



Full wwPDB EM Validation Report ⓘ

Jun 21, 2026 – 05:11 am BST

PDB ID : 7O7Z / pdb_00007o7z
EMDB ID : EMD-12757
Title : Rabbit 80S ribosome stalled close to the mutated SARS-CoV-2 slippery site
by a pseudoknot (classified for pseudoknot)
Authors : Bhatt, P.R.; Scaiola, A.; Leibundgut, M.A.; Atkins, J.F.; Ban, N.
Deposited on : 2021-04-14
Resolution : 2.40 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:

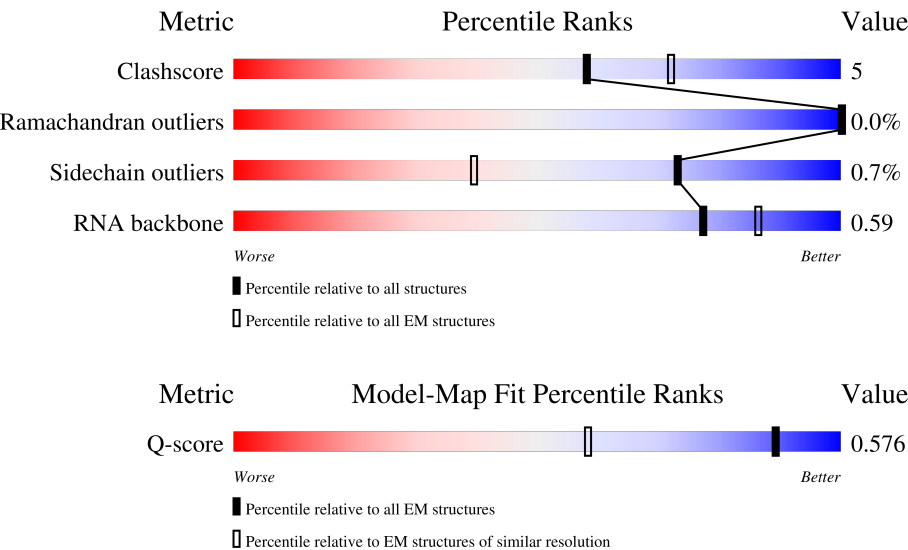
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.40 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	5628 (1.90 - 2.90)

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	A2	1870	
2	AA	84	
3	AB	69	

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Mol	Chain	Length	Quality of chain
4	AC	156	
5	AD	133	
6	AE	115	
7	AF	317	
8	AG	56	
9	AH	220	
10	AI	76	
11	AT	76	
12	AZ	295	
13	Aa	264	
14	Ab	293	
15	Ac	281	
16	Ad	263	
17	Ae	204	
18	Af	249	
19	Ag	432	
20	Ah	208	
21	Ai	194	
22	Aj	165	
23	Ak	158	
24	Al	132	
25	Am	151	
26	An	151	
27	Ao	145	
28	Ap	172	























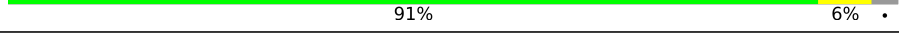


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Mol	Chain	Length	Quality of chain
29	Aq	135	
30	Ar	152	
31	As	145	
32	At	119	
33	Au	83	
34	Av	130	
35	Aw	143	
36	Ax	130	
37	Ay	124	
38	Az	25	
39	B5	4808	
40	B7	120	
41	B8	158	
42	BA	257	
43	BB	403	
44	BC	413	
45	BD	297	
46	BE	291	
47	BF	247	
48	BG	266	
49	BH	192	
50	BI	214	
51	BJ	178	
52	BK	1071	
53	BL	211	

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Mol	Chain	Length	Quality of chain
54	BM	218	
55	BN	204	
56	BO	203	
57	BP	184	
58	BQ	188	
59	BR	196	
60	BS	176	
61	BT	160	
62	BU	128	
63	BV	140	
64	BW	157	
65	BX	156	
66	BY	145	
67	BZ	136	
68	Ba	148	
69	Bb	245	
70	Bc	115	
71	Bd	125	
72	Be	135	
73	Bf	110	
74	Bg	117	
75	Bh	123	
76	Bi	105	
77	Bj	97	
78	Bk	70	

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Mol	Chain	Length	Quality of chain
79	Bl	51	
80	Bm	128	
81	Bo	106	
82	Bp	92	
83	Br	137	
84	Bs	318	
85	Bt	165	
86	Bv	217	

2 Entry composition

There are 92 unique types of molecules in this entry. The entry contains 229742 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 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A2	1770	Total	C	N	O	P	0	0
			37833	16911	6781	12371	1770		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A2	1249	B8N	C	conflict	GB GBCT01000564.1
A2	1338	4AC	C	conflict	GB GBCT01000564.1
A2	1843	4AC	C	conflict	GB GBCT01000564.1

- Molecule 2 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AA	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 3 is a protein called Ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AB	63	Total	C	N	O	S	0	0
			495	302	98	93	2		

- Molecule 4 is a protein called Ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AC	74	Total	C	N	O	S	0	0
			610	385	117	101	7		

- Molecule 5 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AD	57	Total	C	N	O	S	0	0
			457	282	101	73	1		

- Molecule 6 is a protein called Ribosomal protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AE	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

- Molecule 7 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AF	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 8 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AG	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 9 is a RNA chain called mRNA containing SARS-CoV-2 sequence.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AH	95	Total	C	N	O	P	0	0
			2018	901	349	673	95		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AH	3466	U	A	conflict	GB NC_045512.2
AH	3468	A	C	conflict	GB NC_045512.2

- Molecule 10 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AI	76	Total	C	N	O	P	0	0
			939	393	11	459	76		

- Molecule 11 is a RNA chain called P-site Phe-tRNA(Phe).

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AT	76	Total	C	N	O	P	0	0
			1652	746	294	536	76		

- Molecule 12 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AZ	221	Total	C	N	O	S	0	0
			1743	1107	305	323	8		

- Molecule 13 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Aa	224	Total	C	N	O	S	0	0
			1815	1152	328	321	14		

- Molecule 14 is a protein called Ribosomal protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Ab	220	Total	C	N	O	S	0	0
			1706	1105	292	300	9		

- Molecule 15 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Ac	225	Total	C	N	O	S	0	0
			1751	1116	315	313	7		

- Molecule 16 is a protein called Ribosomal protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Ad	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 17 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Ae	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 18 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Af	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 19 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Ag	190	Total	C	N	O	S	0	0
			1529	975	281	272	1		

- Molecule 20 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Ah	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ah	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 21 is a protein called Ribosomal protein S9 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Ai	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 22 is a protein called eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Aj	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 23 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Ak	154	Total	C	N	O	S	0	0
			1262	804	236	216	6		

- Molecule 24 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Al	124	Total	C	N	O	S	0	0
			958	600	170	179	9		

- Molecule 25 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Am	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 26 is a protein called 40S ribosomal protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	An	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 27 is a protein called 40S ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Ao	128	Total	C	N	O	S	0	0
			1048	665	197	179	7		

- Molecule 28 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Ap	141	Total	C	N	O	S	0	0
			1124	715	212	194	3		

- Molecule 29 is a protein called 40S ribosomal protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Aq	134	Total	C	N	O	S	0	0
			1080	678	201	197	4		

- Molecule 30 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ar	148	Total	C	N	O	S	0	0
			1217	763	245	208	1		

- Molecule 31 is a protein called Ribosomal protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	As	143	Total	C	N	O	S	0	0
			1113	698	214	198	3		

- Molecule 32 is a protein called 40S ribosomal protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	At	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 33 is a protein called Ribosomal protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Au	83	Total	C	N	O	S	0	0
			640	394	117	124	5		

- Molecule 34 is a protein called Ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Av	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 35 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Aw	141	Total	C	N	O	S	0	0
			1099	693	219	184	3		

- Molecule 36 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Ax	125	Total	C	N	O	S	0	0
			1015	642	199	169	5		

- Molecule 37 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ay	85	Total	C	N	O	S	0	0
			683	439	128	115	1		

- Molecule 38 is a protein called 60s ribosomal protein l41.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Az	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 39 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	B5	3764	Total	C	N	O	P	0	0
			80772	36003	14762	26243	3764		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B5	3550	UY1	U	conflict	GB GBCN01009604.1

- Molecule 40 is a RNA chain called 5S.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	B7	120	Total	C	N	O	P	0	0
			2570	1141	456	851	122		

- Molecule 41 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	B8	156	Total	C	N	O	P	0	0
			3319	1481	585	1097	156		

- Molecule 42 is a protein called Ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BA	253	Total	C	N	O	S	0	0
			1940	1214	396	324	6		

- Molecule 43 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BB	398	Total	C	N	O	S	0	0
			3206	2042	605	546	13		

- Molecule 44 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BC	362	Total	C	N	O	S	0	0
			2886	1814	577	481	14		

- Molecule 45 is a protein called Ribosomal_L18_c domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BD	294	Total	C	N	O	S	0	0
			2398	1516	439	429	14		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BD	2	AAC	GLY	conflict	UNP G1SYJ6

- Molecule 46 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BE	243	Total	C	N	O	S	0	0
			1960	1258	378	321	3		

- Molecule 47 is a protein called Ribosomal Protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BF	226	Total	C	N	O	S	0	0
			1886	1211	362	304	9		

- Molecule 48 is a protein called Ribosomal protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BG	233	Total	C	N	O	S	0	0
			1877	1197	361	315	4		

- Molecule 49 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BH	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 50 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BI	213	Total	C	N	O	S	0	0
			1717	1086	332	285	14		

- Molecule 51 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BJ	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 52 is a protein called Replicase polyprotein 1ab.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BK	35	Total	C	N	O	S	0	0
			265	163	45	51	6		

- Molecule 53 is a protein called Ribosomal protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BL	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

- Molecule 54 is a protein called Ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BM	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 55 is a protein called Ribosomal protein L15.

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

- Molecule 56 is a protein called Ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BO	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 57 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BP	159	Total	C	N	O	S	0	0
			1289	809	249	222	9		

- Molecule 58 is a protein called Ribosomal Protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	BQ	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

- Molecule 59 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	BR	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 60 is a protein called Ribosomal protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	BS	176	Total	C	N	O	S	0	0
			1457	924	288	234	11		

- Molecule 61 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	BT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 62 is a protein called Ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	BU	99	Total	C	N	O	S	0	0
			806	516	141	147	2		

- Molecule 63 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	BV	139	Total	C	N	O	S	0	0
			1034	648	199	182	5		

- Molecule 64 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	BW	121	Total	C	N	O	S	0	0
			991	619	202	166	4		

- Molecule 65 is a protein called uL23.

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

- Molecule 66 is a protein called Ribosomal protein L26.

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

- Molecule 67 is a protein called 60S ribosomal protein L27.

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

- Molecule 68 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Ba	147	Total	C	N	O	S	0	0
			1163	734	239	186	4		

- Molecule 69 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Bb	108	Total	C	N	O	S	0	0
			881	548	196	134	3		

- Molecule 70 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Bc	108	Total	C	N	O	S	0	0
			836	530	148	151	7		

- Molecule 71 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Bd	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 72 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Be	130	Total	C	N	O	S	0	0
			1070	676	221	168	5		

- Molecule 73 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Bf	110	Total	C	N	O	S	0	0
			884	560	175	144	5		

- Molecule 74 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Bg	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 75 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Bh	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 76 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Bi	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 77 is a protein called Ribosomal protein L37.

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

- Molecule 78 is a protein called eL38.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Bk	24	LYS	ASN	conflict	UNP G1U001

- Molecule 79 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Bl	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 80 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Bm	52	Total	C	N	O	S	0	0
			432	269	90	67	6		

- Molecule 81 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Bo	105	Total	C	N	O	S	0	0
			863	543	175	139	6		

- Molecule 82 is a protein called eL43.

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

- Molecule 83 is a protein called Ribosomal protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Br	126	Total	C	N	O	S	0	0
			1014	629	209	170	6		

- Molecule 84 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Bs	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

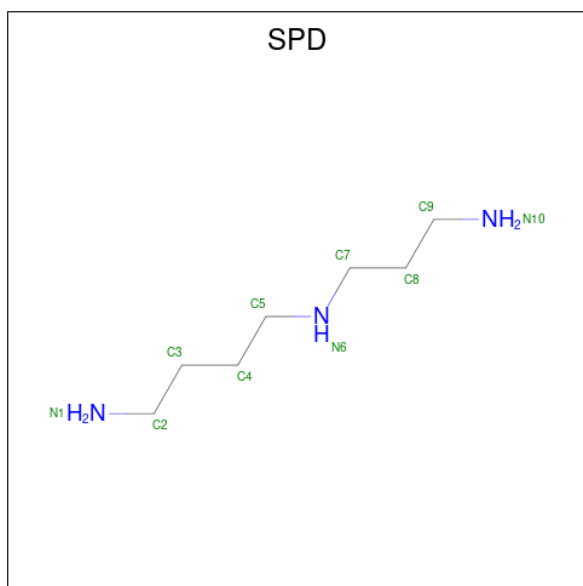
- Molecule 85 is a protein called Ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	Bt	156	Total	C	N	O	S	0	0
			1178	733	221	220	4		

- Molecule 86 is a protein called Ribosomal protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	Bv	212	Total	C	N	O	S	0	0
			1707	1092	308	299	8		

- Molecule 87 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃).



Mol	Chain	Residues	Atoms			AltConf
87	A2	1	Total	C	N	0
			10	7	3	
87	A2	1	Total	C	N	0
			10	7	3	
87	A2	1	Total	C	N	0
			10	7	3	
87	A2	1	Total	C	N	0
			10	7	3	
87	A2	1	Total	C	N	0
			10	7	3	
87	A2	1	Total	C	N	0
			10	7	3	
87	A2	1	Total	C	N	0
			10	7	3	

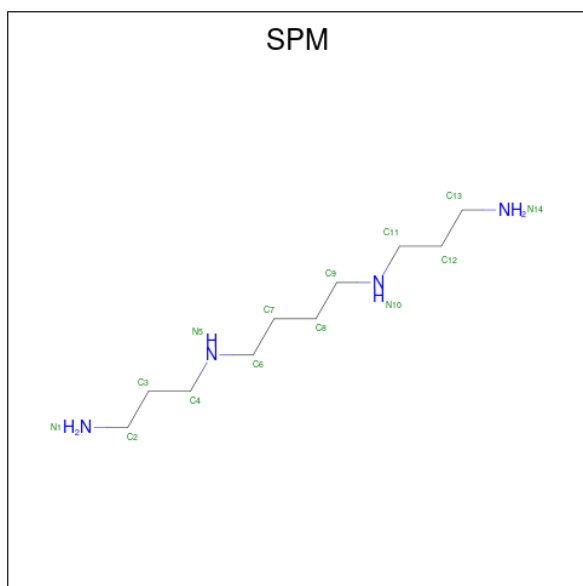
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Mol	Chain	Residues	Atoms			AltConf
87	B5	1	Total	C	N	0
			10	7	3	

- Molecule 88 is SPERMINE (CCD ID: SPM) (formula: $C_{10}H_{26}N_4$).



Mol	Chain	Residues	Atoms			AltConf
88	A2	1	Total	C	N	0
			14	10	4	
88	B5	1	Total	C	N	0
			14	10	4	
88	B5	1	Total	C	N	0
			14	10	4	

- Molecule 89 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
89	A2	109	Total	Mg	0
			109	109	
89	AH	1	Total	Mg	0
			1	1	
89	AT	3	Total	Mg	0
			3	3	
89	Af	1	Total	Mg	0
			1	1	
89	B5	284	Total	Mg	0
			284	284	

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Mol	Chain	Residues	Atoms		AltConf
89	B7	9	Total 9	Mg 9	0
89	B8	9	Total 9	Mg 9	0
89	BP	1	Total 1	Mg 1	0
89	BR	1	Total 1	Mg 1	0
89	BV	1	Total 1	Mg 1	0
89	Ba	1	Total 1	Mg 1	0

- Molecule 90 is UNKNOWN LIGAND (CCD ID: UNX) (formula: X).

Mol	Chain	Residues	Atoms		AltConf
90	A2	60	Total 60	X 60	0
90	AT	4	Total 4	X 4	0
90	Ae	1	Total 1	X 1	0
90	An	1	Total 1	X 1	0
90	Ar	1	Total 1	X 1	0
90	As	1	Total 1	X 1	0
90	B5	225	Total 225	X 225	0
90	B7	6	Total 6	X 6	0
90	B8	8	Total 8	X 8	0
90	BA	3	Total 3	X 3	0
90	BB	4	Total 4	X 4	0
90	BC	1	Total 1	X 1	0
90	BH	1	Total 1	X 1	0

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Mol	Chain	Residues	Atoms		AltConf
90	BI	1	Total 1	X 1	0
90	BL	1	Total 1	X 1	0
90	BN	1	Total 1	X 1	0
90	BQ	2	Total 2	X 2	0
90	BT	2	Total 2	X 2	0
90	Bb	1	Total 1	X 1	0
90	Be	1	Total 1	X 1	0
90	Bf	1	Total 1	X 1	0
90	Bg	1	Total 1	X 1	0
90	Bl	1	Total 1	X 1	0
90	Bo	1	Total 1	X 1	0

- Molecule 91 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
91	AC	1	Total 1	Zn 1	0
91	AE	1	Total 1	Zn 1	0
91	AG	1	Total 1	Zn 1	0
91	Bg	1	Total 1	Zn 1	0
91	Bj	1	Total 1	Zn 1	0
91	Bm	1	Total 1	Zn 1	0
91	Bo	1	Total 1	Zn 1	0
91	Bp	1	Total 1	Zn 1	0

- Molecule 92 is water.

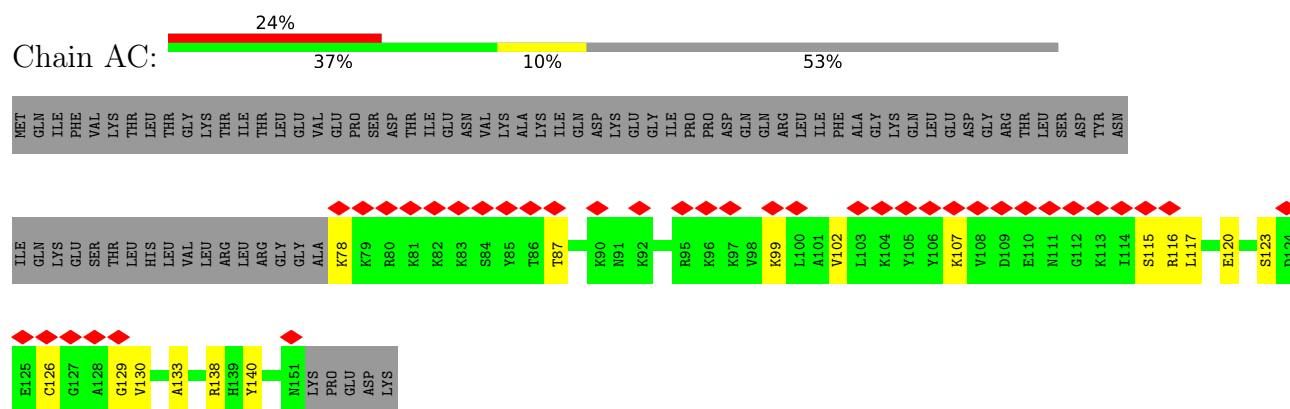
Mol	Chain	Residues	Atoms		AltConf
92	A2	526	Total 526	O 526	0
92	AH	9	Total 9	O 9	0
92	AI	1	Total 1	O 1	0
92	AT	12	Total 12	O 12	0
92	Aa	1	Total 1	O 1	0
92	Ac	1	Total 1	O 1	0
92	Af	3	Total 3	O 3	0
92	Ak	1	Total 1	O 1	0
92	Am	1	Total 1	O 1	0
92	An	2	Total 2	O 2	0
92	Ap	3	Total 3	O 3	0
92	As	2	Total 2	O 2	0
92	At	1	Total 1	O 1	0
92	Aw	3	Total 3	O 3	0
92	B5	1391	Total 1391	O 1391	0
92	B7	45	Total 45	O 45	0
92	B8	50	Total 50	O 50	0
92	BA	10	Total 10	O 10	0
92	BB	5	Total 5	O 5	0
92	BC	7	Total 7	O 7	0
92	BD	1	Total 1	O 1	0

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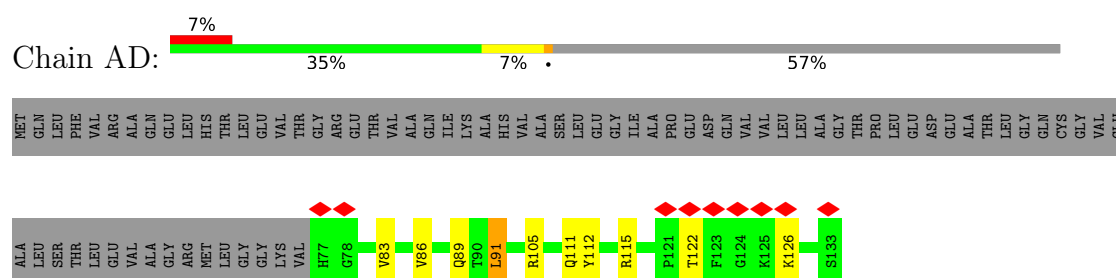
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Mol	Chain	Residues	Atoms		AltConf
92	BF	1	Total 1	O 1	0
92	BH	1	Total 1	O 1	0
92	BI	4	Total 4	O 4	0
92	BL	3	Total 3	O 3	0
92	BN	3	Total 3	O 3	0
92	BO	1	Total 1	O 1	0
92	BP	2	Total 2	O 2	0
92	BR	5	Total 5	O 5	0
92	BV	2	Total 2	O 2	0
92	BX	2	Total 2	O 2	0
92	Ba	6	Total 6	O 6	0
92	Bd	1	Total 1	O 1	0
92	Be	4	Total 4	O 4	0
92	Bg	2	Total 2	O 2	0
92	Bj	3	Total 3	O 3	0
92	Bl	1	Total 1	O 1	0
92	Bo	1	Total 1	O 1	0

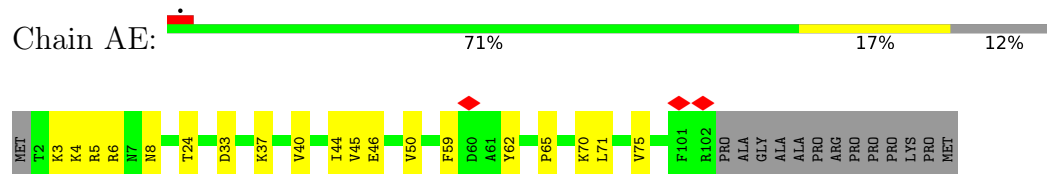
- Molecule 4: Ribosomal protein S27a



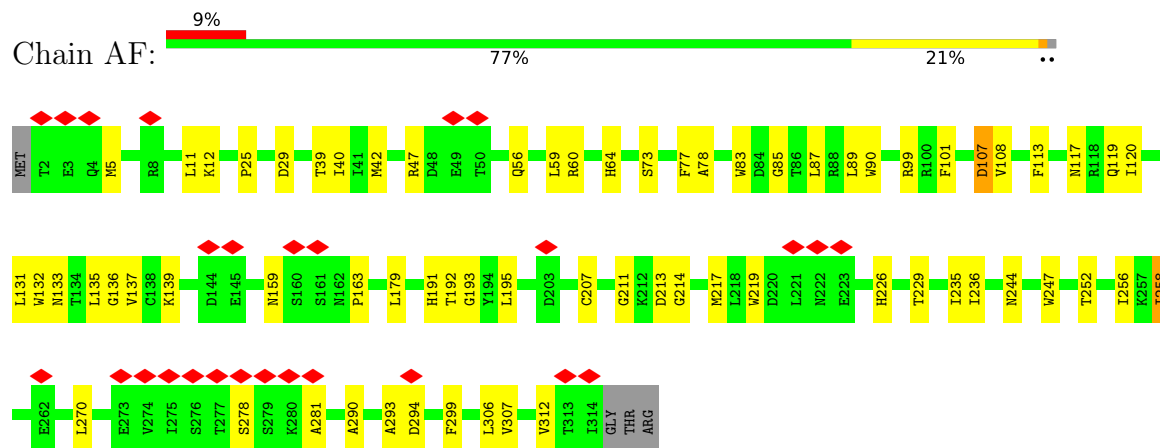
- Molecule 5: 40S ribosomal protein S30



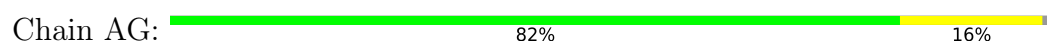
- Molecule 6: Ribosomal protein eS26

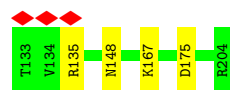


- Molecule 7: RACK1

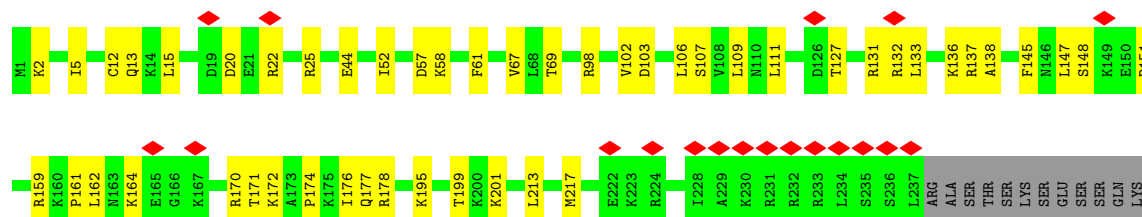
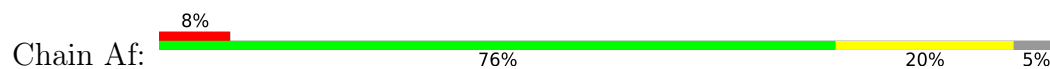


- Molecule 8: uS14

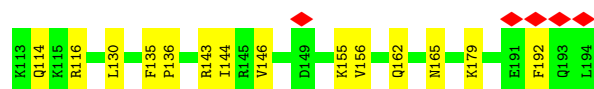
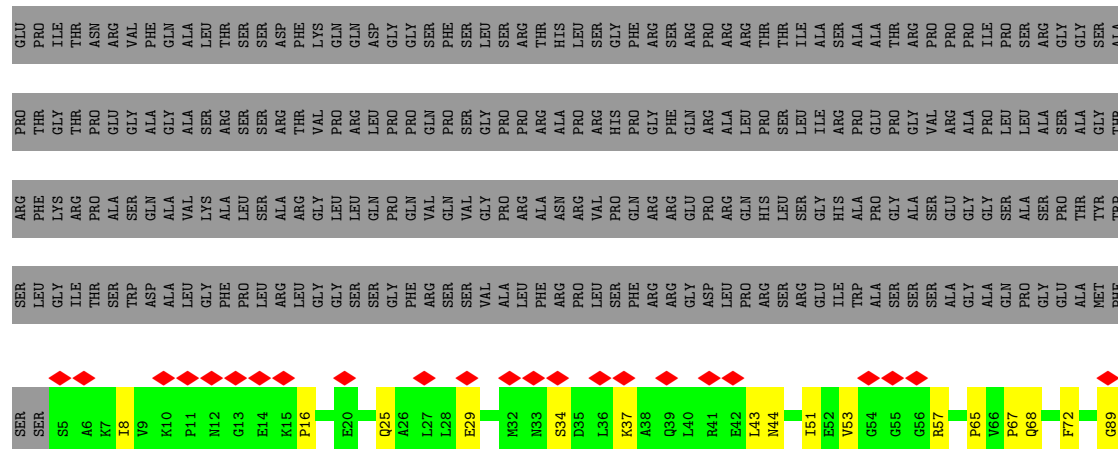
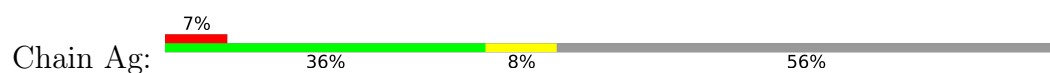




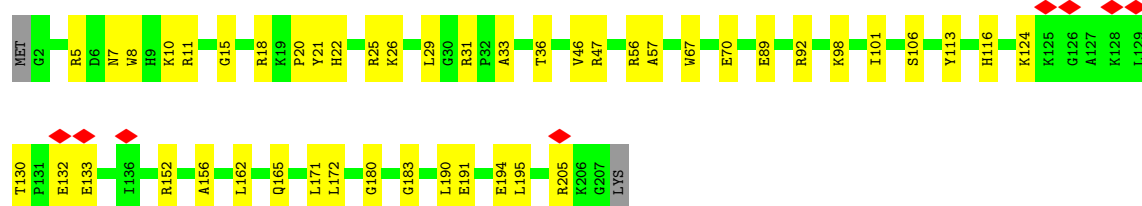
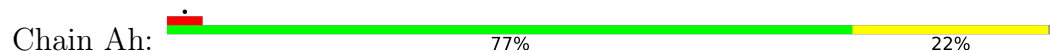
• Molecule 18: 40S ribosomal protein S6



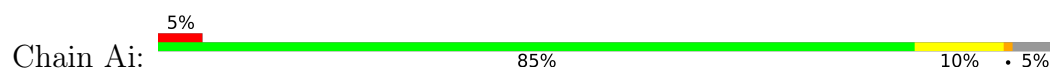
• Molecule 19: 40S ribosomal protein S7



• Molecule 20: 40S ribosomal protein S8

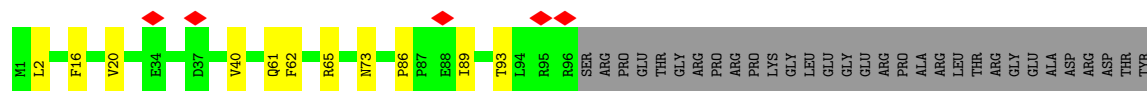


• Molecule 21: Ribosomal protein S9 (Predicted)

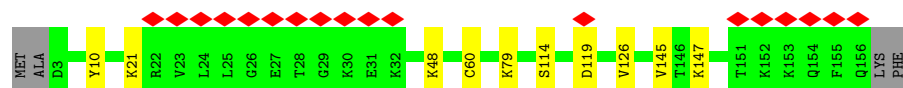
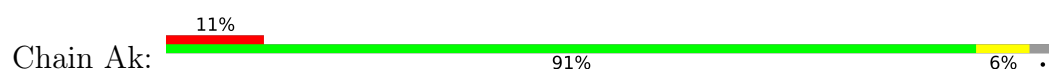




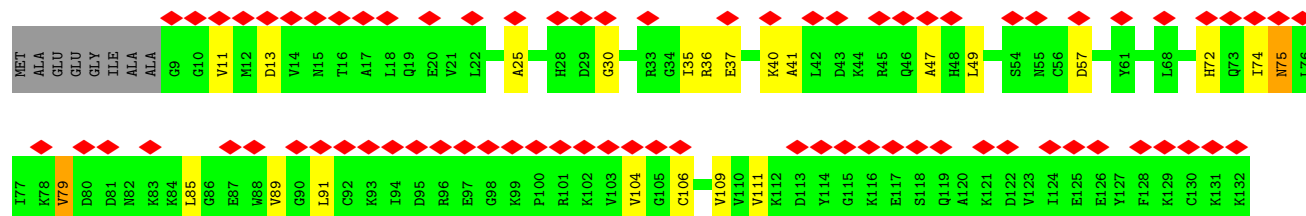
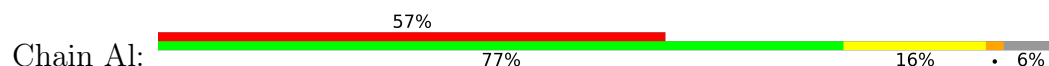
- Molecule 22: eS10



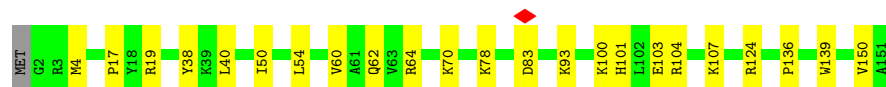
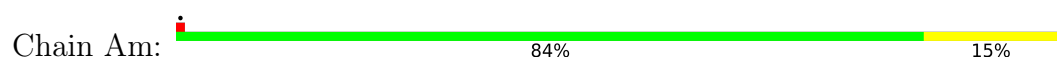
- Molecule 23: 40S ribosomal protein S11



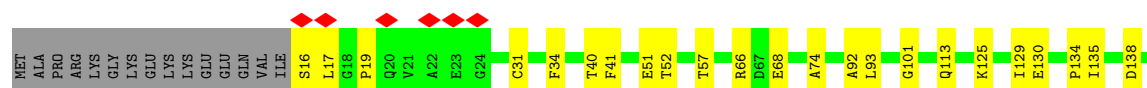
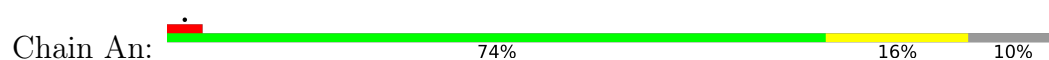
- Molecule 24: 40S ribosomal protein S12



- Molecule 25: uS15




- Molecule 26: 40S ribosomal protein uS11



L151

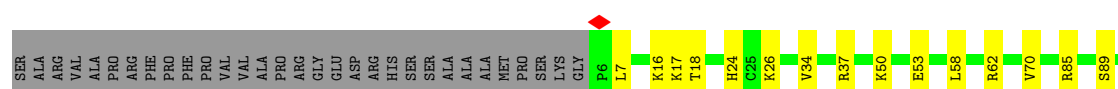
- Molecule 27: 40S ribosomal protein uS19

Chain Ao: 




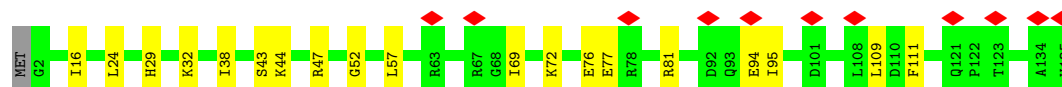
- Molecule 28: uS9

Chain Ap: 




- Molecule 29: 40S ribosomal protein eS17

Chain Aq: 



- Molecule 30: 40S ribosomal protein S18

Chain Ar: 




- Molecule 31: Ribosomal protein eS19

Chain As: 

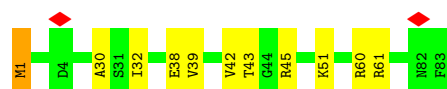
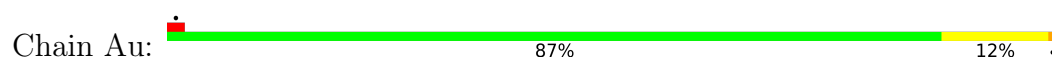


- Molecule 32: 40S ribosomal protein uS10

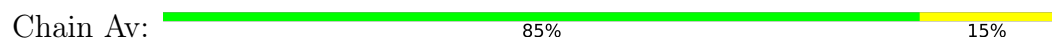
Chain At: 



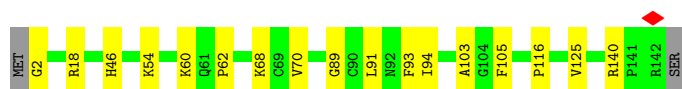
- Molecule 33: Ribosomal protein eS21



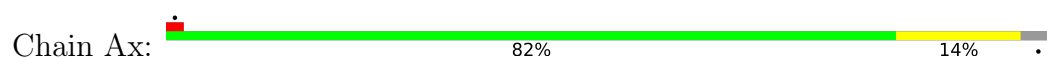
- Molecule 34: Ribosomal protein S15a



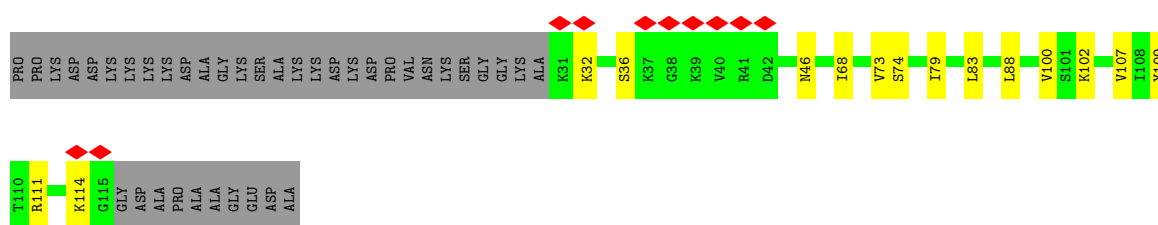
- Molecule 35: 40S ribosomal protein S23



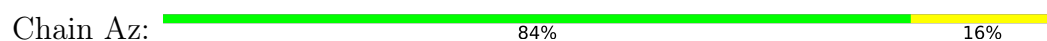
- Molecule 36: 40S ribosomal protein S24



- Molecule 37: 40S ribosomal protein S25

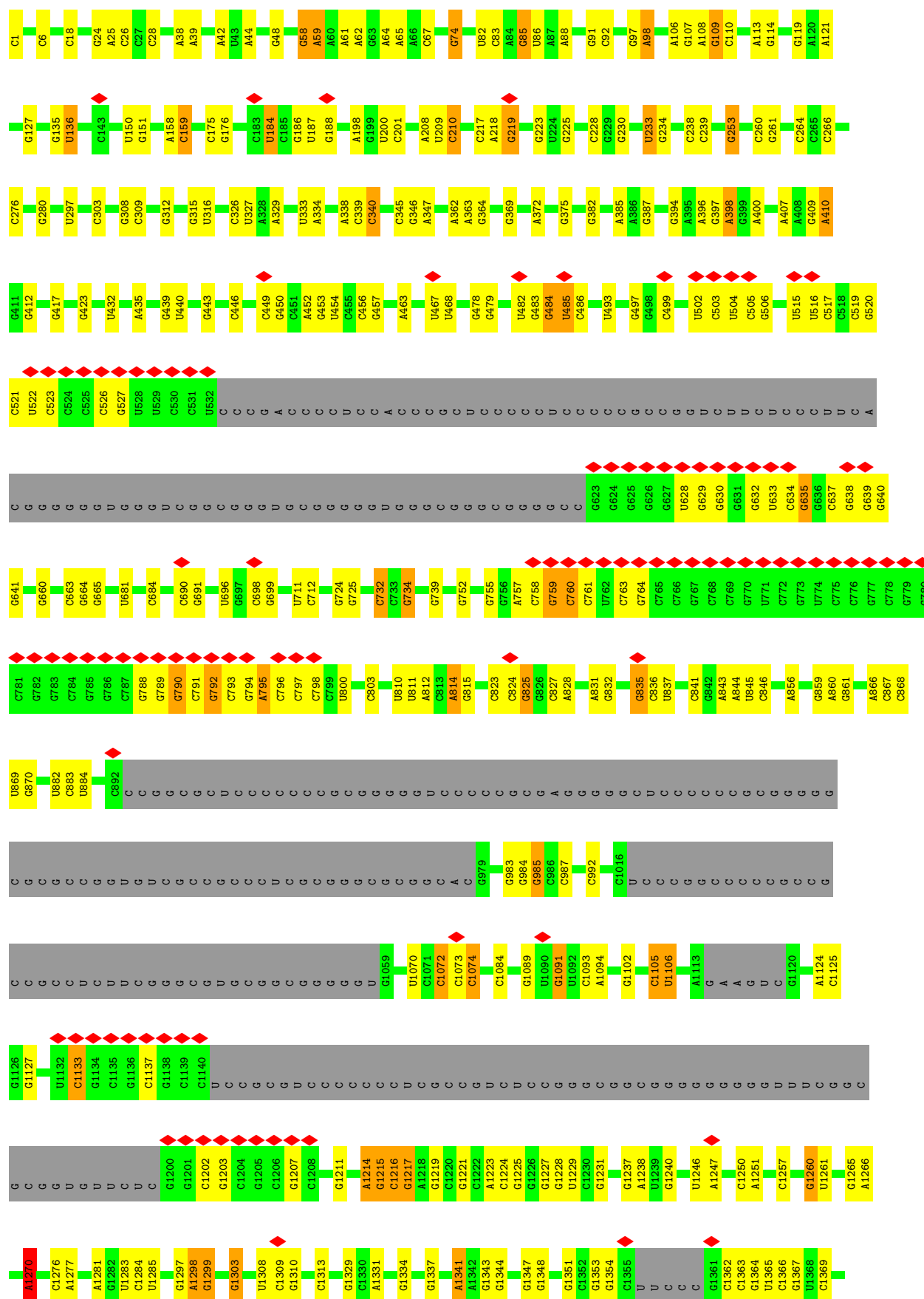


- Molecule 38: 60s ribosomal protein l41



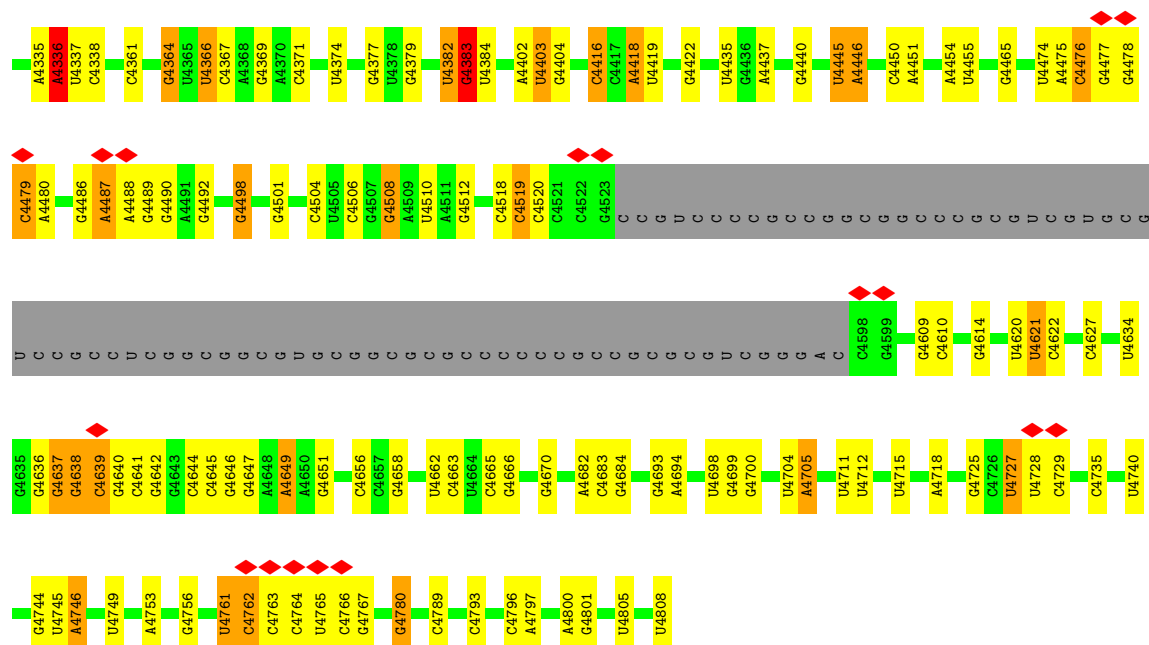
- Molecule 39: 28S rRNA



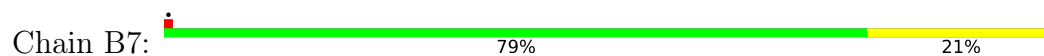




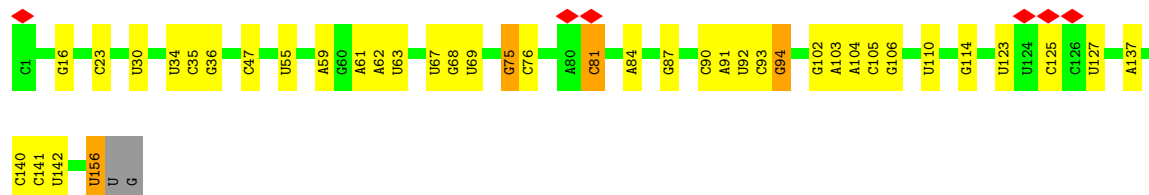
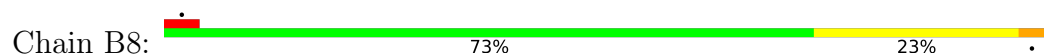




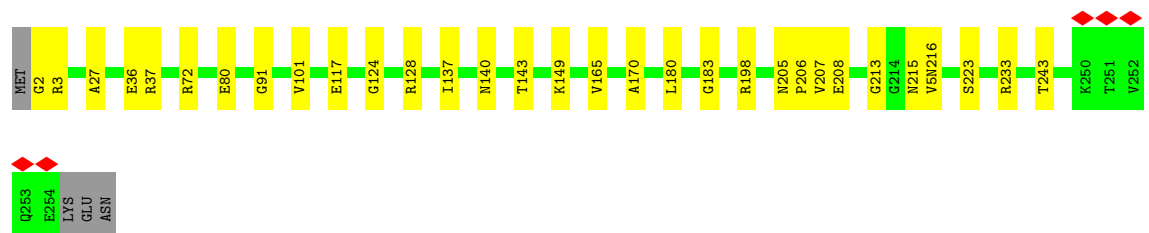
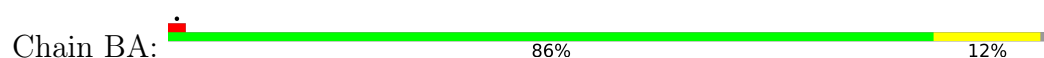
- Molecule 40: 5S




- Molecule 41: 5.8S rRNA

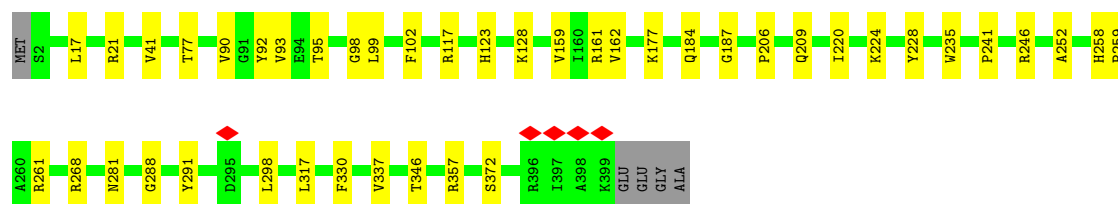


- Molecule 42: Ribosomal protein uL2




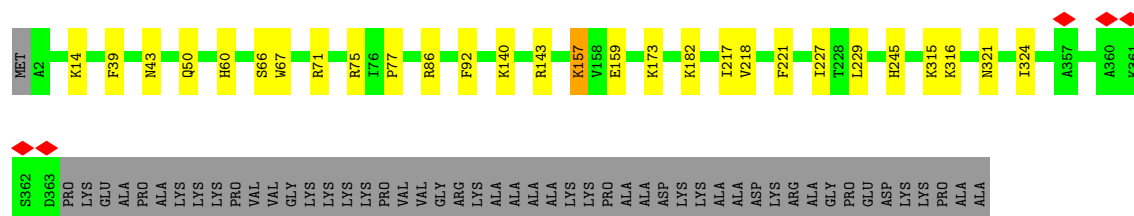
- Molecule 43: Ribosomal protein L3

Chain BB:  88% 11%



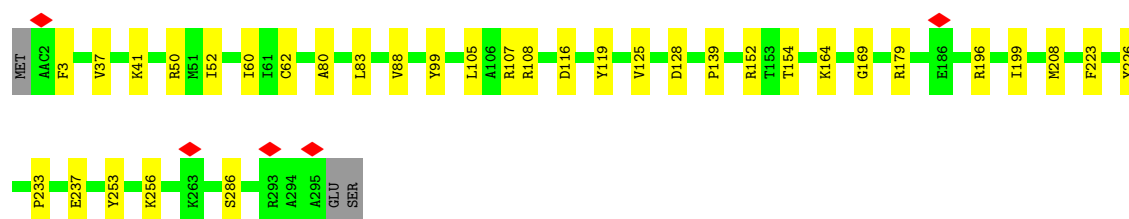
- Molecule 44: 60S ribosomal protein L4

Chain BC:  81% 7% 12%




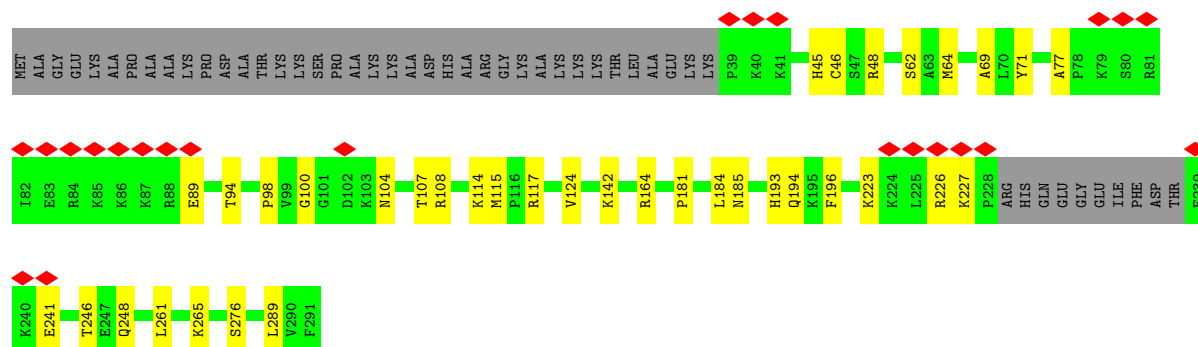
- Molecule 45: Ribosomal_L18_c domain-containing protein

Chain BD:  88% 11%




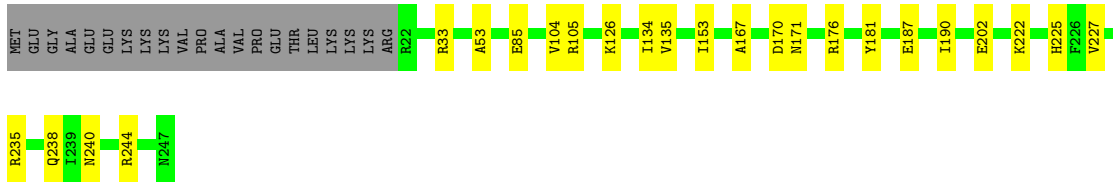
- Molecule 46: 60S ribosomal protein L6

Chain BE:  8% 71% 13% 16%

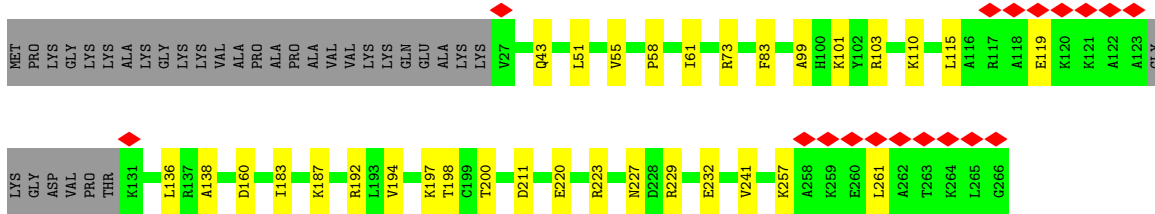
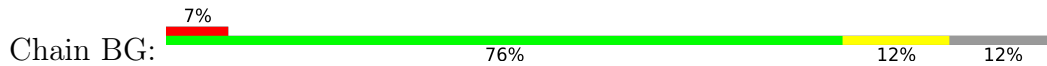


- Molecule 47: Ribosomal Protein uL30

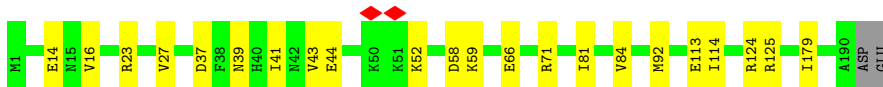
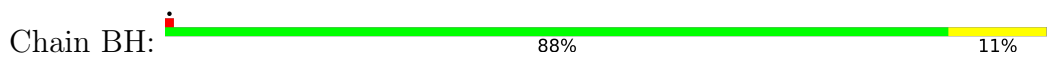
Chain BF:  82% 10% 9%



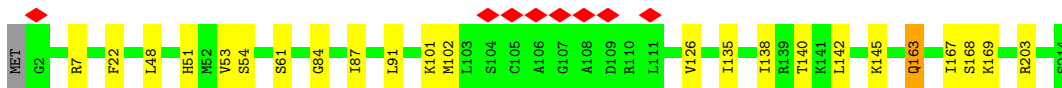
- Molecule 48: Ribosomal protein eL8



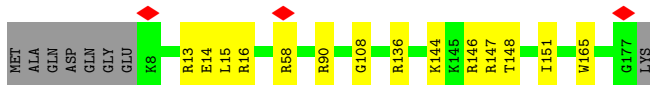
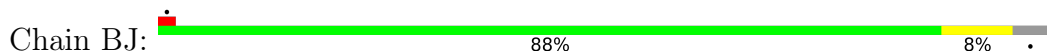
- Molecule 49: 60S ribosomal protein L9



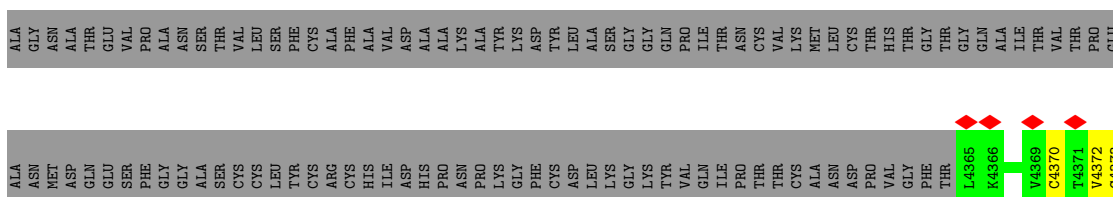
- Molecule 50: 60S ribosomal protein L10

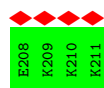


- Molecule 51: Ribosomal protein L11

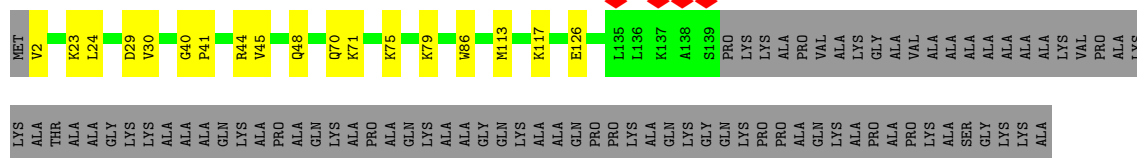


- Molecule 52: Replicase polyprotein 1ab





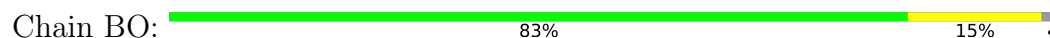
• Molecule 54: Ribosomal protein L14



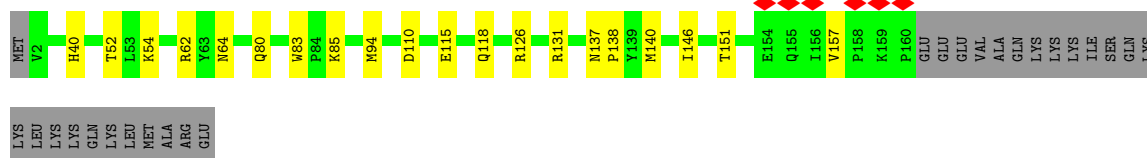
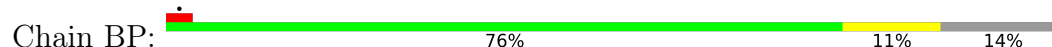
• Molecule 55: Ribosomal protein L15



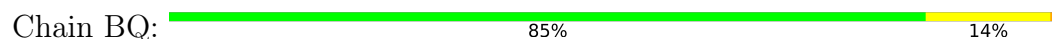
• Molecule 56: Ribosomal protein uL13




• Molecule 57: uL22

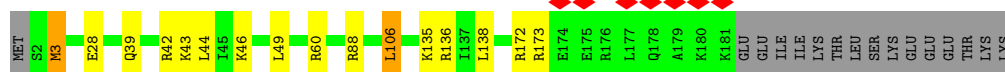


• Molecule 58: Ribosomal Protein eL18



• Molecule 59: 60S ribosomal protein L19

Chain BR:  84% 7% 8%




- Molecule 60: Ribosomal protein eL20

Chain BS:  91% 9%



- Molecule 61: eL21

Chain BT:  88% 12%



- Molecule 62: Ribosomal protein eL22

Chain BU:  66% 12% 23%




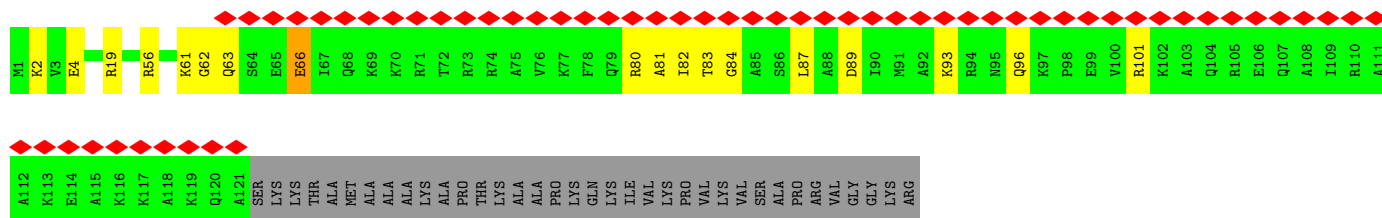
- Molecule 63: Ribosomal protein L23

Chain BV:  6% 91% 9%



- Molecule 64: eL24

Chain BW:  38% 66% 11% 23%



- Molecule 65: uL23

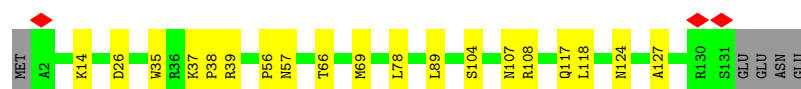
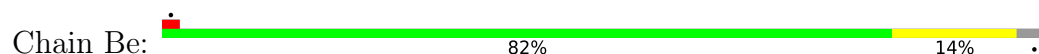
Chain BX:  72% 24%







- Molecule 72: eL32



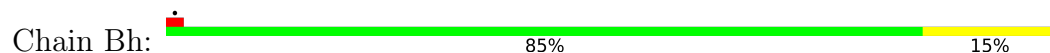
- Molecule 73: eL33



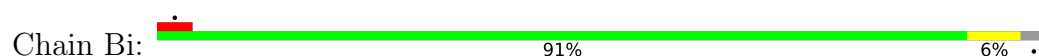
- Molecule 74: 60S ribosomal protein L34



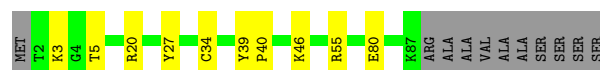
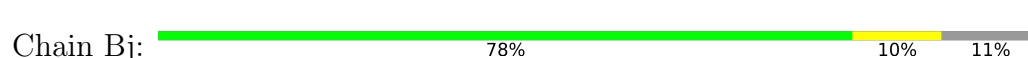
- Molecule 75: uL29



- Molecule 76: 60S ribosomal protein L36



- Molecule 77: Ribosomal protein L37




- Molecule 78: eL38

Chain Bk:  87% 10% ..



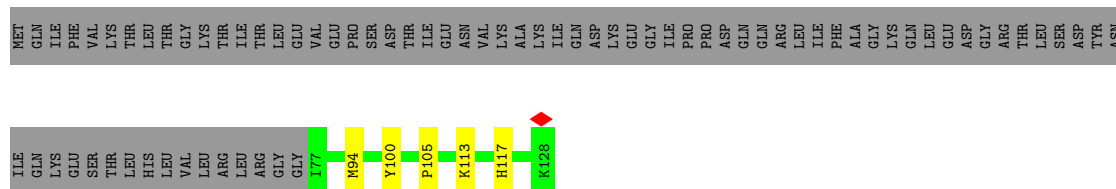
- Molecule 79: eL39

Chain Bl:  78% 18% ..



- Molecule 80: 60S ribosomal protein L40

Chain Bm:  37% 59%



- Molecule 81: eL42

Chain Bo:  88% 11% .




- Molecule 82: eL43

Chain Bp:  91% 8% .



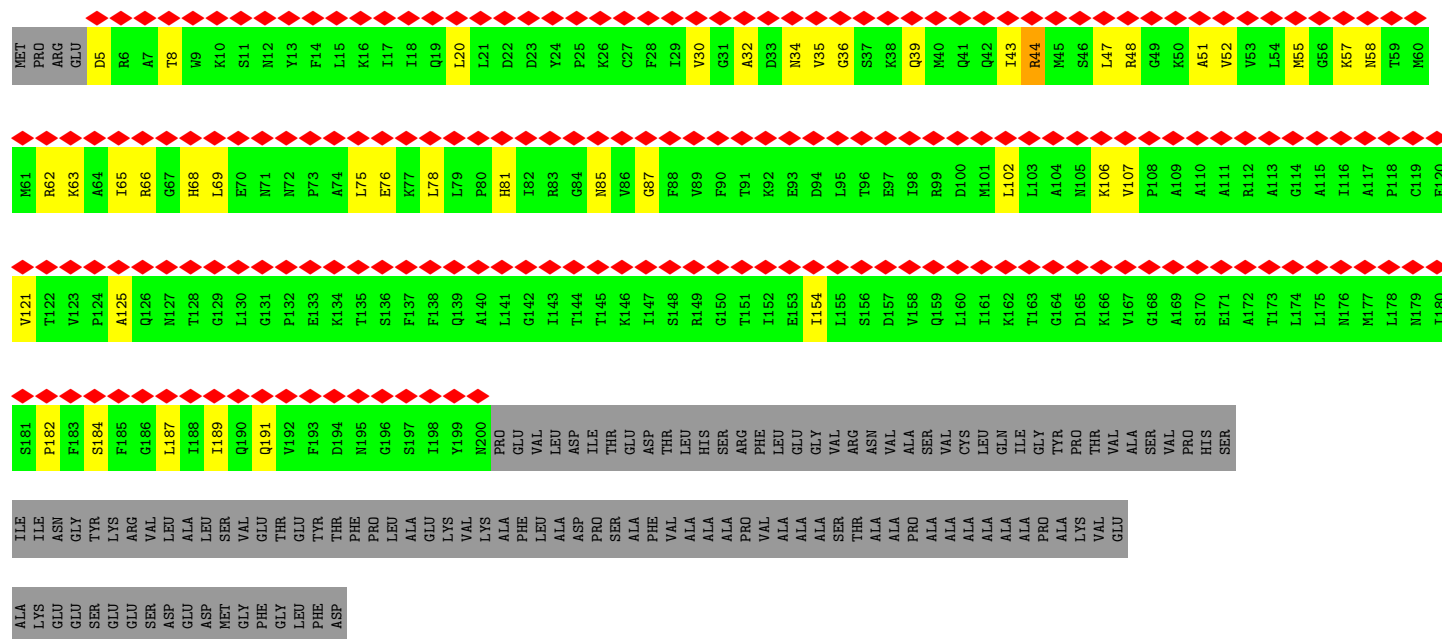
- Molecule 83: Ribosomal protein eL28

Chain Br:  84% 8% 8%

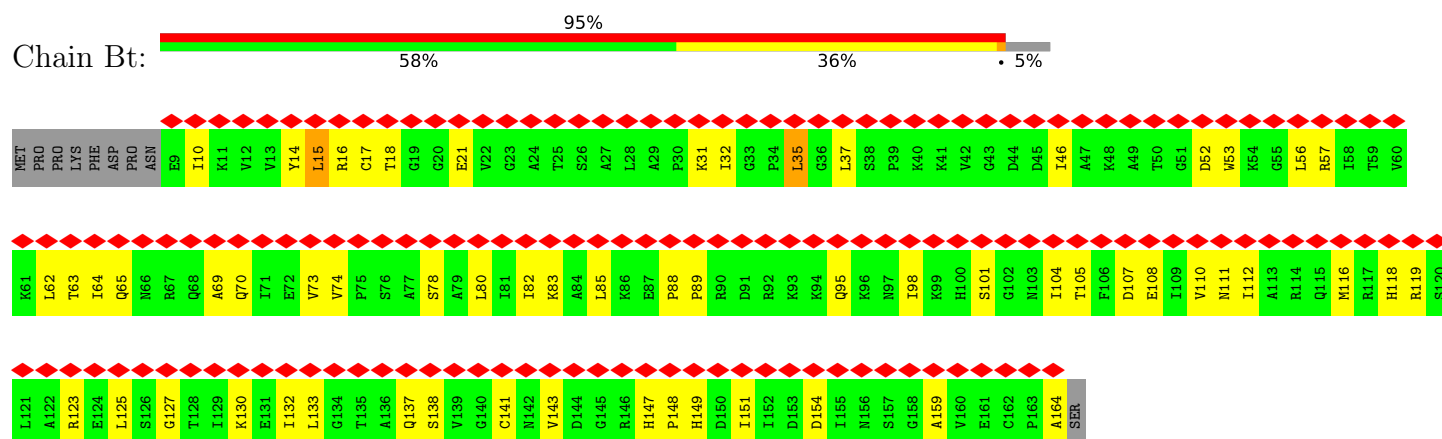


- Molecule 84: 60S acidic ribosomal protein P0

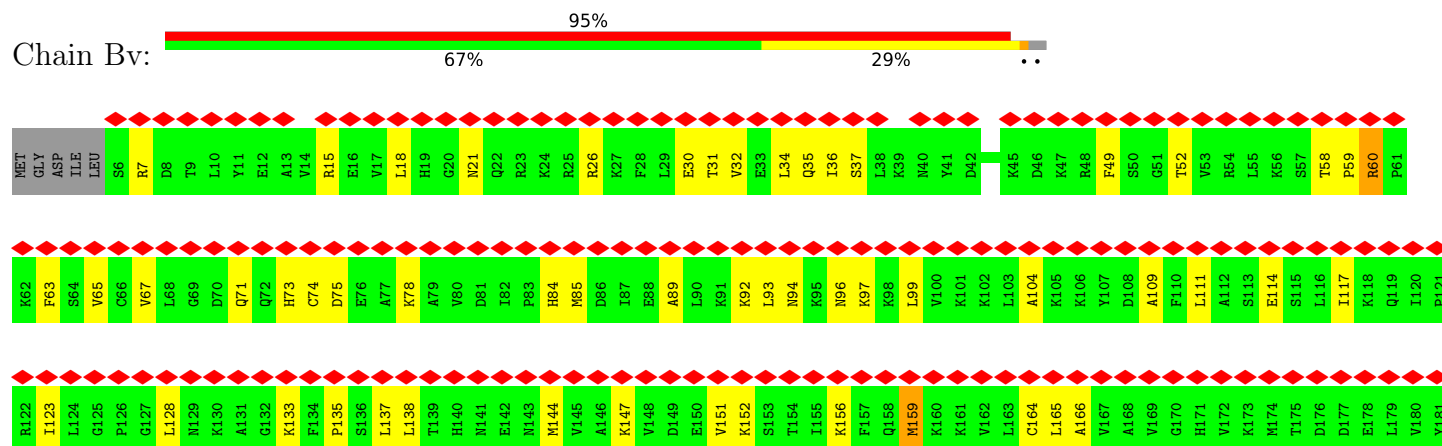
Chain Bs:  62% 49% 13% 38%



• Molecule 85: Ribosomal protein L12



• Molecule 86: Ribosomal protein uL1



N182	I183	H184	L185	A186	V187	N188	F189	L190	V191	S192	L193	L194	K195	K196	N197	W198	Q199	N200	V201	R202	A203	L204	Y205	L206	K207	S208	T209	M210	G211	K212	P213	Q214	R215	L216	Y217
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	171706	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	56604	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	45.454	Depositor
Minimum map value	-18.107	Depositor
Average map value	-0.006	Depositor
Map value standard deviation	0.952	Depositor
Recommended contour level	5	Depositor
Map size (\AA)	593.6, 593.6, 593.6	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, AYA, MLZ, UNX, UY1, ZN, OMG, AME, M2G, UR3, SPM, H2U, 4AC, MG, 1MA, G7M, MA6, PSU, AAC, 5MC, NMM, 6MZ, OMU, HY3, SPD, GTP, 2MG, OMC, M3L, B8N, YYG, V5N, HIC, A2M, SAC

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	A2	0.15	0/40342	0.17	0/62877
2	AA	0.10	0/665	0.27	0/891
3	AB	0.10	0/497	0.23	0/666
4	AC	0.08	0/622	0.24	0/822
5	AD	0.10	0/462	0.25	0/607
6	AE	0.11	0/828	0.23	0/1109
7	AF	0.09	0/2493	0.24	0/3394
8	AG	0.11	0/470	0.26	0/623
9	AH	0.06	0/2253	0.13	0/3508
10	AI	0.15	0/68	0.23	0/103
11	AT	0.16	0/1440	0.14	0/2242
12	AZ	0.10	0/1771	0.23	0/2406
13	Aa	0.11	0/1841	0.24	0/2459
14	Ab	0.11	0/1742	0.26	0/2354
15	Ac	0.10	0/1779	0.24	0/2395
16	Ad	0.11	0/2118	0.26	0/2849
17	Ae	0.10	0/1531	0.27	0/2059
18	Af	0.09	0/1946	0.24	0/2590
19	Ag	0.09	0/1552	0.24	0/2079
20	Ah	0.10	0/1715	0.25	0/2287
21	Ai	0.09	0/1550	0.22	0/2069
22	Aj	0.10	0/834	0.26	0/1125
23	Ak	0.11	0/1284	0.24	0/1717
24	Al	0.08	0/968	0.25	0/1296
25	Am	0.11	0/1232	0.25	0/1656
26	An	0.12	0/1029	0.31	0/1380
27	Ao	0.11	0/1069	0.26	0/1429
28	Ap	0.10	0/1142	0.28	0/1528
29	Aq	0.09	0/1094	0.23	0/1469
30	Ar	0.08	0/1226	0.22	0/1643

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	As	0.10	0/1119	0.24	0/1498
32	At	0.11	0/831	0.24	0/1115
33	Au	0.10	0/636	0.24	0/852
34	Av	0.12	0/1051	0.25	0/1406
35	Aw	0.10	0/1107	0.25	0/1475
36	Ax	0.09	0/1032	0.22	0/1371
37	Ay	0.09	0/691	0.22	0/922
38	Az	0.10	0/240	0.21	0/305
39	B5	0.14	2/87403 (0.0%)	0.18	0/136359
40	B7	0.11	0/2835	0.16	0/4418
41	B8	0.11	0/3635	0.17	0/5661
42	BA	0.13	0/1965	0.29	0/2633
43	BB	0.12	0/3261	0.26	0/4364
44	BC	0.11	0/2932	0.24	0/3939
45	BD	0.11	0/2437	0.24	0/3264
46	BE	0.10	0/1998	0.23	0/2673
47	BF	0.11	0/1922	0.25	0/2563
48	BG	0.11	0/1908	0.24	0/2566
49	BH	0.11	0/1535	0.25	0/2063
50	BI	0.11	0/1756	0.24	0/2346
51	BJ	0.10	0/1385	0.24	0/1852
52	BK	0.10	0/269	0.28	0/361
53	BL	0.11	0/1733	0.23	0/2316
54	BM	0.10	0/1158	0.23	0/1547
55	BN	0.12	0/1746	0.24	0/2338
56	BO	0.12	0/1662	0.23	0/2222
57	BP	0.11	0/1317	0.25	0/1768
58	BQ	0.12	0/1539	0.26	0/2054
59	BR	0.09	0/1524	0.23	0/2013
60	BS	0.12	0/1497	0.24	0/2008
61	BT	0.11	0/1326	0.24	0/1770
62	BU	0.09	0/820	0.24	0/1100
63	BV	0.12	0/1048	0.26	0/1402
64	BW	0.09	0/1006	0.23	0/1334
65	BX	0.10	0/984	0.23	0/1323
66	BY	0.10	0/1132	0.23	0/1504
67	BZ	0.10	0/1130	0.23	0/1507
68	Ba	0.11	0/1179	0.25	0/1572
69	Bb	0.10	0/884	0.27	0/1169
70	Bc	0.10	0/847	0.21	0/1134
71	Bd	0.12	0/903	0.24	0/1216
72	Be	0.11	0/1088	0.25	0/1451
73	Bf	0.12	0/903	0.26	0/1208

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
74	Bg	0.11	0/916	0.25	0/1220
75	Bh	0.09	0/1021	0.21	0/1348
76	Bi	0.09	0/841	0.24	0/1112
77	Bj	0.12	0/720	0.28	0/952
78	Bk	0.09	0/575	0.21	0/761
79	Bl	0.12	0/459	0.25	0/608
80	Bm	0.10	0/426	0.27	0/564
81	Bo	0.12	0/866	0.26	0/1141
82	Bp	0.11	0/718	0.27	0/953
83	Br	0.11	0/1020	0.25	0/1366
84	Bs	0.08	0/1530	0.23	0/2064
85	Bt	0.08	0/1193	0.25	0/1609
86	Bv	0.09	0/1735	0.30	0/2328
All	All	0.13	2/236957 (0.0%)	0.21	0/347620

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
81	Bo	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	B5	4761	U	C4-O4	5.13	1.33	1.23
39	B5	4269	A2M	O3'-P	5.00	1.61	1.56

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
81	Bo	53	MLZ	Mainchain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A2	37833	0	19167	300	0
2	AA	651	0	672	9	0
3	AB	495	0	523	6	0
4	AC	610	0	634	16	0
5	AD	457	0	502	11	0
6	AE	814	0	863	13	0
7	AF	2436	0	2393	43	0
8	AG	459	0	448	7	0
9	AH	2018	0	1018	14	0
10	AI	939	0	618	4	0
11	AT	1652	0	859	12	0
12	AZ	1743	0	1748	22	0
13	Aa	1815	0	1908	24	0
14	Ab	1706	0	1796	16	0
15	Ac	1751	0	1846	23	0
16	Ad	2076	0	2177	18	0
17	Ae	1509	0	1563	21	0
18	Af	1923	0	2089	39	0
19	Ag	1529	0	1627	20	0
20	Ah	1686	0	1772	32	0
21	Ai	1525	0	1640	15	0
22	Aj	810	0	836	9	0
23	Ak	1262	0	1335	7	0
24	Al	958	0	993	18	0
25	Am	1208	0	1293	16	0
26	An	1016	0	1039	18	0
27	Ao	1048	0	1093	10	0
28	Ap	1124	0	1193	19	0
29	Aq	1080	0	1135	13	0
30	Ar	1217	0	1279	18	0
31	As	1113	0	1145	12	0
32	At	821	0	883	8	0
33	Au	640	0	633	7	0
34	Av	1034	0	1080	16	0
35	Aw	1099	0	1162	11	0
36	Ax	1015	0	1086	13	0
37	Ay	683	0	761	10	0
38	Az	239	0	289	5	0
39	B5	80772	0	40876	563	0
40	B7	2570	0	1294	14	0
41	B8	3319	0	1684	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	BA	1940	0	2029	20	0
43	BB	3206	0	3353	30	0
44	BC	2886	0	3057	20	0
45	BD	2398	0	2430	23	0
46	BE	1960	0	2153	24	0
47	BF	1886	0	2008	17	0
48	BG	1877	0	2023	18	0
49	BH	1516	0	1597	14	0
50	BI	1717	0	1763	15	0
51	BJ	1362	0	1399	8	0
52	BK	265	0	254	5	0
53	BL	1702	0	1820	21	0
54	BM	1137	0	1211	14	0
55	BN	1701	0	1749	19	0
56	BO	1630	0	1777	22	0
57	BP	1289	0	1329	15	0
58	BQ	1515	0	1634	21	0
59	BR	1508	0	1664	14	0
60	BS	1457	0	1492	10	0
61	BT	1298	0	1366	16	0
62	BU	806	0	827	9	0
63	BV	1034	0	1097	10	0
64	BW	991	0	1048	12	0
65	BX	967	0	1040	3	0
66	BY	1115	0	1205	13	0
67	BZ	1107	0	1182	11	0
68	Ba	1163	0	1202	16	0
69	Bb	881	0	957	11	0
70	Bc	836	0	888	6	0
71	Bd	888	0	930	11	0
72	Be	1070	0	1165	17	0
73	Bf	884	0	923	11	0
74	Bg	906	0	998	5	0
75	Bh	1013	0	1147	14	0
76	Bi	830	0	916	4	0
77	Bj	705	0	737	8	0
78	Bk	569	0	637	6	0
79	Bl	447	0	479	8	0
80	Bm	432	0	470	3	0
81	Bo	863	0	929	8	0
82	Bp	708	0	756	6	0
83	Br	1014	0	1083	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
84	Bs	1507	0	1564	29	0
85	Bt	1178	0	1235	38	0
86	Bv	1707	0	1815	43	0
87	A2	80	0	152	6	0
87	B5	220	0	418	18	0
88	A2	14	0	26	2	0
88	B5	28	0	52	3	0
89	A2	109	0	0	0	0
89	AH	1	0	0	0	0
89	AT	3	0	0	0	0
89	Af	1	0	0	0	0
89	B5	284	0	0	0	0
89	B7	9	0	0	0	0
89	B8	9	0	0	0	0
89	BP	1	0	0	0	0
89	BR	1	0	0	0	0
89	BV	1	0	0	0	0
89	Ba	1	0	0	0	0
90	A2	60	0	0	0	0
90	AT	4	0	0	0	0
90	Ae	1	0	0	0	0
90	An	1	0	0	0	0
90	Ar	1	0	0	0	0
90	As	1	0	0	0	0
90	B5	225	0	0	0	0
90	B7	6	0	0	0	0
90	B8	8	0	0	0	0
90	BA	3	0	0	0	0
90	BB	4	0	0	0	0
90	BC	1	0	0	0	0
90	BH	1	0	0	0	0
90	BI	1	0	0	0	0
90	BL	1	0	0	0	0
90	BN	1	0	0	0	0
90	BQ	2	0	0	0	0
90	BT	2	0	0	0	0
90	Bb	1	0	0	0	0
90	Be	1	0	0	0	0
90	Bf	1	0	0	0	0
90	Bg	1	0	0	0	0
90	Bl	1	0	0	0	0
90	Bo	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
91	AC	1	0	0	0	0
91	AE	1	0	0	0	0
91	AG	1	0	0	0	0
91	Bg	1	0	0	0	0
91	Bj	1	0	0	0	0
91	Bm	1	0	0	0	0
91	Bo	1	0	0	0	0
91	Bp	1	0	0	0	0
92	A2	526	0	0	9	0
92	AH	9	0	0	0	0
92	AI	1	0	0	1	0
92	AT	12	0	0	0	0
92	Aa	1	0	0	0	0
92	Ac	1	0	0	0	0
92	Af	3	0	0	0	0
92	Ak	1	0	0	0	0
92	Am	1	0	0	0	0
92	An	2	0	0	1	0
92	Ap	3	0	0	0	0
92	As	2	0	0	0	0
92	At	1	0	0	0	0
92	Aw	3	0	0	0	0
92	B5	1391	0	0	11	0
92	B7	45	0	0	2	0
92	B8	50	0	0	0	0
92	BA	10	0	0	1	0
92	BB	5	0	0	0	0
92	BC	7	0	0	0	0
92	BD	1	0	0	0	0
92	BF	1	0	0	0	0
92	BH	1	0	0	0	0
92	BI	4	0	0	0	0
92	BL	3	0	0	0	0
92	BN	3	0	0	0	0
92	BO	1	0	0	0	0
92	BP	2	0	0	0	0
92	BR	5	0	0	0	0
92	BV	2	0	0	1	0
92	BX	2	0	0	0	0
92	Ba	6	0	0	0	0
92	Bd	1	0	0	0	0
92	Be	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
92	Bg	2	0	0	0	0
92	Bj	3	0	0	0	0
92	Bl	1	0	0	0	0
92	Bo	1	0	0	0	0
All	All	229742	0	168938	1699	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 5.

All (1699) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A2:1092:C:HO2'	34:Av:2:VAL:N	1.56	1.03
41:B8:81:C:HO2'	75:Bh:2:ALA:N	1.64	0.94
39:B5:1:C:H42	41:B8:156:U:H3	1.25	0.82
1:A2:929:G:H1	1:A2:1014:U:H3	1.33	0.77
63:BV:50:ASN:ND2	92:BV:301:HOH:O	2.16	0.77
46:BE:227:LYS:HE2	46:BE:241:GLU:H	1.51	0.75
48:BG:58:PRO:HD2	48:BG:61:ILE:HD12	1.68	0.75
2:AA:23:ARG:HH22	2:AA:29:ASN:HD21	1.35	0.75
39:B5:2205:U:H2'	39:B5:2206:A2M:H8	1.69	0.74
1:A2:953:G:H21	26:An:52:THR:HG21	1.55	0.72
28:Ap:58:LEU:HB3	28:Ap:62:ARG:HD2	1.72	0.71
1:A2:926:G:H1	1:A2:1018:U:H3	1.38	0.71
7:AF:247:TRP:HB3	7:AF:258:ILE:HD11	1.71	0.71
84:Bs:47:LEU:HB3	84:Bs:51:ALA:HB3	1.70	0.71
87:B5:4924:SPD:H101	56:BO:91:LYS:HD3	1.55	0.71
13:Aa:44:ILE:HD12	13:Aa:69:VAL:HG21	1.74	0.70
39:B5:2106:A:OP1	83:Br:107:ARG:NH2	2.24	0.70
1:A2:1522:C:OP2	30:Ar:136:THR:OG1	2.10	0.70
39:B5:2444:A:N6	39:B5:2587:A:OP2	2.25	0.70
86:Bv:49:PHE:HB2	86:Bv:159:MET:HG3	1.72	0.70
34:Av:80:ASP:OD1	34:Av:124:LYS:NZ	2.25	0.70
39:B5:1415:C:H5''	58:BQ:144:LYS:HG2	1.73	0.69
57:BP:126:ARG:HG3	57:BP:140:MET:HE1	1.74	0.69
39:B5:1299:G:OP1	58:BQ:108:ARG:NH2	2.24	0.69
1:A2:1491:OMG:HM22	1:A2:1492:G:H5'	1.75	0.69
39:B5:3555:G:N2	39:B5:3555:G:OP2	2.25	0.69
28:Ap:132:PHE:O	28:Ap:140:ARG:NH2	2.25	0.69
1:A2:1021:A:N7	25:Am:70:LYS:NZ	2.40	0.69
39:B5:2541:G:H21	74:Bg:28:ASN:HD21	1.40	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:B5:2548:G:O6	59:BR:46:LYS:NZ	2.26	0.69
71:Bd:64:ILE:HG23	71:Bd:68:LEU:HD23	1.76	0.68
39:B5:264:C:O2	75:Bh:112:ARG:NH2	2.27	0.68
86:Bv:63:PHE:O	86:Bv:152:LYS:NZ	2.26	0.68
24:Al:79:VAL:HG11	24:Al:85:LEU:HB2	1.76	0.68
1:A2:1392:OMC:HM22	1:A2:1393:U:H5'	1.76	0.68
21:Ai:120:ALA:O	21:Ai:125:HIS:ND1	2.24	0.68
1:A2:1397:A:O2'	1:A2:1399:G:N7	2.26	0.68
39:B5:2538:A:OP1	78:Bk:35:LYS:NZ	2.26	0.67
39:B5:3373:U:OP2	39:B5:3378:A:N6	2.24	0.67
39:B5:1133:C:O2	39:B5:1207:G:N2	2.26	0.67
39:B5:3852:G:N2	48:BG:43:GLN:O	2.28	0.67
86:Bv:74:CYS:SG	86:Bv:78:LYS:NZ	2.66	0.67
39:B5:1260:OMG:HM22	39:B5:1261:U:H5'	1.76	0.67
39:B5:4336:A2M:HM'2	39:B5:4337:U:H5'	1.76	0.67
39:B5:632:G:H5''	39:B5:633:U:H5'	1.76	0.67
7:AF:87:LEU:HB2	7:AF:101:PHE:HB2	1.76	0.66
1:A2:46:A:OP2	92:A2:2101:HOH:O	2.13	0.66
84:Bs:65:ILE:HG23	84:Bs:75:LEU:HB3	1.78	0.66
1:A2:577:A2M:HM'2	1:A2:578:U:H5'	1.76	0.66
39:B5:2545:C:OP1	62:BU:101:ARG:NH2	2.29	0.66
84:Bs:48:ARG:HD3	85:Bt:123:ARG:HG2	1.77	0.66
86:Bv:89:ALA:HA	86:Bv:92:LYS:HD3	1.78	0.66
1:A2:941:U:H3	1:A2:1003:U:H3	1.44	0.66
39:B5:4218:G:O2'	80:Bm:100:TYR:O	2.14	0.65
40:B7:105:C:OP2	50:BI:203:ARG:NH1	2.29	0.65
10:AI:76:A:N1	92:AI:101:HOH:O	2.30	0.65
19:Ag:162:GLN:OE1	19:Ag:165:ASN:ND2	2.29	0.65
39:B5:3468:A:OP2	92:B5:5501:HOH:O	2.14	0.65
10:AI:9:N:H1'2	10:AI:45:N:H2'	1.79	0.65
39:B5:2486:G:N7	92:B5:5541:HOH:O	2.29	0.65
39:B5:3991:G:N7	92:B5:5535:HOH:O	2.29	0.65
39:B5:4364:OMG:H5''	63:BV:15:ARG:HB2	1.77	0.65
1:A2:1056:A:N7	92:A2:2115:HOH:O	2.28	0.65
7:AF:256:ILE:HB	7:AF:270:LEU:HB2	1.79	0.65
68:Ba:72:THR:HG22	68:Ba:110:LYS:HB3	1.79	0.65
39:B5:484:G:H3'	39:B5:485:U:H2'	1.79	0.65
39:B5:1810:A2M:HM'2	39:B5:1811:G:H5'	1.79	0.65
39:B5:1915:G:N3	85:Bt:138:SER:OG	2.30	0.65
54:BM:40:GLY:HA3	54:BM:45:VAL:HB	1.79	0.64
39:B5:1605:A:H5''	87:B5:4920:SPD:H22	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:B5:2143:A:N7	44:BC:143:ARG:NH1	2.46	0.64
39:B5:4735:C:OP1	71:Bd:32:ARG:NH1	2.31	0.64
81:Bo:34:TYR:O	81:Bo:39:ARG:NH1	2.29	0.64
1:A2:1052:G:N7	92:A2:2122:HOH:O	2.30	0.64
26:An:34:PHE:HB3	26:An:41:PHE:HB2	1.79	0.64
1:A2:1551:G:H3'	1:A2:1580:A:H61	1.63	0.64
8:AG:44:ARG:NH1	32:At:78:ASP:OD2	2.30	0.64
41:B8:102:G:OP1	77:Bj:20:ARG:NH1	2.30	0.64
43:BB:41:VAL:HA	43:BB:187:GLY:HA3	1.80	0.64
86:Bv:52:THR:HG22	86:Bv:156:LYS:HG2	1.80	0.64
1:A2:165:G:OP2	1:A2:165:G:N2	2.28	0.64
39:B5:4379:G:OP2	87:B5:4917:SPD:N1	2.31	0.64
39:B5:3518:U:OP1	39:B5:4296:G:O2'	2.14	0.64
86:Bv:117:ILE:HD13	86:Bv:137:LEU:HD21	1.78	0.63
7:AF:217:MET:HG2	7:AF:229:THR:HG22	1.80	0.63
39:B5:432:U:O2	87:B5:4924:SPD:N6	2.31	0.63
39:B5:1869:U:OP2	56:BO:49:ARG:NH1	2.30	0.63
72:Be:78:LEU:O	83:Br:20:ARG:NH1	2.31	0.63
84:Bs:102:LEU:HD11	84:Bs:187:LEU:HD12	1.79	0.63
39:B5:2422:G:N2	39:B5:2425:A:OP2	2.24	0.63
39:B5:3456:A2M:HM'2	39:B5:3457:G:H5'	1.80	0.63
12:AZ:94:THR:HG23	12:AZ:186:ARG:HH12	1.64	0.63
62:BU:28:PRO:HB2	62:BU:34:MET:HG2	1.80	0.63
7:AF:120:ILE:HB	7:AF:132:TRP:HB2	1.80	0.62
30:Ar:46:ARG:HG2	31:As:35:ASP:HB2	1.80	0.62
39:B5:198:A:OP2	66:BY:126:ARG:NH2	2.32	0.62
46:BE:115:MET:O	83:Br:87:ARG:NH1	2.31	0.62
86:Bv:111:LEU:HD21	86:Bv:151:VAL:HG21	1.81	0.62
1:A2:397:U:OP2	23:Ak:79:LYS:NZ	2.30	0.62
39:B5:432:U:H1'	87:B5:4924:SPD:HN6	1.64	0.62
30:Ar:98:VAL:HG11	30:Ar:106:LYS:HG3	1.81	0.62
39:B5:4366:OMU:OP2	39:B5:4416:C:N4	2.29	0.62
86:Bv:67:VAL:HG12	86:Bv:84:HIS:HD2	1.64	0.62
39:B5:1297:G:N7	58:BQ:104:ARG:NH2	2.48	0.62
60:BS:173:ASN:ND2	60:BS:175:PHE:O	2.31	0.62
1:A2:1286:G:O2'	4:AC:99:LYS:NZ	2.29	0.62
1:A2:1675:G:N7	28:Ap:17:LYS:NZ	2.47	0.62
5:AD:122:THR:HG21	5:AD:126:LYS:HG2	1.81	0.62
39:B5:2328:U:H3	39:B5:2336:G:H1	1.46	0.62
39:B5:4666:G:N2	39:B5:4666:G:OP2	2.30	0.62
1:A2:228:C:H42	1:A2:902:G:H1'	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A2:1402:A:N6	1:A2:1442:U:O2'	2.33	0.62
13:Aa:92:GLN:NE2	13:Aa:229:MET:SD	2.72	0.62
39:B5:4764:C:O2'	39:B5:4767:G:N3	2.33	0.62
7:AF:29:ASP:OD1	7:AF:47:ARG:NH1	2.27	0.61
39:B5:1399:G:OP2	39:B5:1399:G:N2	2.27	0.61
1:A2:513:A2M:HM'2	1:A2:514:G:H5'	1.80	0.61
39:B5:4292:A:N7	42:BA:215:ASN:ND2	2.48	0.61
7:AF:133:ASN:HB3	7:AF:139:LYS:HE3	1.83	0.61
39:B5:2301:C:H5''	55:BN:67:ARG:HD2	1.82	0.61
42:BA:27:ALA:O	42:BA:128:ARG:NH1	2.30	0.61
1:A2:1355:G:N2	1:A2:1358:A:OP2	2.26	0.61
18:Af:22:ARG:HG2	18:Af:25:ARG:HH22	1.66	0.61
47:BF:104:VAL:HG13	47:BF:135:VAL:HG12	1.83	0.61
1:A2:430:C:O2'	1:A2:812:A:N1	2.33	0.61
11:AT:32:OMC:HM22	11:AT:33:U:H5'	1.81	0.61
86:Bv:114:GLU:HA	86:Bv:137:LEU:HD22	1.83	0.61
1:A2:1285:A:H2'	24:Al:91:LEU:HD21	1.82	0.61
1:A2:1508:G:N2	4:AC:87:THR:O	2.28	0.61
29:Aq:94:GLU:HG2	29:Aq:95:ILE:HG13	1.83	0.61
39:B5:835:G:OP1	54:BM:44:ARG:NH1	2.33	0.60
39:B5:1284:OMC:OP1	68:Ba:6:ARG:NH2	2.33	0.60
1:A2:166:A2M:HM'2	1:A2:167:G:H5'	1.81	0.60
27:Ao:18:ARG:NH1	30:Ar:88:LYS:O	2.34	0.60
53:BL:81:LEU:HD12	53:BL:86:ILE:HB	1.83	0.60
18:Af:148:SER:N	18:Af:151:ASP:OD2	2.32	0.60
10:Al:75:C:O2'	81:Bo:54:PRO:O	2.17	0.60
59:BR:39:GLN:OE1	59:BR:42:ARG:NH1	2.34	0.60
75:Bh:4:ILE:HD12	75:Bh:53:SER:HB3	1.82	0.60
39:B5:2161:G:N2	39:B5:2164:G:OP2	2.33	0.60
39:B5:1960:G:OP1	84:Bs:58:ASN:ND2	2.34	0.60
39:B5:1924:G:H1'	39:B5:1942:G:H2'	1.84	0.60
1:A2:17:C:O2'	1:A2:1195:A:N1	2.35	0.60
1:A2:378:G:H5'	20:Ah:98:LYS:HB3	1.82	0.60
20:Ah:101:ILE:HD12	20:Ah:190:LEU:HD11	1.84	0.60
39:B5:2169:G:OP1	72:Be:108:ARG:NH2	2.34	0.60
1:A2:1245:PSU:H5''	4:AC:78:LYS:HD2	1.84	0.60
7:AF:244:ASN:ND2	7:AF:294:ASP:O	2.35	0.60
39:B5:1620:C:O2'	88:B5:4912:SPM:N1	2.35	0.60
50:BI:87:ILE:HG12	50:BI:138:ILE:HG12	1.84	0.60
64:BW:2:LYS:NZ	64:BW:4:GLU:OE2	2.35	0.60
30:Ar:22:GLY:HA2	30:Ar:56:ALA:HB3	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:B5:184:U:H3	39:B5:253:G:H1	1.50	0.59
1:A2:463:OMC:HM22	1:A2:464:C:H5'	1.84	0.59
39:B5:1846:A:H4'	47:BF:222:LYS:HE3	1.84	0.59
39:B5:1394:U:HO2'	47:BF:33:ARG:HE	1.50	0.59
50:BI:48:LEU:HB2	50:BI:142:LEU:HD23	1.82	0.59
39:B5:369:G:N2	39:B5:372:A:OP2	2.30	0.59
43:BB:92:TYR:HB2	43:BB:159:VAL:HB	1.83	0.59
1:A2:1569:C:OP1	31:As:96:SER:OG	2.21	0.59
9:AH:3537:A:H3'	9:AH:3538:G:H4'	1.85	0.59
51:BJ:146:ARG:HG2	51:BJ:147:ARG:HG3	1.84	0.59
1:A2:840:C:H42	36:Ax:48:TYR:HA	1.67	0.59
1:A2:1131:G:N2	1:A2:1131:G:OP2	2.31	0.59
25:Am:136:PRO:HG2	25:Am:139:TRP:HB2	1.85	0.59
39:B5:1237:G:OP2	39:B5:1237:G:N2	2.28	0.59
49:BH:59:LYS:HE2	49:BH:66:GLU:HB3	1.85	0.59
39:B5:1673:G:N2	39:B5:1674:U:O4	2.27	0.59
39:B5:1694:C:O2	45:BD:3:PHE:N	2.36	0.59
4:AC:116:ARG:NH1	4:AC:120:GLU:OE2	2.36	0.59
39:B5:1606:G:OP2	87:B5:4920:SPD:N1	2.36	0.59
1:A2:747:C:H42	1:A2:796:A:H61	1.51	0.58
1:A2:1758:G:H1	1:A2:1776:U:H3	1.50	0.58
31:As:60:THR:HG23	31:As:75:MET:HE2	1.85	0.58
39:B5:3540:OMC:HM22	39:B5:3541:G:H5'	1.85	0.58
39:B5:3557:A2M:HM'2	39:B5:3558:C:H5'	1.85	0.58
39:B5:4627:C:O2	39:B5:4670:G:N2	2.27	0.58
1:A2:523:A:H5''	21:AI:145:PRO:HD2	1.85	0.58
39:B5:67:C:OP2	39:B5:312:G:N2	2.31	0.58
39:B5:1653:C:O2'	47:BF:176:ARG:NH2	2.36	0.58
51:BJ:144:LYS:O	51:BJ:148:THR:OG1	2.20	0.58
85:Bt:10:ILE:HG12	85:Bt:65:GLN:HG2	1.84	0.58
1:A2:469:A2M:HM'2	1:A2:470:A:H5'	1.85	0.58
16:Ad:11:ARG:HA	16:Ad:28:ALA:HB2	1.85	0.58
67:BZ:92:ASP:HB3	67:BZ:95:VAL:HG12	1.84	0.58
30:Ar:16:LEU:HD21	30:Ar:72:GLN:HE21	1.68	0.58
39:B5:2685:G:HO2'	87:B5:4917:SPD:HN6	1.50	0.58
39:B5:3450:A2M:HM'2	39:B5:3451:A:H5'	1.84	0.58
43:BB:291:TYR:HB3	43:BB:298:LEU:HD11	1.84	0.58
73:Bf:43:LEU:O	73:Bf:109:ARG:NH1	2.33	0.58
26:An:101:GLY:HA3	26:An:134:PRO:HG2	1.86	0.58
39:B5:4287:G:N2	39:B5:4290:A:OP2	2.32	0.58
1:A2:1148:C:OP1	6:AE:6:ARG:NH1	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Af:58:LYS:HA	18:Af:107:SER:HB2	1.84	0.58
23:Ak:119:ASP:O	23:Ak:147:LYS:NZ	2.34	0.58
27:Ao:44:ARG:HH21	27:Ao:53:GLN:HE21	1.50	0.58
39:B5:3562:A2M:HM'2	39:B5:3563:U:H5'	1.86	0.58
41:B8:102:G:OP2	41:B8:104:A:O2'	2.22	0.58
65:BX:82:THR:HG22	65:BX:155:ILE:HG23	1.85	0.58
1:A2:35:C:H2'	1:A2:36:PSU:H6	1.69	0.58
39:B5:1217:G:H4'	46:BE:77:ALA:HB2	1.85	0.58
39:B5:1937:A:N3	39:B5:1958:C:O2'	2.32	0.58
39:B5:2103:C:O2	83:Br:99:LYS:NZ	2.35	0.58
45:BD:62:CYS:HB3	45:BD:105:LEU:HD22	1.85	0.58
42:BA:101:VAL:HG22	42:BA:165:VAL:HG22	1.85	0.57
1:A2:612:G:H4'	5:AD:91:LEU:HD21	1.85	0.57
1:A2:1293:C:N3	4:AC:138:ARG:NH2	2.48	0.57
12:AZ:8:LEU:HD11	33:Au:39:VAL:HG11	1.86	0.57
36:Ax:117:VAL:HG11	36:Ax:125:VAL:HG21	1.86	0.57
39:B5:4416:C:O2'	39:B5:4418:A:OP2	2.18	0.57
16:Ad:45:ILE:HA	16:Ad:61:VAL:HG11	1.86	0.57
21:Ai:107:GLU:O	21:Ai:113:GLN:NE2	2.38	0.57
39:B5:1334:G:N2	39:B5:1337:G:OP2	2.34	0.57
47:BF:126:LYS:HB2	61:BT:133:ALA:HB3	1.86	0.57
86:Bv:183:ILE:HD13	86:Bv:206:ILE:HD13	1.85	0.57
7:AF:78:ALA:HB3	7:AF:90:TRP:HB2	1.85	0.57
63:BV:69:LYS:NZ	63:BV:71:GLU:OE2	2.38	0.57
67:BZ:50:PRO:HD3	67:BZ:68:ILE:HG12	1.86	0.57
17:Ae:129:GLY:HA3	17:Ae:135:ARG:HH22	1.70	0.57
19:Ag:34:SER:HA	19:Ag:37:LYS:HB2	1.85	0.57
29:Aq:44:LYS:HG3	29:Aq:47:ARG:HH21	1.69	0.57
39:B5:3702:G:HO2'	86:Bv:31:THR:HG1	1.51	0.57
39:B5:4403:U:H3	87:B5:4917:SPD:H82	1.69	0.57
18:Af:161:PRO:HD3	64:BW:84:GLY:HA2	1.84	0.57
20:Ah:130:THR:OG1	20:Ah:132:GLU:OE1	2.23	0.57
39:B5:88:A:N7	58:BQ:173:LYS:NZ	2.52	0.57
1:A2:64:A:H2	1:A2:83:A:H62	1.50	0.57
1:A2:437:OMG:HM22	1:A2:438:G:H5'	1.86	0.57
1:A2:944:U:O2'	26:An:135:ILE:O	2.22	0.57
86:Bv:36:ILE:HD11	86:Bv:165:LEU:HD12	1.86	0.57
39:B5:308:G:OP2	39:B5:308:G:N2	2.30	0.57
39:B5:1919:U:O4	85:Bt:57:ARG:NH2	2.38	0.57
39:B5:2194:OMC:HM22	39:B5:2195:U:H5'	1.86	0.57
60:BS:127:MET:HG2	61:BT:153:PRO:HB2	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:Bo:59:LYS:NZ	81:Bo:61:LYS:O	2.37	0.57
1:A2:630:A:O2'	1:A2:632:U:OP1	2.23	0.57
11:AT:20:G:OP2	51:BJ:58:ARG:NH2	2.38	0.57
39:B5:382:G:N1	39:B5:385:A:OP2	2.37	0.57
86:Bv:204:LEU:HD22	86:Bv:216:LEU:HD23	1.87	0.57
12:AZ:37:TYR:OH	12:AZ:57:LYS:NZ	2.35	0.56
16:Ad:124:CYS:HB3	16:Ad:141:THR:HB	1.87	0.56
40:B7:55:A:O2'	51:BJ:151:ILE:O	2.19	0.56
15:Ac:64:ARG:NH1	22:Aj:73:ASN:OD1	2.37	0.56
1:A2:74:G:H2'	1:A2:75:G:H8	1.69	0.56
1:A2:417:U:HO2'	1:A2:653:U:HO2'	1.52	0.56
1:A2:1032:A2M:HM'2	1:A2:1033:C:H5'	1.87	0.56
13:Aa:189:ILE:HB	13:Aa:190:PRO:HD3	1.86	0.56
15:Ac:70:THR:HG22	15:Ac:86:LEU:HD13	1.88	0.56
17:Ae:58:ALA:HB3	17:Ae:62:ARG:HH21	1.71	0.56
20:Ah:56:ARG:NH1	20:Ah:180:GLY:O	2.38	0.56
30:Ar:26:ILE:HG13	30:Ar:45:LEU:HD21	1.87	0.56
39:B5:228:C:O2'	66:BY:14:ASN:ND2	2.38	0.56
39:B5:1763:G:H5''	61:BT:35:LYS:HE3	1.87	0.56
42:BA:140:ASN:ND2	42:BA:143:THR:OG1	2.38	0.56
52:BK:4379:TYR:HB3	79:Bl:46:ARG:HH12	1.71	0.56
85:Bt:63:THR:HB	85:Bt:70:GLN:HB2	1.86	0.56
27:Ao:123:TYR:OH	30:Ar:124:ARG:NH1	2.38	0.56
39:B5:3669:C:H1'	55:BN:125:SER:HB3	1.88	0.56
39:B5:4335:A:N1	39:B5:4367:C:O2'	2.34	0.56
1:A2:1704:OMC:HM22	1:A2:1705:C:H5'	1.88	0.56
14:Ab:102:LEU:HD22	14:Ab:130:ILE:HG12	1.88	0.56
39:B5:3420:U:OP2	42:BA:198:ARG:NH2	2.37	0.56
40:B7:6:C:H4'	45:BD:52:ILE:HD13	1.87	0.56
65:BX:73:HIS:CD2	65:BX:115:LYS:HD3	2.40	0.56
1:A2:912:C:H41	59:BR:173:ARG:HH12	1.54	0.56
1:A2:1092:C:O2'	34:Av:2:VAL:N	2.34	0.56
48:BG:83:PHE:HA	48:BG:183:ILE:HD13	1.88	0.56
85:Bt:116:MET:HG3	85:Bt:132:ILE:HD11	1.87	0.56
1:A2:1390:C:OP1	29:Aq:43:SER:OG	2.20	0.56
12:AZ:33:GLN:HB3	12:AZ:154:LEU:HD12	1.87	0.56
33:Au:43:THR:OG1	33:Au:45:ARG:NH1	2.39	0.56
39:B5:3843:G:H4'	39:B5:3844:C:H5'	1.86	0.56
1:A2:1532:A:H4'	1:A2:1606:G:H4'	1.88	0.56
1:A2:434:A:H5''	20:Ah:22:HIS:HB3	1.88	0.55
53:BL:75:GLY:O	53:BL:102:ARG:NH1	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:BU:100:LEU:HD13	62:BU:112:LEU:HD23	1.87	0.55
63:BV:21:PRO:HA	63:BV:54:ALA:HA	1.88	0.55
7:AF:87:LEU:HD21	7:AF:108:VAL:HG11	1.89	0.55
39:B5:1224:C:O2'	44:BC:321:ASN:OD1	2.24	0.55
39:B5:1638:PSU:OP1	68:Ba:44:ASN:ND2	2.36	0.55
39:B5:3432:C:O2'	39:B5:3506:A:N3	2.35	0.55
39:B5:4269:A2M:H5''	39:B5:4270:G:H5'	1.88	0.55
1:A2:1256:G:OP1	1:A2:1257:G:O2'	2.23	0.55
19:Ag:57:ARG:NH2	19:Ag:89:GLY:O	2.38	0.55
19:Ag:65:PRO:HD2	19:Ag:68:GLN:HE21	1.70	0.55
20:Ah:116:HIS:O	20:Ah:152:ARG:NH2	2.39	0.55
39:B5:2499:U:H5''	67:BZ:38:TYR:HB3	1.89	0.55
19:Ag:144:ILE:HB	34:Av:52:ILE:HB	1.88	0.55
24:Al:75:ASN:N	24:Al:75:ASN:OD1	2.38	0.55
39:B5:1546:U:OP2	39:B5:2699:C:O2'	2.16	0.55
39:B5:3812:G:O6	42:BA:72:ARG:NH2	2.37	0.55
39:B5:4705:A:H5'	43:BB:128:LYS:HG3	1.88	0.55
44:BC:221:PHE:HB3	44:BC:227:ILE:HG21	1.87	0.55
78:Bk:57:LYS:NZ	78:Bk:68:GLU:OE2	2.30	0.55
1:A2:642:A:O2'	1:A2:646:C:OP1	2.23	0.55
39:B5:3619:OMC:HM22	39:B5:3620:G:H5'	1.87	0.55
39:B5:3781:A:H5''	86:Bv:213:PRO:HD3	1.89	0.55
39:B5:4366:OMU:HM22	39:B5:4367:C:H5'	1.87	0.55
60:BS:154:LEU:HB3	60:BS:157:ARG:HD3	1.89	0.55
10:Al:9:N:H4'	10:Al:46:N:H5'	1.89	0.55
39:B5:186:G:N2	39:B5:186:G:OP2	2.37	0.55
39:B5:1665:U:H5'	47:BF:134:ILE:HD11	1.87	0.55
24:Al:49:LEU:HB3	24:Al:111:VAL:HB	1.89	0.55
39:B5:1955:C:H2'	39:B5:1956:A:H8	1.71	0.55
45:BD:125:VAL:HG11	45:BD:199:ILE:HG21	1.89	0.55
62:BU:111:GLU:OE2	62:BU:113:ARG:NE	2.32	0.55
64:BW:96:GLN:O	64:BW:101:ARG:NH2	2.40	0.55
85:Bt:80:LEU:HD13	85:Bt:112:ILE:HG23	1.88	0.55
86:Bv:73:HIS:ND1	86:Bv:144:MET:SD	2.80	0.55
18:Af:5:ILE:HG12	18:Af:111:LEU:HB2	1.89	0.55
28:Ap:53:GLU:OE1	28:Ap:85:ARG:NH2	2.38	0.55
39:B5:407:A:O2'	39:B5:410:A:OP1	2.24	0.55
39:B5:329:A:OP2	87:B5:4907:SPD:N10	2.40	0.55
39:B5:1988:G:HO2'	39:B5:3616:PSU:HO2'	1.54	0.55
45:BD:83:LEU:HB3	45:BD:88:VAL:HB	1.89	0.55
86:Bv:15:ARG:HH21	86:Bv:18:LEU:HB3	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A2:75:G:O2'	1:A2:77:A:OP1	2.24	0.55
1:A2:920:A:O2'	87:A2:1906:SPD:N1	2.40	0.55
1:A2:1680:A:H2'	17:Ae:60:ARG:HD2	1.89	0.55
39:B5:1341:A:N1	39:B5:1453:G:O2'	2.38	0.55
42:BA:3:ARG:HG2	42:BA:207:VAL:HG22	1.88	0.55
7:AF:214:GLY:HA2	7:AF:236:ILE:HG13	1.90	0.54
24:Al:25:ALA:O	24:Al:30:GLY:N	2.35	0.54
39:B5:793:C:N3	39:B5:794:G:N1	2.54	0.54
39:B5:1639:A:OP1	68:Ba:47:LYS:NZ	2.38	0.54
41:B8:81:C:O2'	75:Bh:2:ALA:N	2.36	0.54
1:A2:142:C:N4	1:A2:330:G:OP1	2.37	0.54
1:A2:191:A:H62	1:A2:208:G:H21	1.55	0.54
1:A2:1594:C:H1'	31:As:12:GLN:HE22	1.72	0.54
13:Aa:71:LEU:HD11	13:Aa:189:ILE:HG23	1.88	0.54
39:B5:184:U:H3	39:B5:253:G:H22	1.56	0.54
44:BC:218:VAL:HA	44:BC:229:LEU:HG	1.89	0.54
1:A2:1018:U:OP1	25:Am:62:GLN:NE2	2.41	0.54
1:A2:1547:G:H5'	28:Ap:18:THR:HG21	1.89	0.54
1:A2:1598:C:H4'	1:A2:1604:G:C6	2.43	0.54
12:AZ:177:MET:SD	12:AZ:180:ARG:NH2	2.81	0.54
14:Ab:196:ILE:HB	14:Ab:223:TYR:HB2	1.89	0.54
57:BP:138:PRO:HB3	57:BP:140:MET:HE3	1.88	0.54
1:A2:1448:OMG:HM22	1:A2:1449:A:H5'	1.90	0.54
1:A2:1837:G:OP1	92:A2:2102:HOH:O	2.19	0.54
81:Bo:26:TYR:HB3	81:Bo:67:VAL:HB	1.89	0.54
1:A2:167:G:O3'	64:BW:80:ARG:NH1	2.41	0.54
39:B5:3628:C:O2'	43:BB:268:ARG:NH1	2.37	0.54
51:BJ:14:GLU:OE2	51:BJ:16:ARG:NH2	2.29	0.54
59:BR:44:LEU:HD22	59:BR:49:LEU:HD12	1.89	0.54
60:BS:74:ARG:O	60:BS:76:LYS:NZ	2.37	0.54
86:Bv:85:MET:HE2	86:Bv:93:LEU:HD21	1.90	0.54
39:B5:734:G:OP2	54:BM:71:LYS:NZ	2.39	0.54
43:BB:161:ARG:HG2	43:BB:184:GLN:HA	1.88	0.54
85:Bt:32:ILE:HB	85:Bt:35:LEU:HD11	1.90	0.54
86:Bv:138:LEU:HD21	86:Bv:147:LYS:HG2	1.90	0.54
1:A2:380:C:O2	20:Ah:5:ARG:NE	2.41	0.54
3:AB:27:CYS:SG	17:Ae:126:THR:HG21	2.48	0.54
7:AF:11:LEU:HB2	7:AF:307:VAL:HB	1.89	0.54
39:B5:2515:C:OP1	82:Bp:44:LYS:NZ	2.35	0.54
86:Bv:94:ASN:O	86:Bv:97:LYS:NZ	2.36	0.54
1:A2:1286:G:H1	24:Al:57:ASP:HB2	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Af:98:ARG:NH2	18:Af:103:ASP:OD1	2.37	0.54
39:B5:788:G:H2'	39:B5:789:G:H8	1.71	0.54
39:B5:1772:G:OP1	61:BT:120:LYS:NZ	2.41	0.54
2:AA:67:THR:OG1	2:AA:70:LYS:O	2.26	0.54
3:AB:32:VAL:HG11	3:AB:56:LEU:HD12	1.90	0.54
5:AD:83:VAL:HG22	35:Aw:68:LYS:HE2	1.90	0.54
7:AF:120:ILE:O	7:AF:132:TRP:N	2.38	0.54
11:AT:29:A:H4'	30:Ar:148:VAL:HG11	1.89	0.54
39:B5:1341:A:O2'	39:B5:1422:C:O2'	2.19	0.54
39:B5:1859:C:H3'	39:B5:1860:C:H5''	1.89	0.54
64:BW:81:ALA:HB2	64:BW:87:LEU:HB2	1.90	0.54
83:Br:26:SER:OG	83:Br:28:GLU:OE1	2.17	0.54
1:A2:521:A:O2'	1:A2:826:A:N3	2.41	0.54
1:A2:1417:C:OP1	31:As:129:ARG:NH1	2.41	0.54
7:AF:236:ILE:HG12	7:AF:252:THR:HG22	1.89	0.54
15:Ac:123:LEU:HD22	15:Ac:152:PHE:HB3	1.89	0.54
24:Al:91:LEU:HD22	24:Al:106:CYS:HB2	1.90	0.54
44:BC:140:LYS:HE3	44:BC:245:HIS:HB2	1.90	0.54
45:BD:41:LYS:NZ	61:BT:32:ARG:O	2.31	0.54
1:A2:35:C:H5''	1:A2:580:C:H5''	1.89	0.53
6:AE:3:LYS:NZ	6:AE:8:ASN:OD1	2.41	0.53
12:AZ:77:ILE:HD11	12:AZ:99:ILE:HD12	1.90	0.53
39:B5:2739:G:OP1	59:BR:136:ARG:NH1	2.42	0.53
42:BA:117:GLU:HG2	42:BA:124:GLY:H	1.73	0.53
84:Bs:48:ARG:HH11	85:Bt:123:ARG:HG2	1.73	0.53
84:Bs:68:HIS:HB3	84:Bs:75:LEU:HD22	1.89	0.53
1:A2:126:G:OP2	18:Af:195:LYS:NZ	2.37	0.53
1:A2:153:G:N3	18:Af:13:GLN:NE2	2.55	0.53
18:Af:138:ALA:HA	18:Af:176:ILE:HD11	1.90	0.53
39:B5:239:C:OP1	66:BY:46:SER:OG	2.27	0.53
39:B5:1223:A:O2'	39:B5:1225:G:N7	2.39	0.53
39:B5:1458:A:H62	58:BQ:87:THR:HG21	1.73	0.53
39:B5:2302:G:N2	39:B5:2305:C:OP2	2.41	0.53
72:Be:117:GLN:O	83:Br:119:ARG:NH2	2.41	0.53
39:B5:1105:C:O2	69:Bb:91:ARG:NE	2.35	0.53
39:B5:1879:G:H22	39:B5:4180:C:H5''	1.73	0.53
48:BG:229:ARG:NE	48:BG:232:GLU:OE2	2.41	0.53
9:AH:3464:U:O2'	9:AH:3466:U:OP1	2.25	0.53
12:AZ:184:ARG:HD3	12:AZ:191:ARG:HG2	1.91	0.53
17:Ae:63:LYS:HD2	17:Ae:71:ARG:HH12	1.74	0.53
39:B5:4416:C:O2'	63:BV:15:ARG:NH2	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:Bt:14:TYR:O	85:Bt:31:LYS:NZ	2.42	0.53
85:Bt:18:THR:OG1	85:Bt:21:GLU:O	2.25	0.53
86:Bv:94:ASN:HB2	86:Bv:123:ILE:HB	1.90	0.53
1:A2:78:C:OP1	18:Af:159:ARG:NH2	2.42	0.53
18:Af:2:LYS:HB3	18:Af:15:LEU:HD11	1.89	0.53
20:Ah:57:ALA:HB2	20:Ah:183:GLY:HA2	1.90	0.53
26:An:151:LEU:O	92:An:301:HOH:O	2.17	0.53
39:B5:2651:G:O3'	59:BR:60:ARG:NH1	2.41	0.53
53:BL:178:ALA:N	68:Ba:134:GLU:OE2	2.38	0.53
1:A2:485:A2M:O5'	1:A2:485:A2M:H8	2.09	0.53
1:A2:1606:G:OP1	31:As:84:ARG:NH2	2.41	0.53
39:B5:1453:G:OP1	58:BQ:150:ARG:NH1	2.42	0.53
39:B5:1776:A:OP1	61:BT:108:ARG:NH1	2.41	0.53
39:B5:4138:OMG:HM21	39:B5:4140:A:H2'	1.91	0.53
1:A2:905:A:O2'	23:Ak:48:LYS:NZ	2.41	0.53
1:A2:1311:U:H5''	4:AC:130:VAL:HG13	1.89	0.53
7:AF:163:PRO:HB2	7:AF:179:LEU:HB3	1.90	0.53
87:A2:1903:SPD:N1	30:Ar:133:GLY:O	2.39	0.53
5:AD:86:VAL:HA	5:AD:89:GLN:HE21	1.73	0.53
22:Aj:61:GLN:HE21	22:Aj:62:PHE:H	1.55	0.53
56:BO:61:ARG:HA	56:BO:70:PRO:HD2	1.90	0.53
17:Ae:49:LEU:HD12	28:Ap:50:LYS:HG2	1.91	0.53
28:Ap:34:VAL:HG22	28:Ap:70:VAL:HB	1.91	0.53
39:B5:4073:C:OP1	61:BT:70:HIS:NE2	2.42	0.53
39:B5:4480:A:H61	39:B5:4704:U:H3	1.56	0.53
42:BA:137:ILE:HD11	42:BA:149:LYS:HB2	1.91	0.53
1:A2:90:G:OP2	87:A2:1904:SPD:N10	2.42	0.53
1:A2:74:G:H1	18:Af:171:THR:H	1.58	0.52
1:A2:1118:C:O2'	1:A2:1119:C:O4'	2.27	0.52
21:Ai:170:PRO:O	21:Ai:175:ARG:NH1	2.42	0.52
39:B5:1737:G:O2'	61:BT:60:LYS:NZ	2.42	0.52
45:BD:128:ASP:O	45:BD:164:LYS:NZ	2.38	0.52
67:BZ:12:LEU:HB2	67:BZ:81:MET:HB3	1.90	0.52
1:A2:1034:G:N1	1:A2:1081:A:O2'	2.35	0.52
7:AF:40:ILE:HB	7:AF:59:LEU:HB2	1.91	0.52
19:Ag:143:ARG:HB2	19:Ag:155:LYS:HB2	1.91	0.52
35:Aw:93:PHE:O	35:Aw:140:ARG:NH1	2.42	0.52
39:B5:1072:C:H1'	39:B5:1074:C:C2	2.44	0.52
49:BH:44:GLU:HB3	49:BH:58:ASP:HB2	1.90	0.52
12:AZ:77:ILE:HG13	12:AZ:99:ILE:HB	1.91	0.52
39:B5:1940:G:N2	39:B5:1955:C:O2	2.26	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:BR:106:LEU:HD13	59:BR:138:LEU:HD21	1.91	0.52
24:Al:89:VAL:HG11	24:Al:109:VAL:HG11	1.92	0.52
39:B5:2386:A:H2'	39:B5:2387:G:C8	2.45	0.52
39:B5:4068:G:N2	39:B5:4071:A:OP2	2.41	0.52
39:B5:4745:U:H4'	39:B5:4746:A:H5'	1.90	0.52
75:Bh:13:LYS:NZ	75:Bh:16:GLU:OE2	2.34	0.52
1:A2:956:A:N1	1:A2:969:U:O2'	2.39	0.52
34:Av:104:LEU:HD23	34:Av:125:ILE:HA	1.92	0.52
1:A2:1663:U:O4	1:A2:1664:A:N6	2.41	0.52
39:B5:1394:U:O2'	47:BF:33:ARG:NE	2.35	0.52
39:B5:1789:A:OP2	53:BL:5:ARG:NH2	2.43	0.52
39:B5:1933:C:H2'	39:B5:1934:G:H8	1.75	0.52
39:B5:4727:U:OP2	43:BB:123:HIS:ND1	2.38	0.52
84:Bs:125:ALA:HA	84:Bs:154:ILE:HB	1.92	0.52
1:A2:1014:U:OP1	1:A2:1130:G:O2'	2.26	0.52
63:BV:13:LYS:HB3	63:BV:128:LEU:HD11	1.92	0.52
84:Bs:32:ALA:O	84:Bs:85:ASN:ND2	2.42	0.52
1:A2:68:A:OP2	18:Af:164:LYS:NZ	2.38	0.52
12:AZ:17:LYS:HB3	12:AZ:173:LEU:HD11	1.91	0.52
13:Aa:28:LYS:HB3	13:Aa:48:LEU:HD11	1.92	0.52
39:B5:1458:A:H4'	39:B5:1459:G:H5'	1.90	0.52
57:BP:40:HIS:NE2	57:BP:110:ASP:O	2.38	0.52
60:BS:15:ARG:HB3	60:BS:27:LEU:HD23	1.91	0.52
86:Bv:128:LEU:HD13	86:Bv:135:PRO:HD3	1.92	0.52
17:Ae:102:LEU:HD21	37:Ay:100:VAL:HG21	1.91	0.52
24:Al:11:VAL:HG13	24:Al:13:ASP:H	1.74	0.52
32:At:48:LEU:HD22	32:At:93:SER:HB3	1.92	0.52
39:B5:1070:U:O2	45:BD:286:SER:OG	2.24	0.52
39:B5:3894:C:OP1	67:BZ:59:LYS:NZ	2.39	0.52
65:BX:64:SER:HB2	75:Bh:69:LEU:HD13	1.91	0.52
71:Bd:38:PHE:HB3	71:Bd:78:ARG:HG2	1.92	0.52
84:Bs:65:ILE:HG12	84:Bs:75:LEU:HD23	1.91	0.52
1:A2:1567:G:N7	31:As:101:ARG:NH2	2.57	0.52
39:B5:364:G:O6	77:Bj:55:ARG:NH2	2.35	0.52
39:B5:519:C:H2'	39:B5:520:G:C8	2.45	0.52
39:B5:2552:C:OP2	59:BR:43:LYS:NZ	2.34	0.52
39:B5:4361:C:H5''	43:BB:357:ARG:NE	2.25	0.52
41:B8:75:OMG:OP2	66:BY:74:TYR:OH	2.28	0.52
1:A2:1500:U:H4'	15:Ac:176:LEU:HD13	1.92	0.51
1:A2:1690:C:OP1	87:A2:1901:SPD:N1	2.42	0.51
9:AH:3475:G:H5'	15:Ac:117:ARG:HH21	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:Ay:68:ILE:HB	37:Ay:109:TYR:HB2	1.91	0.51
39:B5:2330:G:H1'	41:B8:125:C:H1'	1.92	0.51
39:B5:4151:G:OP2	50:BI:7:ARG:NH2	2.40	0.51
50:BI:53:VAL:HG11	61:BT:158:PHE:HZ	1.75	0.51
86:Bv:35:GLN:HB2	86:Bv:205:TYR:HB2	1.90	0.51
86:Bv:65:VAL:HG22	86:Bv:109:ALA:HB3	1.91	0.51
39:B5:2110:U:OP1	83:Br:37:SER:OG	2.24	0.51
39:B5:4316:G:H2'	39:B5:4317:A2M:H8	1.92	0.51
84:Bs:20:LEU:HD22	84:Bs:52:VAL:HG11	1.92	0.51
1:A2:65:C:C6	18:Af:174:PRO:HB3	2.45	0.51
1:A2:1076:C:OP1	25:Am:107:LYS:NZ	2.44	0.51
1:A2:1229:A:H2'	1:A2:1230:G:C8	2.45	0.51
1:A2:1827:G:HO2'	39:B5:3491:A:HO2'	1.55	0.51
7:AF:42:MET:O	7:AF:56:GLN:N	2.42	0.51
15:Ac:68:GLU:HG3	22:Aj:93:THR:HG21	1.92	0.51
39:B5:1984:G:O6	39:B5:3602:C:O2'	2.28	0.51
39:B5:2552:C:H5''	59:BR:43:LYS:HD2	1.91	0.51
39:B5:4639:C:O2'	39:B5:4641:C:OP2	2.23	0.51
49:BH:44:GLU:HG3	54:BM:2:VAL:HG22	1.91	0.51
1:A2:1817:G:N7	92:A2:2133:HOH:O	2.34	0.51
39:B5:1879:G:N2	39:B5:4180:C:OP1	2.43	0.51
41:B8:141:C:H5''	55:BN:60:VAL:HG11	1.92	0.51
57:BP:64:ASN:ND2	57:BP:80:GLN:OE1	2.44	0.51
83:Br:82:ILE:HG22	83:Br:89:THR:HG22	1.92	0.51
1:A2:1329:OMG:HM22	1:A2:1330:U:H5'	1.93	0.51
2:AA:11:SER:OG	2:AA:14:GLU:OE1	2.29	0.51
12:AZ:77:ILE:HG21	12:AZ:133:PRO:HG3	1.93	0.51
47:BF:53:ALA:HB2	47:BF:187:GLU:HG3	1.93	0.51
1:A2:64:A:OP1	18:Af:177:GLN:NE2	2.43	0.51
3:AB:29:GLN:NE2	3:AB:66:ARG:O	2.40	0.51
33:Au:32:ILE:HG12	33:Au:60:ARG:HD2	1.92	0.51
36:Ax:39:GLU:OE1	36:Ax:39:GLU:N	2.44	0.51
43:BB:95:THR:OG1	43:BB:98:GLY:O	2.25	0.51
84:Bs:32:ALA:HB1	84:Bs:35:VAL:HG21	1.92	0.51
17:Ae:167:LYS:NZ	17:Ae:175:ASP:OD2	2.31	0.51
39:B5:2684:G:N7	92:B5:5591:HOH:O	2.35	0.51
39:B5:3682:U:H2'	39:B5:3683:G:C8	2.45	0.51
80:Bm:94:MET:HG2	80:Bm:105:PRO:HA	1.93	0.51
1:A2:1674:U:O2'	17:Ae:84:GLY:O	2.24	0.51
3:AB:47:LYS:NZ	17:Ae:125:SER:O	2.40	0.51
39:B5:423:G:OP1	57:BP:62:ARG:NH1	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:B5:1624:A:OP1	69:Bb:18:ARG:NH1	2.43	0.51
39:B5:2678:A:O2'	43:BB:228:TYR:O	2.29	0.51
84:Bs:106:LYS:HB3	84:Bs:184:SER:HB3	1.91	0.51
5:AD:83:VAL:HG11	35:Aw:91:LEU:HB3	1.92	0.51
27:Ao:37:TYR:O	30:Ar:88:LYS:NZ	2.35	0.51
39:B5:4136:A:OP2	92:B5:5502:HOH:O	2.19	0.51
85:Bt:82:ILE:HA	85:Bt:85:LEU:HD12	1.92	0.51
85:Bt:95:GLN:HG3	85:Bt:98:ILE:HG12	1.92	0.51
1:A2:1544:U:H5''	28:Ap:37:ARG:HH12	1.75	0.51
35:Aw:70:VAL:HG11	35:Aw:94:ILE:HG21	1.91	0.51
39:B5:1509:A:OP1	82:Bp:5:THR:OG1	2.28	0.51
39:B5:2146:C:OP1	72:Be:107:ASN:ND2	2.39	0.51
45:BD:152:ARG:HG3	45:BD:154:THR:HG23	1.92	0.51
9:AH:3538:G:H2'	9:AH:3539:G:C8	2.47	0.50
37:Ay:111:ARG:HD2	37:Ay:114:LYS:HE3	1.93	0.50
39:B5:2507:G:H4'	39:B5:2520:G:H4'	1.92	0.50
39:B5:4508:G:OP2	56:BO:37:ARG:NH1	2.38	0.50
53:BL:91:ALA:HB1	53:BL:96:ILE:HB	1.93	0.50
85:Bt:52:ASP:OD1	85:Bt:52:ASP:N	2.42	0.50
1:A2:191:A:H3'	1:A2:192:C:H5''	1.94	0.50
1:A2:1524:C:H4'	30:Ar:148:VAL:HA	1.93	0.50
39:B5:1214:A:H61	39:B5:2054:G:H21	1.57	0.50
39:B5:1811:G:O2'	39:B5:3965:A:N3	2.40	0.50
39:B5:2741:G:OP2	59:BR:135:LYS:NZ	2.37	0.50
39:B5:3480:A:O2'	42:BA:223:SER:OG	2.27	0.50
39:B5:3497:G:O2'	39:B5:3499:C:N4	2.45	0.50
1:A2:64:A:O5'	18:Af:136:LYS:NZ	2.42	0.50
1:A2:231:A:H2'	1:A2:232:A:H8	1.76	0.50
39:B5:2161:G:OP2	72:Be:14:LYS:NZ	2.43	0.50
53:BL:80:GLU:OE2	53:BL:102:ARG:NH2	2.44	0.50
1:A2:28:U:H2'	1:A2:29:G:H8	1.76	0.50
1:A2:943:G:OP1	13:Aa:216:LYS:NZ	2.44	0.50
12:AZ:145:ILE:HG12	12:AZ:159:ILE:HB	1.92	0.50
20:Ah:67:TRP:NE1	20:Ah:191:GLU:OE2	2.39	0.50
39:B5:3694:A:N6	39:B5:3767:G:OP1	2.42	0.50
39:B5:3936:U:OP1	87:B5:4904:SPD:N10	2.45	0.50
39:B5:4636:G:O2'	39:B5:4666:G:N7	2.44	0.50
40:B7:117:G:H5''	45:BD:256:LYS:HD2	1.94	0.50
79:Bl:30:LYS:HB2	79:Bl:33:ASN:HB2	1.92	0.50
84:Bs:66:ARG:HA	84:Bs:69:LEU:HG	1.93	0.50
4:AC:107:LYS:HB3	4:AC:117:LEU:HD11	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:Aq:16:ILE:HG22	29:Aq:24:LEU:HD11	1.93	0.50
39:B5:1701:C:H2'	39:B5:1702:C:C6	2.45	0.50
39:B5:4283:C:H2'	39:B5:4284:G:C8	2.46	0.50
40:B7:23:A:N3	40:B7:118:C:O2'	2.41	0.50
48:BG:73:ARG:NH1	48:BG:241:VAL:O	2.44	0.50
58:BQ:119:LYS:HE3	58:BQ:121:LEU:HD21	1.93	0.50
1:A2:74:G:H1	18:Af:171:THR:N	2.09	0.50
1:A2:799:G:OP1	19:Ag:110:THR:OG1	2.29	0.50
1:A2:1684:C:H5'	17:Ae:130:ARG:HD2	1.93	0.50
7:AF:195:LEU:HA	7:AF:211:GLY:HA3	1.93	0.50
16:Ad:44:LEU:HD21	16:Ad:72:ILE:HD11	1.93	0.50
39:B5:1215:G:H5''	69:Bb:110:ALA:HB1	1.92	0.50
72:Be:89:LEU:HD13	72:Be:118:LEU:HD22	1.93	0.50
1:A2:571:C:O2'	36:Ax:34:THR:O	2.25	0.50
39:B5:519:C:H2'	39:B5:520:G:H8	1.77	0.50
39:B5:4510:U:HO2'	60:BS:174:THR:HG1	1.55	0.50
43:BB:261:ARG:HB2	56:BO:64:THR:HG21	1.93	0.50
50:BI:145:LYS:HE2	50:BI:167:ILE:HG13	1.94	0.50
51:BJ:13:ARG:O	51:BJ:136:ARG:NH1	2.45	0.50
34:Av:14:ILE:HD11	34:Av:27:ILE:HD11	1.94	0.50
39:B5:3886:G:H2'	39:B5:3887:G:H8	1.77	0.50
1:A2:381:G:N1	1:A2:384:G:OP2	2.31	0.50
7:AF:12:LYS:HG2	7:AF:306:LEU:HD22	1.94	0.50
20:Ah:89:GLU:OE1	20:Ah:92:ARG:NH2	2.45	0.50
39:B5:788:G:H2'	39:B5:789:G:C8	2.46	0.50
39:B5:835:G:OP1	54:BM:23:LYS:NZ	2.40	0.50
39:B5:992:C:OP1	39:B5:1106:U:O2'	2.25	0.50
39:B5:4060:C:O2'	69:Bb:36:ASP:OD1	2.27	0.50
53:BL:62:PRO:O	53:BL:63:THR:OG1	2.28	0.50
59:BR:28:GLU:HG3	59:BR:49:LEU:HD22	1.93	0.50
60:BS:147:ASP:HB3	60:BS:150:ILE:HB	1.94	0.50
66:BY:31:SER:HA	66:BY:48:PRO:HA	1.94	0.50
1:A2:1624:A:OP2	87:A2:1903:SPD:N1	2.45	0.49
12:AZ:176:TRP:HE1	12:AZ:197:VAL:HG23	1.77	0.49
28:Ap:101:ASP:OD1	28:Ap:102:GLU:N	2.44	0.49
39:B5:2469:U:O4	62:BU:97:ARG:NH1	2.38	0.49
39:B5:1673:G:HO2'	87:B5:4919:SPD:H101	1.57	0.49
39:B5:1936:U:OP2	85:Bt:123:ARG:NH1	2.45	0.49
1:A2:1513:C:H5''	8:AG:8:TRP:HZ3	1.77	0.49
25:Am:93:LYS:HA	25:Am:150:VAL:HG21	1.94	0.49
39:B5:398:A2M:H8	39:B5:398:A2M:O5'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:B5:3477:U:HO2'	42:BA:243:THR:H	1.59	0.49
57:BP:115:GLU:OE1	57:BP:151:THR:OG1	2.29	0.49
1:A2:869:G:OP2	1:A2:869:G:N2	2.35	0.49
21:Ai:170:PRO:HB3	21:Ai:174:LYS:HE3	1.93	0.49
39:B5:1568:A:H5'	42:BA:183:GLY:HA2	1.93	0.49
39:B5:1757:G:OP2	39:B5:1757:G:N2	2.35	0.49
46:BE:117:ARG:HH21	83:Br:87:ARG:HH22	1.59	0.49
85:Bt:133:LEU:HD11	85:Bt:151:ILE:HG13	1.94	0.49
15:Ac:132:LYS:HE3	15:Ac:191:PRO:HA	1.93	0.49
39:B5:4037:G:H5'	39:B5:4039:PSU:C6	2.47	0.49
49:BH:114:ILE:HB	49:BH:124:ARG:HB2	1.95	0.49
1:A2:99:A2M:HM'2	1:A2:100:U:H5'	1.95	0.49
7:AF:131:LEU:O	7:AF:139:LYS:N	2.42	0.49
39:B5:2691:G:O2'	39:B5:3570:U:O4	2.25	0.49
44:BC:315:LYS:HD2	47:BF:167:ALA:HB1	1.95	0.49
48:BG:99:ALA:HB1	48:BG:136:LEU:HD11	1.95	0.49
1:A2:589:G:OP2	1:A2:589:G:N2	2.40	0.49
1:A2:657:G:H5'	1:A2:663:G:N2	2.28	0.49
5:AD:83:VAL:HG12	35:Aw:89:GLY:HA2	1.95	0.49
9:AH:3511:C:H2'	9:AH:3512:A:H8	1.77	0.49
39:B5:2281:A:O2'	39:B5:2283:U:OP2	2.28	0.49
63:BV:13:LYS:HD2	63:BV:128:LEU:HD21	1.93	0.49
1:A2:1232:C:O2'	1:A2:1254:A:N6	2.46	0.49
1:A2:1843:4AC:O7	38:Az:4:LYS:NZ	2.39	0.49
15:Ac:39:VAL:HG22	15:Ac:48:ILE:HG22	1.95	0.49
20:Ah:162:LEU:HD11	20:Ah:191:GLU:HG2	1.93	0.49
39:B5:638:G:OP2	53:BL:162:LYS:NZ	2.32	0.49
39:B5:1907:G:H2'	39:B5:1908:G:C8	2.48	0.49
39:B5:2712:U:O2'	39:B5:2724:A:N7	2.43	0.49
45:BD:223:PHE:HB3	45:BD:226:TYR:HB2	1.95	0.49
47:BF:235:ARG:HB2	47:BF:238:GLN:HB2	1.95	0.49
50:BI:51:HIS:CD2	50:BI:168:SER:HB2	2.47	0.49
84:Bs:58:ASN:O	84:Bs:62:ARG:HG3	2.13	0.49
85:Bt:107:ASP:HA	85:Bt:110:VAL:HG12	1.94	0.49
8:AG:52:PHE:HB3	32:At:80:PHE:HB3	1.95	0.49
15:Ac:42:THR:OG1	15:Ac:45:ARG:O	2.20	0.49
28:Ap:89:SER:HB3	28:Ap:112:LEU:HD13	1.95	0.49
39:B5:1093:C:H2'	39:B5:1094:A:H8	1.77	0.49
39:B5:1284:OMC:HM22	39:B5:1285:U:H5'	1.95	0.49
39:B5:1671:C:H5''	61:BT:43:LYS:HD2	1.94	0.49
61:BT:18:PRO:HG2	61:BT:21:LYS:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:Bs:30:VAL:HG12	84:Bs:189:ILE:HG12	1.93	0.49
39:B5:1227:G:N1	39:B5:2015:G:OP1	2.38	0.49
39:B5:4328:C:O2'	43:BB:99:LEU:O	2.24	0.49
53:BL:207:VAL:HG12	86:Bv:7:ARG:HH12	1.77	0.49
77:Bj:27:TYR:HA	77:Bj:34:CYS:HA	1.95	0.49
85:Bt:101:SER:HA	85:Bt:141:CYS:HA	1.94	0.49
1:A2:31:U:O2'	1:A2:644:A:N1	2.46	0.48
1:A2:1618:G:N1	1:A2:1621:A:OP2	2.45	0.48
7:AF:39:THR:HG22	7:AF:60:ARG:HG2	1.94	0.48
12:AZ:135:THR:O	12:AZ:138:SER:OG	2.28	0.48
16:Ad:151:ASP:HB3	16:Ad:154:ILE:HG13	1.95	0.48
20:Ah:26:LYS:HG2	20:Ah:29:LEU:HD23	1.96	0.48
42:BA:205:ASN:ND2	92:BA:403:HOH:O	2.45	0.48
43:BB:77:THR:HG21	43:BB:337:VAL:HG22	1.95	0.48
45:BD:196:ARG:NH2	45:BD:237:GLU:OE2	2.43	0.48
46:BE:45:HIS:ND1	46:BE:46:CYS:O	2.40	0.48
13:Aa:99:ASN:OD1	13:Aa:100:PHE:N	2.45	0.48
13:Aa:129:THR:OG1	13:Aa:131:ASP:OD1	2.29	0.48
39:B5:62:A:OP1	55:BN:172:ARG:NH1	2.47	0.48
39:B5:1093:C:H2'	39:B5:1094:A:C8	2.47	0.48
39:B5:1381:G:N1	39:B5:1413:C:OP2	2.36	0.48
39:B5:3450:A2M:H8	39:B5:3450:A2M:O5'	2.13	0.48
39:B5:3954:U:OP1	39:B5:4080:U:O2'	2.22	0.48
39:B5:4314:A:O3'	43:BB:21:ARG:NH2	2.45	0.48
39:B5:4367:C:OP1	63:BV:48:ARG:HD2	2.13	0.48
44:BC:60:HIS:HA	44:BC:92:PHE:HE1	1.78	0.48
1:A2:1805:OMU:HM22	1:A2:1806:G:H5'	1.95	0.48
1:A2:1864:A:OP2	6:AE:4:LYS:NZ	2.44	0.48
18:Af:102:VAL:HG13	18:Af:106:LEU:HD12	1.95	0.48
27:Ao:53:GLN:OE1	27:Ao:53:GLN:N	2.43	0.48
33:Au:38:GLU:OE2	33:Au:51:LYS:NZ	2.42	0.48
39:B5:1503:G:OP1	87:B5:4916:SPD:N10	2.46	0.48
39:B5:1572:G:H1'	39:B5:2356:A:N6	2.28	0.48
64:BW:63:GLN:OE1	64:BW:63:GLN:N	2.46	0.48
84:Bs:5:ASP:HB2	84:Bs:8:THR:HG22	1.96	0.48
5:AD:112:TYR:CG	21:Ai:33:GLY:HA3	2.48	0.48
39:B5:3628:C:HO2'	43:BB:268:ARG:HH12	1.62	0.48
86:Bv:26:ARG:HG3	86:Bv:30:GLU:HG3	1.94	0.48
1:A2:563:U:H2'	1:A2:564:G:C8	2.49	0.48
1:A2:1143:G:OP1	14:Ab:187:ARG:NH1	2.46	0.48
30:Ar:44:VAL:HG11	30:Ar:71:MET:HG3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:B5:1743:A:H5'	39:B5:1745:G:O4'	2.13	0.48
39:B5:4006:U:H2'	39:B5:4007:C:C6	2.48	0.48
67:BZ:51:ARG:HB2	67:BZ:65:ARG:HB3	1.94	0.48
17:Ae:19:LEU:HD21	17:Ae:69:VAL:HG11	1.96	0.48
25:Am:101:HIS:HA	25:Am:104:ARG:HH21	1.78	0.48
36:Ax:21:LYS:HB2	36:Ax:75:ILE:HB	1.95	0.48
39:B5:26:C:O2'	39:B5:338:A:N3	2.42	0.48
39:B5:1680:G:O6	40:B7:103:A:O2'	2.27	0.48
39:B5:4124:A:O2'	39:B5:4125:A:H2'	2.12	0.48
78:Bk:13:LEU:HD23	78:Bk:16:ARG:HH21	1.78	0.48
26:An:40:THR:HG21	26:An:74:ALA:HB2	1.95	0.48
35:Aw:60:LYS:HG3	35:Aw:116:PRO:HG3	1.96	0.48
39:B5:44:A:H5''	88:B5:4915:SPM:H71	1.95	0.48
44:BC:66:SER:HA	44:BC:77:PRO:HA	1.96	0.48
67:BZ:136:PHE:O	74:Bg:78:TYR:OH	2.27	0.48
1:A2:875:G:N3	19:Ag:114:GLN:NE2	2.58	0.48
1:A2:1651:A:H5''	28:Ap:139:ALA:HB2	1.95	0.48
14:Ab:254:ASP:HB2	33:Au:1:AME:HT22	1.96	0.48
16:Ad:100:ARG:HB2	16:Ad:114:ILE:HD13	1.95	0.48
21:Ai:152:ASP:OD1	21:Ai:152:ASP:N	2.42	0.48
32:At:41:ARG:O	32:At:45:GLU:HG2	2.14	0.48
39:B5:684:C:OP2	46:BE:114:LYS:NZ	2.35	0.48
39:B5:755:G:H1	39:B5:800:U:H3	1.61	0.48
39:B5:795:A:H3'	39:B5:796:C:C6	2.49	0.48
39:B5:2257:G:H2'	39:B5:2258:OMU:H6	1.94	0.48
39:B5:3974:OMG:H5''	39:B5:3975:U:O4'	2.14	0.48
39:B5:4663:C:O2	39:B5:4665:C:N4	2.47	0.48
45:BD:108:ARG:CZ	45:BD:253:TYR:HB2	2.44	0.48
56:BO:34:VAL:HG22	56:BO:103:LYS:HB2	1.95	0.48
1:A2:127:C:O2	16:Ad:134:LYS:NZ	2.43	0.48
1:A2:1846:A:H2'	1:A2:1847:G:C8	2.49	0.48
7:AF:73:SER:OG	7:AF:117:ASN:OD1	2.20	0.48
7:AF:101:PHE:CD2	7:AF:136:GLY:HA2	2.49	0.48
39:B5:2363:C:O2	39:B5:2483:G:N2	2.47	0.48
47:BF:153:ILE:HD12	47:BF:190:ILE:HG12	1.95	0.48
50:BI:61:SER:HA	50:BI:126:VAL:HG12	1.96	0.48
85:Bt:15:LEU:HD22	85:Bt:16:ARG:H	1.78	0.48
1:A2:445:G:O6	20:Ah:26:LYS:HE3	2.14	0.48
1:A2:1098:G:H4'	12:AZ:32:PHE:CD1	2.49	0.48
12:AZ:108:PHE:HB2	12:AZ:136:GLU:HG2	1.95	0.48
30:Ar:92:ASP:OD1	30:Ar:92:ASP:N	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Ax:57:VAL:HB	36:Ax:60:PHE:HE2	1.79	0.48
68:Ba:100:ILE:HG13	68:Ba:123:ILE:HB	1.95	0.48
84:Bs:55:MET:HG2	84:Bs:87:GLY:HA2	1.96	0.48
1:A2:43:U:OP2	1:A2:486:A:N6	2.34	0.47
1:A2:121:OMU:HM22	1:A2:122:G:H5'	1.95	0.47
1:A2:168:C:OP1	18:Af:131:ARG:NH2	2.46	0.47
16:Ad:87:MET:HE2	16:Ad:123:LEU:HB2	1.96	0.47
18:Af:20:ASP:OD2	18:Af:22:ARG:NH2	2.47	0.47
20:Ah:106:SER:HB3	20:Ah:171:LEU:HG	1.95	0.47
39:B5:74:G:H5'	53:BL:59:VAL:HB	1.96	0.47
39:B5:1480:A:N7	92:B5:5596:HOH:O	2.35	0.47
39:B5:2400:G:H1	39:B5:2413:U:H3	1.62	0.47
39:B5:2687:A:O2'	39:B5:4377:G:H4'	2.14	0.47
39:B5:4796:C:H2'	39:B5:4797:A:C8	2.48	0.47
44:BC:159:GLU:HA	44:BC:217:ILE:HB	1.95	0.47
53:BL:12:PRO:HB2	53:BL:14:PHE:HD2	1.79	0.47
71:Bd:23:ARG:HG2	71:Bd:121:ASN:HA	1.96	0.47
74:Bg:64:LEU:HD23	74:Bg:67:LEU:HD12	1.96	0.47
85:Bt:147:HIS:CD2	85:Bt:149:HIS:HB2	2.49	0.47
1:A2:658:U:O2	92:A2:2103:HOH:O	2.20	0.47
39:B5:439:G:O3'	73:Bf:91:ASN:ND2	2.47	0.47
39:B5:1922:A:H1'	39:B5:1949:A:H4'	1.95	0.47
39:B5:1934:G:O6	39:B5:1939:G:N2	2.47	0.47
39:B5:2225:A:N1	39:B5:2672:U:O2'	2.45	0.47
46:BE:193:HIS:HB3	46:BE:196:PHE:HD2	1.79	0.47
49:BH:92:MET:HE2	49:BH:179:ILE:HG22	1.95	0.47
86:Bv:114:GLU:N	86:Bv:138:LEU:O	2.44	0.47
1:A2:1038:G:H4'	1:A2:1846:A:H4'	1.96	0.47
1:A2:1607:G:N2	1:A2:1633:G:H1'	2.28	0.47
7:AF:107:ASP:OD1	7:AF:107:ASP:N	2.46	0.47
39:B5:1712:U:H2'	39:B5:1713:C:C6	2.48	0.47
39:B5:1922:A:H4'	39:B5:1923:A:C8	2.49	0.47
39:B5:1935:C:H42	39:B5:1939:G:H22	1.62	0.47
39:B5:2036:A:H3'	39:B5:2037:G:H5'	1.95	0.47
50:BI:91:LEU:HD12	50:BI:135:ILE:HG23	1.95	0.47
1:A2:1764:G:H2'	1:A2:1765:G:C8	2.49	0.47
11:AT:62:C:H2'	11:AT:63:G:H8	1.80	0.47
13:Aa:123:ALA:HB2	13:Aa:165:ARG:HG3	1.96	0.47
20:Ah:124:LYS:HE2	39:B5:4762:C:H5'	1.95	0.47
63:BV:107:ASN:OD1	63:BV:111:GLU:HG2	2.14	0.47
67:BZ:41:ALA:HB2	67:BZ:77:TYR:HE1	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:Bv:73:HIS:HA	86:Bv:144:MET:HE1	1.96	0.47
7:AF:119:GLN:HB3	7:AF:131:LEU:HD11	1.97	0.47
7:AF:278:SER:HB2	7:AF:281:ALA:HB3	1.96	0.47
12:AZ:198:MET:HG2	12:AZ:200:ASP:H	1.80	0.47
13:Aa:44:ILE:HD11	13:Aa:74:LEU:HD21	1.97	0.47
17:Ae:73:THR:O	17:Ae:89:THR:HG21	2.14	0.47
24:Al:41:ALA:HB1	24:Al:47:ALA:HB2	1.96	0.47
39:B5:1283:U:OP1	68:Ba:8:THR:OG1	2.31	0.47
39:B5:1478:A:N3	39:B5:4135:C:O2'	2.47	0.47
39:B5:2022:C:OP2	58:BQ:14:ARG:NH2	2.46	0.47
39:B5:2169:G:H5''	72:Be:127:ALA:HB2	1.95	0.47
39:B5:4620:U:C4	54:BM:113:MET:HG3	2.50	0.47
39:B5:4684:G:N1	73:Bf:3:GLY:O	2.40	0.47
1:A2:1299:G:H4'	27:Ao:78:THR:HA	1.97	0.47
1:A2:1809:U:H2'	1:A2:1810:A:C8	2.50	0.47
2:AA:23:ARG:O	34:Av:60:LYS:NZ	2.47	0.47
4:AC:102:VAL:HG21	24:Al:35:ILE:HG21	1.96	0.47
39:B5:1898:U:H1'	39:B5:1900:G:C2	2.49	0.47
47:BF:105:ARG:NH2	58:BQ:4:ASP:OD1	2.46	0.47
71:Bd:37:GLY:O	71:Bd:41:ARG:HG3	2.14	0.47
73:Bf:36:ARG:NH1	73:Bf:79:GLY:O	2.42	0.47
1:A2:192:C:H4'	1:A2:192:C:OP1	2.15	0.47
1:A2:642:A:OP1	21:Ai:40:LYS:NZ	2.42	0.47
1:A2:1294:A:H61	1:A2:1307:U:H3	1.62	0.47
2:AA:28:PRO:HG3	25:Am:17:PRO:HG3	1.95	0.47
6:AE:44:ILE:HD12	6:AE:65:PRO:HG2	1.96	0.47
37:Ay:79:ILE:HB	37:Ay:83:LEU:HD23	1.97	0.47
38:Az:23:ARG:HH22	39:B5:3514:5MC:P	2.37	0.47
39:B5:1672:G:N3	39:B5:3960:A:H2'	2.30	0.47
39:B5:3805:A:N1	39:B5:3917:C:N4	2.61	0.47
45:BD:119:TYR:OH	45:BD:139:PRO:O	2.33	0.47
51:BJ:15:LEU:HD12	51:BJ:165:TRP:HB2	1.96	0.47
54:BM:29:ASP:OD1	54:BM:30:VAL:N	2.47	0.47
60:BS:99:ASP:OD1	60:BS:100:LEU:N	2.45	0.47
84:Bs:30:VAL:HG21	84:Bs:187:LEU:HD13	1.97	0.47
85:Bt:35:LEU:HD12	85:Bt:37:LEU:H	1.79	0.47
85:Bt:125:LEU:HD12	85:Bt:164:ALA:HB3	1.95	0.47
86:Bv:21:ASN:HB2	86:Bv:26:ARG:HD3	1.96	0.47
1:A2:116:OMU:HM22	1:A2:117:C:H5'	1.96	0.47
7:AF:77:PHE:HB3	7:AF:89:LEU:HD11	1.97	0.47
17:Ae:40:ALA:HB1	17:Ae:45:TYR:CG	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:Aq:57:LEU:HD13	29:Aq:69:ILE:HD11	1.97	0.47
39:B5:136:U:O4	75:Bh:79:LYS:NZ	2.33	0.47
39:B5:639:G:H2'	39:B5:640:G:H8	1.80	0.47
48:BG:103:ARG:NH2	48:BG:192:ARG:O	2.48	0.47
67:BZ:95:VAL:HG13	67:BZ:96:VAL:HG23	1.96	0.47
70:Bc:37:MET:HE3	70:Bc:42:LYS:HB2	1.97	0.47
1:A2:35:C:H2'	1:A2:36:PSU:C6	2.50	0.47
1:A2:798:C:H2'	1:A2:799:G:C4	2.49	0.47
1:A2:1639:G:H4'	37:Ay:36:SER:HB3	1.96	0.47
2:AA:12:PRO:HB3	19:Ag:192:PHE:CG	2.50	0.47
16:Ad:125:LYS:H	16:Ad:142:HIS:HD2	1.63	0.47
20:Ah:113:TYR:OH	20:Ah:156:ALA:O	2.27	0.47
39:B5:696:U:H5'	46:BE:124:VAL:HG21	1.97	0.47
39:B5:1718:PSU:H2'	39:B5:1719:A:C8	2.50	0.47
39:B5:1943:U:H2'	39:B5:1944:G:C8	2.50	0.47
39:B5:3386:G:O2'	39:B5:3425:U:OP1	2.25	0.47
39:B5:3422:U:O2'	39:B5:3549:A:N3	2.36	0.47
39:B5:4089:U:O2'	81:Bo:31:ASP:OD1	2.33	0.47
47:BF:85:GLU:HG3	61:BT:135:PRO:HB3	1.95	0.47
69:Bb:56:LYS:O	69:Bb:60:ASN:ND2	2.36	0.47
1:A2:1063:A:OP1	87:A2:1905:SPD:H52	2.14	0.47
39:B5:1899:A:H1'	84:Bs:63:LYS:HD3	1.97	0.47
39:B5:3599:A2M:HM'3	39:B5:3612:G:N2	2.30	0.47
39:B5:4445:U:H1'	39:B5:4446:A:H5''	1.96	0.47
42:BA:206:PRO:HG3	42:BA:213:GLY:HA3	1.97	0.47
47:BF:240:ASN:O	47:BF:244:ARG:HG2	2.15	0.47
53:BL:42:ARG:HG3	53:BL:45:ARG:HH21	1.79	0.47
1:A2:1600:U:OP2	37:Ay:46:ASN:ND2	2.48	0.46
1:A2:1737:G:H2'	1:A2:1738:G:C8	2.51	0.46
2:AA:84:HIS:OXT	25:Am:19:ARG:NH1	2.48	0.46
20:Ah:205:ARG:NH1	39:B5:2736:U:O3'	2.48	0.46
39:B5:435:A:O2'	72:Be:26:ASP:OD2	2.28	0.46
39:B5:752:G:H1	39:B5:803:C:H42	1.62	0.46
39:B5:1276:C:H2'	39:B5:1277:A:C8	2.50	0.46
86:Bv:104:ALA:O	86:Bv:133:LYS:NZ	2.35	0.46
1:A2:1448:OMG:OP1	32:At:87:ARG:NH2	2.42	0.46
15:Ac:56:GLN:H	15:Ac:56:GLN:HG3	1.44	0.46
39:B5:1532:G:O2'	39:B5:1567:G:H4'	2.15	0.46
39:B5:2216:C:H5'	71:Bd:46:LEU:HD22	1.96	0.46
86:Bv:37:SER:HB2	86:Bv:202:ARG:HB2	1.96	0.46
1:A2:49:C:N4	1:A2:474:A:OP2	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A2:614:G:N2	1:A2:627:G:OP1	2.48	0.46
1:A2:920:A:OP2	25:Am:64:ARG:NH2	2.47	0.46
13:Aa:86:LEU:HB3	13:Aa:98:THR:HB	1.97	0.46
39:B5:48:G:OP1	55:BN:192:TRP:NE1	2.40	0.46
39:B5:238:C:OP2	66:BY:45:ARG:NH2	2.49	0.46
39:B5:1449:U:H2'	39:B5:1450:G:H8	1.79	0.46
7:AF:133:ASN:HD21	7:AF:137:VAL:HB	1.80	0.46
8:AG:22:ARG:NH1	15:Ac:16:ILE:HG21	2.30	0.46
35:Aw:54:LYS:HE3	35:Aw:91:LEU:HG	1.98	0.46
39:B5:150:U:OP2	48:BG:200:THR:OG1	2.24	0.46
39:B5:4051:G:O5'	61:BT:83:LYS:NZ	2.48	0.46
39:B5:4440:G:H4'	49:BH:71:ARG:HH12	1.80	0.46
39:B5:4638:G:H5'	39:B5:4639:C:OP2	2.16	0.46
46:BE:181:PRO:HD2	46:BE:184:LEU:HD12	1.98	0.46
85:Bt:154:ASP:HB3	85:Bt:159:ALA:HB3	1.98	0.46
7:AF:5:MET:HG2	7:AF:312:VAL:HG22	1.98	0.46
7:AF:290:ALA:HB3	7:AF:299:PHE:HB2	1.97	0.46
17:Ae:80:GLY:HA2	17:Ae:83:ASN:ND2	2.31	0.46
25:Am:54:LEU:HB3	25:Am:60:VAL:HB	1.96	0.46
32:At:54:VAL:HG13	32:At:88:LEU:HB2	1.97	0.46
36:Ax:7:ILE:HG22	36:Ax:27:VAL:HG22	1.97	0.46
39:B5:382:G:H4'	39:B5:407:A:N1	2.30	0.46
39:B5:1853:C:H4'	56:BO:89:PRO:HD3	1.97	0.46
39:B5:3403:G:OP1	55:BN:72:LYS:NZ	2.46	0.46
39:B5:4498:G:N7	73:Bf:52:LYS:NZ	2.59	0.46
45:BD:208:MET:HE3	45:BD:233:PRO:HG3	1.97	0.46
71:Bd:59:THR:HG21	71:Bd:103:TYR:HA	1.96	0.46
1:A2:387:C:H5'	20:Ah:7:ASN:HD22	1.80	0.46
1:A2:1229:A:O2'	1:A2:1635:A:N3	2.48	0.46
7:AF:64:HIS:HB3	7:AF:83:TRP:HB2	1.98	0.46
18:Af:162:LEU:HD11	18:Af:172:LYS:HD2	1.98	0.46
26:An:16:SER:OG	26:An:17:LEU:N	2.49	0.46
30:Ar:36:VAL:HG21	30:Ar:71:MET:HE3	1.97	0.46
39:B5:837:U:H5'	54:BM:48:GLN:HG2	1.98	0.46
39:B5:2250:G:OP2	39:B5:2250:G:N2	2.46	0.46
39:B5:4403:U:N3	87:B5:4917:SPD:H82	2.30	0.46
56:BO:54:TYR:OH	56:BO:73:PHE:O	2.33	0.46
1:A2:1184:A:OP1	38:Az:15:ARG:NH1	2.47	0.46
12:AZ:206:ASP:OD1	12:AZ:206:ASP:N	2.42	0.46
39:B5:151:G:OP2	55:BN:4:TYR:OH	2.25	0.46
39:B5:1137:C:H42	39:B5:1203:G:H1	1.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:B5:1829:G:OP2	39:B5:1829:G:N2	2.43	0.46
39:B5:2363:C:H2'	39:B5:2364:G:C8	2.50	0.46
39:B5:4636:G:C2	39:B5:4637:G:H1'	2.50	0.46
46:BE:142:LYS:O	46:BE:194:GLN:NE2	2.41	0.46
73:Bf:41:PHE:HE1	73:Bf:110:ILE:HD13	1.80	0.46
1:A2:909:A:H5''	59:BR:172:ARG:HH12	1.80	0.46
7:AF:60:ARG:HE	28:Ap:97:GLN:HE22	1.63	0.46
7:AF:99:ARG:NH2	7:AF:135:LEU:O	2.47	0.46
12:AZ:79:SER:HA	12:AZ:101:GLY:HA2	1.98	0.46
28:Ap:16:LYS:HD2	28:Ap:16:LYS:HA	1.76	0.46
34:Av:30:CYS:SG	34:Av:31:SER:N	2.88	0.46
39:B5:711:U:H2'	39:B5:712:C:C6	2.51	0.46
39:B5:1693:U:H4'	39:B5:1694:C:H5'	1.98	0.46
39:B5:1907:G:H2'	39:B5:1908:G:H8	1.79	0.46
44:BC:67:TRP:HB3	44:BC:71:ARG:HD3	1.98	0.46
1:A2:390:A:OP2	92:A2:2104:HOH:O	2.21	0.46
4:AC:102:VAL:HG11	24:Al:35:ILE:HB	1.97	0.46
13:Aa:103:MET:HE1	13:Aa:212:VAL:O	2.15	0.46
18:Af:67:VAL:HG12	18:Af:69:THR:HG22	1.97	0.46
25:Am:83:ASP:OD1	25:Am:83:ASP:N	2.48	0.46
39:B5:1588:G:H5'	39:B5:1589:A:OP1	2.16	0.46
44:BC:316:LYS:HB2	44:BC:324:ILE:HG13	1.98	0.46
69:Bb:36:ASP:HB3	69:Bb:39:PHE:HB3	1.96	0.46
86:Bv:187:VAL:HG11	86:Bv:204:LEU:HD11	1.98	0.46
19:Ag:8:ILE:HD13	19:Ag:16:PRO:HB3	1.96	0.46
39:B5:790:G:O2'	39:B5:792:G:O4'	2.30	0.46
39:B5:2536:G:OP2	78:Bk:33:LYS:NZ	2.44	0.46
39:B5:3693:G:O2'	39:B5:3771:G:N2	2.49	0.46
39:B5:3816:C:OP1	42:BA:37:ARG:NH2	2.39	0.46
49:BH:113:GLU:HG2	49:BH:125:ARG:HG2	1.98	0.46
76:Bi:73:ILE:O	76:Bi:77:VAL:HG22	2.16	0.46
1:A2:156:G:OP1	18:Af:2:LYS:NZ	2.41	0.45
1:A2:940:U:OP1	82:Bp:85:ARG:NH2	2.49	0.45
1:A2:953:G:OP1	13:Aa:56:LYS:NZ	2.49	0.45
1:A2:1763:C:H2'	1:A2:1764:G:C8	2.51	0.45
29:Aq:109:LEU:HG	29:Aq:111:PHE:HD2	1.80	0.45
39:B5:394:G:N2	39:B5:397:G:OP2	2.32	0.45
39:B5:811:U:H5	39:B5:814:A:N7	2.14	0.45
39:B5:2252:U:H4'	39:B5:2271:A:H4'	1.98	0.45
39:B5:4202:OMC:HM22	39:B5:4203:PSU:H5''	1.97	0.45
44:BC:39:PHE:O	44:BC:43:ASN:ND2	2.41	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:Ba:36:GLY:HA3	68:Ba:40:HIS:CE1	2.51	0.45
80:Bm:113:LYS:HG2	80:Bm:117:HIS:CE1	2.51	0.45
85:Bt:64:ILE:HA	85:Bt:69:ALA:HA	1.97	0.45
86:Bv:31:THR:HG1	86:Bv:209:THR:HG1	1.63	0.45
18:Af:52:ILE:HG23	18:Af:109:LEU:HD11	1.98	0.45
18:Af:213:LEU:HG	18:Af:217:MET:HE2	1.97	0.45
20:Ah:130:THR:HG23	20:Ah:133:GLU:H	1.82	0.45
21:Ai:138:ARG:NH1	21:Ai:153:SER:OG	2.47	0.45
39:B5:121:A:OP1	48:BG:110:LYS:NZ	2.41	0.45
39:B5:1125:C:H5	46:BE:62:SER:HB2	1.81	0.45
39:B5:1270:A2M:OP2	39:B5:4191:U:O2'	2.27	0.45
39:B5:1838:G:O2'	72:Be:57:ASN:OD1	2.30	0.45
39:B5:2221:G:N2	39:B5:2224:A:OP2	2.46	0.45
86:Bv:71:GLN:O	86:Bv:75:ASP:N	2.41	0.45
1:A2:1143:G:N2	1:A2:1146:A:OP2	2.36	0.45
39:B5:1211:G:N7	69:Bb:111:ARG:NH1	2.62	0.45
39:B5:1303:G:H4'	55:BN:203:TYR:HB2	1.98	0.45
39:B5:4282:OMC:HM22	39:B5:4283:C:H5'	1.98	0.45
39:B5:4487:A:H2'	39:B5:4639:C:H5	1.81	0.45
85:Bt:127:GLY:HA2	85:Bt:130:LYS:HD3	1.98	0.45
1:A2:496:U:H4'	16:Ad:24:THR:HG22	1.97	0.45
1:A2:1085:A:OP1	1:A2:1859:G:O2'	2.30	0.45
1:A2:1233:PSU:H2'	1:A2:1234:G:H8	1.82	0.45
4:AC:133:ALA:N	4:AC:140:TYR:O	2.27	0.45
9:AH:3471:G:H1'	14:Ab:147:VAL:HG11	1.99	0.45
18:Af:131:ARG:O	64:BW:83:THR:N	2.40	0.45
39:B5:1959:U:H5''	84:Bs:57:LYS:HG3	1.98	0.45
39:B5:2101:C:O2	46:BE:94:THR:OG1	2.29	0.45
39:B5:3588:A:H5''	57:BP:83:TRP:O	2.17	0.45
39:B5:4268:G:O2'	39:B5:4271:C:OP2	2.23	0.45
39:B5:4649:A:H4'	43:BB:95:THR:HG22	1.99	0.45
51:BJ:90:ARG:NH2	51:BJ:108:GLY:O	2.49	0.45
72:Be:35:TRP:CZ2	72:Be:56:PRO:HD2	2.51	0.45
1:A2:1338:4AC:H2'	1:A2:1339:G:C8	2.52	0.45
18:Af:131:ARG:HB2	64:BW:82:ILE:HA	1.99	0.45
23:Ak:126:VAL:HG12	23:Ak:145:VAL:HG22	1.99	0.45
39:B5:86:U:OP1	58:BQ:169:SER:OG	2.32	0.45
39:B5:3609:A:OP1	92:B5:5503:HOH:O	2.20	0.45
47:BF:181:TYR:CZ	47:BF:202:GLU:HG2	2.51	0.45
53:BL:90:VAL:O	53:BL:93:THR:OG1	2.35	0.45
55:BN:116:LEU:HD22	55:BN:135:ILE:HD11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:Bv:204:LEU:N	86:Bv:216:LEU:O	2.41	0.45
1:A2:172:OMU:H6	1:A2:315:U:H1'	1.99	0.45
1:A2:508:G:OP2	36:Ax:104:ARG:NH2	2.50	0.45
1:A2:836:C:H2'	1:A2:838:A:N3	2.32	0.45
37:Ay:102:LYS:HD2	37:Ay:107:VAL:HG12	1.97	0.45
39:B5:25:A:N3	39:B5:339:C:O2'	2.46	0.45
39:B5:629:G:H2'	39:B5:630:G:C8	2.51	0.45
49:BH:16:VAL:HG21	49:BH:81:ILE:HG23	1.96	0.45
55:BN:53:TYR:HB2	55:BN:133:ILE:HD13	1.99	0.45
64:BW:56:ARG:HB3	64:BW:61:LYS:HB2	1.99	0.45
86:Bv:207:LYS:HB3	86:Bv:213:PRO:HA	1.98	0.45
1:A2:1240:U:H5''	27:Ao:124:LYS:HD3	1.97	0.45
11:AT:69:C:H2'	11:AT:70:G:C8	2.52	0.45
22:Aj:16:PHE:HE1	22:Aj:89:ILE:HG22	1.82	0.45
39:B5:1866:U:OP1	39:B5:1888:U:O2'	2.29	0.45
39:B5:3789:U:H2'	39:B5:3790:A:C8	2.52	0.45
88:B5:4912:SPM:H22	58:BQ:11:ARG:HB3	1.99	0.45
44:BC:14:LYS:HA	44:BC:173:LYS:HD3	1.99	0.45
45:BD:107:ARG:NH1	45:BD:169:GLY:O	2.46	0.45
46:BE:98:PRO:HA	46:BE:107:THR:HA	1.98	0.45
61:BT:93:ILE:HA	61:BT:96:ILE:HG12	1.98	0.45
75:Bh:6:ALA:O	75:Bh:10:ARG:HG3	2.16	0.45
75:Bh:80:PRO:HD2	75:Bh:83:LEU:HD12	1.99	0.45
1:A2:1446:PSU:O2	1:A2:1447:A:N6	2.50	0.45
9:AH:3454:C:H2'	9:AH:3455:A:C5	2.51	0.45
12:AZ:80:ARG:O	12:AZ:84:GLN:HG3	2.17	0.45
14:Ab:252:THR:OG1	14:Ab:254:ASP:OD1	2.25	0.45
15:Ac:115:VAL:HG11	15:Ac:142:LEU:HD22	1.99	0.45
16:Ad:107:GLY:HA2	16:Ad:189:LEU:HG	1.99	0.45
25:Am:100:LYS:O	25:Am:103:GLU:HG2	2.16	0.45
35:Aw:46:HIS:CD2	35:Aw:103:ALA:HB2	2.52	0.45
39:B5:4159:C:OP2	87:B5:4921:SPD:H92	2.17	0.45
68:Ba:71:PRO:HG2	68:Ba:108:TYR:HA	1.98	0.45
85:Bt:105:THR:HB	85:Bt:108:GLU:HG3	1.98	0.45
86:Bv:35:GLN:HG3	86:Bv:166:ALA:HB2	1.98	0.45
11:AT:51:U:H2'	11:AT:52:G:C8	2.52	0.45
14:Ab:128:VAL:HG11	14:Ab:155:ILE:HG12	1.99	0.45
19:Ag:101:LEU:HB2	19:Ag:116:ARG:HD2	1.99	0.45
39:B5:58:G:H4'	39:B5:59:A:H4'	1.99	0.45
62:BU:80:LYS:HG2	62:BU:110:TYR:CE2	2.52	0.45
70:Bc:99:PRO:HG3	70:Bc:105:ILE:HG13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A2:1233:PSU:H2'	1:A2:1234:G:C8	2.52	0.45
1:A2:1649:G:N7	28:Ap:17:LYS:HE2	2.33	0.45
26:An:92:ALA:HA	26:An:125:LYS:HB2	1.99	0.45
39:B5:362:A:N6	79:Bl:37:TYR:O	2.46	0.45
39:B5:4052:OMU:OP2	58:BQ:159:PRO:HD2	2.17	0.45
39:B5:4476:C:O2'	39:B5:4479:C:N3	2.50	0.45
50:BI:101:LYS:NZ	50:BI:102:MET:O	2.49	0.45
57:BP:131:ARG:HG3	57:BP:137:ASN:ND2	2.32	0.45
68:Ba:13:GLY:O	72:Be:39:ARG:NE	2.44	0.45
68:Ba:85:GLN:HA	68:Ba:88:VAL:HG22	1.99	0.45
1:A2:324:C:H42	1:A2:328:G:N2	2.14	0.44
1:A2:828:A:N7	92:A2:2140:HOH:O	2.36	0.44
1:A2:1540:U:OP1	31:As:44:GLU:N	2.46	0.44
1:A2:1758:G:H2'	1:A2:1759:G:H8	1.81	0.44
21:AI:114:VAL:HG12	21:AI:120:ALA:HB2	1.99	0.44
39:B5:521:C:H2'	39:B5:522:U:C6	2.52	0.44
39:B5:632:G:C2	39:B5:635:G:H1'	2.52	0.44
39:B5:1423:C:OP1	68:Ba:132:ARG:NH2	2.47	0.44
56:BO:74:ARG:NH1	56:BO:145:VAL:O	2.46	0.44
1:A2:28:U:H2'	1:A2:29:G:C8	2.52	0.44
1:A2:447:G:P	20:Ah:47:ARG:HH22	2.39	0.44
1:A2:1448:OMG:P	32:At:87:ARG:HH22	2.40	0.44
39:B5:217:C:OP2	39:B5:219:G:O2'	2.31	0.44
39:B5:827:C:H2'	39:B5:828:A:C8	2.53	0.44
39:B5:3699:G:N2	86:Bv:164:CYS:SG	2.88	0.44
39:B5:4270:G:N3	43:BB:252:ALA:HB1	2.32	0.44
39:B5:4698:U:H2'	39:B5:4699:G:C8	2.52	0.44
41:B8:36:G:C5	75:Bh:89:ARG:HD3	2.53	0.44
66:BY:30:MET:HB3	66:BY:101:PRO:HG2	1.99	0.44
39:B5:1632:PSU:H4'	39:B5:1635:G:N1	2.32	0.44
39:B5:3464:A:H2'	39:B5:3465:A:C8	2.53	0.44
39:B5:4020:A:H2'	39:B5:4021:G:C8	2.52	0.44
58:BQ:106:THR:O	58:BQ:110:ARG:HG3	2.18	0.44
62:BU:47:ILE:HD12	62:BU:63:ILE:HD11	1.98	0.44
1:A2:673:A:OP2	88:A2:1909:SPM:H132	2.18	0.44
1:A2:1009:A:OP2	70:Bc:8:LYS:NZ	2.35	0.44
1:A2:1230:G:OP1	37:Ay:32:LYS:NZ	2.50	0.44
13:Aa:179:ASN:HB3	13:Aa:183:GLU:HB2	2.00	0.44
20:Ah:10:LYS:O	20:Ah:18:ARG:NH1	2.50	0.44
28:Ap:7:LEU:HD23	28:Ap:7:LEU:H	1.83	0.44
34:Av:28:ARG:HB3	34:Av:60:LYS:HG2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:B5:175:C:H2'	39:B5:176:G:C8	2.53	0.44
39:B5:522:U:H2'	39:B5:523:C:C6	2.53	0.44
39:B5:1936:U:H4'	84:Bs:44:ARG:CZ	2.46	0.44
39:B5:2156:A:H5'	39:B5:2157:G:OP2	2.17	0.44
39:B5:4253:A:H2'	39:B5:4254:C:C6	2.53	0.44
43:BB:206:PRO:HG2	43:BB:209:GLN:HG3	1.99	0.44
49:BH:37:ASP:OD2	49:BH:39:ASN:ND2	2.50	0.44
57:BP:64:ASN:O	57:BP:80:GLN:NE2	2.50	0.44
60:BS:93:MET:HE1	60:BS:117:HIS:CE1	2.52	0.44
1:A2:126:G:H8	18:Af:199:THR:HG21	1.83	0.44
6:AE:46:GLU:O	6:AE:50:VAL:HG23	2.18	0.44
14:Ab:191:VAL:HG11	14:Ab:236:PHE:HA	1.99	0.44
17:Ae:14:THR:HB	17:Ae:15:PRO:HD3	2.00	0.44
20:Ah:194:GLU:HG2	23:Ak:10:TYR:CD2	2.53	0.44
39:B5:2272:A:OP1	79:Bl:43:HIS:NE2	2.43	0.44
39:B5:2536:G:H2'	39:B5:2537:G:N2	2.33	0.44
39:B5:2588:A:H2'	39:B5:2589:A:C8	2.52	0.44
76:Bi:26:HIS:O	76:Bi:29:ARG:HG3	2.18	0.44
79:Bl:42:ARG:HG3	79:Bl:47:THR:HG23	1.99	0.44
1:A2:817:A:OP1	21:Ai:10:ARG:NH2	2.51	0.44
19:Ag:25:GLN:O	19:Ag:29:GLU:HG2	2.17	0.44
1:A2:925:G:H5'	25:Am:4:MET:HE3	1.99	0.44
1:A2:1227:G:N1	1:A2:1640:G7M:OP2	2.31	0.44
1:A2:1802:A:H2'	1:A2:1803:C:C6	2.53	0.44
4:AC:107:LYS:HE3	4:AC:115:SER:HB3	2.00	0.44
19:Ag:130:LEU:HD21	19:Ag:156:VAL:HG21	1.98	0.44
20:Ah:172:LEU:HB3	20:Ah:190:LEU:HD12	1.99	0.44
25:Am:4:MET:SD	25:Am:124:ARG:NH2	2.91	0.44
39:B5:175:C:H2'	39:B5:176:G:H8	1.81	0.44
39:B5:1933:C:H2'	39:B5:1934:G:C8	2.52	0.44
39:B5:2704:OMC:HM22	39:B5:2705:G:H5'	2.00	0.44
54:BM:24:LEU:HD11	54:BM:86:TRP:CG	2.52	0.44
58:BQ:122:THR:OG1	58:BQ:124:ASP:OD1	2.34	0.44
75:Bh:67:GLU:HG2	75:Bh:71:LYS:HE3	1.99	0.44
85:Bt:118:HIS:CD2	85:Bt:119:ARG:HG2	2.53	0.44
1:A2:417:U:H2'	1:A2:418:C:O4'	2.17	0.44
1:A2:485:A2M:HM'2	1:A2:486:A:C5	2.53	0.44
1:A2:982:A:H2'	1:A2:983:G:C8	2.53	0.44
1:A2:1100:G:H22	1:A2:1134:A:H2	1.66	0.44
1:A2:1156:U:OP1	14:Ab:185:THR:OG1	2.34	0.44
1:A2:1321:G:H2'	1:A2:1322:G:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AG:3:HIS:HB3	8:AG:6:LEU:HB2	2.00	0.44
39:B5:456:C:H2'	39:B5:457:G:C8	2.53	0.44
39:B5:2118:G:H2'	39:B5:2119:A:C8	2.53	0.44
39:B5:4271:C:OP1	43:BB:246:ARG:NH1	2.40	0.44
43:BB:317:LEU:HB2	43:BB:372:SER:HB2	1.98	0.44
49:BH:41:ILE:HG22	49:BH:43:VAL:HG13	1.99	0.44
85:Bt:104:ILE:HB	85:Bt:143:VAL:HG22	1.99	0.44
1:A2:71:G:O6	18:Af:170:ARG:NH1	2.51	0.44
1:A2:99:A2M:H8	1:A2:99:A2M:O5'	2.18	0.44
1:A2:1011:G:H2'	1:A2:1012:A:C8	2.53	0.44
1:A2:1149:A:H4'	1:A2:1150:A:O4'	2.18	0.44
1:A2:1292:A:N3	4:AC:140:TYR:OH	2.39	0.44
7:AF:159:ASN:HD22	7:AF:159:ASN:H	1.66	0.44
19:Ag:135:PHE:CG	19:Ag:136:PRO:HA	2.53	0.44
30:Ar:46:ARG:HH12	30:Ar:52:LEU:HD11	1.83	0.44
36:Ax:78:SER:OG	36:Ax:80:ASP:OD1	2.28	0.44
39:B5:2322:G:H2'	39:B5:2323:G:H8	1.83	0.44
39:B5:2719:OMG:C8	82:Bp:16:THR:HG22	2.53	0.44
39:B5:3353:A:O2'	39:B5:4404:G:O2'	2.30	0.44
39:B5:4698:U:H2'	39:B5:4699:G:H8	1.82	0.44
48:BG:115:LEU:O	48:BG:119:GLU:HG2	2.18	0.44
68:Ba:89:ASN:OD1	68:Ba:92:LYS:NZ	2.37	0.44
70:Bc:4:ALA:O	70:Bc:7:THR:OG1	2.35	0.44
1:A2:700:C:H2'	1:A2:701:G:C8	2.53	0.43
1:A2:1102:U:H2'	1:A2:1103:G:C8	2.52	0.43
1:A2:1375:C:H2'	1:A2:1376:G:O4'	2.18	0.43
1:A2:1623:U:H3'	1:A2:1624:A:H4'	2.00	0.43
3:AB:21:THR:HB	3:AB:68:LEU:HD21	1.99	0.43
6:AE:45:VAL:HA	26:An:113:GLN:HE22	1.83	0.43
17:Ae:135:ARG:HD3	26:An:66:ARG:NH2	2.33	0.43
39:B5:85:G:O2'	39:B5:97:G:O6	2.33	0.43
39:B5:2573:U:H2'	39:B5:2574:C:C6	2.53	0.43
39:B5:4135:C:H2'	39:B5:4136:A:C8	2.53	0.43
1:A2:533:C:H2'	1:A2:534:A:C8	2.53	0.43
12:AZ:76:VAL:HG12	12:AZ:123:VAL:HB	2.01	0.43
14:Ab:165:VAL:HG21	14:Ab:217:ALA:HB1	1.99	0.43
15:Ac:172:VAL:HG22	15:Ac:185:LYS:HG2	2.00	0.43
15:Ac:206:ASP:OD1	15:Ac:206:ASP:N	2.50	0.43
39:B5:92:C:OP2	39:B5:4087:C:O2'	2.30	0.43
39:B5:732:C:OP1	39:B5:734:G:H4'	2.18	0.43
39:B5:1276:C:H2'	39:B5:1277:A:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:B5:1796:C:H2'	39:B5:1797:A:C8	2.54	0.43
39:B5:1907:G:H4'	84:Bs:34:ASN:HD22	1.82	0.43
39:B5:4204:C:H2'	39:B5:4205:U:C6	2.53	0.43
40:B7:74:A:N1	40:B7:100:A:H5''	2.34	0.43
43:BB:220:ILE:HB	43:BB:346:THR:HB	2.00	0.43
75:Bh:87:LYS:N	77:Bj:80:GLU:OE2	2.38	0.43
84:Bs:39:GLN:HE21	84:Bs:43:ILE:HD11	1.83	0.43
85:Bt:108:GLU:HA	85:Bt:111:ASN:HD21	1.83	0.43
1:A2:665:A:O2'	1:A2:671:A:N1	2.48	0.43
1:A2:1084:A:N7	1:A2:1842:C:O2'	2.48	0.43
1:A2:1780:G:H2'	1:A2:1781:G:C8	2.53	0.43
5:AD:105:ARG:HD3	21:Ai:127:ARG:HD3	2.00	0.43
13:Aa:83:LYS:NZ	26:An:130:GLU:OE2	2.51	0.43
17:Ae:43:GLU:H	17:Ae:43:GLU:CD	2.24	0.43
39:B5:1386:C:H2'	39:B5:1387:G:O4'	2.18	0.43
39:B5:1924:G:N2	39:B5:1924:G:OP1	2.52	0.43
39:B5:2228:U:H4'	59:BR:3:MET:HG2	2.00	0.43
39:B5:2242:G:O2'	39:B5:2665:G:O2'	2.33	0.43
54:BM:126:GLU:HG3	56:BO:185:VAL:HG13	2.01	0.43
57:BP:94:MET:HE1	57:BP:146:ILE:HB	1.99	0.43
86:Bv:205:TYR:HA	86:Bv:214:GLN:O	2.19	0.43
1:A2:27:A2M:HM'2	1:A2:28:U:H5'	2.01	0.43
1:A2:417:U:O2'	1:A2:653:U:O2'	2.25	0.43
9:AH:3473:U:H5''	15:Ac:117:ARG:HH12	1.83	0.43
37:Ay:73:VAL:HG21	37:Ay:88:LEU:HD21	1.99	0.43
39:B5:4371:C:OP1	43:BB:224:LYS:HG3	2.18	0.43
55:BN:28:TRP:O	55:BN:32:GLN:HG2	2.18	0.43
57:BP:40:HIS:CE1	57:BP:157:VAL:HB	2.53	0.43
85:Bt:137:GLN:HB3	85:Bt:148:PRO:HG2	2.00	0.43
86:Bv:60:ARG:H	86:Bv:60:ARG:HG3	1.61	0.43
6:AE:37:LYS:HD2	6:AE:70:LYS:HZ1	1.83	0.43
11:AT:17:H2U:H2'	11:AT:17:H2U:H61	1.65	0.43
13:Aa:48:LEU:O	26:An:51:GLU:HG3	2.18	0.43
20:Ah:11:ARG:NH1	20:Ah:15:GLY:O	2.46	0.43
41:B8:141:C:H2'	41:B8:142:U:C6	2.54	0.43
53:BL:40:GLN:O	53:BL:44:ARG:HG3	2.18	0.43
58:BQ:178:ARG:N	68:Ba:51:GLY:HA2	2.34	0.43
67:BZ:115:LYS:NZ	67:BZ:119:GLU:OE2	2.51	0.43
72:Be:104:SER:O	72:Be:108:ARG:HG3	2.19	0.43
1:A2:1147:C:O2'	1:A2:1151:A:N1	2.46	0.43
1:A2:1590:A:N3	1:A2:1654:U:O2'	2.40	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AA:33:MET:HE2	2:AA:48:SER:HA	2.01	0.43
11:AT:34:OMG:HM22	11:AT:35:A:H5'	2.00	0.43
13:Aa:190:PRO:O	13:Aa:192:SER:N	2.50	0.43
16:Ad:87:MET:HE1	16:Ad:236:ILE:HG21	2.01	0.43
28:Ap:16:LYS:HG3	28:Ap:17:LYS:H	1.84	0.43
33:Au:30:ALA:O	33:Au:60:ARG:HD3	2.18	0.43
39:B5:1225:G:OP1	44:BC:316:LYS:NZ	2.48	0.43
39:B5:1706:A:C5	39:B5:1707:C:H1'	2.53	0.43
39:B5:3791:U:H2'	39:B5:3792:C:C6	2.53	0.43
42:BA:80:GLU:HB2	42:BA:170:ALA:HA	2.01	0.43
56:BO:81:TRP:HB2	56:BO:104:VAL:HG21	2.00	0.43
1:A2:220:U:H2'	1:A2:221:A:C8	2.53	0.43
1:A2:382:C:OP2	20:Ah:31:ARG:NH2	2.52	0.43
1:A2:675:C:H2'	1:A2:676:U:C6	2.53	0.43
1:A2:1776:U:H2'	1:A2:1777:G:C8	2.54	0.43
15:Ac:53:THR:HA	15:Ac:90:LYS:HE2	2.00	0.43
21:Ai:83:ARG:HH21	21:Ai:150:ARG:NH1	2.17	0.43
39:B5:757:A:N6	39:B5:759:G:O6	2.51	0.43
39:B5:1105:C:C5	69:Bb:92:LYS:HD2	2.54	0.43
52:BK:4374:GLY:HA3	57:BP:126:ARG:O	2.19	0.43
55:BN:178:HIS:HA	55:BN:181:HIS:NE2	2.33	0.43
1:A2:65:C:C4	18:Af:133:LEU:HB3	2.54	0.43
1:A2:115:U:H2'	1:A2:116:OMU:C6	2.49	0.43
1:A2:155:G:H4'	18:Af:15:LEU:HD22	2.01	0.43
1:A2:745:G:N3	19:Ag:109:ARG:NH2	2.67	0.43
1:A2:1443:OMU:HM22	1:A2:1444:C:H5'	2.01	0.43
7:AF:25:PRO:HA	7:AF:293:ALA:HB2	2.01	0.43
8:AG:20:SER:OG	22:Aj:65:ARG:NH1	2.51	0.43
14:Ab:169:TYR:OH	14:Ab:175:GLY:O	2.34	0.43
16:Ad:86:PHE:CD2	16:Ad:87:MET:HG2	2.54	0.43
20:Ah:36:THR:OG1	20:Ah:57:ALA:O	2.36	0.43
20:Ah:165:GLN:HE22	20:Ah:195:LEU:HD11	1.84	0.43
24:Al:89:VAL:HG23	24:Al:91:LEU:HB2	2.01	0.43
28:Ap:96:TYR:HA	28:Ap:100:VAL:HG23	2.01	0.43
39:B5:24:G:N7	77:Bj:46:LYS:NZ	2.65	0.43
39:B5:396:A:OP1	92:B5:5505:HOH:O	2.21	0.43
39:B5:664:G:H2'	39:B5:665:G:H8	1.83	0.43
39:B5:1769:G:H4'	69:Bb:68:ARG:CZ	2.47	0.43
40:B7:31:G:N7	92:B7:304:HOH:O	2.36	0.43
58:BQ:35:LEU:O	58:BQ:39:THR:OG1	2.28	0.43
1:A2:1113:U:H1'	13:Aa:146:ARG:HH22	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A2:1565:C:OP1	31:As:121:ARG:NH2	2.52	0.43
6:AE:24:THR:HG21	6:AE:71:LEU:HD22	2.01	0.43
19:Ag:146:VAL:HG12	34:Av:42:MET:HE1	2.01	0.43
39:B5:347:A:O2'	44:BC:50:GLN:NE2	2.52	0.43
39:B5:763:C:H2'	39:B5:764:G:H8	1.84	0.43
39:B5:2028:G:H1	39:B5:2038:C:H41	1.66	0.43
39:B5:4450:C:H2'	39:B5:4451:A:C8	2.53	0.43
46:BE:246:THR:HG22	46:BE:248:GLN:H	1.83	0.43
54:BM:126:GLU:HB3	56:BO:181:ALA:HB1	2.01	0.43
57:BP:54:LYS:HA	57:BP:83:TRP:CD1	2.53	0.43
1:A2:602:OMG:HM22	1:A2:603:G:H5'	2.01	0.43
1:A2:1537:G:H2'	1:A2:1538:A:C8	2.53	0.43
1:A2:1649:G:O2'	1:A2:1675:G:O6	2.32	0.43
11:AT:26:M2G:HM12	11:AT:44:A:H2	1.83	0.43
39:B5:38:A:H5''	68:Ba:35:ALA:HB2	2.01	0.43
39:B5:85:G:N2	39:B5:98:A:OP2	2.39	0.43
39:B5:2338:U:H2'	39:B5:2339:G:H8	1.84	0.43
39:B5:2705:G:O6	87:B5:4913:SPD:N1	2.52	0.43
39:B5:4137:G:OP1	44:BC:75:ARG:NH1	2.41	0.43
39:B5:4693:G:H2'	39:B5:4694:A:C8	2.54	0.43
40:B7:11:A:N1	40:B7:66:G:O2'	2.48	0.43
50:BI:54:SER:HB2	50:BI:135:ILE:HD11	2.00	0.43
63:BV:87:SER:HB3	64:BW:19:ARG:HH21	1.83	0.43
70:Bc:38:ILE:HG21	70:Bc:63:TYR:HB3	2.01	0.43
2:AA:23:ARG:HH22	2:AA:29:ASN:ND2	2.11	0.42
13:Aa:30:TRP:CE2	26:An:19:PRO:HD3	2.54	0.42
28:Ap:24:HIS:HE1	28:Ap:26:LYS:HD3	1.83	0.42
29:Aq:109:LEU:HG	29:Aq:111:PHE:CD2	2.54	0.42
30:Ar:7:GLU:H	30:Ar:7:GLU:CD	2.27	0.42
34:Av:55:ASP:O	34:Av:57:ARG:NH1	2.51	0.42
39:B5:280:G:OP2	55:BN:44:ARG:NH2	2.43	0.42
39:B5:303:C:OP2	55:BN:68:ARG:NH2	2.46	0.42
39:B5:478:G:H2'	39:B5:479:G:C8	2.53	0.42
39:B5:1548:A:H5''	39:B5:2682:U:H5''	2.00	0.42
39:B5:2477:C:H2'	39:B5:2478:U:C6	2.54	0.42
39:B5:3836:G:H2'	39:B5:3837:G:H8	1.83	0.42
48:BG:223:ARG:HG3	48:BG:227:ASN:HB2	2.01	0.42
86:Bv:59:PRO:HG2	86:Bv:63:PHE:HE2	1.84	0.42
1:A2:449:A:H5''	20:Ah:25:ARG:HA	2.01	0.42
1:A2:875:G:H2'	1:A2:876:A:H8	1.83	0.42
1:A2:958:A:OP1	26:An:57:THR:OG1	2.32	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AT:33:U:H4'	11:AT:37:YYG:H243	2.01	0.42
31:As:71:GLY:O	31:As:75:MET:HG2	2.20	0.42
34:Av:45:GLY:O	34:Av:68:ARG:NH2	2.49	0.42
39:B5:760:C:O2	39:B5:792:G:N2	2.44	0.42
39:B5:3439:U:H2'	39:B5:3440:C:C6	2.54	0.42
39:B5:3909:U:H5'	39:B5:3910:C:H5''	2.00	0.42
39:B5:4166:PSU:O2	39:B5:4221:G:N2	2.52	0.42
39:B5:4190:C:OP1	92:B5:5506:HOH:O	2.21	0.42
39:B5:4422:G:OP1	43:BB:281:ASN:ND2	2.42	0.42
1:A2:195:C:H2'	1:A2:196:C:C6	2.54	0.42
1:A2:1222:G:O2'	1:A2:1677:U:O2	2.36	0.42
1:A2:1330:U:O2'	1:A2:1333:A:OP2	2.27	0.42
7:AF:85:GLY:HA2	7:AF:108:VAL:HG23	2.01	0.42
39:B5:478:G:H2'	39:B5:479:G:H8	1.84	0.42
39:B5:2357:G:OP1	74:Bg:17:SER:OG	2.35	0.42
39:B5:3930:G:H5'	42:BA:233:ARG:HB2	2.00	0.42
39:B5:4064:C:H4'	81:Bo:17:LYS:HA	2.01	0.42
42:BA:36:GLU:HA	42:BA:91:GLY:HA2	2.02	0.42
77:Bj:39:TYR:CG	77:Bj:40:PRO:HA	2.54	0.42
1:A2:495:C:N4	1:A2:510:OMG:HN22	2.17	0.42
1:A2:617:A:H1'	5:AD:86:VAL:HG23	2.01	0.42
1:A2:1837:G:OP1	1:A2:1840:U:H4'	2.20	0.42
7:AF:207:CYS:SG	7:AF:219:TRP:HB2	2.58	0.42
26:An:31:CYS:HB2	26:An:93:LEU:HG	2.00	0.42
39:B5:637:C:H2'	39:B5:638:G:C8	2.53	0.42
39:B5:1215:G:O2'	39:B5:1216:C:H5'	2.20	0.42
39:B5:1353:G:H2'	39:B5:1354:G:C8	2.54	0.42
39:B5:1387:G:O2'	39:B5:1407:A:N6	2.52	0.42
39:B5:1611:U:O2'	39:B5:3638:A:N1	2.46	0.42
39:B5:4012:G:N3	39:B5:4012:G:H2'	2.34	0.42
41:B8:92:U:H2'	41:B8:93:C:O4'	2.19	0.42
55:BN:145:ASN:O	55:BN:149:GLN:HG3	2.20	0.42
56:BO:10:ASP:HB2	56:BO:117:ARG:HB3	2.01	0.42
56:BO:130:LYS:HB2	56:BO:133:ARG:HG2	2.01	0.42
78:Bk:36:VAL:HG13	78:Bk:43:TYR:HB2	2.02	0.42
1:A2:824:U:N3	21:Ai:143:ASN:OD1	2.47	0.42
1:A2:1000:G:OP2	92:A2:2105:HOH:O	2.21	0.42
1:A2:1309:U:O2'	1:A2:1310:C:O4'	2.36	0.42
1:A2:1316:U:H4'	22:Aj:2:LEU:HG	2.00	0.42
6:AE:59:PHE:HB2	6:AE:62:TYR:HB2	2.02	0.42
9:AH:3492:C:H2'	9:AH:3493:G:H8	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:Ac:163:PRO:O	15:Ac:167:TYR:HB2	2.20	0.42
29:Aq:77:GLU:OE2	29:Aq:81:ARG:NH2	2.53	0.42
38:Az:23:ARG:NH2	39:B5:3514:5MC:OP1	2.43	0.42
39:B5:1089:G:H2'	39:B5:1091:G:C8	2.55	0.42
39:B5:1250:C:H2'	39:B5:1251:A:C8	2.54	0.42
39:B5:1897:A:O2'	39:B5:1964:A:N1	2.52	0.42
39:B5:3781:A:H2'	39:B5:3782:C:C6	2.54	0.42
39:B5:3836:G:H2'	39:B5:3837:G:C8	2.55	0.42
39:B5:4192:U:O2'	39:B5:4196:U:OP1	2.36	0.42
47:BF:225:HIS:ND1	47:BF:227:VAL:HG22	2.35	0.42
86:Bv:34:LEU:O	86:Bv:166:ALA:HA	2.20	0.42
1:A2:165:G:H2'	1:A2:166:A2M:H8	2.01	0.42
1:A2:1416:C:O2'	31:As:132:ASP:OD2	2.31	0.42
24:Al:72:HIS:CD2	24:Al:74:ILE:HD11	2.54	0.42
39:B5:1437:G:N7	53:BL:188:ASN:ND2	2.68	0.42
39:B5:1471:G:O2'	53:BL:18:TRP:NE1	2.47	0.42
39:B5:1489:A2M:HM'3	39:B5:1592:A:C4	2.54	0.42
39:B5:1542:G:OP1	92:B5:5507:HOH:O	2.22	0.42
39:B5:1815:U:H2'	39:B5:1816:G:C8	2.55	0.42
39:B5:1955:C:H2'	39:B5:1956:A:C8	2.53	0.42
39:B5:3331:A:H2'	39:B5:3332:G:C8	2.55	0.42
39:B5:4017:A:OP1	39:B5:4018:G:N2	2.53	0.42
39:B5:4383:OMG:HM22	39:B5:4384:U:O4'	2.20	0.42
39:B5:4662:U:H2'	39:B5:4663:C:C6	2.55	0.42
40:B7:24:C:H2'	40:B7:25:G:O4'	2.20	0.42
45:BD:179:ARG:HA	45:BD:179:ARG:HD3	1.81	0.42
50:BI:84:GLY:O	50:BI:140:THR:OG1	2.31	0.42
50:BI:163:GLN:HE21	50:BI:163:GLN:HB2	1.67	0.42
55:BN:201:HIS:O	55:BN:204:ARG:NH1	2.44	0.42
56:BO:170:LYS:HE3	56:BO:170:LYS:HB2	1.81	0.42
57:BP:52:THR:HG23	57:BP:85:LYS:HG3	2.00	0.42
1:A2:107:A:H2'	1:A2:108:G:C8	2.54	0.42
1:A2:1089:U:OP1	88:A2:1909:SPM:N14	2.53	0.42
9:AH:3527:U:H2'	9:AH:3528:G:C8	2.54	0.42
30:Ar:48:ALA:HB2	30:Ar:70:ILE:HD12	2.01	0.42
39:B5:18:C:H4'	55:BN:138:PHE:CD1	2.55	0.42
39:B5:1265:G:H2'	39:B5:3608:A:N7	2.35	0.42
39:B5:1363:C:H2'	39:B5:1364:G:C8	2.54	0.42
39:B5:2539:A:H62	78:Bk:35:LYS:NZ	2.17	0.42
39:B5:3600:G:H22	39:B5:3632:G:H1'	1.84	0.42
39:B5:4139:G:O4'	39:B5:4193:5MC:HM52	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:B5:4337:U:H2'	39:B5:4338:C:C6	2.55	0.42
43:BB:17:LEU:HD21	43:BB:235:TRP:HH2	1.85	0.42
45:BD:60:ILE:HB	45:BD:80:ALA:HB2	2.01	0.42
48:BG:187:LYS:HB2	48:BG:198:THR:HG23	2.02	0.42
72:Be:37:LYS:HD2	72:Be:38:PRO:HD2	2.02	0.42
72:Be:66:THR:HA	72:Be:69:MET:HE3	2.01	0.42
1:A2:49:C:H2'	1:A2:473:C:H41	1.84	0.42
1:A2:617:A:OP1	35:Aw:68:LYS:NZ	2.53	0.42
1:A2:1799:C:H2'	1:A2:1800:G:O4'	2.19	0.42
1:A2:1850:G:N3	39:B5:3498:A:O2'	2.48	0.42
18:Af:201:LYS:HE3	18:Af:201:LYS:HB3	1.77	0.42
22:Aj:86:PRO:HG2	22:Aj:89:ILE:HG13	2.02	0.42
39:B5:230:G:OP1	66:BY:15:ARG:NH1	2.46	0.42
39:B5:526:C:H2'	39:B5:527:G:C8	2.55	0.42
39:B5:823:C:OP1	39:B5:825:G:O2'	2.36	0.42
39:B5:1503:G:O2'	39:B5:2655:A:N3	2.46	0.42
39:B5:1927:G:H2'	39:B5:1928:G:H8	1.84	0.42
39:B5:2217:A:H5'	71:Bd:64:ILE:O	2.19	0.42
39:B5:2267:OMG:HM22	39:B5:2269:U:C6	2.55	0.42
39:B5:3374:A:C4	77:Bj:3:LYS:HB3	2.55	0.42
41:B8:30:U:OP1	53:BL:34:ARG:NH2	2.53	0.42
46:BE:261:LEU:HG	46:BE:265:LYS:HE3	2.01	0.42
53:BL:107:THR:HG22	76:Bi:20:ASN:HB3	2.02	0.42
86:Bv:32:VAL:HA	86:Bv:208:SER:HA	2.02	0.42
1:A2:240:G:H2'	1:A2:241:G:C8	2.55	0.42
1:A2:1008:C:H2'	1:A2:1009:A:C8	2.54	0.42
1:A2:1320:U:H2'	1:A2:1321:G:C8	2.55	0.42
1:A2:1486:U:OP1	15:Ac:151:LYS:NZ	2.53	0.42
9:AH:3476:C:H2'	9:AH:3477:G:C8	2.55	0.42
13:Aa:30:TRP:CE2	13:Aa:48:LEU:HD13	2.55	0.42
39:B5:1680:G:N3	39:B5:1720:PSU:H5''	2.33	0.42
39:B5:1689:G:H22	39:B5:1719:A:H2	1.68	0.42
39:B5:2032:G:O2'	39:B5:2100:C:N4	2.52	0.42
39:B5:2719:OMG:HM22	39:B5:2720:G:O5'	2.20	0.42
39:B5:4088:C:O3'	81:Bo:37:GLY:HA3	2.19	0.42
41:B8:47:C:H1'	41:B8:61:A:H2'	2.00	0.42
48:BG:51:LEU:O	48:BG:55:VAL:HG23	2.20	0.42
49:BH:27:VAL:HG12	49:BH:84:VAL:HG21	2.02	0.42
56:BO:47:PHE:HA	56:BO:136:ALA:HB2	2.02	0.42
66:BY:134:LYS:HE3	66:BY:134:LYS:HB3	1.86	0.42
1:A2:14:C:O2'	1:A2:669:A2M:N1	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:Ab:256:TRP:CD2	34:Av:68:ARG:HD2	2.54	0.42
16:Ad:55:ALA:HB1	16:Ad:60:GLU:HB2	2.02	0.42
16:Ad:174:LYS:O	16:Ad:179:ASN:ND2	2.53	0.42
20:Ah:21:TYR:CZ	20:Ah:22:HIS:HD2	2.38	0.42
24:Al:37:GLU:HA	24:Al:40:LYS:HD2	2.01	0.42
29:Aq:29:HIS:HA	29:Aq:32:LYS:HE2	2.02	0.42
39:B5:223:G:H4'	39:B5:225:G:N7	2.35	0.42
39:B5:443:G:H5''	73:Bf:54:LYS:HB3	2.01	0.42
39:B5:640:G:H2'	39:B5:641:G:H8	1.83	0.42
39:B5:1545:C:H5''	39:B5:1546:U:O5'	2.20	0.42
39:B5:2007:C:OP1	73:Bf:15:LYS:NZ	2.50	0.42
39:B5:2018:G:H2'	39:B5:2019:U:C6	2.55	0.42
39:B5:2142:G:OP1	44:BC:182:LYS:NZ	2.41	0.42
39:B5:2465:G:OP2	62:BU:84:LYS:NZ	2.50	0.42
39:B5:3342:A:H2'	39:B5:3343:A:H8	1.85	0.42
39:B5:3676:OMG:HN1	39:B5:3797:U:H3	1.68	0.42
39:B5:4206:U:H2'	39:B5:4207:C:C6	2.55	0.42
39:B5:4712:U:H1'	39:B5:4725:G:C2	2.55	0.42
41:B8:90:C:H2'	41:B8:91:A:C8	2.55	0.42
48:BG:101:LYS:NZ	48:BG:211:ASP:OD1	2.44	0.42
48:BG:257:LYS:O	48:BG:261:LEU:N	2.50	0.42
55:BN:90:ASN:O	81:Bo:48:TYR:OH	2.29	0.42
73:Bf:7:CYS:HB2	73:Bf:103:VAL:HB	2.02	0.42
86:Bv:94:ASN:OD1	86:Bv:97:LYS:NZ	2.35	0.42
1:A2:1260:A:H1'	1:A2:1265:C:N4	2.34	0.41
1:A2:1266:A:H5''	1:A2:1267:C:OP2	2.20	0.41
7:AF:192:THR:N	7:AF:213:ASP:OD2	2.53	0.41
17:Ae:71:ARG:NH2	17:Ae:148:ASN:OD1	2.52	0.41
33:Au:1:AME:HA	33:Au:1:AME:HT23	1.70	0.41
39:B5:108:A:N1	39:B5:333:U:O2'	2.51	0.41
39:B5:340:C:OP2	92:B5:5508:HOH:O	2.22	0.41
39:B5:3497:G:H21	39:B5:3498:A:N6	2.18	0.41
39:B5:3766:C:H2'	39:B5:3767:G:O4'	2.20	0.41
40:B7:117:G:OP1	45:BD:253:TYR:OH	2.35	0.41
49:BH:23:ARG:HE	49:BH:39:ASN:HA	1.84	0.41
52:BK:4370:CYS:SG	52:BK:4372:VAL:HG12	2.60	0.41
56:BO:175:MET:O	56:BO:179:LYS:HG2	2.20	0.41
73:Bf:40:GLU:O	73:Bf:109:ARG:NH2	2.53	0.41
1:A2:4:C:H4'	14:Ab:207:ALA:HB2	2.02	0.41
1:A2:17:C:H2'	1:A2:18:C:C6	2.55	0.41
1:A2:608:U:H2'	15:Ac:143:ARG:HH22	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A2:749:C:H2'	1:A2:750:U:H5''	2.01	0.41
1:A2:1437:C:H2'	1:A2:1438:C:C5	2.55	0.41
3:AB:55:VAL:HB	17:Ae:34:SER:HA	2.02	0.41
16:Ad:125:LYS:H	16:Ad:142:HIS:CD2	2.38	0.41
36:Ax:80:ASP:OD1	36:Ax:81:TYR:N	2.53	0.41
39:B5:690:C:N4	46:BE:226:ARG:HE	2.18	0.41
39:B5:985:G:O6	46:BE:48:ARG:NH2	2.53	0.41
39:B5:1772:G:N2	39:B5:1774:G:O4'	2.53	0.41
39:B5:3388:A:H2'	39:B5:3389:U:C6	2.56	0.41
39:B5:3625:C:O2'	39:B5:4718:A:N1	2.49	0.41
39:B5:4018:G:N2	39:B5:4018:G:OP2	2.31	0.41
43:BB:288:GLY:HA3	43:BB:330:PHE:CE1	2.55	0.41
52:BK:4370:CYS:HB3	52:BK:4373:CYS:SG	2.60	0.41
56:BO:58:LEU:HD12	56:BO:58:LEU:HA	1.94	0.41
72:Be:124:ASN:N	72:Be:124:ASN:OD1	2.52	0.41
1:A2:229:A:H2'	1:A2:230:A:C8	2.54	0.41
1:A2:894:U:H2'	1:A2:895:G:C8	2.55	0.41
1:A2:1459:G:OP1	7:AF:281:ALA:HB2	2.20	0.41
1:A2:1754:C:H2'	1:A2:1755:G:C8	2.56	0.41
14:Ab:192:LEU:HB3	14:Ab:227:ARG:HG2	2.03	0.41
15:Ac:75:LYS:NZ	22:Aj:20:VAL:O	2.47	0.41
19:Ag:51:ILE:HG21	19:Ag:179:LYS:HG2	2.01	0.41
27:Ao:41:GLN:HG3	27:Ao:84:ILE:HD13	2.02	0.41
39:B5:6:C:H5''	48:BG:197:LYS:HB3	2.03	0.41
39:B5:28:C:H4'	39:B5:61:A:H4'	2.02	0.41
39:B5:210:C:OP1	66:BY:59:ARG:NE	2.49	0.41
39:B5:664:G:H2'	39:B5:665:G:C8	2.55	0.41
39:B5:1411:C:H4'	58:BQ:73:PRO:HG2	2.02	0.41
39:B5:1695:U:H2'	39:B5:1696:U:C6	2.55	0.41
39:B5:1696:U:H2'	39:B5:1697:G:C8	2.55	0.41
39:B5:1741:A:H4'	61:BT:105:PHE:CD1	2.54	0.41
39:B5:2497:C:H2'	39:B5:2498:C:C6	2.55	0.41
39:B5:4270:G:C2	43:BB:252:ALA:HB1	2.55	0.41
39:B5:4510:U:O2'	60:BS:174:THR:OG1	2.26	0.41
39:B5:4699:G:H2'	39:B5:4700:G:C8	2.55	0.41
43:BB:258:HIS:HA	43:BB:259:PRO:C	2.44	0.41
53:BL:7:GLY:O	68:Ba:49:HIS:NE2	2.45	0.41
64:BW:89:ASP:O	64:BW:93:LYS:HG2	2.21	0.41
1:A2:360:U:OP2	35:Aw:18:ARG:HD2	2.21	0.41
1:A2:747:C:N4	1:A2:796:A:H61	2.18	0.41
1:A2:887:A:H62	1:A2:901:C:H42	1.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A2:1145:A:H2'	1:A2:1146:A:C8	2.56	0.41
1:A2:1652:A:H1'	17:Ae:83:ASN:HD22	1.85	0.41
12:AZ:59:LEU:O	12:AZ:63:ARG:HG3	2.20	0.41
18:Af:57:ASP:OD1	18:Af:61:PHE:N	2.53	0.41
32:At:56:MET:HB2	32:At:86:LYS:HB3	2.01	0.41
39:B5:92:C:OP1	87:B5:4908:SPD:N10	2.49	0.41
39:B5:1918:A:N1	85:Bt:57:ARG:NH1	2.58	0.41
39:B5:2304:G:H2'	39:B5:2305:C:C6	2.56	0.41
39:B5:4265:C:H5''	39:B5:4266:G:H5''	2.02	0.41
39:B5:4744:G:N2	39:B5:4780:G:O2'	2.53	0.41
56:BO:8:VAL:HG12	56:BO:117:ARG:HG3	2.01	0.41
64:BW:62:GLY:O	64:BW:66:GLU:HG3	2.19	0.41
71:Bd:92:ARG:HA	71:Bd:102:LEU:HD23	2.02	0.41
84:Bs:121:VAL:HG22	84:Bs:182:PRO:HB3	2.03	0.41
85:Bt:17:CYS:SG	85:Bt:18:THR:N	2.93	0.41
1:A2:518:OMC:HM22	1:A2:519:G:H5'	2.02	0.41
1:A2:1244:U:H2'	1:A2:1245:PSU:O4'	2.21	0.41
6:AE:45:VAL:HA	26:An:113:GLN:NE2	2.35	0.41
13:Aa:27:LYS:HA	13:Aa:51:ARG:NH1	2.35	0.41
14:Ab:200:ARG:O	21:Ai:98:LEU:HB3	2.20	0.41
39:B5:109:G:OP2	53:BL:74:ARG:NH2	2.54	0.41
39:B5:114:G:N2	39:B5:158:A:H61	2.19	0.41
39:B5:1928:G:H2'	39:B5:1929:A:C8	2.54	0.41
39:B5:2272:A:H5''	79:Bl:43:HIS:HE2	1.85	0.41
40:B7:48:G:OP1	45:BD:226:TYR:OH	2.38	0.41
46:BE:69:ALA:HA	46:BE:71:TYR:CE2	2.56	0.41
46:BE:164:ARG:NH1	46:BE:276:SER:OG	2.54	0.41
85:Bt:53:TRP:HD1	85:Bt:56:LEU:HB2	1.85	0.41
1:A2:1703:G:C2	1:A2:1704:OMC:H1'	2.56	0.41
1:A2:1833:6MZ:H8	1:A2:1833:6MZ:O5'	2.20	0.41
4:AC:123:SER:HB2	4:AC:126:CYS:SG	2.61	0.41
6:AE:65:PRO:HG3	26:An:129:ILE:O	2.21	0.41
39:B5:327:U:O2'	76:Bi:30:ARG:NH1	2.52	0.41
39:B5:1283:U:H2'	39:B5:1284:OMC:C6	2.55	0.41
39:B5:1520:A:C5	39:B5:1521:C:H1'	2.55	0.41
39:B5:1834:G:H2'	39:B5:1835:A:O4'	2.21	0.41
39:B5:2223:G:N2	39:B5:2267:OMG:H5''	2.35	0.41
39:B5:3643:C:H4'	39:B5:3942:OMG:HM22	2.03	0.41
41:B8:67:U:H2'	41:B8:68:G:H8	1.86	0.41
42:BA:2:GLY:HA2	42:BA:207:VAL:HG23	2.02	0.41
44:BC:71:ARG:NH2	52:BK:4388:GLU:HG3	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:BD:37:VAL:HG12	45:BD:50:ARG:HD3	2.03	0.41
46:BE:164:ARG:O	46:BE:185:ASN:ND2	2.54	0.41
56:BO:9:LEU:HD23	56:BO:118:MET:HB2	2.02	0.41
71:Bd:68:LEU:HA	71:Bd:108:TYR:HB2	2.03	0.41
84:Bs:85:ASN:OD1	84:Bs:85:ASN:N	2.51	0.41
4:AC:102:VAL:HG12	24:Al:36:ARG:NE	2.36	0.41
20:Ah:70:GLU:OE2	23:Ak:21:LYS:NZ	2.44	0.41
25:Am:38:TYR:CZ	25:Am:78:LYS:HG3	2.56	0.41
25:Am:40:LEU:HD12	25:Am:50:ILE:HG23	2.03	0.41
36:Ax:117:VAL:HG23	36:Ax:122:LYS:HG2	2.03	0.41
39:B5:24:G:O2'	39:B5:26:C:N4	2.48	0.41
39:B5:1089:G:H2'	39:B5:1091:G:H8	1.85	0.41
39:B5:1308:U:OP2	53:BL:36:ARG:NH2	2.45	0.41
39:B5:1365:U:H2'	39:B5:1366:C:C6	2.56	0.41
39:B5:1816:G:O6	69:Bb:10:HIS:NE2	2.51	0.41
39:B5:2382:C:H2'	39:B5:2383:C:C6	2.56	0.41
39:B5:2655:A:H5'	59:BR:88:ARG:HG2	2.02	0.41
41:B8:93:C:O2'	41:B8:94:G:H8	2.03	0.41
41:B8:140:C:H2'	41:B8:141:C:C6	2.56	0.41
54:BM:75:LYS:O	54:BM:79:LYS:HG2	2.20	0.41
58:BQ:111:SER:O	58:BQ:115:LYS:HB2	2.20	0.41
70:Bc:38:ILE:HD11	70:Bc:46:VAL:HG21	2.03	0.41
85:Bt:46:ILE:HD11	85:Bt:62:LEU:HD21	2.03	0.41
85:Bt:78:SER:O	85:Bt:82:ILE:HG13	2.21	0.41
1:A2:813:A:H5''	16:Ad:16:LYS:HD2	2.02	0.41
1:A2:1865:U:H3'	6:AE:5:ARG:HH21	1.85	0.41
6:AE:33:ASP:OD1	6:AE:33:ASP:N	2.54	0.41
7:AF:191:HIS:CG	7:AF:195:LEU:HD11	2.56	0.41
9:AH:3488:A:H2'	9:AH:3489:G:H8	1.86	0.41
9:AH:3537:A:C3'	9:AH:3538:G:H4'	2.50	0.41
12:AZ:210:ILE:HG21	29:Aq:81:ARG:HD3	2.03	0.41
13:Aa:2:ALA:HB2	26:An:68:GLU:OE2	2.21	0.41
14:Ab:256:TRP:CG	34:Av:68:ARG:HD2	2.54	0.41
15:Ac:45:ARG:NH2	15:Ac:82:GLY:O	2.53	0.41
39:B5:423:G:N2	57:BP:118:GLN:OE1	2.40	0.41
39:B5:1343:G:H2'	39:B5:1344:G:C8	2.56	0.41
39:B5:3351:G:N7	87:B5:4913:SPD:H72	2.36	0.41
39:B5:4324:G:H2'	39:B5:4325:PSU:C6	2.56	0.41
39:B5:4330:A:H2'	39:B5:4331:U:O4'	2.21	0.41
39:B5:4621:U:OP1	54:BM:117:LYS:NZ	2.49	0.41
40:B7:27:G:H21	40:B7:55:A:N6	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:BU:48:LYS:HG2	62:BU:53:ALA:HB2	2.03	0.41
66:BY:59:ARG:HG3	66:BY:103:LYS:HD2	2.02	0.41
82:Bp:13:LYS:HE3	82:Bp:14:TYR:CZ	2.56	0.41
1:A2:65:C:C2	18:Af:133:LEU:HD22	2.56	0.41
1:A2:380:C:H5'	20:Ah:33:ALA:HA	2.03	0.41
1:A2:583:U:H2'	1:A2:584:A:H5''	2.02	0.41
1:A2:613:U:H4'	5:AD:89:GLN:NE2	2.36	0.41
1:A2:915:U:OP1	19:Ag:67:PRO:HG3	2.21	0.41
1:A2:1162:U:O4	35:Aw:2:GLY:N	2.54	0.41
1:A2:1798:U:H2'	1:A2:1799:C:C6	2.56	0.41
5:AD:111:GLN:O	5:AD:115:ARG:HG2	2.21	0.41
7:AF:193:GLY:N	7:AF:213:ASP:OD1	2.54	0.41
7:AF:226:HIS:NE2	7:AF:229:THR:HG23	2.36	0.41
9:AH:3543:U:H2'	9:AH:3544:U:C6	2.56	0.41
11:AT:62:C:H2'	11:AT:63:G:C8	2.56	0.41
13:Aa:30:TRP:CD2	13:Aa:48:LEU:HD13	2.56	0.41
18:Af:137:ARG:HD3	18:Af:178:ARG:NH2	2.35	0.41
19:Ag:43:LEU:HB3	19:Ag:72:PHE:CE1	2.56	0.41
27:Ao:17:TYR:HB3	27:Ao:25:LEU:HD11	2.03	0.41
27:Ao:24:GLN:O	27:Ao:28:MET:HG3	2.20	0.41
28:Ap:98:LYS:HD2	28:Ap:99:TYR:CZ	2.56	0.41
29:Aq:38:ILE:H	29:Aq:38:ILE:HG13	1.73	0.41
37:Ay:74:SER:OG	37:Ay:79:ILE:O	2.30	0.41
38:Az:16:LYS:HE2	38:Az:16:LYS:HB2	1.91	0.41
39:B5:113:A:H2'	39:B5:114:G:O4'	2.21	0.41
39:B5:158:A:N1	39:B5:276:C:O2'	2.53	0.41
39:B5:345:C:H2'	39:B5:346:G:C8	2.54	0.41
39:B5:417:G:H1'	41:B8:16:G:N2	2.36	0.41
39:B5:456:C:H2'	39:B5:457:G:H8	1.85	0.41
39:B5:882:U:H2'	39:B5:883:C:C6	2.56	0.41
39:B5:1347:G:H1	39:B5:1369:C:H42	1.67	0.41
39:B5:1727:A:H2'	50:BI:22:PHE:CZ	2.56	0.41
39:B5:1805:U:H2'	39:B5:1806:A:O4'	2.20	0.41
39:B5:1908:G:H4'	84:Bs:36:GLY:HA2	2.01	0.41
39:B5:2321:C:H2'	39:B5:2322:G:O4'	2.21	0.41
39:B5:2387:G:H4'	39:B5:2389:G:N7	2.36	0.41
39:B5:3380:A:H1'	39:B5:3517:A2M:N6	2.35	0.41
39:B5:3609:A:N3	39:B5:4147:G:O2'	2.41	0.41
39:B5:3619:OMC:H5''	56:BO:71:TYR:CE2	2.56	0.41
43:BB:93:VAL:HG23	43:BB:102:PHE:HB2	2.03	0.41
43:BB:117:ARG:HA	43:BB:177:LYS:HD3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:BD:116:ASP:N	45:BD:116:ASP:OD1	2.52	0.41
50:BI:169:LYS:NZ	61:BT:157:GLU:OE2	2.33	0.41
56:BO:10:ASP:OD2	56:BO:37:ARG:NH2	2.38	0.41
67:BZ:68:ILE:O	67:BZ:115:LYS:HG3	2.21	0.41
85:Bt:88:PRO:HA	85:Bt:89:PRO:HD3	1.94	0.41
1:A2:875:G:H2'	1:A2:876:A:C8	2.56	0.41
1:A2:1284:C:O2'	1:A2:1314:A:N1	2.48	0.41
1:A2:1433:U:H5''	1:A2:1434:C:OP2	2.21	0.41
29:Aq:72:LYS:O	29:Aq:76:GLU:HG2	2.20	0.41
34:Av:42:MET:HE2	34:Av:42:MET:HB3	1.96	0.41
39:B5:208:A:C2	39:B5:233:U:H5''	2.56	0.41
39:B5:638:G:H2'	39:B5:639:G:C8	2.55	0.41
39:B5:1556:A:OP1	77:Bj:5:THR:OG1	2.31	0.41
39:B5:1753:C:O2'	69:Bb:42:ASN:OD1	2.33	0.41
39:B5:2325:C:H2'	39:B5:2326:G:H8	1.85	0.41
39:B5:3363:U:O2'	39:B5:3537:U:OP1	2.39	0.41
39:B5:3465:A:H2'	39:B5:3466:PSU:O4'	2.21	0.41
39:B5:3664:U:H2'	39:B5:3665:G:C8	2.56	0.41
39:B5:3684:A:H2'	39:B5:3685:G:H8	1.86	0.41
39:B5:4519:C:H2'	39:B5:4520:C:C6	2.56	0.41
40:B7:97:G:N7	92:B7:305:HOH:O	2.37	0.41
41:B8:75:OMG:HM22	41:B8:76:C:O4'	2.20	0.41
46:BE:48:ARG:HB2	46:BE:64:MET:HE1	2.03	0.41
46:BE:89:GLU:CD	46:BE:89:GLU:H	2.28	0.41
73:Bf:41:PHE:O	73:Bf:45:LYS:NZ	2.40	0.41
74:Bg:56:VAL:HG13	74:Bg:72:LYS:HA	2.03	0.41
75:Bh:82:ASP:OD1	75:Bh:82:ASP:N	2.53	0.41
84:Bs:69:LEU:HD22	84:Bs:76:GLU:HB2	2.02	0.41
85:Bt:80:LEU:HA	85:Bt:83:LYS:HE3	2.02	0.41
85:Bt:80:LEU:HD23	85:Bt:83:LYS:HD2	2.03	0.41
1:A2:118:C:H1'	1:A2:446:A:C5	2.56	0.40
1:A2:152:U:H1'	18:Af:132:ARG:HD2	2.03	0.40
1:A2:867:PSU:H2'	1:A2:868:OMG:C8	2.56	0.40
1:A2:1454:C:O2'	29:Aq:52:GLY:HA3	2.22	0.40
19:Ag:44:ASN:OD1	19:Ag:68:GLN:NE2	2.45	0.40
31:As:39:LEU:HD23	31:As:39:LEU:HA	1.84	0.40
39:B5:681:U:OP1	46:BE:100:GLY:N	2.47	0.40
39:B5:2544:U:H2'	39:B5:2545:C:C6	2.56	0.40
39:B5:3693:G:H2'	39:B5:3695:A:N7	2.36	0.40
39:B5:3952:C:HO2'	39:B5:4081:C:HO2'	1.69	0.40
39:B5:4202:OMC:HM21	43:BB:241:PRO:HD3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:B5:4474:U:H4'	39:B5:4705:A:H1'	2.02	0.40
45:BD:99:TYR:HE2	45:BD:164:LYS:HG3	1.86	0.40
49:BH:14:GLU:CD	49:BH:14:GLU:H	2.29	0.40
49:BH:52:LYS:HE2	49:BH:52:LYS:HB3	1.84	0.40
71:Bd:19:GLU:OE1	71:Bd:92:ARG:NH1	2.55	0.40
1:A2:231:A:H2'	1:A2:232:A:C8	2.56	0.40
1:A2:1512:U:H2'	1:A2:1513:C:C6	2.56	0.40
11:AT:58:1MA:O2'	11:AT:60:C:OP2	2.23	0.40
13:Aa:136:ARG:HB3	13:Aa:216:LYS:HB2	2.03	0.40
22:Aj:86:PRO:HD2	22:Aj:89:ILE:HD12	2.02	0.40
23:Ak:60:CYS:SG	23:Ak:114:SER:OG	2.69	0.40
36:Ax:100:LYS:HE2	36:Ax:100:LYS:HB3	1.97	0.40
39:B5:158:A:H5''	39:B5:159:C:H2'	2.03	0.40
39:B5:663:C:H2'	39:B5:664:G:C8	2.56	0.40
39:B5:1388:A:N6	39:B5:1406:G:O2'	2.55	0.40
39:B5:1664:U:H2'	39:B5:1665:U:C6	2.56	0.40
39:B5:1785:G:H2'	39:B5:1786:C:C6	2.57	0.40
39:B5:2119:A:H2'	39:B5:2120:C:O4'	2.22	0.40
39:B5:2387:G:H2'	39:B5:2388:U:O4'	2.21	0.40
39:B5:2602:G:H1'	39:B5:2607:A:H2	1.86	0.40
39:B5:4324:G:H2'	39:B5:4325:PSU:H6	1.86	0.40
41:B8:106:G:H4'	41:B8:137:A:H5'	2.03	0.40
42:BA:180:LEU:HD21	82:Bp:22:LEU:HB3	2.03	0.40
46:BE:104:ASN:OD1	46:BE:108:ARG:NH2	2.55	0.40
1:A2:51:U:H2'	1:A2:52:G:C8	2.57	0.40
1:A2:727:C:N4	1:A2:728:G:O6	2.54	0.40
7:AF:59:LEU:HD23	7:AF:90:TRP:CD2	2.57	0.40
8:AG:30:LEU:HA	8:AG:39:CYS:HA	2.03	0.40
15:Ac:90:LYS:HD3	15:Ac:91:VAL:N	2.35	0.40
20:Ah:8:TRP:CE3	20:Ah:20:PRO:HB3	2.56	0.40
34:Av:86:LEU:HG	34:Av:90:GLN:HE21	1.86	0.40
39:B5:82:U:H2'	39:B5:83:C:O4'	2.22	0.40
39:B5:106:A:H2'	39:B5:107:G:O4'	2.22	0.40
39:B5:260:C:H2'	39:B5:261:G:H8	1.86	0.40
39:B5:375:G:O3'	44:BC:86:ARG:HG2	2.20	0.40
39:B5:1298:A:N1	39:B5:1329:G:O2'	2.53	0.40
39:B5:1313:C:N4	87:B5:4922:SPD:H31	2.37	0.40
39:B5:1688:A:H2'	39:B5:1689:G:C8	2.57	0.40
39:B5:3548:A:OP1	39:B5:3550:UY1:N1	2.55	0.40
39:B5:3934:U:H2'	39:B5:3935:U:C6	2.56	0.40
39:B5:3985:A:H2'	39:B5:3986:G:C8	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:BM:41:PRO:HB3	54:BM:70:GLN:HG3	2.03	0.40
58:BQ:43:PHE:CD2	58:BQ:133:GLY:HA3	2.56	0.40
58:BQ:177:ALA:O	58:BQ:184:ARG:HB2	2.21	0.40
84:Bs:81:HIS:ND1	84:Bs:191:GLN:OE1	2.55	0.40
1:A2:838:A:C6	36:Ax:47:MET:HE3	2.56	0.40
4:AC:102:VAL:HG12	24:Al:36:ARG:HE	1.86	0.40
4:AC:129:GLY:HA3	24:Al:40:LYS:HA	2.03	0.40
18:Af:145:PHE:HB2	18:Af:147:LEU:HG	2.03	0.40
39:B5:345:C:H2'	39:B5:346:G:H8	1.86	0.40
39:B5:1617:C:OP2	72:Be:39:ARG:NH2	2.52	0.40
39:B5:1809:C:H2'	39:B5:1810:A2M:H8	2.02	0.40
39:B5:2110:U:C6	39:B5:2113:G:H4'	2.57	0.40
39:B5:2146:C:H5''	72:Be:104:SER:HB3	2.04	0.40
47:BF:170:ASP:OD1	47:BF:171:ASN:N	2.54	0.40
66:BY:2:LYS:HE3	66:BY:2:LYS:HB3	1.85	0.40
1:A2:62:G:H1'	1:A2:172:OMU:HM23	2.02	0.40
1:A2:126:G:H2'	18:Af:199:THR:HG21	2.04	0.40
1:A2:485:A2M:HM'2	1:A2:486:A:C4	2.57	0.40
1:A2:503:C:O4'	16:Ad:66:MET:HG3	2.21	0.40
1:A2:1434:C:O2'	1:A2:1435:C:O4'	2.39	0.40
15:Ac:48:ILE:HG13	15:Ac:86:LEU:HG	2.04	0.40
18:Af:12:CYS:SG	18:Af:127:THR:HG23	2.62	0.40
39:B5:2249:G:N7	79:Bl:2:SER:N	2.70	0.40
39:B5:4111:C:OP1	58:BQ:184:ARG:NH2	2.54	0.40
44:BC:157:LYS:HE2	44:BC:157:LYS:HB3	1.89	0.40
48:BG:138:ALA:HB2	48:BG:194:VAL:HG11	2.04	0.40
48:BG:160:ASP:OD1	48:BG:160:ASP:N	2.52	0.40
55:BN:143:ARG:NH1	75:Bh:95:LEU:HD23	2.37	0.40
66:BY:55:VAL:HG12	66:BY:106:ILE:HA	2.02	0.40
79:Bl:20:ASN:ND2	79:Bl:42:ARG:O	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AA	81/84 (96%)	79 (98%)	2 (2%)	0	100	100
3	AB	61/69 (88%)	61 (100%)	0	0	100	100
4	AC	72/156 (46%)	70 (97%)	2 (3%)	0	100	100
5	AD	55/133 (41%)	54 (98%)	1 (2%)	0	100	100
6	AE	99/115 (86%)	99 (100%)	0	0	100	100
7	AF	311/317 (98%)	302 (97%)	9 (3%)	0	100	100
8	AG	53/56 (95%)	53 (100%)	0	0	100	100
12	AZ	219/295 (74%)	214 (98%)	5 (2%)	0	100	100
13	Aa	220/264 (83%)	218 (99%)	2 (1%)	0	100	100
14	Ab	218/293 (74%)	217 (100%)	1 (0%)	0	100	100
15	Ac	223/281 (79%)	222 (100%)	1 (0%)	0	100	100
16	Ad	260/263 (99%)	257 (99%)	3 (1%)	0	100	100
17	Ae	189/204 (93%)	186 (98%)	3 (2%)	0	100	100
18	Af	235/249 (94%)	234 (100%)	1 (0%)	0	100	100
19	Ag	188/432 (44%)	186 (99%)	2 (1%)	0	100	100
20	Ah	204/208 (98%)	201 (98%)	3 (2%)	0	100	100
21	Ai	183/194 (94%)	180 (98%)	3 (2%)	0	100	100
22	Aj	94/165 (57%)	91 (97%)	3 (3%)	0	100	100
23	Ak	152/158 (96%)	149 (98%)	3 (2%)	0	100	100
24	Al	122/132 (92%)	119 (98%)	3 (2%)	0	100	100
25	Am	148/151 (98%)	148 (100%)	0	0	100	100
26	An	134/151 (89%)	131 (98%)	3 (2%)	0	100	100
27	Ao	126/145 (87%)	125 (99%)	0	1 (1%)	16	25
28	Ap	139/172 (81%)	135 (97%)	3 (2%)	1 (1%)	18	28
29	Aq	132/135 (98%)	132 (100%)	0	0	100	100
30	Ar	146/152 (96%)	143 (98%)	3 (2%)	0	100	100
31	As	140/145 (97%)	139 (99%)	1 (1%)	0	100	100
32	At	102/119 (86%)	101 (99%)	1 (1%)	0	100	100
33	Au	81/83 (98%)	81 (100%)	0	0	100	100
34	Av	127/130 (98%)	126 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	Aw	138/143 (96%)	136 (99%)	2 (1%)	0	100	100
36	Ax	123/130 (95%)	123 (100%)	0	0	100	100
37	Ay	83/124 (67%)	81 (98%)	2 (2%)	0	100	100
38	Az	23/25 (92%)	23 (100%)	0	0	100	100
42	BA	250/257 (97%)	242 (97%)	8 (3%)	0	100	100
43	BB	395/403 (98%)	391 (99%)	4 (1%)	0	100	100
44	BC	360/413 (87%)	356 (99%)	4 (1%)	0	100	100
45	BD	291/297 (98%)	289 (99%)	2 (1%)	0	100	100
46	BE	239/291 (82%)	233 (98%)	6 (2%)	0	100	100
47	BF	224/247 (91%)	218 (97%)	6 (3%)	0	100	100
48	BG	229/266 (86%)	228 (100%)	1 (0%)	0	100	100
49	BH	188/192 (98%)	188 (100%)	0	0	100	100
50	BI	211/214 (99%)	206 (98%)	5 (2%)	0	100	100
51	BJ	168/178 (94%)	168 (100%)	0	0	100	100
52	BK	33/1071 (3%)	33 (100%)	0	0	100	100
53	BL	208/211 (99%)	205 (99%)	3 (1%)	0	100	100
54	BM	136/218 (62%)	134 (98%)	2 (2%)	0	100	100
55	BN	201/204 (98%)	197 (98%)	4 (2%)	0	100	100
56	BO	197/203 (97%)	195 (99%)	2 (1%)	0	100	100
57	BP	157/184 (85%)	155 (99%)	2 (1%)	0	100	100
58	BQ	185/188 (98%)	182 (98%)	3 (2%)	0	100	100
59	BR	178/196 (91%)	178 (100%)	0	0	100	100
60	BS	174/176 (99%)	174 (100%)	0	0	100	100
61	BT	157/160 (98%)	156 (99%)	1 (1%)	0	100	100
62	BU	97/128 (76%)	96 (99%)	1 (1%)	0	100	100
63	BV	137/140 (98%)	136 (99%)	1 (1%)	0	100	100
64	BW	119/157 (76%)	119 (100%)	0	0	100	100
65	BX	116/156 (74%)	115 (99%)	1 (1%)	0	100	100
66	BY	132/145 (91%)	131 (99%)	1 (1%)	0	100	100
67	BZ	133/136 (98%)	132 (99%)	1 (1%)	0	100	100
68	Ba	144/148 (97%)	138 (96%)	5 (4%)	1 (1%)	18	28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	Bb	103/245 (42%)	99 (96%)	4 (4%)	0	100	100
70	Bc	106/115 (92%)	106 (100%)	0	0	100	100
71	Bd	105/125 (84%)	105 (100%)	0	0	100	100
72	Be	128/135 (95%)	128 (100%)	0	0	100	100
73	Bf	108/110 (98%)	108 (100%)	0	0	100	100
74	Bg	112/117 (96%)	111 (99%)	1 (1%)	0	100	100
75	Bh	120/123 (98%)	119 (99%)	1 (1%)	0	100	100
76	Bi	100/105 (95%)	99 (99%)	1 (1%)	0	100	100
77	Bj	84/97 (87%)	84 (100%)	0	0	100	100
78	Bk	67/70 (96%)	67 (100%)	0	0	100	100
79	Bl	48/51 (94%)	48 (100%)	0	0	100	100
80	Bm	49/128 (38%)	49 (100%)	0	0	100	100
81	Bo	102/106 (96%)	100 (98%)	2 (2%)	0	100	100
82	Bp	89/92 (97%)	86 (97%)	3 (3%)	0	100	100
83	Br	124/137 (90%)	122 (98%)	2 (2%)	0	100	100
84	Bs	194/318 (61%)	189 (97%)	5 (3%)	0	100	100
85	Bt	154/165 (93%)	152 (99%)	2 (1%)	0	100	100
86	Bv	210/217 (97%)	197 (94%)	13 (6%)	0	100	100
All	All	11943/14908 (80%)	11780 (99%)	160 (1%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
27	Ao	137	HIS
28	Ap	100	VAL
68	Ba	15	VAL

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	AA	75/76 (99%)	74 (99%)	1 (1%)	61	80
3	AB	56/62 (90%)	55 (98%)	1 (2%)	51	73
4	AC	67/140 (48%)	67 (100%)	0	100	100
5	AD	47/106 (44%)	46 (98%)	1 (2%)	47	69
6	AE	88/98 (90%)	86 (98%)	2 (2%)	44	66
7	AF	272/275 (99%)	268 (98%)	4 (2%)	57	77
8	AG	48/49 (98%)	48 (100%)	0	100	100
12	AZ	182/243 (75%)	175 (96%)	7 (4%)	29	49
13	Aa	203/231 (88%)	201 (99%)	2 (1%)	68	84
14	Ab	185/223 (83%)	184 (100%)	1 (0%)	81	91
15	Ac	189/232 (82%)	185 (98%)	4 (2%)	47	69
16	Ad	224/225 (100%)	224 (100%)	0	100	100
17	Ae	161/170 (95%)	160 (99%)	1 (1%)	78	89
18	Af	207/218 (95%)	206 (100%)	1 (0%)	81	91
19	Ag	170/360 (47%)	169 (99%)	1 (1%)	78	89
20	Ah	178/180 (99%)	177 (99%)	1 (1%)	78	89
21	Ai	161/168 (96%)	160 (99%)	1 (1%)	78	89
22	Aj	87/136 (64%)	86 (99%)	1 (1%)	65	82
23	Ak	139/142 (98%)	139 (100%)	0	100	100
24	Al	104/108 (96%)	101 (97%)	3 (3%)	37	60
25	Am	130/131 (99%)	130 (100%)	0	100	100
26	An	106/119 (89%)	105 (99%)	1 (1%)	70	85
27	Ao	114/130 (88%)	113 (99%)	1 (1%)	70	85
28	Ap	117/140 (84%)	117 (100%)	0	100	100
29	Aq	120/121 (99%)	120 (100%)	0	100	100
30	Ar	127/131 (97%)	124 (98%)	3 (2%)	43	65
31	As	112/114 (98%)	112 (100%)	0	100	100
32	At	94/107 (88%)	92 (98%)	2 (2%)	47	69
33	Au	67/67 (100%)	65 (97%)	2 (3%)	36	58
34	Av	112/113 (99%)	112 (100%)	0	100	100
35	Aw	112/114 (98%)	110 (98%)	2 (2%)	51	73
36	Ax	107/112 (96%)	107 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	Ay	75/102 (74%)	75 (100%)	0	100	100
38	Az	24/24 (100%)	24 (100%)	0	100	100
42	BA	194/198 (98%)	193 (100%)	1 (0%)	81	91
43	BB	344/347 (99%)	342 (99%)	2 (1%)	78	89
44	BC	302/337 (90%)	301 (100%)	1 (0%)	86	93
45	BD	247/250 (99%)	247 (100%)	0	100	100
46	BE	216/251 (86%)	214 (99%)	2 (1%)	70	85
47	BF	197/215 (92%)	197 (100%)	0	100	100
48	BG	199/223 (89%)	198 (100%)	1 (0%)	81	91
49	BH	169/171 (99%)	169 (100%)	0	100	100
50	BI	180/181 (99%)	179 (99%)	1 (1%)	78	89
51	BJ	143/149 (96%)	143 (100%)	0	100	100
52	BK	30/936 (3%)	30 (100%)	0	100	100
53	BL	175/176 (99%)	173 (99%)	2 (1%)	65	82
54	BM	117/161 (73%)	117 (100%)	0	100	100
55	BN	171/172 (99%)	171 (100%)	0	100	100
56	BO	171/173 (99%)	171 (100%)	0	100	100
57	BP	140/163 (86%)	140 (100%)	0	100	100
58	BQ	164/165 (99%)	161 (98%)	3 (2%)	51	73
59	BR	159/175 (91%)	157 (99%)	2 (1%)	61	80
60	BS	154/154 (100%)	154 (100%)	0	100	100
61	BT	139/140 (99%)	138 (99%)	1 (1%)	76	88
62	BU	88/113 (78%)	88 (100%)	0	100	100
63	BV	106/107 (99%)	106 (100%)	0	100	100
64	BW	100/126 (79%)	99 (99%)	1 (1%)	68	84
65	BX	106/134 (79%)	106 (100%)	0	100	100
66	BY	124/135 (92%)	124 (100%)	0	100	100
67	BZ	117/118 (99%)	117 (100%)	0	100	100
68	Ba	118/119 (99%)	118 (100%)	0	100	100
69	Bb	87/183 (48%)	87 (100%)	0	100	100
70	Bc	92/98 (94%)	91 (99%)	1 (1%)	65	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
71	Bd	98/110 (89%)	98 (100%)	0	100	100
72	Be	116/121 (96%)	116 (100%)	0	100	100
73	Bf	89/89 (100%)	89 (100%)	0	100	100
74	Bg	98/100 (98%)	98 (100%)	0	100	100
75	Bh	109/110 (99%)	109 (100%)	0	100	100
76	Bi	86/89 (97%)	86 (100%)	0	100	100
77	Bj	73/80 (91%)	73 (100%)	0	100	100
78	Bk	64/65 (98%)	63 (98%)	1 (2%)	55	76
79	Bl	47/48 (98%)	45 (96%)	2 (4%)	26	44
80	Bm	47/115 (41%)	47 (100%)	0	100	100
81	Bo	92/93 (99%)	92 (100%)	0	100	100
82	Bp	74/75 (99%)	74 (100%)	0	100	100
83	Br	109/120 (91%)	109 (100%)	0	100	100
84	Bs	164/258 (64%)	161 (98%)	3 (2%)	51	73
85	Bt	128/137 (93%)	124 (97%)	4 (3%)	35	57
86	Bv	191/195 (98%)	186 (97%)	5 (3%)	40	63
All	All	10394/12642 (82%)	10318 (99%)	76 (1%)	73	88

All (76) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AA	74	THR
3	AB	14	VAL
5	AD	91	LEU
6	AE	40	VAL
6	AE	75	VAL
7	AF	107	ASP
7	AF	113	PHE
7	AF	235	ILE
7	AF	258	ILE
12	AZ	28	THR
12	AZ	77	ILE
12	AZ	87	VAL
12	AZ	121	LEU
12	AZ	125	THR
12	AZ	192	GLU

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Mol	Chain	Res	Type
12	AZ	206	ASP
13	Aa	9	LEU
13	Aa	178	THR
14	Ab	121	ARG
15	Ac	46	THR
15	Ac	56	GLN
15	Ac	72	VAL
15	Ac	96	LEU
17	Ae	43	GLU
18	Af	44	GLU
19	Ag	53	VAL
20	Ah	46	VAL
21	Ai	152	ASP
22	Aj	40	VAL
24	Al	75	ASN
24	Al	79	VAL
24	Al	104	VAL
26	An	138	ASP
27	Ao	105	VAL
30	Ar	83	PHE
30	Ar	94	LYS
30	Ar	103	LEU
32	At	54	VAL
32	At	68	THR
33	Au	42	VAL
33	Au	61	ARG
35	Aw	105	PHE
35	Aw	125	VAL
42	BA	208	GLU
43	BB	90	VAL
43	BB	162	VAL
44	BC	157	LYS
46	BE	223	LYS
46	BE	289	LEU
48	BG	220	GLU
50	BI	163	GLN
53	BL	81	LEU
53	BL	115	GLN
58	BQ	14	ARG
58	BQ	82	VAL
58	BQ	115	LYS
59	BR	3	MET

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Mol	Chain	Res	Type
59	BR	106	LEU
61	BT	76	VAL
64	BW	66	GLU
70	Bc	94	LEU
78	Bk	36	VAL
79	Bl	47	THR
79	Bl	51	LEU
84	Bs	44	ARG
84	Bs	78	LEU
84	Bs	107	VAL
85	Bt	15	LEU
85	Bt	35	LEU
85	Bt	73	VAL
85	Bt	74	VAL
86	Bv	58	THR
86	Bv	60	ARG
86	Bv	96	ASN
86	Bv	99	LEU
86	Bv	159	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (108) such sidechains are listed below:

Mol	Chain	Res	Type
2	AA	29	ASN
2	AA	51	GLN
5	AD	89	GLN
6	AE	72	HIS
7	AF	62	HIS
7	AF	147	HIS
7	AF	196	ASN
8	AG	3	HIS
8	AG	28	HIS
12	AZ	9	GLN
12	AZ	193	HIS
13	Aa	76	ASN
13	Aa	158	HIS
13	Aa	160	GLN
16	Ad	142	HIS
16	Ad	157	ASN
16	Ad	201	HIS
17	Ae	65	GLN
17	Ae	118	ASN

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Mol	Chain	Res	Type
19	Ag	91	HIS
20	Ah	7	ASN
20	Ah	116	HIS
20	Ah	167	GLN
22	Aj	50	GLN
22	Aj	61	GLN
22	Aj	66	HIS
22	Aj	77	GLN
22	Aj	84	HIS
23	Ak	11	GLN
23	Ak	18	GLN
23	Ak	19	ASN
23	Ak	39	ASN
24	Al	72	HIS
26	An	113	GLN
27	Ao	32	GLN
27	Ao	104	GLN
28	Ap	24	HIS
28	Ap	86	GLN
28	Ap	97	GLN
28	Ap	114	GLN
29	Aq	121	GLN
30	Ar	72	GLN
31	As	12	GLN
33	Au	35	ASN
34	Av	90	GLN
34	Av	91	ASN
35	Aw	92	ASN
37	Ay	112	ASN
42	BA	22	HIS
42	BA	140	ASN
42	BA	205	ASN
43	BB	186	ASN
43	BB	289	GLN
44	BC	50	GLN
44	BC	85	HIS
44	BC	212	ASN
44	BC	276	ASN
47	BF	115	GLN
47	BF	118	ASN
48	BG	38	ASN
48	BG	64	GLN

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Mol	Chain	Res	Type
48	BG	100	HIS
48	BG	141	ASN
49	BH	98	HIS
50	BI	59	GLN
50	BI	73	ASN
52	BK	4397	GLN
53	BL	104	ASN
54	BM	33	GLN
56	BO	180	GLN
57	BP	34	GLN
57	BP	97	ASN
57	BP	137	ASN
58	BQ	7	HIS
58	BQ	45	GLN
58	BQ	57	ASN
59	BR	75	HIS
59	BR	143	HIS
61	BT	131	GLN
63	BV	50	ASN
64	BW	120	GLN
66	BY	18	HIS
68	Ba	34	ASN
71	Bd	34	HIS
71	Bd	116	ASN
72	Be	23	HIS
72	Be	52	GLN
74	Bg	28	ASN
75	Bh	98	HIS
76	Bi	15	HIS
76	Bi	26	HIS
76	Bi	36	HIS
77	Bj	13	ASN
77	Bj	57	ASN
77	Bj	66	HIS
78	Bk	58	GLN
79	Bl	25	GLN
80	Bm	117	HIS
81	Bo	102	GLN
83	Br	6	GLN
84	Bs	34	ASN
84	Bs	41	GLN
84	Bs	68	HIS

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Mol	Chain	Res	Type
84	Bs	179	ASN
84	Bs	190	GLN
85	Bt	70	GLN
85	Bt	100	HIS
86	Bv	44	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A2	1764/1870 (94%)	226 (12%)	0
10	AI	2/76 (2%)	1 (50%)	0
11	AT	75/76 (98%)	10 (13%)	0
39	B5	3752/4808 (78%)	489 (13%)	3 (0%)
40	B7	118/120 (98%)	8 (6%)	0
41	B8	155/158 (98%)	17 (10%)	0
9	AH	94/220 (42%)	29 (30%)	0
All	All	5960/7328 (81%)	780 (13%)	3 (0%)

All (780) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A2	2	A
1	A2	3	C
1	A2	4	C
1	A2	33	G
1	A2	41	G
1	A2	46	A
1	A2	56	G
1	A2	58	C
1	A2	67	C
1	A2	68	A
1	A2	73	C
1	A2	74	G
1	A2	75	G
1	A2	76	U
1	A2	77	A
1	A2	79	A
1	A2	103	A
1	A2	113	G
1	A2	115	U
1	A2	124	U

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Mol	Chain	Res	Type
1	A2	126	G
1	A2	130	G
1	A2	143	U
1	A2	147	A
1	A2	155	G
1	A2	162	C
1	A2	163	U
1	A2	168	C
1	A2	178	C
1	A2	184	G
1	A2	188	C
1	A2	192	C
1	A2	226	A
1	A2	282	C
1	A2	306	U
1	A2	307	C
1	A2	308	G
1	A2	310	G
1	A2	313	G
1	A2	320	C
1	A2	324	C
1	A2	325	U
1	A2	327	C
1	A2	328	G
1	A2	336	G
1	A2	348	G
1	A2	363	C
1	A2	365	A
1	A2	369	U
1	A2	370	C
1	A2	386	G
1	A2	387	C
1	A2	401	C
1	A2	410	C
1	A2	422	G
1	A2	439	G
1	A2	449	A
1	A2	450	A
1	A2	451	C
1	A2	465	A
1	A2	466	A
1	A2	472	G

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Mol	Chain	Res	Type
1	A2	473	C
1	A2	474	A
1	A2	475	G
1	A2	483	G
1	A2	488	U
1	A2	493	C
1	A2	526	A
1	A2	548	G
1	A2	557	U
1	A2	565	A
1	A2	569	C
1	A2	577	A2M
1	A2	584	A
1	A2	590	G
1	A2	592	U
1	A2	607	G
1	A2	608	U
1	A2	609	C
1	A2	615	C
1	A2	629	A
1	A2	632	U
1	A2	644	A
1	A2	645	OMG
1	A2	656	A
1	A2	661	C
1	A2	669	A2M
1	A2	670	A
1	A2	671	A
1	A2	672	A
1	A2	673	A
1	A2	674	G
1	A2	698	G
1	A2	734	C
1	A2	747	C
1	A2	748	U
1	A2	750	U
1	A2	755	G
1	A2	756	C
1	A2	798	C
1	A2	799	G
1	A2	802	PSU
1	A2	812	A

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Mol	Chain	Res	Type
1	A2	822	G
1	A2	823	PSU
1	A2	831	A
1	A2	832	G
1	A2	837	G
1	A2	838	A
1	A2	839	G
1	A2	840	C
1	A2	841	C
1	A2	842	G
1	A2	848	A
1	A2	860	G
1	A2	871	A
1	A2	873	A
1	A2	879	G
1	A2	886	U
1	A2	892	G
1	A2	910	G
1	A2	914	A
1	A2	915	U
1	A2	921	A
1	A2	923	A
1	A2	934	G
1	A2	944	U
1	A2	956	A
1	A2	964	A
1	A2	972	G
1	A2	991	A
1	A2	993	A
1	A2	1000	G
1	A2	1018	U
1	A2	1024	A
1	A2	1061	A
1	A2	1062	U
1	A2	1063	A
1	A2	1084	A
1	A2	1086	C
1	A2	1116	U
1	A2	1117	C
1	A2	1118	C
1	A2	1119	C
1	A2	1122	G

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Mol	Chain	Res	Type
1	A2	1134	A
1	A2	1145	A
1	A2	1154	C
1	A2	1155	U
1	A2	1196	A
1	A2	1208	G
1	A2	1216	C
1	A2	1225	G
1	A2	1243	U
1	A2	1252	A
1	A2	1254	A
1	A2	1257	G
1	A2	1258	G
1	A2	1260	A
1	A2	1266	A
1	A2	1272	C
1	A2	1275	G
1	A2	1276	G
1	A2	1283	A
1	A2	1303	G
1	A2	1304	C
1	A2	1343	U
1	A2	1349	G
1	A2	1359	U
1	A2	1372	U
1	A2	1373	U
1	A2	1379	A
1	A2	1398	U
1	A2	1403	A
1	A2	1406	A
1	A2	1407	G
1	A2	1419	C
1	A2	1420	C
1	A2	1422	A
1	A2	1424	C
1	A2	1425	G
1	A2	1436	C
1	A2	1438	C
1	A2	1455	A
1	A2	1463	U
1	A2	1464	U
1	A2	1481	A

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Mol	Chain	Res	Type
1	A2	1488	A
1	A2	1490	A
1	A2	1491	OMG
1	A2	1498	G
1	A2	1510	U
1	A2	1522	C
1	A2	1523	A
1	A2	1534	A
1	A2	1553	G
1	A2	1554	C
1	A2	1571	G
1	A2	1581	A
1	A2	1589	A
1	A2	1602	A
1	A2	1622	U
1	A2	1624	A
1	A2	1655	G
1	A2	1666	G
1	A2	1681	G
1	A2	1699	C
1	A2	1700	A
1	A2	1722	U
1	A2	1723	G
1	A2	1749	G
1	A2	1783	G
1	A2	1784	C
1	A2	1785	G
1	A2	1830	G
1	A2	1832	A
1	A2	1837	G
1	A2	1839	U
1	A2	1850	G
1	A2	1852	MA6
1	A2	1862	G
1	A2	1863	G
1	A2	1864	A
1	A2	1865	U
1	A2	1866	C
9	AH	3453	A
9	AH	3454	C
9	AH	3455	A
9	AH	3456	A

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Mol	Chain	Res	Type
9	AH	3465	A
9	AH	3469	G
9	AH	3470	G
9	AH	3471	G
9	AH	3474	U
9	AH	3479	U
9	AH	3480	G
9	AH	3482	A
9	AH	3483	A
9	AH	3485	U
9	AH	3486	G
9	AH	3487	C
9	AH	3488	A
9	AH	3501	C
9	AH	3504	U
9	AH	3516	A
9	AH	3520	G
9	AH	3527	U
9	AH	3531	G
9	AH	3532	U
9	AH	3533	A
9	AH	3534	U
9	AH	3535	A
9	AH	3538	G
9	AH	3540	G
10	AI	76	A
11	AT	16	H2U
11	AT	17	H2U
11	AT	18	G
11	AT	19	G
11	AT	20	G
11	AT	21	A
11	AT	22	G
11	AT	46	G7M
11	AT	48	C
11	AT	76	A
39	B5	39	A
39	B5	42	A
39	B5	58	G
39	B5	59	A
39	B5	64	A
39	B5	65	A

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Mol	Chain	Res	Type
39	B5	74	G
39	B5	85	G
39	B5	91	G
39	B5	98	A
39	B5	109	G
39	B5	110	C
39	B5	119	G
39	B5	127	G
39	B5	135	G
39	B5	136	U
39	B5	159	C
39	B5	184	U
39	B5	187	U
39	B5	188	G
39	B5	200	U
39	B5	201	C
39	B5	209	U
39	B5	210	C
39	B5	218	A
39	B5	219	G
39	B5	233	U
39	B5	234	G
39	B5	253	G
39	B5	266	C
39	B5	297	U
39	B5	309	C
39	B5	315	G
39	B5	316	U
39	B5	326	C
39	B5	334	A
39	B5	340	C
39	B5	363	A
39	B5	387	G
39	B5	409	G
39	B5	410	A
39	B5	412	G
39	B5	440	U
39	B5	446	C
39	B5	449	C
39	B5	450	G
39	B5	452	A
39	B5	453	G

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Mol	Chain	Res	Type
39	B5	454	U
39	B5	463	A
39	B5	467	U
39	B5	468	U
39	B5	482	U
39	B5	483	G
39	B5	484	G
39	B5	485	U
39	B5	486	C
39	B5	493	U
39	B5	497	G
39	B5	499	C
39	B5	502	U
39	B5	503	C
39	B5	504	U
39	B5	505	C
39	B5	506	G
39	B5	515	U
39	B5	516	U
39	B5	517	C
39	B5	628	U
39	B5	634	C
39	B5	635	G
39	B5	660	G
39	B5	691	G
39	B5	698	C
39	B5	699	G
39	B5	724	G
39	B5	725	G
39	B5	732	C
39	B5	734	G
39	B5	739	G
39	B5	758	C
39	B5	759	G
39	B5	760	C
39	B5	761	C
39	B5	790	G
39	B5	791	C
39	B5	792	G
39	B5	795	A
39	B5	797	C
39	B5	798	C

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Mol	Chain	Res	Type
39	B5	810	U
39	B5	812	A
39	B5	814	A
39	B5	815	G
39	B5	824	C
39	B5	825	G
39	B5	831	A
39	B5	832	G
39	B5	835	G
39	B5	836	C
39	B5	841	C
39	B5	843	A
39	B5	844	A
39	B5	845	U
39	B5	846	C
39	B5	856	A
39	B5	859	G
39	B5	860	A
39	B5	861	G
39	B5	866	A
39	B5	867	C
39	B5	868	C
39	B5	869	U
39	B5	870	G
39	B5	884	U
39	B5	983	G
39	B5	984	G
39	B5	985	G
39	B5	987	C
39	B5	1072	C
39	B5	1073	C
39	B5	1074	C
39	B5	1084	C
39	B5	1091	G
39	B5	1102	G
39	B5	1105	C
39	B5	1106	U
39	B5	1124	A
39	B5	1127	G
39	B5	1133	C
39	B5	1202	C
39	B5	1214	A

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Mol	Chain	Res	Type
39	B5	1215	G
39	B5	1216	C
39	B5	1217	G
39	B5	1219	G
39	B5	1221	G
39	B5	1228	G
39	B5	1229	U
39	B5	1231	G
39	B5	1238	A
39	B5	1240	G
39	B5	1246	U
39	B5	1247	A
39	B5	1257	C
39	B5	1270	A2M
39	B5	1281	A
39	B5	1298	A
39	B5	1299	G
39	B5	1303	G
39	B5	1309	C
39	B5	1310	G
39	B5	1331	A
39	B5	1341	A
39	B5	1348	G
39	B5	1351	G
39	B5	1362	C
39	B5	1367	G
39	B5	1375	A
39	B5	1391	C
39	B5	1392	C
39	B5	1393	C
39	B5	1401	C
39	B5	1439	G
39	B5	1452	A
39	B5	1453	G
39	B5	1457	G
39	B5	1469	U
39	B5	1489	A2M
39	B5	1502	A
39	B5	1521	C
39	B5	1533	U
39	B5	1546	U
39	B5	1551	U

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Mol	Chain	Res	Type
39	B5	1579	G
39	B5	1580	OMG
39	B5	1586	A
39	B5	1588	G
39	B5	1589	A
39	B5	1593	A
39	B5	1595	C
39	B5	1596	G
39	B5	1597	A
39	B5	1609	G
39	B5	1616	C
39	B5	1631	C
39	B5	1632	PSU
39	B5	1653	C
39	B5	1657	C
39	B5	1658	C
39	B5	1673	G
39	B5	1694	C
39	B5	1704	A
39	B5	1705	A
39	B5	1726	A
39	B5	1743	A
39	B5	1745	G
39	B5	1751	C
39	B5	1754	G
39	B5	1767	C
39	B5	1774	G
39	B5	1775	G
39	B5	1776	A
39	B5	1781	G
39	B5	1782	A
39	B5	1794	G
39	B5	1808	G
39	B5	1836	A
39	B5	1857	U
39	B5	1859	C
39	B5	1860	C
39	B5	1861	G
39	B5	1870	C
39	B5	1871	A
39	B5	1879	G
39	B5	1887	G

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Mol	Chain	Res	Type
39	B5	1890	G
39	B5	1898	U
39	B5	1899	A
39	B5	1900	G
39	B5	1913	U
39	B5	1914	G
39	B5	1916	C
39	B5	1922	A
39	B5	1923	A
39	B5	1924	G
39	B5	1925	U
39	B5	1926	C
39	B5	1936	U
39	B5	1940	G
39	B5	1942	G
39	B5	1943	U
39	B5	1963	G
39	B5	1965	A
39	B5	1985	G
39	B5	1987	U
39	B5	1994	G
39	B5	1995	G
39	B5	2008	A
39	B5	2023	U
39	B5	2032	G
39	B5	2034	A
39	B5	2037	G
39	B5	2041	G
39	B5	2043	A
39	B5	2044	A
39	B5	2045	G
39	B5	2046	A
39	B5	2047	G
39	B5	2050	U
39	B5	2101	C
39	B5	2132	C
39	B5	2143	A
39	B5	2144	G
39	B5	2156	A
39	B5	2157	G
39	B5	2191	G
39	B5	2194	OMC

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Mol	Chain	Res	Type
39	B5	2203	A
39	B5	2207	OMG
39	B5	2238	A
39	B5	2253	C
39	B5	2264	G
39	B5	2268	U
39	B5	2332	C
39	B5	2333	U
39	B5	2334	C
39	B5	2349	G
39	B5	2356	A
39	B5	2372	A
39	B5	2380	A
39	B5	2386	A
39	B5	2387	G
39	B5	2388	U
39	B5	2390	G
39	B5	2397	U
39	B5	2409	G
39	B5	2416	A
39	B5	2430	A
39	B5	2432	C
39	B5	2444	A
39	B5	2470	C
39	B5	2496	C
39	B5	2503	A
39	B5	2512	C
39	B5	2530	U
39	B5	2537	G
39	B5	2538	A
39	B5	2539	A
39	B5	2546	G
39	B5	2551	U
39	B5	2552	C
39	B5	2553	C
39	B5	2554	G
39	B5	2578	G
39	B5	2586	A
39	B5	2606	U
39	B5	2612	U
39	B5	2631	U
39	B5	2633	U

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Mol	Chain	Res	Type
39	B5	2641	A
39	B5	2646	U
39	B5	2657	C
39	B5	2669	U
39	B5	2670	G
39	B5	2672	U
39	B5	2698	G
39	B5	2745	G
39	B5	3329	G
39	B5	3350	C
39	B5	3358	G
39	B5	3362	A
39	B5	3367	A
39	B5	3376	U
39	B5	3385	A
39	B5	3394	A
39	B5	3396	G
39	B5	3405	C
39	B5	3428	C
39	B5	3443	A
39	B5	3444	A
39	B5	3485	G
39	B5	3492	A2M
39	B5	3493	C
39	B5	3498	A
39	B5	3508	G
39	B5	3509	G
39	B5	3516	A
39	B5	3543	G
39	B5	3544	C
39	B5	3546	U
39	B5	3549	A
39	B5	3551	G
39	B5	3570	U
39	B5	3571	G
39	B5	3572	U
39	B5	3599	A2M
39	B5	3609	A
39	B5	3610	C
39	B5	3611	G
39	B5	3629	G
39	B5	3633	A

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Mol	Chain	Res	Type
39	B5	3638	A
39	B5	3639	G
39	B5	3640	A
39	B5	3647	U
39	B5	3670	G
39	B5	3688	G
39	B5	3689	U
39	B5	3801	A
39	B5	3804	G
39	B5	3823	G
39	B5	3824	C
39	B5	3825	G
39	B5	3832	G
39	B5	3833	A
39	B5	3834	G
39	B5	3846	U
39	B5	3847	C
39	B5	3850	G
39	B5	3855	A
39	B5	3869	G
39	B5	3874	U
39	B5	3875	C
39	B5	3891	C
39	B5	3892	G
39	B5	3896	G
39	B5	3904	C
39	B5	3909	U
39	B5	3916	A
39	B5	3929	G
39	B5	3930	G
39	B5	3937	G
39	B5	3949	A
39	B5	3975	U
39	B5	3979	A
39	B5	3997	A
39	B5	4000	G
39	B5	4004	C
39	B5	4012	G
39	B5	4014	A
39	B5	4017	A
39	B5	4019	A
39	B5	4027	A

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Mol	Chain	Res	Type
39	B5	4037	G
39	B5	4050	A
39	B5	4051	G
39	B5	4052	OMU
39	B5	4060	C
39	B5	4075	G
39	B5	4076	G
39	B5	4078	C
39	B5	4096	C
39	B5	4119	G
39	B5	4122	A
39	B5	4123	G
39	B5	4124	A
39	B5	4126	A
39	B5	4133	C
39	B5	4137	G
39	B5	4140	A
39	B5	4161	A
39	B5	4168	A
39	B5	4194	G
39	B5	4210	A
39	B5	4212	C
39	B5	4221	G
39	B5	4258	U
39	B5	4259	A
39	B5	4261	G
39	B5	4265	C
39	B5	4270	G
39	B5	4274	G
39	B5	4294	A
39	B5	4306	C
39	B5	4313	G
39	B5	4321	G
39	B5	4336	A2M
39	B5	4382	PSU
39	B5	4383	OMG
39	B5	4402	A
39	B5	4403	U
39	B5	4416	C
39	B5	4418	A
39	B5	4437	A
39	B5	4446	A

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Mol	Chain	Res	Type
39	B5	4454	A
39	B5	4455	U
39	B5	4465	G
39	B5	4475	A
39	B5	4476	C
39	B5	4477	G
39	B5	4478	G
39	B5	4479	C
39	B5	4486	G
39	B5	4487	A
39	B5	4488	A
39	B5	4489	G
39	B5	4490	G
39	B5	4492	G
39	B5	4498	G
39	B5	4501	G
39	B5	4504	C
39	B5	4506	C
39	B5	4508	G
39	B5	4512	G
39	B5	4518	C
39	B5	4519	C
39	B5	4609	G
39	B5	4610	C
39	B5	4614	G
39	B5	4621	U
39	B5	4622	C
39	B5	4634	U
39	B5	4637	G
39	B5	4638	G
39	B5	4639	C
39	B5	4640	G
39	B5	4642	G
39	B5	4644	C
39	B5	4645	C
39	B5	4646	G
39	B5	4647	G
39	B5	4649	A
39	B5	4651	G
39	B5	4656	C
39	B5	4658	G
39	B5	4682	A

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Mol	Chain	Res	Type
39	B5	4683	C
39	B5	4705	A
39	B5	4715	U
39	B5	4727	U
39	B5	4728	U
39	B5	4729	C
39	B5	4746	A
39	B5	4753	A
39	B5	4756	G
39	B5	4761	U
39	B5	4762	C
39	B5	4763	C
39	B5	4765	U
39	B5	4766	C
39	B5	4780	G
39	B5	4789	C
39	B5	4793	C
39	B5	4800	A
39	B5	4801	G
39	B5	4805	U
39	B5	4808	U
40	B7	7	G
40	B7	42	A
40	B7	50	A
40	B7	53	U
40	B7	54	A
40	B7	64	G
40	B7	110	G
40	B7	120	U
41	B8	23	C
41	B8	34	U
41	B8	35	C
41	B8	59	A
41	B8	62	A
41	B8	63	U
41	B8	81	C
41	B8	84	A
41	B8	87	G
41	B8	94	G
41	B8	103	A
41	B8	105	C
41	B8	110	U

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Mol	Chain	Res	Type
41	B8	114	G
41	B8	123	U
41	B8	127	U
41	B8	156	U

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
39	B5	1545	C
39	B5	1588	G
39	B5	4445	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	A2	1005	1	18,21,22	1.38	2 (11%)	22,30,33	1.87	3 (13%)
1	OMG	A2	684	1	23,26,27	1.19	3 (13%)	33,38,41	1.96	6 (18%)
1	OMU	A2	1443	1,89	19,22,23	1.22	3 (15%)	26,31,34	1.69	4 (15%)
39	PSU	B5	4107	39	18,21,22	1.37	2 (11%)	22,30,33	1.89	3 (13%)
33	AME	Au	1	33	9,10,11	0.47	0	9,11,13	0.88	1 (11%)
39	OMG	B5	3676	39	23,26,27	1.19	3 (13%)	33,38,41	1.95	6 (18%)
39	PSU	B5	1720	39	18,21,22	1.37	2 (11%)	22,30,33	1.88	3 (13%)
1	A2M	A2	1032	1	22,25,26	1.43	4 (18%)	31,36,39	2.17	10 (32%)
1	OMC	A2	1704	1	19,22,23	0.81	0	26,31,34	0.83	1 (3%)
1	OMU	A2	429	1	19,22,23	1.19	2 (10%)	26,31,34	1.69	5 (19%)
39	A2M	B5	1479	39	22,25,26	1.44	4 (18%)	31,36,39	2.10	10 (32%)
1	PSU	A2	1446	1	18,21,22	1.35	2 (11%)	22,30,33	1.90	3 (13%)
1	A2M	A2	1679	1	22,25,26	1.45	4 (18%)	31,36,39	2.16	10 (32%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
83	SAC	Br	2	83	7,8,9	0.51	0	8,9,11	0.86	1 (12%)
1	OMG	A2	1491	1,89	23,26,27	1.19	3 (13%)	33,38,41	1.97	7 (21%)
1	PSU	A2	823	1	18,21,22	1.37	2 (11%)	22,30,33	1.90	4 (18%)
1	PSU	A2	573	1	18,21,22	1.33	2 (11%)	22,30,33	1.91	4 (18%)
39	OMC	B5	4282	89,39	19,22,23	0.82	0	26,31,34	0.83	0
39	A2M	B5	1489	89,39	22,25,26	1.46	4 (18%)	31,36,39	2.07	9 (29%)
1	MA6	A2	1852	1	23,26,27	1.53	5 (21%)	34,38,41	2.16	11 (32%)
39	OMG	B5	1580	39	23,26,27	1.21	3 (13%)	33,38,41	1.94	6 (18%)
1	OMC	A2	463	1	19,22,23	0.81	0	26,31,34	0.81	0
1	OMC	A2	518	1	19,22,23	0.81	0	26,31,34	0.80	0
39	PSU	B5	3496	39	18,21,22	1.37	2 (11%)	22,30,33	1.92	3 (13%)
39	OMC	B5	4202	39	19,22,23	0.81	0	26,31,34	0.80	0
41	PSU	B8	55	41	18,21,22	1.36	2 (11%)	22,30,33	1.93	4 (18%)
39	PSU	B5	1683	39	18,21,22	1.35	2 (11%)	22,30,33	1.91	4 (18%)
39	OMC	B5	1820	89,39	19,22,23	0.81	0	26,31,34	0.84	0
39	PSU	B5	4045	39	18,21,22	1.36	2 (11%)	22,30,33	1.90	3 (13%)
39	PSU	B5	4188	39	18,21,22	1.36	2 (11%)	22,30,33	1.91	3 (13%)
39	PSU	B5	4177	39	18,21,22	1.36	2 (11%)	22,30,33	1.88	3 (13%)
41	OMG	B8	75	41	23,26,27	1.19	3 (13%)	33,38,41	1.94	6 (18%)
39	OMG	B5	4364	39	23,26,27	1.20	3 (13%)	33,38,41	1.94	6 (18%)
1	A2M	A2	159	1	22,25,26	1.46	4 (18%)	31,36,39	2.16	10 (32%)
39	OMU	B5	4366	39	19,22,23	1.23	3 (15%)	26,31,34	1.71	4 (15%)
39	PSU	B5	4169	39	18,21,22	1.37	2 (11%)	22,30,33	1.88	3 (13%)
39	PSU	B5	4435	39	18,21,22	1.38	2 (11%)	22,30,33	1.91	3 (13%)
39	PSU	B5	1718	39	18,21,22	1.35	2 (11%)	22,30,33	1.89	3 (13%)
11	2MG	AT	10	11	23,26,27	1.26	4 (17%)	32,38,41	2.17	6 (18%)
1	PSU	A2	1348	1	18,21,22	1.36	2 (11%)	22,30,33	1.91	3 (13%)
39	OMC	B5	2208	89,39	19,22,23	0.79	0	26,31,34	0.78	0
39	OMC	B5	3433	39	19,22,23	0.79	0	26,31,34	0.76	0
39	PSU	B5	4039	39	18,21,22	1.37	2 (11%)	22,30,33	1.88	3 (13%)
1	G7M	A2	1640	1,11	23,26,27	2.32	5 (21%)	35,39,42	2.92	10 (28%)
39	UR3	B5	4276	39	19,22,23	0.99	1 (5%)	26,32,35	1.42	1 (3%)
39	PSU	B5	4217	39	18,21,22	1.39	2 (11%)	22,30,33	1.87	3 (13%)
44	AYA	BC	2	44	6,7,8	0.75	0	5,8,10	0.24	0
39	PSU	B5	1801	39	18,21,22	1.36	2 (11%)	22,30,33	1.92	4 (18%)
1	PSU	A2	34	1	18,21,22	1.36	2 (11%)	22,30,33	1.91	4 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
39	PSU	B5	4298	39	18,21,22	1.37	2 (11%)	22,30,33	1.94	4 (18%)
39	OMG	B5	3359	39	23,26,27	1.20	3 (13%)	33,38,41	1.96	6 (18%)
39	PSU	B5	4749	39	18,21,22	1.36	2 (11%)	22,30,33	1.89	3 (13%)
1	PSU	A2	218	1	18,21,22	1.35	2 (11%)	22,30,33	1.91	3 (13%)
39	OMC	B5	3573	39	19,22,23	0.81	0	26,31,34	0.87	1 (3%)
39	OMG	B5	3942	11,39	23,26,27	1.21	3 (13%)	33,38,41	1.97	6 (18%)
39	A2M	B5	3517	39	22,25,26	1.41	4 (18%)	31,36,39	2.24	11 (35%)
39	OMU	B5	3973	39	19,22,23	1.24	3 (15%)	26,31,34	1.69	4 (15%)
39	A2M	B5	3492	1,39	22,25,26	1.46	4 (18%)	31,36,39	2.13	10 (32%)
39	PSU	B5	2351	39	18,21,22	1.36	2 (11%)	22,30,33	1.92	4 (18%)
39	A2M	B5	3599	39	22,25,26	1.46	4 (18%)	31,36,39	2.09	10 (32%)
39	OMC	B5	2667	39	19,22,23	0.81	0	26,31,34	0.82	1 (3%)
39	PSU	B5	3554	39	18,21,22	1.36	2 (11%)	22,30,33	1.86	3 (13%)
39	6MZ	B5	3966	39	22,25,26	1.42	4 (18%)	30,36,39	2.19	9 (30%)
39	PSU	B5	3616	39	18,21,22	1.36	2 (11%)	22,30,33	1.87	3 (13%)
1	OMU	A2	121	1	19,22,23	1.22	3 (15%)	26,31,34	1.69	4 (15%)
1	A2M	A2	591	1	22,25,26	1.46	4 (18%)	31,36,39	2.18	7 (22%)
39	PSU	B5	3462	39	18,21,22	1.34	2 (11%)	22,30,33	1.89	3 (13%)
39	PSU	B5	4374	39	18,21,22	1.37	2 (11%)	22,30,33	1.93	3 (13%)
35	HY3	Aw	62	35	6,8,9	1.90	1 (16%)	5,10,12	1.13	1 (20%)
39	PSU	B5	3447	39	18,21,22	1.36	2 (11%)	22,30,33	1.92	3 (13%)
1	PSU	A2	815	1	18,21,22	1.36	2 (11%)	22,30,33	1.89	3 (13%)
1	PSU	A2	816	1	18,21,22	1.34	2 (11%)	22,30,33	1.91	4 (18%)
39	PSU	B5	4149	39	18,21,22	1.36	2 (11%)	22,30,33	1.94	4 (18%)
39	PSU	B5	4419	39	18,21,22	1.36	2 (11%)	22,30,33	1.92	4 (18%)
1	OMG	A2	437	1	23,26,27	1.21	3 (13%)	33,38,41	1.95	6 (18%)
1	A2M	A2	577	1	22,25,26	1.46	4 (18%)	31,36,39	2.12	10 (32%)
11	H2U	AT	17	11	18,21,22	1.00	2 (11%)	21,30,33	1.72	2 (9%)
11	PSU	AT	28	11	18,21,22	1.36	2 (11%)	22,30,33	1.90	4 (18%)
68	V5N	Ba	39	68	9,11,12	2.14	2 (22%)	9,14,16	1.70	2 (22%)
39	OMU	B5	3657	39	19,22,23	1.24	2 (10%)	26,31,34	1.76	5 (19%)
1	PSU	A2	867	1	18,21,22	1.35	2 (11%)	22,30,33	1.92	4 (18%)
39	PSU	B5	3502	39	18,21,22	1.37	2 (11%)	22,30,33	1.95	4 (18%)
1	OMU	A2	172	1	19,22,23	1.20	3 (15%)	26,31,34	1.72	4 (15%)
39	OMG	B5	1260	39	23,26,27	1.20	3 (13%)	33,38,41	1.98	6 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
39	PSU	B5	4325	39	18,21,22	1.37	2 (11%)	22,30,33	1.92	3 (13%)
1	OMU	A2	1289	1	19,22,23	1.24	3 (15%)	26,31,34	1.69	5 (19%)
39	PSU	B5	3371	39	18,21,22	1.37	2 (11%)	22,30,33	1.88	3 (13%)
39	OMC	B5	2265	89,39	19,22,23	0.82	0	26,31,34	0.86	1 (3%)
30	SAC	Ar	2	30	7,8,9	0.53	0	8,9,11	0.89	1 (12%)
39	PSU	B5	4246	39	18,21,22	1.35	2 (11%)	22,30,33	1.93	3 (13%)
1	PSU	A2	1368	1	18,21,22	1.34	2 (11%)	22,30,33	1.91	3 (13%)
39	A2M	B5	1810	89,39	22,25,26	1.45	4 (18%)	31,36,39	2.17	10 (32%)
39	OMG	B5	3974	39	23,26,27	1.18	3 (13%)	33,38,41	1.92	6 (18%)
11	PSU	AT	27	11	18,21,22	1.35	2 (11%)	22,30,33	1.92	3 (13%)
1	PSU	A2	1047	1	18,21,22	1.36	2 (11%)	22,30,33	1.91	3 (13%)
39	OMG	B5	2267	39	23,26,27	1.21	3 (13%)	33,38,41	1.91	6 (18%)
1	4AC	A2	1843	1	21,24,25	1.01	1 (4%)	29,34,37	1.04	3 (10%)
11	1MA	AT	58	11	21,25,26	1.38	4 (19%)	31,37,40	1.69	5 (16%)
1	B8N	A2	1249	1	24,29,30	1.29	3 (12%)	29,42,45	1.26	3 (10%)
11	OMC	AT	32	11	19,22,23	0.81	0	26,31,34	0.80	0
39	5MC	B5	4193	39	18,22,23	1.00	2 (11%)	26,32,35	1.24	2 (7%)
1	PSU	A2	105	1	18,21,22	1.37	2 (11%)	22,30,33	1.92	3 (13%)
39	PSU	B5	1491	39	18,21,22	1.37	2 (11%)	22,30,33	1.93	4 (18%)
39	PSU	B5	4058	39	18,21,22	1.36	2 (11%)	22,30,33	1.91	3 (13%)
81	MLZ	Bo	53	81	8,9,10	0.48	0	4,9,11	0.10	0
39	PSU	B5	4740	39	18,21,22	1.36	2 (11%)	22,30,33	1.89	3 (13%)
1	PSU	A2	650	1	18,21,22	1.37	2 (11%)	22,30,33	1.94	4 (18%)
39	PSU	B5	1537	39	18,21,22	1.37	2 (11%)	22,30,33	1.89	3 (13%)
80	M3L	Bm	98	80	10,11,12	0.82	0	9,14,16	0.50	0
39	OMG	B5	4369	39	23,26,27	1.20	3 (13%)	33,38,41	1.95	6 (18%)
39	A2M	B5	4336	39	22,25,26	1.46	4 (18%)	31,36,39	2.16	10 (32%)
39	PSU	B5	1731	39	18,21,22	1.35	2 (11%)	22,30,33	1.85	4 (18%)
11	H2U	AT	16	11	18,21,22	0.99	2 (11%)	21,30,33	1.38	2 (9%)
39	PSU	B5	3466	39	18,21,22	1.35	2 (11%)	22,30,33	1.91	4 (18%)
39	OMC	B5	3619	39	19,22,23	0.81	0	26,31,34	0.84	0
39	PSU	B5	3427	39	18,21,22	1.34	2 (11%)	22,30,33	1.92	3 (13%)
39	A2M	B5	3450	39	22,25,26	1.44	4 (18%)	31,36,39	2.09	9 (29%)
39	PSU	B5	1799	39	18,21,22	1.38	2 (11%)	22,30,33	1.90	3 (13%)
39	PSU	B5	1638	39	18,21,22	1.38	2 (11%)	22,30,33	1.90	3 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
39	PSU	B5	2475	39	18,21,22	1.36	2 (11%)	22,30,33	1.87	3 (13%)
39	PSU	B5	4042	39	18,21,22	1.35	2 (11%)	22,30,33	1.93	4 (18%)
39	A2M	B5	398	39	22,25,26	1.46	4 (18%)	31,36,39	2.14	9 (29%)
39	PSU	B5	3576	39	18,21,22	1.38	2 (11%)	22,30,33	1.87	3 (13%)
11	YYG	AT	37	11	37,42,43	1.86	7 (18%)	45,62,65	1.94	10 (22%)
39	OMU	B5	2680	39	19,22,23	1.22	2 (10%)	26,31,34	1.74	5 (19%)
11	G7M	AT	46	11	23,26,27	2.31	5 (21%)	35,39,42	2.95	10 (28%)
1	OMU	A2	1327	1,89	19,22,23	1.19	2 (10%)	26,31,34	1.71	5 (19%)
39	PSU	B5	1721	39	18,21,22	1.36	2 (11%)	22,30,33	1.91	4 (18%)
39	OMC	B5	2194	89,39	19,22,23	0.81	0	26,31,34	0.94	2 (7%)
1	A2M	A2	166	1	22,25,26	1.47	4 (18%)	31,36,39	2.16	10 (32%)
1	PSU	A2	1178	1	18,21,22	1.36	2 (11%)	22,30,33	1.94	3 (13%)
39	PSU	B5	3490	39	18,21,22	1.36	2 (11%)	22,30,33	1.88	4 (18%)
40	GTP	B7	1	40	30,34,34	0.50	0	46,54,54	0.58	0
1	PSU	A2	864	1	18,21,22	1.36	2 (11%)	22,30,33	1.91	3 (13%)
1	PSU	A2	1626	1	18,21,22	1.36	2 (11%)	22,30,33	1.89	3 (13%)
12	SAC	AZ	2	12	7,8,9	0.52	0	8,9,11	0.86	1 (12%)
39	PSU	B5	3585	89,39	18,21,22	1.39	2 (11%)	22,30,33	1.89	3 (13%)
39	OMC	B5	2647	39	19,22,23	0.81	0	26,31,34	0.82	0
1	PSU	A2	610	1	18,21,22	1.36	2 (11%)	22,30,33	1.90	3 (13%)
39	A2M	B5	2658	89,39	22,25,26	1.44	4 (18%)	31,36,39	2.10	8 (25%)
1	OMC	A2	1392	1	19,22,23	0.84	0	26,31,34	0.95	1 (3%)
1	PSU	A2	1644	1,89	18,21,22	1.36	2 (11%)	22,30,33	1.90	3 (13%)
39	OMG	B5	2207	39	23,26,27	1.19	3 (13%)	33,38,41	1.92	6 (18%)
11	OMG	AT	34	9,11	23,26,27	1.19	3 (13%)	33,38,41	1.95	6 (18%)
42	V5N	BA	216	42	9,11,12	2.13	2 (22%)	9,14,16	1.74	2 (22%)
1	PSU	A2	687	1	18,21,22	1.35	2 (11%)	22,30,33	1.90	3 (13%)
1	A2M	A2	27	1,89	22,25,26	1.46	4 (18%)	31,36,39	2.13	10 (32%)
1	OMG	A2	645	1	23,26,27	1.20	3 (13%)	33,38,41	1.95	6 (18%)
39	A2M	B5	4269	89,39	22,25,26	1.45	4 (18%)	31,36,39	2.17	10 (32%)
1	OMU	A2	628	1	19,22,23	1.18	2 (10%)	26,31,34	1.70	5 (19%)
1	4AC	A2	1338	1	21,24,25	1.09	2 (9%)	29,34,37	1.31	3 (10%)
11	5MU	AT	54	11	19,22,23	1.41	6 (31%)	28,32,35	2.05	7 (25%)
39	OMU	B5	2258	39	19,22,23	1.22	2 (10%)	26,31,34	1.68	4 (15%)
31	NMM	As	67	31	9,11,12	0.59	0	6,12,14	0.46	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
39	PSU	B5	4099	39	18,21,22	1.37	2 (11%)	22,30,33	1.92	3 (13%)
1	OMU	A2	116	1	19,22,23	1.21	3 (15%)	26,31,34	1.69	5 (19%)
39	A2M	B5	3557	39	22,25,26	1.46	4 (18%)	31,36,39	2.14	9 (29%)
39	OMC	B5	3540	39	19,22,23	0.79	0	26,31,34	0.77	0
39	PSU	B5	1632	39	18,21,22	1.38	2 (11%)	22,30,33	1.89	4 (18%)
1	PSU	A2	1175	1	18,21,22	1.36	2 (11%)	22,30,33	1.88	3 (13%)
11	1MA	AT	14	11	21,25,26	1.37	4 (19%)	31,37,40	1.68	6 (19%)
1	PSU	A2	407	1	18,21,22	1.36	2 (11%)	22,30,33	1.90	3 (13%)
39	PSU	B5	3494	39	18,21,22	1.37	2 (11%)	22,30,33	1.89	3 (13%)
1	A2M	A2	485	1	22,25,26	1.45	4 (18%)	31,36,39	2.12	9 (29%)
39	OMC	B5	2704	39	19,22,23	0.81	0	26,31,34	0.83	1 (3%)
39	PSU	B5	3652	89,39	18,21,22	1.38	2 (11%)	22,30,33	1.91	3 (13%)
1	PSU	A2	967	1	18,21,22	1.37	2 (11%)	22,30,33	1.89	3 (13%)
39	OMG	B5	3631	39	23,26,27	1.19	3 (13%)	33,38,41	1.95	6 (18%)
1	PSU	A2	682	1	18,21,22	1.38	2 (11%)	22,30,33	1.89	3 (13%)
39	A2M	B5	2206	89,39	22,25,26	1.44	4 (18%)	31,36,39	2.05	9 (29%)
39	OMU	B5	4244	39	19,22,23	1.21	2 (10%)	26,31,34	1.70	4 (15%)
39	OMC	B5	1284	39	19,22,23	0.80	0	26,31,34	0.77	0
39	PSU	B5	4278	39	18,21,22	1.37	2 (11%)	22,30,33	1.88	3 (13%)
39	A2M	B5	1270	39	22,25,26	1.44	4 (18%)	31,36,39	2.10	9 (29%)
11	PSU	AT	39	11	18,21,22	1.36	2 (11%)	22,30,33	1.91	3 (13%)
39	OMG	B5	4383	39	23,26,27	1.20	3 (13%)	33,38,41	1.95	6 (18%)
1	OMG	A2	602	1	23,26,27	1.20	3 (13%)	33,38,41	1.93	6 (18%)
1	MA6	A2	1851	1	23,26,27	1.53	5 (21%)	34,38,41	2.19	12 (35%)
1	PSU	A2	1239	1	18,21,22	1.36	2 (11%)	22,30,33	1.90	4 (18%)
1	A2M	A2	99	1,89	22,25,26	1.46	4 (18%)	31,36,39	2.14	9 (29%)
39	PSU	B5	4322	39	18,21,22	1.35	2 (11%)	22,30,33	1.89	3 (13%)
39	OMG	B5	3476	39	23,26,27	1.19	3 (13%)	33,38,41	1.94	6 (18%)
1	PSU	A2	119	1	18,21,22	1.35	2 (11%)	22,30,33	1.86	3 (13%)
39	UY1	B5	3550	39	19,22,23	1.31	3 (15%)	22,31,34	2.02	5 (22%)
39	OMG	B5	2719	39	23,26,27	1.21	3 (13%)	33,38,41	1.98	6 (18%)
39	A2M	B5	4317	39	22,25,26	1.47	4 (18%)	31,36,39	2.09	9 (29%)
1	PSU	A2	652	1	18,21,22	1.35	2 (11%)	22,30,33	1.91	3 (13%)
1	PSU	A2	1046	1	18,21,22	1.35	2 (11%)	22,30,33	1.89	3 (13%)
1	PSU	A2	1233	1	18,21,22	1.36	2 (11%)	22,30,33	1.90	3 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMU	A2	1805	1	19,22,23	1.23	3 (15%)	26,31,34	1.71	4 (15%)
39	PSU	B5	3583	39	18,21,22	1.38	2 (11%)	22,30,33	1.93	3 (13%)
39	OMU	B5	4052	39	19,22,23	1.23	3 (15%)	26,31,34	1.71	5 (19%)
39	PSU	B5	4267	89,39	18,21,22	1.37	2 (11%)	22,30,33	1.89	5 (22%)
39	OMG	B5	4245	39	23,26,27	1.20	3 (13%)	33,38,41	1.94	6 (18%)
43	HIC	BB	245	43	10,11,12	0.59	0	8,14,16	0.44	0
1	PSU	A2	1245	1	18,21,22	1.34	2 (11%)	22,30,33	1.88	3 (13%)
39	OMG	B5	4138	39	23,26,27	1.19	3 (13%)	33,38,41	1.94	6 (18%)
11	PSU	AT	55	11	18,21,22	1.34	2 (11%)	22,30,33	1.91	4 (18%)
1	A2M	A2	1384	1	22,25,26	1.46	4 (18%)	31,36,39	2.09	10 (32%)
1	PSU	A2	1082	1	18,21,22	1.39	3 (16%)	22,30,33	1.85	3 (13%)
39	OMG	B5	1477	39	23,26,27	1.19	3 (13%)	33,38,41	1.94	6 (18%)
39	A2M	B5	400	39	22,25,26	1.47	4 (18%)	31,36,39	2.10	9 (29%)
39	A2M	B5	3562	39	22,25,26	1.45	4 (18%)	31,36,39	2.14	10 (32%)
39	1MA	B5	1266	89,39	21,25,26	1.36	4 (19%)	31,37,40	1.68	4 (12%)
39	OMC	B5	3601	39	19,22,23	0.81	0	26,31,34	0.80	0
39	OMG	B5	4116	39	23,26,27	1.20	3 (13%)	33,38,41	1.94	6 (18%)
39	PSU	B5	4203	39	18,21,22	1.36	2 (11%)	22,30,33	1.88	3 (13%)
41	PSU	B8	69	41	18,21,22	1.38	2 (11%)	22,30,33	1.93	4 (18%)
39	A2M	B5	2630	89,39	22,25,26	1.44	4 (18%)	31,36,39	2.07	8 (25%)
1	PSU	A2	802	1	18,21,22	1.37	2 (11%)	22,30,33	1.88	3 (13%)
1	OMG	A2	868	1	23,26,27	1.20	3 (13%)	33,38,41	1.94	6 (18%)
1	OMG	A2	1329	1	23,26,27	1.19	3 (13%)	33,38,41	1.94	6 (18%)
39	A2M	B5	2244	89,39	22,25,26	1.45	4 (18%)	31,36,39	2.12	10 (32%)
39	PSU	B5	3369	39	18,21,22	1.38	3 (16%)	22,30,33	1.94	4 (18%)
39	PSU	B5	3500	39	18,21,22	1.37	2 (11%)	22,30,33	1.91	3 (13%)
39	5MC	B5	3514	89,39	18,22,23	0.94	2 (11%)	26,32,35	1.18	3 (11%)
39	PSU	B5	4382	39	18,21,22	1.37	2 (11%)	22,30,33	1.89	4 (18%)
1	PSU	A2	109	1	18,21,22	1.36	2 (11%)	22,30,33	1.90	3 (13%)
39	PSU	B5	4166	39	18,21,22	1.37	2 (11%)	22,30,33	1.86	4 (18%)
69	MLZ	Bb	5	69	8,9,10	0.48	0	4,9,11	0.07	0
1	A2M	A2	513	1	22,25,26	1.46	4 (18%)	31,36,39	2.14	9 (29%)
1	PSU	A2	1693	1	18,21,22	1.37	2 (11%)	22,30,33	1.90	4 (18%)
11	M2G	AT	26	11	24,27,28	1.29	4 (16%)	35,40,43	1.82	6 (17%)
39	OMG	B5	3524	39	23,26,27	1.19	3 (13%)	33,38,41	1.93	6 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	A2	1057	1	18,21,22	1.37	2 (11%)	22,30,33	1.90	3 (13%)
1	OMG	A2	1448	1	23,26,27	1.20	3 (13%)	33,38,41	1.93	6 (18%)
39	PSU	B5	4711	39	18,21,22	1.36	2 (11%)	22,30,33	1.91	4 (18%)
1	OMC	A2	174	1,89	19,22,23	0.80	0	26,31,34	0.78	0
1	A2M	A2	669	1,89	22,25,26	1.44	5 (22%)	31,36,39	2.05	9 (29%)
1	PSU	A2	36	1	18,21,22	1.35	2 (11%)	22,30,33	1.88	3 (13%)
1	PSU	A2	210	1	18,21,22	1.36	2 (11%)	22,30,33	1.86	3 (13%)
1	OMU	A2	355	1	19,22,23	1.24	3 (15%)	26,31,34	1.74	4 (15%)
1	A2M	A2	469	1	22,25,26	1.46	4 (18%)	31,36,39	2.13	10 (32%)
39	A2M	B5	3456	39	22,25,26	1.46	4 (18%)	31,36,39	2.12	10 (32%)
39	OMG	B5	4240	39	23,26,27	1.20	3 (13%)	33,38,41	1.95	6 (18%)
11	5MC	AT	49	11	18,22,23	0.95	2 (11%)	26,32,35	1.13	2 (7%)
1	6MZ	A2	1833	1,89	22,25,26	1.43	4 (18%)	30,36,39	2.13	8 (26%)
1	OMG	A2	510	1,89	23,26,27	1.20	3 (13%)	33,38,41	1.94	6 (18%)
1	PSU	A2	93	1	18,21,22	1.37	2 (11%)	22,30,33	1.90	3 (13%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	A2	1005	1	-	0/7/25/26	0/2/2/2
1	OMG	A2	684	1	-	4/9/27/28	0/3/3/3
1	OMU	A2	1443	1,89	-	1/9/27/28	0/2/2/2
39	PSU	B5	4107	39	-	0/7/25/26	0/2/2/2
33	AME	Au	1	33	-	2/9/10/12	-
39	OMG	B5	3676	39	-	1/9/27/28	0/3/3/3
39	PSU	B5	1720	39	-	0/7/25/26	0/2/2/2
1	A2M	A2	1032	1	-	0/9/27/28	0/3/3/3
1	OMC	A2	1704	1	-	2/9/27/28	0/2/2/2
1	OMU	A2	429	1	-	4/9/27/28	0/2/2/2
39	A2M	B5	1479	39	-	0/9/27/28	0/3/3/3
1	PSU	A2	1446	1	-	0/7/25/26	0/2/2/2
1	A2M	A2	1679	1	-	0/9/27/28	0/3/3/3
83	SAC	Br	2	83	-	0/7/8/10	-
1	OMG	A2	1491	1,89	-	2/9/27/28	0/3/3/3
1	PSU	A2	823	1	-	1/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	A2	573	1	-	0/7/25/26	0/2/2/2
39	OMC	B5	4282	89,39	-	0/9/27/28	0/2/2/2
39	A2M	B5	1489	89,39	-	1/9/27/28	0/3/3/3
1	MA6	A2	1852	1	-	2/11/29/30	0/3/3/3
39	OMG	B5	1580	39	-	0/9/27/28	0/3/3/3
1	OMC	A2	463	1	-	0/9/27/28	0/2/2/2
1	OMC	A2	518	1	-	0/9/27/28	0/2/2/2
39	PSU	B5	3496	39	-	0/7/25/26	0/2/2/2
39	OMC	B5	4202	39	-	1/9/27/28	0/2/2/2
41	PSU	B8	55	41	-	0/7/25/26	0/2/2/2
39	PSU	B5	1683	39	-	0/7/25/26	0/2/2/2
39	OMC	B5	1820	89,39	-	1/9/27/28	0/2/2/2
39	PSU	B5	4045	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	4188	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	4177	39	-	0/7/25/26	0/2/2/2
41	OMG	B8	75	41	-	0/9/27/28	0/3/3/3
39	OMG	B5	4364	39	-	0/9/27/28	0/3/3/3
1	A2M	A2	159	1	-	0/9/27/28	0/3/3/3
39	OMU	B5	4366	39	-	0/9/27/28	0/2/2/2
39	PSU	B5	4169	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	4435	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	1718	39	-	0/7/25/26	0/2/2/2
11	2MG	AT	10	11	-	0/9/27/28	0/3/3/3
1	PSU	A2	1348	1	-	0/7/25/26	0/2/2/2
39	OMC	B5	2208	89,39	-	0/9/27/28	0/2/2/2
39	OMC	B5	3433	39	-	4/9/27/28	0/2/2/2
39	PSU	B5	4039	39	-	0/7/25/26	0/2/2/2
1	G7M	A2	1640	1,11	-	0/7/25/26	0/3/3/3
39	UR3	B5	4276	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	4217	39	-	0/7/25/26	0/2/2/2
44	AYA	BC	2	44	-	0/4/6/8	-
39	PSU	B5	1801	39	-	0/7/25/26	0/2/2/2
1	PSU	A2	34	1	-	0/7/25/26	0/2/2/2
39	PSU	B5	4298	39	-	0/7/25/26	0/2/2/2
39	OMG	B5	3359	39	-	0/9/27/28	0/3/3/3
39	PSU	B5	4749	39	-	0/7/25/26	0/2/2/2
1	PSU	A2	218	1	-	0/7/25/26	0/2/2/2
39	OMC	B5	3573	39	-	0/9/27/28	0/2/2/2
39	OMG	B5	3942	11,39	-	0/9/27/28	0/3/3/3
39	A2M	B5	3517	39	-	2/9/27/28	0/3/3/3
39	OMU	B5	3973	39	-	1/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	A2M	B5	3492	1,39	-	3/9/27/28	0/3/3/3
39	PSU	B5	2351	39	-	0/7/25/26	0/2/2/2
39	A2M	B5	3599	39	-	2/9/27/28	0/3/3/3
39	OMC	B5	2667	39	-	0/9/27/28	0/2/2/2
39	PSU	B5	3554	39	-	0/7/25/26	0/2/2/2
39	6MZ	B5	3966	39	-	0/9/27/28	0/3/3/3
39	PSU	B5	3616	39	-	0/7/25/26	0/2/2/2
1	OMU	A2	121	1	-	1/9/27/28	0/2/2/2
1	A2M	A2	591	1	-	3/9/27/28	0/3/3/3
39	PSU	B5	3462	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	4374	39	-	0/7/25/26	0/2/2/2
35	HY3	Aw	62	35	-	0/1/12/14	0/1/1/1
39	PSU	B5	3447	39	-	0/7/25/26	0/2/2/2
1	PSU	A2	815	1	-	0/7/25/26	0/2/2/2
1	PSU	A2	816	1	-	0/7/25/26	0/2/2/2
39	PSU	B5	4149	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	4419	39	-	0/7/25/26	0/2/2/2
1	OMG	A2	437	1	-	0/9/27/28	0/3/3/3
1	A2M	A2	577	1	-	2/9/27/28	0/3/3/3
11	H2U	AT	17	11	-	6/7/38/39	0/2/2/2
11	PSU	AT	28	11	-	0/7/25/26	0/2/2/2
68	V5N	Ba	39	68	-	1/9/10/12	0/1/1/1
39	OMU	B5	3657	39	-	0/9/27/28	0/2/2/2
1	PSU	A2	867	1	-	0/7/25/26	0/2/2/2
39	PSU	B5	3502	39	-	0/7/25/26	0/2/2/2
1	OMU	A2	172	1	-	0/9/27/28	0/2/2/2
39	OMG	B5	1260	39	-	1/9/27/28	0/3/3/3
39	PSU	B5	4325	39	-	0/7/25/26	0/2/2/2
1	OMU	A2	1289	1	-	0/9/27/28	0/2/2/2
39	PSU	B5	3371	39	-	0/7/25/26	0/2/2/2
39	OMC	B5	2265	89,39	-	1/9/27/28	0/2/2/2
30	SAC	Ar	2	30	-	0/7/8/10	-
39	PSU	B5	4246	39	-	1/7/25/26	0/2/2/2
1	PSU	A2	1368	1	-	0/7/25/26	0/2/2/2
39	A2M	B5	1810	89,39	-	0/9/27/28	0/3/3/3
39	OMG	B5	3974	39	-	0/9/27/28	0/3/3/3
11	PSU	AT	27	11	-	0/7/25/26	0/2/2/2
1	PSU	A2	1047	1	-	0/7/25/26	0/2/2/2
39	OMG	B5	2267	39	-	0/9/27/28	0/3/3/3
1	4AC	A2	1843	1	-	2/11/29/30	0/2/2/2
11	1MA	AT	58	11	-	0/7/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	B8N	A2	1249	1	-	4/16/34/35	0/2/2/2
11	OMC	AT	32	11	-	0/9/27/28	0/2/2/2
39	5MC	B5	4193	39	-	4/7/25/26	0/2/2/2
1	PSU	A2	105	1	-	0/7/25/26	0/2/2/2
39	PSU	B5	1491	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	4058	39	-	0/7/25/26	0/2/2/2
81	MLZ	B _o	53	81	-	0/7/8/10	-
39	PSU	B5	4740	39	-	0/7/25/26	0/2/2/2
1	PSU	A2	650	1	-	0/7/25/26	0/2/2/2
39	PSU	B5	1537	39	-	0/7/25/26	0/2/2/2
80	M3L	B _m	98	80	-	0/9/10/12	-
39	OMG	B5	4369	39	-	1/9/27/28	0/3/3/3
39	A2M	B5	4336	39	-	1/9/27/28	0/3/3/3
39	PSU	B5	1731	39	-	0/7/25/26	0/2/2/2
11	H2U	AT	16	11	-	1/7/38/39	0/2/2/2
39	PSU	B5	3466	39	-	0/7/25/26	0/2/2/2
39	OMC	B5	3619	39	-	2/9/27/28	0/2/2/2
39	PSU	B5	3427	39	-	0/7/25/26	0/2/2/2
39	A2M	B5	3450	39	-	1/9/27/28	0/3/3/3
39	PSU	B5	1799	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	1638	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	2475	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	4042	39	-	0/7/25/26	0/2/2/2
39	A2M	B5	398	39	-	2/9/27/28	0/3/3/3
39	PSU	B5	3576	39	-	1/7/25/26	0/2/2/2
11	YYG	AT	37	11	-	0/24/42/43	0/4/4/4
39	OMU	B5	2680	39	-	1/9/27/28	0/2/2/2
11	G7M	AT	46	11	-	1/7/25/26	0/3/3/3
1	OMU	A2	1327	1,89	-	0/9/27/28	0/2/2/2
39	PSU	B5	1721	39	-	0/7/25/26	0/2/2/2
39	OMC	B5	2194	89,39	-	2/9/27/28	0/2/2/2
1	A2M	A2	166	1	-	0/9/27/28	0/3/3/3
1	PSU	A2	1178	1	-	0/7/25/26	0/2/2/2
39	PSU	B5	3490	39	-	0/7/25/26	0/2/2/2
40	GTP	B7	1	40	-	0/22/38/38	0/3/3/3
1	PSU	A2	864	1	-	0/7/25/26	0/2/2/2
1	PSU	A2	1626	1	-	0/7/25/26	0/2/2/2
12	SAC	AZ	2	12	-	2/7/8/10	-
39	PSU	B5	3585	89,39	-	0/7/25/26	0/2/2/2
39	OMC	B5	2647	39	-	1/9/27/28	0/2/2/2
1	PSU	A2	610	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	A2M	B5	2658	89,39	-	0/9/27/28	0/3/3/3
1	OMC	A2	1392	1	-	1/9/27/28	0/2/2/2
1	PSU	A2	1644	1,89	-	0/7/25/26	0/2/2/2
39	OMG	B5	2207	39	-	2/9/27/28	0/3/3/3
11	OMG	AT	34	9,11	-	0/9/27/28	0/3/3/3
42	V5N	BA	216	42	-	1/9/10/12	0/1/1/1
1	PSU	A2	687	1	-	0/7/25/26	0/2/2/2
1	A2M	A2	27	1,89	-	2/9/27/28	0/3/3/3
1	OMG	A2	645	1	-	4/9/27/28	0/3/3/3
39	A2M	B5	4269	89,39	-	0/9/27/28	0/3/3/3
1	OMU	A2	628	1	-	2/9/27/28	0/2/2/2
1	4AC	A2	1338	1	-	4/11/29/30	0/2/2/2
11	5MU	AT	54	11	-	0/7/25/26	0/2/2/2
39	OMU	B5	2258	39	-	0/9/27/28	0/2/2/2
31	NMM	As	67	31	-	1/9/11/13	-
39	PSU	B5	4099	39	-	0/7/25/26	0/2/2/2
1	OMU	A2	116	1	-	1/9/27/28	0/2/2/2
39	A2M	B5	3557	39	-	1/9/27/28	0/3/3/3
39	OMC	B5	3540	39	-	0/9/27/28	0/2/2/2
39	PSU	B5	1632	39	-	0/7/25/26	0/2/2/2
1	PSU	A2	1175	1	-	0/7/25/26	0/2/2/2
11	1MA	AT	14	11	-	0/7/25/26	0/3/3/3
1	PSU	A2	407	1	-	0/7/25/26	0/2/2/2
39	PSU	B5	3494	39	-	1/7/25/26	0/2/2/2
1	A2M	A2	485	1	-	0/9/27/28	0/3/3/3
39	OMC	B5	2704	39	-	1/9/27/28	0/2/2/2
39	PSU	B5	3652	89,39	-	0/7/25/26	0/2/2/2
1	PSU	A2	967	1	-	0/7/25/26	0/2/2/2
39	OMG	B5	3631	39	-	0/9/27/28	0/3/3/3
1	PSU	A2	682	1	-	0/7/25/26	0/2/2/2
39	A2M	B5	2206	89,39	-	0/9/27/28	0/3/3/3
39	OMU	B5	4244	39	-	0/9/27/28	0/2/2/2
39	OMC	B5	1284	39	-	2/9/27/28	0/2/2/2
39	PSU	B5	4278	39	-	0/7/25/26	0/2/2/2
39	A2M	B5	1270	39	-	0/9/27/28	0/3/3/3
11	PSU	AT	39	11	-	0/7/25/26	0/2/2/2
39	OMG	B5	4383	39	-	0/9/27/28	0/3/3/3
1	OMG	A2	602	1	-	0/9/27/28	0/3/3/3
1	MA6	A2	1851	1	-	0/11/29/30	0/3/3/3
1	PSU	A2	1239	1	-	0/7/25/26	0/2/2/2
1	A2M	A2	99	1,89	-	2/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	PSU	B5	4322	39	-	0/7/25/26	0/2/2/2
39	OMG	B5	3476	39	-	0/9/27/28	0/3/3/3
1	PSU	A2	119	1	-	0/7/25/26	0/2/2/2
39	UY1	B5	3550	39	-	4/9/27/28	0/2/2/2
39	OMG	B5	2719	39	-	0/9/27/28	0/3/3/3
39	A2M	B5	4317	39	-	0/9/27/28	0/3/3/3
1	PSU	A2	652	1	-	0/7/25/26	0/2/2/2
1	PSU	A2	1046	1	-	0/7/25/26	0/2/2/2
1	PSU	A2	1233	1	-	0/7/25/26	0/2/2/2
1	OMU	A2	1805	1	-	2/9/27/28	0/2/2/2
39	PSU	B5	3583	39	-	1/7/25/26	0/2/2/2
39	OMU	B5	4052	39	-	0/9/27/28	0/2/2/2
39	PSU	B5	4267	89,39	-	0/7/25/26	0/2/2/2
39	OMG	B5	4245	39	-	0/9/27/28	0/3/3/3
43	HIC	BB	245	43	-	0/5/6/8	0/1/1/1
1	PSU	A2	1245	1	-	0/7/25/26	0/2/2/2
39	OMG	B5	4138	39	-	0/9/27/28	0/3/3/3
11	PSU	AT	55	11	-	0/7/25/26	0/2/2/2
1	A2M	A2	1384	1	-	0/9/27/28	0/3/3/3
1	PSU	A2	1082	1	-	1/7/25/26	0/2/2/2
39	OMG	B5	1477	39	-	1/9/27/28	0/3/3/3
39	A2M	B5	400	39	-	0/9/27/28	0/3/3/3
39	A2M	B5	3562	39	-	0/9/27/28	0/3/3/3
39	1MA	B5	1266	89,39	-	1/7/25/26	0/3/3/3
39	OMC	B5	3601	39	-	0/9/27/28	0/2/2/2
39	OMG	B5	4116	39	-	0/9/27/28	0/3/3/3
39	PSU	B5	4203	39	-	0/7/25/26	0/2/2/2
41	PSU	B8	69	41	-	0/7/25/26	0/2/2/2
39	A2M	B5	2630	89,39	-	3/9/27/28	0/3/3/3
1	PSU	A2	802	1	-	2/7/25/26	0/2/2/2
1	OMG	A2	868	1	-	0/9/27/28	0/3/3/3
1	OMG	A2	1329	1	-	1/9/27/28	0/3/3/3
39	A2M	B5	2244	89,39	-	0/9/27/28	0/3/3/3
39	PSU	B5	3369	39	-	0/7/25/26	0/2/2/2
39	PSU	B5	3500	39	-	0/7/25/26	0/2/2/2
39	5MC	B5	3514	89,39	-	0/7/25/26	0/2/2/2
39	PSU	B5	4382	39	-	3/7/25/26	0/2/2/2
1	PSU	A2	109	1	-	0/7/25/26	0/2/2/2
39	PSU	B5	4166	39	-	0/7/25/26	0/2/2/2
69	MLZ	Bb	5	69	-	2/7/8/10	-
1	A2M	A2	513	1	-	4/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	A2	1693	1	-	0/7/25/26	0/2/2/2
11	M2G	AT	26	11	-	0/11/29/30	0/3/3/3
39	OMG	B5	3524	39	-	1/9/27/28	0/3/3/3
1	PSU	A2	1057	1	-	0/7/25/26	0/2/2/2
1	OMG	A2	1448	1	-	2/9/27/28	0/3/3/3
39	PSU	B5	4711	39	-	0/7/25/26	0/2/2/2
1	OMC	A2	174	1,89	-	0/9/27/28	0/2/2/2
1	A2M	A2	669	1,89	-	2/9/27/28	0/3/3/3
1	PSU	A2	36	1	-	0/7/25/26	0/2/2/2
1	PSU	A2	210	1	-	0/7/25/26	0/2/2/2
1	OMU	A2	355	1	-	0/9/27/28	0/2/2/2
1	A2M	A2	469	1	-	1/9/27/28	0/3/3/3
39	A2M	B5	3456	39	-	0/9/27/28	0/3/3/3
39	OMG	B5	4240	39	-	0/9/27/28	0/3/3/3
11	5MC	AT	49	11	-	0/7/25/26	0/2/2/2
1	6MZ	A2	1833	1,89	-	2/9/27/28	0/3/3/3
1	OMG	A2	510	1,89	-	0/9/27/28	0/3/3/3
1	PSU	A2	93	1	-	0/7/25/26	0/2/2/2

All (558) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	AT	46	G7M	C8-N7	7.32	1.46	1.33
1	A2	1640	G7M	C8-N7	7.30	1.46	1.33
11	AT	37	YYG	O23-C21	6.57	1.45	1.34
11	AT	37	YYG	O18-C16	5.16	1.45	1.33
68	Ba	39	V5N	CG-ND1	-5.08	1.32	1.37
42	BA	216	V5N	CG-ND1	-5.07	1.32	1.37
1	A2	1640	G7M	C5-N7	-4.73	1.33	1.39
11	AT	46	G7M	C5-N7	-4.68	1.33	1.39
1	A2	591	A2M	C5-C4	4.55	1.47	1.39
39	B5	3492	A2M	C5-C4	4.55	1.47	1.39
1	A2	1852	MA6	C5-C4	4.52	1.47	1.39
1	A2	1851	MA6	C5-C4	4.50	1.47	1.39
39	B5	398	A2M	C5-C4	4.48	1.47	1.39
39	B5	400	A2M	C5-C4	4.48	1.47	1.39
39	B5	4317	A2M	C5-C4	4.47	1.47	1.39
39	B5	3599	A2M	C5-C4	4.47	1.47	1.39
1	A2	1384	A2M	C5-C4	4.47	1.47	1.39
39	B5	3456	A2M	C5-C4	4.46	1.47	1.39
1	A2	27	A2M	C5-C4	4.46	1.47	1.39
1	A2	513	A2M	C5-C4	4.46	1.47	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A2	166	A2M	C5-C4	4.45	1.47	1.39
39	B5	4336	A2M	C5-C4	4.45	1.47	1.39
1	A2	159	A2M	C5-C4	4.45	1.47	1.39
1	A2	577	A2M	C5-C4	4.45	1.47	1.39
1	A2	99	A2M	C5-C4	4.44	1.47	1.39
39	B5	2658	A2M	C5-C4	4.43	1.47	1.39
1	A2	469	A2M	C5-C4	4.43	1.47	1.39
39	B5	4269	A2M	C5-C4	4.43	1.47	1.39
39	B5	3562	A2M	C5-C4	4.42	1.47	1.39
39	B5	3557	A2M	C5-C4	4.41	1.47	1.39
39	B5	3966	6MZ	C5-C4	4.41	1.47	1.39
1	A2	485	A2M	C5-C4	4.40	1.47	1.39
1	A2	1833	6MZ	C5-C4	4.39	1.47	1.39
39	B5	1489	A2M	C5-C4	4.39	1.47	1.39
39	B5	2206	A2M	C5-C4	4.39	1.47	1.39
1	A2	1679	A2M	C5-C4	4.38	1.47	1.39
39	B5	3450	A2M	C5-C4	4.38	1.47	1.39
39	B5	2244	A2M	C5-C4	4.37	1.47	1.39
39	B5	1810	A2M	C5-C4	4.37	1.47	1.39
39	B5	2630	A2M	C5-C4	4.37	1.47	1.39
39	B5	1270	A2M	C5-C4	4.36	1.47	1.39
39	B5	1479	A2M	C5-C4	4.34	1.47	1.39
1	A2	669	A2M	C5-C4	4.32	1.47	1.39
1	A2	1032	A2M	C5-C4	4.31	1.47	1.39
35	Aw	62	HY3	C3-CA	-4.29	1.50	1.55
39	B5	3517	A2M	C5-C4	4.17	1.46	1.39
1	A2	1640	G7M	C8-N9	4.04	1.47	1.35
11	AT	46	G7M	C8-N9	3.99	1.46	1.35
1	A2	1640	G7M	C5-C4	3.74	1.47	1.38
11	AT	46	G7M	C5-C4	3.68	1.47	1.38
11	AT	37	YYG	C6-N1	-3.45	1.34	1.42
39	B5	3550	UY1	C6-C5	3.38	1.39	1.35
11	AT	37	YYG	C5-C4	3.32	1.48	1.38
1	A2	210	PSU	C6-C5	3.21	1.39	1.35
1	A2	867	PSU	C6-C5	3.20	1.39	1.35
1	A2	802	PSU	C6-C5	3.19	1.39	1.35
39	B5	4039	PSU	C6-C5	3.19	1.39	1.35
41	B8	55	PSU	C6-C5	3.18	1.39	1.35
1	A2	1249	B8N	C4-N3	-3.18	1.34	1.40
39	B5	3494	PSU	C6-C5	3.17	1.39	1.35
39	B5	3616	PSU	C6-C5	3.17	1.39	1.35
11	AT	58	1MA	C6-N6	3.16	1.35	1.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	B5	4166	PSU	C6-C5	3.16	1.39	1.35
1	A2	1005	PSU	C6-C5	3.15	1.39	1.35
1	A2	864	PSU	C6-C5	3.14	1.39	1.35
39	B5	1720	PSU	C6-C5	3.14	1.39	1.35
1	A2	610	PSU	C6-C5	3.14	1.39	1.35
1	A2	682	PSU	C6-C5	3.14	1.39	1.35
11	AT	28	PSU	C6-C5	3.14	1.39	1.35
39	B5	4042	PSU	C6-C5	3.14	1.39	1.35
1	A2	1178	PSU	C6-C5	3.13	1.39	1.35
39	B5	1632	PSU	C6-C5	3.13	1.39	1.35
39	B5	4099	PSU	C6-C5	3.13	1.39	1.35
39	B5	1799	PSU	C6-C5	3.13	1.39	1.35
39	B5	4325	PSU	C6-C5	3.13	1.39	1.35
39	B5	4711	PSU	C6-C5	3.13	1.39	1.35
11	AT	14	1MA	C5-C4	3.13	1.47	1.38
39	B5	4749	PSU	C6-C5	3.13	1.39	1.35
39	B5	3496	PSU	C6-C5	3.12	1.39	1.35
11	AT	58	1MA	C5-C4	3.12	1.47	1.38
39	B5	1266	1MA	C6-N6	3.12	1.35	1.28
1	A2	93	PSU	C6-C5	3.12	1.39	1.35
1	A2	1626	PSU	C6-C5	3.12	1.39	1.35
1	A2	1239	PSU	C6-C5	3.12	1.39	1.35
39	B5	4217	PSU	C6-C5	3.12	1.39	1.35
39	B5	3576	PSU	C6-C5	3.12	1.39	1.35
1	A2	967	PSU	C6-C5	3.11	1.38	1.35
39	B5	4374	PSU	C6-C5	3.11	1.38	1.35
1	A2	34	PSU	C6-C5	3.11	1.38	1.35
1	A2	1047	PSU	C6-C5	3.11	1.38	1.35
11	AT	14	1MA	C6-N6	3.11	1.35	1.28
39	B5	2475	PSU	C6-C5	3.10	1.38	1.35
1	A2	1233	PSU	C6-C5	3.10	1.38	1.35
1	A2	1348	PSU	C6-C5	3.10	1.38	1.35
39	B5	4740	PSU	C6-C5	3.10	1.38	1.35
39	B5	3466	PSU	C6-C5	3.09	1.38	1.35
39	B5	1638	PSU	C6-C5	3.09	1.38	1.35
39	B5	1721	PSU	C6-C5	3.09	1.38	1.35
1	A2	105	PSU	C6-C5	3.09	1.38	1.35
39	B5	1731	PSU	C6-C5	3.08	1.38	1.35
39	B5	3554	PSU	C6-C5	3.08	1.38	1.35
1	A2	1693	PSU	C6-C5	3.08	1.38	1.35
39	B5	4267	PSU	C6-C5	3.08	1.38	1.35
39	B5	4435	PSU	C6-C5	3.08	1.38	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	AT	55	PSU	C6-C5	3.08	1.38	1.35
1	A2	650	PSU	C6-C5	3.08	1.38	1.35
39	B5	3500	PSU	C6-C5	3.08	1.38	1.35
1	A2	1057	PSU	C6-C5	3.07	1.38	1.35
1	A2	868	OMG	C5-C4	3.07	1.47	1.38
1	A2	1082	PSU	C6-C5	3.07	1.38	1.35
39	B5	4322	PSU	C6-C5	3.07	1.38	1.35
39	B5	3583	PSU	C6-C5	3.07	1.38	1.35
39	B5	4169	PSU	C6-C5	3.07	1.38	1.35
1	A2	119	PSU	C6-C5	3.07	1.38	1.35
1	A2	1446	PSU	C6-C5	3.06	1.38	1.35
39	B5	1801	PSU	C6-C5	3.06	1.38	1.35
39	B5	1537	PSU	C6-C5	3.06	1.38	1.35
39	B5	3585	PSU	C6-C5	3.06	1.38	1.35
39	B5	4177	PSU	C6-C5	3.06	1.38	1.35
11	AT	27	PSU	C6-C5	3.06	1.38	1.35
1	A2	815	PSU	C6-C5	3.06	1.38	1.35
39	B5	2267	OMG	C5-C4	3.06	1.47	1.38
39	B5	3502	PSU	C6-C5	3.06	1.38	1.35
11	AT	39	PSU	C6-C5	3.06	1.38	1.35
39	B5	4107	PSU	C6-C5	3.05	1.38	1.35
39	B5	2719	OMG	C5-C4	3.05	1.47	1.38
1	A2	823	PSU	C6-C5	3.05	1.38	1.35
39	B5	3676	OMG	C5-C4	3.05	1.47	1.38
11	AT	10	2MG	C5-C4	3.05	1.47	1.38
39	B5	4240	OMG	C5-C4	3.05	1.47	1.38
11	AT	34	OMG	C5-C4	3.05	1.47	1.38
1	A2	218	PSU	C6-C5	3.05	1.38	1.35
39	B5	4382	PSU	C6-C5	3.04	1.38	1.35
39	B5	3447	PSU	C6-C5	3.04	1.38	1.35
1	A2	687	PSU	C6-C5	3.04	1.38	1.35
1	A2	816	PSU	C6-C5	3.04	1.38	1.35
1	A2	1448	OMG	C5-C4	3.04	1.47	1.38
39	B5	4278	PSU	C6-C5	3.04	1.38	1.35
39	B5	4246	PSU	C6-C5	3.04	1.38	1.35
1	A2	1046	PSU	C6-C5	3.04	1.38	1.35
1	A2	573	PSU	C6-C5	3.03	1.38	1.35
39	B5	1683	PSU	C6-C5	3.03	1.38	1.35
39	B5	1580	OMG	C5-C4	3.03	1.47	1.38
39	B5	2351	PSU	C6-C5	3.03	1.38	1.35
39	B5	4045	PSU	C6-C5	3.03	1.38	1.35
39	B5	3490	PSU	C6-C5	3.03	1.38	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A2	1175	PSU	C6-C5	3.03	1.38	1.35
1	A2	510	OMG	C5-C4	3.03	1.47	1.38
1	A2	109	PSU	C6-C5	3.03	1.38	1.35
39	B5	3476	OMG	C5-C4	3.02	1.47	1.38
41	B8	69	PSU	C6-C5	3.02	1.38	1.35
1	A2	652	PSU	C6-C5	3.02	1.38	1.35
39	B5	4298	PSU	C6-C5	3.02	1.38	1.35
39	B5	1491	PSU	C6-C5	3.02	1.38	1.35
1	A2	1644	PSU	C6-C5	3.02	1.38	1.35
1	A2	437	OMG	C5-C4	3.02	1.47	1.38
39	B5	4245	OMG	C5-C4	3.02	1.47	1.38
1	A2	645	OMG	C5-C4	3.02	1.47	1.38
1	A2	602	OMG	C5-C4	3.01	1.47	1.38
39	B5	3942	OMG	C5-C4	3.01	1.47	1.38
39	B5	3524	OMG	C5-C4	3.01	1.47	1.38
1	A2	1368	PSU	C6-C5	3.01	1.38	1.35
39	B5	4149	PSU	C6-C5	3.01	1.38	1.35
1	A2	1329	OMG	C5-C4	3.01	1.47	1.38
39	B5	1718	PSU	C6-C5	3.01	1.38	1.35
39	B5	4058	PSU	C6-C5	3.01	1.38	1.35
11	AT	26	M2G	C5-C4	3.00	1.47	1.38
1	A2	684	OMG	C5-C4	3.00	1.47	1.38
39	B5	3974	OMG	C5-C4	3.00	1.47	1.38
39	B5	3427	PSU	C6-C5	3.00	1.38	1.35
39	B5	3462	PSU	C6-C5	3.00	1.38	1.35
39	B5	1266	1MA	C5-C4	3.00	1.47	1.38
39	B5	3652	PSU	C6-C5	2.99	1.38	1.35
39	B5	4116	OMG	C5-C4	2.99	1.47	1.38
39	B5	4138	OMG	C5-C4	2.99	1.47	1.38
1	A2	407	PSU	C6-C5	2.98	1.38	1.35
39	B5	4419	PSU	C6-C5	2.98	1.38	1.35
39	B5	3371	PSU	C6-C5	2.98	1.38	1.35
1	A2	1245	PSU	C6-C5	2.98	1.38	1.35
39	B5	4383	OMG	C5-C4	2.98	1.47	1.38
39	B5	3359	OMG	C5-C4	2.98	1.47	1.38
39	B5	4364	OMG	C5-C4	2.98	1.47	1.38
39	B5	4188	PSU	C6-C5	2.97	1.38	1.35
39	B5	4203	PSU	C6-C5	2.97	1.38	1.35
1	A2	1491	OMG	C5-C4	2.97	1.47	1.38
39	B5	2207	OMG	C5-C4	2.97	1.47	1.38
41	B8	75	OMG	C5-C4	2.97	1.47	1.38
1	A2	36	PSU	C6-C5	2.96	1.38	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	B5	1477	OMG	C5-C4	2.96	1.47	1.38
39	B5	4369	OMG	C5-C4	2.95	1.47	1.38
39	B5	1260	OMG	C5-C4	2.93	1.46	1.38
42	BA	216	V5N	CD2-NE2	-2.93	1.33	1.37
1	A2	1249	B8N	C6-C5	2.92	1.39	1.34
39	B5	3369	PSU	C6-C5	2.92	1.38	1.35
68	Ba	39	V5N	CD2-NE2	-2.91	1.33	1.37
39	B5	4193	5MC	C6-C5	2.91	1.39	1.34
39	B5	1491	PSU	C4-N3	-2.90	1.33	1.38
1	A2	1338	4AC	C4-N4	-2.90	1.35	1.39
39	B5	3631	OMG	C5-C4	2.90	1.46	1.38
39	B5	3369	PSU	C4-N3	-2.89	1.33	1.38
1	A2	1851	MA6	C5-C6	2.87	1.49	1.41
39	B5	4217	PSU	C4-N3	-2.85	1.33	1.38
39	B5	1799	PSU	C4-N3	-2.84	1.33	1.38
39	B5	3583	PSU	C4-N3	-2.84	1.33	1.38
39	B5	4419	PSU	C4-N3	-2.83	1.33	1.38
39	B5	4298	PSU	C4-N3	-2.83	1.33	1.38
1	A2	407	PSU	C4-N3	-2.82	1.33	1.38
1	A2	1693	PSU	C4-N3	-2.82	1.33	1.38
1	A2	1852	MA6	C5-C6	2.82	1.49	1.41
39	B5	3585	PSU	C4-N3	-2.81	1.33	1.38
39	B5	4435	PSU	C4-N3	-2.81	1.33	1.38
1	A2	864	PSU	C4-N3	-2.81	1.33	1.38
39	B5	1638	PSU	C4-N3	-2.81	1.33	1.38
1	A2	1348	PSU	C4-N3	-2.81	1.33	1.38
39	B5	3490	PSU	C4-N3	-2.81	1.33	1.38
39	B5	3500	PSU	C4-N3	-2.81	1.33	1.38
39	B5	3652	PSU	C4-N3	-2.81	1.33	1.38
1	A2	682	PSU	C4-N3	-2.80	1.33	1.38
1	A2	1175	PSU	C4-N3	-2.80	1.33	1.38
39	B5	4058	PSU	C4-N3	-2.80	1.33	1.38
41	B8	69	PSU	C4-N3	-2.80	1.33	1.38
39	B5	4107	PSU	C4-N3	-2.80	1.33	1.38
39	B5	4740	PSU	C4-N3	-2.79	1.33	1.38
11	AT	37	YYG	C2-N3	-2.79	1.34	1.39
39	B5	1801	PSU	C4-N3	-2.79	1.33	1.38
39	B5	3576	PSU	C4-N3	-2.79	1.33	1.38
39	B5	4045	PSU	C4-N3	-2.79	1.33	1.38
39	B5	2351	PSU	C4-N3	-2.79	1.33	1.38
39	B5	3427	PSU	C4-N3	-2.79	1.33	1.38
39	B5	1731	PSU	C4-N3	-2.79	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A2	1082	PSU	C4-N3	-2.78	1.33	1.38
39	B5	4374	PSU	C4-N3	-2.78	1.33	1.38
1	A2	1005	PSU	C4-N3	-2.78	1.33	1.38
39	B5	4267	PSU	C4-N3	-2.78	1.33	1.38
1	A2	650	PSU	C4-N3	-2.77	1.33	1.38
1	A2	967	PSU	C4-N3	-2.77	1.33	1.38
1	A2	815	PSU	C4-N3	-2.77	1.33	1.38
39	B5	4149	PSU	C4-N3	-2.77	1.33	1.38
39	B5	4203	PSU	C4-N3	-2.77	1.33	1.38
39	B5	4325	PSU	C4-N3	-2.77	1.33	1.38
39	B5	4188	PSU	C4-N3	-2.76	1.33	1.38
39	B5	3502	PSU	C4-N3	-2.76	1.33	1.38
39	B5	1721	PSU	C4-N3	-2.76	1.33	1.38
11	AT	27	PSU	C4-N3	-2.76	1.33	1.38
39	B5	3371	PSU	C4-N3	-2.76	1.33	1.38
1	A2	1245	PSU	C4-N3	-2.76	1.33	1.38
39	B5	4382	PSU	C4-N3	-2.75	1.33	1.38
39	B5	4099	PSU	C4-N3	-2.75	1.33	1.38
1	A2	105	PSU	C4-N3	-2.75	1.33	1.38
39	B5	3616	PSU	C4-N3	-2.75	1.33	1.38
1	A2	1233	PSU	C4-N3	-2.75	1.33	1.38
39	B5	4169	PSU	C4-N3	-2.75	1.33	1.38
1	A2	93	PSU	C4-N3	-2.75	1.33	1.38
39	B5	1683	PSU	C4-N3	-2.75	1.33	1.38
39	B5	3447	PSU	C4-N3	-2.75	1.33	1.38
39	B5	1720	PSU	C4-N3	-2.75	1.33	1.38
1	A2	1047	PSU	C4-N3	-2.75	1.33	1.38
1	A2	109	PSU	C4-N3	-2.75	1.33	1.38
1	A2	34	PSU	C4-N3	-2.75	1.33	1.38
1	A2	652	PSU	C4-N3	-2.75	1.33	1.38
39	B5	1537	PSU	C4-N3	-2.75	1.33	1.38
1	A2	1446	PSU	C4-N3	-2.74	1.33	1.38
11	AT	28	PSU	C4-N3	-2.74	1.33	1.38
39	B5	3496	PSU	C4-N3	-2.74	1.33	1.38
1	A2	1057	PSU	C4-N3	-2.74	1.33	1.38
1	A2	1851	MA6	C6-N6	2.74	1.44	1.36
11	AT	55	PSU	C4-N3	-2.74	1.33	1.38
1	A2	1046	PSU	C4-N3	-2.74	1.33	1.38
1	A2	1239	PSU	C4-N3	-2.74	1.33	1.38
39	B5	4278	PSU	C4-N3	-2.74	1.33	1.38
39	B5	3466	PSU	C4-N3	-2.74	1.33	1.38
1	A2	1178	PSU	C4-N3	-2.74	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	B5	4711	PSU	C4-N3	-2.74	1.33	1.38
39	B5	4042	PSU	C4-N3	-2.73	1.33	1.38
39	B5	2475	PSU	C4-N3	-2.73	1.33	1.38
1	A2	687	PSU	C4-N3	-2.73	1.33	1.38
1	A2	218	PSU	C4-N3	-2.72	1.33	1.38
39	B5	4039	PSU	C4-N3	-2.72	1.33	1.38
39	B5	4749	PSU	C4-N3	-2.72	1.33	1.38
1	A2	166	A2M	C5-C6	2.72	1.48	1.41
1	A2	610	PSU	C4-N3	-2.72	1.33	1.38
39	B5	3462	PSU	C4-N3	-2.72	1.33	1.38
1	A2	1368	PSU	C4-N3	-2.72	1.33	1.38
11	AT	39	PSU	C4-N3	-2.72	1.33	1.38
39	B5	4322	PSU	C4-N3	-2.72	1.33	1.38
1	A2	816	PSU	C4-N3	-2.72	1.33	1.38
41	B8	55	PSU	C4-N3	-2.71	1.33	1.38
1	A2	1644	PSU	C4-N3	-2.71	1.33	1.38
39	B5	3514	5MC	C6-C5	2.71	1.39	1.34
11	AT	26	M2G	C2-N2	2.71	1.40	1.35
1	A2	867	PSU	C4-N3	-2.70	1.33	1.38
1	A2	119	PSU	C4-N3	-2.70	1.33	1.38
1	A2	1626	PSU	C4-N3	-2.70	1.33	1.38
1	A2	513	A2M	C5-C6	2.70	1.48	1.41
39	B5	4246	PSU	C4-N3	-2.70	1.33	1.38
11	AT	49	5MC	C6-C5	2.70	1.39	1.34
39	B5	3554	PSU	C4-N3	-2.69	1.33	1.38
1	A2	159	A2M	C5-C6	2.69	1.48	1.41
39	B5	4166	PSU	C4-N3	-2.69	1.33	1.38
39	B5	4177	PSU	C4-N3	-2.69	1.33	1.38
1	A2	802	PSU	C4-N3	-2.69	1.33	1.38
39	B5	1718	PSU	C4-N3	-2.69	1.33	1.38
1	A2	36	PSU	C4-N3	-2.68	1.33	1.38
39	B5	398	A2M	C5-C6	2.68	1.48	1.41
39	B5	2244	A2M	C5-C6	2.67	1.48	1.41
11	AT	54	5MU	C6-C5	2.67	1.39	1.34
1	A2	577	A2M	C5-C6	2.67	1.48	1.41
11	AT	54	5MU	C4-N3	-2.67	1.33	1.38
1	A2	469	A2M	C5-C6	2.67	1.48	1.41
1	A2	573	PSU	C4-N3	-2.67	1.33	1.38
39	B5	2267	OMG	C6-N1	-2.67	1.33	1.38
39	B5	4244	OMU	C4-N3	-2.66	1.33	1.38
39	B5	3657	OMU	C4-N3	-2.66	1.33	1.38
39	B5	4366	OMU	C4-N3	-2.66	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	B5	1489	A2M	C5-C6	2.65	1.48	1.41
1	A2	591	A2M	C5-C6	2.65	1.48	1.41
39	B5	1479	A2M	C5-C6	2.65	1.48	1.41
39	B5	4317	A2M	C5-C6	2.64	1.48	1.41
39	B5	3494	PSU	C4-N3	-2.64	1.33	1.38
39	B5	400	A2M	C5-C6	2.64	1.48	1.41
39	B5	3550	UY1	C2-N1	2.64	1.40	1.36
39	B5	3942	OMG	C6-N1	-2.64	1.33	1.38
39	B5	2719	OMG	C6-N1	-2.63	1.33	1.38
1	A2	355	OMU	C4-N3	-2.63	1.33	1.38
1	A2	1679	A2M	C5-C6	2.63	1.48	1.41
1	A2	823	PSU	C4-N3	-2.63	1.34	1.38
39	B5	4336	A2M	C5-C6	2.63	1.48	1.41
39	B5	3456	A2M	C5-C6	2.63	1.48	1.41
1	A2	27	A2M	C5-C6	2.62	1.48	1.41
39	B5	3450	A2M	C5-C6	2.62	1.48	1.41
39	B5	1580	OMG	C6-N1	-2.62	1.34	1.38
1	A2	669	A2M	C5-C6	2.62	1.48	1.41
39	B5	3973	OMU	C4-N3	-2.62	1.33	1.38
1	A2	1843	4AC	C4-N4	-2.62	1.35	1.39
1	A2	1384	A2M	C5-C6	2.61	1.48	1.41
39	B5	4052	OMU	C4-N3	-2.61	1.33	1.38
39	B5	3359	OMG	C6-N1	-2.61	1.34	1.38
39	B5	3562	A2M	C5-C6	2.61	1.48	1.41
39	B5	3557	A2M	C5-C6	2.61	1.48	1.41
39	B5	1810	A2M	C5-C6	2.61	1.48	1.41
39	B5	2658	A2M	C5-C6	2.61	1.48	1.41
39	B5	2680	OMU	C4-N3	-2.61	1.33	1.38
1	A2	485	A2M	C5-C6	2.60	1.48	1.41
1	A2	210	PSU	C4-N3	-2.60	1.34	1.38
39	B5	1270	A2M	C5-C6	2.60	1.48	1.41
1	A2	602	OMG	C6-N1	-2.60	1.34	1.38
39	B5	2207	OMG	C6-N1	-2.59	1.34	1.38
1	A2	1491	OMG	C6-N1	-2.59	1.34	1.38
39	B5	4116	OMG	C6-N1	-2.59	1.34	1.38
39	B5	3599	A2M	C5-C6	2.59	1.48	1.41
1	A2	1032	A2M	C5-C6	2.59	1.48	1.41
39	B5	3492	A2M	C5-C6	2.59	1.48	1.41
39	B5	1632	PSU	C4-N3	-2.58	1.34	1.38
1	A2	437	OMG	C6-N1	-2.58	1.34	1.38
1	A2	510	OMG	C6-N1	-2.58	1.34	1.38
39	B5	2258	OMU	C4-N3	-2.57	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	B5	3517	A2M	C5-C6	2.57	1.48	1.41
39	B5	4364	OMG	C6-N1	-2.56	1.34	1.38
39	B5	1260	OMG	C6-N1	-2.56	1.34	1.38
39	B5	4245	OMG	C6-N1	-2.56	1.34	1.38
1	A2	645	OMG	C6-N1	-2.56	1.34	1.38
1	A2	1852	MA6	C6-N6	2.56	1.44	1.36
39	B5	3476	OMG	C6-N1	-2.56	1.34	1.38
39	B5	4138	OMG	C6-N1	-2.56	1.34	1.38
39	B5	4269	A2M	C5-C6	2.55	1.48	1.41
39	B5	4383	OMG	C6-N1	-2.55	1.34	1.38
1	A2	121	OMU	C4-N3	-2.55	1.34	1.38
1	A2	172	OMU	C4-N3	-2.55	1.34	1.38
11	AT	17	H2U	C2-N3	-2.55	1.33	1.38
1	A2	99	A2M	C5-C6	2.54	1.48	1.41
1	A2	1448	OMG	C6-N1	-2.54	1.34	1.38
39	B5	1477	OMG	C6-N1	-2.54	1.34	1.38
1	A2	1443	OMU	C4-N3	-2.54	1.34	1.38
1	A2	429	OMU	C4-N3	-2.53	1.34	1.38
39	B5	4369	OMG	C6-N1	-2.53	1.34	1.38
39	B5	2206	A2M	C5-C6	2.53	1.48	1.41
39	B5	4240	OMG	C6-N1	-2.53	1.34	1.38
1	A2	1805	OMU	C4-N3	-2.53	1.34	1.38
1	A2	1329	OMG	C6-N1	-2.53	1.34	1.38
1	A2	1249	B8N	C2-N3	-2.52	1.34	1.38
1	A2	1289	OMU	C4-N3	-2.52	1.34	1.38
39	B5	3524	OMG	C6-N1	-2.52	1.34	1.38
39	B5	3631	OMG	C6-N1	-2.51	1.34	1.38
11	AT	10	2MG	C6-N1	-2.51	1.34	1.38
11	AT	16	H2U	C2-N3	-2.50	1.33	1.38
39	B5	3966	6MZ	C5-C6	2.50	1.48	1.41
39	B5	2630	A2M	C5-C6	2.50	1.48	1.41
11	AT	26	M2G	C6-N1	-2.50	1.34	1.38
1	A2	1327	OMU	C4-N3	-2.49	1.34	1.38
39	B5	3676	OMG	C6-N1	-2.49	1.34	1.38
39	B5	3974	OMG	C6-N1	-2.48	1.34	1.38
11	AT	34	OMG	C6-N1	-2.48	1.34	1.38
1	A2	868	OMG	C6-N1	-2.47	1.34	1.38
41	B8	75	OMG	C6-N1	-2.47	1.34	1.38
1	A2	116	OMU	C4-N3	-2.47	1.34	1.38
1	A2	684	OMG	C6-N1	-2.47	1.34	1.38
1	A2	1640	G7M	C6-N1	-2.46	1.34	1.38
1	A2	166	A2M	C8-N7	2.43	1.36	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A2	628	OMU	C4-N3	-2.43	1.34	1.38
1	A2	1384	A2M	C8-N7	2.42	1.36	1.31
1	A2	159	A2M	C8-N7	2.41	1.36	1.31
1	A2	1833	6MZ	C5-N7	-2.40	1.34	1.39
1	A2	469	A2M	C8-N7	2.38	1.36	1.31
39	B5	3492	A2M	C8-N7	2.38	1.36	1.31
39	B5	3657	OMU	C2-N3	-2.37	1.33	1.38
11	AT	37	YYG	C5-N7	-2.36	1.34	1.39
39	B5	4336	A2M	C8-N7	2.36	1.36	1.31
11	AT	46	G7M	C6-N1	-2.36	1.34	1.38
39	B5	2244	A2M	C8-N7	2.35	1.36	1.31
1	A2	669	A2M	C8-N7	2.35	1.36	1.31
39	B5	3456	A2M	C8-N7	2.34	1.36	1.31
39	B5	1810	A2M	C8-N7	2.34	1.36	1.31
39	B5	2267	OMG	C5-N7	-2.34	1.34	1.39
39	B5	398	A2M	C8-N7	2.33	1.36	1.31
39	B5	2630	A2M	C5-N7	-2.33	1.34	1.39
39	B5	3517	A2M	C8-N7	2.33	1.36	1.31
11	AT	54	5MU	C6-N1	-2.33	1.34	1.38
39	B5	3557	A2M	C8-N7	2.33	1.36	1.31
1	A2	1679	A2M	C8-N7	2.33	1.36	1.31
1	A2	577	A2M	C8-N7	2.33	1.36	1.31
1	A2	1032	A2M	C8-N7	2.33	1.36	1.31
1	A2	513	A2M	C8-N7	2.32	1.36	1.31
39	B5	400	A2M	C8-N7	2.32	1.36	1.31
39	B5	2206	A2M	C5-N7	-2.32	1.34	1.39
39	B5	4317	A2M	C8-N7	2.32	1.36	1.31
39	B5	1489	A2M	C8-N7	2.31	1.36	1.31
39	B5	3973	OMU	C2-N3	-2.31	1.33	1.38
39	B5	1580	OMG	C5-N7	-2.31	1.34	1.39
39	B5	4193	5MC	C6-N1	-2.30	1.34	1.38
1	A2	591	A2M	C5-N7	-2.30	1.34	1.39
11	AT	17	H2U	C4-N3	-2.30	1.33	1.37
39	B5	4269	A2M	C8-N7	2.30	1.35	1.31
39	B5	1479	A2M	C8-N7	2.30	1.35	1.31
39	B5	3562	A2M	C8-N7	2.30	1.35	1.31
1	A2	1833	6MZ	C5-C6	2.29	1.47	1.41
11	AT	54	5MU	C4-C5	2.29	1.48	1.44
39	B5	3966	6MZ	C5-N7	-2.29	1.34	1.39
11	AT	49	5MC	C6-N1	-2.29	1.34	1.38
11	AT	58	1MA	C2-N3	2.29	1.34	1.30
39	B5	1270	A2M	C8-N7	2.28	1.35	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	B5	3599	A2M	C8-N7	2.28	1.35	1.31
1	A2	591	A2M	C8-N7	2.28	1.35	1.31
39	B5	3557	A2M	C5-N7	-2.28	1.34	1.39
39	B5	3942	OMG	C5-N7	-2.28	1.34	1.39
39	B5	3562	A2M	C5-N7	-2.28	1.34	1.39
1	A2	485	A2M	C8-N7	2.27	1.35	1.31
1	A2	99	A2M	C8-N7	2.27	1.35	1.31
39	B5	1270	A2M	C5-N7	-2.27	1.34	1.39
1	A2	1491	OMG	C5-N7	-2.27	1.34	1.39
39	B5	4244	OMU	C2-N3	-2.27	1.33	1.38
1	A2	27	A2M	C8-N7	2.27	1.35	1.31
1	A2	99	A2M	C5-N7	-2.27	1.34	1.39
39	B5	2658	A2M	C5-N7	-2.26	1.34	1.39
1	A2	1851	MA6	C8-N7	2.26	1.35	1.31
39	B5	3599	A2M	C5-N7	-2.26	1.34	1.39
39	B5	1266	1MA	C5-N7	-2.26	1.34	1.39
39	B5	4317	A2M	C5-N7	-2.26	1.34	1.39
1	A2	116	OMU	C2-N3	-2.26	1.33	1.38
39	B5	3450	A2M	C8-N7	2.26	1.35	1.31
39	B5	2658	A2M	C8-N7	2.25	1.35	1.31
39	B5	3524	OMG	C5-N7	-2.25	1.34	1.39
39	B5	4116	OMG	C5-N7	-2.25	1.34	1.39
39	B5	2206	A2M	C8-N7	2.24	1.35	1.31
39	B5	3550	UY1	C6-N1	-2.24	1.32	1.36
39	B5	1489	A2M	C5-N7	-2.24	1.34	1.39
39	B5	3450	A2M	C5-N7	-2.24	1.34	1.39
11	AT	14	1MA	C2-N3	2.24	1.34	1.30
1	A2	1852	MA6	C8-N7	2.24	1.35	1.31
39	B5	2680	OMU	C2-N3	-2.24	1.34	1.38
1	A2	1679	A2M	C5-N7	-2.24	1.34	1.39
1	A2	1327	OMU	C2-N3	-2.24	1.34	1.38
39	B5	2719	OMG	C5-N7	-2.23	1.34	1.39
39	B5	400	A2M	C5-N7	-2.23	1.34	1.39
39	B5	3514	5MC	C6-N1	-2.23	1.34	1.38
39	B5	4366	OMU	C2-N3	-2.23	1.34	1.38
39	B5	1479	A2M	C5-N7	-2.23	1.34	1.39
1	A2	437	OMG	C5-N7	-2.23	1.34	1.39
39	B5	2258	OMU	C2-N3	-2.22	1.34	1.38
39	B5	4369	OMG	C5-N7	-2.22	1.34	1.39
1	A2	513	A2M	C5-N7	-2.22	1.34	1.39
1	A2	1289	OMU	C2-N1	2.22	1.42	1.38
39	B5	4269	A2M	C5-N7	-2.22	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A2	355	OMU	C2-N3	-2.22	1.34	1.38
1	A2	27	A2M	C5-N7	-2.22	1.34	1.39
1	A2	485	A2M	C5-N7	-2.22	1.34	1.39
11	AT	34	OMG	C5-N7	-2.21	1.34	1.39
39	B5	2244	A2M	C5-N7	-2.21	1.34	1.39
39	B5	4336	A2M	C5-N7	-2.21	1.34	1.39
1	A2	121	OMU	C2-N3	-2.21	1.34	1.38
1	A2	602	OMG	C5-N7	-2.21	1.34	1.39
11	AT	10	2MG	C5-N7	-2.21	1.34	1.39
1	A2	645	OMG	C5-N7	-2.21	1.34	1.39
39	B5	2630	A2M	C8-N7	2.20	1.35	1.31
39	B5	4138	OMG	C5-N7	-2.20	1.34	1.39
39	B5	4052	OMU	C2-N3	-2.20	1.34	1.38
1	A2	577	A2M	C5-N7	-2.20	1.34	1.39
1	A2	469	A2M	C5-N7	-2.20	1.34	1.39
1	A2	1805	OMU	C2-N3	-2.20	1.34	1.38
39	B5	1810	A2M	C5-N7	-2.20	1.34	1.39
39	B5	398	A2M	C5-N7	-2.19	1.34	1.39
39	B5	4364	OMG	C5-N7	-2.19	1.34	1.39
1	A2	628	OMU	C2-N3	-2.19	1.34	1.38
39	B5	2207	OMG	C5-N7	-2.19	1.34	1.39
1	A2	166	A2M	C5-N7	-2.19	1.34	1.39
1	A2	1384	A2M	C5-N7	-2.19	1.34	1.39
39	B5	4240	OMG	C5-N7	-2.19	1.34	1.39
11	AT	14	1MA	C5-N7	-2.19	1.34	1.39
1	A2	1448	OMG	C5-N7	-2.19	1.34	1.39
11	AT	10	2MG	C2-N3	2.19	1.36	1.31
39	B5	1260	OMG	C5-N7	-2.18	1.34	1.39
39	B5	3492	A2M	C5-N7	-2.18	1.34	1.39
39	B5	4245	OMG	C5-N7	-2.18	1.34	1.39
1	A2	510	OMG	C5-N7	-2.18	1.34	1.39
39	B5	3517	A2M	C5-N7	-2.18	1.34	1.39
1	A2	868	OMG	C5-N7	-2.18	1.34	1.39
39	B5	3456	A2M	C5-N7	-2.18	1.34	1.39
1	A2	1329	OMG	C5-N7	-2.18	1.34	1.39
39	B5	3631	OMG	C5-N7	-2.17	1.34	1.39
1	A2	429	OMU	C2-N3	-2.17	1.34	1.38
1	A2	1443	OMU	C2-N3	-2.17	1.34	1.38
1	A2	1289	OMU	C2-N3	-2.17	1.34	1.38
39	B5	1477	OMG	C5-N7	-2.17	1.34	1.39
1	A2	159	A2M	C5-N7	-2.17	1.34	1.39
1	A2	684	OMG	C5-N7	-2.16	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A2	669	A2M	C5-N7	-2.16	1.34	1.39
11	AT	58	1MA	C5-N7	-2.16	1.34	1.39
1	A2	1032	A2M	C5-N7	-2.16	1.34	1.39
39	B5	4383	OMG	C5-N7	-2.16	1.34	1.39
11	AT	16	H2U	C4-N3	-2.15	1.33	1.37
39	B5	3974	OMG	C5-N7	-2.15	1.34	1.39
39	B5	3966	6MZ	C8-N7	2.15	1.35	1.31
41	B8	75	OMG	C5-N7	-2.15	1.34	1.39
11	AT	37	YYG	C2-N1	-2.15	1.35	1.38
1	A2	1852	MA6	C5-N7	-2.15	1.35	1.39
39	B5	3359	OMG	C5-N7	-2.15	1.34	1.39
39	B5	3369	PSU	C2-N3	-2.14	1.33	1.37
11	AT	54	5MU	C2-N1	2.13	1.41	1.38
39	B5	1266	1MA	C2-N3	2.13	1.34	1.30
1	A2	172	OMU	C2-N3	-2.13	1.34	1.38
39	B5	3476	OMG	C5-N7	-2.13	1.35	1.39
11	AT	26	M2G	C5-N7	-2.12	1.35	1.39
39	B5	3676	OMG	C5-N7	-2.11	1.35	1.39
1	A2	1851	MA6	C5-N7	-2.10	1.35	1.39
1	A2	1805	OMU	C2-N1	2.08	1.41	1.38
1	A2	116	OMU	C5-C4	-2.07	1.39	1.43
39	B5	4052	OMU	C5-C4	-2.07	1.39	1.43
1	A2	121	OMU	C5-C4	-2.05	1.39	1.43
1	A2	172	OMU	C5-C4	-2.05	1.39	1.43
1	A2	1338	4AC	C7-N4	-2.05	1.33	1.37
1	A2	1833	6MZ	C8-N7	2.05	1.35	1.31
1	A2	1443	OMU	C5-C4	-2.05	1.39	1.43
39	B5	3973	OMU	C2-N1	2.04	1.41	1.38
11	AT	54	5MU	C2-N3	-2.03	1.34	1.38
1	A2	669	A2M	C4-N9	-2.03	1.33	1.37
1	A2	1082	PSU	C2-N3	-2.03	1.34	1.37
39	B5	4366	OMU	C5-C4	-2.03	1.39	1.43
1	A2	355	OMU	C5-C4	-2.02	1.39	1.43
39	B5	4276	UR3	C2-N1	2.01	1.41	1.38

All (1054) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	AT	46	G7M	CN7-N7-C8	-7.83	112.76	124.84
1	A2	1640	G7M	CN7-N7-C8	-7.73	112.92	124.84
11	AT	10	2MG	C2-N3-C4	7.16	120.91	112.04
11	AT	17	H2U	C4-N3-C2	-7.02	119.97	125.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	591	A2M	C5-C4-N3	-6.82	117.86	126.75
11	AT	46	G7M	C8-N7-C5	6.71	116.18	107.78
11	AT	46	G7M	N9-C8-N7	-6.70	95.62	112.21
1	A2	1833	6MZ	C5-C4-N3	-6.57	118.18	126.75
1	A2	1640	G7M	C8-N7-C5	6.55	115.97	107.78
1	A2	1640	G7M	N9-C8-N7	-6.54	96.03	112.21
39	B5	2719	OMG	C5-C4-N3	-6.42	118.04	128.46
11	AT	46	G7M	N9-C4-N3	6.37	138.73	125.94
1	A2	1640	G7M	N9-C4-N3	6.37	138.72	125.94
39	B5	398	A2M	C5-C4-N3	-6.34	118.48	126.75
39	B5	4336	A2M	C5-C4-N3	-6.32	118.50	126.75
39	B5	3942	OMG	C5-C4-N3	-6.30	118.25	128.46
39	B5	2658	A2M	C5-C4-N3	-6.29	118.55	126.75
39	B5	2267	OMG	C5-C4-N3	-6.26	118.30	128.46
1	A2	166	A2M	C5-C4-N3	-6.26	118.59	126.75
39	B5	3369	PSU	N1-C2-N3	6.25	122.21	115.13
39	B5	1580	OMG	C5-C4-N3	-6.25	118.33	128.46
39	B5	3966	6MZ	C5-C4-N3	-6.24	118.61	126.75
39	B5	4374	PSU	N1-C2-N3	6.22	122.18	115.13
39	B5	3502	PSU	N1-C2-N3	6.20	122.16	115.13
1	A2	99	A2M	C5-C4-N3	-6.20	118.66	126.75
1	A2	513	A2M	C5-C4-N3	-6.20	118.66	126.75
39	B5	3557	A2M	C5-C4-N3	-6.20	118.67	126.75
39	B5	4298	PSU	N1-C2-N3	6.19	122.14	115.13
1	A2	1178	PSU	N1-C2-N3	6.18	122.13	115.13
41	B8	69	PSU	N1-C2-N3	6.18	122.13	115.13
39	B5	400	A2M	C5-C4-N3	-6.17	118.69	126.75
39	B5	4240	OMG	C5-C4-N3	-6.17	118.46	128.46
1	A2	27	A2M	C5-C4-N3	-6.17	118.71	126.75
1	A2	1491	OMG	C5-C4-N3	-6.16	118.47	128.46
39	B5	4325	PSU	N1-C2-N3	6.16	122.11	115.13
39	B5	4246	PSU	N1-C2-N3	6.16	122.10	115.13
39	B5	3583	PSU	N1-C2-N3	6.15	122.10	115.13
1	A2	1679	A2M	C5-C4-N3	-6.15	118.72	126.75
39	B5	4188	PSU	N1-C2-N3	6.15	122.10	115.13
1	A2	159	A2M	C5-C4-N3	-6.15	118.73	126.75
39	B5	4149	PSU	N1-C2-N3	6.15	122.10	115.13
1	A2	650	PSU	N1-C2-N3	6.15	122.09	115.13
1	A2	1384	A2M	C5-C4-N3	-6.14	118.73	126.75
11	AT	34	OMG	C5-C4-N3	-6.14	118.50	128.46
39	B5	3496	PSU	N1-C2-N3	6.14	122.08	115.13
39	B5	3447	PSU	N1-C2-N3	6.14	122.08	115.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	437	OMG	C5-C4-N3	-6.13	118.51	128.46
39	B5	3562	A2M	C5-C4-N3	-6.13	118.75	126.75
39	B5	1801	PSU	N1-C2-N3	6.12	122.07	115.13
39	B5	4042	PSU	N1-C2-N3	6.12	122.06	115.13
39	B5	4711	PSU	N1-C2-N3	6.12	122.06	115.13
1	A2	105	PSU	N1-C2-N3	6.11	122.06	115.13
39	B5	4419	PSU	N1-C2-N3	6.11	122.06	115.13
39	B5	3427	PSU	N1-C2-N3	6.11	122.06	115.13
39	B5	3585	PSU	N1-C2-N3	6.11	122.06	115.13
39	B5	2351	PSU	N1-C2-N3	6.11	122.05	115.13
11	AT	39	PSU	N1-C2-N3	6.11	122.05	115.13
39	B5	4435	PSU	N1-C2-N3	6.11	122.05	115.13
1	A2	469	A2M	C5-C4-N3	-6.11	118.78	126.75
39	B5	3524	OMG	C5-C4-N3	-6.11	118.55	128.46
1	A2	34	PSU	N1-C2-N3	6.11	122.05	115.13
39	B5	3599	A2M	C5-C4-N3	-6.11	118.78	126.75
1	A2	510	OMG	C5-C4-N3	-6.11	118.55	128.46
39	B5	1491	PSU	N1-C2-N3	6.10	122.04	115.13
39	B5	3466	PSU	N1-C2-N3	6.10	122.04	115.13
39	B5	1721	PSU	N1-C2-N3	6.10	122.04	115.13
1	A2	645	OMG	C5-C4-N3	-6.10	118.57	128.46
11	AT	27	PSU	N1-C2-N3	6.10	122.04	115.13
1	A2	1448	OMG	C5-C4-N3	-6.10	118.57	128.46
1	A2	485	A2M	C5-C4-N3	-6.10	118.80	126.75
39	B5	1799	PSU	N1-C2-N3	6.10	122.04	115.13
11	AT	28	PSU	N1-C2-N3	6.10	122.04	115.13
1	A2	602	OMG	C5-C4-N3	-6.09	118.57	128.46
41	B8	55	PSU	N1-C2-N3	6.09	122.03	115.13
39	B5	4317	A2M	C5-C4-N3	-6.09	118.80	126.75
39	B5	4099	PSU	N1-C2-N3	6.09	122.03	115.13
39	B5	4058	PSU	N1-C2-N3	6.09	122.03	115.13
39	B5	4107	PSU	N1-C2-N3	6.09	122.03	115.13
11	AT	10	2MG	C5-C4-N3	-6.09	118.59	128.46
39	B5	4045	PSU	N1-C2-N3	6.08	122.02	115.13
39	B5	3450	A2M	C5-C4-N3	-6.08	118.82	126.75
1	A2	816	PSU	N1-C2-N3	6.08	122.02	115.13
1	A2	1057	PSU	N1-C2-N3	6.08	122.02	115.13
39	B5	3500	PSU	N1-C2-N3	6.08	122.02	115.13
39	B5	4740	PSU	N1-C2-N3	6.08	122.02	115.13
39	B5	4269	A2M	C5-C4-N3	-6.08	118.82	126.75
1	A2	652	PSU	N1-C2-N3	6.08	122.01	115.13
1	A2	1047	PSU	N1-C2-N3	6.08	122.01	115.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	B5	2630	A2M	C5-C4-N3	-6.07	118.83	126.75
39	B5	1479	A2M	C5-C4-N3	-6.07	118.83	126.75
39	B5	1683	PSU	N1-C2-N3	6.07	122.01	115.13
39	B5	4383	OMG	C5-C4-N3	-6.07	118.61	128.46
39	B5	1632	PSU	N1-C2-N3	6.07	122.00	115.13
1	A2	1644	PSU	N1-C2-N3	6.07	122.00	115.13
39	B5	1638	PSU	N1-C2-N3	6.07	122.00	115.13
39	B5	3494	PSU	N1-C2-N3	6.07	122.00	115.13
1	A2	218	PSU	N1-C2-N3	6.06	122.00	115.13
39	B5	1260	OMG	C5-C4-N3	-6.06	118.62	128.46
1	A2	687	PSU	N1-C2-N3	6.06	122.00	115.13
1	A2	1693	PSU	N1-C2-N3	6.06	122.00	115.13
1	A2	967	PSU	N1-C2-N3	6.06	122.00	115.13
39	B5	1720	PSU	N1-C2-N3	6.06	121.99	115.13
39	B5	2206	A2M	C5-C4-N3	-6.06	118.85	126.75
1	A2	867	PSU	N1-C2-N3	6.06	121.99	115.13
39	B5	3371	PSU	N1-C2-N3	6.06	121.99	115.13
41	B8	75	OMG	C5-C4-N3	-6.05	118.64	128.46
39	B5	1537	PSU	N1-C2-N3	6.05	121.99	115.13
1	A2	610	PSU	N1-C2-N3	6.05	121.99	115.13
1	A2	864	PSU	N1-C2-N3	6.05	121.98	115.13
39	B5	3676	OMG	C5-C4-N3	-6.05	118.64	128.46
1	A2	1233	PSU	N1-C2-N3	6.05	121.98	115.13
1	A2	1239	PSU	N1-C2-N3	6.05	121.98	115.13
39	B5	1810	A2M	C5-C4-N3	-6.05	118.86	126.75
1	A2	1626	PSU	N1-C2-N3	6.05	121.98	115.13
39	B5	3652	PSU	N1-C2-N3	6.05	121.98	115.13
39	B5	4382	PSU	N1-C2-N3	6.04	121.98	115.13
1	A2	407	PSU	N1-C2-N3	6.04	121.98	115.13
1	A2	1368	PSU	N1-C2-N3	6.04	121.98	115.13
39	B5	3359	OMG	C5-C4-N3	-6.04	118.66	128.46
39	B5	4245	OMG	C5-C4-N3	-6.04	118.66	128.46
39	B5	4322	PSU	N1-C2-N3	6.04	121.97	115.13
39	B5	2244	A2M	C5-C4-N3	-6.04	118.87	126.75
1	A2	1446	PSU	N1-C2-N3	6.04	121.97	115.13
1	A2	823	PSU	N1-C2-N3	6.04	121.97	115.13
1	A2	109	PSU	N1-C2-N3	6.03	121.97	115.13
1	A2	1348	PSU	N1-C2-N3	6.03	121.97	115.13
39	B5	3476	OMG	C5-C4-N3	-6.03	118.67	128.46
39	B5	4169	PSU	N1-C2-N3	6.03	121.96	115.13
1	A2	93	PSU	N1-C2-N3	6.03	121.96	115.13
39	B5	4217	PSU	N1-C2-N3	6.03	121.96	115.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	AT	55	PSU	N1-C2-N3	6.03	121.96	115.13
1	A2	573	PSU	N1-C2-N3	6.02	121.95	115.13
1	A2	577	A2M	C5-C4-N3	-6.02	118.89	126.75
1	A2	815	PSU	N1-C2-N3	6.02	121.95	115.13
39	B5	4267	PSU	N1-C2-N3	6.01	121.94	115.13
1	A2	868	OMG	C5-C4-N3	-6.01	118.71	128.46
1	A2	1046	PSU	N1-C2-N3	6.01	121.94	115.13
39	B5	3492	A2M	C5-C4-N3	-6.01	118.91	126.75
1	A2	682	PSU	N1-C2-N3	6.00	121.93	115.13
39	B5	4278	PSU	N1-C2-N3	6.00	121.93	115.13
1	A2	802	PSU	N1-C2-N3	6.00	121.93	115.13
1	A2	1329	OMG	C5-C4-N3	-6.00	118.73	128.46
39	B5	4138	OMG	C5-C4-N3	-5.99	118.74	128.46
39	B5	4177	PSU	N1-C2-N3	5.99	121.92	115.13
39	B5	2475	PSU	N1-C2-N3	5.99	121.92	115.13
1	A2	119	PSU	N1-C2-N3	5.99	121.91	115.13
39	B5	3576	PSU	N1-C2-N3	5.99	121.91	115.13
39	B5	1489	A2M	C5-C4-N3	-5.98	118.94	126.75
39	B5	4749	PSU	N1-C2-N3	5.98	121.91	115.13
39	B5	3456	A2M	C5-C4-N3	-5.98	118.95	126.75
39	B5	3490	PSU	N1-C2-N3	5.98	121.90	115.13
39	B5	4364	OMG	C5-C4-N3	-5.97	118.77	128.46
1	A2	36	PSU	N1-C2-N3	5.97	121.89	115.13
1	A2	1032	A2M	C5-C4-N3	-5.97	118.96	126.75
39	B5	4203	PSU	N1-C2-N3	5.97	121.89	115.13
1	A2	684	OMG	C5-C4-N3	-5.96	118.78	128.46
1	A2	210	PSU	N1-C2-N3	5.96	121.89	115.13
39	B5	4116	OMG	C5-C4-N3	-5.96	118.79	128.46
1	A2	1245	PSU	N1-C2-N3	5.96	121.88	115.13
39	B5	1477	OMG	C5-C4-N3	-5.96	118.79	128.46
1	A2	1175	PSU	N1-C2-N3	5.96	121.88	115.13
39	B5	1718	PSU	N1-C2-N3	5.96	121.88	115.13
39	B5	1270	A2M	C5-C4-N3	-5.95	118.98	126.75
39	B5	2207	OMG	C5-C4-N3	-5.95	118.80	128.46
39	B5	4039	PSU	N1-C2-N3	5.95	121.88	115.13
39	B5	3462	PSU	N1-C2-N3	5.95	121.87	115.13
11	AT	26	M2G	C5-C4-N3	-5.95	118.81	128.46
39	B5	3616	PSU	N1-C2-N3	5.93	121.85	115.13
39	B5	4369	OMG	C5-C4-N3	-5.92	118.85	128.46
1	A2	1005	PSU	N1-C2-N3	5.92	121.84	115.13
39	B5	3554	PSU	N1-C2-N3	5.92	121.83	115.13
1	A2	1082	PSU	N1-C2-N3	5.90	121.81	115.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	B5	3517	A2M	C5-C4-N3	-5.89	119.07	126.75
1	A2	1852	MA6	C5-C4-N3	-5.88	119.08	126.75
39	B5	4166	PSU	N1-C2-N3	5.87	121.78	115.13
39	B5	3974	OMG	C5-C4-N3	-5.85	118.97	128.46
39	B5	1731	PSU	N1-C2-N3	5.84	121.75	115.13
39	B5	3631	OMG	C5-C4-N3	-5.84	118.98	128.46
1	A2	1851	MA6	C5-C4-N3	-5.79	119.20	126.75
39	B5	4276	UR3	C4-N3-C2	-5.73	119.17	124.56
1	A2	669	A2M	C5-C4-N3	-5.71	119.31	126.75
11	AT	37	YYG	N9-C4-N3	5.57	138.65	129.44
1	A2	1640	G7M	C5-C4-N3	-5.46	117.67	128.15
1	A2	591	A2M	N3-C4-N9	5.42	136.02	127.08
11	AT	58	1MA	C5-C4-N3	-5.39	119.22	127.26
11	AT	14	1MA	C5-C4-N3	-5.37	119.24	127.26
1	A2	1833	6MZ	N3-C4-N9	5.36	135.92	127.08
39	B5	3550	UY1	C4-N3-C2	-5.36	118.62	126.34
39	B5	1266	1MA	C5-C4-N3	-5.34	119.30	127.26
11	AT	46	G7M	C5-C4-N3	-5.33	117.92	128.15
11	AT	54	5MU	C4-N3-C2	-5.08	120.77	127.35
39	B5	2719	OMG	C2-N3-C4	5.05	121.30	112.30
39	B5	3942	OMG	C2-N3-C4	4.99	121.19	112.30
39	B5	4336	A2M	N3-C4-N9	4.97	135.27	127.08
39	B5	4240	OMG	C2-N3-C4	4.95	121.12	112.30
1	A2	1491	OMG	C2-N3-C4	4.94	121.10	112.30
1	A2	684	OMG	C2-N3-C4	4.93	121.09	112.30
39	B5	4383	OMG	C2-N3-C4	4.92	121.07	112.30
41	B8	75	OMG	C2-N3-C4	4.91	121.06	112.30
39	B5	3476	OMG	C2-N3-C4	4.90	121.04	112.30
39	B5	3966	6MZ	N3-C4-N9	4.90	135.15	127.08
11	AT	34	OMG	C2-N3-C4	4.89	121.02	112.30
1	A2	437	OMG	C2-N3-C4	4.88	121.00	112.30
39	B5	1260	OMG	C2-N3-C4	4.88	121.00	112.30
39	B5	4138	OMG	C2-N3-C4	4.88	121.00	112.30
39	B5	3524	OMG	C2-N3-C4	4.88	120.99	112.30
39	B5	3359	OMG	C2-N3-C4	4.88	120.99	112.30
39	B5	1580	OMG	C2-N3-C4	4.88	120.99	112.30
1	A2	645	OMG	C2-N3-C4	4.87	120.98	112.30
39	B5	4245	OMG	C2-N3-C4	4.87	120.98	112.30
1	A2	602	OMG	C2-N3-C4	4.87	120.98	112.30
39	B5	4364	OMG	C2-N3-C4	4.87	120.97	112.30
1	A2	99	A2M	N3-C4-N9	4.86	135.09	127.08
1	A2	166	A2M	N3-C4-N9	4.86	135.09	127.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	1329	OMG	C2-N3-C4	4.86	120.95	112.30
39	B5	3676	OMG	C2-N3-C4	4.85	120.95	112.30
39	B5	1477	OMG	C2-N3-C4	4.85	120.95	112.30
1	A2	27	A2M	N3-C4-N9	4.84	135.06	127.08
1	A2	868	OMG	C2-N3-C4	4.84	120.93	112.30
39	B5	4116	OMG	C2-N3-C4	4.84	120.92	112.30
39	B5	2658	A2M	N3-C4-N9	4.84	135.06	127.08
1	A2	1679	A2M	N3-C4-N9	4.84	135.05	127.08
39	B5	2207	OMG	C2-N3-C4	4.83	120.91	112.30
39	B5	3557	A2M	N3-C4-N9	4.83	135.05	127.08
1	A2	510	OMG	C2-N3-C4	4.83	120.91	112.30
39	B5	2630	A2M	N3-C4-N9	4.83	135.03	127.08
39	B5	3631	OMG	C2-N3-C4	4.82	120.89	112.30
1	A2	513	A2M	N3-C4-N9	4.82	135.03	127.08
39	B5	2267	OMG	C2-N3-C4	4.82	120.89	112.30
11	AT	16	H2U	C4-N3-C2	-4.82	121.80	125.79
39	B5	4369	OMG	C2-N3-C4	4.82	120.88	112.30
1	A2	485	A2M	N3-C4-N9	4.82	135.02	127.08
39	B5	4317	A2M	N3-C4-N9	4.82	135.02	127.08
39	B5	2719	OMG	N9-C4-N3	4.82	135.61	125.94
1	A2	1448	OMG	C2-N3-C4	4.82	120.88	112.30
1	A2	1491	OMG	N9-C4-N3	4.81	135.60	125.94
39	B5	398	A2M	N3-C4-N9	4.81	135.00	127.08
39	B5	3599	A2M	N3-C4-N9	4.80	134.98	127.08
1	A2	1384	A2M	N3-C4-N9	4.79	134.97	127.08
39	B5	400	A2M	N3-C4-N9	4.79	134.97	127.08
1	A2	159	A2M	N3-C4-N9	4.78	134.97	127.08
39	B5	3974	OMG	C2-N3-C4	4.78	120.82	112.30
39	B5	2206	A2M	N3-C4-N9	4.78	134.96	127.08
11	AT	54	5MU	N3-C2-N1	4.78	121.24	114.89
39	B5	3562	A2M	N3-C4-N9	4.77	134.94	127.08
39	B5	2267	OMG	N9-C4-N3	4.77	135.52	125.94
1	A2	1338	4AC	N4-C4-N3	4.77	121.85	113.85
39	B5	4269	A2M	N3-C4-N9	4.77	134.94	127.08
1	A2	469	A2M	N3-C4-N9	4.75	134.91	127.08
39	B5	3524	OMG	N9-C4-N3	4.75	135.47	125.94
39	B5	3942	OMG	N9-C4-N3	4.75	135.47	125.94
1	A2	577	A2M	N3-C4-N9	4.74	134.89	127.08
39	B5	3450	A2M	N3-C4-N9	4.73	134.87	127.08
39	B5	1580	OMG	N9-C4-N3	4.72	135.42	125.94
39	B5	3456	A2M	N3-C4-N9	4.72	134.86	127.08
39	B5	3492	A2M	N3-C4-N9	4.72	134.86	127.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	B5	1266	1MA	C2-N3-C4	4.70	121.64	112.41
1	A2	1032	A2M	N3-C4-N9	4.69	134.81	127.08
39	B5	2244	A2M	N3-C4-N9	4.68	134.80	127.08
11	AT	14	1MA	C2-N3-C4	4.68	121.60	112.41
11	AT	34	OMG	N9-C4-N3	4.67	135.32	125.94
39	B5	1479	A2M	N3-C4-N9	4.67	134.78	127.08
39	B5	1270	A2M	N3-C4-N9	4.67	134.77	127.08
11	AT	58	1MA	C2-N3-C4	4.66	121.58	112.41
39	B5	1810	A2M	N3-C4-N9	4.66	134.77	127.08
39	B5	3517	A2M	N3-C4-N9	4.66	134.75	127.08
39	B5	1489	A2M	N3-C4-N9	4.64	134.72	127.08
11	AT	10	2MG	N9-C4-N3	4.63	135.24	125.94
39	B5	4240	OMG	N9-C4-N3	4.61	135.20	125.94
1	A2	602	OMG	N9-C4-N3	4.61	135.20	125.94
39	B5	3657	OMU	C4-N3-C2	-4.60	120.52	126.58
39	B5	2680	OMU	C4-N3-C2	-4.59	120.53	126.58
1	A2	437	OMG	N9-C4-N3	4.57	135.12	125.94
1	A2	868	OMG	N9-C4-N3	4.56	135.09	125.94
1	A2	510	OMG	N9-C4-N3	4.55	135.07	125.94
39	B5	1260	OMG	N9-C4-N3	4.55	135.07	125.94
39	B5	4245	OMG	N9-C4-N3	4.55	135.07	125.94
39	B5	4244	OMU	C4-N3-C2	-4.53	120.61	126.58
1	A2	1851	MA6	C2-N1-C6	4.53	122.45	111.75
1	A2	1448	OMG	N9-C4-N3	4.52	135.03	125.94
41	B8	75	OMG	N9-C4-N3	4.52	135.02	125.94
11	AT	26	M2G	C2-N3-C4	4.51	120.86	112.51
1	A2	355	OMU	C4-N3-C2	-4.51	120.63	126.58
39	B5	3476	OMG	N9-C4-N3	4.51	135.00	125.94
39	B5	3676	OMG	N9-C4-N3	4.51	135.00	125.94
1	A2	429	OMU	C4-N3-C2	-4.51	120.63	126.58
39	B5	4116	OMG	N9-C4-N3	4.51	134.99	125.94
1	A2	628	OMU	C4-N3-C2	-4.51	120.64	126.58
1	A2	1327	OMU	C4-N3-C2	-4.50	120.64	126.58
39	B5	1477	OMG	N9-C4-N3	4.50	134.98	125.94
1	A2	645	OMG	N9-C4-N3	4.50	134.98	125.94
39	B5	4138	OMG	N9-C4-N3	4.50	134.97	125.94
11	AT	54	5MU	C5-C4-N3	4.50	119.15	115.31
1	A2	1852	MA6	C2-N1-C6	4.49	122.37	111.75
39	B5	4364	OMG	N9-C4-N3	4.49	134.95	125.94
1	A2	172	OMU	C4-N3-C2	-4.47	120.69	126.58
39	B5	3973	OMU	C4-N3-C2	-4.45	120.72	126.58
39	B5	3359	OMG	N9-C4-N3	4.44	134.86	125.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	684	OMG	N9-C4-N3	4.44	134.85	125.94
1	A2	1329	OMG	N9-C4-N3	4.44	134.85	125.94
39	B5	4383	OMG	N9-C4-N3	4.43	134.84	125.94
39	B5	2258	OMU	C4-N3-C2	-4.43	120.74	126.58
1	A2	669	A2M	N3-C4-N9	4.43	134.38	127.08
39	B5	4366	OMU	C4-N3-C2	-4.43	120.74	126.58
11	AT	26	M2G	N9-C4-N3	4.42	134.81	125.94
39	B5	4369	OMG	N9-C4-N3	4.42	134.81	125.94
39	B5	3550	UY1	N1-C2-N3	4.42	120.14	115.13
39	B5	2207	OMG	N9-C4-N3	4.41	134.79	125.94
1	A2	116	OMU	C4-N3-C2	-4.40	120.78	126.58
1	A2	1805	OMU	C4-N3-C2	-4.38	120.80	126.58
39	B5	4052	OMU	C4-N3-C2	-4.37	120.82	126.58
1	A2	1443	OMU	C4-N3-C2	-4.36	120.83	126.58
1	A2	1852	MA6	N3-C4-N9	4.34	134.24	127.08
39	B5	3974	OMG	N9-C4-N3	4.33	134.64	125.94
1	A2	121	OMU	C4-N3-C2	-4.33	120.87	126.58
1	A2	1640	G7M	C2-N3-C4	4.32	119.99	112.30
11	AT	46	G7M	C8-N9-C4	4.32	118.09	107.16
39	B5	3631	OMG	N9-C4-N3	4.28	134.53	125.94
1	A2	1289	OMU	C4-N3-C2	-4.28	120.94	126.58
1	A2	1851	MA6	N3-C4-N9	4.26	134.10	127.08
11	AT	46	G7M	C2-N3-C4	4.25	119.88	112.30
1	A2	355	OMU	N3-C2-N1	4.24	120.52	114.89
39	B5	2680	OMU	N3-C2-N1	4.23	120.51	114.89
39	B5	3657	OMU	N3-C2-N1	4.23	120.50	114.89
39	B5	4366	OMU	N3-C2-N1	4.16	120.42	114.89
1	A2	116	OMU	N3-C2-N1	4.16	120.41	114.89
39	B5	4193	5MC	C5-C6-N1	-4.15	119.06	123.34
39	B5	4244	OMU	N3-C2-N1	4.15	120.39	114.89
39	B5	3973	OMU	N3-C2-N1	4.14	120.39	114.89
1	A2	1640	G7M	C8-N9-C4	4.13	117.61	107.16
1	A2	591	A2M	C2-N3-C4	4.12	121.49	111.75
39	B5	4052	OMU	N3-C2-N1	4.11	120.34	114.89
39	B5	3502	PSU	C4-N3-C2	-4.11	120.42	126.34
11	AT	37	YYG	O23-C21-N20	4.09	117.98	110.80
39	B5	2258	OMU	N3-C2-N1	4.07	120.30	114.89
1	A2	429	OMU	N3-C2-N1	4.06	120.27	114.89
1	A2	1805	OMU	N3-C2-N1	4.06	120.27	114.89
39	B5	4149	PSU	C4-N3-C2	-4.05	120.50	126.34
1	A2	121	OMU	N3-C2-N1	4.05	120.27	114.89
41	B8	55	PSU	C4-N3-C2	-4.05	120.51	126.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	B5	4099	PSU	C4-N3-C2	-4.04	120.52	126.34
1	A2	1327	OMU	N3-C2-N1	4.04	120.25	114.89
39	B5	1491	PSU	C4-N3-C2	-4.04	120.52	126.34
1	A2	172	OMU	N3-C2-N1	4.04	120.25	114.89
39	B5	3369	PSU	C4-N3-C2	-4.03	120.53	126.34
1	A2	573	PSU	C4-N3-C2	-4.03	120.53	126.34
1	A2	650	PSU	C4-N3-C2	-4.03	120.53	126.34
1	A2	1443	OMU	N3-C2-N1	4.03	120.24	114.89
11	AT	55	PSU	C4-N3-C2	-4.03	120.54	126.34
1	A2	628	OMU	N3-C2-N1	4.02	120.23	114.89
39	B5	4298	PSU	C4-N3-C2	-4.02	120.54	126.34
39	B5	2351	PSU	C4-N3-C2	-4.02	120.55	126.34
39	B5	3583	PSU	C4-N3-C2	-4.02	120.55	126.34
39	B5	1721	PSU	C4-N3-C2	-4.01	120.55	126.34
39	B5	4419	PSU	C4-N3-C2	-4.01	120.56	126.34
1	A2	1178	PSU	C4-N3-C2	-4.01	120.56	126.34
1	A2	867	PSU	C4-N3-C2	-4.01	120.56	126.34
1	A2	1348	PSU	C4-N3-C2	-4.01	120.56	126.34
39	B5	3447	PSU	C4-N3-C2	-4.01	120.56	126.34
1	A2	105	PSU	C4-N3-C2	-4.01	120.57	126.34
1	A2	816	PSU	C4-N3-C2	-4.01	120.57	126.34
1	A2	34	PSU	C4-N3-C2	-4.00	120.58	126.34
39	B5	2658	A2M	C2-N3-C4	4.00	121.19	111.75
39	B5	4042	PSU	C4-N3-C2	-3.98	120.60	126.34
11	AT	27	PSU	C4-N3-C2	-3.98	120.60	126.34
1	A2	1239	PSU	C4-N3-C2	-3.98	120.60	126.34
39	B5	3427	PSU	C4-N3-C2	-3.98	120.60	126.34
1	A2	218	PSU	C4-N3-C2	-3.98	120.61	126.34
39	B5	4325	PSU	C4-N3-C2	-3.98	120.61	126.34
1	A2	1640	G7M	C1'-N9-C8	-3.98	113.31	126.74
11	AT	28	PSU	C4-N3-C2	-3.97	120.61	126.34
1	A2	1368	PSU	C4-N3-C2	-3.97	120.62	126.34
39	B5	1683	PSU	C4-N3-C2	-3.97	120.62	126.34
1	A2	864	PSU	C4-N3-C2	-3.96	120.63	126.34
39	B5	3652	PSU	C4-N3-C2	-3.96	120.63	126.34
39	B5	4711	PSU	C4-N3-C2	-3.96	120.63	126.34
1	A2	687	PSU	C4-N3-C2	-3.96	120.63	126.34
39	B5	4058	PSU	C4-N3-C2	-3.96	120.63	126.34
1	A2	1233	PSU	C4-N3-C2	-3.96	120.64	126.34
39	B5	1801	PSU	C4-N3-C2	-3.96	120.64	126.34
39	B5	3500	PSU	C4-N3-C2	-3.96	120.64	126.34
1	A2	1032	A2M	C2'-C1'-N9	-3.95	106.87	113.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	1446	PSU	C4-N3-C2	-3.95	120.64	126.34
41	B8	69	PSU	C4-N3-C2	-3.95	120.64	126.34
39	B5	4374	PSU	C4-N3-C2	-3.95	120.64	126.34
39	B5	4336	A2M	C2-N3-C4	3.95	121.08	111.75
39	B5	1718	PSU	C4-N3-C2	-3.95	120.65	126.34
1	A2	652	PSU	C4-N3-C2	-3.95	120.65	126.34
1	A2	1289	OMU	N3-C2-N1	3.95	120.13	114.89
1	A2	1693	PSU	C4-N3-C2	-3.94	120.66	126.34
1	A2	166	A2M	C2-N3-C4	3.94	121.07	111.75
1	A2	93	PSU	C4-N3-C2	-3.94	120.66	126.34
1	A2	109	PSU	C4-N3-C2	-3.94	120.66	126.34
1	A2	1046	PSU	C4-N3-C2	-3.94	120.66	126.34
1	A2	407	PSU	C4-N3-C2	-3.94	120.66	126.34
39	B5	4188	PSU	C4-N3-C2	-3.93	120.67	126.34
1	A2	1644	PSU	C4-N3-C2	-3.93	120.68	126.34
39	B5	4267	PSU	C4-N3-C2	-3.93	120.68	126.34
39	B5	4740	PSU	C4-N3-C2	-3.93	120.68	126.34
39	B5	3462	PSU	C4-N3-C2	-3.93	120.68	126.34
39	B5	4749	PSU	C4-N3-C2	-3.92	120.68	126.34
11	AT	39	PSU	C4-N3-C2	-3.92	120.69	126.34
39	B5	4203	PSU	C4-N3-C2	-3.92	120.69	126.34
1	A2	1057	PSU	C4-N3-C2	-3.92	120.69	126.34
39	B5	3966	6MZ	C2-N3-C4	3.92	121.00	111.75
39	B5	4246	PSU	C4-N3-C2	-3.92	120.70	126.34
1	A2	682	PSU	C4-N3-C2	-3.91	120.70	126.34
39	B5	3490	PSU	C4-N3-C2	-3.91	120.70	126.34
1	A2	967	PSU	C4-N3-C2	-3.91	120.70	126.34
39	B5	3466	PSU	C4-N3-C2	-3.91	120.70	126.34
39	B5	3496	PSU	C4-N3-C2	-3.91	120.70	126.34
39	B5	4177	PSU	C4-N3-C2	-3.91	120.70	126.34
1	A2	815	PSU	C4-N3-C2	-3.91	120.71	126.34
39	B5	4039	PSU	C4-N3-C2	-3.91	120.71	126.34
39	B5	1720	PSU	C4-N3-C2	-3.91	120.71	126.34
39	B5	3585	PSU	C4-N3-C2	-3.90	120.71	126.34
39	B5	1537	PSU	C4-N3-C2	-3.90	120.72	126.34
39	B5	398	A2M	C2-N3-C4	3.90	120.97	111.75
1	A2	1245	PSU	C4-N3-C2	-3.90	120.72	126.34
1	A2	610	PSU	C4-N3-C2	-3.89	120.73	126.34
39	B5	2244	A2M	C2-N3-C4	3.89	120.94	111.75
39	B5	4169	PSU	C4-N3-C2	-3.89	120.74	126.34
11	AT	54	5MU	O4-C4-C5	-3.89	120.40	124.90
11	AT	46	G7M	C1'-N9-C8	-3.89	113.62	126.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	B5	4435	PSU	C4-N3-C2	-3.89	120.74	126.34
39	B5	400	A2M	C2-N3-C4	3.88	120.93	111.75
39	B5	4322	PSU	C4-N3-C2	-3.88	120.74	126.34
1	A2	802	PSU	C4-N3-C2	-3.88	120.74	126.34
39	B5	3557	A2M	C2-N3-C4	3.88	120.92	111.75
39	B5	1638	PSU	C4-N3-C2	-3.88	120.75	126.34
39	B5	1731	PSU	C4-N3-C2	-3.88	120.75	126.34
39	B5	4045	PSU	C4-N3-C2	-3.88	120.75	126.34
39	B5	2630	A2M	C2-N3-C4	3.88	120.91	111.75
1	A2	513	A2M	C2-N3-C4	3.88	120.91	111.75
1	A2	1679	A2M	C2-N3-C4	3.88	120.91	111.75
1	A2	485	A2M	C2-N3-C4	3.88	120.91	111.75
1	A2	1047	PSU	C4-N3-C2	-3.88	120.75	126.34
1	A2	1384	A2M	C2-N3-C4	3.87	120.90	111.75
11	AT	37	YYG	O23-C21-O22	-3.87	118.89	124.58
1	A2	1626	PSU	C4-N3-C2	-3.87	120.76	126.34
39	B5	3517	A2M	C2-N3-C4	3.87	120.89	111.75
39	B5	3576	PSU	C4-N3-C2	-3.87	120.77	126.34
1	A2	1851	MA6	C4-C5-N7	-3.87	105.91	110.62
1	A2	1005	PSU	C4-N3-C2	-3.86	120.77	126.34
39	B5	1799	PSU	C4-N3-C2	-3.86	120.78	126.34
39	B5	4107	PSU	C4-N3-C2	-3.86	120.78	126.34
39	B5	4317	A2M	C2-N3-C4	3.85	120.84	111.75
1	A2	27	A2M	C2-N3-C4	3.85	120.84	111.75
39	B5	1810	A2M	C2-N3-C4	3.85	120.84	111.75
1	A2	99	A2M	C2-N3-C4	3.85	120.84	111.75
1	A2	159	A2M	C2-N3-C4	3.85	120.84	111.75
1	A2	469	A2M	C2-N3-C4	3.84	120.83	111.75
39	B5	3456	A2M	C2-N3-C4	3.84	120.82	111.75
1	A2	1175	PSU	C4-N3-C2	-3.84	120.81	126.34
1	A2	577	A2M	C2-N3-C4	3.83	120.81	111.75
39	B5	1479	A2M	C2-N3-C4	3.83	120.80	111.75
39	B5	4278	PSU	C4-N3-C2	-3.83	120.82	126.34
39	B5	3371	PSU	C4-N3-C2	-3.83	120.82	126.34
1	A2	119	PSU	C4-N3-C2	-3.83	120.83	126.34
1	A2	1032	A2M	C2-N3-C4	3.82	120.78	111.75
39	B5	2206	A2M	C2-N3-C4	3.82	120.78	111.75
39	B5	3562	A2M	C2-N3-C4	3.82	120.77	111.75
39	B5	3554	PSU	C4-N3-C2	-3.81	120.85	126.34
39	B5	3616	PSU	C4-N3-C2	-3.81	120.85	126.34
1	A2	823	PSU	C4-N3-C2	-3.81	120.86	126.34
39	B5	4217	PSU	C4-N3-C2	-3.80	120.86	126.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	B5	1270	A2M	C2-N3-C4	3.80	120.73	111.75
39	B5	2475	PSU	C4-N3-C2	-3.80	120.86	126.34
39	B5	1489	A2M	C2-N3-C4	3.80	120.73	111.75
39	B5	3599	A2M	C2-N3-C4	3.80	120.73	111.75
39	B5	3450	A2M	C2-N3-C4	3.80	120.72	111.75
1	A2	36	PSU	C4-N3-C2	-3.79	120.87	126.34
1	A2	1851	MA6	C2-N3-C4	3.79	120.71	111.75
39	B5	3494	PSU	C4-N3-C2	-3.79	120.88	126.34
11	AT	37	YYG	N3-C2-N2	-3.79	121.13	126.59
1	A2	1852	MA6	C2-N3-C4	3.78	120.69	111.75
1	A2	1082	PSU	C4-N3-C2	-3.78	120.89	126.34
39	B5	4269	A2M	C2-N3-C4	3.78	120.69	111.75
1	A2	210	PSU	C4-N3-C2	-3.78	120.89	126.34
1	A2	1833	6MZ	C2-N3-C4	3.77	120.66	111.75
39	B5	4166	PSU	C4-N3-C2	-3.76	120.91	126.34
1	A2	1852	MA6	C4-C5-N7	-3.76	106.05	110.62
39	B5	4382	PSU	C4-N3-C2	-3.75	120.94	126.34
1	A2	1851	MA6	N1-C6-N6	3.74	121.18	117.08
11	AT	37	YYG	C24-O23-C21	3.74	120.08	115.66
39	B5	3492	A2M	C2-N3-C4	3.74	120.58	111.75
1	A2	669	A2M	C2-N3-C4	3.74	120.58	111.75
39	B5	1632	PSU	C4-N3-C2	-3.74	120.96	126.34
39	B5	3657	OMU	C5-C4-N3	3.66	120.31	114.84
39	B5	4244	OMU	C5-C4-N3	3.65	120.30	114.84
1	A2	429	OMU	C5-C4-N3	3.65	120.30	114.84
39	B5	3494	PSU	O2-C2-N1	-3.63	118.80	122.79
39	B5	2258	OMU	C5-C4-N3	3.62	120.25	114.84
1	A2	1327	OMU	C5-C4-N3	3.62	120.25	114.84
39	B5	3973	OMU	C5-C4-N3	3.61	120.25	114.84
1	A2	628	OMU	C5-C4-N3	3.59	120.22	114.84
1	A2	116	OMU	C5-C4-N3	3.59	120.21	114.84
1	A2	1805	OMU	C5-C4-N3	3.59	120.21	114.84
1	A2	1047	PSU	O2-C2-N1	-3.59	118.84	122.79
1	A2	1289	OMU	C5-C4-N3	3.59	120.20	114.84
39	B5	2680	OMU	C5-C4-N3	3.58	120.20	114.84
11	AT	54	5MU	C5-C6-N1	-3.58	119.66	123.34
39	B5	4246	PSU	O2-C2-N1	-3.56	118.87	122.79
39	B5	4269	A2M	C2'-C1'-N9	-3.56	107.54	113.53
1	A2	355	OMU	C5-C4-N3	3.56	120.16	114.84
39	B5	4366	OMU	C5-C4-N3	3.56	120.16	114.84
11	AT	37	YYG	C10-C11-N2	3.55	126.58	119.38
1	A2	121	OMU	C5-C4-N3	3.55	120.15	114.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	1443	OMU	C5-C4-N3	3.55	120.15	114.84
39	B5	4052	OMU	C5-C4-N3	3.54	120.14	114.84
39	B5	4382	PSU	O2-C2-N1	-3.53	118.90	122.79
1	A2	172	OMU	C5-C4-N3	3.53	120.12	114.84
1	A2	36	PSU	O2-C2-N1	-3.52	118.91	122.79
39	B5	4149	PSU	O2-C2-N1	-3.52	118.91	122.79
1	A2	823	PSU	O2-C2-N1	-3.52	118.92	122.79
39	B5	3583	PSU	O2-C2-N1	-3.51	118.93	122.79
39	B5	4278	PSU	O2-C2-N1	-3.51	118.93	122.79
1	A2	159	A2M	C2'-C1'-N9	-3.50	107.64	113.53
1	A2	1640	G7M	CN7-N7-C5	3.49	131.11	126.77
1	A2	650	PSU	O2-C2-N1	-3.49	118.95	122.79
11	AT	39	PSU	O2-C2-N1	-3.49	118.95	122.79
1	A2	1175	PSU	O2-C2-N1	-3.49	118.95	122.79
39	B5	3652	PSU	O2-C2-N1	-3.48	118.96	122.79
39	B5	1718	PSU	O2-C2-N1	-3.48	118.96	122.79
39	B5	4045	PSU	O2-C2-N1	-3.48	118.96	122.79
39	B5	3496	PSU	O2-C2-N1	-3.48	118.96	122.79
39	B5	1632	PSU	O2-C2-N1	-3.47	118.97	122.79
1	A2	1644	PSU	O2-C2-N1	-3.46	118.98	122.79
39	B5	4325	PSU	O2-C2-N1	-3.46	118.98	122.79
11	AT	46	G7M	CN7-N7-C5	3.46	131.07	126.77
1	A2	610	PSU	O2-C2-N1	-3.46	118.98	122.79
39	B5	3514	5MC	C5-C6-N1	-3.46	119.78	123.34
39	B5	3631	OMG	C6-C5-N7	3.46	136.68	130.25
41	B8	69	PSU	O2-C2-N1	-3.46	118.98	122.79
39	B5	1810	A2M	C2'-C1'-N9	-3.45	107.72	113.53
1	A2	210	PSU	O2-C2-N1	-3.45	118.99	122.79
1	A2	1368	PSU	O2-C2-N1	-3.45	118.99	122.79
1	A2	1626	PSU	O2-C2-N1	-3.45	119.00	122.79
1	A2	1178	PSU	O2-C2-N1	-3.44	119.00	122.79
11	AT	27	PSU	O2-C2-N1	-3.44	119.00	122.79
42	BA	216	V5N	CD2-CG-ND1	3.43	110.22	105.71
39	B5	3517	A2M	O4'-C1'-N9	3.43	114.83	108.06
39	B5	1491	PSU	O2-C2-N1	-3.43	119.01	122.79
39	B5	4374	PSU	O2-C2-N1	-3.43	119.01	122.79
1	A2	218	PSU	O2-C2-N1	-3.43	119.02	122.79
1	A2	652	PSU	O2-C2-N1	-3.43	119.02	122.79
39	B5	3502	PSU	O2-C2-N1	-3.43	119.02	122.79
39	B5	3447	PSU	O2-C2-N1	-3.42	119.02	122.79
39	B5	3462	PSU	O2-C2-N1	-3.41	119.03	122.79
1	A2	573	PSU	O2-C2-N1	-3.41	119.03	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	93	PSU	O2-C2-N1	-3.41	119.04	122.79
39	B5	4298	PSU	O2-C2-N1	-3.41	119.04	122.79
39	B5	4042	PSU	O2-C2-N1	-3.41	119.04	122.79
1	A2	407	PSU	O2-C2-N1	-3.40	119.04	122.79
1	A2	687	PSU	O2-C2-N1	-3.40	119.05	122.79
39	B5	4099	PSU	O2-C2-N1	-3.40	119.05	122.79
41	B8	55	PSU	O2-C2-N1	-3.39	119.05	122.79
1	A2	684	OMG	C6-C5-N7	3.39	136.56	130.25
39	B5	3371	PSU	O2-C2-N1	-3.39	119.06	122.79
1	A2	867	PSU	O2-C2-N1	-3.39	119.06	122.79
39	B5	1683	PSU	O2-C2-N1	-3.39	119.06	122.79
39	B5	4749	PSU	O2-C2-N1	-3.39	119.06	122.79
1	A2	34	PSU	O2-C2-N1	-3.38	119.06	122.79
1	A2	109	PSU	O2-C2-N1	-3.38	119.06	122.79
39	B5	398	A2M	C4-C5-N7	-3.38	106.50	110.62
39	B5	4166	PSU	O2-C2-N1	-3.38	119.07	122.79
39	B5	4419	PSU	O2-C2-N1	-3.38	119.07	122.79
39	B5	1489	A2M	C4-C5-N7	-3.37	106.51	110.62
39	B5	1801	PSU	O2-C2-N1	-3.37	119.08	122.79
1	A2	815	PSU	O2-C2-N1	-3.37	119.08	122.79
39	B5	1537	PSU	O2-C2-N1	-3.37	119.08	122.79
39	B5	2351	PSU	O2-C2-N1	-3.37	119.08	122.79
39	B5	3466	PSU	O2-C2-N1	-3.36	119.09	122.79
39	B5	4188	PSU	O2-C2-N1	-3.36	119.09	122.79
11	AT	37	YYG	O18-C16-C15	3.36	120.12	111.52
39	B5	4169	PSU	O2-C2-N1	-3.36	119.09	122.79
1	A2	1249	B8N	C4-N3-C2	-3.36	121.21	125.46
1	A2	105	PSU	O2-C2-N1	-3.36	119.09	122.79
1	A2	1239	PSU	O2-C2-N1	-3.36	119.10	122.79
39	B5	3966	6MZ	C6-C5-N7	3.36	136.02	132.39
39	B5	4435	PSU	O2-C2-N1	-3.35	119.10	122.79
1	A2	802	PSU	O2-C2-N1	-3.35	119.10	122.79
1	A2	1446	PSU	O2-C2-N1	-3.35	119.10	122.79
11	AT	55	PSU	O2-C2-N1	-3.35	119.10	122.79
1	A2	864	PSU	O2-C2-N1	-3.35	119.11	122.79
39	B5	4058	PSU	O2-C2-N1	-3.35	119.11	122.79
39	B5	3550	UY1	CM2-O2'-C2'	-3.35	105.74	114.52
39	B5	4711	PSU	O2-C2-N1	-3.35	119.11	122.79
39	B5	3500	PSU	O2-C2-N1	-3.34	119.11	122.79
11	AT	49	5MC	C5-C6-N1	-3.34	119.90	123.34
39	B5	4039	PSU	O2-C2-N1	-3.34	119.11	122.79
39	B5	2630	A2M	N3-C2-N1	-3.34	123.38	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	B5	3554	PSU	O2-C2-N1	-3.34	119.12	122.79
39	B5	3974	OMG	C6-C5-N7	3.34	136.45	130.25
39	B5	1810	A2M	C4-C5-N7	-3.33	106.56	110.62
1	A2	1693	PSU	O2-C2-N1	-3.33	119.12	122.79
1	A2	1245	PSU	O2-C2-N1	-3.33	119.12	122.79
1	A2	1032	A2M	N3-C2-N1	-3.32	123.40	128.60
39	B5	3557	A2M	C2'-C1'-N9	-3.32	107.93	113.53
39	B5	3517	A2M	N3-C2-N1	-3.32	123.41	128.60
39	B5	1266	1MA	N9-C4-N3	3.32	134.68	126.94
39	B5	3576	PSU	O2-C2-N1	-3.32	119.14	122.79
39	B5	4177	PSU	O2-C2-N1	-3.32	119.14	122.79
39	B5	1479	A2M	C4-C5-N7	-3.32	106.58	110.62
68	Ba	39	V5N	CD2-CG-ND1	3.31	110.06	105.71
39	B5	2475	PSU	O2-C2-N1	-3.31	119.14	122.79
39	B5	4383	OMG	C6-C5-N7	3.31	136.41	130.25
39	B5	1799	PSU	O2-C2-N1	-3.31	119.14	122.79
1	A2	119	PSU	O2-C2-N1	-3.31	119.15	122.79
39	B5	1720	PSU	O2-C2-N1	-3.31	119.15	122.79
1	A2	159	A2M	C4-C5-N7	-3.31	106.59	110.62
11	AT	14	1MA	N9-C4-N3	3.31	134.65	126.94
1	A2	513	A2M	C4-C5-N7	-3.30	106.59	110.62
1	A2	1046	PSU	O2-C2-N1	-3.30	119.15	122.79
39	B5	3359	OMG	C6-C5-N7	3.30	136.39	130.25
1	A2	27	A2M	C4-C5-N7	-3.30	106.60	110.62
39	B5	4369	OMG	C6-C5-N7	3.30	136.39	130.25
1	A2	816	PSU	O2-C2-N1	-3.30	119.16	122.79
39	B5	3585	PSU	O2-C2-N1	-3.29	119.16	122.79
1	A2	469	A2M	C4-C5-N7	-3.29	106.61	110.62
1	A2	166	A2M	C4-C5-N7	-3.29	106.61	110.62
1	A2	1679	A2M	C4-C5-N7	-3.29	106.61	110.62
39	B5	3562	A2M	C4-C5-N7	-3.29	106.61	110.62
39	B5	3966	6MZ	C9-N6-C6	-3.29	120.04	122.87
39	B5	3562	A2M	C2'-C1'-N9	-3.29	107.99	113.53
39	B5	1721	PSU	O2-C2-N1	-3.29	119.17	122.79
39	B5	2244	A2M	N3-C2-N1	-3.29	123.45	128.60
39	B5	2244	A2M	C4-C5-N7	-3.29	106.61	110.62
39	B5	4217	PSU	O2-C2-N1	-3.29	119.17	122.79
39	B5	2658	A2M	N3-C2-N1	-3.29	123.46	128.60
39	B5	3427	PSU	O2-C2-N1	-3.29	119.17	122.79
1	A2	1329	OMG	C6-C5-N7	3.29	136.36	130.25
39	B5	2658	A2M	C4-C5-N7	-3.29	106.62	110.62
1	A2	682	PSU	O2-C2-N1	-3.29	119.17	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	B5	4336	A2M	C4-C5-N7	-3.28	106.62	110.62
1	A2	1057	PSU	O2-C2-N1	-3.28	119.18	122.79
11	AT	26	M2G	C6-C5-N7	3.28	136.35	130.25
1	A2	669	A2M	C4-C5-N7	-3.28	106.62	110.62
39	B5	2207	OMG	C6-C5-N7	3.28	136.34	130.25
39	B5	1638	PSU	O2-C2-N1	-3.28	119.18	122.79
39	B5	4138	OMG	C6-C5-N7	3.28	136.34	130.25
39	B5	4269	A2M	C4-C5-N7	-3.27	106.63	110.62
39	B5	4116	OMG	C6-C5-N7	3.27	136.34	130.25
1	A2	99	A2M	C4-C5-N7	-3.27	106.63	110.62
39	B5	400	A2M	C4-C5-N7	-3.27	106.63	110.62
39	B5	4322	PSU	O2-C2-N1	-3.27	119.19	122.79
39	B5	4364	OMG	C6-C5-N7	3.27	136.33	130.25
1	A2	1005	PSU	O2-C2-N1	-3.27	119.19	122.79
1	A2	577	A2M	C4-C5-N7	-3.27	106.64	110.62
1	A2	1348	PSU	O2-C2-N1	-3.27	119.19	122.79
39	B5	4203	PSU	O2-C2-N1	-3.26	119.20	122.79
39	B5	1810	A2M	N3-C2-N1	-3.26	123.50	128.60
39	B5	3476	OMG	C6-C5-N7	3.26	136.31	130.25
1	A2	967	PSU	O2-C2-N1	-3.26	119.20	122.79
39	B5	3490	PSU	O2-C2-N1	-3.26	119.20	122.79
1	A2	513	A2M	C2'-C1'-N9	-3.26	108.05	113.53
1	A2	485	A2M	N3-C2-N1	-3.26	123.51	128.60
11	AT	58	1MA	N9-C4-N3	3.25	134.52	126.94
1	A2	1233	PSU	O2-C2-N1	-3.25	119.21	122.79
39	B5	3456	A2M	N3-C2-N1	-3.25	123.52	128.60
39	B5	1477	OMG	C6-C5-N7	3.25	136.29	130.25
39	B5	3456	A2M	C4-C5-N7	-3.24	106.67	110.62
1	A2	1679	A2M	N3-C2-N1	-3.24	123.53	128.60
1	A2	645	OMG	C6-C5-N7	3.24	136.27	130.25
39	B5	4267	PSU	O2-C2-N1	-3.24	119.22	122.79
39	B5	4107	PSU	O2-C2-N1	-3.24	119.23	122.79
39	B5	3492	A2M	C2'-C1'-N9	-3.23	108.09	113.53
39	B5	3599	A2M	C4-C5-N7	-3.23	106.68	110.62
1	A2	1032	A2M	C4-C5-N7	-3.23	106.68	110.62
1	A2	1384	A2M	C4-C5-N7	-3.23	106.69	110.62
1	A2	1851	MA6	N1-C2-N3	-3.22	123.56	128.60
39	B5	4336	A2M	N3-C2-N1	-3.22	123.57	128.60
39	B5	3676	OMG	C6-C5-N7	3.22	136.23	130.25
39	B5	3557	A2M	C4-C5-N7	-3.22	106.70	110.62
39	B5	1260	OMG	C6-C5-N7	3.22	136.23	130.25
39	B5	3450	A2M	C4-C5-N7	-3.21	106.70	110.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	577	A2M	N3-C2-N1	-3.21	123.58	128.60
39	B5	400	A2M	N3-C2-N1	-3.21	123.58	128.60
39	B5	2206	A2M	N3-C2-N1	-3.21	123.58	128.60
39	B5	3616	PSU	O2-C2-N1	-3.21	119.26	122.79
1	A2	577	A2M	C2'-C1'-N9	-3.20	108.14	113.53
1	A2	166	A2M	N3-C2-N1	-3.20	123.60	128.60
1	A2	1384	A2M	N3-C2-N1	-3.20	123.60	128.60
39	B5	3517	A2M	C4-C5-N7	-3.20	106.72	110.62
39	B5	4740	PSU	O2-C2-N1	-3.20	119.27	122.79
41	B8	75	OMG	C6-C5-N7	3.20	136.19	130.25
11	AT	28	PSU	O2-C2-N1	-3.20	119.27	122.79
39	B5	1489	A2M	N3-C2-N1	-3.19	123.61	128.60
39	B5	4245	OMG	C6-C5-N7	3.19	136.18	130.25
39	B5	4317	A2M	N3-C2-N1	-3.19	123.61	128.60
39	B5	3966	6MZ	N1-C2-N3	-3.19	123.62	128.60
39	B5	3492	A2M	C4-C5-N7	-3.18	106.74	110.62
39	B5	1270	A2M	N3-C2-N1	-3.18	123.62	128.60
1	A2	591	A2M	N3-C2-N1	-3.18	123.63	128.60
39	B5	4317	A2M	C4-C5-N7	-3.18	106.75	110.62
39	B5	3966	6MZ	C4-C5-N7	-3.17	106.75	110.62
1	A2	469	A2M	N3-C2-N1	-3.17	123.64	128.60
1	A2	510	OMG	C6-C5-N7	3.17	136.15	130.25
39	B5	1270	A2M	C4-C5-N7	-3.17	106.76	110.62
39	B5	4240	OMG	C6-C5-N7	3.16	136.13	130.25
39	B5	3557	A2M	N3-C2-N1	-3.16	123.65	128.60
39	B5	2244	A2M	C2'-C1'-N9	-3.16	108.20	113.53
1	A2	27	A2M	N3-C2-N1	-3.16	123.66	128.60
1	A2	437	OMG	C6-C5-N7	3.16	136.12	130.25
1	A2	99	A2M	N3-C2-N1	-3.16	123.67	128.60
1	A2	602	OMG	C6-C5-N7	3.16	136.12	130.25
1	A2	485	A2M	C4-C5-N7	-3.15	106.78	110.62
1	A2	868	OMG	C6-C5-N7	3.15	136.11	130.25
1	A2	1852	MA6	N1-C2-N3	-3.15	123.67	128.60
39	B5	1479	A2M	N3-C2-N1	-3.14	123.69	128.60
1	A2	513	A2M	N3-C2-N1	-3.14	123.70	128.60
1	A2	1679	A2M	C2'-C1'-N9	-3.14	108.25	113.53
1	A2	669	A2M	N3-C2-N1	-3.13	123.70	128.60
39	B5	3562	A2M	N3-C2-N1	-3.13	123.70	128.60
39	B5	2206	A2M	C4-C5-N7	-3.13	106.81	110.62
1	A2	591	A2M	C4-C5-N7	-3.11	106.83	110.62
39	B5	3492	A2M	N3-C2-N1	-3.11	123.75	128.60
39	B5	3450	A2M	C2'-C1'-N9	-3.10	108.31	113.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	B5	4269	A2M	N3-C2-N1	-3.10	123.75	128.60
1	A2	1448	OMG	C6-C5-N7	3.10	136.02	130.25
1	A2	1851	MA6	C5-N7-C8	3.10	107.91	103.51
39	B5	3369	PSU	O2-C2-N1	-3.10	119.38	122.79
39	B5	398	A2M	N3-C2-N1	-3.09	123.77	128.60
11	AT	34	OMG	C6-C5-N7	3.08	135.98	130.25
1	A2	1249	B8N	N3-C2-N1	3.08	121.11	116.76
39	B5	3599	A2M	N3-C2-N1	-3.08	123.79	128.60
39	B5	3450	A2M	N3-C2-N1	-3.08	123.79	128.60
39	B5	2630	A2M	C4-C5-N7	-3.07	106.88	110.62
1	A2	159	A2M	N3-C2-N1	-3.07	123.80	128.60
11	AT	10	2MG	C6-C5-N7	3.06	135.94	130.25
39	B5	3942	OMG	C6-C5-N7	3.05	135.93	130.25
1	A2	1082	PSU	O2-C2-N1	-3.05	119.43	122.79
39	B5	1731	PSU	O2-C2-N1	-3.04	119.44	122.79
1	A2	172	OMU	O4-C4-C5	-3.04	119.81	125.16
39	B5	2719	OMG	C6-C5-N7	3.03	135.89	130.25
39	B5	398	A2M	C2'-C1'-N9	-3.03	108.42	113.53
1	A2	429	OMU	O4-C4-C5	-3.03	119.83	125.16
39	B5	1270	A2M	C2'-C1'-N9	-3.03	108.43	113.53
1	A2	99	A2M	C2'-C1'-N9	-3.01	108.45	113.53
1	A2	628	OMU	O4-C4-C5	-3.01	119.87	125.16
39	B5	4052	OMU	O4-C4-C5	-3.01	119.87	125.16
1	A2	166	A2M	C2'-C1'-N9	-3.00	108.48	113.53
1	A2	1852	MA6	C5-N7-C8	2.99	107.76	103.51
1	A2	1289	OMU	O4-C4-C5	-2.99	119.90	125.16
1	A2	27	A2M	C2'-C1'-N9	-2.99	108.50	113.53
39	B5	3524	OMG	C6-C5-N7	2.99	135.80	130.25
39	B5	3657	OMU	O4-C4-C5	-2.98	119.92	125.16
39	B5	3517	A2M	C4-N9-C8	2.98	108.96	105.73
1	A2	121	OMU	O4-C4-C5	-2.98	119.92	125.16
39	B5	3550	UY1	C6-C5-C4	2.98	120.28	118.20
1	A2	116	OMU	O4-C4-C5	-2.98	119.92	125.16
39	B5	3456	A2M	C2'-C1'-N9	-2.98	108.52	113.53
1	A2	1327	OMU	O4-C4-C5	-2.97	119.93	125.16
1	A2	1491	OMG	C6-C5-N7	2.97	135.77	130.25
1	A2	355	OMU	O4-C4-C5	-2.97	119.94	125.16
1	A2	1443	OMU	O4-C4-C5	-2.96	119.95	125.16
1	A2	1805	OMU	O4-C4-C5	-2.94	119.99	125.16
39	B5	1580	OMG	C6-C5-N7	2.93	135.70	130.25
1	A2	1833	6MZ	N1-C2-N3	-2.91	124.04	128.60
39	B5	2680	OMU	O4-C4-C5	-2.91	120.04	125.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	B5	2258	OMU	O4-C4-C5	-2.91	120.05	125.16
39	B5	4244	OMU	O4-C4-C5	-2.90	120.05	125.16
1	A2	1833	6MZ	C4-C5-N7	-2.90	107.08	110.62
1	A2	485	A2M	C2'-C1'-N9	-2.87	108.70	113.53
39	B5	4366	OMU	O4-C4-C5	-2.84	120.17	125.16
39	B5	3973	OMU	O4-C4-C5	-2.83	120.18	125.16
1	A2	1679	A2M	C5-N7-C8	2.82	107.52	103.51
1	A2	669	A2M	C4-N9-C8	2.82	108.79	105.73
39	B5	1489	A2M	C5-N7-C8	2.82	107.52	103.51
1	A2	27	A2M	C5-N7-C8	2.82	107.52	103.51
39	B5	4336	A2M	C5-N7-C8	2.81	107.51	103.51
39	B5	1810	A2M	C5-N7-C8	2.80	107.49	103.51
1	A2	159	A2M	C5-N7-C8	2.80	107.48	103.51
39	B5	2267	OMG	C6-C5-N7	2.79	135.44	130.25
1	A2	513	A2M	C5-N7-C8	2.79	107.47	103.51
1	A2	1032	A2M	C4-N9-C8	2.79	108.75	105.73
1	A2	469	A2M	C5-N7-C8	2.79	107.47	103.51
1	A2	166	A2M	C5-N7-C8	2.79	107.47	103.51
39	B5	3562	A2M	C5-N7-C8	2.79	107.47	103.51
39	B5	3517	A2M	C5-N7-C8	2.78	107.46	103.51
39	B5	2244	A2M	C5-N7-C8	2.78	107.46	103.51
1	A2	1843	4AC	N4-C4-N3	2.77	118.50	113.85
1	A2	1852	MA6	N1-C6-N6	2.77	120.11	117.08
1	A2	577	A2M	C5-N7-C8	2.76	107.44	103.51
39	B5	1479	A2M	C5-N7-C8	2.76	107.43	103.51
11	AT	37	YYG	C3-N3-C2	-2.76	114.89	120.42
39	B5	4269	A2M	C5-N7-C8	2.75	107.42	103.51
39	B5	3456	A2M	C4-N9-C8	2.74	108.70	105.73
39	B5	398	A2M	C5-N7-C8	2.74	107.40	103.51
39	B5	2658	A2M	C5-N7-C8	2.74	107.40	103.51
1	A2	99	A2M	C5-N7-C8	2.73	107.38	103.51
39	B5	3456	A2M	C5-N7-C8	2.73	107.38	103.51
39	B5	3517	A2M	C2'-C1'-N9	-2.73	108.94	113.53
39	B5	3631	OMG	C4-C5-N7	-2.72	106.41	110.72
1	A2	577	A2M	C4-N9-C8	2.72	108.67	105.73
39	B5	3599	A2M	C5-N7-C8	2.71	107.36	103.51
1	A2	1384	A2M	C5-N7-C8	2.71	107.36	103.51
1	A2	1032	A2M	C5-N7-C8	2.71	107.36	103.51
39	B5	4269	A2M	C4-N9-C8	2.71	108.66	105.73
39	B5	4383	OMG	C4-C5-N7	-2.71	106.44	110.72
39	B5	400	A2M	C5-N7-C8	2.71	107.36	103.51
1	A2	1679	A2M	C4-N9-C8	2.69	108.64	105.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	B5	4317	A2M	C5-N7-C8	2.69	107.33	103.51
39	B5	3359	OMG	C4-C5-N7	-2.69	106.47	110.72
39	B5	3966	6MZ	C5-N7-C8	2.69	107.32	103.51
1	A2	669	A2M	C5-N7-C8	2.68	107.32	103.51
39	B5	4193	5MC	C5-C4-N3	-2.68	118.78	121.67
1	A2	645	OMG	C4-C5-N7	-2.68	106.48	110.72
39	B5	3557	A2M	C5-N7-C8	2.68	107.31	103.51
1	A2	591	A2M	C5-N7-C8	2.67	107.30	103.51
39	B5	1270	A2M	C5-N7-C8	2.66	107.30	103.51
1	A2	1329	OMG	C4-C5-N7	-2.66	106.51	110.72
39	B5	3450	A2M	C5-N7-C8	2.66	107.29	103.51
39	B5	3492	A2M	C5-N7-C8	2.66	107.28	103.51
1	A2	684	OMG	C4-C5-N7	-2.65	106.52	110.72
39	B5	2206	A2M	C5-N7-C8	2.65	107.28	103.51
39	B5	1489	A2M	C4-N9-C8	2.64	108.59	105.73
11	AT	26	M2G	C4-C5-N7	-2.64	106.55	110.72
1	A2	159	A2M	C4-N9-C8	2.64	108.59	105.73
39	B5	4336	A2M	C2'-C1'-N9	-2.64	109.09	113.53
1	A2	510	OMG	C4-C5-N7	-2.64	106.55	110.72
39	B5	2207	OMG	C4-C5-N7	-2.63	106.55	110.72
39	B5	4336	A2M	C4-N9-C8	2.63	108.58	105.73
39	B5	3974	OMG	C4-C5-N7	-2.63	106.55	110.72
39	B5	4369	OMG	C4-C5-N7	-2.63	106.56	110.72
39	B5	3599	A2M	C4-N9-C8	2.63	108.58	105.73
39	B5	3676	OMG	C4-C5-N7	-2.62	106.57	110.72
1	A2	437	OMG	C4-C5-N7	-2.62	106.57	110.72
39	B5	2630	A2M	C5-N7-C8	2.62	107.24	103.51
1	A2	469	A2M	C4-N9-C8	2.62	108.57	105.73
1	A2	485	A2M	C5-N7-C8	2.62	107.23	103.51
1	A2	1338	4AC	C6-C5-C4	2.62	120.16	116.96
39	B5	1260	OMG	C4-C5-N7	-2.62	106.58	110.72
11	AT	58	1MA	C4-C5-N7	-2.61	106.59	110.72
1	A2	27	A2M	C4-N9-C8	2.61	108.56	105.73
39	B5	1810	A2M	C4-N9-C8	2.61	108.56	105.73
39	B5	4364	OMG	C4-C5-N7	-2.61	106.59	110.72
39	B5	4317	A2M	C4-N9-C8	2.61	108.55	105.73
39	B5	3492	A2M	C4-N9-C8	2.60	108.55	105.73
41	B8	75	OMG	C4-C5-N7	-2.60	106.61	110.72
39	B5	2244	A2M	C4-N9-C8	2.59	108.54	105.73
1	A2	1491	OMG	O6-C6-C5	-2.59	119.73	126.60
39	B5	3476	OMG	C4-C5-N7	-2.59	106.63	110.72
39	B5	4245	OMG	C4-C5-N7	-2.58	106.63	110.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	469	A2M	C2'-C1'-N9	-2.58	109.18	113.53
39	B5	4240	OMG	C4-C5-N7	-2.58	106.64	110.72
1	A2	166	A2M	C4-N9-C8	2.58	108.52	105.73
39	B5	2719	OMG	C4-C5-N7	-2.58	106.64	110.72
1	A2	1384	A2M	C4-N9-C8	2.58	108.52	105.73
1	A2	1448	OMG	C4-C5-N7	-2.57	106.65	110.72
11	AT	46	G7M	O6-C6-C5	-2.57	122.26	128.06
39	B5	4138	OMG	C4-C5-N7	-2.57	106.65	110.72
1	A2	485	A2M	C4-N9-C8	2.57	108.51	105.73
1	A2	1851	MA6	C4-N9-C8	2.57	108.51	105.73
39	B5	4116	OMG	C4-C5-N7	-2.56	106.67	110.72
39	B5	1479	A2M	C4-N9-C8	2.56	108.50	105.73
39	B5	400	A2M	C2'-C1'-N9	-2.56	109.22	113.53
39	B5	1270	A2M	C4-N9-C8	2.56	108.50	105.73
39	B5	1477	OMG	C4-C5-N7	-2.56	106.68	110.72
39	B5	3942	OMG	C4-C5-N7	-2.55	106.68	110.72
1	A2	1833	6MZ	C5-N7-C8	2.55	107.13	103.51
42	BA	216	V5N	O-C-CA	-2.55	118.10	124.78
1	A2	868	OMG	C4-C5-N7	-2.54	106.70	110.72
1	A2	99	A2M	C4-N9-C8	2.54	108.48	105.73
39	B5	3557	A2M	C4-N9-C8	2.54	108.48	105.73
39	B5	2630	A2M	C4-N9-C8	2.53	108.47	105.73
39	B5	3562	A2M	C4-N9-C8	2.53	108.47	105.73
1	A2	602	OMG	C4-C5-N7	-2.53	106.72	110.72
11	AT	34	OMG	C4-C5-N7	-2.52	106.73	110.72
1	A2	1338	4AC	C5-C4-N4	-2.52	118.55	122.92
33	Au	1	AME	O-C-CA	-2.51	118.20	124.78
1	A2	1843	4AC	C6-C5-C4	2.51	120.03	116.96
11	AT	10	2MG	C4-C5-N7	-2.50	106.76	110.72
1	A2	513	A2M	C4-N9-C8	2.50	108.44	105.73
11	AT	14	1MA	C4-C5-N7	-2.50	106.77	110.72
68	Ba	39	V5N	O-C-CA	-2.49	118.24	124.78
39	B5	2206	A2M	C4-N9-C8	2.49	108.43	105.73
39	B5	3514	5MC	C5-C4-N3	-2.48	119.00	121.67
11	AT	49	5MC	C5-C4-N3	-2.48	119.00	121.67
39	B5	1580	OMG	C4-C5-N7	-2.47	106.81	110.72
39	B5	400	A2M	C4-N9-C8	2.47	108.41	105.73
39	B5	3450	A2M	C4-N9-C8	2.47	108.41	105.73
39	B5	4317	A2M	C2'-C1'-N9	-2.47	109.38	113.53
11	AT	37	YYG	O18-C16-O17	-2.46	119.03	123.84
1	A2	1640	G7M	O6-C6-C5	-2.45	122.53	128.06
39	B5	3514	5MC	O2-C2-N3	-2.43	118.37	122.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	1852	MA6	C4-N9-C8	2.41	108.34	105.73
11	AT	16	H2U	C5-C6-N1	-2.41	103.67	111.61
30	Ar	2	SAC	O-C-CA	-2.41	118.46	124.78
1	A2	669	A2M	C6-C5-N7	2.40	136.49	132.02
39	B5	3966	6MZ	C4-N9-C8	2.40	108.33	105.73
1	A2	1384	A2M	C2'-C1'-N9	-2.39	109.51	113.53
39	B5	1266	1MA	C4-C5-N7	-2.39	106.94	110.72
39	B5	2267	OMG	C4-C5-N7	-2.39	106.94	110.72
1	A2	1833	6MZ	C4-N9-C8	2.39	108.31	105.73
39	B5	3517	A2M	C6-C5-N7	2.38	136.45	132.02
39	B5	3524	OMG	C4-C5-N7	-2.37	106.97	110.72
39	B5	3517	A2M	N9-C8-N7	-2.36	110.68	113.91
12	AZ	2	SAC	O-C-CA	-2.35	118.62	124.78
39	B5	2194	OMC	O2-C2-N3	-2.34	118.53	122.33
39	B5	3599	A2M	C2'-C1'-N9	-2.34	109.60	113.53
39	B5	2658	A2M	C4-N9-C8	2.33	108.25	105.73
39	B5	1489	A2M	C6-C5-N7	2.32	136.34	132.02
39	B5	3456	A2M	C6-C5-N7	2.32	136.33	132.02
39	B5	1479	A2M	C2'-C1'-N9	-2.31	109.64	113.53
83	Br	2	SAC	O-C-CA	-2.31	118.73	124.78
39	B5	2244	A2M	C6-C5-N7	2.30	136.31	132.02
39	B5	1810	A2M	C6-C5-N7	2.30	136.31	132.02
39	B5	398	A2M	C4-N9-C8	2.28	108.20	105.73
1	A2	1491	OMG	C4-C5-N7	-2.28	107.11	110.72
39	B5	2206	A2M	C2'-C1'-N9	-2.28	109.69	113.53
39	B5	3550	UY1	O2-C2-N1	-2.28	120.28	122.79
1	A2	591	A2M	C4-N9-C8	2.27	108.19	105.73
1	A2	1289	OMU	C1'-N1-C2	2.27	121.67	117.57
1	A2	469	A2M	C6-C5-N7	2.25	136.21	132.02
39	B5	1270	A2M	C6-C5-N7	2.25	136.21	132.02
1	A2	577	A2M	C6-C5-N7	2.25	136.21	132.02
1	A2	1392	OMC	O2-C2-N3	-2.24	118.69	122.33
39	B5	1479	A2M	C6-C5-N7	2.24	136.20	132.02
1	A2	1851	MA6	C6-C5-N7	2.24	137.04	133.28
1	A2	1032	A2M	C6-C5-N7	2.24	136.19	132.02
35	Aw	62	HY3	O-C-CA	-2.24	118.59	124.83
1	A2	513	A2M	C6-C5-N7	2.23	136.18	132.02
39	B5	2658	A2M	C6-C5-N7	2.23	136.18	132.02
39	B5	3524	OMG	O6-C6-C5	-2.23	120.69	126.60
39	B5	1580	OMG	O6-C6-C5	-2.23	120.70	126.60
1	A2	628	OMU	O2-C2-N1	-2.22	119.84	122.79
11	AT	54	5MU	O2-C2-N1	-2.21	119.84	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	1679	A2M	C6-C5-N7	2.21	136.14	132.02
39	B5	400	A2M	C6-C5-N7	2.21	136.14	132.02
39	B5	3657	OMU	O2-C2-N1	-2.21	119.84	122.79
39	B5	3599	A2M	C6-C5-N7	2.21	136.14	132.02
11	AT	34	OMG	O6-C6-C5	-2.21	120.74	126.60
1	A2	27	A2M	C6-C5-N7	2.21	136.13	132.02
1	A2	166	A2M	C6-C5-N7	2.21	136.13	132.02
1	A2	159	A2M	C6-C5-N7	2.21	136.13	132.02
1	A2	1327	OMU	O2-C2-N1	-2.20	119.86	122.79
1	A2	1384	A2M	C6-C5-N7	2.19	136.10	132.02
39	B5	3562	A2M	C6-C5-N7	2.18	136.09	132.02
39	B5	4269	A2M	C6-C5-N7	2.18	136.08	132.02
39	B5	398	A2M	C6-C5-N7	2.18	136.08	132.02
1	A2	1329	OMG	O6-C6-C5	-2.17	120.84	126.60
11	AT	26	M2G	O6-C6-C5	-2.17	120.84	126.60
1	A2	823	PSU	O4'-C1'-C2'	2.17	108.20	105.14
1	A2	485	A2M	C6-C5-N7	2.17	136.06	132.02
39	B5	4317	A2M	C6-C5-N7	2.17	136.06	132.02
39	B5	2719	OMG	O6-C6-C5	-2.17	120.86	126.60
39	B5	3942	OMG	O6-C6-C5	-2.17	120.86	126.60
39	B5	4116	OMG	O6-C6-C5	-2.16	120.86	126.60
1	A2	669	A2M	N9-C8-N7	-2.16	110.96	113.91
1	A2	1851	MA6	N9-C8-N7	-2.16	110.96	113.91
1	A2	1448	OMG	O6-C6-C5	-2.16	120.87	126.60
11	AT	10	2MG	O6-C6-C5	-2.16	120.88	126.60
39	B5	2265	OMC	O2-C2-N3	-2.16	118.82	122.33
39	B5	2267	OMG	O6-C6-C5	-2.16	120.88	126.60
39	B5	4336	A2M	C6-C5-N7	2.16	136.04	132.02
39	B5	3557	A2M	C6-C5-N7	2.15	136.03	132.02
11	AT	58	1MA	C6-C5-N7	2.15	136.11	132.20
1	A2	868	OMG	O6-C6-C5	-2.15	120.89	126.60
39	B5	3450	A2M	C6-C5-N7	2.15	136.03	132.02
1	A2	1704	OMC	O2-C2-N3	-2.15	118.83	122.33
39	B5	4138	OMG	O6-C6-C5	-2.15	120.90	126.60
39	B5	3573	OMC	O2-C2-N3	-2.15	118.84	122.33
1	A2	1491	OMG	C5-C6-N1	2.15	118.64	113.19
1	A2	1032	A2M	N9-C8-N7	-2.14	110.98	113.91
39	B5	3676	OMG	O6-C6-C5	-2.14	120.92	126.60
39	B5	1260	OMG	O6-C6-C5	-2.14	120.92	126.60
1	A2	437	OMG	O6-C6-C5	-2.14	120.93	126.60
41	B8	75	OMG	O6-C6-C5	-2.14	120.93	126.60
39	B5	2206	A2M	C6-C5-N7	2.14	136.00	132.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	1679	A2M	N9-C8-N7	-2.13	111.00	113.91
1	A2	99	A2M	C6-C5-N7	2.13	135.99	132.02
39	B5	4369	OMG	O6-C6-C5	-2.13	120.95	126.60
39	B5	2194	OMC	C1'-N1-C2	2.13	123.16	118.42
1	A2	684	OMG	O6-C6-C5	-2.12	120.97	126.60
1	A2	1852	MA6	C6-C5-N7	2.12	136.84	133.28
39	B5	3974	OMG	O6-C6-C5	-2.12	120.98	126.60
39	B5	4245	OMG	O6-C6-C5	-2.12	120.99	126.60
39	B5	1477	OMG	O6-C6-C5	-2.12	120.99	126.60
39	B5	2680	OMU	O2-C2-N1	-2.11	119.98	122.79
39	B5	3476	OMG	O6-C6-C5	-2.11	121.00	126.60
39	B5	1810	A2M	N9-C8-N7	-2.11	111.03	113.91
1	A2	602	OMG	O6-C6-C5	-2.11	121.00	126.60
39	B5	3369	PSU	C5-C6-N1	-2.11	118.94	122.11
39	B5	3502	PSU	C5-C6-N1	-2.11	118.95	122.11
1	A2	1833	6MZ	C6-C5-N7	2.11	134.67	132.39
39	B5	4149	PSU	C5-C6-N1	-2.11	118.95	122.11
1	A2	577	A2M	N9-C8-N7	-2.10	111.04	113.91
39	B5	2630	A2M	C6-C5-N7	2.10	135.94	132.02
1	A2	159	A2M	N9-C8-N7	-2.10	111.04	113.91
39	B5	4364	OMG	O6-C6-C5	-2.10	121.03	126.60
39	B5	3631	OMG	O6-C6-C5	-2.10	121.03	126.60
39	B5	4269	A2M	N9-C8-N7	-2.10	111.05	113.91
39	B5	4240	OMG	O6-C6-C5	-2.10	121.04	126.60
39	B5	4166	PSU	O4'-C1'-C2'	2.09	108.10	105.14
1	A2	645	OMG	O6-C6-C5	-2.09	121.04	126.60
39	B5	1489	A2M	N9-C8-N7	-2.09	111.05	113.91
1	A2	469	A2M	N9-C8-N7	-2.09	111.05	113.91
1	A2	429	OMU	O2-C2-N1	-2.09	120.00	122.79
39	B5	3456	A2M	N9-C8-N7	-2.09	111.05	113.91
39	B5	4267	PSU	C5-C6-N1	-2.09	118.97	122.11
1	A2	34	PSU	C5-C6-N1	-2.09	118.98	122.11
1	A2	1249	B8N	C5-C4-N3	2.09	120.03	116.17
39	B5	2244	A2M	N9-C8-N7	-2.08	111.06	113.91
39	B5	4336	A2M	N9-C8-N7	-2.08	111.06	113.91
39	B5	1632	PSU	O4'-C1'-C2'	2.08	108.08	105.14
39	B5	2207	OMG	O6-C6-C5	-2.08	121.08	126.60
39	B5	1721	PSU	C5-C6-N1	-2.08	118.99	122.11
39	B5	3492	A2M	C6-C5-N7	2.08	135.89	132.02
39	B5	3359	OMG	O6-C6-C5	-2.08	121.09	126.60
1	A2	166	A2M	N9-C8-N7	-2.07	111.08	113.91
11	AT	17	H2U	C5-C6-N1	-2.07	104.80	111.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	AT	55	PSU	C5-C6-N1	-2.07	119.01	122.11
39	B5	2704	OMC	O2-C2-N3	-2.07	118.97	122.33
39	B5	1479	A2M	N9-C8-N7	-2.06	111.09	113.91
11	AT	14	1MA	C6-C5-N7	2.06	135.95	132.20
39	B5	4383	OMG	O6-C6-C5	-2.06	121.14	126.60
1	A2	510	OMG	O6-C6-C5	-2.06	121.14	126.60
39	B5	4711	PSU	C5-C6-N1	-2.06	119.02	122.11
1	A2	27	A2M	N9-C8-N7	-2.06	111.10	113.91
11	AT	14	1MA	N1-C2-N3	-2.06	123.55	126.00
39	B5	2351	PSU	C5-C6-N1	-2.05	119.03	122.11
11	AT	37	YYG	C8-N9-C4	2.05	108.54	106.56
39	B5	1491	PSU	C5-C6-N1	-2.05	119.03	122.11
41	B8	55	PSU	C5-C6-N1	-2.05	119.03	122.11
1	A2	573	PSU	C5-C6-N1	-2.05	119.04	122.11
41	B8	69	PSU	O4'-C1'-C2'	2.04	108.03	105.14
1	A2	1693	PSU	C5-C6-N1	-2.04	119.05	122.11
39	B5	1731	PSU	C5-C6-N1	-2.04	119.05	122.11
39	B5	3490	PSU	C5-C6-N1	-2.03	119.06	122.11
1	A2	867	PSU	C5-C6-N1	-2.03	119.06	122.11
1	A2	1384	A2M	N9-C8-N7	-2.03	111.14	113.91
39	B5	4267	PSU	O4'-C1'-C2'	2.03	108.01	105.14
1	A2	1843	4AC	C5-C4-N3	-2.03	119.33	122.59
1	A2	116	OMU	O2-C2-N1	-2.03	120.09	122.79
39	B5	4052	OMU	C1'-N1-C2	2.03	121.24	117.57
39	B5	4419	PSU	C5-C6-N1	-2.02	119.07	122.11
39	B5	3599	A2M	N9-C8-N7	-2.02	111.14	113.91
39	B5	3562	A2M	N9-C8-N7	-2.02	111.15	113.91
11	AT	28	PSU	C5-C6-N1	-2.02	119.08	122.11
1	A2	1851	MA6	C5-C6-N6	-2.02	121.78	125.30
1	A2	816	PSU	C5-C6-N1	-2.02	119.08	122.11
39	B5	4042	PSU	C5-C6-N1	-2.02	119.08	122.11
1	A2	1239	PSU	C5-C6-N1	-2.02	119.08	122.11
39	B5	4382	PSU	O4'-C1'-C2'	2.02	107.99	105.14
1	A2	1852	MA6	N9-C8-N7	-2.01	111.16	113.91
11	AT	54	5MU	C5M-C5-C4	2.01	120.98	118.77
39	B5	1801	PSU	C5-C6-N1	-2.01	119.09	122.11
39	B5	3466	PSU	C5-C6-N1	-2.01	119.09	122.11
39	B5	4298	PSU	C5-C6-N1	-2.01	119.10	122.11
39	B5	3492	A2M	O4'-C1'-N9	2.01	112.01	108.06
39	B5	1683	PSU	C5-C6-N1	-2.01	119.10	122.11
1	A2	650	PSU	C5-C6-N1	-2.00	119.10	122.11
39	B5	2667	OMC	O2-C2-N3	-2.00	119.08	122.33

There are no chirality outliers.

All (134) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A2	429	OMU	C2'-C1'-N1-C2
1	A2	429	OMU	C2'-C1'-N1-C6
1	A2	645	OMG	O4'-C4'-C5'-O5'
1	A2	645	OMG	C3'-C4'-C5'-O5'
1	A2	1833	6MZ	N1-C6-N6-C9
39	B5	3433	OMC	C2'-C1'-N1-C2
39	B5	3433	OMC	C2'-C1'-N1-C6
39	B5	3517	A2M	O4'-C4'-C5'-O5'
39	B5	4336	A2M	C4'-C5'-O5'-P
39	B5	4382	PSU	C3'-C4'-C5'-O5'
39	B5	4382	PSU	O4'-C4'-C5'-O5'
1	A2	1249	B8N	N34-C33-C34-O35
1	A2	1338	4AC	N3-C4-N4-C7
1	A2	1338	4AC	C5-C4-N4-C7
1	A2	1338	4AC	O7-C7-N4-C4
1	A2	1338	4AC	CM7-C7-N4-C4
11	AT	17	H2U	O4'-C4'-C5'-O5'
11	AT	17	H2U	O4'-C1'-N1-C6
11	AT	17	H2U	C2'-C1'-N1-C2
11	AT	17	H2U	C2'-C1'-N1-C6
31	As	67	NMM	O-C-CA-CB
42	BA	216	V5N	O-C-CA-CB
1	A2	513	A2M	O4'-C4'-C5'-O5'
1	A2	669	A2M	O4'-C4'-C5'-O5'
1	A2	669	A2M	C3'-C4'-C5'-O5'
1	A2	684	OMG	O4'-C4'-C5'-O5'
1	A2	1448	OMG	C3'-C4'-C5'-O5'
39	B5	2207	OMG	O4'-C4'-C5'-O5'
11	AT	17	H2U	C3'-C4'-C5'-O5'
33	Au	1	AME	CT2-CT1-N-CA
33	Au	1	AME	OT-CT1-N-CA
1	A2	577	A2M	O4'-C4'-C5'-O5'
1	A2	577	A2M	C3'-C4'-C5'-O5'
39	B5	398	A2M	O4'-C4'-C5'-O5'
39	B5	2207	OMG	C3'-C4'-C5'-O5'
39	B5	3492	A2M	C3'-C4'-C5'-O5'
39	B5	3517	A2M	C3'-C4'-C5'-O5'
1	A2	1249	B8N	N34-C33-C34-O36
1	A2	99	A2M	O4'-C4'-C5'-O5'
1	A2	513	A2M	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
39	B5	4193	5MC	C2'-C1'-N1-C6
1	A2	684	OMG	C3'-C4'-C5'-O5'
1	A2	802	PSU	C3'-C4'-C5'-O5'
39	B5	3492	A2M	O4'-C4'-C5'-O5'
39	B5	3599	A2M	C3'-C4'-C5'-O5'
1	A2	1448	OMG	O4'-C4'-C5'-O5'
1	A2	1704	OMC	O4'-C4'-C5'-O5'
1	A2	1852	MA6	C5-C6-N6-C9
1	A2	802	PSU	O4'-C4'-C5'-O5'
1	A2	1443	OMU	C3'-C2'-O2'-CM2
1	A2	1833	6MZ	C5-C6-N6-C9
39	B5	398	A2M	C3'-C4'-C5'-O5'
11	AT	17	H2U	O4'-C1'-N1-C2
39	B5	2630	A2M	C2'-C1'-N9-C8
12	AZ	2	SAC	C-CA-N-C1A
1	A2	1249	B8N	C32-C33-C34-O36
1	A2	121	OMU	C3'-C2'-O2'-CM2
1	A2	1491	OMG	C3'-C2'-O2'-CM2
1	A2	1805	OMU	C3'-C2'-O2'-CM2
39	B5	2680	OMU	C3'-C2'-O2'-CM2
39	B5	3676	OMG	C3'-C2'-O2'-CM2
39	B5	4193	5MC	O4'-C1'-N1-C6
1	A2	1843	4AC	N3-C4-N4-C7
1	A2	1843	4AC	C5-C4-N4-C7
39	B5	3576	PSU	C4'-C5'-O5'-P
39	B5	4246	PSU	C4'-C5'-O5'-P
39	B5	3599	A2M	O4'-C4'-C5'-O5'
69	Bb	5	MLZ	N-CA-CB-CG
39	B5	4193	5MC	O4'-C1'-N1-C2
39	B5	4193	5MC	C2'-C1'-N1-C2
1	A2	1249	B8N	C32-C33-C34-O35
1	A2	645	OMG	C4'-C5'-O5'-P
39	B5	3550	UY1	C4'-C5'-O5'-P
39	B5	3433	OMC	O4'-C1'-N1-C6
1	A2	1852	MA6	C4'-C5'-O5'-P
11	AT	16	H2U	C4'-C5'-O5'-P
1	A2	429	OMU	O4'-C1'-N1-C6
68	Ba	39	V5N	O2-CB-CG-CD2
1	A2	645	OMG	C3'-C2'-O2'-CM2
39	B5	1260	OMG	C3'-C2'-O2'-CM2
39	B5	1477	OMG	C3'-C2'-O2'-CM2
39	B5	2647	OMC	C3'-C2'-O2'-CM2

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Mol	Chain	Res	Type	Atoms
39	B5	4202	OMC	C3'-C2'-O2'-CM2
39	B5	4369	OMG	C3'-C2'-O2'-CM2
39	B5	3550	UY1	C1'-C2'-O2'-CM2
1	A2	823	PSU	C3'-C4'-C5'-O5'
39	B5	3494	PSU	C3'-C4'-C5'-O5'
39	B5	3550	UY1	O4'-C1'-C5-C4
1	A2	116	OMU	C3'-C2'-O2'-CM2
1	A2	513	A2M	C3'-C2'-O2'-CM'
1	A2	684	OMG	C3'-C2'-O2'-CM2
1	A2	1329	OMG	C3'-C2'-O2'-CM2
39	B5	2265	OMC	C3'-C2'-O2'-CM2
39	B5	3524	OMG	C3'-C2'-O2'-CM2
39	B5	3557	A2M	C3'-C2'-O2'-CM'
1	A2	429	OMU	O4'-C1'-N1-C2
1	A2	628	OMU	C2'-C1'-N1-C6
39	B5	2194	OMC	O4'-C4'-C5'-O5'
1	A2	591	A2M	C2'-C1'-N9-C4
39	B5	2630	A2M	O4'-C1'-N9-C8
39	B5	1266	1MA	C2'-C1'-N9-C8
1	A2	469	A2M	O4'-C4'-C5'-O5'
1	A2	1704	OMC	C3'-C4'-C5'-O5'
69	Bb	5	MLZ	C-CA-CB-CG
39	B5	3433	OMC	O4'-C1'-N1-C2
39	B5	3619	OMC	C4'-C5'-O5'-P
39	B5	3492	A2M	C2'-C1'-N9-C8
1	A2	99	A2M	C3'-C4'-C5'-O5'
1	A2	513	A2M	C1'-C2'-O2'-CM'
1	A2	684	OMG	C1'-C2'-O2'-CM2
39	B5	1284	OMC	C1'-C2'-O2'-CM2
1	A2	628	OMU	O4'-C1'-N1-C6
39	B5	3550	UY1	C3'-C2'-O2'-CM2
1	A2	591	A2M	C2'-C1'-N9-C8
39	B5	4382	PSU	O4'-C1'-C5-C6
39	B5	2194	OMC	C2'-C1'-N1-C2
1	A2	591	A2M	O4'-C1'-N9-C8
1	A2	27	A2M	O4'-C4'-C5'-O5'
1	A2	1805	OMU	O4'-C4'-C5'-O5'
39	B5	1489	A2M	O4'-C4'-C5'-O5'
39	B5	3450	A2M	O4'-C4'-C5'-O5'
39	B5	2630	A2M	C2'-C1'-N9-C4
12	AZ	2	SAC	CB-CA-N-C1A
1	A2	1491	OMG	C4'-C5'-O5'-P

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Mol	Chain	Res	Type	Atoms
1	A2	27	A2M	C3'-C2'-O2'-CM'
39	B5	1284	OMC	C3'-C2'-O2'-CM2
39	B5	1820	OMC	C3'-C2'-O2'-CM2
39	B5	2704	OMC	C3'-C2'-O2'-CM2
39	B5	3619	OMC	C3'-C2'-O2'-CM2
39	B5	3973	OMU	C3'-C2'-O2'-CM2
11	AT	46	G7M	O4'-C4'-C5'-O5'
1	A2	1392	OMC	C2'-C1'-N1-C2
1	A2	1082	PSU	C4'-C5'-O5'-P
39	B5	3583	PSU	C3'-C4'-C5'-O5'

There are no ring outliers.

88 monomers are involved in 111 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A2	1443	OMU	1	0
33	Au	1	AME	2	0
39	B5	3676	OMG	1	0
39	B5	1720	PSU	1	0
1	A2	1032	A2M	1	0
1	A2	1704	OMC	2	0
1	A2	1446	PSU	1	0
1	A2	1491	OMG	1	0
39	B5	4282	OMC	1	0
39	B5	1489	A2M	1	0
1	A2	463	OMC	1	0
1	A2	518	OMC	1	0
39	B5	4202	OMC	2	0
41	B8	75	OMG	2	0
39	B5	4364	OMG	1	0
39	B5	4366	OMU	2	0
39	B5	1718	PSU	1	0
39	B5	4039	PSU	1	0
1	A2	1640	G7M	1	0
39	B5	3942	OMG	1	0
39	B5	3517	A2M	1	0
39	B5	3599	A2M	1	0
39	B5	3616	PSU	1	0
1	A2	121	OMU	1	0
1	A2	437	OMG	1	0
1	A2	577	A2M	1	0
11	AT	17	H2U	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A2	867	PSU	1	0
1	A2	172	OMU	2	0
39	B5	1260	OMG	1	0
39	B5	4325	PSU	2	0
39	B5	1810	A2M	2	0
39	B5	3974	OMG	1	0
39	B5	2267	OMG	2	0
1	A2	1843	4AC	1	0
11	AT	58	1MA	1	0
11	AT	32	OMC	1	0
39	B5	4193	5MC	1	0
39	B5	4336	A2M	1	0
39	B5	3466	PSU	1	0
39	B5	3619	OMC	2	0
39	B5	3450	A2M	2	0
39	B5	1638	PSU	1	0
39	B5	398	A2M	1	0
11	AT	37	YYG	1	0
39	B5	2194	OMC	1	0
1	A2	166	A2M	2	0
1	A2	1392	OMC	1	0
11	AT	34	OMG	1	0
1	A2	27	A2M	1	0
39	B5	4269	A2M	1	0
1	A2	1338	4AC	1	0
39	B5	2258	OMU	1	0
1	A2	116	OMU	2	0
39	B5	3557	A2M	1	0
39	B5	3540	OMC	1	0
39	B5	1632	PSU	1	0
1	A2	485	A2M	3	0
39	B5	2704	OMC	1	0
39	B5	2206	A2M	1	0
39	B5	1284	OMC	3	0
39	B5	1270	A2M	1	0
39	B5	4383	OMG	1	0
1	A2	602	OMG	1	0
1	A2	99	A2M	2	0
39	B5	3550	UY1	1	0
39	B5	2719	OMG	2	0
39	B5	4317	A2M	1	0
1	A2	1233	PSU	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A2	1805	OMU	1	0
39	B5	4052	OMU	1	0
1	A2	1245	PSU	2	0
39	B5	4138	OMG	1	0
39	B5	3562	A2M	1	0
39	B5	4203	PSU	1	0
1	A2	868	OMG	1	0
1	A2	1329	OMG	1	0
39	B5	3514	5MC	2	0
39	B5	4166	PSU	1	0
1	A2	513	A2M	1	0
11	AT	26	M2G	1	0
1	A2	1448	OMG	3	0
1	A2	669	A2M	1	0
1	A2	36	PSU	2	0
1	A2	469	A2M	1	0
39	B5	3456	A2M	1	0
1	A2	1833	6MZ	1	0
1	A2	510	OMG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 790 ligands modelled in this entry, 428 are monoatomic and 329 are unknown - leaving 33 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	$\# Z > 2$
87	SPD	B5	4913	-	9,9,9	0.16	0	8,8,8	0.17	0
87	SPD	A2	1906	-	9,9,9	0.16	0	8,8,8	0.18	0
88	SPM	B5	4912	-	13,13,13	0.15	0	12,12,12	0.23	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	SPD	B5	4902	-	9,9,9	0.15	0	8,8,8	0.23	0
87	SPD	A2	1907	-	9,9,9	0.15	0	8,8,8	0.18	0
87	SPD	B5	4901	-	9,9,9	0.14	0	8,8,8	0.15	0
87	SPD	B5	4904	-	9,9,9	0.15	0	8,8,8	0.19	0
87	SPD	B5	4916	-	9,9,9	0.15	0	8,8,8	0.22	0
87	SPD	B5	4903	-	9,9,9	0.16	0	8,8,8	0.20	0
87	SPD	A2	1902	-	9,9,9	0.15	0	8,8,8	0.15	0
87	SPD	B5	4923	-	9,9,9	0.15	0	8,8,8	0.20	0
87	SPD	A2	1904	-	9,9,9	0.15	0	8,8,8	0.19	0
87	SPD	B5	4919	-	9,9,9	0.15	0	8,8,8	0.21	0
88	SPM	B5	4915	-	13,13,13	0.16	0	12,12,12	0.22	0
87	SPD	B5	4918	-	9,9,9	0.15	0	8,8,8	0.17	0
87	SPD	B5	4922	-	9,9,9	0.15	0	8,8,8	0.17	0
87	SPD	A2	1905	-	9,9,9	0.16	0	8,8,8	0.17	0
87	SPD	B5	4908	-	9,9,9	0.16	0	8,8,8	0.16	0
87	SPD	B5	4914	-	9,9,9	0.15	0	8,8,8	0.17	0
87	SPD	A2	1903	-	9,9,9	0.15	0	8,8,8	0.19	0
87	SPD	A2	1901	-	9,9,9	0.16	0	8,8,8	0.18	0
87	SPD	B5	4909	-	9,9,9	0.16	0	8,8,8	0.19	0
87	SPD	B5	4921	-	9,9,9	0.16	0	8,8,8	0.18	0
87	SPD	B5	4907	-	9,9,9	0.16	0	8,8,8	0.18	0
87	SPD	B5	4911	-	9,9,9	0.15	0	8,8,8	0.17	0
87	SPD	A2	1908	-	9,9,9	0.15	0	8,8,8	0.20	0
87	SPD	B5	4910	-	9,9,9	0.15	0	8,8,8	0.18	0
87	SPD	B5	4920	-	9,9,9	0.15	0	8,8,8	0.23	0
87	SPD	B5	4924	-	9,9,9	0.16	0	8,8,8	0.14	0
87	SPD	B5	4906	-	9,9,9	0.15	0	8,8,8	0.16	0
87	SPD	B5	4905	-	9,9,9	0.16	0	8,8,8	0.21	0
87	SPD	B5	4917	-	9,9,9	0.15	0	8,8,8	0.18	0
88	SPM	A2	1909	-	13,13,13	0.14	0	12,12,12	0.18	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	SPD	B5	4913	-	-	0/7/7/7	-
87	SPD	A2	1906	-	-	1/7/7/7	-
88	SPM	B5	4912	-	-	1/11/11/11	-
87	SPD	B5	4902	-	-	1/7/7/7	-
87	SPD	A2	1907	-	-	1/7/7/7	-
87	SPD	B5	4901	-	-	1/7/7/7	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	SPD	B5	4904	-	-	0/7/7/7	-
87	SPD	B5	4916	-	-	0/7/7/7	-
87	SPD	B5	4903	-	-	2/7/7/7	-
87	SPD	A2	1902	-	-	0/7/7/7	-
87	SPD	B5	4923	-	-	0/7/7/7	-
87	SPD	A2	1904	-	-	0/7/7/7	-
87	SPD	B5	4919	-	-	0/7/7/7	-
88	SPM	B5	4915	-	-	0/11/11/11	-
87	SPD	B5	4918	-	-	0/7/7/7	-
87	SPD	B5	4922	-	-	1/7/7/7	-
87	SPD	A2	1905	-	-	0/7/7/7	-
87	SPD	B5	4908	-	-	0/7/7/7	-
87	SPD	B5	4914	-	-	0/7/7/7	-
87	SPD	A2	1903	-	-	0/7/7/7	-
87	SPD	A2	1901	-	-	1/7/7/7	-
87	SPD	B5	4909	-	-	0/7/7/7	-
87	SPD	B5	4921	-	-	1/7/7/7	-
87	SPD	B5	4907	-	-	0/7/7/7	-
87	SPD	B5	4911	-	-	0/7/7/7	-
87	SPD	A2	1908	-	-	0/7/7/7	-
87	SPD	B5	4910	-	-	1/7/7/7	-
87	SPD	B5	4920	-	-	0/7/7/7	-
87	SPD	B5	4924	-	-	1/7/7/7	-
87	SPD	B5	4906	-	-	1/7/7/7	-
87	SPD	B5	4905	-	-	0/7/7/7	-
87	SPD	B5	4917	-	-	0/7/7/7	-
88	SPM	A2	1909	-	-	1/11/11/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
88	A2	1909	SPM	C12-C11-N10-C9
87	B5	4901	SPD	C4-C5-N6-C7
87	B5	4902	SPD	C2-C3-C4-C5
87	B5	4924	SPD	C2-C3-C4-C5
87	B5	4903	SPD	C2-C3-C4-C5
87	B5	4906	SPD	C2-C3-C4-C5
87	A2	1906	SPD	C8-C7-N6-C5

Continued on next page...

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Mol	Chain	Res	Type	Atoms
87	A2	1907	SPD	C2-C3-C4-C5
87	B5	4910	SPD	C2-C3-C4-C5
87	B5	4922	SPD	C2-C3-C4-C5
87	B5	4921	SPD	C8-C7-N6-C5
88	B5	4912	SPM	C6-C7-C8-C9
87	B5	4903	SPD	C8-C7-N6-C5
87	A2	1901	SPD	C2-C3-C4-C5

There are no ring outliers.

19 monomers are involved in 29 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	B5	4913	SPD	2	0
87	A2	1906	SPD	1	0
88	B5	4912	SPM	2	0
87	B5	4904	SPD	1	0
87	B5	4916	SPD	1	0
87	A2	1904	SPD	1	0
87	B5	4919	SPD	1	0
88	B5	4915	SPM	1	0
87	B5	4922	SPD	1	0
87	A2	1905	SPD	1	0
87	B5	4908	SPD	1	0
87	A2	1903	SPD	2	0
87	A2	1901	SPD	1	0
87	B5	4921	SPD	1	0
87	B5	4907	SPD	1	0
87	B5	4920	SPD	2	0
87	B5	4924	SPD	3	0
87	B5	4917	SPD	4	0
88	A2	1909	SPM	2	0

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.

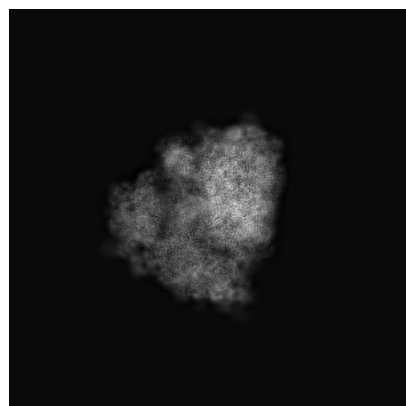
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12757. These allow visual inspection of the internal detail of the map and identification of artifacts.

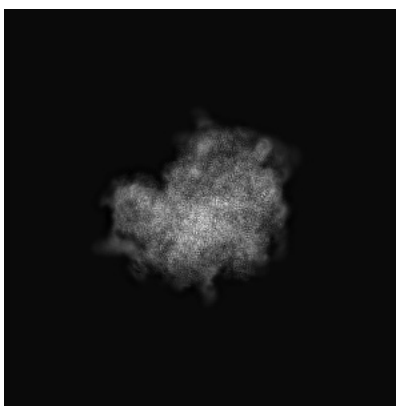
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

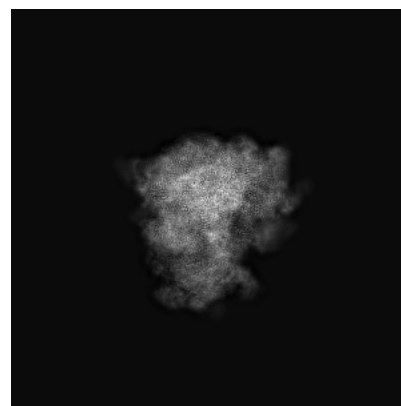
6.1.1 Primary map



X

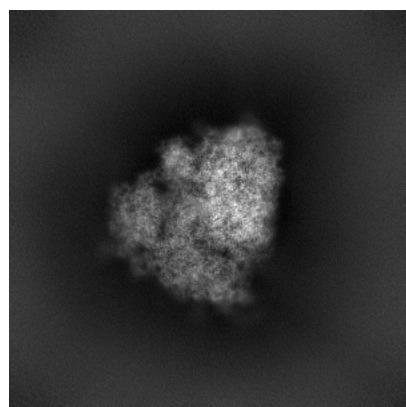


Y

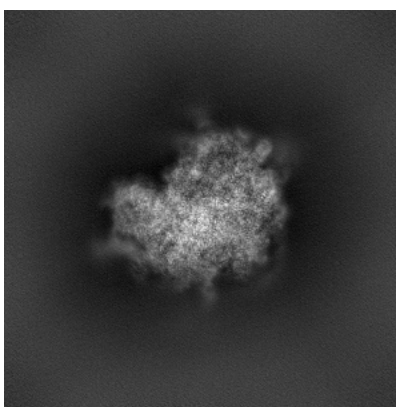


Z

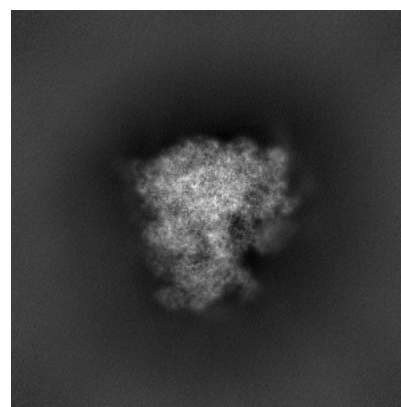
6.1.2 Raw map



X



Y

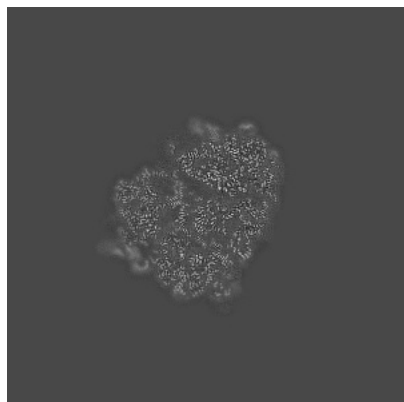


Z

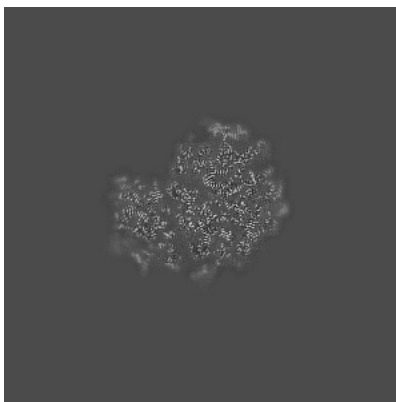
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

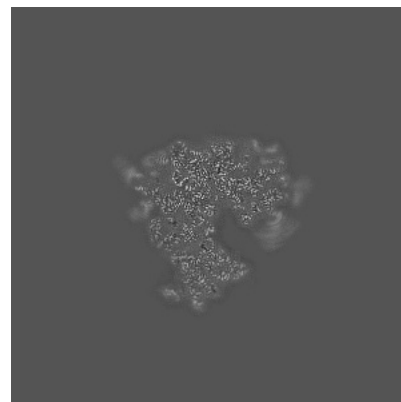
6.2.1 Primary map



X Index: 280

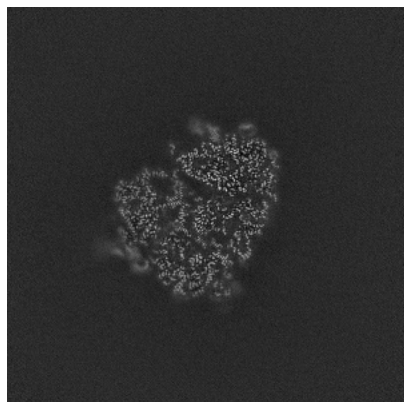


Y Index: 280

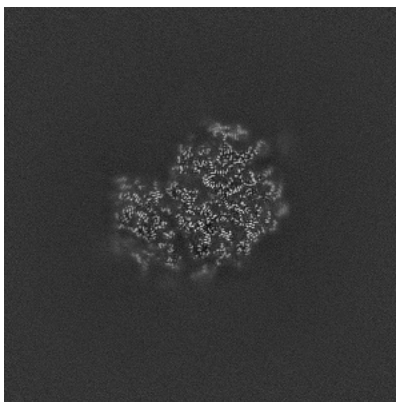


Z Index: 280

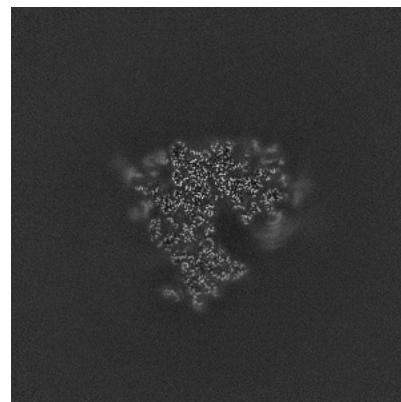
6.2.2 Raw map



X Index: 280



Y Index: 280

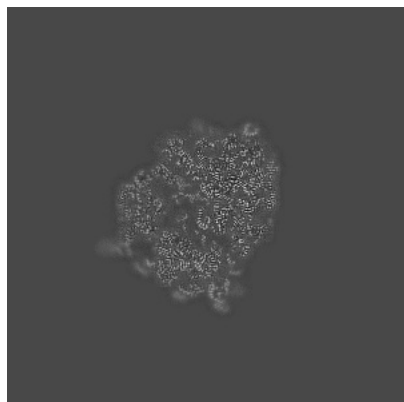


Z Index: 280

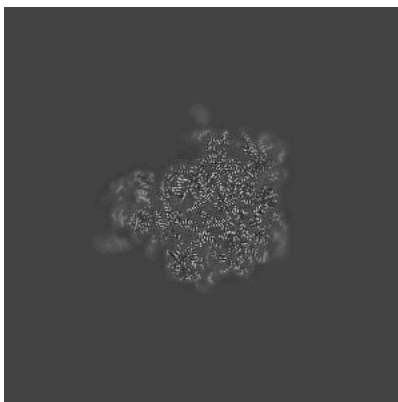
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

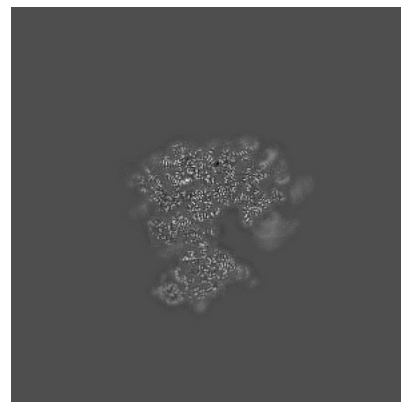
6.3.1 Primary map



X Index: 287

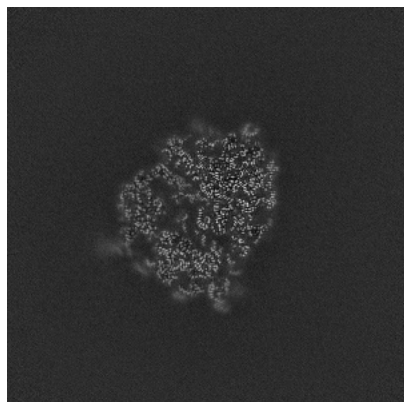


Y Index: 313

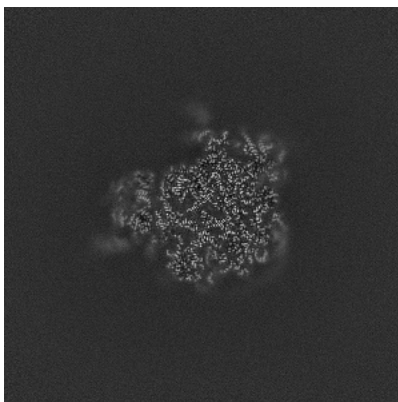


Z Index: 272

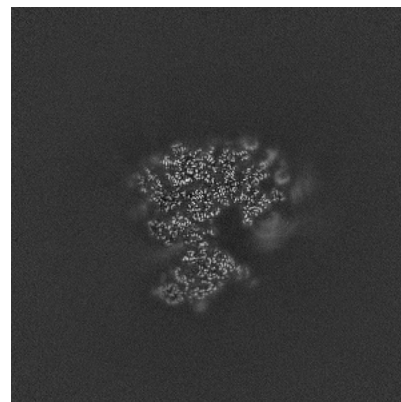
6.3.2 Raw map



X Index: 287



Y Index: 313

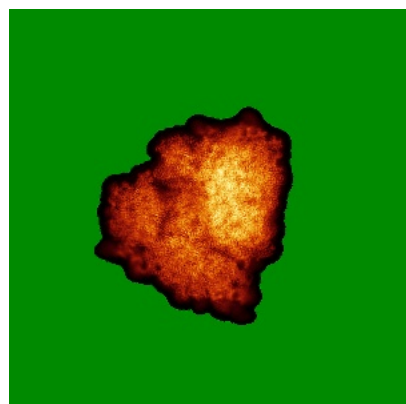


Z Index: 272

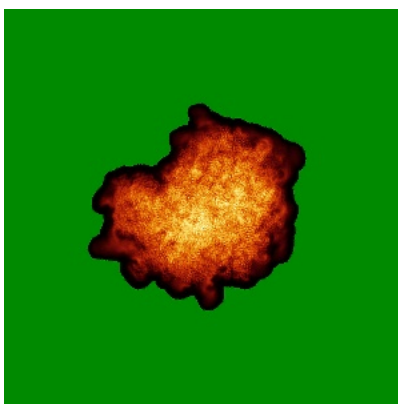
The images above show the largest variance slices of the map in three orthogonal directions.

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

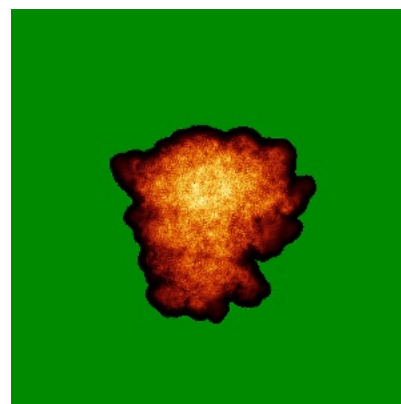
6.4.1 Primary map



X

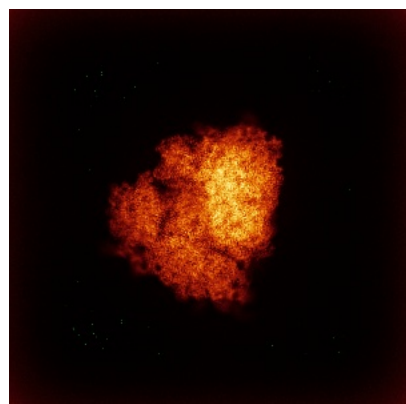


Y

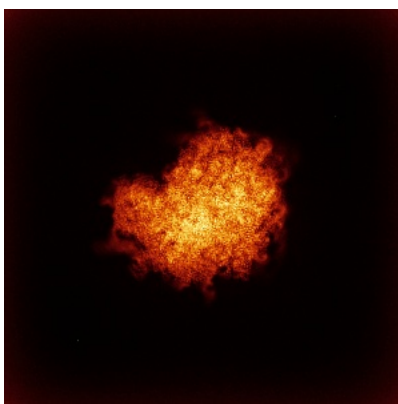


Z

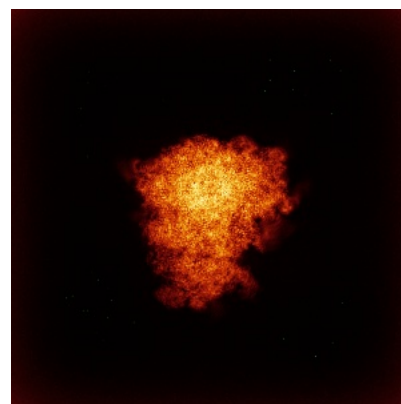
6.4.2 Raw map



X



Y

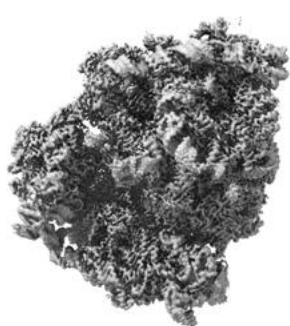


Z

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



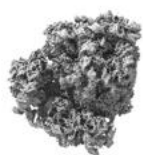
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 5.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

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

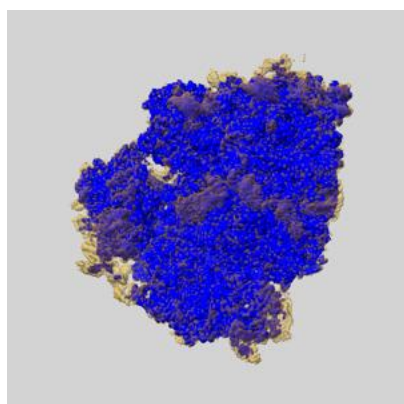
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

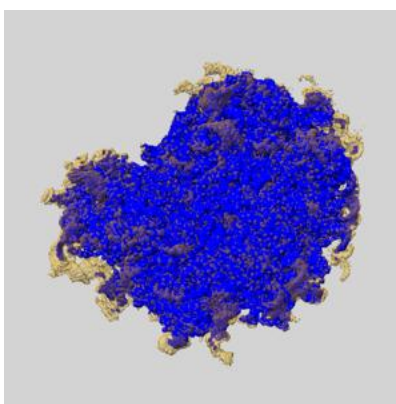
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

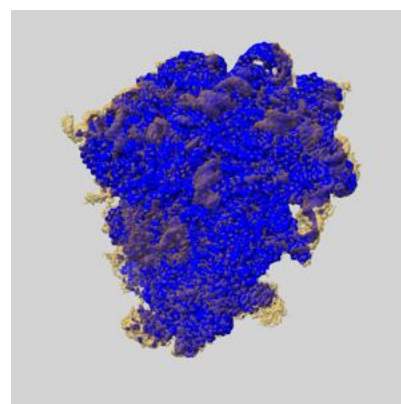
6.6.1 emd_12757_msk_1.map [i](#)



X

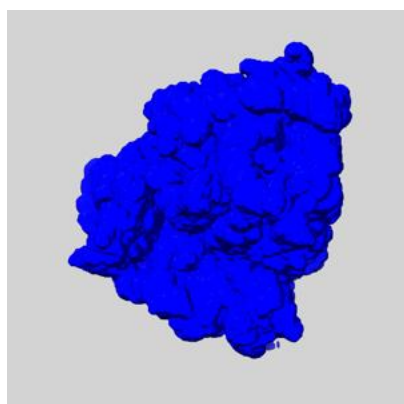


Y

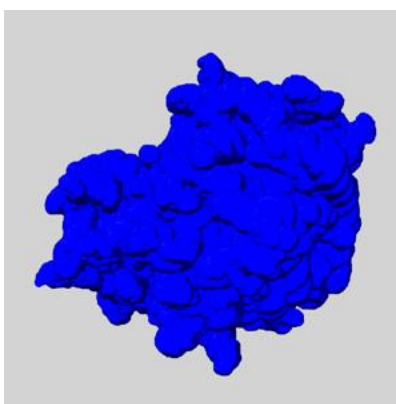


Z

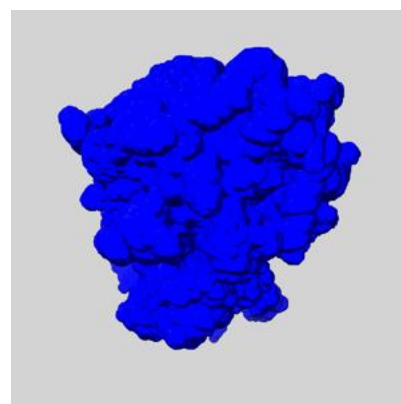
6.6.2 emd_12757_msk_2.map [i](#)



X



Y

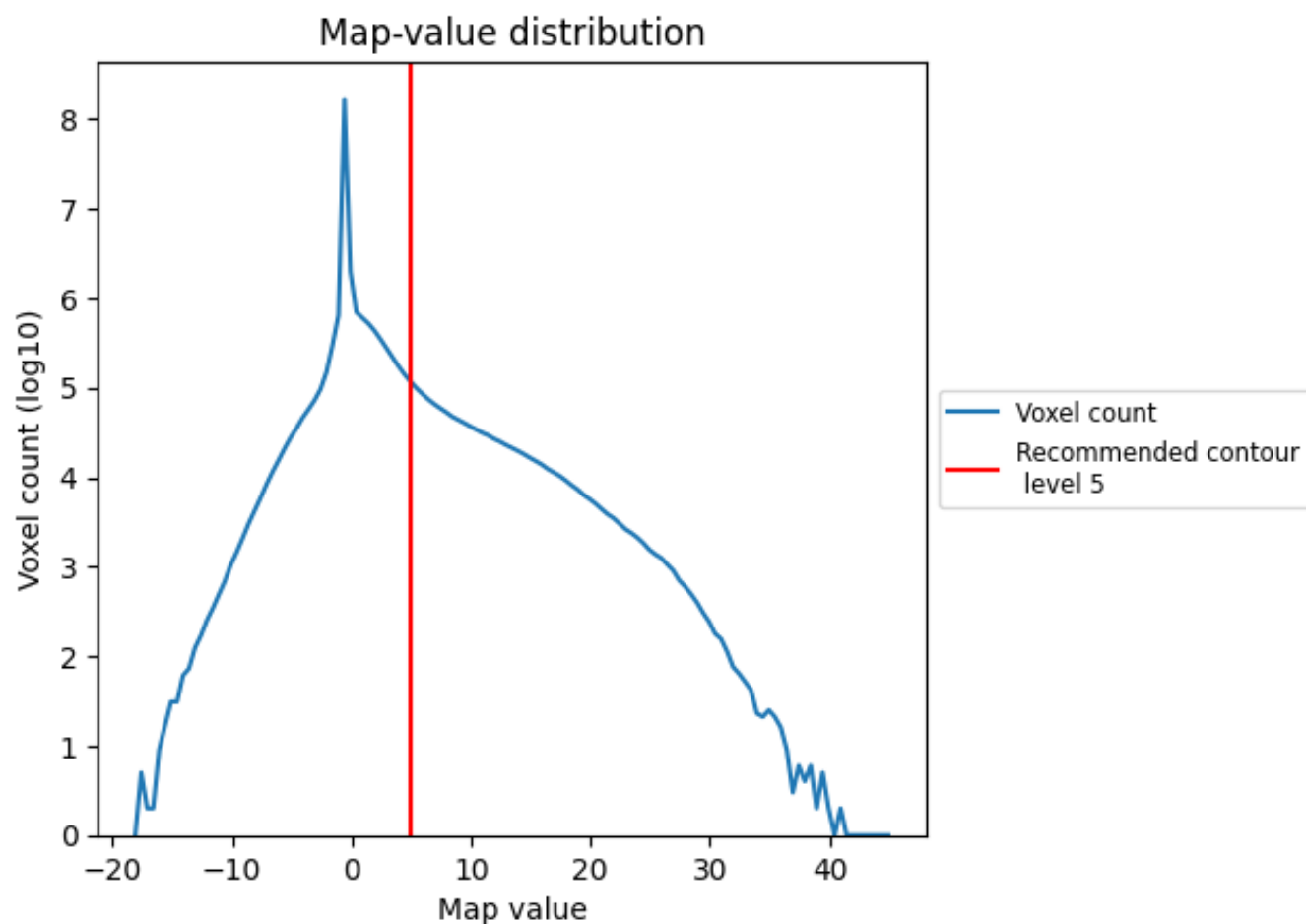


Z

7 Map analysis [i](#)

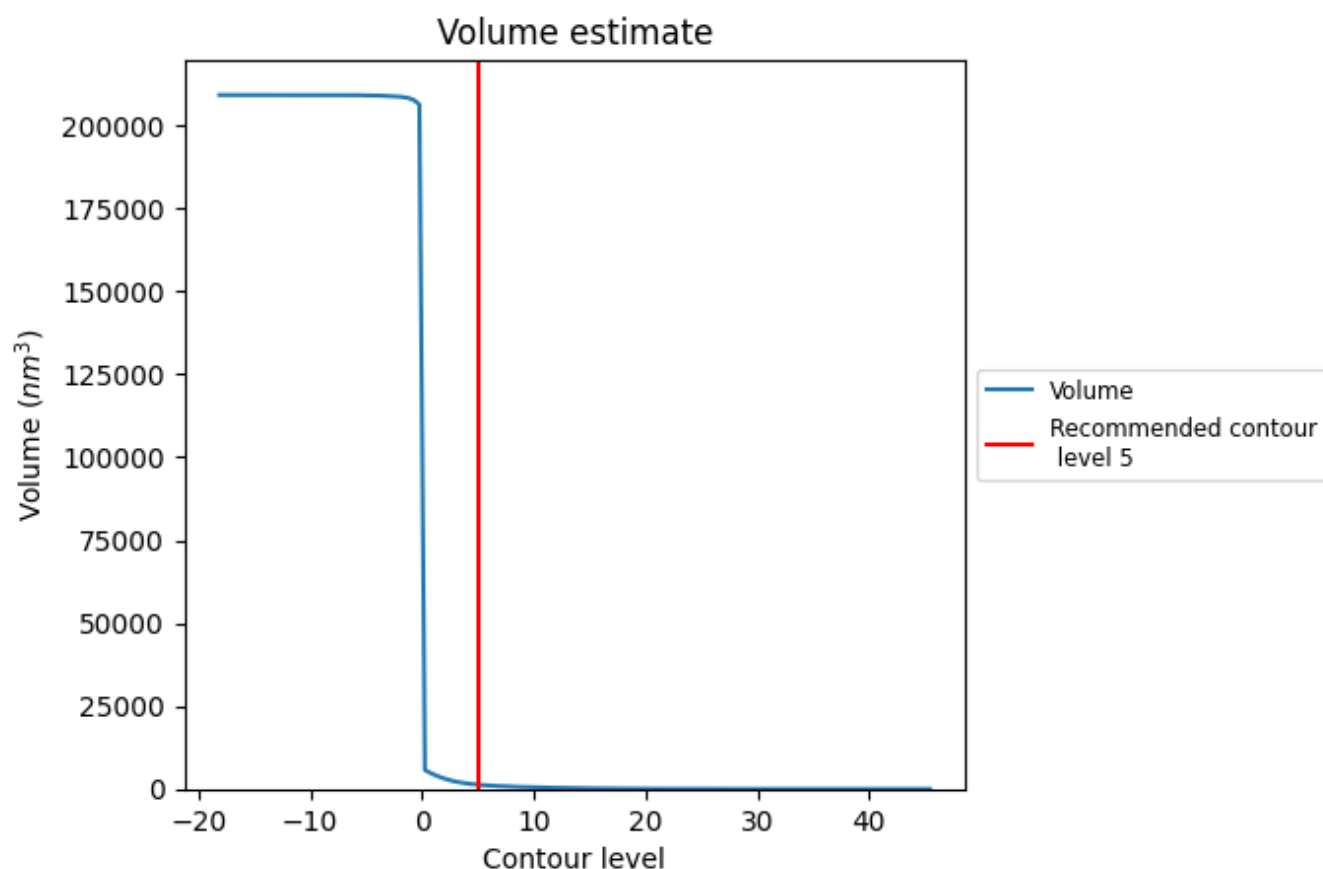
This section contains the results of statistical analysis of the map.

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.

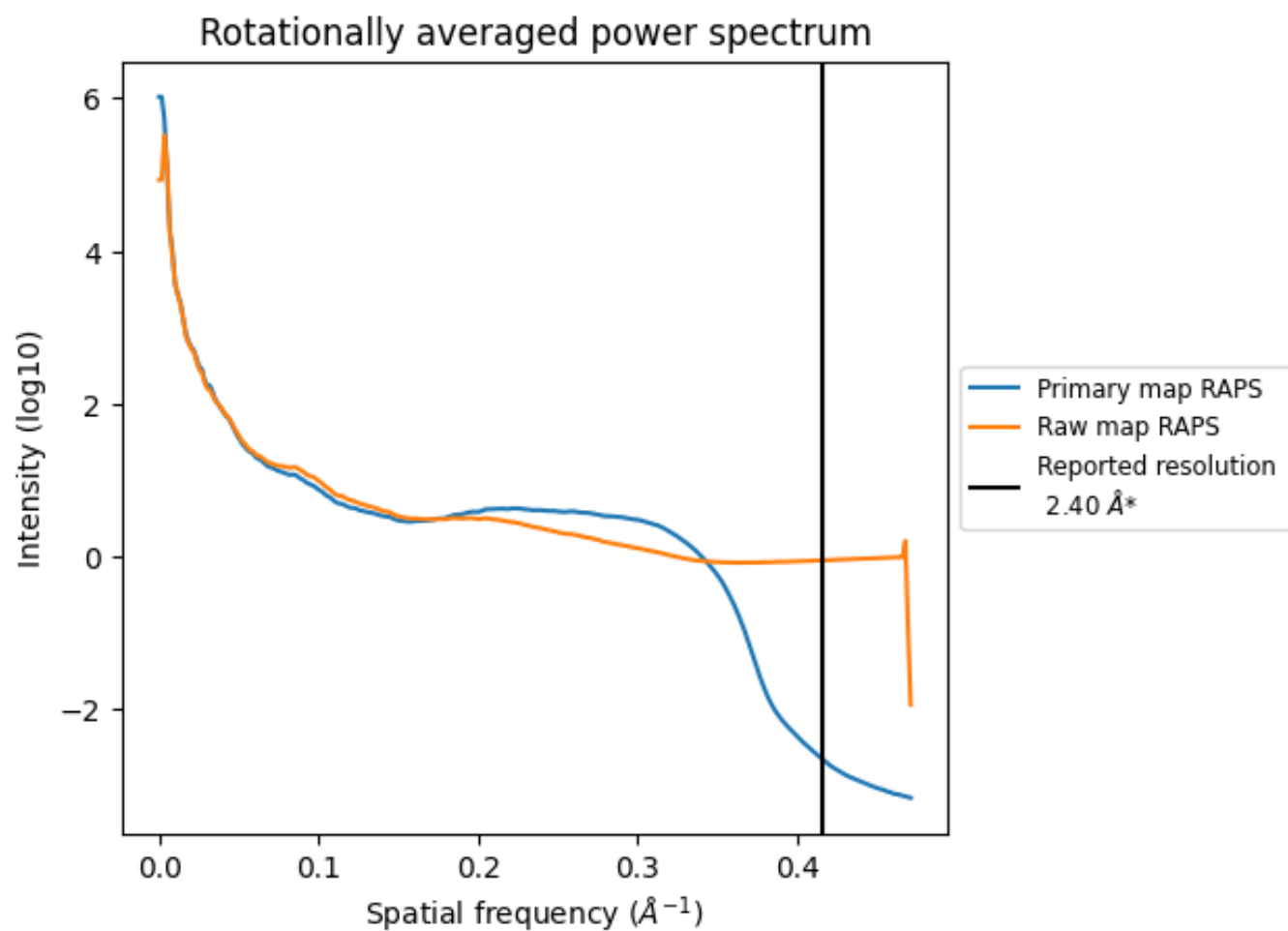
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1298 nm^3 ; this corresponds to an approximate mass of 1172 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 ⓘ

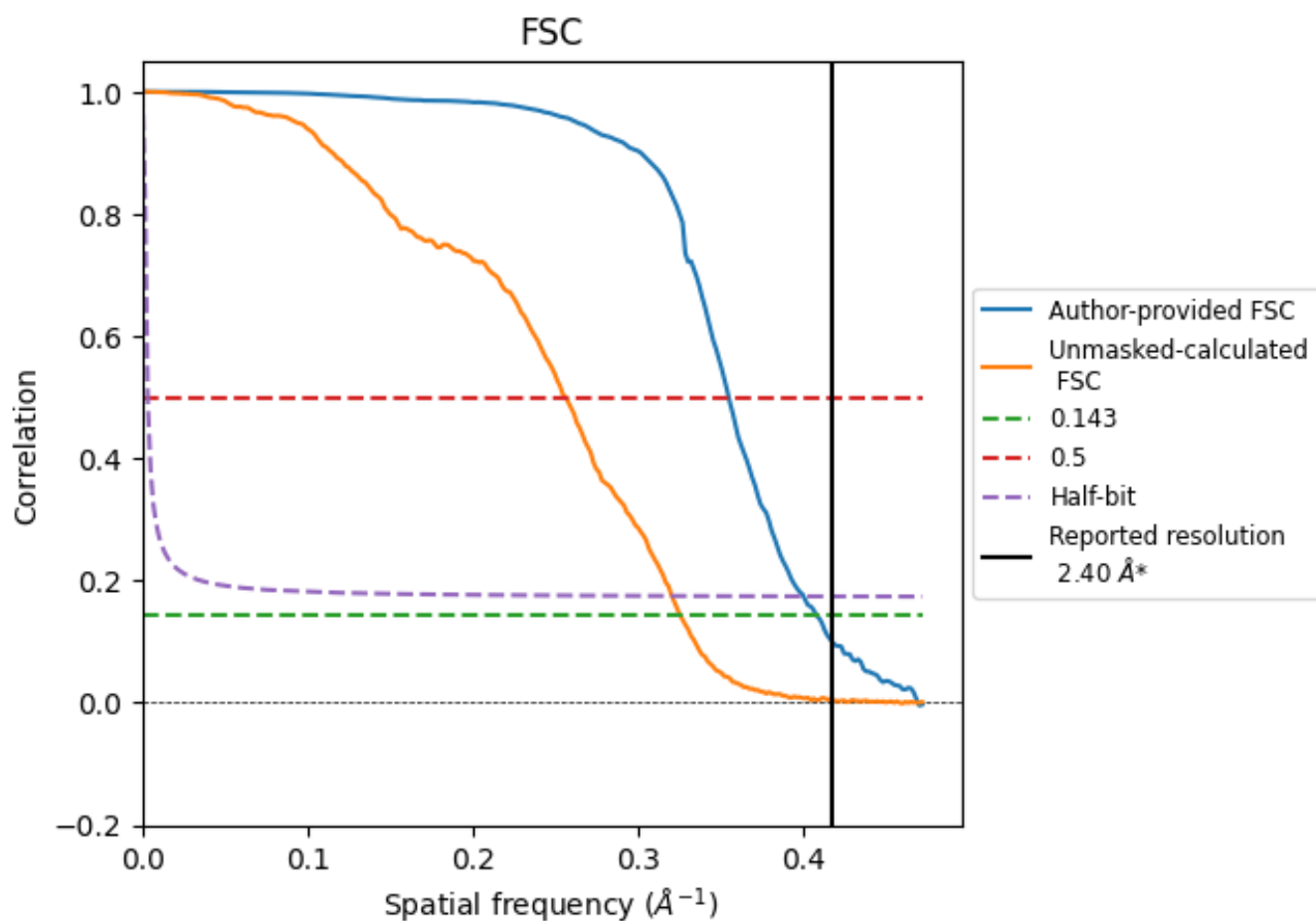


*Reported resolution corresponds to spatial frequency of 0.417 \AA^{-1}

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 0.417 Å⁻¹

8.2 Resolution estimates [i](#)

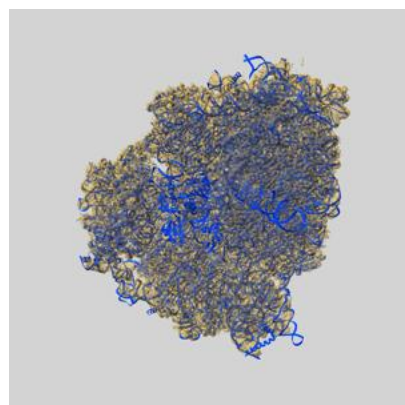
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	2.45	2.82	2.50
Unmasked-calculated*	3.07	3.90	3.12

*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 3.07 differs from the reported value 2.4 by more than 10 %

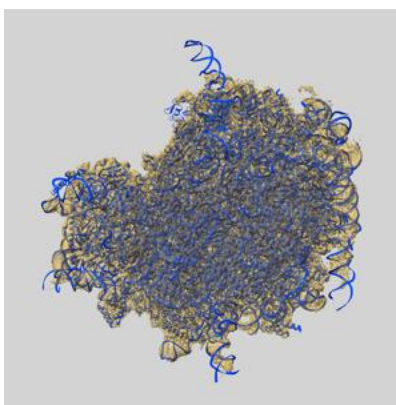
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12757 and PDB model 7O7Z. Per-residue inclusion information can be found in section [3](#) on page [27](#).

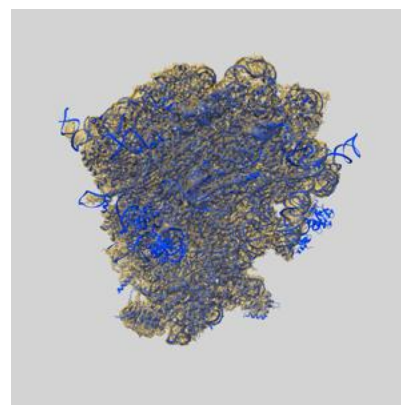
9.1 Map-model overlay [i](#)



X



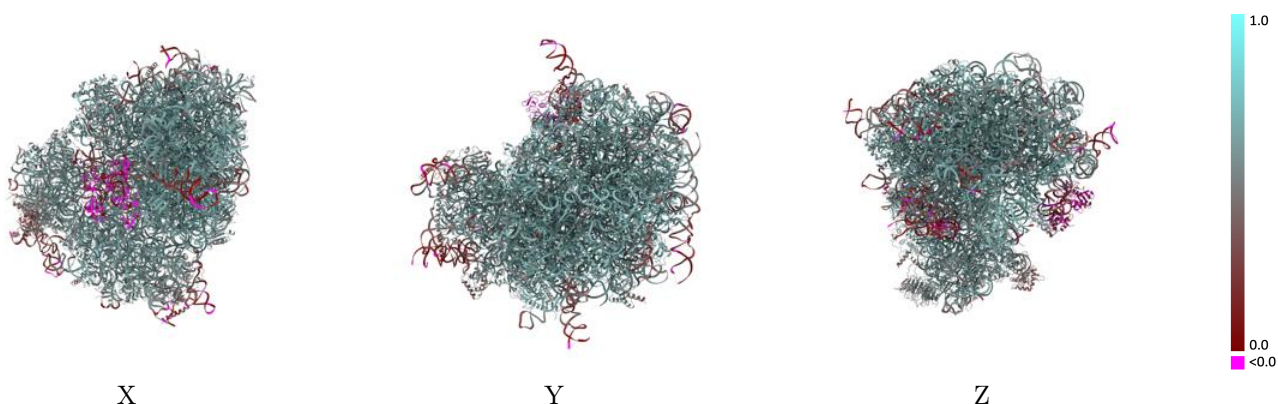
Y



Z

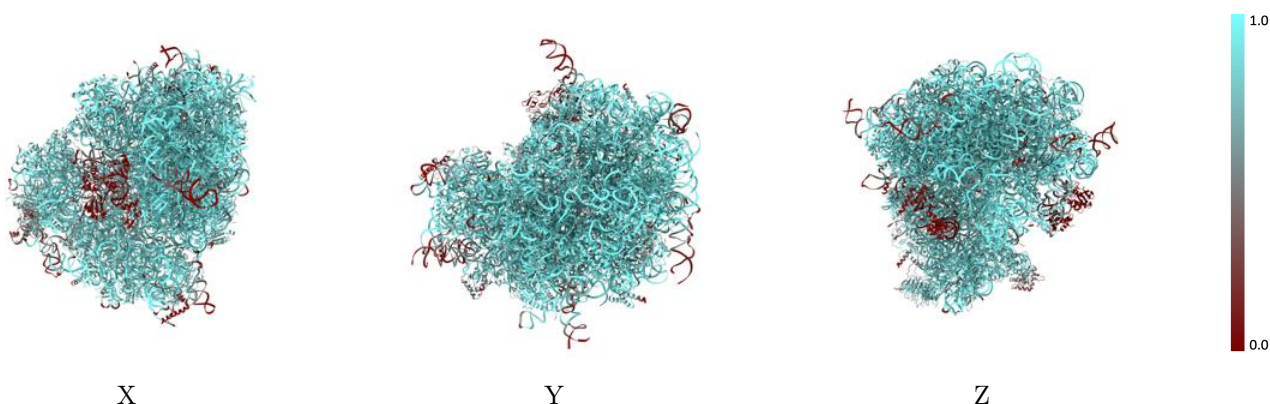
The images above show the 3D surface view of the map at the recommended contour level 5.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



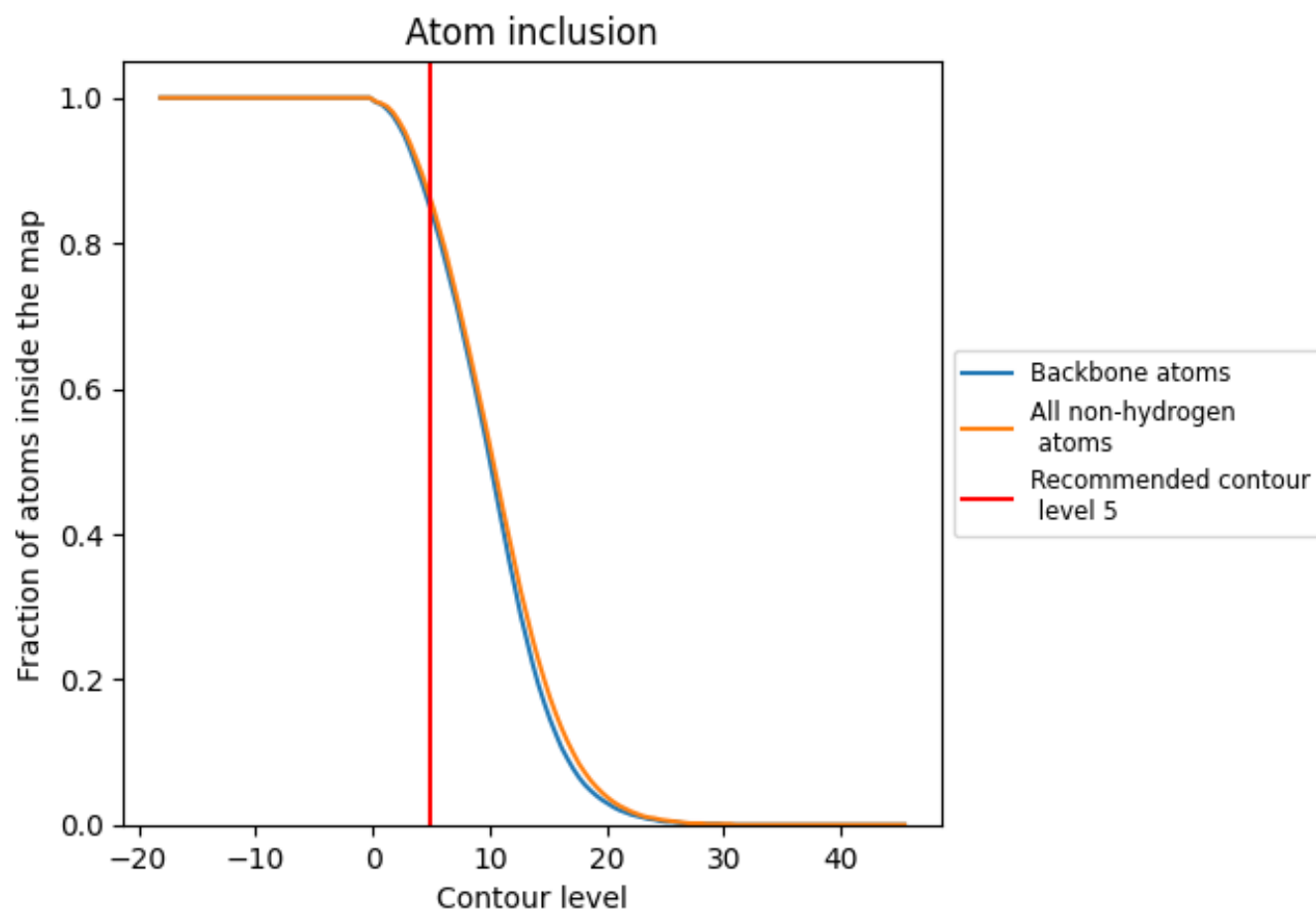
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (5).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 84% of all backbone atoms, 86% 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 (5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8580	 0.5760
A2	 0.9060	 0.5760
AA	 0.7930	 0.5730
AB	 0.7670	 0.5800
AC	 0.4040	 0.3600
AD	 0.7460	 0.5580
AE	 0.8720	 0.6130
AF	 0.7090	 0.4910
AG	 0.9050	 0.6280
AH	 0.4400	 0.2140
AI	 0.4400	 0.3250
AT	 0.8960	 0.6030
AZ	 0.8340	 0.6010
Aa	 0.8400	 0.6110
Ab	 0.8900	 0.6230
Ac	 0.7440	 0.5600
Ad	 0.8750	 0.5940
Ae	 0.8290	 0.6050
Af	 0.7430	 0.4900
Ag	 0.6430	 0.5080
Ah	 0.8560	 0.5960
Ai	 0.8690	 0.6040
Aj	 0.7680	 0.5230
Ak	 0.8180	 0.5960
Al	 0.3160	 0.2940
Am	 0.8860	 0.6270
An	 0.8800	 0.6310
Ao	 0.7990	 0.5420
Ap	 0.8460	 0.5760
Aq	 0.7250	 0.5510
Ar	 0.8200	 0.5640
As	 0.8520	 0.5830
At	 0.7390	 0.5270
Au	 0.8530	 0.6110
Av	 0.9430	 0.6510























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Chain	Atom inclusion	Q-score
Aw	 0.9120	 0.6380
Ax	 0.8280	 0.5500
Ay	 0.7210	 0.5460
Az	 0.8850	 0.6340
B5	 0.9010	 0.5820
B7	 0.9860	 0.6500
B8	 0.9430	 0.6250
BA	 0.9330	 0.6500
BB	 0.9210	 0.6470
BC	 0.9370	 0.6450
BD	 0.9080	 0.6190
BE	 0.8130	 0.5770
BF	 0.9430	 0.6560
BG	 0.8290	 0.5900
BH	 0.8980	 0.6340
BI	 0.8850	 0.6430
BJ	 0.8680	 0.6220
BK	 0.4100	 0.4710
BL	 0.8760	 0.6160
BM	 0.9080	 0.6220
BN	 0.9750	 0.6620
BO	 0.9420	 0.6520
BP	 0.8990	 0.6400
BQ	 0.9400	 0.6520
BR	 0.8630	 0.6040
BS	 0.9460	 0.6560
BT	 0.8890	 0.6210
BU	 0.8210	 0.5660
BV	 0.8840	 0.6410
BW	 0.5050	 0.4500
BX	 0.9030	 0.6360
BY	 0.9010	 0.6330
BZ	 0.9090	 0.6370
Ba	 0.9630	 0.6560
Bb	 0.7560	 0.5580
Bc	 0.8070	 0.5920
Bd	 0.8820	 0.6290
Be	 0.9380	 0.6460
Bf	 0.9500	 0.6570
Bg	 0.9060	 0.6290
Bh	 0.8920	 0.6290
Bi	 0.8670	 0.6150

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Chain	Atom inclusion	Q-score
Bj	 0.9640	 0.6530
Bk	 0.7850	 0.5750
Bl	 0.9280	 0.6400
Bm	 0.9240	 0.6420
Bo	 0.8970	 0.6490
Bp	 0.8950	 0.6420
Br	 0.9360	 0.6430
Bs	 0.0060	 0.0310
Bt	 0.0020	 0.0450
Bv	 0.0720	 0.1750