



Full wwPDB EM Validation Report ⓘ

Jun 21, 2026 – 12:55 pm BST

PDB ID : 8Q7Z / pdb_00008q7z
EMDB ID : EMD-18168
Title : Structure of the G. gallus 80S non-rotated ribosome
Authors : Nurullina, L.; Jenner, L.; Yusupov, M.
Deposited on : 2023-08-17
Resolution : 2.50 Å (reported)
Based on initial model : 7O7Z

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

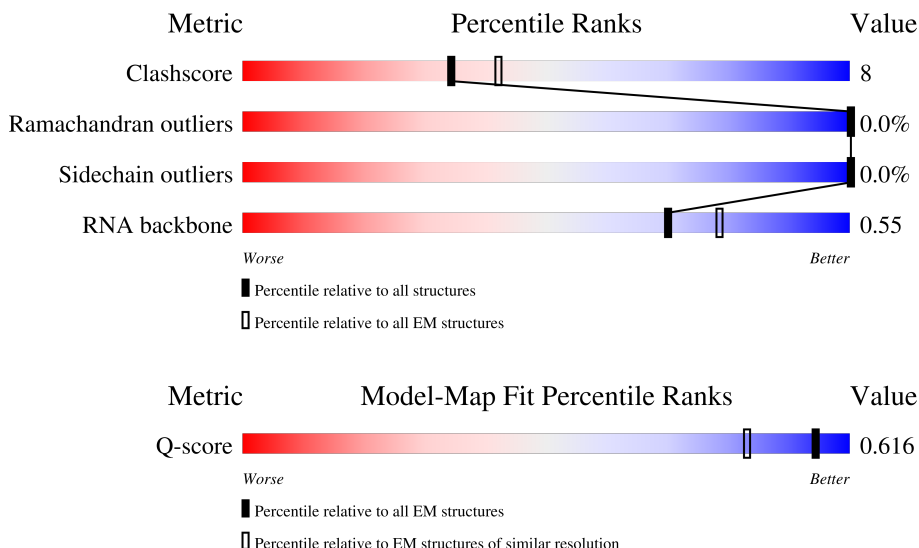
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.50 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	7115 (2.00 - 3.00)

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	B5	4441	
2	B8	157	
3	B7	119	

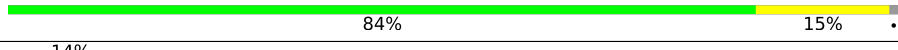
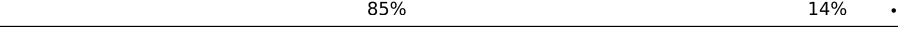
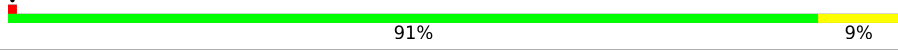
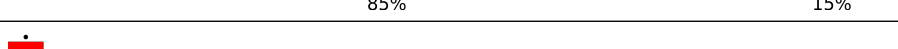
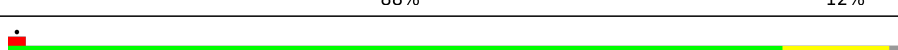
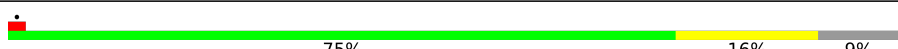
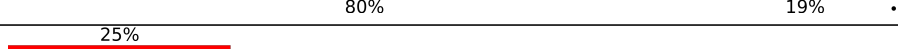
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Mol	Chain	Length	Quality of chain
4	Az	25	
5	BA	257	
6	BB	403	
7	BC	421	
8	BD	297	
9	BE	298	
10	BF	246	
11	BG	266	
12	BH	192	
13	BI	214	
14	BJ	178	
15	BL	211	
16	BM	131	
17	BN	204	
18	BO	203	
19	BP	184	
20	BQ	187	
21	BR	196	
22	BS	176	
23	BT	160	
24	BU	128	
25	BV	140	
26	BW	157	
27	BX	155	
28	BY	145	

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Mol	Chain	Length	Quality of chain
29	BZ	136	
30	Ba	148	
31	Bb	71	
32	Bc	115	
33	Bd	176	
34	Be	135	
35	Bf	110	
36	Bg	117	
37	Bh	123	
38	Bi	105	
39	Bj	97	
40	Bk	70	
41	Bl	51	
42	Bm	128	
43	Bo	105	
44	Bp	92	
45	Br	138	
46	A2	1823	
47	Aa	264	
48	AA	84	
49	AB	69	
50	Ab	264	
51	Ad	263	
52	AD	133	
53	AE	115	

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Mol	Chain	Length	Quality of chain
54	Af	249	
55	Ag	194	
56	Ah	207	
57	Ai	194	
58	Ak	158	
59	Am	151	
60	An	151	
61	At	119	
62	Au	84	
63	Av	130	
64	Aw	143	
65	Ax	131	
66	AZ	296	
67	Ap	146	
68	AC	156	
69	Ae	204	
70	AF	317	
71	AG	171	
72	Aj	165	
73	Al	132	
74	Ao	145	
75	Ar	152	
76	As	145	
77	Ay	125	
78	Ac	243	

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Mol	Chain	Length	Quality of chain
79	V	76	
80	Aq	135	

2 Entry composition [i](#)

There are 83 unique types of molecules in this entry. The entry contains 216968 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 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B5	3562	Total	C	N	O	P	0	0
			76444	34065	13971	24846	3562		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B5	3295	UY1	U	modified residue	GB KT445934.2

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B8	157	Total	C	N	O	P	0	0
			3338	1490	588	1103	157		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B7	119	Total	C	N	O	P	0	0
			2536	1130	449	838	119		

- Molecule 4 is a protein called 60S ribosomal protein L41.

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

- Molecule 5 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	BA	248	Total	C	N	O	S	0	0
			1898	1191	387	314	6		

- Molecule 6 is a protein called Ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	BB	398	Total	C	N	O	S	0	0
			3209	2042	603	550	14		

- Molecule 7 is a protein called 60S ribosomal protein L4 C-terminal domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	BC	361	Total	C	N	O	S	0	0
			2888	1816	574	484	14		

- Molecule 8 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	BD	296	Total	C	N	O	S	0	0
			2388	1506	437	433	12		

- Molecule 9 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	BE	224	Total	C	N	O	S	0	0
			1811	1161	353	295	2		

- Molecule 10 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	BF	234	Total	C	N	O	S	0	0
			1939	1245	377	309	8		

- Molecule 11 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	BG	210	Total	C	N	O	S	0	0
			1704	1089	326	284	5		

- Molecule 12 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	BH	192	Total	C	N	O	S	0	0
			1533	962	288	277	6		

- Molecule 13 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	BI	205	Total	C	N	O	S	0	0
			1654	1050	322	268	14		

- Molecule 14 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	BJ	170	Total	C	N	O	S	0	0
			1362	861	255	241	5		

- Molecule 15 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	BL	210	Total	C	N	O	S	0	0
			1710	1072	354	279	5		

- Molecule 16 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	BM	130	Total	C	N	O	S	0	0
			1077	688	209	172	8		

- Molecule 17 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	BN	203	Total	C	N	O	S	0	0
			1700	1071	359	266	4		

- Molecule 18 is a protein called Ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	BO	201	Total	C	N	O	S	0	0
			1643	1058	321	259	5		

- Molecule 19 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	BP	155	Total	C	N	O	S	0	0
			1259	788	244	218	9		

- Molecule 20 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	BQ	187	Total	C	N	O	S	0	0
			1503	939	314	245	5		

- Molecule 21 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	BR	180	Total	C	N	O	S	0	0
			1503	930	325	238	10		

- Molecule 22 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BS	176	Total	C	N	O	S	0	0
			1464	931	286	236	11		

- Molecule 23 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	BT	159	Total	C	N	O	S	0	0
			1299	825	252	216	6		

- Molecule 24 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BU	100	Total	C	N	O	S	0	0
			817	523	143	149	2		

- Molecule 25 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BV	134	Total	C	N	O	S	0	0
			993	625	187	176	5		

- Molecule 26 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BW	67	Total	C	N	O	S	0	0
			560	356	107	94	3		

- Molecule 27 is a protein called Ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BX	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 28 is a protein called Ribosomal protein L26 like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BY	133	Total	C	N	O	S	0	0
			1106	694	224	185	3		

- Molecule 29 is a protein called Large ribosomal subunit protein eL27.

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

- Molecule 30 is a protein called Ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ba	147	Total	C	N	O	S	0	0
			1179	748	240	187	4		

- Molecule 31 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Bb	70	Total	C	N	O	S	0	0
			582	360	126	94	2		

- Molecule 32 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Bc	95	Total	C	N	O	S	0	0
			738	468	131	133	6		

- Molecule 33 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Bd	105	Total	C	N	O	S	0	0
			867	549	168	148	2		

- Molecule 34 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Be	130	Total	C	N	O	S	0	0
			1074	681	219	169	5		

- Molecule 35 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Bf	110	Total	C	N	O	S	0	0
			886	559	178	144	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Bf	103	VAL	-	insertion	UNP A0A8V0YS49

- Molecule 36 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Bg	108	Total	C	N	O	S	0	0
			860	540	178	137	5		

- Molecule 37 is a protein called Large ribosomal subunit protein uL29.

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

- Molecule 38 is a protein called Large ribosomal subunit protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Bi	100	Total	C	N	O	S	0	0
			821	515	173	127	6		

- Molecule 39 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Bj	86	Total	C	N	O	S	0	0
			704	432	155	112	5		

- Molecule 40 is a protein called 60S ribosomal protein L38.

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

- Molecule 41 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Bl	50	Total	C	N	O	S	0	0
			442	281	96	64	1		

- Molecule 42 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Bm	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 43 is a protein called Ribosomal protein L36a like.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Bo	105	Total	C	N	O	S	0	0
			861	540	177	138	6		

- Molecule 44 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Bp	91	Total	C	N	O	S	0	0
			706	445	134	120	7		

- Molecule 45 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Br	126	Total	C	N	O	S	0	0
			1025	635	218	169	3		

- Molecule 46 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	A2	1676	Total	C	N	O	P	0	0
			35806	16005	6419	11706	1676		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A2	1206	B8N	U	modified residue	GB KT445934.2
A2	1295	4AC	C	modified residue	GB KT445934.2
A2	1796	4AC	C	modified residue	GB KT445934.2

- Molecule 47 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Aa	213	Total	C	N	O	S	0	0
			1730	1098	309	309	14		

- Molecule 48 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	AA	83	Total	C	N	O	S	0	0
			657	410	125	115	7		

- Molecule 49 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	AB	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 50 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Ab	219	Total	C	N	O	S	0	0
			1698	1099	291	299	9		

- Molecule 51 is a protein called Small ribosomal subunit protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Ad	262	Total	C	N	O	S	0	0
			2076	1324	387	357	8		

- Molecule 52 is a protein called Ribosomal protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	AD	57	Total	C	N	O	S	0	0
			452	279	99	73	1		

- Molecule 53 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	AE	99	Total	C	N	O	S	0	0
			793	492	165	131	5		

- Molecule 54 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Af	227	Total	C	N	O	S	0	0
			1838	1144	367	320	7		

- Molecule 55 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Ag	187	Total	C	N	O	S	0	0
			1500	956	276	267	1		

- Molecule 56 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Ah	206	Total	C	N	O	S	0	0
			1685	1059	332	289	5		

- Molecule 57 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Ai	179	Total	C	N	O	S	0	0
			1495	953	299	241	2		

- Molecule 58 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Ak	152	Total	C	N	O	S	0	0
			1236	784	233	213	6		

- Molecule 59 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 60 is a protein called Ribosomal protein S14.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
An	138	IAS	ASP	modified residue	UNP Q5ZHW8

- Molecule 61 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	At	102	Total	C	N	O	S	0	0
			811	508	154	145	4		

- Molecule 62 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Au	84	Total	C	N	O	S	0	0
			640	394	118	124	4		

- Molecule 63 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Av	129	Total	C	N	O	S	0	0
			1035	659	193	177	6		

- Molecule 64 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Aw	142	Total	C	N	O	S	0	0
			1104	696	220	185	3		

- Molecule 65 is a protein called 40S ribosomal protein S24.

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

- Molecule 66 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AZ	207	Total	C	N	O	S	0	0
			1626	1036	287	295	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AZ	2	ACE	-	acetylation	UNP P50890

- Molecule 67 is a protein called Ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Ap	141	Total	C	N	O	S	0	0
			1123	715	212	193	3		

- Molecule 68 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	AC	74	Total	C	N	O	S	0	0
			611	386	117	101	7		

- Molecule 69 is a protein called Ribosomal protein S5.

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

- Molecule 70 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	AF	311	Total	C	N	O	S	0	0
			2420	1526	422	460	12		

- Molecule 71 is a protein called 40S ribosomal protein S29.

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

- Molecule 72 is a protein called Ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Aj	96	Total	C	N	O	S	0	0
			812	532	143	131	6		

- Molecule 73 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Al	118	Total	C	N	O	S	0	0
			916	574	162	172	8		

- Molecule 74 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Ao	127	Total	C	N	O	S	0	0
			1044	663	197	177	7		

- Molecule 75 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Ar	144	Total	C	N	O	S	0	0
			1191	748	241	201	1		

- Molecule 76 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	As	143	Total	C	N	O	S	0	0
			1115	698	216	199	2		

- Molecule 77 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Ay	70	Total	C	N	O	S	0	0
			555	357	101	96	1		

- Molecule 78 is a protein called DNA-(apurinic or apyrimidinic site) lyase.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Ac	225	Total	C	N	O	S	0	0
			1752	1117	315	313	7		

- Molecule 79 is a RNA chain called Phe tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	V	76	Total	C	N	O	P	0	0
			1628	727	302	524	75		

- Molecule 80 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Aq	134	Total	C	N	O	S	0	0
			1081	678	201	197	5		

- Molecule 81 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
81	B5	346	Total	Mg	0
			346	346	
81	B8	9	Total	Mg	0
			9	9	
81	B7	11	Total	Mg	0
			11	11	
81	BA	3	Total	Mg	0
			3	3	
81	BH	1	Total	Mg	0
			1	1	
81	BI	2	Total	Mg	0
			2	2	
81	BN	2	Total	Mg	0
			2	2	
81	BP	2	Total	Mg	0
			2	2	
81	BV	1	Total	Mg	0
			1	1	
81	Ba	1	Total	Mg	0
			1	1	
81	Bb	2	Total	Mg	0
			2	2	
81	Be	1	Total	Mg	0
			1	1	
81	Bf	1	Total	Mg	0
			1	1	
81	Bg	1	Total	Mg	0
			1	1	
81	Bj	1	Total	Mg	0
			1	1	
81	Bo	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
81	A2	104	Total 104	Mg 104	0
81	Ak	1	Total 1	Mg 1	0
81	An	3	Total 3	Mg 3	0
81	As	1	Total 1	Mg 1	0

- Molecule 82 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 83 is water.

Mol	Chain	Residues	Atoms		AltConf
83	B5	4198	Total 4198	O 4198	0
83	B8	72	Total 72	O 72	0
83	B7	30	Total 30	O 30	0
83	Az	5	Total 5	O 5	0
83	BA	28	Total 28	O 28	0
83	BB	49	Total 49	O 49	0

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Mol	Chain	Residues	Atoms		AltConf
83	BC	45	Total 45	O 45	0
83	BD	22	Total 22	O 22	0
83	BE	11	Total 11	O 11	0
83	BF	24	Total 24	O 24	0
83	BG	15	Total 15	O 15	0
83	BH	15	Total 15	O 15	0
83	BI	13	Total 13	O 13	0
83	BJ	3	Total 3	O 3	0
83	BL	29	Total 29	O 29	0
83	BM	6	Total 6	O 6	0
83	BN	29	Total 29	O 29	0
83	BO	19	Total 19	O 19	0
83	BP	23	Total 23	O 23	0
83	BQ	24	Total 24	O 24	0
83	BR	9	Total 9	O 9	0
83	BS	21	Total 21	O 21	0
83	BT	21	Total 21	O 21	0
83	BU	2	Total 2	O 2	0
83	BV	17	Total 17	O 17	0
83	BW	4	Total 4	O 4	0
83	BX	5	Total 5	O 5	0

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Mol	Chain	Residues	Atoms		AltConf
83	BY	11	Total 11	O 11	0
83	BZ	5	Total 5	O 5	0
83	Ba	23	Total 23	O 23	0
83	Bb	11	Total 11	O 11	0
83	Bc	5	Total 5	O 5	0
83	Bd	9	Total 9	O 9	0
83	Be	17	Total 17	O 17	0
83	Bf	25	Total 25	O 25	0
83	Bg	9	Total 9	O 9	0
83	Bh	3	Total 3	O 3	0
83	Bi	8	Total 8	O 8	0
83	Bj	16	Total 16	O 16	0
83	Bl	5	Total 5	O 5	0
83	Bm	5	Total 5	O 5	0
83	Bo	15	Total 15	O 15	0
83	Bp	12	Total 12	O 12	0
83	Br	16	Total 16	O 16	0
83	A2	832	Total 832	O 832	0
83	Aa	10	Total 10	O 10	0
83	AA	8	Total 8	O 8	0
83	AB	1	Total 1	O 1	0

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Mol	Chain	Residues	Atoms		AltConf
83	Ab	11	Total 11	O 11	0
83	Ad	10	Total 10	O 10	0
83	AD	2	Total 2	O 2	0
83	AE	9	Total 9	O 9	0
83	Af	1	Total 1	O 1	0
83	Ah	7	Total 7	O 7	0
83	Ai	7	Total 7	O 7	0
83	Ak	10	Total 10	O 10	0
83	Am	4	Total 4	O 4	0
83	An	7	Total 7	O 7	0
83	At	3	Total 3	O 3	0
83	Au	2	Total 2	O 2	0
83	Av	10	Total 10	O 10	0
83	Aw	8	Total 8	O 8	0
83	Ax	4	Total 4	O 4	0
83	AZ	3	Total 3	O 3	0
83	Ap	1	Total 1	O 1	0
83	Ae	2	Total 2	O 2	0
83	AG	2	Total 2	O 2	0
83	Ar	1	Total 1	O 1	0
83	Ay	4	Total 4	O 4	0

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Mol	Chain	Residues	Atoms		AltConf
83	V	9	Total	O	0
			9	9	
83	Aq	4	Total	O	0
			4	4	

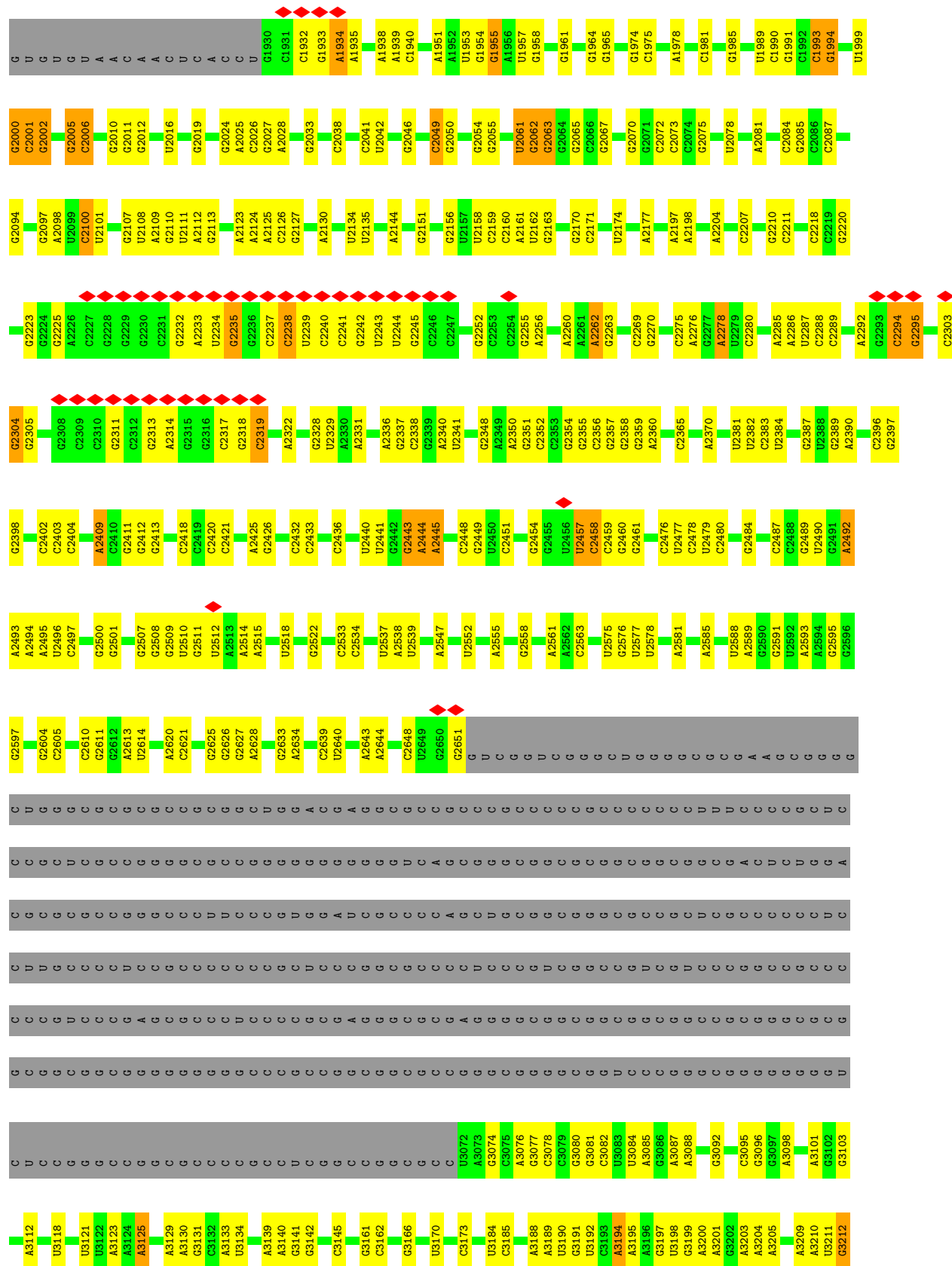
3 Residue-property plots

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

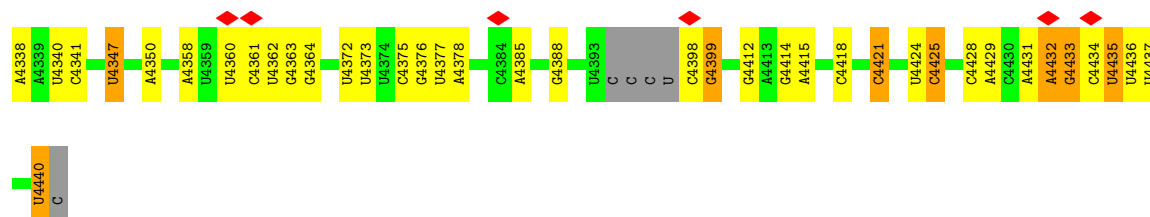
• Molecule 1: 28S rRNA



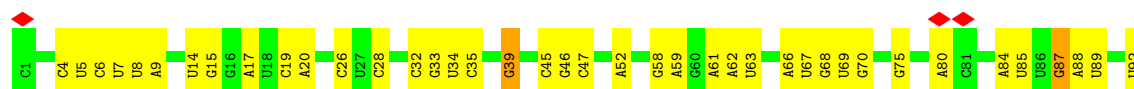




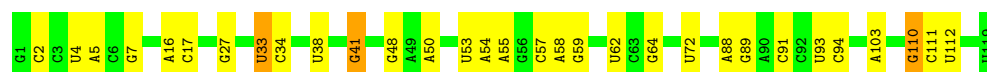
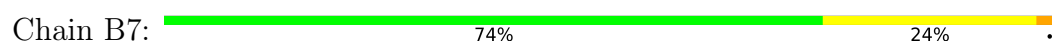




• Molecule 2: 5.8S rRNA



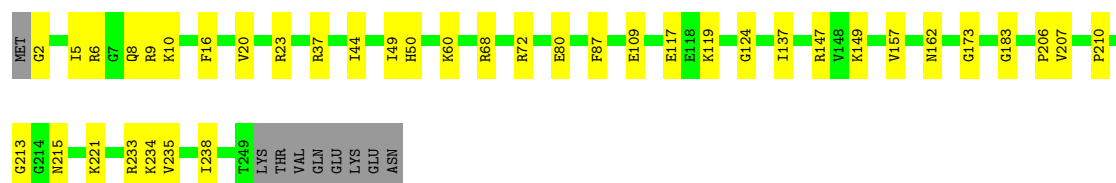
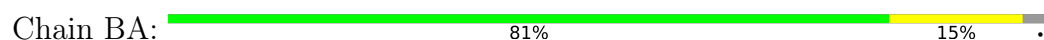
• Molecule 3: 5S rRNA



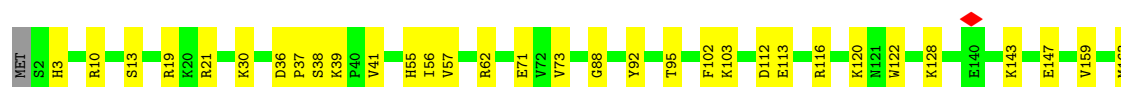
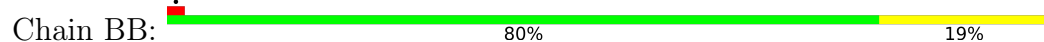
• Molecule 4: 60S ribosomal protein L41



• Molecule 5: 60S ribosomal protein L8

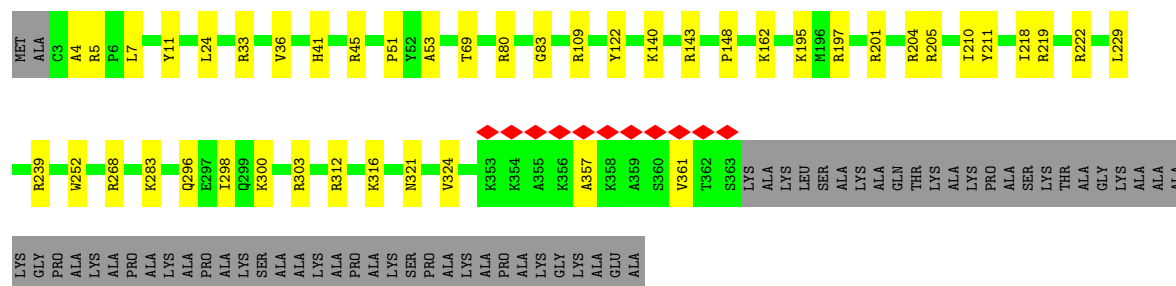


• Molecule 6: Ribosomal protein uL3

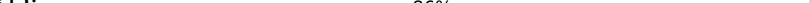


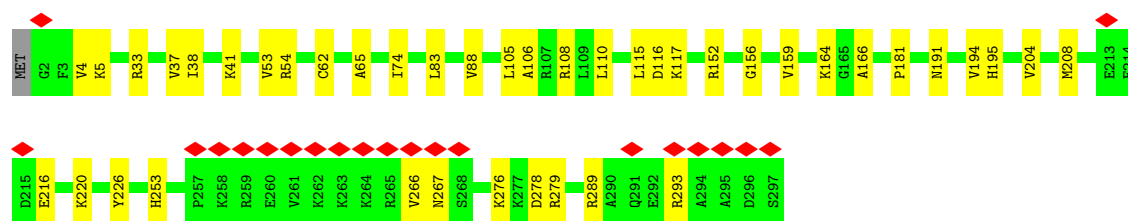
- Molecule 7: 60S ribosomal protein L4 C-terminal domain-containing protein

Chain BC:

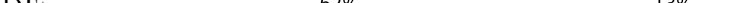


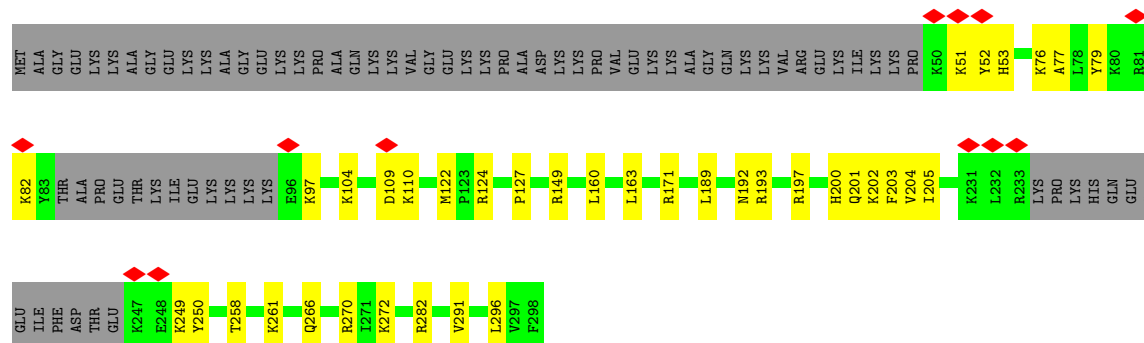
- Molecule 8: Large ribosomal subunit protein uL18

Chain BD: 



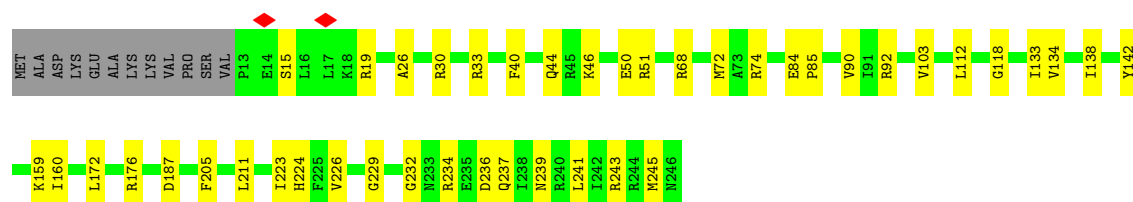
- Molecule 9: 60S ribosomal protein L6

Chain BE:  62% 13% 25%

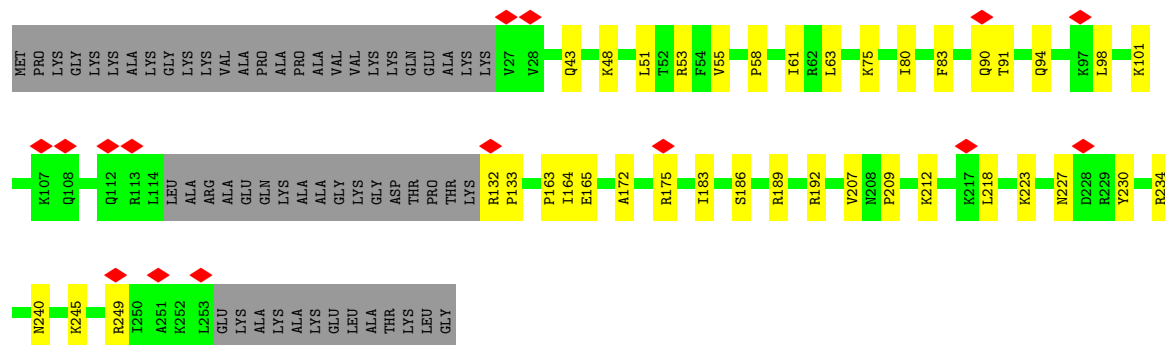


- Molecule 10: Large ribosomal subunit protein uL30

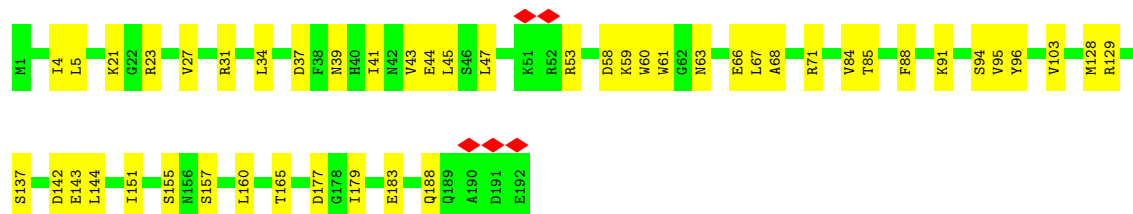
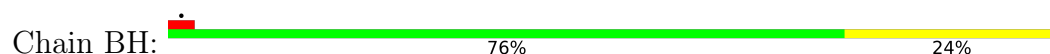
Chain BF: 78% 17% 5%



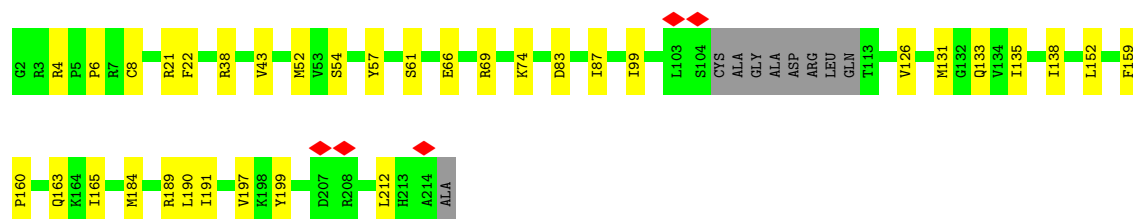
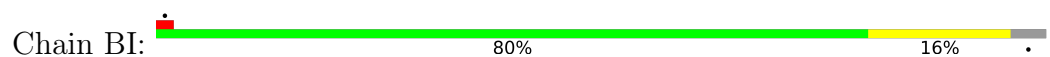
- Molecule 11: Large ribosomal subunit protein eL8



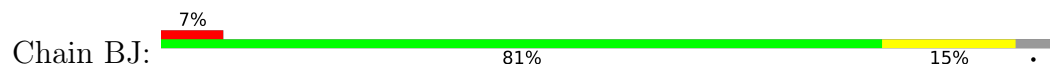
- Molecule 12: 60S ribosomal protein L9

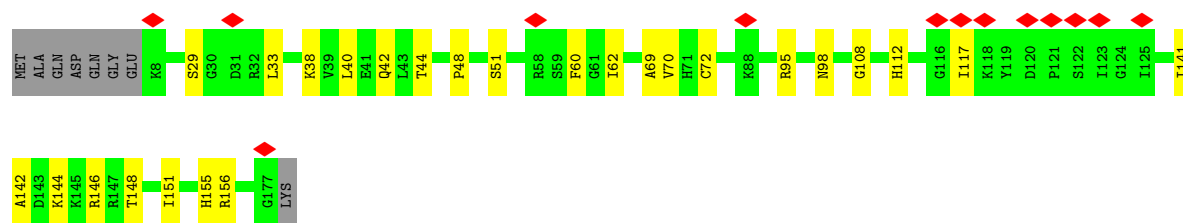


- Molecule 13: Large ribosomal subunit protein uL16

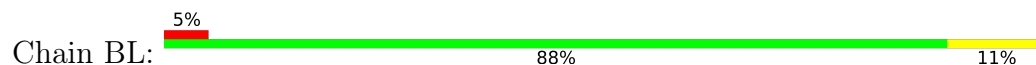


- Molecule 14: 60S ribosomal protein L11

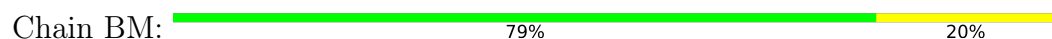




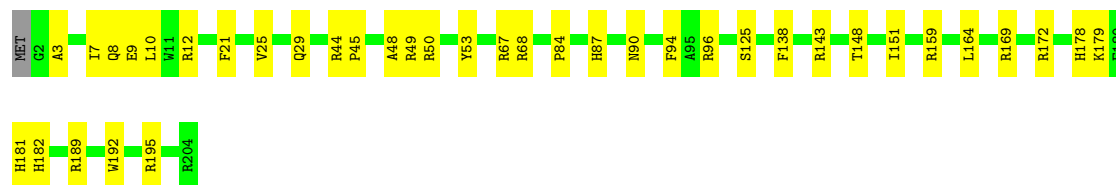
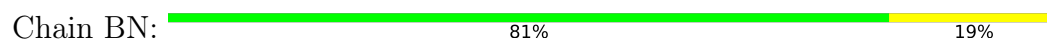
- Molecule 15: Large ribosomal subunit protein eL13



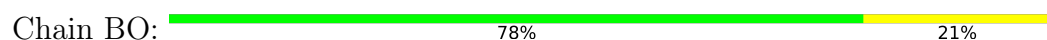
- Molecule 16: 60S ribosomal protein L14



- Molecule 17: Ribosomal protein L15



- Molecule 18: Ribosomal protein uL13



- Molecule 19: 60S ribosomal protein L17



LYS
LYS
LYS
ILE
SER
GLN
LYS
LYS
LEU
LYS
LYS
GLN
LYS
LEU
MET
ALA
ARG
GLU

• Molecule 20: Ribosomal protein L18

Chain BQ: 85% 15%

G2 K9 K12 K15 K19 D22 L35 R38 T39 N40 K49 R65 L72 R75 V82 A102 R112 R115 K132 R143 V148 K154 P159 T163 S169 K173 A177 R179 R184 R188

• Molecule 21: Ribosomal protein L19

Chain BR: 10% 80% 12% 8%

MET S2 N36 S37 Q40 K46 R60 I78 M96 M99 R104 L105 R108 Y109 R117 L138 M139 D157 E160 A161 R162 R163 S164 K165 T166 K167 E168 A169 R170 K171 R172 R173 E174 E175 R176 L177 Q178 A179 K180 K181 GLU GLU ILE ILE LYS THR LEU

SER
LYS
GLU
GLU
THR
LYS
LYS

• Molecule 22: 60S ribosomal protein L18a

Chain BS: 85% 15%

M1 G5 C16 L17 P18 T19 P20 K21 M30 F47 L51 M54 T71 R74 V75 K76 M93 R98 T101 G104 R111 H117 V142 R157 V158 R161 Q162 H163 K164 M173 T174 F175 F176

• Molecule 23: 60S ribosomal protein L21

Chain BT: 78% 21%

MET T2 K5 G6 R17 H22 L27 Y30 M31 R32 I33 Y34 K35 K36 K43 G51 H54 M66 V67 T68 Q69 H70 K78 R79 V80 K81 G82 K83 K87 R88 R92 I93 T96 K97 H98 Q107 R108 E111 K117 K120 E121 K122 G123

I124 W125 V126 K129 R136 L151 A160

• Molecule 24: Large ribosomal subunit protein eL22

Chain BU: 10% 57% 21% 22%

MET ALA PRO VAL LYS LYS PRO ALA ALA LYS GLY GLY LYS LYS LYS Q17 V18 L19 K20 P21 T22 L23 D24 D31 G32 I33 M34 Q35 F39 E40 K48 A53 G54 N55 G58 G59 V60 V61 S66 K67 S68 K69 V72 E75 K80 L83 K84 Y85 L86

T87 K88 K89 R97 D98 W99 V102 N105 Y110 E111 L112 R113 Q116 ILE ASN GLN ASP ASP LYS GLU GLU GLU GLU GLU ASP

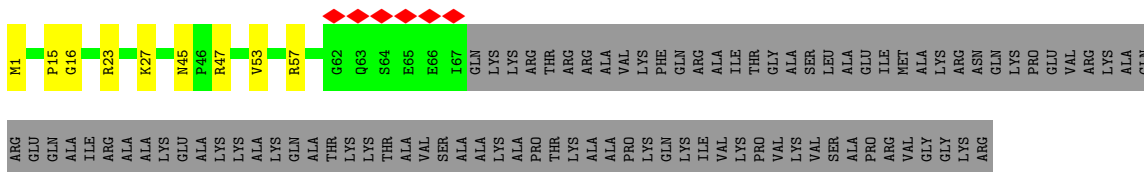
• Molecule 25: Large ribosomal subunit protein uL14

Chain BV:  79% 16% .



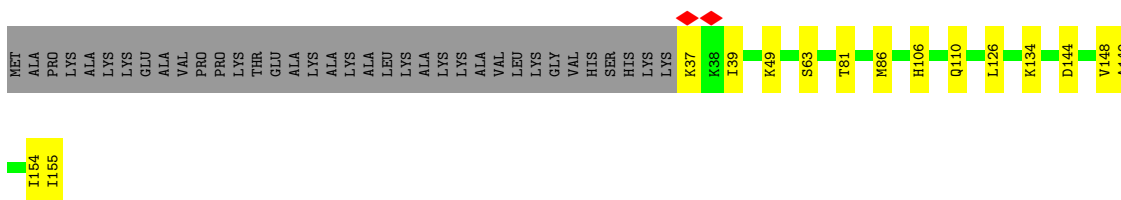
- Molecule 26: Ribosomal protein L24

Chain BW:  37% 6% 57%



- Molecule 27: Ribosomal protein uL23

Chain BX: 67% 10% 23%



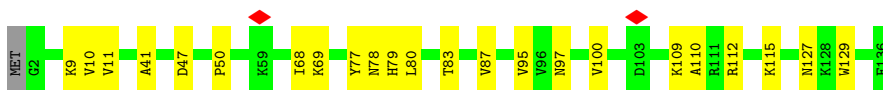
- Molecule 28: Ribosomal protein L26 like 1

Chain BY: 76% 16% 8%



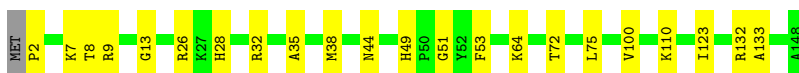
- Molecule 29: Large ribosomal subunit protein eL27

Chain BZ: 82% 17%

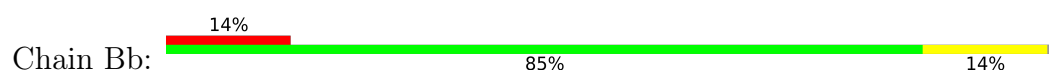


- Molecule 30: Ribosomal protein uL15

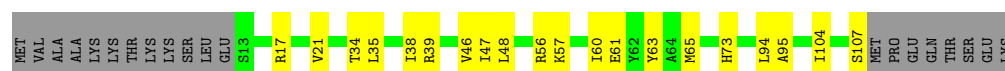
Chain Ba:  84% 15%



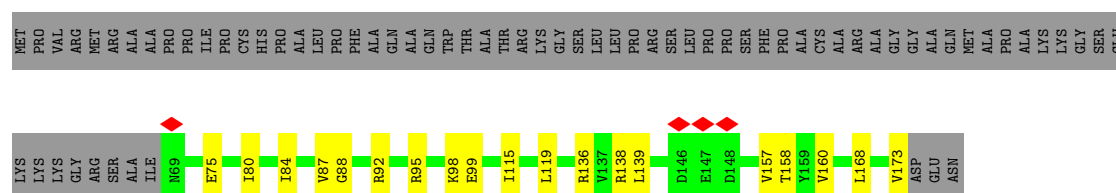
- Molecule 31: 60S ribosomal protein L29



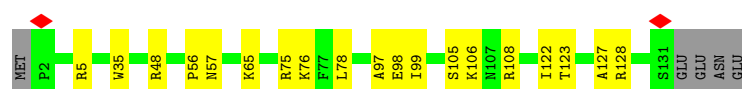
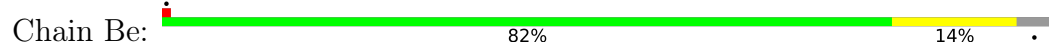
- Molecule 32: Large ribosomal subunit protein eL30



- Molecule 33: 60S ribosomal protein L31



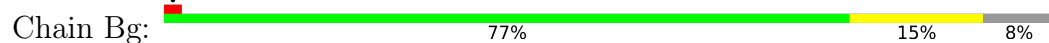
- Molecule 34: Ribosomal protein L32



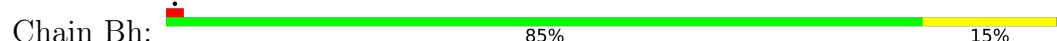
- Molecule 35: 60S ribosomal protein L35a



- Molecule 36: 60S ribosomal protein L34

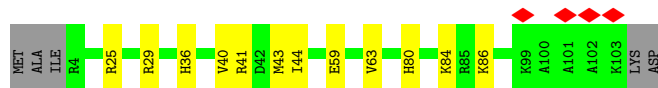
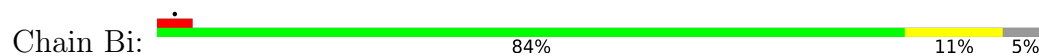


- Molecule 37: Large ribosomal subunit protein uL29

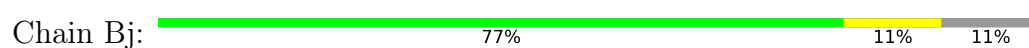




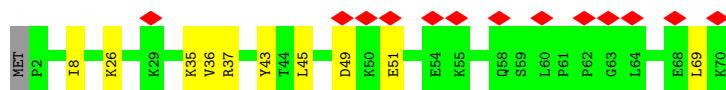
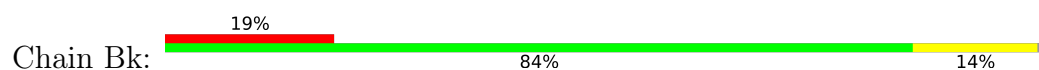
- Molecule 38: Large ribosomal subunit protein eL36



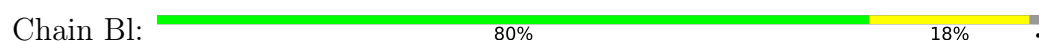
- Molecule 39: Ribosomal protein L37



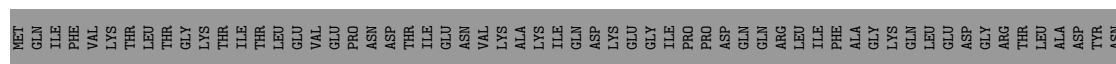
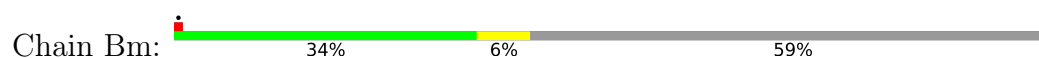
- Molecule 40: 60S ribosomal protein L38



- Molecule 41: Large ribosomal subunit protein eL39



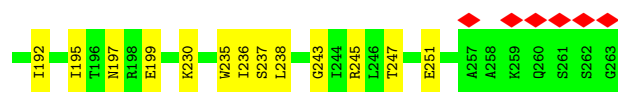
- Molecule 42: Ubiquitin-60S ribosomal protein L40



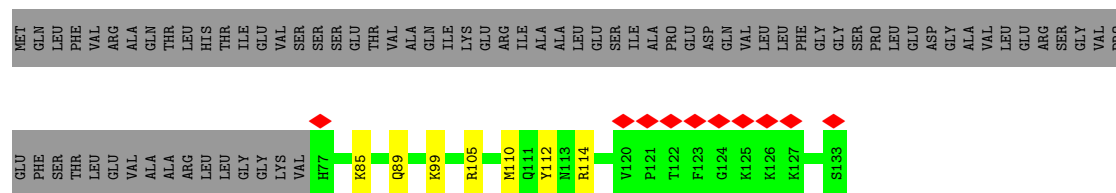
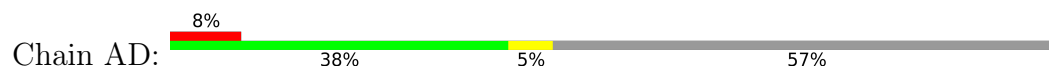
- Molecule 43: Ribosomal protein L36a like



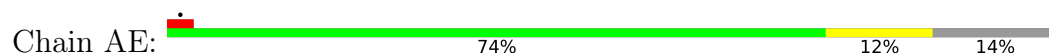




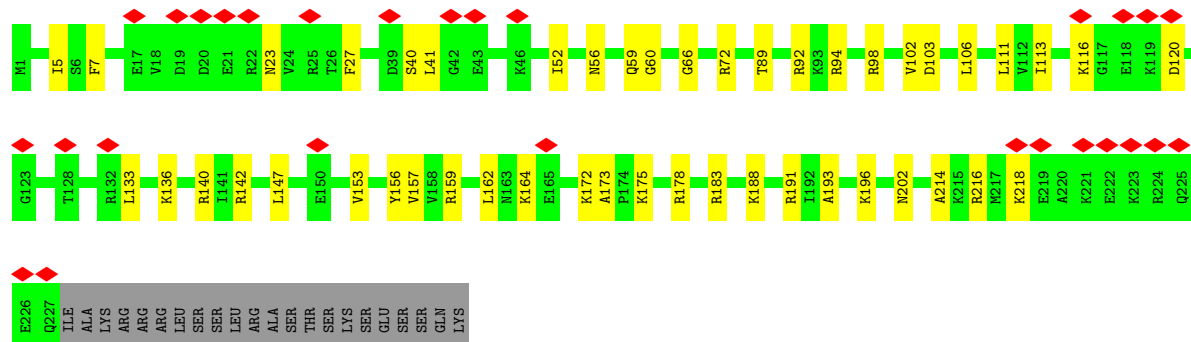
• Molecule 52: Ribosomal protein eS30



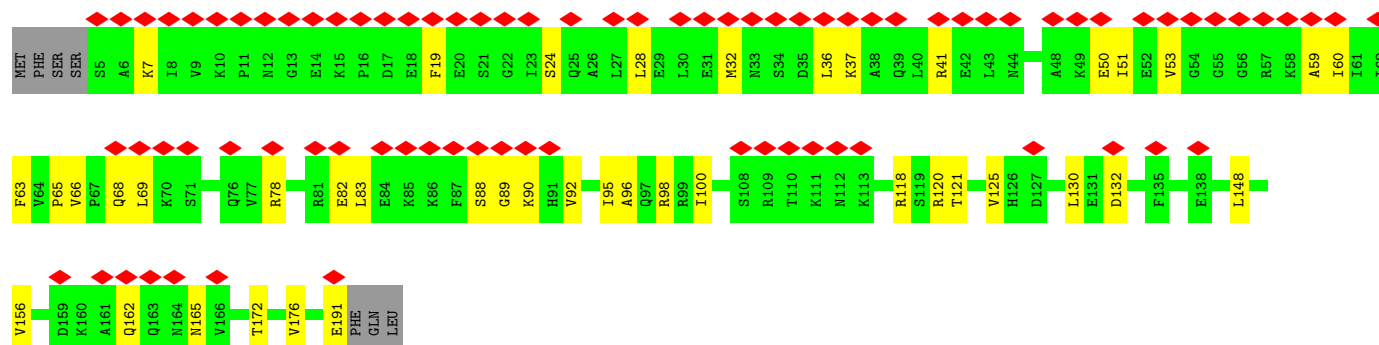
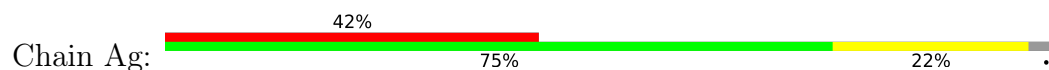
• Molecule 53: 40S ribosomal protein S26



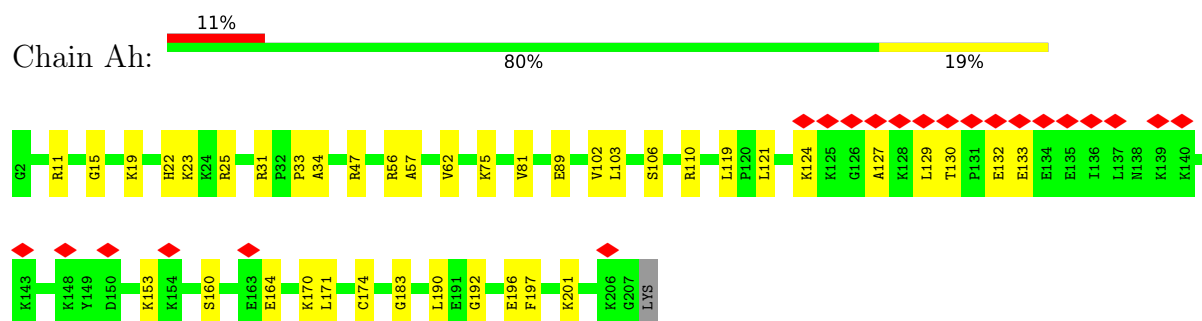
• Molecule 54: Small ribosomal subunit protein eS6



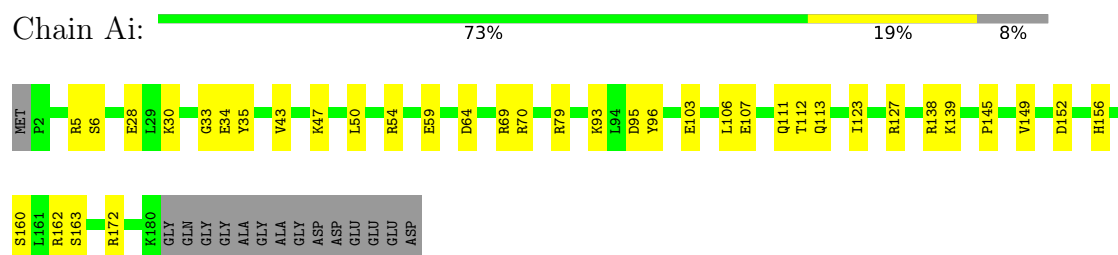
• Molecule 55: 40S ribosomal protein S7



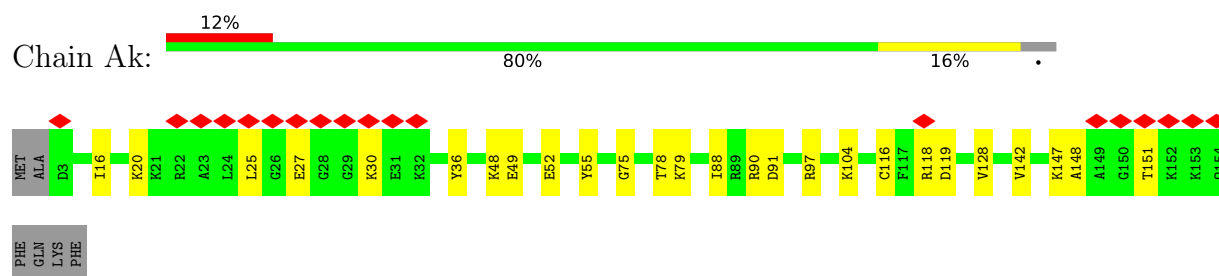
- Molecule 56: 40S ribosomal protein S8



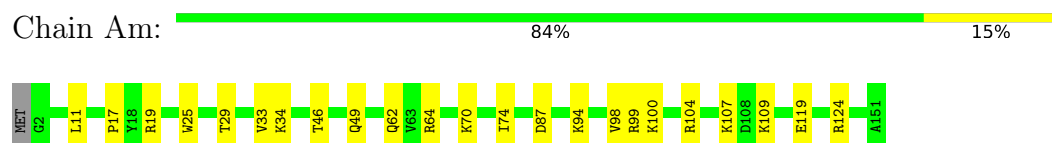
- Molecule 57: 40S ribosomal protein S9



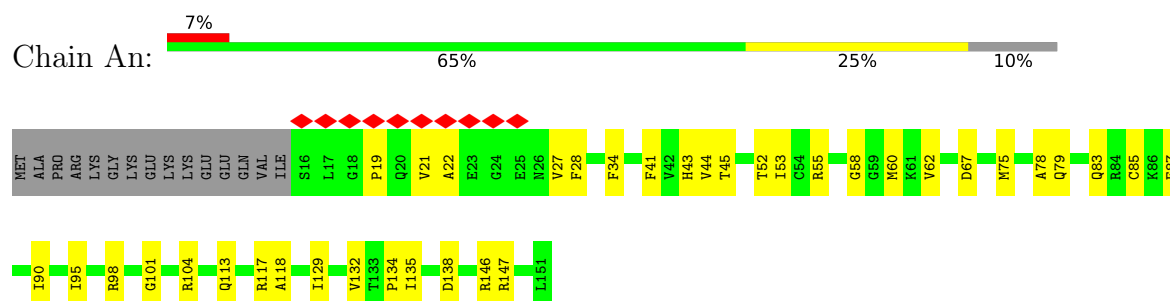
- Molecule 58: 40S ribosomal protein S11



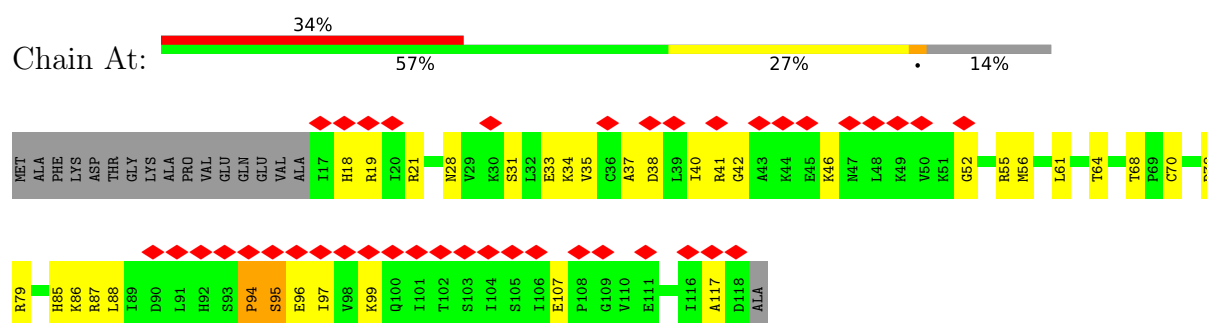
- Molecule 59: Small ribosomal subunit protein uS15



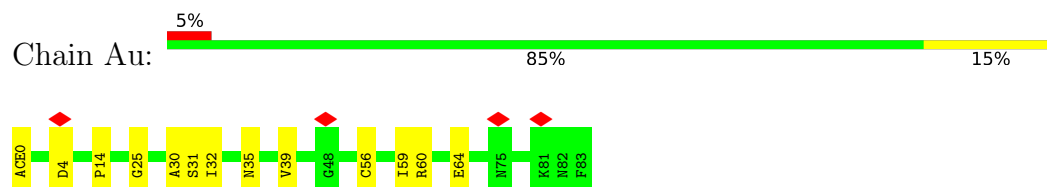
- Molecule 60: Ribosomal protein S14



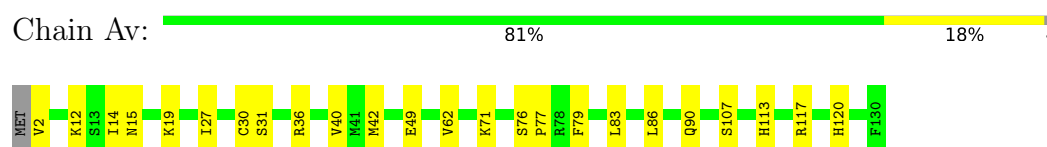
- Molecule 61: 40S ribosomal protein S20



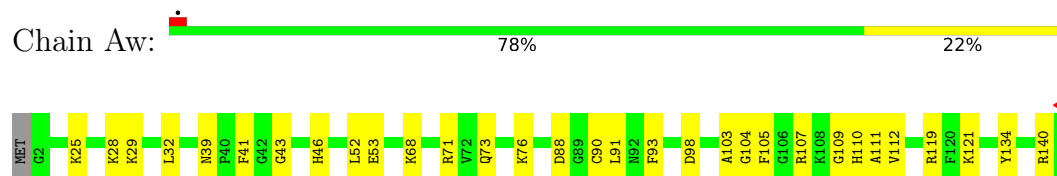
- Molecule 62: Small ribosomal subunit protein eS21



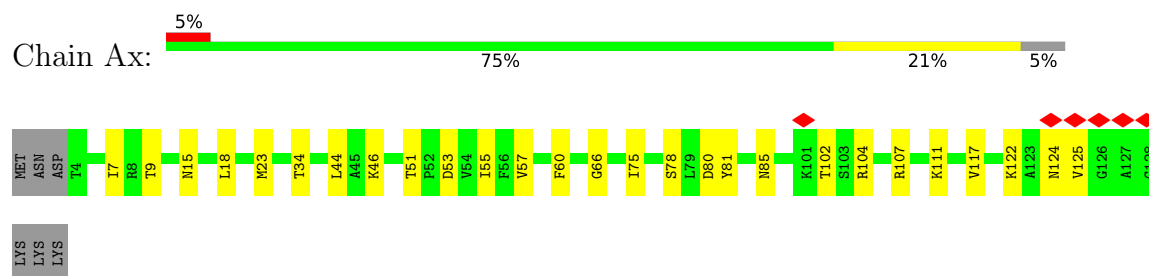
- Molecule 63: 40S ribosomal protein S15a



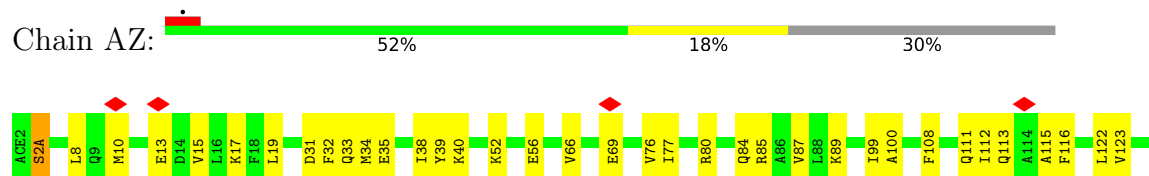
- Molecule 64: Small ribosomal subunit protein uS12

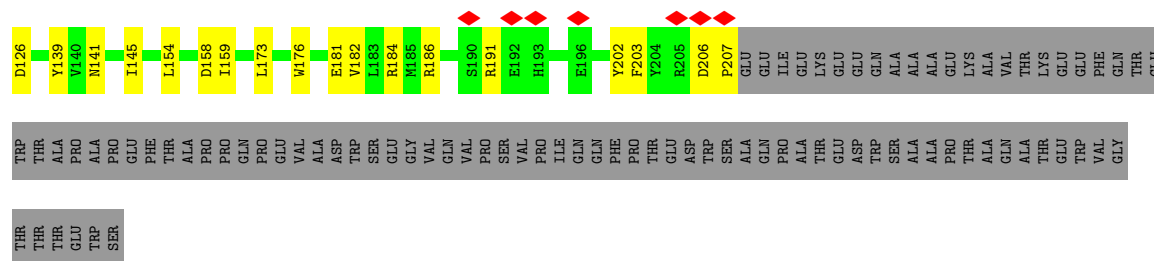


- Molecule 65: 40S ribosomal protein S24

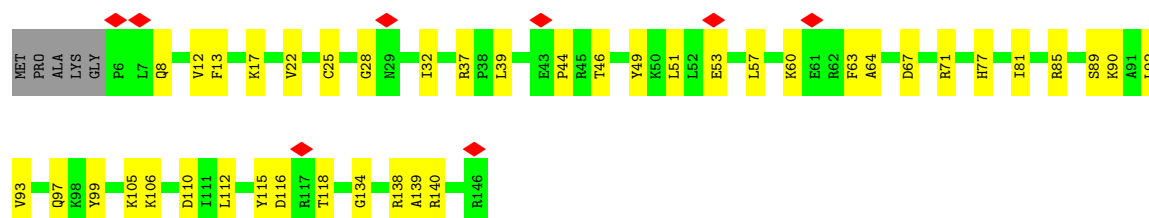
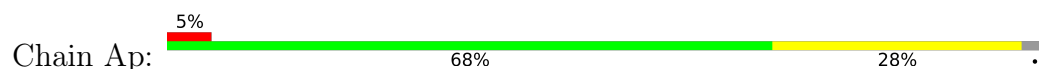


- Molecule 66: Small ribosomal subunit protein uS2

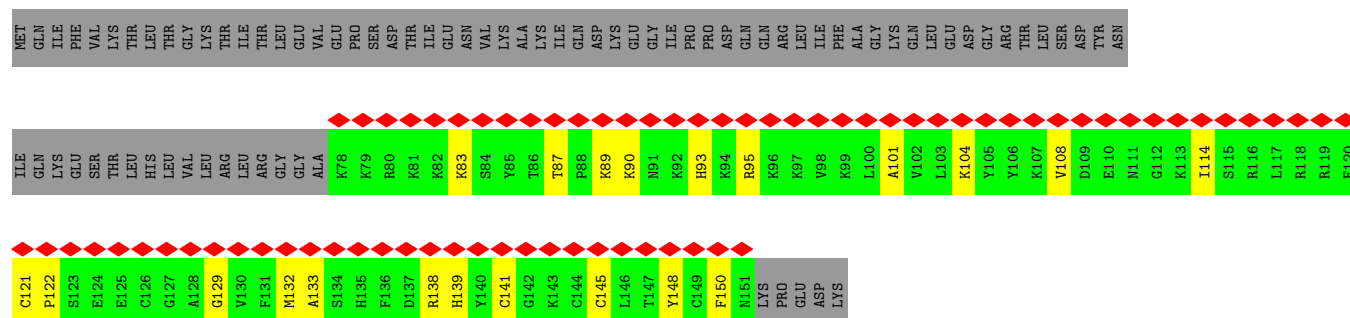
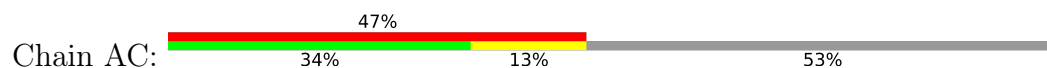




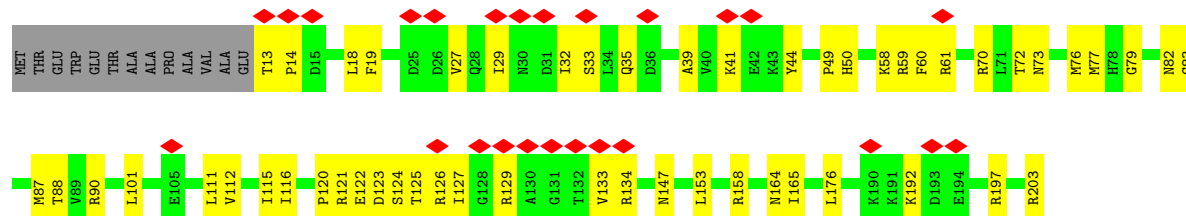
- Molecule 67: Ribosomal protein S16



- Molecule 68: Ubiquitin



- Molecule 69: Ribosomal protein S5

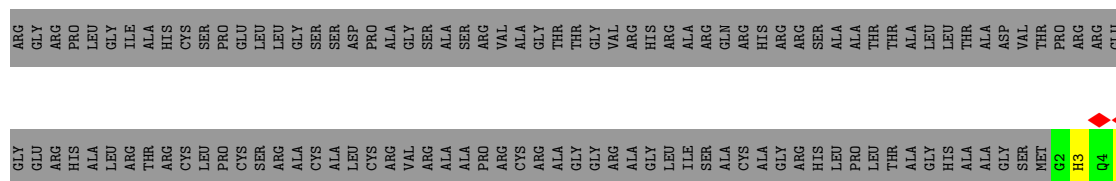


- Molecule 70: Small ribosomal subunit protein RACK1

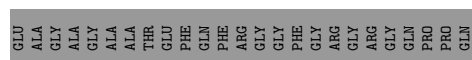
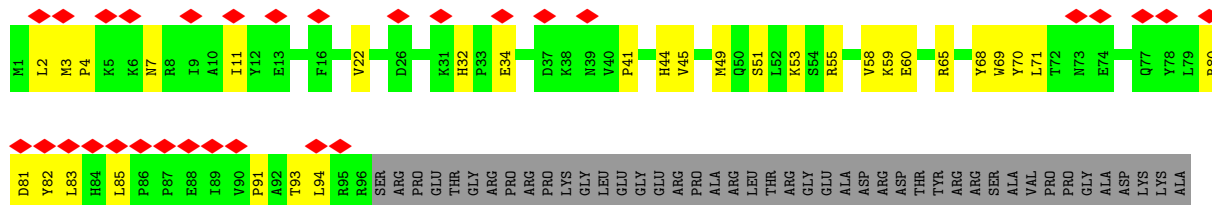




• Molecule 71: 40S ribosomal protein S29



• Molecule 72: Ribosomal protein S10

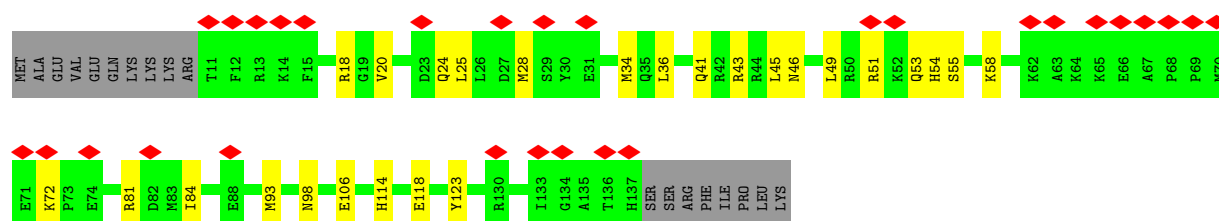
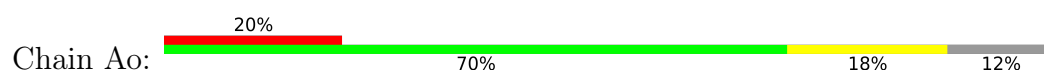


• Molecule 73: Small ribosomal subunit protein eS12

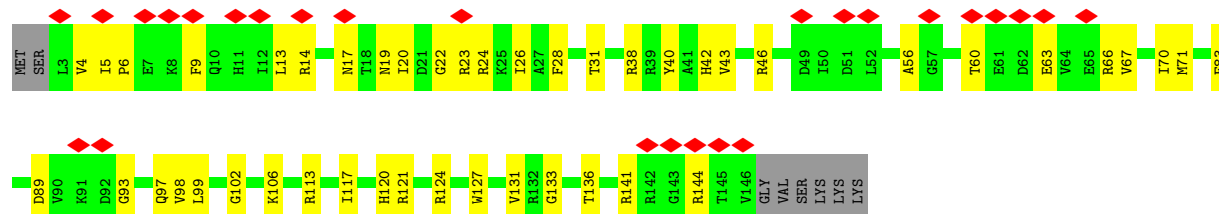




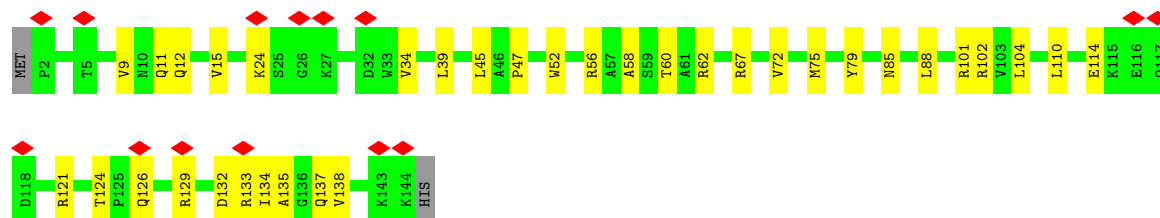
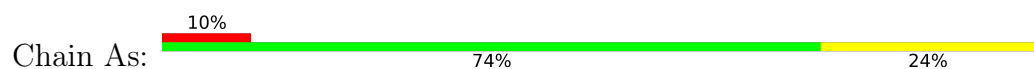
• Molecule 74: Small ribosomal subunit protein uS19



• Molecule 75: 40S ribosomal protein S18

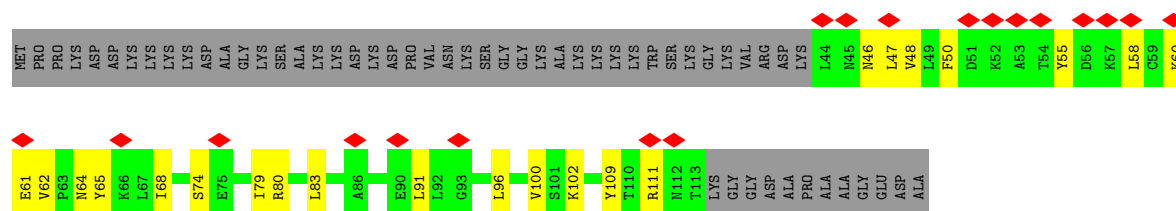


• Molecule 76: 40S ribosomal protein S19

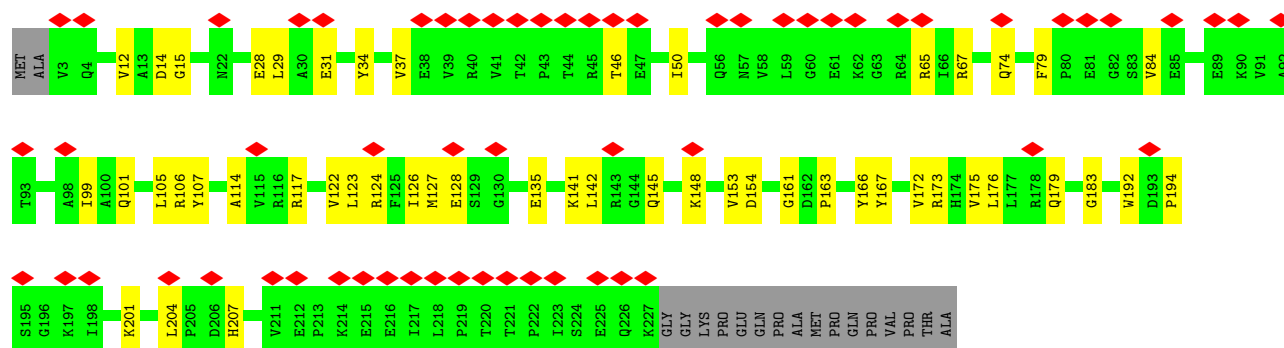
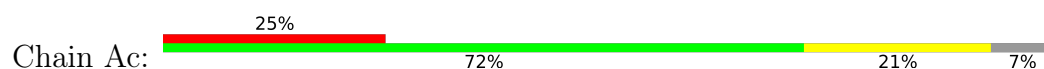


• Molecule 77: 40S ribosomal protein S25

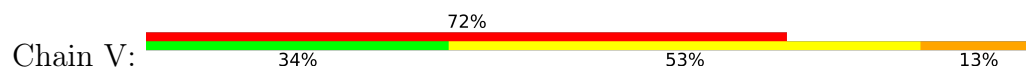




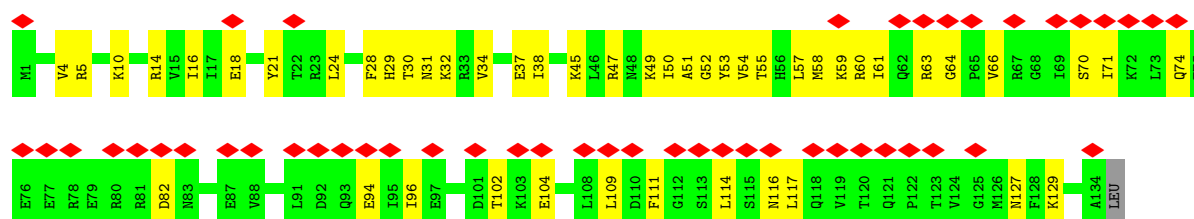
• Molecule 78: DNA-(apurinic or apyrimidinic site) lyase



• Molecule 79: Phe tRNA



• Molecule 80: Small ribosomal subunit protein eS17



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	122598	Depositor
Resolution determination method	FSC 3 SIGMA CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	96000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	2.826	Depositor
Minimum map value	-0.288	Depositor
Average map value	0.021	Depositor
Map value standard deviation	0.063	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	465.74, 465.74, 465.74	wwPDB
Map dimensions	580, 580, 580	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.803, 0.803, 0.803	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NMM, HIC, ZN, PSU, 6MZ, B8N, 4AC, OMU, MG, OMG, MA6, 1MA, UR3, IAS, MLZ, UY1, ACE, OMC, 5MC, A2M

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	B5	0.15	0/83215	0.27	0/129832
2	B8	0.11	0/3656	0.24	0/5693
3	B7	0.12	0/2832	0.24	0/4413
4	Az	0.14	0/240	0.38	0/305
5	BA	0.14	0/1937	0.35	0/2597
6	BB	0.13	0/3264	0.31	0/4363
7	BC	0.13	0/2942	0.31	0/3950
8	BD	0.12	0/2431	0.31	0/3255
9	BE	0.11	0/1845	0.28	0/2466
10	BF	0.15	0/1975	0.34	0/2634
11	BG	0.13	0/1736	0.32	0/2342
12	BH	0.13	0/1552	0.30	0/2086
13	BI	0.13	0/1694	0.30	0/2264
14	BJ	0.12	0/1385	0.33	0/1852
15	BL	0.12	0/1742	0.30	0/2324
16	BM	0.13	0/1097	0.30	0/1460
17	BN	0.13	0/1745	0.29	0/2337
18	BO	0.14	0/1675	0.34	0/2239
19	BP	0.13	0/1285	0.33	0/1723
20	BQ	0.13	0/1527	0.31	0/2038
21	BR	0.14	0/1519	0.31	0/2007
22	BS	0.13	0/1503	0.32	0/2016
23	BT	0.13	0/1327	0.28	0/1771
24	BU	0.14	0/831	0.35	0/1115
25	BV	0.12	0/1007	0.32	0/1350
26	BW	0.12	0/573	0.32	0/763
27	BX	0.11	0/993	0.32	0/1334
28	BY	0.13	0/1123	0.33	0/1493
29	BZ	0.11	0/1130	0.24	0/1507
30	Ba	0.12	0/1209	0.30	0/1615
31	Bb	0.13	0/593	0.34	0/782

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Bc	0.12	0/748	0.29	0/1004
33	Bd	0.13	0/882	0.30	0/1187
34	Be	0.11	0/1093	0.27	0/1457
35	Bf	0.12	0/905	0.29	0/1211
36	Bg	0.12	0/870	0.32	0/1159
37	Bh	0.27	0/1023	0.35	0/1351
38	Bi	0.13	0/832	0.31	0/1100
39	Bj	0.13	0/718	0.35	0/948
40	Bk	0.12	0/575	0.31	0/761
41	Bl	0.12	0/452	0.26	0/596
42	Bm	0.10	0/435	0.29	0/575
43	Bo	0.12	0/864	0.29	0/1139
44	Bp	0.12	0/716	0.30	0/950
45	Br	0.14	0/1042	0.30	0/1398
46	A2	0.14	2/39049 (0.0%)	0.26	0/60848
47	Aa	0.12	0/1757	0.33	0/2352
48	AA	0.10	0/670	0.27	0/897
49	AB	0.11	0/508	0.31	0/680
50	Ab	0.12	0/1734	0.30	0/2342
51	Ad	0.11	0/2118	0.28	0/2848
52	AD	0.09	0/458	0.33	0/602
53	AE	0.12	0/806	0.31	0/1080
54	Af	0.11	0/1861	0.29	0/2481
55	Ag	0.12	0/1522	0.34	0/2039
56	Ah	0.12	0/1715	0.32	0/2289
57	Ai	0.13	0/1520	0.34	0/2030
58	Ak	0.12	0/1257	0.29	0/1680
59	Am	0.11	0/1232	0.25	0/1656
60	An	0.12	0/1020	0.34	0/1366
61	At	0.13	0/821	0.40	0/1103
62	Au	0.12	0/644	0.28	0/863
63	Av	0.13	0/1052	0.30	0/1408
64	Aw	0.19	0/1122	0.39	0/1498
65	Ax	0.11	0/1032	0.27	0/1371
66	AZ	0.14	0/1661	0.33	0/2259
67	Ap	0.13	0/1141	0.36	0/1527
68	AC	0.16	0/623	0.39	0/823
69	Ae	0.13	0/1531	0.37	0/2059
70	AF	0.12	0/2477	0.37	0/3372
71	AG	0.13	0/470	0.32	0/623
72	Aj	0.14	0/836	0.36	0/1128
73	Al	0.18	0/926	0.45	0/1244
74	Ao	0.11	0/1065	0.31	0/1424

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	Ar	0.15	0/1209	0.38	0/1620
76	As	0.17	0/1120	0.36	0/1499
77	Ay	0.20	0/561	0.36	0/755
78	Ac	0.12	0/1780	0.32	0/2396
79	V	0.10	0/1822	0.25	0/2841
80	Aq	0.14	0/1095	0.35	0/1469
All	All	0.14	2/222953 (0.0%)	0.29	0/327234

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	A2	99	A2M	O3'-P	5.04	1.61	1.56
46	A2	1284	OMU	O3'-P	5.03	1.61	1.56

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B5	76444	0	38695	1072	0
2	B8	3338	0	1695	47	0
3	B7	2536	0	1284	24	0
4	Az	239	0	288	6	0
5	BA	1898	0	1995	30	0
6	BB	3209	0	3351	58	0
7	BC	2888	0	3057	46	0
8	BD	2388	0	2424	30	0
9	BE	1811	0	1973	28	0
10	BF	1939	0	2084	30	0
11	BG	1704	0	1821	32	0
12	BH	1533	0	1608	31	0
13	BI	1654	0	1703	24	0
14	BJ	1362	0	1398	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	BL	1710	0	1829	21	0
16	BM	1077	0	1140	23	0
17	BN	1700	0	1746	37	0
18	BO	1643	0	1787	41	0
19	BP	1259	0	1293	16	0
20	BQ	1503	0	1624	25	0
21	BR	1503	0	1656	22	0
22	BS	1464	0	1512	19	0
23	BT	1299	0	1370	29	0
24	BU	817	0	839	22	0
25	BV	993	0	1050	17	0
26	BW	560	0	569	10	0
27	BX	976	0	1053	10	0
28	BY	1106	0	1192	19	0
29	BZ	1107	0	1182	13	0
30	Ba	1179	0	1225	23	0
31	Bb	582	0	614	8	0
32	Bc	738	0	774	14	0
33	Bd	867	0	917	13	0
34	Be	1074	0	1174	15	0
35	Bf	886	0	924	9	0
36	Bg	860	0	955	15	0
37	Bh	1015	0	1148	12	0
38	Bi	821	0	903	13	0
39	Bj	704	0	738	9	0
40	Bk	569	0	637	9	0
41	Bl	442	0	483	6	0
42	Bm	429	0	465	6	0
43	Bo	861	0	930	9	0
44	Bp	706	0	756	8	0
45	Br	1025	0	1087	21	0
46	A2	35806	0	18114	544	0
47	Aa	1730	0	1803	39	0
48	AA	657	0	678	11	0
49	AB	506	0	536	13	0
50	Ab	1698	0	1788	40	0
51	Ad	2076	0	2176	33	0
52	AD	452	0	494	5	0
53	AE	793	0	841	11	0
54	Af	1838	0	1973	33	0
55	Ag	1500	0	1602	28	0
56	Ah	1685	0	1772	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	Ai	1495	0	1615	28	0
58	Ak	1236	0	1306	16	0
59	Am	1208	0	1294	17	0
60	An	1016	0	1038	29	0
61	At	811	0	877	25	0
62	Au	640	0	643	11	0
63	Av	1035	0	1080	22	0
64	Aw	1104	0	1172	20	0
65	Ax	1015	0	1086	19	0
66	AZ	1626	0	1636	41	0
67	Ap	1123	0	1193	29	0
68	AC	611	0	637	21	0
69	Ae	1509	0	1563	43	0
70	AF	2420	0	2380	78	0
71	AG	459	0	448	15	0
72	Aj	812	0	840	22	0
73	Al	916	0	943	38	0
74	Ao	1044	0	1089	21	0
75	Ar	1191	0	1253	33	0
76	As	1115	0	1147	29	0
77	Ay	555	0	608	19	0
78	Ac	1752	0	1848	33	0
79	V	1628	0	826	28	0
80	Aq	1081	0	1138	46	0
81	A2	104	0	0	0	0
81	Ak	1	0	0	0	0
81	An	3	0	0	0	0
81	As	1	0	0	0	0
81	B5	346	0	0	0	0
81	B7	11	0	0	0	0
81	B8	9	0	0	0	0
81	BA	3	0	0	0	0
81	BH	1	0	0	0	0
81	BI	2	0	0	0	0
81	BN	2	0	0	0	0
81	BP	2	0	0	0	0
81	BV	1	0	0	0	0
81	Ba	1	0	0	0	0
81	Bb	2	0	0	0	0
81	Be	1	0	0	0	0
81	Bf	1	0	0	0	0
81	Bg	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
81	Bj	1	0	0	0	0
81	Bo	1	0	0	0	0
82	AE	1	0	0	0	0
82	AG	1	0	0	0	0
82	Bg	1	0	0	0	0
82	Bj	1	0	0	0	0
82	Bm	1	0	0	0	0
82	Bo	1	0	0	0	0
82	Bp	1	0	0	0	0
83	A2	832	0	0	5	0
83	AA	8	0	0	0	0
83	AB	1	0	0	0	0
83	AD	2	0	0	0	0
83	AE	9	0	0	0	0
83	AG	2	0	0	1	0
83	AZ	3	0	0	0	0
83	Aa	10	0	0	0	0
83	Ab	11	0	0	0	0
83	Ad	10	0	0	0	0
83	Ae	2	0	0	0	0
83	Af	1	0	0	0	0
83	Ah	7	0	0	0	0
83	Ai	7	0	0	0	0
83	Ak	10	0	0	0	0
83	Am	4	0	0	0	0
83	An	7	0	0	0	0
83	Ap	1	0	0	0	0
83	Aq	4	0	0	0	0
83	Ar	1	0	0	0	0
83	At	3	0	0	0	0
83	Au	2	0	0	0	0
83	Av	10	0	0	0	0
83	Aw	8	0	0	0	0
83	Ax	4	0	0	0	0
83	Ay	4	0	0	0	0
83	Az	5	0	0	0	0
83	B5	4198	0	0	11	0
83	B7	30	0	0	1	0
83	B8	72	0	0	0	0
83	BA	28	0	0	1	0
83	BB	49	0	0	2	0
83	BC	45	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
83	BD	22	0	0	1	0
83	BE	11	0	0	0	0
83	BF	24	0	0	0	0
83	BG	15	0	0	1	0
83	BH	15	0	0	0	0
83	BI	13	0	0	0	0
83	BJ	3	0	0	0	0
83	BL	29	0	0	0	0
83	BM	6	0	0	0	0
83	BN	29	0	0	1	0
83	BO	19	0	0	0	0
83	BP	23	0	0	0	0
83	BQ	24	0	0	0	0
83	BR	9	0	0	0	0
83	BS	21	0	0	0	0
83	BT	21	0	0	0	0
83	BU	2	0	0	1	0
83	BV	17	0	0	1	0
83	BW	4	0	0	1	0
83	BX	5	0	0	0	0
83	BY	11	0	0	0	0
83	BZ	5	0	0	0	0
83	Ba	23	0	0	1	0
83	Bb	11	0	0	0	0
83	Bc	5	0	0	0	0
83	Bd	9	0	0	0	0
83	Be	17	0	0	0	0
83	Bf	25	0	0	0	0
83	Bg	9	0	0	0	0
83	Bh	3	0	0	0	0
83	Bi	8	0	0	1	0
83	Bj	16	0	0	0	0
83	Bl	5	0	0	0	0
83	Bm	5	0	0	1	0
83	Bo	15	0	0	0	0
83	Bp	12	0	0	0	0
83	Br	16	0	0	1	0
83	V	9	0	0	0	0
All	All	216968	0	156385	2924	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 8.

All (2924) 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:B5:1669:G:H1	1:B5:1679:U:H3	1.04	0.99
1:B5:449:G:H3'	1:B5:450:C:H4'	1.48	0.93
80:Aq:31:ASN:HD22	80:Aq:55:THR:HG22	1.36	0.91
70:AF:173:LEU:HD22	70:AF:189:ILE:HG22	1.52	0.91
76:As:126:GLN:O	76:As:129:ARG:NH1	2.03	0.91
1:B5:2234:U:H3	1:B5:2242:G:H1	1.19	0.90
10:BF:159:LYS:O	10:BF:176:ARG:NH1	2.09	0.85
74:Ao:51:ARG:NH1	74:Ao:55:SER:OG	2.10	0.84
1:B5:279:G:H5''	17:BN:8:GLN:HE22	1.42	0.83
55:Ag:37:LYS:HE2	55:Ag:41:ARG:HE	1.45	0.82
1:B5:457:G:H1	1:B5:639:G:H22	1.28	0.82
1:B5:4137:G:H4'	12:BH:71:ARG:HH12	1.44	0.81
1:B5:629:C:H4'	45:Br:85:ASN:HD22	1.45	0.81
5:BA:137:ILE:HD11	5:BA:149:LYS:HB2	1.63	0.81
64:Aw:109:GLY:O	64:Aw:119:ARG:NH1	2.13	0.81
1:B5:3414:C:H1'	17:BN:125:SER:HB3	1.62	0.80
20:BQ:15:ARG:HH21	20:BQ:19:LYS:H	1.28	0.79
46:A2:1359:A:H4'	61:At:52:GLY:HA3	1.64	0.79
78:Ac:135:GLU:HG3	78:Ac:153:VAL:HG12	1.64	0.79
69:Ae:125:THR:HG22	69:Ae:126:ARG:H	1.48	0.78
67:Ap:97:GLN:HB3	67:Ap:105:LYS:HG3	1.64	0.78
75:Ar:22:GLY:HA2	75:Ar:56:ALA:HB3	1.66	0.78
61:At:19:ARG:NH1	61:At:117:ALA:O	2.17	0.78
51:Ad:133:THR:HG22	51:Ad:134:LYS:HG2	1.65	0.78
1:B5:4021:G:H5''	6:BB:120:LYS:HD2	1.65	0.77
79:V:9:A:O2'	79:V:11:C:N4	2.19	0.76
33:Bd:138:ARG:HH22	33:Bd:173:VAL:HG11	1.48	0.76
69:Ae:73:ASN:HA	69:Ae:76:MET:HE3	1.67	0.76
7:BC:162:LYS:HD2	7:BC:219:ARG:HH21	1.48	0.76
1:B5:1208:G:O6	7:BC:312:ARG:NH2	2.19	0.75
1:B5:3543:G:H1	1:B5:3561:U:H3	1.33	0.75
55:Ag:53:VAL:HG21	55:Ag:172:THR:HG22	1.68	0.75
1:B5:1410:G:OP1	15:BL:190:ARG:NH2	2.20	0.75
3:B7:72:U:O2	3:B7:103:A:N6	2.19	0.75
32:Bc:17:ARG:HH12	32:Bc:107:SER:HB2	1.50	0.75
1:B5:446:U:H3	1:B5:2063:G:H22	1.32	0.74
1:B5:1999:U:H4'	1:B5:2000:G:H3'	1.68	0.74
18:BO:3:GLU:OE1	18:BO:31:ARG:NH2	2.18	0.74
68:AC:101:ALA:HA	68:AC:104:LYS:HZ2	1.51	0.74
47:Aa:121:ILE:HG12	47:Aa:161:VAL:HG13	1.67	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:2591:G:H1	1:B5:3323:U:H3	1.35	0.74
75:Ar:89:ASP:HB3	75:Ar:93:GLY:H	1.52	0.74
1:B5:4060:G:OP2	6:BB:358:ARG:NH2	2.20	0.74
11:BG:189:ARG:HG2	11:BG:192:ARG:HH12	1.52	0.74
32:Bc:47:ILE:HD12	32:Bc:94:LEU:HD11	1.68	0.74
1:B5:74:G:H5''	15:BL:59:VAL:HB	1.68	0.74
1:B5:686:G:H1	1:B5:728:G:H22	1.34	0.74
46:A2:779:G:OP1	57:Ai:79:ARG:NH2	2.20	0.73
1:B5:2012:G:OP1	45:Br:107:ARG:NH2	2.22	0.73
46:A2:939:A:H2'	46:A2:940:G:C8	2.24	0.73
70:AF:220:ASP:HB3	70:AF:223:GLU:HG2	1.70	0.73
46:A2:1410:A:OP1	80:Aq:5:ARG:NH2	2.21	0.73
65:Ax:55:ILE:HG12	65:Ax:75:ILE:HG12	1.69	0.73
79:V:60:C:OP2	79:V:61:C:N4	2.21	0.73
46:A2:1049:C:HO2'	63:Av:2:VAL:N	1.86	0.72
70:AF:17:TRP:HB2	70:AF:36:ARG:HD2	1.70	0.72
49:AB:40:ARG:HH12	60:An:117:ARG:HH21	1.36	0.72
50:Ab:137:ARG:HB2	50:Ab:219:TYR:HD1	1.53	0.72
1:B5:672:A:H62	1:B5:740:G:H21	1.38	0.72
1:B5:1405:U:O2'	1:B5:1407:G:N2	2.22	0.72
1:B5:3118:U:OP2	1:B5:3123:A:N6	2.23	0.72
60:An:21:VAL:HG22	60:An:22:ALA:H	1.54	0.72
1:B5:1295:G:N7	7:BC:239:ARG:NH2	2.37	0.72
46:A2:1491:G:H2'	46:A2:1492:A:H8	1.55	0.72
70:AF:220:ASP:HB2	70:AF:227:LEU:HD11	1.71	0.72
1:B5:4160:A:OP2	6:BB:30:LYS:NZ	2.21	0.72
1:B5:4193:G:N7	35:Bf:66:ARG:NH2	2.37	0.72
1:B5:4277:A:H61	1:B5:4288:G:H1	1.36	0.72
59:Am:100:LYS:HE2	59:Am:104:ARG:HH12	1.54	0.72
76:As:129:ARG:O	76:As:133:ARG:HG2	1.90	0.71
1:B5:184:U:H3	1:B5:254:G:H22	1.38	0.71
1:B5:2225:G:N7	27:BX:49:LYS:NZ	2.38	0.71
64:Aw:98:ASP:OD1	64:Aw:140:ARG:NH2	2.23	0.71
72:Aj:3:MET:HG3	72:Aj:44:HIS:HD2	1.55	0.71
1:B5:4312:G:H5''	9:BE:197:ARG:HE	1.55	0.71
1:B5:4076:G:O2'	1:B5:4078:A:OP2	2.08	0.71
1:B5:4245:G:H1	18:BO:176:ARG:HD3	1.56	0.71
2:B8:124:U:O2'	2:B8:126:C:N4	2.23	0.71
46:A2:917:G:OP1	60:An:104:ARG:NH2	2.24	0.71
46:A2:975:U:OP1	59:Am:62:GLN:NE2	2.24	0.71
46:A2:1462:G:N2	68:AC:87:THR:O	2.24	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A2:1716:U:H3	46:A2:1725:G:H1	1.38	0.71
32:Bc:34:THR:HG23	32:Bc:95:ALA:HB2	1.72	0.70
46:A2:1346:A:H61	78:Ac:161:GLY:HA3	1.54	0.70
46:A2:1602:A:OP1	67:Ap:138:ARG:NH1	2.23	0.70
47:Aa:33:VAL:HG12	47:Aa:44:ILE:HD12	1.73	0.70
1:B5:1218:G:OP2	1:B5:1218:G:N2	2.21	0.70
47:Aa:225:LEU:HG	47:Aa:229:MET:HE1	1.74	0.70
1:B5:2100:OMC:HM22	1:B5:2101:U:H5'	1.73	0.70
1:B5:1812:G:OP1	35:Bf:87:LYS:NZ	2.25	0.70
7:BC:36:VAL:HG11	7:BC:122:TYR:HD2	1.56	0.70
46:A2:1476:C:OP2	75:Ar:136:THR:OG1	2.09	0.70
1:B5:1153:C:H2'	1:B5:1154:G:H8	1.58	0.69
46:A2:1373:C:O2'	76:As:132:ASP:OD2	2.10	0.69
68:AC:108:VAL:HG11	73:Al:63:LYS:HE3	1.74	0.69
16:BM:127:ILE:HD11	18:BO:178:ARG:HG3	1.74	0.69
28:BY:52:ASP:HA	28:BY:69:LYS:HE2	1.74	0.69
51:Ad:179:ASN:ND2	51:Ad:230:LYS:O	2.25	0.69
79:V:22:G:N7	79:V:46:G:N2	2.28	0.69
1:B5:3430:G:H2'	1:B5:3431:A:H8	1.57	0.69
76:As:60:THR:HG23	76:As:75:MET:HE2	1.73	0.69
46:A2:1268:U:H3'	73:Al:36:ARG:HH22	1.56	0.69
52:AD:110:MET:SD	52:AD:114:ARG:NE	2.64	0.69
61:At:79:ARG:NH1	71:AG:56:ASP:OXT	2.26	0.69
1:B5:2269:C:O2	1:B5:2389:G:N2	2.26	0.69
55:Ag:28:LEU:HG	55:Ag:32:MET:HE1	1.75	0.69
66:AZ:19:LEU:HB3	80:Aq:96:ILE:HG21	1.74	0.69
66:AZ:77:ILE:HG12	66:AZ:99:ILE:HB	1.74	0.69
13:BI:87:ILE:HG12	13:BI:138:ILE:HG12	1.73	0.69
46:A2:1186:A:H2'	46:A2:1187:G:C8	2.28	0.69
10:BF:84:GLU:OE2	23:BT:136:ARG:NH2	2.25	0.68
70:AF:312:VAL:HG12	70:AF:314:ILE:H	1.57	0.68
1:B5:2444:A:OP1	40:Bk:35:LYS:NZ	2.26	0.68
1:B5:2454:G:O6	21:BR:46:LYS:NZ	2.25	0.68
20:BQ:40:ASN:OD1	20:BQ:132:LYS:NZ	2.24	0.68
55:Ag:88:SER:HB3	55:Ag:90:LYS:HG3	1.75	0.68
79:V:33:U:O2	79:V:36:A:N7	2.26	0.68
46:A2:877:A:OP2	59:Am:64:ARG:NH1	2.25	0.68
1:B5:3275:U:OP2	25:BV:74:LYS:NZ	2.27	0.68
1:B5:3951:C:H5''	25:BV:43:LYS:HD3	1.75	0.68
18:BO:3:GLU:HG3	18:BO:118:MET:HE2	1.74	0.68
19:BP:94:MET:HE1	19:BP:146:ILE:HB	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A2:544:A:OP1	57:Ai:162:ARG:NH2	2.25	0.68
46:A2:1356:G:H1'	70:AF:63:SER:HB3	1.74	0.68
1:B5:4267:C:O2'	1:B5:4269:G:N7	2.22	0.68
1:B5:3917:A:OP2	1:B5:3919:C:N4	2.27	0.68
16:BM:55:MET:O	22:BS:157:ARG:NH2	2.25	0.68
46:A2:1354:A:O2'	46:A2:1356:G:N7	2.26	0.68
78:Ac:141:LYS:HE2	78:Ac:179:GLN:HB3	1.76	0.68
7:BC:140:LYS:O	7:BC:204:ARG:NH2	2.26	0.68
1:B5:455:U:O4	1:B5:642:G:N2	2.27	0.68
1:B5:495:G:H5''	7:BC:268:ARG:HD3	1.75	0.68
45:Br:62:VAL:HG21	45:Br:93:LEU:HD21	1.75	0.67
1:B5:1257:C:H2'	1:B5:1258:A:H8	1.59	0.67
1:B5:3430:G:H2'	1:B5:3431:A:C8	2.29	0.67
1:B5:1366:G:O2'	1:B5:2002:G:O6	2.12	0.67
46:A2:193:U:O2	46:A2:196:G:O6	2.12	0.67
65:Ax:78:SER:OG	65:Ax:80:ASP:OD1	2.12	0.67
1:B5:1958:G:HO2'	1:B5:3361:U:HO2'	1.42	0.67
1:B5:2507:G:O2'	1:B5:2514:A:N3	2.25	0.67
46:A2:64:A:H2	46:A2:83:A:H62	1.41	0.67
46:A2:1081:C:OP1	47:Aa:151:ARG:NH2	2.27	0.67
1:B5:280:A:OP2	17:BN:8:GLN:NE2	2.27	0.67
50:Ab:225:ASP:HB2	62:Au:0:ACE:H1	1.76	0.67
1:B5:370:G:N2	1:B5:373:A:OP2	2.24	0.67
1:B5:3413:G:N2	17:BN:125:SER:HB2	2.10	0.67
46:A2:109:PSU:OP1	46:A2:769:A:O2'	2.12	0.67
1:B5:1251:A2M:OP2	1:B5:3888:U:O2'	2.11	0.67
1:B5:3989:A:N7	5:BA:215:ASN:ND2	2.42	0.67
33:Bd:115:ILE:HG23	33:Bd:119:LEU:HD23	1.76	0.67
46:A2:1033:C:OP1	59:Am:107:LYS:NZ	2.28	0.67
46:A2:1054:C:H42	46:A2:1094:U:H3	1.41	0.67
53:AE:45:VAL:HG21	53:AE:53:ILE:HD13	1.76	0.67
61:At:85:HIS:HB3	61:At:87:ARG:HH12	1.60	0.67
1:B5:582:C:H5''	15:BL:162:LYS:HE3	1.75	0.66
68:AC:121:CYS:HA	68:AC:132:MET:HE3	1.76	0.66
66:AZ:145:ILE:HG12	66:AZ:159:ILE:HB	1.77	0.66
51:Ad:11:ARG:HA	51:Ad:28:ALA:HB2	1.78	0.66
1:B5:2350:A:N6	1:B5:2493:A:OP2	2.26	0.66
1:B5:2581:A:OP1	33:Bd:98:LYS:NZ	2.27	0.66
1:B5:3500:C:H2'	1:B5:3501:A:C8	2.30	0.66
51:Ad:62:LYS:HA	51:Ad:80:ILE:HD11	1.77	0.66
61:At:38:ASP:OD1	61:At:41:ARG:NH1	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:224:C:C2	7:BC:219:ARG:HD2	2.31	0.66
1:B5:4063:OMU:OP2	1:B5:4113:C:N4	2.26	0.66
70:AF:87:LEU:HB2	70:AF:101:PHE:HB2	1.78	0.66
1:B5:304:C:OP2	17:BN:68:ARG:NH2	2.28	0.66
46:A2:1246:U:N3	46:A2:1269:C:O2	2.29	0.66
47:Aa:148:ASN:OD1	80:Aq:127:ASN:ND2	2.28	0.66
15:BL:125:ILE:HD11	37:Bh:122:LYS:HG3	1.77	0.66
46:A2:910:G:H21	60:An:52:THR:HG21	1.60	0.66
46:A2:1567:G:OP1	74:Ao:18:ARG:NH2	2.29	0.66
1:B5:3536:C:OP1	5:BA:37:ARG:NH1	2.28	0.66
1:B5:4231:G:H5''	18:BO:169:ARG:HH12	1.60	0.66
11:BG:63:LEU:HD21	17:BN:29:GLN:HG3	1.78	0.66
15:BL:63:THR:O	15:BL:65:ARG:N	2.28	0.66
25:BV:42:VAL:HB	25:BV:45:ILE:HD12	1.78	0.66
46:A2:1258:G:H2'	74:Ao:51:ARG:HH21	1.61	0.66
46:A2:1553:G:H3'	77:Ay:80:ARG:HD3	1.78	0.66
1:B5:3532:G:O6	5:BA:72:ARG:NH2	2.27	0.65
1:B5:3984:G:N2	1:B5:3987:A:OP2	2.25	0.65
46:A2:1491:G:H2'	46:A2:1492:A:C8	2.30	0.65
51:Ad:19:MET:SD	51:Ad:108:ARG:NH1	2.69	0.65
60:An:34:PHE:HB3	60:An:41:PHE:HB2	1.77	0.65
1:B5:4300:C:H5''	16:BM:114:LYS:HD2	1.77	0.65
58:Ak:49:GLU:OE1	58:Ak:118:ARG:NH2	2.30	0.65
41:Bl:25:GLN:OE1	41:Bl:28:ARG:NH2	2.30	0.65
51:Ad:100:ARG:HH21	51:Ad:118:GLU:HG2	1.61	0.65
46:A2:390:C:OP1	51:Ad:10:LYS:NZ	2.24	0.65
46:A2:774:PSU:OP1	51:Ad:22:LYS:NZ	2.27	0.65
46:A2:164:G:OP2	46:A2:164:G:N2	2.25	0.65
1:B5:1627:G:H5''	1:B5:1628:U:H5'	1.79	0.65
2:B8:75:OMG:OP2	28:BY:74:TYR:OH	2.14	0.65
46:A2:144:G:O6	54:Af:178:ARG:NH2	2.27	0.65
51:Ad:105:THR:HG21	51:Ad:245:ARG:HA	1.79	0.65
55:Ag:148:LEU:HA	63:Av:42:MET:HE2	1.79	0.65
68:AC:132:MET:HB3	68:AC:139:HIS:HB3	1.79	0.65
3:B7:2:C:H5''	8:BD:266:VAL:HG13	1.79	0.65
46:A2:1331:C:O2'	80:Aq:10:LYS:NZ	2.30	0.65
1:B5:746:U:OP2	16:BM:19:ARG:NH2	2.31	0.65
1:B5:1357:C:H3'	1:B5:1358:G:H4'	1.78	0.65
1:B5:1823:C:H4'	18:BO:89:PRO:HD3	1.78	0.65
1:B5:4363:G:H2'	1:B5:4364:G:C8	2.32	0.65
18:BO:10:ASP:OD2	18:BO:37:ARG:NH2	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:At:95:SER:OG	61:At:99:LYS:NZ	2.28	0.65
1:B5:1370:G:H3'	1:B5:1371:G:H8	1.61	0.64
36:Bg:69:LYS:HG2	36:Bg:73:HIS:CE1	2.32	0.64
46:A2:860:G:H2'	46:A2:861:A:H8	1.62	0.64
1:B5:126:C:H2'	1:B5:127:G:H8	1.62	0.64
1:B5:4358:A:OP2	6:BB:116:ARG:NH2	2.29	0.64
5:BA:173:GLY:O	44:Bp:69:TRP:NE1	2.30	0.64
58:Ak:119:ASP:O	58:Ak:147:LYS:NZ	2.31	0.64
1:B5:3200:A:H2'	1:B5:3201:A2M:H8	1.78	0.64
1:B5:3717:A:H2'	1:B5:3718:G:C8	2.33	0.64
1:B5:4341:C:OP1	19:BP:74:LYS:NZ	2.29	0.64
46:A2:886:G:H2'	46:A2:887:G:C8	2.33	0.64
65:Ax:117:VAL:O	65:Ax:122:LYS:NZ	2.28	0.64
1:B5:1614:G:H5'	20:BQ:15:ARG:HG3	1.78	0.64
1:B5:2244:U:H2'	1:B5:2245:G:C8	2.32	0.64
1:B5:101:A:O2'	15:BL:63:THR:OG1	2.12	0.64
1:B5:1640:C:H5''	23:BT:43:LYS:HD2	1.79	0.64
55:Ag:83:LEU:HD23	55:Ag:92:VAL:HG11	1.80	0.64
14:BJ:95:ARG:O	14:BJ:98:ASN:HB2	1.98	0.64
19:BP:16:LYS:HG2	19:BP:149:ILE:HG12	1.80	0.64
46:A2:913:A:H5''	60:An:60:MET:HE3	1.79	0.64
46:A2:1605:A:H5''	67:Ap:139:ALA:HB2	1.80	0.64
46:A2:1700:A:H1'	54:Af:66:GLY:HA2	1.79	0.64
1:B5:609:G:H2'	1:B5:610:G:H8	1.63	0.63
1:B5:778:C:H4'	1:B5:779:C:H5'	1.81	0.63
1:B5:2218:C:H5	1:B5:2220:G:H1	1.47	0.63
46:A2:491:U:H2'	46:A2:492:A:H8	1.63	0.63
79:V:62:C:H2'	79:V:63:G:H8	1.64	0.63
9:BE:201:GLN:HA	9:BE:204:VAL:HG22	1.81	0.63
1:B5:1500:G:O2'	1:B5:1535:G:H4'	1.99	0.63
1:B5:1676:C:H2'	1:B5:1677:G:C8	2.33	0.63
1:B5:4037:U:H2'	1:B5:4038:G:H8	1.64	0.63
78:Ac:204:LEU:HB2	78:Ac:207:HIS:HB2	1.79	0.63
79:V:16:U:H2'	79:V:17:U:H4'	1.81	0.63
12:BH:91:LYS:HB2	12:BH:183:GLU:HB3	1.81	0.63
46:A2:1808:U:H2'	46:A2:1809:G:H8	1.63	0.63
73:Al:36:ARG:NH1	73:Al:37:GLU:OE2	2.31	0.63
75:Ar:121:ARG:HG3	75:Ar:131:VAL:HB	1.80	0.63
1:B5:3965:G:O2'	1:B5:3968:C:OP2	2.17	0.63
28:BY:74:TYR:HE2	28:BY:77:LYS:HG3	1.63	0.63
54:Af:98:ARG:NH2	54:Af:103:ASP:OD1	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B7:17:C:OP1	14:BJ:156:ARG:NH2	2.31	0.62
11:BG:209:PRO:HA	11:BG:212:LYS:HG3	1.80	0.62
46:A2:1505:G:H3'	46:A2:1534:A:H61	1.64	0.62
1:B5:4137:G:H4'	12:BH:71:ARG:NH1	2.15	0.62
46:A2:978:A:OP2	59:Am:70:LYS:NZ	2.31	0.62
1:B5:1732:G:H5''	23:BT:35:LYS:HE2	1.82	0.62
6:BB:21:ARG:NH2	83:BB:502:HOH:O	2.31	0.62
50:Ab:162:VAL:HG11	50:Ab:207:PHE:HA	1.81	0.62
70:AF:296:GLN:O	70:AF:311:GLN:NE2	2.33	0.62
16:BM:99:GLU:O	16:BM:103:LYS:HG2	1.98	0.62
72:Aj:81:ASP:OD2	73:Al:96:ARG:NH2	2.32	0.62
46:A2:84:A:N3	46:A2:149:A:O2'	2.30	0.62
46:A2:1571:U:OP2	74:Ao:43:ARG:NH2	2.32	0.62
75:Ar:66:ARG:O	75:Ar:70:ILE:HD12	2.00	0.62
78:Ac:74:GLN:NE2	78:Ac:79:PHE:O	2.24	0.62
1:B5:99:A:H3'	1:B5:100:G:H21	1.65	0.62
1:B5:497:G:H22	1:B5:598:G:H1	1.45	0.62
1:B5:2073:C:O2'	34:Be:98:GLU:OE1	2.18	0.62
1:B5:2494:A:H2'	1:B5:2495:A:C8	2.35	0.62
1:B5:3681:G:H2'	1:B5:3682:A:C8	2.35	0.62
6:BB:147:GLU:OE2	6:BB:198:ARG:NH2	2.28	0.62
46:A2:1435:A:O2'	61:At:79:ARG:NH1	2.31	0.62
60:An:101:GLY:HA3	60:An:134:PRO:HG2	1.81	0.62
78:Ac:114:ALA:HB3	78:Ac:117:ARG:HE	1.65	0.62
1:B5:218:A:O2'	1:B5:219:G:N2	2.33	0.62
1:B5:1669:G:O6	1:B5:1679:U:O4	2.18	0.62
1:B5:1849:G:H22	1:B5:3877:C:H5''	1.64	0.62
1:B5:2111:U:H2'	1:B5:2112:A2M:H8	1.81	0.62
37:Bh:13:LYS:HB2	37:Bh:16:GLU:HG3	1.80	0.62
45:Br:122:ARG:NH2	83:Br:201:HOH:O	2.32	0.62
47:Aa:49:VAL:HB	47:Aa:62:LEU:HD13	1.82	0.62
1:B5:62:A:N3	1:B5:77:U:O2'	2.31	0.62
1:B5:2365:C:OP1	21:BR:60:ARG:NH1	2.33	0.62
69:Ae:112:VAL:O	69:Ae:116:ILE:HG12	1.99	0.62
73:Al:15:ASN:O	73:Al:19:GLN:HG2	2.00	0.62
1:B5:3507:C:H2'	1:B5:3508:U:C6	2.35	0.62
5:BA:147:ARG:HG2	5:BA:157:VAL:HG22	1.82	0.62
28:BY:50:ARG:HD2	28:BY:115:ARG:HH11	1.65	0.61
1:B5:1150:G:O2'	8:BD:278:ASP:OD2	2.18	0.61
1:B5:1579:U:OP2	30:Ba:26:ARG:NH2	2.30	0.61
13:BI:38:ARG:HD3	13:BI:83:ASP:HB2	1.79	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:AE:44:ILE:O	60:An:113:GLN:NE2	2.32	0.61
1:B5:424:G:OP1	19:BP:62:ARG:NH1	2.34	0.61
1:B5:1276:G:O6	20:BQ:55:ARG:NH1	2.29	0.61
46:A2:468:G:OP2	65:Ax:104:ARG:NH2	2.33	0.61
46:A2:796:G:O2'	46:A2:797:C:OP1	2.18	0.61
6:BB:92:TYR:HB2	6:BB:159:VAL:HB	1.82	0.61
11:BG:75:LYS:HG2	11:BG:240:ASN:HB2	1.82	0.61
46:A2:494:A:H2'	46:A2:495:G:H8	1.65	0.61
46:A2:1230:C:OP2	68:AC:90:LYS:NZ	2.33	0.61
46:A2:1712:G:O6	46:A2:1729:U:O2	2.18	0.61
49:AB:18:LEU:HD11	49:AB:43:ILE:HD12	1.82	0.61
58:Ak:27:GLU:HB3	58:Ak:30:LYS:HB2	1.82	0.61
1:B5:4272:C:N4	1:B5:4321:U:O4	2.33	0.61
21:BR:176:ARG:NH2	46:A2:867:G:OP1	2.34	0.61
1:B5:3745:U:H4'	23:BT:5:LYS:HD2	1.82	0.61
46:A2:169:A:OP2	54:Af:140:ARG:NH1	2.27	0.61
49:AB:59:LEU:HD11	69:Ae:121:ARG:HH11	1.64	0.61
50:Ab:215:ILE:O	50:Ab:218:THR:OG1	2.13	0.61
1:B5:1223:C:H2'	1:B5:1224:G:C8	2.36	0.61
17:BN:45:PRO:O	17:BN:49:ARG:HG3	2.01	0.61
18:BO:193:THR:HG22	18:BO:197:LYS:HE2	1.83	0.61
72:Aj:58:VAL:HG12	72:Aj:71:LEU:HA	1.82	0.61
46:A2:1599:C:H4'	67:Ap:140:ARG:HB2	1.82	0.61
56:Ah:34:ALA:HB2	56:Ah:56:ARG:HD2	1.81	0.61
1:B5:301:A:H2'	1:B5:302:G:H8	1.65	0.61
1:B5:644:G:OP1	34:Be:5:ARG:NH2	2.34	0.61
1:B5:2648:C:OP1	21:BR:108:ARG:NH2	2.25	0.61
46:A2:523:U:H2'	46:A2:524:G:C8	2.35	0.61
49:AB:67:ARG:O	49:AB:69:ARG:NH1	2.34	0.61
74:Ao:123:TYR:OH	75:Ar:124:ARG:NH1	2.33	0.61
1:B5:629:C:H4'	45:Br:85:ASN:ND2	2.15	0.61
66:AZ:182:VAL:O	66:AZ:186:ARG:HG3	2.01	0.61
69:Ae:70:ARG:NH2	69:Ae:147:ASN:OD1	2.34	0.61
72:Aj:32:HIS:HD2	72:Aj:34:GLU:H	1.47	0.61
80:Aq:10:LYS:HB3	80:Aq:14:ARG:HH12	1.64	0.60
1:B5:194:C:O2	28:BY:121:ARG:NH2	2.34	0.60
1:B5:2494:A:H2'	1:B5:2495:A:H8	1.66	0.60
46:A2:430:A:N6	83:A2:2147:HOH:O	2.34	0.60
46:A2:504:C:H2'	46:A2:505:G:C8	2.36	0.60
46:A2:1799:A:H2'	46:A2:1800:G:C8	2.37	0.60
1:B5:4337:A:H5'	6:BB:128:LYS:HG3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A2:1186:A:H2'	46:A2:1187:G:H8	1.64	0.60
12:BH:37:ASP:OD1	12:BH:39:ASN:ND2	2.33	0.60
1:B5:745:G:H2'	16:BM:19:ARG:HH22	1.65	0.60
46:A2:125:C:OP1	54:Af:202:ASN:ND2	2.31	0.60
46:A2:1217:A:H1'	46:A2:1222:C:H42	1.66	0.60
1:B5:1829:C:H3'	1:B5:1830:C:H5''	1.82	0.60
11:BG:132:ARG:HD3	11:BG:133:PRO:HD2	1.83	0.60
46:A2:818:G:H21	63:Av:107:SER:HB3	1.67	0.60
70:AF:73:SER:OG	70:AF:117:ASN:OD1	2.18	0.60
1:B5:1245:U:O2'	1:B5:1800:A:N1	2.31	0.60
1:B5:2046:G:O2'	7:BC:140:LYS:NZ	2.35	0.60
1:B5:2067:G:N2	1:B5:2070:G:OP2	2.31	0.60
1:B5:3681:G:H2'	1:B5:3682:A:H8	1.67	0.60
1:B5:4113:C:O2'	1:B5:4115:A:OP2	2.19	0.60
9:BE:202:LYS:HE3	35:Bf:107:PRO:HB3	1.84	0.60
22:BS:30:MET:HE1	22:BS:47:PHE:HB3	1.83	0.60
1:B5:1616:U:OP2	20:BQ:49:LYS:NZ	2.34	0.60
1:B5:3551:C:H41	1:B5:3552:G:H21	1.50	0.60
1:B5:3703:U:H2'	1:B5:3704:C:C6	2.37	0.60
50:Ab:219:TYR:OH	62:Au:14:PRO:HD3	2.00	0.60
1:B5:1569:A:O2'	39:Bj:49:TRP:O	2.20	0.60
1:B5:3980:C:H2'	1:B5:3981:G:C8	2.36	0.60
1:B5:4231:G:H5'	18:BO:169:ARG:HH22	1.67	0.60
73:Al:77:ILE:HD11	73:Al:128:PHE:HB2	1.84	0.60
1:B5:502:C:O2'	1:B5:503:G:OP1	2.19	0.59
1:B5:3450:G:H2'	1:B5:3451:G:C8	2.37	0.59
83:B5:4971:HOH:O	16:BM:98:ARG:NH1	2.35	0.59
21:BR:160:GLU:OE1	21:BR:163:ARG:NH2	2.30	0.59
46:A2:1521:G:N7	76:As:101:ARG:NH2	2.50	0.59
57:Ai:28:GLU:OE2	57:Ai:47:LYS:NZ	2.35	0.59
66:AZ:33:GLN:HB3	66:AZ:154:LEU:HD12	1.83	0.59
40:Bk:8:ILE:HG13	40:Bk:45:LEU:HD21	1.85	0.59
46:A2:56:G:OP1	65:Ax:111:LYS:NZ	2.31	0.59
46:A2:574:G:N2	46:A2:587:G:OP1	2.34	0.59
1:B5:4188:G:H22	1:B5:4326:A:H2	1.51	0.59
24:BU:111:GLU:OE2	24:BU:113:ARG:NE	2.31	0.59
1:B5:483:C:O2'	7:BC:296:GLN:HG2	2.03	0.59
5:BA:2:GLY:HA2	5:BA:207:VAL:HG23	1.85	0.59
30:Ba:132:ARG:NH1	83:Ba:302:HOH:O	2.29	0.59
46:A2:1219:C:O2	71:AG:10:HIS:NE2	2.25	0.59
78:Ac:194:PRO:O	78:Ac:201:LYS:NZ	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:V:27:G:H2'	79:V:28:G:C8	2.37	0.59
1:B5:419:A:C2	2:B8:17:A:H1'	2.38	0.59
1:B5:2288:C:H2'	1:B5:2289:C:C6	2.38	0.59
1:B5:3428:G:H2'	1:B5:3429:A:C8	2.38	0.59
1:B5:494:G:H2'	1:B5:495:G:C8	2.38	0.59
1:B5:2207:C:H5''	17:BN:67:ARG:HD2	1.85	0.59
1:B5:3387:C:H2'	1:B5:3388:C:C6	2.37	0.59
6:BB:36:ASP:HB3	6:BB:39:LYS:HD3	1.85	0.59
23:BT:88:ARG:NH1	31:Bb:33:LYS:O	2.36	0.59
79:V:69:C:H2'	79:V:70:G:H8	1.68	0.59
38:Bi:80:HIS:NE2	38:Bi:84:LYS:HE2	2.17	0.59
1:B5:777:G:O2'	1:B5:778:C:O4'	2.21	0.59
1:B5:1133:G:H2'	1:B5:1134:G:H8	1.68	0.59
12:BH:44:GLU:HB3	12:BH:58:ASP:HB2	1.85	0.59
46:A2:788:G:OP1	57:Ai:6:SER:OG	2.21	0.59
46:A2:1161:G:H2'	46:A2:1162:A:C8	2.37	0.59
80:Aq:51:ALA:O	80:Aq:55:THR:HG23	2.01	0.59
1:B5:481:G:OP1	45:Br:67:ARG:NH2	2.32	0.59
1:B5:1514:U:OP2	1:B5:2605:C:O2'	2.13	0.59
3:B7:91:C:O3'	13:BI:131:MET:HE1	2.03	0.59
46:A2:1518:G:OP1	76:As:121:ARG:NH1	2.29	0.59
70:AF:258:ILE:HD11	70:AF:268:ASP:HB3	1.85	0.59
1:B5:1404:C:H2'	1:B5:1405:U:H5'	1.85	0.59
8:BD:204:VAL:HG12	8:BD:208:MET:HE3	1.84	0.59
50:Ab:92:ARG:HH22	50:Ab:116:LYS:HE3	1.68	0.59
1:B5:773:G:OP1	9:BE:97:LYS:NZ	2.35	0.58
1:B5:1221:G:HO2'	1:B5:1222:U:H6	1.51	0.58
1:B5:3433:G:O6	1:B5:3504:A:N1	2.36	0.58
1:B5:3915:G:O2'	42:Bm:100:TYR:O	2.19	0.58
1:B5:4061:OMG:H5''	25:BV:15:ARG:HB2	1.85	0.58
17:BN:138:PHE:HA	17:BN:143:ARG:HD2	1.85	0.58
47:Aa:110:MET:O	47:Aa:114:VAL:HG23	2.03	0.58
1:B5:93:G:H2'	1:B5:94:A:C8	2.38	0.58
2:B8:67:U:H2'	2:B8:68:G:H8	1.67	0.58
26:BW:1:MET:N	83:BW:201:HOH:O	2.34	0.58
46:A2:938:A:H2'	46:A2:939:A:C8	2.38	0.58
54:Af:7:PHE:HB2	54:Af:113:ILE:HD12	1.85	0.58
1:B5:1257:C:H2'	1:B5:1258:A:C8	2.38	0.58
1:B5:1264:U:H2'	1:B5:1265:OMC:C6	2.37	0.58
5:BA:234:LYS:HG2	5:BA:238:ILE:HG12	1.84	0.58
46:A2:1558:G:N2	75:Ar:24:ARG:HH21	2.00	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:Ar:23:ARG:NE	77:Ay:48:VAL:HB	2.18	0.58
1:B5:3703:U:H2'	1:B5:3704:C:H6	1.68	0.58
1:B5:3902:U:H2'	1:B5:3903:U:C6	2.38	0.58
1:B5:4362:U:H2'	1:B5:4363:G:H8	1.67	0.58
3:B7:27:G:OP1	14:BJ:146:ARG:NH2	2.34	0.58
42:Bm:98:LYS:HD2	42:Bm:118:THR:HG21	1.86	0.58
47:Aa:30:TRP:CE2	47:Aa:48:LEU:HD21	2.39	0.58
47:Aa:146:ARG:HB2	47:Aa:149:GLN:HB2	1.85	0.58
79:V:70:G:H2'	79:V:71:G:C8	2.38	0.58
1:B5:4253:C:OP1	16:BM:121:ARG:NH2	2.37	0.58
7:BC:204:ARG:NH1	7:BC:205:ARG:O	2.36	0.58
8:BD:65:ALA:HB2	8:BD:74:ILE:HG13	1.84	0.58
46:A2:106:C:H2'	46:A2:107:A:H8	1.69	0.58
55:Ag:19:PHE:HZ	55:Ag:60:ILE:HG23	1.68	0.58
80:Aq:28:PHE:HA	80:Aq:55:THR:HG21	1.85	0.58
1:B5:2269:C:H2'	1:B5:2270:G:H8	1.69	0.58
47:Aa:46:LYS:HZ1	60:An:21:VAL:HG21	1.69	0.58
1:B5:3682:A:H2'	1:B5:3683:G:C8	2.39	0.58
1:B5:4303:C:H5''	9:BE:272:LYS:NZ	2.19	0.58
70:AF:280:LYS:HE2	80:Aq:63:ARG:NH2	2.19	0.58
71:AG:26:ASN:ND2	83:AG:201:HOH:O	2.36	0.58
1:B5:247:G:N2	28:BY:121:ARG:HH21	2.02	0.58
1:B5:650:A:H2'	1:B5:651:C:C6	2.38	0.58
1:B5:1938:A:H2'	1:B5:1939:A:C8	2.38	0.58
66:AZ:10:MET:HE1	80:Aq:109:LEU:HD23	1.86	0.58
69:Ae:120:PRO:HA	69:Ae:192:LYS:HE2	1.86	0.58
1:B5:1606:PSU:OP1	30:Ba:44:ASN:ND2	2.32	0.58
27:BX:81:THR:HG22	27:BX:154:ILE:HG23	1.86	0.58
46:A2:102:A:H4'	46:A2:104:A:C8	2.39	0.58
46:A2:927:U:OP1	46:A2:928:G:O2'	2.15	0.58
50:Ab:37:LEU:HD11	50:Ab:52:ILE:HG12	1.86	0.58
1:B5:2370:A:OP2	24:BU:110:TYR:OH	2.22	0.57
1:B5:3080:G:H2'	1:B5:3081:G:C8	2.39	0.57
46:A2:1483:G:O2'	46:A2:1621:C:OP1	2.21	0.57
1:B5:1357:C:O2'	1:B5:1360:C:O4'	2.22	0.57
1:B5:3450:G:H2'	1:B5:3451:G:H8	1.67	0.57
1:B5:3506:U:H2'	1:B5:3507:C:C6	2.38	0.57
10:BF:223:ILE:HG13	10:BF:229:GLY:HA3	1.84	0.57
20:BQ:15:ARG:NH2	20:BQ:19:LYS:H	2.01	0.57
58:Ak:20:LYS:HE2	58:Ak:20:LYS:HA	1.86	0.57
70:AF:130:LYS:HG2	70:AF:141:THR:HG22	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:Ar:127:TRP:O	75:Ar:144:ARG:NH2	2.37	0.57
1:B5:457:G:H22	1:B5:639:G:N2	2.03	0.57
1:B5:1223:C:H2'	1:B5:1224:G:H8	1.69	0.57
18:BO:185:VAL:O	18:BO:189:ILE:HG12	2.03	0.57
46:A2:1095:C:H42	46:A2:1106:C:H5	1.52	0.57
74:Ao:34:MET:SD	74:Ao:46:ASN:ND2	2.77	0.57
1:B5:3570:G:O6	36:Bg:101:LYS:NZ	2.26	0.57
46:A2:352:C:H2'	46:A2:353:A:H8	1.68	0.57
46:A2:65:C:H4'	54:Af:172:LYS:HE3	1.86	0.57
46:A2:965:C:H2'	46:A2:966:A:C8	2.40	0.57
1:B5:4265:A:OP1	18:BO:188:LYS:NZ	2.37	0.57
70:AF:150:TRP:HE1	80:Aq:37:GLU:CD	2.12	0.57
8:BD:62:CYS:HB3	8:BD:105:LEU:HD22	1.86	0.57
46:A2:314:C:O2'	46:A2:315:OMU:OP1	2.22	0.57
46:A2:886:G:H1	46:A2:971:U:H3	1.52	0.57
46:A2:1548:C:O2	76:As:12:GLN:NE2	2.37	0.57
47:Aa:40:ASN:N	47:Aa:75:GLN:OE1	2.29	0.57
79:V:69:C:H2'	79:V:70:G:C8	2.39	0.57
83:B7:301:HOH:O	8:BD:276:LYS:NZ	2.37	0.57
10:BF:176:ARG:HG2	10:BF:205:PHE:CD1	2.40	0.57
40:Bk:26:LYS:HB2	40:Bk:69:LEU:HD12	1.85	0.57
43:Bo:70:LEU:HD11	43:Bo:83:LEU:HD22	1.87	0.57
45:Br:26:SER:HB3	45:Br:28:GLU:OE1	2.05	0.57
62:Au:31:SER:O	66:AZ:141:ASN:ND2	2.32	0.57
51:Ad:192:ILE:HB	51:Ad:243:GLY:HA3	1.87	0.57
1:B5:2328:G:N2	1:B5:2331:A:OP2	2.32	0.57
3:B7:93:U:H2'	3:B7:94:C:C6	2.40	0.57
8:BD:156:GLY:HA2	8:BD:181:PRO:HG3	1.86	0.57
32:Bc:57:LYS:O	32:Bc:61:GLU:HG3	2.04	0.57
46:A2:1380:G:O2'	46:A2:1382:G:OP2	2.13	0.57
1:B5:158:A:H5''	1:B5:159:C:H2'	1.87	0.56
1:B5:1808:G:O2'	34:Be:57:ASN:OD1	2.22	0.56
46:A2:901:U:O2'	60:An:135:ILE:O	2.23	0.56
69:Ae:122:GLU:OE2	69:Ae:203:ARG:NH1	2.38	0.56
1:B5:461:C:H2'	1:B5:462:G:H8	1.70	0.56
1:B5:3438:G:O2'	1:B5:3491:G:N2	2.36	0.56
46:A2:1178:A:N3	46:A2:1632:U:O2'	2.33	0.56
46:A2:1498:U:OP1	67:Ap:37:ARG:NH2	2.37	0.56
73:Al:81:ASP:HB3	73:Al:84:LYS:HG2	1.86	0.56
1:B5:3493:G:H21	1:B5:3495:A:H8	1.53	0.56
7:BC:312:ARG:NH2	83:BC:506:HOH:O	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:BI:189:ARG:NH2	13:BI:199:TYR:OH	2.38	0.56
15:BL:64:VAL:HA	15:BL:67:HIS:ND1	2.20	0.56
24:BU:84:LYS:HG2	24:BU:88:LYS:HE2	1.87	0.56
29:BZ:47:ASP:HB3	29:BZ:69:LYS:HG2	1.88	0.56
43:Bo:59:LYS:NZ	43:Bo:61:LYS:O	2.30	0.56
46:A2:601:A:H2'	46:A2:602:A:C8	2.40	0.56
46:A2:1733:G:O2'	46:A2:1734:G:OP1	2.22	0.56
59:Am:99:ARG:NH2	59:Am:119:GLU:OE2	2.36	0.56
70:AF:31:ILE:HG21	70:AF:299:PHE:HE2	1.70	0.56
1:B5:4432:A:H4'	1:B5:4433:G:OP1	2.06	0.56
6:BB:36:ASP:OD2	6:BB:38:SER:OG	2.23	0.56
46:A2:488:C:H2'	46:A2:489:A:H8	1.70	0.56
46:A2:971:U:OP1	46:A2:1087:G:O2'	2.24	0.56
46:A2:1175:A:H2'	46:A2:1176:C:C6	2.40	0.56
50:Ab:166:LEU:HD23	50:Ab:195:THR:HG22	1.88	0.56
71:AG:20:SER:OG	72:Aj:65:ARG:NH1	2.38	0.56
1:B5:2084:C:H2'	1:B5:2085:G:H8	1.70	0.56
46:A2:1463:A:OP1	68:AC:83:LYS:NZ	2.38	0.56
70:AF:11:LEU:HB2	70:AF:307:VAL:HB	1.88	0.56
1:B5:512:U:OP1	15:BL:163:ARG:NH2	2.38	0.56
1:B5:3084:U:H2'	1:B5:3085:A:C8	2.41	0.56
1:B5:3551:C:N4	1:B5:3552:G:N3	2.54	0.56
7:BC:296:GLN:HB3	7:BC:300:LYS:NZ	2.21	0.56
9:BE:200:HIS:HB3	9:BE:203:PHE:HD2	1.71	0.56
51:Ad:79:ASP:HB3	51:Ad:82:TYR:HB2	1.86	0.56
71:AG:22:ARG:HG2	71:AG:38:MET:HG2	1.87	0.56
2:B8:141:C:H2'	2:B8:142:U:C6	2.41	0.56
29:BZ:50:PRO:HD3	29:BZ:68:ILE:HG12	1.88	0.56
46:A2:144:G:H2'	46:A2:145:G:C8	2.41	0.56
1:B5:493:C:H2'	1:B5:494:G:C8	2.40	0.56
1:B5:715:G:H2'	1:B5:716:C:C6	2.41	0.56
1:B5:1384:C:H2'	1:B5:1385:A:H8	1.71	0.56
1:B5:3770:C:OP1	23:BT:70:HIS:NE2	2.38	0.56
5:BA:20:VAL:HA	5:BA:23:ARG:HG3	1.88	0.56
29:BZ:78:ASN:OD1	32:Bc:39:ARG:NH2	2.39	0.56
46:A2:1544:A:N3	46:A2:1608:U:O2'	2.32	0.56
70:AF:217:MET:HE3	70:AF:219:TRP:CH2	2.41	0.56
1:B5:495:G:H1	1:B5:600:C:H42	1.54	0.56
65:Ax:18:LEU:O	65:Ax:85:ASN:ND2	2.38	0.56
72:Aj:51:SER:HB3	72:Aj:55:ARG:HH21	1.71	0.56
74:Ao:114:HIS:ND1	74:Ao:118:GLU:OE1	2.34	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:1599:C:H41	1:B5:3821:A:H5''	1.71	0.56
1:B5:1687:U:H2'	1:B5:1688:A:C8	2.40	0.56
1:B5:2493:A:H2'	1:B5:2494:A:C8	2.40	0.56
46:A2:394:A:H5''	56:Ah:22:HIS:HB3	1.87	0.56
46:A2:954:A:H2'	46:A2:955:A:C8	2.39	0.56
46:A2:1418:U:H4'	46:A2:1419:C:O5'	2.06	0.56
46:A2:1617:U:O4	46:A2:1618:A:N6	2.39	0.56
51:Ad:151:ASP:HB3	51:Ad:154:ILE:HG13	1.87	0.56
57:Ai:103:GLU:O	57:Ai:106:LEU:N	2.38	0.56
1:B5:715:G:H2'	1:B5:716:C:H6	1.71	0.55
1:B5:1426:A:H4'	1:B5:1427:G:H5'	1.86	0.55
1:B5:3081:G:H2'	1:B5:3082:C:C6	2.40	0.55
1:B5:3874:PSU:P	13:BI:6:PRO:HG3	2.46	0.55
1:B5:4325:G:H2'	1:B5:4326:A:C8	2.40	0.55
61:At:18:HIS:HB3	61:At:94:PRO:HG3	1.88	0.55
75:Ar:67:VAL:O	75:Ar:71:MET:HG3	2.06	0.55
8:BD:164:LYS:HG2	8:BD:195:HIS:NE2	2.22	0.55
28:BY:30:MET:HB3	28:BY:101:PRO:HG2	1.88	0.55
1:B5:1446:A:N3	1:B5:3832:C:O2'	2.36	0.55
1:B5:3765:G:N2	1:B5:3768:A:OP2	2.37	0.55
24:BU:97:ARG:NH2	83:BU:201:HOH:O	2.39	0.55
46:A2:860:G:H2'	46:A2:861:A:C8	2.41	0.55
46:A2:1312:G:N2	46:A2:1315:A:OP2	2.30	0.55
46:A2:1550:U:H2'	46:A2:1551:U:C6	2.41	0.55
1:B5:1361:A:H5'	1:B5:1365:C:H42	1.70	0.55
1:B5:1657:A:H2'	1:B5:1658:G:C8	2.42	0.55
1:B5:3209:A:H2'	1:B5:3210:A:C8	2.41	0.55
57:Ai:113:GLN:HG3	57:Ai:149:VAL:HG21	1.88	0.55
72:Aj:60:GLU:HG2	72:Aj:69:TRP:CD1	2.41	0.55
1:B5:1592:A:H4'	1:B5:1608:G:N2	2.22	0.55
1:B5:3413:G:H21	17:BN:125:SER:HB2	1.71	0.55
1:B5:4254:U:O3'	35:Bf:1:MET:N	2.39	0.55
74:Ao:93:MET:HE1	74:Ao:106:GLU:HG2	1.89	0.55
1:B5:2075:G:H5''	34:Be:127:ALA:HB2	1.88	0.55
1:B5:2234:U:H2'	1:B5:2235:G:C8	2.42	0.55
1:B5:3141:G:H2'	1:B5:3142:G:H8	1.71	0.55
46:A2:1543:A:H2'	46:A2:1544:A:C8	2.42	0.55
58:Ak:75:GLY:HA3	58:Ak:88:ILE:HD12	1.88	0.55
1:B5:2356:C:H5''	21:BR:96:MET:HE1	1.88	0.55
1:B5:3821:A:O2'	1:B5:3822:A:H2'	2.07	0.55
1:B5:4081:U:H2'	1:B5:4082:G:N3	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:BB:41:VAL:HA	6:BB:187:GLY:HA3	1.89	0.55
15:BL:56:ARG:NH1	15:BL:74:ARG:O	2.38	0.55
46:A2:488:C:H2'	46:A2:489:A:C8	2.42	0.55
46:A2:491:U:H2'	46:A2:492:A:C8	2.41	0.55
47:Aa:190:PRO:O	47:Aa:195:LYS:NZ	2.39	0.55
1:B5:1842:G:H2'	1:B5:1843:A:C8	2.42	0.55
1:B5:4034:U:H2'	1:B5:4035:C:C6	2.42	0.55
1:B5:4277:A:N6	1:B5:4288:G:H1	2.02	0.55
24:BU:48:LYS:HG2	24:BU:53:ALA:HB2	1.88	0.55
46:A2:617:G:N2	46:A2:624:C:H5''	2.21	0.55
46:A2:832:G:H2'	46:A2:833:A:H8	1.71	0.55
66:AZ:13:GLU:OE2	66:AZ:17:LYS:NZ	2.37	0.55
69:Ae:123:ASP:OD1	69:Ae:124:SER:N	2.35	0.55
80:Aq:10:LYS:HB3	80:Aq:14:ARG:NH1	2.22	0.55
80:Aq:34:VAL:O	80:Aq:38:ILE:HG12	2.07	0.55
1:B5:3694:C:H5''	14:BJ:108:GLY:HA3	1.88	0.55
11:BG:80:ILE:HG23	11:BG:164:ILE:HD13	1.88	0.55
18:BO:3:GLU:HB3	18:BO:31:ARG:HH22	1.72	0.55
46:A2:12:U:H2'	46:A2:13:C:C6	2.41	0.55
46:A2:878:A:O2'	46:A2:880:A:OP1	2.24	0.55
46:A2:1724:G:H2'	46:A2:1725:G:H8	1.72	0.55
51:Ad:54:TYR:O	65:Ax:15:ASN:ND2	2.40	0.55
1:B5:500:G:H2'	1:B5:501:G:C8	2.41	0.55
1:B5:1527:G:H2'	1:B5:1528:G:C8	2.42	0.55
1:B5:1870:G:O2'	1:B5:1933:G:N1	2.35	0.55
1:B5:2269:C:H2'	1:B5:2270:G:C8	2.42	0.55
1:B5:2593:A:O2'	1:B5:4074:G:H4'	2.07	0.55
1:B5:3858:A:H4'	13:BI:74:LYS:HD3	1.88	0.55
8:BD:116:ASP:OD1	8:BD:117:LYS:N	2.40	0.55
41:BI:20:ASN:ND2	41:BI:42:ARG:O	2.31	0.55
46:A2:990:C:H5''	59:Am:109:LYS:HD2	1.89	0.55
46:A2:1553:G:OP1	77:Ay:80:ARG:NH1	2.40	0.55
46:A2:1810:C:H2'	46:A2:1811:G:C8	2.42	0.55
61:At:56:MET:HG3	61:At:86:LYS:HG2	1.89	0.55
1:B5:2238:C:H4'	1:B5:2240:C:N4	2.22	0.54
1:B5:3427:U:H2'	1:B5:3428:G:C8	2.42	0.54
1:B5:3951:C:OP1	25:BV:43:LYS:NZ	2.34	0.54
1:B5:3980:C:H2'	1:B5:3981:G:H8	1.71	0.54
1:B5:4362:U:H2'	1:B5:4363:G:C8	2.41	0.54
7:BC:7:LEU:O	45:Br:71:ARG:NH2	2.40	0.54
12:BH:103:VAL:HG11	12:BH:144:LEU:HD21	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BV:13:LYS:HD3	25:BV:128:LEU:HD11	1.89	0.54
32:Bc:38:ILE:HG21	32:Bc:63:TYR:HB3	1.89	0.54
46:A2:107:A:H2'	46:A2:108:G:C8	2.42	0.54
1:B5:1233:C:H2'	1:B5:1234:C:C6	2.42	0.54
1:B5:1851:A:H2'	1:B5:1852:A:C8	2.42	0.54
7:BC:36:VAL:HG11	7:BC:122:TYR:CD2	2.41	0.54
30:Ba:72:THR:HG22	30:Ba:110:LYS:HB3	1.88	0.54
46:A2:1235:C:H2'	46:A2:1236:A:H8	1.72	0.54
46:A2:1246:U:O4	46:A2:1269:C:N3	2.41	0.54
57:Ai:138:ARG:HH21	57:Ai:152:ASP:C	2.14	0.54
1:B5:3559:U:H2'	1:B5:3560:C:H6	1.73	0.54
24:BU:84:LYS:NZ	24:BU:102:VAL:O	2.38	0.54
69:Ae:39:ALA:HB1	69:Ae:44:TYR:CG	2.42	0.54
77:Ay:68:ILE:HB	77:Ay:109:TYR:HB2	1.90	0.54
78:Ac:99:ILE:HG23	78:Ac:173:ARG:HH12	1.71	0.54
1:B5:267:C:O2'	1:B5:268:G:O5'	2.24	0.54
1:B5:1370:G:H3'	1:B5:1371:G:C8	2.42	0.54
6:BB:112:ASP:O	6:BB:116:ARG:HG3	2.06	0.54
32:Bc:38:ILE:HD11	32:Bc:46:VAL:HG21	1.88	0.54
46:A2:1179:G:O2'	46:A2:1631:U:O2	2.23	0.54
47:Aa:48:LEU:O	47:Aa:65:ARG:NH1	2.36	0.54
70:AF:206:LEU:HA	70:AF:220:ASP:HA	1.90	0.54
73:Al:82:ASN:HA	73:Al:85:LEU:HB3	1.89	0.54
1:B5:1232:A:H2'	1:B5:1233:C:C6	2.43	0.54
1:B5:1732:G:H2'	1:B5:1733:A:C8	2.43	0.54
1:B5:1799:G:OP2	1:B5:1799:G:N2	2.40	0.54
1:B5:3131:G:O2'	1:B5:3170:U:OP1	2.19	0.54
1:B5:4142:U:H1'	1:B5:4143:A:H5''	1.88	0.54
46:A2:1246:U:O2'	46:A2:1273:U:O2'	2.24	0.54
70:AF:240:CYS:HG	70:AF:291:TRP:CD1	2.25	0.54
1:B5:1585:C:H2'	1:B5:1586:C:C6	2.42	0.54
1:B5:3350:G:H2'	1:B5:3351:G:C8	2.42	0.54
2:B8:102:G:OP2	2:B8:104:A:O2'	2.22	0.54
3:B7:110:G:H2'	3:B7:111:C:C6	2.43	0.54
9:BE:51:LYS:HG3	9:BE:52:TYR:CD2	2.43	0.54
11:BG:223:LYS:HD2	11:BG:227:ASN:HB2	1.88	0.54
46:A2:51:U:H2'	46:A2:52:G:C8	2.42	0.54
46:A2:600:C:H2'	46:A2:601:A:H8	1.73	0.54
46:A2:910:G:H2'	46:A2:911:C:C6	2.43	0.54
46:A2:1517:C:H2'	46:A2:1518:G:H8	1.72	0.54
50:Ab:123:ARG:O	50:Ab:127:ILE:HD12	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:Ab:238:GLN:OE1	62:Au:35:ASN:ND2	2.41	0.54
73:Al:42:LEU:O	73:Al:72:HIS:NE2	2.40	0.54
73:Al:95:ASP:OD1	73:Al:96:ARG:N	2.40	0.54
76:As:85:ASN:HB2	76:As:88:LEU:HB2	1.90	0.54
1:B5:617:U:H2'	1:B5:618:C:C6	2.42	0.54
25:BV:85:ARG:NH1	83:BV:304:HOH:O	2.40	0.54
27:BX:106:HIS:O	27:BX:110:GLN:HG3	2.08	0.54
46:A2:489:A:H2'	46:A2:490:A:H8	1.73	0.54
46:A2:1238:G:H2'	46:A2:1239:G:H8	1.71	0.54
75:Ar:38:ARG:HB3	76:As:45:LEU:HD21	1.89	0.54
1:B5:1402:G:H2'	1:B5:1403:C:C6	2.43	0.54
1:B5:4078:A:H3'	1:B5:4079:U:H4'	1.90	0.54
20:BQ:154:LYS:O	20:BQ:163:THR:OG1	2.25	0.54
22:BS:101:THR:HG22	22:BS:104:GLY:H	1.72	0.54
70:AF:259:TRP:HE1	70:AF:266:ILE:HG22	1.73	0.54
1:B5:3671:OMG:H5''	1:B5:3672:U:O4'	2.08	0.54
1:B5:3717:A:H2'	1:B5:3718:G:H8	1.70	0.54
46:A2:1189:C:O2'	46:A2:1211:A:N6	2.41	0.54
46:A2:1751:U:H2'	46:A2:1752:C:C6	2.43	0.54
56:Ah:103:LEU:HD13	56:Ah:170:LYS:HD3	1.90	0.54
1:B5:1258:A:H2'	1:B5:1259:A:C8	2.43	0.54
46:A2:57:U:OP1	46:A2:465:G:O2'	2.26	0.54
46:A2:1184:G:N1	46:A2:1594:G:OP2	2.36	0.54
57:Ai:30:LYS:O	57:Ai:34:GLU:HG2	2.07	0.54
64:Aw:105:PHE:HD1	64:Aw:121:LYS:HB3	1.73	0.54
1:B5:187:C:H5'	1:B5:245:C:H1'	1.90	0.53
1:B5:1093:G:H2'	1:B5:1094:G:C8	2.43	0.53
1:B5:4281:A:H4'	6:BB:95:THR:HG22	1.89	0.53
46:A2:29:G:H2'	46:A2:30:C:C6	2.43	0.53
46:A2:635:C:H2'	46:A2:636:U:C6	2.43	0.53
50:Ab:140:TYR:OH	50:Ab:146:GLY:O	2.25	0.53
72:Aj:3:MET:HE1	72:Aj:11:ILE:HD12	1.89	0.53
1:B5:62:A:OP1	17:BN:172:ARG:NH1	2.36	0.53
1:B5:4037:U:H2'	1:B5:4038:G:C8	2.43	0.53
3:B7:62:U:OP2	8:BD:276:LYS:NZ	2.36	0.53
8:BD:41:LYS:NZ	23:BT:32:ARG:O	2.31	0.53
12:BH:23:ARG:HA	12:BH:45:LEU:HD12	1.90	0.53
12:BH:27:VAL:HG12	12:BH:84:VAL:HG21	1.90	0.53
16:BM:130:LEU:HB3	18:BO:177:LEU:HD11	1.89	0.53
24:BU:24:ASP:HB3	24:BU:111:GLU:HB3	1.89	0.53
46:A2:74:G:O2'	46:A2:76:U:O4	2.27	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A2:328:U:H4'	46:A2:332:A:C8	2.43	0.53
46:A2:1159:U:H2'	46:A2:1160:U:C6	2.43	0.53
46:A2:1763:A:H2'	46:A2:1764:U:C6	2.43	0.53
56:Ah:160:SER:O	56:Ah:164:GLU:HG3	2.07	0.53
70:AF:280:LYS:HE2	80:Aq:63:ARG:HH22	1.73	0.53
1:B5:152:U:OP2	17:BN:49:ARG:NH2	2.39	0.53
1:B5:1403:C:O2'	1:B5:1405:U:OP2	2.20	0.53
1:B5:3387:C:H2'	1:B5:3388:C:H6	1.73	0.53
46:A2:617:G:H5'	46:A2:623:G:N2	2.24	0.53
46:A2:1217:A:H1'	46:A2:1222:C:N4	2.23	0.53
70:AF:214:GLY:HA2	70:AF:236:ILE:HG12	1.90	0.53
1:B5:3184:U:H2'	1:B5:3185:C:C6	2.43	0.53
4:Az:2:ARG:NH2	46:A2:1795:C:H3'	2.23	0.53
11:BG:192:ARG:NH2	83:BG:302:HOH:O	2.35	0.53
46:A2:1073:U:H1'	46:A2:1074:C:H2'	1.89	0.53
46:A2:1175:A:H2'	46:A2:1176:C:H6	1.74	0.53
46:A2:1185:G:C2	46:A2:1186:A:C8	2.97	0.53
50:Ab:158:ARG:HD3	50:Ab:163:LEU:HD12	1.89	0.53
53:AE:10:ARG:HB2	53:AE:33:ASP:OD1	2.07	0.53
61:At:31:SER:O	61:At:34:LYS:HG3	2.07	0.53
69:Ae:126:ARG:HH22	69:Ae:134:ARG:NH1	2.06	0.53
1:B5:159:C:H5''	38:Bi:25:ARG:HD2	1.91	0.53
1:B5:446:U:H3	1:B5:2063:G:N2	2.05	0.53
1:B5:613:C:H2'	1:B5:614:C:C6	2.43	0.53
27:BX:86:MET:HE1	27:BX:154:ILE:HG22	1.91	0.53
36:Bg:83:CYS:SG	36:Bg:86:CYS:HB2	2.49	0.53
46:A2:994:A:H4'	46:A2:1809:G:N2	2.24	0.53
47:Aa:112:SER:O	47:Aa:115:LYS:NZ	2.35	0.53
50:Ab:43:ASP:OD2	50:Ab:243:HIS:NE2	2.35	0.53
63:Av:15:ASN:ND2	63:Av:71:LYS:HA	2.24	0.53
70:AF:88:ARG:NH1	70:AF:97:THR:OG1	2.42	0.53
70:AF:256:ILE:HB	70:AF:270:LEU:HB2	1.89	0.53
76:As:34:VAL:O	76:As:52:TRP:NE1	2.38	0.53
80:Aq:24:LEU:HB2	80:Aq:58:MET:HE2	1.90	0.53
1:B5:2244:U:H2'	1:B5:2245:G:H8	1.71	0.53
1:B5:3848:G:H5'	13:BI:8:CYS:SG	2.49	0.53
2:B8:87:G:OP1	37:Bh:7:ARG:NH2	2.42	0.53
2:B8:96:C:H5''	37:Bh:66:LYS:HG2	1.90	0.53
5:BA:49:ILE:HD13	5:BA:60:LYS:NZ	2.24	0.53
7:BC:80:ARG:HG2	7:BC:80:ARG:HH11	1.74	0.53
21:BR:105:LEU:HD23	21:BR:138:LEU:HD23	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:Bo:54:PRO:O	79:V:75:C:O2'	2.20	0.53
47:Aa:136:ARG:HG2	47:Aa:138:PHE:CE1	2.44	0.53
48:AA:40:CYS:SG	48:AA:41:TYR:N	2.81	0.53
54:Af:116:LYS:NZ	54:Af:120:ASP:OD1	2.41	0.53
74:Ao:34:MET:HE2	74:Ao:45:LEU:HB3	1.89	0.53
75:Ar:14:ARG:HH11	75:Ar:17:ASN:HA	1.74	0.53
78:Ac:37:VAL:HG23	78:Ac:50:ILE:HD13	1.90	0.53
1:B5:1439:G:P	30:Ba:32:ARG:HH21	2.31	0.53
1:B5:2024:G:OP2	7:BC:312:ARG:HD3	2.09	0.53
12:BH:44:GLU:OE2	16:BM:2:VAL:N	2.42	0.53
18:BO:34:VAL:HG22	18:BO:103:LYS:HB2	1.90	0.53
45:Br:58:LYS:O	45:Br:83:ARG:NE	2.39	0.53
46:A2:67:C:C5	54:Af:162:LEU:HB3	2.44	0.53
46:A2:1244:G:O6	73:Al:36:ARG:HB3	2.09	0.53
46:A2:1393:A:H2'	46:A2:1394:A:C8	2.43	0.53
67:Ap:106:LYS:NZ	67:Ap:110:ASP:OD2	2.41	0.53
78:Ac:29:LEU:HB2	78:Ac:34:TYR:HB2	1.89	0.53
80:Aq:102:THR:C	80:Aq:104:GLU:H	2.16	0.53
1:B5:1270:A:H2'	1:B5:1271:C:C6	2.43	0.53
1:B5:1319:G:HO2'	1:B5:1391:C:HO2'	1.49	0.53
1:B5:1384:C:H2'	1:B5:1385:A:C8	2.44	0.53
1:B5:3133:A:H2'	1:B5:3134:U:H6	1.73	0.53
26:BW:45:ASN:HD21	26:BW:47:ARG:HB2	1.74	0.53
46:A2:1246:U:N3	46:A2:1269:C:C2	2.73	0.53
50:Ab:144:LYS:O	62:Au:4:ASP:N	2.36	0.53
1:B5:1471:G:O2'	1:B5:2561:A:N3	2.33	0.53
1:B5:1626:G:H1'	1:B5:1627:G:C8	2.43	0.53
1:B5:2028:A:O2'	34:Be:48:ARG:NH2	2.42	0.53
1:B5:2294:C:H4'	1:B5:2295:G:H5'	1.91	0.53
1:B5:3195:A2M:H2	1:B5:3411:G:C1'	2.39	0.53
6:BB:291:TYR:HB3	6:BB:298:LEU:HD11	1.91	0.53
12:BH:31:ARG:HD2	12:BH:188:GLN:HE22	1.74	0.53
17:BN:9:GLU:HB2	38:Bi:44:ILE:HG13	1.91	0.53
18:BO:9:LEU:HD23	18:BO:118:MET:HB2	1.89	0.53
19:BP:39:MET:HG2	19:BP:43:LYS:HD3	1.91	0.53
46:A2:1410:A:H2'	46:A2:1411:G:H8	1.74	0.53
1:B5:2514:A:H2'	1:B5:2515:A:C8	2.44	0.53
41:Bl:38:ASN:HB3	41:Bl:41:ARG:HG2	1.91	0.53
46:A2:118:C:H1'	46:A2:406:A:C5	2.44	0.53
46:A2:1056:C:H2'	46:A2:1057:G:C8	2.44	0.53
46:A2:1290:A:O2'	78:Ac:145:GLN:O	2.25	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A2:1692:G:OP1	54:Af:94:ARG:NH2	2.39	0.53
66:AZ:184:ARG:HG2	66:AZ:191:ARG:HG2	1.90	0.53
69:Ae:111:LEU:O	69:Ae:115:ILE:HG12	2.09	0.53
1:B5:28:C:H3'	17:BN:189:ARG:NH2	2.24	0.52
1:B5:1633:U:H2'	1:B5:1634:U:H6	1.74	0.52
46:A2:1667:A:H2'	46:A2:1668:C:C6	2.44	0.52
58:Ak:128:VAL:HG12	58:Ak:142:VAL:HA	1.91	0.52
66:AZ:2(A):SER:OG	66:AZ:56:GLU:OE2	2.21	0.52
77:Ay:79:ILE:HB	77:Ay:83:LEU:HD23	1.91	0.52
1:B5:521:C:H2'	1:B5:522:C:O4'	2.09	0.52
1:B5:1585:C:H2'	1:B5:1586:C:H6	1.74	0.52
19:BP:64:ASN:O	19:BP:80:GLN:NE2	2.43	0.52
46:A2:506:A:H2'	46:A2:507:G:C8	2.43	0.52
51:Ad:45:ILE:HA	51:Ad:61:VAL:HG11	1.90	0.52
55:Ag:60:ILE:HB	55:Ag:92:VAL:HG22	1.90	0.52
70:AF:36:ARG:HG2	70:AF:65:PHE:CG	2.44	0.52
75:Ar:5:ILE:HD12	75:Ar:5:ILE:H	1.74	0.52
78:Ac:124:ARG:O	78:Ac:128:GLU:HG3	2.09	0.52
78:Ac:172:VAL:O	78:Ac:173:ARG:NE	2.42	0.52
79:V:27:G:H2'	79:V:28:G:H8	1.73	0.52
1:B5:418:G:OP1	1:B5:2078:U:O2'	2.25	0.52
1:B5:656:U:H2'	1:B5:657:C:C6	2.43	0.52
1:B5:3973:UR3:H2'	1:B5:3974:U:H2'	1.92	0.52
1:B5:4060:G:OP1	6:BB:62:ARG:NH1	2.41	0.52
8:BD:110:LEU:HD22	8:BD:115:LEU:HB2	1.92	0.52
13:BI:43:VAL:HG21	13:BI:197:VAL:HG13	1.91	0.52
20:BQ:178:ARG:H	30:Ba:51:GLY:HA2	1.74	0.52
46:A2:861:A:H2'	46:A2:862:A:C8	2.45	0.52
48:AA:15:GLU:O	48:AA:23:ARG:NE	2.41	0.52
1:B5:1395:C:H2'	1:B5:1396:U:C6	2.44	0.52
1:B5:2457:U:HO2'	1:B5:2458:C:H3'	1.74	0.52
1:B5:2461:G:O6	21:BR:46:LYS:NZ	2.38	0.52
1:B5:2597:G:O2'	1:B5:3315:U:O4	2.23	0.52
3:B7:38:U:N3	3:B7:41:G:OP2	2.32	0.52
16:BM:24:LEU:HD11	16:BM:86:TRP:CG	2.44	0.52
34:Be:99:ILE:HG21	34:Be:108:ARG:HG2	1.92	0.52
46:A2:1762:U:H2'	46:A2:1763:A:C8	2.44	0.52
50:Ab:171:ARG:O	57:Ai:54:ARG:NH2	2.32	0.52
61:At:31:SER:O	61:At:35:VAL:HG23	2.10	0.52
1:B5:23:C:H2'	1:B5:24:G:O4'	2.10	0.52
1:B5:1205:C:O2'	7:BC:321:ASN:OD1	2.20	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:1634:U:H5'	10:BF:133:ILE:HD11	1.90	0.52
1:B5:3935:U:O2'	1:B5:3955:U:O2	2.24	0.52
6:BB:143:LYS:O	6:BB:147:GLU:HG2	2.09	0.52
10:BF:51:ARG:HD3	10:BF:187:ASP:OD1	2.09	0.52
60:An:85:CYS:HB3	60:An:90:ILE:HB	1.92	0.52
73:Al:35:ILE:HG13	73:Al:61:TYR:CE2	2.44	0.52
1:B5:597:C:H2'	1:B5:598:G:H8	1.75	0.52
20:BQ:178:ARG:N	30:Ba:51:GLY:HA2	2.24	0.52
24:BU:86:LEU:HD23	24:BU:89:LYS:HD3	1.91	0.52
26:BW:45:ASN:ND2	26:BW:47:ARG:HB2	2.25	0.52
46:A2:1268:U:H5''	73:Al:36:ARG:NH2	2.24	0.52
68:AC:108:VAL:HA	68:AC:114:ILE:HD12	1.92	0.52
75:Ar:98:VAL:HG11	75:Ar:106:LYS:HG3	1.92	0.52
1:B5:744:C:H4'	1:B5:745:G:C8	2.45	0.52
1:B5:1341:A:H4'	1:B5:1342:G:H5'	1.90	0.52
1:B5:2061:U:H2'	1:B5:2062:G:C8	2.44	0.52
1:B5:3394:A:H2'	1:B5:3395:G:H8	1.75	0.52
1:B5:3400:A:H2'	1:B5:3401:C:C6	2.45	0.52
1:B5:3631:U:H2'	1:B5:3632:U:C6	2.45	0.52
12:BH:59:LYS:HE2	12:BH:66:GLU:HB3	1.90	0.52
18:BO:157:GLU:OE1	18:BO:160:ARG:NH2	2.39	0.52
42:Bm:94:MET:HG2	42:Bm:105:PRO:HA	1.91	0.52
46:A2:315:OMU:OP1	58:Ak:90:ARG:NH2	2.38	0.52
46:A2:1190:U:H2'	46:A2:1191:G:C8	2.45	0.52
61:At:28:ASN:HB3	61:At:31:SER:HB3	1.92	0.52
64:Aw:107:ARG:HB3	64:Aw:110:HIS:HB3	1.91	0.52
1:B5:3195:A2M:H2	1:B5:3411:G:H1'	1.92	0.52
1:B5:3357:G:H2'	1:B5:3358:G:C8	2.44	0.52
1:B5:3489:C:H2'	1:B5:3490:G:H8	1.74	0.52
46:A2:157:A:H2'	46:A2:158:A2M:O4'	2.10	0.52
46:A2:1245:A:H2'	46:A2:1246:U:O4'	2.10	0.52
47:Aa:97:LEU:HB2	47:Aa:228:LEU:HD21	1.92	0.52
54:Af:142:ARG:HG3	54:Af:147:LEU:HB2	1.92	0.52
1:B5:352:C:OP2	7:BC:197:ARG:NH1	2.41	0.52
1:B5:2359:G:H2'	1:B5:2360:A:H8	1.75	0.52
1:B5:3836:G:O4'	1:B5:3890:5MC:HM52	2.10	0.52
1:B5:4228:G:H2'	1:B5:4229:G:C8	2.45	0.52
5:BA:68:ARG:HH11	5:BA:72:ARG:HH21	1.58	0.52
6:BB:228:TYR:CE1	6:BB:270:GLY:HA2	2.44	0.52
24:BU:80:LYS:HG2	24:BU:110:TYR:CE2	2.45	0.52
46:A2:329:U:OP1	46:A2:330:C:O2'	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A2:962:U:H2'	46:A2:963:G:H8	1.74	0.52
46:A2:1523:C:H2'	46:A2:1524:A:C8	2.45	0.52
46:A2:1622:U:H2'	46:A2:1623:C:C6	2.45	0.52
49:AB:21:THR:HB	49:AB:68:LEU:HD11	1.92	0.52
1:B5:162:A:H2'	1:B5:163:A:C8	2.45	0.52
1:B5:2049:C:H41	7:BC:143:ARG:HE	1.58	0.52
5:BA:6:ARG:NH1	83:BA:403:HOH:O	2.40	0.52
11:BG:58:PRO:HD2	11:BG:61:ILE:HD12	1.92	0.52
16:BM:85:LYS:O	16:BM:89:THR:HG23	2.10	0.52
18:BO:54:TYR:OH	18:BO:73:PHE:O	2.28	0.52
56:Ah:174:CYS:HB2	56:Ah:190:LEU:HD21	1.92	0.52
57:Ai:43:VAL:HG12	57:Ai:47:LYS:HE3	1.91	0.52
69:Ae:32:ILE:HD12	69:Ae:35:GLN:HG3	1.91	0.52
80:Aq:50:ILE:O	80:Aq:54:VAL:HG23	2.09	0.52
1:B5:308:A:N3	1:B5:311:G:O2'	2.42	0.51
1:B5:745:G:H2'	16:BM:19:ARG:NH2	2.25	0.51
1:B5:3410:G:H2'	1:B5:3411:G:H8	1.75	0.51
25:BV:48:ARG:NH1	25:BV:49:LEU:HB3	2.25	0.51
46:A2:51:U:H2'	46:A2:52:G:H8	1.75	0.51
46:A2:1500:A:H2'	46:A2:1501:G:C8	2.45	0.51
46:A2:1598:U:H2'	46:A2:1599:C:C6	2.45	0.51
73:Al:28:HIS:NE2	73:Al:116:LYS:HB2	2.24	0.51
1:B5:3373:C:H1'	6:BB:268:ARG:HH22	1.76	0.51
7:BC:218:ILE:O	7:BC:222:ARG:HB3	2.09	0.51
46:A2:1817:A:H1'	53:AE:79:ILE:HD13	1.91	0.51
54:Af:193:ALA:HA	54:Af:196:LYS:HD2	1.91	0.51
55:Ag:88:SER:OG	55:Ag:89:GLY:N	2.41	0.51
70:AF:5:MET:HB2	70:AF:270:LEU:HD21	1.92	0.51
70:AF:219:TRP:HZ3	70:AF:226:HIS:HB2	1.74	0.51
74:Ao:24:GLN:O	74:Ao:28:MET:HG3	2.10	0.51
75:Ar:6:PRO:HB2	75:Ar:9:PHE:HB2	1.91	0.51
1:B5:48:G:OP1	17:BN:192:TRP:NE1	2.41	0.51
1:B5:1439:G:O2'	15:BL:18:TRP:NE1	2.40	0.51
1:B5:1592:A:H4'	1:B5:1608:G:H22	1.75	0.51
1:B5:3204:A:H2'	1:B5:3205:A:C8	2.45	0.51
1:B5:4418:C:O2'	1:B5:4421:C:OP2	2.20	0.51
10:BF:46:LYS:O	10:BF:50:GLU:HG2	2.11	0.51
46:A2:456:U:H2'	46:A2:457:C:O4'	2.10	0.51
46:A2:1265:U:H2'	46:A2:1266:U:C6	2.45	0.51
46:A2:1375:C:O2'	46:A2:1377:C:N4	2.43	0.51
46:A2:1488:A:H2	46:A2:1491:G:N3	2.07	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:Aa:99:ASN:OD1	47:Aa:100:PHE:N	2.40	0.51
70:AF:178:ASN:HB2	70:AF:185:LYS:HD2	1.92	0.51
73:Al:42:LEU:HD23	73:Al:68:LEU:HD23	1.92	0.51
1:B5:68:U:OP1	17:BN:178:HIS:ND1	2.28	0.51
1:B5:520:U:H2'	1:B5:521:C:H6	1.75	0.51
1:B5:677:U:O2'	1:B5:680:C:OP1	2.20	0.51
1:B5:1536:A:H5'	5:BA:183:GLY:HA2	1.92	0.51
1:B5:2340:A:H2'	1:B5:2341:U:H6	1.76	0.51
1:B5:3767:A:H2'	1:B5:3768:A:C8	2.45	0.51
26:BW:23:ARG:HH21	26:BW:27:LYS:HD3	1.76	0.51
33:Bd:87:VAL:HG21	33:Bd:95:ARG:HG2	1.93	0.51
46:A2:982:A:OP2	59:Am:124:ARG:NH2	2.39	0.51
46:A2:1717:C:H2'	46:A2:1718:G:C8	2.45	0.51
47:Aa:108:ASP:OD1	47:Aa:109:LYS:N	2.43	0.51
63:Av:14:ILE:HD11	63:Av:27:ILE:HD11	1.92	0.51
77:Ay:74:SER:OG	77:Ay:79:ILE:O	2.22	0.51
80:Aq:59:LYS:O	80:Aq:63:ARG:NH1	2.41	0.51
2:B8:67:U:H2'	2:B8:68:G:C8	2.46	0.51
19:BP:27:LYS:HE2	19:BP:63:TYR:CD1	2.46	0.51
46:A2:590:A:O2'	46:A2:592:U:OP1	2.28	0.51
46:A2:839:G:N1	46:A2:864:C:O2	2.44	0.51
46:A2:1305:U:H2'	46:A2:1306:G:N3	2.26	0.51
66:AZ:52:LYS:HB2	80:Aq:109:LEU:HG	1.92	0.51
67:Ap:134:GLY:HA3	67:Ap:139:ALA:O	2.11	0.51
1:B5:1641:G:N3	1:B5:3657:A:H2'	2.25	0.51
1:B5:1675:A:C5	1:B5:1676:C:H1'	2.45	0.51
1:B5:3257:G:N2	83:B5:5335:HOH:O	2.42	0.51
1:B5:4123:G:H2'	1:B5:4124:A:C8	2.46	0.51
2:B8:28:C:H4'	7:BC:51:PRO:HG2	1.92	0.51
5:BA:210:PRO:O	5:BA:221:LYS:NZ	2.42	0.51
28:BY:31:SER:HA	28:BY:48:PRO:HA	1.91	0.51
54:Af:5:ILE:HG12	54:Af:111:LEU:HB2	1.91	0.51
55:Ag:98:ARG:NH1	55:Ag:132:ASP:OD2	2.28	0.51
64:Aw:107:ARG:HD3	64:Aw:112:VAL:HG22	1.93	0.51
77:Ay:50:PHE:HB3	77:Ay:55:TYR:HB2	1.91	0.51
1:B5:67:C:OP2	1:B5:313:G:N2	2.43	0.51
1:B5:1710:A:O2'	23:BT:108:ARG:NH2	2.42	0.51
11:BG:227:ASN:OD1	11:BG:230:TYR:OH	2.26	0.51
46:A2:416:A:O2'	46:A2:1690:A:N3	2.36	0.51
46:A2:898:U:H2'	46:A2:899:C:C6	2.46	0.51
46:A2:1411:G:O5'	80:Aq:59:LYS:NZ	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A2:1660:C:H2'	46:A2:1661:G:C8	2.45	0.51
70:AF:164:ILE:HG22	70:AF:178:ASN:HA	1.93	0.51
1:B5:409:A:O2'	1:B5:412:G:OP2	2.23	0.51
1:B5:789:U:H2'	1:B5:790:C:C6	2.45	0.51
1:B5:3198:U:H2'	1:B5:3199:G:H8	1.74	0.51
1:B5:3491:G:H2'	1:B5:3492:U:C6	2.46	0.51
1:B5:3651:U:OP1	1:B5:3777:U:O2'	2.26	0.51
1:B5:3947:C:H2'	1:B5:3948:C:C6	2.45	0.51
1:B5:4358:A:P	6:BB:116:ARG:HH22	2.34	0.51
5:BA:117:GLU:HG2	5:BA:124:GLY:H	1.76	0.51
9:BE:163:LEU:HD11	9:BE:205:ILE:HG13	1.93	0.51
14:BJ:112:HIS:CD2	14:BJ:117:ILE:HG21	2.45	0.51
46:A2:402:C:H2'	46:A2:403:C:C6	2.46	0.51
56:Ah:124:LYS:HB2	56:Ah:127:ALA:HB2	1.92	0.51
69:Ae:129:ARG:HD3	69:Ae:134:ARG:NH1	2.25	0.51
1:B5:691:U:H1'	1:B5:727:A:C8	2.46	0.51
1:B5:1836:U:OP1	1:B5:1858:U:O2'	2.25	0.51
1:B5:3242:G:O2'	1:B5:3244:C:N4	2.44	0.51
8:BD:108:ARG:CZ	8:BD:253:HIS:HB2	2.41	0.51
14:BJ:38:LYS:O	14:BJ:42:GLN:HG3	2.11	0.51
39:Bj:63:ARG:NH1	39:Bj:65:ARG:HH21	2.09	0.51
46:A2:1237:C:H2'	46:A2:1238:G:H8	1.76	0.51
46:A2:1268:U:H3'	73:Al:36:ARG:NH2	2.24	0.51
46:A2:1363:A:H2'	46:A2:1364:G:O4'	2.11	0.51
46:A2:1799:A:H2'	46:A2:1800:G:H8	1.73	0.51
50:Ab:241:THR:HG21	66:AZ:69:GLU:HB2	1.93	0.51
63:Av:86:LEU:HD21	63:Av:113:HIS:HB2	1.92	0.51
1:B5:3084:U:H2'	1:B5:3085:A:H8	1.75	0.51
1:B5:3729:C:H2'	1:B5:3730:G:C8	2.46	0.51
1:B5:3764:U:H2'	1:B5:3765:G:C8	2.46	0.51
1:B5:4008:C:OP1	18:BO:65:ASN:ND2	2.32	0.51
3:B7:55:A:O2'	14:BJ:151:ILE:O	2.20	0.51
7:BC:33:ARG:HG3	7:BC:122:TYR:OH	2.11	0.51
14:BJ:151:ILE:HG22	14:BJ:155:HIS:HB3	1.92	0.51
37:Bh:9:LEU:HA	37:Bh:12:LYS:HD2	1.92	0.51
46:A2:1712:G:O6	46:A2:1729:U:C2	2.64	0.51
59:Am:87:ASP:N	59:Am:87:ASP:OD1	2.44	0.51
68:AC:133:ALA:O	68:AC:139:HIS:ND1	2.39	0.51
1:B5:2413:G:H4'	1:B5:2426:G:H4'	1.93	0.50
1:B5:3347:C:H2'	1:B5:3348:A:H8	1.75	0.50
1:B5:3545:G:H2'	1:B5:3546:A:H8	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:4041:C:H2'	1:B5:4054:A:H61	1.76	0.50
1:B5:4265:A:O2'	1:B5:4267:C:OP1	2.25	0.50
2:B8:141:C:H2'	2:B8:142:U:H6	1.76	0.50
6:BB:19:ARG:HB2	6:BB:234:ARG:NH2	2.26	0.50
6:BB:88:GLY:HA3	6:BB:163:MET:HE2	1.92	0.50
46:A2:1332:C:H2'	46:A2:1333:G:O4'	2.10	0.50
46:A2:1374:C:H2'	46:A2:1375:C:C6	2.46	0.50
46:A2:1488:A:C8	46:A2:1559:G:H1'	2.46	0.50
46:A2:1543:A:N3	46:A2:1609:G:O2'	2.39	0.50
63:Av:90:GLN:OE1	63:Av:117:ARG:NH2	2.30	0.50
67:Ap:53:GLU:HG3	67:Ap:85:ARG:HH21	1.75	0.50
1:B5:109:G:OP2	15:BL:74:ARG:NH2	2.43	0.50
1:B5:175:C:H2'	1:B5:176:G:H8	1.75	0.50
1:B5:485:A:OP1	10:BF:19:ARG:NH2	2.44	0.50
1:B5:1315:A:H2'	1:B5:1316:G:C8	2.46	0.50
1:B5:3594:G:H2'	1:B5:3595:G:C8	2.47	0.50
1:B5:3835:OMG:H2'	1:B5:3890:5MC:HM51	1.94	0.50
1:B5:4264:G:O3'	18:BO:188:LYS:NZ	2.45	0.50
33:Bd:136:ARG:HD3	33:Bd:168:LEU:HD13	1.92	0.50
57:Ai:107:GLU:HA	57:Ai:112:THR:HG21	1.94	0.50
67:Ap:77:HIS:O	67:Ap:81:ILE:HG12	2.11	0.50
68:AC:132:MET:HE1	68:AC:141:CYS:HB2	1.93	0.50
1:B5:1142:U:H2'	1:B5:1143:G:C8	2.45	0.50
1:B5:2558:G:O2'	1:B5:4087:G:OP1	2.26	0.50
1:B5:4217:C:H2'	1:B5:4218:G:C8	2.46	0.50
1:B5:4347:U:OP1	83:B5:4903:HOH:O	2.20	0.50
44:Bp:26:VAL:O	44:Bp:30:GLU:HG3	2.12	0.50
46:A2:1258:G:N3	74:Ao:51:ARG:NH2	2.59	0.50
46:A2:1458:C:H2'	46:A2:1459:U:C6	2.46	0.50
46:A2:1688:U:H2'	46:A2:1689:G:O4'	2.12	0.50
47:Aa:181:LEU:O	47:Aa:185:VAL:HG23	2.11	0.50
80:Aq:18:GLU:HG2	80:Aq:70:SER:H	1.77	0.50
1:B5:365:G:O6	39:Bj:52:LYS:NZ	2.42	0.50
7:BC:41:HIS:CE1	7:BC:45:ARG:HD3	2.45	0.50
8:BD:289:ARG:O	8:BD:293:ARG:HG2	2.11	0.50
13:BI:66:GLU:OE1	13:BI:69:ARG:NH1	2.45	0.50
46:A2:1235:C:H2'	46:A2:1236:A:C8	2.47	0.50
46:A2:1393:A:H2'	46:A2:1394:A:H8	1.77	0.50
46:A2:1451:U:O2'	46:A2:1453:A:OP1	2.27	0.50
46:A2:1628:U:H2'	46:A2:1629:G:O4'	2.12	0.50
46:A2:1810:C:H2'	46:A2:1811:G:H8	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:Ad:151:ASP:OD2	54:Af:216:ARG:NH2	2.45	0.50
60:An:75:MET:SD	60:An:79:GLN:NE2	2.84	0.50
69:Ae:126:ARG:NH1	69:Ae:127:ILE:O	2.44	0.50
72:Aj:22:VAL:HG22	72:Aj:68:TYR:HD1	1.76	0.50
1:B5:412:G:H4'	1:B5:413:G:H5''	1.94	0.50
1:B5:2292:A:H2	1:B5:2522:G:H22	1.59	0.50
1:B5:4414:G:H2'	1:B5:4415:A:C8	2.46	0.50
8:BD:53:VAL:HG11	8:BD:159:VAL:HA	1.93	0.50
9:BE:79:TYR:O	9:BE:82:LYS:NZ	2.29	0.50
46:A2:983:U:H2'	46:A2:984:C:O4'	2.12	0.50
46:A2:1454:U:H4'	78:Ac:176:LEU:HD13	1.93	0.50
55:Ag:65:PRO:HB2	55:Ag:68:GLN:HB2	1.94	0.50
69:Ae:77:MET:HB2	69:Ae:158:ARG:CZ	2.41	0.50
74:Ao:41:GLN:HG3	74:Ao:84:ILE:HD13	1.93	0.50
1:B5:281:G:OP2	17:BN:44:ARG:NH2	2.43	0.50
1:B5:677:U:OP1	1:B5:679:C:O2'	2.25	0.50
1:B5:2329:U:O2'	29:BZ:79:HIS:ND1	2.41	0.50
1:B5:4236:G:H2'	1:B5:4237:U:C6	2.46	0.50
10:BF:239:ASN:O	10:BF:243:ARG:HG2	2.12	0.50
12:BH:94:SER:HB2	12:BH:142:ASP:HB3	1.93	0.50
14:BJ:44:THR:HG21	14:BJ:72:CYS:SG	2.52	0.50
46:A2:1071:A:H2'	46:A2:1072:U:C6	2.47	0.50
46:A2:1157:A:H2'	46:A2:1158:A:C8	2.46	0.50
66:AZ:111:GLN:HG2	66:AZ:112:ILE:HG23	1.94	0.50
79:V:58:A:O2'	79:V:60:C:OP2	2.28	0.50
1:B5:229:G:H5''	28:BY:11:ARG:HG3	1.94	0.50
1:B5:1360:C:H4'	1:B5:1361:A:H2'	1.94	0.50
1:B5:1383:C:H2'	1:B5:1384:C:H6	1.77	0.50
1:B5:2160:C:H2'	1:B5:2161:A:H8	1.77	0.50
1:B5:3563:G:OP2	1:B5:3563:G:N2	2.23	0.50
1:B5:4006:U:C2	1:B5:4007:A:C8	3.00	0.50
1:B5:4006:U:H2'	1:B5:4007:A:H8	1.77	0.50
2:B8:144:C:H2'	2:B8:145:C:C6	2.47	0.50
6:BB:342:LYS:NZ	83:BB:507:HOH:O	2.45	0.50
18:BO:128:ARG:NH1	22:BS:162:GLN:OE1	2.45	0.50
46:A2:5:U:H2'	46:A2:6:G:H8	1.76	0.50
46:A2:900:G:H2'	46:A2:901:U:C6	2.46	0.50
47:Aa:124:HIS:HA	47:Aa:137:LEU:O	2.11	0.50
51:Ad:112:HIS:NE2	51:Ad:237:SER:O	2.44	0.50
80:Aq:29:HIS:HA	80:Aq:32:LYS:HE2	1.94	0.50
80:Aq:114:LEU:HD23	80:Aq:117:LEU:HD11	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:648:C:OP1	35:Bf:89:ARG:NH2	2.44	0.50
1:B5:1540:G:H1'	1:B5:2262:A:N6	2.27	0.50
1:B5:1746:A:OP1	23:BT:108:ARG:NH2	2.44	0.50
1:B5:2204:A:H1'	1:B5:2220:G:C5	2.46	0.50
1:B5:2223:G:H22	1:B5:2252:G:H5''	1.77	0.50
1:B5:2381:U:H2'	1:B5:2382:U:C6	2.47	0.50
1:B5:4228:G:H2'	1:B5:4229:G:H8	1.76	0.50
1:B5:4237:U:H2'	1:B5:4238:C:C6	2.47	0.50
2:B8:45:C:H4'	41:Bl:11:ARG:HD2	1.94	0.50
9:BE:160:LEU:HD13	9:BE:204:VAL:HG21	1.92	0.50
19:BP:54:LYS:HA	19:BP:83:TRP:CD1	2.46	0.50
37:Bh:106:LYS:O	37:Bh:110:LYS:HG2	2.11	0.50
46:A2:1752:C:H2'	46:A2:1753:G:O4'	2.11	0.50
56:Ah:57:ALA:HB2	56:Ah:183:GLY:HA2	1.93	0.50
67:Ap:93:VAL:HG13	67:Ap:105:LYS:HG2	1.94	0.50
73:Al:31:LEU:O	73:Al:31:LEU:HD23	2.11	0.50
73:Al:55:ASN:HB3	73:Al:82:ASN:CG	2.37	0.50
75:Ar:4:VAL:HG12	75:Ar:5:ILE:N	2.26	0.50
1:B5:425:U:H2'	1:B5:426:U:C6	2.47	0.50
1:B5:1222:U:C2	1:B5:1223:C:C5	2.99	0.50
1:B5:2270:G:H5'	1:B5:2389:G:H1'	1.93	0.50
1:B5:3370:C:O2'	1:B5:4350:A:N1	2.45	0.50
32:Bc:48:LEU:HD21	32:Bc:60:ILE:HG21	1.93	0.50
46:A2:17:C:H2'	46:A2:18:C:C6	2.46	0.50
46:A2:1572:G:N1	46:A2:1575:A:OP2	2.44	0.50
47:Aa:136:ARG:HB2	47:Aa:218:LEU:HD11	1.93	0.50
1:B5:72:G:N7	15:BL:67:HIS:HD2	2.09	0.49
1:B5:1361:A:H8	10:BF:33:ARG:HG3	1.77	0.49
1:B5:3617:C:H2'	1:B5:3618:G:H8	1.77	0.49
1:B5:4164:G:H2'	1:B5:4165:U:O4'	2.12	0.49
3:B7:4:U:H2'	3:B7:5:A:H8	1.77	0.49
5:BA:49:ILE:HD13	5:BA:60:LYS:HZ2	1.75	0.49
29:BZ:95:VAL:HG12	29:BZ:110:ALA:HA	1.94	0.49
46:A2:806:U:H2'	46:A2:807:A:H8	1.77	0.49
46:A2:1097:C:H2'	46:A2:1098:G:O4'	2.11	0.49
46:A2:1669:U:H2'	46:A2:1670:A:C8	2.46	0.49
50:Ab:96:LYS:HG2	50:Ab:114:CYS:HB2	1.93	0.49
1:B5:1271:C:H2'	1:B5:1272:G:C8	2.47	0.49
1:B5:2197:A:H2'	1:B5:2198:A:C8	2.47	0.49
1:B5:3199:G:H2'	1:B5:3200:A:H8	1.77	0.49
1:B5:3348:A:H2'	1:B5:3349:A:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:4062:U:H2'	1:B5:4063:OMU:H6	1.95	0.49
3:B7:48:G:H5'	8:BD:226:TYR:HE1	1.76	0.49
7:BC:5:ARG:HD2	7:BC:24:LEU:O	2.12	0.49
20:BQ:72:LEU:HB2	20:BQ:75:ARG:HD2	1.93	0.49
22:BS:98:ARG:HG3	22:BS:142:VAL:HG13	1.94	0.49
34:Be:78:LEU:O	45:Br:20:ARG:NH1	2.43	0.49
46:A2:409:A:H5''	56:Ah:25:ARG:HA	1.93	0.49
46:A2:1179:G:H2'	46:A2:1180:G:C8	2.47	0.49
46:A2:1647:U:H2'	46:A2:1648:G:C8	2.47	0.49
48:AA:67:THR:OG1	48:AA:70:LYS:O	2.29	0.49
51:Ad:173:ILE:HD11	51:Ad:235:TRP:CD2	2.47	0.49
54:Af:59:GLN:OE1	54:Af:72:ARG:NH2	2.44	0.49
78:Ac:163:PRO:O	78:Ac:167:TYR:HB2	2.11	0.49
79:V:23:A:H2'	79:V:24:G:H8	1.77	0.49
1:B5:1119:G:H2'	1:B5:1120:C:C6	2.47	0.49
1:B5:1755:G:H2'	1:B5:1756:C:C6	2.47	0.49
13:BI:152:LEU:HB3	13:BI:165:ILE:HD12	1.94	0.49
27:BX:144:ASP:O	27:BX:148:VAL:HG23	2.12	0.49
32:Bc:17:ARG:HD3	32:Bc:104:ILE:HA	1.94	0.49
43:Bo:82:MET:HE2	43:Bo:82:MET:HA	1.95	0.49
46:A2:1041:A:N7	46:A2:1795:C:O2'	2.41	0.49
46:A2:1113:U:OP1	50:Ab:156:THR:OG1	2.28	0.49
46:A2:1295:4AC:H2'	46:A2:1296:G:C8	2.47	0.49
46:A2:1731:C:H2'	46:A2:1732:C:H6	1.77	0.49
64:Aw:41:PHE:O	64:Aw:76:LYS:NZ	2.32	0.49
80:Aq:58:MET:HA	80:Aq:61:ILE:HG22	1.94	0.49
1:B5:1266:U:H5'	7:BC:109:ARG:HA	1.93	0.49
1:B5:3092:G:N2	83:B5:5344:HOH:O	2.43	0.49
1:B5:3184:U:H2'	1:B5:3185:C:H6	1.77	0.49
46:A2:903:U:H2'	46:A2:904:U:C6	2.48	0.49
46:A2:968:G:H2'	46:A2:969:A:C8	2.48	0.49
46:A2:1468:C:H2'	46:A2:1469:G:H8	1.78	0.49
61:At:46:LYS:HD3	61:At:97:ILE:HD11	1.93	0.49
65:Ax:102:THR:HG23	65:Ax:107:ARG:HE	1.75	0.49
72:Aj:53:LYS:HG3	72:Aj:60:GLU:HG3	1.95	0.49
75:Ar:43:VAL:HG11	75:Ar:83:PHE:CE2	2.47	0.49
1:B5:314:U:H5''	17:BN:179:LYS:HE3	1.95	0.49
1:B5:789:U:H2'	1:B5:790:C:H6	1.78	0.49
1:B5:2278:A:O2'	1:B5:2280:C:OP2	2.30	0.49
1:B5:3211:U:H2'	1:B5:3212:G:H5'	1.94	0.49
1:B5:3950:A:H2'	1:B5:3951:C:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:4291:G:H2'	1:B5:4292:C:C6	2.47	0.49
12:BH:34:LEU:HD12	12:BH:84:VAL:HG13	1.93	0.49
46:A2:503:U:C5	46:A2:504:C:H1'	2.47	0.49
46:A2:600:C:H2'	46:A2:601:A:C8	2.47	0.49
46:A2:1515:U:HO2'	46:A2:1538:C:HO2'	1.49	0.49
50:Ab:155:VAL:HG11	50:Ab:218:THR:HA	1.95	0.49
61:At:33:GLU:OE2	61:At:55:ARG:NH2	2.42	0.49
74:Ao:54:HIS:O	74:Ao:58:LYS:HG3	2.13	0.49
1:B5:1232:A:H2'	1:B5:1233:C:H6	1.77	0.49
1:B5:3433:G:H1	1:B5:3504:A:H2	1.57	0.49
1:B5:3436:U:H3'	1:B5:3437:A:H8	1.76	0.49
1:B5:3502:C:H2'	1:B5:3503:U:C6	2.48	0.49
1:B5:3729:C:H2'	1:B5:3730:G:H8	1.77	0.49
1:B5:4131:C:O2'	12:BH:155:SER:OG	2.29	0.49
2:B8:88:A:H2'	2:B8:89:U:O4'	2.12	0.49
46:A2:595:A:H2'	46:A2:596:G:H8	1.78	0.49
46:A2:1357:C:H4'	70:AF:100:ARG:NH2	2.27	0.49
46:A2:1406:G:OP1	80:Aq:32:LYS:NZ	2.38	0.49
55:Ag:130:LEU:HD21	55:Ag:156:VAL:HG21	1.95	0.49
55:Ag:162:GLN:HB3	55:Ag:165:ASN:HB3	1.92	0.49
60:An:75:MET:HG2	60:An:118:ALA:HB2	1.94	0.49
64:Aw:52:LEU:HD11	64:Aw:73:GLN:HB2	1.94	0.49
70:AF:32:LEU:HD12	70:AF:71:ILE:HG12	1.94	0.49
1:B5:1206:G:OP1	7:BC:316:LYS:NZ	2.39	0.49
1:B5:1516:A:H5''	1:B5:2588:U:H5''	1.95	0.49
1:B5:2041:C:H2'	1:B5:2042:U:C6	2.48	0.49
1:B5:4428:C:H2'	1:B5:4429:A:C8	2.48	0.49
34:Be:105:SER:HB3	34:Be:128:ARG:HB3	1.94	0.49
38:Bi:41:ARG:NH2	83:Bi:202:HOH:O	2.46	0.49
46:A2:28:U:H2'	46:A2:29:G:H8	1.77	0.49
46:A2:1359:A:H2'	46:A2:1360:A:C8	2.47	0.49
46:A2:1515:U:H2'	46:A2:1516:A:H8	1.76	0.49
56:Ah:11:ARG:NH1	56:Ah:15:GLY:O	2.43	0.49
56:Ah:81:VAL:HG22	56:Ah:102:VAL:HG12	1.95	0.49
70:AF:4:GLN:HG3	70:AF:267:VAL:HG22	1.94	0.49
1:B5:1830:C:C6	22:BS:161:ARG:HD3	2.47	0.49
1:B5:2359:G:H2'	1:B5:2360:A:C8	2.48	0.49
1:B5:4363:G:H2'	1:B5:4364:G:H8	1.78	0.49
15:BL:7:GLY:O	30:Ba:49:HIS:NE2	2.42	0.49
49:AB:55:VAL:HB	69:Ae:33:SER:HA	1.95	0.49
55:Ag:66:VAL:HG22	55:Ag:96:ALA:HB1	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:An:98:ARG:HB3	60:An:132:VAL:HG23	1.94	0.49
1:B5:434:A:C2	1:B5:3344:A2M:H4'	2.48	0.49
1:B5:1659:A:H2'	1:B5:1660:G:C8	2.48	0.49
1:B5:2337:G:H4'	1:B5:2338:C:H5'	1.94	0.49
1:B5:3508:U:H2'	1:B5:3509:G:C8	2.48	0.49
1:B5:3608:C:OP1	11:BG:53:ARG:NH2	2.46	0.49
20:BQ:177:ALA:O	20:BQ:184:ARG:HB2	2.12	0.49
46:A2:910:G:OP1	47:Aa:56:LYS:NZ	2.44	0.49
46:A2:1083:C:OP1	80:Aq:129:LYS:HD2	2.13	0.49
46:A2:1793:U:H2'	46:A2:1794:U:C6	2.48	0.49
46:A2:1816:G:OP2	83:A2:2101:HOH:O	2.19	0.49
47:Aa:30:TRP:O	47:Aa:94:LYS:HD2	2.12	0.49
55:Ag:78:ARG:O	55:Ag:82:GLU:HG2	2.12	0.49
66:AZ:176:TRP:HA	66:AZ:202:TYR:CE2	2.48	0.49
1:B5:277:C:H2'	38:Bi:29:ARG:HH12	1.78	0.49
1:B5:326:U:H2'	1:B5:327:C:C6	2.48	0.49
1:B5:3608:C:OP1	11:BG:245:LYS:NZ	2.46	0.49
1:B5:3787:U:H2'	1:B5:3788:C:C6	2.47	0.49
1:B5:4231:G:C5'	18:BO:169:ARG:HH12	2.26	0.49
46:A2:283:C:H2'	46:A2:284:C:C6	2.48	0.49
58:Ak:91:ASP:HB3	58:Ak:104:LYS:HE2	1.94	0.49
61:At:21:ARG:HH11	61:At:88:LEU:HD22	1.78	0.49
67:Ap:32:ILE:HG21	67:Ap:39:LEU:HD22	1.94	0.49
70:AF:206:LEU:HB2	70:AF:219:TRP:O	2.13	0.49
1:B5:1439:G:OP2	30:Ba:32:ARG:NH2	2.46	0.48
1:B5:2389:G:H2'	1:B5:2390:A:C8	2.48	0.48
1:B5:4414:G:H2'	1:B5:4415:A:H8	1.77	0.48
21:BR:172:ARG:HE	21:BR:176:ARG:HH22	1.60	0.48
22:BS:16:CYS:SG	22:BS:54:MET:HG2	2.53	0.48
33:Bd:75:GLU:HG2	33:Bd:138:ARG:HG2	1.93	0.48
38:Bi:80:HIS:HE2	38:Bi:84:LYS:HE2	1.78	0.48
46:A2:494:A:H2'	46:A2:495:G:C8	2.48	0.48
46:A2:887:G:H2'	46:A2:888:C:O4'	2.13	0.48
46:A2:898:U:H3	46:A2:960:U:H3	1.61	0.48
46:A2:1147:A:H2'	46:A2:1148:A:C8	2.48	0.48
46:A2:1812:G:OP2	60:An:146:ARG:NH2	2.37	0.48
49:AB:59:LEU:HD11	69:Ae:121:ARG:NH1	2.27	0.48
67:Ap:60:LYS:O	67:Ap:64:ALA:HB2	2.13	0.48
72:Aj:93:THR:O	78:Ac:67:ARG:NE	2.39	0.48
1:B5:622:C:H2'	1:B5:623:G:O4'	2.13	0.48
1:B5:1366:G:H3'	1:B5:2000:G:H22	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:1991:G:H5''	20:BQ:12:LYS:HD2	1.93	0.48
1:B5:2161:A:H2'	1:B5:2162:U:C6	2.47	0.48
1:B5:3388:C:H2'	1:B5:3389:U:H6	1.79	0.48
1:B5:4159:U:OP1	6:BB:276:HIS:ND1	2.45	0.48
1:B5:4291:G:H2'	1:B5:4292:C:H6	1.78	0.48
3:B7:93:U:H2'	3:B7:94:C:H6	1.78	0.48
6:BB:393:LYS:HA	6:BB:396:ARG:HG2	1.95	0.48
12:BH:85:THR:O	12:BH:188:GLN:NE2	2.45	0.48
28:BY:52:ASP:O	28:BY:108:ARG:NH2	2.46	0.48
46:A2:101:U:H5''	56:Ah:19:LYS:HE3	1.94	0.48
46:A2:499:U:H2'	46:A2:500:C:H6	1.78	0.48
65:Ax:51:THR:OG1	65:Ax:53:ASP:OD1	2.28	0.48
1:B5:65:A:N6	1:B5:75:G:H1'	2.28	0.48
1:B5:519:C:H2'	1:B5:520:U:O4'	2.13	0.48
1:B5:1119:G:H2'	1:B5:1120:C:H6	1.79	0.48
1:B5:1231:C:H2'	1:B5:1232:A:H8	1.78	0.48
1:B5:1595:U:H2'	1:B5:1596:U:C6	2.48	0.48
1:B5:4340:U:H2'	1:B5:4341:C:H6	1.78	0.48
14:BJ:144:LYS:O	14:BJ:148:THR:OG1	2.31	0.48
17:BN:50:ARG:NH1	83:BN:404:HOH:O	2.45	0.48
24:BU:85:TYR:CZ	24:BU:89:LYS:HD2	2.47	0.48
25:BV:34:ALA:HB2	25:BV:72:LEU:HD13	1.95	0.48
46:A2:1237:C:H2'	46:A2:1238:G:C8	2.48	0.48
54:Af:56:ASN:ND2	54:Af:60:GLY:O	2.44	0.48
69:Ae:101:LEU:HD11	77:Ay:100:VAL:HG21	1.95	0.48
70:AF:40:ILE:HD11	70:AF:66:VAL:HG11	1.94	0.48
72:Aj:59:LYS:HG2	72:Aj:70:TYR:HB2	1.95	0.48
79:V:9:A:H8	79:V:23:A:H62	1.60	0.48
79:V:70:G:H2'	79:V:71:G:H8	1.75	0.48
1:B5:2005:G:H2'	1:B5:2006:C:C6	2.48	0.48
1:B5:2024:G:H2'	1:B5:2025:A:C8	2.48	0.48
1:B5:2340:A:H2'	1:B5:2341:U:C6	2.49	0.48
1:B5:3125:A:H1'	1:B5:3262:A2M:N6	2.29	0.48
1:B5:3690:G:H4'	8:BD:4:VAL:HG11	1.95	0.48
1:B5:4068:C:O2'	1:B5:4069:A:H5'	2.13	0.48
12:BH:128:MET:HA	12:BH:128:MET:HE2	1.96	0.48
23:BT:36:LYS:HE2	23:BT:66:ASN:HA	1.95	0.48
46:A2:1582:C:H2'	46:A2:1583:C:H6	1.78	0.48
55:Ag:7:LYS:HB2	55:Ag:24:SER:HB2	1.95	0.48
68:AC:129:GLY:HA3	73:Al:40:LYS:NZ	2.28	0.48
76:As:56:ARG:C	76:As:58:ALA:H	2.22	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:1605:A:H5''	15:BL:3:PRO:O	2.13	0.48
1:B5:2232:G:H2'	1:B5:2233:A:H8	1.78	0.48
1:B5:2479:U:H2'	1:B5:2480:C:C6	2.48	0.48
1:B5:3917:A:H5''	42:Bm:125:LYS:HD2	1.95	0.48
1:B5:4265:A:P	18:BO:188:LYS:HZ1	2.37	0.48
6:BB:57:VAL:HG22	6:BB:73:VAL:HG22	1.94	0.48
22:BS:71:THR:O	22:BS:76:LYS:NZ	2.45	0.48
46:A2:1552:C:H4'	46:A2:1558:G:O6	2.14	0.48
46:A2:1616:A:OP2	71:AG:32:ARG:NH2	2.45	0.48
1:B5:162:A:H2'	1:B5:163:A:H8	1.78	0.48
1:B5:1271:C:H2'	1:B5:1272:G:H8	1.79	0.48
1:B5:1551:C:OP2	5:BA:9:ARG:HD2	2.14	0.48
1:B5:4244:G:H4'	1:B5:4245:G:H5''	1.94	0.48
7:BC:211:TYR:OH	7:BC:218:ILE:HD11	2.13	0.48
33:Bd:80:ILE:O	33:Bd:84:ILE:HG12	2.13	0.48
43:Bo:35:ALA:O	43:Bo:39:ARG:HG3	2.14	0.48
46:A2:883:G:H1	46:A2:975:U:H3	1.62	0.48
46:A2:1608:U:H2'	46:A2:1609:G:C8	2.48	0.48
1:B5:3247:U:H2'	1:B5:3248:C:C6	2.49	0.48
6:BB:102:PHE:CD2	6:BB:103:LYS:HG2	2.48	0.48
77:Ay:47:LEU:HB3	77:Ay:79:ILE:HG22	1.96	0.48
1:B5:759:G:H2'	1:B5:760:G:H8	1.78	0.48
1:B5:1635:U:H2'	1:B5:1636:U:C6	2.48	0.48
1:B5:3627:G:H5'	5:BA:233:ARG:HB2	1.96	0.48
1:B5:4177:A:H2'	1:B5:4178:G:C8	2.48	0.48
4:Az:12:ARG:HG2	4:Az:15:ARG:HH22	1.79	0.48
10:BF:40:PHE:O	10:BF:44:GLN:HG2	2.14	0.48
16:BM:119:ARG:HG3	18:BO:189:ILE:HB	1.95	0.48
25:BV:65:VAL:O	25:BV:73:ARG:HG2	2.14	0.48
51:Ad:197:ASN:ND2	51:Ad:199:GLU:OE2	2.46	0.48
70:AF:174:VAL:HG21	70:AF:219:TRP:HE1	1.79	0.48
1:B5:459:C:OP2	9:BE:124:ARG:NH1	2.46	0.48
1:B5:1481:A:H2'	1:B5:1482:G:H8	1.78	0.48
1:B5:1693:C:OP1	13:BI:133:GLN:NE2	2.39	0.48
1:B5:3195:A2M:H2	1:B5:3411:G:O4'	2.14	0.48
9:BE:171:ARG:O	9:BE:192:ASN:ND2	2.46	0.48
13:BI:54:SER:HB2	13:BI:135:ILE:HD11	1.95	0.48
46:A2:15:U:H2'	46:A2:16:G:O4'	2.13	0.48
48:AA:82:LYS:HD3	59:Am:25:TRP:CD2	2.49	0.48
69:Ae:126:ARG:HH22	69:Ae:134:ARG:CZ	2.27	0.48
75:Ar:4:VAL:HG12	75:Ar:5:ILE:H	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:522:C:H2'	1:B5:523:G:C8	2.49	0.48
1:B5:616:G:H2'	1:B5:617:U:C6	2.49	0.48
1:B5:721:U:H2'	1:B5:722:G:O4'	2.13	0.48
1:B5:2158:U:H4'	1:B5:2177:A:H4'	1.96	0.48
1:B5:3166:G:O2'	1:B5:3295:UY1:OP2	2.26	0.48
1:B5:3536:C:H2'	1:B5:3537:G:H8	1.79	0.48
1:B5:3635:A:H2'	1:B5:3636:C:H6	1.79	0.48
1:B5:4128:U:H2'	1:B5:4129:G:C8	2.49	0.48
2:B8:58:G:N7	39:Bj:63:ARG:NH2	2.47	0.48
76:As:9:VAL:HG11	76:As:135:ALA:O	2.14	0.48
1:B5:397:A:H2'	1:B5:398:G:C8	2.49	0.47
1:B5:408:A:O2'	1:B5:411:A:OP1	2.25	0.47
1:B5:597:C:H2'	1:B5:598:G:C8	2.49	0.47
1:B5:1153:C:H2'	1:B5:1154:G:C8	2.44	0.47
1:B5:1481:A:H2'	1:B5:1482:G:C8	2.49	0.47
1:B5:1802:C:H1'	1:B5:1846:C:O2	2.13	0.47
1:B5:3744:U:H4'	23:BT:54:HIS:CE1	2.49	0.47
22:BS:93:MET:HE1	22:BS:117:HIS:CE1	2.49	0.47
46:A2:1412:U:H2'	46:A2:1413:G:H8	1.78	0.47
46:A2:1486:A:H4'	46:A2:1560:G:H4'	1.96	0.47
46:A2:1613:G:OP2	46:A2:1615:C:N4	2.43	0.47
52:AD:85:LYS:O	52:AD:89:GLN:HG2	2.14	0.47
75:Ar:42:HIS:O	75:Ar:46:ARG:HG2	2.14	0.47
76:As:11:GLN:OE1	76:As:62:ARG:HD2	2.14	0.47
78:Ac:106:ARG:HG3	78:Ac:175:VAL:HG22	1.96	0.47
1:B5:1253:G:O2'	1:B5:2098:A:OP1	2.31	0.47
1:B5:3536:C:H2'	1:B5:3537:G:C8	2.49	0.47
1:B5:3788:C:H2'	1:B5:3789:U:C6	2.49	0.47
1:B5:3901:C:H2'	1:B5:3902:U:C6	2.48	0.47
3:B7:4:U:H2'	3:B7:5:A:C8	2.48	0.47
46:A2:394:A:H2'	46:A2:395:G:C8	2.49	0.47
46:A2:1046:U:H4'	46:A2:1047:G:OP2	2.14	0.47
47:Aa:198:GLU:HB2	47:Aa:210:VAL:HB	1.95	0.47
60:An:58:GLY:O	60:An:62:VAL:HG22	2.14	0.47
76:As:72:VAL:HG21	76:As:101:ARG:HG2	1.96	0.47
1:B5:20:U:H3'	1:B5:21:G:H8	1.80	0.47
1:B5:383:G:N1	1:B5:386:A:OP2	2.38	0.47
1:B5:1616:U:H2'	1:B5:1617:C:O4'	2.14	0.47
1:B5:1649:G:N3	1:B5:1689:U:H5'	2.29	0.47
10:BF:236:ASP:OD2	10:BF:237:GLN:NE2	2.41	0.47
11:BG:94:GLN:HG3	11:BG:218:LEU:HD21	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A2:499:U:H2'	46:A2:500:C:C6	2.48	0.47
46:A2:1186:A:O2'	46:A2:1589:A:N3	2.38	0.47
46:A2:1456:C:H2'	46:A2:1457:C:H6	1.79	0.47
46:A2:1625:C:H2'	46:A2:1626:G:C8	2.48	0.47
46:A2:1636:U:H2'	46:A2:1637:C:C6	2.48	0.47
46:A2:1755:A:H2'	46:A2:1756:C:C6	2.49	0.47
64:Aw:46:HIS:CD2	64:Aw:103:ALA:HB2	2.49	0.47
77:Ay:64:ASN:O	77:Ay:111:ARG:NH1	2.42	0.47
80:Aq:10:LYS:HD3	80:Aq:53:TYR:CE2	2.49	0.47
1:B5:106:A:H2'	1:B5:107:G:O4'	2.14	0.47
1:B5:223:G:H4'	1:B5:225:G:N7	2.29	0.47
1:B5:649:G:H2'	1:B5:650:A:C8	2.50	0.47
1:B5:716:C:H2'	1:B5:717:C:H6	1.80	0.47
1:B5:1851:A:H2'	1:B5:1852:A:H8	1.79	0.47
1:B5:3087:A:O2'	56:Ah:89:GLU:OE2	2.32	0.47
2:B8:5:U:H2'	2:B8:6:C:H6	1.78	0.47
5:BA:44:ILE:HD13	5:BA:87:PHE:CE1	2.49	0.47
13:BI:61:SER:HA	13:BI:126:VAL:HG12	1.94	0.47
37:Bh:80:PRO:O	37:Bh:84:ARG:HG3	2.14	0.47
46:A2:697:A:H4'	46:A2:697:A:OP1	2.14	0.47
46:A2:983:U:OP1	46:A2:1048:C:O2'	2.31	0.47
46:A2:1162:A:OP1	50:Ab:88:ARG:NE	2.44	0.47
46:A2:1162:A:H2'	46:A2:1163:C:C6	2.49	0.47
46:A2:1479:G:N7	75:Ar:141:ARG:NH1	2.63	0.47
55:Ag:51:ILE:HD11	55:Ag:176:VAL:HG22	1.96	0.47
55:Ag:118:ARG:O	55:Ag:121:THR:OG1	2.29	0.47
66:AZ:66:VAL:HG12	66:AZ:182:VAL:HG13	1.96	0.47
76:As:104:LEU:HD22	76:As:121:ARG:HG2	1.96	0.47
1:B5:108:A:N1	1:B5:334:U:O2'	2.47	0.47
1:B5:1556:G:H5'	1:B5:1557:A:OP1	2.15	0.47
1:B5:3161:G:H2'	1:B5:3162:C:C6	2.49	0.47
1:B5:3345:G:H22	1:B5:3377:G:H1'	1.79	0.47
27:BX:86:MET:SD	27:BX:155:ILE:HD11	2.54	0.47
46:A2:1306:G:OP1	50:Ab:92:ARG:NH2	2.48	0.47
50:Ab:224:PRO:HA	50:Ab:227:TRP:CG	2.49	0.47
55:Ag:100:ILE:HG12	55:Ag:125:VAL:HG21	1.96	0.47
69:Ae:126:ARG:HH12	69:Ae:134:ARG:NH1	2.12	0.47
70:AF:30:MET:HA	70:AF:43:TRP:O	2.15	0.47
70:AF:201:SER:OG	70:AF:205:SER:N	2.40	0.47
1:B5:4:G:H2'	1:B5:5:A:H8	1.80	0.47
1:B5:1346:G:N7	83:B5:5166:HOH:O	2.36	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:3617:C:H2'	1:B5:3618:G:C8	2.50	0.47
1:B5:3790:G:H2'	1:B5:3791:A:C8	2.50	0.47
1:B5:4283:G:H2'	1:B5:4284:U:H2'	1.96	0.47
30:Ba:75:LEU:HD11	30:Ba:133:ALA:HA	1.96	0.47
46:A2:542:U:H4'	65:Ax:66:GLY:HA2	1.96	0.47
46:A2:1190:U:H2'	46:A2:1191:G:H8	1.79	0.47
69:Ae:197:ARG:HE	79:V:41:C:H4'	1.78	0.47
80:Aq:71:ILE:HD13	80:Aq:74:GLN:HG3	1.96	0.47
1:B5:37:U:H5''	30:Ba:32:ARG:HD3	1.95	0.47
1:B5:173:C:H2'	1:B5:174:C:H6	1.79	0.47
1:B5:426:U:H2'	1:B5:427:A:H8	1.79	0.47
1:B5:520:U:H2'	1:B5:521:C:C6	2.50	0.47
1:B5:1325:C:H2'	1:B5:1326:G:H8	1.80	0.47
1:B5:1786:G:O6	31:Bb:10:HIS:NE2	2.47	0.47
1:B5:2016:U:C6	1:B5:2019:G:H4'	2.49	0.47
1:B5:2487:C:HO2'	1:B5:2489:G:H8	1.58	0.47
1:B5:3133:A:H2'	1:B5:3134:U:C6	2.50	0.47
1:B5:3247:U:H2'	1:B5:3248:C:H6	1.79	0.47
1:B5:3515:U:H2'	1:B5:3516:U:C6	2.49	0.47
1:B5:3570:G:O3'	36:Bg:90:ARG:NH2	2.47	0.47
1:B5:3900:PSU:H1'	6:BB:252:ALA:HB3	1.96	0.47
1:B5:3921:G:O2'	1:B5:4045:A:N1	2.47	0.47
1:B5:4036:C:H2'	1:B5:4037:U:H6	1.80	0.47
1:B5:4172:A:H5'	1:B5:4336:U:H1'	1.97	0.47
2:B8:47:C:H1'	2:B8:61:A:H2'	1.96	0.47
2:B8:123:U:H2'	2:B8:124:U:H2'	1.97	0.47
6:BB:116:ARG:HG2	6:BB:122:TRP:CD2	2.50	0.47
12:BH:96:TYR:HA	12:BH:177:ASP:OD1	2.15	0.47
13:BI:184:MET:HE2	13:BI:190:LEU:HG	1.97	0.47
27:BX:63:SER:HB2	37:Bh:69:LEU:HD13	1.96	0.47
28:BY:127:GLN:O	28:BY:131:GLU:HG2	2.15	0.47
30:Ba:100:VAL:HG22	30:Ba:123:ILE:HB	1.96	0.47
36:Bg:57:ARG:HG2	36:Bg:59:VAL:HG13	1.96	0.47
46:A2:764:U:H2'	46:A2:765:U:C6	2.50	0.47
46:A2:1353:C:O2'	46:A2:1354:A:H5'	2.14	0.47
55:Ag:66:VAL:HA	55:Ag:69:LEU:HD23	1.96	0.47
56:Ah:130:THR:HG22	56:Ah:132:GLU:OE1	2.15	0.47
66:AZ:123:VAL:HG22	66:AZ:145:ILE:HB	1.95	0.47
69:Ae:32:ILE:HA	69:Ae:35:GLN:HG2	1.97	0.47
70:AF:51:ASN:ND2	70:AF:53:GLY:O	2.47	0.47
70:AF:207:CYS:SG	70:AF:219:TRP:HB2	2.55	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:Aj:82:TYR:HD2	72:Aj:83:LEU:HD12	1.80	0.47
78:Ac:145:GLN:NE2	78:Ac:179:GLN:OE1	2.47	0.47
80:Aq:60:ARG:HH12	80:Aq:66:VAL:HG11	1.80	0.47
1:B5:167:C:H2'	1:B5:168:C:C6	2.50	0.47
1:B5:672:A:N6	1:B5:740:G:H21	2.10	0.47
1:B5:2234:U:O2	1:B5:2242:G:N2	2.35	0.47
1:B5:2382:U:H2'	1:B5:2383:C:H6	1.80	0.47
1:B5:3347:C:H2'	1:B5:3348:A:C8	2.50	0.47
1:B5:3849:U:C2	1:B5:3850:G:C8	3.02	0.47
1:B5:3979:OMC:HM22	1:B5:3980:C:O4'	2.15	0.47
1:B5:4022:PSU:H2'	1:B5:4023:U:C6	2.49	0.47
5:BA:80:GLU:HG3	44:Bp:66:GLY:HA2	1.97	0.47
6:BB:388:PHE:HD1	6:BB:389:MET:HE2	1.80	0.47
12:BH:63:ASN:O	12:BH:67:LEU:HG	2.15	0.47
46:A2:288:G:H2'	46:A2:290:G:C8	2.50	0.47
46:A2:481:A:O2'	46:A2:785:A:N3	2.40	0.47
46:A2:489:A:H2'	46:A2:490:A:C8	2.48	0.47
46:A2:1073:U:O2	46:A2:1074:C:O2'	2.28	0.47
65:Ax:80:ASP:OD1	65:Ax:81:TYR:N	2.47	0.47
1:B5:1697:C:OP1	13:BI:21:ARG:NH2	2.48	0.47
1:B5:2160:C:H2'	1:B5:2161:A:C8	2.50	0.47
1:B5:2318:G:H2'	1:B5:2319:C:C6	2.50	0.47
1:B5:3087:A:H2'	1:B5:3088:A:C8	2.50	0.47
24:BU:22:THR:HG23	24:BU:69:LYS:HG3	1.96	0.47
24:BU:66:SER:OG	24:BU:69:LYS:HB3	2.14	0.47
46:A2:314:C:H2'	46:A2:315:OMU:H6	1.95	0.47
46:A2:1713:G:N2	46:A2:1728:C:N3	2.62	0.47
73:Al:13:ASP:N	73:Al:13:ASP:OD1	2.48	0.47
1:B5:1461:U:H2'	1:B5:1462:G:H8	1.79	0.47
1:B5:1676:C:H2'	1:B5:1677:G:H8	1.79	0.47
1:B5:3096:G:H22	1:B5:3101:A:H1'	1.80	0.47
1:B5:3555:G:H2'	1:B5:3556:G:C8	2.50	0.47
1:B5:3558:C:H2'	1:B5:3559:U:H6	1.78	0.47
1:B5:3701:C:H2'	1:B5:3702:C:H6	1.80	0.47
9:BE:77:ALA:HA	9:BE:79:TYR:CE2	2.50	0.47
9:BE:109:ASP:OD1	9:BE:110:LYS:N	2.48	0.47
12:BH:47:LEU:HB3	12:BH:53:ARG:HH21	1.80	0.47
46:A2:279:C:OP2	54:Af:183:ARG:NH2	2.46	0.47
46:A2:1341:A2M:HM'3	46:A2:1341:A2M:H1'	1.75	0.47
50:Ab:46:ILE:HD11	50:Ab:236:PRO:HB3	1.97	0.47
54:Af:214:ALA:O	54:Af:218:LYS:HG2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:As:114:GLU:HG2	76:As:124:THR:HG22	1.96	0.47
1:B5:7:C:H2'	1:B5:8:U:C6	2.50	0.46
1:B5:1394:U:H2'	1:B5:1395:C:H6	1.81	0.46
1:B5:1417:U:H2'	1:B5:1418:G:H8	1.80	0.46
1:B5:1427:G:H2'	1:B5:1428:C:C6	2.50	0.46
1:B5:1622:C:O2'	1:B5:1624:G:OP2	2.28	0.46
1:B5:1626:G:O2'	1:B5:1628:U:OP1	2.29	0.46
1:B5:1659:A:H2'	1:B5:1660:G:H8	1.80	0.46
1:B5:3194:A:H2'	1:B5:3195:A2M:H8	1.97	0.46
6:BB:379:PHE:HD1	6:BB:384:GLU:HG2	1.80	0.46
8:BD:216:GLU:HG3	8:BD:220:LYS:NZ	2.30	0.46
9:BE:189:LEU:HD12	9:BE:193:ARG:HA	1.96	0.46
32:Bc:35:LEU:HD11	32:Bc:63:TYR:CZ	2.50	0.46
46:A2:1667:A:H2'	46:A2:1668:C:H6	1.80	0.46
46:A2:1691:G:H2'	46:A2:1692:G:C8	2.51	0.46
69:Ae:29:ILE:HG13	69:Ae:112:VAL:HG11	1.95	0.46
73:Al:31:LEU:HD21	73:Al:89:VAL:HG13	1.96	0.46
73:Al:59:PRO:HA	73:Al:62:VAL:HG22	1.96	0.46
1:B5:772:G:H8	1:B5:774:A:N6	2.14	0.46
1:B5:1455:G:OP2	39:Bj:31:LYS:NZ	2.36	0.46
1:B5:1672:G:N2	1:B5:1675:A:OP1	2.49	0.46
1:B5:3616:G:H2'	1:B5:3617:C:C6	2.50	0.46
1:B5:4212:G:H4'	18:BO:176:ARG:HE	1.79	0.46
11:BG:189:ARG:HG2	11:BG:192:ARG:NH1	2.27	0.46
12:BH:129:ARG:HH21	12:BH:160:LEU:HD11	1.80	0.46
23:BT:81:LYS:HG2	31:Bb:16:TRP:CZ2	2.50	0.46
26:BW:23:ARG:NH2	26:BW:27:LYS:HD3	2.30	0.46
46:A2:457:C:OP2	83:A2:2102:HOH:O	2.21	0.46
46:A2:1468:C:P	71:AG:12:ARG:HH22	2.38	0.46
46:A2:1572:G:N7	74:Ao:43:ARG:NH1	2.59	0.46
59:Am:94:LYS:O	59:Am:98:VAL:HG23	2.15	0.46
72:Aj:91:PRO:HD2	72:Aj:94:LEU:HD12	1.97	0.46
1:B5:90:G:OP2	1:B5:92:C:N4	2.40	0.46
1:B5:1280:G:H2'	1:B5:1281:U:C6	2.50	0.46
1:B5:1366:G:H2'	1:B5:1366:G:N3	2.30	0.46
1:B5:1475:G:O2'	1:B5:1497:G:N2	2.33	0.46
1:B5:1686:C:H5''	8:BD:5:LYS:HB2	1.96	0.46
1:B5:2055:G:H1'	1:B5:2081:A:N6	2.30	0.46
1:B5:2451:C:O3'	24:BU:113:ARG:NH1	2.48	0.46
1:B5:3558:C:H2'	1:B5:3559:U:C6	2.50	0.46
6:BB:57:VAL:HG13	26:BW:1:MET:HE3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:BR:36:ASN:OD1	21:BR:40:GLN:NE2	2.48	0.46
22:BS:74:ARG:O	22:BS:76:LYS:NZ	2.46	0.46
37:Bh:33:VAL:O	37:Bh:37:THR:HG23	2.14	0.46
46:A2:39:A:OP1	57:Ai:5:ARG:NH1	2.47	0.46
46:A2:1102:A:H2'	46:A2:1103:A:C8	2.50	0.46
46:A2:1295:4AC:H2'	46:A2:1296:G:H8	1.80	0.46
49:AB:58:LEU:HD23	49:AB:61:SER:HA	1.97	0.46
54:Af:52:ILE:HD13	54:Af:102:VAL:HG21	1.97	0.46
61:At:42:GLY:O	61:At:46:LYS:HG3	2.16	0.46
64:Aw:110:HIS:ND1	64:Aw:111:ALA:O	2.41	0.46
73:Al:82:ASN:OD1	73:Al:83:LYS:N	2.48	0.46
1:B5:153:G:H2'	1:B5:154:G:H8	1.80	0.46
1:B5:771:A:H4'	1:B5:772:G:O5'	2.15	0.46
1:B5:2613:A:H2'	1:B5:2614:U:C6	2.50	0.46
1:B5:3197:G:H1	1:B5:3210:A:H2	1.53	0.46
1:B5:3881:U:H2'	1:B5:3882:U:O4'	2.16	0.46
1:B5:4043:G:O2'	1:B5:4052:G:O6	2.33	0.46
1:B5:4256:G:N7	9:BE:282:ARG:NH2	2.63	0.46
1:B5:4398:C:H2'	1:B5:4398:C:O2	2.14	0.46
6:BB:10:ARG:NH1	6:BB:265:SER:O	2.49	0.46
19:BP:67:VAL:HA	19:BP:82:ARG:NH2	2.31	0.46
34:Be:35:TRP:CZ2	34:Be:56:PRO:HD2	2.50	0.46
46:A2:209:U:H2'	46:A2:210:U:C6	2.50	0.46
46:A2:404:U:H2'	46:A2:405:G:O4'	2.16	0.46
46:A2:595:A:H2'	46:A2:596:G:C8	2.50	0.46
46:A2:1251:A:H1'	68:AC:138:ARG:NE	2.31	0.46
46:A2:1720:C:O2'	46:A2:1722:A:N1	2.37	0.46
46:A2:1723:C:H2'	46:A2:1724:G:C8	2.50	0.46
55:Ag:191:GLU:OE1	55:Ag:191:GLU:N	2.48	0.46
61:At:34:LYS:NZ	61:At:107:GLU:HB2	2.31	0.46
61:At:94:PRO:O	61:At:96:GLU:N	2.48	0.46
78:Ac:99:ILE:HG23	78:Ac:173:ARG:NH1	2.30	0.46
80:Aq:61:ILE:HD12	80:Aq:64:GLY:O	2.14	0.46
1:B5:163:A:H2'	1:B5:164:G:H8	1.80	0.46
1:B5:280:A:C4	17:BN:12:ARG:HG2	2.50	0.46
1:B5:691:U:C2	1:B5:692:G:C8	3.03	0.46
1:B5:746:U:H2'	1:B5:747:C:C6	2.49	0.46
1:B5:3364:OMC:H5''	18:BO:71:TYR:CE2	2.51	0.46
1:B5:4275:G:H2'	1:B5:4276:G:H8	1.80	0.46
6:BB:258:HIS:HA	6:BB:259:PRO:C	2.40	0.46
46:A2:602:A:O2'	46:A2:606:C:OP1	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:Ah:119:LEU:HD11	56:Ah:153:LYS:HG2	1.95	0.46
61:At:37:ALA:HA	61:At:40:ILE:HG22	1.97	0.46
66:AZ:15:VAL:HG21	80:Aq:111:PHE:CE2	2.51	0.46
77:Ay:62:VAL:HG13	77:Ay:68:ILE:HD12	1.97	0.46
80:Aq:96:ILE:HB	80:Aq:117:LEU:HD23	1.96	0.46
1:B5:39:A:H5''	30:Ba:35:ALA:HB1	1.98	0.46
1:B5:163:A:H2'	1:B5:164:G:C8	2.51	0.46
1:B5:2127:G:N2	1:B5:2130:A:OP2	2.47	0.46
2:B8:148:A:H2'	2:B8:149:G:C8	2.51	0.46
6:BB:37:PRO:HA	6:BB:187:GLY:O	2.15	0.46
46:A2:349:U:H2'	46:A2:350:A:C8	2.50	0.46
46:A2:350:A:H2'	46:A2:351:C:C6	2.50	0.46
46:A2:653:G:H2'	46:A2:654:A:C8	2.51	0.46
46:A2:1094:U:H2'	46:A2:1095:C:C6	2.51	0.46
56:Ah:197:PHE:CZ	56:Ah:201:LYS:HE2	2.51	0.46
67:Ap:49:TYR:O	67:Ap:53:GLU:HG2	2.15	0.46
73:Al:22:LEU:HD22	73:Al:109:VAL:HG11	1.97	0.46
80:Aq:24:LEU:HD22	80:Aq:54:VAL:HG11	1.96	0.46
1:B5:1258:A:H2'	1:B5:1259:A:H8	1.80	0.46
1:B5:1395:C:H2'	1:B5:1396:U:H6	1.79	0.46
1:B5:2210:G:H2'	1:B5:2211:C:C6	2.51	0.46
1:B5:2500:G:H2'	1:B5:2501:G:H8	1.81	0.46
1:B5:3858:A:H2'	1:B5:3859:G:O4'	2.15	0.46
1:B5:4221:C:H2'	1:B5:4222:C:C6	2.51	0.46
1:B5:4318:U:H2'	1:B5:4319:C:C6	2.50	0.46
17:BN:3:ALA:O	17:BN:7:ILE:HG13	2.16	0.46
22:BS:51:LEU:HD13	23:BT:151:LEU:HB3	1.97	0.46
46:A2:96:C:H2'	46:A2:97:U:C6	2.51	0.46
46:A2:197:G:H2'	46:A2:198:G:C8	2.51	0.46
46:A2:379:A:H2'	46:A2:380:G:C8	2.51	0.46
46:A2:794:U:C4	46:A2:795:G:H1'	2.50	0.46
46:A2:968:G:H2'	46:A2:969:A:H8	1.81	0.46
46:A2:1736:G:H2'	46:A2:1738:G:C8	2.51	0.46
70:AF:245:ARG:HD2	70:AF:247:TRP:CE3	2.51	0.46
72:Aj:60:GLU:HG2	72:Aj:69:TRP:NE1	2.31	0.46
78:Ac:192:TRP:NE1	78:Ac:201:LYS:O	2.36	0.46
79:V:4:G:H2'	79:V:5:A:C8	2.51	0.46
1:B5:51:A:N7	83:B5:5174:HOH:O	2.36	0.46
1:B5:272:C:H2'	1:B5:273:U:C6	2.51	0.46
1:B5:1347:G:N1	1:B5:1381:C:OP2	2.33	0.46
1:B5:3555:G:H2'	1:B5:3556:G:H8	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:3598:C:H2'	1:B5:3599:G:O4'	2.15	0.46
1:B5:3680:C:OP1	1:B5:3770:C:O2'	2.33	0.46
16:BM:29:ASP:OD2	16:BM:67:SER:OG	2.33	0.46
20:BQ:35:LEU:O	20:BQ:39:THR:OG1	2.20	0.46
46:A2:994:A:H4'	46:A2:1809:G:H21	1.81	0.46
46:A2:1583:C:H2'	46:A2:1584:C:C6	2.50	0.46
48:AA:60:SER:O	48:AA:60:SER:OG	2.34	0.46
50:Ab:176:VAL:O	50:Ab:195:THR:OG1	2.24	0.46
69:Ae:72:THR:O	69:Ae:88:THR:HG21	2.16	0.46
70:AF:84:ASP:N	70:AF:84:ASP:OD1	2.48	0.46
72:Aj:80:ARG:HD3	72:Aj:85:LEU:HB2	1.98	0.46
75:Ar:120:HIS:CE1	75:Ar:124:ARG:HD2	2.51	0.46
1:B5:1954:G:O2'	1:B5:1955:G:H5''	2.16	0.46
1:B5:2445:A:H62	40:Bk:35:LYS:NZ	2.13	0.46
1:B5:4377:U:H4'	1:B5:4378:A:H5'	1.97	0.46
2:B8:127:U:H3'	2:B8:128:C:C6	2.51	0.46
34:Be:97:ALA:HB3	34:Be:122:ILE:HD13	1.98	0.46
36:Bg:73:HIS:HA	36:Bg:80:GLY:HA3	1.98	0.46
46:A2:547:G:H2'	57:Ai:172:ARG:HH12	1.81	0.46
46:A2:1402:G:OP1	61:At:85:HIS:ND1	2.47	0.46
46:A2:1554:U:OP2	77:Ay:46:ASN:ND2	2.39	0.46
46:A2:1732:C:H2'	46:A2:1733:G:C8	2.51	0.46
48:AA:3:LEU:HD13	62:Au:64:GLU:HG3	1.98	0.46
53:AE:46:GLU:O	53:AE:50:VAL:HG13	2.16	0.46
56:Ah:62:VAL:HG21	56:Ah:75:LYS:HE3	1.98	0.46
66:AZ:84:GLN:HG2	66:AZ:100:ALA:HB1	1.97	0.46
67:Ap:116:ASP:OD1	67:Ap:118:THR:OG1	2.34	0.46
80:Aq:16:ILE:HG23	80:Aq:38:ILE:HD11	1.97	0.46
1:B5:1281:U:H2'	1:B5:1282:C:C6	2.51	0.46
1:B5:1583:U:H3'	30:Ba:13:GLY:HA2	1.97	0.46
1:B5:1651:A:N1	1:B5:1697:C:O2'	2.38	0.46
1:B5:2275:C:H2'	1:B5:2276:A:C8	2.51	0.46
1:B5:3203:A:H2'	1:B5:3204:A:C8	2.51	0.46
1:B5:3262:A2M:HM'1	1:B5:3980:C:H1'	1.98	0.46
2:B8:66:A:H2'	2:B8:67:U:C6	2.51	0.46
6:BB:339:GLY:HA3	6:BB:343:ARG:HG2	1.98	0.46
12:BH:4:ILE:HG12	12:BH:61:TRP:CH2	2.51	0.46
22:BS:161:ARG:NH2	22:BS:164:LYS:HD2	2.31	0.46
32:Bc:17:ARG:O	32:Bc:21:VAL:HG23	2.15	0.46
46:A2:196:G:H2'	46:A2:197:G:O4'	2.16	0.46
46:A2:314:C:H2'	46:A2:315:OMU:C6	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A2:341:U:OP1	56:Ah:31:ARG:HD2	2.16	0.46
46:A2:617:G:H21	46:A2:624:C:H5''	1.80	0.46
46:A2:789:C:OP1	51:Ad:21:ASP:HB2	2.16	0.46
46:A2:1446:G:H2'	46:A2:1447:U:C6	2.51	0.46
47:Aa:159:GLN:O	47:Aa:163:GLN:HG3	2.16	0.46
52:AD:105:ARG:HD3	57:Ai:127:ARG:HD3	1.97	0.46
58:Ak:48:LYS:O	58:Ak:52:GLU:HG3	2.16	0.46
69:Ae:58:LYS:HB3	69:Ae:61:ARG:CD	2.46	0.46
71:AG:30:LEU:HA	71:AG:39:CYS:HA	1.98	0.46
1:B5:188:G:H2'	1:B5:188:G:N3	2.31	0.45
1:B5:424:G:H2'	1:B5:425:U:C6	2.51	0.45
1:B5:1142:U:H4'	8:BD:279:ARG:HD2	1.98	0.45
1:B5:1746:A:H5'	23:BT:129:LYS:HE3	1.98	0.45
1:B5:1830:C:C4	16:BM:17:PHE:HB3	2.50	0.45
1:B5:3761:C:O2	43:Bo:18:HIS:HE1	1.99	0.45
1:B5:4127:A:H2'	1:B5:4128:U:O4'	2.16	0.45
1:B5:4243:C:OP2	16:BM:98:ARG:NH2	2.48	0.45
8:BD:41:LYS:HB2	23:BT:68:THR:O	2.17	0.45
12:BH:95:VAL:HG22	42:Bm:82:LEU:HB3	1.98	0.45
13:BI:57:TYR:HB2	13:BI:131:MET:HE2	1.98	0.45
13:BI:212:LEU:HD23	13:BI:212:LEU:HA	1.83	0.45
18:BO:61:ARG:HD2	18:BO:66:PRO:HB3	1.98	0.45
21:BR:170:ARG:HH12	21:BR:173:ARG:HD3	1.81	0.45
33:Bd:95:ARG:O	33:Bd:99:GLU:HG2	2.16	0.45
46:A2:393:G:H2'	46:A2:394:A:C8	2.51	0.45
46:A2:899:C:H2'	46:A2:900:G:C8	2.51	0.45
46:A2:1249:A:O2'	68:AC:145:CYS:SG	2.57	0.45
46:A2:1278:G:H2'	46:A2:1279:G:O4'	2.16	0.45
46:A2:1657:G:H2'	46:A2:1658:OMC:O4'	2.17	0.45
46:A2:1666:U:H2'	46:A2:1667:A:H8	1.81	0.45
66:AZ:76:VAL:HG23	66:AZ:87:VAL:HG13	1.97	0.45
67:Ap:63:PHE:CZ	67:Ap:92:LEU:HD22	2.52	0.45
69:Ae:59:ARG:HG2	69:Ae:60:PHE:CD2	2.51	0.45
70:AF:64:HIS:CG	70:AF:65:PHE:H	2.34	0.45
1:B5:247:G:H22	28:BY:121:ARG:HH21	1.64	0.45
1:B5:1939:A:H2'	1:B5:1940:C:O4'	2.15	0.45
1:B5:3076:A:H2'	1:B5:3077:G:C8	2.51	0.45
1:B5:3299:U:H2'	1:B5:3300:G:O4'	2.16	0.45
1:B5:3492:U:H2'	1:B5:3493:G:O4'	2.16	0.45
4:Az:2:ARG:HD3	4:Az:5:TRP:NE1	2.32	0.45
5:BA:109:GLU:HG2	5:BA:137:ILE:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:BH:41:ILE:HG22	12:BH:43:VAL:HG13	1.97	0.45
25:BV:91:LYS:HA	25:BV:91:LYS:HD2	1.77	0.45
46:A2:305:U:H2'	46:A2:306:U:C6	2.51	0.45
46:A2:1122:G:O2'	46:A2:1123:G:H5'	2.16	0.45
51:Ad:181:CYS:HB3	51:Ad:195:ILE:HD11	1.97	0.45
63:Av:36:ARG:O	63:Av:40:VAL:HG23	2.16	0.45
66:AZ:39:TYR:CE2	66:AZ:40:LYS:HE2	2.51	0.45
70:AF:156:PHE:HE1	70:AF:179:LEU:HD11	1.82	0.45
72:Aj:11:ILE:HD13	72:Aj:45:VAL:HA	1.97	0.45
74:Ao:49:LEU:HD12	74:Ao:53:GLN:HB3	1.98	0.45
74:Ao:51:ARG:NH1	74:Ao:55:SER:HG	2.11	0.45
1:B5:1821:G:N2	18:BO:87:MET:HE2	2.31	0.45
1:B5:4375:C:H2'	1:B5:4376:G:O4'	2.15	0.45
1:B5:4432:A:O3'	1:B5:4433:G:H8	1.99	0.45
12:BH:137:SER:OG	12:BH:143:GLU:HB3	2.15	0.45
21:BR:172:ARG:HB3	21:BR:176:ARG:NH2	2.31	0.45
46:A2:44:U:O2'	46:A2:45:A:H2'	2.17	0.45
46:A2:1365:U:H2'	46:A2:1366:U:C6	2.51	0.45
50:Ab:103:ASP:CG	50:Ab:107:HIS:HB2	2.41	0.45
55:Ag:19:PHE:CZ	55:Ag:60:ILE:HG23	2.49	0.45
62:Au:56:CYS:SG	62:Au:59:ILE:HG12	2.56	0.45
75:Ar:14:ARG:NH2	75:Ar:19:ASN:OD1	2.50	0.45
75:Ar:23:ARG:CZ	77:Ay:48:VAL:HB	2.46	0.45
78:Ac:46:THR:HG23	78:Ac:84:VAL:HG23	1.98	0.45
1:B5:1779:C:H2'	1:B5:1780:A2M:H8	1.99	0.45
1:B5:2156:G:OP2	1:B5:2156:G:N2	2.44	0.45
1:B5:3118:U:H5	1:B5:3123:A:N7	2.14	0.45
1:B5:3550:C:H2'	1:B5:3551:C:C6	2.51	0.45
1:B5:3833:A:H2'	1:B5:3834:G:O4'	2.16	0.45
1:B5:3941:OMU:HM23	1:B5:3943:U:H6	1.82	0.45
5:BA:206:PRO:HG3	5:BA:213:GLY:HA3	1.97	0.45
8:BD:38:ILE:HD12	23:BT:30:TYR:HB2	1.99	0.45
28:BY:50:ARG:HD2	28:BY:115:ARG:NH1	2.30	0.45
46:A2:519:G:H2'	46:A2:520:G:C8	2.52	0.45
46:A2:1629:G:OP1	69:Ae:50:HIS:NE2	2.39	0.45
46:A2:1693:U:H2'	46:A2:1694:C:C6	2.51	0.45
56:Ah:22:HIS:ND1	56:Ah:23:LYS:O	2.41	0.45
64:Aw:90:CYS:HA	64:Aw:93:PHE:HD2	1.82	0.45
65:Ax:57:VAL:HB	65:Ax:60:PHE:HE2	1.81	0.45
67:Ap:44:PRO:HB2	67:Ap:46:THR:HG22	1.99	0.45
69:Ae:58:LYS:HB3	69:Ae:61:ARG:HD2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:As:9:VAL:O	76:As:11:GLN:NE2	2.49	0.45
78:Ac:142:LEU:HB2	78:Ac:148:LYS:HG2	1.97	0.45
80:Aq:21:TYR:CD1	80:Aq:58:MET:HE1	2.51	0.45
1:B5:276:U:H2'	1:B5:277:C:C6	2.52	0.45
1:B5:498:C:H41	1:B5:597:C:H42	1.65	0.45
1:B5:1095:G:N7	9:BE:53:HIS:NE2	2.64	0.45
1:B5:1353:G:H2'	1:B5:1354:G:C8	2.52	0.45
1:B5:1486:A:H2'	1:B5:1487:A:C8	2.51	0.45
1:B5:1490:U:H2'	1:B5:1491:C:H6	1.81	0.45
1:B5:2026:C:H2'	1:B5:2027:G:C8	2.51	0.45
1:B5:3194:A:H2'	1:B5:3195:A2M:C8	2.47	0.45
1:B5:3338:A:H2'	1:B5:3339:A:C8	2.51	0.45
1:B5:3580:C:H2'	1:B5:3581:C:C6	2.52	0.45
1:B5:3651:U:H2'	1:B5:3652:G:H8	1.82	0.45
1:B5:3743:U:OP1	23:BT:87:LYS:HE2	2.17	0.45
1:B5:4099:C:OP1	1:B5:4101:G:H5'	2.16	0.45
17:BN:159:ARG:HB3	17:BN:164:LEU:HB2	1.97	0.45
24:BU:72:VAL:HG21	24:BU:83:LEU:HD11	1.97	0.45
28:BY:80:ILE:HG13	28:BY:82:ILE:HD11	1.97	0.45
46:A2:516:A:OP1	52:AD:99:LYS:NZ	2.28	0.45
46:A2:899:C:H2'	46:A2:900:G:H8	1.82	0.45
46:A2:1179:G:H2'	46:A2:1180:G:H8	1.81	0.45
46:A2:1213:G:OP1	46:A2:1214:G:O2'	2.21	0.45
46:A2:1223:A:H5''	46:A2:1224:C:OP2	2.16	0.45
46:A2:1262:U:OP1	68:AC:93:HIS:ND1	2.47	0.45
56:Ah:106:SER:HB3	56:Ah:171:LEU:HG	1.98	0.45
66:AZ:80:ARG:NH2	66:AZ:126:ASP:HB2	2.30	0.45
72:Aj:4:PRO:HB2	72:Aj:7:ASN:HD22	1.81	0.45
1:B5:2508:G:O2'	1:B5:2509:G:O4'	2.30	0.45
1:B5:3509:G:H2'	1:B5:3510:A:N3	2.31	0.45
1:B5:4151:A:N3	1:B5:4152:U:H5'	2.31	0.45
2:B8:155:C:H2'	2:B8:156:U:O4'	2.17	0.45
6:BB:285:TYR:N	6:BB:332:MET:O	2.49	0.45
12:BH:88:PHE:CE1	12:BH:151:ILE:HD12	2.51	0.45
46:A2:190:A:H3'	46:A2:191:C:H5''	1.99	0.45
46:A2:1172:A:H2'	46:A2:1175:A:N7	2.32	0.45
48:AA:62:ILE:O	48:AA:74:THR:OG1	2.32	0.45
51:Ad:143:ASP:OD1	51:Ad:143:ASP:N	2.44	0.45
60:An:43:HIS:CD2	60:An:55:ARG:HB2	2.52	0.45
70:AF:227:LEU:HB3	70:AF:228:TYR:CD1	2.52	0.45
1:B5:1180:C:H2'	1:B5:1181:G:H8	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:1222:U:H2'	1:B5:1223:C:H6	1.81	0.45
1:B5:1320:A:N1	1:B5:1421:G:O2'	2.47	0.45
1:B5:1609:C:O2'	31:Bb:18:ARG:NH1	2.49	0.45
1:B5:2055:G:OP1	34:Be:128:ARG:NH1	2.46	0.45
1:B5:3407:U:H2'	1:B5:3408:C:C6	2.52	0.45
1:B5:3482:C:H2'	1:B5:3483:G:C8	2.51	0.45
1:B5:3487:G:H2'	1:B5:3487:G:N3	2.31	0.45
1:B5:3682:A:H2'	1:B5:3683:G:H8	1.79	0.45
1:B5:3981:G:H2'	1:B5:3982:U:C6	2.52	0.45
33:Bd:119:LEU:HD22	33:Bd:157:VAL:HG12	1.98	0.45
46:A2:1552:C:H4'	46:A2:1558:G:C6	2.52	0.45
46:A2:1583:C:H2'	46:A2:1584:C:H6	1.80	0.45
47:Aa:81:PHE:O	47:Aa:106:THR:HG23	2.17	0.45
47:Aa:126:ASP:OD1	47:Aa:136:ARG:HD3	2.17	0.45
69:Ae:125:THR:HG22	69:Ae:126:ARG:N	2.24	0.45
71:AG:19:ARG:HD2	71:AG:32:ARG:HD3	1.98	0.45
75:Ar:28:PHE:O	75:Ar:31:THR:OG1	2.35	0.45
1:B5:268:G:H2'	1:B5:269:G:C8	2.52	0.45
1:B5:442:G:H2'	1:B5:443:G:H8	1.81	0.45
1:B5:593:C:OP1	7:BC:268:ARG:NH1	2.45	0.45
1:B5:1490:U:H2'	1:B5:1491:C:C6	2.52	0.45
1:B5:1512:C:H2'	1:B5:1513:C:C6	2.52	0.45
1:B5:2304:G:H2'	1:B5:2305:G:C8	2.52	0.45
1:B5:3087:A:H2'	1:B5:3088:A:H8	1.80	0.45
1:B5:3619:U:H2'	1:B5:3620:C:C6	2.52	0.45
1:B5:4202:G:H2'	1:B5:4203:C:C6	2.52	0.45
1:B5:4245:G:N1	18:BO:176:ARG:HD3	2.27	0.45
2:B8:4:C:H2'	2:B8:5:U:H6	1.81	0.45
3:B7:16:A:H2'	3:B7:17:C:C6	2.52	0.45
18:BO:37:ARG:HG3	18:BO:39:GLU:OE2	2.17	0.45
46:A2:92:A:H1'	51:Ad:3:ARG:HB3	1.99	0.45
46:A2:921:A:H2'	46:A2:922:A:C8	2.52	0.45
50:Ab:56:SER:OG	62:Au:25:GLY:O	2.29	0.45
57:Ai:34:GLU:HG3	57:Ai:35:TYR:CD2	2.52	0.45
68:AC:122:PRO:HG3	68:AC:148:TYR:HE2	1.82	0.45
69:Ae:79:GLY:HA2	69:Ae:82:ASN:ND2	2.31	0.45
79:V:62:C:H2'	79:V:63:G:C8	2.49	0.45
1:B5:18:C:H4'	17:BN:138:PHE:CD2	2.51	0.45
1:B5:175:C:H2'	1:B5:176:G:C8	2.51	0.45
1:B5:617:U:OP1	45:Br:95:HIS:ND1	2.49	0.45
1:B5:1954:G:O6	1:B5:3347:C:O2'	2.34	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:2011:G:N2	9:BE:122:MET:HE1	2.31	0.45
1:B5:2304:G:H2'	1:B5:2305:G:H8	1.81	0.45
1:B5:2585:A:H1'	6:BB:228:TYR:CE2	2.52	0.45
1:B5:4186:G:H2'	1:B5:4187:C:C6	2.52	0.45
7:BC:298:ILE:HD12	20:BQ:35:LEU:HD21	1.99	0.45
16:BM:119:ARG:NE	18:BO:189:ILE:HD12	2.32	0.45
51:Ad:124:CYS:HB3	51:Ad:141:THR:HB	1.99	0.45
53:AE:39:PHE:CD2	53:AE:41:ILE:HD11	2.52	0.45
63:Av:83:LEU:HD23	63:Av:83:LEU:HA	1.89	0.45
69:Ae:87:MET:O	69:Ae:90:ARG:HG2	2.17	0.45
70:AF:72:SER:HB2	70:AF:117:ASN:ND2	2.32	0.45
70:AF:218:LEU:HD11	70:AF:261:LEU:HD22	1.98	0.45
1:B5:1432:C:H5''	30:Ba:2:PRO:HD2	1.99	0.45
1:B5:1672:G:H2'	1:B5:1674:A:H5''	1.99	0.45
1:B5:2223:G:N2	1:B5:2252:G:H5''	2.31	0.45
1:B5:3559:U:H2'	1:B5:3560:C:C6	2.52	0.45
1:B5:3902:U:H2'	1:B5:3903:U:H6	1.81	0.45
1:B5:4021:G:H2'	1:B5:4022:PSU:C6	2.51	0.45
3:B7:55:A:H4'	14:BJ:155:HIS:HB2	1.97	0.45
7:BC:316:LYS:HB2	7:BC:324:VAL:HG21	1.98	0.45
11:BG:172:ALA:HB3	38:Bi:43:MET:HE1	1.99	0.45
21:BR:99:MET:HE2	21:BR:99:MET:HA	1.98	0.45
30:Ba:38:MET:HE2	30:Ba:53:PHE:CD1	2.52	0.45
33:Bd:139:LEU:HD22	33:Bd:157:VAL:HG22	1.99	0.45
36:Bg:106:VAL:HG23	36:Bg:107:LEU:HD12	1.99	0.45
46:A2:16:G:H2'	46:A2:17:C:C6	2.52	0.45
46:A2:197:G:H2'	46:A2:198:G:H8	1.81	0.45
46:A2:283:C:H2'	46:A2:284:C:H6	1.82	0.45
46:A2:1401:A:O2'	46:A2:1402:G:H5''	2.16	0.45
51:Ad:87:MET:HE1	51:Ad:236:ILE:HD13	1.99	0.45
55:Ag:51:ILE:HG13	55:Ag:59:ALA:HB3	1.99	0.45
66:AZ:17:LYS:HD3	66:AZ:173:LEU:HD11	1.99	0.45
67:Ap:8:GLN:HA	67:Ap:99:TYR:CZ	2.52	0.45
73:Al:26:LEU:HD23	73:Al:31:LEU:HD13	1.98	0.45
73:Al:40:LYS:HD3	73:Al:43:ASP:HB2	1.97	0.45
75:Ar:67:VAL:HG12	75:Ar:71:MET:HE3	1.99	0.45
1:B5:1620:G:H3'	1:B5:1621:G:H5'	1.98	0.44
1:B5:2620:A:H2'	1:B5:2621:C:O4'	2.17	0.44
1:B5:3567:C:H5	36:Bg:100:GLN:HG2	1.82	0.44
8:BD:152:ARG:NH1	83:BD:302:HOH:O	2.38	0.44
14:BJ:95:ARG:HH11	14:BJ:95:ARG:HG3	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:BL:187:ALA:HA	15:BL:190:ARG:HG2	1.99	0.44
22:BS:5:GLY:O	22:BS:111:ARG:NH2	2.51	0.44
46:A2:1732:C:C2	46:A2:1733:G:C8	3.05	0.44
47:Aa:164:ILE:HG12	47:Aa:201:CYS:HB3	1.99	0.44
50:Ab:143:ASN:ND2	57:Ai:95:ASP:OD2	2.30	0.44
53:AE:58:VAL:HG21	60:An:28:PHE:HZ	1.83	0.44
1:B5:426:U:H2'	1:B5:427:A:C8	2.52	0.44
1:B5:1775:U:H2'	1:B5:1776:A:O4'	2.17	0.44
1:B5:1776:A:H2'	1:B5:1777:A:C8	2.51	0.44
1:B5:2061:U:H2'	1:B5:2062:G:H8	1.82	0.44
1:B5:2094:G:N7	30:Ba:9:ARG:NH2	2.64	0.44
1:B5:2625:OMG:HM22	1:B5:2626:G:O5'	2.17	0.44
1:B5:3388:C:H2'	1:B5:3389:U:C6	2.52	0.44
1:B5:3394:A:H2'	1:B5:3395:G:C8	2.51	0.44
1:B5:3451:G:H2'	1:B5:3452:C:C6	2.53	0.44
2:B8:4:C:H2'	2:B8:5:U:C6	2.53	0.44
2:B8:92:U:H2'	2:B8:93:C:O4'	2.17	0.44
9:BE:200:HIS:O	9:BE:204:VAL:HG13	2.17	0.44
10:BF:103:VAL:HG13	10:BF:134:VAL:HG12	1.98	0.44
11:BG:172:ALA:C	38:Bi:43:MET:HE1	2.42	0.44
14:BJ:40:LEU:HD12	14:BJ:70:VAL:HG13	1.99	0.44
23:BT:27:LEU:O	23:BT:31:MET:HG3	2.17	0.44
31:Bb:32:LEU:HD13	31:Bb:43:MET:HE1	1.99	0.44
31:Bb:49:HIS:HB3	31:Bb:52:LYS:HD3	1.98	0.44
37:Bh:6:ALA:O	37:Bh:10:ARG:HG2	2.17	0.44
44:Bp:85:ARG:O	44:Bp:89:LEU:HG	2.17	0.44
46:A2:192:C:H2'	46:A2:193:U:O4'	2.18	0.44
46:A2:408:A:H4'	51:Ad:3:ARG:HG2	1.98	0.44
46:A2:696:C:H3'	46:A2:697:A:H5''	1.99	0.44
46:A2:962:U:H2'	46:A2:963:G:C8	2.52	0.44
46:A2:1818:U:OP2	53:AE:4:LYS:NZ	2.39	0.44
47:Aa:52:THR:HG23	47:Aa:57:ILE:HA	1.98	0.44
69:Ae:164:ASN:OD1	69:Ae:165:ILE:N	2.50	0.44
70:AF:91:ASP:HB2	70:AF:98:THR:OG1	2.17	0.44
76:As:75:MET:HE3	76:As:79:TYR:HE2	1.82	0.44
79:V:56:C:N4	79:V:57:G:O6	2.50	0.44
1:B5:261:C:H2'	1:B5:262:G:C8	2.53	0.44
1:B5:287:U:H2'	1:B5:288:U:C6	2.52	0.44
1:B5:442:G:H2'	1:B5:443:G:C8	2.52	0.44
1:B5:452:C:O2'	1:B5:1218:G:H2'	2.17	0.44
1:B5:631:U:H2'	1:B5:632:C:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:2613:A:H2'	1:B5:2614:U:H6	1.83	0.44
1:B5:3850:G:H1'	1:B5:3881:U:C2	2.52	0.44
1:B5:4032:A:N1	1:B5:4064:C:O2'	2.45	0.44
2:B8:153:C:O2'	11:BG:186:SER:HB2	2.17	0.44
7:BC:11:TYR:CZ	7:BC:148:PRO:HB2	2.52	0.44
9:BE:258:THR:O	9:BE:261:LYS:HG3	2.17	0.44
16:BM:118:MET:HG2	18:BO:192:PHE:CZ	2.52	0.44
33:Bd:138:ARG:HG3	33:Bd:160:VAL:CG2	2.47	0.44
46:A2:65:C:C2	54:Af:133:LEU:HD22	2.53	0.44
46:A2:403:C:H2'	46:A2:404:U:C6	2.53	0.44
46:A2:505:G:H2'	46:A2:506:A:C8	2.52	0.44
46:A2:524:G:O2'	46:A2:525:A:H8	2.01	0.44
46:A2:602:A:H2'	46:A2:603:U:O4'	2.17	0.44
46:A2:875:U:H2'	46:A2:876:U:C6	2.52	0.44
46:A2:1682:G:H2'	46:A2:1683:U:C6	2.52	0.44
50:Ab:35:THR:HG22	66:AZ:116:PHE:HE2	1.80	0.44
63:Av:42:MET:HE3	63:Av:49:GLU:HA	2.00	0.44
63:Av:77:PRO:HG2	63:Av:79:PHE:CZ	2.52	0.44
64:Aw:39:ASN:ND2	64:Aw:43:GLY:H	2.15	0.44
73:Al:69:CYS:HA	73:Al:74:ILE:HG12	1.98	0.44
78:Ac:14:ASP:OD1	78:Ac:15:GLY:N	2.51	0.44
78:Ac:105:LEU:HB2	78:Ac:122:VAL:HG21	1.99	0.44
1:B5:430:A:H2'	1:B5:431:G:C8	2.52	0.44
1:B5:1784:C:H2'	1:B5:1785:U:C6	2.52	0.44
1:B5:2356:C:H2'	1:B5:2357:G:H8	1.82	0.44
1:B5:2440:U:H2'	1:B5:2441:U:C6	2.52	0.44
1:B5:2510:U:H4'	1:B5:2511:G:O4'	2.17	0.44
1:B5:3383:A:H2'	7:BC:69:THR:HG21	1.99	0.44
1:B5:3967:G:C2	6:BB:252:ALA:HB1	2.52	0.44
1:B5:4070:U:O2'	6:BB:55:HIS:ND1	2.37	0.44
1:B5:4192:C:O2'	1:B5:4193:G:H5'	2.17	0.44
6:BB:285:TYR:CD1	6:BB:363:ILE:HG13	2.51	0.44
6:BB:288:GLY:HA3	6:BB:330:PHE:CZ	2.52	0.44
9:BE:291:VAL:HG13	9:BE:296:LEU:HD21	2.00	0.44
10:BF:68:ARG:HG2	10:BF:72:MET:HE3	1.99	0.44
10:BF:85:PRO:HG3	10:BF:142:TYR:CE2	2.52	0.44
11:BG:175:ARG:HB2	11:BG:230:TYR:CE1	2.53	0.44
35:Bf:14:TYR:OH	35:Bf:92:LEU:O	2.33	0.44
36:Bg:95:PHE:O	36:Bg:99:GLU:HG2	2.17	0.44
39:Bj:27:TYR:HA	39:Bj:34:CYS:HA	1.98	0.44
46:A2:377:U:HO2'	46:A2:613:U:HO2'	1.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A2:576:C:H2'	46:A2:577:A:O4'	2.17	0.44
46:A2:1364:G:H2'	46:A2:1365:U:C6	2.52	0.44
46:A2:1364:G:N2	46:A2:1397:U:O4	2.50	0.44
46:A2:1777:A:H2'	46:A2:1778:A:C8	2.53	0.44
46:A2:1790:G:OP1	46:A2:1793:U:H4'	2.18	0.44
50:Ab:62:SER:HB3	50:Ab:127:ILE:HG23	1.99	0.44
51:Ad:20:LEU:HD21	51:Ad:46:ILE:HD12	2.00	0.44
57:Ai:111:GLN:NE2	57:Ai:123:ILE:HG13	2.32	0.44
58:Ak:78:THR:HG22	58:Ak:79:LYS:HG3	1.98	0.44
70:AF:42:MET:HE3	70:AF:59:LEU:HD21	2.00	0.44
1:B5:6:C:H2'	1:B5:7:C:H6	1.82	0.44
1:B5:37:U:H2'	1:B5:38:A:O4'	2.16	0.44
1:B5:1181:G:H2'	1:B5:1182:G:C8	2.53	0.44
1:B5:1383:C:H2'	1:B5:1384:C:C6	2.53	0.44
1:B5:2311:G:C6	1:B5:2313:G:H5''	2.52	0.44
1:B5:2477:U:H2'	1:B5:2478:C:C6	2.53	0.44
1:B5:3140:A:N6	1:B5:3611:G:O2'	2.39	0.44
1:B5:3198:U:H2'	1:B5:3199:G:C8	2.52	0.44
1:B5:3213:A:H2'	1:B5:3214:A:C8	2.53	0.44
1:B5:3564:C:O2'	11:BG:43:GLN:NE2	2.39	0.44
1:B5:4364:G:H1	1:B5:4429:A:H2	1.64	0.44
5:BA:5:ILE:HG12	5:BA:8:GLN:HG3	2.00	0.44
6:BB:238:LYS:HB2	6:BB:238:LYS:HE2	1.76	0.44
7:BC:296:GLN:HB3	7:BC:300:LYS:HZ2	1.81	0.44
17:BN:90:ASN:O	43:Bo:48:TYR:OH	2.31	0.44
21:BR:104:ARG:O	21:BR:108:ARG:HG3	2.18	0.44
22:BS:71:THR:HB	22:BS:74:ARG:HD3	1.98	0.44
45:Br:62:VAL:CG2	45:Br:93:LEU:HD21	2.45	0.44
46:A2:483:A:H5''	57:Ai:145:PRO:HD2	1.99	0.44
46:A2:531:C:O2'	65:Ax:34:THR:O	2.28	0.44
46:A2:613:U:H2'	46:A2:614:A:C8	2.52	0.44
55:Ag:63:PHE:HA	55:Ag:95:ILE:O	2.17	0.44
57:Ai:111:GLN:HE21	57:Ai:123:ILE:HG13	1.82	0.44
75:Ar:9:PHE:HZ	75:Ar:23:ARG:HA	1.82	0.44
1:B5:58:G:H4'	1:B5:59:A:H4'	2.00	0.44
1:B5:289:G:H2'	1:B5:290:C:C6	2.53	0.44
1:B5:649:G:H2'	1:B5:650:A:H8	1.80	0.44
1:B5:694:C:H2'	1:B5:695:C:C6	2.53	0.44
1:B5:1264:U:OP1	30:Ba:8:THR:OG1	2.29	0.44
1:B5:1375:C:H2'	1:B5:1376:G:O4'	2.18	0.44
1:B5:1536:A:H5'	5:BA:183:GLY:CA	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:1788:C:O2'	1:B5:1800:A:N3	2.47	0.44
1:B5:1975:C:O2'	35:Bf:79:GLY:HA2	2.17	0.44
1:B5:2317:C:H2'	1:B5:2318:G:H8	1.83	0.44
1:B5:3145:C:H5'	5:BA:8:GLN:O	2.18	0.44
1:B5:3409:U:H2'	1:B5:3410:G:C8	2.53	0.44
1:B5:4147:C:H2'	1:B5:4148:A:C8	2.52	0.44
1:B5:4398:C:H5''	1:B5:4399:G:C8	2.52	0.44
1:B5:4424:U:OP1	1:B5:4425:C:N4	2.51	0.44
13:BI:52:MET:HE1	13:BI:159:PHE:CD2	2.53	0.44
17:BN:48:ALA:HB1	17:BN:53:TYR:HB3	2.00	0.44
25:BV:89:ARG:HB2	25:BV:95:PHE:CE2	2.53	0.44
29:BZ:9:LYS:NZ	29:BZ:83:THR:O	2.38	0.44
46:A2:609:A:H4'	64:Aw:104:GLY:O	2.17	0.44
54:Af:153:VAL:O	54:Af:157:VAL:HG23	2.17	0.44
61:At:61:LEU:HD22	71:AG:34:TYR:CE1	2.52	0.44
69:Ae:133:VAL:C	69:Ae:134:ARG:HG2	2.42	0.44
76:As:24:LYS:HB3	76:As:24:LYS:HE2	1.67	0.44
1:B5:61:A:H5''	17:BN:164:LEU:HD21	1.99	0.44
1:B5:1623:G:H4'	1:B5:1624:G:OP1	2.16	0.44
1:B5:1694:A:H2'	1:B5:1697:C:C5	2.52	0.44
1:B5:2125:A:H2'	1:B5:2126:C:C6	2.52	0.44
1:B5:2288:C:H2'	1:B5:2289:C:H6	1.78	0.44
1:B5:3338:A:H2'	1:B5:3339:A:H8	1.82	0.44
1:B5:3393:G:H2'	1:B5:3394:A:C8	2.52	0.44
1:B5:3410:G:H2'	1:B5:3411:G:C8	2.52	0.44
2:B8:6:C:H2'	2:B8:7:U:H6	1.82	0.44
2:B8:8:U:H2'	2:B8:9:A:C8	2.52	0.44
2:B8:14:U:C4	2:B8:15:G:C6	3.06	0.44
5:BA:210:PRO:HG2	5:BA:235:VAL:HG21	2.00	0.44
11:BG:230:TYR:O	11:BG:234:ARG:HG2	2.18	0.44
20:BQ:112:ARG:HG2	20:BQ:115:ARG:NH2	2.33	0.44
46:A2:106:C:H2'	46:A2:107:A:C8	2.49	0.44
46:A2:341:U:P	56:Ah:56:ARG:HH22	2.40	0.44
46:A2:1051:A:H2'	46:A2:1052:C:H6	1.83	0.44
46:A2:1483:G:H2'	46:A2:1484:C:C6	2.53	0.44
46:A2:1755:A:H2'	46:A2:1756:C:H6	1.82	0.44
49:AB:51:ARG:HG3	69:Ae:60:PHE:CE2	2.53	0.44
64:Aw:68:LYS:HG2	64:Aw:91:LEU:HD22	2.00	0.44
66:AZ:80:ARG:O	66:AZ:84:GLN:HG3	2.17	0.44
70:AF:148:SER:OG	70:AF:171:ASP:OD1	2.35	0.44
78:Ac:163:PRO:HA	78:Ac:166:TYR:CZ	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:1180:C:H2'	1:B5:1181:G:C8	2.53	0.44
1:B5:1252:C:H5''	1:B5:3892:A:OP1	2.17	0.44
1:B5:1263:G:H4'	1:B5:1264:U:H6	1.83	0.44
1:B5:1271:C:OP1	20:BQ:148:VAL:HG12	2.18	0.44
1:B5:1629:G:H2'	1:B5:1630:C:C6	2.53	0.44
1:B5:1670:C:H2'	1:B5:1671:C:C6	2.53	0.44
1:B5:1743:U:N3	23:BT:126:VAL:O	2.39	0.44
1:B5:2072:C:H2'	1:B5:2073:C:H6	1.82	0.44
1:B5:2625:OMG:C8	44:Bp:16:THR:HG22	2.52	0.44
1:B5:4372:PSU:H2'	1:B5:4373:U:O4'	2.18	0.44
1:B5:4431:A:H5''	1:B5:4432:A:C8	2.53	0.44
2:B8:19:C:H2'	2:B8:20:A:C8	2.53	0.44
2:B8:154:G:H2'	2:B8:155:C:C6	2.52	0.44
5:BA:119:LYS:C	5:BA:162:ASN:HD21	2.26	0.44
7:BC:162:LYS:HD2	7:BC:219:ARG:NH2	2.25	0.44
31:Bb:67:LEU:HA	31:Bb:70:LYS:HE2	2.00	0.44
32:Bc:56:ARG:O	32:Bc:60:ILE:HG12	2.17	0.44
43:Bo:12:CYS:O	43:Bo:16:GLY:N	2.49	0.44
44:Bp:86:LEU:HD23	44:Bp:89:LEU:HD12	1.98	0.44
46:A2:1368:C:H2'	46:A2:1369:G:H8	1.82	0.44
62:Au:30:ALA:O	62:Au:60:ARG:HD3	2.17	0.44
70:AF:31:ILE:HG21	70:AF:299:PHE:CE2	2.51	0.44
71:AG:34:TYR:HB3	78:Ac:12:VAL:HG21	1.98	0.44
73:Al:50:CYS:SG	73:Al:52:LEU:HD23	2.57	0.44
1:B5:25:A:C8	1:B5:342:G:C8	3.06	0.44
1:B5:181:C:H2'	1:B5:182:G:C8	2.52	0.44
1:B5:669:G:OP2	10:BF:74:ARG:NE	2.49	0.44
1:B5:1192:A:O2'	10:BF:50:GLU:OE1	2.32	0.44
1:B5:1242:U:H2'	1:B5:1243:C:C6	2.53	0.44
1:B5:1587:U:H2'	1:B5:1588:C:C6	2.53	0.44
1:B5:1804:G:H2'	1:B5:1805:A:O4'	2.17	0.44
1:B5:2113:OMG:HM23	1:B5:2113:OMG:H1'	1.83	0.44
1:B5:2476:C:H2'	1:B5:2477:U:C6	2.53	0.44
1:B5:4435:U:H2'	1:B5:4436:U:C6	2.53	0.44
3:B7:111:C:H2'	3:B7:112:U:O4'	2.18	0.44
10:BF:90:VAL:O	10:BF:118:GLY:HA2	2.18	0.44
25:BV:42:VAL:HG13	25:BV:61:VAL:HG12	1.99	0.44
29:BZ:87:VAL:HG12	29:BZ:127:ASN:CG	2.43	0.44
46:A2:410:A:H4'	51:Ad:3:ARG:HD3	1.99	0.44
46:A2:887:G:N2	46:A2:1062:G:H4'	2.33	0.44
46:A2:1462:G:N7	68:AC:89:LYS:HD2	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A2:1695:C:H2'	46:A2:1696:U:C6	2.53	0.44
46:A2:1732:C:H2'	46:A2:1733:G:H8	1.83	0.44
47:Aa:173:THR:O	47:Aa:177:GLN:HG2	2.17	0.44
50:Ab:165:ARG:HD3	50:Ab:167:ILE:HD11	2.00	0.44
68:AC:101:ALA:HA	68:AC:104:LYS:NZ	2.29	0.44
80:Aq:31:ASN:HA	80:Aq:34:VAL:HG22	1.99	0.44
1:B5:63:G:P	17:BN:169:ARG:HH22	2.41	0.43
1:B5:123:C:H2'	1:B5:124:C:H6	1.83	0.43
1:B5:446:U:H3	1:B5:2063:G:H1	1.64	0.43
1:B5:787:C:H5'	9:BE:52:TYR:HA	2.00	0.43
1:B5:1234:C:H2'	1:B5:1235:C:C6	2.52	0.43
1:B5:1367:G:H5'	10:BF:26:ALA:HB2	2.00	0.43
1:B5:1615:C:H4'	20:BQ:143:ARG:HH22	1.83	0.43
1:B5:1647:G:H2'	1:B5:1648:C:C6	2.53	0.43
1:B5:2643:A:H2'	1:B5:2644:A:C8	2.53	0.43
1:B5:3551:C:H41	1:B5:3552:G:N2	2.13	0.43
1:B5:4071:PSU:H4'	26:BW:16:GLY:O	2.18	0.43
2:B8:140:C:H2'	2:B8:141:C:C6	2.53	0.43
33:Bd:88:GLY:O	33:Bd:92:ARG:HG3	2.18	0.43
40:Bk:49:ASP:HB3	40:Bk:51:GLU:OE1	2.18	0.43
46:A2:5:U:H2'	46:A2:6:G:C8	2.53	0.43
46:A2:17:C:O2'	46:A2:1152:A:N1	2.42	0.43
46:A2:1611:G:H2'	46:A2:1612:G:H8	1.83	0.43
46:A2:1754:A:H3'	46:A2:1755:A:H8	1.83	0.43
60:An:44:VAL:HG12	60:An:53:ILE:HB	1.99	0.43
66:AZ:176:TRP:HA	66:AZ:202:TYR:HE2	1.82	0.43
76:As:134:ILE:O	76:As:138:VAL:HG23	2.18	0.43
78:Ac:105:LEU:HD12	78:Ac:122:VAL:HG21	1.99	0.43
1:B5:268:G:H2'	1:B5:269:G:H8	1.83	0.43
1:B5:1233:C:OP1	18:BO:93:LYS:NZ	2.49	0.43
1:B5:1263:G:H4'	1:B5:1264:U:C6	2.53	0.43
1:B5:1459:U:H2'	1:B5:1460:A:H8	1.82	0.43
1:B5:2000:G:H4'	1:B5:2001:C:H5'	2.00	0.43
1:B5:2016:U:OP1	45:Br:37:SER:HB2	2.19	0.43
1:B5:2403:C:H2'	1:B5:2404:C:H6	1.82	0.43
1:B5:3098:A:C8	1:B5:4085:U:H1'	2.53	0.43
1:B5:3372:G:N2	6:BB:268:ARG:HH21	2.16	0.43
1:B5:4027:C:H2'	1:B5:4028:U:O4'	2.18	0.43
1:B5:4206:U:O2'	22:BS:174:THR:OG1	2.25	0.43
2:B8:26:C:O2'	7:BC:53:ALA:O	2.31	0.43
3:B7:57:C:H2'	3:B7:58:A:H8	1.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:BB:165:HIS:HA	6:BB:179:HIS:O	2.18	0.43
15:BL:17:ASP:OD1	15:BL:20:ARG:NE	2.51	0.43
25:BV:62:MET:HE3	25:BV:76:VAL:HG12	2.00	0.43
28:BY:72:GLN:HB3	28:BY:81:TYR:HB2	1.99	0.43
46:A2:74:G:H2'	46:A2:75:G:O4'	2.19	0.43
46:A2:99:A2M:H8	46:A2:99:A2M:O5'	2.18	0.43
46:A2:697:A:H2'	46:A2:698:G:H4'	1.99	0.43
46:A2:911:C:O2	60:An:55:ARG:NH2	2.50	0.43
46:A2:1112:U:O4	50:Ab:198:ARG:HD2	2.19	0.43
56:Ah:192:GLY:O	56:Ah:196:GLU:HG3	2.18	0.43
62:Au:39:VAL:HG21	66:AZ:8:LEU:HD11	2.00	0.43
65:Ax:46:LYS:HE2	65:Ax:46:LYS:HB3	1.69	0.43
67:Ap:51:LEU:HG	67:Ap:81:ILE:HG23	2.00	0.43
75:Ar:13:LEU:HB2	75:Ar:20:ILE:HB	2.00	0.43
1:B5:470:C:H2'	1:B5:471:A:H8	1.83	0.43
1:B5:1204:C:O2'	1:B5:1206:G:N7	2.39	0.43
1:B5:1229:C:H2'	1:B5:1230:C:C6	2.53	0.43
1:B5:1353:G:H2'	1:B5:1354:G:H8	1.83	0.43
1:B5:1629:G:H2'	1:B5:1630:C:H6	1.81	0.43
1:B5:1635:U:H2'	1:B5:1636:U:H6	1.83	0.43
1:B5:1678:A:C5	1:B5:1679:U:C5	3.06	0.43
1:B5:2448:C:H2'	1:B5:2449:G:H8	1.84	0.43
1:B5:2457:U:O2'	1:B5:2458:C:H3'	2.18	0.43
1:B5:3505:C:H2'	1:B5:3506:U:C5	2.53	0.43
1:B5:3514:U:H2'	1:B5:3515:U:C6	2.53	0.43
1:B5:3822:A:OP1	83:B5:4907:HOH:O	2.21	0.43
1:B5:4338:A:OP2	83:B5:4906:HOH:O	2.21	0.43
10:BF:92:ARG:HB2	10:BF:112:LEU:HB3	2.00	0.43
11:BG:163:PRO:HB2	11:BG:165:GLU:OE1	2.17	0.43
11:BG:223:LYS:HD2	11:BG:227:ASN:CB	2.48	0.43
23:BT:107:GLN:O	23:BT:111:GLU:HG3	2.18	0.43
29:BZ:10:VAL:HG11	29:BZ:129:TRP:HZ3	1.83	0.43
33:Bd:138:ARG:HB2	33:Bd:158:THR:OG1	2.17	0.43
36:Bg:5:LEU:HD11	36:Bg:30:ILE:HG22	2.01	0.43
38:Bi:59:GLU:O	38:Bi:63:VAL:HG22	2.17	0.43
46:A2:91:A:H61	54:Af:89:THR:HG22	1.83	0.43
46:A2:106:C:OP1	46:A2:392:G:O2'	2.34	0.43
46:A2:1238:G:H2'	46:A2:1239:G:C8	2.52	0.43
46:A2:1377:C:H2'	46:A2:1378:G:N7	2.33	0.43
46:A2:1643:C:H2'	46:A2:1644:C:H6	1.83	0.43
46:A2:1808:U:P	60:An:147:ARG:HH22	2.40	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:AF:51:ASN:OD1	70:AF:52:TYR:N	2.52	0.43
70:AF:69:VAL:HG23	70:AF:80:SER:HB2	2.00	0.43
70:AF:157:SER:HB3	70:AF:164:ILE:HG13	2.00	0.43
77:Ay:91:LEU:HD21	77:Ay:96:LEU:HB2	1.99	0.43
1:B5:425:U:H2'	1:B5:426:U:H6	1.84	0.43
1:B5:1252:C:H2'	1:B5:1253:G:C8	2.53	0.43
1:B5:1303:G:H21	1:B5:1304:C:N4	2.17	0.43
1:B5:1321:G:N2	1:B5:1341:A:H5'	2.33	0.43
1:B5:1487:A:H2'	1:B5:1488:A:C8	2.53	0.43
1:B5:3077:G:H2'	1:B5:3078:C:C6	2.54	0.43
1:B5:3891:G:H5''	1:B5:3892:A:H5''	1.99	0.43
1:B5:4006:U:H2'	1:B5:4007:A:C8	2.53	0.43
1:B5:4065:A:H4'	6:BB:13:SER:HB2	1.99	0.43
1:B5:4211:G:OP1	18:BO:168:TYR:OH	2.33	0.43
2:B8:5:U:H2'	2:B8:6:C:C6	2.52	0.43
17:BN:84:PRO:HA	17:BN:87:HIS:CG	2.53	0.43
24:BU:105:ASN:HB2	24:BU:111:GLU:HG2	2.00	0.43
36:Bg:86:CYS:O	36:Bg:90:ARG:HG3	2.18	0.43
46:A2:4:C:H4'	50:Ab:178:ALA:HB2	2.01	0.43
46:A2:53:C:O2'	46:A2:468:G:N7	2.41	0.43
46:A2:377:U:H2'	46:A2:378:C:O4'	2.17	0.43
46:A2:995:G:H4'	46:A2:1799:A:H4'	2.00	0.43
46:A2:1258:G:H2'	74:Ao:51:ARG:NH2	2.32	0.43
46:A2:1336:A:H4'	46:A2:1337:A:O5'	2.18	0.43
46:A2:1674:A:N6	46:A2:1768:G:O2'	2.48	0.43
47:Aa:71:LEU:HD22	47:Aa:84:PHE:HE1	1.83	0.43
51:Ad:247:THR:O	51:Ad:251:GLU:HG3	2.18	0.43
58:Ak:97:ARG:HH11	58:Ak:97:ARG:HG3	1.84	0.43
60:An:45:THR:HA	60:An:52:THR:HA	1.99	0.43
78:Ac:31:GLU:HG3	78:Ac:107:TYR:CZ	2.52	0.43
1:B5:208:A:C2	1:B5:233:U:H5''	2.53	0.43
1:B5:1658:G:H22	1:B5:1688:A:H2	1.66	0.43
1:B5:3405:A:H2'	1:B5:3406:G:O4'	2.18	0.43
1:B5:3874:PSU:H5'	13:BI:160:PRO:HD3	1.99	0.43
2:B8:32:C:H2'	2:B8:33:G:O4'	2.18	0.43
3:B7:88:A:H2'	3:B7:89:G:O4'	2.18	0.43
6:BB:56:ILE:O	6:BB:73:VAL:HA	2.18	0.43
6:BB:113:GLU:OE1	6:BB:167:GLN:HA	2.18	0.43
11:BG:227:ASN:HA	11:BG:230:TYR:CE2	2.53	0.43
13:BI:52:MET:HE3	13:BI:163:GLN:HG2	2.00	0.43
34:Be:98:GLU:HG3	34:Be:123:THR:OG1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A2:72:G:C6	46:A2:74:G:H1'	2.53	0.43
46:A2:81:U:H2'	46:A2:82:G:O4'	2.18	0.43
46:A2:1117:G:OP1	63:Av:76:SER:HB3	2.19	0.43
46:A2:1500:A:H2	46:A2:1626:G:H1'	1.83	0.43
46:A2:1629:G:N7	67:Ap:17:LYS:NZ	2.66	0.43
51:Ad:61:VAL:HG12	51:Ad:80:ILE:HD12	1.99	0.43
67:Ap:53:GLU:O	67:Ap:57:LEU:HB2	2.18	0.43
67:Ap:89:SER:HB3	67:Ap:112:LEU:HD13	1.99	0.43
70:AF:270:LEU:HD22	70:AF:310:TRP:CE3	2.54	0.43
73:Al:49:LEU:HD21	73:Al:51:VAL:HB	2.00	0.43
80:Aq:30:THR:O	80:Aq:34:VAL:HG13	2.18	0.43
1:B5:470:C:H2'	1:B5:471:A:C8	2.54	0.43
1:B5:2348:G:OP1	36:Bg:40:LYS:NZ	2.47	0.43
1:B5:3709:G:H2'	1:B5:3709:G:N3	2.33	0.43
1:B5:4036:C:H2'	1:B5:4037:U:C6	2.52	0.43
2:B8:6:C:H2'	2:B8:7:U:C6	2.53	0.43
29:BZ:68:ILE:O	29:BZ:115:LYS:HG3	2.18	0.43
44:Bp:51:ALA:HB3	44:Bp:54:ILE:HD13	2.01	0.43
46:A2:14:C:H2'	46:A2:15:U:C6	2.53	0.43
46:A2:342:C:H2'	46:A2:343:U:C6	2.53	0.43
46:A2:1645:U:H2'	46:A2:1646:U:C6	2.54	0.43
50:Ab:182:LYS:O	50:Ab:186:MET:HG3	2.18	0.43
70:AF:188:HIS:HB3	70:AF:219:TRP:CZ2	2.53	0.43
70:AF:219:TRP:CZ3	70:AF:226:HIS:HB2	2.54	0.43
1:B5:2072:C:H2'	1:B5:2073:C:C6	2.53	0.43
1:B5:2087:C:H4'	45:Br:12:ASN:O	2.18	0.43
1:B5:2357:G:H2'	1:B5:2358:G:H8	1.82	0.43
1:B5:3716:A:H2'	1:B5:3717:A:C8	2.54	0.43
1:B5:3788:C:H2'	1:B5:3789:U:H6	1.82	0.43
1:B5:4115:A:OP1	25:BV:15:ARG:NH2	2.36	0.43
4:Az:1:MET:HG3	46:A2:1661:G:H5'	2.00	0.43
18:BO:61:ARG:HA	18:BO:70:PRO:HD2	1.99	0.43
21:BR:163:ARG:HH11	46:A2:831:G:H22	1.67	0.43
22:BS:17:LEU:HD21	23:BT:136:ARG:NH1	2.33	0.43
25:BV:87:SER:HA	25:BV:97:TYR:HB3	2.00	0.43
45:Br:101:ARG:HD2	45:Br:101:ARG:HA	1.86	0.43
46:A2:414:C:O2'	54:Af:92:ARG:O	2.25	0.43
46:A2:873:G:OP1	55:Ag:120:ARG:NH1	2.36	0.43
46:A2:1243:G:O5'	73:Al:35:ILE:HG12	2.19	0.43
46:A2:1247:U:H4'	72:Aj:2:LEU:HG	2.01	0.43
46:A2:1250:C:N3	68:AC:138:ARG:NH1	2.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A2:1584:C:H2'	46:A2:1585:A:O4'	2.18	0.43
48:AA:28:PRO:HG3	59:Am:17:PRO:HG3	2.00	0.43
66:AZ:206:ASP:HA	66:AZ:207:PRO:HD2	1.82	0.43
69:Ae:13:THR:HB	69:Ae:14:PRO:HD3	2.00	0.43
69:Ae:18:LEU:HD11	69:Ae:49:PRO:HD3	2.01	0.43
72:Aj:41:PRO:O	72:Aj:45:VAL:HG23	2.18	0.43
78:Ac:101:GLN:HG3	78:Ac:126:ILE:HD11	2.00	0.43
1:B5:301:A:H2'	1:B5:302:G:C8	2.50	0.43
1:B5:1222:U:H2'	1:B5:1223:C:C6	2.54	0.43
1:B5:1365:C:OP2	10:BF:30:ARG:NH2	2.51	0.43
1:B5:2351:G:H2'	1:B5:2352:C:C6	2.53	0.43
1:B5:3400:A:H2'	1:B5:3401:C:H6	1.84	0.43
1:B5:3545:G:H2'	1:B5:3546:A:C8	2.53	0.43
1:B5:3924:U:H2'	1:B5:3925:U:C6	2.53	0.43
1:B5:3986:G:H2'	1:B5:3987:A:C8	2.54	0.43
2:B8:94:G:C5	39:Bj:84:PRO:HD3	2.54	0.43
7:BC:303:ARG:O	20:BQ:38:ARG:NH2	2.37	0.43
9:BE:266:GLN:O	9:BE:270:ARG:HG2	2.18	0.43
17:BN:178:HIS:HA	17:BN:181:HIS:NE2	2.33	0.43
23:BT:80:VAL:O	23:BT:83:LYS:HG2	2.19	0.43
46:A2:1102:A:H8	46:A2:1102:A:OP2	2.01	0.43
50:Ab:79:LYS:HD2	50:Ab:204:LEU:HD13	2.01	0.43
60:An:19:PRO:HG3	60:An:27:VAL:HG21	2.00	0.43
60:An:95:ILE:HB	60:An:129:ILE:HG12	1.99	0.43
66:AZ:89:LYS:NZ	80:Aq:82:ASP:HB3	2.34	0.43
75:Ar:99:LEU:O	75:Ar:102:GLY:N	2.52	0.43
1:B5:173:C:H2'	1:B5:174:C:C6	2.54	0.43
1:B5:3583:G:H2'	1:B5:3584:G:H8	1.84	0.43
5:BA:10:LYS:HA	5:BA:16:PHE:CD2	2.54	0.43
12:BH:37:ASP:CG	12:BH:39:ASN:HD22	2.26	0.43
15:BL:8:MET:HE3	15:BL:8:MET:HB2	1.95	0.43
18:BO:108:ILE:HD12	18:BO:160:ARG:CZ	2.48	0.43
20:BQ:82:VAL:O	20:BQ:102:ALA:HA	2.19	0.43
22:BS:173:ASN:ND2	22:BS:175:PHE:O	2.52	0.43
46:A2:897:U:H2'	46:A2:898:U:C6	2.53	0.43
46:A2:1178:A:H2'	46:A2:1179:G:O4'	2.18	0.43
46:A2:1500:A:C2	46:A2:1626:G:H1'	2.53	0.43
47:Aa:125:VAL:O	47:Aa:136:ARG:HA	2.19	0.43
50:Ab:130:LYS:O	50:Ab:133:ILE:HG12	2.19	0.43
56:Ah:110:ARG:HA	56:Ah:121:LEU:HD23	2.00	0.43
59:Am:34:LYS:HE3	59:Am:74:ILE:HG12	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:AF:223:GLU:HG3	70:AF:225:LYS:HG2	2.00	0.43
70:AF:240:CYS:SG	70:AF:249:CYS:HB2	2.59	0.43
73:Al:38:ALA:O	73:Al:42:LEU:HD13	2.19	0.43
76:As:11:GLN:O	76:As:15:VAL:HG23	2.19	0.43
1:B5:1099:C:H2'	1:B5:1100:G:H8	1.83	0.43
1:B5:1681:U:H2'	1:B5:1682:C:C6	2.54	0.43
1:B5:4193:G:N7	35:Bf:52:LYS:HE3	2.34	0.43
19:BP:92:LEU:HD22	19:BP:96:LYS:NZ	2.34	0.43
46:A2:193:U:H2'	46:A2:194:C:O4'	2.18	0.43
46:A2:208:A:C6	46:A2:209:U:C5	3.07	0.43
46:A2:339:U:O2'	56:Ah:33:PRO:HB3	2.19	0.43
46:A2:1724:G:H2'	46:A2:1725:G:C8	2.53	0.43
48:AA:84:HIS:OXT	59:Am:19:ARG:NH2	2.48	0.43
57:Ai:93:LYS:HB2	57:Ai:96:TYR:CD2	2.53	0.43
58:Ak:25:LEU:HB3	58:Ak:27:GLU:OE1	2.18	0.43
63:Av:30:CYS:SG	63:Av:31:SER:N	2.92	0.43
64:Aw:105:PHE:HA	64:Aw:121:LYS:HD3	2.00	0.43
69:Ae:125:THR:CG2	69:Ae:126:ARG:H	2.24	0.43
70:AF:296:GLN:HG3	70:AF:311:GLN:NE2	2.34	0.43
73:Al:61:TYR:O	73:Al:65:VAL:HG23	2.19	0.43
76:As:75:MET:HE3	76:As:79:TYR:CE2	2.54	0.43
77:Ay:65:TYR:HB2	77:Ay:68:ILE:HD11	2.01	0.43
79:V:51:U:H2'	79:V:52:G:C8	2.54	0.43
80:Aq:45:LYS:HG2	80:Aq:49:LYS:HE2	2.01	0.43
1:B5:727:A:H2'	1:B5:728:G:O4'	2.19	0.42
1:B5:2110:G:O2'	1:B5:3336:G:O6	2.35	0.42
1:B5:3496:A:H1'	1:B5:3497:U:C6	2.54	0.42
2:B8:67:U:OP1	39:Bj:87:LYS:HG2	2.18	0.42
10:BF:15:SER:O	10:BF:19:ARG:HG3	2.19	0.42
14:BJ:60:PHE:HB2	14:BJ:62:ILE:HG12	2.00	0.42
18:BO:142:ALA:HA	18:BO:145:VAL:HG22	2.01	0.42
24:BU:60:VAL:HG23	24:BU:61:VAL:HG23	2.00	0.42
27:BX:37:LYS:C	27:BX:39:ILE:H	2.27	0.42
29:BZ:11:VAL:HG21	29:BZ:80:LEU:HD13	2.01	0.42
32:Bc:57:LYS:HE2	32:Bc:73:HIS:CD2	2.54	0.42
34:Be:76:LYS:O	45:Br:23:GLN:NE2	2.50	0.42
46:A2:67:C:C5	54:Af:164:LYS:HB2	2.54	0.42
46:A2:115:U:H2'	46:A2:116:OMU:C6	2.49	0.42
46:A2:562:OMG:HM23	46:A2:562:OMG:H1'	1.75	0.42
46:A2:1054:C:H2'	46:A2:1055:G:O4'	2.18	0.42
54:Af:102:VAL:HG13	54:Af:106:LEU:HD12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:Aw:53:GLU:HG2	64:Aw:71:ARG:HB2	2.00	0.42
73:Al:42:LEU:HD12	73:Al:47:ALA:CB	2.48	0.42
1:B5:1467:G:H5''	36:Bg:14:ASN:O	2.19	0.42
1:B5:1680:C:H2'	1:B5:1681:U:C6	2.55	0.42
1:B5:1981:C:O2'	10:BF:211:LEU:O	2.37	0.42
1:B5:3651:U:P	23:BT:6:GLY:HA3	2.60	0.42
1:B5:4041:C:H2'	1:B5:4054:A:N6	2.33	0.42
1:B5:4134:A:O2'	12:BH:68:ALA:O	2.27	0.42
6:BB:303:ALA:HB2	6:BB:314:ILE:HA	2.01	0.42
23:BT:17:ARG:HB2	23:BT:22:HIS:CE1	2.53	0.42
46:A2:193:U:O2	46:A2:196:G:C6	2.72	0.42
46:A2:1411:G:H2'	46:A2:1412:U:C6	2.54	0.42
48:AA:64:CYS:HB3	48:AA:73:LEU:HD23	2.00	0.42
64:Aw:28:LYS:HE2	64:Aw:32:LEU:HD22	2.00	0.42
66:AZ:35:GLU:O	66:AZ:38:ILE:HG12	2.19	0.42
70:AF:196:ASN:N	70:AF:210:GLY:O	2.42	0.42
75:Ar:40:TYR:CZ	75:Ar:97:GLN:HG2	2.54	0.42
1:B5:70:A:OP2	30:Ba:64:LYS:NZ	2.50	0.42
1:B5:197:A:N1	1:B5:225:G:O2'	2.44	0.42
1:B5:627:U:OP1	9:BE:104:LYS:NZ	2.47	0.42
1:B5:1269:C:H2'	1:B5:1270:A:C8	2.54	0.42
1:B5:1593:G:O2'	1:B5:1762:G:H4'	2.20	0.42
1:B5:1815:U:H2'	1:B5:1816:A:H8	1.83	0.42
1:B5:2533:C:H2'	1:B5:2534:C:H6	1.84	0.42
1:B5:2610:OMC:H2'	1:B5:2611:G:O4'	2.20	0.42
1:B5:3419:A:H2'	1:B5:3420:A:C8	2.54	0.42
1:B5:3571:C:P	36:Bg:90:ARG:HH22	2.42	0.42
1:B5:4340:U:H2'	1:B5:4341:C:C6	2.54	0.42
3:B7:58:A:H2'	3:B7:59:G:H8	1.85	0.42
38:Bi:86:LYS:HD3	38:Bi:86:LYS:HA	1.85	0.42
46:A2:111:A:H2'	46:A2:112:U:C6	2.54	0.42
46:A2:251:G:H22	46:A2:255:C:H5	1.66	0.42
46:A2:426:A:N6	83:A2:2249:HOH:O	2.51	0.42
67:Ap:12:VAL:HG11	67:Ap:90:LYS:HB3	2.00	0.42
79:V:60:C:H5''	79:V:61:C:C5	2.54	0.42
1:B5:50:C:C2	1:B5:51:A:C8	3.08	0.42
1:B5:502:C:HO2'	1:B5:503:G:P	2.42	0.42
1:B5:735:G:H2'	1:B5:736:G:O4'	2.19	0.42
1:B5:1170:G:H2'	1:B5:1171:C:C6	2.54	0.42
1:B5:1637:A:H2'	1:B5:1638:C:C6	2.55	0.42
1:B5:2240:C:O5'	1:B5:2240:C:H6	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:2420:C:H2'	1:B5:2421:C:C6	2.54	0.42
1:B5:2492:A:H2'	1:B5:2493:A:C8	2.54	0.42
1:B5:2633:G:H2'	1:B5:2634:A:H8	1.83	0.42
1:B5:3242:G:H21	1:B5:3243:A:N6	2.17	0.42
1:B5:3249:U:O2'	1:B5:3250:U:O5'	2.35	0.42
1:B5:3700:A:C2	14:BJ:60:PHE:HB3	2.54	0.42
1:B5:3701:C:C2	1:B5:3702:C:C5	3.08	0.42
1:B5:3779:A:H5''	1:B5:3780:C:H5'	2.00	0.42
1:B5:3958:G:H5''	6:BB:3:HIS:CE1	2.54	0.42
10:BF:241:LEU:O	10:BF:245:MET:HG3	2.19	0.42
11:BG:83:PHE:HA	11:BG:183:ILE:HD13	2.01	0.42
26:BW:53:VAL:O	26:BW:57:ARG:HG2	2.20	0.42
38:Bi:36:HIS:O	38:Bi:40:VAL:HG23	2.20	0.42
45:Br:84:ARG:HE	45:Br:88:ALA:HB1	1.84	0.42
46:A2:305:U:H2'	46:A2:306:U:H6	1.85	0.42
46:A2:493:C:H2'	46:A2:494:A:H8	1.84	0.42
49:AB:33:GLU:HG2	49:AB:41:SER:HB2	2.00	0.42
64:Aw:90:CYS:HA	64:Aw:93:PHE:CD2	2.55	0.42
67:Ap:25:CYS:HA	67:Ap:67:ASP:O	2.20	0.42
70:AF:241:PHE:CE1	70:AF:248:LEU:HD13	2.54	0.42
1:B5:37:U:H5''	30:Ba:32:ARG:CD	2.50	0.42
1:B5:348:A:H2'	1:B5:349:G:C8	2.54	0.42
1:B5:518:C:C4	1:B5:519:C:C4	3.07	0.42
1:B5:1738:G:H2'	1:B5:1739:G:C8	2.54	0.42
1:B5:1974:G:H2'	1:B5:1975:C:O4'	2.19	0.42
1:B5:3432:G:H2'	1:B5:3433:G:C8	2.54	0.42
1:B5:3504:A:H2'	1:B5:3505:C:C6	2.54	0.42
1:B5:3715:G:O2'	1:B5:3716:A:H8	2.03	0.42
1:B5:3787:U:H2'	1:B5:3788:C:H6	1.84	0.42
83:B5:5866:HOH:O	30:Ba:32:ARG:HD2	2.19	0.42
17:BN:94:PHE:CE2	17:BN:96:ARG:HB2	2.55	0.42
18:BO:161:LYS:O	18:BO:165:LYS:HG3	2.20	0.42
24:BU:20:LYS:HB3	24:BU:20:LYS:HE3	1.91	0.42
29:BZ:41:ALA:HB2	29:BZ:77:TYR:HE1	1.84	0.42
32:Bc:65:MET:HE3	32:Bc:65:MET:HB3	1.89	0.42
34:Be:106:LYS:HB3	34:Be:106:LYS:HE2	1.81	0.42
54:Af:147:LEU:HD11	54:Af:156:TYR:HD2	1.84	0.42
58:Ak:16:ILE:HD11	58:Ak:36:TYR:HB2	2.00	0.42
67:Ap:44:PRO:HD3	67:Ap:77:HIS:HB3	2.02	0.42
70:AF:101:PHE:CD2	70:AF:136:GLY:HA2	2.54	0.42
70:AF:236:ILE:HD13	70:AF:252:THR:HA	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:AG:33:LYS:HE2	71:AG:34:TYR:CZ	2.54	0.42
80:Aq:53:TYR:CE2	80:Aq:57:LEU:HD11	2.54	0.42
1:B5:123:C:H2'	1:B5:124:C:C6	2.53	0.42
1:B5:435:A:H2'	1:B5:436:A:O4'	2.20	0.42
1:B5:461:C:H2'	1:B5:462:G:C8	2.53	0.42
1:B5:1266:U:C5'	7:BC:109:ARG:HA	2.49	0.42
1:B5:1417:U:O3'	1:B5:3740:G:H4'	2.19	0.42
1:B5:1961:G:H5'	18:BO:16:LEU:HD23	2.01	0.42
1:B5:2033:G:OP1	30:Ba:7:LYS:NZ	2.44	0.42
1:B5:3199:G:H2'	1:B5:3200:A:C8	2.54	0.42
2:B8:106:G:H4'	2:B8:137:A:H5'	2.01	0.42
6:BB:301:ASN:HB3	6:BB:311:ASP:OD1	2.20	0.42
6:BB:354:GLN:HB3	6:BB:359:ALA:HB1	2.01	0.42
13:BI:191:ILE:HD11	13:BI:212:LEU:HD11	2.00	0.42
14:BJ:141:ILE:HG13	14:BJ:142:ALA:N	2.35	0.42
21:BR:36:ASN:H	21:BR:40:GLN:NE2	2.18	0.42
24:BU:105:ASN:HB2	24:BU:111:GLU:CG	2.49	0.42
46:A2:1173:C:O2'	46:A2:1600:C:OP2	2.32	0.42
46:A2:1266:U:H2'	46:A2:1267:C:C6	2.54	0.42
46:A2:1445:OMG:HM23	46:A2:1445:OMG:H1'	1.90	0.42
46:A2:1610:C:H2'	46:A2:1611:G:H8	1.83	0.42
46:A2:1628:U:O2'	69:Ae:83:GLY:O	2.28	0.42
51:Ad:128:LYS:HG2	51:Ad:140:VAL:HB	2.02	0.42
53:AE:65:PRO:HG3	60:An:129:ILE:O	2.19	0.42
57:Ai:64:ASP:O	57:Ai:70:ARG:HD3	2.20	0.42
66:AZ:10:MET:HE3	80:Aq:111:PHE:HE2	1.84	0.42
66:AZ:108:PHE:HE2	66:AZ:122:LEU:HD21	1.84	0.42
68:AC:139:HIS:NE2	68:AC:150:PHE:HE1	2.17	0.42
79:V:26:G:C2	79:V:27:G:C8	3.08	0.42
1:B5:168:C:H2'	1:B5:169:C:O4'	2.20	0.42
1:B5:288:U:H2'	1:B5:289:G:C8	2.55	0.42
1:B5:343:G:H2'	1:B5:344:C:C6	2.54	0.42
1:B5:602:G:N2	7:BC:4:ALA:HB2	2.35	0.42
1:B5:768:G:O2'	1:B5:2012:G:O6	2.36	0.42
1:B5:1458:C:H2'	1:B5:1459:U:O4'	2.20	0.42
1:B5:1993:C:H4'	1:B5:1994:G:OP2	2.19	0.42
1:B5:3414:C:OP2	1:B5:3415:U:O2'	2.31	0.42
1:B5:3553:A:OP1	1:B5:3554:G:N2	2.53	0.42
1:B5:3696:A:H5'	1:B5:3697:G:C8	2.54	0.42
1:B5:3848:G:O2'	13:BI:4:ARG:NH2	2.45	0.42
1:B5:4009:U:H2'	1:B5:4010:G:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:4325:G:H2'	1:B5:4326:A:H8	1.82	0.42
3:B7:59:G:H1'	8:BD:267:ASN:HB3	2.02	0.42
8:BD:204:VAL:O	8:BD:208:MET:HG3	2.20	0.42
11:BG:51:LEU:O	11:BG:55:VAL:HG23	2.20	0.42
21:BR:109:TYR:OH	21:BR:139:MET:HE3	2.19	0.42
27:BX:126:LEU:HD11	27:BX:134:LYS:HE2	2.02	0.42
46:A2:107:A:H2'	46:A2:108:G:H8	1.84	0.42
46:A2:313:U:H2'	46:A2:314:C:C6	2.54	0.42
46:A2:382:G:H4'	46:A2:621:C:N4	2.34	0.42
46:A2:1105:C:OP1	53:AE:6:ARG:NH1	2.53	0.42
46:A2:1147:A:H2'	46:A2:1148:A:H8	1.83	0.42
46:A2:1556:A:H2'	46:A2:1556:A:N3	2.35	0.42
46:A2:1691:G:H2'	46:A2:1692:G:H8	1.84	0.42
61:At:64:THR:HA	61:At:78:ASP:O	2.19	0.42
67:Ap:13:PHE:HB3	67:Ap:22:VAL:HG22	2.02	0.42
70:AF:31:ILE:HG13	70:AF:43:TRP:CD1	2.54	0.42
70:AF:31:ILE:HG13	70:AF:43:TRP:HD1	1.85	0.42
76:As:102:ARG:HA	76:As:102:ARG:HD3	1.90	0.42
78:Ac:28:GLU:O	78:Ac:65:ARG:NH2	2.52	0.42
1:B5:235:A:P	7:BC:201:ARG:HH22	2.42	0.42
1:B5:261:C:H2'	1:B5:262:G:H8	1.84	0.42
1:B5:1142:U:H2'	1:B5:1143:G:H8	1.83	0.42
1:B5:1677:G:H2'	1:B5:1678:A:H8	1.84	0.42
1:B5:3201:A2M:HM'3	1:B5:3201:A2M:H1'	1.70	0.42
1:B5:3483:G:H2'	1:B5:3484:G:C8	2.54	0.42
1:B5:3602:C:H2'	1:B5:3603:C:C6	2.55	0.42
1:B5:3720:G:H5''	23:BT:17:ARG:HG2	2.02	0.42
1:B5:4275:G:H2'	1:B5:4276:G:C8	2.55	0.42
8:BD:53:VAL:O	8:BD:54:ARG:NH1	2.44	0.42
13:BI:4:ARG:NH1	13:BI:99:ILE:HG13	2.34	0.42
14:BJ:29:SER:HA	14:BJ:33:LEU:HD12	2.00	0.42
21:BR:78:ILE:HD13	21:BR:78:ILE:HA	1.92	0.42
46:A2:469:A:H3'	46:A2:470:OMG:H8	1.85	0.42
46:A2:1055:G:H4'	66:AZ:32:PHE:CD1	2.55	0.42
46:A2:1351:G:H2'	46:A2:1352:G:C8	2.55	0.42
46:A2:1519:C:P	76:As:121:ARG:HH22	2.42	0.42
50:Ab:61:GLU:HB3	50:Ab:63:GLU:OE1	2.20	0.42
54:Af:27:PHE:HE2	54:Af:41:LEU:HD21	1.84	0.42
66:AZ:184:ARG:HB3	66:AZ:191:ARG:NH1	2.35	0.42
70:AF:27:PHE:HB2	70:AF:30:MET:HG3	2.01	0.42
70:AF:234:ASP:OD1	70:AF:252:THR:OG1	2.23	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:AG:17:GLY:HA2	71:AG:27:ARG:NH1	2.35	0.42
1:B5:6:C:H2'	1:B5:7:C:C6	2.54	0.42
1:B5:1155:C:H2'	1:B5:1156:C:C6	2.55	0.42
1:B5:1989:U:H2'	1:B5:1990:C:C6	2.55	0.42
1:B5:2171:OMC:HM23	1:B5:2171:OMC:H1'	1.70	0.42
1:B5:2443:G:H5'	1:B5:2444:A:C2	2.55	0.42
1:B5:2595:G:O2'	25:BV:19:GLY:O	2.30	0.42
1:B5:3532:G:O6	5:BA:68:ARG:HD2	2.19	0.42
1:B5:4091:A:H2'	1:B5:4092:G:H8	1.84	0.42
1:B5:4220:C:H2'	1:B5:4221:C:C6	2.55	0.42
2:B8:70:G:H5''	28:BY:27:ARG:CZ	2.50	0.42
8:BD:33:ARG:O	8:BD:37:VAL:HG22	2.20	0.42
8:BD:83:LEU:HB3	8:BD:88:VAL:HB	2.01	0.42
9:BE:249:LYS:NZ	9:BE:250:TYR:O	2.43	0.42
10:BF:160:ILE:HD13	10:BF:172:LEU:HD22	2.01	0.42
11:BG:165:GLU:HB3	17:BN:10:LEU:HD23	2.01	0.42
14:BJ:51:SER:HB3	14:BJ:69:ALA:HB3	2.00	0.42
15:BL:61:CYS:HB2	15:BL:66:TYR:O	2.20	0.42
46:A2:57:U:O2'	46:A2:460:G:N3	2.53	0.42
46:A2:129:C:H4'	46:A2:130:C:H5'	2.02	0.42
46:A2:207:C:C4	46:A2:208:A:N7	2.87	0.42
46:A2:922:A:H2'	46:A2:923:U:H6	1.84	0.42
46:A2:1181:A:H2'	46:A2:1182:G:O4'	2.20	0.42
46:A2:1269:C:H42	68:AC:95:ARG:HH21	1.67	0.42
46:A2:1431:A:H4'	46:A2:1432:U:H5''	2.02	0.42
46:A2:1666:U:H2'	46:A2:1667:A:C8	2.54	0.42
58:AK:97:ARG:HG3	58:AK:97:ARG:NH1	2.35	0.42
60:AN:62:VAL:HG21	60:AN:67:ASP:C	2.45	0.42
67:AP:28:GLY:HA3	67:AP:67:ASP:CG	2.45	0.42
70:AF:246:TYR:CE2	70:AF:261:LEU:HB2	2.55	0.42
1:B5:1234:C:H2'	1:B5:1235:C:H6	1.85	0.42
1:B5:1841:A:H2'	1:B5:1842:G:C8	2.55	0.42
1:B5:2111:U:H5''	19:BP:66:GLY:HA3	2.01	0.42
1:B5:2123:A:H2'	1:B5:2124:A:C8	2.55	0.42
1:B5:3676:A:C5	1:B5:3678:G:C8	3.08	0.42
1:B5:3907:A:N3	1:B5:3907:A:H2'	2.35	0.42
10:BF:134:VAL:HG23	10:BF:138:ILE:HD13	2.02	0.42
46:A2:207:C:C2	46:A2:208:A:C8	3.08	0.42
46:A2:991:G:N1	46:A2:1038:A:O2'	2.39	0.42
46:A2:1435:A:O2'	71:AG:56:ASP:OXT	2.27	0.42
46:A2:1668:C:H2'	46:A2:1669:U:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:Ab:224:PRO:HA	50:Ab:227:TRP:CD2	2.55	0.42
57:Ai:50:LEU:O	57:Ai:54:ARG:HG3	2.20	0.42
62:Au:32:ILE:HD13	66:AZ:158:ASP:CG	2.45	0.42
65:Ax:57:VAL:HB	65:Ax:60:PHE:CE2	2.54	0.42
72:Aj:3:MET:CE	72:Aj:11:ILE:HD12	2.50	0.42
75:Ar:113:ARG:O	75:Ar:117:ILE:HG12	2.20	0.42
1:B5:271:G:H2'	1:B5:272:C:C6	2.55	0.41
1:B5:476:G:H2'	1:B5:477:G:H8	1.85	0.41
1:B5:2425:A:C4	1:B5:2426:G:C8	3.08	0.41
1:B5:3250:U:H2'	1:B5:3252:A:OP2	2.20	0.41
1:B5:3333:A:H5''	19:BP:83:TRP:O	2.20	0.41
1:B5:3428:G:H2'	1:B5:3429:A:H8	1.84	0.41
1:B5:4265:A:H1'	1:B5:4268:G:N7	2.35	0.41
17:BN:9:GLU:CB	38:Bi:44:ILE:HG13	2.50	0.41
23:BT:51:GLY:HA3	23:BT:92:ARG:HG3	2.00	0.41
28:BY:54:GLU:HB2	28:BY:108:ARG:HB3	2.01	0.41
38:Bi:80:HIS:CD2	38:Bi:84:LYS:HE2	2.55	0.41
46:A2:352:C:H2'	46:A2:353:A:C8	2.51	0.41
46:A2:1106:C:OP1	53:AE:6:ARG:NH2	2.50	0.41
46:A2:1229:C:H5'	68:AC:90:LYS:NZ	2.35	0.41
46:A2:1365:U:H4'	67:Ap:71:ARG:CZ	2.50	0.41
50:Ab:65:ILE:HG13	50:Ab:130:LYS:O	2.20	0.41
64:Aw:25:LYS:O	64:Aw:29:LYS:HG2	2.20	0.41
69:Ae:121:ARG:HH21	69:Ae:192:LYS:HZ2	1.68	0.41
74:Ao:20:VAL:HG12	74:Ao:25:LEU:HG	2.01	0.41
1:B5:1696:A:H2'	13:Bi:22:PHE:CZ	2.55	0.41
1:B5:2243:U:H2'	1:B5:2244:U:O4'	2.20	0.41
1:B5:2403:C:H2'	1:B5:2404:C:C6	2.54	0.41
1:B5:3370:C:H2'	1:B5:3371:A:C8	2.55	0.41
1:B5:3835:OMG:HM21	1:B5:3837:A:H2'	2.01	0.41
1:B5:4303:C:O2'	1:B5:4304:C:H5'	2.19	0.41
4:Az:11:ARG:NH2	46:A2:1798:U:OP1	2.53	0.41
10:BF:224:HIS:ND1	10:BF:226:VAL:HG22	2.35	0.41
14:BJ:48:PRO:HB2	14:BJ:70:VAL:HG22	2.02	0.41
17:BN:21:PHE:O	17:BN:25:VAL:HG22	2.19	0.41
18:BO:127:VAL:HG13	22:BS:158:VAL:HG13	2.01	0.41
24:BU:84:LYS:HB2	24:BU:110:TYR:CE2	2.54	0.41
29:BZ:97:ASN:O	29:BZ:100:VAL:HG22	2.20	0.41
39:Bj:39:TYR:CG	39:Bj:40:PRO:HA	2.55	0.41
40:Bk:8:ILE:H	40:Bk:8:ILE:HD12	1.83	0.41
46:A2:478:C:H2'	46:A2:479:G:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A2:911:C:H2'	46:A2:912:U:C6	2.55	0.41
46:A2:1051:A:H2'	46:A2:1052:C:C6	2.54	0.41
49:AB:16:LYS:HB3	49:AB:31:ARG:HB3	2.01	0.41
51:Ad:173:ILE:HD11	51:Ad:235:TRP:CE2	2.56	0.41
59:Am:29:THR:O	59:Am:33:VAL:HG23	2.19	0.41
66:AZ:89:LYS:HB3	66:AZ:202:TYR:CE1	2.55	0.41
67:Ap:57:LEU:HD11	67:Ap:115:TYR:CG	2.55	0.41
74:Ao:81:ARG:NH1	74:Ao:98:ASN:HA	2.35	0.41
1:B5:2:G:H2'	1:B5:3:C:C6	2.56	0.41
1:B5:517:G:H1	1:B5:583:C:H42	1.67	0.41
1:B5:1157:C:H5'	1:B5:1158:C:OP2	2.21	0.41
1:B5:1486:A:N6	46:A2:986:A:N1	2.67	0.41
1:B5:1785:U:H2'	1:B5:1786:G:C8	2.55	0.41
1:B5:3141:G:H2'	1:B5:3142:G:C8	2.52	0.41
1:B5:3239:U:C2	1:B5:3240:A:C8	3.09	0.41
1:B5:3321:U:OP2	83:B5:4908:HOH:O	2.21	0.41
1:B5:3423:G:H2'	1:B5:3424:A:C8	2.55	0.41
1:B5:3483:G:H2'	1:B5:3484:G:H8	1.85	0.41
1:B5:3621:A:H2'	1:B5:3622:G:C8	2.55	0.41
6:BB:224:LYS:HG2	6:BB:340:THR:HG22	2.02	0.41
8:BD:191:ASN:ND2	8:BD:194:VAL:HG23	2.35	0.41
11:BG:91:THR:HA	11:BG:94:GLN:HG2	2.02	0.41
11:BG:186:SER:O	11:BG:189:ARG:N	2.53	0.41
18:BO:74:ARG:O	18:BO:142:ALA:HB1	2.19	0.41
22:BS:19:THR:C	22:BS:21:LYS:H	2.29	0.41
24:BU:33:ILE:HD12	24:BU:99:TRP:HE1	1.85	0.41
34:Be:65:LYS:O	34:Be:75:ARG:NH2	2.52	0.41
37:Bh:29:SER:O	37:Bh:33:VAL:HG23	2.21	0.41
40:Bk:36:VAL:HG12	40:Bk:43:TYR:HB2	2.03	0.41
45:Br:59:GLY:HA3	45:Br:83:ARG:HG2	2.01	0.41
46:A2:901:U:C2	46:A2:902:A:C8	3.07	0.41
46:A2:1693:U:H2'	46:A2:1694:C:H6	1.85	0.41
47:Aa:109:LYS:HE3	47:Aa:113:MET:SD	2.60	0.41
57:Ai:160:SER:HB3	57:Ai:163:SER:HB2	2.02	0.41
60:An:78:ALA:HB3	60:An:118:ALA:HB3	2.03	0.41
70:AF:47:ARG:HA	70:AF:52:TYR:HA	2.03	0.41
79:V:23:A:H2'	79:V:24:G:C8	2.55	0.41
1:B5:99:A:H2'	1:B5:100:G:N3	2.36	0.41
1:B5:132:G:H2'	1:B5:133:C:O4'	2.20	0.41
1:B5:280:A:N1	1:B5:307:A:H5''	2.35	0.41
1:B5:670:G:C6	1:B5:742:A:C4	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:1277:C:H2'	1:B5:1278:G:O4'	2.19	0.41
1:B5:1360:C:O2'	1:B5:1361:A:H5''	2.21	0.41
1:B5:2639:C:H2'	1:B5:2640:U:C6	2.55	0.41
1:B5:3436:U:H3'	1:B5:3437:A:C8	2.55	0.41
1:B5:3522:C:H2'	1:B5:3523:U:C6	2.55	0.41
1:B5:3562:C:O2'	1:B5:3563:G:H5'	2.20	0.41
1:B5:4050:A:H8	1:B5:4050:A:O5'	2.03	0.41
1:B5:4181:C:OP1	1:B5:4440:U:O2'	2.38	0.41
1:B5:4204:G:H2'	1:B5:4205:A:H8	1.86	0.41
2:B8:75:OMG:HM23	2:B8:75:OMG:H1'	1.87	0.41
2:B8:93:C:O2'	2:B8:94:G:H8	2.03	0.41
3:B7:33:U:H2'	3:B7:34:C:C6	2.55	0.41
17:BN:182:HIS:HA	17:BN:195:ARG:HH12	1.85	0.41
19:BP:27:LYS:O	19:BP:31:GLU:HG2	2.21	0.41
46:A2:65:C:OP1	54:Af:136:LYS:NZ	2.40	0.41
46:A2:214:C:H2'	46:A2:215:A:C8	2.55	0.41
46:A2:653:G:H2'	46:A2:654:A:H8	1.84	0.41
46:A2:696:C:H3'	46:A2:697:A:C5'	2.50	0.41
46:A2:1408:C:O2'	80:Aq:52:GLY:HA3	2.19	0.41
46:A2:1496:G:OP1	76:As:56:ARG:NE	2.32	0.41
46:A2:1631:U:H2'	46:A2:1632:U:O4'	2.21	0.41
46:A2:1643:C:H2'	46:A2:1644:C:C6	2.54	0.41
63:Av:12:LYS:HA	63:Av:12:LYS:HD3	1.85	0.41
70:AF:192:THR:OG1	70:AF:213:ASP:OD2	2.33	0.41
70:AF:223:GLU:HG3	70:AF:225:LYS:H	1.85	0.41
1:B5:35:U:H4'	1:B5:1448:A:N1	2.35	0.41
1:B5:88:A:N7	20:BQ:173:LYS:NZ	2.69	0.41
1:B5:486:G:C2'	1:B5:487:G:H5'	2.51	0.41
1:B5:720:G:H2'	1:B5:721:U:H6	1.84	0.41
1:B5:1427:G:H2'	1:B5:1428:C:H6	1.85	0.41
1:B5:1515:G:O2'	1:B5:2589:A:OP1	2.36	0.41
1:B5:2285:A:P	40:Bk:37:ARG:HH11	2.44	0.41
1:B5:2411:G:H2'	1:B5:2412:G:C8	2.55	0.41
1:B5:2445:A:H62	40:Bk:35:LYS:HZ2	1.68	0.41
1:B5:3924:U:H2'	1:B5:3925:U:H6	1.85	0.41
2:B8:85:U:H5'	2:B8:87:G:O4'	2.21	0.41
3:B7:57:C:H2'	3:B7:58:A:C8	2.55	0.41
12:BH:128:MET:SD	12:BH:157:SER:HB3	2.60	0.41
23:BT:93:ILE:HA	23:BT:96:ILE:HG12	2.01	0.41
46:A2:98:C:H2'	46:A2:387:A:H4'	2.03	0.41
46:A2:1647:U:H2'	46:A2:1648:G:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:AA:8:LEU:HG	63:Av:62:VAL:HG11	2.01	0.41
52:AD:112:TYR:CG	57:Ai:33:GLY:HA3	2.55	0.41
55:Ag:50:GLU:O	55:Ag:50:GLU:HG2	2.21	0.41
57:Ai:107:GLU:O	57:Ai:113:GLN:NE2	2.43	0.41
61:At:68:THR:HG23	61:At:70:CYS:O	2.20	0.41
63:Av:77:PRO:HG2	63:Av:79:PHE:CE2	2.55	0.41
1:B5:99:A:H4'	17:BN:181:HIS:CD2	2.55	0.41
1:B5:1133:G:H2'	1:B5:1134:G:C8	2.53	0.41
1:B5:1398:G:H2'	1:B5:1399:C:C6	2.55	0.41
1:B5:3374:G:OP1	6:BB:250:LYS:HD2	2.20	0.41
1:B5:3662:A:H2'	1:B5:3663:6MZ:C8	2.50	0.41
1:B5:3862:U:C4	1:B5:3863:U:C5	3.09	0.41
1:B5:4286:G:O2'	1:B5:4287:C:H5''	2.20	0.41
7:BC:210:ILE:HG21	7:BC:252:TRP:CZ3	2.55	0.41
7:BC:218:ILE:HA	7:BC:229:LEU:HG	2.03	0.41
7:BC:283:LYS:NZ	20:BQ:22:ASP:OD2	2.38	0.41
11:BG:48:LYS:HD3	11:BG:48:LYS:HA	1.86	0.41
20:BQ:9:LYS:HB3	20:BQ:9:LYS:HE2	1.77	0.41
46:A2:263:A:H2'	46:A2:264:A:O4'	2.20	0.41
46:A2:1161:G:H2'	46:A2:1162:A:H8	1.82	0.41
46:A2:1323:G:H2'	46:A2:1324:G:H8	1.85	0.41
46:A2:1517:C:H2'	46:A2:1518:G:C8	2.53	0.41
46:A2:1578:A:O5'	75:Ar:133:GLY:HA3	2.21	0.41
46:A2:1582:C:H2'	46:A2:1583:C:C6	2.54	0.41
55:Ag:60:ILE:HD11	55:Ag:90:LYS:HE2	2.01	0.41
63:Av:83:LEU:HD11	63:Av:120:HIS:HA	2.03	0.41
66:AZ:31:ASP:HB3	66:AZ:34:MET:HB2	2.03	0.41
66:AZ:85:ARG:NH1	66:AZ:203:PHE:O	2.48	0.41
67:Ap:57:LEU:HD11	67:Ap:115:TYR:CD2	2.56	0.41
70:AF:31:ILE:HD13	70:AF:299:PHE:CE2	2.55	0.41
70:AF:145:GLU:HG2	70:AF:177:TRP:HH2	1.86	0.41
79:V:2:C:H2'	79:V:3:C:C6	2.56	0.41
79:V:65:G:H2'	79:V:66:U:C6	2.56	0.41
1:B5:382:U:H2'	1:B5:383:G:O4'	2.20	0.41
1:B5:629:C:OP1	45:Br:87:ARG:NH1	2.50	0.41
1:B5:1433:G:H2'	1:B5:1434:U:C6	2.56	0.41
1:B5:1587:U:H2'	1:B5:1588:C:H6	1.85	0.41
1:B5:1825:G:O6	35:Bf:18:LEU:HB2	2.21	0.41
1:B5:3373:C:H1'	6:BB:268:ARG:NH2	2.34	0.41
1:B5:3522:C:O3'	11:BG:249:ARG:NH2	2.54	0.41
1:B5:3548:C:H2'	1:B5:3549:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:3651:U:H2'	1:B5:3652:G:C8	2.55	0.41
1:B5:3903:U:H2'	1:B5:3904:C:H6	1.86	0.41
1:B5:4071:PSU:H2'	1:B5:4072:U:C6	2.55	0.41
21:BR:172:ARG:O	21:BR:176:ARG:HG3	2.20	0.41
27:BX:149:ALA:HB1	27:BX:154:ILE:HB	2.02	0.41
46:A2:493:C:H2'	46:A2:494:A:C8	2.56	0.41
46:A2:976:U:H2'	46:A2:977:C:H6	1.85	0.41
46:A2:1081:C:P	47:Aa:151:ARG:HH22	2.43	0.41
46:A2:1139:A:H2'	46:A2:1140:A:C8	2.56	0.41
46:A2:1307:G:H2'	46:A2:1308:U:C6	2.55	0.41
46:A2:1421:G:H4'	80:Aq:4:VAL:HG22	2.03	0.41
46:A2:1493:C:H2'	46:A2:1494:U:C6	2.55	0.41
59:Am:46:THR:OG1	59:Am:49:GLN:HG3	2.21	0.41
70:AF:269:GLU:OE1	70:AF:271:LYS:HB2	2.21	0.41
1:B5:212:A:H2'	1:B5:213:G:H8	1.86	0.41
1:B5:618:C:H2'	1:B5:619:G:H8	1.86	0.41
1:B5:1231:C:H2'	1:B5:1232:A:C8	2.54	0.41
1:B5:1324:C:H2'	1:B5:1325:C:C6	2.56	0.41
1:B5:2107:G:H2'	1:B5:2108:U:O4'	2.20	0.41
1:B5:2409:A:OP1	21:BR:117:ARG:NH1	2.53	0.41
1:B5:3749:OMU:OP2	20:BQ:159:PRO:HD2	2.21	0.41
1:B5:4337:A:H2'	1:B5:4338:A:O4'	2.21	0.41
12:BH:5:LEU:HB2	12:BH:60:TRP:CZ3	2.55	0.41
16:BM:12:ILE:HD11	16:BM:62:LEU:HG	2.03	0.41
17:BN:148:THR:O	17:BN:151:ILE:HG22	2.20	0.41
18:BO:155:THR:HG22	18:BO:159:LYS:NZ	2.36	0.41
24:BU:24:ASP:HB3	24:BU:111:GLU:CB	2.51	0.41
30:Ba:28:HIS:CE1	30:Ba:32:ARG:NH1	2.89	0.41
42:Bm:102:ARG:NH1	83:Bm:301:HOH:O	2.52	0.41
46:A2:120:U:H2'	46:A2:121:OMU:H6	2.02	0.41
46:A2:498:C:H2'	46:A2:499:U:C6	2.56	0.41
46:A2:516:A:C8	46:A2:550:G:H5'	2.56	0.41
46:A2:963:G:H2'	46:A2:964:C:H6	1.86	0.41
46:A2:1087:G:H4'	59:Am:11:LEU:HD23	2.02	0.41
46:A2:1292:G:O3'	78:Ac:183:GLY:HA3	2.21	0.41
46:A2:1435:A:HO2'	61:At:79:ARG:NH1	2.19	0.41
46:A2:1513:C:H2'	46:A2:1514:C:C6	2.56	0.41
46:A2:1551:U:H2'	46:A2:1552:C:O4'	2.20	0.41
50:Ab:37:LEU:HD21	50:Ab:52:ILE:HD13	2.02	0.41
56:Ah:129:LEU:O	56:Ah:133:GLU:HB2	2.21	0.41
61:At:56:MET:HE2	61:At:56:MET:HA	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:Ax:7:ILE:HD12	65:Ax:44:LEU:HD23	2.03	0.41
73:Al:52:LEU:HG	73:Al:65:VAL:HG21	2.03	0.41
75:Ar:26:ILE:HD13	75:Ar:56:ALA:HA	2.02	0.41
1:B5:36:U:OP1	1:B5:1574:G:N2	2.45	0.41
1:B5:86:U:H2'	1:B5:87:A:C8	2.55	0.41
1:B5:222:C:H2'	1:B5:223:G:O4'	2.21	0.41
1:B5:495:G:H5'	7:BC:268:ARG:HB2	2.01	0.41
1:B5:786:C:OP2	9:BE:76:LYS:HD3	2.21	0.41
1:B5:1186:C:H4'	1:B5:1187:G:C5	2.55	0.41
1:B5:1299:G:H2'	1:B5:1300:C:C6	2.56	0.41
1:B5:1366:G:H4'	1:B5:1367:G:O5'	2.21	0.41
1:B5:1470:A:H2'	1:B5:1471:G:O4'	2.21	0.41
1:B5:1514:U:H5''	1:B5:3970:G:OP1	2.20	0.41
1:B5:2134:U:H2'	1:B5:2135:U:C6	2.56	0.41
1:B5:2162:U:H2'	1:B5:2163:G:H8	1.86	0.41
1:B5:2354:G:H2'	1:B5:2355:G:C8	2.56	0.41
1:B5:2383:C:H2'	1:B5:2384:U:H6	1.86	0.41
1:B5:2593:A:N6	1:B5:3316:G:O2'	2.54	0.41
1:B5:3080:G:O2'	1:B5:3081:G:O4'	2.35	0.41
1:B5:3210:A:H2'	1:B5:3211:U:O4'	2.21	0.41
1:B5:3249:U:H4'	1:B5:3250:U:OP1	2.21	0.41
1:B5:3263:U:O2	1:B5:3291:U:H4'	2.21	0.41
1:B5:3263:U:OP1	1:B5:3993:G:O2'	2.24	0.41
1:B5:3332:C:H2'	1:B5:3333:A:H8	1.86	0.41
1:B5:3442:A:N6	1:B5:3493:G:H1'	2.36	0.41
1:B5:3744:U:OP1	23:BT:78:LYS:NZ	2.53	0.41
1:B5:3929:C:H2'	1:B5:3930:A:O4'	2.20	0.41
1:B5:4187:C:N3	83:B5:5195:HOH:O	2.37	0.41
7:BC:195:LYS:O	83:BC:501:HOH:O	2.22	0.41
7:BC:357:ALA:O	7:BC:361:VAL:HG23	2.20	0.41
10:BF:234:ARG:HD3	10:BF:237:GLN:HB2	2.03	0.41
24:BU:23:LEU:HD23	24:BU:39:PHE:CE2	2.56	0.41
29:BZ:109:LYS:HG3	29:BZ:112:ARG:NH2	2.35	0.41
44:Bp:29:ILE:HG23	44:Bp:69:TRP:CG	2.56	0.41
46:A2:64:A:O5'	54:Af:136:LYS:NZ	2.51	0.41
46:A2:77:A:H2	54:Af:175:LYS:HG3	1.86	0.41
46:A2:260:G:OP1	51:Ad:134:LYS:N	2.25	0.41
46:A2:1001:G:H2'	46:A2:1002:G:O4'	2.20	0.41
46:A2:1277:U:H2'	46:A2:1278:G:C8	2.56	0.41
46:A2:1311:A:OP1	66:AZ:139:TYR:OH	2.32	0.41
46:A2:1412:U:H2'	46:A2:1413:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:A2:1549:A:O3'	77:Ay:102:LYS:NZ	2.54	0.41
46:A2:1721:C:H4'	46:A2:1722:A:C2	2.55	0.41
46:A2:1725:G:C2	46:A2:1726:C:C5	3.08	0.41
46:A2:1726:C:H2'	46:A2:1727:C:O4'	2.20	0.41
47:Aa:103:MET:HE1	47:Aa:212:VAL:O	2.21	0.41
50:Ab:47:LYS:HA	50:Ab:47:LYS:HD3	1.87	0.41
60:An:83:GLN:O	60:An:87:GLU:HG3	2.20	0.41
66:AZ:113:GLN:C	66:AZ:115:ALA:H	2.29	0.41
70:AF:8:ARG:HB2	70:AF:311:GLN:HB2	2.03	0.41
76:As:134:ILE:O	76:As:137:GLN:HG2	2.21	0.41
78:Ac:123:LEU:O	78:Ac:127:MET:HG2	2.21	0.41
80:Aq:94:GLU:O	80:Aq:116:ASN:ND2	2.34	0.41
1:B5:273:U:H2'	1:B5:274:U:C6	2.55	0.41
1:B5:426:U:OP1	19:BP:37:LYS:NZ	2.53	0.41
1:B5:493:C:H2'	1:B5:494:G:H8	1.81	0.41
1:B5:765:A:H1'	1:B5:1985:G:H5''	2.02	0.41
1:B5:1221:G:O2'	1:B5:1222:U:H6	2.04	0.41
1:B5:1372:C:OP1	20:BQ:40:ASN:ND2	2.52	0.41
1:B5:1428:C:H2'	1:B5:1429:G:C8	2.56	0.41
1:B5:2432:C:H2'	1:B5:2433:C:C6	2.56	0.41
1:B5:3197:G:H22	1:B5:3210:A:H2	1.68	0.41
1:B5:3370:C:H2'	1:B5:3371:A:H8	1.86	0.41
1:B5:3539:G:H2'	1:B5:3540:G:H8	1.86	0.41
1:B5:3763:G:H2'	1:B5:3764:U:C6	2.56	0.41
1:B5:3936:U:H2'	1:B5:3937:OMG:H8	1.85	0.41
2:B8:39:G:H1'	2:B8:103:A:N6	2.36	0.41
3:B7:58:A:H2'	3:B7:59:G:C8	2.55	0.41
8:BD:106:ALA:HB2	8:BD:166:ALA:HA	2.03	0.41
10:BF:224:HIS:NE2	10:BF:232:GLY:HA3	2.36	0.41
16:BM:40:GLY:HA3	16:BM:45:VAL:HB	2.02	0.41
26:BW:1:MET:HB2	26:BW:15:PRO:HG3	2.03	0.41
28:BY:22:PRO:O	28:BY:26:ARG:HG3	2.20	0.41
46:A2:198:G:H2'	46:A2:199:G:O4'	2.21	0.41
46:A2:443:G:OP1	64:Aw:76:LYS:HA	2.21	0.41
46:A2:636:U:H2'	46:A2:637:C:H6	1.85	0.41
46:A2:839:G:H1	46:A2:863:A:N6	2.18	0.41
46:A2:977:C:H2'	46:A2:978:A:O4'	2.21	0.41
46:A2:1634:A:H2'	69:Ae:59:ARG:HD2	2.03	0.41
46:A2:1658:OMC:H2'	46:A2:1659:C:O4'	2.21	0.41
46:A2:1779:A:HO2'	46:A2:1780:G:P	2.43	0.41
54:Af:188:LYS:HG3	54:Af:191:ARG:NH2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:Av:15:ASN:OD1	63:Av:19:LYS:NZ	2.54	0.41
70:AF:228:TYR:CZ	70:AF:264:LYS:HE3	2.56	0.41
73:Al:51:VAL:HA	73:Al:77:ILE:O	2.21	0.41
73:Al:87:GLU:HG3	73:Al:103:VAL:HG21	2.03	0.41
74:Ao:18:ARG:NH1	74:Ao:36:LEU:O	2.53	0.41
76:As:39:LEU:HG	76:As:47:PRO:HG3	2.02	0.41
76:As:110:LEU:O	76:As:110:LEU:HD23	2.19	0.41
80:Aq:32:LYS:HE2	80:Aq:32:LYS:HB3	1.81	0.41
1:B5:35:U:H4'	1:B5:1448:A:C2	2.56	0.40
1:B5:152:U:P	17:BN:49:ARG:HH12	2.44	0.40
1:B5:386:A:H1'	1:B5:387:A:H5''	2.03	0.40
1:B5:461:C:C2	1:B5:462:G:C8	3.09	0.40
1:B5:495:G:H1	1:B5:600:C:N4	2.17	0.40
1:B5:743:U:H4'	1:B5:744:C:H5''	2.02	0.40
1:B5:1181:G:H2'	1:B5:1182:G:H8	1.86	0.40
1:B5:1436:C:H4'	15:BL:4:SER:HB2	2.02	0.40
1:B5:1511:U:H2'	1:B5:1512:C:C6	2.56	0.40
1:B5:1513:C:H5''	1:B5:1514:U:O5'	2.20	0.40
1:B5:1721:U:H4'	31:Bb:49:HIS:O	2.21	0.40
1:B5:2496:U:H2'	1:B5:2497:C:C6	2.55	0.40
1:B5:3129:A:H2'	1:B5:3130:A:C5	2.56	0.40
11:BG:98:LEU:HA	11:BG:101:LYS:NZ	2.36	0.40
12:BH:165:THR:HG21	12:BH:179:ILE:HG13	2.03	0.40
21:BR:177:LEU:HA	21:BR:180:LYS:HB2	2.02	0.40
23:BT:33:ILE:O	23:BT:98:HIS:NE2	2.53	0.40
28:BY:74:TYR:CE2	28:BY:77:LYS:HE2	2.56	0.40
36:Bg:69:LYS:O	36:Bg:73:HIS:ND1	2.54	0.40
45:Br:58:LYS:HD2	45:Br:58:LYS:HA	1.94	0.40
46:A2:1025:C:H2'	46:A2:1026:G:O4'	2.20	0.40
46:A2:1115:G:O2'	63:Av:76:SER:N	2.54	0.40
51:Ad:192:ILE:HD13	51:Ad:238:LEU:HD13	2.02	0.40
63:Av:36:ARG:HA	63:Av:36:ARG:HE	1.86	0.40
65:Ax:9:THR:HG23	65:Ax:23:MET:HG3	2.03	0.40
65:Ax:124:ASN:OD1	65:Ax:125:VAL:N	2.53	0.40
69:Ae:18:LEU:HG	69:Ae:19:PHE:CD2	2.55	0.40
70:AF:19:THR:O	70:AF:288:SER:HB2	2.21	0.40
74:Ao:72:LYS:HD3	74:Ao:72:LYS:HA	1.90	0.40
78:Ac:123:LEU:HD21	78:Ac:154:ASP:CB	2.50	0.40
1:B5:369:C:O4'	7:BC:83:GLY:HA3	2.21	0.40
1:B5:494:G:H2'	1:B5:495:G:H8	1.84	0.40
1:B5:1357:C:H3'	1:B5:1358:G:C4'	2.48	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B5:2287:U:H2'	1:B5:2288:C:C6	2.57	0.40
1:B5:2356:C:H2'	1:B5:2357:G:C8	2.56	0.40
1:B5:2490:U:H2'	5:BA:50:HIS:CD2	2.55	0.40
4:Az:16:LYS:HB3	4:Az:16:LYS:HE2	1.88	0.40
16:BM:74:ARG:O	16:BM:78:GLU:HG3	2.21	0.40
21:BR:37:SER:H	21:BR:40:GLN:HE21	1.68	0.40
46:A2:407:G:P	56:Ah:47:ARG:HH12	2.44	0.40
46:A2:889:C:H5''	47:Aa:157:GLN:OE1	2.20	0.40
46:A2:1306:G:C8	46:A2:1307:G:C8	3.09	0.40
54:Af:23:ASN:O	54:Af:40:SER:OG	2.34	0.40
66:AZ:108:PHE:CE2	66:AZ:122:LEU:HD21	2.56	0.40
70:AF:154:VAL:O	70:AF:155:ARG:HD3	2.21	0.40
75:Ar:60:THR:OG1	75:Ar:63:GLU:OE1	2.31	0.40
77:Ay:50:PHE:CE2	77:Ay:83:LEU:HD11	2.56	0.40
79:V:16:U:C2	79:V:61:C:H5'	2.56	0.40
80:Aq:32:LYS:HD2	80:Aq:47:ARG:HH11	1.85	0.40
1:B5:86:U:OP1	20:BQ:169:SER:OG	2.32	0.40
1:B5:170:A:H2'	1:B5:171:U:C6	2.56	0.40
1:B5:578:C:N4	1:B5:579:G:O6	2.54	0.40
1:B5:1394:U:H2'	1:B5:1395:C:C6	2.56	0.40
1:B5:2627:G:OP2	1:B5:2628:A:O2'	2.29	0.40
1:B5:3528:C:H2'	1:B5:3529:G:H8	1.85	0.40
1:B5:4070:U:H4'	6:BB:373:LYS:HE3	2.03	0.40
1:B5:4134:A:H2'	1:B5:4135:A:O4'	2.22	0.40
1:B5:4294:U:H2'	1:B5:4295:C:C6	2.57	0.40
2:B8:7:U:H2'	2:B8:8:U:C6	2.57	0.40
2:B8:46:G:OP1	41:Bl:18:LYS:NZ	2.42	0.40
9:BE:127:PRO:O	45:Br:112:ARG:NH1	2.42	0.40
11:BG:207:VAL:HG13	11:BG:212:LYS:HG2	2.03	0.40
15:BL:115:GLN:O	15:BL:119:GLU:HG2	2.22	0.40
46:A2:26:U:H2'	46:A2:27:A2M:H8	2.03	0.40
46:A2:396:A:N6	83:A2:2262:HOH:O	2.53	0.40
46:A2:1568:G:C2	46:A2:1582:C:C2	3.09	0.40
49:AB:13:ARG:C	49:AB:32:VAL:HG23	2.46	0.40
55:Ag:36:LEU:HB3	55:Ag:37:LYS:H	1.76	0.40
57:Ai:111:GLN:NE2	57:Ai:127:ARG:HB2	2.36	0.40
57:Ai:138:ARG:HD3	57:Ai:156:HIS:CG	2.56	0.40
58:Ak:55:TYR:OH	58:Ak:116:CYS:HB3	2.20	0.40
58:Ak:148:ALA:HB3	58:Ak:151:THR:HG21	2.03	0.40
64:Aw:88:ASP:O	64:Aw:134:TYR:HE1	2.04	0.40
69:Ae:27:VAL:HG23	69:Ae:41:LYS:HE2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:Ay:58:LEU:HG	77:Ay:62:VAL:HG21	2.01	0.40
1:B5:456:C:H2'	1:B5:457:G:C8	2.55	0.40
1:B5:686:G:O2'	1:B5:688:A:O5'	2.32	0.40
1:B5:2025:A:H2'	1:B5:2026:C:O4'	2.20	0.40
1:B5:2397:G:H2'	1:B5:2398:G:H8	1.86	0.40
1:B5:2538:A:H1'	41:Bl:45:ARG:HH22	1.85	0.40
1:B5:3421:G:H4'	47:Aa:54:GLY:HA2	2.02	0.40
1:B5:3679:G:H4'	1:B5:3771:G:O2'	2.21	0.40
1:B5:3706:C:H2'	1:B5:3707:G:O4'	2.21	0.40
1:B5:3889:U:O2'	1:B5:3893:U:OP1	2.37	0.40
1:B5:4235:G:OP2	12:BH:21:LYS:NZ	2.37	0.40
6:BB:294:LYS:HD2	6:BB:294:LYS:HA	1.92	0.40
10:BF:92:ARG:NH1	10:BF:112:LEU:O	2.48	0.40
15:BL:62:PRO:O	15:BL:63:THR:OG1	2.40	0.40
19:BP:10:ASN:HB2	19:BP:13:LYS:HB2	2.03	0.40
43:Bo:30:LYS:NZ	79:V:1:G:O3'	2.54	0.40
46:A2:12:U:H2'	46:A2:13:C:H6	1.84	0.40
46:A2:85:A:H2'	46:A2:86:C:H6	1.87	0.40
46:A2:613:U:H2'	46:A2:614:A:H8	1.86	0.40
46:A2:801:C:H2'	46:A2:802:G:O4'	2.22	0.40
46:A2:994:A:N3	46:A2:1798:U:O2'	2.55	0.40
46:A2:1718:G:C6	46:A2:1724:G:N1	2.90	0.40
47:Aa:189:ILE:HB	47:Aa:190:PRO:HD3	2.04	0.40
54:Af:159:ARG:HE	54:Af:173:ALA:HB2	1.86	0.40
63:Av:15:ASN:HD21	63:Av:71:LYS:HA	1.84	0.40
65:Ax:53:ASP:OD1	65:Ax:53:ASP:N	2.51	0.40
66:AZ:181:GLU:CD	66:AZ:191:ARG:HH22	2.30	0.40
70:AF:252:THR:HG21	70:AF:257:LYS:HG2	2.03	0.40
71:AG:3:HIS:HD2	71:AG:5:GLN:HB2	1.85	0.40
77:Ay:60:LYS:HG3	77:Ay:61:GLU:HG3	2.03	0.40
1:B5:21:G:H1'	2:B8:103:A:N3	2.36	0.40
1:B5:185:C:C2	1:B5:186:U:H1'	2.57	0.40
1:B5:212:A:H2'	1:B5:213:G:C8	2.57	0.40
1:B5:651:C:OP1	9:BE:149:ARG:NE	2.49	0.40
1:B5:727:A:N3	16:BM:65:PRO:HG3	2.37	0.40
1:B5:1513:C:H3'	1:B5:1514:U:H4'	2.03	0.40
1:B5:1738:G:H2'	1:B5:1739:G:H8	1.86	0.40
1:B5:1867:C:O2'	1:B5:1934:A:N1	2.50	0.40
1:B5:2605:C:O2	6:BB:242:ARG:NH2	2.46	0.40
1:B5:3512:C:H2'	1:B5:3513:G:C8	2.56	0.40
1:B5:3560:C:C2	1:B5:3561:U:C5	3.10	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:BB:71:GLU:OE1	26:BW:1:MET:HG2	2.21	0.40
19:BP:78:TRP:CD1	19:BP:80:GLN:H	2.40	0.40
37:Bh:52:LYS:HA	37:Bh:52:LYS:HD3	1.91	0.40
46:A2:610:PSU:H2'	46:A2:611:A:H8	1.87	0.40
46:A2:1117:G:P	63:Av:76:SER:HB3	2.62	0.40
46:A2:1271:A:OP2	73:Al:33:ARG:NH1	2.54	0.40
46:A2:1518:G:H2'	46:A2:1519:C:H6	1.86	0.40
47:Aa:120:MET:HB2	47:Aa:142:PHE:CD2	2.57	0.40
49:AB:40:ARG:NH1	60:An:117:ARG:HH21	2.11	0.40
57:Ai:59:GLU:OE2	57:Ai:69:ARG:NH2	2.55	0.40
69:Ae:153:LEU:HD22	69:Ae:176:LEU:HD23	2.03	0.40
72:Aj:45:VAL:HG13	72:Aj:49:MET:HE1	2.03	0.40
73:Al:35:ILE:HD11	73:Al:107:SER:OG	2.22	0.40
76:As:104:LEU:HD13	76:As:121:ARG:HD3	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	Az	23/25 (92%)	23 (100%)	0	0	100	100
5	BA	246/257 (96%)	238 (97%)	8 (3%)	0	100	100
6	BB	395/403 (98%)	388 (98%)	7 (2%)	0	100	100
7	BC	359/421 (85%)	353 (98%)	6 (2%)	0	100	100
8	BD	294/297 (99%)	284 (97%)	10 (3%)	0	100	100
9	BE	218/298 (73%)	215 (99%)	3 (1%)	0	100	100
10	BF	232/246 (94%)	225 (97%)	7 (3%)	0	100	100
11	BG	206/266 (77%)	201 (98%)	5 (2%)	0	100	100
12	BH	190/192 (99%)	190 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	BI	201/214 (94%)	197 (98%)	4 (2%)	0	100	100
14	BJ	168/178 (94%)	165 (98%)	3 (2%)	0	100	100
15	BL	208/211 (99%)	202 (97%)	5 (2%)	1 (0%)	24	43
16	BM	128/131 (98%)	126 (98%)	2 (2%)	0	100	100
17	BN	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
18	BO	199/203 (98%)	196 (98%)	3 (2%)	0	100	100
19	BP	153/184 (83%)	151 (99%)	2 (1%)	0	100	100
20	BQ	185/187 (99%)	183 (99%)	2 (1%)	0	100	100
21	BR	178/196 (91%)	177 (99%)	1 (1%)	0	100	100
22	BS	174/176 (99%)	170 (98%)	4 (2%)	0	100	100
23	BT	157/160 (98%)	155 (99%)	2 (1%)	0	100	100
24	BU	98/128 (77%)	94 (96%)	4 (4%)	0	100	100
25	BV	132/140 (94%)	131 (99%)	1 (1%)	0	100	100
26	BW	65/157 (41%)	65 (100%)	0	0	100	100
27	BX	117/155 (76%)	113 (97%)	4 (3%)	0	100	100
28	BY	131/145 (90%)	129 (98%)	2 (2%)	0	100	100
29	BZ	133/136 (98%)	130 (98%)	3 (2%)	0	100	100
30	Ba	145/148 (98%)	142 (98%)	3 (2%)	0	100	100
31	Bb	68/71 (96%)	66 (97%)	2 (3%)	0	100	100
32	Bc	93/115 (81%)	93 (100%)	0	0	100	100
33	Bd	103/176 (58%)	101 (98%)	2 (2%)	0	100	100
34	Be	128/135 (95%)	126 (98%)	2 (2%)	0	100	100
35	Bf	108/110 (98%)	107 (99%)	1 (1%)	0	100	100
36	Bg	106/117 (91%)	105 (99%)	1 (1%)	0	100	100
37	Bh	120/123 (98%)	117 (98%)	3 (2%)	0	100	100
38	Bi	98/105 (93%)	96 (98%)	2 (2%)	0	100	100
39	Bj	84/97 (87%)	84 (100%)	0	0	100	100
40	Bk	67/70 (96%)	66 (98%)	1 (2%)	0	100	100
41	Bl	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
42	Bm	50/128 (39%)	50 (100%)	0	0	100	100
43	Bo	102/105 (97%)	100 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	Bp	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
45	Br	124/138 (90%)	121 (98%)	3 (2%)	0	100	100
47	Aa	211/264 (80%)	207 (98%)	4 (2%)	0	100	100
48	AA	81/84 (96%)	78 (96%)	3 (4%)	0	100	100
49	AB	62/69 (90%)	59 (95%)	3 (5%)	0	100	100
50	Ab	217/264 (82%)	215 (99%)	2 (1%)	0	100	100
51	Ad	260/263 (99%)	254 (98%)	6 (2%)	0	100	100
52	AD	55/133 (41%)	53 (96%)	2 (4%)	0	100	100
53	AE	97/115 (84%)	96 (99%)	1 (1%)	0	100	100
54	Af	225/249 (90%)	224 (100%)	1 (0%)	0	100	100
55	Ag	185/194 (95%)	175 (95%)	10 (5%)	0	100	100
56	Ah	204/207 (99%)	193 (95%)	11 (5%)	0	100	100
57	Ai	177/194 (91%)	173 (98%)	3 (2%)	1 (1%)	21	38
58	Ak	150/158 (95%)	147 (98%)	3 (2%)	0	100	100
59	Am	148/151 (98%)	148 (100%)	0	0	100	100
60	An	132/151 (87%)	122 (92%)	10 (8%)	0	100	100
61	At	100/119 (84%)	85 (85%)	13 (13%)	2 (2%)	6	10
62	Au	82/84 (98%)	81 (99%)	1 (1%)	0	100	100
63	Av	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
64	Aw	140/143 (98%)	134 (96%)	6 (4%)	0	100	100
65	Ax	123/131 (94%)	123 (100%)	0	0	100	100
66	AZ	205/296 (69%)	198 (97%)	7 (3%)	0	100	100
67	Ap	139/146 (95%)	128 (92%)	11 (8%)	0	100	100
68	AC	72/156 (46%)	62 (86%)	10 (14%)	0	100	100
69	Ae	189/204 (93%)	179 (95%)	10 (5%)	0	100	100
70	AF	309/317 (98%)	288 (93%)	21 (7%)	0	100	100
71	AG	53/171 (31%)	52 (98%)	1 (2%)	0	100	100
72	Aj	94/165 (57%)	92 (98%)	2 (2%)	0	100	100
73	Al	116/132 (88%)	102 (88%)	14 (12%)	0	100	100
74	Ao	125/145 (86%)	118 (94%)	7 (6%)	0	100	100
75	Ar	142/152 (93%)	131 (92%)	11 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
76	As	140/145 (97%)	136 (97%)	4 (3%)	0	100	100
77	Ay	68/125 (54%)	68 (100%)	0	0	100	100
78	Ac	223/243 (92%)	221 (99%)	2 (1%)	0	100	100
80	Aq	132/135 (98%)	122 (92%)	10 (8%)	0	100	100
All	All	11107/12726 (87%)	10791 (97%)	312 (3%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	BL	64	VAL
57	Ai	139	LYS
61	At	95	SER
61	At	94	PRO

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	
4	Az	24/24 (100%)	24 (100%)	0	100	100
5	BA	190/199 (96%)	190 (100%)	0	100	100
6	BB	346/349 (99%)	346 (100%)	0	100	100
7	BC	305/338 (90%)	305 (100%)	0	100	100
8	BD	248/249 (100%)	248 (100%)	0	100	100
9	BE	195/256 (76%)	195 (100%)	0	100	100
10	BF	201/211 (95%)	201 (100%)	0	100	100
11	BG	186/225 (83%)	185 (100%)	1 (0%)	81	92
12	BH	171/171 (100%)	171 (100%)	0	100	100
13	BI	173/178 (97%)	173 (100%)	0	100	100
14	BJ	142/148 (96%)	142 (100%)	0	100	100
15	BL	177/178 (99%)	177 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	BM	112/113 (99%)	112 (100%)	0	100	100
17	BN	171/172 (99%)	171 (100%)	0	100	100
18	BO	172/173 (99%)	172 (100%)	0	100	100
19	BP	136/163 (83%)	135 (99%)	1 (1%)	76	89
20	BQ	159/159 (100%)	159 (100%)	0	100	100
21	BR	159/175 (91%)	159 (100%)	0	100	100
22	BS	157/157 (100%)	157 (100%)	0	100	100
23	BT	139/140 (99%)	139 (100%)	0	100	100
24	BU	90/113 (80%)	90 (100%)	0	100	100
25	BV	102/107 (95%)	102 (100%)	0	100	100
26	BW	59/127 (46%)	59 (100%)	0	100	100
27	BX	107/134 (80%)	107 (100%)	0	100	100
28	BY	123/135 (91%)	123 (100%)	0	100	100
29	BZ	117/118 (99%)	117 (100%)	0	100	100
30	Ba	121/122 (99%)	121 (100%)	0	100	100
31	Bb	61/62 (98%)	61 (100%)	0	100	100
32	Bc	80/98 (82%)	80 (100%)	0	100	100
33	Bd	95/148 (64%)	95 (100%)	0	100	100
34	Be	118/123 (96%)	118 (100%)	0	100	100
35	Bf	89/89 (100%)	89 (100%)	0	100	100
36	Bg	93/101 (92%)	93 (100%)	0	100	100
37	Bh	109/110 (99%)	109 (100%)	0	100	100
38	Bi	85/89 (96%)	85 (100%)	0	100	100
39	Bj	73/80 (91%)	73 (100%)	0	100	100
40	Bk	64/65 (98%)	64 (100%)	0	100	100
41	Bl	47/48 (98%)	47 (100%)	0	100	100
42	Bm	48/115 (42%)	48 (100%)	0	100	100
43	Bo	92/92 (100%)	92 (100%)	0	100	100
44	Bp	74/75 (99%)	74 (100%)	0	100	100
45	Br	111/118 (94%)	111 (100%)	0	100	100
47	Aa	194/228 (85%)	194 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	AA	75/76 (99%)	75 (100%)	0	100	100
49	AB	57/62 (92%)	57 (100%)	0	100	100
50	Ab	185/214 (86%)	185 (100%)	0	100	100
51	Ad	223/224 (100%)	223 (100%)	0	100	100
52	AD	46/108 (43%)	46 (100%)	0	100	100
53	AE	87/99 (88%)	87 (100%)	0	100	100
54	Af	199/219 (91%)	199 (100%)	0	100	100
55	Ag	167/174 (96%)	167 (100%)	0	100	100
56	Ah	177/178 (99%)	177 (100%)	0	100	100
57	Ai	160/168 (95%)	160 (100%)	0	100	100
58	Ak	135/140 (96%)	135 (100%)	0	100	100
59	Am	130/131 (99%)	130 (100%)	0	100	100
60	An	105/118 (89%)	105 (100%)	0	100	100
61	At	94/106 (89%)	94 (100%)	0	100	100
62	Au	69/69 (100%)	69 (100%)	0	100	100
63	Av	112/113 (99%)	112 (100%)	0	100	100
64	Aw	114/115 (99%)	114 (100%)	0	100	100
65	Ax	107/113 (95%)	107 (100%)	0	100	100
66	AZ	172/245 (70%)	171 (99%)	1 (1%)	78	91
67	Ap	116/119 (98%)	116 (100%)	0	100	100
68	AC	67/140 (48%)	67 (100%)	0	100	100
69	Ae	161/170 (95%)	161 (100%)	0	100	100
70	AF	270/275 (98%)	270 (100%)	0	100	100
71	AG	48/130 (37%)	48 (100%)	0	100	100
72	Aj	88/136 (65%)	88 (100%)	0	100	100
73	Al	100/109 (92%)	100 (100%)	0	100	100
74	Ao	113/130 (87%)	113 (100%)	0	100	100
75	Ar	125/132 (95%)	125 (100%)	0	100	100
76	As	112/114 (98%)	112 (100%)	0	100	100
77	Ay	61/102 (60%)	61 (100%)	0	100	100
78	Ac	189/202 (94%)	189 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
80	Aq	120/121 (99%)	120 (100%)	0	100	100
All	All	9699/10827 (90%)	9696 (100%)	3 (0%)	100	100

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	BG	90	GLN
19	BP	93	HIS
66	AZ	2(A)	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (106) such sidechains are listed below:

Mol	Chain	Res	Type
5	BA	140	ASN
6	BB	236	HIS
6	BB	376	HIS
7	BC	38	ASN
7	BC	187	GLN
7	BC	329	ASN
8	BD	45	ASN
8	BD	225	GLN
8	BD	229	ASN
10	BF	124	ASN
10	BF	233	ASN
10	BF	246	ASN
11	BG	195	HIS
12	BH	39	ASN
12	BH	78	GLN
12	BH	102	ASN
12	BH	106	GLN
12	BH	188	GLN
13	BI	59	GLN
15	BL	19	GLN
15	BL	67	HIS
16	BM	20	HIS
17	BN	8	GLN
18	BO	26	GLN
18	BO	180	GLN
18	BO	184	ASN
19	BP	10	ASN
19	BP	21	ASN

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Mol	Chain	Res	Type
19	BP	133	HIS
19	BP	155	GLN
21	BR	40	GLN
21	BR	178	GLN
22	BS	50	GLN
23	BT	50	GLN
23	BT	131	GLN
24	BU	94	ASN
25	BV	27	ASN
28	BY	14	ASN
28	BY	43	ASN
28	BY	61	HIS
28	BY	96	HIS
30	Ba	34	ASN
30	Ba	60	HIS
31	Bb	17	HIS
31	Bb	19	ASN
31	Bb	60	ASN
32	Bc	19	GLN
33	Bd	130	ASN
33	Bd	172	ASN
34	Be	52	GLN
34	Be	126	ASN
35	Bf	20	ASN
35	Bf	55	ASN
37	Bh	20	GLN
37	Bh	101	ASN
38	Bi	20	ASN
39	Bj	57	ASN
41	Bl	17	GLN
41	Bl	33	ASN
42	Bm	84	GLN
43	Bo	34	HIS
44	Bp	56	HIS
45	Br	21	ASN
47	Aa	158	HIS
47	Aa	163	GLN
49	AB	29	GLN
50	Ab	86	GLN
51	Ad	161	GLN
51	Ad	179	ASN
51	Ad	188	ASN

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Mol	Chain	Res	Type
52	AD	89	GLN
53	AE	25	ASN
53	AE	72	HIS
54	Af	105	ASN
54	Af	225	GLN
55	Ag	39	GLN
56	Ah	52	ASN
56	Ah	146	GLN
59	Am	69	ASN
60	An	32	HIS
62	Au	33	GLN
62	Au	49	GLN
62	Au	75	ASN
63	Av	24	GLN
64	Aw	16	HIS
65	Ax	63	HIS
66	AZ	113	GLN
66	AZ	132	GLN
67	Ap	48	GLN
69	Ae	117	ASN
69	Ae	202	ASN
70	AF	222	ASN
70	AF	296	GLN
70	AF	311	GLN
71	AG	16	GLN
71	AG	26	ASN
72	Aj	32	HIS
72	Aj	61	GLN
72	Aj	66	HIS
74	Ao	35	GLN
74	Ao	46	ASN
75	Ar	17	ASN
77	Ay	112	ASN
80	Aq	31	ASN
80	Aq	93	GLN
80	Aq	118	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	B5	3554/4441 (80%)	559 (15%)	23 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B8	156/157 (99%)	16 (10%)	0
3	B7	118/119 (99%)	8 (6%)	0
46	A2	1670/1823 (91%)	297 (17%)	3 (0%)
79	V	75/76 (98%)	26 (34%)	1 (1%)
All	All	5573/6616 (84%)	906 (16%)	27 (0%)

All (906) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	B5	39	A
1	B5	42	A
1	B5	58	G
1	B5	59	A
1	B5	64	A
1	B5	65	A
1	B5	66	A
1	B5	71	C
1	B5	72	G
1	B5	73	A
1	B5	85	G
1	B5	91	G
1	B5	98	A
1	B5	109	G
1	B5	110	C
1	B5	119	G
1	B5	120	A
1	B5	135	G
1	B5	142	G
1	B5	143	C
1	B5	159	C
1	B5	172	C
1	B5	181	C
1	B5	182	G
1	B5	184	U
1	B5	187	C
1	B5	188	G
1	B5	200	U
1	B5	201	C
1	B5	209	U
1	B5	210	C
1	B5	216	C
1	B5	217	C

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Mol	Chain	Res	Type
1	B5	218	A
1	B5	219	G
1	B5	220	C
1	B5	233	U
1	B5	234	G
1	B5	256	C
1	B5	267	C
1	B5	268	G
1	B5	269	G
1	B5	298	U
1	B5	316	G
1	B5	317	U
1	B5	327	C
1	B5	335	A
1	B5	341	C
1	B5	364	A
1	B5	388	G
1	B5	410	G
1	B5	411	A
1	B5	413	G
1	B5	433	U
1	B5	445	G
1	B5	450	C
1	B5	451	G
1	B5	453	A
1	B5	454	G
1	B5	455	U
1	B5	457	G
1	B5	464	A
1	B5	468	U
1	B5	473	C
1	B5	482	C
1	B5	484	A
1	B5	485	A
1	B5	486	G
1	B5	487	G
1	B5	488	U
1	B5	490	G
1	B5	494	G
1	B5	495	G
1	B5	503	G
1	B5	511	A

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Mol	Chain	Res	Type
1	B5	515	C
1	B5	517	G
1	B5	518	C
1	B5	523	G
1	B5	524	C
1	B5	578	C
1	B5	579	G
1	B5	583	C
1	B5	584	G
1	B5	595	C
1	B5	600	C
1	B5	604	C
1	B5	605	G
1	B5	606	U
1	B5	607	C
1	B5	624	C
1	B5	626	U
1	B5	629	C
1	B5	635	C
1	B5	636	G
1	B5	642	G
1	B5	643	C
1	B5	668	G
1	B5	669	G
1	B5	670	G
1	B5	677	U
1	B5	679	C
1	B5	682	G
1	B5	684	G
1	B5	687	C
1	B5	688	A
1	B5	723	U
1	B5	725	A
1	B5	726	U
1	B5	727	A
1	B5	731	G
1	B5	736	G
1	B5	742	A
1	B5	745	G
1	B5	746	U
1	B5	752	A
1	B5	753	A

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Mol	Chain	Res	Type
1	B5	754	U
1	B5	765	A
1	B5	767	G
1	B5	768	G
1	B5	769	A
1	B5	771	A
1	B5	772	G
1	B5	774	A
1	B5	776	C
1	B5	778	C
1	B5	789	U
1	B5	1095	G
1	B5	1097	G
1	B5	1099	C
1	B5	1106	G
1	B5	1107	C
1	B5	1109	G
1	B5	1110	G
1	B5	1115	C
1	B5	1128	C
1	B5	1133	G
1	B5	1135	G
1	B5	1145	G
1	B5	1147	U
1	B5	1148	C
1	B5	1152	G
1	B5	1158	C
1	B5	1162	C
1	B5	1184	C
1	B5	1185	U
1	B5	1187	G
1	B5	1192	A
1	B5	1195	C
1	B5	1197	A
1	B5	1198	G
1	B5	1200	G
1	B5	1201	C
1	B5	1202	G
1	B5	1205	C
1	B5	1209	G
1	B5	1210	U
1	B5	1212	C

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Mol	Chain	Res	Type
1	B5	1221	G
1	B5	1222	U
1	B5	1227	U
1	B5	1238	C
1	B5	1251	A2M
1	B5	1262	A
1	B5	1279	A
1	B5	1280	G
1	B5	1284	G
1	B5	1291	G
1	B5	1310	A
1	B5	1317	G
1	B5	1320	A
1	B5	1339	U
1	B5	1357	C
1	B5	1358	G
1	B5	1359	G
1	B5	1360	C
1	B5	1361	A
1	B5	1362	G
1	B5	1363	G
1	B5	1364	C
1	B5	1366	G
1	B5	1367	G
1	B5	1368	A
1	B5	1369	A
1	B5	1371	G
1	B5	1376	G
1	B5	1380	G
1	B5	1405	U
1	B5	1420	A
1	B5	1421	G
1	B5	1425	G
1	B5	1437	U
1	B5	1448	A
1	B5	1457	A2M
1	B5	1470	A
1	B5	1486	A
1	B5	1489	C
1	B5	1501	U
1	B5	1514	U
1	B5	1519	U

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Mol	Chain	Res	Type
1	B5	1547	G
1	B5	1548	OMG
1	B5	1554	A
1	B5	1556	G
1	B5	1557	A
1	B5	1561	A
1	B5	1563	C
1	B5	1564	G
1	B5	1565	A
1	B5	1577	G
1	B5	1584	C
1	B5	1593	G
1	B5	1599	C
1	B5	1600	PSU
1	B5	1603	G
1	B5	1621	G
1	B5	1623	G
1	B5	1624	G
1	B5	1625	C
1	B5	1626	G
1	B5	1627	G
1	B5	1628	U
1	B5	1631	A
1	B5	1642	G
1	B5	1648	C
1	B5	1663	C
1	B5	1668	G
1	B5	1672	G
1	B5	1673	A
1	B5	1674	A
1	B5	1680	C
1	B5	1695	A
1	B5	1712	A
1	B5	1719	G
1	B5	1723	G
1	B5	1724	C
1	B5	1728	C
1	B5	1741	C
1	B5	1742	G
1	B5	1743	U
1	B5	1745	G
1	B5	1746	A

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Mol	Chain	Res	Type
1	B5	1751	G
1	B5	1752	A
1	B5	1764	G
1	B5	1778	G
1	B5	1791	U
1	B5	1801	A
1	B5	1806	A
1	B5	1827	U
1	B5	1829	C
1	B5	1830	C
1	B5	1831	G
1	B5	1840	C
1	B5	1841	A
1	B5	1849	G
1	B5	1857	G
1	B5	1860	G
1	B5	1868	U
1	B5	1870	G
1	B5	1871	A
1	B5	1874	G
1	B5	1932	C
1	B5	1934	A
1	B5	1935	A
1	B5	1951	A
1	B5	1953	U
1	B5	1955	G
1	B5	1957	U
1	B5	1964	G
1	B5	1965	G
1	B5	1978	A
1	B5	1993	C
1	B5	1994	G
1	B5	2001	C
1	B5	2002	G
1	B5	2006	C
1	B5	2010	G
1	B5	2038	C
1	B5	2049	C
1	B5	2050	G
1	B5	2054	G
1	B5	2062	G
1	B5	2063	G

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Mol	Chain	Res	Type
1	B5	2065	G
1	B5	2097	G
1	B5	2100	OMC
1	B5	2109	A
1	B5	2144	A
1	B5	2151	G
1	B5	2159	C
1	B5	2170	G
1	B5	2174	U
1	B5	2235	G
1	B5	2237	C
1	B5	2238	C
1	B5	2239	U
1	B5	2241	C
1	B5	2255	G
1	B5	2256	A
1	B5	2260	A
1	B5	2262	A
1	B5	2263	G
1	B5	2278	A
1	B5	2286	A
1	B5	2294	C
1	B5	2295	G
1	B5	2303	C
1	B5	2304	G
1	B5	2314	A
1	B5	2319	C
1	B5	2322	A
1	B5	2336	A
1	B5	2387	G
1	B5	2396	C
1	B5	2402	C
1	B5	2409	A
1	B5	2418	C
1	B5	2436	C
1	B5	2443	G
1	B5	2444	A
1	B5	2445	A
1	B5	2457	U
1	B5	2458	C
1	B5	2459	C
1	B5	2460	G

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Mol	Chain	Res	Type
1	B5	2484	G
1	B5	2492	A
1	B5	2512	U
1	B5	2518	U
1	B5	2537	U
1	B5	2539	U
1	B5	2547	A
1	B5	2552	U
1	B5	2555	A
1	B5	2563	C
1	B5	2575	U
1	B5	2576	G
1	B5	2577	U
1	B5	2578	U
1	B5	2604	G
1	B5	2651	G
1	B5	3074	G
1	B5	3095	C
1	B5	3103	G
1	B5	3112	A
1	B5	3121	U
1	B5	3125	A
1	B5	3139	A
1	B5	3173	C
1	B5	3188	A
1	B5	3189	A
1	B5	3190	U
1	B5	3191	G
1	B5	3194	A
1	B5	3212	G
1	B5	3230	G
1	B5	3237	A
1	B5	3246	C
1	B5	3250	U
1	B5	3253	G
1	B5	3254	G
1	B5	3262	A2M
1	B5	3263	U
1	B5	3288	G
1	B5	3291	U
1	B5	3294	A
1	B5	3296	G

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Mol	Chain	Res	Type
1	B5	3300	G
1	B5	3301	A
1	B5	3315	U
1	B5	3316	G
1	B5	3317	U
1	B5	3321	U
1	B5	3328	U
1	B5	3354	A
1	B5	3355	C
1	B5	3356	G
1	B5	3369	U
1	B5	3374	G
1	B5	3375	G
1	B5	3378	A
1	B5	3382	A
1	B5	3383	A
1	B5	3384	G
1	B5	3385	A
1	B5	3392	U
1	B5	3425	C
1	B5	3430	G
1	B5	3433	G
1	B5	3434	U
1	B5	3435	G
1	B5	3437	A
1	B5	3442	A
1	B5	3443	A
1	B5	3444	G
1	B5	3449	A
1	B5	3485	C
1	B5	3487	G
1	B5	3488	C
1	B5	3489	C
1	B5	3494	A
1	B5	3495	A
1	B5	3504	A
1	B5	3506	U
1	B5	3510	A
1	B5	3513	G
1	B5	3516	U
1	B5	3524	U
1	B5	3544	C

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Mol	Chain	Res	Type
1	B5	3552	G
1	B5	3553	A
1	B5	3554	G
1	B5	3566	U
1	B5	3567	C
1	B5	3569	G
1	B5	3570	G
1	B5	3575	A
1	B5	3586	G
1	B5	3588	G
1	B5	3589	C
1	B5	3593	G
1	B5	3601	C
1	B5	3605	C
1	B5	3606	U
1	B5	3613	A
1	B5	3626	G
1	B5	3627	G
1	B5	3634	G
1	B5	3646	A
1	B5	3664	C
1	B5	3668	G
1	B5	3672	U
1	B5	3676	A
1	B5	3692	G
1	B5	3694	C
1	B5	3697	G
1	B5	3709	G
1	B5	3711	A
1	B5	3714	A
1	B5	3716	A
1	B5	3724	A
1	B5	3732	U
1	B5	3734	G
1	B5	3747	A
1	B5	3748	G
1	B5	3757	C
1	B5	3772	G
1	B5	3773	G
1	B5	3775	C
1	B5	3782	A
1	B5	3792	C

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Mol	Chain	Res	Type
1	B5	3793	U
1	B5	3797	U
1	B5	3816	G
1	B5	3819	A
1	B5	3820	G
1	B5	3821	A
1	B5	3823	A
1	B5	3830	C
1	B5	3834	G
1	B5	3837	A
1	B5	3848	G
1	B5	3863	U
1	B5	3865	A
1	B5	3869	C
1	B5	3887	C
1	B5	3891	G
1	B5	3907	A
1	B5	3918	G
1	B5	3953	A
1	B5	3955	U
1	B5	3956	A
1	B5	3958	G
1	B5	3962	C
1	B5	3967	G
1	B5	3991	A
1	B5	4003	C
1	B5	4010	G
1	B5	4018	G
1	B5	4033	A2M
1	B5	4069	A
1	B5	4079	U
1	B5	4080	OMG
1	B5	4099	C
1	B5	4100	U
1	B5	4113	C
1	B5	4115	A
1	B5	4134	A
1	B5	4143	A
1	B5	4151	A
1	B5	4152	U
1	B5	4163	C
1	B5	4172	A

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Mol	Chain	Res	Type
1	B5	4173	C
1	B5	4174	C
1	B5	4175	G
1	B5	4176	C
1	B5	4179	C
1	B5	4182	C
1	B5	4183	G
1	B5	4184	A
1	B5	4185	G
1	B5	4188	G
1	B5	4194	G
1	B5	4197	G
1	B5	4200	U
1	B5	4201	C
1	B5	4202	G
1	B5	4204	G
1	B5	4208	G
1	B5	4215	G
1	B5	4216	C
1	B5	4219	C
1	B5	4225	U
1	B5	4227	G
1	B5	4232	G
1	B5	4242	G
1	B5	4243	C
1	B5	4254	U
1	B5	4255	C
1	B5	4266	C
1	B5	4267	C
1	B5	4268	G
1	B5	4269	G
1	B5	4271	G
1	B5	4272	C
1	B5	4273	G
1	B5	4274	C
1	B5	4277	A
1	B5	4278	C
1	B5	4281	A
1	B5	4286	G
1	B5	4288	G
1	B5	4296	U
1	B5	4297	C

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Mol	Chain	Res	Type
1	B5	4305	G
1	B5	4307	G
1	B5	4314	A
1	B5	4315	U
1	B5	4334	G
1	B5	4335	C
1	B5	4337	A
1	B5	4347	U
1	B5	4360	U
1	B5	4361	C
1	B5	4385	A
1	B5	4388	G
1	B5	4399	G
1	B5	4412	G
1	B5	4421	C
1	B5	4425	C
1	B5	4432	A
1	B5	4433	G
1	B5	4434	C
1	B5	4435	U
1	B5	4437	U
1	B5	4440	U
2	B8	34	U
2	B8	35	C
2	B8	39	G
2	B8	52	A
2	B8	59	A
2	B8	62	A
2	B8	63	U
2	B8	80	A
2	B8	84	A
2	B8	87	G
2	B8	94	G
2	B8	103	A
2	B8	105	C
2	B8	110	U
2	B8	114	G
2	B8	125	C
3	B7	7	G
3	B7	33	U
3	B7	41	G
3	B7	50	A

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Mol	Chain	Res	Type
3	B7	53	U
3	B7	54	A
3	B7	64	G
3	B7	110	G
46	A2	2	A
46	A2	3	C
46	A2	23	G
46	A2	25	A
46	A2	33	G
46	A2	41	G
46	A2	44	U
46	A2	46	A
46	A2	56	G
46	A2	59	U
46	A2	67	C
46	A2	68	A
46	A2	71	G
46	A2	74	G
46	A2	76	U
46	A2	77	A
46	A2	79	A
46	A2	103	A
46	A2	113	G
46	A2	114	G
46	A2	116	OMU
46	A2	126	G
46	A2	128	U
46	A2	129	C
46	A2	141	C
46	A2	142	U
46	A2	148	A
46	A2	154	G
46	A2	161	C
46	A2	162	U
46	A2	174	A
46	A2	177	C
46	A2	183	A
46	A2	191	C
46	A2	194	C
46	A2	260	G
46	A2	264	A
46	A2	267	U

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Mol	Chain	Res	Type
46	A2	268	C
46	A2	271	G
46	A2	274	G
46	A2	281	C
46	A2	286	C
46	A2	288	G
46	A2	291	G
46	A2	308	G
46	A2	315	OMU
46	A2	323	C
46	A2	325	A
46	A2	330	C
46	A2	342	C
46	A2	346	G
46	A2	347	C
46	A2	361	C
46	A2	368	A
46	A2	370	C
46	A2	381	G
46	A2	382	G
46	A2	389	OMU
46	A2	390	C
46	A2	399	G
46	A2	409	A
46	A2	410	A
46	A2	411	C
46	A2	425	A
46	A2	432	G
46	A2	433	C
46	A2	434	A
46	A2	435	G
46	A2	443	G
46	A2	448	U
46	A2	453	C
46	A2	461	A
46	A2	468	G
46	A2	469	A
46	A2	477	A
46	A2	497	A
46	A2	508	G
46	A2	511	C
46	A2	516	A

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Mol	Chain	Res	Type
46	A2	520	G
46	A2	524	G
46	A2	525	A
46	A2	529	C
46	A2	531	C
46	A2	537	A
46	A2	544	A
46	A2	548	A
46	A2	550	G
46	A2	552	U
46	A2	556	U
46	A2	565	A
46	A2	567	G
46	A2	569	C
46	A2	570	U
46	A2	575	C
46	A2	578	G
46	A2	582	C
46	A2	589	A
46	A2	592	U
46	A2	604	A
46	A2	605	OMG
46	A2	616	A
46	A2	621	C
46	A2	625	A
46	A2	629	A2M
46	A2	630	A
46	A2	632	A
46	A2	633	A
46	A2	634	G
46	A2	694	C
46	A2	695	C
46	A2	696	C
46	A2	697	A
46	A2	698	G
46	A2	761	U
46	A2	771	A
46	A2	774	PSU
46	A2	781	G
46	A2	782	PSU
46	A2	790	A
46	A2	791	G

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Mol	Chain	Res	Type
46	A2	796	G
46	A2	797	C
46	A2	798	C
46	A2	799	G
46	A2	805	A
46	A2	826	G
46	A2	828	A
46	A2	829	U
46	A2	837	C
46	A2	839	G
46	A2	846	U
46	A2	858	C
46	A2	863	A
46	A2	865	G
46	A2	867	G
46	A2	871	A
46	A2	875	U
46	A2	878	A
46	A2	880	A
46	A2	888	C
46	A2	891	G
46	A2	901	U
46	A2	913	A
46	A2	929	G
46	A2	936	G
46	A2	948	A
46	A2	950	A
46	A2	975	U
46	A2	981	A
46	A2	1019	U
46	A2	1020	A
46	A2	1041	A
46	A2	1043	C
46	A2	1047	G
46	A2	1073	U
46	A2	1074	C
46	A2	1075	C
46	A2	1076	C
46	A2	1079	G
46	A2	1091	A
46	A2	1096	C
46	A2	1097	C

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Mol	Chain	Res	Type
46	A2	1102	A
46	A2	1107	A
46	A2	1111	C
46	A2	1112	U
46	A2	1124	G
46	A2	1153	A
46	A2	1165	G
46	A2	1166	A
46	A2	1168	G
46	A2	1169	G
46	A2	1173	C
46	A2	1182	G
46	A2	1200	U
46	A2	1209	A
46	A2	1211	A
46	A2	1214	G
46	A2	1215	G
46	A2	1217	A
46	A2	1223	A
46	A2	1229	C
46	A2	1232	G
46	A2	1233	G
46	A2	1240	A
46	A2	1243	G
46	A2	1244	G
46	A2	1245	A
46	A2	1254	U
46	A2	1260	G
46	A2	1261	C
46	A2	1268	U
46	A2	1269	C
46	A2	1270	G
46	A2	1271	A
46	A2	1276	G
46	A2	1300	U
46	A2	1306	G
46	A2	1316	U
46	A2	1329	U
46	A2	1330	U
46	A2	1336	A
46	A2	1340	A
46	A2	1342	C

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Mol	Chain	Res	Type
46	A2	1355	U
46	A2	1360	A
46	A2	1361	C
46	A2	1362	U
46	A2	1363	A
46	A2	1364	G
46	A2	1376	C
46	A2	1377	C
46	A2	1379	A
46	A2	1381	C
46	A2	1382	G
46	A2	1383	G
46	A2	1391	C
46	A2	1392	C
46	A2	1394	A
46	A2	1408	C
46	A2	1409	A
46	A2	1410	A
46	A2	1411	G
46	A2	1418	U
46	A2	1419	C
46	A2	1420	A
46	A2	1435	A
46	A2	1442	A
46	A2	1444	A
46	A2	1445	OMG
46	A2	1450	G
46	A2	1452	G
46	A2	1453	A
46	A2	1464	U
46	A2	1475	G
46	A2	1476	C
46	A2	1488	A
46	A2	1499	C
46	A2	1503	U
46	A2	1508	U
46	A2	1510	U
46	A2	1515	U
46	A2	1525	G
46	A2	1534	A
46	A2	1535	A
46	A2	1540	U

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Mol	Chain	Res	Type
46	A2	1541	U
46	A2	1543	A
46	A2	1551	U
46	A2	1556	A
46	A2	1559	G
46	A2	1572	G
46	A2	1576	U
46	A2	1578	A
46	A2	1609	G
46	A2	1616	A
46	A2	1620	G
46	A2	1626	G
46	A2	1653	C
46	A2	1654	A
46	A2	1676	U
46	A2	1677	G
46	A2	1681	G
46	A2	1707	C
46	A2	1710	G
46	A2	1713	G
46	A2	1714	G
46	A2	1715	G
46	A2	1720	C
46	A2	1721	C
46	A2	1722	A
46	A2	1729	U
46	A2	1730	G
46	A2	1734	G
46	A2	1735	A
46	A2	1736	G
46	A2	1737	C
46	A2	1738	G
46	A2	1739	U
46	A2	1754	A
46	A2	1769	A
46	A2	1779	A
46	A2	1780	G
46	A2	1783	G
46	A2	1785	A
46	A2	1789	A
46	A2	1790	G
46	A2	1792	U

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Mol	Chain	Res	Type
46	A2	1803	G
46	A2	1805	MA6
46	A2	1815	G
46	A2	1816	G
46	A2	1817	A
46	A2	1818	U
46	A2	1819	C
79	V	7	A
79	V	8	U
79	V	9	A
79	V	10	G
79	V	16	U
79	V	17	U
79	V	18	G
79	V	20	G
79	V	22	G
79	V	27	G
79	V	31	A
79	V	32	C
79	V	36	A
79	V	37	G
79	V	38	A
79	V	40	C
79	V	41	C
79	V	45	G
79	V	46	G
79	V	47	U
79	V	49	C
79	V	53	G
79	V	59	U
79	V	60	C
79	V	61	C
79	V	76	A

All (27) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	B5	119	G
1	B5	216	C
1	B5	489	C
1	B5	502	C
1	B5	771	A

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Mol	Chain	Res	Type
1	B5	777	G
1	B5	1197	A
1	B5	1358	G
1	B5	1366	G
1	B5	1513	C
1	B5	1556	G
1	B5	1626	G
1	B5	1993	C
1	B5	2000	G
1	B5	2005	G
1	B5	2061	U
1	B5	3245	U
1	B5	3249	U
1	B5	4142	U
1	B5	4182	C
1	B5	4231	G
1	B5	4304	C
1	B5	4432	A
46	A2	1418	U
46	A2	1733	G
46	A2	1779	A
79	V	8	U

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

142 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	B5	3736	1	18,21,22	0.49	0	22,30,33	0.55	0
1	PSU	B5	1771	1	18,21,22	0.47	0	22,30,33	0.61	0
1	A2M	B5	3195	1	22,25,26	0.09	0	31,36,39	0.21	0
1	PSU	B5	1600	1	18,21,22	0.66	1 (5%)	22,30,33	0.59	0
1	OMG	B5	3813	1	23,26,27	0.28	0	33,38,41	0.39	0
1	PSU	B5	4071	1	18,21,22	0.51	0	22,30,33	0.57	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
60	IAS	An	138	60	6,7,8	1.05	0	6,8,10	1.30	1 (16%)
1	PSU	B5	3397	1,81	18,21,22	0.47	0	22,30,33	0.59	0
1	PSU	B5	1769	1	18,21,22	0.49	0	22,30,33	0.57	0
1	OMG	B5	3376	1,81	23,26,27	0.31	0	33,38,41	0.49	0
1	A2M	B5	1251	1	22,25,26	0.07	0	31,36,39	0.23	0
1	PSU	B5	3874	1	18,21,22	0.47	0	22,30,33	0.60	0
1	PSU	B5	3192	1	18,21,22	0.54	0	22,30,33	0.59	1 (4%)
1	OMG	B5	4080	1	23,26,27	0.29	0	33,38,41	0.35	0
1	A2M	B5	2564	1	22,25,26	0.08	0	31,36,39	0.20	0
46	OMG	A2	605	46	23,26,27	0.28	0	33,38,41	0.44	0
1	OMC	B5	3979	1	19,22,23	0.32	0	26,31,34	0.47	0
2	OMG	B8	75	2	23,26,27	0.29	0	33,38,41	0.39	0
46	OMU	A2	315	46	19,22,23	0.33	0	26,31,34	0.64	0
1	5MC	B5	3259	1,81	18,22,23	0.29	0	26,32,35	0.43	0
1	PSU	B5	3739	1	18,21,22	0.47	0	22,30,33	0.62	0
6	HIC	BB	245	6	10,11,12	1.55	2 (20%)	8,14,16	0.97	0
1	1MA	B5	1247	1,81	21,25,26	0.30	0	31,37,40	0.46	0
1	PSU	B5	3975	1	18,21,22	0.52	0	22,30,33	0.55	0
1	PSU	B5	3846	1	18,21,22	0.49	0	22,30,33	0.58	0
1	A2M	B5	3201	1	22,25,26	0.07	0	31,36,39	0.18	0
46	MA6	A2	1804	46	23,26,27	0.32	0	34,38,41	0.66	1 (2%)
46	A2M	A2	989	46	22,25,26	0.08	0	31,36,39	0.35	0
1	5MC	B5	3890	1	18,22,23	0.34	0	26,32,35	0.63	0
46	PSU	A2	774	46	18,21,22	0.47	0	22,30,33	0.60	0
1	OMC	B5	3178	1,81	19,22,23	0.26	0	26,31,34	0.47	0
46	A2M	A2	1341	46	22,25,26	0.09	0	31,36,39	0.23	0
46	B8N	A2	1206	46	24,29,30	0.58	0	29,42,45	0.64	0
1	PSU	B5	1690	1	18,21,22	0.47	0	22,30,33	0.59	0
46	6MZ	A2	1786	46,81	22,25,26	0.31	0	30,36,39	0.41	0
1	OMC	B5	1790	1,81	19,22,23	0.29	0	26,31,34	0.59	0
46	PSU	A2	647	46	18,21,22	0.47	0	22,30,33	0.57	0
1	PSU	B5	4019	1	18,21,22	0.48	0	22,30,33	0.58	0
1	PSU	B5	3995	1	18,21,22	0.48	0	22,30,33	0.60	0
46	A2M	A2	27	46,81	22,25,26	0.06	0	31,36,39	0.27	0
1	A2M	B5	3307	1	22,25,26	0.08	0	31,36,39	0.37	0
1	PSU	B5	4343	1	18,21,22	0.48	0	22,30,33	0.59	0
46	A2M	A2	158	46	22,25,26	0.08	0	31,36,39	0.17	0
1	OMC	B5	2171	1,81	19,22,23	0.29	0	26,31,34	0.40	0
46	OMG	A2	470	46,81	23,26,27	0.28	0	33,38,41	0.39	0
46	OMG	A2	562	46	23,26,27	0.28	0	33,38,41	0.34	0
46	PSU	A2	610	46	18,21,22	0.46	0	22,30,33	0.61	0
46	PSU	A2	109	46,81	18,21,22	0.50	0	22,30,33	0.57	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMC	B5	2610	1	19,22,23	0.28	0	26,31,34	0.34	0
1	OMC	B5	3364	1	19,22,23	0.31	0	26,31,34	0.47	0
1	OMG	B5	2113	1	23,26,27	0.28	0	33,38,41	0.38	0
1	OMG	B5	3937	1	23,26,27	0.29	0	33,38,41	0.43	0
1	OMG	B5	3835	1	23,26,27	0.27	0	33,38,41	0.38	0
46	A2M	A2	165	46	22,25,26	0.08	0	31,36,39	0.39	0
46	OMU	A2	121	46	19,22,23	0.29	0	26,31,34	0.46	0
1	OMG	B5	3104	1	23,26,27	0.30	0	33,38,41	0.52	0
1	PSU	B5	4116	1	18,21,22	0.48	0	22,30,33	0.59	0
1	PSU	B5	3885	1	18,21,22	0.52	0	22,30,33	0.62	1 (4%)
1	A2M	B5	1780	1,81	22,25,26	0.08	0	31,36,39	0.48	0
1	PSU	B5	3964	1,81	18,21,22	0.51	0	22,30,33	0.59	0
46	OMC	A2	173	46	19,22,23	0.29	0	26,31,34	0.45	0
46	4AC	A2	1796	46	21,24,25	0.30	0	29,34,37	0.30	0
1	OMG	B5	4061	1	23,26,27	0.28	0	33,38,41	0.43	0
1	A2M	B5	2112	1,81	22,25,26	0.07	0	31,36,39	0.20	0
1	OMU	B5	3402	1	19,22,23	0.29	0	26,31,34	0.48	0
1	OMG	B5	3269	1	23,26,27	0.28	0	33,38,41	0.34	0
1	OMC	B5	3285	1	19,22,23	0.30	0	26,31,34	0.36	0
46	OMG	A2	644	46	23,26,27	0.33	0	33,38,41	0.38	0
1	PSU	B5	4022	1	18,21,22	0.49	0	22,30,33	0.57	0
46	A2M	A2	551	46	22,25,26	0.12	0	31,36,39	0.33	0
1	OMG	B5	1548	1,81	23,26,27	0.30	0	33,38,41	0.42	0
1	OMG	B5	3942	1	23,26,27	0.28	0	33,38,41	0.40	0
1	A2M	B5	1447	1	22,25,26	0.12	0	31,36,39	0.33	0
1	OMG	B5	3671	1	23,26,27	0.26	0	33,38,41	0.45	0
1	PSU	B5	4132	1	18,21,22	0.47	0	22,30,33	0.61	0
1	PSU	B5	3755	1	18,21,22	0.48	0	22,30,33	0.58	0
1	PSU	B5	3796	1	18,21,22	0.47	0	22,30,33	0.58	0
1	OMG	B5	2625	1	23,26,27	0.28	0	33,38,41	0.38	0
1	OMU	B5	3749	1	19,22,23	0.30	0	26,31,34	0.45	0
1	UY1	B5	3295	1,81	19,22,23	0.50	0	22,31,34	0.54	0
1	PSU	B5	1606	1,81	18,21,22	0.49	0	22,30,33	0.59	0
46	PSU	A2	782	46	18,21,22	0.60	1 (5%)	22,30,33	0.67	1 (4%)
1	OMG	B5	1445	1	23,26,27	0.29	0	33,38,41	0.48	0
1	A2M	B5	401	1	22,25,26	0.09	0	31,36,39	0.19	0
1	PSU	B5	1700	1	18,21,22	0.52	0	22,30,33	0.56	0
46	OMU	A2	389	46	19,22,23	0.32	0	26,31,34	0.50	0
46	PSU	A2	258	46	18,21,22	0.48	0	22,30,33	0.57	0
1	A2M	B5	2536	1,81	22,25,26	0.08	0	31,36,39	0.21	0
1	OMG	B5	3639	1	23,26,27	0.28	0	33,38,41	0.36	0
1	A2M	B5	1457	1,81	22,25,26	0.07	0	31,36,39	0.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMC	B5	2100	1	19,22,23	0.32	0	26,31,34	0.42	0
1	OMC	B5	2553	1	19,22,23	0.28	0	26,31,34	0.39	0
46	PSU	A2	642	46	18,21,22	0.49	0	22,30,33	0.59	0
1	PSU	B5	3742	1	18,21,22	0.50	0	22,30,33	0.56	0
46	MA6	A2	1805	46	23,26,27	0.31	0	34,38,41	0.67	1 (2%)
1	OMU	B5	4063	1	19,22,23	0.31	0	26,31,34	0.54	0
1	OMC	B5	1265	1	19,22,23	0.28	0	26,31,34	0.42	0
46	OMC	A2	1658	46	19,22,23	0.27	0	26,31,34	0.42	0
1	OMU	B5	2586	1	19,22,23	0.32	0	26,31,34	0.55	0
1	PSU	B5	1652	1	18,21,22	0.48	0	22,30,33	0.57	0
1	A2M	B5	4014	1	22,25,26	0.09	0	31,36,39	0.25	0
1	PSU	B5	3116	1	18,21,22	0.50	0	22,30,33	0.58	0
1	A2M	B5	3966	1,81	22,25,26	0.08	0	31,36,39	0.52	1 (3%)
46	OMG	A2	1286	46	23,26,27	0.28	0	33,38,41	0.37	0
1	OMG	B5	1241	1	23,26,27	0.33	0	33,38,41	0.49	0
46	PSU	A2	1039	46	18,21,22	0.60	1 (5%)	22,30,33	0.65	0
1	PSU	B5	4372	1,81	18,21,22	0.50	0	22,30,33	0.58	0
1	A2M	B5	399	1	22,25,26	0.08	0	31,36,39	0.23	0
43	MLZ	B _o	53	43	8,9,10	0.73	0	4,9,11	0.64	0
1	PSU	B5	3172	1,81	18,21,22	0.49	0	22,30,33	0.60	0
46	OMU	A2	171	46	19,22,23	0.25	0	26,31,34	0.55	0
1	OMC	B5	3899	1	19,22,23	0.29	0	26,31,34	0.37	0
1	OMC	B5	3318	1	19,22,23	0.28	0	26,31,34	0.41	0
1	OMG	B5	2173	1	23,26,27	0.27	0	33,38,41	0.35	0
46	OMG	A2	1445	46,81	23,26,27	0.27	0	33,38,41	0.38	0
46	OMU	A2	116	46	19,22,23	0.28	0	26,31,34	0.42	0
46	PSU	A2	775	46	18,21,22	0.46	0	22,30,33	0.58	0
1	A2M	B5	3302	1	22,25,26	0.07	0	31,36,39	0.26	0
46	A2M	A2	99	46,81	22,25,26	0.08	0	31,36,39	0.29	0
1	OMC	B5	3346	1	19,22,23	0.28	0	26,31,34	0.44	0
1	OMU	B5	3670	1	19,22,23	0.31	0	26,31,34	0.47	0
1	6MZ	B5	3663	1	22,25,26	0.30	0	30,36,39	0.34	0
1	PSU	B5	3866	1	18,21,22	0.49	0	22,30,33	0.57	0
1	A2M	B5	3344	1	22,25,26	0.09	0	31,36,39	0.23	0
1	A2M	B5	4033	1	22,25,26	0.09	0	31,36,39	0.27	0
46	A2M	A2	629	46,81	22,25,26	0.11	0	31,36,39	0.28	0
1	PSU	B5	3900	1	18,21,22	0.51	0	22,30,33	0.59	1 (4%)
1	PSU	B5	3804	1	18,21,22	0.46	0	22,30,33	0.58	0
1	OMU	B5	3941	1	19,22,23	0.30	0	26,31,34	0.47	0
46	4AC	A2	1295	46	21,24,25	0.33	0	29,34,37	0.41	0
46	A2M	A2	445	46	22,25,26	0.07	0	31,36,39	0.25	0
1	A2M	B5	3262	1,81	22,25,26	0.11	0	31,36,39	0.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
46	PSU	A2	93	46	18,21,22	0.50	0	22,30,33	0.56	0
1	OMG	B5	3221	1	23,26,27	0.28	0	33,38,41	0.41	0
2	PSU	B8	55	2	18,21,22	0.45	0	22,30,33	0.61	0
1	OMG	B5	4066	1	23,26,27	0.30	0	33,38,41	0.49	0
46	OMU	A2	1284	46	19,22,23	0.24	0	26,31,34	0.47	0
1	UR3	B5	3973	1	19,22,23	0.30	0	26,32,35	0.31	0
46	PSU	A2	1132	46,81	18,21,22	0.48	0	22,30,33	0.58	0
76	NMM	As	67	76	9,11,12	1.59	1 (11%)	6,12,14	3.56	2 (33%)
1	PSU	B5	3114	1,81	18,21,22	0.45	0	22,30,33	0.63	0
2	PSU	B8	69	2,81	18,21,22	0.54	0	22,30,33	0.66	1 (4%)

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	B5	3736	1	-	0/7/25/26	0/2/2/2
1	PSU	B5	1771	1	-	0/7/25/26	0/2/2/2
1	A2M	B5	3195	1	-	0/9/27/28	0/3/3/3
1	PSU	B5	1600	1	-	0/7/25/26	0/2/2/2
1	OMG	B5	3813	1	-	1/9/27/28	0/3/3/3
1	PSU	B5	4071	1	-	0/7/25/26	0/2/2/2
60	IAS	An	138	60	-	3/7/7/8	-
1	PSU	B5	3397	1,81	-	0/7/25/26	0/2/2/2
1	PSU	B5	1769	1	-	0/7/25/26	0/2/2/2
1	OMG	B5	3376	1,81	-	0/9/27/28	0/3/3/3
1	A2M	B5	1251	1	-	1/9/27/28	0/3/3/3
1	PSU	B5	3874	1	-	0/7/25/26	0/2/2/2
1	PSU	B5	3192	1	-	0/7/25/26	0/2/2/2
1	OMG	B5	4080	1	-	0/9/27/28	0/3/3/3
1	A2M	B5	2564	1	-	0/9/27/28	0/3/3/3
46	OMG	A2	605	46	-	3/9/27/28	0/3/3/3
1	OMC	B5	3979	1	-	0/9/27/28	0/2/2/2
2	OMG	B8	75	2	-	0/9/27/28	0/3/3/3
46	OMU	A2	315	46	-	2/9/27/28	0/2/2/2
1	5MC	B5	3259	1,81	-	0/7/25/26	0/2/2/2
1	PSU	B5	3739	1	-	0/7/25/26	0/2/2/2
6	HIC	BB	245	6	-	0/5/6/8	0/1/1/1
1	1MA	B5	1247	1,81	-	2/7/25/26	0/3/3/3
1	PSU	B5	3975	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	B5	3846	1	-	0/7/25/26	0/2/2/2
1	A2M	B5	3201	1	-	1/9/27/28	0/3/3/3
46	MA6	A2	1804	46	-	0/11/29/30	0/3/3/3
46	A2M	A2	989	46	-	0/9/27/28	0/3/3/3
1	5MC	B5	3890	1	-	3/7/25/26	0/2/2/2
46	PSU	A2	774	46	-	3/7/25/26	0/2/2/2
1	OMC	B5	3178	1,81	-	4/9/27/28	0/2/2/2
46	A2M	A2	1341	46	-	1/9/27/28	0/3/3/3
46	B8N	A2	1206	46	-	4/16/34/35	0/2/2/2
1	PSU	B5	1690	1	-	0/7/25/26	0/2/2/2
46	6MZ	A2	1786	46,81	-	0/9/27/28	0/3/3/3
1	OMC	B5	1790	1,81	-	0/9/27/28	0/2/2/2
46	PSU	A2	647	46	-	0/7/25/26	0/2/2/2
1	PSU	B5	4019	1	-	0/7/25/26	0/2/2/2
1	PSU	B5	3995	1	-	0/7/25/26	0/2/2/2
46	A2M	A2	27	46,81	-	0/9/27/28	0/3/3/3
1	A2M	B5	3307	1	-	0/9/27/28	0/3/3/3
1	PSU	B5	4343	1	-	0/7/25/26	0/2/2/2
46	A2M	A2	158	46	-	0/9/27/28	0/3/3/3
1	OMC	B5	2171	1,81	-	3/9/27/28	0/2/2/2
46	OMG	A2	470	46,81	-	0/9/27/28	0/3/3/3
46	OMG	A2	562	46	-	1/9/27/28	0/3/3/3
46	PSU	A2	610	46	-	0/7/25/26	0/2/2/2
46	PSU	A2	109	46,81	-	0/7/25/26	0/2/2/2
1	OMC	B5	2610	1	-	0/9/27/28	0/2/2/2
1	OMC	B5	3364	1	-	0/9/27/28	0/2/2/2
1	OMG	B5	2113	1	-	2/9/27/28	0/3/3/3
1	OMG	B5	3937	1	-	1/9/27/28	0/3/3/3
1	OMG	B5	3835	1	-	0/9/27/28	0/3/3/3
46	A2M	A2	165	46	-	0/9/27/28	0/3/3/3
46	OMU	A2	121	46	-	0/9/27/28	0/2/2/2
1	OMG	B5	3104	1	-	0/9/27/28	0/3/3/3
1	PSU	B5	4116	1	-	0/7/25/26	0/2/2/2
1	PSU	B5	3885	1	-	0/7/25/26	0/2/2/2
1	A2M	B5	1780	1,81	-	0/9/27/28	0/3/3/3
1	PSU	B5	3964	1,81	-	2/7/25/26	0/2/2/2
46	OMC	A2	173	46	-	0/9/27/28	0/2/2/2
46	4AC	A2	1796	46	-	0/11/29/30	0/2/2/2
1	OMG	B5	4061	1	-	0/9/27/28	0/3/3/3
1	A2M	B5	2112	1,81	-	1/9/27/28	0/3/3/3
1	OMU	B5	3402	1	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMG	B5	3269	1	-	0/9/27/28	0/3/3/3
1	OMC	B5	3285	1	-	0/9/27/28	0/2/2/2
46	OMG	A2	644	46	-	0/9/27/28	0/3/3/3
1	PSU	B5	4022	1	-	0/7/25/26	0/2/2/2
46	A2M	A2	551	46	-	1/9/27/28	0/3/3/3
1	OMG	B5	1548	1,81	-	1/9/27/28	0/3/3/3
1	OMG	B5	3942	1	-	0/9/27/28	0/3/3/3
1	A2M	B5	1447	1	-	1/9/27/28	0/3/3/3
1	OMG	B5	3671	1	-	0/9/27/28	0/3/3/3
1	PSU	B5	4132	1	-	0/7/25/26	0/2/2/2
1	PSU	B5	3755	1	-	0/7/25/26	0/2/2/2
1	PSU	B5	3796	1	-	0/7/25/26	0/2/2/2
1	OMG	B5	2625	1	-	0/9/27/28	0/3/3/3
1	OMU	B5	3749	1	-	0/9/27/28	0/2/2/2
1	UY1	B5	3295	1,81	-	2/9/27/28	0/2/2/2
1	PSU	B5	1606	1,81	-	0/7/25/26	0/2/2/2
46	PSU	A2	782	46	-	0/7/25/26	0/2/2/2
1	OMG	B5	1445	1	-	0/9/27/28	0/3/3/3
1	A2M	B5	401	1	-	0/9/27/28	0/3/3/3
1	PSU	B5	1700	1	-	0/7/25/26	0/2/2/2
46	OMU	A2	389	46	-	7/9/27/28	0/2/2/2
46	PSU	A2	258	46	-	0/7/25/26	0/2/2/2
1	A2M	B5	2536	1,81	-	3/9/27/28	0/3/3/3
1	OMG	B5	3639	1	-	1/9/27/28	0/3/3/3
1	A2M	B5	1457	1,81	-	2/9/27/28	0/3/3/3
1	OMC	B5	2100	1	-	3/9/27/28	0/2/2/2
1	OMC	B5	2553	1	-	0/9/27/28	0/2/2/2
46	PSU	A2	642	46	-	0/7/25/26	0/2/2/2
1	PSU	B5	3742	1	-	0/7/25/26	0/2/2/2
46	MA6	A2	1805	46	-	1/11/29/30	0/3/3/3
1	OMU	B5	4063	1	-	0/9/27/28	0/2/2/2
1	OMC	B5	1265	1	-	0/9/27/28	0/2/2/2
46	OMC	A2	1658	46	-	0/9/27/28	0/2/2/2
1	OMU	B5	2586	1	-	0/9/27/28	0/2/2/2
1	PSU	B5	1652	1	-	0/7/25/26	0/2/2/2
1	A2M	B5	4014	1	-	0/9/27/28	0/3/3/3
1	PSU	B5	3116	1	-	0/7/25/26	0/2/2/2
1	A2M	B5	3966	1,81	-	0/9/27/28	0/3/3/3
46	OMG	A2	1286	46	-	0/9/27/28	0/3/3/3
1	OMG	B5	1241	1	-	0/9/27/28	0/3/3/3
46	PSU	A2	1039	46	-	1/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	B5	4372	1,81	-	0/7/25/26	0/2/2/2
1	A2M	B5	399	1	-	1/9/27/28	0/3/3/3
43	MLZ	B _o	53	43	-	3/7/8/10	-
1	PSU	B5	3172	1,81	-	0/7/25/26	0/2/2/2
46	OMU	A2	171	46	-	0/9/27/28	0/2/2/2
1	OMC	B5	3899	1	-	0/9/27/28	0/2/2/2
1	OMC	B5	3318	1	-	0/9/27/28	0/2/2/2
1	OMG	B5	2173	1	-	0/9/27/28	0/3/3/3
46	OMG	A2	1445	46,81	-	1/9/27/28	0/3/3/3
46	OMU	A2	116	46	-	2/9/27/28	0/2/2/2
46	PSU	A2	775	46	-	0/7/25/26	0/2/2/2
1	A2M	B5	3302	1	-	0/9/27/28	0/3/3/3
46	A2M	A2	99	46,81	-	0/9/27/28	0/3/3/3
1	OMC	B5	3346	1	-	1/9/27/28	0/2/2/2
1	OMU	B5	3670	1	-	0/9/27/28	0/2/2/2
1	6MZ	B5	3663	1	-	0/9/27/28	0/3/3/3
1	PSU	B5	3866	1	-	0/7/25/26	0/2/2/2
1	A2M	B5	3344	1	-	1/9/27/28	0/3/3/3
1	A2M	B5	4033	1	-	1/9/27/28	0/3/3/3
46	A2M	A2	629	46,81	-	3/9/27/28	0/3/3/3
1	PSU	B5	3900	1	-	0/7/25/26	0/2/2/2
1	PSU	B5	3804	1	-	0/7/25/26	0/2/2/2
1	OMU	B5	3941	1	-	0/9/27/28	0/2/2/2
46	4AC	A2	1295	46	-	2/11/29/30	0/2/2/2
46	A2M	A2	445	46	-	0/9/27/28	0/3/3/3
1	A2M	B5	3262	1,81	-	2/9/27/28	0/3/3/3
46	PSU	A2	93	46	-	0/7/25/26	0/2/2/2
1	OMG	B5	3221	1	-	0/9/27/28	0/3/3/3
2	PSU	B8	55	2	-	0/7/25/26	0/2/2/2
1	OMG	B5	4066	1	-	0/9/27/28	0/3/3/3
46	OMU	A2	1284	46	-	0/9/27/28	0/2/2/2
1	UR3	B5	3973	1	-	0/7/25/26	0/2/2/2
46	PSU	A2	1132	46,81	-	0/7/25/26	0/2/2/2
76	NMM	A _s	67	76	-	5/9/11/13	-
1	PSU	B5	3114	1,81	-	0/7/25/26	0/2/2/2
2	PSU	B8	69	2,81	-	0/7/25/26	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
76	A _s	67	NMM	CZ-NH2	4.34	1.44	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	BB	245	HIC	CD2-CG	3.04	1.41	1.36
1	B5	1600	PSU	O4'-C1'	-2.35	1.40	1.43
46	A2	782	PSU	O4'-C1'	-2.17	1.40	1.43
46	A2	1039	PSU	O4'-C1'	-2.16	1.40	1.43
6	BB	245	HIC	CD2-NE2	2.02	1.39	1.36

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
76	As	67	NMM	NE-CZ-NH2	-7.62	112.49	119.48
76	As	67	NMM	NE-CZ-NH1	4.12	127.97	120.26
46	A2	1804	MA6	C2-N1-C6	2.46	117.57	111.75
46	A2	1805	MA6	C2-N1-C6	2.42	117.46	111.75
60	An	138	IAS	OD1-CG-CB	-2.40	118.43	125.43
2	B8	69	PSU	O4'-C1'-C2'	2.25	108.31	105.14
46	A2	782	PSU	O4'-C1'-C2'	2.15	108.18	105.14
1	B5	3885	PSU	O4'-C1'-C2'	2.14	108.17	105.14
1	B5	3966	A2M	C2'-C3'-C4'	-2.06	97.52	101.99
1	B5	3900	PSU	O4'-C1'-C2'	2.04	108.02	105.14
1	B5	3192	PSU	O4'-C1'-C2'	2.02	107.99	105.14

There are no chirality outliers.

All (83) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B5	2171	OMC	C1'-C2'-O2'-CM2
1	B5	3178	OMC	C2'-C1'-N1-C2
1	B5	3178	OMC	C2'-C1'-N1-C6
1	B5	3201	A2M	C1'-C2'-O2'-CM'
1	B5	3639	OMG	C1'-C2'-O2'-CM2
1	B5	4033	A2M	C4'-C5'-O5'-P
43	Bo	53	MLZ	N-CA-CB-CG
43	Bo	53	MLZ	C-CA-CB-CG
46	A2	116	OMU	C3'-C4'-C5'-O5'
46	A2	116	OMU	O4'-C4'-C5'-O5'
46	A2	389	OMU	C3'-C4'-C5'-O5'
46	A2	389	OMU	O4'-C4'-C5'-O5'
46	A2	562	OMG	C1'-C2'-O2'-CM2
46	A2	605	OMG	O4'-C4'-C5'-O5'
46	A2	774	PSU	C2'-C1'-C5-C4
46	A2	774	PSU	C3'-C4'-C5'-O5'
46	A2	1341	A2M	C1'-C2'-O2'-CM'

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Mol	Chain	Res	Type	Atoms
60	An	138	IAS	N-CA-CB-CG
60	An	138	IAS	C-CA-CB-CG
60	An	138	IAS	CA-CB-CG-OD1
76	As	67	NMM	C-CA-CB-CG
76	As	67	NMM	N-CA-CB-CG
76	As	67	NMM	O-C-CA-CB
46	A2	605	OMG	C3'-C4'-C5'-O5'
46	A2	774	PSU	O4'-C4'-C5'-O5'
46	A2	1206	B8N	N34-C33-C34-O36
76	As	67	NMM	NE-CD-CG-CB
1	B5	2113	OMG	O4'-C4'-C5'-O5'
1	B5	1548	OMG	C3'-C2'-O2'-CM2
46	A2	315	OMU	O4'-C4'-C5'-O5'
1	B5	2113	OMG	C3'-C4'-C5'-O5'
46	A2	389	OMU	C2'-C1'-N1-C6
1	B5	2171	OMC	O4'-C4'-C5'-O5'
46	A2	1206	B8N	N34-C33-C34-O35
46	A2	1295	4AC	O7-C7-N4-C4
46	A2	1295	4AC	CM7-C7-N4-C4
1	B5	1457	A2M	C4'-C5'-O5'-P
46	A2	629	A2M	O4'-C4'-C5'-O5'
1	B5	399	A2M	C1'-C2'-O2'-CM'
1	B5	3890	5MC	O4'-C1'-N1-C6
43	Bo	53	MLZ	CA-CB-CG-CD
46	A2	605	OMG	C4'-C5'-O5'-P
46	A2	1206	B8N	C31-C32-C33-C34
1	B5	2536	A2M	C2'-C1'-N9-C8
1	B5	3813	OMG	C3'-C2'-O2'-CM2
46	A2	1805	MA6	C4'-C5'-O5'-P
1	B5	3295	UY1	C4'-C5'-O5'-P
1	B5	2171	OMC	C3'-C4'-C5'-O5'
76	As	67	NMM	CA-CB-CG-CD
1	B5	3178	OMC	O4'-C1'-N1-C6
46	A2	1445	OMG	C4'-C5'-O5'-P
46	A2	389	OMU	O4'-C1'-N1-C6
1	B5	3890	5MC	C2'-C1'-N1-C6
1	B5	1251	A2M	C4'-C5'-O5'-P
1	B5	3346	OMC	C3'-C2'-O2'-CM2
1	B5	3178	OMC	O4'-C1'-N1-C2
46	A2	315	OMU	C3'-C4'-C5'-O5'
1	B5	2536	A2M	C2'-C1'-N9-C4
1	B5	1247	1MA	C2'-C1'-N9-C4

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Mol	Chain	Res	Type	Atoms
1	B5	2100	OMC	O4'-C4'-C5'-O5'
1	B5	3890	5MC	O4'-C1'-N1-C2
1	B5	2100	OMC	C2'-C1'-N1-C6
1	B5	3964	PSU	O4'-C1'-C5-C4
1	B5	3295	UY1	O4'-C1'-C5-C4
46	A2	1206	B8N	O4'-C1'-C5-C4
1	B5	1447	A2M	O4'-C1'-N9-C8
1	B5	1247	1MA	C2'-C1'-N9-C8
46	A2	389	OMU	O4'-C1'-N1-C2
46	A2	389	OMU	C2'-C1'-N1-C2
46	A2	629	A2M	C2'-C1'-N9-C8
1	B5	3262	A2M	C3'-C2'-O2'-CM'
1	B5	2536	A2M	O4'-C1'-N9-C8
46	A2	629	A2M	C3'-C4'-C5'-O5'
1	B5	3964	PSU	O4'-C1'-C5-C6
1	B5	2100	OMC	C2'-C1'-N1-C2
46	A2	551	A2M	O4'-C1'-N9-C8
1	B5	1457	A2M	O4'-C4'-C5'-O5'
1	B5	3262	A2M	O4'-C4'-C5'-O5'
1	B5	3344	A2M	C3'-C4'-C5'-O5'
1	B5	2112	A2M	C3'-C2'-O2'-CM'
1	B5	3937	OMG	C3'-C2'-O2'-CM2
46	A2	389	OMU	C4'-C5'-O5'-P
46	A2	1039	PSU	C4'-C5'-O5'-P

There are no ring outliers.

48 monomers are involved in 66 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B5	3195	A2M	5	0
1	B5	4071	PSU	2	0
1	B5	1251	A2M	1	0
1	B5	3874	PSU	2	0
1	B5	3979	OMC	1	0
2	B8	75	OMG	2	0
46	A2	315	OMU	4	0
1	B5	3201	A2M	2	0
1	B5	3890	5MC	2	0
46	A2	774	PSU	1	0
46	A2	1341	A2M	1	0
46	A2	27	A2M	1	0
46	A2	158	A2M	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B5	2171	OMC	1	0
46	A2	470	OMG	1	0
46	A2	562	OMG	1	0
46	A2	610	PSU	1	0
46	A2	109	PSU	1	0
1	B5	2610	OMC	1	0
1	B5	3364	OMC	1	0
1	B5	2113	OMG	1	0
1	B5	3937	OMG	1	0
1	B5	3835	OMG	2	0
46	A2	121	OMU	1	0
1	B5	1780	A2M	1	0
1	B5	4061	OMG	1	0
1	B5	2112	A2M	1	0
1	B5	4022	PSU	2	0
1	B5	3671	OMG	1	0
1	B5	2625	OMG	2	0
1	B5	3749	OMU	1	0
1	B5	3295	UY1	1	0
1	B5	1606	PSU	1	0
1	B5	2100	OMC	1	0
1	B5	4063	OMU	2	0
1	B5	1265	OMC	1	0
46	A2	1658	OMC	2	0
1	B5	4372	PSU	1	0
46	A2	1445	OMG	1	0
46	A2	116	OMU	1	0
46	A2	99	A2M	1	0
1	B5	3663	6MZ	1	0
1	B5	3344	A2M	1	0
1	B5	3900	PSU	1	0
1	B5	3941	OMU	1	0
46	A2	1295	4AC	2	0
1	B5	3262	A2M	2	0
1	B5	3973	UR3	1	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 501 ligands modelled in this entry, 501 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

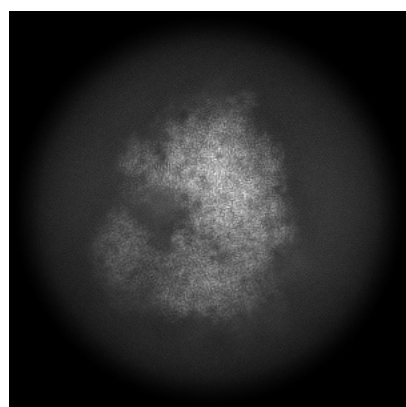
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-18168. These allow visual inspection of the internal detail of the map and identification of artifacts.

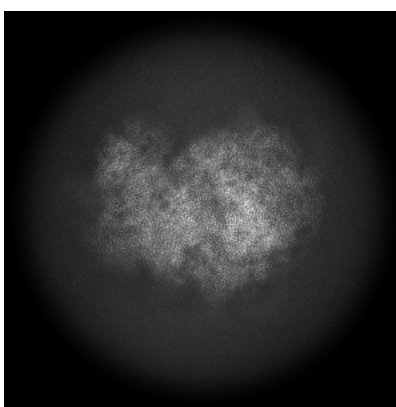
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

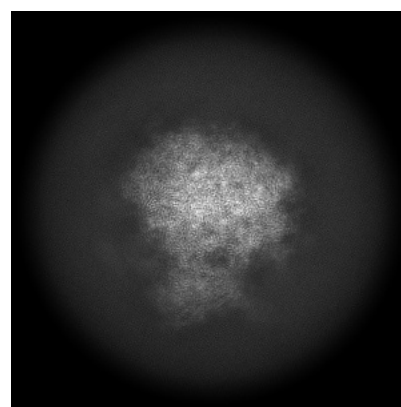
6.1.1 Primary map



X



Y

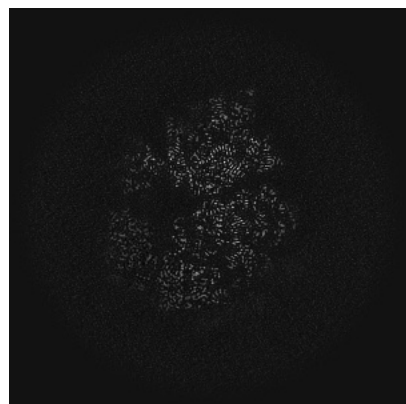


Z

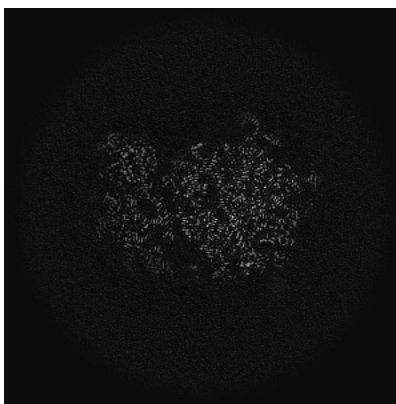
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

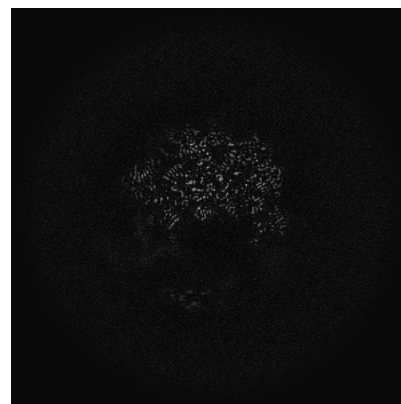
6.2.1 Primary map



X Index: 290



Y Index: 290

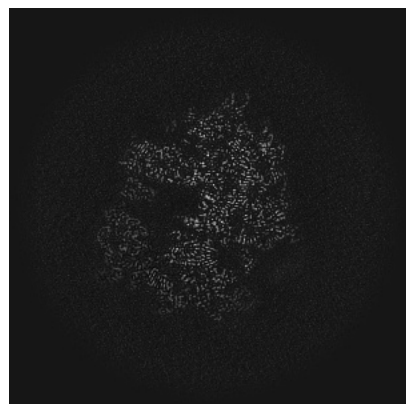


Z Index: 290

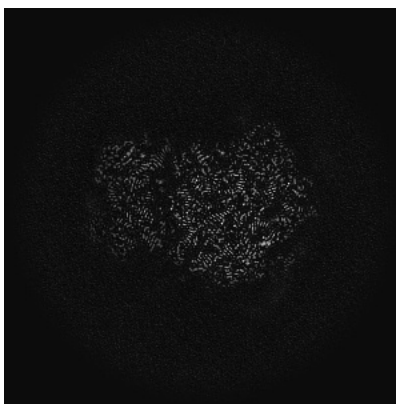
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

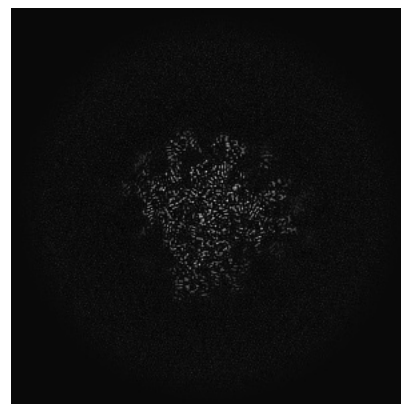
6.3.1 Primary map



X Index: 270



Y Index: 300

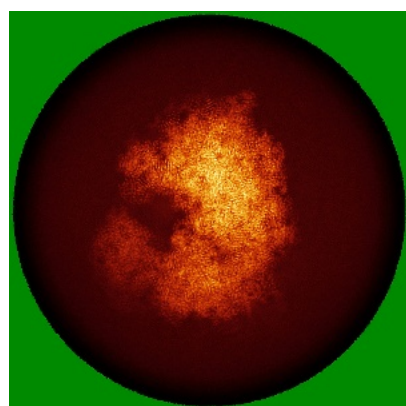


Z Index: 348

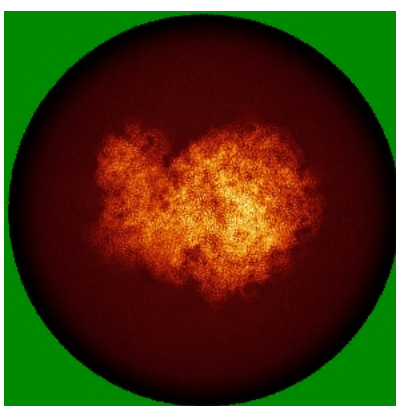
The images above show the largest variance slices of the map in three orthogonal directions.

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

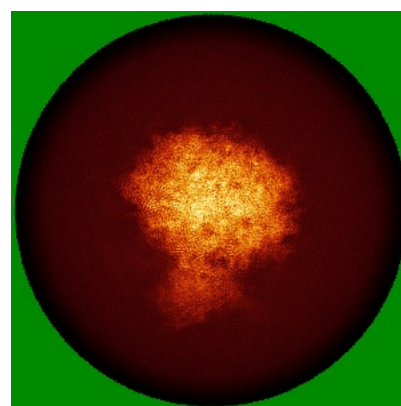
6.4.1 Primary map



X



Y

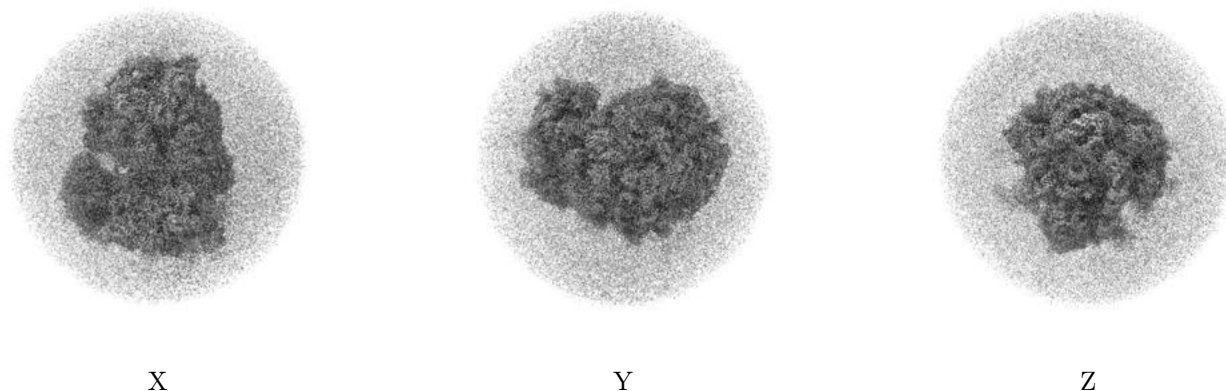


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

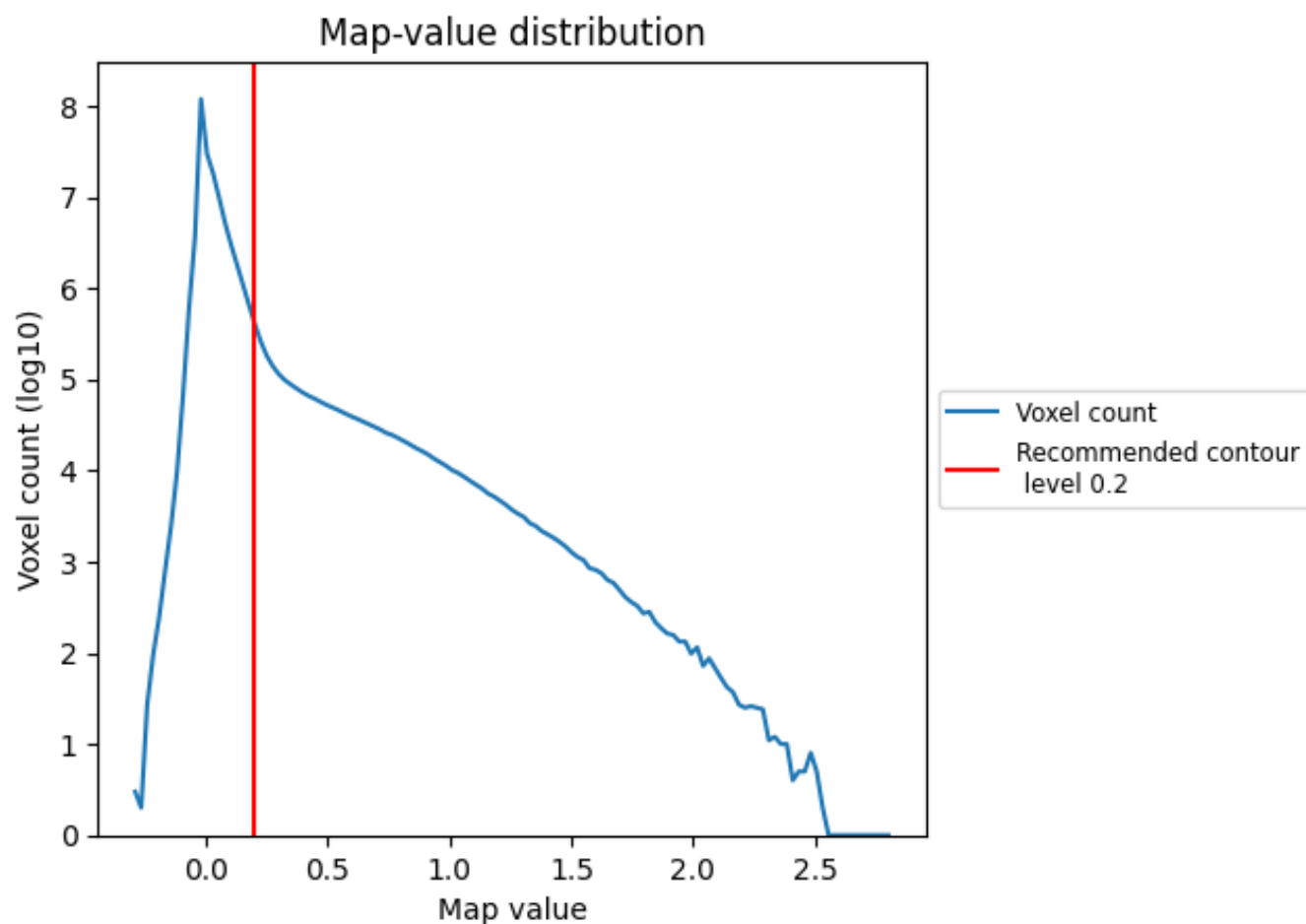
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

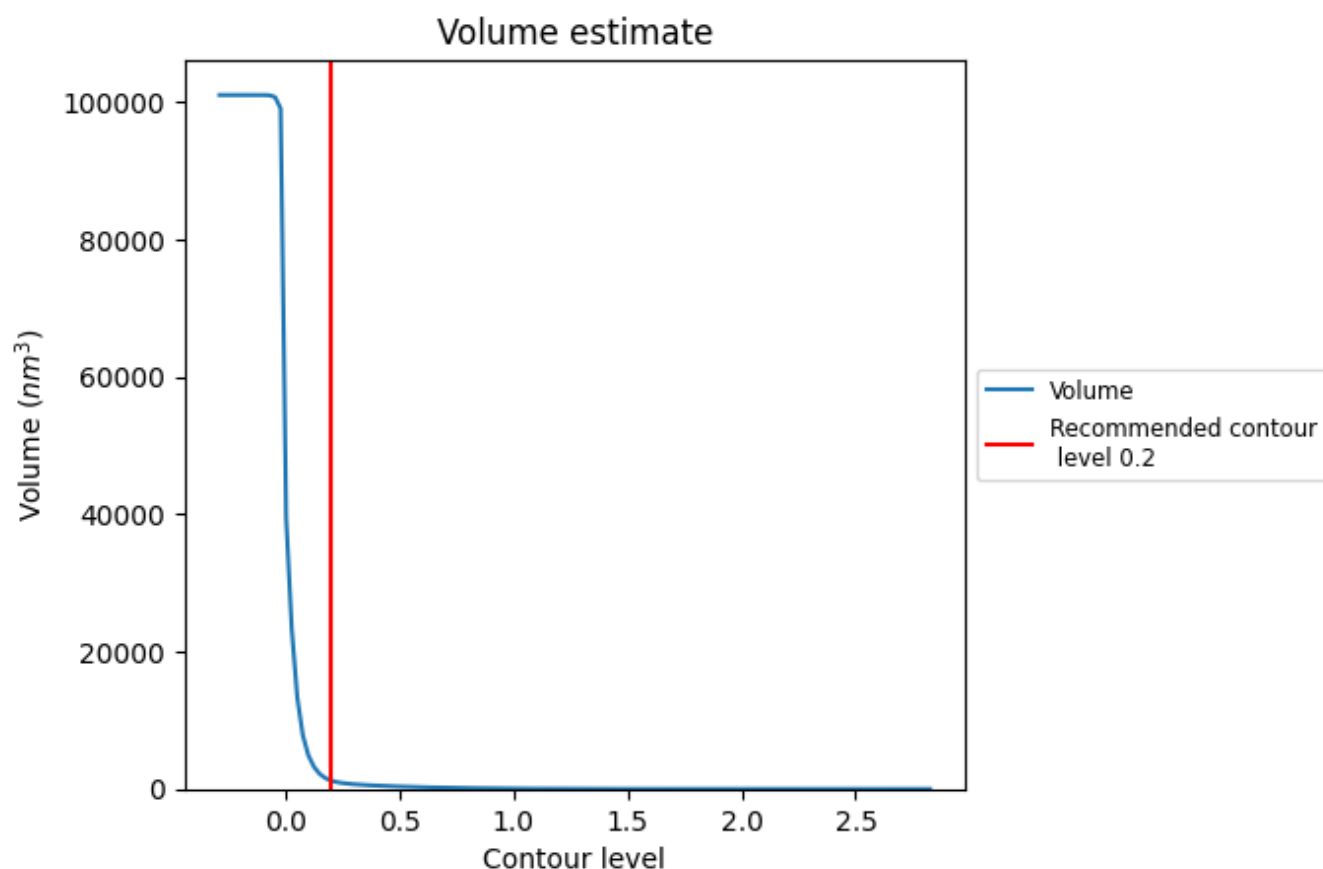
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

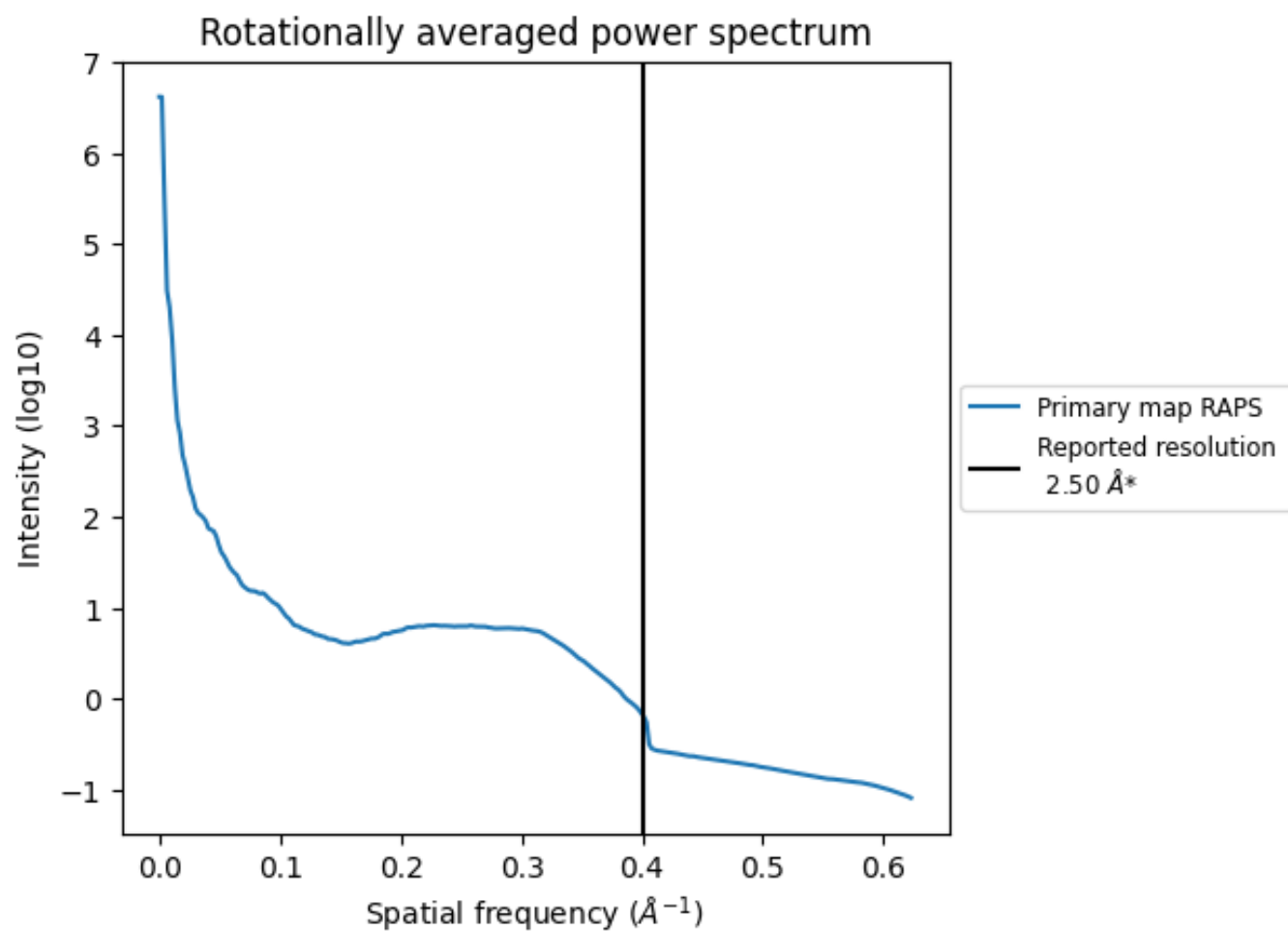
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1226 nm^3 ; this corresponds to an approximate mass of 1108 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 0.400 Å⁻¹

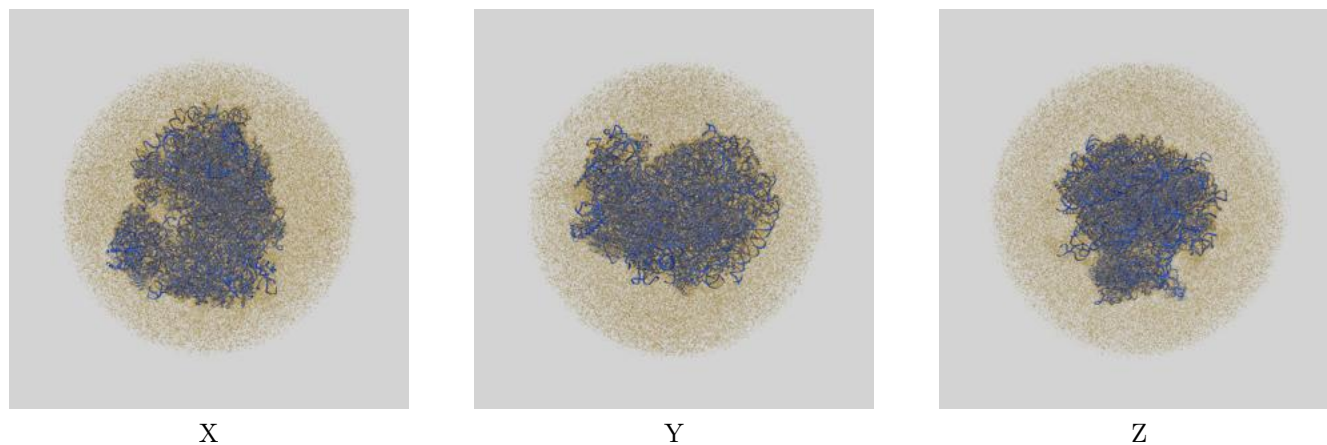
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

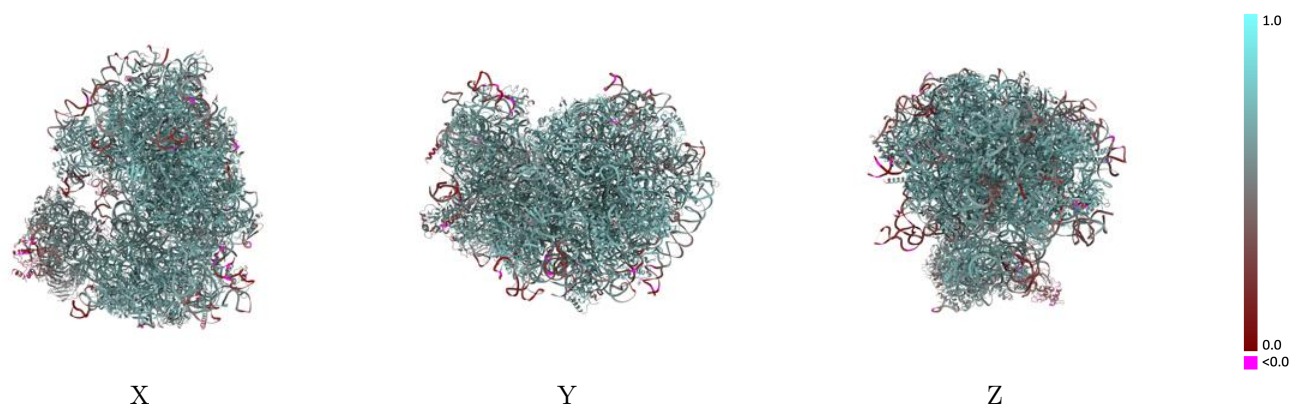
This section contains information regarding the fit between EMDB map EMD-18168 and PDB model 8Q7Z. Per-residue inclusion information can be found in section [3](#) on page [25](#).

9.1 Map-model overlay [i](#)



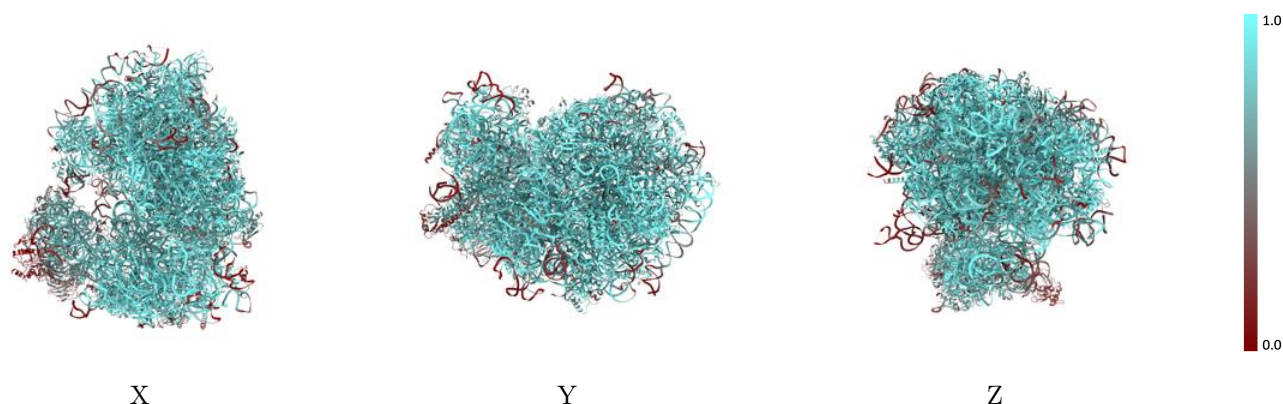
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



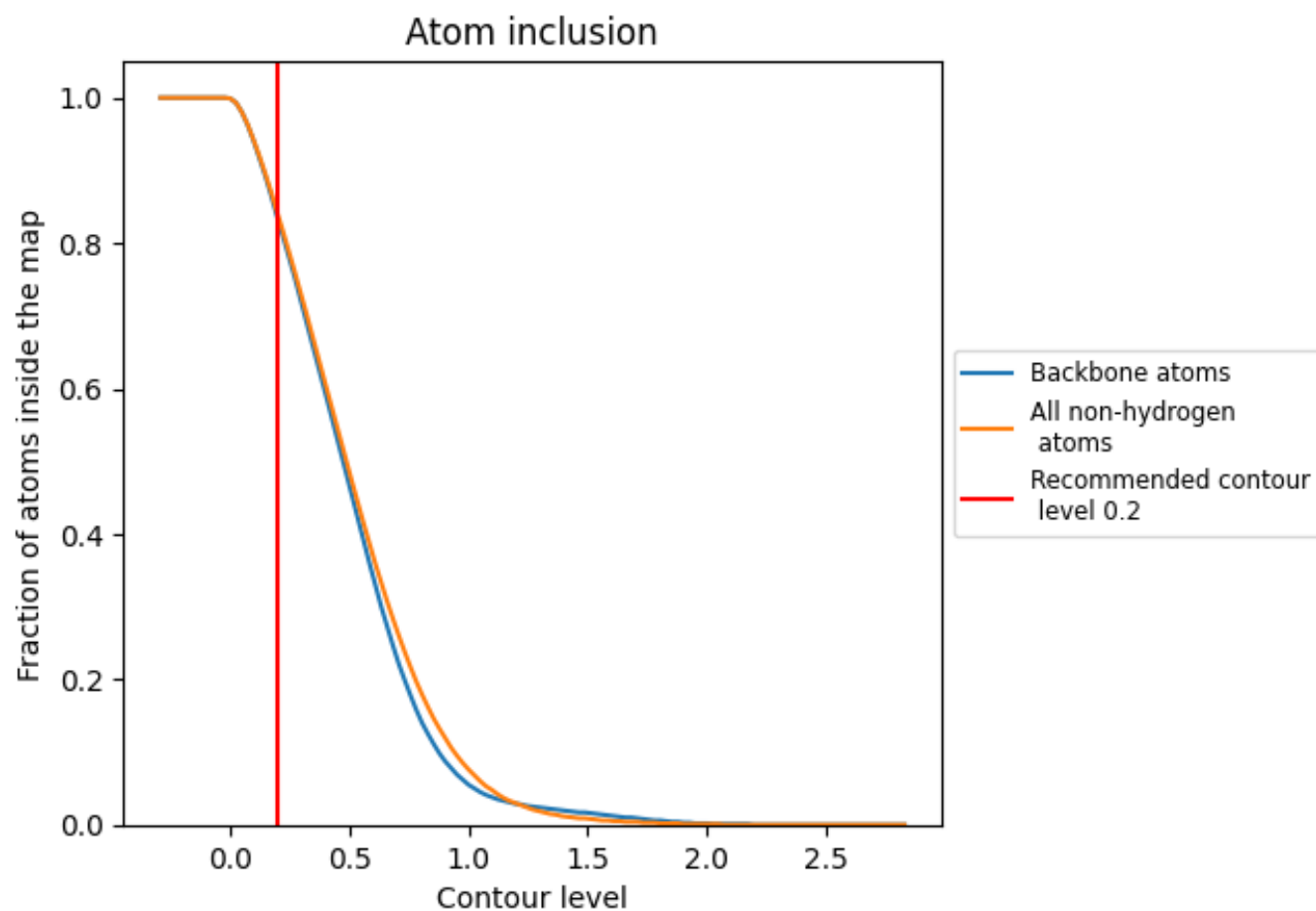
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8420	 0.6160
A2	 0.8570	 0.5980
AA	 0.7270	 0.5760
AB	 0.5470	 0.5230
AC	 0.0390	 0.2340
AD	 0.6930	 0.5710
AE	 0.8700	 0.6600
AF	 0.3390	 0.4560
AG	 0.7830	 0.5950
AZ	 0.7970	 0.6150
Aa	 0.8260	 0.6260
Ab	 0.8670	 0.6510
Ac	 0.5510	 0.5170
Ad	 0.9170	 0.6570
Ae	 0.6880	 0.5580
Af	 0.7370	 0.5630
Ag	 0.4980	 0.5000
Ah	 0.8280	 0.6260
Ai	 0.9040	 0.6480
Aj	 0.5370	 0.4940
Ak	 0.8490	 0.6430
Al	 0.0370	 0.1750
Am	 0.8760	 0.6570
An	 0.8480	 0.6360
Ao	 0.6100	 0.5240
Ap	 0.7430	 0.5710
Aq	 0.5090	 0.4910
Ar	 0.6520	 0.5250
As	 0.7210	 0.5640
At	 0.5200	 0.4930
Au	 0.8220	 0.6340
Av	 0.9390	 0.6780
Aw	 0.8880	 0.6570
Ax	 0.8710	 0.6350
Ay	 0.5310	 0.4860



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Chain	Atom inclusion	Q-score
Az	 0.9080	 0.6760
B5	 0.8680	 0.6130
B7	 0.9750	 0.6660
B8	 0.9150	 0.6420
BA	 0.9740	 0.7140
BB	 0.9450	 0.6970
BC	 0.9460	 0.6910
BD	 0.8490	 0.6340
BE	 0.8670	 0.6410
BF	 0.9480	 0.7040
BG	 0.8200	 0.6240
BH	 0.9100	 0.6640
BI	 0.9190	 0.6740
BJ	 0.7960	 0.6130
BL	 0.8780	 0.6500
BM	 0.9390	 0.6820
BN	 0.9880	 0.7210
BO	 0.9470	 0.6880
BP	 0.9440	 0.6960
BQ	 0.9700	 0.7140
BR	 0.8300	 0.6260
BS	 0.9650	 0.7020
BT	 0.9000	 0.6770
BU	 0.6920	 0.5570
BV	 0.9460	 0.7040
BW	 0.8520	 0.6440
BX	 0.9070	 0.6730
BY	 0.9190	 0.6660
BZ	 0.8970	 0.6590
Ba	 0.9750	 0.7190
Bb	 0.8190	 0.6220
Bc	 0.9170	 0.6690
Bd	 0.8960	 0.6670
Be	 0.9630	 0.7080
Bf	 0.9610	 0.7170
Bg	 0.9240	 0.6820
Bh	 0.9020	 0.6650
Bi	 0.8940	 0.6560
Bj	 0.9780	 0.7030
Bk	 0.7090	 0.5970
Bl	 0.9080	 0.6780
Bm	 0.9300	 0.6810

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Chain	Atom inclusion	Q-score
Bo	 0.9070	 0.6850
Bp	 0.9270	 0.6870
Br	 0.9320	 0.6860
V	 0.3470	 0.3090