:ILE:HG23	1.78	0.41
59:CC:705:GLU:HB3	59:CC:794:LEU:N	2.36	0.41
59:CC:734:ILE:HG23	59:CC:734:ILE:HD12	1.77	0.41
60:CD:80:HIS:O	60:CD:83:VAL:HG22	2.21	0.41
60:CD:416:ILE:O	60:CD:416:ILE:HG23	2.15	0.41
60:CD:605:LEU:HD12	60:CD:605:LEU:HA	1.84	0.41
1:AA:996:A:C4	1:AA:997:U:C5	3.08	0.41
1:AA:1428:A:H2'	1:AA:1429:A:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AK:108:THR:OG1	11:AK:109:ASN:N	2.54	0.41
24:AX:16:H2U:HN3	24:AX:59:U:H3	1.69	0.41
25:BA:309:A:N3	25:BA:329:G:O2'	2.43	0.41
25:BA:1071:G:N2	25:BA:1089:A:O2'	2.54	0.41
25:BA:2514:U:H2'	25:BA:2515:C:C6	2.56	0.41
27:BC:37:ASN:HB2	27:BC:62:TYR:HB2	2.02	0.41
30:BF:126:GLY:O	30:BF:127:ASN:ND2	2.54	0.41
33:BK:122:LEU:C	33:BK:123:LYS:HG2	2.46	0.41
38:BP:48:LEU:HD23	38:BP:48:LEU:HA	1.89	0.41
58:CB:66:HIS:CE1	58:CB:68:TYR:HD1	2.39	0.41
59:CC:150:HIS:ND1	59:CC:150:HIS:O	2.54	0.41
59:CC:447:HIS:C	59:CC:449:GLY:H	2.28	0.41
59:CC:456:VAL:C	59:CC:458:GLU:H	2.29	0.41
59:CC:675:ASP:OD1	59:CC:676:ALA:N	2.54	0.41
60:CD:442:ILE:HA	60:CD:442:ILE:HD13	1.89	0.41
60:CD:442:ILE:HG23	60:CD:442:ILE:HD12	1.64	0.41
60:CD:699:ASP:HA	60:CD:702:GLN:HG2	2.03	0.41
60:CD:1175:LEU:HB2	60:CD:1190:ILE:HD12	2.02	0.41
1:AA:1315:U:H2'	1:AA:1316:G:O4'	2.21	0.40
2:AB:132:LYS:HA	2:AB:132:LYS:HE3	2.03	0.40
2:AB:165:ASP:O	2:AB:169:GLU:HG2	2.21	0.40
6:AF:82:ASP:OD1	6:AF:82:ASP:N	2.54	0.40
13:AM:12:HIS:O	13:AM:44:LYS:HD2	2.21	0.40
25:BA:278:A:N1	25:BA:361:G:O2'	2.35	0.40
25:BA:958:U:H2'	26:BB:89:U:C2	2.56	0.40
25:BA:2112:G:H3'	25:BA:2113:U:C5	2.56	0.40
34:BL:41:ILE:HD11	34:BL:86:LEU:HD22	2.02	0.40
58:CA:188:GLU:O	58:CA:199:ASP:HA	2.21	0.40
60:CD:119:SER:OG	60:CD:120:LEU:N	2.50	0.40
60:CD:798:ARG:O	60:CD:799:ARG:C	2.62	0.40
1:AA:1014:A:N3	1:AA:1219:A:H1'	2.37	0.40
1:AA:1150:A:N6	1:AA:1151:A:N6	2.69	0.40
1:AA:1236:A:H4'	1:AA:1304:G:H4'	2.03	0.40
2:AB:222:ARG:HA	61:CE:62:GLN:OE1	2.22	0.40
6:AF:38:ARG:O	6:AF:38:ARG:HG3	2.17	0.40
10:AJ:12:ALA:HB2	10:AJ:18:ILE:HD13	2.03	0.40
25:BA:2029:G:N1	25:BA:2033:A:OP2	2.31	0.40
25:BA:2111:U:O2'	25:BA:2112:G:H5'	2.21	0.40
25:BA:2898:U:O2'	33:BK:134:ALA:O	2.32	0.40
44:BV:96:PHE:O	44:BV:100:SER:HA	2.21	0.40
59:CC:145:ILE:HD12	59:CC:145:ILE:N	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:CC:675:ASP:OD1	59:CC:675:ASP:C	2.63	0.40
1:AA:1492:A:OP1	12:AL:44:LYS:N	2.54	0.40
3:AC:128:VAL:HG12	3:AC:129:MET:N	2.36	0.40
11:AK:17:SER:O	11:AK:80:LYS:N	2.41	0.40
13:AM:54:ASP:OD1	13:AM:54:ASP:C	2.64	0.40
16:AP:6:LEU:HD23	16:AP:19:VAL:HG22	2.02	0.40
25:BA:1173:U:C4	25:BA:1176:U:O2	2.75	0.40
25:BA:1486:U:H2'	25:BA:1487:U:H6	1.86	0.40
25:BA:2198:A:N3	32:BH:29:PHE:HB2	2.36	0.40
38:BP:28:VAL:HG11	38:BP:103:VAL:HG22	2.02	0.40
57:CT:5:DG:H2'	57:CT:6:DA:O4'	2.21	0.40
59:CC:647:ARG:C	59:CC:649:GLN:H	2.30	0.40
59:CC:693:LEU:HA	59:CC:693:LEU:HD12	1.85	0.40
59:CC:783:LEU:HD23	59:CC:783:LEU:HA	1.83	0.40
60:CD:1226:VAL:O	60:CD:1229:VAL:HG12	2.21	0.40
1:AA:501:C:H2'	1:AA:502:A:H8	1.86	0.40
17:AQ:81:LYS:HB2	17:AQ:81:LYS:HE2	1.63	0.40
19:AS:67:VAL:HG21	55:B7:57:VAL:HG22	2.03	0.40
22:AV:53:G:OP1	59:CC:1065:LYS:NZ	2.53	0.40
24:AX:2:C:H2'	24:AX:3:C:C6	2.56	0.40
25:BA:81:G:H2'	25:BA:82:U:O4'	2.21	0.40
25:BA:1275:A:OP2	25:BA:1646:C:N4	2.35	0.40
25:BA:1421:G:C2	25:BA:1422:G:C8	3.10	0.40
25:BA:1596:A:O2'	25:BA:1597:A:O4'	2.39	0.40
25:BA:1720:U:H2'	25:BA:1721:G:O4'	2.22	0.40
32:BH:15:LEU:HD21	32:BH:55:GLU:HB3	2.04	0.40
56:CN:27:DA:C4	56:CN:28:DA:N7	2.89	0.40
58:CA:98:VAL:HG22	58:CA:99:ILE:N	2.37	0.40
58:CA:180:VAL:HG12	58:CA:207:THR:HG22	2.02	0.40
59:CC:678:ARG:NH1	59:CC:681:MET:SD	2.94	0.40
59:CC:1082:ILE:HD13	59:CC:1082:ILE:HG21	1.86	0.40
60:CD:1044:GLN:O	60:CD:1067:ARG:HG2	2.21	0.40
1:AA:736:C:H2'	1:AA:737:C:C6	2.57	0.40
1:AA:1412:C:H2'	1:AA:1413:A:C8	2.57	0.40
11:AK:35:THR:HG1	11:AK:40:ASN:C	2.22	0.40
20:AT:25:ARG:HH11	20:AT:25:ARG:HG2	1.87	0.40
25:BA:44:A:H2'	25:BA:45:G:O4'	2.22	0.40
25:BA:848:C:H2'	25:BA:849:A:C8	2.56	0.40
25:BA:883:G:H2'	25:BA:884:U:C6	2.57	0.40
25:BA:1599:U:H2'	25:BA:1600:C:H6	1.86	0.40
25:BA:2101:A:N6	25:BA:2102:G:O6	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2119:A:N7	25:BA:2170:A:H2	2.19	0.40
26:BB:52:A:N7	38:BP:64:TYR:OH	2.44	0.40
27:BC:78:VAL:HG21	27:BC:110:LEU:HD21	2.04	0.40
39:BQ:40:LEU:HD23	39:BQ:40:LEU:HA	1.91	0.40
49:B1:10:THR:HG22	49:B1:11:ARG:N	2.36	0.40
59:CC:746:ALA:HB2	59:CC:967:LEU:HD21	2.02	0.40
59:CC:951:MET:O	59:CC:955:GLN:HG2	2.21	0.40
59:CC:1211:ARG:NH1	59:CC:1220:GLN:OE1	2.52	0.40
59:CC:1254:VAL:HG13	59:CC:1255:THR:N	2.37	0.40
60:CD:157:GLN:CG	60:CD:158:GLN:H	2.34	0.40
60:CD:326:SER:O	60:CD:327:LEU:C	2.65	0.40
60:CD:572:THR:HG23	60:CD:573:THR:N	2.36	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AB	224/241 (93%)	210 (94%)	13 (6%)	1 (0%)	30	65
3	AC	207/233 (89%)	197 (95%)	6 (3%)	4 (2%)	6	30
4	AD	203/206 (98%)	192 (95%)	10 (5%)	1 (0%)	24	60
5	AE	154/167 (92%)	145 (94%)	7 (4%)	2 (1%)	9	38
6	AF	102/131 (78%)	97 (95%)	5 (5%)	0	100	100
7	AG	152/156 (97%)	144 (95%)	6 (4%)	2 (1%)	9	38
8	AH	127/130 (98%)	119 (94%)	8 (6%)	0	100	100
9	AI	126/130 (97%)	111 (88%)	12 (10%)	3 (2%)	4	24
10	AJ	98/103 (95%)	90 (92%)	5 (5%)	3 (3%)	3	19
11	AK	115/129 (89%)	100 (87%)	14 (12%)	1 (1%)	14	48

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	AL	119/124 (96%)	109 (92%)	8 (7%)	2 (2%)	7	32
13	AM	113/118 (96%)	108 (96%)	5 (4%)	0	100	100
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%)	78 (98%)	2 (2%)	0	100	100
17	AQ	78/84 (93%)	73 (94%)	5 (6%)	0	100	100
18	AR	64/75 (85%)	61 (95%)	2 (3%)	1 (2%)	7	34
19	AS	81/92 (88%)	80 (99%)	1 (1%)	0	100	100
20	AT	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
21	AU	68/71 (96%)	68 (100%)	0	0	100	100
27	BC	270/273 (99%)	249 (92%)	18 (7%)	3 (1%)	11	43
28	BD	206/209 (99%)	196 (95%)	9 (4%)	1 (0%)	24	60
29	BE	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
30	BF	176/179 (98%)	163 (93%)	10 (6%)	3 (2%)	7	32
31	BG	173/177 (98%)	159 (92%)	13 (8%)	1 (1%)	21	56
32	BH	147/149 (99%)	134 (91%)	10 (7%)	3 (2%)	6	28
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	36
36	BN	133/136 (98%)	128 (96%)	5 (4%)	0	100	100
37	BO	118/127 (93%)	108 (92%)	10 (8%)	0	100	100
38	BP	115/117 (98%)	106 (92%)	8 (7%)	1 (1%)	14	48
39	BQ	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
40	BR	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
41	BS	101/103 (98%)	97 (96%)	3 (3%)	1 (1%)	12	45
42	BT	108/110 (98%)	103 (95%)	5 (5%)	0	100	100
43	BU	94/100 (94%)	88 (94%)	5 (5%)	1 (1%)	11	43
44	BV	101/104 (97%)	97 (96%)	3 (3%)	1 (1%)	12	45
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	BZ	60/63 (95%)	58 (97%)	2 (3%)	0	100	100
49	B1	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
50	B2	54/57 (95%)	54 (100%)	0	0	100	100
51	B3	51/55 (93%)	47 (92%)	4 (8%)	0	100	100
52	B4	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
53	B5	62/65 (95%)	58 (94%)	3 (5%)	1 (2%)	7	34
54	B6	36/50 (72%)	35 (97%)	1 (3%)	0	100	100
55	B7	68/70 (97%)	61 (90%)	7 (10%)	0	100	100
58	CA	227/329 (69%)	217 (96%)	10 (4%)	0	100	100
58	CB	215/329 (65%)	203 (94%)	11 (5%)	1 (0%)	24	60
59	CC	1316/1342 (98%)	1197 (91%)	110 (8%)	9 (1%)	18	53
60	CD	1327/1407 (94%)	1222 (92%)	95 (7%)	10 (1%)	16	50
61	CE	59/91 (65%)	53 (90%)	4 (7%)	2 (3%)	3	17
All	All	8766/9396 (93%)	8198 (94%)	508 (6%)	60 (1%)	20	53

All (60) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	AG	56	LYS
9	AI	56	ASP
10	AJ	57	VAL
11	AK	93	ARG
12	AL	88	LYS
12	AL	102	LEU
31	BG	47	ASP
32	BH	89	LYS
53	B5	32	ILE
59	CC	165	HIS
60	CD	1159	ILE
3	AC	51	SER
3	AC	80	LYS
9	AI	13	LYS
27	BC	241	GLY
30	BF	62	GLY
32	BH	15	LEU
35	BM	36	LYS
58	CB	155	ALA

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Mol	Chain	Res	Type
59	CC	47	TYR
60	CD	1051	ASP
28	BD	149	ASN
38	BP	100	HIS
41	BS	53	PHE
59	CC	258	ASN
59	CC	1177	ARG
60	CD	119	SER
60	CD	121	PRO
60	CD	712	GLN
60	CD	854	ALA
60	CD	1200	GLU
2	AB	165	ASP
3	AC	14	ILE
5	AE	90	THR
7	AG	130	ASN
9	AI	14	SER
10	AJ	58	ASN
18	AR	72	ASP
30	BF	177	PHE
32	BH	76	GLU
59	CC	282	VAL
59	CC	596	ASP
59	CC	1153	ALA
60	CD	586	GLY
4	AD	43	ALA
35	BM	99	ASN
43	BU	3	ARG
44	BV	8	ASP
61	CE	16	ARG
3	AC	60	PRO
10	AJ	78	GLU
27	BC	197	ASN
27	BC	233	GLY
59	CC	1223	ARG
60	CD	312	ARG
61	CE	4	VAL
5	AE	108	GLY
30	BF	176	PRO
59	CC	1186	VAL
60	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%)	171 (91%)	16 (9%)	10	36
3	AC	171/190 (90%)	160 (94%)	11 (6%)	16	48
4	AD	172/173 (99%)	163 (95%)	9 (5%)	21	55
5	AE	118/126 (94%)	105 (89%)	13 (11%)	6	25
6	AF	91/112 (81%)	85 (93%)	6 (7%)	15	46
7	AG	127/129 (98%)	121 (95%)	6 (5%)	23	58
8	AH	104/105 (99%)	96 (92%)	8 (8%)	12	40
9	AI	106/107 (99%)	99 (93%)	7 (7%)	15	46
10	AJ	87/90 (97%)	80 (92%)	7 (8%)	11	38
11	AK	90/99 (91%)	84 (93%)	6 (7%)	15	46
12	AL	102/103 (99%)	96 (94%)	6 (6%)	18	50
13	AM	93/96 (97%)	87 (94%)	6 (6%)	15	47
14	AN	83/84 (99%)	79 (95%)	4 (5%)	23	57
15	AO	76/77 (99%)	73 (96%)	3 (4%)	28	62
16	AP	65/65 (100%)	61 (94%)	4 (6%)	16	49
17	AQ	74/78 (95%)	71 (96%)	3 (4%)	27	61
18	AR	57/65 (88%)	55 (96%)	2 (4%)	32	65
19	AS	72/79 (91%)	70 (97%)	2 (3%)	38	70
20	AT	65/66 (98%)	61 (94%)	4 (6%)	16	49
21	AU	60/61 (98%)	54 (90%)	6 (10%)	7	29
27	BC	217/218 (100%)	213 (98%)	4 (2%)	51	77
28	BD	163/163 (100%)	157 (96%)	6 (4%)	30	64
29	BE	165/165 (100%)	154 (93%)	11 (7%)	15	46
30	BF	149/150 (99%)	135 (91%)	14 (9%)	8	32
31	BG	136/138 (99%)	124 (91%)	12 (9%)	9	35
32	BH	114/114 (100%)	106 (93%)	8 (7%)	14	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	BK	116/116 (100%)	109 (94%)	7 (6%)	17	50
34	BL	104/104 (100%)	99 (95%)	5 (5%)	23	57
35	BM	103/103 (100%)	93 (90%)	10 (10%)	8	30
36	BN	108/108 (100%)	102 (94%)	6 (6%)	19	52
37	BO	100/103 (97%)	95 (95%)	5 (5%)	22	56
38	BP	87/87 (100%)	81 (93%)	6 (7%)	14	45
39	BQ	99/100 (99%)	88 (89%)	11 (11%)	6	25
40	BR	89/90 (99%)	85 (96%)	4 (4%)	24	59
41	BS	84/84 (100%)	78 (93%)	6 (7%)	13	43
42	BT	93/93 (100%)	89 (96%)	4 (4%)	26	60
43	BU	83/84 (99%)	79 (95%)	4 (5%)	23	57
44	BV	84/85 (99%)	77 (92%)	7 (8%)	10	37
45	BW	78/78 (100%)	73 (94%)	5 (6%)	16	48
46	BX	58/63 (92%)	57 (98%)	1 (2%)	53	78
47	BY	67/68 (98%)	62 (92%)	5 (8%)	12	41
48	BZ	54/55 (98%)	52 (96%)	2 (4%)	30	64
49	B1	48/49 (98%)	46 (96%)	2 (4%)	26	61
50	B2	47/48 (98%)	46 (98%)	1 (2%)	47	75
51	B3	48/49 (98%)	43 (90%)	5 (10%)	7	28
52	B4	37/38 (97%)	35 (95%)	2 (5%)	20	53
53	B5	51/52 (98%)	48 (94%)	3 (6%)	18	50
54	B6	34/44 (77%)	32 (94%)	2 (6%)	18	50
55	B7	62/62 (100%)	59 (95%)	3 (5%)	23	57
58	CA	197/286 (69%)	192 (98%)	5 (2%)	42	72
58	CB	187/286 (65%)	177 (95%)	10 (5%)	20	54
59	CC	1139/1157 (98%)	1094 (96%)	45 (4%)	28	62
60	CD	1118/1168 (96%)	1094 (98%)	24 (2%)	47	75
61	CE	52/75 (69%)	50 (96%)	2 (4%)	29	63
All	All	7371/7787 (95%)	6995 (95%)	376 (5%)	23	55

All (376) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AB	47	VAL
2	AB	59	LYS
2	AB	63	ARG
2	AB	64	LYS
2	AB	68	LEU
2	AB	74	ARG
2	AB	117	LEU
2	AB	128	LYS
2	AB	129	LEU
2	AB	132	LYS
2	AB	135	LEU
2	AB	161	LEU
2	AB	169	GLU
2	AB	186	ILE
2	AB	220	THR
2	AB	221	VAL
3	AC	14	ILE
3	AC	28	GLU
3	AC	33	LEU
3	AC	35	SER
3	AC	93	ASP
3	AC	121	THR
3	AC	153	VAL
3	AC	154	SER
3	AC	165	THR
3	AC	172	ARG
3	AC	185	ASN
4	AD	17	THR
4	AD	47	ARG
4	AD	138	SER
4	AD	156	LYS
4	AD	167	LYS
4	AD	179	GLU
4	AD	181	THR
4	AD	194	ASP
4	AD	197	GLU
5	AE	10	GLU
5	AE	15	LEU
5	AE	18	VAL
5	AE	34	THR
5	AE	39	VAL
5	AE	81	LEU
5	AE	93	ARG

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Mol	Chain	Res	Type
5	AE	94	VAL
5	AE	134	ILE
5	AE	138	ARG
5	AE	141	ILE
5	AE	142	ASP
5	AE	146	ASN
6	AF	7	VAL
6	AF	24	ARG
6	AF	38	ARG
6	AF	44	ARG
6	AF	71	ILE
6	AF	100	SER
7	AG	7	ILE
7	AG	80	VAL
7	AG	123	GLU
7	AG	130	ASN
7	AG	133	THR
7	AG	146	GLU
8	AH	3	MET
8	AH	55	THR
8	AH	72	VAL
8	AH	76	GLN
8	AH	90	ASP
8	AH	96	MET
8	AH	107	SER
8	AH	121	LEU
9	AI	41	ARG
9	AI	42	GLU
9	AI	48	VAL
9	AI	49	ARG
9	AI	57	MET
9	AI	111	VAL
9	AI	123	ARG
10	AJ	16	ARG
10	AJ	18	ILE
10	AJ	36	VAL
10	AJ	37	ARG
10	AJ	44	THR
10	AJ	75	ASP
10	AJ	96	VAL
11	AK	13	ARG
11	AK	16	VAL

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Mol	Chain	Res	Type
11	AK	76	GLU
11	AK	84	VAL
11	AK	108	THR
11	AK	116	ILE
12	AL	5	ASN
12	AL	16	VAL
12	AL	24	LEU
12	AL	40	THR
12	AL	90	LEU
12	AL	102	LEU
13	AM	11	ASP
13	AM	16	VAL
13	AM	89	LEU
13	AM	93	ARG
13	AM	104	THR
13	AM	107	ARG
14	AN	11	VAL
14	AN	89	MET
14	AN	92	GLU
14	AN	100	SER
15	AO	40	GLN
15	AO	64	ARG
15	AO	73	LYS
16	AP	42	ILE
16	AP	45	GLU
16	AP	50	THR
16	AP	77	GLU
17	AQ	4	LYS
17	AQ	48	ASP
17	AQ	75	LEU
18	AR	55	LEU
18	AR	71	THR
19	AS	31	LEU
19	AS	79	THR
20	AT	6	SER
20	AT	10	ARG
20	AT	24	ARG
20	AT	48	GLN
21	AU	4	ILE
21	AU	13	ASP
21	AU	18	ARG
21	AU	28	VAL

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Mol	Chain	Res	Type
21	AU	29	LEU
21	AU	69	ARG
27	BC	3	VAL
27	BC	14	ARG
27	BC	129	THR
27	BC	130	LEU
28	BD	13	ARG
28	BD	29	VAL
28	BD	30	GLU
28	BD	43	ASP
28	BD	56	LYS
28	BD	157	LYS
29	BE	4	VAL
29	BE	13	THR
29	BE	21	ARG
29	BE	22	ASP
29	BE	40	ARG
29	BE	57	LYS
29	BE	77	ILE
29	BE	88	ARG
29	BE	111	GLU
29	BE	136	GLN
29	BE	153	LEU
30	BF	6	ASP
30	BF	14	LYS
30	BF	49	LEU
30	BF	57	LEU
30	BF	60	ILE
30	BF	92	ARG
30	BF	98	GLU
30	BF	115	ARG
30	BF	123	ASP
30	BF	133	ARG
30	BF	140	GLU
30	BF	141	ILE
30	BF	158	THR
30	BF	159	THR
31	BG	16	ASP
31	BG	32	GLU
31	BG	36	THR
31	BG	84	THR
31	BG	95	ARG

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Mol	Chain	Res	Type
31	BG	110	SER
31	BG	127	THR
31	BG	141	ILE
31	BG	167	GLU
31	BG	168	VAL
31	BG	170	ARG
31	BG	176	LYS
32	BH	3	VAL
32	BH	15	LEU
32	BH	40	THR
32	BH	66	ASN
32	BH	75	LEU
32	BH	87	GLU
32	BH	129	GLU
32	BH	133	GLN
33	BK	1	MET
33	BK	57	LEU
33	BK	90	GLU
33	BK	108	MET
33	BK	123	LYS
33	BK	129	GLU
33	BK	142	ILE
34	BL	17	ARG
34	BL	41	ILE
34	BL	58	LEU
34	BL	67	LYS
34	BL	99	ILE
35	BM	30	THR
35	BM	40	SER
35	BM	67	THR
35	BM	70	LYS
35	BM	76	GLU
35	BM	78	ARG
35	BM	79	LEU
35	BM	84	LYS
35	BM	115	GLU
35	BM	118	THR
36	BN	16	ARG
36	BN	18	ARG
36	BN	47	GLU
36	BN	55	ARG
36	BN	100	LYS

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Mol	Chain	Res	Type
36	BN	110	GLU
37	BO	2	ARG
37	BO	13	ASN
37	BO	63	ARG
37	BO	65	LEU
37	BO	69	ARG
38	BP	1	MET
38	BP	13	ARG
38	BP	47	VAL
38	BP	52	SER
38	BP	115	LEU
38	BP	116	GLN
39	BQ	27	GLU
39	BQ	38	LYS
39	BQ	40	LEU
39	BQ	66	ASN
39	BQ	80	VAL
39	BQ	88	ARG
39	BQ	89	ARG
39	BQ	96	LYS
39	BQ	110	ILE
39	BQ	111	LYS
39	BQ	113	ARG
40	BR	11	ARG
40	BR	51	ARG
40	BR	59	GLN
40	BR	91	ASP
41	BS	10	LYS
41	BS	20	VAL
41	BS	31	GLU
41	BS	39	LEU
41	BS	48	LYS
41	BS	73	LYS
42	BT	19	LEU
42	BT	29	VAL
42	BT	41	LYS
42	BT	110	ARG
43	BU	1	MET
43	BU	12	ARG
43	BU	53	VAL
43	BU	89	GLU
44	BV	7	ARG

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Mol	Chain	Res	Type
44	BV	9	ASP
44	BV	43	LYS
44	BV	46	GLN
44	BV	52	LEU
44	BV	72	ILE
44	BV	101	GLU
45	BW	40	ILE
45	BW	41	GLU
45	BW	45	ASP
45	BW	62	THR
45	BW	65	VAL
46	BX	70	GLU
47	BY	2	SER
47	BY	25	THR
47	BY	33	LEU
47	BY	48	THR
47	BY	71	LEU
48	BZ	58	ASN
48	BZ	59	GLU
49	B1	8	THR
49	B1	10	THR
50	B2	12	LYS
51	B3	5	ILE
51	B3	10	LYS
51	B3	23	THR
51	B3	32	GLU
51	B3	50	LYS
52	B4	15	SER
52	B4	22	MET
53	B5	32	ILE
53	B5	54	ASP
53	B5	55	LEU
54	B6	12	ARG
54	B6	26	ILE
55	B7	10	GLU
55	B7	21	VAL
55	B7	32	LEU
58	CA	7	GLU
58	CA	13	LEU
58	CA	74	VAL
58	CA	101	THR
58	CA	224	LEU

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Mol	Chain	Res	Type
58	CB	41	ASN
58	CB	48	LEU
58	CB	66	HIS
58	CB	76	GLU
58	CB	83	LEU
58	CB	170	ARG
58	CB	174	ASP
58	CB	187	VAL
58	CB	191	ARG
58	CB	214	GLU
59	CC	20	GLN
59	CC	47	TYR
59	CC	65	ASN
59	CC	108	GLU
59	CC	116	ASP
59	CC	150	HIS
59	CC	193	ASN
59	CC	262	TYR
59	CC	292	ILE
59	CC	316	GLU
59	CC	369	MET
59	CC	524	ILE
59	CC	529	ARG
59	CC	562	GLU
59	CC	568	ASN
59	CC	569	ILE
59	CC	575	LEU
59	CC	657	THR
59	CC	726	TYR
59	CC	736	VAL
59	CC	745	GLU
59	CC	772	SER
59	CC	800	MET
59	CC	815	SER
59	CC	822	VAL
59	CC	830	THR
59	CC	843	THR
59	CC	856	ASN
59	CC	888	THR
59	CC	1002	LEU
59	CC	1005	GLU
59	CC	1022	LYS

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Mol	Chain	Res	Type
59	CC	1050	VAL
59	CC	1076	ILE
59	CC	1083	GLU
59	CC	1223	ARG
59	CC	1240	ASP
59	CC	1247	SER
59	CC	1250	SER
59	CC	1287	LEU
59	CC	1291	LEU
59	CC	1298	VAL
59	CC	1304	MET
59	CC	1336	ASN
59	CC	1340	GLU
60	CD	157	GLN
60	CD	158	GLN
60	CD	244	VAL
60	CD	255	LEU
60	CD	416	ILE
60	CD	418	GLU
60	CD	488	ASN
60	CD	592	VAL
60	CD	709	ARG
60	CD	802	ASP
60	CD	826	ILE
60	CD	839	VAL
60	CD	856	ILE
60	CD	1041	ILE
60	CD	1046	ILE
60	CD	1141	VAL
60	CD	1144	LEU
60	CD	1163	VAL
60	CD	1165	PHE
60	CD	1167	LYS
60	CD	1195	GLN
60	CD	1237	VAL
60	CD	1261	LEU
60	CD	1334	GLU
61	CE	3	ARG
61	CE	44	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (63) such sidechains are listed below:

Mol	Chain	Res	Type
2	AB	58	ASN
3	AC	25	ASN
4	AD	126	ASN
5	AE	135	ASN
6	AF	58	HIS
6	AF	94	HIS
7	AG	130	ASN
8	AH	16	ASN
9	AI	5	GLN
9	AI	75	GLN
9	AI	110	GLN
10	AJ	4	GLN
11	AK	118	HIS
11	AK	119	ASN
12	AL	77	HIS
13	AM	12	HIS
15	AO	35	GLN
15	AO	38	HIS
17	AQ	31	HIS
27	BC	128	ASN
27	BC	239	ASN
28	BD	94	GLN
28	BD	140	HIS
28	BD	148	GLN
29	BE	46	GLN
30	BF	81	GLN
30	BF	127	ASN
32	BH	28	ASN
32	BH	73	ASN
33	BK	47	HIS
36	BN	22	GLN
36	BN	97	GLN
37	BO	9	GLN
37	BO	31	HIS
38	BP	104	GLN
39	BQ	75	GLN
40	BR	72	ASN
41	BS	43	ASN
43	BU	28	ASN
43	BU	48	GLN
44	BV	54	GLN
45	BW	75	GLN
46	BX	76	ASN

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Mol	Chain	Res	Type
49	B1	20	HIS
52	B4	6	GLN
58	CA	194	GLN
59	CC	60	GLN
59	CC	238	GLN
59	CC	494	ASN
59	CC	518	ASN
59	CC	573	ASN
59	CC	686	GLN
59	CC	955	GLN
59	CC	1008	GLN
59	CC	1111	GLN
60	CD	469	HIS
60	CD	477	GLN
60	CD	792	ASN
60	CD	861	ASN
60	CD	929	GLN
60	CD	1227	HIS
61	CE	7	GLN
61	CE	62	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1532/1542 (99%)	297 (19%)	28 (1%)
22	AV	25/53 (47%)	9 (36%)	1 (4%)
23	AW	76/77 (98%)	23 (30%)	8 (10%)
24	AX	75/76 (98%)	18 (24%)	1 (1%)
25	BA	2899/2904 (99%)	570 (19%)	65 (2%)
26	BB	120/120 (100%)	12 (10%)	1 (0%)
All	All	4727/4772 (99%)	929 (19%)	104 (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	22	G
1	AA	29	U
1	AA	32	A

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Mol	Chain	Res	Type
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	72	A
1	AA	74	A
1	AA	75	G
1	AA	76	G
1	AA	80	C
1	AA	81	A
1	AA	82	G
1	AA	83	C
1	AA	84	U
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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	463	U
1	AA	464	U
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	530	G
1	AA	531	U
1	AA	532	A
1	AA	533	A
1	AA	547	A
1	AA	559	A
1	AA	568	G
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

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Mol	Chain	Res	Type
1	AA	633	G
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	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	843	U
1	AA	844	G
1	AA	845	A
1	AA	846	G
1	AA	847	G
1	AA	849	G
1	AA	874	G
1	AA	887	G
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	969	A

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Mol	Chain	Res	Type
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	1008	U
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	1037	C
1	AA	1043	G
1	AA	1044	A
1	AA	1046	A
1	AA	1065	U
1	AA	1084	G
1	AA	1085	U
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	1137	C
1	AA	1139	G
1	AA	1140	C
1	AA	1141	C

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Mol	Chain	Res	Type
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	1168	U
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	1215	G
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	1275	A
1	AA	1277	C
1	AA	1278	G
1	AA	1279	G
1	AA	1280	A
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

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Mol	Chain	Res	Type
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	1446	A
1	AA	1447	A
1	AA	1448	C
1	AA	1452	C
1	AA	1453	G
1	AA	1487	G
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	16	A
22	AV	24	A
22	AV	26	A

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Mol	Chain	Res	Type
22	AV	27	C
22	AV	44	A
22	AV	45	C
22	AV	46	G
22	AV	49	G
22	AV	53	G
23	AW	6	G
23	AW	9	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	37	A
23	AW	47	U
23	AW	48	C
23	AW	49	G
23	AW	57	A
23	AW	59	A
23	AW	74	C
23	AW	75	C
23	AW	76	A
24	AX	5	G
24	AX	6	G
24	AX	8	4SU
24	AX	9	A
24	AX	11	C
24	AX	15	G
24	AX	16	H2U
24	AX	17	C
24	AX	18	G
24	AX	20	H2U
24	AX	22	G
24	AX	45	U
24	AX	46	G7M

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Mol	Chain	Res	Type
24	AX	47	3AU
24	AX	48	C
24	AX	49	C
24	AX	58	A
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	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
25	BA	102	U
25	BA	103	A
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	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

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Mol	Chain	Res	Type
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	264	C
25	BA	265	A
25	BA	266	G
25	BA	270	A
25	BA	271	G
25	BA	272	A
25	BA	276	U
25	BA	277	G
25	BA	278	A
25	BA	285	G
25	BA	291	G
25	BA	302	C
25	BA	310	A
25	BA	311	A
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	372	G
25	BA	386	G
25	BA	396	G
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	457	A
25	BA	477	A

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Mol	Chain	Res	Type
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	509	C
25	BA	531	C
25	BA	532	A
25	BA	533	G
25	BA	544	G
25	BA	550	U
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
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

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Mol	Chain	Res	Type
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	845	A
25	BA	846	U
25	BA	858	G
25	BA	859	G
25	BA	869	G
25	BA	878	A
25	BA	881	G
25	BA	883	G
25	BA	884	U
25	BA	885	C
25	BA	886	A
25	BA	887	U
25	BA	890	C
25	BA	891	G
25	BA	892	A
25	BA	895	U
25	BA	896	A
25	BA	897	C
25	BA	898	C
25	BA	899	A
25	BA	910	A
25	BA	914	G
25	BA	931	U
25	BA	933	A

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Mol	Chain	Res	Type
25	BA	940	G
25	BA	941	A
25	BA	945	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
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	1066	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	1078	U
25	BA	1083	U
25	BA	1087	G
25	BA	1088	A
25	BA	1090	A

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Mol	Chain	Res	Type
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	1175	A
25	BA	1176	U
25	BA	1177	G
25	BA	1178	C
25	BA	1180	U
25	BA	1186	G
25	BA	1212	G
25	BA	1236	G
25	BA	1238	G
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	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

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Mol	Chain	Res	Type
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
25	BA	1493	C
25	BA	1495	A
25	BA	1497	U
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

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Mol	Chain	Res	Type
25	BA	1580	A
25	BA	1581	G
25	BA	1583	A
25	BA	1584	U
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	1619	G
25	BA	1630	A
25	BA	1647	U
25	BA	1648	U
25	BA	1649	G
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

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Mol	Chain	Res	Type
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	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
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

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Mol	Chain	Res	Type
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	2095	A
25	BA	2097	A
25	BA	2099	U
25	BA	2100	G
25	BA	2101	A
25	BA	2102	G
25	BA	2107	G
25	BA	2109	U
25	BA	2110	G
25	BA	2111	U
25	BA	2113	U
25	BA	2115	G
25	BA	2116	G
25	BA	2117	A
25	BA	2118	U
25	BA	2119	A
25	BA	2120	G
25	BA	2121	G
25	BA	2123	G
25	BA	2124	G
25	BA	2125	G
25	BA	2126	A
25	BA	2127	G
25	BA	2129	C
25	BA	2131	U

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Mol	Chain	Res	Type
25	BA	2132	U
25	BA	2133	G
25	BA	2135	A
25	BA	2136	G
25	BA	2137	U
25	BA	2138	G
25	BA	2139	U
25	BA	2140	G
25	BA	2148	G
25	BA	2150	C
25	BA	2157	G
25	BA	2159	G
25	BA	2162	G
25	BA	2164	C
25	BA	2165	C
25	BA	2167	U
25	BA	2169	A
25	BA	2170	A
25	BA	2171	A
25	BA	2172	U
25	BA	2173	A
25	BA	2177	C
25	BA	2181	U
25	BA	2182	U
25	BA	2183	A
25	BA	2188	U
25	BA	2189	U
25	BA	2191	A
25	BA	2192	U
25	BA	2193	G
25	BA	2194	U
25	BA	2197	U
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

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Mol	Chain	Res	Type
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	2361	G
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
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

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Mol	Chain	Res	Type
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	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	2602	A
25	BA	2609	U
25	BA	2610	C
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

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Mol	Chain	Res	Type
25	BA	2744	G
25	BA	2748	A
25	BA	2757	A
25	BA	2762	C
25	BA	2778	A
25	BA	2791	G
25	BA	2797	U
25	BA	2798	U
25	BA	2799	G
25	BA	2801	G
25	BA	2818	U
25	BA	2820	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	2873	A
25	BA	2874	C
25	BA	2879	A
25	BA	2880	C
25	BA	2883	A
25	BA	2884	U
25	BA	2885	G
25	BA	2886	A
25	BA	2891	U
25	BA	2902	C
25	BA	2903	U
26	BB	13	G
26	BB	16	G
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	89	U
26	BB	90	C
26	BB	99	A
26	BB	109	A

All (104) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	4	U
1	AA	70	U
1	AA	147	G
1	AA	181	A
1	AA	182	A
1	AA	183	C
1	AA	197	A
1	AA	209	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	1166	G
1	AA	1167	A
1	AA	1196	A
1	AA	1211	U
1	AA	1213	A
1	AA	1214	C
1	AA	1299	A
1	AA	1363	A
1	AA	1396	A
1	AA	1447	A
22	AV	43	A
23	AW	15	G
23	AW	16	C
23	AW	18	G
23	AW	19	G
23	AW	20	H2U
23	AW	21	A
23	AW	47	U
23	AW	60	U
24	AX	19	G
25	BA	33	C
25	BA	62	U
25	BA	71	A
25	BA	101	A
25	BA	138	U

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Mol	Chain	Res	Type
25	BA	140	C
25	BA	199	A
25	BA	271	G
25	BA	310	A
25	BA	404	A
25	BA	503	A
25	BA	549	C
25	BA	685	A
25	BA	764	A
25	BA	776	G
25	BA	784	G
25	BA	885	C
25	BA	890	C
25	BA	895	U
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	1077	A
25	BA	1109	C
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	1379	U
25	BA	1395	A
25	BA	1405	U
25	BA	1407	G
25	BA	1434	A
25	BA	1490	A
25	BA	1494	A
25	BA	1509	A
25	BA	1583	A
25	BA	1584	U
25	BA	1608	A
25	BA	1913	A
25	BA	1918	A
25	BA	2062	A

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Mol	Chain	Res	Type
25	BA	2191	A
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	2602	A
25	BA	2610	C
25	BA	2756	U
25	BA	2797	U
25	BA	2798	U
25	BA	2873	A
26	BB	1	U

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

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	UR3	AA	1498	1	19,22,23	2.50	6 (31%)	26,32,35	1.25	2 (7%)
25	PSU	BA	2580	25	18,21,22	1.09	3 (16%)	22,30,33	2.07	6 (27%)
25	G7M	BA	2069	25	23,26,27	2.55	9 (39%)	35,39,42	2.49	13 (37%)
25	5MU	BA	1939	62,25	19,22,23	1.46	4 (21%)	28,32,35	2.32	6 (21%)
25	6MZ	BA	1618	25	22,25,26	2.55	5 (22%)	30,36,39	2.66	10 (33%)
1	5MC	AA	1407	1	18,22,23	3.77	7 (38%)	26,32,35	1.07	2 (7%)
23	4SU	AW	8	23	18,21,22	4.08	8 (44%)	26,30,33	2.30	5 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
25	5MU	BA	747	25	19,22,23	1.40	4 (21%)	28,32,35	2.28	6 (21%)
25	6MZ	BA	2030	25	22,25,26	2.61	5 (22%)	30,36,39	2.51	11 (36%)
24	H2U	AX	20	24	18,21,22	3.12	5 (27%)	21,30,33	1.95	5 (23%)
25	PSU	BA	2457	25	18,21,22	1.12	2 (11%)	22,30,33	2.00	5 (22%)
25	OMC	BA	2498	62,25	19,22,23	2.81	7 (36%)	26,31,34	0.96	1 (3%)
24	5MU	AX	54	24	19,22,23	1.36	5 (26%)	28,32,35	2.06	7 (25%)
24	PSU	AX	55	24	18,21,22	1.05	1 (5%)	22,30,33	1.87	5 (22%)
24	3AU	AX	47	24	18,21,29	3.43	8 (44%)	26,30,43	1.72	5 (19%)
25	1MG	BA	745	25	22,26,27	2.67	6 (27%)	33,39,42	1.82	8 (24%)
28	MEQ	BD	150	28	8,9,10	0.89	0	5,10,12	0.55	0
1	2MG	AA	966	1	23,26,27	2.76	9 (39%)	32,38,41	2.93	13 (40%)
1	PSU	AA	516	1	18,21,22	1.14	2 (11%)	22,30,33	2.15	6 (27%)
24	G7M	AX	46	24	23,26,27	3.75	12 (52%)	35,39,42	1.62	7 (20%)
25	PSU	BA	2504	25	18,21,22	1.04	1 (5%)	22,30,33	1.91	4 (18%)
1	4OC	AA	1402	62,1	20,23,24	3.24	9 (45%)	26,32,35	0.97	1 (3%)
24	4SU	AX	8	24	18,21,22	4.08	8 (44%)	26,30,33	2.34	5 (19%)
25	5MC	BA	1962	25	18,22,23	3.75	7 (38%)	26,32,35	1.08	4 (15%)
23	OMC	AW	32	23	19,22,23	2.81	8 (42%)	26,31,34	0.78	0
25	PSU	BA	2604	25	18,21,22	1.05	1 (5%)	22,30,33	1.91	5 (22%)
1	G7M	AA	527	1	23,26,27	2.47	9 (39%)	35,39,42	2.48	12 (34%)
24	PSU	AX	32	24	18,21,22	1.01	1 (5%)	22,30,33	1.72	4 (18%)
24	MIA	AX	37	24	26,29,32	2.87	5 (19%)	37,41,47	2.70	16 (43%)
24	PSU	AX	39	24	18,21,22	1.05	1 (5%)	22,30,33	1.85	5 (22%)
25	PSU	BA	955	25	18,21,22	1.11	2 (11%)	22,30,33	1.94	5 (22%)
12	D2T	AL	89	12	7,9,10	1.01	0	6,11,13	2.45	4 (66%)
25	OMU	BA	2552	25	19,22,23	2.83	7 (36%)	26,31,34	1.76	4 (15%)
1	2MG	AA	1516	1	23,26,27	2.67	9 (39%)	32,38,41	2.71	13 (40%)
23	H2U	AW	20	23	18,21,22	3.00	5 (27%)	21,30,33	2.25	6 (28%)
25	2MG	BA	1835	25	23,26,27	2.72	9 (39%)	32,38,41	2.92	13 (40%)
25	2MG	BA	2445	25	23,26,27	2.68	9 (39%)	32,38,41	2.84	14 (43%)
25	OMG	BA	2251	23,25	23,26,27	2.45	9 (39%)	33,38,41	2.01	11 (33%)
25	3TD	BA	1915	25	18,22,23	4.42	10 (55%)	22,32,35	2.19	4 (18%)
23	5MU	AW	54	23	19,22,23	1.39	5 (26%)	28,32,35	2.11	6 (21%)
1	5MC	AA	967	1	18,22,23	3.75	7 (38%)	26,32,35	1.04	2 (7%)
36	4D4	BN	81	36	9,11,12	2.51	3 (33%)	8,13,15	0.83	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MA6	AA	1518	1	23,26,27	1.58	5 (21%)	34,38,41	3.78	11 (32%)
1	2MG	AA	1207	62,1	23,26,27	2.73	9 (39%)	32,38,41	2.79	13 (40%)
25	PSU	BA	746	62,25	18,21,22	1.07	3 (16%)	22,30,33	1.97	7 (31%)
25	PSU	BA	2605	25	18,21,22	1.08	2 (11%)	22,30,33	1.90	4 (18%)
1	MA6	AA	1519	1	23,26,27	1.58	5 (21%)	34,38,41	3.78	11 (32%)
25	H2U	BA	2449	25	18,21,22	2.85	5 (27%)	21,30,33	2.13	5 (23%)
24	H2U	AX	16	24	18,21,22	3.02	5 (27%)	21,30,33	2.05	5 (23%)
25	PSU	BA	1917	25	18,21,22	1.07	2 (11%)	22,30,33	1.87	5 (22%)
25	2MA	BA	2503	62,25	22,25,26	3.97	10 (45%)	33,37,40	2.55	10 (30%)
25	PSU	BA	1911	25	18,21,22	1.09	1 (5%)	22,30,33	1.85	4 (18%)
23	PSU	AW	55	23	18,21,22	1.07	1 (5%)	22,30,33	1.86	6 (27%)

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	UR3	AA	1498	1	-	0/7/25/26	0/2/2/2
25	PSU	BA	2580	25	-	0/7/25/26	0/2/2/2
25	G7M	BA	2069	25	-	2/7/25/26	0/3/3/3
25	5MU	BA	1939	62,25	-	2/7/25/26	0/2/2/2
25	6MZ	BA	1618	25	-	3/9/27/28	0/3/3/3
1	5MC	AA	1407	1	-	0/7/25/26	0/2/2/2
23	4SU	AW	8	23	-	0/7/25/26	0/2/2/2
25	5MU	BA	747	25	-	0/7/25/26	0/2/2/2
25	6MZ	BA	2030	25	-	2/9/27/28	0/3/3/3
24	H2U	AX	20	24	-	3/7/38/39	0/2/2/2
25	PSU	BA	2457	25	-	0/7/25/26	0/2/2/2
25	OMC	BA	2498	62,25	-	2/9/27/28	0/2/2/2
24	5MU	AX	54	24	-	0/7/25/26	0/2/2/2
24	PSU	AX	55	24	-	1/7/25/26	0/2/2/2
24	3AU	AX	47	24	-	2/7/25/35	0/2/2/2
25	1MG	BA	745	25	-	0/7/25/26	0/3/3/3
28	MEQ	BD	150	28	-	2/8/9/11	-
1	2MG	AA	966	1	-	2/9/27/28	0/3/3/3
1	PSU	AA	516	1	-	2/7/25/26	0/2/2/2
24	G7M	AX	46	24	-	3/7/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	PSU	BA	2504	25	-	0/7/25/26	0/2/2/2
1	4OC	AA	1402	62,1	-	0/9/29/30	0/2/2/2
24	4SU	AX	8	24	-	2/7/25/26	0/2/2/2
25	5MC	BA	1962	25	-	0/7/25/26	0/2/2/2
23	OMC	AW	32	23	-	0/9/27/28	0/2/2/2
25	PSU	BA	2604	25	-	0/7/25/26	0/2/2/2
1	G7M	AA	527	1	-	1/7/25/26	0/3/3/3
24	PSU	AX	32	24	-	0/7/25/26	0/2/2/2
24	MIA	AX	37	24	-	4/13/31/34	0/3/3/3
24	PSU	AX	39	24	-	0/7/25/26	0/2/2/2
25	PSU	BA	955	25	-	0/7/25/26	0/2/2/2
12	D2T	AL	89	12	-	1/7/12/14	-
25	OMU	BA	2552	25	-	2/9/27/28	0/2/2/2
1	2MG	AA	1516	1	-	0/9/27/28	0/3/3/3
23	H2U	AW	20	23	-	2/7/38/39	0/2/2/2
25	2MG	BA	1835	25	-	0/9/27/28	0/3/3/3
25	2MG	BA	2445	25	-	2/9/27/28	0/3/3/3
25	OMG	BA	2251	23,25	-	1/9/27/28	0/3/3/3
25	3TD	BA	1915	25	-	2/7/25/26	0/2/2/2
23	5MU	AW	54	23	-	0/7/25/26	0/2/2/2
1	5MC	AA	967	1	-	3/7/25/26	0/2/2/2
36	4D4	BN	81	36	-	7/11/12/14	-
1	MA6	AA	1518	1	-	0/11/29/30	0/3/3/3
1	2MG	AA	1207	62,1	-	1/9/27/28	0/3/3/3
25	PSU	BA	746	62,25	-	2/7/25/26	0/2/2/2
25	PSU	BA	2605	25	-	0/7/25/26	0/2/2/2
1	MA6	AA	1519	1	-	3/11/29/30	0/3/3/3
25	H2U	BA	2449	25	-	0/7/38/39	0/2/2/2
24	H2U	AX	16	24	-	3/7/38/39	0/2/2/2
25	PSU	BA	1917	25	-	2/7/25/26	0/2/2/2
25	2MA	BA	2503	62,25	-	2/7/25/26	0/3/3/3
25	PSU	BA	1911	25	-	1/7/25/26	0/2/2/2
23	PSU	AW	55	23	-	0/7/25/26	0/2/2/2

All (281) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	BA	2503	2MA	C4-N3	12.19	1.49	1.34
25	BA	1915	3TD	C6-C5	11.77	1.49	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	AX	46	G7M	C8-N7	10.68	1.52	1.33
25	BA	2030	6MZ	C6-N6	10.26	1.45	1.34
25	BA	1618	6MZ	C6-N6	10.15	1.45	1.34
24	AX	37	MIA	C13-C14	9.69	1.60	1.32
25	BA	1915	3TD	C2-N1	9.63	1.49	1.37
1	AA	1407	5MC	C6-C5	9.59	1.50	1.34
24	AX	20	H2U	C2-N1	9.57	1.49	1.35
23	AW	20	H2U	C2-N1	9.32	1.48	1.35
24	AX	16	H2U	C2-N1	9.27	1.48	1.35
1	AA	967	5MC	C6-C5	9.23	1.49	1.34
23	AW	8	4SU	C4-N3	9.23	1.47	1.37
25	BA	1962	5MC	C6-C5	9.19	1.49	1.34
24	AX	37	MIA	C6-N6	9.10	1.48	1.34
24	AX	8	4SU	C4-N3	9.08	1.47	1.37
25	BA	2449	H2U	C2-N1	8.27	1.47	1.35
1	AA	966	2MG	C2-N3	7.92	1.47	1.31
25	BA	745	1MG	C2-N3	7.67	1.48	1.34
25	BA	1835	2MG	C2-N3	7.66	1.46	1.31
24	AX	47	3AU	C2-N1	7.63	1.50	1.38
24	AX	8	4SU	C2-N1	7.59	1.50	1.38
1	AA	1207	2MG	C2-N3	7.50	1.46	1.31
25	BA	2445	2MG	C2-N3	7.50	1.46	1.31
23	AW	8	4SU	C2-N1	7.39	1.50	1.38
1	AA	1516	2MG	C2-N3	7.11	1.45	1.31
25	BA	2503	2MA	C6-N1	7.10	1.45	1.35
24	AX	47	3AU	C6-C5	7.07	1.51	1.35
1	AA	967	5MC	C4-N3	7.04	1.46	1.34
25	BA	1962	5MC	C4-N3	7.03	1.46	1.34
25	BA	2503	2MA	C2-N3	6.72	1.46	1.34
1	AA	1407	5MC	C4-N3	6.66	1.45	1.34
24	AX	20	H2U	C2-N3	6.63	1.49	1.38
1	AA	1402	4OC	C4-N3	6.53	1.44	1.32
23	AW	8	4SU	C2-N3	6.48	1.49	1.38
24	AX	47	3AU	C2-N3	6.48	1.49	1.38
24	AX	8	4SU	C2-N3	6.45	1.49	1.38
25	BA	2251	OMG	C4-N3	6.41	1.49	1.34
25	BA	1962	5MC	C2-N3	6.40	1.49	1.36
1	AA	967	5MC	C2-N3	6.30	1.49	1.36
1	AA	1407	5MC	C2-N3	6.28	1.49	1.36
25	BA	2552	OMU	C2-N3	6.27	1.49	1.38
24	AX	16	H2U	C2-N3	6.27	1.49	1.38
1	AA	1402	4OC	C6-C5	6.19	1.49	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AW	20	H2U	C2-N3	6.18	1.49	1.38
1	AA	1498	UR3	C2-N1	6.15	1.47	1.38
25	BA	2449	H2U	C2-N3	6.08	1.48	1.38
24	AX	8	4SU	C6-C5	6.01	1.49	1.35
23	AW	8	4SU	C6-C5	6.00	1.49	1.35
25	BA	2498	OMC	C2-N3	5.95	1.48	1.36
23	AW	32	OMC	C2-N3	5.94	1.48	1.36
25	BA	1915	3TD	C6-N1	5.87	1.46	1.36
36	BN	81	4D4	CZ-NE	5.86	1.44	1.33
24	AX	46	G7M	C4-N3	5.84	1.48	1.34
25	BA	2552	OMU	C6-C5	5.84	1.48	1.35
24	AX	46	G7M	C2-N3	5.84	1.47	1.33
25	BA	745	1MG	C4-N3	5.83	1.48	1.34
25	BA	2069	G7M	C4-N3	5.74	1.47	1.34
1	AA	1498	UR3	C6-C5	5.73	1.48	1.35
25	BA	2503	2MA	C2-N1	5.73	1.44	1.34
25	BA	2498	OMC	C6-C5	5.65	1.48	1.35
1	AA	1402	4OC	C2-N3	5.65	1.47	1.36
23	AW	32	OMC	C6-C5	5.62	1.48	1.35
23	AW	8	4SU	C4-S4	-5.57	1.57	1.68
24	AX	8	4SU	C5-C4	5.57	1.49	1.42
24	AX	46	G7M	C8-N9	5.51	1.51	1.35
1	AA	527	G7M	C4-N3	5.49	1.47	1.34
24	AX	8	4SU	C4-S4	-5.43	1.58	1.68
25	BA	2069	G7M	C5-N7	-5.43	1.32	1.39
23	AW	8	4SU	C5-C4	5.42	1.49	1.42
1	AA	527	G7M	C5-N7	-5.40	1.32	1.39
25	BA	1962	5MC	C4-N4	5.26	1.47	1.34
1	AA	1407	5MC	C4-N4	5.19	1.47	1.34
25	BA	2251	OMG	C2-N2	5.17	1.46	1.34
1	AA	967	5MC	C4-N4	5.15	1.47	1.34
25	BA	745	1MG	C2-N2	5.12	1.43	1.34
24	AX	20	H2U	C4-N3	5.10	1.46	1.37
1	AA	1207	2MG	C4-N3	5.08	1.46	1.34
1	AA	966	2MG	C4-N3	5.08	1.46	1.34
24	AX	47	3AU	C4-N3	5.07	1.47	1.38
25	BA	2445	2MG	C4-N3	5.07	1.46	1.34
25	BA	1915	3TD	C1'-C5	-5.05	1.38	1.50
25	BA	1835	2MG	C4-N3	5.04	1.46	1.34
1	AA	1402	4OC	O2-C2	-5.00	1.14	1.23
25	BA	2251	OMG	C2-N3	4.97	1.45	1.33
25	BA	2552	OMU	C2-N1	4.92	1.46	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	1407	5MC	C6-N1	4.85	1.46	1.38
1	AA	967	5MC	C6-N1	4.82	1.46	1.38
24	AX	46	G7M	C2-N2	4.81	1.45	1.34
24	AX	16	H2U	C4-N3	4.78	1.45	1.37
24	AX	46	G7M	C5-N7	4.78	1.44	1.39
25	BA	1962	5MC	C6-N1	4.78	1.46	1.38
1	AA	1516	2MG	C4-N3	4.76	1.45	1.34
23	AW	20	H2U	C4-N3	4.73	1.45	1.37
25	BA	2069	G7M	C2-N3	4.72	1.44	1.33
1	AA	966	2MG	C2-N2	4.68	1.43	1.33
23	AW	32	OMC	C4-N4	4.68	1.44	1.33
1	AA	1402	4OC	C4-N4	4.68	1.45	1.35
25	BA	2498	OMC	C4-N4	4.67	1.44	1.33
25	BA	2498	OMC	C4-N3	4.63	1.43	1.34
23	AW	32	OMC	C4-N3	4.61	1.43	1.34
25	BA	2503	2MA	C5-C6	4.47	1.53	1.41
25	BA	2069	G7M	C2-N2	4.42	1.44	1.34
25	BA	2449	H2U	C4-N3	4.42	1.45	1.37
1	AA	527	G7M	C2-N3	4.40	1.43	1.33
1	AA	1498	UR3	C2-N3	4.40	1.47	1.39
1	AA	1516	2MG	C2-N2	4.37	1.43	1.33
1	AA	1207	2MG	C2-N2	4.36	1.43	1.33
25	BA	1962	5MC	C2-N1	4.32	1.49	1.40
25	BA	1915	3TD	C2-N3	4.30	1.48	1.38
1	AA	1407	5MC	C2-N1	4.26	1.49	1.40
1	AA	527	G7M	C2-N2	4.17	1.44	1.34
25	BA	2445	2MG	C2-N2	4.17	1.42	1.33
25	BA	1835	2MG	C2-N2	4.11	1.42	1.33
24	AX	46	G7M	C2-N1	4.05	1.47	1.37
25	BA	1835	2MG	O6-C6	-4.03	1.15	1.23
1	AA	1402	4OC	C5-C4	4.03	1.49	1.40
1	AA	967	5MC	C2-N1	4.02	1.48	1.40
23	AW	32	OMC	C2-N1	4.00	1.48	1.40
25	BA	2445	2MG	O6-C6	-3.99	1.16	1.23
25	BA	2552	OMU	O4-C4	-3.95	1.16	1.24
1	AA	1516	2MG	O6-C6	-3.95	1.16	1.23
25	BA	2498	OMC	C2-N1	3.92	1.48	1.40
1	AA	1207	2MG	O6-C6	-3.92	1.16	1.23
25	BA	2552	OMU	C4-N3	3.78	1.45	1.38
1	AA	1516	2MG	C2-N1	3.77	1.42	1.36
1	AA	966	2MG	O6-C6	-3.73	1.16	1.23
1	AA	966	2MG	C2-N1	3.72	1.42	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	BA	2503	2MA	C8-N7	3.70	1.38	1.31
25	BA	1835	2MG	C2-N1	3.68	1.42	1.36
24	AX	46	G7M	C5-C6	3.68	1.53	1.43
1	AA	1207	2MG	C2-N1	3.65	1.42	1.36
25	BA	2552	OMU	O2-C2	-3.61	1.16	1.23
1	AA	1402	4OC	C2-N1	3.61	1.47	1.40
24	AX	46	G7M	O6-C6	-3.61	1.16	1.23
25	BA	745	1MG	C5-N7	-3.52	1.32	1.39
25	BA	2445	2MG	C2-N1	3.51	1.42	1.36
1	AA	1519	MA6	C6-N6	3.50	1.47	1.36
25	BA	1915	3TD	O2-C2	-3.49	1.16	1.23
25	BA	1835	2MG	C5-N7	-3.48	1.32	1.39
25	BA	2445	2MG	C5-N7	-3.46	1.32	1.39
1	AA	1518	MA6	C5-C4	-3.46	1.32	1.39
25	BA	1939	5MU	C4-N3	-3.43	1.32	1.38
25	BA	2030	6MZ	C5-C4	-3.43	1.32	1.39
1	AA	1516	2MG	C5-N7	-3.43	1.32	1.39
1	AA	1519	MA6	C5-C4	-3.42	1.32	1.39
1	AA	1207	2MG	C5-N7	-3.40	1.32	1.39
24	AX	47	3AU	C6-N1	3.39	1.46	1.38
1	AA	1518	MA6	C6-N6	3.38	1.46	1.36
25	BA	1618	6MZ	C5-C4	-3.30	1.32	1.39
1	AA	1516	2MG	C4-N9	-3.29	1.29	1.38
24	AX	8	4SU	O2-C2	-3.27	1.17	1.23
1	AA	966	2MG	C5-N7	-3.26	1.32	1.39
36	BN	81	4D4	CZ-NH2	3.25	1.45	1.32
23	AW	8	4SU	O2-C2	-3.24	1.17	1.23
24	AX	46	G7M	C6-N1	3.22	1.44	1.38
24	AX	55	PSU	C6-C5	3.21	1.39	1.35
1	AA	527	G7M	C5-C6	3.20	1.52	1.43
25	BA	2069	G7M	C5-C6	3.20	1.52	1.43
1	AA	1402	4OC	CM4-N4	3.19	1.51	1.45
25	BA	747	5MU	C4-N3	-3.19	1.32	1.38
24	AX	39	PSU	C6-C5	3.17	1.39	1.35
23	AW	55	PSU	C6-C5	3.15	1.39	1.35
25	BA	745	1MG	C5-C6	3.14	1.53	1.45
25	BA	2251	OMG	C5-N7	-3.13	1.33	1.39
24	AX	8	4SU	C6-N1	3.08	1.45	1.38
23	AW	32	OMC	O2-C2	-3.06	1.18	1.23
25	BA	1915	3TD	O4-C4	-3.05	1.16	1.23
23	AW	8	4SU	C6-N1	3.04	1.45	1.38
25	BA	2498	OMC	O2-C2	-3.04	1.18	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	BA	2503	2MA	C6-N6	-3.03	1.26	1.34
1	AA	1518	MA6	C8-N9	-2.94	1.32	1.37
1	AA	1207	2MG	C4-N9	-2.93	1.30	1.38
24	AX	47	3AU	O4-C4	-2.93	1.18	1.24
24	AX	32	PSU	C6-C5	2.91	1.38	1.35
1	AA	527	G7M	C4-N9	-2.91	1.30	1.38
24	AX	37	MIA	C4-N9	-2.89	1.31	1.37
25	BA	1939	5MU	C6-N1	-2.89	1.33	1.38
1	AA	967	5MC	O2-C2	-2.88	1.18	1.23
1	AA	516	PSU	C6-C5	2.88	1.38	1.35
25	BA	1911	PSU	C6-C5	2.88	1.38	1.35
1	AA	527	G7M	O6-C6	-2.87	1.18	1.23
25	BA	2498	OMC	C6-N1	2.86	1.44	1.38
25	BA	2069	G7M	O6-C6	-2.85	1.18	1.23
25	BA	747	5MU	C6-N1	-2.85	1.33	1.38
24	AX	47	3AU	C5-C4	2.83	1.49	1.43
1	AA	1402	4OC	C6-N1	2.83	1.44	1.38
25	BA	2504	PSU	C6-C5	2.82	1.38	1.35
25	BA	1939	5MU	C2-N3	-2.82	1.32	1.38
24	AX	37	MIA	C5-C4	-2.82	1.33	1.39
25	BA	1618	6MZ	C5-N7	-2.81	1.33	1.39
23	AW	54	5MU	C4-N3	-2.81	1.33	1.38
25	BA	2069	G7M	C4-N9	-2.81	1.30	1.38
24	AX	54	5MU	C4-N3	-2.80	1.33	1.38
25	BA	2604	PSU	C6-C5	2.80	1.38	1.35
25	BA	2030	6MZ	C5-N7	-2.79	1.33	1.39
1	AA	1519	MA6	C8-N9	-2.79	1.32	1.37
1	AA	1407	5MC	O2-C2	-2.77	1.18	1.23
25	BA	1917	PSU	C6-C5	2.74	1.38	1.35
1	AA	1519	MA6	C10-N6	2.74	1.52	1.45
1	AA	966	2MG	C4-N9	-2.73	1.31	1.38
25	BA	2251	OMG	O6-C6	-2.72	1.18	1.23
25	BA	1618	6MZ	C8-N9	-2.72	1.32	1.37
25	BA	2445	2MG	C4-N9	-2.72	1.31	1.38
1	AA	1518	MA6	C10-N6	2.71	1.51	1.45
25	BA	2030	6MZ	C8-N9	-2.70	1.32	1.37
25	BA	1835	2MG	C4-N9	-2.70	1.31	1.38
23	AW	32	OMC	C6-N1	2.70	1.44	1.38
25	BA	1962	5MC	O2-C2	-2.69	1.18	1.23
24	AX	37	MIA	C5-N7	-2.69	1.33	1.39
25	BA	955	PSU	C6-C5	2.67	1.38	1.35
1	AA	966	2MG	C6-N1	2.66	1.43	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	1498	UR3	O4-C4	-2.65	1.17	1.23
25	BA	1915	3TD	C10-N3	2.63	1.51	1.47
25	BA	2580	PSU	C6-C5	2.62	1.38	1.35
25	BA	1835	2MG	C6-N1	2.61	1.43	1.38
25	BA	2503	2MA	C5-N7	-2.60	1.34	1.39
25	BA	2449	H2U	O4-C4	-2.60	1.18	1.23
25	BA	2449	H2U	O2-C2	-2.59	1.18	1.23
1	AA	1207	2MG	C6-N1	2.57	1.43	1.38
24	AX	47	3AU	O2-C2	-2.56	1.18	1.23
25	BA	2457	PSU	C6-C5	2.54	1.38	1.35
25	BA	2069	G7M	C2-N1	2.52	1.43	1.37
24	AX	54	5MU	C6-N1	-2.51	1.33	1.38
25	BA	747	5MU	C2-N3	-2.51	1.33	1.38
25	BA	1915	3TD	C4-N3	2.50	1.45	1.40
1	AA	1516	2MG	C6-N1	2.49	1.43	1.38
25	BA	746	PSU	C6-C5	2.47	1.38	1.35
25	BA	2503	2MA	C8-N9	-2.47	1.33	1.37
25	BA	2030	6MZ	C6-N1	-2.45	1.31	1.35
23	AW	54	5MU	C6-N1	-2.43	1.33	1.38
1	AA	1498	UR3	O2-C2	-2.43	1.18	1.22
1	AA	1498	UR3	C6-N1	2.41	1.43	1.38
25	BA	2251	OMG	C2-N1	2.41	1.43	1.37
25	BA	1939	5MU	C6-C5	2.41	1.38	1.34
25	BA	2503	2MA	CM2-C2	2.40	1.56	1.49
25	BA	2445	2MG	C6-N1	2.40	1.43	1.38
24	AX	16	H2U	O2-C2	-2.39	1.18	1.23
25	BA	747	5MU	C6-C5	2.39	1.38	1.34
23	AW	54	5MU	C6-C5	2.36	1.38	1.34
25	BA	2605	PSU	C6-C5	2.36	1.38	1.35
1	AA	1518	MA6	C5-N7	-2.35	1.34	1.39
23	AW	20	H2U	O2-C2	-2.34	1.18	1.23
36	BN	81	4D4	CZ-NH1	-2.34	1.25	1.34
1	AA	527	G7M	C2-N1	2.34	1.43	1.37
25	BA	2445	2MG	C5-C6	2.33	1.53	1.44
24	AX	46	G7M	C4-N9	2.32	1.44	1.38
25	BA	2605	PSU	C4-C5	-2.32	1.37	1.44
24	AX	20	H2U	O2-C2	-2.30	1.18	1.23
25	BA	2069	G7M	C6-N1	2.30	1.43	1.38
24	AX	54	5MU	C2-N3	-2.29	1.33	1.38
1	AA	1207	2MG	C5-C6	2.28	1.52	1.44
25	BA	746	PSU	C4-C5	-2.27	1.37	1.44
25	BA	2251	OMG	C5-C6	2.27	1.52	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	BA	2552	OMU	C6-N1	2.27	1.43	1.38
25	BA	1915	3TD	O4'-C1'	-2.27	1.40	1.43
23	AW	54	5MU	C2-N3	-2.25	1.34	1.38
1	AA	1516	2MG	C5-C6	2.24	1.52	1.44
1	AA	1519	MA6	C5-N7	-2.24	1.34	1.39
24	AX	16	H2U	O4-C4	-2.23	1.18	1.23
1	AA	516	PSU	C4-C5	-2.22	1.37	1.44
25	BA	2251	OMG	C6-N1	2.22	1.43	1.38
23	AW	54	5MU	C4-C5	2.21	1.48	1.44
25	BA	1835	2MG	C5-C6	2.21	1.52	1.44
25	BA	1618	6MZ	C6-N1	-2.19	1.31	1.35
25	BA	2251	OMG	C4-N9	-2.19	1.32	1.38
1	AA	966	2MG	C5-C6	2.18	1.52	1.44
24	AX	54	5MU	C6-C5	2.18	1.38	1.34
24	AX	46	G7M	C5-C4	2.13	1.43	1.38
25	BA	746	PSU	O4'-C1'	-2.12	1.40	1.43
24	AX	20	H2U	O4-C4	-2.10	1.19	1.23
1	AA	527	G7M	C6-N1	2.10	1.42	1.38
23	AW	20	H2U	O4-C4	-2.09	1.19	1.23
25	BA	2457	PSU	C4-C5	-2.09	1.38	1.44
25	BA	745	1MG	C4-N9	-2.08	1.32	1.38
25	BA	955	PSU	C4-C5	-2.08	1.38	1.44
23	AW	32	OMC	C5-C4	2.08	1.47	1.42
25	BA	2580	PSU	O4'-C1'	-2.07	1.41	1.43
25	BA	2580	PSU	C4-C5	-2.07	1.38	1.44
25	BA	1917	PSU	O4'-C1'	-2.06	1.41	1.43
24	AX	54	5MU	C4-C5	2.02	1.48	1.44

All (342) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1519	MA6	N1-C6-N6	-16.05	99.54	117.08
1	AA	1518	MA6	N1-C6-N6	-15.92	99.67	117.08
1	AA	1519	MA6	C5-C6-N6	8.66	140.39	125.30
1	AA	966	2MG	C1'-N9-C8	-8.35	102.93	126.70
1	AA	1518	MA6	C5-C6-N6	8.30	139.76	125.30
24	AX	8	4SU	C4-N3-C2	-8.27	119.31	127.34
24	AX	37	MIA	C12-C13-C14	-8.16	111.27	127.14
23	AW	8	4SU	C4-N3-C2	-8.08	119.49	127.34
25	BA	1835	2MG	C1'-N9-C8	-7.80	104.48	126.70
23	AW	20	H2U	C4-N3-C2	-7.43	119.63	125.79
25	BA	2449	H2U	C4-N3-C2	-7.37	119.67	125.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1516	2MG	C1'-N9-C8	-7.22	106.15	126.70
25	BA	2445	2MG	C1'-N9-C8	-7.17	106.30	126.70
24	AX	16	H2U	C4-N3-C2	-7.16	119.86	125.79
1	AA	1207	2MG	C1'-N9-C8	-7.10	106.50	126.70
1	AA	966	2MG	C1'-N9-C4	7.06	147.47	126.50
25	BA	1835	2MG	C1'-N9-C4	7.05	147.46	126.50
25	BA	1915	3TD	N1-C2-N3	6.93	121.61	116.14
25	BA	2030	6MZ	C9-N6-C6	-6.86	116.97	122.87
25	BA	2503	2MA	C1'-N9-C8	-6.80	111.78	127.14
24	AX	20	H2U	C4-N3-C2	-6.68	120.25	125.79
25	BA	2445	2MG	C2-N3-C4	6.55	120.16	112.04
1	AA	1207	2MG	C2-N3-C4	6.50	120.10	112.04
25	BA	2445	2MG	C1'-N9-C4	6.49	145.77	126.50
1	AA	1516	2MG	C1'-N9-C4	6.42	145.56	126.50
25	BA	1835	2MG	C2-N3-C4	6.35	119.91	112.04
1	AA	966	2MG	C2-N3-C4	6.28	119.82	112.04
25	BA	1618	6MZ	C9-N6-C6	-6.22	117.51	122.87
25	BA	2069	G7M	C1'-N9-C8	-6.13	106.06	126.74
1	AA	1207	2MG	C1'-N9-C4	6.11	144.66	126.50
25	BA	2503	2MA	N9-C8-N7	-6.05	105.64	113.91
1	AA	527	G7M	C1'-N9-C8	-6.04	106.33	126.74
1	AA	1516	2MG	C2-N3-C4	6.01	119.49	112.04
25	BA	1618	6MZ	C5-C4-N3	-5.97	118.97	126.75
25	BA	1939	5MU	C4-N3-C2	-5.85	119.77	127.35
25	BA	2069	G7M	C1'-N9-C4	5.74	143.54	126.50
25	BA	747	5MU	C4-N3-C2	-5.73	119.93	127.35
1	AA	527	G7M	C1'-N9-C4	5.73	143.52	126.50
24	AX	8	4SU	C5-C4-N3	5.68	119.96	114.69
25	BA	1618	6MZ	N1-C2-N3	-5.62	119.81	128.60
1	AA	1518	MA6	N1-C2-N3	-5.60	119.85	128.60
1	AA	1519	MA6	N1-C2-N3	-5.58	119.87	128.60
25	BA	1939	5MU	N3-C2-N1	5.57	122.28	114.89
23	AW	8	4SU	C5-C4-N3	5.54	119.83	114.69
24	AX	37	MIA	N3-C2-N1	-5.51	119.98	128.60
1	AA	1518	MA6	C5-C4-N3	-5.45	119.63	126.75
25	BA	2030	6MZ	N1-C2-N3	-5.43	120.11	128.60
25	BA	2552	OMU	C4-N3-C2	-5.36	119.51	126.58
25	BA	747	5MU	N3-C2-N1	5.36	122.00	114.89
1	AA	527	G7M	CN7-N7-C5	5.24	133.28	126.77
25	BA	745	1MG	C5-C4-N3	-5.20	120.02	128.46
23	AW	54	5MU	C4-N3-C2	-5.16	120.67	127.35
24	AX	37	MIA	C5-C4-N3	-5.16	120.02	126.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	AX	54	5MU	C4-N3-C2	-5.12	120.72	127.35
25	BA	2605	PSU	C4-N3-C2	-5.12	118.96	126.34
25	BA	2069	G7M	CN7-N7-C5	5.12	133.12	126.77
25	BA	2457	PSU	N1-C2-N3	5.06	120.86	115.13
1	AA	516	PSU	C4-N3-C2	-5.03	119.09	126.34
25	BA	2030	6MZ	N9-C8-N7	-5.03	107.03	113.91
1	AA	1519	MA6	C5-C4-N3	-5.02	120.20	126.75
25	BA	2445	2MG	C2-N1-C6	-5.01	118.71	124.48
24	AX	47	3AU	C4-N3-C2	-5.01	119.97	126.58
25	BA	1835	2MG	C2-N1-C6	-5.01	118.71	124.48
1	AA	516	PSU	N1-C2-N3	5.01	120.81	115.13
25	BA	955	PSU	N1-C2-N3	5.01	120.80	115.13
25	BA	2604	PSU	N1-C2-N3	4.99	120.79	115.13
25	BA	2457	PSU	C4-N3-C2	-4.99	119.15	126.34
25	BA	955	PSU	C4-N3-C2	-4.97	119.17	126.34
25	BA	1939	5MU	C5-C6-N1	-4.95	118.24	123.34
25	BA	2580	PSU	C4-N3-C2	-4.84	119.36	126.34
25	BA	1911	PSU	C4-N3-C2	-4.83	119.38	126.34
25	BA	2580	PSU	N1-C2-N3	4.81	120.58	115.13
25	BA	1939	5MU	C5-C4-N3	4.80	119.41	115.31
25	BA	1917	PSU	N1-C2-N3	4.80	120.57	115.13
24	AX	54	5MU	N3-C2-N1	4.79	121.25	114.89
25	BA	2504	PSU	C4-N3-C2	-4.79	119.44	126.34
25	BA	2604	PSU	C4-N3-C2	-4.77	119.46	126.34
25	BA	1911	PSU	N1-C2-N3	4.76	120.52	115.13
1	AA	1207	2MG	C2-N1-C6	-4.74	119.02	124.48
25	BA	1915	3TD	C4-N3-C2	-4.74	119.46	124.61
23	AW	54	5MU	N3-C2-N1	4.74	121.18	114.89
24	AX	55	PSU	N1-C2-N3	4.71	120.47	115.13
24	AX	37	MIA	N9-C8-N7	-4.70	107.48	113.91
24	AX	39	PSU	C4-N3-C2	-4.70	119.57	126.34
24	AX	55	PSU	C4-N3-C2	-4.69	119.59	126.34
25	BA	2503	2MA	C4-N9-C1'	4.68	137.74	126.59
25	BA	747	5MU	C5-C4-N3	4.68	119.30	115.31
25	BA	2503	2MA	C5-C4-N3	-4.66	121.95	127.19
25	BA	2504	PSU	N1-C2-N3	4.65	120.40	115.13
24	AX	39	PSU	N1-C2-N3	4.65	120.40	115.13
25	BA	746	PSU	C4-N3-C2	-4.61	119.69	126.34
25	BA	2605	PSU	N1-C2-N3	4.57	120.31	115.13
25	BA	747	5MU	C5-C6-N1	-4.56	118.65	123.34
24	AX	32	PSU	C4-N3-C2	-4.55	119.78	126.34
23	AW	54	5MU	C5-C4-N3	4.53	119.18	115.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1516	2MG	C2-N1-C6	-4.51	119.29	124.48
23	AW	55	PSU	C4-N3-C2	-4.50	119.85	126.34
25	BA	2030	6MZ	C5-C4-N3	-4.49	120.89	126.75
25	BA	2445	2MG	C5-C4-N3	-4.47	121.21	128.46
25	BA	2251	OMG	C5-C4-N3	-4.46	121.22	128.46
1	AA	1498	UR3	C4-N3-C2	-4.46	120.37	124.56
24	AX	54	5MU	C5-C4-N3	4.45	119.11	115.31
25	BA	1917	PSU	C4-N3-C2	-4.45	119.93	126.34
1	AA	1518	MA6	N9-C8-N7	-4.44	107.84	113.91
1	AA	966	2MG	C2-N1-C6	-4.44	119.37	124.48
1	AA	1519	MA6	N9-C8-N7	-4.41	107.88	113.91
24	AX	37	MIA	C15-C14-C13	-4.41	109.90	122.65
1	AA	527	G7M	CN7-N7-C8	-4.40	118.05	124.84
25	BA	1618	6MZ	N9-C8-N7	-4.40	107.90	113.91
24	AX	46	G7M	C2-N3-C4	4.39	120.12	112.30
25	BA	2503	2MA	C4-N9-C8	4.37	110.47	105.73
25	BA	1835	2MG	C5-C4-N3	-4.37	121.37	128.46
24	AX	47	3AU	N3-C2-N1	4.37	120.69	114.89
24	AX	32	PSU	N1-C2-N3	4.36	120.07	115.13
25	BA	1835	2MG	CM2-N2-C2	-4.30	114.36	123.86
25	BA	2069	G7M	CN7-N7-C8	-4.29	118.22	124.84
25	BA	2069	G7M	C2-N3-C4	4.26	119.88	112.30
25	BA	746	PSU	N1-C2-N3	4.24	119.93	115.13
25	BA	1939	5MU	O4-C4-C5	-4.09	120.16	124.90
25	BA	2251	OMG	C2-N3-C4	4.09	119.59	112.30
24	AX	8	4SU	N3-C2-N1	4.09	120.32	114.89
23	AW	55	PSU	N1-C2-N3	4.09	119.76	115.13
1	AA	966	2MG	C5-C4-N3	-4.08	121.84	128.46
25	BA	2069	G7M	C5-C6-N1	4.08	120.31	111.79
25	BA	1618	6MZ	C4-C5-C6	4.06	119.96	116.81
25	BA	747	5MU	O4-C4-C5	-4.06	120.20	124.90
1	AA	1207	2MG	C5-C4-N3	-4.02	121.94	128.46
25	BA	1618	6MZ	N3-C4-N9	4.02	133.70	127.08
1	AA	527	G7M	C5-C6-N1	4.01	120.15	111.79
25	BA	2251	OMG	C1'-N9-C8	-3.99	115.33	126.70
23	AW	8	4SU	N3-C2-N1	3.98	120.17	114.89
1	AA	527	G7M	C2-N3-C4	3.95	119.34	112.30
25	BA	2552	OMU	N3-C2-N1	3.94	120.12	114.89
24	AX	46	G7M	C5-C6-N1	3.94	120.02	111.79
25	BA	1618	6MZ	C2-N3-C4	3.93	121.04	111.75
25	BA	2251	OMG	N9-C8-N7	-3.92	106.01	113.39
24	AX	37	MIA	C16-C14-C13	-3.91	111.36	122.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	AX	54	5MU	O4-C4-C5	-3.90	120.38	124.90
24	AX	46	G7M	C5-C4-N3	-3.88	120.70	128.15
1	AA	1518	MA6	N3-C4-N9	3.88	133.48	127.08
23	AW	54	5MU	C5-C6-N1	-3.88	119.35	123.34
24	AX	37	MIA	C4-C5-C6	3.84	119.79	116.81
23	AW	54	5MU	O4-C4-C5	-3.84	120.45	124.90
25	BA	745	1MG	N9-C4-N3	3.81	133.59	125.94
1	AA	1518	MA6	C4-C5-C6	3.74	120.07	115.88
25	BA	2503	2MA	C5-N7-C8	3.71	108.78	103.51
1	AA	527	G7M	O6-C6-C5	-3.69	119.73	128.06
1	AA	966	2MG	N9-C8-N7	-3.68	106.46	113.39
1	AA	1207	2MG	N9-C8-N7	-3.68	106.46	113.39
23	AW	20	H2U	N3-C2-N1	3.66	120.52	116.65
25	BA	2069	G7M	O6-C6-C5	-3.65	119.83	128.06
1	AA	1516	2MG	C5-C4-N3	-3.64	122.56	128.46
25	BA	2445	2MG	CM2-N2-C2	-3.63	115.85	123.86
1	AA	1519	MA6	C4-C5-C6	3.62	119.93	115.88
1	AA	1518	MA6	C2-N3-C4	3.61	120.29	111.75
12	AL	89	D2T	CB1-SB-CB	3.59	108.94	102.44
25	BA	2552	OMU	C5-C4-N3	3.56	120.16	114.84
24	AX	37	MIA	C2-N3-C4	3.53	120.09	111.75
1	AA	1519	MA6	C2-N1-C6	3.53	120.08	111.75
23	AW	8	4SU	C5-C4-S4	-3.52	119.93	124.47
25	BA	747	5MU	O2-C2-N1	-3.50	118.13	122.79
24	AX	54	5MU	C5-C6-N1	-3.50	119.74	123.34
25	BA	2030	6MZ	C5-N7-C8	3.47	108.44	103.51
25	BA	745	1MG	C2-N3-C4	3.47	119.78	111.98
25	BA	2503	2MA	N3-C2-N1	-3.46	119.36	125.72
1	AA	1519	MA6	C2-N3-C4	3.43	119.86	111.75
25	BA	745	1MG	N9-C8-N7	-3.43	106.93	113.39
1	AA	1516	2MG	CM2-N2-C2	-3.39	116.36	123.86
24	AX	8	4SU	C5-C4-S4	-3.38	120.12	124.47
1	AA	1207	2MG	CM2-N2-C2	-3.34	116.49	123.86
1	AA	1518	MA6	C2-N1-C6	3.32	119.59	111.75
25	BA	2445	2MG	N9-C8-N7	-3.31	107.15	113.39
25	BA	2030	6MZ	C2-N3-C4	3.29	119.53	111.75
1	AA	1407	5MC	C5-C6-N1	-3.28	119.96	123.34
24	AX	16	H2U	N3-C2-N1	3.28	120.12	116.65
1	AA	1516	2MG	N9-C8-N7	-3.28	107.22	113.39
25	BA	1835	2MG	N9-C8-N7	-3.27	107.23	113.39
1	AA	1519	MA6	N3-C4-N9	3.26	132.45	127.08
1	AA	527	G7M	C2-N1-C6	-3.24	119.20	125.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	2069	G7M	C5-C4-N3	-3.22	121.97	128.15
1	AA	527	G7M	C5-C4-N3	-3.22	121.97	128.15
24	AX	20	H2U	N3-C2-N1	3.20	120.04	116.65
24	AX	47	3AU	C5-C4-N3	3.16	119.57	114.84
24	AX	37	MIA	C5-N7-C8	3.15	107.98	103.51
12	AL	89	D2T	OD2-CG-CB	3.14	119.93	113.15
25	BA	2449	H2U	N3-C2-N1	3.10	119.94	116.65
25	BA	1915	3TD	C6-C5-C4	3.10	120.36	118.22
25	BA	2503	2MA	CM2-C2-N1	3.10	121.98	117.15
24	AX	37	MIA	N3-C4-N9	3.09	132.17	127.08
25	BA	1939	5MU	O2-C2-N1	-3.09	118.69	122.79
25	BA	745	1MG	C1'-N9-C4	-3.08	117.35	126.50
24	AX	55	PSU	O2-C2-N1	-3.07	119.41	122.79
25	BA	2604	PSU	O2-C2-N1	-3.06	119.42	122.79
25	BA	1618	6MZ	C5-N7-C8	3.06	107.85	103.51
25	BA	1917	PSU	C6-N1-C2	-3.05	119.57	122.68
24	AX	46	G7M	O6-C6-C5	-3.03	121.23	128.06
1	AA	967	5MC	C5-C6-N1	-3.02	120.23	123.34
1	AA	1207	2MG	C5-C6-N1	3.01	120.84	113.19
25	BA	2445	2MG	C5-C6-N1	2.97	120.74	113.19
25	BA	2449	H2U	C5-C4-N3	2.97	119.98	116.65
25	BA	2069	G7M	C2-N1-C6	-2.96	119.70	125.10
25	BA	2030	6MZ	C4-C5-C6	2.95	119.10	116.81
25	BA	1835	2MG	C5-C6-N1	2.91	120.59	113.19
1	AA	516	PSU	O2-C2-N1	-2.91	119.59	122.79
25	BA	2457	PSU	O2-C2-N1	-2.90	119.59	122.79
25	BA	2552	OMU	O4-C4-C5	-2.90	120.05	125.16
1	AA	516	PSU	O4'-C1'-C2'	2.90	109.23	105.14
25	BA	2030	6MZ	C4-N9-C8	2.89	108.86	105.73
25	BA	2251	OMG	C2-N1-C6	-2.89	119.84	125.10
25	BA	2251	OMG	N9-C4-N3	2.87	131.71	125.94
1	AA	1518	MA6	C4-N9-C8	2.86	108.82	105.73
24	AX	16	H2U	C5-C4-N3	2.86	119.86	116.65
25	BA	2449	H2U	O2-C2-N1	-2.85	119.53	123.11
1	AA	966	2MG	C5-C6-N1	2.85	120.42	113.19
25	BA	2580	PSU	O4'-C1'-C2'	2.83	109.14	105.14
24	AX	46	G7M	C2-N1-C6	-2.83	119.93	125.10
24	AX	39	PSU	O2-C2-N1	-2.81	119.69	122.79
24	AX	47	3AU	O4-C4-C5	-2.80	120.24	125.16
24	AX	20	H2U	C5-C6-N1	2.79	120.82	111.61
23	AW	20	H2U	C5-C4-N3	2.78	119.77	116.65
1	AA	1519	MA6	C5-N7-C8	2.76	107.42	103.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1518	MA6	C5-N7-C8	2.75	107.42	103.51
1	AA	1516	2MG	C5-C6-N1	2.75	120.17	113.19
25	BA	2251	OMG	C5-C6-N1	2.75	120.16	113.19
1	AA	966	2MG	O6-C6-C5	-2.74	119.34	126.60
1	AA	966	2MG	N1-C2-N3	-2.74	119.72	123.95
25	BA	1917	PSU	O2-C2-N1	-2.72	119.80	122.79
1	AA	1207	2MG	N1-C2-N3	-2.70	119.78	123.95
25	BA	746	PSU	O2'-C2'-C3'	2.69	120.52	111.82
23	AW	20	H2U	O2-C2-N1	-2.69	119.73	123.11
25	BA	745	1MG	C5-C6-N1	2.68	120.09	114.91
25	BA	2069	G7M	N9-C8-N7	-2.68	105.59	112.21
1	AA	516	PSU	C6-N1-C2	-2.68	119.95	122.68
1	AA	1519	MA6	C4-N9-C8	2.67	108.63	105.73
25	BA	2251	OMG	C1'-N9-C4	2.66	134.41	126.50
24	AX	16	H2U	C5-C6-N1	2.66	120.36	111.61
25	BA	1618	6MZ	C5-C6-N1	2.64	121.01	118.20
25	BA	2503	2MA	C4-C5-N7	-2.61	107.43	110.62
1	AA	527	G7M	N9-C8-N7	-2.61	105.77	112.21
24	AX	37	MIA	C4-N9-C8	2.60	108.55	105.73
25	BA	2449	H2U	C5-C6-N1	2.60	120.18	111.61
1	AA	527	G7M	N2-C2-N1	2.60	122.25	116.71
25	BA	2580	PSU	O2-C2-N1	-2.60	119.93	122.79
25	BA	2580	PSU	C6-N1-C2	-2.57	120.05	122.68
1	AA	1207	2MG	O6-C6-C5	-2.56	119.81	126.60
1	AA	1516	2MG	O6-C6-C5	-2.56	119.81	126.60
23	AW	55	PSU	O2-C2-N1	-2.55	119.98	122.79
25	BA	1618	6MZ	C4-N9-C8	2.54	108.49	105.73
25	BA	2069	G7M	N2-C2-N1	2.54	122.13	116.71
25	BA	2605	PSU	O2-C2-N1	-2.54	119.99	122.79
25	BA	2498	OMC	O3'-C3'-C2'	2.53	118.35	111.17
1	AA	966	2MG	CM2-N2-C2	-2.51	118.32	123.86
25	BA	2504	PSU	O2-C2-N1	-2.50	120.04	122.79
25	BA	1835	2MG	O6-C6-C5	-2.50	119.97	126.60
23	AW	20	H2U	C5-C6-N1	2.50	119.84	111.61
25	BA	2604	PSU	C6-N1-C2	-2.45	120.18	122.68
1	AA	1516	2MG	N1-C2-N3	-2.45	120.17	123.95
24	AX	20	H2U	C5-C4-N3	2.44	119.39	116.65
25	BA	2251	OMG	C8-N7-C5	2.44	108.66	104.24
25	BA	2030	6MZ	N3-C4-N9	2.44	131.10	127.08
25	BA	2503	2MA	N3-C4-N9	2.43	130.37	126.99
25	BA	746	PSU	C6-C5-C4	2.43	119.90	118.20
25	BA	2030	6MZ	C4-C5-N7	-2.43	107.66	110.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	1962	5MC	C5-C6-N1	-2.43	120.84	123.34
25	BA	955	PSU	O2-C2-N1	-2.42	120.13	122.79
24	AX	37	MIA	C16-C14-C15	-2.42	109.27	114.60
25	BA	2445	2MG	C4-C5-N7	-2.41	106.91	110.72
25	BA	2580	PSU	C3'-C2'-C1'	2.40	104.43	101.64
24	AX	46	G7M	N9-C8-N7	-2.39	106.29	112.21
1	AA	1402	4OC	C6-C5-C4	2.39	119.89	116.96
25	BA	2445	2MG	O6-C6-C5	-2.38	120.29	126.60
24	AX	54	5MU	O2-C2-N1	-2.38	119.63	122.79
25	BA	2457	PSU	C6-N1-C2	-2.37	120.26	122.68
25	BA	2445	2MG	N1-C2-N3	-2.37	120.29	123.95
24	AX	39	PSU	C6-N1-C2	-2.36	120.27	122.68
25	BA	1835	2MG	N1-C2-N3	-2.34	120.33	123.95
25	BA	2069	G7M	N9-C4-N3	2.34	130.63	125.94
25	BA	746	PSU	C3'-C2'-C1'	2.34	104.36	101.64
25	BA	955	PSU	C6-N1-C2	-2.33	120.30	122.68
25	BA	2251	OMG	O6-C6-C5	-2.32	120.44	126.60
24	AX	16	H2U	O2-C2-N1	-2.32	120.20	123.11
25	BA	1911	PSU	O2-C2-N1	-2.31	120.24	122.79
1	AA	1207	2MG	C8-N7-C5	2.31	108.42	104.24
25	BA	746	PSU	O2-C2-N1	-2.30	120.25	122.79
25	BA	2445	2MG	C8-N7-C5	2.30	108.41	104.24
24	AX	32	PSU	O2-C2-N1	-2.29	120.27	122.79
1	AA	966	2MG	O3'-C3'-C4'	2.28	117.66	111.05
24	AX	55	PSU	C6-N1-C2	-2.27	120.36	122.68
23	AW	55	PSU	C3'-C2'-C1'	2.26	104.27	101.64
25	BA	1835	2MG	C4-C5-N7	-2.26	107.15	110.72
1	AA	1207	2MG	C6-C5-N7	2.26	134.44	130.25
23	AW	8	4SU	O2-C2-N1	-2.25	119.79	122.79
25	BA	1915	3TD	O4'-C1'-C2'	2.25	108.31	105.14
1	AA	1516	2MG	C6-C5-N7	2.24	134.42	130.25
1	AA	516	PSU	C3'-C2'-C1'	2.23	104.24	101.64
23	AW	54	5MU	O2-C2-N1	-2.22	119.83	122.79
25	BA	2251	OMG	C8-N9-C4	2.21	110.25	106.05
25	BA	1835	2MG	C8-N7-C5	2.20	108.23	104.24
1	AA	1207	2MG	C4-C5-N7	-2.20	107.23	110.72
1	AA	966	2MG	N9-C4-N3	2.19	130.34	125.94
25	BA	2445	2MG	C5-C4-N9	2.19	109.60	105.63
1	AA	1516	2MG	C4-C5-N7	-2.18	107.27	110.72
24	AX	20	H2U	O2-C2-N1	-2.18	120.37	123.11
25	BA	1917	PSU	O4'-C1'-C2'	2.18	108.22	105.14
24	AX	55	PSU	C6-C5-C4	2.18	119.72	118.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	AX	46	G7M	C5-C4-N9	2.18	110.66	105.89
24	AX	37	MIA	C1'-N9-C8	-2.17	122.23	127.14
24	AX	37	MIA	C5-C6-N1	2.17	120.52	118.20
1	AA	527	G7M	N9-C4-N3	2.17	130.29	125.94
25	BA	1911	PSU	C6-N1-C2	-2.15	120.48	122.68
12	AL	89	D2T	CB-CA-N	2.14	113.67	109.10
1	AA	1516	2MG	C5-C4-N9	2.14	109.52	105.63
24	AX	8	4SU	O2-C2-N1	-2.13	119.95	122.79
1	AA	966	2MG	C8-N7-C5	2.13	108.09	104.24
25	BA	1962	5MC	C1'-N1-C6	-2.13	117.58	121.12
25	BA	2445	2MG	C6-C5-N7	2.12	134.20	130.25
25	BA	2457	PSU	O4'-C1'-C2'	2.12	108.13	105.14
25	BA	2504	PSU	C6-N1-C2	-2.12	120.52	122.68
25	BA	2030	6MZ	C5-C6-N1	2.10	120.44	118.20
23	AW	55	PSU	C6-N1-C2	-2.09	120.55	122.68
25	BA	745	1MG	C1'-N9-C8	2.08	132.63	126.70
1	AA	967	5MC	CM5-C5-C6	-2.08	120.07	122.85
25	BA	2069	G7M	N1-C2-N3	-2.07	119.46	123.32
12	AL	89	D2T	O-C-CA	-2.06	119.37	124.78
1	AA	1407	5MC	CM5-C5-C6	-2.06	120.10	122.85
25	BA	2605	PSU	C6-N1-C2	-2.06	120.58	122.68
25	BA	1835	2MG	C5-C4-N9	2.05	109.35	105.63
25	BA	745	1MG	C8-N7-C5	2.04	107.94	104.24
23	AW	55	PSU	O4'-C1'-C2'	2.04	108.02	105.14
25	BA	1962	5MC	C1'-N1-C2	2.04	122.97	118.42
24	AX	39	PSU	C6-C5-C4	2.02	119.61	118.20
25	BA	1962	5MC	CM5-C5-C6	-2.02	120.15	122.85
1	AA	1498	UR3	C1'-N1-C2	2.02	120.40	116.99
24	AX	47	3AU	O2-C2-N1	-2.02	120.10	122.79
25	BA	2604	PSU	C6-C5-C4	2.02	119.61	118.20
23	AW	20	H2U	O5'-C5'-C4'	2.01	115.84	108.99
25	BA	746	PSU	C6-N1-C2	-2.01	120.63	122.68
24	AX	37	MIA	C4-C5-N7	-2.01	108.17	110.62
24	AX	32	PSU	C6-N1-C2	-2.01	120.63	122.68
25	BA	955	PSU	C6-C5-C4	2.01	119.60	118.20
24	AX	37	MIA	C12-N6-C6	-2.00	119.58	122.55
24	AX	54	5MU	C5M-C5-C4	2.00	120.97	118.77

There are no chirality outliers.

All (67) 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	1519	MA6	O4'-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	CA-CB-CG-CD
36	BN	81	4D4	OB-CB-CG-CD
23	AW	20	H2U	O4'-C4'-C5'-O5'
24	AX	37	MIA	C12-C13-C14-C15
24	AX	37	MIA	C12-C13-C14-C16
24	AX	46	G7M	O4'-C4'-C5'-O5'
24	AX	46	G7M	C3'-C4'-C5'-O5'
25	BA	746	PSU	C2'-C1'-C5-C6
25	BA	1618	6MZ	C3'-C4'-C5'-O5'
25	BA	1915	3TD	O4'-C1'-C5-C4
25	BA	1915	3TD	O4'-C1'-C5-C6
25	BA	2251	OMG	C1'-C2'-O2'-CM2
25	BA	2552	OMU	O4'-C4'-C5'-O5'
1	AA	967	5MC	O4'-C4'-C5'-O5'
1	AA	967	5MC	C3'-C4'-C5'-O5'
1	AA	1519	MA6	C3'-C4'-C5'-O5'
23	AW	20	H2U	C3'-C4'-C5'-O5'
24	AX	8	4SU	C3'-C4'-C5'-O5'
24	AX	8	4SU	O4'-C4'-C5'-O5'
24	AX	47	3AU	C3'-C4'-C5'-O5'
24	AX	47	3AU	O4'-C4'-C5'-O5'
25	BA	1618	6MZ	O4'-C4'-C5'-O5'
25	BA	1917	PSU	O4'-C4'-C5'-O5'
25	BA	2503	2MA	O4'-C4'-C5'-O5'
25	BA	2503	2MA	C3'-C4'-C5'-O5'
25	BA	2552	OMU	C3'-C4'-C5'-O5'
28	BD	150	MEQ	OE1-CD-CG-CB
28	BD	150	MEQ	NE2-CD-CG-CB
1	AA	516	PSU	C3'-C4'-C5'-O5'
25	BA	1917	PSU	C3'-C4'-C5'-O5'
25	BA	2030	6MZ	O4'-C4'-C5'-O5'
25	BA	2445	2MG	C3'-C4'-C5'-O5'
24	AX	16	H2U	O4'-C4'-C5'-O5'
25	BA	2498	OMC	O4'-C4'-C5'-O5'
1	AA	1207	2MG	O4'-C4'-C5'-O5'
24	AX	37	MIA	C5-C6-N6-C12

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Mol	Chain	Res	Type	Atoms
24	AX	37	MIA	N1-C6-N6-C12
1	AA	516	PSU	O4'-C4'-C5'-O5'
25	BA	2498	OMC	C3'-C4'-C5'-O5'
24	AX	16	H2U	C3'-C4'-C5'-O5'
24	AX	16	H2U	C4'-C5'-O5'-P
25	BA	2445	2MG	O4'-C4'-C5'-O5'
25	BA	1911	PSU	O4'-C4'-C5'-O5'
25	BA	2030	6MZ	C3'-C4'-C5'-O5'
25	BA	1939	5MU	O4'-C4'-C5'-O5'
24	AX	46	G7M	C4'-C5'-O5'-P
25	BA	2069	G7M	C4'-C5'-O5'-P
24	AX	55	PSU	O4'-C1'-C5-C4
36	BN	81	4D4	CG-CD-NE-CZ
25	BA	1618	6MZ	C2'-C1'-N9-C8
12	AL	89	D2T	CG-CB-SB-CB1
24	AX	20	H2U	O4'-C1'-N1-C6
25	BA	746	PSU	O4'-C1'-C5-C6
1	AA	1519	MA6	C4'-C5'-O5'-P
25	BA	1939	5MU	C3'-C4'-C5'-O5'
25	BA	2069	G7M	O4'-C4'-C5'-O5'
24	AX	20	H2U	C2'-C1'-N1-C2
1	AA	527	G7M	C4'-C5'-O5'-P
1	AA	967	5MC	C4'-C5'-O5'-P
24	AX	20	H2U	C4'-C5'-O5'-P

There are no ring outliers.

21 monomers are involved in 32 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	AA	1498	UR3	1	0
25	BA	2069	G7M	2	0
25	BA	2030	6MZ	1	0
24	AX	54	5MU	1	0
28	BD	150	MEQ	3	0
1	AA	966	2MG	2	0
24	AX	8	4SU	1	0
1	AA	527	G7M	2	0
24	AX	37	MIA	3	0
12	AL	89	D2T	2	0
1	AA	1516	2MG	1	0
23	AW	20	H2U	2	0
25	BA	2251	OMG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	BA	1915	3TD	1	0
1	AA	967	5MC	1	0
25	BA	2605	PSU	1	0
1	AA	1519	MA6	1	0
24	AX	16	H2U	3	0
25	BA	1917	PSU	3	0
25	BA	2503	2MA	1	0
23	AW	55	PSU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 492 ligands modelled in this entry, 491 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	$\# Z > 2$
63	PHE	AX	101	24	10,11,12	0.62	0	10,13,15	0.22	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
63	PHE	AX	101	24	-	0/5/6/8	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
63	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
60	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

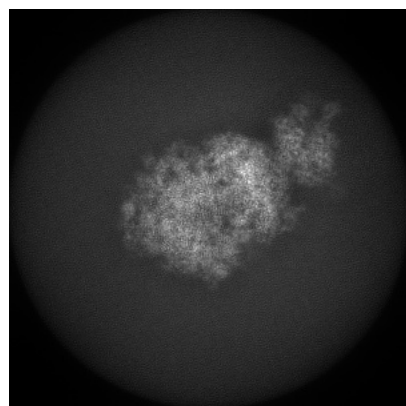
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11426. These allow visual inspection of the internal detail of the map and identification of artifacts.

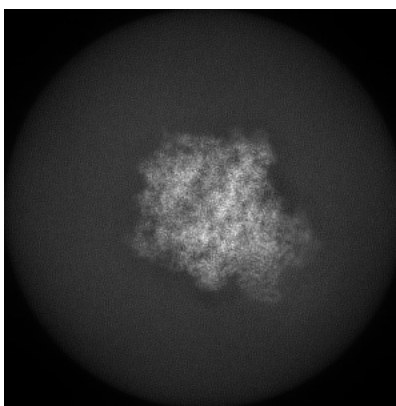
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

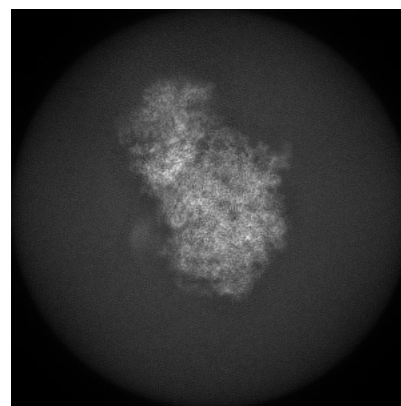
6.1.1 Primary map



X

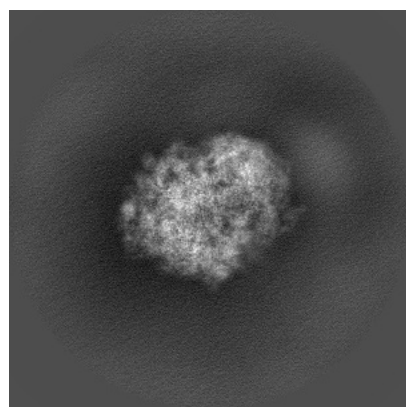


Y

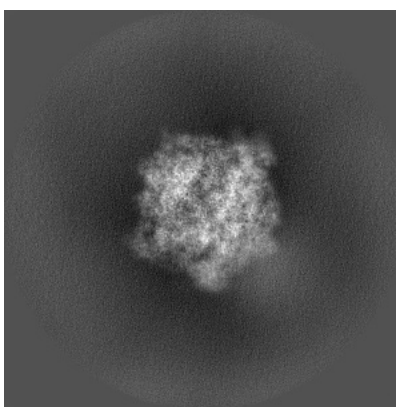


Z

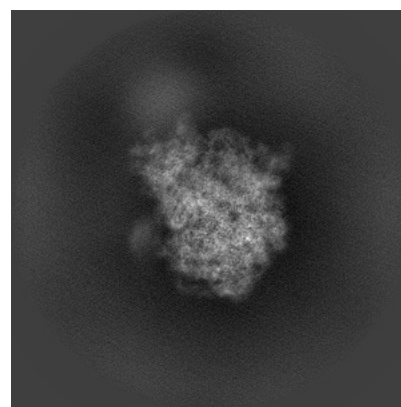
6.1.2 Raw map



X



Y

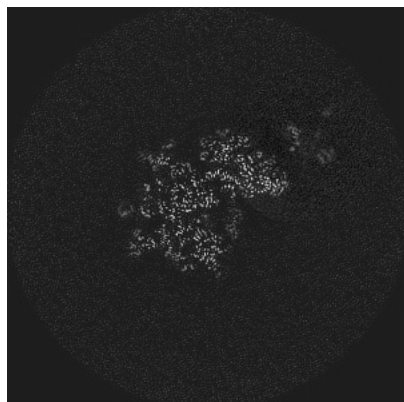


Z

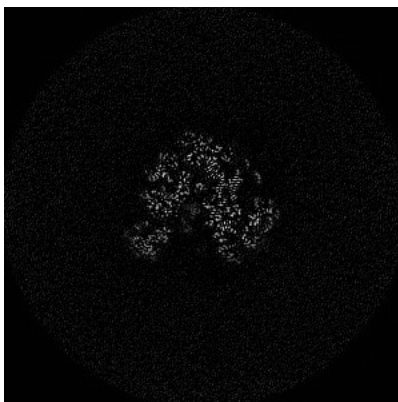
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

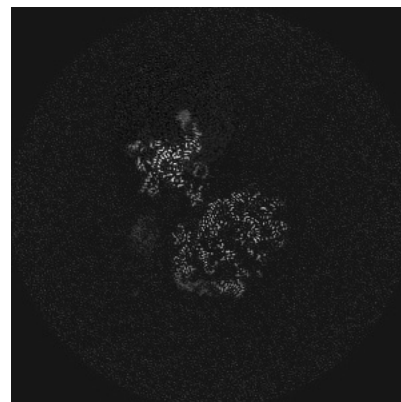
6.2.1 Primary map



X Index: 260

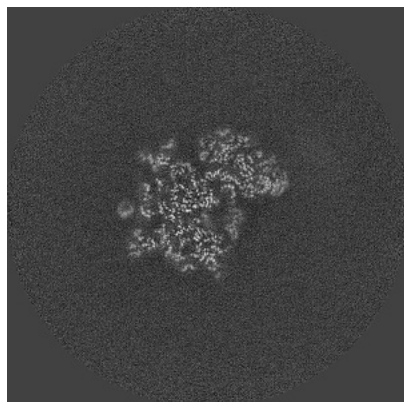


Y Index: 260

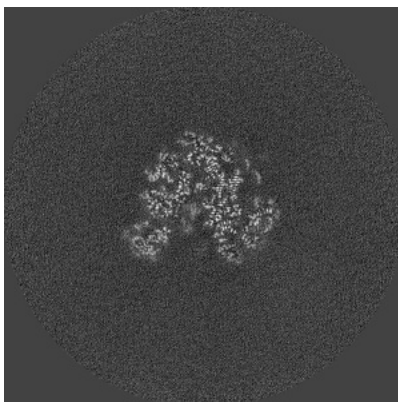


Z Index: 260

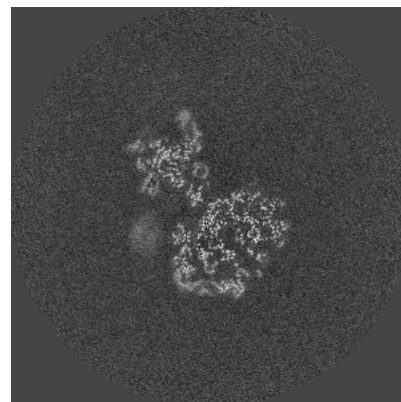
6.2.2 Raw map



X Index: 260



Y Index: 260

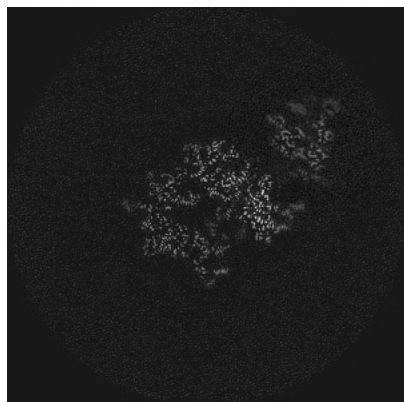


Z Index: 260

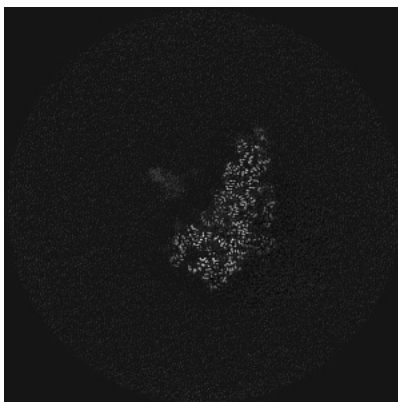
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

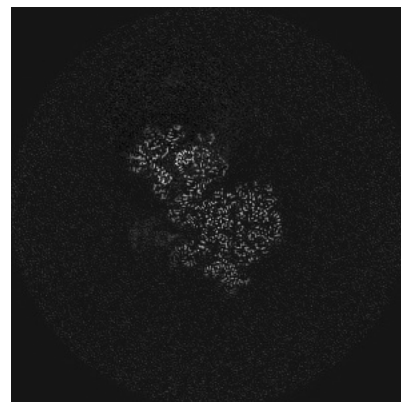
6.3.1 Primary map



X Index: 227

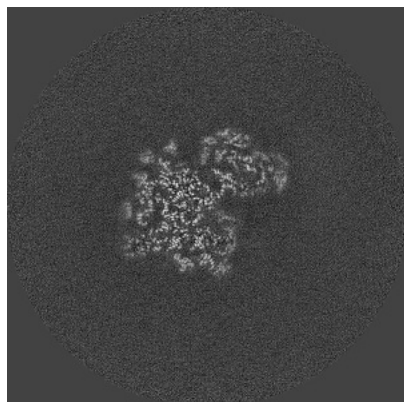


Y Index: 312

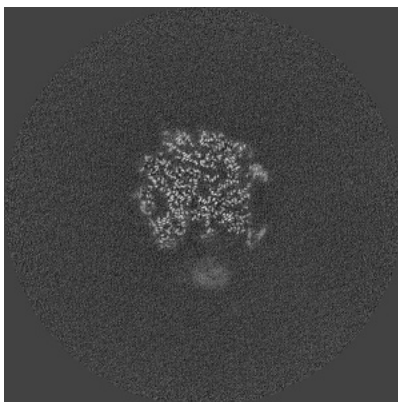


Z Index: 277

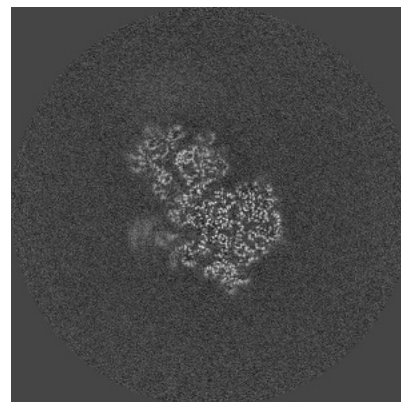
6.3.2 Raw map



X Index: 266



Y Index: 231

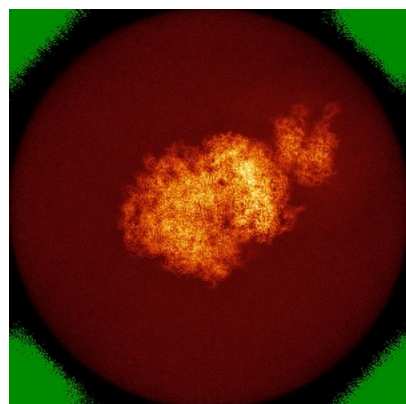


Z Index: 277

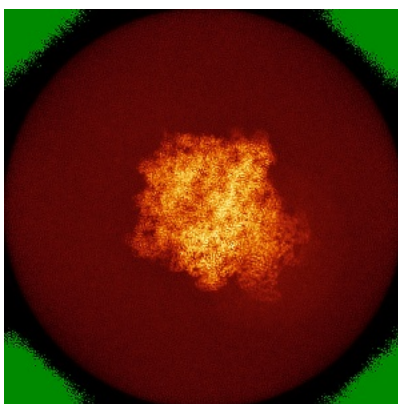
The images above show the largest variance slices of the map in three orthogonal directions.

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

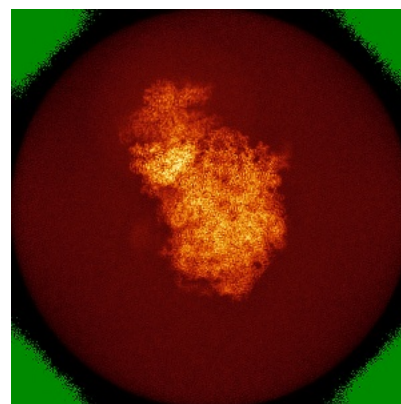
6.4.1 Primary map



X

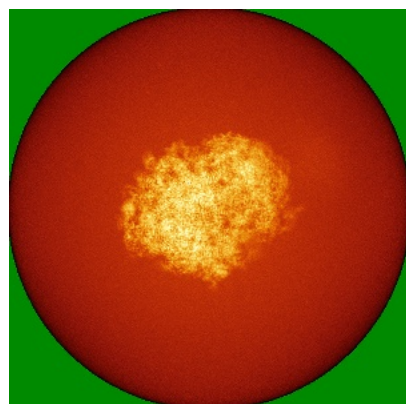


Y

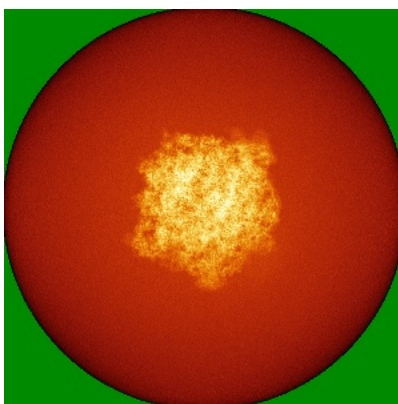


Z

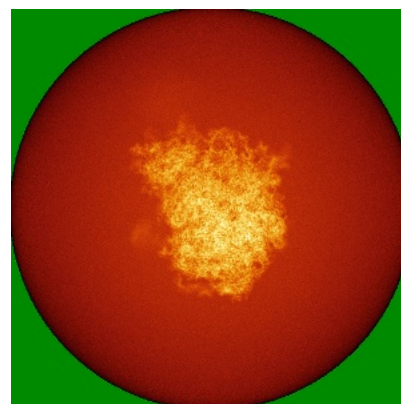
6.4.2 Raw map



X



Y

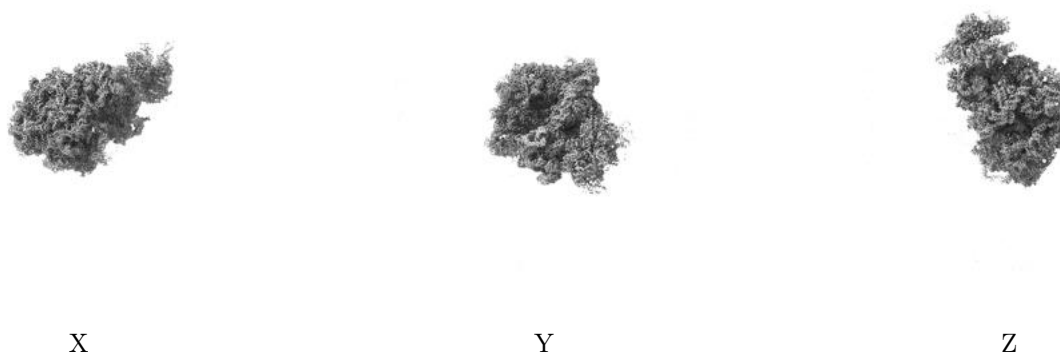


Z

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.

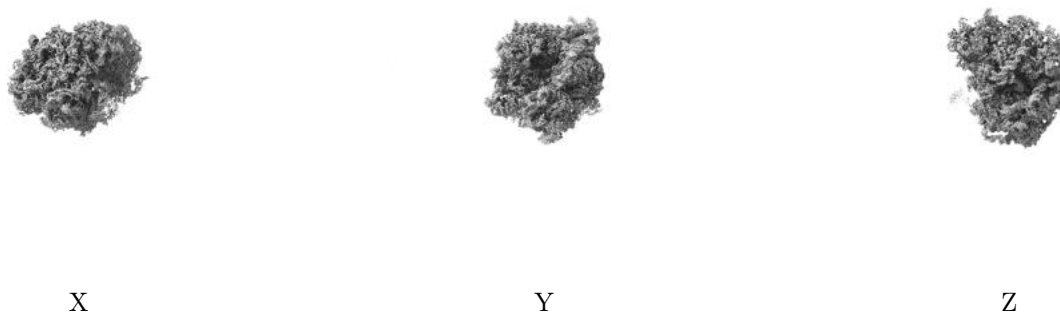
6.5 Orthogonal surface views [i](#)

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.

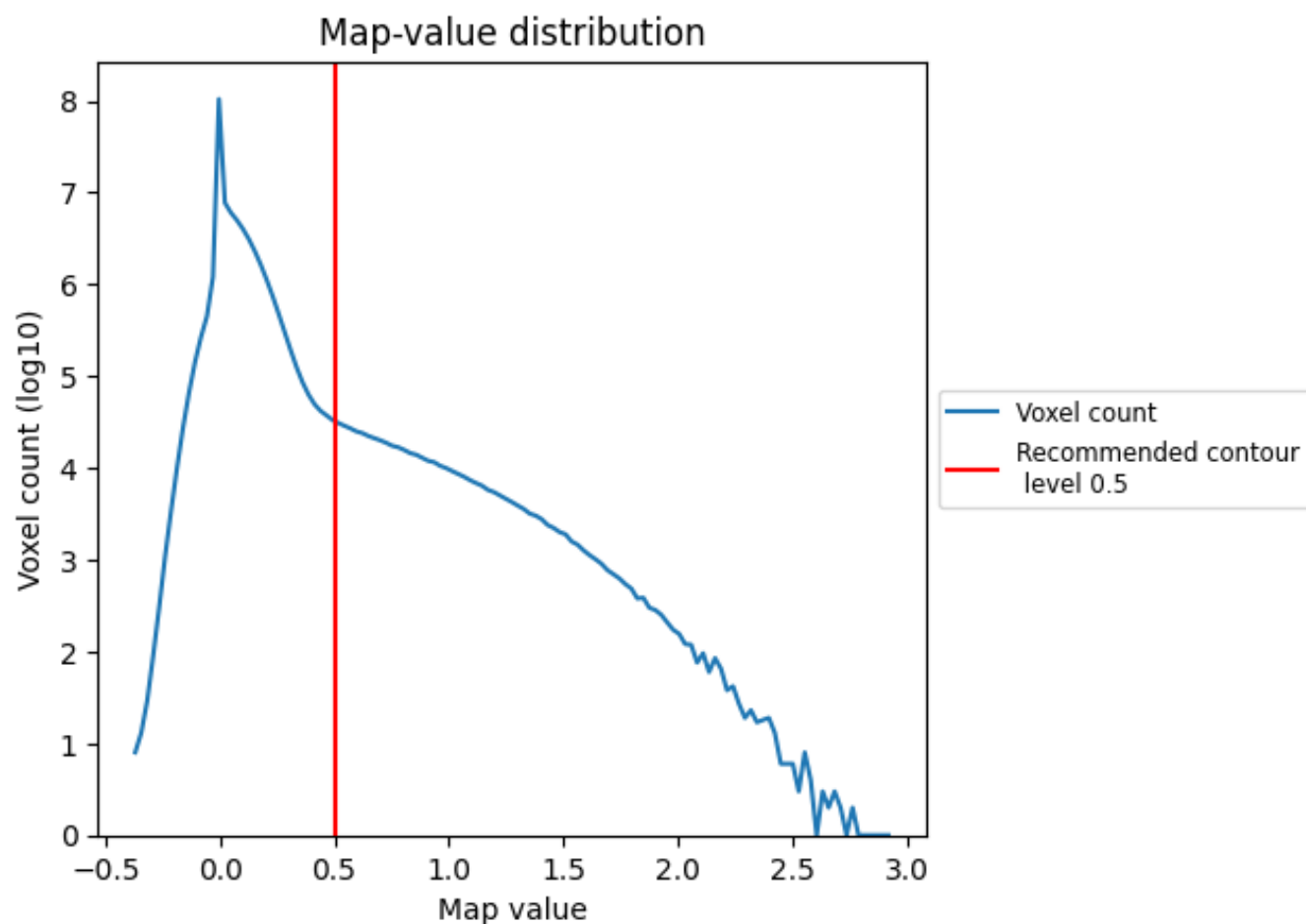
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

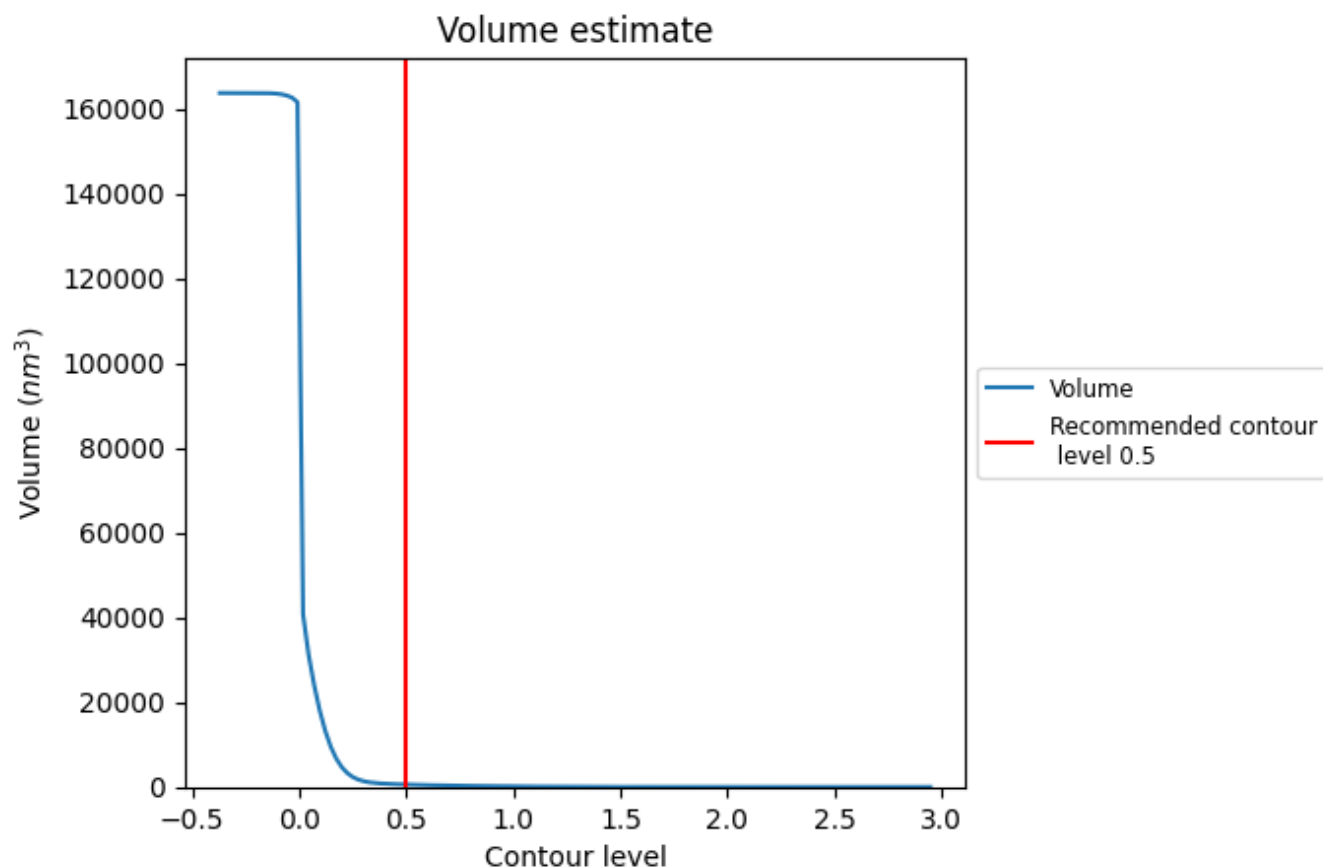
This section contains the results of statistical analysis of the map.

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.

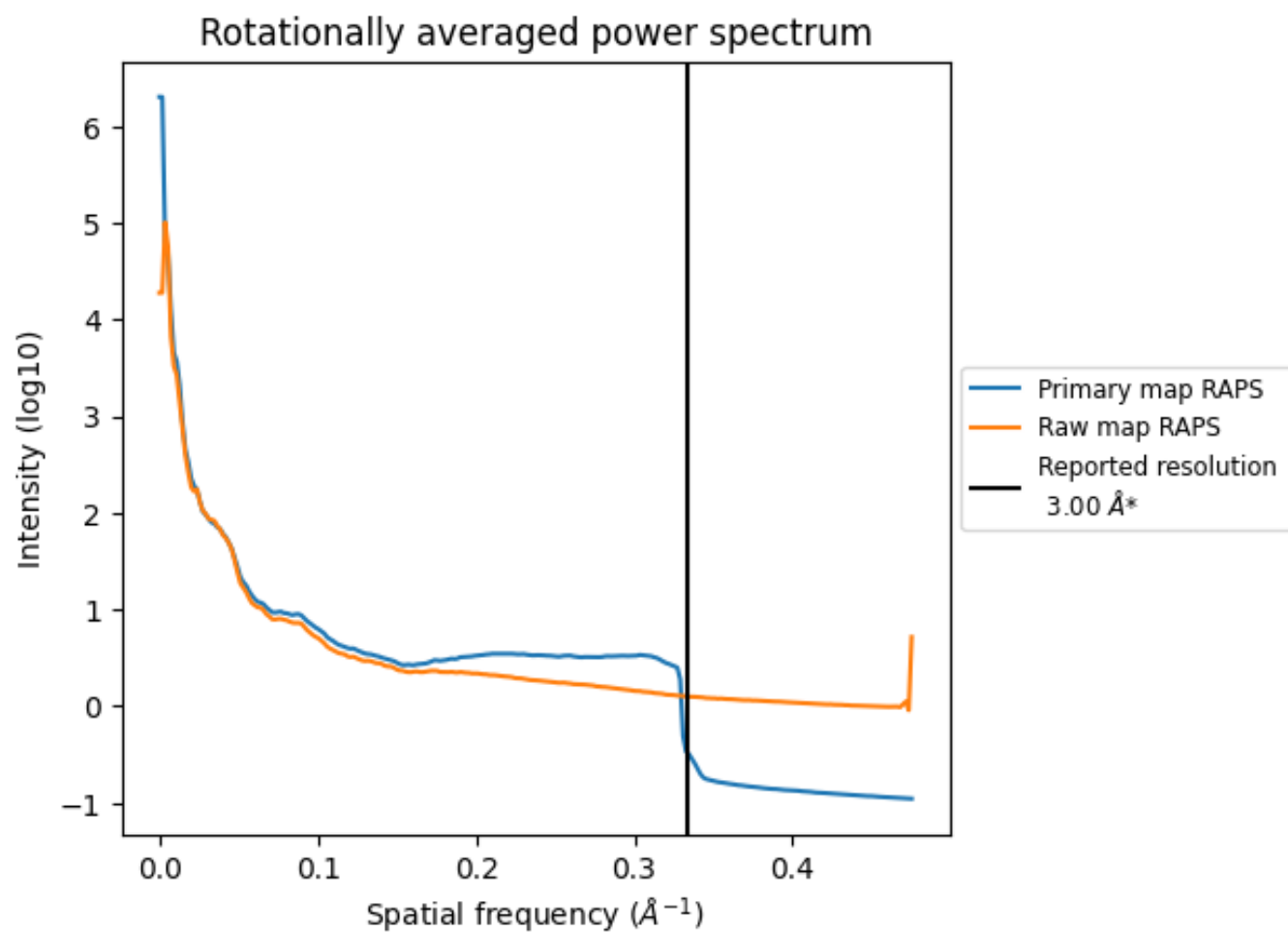
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 568 nm³; this corresponds to an approximate mass of 513 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 ⓘ

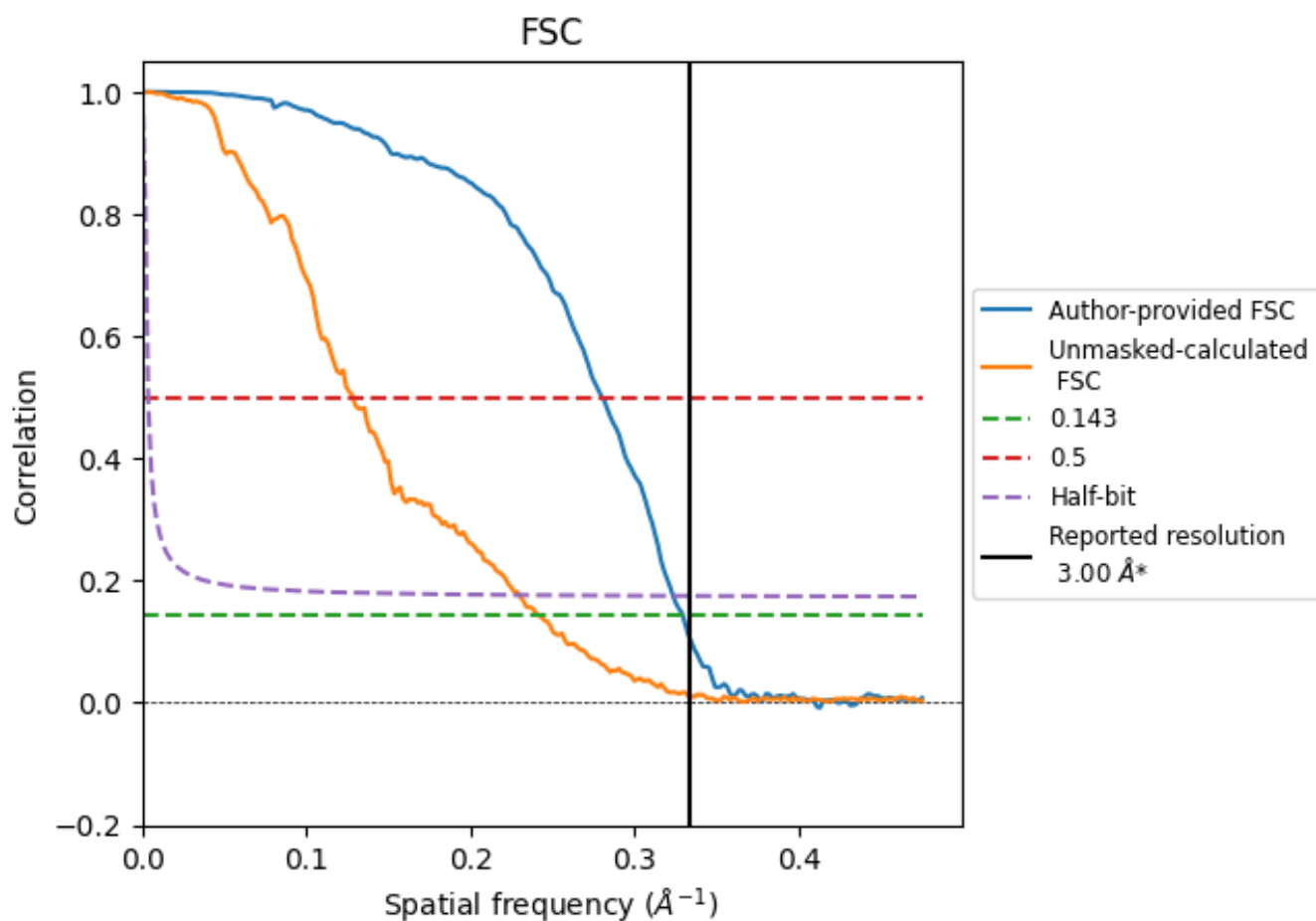


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

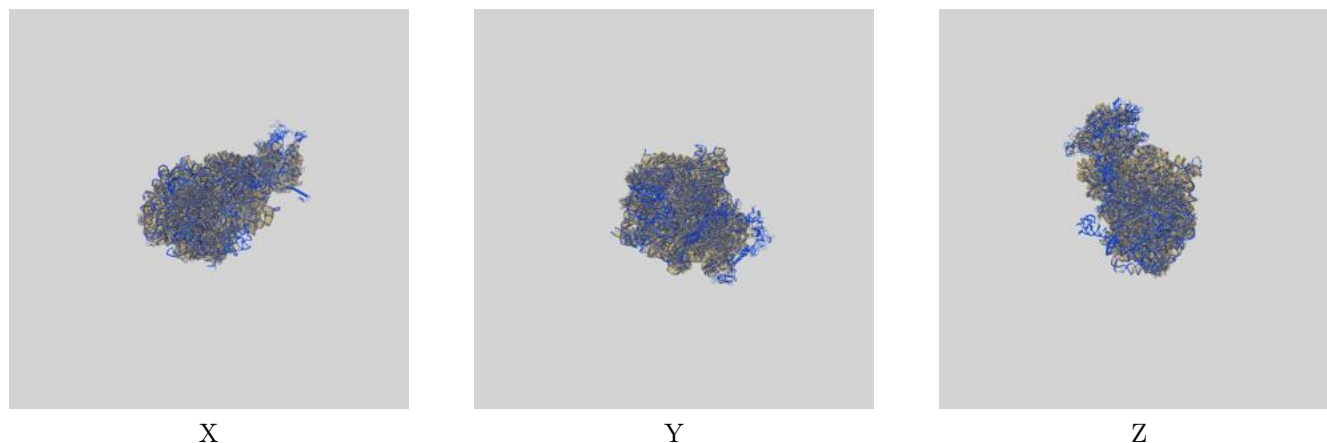
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.04	3.57	3.09
Unmasked-calculated*	4.14	7.79	4.35

*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 4.14 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

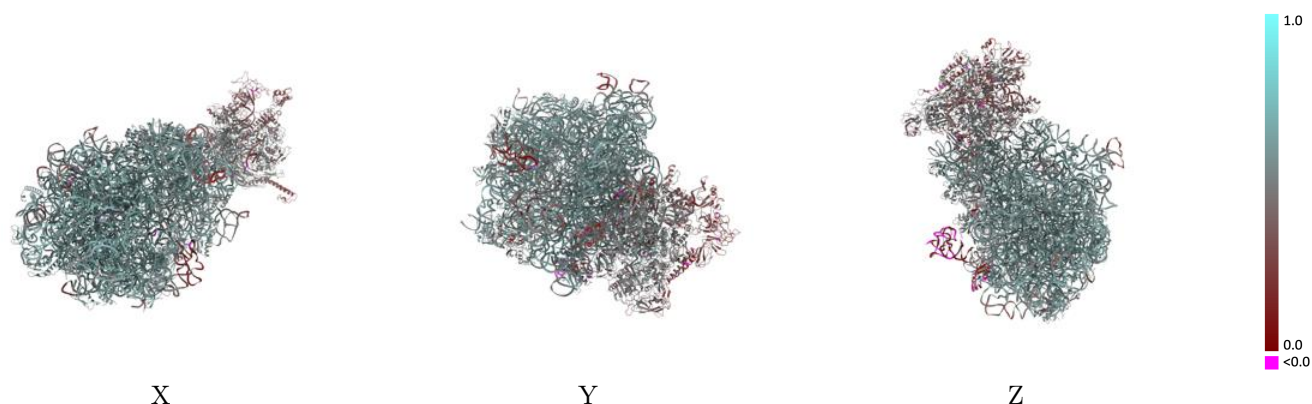
This section contains information regarding the fit between EMDB map EMD-11426 and PDB model 6ZU1. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



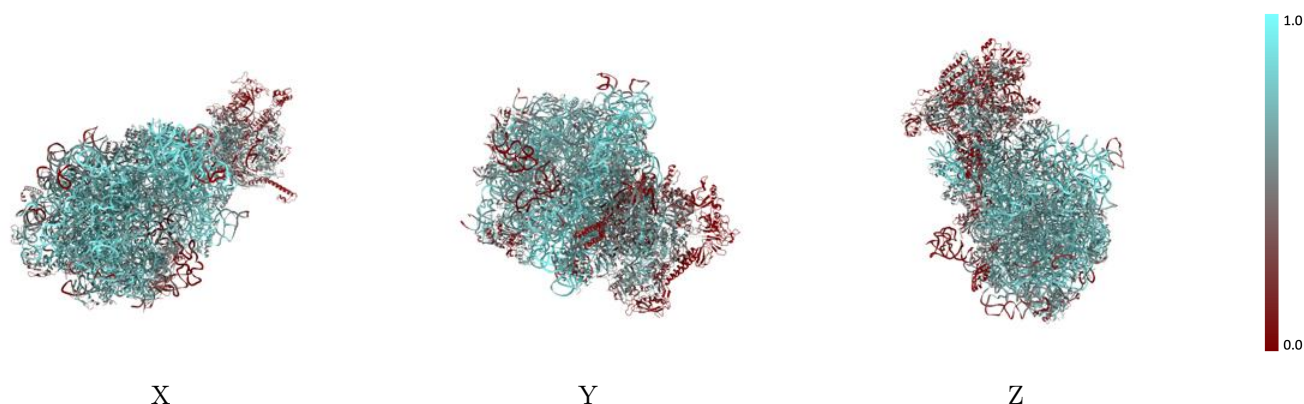
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



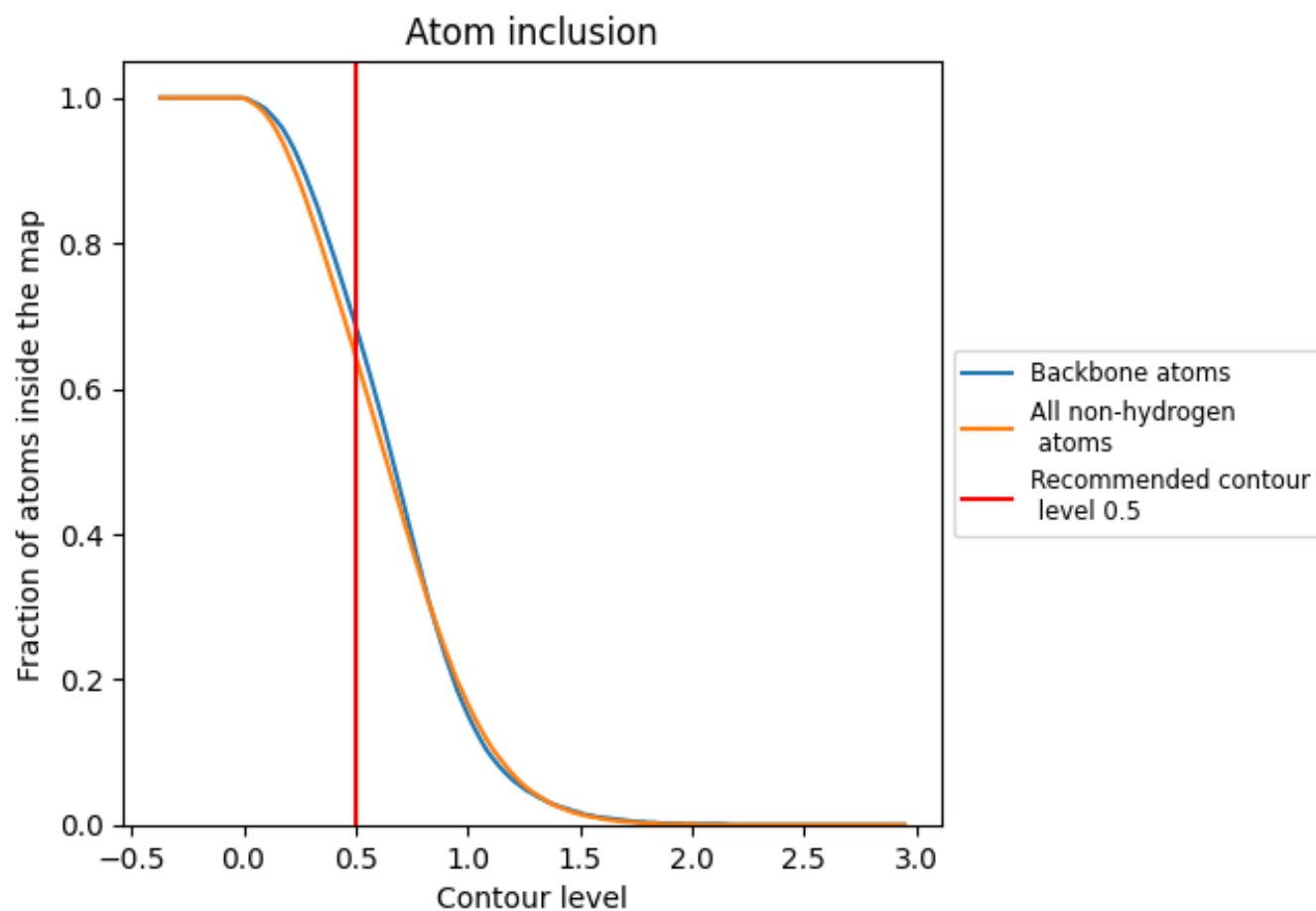
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 [i](#)



At the recommended contour level, 69% of all backbone atoms, 64% 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	 0.6450	 0.5460
AA	 0.8610	 0.5860
AB	 0.2090	 0.4790
AC	 0.7050	 0.5710
AD	 0.5130	 0.5390
AE	 0.6150	 0.5650
AF	 0.4440	 0.5200
AG	 0.5650	 0.5210
AH	 0.6200	 0.5730
AI	 0.7820	 0.5740
AJ	 0.5560	 0.5130
AK	 0.5130	 0.5450
AL	 0.6510	 0.5810
AM	 0.6830	 0.5500
AN	 0.7850	 0.5850
AO	 0.5730	 0.5670
AP	 0.6920	 0.5730
AQ	 0.6120	 0.5600
AR	 0.4900	 0.4880
AS	 0.7710	 0.5720
AT	 0.6730	 0.5650
AU	 0.2410	 0.4860
AV	 0.4880	 0.4840
AW	 0.4880	 0.5310
AX	 0.2890	 0.5250
B1	 0.5790	 0.5800
B2	 0.6030	 0.5850
B3	 0.1590	 0.5180
B4	 0.7200	 0.6100
B5	 0.6820	 0.6140
B6	 0.6640	 0.5950
B7	 0.0670	 0.4030
BA	 0.7310	 0.5750
BB	 0.6990	 0.5900
BC	 0.6560	 0.6040



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Chain	Atom inclusion	Q-score
BD	 0.6460	 0.5980
BE	 0.5100	 0.5700
BF	 0.2480	 0.4980
BG	 0.3540	 0.5290
BH	 0.0320	 0.2420
BK	 0.6590	 0.5930
BL	 0.6120	 0.5920
BM	 0.5930	 0.5850
BN	 0.6300	 0.6000
BO	 0.7020	 0.6090
BP	 0.5320	 0.5620
BQ	 0.5880	 0.5860
BR	 0.6840	 0.6000
BS	 0.5970	 0.5870
BT	 0.6080	 0.5860
BU	 0.4880	 0.5470
BV	 0.4720	 0.5520
BW	 0.5430	 0.5580
BX	 0.6440	 0.6050
BY	 0.6010	 0.5930
BZ	 0.4440	 0.5440
CA	 0.4070	 0.4390
CB	 0.2010	 0.4080
CC	 0.4200	 0.4390
CD	 0.3200	 0.4070
CE	 0.0000	 0.2060
CN	 0.1570	 0.2870
CT	 0.3710	 0.3690