



Full wwPDB EM Validation Report ⓘ

Jun 23, 2026 – 02:02 PM JST

PDB ID : 8IDY / pdb_00008idy
EMDB ID : EMD-35371
Title : human nuclear pre-60S ribosomal particle - State F
Authors : Zhang, Y.; Gao, N.
Deposited on : 2023-02-14
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

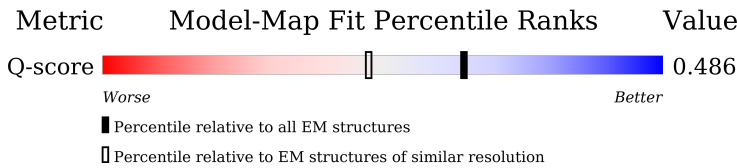
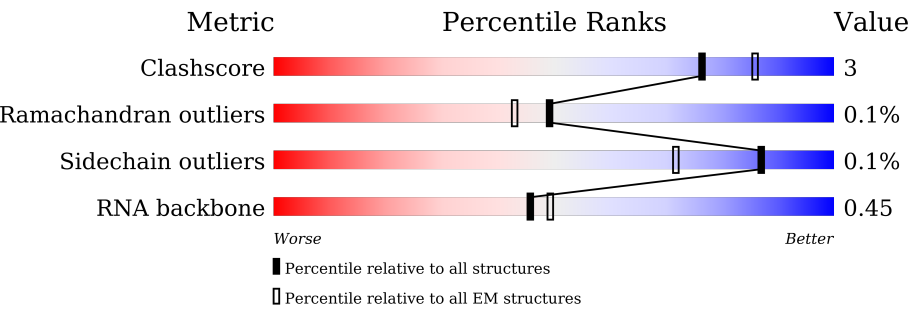
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.00 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	5	120	82% 18%
2	6	245	7% 92% 7%
3	7	163	75% 8% 17%

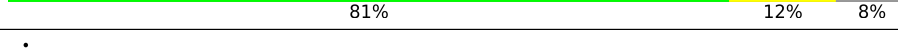
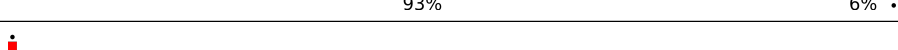
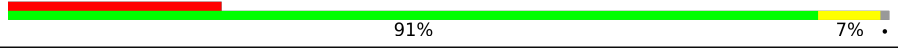
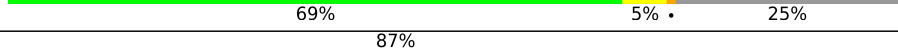
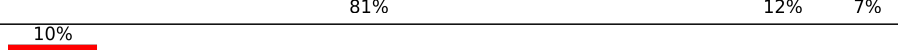
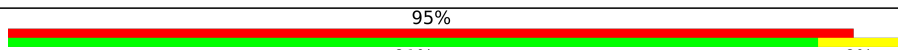
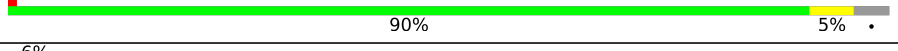
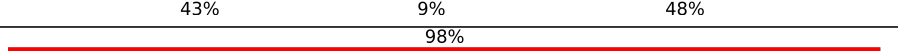
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Mol	Chain	Length	Quality of chain
4	8	156	
5	9	134	
6	B	403	
7	C	159	
8	D	427	
9	E	115	
10	F	117	
11	G	266	
12	H	123	
13	I	192	
14	K	105	
15	L	148	
16	M	97	
17	N	178	
18	O	70	
19	P	51	
20	Q	211	
21	S	215	
22	U	204	
23	V	203	
24	W	106	
25	X	92	
26	Z	188	
27	a	196	
28	b	176	

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Mol	Chain	Length	Quality of chain
29	c	160	
30	e	140	
31	g	156	
32	h	145	
33	i	136	
34	l	137	
35	m	257	
36	n	110	
37	o	288	
38	p	248	
39	r	297	
40	A	731	
41	R	203	
42	J	239	
43	T	99	
44	2	5054	
45	y	165	
46	4	634	
47	d	128	
48	j	125	
49	k	135	
50	Y	184	
51	z	129	
52	t	217	
53	u	687	

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Mol	Chain	Length	Quality of chain
54	v	260	13%8%5%87%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 155910 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 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 2 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	6	244	Total	C	N	O	S	0	0
			1852	1149	318	372	13		

- Molecule 3 is a protein called Probable ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	7	135	Total	C	N	O	S	0	0
			1159	737	225	187	10		

- Molecule 4 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	8	156	Total	C	N	O	P	0	0
			3315	1481	585	1094	155		

- Molecule 5 is a protein called Zinc finger protein 593.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	9	97	Total	C	N	O	S	0	0
			793	484	171	134	4		

- Molecule 6 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	402	Total	C	N	O	S	1	0
			3244	2065	609	556	14		

- Molecule 7 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	93	Total	C	N	O	S	0	0
			764	476	167	117	4		

- Molecule 8 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	358	Total	C	N	O	S	0	0
			2853	1797	570	473	13		

- Molecule 9 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 10 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	109	Total	C	N	O	S	0	0
			868	544	179	139	6		

- Molecule 11 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G	241	Total	C	N	O	S	1	0
			1935	1233	374	324	4		

- Molecule 12 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 13 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	I	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 14 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 15 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 16 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 17 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	165	Total	C	N	O	S	0	0
			1319	836	245	233	5		

- Molecule 18 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	O	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 19 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	P	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 20 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Q	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 21 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S	135	Total	C	N	O	S	0	0
			1111	713	213	178	7		

- Molecule 22 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 23 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 24 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	100	Total	C	N	O	S	0	0
			818	512	168	132	6		

- Molecule 25 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 26 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 27 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	148	Total	C	N	O	S	0	0
			1239	772	266	192	9		

- Molecule 28 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	176	Total	C	N	O	S	0	0
			1461	930	284	236	11		

- Molecule 29 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	155	Total	C	N	O	S	0	0
			1264	801	248	210	5		

- Molecule 30 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 31 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	g	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 32 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	h	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 33 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	i	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 34 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	l	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 35 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	m	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 36 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	n	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 37 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	o	235	Total	C	N	O	S	0	0
			1897	1217	360	316	4		

- Molecule 38 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	p	225	Total	C	N	O	S	1	0
			1878	1207	361	301	9		

- Molecule 39 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	r	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 40 is a protein called G Protein Nucleolar 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	A	307	Total	C	N	O	S	0	0
			2460	1576	419	457	8		

- Molecule 41 is a protein called Translation machinery-associated protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	R	153	Total	C	N	O	S	0	0
			1296	810	248	233	5		

- Molecule 42 is a protein called mRNA turnover protein 4 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	J	223	Total	C	N	O	S	0	0
			1809	1140	309	349	11		

- Molecule 43 is a protein called Leydig cell tumor 10 kDa protein homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	T	44	Total	C	N	O	S	0	0
			343	215	71	56	1		

- Molecule 44 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	2	3641	Total	C	N	O	P	0	0
			77442	34506	14094	25202	3640		

- Molecule 45 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	y	165	Total	C	N	O	S	0	0
			1250	779	232	234	5		

- Molecule 46 is a protein called GTP-binding protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	4	611	Total	C	N	O	S	0	0
			5016	3151	918	920	27		

- Molecule 47 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	d	104	Total	C	N	O	S	0	0
			850	542	149	157	2		

- Molecule 48 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	j	111	Total	C	N	O	S	0	0
			918	578	178	160	2		

- Molecule 49 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	k	129	Total	C	N	O	S	0	0
			1064	673	220	166	5		

- Molecule 50 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Y	167	Total	C	N	O	S	0	0
			1355	848	260	238	9		

- Molecule 51 is a protein called Protein LLP homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	z	67	Total	C	N	O	S	0	0
			581	363	128	88	2		

- Molecule 52 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	t	212	Total	C	N	O	S	0	0
			1708	1092	308	300	8		

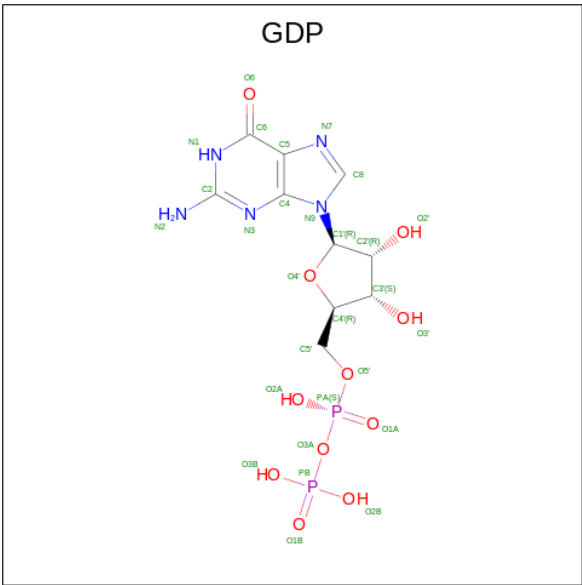
- Molecule 53 is a protein called Protein SDA1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	u	554	Total	C	N	O	S	0	0
			4536	2890	810	804	32		

- Molecule 54 is a protein called Ribosome biogenesis protein NSA2 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	v	35	Total	C	N	O	0	0
			316	196	68	52		

- Molecule 55 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



Mol	Chain	Residues	Atoms					AltConf
55	A	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	A	1	Total	Mg	0
			1	1	

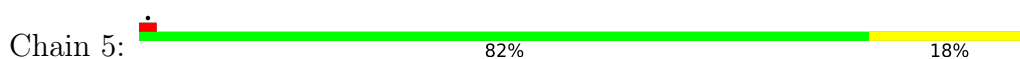
- Molecule 57 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
57	A	1	Total	K	0
			1	1	

3 Residue-property plots [i](#)

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

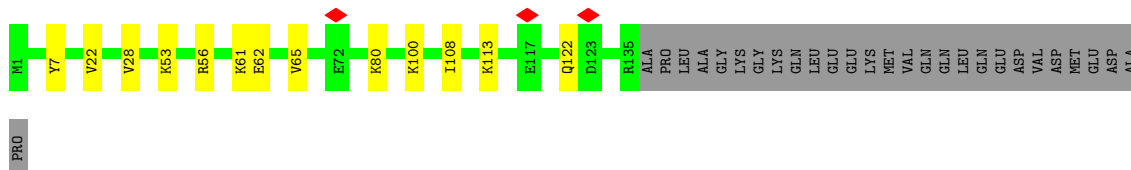
- Molecule 1: 5S rRNA



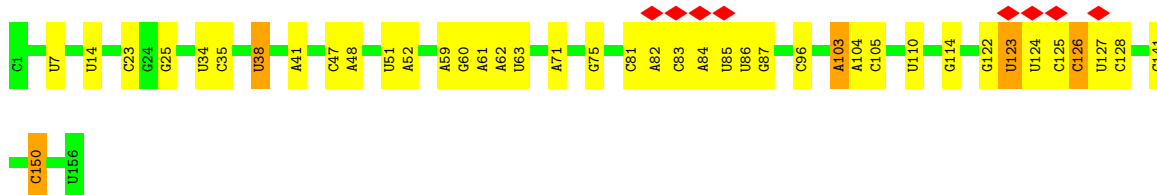
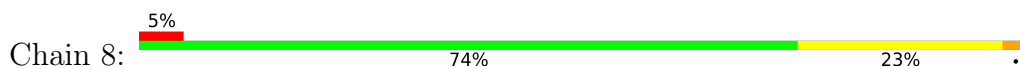
- Molecule 2: Eukaryotic translation initiation factor 6



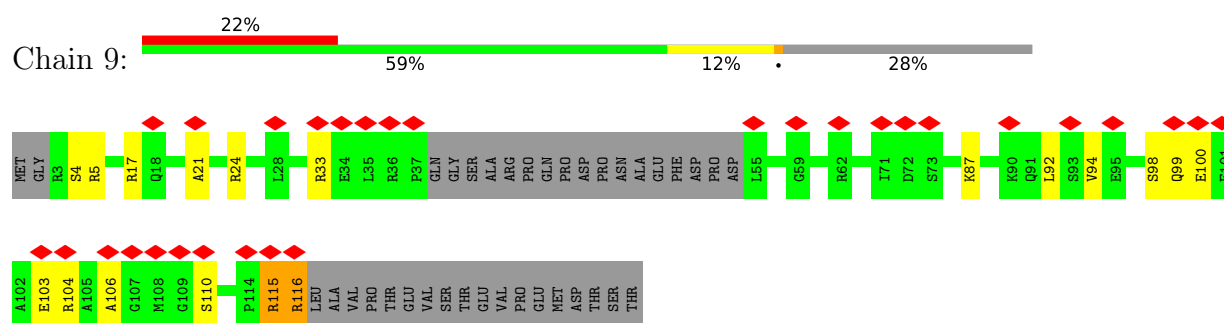
- Molecule 3: Probable ribosome biogenesis protein RLP24



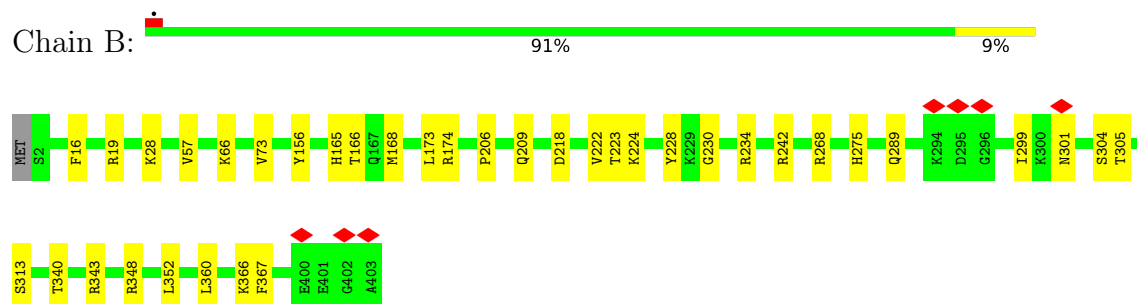
- Molecule 4: 5.8S rRNA



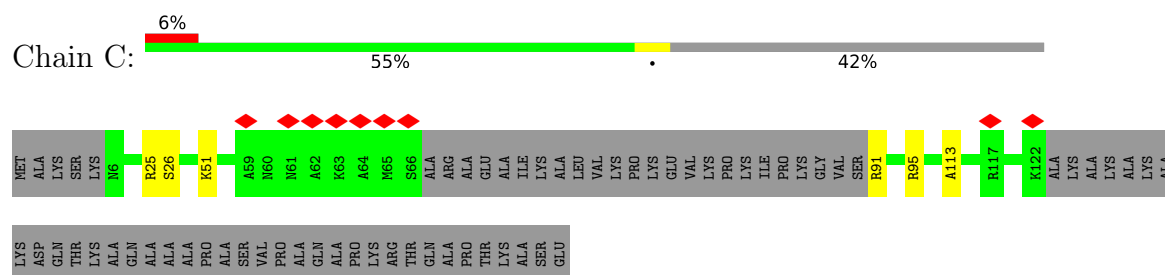
- Molecule 5: Zinc finger protein 593



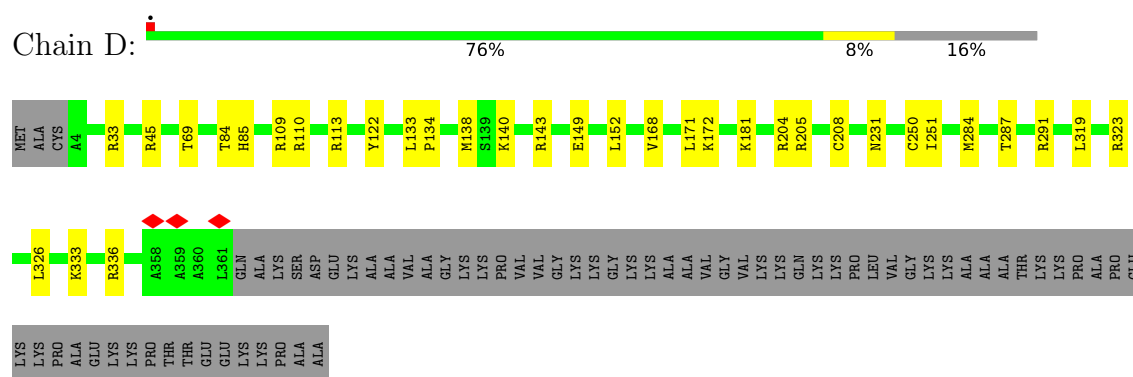
- Molecule 6: 60S ribosomal protein L3



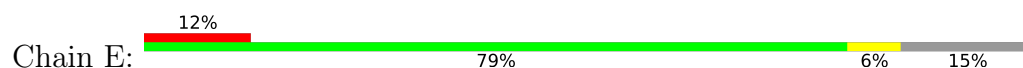
- Molecule 7: 60S ribosomal protein L29

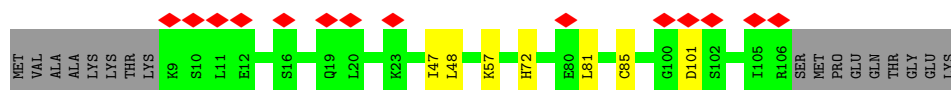


- Molecule 8: 60S ribosomal protein L4

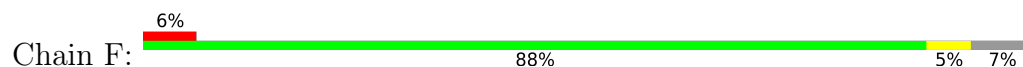


- Molecule 9: 60S ribosomal protein L30

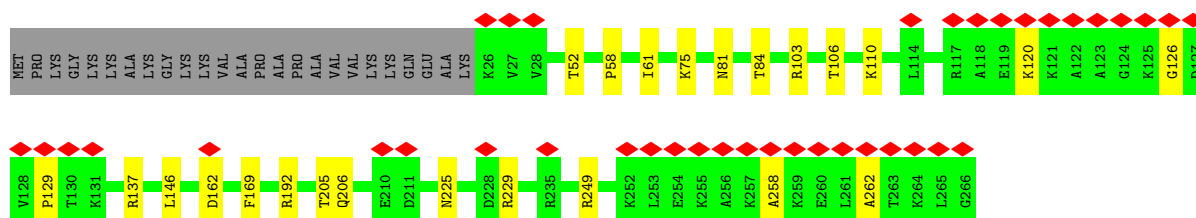
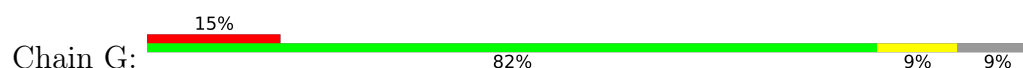




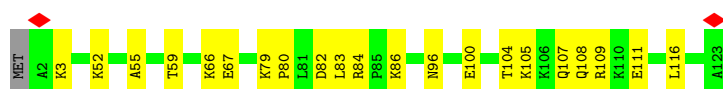
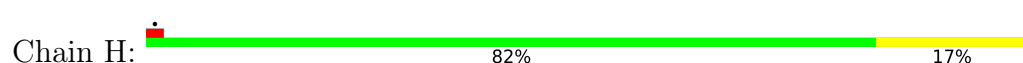
- Molecule 10: 60S ribosomal protein L34



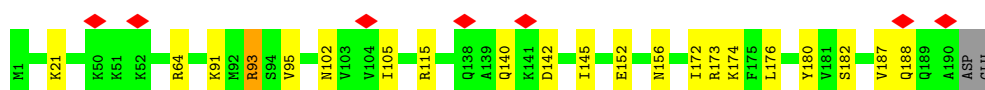
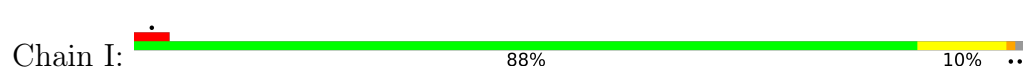
- Molecule 11: 60S ribosomal protein L7a



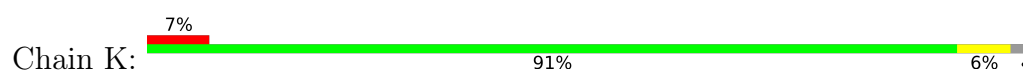
- Molecule 12: 60S ribosomal protein L35



- Molecule 13: 60S ribosomal protein L9

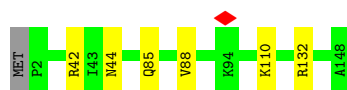


- Molecule 14: 60S ribosomal protein L36



- Molecule 15: 60S ribosomal protein L27a





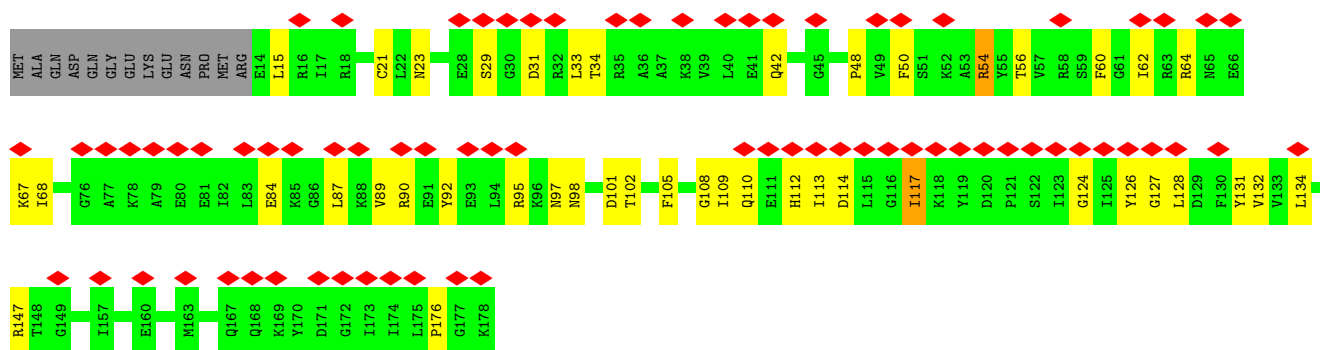
- Molecule 16: 60S ribosomal protein L37

Chain M: 74% 14% 11%



- Molecule 17: 60S ribosomal protein L11

Chain N: 42% 68% 24% 7%



- Molecule 18: 60S ribosomal protein L38

Chain O: 16% 91% 7%



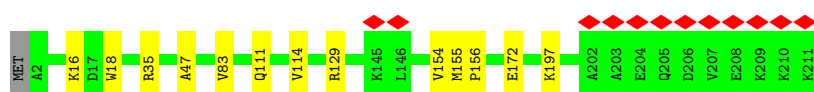
- Molecule 19: 60S ribosomal protein L39

Chain P: 84% 14%

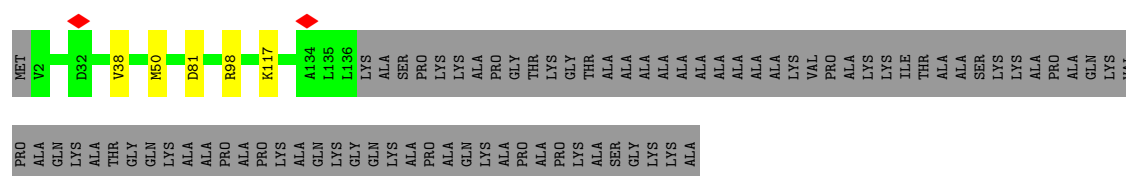


- Molecule 20: 60S ribosomal protein L13

Chain Q: 6% 93% 6%



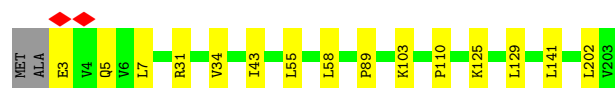
- Molecule 21: 60S ribosomal protein L14



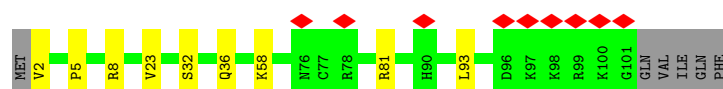
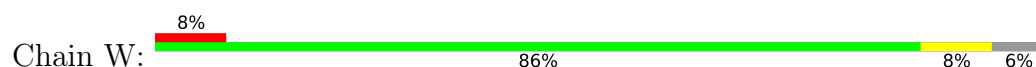
- Molecule 22: 60S ribosomal protein L15



- Molecule 23: 60S ribosomal protein L13a



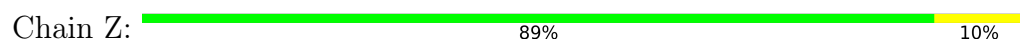
- Molecule 24: 60S ribosomal protein L36a



- Molecule 25: 60S ribosomal protein L37a



- Molecule 26: 60S ribosomal protein L18



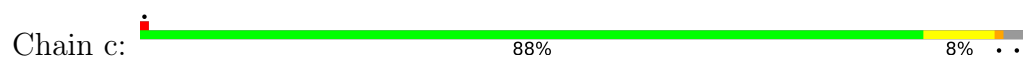
- Molecule 27: 60S ribosomal protein L19



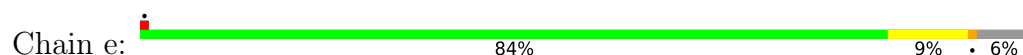
- Molecule 28: 60S ribosomal protein L18a



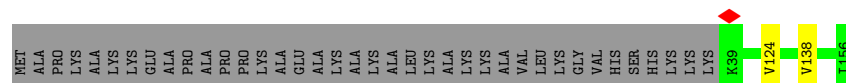
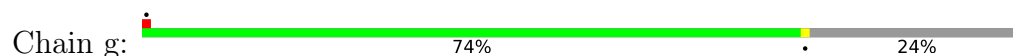
- Molecule 29: 60S ribosomal protein L21



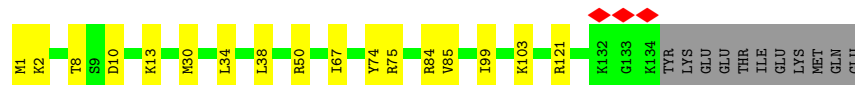
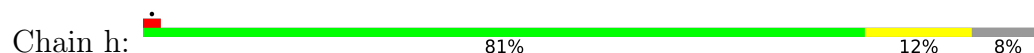
- Molecule 30: 60S ribosomal protein L23



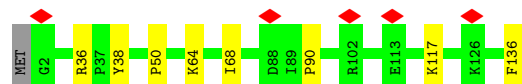
- Molecule 31: 60S ribosomal protein L23a



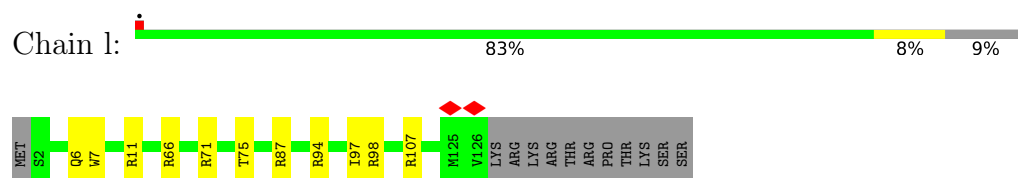
- Molecule 32: 60S ribosomal protein L26



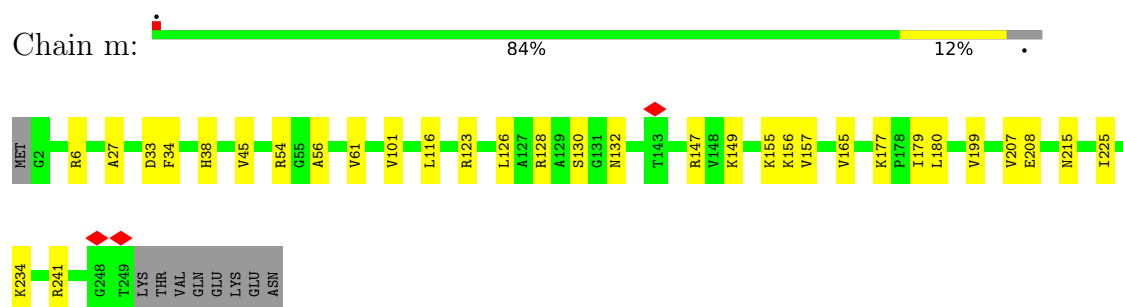
- Molecule 33: 60S ribosomal protein L27



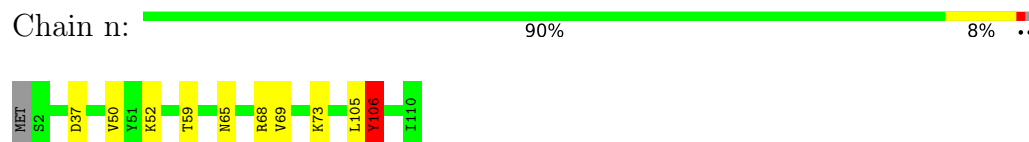
- Molecule 34: 60S ribosomal protein L28



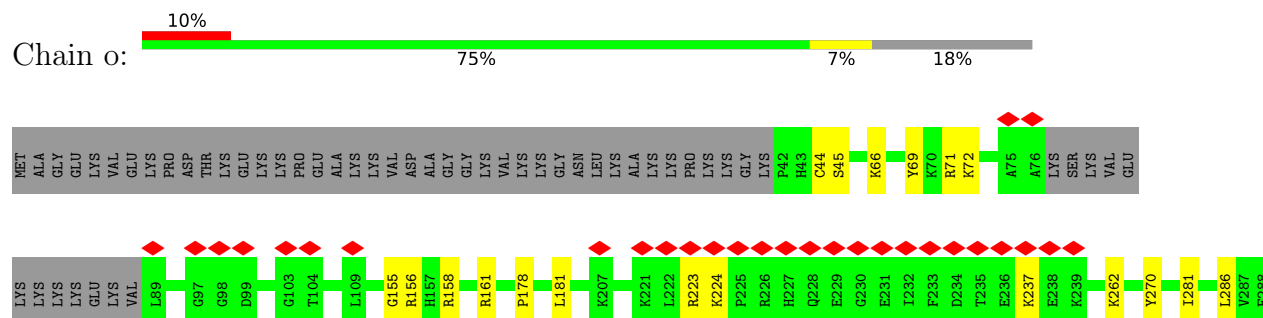
- Molecule 35: 60S ribosomal protein L8



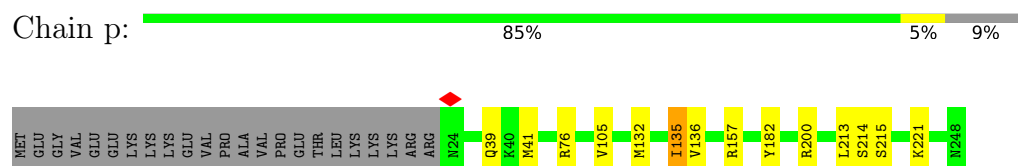
- Molecule 36: 60S ribosomal protein L35a



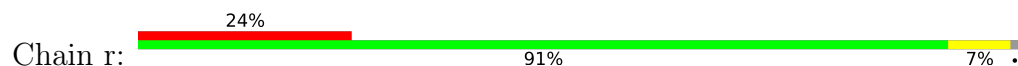
- Molecule 37: 60S ribosomal protein L6



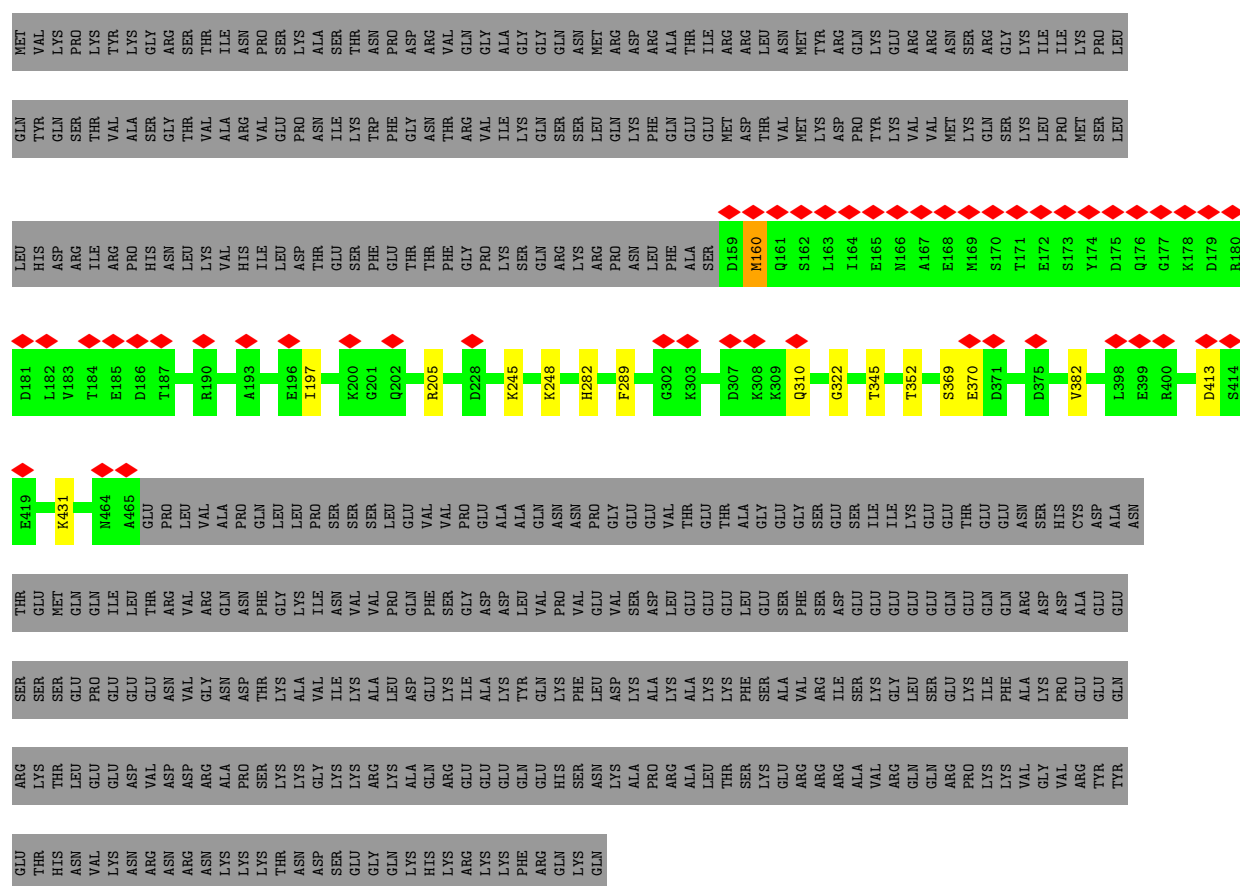
- Molecule 38: 60S ribosomal protein L7



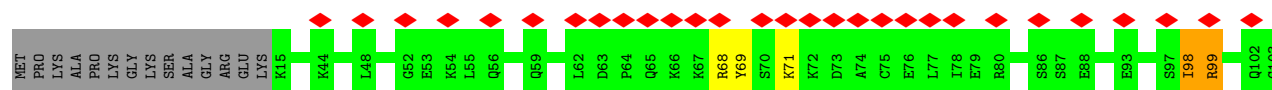
- Molecule 39: 60S ribosomal protein L5

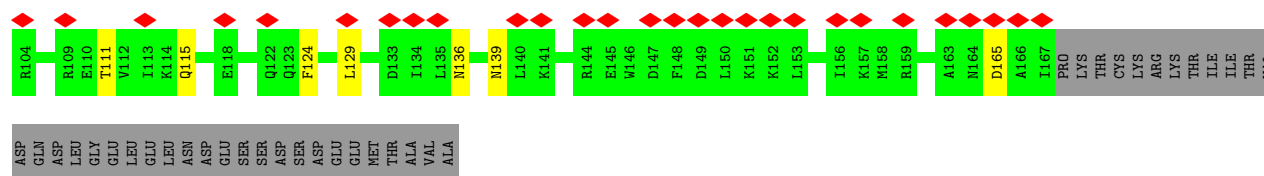


- Molecule 40: G Protein Nucleolar 2

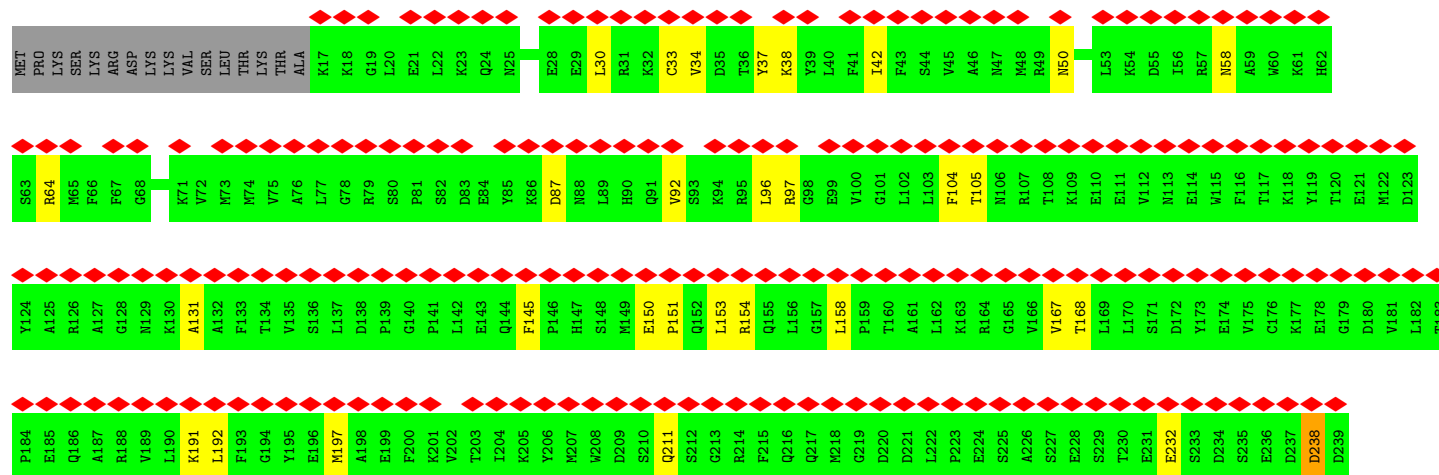
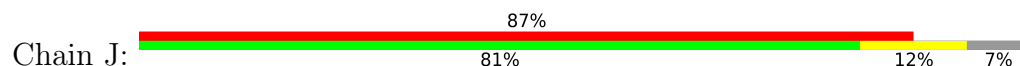


- Molecule 41: Translation machinery-associated protein 16

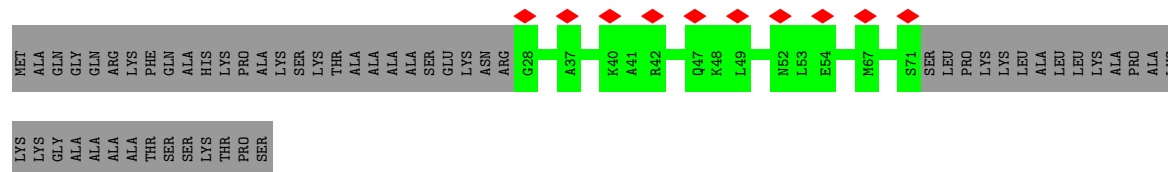




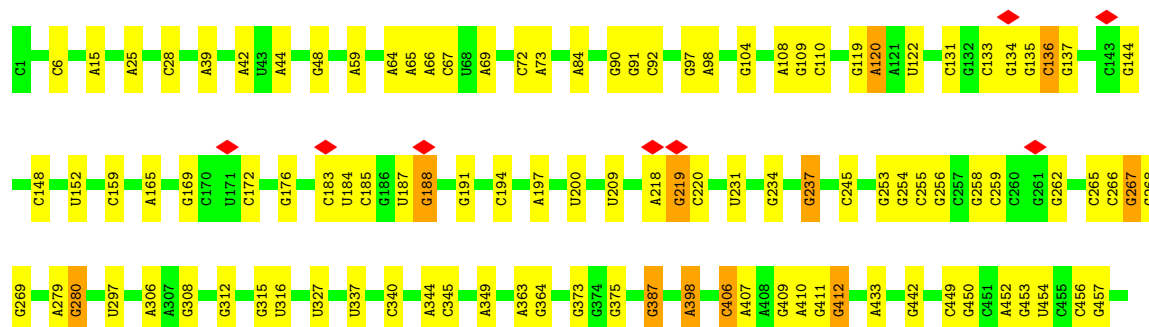
• Molecule 42: mRNA turnover protein 4 homolog



• Molecule 43: Leydig cell tumor 10 kDa protein homolog



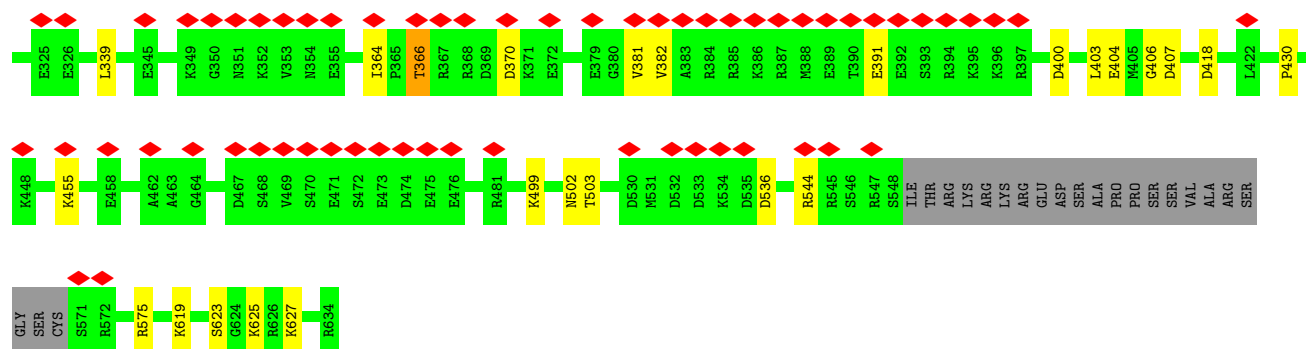
• Molecule 44: 28S rRNA



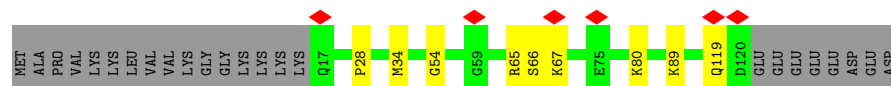
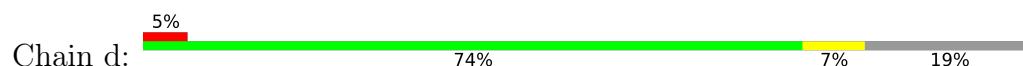




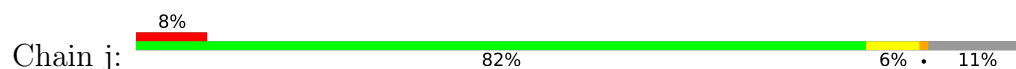




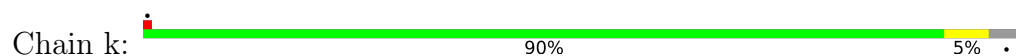
- Molecule 47: 60S ribosomal protein L22



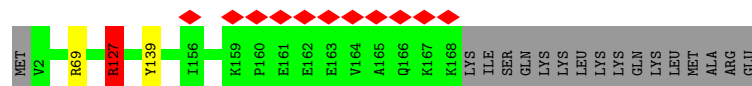
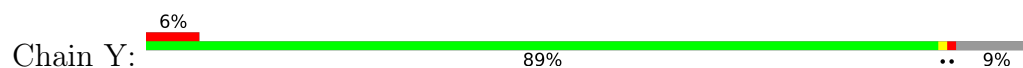
- Molecule 48: 60S ribosomal protein L31



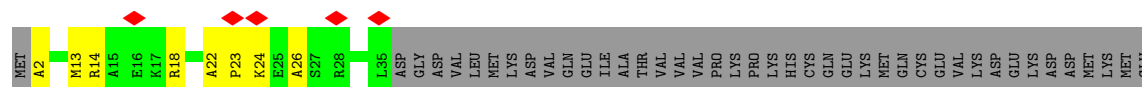
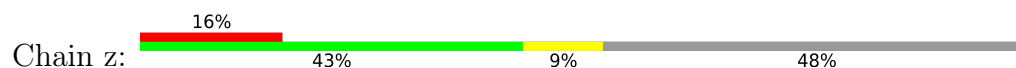
- Molecule 49: 60S ribosomal protein L32

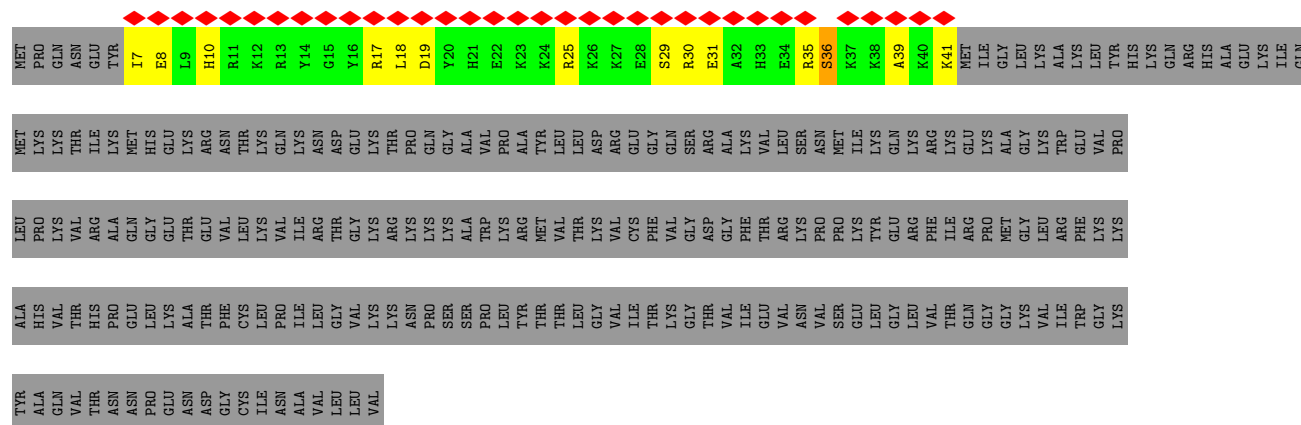


- Molecule 50: 60S ribosomal protein L17



- Molecule 51: Protein LLP homolog





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	41193	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 ($e^-/\text{\AA}^2$)	1.8	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.223	Depositor
Minimum map value	-0.065	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.0365	Depositor
Map size (Å)	548.0, 548.0, 548.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.37, 1.37, 1.37	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: A2M, B9B, 5MC, B8T, OMG, OMU, P7G, BGH, MHG, E6G, B8H, GDP, E7G, M7A, 1MA, B9H, 5MU, UR3, 2MG, I4U, P4U, B8Q, K, 6MZ, OMC, 7MG, MG, B8K, B8W

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	5	0.22	0/2858	0.39	0/4455
2	6	0.30	0/1877	0.71	0/2554
3	7	0.34	0/1181	0.74	2/1563 (0.1%)
4	8	0.24	0/3679	0.43	0/5732
5	9	0.33	0/808	0.85	4/1076 (0.4%)
6	B	0.28	0/3315	0.70	3/4435 (0.1%)
7	C	0.27	0/777	0.70	0/1026
8	D	0.28	0/2907	0.69	4/3905 (0.1%)
9	E	0.30	0/774	0.66	0/1038
10	F	0.26	0/878	0.65	0/1170
11	G	0.33	0/1971	0.71	4/2651 (0.2%)
12	H	0.33	0/1023	0.72	3/1351 (0.2%)
13	I	0.31	0/1537	0.72	3/2066 (0.1%)
14	K	0.27	0/843	0.63	0/1115
15	L	0.23	0/1191	0.55	0/1591
16	M	0.26	0/720	0.70	2/952 (0.2%)
17	N	0.39	0/1341	1.02	4/1793 (0.2%)
18	O	0.32	0/575	0.74	0/761
19	P	0.27	0/454	0.57	0/599
20	Q	0.31	0/1732	0.67	1/2315 (0.0%)
21	S	0.33	0/1133	0.71	0/1516
22	U	0.23	0/1746	0.54	0/2338
23	V	0.28	0/1682	0.60	1/2250 (0.0%)
24	W	0.26	0/831	0.68	2/1095 (0.2%)
25	X	0.26	0/718	0.56	0/953
26	Z	0.24	0/1537	0.56	0/2052
27	a	0.32	0/1255	0.75	2/1662 (0.1%)
28	b	0.25	0/1501	0.55	0/2013
29	c	0.28	0/1291	0.71	3/1725 (0.2%)
30	e	0.27	0/993	0.71	3/1332 (0.2%)
31	g	0.24	0/984	0.51	0/1323

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	h	0.26	0/1132	0.61	0/1504
33	i	0.28	0/1130	0.65	0/1507
34	l	0.27	0/1017	0.63	0/1364
35	m	0.27	0/1936	0.65	2/2596 (0.1%)
36	n	0.24	0/895	0.70	3/1198 (0.3%)
37	o	0.27	0/1935	0.69	0/2596
38	p	0.34	0/1916	0.70	4/2553 (0.2%)
39	r	0.28	0/2428	0.68	2/3252 (0.1%)
40	A	0.28	0/2515	0.59	0/3403
41	R	0.36	0/1317	0.72	2/1757 (0.1%)
42	J	0.34	0/1844	0.74	2/2476 (0.1%)
43	T	0.28	0/345	0.76	0/455
44	2	0.24	5/84533 (0.0%)	0.45	31/131714 (0.0%)
45	y	0.30	0/1269	0.73	0/1712
46	4	0.33	0/5099	0.82	12/6840 (0.2%)
47	d	0.34	0/864	0.85	4/1160 (0.3%)
48	j	0.30	0/933	0.70	0/1256
49	k	0.29	0/1082	0.65	0/1443
50	Y	0.25	0/1383	0.61	1/1856 (0.1%)
51	z	0.36	0/587	0.85	2/767 (0.3%)
52	t	0.26	0/1736	0.64	1/2328 (0.0%)
53	u	0.31	2/4614 (0.0%)	0.66	3/6191 (0.0%)
54	v	0.28	0/321	0.40	0/418
All	All	0.27	7/164943 (0.0%)	0.56	110/240753 (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
6	B	0	1
11	G	0	1
17	N	0	1
20	Q	0	1
29	c	0	1
30	e	0	1
35	m	0	2
36	n	0	1
42	J	0	1
50	Y	0	1
53	u	0	3
All	All	0	14

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
53	u	668	PHE	CD2-CE2	7.62	1.61	1.38
44	2	4060	U	O3'-P	5.72	1.69	1.61
53	u	668	PHE	CE2-CZ	5.66	1.55	1.38
44	2	4062	A	O3'-P	5.53	1.69	1.61
44	2	4063	U	O5'-C5'	5.41	1.50	1.42
44	2	4061	G	O3'-P	5.35	1.69	1.61
44	2	2401	A2M	O3'-P	5.16	1.61	1.56

All (110) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2	4192	A	P-O3'-C3'	-9.59	105.82	120.20
44	2	4062	A	C4'-C3'-O3'	9.38	123.47	109.40
44	2	4200	G	P-O3'-C3'	-9.38	106.14	120.20
44	2	4061	G	C4'-C3'-O3'	9.22	123.22	109.40
44	2	4202	U	P-O3'-C3'	-9.06	106.61	120.20
46	4	503	THR	CA-C-N	8.83	137.60	121.70
46	4	503	THR	C-N-CA	8.83	137.60	121.70
36	n	105	LEU	CA-C-N	8.26	141.94	121.80
36	n	105	LEU	C-N-CA	8.26	141.94	121.80
27	a	78	ILE	N-CA-C	-7.96	105.46	111.90
44	2	4201	G	P-O3'-C3'	-7.64	108.74	120.20
44	2	4197	G	P-O3'-C3'	-7.53	108.91	120.20
16	M	82	THR	CA-C-N	7.51	131.15	120.49
16	M	82	THR	C-N-CA	7.51	131.15	120.49
44	2	4195	G	P-O3'-C3'	-7.51	108.94	120.20
46	4	406	GLY	CA-C-N	7.50	135.87	121.54
46	4	406	GLY	C-N-CA	7.50	135.87	121.54
17	N	113	ILE	CG1-CB-CG2	-7.47	88.28	110.70
44	2	4198	G	P-O3'-C3'	-7.45	109.02	120.20
36	n	106	TYR	N-CA-C	7.45	126.26	109.81
53	u	668	PHE	CZ-CE2-CD2	-7.24	106.96	120.00
44	2	4193	C	P-O3'-C3'	-7.06	109.61	120.20
6	B	304	SER	CA-C-N	7.00	133.53	122.61
6	B	304	SER	C-N-CA	7.00	133.53	122.61
44	2	4063	U	C4'-C3'-O3'	6.95	123.43	113.00
46	4	41	HIS	CA-C-N	6.88	134.68	121.54
46	4	41	HIS	C-N-CA	6.88	134.68	121.54
44	2	4381	A	C2'-C3'-O3'	-6.84	103.44	113.70
44	2	4196	G	P-O3'-C3'	-6.82	109.98	120.20
29	c	118	GLU	N-CA-CB	6.53	120.26	110.53
46	4	230	LEU	CA-CB-CG	6.50	139.05	116.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	e	90	ARG	CA-C-N	6.49	133.94	121.54
30	e	90	ARG	C-N-CA	6.49	133.94	121.54
3	7	7	TYR	CA-C-N	6.48	133.92	121.54
3	7	7	TYR	C-N-CA	6.48	133.92	121.54
46	4	391	GLU	CA-C-N	6.45	133.85	121.54
46	4	391	GLU	C-N-CA	6.45	133.85	121.54
53	u	74	LEU	CA-CB-CG	6.39	138.66	116.30
44	2	495	C	N1-C1'-C2'	6.37	121.55	112.00
47	d	54	GLY	CA-C-N	6.15	132.20	122.61
47	d	54	GLY	C-N-CA	6.15	132.20	122.61
47	d	66	SER	CA-C-N	6.11	133.21	121.54
47	d	66	SER	C-N-CA	6.11	133.21	121.54
44	2	4194	U	P-O3'-C3'	-6.05	111.12	120.20
8	D	319	LEU	CA-CB-CG	6.03	137.40	116.30
44	2	2760	G	P-O3'-C3'	6.02	129.23	120.20
46	4	430	PRO	CA-C-N	6.01	133.01	121.54
46	4	430	PRO	C-N-CA	6.01	133.01	121.54
52	t	197	ASN	CB-CA-C	-6.00	109.67	116.63
8	D	171	LEU	CA-CB-CG	5.98	137.22	116.30
44	2	914	U	P-O3'-C3'	5.97	129.16	120.20
12	H	67	GLU	N-CA-CB	5.85	119.35	110.28
17	N	84	GLU	N-CA-CB	5.80	119.26	110.28
42	J	238	ASP	CA-C-N	5.79	132.13	121.70
42	J	238	ASP	C-N-CA	5.79	132.13	121.70
13	I	188	GLN	CA-CB-CG	5.78	125.65	114.10
44	2	2033	A	P-O3'-C3'	5.76	128.84	120.20
53	u	326	GLY	N-CA-C	5.71	126.71	113.18
44	2	1980	U	P-O3'-C3'	5.68	128.72	120.20
6	B	360	LEU	CA-CB-CG	5.64	136.06	116.30
39	r	191	ASN	CA-C-N	5.64	132.31	121.54
39	r	191	ASN	C-N-CA	5.64	132.31	121.54
11	G	169	PHE	CA-C-N	5.59	127.07	120.09
11	G	169	PHE	C-N-CA	5.59	127.07	120.09
44	2	4199	C	P-O3'-C3'	-5.59	111.82	120.20
44	2	4204	C	C2'-C3'-O3'	-5.50	105.44	113.70
44	2	3905	A	P-O3'-C3'	5.49	128.43	120.20
11	G	129	PRO	CA-C-N	5.47	130.12	122.08
11	G	129	PRO	C-N-CA	5.47	130.12	122.08
44	2	485	C	C2-N1-C1'	5.46	135.18	118.80
13	I	187	VAL	CA-C-N	5.46	131.96	121.54
13	I	187	VAL	C-N-CA	5.46	131.96	121.54
44	2	406	C	C2'-C3'-O3'	5.42	121.84	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	a	113	LYS	CA-CB-CG	5.40	124.89	114.10
44	2	406	C	P-O3'-C3'	5.38	128.26	120.20
41	R	98	ILE	CA-C-N	5.35	131.77	121.54
41	R	98	ILE	C-N-CA	5.35	131.77	121.54
44	2	4191	G	C2'-C3'-O3'	5.32	117.48	109.50
12	H	100	GLU	N-CA-CB	5.30	119.32	110.41
44	2	2015	U	P-O3'-C3'	5.28	128.12	120.20
50	Y	127	ARG	CG-CD-NE	5.28	123.62	112.00
44	2	4063	U	C2'-C3'-O3'	-5.27	105.80	113.70
23	V	110	PRO	N-CA-C	5.26	117.11	110.70
29	c	80	VAL	N-CA-C	-5.26	102.14	109.45
46	4	12	VAL	CA-CB-CG1	5.24	119.31	110.40
38	p	135	ILE	CA-C-N	-5.23	116.73	121.65
38	p	135	ILE	C-N-CA	-5.23	116.73	121.65
44	2	1676	C	P-O3'-C3'	5.23	128.04	120.20
8	D	231	ASN	CA-C-N	5.22	131.37	121.97
8	D	231	ASN	C-N-CA	5.22	131.37	121.97
5	9	4	SER	CA-C-N	5.20	133.27	122.41
5	9	4	SER	C-N-CA	5.20	133.27	122.41
29	c	118	GLU	CA-CB-CG	5.19	124.48	114.10
44	2	4913	G	P-O3'-C3'	5.18	127.98	120.20
38	p	221	LYS	CA-C-N	5.13	133.99	122.19
38	p	221	LYS	C-N-CA	5.13	133.99	122.19
51	z	23	PRO	CA-C-N	5.09	131.26	121.54
51	z	23	PRO	C-N-CA	5.09	131.26	121.54
35	m	179	ILE	CA-C-N	5.07	131.23	121.54
35	m	179	ILE	C-N-CA	5.07	131.23	121.54
30	e	90	ARG	CA-CB-CG	5.07	124.24	114.10
12	H	67	GLU	CA-CB-CG	5.06	124.23	114.10
5	9	98	SER	CA-C-N	5.06	131.21	121.54
5	9	98	SER	C-N-CA	5.06	131.21	121.54
24	W	32	SER	CA-C-N	5.03	131.15	121.54
24	W	32	SER	C-N-CA	5.03	131.15	121.54
44	2	4382	G	C2'-C3'-O3'	-5.03	106.16	113.70
20	Q	47	ALA	N-CA-C	5.02	120.91	109.81
17	N	54	ARG	CA-C-N	5.02	128.79	121.31
17	N	54	ARG	C-N-CA	5.02	128.79	121.31

There are no chirality outliers.

All (14) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	B	16	PHE	Peptide
11	G	162	ASP	Peptide
42	J	238	ASP	Peptide
17	N	117	ILE	Peptide
20	Q	154	VAL	Peptide
50	Y	127	ARG	Sidechain
29	c	80	VAL	Peptide
30	e	96	LEU	Peptide
35	m	132	ASN	Peptide
35	m	54	ARG	Peptide
36	n	106	TYR	Peptide
53	u	325	VAL	Peptide
53	u	606	PRO	Peptide
53	u	66	ILE	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	5	2558	0	1296	5	0
2	6	1852	0	1828	12	0
3	7	1159	0	1224	10	0
4	8	3315	0	1685	17	0
5	9	793	0	807	12	0
6	B	3244	0	3389	24	0
7	C	764	0	822	5	0
8	D	2853	0	3028	21	0
9	E	764	0	804	4	0
10	F	868	0	963	4	0
11	G	1935	0	2087	14	0
12	H	1015	0	1148	15	0
13	I	1518	0	1601	46	0
14	K	832	0	917	4	0
15	L	1162	0	1213	5	0
16	M	705	0	741	10	0
17	N	1319	0	1356	59	0
18	O	569	0	637	3	0
19	P	444	0	483	6	0
20	Q	1701	0	1818	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	S	1111	0	1174	4	0
22	U	1701	0	1749	13	0
23	V	1650	0	1794	8	0
24	W	818	0	888	7	0
25	X	708	0	760	4	0
26	Z	1513	0	1628	12	0
27	a	1239	0	1363	9	0
28	b	1461	0	1502	11	0
29	c	1264	0	1337	11	0
30	e	979	0	1039	9	0
31	g	967	0	1040	1	0
32	h	1115	0	1205	13	0
33	i	1107	0	1182	5	0
34	l	1002	0	1068	9	0
35	m	1898	0	1993	19	0
36	n	876	0	912	6	0
37	o	1897	0	2046	12	0
38	p	1878	0	2009	8	0
39	r	2382	0	2410	13	0
40	A	2460	0	2489	14	0
41	R	1296	0	1324	6	0
42	J	1809	0	1783	21	0
43	T	343	0	390	0	0
44	2	77442	0	38788	392	0
45	y	1250	0	1305	9	0
46	4	5016	0	5153	31	0
47	d	850	0	868	5	0
48	j	918	0	964	6	0
49	k	1064	0	1160	5	0
50	Y	1355	0	1390	2	0
51	z	581	0	656	7	0
52	t	1708	0	1815	12	0
53	u	4536	0	4714	75	0
54	v	316	0	332	57	0
55	A	28	0	12	1	0
56	A	1	0	0	1	0
57	A	1	0	0	0	0
All	All	155910	0	118089	793	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 3.

All (793) 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)
44:2:4083:5MU:C5	44:2:4083:5MU:C4	1.79	1.67
44:2:1860:B8H:C5	44:2:1860:B8H:C4	1.82	1.57
44:2:4296:B8H:C5	44:2:4296:B8H:C4	1.82	1.53
44:2:4199:C:N3	53:u:647:LYS:HA	1.30	1.45
44:2:4197:G:C6	53:u:655:ARG:NH2	1.98	1.32
44:2:4287:G:OP1	53:u:426:LYS:HB2	1.21	1.28
13:I:180:TYR:CE2	54:v:19:ASP:CG	2.10	1.27
44:2:4199:C:O2	53:u:647:LYS:CG	1.81	1.27
17:N:23:ASN:ND2	44:2:4258:C:O2'	1.69	1.25
17:N:101:ASP:N	44:2:4248:A:O2'	1.69	1.23
13:I:180:TYR:CE2	54:v:19:ASP:OD2	1.95	1.19
13:I:180:TYR:CD2	54:v:19:ASP:CG	2.24	1.15
44:2:4199:C:O2	53:u:647:LYS:CB	1.95	1.13
44:2:4199:C:O2	53:u:647:LYS:HG2	1.43	1.11
44:2:4271:A:H4'	53:u:610:LYS:HE2	1.24	1.09
44:2:4197:G:C5	53:u:655:ARG:NH2	2.23	1.07
44:2:4199:C:N3	53:u:647:LYS:CA	2.23	1.01
13:I:180:TYR:HE2	54:v:19:ASP:OD2	1.35	1.01
17:N:98:ASN:HB2	44:2:4250:G:H5''	1.43	1.01
17:N:131:TYR:HE2	44:2:4260:U:O2'	1.43	1.00
13:I:176:LEU:HB2	54:v:17:ARG:HD3	1.41	1.00
17:N:131:TYR:HE2	44:2:4260:U:HO2'	1.00	0.98
17:N:98:ASN:CB	44:2:4250:G:H5''	1.94	0.98
44:2:4199:C:O2	53:u:647:LYS:HB3	1.63	0.96
13:I:180:TYR:CE2	54:v:19:ASP:OD1	2.17	0.96
40:A:345:THR:HG1	56:A:802:MG:MG	0.56	0.95
44:2:4287:G:OP1	53:u:426:LYS:CB	2.14	0.95
17:N:131:TYR:CE2	44:2:4260:U:O2'	2.19	0.94
44:2:4199:C:C2	53:u:647:LYS:HA	2.06	0.91
44:2:4192:A:H1'	53:u:685:ARG:CD	2.01	0.90
17:N:128:LEU:O	44:2:4251:A:N7	2.06	0.89
44:2:4697:U:H5'	54:v:29:SER:CB	2.03	0.87
13:I:180:TYR:CD2	54:v:19:ASP:OD2	2.23	0.87
13:I:176:LEU:HD13	54:v:17:ARG:HA	1.56	0.86
44:2:4203:A:H5''	53:u:628:VAL:CG1	2.05	0.85
44:2:4199:C:C2	53:u:647:LYS:CB	2.61	0.84
44:2:4233:A:O5'	53:u:605:LYS:HD2	1.78	0.84
44:2:4197:G:N1	53:u:655:ARG:NH2	2.12	0.84
44:2:4697:U:H5'	54:v:29:SER:OG	1.79	0.83
44:2:4697:U:OP1	54:v:25:ARG:NH2	2.11	0.82
17:N:98:ASN:O	44:2:4249:G:O2'	1.98	0.81
17:N:95:ARG:NH2	44:2:4251:A:OP2	2.13	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:U:165:THR:O	22:U:169:ARG:HB2	1.81	0.81
17:N:98:ASN:HB2	44:2:4250:G:C5'	2.11	0.80
17:N:101:ASP:HB2	44:2:4248:A:O2'	1.82	0.79
13:I:93:ARG:HD3	54:v:18:LEU:HD13	1.64	0.79
17:N:54:ARG:NH2	44:2:4258:C:OP2	2.17	0.78
17:N:60:PHE:CE1	44:2:4257:A:C6	2.71	0.78
44:2:4199:C:C2	53:u:647:LYS:CA	2.66	0.78
44:2:4067:U:H3'	44:2:4068:U:H5''	1.65	0.77
44:2:4199:C:C2	53:u:647:LYS:HG2	2.19	0.77
13:I:174:LYS:HZ2	54:v:10:HIS:HB2	1.50	0.76
13:I:93:ARG:CD	13:I:182:SER:HB3	2.16	0.76
44:2:4192:A:H1'	53:u:685:ARG:HD2	1.68	0.75
44:2:3953:G:C2	44:2:3954:A:H1'	2.20	0.75
44:2:4192:A:C1'	53:u:685:ARG:CD	2.64	0.75
13:I:176:LEU:HB2	54:v:17:ARG:CD	2.16	0.75
44:2:4233:A:H5'	53:u:605:LYS:HB3	1.70	0.74
17:N:60:PHE:CZ	44:2:4257:A:N1	2.56	0.73
40:A:310:GLN:HG3	44:2:4198:G:N2	2.03	0.73
44:2:1872:G:O2'	44:2:4219:A:N3	2.21	0.73
16:M:2:THR:N	44:2:3642:A:HO2'	1.84	0.73
44:2:4192:A:H1'	53:u:685:ARG:HD3	1.70	0.72
44:2:4192:A:C1'	53:u:685:ARG:HD2	2.19	0.72
44:2:4271:A:C4'	53:u:610:LYS:HE2	2.13	0.72
44:2:4197:G:C2	53:u:655:ARG:NH2	2.57	0.72
2:6:39:GLU:O	2:6:43:SER:HB2	1.90	0.71
13:I:93:ARG:CD	54:v:18:LEU:HD13	2.21	0.71
13:I:95:VAL:HG13	54:v:18:LEU:HD11	1.73	0.70
40:A:322:GLY:HA2	55:A:801:GDP:O2A	1.92	0.70
17:N:101:ASP:CA	44:2:4248:A:O2'	2.40	0.69
40:A:310:GLN:HG3	44:2:4198:G:H21	1.56	0.69
44:2:4068:U:H4'	44:2:4068:U:OP1	1.90	0.69
44:2:4199:C:C2	53:u:647:LYS:HB3	2.27	0.69
44:2:4197:G:C4	53:u:655:ARG:NH2	2.60	0.68
44:2:4697:U:C4'	54:v:29:SER:OG	2.41	0.68
44:2:4192:A:C1'	53:u:685:ARG:HD3	2.23	0.68
44:2:4199:C:O2	53:u:647:LYS:CD	2.42	0.67
13:I:93:ARG:NE	54:v:18:LEU:HD13	2.09	0.67
44:2:4203:A:H5''	53:u:628:VAL:HG13	1.75	0.67
17:N:98:ASN:HA	44:2:4249:G:O3'	1.93	0.66
44:2:3950:U:H2'	44:2:3951:G:O4'	1.96	0.66
44:2:4198:G:H4'	53:u:651:PHE:CG	2.30	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:2:4697:U:C5'	54:v:29:SER:OG	2.44	0.66
17:N:127:GLY:HA3	44:2:4251:A:C6	2.31	0.65
13:I:176:LEU:HD13	54:v:17:ARG:CA	2.26	0.65
13:I:174:LYS:NZ	54:v:10:HIS:HB2	2.10	0.65
13:I:180:TYR:HE2	54:v:19:ASP:CG	1.74	0.65
17:N:101:ASP:CB	44:2:4248:A:O2'	2.45	0.64
17:N:98:ASN:CB	44:2:4250:G:C5'	2.72	0.64
44:2:961:G:N2	44:2:964:A:N6	2.45	0.64
13:I:93:ARG:HD2	13:I:182:SER:HB3	1.79	0.64
5:9:94:VAL:HA	5:9:116:ARG:C	2.23	0.64
44:2:1739:G:H22	44:2:1790:U:H3	1.44	0.64
13:I:174:LYS:HZ1	54:v:10:HIS:CD2	2.16	0.63
44:2:4234:A:OP1	53:u:606:PRO:O	2.16	0.63
44:2:4065:G:H3'	44:2:4066:U:H5''	1.80	0.62
2:6:129:LEU:O	2:6:133:LEU:HB2	1.99	0.62
17:N:101:ASP:HB2	44:2:4248:A:C1'	2.30	0.62
44:2:3955:G:H4'	44:2:4057:C:H2'	1.81	0.62
44:2:4234:A:OP2	53:u:607:LYS:HD3	2.00	0.62
44:2:4697:U:C5'	54:v:29:SER:CB	2.77	0.62
44:2:4067:U:H3'	44:2:4068:U:C5'	2.30	0.61
44:2:1948:G:OP1	54:v:36:SER:HB2	2.01	0.61
44:2:3955:G:OP2	44:2:3955:G:H8	1.82	0.61
19:P:21:ARG:HH21	46:4:575:ARG:HD2	1.66	0.61
17:N:128:LEU:O	44:2:4251:A:C8	2.52	0.61
44:2:4199:C:C2	53:u:647:LYS:CG	2.78	0.61
44:2:2362:U:H2'	44:2:2363:A2M:H8	1.83	0.61
44:2:4202:U:H2'	44:2:4203:A:C8	2.35	0.60
44:2:4698:C:OP1	54:v:30:ARG:HD3	2.01	0.60
17:N:60:PHE:CE1	44:2:4257:A:N1	2.69	0.60
44:2:961:G:N2	44:2:964:A:C6	2.69	0.60
13:I:180:TYR:CD2	54:v:19:ASP:CB	2.83	0.60
44:2:3960:A:C5	44:2:4043:G:O6	2.55	0.60
17:N:95:ARG:HH21	44:2:4251:A:P	2.24	0.60
44:2:4697:U:C5'	54:v:29:SER:HB3	2.32	0.60
44:2:4468:U:HO2'	51:z:2:ALA:N	2.00	0.59
26:Z:12:LYS:HD2	26:Z:14:ARG:HH21	1.67	0.59
44:2:4195:G:H5''	44:2:4195:G:H8	1.67	0.59
44:2:4197:G:C2	53:u:655:ARG:NH1	2.71	0.59
53:u:606:PRO:HB2	53:u:608:SER:HB3	1.84	0.59
44:2:4697:U:H5'	54:v:29:SER:HB3	1.82	0.59
44:2:4200:G:HO2'	44:2:4201:G:H8	1.49	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:D:291:ARG:NH1	44:2:667:A:N7	2.52	0.58
16:M:54:LYS:O	16:M:58:THR:HB	2.03	0.58
44:2:3951:G:N1	44:2:4060:U:N3	2.50	0.58
44:2:3960:A:N7	44:2:4043:G:O6	2.36	0.58
44:2:4233:A:C5'	53:u:605:LYS:HB3	2.33	0.58
46:4:257:LEU:HD21	46:4:296:ILE:HB	1.85	0.58
17:N:101:ASP:N	44:2:4248:A:HO2'	1.94	0.58
44:2:4195:G:C6	53:u:647:LYS:NZ	2.72	0.58
44:2:3946:G:H1	44:2:4067:U:H3	1.52	0.58
35:m:45:VAL:HG12	35:m:61:VAL:HG22	1.85	0.57
39:r:76:CYS:SG	39:r:112:ARG:NH1	2.78	0.57
4:8:83:C:H42	32:h:50:ARG:HH12	1.51	0.57
44:2:4697:U:O3'	54:v:30:ARG:HG3	2.03	0.57
13:I:180:TYR:HD2	54:v:19:ASP:CG	2.00	0.57
41:R:71:LYS:HD3	41:R:165:ASP:HB3	1.86	0.57
17:N:60:PHE:CE1	44:2:4257:A:N6	2.73	0.57
46:4:400:ASP:O	46:4:404:GLU:HB2	2.04	0.57
44:2:3946:G:H22	44:2:4068:U:H1'	1.68	0.56
17:N:56:THR:H	17:N:64:ARG:HH21	1.54	0.56
26:Z:81:VAL:HG12	26:Z:101:CYS:HB3	1.86	0.56
44:2:4291:G:H4'	44:2:4292:A:H5''	1.86	0.56
42:J:64:ARG:HG2	42:J:104:PHE:HB2	1.86	0.56
17:N:95:ARG:NH2	44:2:4251:A:P	2.78	0.56
44:2:4188:U:H2'	44:2:4189:U:C6	2.41	0.56
13:I:93:ARG:HD3	54:v:18:LEU:CD1	2.33	0.56
44:2:495:C:O2	44:2:497:G:N2	2.38	0.56
44:2:1098:G:H1	44:2:1197:C:H42	1.54	0.56
35:m:215:ASN:HD22	44:2:4546:A:H62	1.54	0.56
4:8:96:C:H5''	12:H:66:LYS:HD2	1.88	0.55
18:O:24:LYS:HB2	18:O:35:LYS:HB2	1.88	0.55
24:W:8:ARG:NH2	44:2:4232:U:O4	2.40	0.55
44:2:3722:G:H2'	44:2:3723:A2M:H8	1.89	0.55
17:N:29:SER:HA	17:N:33:LEU:HD23	1.88	0.55
28:b:19:THR:HG23	28:b:22:CYS:H	1.71	0.55
17:N:98:ASN:HB3	44:2:4250:G:H5''	1.86	0.55
44:2:4196:G:H8	44:2:4196:G:OP2	1.89	0.55
44:2:4066:U:H2'	44:2:4067:U:C6	2.42	0.55
42:J:50:ASN:ND2	44:2:1969:G:O2'	2.40	0.55
44:2:4195:G:H3'	44:2:4196:G:C8	2.42	0.55
17:N:98:ASN:HA	44:2:4250:G:P	2.47	0.54
44:2:4192:A:O4'	53:u:685:ARG:HD2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:67:ILE:HD11	26:Z:95:VAL:HG23	1.88	0.54
52:t:54:ARG:HD2	52:t:150:GLU:HG3	1.89	0.54
35:m:116:LEU:HB2	35:m:126:LEU:HB2	1.90	0.54
44:2:4056:A:H2'	44:2:4057:C:H5''	1.90	0.54
8:D:152:LEU:HD23	8:D:251:ILE:HG12	1.90	0.54
13:I:174:LYS:HZ2	54:v:10:HIS:CB	2.19	0.54
44:2:4197:G:C2	53:u:655:ARG:CZ	2.91	0.54
23:V:34:VAL:HG12	23:V:103:LYS:HB2	1.89	0.54
27:a:98:ARG:NH2	27:a:130:ASN:OD1	2.41	0.54
5:9:100:GLU:OE1	5:9:104:ARG:NH1	2.41	0.54
28:b:77:ASN:ND2	28:b:137:CYS:SG	2.81	0.54
44:2:1992:U:H5'	44:2:1993:C:H5'	1.89	0.54
32:h:8:THR:HG21	32:h:13:LYS:HD2	1.90	0.54
44:2:4198:G:H4'	53:u:651:PHE:CD2	2.43	0.53
17:N:112:HIS:HD2	17:N:126:TYR:H	1.56	0.53
44:2:4199:C:C4	53:u:647:LYS:HA	2.29	0.53
11:G:137[A]:ARG:HD2	11:G:146:LEU:HD11	1.90	0.53
22:U:125:SER:HB3	44:2:3937:C:H1'	1.90	0.53
25:X:29:ILE:HG21	35:m:177:LYS:HB2	1.90	0.53
29:c:4:THR:OG1	44:2:4208:U:OP2	2.18	0.53
42:J:96:LEU:O	42:J:97:ARG:NH1	2.42	0.53
44:2:4195:G:H5''	44:2:4195:G:C8	2.43	0.53
44:2:1972:G:H1	44:2:1994:C:H5	1.57	0.53
44:2:4613:C:H4'	51:z:13:MET:HE2	1.90	0.53
2:6:126:GLU:OE2	2:6:139:ARG:NH1	2.41	0.53
41:R:98:ILE:HG22	41:R:99:ARG:HG2	1.91	0.53
17:N:60:PHE:CZ	44:2:4257:A:C2	2.97	0.53
8:D:284:MET:HE2	8:D:287:THR:HA	1.91	0.53
26:Z:53:MET:HE3	44:2:1692:C:H5''	1.90	0.53
44:2:2562:G:N2	44:2:2565:A:OP2	2.42	0.53
17:N:131:TYR:CZ	44:2:4260:U:H1'	2.44	0.53
28:b:29:ARG:HG3	29:c:148:PRO:HB2	1.91	0.53
35:m:215:ASN:ND2	44:2:4546:A:N7	2.56	0.53
44:2:3616:U:OP2	44:2:3617:G:N2	2.41	0.53
32:h:34:LEU:HD23	32:h:38:LEU:HB3	1.90	0.52
44:2:2007:G:H21	44:2:2012:A:H62	1.56	0.52
44:2:3641:U:OP2	44:2:3646:A:N6	2.42	0.52
17:N:23:ASN:HD21	44:2:4258:C:C2'	2.06	0.52
24:W:81:ARG:NH2	44:2:4294:C:OP1	2.42	0.52
42:J:151:PRO:HG3	42:J:154:ARG:HH21	1.73	0.52
1:5:74:A:N3	28:b:53:LYS:NZ	2.57	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:B:230:GLY:O	6:B:234:ARG:HB2	2.09	0.52
29:c:114:GLN:HA	29:c:117:LYS:HG2	1.92	0.52
44:2:1256:G:OP2	44:2:1257:A:N6	2.42	0.52
40:A:352:THR:HG23	44:2:4539:U:H5''	1.92	0.52
44:2:3960:A:N7	44:2:4043:G:C6	2.78	0.52
2:6:119:PRO:O	2:6:139:ARG:NH2	2.43	0.52
54:v:31:GLU:OE2	54:v:35:ARG:NH2	2.42	0.52
28:b:13:VAL:HG22	28:b:29:ARG:HG2	1.92	0.52
44:2:4698:C:C5	54:v:30:ARG:NH1	2.77	0.52
14:K:30:ARG:NH1	44:2:327:U:O2'	2.43	0.52
23:V:3:GLU:OE2	23:V:5:GLN:NE2	2.43	0.52
37:o:44:CYS:SG	37:o:45:SER:N	2.81	0.52
45:y:41:LYS:NZ	45:y:67:ARG:O	2.43	0.52
42:J:33:CYS:O	42:J:37:TYR:HB2	2.10	0.52
4:8:103:A:OP1	16:M:21:ARG:NH2	2.43	0.51
6:B:66:LYS:NZ	30:e:12:ALA:O	2.42	0.51
9:E:48:LEU:HD13	9:E:57:LYS:HG3	1.92	0.51
44:2:4192:A:O4'	53:u:685:ARG:CD	2.58	0.51
52:t:113:SER:HA	52:t:138:LEU:HB3	1.91	0.51
6:B:156:TYR:OH	44:2:4912:G:N2	2.44	0.51
8:D:140:LYS:O	8:D:204:ARG:NH2	2.44	0.51
17:N:105:PHE:HB3	17:N:132:VAL:HB	1.92	0.51
39:r:156:GLY:HA2	39:r:181:PRO:HG3	1.93	0.51
42:J:33:CYS:O	42:J:37:TYR:CB	2.58	0.51
5:9:116:ARG:HH11	5:9:116:ARG:HB3	1.74	0.51
22:U:47:LYS:NZ	44:2:280:G:OP1	2.44	0.51
44:2:517:C:H5	44:2:645:G:H21	1.57	0.51
44:2:4286:C:O2'	53:u:424:LYS:NZ	2.43	0.51
19:P:48:LYS:NZ	44:2:2406:G:O2'	2.44	0.51
28:b:127:MET:HE1	29:c:155:PRO:HG3	1.93	0.51
29:c:130:ARG:NH1	44:2:1837:A:OP2	2.44	0.51
32:h:1:MET:HE3	32:h:2:LYS:H	1.75	0.51
46:4:121:ASP:HB2	46:4:125:ARG:HG3	1.91	0.51
53:u:639:SER:OG	53:u:640:SER:N	2.43	0.51
13:I:152:GLU:O	13:I:156:ASN:HB2	2.10	0.51
15:L:42:ARG:NH1	44:2:4376:A:O2'	2.44	0.51
44:2:3955:G:N2	44:2:3967:G:O4'	2.44	0.51
44:2:4200:G:O2'	44:2:4201:G:H8	1.94	0.51
53:u:57:ALA:HB1	53:u:99:THR:HG21	1.93	0.51
13:I:174:LYS:NZ	54:v:10:HIS:CD2	2.78	0.51
16:M:20:ARG:NH2	16:M:39:TYR:OH	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:e:15:ARG:HB2	44:2:4618:G:H5''	1.92	0.51
44:2:4199:C:H4'	44:2:4200:G:H5'	1.91	0.51
52:t:38:LEU:HD22	52:t:194:LEU:HD21	1.93	0.51
8:D:109:ARG:NH2	44:2:2343:G:OP2	2.44	0.51
10:F:76:ARG:NH1	44:2:2583:C:OP2	2.43	0.51
30:e:90:ARG:HD2	30:e:123:LYS:HD2	1.92	0.51
32:h:67:ILE:O	32:h:84:ARG:NH2	2.44	0.51
45:y:114:ARG:NH2	45:y:165:SER:O	2.44	0.51
3:7:56:ARG:HE	3:7:61:LYS:HG3	1.76	0.51
44:2:3948:C:H2'	44:2:3949:A:N7	2.26	0.51
13:I:140:GLN:NE2	13:I:142:ASP:OD1	2.42	0.51
44:2:2418:A:N1	44:2:2429:A:O2'	2.44	0.51
44:2:4698:C:OP1	54:v:30:ARG:CD	2.59	0.51
27:a:101:ILE:HG13	27:a:104:ARG:HH21	1.76	0.51
44:2:1316:OMG:OP1	49:k:43:ASN:ND2	2.44	0.51
37:o:69:TYR:O	37:o:72:LYS:NZ	2.43	0.50
46:4:230:LEU:O	46:4:233:ARG:NH1	2.43	0.50
4:8:81:C:OP1	12:H:3:LYS:NZ	2.45	0.50
4:8:126:C:H3'	44:2:2493:G:H21	1.75	0.50
13:I:180:TYR:HD2	54:v:19:ASP:HB3	1.76	0.50
18:O:51:GLU:O	18:O:55:LYS:NZ	2.44	0.50
44:2:664:G:N2	44:2:666:G:O6	2.43	0.50
44:2:1865:G:H21	44:2:1868:A:H62	1.59	0.50
35:m:101:VAL:HG22	35:m:165:VAL:HG22	1.93	0.50
5:9:21:ALA:HB3	5:9:24:ARG:HB2	1.93	0.50
11:G:58:PRO:HG2	11:G:61:ILE:HD12	1.92	0.50
13:I:102:ASN:HB3	13:I:115:ARG:HB3	1.94	0.50
26:Z:53:MET:HE2	26:Z:57:ASN:HB3	1.92	0.50
38:p:105:VAL:HG13	38:p:136:VAL:HG12	1.94	0.50
44:2:3620:G:OP1	44:2:3622:C:N4	2.43	0.50
3:7:62:GLU:HG2	3:7:108:ILE:HD11	1.94	0.50
12:H:109:ARG:NH1	44:2:267:G:OP1	2.45	0.50
13:I:180:TYR:CD2	54:v:19:ASP:HB3	2.47	0.50
44:2:2601:A:N6	44:2:2744:A:OP2	2.43	0.50
2:6:9:ASN:ND2	44:2:4596:C:OP1	2.43	0.50
6:B:174:ARG:NH1	44:2:4985:U:O2	2.45	0.50
15:L:132:ARG:NH2	44:2:1468:C:OP1	2.44	0.50
17:N:131:TYR:CE2	44:2:4260:U:H1'	2.46	0.50
21:S:38:VAL:HG21	21:S:50:MET:HE2	1.92	0.50
23:V:89:PRO:HD3	44:2:1914:C:H4'	1.94	0.50
27:a:105:LEU:HD22	27:a:135:LYS:HG3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:l:94:ARG:NH1	44:2:2262:G:OP1	2.44	0.50
46:4:418:ASP:OD1	46:4:418:ASP:N	2.44	0.50
46:4:499:LYS:O	46:4:502:ASN:ND2	2.44	0.50
4:8:123:U:O2'	4:8:126:C:N4	2.45	0.50
44:2:1552:G:O2'	44:2:1574:B9B:N2	2.45	0.50
44:2:1913:C:O2	44:2:2050:OMG:N2	2.41	0.50
44:2:2777:G:H5''	44:2:2778:G:H5'	1.93	0.50
44:2:4570:G:H2'	44:2:4571:A2M:H8	1.94	0.50
6:B:242:ARG:NH2	44:2:2856:C:O2	2.43	0.50
15:L:44:ASN:ND2	44:2:1683:U:OP1	2.45	0.50
44:2:4915:G:OP2	51:z:111:LYS:NZ	2.45	0.50
49:k:99:ILE:HG21	49:k:108:ARG:HG3	1.94	0.50
7:C:25:ARG:NH1	7:C:26:SER:O	2.44	0.50
1:5:6:C:O2'	39:r:50:ARG:NH2	2.45	0.49
17:N:112:HIS:NE2	17:N:124:GLY:O	2.42	0.49
28:b:15:ARG:HB3	28:b:27:LEU:HD23	1.94	0.49
44:2:3958:G:O2'	53:u:170:ARG:NH2	2.45	0.49
44:2:3976:C:N4	44:2:4035:G:OP2	2.45	0.49
48:j:18:ASN:O	48:j:90:ARG:NH2	2.45	0.49
17:N:101:ASP:HB2	44:2:4248:A:C2'	2.42	0.49
3:7:53:LYS:HG2	5:9:106:ALA:HB2	1.94	0.49
30:e:51:ARG:NH1	44:2:4620:OMU:OP1	2.45	0.49
46:4:85:ILE:HD13	46:4:238:MET:HB3	1.95	0.49
47:d:65:ARG:HG2	47:d:67:LYS:H	1.77	0.49
6:B:352:LEU:HD13	51:z:18:ARG:HH21	1.77	0.49
8:D:204:ARG:NH1	8:D:205:ARG:O	2.45	0.49
17:N:95:ARG:NH1	17:N:97:ASN:OD1	2.46	0.49
21:S:117:LYS:NZ	44:2:4882:U:OP1	2.45	0.49
40:A:205:ARG:NH2	44:2:4499:G:O6	2.46	0.49
40:A:310:GLN:CG	44:2:4198:G:H21	2.22	0.49
44:2:2020:U:H2'	44:2:2021:G:H8	1.77	0.49
44:2:4191:G:H1'	44:2:4192:A:C5'	2.43	0.49
7:C:113:ALA:HB2	38:p:41:MET:HE2	1.94	0.49
11:G:120:LYS:NZ	11:G:126:GLY:O	2.44	0.49
20:Q:16:LYS:NZ	44:2:97:G:OP1	2.43	0.49
28:b:71:SER:O	28:b:76:LYS:NZ	2.45	0.49
42:J:42:ILE:HD11	42:J:92:VAL:HG13	1.93	0.49
44:2:1207:C:H2'	44:2:1208:G:H8	1.78	0.49
19:P:41:ARG:NH1	44:2:2431:A:OP1	2.44	0.49
34:l:98:ARG:NH2	44:2:2262:G:OP2	2.44	0.49
44:2:4698:C:H5	54:v:30:ARG:NH1	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:i:36:ARG:NH1	33:i:38:TYR:OH	2.44	0.49
8:D:323:ARG:NH1	44:2:1279:A:O2'	2.45	0.49
21:S:81:ASP:OD1	21:S:81:ASP:N	2.46	0.49
32:h:1:MET:HE2	44:2:1368:A:H1'	1.95	0.49
8:D:208:CYS:HB3	8:D:250:CYS:HA	1.94	0.49
13:I:180:TYR:HD2	54:v:19:ASP:CB	2.24	0.49
42:J:168:THR:HG23	45:y:1:MET:HE3	1.94	0.49
52:t:7:ARG:NH2	53:u:548:SER:O	2.45	0.49
16:M:55:ARG:NH2	44:2:364:G:O6	2.46	0.48
34:l:87:ARG:NH1	44:2:690:C:OP1	2.45	0.48
44:2:67:C:OP2	44:2:312:G:N2	2.45	0.48
44:2:187:U:O4	44:2:245:C:N4	2.45	0.48
44:2:3949:A:N3	44:2:3949:A:H2'	2.27	0.48
53:u:415:GLN:HG2	53:u:448:GLN:HE22	1.78	0.48
13:I:93:ARG:NE	13:I:182:SER:HB3	2.28	0.48
26:Z:71:LYS:NZ	44:2:1419:G:OP1	2.46	0.48
26:Z:157:GLY:O	26:Z:188:ASN:ND2	2.46	0.48
44:2:3972:A:H1'	44:2:4050:A:H61	1.79	0.48
52:t:120:ILE:HG13	52:t:121:PRO:HD3	1.95	0.48
3:7:22:VAL:HG22	3:7:28:VAL:HG12	1.96	0.48
11:G:249:ARG:NH2	44:2:4074:C:O3'	2.45	0.48
22:U:193:ARG:NH2	44:2:28:C:OP2	2.42	0.48
39:r:193:GLU:OE1	39:r:196:ARG:NH2	2.47	0.48
44:2:4068:U:C4	44:2:4069:U:C4	3.01	0.48
1:5:7:G:OP1	39:r:33:ARG:NH1	2.46	0.48
6:B:218:ASP:OD2	6:B:348:ARG:NH1	2.47	0.48
17:N:60:PHE:CD1	44:2:4257:A:C6	3.01	0.48
20:Q:35:ARG:NH2	44:2:337:U:OP1	2.44	0.48
22:U:68:ARG:NH1	22:U:124:ASP:O	2.46	0.48
37:o:156:ARG:NH1	44:2:4940:C:OP1	2.47	0.48
2:6:214:GLU:HA	2:6:217:VAL:HG12	1.96	0.48
38:p:182:TYR:HB3	38:p:200:ARG:HG3	1.96	0.48
44:2:2459:G:N2	44:2:2462:C:OP2	2.45	0.48
44:2:4189:U:H1'	44:2:4380:A:C4	2.48	0.48
9:E:101:ASP:N	9:E:101:ASP:OD1	2.46	0.48
30:e:83:ARG:NH1	30:e:120:PRO:O	2.46	0.48
34:l:107:ARG:NH2	44:2:2263:A:OP1	2.47	0.48
42:J:191:LYS:NZ	44:2:2012:A:O3'	2.47	0.48
44:2:3717:A:H2'	44:2:3718:A2M:H8	1.95	0.48
46:4:226:LEU:O	46:4:233:ARG:NH2	2.47	0.48
13:I:142:ASP:OD1	13:I:142:ASP:N	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:Q:111:GLN:HA	20:Q:114:VAL:HG12	1.95	0.48
35:m:27:ALA:O	35:m:128:ARG:NH1	2.46	0.48
27:a:39:GLN:NE2	44:2:2711:G:OP2	2.46	0.48
38:p:132:MET:HA	38:p:135:ILE:HD12	1.94	0.48
12:H:96:ASN:ND2	44:2:136:C:OP1	2.46	0.48
25:X:38:THR:HA	25:X:45:THR:HA	1.95	0.48
50:Y:127:ARG:HD2	50:Y:139:TYR:HD2	1.79	0.48
13:I:64:ARG:NH1	44:2:4693:C:OP1	2.47	0.48
17:N:109:ILE:HD12	17:N:128:LEU:HD11	1.96	0.48
44:2:2845:A:H61	44:2:3843:C:H42	1.60	0.48
8:D:168:VAL:O	8:D:172:LYS:HB2	2.14	0.47
12:H:116:LEU:O	20:Q:129:ARG:NH1	2.47	0.47
33:i:90:PRO:O	33:i:117:LYS:NZ	2.46	0.47
44:2:4453:C:OP1	44:2:4519:C:N4	2.47	0.47
44:2:4980:C:N3	50:Y:69:ARG:NH2	2.60	0.47
17:N:48:PRO:HG2	17:N:50:PHE:HE1	1.79	0.47
23:V:7:LEU:HD22	23:V:31:ARG:HH21	1.78	0.47
35:m:123:ARG:NH2	44:2:4083:5MU:OP1	2.48	0.47
44:2:961:G:C2	44:2:964:A:N6	2.82	0.47
13:I:176:LEU:HA	54:v:17:ARG:CZ	2.45	0.47
15:L:110:LYS:NZ	44:2:1396:G:N7	2.53	0.47
42:J:232:GLU:OE2	44:2:1965:G:N2	2.47	0.47
44:2:1595:G:H1'	44:2:1597:G:H21	1.79	0.47
22:U:73:ARG:HD2	22:U:89:VAL:HG12	1.97	0.47
26:Z:39:THR:HG22	26:Z:41:SER:H	1.80	0.47
44:2:2486:G:O6	44:2:2492:C:N4	2.46	0.47
47:d:28:PRO:HB2	47:d:34:MET:HG2	1.97	0.47
4:8:38:U:O2'	12:H:86:LYS:NZ	2.47	0.47
7:C:91:ARG:NH2	44:2:1214:C:OP2	2.48	0.47
36:n:68:ARG:NH1	44:2:442:G:OP1	2.44	0.47
37:o:155:GLY:O	37:o:158:ARG:NH1	2.47	0.47
44:2:4204:C:H4'	53:u:629:ARG:HH21	1.80	0.47
4:8:47:C:H1'	4:8:61:A:H2'	1.96	0.47
13:I:95:VAL:HG13	54:v:18:LEU:CD1	2.44	0.47
19:P:28:ARG:NH1	19:P:36:ARG:O	2.45	0.47
29:c:51:GLY:HA3	29:c:92:ARG:HG3	1.97	0.47
37:o:281:ILE:HD12	37:o:286:LEU:HD11	1.97	0.47
44:2:2872:C:HO2'	44:2:3823:G:HO2'	1.58	0.47
44:2:4478:G:N2	44:2:4608:G:O2'	2.48	0.47
48:j:111:VAL:HG21	48:j:117:LEU:HD21	1.96	0.47
6:B:19:ARG:NH2	44:2:4623:OMG:OP1	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:B:28:LYS:NZ	44:2:4582:C:OP2	2.46	0.47
7:C:51:LYS:NZ	44:2:1401:C:OP2	2.43	0.47
22:U:90:ASN:ND2	44:2:3928:A:OP1	2.44	0.47
38:p:39:GLN:OE1	44:2:1703:C:O2'	2.32	0.47
39:r:23:ARG:O	39:r:23:ARG:NH1	2.48	0.47
44:2:3855:C:H2'	44:2:3856:A:H8	1.80	0.47
46:4:73:ASP:OD1	46:4:73:ASP:N	2.46	0.47
46:4:292:ASP:OD1	46:4:292:ASP:N	2.45	0.47
6:B:57:VAL:HG22	6:B:367:PHE:HB3	1.97	0.47
12:H:82:ASP:OD1	12:H:82:ASP:N	2.47	0.47
17:N:105:PHE:O	17:N:132:VAL:N	2.48	0.47
18:O:17:ARG:NH2	44:2:2772:C:O2'	2.48	0.47
44:2:2521:G:H2'	44:2:2522:7MG:H82	1.95	0.47
44:2:3953:G:H2'	44:2:3954:A:O4'	2.14	0.47
44:2:4475:G:O6	54:v:8:GLU:HG3	2.14	0.47
32:h:85:VAL:HG11	32:h:99:ILE:HD11	1.96	0.47
44:2:4058:U:O4'	53:u:155:ASN:HB2	2.15	0.47
5:9:33:ARG:HH22	5:9:92:LEU:HA	1.80	0.47
23:V:43:ILE:HD12	23:V:141:LEU:HD21	1.97	0.47
34:l:7:TRP:O	34:l:11:ARG:HB2	2.14	0.47
44:2:4065:G:N2	44:2:4066:U:H1'	2.29	0.47
6:B:206:PRO:HG2	6:B:209:GLN:HG3	1.97	0.46
42:J:38:LYS:HE3	42:J:211:GLN:HB2	1.97	0.46
44:2:4698:C:C6	54:v:30:ARG:HD3	2.50	0.46
52:t:129:ASN:ND2	53:u:329:GLU:OE1	2.46	0.46
35:m:149:LYS:HB3	35:m:155:LYS:HD3	1.97	0.46
44:2:2092:G:O2'	44:2:2262:G:N2	2.48	0.46
44:2:4188:U:O2'	44:2:4189:U:H5'	2.15	0.46
46:4:381:VAL:HG23	46:4:382:VAL:HG13	1.97	0.46
44:2:1701:A:N7	44:2:1703:C:N4	2.63	0.46
44:2:4199:C:O2	53:u:647:LYS:HD3	2.14	0.46
45:y:107:ASP:OD1	45:y:107:ASP:N	2.47	0.46
46:4:227:ASP:OD1	46:4:227:ASP:N	2.49	0.46
48:j:123:ASP:OD1	48:j:123:ASP:N	2.48	0.46
42:J:150:GLU:HB2	42:J:167:VAL:HG22	1.98	0.46
44:2:1969:G:H1	44:2:2018:C:H42	1.62	0.46
44:2:3950:U:H2'	44:2:3951:G:C1'	2.45	0.46
44:2:4203:A:H4'	44:2:4203:A:OP1	2.15	0.46
8:D:181:LYS:NZ	44:2:219:G:O6	2.49	0.46
9:E:47:ILE:HG12	9:E:72:HIS:HB3	1.96	0.46
11:G:225:ASN:O	11:G:229:ARG:NH1	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:85:GLN:HA	15:L:88:VAL:HG12	1.96	0.46
28:b:1:MET:HE3	28:b:35:PRO:HD3	1.96	0.46
44:2:4418:G:N2	44:2:4422:A:O3'	2.47	0.46
3:7:65:VAL:HG22	5:9:110:SER:HB3	1.98	0.46
6:B:224:LYS:HG2	6:B:340:THR:HB	1.98	0.46
6:B:289:GLN:OE1	6:B:301:ASN:ND2	2.49	0.46
11:G:205:THR:OG1	11:G:206:GLN:N	2.49	0.46
13:I:172:ILE:HB	54:v:17:ARG:HH21	1.79	0.46
32:h:103:LYS:NZ	44:2:231:U:O2	2.47	0.46
39:r:215:ASP:N	39:r:215:ASP:OD1	2.49	0.46
5:9:5:ARG:NH2	44:2:1590:C:O2'	2.49	0.46
23:V:125:LYS:HG2	23:V:129:LEU:HD12	1.98	0.46
44:2:990:C:H2'	44:2:992:C:H5''	1.98	0.46
44:2:1895:G:O2'	44:2:1907:A:N3	2.46	0.46
10:F:15:THR:O	10:F:19:LYS:NZ	2.49	0.46
21:S:98:ARG:NH1	44:2:4872:2MG:O6	2.48	0.46
28:b:66:GLN:O	44:2:729:2MG:N2	2.44	0.46
44:2:1480:C:O2'	44:2:1482:G:OP2	2.34	0.46
44:2:4670:C:O2'	44:2:4672:A:OP2	2.34	0.46
51:z:22:ALA:O	51:z:26:ALA:HB3	2.16	0.46
6:B:234:ARG:NH1	6:B:268:ARG:O	2.49	0.46
44:2:508:G:O2'	44:2:510:U:OP2	2.33	0.46
44:2:1279:A:O2'	44:2:1281:G:N7	2.46	0.46
44:2:2859:G:N2	44:2:3837:C:O2	2.44	0.46
44:2:3969:G:O6	44:2:4051:C:N4	2.49	0.46
13:I:95:VAL:HG11	54:v:18:LEU:HG	1.97	0.46
16:M:27:TYR:HA	16:M:34:CYS:HA	1.96	0.46
25:X:59:SER:O	44:2:2652:G:N2	2.49	0.46
38:p:76:ARG:NE	44:2:730:G:OP2	2.47	0.46
44:2:188:G:N2	44:2:191:G:O6	2.49	0.46
44:2:4200:G:O2'	44:2:4201:G:O5'	2.34	0.46
13:I:93:ARG:CZ	54:v:18:LEU:HB3	2.47	0.45
20:Q:197:LYS:HD2	44:2:4358:U:H4'	1.98	0.45
35:m:56:ALA:HB2	35:m:130:SER:HB3	1.98	0.45
4:8:150:C:N4	11:G:52:THR:O	2.48	0.45
6:B:299:ILE:HB	6:B:313:SER:HB3	1.98	0.45
7:C:95:ARG:NH1	44:2:1265:G:OP1	2.43	0.45
35:m:207:VAL:HG13	35:m:208:GLU:HG3	1.97	0.45
41:R:136:ASN:HB3	41:R:139:ASN:HB2	1.99	0.45
42:J:145:PHE:HZ	42:J:192:LEU:HB2	1.81	0.45
44:2:387:G:O2'	44:2:412:G:N1	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:y:79:ALA:HA	45:y:82:ILE:HD12	1.98	0.45
16:M:52:LYS:NZ	44:2:375:G:OP2	2.42	0.45
44:2:1931:C:N4	44:2:2040:A:O2'	2.49	0.45
44:2:3969:G:O2'	44:2:4054:C:N4	2.50	0.45
8:D:336:ARG:NH1	44:2:947:C:OP1	2.50	0.45
17:N:31:ASP:OD1	17:N:31:ASP:N	2.49	0.45
20:Q:18:TRP:NE1	44:2:1516:G:O2'	2.47	0.45
33:i:50:PRO:HD3	33:i:68:ILE:HG12	1.97	0.45
40:A:413:ASP:OD1	40:A:413:ASP:N	2.49	0.45
44:2:2621:A:OP1	47:d:80:LYS:NZ	2.49	0.45
46:4:196:GLN:HG2	46:4:201:THR:HB	1.99	0.45
44:2:2630:U:O4	47:d:89:LYS:NZ	2.48	0.45
44:2:4253:A:N3	44:2:4254:G:N2	2.65	0.45
44:2:4678:G:OP1	51:z:14:ARG:NH1	2.50	0.45
4:8:141:C:OP1	22:U:38:ARG:NH1	2.50	0.45
38:p:214:SER:OG	38:p:215:SER:N	2.50	0.45
39:r:62:CYS:HB3	39:r:105:LEU:HD22	1.98	0.45
6:B:165:HIS:ND1	6:B:166:THR:O	2.49	0.45
6:B:223:THR:HB	6:B:275:HIS:H	1.81	0.45
8:D:149:GLU:OE2	34:l:71:ARG:NH1	2.50	0.45
41:R:68:ARG:NH1	41:R:69:TYR:O	2.50	0.45
44:2:4065:G:H2'	44:2:4066:U:O4'	2.16	0.45
44:2:4191:G:O2'	44:2:4192:A:P	2.74	0.45
13:I:21:LYS:NZ	44:2:4863:G:OP1	2.46	0.44
17:N:62:ILE:HG12	17:N:68:ILE:HG21	1.98	0.44
17:N:147:ARG:HE	39:r:27:LYS:HE2	1.81	0.44
22:U:116:LEU:HD22	22:U:135:ILE:HD11	1.99	0.44
44:2:4221:C:C6	53:u:679:LEU:HD22	2.52	0.44
3:7:122:GLN:HE22	44:2:5010:U:H1'	1.81	0.44
12:H:80:PRO:HD2	12:H:83:LEU:HD12	1.98	0.44
22:U:44:ARG:NH1	22:U:120:TRP:O	2.48	0.44
42:J:37:TYR:OH	42:J:105:THR:N	2.50	0.44
44:2:496:G:H1	44:2:658:C:HO2'	1.66	0.44
44:2:1871:A2M:H5''	53:u:676:ARG:HH12	1.66	0.44
44:2:1948:G:OP1	54:v:36:SER:CB	2.64	0.44
40:A:160:MET:HE1	46:4:277:PRO:HB2	1.99	0.44
44:2:1332:C:H2'	44:2:1333:A:H8	1.81	0.44
44:2:4203:A:C5'	53:u:628:VAL:HG13	2.44	0.44
6:B:57:VAL:HG23	6:B:366:LYS:HB3	2.00	0.44
8:D:84:THR:OG1	8:D:85:HIS:N	2.49	0.44
33:i:64:LYS:HA	33:i:64:LYS:HD2	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:2:5022:U:O2'	44:2:5025:C:N4	2.45	0.44
46:4:230:LEU:HD12	46:4:231:GLU:H	1.83	0.44
29:c:142:ARG:NH1	44:2:1090:G:OP1	2.49	0.44
37:o:262:LYS:NZ	44:2:4933:C:OP2	2.49	0.44
46:4:455:LYS:HE3	46:4:455:LYS:HB2	1.80	0.44
13:I:91:LYS:HG2	13:I:145:ILE:HG22	1.99	0.44
23:V:55:LEU:HD23	23:V:58:LEU:HD12	2.00	0.44
31:g:124:VAL:HG22	31:g:138:VAL:HG23	2.00	0.44
44:2:3932:U:H2'	44:2:3933:G:H8	1.83	0.44
44:2:4698:C:H41	54:v:30:ARG:NH1	2.16	0.44
41:R:124:PHE:HB2	41:R:129:LEU:HG	1.99	0.44
44:2:495:C:C2	44:2:497:G:N2	2.85	0.44
44:2:1945:G:N2	54:v:39:ALA:O	2.50	0.44
44:2:4066:U:H2'	44:2:4067:U:O4'	2.17	0.44
4:8:75:G:OP2	32:h:74:TYR:OH	2.35	0.44
5:9:115:ARG:O	5:9:116:ARG:C	2.61	0.44
8:D:33:ARG:HG3	8:D:122:TYR:HE2	1.83	0.44
8:D:110:ARG:O	8:D:113:ARG:NH1	2.49	0.44
35:m:156:LYS:NZ	44:2:3662:A:OP2	2.44	0.44
40:A:245:LYS:HG2	40:A:248:LYS:HE3	1.99	0.44
44:2:1245:C:H2'	44:2:1246:G:H8	1.83	0.44
44:2:1437:C:H1'	44:2:2098:G:H3'	2.00	0.44
3:7:100:LYS:HE2	3:7:100:LYS:HB3	1.76	0.44
6:B:168:MET:HE1	6:B:173:LEU:HD12	2.00	0.44
17:N:101:ASP:HB2	44:2:4248:A:C4'	2.48	0.44
20:Q:83:VAL:HG12	20:Q:114:VAL:HG21	2.00	0.44
37:o:66:LYS:O	37:o:71:ARG:NH2	2.50	0.44
44:2:4188:U:H2'	44:2:4189:U:H6	1.82	0.44
44:2:4477:A:N7	46:4:7:LYS:NZ	2.66	0.44
53:u:332:LEU:HD12	53:u:332:LEU:HA	1.92	0.44
26:Z:45:GLN:HE22	44:2:1698:C:H42	1.66	0.43
27:a:135:LYS:NZ	44:2:2898:G:OP2	2.50	0.43
44:2:4195:G:N1	53:u:647:LYS:NZ	2.66	0.43
46:4:364:ILE:HG22	46:4:366:THR:H	1.83	0.43
46:4:400:ASP:HA	46:4:403:LEU:HG	2.00	0.43
53:u:426:LYS:HB3	53:u:604:LYS:HE3	1.99	0.43
13:I:174:LYS:NZ	54:v:10:HIS:CG	2.86	0.43
22:U:113:LEU:HB2	22:U:134:LEU:HD12	2.00	0.43
42:J:87:ASP:OD1	42:J:87:ASP:N	2.49	0.43
24:W:2:VAL:HG23	44:2:4231:C:OP2	2.18	0.43
27:a:105:LEU:HD13	27:a:135:LYS:HE3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:o:223:ARG:HA	37:o:224:LYS:HA	1.83	0.43
44:2:90:G:OP2	44:2:92:C:N4	2.49	0.43
52:t:87:ILE:HA	52:t:90:LEU:HD12	1.99	0.43
1:5:13:A:OP2	1:5:66:G:N2	2.47	0.43
3:7:80:LYS:HE2	3:7:80:LYS:HB2	1.81	0.43
12:H:52:LYS:HA	12:H:52:LYS:HD3	1.87	0.43
17:N:23:ASN:ND2	44:2:4258:C:C2'	2.75	0.43
17:N:42:GLN:HB3	17:N:117:ILE:HD12	2.01	0.43
29:c:111:GLU:HA	29:c:114:GLN:HG3	2.00	0.43
44:2:753:C:H41	44:2:910:G:H1	1.65	0.43
44:2:3658:C:H2'	44:2:3659:G:H8	1.82	0.43
44:2:3967:G:C5	44:2:4057:C:N3	2.87	0.43
44:2:4195:G:C2	44:2:4200:G:C5	3.06	0.43
49:k:82:VAL:HG13	49:k:114:ARG:HG2	2.00	0.43
52:t:43:PRO:HB2	52:t:48:ARG:HE	1.83	0.43
25:X:18:TYR:HB3	35:m:180:LEU:HD22	2.01	0.43
35:m:34:PHE:O	35:m:38:HIS:HB2	2.18	0.43
35:m:147:ARG:HB3	35:m:157:VAL:HG22	2.01	0.43
44:2:2469:C:H5	44:2:2471:G:H1	1.67	0.43
44:2:4197:G:C4	53:u:655:ARG:CZ	3.01	0.43
46:4:619:LYS:O	46:4:623:SER:HB2	2.19	0.43
4:8:41:A:HO2'	16:M:59:THR:HG1	1.66	0.43
5:9:99:GLN:NE2	5:9:103:GLU:OE1	2.50	0.43
16:M:49:TRP:O	44:2:1646:A:O2'	2.33	0.43
44:2:1195:G:N3	44:2:1195:G:H2'	2.33	0.43
46:4:250:ALA:HB2	46:4:339:LEU:HB2	2.00	0.43
52:t:103:LEU:HA	52:t:106:LYS:HE3	2.00	0.43
12:H:108:GLN:HA	12:H:111:GLU:HG2	2.00	0.43
27:a:92:LYS:NZ	44:2:1574:B9B:OP2	2.52	0.43
32:h:30:MET:HE1	32:h:75:ARG:HG2	2.00	0.43
45:y:75:PRO:HB2	45:y:80:LEU:HD21	1.99	0.43
52:t:204:LEU:HD13	52:t:217:TYR:HB3	2.01	0.43
9:E:81:LEU:O	9:E:85:CYS:HB2	2.18	0.43
12:H:96:ASN:HD22	44:2:136:C:H5''	1.83	0.43
17:N:89:VAL:HG21	17:N:114:ASP:HB2	1.99	0.43
53:u:196:ALA:HB2	53:u:289:LEU:HD22	1.99	0.43
4:8:7:U:O2'	44:2:1305:C:OP1	2.35	0.43
8:D:45:ARG:NH2	44:2:2295:C:O2'	2.52	0.43
32:h:121:ARG:NH1	44:2:194:C:O2	2.52	0.43
35:m:241:ARG:NH1	44:2:3659:G:OP1	2.51	0.43
36:n:59:THR:OG1	36:n:65:ASN:OD1	2.37	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:n:73:LYS:HD3	44:2:952:G:H5''	2.00	0.43
41:R:111:THR:O	41:R:115:GLN:OE1	2.36	0.43
44:2:4697:U:H4'	54:v:29:SER:OG	2.16	0.43
24:W:58:LYS:HD3	24:W:58:LYS:HA	1.92	0.43
44:2:753:C:H5	44:2:910:G:H22	1.66	0.43
44:2:1255:A:OP1	44:2:1257:A:N6	2.46	0.43
44:2:1303:A:O2'	44:2:2314:G:OP1	2.37	0.43
3:7:113:LYS:HB3	3:7:113:LYS:HE2	1.83	0.42
6:B:301:ASN:OD1	6:B:301:ASN:N	2.52	0.42
36:n:50:VAL:HG22	36:n:69:VAL:HG23	2.00	0.42
42:J:34:VAL:HA	42:J:37:TYR:HB3	2.01	0.42
42:J:153:LEU:HD13	42:J:158:LEU:HD22	2.01	0.42
44:2:679:C:H2'	44:2:680:G:H8	1.83	0.42
44:2:3923:A:H5''	53:u:635:ASN:HD22	1.84	0.42
2:6:236:MET:HB2	2:6:239:SER:HB2	2.01	0.42
3:7:61:LYS:H	3:7:61:LYS:HG2	1.63	0.42
6:B:222:VAL:O	6:B:343:ARG:NH1	2.53	0.42
6:B:305:THR:O	6:B:305:THR:OG1	2.34	0.42
8:D:69:THR:OG1	44:2:4390:A:OP1	2.37	0.42
32:h:8:THR:HB	32:h:10:ASP:H	1.85	0.42
44:2:3720:G:H22	44:2:3733:A:H2	1.67	0.42
11:G:81:ASN:O	11:G:84:THR:OG1	2.37	0.42
26:Z:159:PRO:HA	26:Z:160:HIS:HA	1.81	0.42
30:e:64:THR:HG22	30:e:76:VAL:HG22	2.02	0.42
44:2:1556:C:O2'	44:2:2669:C:OP1	2.37	0.42
44:2:3971:G:H21	44:2:3973:G:H1'	1.84	0.42
51:z:90:HIS:O	51:z:92:GLN:NE2	2.49	0.42
2:6:155:SER:OG	2:6:156:ASN:N	2.48	0.42
44:2:3950:U:H2'	44:2:3951:G:C8	2.54	0.42
44:2:3953:G:N3	44:2:3954:A:H1'	2.34	0.42
35:m:6:ARG:NH2	35:m:199:VAL:O	2.52	0.42
44:2:1366:G:O2'	44:2:1367:C:O2	2.37	0.42
44:2:1865:G:N2	44:2:1868:A:H62	2.17	0.42
44:2:3619:G:H22	44:2:3624:A:H1'	1.84	0.42
44:2:3977:C:N4	44:2:4032:G:O5'	2.53	0.42
44:2:4637:OMG:H1'	44:2:4637:OMG:HM23	1.79	0.42
53:u:623:ASP:OD1	53:u:623:ASP:N	2.45	0.42
4:8:126:C:OP2	44:2:2488:C:N4	2.53	0.42
11:G:106:THR:O	11:G:110:LYS:HB2	2.20	0.42
44:2:4066:U:H4'	44:2:4066:U:OP1	2.20	0.42
45:y:103:ASN:HA	45:y:142:ASN:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:4:536:ASP:OD1	46:4:536:ASP:N	2.47	0.42
53:u:196:ALA:O	53:u:200:ASN:ND2	2.51	0.42
40:A:282:HIS:HB3	40:A:289:PHE:HB3	2.02	0.42
44:2:3975:C:H5''	44:2:4031:U:H5'	2.01	0.42
44:2:4068:U:H2'	44:2:4069:U:O4'	2.20	0.42
44:2:4620:OMU:H1'	44:2:4620:OMU:HM23	1.82	0.42
52:t:104:ALA:O	52:t:133:LYS:NZ	2.50	0.42
12:H:104:THR:HG23	12:H:107:GLN:H	1.85	0.42
14:K:2:ALA:HB3	20:Q:172:GLU:HG3	2.00	0.42
23:V:202:LEU:H	44:2:4872:2MG:HM21	1.84	0.42
44:2:1444:G:H22	44:2:2103:G:H1	1.68	0.42
44:2:4204:C:O2'	44:2:4205:A:O5'	2.37	0.42
46:4:179:VAL:O	46:4:289:ASN:ND2	2.51	0.42
46:4:206:PHE:HB2	46:4:221:ASP:HB3	2.01	0.42
48:j:100:ASN:C	48:j:100:ASN:HD22	2.27	0.42
6:B:57:VAL:HG12	6:B:73:VAL:HG22	2.01	0.42
6:B:228:TYR:O	44:2:2835:A:O2'	2.35	0.42
12:H:105:LYS:HA	12:H:108:GLN:HG2	2.02	0.42
19:P:9:ILE:HG23	19:P:51:LEU:HD21	2.02	0.42
22:U:98:LEU:HA	22:U:101:VAL:HG12	2.01	0.42
30:e:37:LEU:HD21	30:e:105:ILE:HD11	2.02	0.42
37:o:178:PRO:HB2	37:o:181:LEU:HD23	2.02	0.42
44:2:2324:C:O2'	49:k:98:GLU:OE1	2.35	0.42
44:2:4187:G:H2'	44:2:4188:U:C6	2.55	0.42
54:v:41:LYS:HA	54:v:41:LYS:HD2	1.85	0.42
4:8:122:G:H1	4:8:128:C:H42	1.67	0.42
5:9:87:LYS:NZ	44:2:3614:G:N7	2.67	0.42
11:G:258:ALA:O	11:G:262:ALA:HB3	2.20	0.42
13:I:93:ARG:CZ	54:v:18:LEU:HD13	2.49	0.42
17:N:31:ASP:HA	17:N:34:THR:HG22	2.02	0.42
17:N:102:THR:HG21	44:2:4261:C:O2'	2.19	0.42
44:2:1168:G:C6	44:2:1194:G:C5	3.08	0.42
44:2:4203:A:N6	53:u:630:LYS:HG2	2.35	0.42
48:j:64:ILE:HG23	48:j:68:LEU:HD23	2.00	0.42
1:5:60:G:H2'	1:5:61:G:H8	1.84	0.41
13:I:105:ILE:HD12	13:I:105:ILE:HA	1.95	0.41
35:m:33:ASP:N	35:m:33:ASP:OD1	2.52	0.41
36:n:52:LYS:NZ	44:2:4751:G:N7	2.68	0.41
37:o:161:ARG:NH1	37:o:270:TYR:O	2.53	0.41
10:F:41:ALA:O	10:F:52:ARG:NH1	2.44	0.41
17:N:110:GLN:HG2	44:2:4251:A:H1'	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:p:157:ARG:HD2	38:p:213:LEU:HD23	2.01	0.41
42:J:131:ALA:HA	42:J:197:MET:HG2	2.02	0.41
44:2:3951:G:O6	44:2:4060:U:O4	2.37	0.41
2:6:56:CYS:SG	30:e:123:LYS:NZ	2.81	0.41
12:H:55:ALA:O	12:H:59:THR:OG1	2.35	0.41
14:K:56:ARG:HA	14:K:59:GLU:HG2	2.01	0.41
44:2:2848:G:O2'	44:2:3838:U:O4	2.35	0.41
46:4:544:ARG:HH21	47:d:119:GLN:HB3	1.84	0.41
52:t:107:TYR:O	52:t:133:LYS:NZ	2.44	0.41
4:8:51:U:OP2	19:P:21:ARG:NH2	2.53	0.41
11:G:103:ARG:NH2	11:G:192:ARG:O	2.54	0.41
14:K:33:LEU:HD21	14:K:38:LYS:HB2	2.02	0.41
17:N:15:LEU:HD11	17:N:134:LEU:HB3	2.01	0.41
24:W:5:PRO:HD3	44:2:4232:U:O2'	2.20	0.41
42:J:58:ASN:OD1	45:y:123:ARG:NH1	2.53	0.41
44:2:4203:A:C5'	53:u:628:VAL:CG1	2.89	0.41
44:2:4373:G:H22	53:u:627:PHE:HD1	1.68	0.41
44:2:4740:G:H1'	44:2:4742:G:H5''	2.02	0.41
46:4:135:GLY:O	46:4:139:THR:OG1	2.38	0.41
53:u:399:LYS:HE2	53:u:399:LYS:HB3	1.91	0.41
5:9:17:ARG:NH2	44:2:2860:C:OP1	2.51	0.41
8:D:133:LEU:HD13	34:l:6:GLN:HE21	1.86	0.41
17:N:60:PHE:CE2	44:2:4257:A:C2	3.09	0.41
22:U:140:LYS:HA	22:U:143:ARG:HB3	2.02	0.41
37:o:181:LEU:O	44:2:4883:C:N4	2.50	0.41
40:A:197:ILE:HD13	40:A:382:VAL:HG13	2.03	0.41
46:4:370:ASP:OD1	46:4:370:ASP:N	2.54	0.41
46:4:625:LYS:HG3	46:4:627:LYS:HE3	2.01	0.41
53:u:127:ARG:HH11	53:u:173:ASN:HB2	1.85	0.41
8:D:326:LEU:HD21	8:D:333:LYS:HB2	2.03	0.41
17:N:90:ARG:NH1	17:N:108:GLY:O	2.54	0.41
26:Z:72:LEU:HB2	26:Z:75:ARG:HD2	2.03	0.41
29:c:130:ARG:NH2	44:2:1802:A:N3	2.69	0.41
44:2:3683:C:H2'	53:u:4:ARG:HH21	1.85	0.41
4:8:83:C:N3	32:h:50:ARG:NH2	2.68	0.41
13:I:173:ARG:HD2	54:v:7:ILE:HG21	2.01	0.41
24:W:23:VAL:HG23	24:W:93:LEU:HD11	2.01	0.41
34:l:66:ARG:NH1	34:l:75:THR:O	2.53	0.41
44:2:120:A:N1	44:2:148:C:O2'	2.49	0.41
44:2:4448:G:H22	44:2:4502:C:H5	1.69	0.41
53:u:374:LEU:HD22	53:u:398:ILE:HG12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:D:134:PRO:O	8:D:138:MET:HB2	2.21	0.41
13:I:180:TYR:OH	54:v:17:ARG:HD2	2.21	0.41
20:Q:155:MET:HA	20:Q:156:PRO:HD3	1.77	0.41
35:m:225:ILE:HG12	35:m:234:LYS:HA	2.03	0.41
37:o:237:LYS:HB2	37:o:237:LYS:HE2	1.89	0.41
44:2:2877:G:N2	44:2:3824:A:O2'	2.51	0.41
53:u:609:ASP:OD1	53:u:609:ASP:N	2.53	0.41
2:6:93:GLN:HB2	2:6:132:VAL:HG13	2.03	0.41
10:F:33:LEU:HD23	10:F:33:LEU:HA	1.96	0.41
27:a:6:LEU:O	27:a:10:LEU:HB2	2.21	0.41
33:i:136:PHE:OXT	44:2:4122:G:O2'	2.37	0.41
39:r:84:PRO:HB3	39:r:89:LYS:HG3	2.03	0.41
42:J:30:LEU:HG	42:J:64:ARG:HH21	1.86	0.41
44:2:1478:C:H2'	44:2:1479:G:H8	1.86	0.41
44:2:4221:C:H42	53:u:682:LYS:HE2	1.86	0.41
2:6:39:GLU:O	2:6:43:SER:CB	2.66	0.41
11:G:137[B]:ARG:HD3	11:G:146:LEU:HD11	2.03	0.41
29:c:100:LYS:HB2	44:2:1730:U:H4'	2.01	0.41
39:r:282:GLN:HA	39:r:285:ALA:HB3	2.03	0.41
44:2:2045:G:N2	44:2:2046:G:N7	2.68	0.41
44:2:4193:C:H2'	44:2:4194:U:C6	2.56	0.41
49:k:26:ASP:OD1	49:k:26:ASP:N	2.53	0.41
16:M:67:LEU:HD23	16:M:67:LEU:HA	1.97	0.40
24:W:36:GLN:HG2	44:2:4363:A:H5''	2.03	0.40
44:2:308:G:OP2	44:2:308:G:N2	2.44	0.40
44:2:4058:U:H4'	53:u:153:LYS:O	2.21	0.40
45:y:25:THR:HG21	45:y:40:LYS:HZ1	1.87	0.40
46:4:176:TYR:OH	46:4:256:ASP:OD1	2.37	0.40
46:4:248:ARG:HB3	46:4:249:ALA:H	1.76	0.40
17:N:87:LEU:HD12	17:N:92:TYR:HA	2.03	0.40
40:A:431:LYS:HA	40:A:431:LYS:HD3	1.97	0.40
44:2:1994:C:H2'	44:2:1995:G:H8	1.86	0.40
2:6:201:ASP:OD1	2:6:201:ASP:N	2.48	0.40
11:G:258:ALA:O	11:G:262:ALA:CB	2.69	0.40
12:H:79:LYS:O	12:H:84:ARG:NH2	2.53	0.40
34:l:97:ILE:HG21	34:l:107:ARG:HB2	2.03	0.40
42:J:50:ASN:OD1	44:2:1998:A:N6	2.54	0.40
44:2:268:G:H2'	44:2:269:G:H8	1.86	0.40
44:2:4202:U:H5''	44:2:4202:U:H6	1.86	0.40
27:a:96:MET:HE3	27:a:96:MET:HB2	1.94	0.40
39:r:273:LEU:HA	39:r:276:LYS:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:r:277:LYS:HA	39:r:280:VAL:HG12	2.02	0.40
44:2:3654:G:O2'	44:2:3693:U:OP1	2.39	0.40
44:2:4301:U:OP2	44:2:4303:C:N4	2.55	0.40
8:D:143:ARG:HD3	8:D:143:ARG:HA	1.94	0.40
11:G:75:LYS:HE3	11:G:75:LYS:HB2	1.90	0.40
17:N:67:LYS:HE3	17:N:67:LYS:HB3	1.90	0.40
26:Z:43:PHE:HZ	26:Z:81:VAL:HG21	1.86	0.40
28:b:51:LEU:HD13	29:c:151:LEU:HD23	2.04	0.40
30:e:69:LYS:HD3	30:e:69:LYS:HA	1.94	0.40
36:n:37:ASP:OD1	36:n:37:ASP:N	2.54	0.40
40:A:369:SER:OG	40:A:370:GLU:N	2.53	0.40
44:2:2528:G:H4'	44:2:2783:A:H4'	2.03	0.40
44:2:4996:C:OP1	48:j:32:ARG:NH1	2.48	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	6	242/245 (99%)	225 (93%)	17 (7%)	0	100	100
3	7	133/163 (82%)	129 (97%)	4 (3%)	0	100	100
5	9	93/134 (69%)	81 (87%)	12 (13%)	0	100	100
6	B	401/403 (100%)	376 (94%)	25 (6%)	0	100	100
7	C	89/159 (56%)	87 (98%)	2 (2%)	0	100	100
8	D	356/427 (83%)	331 (93%)	25 (7%)	0	100	100
9	E	96/115 (84%)	92 (96%)	4 (4%)	0	100	100
10	F	107/117 (92%)	104 (97%)	3 (3%)	0	100	100
11	G	240/266 (90%)	229 (95%)	11 (5%)	0	100	100
12	H	120/123 (98%)	116 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	I	188/192 (98%)	178 (95%)	10 (5%)	0	100	100
14	K	100/105 (95%)	95 (95%)	5 (5%)	0	100	100
15	L	145/148 (98%)	135 (93%)	10 (7%)	0	100	100
16	M	84/97 (87%)	78 (93%)	6 (7%)	0	100	100
17	N	163/178 (92%)	140 (86%)	21 (13%)	2 (1%)	10	40
18	O	67/70 (96%)	63 (94%)	4 (6%)	0	100	100
19	P	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
20	Q	208/211 (99%)	195 (94%)	13 (6%)	0	100	100
21	S	133/215 (62%)	127 (96%)	6 (4%)	0	100	100
22	U	201/204 (98%)	192 (96%)	9 (4%)	0	100	100
23	V	199/203 (98%)	193 (97%)	6 (3%)	0	100	100
24	W	98/106 (92%)	94 (96%)	4 (4%)	0	100	100
25	X	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
26	Z	185/188 (98%)	180 (97%)	5 (3%)	0	100	100
27	a	146/196 (74%)	140 (96%)	6 (4%)	0	100	100
28	b	174/176 (99%)	168 (97%)	6 (3%)	0	100	100
29	c	153/160 (96%)	149 (97%)	4 (3%)	0	100	100
30	e	129/140 (92%)	114 (88%)	15 (12%)	0	100	100
31	g	116/156 (74%)	113 (97%)	3 (3%)	0	100	100
32	h	132/145 (91%)	130 (98%)	2 (2%)	0	100	100
33	i	133/136 (98%)	121 (91%)	12 (9%)	0	100	100
34	l	123/137 (90%)	117 (95%)	6 (5%)	0	100	100
35	m	246/257 (96%)	216 (88%)	30 (12%)	0	100	100
36	n	107/110 (97%)	103 (96%)	3 (3%)	1 (1%)	14	48
37	o	231/288 (80%)	215 (93%)	16 (7%)	0	100	100
38	p	224/248 (90%)	213 (95%)	11 (5%)	0	100	100
39	r	291/297 (98%)	278 (96%)	13 (4%)	0	100	100
40	A	305/731 (42%)	296 (97%)	8 (3%)	1 (0%)	36	70
41	R	151/203 (74%)	143 (95%)	7 (5%)	1 (1%)	18	53
42	J	221/239 (92%)	209 (95%)	12 (5%)	0	100	100
43	T	42/99 (42%)	42 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	y	163/165 (99%)	159 (98%)	4 (2%)	0	100	100
46	4	607/634 (96%)	559 (92%)	45 (7%)	3 (0%)	24	60
47	d	102/128 (80%)	94 (92%)	8 (8%)	0	100	100
48	j	109/125 (87%)	103 (94%)	6 (6%)	0	100	100
49	k	127/135 (94%)	121 (95%)	6 (5%)	0	100	100
50	Y	165/184 (90%)	154 (93%)	11 (7%)	0	100	100
51	z	63/129 (49%)	60 (95%)	2 (3%)	1 (2%)	7	34
52	t	210/217 (97%)	201 (96%)	9 (4%)	0	100	100
53	u	546/687 (80%)	515 (94%)	30 (6%)	1 (0%)	43	76
54	v	33/260 (13%)	33 (100%)	0	0	100	100
All	All	8834/10594 (83%)	8338 (94%)	486 (6%)	10 (0%)	49	80

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	N	176	PRO
36	n	106	TYR
40	A	160	MET
53	u	326	GLY
17	N	21	CYS
51	z	24	LYS
46	4	88	ASP
41	R	99	ARG
46	4	407	ASP
46	4	366	THR

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	6	212/213 (100%)	212 (100%)	0	100	100
3	7	126/149 (85%)	126 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	9	82/114 (72%)	80 (98%)	2 (2%)	43	73
6	B	349/349 (100%)	349 (100%)	0	100	100
7	C	78/126 (62%)	78 (100%)	0	100	100
8	D	298/348 (86%)	298 (100%)	0	100	100
9	E	83/97 (86%)	83 (100%)	0	100	100
10	F	94/100 (94%)	94 (100%)	0	100	100
11	G	204/223 (92%)	204 (100%)	0	100	100
12	H	109/110 (99%)	109 (100%)	0	100	100
13	I	169/171 (99%)	168 (99%)	1 (1%)	78	88
14	K	86/89 (97%)	86 (100%)	0	100	100
15	L	120/121 (99%)	120 (100%)	0	100	100
16	M	73/80 (91%)	73 (100%)	0	100	100
17	N	138/149 (93%)	138 (100%)	0	100	100
18	O	64/65 (98%)	64 (100%)	0	100	100
19	P	47/48 (98%)	47 (100%)	0	100	100
20	Q	176/177 (99%)	176 (100%)	0	100	100
21	S	115/161 (71%)	115 (100%)	0	100	100
22	U	171/172 (99%)	171 (100%)	0	100	100
23	V	173/174 (99%)	173 (100%)	0	100	100
24	W	88/94 (94%)	88 (100%)	0	100	100
25	X	74/75 (99%)	74 (100%)	0	100	100
26	Z	164/165 (99%)	164 (100%)	0	100	100
27	a	133/175 (76%)	133 (100%)	0	100	100
28	b	157/157 (100%)	157 (100%)	0	100	100
29	c	136/140 (97%)	136 (100%)	0	100	100
30	e	101/107 (94%)	101 (100%)	0	100	100
31	g	106/133 (80%)	106 (100%)	0	100	100
32	h	124/135 (92%)	124 (100%)	0	100	100
33	i	117/118 (99%)	117 (100%)	0	100	100
34	l	109/121 (90%)	109 (100%)	0	100	100
35	m	190/199 (96%)	190 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	n	88/89 (99%)	88 (100%)	0	100	100
37	o	208/252 (82%)	208 (100%)	0	100	100
38	p	195/215 (91%)	195 (100%)	0	100	100
39	r	246/250 (98%)	246 (100%)	0	100	100
40	A	272/654 (42%)	272 (100%)	0	100	100
41	R	141/184 (77%)	141 (100%)	0	100	100
42	J	199/214 (93%)	199 (100%)	0	100	100
43	T	37/76 (49%)	37 (100%)	0	100	100
45	y	137/137 (100%)	137 (100%)	0	100	100
46	4	554/574 (96%)	554 (100%)	0	100	100
47	d	94/115 (82%)	94 (100%)	0	100	100
48	j	101/110 (92%)	100 (99%)	1 (1%)	68	84
49	k	115/121 (95%)	115 (100%)	0	100	100
50	Y	147/163 (90%)	147 (100%)	0	100	100
51	z	61/115 (53%)	61 (100%)	0	100	100
52	t	191/196 (97%)	191 (100%)	0	100	100
53	u	509/629 (81%)	509 (100%)	0	100	100
54	v	32/228 (14%)	31 (97%)	1 (3%)	35	68
All	All	7793/9177 (85%)	7788 (100%)	5 (0%)	87	93

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	9	115	ARG
5	9	116	ARG
13	I	93	ARG
48	j	100	ASN
54	v	36	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (95) such sidechains are listed below:

Mol	Chain	Res	Type
2	6	140	GLN
2	6	157	GLN
2	6	178	GLN

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Mol	Chain	Res	Type
3	7	122	GLN
3	7	130	ASN
3	7	132	HIS
5	9	79	HIS
6	B	11	HIS
6	B	109	HIS
6	B	354	GLN
7	C	11	ASN
7	C	19	ASN
8	D	347	HIS
9	E	15	ASN
9	E	40	GLN
10	F	110	GLN
11	G	85	GLN
11	G	149	ASN
12	H	96	ASN
13	I	39	ASN
13	I	156	ASN
13	I	162	GLN
13	I	189	GLN
14	K	15	HIS
15	L	19	HIS
15	L	44	ASN
15	L	60	HIS
16	M	57	ASN
17	N	23	ASN
19	P	25	GLN
19	P	33	ASN
20	Q	175	ASN
22	U	109	HIS
23	V	50	ASN
23	V	63	ASN
24	W	3	ASN
26	Z	7	HIS
26	Z	21	GLN
26	Z	45	GLN
28	b	50	GLN
28	b	77	ASN
29	c	98	HIS
30	e	27	ASN
30	e	135	ASN
32	h	14	ASN

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Mol	Chain	Res	Type
32	h	20	ASN
32	h	40	GLN
32	h	65	GLN
32	h	91	ASN
33	i	127	ASN
34	l	6	GLN
34	l	31	ASN
35	m	140	ASN
35	m	215	ASN
36	n	21	GLN
36	n	56	ASN
38	p	24	ASN
38	p	99	ASN
38	p	241	ASN
38	p	248	ASN
39	r	111	ASN
39	r	122	GLN
41	R	61	HIS
45	y	103	ASN
46	4	5	ASN
46	4	64	GLN
46	4	274	ASN
46	4	311	GLN
46	4	361	HIS
46	4	482	GLN
46	4	502	ASN
47	d	94	ASN
48	j	34	HIS
48	j	100	ASN
49	k	57	ASN
49	k	63	ASN
49	k	80	HIS
50	Y	40	HIS
50	Y	116	HIS
50	Y	166	GLN
52	t	71	GLN
53	u	18	ASN
53	u	34	GLN
53	u	36	ASN
53	u	50	ASN
53	u	65	GLN
53	u	68	HIS

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Mol	Chain	Res	Type
53	u	76	ASN
53	u	288	HIS
53	u	328	HIS
53	u	363	HIS
53	u	448	GLN
53	u	603	HIS
53	u	635	ASN
54	v	10	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	119/120 (99%)	14 (11%)	0
4	8	155/156 (99%)	28 (18%)	0
44	2	3569/5054 (70%)	870 (24%)	22 (0%)
All	All	3843/5330 (72%)	912 (23%)	22 (0%)

All (912) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	11	A
1	5	22	A
1	5	24	C
1	5	33	U
1	5	40	U
1	5	41	G
1	5	48	G
1	5	53	U
1	5	63	C
1	5	64	G
1	5	100	A
1	5	109	U
1	5	110	G
1	5	120	U
4	8	23	C
4	8	25	G
4	8	34	U
4	8	35	C
4	8	38	U
4	8	48	A
4	8	52	A

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Mol	Chain	Res	Type
4	8	59	A
4	8	60	G
4	8	62	A
4	8	63	U
4	8	71	A
4	8	82	A
4	8	84	A
4	8	85	U
4	8	86	U
4	8	87	G
4	8	103	A
4	8	104	A
4	8	105	C
4	8	110	U
4	8	114	G
4	8	123	U
4	8	124	U
4	8	125	C
4	8	126	C
4	8	127	U
4	8	150	C
44	2	6	C
44	2	15	A
44	2	25	A
44	2	39	A
44	2	42	A
44	2	44	A
44	2	48	G
44	2	59	A
44	2	64	A
44	2	65	A
44	2	66	A
44	2	69	A
44	2	72	C
44	2	73	A
44	2	84	A
44	2	91	G
44	2	98	A
44	2	104	G
44	2	108	A
44	2	109	G
44	2	110	C

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Mol	Chain	Res	Type
44	2	119	G
44	2	120	A
44	2	122	U
44	2	131	C
44	2	133	C
44	2	134	G
44	2	135	G
44	2	136	C
44	2	137	G
44	2	144	G
44	2	152	U
44	2	159	C
44	2	165	A
44	2	169	G
44	2	172	C
44	2	176	G
44	2	183	C
44	2	184	U
44	2	185	C
44	2	188	G
44	2	197	A
44	2	200	U
44	2	209	U
44	2	218	A
44	2	219	G
44	2	220	C
44	2	234	G
44	2	237	B9B
44	2	253	G
44	2	254	G
44	2	255	C
44	2	256	G
44	2	258	G
44	2	259	C
44	2	262	G
44	2	265	C
44	2	266	C
44	2	267	G
44	2	279	A
44	2	280	G
44	2	297	U
44	2	306	A

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Mol	Chain	Res	Type
44	2	315	G
44	2	316	U
44	2	340	C
44	2	344	A
44	2	345	C
44	2	349	A
44	2	363	A
44	2	387	G
44	2	398	A2M
44	2	406	C
44	2	407	A
44	2	409	G
44	2	410	A
44	2	411	G
44	2	412	G
44	2	433	A
44	2	449	C
44	2	450	G
44	2	452	A
44	2	453	G
44	2	454	U
44	2	456	C
44	2	457	G
44	2	465	G
44	2	467	U
44	2	468	U
44	2	483	G
44	2	484	U
44	2	485	C
44	2	486	C
44	2	489	C
44	2	491	G
44	2	495	C
44	2	496	G
44	2	497	G
44	2	498	C
44	2	499	G
44	2	500	G
44	2	504	G
44	2	505	G
44	2	509	A
44	2	510	U

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Mol	Chain	Res	Type
44	2	512	U
44	2	513	U
44	2	514	U
44	2	515	C
44	2	518	G
44	2	519	C
44	2	644	G
44	2	646	G
44	2	648	G
44	2	657	C
44	2	659	G
44	2	662	C
44	2	667	A
44	2	668	C
44	2	669	C
44	2	685	C
44	2	686	A
44	2	688	U
44	2	692	A
44	2	696	C
44	2	697	G
44	2	704	C
44	2	708	G
44	2	731	G
44	2	738	C
44	2	739	G
44	2	740	G
44	2	742	G
44	2	759	G
44	2	904	C
44	2	905	C
44	2	909	A
44	2	910	G
44	2	913	U
44	2	914	U
44	2	915	A
44	2	916	C
44	2	917	A
44	2	918	G
44	2	923	C
44	2	924	C
44	2	925	C

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Mol	Chain	Res	Type
44	2	926	G
44	2	932	A
44	2	933	G
44	2	934	C
44	2	935	A
44	2	936	C
44	2	937	U
44	2	941	C
44	2	943	A
44	2	944	A
44	2	945	U
44	2	946	C
44	2	956	A
44	2	959	G
44	2	960	A
44	2	961	G
44	2	962	C
44	2	963	G
44	2	964	A
44	2	965	G
44	2	966	A
44	2	967	C
44	2	969	C
44	2	970	G
44	2	971	U
44	2	972	C
44	2	982	U
44	2	984	C
44	2	988	C
44	2	989	U
44	2	990	C
44	2	991	C
44	2	992	C
44	2	993	G
44	2	994	G
44	2	995	C
44	2	996	G
44	2	1048	G
44	2	1049	C
44	2	1050	C
44	2	1051	G
44	2	1066	G

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Mol	Chain	Res	Type
44	2	1068	G
44	2	1070	G
44	2	1071	C
44	2	1072	C
44	2	1082	C
44	2	1083	U
44	2	1095	A
44	2	1100	U
44	2	1168	G
44	2	1173	G
44	2	1176	C
44	2	1178	G
44	2	1179	U
44	2	1180	C
44	2	1181	C
44	2	1182	C
44	2	1183	C
44	2	1187	G
44	2	1195	G
44	2	1198	G
44	2	1200	G
44	2	1202	C
44	2	1203	G
44	2	1209	U
44	2	1211	G
44	2	1215	C
44	2	1216	C
44	2	1218	G
44	2	1220	G
44	2	1222	A
44	2	1235	G
44	2	1241	C
44	2	1245	C
44	2	1253	G
44	2	1254	A
44	2	1255	A
44	2	1260	G
44	2	1266	G
44	2	1269	G
44	2	1271	G
44	2	1272	C
44	2	1275	G

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Mol	Chain	Res	Type
44	2	1280	C
44	2	1283	G
44	2	1284	G
44	2	1287	G
44	2	1289	C
44	2	1294	A
44	2	1295	C
44	2	1296	G
44	2	1301	C
44	2	1302	U
44	2	1303	A
44	2	1314	C
44	2	1318	C
44	2	1320	U
44	2	1321	G
44	2	1322	A
44	2	1326	A2M
44	2	1354	A
44	2	1358	G
44	2	1359	G
44	2	1365	C
44	2	1366	G
44	2	1367	C
44	2	1370	G
44	2	1371	A
44	2	1377	G
44	2	1378	C
44	2	1379	C
44	2	1381	U
44	2	1387	A
44	2	1394	G
44	2	1397	A
44	2	1398	A
44	2	1402	C
44	2	1404	G
44	2	1407	C
44	2	1409	C
44	2	1410	U
44	2	1414	C
44	2	1417	C
44	2	1419	G
44	2	1420	A

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Mol	Chain	Res	Type
44	2	1425	G
44	2	1439	C
44	2	1441	C
44	2	1442	C
44	2	1444	G
44	2	1446	C
44	2	1447	C
44	2	1448	G
44	2	1482	G
44	2	1483	C
44	2	1497	A
44	2	1498	G
44	2	1502	G
44	2	1503	A
44	2	1525	A
44	2	1534	A2M
44	2	1547	A
44	2	1564	A
44	2	1574	B9B
44	2	1578	U
44	2	1592	G
44	2	1596	U
44	2	1612	G
44	2	1613	A
44	2	1624	G
44	2	1625	OMG
44	2	1626	G
44	2	1631	A
44	2	1633	G
44	2	1634	A
44	2	1637	A
44	2	1638	A
44	2	1641	G
44	2	1642	A
44	2	1650	A
44	2	1654	G
44	2	1661	C
44	2	1676	C
44	2	1677	U
44	2	1678	C
44	2	1691	G
44	2	1694	C

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Mol	Chain	Res	Type
44	2	1697	G
44	2	1699	A
44	2	1700	G
44	2	1701	A
44	2	1703	C
44	2	1704	C
44	2	1705	G
44	2	1707	C
44	2	1715	C
44	2	1716	G
44	2	1718	C
44	2	1719	A
44	2	1724	G
44	2	1726	U
44	2	1734	G
44	2	1790	U
44	2	1797	E7G
44	2	1803	G
44	2	1804	A
44	2	1806	G
44	2	1810	G
44	2	1815	G
44	2	1821	G
44	2	1822	U
44	2	1834	U
44	2	1836	G
44	2	1837	A
44	2	1842	G
44	2	1843	A
44	2	1854	G
44	2	1855	G
44	2	1866	UR3
44	2	1867	A
44	2	1869	G
44	2	1870	C
44	2	1881	C
44	2	1883	OMG
44	2	1891	A
44	2	1897	A
44	2	1916	G
44	2	1918	U
44	2	1919	G

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Mol	Chain	Res	Type
44	2	1920	C
44	2	1922	G
44	2	1925	G
44	2	1931	C
44	2	1932	A
44	2	1938	C
44	2	1948	G
44	2	1958	A
44	2	1960	A
44	2	1961	G
44	2	1962	A
44	2	1971	C
44	2	1972	G
44	2	1974	U
44	2	1980	U
44	2	1981	G
44	2	1982	G
44	2	1983	A
44	2	1984	A
44	2	1985	G
44	2	1991	A
44	2	2001	G
44	2	2002	A
44	2	2003	G
44	2	2004	U
44	2	2008	U
44	2	2011	C
44	2	2015	U
44	2	2016	C
44	2	2024	G
44	2	2025	A
44	2	2026	A
44	2	2033	A
44	2	2034	G
44	2	2044	U
44	2	2046	G
44	2	2048	U
44	2	2055	G
44	2	2056	G
44	2	2069	A
44	2	2071	A
44	2	2084	C

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Mol	Chain	Res	Type
44	2	2085	G
44	2	2090	U
44	2	2091	C
44	2	2092	G
44	2	2093	A
44	2	2095	A
44	2	2097	U
44	2	2098	G
44	2	2100	A
44	2	2101	C
44	2	2104	G
44	2	2105	A
44	2	2106	G
44	2	2108	G
44	2	2110	C
44	2	2111	G
44	2	2112	G
44	2	2113	C
44	2	2250	C
44	2	2251	G
44	2	2252	G
44	2	2253	A
44	2	2255	C
44	2	2256	C
44	2	2258	C
44	2	2259	G
44	2	2260	C
44	2	2263	A
44	2	2269	C
44	2	2289	C
44	2	2300	A
44	2	2301	G
44	2	2306	G
44	2	2313	A
44	2	2316	G
44	2	2331	G
44	2	2333	G
44	2	2346	C
44	2	2348	G
44	2	2351	C
44	2	2364	OMG
44	2	2369	U

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Mol	Chain	Res	Type
44	2	2395	A
44	2	2416	G
44	2	2417	A
44	2	2424	OMG
44	2	2425	U
44	2	2437	C
44	2	2441	C
44	2	2447	U
44	2	2450	G
44	2	2453	A
44	2	2464	C
44	2	2465	C
44	2	2469	C
44	2	2471	G
44	2	2475	G
44	2	2479	G
44	2	2483	G
44	2	2484	A
44	2	2485	U
44	2	2487	G
44	2	2489	C
44	2	2490	U
44	2	2491	C
44	2	2493	G
44	2	2495	U
44	2	2503	G
44	2	2504	C
44	2	2505	C
44	2	2511	A
44	2	2512	A
44	2	2513	A
44	2	2519	U
44	2	2529	A
44	2	2544	G
44	2	2546	G
44	2	2547	G
44	2	2554	U
44	2	2555	G
44	2	2559	G
44	2	2560	C
44	2	2566	G
44	2	2573	A

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Mol	Chain	Res	Type
44	2	2583	C
44	2	2586	G
44	2	2587	A
44	2	2589	C
44	2	2600	A
44	2	2601	A
44	2	2627	C
44	2	2638	G
44	2	2652	G
44	2	2653	C
44	2	2662	G
44	2	2669	C
44	2	2670	C
44	2	2675	G
44	2	2687	U
44	2	2694	G
44	2	2695	A
44	2	2696	A
44	2	2705	G
44	2	2707	U
44	2	2708	U
44	2	2710	C
44	2	2711	G
44	2	2719	C
44	2	2721	G
44	2	2724	G
44	2	2726	G
44	2	2739	C
44	2	2742	G
44	2	2743	A
44	2	2756	G
44	2	2761	U
44	2	2763	U
44	2	2764	A
44	2	2769	U
44	2	2770	C
44	2	2787	A
44	2	2788	U
44	2	2789	A
44	2	2790	U
44	2	2799	G
44	2	2814	C

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Mol	Chain	Res	Type
44	2	2815	A
44	2	2826	U
44	2	2827	G
44	2	2845	A
44	2	2855	G
44	2	2877	G
44	2	2897	G
44	2	2900	U
44	2	2901	G
44	2	2903	G
44	2	2904	U
44	2	2905	C
44	2	2906	G
44	2	2908	U
44	2	3585	G
44	2	3591	C
44	2	3595	U
44	2	3596	A
44	2	3597	G
44	2	3598	C
44	2	3599	A
44	2	3605	C
44	2	3606	U
44	2	3616	U
44	2	3626	G
44	2	3635	A
44	2	3638	G
44	2	3644	U
44	2	3648	A
44	2	3662	A
44	2	3670	C
44	2	3672	G
44	2	3673	C
44	2	3680	U
44	2	3682	A
44	2	3683	C
44	2	3691	G
44	2	3696	C
44	2	3697	U
44	2	3698	G
44	2	3709	U
44	2	3710	G

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Mol	Chain	Res	Type
44	2	3711	A
44	2	3712	A
44	2	3729	U
44	2	3735	G
44	2	3736	A
44	2	3748	A
44	2	3824	A
44	2	3838	U
44	2	3839	G
44	2	3840	U
44	2	3867	A2M
44	2	3871	A
44	2	3876	A
44	2	3877	A
44	2	3878	C
44	2	3879	G
44	2	3880	P7G
44	2	3892	U
44	2	3897	B8K
44	2	3903	A
44	2	3904	G
44	2	3905	A
44	2	3906	A
44	2	3914	U
44	2	3915	U
44	2	3923	A
44	2	3938	G
44	2	3939	G
44	2	3942	A
44	2	3944	G
44	2	3945	A
44	2	3946	G
44	2	3948	C
44	2	3949	A
44	2	3950	U
44	2	3951	G
44	2	3955	G
44	2	3956	G
44	2	3957	U
44	2	3958	G
44	2	3959	U
44	2	3960	A

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Mol	Chain	Res	Type
44	2	3961	G
44	2	3962	A
44	2	3963	A
44	2	3964	U
44	2	3965	A
44	2	3966	A
44	2	3968	U
44	2	3969	G
44	2	3970	G
44	2	3971	G
44	2	3972	A
44	2	3973	G
44	2	3974	G
44	2	3975	C
44	2	3977	C
44	2	4035	G
44	2	4036	G
44	2	4038	C
44	2	4039	G
44	2	4041	C
44	2	4042	G
44	2	4043	G
44	2	4045	G
44	2	4046	A
44	2	4048	A
44	2	4049	U
44	2	4050	A
44	2	4051	C
44	2	4052	C
44	2	4053	A
44	2	4055	U
44	2	4056	A
44	2	4057	C
44	2	4058	U
44	2	4059	C
44	2	4061	G
44	2	4062	A
44	2	4063	U
44	2	4064	C
44	2	4065	G
44	2	4066	U
44	2	4068	U

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Mol	Chain	Res	Type
44	2	4076	G
44	2	4084	G
44	2	4095	G
44	2	4099	G
44	2	4100	C
44	2	4102	C
44	2	4103	C
44	2	4104	G
44	2	4105	A
44	2	4110	C
44	2	4111	U
44	2	4112	C
44	2	4115	G
44	2	4116	C
44	2	4117	U
44	2	4119	C
44	2	4135	G
44	2	4137	C
44	2	4139	G
44	2	4140	C
44	2	4141	G
44	2	4142	C
44	2	4143	G
44	2	4144	C
44	2	4150	G
44	2	4162	C
44	2	4163	U
44	2	4170	A
44	2	4183	G
44	2	4184	G
44	2	4189	U
44	2	4190	U
44	2	4191	G
44	2	4192	A
44	2	4195	G
44	2	4196	G
44	2	4197	G
44	2	4201	G
44	2	4202	U
44	2	4203	A
44	2	4204	C
44	2	4212	A

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Mol	Chain	Res	Type
44	2	4225	G
44	2	4226	G
44	2	4229	U
44	2	4233	A
44	2	4234	A
44	2	4247	G
44	2	4249	G
44	2	4251	A
44	2	4254	G
44	2	4256	A
44	2	4258	C
44	2	4260	U
44	2	4265	U
44	2	4268	A
44	2	4271	A
44	2	4273	A
44	2	4279	A
44	2	4281	A
44	2	4291	G
44	2	4292	A
44	2	4293	U
44	2	4294	C
44	2	4295	U
44	2	4296	B8H
44	2	4304	A
44	2	4305	G
44	2	4314	C
44	2	4319	C
44	2	4329	G
44	2	4330	G
44	2	4332	C
44	2	4339	A
44	2	4349	C
44	2	4354	U
44	2	4364	G
44	2	4373	G
44	2	4377	G
44	2	4378	A
44	2	4379	A
44	2	4380	A
44	2	4381	A
44	2	4382	G

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Mol	Chain	Res	Type
44	2	4383	U
44	2	4387	C
44	2	4396	A
44	2	4415	1MA
44	2	4418	G
44	2	4422	A
44	2	4424	A
44	2	4428	A
44	2	4436	U
44	2	4437	U
44	2	4451	G
44	2	4452	U
44	2	4453	C
44	2	4464	A
44	2	4465	U
44	2	4466	C
44	2	4475	G
44	2	4484	A
44	2	4488	A
44	2	4498	U
44	2	4499	G
44	2	4505	C
44	2	4512	U
44	2	4513	A
44	2	4518	A
44	2	4519	C
44	2	4523	A2M
44	2	4524	G
44	2	4529	B8W
44	2	4545	G
44	2	4548	A
44	2	4549	G
44	2	4555	U
44	2	4556	U
44	2	4557	U
44	2	4558	U
44	2	4560	C
44	2	4575	G
44	2	4584	A
44	2	4589	A
44	2	4590	A
44	2	4599	A

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Mol	Chain	Res	Type
44	2	4600	G
44	2	4601	U
44	2	4606	G
44	2	4607	A
44	2	4608	G
44	2	4635	A
44	2	4636	U
44	2	4637	OMG
44	2	4656	A
44	2	4657	U
44	2	4670	C
44	2	4672	A
44	2	4678	G
44	2	4687	A
44	2	4693	C
44	2	4694	G
44	2	4695	C
44	2	4698	C
44	2	4700	A
44	2	4708	A
44	2	4709	U
44	2	4719	G
44	2	4720	C
44	2	4721	G
44	2	4730	C
44	2	4731	G
44	2	4733	C
44	2	4734	A
44	2	4735	G
44	2	4740	G
44	2	4741	C
44	2	4742	G
44	2	4745	G
44	2	4754	G
44	2	4757	C
44	2	4759	C
44	2	4761	G
44	2	4764	A
44	2	4765	G
44	2	4771	C
44	2	4773	C
44	2	4775	C

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Mol	Chain	Res	Type
44	2	4776	G
44	2	4859	C
44	2	4870	OMG
44	2	4871	C
44	2	4872	2MG
44	2	4874	A
44	2	4877	G
44	2	4882	U
44	2	4883	C
44	2	4889	G
44	2	4895	C
44	2	4900	C
44	2	4901	G
44	2	4910	G
44	2	4912	G
44	2	4914	C
44	2	4915	G
44	2	4927	G
44	2	4928	C
44	2	4934	A
44	2	4938	A
44	2	4940	C
44	2	4941	G
44	2	4943	A
44	2	4949	G
44	2	4960	G
44	2	4976	U
44	2	4989	U
44	2	4990	C
44	2	4991	U
44	2	4993	G
44	2	5013	C
44	2	5014	A
44	2	5017	G
44	2	5021	C
44	2	5022	U
44	2	5026	U
44	2	5027	C
44	2	5028	G
44	2	5030	U
44	2	5031	G
44	2	5034	A

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Mol	Chain	Res	Type
44	2	5040	U
44	2	5041	G
44	2	5047	C
44	2	5050	C
44	2	5054	C
44	2	5055	G
44	2	5058	A
44	2	5062	G
44	2	5069	U

All (22) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
44	2	406	C
44	2	914	U
44	2	1676	C
44	2	1980	U
44	2	2015	U
44	2	2033	A
44	2	2760	G
44	2	3596	A
44	2	3905	A
44	2	3945	A
44	2	3954	A
44	2	4063	U
44	2	4191	G
44	2	4195	G
44	2	4202	U
44	2	4204	C
44	2	4380	A
44	2	4382	G
44	2	4498	U
44	2	4555	U
44	2	4699	U
44	2	4913	G

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

78 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
44	2MG	2	729	44	23,26,27	2.97	7 (30%)	32,38,41	2.34	10 (31%)
44	P7G	2	3880	44	24,28,29	4.09	11 (45%)	27,41,44	1.47	4 (14%)
44	B9B	2	2754	44	25,28,29	1.73	6 (24%)	35,40,43	5.15	11 (31%)
4	OMU	8	14	4,44	19,22,23	2.99	8 (42%)	26,31,34	1.78	5 (19%)
44	UR3	2	1866	44	19,22,23	2.95	6 (31%)	26,32,35	2.11	6 (23%)
44	B8W	2	4529	44	23,26,27	2.78	6 (26%)	33,38,41	2.68	15 (45%)
44	UR3	2	4530	44	19,22,23	2.86	6 (31%)	26,32,35	1.28	2 (7%)
44	P4U	2	1348	44	21,24,25	3.62	8 (38%)	27,33,36	1.06	1 (3%)
44	M7A	2	4564	44	20,25,26	1.99	3 (15%)	28,37,40	3.87	7 (25%)
44	OMG	2	4870	44	23,26,27	2.68	8 (34%)	33,38,41	2.96	10 (30%)
44	BGH	2	3899	44	25,29,30	4.62	17 (68%)	31,43,46	2.59	12 (38%)
44	OMG	2	2424	44	23,26,27	2.69	8 (34%)	33,38,41	2.77	9 (27%)
44	OMG	2	4623	44	23,26,27	2.65	8 (34%)	33,38,41	2.76	12 (36%)
44	A2M	2	2401	44	22,25,26	3.21	9 (40%)	31,36,39	3.00	11 (35%)
44	OMG	2	2364	44	23,26,27	2.67	8 (34%)	33,38,41	2.73	11 (33%)
44	2MG	2	4872	44	23,26,27	2.89	9 (39%)	32,38,41	2.34	10 (31%)
44	B8T	2	4671	44	19,22,23	3.59	8 (42%)	26,31,34	0.93	1 (3%)
44	B8W	2	4185	44	23,26,27	2.75	6 (26%)	33,38,41	2.64	13 (39%)
44	OMC	2	3887	44	19,22,23	3.03	8 (42%)	26,31,34	0.83	1 (3%)
44	B8K	2	3897	44	24,28,29	3.43	11 (45%)	30,42,45	2.51	11 (36%)
44	OMG	2	1522	44	23,26,27	2.63	8 (34%)	33,38,41	2.77	11 (33%)
44	A2M	2	4571	44	22,25,26	3.16	9 (40%)	31,36,39	2.96	10 (32%)
44	OMC	2	2365	44	19,22,23	3.00	8 (42%)	26,31,34	0.76	0
44	OMG	2	1625	44	23,26,27	2.71	8 (34%)	33,38,41	2.74	10 (30%)
44	B8W	2	2380	44	23,26,27	2.71	5 (21%)	33,38,41	2.56	14 (42%)
44	OMC	2	4536	44	19,22,23	2.98	8 (42%)	26,31,34	1.13	3 (11%)
44	6MZ	2	4220	44	22,25,26	2.58	4 (18%)	30,36,39	3.40	10 (33%)
44	B8K	2	4690	44	24,28,29	3.42	11 (45%)	30,42,45	2.59	11 (36%)
44	B8Q	2	1456	44	17,22,23	2.95	5 (29%)	22,32,35	2.30	6 (27%)
44	A2M	2	1326	44	22,25,26	3.20	9 (40%)	31,36,39	3.02	11 (35%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
44	OMG	2	2773	44	23,26,27	2.70	8 (34%)	33,38,41	2.74	11 (33%)
44	OMU	2	4620	44	19,22,23	2.97	8 (42%)	26,31,34	1.69	4 (15%)
44	A2M	2	3825	44	22,25,26	3.18	9 (40%)	31,36,39	2.96	10 (32%)
44	B8H	2	4296	44	20,22,23	6.62	6 (30%)	21,32,35	2.39	5 (23%)
44	A2M	2	3867	44	22,25,26	3.15	9 (40%)	31,36,39	3.00	10 (32%)
44	OMG	2	1883	44	23,26,27	2.71	8 (34%)	33,38,41	2.74	11 (33%)
44	OMC	2	2861	44	19,22,23	3.06	8 (42%)	26,31,34	1.18	3 (11%)
44	I4U	2	1659	44	21,24,25	3.59	9 (42%)	27,34,37	1.20	1 (3%)
44	B8H	2	1860	44	20,22,23	6.60	6 (30%)	21,32,35	2.36	5 (23%)
44	B9B	2	1574	44	25,28,29	1.72	6 (24%)	35,40,43	5.15	11 (31%)
44	B8T	2	4483	44	19,22,23	3.65	8 (42%)	26,31,34	1.31	3 (11%)
44	OMG	2	1316	44	23,26,27	2.66	8 (34%)	33,38,41	2.74	12 (36%)
44	B8W	2	4472	44	23,26,27	2.78	6 (26%)	33,38,41	2.67	14 (42%)
44	A2M	2	1871	44	22,25,26	3.20	9 (40%)	31,36,39	3.05	11 (35%)
44	E7G	2	1797	44	24,27,28	4.07	11 (45%)	30,40,43	2.18	9 (30%)
44	OMU	2	4306	44	19,22,23	3.04	8 (42%)	26,31,34	1.69	4 (15%)
44	OMG	2	4494	44	23,26,27	2.67	8 (34%)	33,38,41	2.75	9 (27%)
44	MHG	2	4371	44	29,32,33	3.93	11 (37%)	34,46,49	2.37	12 (35%)
44	5MC	2	4335	44	18,22,23	3.59	7 (38%)	26,32,35	1.11	2 (7%)
44	OMG	2	4637	44	23,26,27	2.68	8 (34%)	33,38,41	2.76	10 (30%)
44	1MA	2	4415	44	21,25,26	3.02	5 (23%)	31,37,40	1.83	7 (22%)
44	A2M	2	4523	44	22,25,26	3.16	9 (40%)	31,36,39	3.04	11 (35%)
44	2MG	2	1517	44	23,26,27	2.99	8 (34%)	32,38,41	2.53	8 (25%)
44	E7G	2	2297	44	24,27,28	4.02	11 (45%)	30,40,43	2.15	10 (33%)
44	A2M	2	398	44	22,25,26	3.20	9 (40%)	31,36,39	2.93	10 (32%)
44	OMC	2	2804	44	19,22,23	2.91	8 (42%)	26,31,34	1.36	3 (11%)
44	UR3	2	4597	44	19,22,23	2.78	7 (36%)	26,32,35	1.93	4 (15%)
44	OMG	2	373	44	23,26,27	2.67	8 (34%)	33,38,41	2.67	13 (39%)
44	7MG	2	2522	44	22,26,27	3.73	10 (45%)	29,39,42	1.96	9 (31%)
44	OMG	2	4370	44	23,26,27	2.67	8 (34%)	33,38,41	2.73	11 (33%)
44	OMC	2	3909	44	19,22,23	3.01	8 (42%)	26,31,34	1.24	5 (19%)
44	A2M	2	3723	44	22,25,26	3.16	9 (40%)	31,36,39	2.95	10 (32%)
44	2MG	2	978	44	23,26,27	3.01	8 (34%)	32,38,41	2.16	10 (31%)
44	A2M	2	1534	44	22,25,26	3.18	9 (40%)	31,36,39	3.04	10 (32%)
44	7MG	2	1605	44	22,26,27	3.82	10 (45%)	29,39,42	1.96	9 (31%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
44	B8W	2	4129	44	23,26,27	2.83	6 (26%)	33,38,41	2.59	12 (36%)
44	A2M	2	2363	44	22,25,26	3.19	9 (40%)	31,36,39	2.95	11 (35%)
44	OMC	2	3869	44	19,22,23	3.06	8 (42%)	26,31,34	1.56	4 (15%)
44	B9H	2	2786	44	20,25,26	3.28	5 (25%)	22,35,38	2.40	7 (31%)
44	P7G	2	1909	44	24,28,29	4.05	11 (45%)	27,41,44	1.55	3 (11%)
44	E6G	2	4355	44	24,27,28	2.02	4 (16%)	34,39,42	2.82	14 (41%)
44	OMC	2	3701	44	19,22,23	2.99	8 (42%)	26,31,34	0.78	0
44	A2M	2	3718	44	22,25,26	3.19	9 (40%)	31,36,39	2.86	10 (32%)
44	7MG	2	4550	44	22,26,27	3.82	10 (45%)	29,39,42	1.92	8 (27%)
44	OMG	2	2050	44	23,26,27	2.65	8 (34%)	33,38,41	2.75	10 (30%)
44	B9B	2	237	44	25,28,29	1.74	6 (24%)	35,40,43	5.19	12 (34%)
44	A2M	2	1524	44	22,25,26	3.20	9 (40%)	31,36,39	3.01	11 (35%)
44	5MU	2	4083	44	19,22,23	7.22	8 (42%)	28,32,35	3.42	10 (35%)

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
44	2MG	2	729	44	-	2/9/27/28	0/3/3/3
44	P7G	2	3880	44	-	4/10/40/41	0/3/3/3
44	B9B	2	2754	44	-	2/11/29/30	0/3/3/3
4	OMU	8	14	4,44	-	1/9/27/28	0/2/2/2
44	UR3	2	1866	44	-	3/7/25/26	0/2/2/2
44	B8W	2	4529	44	-	0/9/27/28	0/3/3/3
44	UR3	2	4530	44	-	0/7/25/26	0/2/2/2
44	P4U	2	1348	44	-	1/10/29/30	0/2/2/2
44	M7A	2	4564	44	-	0/7/37/38	0/3/3/3
44	OMG	2	4870	44	-	3/9/27/28	0/3/3/3
44	BGH	2	3899	44	-	1/13/43/44	0/3/3/3
44	OMG	2	2424	44	-	2/9/27/28	0/3/3/3
44	OMG	2	4623	44	-	1/9/27/28	0/3/3/3
44	A2M	2	2401	44	-	1/9/27/28	0/3/3/3
44	OMG	2	2364	44	-	2/9/27/28	0/3/3/3
44	2MG	2	4872	44	-	2/9/27/28	0/3/3/3
44	B8T	2	4671	44	-	0/7/27/28	0/2/2/2
44	B8W	2	4185	44	-	2/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
44	OMC	2	3887	44	-	1/9/27/28	0/2/2/2
44	B8K	2	3897	44	-	3/11/41/42	0/3/3/3
44	OMG	2	1522	44	-	0/9/27/28	0/3/3/3
44	A2M	2	4571	44	-	0/9/27/28	0/3/3/3
44	OMC	2	2365	44	-	0/9/27/28	0/2/2/2
44	OMG	2	1625	44	-	3/9/27/28	0/3/3/3
44	B8W	2	2380	44	-	2/9/27/28	0/3/3/3
44	OMC	2	4536	44	-	0/9/27/28	0/2/2/2
44	6MZ	2	4220	44	-	1/9/27/28	0/3/3/3
44	B8K	2	4690	44	-	0/11/41/42	0/3/3/3
44	B8Q	2	1456	44	-	0/7/42/43	0/2/2/2
44	A2M	2	1326	44	-	3/9/27/28	0/3/3/3
44	OMG	2	2773	44	-	0/9/27/28	0/3/3/3
44	OMU	2	4620	44	-	0/9/27/28	0/2/2/2
44	A2M	2	3825	44	-	0/9/27/28	0/3/3/3
44	B8H	2	4296	44	-	2/7/25/26	0/2/2/2
44	A2M	2	3867	44	-	2/9/27/28	0/3/3/3
44	OMG	2	1883	44	-	2/9/27/28	0/3/3/3
44	OMC	2	2861	44	-	0/9/27/28	0/2/2/2
44	I4U	2	1659	44	-	2/9/29/30	0/2/2/2
44	B8H	2	1860	44	-	2/7/25/26	0/2/2/2
44	B9B	2	1574	44	-	3/11/29/30	0/3/3/3
44	B8T	2	4483	44	-	0/7/27/28	0/2/2/2
44	OMG	2	1316	44	-	0/9/27/28	0/3/3/3
44	B8W	2	4472	44	-	2/9/27/28	0/3/3/3
44	A2M	2	1871	44	-	0/9/27/28	0/3/3/3
44	E7G	2	1797	44	-	2/9/39/40	0/3/3/3
44	OMU	2	4306	44	-	0/9/27/28	0/2/2/2
44	OMG	2	4494	44	-	0/9/27/28	0/3/3/3
44	MHG	2	4371	44	-	3/16/46/47	0/3/3/3
44	5MC	2	4335	44	-	0/7/25/26	0/2/2/2
44	OMG	2	4637	44	-	3/9/27/28	0/3/3/3
44	1MA	2	4415	44	-	3/7/25/26	0/3/3/3
44	A2M	2	4523	44	-	4/9/27/28	0/3/3/3
44	2MG	2	1517	44	-	0/9/27/28	0/3/3/3
44	E7G	2	2297	44	-	1/9/39/40	0/3/3/3
44	A2M	2	398	44	-	2/9/27/28	0/3/3/3
44	OMC	2	2804	44	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
44	UR3	2	4597	44	-	0/7/25/26	0/2/2/2
44	OMG	2	373	44	-	1/9/27/28	0/3/3/3
44	7MG	2	2522	44	-	0/7/37/38	0/3/3/3
44	OMG	2	4370	44	-	1/9/27/28	0/3/3/3
44	OMC	2	3909	44	-	1/9/27/28	0/2/2/2
44	A2M	2	3723	44	-	2/9/27/28	0/3/3/3
44	2MG	2	978	44	-	0/9/27/28	0/3/3/3
44	A2M	2	1534	44	-	1/9/27/28	0/3/3/3
44	7MG	2	1605	44	-	0/7/37/38	0/3/3/3
44	B8W	2	4129	44	-	2/9/27/28	0/3/3/3
44	A2M	2	2363	44	-	0/9/27/28	0/3/3/3
44	OMC	2	3869	44	-	4/9/27/28	0/2/2/2
44	B9H	2	2786	44	-	0/12/47/48	0/2/2/2
44	P7G	2	1909	44	-	3/10/40/41	0/3/3/3
44	E6G	2	4355	44	-	2/10/28/29	0/3/3/3
44	OMC	2	3701	44	-	4/9/27/28	0/2/2/2
44	A2M	2	3718	44	-	0/9/27/28	0/3/3/3
44	7MG	2	4550	44	-	0/7/37/38	0/3/3/3
44	OMG	2	2050	44	-	0/9/27/28	0/3/3/3
44	B9B	2	237	44	-	5/11/29/30	0/3/3/3
44	A2M	2	1524	44	-	2/9/27/28	0/3/3/3
44	5MU	2	4083	44	-	0/7/25/26	0/2/2/2

All (625) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	2	4083	5MU	C4-C5	20.79	1.79	1.44
44	2	4296	B8H	C6-C5	-16.51	1.11	1.34
44	2	1860	B8H	C6-C5	-16.35	1.12	1.34
44	2	4083	5MU	C6-N1	15.93	1.65	1.38
44	2	4296	B8H	C4-N3	-15.73	1.09	1.38
44	2	1860	B8H	C4-N3	-15.64	1.09	1.38
44	2	1860	B8H	C4-C5	13.38	1.82	1.44
44	2	4296	B8H	C4-C5	13.26	1.82	1.44
44	2	1860	B8H	C6-N1	12.26	1.66	1.36
44	2	4296	B8H	C6-N1	12.25	1.66	1.36
44	2	4083	5MU	C6-C5	-11.51	1.15	1.34
44	2	4083	5MU	C4-N3	-11.13	1.18	1.38
44	2	4220	6MZ	C6-N6	10.80	1.45	1.34
44	2	1659	I4U	C4-N3	10.76	1.45	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	2	1348	P4U	C4-N3	10.57	1.45	1.31
44	2	2786	B9H	C2-N3	9.97	1.49	1.37
44	2	4415	1MA	C2-N3	9.71	1.48	1.30
44	2	2297	E7G	C5-N7	9.70	1.46	1.35
44	2	3880	P7G	C5-N7	9.53	1.46	1.35
44	2	1797	E7G	C5-N7	9.50	1.46	1.35
44	2	4371	MHG	C8-N9	9.39	1.51	1.46
44	2	4129	B8W	O6-C6	9.38	1.50	1.35
44	2	3897	B8K	C8-N9	9.30	1.51	1.46
44	2	4550	7MG	C8-N9	9.29	1.51	1.46
44	2	1909	P7G	C8-N9	9.27	1.51	1.46
44	2	1797	E7G	C8-N9	9.25	1.51	1.46
44	2	1909	P7G	C5-N7	9.23	1.45	1.35
44	2	4690	B8K	C8-N9	9.19	1.51	1.46
44	2	1605	7MG	C8-N9	9.18	1.51	1.46
44	2	4335	5MC	C6-C5	9.05	1.49	1.34
44	2	3899	BGH	C8-N9	9.01	1.51	1.46
44	2	2297	E7G	C8-N9	8.92	1.50	1.46
44	2	1524	A2M	C3'-C4'	-8.91	1.30	1.53
44	2	4371	MHG	C5-N7	8.89	1.45	1.35
44	2	3899	BGH	O4'-C1'	8.89	1.63	1.42
44	2	1326	A2M	C3'-C4'	-8.83	1.30	1.53
44	2	398	A2M	C3'-C4'	-8.82	1.30	1.53
44	2	3867	A2M	C3'-C4'	-8.81	1.30	1.53
44	2	1871	A2M	C3'-C4'	-8.80	1.30	1.53
44	2	3899	BGH	C2'-C1'	-8.79	1.30	1.53
44	2	4550	7MG	C5-N7	8.78	1.45	1.35
44	2	4472	B8W	O6-C6	8.74	1.48	1.35
44	2	2363	A2M	C3'-C4'	-8.72	1.30	1.53
44	2	4529	B8W	O6-C6	8.72	1.48	1.35
44	2	4571	A2M	C3'-C4'	-8.72	1.30	1.53
44	2	3825	A2M	C3'-C4'	-8.72	1.30	1.53
44	2	4185	B8W	O6-C6	8.71	1.48	1.35
44	2	2401	A2M	C3'-C4'	-8.70	1.30	1.53
44	2	1534	A2M	C3'-C4'	-8.69	1.30	1.53
44	2	3718	A2M	C3'-C4'	-8.68	1.30	1.53
44	2	3723	A2M	C3'-C4'	-8.67	1.30	1.53
44	2	1605	7MG	C5-N7	8.67	1.45	1.35
44	2	2522	7MG	C5-N7	8.66	1.45	1.35
44	2	3880	P7G	C8-N9	8.62	1.50	1.46
44	2	4523	A2M	C3'-C4'	-8.56	1.31	1.53
44	2	2522	7MG	C8-N9	8.55	1.50	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	2	2380	B8W	O6-C6	8.52	1.48	1.35
44	2	1456	B8Q	C6-C5	8.29	1.52	1.33
44	2	4371	MHG	C2-N3	8.16	1.47	1.31
44	2	978	2MG	C2-N3	8.08	1.47	1.31
44	2	4129	B8W	C2-N2	8.04	1.50	1.33
44	2	4472	B8W	C2-N2	8.01	1.49	1.33
44	2	4529	B8W	C2-N2	8.00	1.49	1.33
44	2	4185	B8W	C2-N2	7.93	1.49	1.33
44	2	729	2MG	C2-N3	7.92	1.47	1.31
44	2	1517	2MG	C2-N3	7.89	1.47	1.31
44	2	2380	B8W	C2-N2	7.84	1.49	1.33
44	2	4872	2MG	C2-N3	7.77	1.46	1.31
44	2	398	A2M	O4'-C4'	7.76	1.62	1.45
44	2	1871	A2M	O4'-C4'	7.73	1.62	1.45
44	2	3718	A2M	O4'-C4'	7.73	1.62	1.45
44	2	2401	A2M	O4'-C4'	7.69	1.62	1.45
44	2	1326	A2M	O4'-C4'	7.69	1.62	1.45
44	2	1534	A2M	O4'-C4'	7.67	1.62	1.45
44	2	4523	A2M	O4'-C4'	7.62	1.62	1.45
44	2	3825	A2M	O4'-C4'	7.61	1.62	1.45
44	2	2363	A2M	O4'-C4'	7.60	1.62	1.45
44	2	3899	BGH	O4'-C4'	-7.58	1.28	1.45
44	2	4483	B8T	C2-N3	7.51	1.51	1.36
44	2	3723	A2M	O4'-C4'	7.50	1.61	1.45
44	2	1524	A2M	O4'-C4'	7.46	1.61	1.45
44	2	4571	A2M	O4'-C4'	7.45	1.61	1.45
44	2	4671	B8T	C2-N3	7.24	1.51	1.36
44	2	3867	A2M	O4'-C4'	7.22	1.61	1.45
44	2	4483	B8T	C4-N3	7.17	1.45	1.32
44	2	4306	OMU	C2-N1	7.16	1.49	1.38
44	2	2786	B9H	C2-N1	7.11	1.48	1.38
44	2	1866	UR3	C2-N1	7.10	1.48	1.38
4	8	14	OMU	C2-N1	7.06	1.49	1.38
44	2	4620	OMU	C2-N1	7.06	1.49	1.38
44	2	4671	B8T	C4-N3	7.05	1.45	1.32
44	2	4415	1MA	C4-N3	7.00	1.50	1.35
44	2	1517	2MG	C4-N3	6.97	1.50	1.34
44	2	2786	B9H	C6-C5	6.93	1.48	1.33
44	2	4671	B8T	C6-C5	6.90	1.51	1.35
44	2	4530	UR3	C2-N1	6.81	1.48	1.38
44	2	1866	UR3	C6-C5	6.81	1.50	1.35
44	2	729	2MG	C4-N3	6.79	1.50	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	2	4597	UR3	C6-C5	6.77	1.50	1.35
44	2	1517	2MG	C2-N2	6.76	1.48	1.33
44	2	978	2MG	C2-N2	6.75	1.48	1.33
44	2	4530	UR3	C6-C5	6.72	1.50	1.35
44	2	4306	OMU	C2-N3	6.71	1.49	1.38
44	2	4483	B8T	C6-C5	6.69	1.50	1.35
44	2	729	2MG	C2-N2	6.67	1.48	1.33
44	2	4690	B8K	C2-N3	6.66	1.49	1.33
44	2	3897	B8K	C2-N3	6.63	1.49	1.33
4	8	14	OMU	C2-N3	6.60	1.49	1.38
44	2	978	2MG	C4-N3	6.60	1.49	1.34
44	2	3909	OMC	C6-C5	6.57	1.50	1.35
44	2	1456	B8Q	C2-N3	6.56	1.46	1.35
44	2	4371	MHG	C8-N7	6.53	1.51	1.45
44	2	4620	OMU	C2-N3	6.53	1.49	1.38
44	2	4335	5MC	C4-N3	6.49	1.45	1.34
44	2	2861	OMC	C2-N3	6.42	1.49	1.36
44	2	3887	OMC	C2-N3	6.42	1.49	1.36
44	2	3880	P7G	C4-N9	6.39	1.44	1.35
44	2	3869	OMC	C2-N3	6.38	1.49	1.36
44	2	3880	P7G	C4-N3	6.38	1.48	1.37
44	2	1909	P7G	C4-N9	6.38	1.44	1.35
44	2	4872	2MG	C2-N2	6.36	1.47	1.33
44	2	2297	E7G	C8-N7	6.35	1.51	1.45
44	2	1659	I4U	C2-N3	6.34	1.49	1.36
44	2	1625	OMG	C2-N3	6.31	1.48	1.33
44	2	4536	OMC	C2-N3	6.31	1.49	1.36
44	2	2365	OMC	C2-N3	6.30	1.49	1.36
44	2	1909	P7G	C4-N3	6.29	1.48	1.37
44	2	4371	MHG	C2-N1	6.28	1.46	1.36
44	2	4483	B8T	C4-N4	6.28	1.48	1.35
44	2	3701	OMC	C2-N3	6.28	1.49	1.36
44	2	1797	E7G	C4-N9	6.27	1.45	1.37
44	2	1625	OMG	C4-N3	6.27	1.49	1.34
44	2	4870	OMG	C2-N3	6.27	1.48	1.33
44	2	1348	P4U	C2-N3	6.26	1.49	1.36
44	2	1883	OMG	C2-N3	6.25	1.48	1.33
44	2	4671	B8T	C4-N4	6.19	1.48	1.35
44	2	2773	OMG	C2-N3	6.19	1.48	1.33
44	2	4335	5MC	C2-N3	6.19	1.48	1.36
44	2	2424	OMG	C2-N3	6.18	1.48	1.33
44	2	1883	OMG	C4-N3	6.17	1.48	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	2	4870	OMG	C4-N3	6.17	1.48	1.34
44	2	1797	E7G	C8-N7	6.16	1.51	1.45
44	2	4597	UR3	C2-N3	6.15	1.50	1.39
44	2	2773	OMG	C4-N3	6.12	1.48	1.34
44	2	4637	OMG	C2-N3	6.12	1.47	1.33
44	2	2424	OMG	C4-N3	6.11	1.48	1.34
44	2	1659	I4U	C6-C5	6.11	1.49	1.35
44	2	4637	OMG	C4-N3	6.11	1.48	1.34
44	2	2364	OMG	C2-N3	6.07	1.47	1.33
44	2	2804	OMC	C2-N3	6.07	1.48	1.36
44	2	4494	OMG	C4-N3	6.07	1.48	1.34
44	2	3701	OMC	C6-C5	6.07	1.49	1.35
44	2	3880	P7G	C8-N7	6.07	1.51	1.45
44	2	1625	OMG	C2-N2	6.06	1.48	1.34
44	2	4872	2MG	C4-N3	6.06	1.48	1.34
44	2	2773	OMG	C2-N2	6.05	1.48	1.34
44	2	1316	OMG	C2-N3	6.05	1.47	1.33
44	2	4370	OMG	C4-N3	6.05	1.48	1.34
44	2	4494	OMG	C2-N3	6.05	1.47	1.33
44	2	1883	OMG	C2-N2	6.04	1.48	1.34
44	2	1348	P4U	C6-C5	6.04	1.49	1.35
44	2	4355	E6G	C2-N2	6.02	1.45	1.33
44	2	2364	OMG	C4-N3	6.02	1.48	1.34
44	2	4370	OMG	C2-N3	6.02	1.47	1.33
44	2	2050	OMG	C2-N3	6.01	1.47	1.33
44	2	3887	OMC	C6-C5	6.01	1.49	1.35
44	2	2424	OMG	C2-N2	6.00	1.48	1.34
44	2	3899	BGH	C4-N9	6.00	1.44	1.37
44	2	2050	OMG	C4-N3	6.00	1.48	1.34
44	2	4870	OMG	C2-N2	5.99	1.48	1.34
44	2	373	OMG	C2-N2	5.98	1.48	1.34
44	2	373	OMG	C2-N3	5.98	1.47	1.33
44	2	4623	OMG	C4-N3	5.98	1.48	1.34
44	2	2365	OMC	C6-C5	5.98	1.49	1.35
44	2	3880	P7G	C2-N2	5.98	1.48	1.34
44	2	1909	P7G	C2-N2	5.97	1.48	1.34
44	2	1866	UR3	C2-N3	5.95	1.50	1.39
44	2	2861	OMC	C6-C5	5.95	1.48	1.35
44	2	4370	OMG	C2-N2	5.94	1.48	1.34
44	2	1316	OMG	C4-N3	5.94	1.48	1.34
44	2	2364	OMG	C2-N2	5.94	1.48	1.34
44	2	4623	OMG	C2-N2	5.94	1.48	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	2	373	OMG	C4-N3	5.94	1.48	1.34
44	2	4536	OMC	C6-C5	5.93	1.48	1.35
44	2	4637	OMG	C2-N2	5.93	1.48	1.34
44	2	2050	OMG	C2-N2	5.90	1.48	1.34
44	2	1316	OMG	C2-N2	5.89	1.48	1.34
44	2	1522	OMG	C4-N3	5.88	1.48	1.34
44	2	1522	OMG	C2-N3	5.87	1.47	1.33
44	2	4494	OMG	C2-N2	5.86	1.48	1.34
44	2	4623	OMG	C2-N3	5.86	1.47	1.33
44	2	4597	UR3	C2-N1	5.85	1.46	1.38
44	2	1797	E7G	C4-N3	5.83	1.48	1.34
44	2	1522	OMG	C2-N2	5.83	1.48	1.34
44	2	4355	E6G	O6-C6	5.81	1.43	1.35
44	2	2804	OMC	C6-C5	5.79	1.48	1.35
44	2	3869	OMC	C6-C5	5.79	1.48	1.35
44	2	4530	UR3	C2-N3	5.77	1.50	1.39
44	2	2297	E7G	C4-N3	5.75	1.47	1.34
44	2	1797	E7G	C2-N3	5.73	1.47	1.33
44	2	2754	B9B	C2-N2	5.72	1.45	1.33
44	2	2297	E7G	C4-N9	5.71	1.44	1.37
44	2	4306	OMU	C6-C5	5.69	1.48	1.35
44	2	3897	B8K	C4-N9	5.69	1.44	1.37
44	2	2297	E7G	C2-N3	5.67	1.46	1.33
44	2	4371	MHG	C2-N2	5.66	1.46	1.33
44	2	4550	7MG	C2-N3	5.65	1.46	1.33
44	2	3899	BGH	C2-N3	5.64	1.46	1.33
44	2	3869	OMC	C2-N1	5.64	1.52	1.40
44	2	3899	BGH	C4-N3	5.63	1.47	1.34
44	2	1605	7MG	C2-N3	5.62	1.46	1.33
44	2	2522	7MG	C2-N3	5.61	1.46	1.33
44	2	4690	B8K	C4-N9	5.61	1.44	1.37
44	2	4371	MHG	C4-N9	5.61	1.44	1.37
44	2	4564	M7A	C4-N9	5.61	1.48	1.38
44	2	237	B9B	C2-N2	5.61	1.45	1.33
44	2	1574	B9B	C2-N2	5.58	1.45	1.33
44	2	4620	OMU	C6-C5	5.52	1.47	1.35
44	2	3909	OMC	C2-N3	5.52	1.47	1.36
44	2	4371	MHG	C4-N3	5.51	1.47	1.34
44	2	4550	7MG	C4-N3	5.50	1.47	1.34
44	2	2522	7MG	C4-N3	5.48	1.47	1.34
4	8	14	OMU	C6-C5	5.47	1.47	1.35
44	2	1605	7MG	C4-N3	5.46	1.47	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	2	3909	OMC	C4-N4	5.43	1.46	1.33
44	2	3880	P7G	C2-N1	5.42	1.46	1.33
44	2	1909	P7G	C8-N7	5.29	1.50	1.45
44	2	4483	B8T	C2-N1	5.26	1.51	1.40
44	2	1605	7MG	C4-N9	5.21	1.43	1.37
44	2	1909	P7G	C2-N1	5.19	1.45	1.33
44	2	2297	E7G	C2-N2	5.19	1.46	1.34
44	2	1797	E7G	C2-N2	5.18	1.46	1.34
44	2	2365	OMC	C4-N3	5.15	1.44	1.34
44	2	2861	OMC	C4-N3	5.12	1.44	1.34
44	2	3887	OMC	C4-N3	5.12	1.44	1.34
44	2	2861	OMC	C2-N1	5.11	1.51	1.40
44	2	3701	OMC	C4-N3	5.06	1.44	1.34
44	2	2522	7MG	C4-N9	5.04	1.43	1.37
44	2	1348	P4U	O4-C4	5.00	1.40	1.35
44	2	4550	7MG	C4-N9	4.99	1.43	1.37
44	2	2804	OMC	C2-N1	4.92	1.50	1.40
44	2	3869	OMC	C4-N4	4.88	1.45	1.33
44	2	2861	OMC	C4-N4	4.87	1.45	1.33
44	2	3899	BGH	C2-N2	4.86	1.45	1.34
44	2	4536	OMC	C4-N4	4.86	1.45	1.33
44	2	3869	OMC	C4-N3	4.86	1.44	1.34
44	2	2365	OMC	C4-N4	4.84	1.45	1.33
44	2	4536	OMC	C2-N1	4.83	1.50	1.40
44	2	4536	OMC	C4-N3	4.83	1.44	1.34
44	2	1456	B8Q	C2-N1	4.83	1.45	1.38
44	2	3701	OMC	C4-N4	4.81	1.45	1.33
44	2	3887	OMC	C4-N4	4.80	1.45	1.33
44	2	2804	OMC	C4-N4	4.79	1.45	1.33
44	2	2522	7MG	C2-N2	4.78	1.45	1.34
44	2	4550	7MG	C2-N2	4.78	1.45	1.34
44	2	1605	7MG	C2-N2	4.77	1.45	1.34
44	2	3867	A2M	O4'-C1'	-4.72	1.30	1.42
44	2	1524	A2M	O4'-C1'	-4.69	1.30	1.42
44	2	2401	A2M	O4'-C1'	-4.69	1.30	1.42
44	2	4571	A2M	O4'-C1'	-4.68	1.30	1.42
44	2	1659	I4U	C5-C4	4.68	1.49	1.43
44	2	3887	OMC	C2-N1	4.67	1.50	1.40
44	2	1326	A2M	O4'-C1'	-4.66	1.31	1.42
44	2	4671	B8T	C2-N1	4.63	1.50	1.40
44	2	2804	OMC	C4-N3	4.60	1.43	1.34
44	2	3723	A2M	O4'-C1'	-4.59	1.31	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	2	3899	BGH	C5-N7	4.58	1.47	1.39
44	2	4523	A2M	O4'-C1'	-4.58	1.31	1.42
44	2	1871	A2M	C6-N6	4.57	1.45	1.34
44	2	2363	A2M	O4'-C1'	-4.57	1.31	1.42
44	2	1524	A2M	C6-N6	4.56	1.45	1.34
44	2	3723	A2M	C6-N6	4.55	1.45	1.34
44	2	3718	A2M	C6-N6	4.55	1.45	1.34
44	2	3825	A2M	O4'-C1'	-4.55	1.31	1.42
44	2	3909	OMC	C4-N3	4.54	1.43	1.34
44	2	1534	A2M	O4'-C1'	-4.53	1.31	1.42
44	2	1326	A2M	C6-N6	4.53	1.45	1.34
44	2	4571	A2M	C6-N6	4.53	1.45	1.34
44	2	398	A2M	O4'-C1'	-4.52	1.31	1.42
44	2	4335	5MC	C6-N1	4.52	1.45	1.38
44	2	4523	A2M	C6-N6	4.51	1.45	1.34
44	2	3718	A2M	O4'-C1'	-4.51	1.31	1.42
44	2	3825	A2M	C6-N6	4.51	1.45	1.34
44	2	398	A2M	C6-N6	4.50	1.45	1.34
44	2	3867	A2M	C6-N6	4.50	1.45	1.34
44	2	2363	A2M	C6-N6	4.50	1.45	1.34
44	2	2365	OMC	C2-N1	4.49	1.49	1.40
44	2	4690	B8K	C4-N3	4.48	1.44	1.34
44	2	4335	5MC	C2-N1	4.47	1.49	1.40
44	2	2401	A2M	C6-N6	4.47	1.45	1.34
44	2	3897	B8K	C4-N3	4.46	1.44	1.34
44	2	1348	P4U	C5-C4	4.45	1.48	1.43
44	2	1860	B8H	C2-N3	4.44	1.45	1.38
44	2	1534	A2M	C6-N6	4.42	1.45	1.34
44	2	4335	5MC	C4-N4	4.41	1.45	1.34
44	2	1871	A2M	O4'-C1'	-4.40	1.31	1.42
44	2	4296	B8H	C2-N3	4.39	1.45	1.38
44	2	4083	5MU	C2-N3	4.38	1.45	1.38
44	2	3701	OMC	C2-N1	4.38	1.49	1.40
44	2	4415	1MA	C5-C6	4.37	1.55	1.43
44	2	3909	OMC	C2-N1	4.35	1.49	1.40
44	2	3897	B8K	C5-C6	4.33	1.54	1.43
44	2	4564	M7A	C6-N6	4.32	1.45	1.34
44	2	1348	P4U	C2-N1	4.32	1.49	1.40
44	2	978	2MG	C2-N1	4.29	1.43	1.36
44	2	4690	B8K	C5-N7	4.29	1.47	1.39
44	2	1659	I4U	C2-N1	4.27	1.49	1.40
44	2	4415	1MA	C2-N1	4.24	1.43	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	2	3897	B8K	C5-N7	4.23	1.46	1.39
44	2	4872	2MG	C2-N1	4.21	1.43	1.36
44	2	3899	BGH	C5-C6	4.21	1.54	1.43
44	2	4690	B8K	C5-C6	4.20	1.54	1.43
44	2	729	2MG	C2-N1	4.16	1.43	1.36
44	2	4306	OMU	C4-N3	4.13	1.46	1.38
4	8	14	OMU	C4-N3	4.08	1.45	1.38
44	2	1517	2MG	C2-N1	4.03	1.43	1.36
44	2	4564	M7A	C5-N7	3.97	1.49	1.39
44	2	4620	OMU	C4-N3	3.94	1.45	1.38
44	2	4671	B8T	C5-C4	3.87	1.49	1.40
44	2	1625	OMG	C5-N7	-3.87	1.31	1.39
44	2	1883	OMG	C5-N7	-3.85	1.31	1.39
44	2	1797	E7G	C5-C6	3.85	1.53	1.43
44	2	2364	OMG	C5-N7	-3.83	1.31	1.39
44	2	4494	OMG	C5-N7	-3.81	1.31	1.39
44	2	1316	OMG	C5-N7	-3.81	1.31	1.39
44	2	4371	MHG	C5-C6	3.80	1.53	1.43
44	2	2424	OMG	C5-N7	-3.80	1.31	1.39
44	2	2297	E7G	C5-C6	3.79	1.53	1.43
44	2	1522	OMG	C5-N7	-3.78	1.31	1.39
44	2	3880	P7G	C2-N3	3.77	1.47	1.37
44	2	2050	OMG	C5-N7	-3.77	1.31	1.39
44	2	4637	OMG	C5-N7	-3.75	1.31	1.39
44	2	1605	7MG	C5-C6	3.74	1.53	1.43
44	2	1909	P7G	C2-N3	3.73	1.46	1.37
44	2	2773	OMG	C5-N7	-3.71	1.31	1.39
44	2	4550	7MG	C5-C6	3.71	1.53	1.43
44	2	3899	BGH	O2'-C2'	3.69	1.52	1.42
44	2	4870	OMG	C5-N7	-3.69	1.31	1.39
44	2	3880	P7G	C6-N1	3.69	1.44	1.38
44	2	4370	OMG	C5-N7	-3.64	1.32	1.39
44	2	373	OMG	C5-N7	-3.63	1.32	1.39
44	2	1605	7MG	C2-N1	3.60	1.46	1.37
44	2	4690	B8K	C71-N7	3.60	1.47	1.39
44	2	3897	B8K	C6-N1	3.59	1.45	1.38
44	2	2522	7MG	C5-C6	3.59	1.52	1.43
44	2	4623	OMG	C5-N7	-3.58	1.32	1.39
44	2	2522	7MG	C2-N1	3.57	1.46	1.37
44	2	4690	B8K	C6-N1	3.56	1.45	1.38
44	2	3899	BGH	C71-N7	3.55	1.47	1.39
44	2	1797	E7G	C2-N1	3.55	1.46	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	2	4483	B8T	C5-C4	3.53	1.48	1.40
44	2	2297	E7G	C2-N1	3.53	1.46	1.37
44	2	4690	B8K	C2-N2	3.52	1.42	1.34
44	2	3909	OMC	C6-N1	3.52	1.46	1.38
44	2	1909	P7G	C6-N1	3.51	1.44	1.38
44	2	3897	B8K	C2-N2	3.50	1.42	1.34
44	2	3897	B8K	C71-N7	3.47	1.47	1.39
44	2	4550	7MG	C2-N1	3.46	1.46	1.37
44	2	2754	B9B	O6-C6	3.45	1.40	1.35
44	2	237	B9B	O6-C6	3.44	1.40	1.35
44	2	3869	OMC	C6-N1	3.43	1.46	1.38
44	2	1866	UR3	C6-N1	3.40	1.46	1.38
44	2	1348	P4U	C6-N1	3.38	1.46	1.38
44	2	3880	P7G	C5-C4	3.38	1.44	1.37
44	2	3887	OMC	C6-N1	3.38	1.46	1.38
44	2	4530	UR3	C6-N1	3.38	1.46	1.38
44	2	4483	B8T	C6-N1	3.37	1.46	1.38
44	2	2297	E7G	C6-N1	3.35	1.45	1.38
44	2	3899	BGH	C2-N1	3.34	1.45	1.37
44	2	373	OMG	C6-N1	3.34	1.45	1.38
44	2	3899	BGH	C6-N1	3.33	1.45	1.38
44	2	1797	E7G	C6-N1	3.32	1.45	1.38
44	2	1909	P7G	C5-C4	3.32	1.44	1.37
44	2	1605	7MG	C6-N1	3.32	1.45	1.38
44	2	4083	5MU	C2-N1	3.30	1.43	1.38
44	2	1659	I4U	C6-N1	3.29	1.45	1.38
44	2	4371	MHG	C6-N1	3.27	1.44	1.38
44	2	4494	OMG	C6-N1	3.26	1.44	1.38
44	2	4690	B8K	C2-N1	3.26	1.45	1.37
44	2	3897	B8K	C2-N1	3.26	1.45	1.37
44	2	1574	B9B	O6-C6	3.25	1.40	1.35
44	2	2861	OMC	C6-N1	3.25	1.45	1.38
44	2	2522	7MG	C6-N1	3.23	1.44	1.38
44	2	4370	OMG	C6-N1	3.23	1.44	1.38
44	2	2365	OMC	C6-N1	3.23	1.45	1.38
44	2	4550	7MG	C6-N1	3.22	1.44	1.38
44	2	1883	OMG	O6-C6	-3.22	1.17	1.23
44	2	4623	OMG	C6-N1	3.21	1.44	1.38
44	2	4671	B8T	C6-N1	3.20	1.45	1.38
44	2	2773	OMG	C6-N1	3.20	1.44	1.38
44	2	1316	OMG	C6-N1	3.16	1.44	1.38
44	2	4355	E6G	C5-C4	-3.16	1.33	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	2	1909	P7G	O6-C6	-3.16	1.18	1.23
44	2	4637	OMG	C6-N1	3.16	1.44	1.38
44	2	1517	2MG	C5-N7	-3.16	1.33	1.39
44	2	4597	UR3	C6-N1	3.15	1.45	1.38
44	2	4623	OMG	O6-C6	-3.15	1.17	1.23
44	2	1522	OMG	C6-N1	3.15	1.44	1.38
44	2	3701	OMC	C6-N1	3.15	1.45	1.38
44	2	2424	OMG	C6-N1	3.14	1.44	1.38
44	2	4370	OMG	O6-C6	-3.12	1.17	1.23
44	2	4870	OMG	O6-C6	-3.12	1.17	1.23
44	2	1522	OMG	O6-C6	-3.12	1.17	1.23
44	2	2364	OMG	C6-N1	3.11	1.44	1.38
44	2	1316	OMG	O6-C6	-3.11	1.17	1.23
44	2	2424	OMG	O6-C6	-3.11	1.17	1.23
44	2	4536	OMC	C6-N1	3.11	1.45	1.38
44	2	3880	P7G	O6-C6	-3.10	1.18	1.23
44	2	1883	OMG	C6-N1	3.10	1.44	1.38
44	2	1625	OMG	O6-C6	-3.08	1.17	1.23
44	2	2401	A2M	O3'-C3'	3.08	1.50	1.43
44	2	2050	OMG	O6-C6	-3.07	1.17	1.23
44	2	4529	B8W	C5-N7	-3.06	1.33	1.39
44	2	2364	OMG	O6-C6	-3.06	1.17	1.23
44	2	1625	OMG	C6-N1	3.06	1.44	1.38
44	2	4494	OMG	O6-C6	-3.05	1.17	1.23
44	2	2773	OMG	O6-C6	-3.05	1.17	1.23
44	2	373	OMG	O6-C6	-3.04	1.17	1.23
44	2	4637	OMG	O6-C6	-3.04	1.17	1.23
44	2	4472	B8W	C5-N7	-3.04	1.33	1.39
44	2	2050	OMG	C6-N1	3.03	1.44	1.38
44	2	729	2MG	C5-N7	-3.02	1.33	1.39
44	2	1534	A2M	O3'-C3'	3.01	1.50	1.43
44	2	2804	OMC	C6-N1	3.00	1.45	1.38
44	2	4185	B8W	C5-N7	-2.99	1.33	1.39
44	2	4620	OMU	O4-C4	-2.95	1.18	1.24
44	2	3899	BGH	O3'-C3'	-2.95	1.36	1.43
44	2	1574	B9B	C5-C4	-2.95	1.33	1.39
44	2	2380	B8W	C5-C4	-2.95	1.33	1.39
4	8	14	OMU	O4-C4	-2.94	1.18	1.24
44	2	237	B9B	C5-C4	-2.94	1.33	1.39
44	2	3718	A2M	O3'-C3'	2.92	1.49	1.43
44	2	4083	5MU	O4-C4	-2.92	1.18	1.23
44	2	4872	2MG	C5-N7	-2.92	1.33	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	2	1871	A2M	O3'-C3'	2.91	1.49	1.43
44	2	2363	A2M	O3'-C3'	2.91	1.49	1.43
44	2	1659	I4U	O4-C4	2.90	1.41	1.35
44	2	3867	A2M	O3'-C3'	2.90	1.49	1.43
44	2	4472	B8W	C5-C4	-2.89	1.33	1.39
44	2	4306	OMU	O4-C4	-2.88	1.18	1.24
44	2	3897	B8K	C5-C4	2.87	1.47	1.38
44	2	3825	A2M	O3'-C3'	2.87	1.49	1.43
44	2	1326	A2M	O3'-C3'	2.87	1.49	1.43
44	2	4870	OMG	C6-N1	2.87	1.44	1.38
44	2	4523	A2M	O3'-C3'	2.87	1.49	1.43
44	2	978	2MG	C5-N7	-2.87	1.33	1.39
44	2	4306	OMU	C6-N1	2.86	1.44	1.38
44	2	398	A2M	O3'-C3'	2.85	1.49	1.43
44	2	3723	A2M	O3'-C3'	2.85	1.49	1.43
44	2	2380	B8W	C5-N7	-2.83	1.33	1.39
44	2	4529	B8W	C5-C4	-2.83	1.33	1.39
44	2	2401	A2M	C5-C4	-2.83	1.33	1.39
44	2	1524	A2M	O3'-C3'	2.82	1.49	1.43
44	2	4220	6MZ	C5-C4	-2.82	1.33	1.39
44	2	4671	B8T	O2-C2	-2.82	1.18	1.23
44	2	4690	B8K	C5-C4	2.81	1.47	1.38
44	2	3909	OMC	C5-C4	2.81	1.49	1.42
44	2	4872	2MG	C5-C6	2.77	1.54	1.44
44	2	4083	5MU	O2-C2	-2.77	1.18	1.23
44	2	3899	BGH	O6-C6	-2.76	1.18	1.23
44	2	4571	A2M	O3'-C3'	2.76	1.49	1.43
44	2	1348	P4U	O2-C2	-2.76	1.18	1.23
44	2	3701	OMC	O2-C2	-2.75	1.18	1.23
44	2	1871	A2M	C5-C4	-2.75	1.33	1.39
44	2	2754	B9B	C5-C4	-2.75	1.33	1.39
44	2	1659	I4U	O2-C2	-2.75	1.18	1.23
44	2	2365	OMC	O2-C2	-2.75	1.18	1.23
44	2	237	B9B	C5-N7	-2.74	1.33	1.39
44	2	978	2MG	C5-C6	2.74	1.54	1.44
44	2	3825	A2M	C5-C4	-2.73	1.33	1.39
4	8	14	OMU	C6-N1	2.73	1.44	1.38
44	2	4185	B8W	C5-C4	-2.72	1.33	1.39
44	2	2363	A2M	C5-C4	-2.72	1.33	1.39
44	2	1534	A2M	C5-C4	-2.72	1.33	1.39
44	2	729	2MG	C5-C6	2.72	1.54	1.44
44	2	2804	OMC	O2-C2	-2.70	1.18	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	2	2754	B9B	C5-N7	-2.70	1.33	1.39
44	2	4571	A2M	C5-C4	-2.69	1.34	1.39
44	2	1574	B9B	C5-N7	-2.69	1.33	1.39
44	2	1517	2MG	C5-C6	2.69	1.54	1.44
44	2	4220	6MZ	C5-N7	-2.68	1.34	1.39
44	2	1524	A2M	O2'-C2'	-2.66	1.35	1.42
44	2	2401	A2M	O2'-C2'	-2.66	1.35	1.42
44	2	398	A2M	C5-C4	-2.66	1.34	1.39
44	2	4620	OMU	C6-N1	2.65	1.44	1.38
44	2	4523	A2M	C5-C4	-2.65	1.34	1.39
44	2	1524	A2M	C5-C4	-2.65	1.34	1.39
44	2	1659	I4U	O4-C41	-2.64	1.41	1.47
44	2	4483	B8T	O2-C2	-2.64	1.18	1.23
44	2	3718	A2M	C5-C4	-2.63	1.34	1.39
44	2	2363	A2M	O2'-C2'	-2.63	1.35	1.42
44	2	4523	A2M	O2'-C2'	-2.62	1.35	1.42
44	2	4623	OMG	C5-C6	2.62	1.54	1.44
44	2	978	2MG	C6-N1	2.61	1.43	1.38
44	2	2773	OMG	C5-C6	2.61	1.54	1.44
44	2	2522	7MG	O6-C6	-2.60	1.18	1.23
44	2	398	A2M	O2'-C2'	-2.60	1.35	1.42
44	2	1316	OMG	C5-C6	2.60	1.54	1.44
44	2	4370	OMG	C5-C6	2.60	1.54	1.44
44	2	1326	A2M	O2'-C2'	-2.60	1.36	1.42
44	2	2861	OMC	O2-C2	-2.60	1.18	1.23
44	2	2050	OMG	C5-C6	2.60	1.54	1.44
44	2	2363	A2M	C8-N9	-2.59	1.32	1.37
44	2	2364	OMG	C5-C6	2.58	1.54	1.44
44	2	373	OMG	C2-N1	2.58	1.44	1.37
44	2	373	OMG	C5-C6	2.58	1.54	1.44
44	2	3723	A2M	C5-C4	-2.57	1.34	1.39
44	2	3887	OMC	O2-C2	-2.57	1.18	1.23
44	2	4637	OMG	C5-C6	2.57	1.53	1.44
44	2	3718	A2M	O2'-C2'	-2.57	1.36	1.42
44	2	1534	A2M	O2'-C2'	-2.57	1.36	1.42
44	2	3909	OMC	O2-C2	-2.57	1.18	1.23
44	2	1522	OMG	C5-C6	2.56	1.53	1.44
44	2	4536	OMC	O2-C2	-2.56	1.19	1.23
44	2	3825	A2M	O2'-C2'	-2.56	1.36	1.42
44	2	4129	B8W	C5-N7	-2.55	1.34	1.39
44	2	4870	OMG	C5-C6	2.55	1.53	1.44
44	2	3701	OMC	C5-C4	2.55	1.48	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	2	4494	OMG	C5-C6	2.54	1.53	1.44
44	2	3867	A2M	O2'-C2'	-2.54	1.36	1.42
44	2	4872	2MG	C6-N1	2.54	1.43	1.38
44	2	3869	OMC	O2-C2	-2.54	1.19	1.23
44	2	1605	7MG	O6-C6	-2.54	1.18	1.23
44	2	3718	A2M	C8-N9	-2.54	1.33	1.37
44	2	3867	A2M	C5-C4	-2.53	1.34	1.39
44	2	4370	OMG	C2-N1	2.53	1.43	1.37
44	2	4335	5MC	O2-C2	-2.53	1.19	1.23
44	2	1625	OMG	C5-C6	2.52	1.53	1.44
44	2	4494	OMG	C2-N1	2.52	1.43	1.37
44	2	2773	OMG	C2-N1	2.52	1.43	1.37
44	2	1871	A2M	O2'-C2'	-2.52	1.36	1.42
44	2	2297	E7G	O6-C6	-2.51	1.18	1.23
44	2	2364	OMG	C2-N1	2.50	1.43	1.37
44	2	1534	A2M	C8-N9	-2.50	1.33	1.37
4	8	14	OMU	O2-C2	-2.50	1.18	1.23
44	2	1625	OMG	C2-N1	2.49	1.43	1.37
44	2	4872	2MG	C4-N9	-2.48	1.31	1.38
44	2	1522	OMG	C2-N1	2.48	1.43	1.37
44	2	1326	A2M	C5-C4	-2.48	1.34	1.39
44	2	1883	OMG	C2-N1	2.47	1.43	1.37
44	2	4571	A2M	C8-N9	-2.46	1.33	1.37
44	2	4529	B8W	C8-N9	-2.46	1.33	1.37
44	2	3723	A2M	O2'-C2'	-2.46	1.36	1.42
44	2	2424	OMG	C5-C6	2.46	1.53	1.44
44	2	4623	OMG	C2-N1	2.45	1.43	1.37
44	2	3887	OMC	C5-C4	2.45	1.48	1.42
44	2	2050	OMG	C2-N1	2.45	1.43	1.37
44	2	4550	7MG	O6-C6	-2.44	1.18	1.23
44	2	3718	A2M	C5-N7	-2.44	1.34	1.39
44	2	4637	OMG	C2-N1	2.44	1.43	1.37
44	2	3723	A2M	C8-N9	-2.43	1.33	1.37
44	2	4571	A2M	O2'-C2'	-2.43	1.36	1.42
44	2	4620	OMU	O2-C2	-2.43	1.18	1.23
44	2	1797	E7G	O6-C6	-2.42	1.19	1.23
44	2	2401	A2M	C8-N9	-2.42	1.33	1.37
44	2	4306	OMU	C5-C4	2.42	1.49	1.43
44	2	2424	OMG	C2-N1	2.41	1.43	1.37
44	2	2861	OMC	C5-C4	2.41	1.48	1.42
44	2	1316	OMG	C2-N1	2.40	1.43	1.37
44	2	2365	OMC	C5-C4	2.40	1.48	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	2	1883	OMG	C5-C6	2.40	1.53	1.44
44	2	1866	UR3	C4-N3	2.40	1.46	1.40
44	2	4129	B8W	C5-C4	-2.40	1.34	1.39
44	2	1456	B8Q	C6-N1	2.38	1.43	1.38
44	2	4870	OMG	C2-N1	2.37	1.43	1.37
44	2	1517	2MG	C6-N1	2.37	1.43	1.38
44	2	4306	OMU	O2-C2	-2.36	1.18	1.23
44	2	2363	A2M	C5-N7	-2.36	1.34	1.39
44	2	1524	A2M	C8-N9	-2.35	1.33	1.37
44	2	3825	A2M	C8-N9	-2.35	1.33	1.37
44	2	1871	A2M	C8-N9	-2.34	1.33	1.37
44	2	398	A2M	C8-N9	-2.34	1.33	1.37
44	2	4129	B8W	C8-N9	-2.34	1.33	1.37
4	8	14	OMU	C5-C4	2.33	1.48	1.43
44	2	1326	A2M	C8-N9	-2.33	1.33	1.37
44	2	4371	MHG	O6-C6	-2.33	1.19	1.23
44	2	1326	A2M	C5-N7	-2.32	1.34	1.39
44	2	4523	A2M	C8-N9	-2.32	1.33	1.37
44	2	3867	A2M	C8-N9	-2.32	1.33	1.37
44	2	1866	UR3	C5-C4	2.32	1.49	1.43
44	2	4597	UR3	C5-C4	2.31	1.49	1.43
44	2	1871	A2M	C5-N7	-2.29	1.34	1.39
44	2	4571	A2M	C5-N7	-2.29	1.34	1.39
44	2	4620	OMU	C5-C4	2.29	1.48	1.43
44	2	4530	UR3	C4-N3	2.29	1.45	1.40
44	2	398	A2M	C5-N7	-2.29	1.34	1.39
44	2	2401	A2M	C5-N7	-2.28	1.34	1.39
44	2	729	2MG	C6-N1	2.26	1.43	1.38
44	2	3867	A2M	C5-N7	-2.25	1.34	1.39
44	2	4536	OMC	C5-C4	2.25	1.48	1.42
44	2	2786	B9H	C6-N1	2.24	1.43	1.38
44	2	1534	A2M	C5-N7	-2.23	1.34	1.39
44	2	1524	A2M	C5-N7	-2.23	1.34	1.39
44	2	3723	A2M	C5-N7	-2.22	1.34	1.39
44	2	3825	A2M	C5-N7	-2.20	1.34	1.39
44	2	4597	UR3	C4-N3	2.19	1.45	1.40
44	2	2380	B8W	C8-N9	-2.19	1.33	1.37
44	2	4185	B8W	C8-N9	-2.19	1.33	1.37
44	2	3899	BGH	C5-C4	2.17	1.45	1.38
44	2	978	2MG	C4-N9	-2.17	1.32	1.38
44	2	237	B9B	C8-N9	-2.17	1.33	1.37
44	2	4530	UR3	C5-C4	2.17	1.49	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	2	1574	B9B	C5-C6	-2.16	1.37	1.41
44	2	4185	B8W	C4-N3	2.16	1.37	1.34
44	2	4523	A2M	C5-N7	-2.14	1.35	1.39
44	2	4415	1MA	CM1-N1	2.14	1.51	1.46
44	2	4220	6MZ	C8-N9	-2.14	1.33	1.37
44	2	1456	B8Q	O2-C2	-2.13	1.18	1.22
44	2	2754	B9B	C5-C6	-2.12	1.37	1.41
44	2	4296	B8H	O4-C4	-2.12	1.19	1.23
44	2	2754	B9B	C8-N9	-2.09	1.33	1.37
44	2	4597	UR3	O2-C2	-2.09	1.18	1.22
44	2	4472	B8W	C4-N3	2.08	1.36	1.34
44	2	237	B9B	C5-C6	-2.08	1.37	1.41
44	2	4355	E6G	C8-N9	-2.07	1.33	1.37
44	2	3869	OMC	C5-C4	2.07	1.47	1.42
44	2	1517	2MG	O6-C6	-2.07	1.19	1.23
44	2	4129	B8W	C4-N3	2.07	1.36	1.34
44	2	4872	2MG	O6-C6	-2.06	1.19	1.23
44	2	2786	B9H	C31-N3	-2.04	1.43	1.46
44	2	1574	B9B	C8-N9	-2.04	1.33	1.37
44	2	4529	B8W	C4-N3	2.03	1.36	1.34
44	2	2804	OMC	C5-C4	2.03	1.47	1.42
44	2	1860	B8H	O4-C4	-2.01	1.19	1.23
44	2	4472	B8W	C8-N9	-2.01	1.33	1.37

All (647) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2	237	B9B	O6-C6-C5	21.20	143.41	116.57
44	2	1574	B9B	O6-C6-C5	21.15	143.35	116.57
44	2	2754	B9B	O6-C6-C5	21.06	143.23	116.57
44	2	1574	B9B	O6-C6-N1	-18.18	94.67	120.00
44	2	237	B9B	O6-C6-N1	-18.06	94.84	120.00
44	2	2754	B9B	O6-C6-N1	-18.00	94.92	120.00
44	2	4564	M7A	C5-C6-N6	13.69	147.13	123.74
44	2	4564	M7A	N6-C6-N1	-11.53	93.11	118.35
44	2	4083	5MU	C5-C4-N3	10.27	124.08	115.31
44	2	4870	OMG	C1'-N9-C8	-9.42	99.89	126.70
44	2	4870	OMG	C1'-N9-C4	9.36	154.30	126.50
44	2	4220	6MZ	C4-N9-C1'	-9.35	104.32	126.59
44	2	4220	6MZ	C1'-N9-C8	9.24	148.00	127.14
44	2	2424	OMG	C1'-N9-C4	8.66	152.23	126.50
44	2	4494	OMG	C1'-N9-C4	8.64	152.15	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2	1522	OMG	C1'-N9-C4	8.58	152.00	126.50
44	2	2050	OMG	C1'-N9-C4	8.55	151.90	126.50
44	2	2424	OMG	C1'-N9-C8	-8.50	102.51	126.70
44	2	1625	OMG	C1'-N9-C4	8.49	151.72	126.50
44	2	4370	OMG	C1'-N9-C4	8.41	151.49	126.50
44	2	2364	OMG	C1'-N9-C4	8.40	151.45	126.50
44	2	1522	OMG	C1'-N9-C8	-8.38	102.84	126.70
44	2	4623	OMG	C1'-N9-C4	8.37	151.36	126.50
44	2	4637	OMG	C1'-N9-C4	8.36	151.33	126.50
44	2	4623	OMG	C1'-N9-C8	-8.35	102.94	126.70
44	2	2773	OMG	C1'-N9-C4	8.34	151.29	126.50
44	2	1316	OMG	C1'-N9-C4	8.27	151.06	126.50
44	2	2050	OMG	C1'-N9-C8	-8.26	103.18	126.70
44	2	4370	OMG	C1'-N9-C8	-8.24	103.23	126.70
44	2	4494	OMG	C1'-N9-C8	-8.22	103.31	126.70
44	2	1883	OMG	C1'-N9-C4	8.21	150.89	126.50
44	2	4083	5MU	C5-C6-N1	-8.18	114.92	123.34
44	2	4637	OMG	C1'-N9-C8	-8.15	103.49	126.70
44	2	1883	OMG	C1'-N9-C8	-8.07	103.72	126.70
44	2	1316	OMG	C1'-N9-C8	-8.06	103.76	126.70
44	2	2773	OMG	C1'-N9-C8	-8.05	103.78	126.70
44	2	1625	OMG	C1'-N9-C8	-8.03	103.84	126.70
44	2	2364	OMG	C1'-N9-C8	-8.01	103.90	126.70
44	2	1517	2MG	C2-N3-C4	7.93	121.88	112.04
44	2	373	OMG	C1'-N9-C4	7.77	149.59	126.50
44	2	373	OMG	C1'-N9-C8	-7.77	104.59	126.70
44	2	4597	UR3	C4-N3-C2	-7.76	117.26	124.56
44	2	4185	B8W	C5-C4-N3	-7.56	118.69	127.19
44	2	4083	5MU	C4-N3-C2	-7.21	118.01	127.35
44	2	1534	A2M	N6-C6-N1	-7.17	102.64	118.35
44	2	4472	B8W	C5-C4-N3	-7.16	119.13	127.19
44	2	729	2MG	C2-N3-C4	7.13	120.88	112.04
44	2	4355	E6G	N2-C2-N3	7.00	128.13	117.25
44	2	1326	A2M	N6-C6-N1	-6.91	103.21	118.35
44	2	4523	A2M	N6-C6-N1	-6.88	103.29	118.35
44	2	1517	2MG	C5-C4-N3	-6.85	117.34	128.46
44	2	237	B9B	C5-C4-N3	-6.84	119.50	127.19
44	2	1524	A2M	N6-C6-N1	-6.81	103.43	118.35
44	2	4529	B8W	C5-C4-N3	-6.81	119.53	127.19
44	2	3867	A2M	N6-C6-N1	-6.80	103.45	118.35
44	2	2754	B9B	C5-C4-N3	-6.78	119.56	127.19
44	2	398	A2M	N6-C6-N1	-6.78	103.50	118.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2	4296	B8H	C4-N3-C2	-6.78	118.58	127.35
44	2	2786	B9H	C6-N1-C2	-6.77	115.72	121.79
44	2	1871	A2M	N6-C6-N1	-6.77	103.52	118.35
44	2	3718	A2M	N6-C6-N1	-6.77	103.53	118.35
44	2	4571	A2M	N6-C6-N1	-6.74	103.59	118.35
44	2	3825	A2M	N6-C6-N1	-6.73	103.61	118.35
44	2	2363	A2M	N6-C6-N1	-6.73	103.62	118.35
44	2	4129	B8W	C5-C4-N3	-6.72	119.63	127.19
44	2	2401	A2M	N6-C6-N1	-6.71	103.66	118.35
44	2	4371	MHG	C2-N3-C4	6.69	120.34	112.04
44	2	4355	E6G	C5-C4-N3	-6.69	119.67	127.19
44	2	3723	A2M	N6-C6-N1	-6.66	103.76	118.35
44	2	4355	E6G	O6-C6-N1	6.61	129.20	120.00
44	2	4872	2MG	C2-N3-C4	6.56	120.17	112.04
44	2	1860	B8H	C4-N3-C2	-6.54	118.88	127.35
44	2	1871	A2M	N3-C2-N1	-6.54	118.37	128.60
44	2	978	2MG	C2-N3-C4	6.50	120.10	112.04
44	2	2380	B8W	C5-C4-N3	-6.49	119.89	127.19
44	2	4220	6MZ	N1-C2-N3	-6.48	118.46	128.60
44	2	4529	B8W	N2-C2-N3	6.44	127.27	117.25
44	2	1574	B9B	C5-C4-N3	-6.40	119.99	127.19
44	2	4129	B8W	N2-C2-N3	6.37	127.17	117.25
44	2	2380	B8W	N2-C2-N3	6.37	127.15	117.25
44	2	4690	B8K	C72-C71-N7	6.33	128.39	118.86
44	2	2401	A2M	N3-C2-N1	-6.31	118.73	128.60
44	2	3825	A2M	N3-C2-N1	-6.30	118.75	128.60
44	2	398	A2M	N3-C2-N1	-6.29	118.76	128.60
44	2	729	2MG	C5-C4-N3	-6.29	118.26	128.46
44	2	4185	B8W	N2-C2-N3	6.26	127.00	117.25
44	2	4523	A2M	N3-C2-N1	-6.24	118.84	128.60
44	2	1534	A2M	N3-C2-N1	-6.24	118.84	128.60
44	2	4220	6MZ	C5-C4-N3	-6.23	118.62	126.75
44	2	3723	A2M	N3-C2-N1	-6.23	118.86	128.60
44	2	1524	A2M	N3-C2-N1	-6.22	118.88	128.60
44	2	4571	A2M	N3-C2-N1	-6.21	118.88	128.60
44	2	1326	A2M	N3-C2-N1	-6.21	118.89	128.60
44	2	4564	M7A	N3-C2-N1	-6.21	118.89	128.60
44	2	2363	A2M	N3-C2-N1	-6.20	118.90	128.60
44	2	3897	B8K	C72-C71-N7	6.16	128.12	118.86
44	2	3825	A2M	N9-C8-N7	-6.12	105.54	113.91
44	2	4523	A2M	N9-C8-N7	-6.11	105.56	113.91
44	2	1534	A2M	C5-C6-N6	6.08	136.66	123.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2	1871	A2M	N9-C8-N7	-6.07	105.61	113.91
44	2	3867	A2M	N3-C2-N1	-6.07	119.11	128.60
44	2	2401	A2M	N9-C8-N7	-6.03	105.66	113.91
44	2	4472	B8W	N2-C2-N3	6.02	126.62	117.25
44	2	3899	BGH	C72-C71-N7	5.98	127.86	118.86
44	2	4690	B8K	C5-C6-N1	5.98	121.53	110.99
44	2	1326	A2M	C5-C6-N6	5.96	136.40	123.43
44	2	4472	B8W	O6-C6-N1	5.94	127.20	119.01
44	2	3718	A2M	C5-C6-N6	5.93	136.34	123.43
44	2	4523	A2M	C5-C6-N6	5.92	136.32	123.43
44	2	1871	A2M	C5-C6-N6	5.91	136.29	123.43
44	2	398	A2M	C5-C6-N6	5.90	136.27	123.43
44	2	3718	A2M	N3-C2-N1	-5.90	119.38	128.60
44	2	1524	A2M	N9-C8-N7	-5.89	105.86	113.91
44	2	4571	A2M	N9-C8-N7	-5.88	105.87	113.91
44	2	3723	A2M	N9-C8-N7	-5.87	105.88	113.91
44	2	3867	A2M	C5-C6-N6	5.86	136.18	123.43
44	2	3867	A2M	N9-C8-N7	-5.83	105.94	113.91
44	2	1524	A2M	C5-C6-N6	5.83	136.11	123.43
44	2	1534	A2M	N9-C8-N7	-5.82	105.95	113.91
44	2	2786	B9H	C31-N3-C2	5.80	124.46	117.21
44	2	4571	A2M	C5-C6-N6	5.80	136.05	123.43
44	2	3825	A2M	C5-C6-N6	5.78	136.00	123.43
44	2	3723	A2M	C5-C6-N6	5.74	135.92	123.43
44	2	2363	A2M	C5-C6-N6	5.74	135.92	123.43
44	2	3899	BGH	C5-C6-N1	5.74	121.10	110.99
44	2	2401	A2M	C5-C6-N6	5.73	135.91	123.43
44	2	398	A2M	N9-C8-N7	-5.71	106.10	113.91
44	2	2363	A2M	N9-C8-N7	-5.70	106.12	113.91
44	2	3897	B8K	C5-C6-N1	5.69	121.02	110.99
44	2	4296	B8H	N3-C2-N1	5.69	121.29	115.14
44	2	1860	B8H	N3-C2-N1	5.66	121.26	115.14
44	2	1456	B8Q	N3-C2-N1	5.66	123.78	117.13
44	2	1326	A2M	N9-C8-N7	-5.62	106.23	113.91
44	2	3718	A2M	N9-C8-N7	-5.50	106.39	113.91
44	2	1866	UR3	O3'-C3'-C2'	5.48	129.55	111.82
44	2	1625	OMG	C5-C4-N3	-5.44	119.63	128.46
44	2	3825	A2M	C4-N9-C8	5.39	111.57	105.73
44	2	1871	A2M	C4-N9-C8	5.37	111.55	105.73
44	2	2401	A2M	C4-N9-C8	5.36	111.53	105.73
44	2	4870	OMG	C5-C4-N3	-5.36	119.77	128.46
44	2	4523	A2M	C4-N9-C8	5.31	111.49	105.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2	4872	2MG	C5-C4-N3	-5.29	119.88	128.46
44	2	978	2MG	C5-C4-N3	-5.27	119.91	128.46
44	2	3723	A2M	C4-N9-C8	5.25	111.42	105.73
44	2	1797	E7G	C5-C6-N1	5.23	120.20	110.99
44	2	4564	M7A	N3-C4-N9	5.20	133.44	126.87
44	2	4306	OMU	C4-N3-C2	-5.20	119.72	126.58
4	8	14	OMU	C4-N3-C2	-5.20	119.72	126.58
44	2	4371	MHG	C5-C6-N1	5.20	120.15	110.99
44	2	2297	E7G	C5-C6-N1	5.19	120.14	110.99
44	2	4571	A2M	C4-N9-C8	5.18	111.34	105.73
44	2	1883	OMG	C5-C4-N3	-5.18	120.06	128.46
44	2	4494	OMG	C5-C4-N3	-5.16	120.09	128.46
44	2	4872	2MG	C2-N1-C6	-5.16	118.55	124.48
44	2	1456	B8Q	C31-N3-C4	5.15	122.02	114.25
44	2	4637	OMG	C5-C4-N3	-5.14	120.12	128.46
44	2	3880	P7G	C4-C5-N7	5.14	109.38	106.67
44	2	4185	B8W	N3-C4-N9	5.13	134.10	126.99
44	2	1524	A2M	C4-N9-C8	5.12	111.28	105.73
44	2	2773	OMG	C5-C4-N3	-5.11	120.18	128.46
44	2	2364	OMG	C5-C4-N3	-5.10	120.18	128.46
44	2	4620	OMU	C4-N3-C2	-5.10	119.85	126.58
44	2	2050	OMG	C5-C4-N3	-5.10	120.19	128.46
44	2	3867	A2M	C4-N9-C8	5.09	111.24	105.73
44	2	4083	5MU	N3-C2-N1	5.05	121.60	114.89
44	2	1316	OMG	C5-C4-N3	-5.04	120.29	128.46
44	2	2424	OMG	C5-C4-N3	-5.04	120.29	128.46
44	2	3899	BGH	C2-N3-C4	5.03	121.25	112.30
44	2	1909	P7G	C4-C5-N7	5.00	109.31	106.67
44	2	1534	A2M	C4-N9-C8	5.00	111.14	105.73
44	2	1456	B8Q	O2-C2-N3	-4.99	115.62	122.95
44	2	2363	A2M	C4-N9-C8	4.98	111.12	105.73
44	2	2754	B9B	N2-C2-N3	4.97	124.98	117.25
44	2	2297	E7G	C4-C5-N7	4.96	109.32	104.91
44	2	237	B9B	N2-C2-N3	4.94	124.93	117.25
44	2	1517	2MG	N9-C4-N3	4.92	135.83	125.94
44	2	4529	B8W	O6-C6-N1	4.91	125.79	119.01
44	2	1605	7MG	C5-C6-N1	4.91	119.64	110.99
44	2	1326	A2M	C5-C4-N3	-4.90	120.36	126.75
44	2	4185	B8W	O6-C6-N1	4.89	125.76	119.01
44	2	1866	UR3	C4-N3-C2	-4.88	119.97	124.56
44	2	4690	B8K	C2-N3-C4	4.88	120.99	112.30
44	2	1522	OMG	C5-C4-N3	-4.87	120.56	128.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2	398	A2M	C4-N9-C8	4.85	110.99	105.73
44	2	1517	2MG	C2-N1-C6	-4.85	118.90	124.48
44	2	4415	1MA	N1-C2-N3	-4.84	120.24	126.00
44	2	3897	B8K	C2-N3-C4	4.84	120.92	112.30
44	2	2522	7MG	C5-C6-N1	4.83	119.50	110.99
44	2	4370	OMG	C5-C4-N3	-4.83	120.63	128.46
44	2	1326	A2M	C4-N9-C8	4.79	110.92	105.73
44	2	1574	B9B	N2-C2-N3	4.79	124.70	117.25
44	2	4371	MHG	C4-C5-N7	4.78	109.16	104.91
44	2	1797	E7G	C4-C5-N7	4.77	109.16	104.91
44	2	4472	B8W	N3-C4-N9	4.77	133.61	126.99
44	2	4415	1MA	C5-C4-N3	-4.76	120.16	127.26
44	2	4550	7MG	C5-C6-N1	4.76	119.38	110.99
44	2	3718	A2M	C4-N9-C8	4.75	110.88	105.73
44	2	729	2MG	C2-N1-C6	-4.73	119.03	124.48
44	2	1797	E7G	C2-N3-C4	4.73	120.72	112.30
44	2	3869	OMC	O2-C2-N3	-4.72	114.65	122.33
44	2	4623	OMG	C5-C4-N3	-4.71	120.82	128.46
44	2	4355	E6G	O6-C6-C5	-4.69	110.63	116.57
44	2	1866	UR3	O3'-C3'-C4'	4.64	124.48	111.05
44	2	2297	E7G	C2-N3-C4	4.64	120.56	112.30
44	2	1534	A2M	C5-C4-N3	-4.61	120.74	126.75
44	2	4083	5MU	C5M-C5-C6	-4.61	116.70	122.85
44	2	4129	B8W	C61-O6-C6	4.58	121.75	117.21
44	2	4530	UR3	C4-N3-C2	-4.58	120.25	124.56
44	2	3867	A2M	C5-C4-N3	-4.56	120.80	126.75
44	2	373	OMG	C5-C4-N3	-4.56	121.07	128.46
44	2	2363	A2M	C5-C4-N3	-4.55	120.81	126.75
44	2	237	B9B	N3-C4-N9	4.54	133.29	126.99
44	2	4870	OMG	C2-N3-C4	4.54	120.39	112.30
44	2	1625	OMG	C2-N3-C4	4.53	120.37	112.30
44	2	2773	OMG	C2-N3-C4	4.53	120.37	112.30
44	2	1316	OMG	C2-N3-C4	4.52	120.35	112.30
44	2	4637	OMG	C2-N3-C4	4.52	120.34	112.30
44	2	398	A2M	C5-C4-N3	-4.49	120.89	126.75
44	2	2364	OMG	C2-N3-C4	4.47	120.27	112.30
44	2	1883	OMG	C2-N3-C4	4.46	120.25	112.30
44	2	4523	A2M	C5-C4-N3	-4.45	120.95	126.75
44	2	4220	6MZ	C2-N3-C4	4.44	122.24	111.75
44	2	4571	A2M	C5-C4-N3	-4.44	120.96	126.75
44	2	2754	B9B	N3-C4-N9	4.44	133.15	126.99
44	2	2424	OMG	C2-N3-C4	4.43	120.20	112.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2	4623	OMG	C2-N3-C4	4.43	120.19	112.30
44	2	1524	A2M	C5-C4-N3	-4.42	120.98	126.75
44	2	2050	OMG	C2-N3-C4	4.42	120.17	112.30
44	2	4494	OMG	C2-N3-C4	4.41	120.15	112.30
44	2	4370	OMG	C2-N3-C4	4.40	120.13	112.30
44	2	3723	A2M	C5-C4-N3	-4.39	121.03	126.75
44	2	1659	I4U	C5-C4-N3	-4.36	118.27	124.91
44	2	373	OMG	C2-N3-C4	4.34	120.03	112.30
44	2	978	2MG	C2-N1-C6	-4.34	119.49	124.48
44	2	4872	2MG	CM2-N2-C2	-4.33	114.29	123.86
44	2	3867	A2M	C1'-N9-C8	-4.32	117.38	127.14
44	2	4690	B8K	C4-C5-N7	4.31	108.74	104.91
44	2	1522	OMG	C2-N3-C4	4.30	119.97	112.30
44	2	2380	B8W	N9-C8-N7	-4.29	108.05	113.91
44	2	3718	A2M	C5-C4-N3	-4.29	121.15	126.75
44	2	2522	7MG	C2-N3-C4	4.29	119.94	112.30
44	2	3825	A2M	C5-C4-N3	-4.28	121.16	126.75
44	2	1326	A2M	C1'-N9-C8	-4.28	117.47	127.14
44	2	2363	A2M	C1'-N9-C8	-4.26	117.51	127.14
44	2	2401	A2M	C5-C4-N3	-4.26	121.19	126.75
44	2	4550	7MG	C2-N3-C4	4.26	119.89	112.30
44	2	1871	A2M	C5-C4-N3	-4.25	121.20	126.75
44	2	3899	BGH	N9-C8-N7	4.25	109.04	103.33
44	2	729	2MG	N9-C4-N3	4.25	134.47	125.94
44	2	1605	7MG	C2-N3-C4	4.25	119.86	112.30
44	2	4220	6MZ	N3-C4-N9	4.24	134.07	127.08
44	2	3899	BGH	C5-C4-N9	4.23	111.83	106.35
44	2	1574	B9B	N9-C8-N7	-4.21	108.15	113.91
44	2	4355	E6G	N9-C8-N7	-4.18	108.20	113.91
44	2	237	B9B	N9-C8-N7	-4.18	108.20	113.91
44	2	3899	BGH	C4-C5-N7	4.16	108.61	104.91
44	2	4129	B8W	N9-C8-N7	-4.16	108.22	113.91
44	2	4571	A2M	C1'-N9-C8	-4.13	117.81	127.14
44	2	1326	A2M	N3-C4-N9	4.13	133.88	127.08
44	2	3897	B8K	C5-C4-N9	4.08	111.65	106.35
44	2	1797	E7G	C5-C4-N3	-4.06	120.40	128.13
44	2	4355	E6G	N3-C4-N9	4.05	132.61	126.99
44	2	3723	A2M	C1'-N9-C8	-4.05	117.99	127.14
44	2	4690	B8K	C5-C4-N9	4.03	111.58	106.35
44	2	1534	A2M	C1'-N9-C8	-4.03	118.03	127.14
44	2	2804	OMC	O2-C2-N3	-4.00	115.82	122.33
44	2	1574	B9B	N3-C4-N9	3.98	132.52	126.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2	1524	A2M	C1'-N9-C8	-3.98	118.15	127.14
44	2	4415	1MA	C2-N3-C4	3.96	120.20	112.41
44	2	1456	B8Q	C6-N1-C2	-3.95	118.25	121.79
44	2	4083	5MU	O4-C4-C5	-3.95	120.32	124.90
44	2	3867	A2M	N3-C4-N9	3.94	133.58	127.08
44	2	4529	B8W	N3-C4-N9	3.93	132.45	126.99
44	2	3897	B8K	C4-C5-N7	3.93	108.41	104.91
44	2	1534	A2M	N3-C4-N9	3.92	133.55	127.08
44	2	2363	A2M	N3-C4-N9	3.92	133.54	127.08
44	2	3723	A2M	N3-C4-N9	3.90	133.51	127.08
44	2	4220	6MZ	N9-C8-N7	-3.89	108.59	113.91
44	2	4523	A2M	C1'-N9-C8	-3.89	118.35	127.14
44	2	4571	A2M	N3-C4-N9	3.86	133.44	127.08
44	2	1866	UR3	O2'-C2'-C3'	3.84	124.25	111.82
44	2	4523	A2M	N3-C4-N9	3.83	133.39	127.08
44	2	2754	B9B	N9-C8-N7	-3.81	108.70	113.91
44	2	1871	A2M	N3-C4-N9	3.81	133.36	127.08
44	2	4129	B8W	N3-C4-N9	3.81	132.27	126.99
44	2	4306	OMU	N3-C2-N1	3.80	119.93	114.89
44	2	1524	A2M	N3-C4-N9	3.79	133.32	127.08
44	2	2401	A2M	N3-C4-N9	3.78	133.31	127.08
44	2	4185	B8W	N9-C8-N7	-3.78	108.75	113.91
44	2	2786	B9H	O3'-C3'-C2'	3.78	121.89	111.17
44	2	4371	MHG	C5-C4-N3	-3.77	120.94	128.13
44	2	3825	A2M	N3-C4-N9	3.77	133.29	127.08
44	2	4472	B8W	O6-C6-C5	-3.77	112.25	116.97
44	2	3718	A2M	C1'-N9-C8	-3.76	118.65	127.14
44	2	2380	B8W	N3-C4-N9	3.76	132.20	126.99
44	2	1326	A2M	C2-N3-C4	3.74	120.60	111.75
44	2	398	A2M	N3-C4-N9	3.74	133.25	127.08
44	2	398	A2M	C1'-N9-C8	-3.74	118.70	127.14
44	2	2297	E7G	C5-C4-N3	-3.73	121.02	128.13
44	2	2380	B8W	O6-C6-N1	3.73	124.15	119.01
44	2	3825	A2M	C1'-N9-C8	-3.72	118.74	127.14
44	2	4690	B8K	N9-C8-N7	3.72	108.32	103.33
44	2	1534	A2M	C2-N3-C4	3.71	120.53	111.75
44	2	4523	A2M	C5-N7-C8	3.70	108.77	103.51
4	8	14	OMU	N3-C2-N1	3.69	119.79	114.89
44	2	4472	B8W	N9-C8-N7	-3.69	108.87	113.91
44	2	1605	7MG	C5-C4-N9	3.67	111.11	106.35
44	2	1348	P4U	C5-C4-N3	-3.67	119.33	124.91
44	2	4620	OMU	N3-C2-N1	3.66	119.75	114.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2	1871	A2M	C1'-N9-C8	-3.66	118.88	127.14
44	2	2401	A2M	C1'-N9-C8	-3.64	118.91	127.14
44	2	4523	A2M	C2-N3-C4	3.63	120.33	111.75
44	2	4571	A2M	C2-N3-C4	3.62	120.31	111.75
44	2	2363	A2M	C2-N3-C4	3.62	120.29	111.75
44	2	398	A2M	C2-N3-C4	3.61	120.28	111.75
44	2	1871	A2M	C2-N3-C4	3.61	120.28	111.75
44	2	3718	A2M	N3-C4-N9	3.61	133.03	127.08
44	2	3867	A2M	C2-N3-C4	3.61	120.27	111.75
44	2	1524	A2M	C2-N3-C4	3.60	120.26	111.75
44	2	3723	A2M	C2-N3-C4	3.59	120.24	111.75
44	2	3825	A2M	C5-N7-C8	3.59	108.61	103.51
44	2	4129	B8W	C5-N7-C8	3.59	108.61	103.51
44	2	4371	MHG	C2-N1-C6	-3.59	120.35	124.48
44	2	2401	A2M	C2-N3-C4	3.58	120.20	111.75
44	2	3825	A2M	C2-N3-C4	3.58	120.20	111.75
44	2	237	B9B	N3-C2-N1	-3.58	119.81	125.42
44	2	1534	A2M	C5-N7-C8	3.56	108.57	103.51
44	2	4129	B8W	N1-C2-N3	-3.56	119.84	125.42
44	2	2522	7MG	C5-C4-N9	3.55	110.96	106.35
44	2	3899	BGH	C5-C4-N3	-3.55	121.36	128.13
44	2	4296	B8H	C5-C4-N3	3.54	124.59	116.58
44	2	3897	B8K	N9-C8-N7	3.53	108.06	103.33
44	2	2522	7MG	C5-C4-N3	-3.51	121.45	128.13
44	2	1871	A2M	C5-N7-C8	3.50	108.48	103.51
44	2	4571	A2M	C5-N7-C8	3.50	108.48	103.51
44	2	3867	A2M	C5-N7-C8	3.50	108.48	103.51
44	2	4355	E6G	N3-C2-N1	-3.49	119.94	125.42
44	2	2380	B8W	C61-O6-C6	-3.49	113.76	117.21
44	2	4371	MHG	C72-C71-N7	-3.48	108.99	112.41
44	2	1524	A2M	C5-N7-C8	3.47	108.44	103.51
44	2	1860	B8H	C5-C4-N3	3.46	124.41	116.58
44	2	1605	7MG	C5-C4-N3	-3.46	121.55	128.13
44	2	2401	A2M	C5-N7-C8	3.46	108.42	103.51
44	2	1326	A2M	C5-N7-C8	3.44	108.40	103.51
44	2	3723	A2M	C5-N7-C8	3.44	108.39	103.51
4	8	14	OMU	C5-C4-N3	3.43	119.97	114.84
44	2	398	A2M	C5-N7-C8	3.43	108.38	103.51
44	2	4564	M7A	C2-N3-C4	3.43	119.84	111.75
44	2	4355	E6G	N2-C2-N1	-3.42	111.93	117.25
44	2	1797	E7G	C5-C4-N9	3.42	110.79	106.35
44	2	4415	1MA	N9-C8-N7	-3.42	106.94	113.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2	1574	B9B	N3-C2-N1	-3.42	120.05	125.42
44	2	2754	B9B	N3-C2-N1	-3.42	120.05	125.42
44	2	4550	7MG	C5-C4-N9	3.42	110.79	106.35
44	2	3718	A2M	C2-N3-C4	3.41	119.80	111.75
44	2	2363	A2M	C5-N7-C8	3.40	108.35	103.51
44	2	3869	OMC	C1'-N1-C2	3.40	126.01	118.42
44	2	4185	B8W	N1-C2-N3	-3.40	120.09	125.42
44	2	4220	6MZ	C4-C5-C6	3.40	119.44	116.81
44	2	4083	5MU	C5M-C5-C4	3.39	122.50	118.77
44	2	2297	E7G	C5-C4-N9	3.38	110.73	106.35
44	2	4529	B8W	C4-N9-C1'	-3.37	118.57	126.59
44	2	2380	B8W	N1-C2-N3	-3.35	120.17	125.42
44	2	4529	B8W	C1'-N9-C8	3.35	134.69	127.14
44	2	4371	MHG	C5-C4-N9	3.35	110.69	106.35
44	2	4620	OMU	C5-C4-N3	3.35	119.84	114.84
44	2	4529	B8W	N1-C2-N3	-3.34	120.17	125.42
44	2	4690	B8K	C6-C5-C4	-3.32	115.78	122.62
44	2	4083	5MU	C6-C5-C4	3.31	120.80	118.03
44	2	4472	B8W	N1-C2-N3	-3.29	120.26	125.42
44	2	4306	OMU	C5-C4-N3	3.28	119.75	114.84
44	2	4550	7MG	C5-C4-N3	-3.28	121.88	128.13
44	2	4870	OMG	C2-N1-C6	-3.28	119.12	125.10
44	2	3718	A2M	C5-N7-C8	3.27	108.15	103.51
44	2	2401	A2M	C2'-C1'-N9	-3.27	108.03	113.53
44	2	1909	P7G	N9-C8-N7	3.25	108.03	103.38
44	2	1883	OMG	C2-N1-C6	-3.23	119.22	125.10
44	2	3897	B8K	C6-C5-C4	-3.21	115.99	122.62
44	2	2861	OMC	O2-C2-N3	-3.21	117.10	122.33
44	2	4637	OMG	C2-N1-C6	-3.21	119.25	125.10
44	2	2050	OMG	C2-N1-C6	-3.20	119.26	125.10
44	2	978	2MG	N9-C4-N3	3.20	132.36	125.94
44	2	1522	OMG	C2-N1-C6	-3.19	119.28	125.10
44	2	2364	OMG	C2-N1-C6	-3.17	119.31	125.10
44	2	1316	OMG	C2-N1-C6	-3.17	119.32	125.10
44	2	4529	B8W	N9-C8-N7	-3.16	109.59	113.91
44	2	1625	OMG	C2-N1-C6	-3.16	119.35	125.10
44	2	3897	B8K	C5-C4-N3	-3.13	122.16	128.13
44	2	4690	B8K	C5-C4-N3	-3.13	122.17	128.13
44	2	4494	OMG	C2-N1-C6	-3.12	119.42	125.10
44	2	1871	A2M	C2'-C1'-N9	-3.11	108.30	113.53
44	2	2773	OMG	C2-N1-C6	-3.10	119.44	125.10
44	2	4355	E6G	C61-O6-C6	-3.09	114.59	117.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2	2380	B8W	C5-N7-C8	3.09	107.89	103.51
44	2	4536	OMC	O2-C2-N3	-3.08	117.31	122.33
44	2	373	OMG	C2-N1-C6	-3.06	119.53	125.10
44	2	2424	OMG	C2-N1-C6	-3.05	119.54	125.10
44	2	4220	6MZ	C5-N7-C8	3.03	107.81	103.51
44	2	4529	B8W	N2-C2-N1	-3.02	112.55	117.25
44	2	4623	OMG	C2-N1-C6	-2.99	119.64	125.10
44	2	4355	E6G	C5-N7-C8	2.99	107.75	103.51
44	2	2522	7MG	N9-C8-N7	2.98	107.64	103.38
4	8	14	OMU	O4-C4-C5	-2.98	119.92	125.16
44	2	4370	OMG	C2-N1-C6	-2.97	119.68	125.10
44	2	3899	BGH	C6-C5-C4	-2.95	116.53	122.62
44	2	2380	B8W	N2-C2-N1	-2.94	112.68	117.25
44	2	4129	B8W	C2-N1-C6	2.94	120.60	115.93
44	2	2861	OMC	C1'-N1-C2	2.93	124.95	118.42
44	2	1517	2MG	C5-C6-N1	2.92	120.61	113.19
44	2	4620	OMU	O4-C4-C5	-2.92	120.02	125.16
44	2	3869	OMC	O2-C2-N1	2.92	124.92	118.89
44	2	2380	B8W	C4-N9-C1'	-2.91	119.65	126.59
44	2	4872	2MG	N9-C8-N7	-2.90	107.93	113.39
44	2	978	2MG	N9-C8-N7	-2.89	107.95	113.39
44	2	4870	OMG	C5-C6-N1	2.89	120.52	113.19
44	2	1883	OMG	O6-C6-C5	-2.88	118.95	126.60
44	2	237	B9B	C5-N7-C8	2.87	107.59	103.51
44	2	1909	P7G	C71-N7-C5	2.87	131.32	124.52
44	2	4185	B8W	C5-N7-C8	2.85	107.55	103.51
44	2	4550	7MG	C4-C5-N7	2.84	109.48	105.53
44	2	1883	OMG	C5-C6-N1	2.83	120.39	113.19
44	2	4129	B8W	C5-C6-N1	-2.82	119.54	123.46
44	2	1860	B8H	O2-C2-N1	-2.80	119.72	122.87
44	2	2804	OMC	O2-C2-N1	2.80	124.67	118.89
44	2	4306	OMU	O4-C4-C5	-2.79	120.25	125.16
44	2	1605	7MG	N9-C8-N7	2.79	107.37	103.38
44	2	4185	B8W	N2-C2-N1	-2.79	112.92	117.25
44	2	2522	7MG	C4-C5-N7	2.79	109.40	105.53
44	2	3899	BGH	O6-C6-N1	-2.79	114.77	120.12
44	2	4637	OMG	C5-C6-N1	2.79	120.26	113.19
44	2	1574	B9B	C5-N7-C8	2.78	107.46	103.51
44	2	4597	UR3	C6-N1-C2	-2.78	119.30	121.79
44	2	4872	2MG	C5-C6-N1	2.77	120.23	113.19
44	2	1522	OMG	C5-C4-N9	2.77	110.65	105.63
44	2	3909	OMC	C5-C4-N4	2.76	124.92	120.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2	4083	5MU	O2-C2-N1	-2.76	119.11	122.79
44	2	4872	2MG	N9-C4-N3	2.76	131.49	125.94
44	2	729	2MG	C5-C6-N1	2.76	120.20	113.19
44	2	3909	OMC	O2-C2-N3	-2.75	117.86	122.33
44	2	2364	OMG	C5-C4-N9	2.75	110.61	105.63
44	2	1625	OMG	C5-C6-N1	2.75	120.17	113.19
44	2	4597	UR3	C3U-N3-C2	2.74	122.12	117.31
44	2	2424	OMG	C5-C6-N1	2.74	120.15	113.19
44	2	4129	B8W	N2-C2-N1	-2.74	112.99	117.25
44	2	1316	OMG	C5-C4-N9	2.73	110.59	105.63
44	2	2773	OMG	C5-C6-N1	2.73	120.12	113.19
44	2	1860	B8H	O4-C4-N3	-2.72	114.90	120.12
44	2	1316	OMG	C5-C6-N1	2.70	120.06	113.19
44	2	4483	B8T	O2-C2-N3	-2.70	117.94	122.33
44	2	4483	B8T	O3'-C3'-C2'	2.70	120.55	111.82
44	2	2364	OMG	C5-C6-N1	2.69	120.03	113.19
44	2	2050	OMG	C5-C6-N1	2.69	120.03	113.19
44	2	2050	OMG	C5-C4-N9	2.69	110.52	105.63
44	2	4129	B8W	C4-C5-N7	-2.69	107.34	110.62
44	2	1605	7MG	C4-C5-N7	2.69	109.27	105.53
44	2	978	2MG	C5-C6-N1	2.69	120.02	113.19
44	2	2804	OMC	C1'-N1-C2	2.69	124.42	118.42
44	2	4671	B8T	C6-C5-C4	2.68	120.24	116.96
44	2	4371	MHG	N1-C2-N3	-2.68	119.81	123.95
44	2	373	OMG	C5-C6-N1	2.67	119.98	113.19
44	2	3880	P7G	N9-C8-N7	2.67	107.20	103.38
44	2	3897	B8K	O6-C6-N1	-2.66	115.02	120.12
44	2	4472	B8W	N2-C2-N1	-2.66	113.12	117.25
44	2	1456	B8Q	C1'-N1-C2	2.66	121.47	116.99
44	2	4623	OMG	C5-C6-N1	2.65	119.93	113.19
44	2	4220	6MZ	C5-C6-N1	2.65	121.03	118.20
44	2	1517	2MG	O6-C6-C5	-2.65	119.57	126.60
44	2	1797	E7G	C2-N1-C6	-2.65	120.28	125.10
44	2	4623	OMG	C5-C4-N9	2.64	110.42	105.63
44	2	4494	OMG	C5-C4-N9	2.64	110.41	105.63
44	2	4370	OMG	C5-C6-N1	2.63	119.88	113.19
44	2	373	OMG	C5-C4-N9	2.63	110.41	105.63
44	2	2754	B9B	C5-N7-C8	2.63	107.24	103.51
44	2	4370	OMG	C5-C4-N9	2.63	110.39	105.63
44	2	4472	B8W	C6-C5-N7	-2.62	130.15	133.63
44	2	2773	OMG	C5-C4-N9	2.62	110.39	105.63
44	2	1522	OMG	C5-C6-N1	2.62	119.84	113.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2	1625	OMG	O6-C6-C5	-2.61	119.67	126.60
44	2	4185	B8W	O6-C6-C5	-2.61	113.69	116.97
44	2	4296	B8H	O2-C2-N1	-2.61	119.93	122.87
44	2	4690	B8K	O6-C6-N1	-2.61	115.11	120.12
44	2	4296	B8H	O4-C4-N3	-2.61	115.11	120.12
44	2	4870	OMG	O6-C6-C5	-2.61	119.68	126.60
44	2	4472	B8W	C5-N7-C8	2.61	107.22	103.51
44	2	4637	OMG	O4'-C1'-N9	2.61	114.32	108.36
44	2	4335	5MC	C5-C6-N1	-2.60	120.66	123.34
44	2	729	2MG	N9-C8-N7	-2.59	108.52	113.39
44	2	1797	E7G	N9-C8-N7	2.58	107.07	103.38
44	2	4494	OMG	C5-C6-N1	2.58	119.75	113.19
44	2	4637	OMG	C5-C4-N9	2.57	110.30	105.63
44	2	2424	OMG	O6-C6-C5	-2.57	119.78	126.60
44	2	1517	2MG	N1-C2-N3	-2.57	119.98	123.95
44	2	2786	B9H	O3'-C3'-C4'	2.57	118.47	111.05
44	2	1456	B8Q	C31-N3-C2	2.57	121.52	117.79
44	2	2297	E7G	N9-C8-N7	2.56	107.03	103.38
44	2	4550	7MG	N9-C8-N7	2.55	107.02	103.38
44	2	4690	B8K	C2-N1-C6	-2.53	120.48	125.10
44	2	4415	1MA	N9-C4-N3	2.53	132.84	126.94
44	2	4872	2MG	O6-C6-C5	-2.53	119.89	126.60
44	2	4637	OMG	O6-C6-C5	-2.53	119.89	126.60
44	2	1625	OMG	C5-C4-N9	2.52	110.21	105.63
44	2	237	B9B	C2-N3-C4	2.52	120.86	113.89
44	2	4530	UR3	C6-N1-C2	-2.51	119.54	121.79
44	2	2786	B9H	C1'-N1-C6	2.50	126.30	120.84
44	2	2364	OMG	O6-C6-C5	-2.50	119.96	126.60
44	2	2773	OMG	O6-C6-C5	-2.50	119.96	126.60
44	2	1316	OMG	O4'-C1'-N9	2.50	114.07	108.36
44	2	4185	B8W	C2-N3-C4	2.48	120.75	113.89
44	2	373	OMG	O6-C6-C5	-2.48	120.02	126.60
44	2	1316	OMG	O6-C6-C5	-2.48	120.02	126.60
4	8	14	OMU	C1'-N1-C2	2.47	122.05	117.57
44	2	2050	OMG	O6-C6-C5	-2.47	120.05	126.60
44	2	4529	B8W	C5-N7-C8	2.47	107.02	103.51
44	2	729	2MG	O6-C6-C5	-2.46	120.07	126.60
44	2	4415	1MA	C1'-N9-C4	-2.46	119.19	126.50
44	2	4370	OMG	O6-C6-C5	-2.46	120.08	126.60
44	2	4494	OMG	O6-C6-C5	-2.46	120.09	126.60
44	2	4355	E6G	C2-N1-C6	2.45	119.82	115.93
44	2	4483	B8T	O3'-C3'-C4'	2.45	118.12	111.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2	2297	E7G	C2-N1-C6	-2.45	120.64	125.10
44	2	373	OMG	O4'-C1'-N9	2.43	113.92	108.36
44	2	4529	B8W	C2-N1-C6	2.43	119.79	115.93
44	2	4623	OMG	O6-C6-C5	-2.43	120.16	126.60
44	2	4529	B8W	C5-C6-N1	-2.42	120.09	123.46
44	2	2754	B9B	C2-N3-C4	2.42	120.59	113.89
44	2	3899	BGH	C2-N1-C6	-2.42	120.69	125.10
44	2	1524	A2M	C4'-O4'-C1'	-2.41	104.14	109.47
44	2	1605	7MG	C2-N1-C6	-2.41	120.70	125.10
44	2	1522	OMG	O6-C6-C5	-2.41	120.21	126.60
44	2	1883	OMG	C2'-C1'-N9	-2.40	109.56	114.22
44	2	4129	B8W	C2-N3-C4	2.40	120.53	113.89
44	2	1574	B9B	C2-N3-C4	2.40	120.52	113.89
44	2	3869	OMC	C6-N1-C2	-2.39	116.34	120.49
44	2	4623	OMG	O4'-C1'-N9	2.39	113.82	108.36
44	2	978	2MG	N1-C2-N3	-2.38	120.26	123.95
44	2	1574	B9B	C61-O6-C6	-2.38	112.93	117.47
44	2	1866	UR3	O2'-C2'-C1'	2.38	117.99	110.02
44	2	2364	OMG	O4'-C1'-N9	2.38	113.80	108.36
44	2	4623	OMG	N2-C2-N1	2.37	121.76	116.71
44	2	4355	E6G	C5-C6-N1	-2.37	120.17	123.46
44	2	237	B9B	C61-O6-C6	-2.36	112.97	117.47
44	2	4185	B8W	C6-C5-N7	-2.36	130.50	133.63
44	2	4083	5MU	O4-C4-N3	-2.36	115.60	120.12
44	2	373	OMG	N2-C2-N1	2.35	121.72	116.71
44	2	2380	B8W	C1'-N9-C8	2.35	132.44	127.14
44	2	978	2MG	O6-C6-C5	-2.35	120.38	126.60
44	2	2424	OMG	C5-C4-N9	2.34	109.88	105.63
44	2	3897	B8K	C2-N1-C6	-2.34	120.84	125.10
44	2	2050	OMG	O4'-C1'-N9	2.34	113.70	108.36
44	2	2380	B8W	C2-N1-C6	2.34	119.64	115.93
44	2	4355	E6G	C2-N3-C4	2.33	120.33	113.89
44	2	4870	OMG	N9-C4-N3	2.33	130.62	125.94
44	2	1883	OMG	C5-C4-N9	2.32	109.83	105.63
44	2	4371	MHG	N9-C8-N7	2.31	106.68	103.38
44	2	237	B9B	C4-N9-C8	2.31	108.23	105.73
44	2	4494	OMG	O4'-C1'-N9	2.31	113.64	108.36
44	2	4564	M7A	C5-C4-N3	-2.31	121.21	126.62
44	2	4472	B8W	C2-N3-C4	2.31	120.26	113.89
44	2	373	OMG	C2'-C1'-N9	-2.30	109.76	114.22
44	2	1574	B9B	C4-N9-C8	2.30	108.22	105.73
44	2	373	OMG	N9-C8-N7	-2.30	109.07	113.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2	1316	OMG	C4-C5-N7	-2.29	107.09	110.72
44	2	4415	1MA	C8-N7-C5	2.29	108.38	104.24
44	2	3899	BGH	N1-C2-N3	-2.29	119.06	123.32
44	2	4690	B8K	N1-C2-N3	-2.29	119.06	123.32
44	2	4623	OMG	C4-C5-N7	-2.28	107.11	110.72
44	2	3897	B8K	N1-C2-N3	-2.28	119.07	123.32
44	2	3880	P7G	C71-N7-C5	2.27	129.90	124.52
44	2	4335	5MC	CM5-C5-C6	-2.27	119.82	122.85
44	2	4529	B8W	O6-C6-C5	-2.27	114.12	116.97
44	2	4371	MHG	O6-C6-C5	-2.27	121.98	127.54
44	2	2424	OMG	O4'-C1'-N9	2.27	113.54	108.36
44	2	729	2MG	N1-C2-N3	-2.26	120.46	123.95
44	2	2786	B9H	O2-C2-N3	-2.25	119.22	122.07
44	2	4550	7MG	C6-C5-C4	-2.25	117.98	122.62
44	2	1883	OMG	O4'-C1'-N9	2.25	113.50	108.36
44	2	1517	2MG	N9-C8-N7	-2.25	109.16	113.39
44	2	2754	B9B	C61-O6-C6	-2.25	113.19	117.47
44	2	1522	OMG	C4-C5-N7	-2.24	107.17	110.72
44	2	373	OMG	C4-C5-N7	-2.24	107.17	110.72
44	2	1797	E7G	N9-C4-N3	2.23	128.81	125.47
44	2	4370	OMG	O4'-C1'-N9	2.23	113.47	108.36
44	2	2380	B8W	C2-N3-C4	2.23	120.06	113.89
44	2	4536	OMC	O2-C2-N1	2.23	123.50	118.89
44	2	2786	B9H	O2-C2-N1	-2.22	117.51	122.72
44	2	2522	7MG	C2-N1-C6	-2.22	121.05	125.10
44	2	4529	B8W	C2-N3-C4	2.21	120.00	113.89
44	2	1522	OMG	O4'-C1'-N9	2.21	113.41	108.36
44	2	1316	OMG	N2-C2-N1	2.21	121.42	116.71
44	2	1625	OMG	O4'-C1'-N9	2.21	113.41	108.36
44	2	4523	A2M	C2'-C1'-N9	-2.20	109.83	113.53
44	2	4623	OMG	N9-C8-N7	-2.20	109.25	113.39
44	2	4870	OMG	C5-C4-N9	2.20	109.62	105.63
44	2	2297	E7G	O6-C6-C5	-2.18	122.20	127.54
44	2	4472	B8W	C4-N9-C1'	-2.18	121.41	126.59
44	2	3909	OMC	C4-N3-C2	2.17	123.77	120.25
44	2	4536	OMC	C1'-N1-C2	2.17	123.27	118.42
44	2	1522	OMG	N2-C2-N1	2.17	121.34	116.71
44	2	2297	E7G	C6-C5-C4	-2.16	118.16	122.62
44	2	3899	BGH	O4'-C1'-N9	2.16	112.24	109.30
44	2	4185	B8W	C2-N1-C6	2.16	119.36	115.93
44	2	1797	E7G	O6-C6-C5	-2.15	122.26	127.54
44	2	4550	7MG	N1-C2-N3	-2.15	119.31	123.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2	4370	OMG	C4-C5-N7	-2.15	107.32	110.72
44	2	2380	B8W	C5-C6-N1	-2.14	120.48	123.46
44	2	4637	OMG	C4-C5-N7	-2.13	107.34	110.72
44	2	4370	OMG	N2-C2-N1	2.13	121.24	116.71
44	2	2364	OMG	C4-C5-N7	-2.12	107.36	110.72
44	2	4870	OMG	N9-C8-N7	-2.12	109.39	113.39
44	2	4371	MHG	C71-N7-C5	2.12	129.54	124.52
44	2	4564	M7A	C71-N7-C5	-2.12	115.88	124.01
44	2	4355	E6G	C4-N9-C8	2.11	108.01	105.73
44	2	4872	2MG	C8-N7-C5	2.11	108.05	104.24
44	2	1625	OMG	N9-C4-N3	2.10	130.16	125.94
44	2	1326	A2M	C4-N9-C1'	2.10	131.60	126.59
44	2	2861	OMC	O2-C2-N1	2.10	123.23	118.89
44	2	2050	OMG	C4-C5-N7	-2.10	107.40	110.72
44	2	1605	7MG	C6-C5-C4	-2.10	118.30	122.62
44	2	4472	B8W	C5-C6-N1	-2.10	120.55	123.46
44	2	4185	B8W	C5-C6-N1	-2.09	120.55	123.46
44	2	1866	UR3	C6-N1-C2	-2.09	119.91	121.79
44	2	978	2MG	C8-N7-C5	2.09	108.03	104.24
44	2	2773	OMG	C4-C5-N7	-2.09	107.42	110.72
44	2	978	2MG	CM2-N2-C2	-2.09	119.26	123.86
44	2	729	2MG	C8-N7-C5	2.07	108.00	104.24
44	2	1883	OMG	N9-C4-N3	2.07	130.10	125.94
44	2	2297	E7G	N1-C2-N3	-2.06	119.47	123.32
44	2	3887	OMC	O2-C2-N3	-2.06	118.98	122.33
44	2	1316	OMG	N9-C8-N7	-2.06	109.51	113.39
44	2	4597	UR3	O2-C2-N3	-2.05	118.45	121.34
44	2	2364	OMG	N2-C2-N1	2.05	121.07	116.71
44	2	4872	2MG	C1'-N9-C4	-2.05	120.42	126.50
44	2	1605	7MG	O6-C6-C5	-2.05	122.52	127.54
44	2	2522	7MG	C6-C5-C4	-2.05	118.40	122.62
44	2	4371	MHG	C6-C5-C4	-2.04	118.42	122.62
44	2	4472	B8W	C2-N1-C6	2.04	119.16	115.93
44	2	729	2MG	CM2-N2-C2	-2.03	119.38	123.86
44	2	2773	OMG	N2-C2-N1	2.03	121.03	116.71
44	2	3909	OMC	C5-C4-N3	-2.02	117.89	121.33
44	2	2773	OMG	C2'-C1'-N9	-2.02	110.31	114.22
44	2	2522	7MG	O6-C6-C5	-2.01	122.60	127.54
44	2	3909	OMC	O2-C2-N1	2.01	123.05	118.89
44	2	4529	B8W	C6-C5-N7	-2.01	130.96	133.63
44	2	237	B9B	C1'-N9-C8	-2.01	122.60	127.14
44	2	3880	P7G	N3-C2-N1	-2.01	119.58	123.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2	2754	B9B	C4-N9-C8	2.00	107.90	105.73
44	2	2363	A2M	C4-N9-C1'	2.00	131.37	126.59

There are no chirality outliers.

All (101) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	8	14	OMU	C1'-C2'-O2'-CM2
44	2	237	B9B	C5-C6-O6-C61
44	2	237	B9B	N1-C6-O6-C61
44	2	237	B9B	C3'-C4'-C5'-O5'
44	2	237	B9B	O4'-C4'-C5'-O5'
44	2	237	B9B	C62-C61-O6-C6
44	2	398	A2M	O4'-C4'-C5'-O5'
44	2	1348	P4U	N3-C4-O4-C41
44	2	1574	B9B	C5-C6-O6-C61
44	2	1574	B9B	N1-C6-O6-C61
44	2	1625	OMG	C3'-C4'-C5'-O5'
44	2	1797	E7G	O4'-C4'-C5'-O5'
44	2	1883	OMG	C3'-C4'-C5'-O5'
44	2	2364	OMG	O4'-C4'-C5'-O5'
44	2	2380	B8W	C5-C6-O6-C61
44	2	2424	OMG	C3'-C4'-C5'-O5'
44	2	2754	B9B	C5-C6-O6-C61
44	2	2754	B9B	N1-C6-O6-C61
44	2	3867	A2M	O4'-C4'-C5'-O5'
44	2	3867	A2M	C3'-C4'-C5'-O5'
44	2	3869	OMC	O4'-C1'-N1-C2
44	2	3869	OMC	O4'-C1'-N1-C6
44	2	3880	P7G	O4'-C4'-C5'-O5'
44	2	3897	B8K	O4'-C4'-C5'-O5'
44	2	4129	B8W	C5-C6-O6-C61
44	2	4129	B8W	N1-C6-O6-C61
44	2	4185	B8W	C5-C6-O6-C61
44	2	4220	6MZ	N1-C6-N6-C9
44	2	4355	E6G	C5-C6-O6-C61
44	2	4355	E6G	N1-C6-O6-C61
44	2	4472	B8W	C5-C6-O6-C61
44	2	4472	B8W	N1-C6-O6-C61
44	2	4637	OMG	C1'-C2'-O2'-CM2
44	2	4870	OMG	O4'-C4'-C5'-O5'
44	2	4870	OMG	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
44	2	398	A2M	C3'-C4'-C5'-O5'
44	2	1326	A2M	C3'-C4'-C5'-O5'
44	2	1883	OMG	O4'-C4'-C5'-O5'
44	2	2364	OMG	C3'-C4'-C5'-O5'
44	2	2424	OMG	O4'-C4'-C5'-O5'
44	2	3880	P7G	C3'-C4'-C5'-O5'
44	2	3897	B8K	C3'-C4'-C5'-O5'
44	2	4637	OMG	O4'-C4'-C5'-O5'
44	2	4872	2MG	O4'-C4'-C5'-O5'
44	2	2380	B8W	N1-C6-O6-C61
44	2	3880	P7G	N7-C71-C72-C73
44	2	729	2MG	O4'-C4'-C5'-O5'
44	2	1326	A2M	O4'-C4'-C5'-O5'
44	2	1625	OMG	O4'-C4'-C5'-O5'
44	2	1797	E7G	C3'-C4'-C5'-O5'
44	2	1866	UR3	O4'-C4'-C5'-O5'
44	2	1909	P7G	O4'-C4'-C5'-O5'
44	2	3723	A2M	O4'-C4'-C5'-O5'
44	2	4415	1MA	O4'-C4'-C5'-O5'
44	2	4872	2MG	C3'-C4'-C5'-O5'
44	2	4185	B8W	N1-C6-O6-C61
44	2	3869	OMC	C2'-C1'-N1-C6
44	2	1866	UR3	C3'-C4'-C5'-O5'
44	2	4415	1MA	C3'-C4'-C5'-O5'
44	2	1909	P7G	C3'-C4'-C5'-O5'
44	2	4523	A2M	O4'-C4'-C5'-O5'
44	2	4637	OMG	C3'-C4'-C5'-O5'
44	2	1574	B9B	C62-C61-O6-C6
44	2	3701	OMC	C2'-C1'-N1-C6
44	2	4523	A2M	C3'-C4'-C5'-O5'
44	2	4371	MHG	C2'-C1'-N9-C8
44	2	4296	B8H	O4'-C4'-C5'-O5'
44	2	4523	A2M	C3'-C2'-O2'-CM'
44	2	1860	B8H	O4'-C4'-C5'-O5'
44	2	729	2MG	C3'-C4'-C5'-O5'
44	2	4296	B8H	C3'-C4'-C5'-O5'
44	2	3869	OMC	C2'-C1'-N1-C2
44	2	4370	OMG	C3'-C2'-O2'-CM2
44	2	1326	A2M	C4'-C5'-O5'-P
44	2	1625	OMG	C4'-C5'-O5'-P
44	2	4870	OMG	C4'-C5'-O5'-P
44	2	3880	P7G	C72-C71-N7-C8

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Mol	Chain	Res	Type	Atoms
44	2	3897	B8K	C4'-C5'-O5'-P
44	2	3701	OMC	O4'-C1'-N1-C6
44	2	3701	OMC	C2'-C1'-N1-C2
44	2	373	OMG	C4'-C5'-O5'-P
44	2	3887	OMC	C4'-C5'-O5'-P
44	2	1534	A2M	O4'-C4'-C5'-O5'
44	2	2297	E7G	C72-C71-N7-C8
44	2	4371	MHG	O4'-C4'-C5'-O5'
44	2	3701	OMC	O4'-C1'-N1-C2
44	2	1909	P7G	C72-C71-N7-C8
44	2	2401	A2M	C3'-C2'-O2'-CM'
44	2	3909	OMC	O4'-C4'-C5'-O5'
44	2	3899	BGH	O4'-C4'-C5'-O5'
44	2	4371	MHG	O4'-C1'-N9-C8
44	2	1524	A2M	O4'-C1'-N9-C8
44	2	3723	A2M	C3'-C4'-C5'-O5'
44	2	4623	OMG	C1'-C2'-O2'-CM2
44	2	1524	A2M	C3'-C2'-O2'-CM'
44	2	1866	UR3	C4'-C5'-O5'-P
44	2	4415	1MA	C4'-C5'-O5'-P
44	2	1860	B8H	C3'-C4'-C5'-O5'
44	2	1659	I4U	C42-C41-O4-C4
44	2	1659	I4U	C43-C41-O4-C4
44	2	4523	A2M	C4'-C5'-O5'-P

There are no ring outliers.

17 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
44	2	729	2MG	1	0
44	2	4623	OMG	1	0
44	2	4872	2MG	2	0
44	2	4571	A2M	1	0
44	2	4620	OMU	2	0
44	2	4296	B8H	1	0
44	2	1860	B8H	1	0
44	2	1574	B9B	2	0
44	2	1316	OMG	1	0
44	2	1871	A2M	1	0
44	2	4637	OMG	1	0
44	2	2522	7MG	1	0
44	2	3723	A2M	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
44	2	2363	A2M	1	0
44	2	3718	A2M	1	0
44	2	2050	OMG	1	0
44	2	4083	5MU	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 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	$\# Z > 2$
55	GDP	A	801	56,57	28,30,30	1.27	3 (10%)	44,47,47	1.91	9 (20%)

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
55	GDP	A	801	56,57	-	2/16/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	A	801	GDP	C6-N1	-3.31	1.32	1.38
55	A	801	GDP	C5-N7	-2.51	1.34	1.39
55	A	801	GDP	C5-C4	2.34	1.45	1.38

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	A	801	GDP	C5-C4-N3	-6.17	118.45	128.46
55	A	801	GDP	C2-N3-C4	4.98	121.17	112.30
55	A	801	GDP	N9-C4-N3	4.62	135.22	125.94
55	A	801	GDP	PA-O3A-PB	-3.52	120.74	132.83
55	A	801	GDP	C6-C5-N7	3.09	136.00	130.25
55	A	801	GDP	C4-C5-N7	-2.54	106.70	110.72
55	A	801	GDP	O3B-PB-O2B	2.35	116.63	107.64
55	A	801	GDP	C3'-C2'-C1'	2.35	105.89	101.43
55	A	801	GDP	O6-C6-C5	-2.14	120.91	126.60

There are no chirality outliers.

All (2) torsion outliers are listed below:

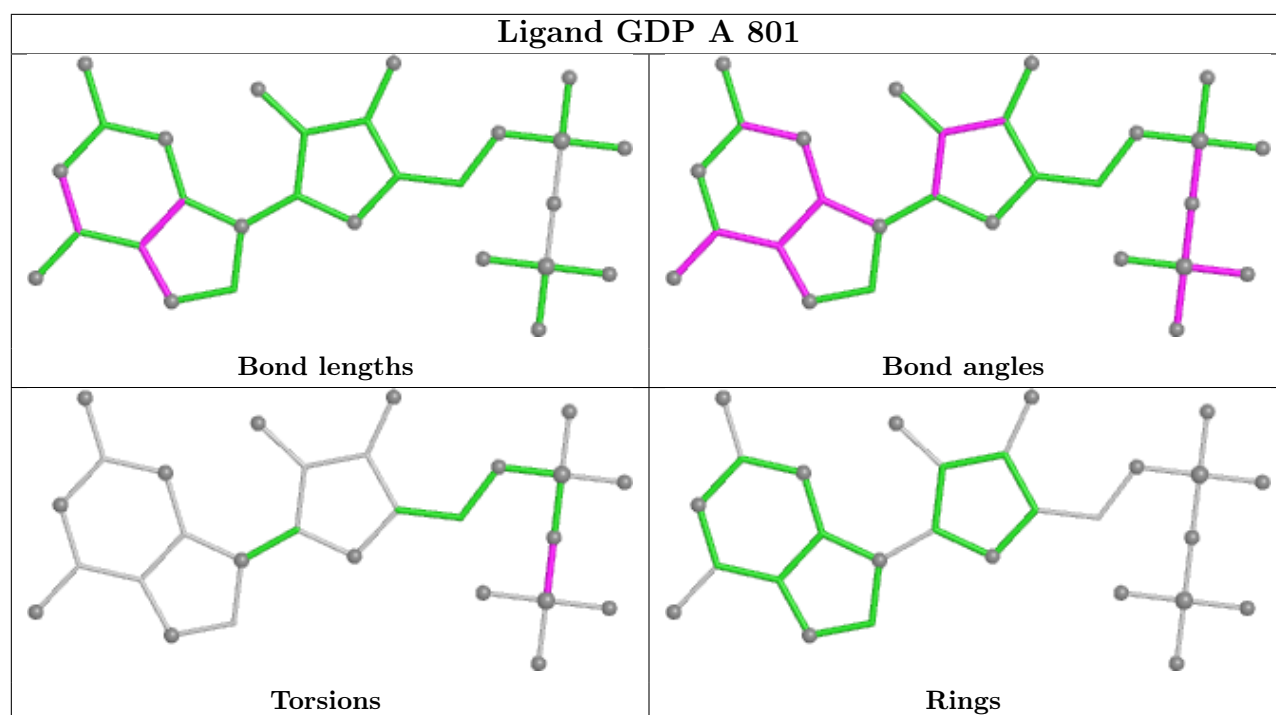
Mol	Chain	Res	Type	Atoms
55	A	801	GDP	PA-O3A-PB-O2B
55	A	801	GDP	PA-O3A-PB-O1B

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
55	A	801	GDP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

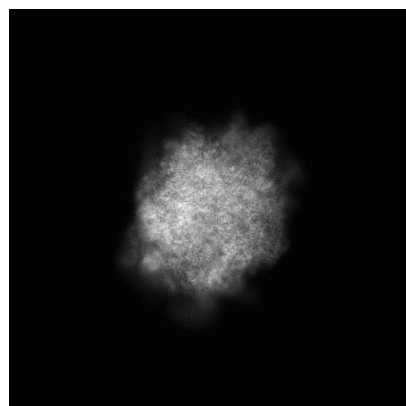
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35371. These allow visual inspection of the internal detail of the map and identification of artifacts.

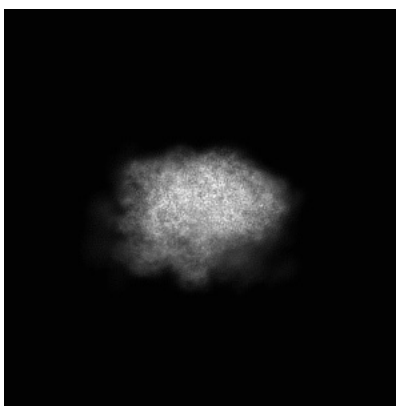
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

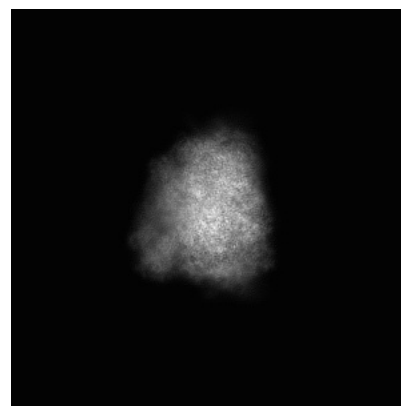
6.1.1 Primary map



X

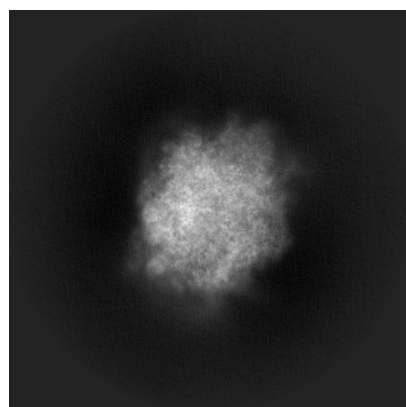


Y

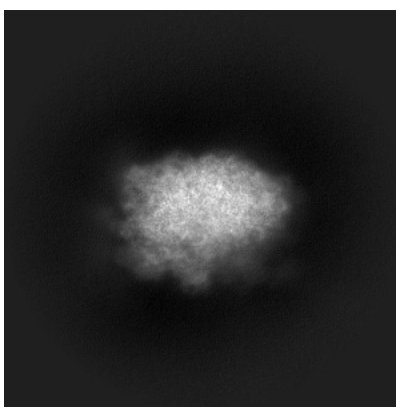


Z

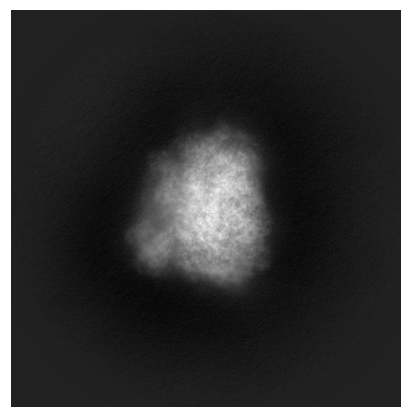
6.1.2 Raw map



X



Y

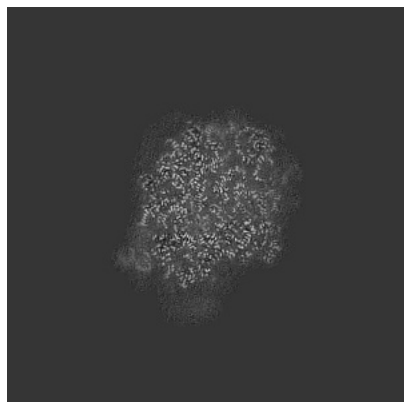


Z

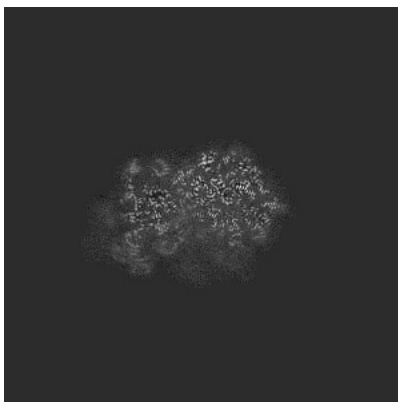
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

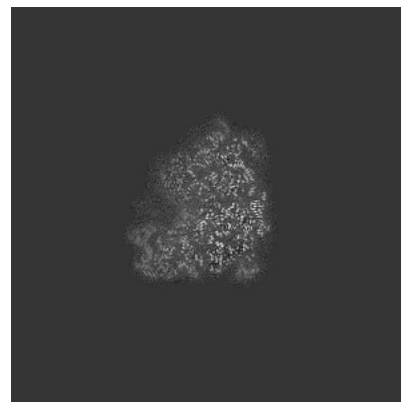
6.2.1 Primary map



X Index: 200

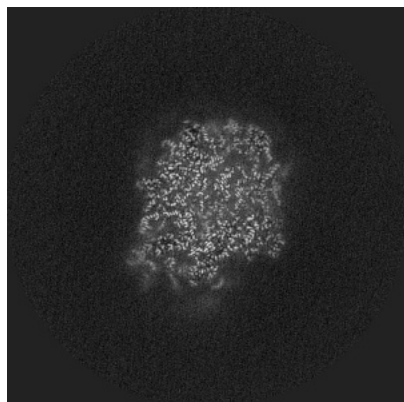


Y Index: 200

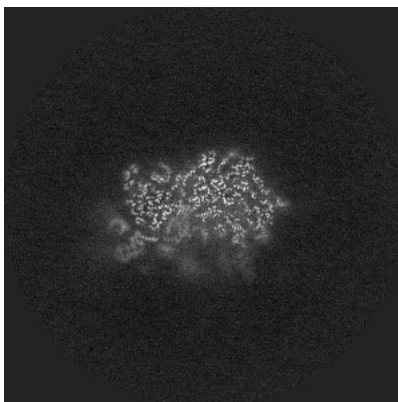


Z Index: 200

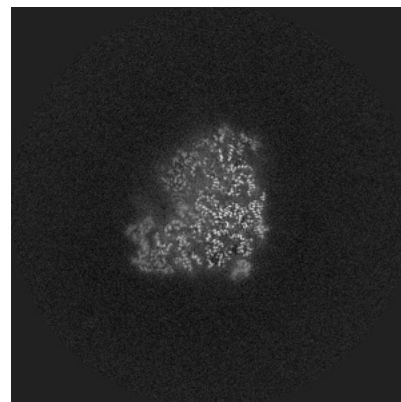
6.2.2 Raw map



X Index: 200



Y Index: 200

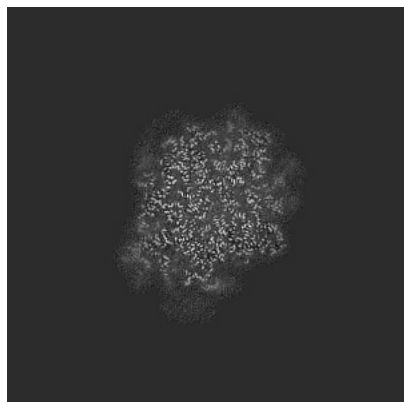


Z Index: 200

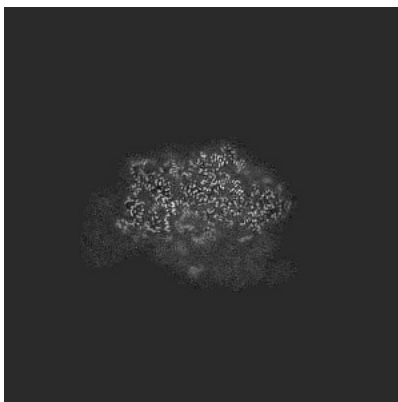
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

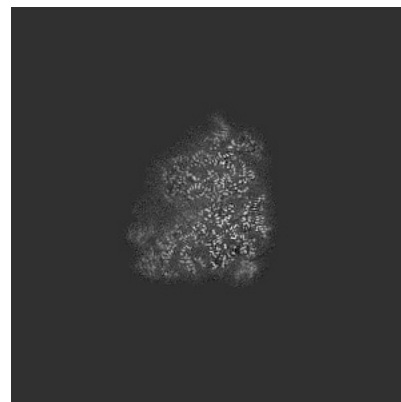
6.3.1 Primary map



X Index: 206

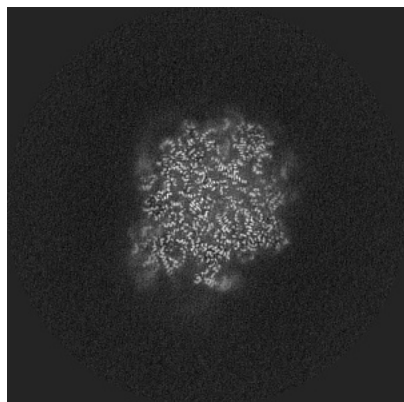


Y Index: 182

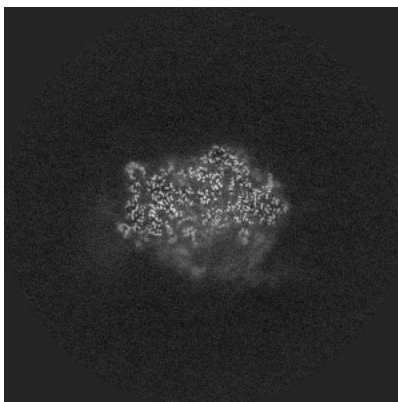


Z Index: 202

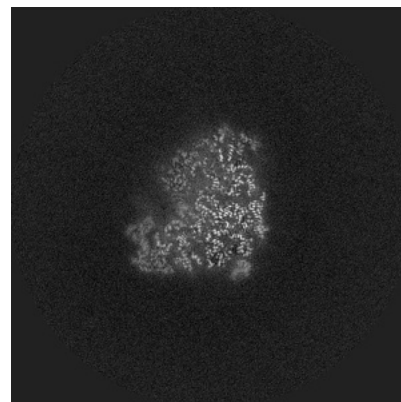
6.3.2 Raw map



X Index: 205



Y Index: 189

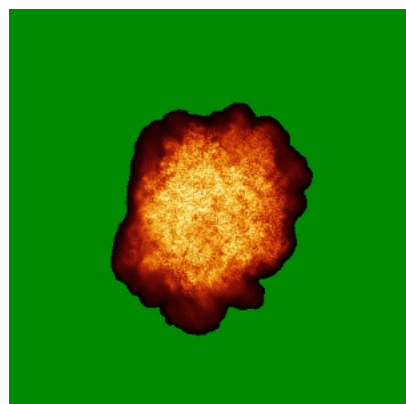


Z Index: 200

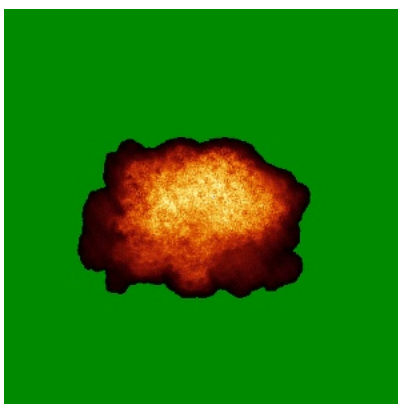
The images above show the largest variance slices of the map in three orthogonal directions.

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

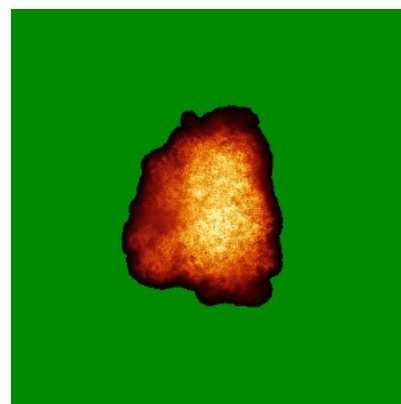
6.4.1 Primary map



X

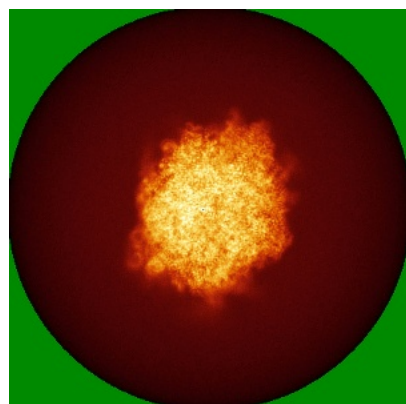


Y

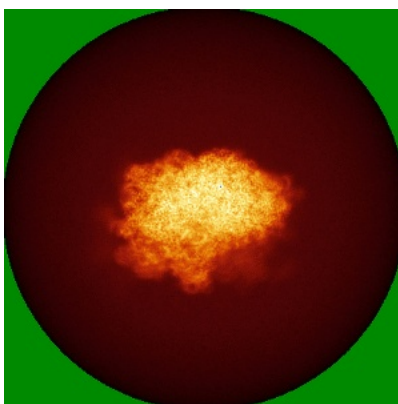


Z

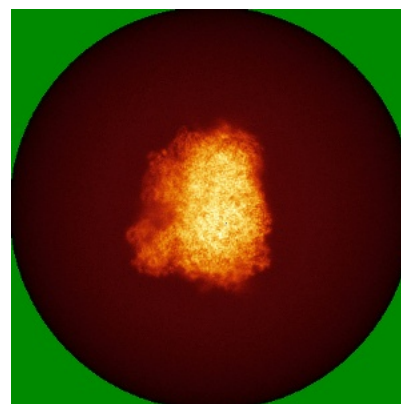
6.4.2 Raw map



X



Y

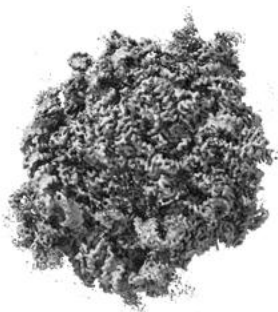


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



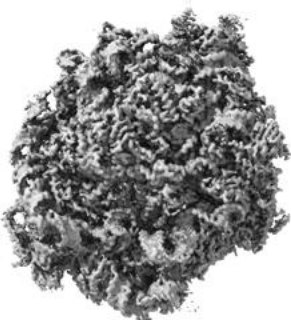
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0365. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

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

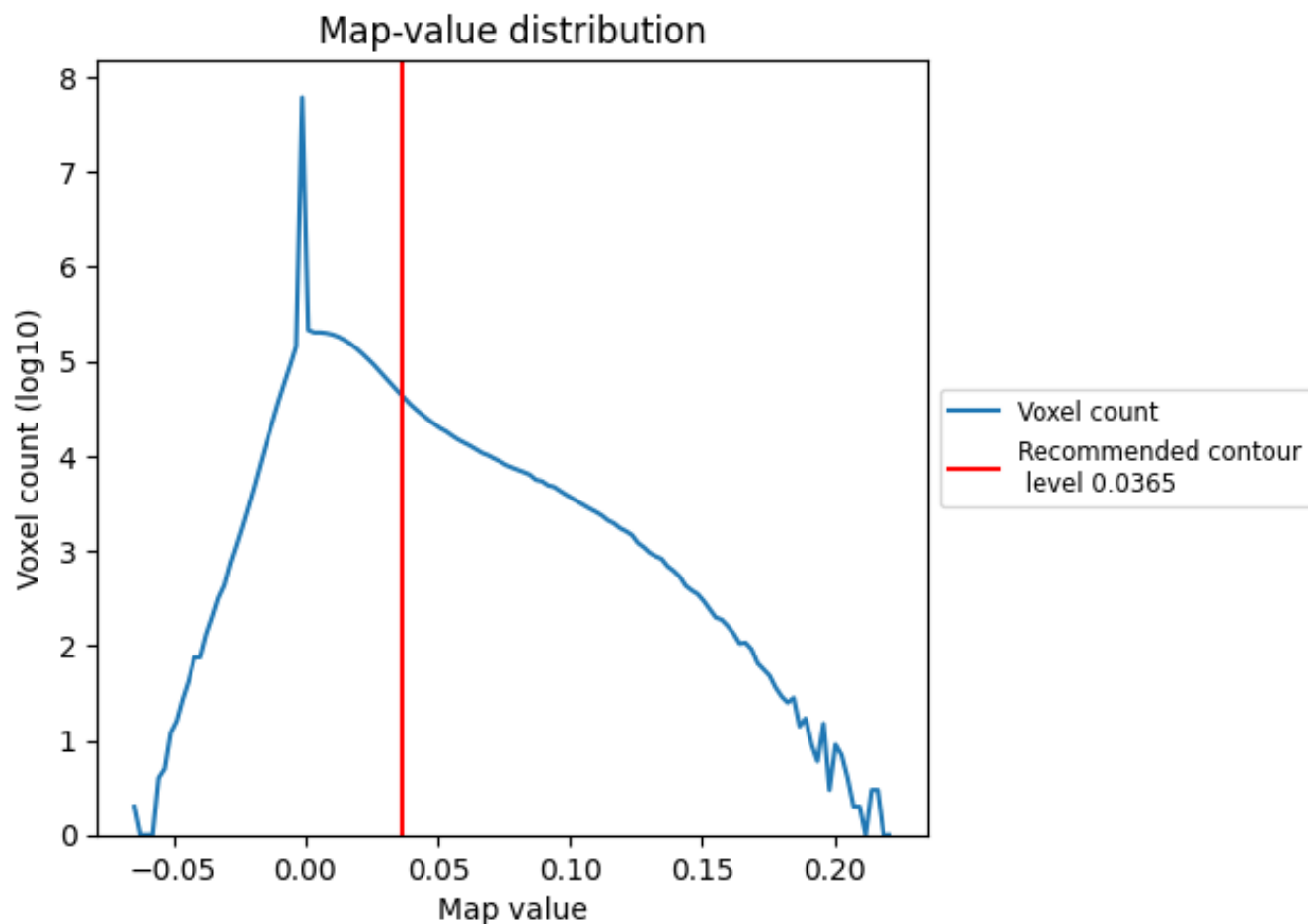
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

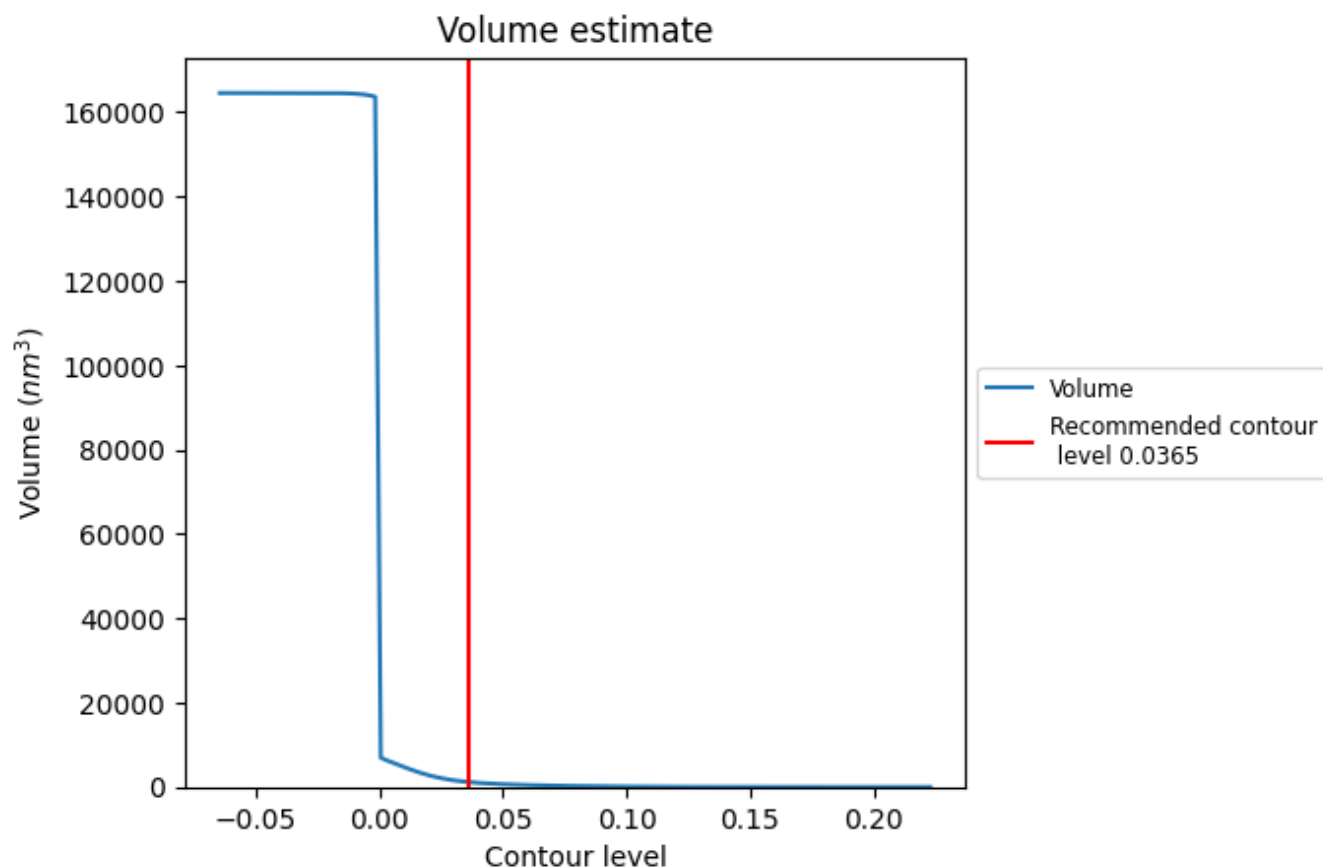
This section contains the results of statistical analysis of the map.

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.

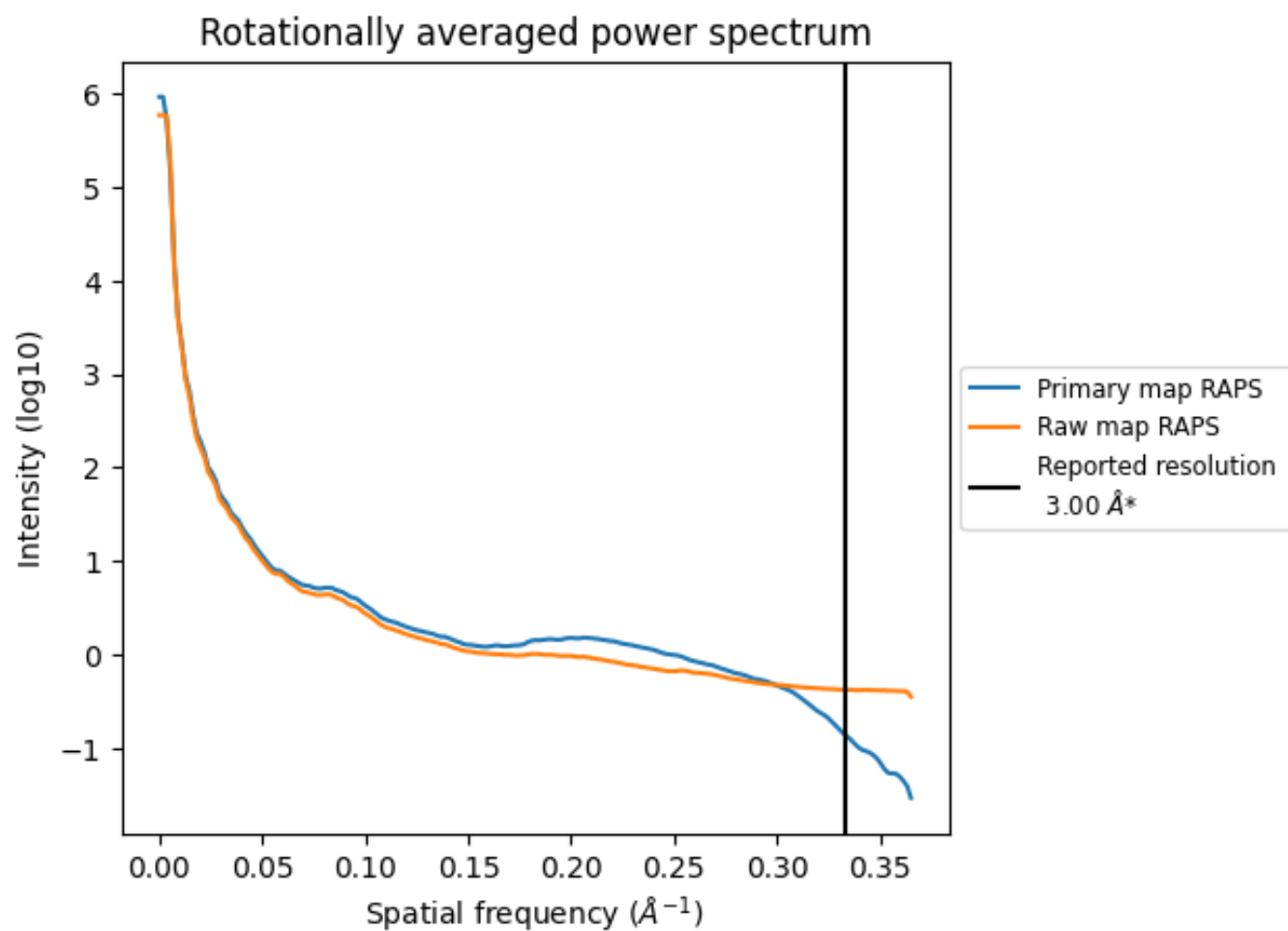
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1145 nm³; this corresponds to an approximate mass of 1034 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 ⓘ

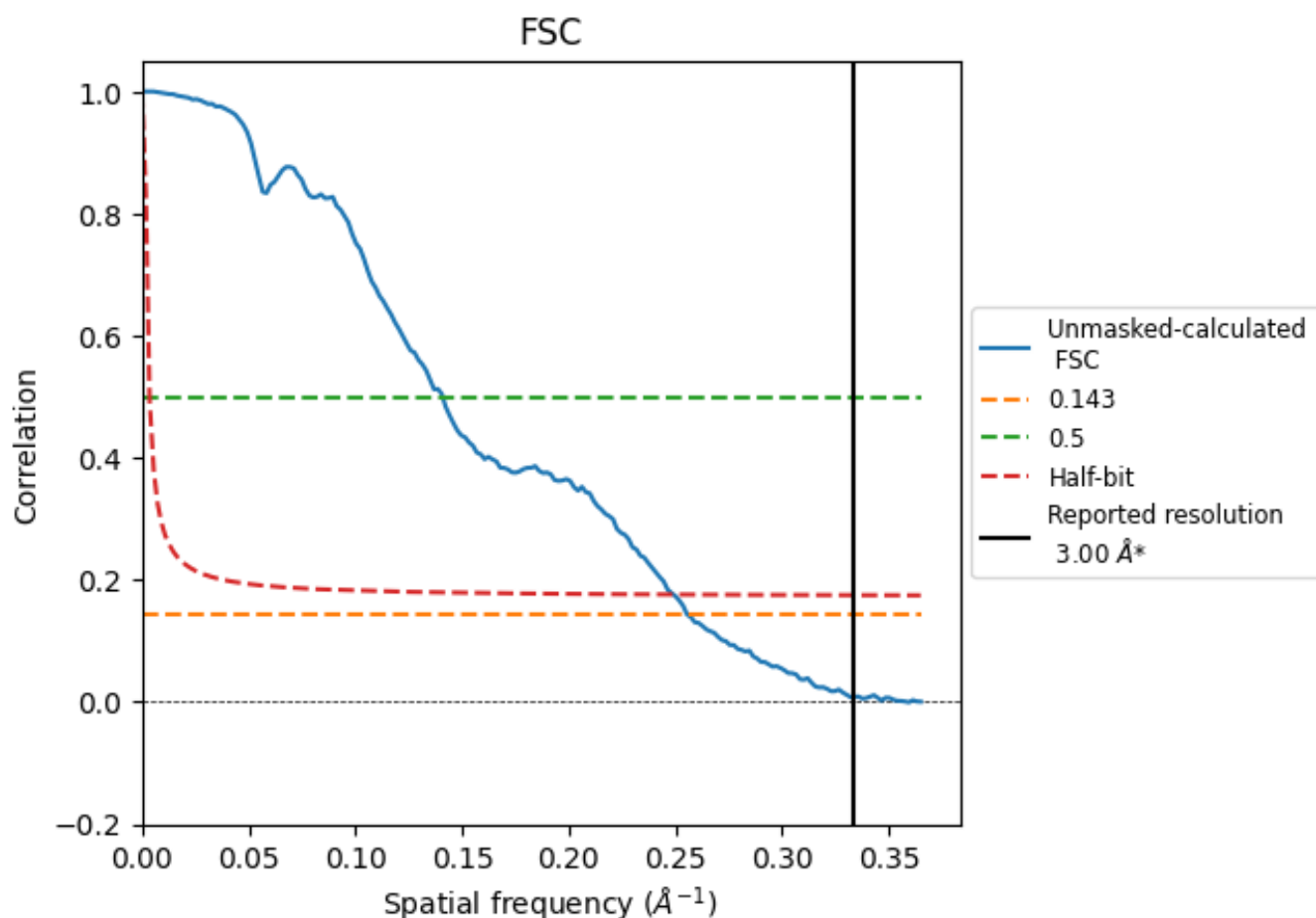


*Reported resolution corresponds to spatial frequency of 0.333 $\text{\AA}^{-1}$

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](#)

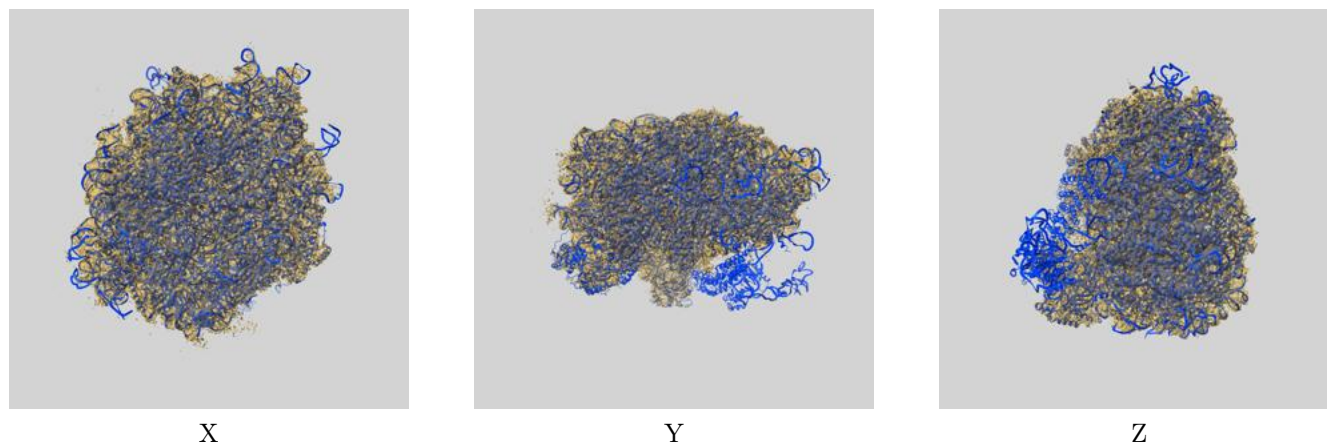
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.91	7.10	4.01

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

9 Map-model fit [i](#)

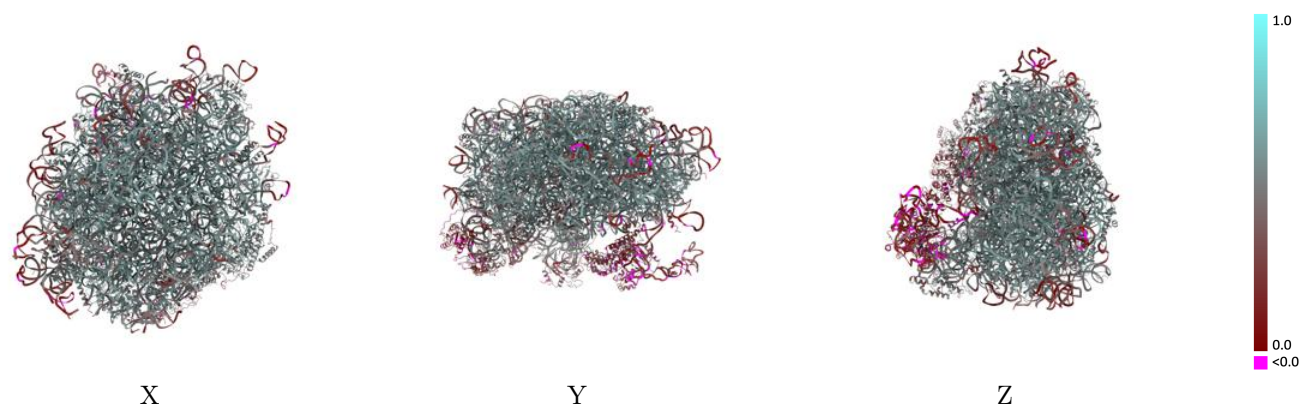
This section contains information regarding the fit between EMDB map EMD-35371 and PDB model 8IDY. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



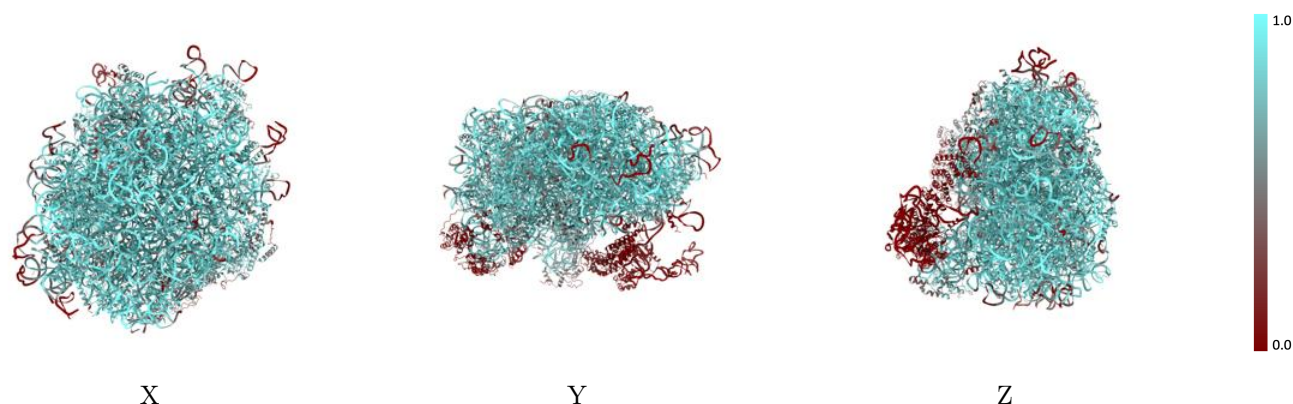
The images above show the 3D surface view of the map at the recommended contour level 0.0365 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



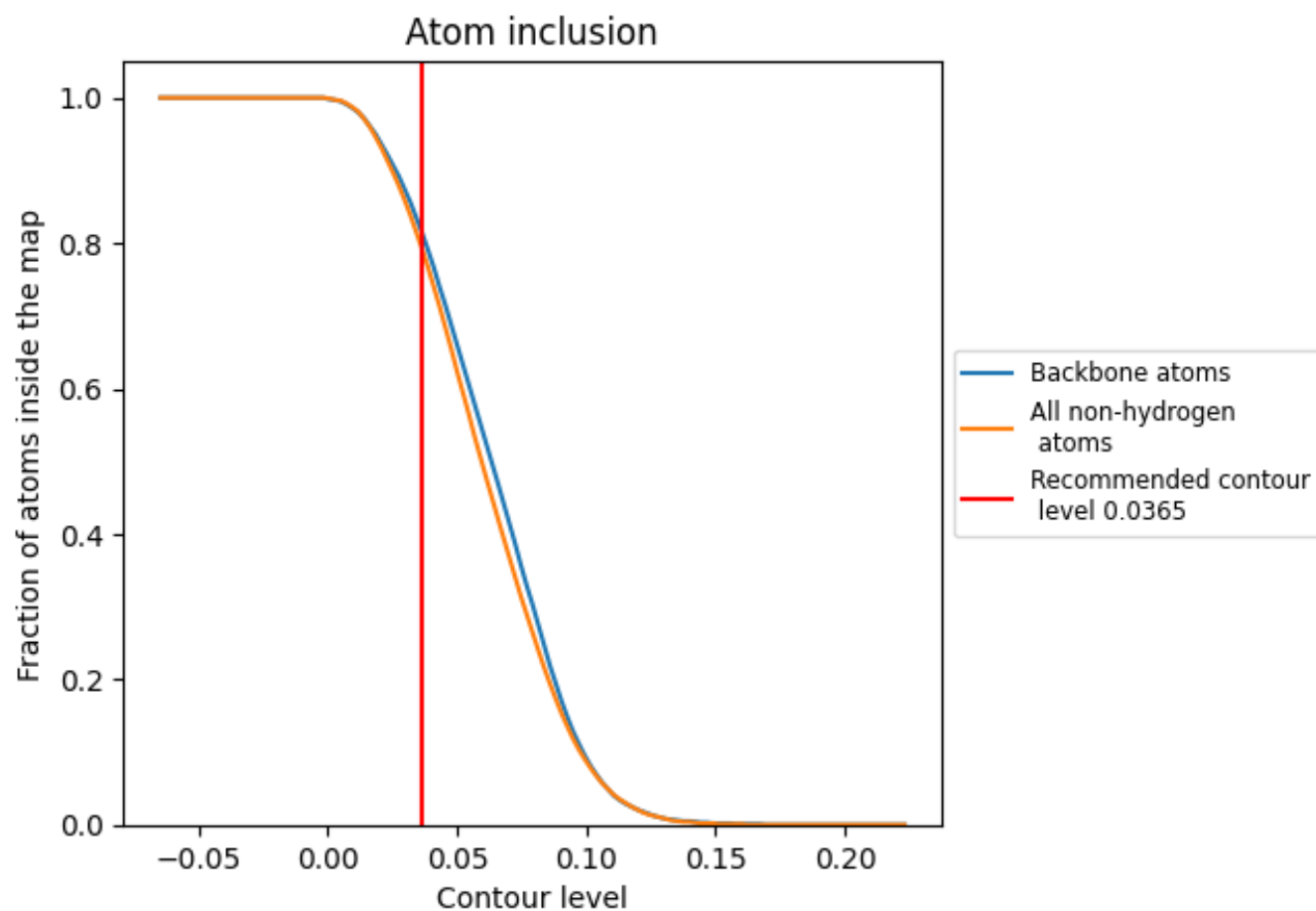
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0365).

9.4 Atom inclusion ⓘ



At the recommended contour level, 82% of all backbone atoms, 79% 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 (0.0365) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7920	 0.4860
2	 0.8620	 0.4910
4	 0.6540	 0.4620
5	 0.9190	 0.4800
6	 0.7350	 0.5080
7	 0.8090	 0.5400
8	 0.9440	 0.5440
9	 0.5540	 0.4670
A	 0.6590	 0.4950
B	 0.9060	 0.5680
C	 0.7520	 0.4750
D	 0.9290	 0.5640
E	 0.6830	 0.5060
F	 0.8820	 0.5540
G	 0.7040	 0.4800
H	 0.8700	 0.5420
I	 0.8030	 0.5240
J	 0.1120	 0.1850
K	 0.8360	 0.5280
L	 0.9320	 0.5790
M	 0.9660	 0.5810
N	 0.4190	 0.3070
O	 0.6770	 0.4920
P	 0.9760	 0.5780
Q	 0.8420	 0.5250
R	 0.4700	 0.4450
S	 0.8970	 0.5510
T	 0.6060	 0.4370
U	 0.9680	 0.5860
V	 0.9220	 0.5660
W	 0.7290	 0.5170
X	 0.8050	 0.5360
Y	 0.8660	 0.5560
Z	 0.9480	 0.5890
a	 0.8740	 0.5430



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Chain	Atom inclusion	Q-score
b	 0.9330	 0.5780
c	 0.8790	 0.5320
d	 0.7520	 0.5180
e	 0.8800	 0.5480
g	 0.8960	 0.5580
h	 0.8860	 0.5570
i	 0.7600	 0.5220
j	 0.8340	 0.5350
k	 0.9400	 0.5790
l	 0.9250	 0.5640
m	 0.9030	 0.5600
n	 0.9530	 0.5870
o	 0.7650	 0.4980
p	 0.9150	 0.5590
r	 0.6190	 0.4250
t	 0.0010	 0.1380
u	 0.0710	 0.2110
v	 0.0860	 0.2300
y	 0.1120	 0.2100
z	 0.5670	 0.4230