



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 10:43 AM UTC

PDB ID : 6OLG / pdb_00006olg
EMDB ID : EMD-0601
Title : Human ribosome nascent chain complex stalled by a drug-like small molecule
(CDH1_RNC with PP tRNA)
Authors : Li, W.; Cate, J.H.D.
Deposited on : 2019-04-16
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

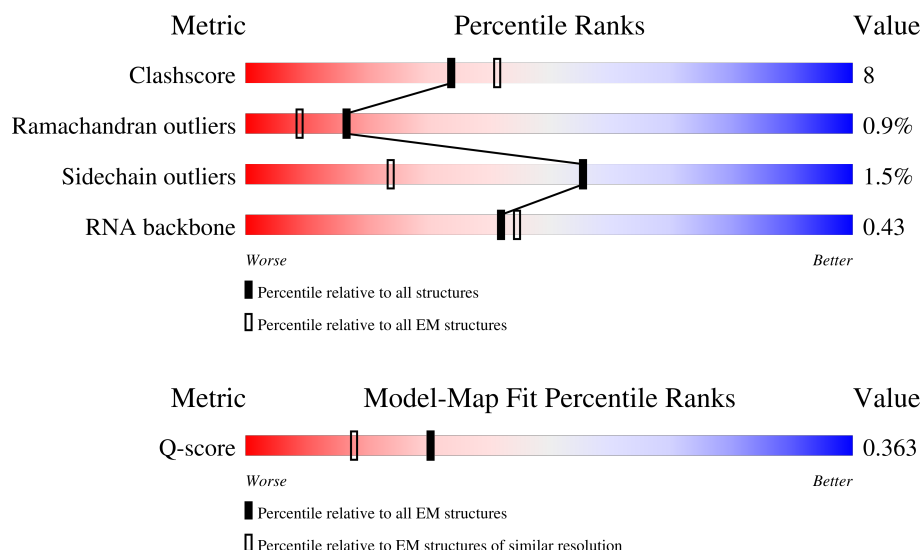
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AA	257	
2	BA	215	
3	AB	394	

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Mol	Chain	Length	Quality of chain
4	BB	212	
5	AC	363	
6	BC	222	
7	A3	157	
8	A4	119	
9	AD	294	
10	AE	194	
11	AF	234	
12	AG	234	
13	AH	191	
14	AI	211	
15	AJ	169	
16	AK	109	
17	AL	205	
18	AM	139	
19	AN	203	
20	AO	195	
21	AP	153	
22	AQ	187	
23	AR	181	
24	AS	175	
25	AT	157	
26	AU	99	
27	AV	129	
28	AW	121	

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Mol	Chain	Length	Quality of chain
29	AX	117	
30	AY	127	
31	AZ	134	
32	Aa	147	
33	Ab	121	
34	Ac	103	
35	Ad	106	
36	Ae	129	
37	Af	109	
38	Ag	114	
39	Ah	122	
40	Ai	97	
41	Aj	84	
42	Ak	69	
43	Al	50	
44	Am	50	
45	An	25	
46	Ao	105	
47	Ap	91	
48	Aq	138	
49	At	122	
50	Au	217	
51	A2	3612	
52	B1	1708	
53	BD	220	

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Mol	Chain	Length	Quality of chain
54	BE	257	32% 79% 21%
55	BF	190	53% 77% 23%
56	BG	232	51% 80% 19%
57	BH	183	50% 80% 19%
58	BI	207	28% 77% 20%
59	BJ	179	36% 80% 18%
60	BK	98	71% 71% 28%
61	BL	153	30% 83% 16%
62	BM	120	99% 79% 21%
63	BN	149	24% 83% 17%
64	BO	136	30% 86% 13%
65	BP	120	61% 61% 29% 8%
66	BQ	139	52% 83% 17%
67	BR	125	55% 80% 18%
68	BS	139	58% 81% 17%
69	BT	143	53% 76% 23%
70	BU	97	59% 87% 13%
71	BV	81	41% 91% 9%
72	BW	129	15% 81% 18%
73	BX	139	20% 78% 22%
74	BY	125	38% 85% 15%
75	BZ	86	70% 87% 13%
76	Ba	97	25% 70% 30%
77	Bb	80	42% 90% 10%
78	Bc	62	53% 68% 31%

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Mol	Chain	Length	Quality of chain
79	Bd	51	
80	Be	55	
81	Bf	73	
82	Bg	314	
83	Bv	76	
84	Bx	16	
85	A	39	

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 216796 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 protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	252	Total	C	N	O	S	0	0
			1930	1209	395	320	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	BA	215	Total	C	N	O	S	0	0
			1704	1083	298	315	8		

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AB	394	Total	C	N	O	S	0	0
			3178	2024	596	544	14		

- Molecule 4 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	BB	212	Total	C	N	O	S	0	0
			1722	1093	308	307	14		

- Molecule 5 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AC	363	Total	C	N	O	S	0	0
			2888	1817	577	480	14		

- Molecule 6 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	BC	222	Total	C	N	O	S	0	0
			1724	1114	296	304	10		

- Molecule 7 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A3	157	Total	C	N	O	P	0	0
			3337	1489	587	1104	157		

- Molecule 8 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A4	119	Total	C	N	O	P	0	0
			2541	1132	454	836	119		

- Molecule 9 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AD	294	Total	C	N	O	S	0	0
			2392	1510	436	432	14		

- Molecule 10 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AE	194	Total	C	N	O	S	0	0
			1571	1013	294	263	1		

- Molecule 11 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AF	234	Total	C	N	O	S	0	0
			1950	1252	376	313	9		

- Molecule 12 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AG	234	Total	C	N	O	S	0	0
			1880	1197	362	317	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AH	191	Total	C	N	O	S	0	0
			1526	960	285	275	6		

- Molecule 14 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AI	208	Total	C	N	O	S	0	0
			1692	1074	327	278	13		

- Molecule 15 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AJ	169	Total	C	N	O	S	0	0
			1353	855	252	240	6		

- Molecule 16 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AK	109	Total	C	N	O	S	0	0
			872	554	159	151	8		

- Molecule 17 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AL	205	Total	C	N	O	S	0	0
			1657	1036	344	273	4		

- Molecule 18 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 19 is a protein called 60S ribosomal protein L15.

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

- Molecule 20 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AO	195	Total	C	N	O	S	0	0
			1606	1034	315	252	5		

- Molecule 21 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 22 is a protein called 60S ribosomal protein L18.

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

- Molecule 23 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AR	181	Total	C	N	O	S	0	0
			1517	938	329	241	9		

- Molecule 24 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AS	175	Total	C	N	O	S	0	0
			1449	921	283	234	11		

- Molecule 25 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AT	157	Total	C	N	O	S	0	0
			1284	815	250	214	5		

- Molecule 26 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AU	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

- Molecule 27 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AV	129	Total	C	N	O	S	0	0
			969	613	182	169	5		

- Molecule 28 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AW	121	Total	C	N	O	S	0	0
			989	617	202	167	3		

- Molecule 29 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AX	117	Total	C	N	O	S	0	0
			958	612	180	165	1		

- Molecule 30 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AY	127	Total	C	N	O	S	0	0
			1064	668	216	177	3		

- Molecule 31 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AZ	134	Total	C	N	O	S	0	0
			1103	712	207	181	3		

- Molecule 32 is a protein called 60S ribosomal protein L27a.

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

- Molecule 33 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ab	68	Total	C	N	O	S	0	0
			559	344	122	90	3		

- Molecule 34 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ac	103	Total	C	N	O	S	0	0
			801	508	141	145	7		

- Molecule 35 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Ad	106	Total	C	N	O	S	0	0
			879	555	170	152	2		

- Molecule 36 is a protein called 60S ribosomal protein L32.

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

- Molecule 37 is a protein called 60S ribosomal protein L35a.

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

- Molecule 38 is a protein called 60S ribosomal protein L34.

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

- Molecule 39 is a protein called 60S ribosomal protein L35.

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

- Molecule 40 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ai	97	Total	C	N	O	S	0	0
			794	497	168	124	5		

- Molecule 41 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Aj	84	Total	C	N	O	S	0	0
			689	423	152	109	5		

- Molecule 42 is a protein called 60S ribosomal protein L38.

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

- Molecule 43 is a protein called 60S ribosomal protein L39.

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

- Molecule 44 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Am	50	Total	C	N	O	S	0	0
			411	254	87	64	6		

- Molecule 45 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	An	25	Total	C	N	O	S	0	0
			240	145	64	28	3		

- Molecule 46 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Ao	105	Total	C	N	O	S	0	0
			863	542	175	140	6		

- Molecule 47 is a protein called 60S ribosomal protein L37a.

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

- Molecule 48 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Aq	138	Total	C	N	O	S	0	0
			1046	654	196	193	3		

- Molecule 49 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	At	122	Total	C	N	O	S	0	0
			980	607	204	165	4		

- Molecule 50 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Au	217	Total	C	N	O	S	0	0
			1744	1114	314	307	9		

- Molecule 51 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	A2	3612	Total	C	N	O	P	0	0
			77427	34482	14158	25175	3612		

- Molecule 52 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	B1	1708	Total	C	N	O	P	0	0
			36456	16274	6546	11928	1708		

- Molecule 53 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BD	220	Total	C	N	O	S	0	0
			1709	1090	308	304	7		

- Molecule 54 is a protein called 40S ribosomal protein S4, Y isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BE	257	Total	C	N	O	S	0	0
			2031	1298	381	344	8		

- Molecule 55 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BF	190	Total	C	N	O	S	0	0
			1502	939	285	271	7		

- Molecule 56 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BG	232	Total	C	N	O	S	0	0
			1884	1176	379	322	7		

- Molecule 57 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BH	183	Total	C	N	O	S	0	0
			1479	941	272	265	1		

- Molecule 58 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	BI	207	Total	C	N	O	S	0	0
			1696	1064	334	293	5		

- Molecule 59 is a protein called 40S ribosomal protein S9.

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

- Molecule 60 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	BK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 61 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	BL	153	Total	C	N	O	S	0	0
			1258	804	235	213	6		

- Molecule 62 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	BM	120	Total	C	N	O	S	0	0
			931	584	164	174	9		

- Molecule 63 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	BN	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 64 is a protein called 40S ribosomal protein S14.

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

- Molecule 65 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	BP	120	Total	C	N	O	S	0	0
			999	636	188	168	7		

- Molecule 66 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	BQ	139	Total	C	N	O	S	0	0
			1109	704	210	192	3		

- Molecule 67 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	BR	125	Total	C	N	O	S	0	0
			1011	634	187	186	4		

- Molecule 68 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	BS	139	Total	C	N	O	S	0	0
			1154	725	233	195	1		

- Molecule 69 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	BT	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 70 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	BU	97	Total	C	N	O	S	0	0
			769	483	144	138	4		

- Molecule 71 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	BV	81	Total	C	N	O	S	0	0
			617	380	114	118	5		

- Molecule 72 is a protein called 40S ribosomal protein S15a.

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

- Molecule 73 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	BX	139	Total	C	N	O	S	0	0
			1080	682	214	181	3		

- Molecule 74 is a protein called 40S ribosomal protein S24.

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

- Molecule 75 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	BZ	86	Total	C	N	O	S	0	0
			688	442	129	116	1		

- Molecule 76 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Ba	97	Total	C	N	O	S	0	0
			774	481	160	128	5		

- Molecule 77 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Bb	80	Total	C	N	O	S	0	0
			625	391	116	111	7		

- Molecule 78 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Bc	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 79 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Bd	51	Total	C	N	O	S	0	0
			427	269	87	66	5		

- Molecule 80 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Be	55	Total	C	N	O	S	0	0
			437	272	96	68	1		

- Molecule 81 is a protein called 40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Bf	73	Total	C	N	O	S	0	0
			601	379	115	100	7		

- Molecule 82 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Bg	314	Total	C	N	O	S	0	0
			2440	1537	425	466	12		

- Molecule 83 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Bv	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		

- Molecule 84 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Bx	16	Total	C	N	O	P	0	0
			320	144	32	128	16		

- Molecule 85 is a protein called Cadherin-1.

Mol	Chain	Residues	Atoms				AltConf	Trace
85	A	39	Total	C	N	O	0	0
			190	112	39	39		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	6	ALA	-	insertion	UNP P12830
A	10	GLU	VAL	conflict	UNP P12830

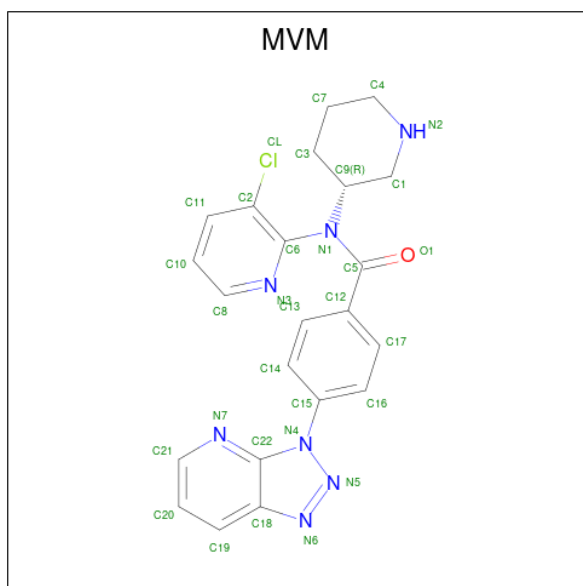
- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	AB	2	Total	Mg	0
			2	2	
86	A3	6	Total	Mg	0
			6	6	
86	A4	9	Total	Mg	0
			9	9	
86	AP	1	Total	Mg	0
			1	1	
86	AY	1	Total	Mg	0
			1	1	
86	Aa	1	Total	Mg	0
			1	1	
86	Ae	1	Total	Mg	0
			1	1	
86	A2	226	Total	Mg	0
			226	226	
86	B1	75	Total	Mg	0
			75	75	
86	BI	1	Total	Mg	0
			1	1	
86	Ba	1	Total	Mg	0
			1	1	
86	Bv	2	Total	Mg	0
			2	2	

- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
87	Aj	1	Total	Zn	0
			1	1	
87	Ao	1	Total	Zn	0
			1	1	
87	Ap	1	Total	Zn	0
			1	1	
87	Ba	1	Total	Zn	0
			1	1	
87	Bd	1	Total	Zn	0
			1	1	

- Molecule 88 is N-(3-chloropyridin-2-yl)-N-[(3R)-piperidin-3-yl]-4-(3H-[1,2,3]triazolo[4,5-b]pyridin-3-yl)benzamide (CCD ID: MVM) (formula: C₂₂H₂₀ClN₇O).

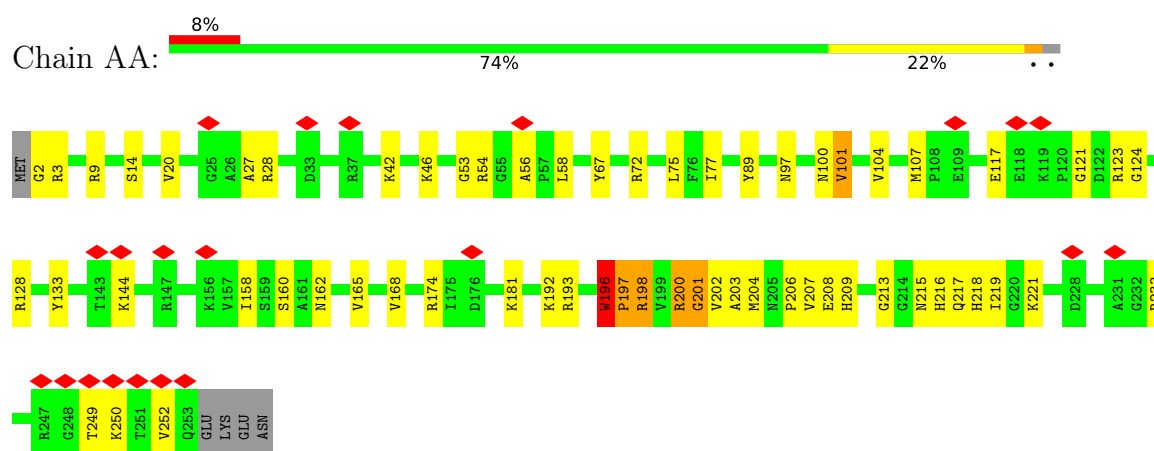


Mol	Chain	Residues	Atoms					AltConf
88	A2	1	Total	C	Cl	N	O	0
			31	22	1	7	1	

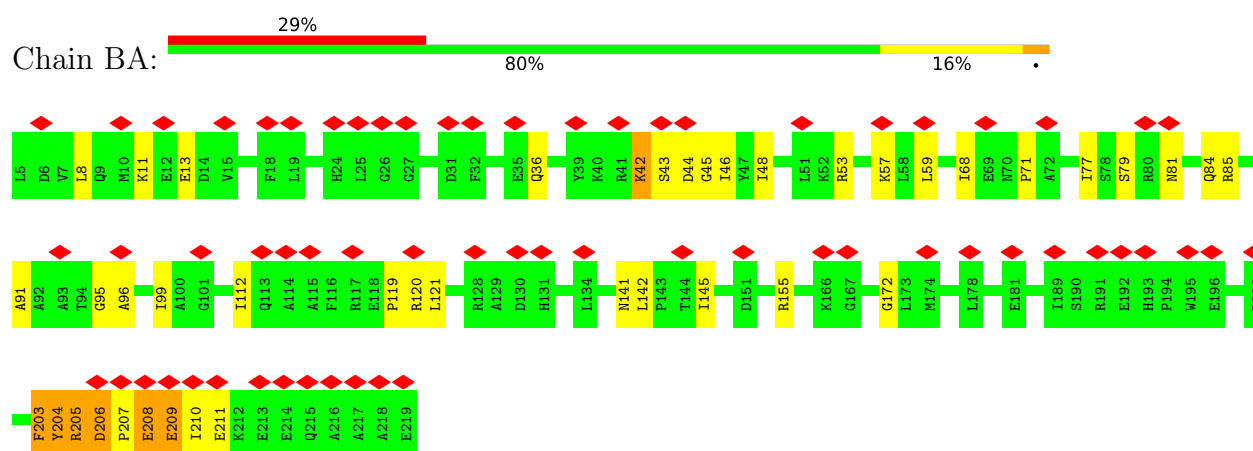
3 Residue-property plots

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.

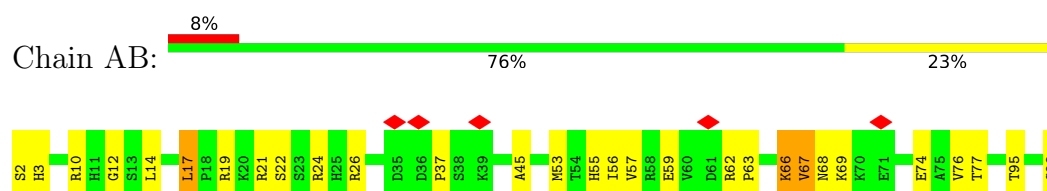
• Molecule 1: 60S ribosomal protein L8

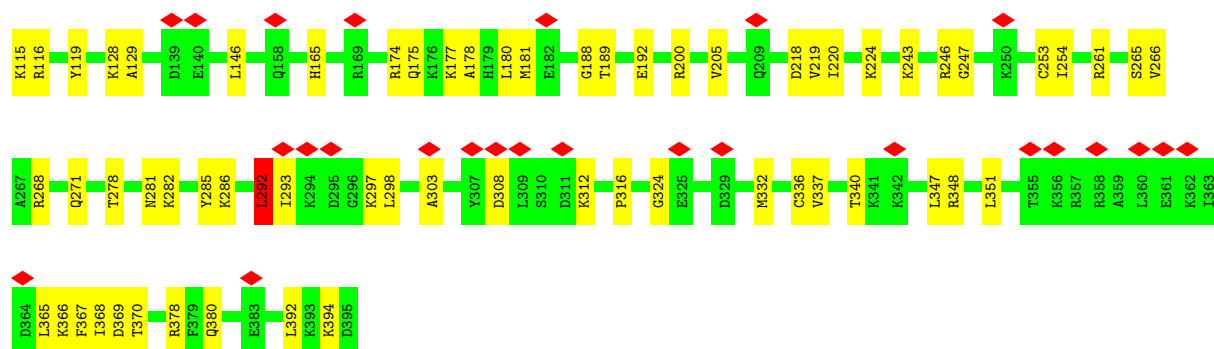


• Molecule 2: 40S ribosomal protein SA



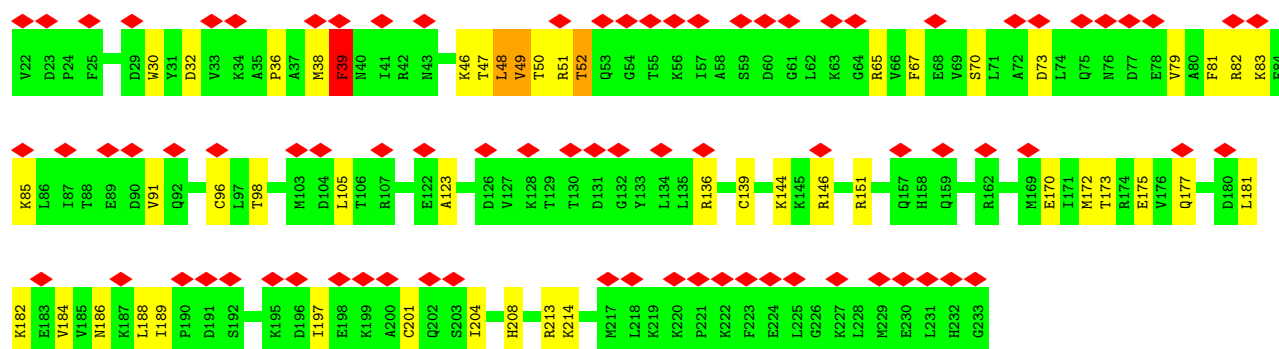
• Molecule 3: 60S ribosomal protein L3





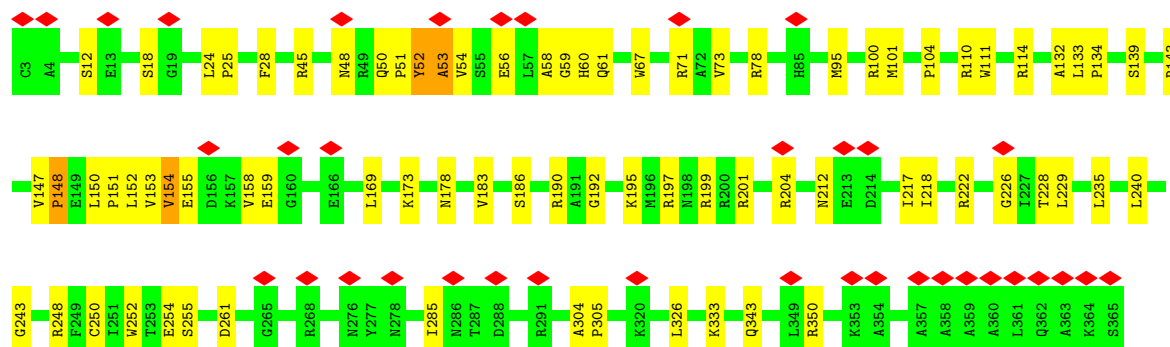
• Molecule 4: 40S ribosomal protein S3a

Chain BB: .



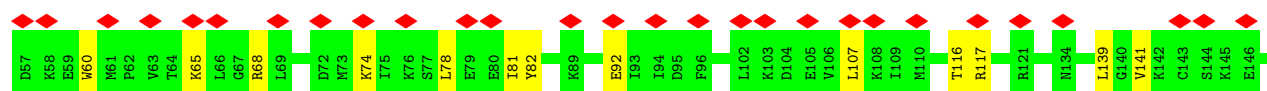
• Molecule 5: 60S ribosomal protein L4

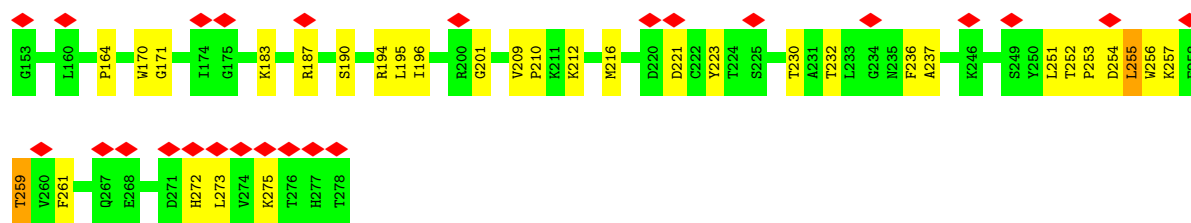
Chain AC: .



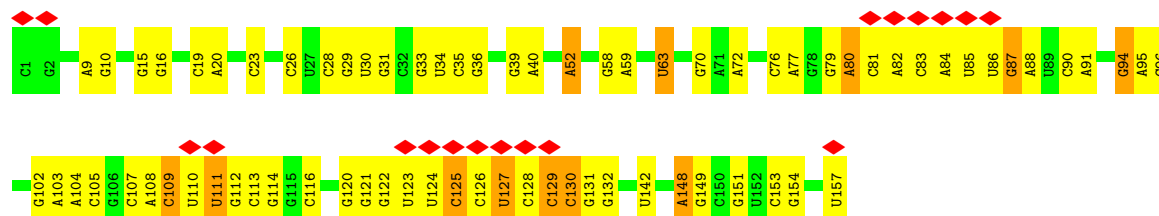
• Molecule 6: 40S ribosomal protein S2

Chain BC: .

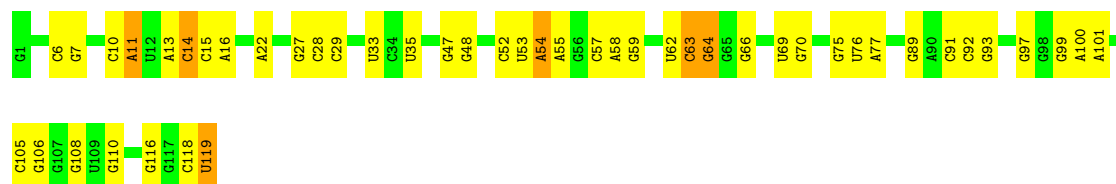




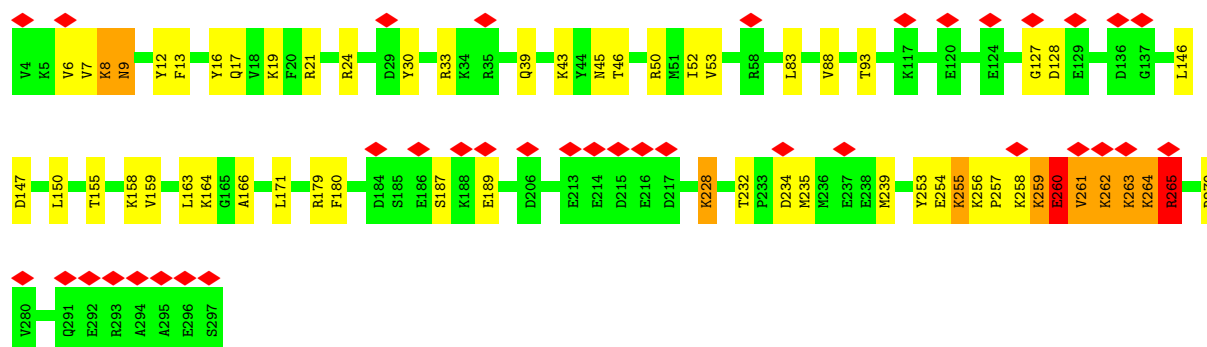
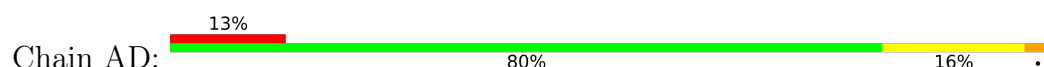
• Molecule 7: 5.8S ribosomal RNA



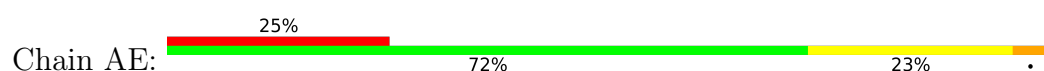
• Molecule 8: 5S ribosomal RNA

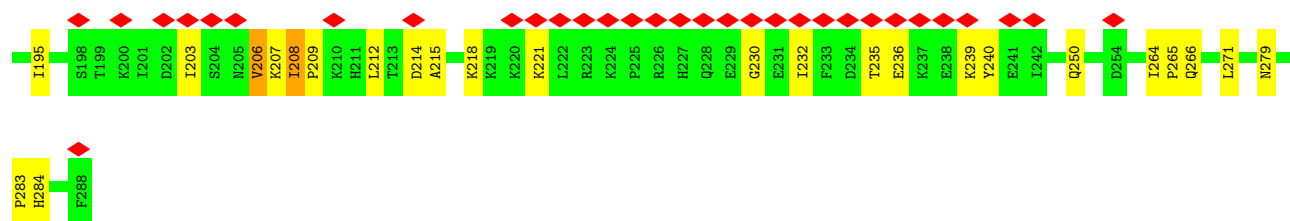


• Molecule 9: 60S ribosomal protein L5

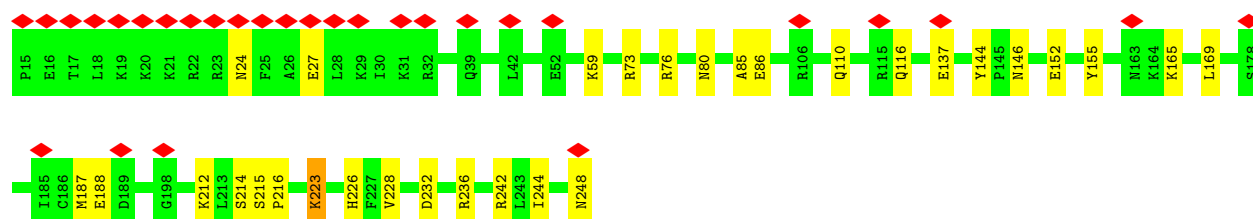
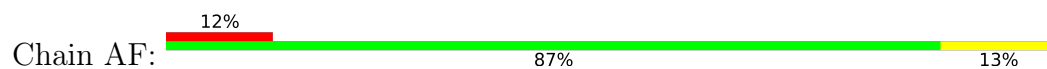


• Molecule 10: 60S ribosomal protein L6

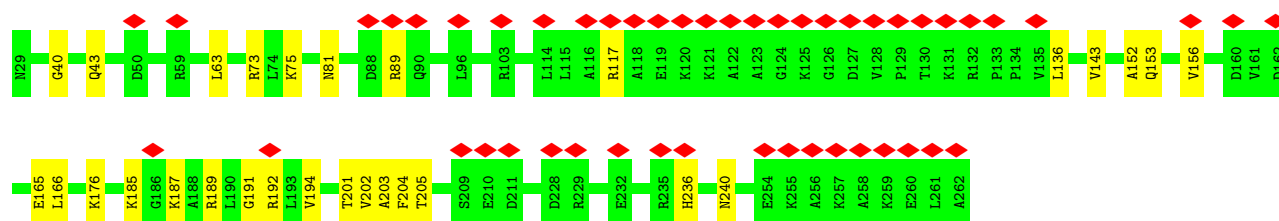
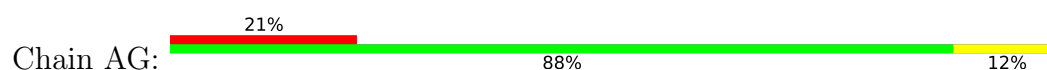




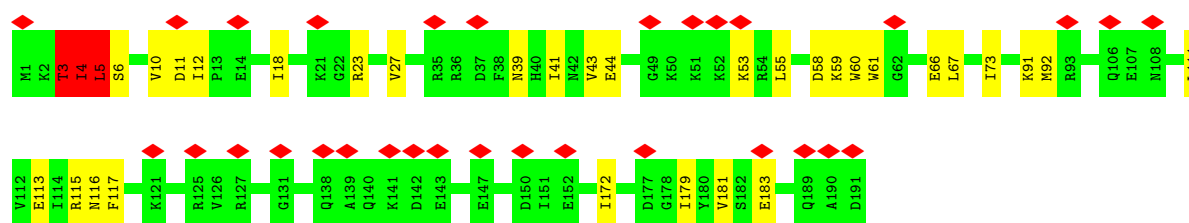
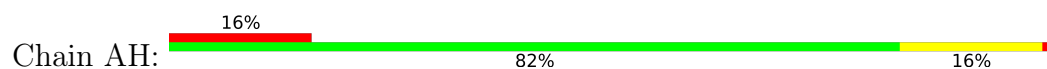
- Molecule 11: 60S ribosomal protein L7



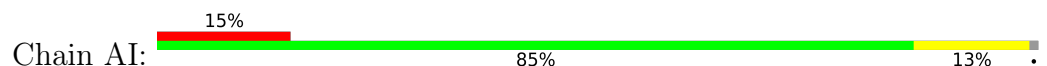
- Molecule 12: 60S ribosomal protein L7a

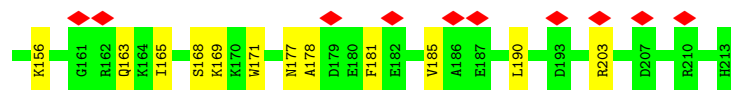


- Molecule 13: 60S ribosomal protein L9

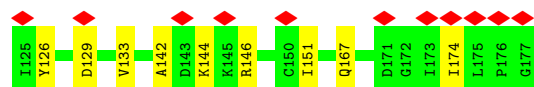
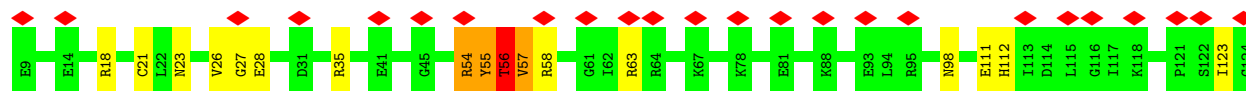
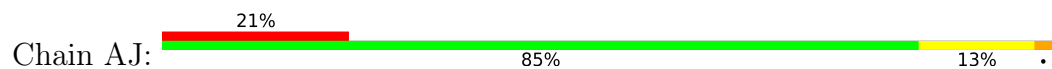


- Molecule 14: 60S ribosomal protein L10

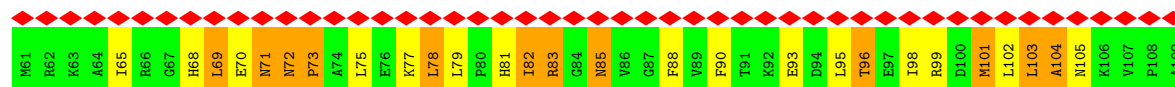
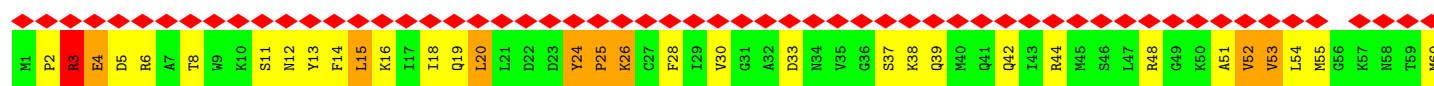




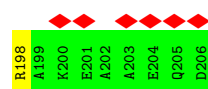
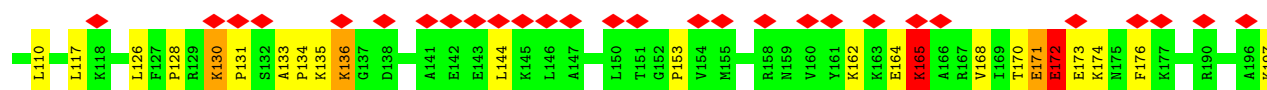
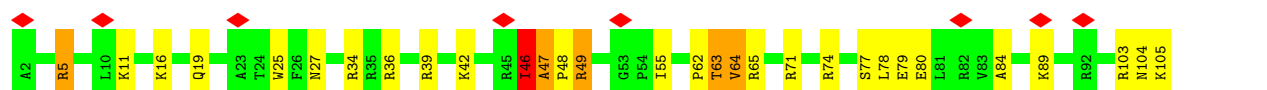
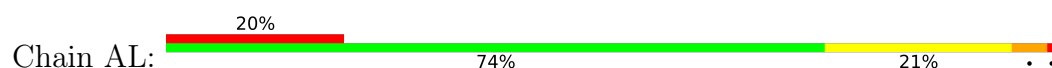
- Molecule 15: 60S ribosomal protein L11



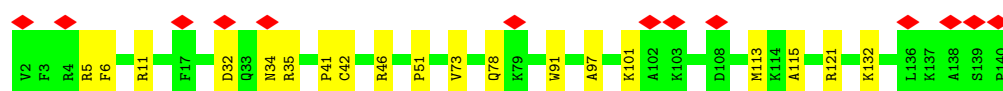
- Molecule 16: 60S acidic ribosomal protein P0



- Molecule 17: 60S ribosomal protein L13

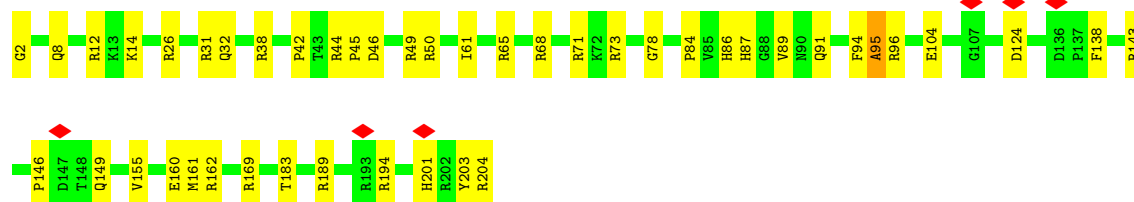


- Molecule 18: 60S ribosomal protein L14



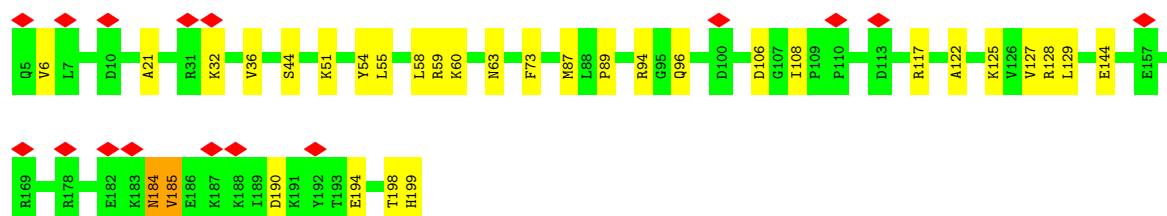
- Molecule 19: 60S ribosomal protein L15

Chain AN:  78% 22%



- Molecule 20: 60S ribosomal protein L13a

Chain AO:  8% 84% 15%



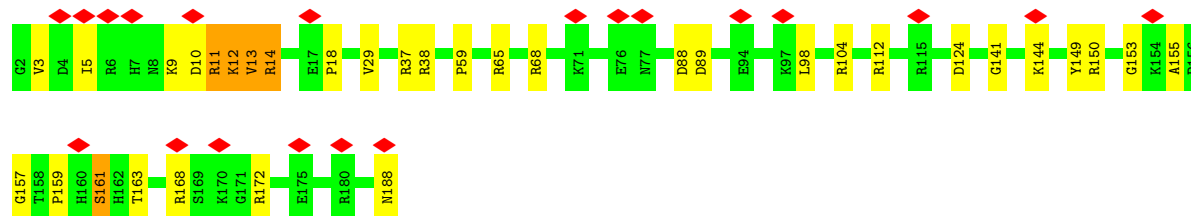
- Molecule 21: 60S ribosomal protein L17

Chain AP:  10% 88% 12%



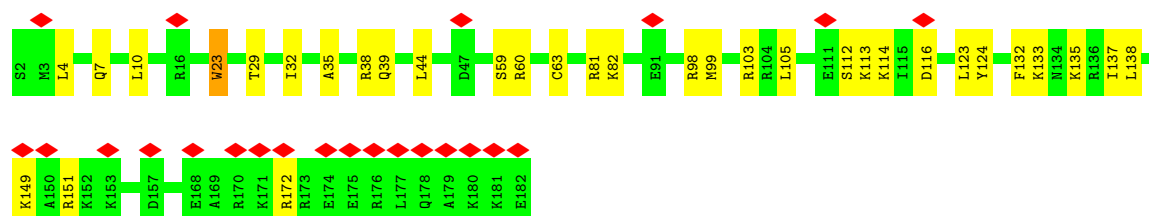
- Molecule 22: 60S ribosomal protein L18

Chain AQ:  11% 82% 16%

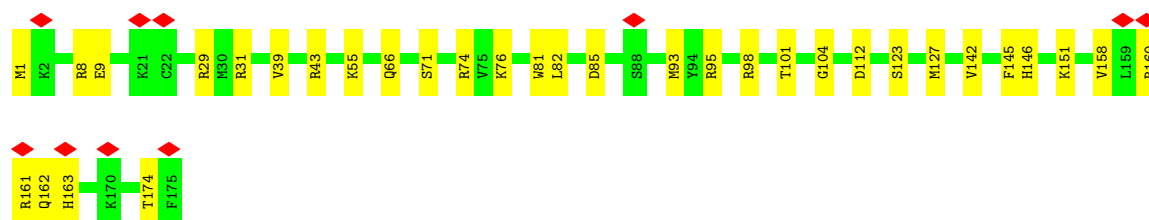
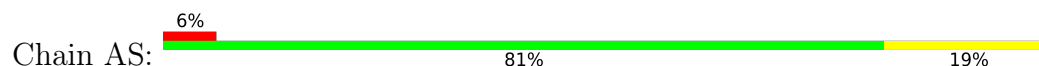


- Molecule 23: 60S ribosomal protein L19

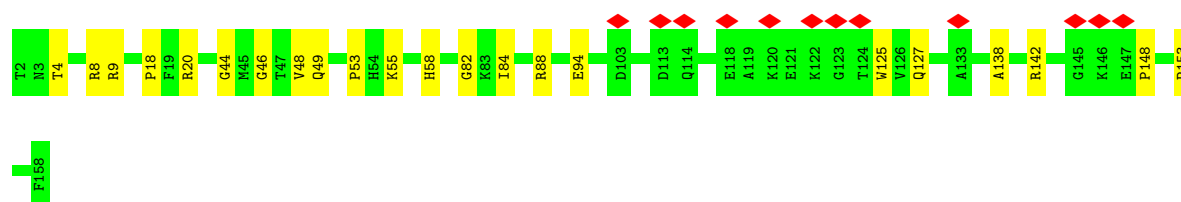
Chain AR:  13% 82% 18%



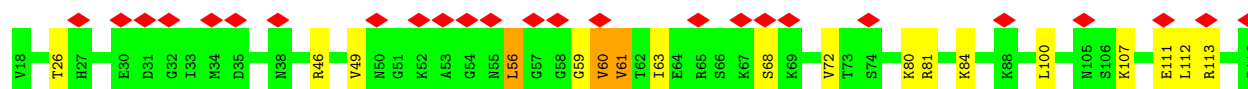
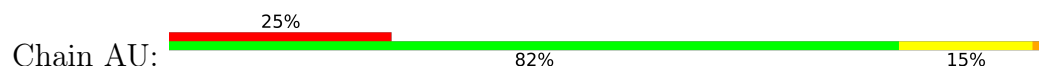
- Molecule 24: 60S ribosomal protein L18a



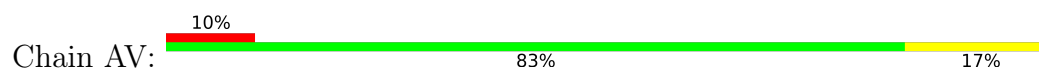
- Molecule 25: 60S ribosomal protein L21



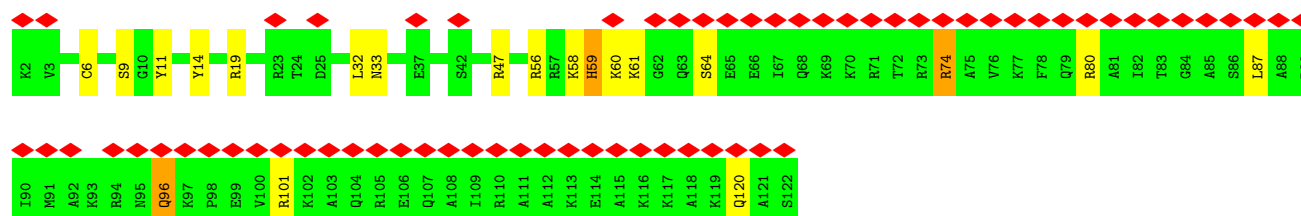
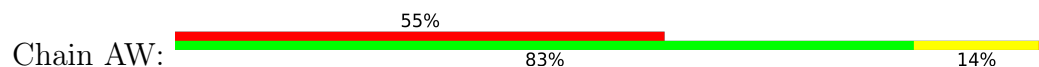
- Molecule 26: 60S ribosomal protein L22



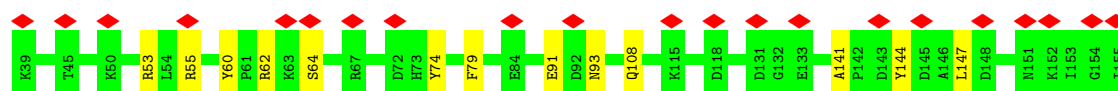
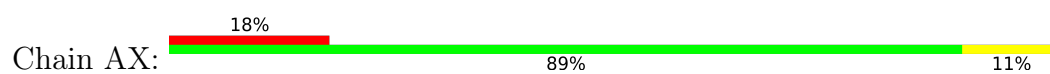
- Molecule 27: 60S ribosomal protein L23



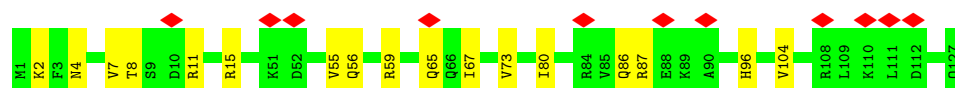
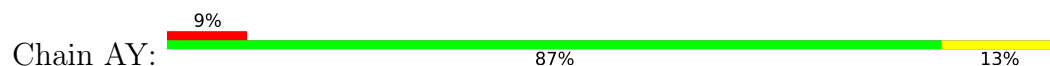
- Molecule 28: 60S ribosomal protein L24



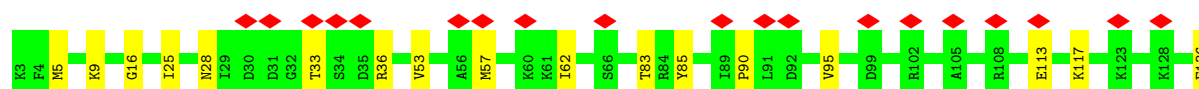
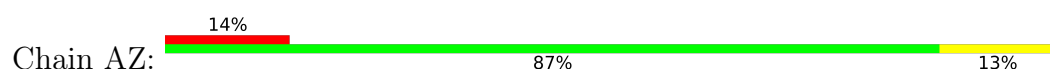
- Molecule 29: 60S ribosomal protein L23a



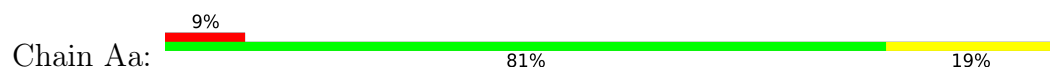
- Molecule 30: 60S ribosomal protein L26



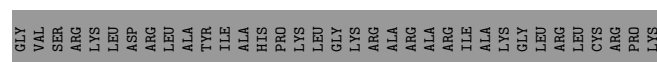
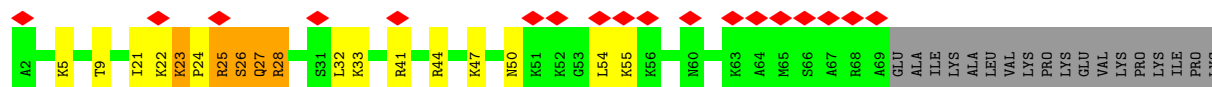
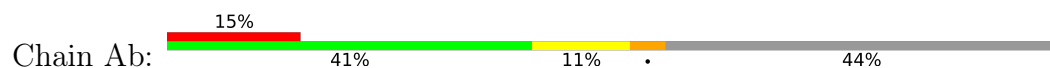
- Molecule 31: 60S ribosomal protein L27



- Molecule 32: 60S ribosomal protein L27a



- Molecule 33: 60S ribosomal protein L29

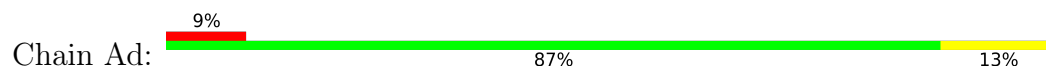


- Molecule 34: 60S ribosomal protein L30

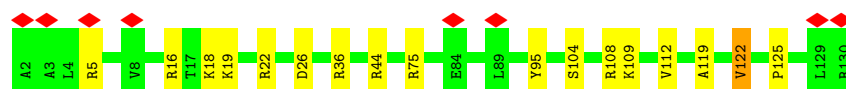




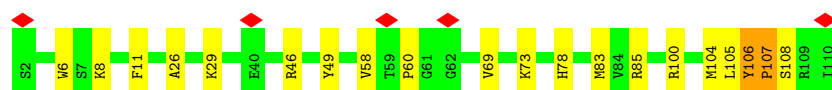
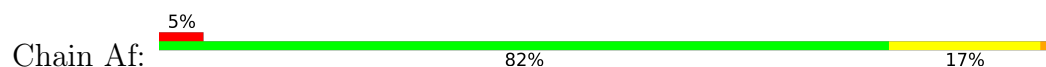
- Molecule 35: 60S ribosomal protein L31



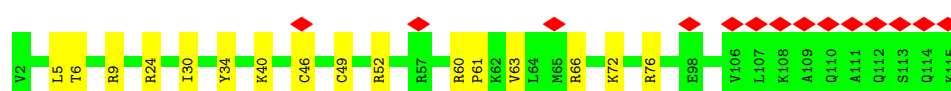
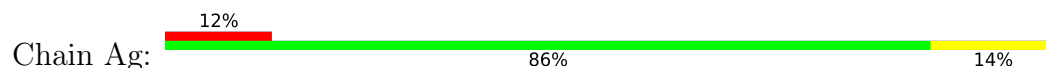
- Molecule 36: 60S ribosomal protein L32



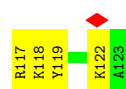
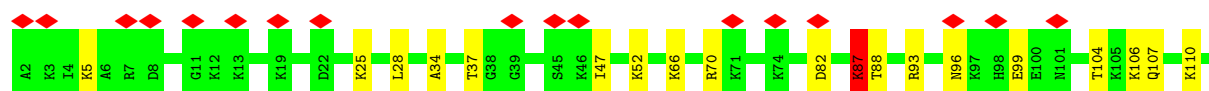
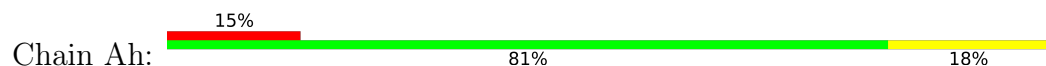
- Molecule 37: 60S ribosomal protein L35a



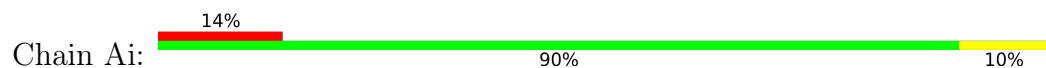
- Molecule 38: 60S ribosomal protein L34



- Molecule 39: 60S ribosomal protein L35



- Molecule 40: 60S ribosomal protein L36

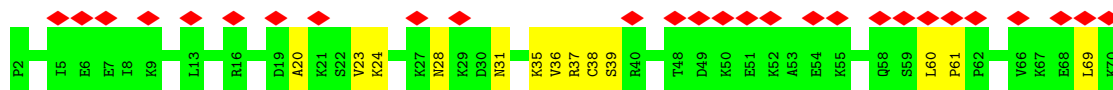
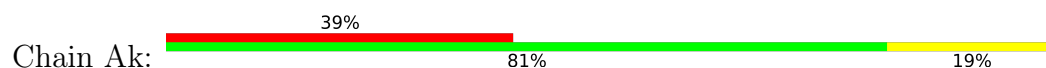




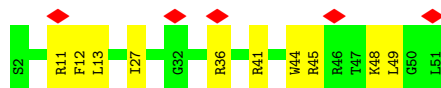
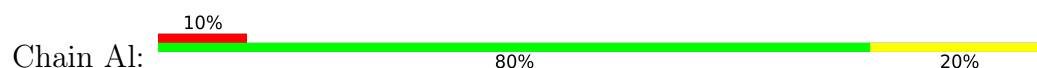
- Molecule 41: 60S ribosomal protein L37



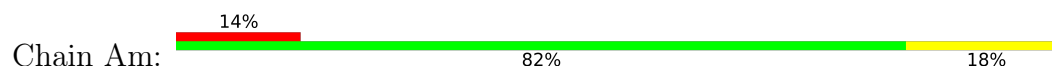
- Molecule 42: 60S ribosomal protein L38



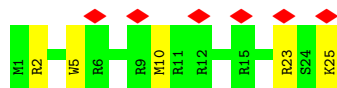
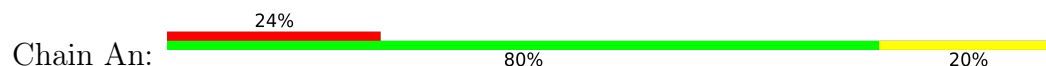
- Molecule 43: 60S ribosomal protein L39



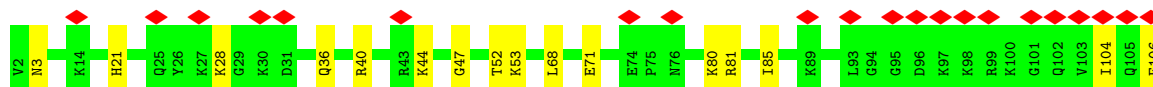
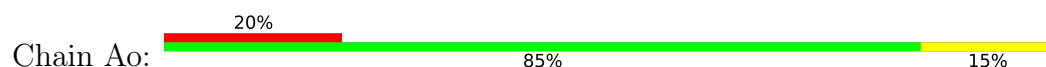
- Molecule 44: 60S ribosomal protein L40



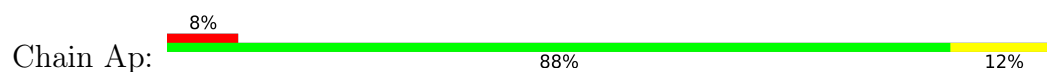
- Molecule 45: 60S ribosomal protein L41



- Molecule 46: 60S ribosomal protein L36a



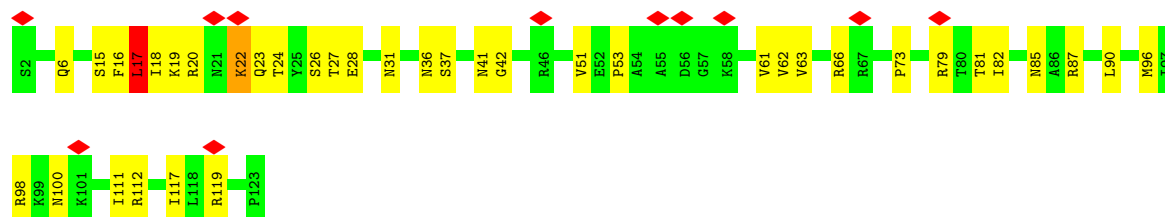
- Molecule 47: 60S ribosomal protein L37a



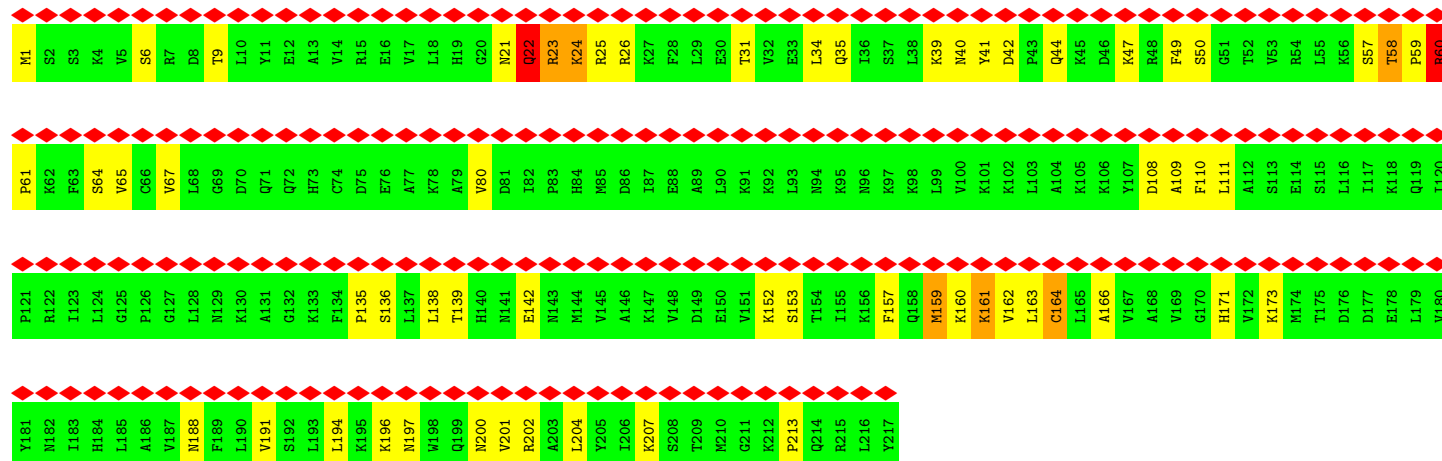
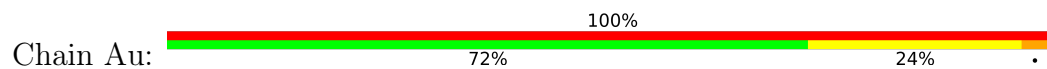
• Molecule 48: 60S ribosomal protein L12



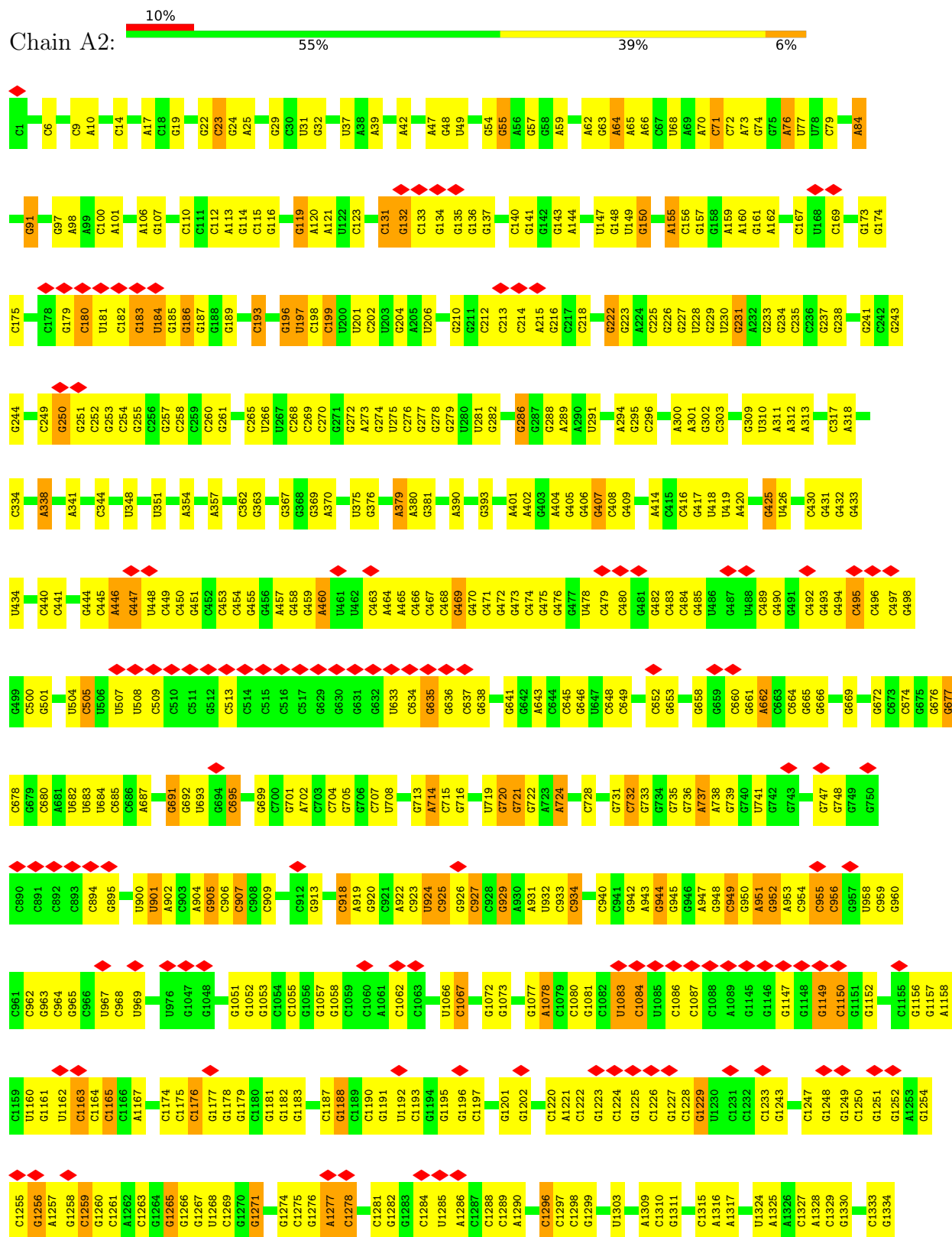
• Molecule 49: 60S ribosomal protein L28



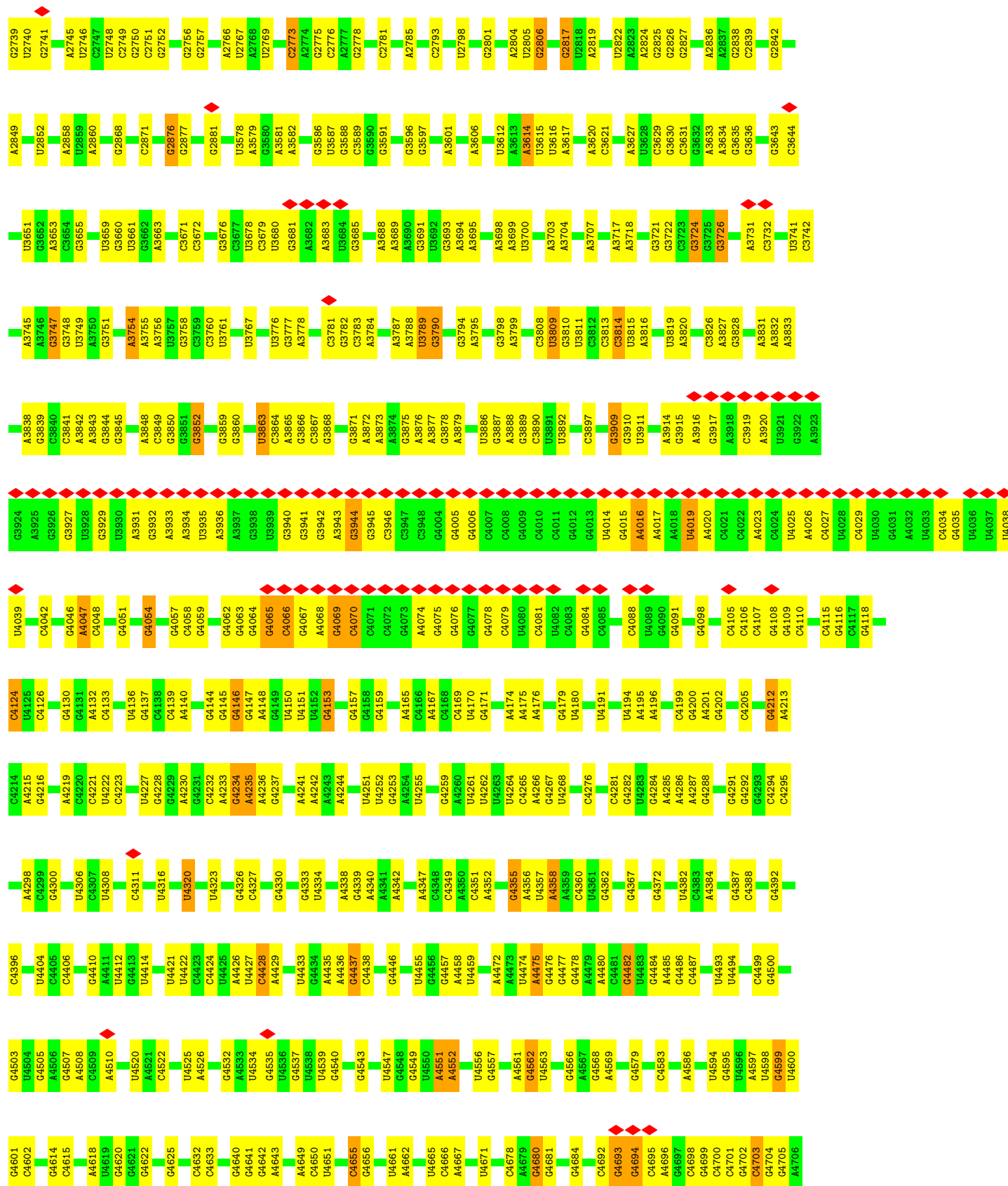
• Molecule 50: 60S ribosomal protein L10a

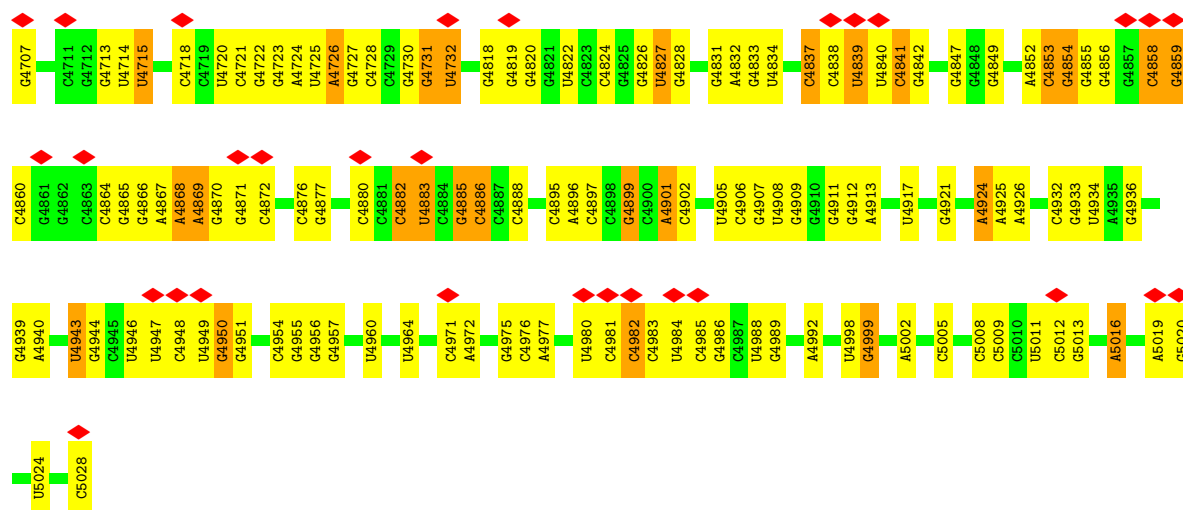


• Molecule 51: 28S ribosomal RNA

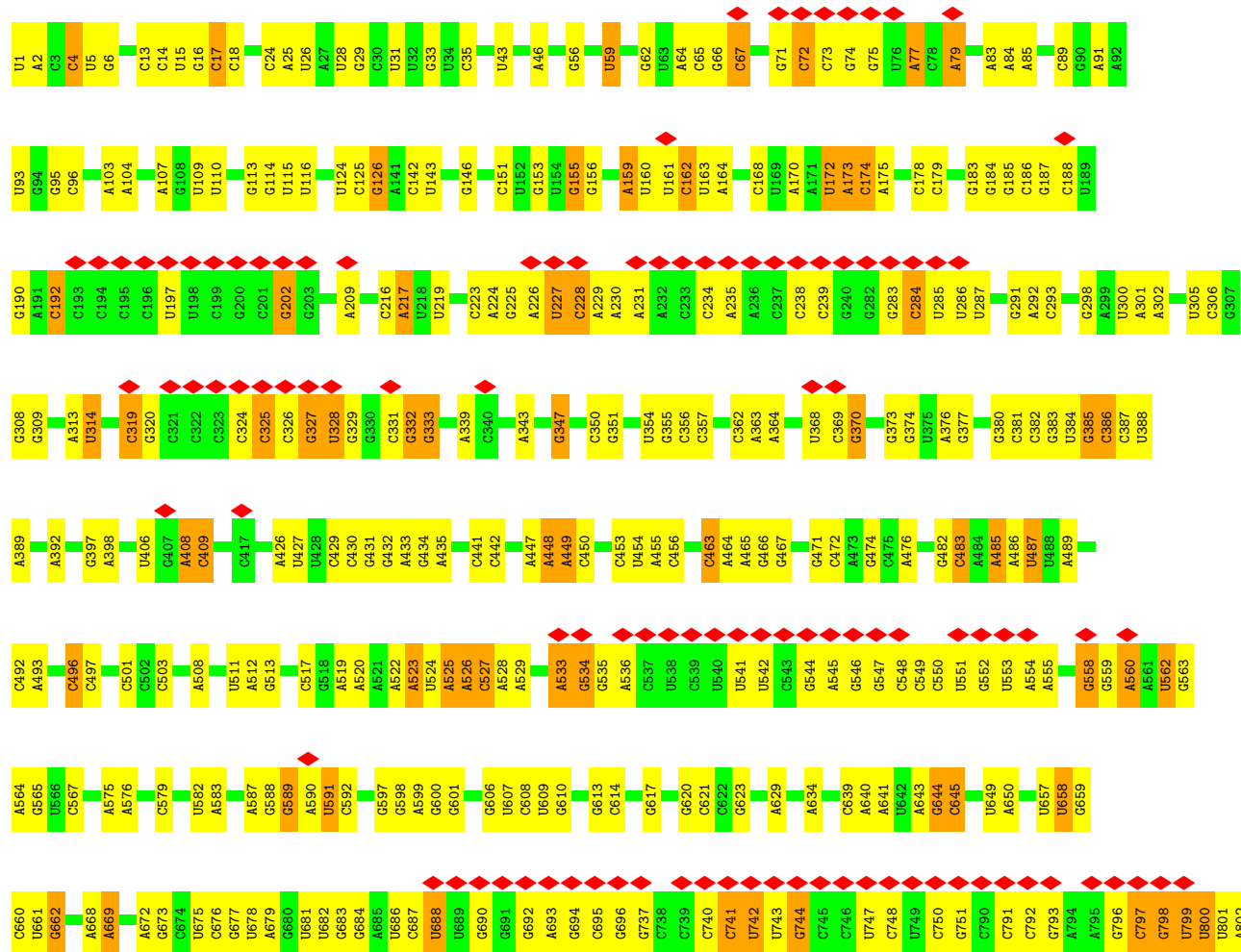


U2645	G1335	G1609	G1912	A1980	G2366	U2464	C2547	U2645
C2646	G1336	C1610	A1913	G1981	C2372	G2465	G2548	C2646
G2647	A1337	A1612	G1914	G1982	G2373	G2466	U2549	G2647
	G1341	A1613	A1915	A1983	A2374	G2467	G2557	
G2652	G1342	A1614	C1916	G1984	U2377	C2468	A2560	G2652
A2653	G1343	G1615	C1919	U1985	G2380	U2469	A2561	A2653
G2665	C1346	A1616	A1920	G1986	A2381	C2470	C2562	G2665
U2666	U1347	C1619	G1921	U1987	G2382	G2471	G2563	U2666
C2667	C1348	A1620	U1928	G1988	C2383	C2472	C2564	C2667
G2673	G1433	G1621	G1929	U1989	A2384	U2473	G2565	G2673
A2674	A1435	C1622	U1930	A1990	G2385	U2474	A2566	A2674
A2675	G1436	G1623	U1931	A1991	G2386	G2475	C2567	A2675
A2676	G1437	A1624	G1932	A1992	U2387		G2568	A2676
		U1830	G1933	C1993	G2388	G2482	G2569	
G2682	G1363	A1625	U1934	A1994	C2389	C2483	G2575	G2682
U2686	A1366	C1626	U1938	C1995	A2279	G2484	G2576	U2686
U2687	G1362	A1627	A1939	U1996	G2280	A2485	A2579	U2687
C2688	G1363	U1632	U1940	C1997	G2281	G2486	A2580	C2688
G2690	U1364	A1628	A1941	A1998	C2282	A2490	G2584	G2690
C2691	G1365	U1636	U1942	C1999	U2283	A2491	G2585	C2691
G2692	G1366	G1642	A1943	U2001	G2285	C2400	G2586	G2692
C2693	U1450	U1643	A1945	U2002	A2292	A2401	G2587	C2693
G2694	U1483	C1648	A1946	G2003	G2301	A2410	A2588	G2694
		G1652	G1946	C2004	G2304	G2416	A2590	
C2698	G1370	U1551	A1948	U2007	G2310	C2420	A2599	C2698
G2699	A1370	G1552	G1949	A2007	C2313	U2426	A2600	G2699
G2700	C1460	G1556	G1950	G2015	G2314	G2429	G2601	G2700
A2704	G1461	U1572	A1951	G2016	G2315	A2430	A2602	A2704
G2705	C1467	C1572	G1952	G2017	G2324	G2431	G2606	G2705
C2706	U1479	U1573	G1953	U2021	G2325	A2436	U2609	C2706
	C1468	C1472	G1954	A2022	A2326	C2437	U2610	
U2709	G1473	G1474	U1955	U2025	G2327	G2438	U2611	U2709
G2710	C1384	C1385	G1956	G2026	U2330	U2439	U2612	G2710
G2715	G1385	A1380	G1957	G2027	U2331	G2441	C2613	G2715
C2716	A1381	U1583	G1958	U2029	U2332	G2442	G2617	C2716
G2717	G1382	C1483	C1959	U2033	G2333	U2447	U2618	G2717
C2718	C1390	G1484	A1960	G2034	A2339	G2450	G2619	C2718
U2719	G1391	A1485	U1961	U2035	G2340	A2451	G2626	U2719
U2720	C1392	G1486	G1962	G2036	A2347	A2452	G2627	U2720
G2721	U1393	C1487	A1963	G2037	A2354	G2453	A2628	G2721
A2722	G1488	U1394	A1964	C2043	A2355	G2454	G2629	A2722
A2723	C1489	C1592	A1965	A2050	A2358	A2456	G2630	A2723
	U1395	C1396	U1967	G2060	U2363	C2457	A2631	
C2727	C1490	C1491	C1968	U2061	U2364	G2461	G2632	C2727
C2728	G1492	G1499	G1969	C2062	U2365	A2462	C2633	C2728
G2729	U1501	G1606	G1970	G2065		A2463	C2634	G2729
	G1498	G1607	A1971	G2066			G2637	
G2732	G1499	G1608	A1972	G2067			A2638	G2732
G2733	G1500		U1904	U2246			G2641	G2733
A2734	G1501		C1905	A2247			A2734	A2734
G2735			G1906				G2642	G2735
A2736			U1911					A2736

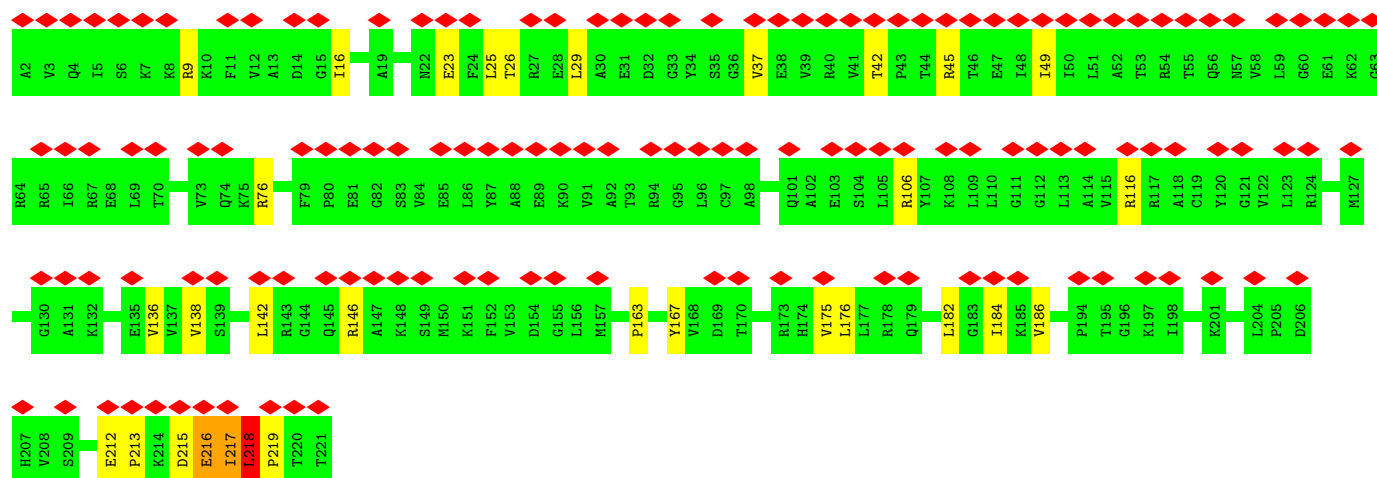




• Molecule 52: 18S ribosomal RNA

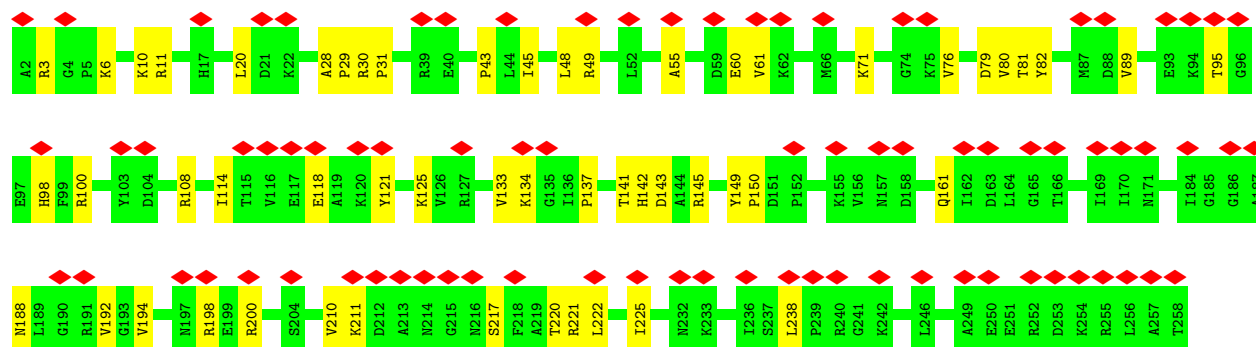






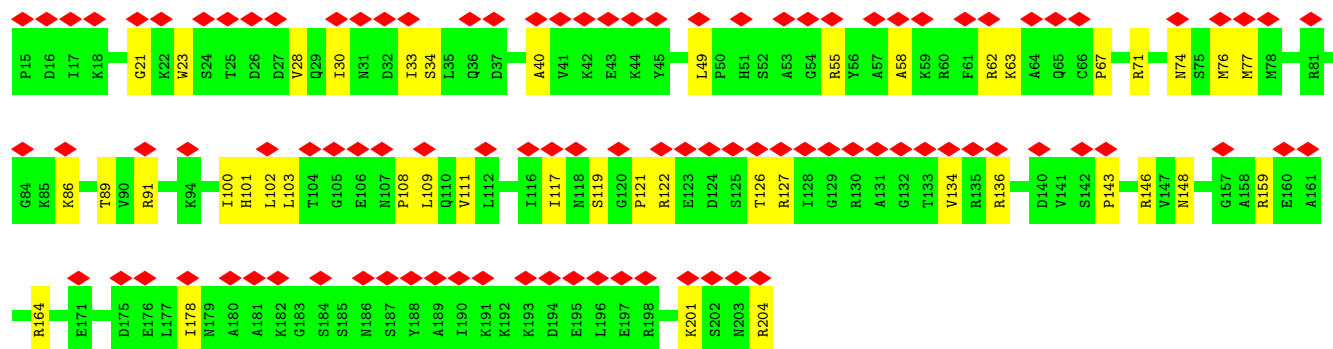
- Molecule 54: 40S ribosomal protein S4, Y isoform 1

Chain BE: 32% 79% 21%



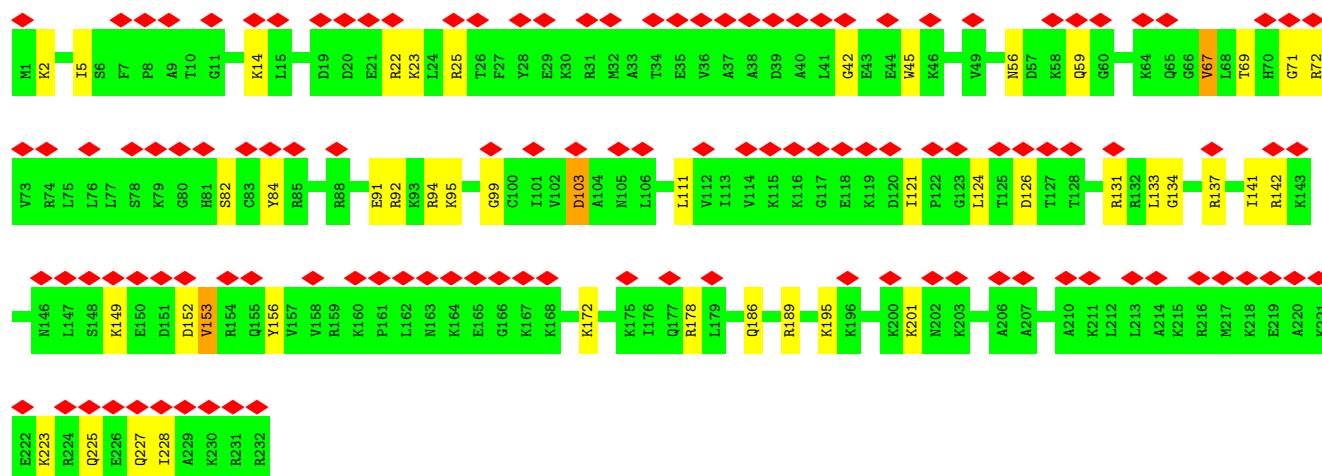
- Molecule 55: 40S ribosomal protein S5

Chain BF: 53% 77% 23%

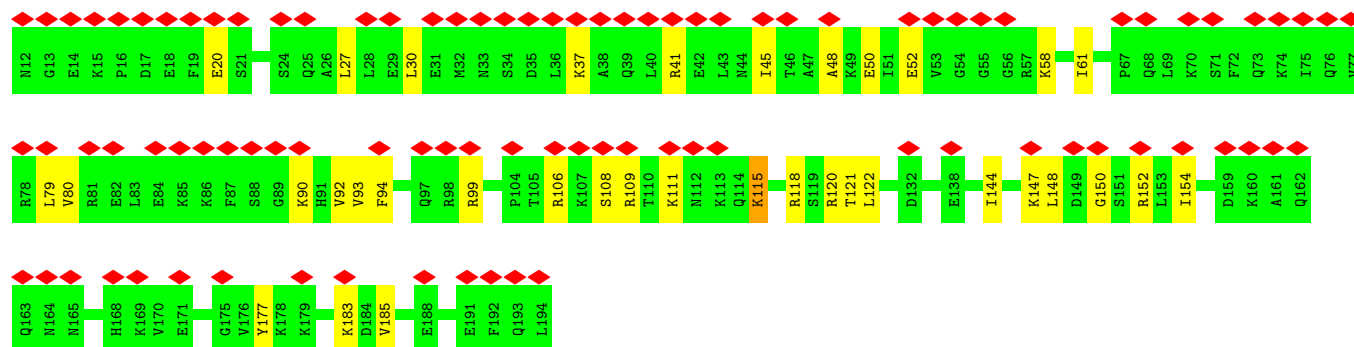
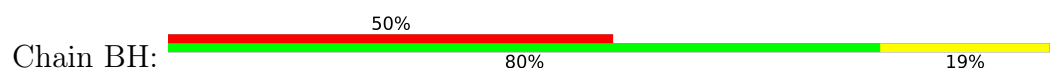


- Molecule 56: 40S ribosomal protein S6

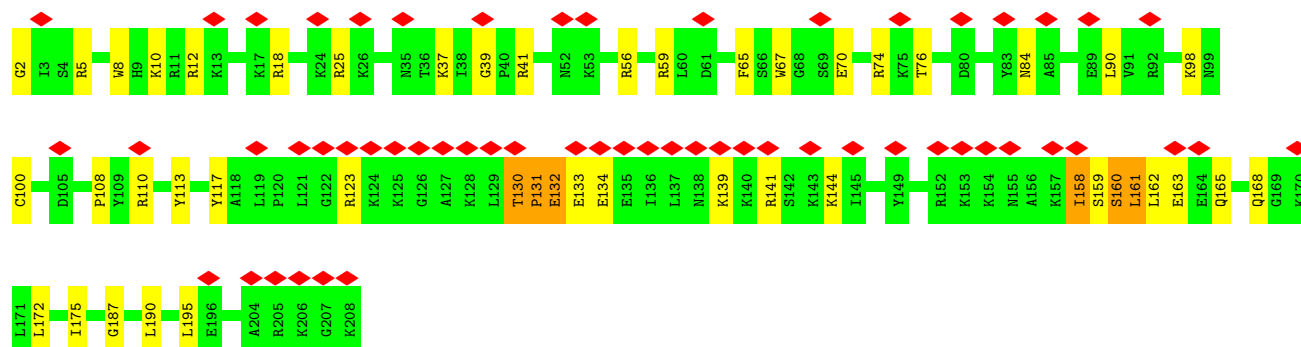
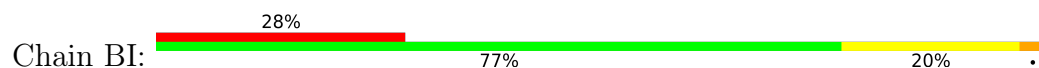
Chain BG: 51% 80% 19%



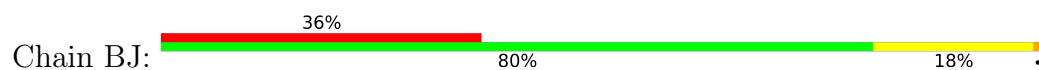
- Molecule 57: 40S ribosomal protein S7

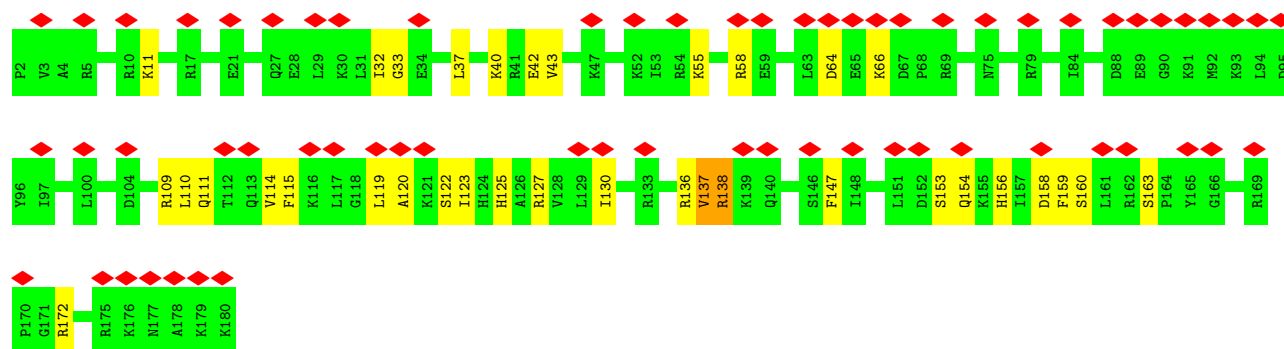


- Molecule 58: 40S ribosomal protein S8

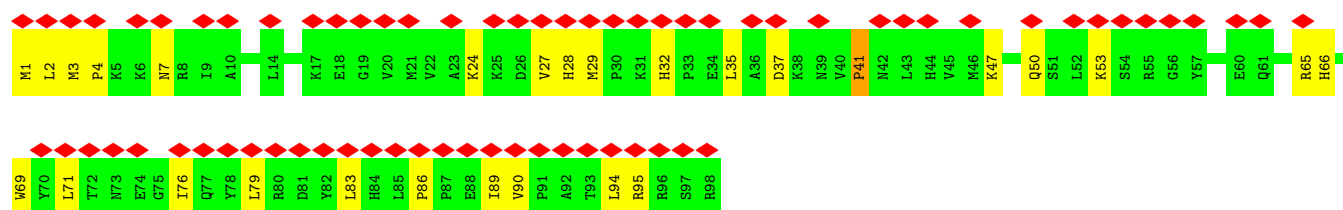
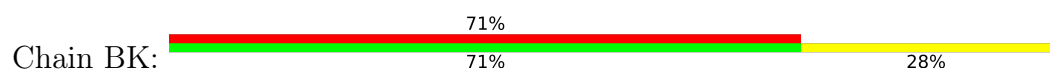


- Molecule 59: 40S ribosomal protein S9

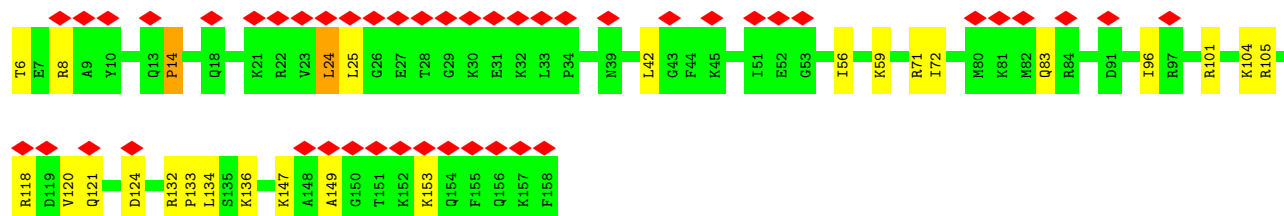
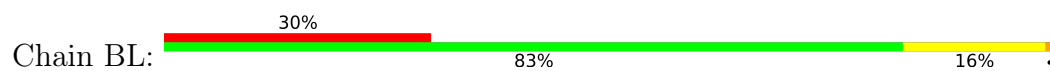




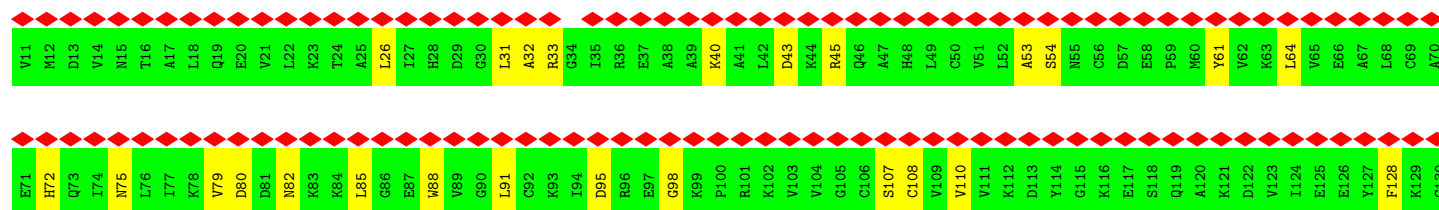
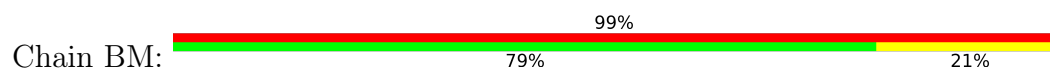
• Molecule 60: 40S ribosomal protein S10



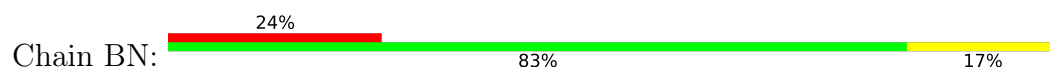
• Molecule 61: 40S ribosomal protein S11

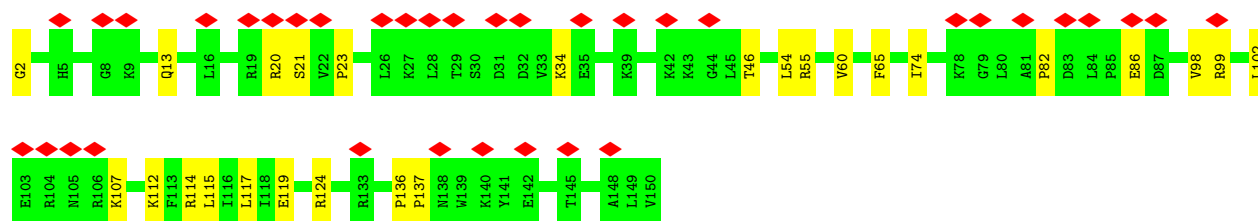


• Molecule 62: 40S ribosomal protein S12

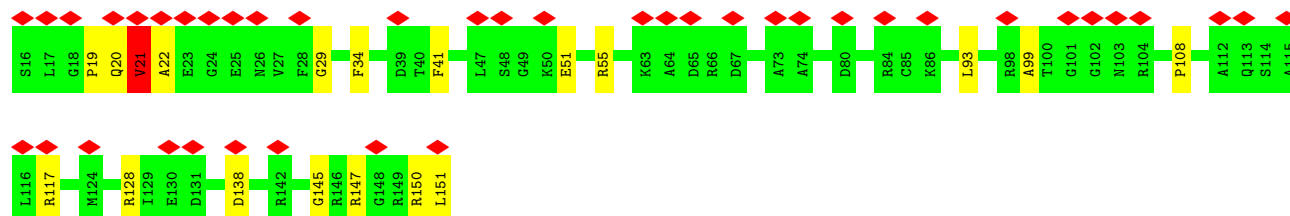
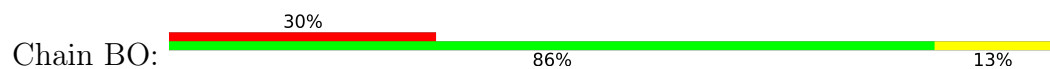


• Molecule 63: 40S ribosomal protein S13

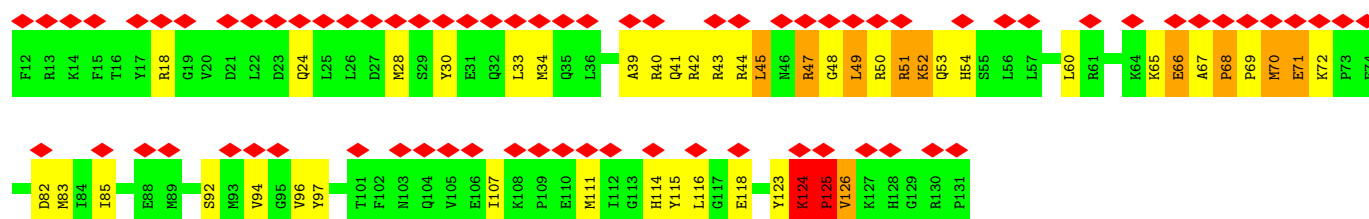




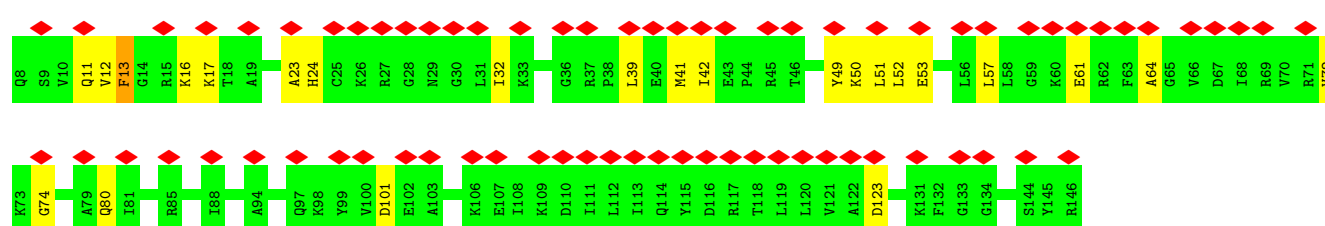
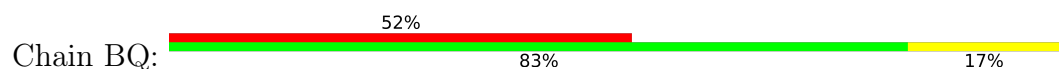
• Molecule 64: 40S ribosomal protein S14



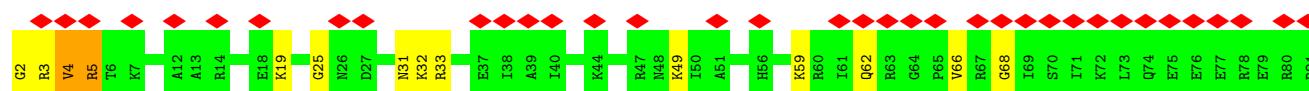
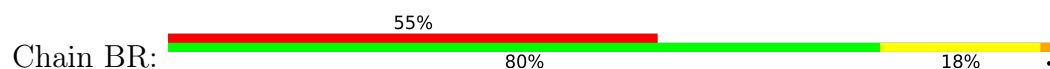
• Molecule 65: 40S ribosomal protein S15

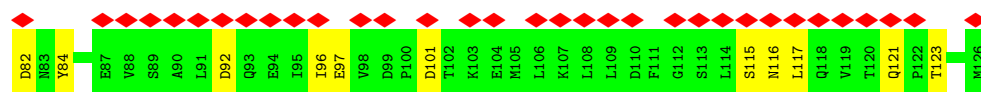


• Molecule 66: 40S ribosomal protein S16



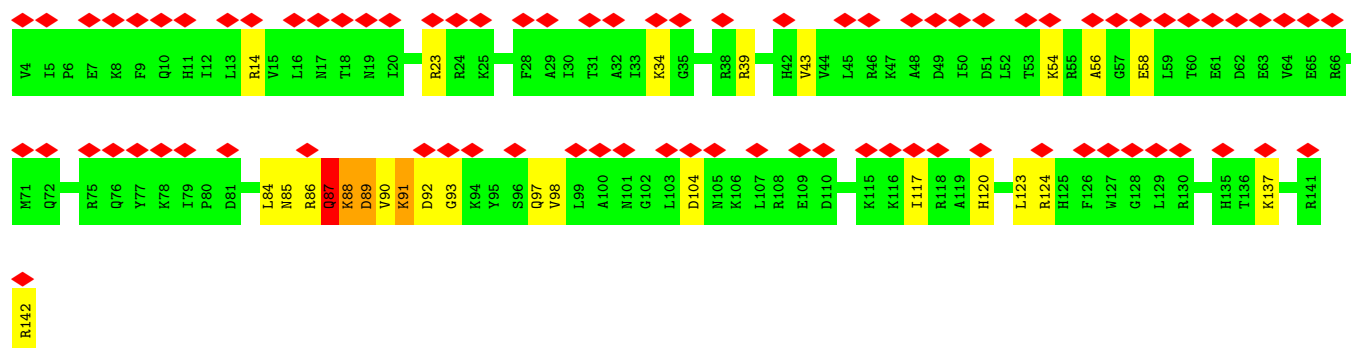
• Molecule 67: 40S ribosomal protein S17





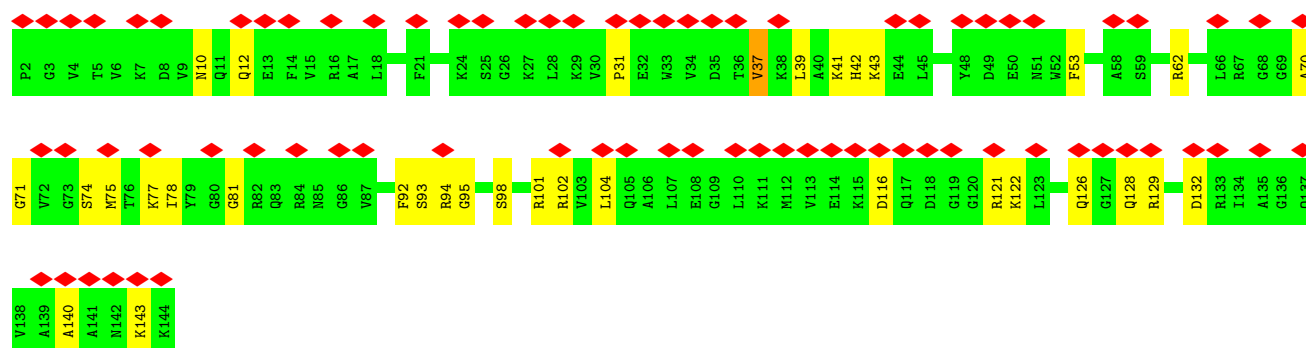
• Molecule 68: 40S ribosomal protein S18

Chain BS: 58% 81% 17% ..



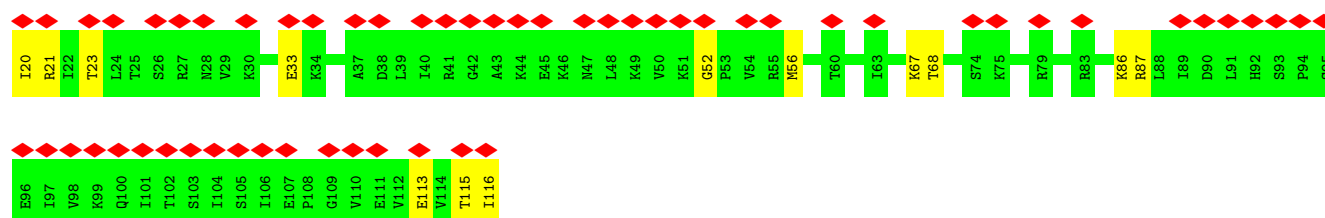
• Molecule 69: 40S ribosomal protein S19

Chain BT: 53% 76% 23% .



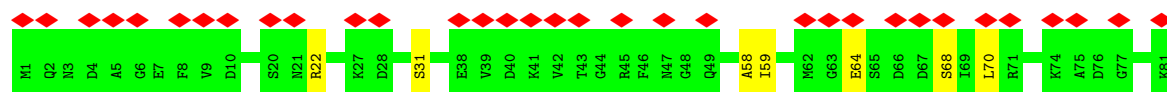
• Molecule 70: 40S ribosomal protein S20

Chain BU: 59% 87% 13%



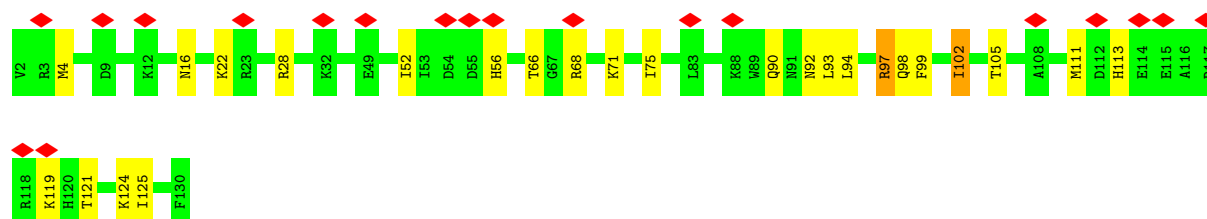
• Molecule 71: 40S ribosomal protein S21

Chain BV: 41% 91% 9%



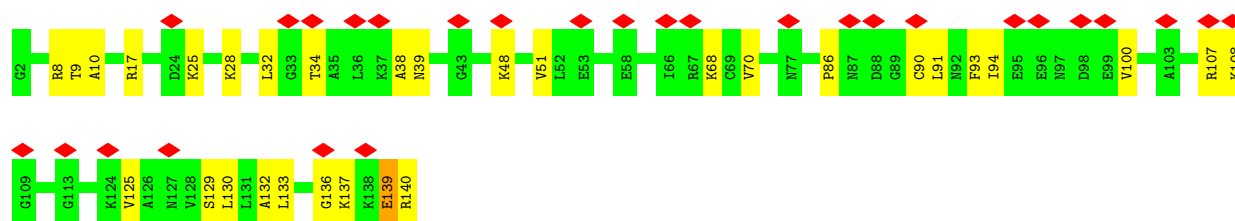
- Molecule 72: 40S ribosomal protein S15a

Chain BW: 15% 81% 18%



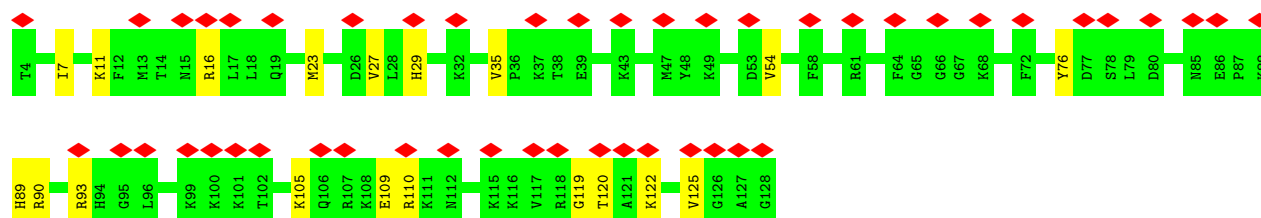
- Molecule 73: 40S ribosomal protein S23

Chain BX: 20% 78% 22%



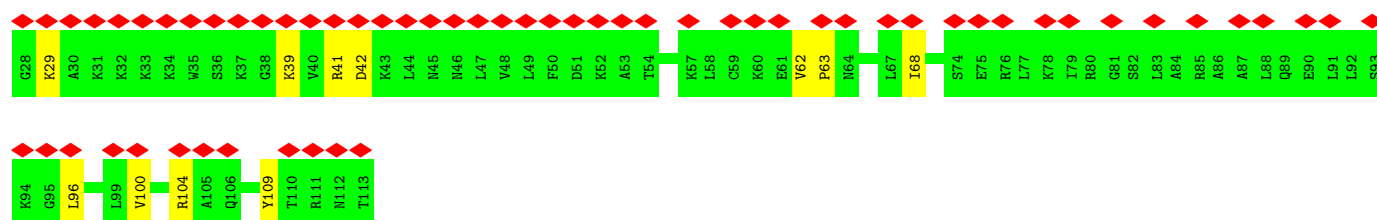
- Molecule 74: 40S ribosomal protein S24

Chain BY: 38% 85% 15%

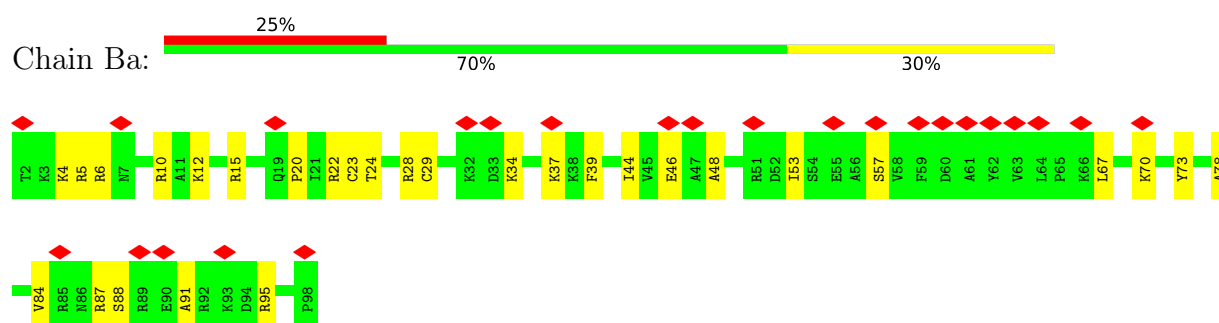


- Molecule 75: 40S ribosomal protein S25

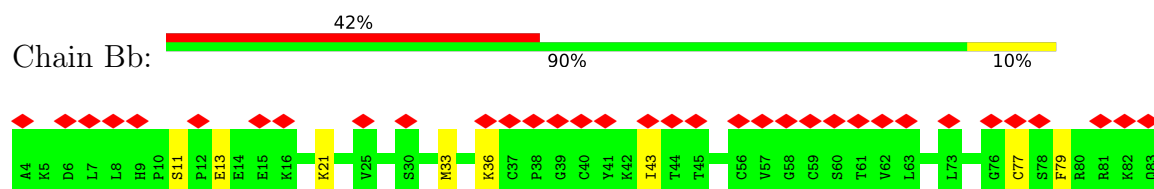
Chain BZ: 70% 87% 13%



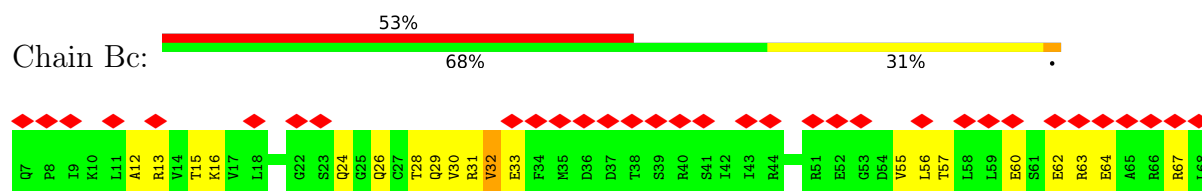
- Molecule 76: 40S ribosomal protein S26



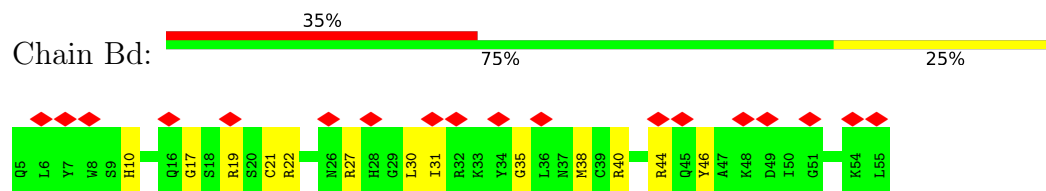
- Molecule 77: 40S ribosomal protein S27



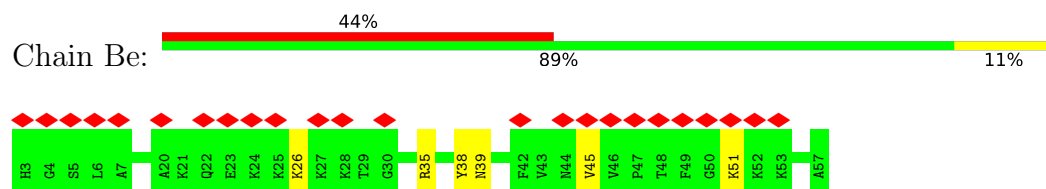
- Molecule 78: 40S ribosomal protein S28



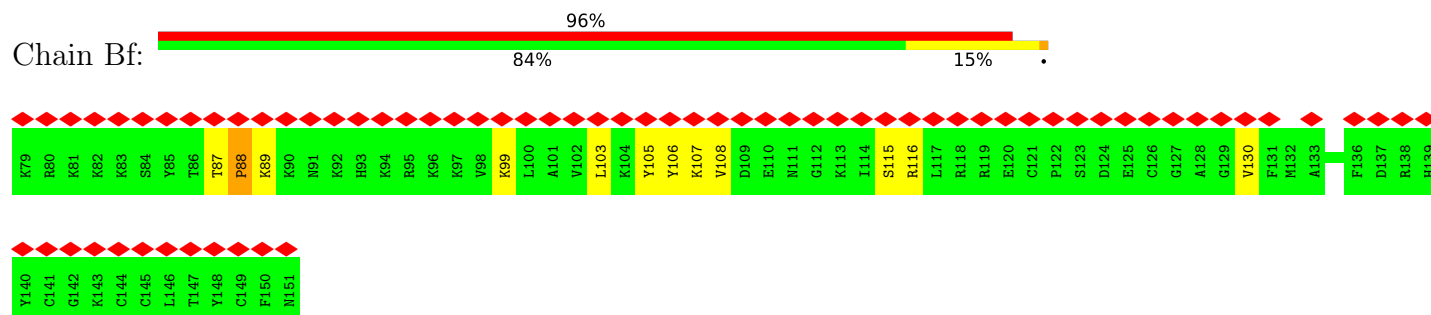
- Molecule 79: 40S ribosomal protein S29



- Molecule 80: 40S ribosomal protein S30

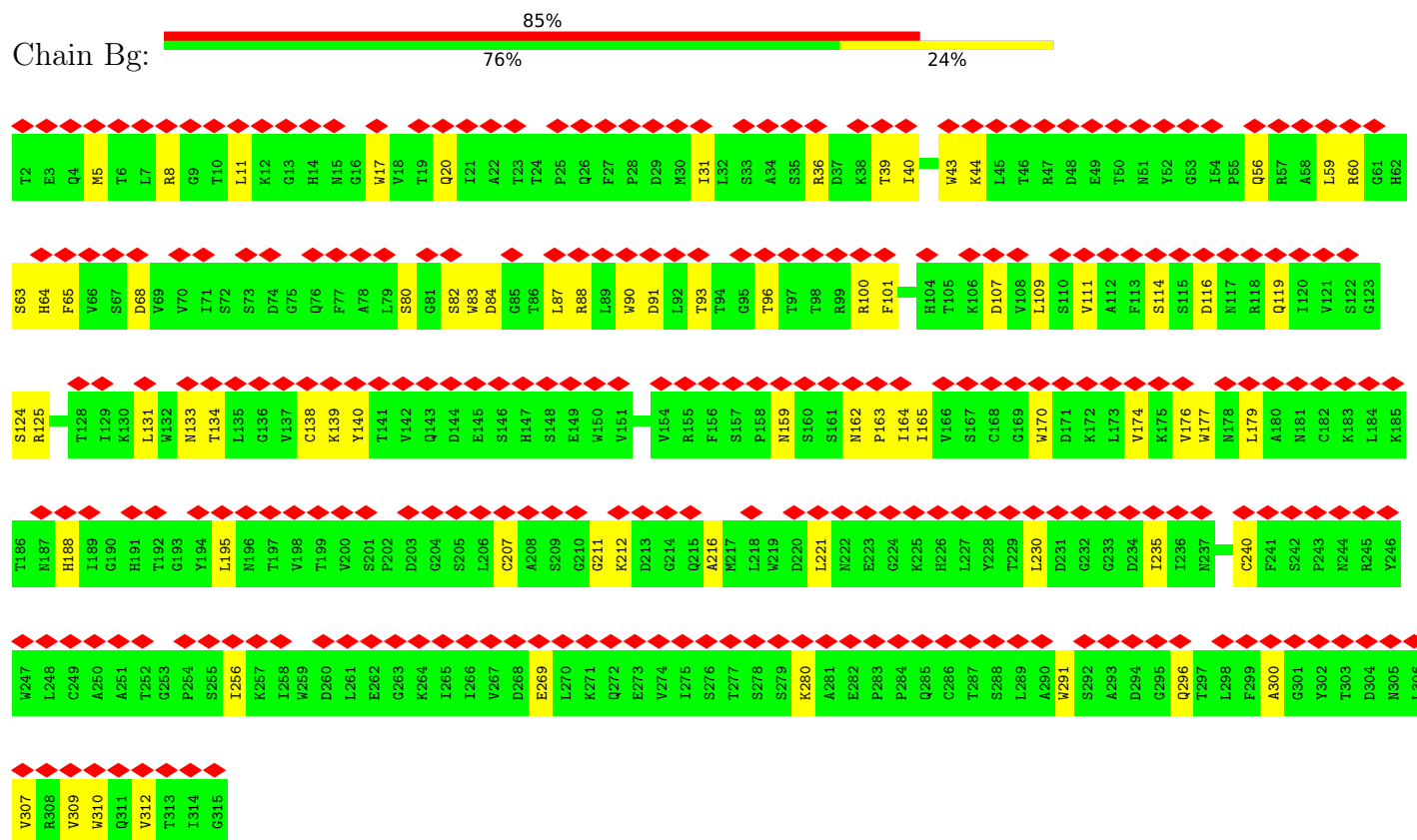


- Molecule 81: 40S ribosomal protein S27a



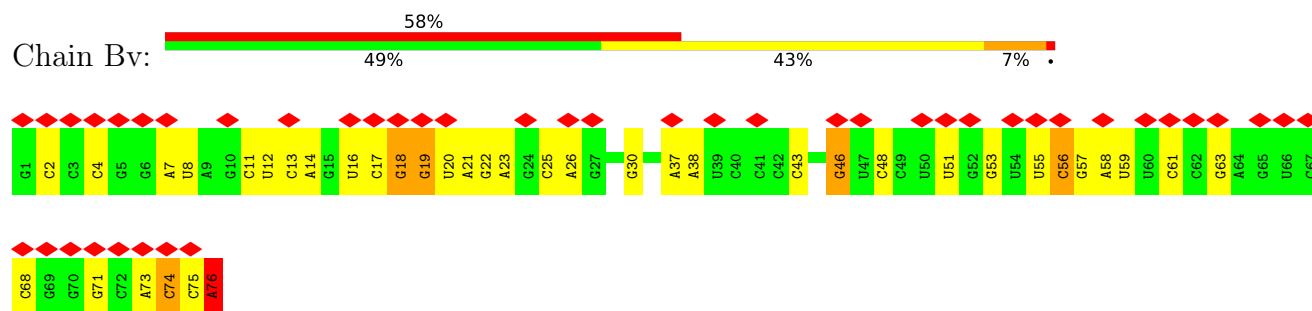
- Molecule 82: Receptor of activated protein C kinase 1

Chain Bg:



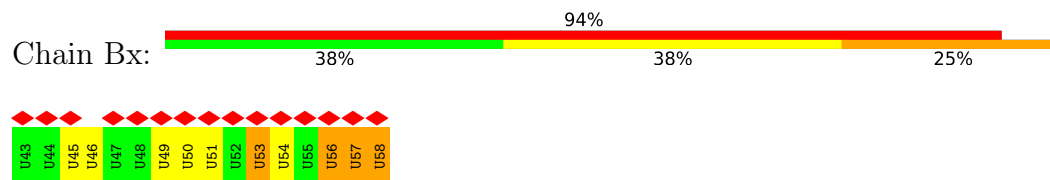
- Molecule 83: tRNA

Chain Bv:



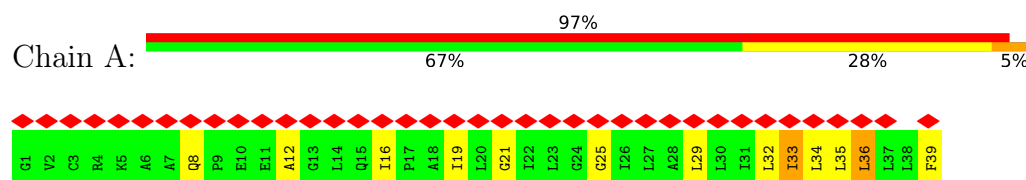
- Molecule 84: mRNA

Chain Bx:



- Molecule 85: Cadherin-1

Chain A:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	16594	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.107	Depositor
Minimum map value	-0.054	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.02	Depositor
Map size ($\text{\AA}$)	471.5, 471.5, 471.5	wwPDB
Map dimensions	410, 410, 410	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.15, 1.15, 1.15	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, MVM

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	AA	0.36	0/1968	0.72	3/2639 (0.1%)
2	BA	0.33	0/1741	0.67	0/2366
3	AB	0.37	0/3246	0.72	1/4345 (0.0%)
4	BB	0.31	0/1749	0.76	2/2340 (0.1%)
5	AC	0.34	0/2942	0.73	2/3951 (0.1%)
6	BC	0.31	0/1761	0.67	0/2379
7	A3	0.32	0/3726	0.44	0/5804
8	A4	0.31	0/2839	0.43	0/4425
9	AD	0.31	0/2437	0.68	2/3262 (0.1%)
10	AE	0.31	0/1603	0.81	3/2153 (0.1%)
11	AF	0.35	0/1986	0.72	1/2644 (0.0%)
12	AG	0.31	0/1913	0.70	0/2576
13	AH	0.31	0/1545	0.72	2/2077 (0.1%)
14	AI	0.32	0/1730	0.72	0/2311
15	AJ	0.30	0/1376	0.70	0/1841
16	AK	0.36	0/886	1.20	6/1188 (0.5%)
17	AL	0.35	0/1688	0.80	0/2260
18	AM	0.34	0/1161	0.69	0/1554
19	AN	0.39	0/1746	0.70	0/2338
20	AO	0.36	0/1638	0.70	1/2191 (0.0%)
21	AP	0.35	0/1268	0.63	0/1701
22	AQ	0.36	0/1537	0.83	3/2052 (0.1%)
23	AR	0.32	0/1533	0.74	1/2025 (0.0%)
24	AS	0.35	0/1488	0.65	0/1997
25	AT	0.34	0/1312	0.62	0/1753
26	AU	0.29	0/822	0.61	0/1103
27	AV	0.33	0/983	0.62	0/1319
28	AW	0.34	0/1004	0.85	6/1332 (0.5%)
29	AX	0.30	0/975	0.63	0/1312
30	AY	0.32	0/1081	0.63	0/1439
31	AZ	0.30	0/1126	0.70	0/1502
32	Aa	0.38	0/1191	0.70	0/1591

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Ab	0.31	0/569	0.75	0/750
34	Ac	0.30	0/812	0.65	0/1089
35	Ad	0.32	0/894	0.67	0/1204
36	Ae	0.33	0/1082	0.72	1/1443 (0.1%)
37	Af	0.39	0/895	0.82	3/1198 (0.3%)
38	Ag	0.34	0/916	0.71	0/1220
39	Ah	0.29	0/1023	0.65	0/1351
40	Ai	0.31	0/805	0.73	0/1065
41	Aj	0.37	0/703	0.87	0/929
42	Ak	0.27	0/575	0.74	0/761
43	Al	0.31	0/454	0.64	0/599
44	Am	0.33	0/417	0.82	0/553
45	An	0.31	0/241	0.72	0/305
46	Ao	0.32	0/877	0.73	0/1156
47	Ap	0.36	0/718	0.75	0/953
48	Aq	0.34	0/1058	1.08	6/1424 (0.4%)
49	At	0.38	0/995	0.94	5/1334 (0.4%)
50	Au	0.28	0/1772	0.75	3/2375 (0.1%)
51	A2	0.32	0/86613	0.44	0/135108
52	B1	0.27	0/40767	0.44	4/63536 (0.0%)
53	BD	0.29	1/1736 (0.1%)	0.63	0/2338
54	BE	0.30	0/2072	0.71	2/2793 (0.1%)
55	BF	0.29	0/1524	0.70	0/2048
56	BG	0.26	0/1907	0.69	1/2538 (0.0%)
57	BH	0.27	0/1501	0.67	0/2009
58	BI	0.32	0/1725	0.79	2/2298 (0.1%)
59	BJ	0.31	0/1520	0.75	0/2030
60	BK	0.30	0/851	0.78	0/1147
61	BL	0.32	0/1281	0.76	4/1710 (0.2%)
62	BM	0.23	0/941	0.67	0/1264
63	BN	0.31	0/1226	0.74	2/1649 (0.1%)
64	BO	0.31	0/1029	0.76	0/1380
65	BP	0.30	0/1019	0.93	3/1361 (0.2%)
66	BQ	0.29	0/1126	0.75	1/1506 (0.1%)
67	BR	0.27	0/1023	0.78	2/1373 (0.1%)
68	BS	0.25	0/1172	0.69	0/1570
69	BT	0.28	0/1131	0.70	0/1515
70	BU	0.26	0/778	0.61	0/1045
71	BV	0.28	0/623	0.70	0/833
72	BW	0.32	0/1051	0.68	0/1406
73	BX	0.31	0/1097	0.73	0/1464
74	BY	0.30	0/1032	0.73	0/1371
75	BZ	0.29	0/696	0.80	0/929

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Ba	0.33	0/786	0.75	0/1053
77	Bb	0.26	0/637	0.64	0/854
78	Bc	0.27	0/490	0.67	0/656
79	Bd	0.35	0/437	0.81	0/580
80	Be	0.29	0/443	0.77	1/583 (0.2%)
81	Bf	0.23	0/613	0.72	0/811
82	Bg	0.25	0/2497	0.60	0/3399
83	Bv	0.34	1/1813 (0.1%)	0.50	3/2823 (0.1%)
84	Bx	0.23	0/351	0.48	0/540
85	A	0.50	1/189 (0.5%)	1.04	2/260 (0.8%)
All	All	0.31	3/232504 (0.0%)	0.57	78/341259 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	BB	0	1
9	AD	0	1
13	AH	0	1
29	AX	0	1
All	All	0	4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	Bv	73	A	O3'-P	11.22	1.77	1.61
85	A	16	ILE	C-N	5.56	1.38	1.33
53	BD	212	GLU	C-N	5.07	1.40	1.33

All (78) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	BP	124	LYS	CA-C-N	12.33	135.25	119.84
65	BP	124	LYS	C-N-CA	12.33	135.25	119.84
16	AK	24	TYR	CA-C-N	10.66	133.17	119.84
16	AK	24	TYR	C-N-CA	10.66	133.17	119.84
16	AK	24	TYR	N-CA-C	9.62	120.52	108.11
83	Bv	74	C	C1'-C2'-O2'	-8.33	95.91	108.40
13	AH	5	LEU	N-CA-C	7.53	121.84	111.90
37	Af	58	VAL	N-CA-C	7.45	117.62	108.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	196	TRP	CA-C-N	7.39	129.08	119.84
1	AA	196	TRP	C-N-CA	7.39	129.08	119.84
28	AW	59	HIS	CA-C-N	7.22	135.33	121.54
28	AW	59	HIS	C-N-CA	7.22	135.33	121.54
37	Af	58	VAL	CA-C-N	7.04	138.99	121.80
37	Af	58	VAL	C-N-CA	7.04	138.99	121.80
83	Bv	73	A	O3'-P-O5'	6.98	114.47	104.00
22	AQ	98	LEU	N-CA-C	6.88	119.18	110.24
5	AC	73	VAL	N-CA-C	6.80	117.31	110.23
66	BQ	101	ASP	N-CA-C	6.66	118.92	110.33
28	AW	96	GLN	CA-C-N	6.59	130.69	120.60
28	AW	96	GLN	C-N-CA	6.59	130.69	120.60
54	BE	29	PRO	CA-C-N	-6.37	112.29	121.20
54	BE	29	PRO	C-N-CA	-6.37	112.29	121.20
13	AH	4	ILE	N-CA-C	6.35	116.97	108.27
58	BI	130	THR	CA-C-N	6.26	127.66	119.84
58	BI	130	THR	C-N-CA	6.26	127.66	119.84
56	BG	103	ASP	CA-C-O	-6.25	111.58	120.51
10	AE	230	GLY	N-CA-C	5.99	119.89	112.64
28	AW	74	ARG	N-CA-C	5.99	117.91	110.91
52	B1	1756	C	C2'-C3'-O3'	5.97	118.46	109.50
61	BL	120	VAL	CA-C-N	5.92	130.14	121.31
61	BL	120	VAL	C-N-CA	5.92	130.14	121.31
5	AC	59	GLY	N-CA-C	-5.85	105.42	115.61
49	At	85	ASN	CA-C-N	5.80	132.62	121.54
49	At	85	ASN	C-N-CA	5.80	132.62	121.54
83	Bv	76	A	C2'-C3'-O3'	5.74	118.10	109.50
50	Au	80	VAL	CA-C-N	5.69	130.66	122.35
50	Au	80	VAL	C-N-CA	5.69	130.66	122.35
49	At	22	LYS	N-CA-CB	5.69	115.31	109.51
49	At	20	ARG	CA-C-N	5.64	132.31	121.54
49	At	20	ARG	C-N-CA	5.64	132.31	121.54
48	Aq	77	ALA	CA-C-N	5.59	132.22	121.54
48	Aq	77	ALA	C-N-CA	5.59	132.22	121.54
16	AK	20	LEU	N-CA-C	-5.58	106.26	112.57
1	AA	20	VAL	N-CA-CB	-5.57	105.87	112.39
22	AQ	159	PRO	CA-C-N	5.56	132.16	121.54
22	AQ	159	PRO	C-N-CA	5.56	132.16	121.54
52	B1	227	U	P-O3'-C3'	5.55	128.52	120.20
48	Aq	120	SER	N-CA-C	-5.48	107.84	114.75
11	AF	165	LYS	CA-CB-CG	5.42	124.95	114.10
85	A	19	ILE	CA-C-N	5.41	131.88	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	A	19	ILE	C-N-CA	5.41	131.88	121.54
52	B1	1756	C	P-O3'-C3'	5.39	128.29	120.20
67	BR	4	VAL	CA-C-N	5.39	131.83	121.54
67	BR	4	VAL	C-N-CA	5.39	131.83	121.54
50	Au	160	LYS	CB-CA-C	-5.38	110.36	116.54
16	AK	15	LEU	N-CA-C	-5.34	106.07	113.18
61	BL	24	LEU	N-CA-C	-5.33	107.33	113.88
10	AE	125	LEU	CA-C-N	5.24	131.55	121.54
10	AE	125	LEU	C-N-CA	5.24	131.55	121.54
16	AK	75	LEU	N-CA-C	-5.23	105.77	113.61
9	AD	228	LYS	CA-C-N	-5.16	115.39	121.90
9	AD	228	LYS	C-N-CA	-5.16	115.39	121.90
3	AB	292	LEU	CA-CB-CG	5.15	134.31	116.30
23	AR	23	TRP	N-CA-C	5.14	116.34	108.52
61	BL	121	GLN	N-CA-C	5.14	117.54	110.35
63	BN	82	PRO	CA-C-N	5.14	131.35	121.54
63	BN	82	PRO	C-N-CA	5.14	131.35	121.54
36	Ae	19	LYS	CA-CB-CG	5.10	124.31	114.10
52	B1	227	U	C2'-C3'-O3'	5.10	117.15	109.50
65	BP	125	PRO	N-CA-C	5.09	122.96	112.47
80	Be	45	VAL	N-CA-CB	-5.09	106.61	112.21
4	BB	175	GLU	CA-C-N	-5.08	117.73	122.66
4	BB	175	GLU	C-N-CA	-5.08	117.73	122.66
28	AW	60	LYS	N-CA-C	-5.07	100.01	110.80
20	AO	94	ARG	N-CA-C	-5.02	106.30	112.72
48	Aq	112	ILE	N-CA-C	-5.02	106.55	111.77
48	Aq	127	GLY	CA-C-N	5.01	127.24	120.38
48	Aq	127	GLY	C-N-CA	5.01	127.24	120.38

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	AD	228	LYS	Peptide
13	AH	116	ASN	Peptide
29	AX	79	PHE	Peptide
4	BB	39	PHE	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	1930	0	2030	67	0
2	BA	1704	0	1703	61	0
3	AB	3178	0	3314	82	0
4	BB	1722	0	1794	64	0
5	AC	2888	0	3064	92	0
6	BC	1724	0	1808	57	0
7	A3	3337	0	1692	38	0
8	A4	2541	0	1285	30	0
9	AD	2392	0	2425	76	0
10	AE	1571	0	1700	49	0
11	AF	1950	0	2093	23	0
12	AG	1880	0	2018	21	0
13	AH	1526	0	1605	29	0
14	AI	1692	0	1744	18	0
15	AJ	1353	0	1386	29	0
16	AK	872	0	916	79	0
17	AL	1657	0	1764	93	0
18	AM	1138	0	1204	14	0
19	AN	1701	0	1749	44	0
20	AO	1606	0	1745	25	0
21	AP	1242	0	1269	12	0
22	AQ	1513	0	1628	30	0
23	AR	1517	0	1670	23	0
24	AS	1449	0	1493	26	0
25	AT	1284	0	1352	21	0
26	AU	808	0	831	21	0
27	AV	969	0	1031	27	0
28	AW	989	0	1041	14	0
29	AX	958	0	1029	10	0
30	AY	1064	0	1145	13	0
31	AZ	1103	0	1179	10	0
32	Aa	1162	0	1212	21	0
33	Ab	559	0	590	31	0
34	Ac	801	0	845	33	0
35	Ad	879	0	924	9	0
36	Ae	1064	0	1160	13	0
37	Af	876	0	912	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	Ag	906	0	1002	12	0
39	Ah	1015	0	1148	33	0
40	Ai	794	0	870	8	0
41	Aj	689	0	717	32	0
42	Ak	569	0	637	9	0
43	Al	444	0	483	8	0
44	Am	411	0	443	7	0
45	An	240	0	289	6	0
46	Ao	863	0	929	11	0
47	Ap	708	0	757	7	0
48	Aq	1046	0	1116	60	0
49	At	980	0	1041	33	0
50	Au	1744	0	1859	59	0
51	A2	77427	0	39116	858	0
52	B1	36456	0	18411	403	0
53	BD	1709	0	1803	27	0
54	BE	2031	0	2138	32	0
55	BF	1502	0	1556	31	0
56	BG	1884	0	2044	34	0
57	BH	1479	0	1564	25	0
58	BI	1696	0	1784	43	0
59	BJ	1495	0	1615	52	0
60	BK	827	0	854	19	0
61	BL	1258	0	1334	17	0
62	BM	931	0	961	14	0
63	BN	1202	0	1289	16	0
64	BO	1016	0	1039	22	0
65	BP	999	0	1046	79	0
66	BQ	1109	0	1174	16	0
67	BR	1011	0	1063	20	0
68	BS	1154	0	1209	34	0
69	BT	1112	0	1146	25	0
70	BU	769	0	837	10	0
71	BV	617	0	622	6	0
72	BW	1034	0	1080	51	0
73	BX	1080	0	1147	37	0
74	BY	1015	0	1086	12	0
75	BZ	688	0	766	7	0
76	Ba	774	0	822	20	0
77	Bb	625	0	646	4	0
78	Bc	488	0	514	28	0
79	Bd	427	0	428	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	Be	437	0	483	7	0
81	Bf	601	0	623	10	0
82	Bg	2440	0	2396	43	0
83	Bv	1623	0	821	16	0
84	Bx	320	0	161	10	0
85	A	190	0	98	14	0
86	A2	226	0	0	0	0
86	A3	6	0	0	0	0
86	A4	9	0	0	0	0
86	AB	2	0	0	0	0
86	AP	1	0	0	0	0
86	AY	1	0	0	0	0
86	Aa	1	0	0	0	0
86	Ae	1	0	0	0	0
86	B1	75	0	0	0	0
86	BI	1	0	0	0	0
86	Ba	1	0	0	0	0
86	Bv	2	0	0	0	0
87	Aj	1	0	0	0	0
87	Ao	1	0	0	0	0
87	Ap	1	0	0	0	0
87	Ba	1	0	0	0	0
87	Bd	1	0	0	0	0
88	A2	31	0	0	7	0
All	All	216796	0	161317	3005	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 (3005) 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)
34:Ac:17:ARG:CB	34:Ac:104:ILE:HD11	1.27	1.53
17:AL:165:LYS:CE	51:A2:505:C:H5''	1.34	1.53
4:BB:30:TRP:CH2	4:BB:48:LEU:HD21	1.42	1.53
17:AL:165:LYS:HE3	51:A2:505:C:C5'	1.37	1.50
17:AL:133:ALA:HB2	17:AL:136:LYS:CE	1.43	1.49
4:BB:47:THR:C	4:BB:48:LEU:HD12	1.34	1.48
34:Ac:17:ARG:CB	34:Ac:104:ILE:CD1	1.91	1.47
59:BJ:136:ARG:CD	59:BJ:159:PHE:HA	1.41	1.46
4:BB:30:TRP:CZ2	4:BB:48:LEU:HD21	1.49	1.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:BP:50:ARG:CG	65:BP:52:LYS:HE3	1.46	1.45
59:BJ:138:ARG:HE	59:BJ:156:HIS:CD2	1.35	1.45
65:BP:50:ARG:HD2	65:BP:52:LYS:CE	1.44	1.44
3:AB:67:VAL:CG1	27:AV:91:LYS:HD2	1.48	1.43
1:AA:196:TRP:HB3	1:AA:197:PRO:CD	1.44	1.42
17:AL:165:LYS:CD	51:A2:505:C:H5''	1.51	1.41
39:Ah:87:LYS:NZ	41:Aj:78:PHE:CB	1.83	1.41
34:Ac:17:ARG:HB3	34:Ac:104:ILE:CD1	1.50	1.40
17:AL:165:LYS:CE	51:A2:505:C:C5'	1.92	1.40
39:Ah:87:LYS:NZ	41:Aj:78:PHE:HB2	1.27	1.38
10:AE:136:HIS:CD2	51:A2:702:A:C4'	2.05	1.37
48:Aq:16:ARG:NH1	48:Aq:58:ILE:HD12	1.34	1.37
64:BO:21:VAL:CG1	64:BO:22:ALA:H	1.31	1.36
17:AL:165:LYS:CD	51:A2:505:C:C5'	2.02	1.35
51:A2:4493:U:N1	85:A:39:PHE:CB	1.87	1.35
3:AB:67:VAL:HG13	27:AV:91:LYS:CD	1.57	1.32
17:AL:165:LYS:HD2	51:A2:505:C:O5'	1.16	1.31
48:Aq:16:ARG:HH12	48:Aq:58:ILE:CD1	1.42	1.30
39:Ah:87:LYS:HZ3	41:Aj:78:PHE:CB	1.35	1.30
51:A2:4493:U:C1'	85:A:39:PHE:CB	2.10	1.30
73:BX:139:GLU:OE2	73:BX:140:ARG:N	1.64	1.29
59:BJ:136:ARG:CD	59:BJ:158:ASP:O	1.80	1.28
50:Au:60:ARG:HB3	50:Au:61:PRO:CD	1.64	1.27
65:BP:50:ARG:CD	65:BP:52:LYS:HE3	1.63	1.27
49:At:17:LEU:CD1	49:At:36:ASN:ND2	1.97	1.27
15:AJ:56:THR:O	15:AJ:57:VAL:CG2	1.81	1.27
2:BA:208:GLU:OE2	2:BA:209:GLU:N	1.66	1.26
17:AL:133:ALA:CB	17:AL:136:LYS:CE	2.13	1.25
59:BJ:136:ARG:HD3	59:BJ:159:PHE:CA	1.65	1.25
17:AL:133:ALA:CB	17:AL:136:LYS:HE2	1.65	1.23
48:Aq:60:VAL:HG22	48:Aq:73:VAL:CG1	1.68	1.23
16:AK:72:ASN:HB3	16:AK:73:PRO:CD	1.66	1.23
81:Bf:88:PRO:O	81:Bf:89:LYS:HD2	1.37	1.23
37:Af:106:TYR:HB3	37:Af:107:PRO:CD	1.68	1.22
65:BP:68:PRO:HG2	65:BP:69:PRO:CD	1.68	1.22
73:BX:139:GLU:OE2	73:BX:140:ARG:HB2	1.39	1.21
15:AJ:56:THR:O	15:AJ:57:VAL:HG22	1.37	1.20
4:BB:30:TRP:CZ3	4:BB:48:LEU:HD11	1.75	1.20
2:BA:206:ASP:CG	2:BA:207:PRO:HD3	1.68	1.19
17:AL:47:ALA:CB	17:AL:48:PRO:CD	2.21	1.19
73:BX:139:GLU:OE2	73:BX:140:ARG:CB	1.90	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:At:17:LEU:HD11	49:At:36:ASN:ND2	1.56	1.18
17:AL:47:ALA:CB	17:AL:48:PRO:HD3	1.67	1.18
4:BB:48:LEU:O	64:BO:51:GLU:HG3	1.39	1.17
6:BC:256:TRP:CZ2	72:BW:68:ARG:CB	2.26	1.17
65:BP:50:ARG:CD	65:BP:52:LYS:CE	2.18	1.17
73:BX:139:GLU:OE2	73:BX:140:ARG:CA	1.93	1.17
5:AC:134:PRO:HG3	5:AC:150:LEU:CD1	1.75	1.17
65:BP:44:ARG:O	65:BP:48:GLY:N	1.78	1.16
4:BB:30:TRP:CZ2	4:BB:48:LEU:CD2	2.29	1.16
16:AK:101:MET:O	16:AK:105:ASN:HB2	1.43	1.15
65:BP:44:ARG:O	65:BP:48:GLY:CA	1.94	1.15
59:BJ:138:ARG:NE	59:BJ:156:HIS:CD2	2.15	1.15
10:AE:136:HIS:CD2	51:A2:702:A:H4'	1.71	1.15
1:AA:196:TRP:CB	1:AA:197:PRO:CD	2.21	1.14
25:AT:84:ILE:HD11	33:Ab:23:LYS:HE2	1.26	1.14
48:Aq:60:VAL:HG22	48:Aq:73:VAL:HG12	1.28	1.14
50:Au:31:THR:HB	50:Au:60:ARG:HH12	1.09	1.14
50:Au:31:THR:HB	50:Au:60:ARG:NH1	1.62	1.14
53:BD:116:ARG:NE	84:Bx:56:U:O4	1.81	1.13
6:BC:256:TRP:HZ2	72:BW:68:ARG:CB	1.60	1.13
5:AC:53:ALA:HB3	51:A2:344:C:H1'	1.25	1.13
17:AL:47:ALA:HB1	17:AL:48:PRO:CD	1.79	1.13
37:Af:106:TYR:CB	37:Af:107:PRO:HD3	1.79	1.13
48:Aq:21:GLU:HB3	48:Aq:50:THR:OG1	1.49	1.13
16:AK:72:ASN:CB	16:AK:73:PRO:HD3	1.78	1.12
6:BC:256:TRP:CZ2	72:BW:68:ARG:HB2	1.84	1.12
9:AD:8:LYS:HE2	9:AD:8:LYS:HA	1.25	1.12
39:Ah:87:LYS:HZ3	41:Aj:78:PHE:HB3	1.03	1.12
65:BP:68:PRO:HG2	65:BP:69:PRO:HD2	1.23	1.11
53:BD:218:LEU:H	53:BD:219:PRO:CD	1.63	1.11
1:AA:198:ARG:HH21	1:AA:198:ARG:HB2	1.11	1.11
4:BB:47:THR:O	4:BB:48:LEU:HD12	1.47	1.11
4:BB:30:TRP:CH2	4:BB:48:LEU:CD2	2.34	1.10
2:BA:43:SER:OG	67:BR:121:GLN:HB2	1.49	1.10
17:AL:165:LYS:HE3	51:A2:505:C:H5'	1.27	1.10
64:BO:21:VAL:HG12	64:BO:22:ALA:N	1.39	1.10
26:AU:60:VAL:O	26:AU:61:VAL:O	1.67	1.09
34:Ac:17:ARG:HB2	34:Ac:104:ILE:CD1	1.66	1.09
48:Aq:21:GLU:OE1	48:Aq:50:THR:HB	1.52	1.09
58:BI:132:GLU:HB3	58:BI:134:GLU:HG2	1.27	1.09
17:AL:165:LYS:HD2	51:A2:505:C:C5'	1.73	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AJ:56:THR:CG2	15:AJ:63:ARG:HA	1.82	1.08
59:BJ:136:ARG:CD	59:BJ:159:PHE:CA	2.28	1.08
17:AL:133:ALA:HB2	17:AL:136:LYS:HE2	1.21	1.08
1:AA:196:TRP:HB3	1:AA:197:PRO:HD2	1.07	1.07
5:AC:154:VAL:HG21	5:AC:158:VAL:HG21	1.35	1.06
1:AA:196:TRP:HB3	1:AA:197:PRO:HD3	1.33	1.06
17:AL:133:ALA:CA	17:AL:136:LYS:HE2	1.84	1.06
34:Ac:99:PRO:HG3	34:Ac:105:ILE:HD11	1.35	1.06
65:BP:44:ARG:O	65:BP:48:GLY:HA3	1.56	1.06
4:BB:47:THR:C	4:BB:48:LEU:CD1	2.28	1.05
17:AL:133:ALA:HB2	17:AL:136:LYS:HE3	1.12	1.05
59:BJ:136:ARG:HD3	59:BJ:159:PHE:HA	1.05	1.05
59:BJ:136:ARG:CG	59:BJ:158:ASP:O	2.05	1.04
16:AK:30:VAL:HG23	16:AK:102:LEU:HD11	1.37	1.03
6:BC:256:TRP:HE1	72:BW:68:ARG:CD	1.72	1.03
6:BC:256:TRP:CH2	72:BW:66:THR:HG21	1.93	1.03
51:A2:4493:U:C6	85:A:39:PHE:CB	2.40	1.03
17:AL:165:LYS:HD2	51:A2:505:C:P	1.99	1.03
17:AL:130:LYS:HB3	17:AL:131:PRO:HD2	1.40	1.02
17:AL:165:LYS:CD	51:A2:505:C:O5'	2.01	1.02
51:A2:4347:A:N6	83:Bv:76:A:OP1	1.93	1.02
9:AD:9:ASN:OD1	9:AD:12:TYR:CG	2.12	1.02
6:BC:256:TRP:NE1	72:BW:68:ARG:HD3	1.75	1.01
10:AE:136:HIS:HD2	51:A2:702:A:H4'	0.99	1.01
59:BJ:136:ARG:HD3	59:BJ:158:ASP:O	1.59	1.01
59:BJ:138:ARG:NH2	59:BJ:156:HIS:NE2	2.08	1.01
19:AN:71:ARG:HD2	19:AN:94:PHE:HB2	1.43	1.01
65:BP:68:PRO:CG	65:BP:69:PRO:CD	2.39	1.01
15:AJ:56:THR:HG21	15:AJ:63:ARG:HA	1.43	1.01
51:A2:1871:G:H1	51:A2:1920:A:N6	1.59	1.01
5:AC:53:ALA:CB	51:A2:344:C:H1'	1.91	1.00
48:Aq:21:GLU:OE1	48:Aq:50:THR:CB	2.09	1.00
59:BJ:136:ARG:HD2	59:BJ:159:PHE:HA	1.38	1.00
50:Au:60:ARG:HB3	50:Au:61:PRO:HD3	1.03	1.00
65:BP:50:ARG:HD2	65:BP:52:LYS:HE2	1.00	1.00
2:BA:206:ASP:HB3	2:BA:207:PRO:HD2	1.41	1.00
10:AE:203:ILE:O	10:AE:206:VAL:HG23	1.61	1.00
3:AB:67:VAL:HG13	27:AV:91:LYS:HD2	1.05	0.99
16:AK:82:ILE:HG22	51:A2:2003:C:OP1	1.62	0.99
65:BP:50:ARG:CG	65:BP:52:LYS:CE	2.40	0.99
37:Af:46:ARG:HD2	37:Af:106:TYR:HD2	1.22	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BA:206:ASP:CB	2:BA:207:PRO:CD	2.40	0.99
51:A2:4703:C:H42	51:A2:4917:U:H3	1.04	0.99
4:BB:30:TRP:CZ3	4:BB:48:LEU:HD21	1.96	0.98
17:AL:165:LYS:CE	51:A2:505:C:H5'	1.82	0.98
37:Af:106:TYR:CB	37:Af:107:PRO:CD	2.34	0.98
2:BA:85:ARG:HH12	2:BA:205:ARG:HB2	1.24	0.98
3:AB:67:VAL:HG11	27:AV:91:LYS:HD2	1.41	0.98
65:BP:50:ARG:HG3	65:BP:52:LYS:HE3	1.42	0.98
15:AJ:56:THR:O	15:AJ:57:VAL:HG23	1.63	0.98
17:AL:133:ALA:CB	17:AL:136:LYS:HE3	1.86	0.98
52:B1:1396:A:H2	52:B1:1449:G:N1	1.62	0.97
59:BJ:138:ARG:HE	59:BJ:156:HIS:CG	1.81	0.97
49:At:17:LEU:HD11	49:At:36:ASN:HD22	1.11	0.97
51:A2:455:G:H1	51:A2:687:A:H2	1.05	0.97
2:BA:206:ASP:HB3	2:BA:207:PRO:CD	1.94	0.97
5:AC:134:PRO:CG	5:AC:150:LEU:HD11	1.94	0.97
2:BA:208:GLU:CD	2:BA:209:GLU:H	1.71	0.97
51:A2:4493:U:C2	85:A:39:PHE:CB	2.48	0.97
10:AE:136:HIS:HD2	51:A2:702:A:C4'	1.55	0.97
51:A2:2431:G:H21	51:A2:2486:A:H62	1.01	0.96
2:BA:81:ASN:O	2:BA:204:TYR:CE1	2.17	0.96
1:AA:196:TRP:CZ3	51:A2:1595:A:C2	2.53	0.96
52:B1:1324:G:H1	52:B1:1504:U:H3	0.96	0.95
83:Bv:76:A:O3'	85:A:39:PHE:C	2.09	0.95
17:AL:130:LYS:HB3	17:AL:131:PRO:CD	1.96	0.95
1:AA:196:TRP:CB	1:AA:197:PRO:HD3	1.90	0.95
2:BA:208:GLU:CD	2:BA:209:GLU:N	2.24	0.95
16:AK:24:TYR:CD1	16:AK:90:PHE:CD2	2.54	0.95
17:AL:170:THR:O	17:AL:174:LYS:NZ	1.99	0.95
6:BC:256:TRP:HE1	72:BW:68:ARG:HD3	1.29	0.95
51:A2:4493:U:O4'	85:A:39:PHE:CB	2.14	0.95
16:AK:79:LEU:HG	16:AK:83:ARG:HH12	1.29	0.95
51:A2:161:G:H1	51:A2:266:U:H3	0.97	0.95
3:AB:67:VAL:HG13	27:AV:91:LYS:CE	1.96	0.94
1:AA:196:TRP:CG	1:AA:197:PRO:HD3	2.02	0.94
4:BB:49:VAL:HG13	4:BB:65:ARG:HH22	1.31	0.94
51:A2:465:A:H62	51:A2:677:G:N2	1.64	0.94
48:Aq:21:GLU:CB	48:Aq:50:THR:OG1	2.15	0.94
2:BA:206:ASP:CG	2:BA:207:PRO:CD	2.41	0.94
5:AC:134:PRO:HG3	5:AC:150:LEU:HD12	1.47	0.94
15:AJ:56:THR:C	15:AJ:57:VAL:HG23	1.92	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:BB:30:TRP:CE2	4:BB:48:LEU:HD21	2.02	0.93
39:Ah:87:LYS:NZ	41:Aj:78:PHE:O	2.01	0.93
5:AC:53:ALA:HB2	51:A2:344:C:O2	1.68	0.93
52:B1:1396:A:C2	52:B1:1449:G:N1	2.34	0.93
51:A2:1871:G:H1	51:A2:1920:A:H61	1.08	0.92
65:BP:68:PRO:HG2	65:BP:69:PRO:HD3	1.48	0.92
59:BJ:136:ARG:HD3	59:BJ:158:ASP:C	1.93	0.92
34:Ac:17:ARG:CB	34:Ac:104:ILE:HD13	1.99	0.92
65:BP:68:PRO:CB	65:BP:69:PRO:HD3	1.99	0.92
5:AC:134:PRO:CG	5:AC:150:LEU:CD1	2.46	0.92
16:AK:30:VAL:CG2	16:AK:102:LEU:HD11	1.98	0.92
78:Bc:12:ALA:HB1	78:Bc:32:VAL:HB	1.51	0.92
51:A2:465:A:H62	51:A2:677:G:H21	1.02	0.92
49:At:17:LEU:CD1	49:At:36:ASN:HD22	1.71	0.92
53:BD:218:LEU:N	53:BD:219:PRO:HD2	1.84	0.92
78:Bc:16:LYS:HD3	78:Bc:31:ARG:NH2	1.83	0.92
9:AD:259:LYS:HG3	9:AD:261:VAL:CG2	1.98	0.92
37:Af:106:TYR:HB3	37:Af:107:PRO:HD3	0.92	0.92
2:BA:208:GLU:OE2	2:BA:209:GLU:CA	2.17	0.91
17:AL:47:ALA:HB1	17:AL:48:PRO:HD3	0.93	0.91
59:BJ:136:ARG:HG2	59:BJ:159:PHE:HB3	1.52	0.91
1:AA:200:ARG:NH1	51:A2:3661:U:OP2	2.02	0.91
2:BA:208:GLU:O	2:BA:211:GLU:N	2.03	0.91
15:AJ:56:THR:C	15:AJ:57:VAL:CG2	2.43	0.91
52:B1:1050:A:H62	52:B1:1068:G:N2	1.67	0.91
26:AU:49:VAL:HG11	26:AU:59:GLY:HA3	1.50	0.91
49:At:17:LEU:CD1	49:At:36:ASN:HD21	1.83	0.91
50:Au:60:ARG:CB	50:Au:61:PRO:HD3	1.99	0.91
65:BP:68:PRO:CG	65:BP:69:PRO:HD3	2.00	0.91
16:AK:4:GLU:HG2	16:AK:6:ARG:H	1.32	0.90
59:BJ:136:ARG:HG3	59:BJ:158:ASP:O	1.68	0.90
51:A2:4703:C:N4	51:A2:4917:U:H3	1.69	0.90
37:Af:46:ARG:HD2	37:Af:106:TYR:CD2	2.06	0.90
59:BJ:136:ARG:NE	59:BJ:158:ASP:O	2.03	0.90
65:BP:68:PRO:HB2	65:BP:69:PRO:HD3	1.51	0.90
48:Aq:59:THR:HG21	48:Aq:74:VAL:C	1.97	0.90
51:A2:724:A:H62	51:A2:918:C:H42	1.18	0.90
17:AL:165:LYS:HD3	51:A2:505:C:H5"	1.54	0.89
65:BP:51:ARG:O	65:BP:54:HIS:N	2.04	0.89
1:AA:198:ARG:HB2	1:AA:198:ARG:NH2	1.87	0.89
4:BB:47:THR:O	4:BB:48:LEU:CD1	2.18	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:AD:256:LYS:HG2	9:AD:257:PRO:HD2	1.55	0.88
53:BD:218:LEU:N	53:BD:219:PRO:CD	2.32	0.88
16:AK:101:MET:O	16:AK:105:ASN:CB	2.21	0.88
17:AL:47:ALA:HB3	17:AL:48:PRO:CD	2.03	0.88
48:Aq:60:VAL:HG22	48:Aq:73:VAL:HG11	1.54	0.88
51:A2:465:A:N6	51:A2:677:G:H21	1.71	0.88
2:BA:205:ARG:NH2	67:BR:84:TYR:CD2	2.40	0.87
48:Aq:60:VAL:CG2	48:Aq:73:VAL:HG12	2.04	0.87
1:AA:200:ARG:O	1:AA:203:ALA:N	2.07	0.87
16:AK:25:PRO:O	16:AK:26:LYS:HB2	1.71	0.87
52:B1:1050:A:H62	52:B1:1068:G:H21	0.91	0.87
15:AJ:56:THR:CG2	15:AJ:63:ARG:CA	2.51	0.87
5:AC:134:PRO:CA	5:AC:150:LEU:HD11	2.04	0.86
16:AK:24:TYR:CD1	16:AK:90:PHE:HD2	1.92	0.86
10:AE:208:ILE:HD12	10:AE:209:PRO:HD2	1.55	0.86
49:At:17:LEU:HD12	49:At:36:ASN:ND2	1.87	0.86
53:BD:218:LEU:H	53:BD:219:PRO:HD2	1.36	0.86
51:A2:1083:U:H3	51:A2:1178:G:H1	1.21	0.86
6:BC:256:TRP:CZ2	72:BW:68:ARG:CG	2.58	0.86
65:BP:68:PRO:CG	65:BP:69:PRO:HD2	2.00	0.86
6:BC:256:TRP:CZ3	72:BW:66:THR:HG21	2.11	0.86
19:AN:71:ARG:CD	19:AN:94:PHE:HB2	2.06	0.86
6:BC:256:TRP:CZ2	72:BW:68:ARG:HG2	2.11	0.85
59:BJ:136:ARG:HD3	59:BJ:159:PHE:N	1.89	0.85
9:AD:8:LYS:HA	9:AD:8:LYS:CE	2.02	0.85
16:AK:72:ASN:HB3	16:AK:73:PRO:HD3	0.87	0.85
51:A2:455:G:N1	51:A2:687:A:C2	2.43	0.85
15:AJ:56:THR:HG23	15:AJ:63:ARG:CA	2.06	0.85
5:AC:150:LEU:CB	5:AC:151:PRO:HD3	2.05	0.85
50:Au:23:ARG:O	50:Au:24:LYS:C	2.19	0.85
65:BP:50:ARG:HG2	65:BP:52:LYS:HE3	1.54	0.85
17:AL:130:LYS:HD2	17:AL:130:LYS:N	1.88	0.85
69:BT:81:GLY:HA3	69:BT:93:SER:O	1.76	0.85
13:AH:4:ILE:HG23	13:AH:61:TRP:CZ3	2.11	0.85
52:B1:1050:A:N6	52:B1:1068:G:H21	1.74	0.84
59:BJ:136:ARG:CG	59:BJ:158:ASP:C	2.49	0.84
52:B1:1396:A:H2	52:B1:1449:G:H1	0.91	0.84
9:AD:259:LYS:HG3	9:AD:261:VAL:HG23	1.59	0.84
9:AD:9:ASN:OD1	9:AD:12:TYR:CB	2.24	0.84
50:Au:59:PRO:HG3	50:Au:152:LYS:O	1.78	0.84
58:BI:132:GLU:HB3	58:BI:134:GLU:CG	2.08	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:BP:68:PRO:CB	65:BP:69:PRO:CD	2.56	0.84
6:BC:256:TRP:HZ2	72:BW:68:ARG:HB3	1.39	0.84
59:BJ:136:ARG:CD	59:BJ:158:ASP:C	2.50	0.84
65:BP:50:ARG:CD	65:BP:52:LYS:HE2	1.95	0.84
2:BA:81:ASN:O	2:BA:204:TYR:HE1	1.58	0.84
34:Ac:17:ARG:HD2	34:Ac:103:ASP:OD1	1.76	0.84
68:BS:90:VAL:C	68:BS:92:ASP:H	1.86	0.83
78:Bc:16:LYS:CD	78:Bc:31:ARG:NH2	2.40	0.83
51:A2:2431:G:N2	51:A2:2486:A:H62	1.76	0.83
78:Bc:12:ALA:CB	78:Bc:32:VAL:HB	2.08	0.83
17:AL:133:ALA:HA	17:AL:136:LYS:HE2	1.59	0.83
6:BC:256:TRP:HZ2	72:BW:68:ARG:CG	1.90	0.83
3:AB:67:VAL:CG1	27:AV:91:LYS:CD	2.32	0.83
51:A2:1977:C:N4	51:A2:1981:G:H22	1.77	0.82
81:Bf:88:PRO:C	81:Bf:89:LYS:HD2	2.04	0.82
78:Bc:16:LYS:CD	78:Bc:31:ARG:HH22	1.92	0.82
4:BB:30:TRP:CE2	4:BB:48:LEU:CD2	2.63	0.82
13:AH:5:LEU:HB3	13:AH:60:TRP:CZ3	2.15	0.82
48:Aq:21:GLU:OE1	48:Aq:50:THR:CG2	2.28	0.82
51:A2:1977:C:H42	51:A2:1981:G:N2	1.78	0.82
26:Au:56:LEU:HD11	26:Au:61:VAL:CB	2.00	0.82
50:Au:60:ARG:CB	50:Au:61:PRO:CD	2.52	0.82
4:BB:30:TRP:CZ3	4:BB:48:LEU:CD1	2.59	0.81
50:Au:44:GLN:OE1	50:Au:161:LYS:NZ	2.12	0.81
51:A2:724:A:H62	51:A2:918:C:N4	1.78	0.81
5:AC:218:ILE:O	5:AC:222:ARG:HB2	1.79	0.81
58:BI:158:ILE:HD11	58:BI:163:GLU:HG2	1.62	0.81
17:AL:63:THR:HG21	32:Aa:66:ASN:ND2	1.96	0.81
17:AL:171:GLU:O	17:AL:173:GLU:N	2.13	0.81
26:Au:59:GLY:O	26:Au:61:VAL:N	2.13	0.81
25:AT:84:ILE:HD11	33:Ab:23:LYS:CE	2.07	0.81
50:Au:59:PRO:O	50:Au:61:PRO:HD2	1.79	0.81
3:AB:63:PRO:HA	3:AB:68:ASN:ND2	1.95	0.81
51:A2:2462:G:H1	51:A2:2474:U:H3	1.29	0.81
73:BX:139:GLU:CD	73:BX:140:ARG:N	2.39	0.81
4:BB:48:LEU:O	64:BO:51:GLU:CG	2.27	0.80
5:AC:134:PRO:N	5:AC:150:LEU:HD11	1.97	0.80
48:Aq:21:GLU:O	48:Aq:23:GLY:N	2.15	0.80
51:A2:4234:G:N1	51:A2:4298:A:C2	2.49	0.80
9:AD:262:LYS:NZ	9:AD:262:LYS:H	1.78	0.80
16:AK:24:TYR:CE1	16:AK:90:PHE:CD2	2.69	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:Ab:28:ARG:HH11	33:Ab:28:ARG:HG3	1.47	0.80
83:Bv:76:A:HO3'	85:A:39:PHE:C	1.84	0.80
65:BP:18:ARG:NH2	68:BS:89:ASP:OD2	2.06	0.80
2:BA:85:ARG:HG2	2:BA:204:TYR:HA	1.62	0.80
39:Ah:87:LYS:HZ2	41:Aj:78:PHE:HB2	0.91	0.80
3:AB:67:VAL:CG2	27:AV:14:PHE:HZ	1.94	0.80
51:A2:4433:U:H3	51:A2:4446:G:H1	1.30	0.80
5:AC:154:VAL:CG2	5:AC:158:VAL:HG21	2.13	0.79
16:AK:65:ILE:O	16:AK:69:LEU:HB2	1.83	0.79
51:A2:2431:G:H21	51:A2:2486:A:N6	1.81	0.79
52:B1:924:G:H1	52:B1:1018:U:H3	1.28	0.79
64:BO:21:VAL:CG1	64:BO:22:ALA:N	2.03	0.79
5:AC:48:ASN:ND2	51:A2:1353:G:OP1	2.13	0.79
16:AK:82:ILE:CG2	51:A2:2003:C:OP1	2.31	0.79
16:AK:79:LEU:HG	16:AK:83:ARG:NH1	1.98	0.79
50:Au:67:VAL:HA	50:Au:111:LEU:O	1.83	0.79
1:AA:196:TRP:HZ3	51:A2:1595:A:C2	1.98	0.78
22:AQ:11:ARG:HG2	22:AQ:11:ARG:HH11	1.48	0.78
10:AE:208:ILE:HD12	10:AE:209:PRO:CD	2.14	0.78
17:AL:165:LYS:HE3	51:A2:505:C:H5''	0.99	0.78
53:BD:218:LEU:H	53:BD:219:PRO:HD3	1.46	0.78
1:AA:196:TRP:HZ3	51:A2:1595:A:N3	1.82	0.78
1:AA:196:TRP:CD2	1:AA:197:PRO:HD3	2.19	0.78
16:AK:69:LEU:HD12	16:AK:71:ASN:H	1.48	0.78
1:AA:200:ARG:O	1:AA:202:VAL:N	2.16	0.78
17:AL:49:ARG:NH1	39:Ah:118:LYS:HA	1.99	0.78
34:Ac:17:ARG:HB2	34:Ac:104:ILE:HD12	1.62	0.78
16:AK:25:PRO:O	16:AK:26:LYS:CB	2.32	0.77
16:AK:48:ARG:HA	16:AK:51:ALA:HB2	1.66	0.77
2:BA:203:PHE:O	2:BA:204:TYR:HB2	1.83	0.77
17:AL:49:ARG:HH12	39:Ah:118:LYS:HA	1.48	0.77
16:AK:102:LEU:C	16:AK:104:ALA:H	1.91	0.77
51:A2:4493:U:H1'	85:A:39:PHE:CB	2.15	0.77
59:BJ:138:ARG:HH21	59:BJ:156:HIS:CD2	2.03	0.76
25:AT:84:ILE:CD1	33:Ab:23:LYS:HE2	2.10	0.76
48:Aq:50:THR:O	48:Aq:54:LYS:HB3	1.84	0.76
5:AC:150:LEU:HB3	5:AC:151:PRO:HD3	1.68	0.76
51:A2:3936:A:H61	51:A2:4015:G:H21	1.32	0.76
52:B1:885:U:H3	52:B1:901:G:H1	1.32	0.76
4:BB:30:TRP:CE3	4:BB:48:LEU:HD11	2.20	0.76
4:BB:47:THR:CA	4:BB:48:LEU:HD12	2.15	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AH:5:LEU:HB3	13:AH:60:TRP:CE3	2.21	0.76
8:A4:116:G:P	9:AD:255:LYS:NZ	2.59	0.76
34:Ac:103:ASP:HB3	34:Ac:106:ARG:NH1	2.00	0.76
51:A2:478:U:H3	51:A2:665:G:H22	1.32	0.76
1:AA:196:TRP:CB	1:AA:197:PRO:HD2	1.97	0.76
48:Aq:16:ARG:CZ	48:Aq:58:ILE:HD12	2.16	0.75
6:BC:256:TRP:NE1	72:BW:68:ARG:CD	2.42	0.75
10:AE:154:THR:HG21	37:Af:106:TYR:HE1	1.51	0.75
2:BA:85:ARG:NH1	2:BA:205:ARG:HB2	1.99	0.75
6:BC:256:TRP:CZ2	72:BW:68:ARG:HB3	2.17	0.75
39:Ah:87:LYS:HZ2	41:Aj:78:PHE:CB	1.71	0.75
50:Au:163:LEU:O	50:Au:164:CYS:HB2	1.85	0.75
1:AA:198:ARG:HH21	1:AA:198:ARG:CB	1.98	0.75
50:Au:159:MET:O	50:Au:159:MET:HG2	1.85	0.75
52:B1:1611:G:O2'	68:BS:87:GLN:HB2	1.86	0.75
5:AC:148:PRO:O	49:At:73:PRO:HD2	1.87	0.75
2:BA:42:LYS:HB2	2:BA:46:ILE:O	1.87	0.75
33:Ab:23:LYS:HG3	33:Ab:24:PRO:CD	2.17	0.74
51:A2:1576:C:H41	88:A2:5327:MVM:C4	1.99	0.74
50:Au:21:ASN:O	50:Au:22:GLN:HB2	1.88	0.74
33:Ab:28:ARG:HG3	33:Ab:28:ARG:NH1	2.00	0.74
2:BA:43:SER:OG	67:BR:121:GLN:CB	2.35	0.74
65:BP:49:LEU:HD22	65:BP:49:LEU:N	2.02	0.74
26:AU:60:VAL:O	26:AU:61:VAL:C	2.31	0.74
53:BD:42:THR:HB	53:BD:45:ARG:O	1.87	0.74
17:AL:42:LYS:O	17:AL:46:ILE:HG13	1.88	0.74
5:AC:53:ALA:HB2	51:A2:344:C:C2	2.23	0.73
49:At:28:GLU:OE1	49:At:31:ASN:ND2	2.21	0.73
51:A2:4715:U:H3	51:A2:4837:C:N4	1.86	0.73
2:BA:85:ARG:NH1	2:BA:205:ARG:H	1.86	0.73
5:AC:134:PRO:HG3	5:AC:150:LEU:HD11	1.55	0.73
9:AD:259:LYS:CG	9:AD:261:VAL:HG23	2.18	0.73
17:AL:47:ALA:HB3	17:AL:48:PRO:HD2	1.69	0.73
51:A2:3936:A:H61	51:A2:4015:G:N2	1.85	0.73
8:A4:116:G:OP2	9:AD:255:LYS:NZ	2.21	0.73
9:AD:235:MET:O	9:AD:239:MET:HB2	1.89	0.73
16:AK:72:ASN:CB	16:AK:73:PRO:CD	2.43	0.73
5:AC:53:ALA:CB	51:A2:344:C:O2	2.36	0.73
39:Ah:87:LYS:NZ	41:Aj:78:PHE:HB3	1.74	0.73
81:Bf:87:THR:N	81:Bf:88:PRO:HD3	2.04	0.73
34:Ac:17:ARG:HG3	34:Ac:104:ILE:HD13	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:Bc:16:LYS:HD3	78:Bc:31:ARG:CZ	2.18	0.73
51:A2:4849:G:H1	51:A2:4886:C:H42	1.34	0.72
52:B1:31:U:OP1	73:BX:137:LYS:HE3	1.88	0.72
59:BJ:136:ARG:CG	59:BJ:159:PHE:HA	2.19	0.72
51:A2:724:A:N6	51:A2:918:C:H42	1.87	0.72
52:B1:1650:A:H62	52:B1:1674:G:H21	1.38	0.72
48:Aq:16:ARG:NH1	48:Aq:58:ILE:CD1	2.17	0.72
16:AK:18:ILE:HD12	16:AK:68:HIS:CD2	2.23	0.72
51:A2:4715:U:N3	51:A2:4837:C:N4	2.37	0.72
9:AD:263:LYS:HB3	9:AD:265:ARG:NH2	2.04	0.72
51:A2:455:G:N1	51:A2:687:A:H2	1.82	0.72
9:AD:263:LYS:HB3	9:AD:265:ARG:HH21	1.54	0.72
10:AE:153:LEU:HD13	37:Af:105:LEU:O	1.90	0.72
16:AK:2:PRO:O	16:AK:3:ARG:HB2	1.89	0.72
3:AB:66:LYS:HG2	3:AB:66:LYS:O	1.90	0.71
59:BJ:138:ARG:HG2	59:BJ:138:ARG:HH11	1.55	0.71
16:AK:69:LEU:HD12	16:AK:69:LEU:C	2.14	0.71
54:BE:89:VAL:HG13	54:BE:98:HIS:HE1	1.55	0.71
33:Ab:23:LYS:HG3	33:Ab:24:PRO:HD2	1.73	0.71
5:AC:50:GLN:HB3	5:AC:51:PRO:HD2	1.72	0.71
17:AL:126:LEU:HD11	17:AL:135:LYS:HB2	1.73	0.70
1:AA:200:ARG:HG2	1:AA:200:ARG:HH11	1.56	0.70
82:Bg:87:LEU:HB2	82:Bg:101:PHE:HB2	1.72	0.70
9:AD:262:LYS:HD3	9:AD:262:LYS:N	2.06	0.70
52:B1:528:A:N7	52:B1:558:G:N2	2.40	0.70
33:Ab:23:LYS:CG	33:Ab:24:PRO:HD2	2.21	0.70
26:AU:49:VAL:HG21	26:AU:56:LEU:HG	1.73	0.70
34:Ac:17:ARG:CG	34:Ac:104:ILE:HD13	2.20	0.70
52:B1:377:G:H5''	58:BI:98:LYS:HB3	1.74	0.70
10:AE:209:PRO:HB2	10:AE:212:LEU:HD22	1.73	0.70
58:BI:132:GLU:O	58:BI:134:GLU:HG2	1.92	0.70
8:A4:116:G:P	9:AD:255:LYS:HZ1	2.13	0.69
9:AD:263:LYS:CB	9:AD:265:ARG:HH21	2.05	0.69
59:BJ:136:ARG:HG2	59:BJ:159:PHE:CB	2.21	0.69
65:BP:50:ARG:HG3	65:BP:52:LYS:HG3	1.74	0.69
3:AB:67:VAL:HG13	27:AV:91:LYS:HE3	1.74	0.69
69:BT:77:LYS:HE2	69:BT:94:ARG:HE	1.56	0.69
68:BS:90:VAL:CG2	68:BS:93:GLY:H	2.06	0.69
69:BT:81:GLY:O	69:BT:92:PHE:HA	1.93	0.69
3:AB:247:GLY:HA2	51:A2:2817:G:H5'	1.74	0.69
49:At:28:GLU:OE2	49:At:41:ASN:ND2	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:BS:90:VAL:O	68:BS:92:ASP:N	2.25	0.69
15:AJ:54:ARG:HG2	15:AJ:54:ARG:HH11	1.58	0.69
65:BP:50:ARG:HG3	65:BP:52:LYS:CE	2.18	0.68
59:BJ:138:ARG:CZ	59:BJ:156:HIS:CD2	2.75	0.68
50:Au:59:PRO:CG	50:Au:152:LYS:O	2.40	0.68
52:B1:442:C:H42	52:B1:449:A:H62	1.39	0.68
52:B1:925:G:H1	52:B1:1017:U:H3	1.40	0.68
59:BJ:37:LEU:HD23	59:BJ:42:GLU:HG3	1.75	0.68
5:AC:134:PRO:CD	5:AC:150:LEU:HD11	2.24	0.68
51:A2:904:A:N3	51:A2:905:G:N2	2.40	0.68
51:A2:1084:C:N4	51:A2:1178:G:N3	2.42	0.68
51:A2:1289:C:H2'	51:A2:1290:A:H8	1.58	0.68
14:AI:185:VAL:HG12	14:AI:190:LEU:HB2	1.75	0.67
51:A2:3726:G:N1	51:A2:3741:U:N3	2.40	0.67
64:BO:21:VAL:HG12	64:BO:22:ALA:H	0.54	0.67
5:AC:134:PRO:CD	5:AC:150:LEU:CD1	2.73	0.67
51:A2:123:C:H42	51:A2:144:A:H61	1.39	0.67
51:A2:3936:A:N6	51:A2:4015:G:H21	1.92	0.67
48:Aq:21:GLU:OE1	48:Aq:50:THR:HG21	1.92	0.67
52:B1:875:A:N6	52:B1:912:C:N4	2.41	0.67
7:A3:109:C:H3'	41:Aj:20:ARG:HH22	1.59	0.67
6:BC:256:TRP:HE1	72:BW:68:ARG:CG	2.08	0.67
52:B1:1144:A:H5'	52:B1:1355:C:H41	1.59	0.67
34:Ac:17:ARG:HB3	34:Ac:104:ILE:HD11	0.69	0.67
5:AC:154:VAL:HG21	5:AC:158:VAL:CG2	2.19	0.67
16:AK:102:LEU:HD23	16:AK:102:LEU:O	1.95	0.67
17:AL:63:THR:O	17:AL:65:ARG:N	2.28	0.67
59:BJ:136:ARG:HG3	59:BJ:158:ASP:C	2.16	0.67
5:AC:134:PRO:CB	5:AC:150:LEU:HD11	2.24	0.66
48:Aq:59:THR:HG21	48:Aq:75:PRO:N	2.09	0.66
51:A2:4854:G:H22	51:A2:4883:U:H1'	1.60	0.66
57:BH:37:LYS:O	57:BH:41:ARG:HB2	1.94	0.66
78:Bc:32:VAL:O	78:Bc:33:GLU:HG3	1.96	0.66
15:AJ:56:THR:HG21	15:AJ:63:ARG:CA	2.20	0.66
52:B1:1101:U:H2'	52:B1:1102:G:H8	1.58	0.66
3:AB:174:ARG:HH12	51:A2:4932:C:H4'	1.61	0.66
9:AD:260:GLU:C	9:AD:262:LYS:HD3	2.21	0.66
4:BB:48:LEU:HD12	4:BB:48:LEU:N	2.07	0.66
6:BC:256:TRP:CE2	72:BW:68:ARG:HG2	2.31	0.66
9:AD:9:ASN:OD1	9:AD:12:TYR:CD2	2.49	0.66
58:BI:158:ILE:CD1	58:BI:163:GLU:N	2.58	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:Aj:46:LYS:NZ	51:A2:24:G:N7	2.44	0.66
52:B1:1735:A:H62	52:B1:1799:G:H21	1.44	0.66
6:BC:171:GLY:HA2	72:BW:98:GLN:HE22	1.60	0.65
21:AP:80:GLN:NE2	51:A2:3863:U:O2'	2.29	0.65
50:Au:67:VAL:HG22	50:Au:111:LEU:HB2	1.79	0.65
51:A2:2464:U:H3	51:A2:2472:G:H1	1.44	0.65
52:B1:1300:U:C4	65:BP:51:ARG:HD3	2.31	0.65
5:AC:71:ARG:HD2	85:A:25:GLY:O	1.96	0.65
28:AW:61:LYS:H	28:AW:64:SER:HB3	1.60	0.65
3:AB:63:PRO:HA	3:AB:68:ASN:HD22	1.61	0.65
17:AL:63:THR:HG21	32:Aa:66:ASN:HD21	1.60	0.65
34:Ac:17:ARG:CG	34:Ac:104:ILE:CD1	2.74	0.65
52:B1:1280:G:H1	52:B1:1317:C:H42	1.43	0.65
55:BF:63:LYS:HG2	55:BF:71:ARG:HH12	1.62	0.65
16:AK:102:LEU:O	16:AK:104:ALA:N	2.29	0.65
19:AN:49:ARG:NH2	51:A2:150:G:OP2	2.30	0.65
68:BS:90:VAL:C	68:BS:92:ASP:N	2.55	0.65
22:AQ:11:ARG:HG2	22:AQ:11:ARG:NH1	2.10	0.65
59:BJ:138:ARG:NH2	59:BJ:156:HIS:CD2	2.63	0.65
52:B1:380:G:OP1	58:BI:56:ARG:NH2	2.30	0.65
11:AF:232:ASP:OD1	11:AF:236:ARG:NH2	2.29	0.65
20:AO:6:VAL:HA	20:AO:32:LYS:O	1.97	0.65
83:Bv:51:U:H3	83:Bv:63:G:H1	1.43	0.65
51:A2:4951:G:H1	51:A2:5016:A:H61	1.43	0.65
11:AF:116:GLN:HE22	11:AF:212:LYS:HE3	1.62	0.64
16:AK:69:LEU:HD12	16:AK:71:ASN:N	2.11	0.64
17:AL:42:LYS:O	17:AL:46:ILE:CG1	2.45	0.64
58:BI:158:ILE:CD1	58:BI:163:GLU:HG2	2.28	0.64
16:AK:71:ASN:O	16:AK:73:PRO:HD2	1.97	0.64
65:BP:65:LYS:C	65:BP:67:ALA:H	2.05	0.64
25:AT:8:ARG:NH2	51:A2:4295:C:O2	2.28	0.64
22:AQ:11:ARG:HB2	51:A2:2062:C:H4'	1.79	0.64
78:Bc:60:GLU:HG2	78:Bc:62:GLU:H	1.62	0.64
24:AS:81:TRP:HB3	24:AS:127:MET:HE3	1.80	0.64
58:BI:160:SER:O	58:BI:163:GLU:N	2.31	0.64
24:AS:98:ARG:NH2	51:A2:737:A:N1	2.45	0.64
52:B1:1152:U:H1'	72:BW:16:ASN:HD21	1.62	0.64
71:BV:59:ILE:HG23	71:BV:64:GLU:HB3	1.78	0.64
5:AC:132:ALA:O	5:AC:150:LEU:HD13	1.97	0.64
10:AE:154:THR:HG21	37:Af:106:TYR:CE1	2.32	0.64
16:AK:69:LEU:CD1	16:AK:71:ASN:H	2.11	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AR:133:LYS:H	23:AR:137:ILE:HD11	1.63	0.64
52:B1:186:C:H2'	52:B1:187:G:H8	1.63	0.64
1:AA:198:ARG:HG3	1:AA:198:ARG:O	1.98	0.64
16:AK:69:LEU:HD12	16:AK:71:ASN:HB2	1.79	0.64
26:AU:56:LEU:HD11	26:AU:61:VAL:HB	1.80	0.64
73:BX:139:GLU:CD	73:BX:140:ARG:H	2.01	0.64
74:BY:110:ARG:NH1	74:BY:125:VAL:O	2.31	0.64
34:Ac:107:SER:HB3	34:Ac:108:MET:SD	2.38	0.64
48:Aq:21:GLU:C	48:Aq:23:GLY:H	2.06	0.64
22:AQ:65:ARG:NH2	51:A2:1441:A:OP1	2.31	0.63
33:Ab:41:ARG:NH1	51:A2:1474:G:O2'	2.31	0.63
51:A2:4535:G:N2	51:A2:4684:G:OP2	2.31	0.63
3:AB:59:GLU:HB2	3:AB:366:LYS:HE3	1.78	0.63
51:A2:904:A:N7	51:A2:907:C:N4	2.46	0.63
55:BF:21:GLY:H	55:BF:23:TRP:HD1	1.47	0.63
3:AB:2:SER:N	51:A2:4482:G:N7	2.46	0.63
51:A2:63:G:H21	51:A2:64:A:H62	1.47	0.63
51:A2:4062:G:H3'	51:A2:4063:G:H21	1.63	0.63
51:A2:4854:G:N7	51:A2:4882:C:N4	2.46	0.63
73:BX:132:ALA:O	73:BX:137:LYS:HB2	1.98	0.63
14:AI:14:ASN:ND2	51:A2:1845:G:OP2	2.31	0.63
48:Aq:21:GLU:HG3	48:Aq:22:VAL:HG13	1.80	0.63
51:A2:1083:U:O2	51:A2:1178:G:N2	2.22	0.63
68:BS:87:GLN:OE1	68:BS:87:GLN:HA	1.99	0.63
39:Ah:87:LYS:HZ3	41:Aj:78:PHE:CA	2.11	0.63
78:Bc:32:VAL:HG11	78:Bc:56:LEU:HB3	1.81	0.63
3:AB:292:LEU:HD13	3:AB:293:ILE:HG13	1.80	0.63
34:Ac:45:LEU:HG	34:Ac:105:ILE:HG23	1.78	0.63
2:BA:85:ARG:HH11	2:BA:205:ARG:H	1.46	0.63
16:AK:69:LEU:CD1	16:AK:71:ASN:HB2	2.28	0.63
52:B1:1143:A:O3'	52:B1:1355:C:N4	2.32	0.63
56:BG:142:ARG:HH22	56:BG:149:LYS:HA	1.64	0.63
1:AA:196:TRP:CZ3	51:A2:1595:A:N3	2.63	0.63
6:BC:171:GLY:HA2	72:BW:98:GLN:NE2	2.13	0.63
24:AS:82:LEU:HB2	24:AS:93:MET:HB3	1.80	0.63
50:Au:57:SER:O	50:Au:58:THR:HG22	1.99	0.63
64:BO:34:PHE:HB3	64:BO:41:PHE:HB2	1.80	0.63
65:BP:24:GLN:O	65:BP:28:MET:HB2	1.99	0.63
65:BP:50:ARG:HH11	65:BP:52:LYS:CE	2.11	0.63
24:AS:101:THR:HG23	24:AS:104:GLY:H	1.64	0.63
41:Aj:36:LYS:HE2	41:Aj:57:ASN:HD21	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BA:208:GLU:O	2:BA:209:GLU:C	2.42	0.62
9:AD:262:LYS:H	9:AD:262:LYS:HZ3	1.43	0.62
50:AU:21:ASN:HD22	50:AU:22:GLN:NE2	1.97	0.62
52:B1:392:A:O2'	61:BL:83:GLN:NE2	2.32	0.62
52:B1:1610:G:N2	68:BS:85:ASN:OD1	2.31	0.62
7:A3:63:U:O2'	39:Ah:52:LYS:NZ	2.32	0.62
51:A2:1576:C:C5	88:A2:5327:MVM:N2	2.66	0.62
58:BI:113:TYR:O	58:BI:117:TYR:HB2	1.99	0.62
59:BJ:136:ARG:CG	59:BJ:159:PHE:CA	2.75	0.62
4:BB:123:ALA:HB3	4:BB:139:CYS:HB3	1.81	0.62
16:AK:102:LEU:C	16:AK:104:ALA:N	2.57	0.62
2:BA:45:GLY:O	2:BA:46:ILE:HD13	1.99	0.62
3:AB:63:PRO:CA	3:AB:68:ASN:ND2	2.62	0.62
12:AG:166:LEU:HD21	19:AN:45:PRO:HG2	1.82	0.62
48:Aq:60:VAL:CG1	48:Aq:71:ILE:HG22	2.29	0.62
52:B1:879:C:H3'	52:B1:880:G:H21	1.64	0.62
5:AC:51:PRO:O	5:AC:111:TRP:CZ2	2.52	0.62
72:BW:68:ARG:NH1	72:BW:68:ARG:O	2.31	0.62
18:AM:6:PHE:O	18:AM:11:ARG:NH1	2.32	0.62
55:BF:71:ARG:NH2	55:BF:148:ASN:OD1	2.32	0.62
2:BA:203:PHE:O	2:BA:204:TYR:CB	2.45	0.62
51:A2:3726:G:N2	51:A2:3741:U:O2	2.32	0.62
54:BE:141:THR:HG22	54:BE:143:ASP:H	1.64	0.62
51:A2:455:G:O6	51:A2:687:A:N1	2.32	0.62
54:BE:198:ARG:HH12	54:BE:200:ARG:HH11	1.48	0.62
63:BN:20:ARG:HH21	72:BW:56:HIS:HE1	1.47	0.62
36:Ae:22:ARG:HE	36:Ae:36:ARG:HB3	1.65	0.62
51:A2:2001:U:H2'	51:A2:2002:G:H8	1.64	0.62
51:A2:2474:U:H2'	51:A2:2475:G:H8	1.65	0.62
67:BR:97:GLU:HA	67:BR:117:LEU:HD23	1.81	0.62
2:BA:42:LYS:HD3	2:BA:48:ILE:HD11	1.80	0.62
2:BA:68:ILE:HD13	2:BA:120:ARG:HH11	1.65	0.62
13:AH:5:LEU:HD12	13:AH:5:LEU:O	2.00	0.62
25:AT:9:ARG:NH2	51:A2:4180:U:OP2	2.32	0.62
27:AV:48:ARG:NH1	51:A2:4583:C:OP1	2.33	0.62
58:BI:130:THR:HB	58:BI:131:PRO:HD2	1.80	0.62
65:BP:49:LEU:O	65:BP:49:LEU:HD23	2.00	0.62
82:Bg:163:PRO:HB2	82:Bg:179:LEU:HB2	1.82	0.62
5:AC:150:LEU:CB	5:AC:151:PRO:CD	2.76	0.61
21:AP:10:ASN:HD21	21:AP:13:LYS:HE2	1.65	0.61
48:Aq:103:ASN:ND2	48:Aq:141:CYS:SG	2.73	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:A2:4234:G:N1	51:A2:4298:A:H2	1.96	0.61
51:A2:4234:G:H1	51:A2:4298:A:H2	1.39	0.61
52:B1:190:G:O2'	52:B1:209:A:N6	2.33	0.61
56:BG:69:THR:HG22	56:BG:71:GLY:H	1.65	0.61
48:Aq:60:VAL:HG13	48:Aq:71:ILE:HG22	1.81	0.61
52:B1:1094:C:OP1	72:BW:28:ARG:NH2	2.33	0.61
65:BP:50:ARG:HH11	65:BP:52:LYS:NZ	1.97	0.61
10:AE:203:ILE:O	10:AE:206:VAL:CG2	2.42	0.61
28:AW:96:GLN:O	28:AW:101:ARG:NH1	2.34	0.61
64:BO:145:GLY:O	76:Ba:22:ARG:NH1	2.33	0.61
72:BW:102:ILE:HB	72:BW:113:HIS:HB2	1.82	0.61
22:AQ:18:PRO:HG3	22:AQ:29:VAL:HG21	1.80	0.61
50:Au:111:LEU:HB3	50:Au:138:LEU:HD11	1.81	0.61
65:BP:85:ILE:HD11	65:BP:116:LEU:HD21	1.82	0.61
3:AB:246:ARG:NH2	51:A2:4520:U:OP2	2.33	0.61
5:AC:195:LYS:NZ	51:A2:2313:C:OP2	2.32	0.61
51:A2:920:G:N2	51:A2:925:C:O2'	2.33	0.61
59:BJ:136:ARG:HH11	59:BJ:160:SER:H	1.47	0.61
67:BR:66:VAL:HG12	67:BR:68:GLY:H	1.64	0.61
4:BB:30:TRP:HZ3	4:BB:48:LEU:HD11	1.58	0.61
42:Ak:24:LYS:HD3	42:Ak:69:LEU:HD11	1.83	0.61
69:BT:70:ALA:HB3	69:BT:121:ARG:HE	1.65	0.61
8:A4:14:C:OP1	9:AD:24:ARG:NH1	2.34	0.61
65:BP:18:ARG:NH1	68:BS:89:ASP:HB2	2.14	0.61
9:AD:259:LYS:CG	9:AD:261:VAL:CG2	2.77	0.61
52:B1:649:U:H2'	52:B1:650:A:H8	1.64	0.61
33:Ab:21:ILE:HG22	33:Ab:21:ILE:O	2.01	0.61
51:A2:162:A:H61	51:A2:265:C:H42	1.48	0.61
6:BC:256:TRP:NE1	72:BW:68:ARG:CG	2.64	0.61
10:AE:136:HIS:CD2	51:A2:702:A:O2'	2.51	0.61
19:AN:71:ARG:HD2	19:AN:94:PHE:CB	2.26	0.61
51:A2:1955:U:C4	51:A2:1983:A:N7	2.68	0.61
52:B1:454:U:H5''	56:BG:94:ARG:HG2	1.82	0.61
1:AA:200:ARG:C	1:AA:202:VAL:N	2.58	0.60
2:BA:206:ASP:CB	2:BA:207:PRO:HD2	2.15	0.60
3:AB:26:ARG:NH1	3:AB:181:MET:SD	2.74	0.60
3:AB:253:CYS:SG	51:A2:4482:G:N2	2.74	0.60
45:An:23:ARG:NH1	51:A2:3778:A:OP1	2.33	0.60
52:B1:1300:U:C4	65:BP:51:ARG:CD	2.84	0.60
52:B1:1854:U:H2'	52:B1:1855:G:H8	1.64	0.60
51:A2:2618:U:HO2'	51:A2:2673:G:H1	1.49	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:BP:30:TYR:HA	65:BP:33:LEU:HG	1.82	0.60
4:BB:82:ARG:NH2	4:BB:188:LEU:O	2.34	0.60
9:AD:7:VAL:O	9:AD:7:VAL:HG12	2.00	0.60
9:AD:93:THR:O	9:AD:158:LYS:NZ	2.35	0.60
11:AF:76:ARG:HD3	51:A2:719:U:H5''	1.83	0.60
15:AJ:167:GLN:HE21	15:AJ:174:ILE:HG13	1.65	0.60
16:AK:18:ILE:CD1	16:AK:68:HIS:CD2	2.84	0.60
17:AL:63:THR:C	17:AL:65:ARG:N	2.58	0.60
41:Aj:13:ASN:ND2	51:A2:1600:G:OP1	2.34	0.60
52:B1:1450:G:H5''	67:BR:33:ARG:HH22	1.66	0.60
52:B1:1748:G:H1	52:B1:1786:U:H3	1.48	0.60
72:BW:98:GLN:OE1	72:BW:98:GLN:HA	1.99	0.60
3:AB:282:LYS:NZ	3:AB:336:CYS:O	2.35	0.60
16:AK:102:LEU:C	16:AK:102:LEU:HD23	2.26	0.60
32:Aa:132:ARG:NH2	51:A2:1450:C:OP1	2.34	0.60
35:Ad:28:ASN:HD22	35:Ad:31:LYS:HZ2	1.48	0.60
51:A2:2756:G:H5''	51:A2:2757:G:H5'	1.82	0.60
74:BY:29:HIS:HE1	74:BY:35:VAL:HG23	1.66	0.60
78:Bc:29:GLN:HE22	78:Bc:67:ARG:HB2	1.65	0.60
3:AB:56:ILE:HD12	3:AB:76:VAL:HG21	1.83	0.60
18:AM:132:LYS:NZ	51:A2:4853:C:OP1	2.34	0.60
49:At:27:THR:O	49:At:27:THR:HG22	2.02	0.60
50:Au:139:THR:HB	50:Au:142:GLU:HB2	1.84	0.60
51:A2:3663:A:H62	51:A2:3794:G:H21	1.50	0.60
51:A2:3758:G:H21	51:A2:3760:C:H42	1.47	0.60
52:B1:104:A:OP1	58:BI:12:ARG:NH1	2.34	0.60
52:B1:1396:A:N1	52:B1:1449:G:O6	2.34	0.60
52:B1:1659:U:H5'	79:Bd:30:LEU:HD13	1.83	0.60
60:BK:4:PRO:HG2	60:BK:7:ASN:HB2	1.84	0.60
82:Bg:195:LEU:HA	82:Bg:211:GLY:HA3	1.81	0.60
25:AT:88:ARG:NH2	33:Ab:33:LYS:O	2.35	0.60
32:Aa:44:ASN:O	32:Aa:48:TYR:HB2	2.02	0.60
16:AK:83:ARG:HG3	51:A2:2003:C:H5'	1.83	0.60
34:Ac:51:ASN:ND2	34:Ac:77:ASN:OD1	2.35	0.60
51:A2:294:A:H2'	51:A2:295:G:H8	1.66	0.60
51:A2:447:G:O6	51:A2:1277:A:N6	2.34	0.60
65:BP:111:MET:HG2	68:BS:117:ILE:HG23	1.83	0.60
29:AX:91:GLU:HG3	29:AX:147:LEU:HD21	1.83	0.60
38:Ag:76:ARG:NH2	51:A2:2562:C:OP2	2.29	0.60
51:A2:1955:U:O4	51:A2:1983:A:N7	2.35	0.60
59:BJ:110:LEU:HB2	59:BJ:147:PHE:HB3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AK:78:LEU:HD23	16:AK:79:LEU:H	1.66	0.60
52:B1:1615:U:OP2	65:BP:43:ARG:NH2	2.35	0.60
3:AB:53:MET:HG2	3:AB:77:THR:HG22	1.83	0.59
50:Au:23:ARG:O	50:Au:25:ARG:N	2.35	0.59
50:Au:163:LEU:HB2	51:A2:4025:U:O2'	2.02	0.59
51:A2:1176:C:H2'	51:A2:1177:G:H8	1.67	0.59
52:B1:1171:G:N2	52:B1:1188:A:OP2	2.35	0.59
52:B1:1565:C:OP2	69:BT:101:ARG:NH1	2.35	0.59
6:BC:256:TRP:NE1	72:BW:68:ARG:HG2	2.17	0.59
8:A4:6:C:H4'	9:AD:52:ILE:HD13	1.84	0.59
10:AE:186:LEU:HD13	10:AE:250:GLN:HG2	1.85	0.59
33:Ab:28:ARG:HH11	33:Ab:28:ARG:CG	2.14	0.59
76:Ba:20:PRO:HB2	76:Ba:29:CYS:HB2	1.84	0.59
76:Ba:88:SER:H	76:Ba:91:ALA:HB3	1.67	0.59
5:AC:150:LEU:HB2	5:AC:151:PRO:HD3	1.81	0.59
7:A3:96:C:H5'	39:Ah:66:LYS:HE3	1.83	0.59
7:A3:122:G:N2	7:A3:129:C:O2'	2.35	0.59
17:AL:64:VAL:HG12	51:A2:71:C:H5'	1.85	0.59
52:B1:575:A:OP1	74:BY:93:ARG:NH1	2.34	0.59
9:AD:263:LYS:CB	9:AD:265:ARG:HE	2.15	0.59
10:AE:188:ARG:NH1	10:AE:214:ASP:OD1	2.35	0.59
46:Ao:3:ASN:HB3	51:A2:4194:U:H5'	1.84	0.59
51:A2:484:C:H2'	51:A2:485:G:H8	1.66	0.59
59:BJ:138:ARG:NE	59:BJ:156:HIS:CG	2.59	0.59
5:AC:143:ARG:NH1	51:A2:2279:A:N7	2.50	0.59
7:A3:58:G:O6	41:Aj:63:ARG:NH2	2.35	0.59
19:AN:96:ARG:NH1	51:A2:29:G:O2'	2.36	0.59
30:AY:59:ARG:HH12	51:A2:196:G:H2'	1.67	0.59
38:Ag:40:LYS:HD2	38:Ag:52:ARG:HH21	1.68	0.59
40:Ai:82:ARG:HH12	51:A2:277:G:H1'	1.66	0.59
41:Aj:75:ARG:NH2	51:A2:338:A:OP1	2.34	0.59
52:B1:650:A:OP2	73:BX:107:ARG:NH1	2.35	0.59
52:B1:1351:G:H1	52:B1:1360:U:H3	1.48	0.59
69:BT:71:GLY:H	69:BT:74:SER:HB2	1.67	0.59
45:An:2:ARG:NH2	52:B1:1841:C:OP2	2.36	0.59
51:A2:4355:G:N2	51:A2:4358:A:OP2	2.35	0.59
52:B1:973:C:O2	64:BO:55:ARG:NH2	2.35	0.59
52:B1:1280:G:H2'	52:B1:1281:G:H8	1.66	0.59
72:BW:75:ILE:HD12	72:BW:125:ILE:HG21	1.84	0.59
1:AA:117:GLU:HB2	1:AA:162:ASN:HB2	1.85	0.59
65:BP:114:HIS:ND1	65:BP:118:GLU:OE1	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:Ab:23:LYS:HG3	33:Ab:24:PRO:HD3	1.84	0.59
51:A2:4698:C:H2'	51:A2:4699:G:H8	1.68	0.59
52:B1:15:U:O2'	52:B1:669:A:N6	2.35	0.59
56:BG:137:ARG:HG3	56:BG:178:ARG:HG3	1.84	0.59
4:BB:30:TRP:CZ3	4:BB:48:LEU:CD2	2.74	0.59
34:Ac:47:ILE:HB	34:Ac:94:LEU:HB2	1.85	0.59
2:BA:81:ASN:O	2:BA:204:TYR:CD1	2.56	0.59
17:AL:65:ARG:NH2	51:A2:1365:G:OP1	2.36	0.59
24:AS:74:ARG:HH12	51:A2:909:C:H4'	1.68	0.59
51:A2:1679:G:N2	51:A2:2065:C:OP1	2.36	0.59
59:BJ:136:ARG:HG2	59:BJ:159:PHE:CA	2.33	0.59
72:BW:94:LEU:HD12	72:BW:97:ARG:HH12	1.68	0.59
16:AK:103:LEU:O	16:AK:104:ALA:HB2	2.02	0.58
50:Au:25:ARG:NH1	50:Au:26:ARG:O	2.36	0.58
50:Au:201:VAL:HG11	50:Au:204:LEU:HD23	1.83	0.58
51:A2:704:C:H2'	51:A2:705:G:H8	1.68	0.58
52:B1:234:C:H2'	52:B1:235:A:H8	1.67	0.58
52:B1:797:C:O2	52:B1:798:G:N2	2.36	0.58
9:AD:262:LYS:NZ	9:AD:262:LYS:O	2.35	0.58
9:AD:263:LYS:HA	9:AD:263:LYS:HE3	1.84	0.58
25:AT:82:GLY:O	33:Ab:21:ILE:HD13	2.03	0.58
49:At:87:ARG:NH1	51:A2:682:U:OP1	2.36	0.58
52:B1:162:C:O3'	56:BG:95:LYS:NZ	2.36	0.58
42:Ak:20:ALA:HA	42:Ak:38:CYS:HA	1.84	0.58
49:At:26:SER:HB3	49:At:36:ASN:HA	1.86	0.58
50:Au:59:PRO:O	50:Au:61:PRO:CD	2.51	0.58
51:A2:132:G:O6	51:A2:136:G:N2	2.36	0.58
51:A2:404:A:O2'	51:A2:408:C:O2'	2.21	0.58
52:B1:24:C:OP1	59:BJ:11:LYS:NZ	2.37	0.58
59:BJ:138:ARG:HH11	59:BJ:138:ARG:CG	2.14	0.58
60:BK:65:ARG:NH2	79:Bd:21:CYS:O	2.36	0.58
65:BP:34:MET:HG3	65:BP:45:LEU:HD13	1.85	0.58
1:AA:158:ILE:HD12	1:AA:162:ASN:HD21	1.68	0.58
3:AB:37:PRO:HA	3:AB:188:GLY:HA2	1.86	0.58
4:BB:36:PRO:HD3	4:BB:98:THR:HG23	1.84	0.58
9:AD:166:ALA:HB1	9:AD:171:LEU:HD12	1.84	0.58
16:AK:18:ILE:CD1	16:AK:68:HIS:HD2	2.16	0.58
34:Ac:29:LEU:HD22	34:Ac:91:VAL:HG21	1.85	0.58
50:Au:42:ASP:H	50:Au:47:LYS:HD2	1.69	0.58
51:A2:2590:A:H5'	51:A2:2667:G:H4'	1.84	0.58
51:A2:4730:G:H1	51:A2:4822:U:H3	1.49	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:B1:913:A:OP2	57:BH:99:ARG:NH1	2.37	0.58
53:BD:25:LEU:O	53:BD:29:LEU:HB2	2.02	0.58
74:BY:105:LYS:O	74:BY:109:GLU:HB2	2.03	0.58
4:BB:173:THR:O	4:BB:177:GLN:HB3	2.03	0.58
17:AL:135:LYS:O	17:AL:136:LYS:HB3	2.04	0.58
48:Aq:31:LYS:HE3	48:Aq:39:PRO:HD3	1.86	0.58
51:A2:1576:C:N4	88:A2:5327:MVM:N2	2.52	0.58
65:BP:68:PRO:HB2	65:BP:69:PRO:CD	2.26	0.58
1:AA:174:ARG:NH2	51:A2:3655:G:OP1	2.37	0.58
2:BA:79:SER:O	2:BA:84:GLN:NE2	2.36	0.58
15:AJ:21:CYS:SG	51:A2:4221:C:O2'	2.60	0.58
30:AY:8:THR:O	51:A2:223:G:N2	2.37	0.58
50:Au:163:LEU:O	50:Au:164:CYS:CB	2.52	0.58
51:A2:1149:G:N3	51:A2:1150:C:O2'	2.35	0.58
51:A2:1576:C:H5	88:A2:5327:MVM:N2	2.02	0.58
1:AA:181:LYS:NZ	51:A2:1559:G:OP2	2.37	0.58
4:BB:49:VAL:HG13	4:BB:65:ARG:NH2	2.11	0.58
8:A4:75:G:N2	8:A4:100:A:OP2	2.36	0.58
40:Ai:65:LYS:HG3	40:Ai:67:LYS:H	1.68	0.58
68:BS:90:VAL:HG23	68:BS:93:GLY:H	1.67	0.58
81:Bf:105:TYR:HB3	81:Bf:116:ARG:HH12	1.68	0.58
3:AB:67:VAL:CG2	27:AV:14:PHE:CZ	2.81	0.58
16:AK:4:GLU:O	16:AK:6:ARG:N	2.36	0.58
48:Aq:40:LYS:HD3	48:Aq:41:LYS:HG3	1.84	0.58
50:Au:59:PRO:HG3	50:Au:153:SER:HA	1.86	0.58
5:AC:304:ALA:O	22:AQ:38:ARG:NH1	2.37	0.58
9:AD:259:LYS:HG3	9:AD:261:VAL:HG21	1.84	0.58
10:AE:279:ASN:HB2	51:A2:4715:U:H5	1.69	0.58
18:AM:34:ASN:ND2	51:A2:1905:C:OP1	2.37	0.58
48:Aq:58:ILE:HG22	48:Aq:75:PRO:HB3	1.86	0.58
48:Aq:143:VAL:O	48:Aq:144:ASP:HB2	2.03	0.58
49:At:19:LYS:HG2	49:At:24:THR:HG22	1.85	0.58
51:A2:894:C:H2'	51:A2:895:G:H8	1.68	0.58
51:A2:1498:G:H2'	51:A2:1500:A:H62	1.69	0.58
51:A2:2586:C:H2'	51:A2:2587:G:H8	1.69	0.58
15:AJ:111:GLU:OE1	68:BS:14:ARG:NH2	2.35	0.57
22:AQ:11:ARG:O	22:AQ:11:ARG:HG3	2.02	0.57
34:Ac:21:VAL:HG11	34:Ac:96:ILE:HD12	1.85	0.57
51:A2:1981:G:H5''	51:A2:1982:G:H5'	1.86	0.57
53:BD:106:ARG:HG3	53:BD:175:VAL:HG22	1.85	0.57
58:BI:130:THR:HB	58:BI:131:PRO:CD	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:BT:75:MET:SD	69:BT:121:ARG:NH1	2.77	0.57
2:BA:42:LYS:NZ	2:BA:48:ILE:HD11	2.19	0.57
18:AM:42:CYS:SG	18:AM:78:GLN:NE2	2.77	0.57
19:AN:169:ARG:NH1	51:A2:63:G:OP2	2.37	0.57
30:AY:56:GLN:HE21	30:AY:65:GLN:H	1.52	0.57
49:At:63:VAL:HG22	49:At:79:ARG:HG2	1.85	0.57
51:A2:2314:C:H2'	51:A2:2315:G:H8	1.69	0.57
52:B1:1261:C:O2	79:Bd:10:HIS:NE2	2.28	0.57
52:B1:1544:C:O2'	66:BQ:80:GLN:NE2	2.37	0.57
52:B1:923:G:OP1	63:BN:2:GLY:N	2.37	0.57
57:BH:50:GLU:OE2	57:BH:90:LYS:NZ	2.36	0.57
73:BX:132:ALA:CA	73:BX:137:LYS:HB2	2.33	0.57
80:Be:51:LYS:HZ2	84:Bx:58:U:H5	1.49	0.57
2:BA:85:ARG:NH1	2:BA:205:ARG:N	2.51	0.57
6:BC:230:THR:HG21	52:B1:4:C:H5'	1.86	0.57
17:AL:133:ALA:HB1	17:AL:136:LYS:CG	2.35	0.57
50:Au:50:SER:HA	50:Au:157:PHE:O	2.04	0.57
51:A2:2466:G:N2	51:A2:2469:U:O4	2.38	0.57
58:BI:132:GLU:OE1	58:BI:132:GLU:HA	2.03	0.57
1:AA:144:LYS:HB3	1:AA:160:SER:HB3	1.86	0.57
6:BC:194:ARG:NH1	52:B1:1156:U:O4	2.37	0.57
19:AN:201:HIS:CD2	19:AN:203:TYR:H	2.22	0.57
48:Aq:78:SER:HA	48:Aq:81:ILE:HG22	1.86	0.57
53:BD:163:PRO:O	53:BD:167:TYR:HB2	2.04	0.57
6:BC:252:THR:HG23	6:BC:255:LEU:HB2	1.86	0.57
6:BC:256:TRP:CE2	72:BW:68:ARG:CG	2.87	0.57
7:A3:15:G:H1'	51:A2:414:A:H61	1.68	0.57
11:AF:80:ASN:HD21	25:AT:142:ARG:HA	1.68	0.57
19:AN:8:GLN:NE2	51:A2:273:A:OP2	2.33	0.57
52:B1:67:C:OP2	56:BG:172:LYS:NZ	2.38	0.57
52:B1:370:G:O2'	58:BI:10:LYS:NZ	2.37	0.57
17:AL:11:LYS:H	22:AQ:168:ARG:HH22	1.51	0.57
33:Ab:5:LYS:NZ	51:A2:1854:A:OP2	2.34	0.57
51:A2:445:C:N4	51:A2:1278:C:N3	2.52	0.57
65:BP:50:ARG:HG2	65:BP:50:ARG:HH11	1.69	0.57
72:BW:94:LEU:CD1	72:BW:97:ARG:HH12	2.17	0.57
51:A2:3919:C:H2'	51:A2:3920:A:H8	1.69	0.57
56:BG:142:ARG:NH1	56:BG:152:ASP:OD1	2.37	0.57
68:BS:43:VAL:HG22	69:BT:37:VAL:HG21	1.87	0.57
1:AA:2:GLY:N	51:A2:4147:G:OP1	2.38	0.57
1:AA:196:TRP:CE3	1:AA:197:PRO:HD3	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:AQ:13:VAL:O	51:A2:1673:G:H5''	2.04	0.57
23:AR:99:MET:HE3	23:AR:103:ARG:HH11	1.70	0.57
50:Au:57:SER:C	50:Au:58:THR:CG2	2.78	0.57
51:A2:2304:C:H2'	51:A2:2305:G:H8	1.69	0.57
80:Be:51:LYS:NZ	84:Bx:58:U:H5	2.03	0.57
5:AC:54:VAL:HG12	5:AC:56:GLU:HB2	1.86	0.57
10:AE:187:ARG:HE	51:A2:4899:G:H4'	1.70	0.57
51:A2:1912:C:N4	51:A2:2021:A:O2'	2.38	0.57
51:A2:2026:G:N2	51:A2:2027:G:N7	2.52	0.57
51:A2:3612:U:OP2	51:A2:3617:A:N6	2.38	0.57
53:BD:116:ARG:CB	84:Bx:57:U:O4	2.53	0.57
63:BN:13:GLN:OE1	77:Bb:21:LYS:NZ	2.36	0.57
52:B1:305:U:O2'	58:BI:41:ARG:NH1	2.38	0.56
52:B1:582:U:H2'	52:B1:583:A:H8	1.70	0.56
52:B1:1076:G:OP2	63:BN:107:LYS:NZ	2.36	0.56
54:BE:80:VAL:HG13	54:BE:81:THR:HG23	1.87	0.56
1:AA:133:TYR:HB3	1:AA:168:VAL:HG12	1.87	0.56
10:AE:283:PRO:O	10:AE:284:HIS:ND1	2.38	0.56
25:AT:55:LYS:NZ	51:A2:4179:G:OP1	2.37	0.56
55:BF:103:LEU:HD22	55:BF:178:ILE:HD13	1.86	0.56
55:BF:127:ARG:HG2	55:BF:134:VAL:HG11	1.86	0.56
60:BK:1:MET:O	60:BK:47:LYS:NZ	2.38	0.56
65:BP:49:LEU:HD22	65:BP:49:LEU:H	1.67	0.56
6:BC:60:TRP:HE1	6:BC:92:GLU:HB2	1.69	0.56
13:AH:92:MET:HG2	13:AH:181:VAL:HA	1.87	0.56
17:AL:42:LYS:NZ	51:A2:107:G:OP2	2.39	0.56
22:AQ:3:VAL:HG21	51:A2:2256:C:H5'	1.88	0.56
22:AQ:37:ARG:NH1	51:A2:2067:G:OP2	2.38	0.56
52:B1:523:A:OP1	59:BJ:127:ARG:NH2	2.37	0.56
52:B1:1854:U:OP1	64:BO:150:ARG:NH1	2.39	0.56
55:BF:76:MET:O	55:BF:159:ARG:NH2	2.38	0.56
41:Aj:56:ARG:NH2	51:A2:369:G:N7	2.53	0.56
52:B1:677:G:H21	52:B1:1028:A:H62	1.54	0.56
55:BF:126:THR:OG1	78:Bc:26:GLN:NE2	2.39	0.56
63:BN:21:SER:HA	63:BN:65:PHE:HB3	1.87	0.56
66:BQ:13:PHE:N	66:BQ:13:PHE:CD1	2.73	0.56
8:A4:116:G:P	9:AD:255:LYS:HZ3	2.28	0.56
9:AD:8:LYS:HE2	9:AD:8:LYS:CA	2.18	0.56
15:AJ:35:ARG:HD3	15:AJ:123:ILE:HA	1.87	0.56
16:AK:77:LYS:O	16:AK:81:HIS:HB2	2.06	0.56
24:AS:160:ARG:HE	24:AS:163:HIS:HB3	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:A2:4692:C:H1'	51:A2:4693:G:H2'	1.87	0.56
52:B1:95:G:OP1	54:BE:10:LYS:NZ	2.39	0.56
52:B1:1822:A:H3'	52:B1:1823:A:H2'	1.88	0.56
62:BM:32:ALA:HB3	62:BM:110:VAL:HB	1.88	0.56
68:BS:84:LEU:HD22	68:BS:97:GLN:HB2	1.87	0.56
5:AC:134:PRO:CG	5:AC:150:LEU:HD12	2.21	0.56
51:A2:963:G:H1	51:A2:1261:C:H42	1.53	0.56
52:B1:801:U:H2'	52:B1:802:A:H8	1.70	0.56
54:BE:45:ILE:O	54:BE:49:ARG:HB3	2.04	0.56
85:A:8:GLN:O	85:A:12:ALA:HB2	2.05	0.56
9:AD:263:LYS:HB3	9:AD:265:ARG:HE	1.71	0.56
9:AD:263:LYS:HB3	9:AD:265:ARG:NE	2.19	0.56
24:AS:127:MET:HA	25:AT:153:PRO:HG2	1.88	0.56
32:Aa:2:PRO:HG2	51:A2:1491:C:H5''	1.88	0.56
51:A2:1838:C:H2'	51:A2:1839:A:H8	1.70	0.56
51:A2:2372:C:OP2	51:A2:2373:G:N2	2.38	0.56
52:B1:71:G:OP2	52:B1:72:C:N4	2.39	0.56
52:B1:1102:G:H1	52:B1:1130:G:H22	1.53	0.56
52:B1:1862:G:O6	76:Ba:34:LYS:NZ	2.38	0.56
2:BA:85:ARG:NH2	67:BR:82:ASP:O	2.39	0.56
35:Ad:32:ARG:NH1	51:A2:4954:C:OP1	2.34	0.56
42:Ak:60:LEU:HD22	42:Ak:61:PRO:HD2	1.88	0.56
51:A2:4150:U:H2'	51:A2:4151:U:H6	1.70	0.56
52:B1:126:G:H5'	56:BG:195:LYS:HD2	1.87	0.56
73:BX:94:ILE:HG12	73:BX:125:VAL:HG21	1.88	0.56
82:Bg:44:LYS:HG3	82:Bg:56:GLN:HG3	1.88	0.56
5:AC:153:VAL:O	5:AC:153:VAL:HG12	2.05	0.56
9:AD:21:ARG:HA	9:AD:24:ARG:HH21	1.71	0.56
28:AW:6:CYS:HG	28:AW:9:SER:HG	1.51	0.56
28:AW:80:ARG:HA	28:AW:87:LEU:HD21	1.88	0.56
38:Ag:60:ARG:HD3	38:Ag:61:PRO:HD2	1.87	0.56
38:Ag:63:VAL:HG13	38:Ag:66:ARG:HH21	1.70	0.56
48:Aq:16:ARG:HG2	48:Aq:58:ILE:O	2.06	0.56
50:Au:161:LYS:HG3	50:Au:161:LYS:O	2.04	0.56
51:A2:2499:C:H5	51:A2:2514:G:H22	1.54	0.56
52:B1:1566:G:N7	69:BT:101:ARG:NH2	2.53	0.56
9:AD:263:LYS:HB3	9:AD:265:ARG:CZ	2.36	0.56
22:AQ:144:LYS:HA	22:AQ:149:TYR:HD2	1.71	0.56
51:A2:2390:C:H2'	51:A2:2391:A:H8	1.71	0.56
51:A2:2576:G:H1	51:A2:2727:C:H5	1.52	0.56
52:B1:434:G:OP2	58:BI:25:ARG:NH2	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:B1:846:G:OP2	54:BE:108:ARG:NH2	2.38	0.56
57:BH:61:ILE:HG22	57:BH:93:VAL:HB	1.86	0.56
65:BP:51:ARG:HA	65:BP:54:HIS:HB3	1.88	0.56
1:AA:46:LYS:NZ	38:Ag:46:CYS:SG	2.70	0.55
7:A3:132:G:OP1	29:AX:108:GLN:NE2	2.39	0.55
51:A2:476:G:H22	51:A2:666:G:H22	1.54	0.55
52:B1:156:G:OP1	56:BG:2:LYS:NZ	2.38	0.55
82:Bg:40:ILE:HB	82:Bg:59:LEU:HB2	1.88	0.55
2:BA:205:ARG:NH2	67:BR:84:TYR:CG	2.75	0.55
22:AQ:172:ARG:HD2	32:Aa:57:GLY:HA3	1.87	0.55
30:AY:15:ARG:NH1	51:A2:226:G:OP1	2.38	0.55
36:Ae:16:ARG:NH2	51:A2:432:G:OP1	2.40	0.55
39:Ah:87:LYS:NZ	41:Aj:78:PHE:C	2.65	0.55
52:B1:1277:C:H2'	52:B1:1278:A:H8	1.72	0.55
55:BF:86:LYS:HA	55:BF:89:THR:HG22	1.88	0.55
82:Bg:212:LYS:HA	82:Bg:235:ILE:HG13	1.89	0.55
4:BB:47:THR:O	4:BB:48:LEU:CG	2.54	0.55
7:A3:9:A:H2'	7:A3:10:G:H8	1.71	0.55
7:A3:111:U:O4	43:Al:11:ARG:NH1	2.40	0.55
16:AK:85:ASN:OD1	16:AK:85:ASN:N	2.37	0.55
46:Ao:104:ILE:HG22	46:Ao:106:PHE:H	1.70	0.55
51:A2:2066:G:H2'	51:A2:2067:G:H8	1.71	0.55
52:B1:658:U:O2	73:BX:17:ARG:NH1	2.38	0.55
82:Bg:109:LEU:HD21	82:Bg:125:ARG:HH21	1.71	0.55
2:BA:71:PRO:HB2	2:BA:95:GLY:HA3	1.89	0.55
3:AB:348:ARG:HH12	3:AB:351:LEU:HD23	1.71	0.55
12:AG:153:GLN:N	12:AG:204:PHE:O	2.37	0.55
51:A2:2838:G:N2	51:A2:3808:C:O2	2.39	0.55
51:A2:4602:C:N3	51:A2:4622:G:N2	2.55	0.55
52:B1:65:C:N4	56:BG:134:GLY:O	2.37	0.55
52:B1:1535:U:O4	55:BF:159:ARG:NE	2.38	0.55
63:BN:99:ARG:NH2	63:BN:119:GLU:OE2	2.40	0.55
73:BX:93:PHE:O	73:BX:140:ARG:NH1	2.39	0.55
3:AB:100:ARG:NE	51:A2:4869:A:OP2	2.39	0.55
4:BB:30:TRP:CE3	4:BB:48:LEU:CD1	2.88	0.55
13:AH:44:GLU:HB3	13:AH:58:ASP:O	2.06	0.55
50:Au:34:LEU:O	50:Au:166:ALA:HA	2.07	0.55
51:A2:476:G:H1	51:A2:666:G:H22	1.54	0.55
51:A2:489:C:H2'	51:A2:490:G:H8	1.70	0.55
73:BX:68:LYS:HD3	73:BX:91:LEU:HD22	1.88	0.55
82:Bg:240:CYS:HG	82:Bg:291:TRP:CD1	2.25	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AB:308:ASP:OD2	3:AB:312:LYS:NZ	2.39	0.55
5:AC:114:ARG:NH1	51:A2:1342:G:N3	2.55	0.55
5:AC:154:VAL:HG23	5:AC:155:GLU:N	2.21	0.55
16:AK:30:VAL:CG2	16:AK:102:LEU:CD1	2.80	0.55
17:AL:63:THR:C	17:AL:65:ARG:H	2.14	0.55
23:AR:103:ARG:NH2	51:A2:2645:U:OP2	2.40	0.55
23:AR:103:ARG:NH2	23:AR:124:TYR:OH	2.40	0.55
25:AT:82:GLY:O	33:Ab:21:ILE:CD1	2.54	0.55
45:An:10:MET:HE2	52:B1:1172:U:H4'	1.88	0.55
50:Au:196:LYS:NZ	51:A2:3695:A:O2'	2.39	0.55
51:A2:1397:C:H2'	51:A2:1398:G:H8	1.71	0.55
51:A2:4980:U:N3	51:A2:4983:C:N4	2.54	0.55
52:B1:64:A:H2	52:B1:83:A:H62	1.52	0.55
52:B1:527:C:OP1	80:Be:35:ARG:NH1	2.39	0.55
79:Bd:19:ARG:NH2	79:Bd:31:ILE:O	2.40	0.55
3:AB:2:SER:O	3:AB:3:HIS:ND1	2.40	0.55
17:AL:16:LYS:NZ	51:A2:97:G:OP1	2.38	0.55
41:Aj:2:THR:N	51:A2:3614:A:OP1	2.40	0.55
52:B1:441:C:OP1	58:BI:2:GLY:N	2.40	0.55
52:B1:1058:A:OP1	83:Bv:38:A:O2'	2.25	0.55
53:BD:116:ARG:HB3	84:Bx:57:U:O4	2.07	0.55
69:BT:104:LEU:HD21	69:BT:121:ARG:HD3	1.89	0.55
8:A4:28:C:OP1	15:AJ:144:LYS:NZ	2.35	0.55
12:AG:81:ASN:ND2	12:AG:236:HIS:O	2.39	0.55
52:B1:658:U:H1'	73:BX:17:ARG:HH12	1.72	0.55
52:B1:875:A:H61	52:B1:912:C:N4	2.05	0.55
52:B1:1048:G:N1	52:B1:1069:U:OP2	2.39	0.55
52:B1:1348:G:H1	52:B1:1381:G:H1	1.53	0.55
58:BI:100:CYS:HB3	58:BI:175:ILE:HD12	1.89	0.55
76:Ba:44:ILE:HG22	76:Ba:67:LEU:HB2	1.89	0.55
3:AB:286:LYS:H	3:AB:332:MET:HB3	1.71	0.55
4:BB:30:TRP:CE3	4:BB:48:LEU:CG	2.90	0.55
6:BC:171:GLY:CA	72:BW:98:GLN:HE22	2.20	0.55
13:AH:92:MET:HE2	13:AH:179:ILE:HG22	1.89	0.55
14:AI:156:LYS:NZ	14:AI:163:GLN:O	2.40	0.55
17:AL:172:GLU:O	17:AL:176:PHE:CB	2.55	0.55
34:Ac:17:ARG:CD	34:Ac:103:ASP:OD1	2.51	0.55
51:A2:1977:C:N4	51:A2:1981:G:N2	2.42	0.55
51:A2:3787:A:O2'	51:A2:3790:G:N3	2.39	0.55
51:A2:4853:C:H2'	51:A2:4854:G:H4'	1.87	0.55
52:B1:525:A:H2'	52:B1:526:A:C8	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:AD:264:LYS:HB3	9:AD:264:LYS:HZ3	1.72	0.55
19:AN:84:PRO:HA	19:AN:87:HIS:HD2	1.71	0.55
21:AP:62:ARG:NH1	51:A2:417:G:OP1	2.38	0.55
52:B1:1838:U:H5'	64:BO:151:LEU:HD22	1.89	0.55
65:BP:96:VAL:HG11	65:BP:116:LEU:O	2.07	0.55
4:BB:32:ASP:HB3	4:BB:46:LYS:HE2	1.88	0.54
6:BC:212:LYS:HG3	6:BC:216:MET:HE2	1.89	0.54
13:AH:12:ILE:HB	13:AH:53:LYS:O	2.07	0.54
34:Ac:103:ASP:HB3	34:Ac:106:ARG:HH11	1.73	0.54
44:Am:102:ARG:NH2	51:A2:4435:A:OP1	2.39	0.54
51:A2:2381:G:H2'	51:A2:2382:A:H8	1.72	0.54
52:B1:1208:A:O2'	52:B1:1835:A:N1	2.40	0.54
52:B1:1218:C:O2'	78:Bc:24:GLN:NE2	2.40	0.54
82:Bg:124:SER:OG	82:Bg:125:ARG:N	2.40	0.54
82:Bg:296:GLN:NE2	82:Bg:312:VAL:O	2.40	0.54
2:BA:204:TYR:C	2:BA:204:TYR:CD2	2.85	0.54
3:AB:254:ILE:HG23	3:AB:266:VAL:HG11	1.89	0.54
16:AK:24:TYR:C	16:AK:24:TYR:CD2	2.86	0.54
22:AQ:150:ARG:NH1	51:A2:1480:G:OP1	2.40	0.54
32:Aa:95:THR:HG23	32:Aa:97:ALA:H	1.72	0.54
33:Ab:55:LYS:NZ	51:A2:1385:C:OP1	2.38	0.54
51:A2:943:A:H5''	51:A2:944:G:H5'	1.88	0.54
52:B1:168:C:H4'	56:BG:131:ARG:HD2	1.89	0.54
52:B1:382:C:H41	58:BI:5:ARG:HH22	1.53	0.54
53:BD:116:ARG:CD	84:Bx:56:U:O4	2.52	0.54
66:BQ:11:GLN:HE21	66:BQ:24:HIS:HD2	1.56	0.54
67:BR:62:GLN:O	82:Bg:280:LYS:NZ	2.41	0.54
74:BY:7:ILE:HG12	74:BY:27:VAL:HG22	1.89	0.54
1:AA:117:GLU:O	1:AA:162:ASN:ND2	2.40	0.54
2:BA:205:ARG:HH11	2:BA:205:ARG:CG	2.21	0.54
3:AB:21:ARG:HE	3:AB:271:GLN:HE22	1.55	0.54
19:AN:31:ARG:NH1	19:AN:124:ASP:OD2	2.40	0.54
25:AT:125:TRP:NE1	25:AT:127:GLN:OE1	2.41	0.54
38:Ag:6:THR:HG21	51:A2:2380:A:H1'	1.90	0.54
51:A2:3671:C:O2'	51:A2:3745:A:N3	2.38	0.54
2:BA:155:ARG:NH2	52:B1:1137:U:O2'	2.39	0.54
7:A3:127:U:O4	7:A3:129:C:N4	2.41	0.54
11:AF:152:GLU:OE1	11:AF:248:ASN:ND2	2.40	0.54
16:AK:82:ILE:HG22	16:AK:83:ARG:N	2.22	0.54
52:B1:681:U:H4'	73:BX:9:THR:HG22	1.88	0.54
1:AA:206:PRO:HG3	1:AA:213:GLY:HA3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AB:261:ARG:HD2	51:A2:3841:C:H4'	1.89	0.54
48:Aq:21:GLU:HB3	48:Aq:50:THR:CB	2.37	0.54
48:Aq:55:GLY:HA3	48:Aq:90:ARG:HH22	1.72	0.54
51:A2:500:C:O2	51:A2:646:G:N2	2.34	0.54
65:BP:50:ARG:HH11	65:BP:52:LYS:HE3	1.71	0.54
82:Bg:159:ASN:HD22	82:Bg:162:ASN:HD21	1.54	0.54
83:Bv:21:A:N6	83:Bv:46:G:O2'	2.41	0.54
4:BB:70:SER:OG	64:BO:128:ARG:NH1	2.40	0.54
4:BB:105:LEU:HD13	4:BB:213:ARG:HA	1.89	0.54
7:A3:52:A:H62	43:Al:27:ILE:HD13	1.72	0.54
12:AG:73:ARG:NH2	51:A2:4124:C:N3	2.51	0.54
37:Af:46:ARG:HH12	51:A2:699:G:H5''	1.73	0.54
46:Ao:21:HIS:HA	46:Ao:71:GLU:O	2.08	0.54
48:Aq:116:MET:HE1	48:Aq:132:ILE:HD12	1.90	0.54
51:A2:454:C:H2'	51:A2:455:G:H8	1.72	0.54
51:A2:4556:U:H2'	51:A2:4557:G:H8	1.72	0.54
52:B1:116:U:H3	52:B1:347:G:H1	1.53	0.54
52:B1:332:G:O2'	52:B1:333:G:N7	2.40	0.54
52:B1:986:G:OP2	52:B1:988:C:N4	2.41	0.54
52:B1:1456:G:OP1	67:BR:59:LYS:NZ	2.39	0.54
54:BE:121:TYR:HB3	54:BE:161:GLN:HE21	1.71	0.54
54:BE:133:VAL:HG12	54:BE:134:LYS:HG3	1.89	0.54
55:BF:23:TRP:HH2	55:BF:101:HIS:HB2	1.71	0.54
55:BF:122:ARG:HD3	78:Bc:57:THR:HG21	1.88	0.54
55:BF:204:ARG:HG3	78:Bc:63:ARG:HH21	1.71	0.54
82:Bg:20:GLN:HG3	82:Bg:68:ASP:HA	1.88	0.54
1:AA:221:LYS:HE2	1:AA:233:ARG:HH12	1.72	0.54
3:AB:115:LYS:NZ	3:AB:129:ALA:O	2.39	0.54
8:A4:52:C:O2'	8:A4:54:A:N7	2.40	0.54
15:AJ:54:ARG:HG2	15:AJ:54:ARG:NH1	2.22	0.54
16:AK:18:ILE:HB	16:AK:68:HIS:CD2	2.43	0.54
51:A2:180:C:N4	51:A2:250:G:O6	2.40	0.54
51:A2:715:C:H2'	51:A2:716:G:H8	1.72	0.54
51:A2:1233:C:O2	51:A2:1243:G:N2	2.41	0.54
51:A2:1297:C:OP1	51:A2:3852:G:N2	2.41	0.54
51:A2:4234:G:C6	51:A2:4298:A:N1	2.76	0.54
52:B1:59:U:N3	52:B1:62:G:OP1	2.41	0.54
52:B1:524:U:OP1	52:B1:525:A:O2'	2.26	0.54
73:BX:39:ASN:HB2	73:BX:108:LYS:HE3	1.90	0.54
13:AH:4:ILE:CG2	13:AH:61:TRP:CZ3	2.88	0.54
17:AL:162:LYS:O	32:Aa:105:ARG:NH2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:A2:3767:U:HO2'	52:B1:1720:U:HO2'	1.55	0.54
52:B1:686:U:O2	57:BH:118:ARG:NH1	2.38	0.54
52:B1:955:A:N7	52:B1:969:U:N3	2.56	0.54
58:BI:160:SER:O	58:BI:162:LEU:N	2.41	0.54
68:BS:39:ARG:HH12	69:BT:39:LEU:HD22	1.73	0.54
14:AI:177:ASN:O	14:AI:181:PHE:HB2	2.08	0.54
15:AJ:35:ARG:HB3	15:AJ:123:ILE:HG23	1.88	0.54
41:Aj:14:LYS:HE3	51:A2:2384:G:H5''	1.89	0.54
42:Ak:23:VAL:HG22	42:Ak:36:VAL:HG22	1.88	0.54
47:Ap:48:LYS:NZ	51:A2:2715:G:OP2	2.40	0.54
49:At:61:VAL:HG12	49:At:81:THR:HG22	1.89	0.54
51:A2:3635:G:H2'	51:A2:3636:G:H8	1.72	0.54
2:BA:112:ILE:HG21	52:B1:1349:G:H21	1.73	0.54
33:Ab:50:ASN:OD1	51:A2:1808:G:N2	2.35	0.54
52:B1:692:G:H2'	52:B1:693:A:H8	1.72	0.54
52:B1:1467:C:OP1	67:BR:2:GLY:N	2.40	0.54
58:BI:139:LYS:HB3	58:BI:144:LYS:HB2	1.90	0.54
4:BB:91:VAL:HA	4:BB:96:CYS:HA	1.89	0.53
4:BB:144:LYS:HB2	4:BB:208:HIS:HB2	1.89	0.53
8:A4:92:C:H2'	8:A4:93:G:H8	1.72	0.53
17:AL:25:TRP:HB2	19:AN:201:HIS:HA	1.90	0.53
20:AO:55:LEU:HD12	20:AO:58:LEU:HD12	1.90	0.53
34:Ac:50:ASN:HB2	34:Ac:76:GLY:H	1.74	0.53
50:Au:39:LYS:HD2	50:Au:40:ASN:HB2	1.90	0.53
51:A2:3688:A:H2'	51:A2:3689:A:H8	1.74	0.53
51:A2:3819:U:H2'	51:A2:3820:A:H8	1.73	0.53
52:B1:1010:G:H2'	52:B1:1011:A:H8	1.72	0.53
52:B1:1454:A:N1	52:B1:1476:A:O2'	2.40	0.53
58:BI:65:PHE:HA	58:BI:187:GLY:O	2.08	0.53
82:Bg:170:TRP:NE1	82:Bg:195:LEU:O	2.40	0.53
3:AB:62:ARG:C	3:AB:68:ASN:HD22	2.16	0.53
5:AC:52:TYR:C	5:AC:52:TYR:CD1	2.85	0.53
5:AC:134:PRO:N	5:AC:150:LEU:CD1	2.71	0.53
16:AK:4:GLU:HB2	16:AK:11:SER:HB3	1.90	0.53
52:B1:383:G:H21	61:BL:133:PRO:HG2	1.72	0.53
1:AA:200:ARG:C	1:AA:202:VAL:H	2.16	0.53
8:A4:13:A:OP2	8:A4:66:G:N2	2.41	0.53
16:AK:103:LEU:O	16:AK:103:LEU:HD23	2.09	0.53
25:AT:46:GLY:O	25:AT:49:GLN:NE2	2.41	0.53
51:A2:1576:C:H5	88:A2:5327:MVM:C1	2.22	0.53
52:B1:386:C:H1'	58:BI:5:ARG:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:B1:1786:U:H2'	52:B1:1787:G:H8	1.73	0.53
78:Bc:13:ARG:O	78:Bc:32:VAL:O	2.27	0.53
20:AO:96:GLN:HE22	51:A2:425:G:H22	1.56	0.53
24:AS:9:GLU:OE2	24:AS:31:ARG:NE	2.41	0.53
39:Ah:87:LYS:HZ3	41:Aj:78:PHE:C	2.17	0.53
51:A2:193:C:O2	51:A2:218:C:O2'	2.20	0.53
52:B1:1189:A:H4'	73:BX:34:THR:HG21	1.90	0.53
56:BG:186:GLN:HB3	56:BG:189:ARG:HH21	1.72	0.53
60:BK:35:LEU:HG	60:BK:37:ASP:H	1.74	0.53
60:BK:83:LEU:HA	60:BK:86:PRO:HD2	1.89	0.53
2:BA:8:LEU:HD13	2:BA:59:LEU:HD11	1.90	0.53
3:AB:365:LEU:HD13	3:AB:368:ILE:HD11	1.91	0.53
6:BC:187:ARG:NH2	52:B1:1143:A:OP2	2.42	0.53
7:A3:94:G:OP2	41:Aj:72:ARG:NH1	2.41	0.53
17:AL:168:VAL:HA	32:Aa:97:ALA:HA	1.91	0.53
23:AR:98:ARG:HH21	23:AR:133:LYS:HA	1.74	0.53
44:Am:100:TYR:OH	51:A2:4387:G:OP1	2.26	0.53
51:A2:451:G:H1	51:A2:691:G:H1	1.57	0.53
52:B1:562:U:H2'	52:B1:563:G:H8	1.73	0.53
61:BL:104:LYS:HZ1	73:BX:8:ARG:HD3	1.73	0.53
73:BX:90:CYS:HA	73:BX:93:PHE:HB2	1.91	0.53
4:BB:32:ASP:HA	4:BB:46:LYS:HG2	1.91	0.53
6:BC:253:PRO:HD3	72:BW:68:ARG:HH21	1.74	0.53
6:BC:256:TRP:HZ2	72:BW:68:ARG:HG2	1.57	0.53
11:AF:24:ASN:ND2	11:AF:27:GLU:OE2	2.39	0.53
45:An:2:ARG:HH11	45:An:5:TRP:HE1	1.56	0.53
51:A2:1324:U:H2'	51:A2:1325:A:H8	1.74	0.53
51:A2:1988:G:H21	51:A2:1993:A:H62	1.57	0.53
52:B1:948:C:H2'	52:B1:949:G:H8	1.74	0.53
3:AB:62:ARG:C	3:AB:68:ASN:ND2	2.66	0.53
6:BC:183:LYS:HA	6:BC:195:LEU:O	2.08	0.53
9:AD:17:GLN:HE21	25:AT:20:ARG:HA	1.72	0.53
14:AI:97:ILE:HG13	14:AI:123:GLN:HB3	1.91	0.53
19:AN:94:PHE:CZ	19:AN:96:ARG:HB2	2.44	0.53
23:AR:172:ARG:HH12	52:B1:908:A:H5''	1.74	0.53
30:AY:11:ARG:NH1	51:A2:225:C:OP1	2.41	0.53
47:Ap:42:CYS:SG	47:Ap:59:SER:OG	2.67	0.53
51:A2:1067:C:N3	51:A2:1197:C:N4	2.57	0.53
51:A2:1851:C:H2'	51:A2:1852:A:H8	1.74	0.53
52:B1:748:C:H1'	52:B1:750:C:H41	1.74	0.53
52:B1:1215:C:H41	52:B1:1646:C:H5	1.54	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:B1:1866:A:H1'	76:Ba:95:ARG:HA	1.90	0.53
5:AC:204:ARG:NH1	51:A2:2278:G:OP2	2.42	0.53
12:AG:152:ALA:HA	12:AG:205:THR:HG22	1.91	0.53
23:AR:7:GLN:NE2	23:AR:35:ALA:O	2.39	0.53
46:Ao:36:GLN:HE21	46:Ao:40:ARG:HH22	1.56	0.53
52:B1:511:U:O2'	52:B1:576:A:N6	2.41	0.53
52:B1:913:A:H2'	57:BH:120:ARG:HH12	1.73	0.53
52:B1:1189:A:H2'	52:B1:1190:A:H8	1.74	0.53
80:Be:51:LYS:NZ	84:Bx:58:U:C5	2.73	0.53
82:Bg:17:TRP:H	82:Bg:36:ARG:HB2	1.74	0.53
23:AR:116:ASP:OD2	23:AR:149:LYS:NZ	2.42	0.53
32:Aa:114:LYS:O	32:Aa:136:LYS:NZ	2.42	0.53
51:A2:376:G:N1	51:A2:379:A:OP2	2.42	0.53
51:A2:493:G:OP2	51:A2:495:C:N4	2.42	0.53
51:A2:2332:U:H2'	51:A2:2333:G:H8	1.73	0.53
52:B1:990:A:OP1	76:Ba:37:LYS:NZ	2.36	0.53
10:AE:133:PHE:HA	10:AE:136:HIS:HD1	1.74	0.53
10:AE:153:LEU:HD11	10:AE:195:ILE:HG13	1.90	0.53
16:AK:93:GLU:HB3	16:AK:98:ILE:HD11	1.91	0.53
24:AS:29:ARG:HB2	25:AT:148:PRO:HB2	1.91	0.53
34:Ac:103:ASP:OD1	34:Ac:103:ASP:N	2.42	0.53
51:A2:3832:A:H2'	51:A2:3833:A:H8	1.73	0.53
52:B1:326:C:O2	52:B1:328:U:N3	2.42	0.53
52:B1:448:A:OP1	58:BI:25:ARG:NH1	2.42	0.53
52:B1:483:C:H5'	73:BX:48:LYS:HG3	1.90	0.53
52:B1:1513:C:H2'	52:B1:1514:G:H8	1.73	0.53
66:BQ:53:GLU:O	66:BQ:57:LEU:HB2	2.09	0.53
78:Bc:28:THR:HG22	78:Bc:30:VAL:CG1	2.39	0.53
4:BB:214:LYS:NZ	52:B1:943:U:OP1	2.41	0.52
6:BC:256:TRP:HE1	72:BW:68:ARG:HG2	1.74	0.52
8:A4:119:U:H2'	9:AD:262:LYS:HB2	1.90	0.52
9:AD:128:ASP:O	9:AD:164:LYS:NZ	2.39	0.52
17:AL:128:PRO:HD2	17:AL:136:LYS:HD3	1.92	0.52
19:AN:68:ARG:NH1	51:A2:296:C:OP1	2.42	0.52
36:Ae:112:VAL:HG23	36:Ae:122:VAL:HG11	1.91	0.52
45:An:25:LYS:NZ	51:A2:2852:U:OP1	2.39	0.52
52:B1:742:U:H3	57:BH:122:LEU:HD22	1.73	0.52
65:BP:65:LYS:O	65:BP:67:ALA:N	2.42	0.52
68:BS:23:ARG:HA	68:BS:56:ALA:HB3	1.91	0.52
70:BU:20:ILE:HA	70:BU:115:THR:O	2.09	0.52
1:AA:174:ARG:HA	47:Ap:69:TRP:HE1	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:AN:204:ARG:NH1	51:A2:1324:U:O3'	2.41	0.52
20:AO:117:ARG:NH2	51:A2:4721:C:OP1	2.43	0.52
22:AQ:155:ALA:O	22:AQ:161:SER:OG	2.27	0.52
26:AU:84:LYS:NZ	51:A2:2601:G:OP2	2.41	0.52
51:A2:4666:C:H2'	51:A2:4667:A:H8	1.74	0.52
52:B1:1808:U:H2'	52:B1:1809:A:H8	1.73	0.52
70:BU:56:MET:HB2	70:BU:86:LYS:HB3	1.92	0.52
7:A3:31:G:OP2	17:AL:34:ARG:NH2	2.39	0.52
16:AK:44:ARG:HH11	51:A2:1977:C:H5''	1.74	0.52
23:AR:105:LEU:HD23	23:AR:138:LEU:HD12	1.90	0.52
48:Aq:21:GLU:HB2	48:Aq:50:THR:OG1	2.04	0.52
51:A2:216:G:H22	51:A2:233:G:H1	1.58	0.52
52:B1:284:C:OP1	52:B1:891:G:O2'	2.28	0.52
52:B1:1033:G:N1	52:B1:1080:A:O2'	2.34	0.52
58:BI:158:ILE:HD11	58:BI:163:GLU:CG	2.35	0.52
74:BY:54:VAL:HG22	74:BY:76:TYR:HB2	1.91	0.52
5:AC:45:ARG:NH2	51:A2:2274:C:O2'	2.41	0.52
5:AC:150:LEU:HB3	5:AC:151:PRO:CD	2.39	0.52
5:AC:186:SER:HB2	5:AC:204:ARG:HE	1.75	0.52
5:AC:305:PRO:HA	22:AQ:38:ARG:HH12	1.73	0.52
18:AM:91:TRP:HE1	51:A2:4827:U:H3'	1.75	0.52
19:AN:73:ARG:NH1	19:AN:86:HIS:O	2.43	0.52
51:A2:3915:G:H1	51:A2:4039:U:H3	1.55	0.52
51:A2:4139:C:H2'	51:A2:4140:A:H8	1.74	0.52
58:BI:37:LYS:HB2	58:BI:59:ARG:HB3	1.92	0.52
65:BP:123:TYR:OH	68:BS:124:ARG:NH1	2.41	0.52
70:BU:20:ILE:HG13	70:BU:116:ILE:HA	1.91	0.52
70:BU:33:GLU:OE2	70:BU:87:ARG:NH2	2.41	0.52
70:BU:68:THR:O	79:Bd:40:ARG:NH1	2.36	0.52
2:BA:42:LYS:CD	2:BA:48:ILE:HD11	2.39	0.52
9:AD:150:LEU:HD12	15:AJ:146:ARG:HG3	1.92	0.52
13:AH:41:ILE:HD13	13:AH:73:ILE:HD11	1.90	0.52
18:AM:115:ALA:HB1	20:AO:190:ASP:HB3	1.91	0.52
19:AN:42:PRO:HG3	19:AN:61:ILE:HG13	1.91	0.52
20:AO:63:ASN:ND2	51:A2:2026:G:OP1	2.41	0.52
51:A2:3815:U:H2'	51:A2:3816:A:H8	1.74	0.52
51:A2:4731:G:N2	51:A2:4732:U:O4	2.36	0.52
52:B1:658:U:O3'	73:BX:17:ARG:NH2	2.42	0.52
54:BE:11:ARG:HA	54:BE:28:ALA:HB2	1.92	0.52
61:BL:147:LYS:HG2	61:BL:149:ALA:H	1.74	0.52
68:BS:120:HIS:HA	68:BS:123:LEU:HB2	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:Bv:2:C:H42	83:Bv:71:G:H1	1.56	0.52
1:AA:117:GLU:HG2	1:AA:124:GLY:H	1.74	0.52
13:AH:172:ILE:HD11	44:Am:102:ARG:HH22	1.74	0.52
27:AV:31:ASN:ND2	27:AV:115:SER:OG	2.38	0.52
34:Ac:90:ARG:NH2	51:A2:2652:G:OP1	2.42	0.52
51:A2:2626:A:H62	51:A2:2665:G:H8	1.58	0.52
51:A2:3631:C:H2'	51:A2:3653:A:H61	1.74	0.52
51:A2:4382:U:O4	51:A2:4437:G:N2	2.42	0.52
52:B1:928:G:H1	52:B1:1013:U:H3	1.56	0.52
60:BK:3:MET:N	60:BK:3:MET:SD	2.83	0.52
4:BB:30:TRP:CE3	4:BB:48:LEU:HD21	2.43	0.52
17:AL:63:THR:O	17:AL:64:VAL:C	2.51	0.52
23:AR:151:ARG:HH12	61:BL:118:ARG:HD3	1.74	0.52
42:Ak:38:CYS:SG	42:Ak:39:SER:N	2.79	0.52
46:Ao:44:LYS:NZ	51:A2:91:G:OP1	2.35	0.52
51:A2:113:A:H62	51:A2:155:A:H2	1.57	0.52
73:BX:139:GLU:CG	73:BX:140:ARG:N	2.73	0.52
78:Bc:15:THR:HG22	78:Bc:16:LYS:HG3	1.91	0.52
1:AA:42:LYS:HG3	1:AA:89:TYR:HE1	1.74	0.52
1:AA:200:ARG:HH11	1:AA:200:ARG:CG	2.20	0.52
3:AB:67:VAL:HG21	27:AV:14:PHE:HZ	1.71	0.52
10:AE:123:ARG:HH22	10:AE:126:LEU:HD21	1.75	0.52
43:Al:44:TRP:O	43:Al:48:LYS:NZ	2.42	0.52
51:A2:173:G:N1	51:A2:255:G:O6	2.42	0.52
51:A2:473:G:H1	51:A2:669:G:N2	2.08	0.52
51:A2:1373:G:N2	51:A2:1376:G:OP2	2.39	0.52
53:BD:142:LEU:HD21	53:BD:182:LEU:HD21	1.92	0.52
83:Bv:18:G:O6	83:Bv:55:U:O2'	2.28	0.52
1:AA:198:ARG:NH1	51:A2:3659:U:OP2	2.43	0.52
9:AD:50:ARG:NH2	9:AD:147:ASP:OD2	2.41	0.52
12:AG:136:LEU:HD13	12:AG:202:VAL:HG13	1.92	0.52
33:Ab:23:LYS:CG	33:Ab:24:PRO:CD	2.84	0.52
50:Au:21:ASN:HD22	50:Au:22:GLN:HE21	1.58	0.52
51:A2:317:C:H2'	51:A2:318:A:H8	1.75	0.52
51:A2:633:U:H4'	51:A2:634:C:H5'	1.91	0.52
51:A2:942:G:O2'	51:A2:944:G:N2	2.42	0.52
51:A2:4234:G:O6	51:A2:4298:A:N1	2.43	0.52
52:B1:1753:C:H2'	52:B1:1754:G:H8	1.73	0.52
56:BG:22:ARG:HG2	56:BG:25:ARG:HH21	1.75	0.52
59:BJ:137:VAL:O	59:BJ:137:VAL:HG12	2.08	0.52
65:BP:50:ARG:HG2	65:BP:50:ARG:NH1	2.22	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:BS:90:VAL:HG22	68:BS:93:GLY:H	1.75	0.52
3:AB:56:ILE:HG12	3:AB:368:ILE:HG12	1.91	0.52
6:BC:256:TRP:HH2	72:BW:66:THR:HG21	1.66	0.52
7:A3:30:U:H2'	7:A3:31:G:H8	1.75	0.52
12:AG:143:VAL:HG22	12:AG:203:ALA:HB2	1.90	0.52
16:AK:15:LEU:O	16:AK:19:GLN:HB3	2.10	0.52
33:Ab:26:SER:O	33:Ab:26:SER:OG	2.26	0.52
46:Ao:81:ARG:NH2	51:A2:4255:U:O2'	2.43	0.52
51:A2:463:C:H3'	51:A2:464:A:H8	1.75	0.52
52:B1:93:U:OP2	54:BE:3:ARG:NH2	2.40	0.52
78:Bc:16:LYS:HD3	78:Bc:31:ARG:HH22	1.55	0.52
5:AC:183:VAL:HG11	5:AC:226:GLY:HA3	1.92	0.51
9:AD:235:MET:O	9:AD:239:MET:CB	2.57	0.51
18:AM:101:LYS:HB2	20:AO:198:THR:HG21	1.91	0.51
22:AQ:157:GLY:O	22:AQ:188:ASN:ND2	2.42	0.51
52:B1:1617:G:O6	65:BP:40:ARG:NH2	2.43	0.51
62:BM:43:ASP:OD2	81:Bf:106:TYR:OH	2.27	0.51
62:BM:82:ASN:ND2	62:BM:107:SER:OG	2.43	0.51
15:AJ:58:ARG:NH2	83:Bv:20:U:OP1	2.41	0.51
17:AL:80:GLU:OE2	17:AL:104:ASN:ND2	2.43	0.51
17:AL:133:ALA:N	17:AL:134:PRO:HD3	2.25	0.51
26:AU:46:ARG:NH2	51:A2:2609:U:OP2	2.42	0.51
51:A2:4858:C:H2'	51:A2:4859:G:H4'	1.92	0.51
52:B1:383:G:O3'	61:BL:132:ARG:NH1	2.43	0.51
54:BE:100:ARG:NH2	54:BE:118:GLU:O	2.43	0.51
63:BN:34:LYS:HE3	63:BN:74:ILE:HG23	1.91	0.51
2:BA:11:LYS:HE3	2:BA:13:GLU:HB3	1.91	0.51
3:AB:119:TYR:OH	3:AB:129:ALA:N	2.43	0.51
3:AB:268:ARG:NH1	51:A2:3867:C:O2'	2.34	0.51
49:At:82:ILE:HG12	51:A2:672:G:H5'	1.90	0.51
52:B1:551:U:OP1	80:Be:39:ASN:ND2	2.43	0.51
56:BG:84:TYR:OH	56:BG:91:GLU:O	2.29	0.51
58:BI:172:LEU:HB3	58:BI:190:LEU:HD12	1.93	0.51
61:BL:6:THR:OG1	61:BL:8:ARG:NH1	2.42	0.51
64:BO:117:ARG:NH2	78:Bc:64:GLU:OE1	2.43	0.51
77:Bb:33:MET:HB2	77:Bb:79:PHE:HB2	1.93	0.51
82:Bg:119:GLN:HB3	82:Bg:131:LEU:HD21	1.93	0.51
19:AN:65:ARG:NH2	51:A2:2436:G:OP1	2.40	0.51
48:Aq:64:ILE:HG13	48:Aq:69:ALA:HA	1.92	0.51
51:A2:459:G:H1	51:A2:683:U:H3	1.59	0.51
51:A2:2438:G:N2	51:A2:2441:C:OP2	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:192:LYS:HB3	1:AA:193:ARG:HE	1.76	0.51
16:AK:24:TYR:HD1	16:AK:90:PHE:CD2	2.26	0.51
35:Ad:19:GLU:HB3	35:Ad:21:VAL:HG13	1.92	0.51
39:Ah:87:LYS:NZ	41:Aj:78:PHE:CA	2.68	0.51
51:A2:1871:G:N1	51:A2:1920:A:N6	2.43	0.51
51:A2:2254:G:H2'	51:A2:2255:A:C8	2.44	0.51
51:A2:2827:G:O2'	51:A2:3809:U:O4	2.25	0.51
52:B1:1079:C:O2'	52:B1:1182:A:N1	2.42	0.51
52:B1:1445:U:O4	52:B1:1446:A:N6	2.43	0.51
56:BG:23:LYS:HG3	56:BG:42:GLY:H	1.74	0.51
71:BV:64:GLU:O	71:BV:68:SER:HB2	2.10	0.51
5:AC:147:VAL:HG13	5:AC:148:PRO:HD2	1.93	0.51
9:AD:262:LYS:N	9:AD:262:LYS:CD	2.73	0.51
16:AK:11:SER:HA	16:AK:14:PHE:HB2	1.92	0.51
21:AP:52:THR:O	21:AP:85:LYS:NZ	2.43	0.51
24:AS:95:ARG:NH2	24:AS:112:ASP:OD2	2.44	0.51
51:A2:455:G:C6	51:A2:687:A:N1	2.78	0.51
51:A2:458:G:H1	51:A2:684:U:H3	1.59	0.51
51:A2:920:G:H2'	51:A2:927:C:H41	1.75	0.51
51:A2:2586:C:H2'	51:A2:2587:G:C8	2.45	0.51
51:A2:4098:G:O6	51:A2:4118:G:N2	2.44	0.51
52:B1:28:U:H2'	52:B1:29:G:H8	1.76	0.51
57:BH:150:GLY:O	57:BH:152:ARG:NH1	2.43	0.51
78:Bc:16:LYS:CG	78:Bc:31:ARG:NH2	2.73	0.51
2:BA:36:GLN:O	2:BA:53:ARG:NH1	2.44	0.51
39:Ah:106:LYS:NZ	51:A2:112:C:OP2	2.43	0.51
51:A2:1072:G:H2'	51:A2:1073:G:H8	1.74	0.51
51:A2:2390:C:H2'	51:A2:2391:A:C8	2.46	0.51
52:B1:56:G:H1	52:B1:89:C:H41	1.58	0.51
53:BD:16:ILE:HG21	79:Bd:22:ARG:HH11	1.75	0.51
61:BL:24:LEU:HD12	61:BL:25:LEU:HG	1.93	0.51
69:BT:41:LYS:HB3	69:BT:95:GLY:HA2	1.91	0.51
78:Bc:16:LYS:HD2	78:Bc:31:ARG:HH22	1.73	0.51
17:AL:133:ALA:HB1	17:AL:136:LYS:CE	2.29	0.51
23:AR:39:GLN:NE2	51:A2:2689:C:OP2	2.35	0.51
51:A2:1514:G:N2	51:A2:1619:A:OP2	2.37	0.51
51:A2:2569:G:H21	51:A2:2734:A:H62	1.57	0.51
52:B1:1023:A:OP2	63:BN:124:ARG:NH1	2.43	0.51
54:BE:31:PRO:HG3	54:BE:43:PRO:HG3	1.92	0.51
55:BF:204:ARG:NH1	78:Bc:60:GLU:OE1	2.43	0.51
56:BG:45:TRP:HE1	56:BG:121:ILE:HG12	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:BU:67:LYS:HA	79:Bd:44:ARG:HD2	1.93	0.51
77:Bb:36:LYS:HG2	77:Bb:43:ILE:HG12	1.92	0.51
82:Bg:107:ASP:HB2	82:Bg:125:ARG:HB2	1.93	0.51
17:AL:130:LYS:CB	17:AL:131:PRO:CD	2.73	0.51
51:A2:1717:U:H2'	51:A2:1718:A:H8	1.76	0.51
51:A2:1919:C:H4'	51:A2:1920:A:H5'	1.93	0.51
51:A2:4005:G:H2'	51:A2:4006:G:C8	2.46	0.51
52:B1:454:U:H2'	52:B1:455:A:C8	2.45	0.51
59:BJ:114:VAL:HG12	59:BJ:120:ALA:HB2	1.93	0.51
65:BP:51:ARG:HB2	65:BP:51:ARG:CZ	2.36	0.51
65:BP:92:SER:H	65:BP:107:ILE:HB	1.75	0.51
82:Bg:140:TYR:OH	82:Bg:179:LEU:O	2.28	0.51
3:AB:14:LEU:HD11	3:AB:265:SER:HA	1.93	0.51
33:Ab:50:ASN:O	33:Ab:54:LEU:HB2	2.11	0.51
46:Ao:47:GLY:HA2	51:A2:282:G:H5'	1.92	0.51
51:A2:68:U:O2'	51:A2:100:C:O2'	2.27	0.51
51:A2:430:C:H2'	51:A2:431:G:H8	1.75	0.51
51:A2:2749:C:H2'	51:A2:2750:G:H8	1.77	0.51
52:B1:453:C:O2'	56:BG:92:ARG:O	2.28	0.51
52:B1:1314:U:C2	60:BK:2:LEU:HB2	2.46	0.51
19:AN:155:VAL:HG12	51:A2:57:G:H4'	1.93	0.50
48:Aq:17:CYS:SG	51:A2:1961:U:N3	2.84	0.50
48:Aq:60:VAL:CG2	48:Aq:73:VAL:CG1	2.62	0.50
49:At:90:LEU:HD11	49:At:111:ILE:HG23	1.92	0.50
51:A2:3629:C:H2'	51:A2:3630:G:H8	1.75	0.50
59:BJ:64:ASP:OD2	59:BJ:66:LYS:NZ	2.44	0.50
73:BX:100:VAL:HG22	73:BX:125:VAL:HG22	1.93	0.50
78:Bc:13:ARG:N	78:Bc:32:VAL:O	2.44	0.50
3:AB:74:GLU:OE1	3:AB:285:TYR:OH	2.26	0.50
5:AC:154:VAL:HG23	5:AC:155:GLU:O	2.12	0.50
16:AK:78:LEU:O	16:AK:81:HIS:N	2.44	0.50
39:Ah:28:LEU:HD22	39:Ah:47:ILE:HD11	1.93	0.50
51:A2:62:A:N3	51:A2:77:U:O2'	2.39	0.50
51:A2:924:U:H4'	51:A2:925:C:H4'	1.93	0.50
52:B1:1329:U:O2'	52:B1:1332:A:OP2	2.28	0.50
53:BD:23:GLU:HA	53:BD:26:THR:HG22	1.93	0.50
73:BX:132:ALA:HA	73:BX:137:LYS:HB2	1.92	0.50
78:Bc:32:VAL:HG11	78:Bc:56:LEU:CB	2.41	0.50
9:AD:12:TYR:O	9:AD:16:TYR:HB2	2.12	0.50
13:AH:61:TRP:HA	13:AH:61:TRP:CE3	2.44	0.50
41:Aj:12:ARG:NH2	51:A2:1599:G:O3'	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:Ao:28:LYS:O	51:A2:4306:U:O2'	2.29	0.50
51:A2:301:A:N7	51:A2:302:G:N1	2.60	0.50
51:A2:1731:A:H2'	51:A2:1732:G:H8	1.75	0.50
51:A2:2673:G:H4'	51:A2:2674:A:H5'	1.93	0.50
52:B1:228:C:H42	52:B1:901:G:H1'	1.76	0.50
52:B1:1256:G:H5''	79:Bd:40:ARG:HE	1.77	0.50
52:B1:1655:C:H2'	52:B1:1656:G:H8	1.76	0.50
65:BP:50:ARG:NH1	65:BP:52:LYS:NZ	2.60	0.50
3:AB:200:ARG:HH22	3:AB:205:VAL:HG22	1.75	0.50
13:AH:11:ASP:OD1	13:AH:11:ASP:N	2.44	0.50
16:AK:33:ASP:O	51:A2:1949:G:O2'	2.30	0.50
48:Aq:50:THR:O	48:Aq:54:LYS:CB	2.58	0.50
48:Aq:59:THR:CG2	48:Aq:75:PRO:HG3	2.41	0.50
49:At:112:ARG:NH2	51:A2:949:C:O2	2.45	0.50
50:Au:49:PHE:N	50:Au:159:MET:SD	2.74	0.50
51:A2:2826:G:O6	51:A2:3813:C:N4	2.44	0.50
6:BC:259:THR:HG23	6:BC:261:PHE:CE2	2.46	0.50
10:AE:128:HIS:CE1	51:A2:1265:G:N7	2.80	0.50
12:AG:143:VAL:HG21	12:AG:201:THR:HB	1.94	0.50
33:Ab:28:ARG:NH2	51:A2:1787:A:H4'	2.26	0.50
51:A2:2575:G:H2'	51:A2:2576:G:H8	1.75	0.50
52:B1:551:U:H2'	52:B1:552:G:C8	2.47	0.50
52:B1:1228:A:H2'	52:B1:1229:G:H8	1.75	0.50
53:BD:213:PRO:HG3	67:BR:19:LYS:HD2	1.94	0.50
65:BP:51:ARG:C	65:BP:54:HIS:H	2.17	0.50
85:A:32:LEU:O	85:A:34:LEU:N	2.44	0.50
5:AC:60:HIS:HE1	5:AC:100:ARG:HE	1.60	0.50
10:AE:132:PRO:HG3	51:A2:1271:G:C2	2.47	0.50
23:AR:4:LEU:HD11	23:AR:29:THR:HG23	1.92	0.50
37:Af:8:LYS:HB3	37:Af:100:ARG:HH11	1.76	0.50
50:Au:111:LEU:HD22	50:Au:138:LEU:HD21	1.94	0.50
51:A2:1051:G:H2'	51:A2:1052:G:H8	1.76	0.50
51:A2:2447:U:H2'	51:A2:2485:G:H22	1.77	0.50
52:B1:172:U:OP1	52:B1:314:U:O2'	2.29	0.50
52:B1:563:G:H2'	52:B1:564:A:H8	1.76	0.50
52:B1:1197:G:H2'	52:B1:1198:G:H8	1.77	0.50
65:BP:71:GLU:O	65:BP:72:LYS:C	2.53	0.50
1:AA:3:ARG:HH21	51:A2:1615:G:H21	1.60	0.50
1:AA:77:ILE:HD11	1:AA:128:ARG:HE	1.77	0.50
9:AD:53:VAL:HB	9:AD:159:VAL:HG23	1.94	0.50
13:AH:4:ILE:HG23	13:AH:61:TRP:CE3	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AK:15:LEU:O	16:AK:19:GLN:CB	2.60	0.50
41:Aj:36:LYS:HA	41:Aj:45:ARG:HH21	1.75	0.50
51:A2:416:C:H2'	51:A2:417:G:H8	1.77	0.50
51:A2:1658:C:O2	51:A2:4153:G:O2'	2.30	0.50
54:BE:6:LYS:HB2	54:BE:30:ARG:HH12	1.77	0.50
58:BI:39:GLY:H	58:BI:59:ARG:HB2	1.76	0.50
60:BK:50:GLN:HA	60:BK:53:LYS:HG2	1.92	0.50
82:Bg:31:ILE:HB	82:Bg:43:TRP:HB2	1.92	0.50
14:AI:169:LYS:NZ	14:AI:177:ASN:OD1	2.43	0.50
24:AS:142:VAL:O	24:AS:146:HIS:ND1	2.43	0.50
51:A2:4264:U:OP2	51:A2:4265:C:N4	2.45	0.50
52:B1:1228:A:H2'	52:B1:1229:G:C8	2.47	0.50
52:B1:1447:G:H2'	52:B1:1448:A:H8	1.77	0.50
8:A4:118:C:OP1	9:AD:256:LYS:NZ	2.38	0.50
10:AE:209:PRO:O	10:AE:212:LEU:HD23	2.11	0.50
13:AH:23:ARG:NH2	13:AH:39:ASN:OD1	2.42	0.50
19:AN:78:GLY:HA2	19:AN:89:VAL:HG21	1.94	0.50
49:At:98:ARG:NH2	51:A2:952:G:OP1	2.45	0.50
51:A2:2673:G:OP2	51:A2:2675:A:N6	2.44	0.50
51:A2:4284:G:N2	51:A2:4287:A:OP2	2.44	0.50
52:B1:1148:A:OP1	76:Ba:6:ARG:NH2	2.45	0.50
52:B1:1860:A:OP2	76:Ba:10:ARG:NH1	2.44	0.50
62:BM:26:LEU:HD23	62:BM:31:LEU:HD12	1.93	0.50
5:AC:235:LEU:HD22	5:AC:240:LEU:HD11	1.94	0.49
8:A4:100:A:H2'	8:A4:101:A:H8	1.77	0.49
11:AF:59:LYS:NZ	51:A2:1195:G:OP1	2.43	0.49
15:AJ:18:ARG:HB3	15:AJ:133:VAL:HG23	1.94	0.49
17:AL:84:ALA:HB2	17:AL:117:LEU:HD13	1.94	0.49
17:AL:103:ARG:HH12	17:AL:105:LYS:HE2	1.77	0.49
19:AN:95:ALA:O	51:A2:294:A:H5'	2.12	0.49
37:Af:49:TYR:O	37:Af:69:VAL:HA	2.12	0.49
51:A2:159:A:H61	51:A2:268:C:H42	1.59	0.49
52:B1:1:U:H5'	52:B1:2:A:H5''	1.94	0.49
52:B1:1650:A:H62	52:B1:1674:G:N2	2.07	0.49
56:BG:153:VAL:HG23	56:BG:156:TYR:HB2	1.94	0.49
81:Bf:99:LYS:HB3	81:Bf:103:LEU:HD11	1.94	0.49
85:A:35:LEU:O	85:A:36:LEU:CB	2.59	0.49
3:AB:3:HIS:ND1	51:A2:4478:G:OP2	2.42	0.49
5:AC:154:VAL:CG2	5:AC:158:VAL:CG2	2.84	0.49
13:AH:5:LEU:O	13:AH:6:SER:C	2.52	0.49
24:AS:93:MET:HG3	51:A2:1933:G:H4'	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Aa:117:LEU:HD12	32:Aa:118:PRO:HD2	1.93	0.49
35:Ad:64:ILE:HG22	35:Ad:106:VAL:HB	1.95	0.49
41:Aj:52:LYS:NZ	51:A2:369:G:OP2	2.45	0.49
51:A2:637:C:H2'	51:A2:638:G:H8	1.77	0.49
52:B1:677:G:N1	52:B1:1027:A:OP2	2.32	0.49
66:BQ:11:GLN:HA	66:BQ:23:ALA:O	2.11	0.49
66:BQ:42:ILE:HD13	66:BQ:51:LEU:HD13	1.92	0.49
16:AK:4:GLU:C	16:AK:6:ARG:N	2.71	0.49
51:A2:132:G:N2	51:A2:135:G:O6	2.44	0.49
51:A2:281:U:H2'	51:A2:282:G:H8	1.77	0.49
51:A2:4525:U:H2'	51:A2:4526:A:H8	1.76	0.49
59:BJ:55:LYS:HE2	59:BJ:58:ARG:HH22	1.77	0.49
63:BN:54:LEU:HB3	63:BN:60:VAL:HB	1.92	0.49
65:BP:41:GLN:HE21	65:BP:115:TYR:HE1	1.58	0.49
7:A3:102:G:OP2	7:A3:104:A:O2'	2.28	0.49
11:AF:155:TYR:OH	11:AF:188:GLU:OE2	2.31	0.49
12:AG:156:VAL:HB	12:AG:202:VAL:HB	1.95	0.49
41:Aj:34:CYS:HB3	41:Aj:39:TYR:H	1.77	0.49
49:At:37:SER:HA	51:A2:2246:U:H5'	1.93	0.49
51:A2:446:A:OP2	51:A2:1276:G:O2'	2.26	0.49
52:B1:5:U:H2'	52:B1:6:G:C8	2.48	0.49
52:B1:639:C:H2'	52:B1:640:A:H8	1.75	0.49
52:B1:1266:C:N3	52:B1:1517:G:N2	2.61	0.49
56:BG:186:GLN:HA	56:BG:189:ARG:HE	1.78	0.49
69:BT:116:ASP:HB2	69:BT:122:LYS:HD3	1.94	0.49
75:BZ:68:ILE:HB	75:BZ:109:TYR:HB2	1.92	0.49
4:BB:30:TRP:CE2	4:BB:48:LEU:HD23	2.47	0.49
4:BB:173:THR:O	4:BB:177:GLN:CB	2.60	0.49
9:AD:155:THR:HG22	9:AD:179:ARG:HA	1.93	0.49
10:AE:203:ILE:HG13	10:AE:206:VAL:HG21	1.95	0.49
51:A2:2465:G:H2'	51:A2:2466:G:H8	1.78	0.49
51:A2:2498:U:O2'	51:A2:2509:U:O2	2.31	0.49
51:A2:4493:U:H4'	51:A2:4494:U:H5'	1.94	0.49
51:A2:4943:U:H2'	51:A2:4944:G:H8	1.77	0.49
52:B1:109:U:O2'	61:BL:71:ARG:NH2	2.45	0.49
52:B1:808:A:OP1	54:BE:188:ASN:ND2	2.38	0.49
66:BQ:41:MET:HE2	69:BT:10:ASN:HA	1.95	0.49
77:Bb:11:SER:OG	77:Bb:13:GLU:OE1	2.30	0.49
4:BB:181:LEU:HA	4:BB:184:VAL:HG22	1.94	0.49
5:AC:12:SER:OG	5:AC:18:SER:OG	2.31	0.49
7:A3:116:C:O2'	29:AX:55:ARG:NH1	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A4:105:C:H2'	8:A4:106:G:H8	1.76	0.49
16:AK:99:ARG:NH1	16:AK:103:LEU:HD12	2.27	0.49
30:AY:55:VAL:HG13	30:AY:104:VAL:HG13	1.94	0.49
51:A2:175:C:O2	51:A2:254:C:N4	2.45	0.49
51:A2:1491:C:H2'	51:A2:1492:G:H8	1.77	0.49
51:A2:2562:C:H2'	51:A2:2563:G:H8	1.77	0.49
51:A2:4703:C:N3	51:A2:4917:U:O2	2.46	0.49
65:BP:50:ARG:HG3	65:BP:52:LYS:CG	2.40	0.49
4:BB:30:TRP:CZ3	4:BB:48:LEU:CG	2.95	0.49
12:AG:187:LYS:NZ	51:A2:148:G:O6	2.39	0.49
15:AJ:26:VAL:HG12	15:AJ:28:GLU:H	1.78	0.49
16:AK:4:GLU:C	16:AK:6:ARG:H	2.21	0.49
17:AL:165:LYS:CB	17:AL:165:LYS:NZ	2.73	0.49
31:AZ:16:GLY:HA3	51:A2:2560:A:H5'	1.95	0.49
35:Ad:30:HIS:NE2	51:A2:4599:G:OP1	2.41	0.49
51:A2:289:A:N6	51:A2:4323:U:O2'	2.46	0.49
51:A2:1627:C:H2'	51:A2:1628:A:C8	2.47	0.49
51:A2:3841:C:H2'	51:A2:3842:A:H8	1.77	0.49
52:B1:456:C:O2'	52:B1:1801:A:O2'	2.27	0.49
52:B1:744:G:H1'	57:BH:108:SER:HA	1.95	0.49
52:B1:982:G:H2'	52:B1:983:A:C8	2.47	0.49
52:B1:1808:U:H2'	52:B1:1809:A:C8	2.47	0.49
55:BF:49:LEU:HD12	66:BQ:50:LYS:HB2	1.95	0.49
65:BP:49:LEU:N	65:BP:49:LEU:CD2	2.73	0.49
68:BS:86:ARG:HB2	68:BS:98:VAL:HG13	1.93	0.49
1:AA:200:ARG:O	1:AA:201:GLY:C	2.56	0.49
5:AC:147:VAL:O	5:AC:148:PRO:O	2.29	0.49
7:A3:36:G:OP2	39:Ah:88:THR:OG1	2.28	0.49
26:AU:80:LYS:NZ	26:AU:107:LYS:O	2.45	0.49
51:A2:1928:U:O2	51:A2:4655:C:N4	2.43	0.49
51:A2:4727:G:H2'	51:A2:4728:C:H6	1.78	0.49
52:B1:168:C:O2'	56:BG:133:LEU:O	2.31	0.49
79:Bd:38:MET:HE1	79:Bd:46:TYR:HD2	1.78	0.49
82:Bg:39:THR:HG22	82:Bg:60:ARG:HD3	1.95	0.49
5:AC:58:ALA:HB1	5:AC:60:HIS:H	1.78	0.49
8:A4:77:A:H62	8:A4:99:G:H21	1.59	0.49
9:AD:30:TYR:HA	9:AD:33:ARG:HB3	1.95	0.49
48:Aq:143:VAL:HG22	48:Aq:144:ASP:N	2.28	0.49
51:A2:161:G:O6	51:A2:266:U:O4	2.31	0.49
51:A2:4707:G:H21	51:A2:4912:G:H1	1.59	0.49
51:A2:4885:G:OP2	51:A2:4885:G:N2	2.38	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:B1:688:U:OP1	57:BH:121:THR:OG1	2.30	0.49
52:B1:835:C:O2'	52:B1:839:C:OP2	2.30	0.49
52:B1:1864:U:H3'	76:Ba:5:ARG:HH21	1.76	0.49
78:Bc:13:ARG:O	78:Bc:32:VAL:C	2.56	0.49
3:AB:95:THR:HG22	51:A2:4868:A:H5''	1.95	0.49
20:AO:184:ASN:HD22	20:AO:185:VAL:HG23	1.77	0.49
22:AQ:104:ARG:NH2	51:A2:1336:G:O6	2.46	0.49
35:Ad:26:THR:HG23	35:Ad:85:ARG:HH11	1.78	0.49
51:A2:3688:A:H2'	51:A2:3689:A:C8	2.48	0.49
1:AA:217:GLN:NE2	51:A2:3621:C:OP1	2.42	0.48
1:AA:249:THR:OG1	52:B1:1043:G:O2'	2.30	0.48
6:BC:65:LYS:HA	6:BC:68:ARG:HE	1.78	0.48
14:AI:38:ARG:HE	14:AI:83:ASP:HB3	1.78	0.48
14:AI:152:LEU:HB2	14:AI:165:ILE:HD12	1.95	0.48
39:Ah:96:ASN:HB3	39:Ah:99:GLU:H	1.78	0.48
48:Aq:59:THR:HG22	48:Aq:75:PRO:HG3	1.94	0.48
49:At:51:VAL:HG12	49:At:62:VAL:HG22	1.94	0.48
51:A2:1576:C:N4	88:A2:5327:MVM:C4	2.73	0.48
51:A2:3660:G:O2'	51:A2:3789:U:OP2	2.30	0.48
51:A2:4015:G:H2'	51:A2:4016:A:H2'	1.95	0.48
52:B1:1648:G:N2	52:B1:1675:A:OP2	2.42	0.48
52:B1:1658:G:OP2	52:B1:1660:C:N4	2.45	0.48
53:BD:76:ARG:HE	60:BK:66:HIS:CE1	2.31	0.48
54:BE:222:LEU:HA	54:BE:225:ILE:HD12	1.95	0.48
58:BI:158:ILE:HD12	58:BI:163:GLU:N	2.28	0.48
82:Bg:82:SER:OG	82:Bg:83:TRP:N	2.43	0.48
82:Bg:88:ARG:HH21	82:Bg:100:ARG:HE	1.61	0.48
5:AC:50:GLN:HB3	5:AC:51:PRO:CD	2.43	0.48
5:AC:54:VAL:O	7:A3:26:C:O2'	2.31	0.48
5:AC:326:LEU:HD21	5:AC:333:LYS:HB2	1.95	0.48
14:AI:79:SER:HB3	14:AI:147:HIS:HD2	1.78	0.48
17:AL:5:ARG:NH1	51:A2:1666:A:OP2	2.46	0.48
21:AP:97:ASN:HD21	51:A2:393:G:H1'	1.77	0.48
51:A2:3693:G:H2'	51:A2:3694:A:H8	1.78	0.48
52:B1:332:G:N7	56:BG:189:ARG:NH2	2.61	0.48
52:B1:363:A:N1	52:B1:397:G:O2'	2.41	0.48
52:B1:1452:A:H61	52:B1:1473:G:H8	1.58	0.48
52:B1:1722:G:O6	52:B1:1812:U:O2	2.31	0.48
69:BT:128:GLN:O	69:BT:132:ASP:HB2	2.13	0.48
1:AA:27:ALA:HB3	1:AA:128:ARG:HH21	1.77	0.48
2:BA:44:ASP:O	2:BA:46:ILE:HG12	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AB:165:HIS:HB2	3:AB:178:ALA:HB1	1.95	0.48
16:AK:69:LEU:CD1	16:AK:71:ASN:CB	2.91	0.48
36:Ae:44:ARG:NH2	51:A2:1298:C:OP1	2.46	0.48
41:Aj:58:THR:HG22	51:A2:23:C:H5''	1.95	0.48
51:A2:2347:A:H3'	51:A2:2806:G:H22	1.78	0.48
52:B1:5:U:H2'	52:B1:6:G:H8	1.78	0.48
57:BH:177:TYR:HE2	57:BH:183:LYS:HB2	1.78	0.48
82:Bg:174:VAL:HB	82:Bg:188:HIS:HB2	1.95	0.48
4:BB:30:TRP:CE3	4:BB:48:LEU:HG	2.49	0.48
4:BB:151:ARG:NH2	52:B1:1123:C:OP1	2.46	0.48
9:AD:256:LYS:HG2	9:AD:257:PRO:CD	2.37	0.48
9:AD:263:LYS:HE3	9:AD:263:LYS:CA	2.42	0.48
11:AF:232:ASP:O	11:AF:236:ARG:NH2	2.47	0.48
31:AZ:83:THR:HG23	31:AZ:85:TYR:H	1.78	0.48
37:Af:105:LEU:O	37:Af:106:TYR:O	2.31	0.48
48:Aq:35:LEU:HD13	48:Aq:36:GLY:H	1.77	0.48
51:A2:1315:C:H2'	51:A2:1316:A:C8	2.49	0.48
51:A2:3581:A:H2'	51:A2:3582:A:H8	1.77	0.48
51:A2:3721:G:H2'	51:A2:3722:G:H8	1.79	0.48
52:B1:406:U:H2'	52:B1:408:A:H8	1.79	0.48
52:B1:600:G:H2'	52:B1:601:G:H8	1.79	0.48
54:BE:55:ALA:HB1	54:BE:60:GLU:HB3	1.95	0.48
60:BK:90:VAL:O	60:BK:95:ARG:NH2	2.46	0.48
64:BO:21:VAL:HG13	64:BO:22:ALA:N	2.15	0.48
1:AA:14:SER:OG	51:A2:1610:C:OP1	2.31	0.48
6:BC:78:LEU:HD12	6:BC:81:ILE:HD12	1.95	0.48
21:AP:3:ARG:O	21:AP:18:ARG:NH2	2.47	0.48
27:AV:43:LYS:HD3	27:AV:62:MET:HE2	1.95	0.48
51:A2:1163:C:O2'	51:A2:1165:C:N4	2.47	0.48
51:A2:1315:C:H2'	51:A2:1316:A:H8	1.79	0.48
51:A2:2274:C:H2'	51:A2:2275:G:H8	1.78	0.48
51:A2:2465:G:H2'	51:A2:2466:G:C8	2.48	0.48
51:A2:4841:C:H2'	51:A2:4842:G:H8	1.78	0.48
52:B1:885:U:H2'	52:B1:886:A:H8	1.78	0.48
52:B1:1144:A:N3	52:B1:1199:A:O2'	2.46	0.48
52:B1:1226:G:N1	52:B1:1639:G:OP2	2.36	0.48
65:BP:65:LYS:C	65:BP:67:ALA:N	2.71	0.48
2:BA:119:PRO:HG2	2:BA:142:LEU:HD22	1.95	0.48
4:BB:30:TRP:CZ2	4:BB:48:LEU:HD23	2.40	0.48
4:BB:38:MET:HE1	4:BB:182:LYS:HG2	1.96	0.48
4:BB:170:GLU:O	4:BB:173:THR:OG1	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:BC:139:LEU:HD11	6:BC:237:ALA:HB1	1.95	0.48
19:AN:189:ARG:NH2	51:A2:29:G:OP2	2.47	0.48
22:AQ:161:SER:OG	22:AQ:163:THR:OG1	2.31	0.48
50:Au:21:ASN:O	50:Au:22:GLN:CB	2.60	0.48
51:A2:241:G:OP1	51:A2:241:G:N2	2.47	0.48
51:A2:1281:C:H2'	51:A2:1282:G:H8	1.78	0.48
51:A2:2365:U:H2'	51:A2:2366:G:H8	1.79	0.48
51:A2:2536:G:H1	51:A2:2549:U:H3	1.61	0.48
51:A2:3864:C:H2'	51:A2:3865:A:H8	1.79	0.48
52:B1:496:C:H2'	52:B1:497:C:H6	1.79	0.48
52:B1:639:C:H2'	52:B1:640:A:C8	2.49	0.48
54:BE:194:VAL:N	54:BE:211:LYS:O	2.40	0.48
65:BP:115:TYR:N	65:BP:115:TYR:CD1	2.77	0.48
67:BR:115:SER:OG	67:BR:116:ASN:N	2.40	0.48
3:AB:378:ARG:HG3	28:AW:32:LEU:HD21	1.95	0.48
5:AC:24:LEU:HD12	5:AC:25:PRO:HD2	1.96	0.48
5:AC:178:ASN:OD1	51:A2:2279:A:N6	2.46	0.48
7:A3:90:C:H2'	7:A3:91:A:C8	2.49	0.48
9:AD:256:LYS:CG	9:AD:257:PRO:HD2	2.34	0.48
19:AN:91:GLN:NE2	51:A2:4139:C:OP2	2.43	0.48
51:A2:475:G:H2'	51:A2:476:G:C8	2.49	0.48
51:A2:475:G:H2'	51:A2:476:G:H8	1.77	0.48
51:A2:3578:U:H2'	51:A2:3579:A:H8	1.79	0.48
52:B1:659:G:O2'	52:B1:662:G:O2'	2.26	0.48
2:BA:42:LYS:HG3	67:BR:101:ASP:OD2	2.13	0.48
5:AC:25:PRO:HB3	5:AC:261:ASP:HB2	1.96	0.48
11:AF:242:ARG:NH2	51:A2:929:G:OP2	2.47	0.48
13:AH:59:LYS:HE2	13:AH:66:GLU:HB3	1.95	0.48
17:AL:144:LEU:HD21	39:Ah:122:LYS:H	1.79	0.48
17:AL:172:GLU:HA	17:AL:172:GLU:OE2	2.13	0.48
28:AW:120:GLN:HG3	52:B1:327:G:H5''	1.95	0.48
32:Aa:64:LYS:NZ	51:A2:70:A:OP2	2.43	0.48
49:At:17:LEU:HD13	49:At:36:ASN:HD21	1.72	0.48
51:A2:4058:C:H2'	51:A2:4059:G:C8	2.48	0.48
52:B1:300:U:H2'	52:B1:301:A:H8	1.79	0.48
52:B1:522:A:N6	52:B1:644:G:OP1	2.46	0.48
52:B1:609:U:H2'	52:B1:610:G:H8	1.79	0.48
52:B1:640:A:H2'	52:B1:641:A:C8	2.48	0.48
52:B1:1592:C:H5''	55:BF:91:ARG:HH22	1.78	0.48
52:B1:1593:C:O2	69:BT:12:GLN:NE2	2.38	0.48
4:BB:30:TRP:CD2	4:BB:48:LEU:HD21	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:BC:256:TRP:CH2	72:BW:66:THR:CG2	2.84	0.48
8:A4:35:U:O2'	9:AD:155:THR:O	2.28	0.48
8:A4:62:U:O2'	8:A4:64:G:O4'	2.32	0.48
17:AL:49:ARG:NH1	39:Ah:117:ARG:O	2.47	0.48
18:AM:46:ARG:NH2	51:A2:925:C:O5'	2.47	0.48
22:AQ:88:ASP:OD1	22:AQ:112:ARG:NH2	2.47	0.48
52:B1:43:U:OP2	52:B1:485:A:N6	2.46	0.48
52:B1:159:A:N6	56:BG:59:GLN:OE1	2.46	0.48
52:B1:527:C:H2'	52:B1:528:A:C4	2.48	0.48
52:B1:1300:U:N3	65:BP:51:ARG:NE	2.62	0.48
52:B1:1612:G:O2'	68:BS:87:GLN:HG3	2.14	0.48
76:Ba:53:ILE:O	76:Ba:57:SER:HB2	2.13	0.48
5:AC:28:PHE:HD1	5:AC:132:ALA:HB2	1.79	0.48
6:BC:259:THR:HG21	6:BC:261:PHE:CZ	2.49	0.48
7:A3:113:C:OP2	51:A2:2757:G:N2	2.47	0.48
24:AS:71:SER:O	24:AS:76:LYS:NZ	2.47	0.48
33:Ab:47:LYS:HA	33:Ab:50:ASN:HD22	1.79	0.48
51:A2:2401:C:O2'	51:A2:3828:G:O2'	2.27	0.48
52:B1:28:U:H2'	52:B1:29:G:C8	2.49	0.48
52:B1:588:G:N2	52:B1:589:G:O6	2.44	0.48
52:B1:870:A:OP1	61:BL:153:LYS:NZ	2.47	0.48
53:BD:217:ILE:H	53:BD:217:ILE:HG12	1.44	0.48
10:AE:221:LYS:HA	10:AE:235:THR:HG21	1.96	0.47
17:AL:80:GLU:HG2	17:AL:110:LEU:HD12	1.95	0.47
20:AO:60:LYS:NZ	51:A2:2027:G:O5'	2.46	0.47
27:AV:46:LYS:NZ	51:A2:4472:A:N7	2.55	0.47
31:AZ:33:THR:HB	31:AZ:36:ARG:H	1.79	0.47
51:A2:735:G:H2'	51:A2:736:G:C8	2.49	0.47
51:A2:964:C:H2'	51:A2:965:G:C8	2.48	0.47
51:A2:2022:A:N7	51:A2:4396:C:O2'	2.47	0.47
52:B1:56:G:H22	52:B1:89:C:H5	1.60	0.47
52:B1:486:A:O2'	52:B1:487:U:O2	2.29	0.47
53:BD:116:ARG:CZ	84:Bx:56:U:O4	2.57	0.47
59:BJ:138:ARG:CG	59:BJ:138:ARG:NH1	2.73	0.47
1:AA:215:ASN:ND2	51:A2:4508:A:N7	2.62	0.47
3:AB:189:THR:N	3:AB:192:GLU:OE2	2.45	0.47
5:AC:134:PRO:HA	5:AC:150:LEU:HD11	1.94	0.47
5:AC:343:GLN:HE22	51:A2:934:C:H1'	1.79	0.47
10:AE:131:LYS:HB2	10:AE:131:LYS:HE3	1.69	0.47
12:AG:176:LYS:NZ	40:Ai:46:GLU:OE2	2.37	0.47
14:AI:7:ARG:NH2	51:A2:4367:G:OP1	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AK:55:MET:HB2	16:AK:88:PHE:HB2	1.95	0.47
36:Ae:104:SER:O	36:Ae:108:ARG:HB2	2.14	0.47
51:A2:3849:C:O2	51:A2:4362:G:O2'	2.32	0.47
51:A2:4351:C:H2'	51:A2:4352:A:C8	2.49	0.47
52:B1:319:C:H2'	52:B1:320:G:C8	2.49	0.47
6:BC:252:THR:OG1	6:BC:254:ASP:OD1	2.26	0.47
13:AH:5:LEU:H	13:AH:60:TRP:HA	1.79	0.47
51:A2:1375:A:N6	51:A2:1453:U:OP1	2.45	0.47
51:A2:1804:U:H2'	51:A2:1805:G:H8	1.78	0.47
51:A2:3892:U:H1'	51:A2:4505:G:H21	1.79	0.47
52:B1:29:G:H4'	73:BX:129:SER:HB3	1.96	0.47
55:BF:30:ILE:HG23	55:BF:117:ILE:HD11	1.96	0.47
55:BF:58:ALA:HB3	55:BF:62:ARG:HD3	1.96	0.47
56:BG:14:LYS:HB2	56:BG:124:LEU:HD21	1.95	0.47
60:BK:24:LYS:HA	60:BK:66:HIS:HA	1.95	0.47
7:A3:153:C:H5''	12:AG:185:LYS:HE2	1.97	0.47
10:AE:128:HIS:NE2	51:A2:1265:G:N7	2.63	0.47
14:AI:47:PRO:HD2	14:AI:141:LYS:HA	1.96	0.47
16:AK:83:ARG:CG	51:A2:2003:C:H5'	2.44	0.47
21:AP:37:LYS:NZ	51:A2:418:U:O3'	2.47	0.47
35:Ad:115:LYS:NZ	51:A2:5002:A:OP2	2.40	0.47
39:Ah:104:THR:HG23	39:Ah:107:GLN:H	1.79	0.47
47:Ap:38:THR:HA	47:Ap:45:THR:HA	1.96	0.47
48:Aq:60:VAL:HA	48:Aq:73:VAL:HG12	1.96	0.47
51:A2:3724:G:OP2	51:A2:3747:G:O2'	2.31	0.47
51:A2:4115:C:H2'	51:A2:4116:G:H8	1.79	0.47
51:A2:4136:U:H2'	51:A2:4137:G:H8	1.78	0.47
51:A2:4980:U:N3	51:A2:4983:C:C4	2.82	0.47
52:B1:197:U:H3	52:B1:202:G:H1	1.63	0.47
52:B1:1401:A:H4'	70:BU:52:GLY:HA3	1.97	0.47
55:BF:55:ARG:NE	66:BQ:123:ASP:OD2	2.47	0.47
64:BO:138:ASP:OD1	64:BO:138:ASP:N	2.45	0.47
65:BP:50:ARG:HG3	65:BP:52:LYS:CD	2.43	0.47
7:A3:19:C:H2'	7:A3:20:A:H8	1.79	0.47
7:A3:125:C:O2'	7:A3:126:C:O2	2.25	0.47
13:AH:43:VAL:HG22	13:AH:59:LYS:HD2	1.97	0.47
27:AV:105:ILE:HG23	27:AV:113:LYS:HB3	1.97	0.47
32:Aa:16:SER:OG	51:A2:2262:G:OP1	2.31	0.47
49:At:66:ARG:NH1	51:A2:473:G:OP1	2.47	0.47
51:A2:476:G:H1	51:A2:666:G:H1	1.61	0.47
51:A2:2617:G:H21	51:A2:2676:A:H62	1.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:A2:4281:C:H2'	51:A2:4282:G:H8	1.79	0.47
52:B1:1735:A:H62	52:B1:1799:G:N2	2.11	0.47
55:BF:108:PRO:HA	55:BF:111:VAL:HG22	1.97	0.47
4:BB:79:VAL:HG21	4:BB:82:ARG:HD3	1.95	0.47
6:BC:170:TRP:O	72:BW:97:ARG:HB2	2.15	0.47
9:AD:83:LEU:HB3	9:AD:88:VAL:HB	1.96	0.47
18:AM:113:MET:HE1	51:A2:4839:U:H3'	1.96	0.47
19:AN:2:GLY:N	51:A2:115:C:OP1	2.47	0.47
19:AN:12:ARG:HD2	51:A2:273:A:C8	2.48	0.47
19:AN:31:ARG:NH2	51:A2:4047:A:O3'	2.47	0.47
39:Ah:93:ARG:NH2	51:A2:19:G:OP2	2.46	0.47
51:A2:3698:A:H2'	51:A2:3699:A:C8	2.49	0.47
51:A2:4058:C:H2'	51:A2:4059:G:H8	1.78	0.47
54:BE:95:THR:HG22	74:BY:16:ARG:HB2	1.95	0.47
57:BH:27:LEU:HD12	57:BH:45:ILE:HD11	1.96	0.47
58:BI:158:ILE:CD1	58:BI:162:LEU:HB2	2.43	0.47
1:AA:97:ASN:H	1:AA:100:ASN:HD22	1.63	0.47
2:BA:141:ASN:ND2	71:BV:31:SER:O	2.42	0.47
3:AB:67:VAL:HG21	27:AV:14:PHE:CZ	2.50	0.47
7:A3:148:A:H2'	7:A3:149:G:C8	2.50	0.47
8:A4:55:A:O2'	15:AJ:151:ILE:O	2.30	0.47
9:AD:146:LEU:HD11	9:AD:163:LEU:HG	1.96	0.47
9:AD:262:LYS:H	9:AD:262:LYS:HZ2	1.59	0.47
10:AE:136:HIS:HE1	51:A2:701:G:H21	1.62	0.47
19:AN:161:MET:SD	51:A2:54:G:O2'	2.71	0.47
20:AO:59:ARG:NH2	51:A2:4424:C:OP1	2.47	0.47
33:Ab:27:GLN:HE21	33:Ab:27:GLN:HB2	1.61	0.47
36:Ae:75:ARG:HD2	36:Ae:95:TYR:HE1	1.80	0.47
42:Ak:24:LYS:HB2	42:Ak:35:LYS:HB2	1.96	0.47
42:Ak:37:ARG:NH1	51:A2:2516:A:OP2	2.42	0.47
50:Au:41:TYR:OH	50:Au:200:ASN:ND2	2.48	0.47
51:A2:1327:C:H2'	51:A2:1328:A:C8	2.50	0.47
51:A2:1782:U:H2'	51:A2:1783:A:H8	1.79	0.47
51:A2:1914:G:H2'	51:A2:1915:A:C8	2.49	0.47
51:A2:2535:G:H2'	51:A2:2536:G:H8	1.79	0.47
51:A2:3703:A:H2'	51:A2:3704:A:C8	2.50	0.47
51:A2:3754:A:H2	51:A2:3761:U:H3	1.61	0.47
51:A2:3909:G:N2	51:A2:4133:C:OP2	2.47	0.47
51:A2:4065:G:N3	51:A2:4066:C:N4	2.63	0.47
51:A2:4235:A:H2'	51:A2:4236:A:C8	2.50	0.47
51:A2:4597:A:H2	51:A2:4625:G:H21	1.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:A2:4912:G:H2'	51:A2:4913:A:H8	1.80	0.47
52:B1:384:U:O4	58:BI:5:ARG:NH1	2.48	0.47
52:B1:982:G:H21	52:B1:1045:U:H1'	1.80	0.47
52:B1:1204:A:O2'	52:B1:1700:C:OP2	2.29	0.47
52:B1:1616:U:H3	52:B1:1620:A:H62	1.60	0.47
52:B1:1692:U:H2'	52:B1:1693:G:C8	2.50	0.47
59:BJ:138:ARG:HH21	59:BJ:156:HIS:CE1	2.16	0.47
61:BL:124:ASP:OD1	61:BL:124:ASP:N	2.44	0.47
62:BM:53:ALA:HA	62:BM:79:VAL:O	2.15	0.47
68:BS:88:LYS:HE3	68:BS:88:LYS:HB3	1.74	0.47
1:AA:207:VAL:HG23	1:AA:208:GLU:HG3	1.97	0.47
5:AC:95:MET:SD	5:AC:95:MET:N	2.79	0.47
13:AH:3:THR:O	13:AH:61:TRP:CE3	2.68	0.47
26:AU:49:VAL:HG21	26:AU:61:VAL:HG21	1.96	0.47
33:Ab:50:ASN:O	33:Ab:54:LEU:CB	2.63	0.47
52:B1:192:C:H41	58:BI:141:ARG:HG3	1.80	0.47
52:B1:562:U:H2'	52:B1:563:G:C8	2.50	0.47
52:B1:591:U:H3	80:Be:26:LYS:HE2	1.80	0.47
52:B1:1013:U:OP1	52:B1:1129:G:O2'	2.32	0.47
52:B1:1183:A:H2'	52:B1:1184:G:H8	1.79	0.47
52:B1:1600:G:OP2	75:BZ:39:LYS:NZ	2.43	0.47
1:AA:200:ARG:NH1	1:AA:200:ARG:CG	2.78	0.47
2:BA:206:ASP:OD1	2:BA:207:PRO:HD3	2.10	0.47
5:AC:350:ARG:HH11	51:A2:714:A:H5''	1.80	0.47
19:AN:44:ARG:NH2	51:A2:274:G:OP2	2.47	0.47
20:AO:125:LYS:HG3	20:AO:129:LEU:HD12	1.96	0.47
29:AX:64:SER:OG	39:Ah:82:ASP:OD1	2.29	0.47
48:Aq:10:ILE:HG22	48:Aq:64:ILE:HB	1.97	0.47
51:A2:1329:C:H2'	51:A2:1330:G:H8	1.80	0.47
51:A2:1485:A:H4'	51:A2:1486:G:H5'	1.97	0.47
69:BT:41:LYS:HD2	69:BT:81:GLY:HA2	1.97	0.47
8:A4:99:G:OP2	24:AS:55:LYS:NZ	2.39	0.47
10:AE:152:ILE:O	10:AE:159:GLY:N	2.48	0.47
51:A2:193:C:H41	51:A2:238:G:H1	1.62	0.47
51:A2:1327:C:H2'	51:A2:1328:A:H8	1.80	0.47
51:A2:1607:G:N1	51:A2:3889:G:OP1	2.41	0.47
51:A2:2522:A:H2	51:A2:2752:G:H22	1.62	0.47
51:A2:4726:A:H61	51:A2:4826:G:H22	1.63	0.47
52:B1:1499:U:H4'	53:BD:176:LEU:HD13	1.97	0.47
73:BX:132:ALA:HB1	73:BX:137:LYS:HB3	1.97	0.47
1:AA:67:TYR:OH	51:A2:4057:G:N7	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AB:67:VAL:HG22	27:AV:14:PHE:CZ	2.49	0.46
9:AD:46:THR:HG21	51:A2:1800:G:H4'	1.97	0.46
9:AD:260:GLU:O	9:AD:261:VAL:C	2.58	0.46
11:AF:228:VAL:HA	24:AS:39:VAL:HG22	1.96	0.46
20:AO:51:LYS:O	20:AO:55:LEU:HB2	2.15	0.46
23:AR:60:ARG:O	23:AR:63:CYS:N	2.48	0.46
25:AT:48:VAL:HG21	25:AT:94:GLU:HG2	1.97	0.46
26:AU:111:GLU:OE1	26:AU:113:ARG:NH2	2.48	0.46
27:AV:31:ASN:HD21	27:AV:115:SER:HG	1.58	0.46
51:A2:747:G:H2'	51:A2:748:G:H8	1.79	0.46
51:A2:2728:C:H2'	51:A2:2729:G:C8	2.50	0.46
52:B1:1015:U:O2'	63:BN:55:ARG:NH1	2.47	0.46
52:B1:1711:U:H2'	52:B1:1712:A:H8	1.79	0.46
52:B1:1863:A:OP2	76:Ba:4:LYS:NZ	2.41	0.46
56:BG:223:LYS:O	56:BG:227:GLN:NE2	2.48	0.46
68:BS:90:VAL:CG2	68:BS:93:GLY:N	2.75	0.46
82:Bg:216:ALA:HB3	82:Bg:230:LEU:HB2	1.96	0.46
3:AB:14:LEU:O	51:A2:4549:G:O2'	2.33	0.46
13:AH:3:THR:O	13:AH:61:TRP:HE3	1.97	0.46
17:AL:133:ALA:HB1	17:AL:136:LYS:HG3	1.97	0.46
50:Au:57:SER:C	50:Au:58:THR:HG22	2.40	0.46
51:A2:186:G:H2'	51:A2:187:G:H8	1.80	0.46
51:A2:1966:G:O2'	51:A2:1984:G:OP2	2.31	0.46
51:A2:4232:C:H5''	51:A2:4233:A:H5''	1.97	0.46
51:A2:4988:U:H2'	51:A2:4989:G:H8	1.79	0.46
52:B1:1692:U:H2'	52:B1:1693:G:H8	1.81	0.46
58:BI:67:TRP:CD1	58:BI:70:GLU:H	2.33	0.46
73:BX:28:LYS:O	73:BX:32:LEU:HB3	2.15	0.46
2:BA:42:LYS:HD3	2:BA:48:ILE:CD1	2.46	0.46
17:AL:197:LYS:HD3	51:A2:4320:U:H4'	1.97	0.46
18:AM:35:ARG:HA	18:AM:51:PRO:HA	1.96	0.46
19:AN:32:GLN:NE2	51:A2:4048:C:OP1	2.48	0.46
28:AW:6:CYS:SG	28:AW:9:SER:OG	2.64	0.46
28:AW:47:ARG:HB3	28:AW:58:LYS:HD2	1.97	0.46
51:A2:1365:G:H2'	51:A2:1366:G:H8	1.80	0.46
51:A2:2824:A:H61	51:A2:3814:C:H42	1.64	0.46
51:A2:3826:C:H2'	51:A2:3827:A:H8	1.81	0.46
52:B1:792:C:H2'	52:B1:793:G:H8	1.79	0.46
2:BA:91:ALA:HA	2:BA:96:ALA:HB3	1.97	0.46
7:A3:126:C:OP2	7:A3:129:C:N4	2.42	0.46
16:AK:81:HIS:ND1	16:AK:81:HIS:C	2.73	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AK:83:ARG:HG3	51:A2:2003:C:C5'	2.45	0.46
25:AT:84:ILE:HD11	33:Ab:23:LYS:CD	2.45	0.46
27:AV:84:GLN:HE21	27:AV:86:LYS:HB3	1.79	0.46
51:A2:2868:G:H21	51:A2:4992:A:H8	1.61	0.46
51:A2:4144:G:O2'	51:A2:4146:G:N7	2.48	0.46
52:B1:151:C:OP1	74:BY:120:THR:OG1	2.32	0.46
52:B1:1354:G:O2'	52:B1:1356:G:O6	2.31	0.46
52:B1:1539:U:H2'	52:B1:1540:G:C8	2.50	0.46
54:BE:192:VAL:HG21	54:BE:238:LEU:HD11	1.98	0.46
82:Bg:164:ILE:HG23	82:Bg:176:VAL:HG13	1.96	0.46
3:AB:22:SER:OG	3:AB:24:ARG:O	2.30	0.46
5:AC:192:GLY:O	5:AC:195:LYS:NZ	2.39	0.46
6:BC:201:GLY:N	6:BC:221:ASP:OD2	2.46	0.46
7:A3:29:G:H5''	17:AL:27:ASN:HB3	1.98	0.46
7:A3:87:G:OP2	39:Ah:5:LYS:NZ	2.48	0.46
9:AD:187:SER:OG	9:AD:189:GLU:OE1	2.28	0.46
21:AP:40:HIS:HE1	21:AP:111:SER:HA	1.80	0.46
27:AV:27:ASN:O	27:AV:102:ALA:HA	2.16	0.46
36:Ae:119:ALA:HB3	49:At:119:ARG:HH22	1.79	0.46
37:Af:73:LYS:NZ	51:A2:940:C:OP1	2.42	0.46
50:Au:22:GLN:N	50:Au:22:GLN:CD	2.73	0.46
51:A2:222:G:OP1	51:A2:238:G:N2	2.41	0.46
51:A2:1731:A:H2'	51:A2:1732:G:C8	2.50	0.46
51:A2:2876:G:H2'	51:A2:2877:G:H8	1.80	0.46
51:A2:4499:C:H2'	51:A2:4500:G:C8	2.51	0.46
52:B1:433:A:H2'	52:B1:434:G:C8	2.51	0.46
52:B1:1533:A:OP1	55:BF:164:ARG:NH2	2.41	0.46
65:BP:83:MET:O	65:BP:115:TYR:HB3	2.15	0.46
2:BA:205:ARG:CG	2:BA:205:ARG:NH1	2.78	0.46
14:AI:103:LEU:HD22	14:AI:108:ALA:HA	1.98	0.46
16:AK:18:ILE:HD12	16:AK:68:HIS:NE2	2.31	0.46
39:Ah:34:ALA:HA	39:Ah:37:THR:HG22	1.97	0.46
51:A2:1228:C:H2'	51:A2:1229:G:C8	2.51	0.46
51:A2:3678:U:H2'	51:A2:3679:C:C6	2.51	0.46
51:A2:4170:U:H2'	51:A2:4171:G:C8	2.50	0.46
55:BF:201:LYS:HD2	55:BF:204:ARG:HE	1.80	0.46
82:Bg:11:LEU:HB2	82:Bg:307:VAL:HB	1.98	0.46
3:AB:55:HIS:ND1	3:AB:369:ASP:OD2	2.39	0.46
4:BB:139:CYS:HB2	4:BB:172:MET:HE1	1.98	0.46
5:AC:133:LEU:HD13	49:At:6:GLN:HE21	1.80	0.46
10:AE:190:HIS:CD2	10:AE:192:LYS:H	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AH:3:THR:OG1	13:AH:67:LEU:HD11	2.15	0.46
17:AL:172:GLU:O	17:AL:176:PHE:HB2	2.16	0.46
44:Am:104:HIS:CD2	44:Am:106:ARG:H	2.34	0.46
51:A2:469:G:H1	51:A2:672:G:H1	1.63	0.46
51:A2:713:G:H2'	51:A2:714:A:C8	2.51	0.46
51:A2:2022:A:H62	51:A2:4396:C:H1'	1.80	0.46
51:A2:3916:A:H2'	51:A2:3917:G:H8	1.81	0.46
51:A2:4038:U:H2'	51:A2:4039:U:H6	1.81	0.46
51:A2:4475:A:H2'	51:A2:4476:G:H8	1.81	0.46
51:A2:4539:U:H2'	51:A2:4540:G:C8	2.51	0.46
52:B1:216:C:O2'	52:B1:217:A:O4'	2.34	0.46
52:B1:740:C:O2'	52:B1:741:C:O2	2.34	0.46
55:BF:40:ALA:HB3	55:BF:67:PRO:HA	1.96	0.46
62:BM:61:TYR:OH	62:BM:108:CYS:SG	2.68	0.46
75:BZ:41:ARG:HH11	75:BZ:42:ASP:HB2	1.80	0.46
2:BA:77:ILE:HG12	2:BA:99:ILE:HG23	1.97	0.46
10:AE:239:LYS:NZ	51:A2:4897:C:O2	2.49	0.46
19:AN:50:ARG:HA	51:A2:113:A:H1'	1.97	0.46
25:AT:44:GLY:H	25:AT:58:HIS:CE1	2.34	0.46
41:Aj:22:CYS:SG	41:Aj:24:SER:OG	2.68	0.46
49:At:26:SER:HB3	49:At:36:ASN:CA	2.45	0.46
52:B1:1314:U:H1'	60:BK:2:LEU:HD13	1.98	0.46
52:B1:1488:C:H3'	52:B1:1489:A:H4'	1.97	0.46
73:BX:132:ALA:C	73:BX:137:LYS:HB2	2.41	0.46
82:Bg:5:MET:HB3	82:Bg:310:TRP:HB3	1.97	0.46
2:BA:42:LYS:HD3	2:BA:48:ILE:CG1	2.46	0.46
7:A3:130:C:H2'	7:A3:131:G:H8	1.80	0.46
15:AJ:142:ALA:HB2	15:AJ:151:ILE:HD11	1.98	0.46
51:A2:1072:G:H2'	51:A2:1073:G:C8	2.51	0.46
51:A2:2500:G:H2'	51:A2:2501:G:H8	1.81	0.46
51:A2:3578:U:H2'	51:A2:3579:A:C8	2.50	0.46
51:A2:4566:G:N2	51:A2:4569:A:OP2	2.48	0.46
51:A2:4932:C:N4	51:A2:4933:G:O6	2.49	0.46
52:B1:558:G:H2'	52:B1:559:G:C8	2.51	0.46
58:BI:84:ASN:HD22	58:BI:90:LEU:HB2	1.81	0.46
59:BJ:37:LEU:HD22	59:BJ:43:VAL:HG22	1.98	0.46
65:BP:39:ALA:HA	65:BP:42:ARG:HE	1.81	0.46
69:BT:126:GLN:OE1	69:BT:129:ARG:NH2	2.49	0.46
4:BB:70:SER:HA	4:BB:83:LYS:HA	1.97	0.46
5:AC:61:GLN:HE21	41:Aj:55:ARG:HH12	1.64	0.46
6:BC:210:PRO:HD3	6:BC:236:PHE:HE2	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:AD:127:GLY:HA2	9:AD:164:LYS:HE2	1.98	0.46
16:AK:71:ASN:O	16:AK:73:PRO:CD	2.63	0.46
20:AO:21:ALA:HA	20:AO:87:MET:HE1	1.98	0.46
35:Ad:25:TYR:HD2	35:Ad:88:LEU:HD13	1.79	0.46
48:Aq:81:ILE:HG13	48:Aq:139:VAL:HG21	1.98	0.46
51:A2:84:A:H61	51:A2:98:A:H5''	1.81	0.46
51:A2:4955:G:H2'	51:A2:4956:G:H8	1.80	0.46
52:B1:1786:U:H2'	52:B1:1787:G:C8	2.51	0.46
54:BE:220:THR:OG1	54:BE:221:ARG:N	2.48	0.46
62:BM:45:ARG:HE	62:BM:72:HIS:HD2	1.63	0.46
65:BP:18:ARG:HD3	68:BS:89:ASP:HB2	1.52	0.46
82:Bg:64:HIS:HB3	82:Bg:83:TRP:HB2	1.98	0.46
82:Bg:133:ASN:HD22	82:Bg:134:THR:H	1.64	0.46
3:AB:67:VAL:HG22	27:AV:14:PHE:HZ	1.80	0.45
26:AU:56:LEU:CD1	26:AU:61:VAL:CB	2.71	0.45
36:Ae:26:ASP:OD1	36:Ae:26:ASP:N	2.48	0.45
37:Af:11:PHE:HE1	37:Af:26:ALA:HB1	1.81	0.45
38:Ag:9:ARG:HG3	38:Ag:34:TYR:HE2	1.79	0.45
48:Aq:59:THR:HG21	48:Aq:75:PRO:CA	2.46	0.45
51:A2:660:C:O2'	51:A2:662:A:OP2	2.34	0.45
51:A2:1316:A:H2'	51:A2:1317:A:H8	1.81	0.45
51:A2:4200:G:H2'	51:A2:4201:A:H8	1.81	0.45
51:A2:4701:C:H2'	51:A2:4702:G:C8	2.51	0.45
51:A2:4980:U:C4	51:A2:4983:C:N4	2.84	0.45
52:B1:406:U:O2'	52:B1:408:A:OP1	2.33	0.45
52:B1:1041:G:H2'	52:B1:1042:A:H8	1.81	0.45
71:BV:64:GLU:O	71:BV:68:SER:CB	2.65	0.45
5:AC:243:GLY:O	51:A2:2275:G:N2	2.43	0.45
8:A4:63:C:H5'	8:A4:64:G:H5''	1.99	0.45
10:AE:203:ILE:CG1	10:AE:206:VAL:HG21	2.47	0.45
17:AL:55:ILE:HA	17:AL:153:PRO:HG2	1.97	0.45
19:AN:46:ASP:OD1	19:AN:46:ASP:N	2.49	0.45
27:AV:51:ARG:NH1	51:A2:3814:C:OP1	2.49	0.45
31:AZ:5:MET:O	31:AZ:28:ASN:ND2	2.49	0.45
43:Al:36:ARG:NH1	51:A2:407:G:O5'	2.43	0.45
49:At:62:VAL:HG11	49:At:96:MET:HE1	1.98	0.45
51:A2:202:C:O2'	51:A2:204:G:N7	2.39	0.45
51:A2:747:G:H2'	51:A2:748:G:C8	2.52	0.45
51:A2:1324:U:H2'	51:A2:1325:A:C8	2.51	0.45
51:A2:1329:C:H2'	51:A2:1330:G:C8	2.51	0.45
51:A2:4939:G:H3'	51:A2:4940:A:H8	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:B1:1256:G:N2	79:Bd:30:LEU:O	2.48	0.45
52:B1:1651:A:H2'	52:B1:1652:G:H8	1.80	0.45
12:AG:75:LYS:HG2	12:AG:240:ASN:HB2	1.98	0.45
15:AJ:27:GLY:HA2	51:A2:4219:A:H2	1.81	0.45
24:AS:142:VAL:HG12	24:AS:146:HIS:CE1	2.51	0.45
29:AX:74:TYR:HB2	39:Ah:25:LYS:HD3	1.98	0.45
45:An:2:ARG:NH1	45:An:5:TRP:HE1	2.14	0.45
51:A2:66:A:N6	51:A2:276:C:O2'	2.48	0.45
51:A2:2575:G:H2'	51:A2:2576:G:C8	2.51	0.45
51:A2:2599:G:H2'	51:A2:2600:A:H8	1.81	0.45
51:A2:2773:C:N4	85:A:21:GLY:O	2.45	0.45
52:B1:380:G:N1	52:B1:383:G:OP2	2.45	0.45
52:B1:1396:A:N1	52:B1:1449:G:C6	2.84	0.45
60:BK:53:LYS:HE2	60:BK:69:TRP:HE1	1.81	0.45
61:BL:96:ILE:HD12	73:BX:10:ALA:HB1	1.99	0.45
1:AA:9:ARG:NH2	51:A2:1611:G:O6	2.49	0.45
3:AB:224:LYS:HG2	3:AB:340:THR:HG22	1.98	0.45
5:AC:110:ARG:NH2	51:A2:1490:A:OP1	2.44	0.45
13:AH:61:TRP:HA	13:AH:61:TRP:HE3	1.82	0.45
21:AP:78:TRP:CD1	21:AP:80:GLN:H	2.35	0.45
22:AQ:68:ARG:HH22	51:A2:1483:C:H5''	1.80	0.45
32:Aa:82:VAL:HG21	32:Aa:101:ILE:HG12	1.99	0.45
52:B1:687:C:N3	57:BH:118:ARG:NH2	2.65	0.45
52:B1:1189:A:H2'	52:B1:1190:A:C8	2.52	0.45
55:BF:134:VAL:HG12	55:BF:136:ARG:H	1.81	0.45
57:BH:37:LYS:O	57:BH:41:ARG:CB	2.65	0.45
64:BO:147:ARG:HA	76:Ba:28:ARG:HG3	1.99	0.45
65:BP:85:ILE:HD11	65:BP:116:LEU:CD2	2.45	0.45
82:Bg:91:ASP:OD2	82:Bg:93:THR:OG1	2.32	0.45
5:AC:51:PRO:HG2	7:A3:28:C:H4'	1.98	0.45
16:AK:28:PHE:O	16:AK:88:PHE:HA	2.15	0.45
17:AL:89:LYS:HZ2	39:Ah:110:LYS:HG2	1.81	0.45
17:AL:172:GLU:O	17:AL:176:PHE:HB3	2.17	0.45
26:AU:49:VAL:CG2	26:AU:56:LEU:HG	2.46	0.45
51:A2:401:A:N7	51:A2:404:A:N6	2.64	0.45
51:A2:1980:A:H2'	51:A2:1981:G:C4	2.52	0.45
51:A2:3864:C:H2'	51:A2:3865:A:C8	2.52	0.45
51:A2:4499:C:H2'	51:A2:4500:G:H8	1.82	0.45
52:B1:14:C:H2'	52:B1:15:U:C6	2.51	0.45
52:B1:124:U:OP1	56:BG:201:LYS:NZ	2.42	0.45
52:B1:678:U:H2'	52:B1:679:A:H8	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:B1:918:U:O2'	52:B1:919:A:O4'	2.34	0.45
56:BG:5:ILE:HD13	56:BG:45:TRP:HH2	1.82	0.45
62:BM:54:SER:HB2	62:BM:80:ASP:HA	1.99	0.45
4:BB:186:ASN:HA	4:BB:189:ILE:HD12	1.98	0.45
14:AI:79:SER:HB3	14:AI:147:HIS:CD2	2.52	0.45
51:A2:471:C:N4	51:A2:472:G:O6	2.49	0.45
51:A2:1310:C:H2'	51:A2:1311:G:C8	2.52	0.45
51:A2:1540:A:H2'	51:A2:1541:G:H8	1.80	0.45
51:A2:1962:G:O6	51:A2:1968:C:N4	2.47	0.45
51:A2:4200:G:H2'	51:A2:4201:A:C8	2.52	0.45
52:B1:1311:C:OP1	62:BM:40:LYS:NZ	2.48	0.45
62:BM:95:ASP:OD1	62:BM:98:GLY:N	2.47	0.45
68:BS:90:VAL:HG22	68:BS:93:GLY:N	2.32	0.45
69:BT:53:PHE:HD1	69:BT:102:ARG:HH22	1.62	0.45
1:AA:54:ARG:HG2	1:AA:56:ALA:H	1.82	0.45
2:BA:172:GLY:HA3	2:BA:203:PHE:HD1	1.81	0.45
2:BA:208:GLU:O	2:BA:210:ILE:N	2.49	0.45
3:AB:219:VAL:HG11	3:AB:337:VAL:HG13	1.99	0.45
10:AE:131:LYS:HG2	10:AE:135:GLN:HB2	1.99	0.45
10:AE:149:ILE:HD12	10:AE:271:LEU:HD21	1.99	0.45
11:AF:85:ALA:HB2	25:AT:138:ALA:HB2	1.99	0.45
34:Ac:35:LEU:HA	34:Ac:38:ILE:HG22	1.98	0.45
43:Al:12:PHE:HE2	43:Al:49:LEU:HD13	1.82	0.45
51:A2:1414:C:H42	51:A2:1435:A:H61	1.63	0.45
51:A2:1585:C:H2'	51:A2:1586:G:H8	1.81	0.45
51:A2:4642:G:H2'	51:A2:4643:A:C8	2.52	0.45
51:A2:4876:C:H2'	51:A2:4877:G:C8	2.52	0.45
52:B1:155:G:H21	56:BG:56:ASN:HD21	1.64	0.45
52:B1:980:A:H2'	52:B1:981:A:C8	2.52	0.45
52:B1:1286:G:N2	52:B1:1312:G:O6	2.50	0.45
61:BL:14:PRO:HG3	61:BL:56:ILE:HG23	1.99	0.45
69:BT:39:LEU:HD12	69:BT:43:LYS:H	1.82	0.45
4:BB:50:THR:HB	4:BB:51:ARG:H	1.58	0.45
4:BB:197:ILE:O	4:BB:201:CYS:HB2	2.16	0.45
9:AD:232:THR:HG23	9:AD:235:MET:HB2	1.99	0.45
51:A2:469:G:H22	51:A2:672:G:H22	1.65	0.45
51:A2:701:G:H2'	51:A2:702:A:C8	2.51	0.45
51:A2:920:G:N2	51:A2:925:C:HO2'	2.15	0.45
51:A2:1416:A:H3'	51:A2:1417:G:H8	1.81	0.45
51:A2:1627:C:H2'	51:A2:1628:A:H8	1.81	0.45
51:A2:2354:A:H2'	51:A2:2355:A:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:A2:4723:G:N2	51:A2:4727:G:O2'	2.49	0.45
52:B1:598:G:H2'	52:B1:599:A:H8	1.81	0.45
52:B1:1856:C:H2'	52:B1:1857:G:C8	2.52	0.45
55:BF:143:PRO:HB3	55:BF:146:ARG:HH21	1.82	0.45
66:BQ:16:LYS:HG3	66:BQ:17:LYS:H	1.82	0.45
66:BQ:61:GLU:HA	66:BQ:64:ALA:HB3	1.98	0.45
1:AA:216:HIS:HB2	1:AA:218:HIS:HD2	1.82	0.45
5:AC:190:ARG:NH1	51:A2:2274:C:OP1	2.50	0.45
6:BC:196:ILE:HB	6:BC:223:TYR:HB2	1.99	0.45
11:AF:216:PRO:O	51:A2:1886:U:O2'	2.33	0.45
11:AF:223:LYS:HD2	51:A2:1888:A:H4'	1.98	0.45
17:AL:19:GLN:NE2	51:A2:1500:A:H61	2.15	0.45
26:AU:56:LEU:HD11	26:AU:61:VAL:HG21	1.17	0.45
51:A2:635:G:H2'	51:A2:636:G:H8	1.82	0.45
51:A2:1576:C:O2'	51:A2:1579:G:O2'	2.33	0.45
51:A2:1784:A:H5''	51:A2:1785:G:H5'	1.98	0.45
51:A2:2626:A:H3'	51:A2:2627:G:H8	1.81	0.45
52:B1:682:U:O2'	72:BW:4:MET:SD	2.66	0.45
52:B1:1781:A:H2'	52:B1:1782:G:C8	2.52	0.45
53:BD:136:VAL:HG22	53:BD:186:VAL:HG22	1.98	0.45
57:BH:79:LEU:HD22	57:BH:94:PHE:HZ	1.82	0.45
58:BI:76:THR:HG23	58:BI:108:PRO:HG2	1.99	0.45
58:BI:165:GLN:HE22	58:BI:195:LEU:HD11	1.82	0.45
1:AA:196:TRP:CG	1:AA:197:PRO:CD	2.79	0.45
3:AB:63:PRO:CA	3:AB:68:ASN:HD22	2.27	0.45
15:AJ:55:TYR:O	15:AJ:55:TYR:CD2	2.70	0.45
19:AN:94:PHE:CD2	19:AN:94:PHE:O	2.70	0.45
24:AS:98:ARG:HH11	24:AS:145:PHE:HB3	1.81	0.45
26:AU:100:LEU:HD23	26:AU:112:LEU:HB3	1.99	0.45
33:Ab:44:ARG:NE	51:A2:1447:G:OP1	2.50	0.45
37:Af:106:TYR:HB2	37:Af:107:PRO:CD	2.37	0.45
50:Au:26:ARG:NE	51:A2:3946:C:OP1	2.50	0.45
51:A2:472:G:H2'	51:A2:473:G:C8	2.52	0.45
51:A2:1281:C:H2'	51:A2:1282:G:C8	2.53	0.45
51:A2:1566:G:N1	51:A2:1592:C:O2	2.49	0.45
51:A2:3940:G:H2'	51:A2:3941:G:H8	1.82	0.45
51:A2:4199:C:H2'	51:A2:4200:G:C8	2.52	0.45
52:B1:223:C:H2'	52:B1:224:A:C8	2.51	0.45
52:B1:385:G:H3'	61:BL:136:LYS:HB2	1.98	0.45
52:B1:1156:U:OP1	72:BW:71:LYS:NZ	2.36	0.45
52:B1:1775:U:H2'	52:B1:1776:G:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:BH:80:VAL:HG23	57:BH:92:VAL:HB	1.98	0.45
60:BK:32:HIS:CE1	60:BK:41:PRO:HB3	2.52	0.45
65:BP:49:LEU:HA	65:BP:53:GLN:OE1	2.17	0.45
83:Bv:19:G:O4'	83:Bv:57:G:N2	2.50	0.45
9:AD:9:ASN:OD1	9:AD:12:TYR:HB3	2.16	0.44
9:AD:264:LYS:HD2	9:AD:264:LYS:H	1.82	0.44
9:AD:279:ARG:HE	51:A2:1160:U:H4'	1.82	0.44
16:AK:13:TYR:OH	51:A2:1980:A:OP1	2.29	0.44
22:AQ:59:PRO:HG2	22:AQ:141:GLY:HA3	1.97	0.44
30:AY:87:ARG:NH2	51:A2:380:A:O4'	2.50	0.44
34:Ac:105:ILE:O	34:Ac:109:PRO:HD2	2.17	0.44
44:Am:104:HIS:HB3	44:Am:107:ALA:HB2	1.98	0.44
49:At:22:LYS:HD2	49:At:22:LYS:HA	1.76	0.44
51:A2:312:A:H2'	51:A2:313:A:H8	1.81	0.44
51:A2:1838:C:H2'	51:A2:1839:A:C8	2.52	0.44
51:A2:2254:G:H2'	51:A2:2255:A:H8	1.82	0.44
51:A2:2849:A:OP2	51:A2:2858:A:N6	2.50	0.44
51:A2:3659:U:H2'	51:A2:3660:G:H8	1.82	0.44
51:A2:4539:U:H2'	51:A2:4540:G:H8	1.81	0.44
51:A2:4925:A:H2'	51:A2:4926:A:H8	1.83	0.44
54:BE:137:PRO:HG2	54:BE:149:TYR:HA	1.99	0.44
56:BG:67:VAL:HG13	56:BG:99:GLY:HA2	1.99	0.44
67:BR:92:ASP:HB2	67:BR:96:ILE:HD11	2.00	0.44
5:AC:212:ASN:OD1	5:AC:255:SER:OG	2.26	0.44
10:AE:128:HIS:NE2	51:A2:1265:G:C8	2.86	0.44
17:AL:36:ARG:NH2	51:A2:1347:U:O4	2.50	0.44
19:AN:14:LYS:HD2	51:A2:274:G:C5	2.52	0.44
37:Af:78:HIS:HB2	37:Af:85:ARG:HG3	1.97	0.44
48:Aq:59:THR:CG2	48:Aq:75:PRO:CA	2.95	0.44
50:Au:60:ARG:NH1	50:Au:60:ARG:HG3	2.31	0.44
51:A2:131:C:N4	51:A2:137:G:O6	2.37	0.44
51:A2:2569:G:N2	51:A2:2734:A:H62	2.16	0.44
51:A2:4136:U:H2'	51:A2:4137:G:C8	2.52	0.44
52:B1:373:G:H2'	52:B1:374:G:H8	1.82	0.44
52:B1:442:C:N4	52:B1:449:A:H62	2.10	0.44
52:B1:942:G:H2'	52:B1:943:U:C6	2.52	0.44
54:BE:11:ARG:HD2	54:BE:20:LEU:HB3	1.99	0.44
65:BP:44:ARG:C	65:BP:48:GLY:H	2.16	0.44
65:BP:50:ARG:CG	65:BP:52:LYS:HG3	2.47	0.44
73:BX:130:LEU:HD23	73:BX:133:LEU:HD12	1.99	0.44
5:AC:134:PRO:CD	5:AC:150:LEU:HD12	2.45	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:Af:29:LYS:HB2	37:Af:83:MET:HE2	1.98	0.44
51:A2:450:C:H2'	51:A2:451:G:H8	1.81	0.44
51:A2:2534:G:H2'	51:A2:2535:G:C8	2.53	0.44
51:A2:4199:C:H2'	51:A2:4200:G:H8	1.82	0.44
51:A2:4201:A:H2'	51:A2:4202:G:H8	1.82	0.44
51:A2:4457:G:H2'	51:A2:4458:A:H8	1.82	0.44
52:B1:661:U:O2'	72:BW:92:ASN:ND2	2.38	0.44
52:B1:1663:A:H4'	52:B1:1664:A:H5'	1.99	0.44
53:BD:138:VAL:HG22	53:BD:184:ILE:HG22	1.97	0.44
63:BN:46:THR:HG23	63:BN:86:GLU:HG2	2.00	0.44
78:Bc:16:LYS:HD3	78:Bc:31:ARG:NH1	2.31	0.44
3:AB:95:THR:OG1	3:AB:98:GLY:N	2.50	0.44
4:BB:36:PRO:HG2	4:BB:39:PHE:HE2	1.82	0.44
5:AC:250:CYS:SG	5:AC:252:TRP:NE1	2.90	0.44
10:AE:138:ARG:HD3	10:AE:138:ARG:HA	1.50	0.44
19:AN:146:PRO:HA	19:AN:149:GLN:HG3	1.99	0.44
20:AO:51:LYS:NZ	20:AO:144:GLU:OE2	2.41	0.44
30:AY:4:ASN:HB2	30:AY:7:VAL:HG12	1.99	0.44
35:Ad:79:ASN:ND2	51:A2:4615:C:OP1	2.51	0.44
51:A2:1296:C:O2	51:A2:3852:G:O2'	2.34	0.44
51:A2:1382:G:H2'	51:A2:1383:G:H8	1.82	0.44
51:A2:2728:C:H2'	51:A2:2729:G:H8	1.80	0.44
51:A2:3887:G:H2'	51:A2:3888:A:H8	1.82	0.44
51:A2:3914:A:H2'	51:A2:3915:G:C8	2.51	0.44
51:A2:4666:C:H2'	51:A2:4667:A:C8	2.52	0.44
52:B1:1284:A:OP2	52:B1:1285:G:O2'	2.32	0.44
54:BE:125:LYS:H	54:BE:142:HIS:CE1	2.35	0.44
59:BJ:109:ARG:HH12	59:BJ:111:GLN:HE21	1.65	0.44
7:A3:153:C:H2'	7:A3:154:G:C8	2.52	0.44
10:AE:177:GLY:HA3	10:AE:184:VAL:HB	1.98	0.44
10:AE:264:ILE:HA	10:AE:265:PRO:HD3	1.85	0.44
16:AK:24:TYR:HD1	16:AK:90:PHE:HD2	1.58	0.44
27:AV:83:ARG:NH1	27:AV:120:PRO:O	2.49	0.44
31:AZ:136:PHE:O	51:A2:4091:G:O2'	2.36	0.44
36:Ae:18:LYS:NZ	51:A2:433:G:OP2	2.50	0.44
44:Am:97:ARG:NH1	44:Am:121:LEU:O	2.51	0.44
50:Au:1:MET:HG3	50:Au:202:ARG:HG3	1.99	0.44
51:A2:226:G:N2	51:A2:235:C:O2	2.50	0.44
51:A2:1436:G:H2'	51:A2:1437:G:H8	1.83	0.44
51:A2:3887:G:H2'	51:A2:3888:A:C8	2.52	0.44
51:A2:4159:G:H1	83:Bv:74:C:H42	1.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:A2:4715:U:C4	51:A2:4837:C:N4	2.85	0.44
51:A2:4841:C:H2'	51:A2:4842:G:C8	2.53	0.44
52:B1:641:A:O2'	52:B1:645:C:OP1	2.32	0.44
52:B1:941:C:H2'	52:B1:942:G:H8	1.83	0.44
52:B1:1018:U:H2'	52:B1:1019:C:H6	1.82	0.44
59:BJ:111:GLN:HB3	59:BJ:130:ILE:HD13	1.99	0.44
64:BO:20:GLN:OE1	64:BO:20:GLN:HA	2.18	0.44
72:BW:111:MET:HE1	72:BW:119:LYS:HG2	2.00	0.44
3:AB:220:ILE:HG12	3:AB:278:THR:HG22	1.98	0.44
12:AG:191:GLY:HA2	12:AG:194:VAL:HG12	2.00	0.44
13:AH:18:ILE:HG13	13:AH:27:VAL:HG22	2.00	0.44
20:AO:44:SER:OG	51:A2:2035:U:OP2	2.36	0.44
20:AO:122:ALA:HB2	24:AS:162:GLN:HG3	2.00	0.44
22:AQ:89:ASP:O	22:AQ:112:ARG:NH2	2.50	0.44
30:AY:86:GLN:HE22	30:AY:96:HIS:CE1	2.36	0.44
37:Af:106:TYR:OH	51:A2:4901:A:H4'	2.18	0.44
49:At:53:PRO:HB3	49:At:117:ILE:HD11	2.00	0.44
51:A2:466:C:H2'	51:A2:467:C:C6	2.53	0.44
51:A2:652:C:H2'	51:A2:653:G:C8	2.53	0.44
51:A2:1157:G:H2'	51:A2:1158:A:C8	2.53	0.44
51:A2:1375:A:H2'	51:A2:1376:G:C8	2.53	0.44
51:A2:4115:C:H2'	51:A2:4116:G:C8	2.52	0.44
51:A2:4600:U:H2'	51:A2:4601:G:C8	2.53	0.44
52:B1:907:G:H2'	52:B1:908:A:C8	2.53	0.44
52:B1:981:A:H2'	52:B1:982:G:C8	2.52	0.44
52:B1:987:A:H4'	76:Ba:70:LYS:HG3	1.98	0.44
52:B1:1523:C:OP1	68:BS:142:ARG:N	2.48	0.44
52:B1:1539:U:H2'	52:B1:1540:G:H8	1.83	0.44
66:BQ:17:LYS:HE2	66:BQ:17:LYS:HB3	1.76	0.44
2:BA:208:GLU:OE2	2:BA:209:GLU:HA	2.08	0.44
7:A3:19:C:H2'	7:A3:20:A:C8	2.52	0.44
11:AF:24:ASN:HA	11:AF:27:GLU:HG2	1.99	0.44
11:AF:169:LEU:HD13	11:AF:187:MET:HE2	2.00	0.44
19:AN:138:PHE:HA	19:AN:143:ARG:HD2	1.99	0.44
23:AR:105:LEU:HD22	23:AR:135:LYS:HG3	1.99	0.44
29:AX:60:TYR:OH	29:AX:62:ARG:NH1	2.51	0.44
31:AZ:9:LYS:HB3	31:AZ:25:ILE:HD12	1.99	0.44
50:Au:159:MET:HE3	50:Au:159:MET:HB3	1.68	0.44
51:A2:2709:U:H2'	51:A2:2710:C:C6	2.53	0.44
51:A2:2736:A:O2'	51:A2:2745:A:O2'	2.34	0.44
51:A2:4436:A:OP2	51:A2:4438:C:N4	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:BH:20:GLU:HG2	57:BH:48:ALA:HB3	2.00	0.44
82:Bg:133:ASN:HB2	82:Bg:138:CYS:HB2	1.99	0.44
2:BA:42:LYS:HZ2	2:BA:48:ILE:HD11	1.82	0.44
5:AC:139:SER:O	49:At:15:SER:N	2.47	0.44
5:AC:201:ARG:NH2	51:A2:231:G:OP1	2.43	0.44
11:AF:244:ILE:O	11:AF:248:ASN:HB2	2.17	0.44
16:AK:16:LYS:O	16:AK:20:LEU:HB2	2.17	0.44
19:AN:194:ARG:NH1	51:A2:79:C:OP2	2.47	0.44
28:AW:11:TYR:OH	51:A2:4999:G:N2	2.50	0.44
48:Aq:136:ALA:HB1	48:Aq:139:VAL:HB	2.00	0.44
51:A2:1057:G:H2'	51:A2:1058:G:C8	2.53	0.44
51:A2:1394:C:H2'	51:A2:1395:G:C8	2.53	0.44
51:A2:4351:C:H2'	51:A2:4352:A:H8	1.83	0.44
52:B1:173:A:H2'	52:B1:174:C:H6	1.82	0.44
52:B1:658:U:O2	52:B1:659:G:N2	2.50	0.44
52:B1:1234:C:H2'	52:B1:1235:G:H8	1.83	0.44
72:BW:90:GLN:HE21	72:BW:113:HIS:CE1	2.36	0.44
74:BY:11:LYS:O	74:BY:23:MET:HA	2.18	0.44
8:A4:15:C:H2'	8:A4:16:A:C8	2.53	0.44
9:AD:8:LYS:CE	9:AD:8:LYS:CA	2.86	0.44
17:AL:71:ARG:NH2	51:A2:74:G:O3'	2.48	0.44
48:Aq:16:ARG:HA	48:Aq:16:ARG:HD2	1.85	0.44
51:A2:1525:G:OP1	51:A2:2493:G:O2'	2.33	0.44
51:A2:1539:C:H2'	51:A2:1540:A:C8	2.52	0.44
51:A2:1953:G:N1	51:A2:1954:G:O6	2.51	0.44
51:A2:2274:C:H2'	51:A2:2275:G:C8	2.53	0.44
52:B1:231:A:OP2	52:B1:889:U:O2'	2.35	0.44
52:B1:388:U:H2'	52:B1:389:A:C8	2.53	0.44
52:B1:409:C:H42	52:B1:431:G:H1	1.65	0.44
52:B1:1144:A:H2'	52:B1:1145:A:C8	2.53	0.44
52:B1:1856:C:H2'	52:B1:1857:G:H8	1.83	0.44
54:BE:45:ILE:O	54:BE:49:ARG:CB	2.66	0.44
64:BO:21:VAL:O	64:BO:22:ALA:C	2.61	0.44
69:BT:75:MET:HA	69:BT:78:ILE:HD12	2.00	0.44
82:Bg:256:ILE:O	82:Bg:269:GLU:HA	2.18	0.44
5:AC:53:ALA:HB2	51:A2:344:C:H1'	1.90	0.43
8:A4:11:A:N6	9:AD:13:PHE:O	2.51	0.43
9:AD:9:ASN:OD1	9:AD:12:TYR:HB2	2.10	0.43
16:AK:8:THR:HA	16:AK:12:ASN:HD22	1.83	0.43
23:AR:82:LYS:O	51:A2:2842:G:O2'	2.34	0.43
30:AY:2:LYS:HD2	30:AY:7:VAL:HG13	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:A2:4222:U:H2'	51:A2:4223:C:H6	1.82	0.43
52:B1:75:G:N2	52:B1:77:A:O5'	2.51	0.43
52:B1:512:A:H2'	52:B1:513:G:H8	1.83	0.43
52:B1:527:C:O2	52:B1:559:G:N2	2.51	0.43
54:BE:114:ILE:HD12	54:BE:114:ILE:HA	1.89	0.43
55:BF:121:PRO:O	55:BF:146:ARG:HG2	2.18	0.43
60:BK:71:LEU:HD21	60:BK:79:LEU:HD11	2.00	0.43
60:BK:89:ILE:HG23	60:BK:95:ARG:HH22	1.83	0.43
63:BN:114:ARG:HD3	63:BN:117:LEU:HD12	2.00	0.43
1:AA:101:VAL:HA	1:AA:165:VAL:HA	2.00	0.43
4:BB:73:ASP:OD1	4:BB:73:ASP:N	2.50	0.43
8:A4:92:C:H2'	8:A4:93:G:C8	2.52	0.43
10:AE:266:GLN:HE22	51:A2:4888:C:H5''	1.82	0.43
11:AF:137:GLU:HB3	11:AF:226:HIS:HE1	1.83	0.43
14:AI:51:HIS:CD2	14:AI:168:SER:HB2	2.53	0.43
15:AJ:23:ASN:HB3	15:AJ:129:ASP:HB3	2.00	0.43
17:AL:74:ARG:NH1	51:A2:76:A:OP2	2.50	0.43
36:Ae:109:LYS:HA	36:Ae:112:VAL:HG12	2.00	0.43
50:Au:65:VAL:HG22	50:Au:109:ALA:HB3	2.01	0.43
51:A2:159:A:H2'	51:A2:160:A:H8	1.84	0.43
51:A2:278:G:H2'	51:A2:279:G:H8	1.83	0.43
52:B1:324:C:H2'	52:B1:325:C:H3'	2.00	0.43
52:B1:940:U:H3	52:B1:1002:U:H3	1.64	0.43
66:BQ:32:ILE:HD13	66:BQ:39:LEU:HD13	2.00	0.43
69:BT:41:LYS:HG3	69:BT:42:HIS:H	1.83	0.43
78:Bc:13:ARG:HB3	78:Bc:55:VAL:HG22	1.99	0.43
3:AB:45:ALA:HA	3:AB:347:LEU:O	2.18	0.43
3:AB:324:GLY:HA2	51:A2:5009:C:H4'	2.00	0.43
8:A4:105:C:OP2	14:AI:203:ARG:NH1	2.32	0.43
16:AK:20:LEU:O	16:AK:24:TYR:CE1	2.72	0.43
19:AN:124:ASP:OD1	19:AN:124:ASP:N	2.52	0.43
29:AX:93:ASN:ND2	51:A2:2511:C:O2'	2.51	0.43
33:Ab:9:THR:N	51:A2:1855:A:OP1	2.49	0.43
50:Au:171:HIS:HD2	50:Au:173:LYS:HB2	1.83	0.43
51:A2:243:G:H2'	51:A2:244:G:C8	2.53	0.43
51:A2:1826:U:H2'	51:A2:1827:G:H8	1.83	0.43
51:A2:2529:G:H2'	51:A2:2530:A:H8	1.82	0.43
51:A2:2749:C:H2'	51:A2:2750:G:C8	2.53	0.43
51:A2:4201:A:H2'	51:A2:4202:G:C8	2.53	0.43
57:BH:147:LYS:HG2	57:BH:148:LEU:H	1.83	0.43
59:BJ:119:LEU:HD21	59:BJ:159:PHE:HE1	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:BN:136:PRO:HA	63:BN:137:PRO:HD3	1.87	0.43
65:BP:70:MET:HE2	65:BP:70:MET:HB2	1.91	0.43
76:Ba:12:LYS:HG3	76:Ba:15:ARG:HB2	1.99	0.43
1:AA:72:ARG:NH2	51:A2:4054:G:O6	2.52	0.43
6:BC:259:THR:CG2	6:BC:261:PHE:CE2	3.01	0.43
9:AD:234:ASP:OD1	9:AD:234:ASP:N	2.50	0.43
21:AP:60:PHE:HD2	21:AP:67:VAL:HG21	1.84	0.43
24:AS:174:THR:HG1	51:A2:4724:A:HO2'	1.62	0.43
51:A2:721:G:H2'	51:A2:722:G:C8	2.53	0.43
51:A2:1316:A:H2'	51:A2:1317:A:C8	2.54	0.43
51:A2:1540:A:H2'	51:A2:1541:G:C8	2.53	0.43
51:A2:1955:U:N3	51:A2:1983:A:C8	2.87	0.43
52:B1:688:U:H1'	52:B1:742:U:C4	2.53	0.43
57:BH:144:ILE:HB	72:BW:52:ILE:HB	2.00	0.43
58:BI:161:LEU:HB3	58:BI:195:LEU:HD23	2.01	0.43
64:BO:99:ALA:HB2	64:BO:108:PRO:HA	1.98	0.43
11:AF:214:SER:OG	11:AF:215:SER:N	2.52	0.43
13:AH:91:LYS:HB2	13:AH:183:GLU:HB3	2.01	0.43
18:AM:97:ALA:HB1	20:AO:198:THR:HG23	2.00	0.43
21:AP:29:THR:HA	21:AP:32:THR:HG22	2.01	0.43
22:AQ:144:LYS:HB3	51:A2:1442:C:H5''	2.01	0.43
50:Au:207:LYS:HG2	50:Au:213:PRO:HA	2.00	0.43
51:A2:268:C:H2'	51:A2:269:C:H6	1.83	0.43
51:A2:963:G:H1	51:A2:1261:C:N4	2.15	0.43
51:A2:1963:G:H1	51:A2:1968:C:N4	2.16	0.43
51:A2:4507:G:H2'	51:A2:4508:A:H8	1.84	0.43
52:B1:234:C:H2'	52:B1:235:A:C8	2.50	0.43
52:B1:388:U:H2'	52:B1:389:A:H8	1.84	0.43
52:B1:519:A:H2'	52:B1:520:A:H8	1.84	0.43
6:BC:65:LYS:HB2	6:BC:68:ARG:HH21	1.83	0.43
24:AS:8:ARG:HD3	24:AS:66:GLN:HE22	1.84	0.43
51:A2:183:G:H21	51:A2:184:U:H1'	1.84	0.43
51:A2:715:C:H2'	51:A2:716:G:C8	2.52	0.43
51:A2:732:C:H2'	51:A2:733:G:C8	2.54	0.43
51:A2:1224:C:OP1	51:A2:1252:G:N2	2.43	0.43
51:A2:3726:G:H21	83:Bv:12:U:H4'	1.83	0.43
51:A2:3741:U:H2'	51:A2:3742:C:C6	2.53	0.43
51:A2:4038:U:H2'	51:A2:4039:U:C6	2.53	0.43
51:A2:4722:G:H2'	51:A2:4723:G:C8	2.54	0.43
52:B1:35:C:H5''	52:B1:579:C:H5''	2.01	0.43
54:BE:79:ASP:HB3	54:BE:82:TYR:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:BF:21:GLY:H	55:BF:23:TRP:CD1	2.33	0.43
57:BH:27:LEU:HD23	57:BH:30:LEU:HD12	1.99	0.43
68:BS:90:VAL:HG23	68:BS:92:ASP:H	1.83	0.43
1:AA:196:TRP:CH2	51:A2:1595:A:C2	3.05	0.43
6:BC:252:THR:HA	6:BC:253:PRO:HD3	1.88	0.43
13:AH:23:ARG:HE	13:AH:39:ASN:HA	1.84	0.43
16:AK:95:LEU:HB3	16:AK:96:THR:H	1.65	0.43
17:AL:165:LYS:HE2	17:AL:165:LYS:HB3	1.66	0.43
23:AR:123:LEU:HD23	23:AR:123:LEU:HA	1.86	0.43
51:A2:186:G:H2'	51:A2:187:G:C8	2.54	0.43
51:A2:1258:G:H1'	51:A2:1259:C:C6	2.53	0.43
51:A2:1397:C:H2'	51:A2:1398:G:C8	2.53	0.43
51:A2:1989:U:O2	51:A2:1993:A:N6	2.51	0.43
51:A2:4170:U:H2'	51:A2:4171:G:H8	1.84	0.43
52:B1:1017:U:H5'	63:BN:55:ARG:HD3	2.00	0.43
52:B1:1748:G:N2	52:B1:1786:U:O2	2.35	0.43
53:BD:9:ARG:HH21	79:Bd:35:GLY:HA2	1.84	0.43
61:BL:59:LYS:HD3	61:BL:134:LEU:HD23	1.99	0.43
64:BO:29:GLY:O	64:BO:93:LEU:HA	2.19	0.43
71:BV:22:ARG:HH22	71:BV:58:ALA:HB3	1.84	0.43
2:BA:121:LEU:HD21	2:BA:145:ILE:HD12	2.01	0.43
4:BB:204:ILE:O	52:B1:1121:G:O2'	2.36	0.43
9:AD:19:LYS:NZ	51:A2:4241:A:O2'	2.52	0.43
9:AD:264:LYS:HB3	9:AD:264:LYS:NZ	2.33	0.43
10:AE:110:ARG:NH1	51:A2:955:C:OP1	2.45	0.43
22:AQ:9:LYS:O	22:AQ:9:LYS:HG2	2.18	0.43
51:A2:440:C:H2'	51:A2:441:C:C6	2.54	0.43
51:A2:500:C:H2'	51:A2:501:G:H8	1.84	0.43
51:A2:900:U:H2'	51:A2:901:U:C6	2.53	0.43
51:A2:2617:G:N2	51:A2:2676:A:H62	2.17	0.43
51:A2:3931:A:N3	51:A2:4014:U:O2'	2.51	0.43
51:A2:4484:G:O2'	51:A2:4487:C:OP2	2.28	0.43
52:B1:533:A:O2'	52:B1:534:G:N7	2.51	0.43
52:B1:984:C:O2'	64:BO:138:ASP:O	2.36	0.43
82:Bg:63:SER:HB2	82:Bg:84:ASP:HB3	2.01	0.43
3:AB:116:ARG:HG2	3:AB:177:LYS:HG2	2.00	0.43
4:BB:30:TRP:CD2	4:BB:48:LEU:CD2	3.01	0.43
5:AC:101:MET:HE2	5:AC:104:PRO:HA	2.00	0.43
6:BC:65:LYS:HG3	6:BC:273:LEU:HD22	2.01	0.43
6:BC:256:TRP:CE2	72:BW:68:ARG:HB2	2.44	0.43
8:A4:15:C:H2'	8:A4:16:A:H8	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AI:118:ALA:O	51:A2:1845:G:O2'	2.32	0.43
20:AO:36:VAL:HG12	20:AO:108:ILE:HG12	2.01	0.43
27:AV:14:PHE:HE2	27:AV:91:LYS:HD3	1.84	0.43
32:Aa:6:ARG:HG3	32:Aa:8:THR:H	1.84	0.43
33:Ab:25:ARG:HE	33:Ab:27:GLN:HE22	1.66	0.43
48:Aq:41:LYS:HZ2	48:Aq:70:GLN:HG3	1.82	0.43
50:Au:188:ASN:HA	50:Au:191:VAL:HG22	2.00	0.43
51:A2:1443:C:H2'	51:A2:1444:A:H8	1.82	0.43
51:A2:1831:A:N3	51:A2:2262:G:O2'	2.52	0.43
51:A2:1836:G:O6	51:A2:1861:G:N2	2.51	0.43
51:A2:4547:U:O4	51:A2:4680:G:N2	2.52	0.43
52:B1:96:C:H41	52:B1:434:G:H1	1.67	0.43
57:BH:154:ILE:HB	57:BH:185:VAL:HG12	1.99	0.43
72:BW:94:LEU:HD12	72:BW:97:ARG:NH1	2.34	0.43
74:BY:119:GLY:H	74:BY:122:LYS:HZ2	1.67	0.43
76:Ba:46:GLU:HG3	76:Ba:48:ALA:H	1.84	0.43
83:Bv:56:C:H2'	83:Bv:57:G:H8	1.84	0.43
84:Bx:58:U:O2	84:Bx:58:U:O2'	2.27	0.43
1:AA:53:GLY:O	1:AA:192:LYS:NZ	2.46	0.43
2:BA:57:LYS:HZ3	71:BV:70:LEU:HB3	1.83	0.43
6:BC:251:LEU:HD13	72:BW:68:ARG:HD2	2.01	0.43
19:AN:94:PHE:O	19:AN:94:PHE:CG	2.70	0.43
34:Ac:77:ASN:N	34:Ac:80:GLU:OE2	2.50	0.43
36:Ae:122:VAL:HG13	36:Ae:125:PRO:HB3	2.01	0.43
50:Au:60:ARG:HH11	50:Au:60:ARG:CG	2.31	0.43
51:A2:951:A:H2'	51:A2:952:G:H2'	2.01	0.43
51:A2:1174:C:H2'	51:A2:1175:C:C6	2.53	0.43
51:A2:2652:G:H5''	51:A2:2653:A:H3'	2.00	0.43
51:A2:3839:G:H22	51:A2:3871:G:H1'	1.84	0.43
51:A2:4551:A:H8	51:A2:4552:A:H1'	1.84	0.43
52:B1:609:U:H2'	52:B1:610:G:C8	2.54	0.43
52:B1:1407:U:H2'	52:B1:1408:U:C6	2.54	0.43
53:BD:146:ARG:HH22	84:Bx:53:U:H5''	1.83	0.43
73:BX:132:ALA:HB1	73:BX:137:LYS:CB	2.48	0.43
7:A3:79:G:H2'	7:A3:80:A:C4	2.53	0.42
9:AD:39:GLN:NE2	9:AD:43:LYS:HD2	2.34	0.42
23:AR:32:ILE:HD13	23:AR:44:LEU:HD13	2.01	0.42
25:AT:4:THR:HG22	51:A2:4169:C:H5''	2.01	0.42
40:Ai:23:LYS:HA	40:Ai:24:PRO:HD3	1.92	0.42
47:Ap:32:SER:HB3	47:Ap:70:THR:HG22	2.01	0.42
51:A2:114:G:H21	51:A2:270:C:H4'	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:A2:286:G:H21	51:A2:288:G:H22	1.67	0.42
51:A2:1572:C:H4'	51:A2:2836:A:H5'	2.01	0.42
51:A2:1670:G:H2'	51:A2:1671:G:C8	2.54	0.42
51:A2:1976:G:O6	51:A2:1981:G:N2	2.53	0.42
51:A2:3726:G:O6	51:A2:3741:U:O4	2.37	0.42
51:A2:3942:G:H22	51:A2:4019:U:H5'	1.84	0.42
51:A2:4236:A:H2'	51:A2:4237:G:C8	2.54	0.42
52:B1:695:C:H3'	52:B1:696:G:H8	1.84	0.42
52:B1:1454:A:N6	52:B1:1477:U:OP2	2.52	0.42
52:B1:1612:G:C1'	68:BS:87:GLN:HG3	2.49	0.42
70:BU:23:THR:HB	70:BU:113:GLU:HB2	2.02	0.42
82:Bg:300:ALA:HB3	82:Bg:310:TRP:HZ3	1.84	0.42
3:AB:297:LYS:HG3	3:AB:298:LEU:H	1.84	0.42
5:AC:285:ILE:N	22:AQ:124:ASP:OD2	2.52	0.42
7:A3:96:C:OP1	39:Ah:70:ARG:NH2	2.52	0.42
20:AO:128:ARG:HH22	24:AS:161:ARG:NH1	2.17	0.42
28:AW:56:ARG:NH2	51:A2:4999:G:N7	2.67	0.42
36:Ae:44:ARG:NH1	51:A2:1298:C:OP2	2.53	0.42
42:Ak:23:VAL:HA	42:Ak:35:LYS:O	2.19	0.42
43:Al:41:ARG:HH22	51:A2:2410:A:P	2.42	0.42
50:Au:110:PHE:HB3	50:Au:135:PRO:HB3	2.01	0.42
51:A2:440:C:H2'	51:A2:441:C:H6	1.84	0.42
51:A2:707:C:H2'	51:A2:708:U:C6	2.54	0.42
51:A2:1187:C:H2'	51:A2:1188:G:C8	2.53	0.42
51:A2:3843:A:H2'	51:A2:3844:G:H8	1.84	0.42
51:A2:4326:G:H2'	51:A2:4327:C:H6	1.84	0.42
52:B1:164:A:H5''	56:BG:82:SER:HB2	2.00	0.42
52:B1:868:G:C2	57:BH:115:LYS:HG3	2.54	0.42
52:B1:1347:U:H2'	52:B1:1348:G:C8	2.54	0.42
52:B1:1593:C:OP2	75:BZ:104:ARG:NH2	2.52	0.42
59:BJ:153:SER:OG	59:BJ:154:GLN:N	2.52	0.42
66:BQ:72:VAL:HG12	66:BQ:74:GLY:H	1.84	0.42
76:Ba:23:CYS:SG	76:Ba:24:THR:N	2.92	0.42
83:Bv:25:C:H2'	83:Bv:26:A:H8	1.84	0.42
3:AB:68:ASN:OD1	3:AB:69:LYS:HG2	2.18	0.42
4:BB:146:ARG:HD2	52:B1:1123:C:H1'	2.01	0.42
12:AG:117:ARG:HH22	51:A2:119:G:H22	1.67	0.42
20:AO:194:GLU:HG3	20:AO:199:HIS:HA	2.02	0.42
22:AQ:12:LYS:NZ	22:AQ:14:ARG:HD3	2.34	0.42
22:AQ:12:LYS:HD2	22:AQ:14:ARG:HH11	1.84	0.42
30:AY:56:GLN:HB2	30:AY:67:ILE:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:A2:106:A:H2'	51:A2:107:G:O4'	2.20	0.42
51:A2:1333:C:H2'	51:A2:1334:G:C8	2.55	0.42
51:A2:4818:G:H2'	51:A2:4819:G:C8	2.54	0.42
51:A2:4912:G:H2'	51:A2:4913:A:C8	2.54	0.42
52:B1:979:C:H2'	52:B1:980:A:C8	2.54	0.42
3:AB:174:ARG:HH22	51:A2:4932:C:H1'	1.83	0.42
6:BC:272:HIS:HA	6:BC:275:LYS:HG2	2.02	0.42
7:A3:70:G:O2'	7:A3:87:G:N2	2.52	0.42
11:AF:152:GLU:HB3	11:AF:248:ASN:HD21	1.84	0.42
12:AG:40:GLY:HA3	12:AG:43:GLN:HE21	1.83	0.42
12:AG:192:ARG:HD3	12:AG:192:ARG:HA	1.81	0.42
13:AH:3:THR:O	13:AH:61:TRP:HA	2.20	0.42
20:AO:89:PRO:HD3	51:A2:1895:C:H4'	2.00	0.42
32:Aa:4:ARG:HA	32:Aa:9:ARG:HE	1.84	0.42
49:At:100:ASN:ND2	51:A2:474:C:O2	2.53	0.42
51:A2:379:A:N1	51:A2:405:G:N2	2.67	0.42
51:A2:684:U:H2'	51:A2:685:C:H6	1.85	0.42
51:A2:1182:G:H2'	51:A2:1183:G:C8	2.53	0.42
51:A2:1895:C:H5''	51:A2:1896:C:H2'	2.01	0.42
51:A2:2565:G:N7	51:A2:2566:A:N6	2.67	0.42
52:B1:291:G:OP2	54:BE:200:ARG:NH2	2.52	0.42
52:B1:463:C:O2'	52:B1:466:G:O6	2.28	0.42
52:B1:1300:U:N3	65:BP:51:ARG:CD	2.82	0.42
52:B1:1413:G:H2'	52:B1:1414:A:C8	2.54	0.42
52:B1:1447:G:H2'	52:B1:1448:A:C8	2.52	0.42
52:B1:1653:U:H2'	52:B1:1654:G:C8	2.54	0.42
52:B1:1854:U:H5''	64:BO:150:ARG:HH12	1.84	0.42
55:BF:100:ILE:HB	55:BF:108:PRO:HB3	2.00	0.42
65:BP:94:VAL:HG11	65:BP:116:LEU:HD13	2.01	0.42
67:BR:25:GLY:O	67:BR:31:ASN:ND2	2.48	0.42
73:BX:107:ARG:HD2	73:BX:107:ARG:HA	1.86	0.42
82:Bg:107:ASP:O	82:Bg:124:SER:OG	2.31	0.42
3:AB:17:LEU:O	3:AB:19:ARG:N	2.52	0.42
3:AB:218:ASP:OD1	3:AB:281:ASN:N	2.42	0.42
3:AB:316:PRO:HA	3:AB:370:THR:HB	2.01	0.42
4:BB:67:PHE:O	4:BB:85:LYS:HA	2.19	0.42
9:AD:260:GLU:C	9:AD:261:VAL:HG23	2.43	0.42
15:AJ:98:ASN:HD22	51:A2:4212:G:H5'	1.84	0.42
19:AN:94:PHE:CE2	19:AN:96:ARG:HB2	2.54	0.42
40:Ai:29:ARG:HD2	40:Ai:32:ARG:HG3	2.02	0.42
49:At:22:LYS:HB3	49:At:23:GLN:H	1.47	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:A2:1460:C:H2'	51:A2:1461:G:H8	1.84	0.42
51:A2:1487:C:H2'	51:A2:1488:G:C8	2.55	0.42
51:A2:1744:C:H2'	51:A2:1745:C:C6	2.54	0.42
51:A2:1975:C:H2'	51:A2:1976:G:H8	1.85	0.42
51:A2:2455:G:H2'	51:A2:2456:A:C8	2.55	0.42
51:A2:2601:G:H2'	51:A2:2602:A:C8	2.54	0.42
51:A2:4069:G:N7	51:A2:4070:C:N4	2.67	0.42
51:A2:4428:C:H2'	51:A2:4429:A:H8	1.83	0.42
51:A2:4982:C:O2'	58:BI:168:GLN:O	2.36	0.42
52:B1:96:C:H5	52:B1:434:G:H22	1.66	0.42
52:B1:799:U:H2'	52:B1:800:U:C6	2.55	0.42
53:BD:215:ASP:HB3	53:BD:216:GLU:H	1.73	0.42
58:BI:8:TRP:HB2	58:BI:18:ARG:NH1	2.34	0.42
4:BB:81:PHE:HD2	4:BB:82:ARG:HG3	1.85	0.42
7:A3:90:C:H2'	7:A3:91:A:H8	1.83	0.42
16:AK:30:VAL:HG21	16:AK:102:LEU:HD11	1.94	0.42
27:AV:13:LYS:HB2	27:AV:128:LEU:HD21	2.01	0.42
29:AX:141:ALA:HB3	29:AX:144:TYR:HD2	1.85	0.42
30:AY:73:VAL:HG22	30:AY:80:ILE:HG22	2.02	0.42
34:Ac:62:TYR:HA	34:Ac:65:MET:HG2	2.01	0.42
48:Aq:22:VAL:CG2	48:Aq:25:THR:O	2.66	0.42
50:Au:21:ASN:C	50:Au:22:GLN:NE2	2.77	0.42
50:Au:31:THR:HA	50:Au:171:HIS:HA	2.01	0.42
51:A2:197:U:H5	51:A2:210:G:H22	1.67	0.42
51:A2:1255:C:OP2	51:A2:1256:G:N1	2.52	0.42
51:A2:1577:G:H21	88:A2:5327:MVM:C8	2.33	0.42
51:A2:4726:A:N6	51:A2:4826:G:H22	2.18	0.42
52:B1:84:A:O3'	74:BY:122:LYS:NZ	2.48	0.42
52:B1:598:G:H2'	52:B1:599:A:C8	2.55	0.42
52:B1:600:G:H2'	52:B1:601:G:C8	2.55	0.42
52:B1:935:G:H2'	52:B1:936:G:H8	1.85	0.42
52:B1:1622:U:O5'	68:BS:120:HIS:NE2	2.42	0.42
54:BE:71:LYS:HA	54:BE:76:VAL:HA	2.01	0.42
59:BJ:33:GLY:HA3	80:Be:38:TYR:CG	2.55	0.42
69:BT:98:SER:O	69:BT:102:ARG:HB2	2.20	0.42
75:BZ:63:PRO:HG3	75:BZ:96:LEU:HD21	2.01	0.42
3:AB:10:ARG:NH1	3:AB:12:GLY:O	2.53	0.42
10:AE:215:ALA:HA	10:AE:218:LYS:HE3	2.01	0.42
27:AV:80:VAL:HG23	27:AV:106:VAL:HG11	2.01	0.42
48:Aq:35:LEU:HD12	48:Aq:37:LEU:HB3	2.00	0.42
51:A2:425:G:C8	51:A2:3859:G:H2'	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:A2:430:C:H2'	51:A2:431:G:C8	2.55	0.42
51:A2:2499:C:H2'	51:A2:2500:G:H8	1.85	0.42
51:A2:4534:U:H2'	51:A2:4535:G:C8	2.54	0.42
52:B1:16:G:H5'	52:B1:669:A:H61	1.85	0.42
52:B1:562:U:OP1	59:BJ:163:SER:OG	2.32	0.42
52:B1:683:G:N2	52:B1:1022:U:OP2	2.40	0.42
52:B1:878:G:H22	52:B1:908:A:H2	1.68	0.42
52:B1:1454:A:H2'	67:BR:3:ARG:HD3	2.01	0.42
56:BG:5:ILE:HG12	56:BG:111:LEU:HD12	2.02	0.42
60:BK:27:VAL:O	60:BK:29:MET:N	2.52	0.42
16:AK:39:GLN:HA	16:AK:42:GLN:HB2	2.01	0.42
17:AL:77:SER:O	17:AL:79:GLU:N	2.53	0.42
17:AL:165:LYS:HE2	51:A2:505:C:H5'	1.89	0.42
43:Al:45:ARG:HH21	51:A2:2775:G:H5'	1.84	0.42
46:Ao:68:LEU:HD11	46:Ao:85:ILE:HD11	2.02	0.42
46:Ao:80:LYS:O	51:A2:4308:U:O2'	2.30	0.42
48:Aq:50:THR:O	48:Aq:54:LYS:CA	2.67	0.42
50:Au:64:SER:O	50:Au:108:ASP:N	2.52	0.42
51:A2:317:C:H2'	51:A2:318:A:C8	2.53	0.42
51:A2:964:C:H2'	51:A2:965:G:H8	1.85	0.42
51:A2:1599:G:H2'	51:A2:1600:G:H8	1.85	0.42
51:A2:3832:A:H2'	51:A2:3833:A:C8	2.52	0.42
51:A2:3841:C:H2'	51:A2:3842:A:C8	2.55	0.42
52:B1:1096:G:OP2	72:BW:22:LYS:NZ	2.50	0.42
52:B1:1268:C:O2	65:BP:97:TYR:OH	2.37	0.42
52:B1:1324:G:N2	52:B1:1504:U:O2	2.36	0.42
52:B1:1542:C:H5''	69:BT:62:ARG:NH1	2.35	0.42
52:B1:1618:C:H2'	52:B1:1619:A:C8	2.55	0.42
57:BH:109:ARG:HH11	57:BH:111:LYS:HA	1.84	0.42
3:AB:392:LEU:HD22	3:AB:394:LYS:HE3	2.01	0.42
10:AE:240:TYR:HE1	51:A2:4897:C:H4'	1.85	0.42
12:AG:89:ARG:HH12	12:AG:185:LYS:HD3	1.84	0.42
14:AI:54:SER:HA	14:AI:163:GLN:HB2	2.02	0.42
20:AO:106:ASP:N	20:AO:106:ASP:OD1	2.52	0.42
24:AS:85:ASP:HB3	24:AS:123:SER:HB3	2.01	0.42
24:AS:151:LYS:HE2	24:AS:151:LYS:HB2	1.93	0.42
26:AU:26:THR:HA	26:AU:68:SER:HB2	2.02	0.42
51:A2:362:C:N4	51:A2:363:G:O6	2.52	0.42
51:A2:2060:G:H2'	51:A2:2061:U:C6	2.55	0.42
51:A2:3635:G:H2'	51:A2:3636:G:C8	2.54	0.42
51:A2:3815:U:H2'	51:A2:3816:A:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:A2:4414:U:OP2	51:A2:4484:G:N2	2.42	0.42
51:A2:4819:G:H2'	51:A2:4820:G:H8	1.85	0.42
51:A2:4976:C:H2'	51:A2:4977:A:H8	1.85	0.42
52:B1:350:C:O2'	52:B1:383:G:N2	2.53	0.42
52:B1:356:C:OP1	61:BL:105:ARG:NH2	2.52	0.42
52:B1:1451:G:OP1	67:BR:32:LYS:NZ	2.40	0.42
59:BJ:32:ILE:HD11	59:BJ:40:LYS:HG2	2.01	0.42
60:BK:76:ILE:HD13	60:BK:94:LEU:HD22	2.02	0.42
68:BS:54:LYS:NZ	68:BS:58:GLU:O	2.52	0.42
70:BU:21:ARG:HG2	70:BU:115:THR:HB	2.02	0.42
1:AA:104:VAL:HA	1:AA:107:MET:HE3	2.02	0.42
10:AE:123:ARG:HH21	51:A2:956:C:H5'	1.84	0.42
10:AE:131:LYS:HG2	10:AE:135:GLN:CB	2.50	0.42
17:AL:42:LYS:O	17:AL:46:ILE:HG12	2.20	0.42
19:AN:155:VAL:O	19:AN:162:ARG:NH2	2.39	0.42
23:AR:172:ARG:NH1	52:B1:908:A:H5''	2.34	0.42
50:Au:60:ARG:HD2	50:Au:61:PRO:HD3	2.00	0.42
51:A2:419:U:H2'	51:A2:420:A:H8	1.84	0.42
51:A2:450:C:H2'	51:A2:451:G:C8	2.55	0.42
51:A2:2610:U:H5''	51:A2:2611:U:H5'	2.02	0.42
51:A2:2645:U:O2'	51:A2:2647:G:N7	2.37	0.42
51:A2:2693:G:H2'	51:A2:2694:G:H8	1.85	0.42
51:A2:4286:A:H2'	51:A2:4287:A:C8	2.55	0.42
51:A2:4503:G:O2'	51:A2:4505:G:O6	2.37	0.42
51:A2:4562:G:H1'	51:A2:4563:U:H5	1.85	0.42
52:B1:300:U:H2'	52:B1:301:A:C8	2.55	0.42
52:B1:694:G:N1	52:B1:737:G:O6	2.53	0.42
52:B1:894:G:H2'	52:B1:895:G:C8	2.54	0.42
81:Bf:87:THR:N	81:Bf:88:PRO:CD	2.81	0.42
82:Bg:65:PHE:HB2	82:Bg:83:TRP:CD1	2.55	0.42
1:AA:58:LEU:HD11	1:AA:75:LEU:HD23	2.02	0.41
1:AA:117:GLU:OE1	1:AA:121:GLY:N	2.42	0.41
5:AC:132:ALA:O	5:AC:150:LEU:CD1	2.67	0.41
5:AC:147:VAL:CG1	5:AC:148:PRO:HD2	2.49	0.41
6:BC:82:TYR:CZ	6:BC:164:PRO:HD3	2.55	0.41
11:AF:110:GLN:HE21	22:AQ:5:ILE:HG23	1.85	0.41
20:AO:194:GLU:O	20:AO:199:HIS:N	2.52	0.41
48:Aq:7:PRO:HB2	48:Aq:8:ASN:H	1.66	0.41
51:A2:1551:U:H2'	51:A2:1552:G:H8	1.85	0.41
51:A2:1607:G:N2	51:A2:4148:A:OP1	2.44	0.41
51:A2:1621:U:N3	51:A2:1625:A:O2'	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:A2:2464:U:H2'	51:A2:2465:G:C8	2.55	0.41
51:A2:2474:U:H2'	51:A2:2475:G:C8	2.49	0.41
51:A2:2535:G:H2'	51:A2:2536:G:C8	2.54	0.41
51:A2:3581:A:H2'	51:A2:3582:A:C8	2.55	0.41
51:A2:3693:G:H2'	51:A2:3694:A:C8	2.54	0.41
52:B1:431:G:H2'	52:B1:432:G:H8	1.85	0.41
52:B1:948:C:H2'	52:B1:949:G:C8	2.54	0.41
52:B1:1061:U:O2	52:B1:1848:U:O2'	2.38	0.41
52:B1:1686:G:H2'	52:B1:1687:C:H6	1.85	0.41
59:BJ:122:SER:O	59:BJ:125:HIS:N	2.50	0.41
62:BM:33:ARG:HD2	62:BM:91:LEU:HD21	2.02	0.41
81:Bf:107:LYS:HB3	81:Bf:115:SER:HB3	2.02	0.41
1:AA:219:ILE:HG22	1:AA:221:LYS:H	1.86	0.41
5:AC:169:LEU:HD11	5:AC:173:LYS:HE3	2.02	0.41
6:BC:232:THR:OG1	52:B1:13:C:OP1	2.31	0.41
10:AE:136:HIS:HB3	10:AE:137:VAL:H	1.56	0.41
13:AH:113:GLU:OE2	13:AH:115:ARG:NH2	2.52	0.41
23:AR:59:SER:HA	51:A2:2613:C:H5'	2.02	0.41
40:Ai:76:ARG:HD3	40:Ai:76:ARG:HA	1.85	0.41
48:Aq:40:LYS:HB2	48:Aq:68:GLN:HB2	2.02	0.41
48:Aq:60:VAL:CA	48:Aq:73:VAL:HG12	2.50	0.41
51:A2:500:C:H2'	51:A2:501:G:C8	2.55	0.41
51:A2:1539:C:H2'	51:A2:1540:A:H8	1.84	0.41
51:A2:2521:G:H2'	51:A2:2522:A:C8	2.55	0.41
51:A2:4261:U:H2'	51:A2:4262:U:H6	1.84	0.41
52:B1:184:G:H2'	52:B1:185:G:C4	2.55	0.41
52:B1:560:A:H5'	59:BJ:172:ARG:N	2.35	0.41
52:B1:1208:A:H2'	52:B1:1209:A:H8	1.84	0.41
52:B1:1310:U:H5'	81:Bf:130:VAL:HG13	2.02	0.41
65:BP:51:ARG:O	65:BP:52:LYS:C	2.63	0.41
66:BQ:49:TYR:HA	66:BQ:52:LEU:HD12	2.02	0.41
69:BT:140:ALA:HA	69:BT:143:LYS:HE3	2.01	0.41
78:Bc:32:VAL:C	78:Bc:33:GLU:O	2.61	0.41
4:BB:136:ARG:NH1	52:B1:942:G:OP1	2.53	0.41
9:AD:164:LYS:HB2	9:AD:180:PHE:HE1	1.85	0.41
16:AK:24:TYR:CD2	16:AK:24:TYR:O	2.73	0.41
17:AL:49:ARG:HG2	39:Ah:119:TYR:CZ	2.55	0.41
18:AM:32:ASP:OD1	18:AM:32:ASP:N	2.53	0.41
24:AS:174:THR:OG1	51:A2:4724:A:O2'	2.37	0.41
27:AV:87:SER:HB3	28:AW:19:ARG:HH21	1.86	0.41
28:AW:74:ARG:NH2	52:B1:1748:G:OP1	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Ah:47:ILE:HD12	39:Ah:47:ILE:HA	1.90	0.41
48:Aq:142:ASN:ND2	48:Aq:144:ASP:OD1	2.53	0.41
50:Au:34:LEU:HD11	50:Au:204:LEU:HD13	2.02	0.41
51:A2:1827:G:H2'	51:A2:1828:C:C6	2.55	0.41
51:A2:1830:U:HO2'	51:A2:1831:A:H8	1.68	0.41
51:A2:2601:G:H2'	51:A2:2602:A:H8	1.85	0.41
51:A2:2633:C:H2'	51:A2:2634:C:H6	1.85	0.41
51:A2:4421:U:H2'	51:A2:4422:U:C6	2.55	0.41
51:A2:4819:G:H2'	51:A2:4820:G:C8	2.54	0.41
51:A2:4980:U:C2	51:A2:4983:C:N3	2.87	0.41
52:B1:178:C:H2'	52:B1:179:C:H6	1.84	0.41
52:B1:894:G:H2'	52:B1:895:G:H8	1.85	0.41
52:B1:1205:C:H2'	52:B1:1206:G:H8	1.85	0.41
53:BD:37:VAL:HA	53:BD:49:ILE:O	2.20	0.41
82:Bg:114:SER:OG	82:Bg:116:ASP:OD1	2.29	0.41
3:AB:292:LEU:HD13	3:AB:293:ILE:H	1.85	0.41
6:BC:74:LYS:HA	6:BC:74:LYS:HD3	1.90	0.41
8:A4:57:C:H2'	8:A4:58:A:H8	1.84	0.41
17:AL:126:LEU:HD13	39:Ah:117:ARG:HH21	1.85	0.41
17:AL:198:ARG:HD3	51:A2:1467:C:H41	1.84	0.41
18:AM:41:PRO:HG3	18:AM:73:VAL:HG12	2.01	0.41
26:AU:63:ILE:HG12	26:AU:72:VAL:HG12	2.02	0.41
51:A2:431:G:H2'	51:A2:432:G:H8	1.85	0.41
51:A2:637:C:H2'	51:A2:638:G:C8	2.54	0.41
51:A2:2641:G:H2'	51:A2:2642:G:H8	1.85	0.41
51:A2:3940:G:H2'	51:A2:3941:G:C8	2.56	0.41
52:B1:1010:G:H2'	52:B1:1011:A:C8	2.55	0.41
52:B1:1280:G:H2'	52:B1:1281:G:C8	2.52	0.41
55:BF:28:VAL:HG21	55:BF:109:LEU:HD23	2.01	0.41
55:BF:33:ILE:HG22	55:BF:34:SER:H	1.85	0.41
55:BF:102:LEU:HD11	75:BZ:100:VAL:HG21	2.03	0.41
59:BJ:115:PHE:HE1	59:BJ:122:SER:H	1.68	0.41
82:Bg:207:CYS:HB2	82:Bg:221:LEU:HB2	2.01	0.41
1:AA:28:ARG:HB3	1:AA:123:ARG:HB3	2.03	0.41
2:BA:155:ARG:HH12	52:B1:1137:U:H4'	1.85	0.41
3:AB:243:LYS:NZ	51:A2:1573:U:OP2	2.54	0.41
5:AC:60:HIS:CE1	5:AC:100:ARG:HE	2.38	0.41
7:A3:85:U:H2'	7:A3:86:U:H2'	2.01	0.41
13:AH:10:VAL:HB	13:AH:55:LEU:HB3	2.02	0.41
31:AZ:90:PRO:O	31:AZ:117:LYS:NZ	2.48	0.41
34:Ac:17:ARG:HB3	34:Ac:102:SER:OG	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:Aj:33:THR:OG1	41:Aj:34:CYS:N	2.54	0.41
50:Au:35:GLN:HG3	50:Au:166:ALA:HB2	2.02	0.41
51:A2:249:C:H2'	51:A2:250:G:C8	2.55	0.41
51:A2:1804:U:H2'	51:A2:1805:G:C8	2.55	0.41
51:A2:1868:G:H21	51:A2:1919:C:N4	2.18	0.41
51:A2:2822:U:O2'	51:A2:4594:U:OP1	2.38	0.41
51:A2:3944:G:H2'	51:A2:3945:G:H8	1.85	0.41
51:A2:4650:C:H2'	51:A2:4651:U:C6	2.56	0.41
51:A2:4853:C:N4	51:A2:4854:G:N3	2.68	0.41
52:B1:792:C:H2'	52:B1:793:G:C8	2.55	0.41
52:B1:1124:C:O2'	67:BR:123:THR:O	2.38	0.41
52:B1:1404:U:OP2	70:BU:21:ARG:NH2	2.41	0.41
52:B1:1713:C:H2'	52:B1:1714:U:H6	1.86	0.41
54:BE:141:THR:HB	54:BE:145:ARG:H	1.86	0.41
68:BS:142:ARG:HD2	75:BZ:29:LYS:HG2	2.01	0.41
73:BX:25:LYS:HA	73:BX:28:LYS:HE2	2.02	0.41
76:Ba:73:TYR:HB3	76:Ba:78:ALA:HB2	2.02	0.41
82:Bg:109:LEU:HD23	82:Bg:109:LEU:HA	1.92	0.41
4:BB:48:LEU:CD1	4:BB:48:LEU:N	2.73	0.41
5:AC:197:ARG:H	5:AC:197:ARG:HG2	1.70	0.41
5:AC:235:LEU:O	51:A2:1356:A:O2'	2.38	0.41
9:AD:45:ASN:ND2	51:A2:1805:G:O3'	2.51	0.41
10:AE:141:ARG:HH12	10:AE:192:LYS:HA	1.84	0.41
15:AJ:112:HIS:HD2	15:AJ:126:TYR:H	1.68	0.41
25:AT:9:ARG:HG2	25:AT:55:LYS:HE2	2.02	0.41
31:AZ:62:ILE:HD12	31:AZ:62:ILE:HA	1.90	0.41
51:A2:1275:C:H2'	51:A2:1276:G:N3	2.36	0.41
52:B1:900:C:H2'	52:B1:901:G:H8	1.85	0.41
57:BH:52:GLU:HG3	57:BH:58:LYS:HE3	2.03	0.41
58:BI:74:ARG:HA	58:BI:74:ARG:HD3	1.92	0.41
61:BL:42:LEU:HD21	61:BL:72:ILE:HD11	2.03	0.41
63:BN:102:LEU:HD11	63:BN:112:LYS:HA	2.02	0.41
73:BX:34:THR:O	73:BX:38:ALA:CB	2.69	0.41
73:BX:139:GLU:OE2	73:BX:140:ARG:C	2.61	0.41
9:AD:8:LYS:HB3	9:AD:9:ASN:H	1.55	0.41
14:AI:171:TRP:HB2	14:AI:178:ALA:HA	2.03	0.41
17:AL:39:ARG:NH2	51:A2:1346:C:OP2	2.52	0.41
17:AL:110:LEU:HD22	40:Ai:20:ASN:HD21	1.85	0.41
26:AU:49:VAL:HG21	26:AU:56:LEU:CG	2.47	0.41
32:Aa:99:PRO:HG2	32:Aa:122:VAL:HG12	2.01	0.41
44:Am:78:ILE:HG12	44:Am:83:ARG:HD2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:A2:1417:G:H2'	51:A2:1418:G:H8	1.86	0.41
51:A2:3844:G:H2'	51:A2:3845:G:C8	2.56	0.41
52:B1:429:C:H2'	52:B1:430:C:H6	1.85	0.41
52:B1:876:C:H2'	52:B1:877:C:C6	2.56	0.41
65:BP:50:ARG:HH11	65:BP:52:LYS:HZ2	1.62	0.41
66:BQ:53:GLU:O	66:BQ:57:LEU:CB	2.69	0.41
3:AB:119:TYR:HE1	51:A2:4925:A:H5''	1.86	0.41
5:AC:326:LEU:HA	5:AC:326:LEU:HD23	1.88	0.41
21:AP:6:LEU:HD23	21:AP:116:HIS:HB2	2.01	0.41
23:AR:10:LEU:HD11	23:AR:38:ARG:HG2	2.03	0.41
23:AR:132:PHE:CD2	23:AR:138:LEU:HD23	2.55	0.41
26:AU:56:LEU:CD1	26:AU:61:VAL:HB	2.47	0.41
33:Ab:23:LYS:CB	33:Ab:24:PRO:CD	2.98	0.41
37:Af:6:TRP:HB3	37:Af:104:MET:SD	2.60	0.41
43:Al:13:LEU:HD21	51:A2:2386:G:C4	2.56	0.41
47:Ap:6:LYS:HG3	47:Ap:7:LYS:HG3	2.03	0.41
51:A2:664:C:H2'	51:A2:665:G:C8	2.56	0.41
51:A2:1227:G:H21	51:A2:1228:C:H41	1.69	0.41
51:A2:1863:U:OP1	51:A2:2259:G:O2'	2.35	0.41
51:A2:2001:U:H2'	51:A2:2002:G:C8	2.51	0.41
51:A2:2364:U:H2'	51:A2:2365:U:C6	2.55	0.41
51:A2:3726:G:N1	51:A2:3741:U:C2	2.89	0.41
51:A2:4911:G:H2'	51:A2:4912:G:C8	2.55	0.41
52:B1:1139:C:H42	52:B1:1149:A:N6	2.19	0.41
56:BG:225:GLN:HA	56:BG:228:ILE:HD12	2.02	0.41
72:BW:105:THR:N	72:BW:124:LYS:O	2.52	0.41
83:Bv:19:G:O5'	83:Bv:57:G:N2	2.54	0.41
2:BA:42:LYS:HE2	2:BA:46:ILE:HB	2.01	0.41
3:AB:57:VAL:HB	3:AB:367:PHE:HB3	2.03	0.41
3:AB:369:ASP:OD1	3:AB:369:ASP:N	2.53	0.41
3:AB:380:GLN:HB2	28:AW:14:TYR:HE2	1.86	0.41
5:AC:199:ARG:NH1	51:A2:2274:C:H5''	2.36	0.41
5:AC:228:THR:OG1	5:AC:248:ARG:NH2	2.49	0.41
6:BC:107:LEU:HD22	6:BC:209:VAL:HG13	2.02	0.41
6:BC:116:THR:HG22	6:BC:117:ARG:H	1.86	0.41
10:AE:113:PRO:HB3	51:A2:453:C:H5'	2.03	0.41
12:AG:165:GLU:OE1	19:AN:26:ARG:NH2	2.53	0.41
17:AL:130:LYS:N	17:AL:130:LYS:CD	2.73	0.41
17:AL:165:LYS:CD	51:A2:505:C:P	2.91	0.41
24:AS:1:MET:HG3	24:AS:43:ARG:HH21	1.85	0.41
31:AZ:95:VAL:HG11	31:AZ:113:GLU:HG3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Aa:79:TRP:HE1	32:Aa:118:PRO:HD2	1.85	0.41
36:Ae:5:ARG:NH1	51:A2:695:C:OP1	2.53	0.41
37:Af:46:ARG:CD	37:Af:106:TYR:HD2	2.10	0.41
41:Aj:49:TRP:O	51:A2:1628:A:O2'	2.33	0.41
46:Ao:52:THR:OG1	46:Ao:53:LYS:N	2.54	0.41
48:Aq:103:ASN:CG	48:Aq:141:CYS:SG	3.04	0.41
48:Aq:113:ALA:HA	48:Aq:116:MET:HE2	2.03	0.41
48:Aq:141:CYS:SG	48:Aq:141:CYS:O	2.79	0.41
51:A2:174:G:H22	51:A2:254:C:H41	1.66	0.41
51:A2:736:G:O6	51:A2:904:A:N6	2.50	0.41
51:A2:944:G:O2'	51:A2:945:G:O4'	2.39	0.41
51:A2:1782:U:H2'	51:A2:1783:A:C8	2.56	0.41
51:A2:1806:G:H2'	51:A2:1807:A:C8	2.55	0.41
51:A2:2332:U:H2'	51:A2:2333:G:C8	2.54	0.41
51:A2:3694:A:H2'	51:A2:3695:A:H8	1.84	0.41
51:A2:3726:G:C2	51:A2:3741:U:O2	2.74	0.41
51:A2:3915:G:H22	51:A2:4039:U:H3	1.69	0.41
51:A2:3932:G:H1	51:A2:3934:A:H3'	1.86	0.41
51:A2:4693:G:H1'	51:A2:4694:G:H2'	2.03	0.41
52:B1:511:U:H2'	52:B1:512:A:C8	2.55	0.41
52:B1:864:A:H2'	52:B1:865:A:H8	1.84	0.41
52:B1:1513:C:H2'	52:B1:1514:G:C8	2.55	0.41
52:B1:1536:G:H2'	52:B1:1537:A:C8	2.55	0.41
54:BE:48:LEU:HD12	54:BE:61:VAL:HG13	2.03	0.41
58:BI:110:ARG:HH11	58:BI:123:ARG:HH11	1.69	0.41
62:BM:64:LEU:HD23	81:Bf:108:VAL:HG23	2.03	0.41
62:BM:75:ASN:HB3	62:BM:128:PHE:CE2	2.56	0.41
65:BP:44:ARG:NH2	65:BP:82:ASP:O	2.53	0.41
65:BP:47:ARG:O	65:BP:47:ARG:HG3	2.21	0.41
68:BS:34:LYS:NZ	68:BS:104:ASP:OD2	2.54	0.41
72:BW:75:ILE:HD11	72:BW:93:LEU:HD11	2.02	0.41
79:Bd:17:GLY:O	79:Bd:27:ARG:NH1	2.53	0.41
82:Bg:8:ARG:HB3	82:Bg:309:VAL:HG23	2.01	0.41
82:Bg:80:SER:OG	82:Bg:90:TRP:NE1	2.43	0.41
9:AD:259:LYS:HG2	9:AD:261:VAL:HG23	1.99	0.41
11:AF:86:GLU:OE2	11:AF:144:TYR:OH	2.29	0.41
12:AG:63:LEU:HD23	12:AG:63:LEU:HA	1.90	0.41
29:AX:60:TYR:OH	51:A2:17:A:OP2	2.37	0.41
51:A2:160:A:H2'	51:A2:161:G:H8	1.86	0.41
51:A2:1388:C:H2'	51:A2:1389:G:C8	2.56	0.41
51:A2:1621:U:H3	51:A2:1625:A:HO2'	1.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:A2:3634:A:N6	51:A2:4130:G:O2'	2.54	0.41
52:B1:354:U:H2'	52:B1:355:G:C8	2.56	0.41
52:B1:466:G:O2'	56:BG:72:ARG:NH1	2.52	0.41
52:B1:941:C:H2'	52:B1:942:G:C8	2.55	0.41
52:B1:1236:G:O6	68:BS:137:LYS:NZ	2.54	0.41
54:BE:210:VAL:O	54:BE:217:SER:HA	2.20	0.41
65:BP:124:LYS:HA	65:BP:125:PRO:HD2	1.55	0.41
67:BR:5:ARG:HG2	67:BR:49:LYS:HD2	2.03	0.41
82:Bg:138:CYS:SG	82:Bg:139:LYS:N	2.94	0.41
85:A:32:LEU:O	85:A:33:ILE:C	2.64	0.41
5:AC:67:TRP:NE1	5:AC:78:ARG:HG3	2.35	0.40
8:A4:77:A:H62	8:A4:99:G:N2	2.19	0.40
10:AE:232:ILE:HG22	10:AE:236:GLU:HB2	2.04	0.40
11:AF:73:ARG:HD3	51:A2:720:G:C6	2.56	0.40
12:AG:185:LYS:O	12:AG:189:ARG:NH2	2.54	0.40
16:AK:60:MET:HA	51:A2:1941:A:H4'	2.03	0.40
18:AM:121:ARG:HD2	51:A2:4886:C:H1'	2.01	0.40
20:AO:127:VAL:HA	24:AS:158:VAL:HG21	2.03	0.40
22:AQ:153:GLY:HA3	22:AQ:163:THR:HG21	2.02	0.40
38:Ag:72:LYS:NZ	51:A2:2728:C:O3'	2.49	0.40
51:A2:459:G:H2'	51:A2:460:A:C8	2.56	0.40
51:A2:1080:C:H2'	51:A2:1081:G:C8	2.55	0.40
51:A2:1259:C:H2'	51:A2:1260:G:C8	2.56	0.40
51:A2:3629:C:H2'	51:A2:3630:G:C8	2.55	0.40
51:A2:3680:U:H2'	51:A2:3681:G:C4	2.56	0.40
51:A2:3691:G:H22	51:A2:3704:A:H2	1.69	0.40
51:A2:3776:U:H2'	51:A2:3777:G:H8	1.85	0.40
51:A2:4950:G:H2'	51:A2:4951:G:C8	2.56	0.40
52:B1:71:G:H1'	52:B1:79:A:N6	2.36	0.40
52:B1:1547:C:H1'	52:B1:1670:C:H4'	2.02	0.40
55:BF:74:ASN:HA	55:BF:77:MET:HE2	2.03	0.40
58:BI:110:ARG:HH11	58:BI:123:ARG:NH1	2.19	0.40
60:BK:50:GLN:HA	60:BK:53:LYS:HE3	2.04	0.40
62:BM:85:LEU:HA	62:BM:88:TRP:HD1	1.86	0.40
3:AB:303:ALA:HB1	3:AB:368:ILE:HB	2.03	0.40
4:BB:30:TRP:CD2	4:BB:48:LEU:HG	2.55	0.40
5:AC:110:ARG:HH22	51:A2:1490:A:P	2.43	0.40
6:BC:190:SER:HB3	52:B1:1143:A:H5'	2.02	0.40
16:AK:52:VAL:HB	16:AK:53:VAL:H	1.72	0.40
17:AL:171:GLU:H	17:AL:171:GLU:HG2	1.66	0.40
20:AO:54:TYR:OH	20:AO:73:PHE:O	2.39	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:AU:81:ARG:NH2	51:A2:2600:A:N7	2.70	0.40
31:AZ:57:MET:HB3	31:AZ:62:ILE:HD13	2.04	0.40
38:Ag:24:ARG:HD3	51:A2:2617:G:H4'	2.03	0.40
38:Ag:76:ARG:HH21	51:A2:2561:A:P	2.44	0.40
42:Ak:28:ASN:HB3	42:Ak:31:ASN:O	2.20	0.40
48:Aq:41:LYS:HD2	48:Aq:70:GLN:HG3	2.03	0.40
50:Au:6:SER:OG	50:Au:9:THR:OG1	2.34	0.40
50:Au:111:LEU:HD23	50:Au:136:SER:HB3	2.03	0.40
51:A2:1258:G:H4'	51:A2:1259:C:H5'	2.04	0.40
51:A2:1298:C:N4	51:A2:1299:G:O6	2.54	0.40
51:A2:1491:C:H2'	51:A2:1492:G:C8	2.56	0.40
51:A2:1551:U:H2'	51:A2:1552:G:C8	2.56	0.40
51:A2:1810:C:H2'	51:A2:1811:G:C8	2.57	0.40
51:A2:1933:G:H2'	51:A2:1934:U:C6	2.56	0.40
51:A2:2354:A:H2'	51:A2:2355:A:C8	2.56	0.40
51:A2:4157:G:O2'	51:A2:4404:U:OP1	2.29	0.40
52:B1:804:U:O2'	72:BW:121:THR:O	2.29	0.40
63:BN:98:VAL:HG12	63:BN:115:LEU:HD12	2.02	0.40
76:Ba:39:PHE:CD1	76:Ba:70:LYS:HD2	2.56	0.40
83:Bv:22:G:H2'	83:Bv:23:A:H8	1.85	0.40
1:AA:250:LYS:HG2	1:AA:252:VAL:HG23	2.03	0.40
3:AB:128:LYS:HG3	51:A2:4924:A:H5'	2.03	0.40
3:AB:165:HIS:HB3	3:AB:180:LEU:HD23	2.03	0.40
3:AB:175:GLN:HG3	51:A2:4943:U:H4'	2.03	0.40
3:AB:378:ARG:HH21	28:AW:33:ASN:HD21	1.69	0.40
7:A3:142:U:P	19:AN:38:ARG:HH22	2.44	0.40
8:A4:69:U:H2'	8:A4:70:G:H8	1.87	0.40
19:AN:104:GLU:HA	19:AN:160:GLU:HG3	2.01	0.40
34:Ac:20:LEU:HD23	34:Ac:20:LEU:HA	1.90	0.40
34:Ac:48:LEU:HD21	34:Ac:60:ILE:HG21	2.03	0.40
38:Ag:5:LEU:HD13	38:Ag:30:ILE:HG22	2.03	0.40
51:A2:470:G:H2'	51:A2:471:C:C6	2.57	0.40
51:A2:3919:C:H2'	51:A2:3920:A:C8	2.53	0.40
52:B1:935:G:H2'	52:B1:936:G:C8	2.56	0.40
52:B1:1491:G:H2'	52:B1:1492:U:C6	2.56	0.40
52:B1:1612:G:H1'	68:BS:87:GLN:HG2	2.03	0.40
52:B1:1615:U:H2'	52:B1:1616:U:H6	1.86	0.40
52:B1:1656:G:H2'	52:B1:1657:G:H8	1.87	0.40
56:BG:126:ASP:OD1	56:BG:126:ASP:N	2.53	0.40
74:BY:89:HIS:CE1	74:BY:90:ARG:HG3	2.56	0.40
82:Bg:165:ILE:HG13	82:Bg:177:TRP:HB2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AC:154:VAL:O	5:AC:254:GLU:HG3	2.22	0.40
5:AC:159:GLU:HA	5:AC:217:ILE:HD13	2.03	0.40
7:A3:76:C:H2'	7:A3:77:A:C8	2.57	0.40
17:AL:135:LYS:O	17:AL:136:LYS:CB	2.69	0.40
19:AN:8:GLN:HE22	51:A2:272:G:H4'	1.86	0.40
23:AR:23:TRP:HH2	23:AR:32:ILE:HG21	1.87	0.40
23:AR:81:ARG:NH2	51:A2:3579:A:OP2	2.50	0.40
29:AX:53:ARG:NH2	51:A2:2454:G:N7	2.69	0.40
32:Aa:95:THR:OG1	32:Aa:96:GLY:N	2.55	0.40
33:Ab:23:LYS:HB2	33:Ab:23:LYS:HE3	1.71	0.40
34:Ac:7:THR:OG1	34:Ac:8:LYS:N	2.55	0.40
51:A2:467:C:H2'	51:A2:468:C:C6	2.57	0.40
51:A2:1310:C:H2'	51:A2:1311:G:H8	1.87	0.40
51:A2:1648:C:O2'	51:A2:1670:G:OP1	2.35	0.40
52:B1:661:U:H5''	52:B1:662:G:H2'	2.03	0.40
52:B1:802:A:H62	57:BH:106:ARG:HH12	1.70	0.40
52:B1:996:A:H2'	52:B1:997:A:C8	2.57	0.40
52:B1:1865:C:OP1	76:Ba:87:ARG:NH2	2.48	0.40
72:BW:99:PHE:CD1	72:BW:99:PHE:N	2.89	0.40
1:AA:204:MET:HE2	1:AA:209:HIS:HB2	2.02	0.40
4:BB:47:THR:O	4:BB:48:LEU:HG	2.21	0.40
8:A4:100:A:H2'	8:A4:101:A:C8	2.56	0.40
16:AK:37:SER:OG	16:AK:38:LYS:N	2.53	0.40
17:AL:171:GLU:C	17:AL:173:GLU:N	2.78	0.40
30:AY:80:ILE:HD11	30:AY:104:VAL:HG21	2.03	0.40
32:Aa:7:LYS:HE2	32:Aa:11:LEU:HD11	2.04	0.40
32:Aa:32:ARG:HD2	51:A2:37:U:H4'	2.03	0.40
34:Ac:104:ILE:H	34:Ac:104:ILE:HG12	1.63	0.40
38:Ag:49:CYS:HA	47:Ap:61:MET:HG3	2.04	0.40
40:Ai:82:ARG:NH1	51:A2:277:G:H1'	2.36	0.40
41:Aj:43:ARG:NH2	51:A2:55:G:OP1	2.41	0.40
49:At:41:ASN:HD22	49:At:42:GLY:H	1.68	0.40
51:A2:198:C:H2'	51:A2:199:C:C6	2.56	0.40
51:A2:476:G:H22	51:A2:666:G:N2	2.19	0.40
51:A2:1077:G:H2'	51:A2:1078:A:C8	2.57	0.40
51:A2:1508:G:H2'	51:A2:1509:A:H8	1.87	0.40
51:A2:1545:A:H2'	51:A2:1546:A:H8	1.86	0.40
52:B1:17:C:H2'	52:B1:18:C:H6	1.86	0.40
52:B1:675:U:H2'	52:B1:676:C:H6	1.87	0.40
52:B1:1112:U:H2'	52:B1:1113:A:C8	2.56	0.40
52:B1:1711:U:H2'	52:B1:1712:A:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:BG:141:ILE:HG21	56:BG:153:VAL:HG21	2.03	0.40
65:BP:50:ARG:NH1	65:BP:52:LYS:CE	2.83	0.40
73:BX:51:VAL:HG22	73:BX:70:VAL:HG11	2.03	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	
1	AA	250/257 (97%)	223 (89%)	24 (10%)	3 (1%)	10	35
2	BA	213/215 (99%)	196 (92%)	13 (6%)	4 (2%)	6	26
3	AB	392/394 (100%)	363 (93%)	29 (7%)	0	100	100
4	BB	210/212 (99%)	181 (86%)	27 (13%)	2 (1%)	12	40
5	AC	361/363 (99%)	333 (92%)	26 (7%)	2 (1%)	21	50
6	BC	220/222 (99%)	205 (93%)	15 (7%)	0	100	100
9	AD	292/294 (99%)	261 (89%)	27 (9%)	4 (1%)	9	31
10	AE	192/194 (99%)	159 (83%)	29 (15%)	4 (2%)	5	24
11	AF	232/234 (99%)	211 (91%)	20 (9%)	1 (0%)	30	59
12	AG	232/234 (99%)	211 (91%)	21 (9%)	0	100	100
13	AH	189/191 (99%)	178 (94%)	9 (5%)	2 (1%)	11	38
14	AI	204/211 (97%)	182 (89%)	22 (11%)	0	100	100
15	AJ	167/169 (99%)	153 (92%)	12 (7%)	2 (1%)	10	35
16	AK	107/109 (98%)	59 (55%)	35 (33%)	13 (12%)	0	1
17	AL	203/205 (99%)	166 (82%)	28 (14%)	9 (4%)	2	13
18	AM	137/139 (99%)	125 (91%)	12 (9%)	0	100	100
19	AN	201/203 (99%)	184 (92%)	16 (8%)	1 (0%)	24	54

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	AO	193/195 (99%)	180 (93%)	13 (7%)	0	100	100
21	AP	151/153 (99%)	147 (97%)	4 (3%)	0	100	100
22	AQ	185/187 (99%)	159 (86%)	25 (14%)	1 (0%)	24	54
23	AR	179/181 (99%)	169 (94%)	9 (5%)	1 (1%)	21	50
24	AS	173/175 (99%)	162 (94%)	11 (6%)	0	100	100
25	AT	155/157 (99%)	140 (90%)	13 (8%)	2 (1%)	9	33
26	AU	97/99 (98%)	87 (90%)	8 (8%)	2 (2%)	5	24
27	AV	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
28	AW	119/121 (98%)	105 (88%)	13 (11%)	1 (1%)	16	44
29	AX	115/117 (98%)	110 (96%)	5 (4%)	0	100	100
30	AY	125/127 (98%)	118 (94%)	7 (6%)	0	100	100
31	AZ	132/134 (98%)	117 (89%)	15 (11%)	0	100	100
32	Aa	145/147 (99%)	128 (88%)	17 (12%)	0	100	100
33	Ab	66/121 (54%)	56 (85%)	9 (14%)	1 (2%)	8	30
34	Ac	101/103 (98%)	96 (95%)	3 (3%)	2 (2%)	6	25
35	Ad	104/106 (98%)	99 (95%)	5 (5%)	0	100	100
36	Ae	127/129 (98%)	113 (89%)	14 (11%)	0	100	100
37	Af	107/109 (98%)	95 (89%)	9 (8%)	3 (3%)	4	19
38	Ag	112/114 (98%)	101 (90%)	11 (10%)	0	100	100
39	Ah	120/122 (98%)	111 (92%)	8 (7%)	1 (1%)	16	44
40	Ai	95/97 (98%)	86 (90%)	9 (10%)	0	100	100
41	Aj	82/84 (98%)	75 (92%)	7 (8%)	0	100	100
42	Ak	67/69 (97%)	63 (94%)	4 (6%)	0	100	100
43	Al	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
44	Am	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
45	An	23/25 (92%)	23 (100%)	0	0	100	100
46	Ao	103/105 (98%)	93 (90%)	10 (10%)	0	100	100
47	Ap	89/91 (98%)	80 (90%)	9 (10%)	0	100	100
48	Aq	136/138 (99%)	94 (69%)	38 (28%)	4 (3%)	3	19
49	At	120/122 (98%)	102 (85%)	16 (13%)	2 (2%)	7	28
50	Au	215/217 (99%)	193 (90%)	18 (8%)	4 (2%)	6	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	BD	218/220 (99%)	202 (93%)	15 (7%)	1 (0%)	24	54
54	BE	255/257 (99%)	235 (92%)	19 (8%)	1 (0%)	30	59
55	BF	188/190 (99%)	171 (91%)	17 (9%)	0	100	100
56	BG	230/232 (99%)	208 (90%)	21 (9%)	1 (0%)	30	59
57	BH	181/183 (99%)	166 (92%)	14 (8%)	1 (1%)	21	50
58	BI	205/207 (99%)	175 (85%)	26 (13%)	4 (2%)	6	25
59	BJ	177/179 (99%)	151 (85%)	25 (14%)	1 (1%)	21	50
60	BK	96/98 (98%)	82 (85%)	12 (12%)	2 (2%)	5	24
61	BL	151/153 (99%)	132 (87%)	18 (12%)	1 (1%)	18	47
62	BM	118/120 (98%)	112 (95%)	6 (5%)	0	100	100
63	BN	147/149 (99%)	129 (88%)	17 (12%)	1 (1%)	18	47
64	BO	134/136 (98%)	119 (89%)	13 (10%)	2 (2%)	8	30
65	BP	118/120 (98%)	101 (86%)	12 (10%)	5 (4%)	2	14
66	BQ	137/139 (99%)	127 (93%)	10 (7%)	0	100	100
67	BR	123/125 (98%)	105 (85%)	16 (13%)	2 (2%)	7	29
68	BS	137/139 (99%)	118 (86%)	16 (12%)	3 (2%)	5	24
69	BT	141/143 (99%)	129 (92%)	11 (8%)	1 (1%)	18	47
70	BU	95/97 (98%)	91 (96%)	4 (4%)	0	100	100
71	BV	79/81 (98%)	75 (95%)	4 (5%)	0	100	100
72	BW	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
73	BX	137/139 (99%)	124 (90%)	11 (8%)	2 (2%)	8	30
74	BY	123/125 (98%)	108 (88%)	15 (12%)	0	100	100
75	BZ	84/86 (98%)	74 (88%)	10 (12%)	0	100	100
76	Ba	95/97 (98%)	87 (92%)	8 (8%)	0	100	100
77	Bb	78/80 (98%)	71 (91%)	7 (9%)	0	100	100
78	Bc	60/62 (97%)	55 (92%)	5 (8%)	0	100	100
79	Bd	49/51 (96%)	43 (88%)	6 (12%)	0	100	100
80	Be	53/55 (96%)	51 (96%)	2 (4%)	0	100	100
81	Bf	71/73 (97%)	64 (90%)	6 (8%)	1 (1%)	9	31
82	Bg	312/314 (99%)	281 (90%)	31 (10%)	0	100	100
85	A	37/39 (95%)	20 (54%)	14 (38%)	3 (8%)	1	4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	11617/11838 (98%)	10430 (90%)	1084 (9%)	103 (1%)	16	42

All (103) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AA	196	TRP
1	AA	197	PRO
1	AA	201	GLY
2	BA	206	ASP
5	AC	148	PRO
9	AD	265	ARG
10	AE	133	PHE
15	AJ	57	VAL
16	AK	5	ASP
16	AK	25	PRO
16	AK	26	LYS
16	AK	72	ASN
16	AK	103	LEU
16	AK	104	ALA
17	AL	46	ILE
17	AL	47	ALA
17	AL	62	PRO
17	AL	172	GLU
19	AN	95	ALA
23	AR	112	SER
26	AU	61	VAL
34	Ac	102	SER
37	Af	106	TYR
48	Aq	22	VAL
48	Aq	58	ILE
49	At	17	LEU
50	Au	60	ARG
50	Au	164	CYS
53	BD	218	LEU
58	BI	133	GLU
58	BI	160	SER
58	BI	161	LEU
68	BS	89	ASP
68	BS	91	LYS
2	BA	203	PHE
2	BA	204	TYR
5	AC	53	ALA

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Mol	Chain	Res	Type
9	AD	253	TYR
17	AL	136	LYS
17	AL	165	LYS
50	Au	24	LYS
60	BK	41	PRO
64	BO	21	VAL
65	BP	66	GLU
68	BS	87	GLN
69	BT	31	PRO
85	A	33	ILE
9	AD	258	LYS
10	AE	127	SER
10	AE	128	HIS
13	AH	117	PHE
15	AJ	56	THR
17	AL	64	VAL
22	AQ	161	SER
26	AU	60	VAL
33	Ab	25	ARG
49	At	16	PHE
61	BL	14	PRO
63	BN	23	PRO
64	BO	19	PRO
65	BP	52	LYS
65	BP	68	PRO
65	BP	125	PRO
67	BR	5	ARG
2	BA	209	GLU
4	BB	39	PHE
4	BB	52	THR
16	AK	3	ARG
16	AK	78	LEU
17	AL	5	ARG
17	AL	78	LEU
25	AT	18	PRO
37	Af	107	PRO
57	BH	115	LYS
58	BI	131	PRO
59	BJ	123	ILE
60	BK	28	HIS
67	BR	4	VAL
73	BX	136	GLY

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Mol	Chain	Res	Type
9	AD	260	GLU
13	AH	3	THR
16	AK	82	ILE
16	AK	96	THR
25	AT	53	PRO
34	Ac	108	MET
39	Ah	87	LYS
50	Au	22	GLN
54	BE	150	PRO
56	BG	103	ASP
65	BP	126	VAL
81	Bf	88	PRO
85	A	36	LEU
11	AF	223	LYS
28	AW	59	HIS
48	Aq	88	PRO
85	A	29	LEU
73	BX	86	PRO
10	AE	185	PRO
16	AK	73	PRO
37	Af	60	PRO
16	AK	52	VAL
16	AK	53	VAL
48	Aq	60	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AA	194/199 (98%)	191 (98%)	3 (2%)	57	69
2	BA	180/180 (100%)	177 (98%)	3 (2%)	53	67
3	AB	343/343 (100%)	338 (98%)	5 (2%)	57	69
4	BB	193/193 (100%)	190 (98%)	3 (2%)	55	68
5	AC	302/302 (100%)	298 (99%)	4 (1%)	61	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	BC	188/188 (100%)	184 (98%)	4 (2%)	47	64
9	AD	248/248 (100%)	236 (95%)	12 (5%)	23	50
10	AE	174/174 (100%)	164 (94%)	10 (6%)	18	45
11	AF	203/203 (100%)	202 (100%)	1 (0%)	81	81
12	AG	199/199 (100%)	199 (100%)	0	100	100
13	AH	170/170 (100%)	166 (98%)	4 (2%)	43	62
14	AI	178/179 (99%)	178 (100%)	0	100	100
15	AJ	142/142 (100%)	139 (98%)	3 (2%)	47	64
16	AK	95/95 (100%)	86 (90%)	9 (10%)	8	29
17	AL	171/171 (100%)	163 (95%)	8 (5%)	23	50
18	AM	118/118 (100%)	117 (99%)	1 (1%)	73	77
19	AN	171/171 (100%)	170 (99%)	1 (1%)	78	80
20	AO	168/168 (100%)	166 (99%)	2 (1%)	63	72
21	AP	134/134 (100%)	134 (100%)	0	100	100
22	AQ	164/164 (100%)	159 (97%)	5 (3%)	36	59
23	AR	160/160 (100%)	158 (99%)	2 (1%)	61	71
24	AS	156/156 (100%)	156 (100%)	0	100	100
25	AT	138/138 (100%)	138 (100%)	0	100	100
26	AU	89/89 (100%)	88 (99%)	1 (1%)	65	74
27	AV	100/100 (100%)	100 (100%)	0	100	100
28	AW	100/100 (100%)	100 (100%)	0	100	100
29	AX	105/105 (100%)	105 (100%)	0	100	100
30	AY	119/119 (100%)	119 (100%)	0	100	100
31	AZ	117/117 (100%)	116 (99%)	1 (1%)	70	76
32	Aa	120/120 (100%)	120 (100%)	0	100	100
33	Ab	58/101 (57%)	52 (90%)	6 (10%)	7	24
34	Ac	88/88 (100%)	84 (96%)	4 (4%)	24	51
35	Ad	97/97 (100%)	97 (100%)	0	100	100
36	Ae	115/115 (100%)	114 (99%)	1 (1%)	70	76
37	Af	88/88 (100%)	87 (99%)	1 (1%)	65	74
38	Ag	98/98 (100%)	98 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	Ah	109/109 (100%)	108 (99%)	1 (1%)	70	76
40	Ai	83/83 (100%)	83 (100%)	0	100	100
41	Aj	71/71 (100%)	70 (99%)	1 (1%)	59	70
42	Ak	64/64 (100%)	64 (100%)	0	100	100
43	Al	47/47 (100%)	47 (100%)	0	100	100
44	Am	46/46 (100%)	46 (100%)	0	100	100
45	An	24/24 (100%)	24 (100%)	0	100	100
46	Ao	93/93 (100%)	93 (100%)	0	100	100
47	Ap	74/74 (100%)	74 (100%)	0	100	100
48	Aq	114/114 (100%)	109 (96%)	5 (4%)	25	51
49	At	106/106 (100%)	104 (98%)	2 (2%)	50	66
50	Au	196/196 (100%)	187 (95%)	9 (5%)	24	50
53	BD	183/183 (100%)	180 (98%)	3 (2%)	55	68
54	BE	220/220 (100%)	220 (100%)	0	100	100
55	BF	160/160 (100%)	159 (99%)	1 (1%)	78	80
56	BG	202/202 (100%)	200 (99%)	2 (1%)	68	75
57	BH	164/164 (100%)	164 (100%)	0	100	100
58	BI	179/179 (100%)	176 (98%)	3 (2%)	53	67
59	BJ	160/160 (100%)	158 (99%)	2 (1%)	61	71
60	BK	89/89 (100%)	89 (100%)	0	100	100
61	BL	138/138 (100%)	137 (99%)	1 (1%)	76	78
62	BM	102/102 (100%)	102 (100%)	0	100	100
63	BN	130/130 (100%)	130 (100%)	0	100	100
64	BO	106/106 (100%)	105 (99%)	1 (1%)	70	76
65	BP	109/109 (100%)	99 (91%)	10 (9%)	8	29
66	BQ	115/115 (100%)	113 (98%)	2 (2%)	53	67
67	BR	113/113 (100%)	113 (100%)	0	100	100
68	BS	121/121 (100%)	118 (98%)	3 (2%)	42	62
69	BT	113/113 (100%)	112 (99%)	1 (1%)	70	76
70	BU	90/90 (100%)	90 (100%)	0	100	100
71	BV	65/65 (100%)	65 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
72	BW	112/112 (100%)	110 (98%)	2 (2%)	51	67
73	BX	111/111 (100%)	110 (99%)	1 (1%)	70	76
74	BY	107/107 (100%)	107 (100%)	0	100	100
75	BZ	75/75 (100%)	74 (99%)	1 (1%)	61	71
76	Ba	84/84 (100%)	83 (99%)	1 (1%)	63	72
77	Bb	72/72 (100%)	71 (99%)	1 (1%)	59	70
78	Bc	55/55 (100%)	54 (98%)	1 (2%)	51	67
79	Bd	45/45 (100%)	45 (100%)	0	100	100
80	Be	44/44 (100%)	44 (100%)	0	100	100
81	Bf	66/66 (100%)	66 (100%)	0	100	100
82	Bg	272/272 (100%)	270 (99%)	2 (1%)	76	78
All	All	10112/10161 (100%)	9962 (98%)	150 (2%)	55	69

All (150) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AA	101	VAL
1	AA	198	ARG
1	AA	200	ARG
2	BA	42	LYS
2	BA	205	ARG
2	BA	208	GLU
3	AB	17	LEU
3	AB	66	LYS
3	AB	67	VAL
3	AB	146	LEU
3	AB	292	LEU
4	BB	48	LEU
4	BB	49	VAL
4	BB	52	THR
5	AC	52	TYR
5	AC	152	LEU
5	AC	154	VAL
5	AC	229	LEU
6	BC	141	VAL
6	BC	255	LEU
6	BC	257	LYS
6	BC	259	THR

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Mol	Chain	Res	Type
9	AD	6	VAL
9	AD	8	LYS
9	AD	9	ASN
9	AD	254	GLU
9	AD	255	LYS
9	AD	259	LYS
9	AD	260	GLU
9	AD	261	VAL
9	AD	262	LYS
9	AD	263	LYS
9	AD	264	LYS
9	AD	265	ARG
10	AE	128	HIS
10	AE	130	LYS
10	AE	131	LYS
10	AE	135	GLN
10	AE	136	HIS
10	AE	137	VAL
10	AE	138	ARG
10	AE	206	VAL
10	AE	207	LYS
10	AE	208	ILE
11	AF	146	ASN
13	AH	3	THR
13	AH	4	ILE
13	AH	5	LEU
13	AH	111	LEU
15	AJ	54	ARG
15	AJ	55	TYR
15	AJ	56	THR
16	AK	3	ARG
16	AK	4	GLU
16	AK	54	LEU
16	AK	69	LEU
16	AK	70	GLU
16	AK	71	ASN
16	AK	83	ARG
16	AK	85	ASN
16	AK	101	MET
17	AL	46	ILE
17	AL	49	ARG
17	AL	63	THR

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Mol	Chain	Res	Type
17	AL	130	LYS
17	AL	164	GLU
17	AL	165	LYS
17	AL	171	GLU
17	AL	172	GLU
18	AM	5	ARG
19	AN	183	THR
20	AO	184	ASN
20	AO	185	VAL
22	AQ	10	ASP
22	AQ	11	ARG
22	AQ	12	LYS
22	AQ	13	VAL
22	AQ	14	ARG
23	AR	113	LYS
23	AR	114	LYS
26	AU	56	LEU
31	AZ	53	VAL
33	Ab	22	LYS
33	Ab	23	LYS
33	Ab	26	SER
33	Ab	27	GLN
33	Ab	28	ARG
33	Ab	32	LEU
34	Ac	102	SER
34	Ac	105	ILE
34	Ac	106	ARG
34	Ac	107	SER
36	Ae	122	VAL
37	Af	108	SER
39	Ah	87	LYS
41	Aj	67	LEU
48	Aq	22	VAL
48	Aq	35	LEU
48	Aq	58	ILE
48	Aq	59	THR
48	Aq	143	VAL
49	At	17	LEU
49	At	18	ILE
50	Au	22	GLN
50	Au	23	ARG
50	Au	58	THR

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Mol	Chain	Res	Type
50	Au	60	ARG
50	Au	159	MET
50	Au	161	LYS
50	Au	162	VAL
50	Au	194	LEU
50	Au	197	ASN
53	BD	216	GLU
53	BD	217	ILE
53	BD	218	LEU
55	BF	119	SER
56	BG	67	VAL
56	BG	153	VAL
58	BI	132	GLU
58	BI	158	ILE
58	BI	159	SER
59	BJ	137	VAL
59	BJ	138	ARG
61	BL	101	ARG
64	BO	21	VAL
65	BP	45	LEU
65	BP	47	ARG
65	BP	49	LEU
65	BP	51	ARG
65	BP	60	LEU
65	BP	66	GLU
65	BP	70	MET
65	BP	71	GLU
65	BP	124	LYS
65	BP	126	VAL
66	BQ	12	VAL
66	BQ	13	PHE
68	BS	87	GLN
68	BS	88	LYS
68	BS	91	LYS
69	BT	37	VAL
72	BW	97	ARG
72	BW	102	ILE
73	BX	139	GLU
75	BZ	62	VAL
76	Ba	84	VAL
77	Bb	77	CYS
78	Bc	32	VAL

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Mol	Chain	Res	Type
82	Bg	96	THR
82	Bg	111	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (190) such sidechains are listed below:

Mol	Chain	Res	Type
1	AA	22	HIS
1	AA	97	ASN
1	AA	132	ASN
1	AA	162	ASN
1	AA	209	HIS
1	AA	218	HIS
2	BA	36	GLN
2	BA	149	ASN
3	AB	68	ASN
3	AB	158	GLN
3	AB	167	GLN
3	AB	245	HIS
3	AB	322	HIS
4	BB	40	ASN
4	BB	75	GLN
4	BB	76	ASN
4	BB	177	GLN
5	AC	38	ASN
5	AC	94	ASN
5	AC	112	HIS
5	AC	215	ASN
5	AC	343	GLN
5	AC	346	ASN
5	AC	347	HIS
6	BC	113	GLN
6	BC	134	ASN
6	BC	178	HIS
9	AD	17	GLN
9	AD	138	GLN
9	AD	191	ASN
9	AD	198	HIS
10	AE	190	HIS
10	AE	205	ASN
10	AE	266	GLN
10	AE	279	ASN
11	AF	116	GLN

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Mol	Chain	Res	Type
11	AF	146	ASN
11	AF	226	HIS
12	AG	149	ASN
13	AH	98	HIS
13	AH	140	GLN
14	AI	14	ASN
14	AI	51	HIS
14	AI	147	HIS
14	AI	166	HIS
15	AJ	71	HIS
15	AJ	155	HIS
15	AJ	167	GLN
16	AK	12	ASN
16	AK	68	HIS
17	AL	19	GLN
17	AL	159	ASN
17	AL	175	ASN
18	AM	70	GLN
18	AM	78	GLN
18	AM	125	ASN
19	AN	87	HIS
19	AN	158	HIS
19	AN	182	HIS
19	AN	196	ASN
19	AN	201	HIS
20	AO	42	ASN
20	AO	65	ASN
20	AO	96	GLN
20	AO	184	ASN
21	AP	34	GLN
21	AP	40	HIS
21	AP	75	GLN
21	AP	80	GLN
21	AP	97	ASN
21	AP	133	HIS
22	AQ	7	HIS
24	AS	66	GLN
25	AT	22	HIS
25	AT	98	HIS
26	AU	50	ASN
26	AU	55	ASN
27	AV	101	ASN

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Mol	Chain	Res	Type
27	AV	135	ASN
28	AW	45	ASN
28	AW	95	ASN
28	AW	96	GLN
29	AX	107	HIS
30	AY	4	ASN
30	AY	20	ASN
30	AY	40	GLN
30	AY	56	GLN
30	AY	61	HIS
30	AY	86	GLN
31	AZ	40	HIS
32	Aa	40	HIS
32	Aa	49	HIS
32	Aa	60	HIS
32	Aa	66	ASN
33	Ab	12	GLN
33	Ab	27	GLN
33	Ab	60	ASN
33	Ab	61	ASN
34	Ac	72	HIS
35	Ad	28	ASN
35	Ad	34	HIS
35	Ad	79	ASN
36	Ae	24	GLN
36	Ae	52	GLN
36	Ae	107	ASN
37	Af	99	HIS
38	Ag	73	HIS
39	Ah	98	HIS
41	Aj	57	ASN
43	Al	20	ASN
43	Al	43	HIS
44	Am	90	ASN
44	Am	120	ASN
46	Ao	3	ASN
46	Ao	19	GLN
46	Ao	36	GLN
48	Aq	8	ASN
48	Aq	70	GLN
48	Aq	97	ASN
48	Aq	103	ASN

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Mol	Chain	Res	Type
48	Aq	111	ASN
48	Aq	118	HIS
49	At	36	ASN
49	At	41	ASN
49	At	100	ASN
50	Au	21	ASN
50	Au	22	GLN
50	Au	35	GLN
50	Au	40	ASN
50	Au	84	HIS
50	Au	197	ASN
53	BD	74	GLN
53	BD	159	HIS
54	BE	98	HIS
54	BE	138	HIS
54	BE	161	GLN
54	BE	197	ASN
54	BE	230	ASN
55	BF	65	GLN
55	BF	82	ASN
55	BF	114	ASN
55	BF	203	ASN
56	BG	202	ASN
56	BG	227	GLN
57	BH	91	HIS
58	BI	84	ASN
58	BI	165	GLN
59	BJ	156	HIS
60	BK	32	HIS
60	BK	50	GLN
61	BL	83	GLN
62	BM	15	ASN
62	BM	73	GLN
63	BN	58	HIS
63	BN	105	ASN
64	BO	32	HIS
65	BP	41	GLN
65	BP	54	HIS
65	BP	128	HIS
66	BQ	24	HIS
66	BQ	80	GLN
66	BQ	86	GLN

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Mol	Chain	Res	Type
67	BR	121	GLN
68	BS	11	HIS
68	BS	17	ASN
68	BS	42	HIS
68	BS	76	GLN
69	BT	91	HIS
72	BW	5	ASN
72	BW	15	ASN
72	BW	16	ASN
72	BW	24	GLN
72	BW	44	HIS
72	BW	70	ASN
72	BW	90	GLN
72	BW	98	GLN
73	BX	23	HIS
73	BX	127	ASN
74	BY	15	ASN
74	BY	29	HIS
74	BY	89	HIS
75	BZ	106	GLN
75	BZ	112	ASN
78	Bc	24	GLN
78	Bc	26	GLN
78	Bc	29	GLN
79	Bd	28	HIS
82	Bg	133	ASN
82	Bg	143	GLN
82	Bg	159	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	A2	3600/3612 (99%)	865 (24%)	15 (0%)
52	B1	1701/1708 (99%)	408 (23%)	10 (0%)
7	A3	156/157 (99%)	41 (26%)	3 (1%)
8	A4	118/119 (99%)	22 (18%)	0
83	Bv	75/76 (98%)	23 (30%)	0
84	Bx	15/16 (93%)	10 (66%)	0
All	All	5665/5688 (99%)	1369 (24%)	28 (0%)

All (1369) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	A3	16	G
7	A3	23	C
7	A3	33	G
7	A3	34	U
7	A3	35	C
7	A3	39	G
7	A3	40	A
7	A3	52	A
7	A3	59	A
7	A3	63	U
7	A3	72	A
7	A3	80	A
7	A3	81	C
7	A3	82	A
7	A3	83	C
7	A3	84	A
7	A3	87	G
7	A3	88	A
7	A3	94	G
7	A3	95	A
7	A3	103	A
7	A3	105	C
7	A3	107	C
7	A3	108	A
7	A3	109	C
7	A3	110	U
7	A3	111	U
7	A3	112	G
7	A3	114	G
7	A3	120	G
7	A3	121	G
7	A3	123	U
7	A3	124	U
7	A3	125	C
7	A3	127	U
7	A3	128	C
7	A3	129	C
7	A3	130	C
7	A3	148	A
7	A3	151	G
7	A3	157	U
8	A4	7	G
8	A4	10	C

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Mol	Chain	Res	Type
8	A4	11	A
8	A4	14	C
8	A4	22	A
8	A4	27	G
8	A4	29	C
8	A4	33	U
8	A4	47	G
8	A4	48	G
8	A4	53	U
8	A4	54	A
8	A4	59	G
8	A4	63	C
8	A4	64	G
8	A4	76	U
8	A4	89	G
8	A4	91	C
8	A4	97	G
8	A4	108	G
8	A4	110	G
8	A4	119	U
51	A2	6	C
51	A2	9	C
51	A2	10	A
51	A2	14	C
51	A2	22	G
51	A2	23	C
51	A2	25	A
51	A2	32	G
51	A2	39	A
51	A2	42	A
51	A2	47	A
51	A2	48	G
51	A2	49	U
51	A2	55	G
51	A2	59	A
51	A2	64	A
51	A2	65	A
51	A2	71	C
51	A2	72	C
51	A2	73	A
51	A2	76	A
51	A2	84	A

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Mol	Chain	Res	Type
51	A2	91	G
51	A2	101	A
51	A2	110	C
51	A2	116	G
51	A2	119	G
51	A2	120	A
51	A2	121	A
51	A2	131	C
51	A2	132	G
51	A2	133	C
51	A2	134	G
51	A2	140	C
51	A2	141	G
51	A2	143	G
51	A2	147	U
51	A2	149	U
51	A2	150	G
51	A2	155	A
51	A2	156	C
51	A2	157	G
51	A2	167	C
51	A2	169	C
51	A2	179	G
51	A2	180	C
51	A2	181	U
51	A2	182	C
51	A2	183	G
51	A2	184	U
51	A2	185	G
51	A2	186	G
51	A2	189	G
51	A2	193	C
51	A2	196	G
51	A2	197	U
51	A2	199	C
51	A2	201	U
51	A2	206	U
51	A2	212	C
51	A2	213	C
51	A2	214	C
51	A2	215	A
51	A2	222	G

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Mol	Chain	Res	Type
51	A2	227	G
51	A2	228	U
51	A2	229	G
51	A2	230	U
51	A2	231	G
51	A2	234	G
51	A2	237	G
51	A2	250	G
51	A2	251	G
51	A2	252	C
51	A2	253	G
51	A2	257	G
51	A2	258	C
51	A2	260	C
51	A2	261	G
51	A2	275	U
51	A2	286	G
51	A2	291	U
51	A2	300	A
51	A2	303	C
51	A2	309	G
51	A2	310	U
51	A2	311	A
51	A2	334	C
51	A2	338	A
51	A2	341	A
51	A2	348	U
51	A2	351	U
51	A2	354	A
51	A2	357	A
51	A2	367	G
51	A2	370	A
51	A2	375	U
51	A2	379	A
51	A2	381	G
51	A2	390	A
51	A2	402	A
51	A2	406	G
51	A2	407	G
51	A2	409	G
51	A2	425	G
51	A2	426	U

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Mol	Chain	Res	Type
51	A2	434	U
51	A2	444	G
51	A2	446	A
51	A2	447	G
51	A2	448	U
51	A2	449	C
51	A2	457	A
51	A2	460	A
51	A2	469	G
51	A2	479	C
51	A2	480	C
51	A2	482	G
51	A2	483	C
51	A2	492	C
51	A2	494	G
51	A2	495	C
51	A2	496	C
51	A2	497	C
51	A2	498	G
51	A2	504	U
51	A2	505	C
51	A2	507	U
51	A2	508	U
51	A2	509	C
51	A2	513	C
51	A2	635	G
51	A2	641	G
51	A2	643	A
51	A2	645	C
51	A2	648	C
51	A2	649	C
51	A2	658	G
51	A2	661	G
51	A2	662	A
51	A2	674	C
51	A2	676	G
51	A2	677	G
51	A2	678	C
51	A2	680	C
51	A2	691	G
51	A2	692	G
51	A2	693	U

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Mol	Chain	Res	Type
51	A2	695	C
51	A2	714	A
51	A2	720	G
51	A2	721	G
51	A2	724	A
51	A2	728	C
51	A2	731	G
51	A2	732	C
51	A2	737	A
51	A2	738	A
51	A2	739	G
51	A2	741	U
51	A2	902	A
51	A2	905	G
51	A2	906	C
51	A2	907	C
51	A2	913	G
51	A2	918	C
51	A2	919	A
51	A2	922	A
51	A2	923	C
51	A2	924	U
51	A2	925	C
51	A2	926	G
51	A2	927	C
51	A2	929	G
51	A2	931	A
51	A2	932	U
51	A2	933	C
51	A2	934	C
51	A2	944	G
51	A2	947	A
51	A2	948	G
51	A2	949	C
51	A2	950	G
51	A2	951	A
51	A2	952	G
51	A2	953	A
51	A2	954	C
51	A2	955	C
51	A2	956	C
51	A2	958	U

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Mol	Chain	Res	Type
51	A2	960	G
51	A2	962	C
51	A2	967	U
51	A2	968	C
51	A2	969	U
51	A2	1053	G
51	A2	1055	C
51	A2	1062	C
51	A2	1066	U
51	A2	1067	C
51	A2	1078	A
51	A2	1083	U
51	A2	1084	C
51	A2	1086	C
51	A2	1087	C
51	A2	1147	G
51	A2	1149	G
51	A2	1150	C
51	A2	1152	G
51	A2	1156	G
51	A2	1161	G
51	A2	1162	U
51	A2	1163	C
51	A2	1164	C
51	A2	1165	C
51	A2	1167	A
51	A2	1176	C
51	A2	1179	G
51	A2	1181	G
51	A2	1188	G
51	A2	1190	C
51	A2	1191	G
51	A2	1192	U
51	A2	1193	C
51	A2	1196	G
51	A2	1201	G
51	A2	1202	G
51	A2	1220	C
51	A2	1221	A
51	A2	1222	C
51	A2	1223	G
51	A2	1225	G

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Mol	Chain	Res	Type
51	A2	1226	C
51	A2	1229	G
51	A2	1247	C
51	A2	1248	G
51	A2	1249	G
51	A2	1250	C
51	A2	1251	G
51	A2	1254	G
51	A2	1256	G
51	A2	1257	A
51	A2	1259	C
51	A2	1263	C
51	A2	1265	G
51	A2	1266	G
51	A2	1267	G
51	A2	1268	U
51	A2	1269	C
51	A2	1271	G
51	A2	1274	G
51	A2	1277	A
51	A2	1278	C
51	A2	1284	C
51	A2	1285	U
51	A2	1286	A
51	A2	1288	C
51	A2	1296	C
51	A2	1303	U
51	A2	1309	A
51	A2	1337	A
51	A2	1341	G
51	A2	1342	G
51	A2	1343	G
51	A2	1348	C
51	A2	1349	G
51	A2	1350	C
51	A2	1353	G
51	A2	1360	G
51	A2	1361	C
51	A2	1362	C
51	A2	1364	U
51	A2	1370	A
51	A2	1373	G

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Mol	Chain	Res	Type
51	A2	1374	A
51	A2	1377	G
51	A2	1380	A
51	A2	1381	A
51	A2	1392	C
51	A2	1393	U
51	A2	1394	C
51	A2	1403	A
51	A2	1421	U
51	A2	1423	U
51	A2	1426	A
51	A2	1429	C
51	A2	1430	C
51	A2	1433	C
51	A2	1463	C
51	A2	1464	G
51	A2	1465	C
51	A2	1466	G
51	A2	1467	C
51	A2	1468	C
51	A2	1472	G
51	A2	1479	A
51	A2	1480	G
51	A2	1483	C
51	A2	1485	A
51	A2	1499	G
51	A2	1500	A
51	A2	1501	C
51	A2	1505	A
51	A2	1506	A
51	A2	1507	A
51	A2	1516	A
51	A2	1517	C
51	A2	1525	G
51	A2	1531	G
51	A2	1548	C
51	A2	1556	G
51	A2	1559	G
51	A2	1563	G
51	A2	1573	U
51	A2	1578	U
51	A2	1579	G

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Mol	Chain	Res	Type
51	A2	1583	A
51	A2	1589	C
51	A2	1595	A
51	A2	1606	G
51	A2	1607	G
51	A2	1608	G
51	A2	1613	A
51	A2	1615	G
51	A2	1616	A
51	A2	1620	A
51	A2	1623	G
51	A2	1631	U
51	A2	1632	A
51	A2	1636	G
51	A2	1642	U
51	A2	1643	C
51	A2	1652	G
51	A2	1661	A
51	A2	1663	G
51	A2	1666	A
51	A2	1673	G
51	A2	1679	G
51	A2	1680	C
51	A2	1701	A
51	A2	1706	G
51	A2	1711	A
51	A2	1713	C
51	A2	1717	U
51	A2	1722	C
51	A2	1723	G
51	A2	1728	A
51	A2	1736	U
51	A2	1737	C
51	A2	1746	G
51	A2	1747	A
51	A2	1748	A
51	A2	1751	G
51	A2	1762	A
51	A2	1763	U
51	A2	1767	C
51	A2	1769	A
51	A2	1776	A

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Mol	Chain	Res	Type
51	A2	1779	G
51	A2	1785	G
51	A2	1786	A
51	A2	1787	A
51	A2	1788	G
51	A2	1794	C
51	A2	1814	G
51	A2	1815	U
51	A2	1816	G
51	A2	1817	G
51	A2	1818	A
51	A2	1822	C
51	A2	1823	G
51	A2	1835	G
51	A2	1836	G
51	A2	1850	G
51	A2	1862	C
51	A2	1863	U
51	A2	1869	A
51	A2	1873	A
51	A2	1880	G
51	A2	1896	C
51	A2	1897	G
51	A2	1902	C
51	A2	1903	G
51	A2	1906	G
51	A2	1911	U
51	A2	1912	C
51	A2	1913	A
51	A2	1920	A
51	A2	1921	G
51	A2	1928	U
51	A2	1929	G
51	A2	1930	U
51	A2	1932	G
51	A2	1939	A
51	A2	1940	U
51	A2	1941	A
51	A2	1942	G
51	A2	1943	A
51	A2	1945	A
51	A2	1956	G

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Mol	Chain	Res	Type
51	A2	1959	C
51	A2	1961	U
51	A2	1962	G
51	A2	1963	G
51	A2	1964	A
51	A2	1965	A
51	A2	1968	C
51	A2	1973	U
51	A2	1974	C
51	A2	1978	U
51	A2	1979	A
51	A2	1980	A
51	A2	1982	G
51	A2	1983	A
51	A2	1984	G
51	A2	1985	U
51	A2	1989	U
51	A2	1991	A
51	A2	2000	C
51	A2	2003	C
51	A2	2007	A
51	A2	2015	G
51	A2	2025	U
51	A2	2027	G
51	A2	2029	U
51	A2	2033	G
51	A2	2035	U
51	A2	2036	G
51	A2	2037	G
51	A2	2043	C
51	A2	2050	A
51	A2	2246	U
51	A2	2247	A
51	A2	2251	C
51	A2	2268	C
51	A2	2279	A
51	A2	2280	G
51	A2	2282	C
51	A2	2283	U
51	A2	2284	U
51	A2	2285	G
51	A2	2292	A

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Mol	Chain	Res	Type
51	A2	2301	G
51	A2	2310	G
51	A2	2324	G
51	A2	2325	C
51	A2	2327	G
51	A2	2330	C
51	A2	2339	A
51	A2	2340	G
51	A2	2358	A
51	A2	2363	U
51	A2	2374	A
51	A2	2377	U
51	A2	2389	C
51	A2	2397	A
51	A2	2400	G
51	A2	2401	C
51	A2	2416	C
51	A2	2420	C
51	A2	2426	U
51	A2	2429	G
51	A2	2442	G
51	A2	2450	G
51	A2	2451	A
51	A2	2453	G
51	A2	2467	C
51	A2	2469	U
51	A2	2470	C
51	A2	2474	U
51	A2	2482	G
51	A2	2483	C
51	A2	2485	G
51	A2	2490	A
51	A2	2492	A
51	A2	2521	G
51	A2	2524	U
51	A2	2525	G
51	A2	2527	C
51	A2	2532	A
51	A2	2533	U
51	A2	2557	G
51	A2	2565	G
51	A2	2566	A

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Mol	Chain	Res	Type
51	A2	2568	C
51	A2	2579	A
51	A2	2580	A
51	A2	2584	G
51	A2	2585	G
51	A2	2600	A
51	A2	2606	C
51	A2	2617	G
51	A2	2619	G
51	A2	2632	C
51	A2	2637	G
51	A2	2638	A
51	A2	2648	C
51	A2	2665	G
51	A2	2666	U
51	A2	2673	G
51	A2	2674	A
51	A2	2675	A
51	A2	2676	A
51	A2	2682	G
51	A2	2689	C
51	A2	2690	G
51	A2	2691	G
51	A2	2698	C
51	A2	2699	C
51	A2	2700	G
51	A2	2704	A
51	A2	2705	G
51	A2	2706	C
51	A2	2717	C
51	A2	2718	C
51	A2	2719	U
51	A2	2720	U
51	A2	2722	A
51	A2	2723	A
51	A2	2732	G
51	A2	2739	G
51	A2	2740	U
51	A2	2741	G
51	A2	2746	U
51	A2	2748	U
51	A2	2751	C

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Mol	Chain	Res	Type
51	A2	2766	A
51	A2	2767	U
51	A2	2769	U
51	A2	2773	C
51	A2	2776	C
51	A2	2778	G
51	A2	2781	C
51	A2	2785	A
51	A2	2793	C
51	A2	2798	U
51	A2	2801	G
51	A2	2804	A
51	A2	2805	U
51	A2	2806	G
51	A2	2817	G
51	A2	2819	A
51	A2	2825	G
51	A2	2839	C
51	A2	2860	A
51	A2	2871	C
51	A2	2876	G
51	A2	2881	G
51	A2	3586	G
51	A2	3587	U
51	A2	3588	G
51	A2	3589	C
51	A2	3591	G
51	A2	3596	G
51	A2	3597	G
51	A2	3601	A
51	A2	3606	A
51	A2	3614	A
51	A2	3615	U
51	A2	3616	U
51	A2	3620	A
51	A2	3627	A
51	A2	3633	A
51	A2	3643	G
51	A2	3644	C
51	A2	3651	U
51	A2	3672	C
51	A2	3676	G

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Mol	Chain	Res	Type
51	A2	3683	A
51	A2	3685	G
51	A2	3700	U
51	A2	3707	A
51	A2	3717	A
51	A2	3718	A
51	A2	3724	G
51	A2	3726	G
51	A2	3731	A
51	A2	3732	C
51	A2	3747	G
51	A2	3748	G
51	A2	3749	U
51	A2	3751	G
51	A2	3754	A
51	A2	3755	A
51	A2	3756	A
51	A2	3781	C
51	A2	3782	G
51	A2	3783	C
51	A2	3784	A
51	A2	3788	A
51	A2	3789	U
51	A2	3790	G
51	A2	3795	A
51	A2	3798	G
51	A2	3799	A
51	A2	3809	U
51	A2	3810	G
51	A2	3811	U
51	A2	3814	C
51	A2	3831	A
51	A2	3838	A
51	A2	3848	A
51	A2	3850	G
51	A2	3852	G
51	A2	3860	G
51	A2	3863	U
51	A2	3866	G
51	A2	3868	G
51	A2	3872	A
51	A2	3873	A

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Mol	Chain	Res	Type
51	A2	3875	G
51	A2	3876	A
51	A2	3877	A
51	A2	3878	G
51	A2	3879	A
51	A2	3886	U
51	A2	3890	C
51	A2	3897	C
51	A2	3909	G
51	A2	3910	G
51	A2	3911	U
51	A2	3927	G
51	A2	3929	G
51	A2	3933	A
51	A2	3935	U
51	A2	3943	A
51	A2	3944	G
51	A2	4016	A
51	A2	4017	A
51	A2	4019	U
51	A2	4020	A
51	A2	4023	A
51	A2	4026	A
51	A2	4027	C
51	A2	4029	C
51	A2	4034	C
51	A2	4035	G
51	A2	4042	C
51	A2	4046	G
51	A2	4047	A
51	A2	4051	G
51	A2	4054	G
51	A2	4064	G
51	A2	4065	G
51	A2	4066	C
51	A2	4067	G
51	A2	4068	A
51	A2	4069	G
51	A2	4070	C
51	A2	4074	A
51	A2	4075	G
51	A2	4076	G

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Mol	Chain	Res	Type
51	A2	4078	G
51	A2	4079	C
51	A2	4081	C
51	A2	4084	G
51	A2	4088	C
51	A2	4105	C
51	A2	4106	C
51	A2	4107	C
51	A2	4108	G
51	A2	4109	G
51	A2	4110	C
51	A2	4124	C
51	A2	4126	C
51	A2	4132	A
51	A2	4145	G
51	A2	4146	G
51	A2	4153	G
51	A2	4165	A
51	A2	4167	A
51	A2	4174	A
51	A2	4175	A
51	A2	4176	A
51	A2	4191	U
51	A2	4195	A
51	A2	4196	A
51	A2	4205	C
51	A2	4212	G
51	A2	4213	A
51	A2	4215	A
51	A2	4216	G
51	A2	4227	U
51	A2	4228	G
51	A2	4230	A
51	A2	4234	G
51	A2	4235	A
51	A2	4242	A
51	A2	4244	A
51	A2	4251	U
51	A2	4252	U
51	A2	4253	G
51	A2	4259	G
51	A2	4266	A

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Mol	Chain	Res	Type
51	A2	4267	G
51	A2	4268	U
51	A2	4276	C
51	A2	4285	A
51	A2	4288	G
51	A2	4291	G
51	A2	4292	G
51	A2	4294	C
51	A2	4300	G
51	A2	4311	C
51	A2	4316	U
51	A2	4320	U
51	A2	4330	G
51	A2	4333	G
51	A2	4334	U
51	A2	4338	A
51	A2	4339	G
51	A2	4340	A
51	A2	4342	A
51	A2	4349	C
51	A2	4355	G
51	A2	4356	A
51	A2	4357	U
51	A2	4358	A
51	A2	4360	C
51	A2	4372	G
51	A2	4384	A
51	A2	4388	C
51	A2	4392	G
51	A2	4406	C
51	A2	4410	G
51	A2	4412	U
51	A2	4426	A
51	A2	4427	U
51	A2	4428	C
51	A2	4437	G
51	A2	4455	U
51	A2	4459	U
51	A2	4474	U
51	A2	4475	A
51	A2	4477	G
51	A2	4480	A

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Mol	Chain	Res	Type
51	A2	4482	G
51	A2	4485	A
51	A2	4486	G
51	A2	4510	A
51	A2	4522	C
51	A2	4532	G
51	A2	4537	G
51	A2	4543	G
51	A2	4551	A
51	A2	4552	A
51	A2	4561	A
51	A2	4562	G
51	A2	4568	G
51	A2	4579	G
51	A2	4586	A
51	A2	4595	G
51	A2	4598	U
51	A2	4599	G
51	A2	4614	G
51	A2	4618	A
51	A2	4620	G
51	A2	4632	C
51	A2	4633	C
51	A2	4640	G
51	A2	4641	G
51	A2	4649	A
51	A2	4655	C
51	A2	4656	G
51	A2	4662	A
51	A2	4665	U
51	A2	4671	U
51	A2	4678	C
51	A2	4680	G
51	A2	4681	G
51	A2	4693	G
51	A2	4694	G
51	A2	4695	C
51	A2	4696	A
51	A2	4700	C
51	A2	4703	C
51	A2	4704	G
51	A2	4705	G

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Mol	Chain	Res	Type
51	A2	4713	G
51	A2	4714	U
51	A2	4715	U
51	A2	4718	C
51	A2	4720	U
51	A2	4725	U
51	A2	4726	A
51	A2	4731	G
51	A2	4732	U
51	A2	4824	C
51	A2	4827	U
51	A2	4828	G
51	A2	4831	G
51	A2	4832	A
51	A2	4833	G
51	A2	4834	U
51	A2	4837	C
51	A2	4838	C
51	A2	4839	U
51	A2	4840	U
51	A2	4841	C
51	A2	4847	G
51	A2	4852	A
51	A2	4853	C
51	A2	4854	G
51	A2	4855	G
51	A2	4856	G
51	A2	4858	C
51	A2	4859	G
51	A2	4860	C
51	A2	4864	C
51	A2	4865	G
51	A2	4866	G
51	A2	4867	A
51	A2	4868	A
51	A2	4869	A
51	A2	4870	G
51	A2	4871	G
51	A2	4872	C
51	A2	4880	C
51	A2	4882	C
51	A2	4883	U

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Mol	Chain	Res	Type
51	A2	4885	G
51	A2	4886	C
51	A2	4895	C
51	A2	4896	A
51	A2	4899	G
51	A2	4901	A
51	A2	4902	C
51	A2	4905	U
51	A2	4906	C
51	A2	4907	G
51	A2	4908	U
51	A2	4909	G
51	A2	4921	G
51	A2	4924	A
51	A2	4934	U
51	A2	4936	G
51	A2	4943	U
51	A2	4946	U
51	A2	4947	U
51	A2	4948	C
51	A2	4949	U
51	A2	4950	G
51	A2	4957	G
51	A2	4960	U
51	A2	4964	U
51	A2	4971	C
51	A2	4972	A
51	A2	4975	G
51	A2	4981	C
51	A2	4982	C
51	A2	4984	U
51	A2	4985	C
51	A2	4986	G
51	A2	4998	U
51	A2	4999	G
51	A2	5005	C
51	A2	5008	C
51	A2	5011	U
51	A2	5012	C
51	A2	5013	G
51	A2	5016	A
51	A2	5019	A

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Mol	Chain	Res	Type
51	A2	5020	G
51	A2	5024	U
51	A2	5028	C
52	B1	4	C
52	B1	17	C
52	B1	25	A
52	B1	26	U
52	B1	33	G
52	B1	46	A
52	B1	59	U
52	B1	66	G
52	B1	67	C
52	B1	72	C
52	B1	73	C
52	B1	74	G
52	B1	77	A
52	B1	79	A
52	B1	85	A
52	B1	91	A
52	B1	103	A
52	B1	107	A
52	B1	110	U
52	B1	113	G
52	B1	114	G
52	B1	115	U
52	B1	125	C
52	B1	126	G
52	B1	142	C
52	B1	143	U
52	B1	146	G
52	B1	153	G
52	B1	155	G
52	B1	159	A
52	B1	160	U
52	B1	161	U
52	B1	162	C
52	B1	163	U
52	B1	170	A
52	B1	172	U
52	B1	173	A
52	B1	174	C
52	B1	175	A

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Mol	Chain	Res	Type
52	B1	183	G
52	B1	188	C
52	B1	192	C
52	B1	202	G
52	B1	217	A
52	B1	219	U
52	B1	225	G
52	B1	226	A
52	B1	227	U
52	B1	228	C
52	B1	229	A
52	B1	230	A
52	B1	238	C
52	B1	239	C
52	B1	283	G
52	B1	284	C
52	B1	285	U
52	B1	286	U
52	B1	287	U
52	B1	292	A
52	B1	293	C
52	B1	298	G
52	B1	302	A
52	B1	306	C
52	B1	308	G
52	B1	309	G
52	B1	313	A
52	B1	314	U
52	B1	319	C
52	B1	325	C
52	B1	327	G
52	B1	328	U
52	B1	329	G
52	B1	331	C
52	B1	332	G
52	B1	333	G
52	B1	339	A
52	B1	343	A
52	B1	347	G
52	B1	351	G
52	B1	357	C
52	B1	362	C

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Mol	Chain	Res	Type
52	B1	364	A
52	B1	368	U
52	B1	369	C
52	B1	370	G
52	B1	376	A
52	B1	381	C
52	B1	385	G
52	B1	386	C
52	B1	387	C
52	B1	398	A
52	B1	408	A
52	B1	409	C
52	B1	426	A
52	B1	427	U
52	B1	435	A
52	B1	447	A
52	B1	448	A
52	B1	449	A
52	B1	450	C
52	B1	463	C
52	B1	464	A
52	B1	465	A
52	B1	467	G
52	B1	471	G
52	B1	472	C
52	B1	474	G
52	B1	476	A
52	B1	482	G
52	B1	483	C
52	B1	485	A
52	B1	487	U
52	B1	489	A
52	B1	492	C
52	B1	493	A
52	B1	496	C
52	B1	501	C
52	B1	503	C
52	B1	508	A
52	B1	517	C
52	B1	523	A
52	B1	525	A
52	B1	526	A

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Mol	Chain	Res	Type
52	B1	527	C
52	B1	529	A
52	B1	533	A
52	B1	534	G
52	B1	535	G
52	B1	536	A
52	B1	541	U
52	B1	542	U
52	B1	544	G
52	B1	545	A
52	B1	546	G
52	B1	547	G
52	B1	548	C
52	B1	549	C
52	B1	550	C
52	B1	553	U
52	B1	554	A
52	B1	555	A
52	B1	558	G
52	B1	560	A
52	B1	562	U
52	B1	565	G
52	B1	567	C
52	B1	587	A
52	B1	589	G
52	B1	590	A
52	B1	591	U
52	B1	592	C
52	B1	597	G
52	B1	606	G
52	B1	607	U
52	B1	608	C
52	B1	613	G
52	B1	614	C
52	B1	617	G
52	B1	620	G
52	B1	621	C
52	B1	623	G
52	B1	629	A
52	B1	634	A
52	B1	643	A
52	B1	644	G

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Mol	Chain	Res	Type
52	B1	645	C
52	B1	657	U
52	B1	658	U
52	B1	660	C
52	B1	662	G
52	B1	668	A
52	B1	669	A
52	B1	672	A
52	B1	673	G
52	B1	684	G
52	B1	688	U
52	B1	690	G
52	B1	741	C
52	B1	742	U
52	B1	743	U
52	B1	744	G
52	B1	747	U
52	B1	751	G
52	B1	791	C
52	B1	796	G
52	B1	797	C
52	B1	798	G
52	B1	799	U
52	B1	800	U
52	B1	806	U
52	B1	808	A
52	B1	810	A
52	B1	811	A
52	B1	821	G
52	B1	827	A
52	B1	836	G
52	B1	837	A
52	B1	839	C
52	B1	841	G
52	B1	847	A
52	B1	848	U
52	B1	868	G
52	B1	870	A
52	B1	871	U
52	B1	874	G
52	B1	885	U
52	B1	888	U

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Mol	Chain	Res	Type
52	B1	890	U
52	B1	891	G
52	B1	913	A
52	B1	914	U
52	B1	917	U
52	B1	919	A
52	B1	920	A
52	B1	928	G
52	B1	929	G
52	B1	933	G
52	B1	943	U
52	B1	950	C
52	B1	955	A
52	B1	956	G
52	B1	958	G
52	B1	959	G
52	B1	960	U
52	B1	962	A
52	B1	963	A
52	B1	969	U
52	B1	975	G
52	B1	988	C
52	B1	990	A
52	B1	991	G
52	B1	992	A
52	B1	1002	U
52	B1	1008	A
52	B1	1017	U
52	B1	1021	U
52	B1	1023	A
52	B1	1044	G
52	B1	1053	C
52	B1	1057	C
52	B1	1060	A
52	B1	1061	U
52	B1	1062	A
52	B1	1076	G
52	B1	1077	A
52	B1	1085	C
52	B1	1088	U
52	B1	1100	A
52	B1	1109	C

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Mol	Chain	Res	Type
52	B1	1110	G
52	B1	1113	A
52	B1	1114	U
52	B1	1115	U
52	B1	1116	C
52	B1	1117	C
52	B1	1119	A
52	B1	1120	U
52	B1	1121	G
52	B1	1123	C
52	B1	1133	A
52	B1	1140	G
52	B1	1146	C
52	B1	1149	A
52	B1	1150	A
52	B1	1156	U
52	B1	1157	G
52	B1	1163	C
52	B1	1170	A
52	B1	1195	A
52	B1	1199	A
52	B1	1203	G
52	B1	1207	G
52	B1	1215	C
52	B1	1224	G
52	B1	1242	U
52	B1	1251	A
52	B1	1253	A
52	B1	1256	G
52	B1	1257	G
52	B1	1258	A
52	B1	1259	A
52	B1	1261	C
52	B1	1271	C
52	B1	1275	G
52	B1	1276	A
52	B1	1285	G
52	B1	1286	G
52	B1	1287	A
52	B1	1288	U
52	B1	1289	U
52	B1	1290	G

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Mol	Chain	Res	Type
52	B1	1297	U
52	B1	1301	A
52	B1	1302	G
52	B1	1303	C
52	B1	1312	G
52	B1	1313	A
52	B1	1314	U
52	B1	1320	G
52	B1	1330	G
52	B1	1331	C
52	B1	1332	A
52	B1	1342	U
52	B1	1352	G
52	B1	1371	U
52	B1	1372	U
52	B1	1373	C
52	B1	1378	A
52	B1	1381	G
52	B1	1382	A
52	B1	1394	G
52	B1	1397	U
52	B1	1398	G
52	B1	1399	C
52	B1	1401	A
52	B1	1406	G
52	B1	1417	C
52	B1	1418	C
52	B1	1420	G
52	B1	1421	A
52	B1	1424	G
52	B1	1426	U
52	B1	1439	A
52	B1	1442	U
52	B1	1444	U
52	B1	1454	A
52	B1	1455	A
52	B1	1461	G
52	B1	1462	U
52	B1	1463	U
52	B1	1477	U
52	B1	1478	U
52	B1	1480	A

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Mol	Chain	Res	Type
52	B1	1484	A
52	B1	1489	A
52	B1	1494	U
52	B1	1495	G
52	B1	1497	G
52	B1	1498	A
52	B1	1507	G
52	B1	1512	C
52	B1	1519	U
52	B1	1520	G
52	B1	1521	C
52	B1	1522	A
52	B1	1531	A
52	B1	1533	A
52	B1	1537	A
52	B1	1544	C
52	B1	1548	G
52	B1	1553	C
52	B1	1554	C
52	B1	1555	U
52	B1	1558	C
52	B1	1560	U
52	B1	1573	G
52	B1	1580	A
52	B1	1582	C
52	B1	1584	G
52	B1	1585	U
52	B1	1586	U
52	B1	1587	G
52	B1	1588	A
52	B1	1601	A
52	B1	1604	G
52	B1	1606	G
52	B1	1618	C
52	B1	1620	A
52	B1	1621	U
52	B1	1622	U
52	B1	1623	A
52	B1	1624	U
52	B1	1660	C
52	B1	1661	A
52	B1	1662	U

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Mol	Chain	Res	Type
52	B1	1663	A
52	B1	1665	G
52	B1	1671	G
52	B1	1678	A
52	B1	1695	A
52	B1	1699	A
52	B1	1703	C
52	B1	1721	U
52	B1	1722	G
52	B1	1737	G
52	B1	1756	C
52	B1	1757	G
52	B1	1776	G
52	B1	1779	G
52	B1	1782	G
52	B1	1783	C
52	B1	1784	G
52	B1	1801	A
52	B1	1811	C
52	B1	1823	A
52	B1	1829	G
52	B1	1834	A
52	B1	1838	U
52	B1	1849	G
52	B1	1851	A
52	B1	1852	C
52	B1	1860	A
52	B1	1861	G
52	B1	1862	G
52	B1	1863	A
52	B1	1865	C
52	B1	1866	A
52	B1	1869	A
83	Bv	4	C
83	Bv	7	A
83	Bv	8	U
83	Bv	11	C
83	Bv	13	C
83	Bv	14	A
83	Bv	16	U
83	Bv	17	C
83	Bv	18	G

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Mol	Chain	Res	Type
83	Bv	19	G
83	Bv	30	G
83	Bv	37	A
83	Bv	43	C
83	Bv	46	G
83	Bv	48	C
83	Bv	53	G
83	Bv	56	C
83	Bv	58	A
83	Bv	59	U
83	Bv	61	C
83	Bv	68	C
83	Bv	75	C
83	Bv	76	A
84	Bx	45	U
84	Bx	46	U
84	Bx	49	U
84	Bx	50	U
84	Bx	51	U
84	Bx	53	U
84	Bx	54	U
84	Bx	56	U
84	Bx	57	U
84	Bx	58	U

All (28) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	A3	33	G
7	A3	39	G
7	A3	108	A
51	A2	31	U
51	A2	71	C
51	A2	227	G
51	A2	228	U
51	A2	901	U
51	A2	959	C
51	A2	1500	A
51	A2	2717	C
51	A2	3755	A
51	A2	4107	C
51	A2	4661	U

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Mol	Chain	Res	Type
51	A2	4865	G
51	A2	4870	G
51	A2	4907	G
51	A2	4946	U
52	B1	173	A
52	B1	227	U
52	B1	286	U
52	B1	369	C
52	B1	644	G
52	B1	797	C
52	B1	1139	C
52	B1	1398	G
52	B1	1554	C
52	B1	1756	C

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 332 ligands modelled in this entry, 331 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
88	MVM	A2	5327	-	35,35,35	1.95	4 (11%)	44,49,49	2.75	17 (38%)

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
88	MVM	A2	5327	-	-	2/20/28/28	0/5/5/5

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
88	A2	5327	MVM	N4-N5	-7.18	1.30	1.38
88	A2	5327	MVM	C5-N1	6.30	1.46	1.37
88	A2	5327	MVM	C6-N1	2.58	1.45	1.39
88	A2	5327	MVM	C12-C5	2.39	1.54	1.50

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
88	A2	5327	MVM	N7-C22-N4	7.36	134.16	125.88
88	A2	5327	MVM	C15-N4-C22	-7.23	124.12	130.55
88	A2	5327	MVM	C15-N4-N5	6.43	125.04	119.25
88	A2	5327	MVM	C7-C3-C9	4.54	119.43	110.81
88	A2	5327	MVM	C18-C22-N7	-4.37	121.17	127.18
88	A2	5327	MVM	C6-N1-C5	-4.32	117.76	122.94
88	A2	5327	MVM	C19-C18-N6	4.04	135.76	130.50
88	A2	5327	MVM	N3-C6-N1	3.75	120.36	116.35
88	A2	5327	MVM	C1-C9-N1	-3.69	106.90	116.16
88	A2	5327	MVM	C12-C5-N1	3.34	122.79	118.36
88	A2	5327	MVM	C21-N7-C22	3.33	122.58	115.05
88	A2	5327	MVM	C8-N3-C6	2.99	121.82	115.05
88	A2	5327	MVM	C11-C2-C6	2.50	120.83	118.51
88	A2	5327	MVM	C6-N1-C9	2.45	122.05	118.40
88	A2	5327	MVM	C20-C21-N7	-2.23	119.90	123.42
88	A2	5327	MVM	C2-C6-N3	-2.22	119.54	123.00
88	A2	5327	MVM	C3-C9-C1	2.02	113.22	110.81

There are no chirality outliers.

All (2) torsion outliers are listed below:

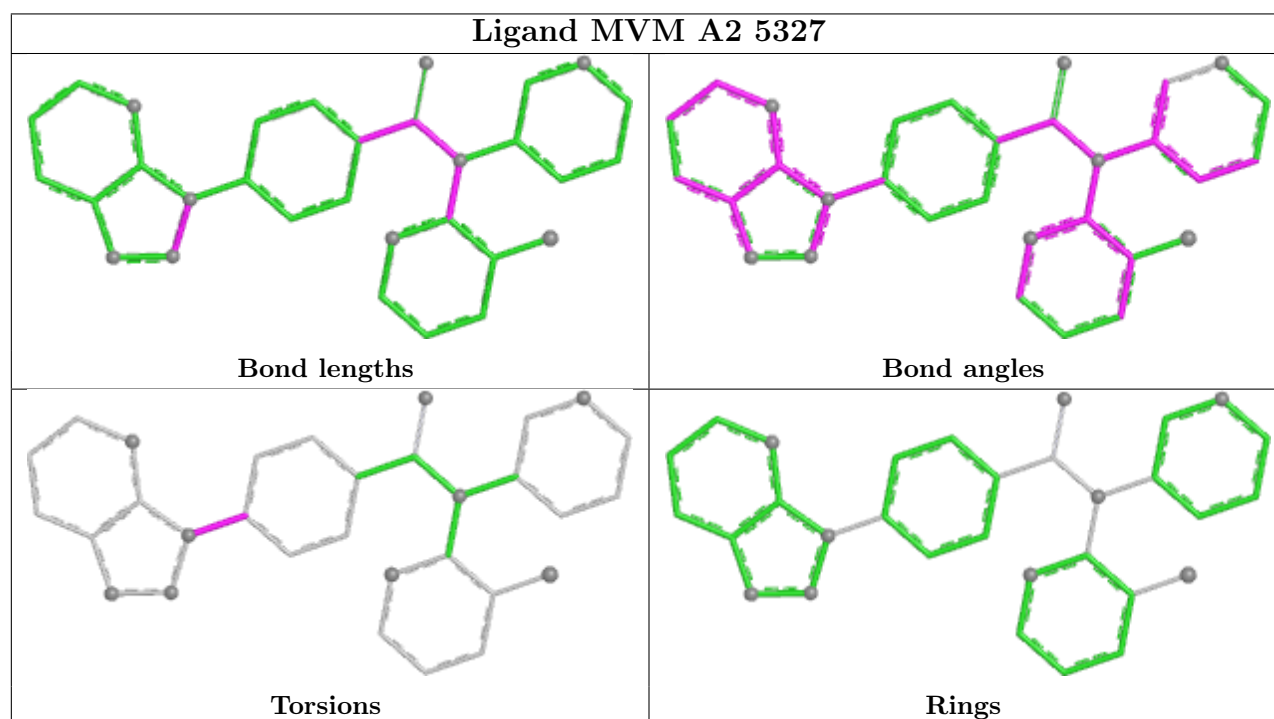
Mol	Chain	Res	Type	Atoms
88	A2	5327	MVM	C16-C15-N4-C22
88	A2	5327	MVM	C14-C15-N4-C22

There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
88	A2	5327	MVM	7	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
51	A2	11
52	B1	6
83	Bv	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B1	126:G	O3'	141:A	P	20.56
1	B1	1757:G	O3'	1775:U	P	18.28
1	A2	3948:C	O3'	4004:G	P	18.11
1	B1	751:G	O3'	790:C	P	17.98
1	A2	4734:C	O3'	4818:G	P	17.83
1	A2	750:G	O3'	890:C	P	17.39
1	A2	1680:C	O3'	1699:C	P	17.31
1	B1	1426:U	O3'	1438:A	P	17.22
1	A2	1233:C	O3'	1243:G	P	17.05
1	A2	517:C	O3'	629:G	P	17.01
1	B1	240:G	O3'	282:G	P	16.73
1	A2	2881:G	O3'	3569:C	P	16.22
1	A2	976:U	O3'	1047:G	P	15.81
1	A2	1089:A	O3'	1145:G	P	15.47
1	B1	696:G	O3'	737:G	P	15.40
1	A2	2068:C	O3'	2245:C	P	14.47
1	A2	1202:G	O3'	1216:G	P	13.43
1	Bv	73:A	O3'	74:C	P	1.78

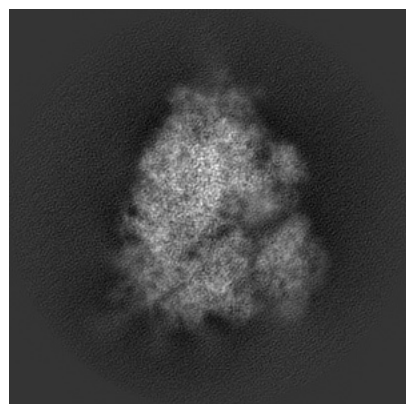
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0601. These allow visual inspection of the internal detail of the map and identification of artifacts.

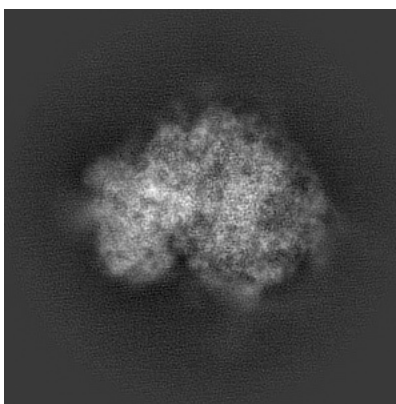
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

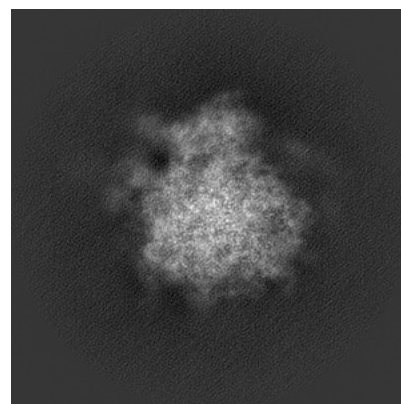
6.1.1 Primary map



X

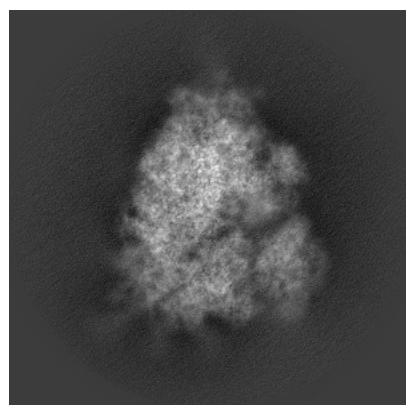


Y

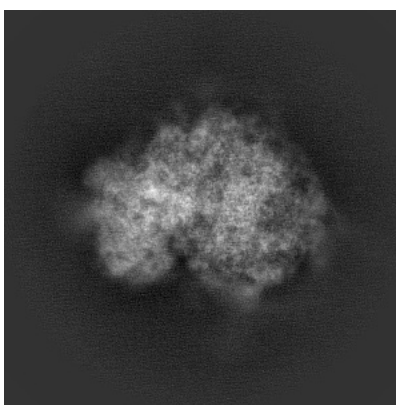


Z

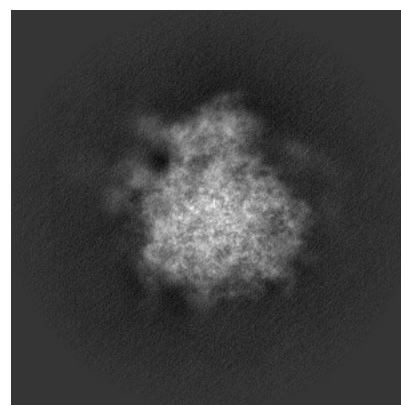
6.1.2 Raw map



X



Y

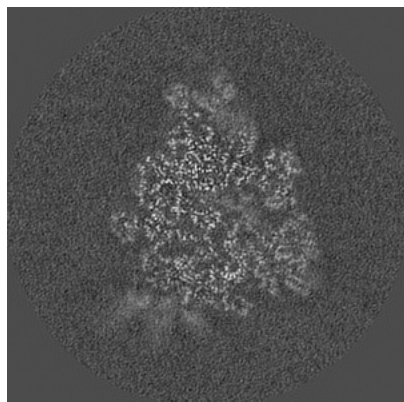


Z

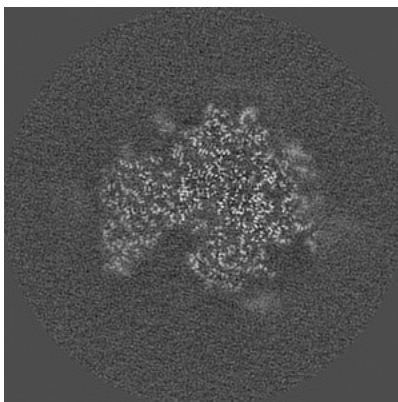
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

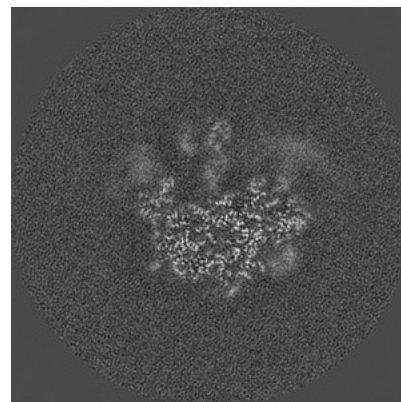
6.2.1 Primary map



X Index: 205

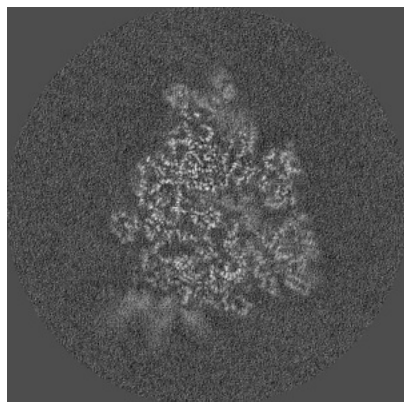


Y Index: 205

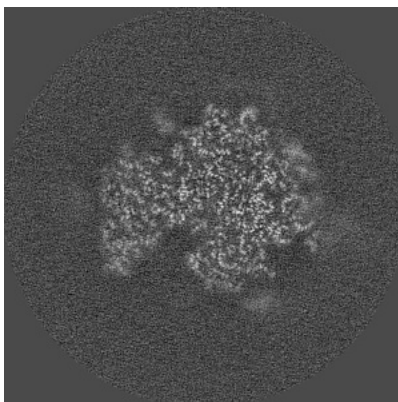


Z Index: 205

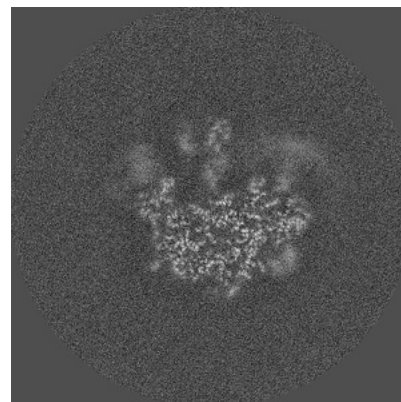
6.2.2 Raw map



X Index: 205



Y Index: 205

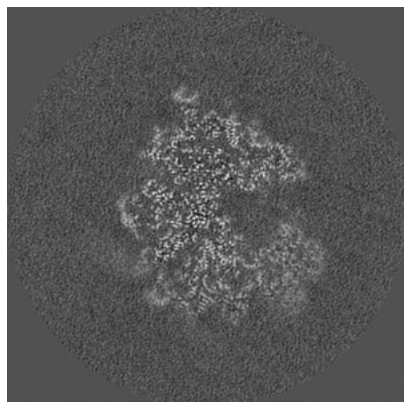


Z Index: 205

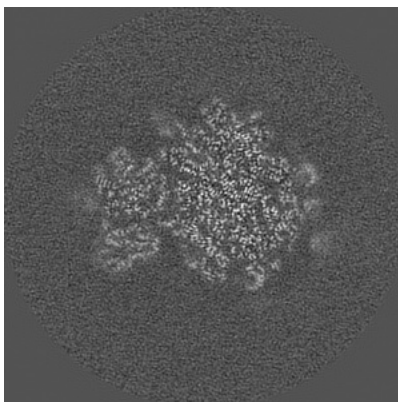
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

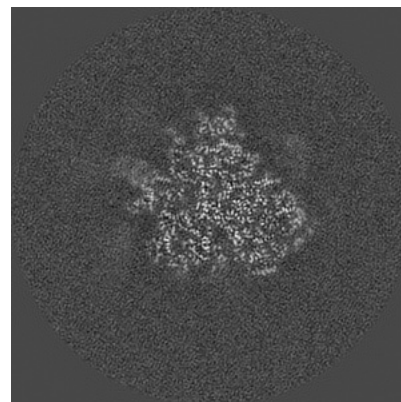
6.3.1 Primary map



X Index: 225

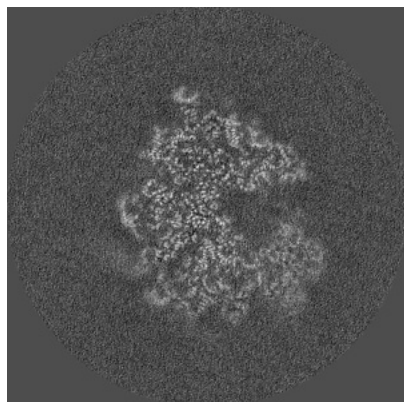


Y Index: 197

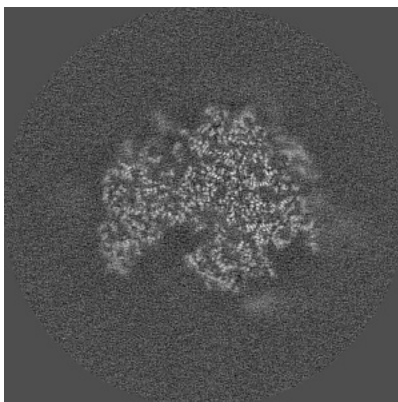


Z Index: 234

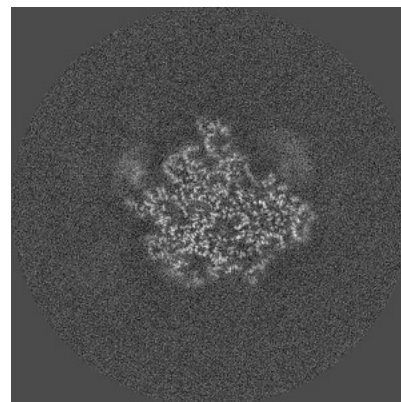
6.3.2 Raw map



X Index: 225



Y Index: 207

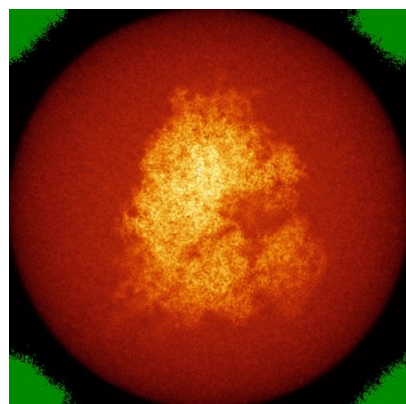


Z Index: 225

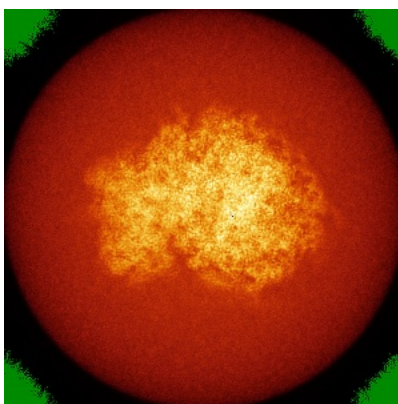
The images above show the largest variance slices of the map in three orthogonal directions.

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

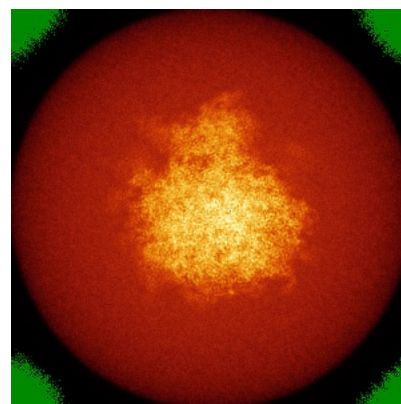
6.4.1 Primary map



X

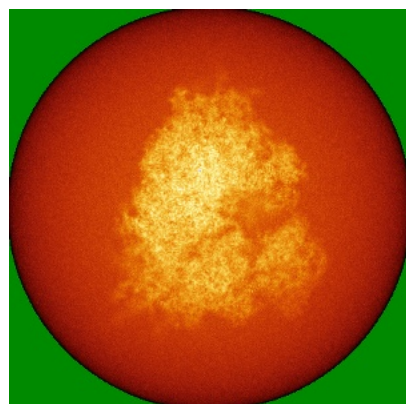


Y

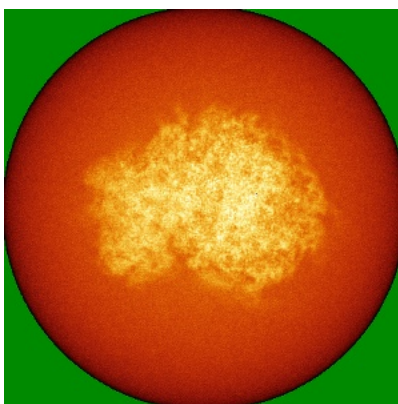


Z

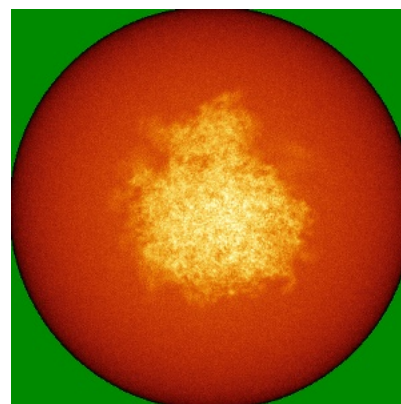
6.4.2 Raw map



X



Y

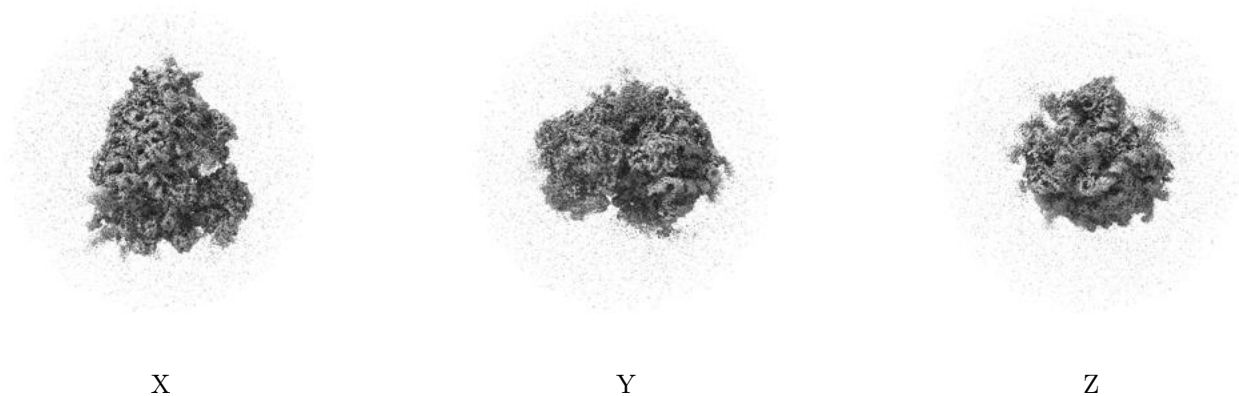


Z

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

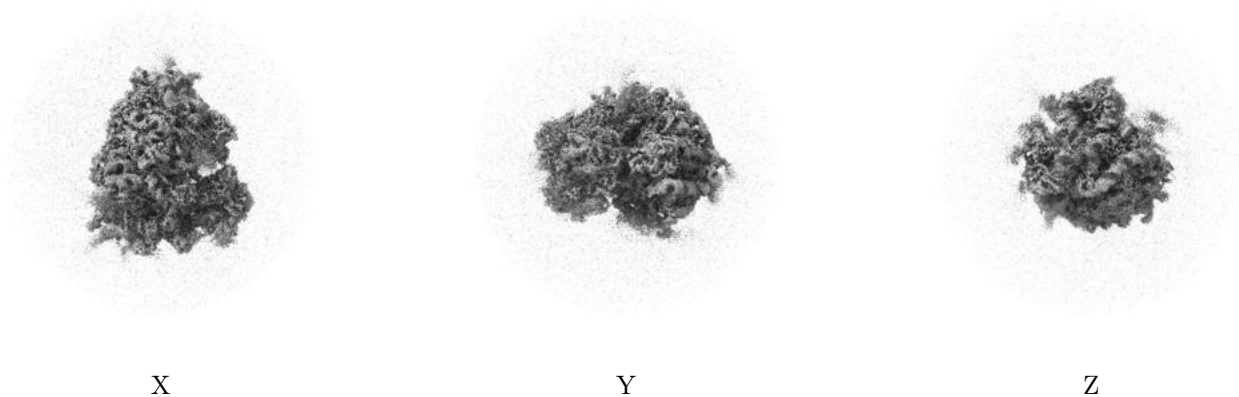
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

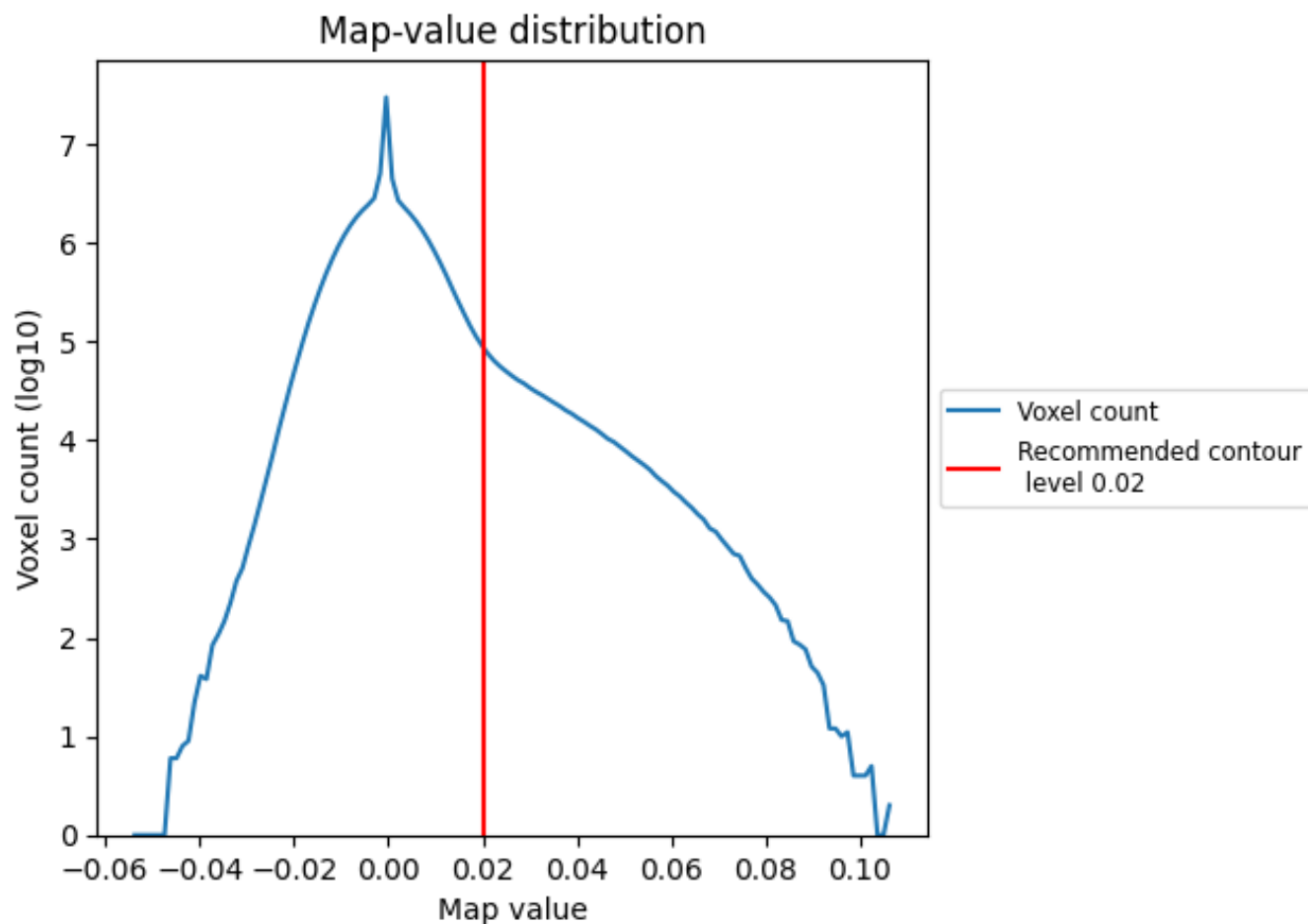
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

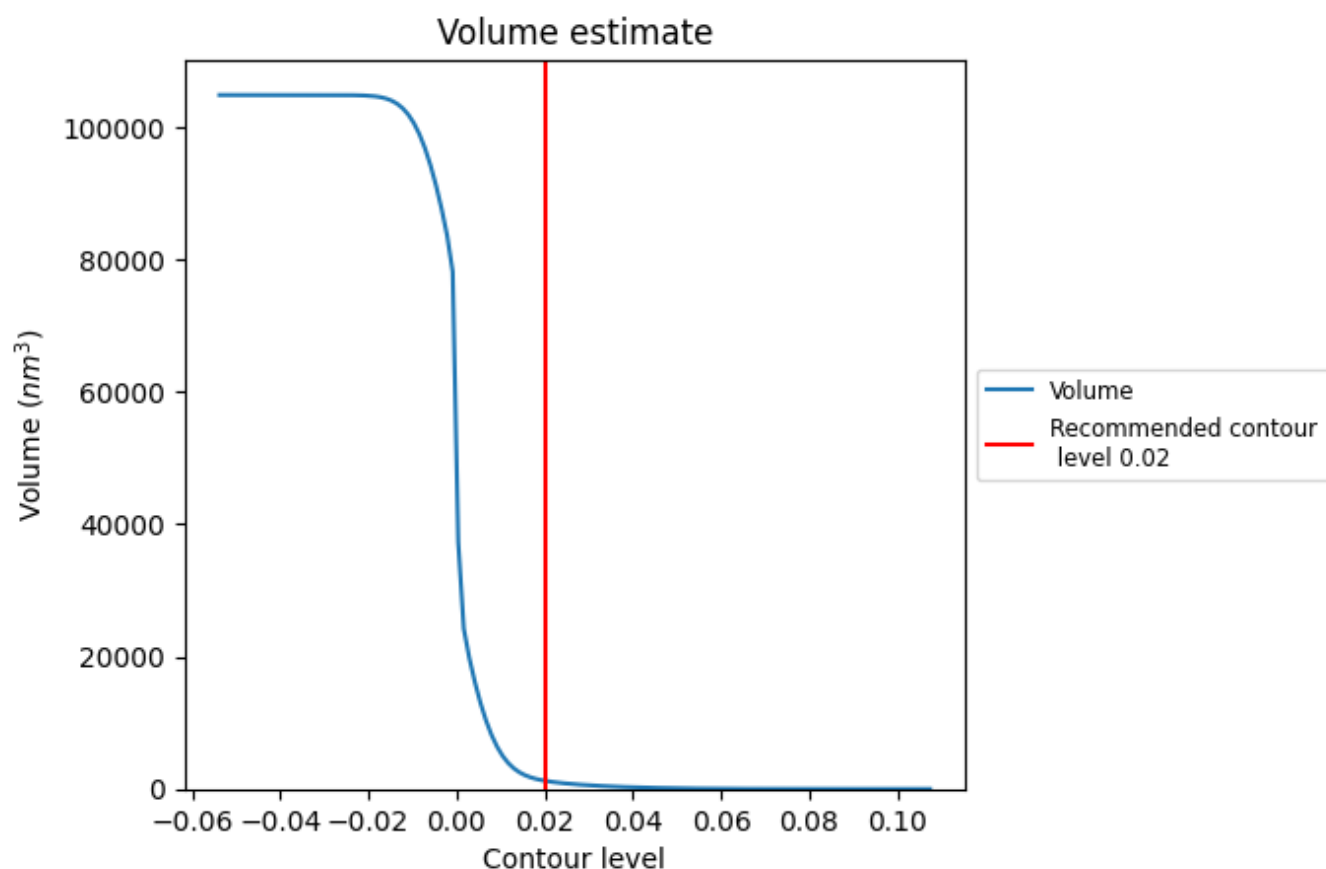
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

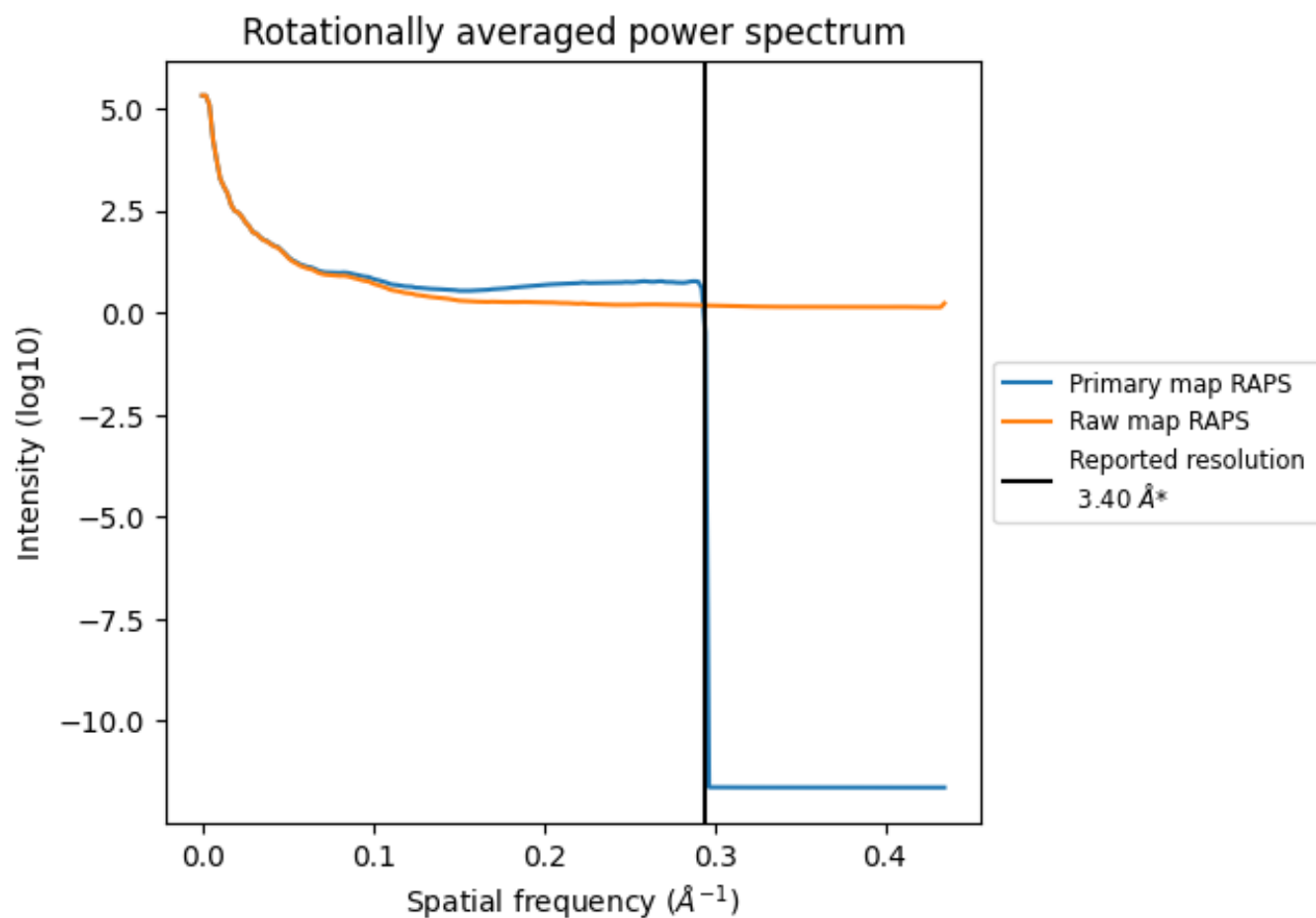
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1242 nm^3 ; this corresponds to an approximate mass of 1122 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 ⓘ

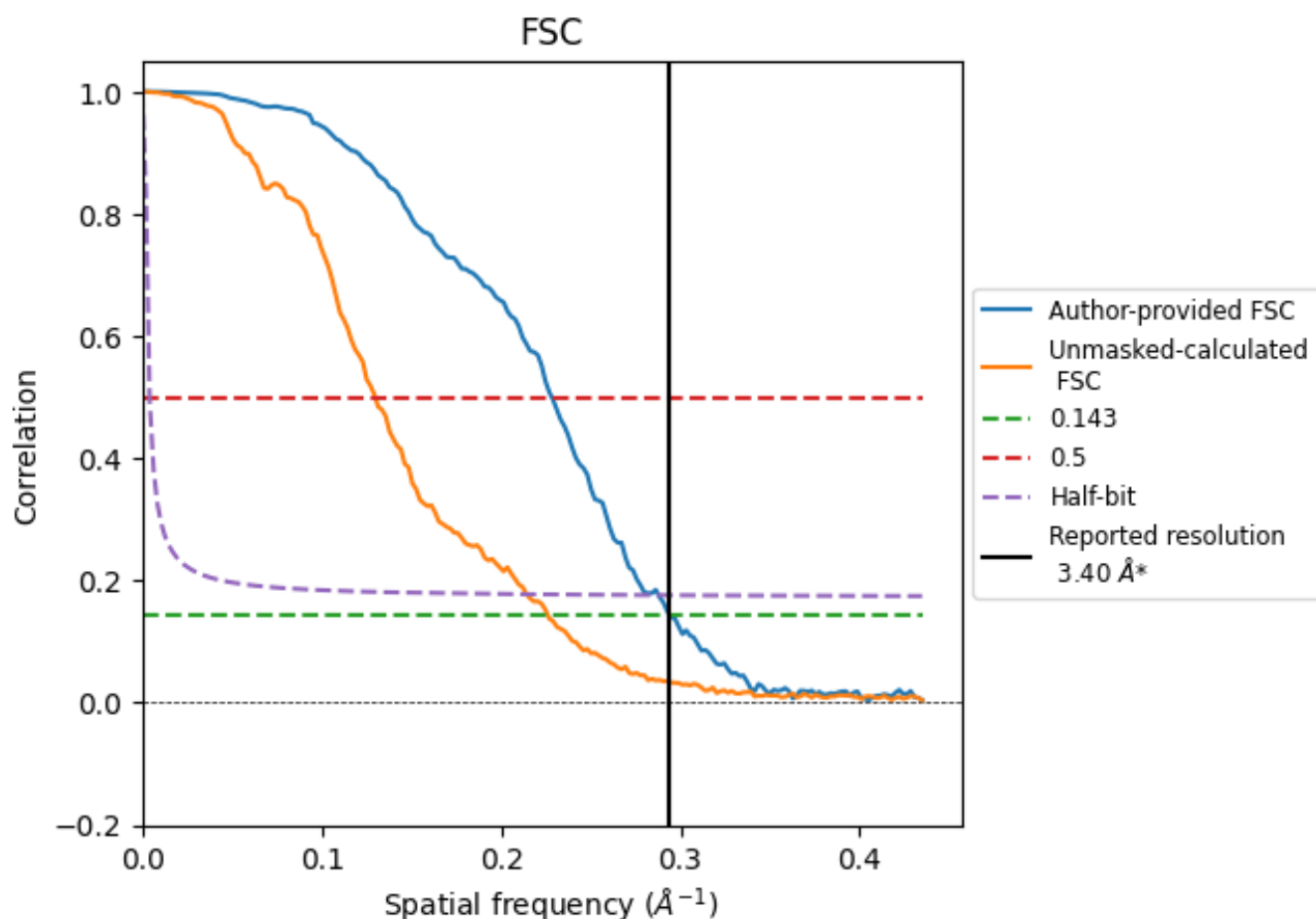


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

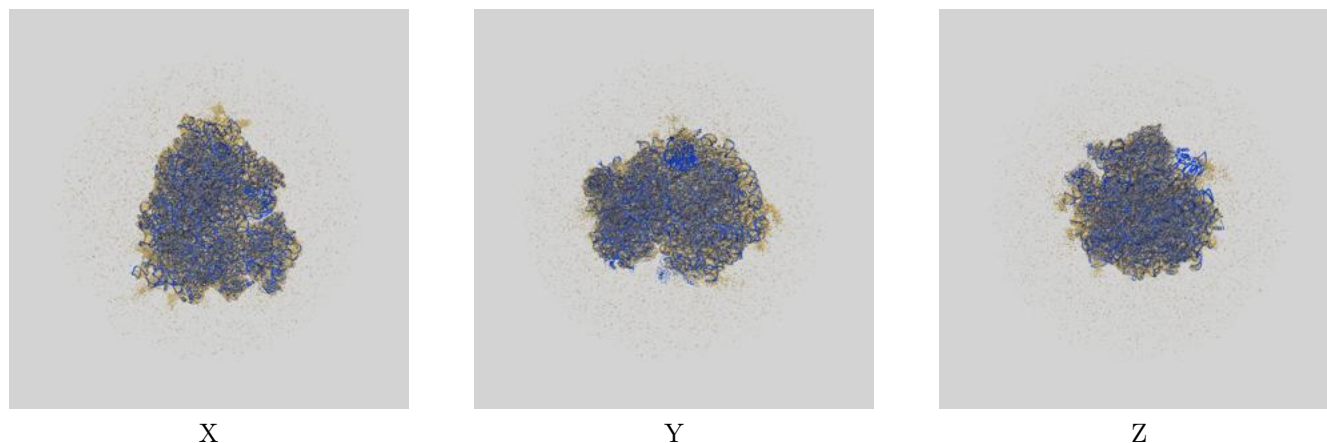
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.40	4.38	3.47
Unmasked-calculated*	4.42	7.70	4.67

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.42 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

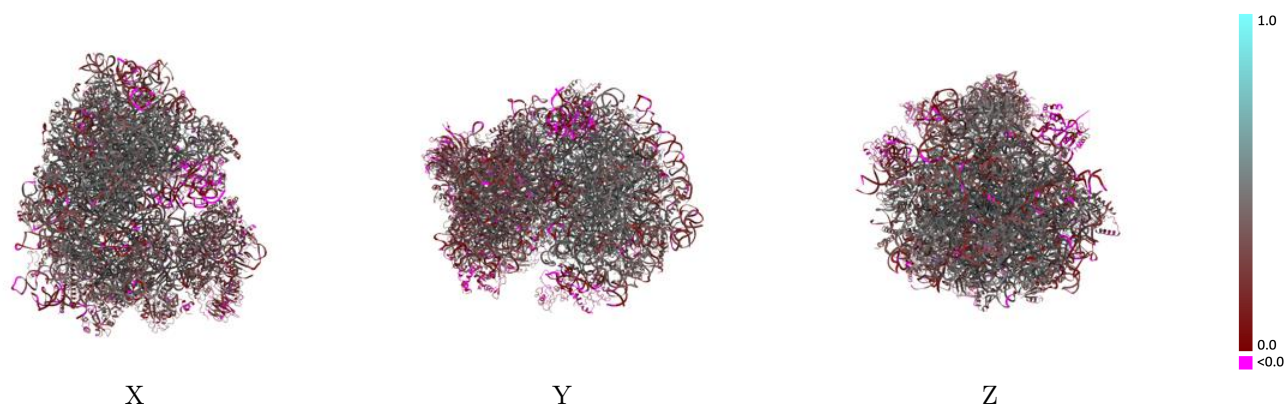
This section contains information regarding the fit between EMDB map EMD-0601 and PDB model 6OLG. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



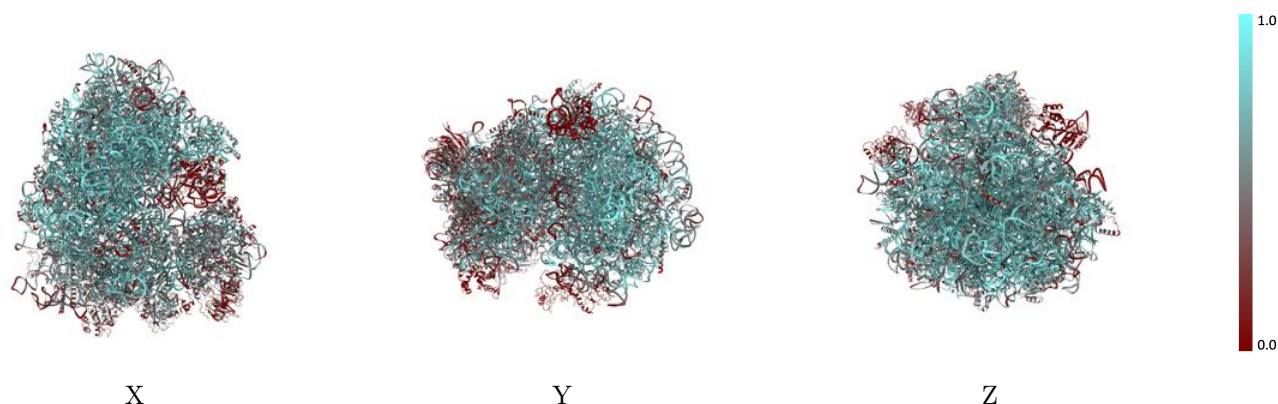
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



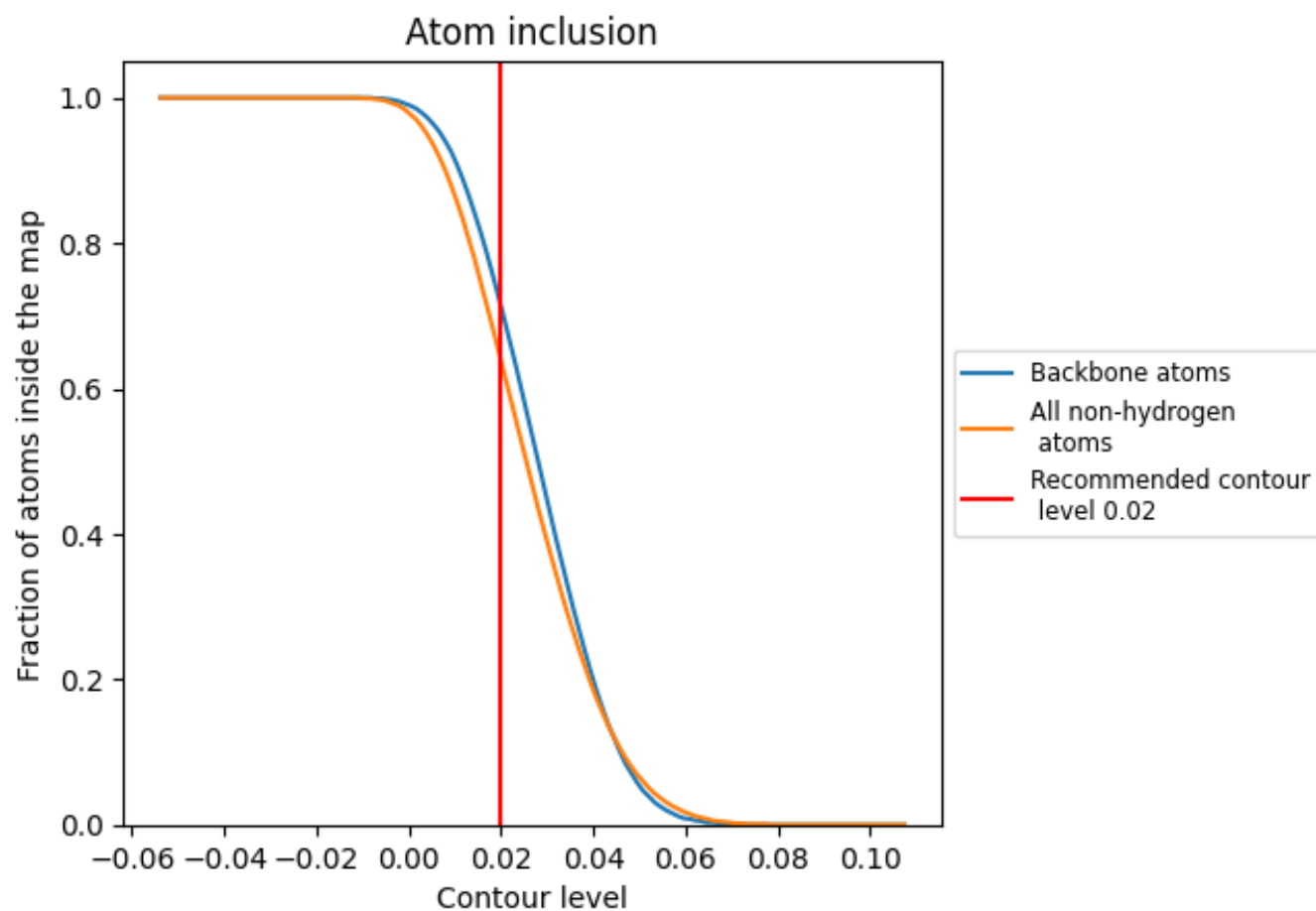
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 64% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6390	 0.3630
A	 0.0740	 0.0960
A2	 0.7520	 0.3930
A3	 0.7640	 0.4020
A4	 0.8630	 0.4520
AA	 0.6720	 0.4320
AB	 0.6500	 0.4280
AC	 0.6680	 0.4320
AD	 0.6230	 0.3830
AE	 0.5410	 0.3590
AF	 0.6380	 0.4090
AG	 0.5640	 0.3510
AH	 0.5730	 0.3930
AI	 0.6200	 0.4030
AJ	 0.5680	 0.3670
AK	 0.0390	 0.0470
AL	 0.5950	 0.3720
AM	 0.6480	 0.4040
AN	 0.7230	 0.4480
AO	 0.6530	 0.4190
AP	 0.6600	 0.4370
AQ	 0.6480	 0.4270
AR	 0.6270	 0.3870
AS	 0.6740	 0.4430
AT	 0.6590	 0.4100
AU	 0.5420	 0.3530
AV	 0.6480	 0.4400
AW	 0.3730	 0.2640
AX	 0.6000	 0.4040
AY	 0.6600	 0.4130
AZ	 0.6230	 0.3660
Aa	 0.6950	 0.4390
Ab	 0.5880	 0.3580
Ac	 0.5820	 0.3890
Ad	 0.6390	 0.4050



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Chain	Atom inclusion	Q-score
Ae	 0.6820	 0.4450
Af	 0.7040	 0.4620
Ag	 0.6200	 0.4080
Ah	 0.6070	 0.3720
Ai	 0.6190	 0.3560
Aj	 0.7170	 0.4510
Ak	 0.5040	 0.3110
Al	 0.6550	 0.4200
Am	 0.6450	 0.4080
An	 0.5520	 0.3670
Ao	 0.5720	 0.3850
Ap	 0.6530	 0.4230
Aq	 0.0210	 0.0630
At	 0.6650	 0.4220
Au	 0.0060	 0.0330
B1	 0.6890	 0.3570
BA	 0.5000	 0.3260
BB	 0.4860	 0.3100
BC	 0.5440	 0.3690
BD	 0.3340	 0.2720
BE	 0.5130	 0.3530
BF	 0.4070	 0.2760
BG	 0.3960	 0.2560
BH	 0.3740	 0.2540
BI	 0.5100	 0.3430
BJ	 0.5030	 0.3120
BK	 0.2780	 0.2000
BL	 0.5170	 0.3390
BM	 0.0410	 0.0730
BN	 0.5380	 0.3460
BO	 0.5330	 0.3590
BP	 0.3710	 0.2340
BQ	 0.4110	 0.2550
BR	 0.3540	 0.2520
BS	 0.3930	 0.2800
BT	 0.3690	 0.2290
BU	 0.3720	 0.2510
BV	 0.4860	 0.3190
BW	 0.5830	 0.3830
BX	 0.5610	 0.3700
BY	 0.4570	 0.2880
BZ	 0.3060	 0.2130

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Chain	Atom inclusion	Q-score
Ba	 0.5610	 0.3270
Bb	 0.4550	 0.3050
Bc	 0.3660	 0.2670
Bd	 0.4540	 0.3030
Be	 0.4120	 0.2940
Bf	 0.0920	 0.1090
Bg	 0.2130	 0.1920
Bv	 0.3690	 0.2530
Bx	 0.0910	 0.0900