



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 05:45 PM UTC

PDB ID : 7ZPQ / pdb_00007zpq
EMDB ID : EMD-14861
Title : Structure of the RQT-bound 80S ribosome from *S. cerevisiae* (C1)
Authors : Best, K.M.; Ikeuchi, K.; Kater, L.; Best, D.M.; Musial, J.; Matsuo, Y.; Berninghausen, O.; Becker, T.; Inada, T.; Beckmann, R.
Deposited on : 2022-04-28
Resolution : 3.47 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
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

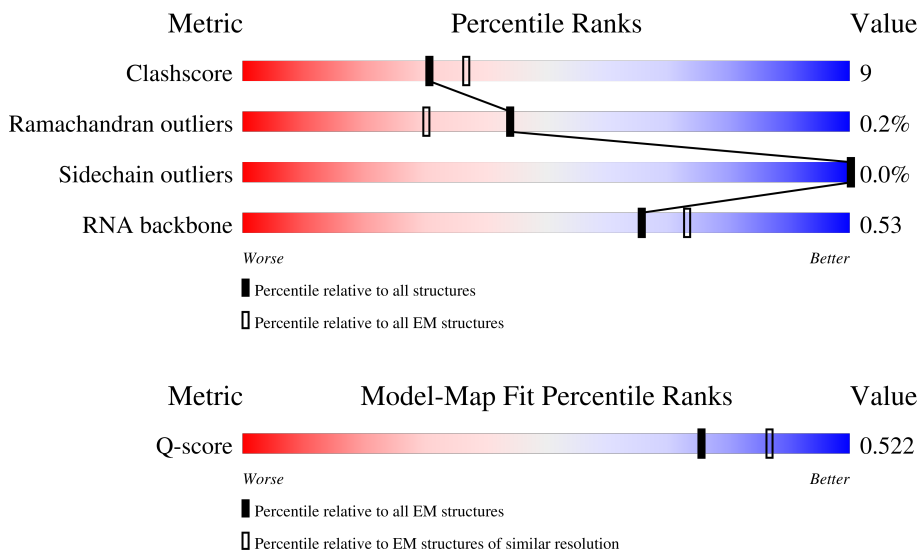
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.47 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	13733 (2.97 - 3.97)

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	2	1798	
2	3	158	
3	4	121	

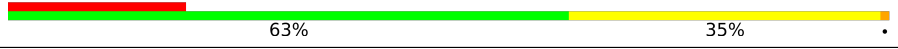
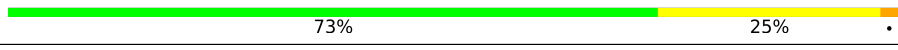
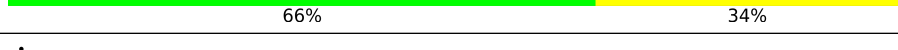
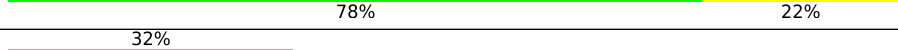
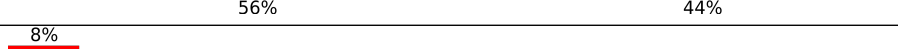
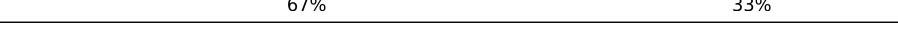
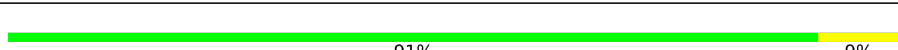
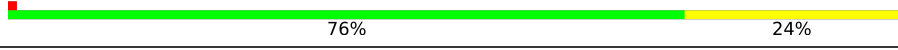
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Mol	Chain	Length	Quality of chain
4	5	3396	
5	6	76	
6	AA	206	
7	AB	255	
8	AC	216	
9	AD	222	
10	AE	258	
11	AF	206	
12	AG	228	
13	AH	184	
14	AI	200	
15	AJ	184	
16	AK	92	
17	AL	144	
18	AM	121	
19	AN	150	
20	AO	127	
21	AP	117	
22	AQ	141	
23	AR	136	
24	AS	145	
25	AT	143	
26	AU	100	
27	AV	87	
28	AW	129	

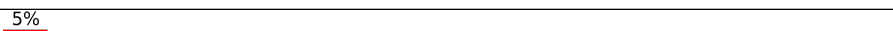
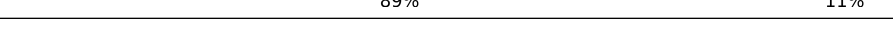
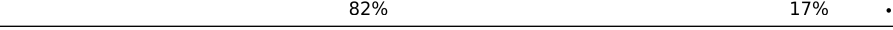
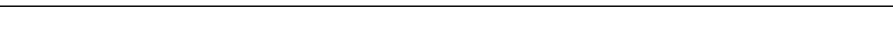
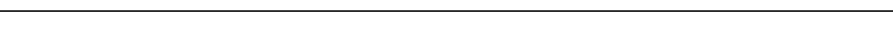
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Mol	Chain	Length	Quality of chain
29	AX	144	
30	AY	134	
31	AZ	82	
32	Aa	97	
33	Ab	81	
34	Ac	63	
35	Ad	53	
36	Ae	60	
37	Af	73	
38	Ag	312	
39	BA	251	
40	BB	386	
41	BC	361	
42	BD	294	
43	BE	176	
44	BF	222	
45	BG	233	
46	BH	191	
47	BI	218	
48	BJ	169	
49	BK	193	
50	BL	136	
51	BM	203	
52	BN	197	
53	BO	183	

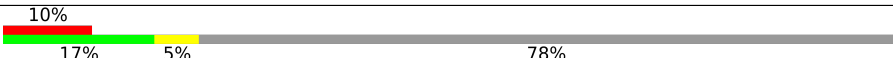
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Mol	Chain	Length	Quality of chain
54	BP	185	 81% 19%
55	BQ	188	 78% 22%
56	BR	171	 80% 20%
57	BS	159	 81% 19%
58	BT	100	 71% 29%
59	BU	136	 82% 18%
60	BV	126	 5% 89% 11%
61	BW	121	 82% 17%
62	BX	125	 77% 23%
63	BY	135	 80% 20%
64	BZ	148	 70% 30%
65	Ba	58	 86% 14%
66	Bb	96	 76% 24%
67	Bc	109	 5% 84% 16%
68	Bd	127	 86% 14%
69	Be	106	 82% 18%
70	Bf	112	 87% 13%
71	Bg	119	 89% 11%
72	Bh	99	 92% 8%
73	Bi	85	 73% 27%
74	Bj	77	 74% 26%
75	Bk	50	 86% 14%
76	Bl	52	 77% 23%
77	Bm	25	 88% 12%
78	Bn	103	 85% 15%

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Mol	Chain	Length	Quality of chain
79	Bo	91	 85% 15%
80	CA	1967	 23% 60% 28% 11%
81	CB	297	 100% 27%
82	CC	530	 10% 17% 5% 78%

2 Entry composition

There are 84 unique types of molecules in this entry. The entry contains 218512 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1771	Total	C	N	O	P	0	0
			37739	16872	6683	12413	1771		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 4 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	5	3184	Total	C	N	O	P	0	0
			68091	30415	12259	22233	3184		

- Molecule 5 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	6	76	Total	C	N	O	P	0	0
			1619	722	288	533	76		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
6	34	U	G	conflict	GB 176436

- Molecule 6 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AA	206	Total	C	N	O	S	0	0
			1603	1030	284	287	2		

- Molecule 7 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AB	226	Total	C	N	O	S	0	0
			1798	1139	330	325	4		

- Molecule 8 is a protein called RPS2 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AC	216	Total	C	N	O	S	0	0
			1626	1042	287	295	2		

- Molecule 9 is a protein called RPS3 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AD	222	Total	C	N	O	S	0	0
			1729	1098	312	313	6		

- Molecule 10 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AE	258	Total	C	N	O	S	0	0
			2056	1308	387	358	3		

- Molecule 11 is a protein called Rps5p.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AF	206	Total	C	N	O	S	0	0
			1605	1005	299	298	3		

- Molecule 12 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AG	228	Total	C	N	O	S	0	0
			1815	1138	351	323	3		

- Molecule 13 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	AH	184	Total	C	N	O		
			1473	946	263	264	0	0

- Molecule 14 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AI	187	Total	C	N	O	S		
			1476	916	295	263	2	0	0

- Molecule 15 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AJ	184	Total	C	N	O	S		
			1479	935	285	258	1	0	0

- Molecule 16 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AK	92	Total	C	N	O	S		
			752	487	122	141	2	0	0

- Molecule 17 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AL	144	Total	C	N	O	S		
			1159	742	219	195	3	0	0

- Molecule 18 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AM	121	Total	C	N	O	S		
			875	551	153	169	2	0	0

- Molecule 19 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AN	150	Total	C	N	O	S		
			1192	759	224	207	2	0	0

- Molecule 20 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AO	127	Total	C	N	O	S	0	0
			926	569	185	169	3		

- Molecule 21 is a protein called RPS15 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AP	117	Total	C	N	O	S	0	0
			916	583	171	155	7		

- Molecule 22 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AQ	141	Total	C	N	O	S	0	0
			1105	708	203	194			

- Molecule 23 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AR	121	Total	C	N	O	S	0	0
			948	596	179	171	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AR	136	VAL	ASN	conflict	UNP P14127

- Molecule 24 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AS	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 25 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AT	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 26 is a protein called RPS20 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AU	100	Total	C	N	O	S	0	0
			797	506	144	146	1		

- Molecule 27 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AV	87	Total	C	N	O	S	0	0
			673	415	125	131	2		

- Molecule 28 is a protein called RPS22A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AW	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 29 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AX	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 30 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	AY	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 31 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	AZ	82	Total	C	N	O	0	0
			651	416	123	112		

- Molecule 32 is a protein called RPS26B isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Aa	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 33 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ab	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 34 is a protein called RPS28A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ac	63	Total	C	N	O	S	0	0
			491	303	96	91	1		

- Molecule 35 is a protein called RPS29A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Ad	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 36 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Ae	60	Total	C	N	O	S	0	0
			472	298	97	76	1		

- Molecule 37 is a protein called RPS31 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Af	73	Total	C	N	O	S	0	0
			556	352	105	95	4		

- Molecule 38 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Ag	312	Total	C	N	O	S	0	0
			2383	1514	409	452	8		

- Molecule 39 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BA	251	Total	C	N	O	S	0	0
			1899	1182	385	331	1		

- Molecule 40 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BB	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 41 is a protein called RPL4A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BC	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 42 is a protein called RPL5 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BD	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 43 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BE	167	Total	C	N	O	S	0	0
			1305	841	234	229	1		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BE	1	MET	-	initiating methionine	UNP P05739
BE	146	ILE	LEU	conflict	UNP P05739
BE	173	MET	LEU	conflict	UNP P05739

- Molecule 44 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BF	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 45 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BG	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 46 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BH	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 47 is a protein called RPL10 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BI	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		

- Molecule 48 is a protein called RPL11B isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BJ	169	Total	C	N	O	S	0	0
			1350	846	253	247	4		

- Molecule 49 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BK	193	Total	C	N	O		0	0
			1543	962	315	266			

- Molecule 50 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BL	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 51 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BM	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 52 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BN	197	Total	C	N	O	S	197	0
			1555	1003	289	262	1		

- Molecule 53 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	BO	183	Total	C	N	O	0	0
			1416	879	284	253		

- Molecule 54 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BP	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 55 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	BQ	188	Total	C	N	O	0	0
			1515	932	323	260		

- Molecule 56 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BR	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 57 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BS	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 58 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
58	BT	100	Total	C	N	O	0	0
			796	516	131	149		

- Molecule 59 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	BU	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 60 is a protein called RPL24A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	BV	126	Total	C	N	O	S	0	0
			836	525	165	145	1		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BV	104	GLN	ASN	conflict	UNP A0A6A5PY83
BV	109	GLN	LEU	conflict	UNP A0A6A5PY83
BV	112	ASP	ASN	conflict	UNP A0A6A5PY83
BV	119	ALA	GLU	conflict	UNP A0A6A5PY83

- Molecule 61 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	BW	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 62 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	BX	125	Total	C	N	O		0	0
			984	620	191	173			

- Molecule 63 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	BY	135	Total	C	N	O		0	0
			1092	710	202	180			

- Molecule 64 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	BZ	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 65 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Ba	58	Total	C	N	O		0	0
			462	289	100	73			

- Molecule 66 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Bb	96	Total	C	N	O	S	0	0
			737	476	123	137	1		

- Molecule 67 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Bc	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 68 is a protein called RPL32 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Bd	127	Total	C	N	O	S	0	0
			1017	644	205	167	1		

- Molecule 69 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Be	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 70 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Bf	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 71 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Bg	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 72 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Bh	99	Total	C	N	O	S	0	0
			766	478	154	132	2		

- Molecule 73 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Bi	85	Total	C	N	O	S	0	0
			670	408	146	111	5		

- Molecule 74 is a protein called RPL38 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Bj	77	Total	C	N	O		0	0
			612	391	115	106			

- Molecule 75 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Bk	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 76 is a protein called 60S ribosomal protein L40-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Bl	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 77 is a protein called RPL41A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Bm	25	Total	C	N	O	S	0	0
			229	139	62	27	1		

- Molecule 78 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Bn	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

- Molecule 79 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Bo	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 80 is a protein called SLH1 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	CA	1742	Total	C	N	O	S	0	0
			14008	8959	2378	2596	75		

- Molecule 81 is a protein called RQC trigger complex subunit CUE3.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	CB	297	Total	C	N	O	S	0	0
			2415	1568	414	427	6		

- Molecule 82 is a protein called RQT4 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	CC	114	Total	C	N	O	S	0	0
			886	539	167	172	8		

- Molecule 83 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
83	2	84	Total	Mg	0
			84	84	
83	AQ	1	Total	Mg	0
			1	1	
83	AT	1	Total	Mg	0
			1	1	

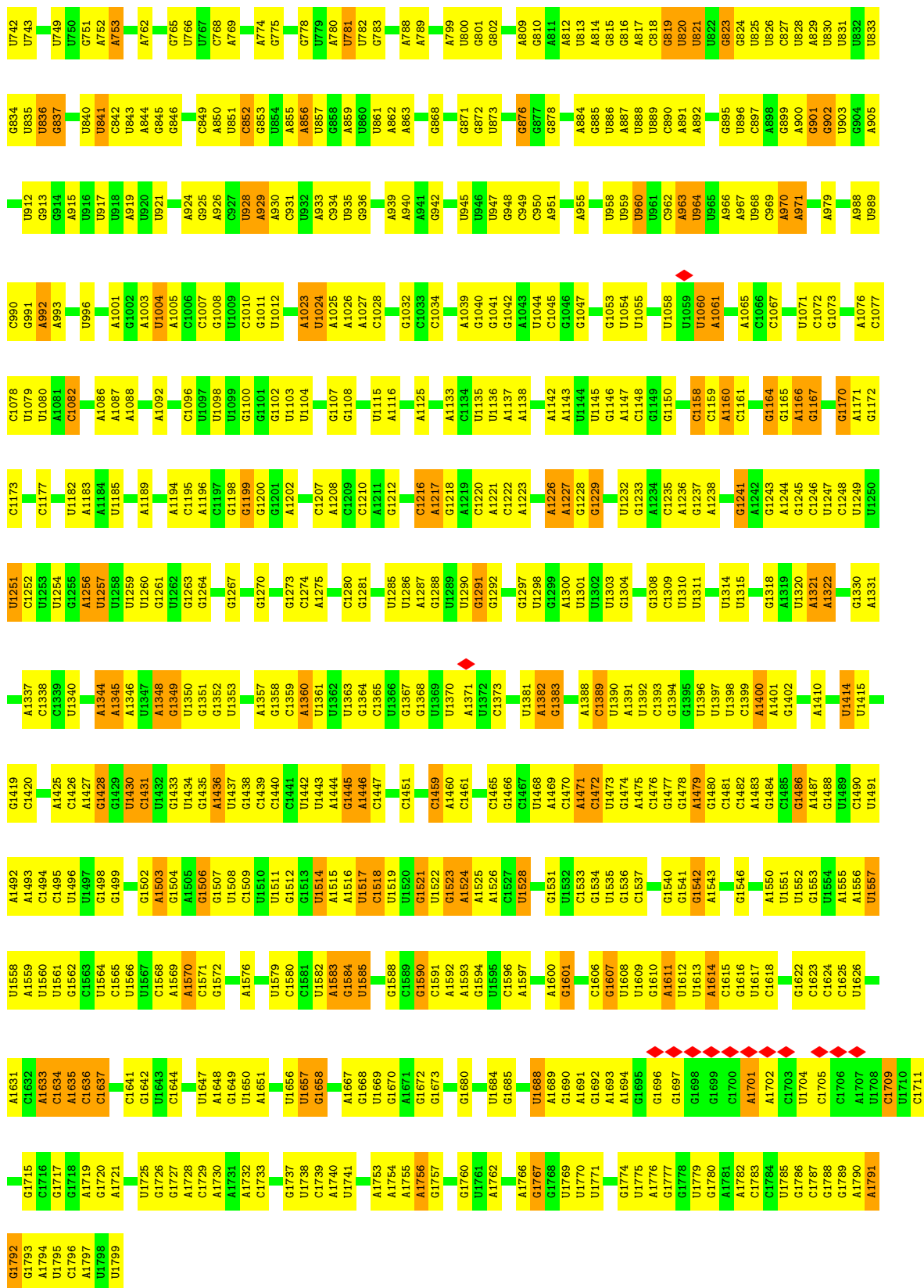
- Molecule 84 is ZINC ION (CCD ID: ZN) (formula: Zn).

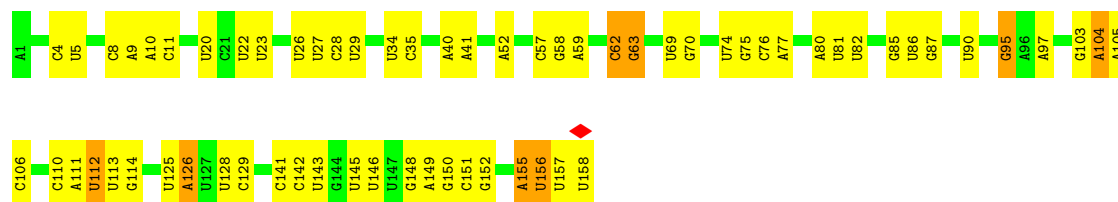
Mol	Chain	Residues	Atoms		AltConf
84	Ad	1	Total	Zn	0
			1	1	
84	Af	1	Total	Zn	0
			1	1	
84	Bf	1	Total	Zn	0
			1	1	
84	Bi	1	Total	Zn	0
			1	1	
84	Bl	1	Total	Zn	0
			1	1	
84	Bn	1	Total	Zn	0
			1	1	
84	Bo	1	Total	Zn	0
			1	1	

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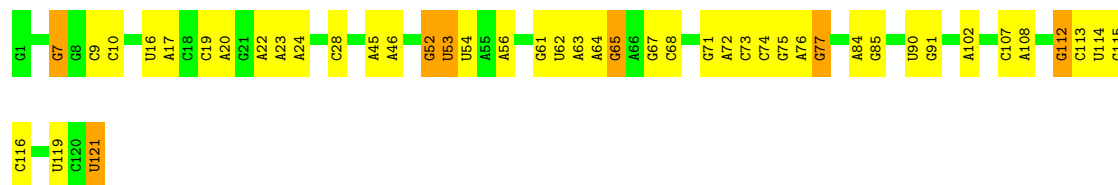
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
84	CC	2	2	2	0





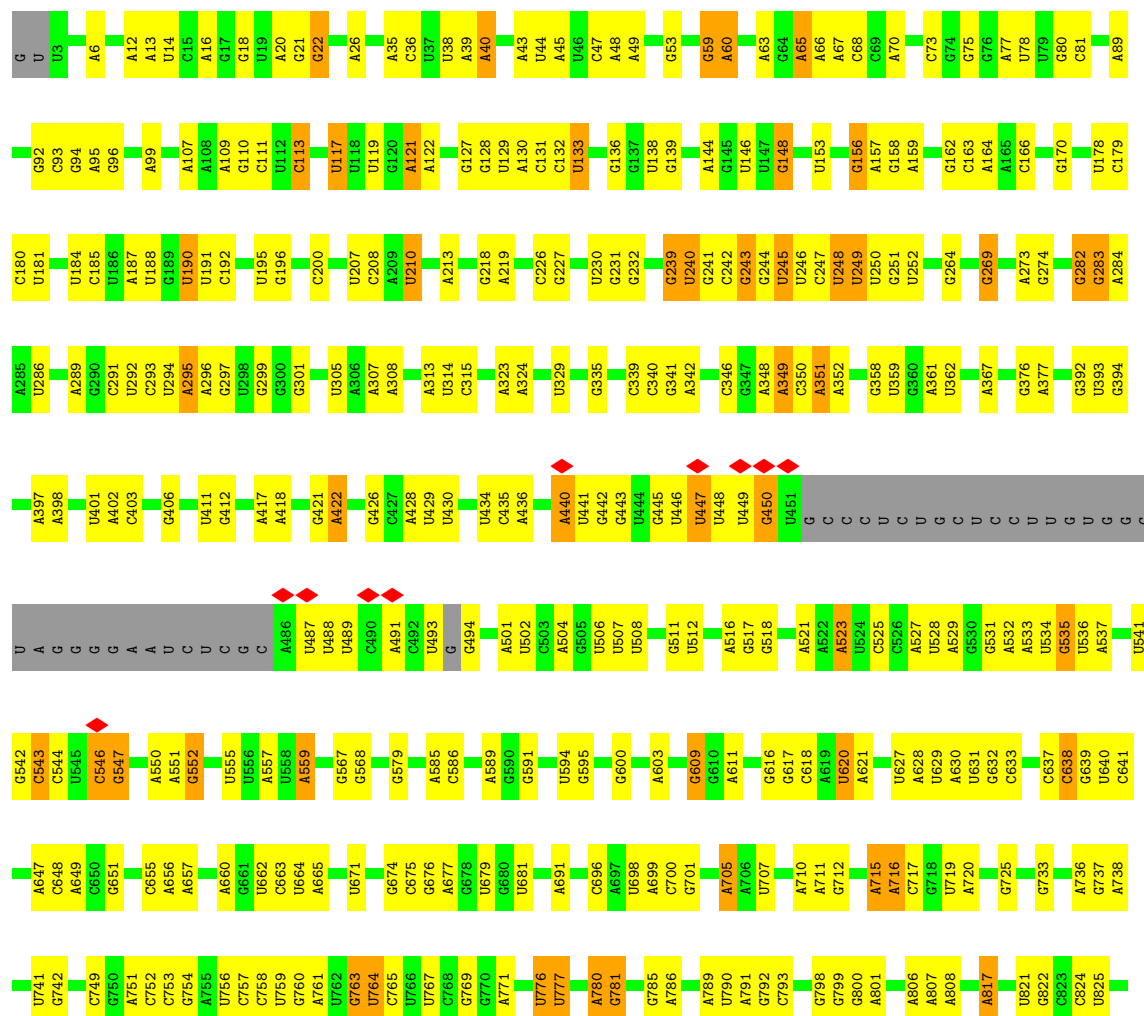
• Molecule 3: 5S ribosomal RNA

Chain 4: 63% 31% 6%



• Molecule 4: 25S ribosomal RNA

Chain 5: 53% 34% 6% 6%

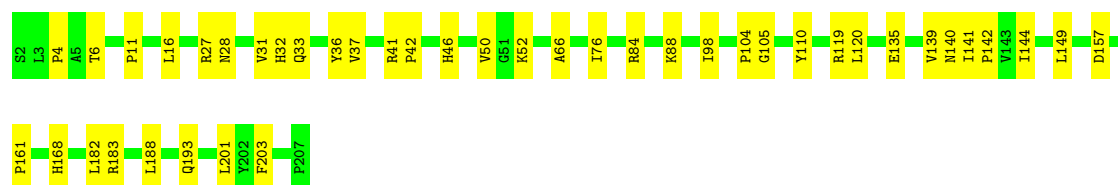
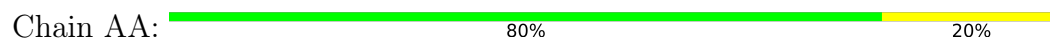




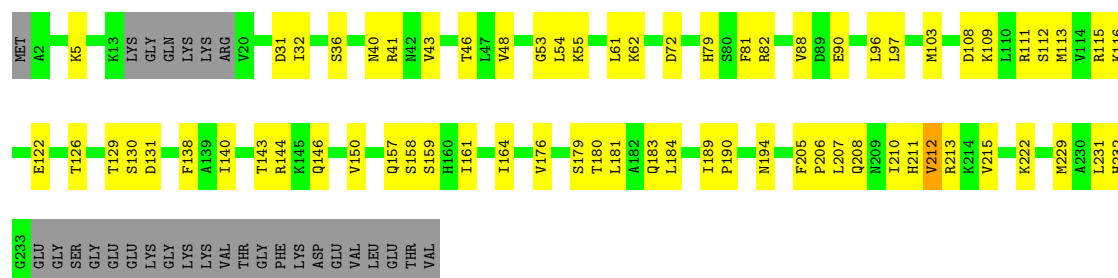
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U3312	A3139	C3228	C2941	U2861	C2756	G2663	A2554	A2413	G2315	U2194	C2097
U3313	A3033	G3229	C2942	U2862	C2757		C2555	C2414		G2195	C2098
A3316	C3034	G3230	G2943	U2863	U2757	U2668	C2556	C2415	U2334	A2198	C2101
U3317	U3041	G3231	G2944	U2864	U2758	U2669	U2557	C2416	G2335	U2102	U2102
G3317	U3042	G3232	G2945	U2865	U2759		U2558	U2417	U2336	U2103	U2103
U3318	U3047	G3233	A2946	U2866	C2760	G2672	U2559	U2418	U2337	G2206	G2106
U3319	U3048	A3234	C2947	C2867	C2761	A2673	A2561	C2419	C2338	A2207	A2107
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A3323	U3051	A3243	C2960	C2871	A2769	A2677		U2423	U2342	U2211	
U3329	G3053	A3244	G2961	A2872		A2678	C2568	A2424	A2345	G2212	
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	C3206	C3206	U3014	C2931	U2714				G2383		
	G3207	G3207	G3015	U2932	U2715				A2384		
	A3210	A3210	A3016	A2933	U2716				G2385		
	U3302	U3302	A3017	U2934	A2717				A2386		
	G3303	G3303	A3018	U2935	G2718				A2387		
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			G3233	C2956	U2739				A2406		
			G3234	C2957	U2740				C2407		
			G3235	C2958	U2741				U2408		
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			G3298	C3021	U2804						
			G3299	C3022	U2805						
			G3300	C3023	U2806						
			G3301	C3024	U2807						
			G3302	C3025	U2808						
			G3303	C3026	U2809						
			G3304	C3027	U2810						
			G3305	C3028	U2811						
			G3306	C3029	U2812						
			G3307	C3030	U2813						
			G3308	C3031	U2814						
			G3309	C3032	U2815						
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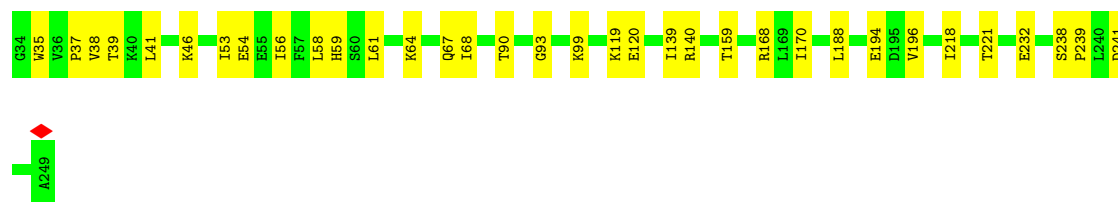
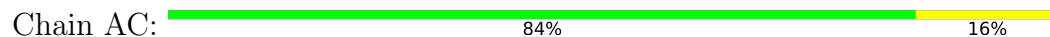
- Molecule 6: 40S ribosomal protein S0-A



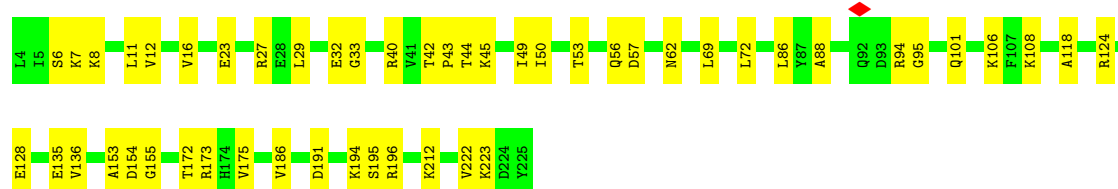
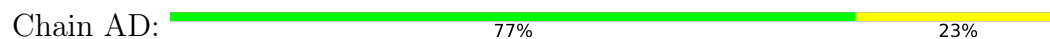
- Molecule 7: 40S ribosomal protein S1



- Molecule 8: RPS2 isoform 1

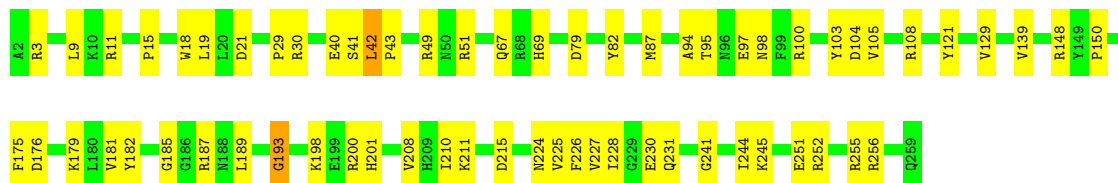


- Molecule 9: RPS3 isoform 1



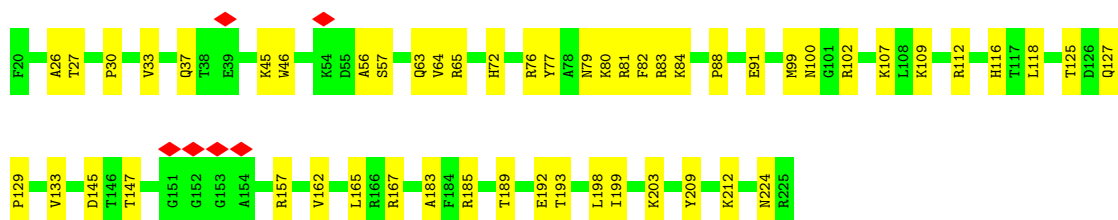
- Molecule 10: 40S ribosomal protein S4-A

Chain AE:  75% 24%



- Molecule 11: Rps5p

Chain AF:  75% 25%



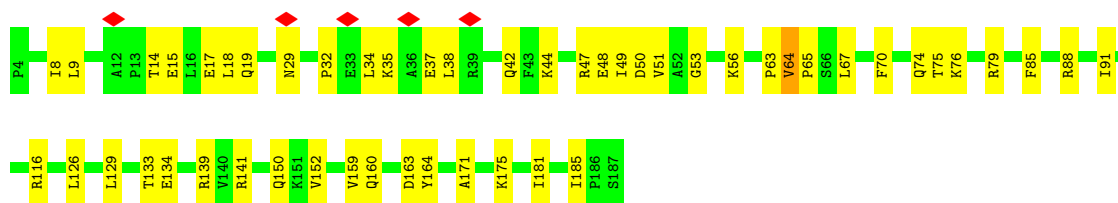
- Molecule 12: 40S ribosomal protein S6-A

Chain AG:  67% 32%



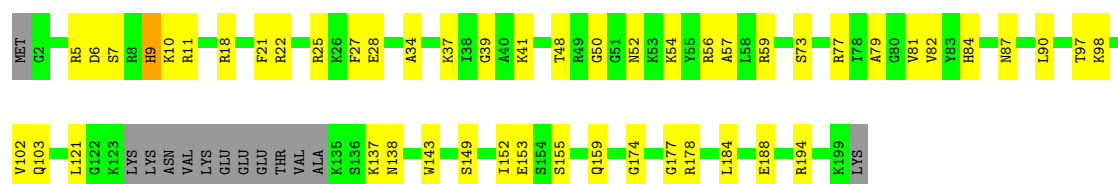
- Molecule 13: 40S ribosomal protein S7-A

Chain AH:  72% 28%

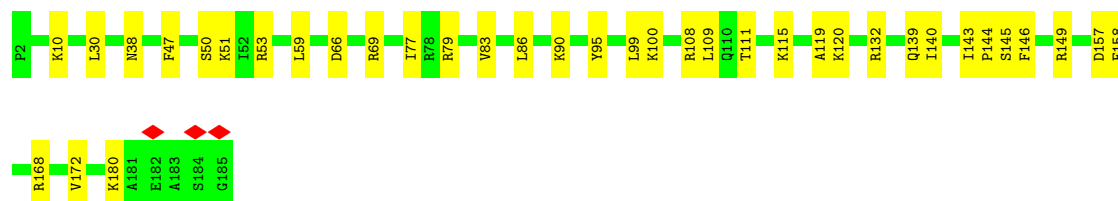
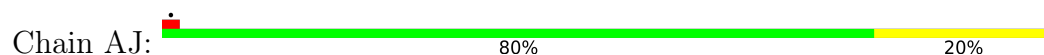


- Molecule 14: 40S ribosomal protein S8

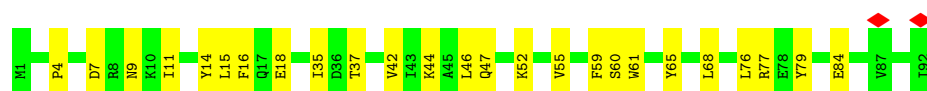
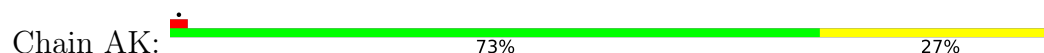
Chain AI:  68% 24% 6%



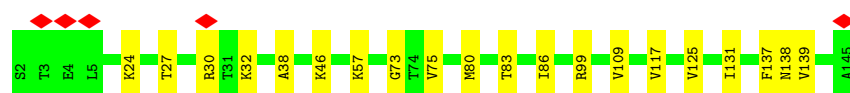
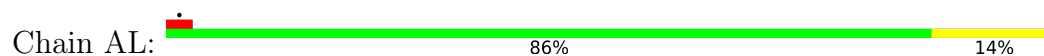
- Molecule 15: 40S ribosomal protein S9-A



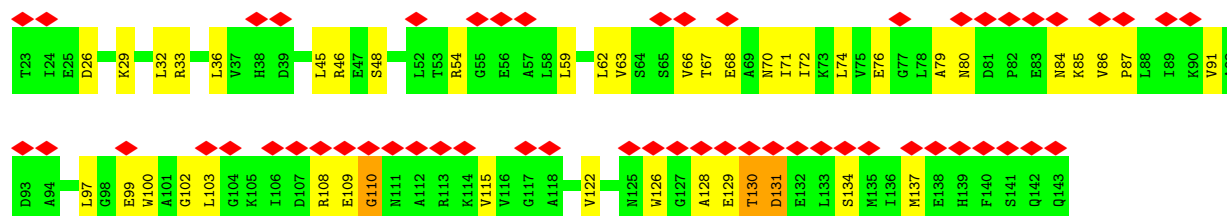
- Molecule 16: 40S ribosomal protein S10-A



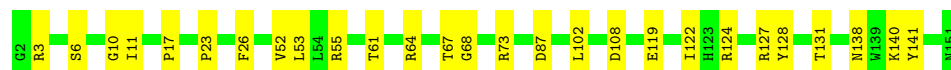
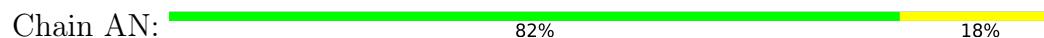
- Molecule 17: 40S ribosomal protein S11-A



- Molecule 18: 40S ribosomal protein S12

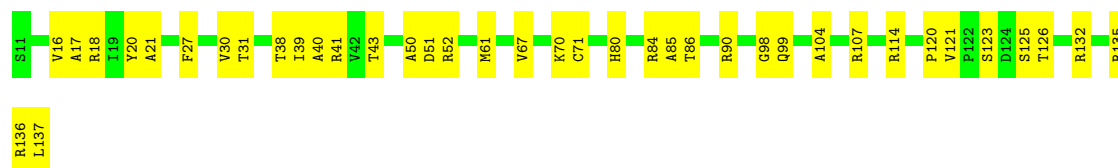


- Molecule 19: 40S ribosomal protein S13



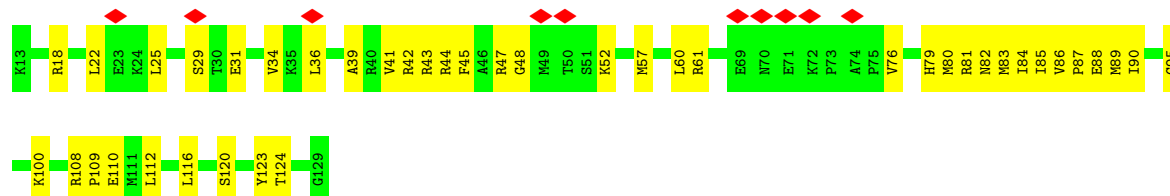
- Molecule 20: 40S ribosomal protein S14-B

Chain AO:  69% 31%



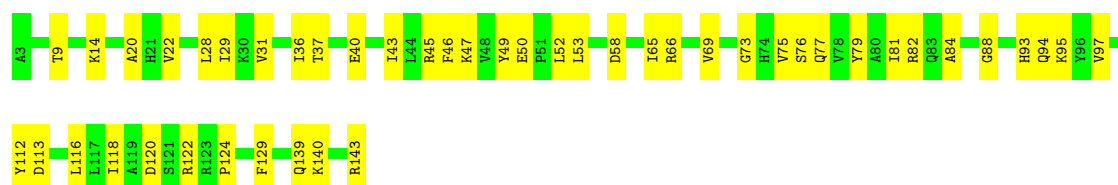
- Molecule 21: RPS15 isoform 1

Chain AP:  9% 64% 36%



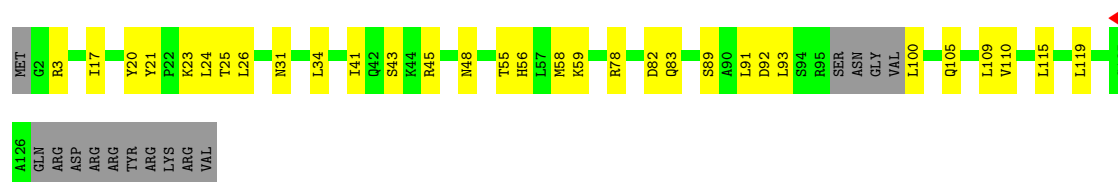
- Molecule 22: 40S ribosomal protein S16-A

Chain AQ:  67% 33%



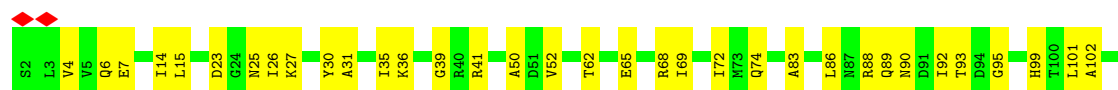
- Molecule 23: 40S ribosomal protein S17-B

Chain AR:  66% 23% 11%



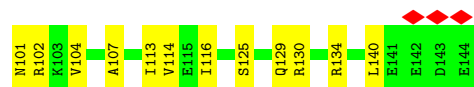
- Molecule 24: 40S ribosomal protein S18-A

Chain AS:  66% 34%

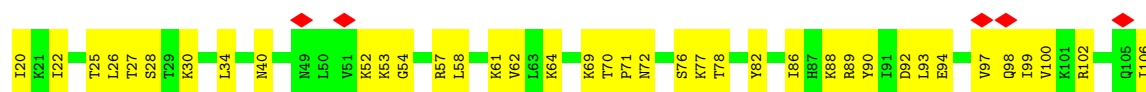




- Molecule 25: 40S ribosomal protein S19-A



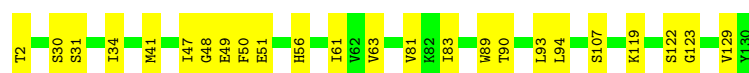
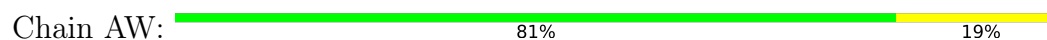
- Molecule 26: RPS20 isoform 1



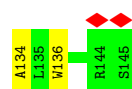
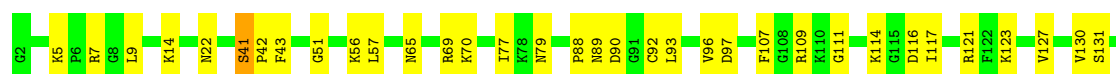
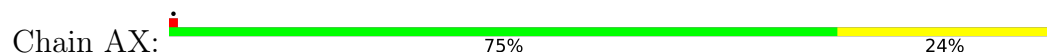
- Molecule 27: 40S ribosomal protein S21-A



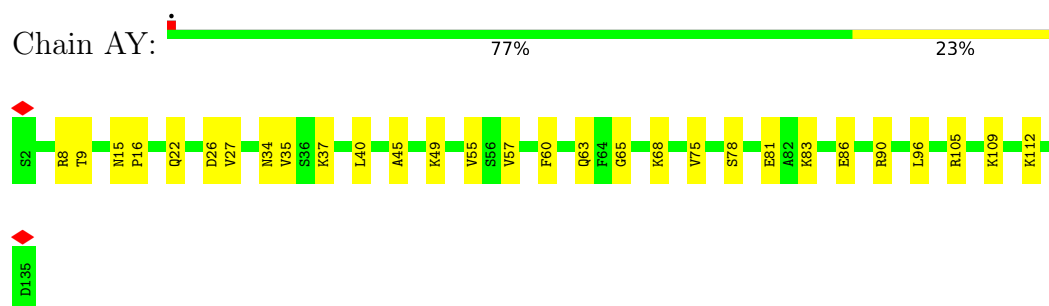
- Molecule 28: RPS22A isoform 1



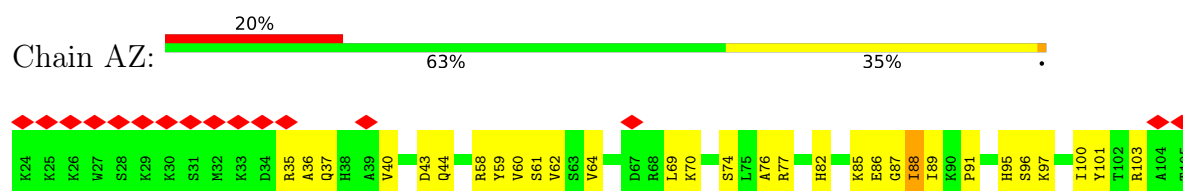
- Molecule 29: 40S ribosomal protein S23-A



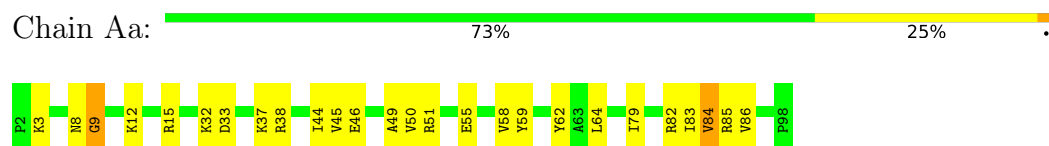
- Molecule 30: 40S ribosomal protein S24-A



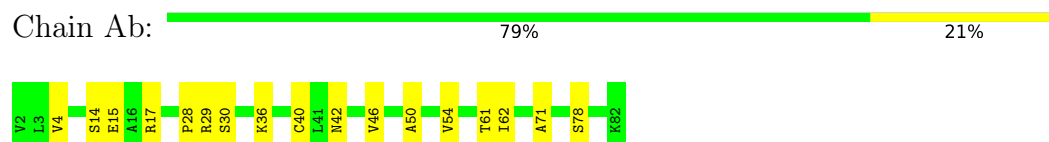
- Molecule 31: 40S ribosomal protein S25



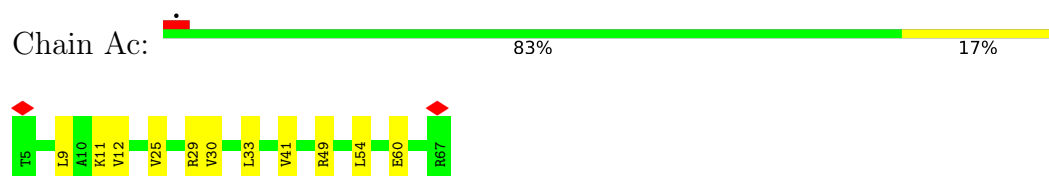
- Molecule 32: RPS26B isoform 1



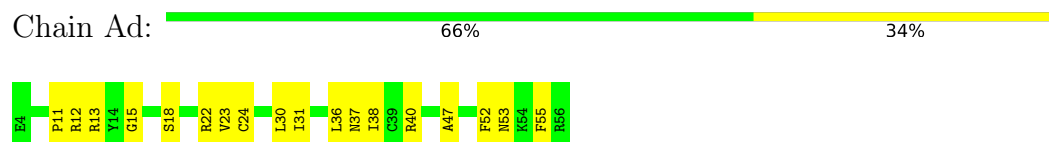
- Molecule 33: 40S ribosomal protein S27-A



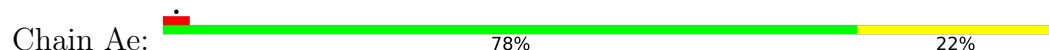
- Molecule 34: RPS28A isoform 1

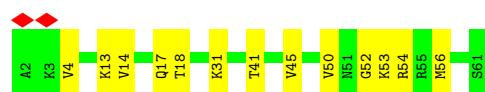


- Molecule 35: RPS29A isoform 1

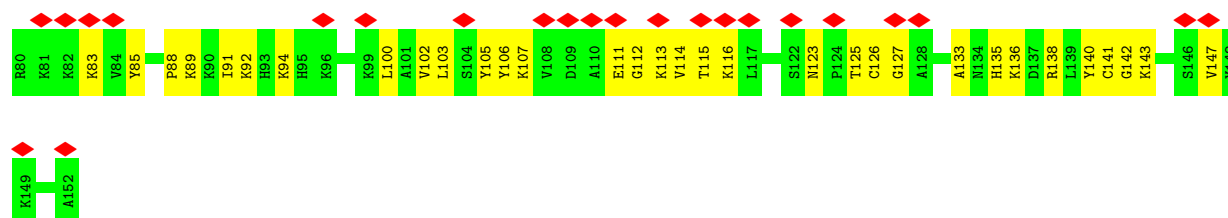


- Molecule 36: 40S ribosomal protein S30-A

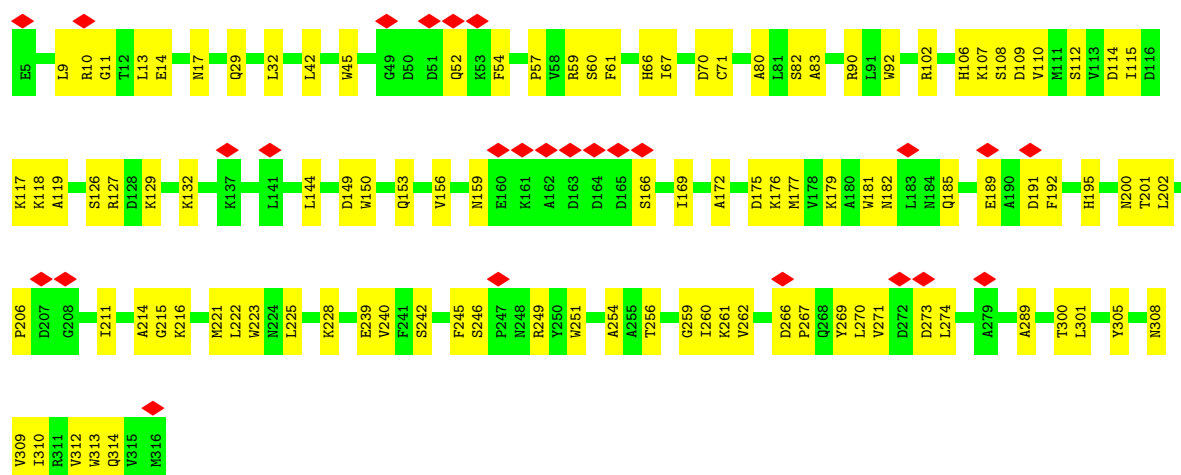




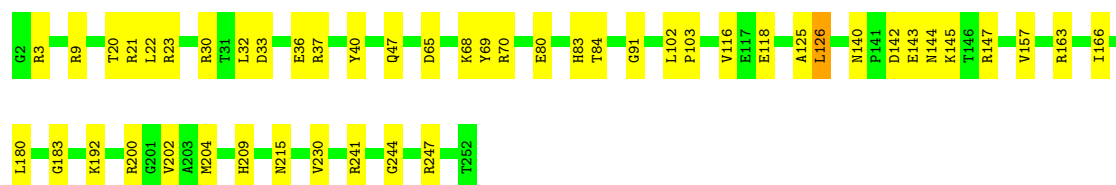
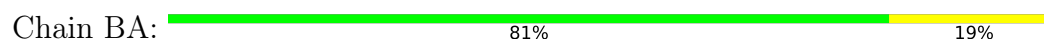
- Molecule 37: RPS31 isoform 1



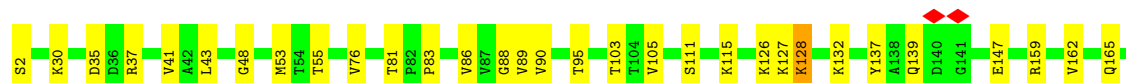
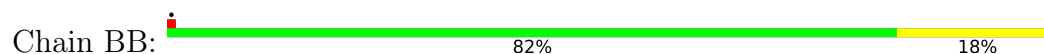
- Molecule 38: Guanine nucleotide-binding protein subunit beta-like protein

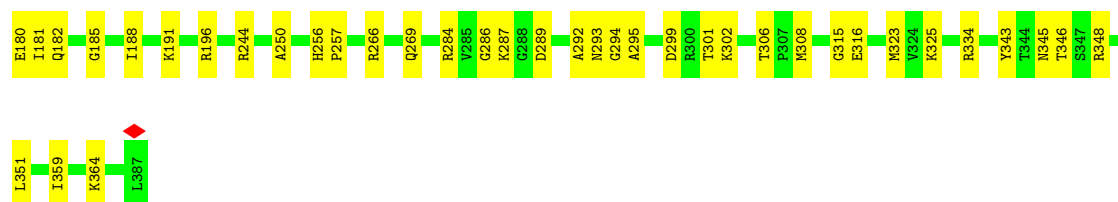


- Molecule 39: 60S ribosomal protein L2-A



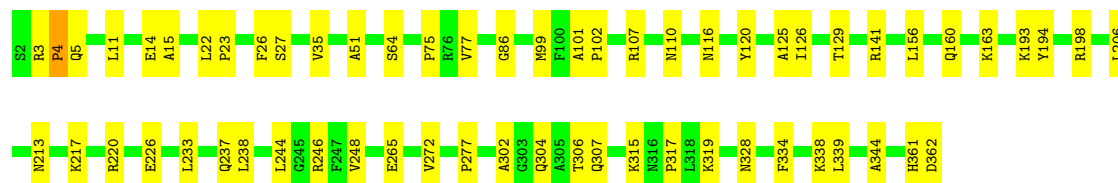
- Molecule 40: 60S ribosomal protein L3





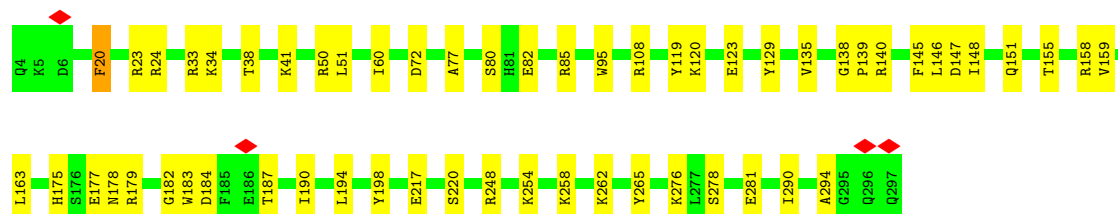
- Molecule 41: RPL4A isoform 1

Chain BC: 83% 17%



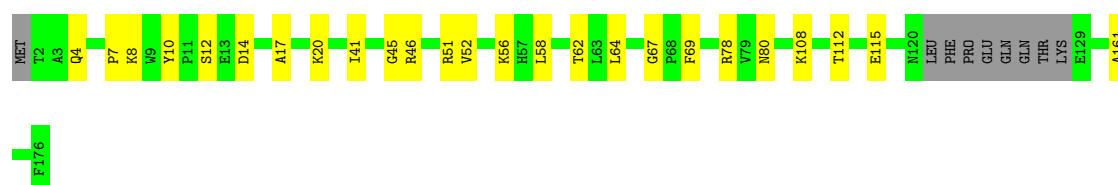
- Molecule 42: RPL5 isoform 1

Chain BD: 81% 19%



- Molecule 43: 60S ribosomal protein L6-B

Chain BE: 81% 14% 5%



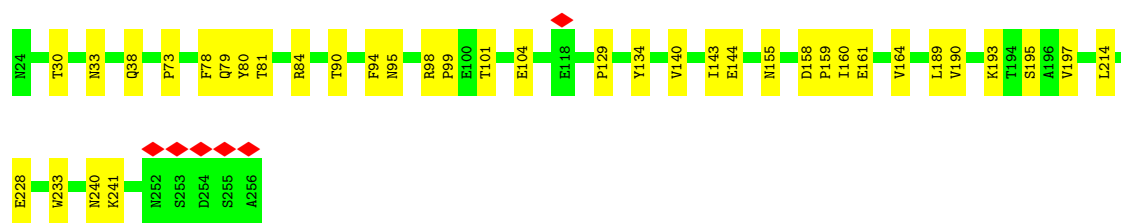
- Molecule 44: 60S ribosomal protein L7-A

Chain BF: 91% 9%

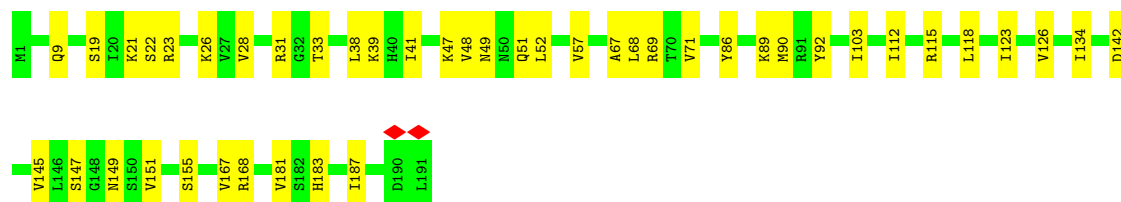
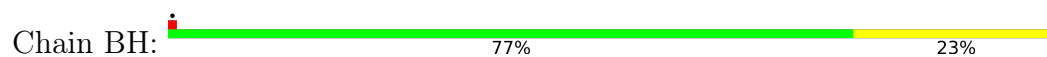


- Molecule 45: 60S ribosomal protein L8-A

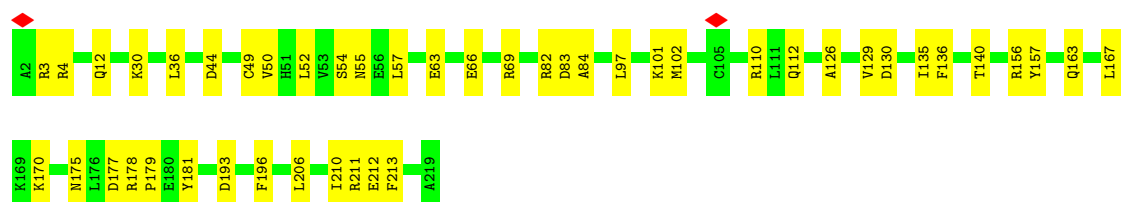
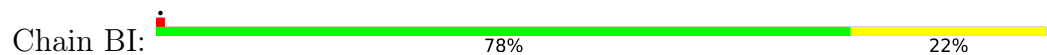
Chain BG: 84% 16%



- Molecule 46: 60S ribosomal protein L9-A



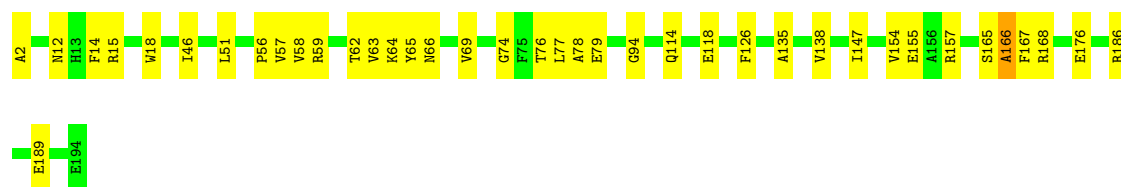
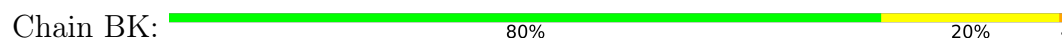
- Molecule 47: RPL10 isoform 1



- Molecule 48: RPL11B isoform 1



- Molecule 49: 60S ribosomal protein L13-A



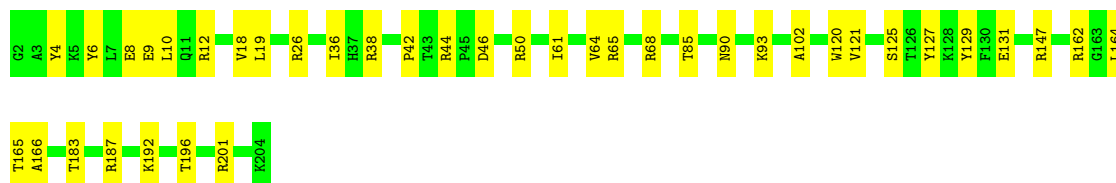
- Molecule 50: 60S ribosomal protein L14-A

Chain BL:  76% 24%



- Molecule 51: 60S ribosomal protein L15-A

Chain BM:  81% 19%



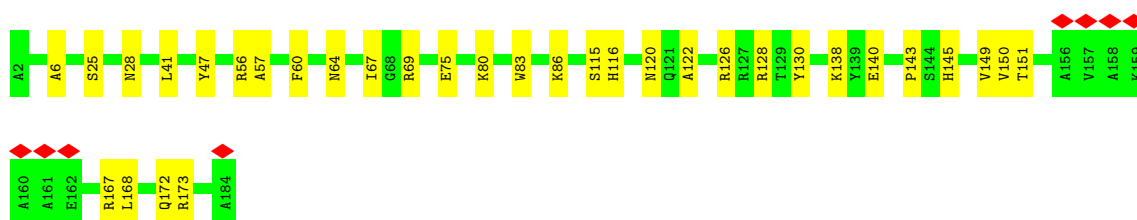
- Molecule 52: 60S ribosomal protein L16-A

Chain BN:  85% 15%



- Molecule 53: 60S ribosomal protein L17-A

Chain BO:  82% 18%



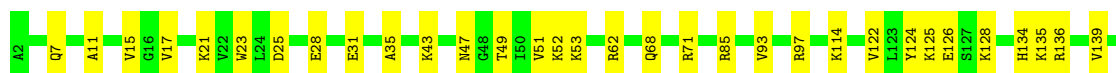
- Molecule 54: 60S ribosomal protein L18-A

Chain BP:  81% 19%

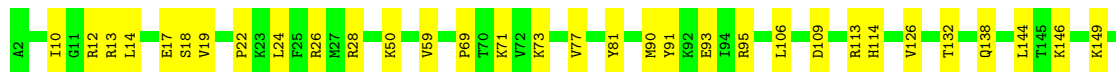
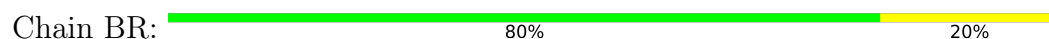


- Molecule 55: 60S ribosomal protein L19-A

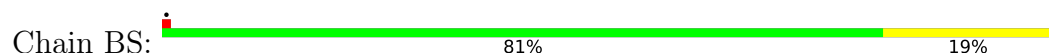
Chain BQ:  78% 22%



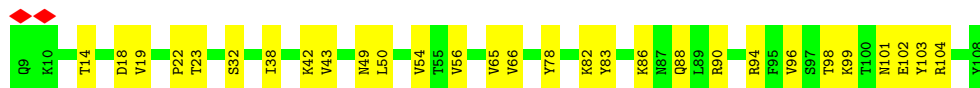
- Molecule 56: 60S ribosomal protein L20-A



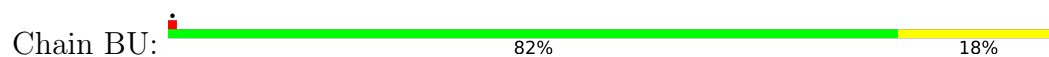
- Molecule 57: 60S ribosomal protein L21-A



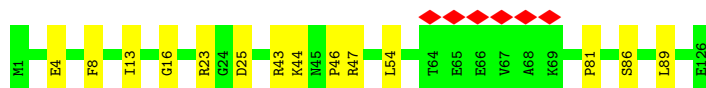
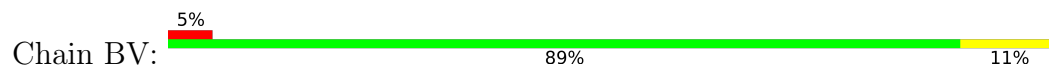
- Molecule 58: 60S ribosomal protein L22-A



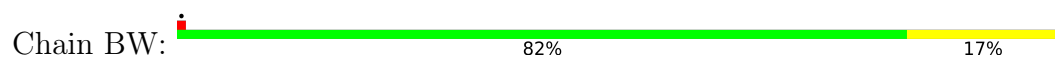
- Molecule 59: 60S ribosomal protein L23-A

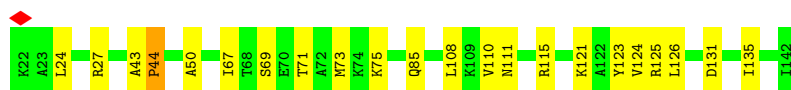


- Molecule 60: RPL24A isoform 1



- Molecule 61: 60S ribosomal protein L25





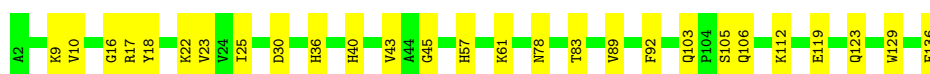
- Molecule 62: 60S ribosomal protein L26-A

Chain BX: 77% 23%



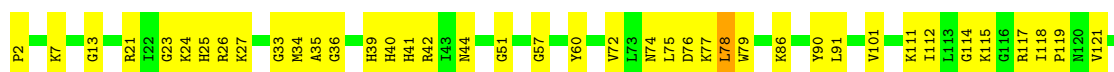
- Molecule 63: 60S ribosomal protein L27-A

Chain BY: 80% 20%



- Molecule 64: 60S ribosomal protein L28

Chain BZ: 70% 30%



- Molecule 65: 60S ribosomal protein L29

Chain Ba: 86% 14%



- Molecule 66: 60S ribosomal protein L30

Chain Bb: 76% 24%



- Molecule 67: 60S ribosomal protein L31-A

Chain Bc: 5% 84% 16%



- Molecule 68: RPL32 isoform 1

Chain Bd:  86% 14%



- Molecule 69: 60S ribosomal protein L33-A

Chain Be:  82% 18%



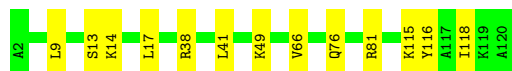
- Molecule 70: 60S ribosomal protein L34-A

Chain Bf:  87% 13%

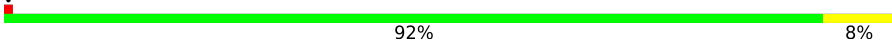


- Molecule 71: 60S ribosomal protein L35-A

Chain Bg:  89% 11%



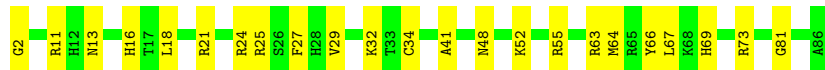
- Molecule 72: 60S ribosomal protein L36-A

Chain Bh:  92% 8%



- Molecule 73: 60S ribosomal protein L37-A

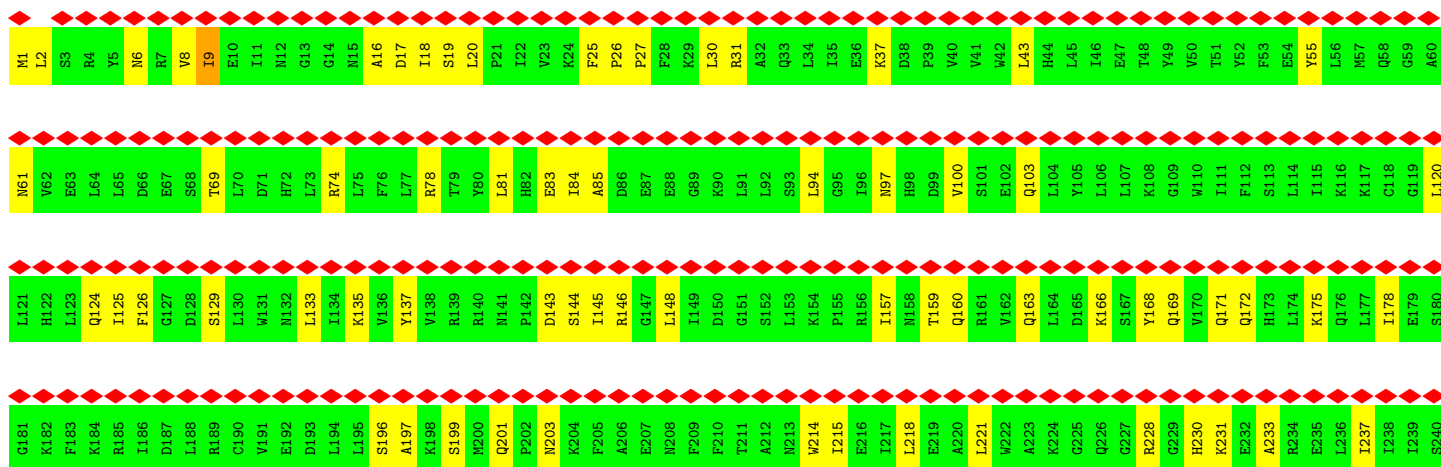
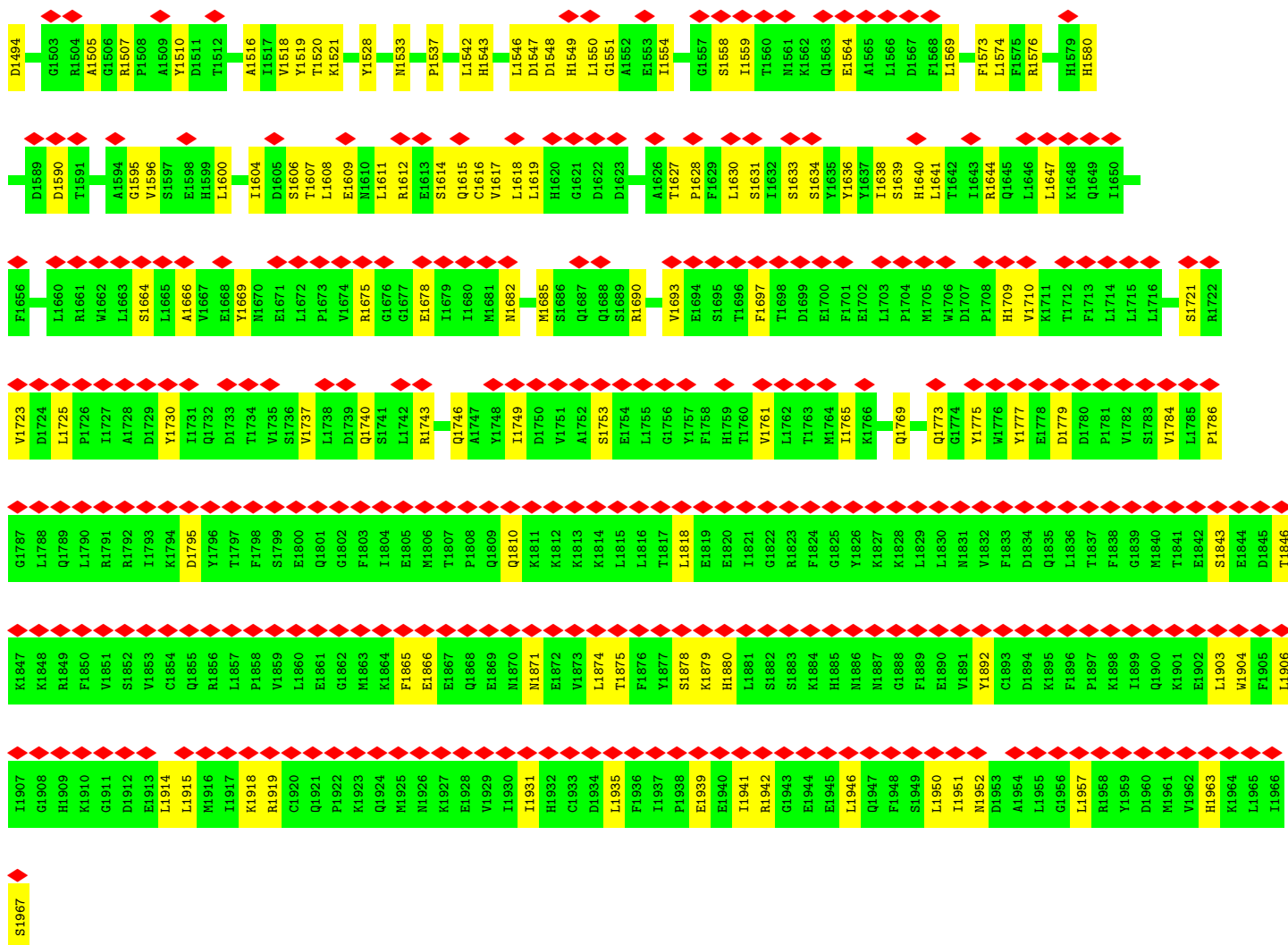
Chain Bi:  73% 27%

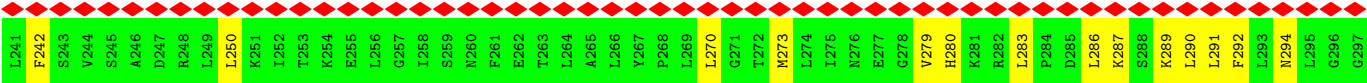


- Molecule 74: RPL38 isoform 1

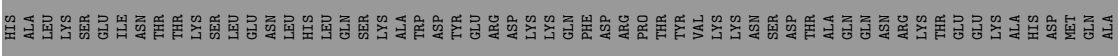
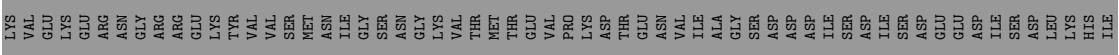
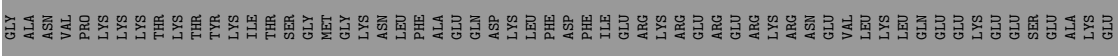
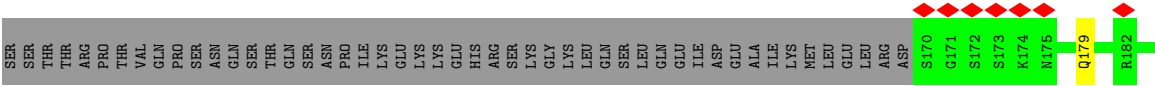
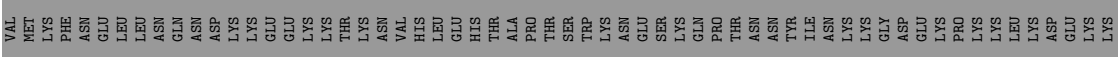
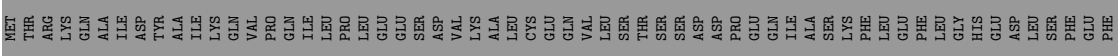
Chain Bj:  74% 26%







• Molecule 82: RQT4 isoform 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	194186	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	43.6	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	7.920	Depositor
Minimum map value	-1.030	Depositor
Average map value	0.016	Depositor
Map value standard deviation	0.145	Depositor
Recommended contour level	0.4	Depositor
Map size (Å)	585.19995, 585.19995, 585.19995	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	2	0.14	0/42211	0.28	0/65773
2	3	0.17	0/3746	0.28	0/5832
3	4	0.15	0/2883	0.23	0/4491
4	5	0.17	0/76214	0.28	0/118821
5	6	0.08	0/1808	0.20	0/2816
6	AA	0.13	0/1644	0.34	0/2249
7	AB	0.16	0/1823	0.44	0/2447
8	AC	0.15	0/1656	0.31	0/2251
9	AD	0.11	0/1754	0.28	0/2361
10	AE	0.16	0/2097	0.38	1/2823 (0.0%)
11	AF	0.13	0/1625	0.35	0/2197
12	AG	0.14	0/1839	0.38	0/2460
13	AH	0.14	0/1498	0.40	0/2019
14	AI	0.15	0/1501	0.41	0/2006
15	AJ	0.14	0/1504	0.36	0/2016
16	AK	0.11	0/769	0.33	0/1039
17	AL	0.16	0/1185	0.34	0/1598
18	AM	0.14	0/883	0.53	0/1199
19	AN	0.15	0/1215	0.39	0/1638
20	AO	0.16	0/937	0.38	0/1261
21	AP	0.13	0/936	0.37	0/1259
22	AQ	0.13	0/1125	0.38	1/1510 (0.1%)
23	AR	0.14	0/957	0.40	0/1283
24	AS	0.11	0/1211	0.36	0/1628
25	AT	0.14	0/1130	0.37	0/1517
26	AU	0.14	0/807	0.36	0/1091
27	AV	0.18	0/682	0.34	0/921
28	AW	0.17	0/1038	0.36	0/1395
29	AX	0.17	0/1139	0.44	0/1518
30	AY	0.13	0/1087	0.33	0/1449
31	AZ	0.13	0/661	0.45	1/888 (0.1%)
32	Aa	0.18	0/782	0.60	0/1047

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
33	Ab	0.14	0/620	0.38	0/838
34	Ac	0.12	0/493	0.30	0/663
35	Ad	0.12	0/452	0.30	0/600
36	Ae	0.17	0/480	0.40	0/639
37	Af	0.19	0/567	0.65	0/764
38	Ag	0.12	0/2436	0.36	0/3318
39	BA	0.18	0/1933	0.37	0/2598
40	BB	0.16	0/3146	0.34	0/4228
41	BC	0.16	0/2800	0.36	0/3790
42	BD	0.14	0/2400	0.33	0/3239
43	BE	0.14	0/1327	0.33	0/1790
44	BF	0.15	0/1821	0.29	0/2451
45	BG	0.16	0/1836	0.36	0/2481
46	BH	0.13	0/1529	0.29	0/2060
47	BI	0.14	0/1801	0.31	0/2416
48	BJ	0.12	0/1371	0.33	0/1838
49	BK	0.16	0/1568	0.38	0/2106
50	BL	0.13	0/1068	0.31	0/1438
51	BM	0.16	0/1757	0.33	0/2354
52	BN	0.15	0/1585	0.31	0/2128
53	BO	0.15	0/1439	0.33	0/1938
54	BP	0.15	0/1465	0.31	0/1965
55	BQ	0.14	0/1532	0.32	0/2043
56	BR	0.16	0/1473	0.30	0/1980
57	BS	0.17	0/1300	0.33	0/1743
58	BT	0.13	0/812	0.36	0/1099
59	BU	0.14	0/1018	0.27	0/1369
60	BV	0.13	0/850	0.32	0/1152
61	BW	0.15	0/979	0.32	0/1321
62	BX	0.15	0/995	0.28	0/1329
63	BY	0.15	0/1118	0.35	0/1497
64	BZ	0.19	0/1204	0.42	0/1612
65	Ba	0.14	0/473	0.33	0/629
66	Bb	0.15	0/745	0.28	0/1001
67	Bc	0.14	0/890	0.29	0/1196
68	Bd	0.15	0/1038	0.32	0/1390
69	Be	0.16	0/868	0.29	0/1168
70	Bf	0.16	0/890	0.30	0/1189
71	Bg	0.13	0/978	0.29	0/1301
72	Bh	0.13	0/772	0.27	0/1026
73	Bi	0.17	0/685	0.33	0/908
74	Bj	0.13	0/618	0.29	0/826
75	Bk	0.15	0/443	0.27	0/588

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Bl	0.14	0/423	0.32	0/562
77	Bm	0.13	0/230	0.25	0/296
78	Bn	0.15	0/836	0.33	0/1104
79	Bo	0.15	0/701	0.31	0/934
80	CA	0.11	0/14309	0.34	1/19348 (0.0%)
81	CB	0.08	0/2463	0.25	0/3324
82	CC	0.09	0/897	0.33	0/1203
All	All	0.15	0/233781	0.31	4/341583 (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
7	AB	0	2
10	AE	0	1
12	AG	0	1
13	AH	0	1
18	AM	0	2
22	AQ	0	1
29	AX	0	2
31	AZ	0	1
32	Aa	0	1
40	BB	0	1
45	BG	0	1
52	BN	0	1
61	BW	0	1
65	Ba	0	2
All	All	0	18

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	AZ	88	ILE	N-CA-C	-5.92	106.95	111.62
80	CA	1117	LYS	N-CA-C	-5.34	104.03	110.44
10	AE	193	GLY	N-CA-C	5.29	125.71	113.18
22	AQ	43	ILE	N-CA-C	-5.21	108.76	113.71

There are no chirality outliers.

All (18) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	AB	211	HIS	Peptide
7	AB	81	PHE	Peptide
10	AE	42	LEU	Peptide
12	AG	68	LEU	Peptide
13	AH	64	VAL	Peptide
18	AM	110	GLY	Peptide
18	AM	130	THR	Peptide
22	AQ	40	GLU	Peptide
29	AX	41	SER	Peptide
29	AX	88	PRO	Peptide
31	AZ	69	LEU	Peptide
32	Aa	9	GLY	Peptide
40	BB	127	LYS	Peptide
45	BG	30	THR	Peptide
52	BN	110[A]	PRO	Peptide
61	BW	43	ALA	Peptide
65	Ba	19	ASN	Peptide
65	Ba	20	GLY	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	37739	0	18988	658	0
2	3	3353	0	1695	50	0
3	4	2579	0	1304	32	0
4	5	68091	0	34217	828	0
5	6	1619	0	821	19	0
6	AA	1603	0	1610	36	0
7	AB	1798	0	1890	51	0
8	AC	1626	0	1715	26	0
9	AD	1729	0	1812	39	0
10	AE	2056	0	2140	42	0
11	AF	1605	0	1669	42	0
12	AG	1815	0	1894	66	0
13	AH	1473	0	1555	39	0
14	AI	1476	0	1501	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	AJ	1479	0	1556	28	0
16	AK	752	0	719	18	0
17	AL	1159	0	1225	15	0
18	AM	875	0	878	34	0
19	AN	1192	0	1255	24	0
20	AO	926	0	950	32	0
21	AP	916	0	941	35	0
22	AQ	1105	0	1166	44	0
23	AR	948	0	990	29	0
24	AS	1192	0	1222	32	0
25	AT	1112	0	1124	36	0
26	AU	797	0	863	45	0
27	AV	673	0	662	24	0
28	AW	1021	0	1060	19	0
29	AX	1121	0	1196	25	0
30	AY	1073	0	1132	24	0
31	AZ	651	0	682	19	0
32	Aa	769	0	818	28	0
33	Ab	610	0	633	10	0
34	Ac	491	0	524	8	0
35	Ad	442	0	428	17	0
36	Ae	472	0	521	9	0
37	Af	556	0	547	32	0
38	Ag	2383	0	2332	72	0
39	BA	1899	0	1957	39	0
40	BB	3075	0	3142	50	0
41	BC	2748	0	2859	45	0
42	BD	2351	0	2294	44	0
43	BE	1305	0	1370	18	0
44	BF	1784	0	1862	15	0
45	BG	1804	0	1877	26	0
46	BH	1508	0	1572	30	0
47	BI	1764	0	1804	33	0
48	BJ	1350	0	1381	36	0
49	BK	1543	0	1608	30	0
50	BL	1053	0	1149	23	0
51	BM	1720	0	1779	32	0
52	BN	1555	0	1659	19	0
53	BO	1416	0	1433	21	0
54	BP	1441	0	1543	27	0
55	BQ	1515	0	1606	32	0
56	BR	1437	0	1475	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	BS	1276	0	1323	24	0
58	BT	796	0	812	22	0
59	BU	1003	0	1048	14	0
60	BV	836	0	709	12	0
61	BW	964	0	1025	14	0
62	BX	984	0	1075	22	0
63	BY	1092	0	1155	23	0
64	BZ	1173	0	1215	46	0
65	Ba	462	0	491	6	0
66	Bb	737	0	792	18	0
67	Bc	876	0	912	10	0
68	Bd	1017	0	1081	14	0
69	Be	850	0	880	13	0
70	Bf	880	0	941	14	0
71	Bg	969	0	1078	10	0
72	Bh	766	0	844	8	0
73	Bi	670	0	673	17	0
74	Bj	612	0	682	13	0
75	Bk	436	0	475	6	0
76	Bl	417	0	455	9	0
77	Bm	229	0	273	3	0
78	Bn	824	0	888	12	0
79	Bo	694	0	735	11	0
80	CA	14008	0	14058	395	0
81	CB	2415	0	2508	55	0
82	CC	886	0	857	21	0
83	2	84	0	0	0	0
83	AQ	1	0	0	0	0
83	AT	1	0	0	0	0
84	Ad	1	0	0	0	0
84	Af	1	0	0	0	0
84	Bf	1	0	0	0	0
84	Bi	1	0	0	0	0
84	Bl	1	0	0	0	0
84	Bn	1	0	0	0	0
84	Bo	1	0	0	0	0
84	CC	2	0	0	0	0
All	All	218512	0	165590	3384	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 9.

All (3384) 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)
5:6:5:U:H3	5:6:68:G:H1	0.99	0.96
1:2:1588:G:H1	1:2:1608:U:H3	1.18	0.91
4:5:1018:G:H1	4:5:1034:U:H3	0.95	0.91
12:AG:23:ARG:NH1	12:AG:40:ALA:O	2.07	0.88
1:2:555:A:N7	1:2:590:C:O2'	2.08	0.86
1:2:1135:U:OP2	29:AX:121:ARG:NH2	2.08	0.86
1:2:521:A:N3	30:AY:34:ASN:ND2	2.24	0.84
29:AX:111:GLY:O	29:AX:121:ARG:NH1	2.11	0.84
1:2:1673:G:H1	1:2:1728:A:H2	1.26	0.83
80:CA:590:ILE:HA	80:CA:594:GLY:HA3	1.61	0.83
7:AB:212:VAL:HG13	7:AB:213:ARG:H	1.44	0.83
38:Ag:117:LYS:HD3	38:Ag:118:LYS:HG3	1.60	0.82
4:5:1724:U:OP2	55:BQ:128:LYS:NZ	2.12	0.82
81:CB:100:VAL:HA	81:CB:103:GLN:HE21	1.44	0.82
4:5:1257:C:N3	4:5:1261:G:N1	2.27	0.81
1:2:895:G:H1	1:2:917:U:H3	1.29	0.81
80:CA:424:LEU:HB3	80:CA:460:ILE:HG22	1.63	0.80
7:AB:144:ARG:HB3	7:AB:208:GLN:HG2	1.61	0.80
62:BX:74:TYR:HE2	62:BX:77:LYS:HG3	1.45	0.80
1:2:1672:G:H2'	1:2:1673:G:C8	2.18	0.79
32:Aa:32:LYS:O	32:Aa:37:LYS:NZ	2.16	0.79
2:3:110:C:O2'	2:3:112:U:OP2	2.00	0.79
12:AG:142:ARG:HE	12:AG:149:LYS:HA	1.48	0.79
4:5:3268:A:OP1	43:BE:46:ARG:NH2	2.16	0.79
14:AI:57:ALA:HB2	14:AI:177:GLY:HA2	1.65	0.78
80:CA:1160:VAL:HA	80:CA:1324:TYR:HB3	1.65	0.78
1:2:1247:U:O2'	37:Af:92:LYS:NZ	2.16	0.78
37:Af:113:LYS:HZ3	37:Af:114:VAL:H	1.31	0.78
1:2:992:A:H2	1:2:1012:U:H3	1.30	0.77
52:BN:27[A]:LEU:O	52:BN:101[A]:ARG:NH1	2.18	0.77
59:BU:81:GLN:O	59:BU:98:ASN:ND2	2.18	0.77
6:AA:88:LYS:HD3	6:AA:201:LEU:HG	1.67	0.77
24:AS:86:LEU:HD22	24:AS:99:HIS:HB2	1.66	0.77
80:CA:1554:ILE:HD11	80:CA:1559:ILE:HB	1.67	0.77
46:BH:89:LYS:HG2	46:BH:145:VAL:HG12	1.67	0.77
80:CA:1380:ARG:HH12	81:CB:1:MET:HG3	1.50	0.76
26:AU:98:GLN:HG2	26:AU:99:ILE:HD12	1.67	0.76
20:AO:20:TYR:HB3	20:AO:27:PHE:HB2	1.66	0.76
44:BF:110:ARG:HE	54:BP:3:ILE:HG12	1.51	0.75
80:CA:1009:THR:HB	80:CA:1108:ASN:HA	1.68	0.75
1:2:1267:G:H1	1:2:1442:U:H3	1.34	0.75
80:CA:500:GLN:HB2	80:CA:682:ILE:HG22	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:284:A:OP2	78:Bn:41:ARG:NH1	2.19	0.75
48:BJ:32:ARG:HB3	48:BJ:120:ILE:HG23	1.68	0.75
4:5:2948:C:OP1	40:BB:244:ARG:NH2	2.18	0.75
4:5:640:U:OP1	64:BZ:21:ARG:NH2	2.19	0.74
71:Bg:76:GLN:O	71:Bg:81:ARG:NH1	2.20	0.74
4:5:1639:C:OP2	70:Bf:74:ARG:NH2	2.18	0.74
4:5:68:C:OP2	4:5:301:G:N2	2.20	0.74
2:3:63:G:O2'	71:Bg:49:LYS:NZ	2.20	0.74
4:5:1661:G:H2'	4:5:1662:G:C8	2.22	0.74
24:AS:92:ILE:HG23	24:AS:93:THR:HG23	1.69	0.74
47:BI:177:ASP:OD1	47:BI:178:ARG:N	2.22	0.73
1:2:871:G:H2'	1:2:872:G:C8	2.23	0.73
1:2:1614:A:OP2	11:AF:84:LYS:NZ	2.21	0.73
1:2:967:A:OP2	19:AN:124:ARG:NH2	2.21	0.73
1:2:488:G:N1	1:2:499:U:O4	2.22	0.73
46:BH:57:VAL:HG23	46:BH:68:LEU:HD13	1.71	0.73
4:5:1348:U:OP1	54:BP:39:ARG:NH1	2.22	0.73
27:AV:74:GLN:NE2	27:AV:80:LYS:O	2.22	0.73
42:BD:155:THR:HG23	42:BD:179:ARG:HH11	1.50	0.72
2:3:75:G:OP2	62:BX:74:TYR:OH	2.06	0.72
4:5:3116:G:H4'	46:BH:69:ARG:HH22	1.52	0.72
48:BJ:49:LYS:HB3	48:BJ:62:ASN:HA	1.71	0.72
56:BR:91:TYR:OH	56:BR:93:GLU:OE1	2.04	0.72
1:2:1160:A:H2'	1:2:1161:C:H6	1.52	0.72
24:AS:14:ILE:HG12	24:AS:23:ASP:HA	1.71	0.72
9:AD:8:LYS:HE2	26:AU:61:LYS:HD3	1.70	0.72
38:Ag:266:ASP:OD1	38:Ag:267:PRO:HD3	1.90	0.72
1:2:142:G:OP2	12:AG:139:ASN:ND2	2.22	0.72
14:AI:82:VAL:HG11	14:AI:103:GLN:HE21	1.55	0.72
1:2:647:G:H22	1:2:687:G:H1	1.35	0.72
4:5:938:C:OP2	64:BZ:26:ARG:NH1	2.22	0.72
32:Aa:82:ARG:HD3	32:Aa:85:ARG:HH22	1.52	0.72
1:2:495:C:N4	80:CA:934:GLU:O	2.23	0.72
1:2:895:G:H21	20:AO:38:THR:HG21	1.55	0.72
1:2:1034:C:HO2'	28:AW:2:THR:N	1.88	0.72
7:AB:143:THR:HB	7:AB:205:PHE:HE2	1.55	0.72
32:Aa:37:LYS:O	32:Aa:38:ARG:NH1	2.22	0.72
19:AN:23:PRO:HD2	19:AN:26:PHE:HB2	1.71	0.71
7:AB:61:LEU:HD21	7:AB:96:LEU:HD22	1.72	0.71
1:2:1785:U:OP1	20:AO:136:ARG:NH2	2.23	0.71
4:5:824:C:H5''	39:BA:21:ARG:HG3	1.70	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:BH:23:ARG:HE	46:BH:39:LYS:HA	1.56	0.71
1:2:1673:G:O6	1:2:1728:A:N1	2.23	0.71
4:5:1348:U:O2	4:5:1349:G:N2	2.23	0.71
7:AB:48:VAL:HG21	7:AB:61:LEU:HD12	1.71	0.71
9:AD:11:LEU:HD12	26:AU:86:ILE:HG12	1.72	0.71
40:BB:188:ILE:HA	40:BB:191:LYS:HB2	1.73	0.71
80:CA:889:ASP:HB3	80:CA:892:LEU:HB2	1.72	0.71
80:CA:1551:GLY:HA2	80:CA:1554:ILE:HG22	1.73	0.71
1:2:1465:C:OP1	22:AQ:139:GLN:NE2	2.23	0.71
1:2:1789:G:OP2	20:AO:132:ARG:NH2	2.21	0.71
1:2:1:U:O4	15:AJ:53:ARG:NH2	2.23	0.71
80:CA:818:MET:HG3	82:CC:370:ARG:HH22	1.55	0.71
10:AE:181:VAL:HG12	10:AE:227:VAL:HG12	1.73	0.71
24:AS:65:GLU:HG3	24:AS:68:ARG:HH21	1.56	0.71
1:2:142:G:H22	1:2:173:A:H2	1.37	0.70
1:2:207:U:O2	14:AI:178:ARG:NH2	2.23	0.70
4:5:170:G:H1	4:5:248:U:H3	1.36	0.70
80:CA:378:ARG:HH21	80:CA:386:LEU:HD13	1.56	0.70
1:2:1229:G:H21	1:2:1256:A:H62	1.36	0.70
80:CA:813:GLU:O	82:CC:370:ARG:NH1	2.24	0.70
35:Ad:36:LEU:HD12	35:Ad:38:ILE:H	1.54	0.70
1:2:1797:A:N6	32:Aa:84:VAL:O	2.24	0.70
1:2:1365:C:OP1	22:AQ:66:ARG:NH2	2.24	0.70
80:CA:1037:VAL:HG21	80:CA:1066:MET:HE1	1.72	0.70
80:CA:503:GLY:HA3	80:CA:690:LEU:HD12	1.73	0.70
40:BB:188:ILE:HG22	40:BB:191:LYS:HD2	1.72	0.70
1:2:55:A:OP1	30:AY:112:LYS:NZ	2.25	0.70
4:5:1940:G:H21	4:5:3362:A:H8	1.40	0.69
55:BQ:134:HIS:CE1	55:BQ:136:ARG:HB3	2.26	0.69
80:CA:810:GLU:OE2	82:CC:377:GLN:NE2	2.25	0.69
41:BC:328:ASN:OD1	44:BF:48:ASN:ND2	2.24	0.69
80:CA:546:VAL:HG12	80:CA:550:ARG:HH22	1.58	0.69
4:5:2895:G:O2'	76:BI:100:TYR:O	2.11	0.69
23:AR:20:TYR:HD1	23:AR:23:LYS:HG3	1.57	0.69
1:2:1594:G:OP2	1:2:1596:C:N4	2.25	0.69
32:Aa:83:ILE:O	32:Aa:85:ARG:N	2.21	0.69
32:Aa:85:ARG:HG3	32:Aa:86:VAL:H	1.57	0.69
73:Bi:21:ARG:NH1	73:Bi:41:ALA:O	2.25	0.69
1:2:225:A:N6	1:2:837:G:O6	2.25	0.69
4:5:282:G:O2'	4:5:283:G:OP2	2.09	0.69
9:AD:95:GLY:HA2	9:AD:101:GLN:HE21	1.56	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:BB:284:ARG:NH1	40:BB:293:ASN:O	2.26	0.69
54:BP:62:VAL:HG13	54:BP:66:ARG:HD2	1.75	0.69
80:CA:1164:THR:HG22	80:CA:1165:GLY:H	1.57	0.69
80:CA:1357:LYS:HG3	80:CA:1361:MET:HE1	1.74	0.69
1:2:1487:A:OP2	9:AD:8:LYS:NZ	2.26	0.69
2:3:58:G:O6	73:Bi:63:ARG:NH1	2.26	0.69
10:AE:185:GLY:H	10:AE:189:LEU:HD13	1.58	0.69
80:CA:683:LEU:HD21	80:CA:693:TYR:HD2	1.58	0.69
13:AH:32:PRO:HA	13:AH:35:LYS:HG3	1.74	0.69
9:AD:62:ASN:H	80:CA:921:LYS:HE3	1.58	0.68
1:2:1555:A:O3'	21:AP:44:ARG:NH1	2.27	0.68
4:5:2600:C:OP1	51:BM:93:LYS:NZ	2.26	0.68
30:AY:86:GLU:OE2	30:AY:90:ARG:NH1	2.26	0.68
41:BC:361:HIS:O	56:BR:28:ARG:NH1	2.27	0.68
57:BS:18:ASP:HB2	57:BS:21:LYS:HB2	1.75	0.68
57:BS:14:MET:HE1	57:BS:55:LYS:HB2	1.75	0.68
2:3:112:U:H3'	75:Bk:8:ARG:HH12	1.57	0.68
4:5:1949:G:OP2	55:BQ:135:LYS:NZ	2.26	0.68
30:AY:55:VAL:HG22	30:AY:75:VAL:HG22	1.73	0.68
38:Ag:156:VAL:HG12	38:Ag:169:ILE:HG22	1.75	0.68
45:BG:95:ASN:OD1	45:BG:98:ARG:NH2	2.26	0.68
66:Bb:57:GLU:OE2	66:Bb:69:TYR:OH	2.11	0.68
4:5:860:G:OP1	79:Bo:17:ARG:NH1	2.26	0.68
4:5:992:A:H5''	57:BS:43:LYS:HD2	1.75	0.68
80:CA:1682:ASN:HA	80:CA:1685:MET:HE2	1.76	0.68
80:CA:549:ALA:HB2	80:CA:597:ILE:HD11	1.75	0.68
1:2:1297:G:N2	1:2:1300:A:OP2	2.25	0.68
1:2:1791:A:H3'	32:Aa:8:ASN:HB3	1.76	0.68
1:2:897:C:O2	20:AO:41:ARG:NH2	2.27	0.68
24:AS:140:THR:HA	24:AS:143:ARG:HH21	1.59	0.68
20:AO:99:GLN:NE2	32:Aa:45:VAL:O	2.27	0.67
1:2:17:C:O2'	1:2:1137:A:N1	2.26	0.67
1:2:1445:G:N2	37:Af:88:PRO:O	2.27	0.67
30:AY:37:LYS:HA	30:AY:40:LEU:HB2	1.75	0.67
37:Af:106:TYR:C	37:Af:107:LYS:HD3	2.19	0.67
80:CA:596:GLY:HA2	80:CA:622:LEU:HG	1.76	0.67
38:Ag:192:PHE:HB3	38:Ag:223:TRP:HZ3	1.59	0.67
9:AD:50:ILE:HD11	9:AD:86:LEU:HD23	1.76	0.67
12:AG:157:VAL:HG22	12:AG:175:ILE:HD11	1.76	0.67
6:AA:31:VAL:HG12	6:AA:33:GLN:H	1.58	0.67
59:BU:14:SER:O	59:BU:81:GLN:NE2	2.26	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:996:U:O2	1:2:1008:G:N2	2.25	0.67
4:5:2440:G:H4'	7:AB:53:GLY:HA3	1.77	0.67
25:AT:97:SER:O	25:AT:101:ASN:ND2	2.28	0.67
62:BX:74:TYR:CE2	62:BX:77:LYS:HG3	2.29	0.67
82:CC:186:PHE:HD1	82:CC:201:VAL:HA	1.60	0.67
1:2:163:G:N2	1:2:163:G:OP2	2.28	0.67
1:2:472:U:O2'	1:2:769:A:N3	2.26	0.67
2:3:142:C:OP1	51:BM:38:ARG:NH1	2.27	0.67
4:5:2111:G:H1'	60:BV:44:LYS:HD2	1.77	0.67
14:AI:79:ALA:HB3	14:AI:103:GLN:HB2	1.76	0.67
63:BY:105:SER:OG	63:BY:106:GLN:OE1	2.13	0.67
1:2:1690:G:H2'	1:2:1691:A:H8	1.59	0.66
80:CA:348:LYS:HG3	80:CA:420:LYS:HB3	1.76	0.66
5:6:33:U:OP2	22:AQ:143:ARG:NH2	2.28	0.66
7:AB:194:ASN:ND2	7:AB:210:ILE:O	2.28	0.66
80:CA:777:ARG:HE	80:CA:809:ASN:HD22	1.42	0.66
4:5:1717:U:H2'	4:5:1718:G:C8	2.30	0.66
4:5:3042:U:OP2	4:5:3092:C:N4	2.28	0.66
47:BI:211:ARG:HH22	47:BI:212:GLU:HB2	1.61	0.66
75:Bk:23:LEU:HD11	75:Bk:35:ILE:HG22	1.75	0.66
1:2:1610:G:OP1	11:AF:72:HIS:NE2	2.28	0.66
80:CA:624:CYS:SG	80:CA:625:THR:N	2.64	0.66
2:3:103:G:OP2	2:3:105:A:O2'	2.14	0.66
64:BZ:24:LYS:O	64:BZ:26:ARG:HG2	1.95	0.66
80:CA:1122:PRO:O	80:CA:1124:SER:N	2.29	0.66
1:2:821:U:O4	1:2:852:C:N3	2.29	0.66
4:5:3139:A:OP2	40:BB:30:LYS:NZ	2.26	0.66
1:2:1565:C:OP1	24:AS:41:ARG:NH1	2.29	0.66
12:AG:68:LEU:HB3	12:AG:69:LEU:HD23	1.78	0.66
80:CA:1417:GLN:O	80:CA:1441:LYS:NZ	2.29	0.66
4:5:2960:C:H2'	4:5:2961:G:C8	2.31	0.66
1:2:636:A:H5''	28:AW:31:SER:HB2	1.76	0.66
4:5:184:U:H3	4:5:232:G:H1	1.43	0.66
4:5:798:G:H4'	49:BK:15:ARG:HE	1.61	0.66
4:5:2392:C:O2'	40:BB:266:ARG:NH1	2.28	0.66
22:AQ:95:LYS:O	38:Ag:59:ARG:NH2	2.23	0.66
80:CA:261:ASN:HD22	80:CA:491:SER:HB3	1.61	0.66
1:2:862:A:OP2	19:AN:64:ARG:NH1	2.21	0.65
80:CA:535:VAL:HG12	80:CA:638:CYS:HB3	1.78	0.65
45:BG:78:PHE:O	45:BG:79:GLN:HG3	1.96	0.65
4:5:289:A:O2'	51:BM:93:LYS:O	2.15	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:1244:A:O2'	4:5:1247:U:OP1	2.14	0.65
4:5:2185:G:O2'	4:5:2314:U:OP2	2.14	0.65
18:AM:131:ASP:HA	18:AM:134:SER:HB2	1.78	0.65
24:AS:83:ALA:O	24:AS:89:GLN:NE2	2.29	0.65
43:BE:52:VAL:HG23	43:BE:67:GLY:HA2	1.78	0.65
2:3:22:U:O4	4:5:341:G:O2'	2.13	0.65
4:5:1778:G:O2'	4:5:1780:G:OP2	2.14	0.65
4:5:2568:C:O2'	4:5:2569:A:O4'	2.14	0.65
42:BD:135:VAL:HG13	42:BD:138:GLY:HA3	1.78	0.65
54:BP:152:HIS:ND1	54:BP:162:ALA:O	2.26	0.65
80:CA:1268:ILE:HG12	80:CA:1303:SER:HB3	1.79	0.65
4:5:2138:A:HO2'	73:Bi:2:GLY:N	1.94	0.65
1:2:322:G:O2'	1:2:323:A:OP2	2.13	0.65
1:2:514:G:H2'	1:2:515:A:H8	1.62	0.65
1:2:1727:G:H2'	1:2:1728:A:C8	2.31	0.65
21:AP:57:MET:HG2	21:AP:61:ARG:HH12	1.62	0.65
45:BG:158:ASP:HB3	45:BG:159:PRO:HD3	1.77	0.65
50:BL:50:LYS:NZ	50:BL:82:SER:O	2.29	0.65
80:CA:1616:CYS:HB3	80:CA:1630:LEU:HG	1.78	0.65
4:5:618:C:OP1	53:BO:173:ARG:NH2	2.30	0.65
14:AI:153:GLU:HG2	14:AI:155:SER:H	1.62	0.65
80:CA:430:HIS:HB3	80:CA:464:SER:HB2	1.77	0.65
1:2:58:U:O2'	1:2:451:A:N3	2.30	0.65
10:AE:18:TRP:NE1	10:AE:41:SER:O	2.30	0.65
58:BT:86:LYS:O	58:BT:88:GLN:NE2	2.29	0.65
10:AE:100:ARG:NH2	10:AE:121:TYR:O	2.30	0.64
39:BA:33:ASP:O	39:BA:37:ARG:NH1	2.30	0.64
1:2:868:G:H1	1:2:960:U:H3	1.45	0.64
4:5:148:G:OP2	51:BM:4:TYR:OH	2.14	0.64
17:AL:73:GLY:HA3	17:AL:86:ILE:HD12	1.79	0.64
24:AS:35:ILE:HG23	24:AS:102:ALA:HB2	1.79	0.64
53:BO:60:PHE:HB3	53:BO:64:ASN:HB3	1.78	0.64
1:2:1414:U:H5'	23:AR:3:ARG:HH21	1.61	0.64
4:5:449:U:O2'	4:5:450:G:N2	2.30	0.64
4:5:600:G:N2	4:5:603:A:OP2	2.30	0.64
4:5:900:G:H1'	4:5:1589:A:N6	2.12	0.64
4:5:3205:G:OP2	4:5:3206:C:N4	2.31	0.64
1:2:1436:A:OP2	9:AD:27:ARG:NH2	2.25	0.64
2:3:8:C:H2'	2:3:9:A:C8	2.33	0.64
4:5:1896:A:H61	4:5:2339:C:H42	1.44	0.64
43:BE:12:SER:OG	43:BE:14:ASP:OD1	2.16	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:Bj:5:ILE:HD11	74:Bj:11:PHE:HD2	1.61	0.64
1:2:458:G:OP1	30:AY:109:LYS:NZ	2.30	0.64
4:5:2681:U:H5'	48:BJ:65:ILE:HD11	1.78	0.64
16:AK:77:ARG:HD3	16:AK:84:GLU:HA	1.79	0.64
47:BI:177:ASP:OD1	47:BI:179:PRO:HD2	1.97	0.64
50:BL:48:GLY:HA3	50:BL:53:VAL:HB	1.80	0.64
80:CA:1157:ASN:ND2	80:CA:1316:LEU:O	2.30	0.64
80:CA:1346:LEU:HD13	80:CA:1350:PRO:HB2	1.79	0.64
1:2:1040:G:H5'	6:AA:32:HIS:HD2	1.62	0.64
4:5:1786:G:H2'	4:5:1787:A:C8	2.32	0.64
11:AF:63:GLN:NE2	11:AF:64:VAL:O	2.31	0.64
54:BP:123:THR:OG1	54:BP:125:ASP:OD1	2.15	0.64
80:CA:1041:GLU:HG2	80:CA:1048:LEU:HD11	1.79	0.64
1:2:1108:G:H1	29:AX:22:ASN:HD22	1.46	0.64
1:2:1256:A:H4'	1:2:1257:U:O5'	1.98	0.64
4:5:2960:C:H2'	4:5:2961:G:H8	1.60	0.64
10:AE:208:VAL:HG11	10:AE:225:VAL:HG21	1.79	0.64
22:AQ:22:VAL:HG22	22:AQ:65:ILE:HG12	1.80	0.64
79:Bo:9:GLY:HA3	79:Bo:27:LYS:HE3	1.79	0.64
4:5:655:C:H2'	4:5:656:A:H8	1.62	0.64
14:AI:155:SER:O	14:AI:159:GLN:NE2	2.31	0.64
63:BY:103:GLN:NE2	63:BY:105:SER:OG	2.30	0.64
1:2:78:A:H5''	12:AG:159:ARG:HH12	1.62	0.63
1:2:143:G:OP2	12:AG:139:ASN:ND2	2.32	0.63
1:2:1584:G:HO2'	1:2:1610:G:H1	1.44	0.63
4:5:40:A:H5''	64:BZ:35:ALA:HB1	1.80	0.63
4:5:1474:A:O2'	67:Bc:57:GLN:NE2	2.31	0.63
6:AA:119:ARG:NH1	8:AC:241:ASP:OD1	2.29	0.63
25:AT:86:ARG:HD2	25:AT:92:LYS:HG2	1.79	0.63
80:CA:734:LEU:O	80:CA:737:THR:OG1	2.16	0.63
80:CA:1480:THR:HG21	80:CA:1520:THR:HG23	1.79	0.63
4:5:761:A:C2	4:5:771:A:H1'	2.33	0.63
11:AF:183:ALA:HB2	11:AF:193:THR:HG21	1.80	0.63
80:CA:785:VAL:HB	80:CA:794:ILE:HB	1.80	0.63
80:CA:1194:MET:HE3	80:CA:1195:LYS:HG2	1.80	0.63
81:CB:43:LEU:HD12	81:CB:103:GLN:HE22	1.62	0.63
4:5:716:A:OP1	4:5:752:C:O2'	2.16	0.63
28:AW:90:THR:HG23	28:AW:94:LEU:HD12	1.79	0.63
80:CA:468:PRO:HB3	80:CA:700:GLN:HB3	1.79	0.63
80:CA:1249:ARG:NH1	80:CA:1633:SER:O	2.31	0.63
1:2:153:G:H21	12:AG:56:ASN:HD21	1.46	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AF:84:LYS:HE3	11:AF:165:LEU:HD21	1.80	0.63
81:CB:160:GLN:HE22	81:CB:163:GLN:HG3	1.63	0.63
1:2:992:A:O2'	1:2:1785:U:O2	2.15	0.63
1:2:1060:U:H3'	1:2:1061:A:H5''	1.79	0.63
4:5:792:G:H5''	64:BZ:2:PRO:HD2	1.80	0.63
4:5:3252:G:H2'	4:5:3253:G:H8	1.64	0.63
26:AU:52:LYS:HZ3	26:AU:54:GLY:HA2	1.64	0.63
37:Af:106:TYR:O	37:Af:107:LYS:HD3	1.98	0.63
1:2:284:G:OP1	12:AG:196:ARG:NH2	2.28	0.63
1:2:1195:C:OP1	26:AU:77:LYS:NZ	2.26	0.63
4:5:559:A:O2'	50:BL:84:LYS:NZ	2.28	0.63
4:5:3295:A:H2'	4:5:3296:A:C8	2.34	0.63
54:BP:98:LYS:NZ	54:BP:118:GLY:O	2.32	0.63
1:2:482:U:H2'	1:2:483:A:H8	1.64	0.63
20:AO:135:ARG:HH12	20:AO:137:LEU:HD13	1.63	0.63
39:BA:40:TYR:HA	39:BA:91:GLY:HA3	1.81	0.63
4:5:567:G:H2'	4:5:568:G:C8	2.34	0.62
4:5:664:U:H2'	4:5:665:A:C8	2.34	0.62
4:5:2890:A:O2'	4:5:2933:A:N3	2.32	0.62
4:5:3275:U:O2'	69:Be:99:ARG:NH1	2.32	0.62
47:BI:211:ARG:NH2	47:BI:212:GLU:HB2	2.13	0.62
1:2:511:A:H5''	15:AJ:172:VAL:HG23	1.81	0.62
25:AT:31:PRO:HG2	25:AT:34:VAL:HB	1.81	0.62
60:BV:23:ARG:NH2	60:BV:25:ASP:OD2	2.31	0.62
80:CA:1264:ILE:HG22	80:CA:1300:LEU:HB3	1.81	0.62
1:2:680:U:O4	1:2:682:C:N4	2.31	0.62
1:2:1480:G:OP1	25:AT:63:ARG:NH2	2.30	0.62
7:AB:5:LYS:NZ	20:AO:51:ASP:OD1	2.30	0.62
12:AG:22:HIS:C	12:AG:25:ARG:HH12	2.07	0.62
4:5:1079:A:H4'	42:BD:140:ARG:O	1.99	0.62
42:BD:182:GLY:HA2	42:BD:194:LEU:HD23	1.80	0.62
80:CA:1119:ARG:NE	82:CC:191:ASN:OD1	2.28	0.62
1:2:487:G:H2'	1:2:488:G:C8	2.34	0.62
10:AE:251:GLU:OE2	10:AE:255:ARG:NH2	2.31	0.62
1:2:534:A:OP1	15:AJ:168:ARG:NH1	2.32	0.62
1:2:1459:C:OP2	24:AS:138:THR:OG1	2.17	0.62
2:3:9:A:H2'	2:3:10:A:C8	2.34	0.62
35:Ad:12:ARG:HH11	35:Ad:12:ARG:HG3	1.64	0.62
46:BH:103:ILE:HD12	46:BH:134:ILE:HD11	1.81	0.62
61:BW:50:ALA:HB1	71:Bg:66:VAL:HG11	1.80	0.62
1:2:78:A:H2'	1:2:79:C:C6	2.35	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:590:C:H2'	1:2:591:A:C8	2.34	0.62
9:AD:124:ARG:NH2	9:AD:128:GLU:OE2	2.33	0.62
10:AE:11:ARG:NH1	10:AE:21:ASP:O	2.31	0.62
38:Ag:110:VAL:HA	38:Ag:126:SER:HA	1.82	0.62
41:BC:126:ILE:O	41:BC:129:THR:OG1	2.16	0.62
74:Bj:33:LYS:HA	74:Bj:33:LYS:HE3	1.82	0.62
1:2:496:G:H2'	1:2:497:G:C8	2.35	0.62
4:5:2931:C:H5''	59:BU:40:LYS:HD3	1.81	0.62
24:AS:90:ASN:HA	24:AS:95:GLY:HA2	1.81	0.62
37:Af:113:LYS:NZ	37:Af:114:VAL:H	1.96	0.62
51:BM:36:ILE:HG12	51:BM:64:VAL:HG23	1.82	0.62
71:Bg:38:ARG:HE	71:Bg:41:LEU:HD13	1.65	0.62
1:2:1474:G:O6	31:AZ:97:LYS:NZ	2.31	0.62
80:CA:502:LEU:HB2	80:CA:684:CYS:HA	1.82	0.62
1:2:495:C:H42	80:CA:935:LYS:HA	1.64	0.62
41:BC:338:LYS:HA	41:BC:338:LYS:HE3	1.81	0.62
57:BS:84:TYR:HB2	65:Ba:24:PRO:HD3	1.81	0.62
63:BY:9:LYS:HB3	63:BY:25:ILE:HD12	1.82	0.62
80:CA:1162:SER:O	80:CA:1168:LYS:NZ	2.33	0.62
1:2:1556:A:H4'	1:2:1557:U:H5	1.65	0.61
55:BQ:152:GLU:OE2	55:BQ:156:ASN:ND2	2.33	0.61
60:BV:86:SER:O	60:BV:89:LEU:N	2.33	0.61
4:5:518:G:OP2	4:5:518:G:N2	2.24	0.61
4:5:838:G:O6	79:Bo:4:ARG:NH1	2.30	0.61
4:5:1667:A:H2'	4:5:1668:G:C8	2.35	0.61
4:5:2155:G:OP1	39:BA:241:ARG:NH1	2.33	0.61
4:5:2440:G:H2'	4:5:2441:A:C8	2.35	0.61
4:5:2767:U:O2'	78:Bn:30:ALA:O	2.17	0.61
4:5:2945:G:O2'	4:5:2948:C:OP2	2.15	0.61
37:Af:113:LYS:NZ	37:Af:114:VAL:O	2.22	0.61
4:5:1629:U:OP2	63:BY:112:LYS:NZ	2.34	0.61
10:AE:9:LEU:HB2	10:AE:30:ARG:HG3	1.82	0.61
10:AE:19:LEU:HD11	10:AE:108:ARG:HD2	1.82	0.61
59:BU:80:ARG:NH1	59:BU:117:PRO:O	2.31	0.61
80:CA:1271:LEU:HA	80:CA:1276:GLY:HA3	1.82	0.61
80:CA:1282:ILE:HG22	80:CA:1286:MET:HE1	1.82	0.61
80:CA:1769:GLN:NE2	80:CA:1952:ASN:O	2.30	0.61
21:AP:123:TYR:OH	24:AS:126:ARG:NH1	2.33	0.61
1:2:924:A:H2'	1:2:925:G:C8	2.35	0.61
18:AM:54:ARG:HH12	37:Af:127:GLY:HA3	1.65	0.61
68:Bd:4:LEU:HD12	68:Bd:5:PRO:HD2	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:CA:1262:LEU:HD13	80:CA:1298:ARG:HB3	1.83	0.61
80:CA:1761:VAL:HG21	80:CA:1914:LEU:HD22	1.82	0.61
4:5:243:G:OP1	71:Bg:115:LYS:NZ	2.31	0.61
27:AV:74:GLN:HA	27:AV:79:LEU:HB3	1.83	0.61
30:AY:26:ASP:OD1	30:AY:68:LYS:NZ	2.33	0.61
38:Ag:289:ALA:HA	38:Ag:305:TYR:HA	1.83	0.61
1:2:29:U:H2'	1:2:30:G:H8	1.65	0.61
1:2:1041:G:H2'	1:2:1042:G:C8	2.35	0.61
4:5:1682:U:O4	58:BT:90:ARG:NH1	2.34	0.61
11:AF:157:ARG:HB3	11:AF:224:ASN:HD21	1.65	0.61
29:AX:109:ARG:HG3	29:AX:114:LYS:HA	1.81	0.61
32:Aa:44:ILE:HG23	32:Aa:45:VAL:HG13	1.82	0.61
1:2:1171:A:H2'	1:2:1172:G:C8	2.35	0.61
3:4:28:C:OP1	48:BJ:137:ARG:NH1	2.32	0.61
19:AN:52:VAL:HG23	19:AN:55:ARG:HH21	1.66	0.61
21:AP:90:ILE:HD13	21:AP:109:PRO:HB3	1.83	0.61
70:Bf:79:SER:OG	70:Bf:80:ARG:NH1	2.34	0.61
1:2:159:U:O2'	12:AG:87:ARG:NH1	2.34	0.61
47:BI:30:LYS:HG3	47:BI:63:GLU:HB3	1.81	0.61
64:BZ:86:LYS:HA	64:BZ:86:LYS:HE3	1.82	0.61
80:CA:380:LEU:HB2	80:CA:399:THR:HG22	1.83	0.61
80:CA:602:MET:SD	80:CA:602:MET:N	2.74	0.61
80:CA:1664:SER:O	80:CA:1709:HIS:ND1	2.30	0.61
4:5:1724:U:O4	55:BQ:125:LYS:NZ	2.34	0.61
14:AI:84:HIS:NE2	14:AI:97:THR:OG1	2.32	0.61
15:AJ:86:LEU:HD13	15:AJ:99:LEU:HD21	1.82	0.61
15:AJ:109:LEU:HB2	15:AJ:146:PHE:HB3	1.82	0.61
18:AM:76:GLU:O	18:AM:80:ASN:ND2	2.34	0.61
22:AQ:47:LYS:HE3	22:AQ:82:ARG:NH1	2.16	0.61
51:BM:192:LYS:O	51:BM:196:THR:OG1	2.19	0.61
80:CA:378:ARG:NH1	80:CA:394:THR:OG1	2.34	0.61
1:2:388:G:OP1	1:2:423:G:O2'	2.19	0.60
6:AA:84:ARG:NH1	6:AA:203:PHE:O	2.34	0.60
64:BZ:75:LEU:HG	64:BZ:114:GLY:HA2	1.83	0.60
1:2:886:U:O2'	20:AO:121:VAL:O	2.19	0.60
1:2:1610:G:N7	22:AQ:14:LYS:NZ	2.43	0.60
1:2:1693:A:N1	1:2:1709:C:N4	2.49	0.60
4:5:2181:C:OP1	39:BA:192:LYS:NZ	2.32	0.60
81:CB:26:PRO:HB3	81:CB:30:LEU:HD23	1.83	0.60
1:2:1170:G:N2	1:2:1571:C:O2'	2.33	0.60
1:2:1524:A:H2'	1:2:1525:A:C8	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1555:A:OP1	21:AP:47:ARG:NE	2.33	0.60
13:AH:9:LEU:HD11	13:AH:17:GLU:HG3	1.81	0.60
38:Ag:80:ALA:HB3	38:Ag:92:TRP:HB2	1.83	0.60
40:BB:126:LYS:HB2	40:BB:128:LYS:HG2	1.84	0.60
47:BI:3:ARG:NE	47:BI:63:GLU:OE2	2.34	0.60
81:CB:18:ILE:O	81:CB:69:THR:OG1	2.18	0.60
1:2:31:C:O2'	1:2:547:U:OP1	2.19	0.60
1:2:878:G:O2'	19:AN:108:ASP:OD1	2.15	0.60
3:4:7:G:OP1	42:BD:33:ARG:NH1	2.33	0.60
22:AQ:94:GLN:NE2	38:Ag:60:SER:O	2.35	0.60
34:Ac:30:VAL:HG11	34:Ac:54:LEU:HD12	1.82	0.60
70:Bf:91:ARG:HG2	70:Bf:95:ILE:HD11	1.84	0.60
4:5:1238:C:N4	4:5:1245:A:OP2	2.35	0.60
13:AH:67:LEU:HD13	13:AH:94:ALA:HB2	1.84	0.60
18:AM:62:LEU:HD21	18:AM:72:ILE:HG12	1.84	0.60
41:BC:334:PHE:HA	41:BC:339:LEU:HD12	1.83	0.60
80:CA:791:MET:H	80:CA:791:MET:HE2	1.66	0.60
1:2:591:A:H2'	1:2:592:A:C8	2.37	0.60
4:5:394:G:N1	4:5:397:A:OP2	2.34	0.60
4:5:2969:A:N7	39:BA:215:ASN:ND2	2.48	0.60
4:5:3295:A:H2'	4:5:3296:A:H8	1.67	0.60
6:AA:120:LEU:HD12	6:AA:142:PRO:HB2	1.83	0.60
7:AB:112:SER:O	7:AB:115:ARG:NH1	2.35	0.60
12:AG:135:PRO:HB2	12:AG:141:ILE:HD13	1.84	0.60
1:2:24:U:OP1	15:AJ:10:LYS:NZ	2.34	0.60
4:5:595:G:H1	4:5:609:G:H5''	1.65	0.60
4:5:655:C:H2'	4:5:656:A:C8	2.37	0.60
4:5:1814:A:H4'	4:5:1815:U:H5'	1.81	0.60
4:5:2213:A:H2'	4:5:2214:A:C8	2.37	0.60
38:Ag:42:LEU:HD21	38:Ag:82:SER:HB3	1.83	0.60
80:CA:1349:CYS:SG	81:CB:37:LYS:NZ	2.66	0.60
1:2:1160:A:H2'	1:2:1161:C:C6	2.35	0.60
9:AD:191:ASP:OD2	9:AD:194:LYS:NZ	2.34	0.60
80:CA:1248:SER:O	80:CA:1251:TRP:HD1	1.83	0.60
4:5:190:U:H2'	62:BX:60:ARG:HH22	1.66	0.60
4:5:966:U:OP1	64:BZ:44:ASN:ND2	2.34	0.60
4:5:3016:A:H2'	4:5:3017:A:C8	2.37	0.60
4:5:3114:A:OP1	46:BH:69:ARG:NH1	2.34	0.60
15:AJ:139:GLN:NE2	15:AJ:140:ILE:O	2.35	0.60
45:BG:144:GLU:OE2	72:Bh:36:ARG:NH1	2.35	0.60
78:Bn:28:TYR:HB3	78:Bn:69:VAL:HB	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:Bn:71:ARG:HH21	78:Bn:80:ARG:HH11	1.49	0.60
80:CA:1041:GLU:HB3	80:CA:1077:PRO:HG3	1.84	0.60
9:AD:94:ARG:NH1	80:CA:969:GLU:OE2	2.31	0.60
26:AU:102:ARG:O	80:CA:1105:ARG:NH1	2.34	0.60
30:AY:57:VAL:HB	30:AY:60:PHE:HE2	1.66	0.60
82:CC:210:CYS:HB3	82:CC:215:GLU:H	1.67	0.60
1:2:1488:G:H3'	1:2:1515:A:H61	1.67	0.59
4:5:2772:C:OP1	78:Bn:15:LYS:NZ	2.30	0.59
4:5:3198:U:O2	46:BH:21:LYS:N	2.34	0.59
6:AA:11:PRO:HA	23:AR:115:LEU:HD21	1.82	0.59
24:AS:62:THR:OG1	24:AS:65:GLU:OE1	2.16	0.59
39:BA:68:LYS:HD3	39:BA:70:ARG:HE	1.66	0.59
52:BN:121[A]:PRO:HA	52:BN:124[A]:LEU:HD12	1.83	0.59
80:CA:510:SER:O	80:CA:513:SER:OG	2.16	0.59
29:AX:70:LYS:HB3	29:AX:93:LEU:HD22	1.83	0.59
4:5:94:G:H2'	4:5:95:A:C8	2.37	0.59
4:5:1498:A:H2'	4:5:1499:C:C6	2.37	0.59
13:AH:70:PHE:HB3	13:AH:74:GLN:HE21	1.66	0.59
28:AW:31:SER:H	28:AW:34:ILE:HD12	1.67	0.59
46:BH:31:ARG:NH1	46:BH:149:ASN:OD1	2.35	0.59
64:BZ:112:ILE:HB	64:BZ:130:VAL:HG12	1.83	0.59
80:CA:349:VAL:HB	80:CA:396:VAL:HG22	1.83	0.59
3:4:77:G:O4'	56:BR:50:LYS:NZ	2.35	0.59
31:AZ:36:ALA:HB1	31:AZ:70:LYS:HZ3	1.67	0.59
4:5:3050:U:O2'	60:BV:16:GLY:O	2.16	0.59
4:5:3252:G:H2'	4:5:3253:G:C8	2.37	0.59
1:2:706:A:H61	1:2:731:C:H5''	1.67	0.59
4:5:733:G:N2	4:5:736:A:OP2	2.30	0.59
41:BC:193:LYS:HA	41:BC:198:ARG:HA	1.84	0.59
1:2:1585:U:H3	1:2:1611:A:H2	1.48	0.59
4:5:617:G:OP1	43:BE:108:LYS:NZ	2.36	0.59
4:5:638:C:H2'	4:5:639:G:H8	1.68	0.59
4:5:1194:G:H2'	4:5:1195:A:C8	2.38	0.59
13:AH:44:LYS:HD3	13:AH:63:PRO:HB3	1.84	0.59
22:AQ:82:ARG:NH2	22:AQ:113:ASP:OD2	2.35	0.59
54:BP:76:ALA:HA	54:BP:79:LYS:HD2	1.84	0.59
64:BZ:78:LEU:HD13	64:BZ:118:ILE:HG21	1.83	0.59
4:5:2697:A:H2'	4:5:2698:G:C8	2.38	0.59
4:5:3174:A:OP1	69:Be:97:SER:OG	2.19	0.59
13:AH:64:VAL:HB	13:AH:94:ALA:HB1	1.83	0.59
32:Aa:83:ILE:HG22	32:Aa:84:VAL:H	1.68	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:BJ:143:ARG:NH1	48:BJ:144:CYS:SG	2.75	0.59
51:BM:44:ARG:NH1	51:BM:120:TRP:O	2.36	0.59
1:2:16:G:H2'	1:2:17:C:C6	2.38	0.59
4:5:1114:U:OP1	64:BZ:23:GLY:N	2.35	0.59
4:5:1352:A:H4'	4:5:1353:U:H5'	1.85	0.59
4:5:1657:C:O2'	4:5:1797:A:OP2	2.14	0.59
11:AF:99:MET:HG3	11:AF:100:ASN:H	1.68	0.59
38:Ag:216:LYS:HA	38:Ag:239:GLU:HG2	1.84	0.59
56:BR:132:THR:HG23	56:BR:144:LEU:HD23	1.85	0.59
1:2:61:A:O2'	1:2:62:A:O4'	2.21	0.59
1:2:540:G:N2	1:2:542:A:N7	2.49	0.59
4:5:1477:A:OP1	4:5:3075:G:O2'	2.19	0.59
4:5:2177:G:N2	39:BA:118:GLU:OE2	2.36	0.59
1:2:751:G:H2'	1:2:752:A:H8	1.67	0.58
62:BX:59:VAL:O	62:BX:64:LYS:NZ	2.30	0.58
80:CA:1543:HIS:HA	80:CA:1546:LEU:HB3	1.85	0.58
2:3:155:A:H5''	45:BG:84:ARG:HH22	1.68	0.58
3:4:121:U:OP2	42:BD:265:TYR:OH	2.18	0.58
4:5:705:A:N7	64:BZ:74:ASN:ND2	2.42	0.58
10:AE:40:GLU:HG2	10:AE:40:GLU:O	2.02	0.58
13:AH:50:ASP:HA	13:AH:56:LYS:HG3	1.84	0.58
13:AH:126:LEU:HD21	13:AH:152:VAL:HG21	1.84	0.58
56:BR:26:ARG:NH1	57:BS:150:THR:OG1	2.35	0.58
70:Bf:91:ARG:O	70:Bf:95:ILE:HD12	2.04	0.58
80:CA:898:TYR:O	80:CA:902:ASN:ND2	2.36	0.58
1:2:153:G:H1	1:2:161:U:H3	1.50	0.58
4:5:1253:U:N3	4:5:1264:G:OP1	2.37	0.58
4:5:2452:G:H2'	4:5:2494:A:H61	1.67	0.58
49:BK:165:SER:O	49:BK:167:PHE:N	2.37	0.58
66:Bb:51:LEU:HD13	70:Bf:91:ARG:HG3	1.84	0.58
4:5:3166:C:H2'	4:5:3167:A:H8	1.68	0.58
18:AM:126:TRP:HD1	18:AM:128:ALA:HB3	1.69	0.58
46:BH:92:TYR:HB2	46:BH:142:ASP:HB3	1.85	0.58
54:BP:36:LEU:O	54:BP:40:THR:OG1	2.15	0.58
58:BT:32:SER:OG	58:BT:83:TYR:OH	2.19	0.58
4:5:1534:A:H2'	4:5:1535:A:C8	2.39	0.58
7:AB:103:MET:HB3	7:AB:215:VAL:HG12	1.85	0.58
13:AH:91:ILE:HG21	13:AH:129:LEU:HD12	1.85	0.58
40:BB:299:ASP:OD2	40:BB:301:THR:OG1	2.16	0.58
41:BC:237:GLN:O	41:BC:246:ARG:NH1	2.37	0.58
46:BH:90:MET:HE3	46:BH:181:VAL:HG23	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:BQ:153:LYS:NZ	55:BQ:157:GLU:OE1	2.36	0.58
1:2:687:G:H5'	28:AW:119:LYS:HG3	1.83	0.58
4:5:1203:A:H2'	4:5:1204:A:C8	2.39	0.58
4:5:3329:U:H5''	40:BB:308:MET:HE2	1.84	0.58
38:Ag:13:LEU:HB2	38:Ag:310:ILE:HB	1.86	0.58
42:BD:50:ARG:NH2	42:BD:72:ASP:OD2	2.36	0.58
58:BT:18:ASP:HB3	58:BT:104:ARG:HB3	1.84	0.58
1:2:1397:U:O2'	1:2:1400:A:N6	2.37	0.58
4:5:243:G:H2'	4:5:244:G:H8	1.68	0.58
4:5:896:A:H5'	39:BA:183:GLY:HA2	1.86	0.58
17:AL:57:LYS:HG2	17:AL:131:ILE:HD12	1.84	0.58
20:AO:86:THR:HG21	20:AO:90:ARG:HD3	1.85	0.58
40:BB:346:THR:HB	40:BB:351:LEU:HD11	1.85	0.58
80:CA:408:THR:OG1	80:CA:446:ARG:NH1	2.32	0.58
1:2:1479:A:OP1	25:AT:57:ARG:NE	2.29	0.58
4:5:2129:U:H2'	4:5:2130:G:C8	2.37	0.58
7:AB:62:LYS:HE2	7:AB:90:GLU:HA	1.85	0.58
9:AD:124:ARG:NH1	80:CA:971:GLU:OE2	2.36	0.58
12:AG:70:PRO:HD3	12:AG:101:ILE:HD12	1.85	0.58
42:BD:60:ILE:HB	42:BD:80:SER:HB3	1.84	0.58
80:CA:355:LEU:HG	80:CA:356:LYS:H	1.69	0.58
81:CB:81:LEU:HD12	81:CB:84:ILE:HD11	1.84	0.58
1:2:1235:C:N3	37:Af:138:ARG:NH1	2.51	0.58
1:2:1300:A:OP1	8:AC:99:LYS:NZ	2.37	0.58
66:Bb:43:ILE:HG12	66:Bb:68:TYR:HB3	1.86	0.58
1:2:1067:C:H5''	7:AB:150:VAL:HG23	1.85	0.58
2:3:8:C:H2'	2:3:9:A:H8	1.68	0.58
4:5:662:U:H2'	4:5:663:C:C6	2.39	0.58
12:AG:32:ILE:HD11	12:AG:63:MET:HE3	1.86	0.58
13:AH:63:PRO:C	13:AH:65:PRO:HD3	2.29	0.58
81:CB:78:ARG:NH2	81:CB:124:GLN:O	2.35	0.58
1:2:1331:A:OP1	23:AR:45:ARG:NH1	2.37	0.57
3:4:62:U:O4	3:4:63:A:N6	2.36	0.57
4:5:3354:U:O2	14:AI:77:ARG:NH1	2.37	0.57
53:BO:128:ARG:NH2	53:BO:130:TYR:OH	2.37	0.57
80:CA:1007:ILE:HG22	80:CA:1537:PRO:HG2	1.86	0.57
1:2:129:U:O2'	1:2:131:C:N4	2.31	0.57
1:2:749:U:H5''	28:AW:83:ILE:HB	1.86	0.57
1:2:830:U:H2'	1:2:831:U:C6	2.39	0.57
1:2:1641:C:H2'	1:2:1642:G:C8	2.39	0.57
4:5:656:A:H2'	4:5:657:A:C8	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:994:G:N2	4:5:995:U:O4	2.29	0.57
4:5:3016:A:H2'	4:5:3017:A:H8	1.68	0.57
10:AE:97:GLU:C	10:AE:98:ASN:HD22	2.12	0.57
11:AF:64:VAL:O	11:AF:65:ARG:HD3	2.04	0.57
42:BD:155:THR:HG22	42:BD:179:ARG:HA	1.84	0.57
42:BD:278:SER:HB3	42:BD:281:GLU:HG2	1.87	0.57
4:5:1039:U:H2'	4:5:1040:A:H8	1.69	0.57
4:5:2869:U:O2'	4:5:2873:U:OP1	2.23	0.57
4:5:3092:C:O2'	4:5:3094:A:OP2	2.20	0.57
13:AH:48:GLU:OE2	13:AH:88:ARG:NH1	2.37	0.57
19:AN:3:ARG:HB3	19:AN:6:SER:HB3	1.87	0.57
42:BD:290:ILE:HD11	47:BI:206:LEU:HD11	1.87	0.57
51:BM:121:VAL:HG11	51:BM:131:GLU:HG3	1.85	0.57
76:BI:79:GLU:O	76:BI:82:LEU:N	2.35	0.57
2:3:69:U:H2'	2:3:70:G:O4'	2.04	0.57
4:5:914:A:C2	39:BA:204:MET:HG2	2.39	0.57
4:5:1825:G:OP1	74:Bj:48:SER:OG	2.22	0.57
4:5:2266:U:O2'	5:6:12:C:O2'	2.23	0.57
4:5:3121:U:H1'	4:5:3122:A:H5''	1.86	0.57
29:AX:41:SER:O	29:AX:43:PHE:N	2.37	0.57
42:BD:120:LYS:O	42:BD:248:ARG:NH1	2.36	0.57
48:BJ:29:ARG:HG2	48:BJ:123:PHE:HZ	1.69	0.57
80:CA:277:HIS:HA	80:CA:280:LYS:HG2	1.87	0.57
80:CA:1190:TYR:HB3	80:CA:1238:ILE:HG13	1.87	0.57
1:2:76:A:N3	1:2:80:A:N6	2.52	0.57
1:2:1358:G:H4'	25:AT:130:ARG:HB3	1.86	0.57
4:5:208:C:OP2	41:BC:163:LYS:NZ	2.37	0.57
4:5:2104:A:OP1	55:BQ:85:ARG:NH2	2.38	0.57
6:AA:4:PRO:HG2	6:AA:6:THR:HG22	1.86	0.57
9:AD:72:LEU:HD22	16:AK:65:TYR:HD2	1.70	0.57
38:Ag:83:ALA:HB1	38:Ag:110:VAL:HG13	1.87	0.57
80:CA:697:ILE:HG23	80:CA:698:THR:HG23	1.86	0.57
1:2:69:G:H1	1:2:82:U:H3	1.52	0.57
1:2:332:U:OP1	14:AI:56:ARG:NH2	2.32	0.57
4:5:63:A:N3	4:5:78:U:O2'	2.36	0.57
4:5:2930:A:H2'	4:5:2931:C:C6	2.39	0.57
4:5:3067:C:H3'	55:BQ:62:ARG:HH22	1.68	0.57
62:BX:17:LYS:O	62:BX:21:THR:OG1	2.17	0.57
1:2:1490:C:H5'	1:2:1492:A:H1'	1.87	0.57
4:5:163:C:H2'	4:5:164:A:C8	2.40	0.57
11:AF:72:HIS:O	22:AQ:47:LYS:NZ	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:AU:53:LYS:HE2	26:AU:53:LYS:HA	1.87	0.57
26:AU:71:PRO:O	35:Ad:40:ARG:NH2	2.36	0.57
45:BG:94:PHE:HB3	45:BG:189:LEU:HD21	1.85	0.57
61:BW:108:LEU:HD23	61:BW:125:ARG:HD3	1.87	0.57
80:CA:1569:LEU:HD23	80:CA:1604:ILE:HD11	1.87	0.57
80:CA:432:LEU:HA	80:CA:437:GLY:HA3	1.87	0.57
1:2:523:G:H22	1:2:527:A:H3'	1.69	0.57
4:5:2901:G:O2'	4:5:3024:A:N1	2.37	0.57
13:AH:37:GLU:HG2	13:AH:38:LEU:HD12	1.87	0.57
29:AX:65:ASN:ND2	29:AX:116:ASP:OD2	2.38	0.57
1:2:68:A:H5'	12:AG:160:ARG:HH22	1.70	0.57
80:CA:248:HIS:O	80:CA:505:ARG:NH1	2.37	0.57
81:CB:125:ILE:O	81:CB:166:LYS:NZ	2.37	0.57
1:2:1477:G:H2'	1:2:1478:G:H8	1.70	0.56
4:5:1110:U:H2'	4:5:1111:U:C6	2.40	0.56
4:5:1909:A:H2'	4:5:1910:A:C8	2.40	0.56
20:AO:21:ALA:HB2	20:AO:98:GLY:HA3	1.86	0.56
22:AQ:47:LYS:HE3	22:AQ:82:ARG:HH12	1.70	0.56
37:Af:133:ALA:N	37:Af:140:TYR:O	2.37	0.56
38:Ag:182:ASN:ND2	38:Ag:185:GLN:OE1	2.38	0.56
1:2:629:U:H2'	1:2:630:A:H5'	1.87	0.56
1:2:1365:C:H5''	22:AQ:66:ARG:HH21	1.70	0.56
4:5:2795:U:OP1	78:Bn:61:LYS:NZ	2.38	0.56
32:Aa:12:LYS:HG3	32:Aa:15:ARG:HB2	1.88	0.56
40:BB:294:GLY:HA2	40:BB:359:ILE:HD12	1.86	0.56
80:CA:399:THR:HG21	80:CA:404:TRP:HD1	1.70	0.56
80:CA:695:SER:HA	80:CA:699:GLN:HB2	1.88	0.56
1:2:250:C:H2'	1:2:251:A:H8	1.70	0.56
1:2:1202:A:H1'	1:2:1207:C:H42	1.70	0.56
4:5:585:A:H2'	4:5:586:C:C6	2.40	0.56
4:5:675:C:O2'	4:5:679:U:OP1	2.22	0.56
4:5:1277:C:O2'	4:5:1278:A:O5'	2.21	0.56
4:5:2510:U:H2'	4:5:2511:A:H8	1.70	0.56
4:5:2555:G:O2'	63:BY:136:PHE:O	2.19	0.56
4:5:2662:G:H2'	4:5:2663:G:C8	2.39	0.56
4:5:2842:U:OP1	4:5:2844:C:N4	2.34	0.56
11:AF:63:GLN:HB3	11:AF:88:PRO:HA	1.86	0.56
41:BC:11:LEU:HD21	41:BC:156:LEU:HB2	1.86	0.56
1:2:144:U:O4	12:AG:137:ARG:NH2	2.21	0.56
4:5:531:G:H2'	4:5:532:A:C8	2.40	0.56
4:5:1029:G:H2'	4:5:1030:A:H8	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:2282:U:OP1	4:5:2973:G:O2'	2.23	0.56
7:AB:36:SER:HA	7:AB:41:ARG:HH12	1.70	0.56
14:AI:56:ARG:NH1	14:AI:174:GLY:O	2.35	0.56
21:AP:61:ARG:NH2	21:AP:88:GLU:OE2	2.38	0.56
27:AV:74:GLN:HE22	27:AV:83:TRP:H	1.53	0.56
1:2:513:U:H2'	1:2:514:G:C8	2.40	0.56
1:2:1183:A:N3	1:2:1210:C:O2'	2.35	0.56
2:3:9:A:H2'	2:3:10:A:H8	1.69	0.56
4:5:1310:G:O2'	4:5:2380:U:O2'	2.16	0.56
4:5:2538:U:O2'	4:5:2541:U:N3	2.36	0.56
11:AF:64:VAL:C	11:AF:65:ARG:HD3	2.31	0.56
16:AK:16:PHE:HB2	16:AK:76:LEU:HD23	1.86	0.56
18:AM:33:ARG:NH2	18:AM:99:GLU:O	2.36	0.56
1:2:887:A:H5''	20:AO:120:PRO:HB2	1.88	0.56
1:2:1502:G:N7	25:AT:102:ARG:NH2	2.53	0.56
1:2:1691:A:H2'	1:2:1692:G:H8	1.70	0.56
4:5:53:G:OP2	73:BI:48:ASN:ND2	2.31	0.56
4:5:1596:C:H2'	4:5:1597:C:C6	2.40	0.56
6:AA:120:LEU:HD21	6:AA:144:ILE:HD12	1.87	0.56
41:BC:125:ALA:HB1	41:BC:238:LEU:HB3	1.87	0.56
52:BN:61[A]:ALA:HA	52:BN:70[A]:PRO:HD2	1.87	0.56
57:BS:70:SER:OG	57:BS:92:ARG:NH1	2.38	0.56
63:BY:103:GLN:NE2	63:BY:106:GLN:OE1	2.38	0.56
1:2:1027:A:OP1	1:2:1789:G:O2'	2.21	0.56
4:5:656:A:H2'	4:5:657:A:H8	1.69	0.56
4:5:700:C:H2'	4:5:701:G:H8	1.69	0.56
4:5:1152:G:N2	4:5:1152:G:OP2	2.34	0.56
4:5:1244:A:N6	4:5:1271:A:OP1	2.38	0.56
4:5:3233:C:H2'	4:5:3234:A:C8	2.40	0.56
6:AA:105:GLY:N	6:AA:135:GLU:OE2	2.36	0.56
40:BB:196:ARG:O	40:BB:196:ARG:NH1	2.36	0.56
1:2:144:U:H2'	1:2:145:A:C8	2.41	0.56
1:2:399:A:H4'	10:AE:3:ARG:HG2	1.88	0.56
1:2:474:A:H5''	15:AJ:144:PRO:HD2	1.86	0.56
1:2:1504:G:OP1	25:AT:97:SER:OG	2.21	0.56
6:AA:140:ASN:ND2	27:AV:31:SER:O	2.26	0.56
29:AX:56:LYS:HE2	29:AX:96:VAL:HG23	1.88	0.56
30:AY:37:LYS:HD2	30:AY:57:VAL:HG23	1.87	0.56
32:Aa:45:VAL:HG23	32:Aa:46:GLU:H	1.71	0.56
50:BL:14:LEU:HD13	56:BR:149:LYS:HD3	1.86	0.56
80:CA:470:PHE:HA	80:CA:473:VAL:HG22	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:CA:921:LYS:HA	80:CA:924:ASN:HB2	1.87	0.56
80:CA:1818:LEU:HB2	80:CA:1957:LEU:HD21	1.88	0.56
82:CC:186:PHE:HD2	82:CC:189:ALA:H	1.52	0.56
1:2:625:C:H2'	1:2:626:U:C6	2.41	0.56
1:2:704:C:N4	1:2:732:G:O2'	2.39	0.56
4:5:2768:U:H2'	4:5:2769:A:H8	1.70	0.56
11:AF:79:ASN:HB2	11:AF:83:ARG:HH12	1.70	0.56
41:BC:160:GLN:NE2	41:BC:213:ASN:O	2.39	0.56
57:BS:39:ILE:HD13	57:BS:102:ARG:HG2	1.88	0.56
1:2:89:G:H21	1:2:452:A:H5'	1.70	0.56
1:2:219:A:OP1	12:AG:227:ARG:NH1	2.39	0.56
4:5:1039:U:H2'	4:5:1040:A:C8	2.39	0.56
4:5:1354:G:O2'	43:BE:8:LYS:NZ	2.39	0.56
4:5:2897:A:OP2	4:5:2899:C:N4	2.38	0.56
4:5:3002:C:O2'	40:BB:180:GLU:OE2	2.15	0.56
64:BZ:39:HIS:O	64:BZ:42:ARG:N	2.38	0.56
74:Bj:32:ASN:OD1	74:Bj:33:LYS:N	2.39	0.56
80:CA:504:CYS:SG	80:CA:505:ARG:N	2.78	0.56
1:2:885:G:H2'	1:2:886:U:C6	2.41	0.55
1:2:1108:G:H1	29:AX:22:ASN:ND2	2.03	0.55
4:5:185:C:OP1	62:BX:122:LYS:NZ	2.39	0.55
4:5:2112:U:H4'	4:5:2113:A:H5'	1.86	0.55
47:BI:49:CYS:HB3	47:BI:168:SER:HB3	1.88	0.55
1:2:520:A:H2'	1:2:521:A:C8	2.41	0.55
1:2:800:U:H2'	1:2:801:G:C8	2.41	0.55
1:2:1216:C:H2'	1:2:1444:A:N1	2.20	0.55
1:2:1251:U:O2	37:Af:135:HIS:NE2	2.34	0.55
4:5:638:C:H2'	4:5:639:G:C8	2.41	0.55
4:5:1799:A:H2'	4:5:1800:A:C8	2.42	0.55
11:AF:45:LYS:HE3	11:AF:46:TRP:CZ2	2.41	0.55
18:AM:134:SER:HA	18:AM:137:MET:HE1	1.89	0.55
48:BJ:10:ARG:NH2	48:BJ:151:SER:O	2.38	0.55
80:CA:1315:TRP:HB2	80:CA:1576:ARG:HG3	1.88	0.55
81:CB:74:ARG:HH21	81:CB:78:ARG:HH21	1.54	0.55
1:2:753:A:OP1	10:AE:187:ARG:N	2.40	0.55
2:3:57:C:H4'	2:3:63:G:N7	2.20	0.55
4:5:121:A:C2	45:BG:129:PRO:HG3	2.42	0.55
4:5:2357:A:H2'	4:5:2358:A:C8	2.40	0.55
13:AH:34:LEU:HD13	13:AH:38:LEU:HD22	1.88	0.55
38:Ag:200:ASN:H	38:Ag:215:GLY:HA2	1.72	0.55
38:Ag:211:ILE:HG23	38:Ag:225:LEU:HD22	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:BY:57:HIS:HB3	63:BY:61:LYS:HB3	1.87	0.55
80:CA:509:GLY:O	80:CA:514:LYS:NZ	2.39	0.55
4:5:359:U:HO2'	73:Bi:16:HIS:HD1	1.55	0.55
4:5:528:U:H2'	4:5:529:A:H8	1.70	0.55
4:5:3151:U:OP2	40:BB:132:LYS:NZ	2.30	0.55
80:CA:1383:ARG:NE	80:CA:1422:THR:OG1	2.40	0.55
1:2:12:U:H2'	1:2:13:C:C6	2.41	0.55
1:2:1415:U:OP1	23:AR:45:ARG:NH2	2.40	0.55
4:5:315:C:OP2	72:Bh:28:TYR:OH	2.21	0.55
4:5:1721:U:OP2	55:BQ:124:TYR:OH	2.19	0.55
4:5:2662:G:H2'	4:5:2663:G:H8	1.72	0.55
5:6:57:A:O2'	48:BJ:55:ARG:NH2	2.40	0.55
7:AB:158:SER:HA	7:AB:161:ILE:HD12	1.88	0.55
7:AB:176:VAL:HG22	7:AB:184:LEU:HD21	1.88	0.55
34:Ac:9:LEU:HB3	34:Ac:33:LEU:HD12	1.88	0.55
51:BM:46:ASP:OD2	51:BM:50:ARG:NH2	2.39	0.55
56:BR:71:LYS:HE3	56:BR:73:LYS:HD2	1.88	0.55
80:CA:467:LEU:HD12	80:CA:468:PRO:HD2	1.88	0.55
82:CC:201:VAL:HG23	82:CC:202:ILE:HD12	1.87	0.55
1:2:329:G:H5''	14:AI:98:LYS:HB3	1.88	0.55
4:5:800:G:H22	41:BC:101:ALA:HA	1.72	0.55
4:5:1264:G:N2	4:5:1265:U:O4	2.40	0.55
4:5:1580:A:OP2	4:5:2522:G:N2	2.37	0.55
4:5:2307:G:O2'	4:5:2310:U:OP2	2.22	0.55
18:AM:76:GLU:HA	18:AM:79:ALA:HB3	1.88	0.55
18:AM:103:LEU:HD11	18:AM:115:VAL:HG23	1.89	0.55
21:AP:22:LEU:HA	21:AP:25:LEU:HG	1.89	0.55
45:BG:81:THR:HG22	45:BG:155:ASN:HD21	1.71	0.55
56:BR:138:GLN:NE2	56:BR:138:GLN:O	2.40	0.55
80:CA:963:SER:O	80:CA:967:LEU:HD23	2.07	0.55
80:CA:1340:ASP:HB2	80:CA:1519:TYR:HD2	1.71	0.55
1:2:1071:U:H2'	1:2:1072:C:C6	2.41	0.55
1:2:1474:G:H2'	1:2:1475:A:H8	1.71	0.55
4:5:2882:U:H2'	4:5:2883:U:C6	2.42	0.55
38:Ag:9:LEU:HD13	38:Ag:313:TRP:HE1	1.71	0.55
58:BT:56:VAL:HG22	58:BT:65:VAL:HG22	1.89	0.55
4:5:1028:U:O4	48:BJ:94:ARG:NH1	2.37	0.55
4:5:1727:G:OP1	79:Bo:44:LYS:NZ	2.34	0.55
4:5:2369:G:H2'	4:5:2370:G:C8	2.42	0.55
4:5:3294:A:H5'	40:BB:128:LYS:HG3	1.88	0.55
6:AA:84:ARG:HE	6:AA:88:LYS:HZ3	1.54	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AH:141:ARG:HG2	28:AW:51:GLU:OE1	2.06	0.55
80:CA:1618:LEU:HD23	80:CA:1627:THR:HG21	1.89	0.55
1:2:494:U:N3	80:CA:881:TYR:OH	2.40	0.55
1:2:992:A:OP2	1:2:1011:G:N2	2.34	0.55
1:2:1474:G:H2'	1:2:1475:A:C8	2.41	0.55
4:5:406:G:OP1	4:5:1415:U:O2'	2.23	0.55
9:AD:154:ASP:OD1	9:AD:155:GLY:N	2.38	0.55
40:BB:83:PRO:O	40:BB:165:GLN:NE2	2.38	0.55
63:BY:57:HIS:HD2	63:BY:61:LYS:HD3	1.72	0.55
80:CA:288:LEU:HB2	80:CA:292:GLN:HE21	1.72	0.55
80:CA:1942:ARG:HB3	80:CA:1967:SER:HA	1.89	0.55
1:2:447:U:OP1	10:AE:49:ARG:NH1	2.39	0.55
1:2:962:C:H2'	1:2:963:A:O4'	2.07	0.55
1:2:1523:G:N2	1:2:1523:G:OP2	2.40	0.55
14:AI:39:GLY:O	14:AI:59:ARG:HB3	2.07	0.55
17:AL:109:VAL:HG12	17:AL:137:PHE:HB2	1.89	0.55
32:Aa:85:ARG:HG3	32:Aa:86:VAL:N	2.22	0.55
39:BA:83:HIS:HB3	79:Bo:64:VAL:HG22	1.88	0.55
80:CA:1547:ASP:HA	80:CA:1550:LEU:HD23	1.89	0.55
80:CA:1690:ARG:NH2	80:CA:1777:TYR:OH	2.40	0.55
2:3:142:C:H2'	2:3:143:U:C6	2.42	0.54
4:5:536:U:H2'	4:5:537:A:H8	1.72	0.54
4:5:715:A:H5''	64:BZ:115:LYS:HA	1.89	0.54
4:5:1054:A:H5''	4:5:2637:A:H61	1.71	0.54
9:AD:29:LEU:HB3	9:AD:32:GLU:HB2	1.88	0.54
13:AH:15:GLU:O	13:AH:19:GLN:NE2	2.39	0.54
55:BQ:15:VAL:HG23	55:BQ:17:VAL:HG22	1.88	0.54
1:2:1382:A:O2'	1:2:1383:G:OP1	2.21	0.54
4:5:1015:U:O2	4:5:1017:C:O2'	2.26	0.54
4:5:2419:A:H2'	4:5:2420:C:C6	2.42	0.54
6:AA:16:LEU:HD22	23:AR:91:LEU:HD23	1.89	0.54
9:AD:33:GLY:HA3	9:AD:53:THR:HG22	1.89	0.54
11:AF:26:ALA:HB3	22:AQ:28:LEU:HB3	1.90	0.54
17:AL:46:LYS:H	17:AL:46:LYS:HD2	1.72	0.54
29:AX:127:VAL:O	29:AX:130:VAL:HG12	2.07	0.54
38:Ag:267:PRO:HB2	38:Ag:269:TYR:HD1	1.72	0.54
42:BD:95:TRP:CE3	42:BD:198:TYR:HB3	2.42	0.54
48:BJ:15:GLU:OE1	48:BJ:132:ASN:ND2	2.40	0.54
56:BR:81:TYR:CE1	56:BR:90:MET:HE3	2.42	0.54
64:BZ:77:LYS:C	64:BZ:79:TRP:H	2.15	0.54
4:5:874:U:N3	4:5:2978:U:OP1	2.36	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:1108:U:H2'	4:5:1109:U:C6	2.42	0.54
42:BD:95:TRP:CZ3	42:BD:198:TYR:HB3	2.42	0.54
62:BX:55:GLU:HG3	62:BX:69:LYS:HZ3	1.72	0.54
80:CA:644:THR:O	80:CA:645:GLN:NE2	2.40	0.54
1:2:1247:U:H2'	1:2:1248:C:C6	2.42	0.54
4:5:887:G:H2'	4:5:888:A:C8	2.42	0.54
14:AI:152:ILE:HG13	14:AI:153:GLU:H	1.72	0.54
26:AU:25:THR:OG1	26:AU:115:GLU:OE1	2.25	0.54
26:AU:97:VAL:HA	26:AU:100:VAL:HG22	1.89	0.54
37:Af:100:LEU:HD12	37:Af:103:LEU:HD11	1.89	0.54
38:Ag:221:MET:SD	38:Ag:223:TRP:NE1	2.81	0.54
47:BI:212:GLU:HG2	47:BI:213:PHE:CD2	2.42	0.54
81:CB:74:ARG:NH1	81:CB:124:GLN:OE1	2.40	0.54
4:5:1278:A:O2'	4:5:1279:C:O5'	2.25	0.54
6:AA:183:ARG:NH2	6:AA:193:GLN:O	2.41	0.54
11:AF:76:ARG:O	11:AF:83:ARG:NH2	2.34	0.54
24:AS:50:ALA:HB2	24:AS:72:ILE:HD12	1.90	0.54
26:AU:106:ILE:HG13	26:AU:107:THR:HG23	1.90	0.54
29:AX:131:SER:O	29:AX:134:ALA:N	2.40	0.54
80:CA:1400:ARG:HH12	80:CA:1428:GLN:HB3	1.72	0.54
1:2:1591:C:H2'	1:2:1592:A:H8	1.71	0.54
1:2:1755:A:H2'	4:5:2256:A:N6	2.23	0.54
3:4:112:G:H2'	3:4:113:C:C6	2.43	0.54
4:5:534:U:H1'	56:BR:146:LYS:HD2	1.89	0.54
4:5:1336:U:H2'	4:5:1337:A:H8	1.72	0.54
4:5:2800:G:O6	64:BZ:42:ARG:NH2	2.40	0.54
40:BB:159:ARG:HG2	40:BB:182:GLN:HA	1.90	0.54
41:BC:99:MET:HE2	41:BC:102:PRO:HA	1.89	0.54
80:CA:1628:PRO:HA	80:CA:1631:SER:HB3	1.89	0.54
1:2:487:G:H2'	1:2:488:G:H8	1.73	0.54
4:5:1748:G:OP2	74:Bj:42:LYS:NZ	2.39	0.54
4:5:1765:U:H5'	55:BQ:43:LYS:HZ1	1.72	0.54
4:5:2228:A:H2'	4:5:2229:A:C8	2.42	0.54
4:5:2427:U:H2'	4:5:2428:U:C6	2.43	0.54
4:5:3165:A:H2'	4:5:3166:C:C6	2.43	0.54
16:AK:35:ILE:HG22	16:AK:37:THR:HG22	1.90	0.54
38:Ag:256:THR:OG1	38:Ag:259:GLY:O	2.21	0.54
42:BD:85:ARG:HH12	42:BD:254:LYS:H	1.53	0.54
66:Bb:36:GLN:OE1	66:Bb:38:LYS:NZ	2.38	0.54
80:CA:999:ASN:ND2	80:CA:1021:ASP:OD2	2.36	0.54
80:CA:1903:LEU:HD11	80:CA:1919:ARG:HB3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:765:C:N4	49:BK:176:GLU:OE2	2.40	0.54
4:5:911:C:H42	39:BA:3:ARG:HD3	1.73	0.54
4:5:2446:U:O2'	4:5:2447:A:OP1	2.24	0.54
10:AE:129:VAL:HG22	10:AE:139:VAL:HG12	1.90	0.54
12:AG:47:GLY:O	12:AG:115:LYS:NZ	2.32	0.54
22:AQ:93:HIS:HA	22:AQ:97:VAL:HB	1.89	0.54
38:Ag:127:ARG:HA	38:Ag:150:TRP:HB2	1.90	0.54
41:BC:317:PRO:C	41:BC:319:LYS:H	2.15	0.54
42:BD:20:PHE:O	42:BD:24:ARG:NH2	2.41	0.54
46:BH:41:ILE:HD13	46:BH:71:VAL:HG22	1.90	0.54
59:BU:54:LEU:HD11	59:BU:119:GLY:HA3	1.90	0.54
78:Bn:2:VAL:N	78:Bn:90:HIS:O	2.41	0.54
80:CA:495:LYS:NZ	80:CA:674:PHE:O	2.41	0.54
1:2:30:G:H2'	1:2:31:C:C6	2.42	0.54
1:2:68:A:N6	12:AG:132:ARG:O	2.41	0.54
4:5:528:U:H2'	4:5:529:A:C8	2.43	0.54
4:5:710:A:H2'	4:5:711:A:C8	2.43	0.54
4:5:1246:G:O2'	4:5:1247:U:O4'	2.26	0.54
8:AC:119:LYS:HG3	8:AC:120:GLU:OE1	2.08	0.54
16:AK:14:TYR:HD1	16:AK:35:ILE:HD11	1.73	0.54
25:AT:84:LYS:HB3	25:AT:94:ILE:HD12	1.90	0.54
39:BA:30:ARG:O	39:BA:163:ARG:NH2	2.30	0.54
80:CA:910:LEU:HD23	80:CA:913:ILE:HD12	1.90	0.54
80:CA:1201:ARG:HH21	80:CA:1205:TRP:HH2	1.54	0.54
80:CA:1879:LYS:NZ	80:CA:1880:HIS:O	2.37	0.54
4:5:633:C:O2'	69:Be:21:ARG:O	2.25	0.54
4:5:640:U:H2'	4:5:641:C:C6	2.42	0.54
4:5:1747:G:H21	74:Bj:2:ALA:HA	1.73	0.54
1:2:397:A:H4'	14:AI:50:GLY:HA2	1.89	0.53
1:2:1785:U:H2'	1:2:1786:G:H8	1.73	0.53
2:3:150:G:OP1	61:BW:27:ARG:NH2	2.39	0.53
3:4:84:A:H2'	3:4:85:G:C8	2.43	0.53
4:5:2440:G:H2'	4:5:2441:A:H8	1.73	0.53
49:BK:62:THR:O	49:BK:64:LYS:N	2.40	0.53
52:BN:110[A]:PRO:O	52:BN:112[A]:TYR:N	2.40	0.53
56:BR:109:ASP:OD2	56:BR:113:ARG:NH1	2.41	0.53
80:CA:271:LYS:HG3	80:CA:273:SER:H	1.74	0.53
80:CA:1614:SER:HA	80:CA:1644:ARG:HB3	1.91	0.53
1:2:169:A:OP2	12:AG:137:ARG:NH2	2.37	0.53
1:2:482:U:H2'	1:2:483:A:C8	2.44	0.53
1:2:947:U:H2'	1:2:948:G:H8	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1590:G:OP1	25:AT:91:TYR:HB2	2.09	0.53
2:3:145:U:H2'	2:3:146:U:C6	2.44	0.53
4:5:1695:U:O2'	4:5:1749:A:N1	2.37	0.53
4:5:3379:C:H4'	40:BB:315:GLY:HA2	1.91	0.53
9:AD:172:THR:O	9:AD:173:ARG:NH1	2.39	0.53
10:AE:175:PHE:HE1	10:AE:198:LYS:HD2	1.73	0.53
54:BP:19:PRO:HD3	54:BP:53:PHE:CD1	2.43	0.53
80:CA:425:ILE:HA	80:CA:461:ILE:HG22	1.91	0.53
80:CA:1001:GLU:HB2	80:CA:1017:ALA:HB3	1.90	0.53
1:2:1220:C:H5''	16:AK:52:LYS:HE3	1.91	0.53
1:2:1483:A:N3	1:2:1607:G:O2'	2.31	0.53
3:4:90:U:H2'	3:4:91:G:O4'	2.08	0.53
4:5:1480:G:O2'	4:5:1871:U:O4	2.19	0.53
4:5:2366:C:H2'	4:5:2367:A:H8	1.73	0.53
12:AG:88:ARG:HB3	12:AG:91:GLU:HB2	1.89	0.53
51:BM:18:VAL:HG13	51:BM:19:LEU:HD12	1.90	0.53
66:Bb:52:ARG:HH11	66:Bb:52:ARG:HG3	1.73	0.53
80:CA:825:GLU:HG3	80:CA:929:ILE:HD11	1.90	0.53
80:CA:1401:ARG:HH22	80:CA:1457:ILE:HD11	1.72	0.53
80:CA:1487:ILE:HD11	80:CA:1491:ARG:HB2	1.90	0.53
1:2:205:U:H2'	1:2:206:A:H8	1.73	0.53
1:2:265:A:OP2	12:AG:194:LYS:NZ	2.39	0.53
1:2:447:U:H2'	1:2:448:C:O4'	2.08	0.53
4:5:1724:U:H1'	4:5:1725:C:C6	2.43	0.53
7:AB:144:ARG:HB3	7:AB:208:GLN:CG	2.35	0.53
21:AP:76:VAL:O	21:AP:95:GLY:N	2.35	0.53
26:AU:52:LYS:NZ	26:AU:54:GLY:HA2	2.23	0.53
27:AV:79:LEU:HG	27:AV:80:LYS:H	1.73	0.53
37:Af:141:CYS:SG	37:Af:142:GLY:N	2.81	0.53
80:CA:1000:ILE:HD11	80:CA:1084:VAL:HG12	1.90	0.53
80:CA:1363:ILE:HD11	80:CA:1374:ILE:HD11	1.91	0.53
1:2:1693:A:H2'	1:2:1694:A:H8	1.74	0.53
4:5:435:C:H2'	4:5:436:A:H8	1.74	0.53
4:5:616:G:H2'	4:5:617:G:C8	2.43	0.53
7:AB:129:THR:HG22	7:AB:176:VAL:HG13	1.89	0.53
80:CA:550:ARG:HA	80:CA:553:ILE:HG22	1.90	0.53
81:CB:218:LEU:HD13	81:CB:237:ILE:HB	1.91	0.53
82:CC:326:LEU:O	82:CC:329:GLN:NE2	2.42	0.53
1:2:140:A:OP2	1:2:140:A:H4'	2.08	0.53
1:2:1393:C:H2'	1:2:1394:G:H8	1.73	0.53
1:2:1617:U:H2'	1:2:1618:C:C6	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:9:C:OP1	57:BS:28:SER:OG	2.27	0.53
9:AD:136:VAL:HG22	9:AD:186:VAL:HG22	1.91	0.53
31:AZ:35:ARG:O	31:AZ:37:GLN:NE2	2.35	0.53
54:BP:19:PRO:HB3	54:BP:53:PHE:HA	1.90	0.53
56:BR:24:LEU:HD11	56:BR:59:VAL:HG21	1.89	0.53
57:BS:17:ARG:HG2	57:BS:22:HIS:HA	1.89	0.53
70:Bf:10:ARG:HH21	75:Bk:3:ALA:HB1	1.73	0.53
80:CA:525:LEU:HD11	80:CA:621:VAL:HG21	1.90	0.53
4:5:1460:A:H2'	4:5:1461:A:H8	1.74	0.53
4:5:1799:A:H2'	4:5:1800:A:H8	1.72	0.53
4:5:2242:A:H5''	39:BA:244:GLY:HA3	1.91	0.53
40:BB:292:ALA:HB1	40:BB:295:ALA:HB3	1.91	0.53
67:Bc:55:LEU:HB2	67:Bc:95:PRO:HD3	1.90	0.53
80:CA:1878:SER:HB3	80:CA:1931:ILE:HB	1.89	0.53
1:2:479:C:O3'	15:AJ:120:LYS:NZ	2.42	0.53
1:2:903:U:O2'	1:2:905:A:N7	2.34	0.53
1:2:1229:G:N2	1:2:1256:A:H62	2.07	0.53
1:2:1360:A:H2	1:2:1364:G:C6	2.26	0.53
1:2:1389:C:N4	1:2:1391:A:O4'	2.41	0.53
1:2:1487:A:H2'	1:2:1488:G:C8	2.44	0.53
4:5:1176:C:H2'	4:5:1177:G:N2	2.24	0.53
4:5:1562:C:H2'	4:5:1563:C:C6	2.44	0.53
4:5:1757:A:H5''	58:BT:94:ARG:HH22	1.72	0.53
4:5:2661:G:H2'	4:5:2662:G:H8	1.74	0.53
23:AR:24:LEU:HD23	23:AR:34:LEU:HD22	1.91	0.53
39:BA:47:GLN:HA	39:BA:84:THR:HG22	1.91	0.53
53:BO:168:LEU:HD12	53:BO:172:GLN:HB3	1.90	0.53
64:BZ:77:LYS:O	64:BZ:79:TRP:N	2.42	0.53
1:2:567:A:H1'	36:Ae:14:VAL:HG23	1.89	0.53
1:2:1531:G:N2	25:AT:48:GLN:OE1	2.41	0.53
4:5:1101:G:OP2	44:BF:196:LYS:NZ	2.37	0.53
4:5:1573:G:H2'	4:5:1574:C:O4'	2.09	0.53
4:5:2441:A:H2'	4:5:2442:G:H8	1.74	0.53
4:5:2442:G:H1	4:5:2505:U:H3	1.56	0.53
4:5:3319:U:O2'	4:5:3320:A:OP1	2.24	0.53
6:AA:84:ARG:HE	6:AA:88:LYS:NZ	2.06	0.53
9:AD:88:ALA:O	80:CA:1079:GLN:NE2	2.37	0.53
9:AD:95:GLY:HA2	9:AD:101:GLN:NE2	2.24	0.53
12:AG:24:ILE:O	12:AG:26:VAL:N	2.42	0.53
24:AS:52:VAL:HG21	24:AS:69:ILE:HD11	1.91	0.53
40:BB:76:VAL:HG12	40:BB:325:LYS:HA	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:Bb:17:VAL:HG11	66:Bb:92:ILE:HD12	1.91	0.53
69:Be:49:ILE:HD11	69:Be:71:VAL:HG22	1.90	0.53
80:CA:356:LYS:HG3	80:CA:381:THR:HB	1.90	0.53
80:CA:748:PHE:HZ	80:CA:754:TRP:HD1	1.54	0.53
82:CC:366:SER:HB2	82:CC:368:ARG:NH1	2.24	0.53
1:2:1104:U:OP1	29:AX:14:LYS:NZ	2.41	0.53
4:5:297:G:O6	51:BM:12:ARG:NH1	2.41	0.53
4:5:1240:A:H61	4:5:1244:A:H2'	1.74	0.53
4:5:2500:A:O2'	4:5:2501:U:OP1	2.27	0.53
4:5:2736:A:OP1	57:BS:92:ARG:NH2	2.42	0.53
21:AP:39:ALA:HA	21:AP:42:ARG:HE	1.73	0.53
38:Ag:42:LEU:HB2	38:Ag:61:PHE:HB2	1.91	0.53
80:CA:433:HIS:O	80:CA:706:ARG:NH2	2.42	0.53
80:CA:481:ARG:HH11	80:CA:485:MET:HG3	1.74	0.53
80:CA:1675:ARG:NH1	80:CA:1678:GLU:OE2	2.36	0.53
1:2:539:G:O2'	1:2:540:G:O5'	2.23	0.52
1:2:936:G:N7	32:Aa:15:ARG:NH2	2.57	0.52
4:5:292:U:OP2	51:BM:68:ARG:NH2	2.40	0.52
4:5:541:U:H2'	4:5:542:G:C8	2.44	0.52
4:5:2986:U:H2'	4:5:2987:A:H8	1.74	0.52
30:AY:8:ARG:NH2	30:AY:26:ASP:OD2	2.38	0.52
32:Aa:46:GLU:HB2	32:Aa:49:ALA:H	1.73	0.52
45:BG:195:SER:OG	45:BG:197:VAL:O	2.27	0.52
76:Bl:98:LYS:HG3	76:Bl:118:THR:HG21	1.90	0.52
4:5:144:A:OP1	45:BG:193:LYS:NZ	2.29	0.52
4:5:620:U:H1'	69:Be:60:ARG:HH22	1.75	0.52
4:5:1420:C:OP2	41:BC:193:LYS:NZ	2.43	0.52
4:5:2137:U:OP2	4:5:2142:A:N6	2.33	0.52
4:5:2961:G:H2'	4:5:2962:U:C6	2.44	0.52
26:AU:20:ILE:N	26:AU:94:GLU:OE1	2.41	0.52
53:BO:122:ALA:HB3	53:BO:143:PRO:HB2	1.92	0.52
78:Bn:26:THR:HA	78:Bn:93:LEU:HD11	1.91	0.52
80:CA:381:THR:C	80:CA:384:MET:HE1	2.33	0.52
80:CA:1141:ASN:HB3	80:CA:1143:MET:SD	2.49	0.52
80:CA:1374:ILE:HB	80:CA:1459:ILE:HG12	1.90	0.52
1:2:733:A:N3	1:2:736:C:N4	2.56	0.52
1:2:836:U:H2'	1:2:837:G:C8	2.45	0.52
1:2:1164:G:H2'	1:2:1165:G:H8	1.73	0.52
4:5:1088:U:C2	4:5:1089:G:C8	2.97	0.52
4:5:2496:C:H2'	4:5:2497:U:C6	2.44	0.52
4:5:2940:A:OP2	40:BB:2:SER:N	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:3322:A:H2'	4:5:3323:A:C8	2.44	0.52
20:AO:107:ARG:NH1	34:Ac:60:GLU:OE1	2.43	0.52
23:AR:20:TYR:O	23:AR:23:LYS:HB2	2.09	0.52
29:AX:89:ASN:HB2	29:AX:92:CYS:SG	2.49	0.52
80:CA:935:LYS:HB2	80:CA:1090:ILE:HD11	1.92	0.52
80:CA:962:PRO:HG2	80:CA:967:LEU:HD21	1.90	0.52
80:CA:998:ILE:HG21	80:CA:1018:LEU:HD23	1.92	0.52
1:2:329:G:H2'	1:2:330:G:H8	1.75	0.52
1:2:939:A:H2'	1:2:940:A:C8	2.44	0.52
1:2:1259:U:H2'	1:2:1260:U:C6	2.45	0.52
4:5:2177:G:O2'	39:BA:126:LEU:HA	2.09	0.52
5:6:8:U:O2'	5:6:21:A:N1	2.42	0.52
8:AC:35:TRP:CE2	8:AC:37:PRO:HB3	2.43	0.52
26:AU:70:THR:O	35:Ad:40:ARG:NH1	2.35	0.52
38:Ag:262:VAL:HG13	38:Ag:271:VAL:HB	1.90	0.52
51:BM:183:THR:HG22	51:BM:187:ARG:HB2	1.91	0.52
58:BT:98:THR:C	58:BT:99:LYS:HD2	2.35	0.52
80:CA:428:GLU:OE1	80:CA:430:HIS:NE2	2.35	0.52
80:CA:1434:HIS:CG	80:CA:1464:LEU:HD21	2.45	0.52
1:2:555:A:O2'	1:2:556:A:O5'	2.20	0.52
1:2:623:A:N6	1:2:970:A:OP1	2.40	0.52
1:2:1251:U:H1'	37:Af:135:HIS:CD2	2.44	0.52
4:5:1389:G:H5''	68:Bd:101:SER:HB3	1.92	0.52
4:5:1659:U:H2'	4:5:1660:C:C6	2.44	0.52
4:5:1791:C:H2'	4:5:1792:C:C6	2.44	0.52
4:5:2357:A:H2'	4:5:2358:A:H8	1.74	0.52
4:5:2441:A:H2'	4:5:2442:G:C8	2.45	0.52
13:AH:76:LYS:HA	13:AH:79:ARG:NH1	2.24	0.52
51:BM:9:GLU:HB2	72:Bh:44:VAL:HG21	1.91	0.52
80:CA:1190:TYR:N	80:CA:1237:VAL:O	2.36	0.52
81:CB:2:LEU:O	81:CB:37:LYS:NZ	2.43	0.52
1:2:258:C:O2	14:AI:178:ARG:NH1	2.39	0.52
1:2:590:C:H2'	1:2:591:A:H8	1.74	0.52
4:5:966:U:H2'	4:5:967:A:C8	2.45	0.52
4:5:2522:G:O6	39:BA:70:ARG:NH2	2.43	0.52
10:AE:211:LYS:NZ	10:AE:215:ASP:OD1	2.29	0.52
22:AQ:45:ARG:HG2	22:AQ:49:TYR:CE2	2.45	0.52
42:BD:50:ARG:NH1	42:BD:147:ASP:OD2	2.43	0.52
59:BU:86:ARG:HH11	59:BU:90:GLY:HA2	1.73	0.52
67:Bc:7:VAL:HG13	67:Bc:78:LYS:HA	1.92	0.52
80:CA:1183:PHE:HB2	80:CA:1186:LYS:HE3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:705:U:O2'	1:2:706:A:O5'	2.22	0.52
4:5:188:U:O2'	4:5:207:U:O2	2.24	0.52
4:5:2942:C:H5''	4:5:2943:G:H5''	1.91	0.52
49:BK:76:THR:O	49:BK:79:GLU:N	2.31	0.52
80:CA:1616:CYS:O	80:CA:1627:THR:OG1	2.19	0.52
80:CA:1866:GLU:HB2	80:CA:1875:THR:HB	1.92	0.52
82:CC:207:LYS:NZ	82:CC:209:LYS:O	2.41	0.52
1:2:304:U:H2'	1:2:305:C:C6	2.45	0.52
1:2:853:G:O5'	55:BQ:173:ARG:NH2	2.43	0.52
1:2:925:G:H2'	1:2:926:A:C8	2.45	0.52
1:2:1648:A:H2'	1:2:1649:G:C8	2.43	0.52
4:5:1084:A:H2'	4:5:1085:A:C8	2.45	0.52
4:5:1206:G:OP1	47:BI:157:TYR:OH	2.22	0.52
4:5:1553:U:H4'	4:5:1554:U:H5'	1.92	0.52
8:AC:168:ARG:HD3	8:AC:170:ILE:HD11	1.91	0.52
25:AT:29:GLU:HG2	25:AT:107:ALA:HB2	1.92	0.52
29:AX:107:PHE:CD1	29:AX:123:LYS:HB3	2.44	0.52
59:BU:15:LEU:HD13	59:BU:51:ALA:HB3	1.91	0.52
80:CA:544:GLU:HA	80:CA:547:LYS:HB3	1.91	0.52
80:CA:838:PHE:HE1	80:CA:899:VAL:HA	1.74	0.52
80:CA:1177:TRP:O	80:CA:1181:LYS:NZ	2.42	0.52
4:5:1390:A:N6	4:5:1418:A:O2'	2.42	0.52
4:5:1460:A:H2'	4:5:1461:A:C8	2.45	0.52
4:5:1597:C:H5'	4:5:1696:A:H1'	1.92	0.52
4:5:1805:C:H2'	4:5:1806:A:H8	1.75	0.52
4:5:2424:A:OP1	51:BM:90:ASN:ND2	2.42	0.52
7:AB:146:GLN:HE21	7:AB:206:PRO:HG3	1.74	0.52
9:AD:62:ASN:N	80:CA:921:LYS:HE3	2.22	0.52
10:AE:148:ARG:NH2	12:AG:201:GLN:OE1	2.40	0.52
36:Ae:41:THR:HA	36:Ae:45:VAL:HG22	1.92	0.52
50:BL:17:VAL:HG21	50:BL:74:ARG:HG3	1.90	0.52
55:BQ:134:HIS:HE1	55:BQ:136:ARG:HB3	1.70	0.52
80:CA:1423:LEU:HD11	80:CA:1438:LEU:HD13	1.91	0.52
1:2:332:U:O2'	14:AI:5:ARG:NH2	2.43	0.52
1:2:841:U:H2'	1:2:842:C:C6	2.45	0.52
1:2:1437:U:H2'	1:2:1438:G:C8	2.45	0.52
18:AM:126:TRP:CD1	18:AM:128:ALA:HB3	2.45	0.52
27:AV:17:CYS:HB2	27:AV:56:SER:HB3	1.92	0.52
38:Ag:159:ASN:ND2	38:Ag:166:SER:O	2.43	0.52
80:CA:1202:VAL:HG22	80:CA:1238:ILE:HD13	1.92	0.52
81:CB:143:ASP:OD1	81:CB:144:SER:N	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:546:C:H5'	4:5:547:G:C4	2.45	0.51
4:5:1087:G:OP1	65:Ba:29:TYR:OH	2.24	0.51
4:5:2407:C:H2'	4:5:2408:U:H6	1.75	0.51
7:AB:229:MET:HA	7:AB:229:MET:HE3	1.92	0.51
21:AP:85:ILE:HG22	21:AP:112:LEU:HD23	1.90	0.51
22:AQ:73:GLY:O	22:AQ:76:SER:N	2.41	0.51
81:CB:215:ILE:HG21	81:CB:270:LEU:HD23	1.91	0.51
1:2:1145:U:H5	1:2:1633:A:N1	2.08	0.51
1:2:1389:C:OP1	23:AR:48:ASN:ND2	2.32	0.51
4:5:1521:G:H5'	61:BW:71:THR:HG21	1.93	0.51
4:5:1807:G:O2'	4:5:2559:U:O4	2.28	0.51
4:5:1913:A:N3	4:5:2120:A:H2'	2.25	0.51
4:5:3160:U:H2'	4:5:3161:C:C6	2.45	0.51
12:AG:48:TYR:OH	12:AG:116:LYS:NZ	2.36	0.51
12:AG:163:THR:HG22	12:AG:168:THR:HG22	1.92	0.51
24:AS:74:GLN:HG2	24:AS:101:LEU:HD21	1.92	0.51
30:AY:78:SER:OG	30:AY:81:GLU:OE1	2.21	0.51
36:Ae:50:VAL:HA	36:Ae:54:ARG:HA	1.93	0.51
80:CA:763:LEU:HB3	80:CA:766:ARG:HB3	1.91	0.51
80:CA:1250:ASN:OD1	80:CA:1253:THR:OG1	2.28	0.51
80:CA:1638:ILE:HG22	80:CA:1640:HIS:H	1.75	0.51
1:2:153:G:H2'	1:2:154:G:H8	1.76	0.51
1:2:386:G:OP2	14:AI:25:ARG:NH2	2.43	0.51
1:2:788:A:H2'	10:AE:19:LEU:HD22	1.93	0.51
1:2:895:G:N2	20:AO:38:THR:HG21	2.25	0.51
1:2:1483:A:H2'	1:2:1484:G:C8	2.45	0.51
9:AD:7:LYS:HD2	26:AU:27:THR:HG21	1.91	0.51
12:AG:2:LYS:HB3	12:AG:108:VAL:HG23	1.92	0.51
12:AG:142:ARG:O	12:AG:146:GLY:N	2.35	0.51
1:2:835:U:H2'	1:2:836:U:H5	1.75	0.51
4:5:422:A:N1	4:5:2362:C:O2'	2.36	0.51
4:5:2504:U:H2'	4:5:2505:U:C6	2.46	0.51
4:5:2883:U:H2'	4:5:2884:C:H6	1.74	0.51
7:AB:32:ILE:HD11	7:AB:46:THR:HG23	1.92	0.51
48:BJ:109:HIS:NE2	48:BJ:114:ILE:HG21	2.26	0.51
80:CA:345:ASP:OD1	80:CA:420:LYS:NZ	2.43	0.51
80:CA:656:ASP:OD2	80:CA:689:ARG:NH2	2.44	0.51
1:2:514:G:H2'	1:2:515:A:C8	2.45	0.51
1:2:623:A:O2'	1:2:624:G:OP1	2.24	0.51
1:2:751:G:H2'	1:2:752:A:C8	2.45	0.51
1:2:1476:C:O2'	25:AT:45:MET:SD	2.68	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:3:149:A:H2'	2:3:150:G:C8	2.45	0.51
4:5:107:A:O2'	4:5:324:A:N3	2.34	0.51
4:5:138:U:H2'	4:5:139:G:H8	1.76	0.51
4:5:1895:A:O2'	4:5:3053:G:H4'	2.11	0.51
4:5:3110:C:O3'	46:BH:155:SER:OG	2.28	0.51
21:AP:83:MET:SD	21:AP:116:LEU:HB2	2.49	0.51
24:AS:117:LYS:O	24:AS:120:ARG:NH1	2.43	0.51
37:Af:125:THR:OG1	37:Af:143:LYS:NZ	2.43	0.51
38:Ag:11:GLY:HA2	38:Ag:52:GLN:HA	1.91	0.51
39:BA:180:LEU:HD11	79:Bo:26:VAL:HG21	1.92	0.51
43:BE:4:GLN:HB2	68:Bd:75:LEU:HB2	1.93	0.51
47:BI:101:LYS:HE2	47:BI:101:LYS:HA	1.92	0.51
53:BO:47:TYR:OH	53:BO:57:ALA:O	2.28	0.51
61:BW:131:ASP:N	61:BW:131:ASP:OD1	2.43	0.51
80:CA:1319:LYS:HE3	80:CA:1321:HIS:HB2	1.92	0.51
4:5:716:A:C6	64:BZ:117:ARG:HG3	2.46	0.51
18:AM:91:VAL:HG21	18:AM:97:LEU:HD13	1.93	0.51
29:AX:41:SER:O	29:AX:41:SER:OG	2.26	0.51
38:Ag:222:LEU:C	38:Ag:223:TRP:HD1	2.19	0.51
39:BA:102:LEU:HD13	39:BA:166:ILE:HD11	1.93	0.51
63:BY:10:VAL:O	63:BY:83:THR:OG1	2.19	0.51
71:Bg:9:LEU:HB3	71:Bg:17:LEU:HD21	1.93	0.51
80:CA:1389:LEU:HD21	80:CA:1457:ILE:HD13	1.93	0.51
80:CA:1871:ASN:ND2	80:CA:1967:SER:O	2.44	0.51
1:2:189:C:H2'	1:2:190:C:C6	2.45	0.51
1:2:1202:A:H1'	1:2:1207:C:N4	2.26	0.51
1:2:1609:U:H5''	22:AQ:75:VAL:HB	1.92	0.51
1:2:1753:A:H2'	1:2:1754:A:C8	2.46	0.51
2:3:40:A:H2'	2:3:41:A:C8	2.45	0.51
4:5:627:U:H2'	4:5:628:A:C8	2.46	0.51
4:5:3164:C:O2'	4:5:3165:A:H8	1.93	0.51
32:Aa:82:ARG:HD3	32:Aa:85:ARG:NH2	2.22	0.51
47:BI:102:MET:HE3	47:BI:112:GLN:HE21	1.75	0.51
49:BK:62:THR:O	49:BK:65:TYR:N	2.32	0.51
55:BQ:21:LYS:HA	55:BQ:53:LYS:HD3	1.93	0.51
62:BX:41:ALA:O	62:BX:125:LYS:NZ	2.31	0.51
63:BY:23:VAL:HG12	63:BY:45:GLY:HA3	1.92	0.51
80:CA:553:ILE:HG13	80:CA:593:PHE:HB3	1.92	0.51
80:CA:765:GLU:OE2	81:CB:228:ARG:NH1	2.44	0.51
1:2:523:G:H1	1:2:527:A:H5''	1.76	0.51
1:2:1241:G:N3	21:AP:79:HIS:ND1	2.59	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:1188:U:OP1	4:5:1210:U:O2'	2.24	0.51
4:5:2352:A:H5''	53:BO:83:TRP:O	2.11	0.51
8:AC:90:THR:OG1	8:AC:93:GLY:O	2.25	0.51
80:CA:1336:LYS:O	80:CA:1516:ALA:N	2.44	0.51
1:2:200:A:H2'	1:2:201:G:H8	1.76	0.51
4:5:3013:U:H2'	4:5:3014:U:C6	2.46	0.51
5:6:8:U:O2	5:6:15:A:N6	2.44	0.51
16:AK:46:LEU:HD12	16:AK:55:VAL:HG21	1.93	0.51
48:BJ:90:GLN:HE21	48:BJ:172:LEU:HD21	1.76	0.51
49:BK:2:ALA:HB3	64:BZ:41:HIS:CE1	2.46	0.51
49:BK:114:GLN:NE2	49:BK:118:GLU:OE2	2.41	0.51
62:BX:86:THR:HG22	62:BX:96:PRO:HA	1.92	0.51
63:BY:103:GLN:HE21	63:BY:106:GLN:HE22	1.59	0.51
80:CA:282:VAL:O	80:CA:369:LYS:NZ	2.41	0.51
1:2:579:A:N6	1:2:1438:G:O2'	2.44	0.51
1:2:903:U:H5''	20:AO:135:ARG:HH21	1.76	0.51
1:2:1472:C:OP1	11:AF:102:ARG:NH2	2.38	0.51
1:2:1648:A:H2'	1:2:1649:G:H8	1.76	0.51
4:5:2406:C:H2'	4:5:2407:C:C6	2.46	0.51
27:AV:53:TYR:OH	27:AV:76:ASP:OD1	2.28	0.51
40:BB:35:ASP:OD2	40:BB:191:LYS:NZ	2.30	0.51
67:Bc:4:LEU:O	67:Bc:79:ARG:NH1	2.44	0.51
69:Be:16:TYR:OH	69:Be:89:LEU:O	2.23	0.51
80:CA:1590:ASP:HB3	80:CA:1595:GLY:HA3	1.93	0.51
1:2:406:U:H2'	1:2:407:A:C8	2.46	0.50
1:2:495:C:H4'	1:2:496:G:C8	2.47	0.50
1:2:1461:C:OP1	24:AS:145:ARG:NH1	2.45	0.50
1:2:1471:A:H2	1:2:1474:G:N3	2.09	0.50
4:5:504:A:O2'	41:BC:315:LYS:NZ	2.44	0.50
4:5:799:G:H2'	4:5:801:A:H62	1.75	0.50
4:5:1219:C:H4'	4:5:1223:A:H5'	1.92	0.50
4:5:2351:U:H2'	4:5:2352:A:H8	1.76	0.50
4:5:2986:U:H2'	4:5:2987:A:C8	2.46	0.50
9:AD:212:LYS:HE2	9:AD:212:LYS:HA	1.93	0.50
13:AH:141:ARG:NH1	28:AW:49:GLU:OE2	2.44	0.50
21:AP:18:ARG:HB2	21:AP:36:LEU:HD12	1.94	0.50
23:AR:21:TYR:HD1	23:AR:58:MET:HE1	1.76	0.50
38:Ag:149:ASP:H	38:Ag:175:ASP:CG	2.19	0.50
80:CA:572:LYS:HA	80:CA:575:TYR:HB3	1.93	0.50
80:CA:791:MET:HE2	80:CA:791:MET:N	2.26	0.50
80:CA:948:ASP:O	80:CA:987:ARG:NH2	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:CA:1596:VAL:HG12	80:CA:1600:LEU:HD23	1.92	0.50
81:CB:27:PRO:O	81:CB:31:ARG:HG2	2.11	0.50
1:2:523:G:H21	1:2:528:U:H5	1.59	0.50
1:2:706:A:H2	1:2:732:G:H4'	1.75	0.50
3:4:53:U:H4'	48:BJ:8:PRO:HB2	1.93	0.50
4:5:2883:U:H2'	4:5:2884:C:C6	2.46	0.50
18:AM:131:ASP:O	18:AM:134:SER:N	2.41	0.50
37:Af:111:GLU:N	37:Af:112:GLY:HA2	2.26	0.50
60:BV:4:GLU:HB2	60:BV:13:ILE:HB	1.91	0.50
80:CA:1494:ASP:N	80:CA:1494:ASP:OD1	2.44	0.50
1:2:612:U:OP2	29:AX:5:LYS:NZ	2.43	0.50
1:2:925:G:H2'	1:2:926:A:H8	1.77	0.50
2:3:75:G:OP1	75:Bk:31:THR:N	2.40	0.50
3:4:61:G:OP1	42:BD:276:LYS:NZ	2.26	0.50
4:5:1064:A:H4'	4:5:1065:A:O5'	2.10	0.50
4:5:1203:A:H2'	4:5:1204:A:H8	1.76	0.50
4:5:1355:A:H4'	4:5:1356:U:O5'	2.11	0.50
4:5:3294:A:H2'	4:5:3295:A:O4'	2.11	0.50
4:5:3306:U:OP1	40:BB:269:GLN:NE2	2.40	0.50
9:AD:29:LEU:HD21	9:AD:69:LEU:HD11	1.91	0.50
11:AF:91:GLU:OE2	11:AF:107:LYS:NZ	2.35	0.50
13:AH:75:THR:O	13:AH:79:ARG:NH1	2.44	0.50
13:AH:133:THR:OG1	13:AH:134:GLU:N	2.44	0.50
13:AH:163:ASP:OD1	13:AH:164:TYR:N	2.44	0.50
20:AO:17:ALA:N	20:AO:80:HIS:O	2.31	0.50
27:AV:4:ASP:OD2	27:AV:5:LYS:N	2.43	0.50
32:Aa:51:ARG:NH1	32:Aa:55:GLU:OE2	2.43	0.50
39:BA:200:ARG:HB3	39:BA:202:VAL:HG12	1.92	0.50
40:BB:48:GLY:HA3	40:BB:81:THR:HG22	1.93	0.50
53:BO:116:HIS:HB3	53:BO:149:VAL:HB	1.93	0.50
55:BQ:28:GLU:HB3	55:BQ:31:GLU:HB3	1.92	0.50
80:CA:416:ASP:N	80:CA:416:ASP:OD1	2.43	0.50
80:CA:853:ARG:HH12	80:CA:888:PHE:HE2	1.58	0.50
80:CA:858:SER:HB2	80:CA:880:ALA:HA	1.92	0.50
1:2:154:G:OP1	12:AG:2:LYS:NZ	2.37	0.50
1:2:1546:G:O2'	24:AS:88:ARG:NH1	2.45	0.50
2:3:156:U:H2'	2:3:157:U:C5	2.46	0.50
4:5:1562:C:O2'	4:5:1563:C:O5'	2.30	0.50
4:5:2216:G:H22	4:5:2229:A:H2	1.59	0.50
4:5:3234:A:H61	4:5:3253:G:H1	1.58	0.50
7:AB:179:SER:HB2	7:AB:183:GLN:HB2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:AQ:120:ASP:OD1	22:AQ:120:ASP:N	2.42	0.50
24:AS:115:ARG:HA	24:AS:118:LYS:HE3	1.92	0.50
32:Aa:50:VAL:HG12	32:Aa:64:LEU:HD11	1.92	0.50
38:Ag:267:PRO:HB2	38:Ag:269:TYR:CD1	2.45	0.50
80:CA:232:GLN:O	80:CA:233:LYS:HG3	2.11	0.50
80:CA:575:TYR:O	80:CA:578:SER:OG	2.29	0.50
1:2:1164:G:H2'	1:2:1165:G:C8	2.47	0.50
1:2:1198:G:OP1	1:2:1199:G:O2'	2.20	0.50
4:5:153:U:H4'	4:5:158:G:H4'	1.93	0.50
4:5:536:U:H2'	4:5:537:A:C8	2.47	0.50
4:5:1658:G:H2'	4:5:1659:U:C6	2.47	0.50
4:5:2724:U:OP2	4:5:2726:C:N4	2.45	0.50
6:AA:37:VAL:HG13	6:AA:46:HIS:HB3	1.93	0.50
9:AD:23:GLU:OE1	16:AK:61:TRP:NE1	2.27	0.50
20:AO:30:VAL:HG11	20:AO:71:CYS:SG	2.51	0.50
27:AV:3:ASN:ND2	27:AV:7:GLN:OE1	2.45	0.50
38:Ag:10:ARG:HB2	38:Ag:314:GLN:HE22	1.75	0.50
38:Ag:254:ALA:O	38:Ag:261:LYS:N	2.36	0.50
42:BD:41:LYS:HD2	57:BS:93:VAL:HG11	1.94	0.50
45:BG:101:THR:HG23	45:BG:104:GLU:H	1.77	0.50
46:BH:38:LEU:HB3	46:BH:41:ILE:HD12	1.94	0.50
80:CA:323:THR:HG21	80:CA:461:ILE:HD12	1.92	0.50
1:2:1521:G:O6	25:AT:68:ARG:NH2	2.43	0.50
4:5:314:U:H2'	4:5:315:C:C6	2.47	0.50
4:5:651:G:O2'	4:5:1435:A:OP1	2.30	0.50
4:5:749:C:H5''	65:Ba:32:LEU:HD12	1.92	0.50
4:5:834:U:H2'	4:5:835:G:O4'	2.11	0.50
4:5:1072:G:H2'	4:5:1073:U:C6	2.47	0.50
4:5:1896:A:H61	4:5:2339:C:N4	2.10	0.50
17:AL:99:ARG:HB2	29:AX:9:LEU:O	2.12	0.50
41:BC:3:ARG:NH2	41:BC:27:SER:OG	2.44	0.50
53:BO:25:SER:HB2	53:BO:28:ASN:HB2	1.93	0.50
53:BO:67:ILE:HD11	53:BO:80:LYS:HB3	1.94	0.50
54:BP:94:PHE:CZ	64:BZ:119:PRO:HD3	2.47	0.50
1:2:950:C:H2'	1:2:951:A:C8	2.46	0.50
1:2:1226:A:H4'	1:2:1227:A:OP1	2.12	0.50
1:2:1673:G:C6	1:2:1728:A:N1	2.79	0.50
2:3:26:U:O2'	41:BC:51:ALA:O	2.29	0.50
4:5:2342:U:OP1	4:5:3089:C:O2'	2.29	0.50
4:5:3215:A:C8	50:BL:121:MET:HE3	2.46	0.50
6:AA:36:TYR:CD2	6:AA:161:PRO:HG3	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AB:36:SER:HA	7:AB:41:ARG:HH22	1.75	0.50
18:AM:48:SER:HB3	18:AM:122:VAL:HG23	1.93	0.50
48:BJ:101:ASN:OD1	48:BJ:130:VAL:HA	2.11	0.50
49:BK:56:PRO:HG3	49:BK:74:GLY:O	2.12	0.50
49:BK:59:ARG:NH2	49:BK:66:ASN:O	2.45	0.50
80:CA:258:GLN:HE22	80:CA:492:PHE:HD1	1.59	0.50
80:CA:1266:ASP:HA	80:CA:1302:MET:HB2	1.93	0.50
1:2:1247:U:H5''	37:Af:94:LYS:N	2.27	0.50
1:2:1247:U:H5''	37:Af:94:LYS:H	1.77	0.50
1:2:1690:G:H2'	1:2:1691:A:C8	2.44	0.50
4:5:1756:C:H2'	4:5:1757:A:H8	1.75	0.50
4:5:2266:U:HO2'	5:6:12:C:HO2'	1.57	0.50
4:5:2514:U:OP2	4:5:2586:G:N2	2.45	0.50
6:AA:52:LYS:HG2	27:AV:82:VAL:HG12	1.93	0.50
39:BA:32:LEU:HD13	39:BA:163:ARG:HD3	1.92	0.50
40:BB:103:THR:OG1	40:BB:147:GLU:OE2	2.27	0.50
54:BP:170:ARG:O	54:BP:171:LYS:HG2	2.12	0.50
80:CA:1004:ILE:HG13	80:CA:1014:ILE:HG12	1.93	0.50
4:5:1119:C:H2'	4:5:1120:A:H8	1.76	0.50
4:5:1523:U:O4	61:BW:75:LYS:NZ	2.41	0.50
4:5:2565:U:H3	4:5:2576:G:H1	1.60	0.50
4:5:2843:U:OP2	4:5:2844:C:N4	2.28	0.50
5:6:60:U:H5''	5:6:61:C:H5	1.77	0.50
10:AE:200:ARG:HG3	10:AE:200:ARG:HH11	1.76	0.50
11:AF:118:LEU:HG	11:AF:129:PRO:HB2	1.94	0.50
15:AJ:132:ARG:HH21	30:AY:65:GLY:HA2	1.77	0.50
26:AU:25:THR:HG22	26:AU:90:TYR:HB3	1.93	0.50
26:AU:99:ILE:HA	26:AU:102:ARG:HG2	1.94	0.50
49:BK:59:ARG:HD2	49:BK:69:VAL:HG12	1.93	0.50
58:BT:94:ARG:HH21	58:BT:96:VAL:HG22	1.77	0.50
80:CA:948:ASP:OD1	80:CA:948:ASP:N	2.45	0.50
80:CA:1550:LEU:HD22	80:CA:1607:THR:HB	1.94	0.50
1:2:227:U:H2'	1:2:228:G:H8	1.77	0.49
1:2:329:G:H2'	1:2:330:G:C8	2.46	0.49
1:2:1550:A:OP2	21:AP:42:ARG:NH2	2.44	0.49
4:5:417:A:H2'	4:5:418:A:C8	2.47	0.49
4:5:1334:U:H2'	4:5:1335:C:C6	2.47	0.49
4:5:2309:A:N3	4:5:2961:G:O2'	2.40	0.49
12:AG:70:PRO:HA	12:AG:98:ARG:HH12	1.77	0.49
16:AK:9:ASN:OD1	16:AK:79:TYR:OH	2.22	0.49
42:BD:217:GLU:O	42:BD:220:SER:OG	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:Bi:18:LEU:HA	73:Bi:25:ARG:HA	1.93	0.49
73:Bi:64:MET:HE2	73:Bi:67:LEU:HB3	1.94	0.49
80:CA:1164:THR:HG22	80:CA:1165:GLY:N	2.26	0.49
1:2:142:G:N2	1:2:173:A:H2	2.08	0.49
1:2:1725:U:H2'	1:2:1726:G:C8	2.47	0.49
4:5:1157:G:H2'	4:5:1158:A:O4'	2.12	0.49
4:5:2096:A:H2'	4:5:2097:U:C6	2.47	0.49
4:5:2516:U:O2	4:5:2594:C:N4	2.45	0.49
4:5:2737:C:O2'	65:Ba:36:ASP:OD1	2.25	0.49
6:AA:52:LYS:HA	27:AV:82:VAL:HG12	1.95	0.49
9:AD:40:ARG:HG3	26:AU:110:PRO:HA	1.93	0.49
11:AF:80:LYS:HE2	11:AF:83:ARG:HH11	1.77	0.49
12:AG:43:ASP:HA	12:AG:46:LYS:HE3	1.94	0.49
17:AL:80:MET:HB2	17:AL:83:THR:O	2.12	0.49
18:AM:26:ASP:OD1	18:AM:29:LYS:NZ	2.45	0.49
31:AZ:61:SER:H	31:AZ:64:VAL:HB	1.77	0.49
38:Ag:115:ILE:HD11	38:Ag:119:ALA:HA	1.94	0.49
45:BG:144:GLU:OE2	51:BM:6:TYR:OH	2.22	0.49
56:BR:12:ARG:HD2	56:BR:22:PRO:HD2	1.94	0.49
80:CA:994:ARG:HD3	80:CA:1023:VAL:HG13	1.94	0.49
1:2:1579:U:H2'	1:2:1580:C:C6	2.48	0.49
4:5:44:U:OP1	51:BM:85:THR:HG23	2.12	0.49
4:5:837:A:OP1	79:Bo:5:THR:OG1	2.26	0.49
4:5:1329:U:OP1	69:Be:17:GLN:NE2	2.41	0.49
4:5:1696:A:H2'	4:5:1697:A:C8	2.47	0.49
25:AT:24:ARG:NH1	25:AT:25:GLN:HE21	2.11	0.49
42:BD:95:TRP:CD1	42:BD:158:ARG:HA	2.47	0.49
80:CA:583:ARG:HH21	80:CA:609:LEU:HD22	1.75	0.49
80:CA:1379:ARG:HH11	80:CA:1435:HIS:HD2	1.60	0.49
4:5:73:C:C4	72:Bh:15:LYS:HD3	2.47	0.49
4:5:2880:U:OP1	59:BU:47:ASN:ND2	2.37	0.49
12:AG:67:VAL:O	12:AG:68:LEU:HG	2.12	0.49
46:BH:23:ARG:NE	46:BH:39:LYS:HA	2.24	0.49
80:CA:439:VAL:O	80:CA:442:THR:OG1	2.28	0.49
80:CA:711:LEU:HD22	80:CA:770:MET:HE2	1.95	0.49
80:CA:1546:LEU:HA	80:CA:1549:HIS:CE1	2.47	0.49
80:CA:1636:TYR:OH	80:CA:1743:ARG:O	2.28	0.49
80:CA:1795:ASP:O	80:CA:1810:GLN:NE2	2.46	0.49
80:CA:1906:LEU:HB3	80:CA:1918:LYS:HB3	1.94	0.49
1:2:217:A:H3'	1:2:218:A:H5''	1.94	0.49
1:2:1606:C:H2'	1:2:1607:G:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:45:A:OP1	42:BD:151:GLN:NE2	2.44	0.49
4:5:351:A:N6	75:Bk:35:ILE:HG23	2.28	0.49
4:5:1743:G:H2'	4:5:1744:G:H8	1.78	0.49
4:5:2430:A:H2'	4:5:2431:C:C6	2.47	0.49
4:5:3259:U:H5''	4:5:3261:C:H5	1.77	0.49
22:AQ:46:PHE:HA	22:AQ:49:TYR:CD2	2.47	0.49
39:BA:142:ASP:N	39:BA:142:ASP:OD1	2.44	0.49
42:BD:146:LEU:HD22	42:BD:163:LEU:HB2	1.95	0.49
64:BZ:39:HIS:O	64:BZ:41:HIS:N	2.46	0.49
80:CA:446:ARG:NE	80:CA:718:GLU:OE2	2.46	0.49
80:CA:921:LYS:HG3	80:CA:1045:SER:HB2	1.93	0.49
80:CA:1171:VAL:HA	80:CA:1174:LEU:HD23	1.93	0.49
81:CB:8:VAL:O	81:CB:9:ILE:HG22	2.13	0.49
1:2:1232:U:H2'	1:2:1233:G:C8	2.47	0.49
1:2:1401:A:OP1	23:AR:56:HIS:NE2	2.34	0.49
4:5:952:A:H4'	4:5:968:G:N2	2.27	0.49
19:AN:87:ASP:N	19:AN:87:ASP:OD1	2.43	0.49
20:AO:125:SER:OG	20:AO:126:THR:N	2.45	0.49
38:Ag:114:ASP:OD2	38:Ag:156:VAL:HG22	2.13	0.49
43:BE:56:LYS:HB3	43:BE:64:LEU:HB3	1.95	0.49
46:BH:89:LYS:HE2	46:BH:183:HIS:HB3	1.94	0.49
80:CA:1559:ILE:HG23	80:CA:1564:GLU:HG3	1.93	0.49
81:CB:81:LEU:HD21	81:CB:133:LEU:HB2	1.94	0.49
1:2:347:G:H5'	17:AL:80:MET:HE3	1.94	0.49
1:2:1701:A:H2'	1:2:1702:A:C8	2.48	0.49
4:5:1419:A:H5''	41:BC:193:LYS:HE3	1.93	0.49
4:5:2611:U:H2'	4:5:2612:U:C6	2.48	0.49
6:AA:76:ILE:HG12	6:AA:98:ILE:HB	1.93	0.49
8:AC:35:TRP:CE2	8:AC:67:GLN:HB2	2.48	0.49
8:AC:54:GLU:HG2	27:AV:11:LEU:HD13	1.93	0.49
12:AG:14:LYS:HE2	12:AG:16:PHE:HE1	1.76	0.49
18:AM:74:LEU:HD21	37:Af:106:TYR:HD2	1.76	0.49
27:AV:32:VAL:HG22	27:AV:60:ARG:HD2	1.94	0.49
31:AZ:88:ILE:HG22	31:AZ:89:ILE:HG23	1.95	0.49
41:BC:3:ARG:HB3	41:BC:22:LEU:HB2	1.94	0.49
46:BH:147:SER:HB2	46:BH:187:ILE:HD11	1.95	0.49
1:2:68:A:H5'	12:AG:160:ARG:HH12	1.77	0.49
1:2:623:A:H3'	1:2:624:G:H5''	1.95	0.49
1:2:628:G:H21	1:2:971:A:H62	1.59	0.49
4:5:39:A:H5''	64:BZ:35:ALA:HB2	1.95	0.49
4:5:307:A:H2'	4:5:308:A:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:876:A:H5''	4:5:1890:U:H5''	1.95	0.49
4:5:3273:A:H5'	43:BE:45:GLY:HA2	1.95	0.49
18:AM:59:LEU:HA	18:AM:87:PRO:HB2	1.95	0.49
21:AP:108:ARG:HB3	21:AP:110:GLU:OE1	2.13	0.49
41:BC:226:GLU:OE1	41:BC:237:GLN:NE2	2.41	0.49
43:BE:51:ARG:NH1	43:BE:161:ALA:O	2.46	0.49
81:CB:197:ALA:HB2	81:CB:203:ASN:HB2	1.94	0.49
1:2:343:C:H2'	1:2:344:A:H8	1.78	0.49
1:2:1382:A:H2'	1:2:1383:G:C8	2.48	0.49
3:4:64:A:H5'	3:4:65:G:H5''	1.95	0.49
4:5:428:A:H2'	4:5:429:U:C6	2.47	0.49
4:5:435:C:H2'	4:5:436:A:C8	2.48	0.49
4:5:769:G:O2'	49:BK:168:ARG:NH1	2.42	0.49
4:5:2406:C:H2'	4:5:2407:C:H6	1.78	0.49
12:AG:57:ASP:HA	12:AG:106:LEU:HA	1.95	0.49
15:AJ:47:PHE:O	15:AJ:51:LYS:HG2	2.13	0.49
15:AJ:180:LYS:H	15:AJ:180:LYS:HD2	1.78	0.49
20:AO:61:MET:HG3	20:AO:104:ALA:HB2	1.94	0.49
47:BI:12:GLN:NE2	47:BI:129:VAL:O	2.46	0.49
64:BZ:76:ASP:OD2	64:BZ:76:ASP:N	2.46	0.49
80:CA:497:LEU:HD21	80:CA:666:PHE:HB3	1.95	0.49
80:CA:1004:ILE:HD11	80:CA:1012:MET:HG3	1.94	0.49
81:CB:146:ARG:NH2	81:CB:196:SER:O	2.46	0.49
1:2:29:U:H2'	1:2:30:G:C8	2.45	0.49
1:2:130:C:H4'	1:2:176:C:H5'	1.95	0.49
1:2:872:G:H2'	1:2:873:U:O4'	2.12	0.49
1:2:947:U:H2'	1:2:948:G:C8	2.48	0.49
1:2:1437:U:H2'	1:2:1438:G:H8	1.78	0.49
1:2:1556:A:H4'	1:2:1557:U:C5	2.47	0.49
4:5:2573:G:H2'	4:5:2574:G:H8	1.78	0.49
4:5:2746:A:H5''	42:BD:178:ASN:HD21	1.78	0.49
8:AC:140:ARG:HB3	8:AC:221:THR:HB	1.95	0.49
12:AG:64:LYS:HB2	12:AG:97:VAL:HG21	1.95	0.49
12:AG:145:PHE:HB2	12:AG:147:LEU:HG	1.94	0.49
17:AL:27:THR:H	17:AL:30:ARG:NH1	2.10	0.49
27:AV:60:ARG:HA	27:AV:65:SER:HB2	1.94	0.49
30:AY:83:LYS:NZ	30:AY:96:LEU:O	2.41	0.49
38:Ag:45:TRP:CZ3	38:Ag:57:PRO:HD3	2.48	0.49
38:Ag:192:PHE:HB3	38:Ag:223:TRP:CZ3	2.42	0.49
38:Ag:201:THR:HG21	38:Ag:242:SER:HA	1.95	0.49
80:CA:1144:GLN:O	80:CA:1147:THR:N	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:CA:1639:SER:O	80:CA:1641:LEU:N	2.41	0.49
1:2:66:U:H5''	12:AG:173:PRO:HA	1.95	0.48
1:2:522:U:H5''	30:AY:37:LYS:HG3	1.95	0.48
1:2:541:A:O2'	1:2:542:A:OP1	2.28	0.48
1:2:1776:A:H2'	1:2:1777:G:C8	2.47	0.48
4:5:1666:G:H2'	4:5:1667:A:C8	2.48	0.48
4:5:2407:C:H2'	4:5:2408:U:C6	2.47	0.48
31:AZ:95:HIS:ND1	31:AZ:96:SER:O	2.46	0.48
32:Aa:83:ILE:HG22	32:Aa:84:VAL:HG13	1.95	0.48
38:Ag:172:ALA:HB3	38:Ag:202:LEU:HD22	1.94	0.48
47:BI:84:ALA:O	47:BI:140:THR:OG1	2.26	0.48
49:BK:138:VAL:HG22	71:Bg:118:ILE:HG23	1.95	0.48
52:BN:47[A]:PHE:HE1	52:BN:141[A]:LEU:HA	1.78	0.48
55:BQ:43:LYS:O	55:BQ:47:ASN:ND2	2.46	0.48
63:BY:17:ARG:NH2	63:BY:18:TYR:OH	2.46	0.48
80:CA:534:GLN:HB2	80:CA:637:ASP:HB2	1.94	0.48
80:CA:738:TYR:CZ	80:CA:742:ARG:HD3	2.47	0.48
80:CA:1289:ILE:O	80:CA:1293:THR:OG1	2.19	0.48
1:2:1647:U:H2'	1:2:1648:A:C8	2.48	0.48
4:5:900:G:H1'	4:5:1589:A:H61	1.76	0.48
4:5:1688:U:H2'	4:5:1689:U:C6	2.49	0.48
10:AE:19:LEU:HB2	10:AE:51:ARG:NH2	2.28	0.48
12:AG:21:GLU:HA	12:AG:24:ILE:HD13	1.94	0.48
12:AG:102:VAL:HG13	12:AG:106:LEU:HD12	1.95	0.48
18:AM:70:ASN:OD1	18:AM:71:ILE:N	2.44	0.48
22:AQ:29:ILE:HG21	22:AQ:36:ILE:HD12	1.95	0.48
38:Ag:9:LEU:HA	38:Ag:313:TRP:CD1	2.49	0.48
38:Ag:300:THR:HG22	38:Ag:314:GLN:HB3	1.94	0.48
42:BD:77:ALA:O	42:BD:108:ARG:NH1	2.44	0.48
48:BJ:109:HIS:HD1	48:BJ:123:PHE:C	2.22	0.48
59:BU:6:ALA:HB1	59:BU:125:LEU:HD11	1.95	0.48
80:CA:1865:PHE:CE2	80:CA:1963:HIS:HB2	2.48	0.48
1:2:689:G:H2'	1:2:690:G:H8	1.77	0.48
1:2:884:A:H2'	1:2:885:G:C8	2.48	0.48
1:2:1740:A:H2'	1:2:1741:U:C6	2.48	0.48
4:5:2206:G:H21	4:5:2207:A:N6	2.11	0.48
4:5:2446:U:HO2'	4:5:2447:A:P	2.35	0.48
4:5:3094:A:H2'	4:5:3095:U:C6	2.48	0.48
4:5:3110:C:H2'	4:5:3111:U:C6	2.48	0.48
38:Ag:14:GLU:HG3	38:Ag:309:VAL:HG12	1.95	0.48
43:BE:41:ILE:HG12	43:BE:51:ARG:HG2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:BQ:47:ASN:OD1	55:BQ:49:THR:OG1	2.28	0.48
81:CB:137:TYR:HB2	81:CB:145:ILE:HD11	1.96	0.48
1:2:385:A:H5''	14:AI:22:ARG:HG2	1.95	0.48
1:2:680:U:H2'	1:2:681:U:H5	1.78	0.48
1:2:959:U:H6	19:AN:61:THR:HB	1.78	0.48
3:4:10:C:N3	42:BD:20:PHE:HB3	2.27	0.48
3:4:71:G:H2'	3:4:72:A:C8	2.48	0.48
4:5:620:U:H5'	53:BO:167:ARG:NH2	2.28	0.48
4:5:664:U:H2'	4:5:665:A:H8	1.78	0.48
4:5:799:G:O2'	49:BK:18:TRP:NE1	2.44	0.48
4:5:1367:G:OP1	68:Bd:45:ARG:NH2	2.43	0.48
4:5:2167:A:H2'	4:5:2168:A:C8	2.48	0.48
6:AA:37:VAL:HG22	6:AA:149:LEU:HD13	1.95	0.48
16:AK:44:LYS:HA	16:AK:47:GLN:HB3	1.96	0.48
22:AQ:50:GLU:OE2	22:AQ:112:TYR:OH	2.26	0.48
34:Ac:12:VAL:HG22	34:Ac:30:VAL:HG12	1.95	0.48
51:BM:64:VAL:HG11	51:BM:102:ALA:HB1	1.96	0.48
1:2:732:G:O2'	1:2:734:A:N6	2.46	0.48
1:2:931:C:H5''	7:AB:116:LYS:HB3	1.96	0.48
1:2:1054:U:H2'	1:2:1055:U:C6	2.49	0.48
1:2:1435:G:C4	16:AK:59:PHE:HE2	2.31	0.48
2:3:74:U:C4	62:BX:74:TYR:HD1	2.32	0.48
4:5:75:G:H5''	49:BK:58:VAL:CG2	2.44	0.48
4:5:525:C:OP2	50:BL:77:ARG:NH2	2.43	0.48
4:5:1756:C:H2'	4:5:1757:A:C8	2.49	0.48
4:5:1927:G:C8	79:Bo:16:VAL:HG12	2.48	0.48
4:5:2160:G:H2'	4:5:2161:G:H8	1.78	0.48
4:5:3157:U:H4'	4:5:3158:G:H5'	1.96	0.48
36:Ae:14:VAL:O	36:Ae:18:THR:HG23	2.13	0.48
39:BA:32:LEU:HD12	39:BA:36:GLU:HB2	1.96	0.48
42:BD:51:LEU:N	42:BD:145:PHE:O	2.43	0.48
80:CA:1008:THR:OG1	80:CA:1011:VAL:HG22	2.13	0.48
80:CA:1380:ARG:NH2	81:CB:2:LEU:HB3	2.28	0.48
82:CC:350:ASP:OD1	82:CC:351:ASN:N	2.40	0.48
1:2:1553:G:N2	1:2:1556:A:OP2	2.46	0.48
4:5:789:A:H2'	4:5:790:U:H6	1.78	0.48
4:5:1724:U:O2'	4:5:1725:C:OP2	2.25	0.48
12:AG:174:LYS:O	12:AG:175:ILE:HD13	2.13	0.48
23:AR:26:LEU:HD23	23:AR:58:MET:HB3	1.96	0.48
45:BG:160:ILE:O	45:BG:164:VAL:HG13	2.13	0.48
46:BH:28:VAL:HG22	46:BH:33:THR:HG22	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:BP:176:ARG:HA	54:BP:182:LYS:O	2.13	0.48
69:Be:48:ARG:NH1	69:Be:70:LYS:HE2	2.29	0.48
80:CA:263:ASN:HA	80:CA:266:TYR:CZ	2.48	0.48
80:CA:1338:TYR:O	80:CA:1518:VAL:HG22	2.13	0.48
80:CA:1693:VAL:HG21	80:CA:1710:VAL:HG13	1.95	0.48
82:CC:329:GLN:HA	82:CC:332:LEU:HB3	1.94	0.48
1:2:607:G:H5'	1:2:613:G:N2	2.27	0.48
1:2:1173:C:OP1	24:AS:132:ARG:NH2	2.46	0.48
1:2:1228:G:H5'	18:AM:45:LEU:HD22	1.94	0.48
4:5:1129:A:H2'	4:5:1130:A:C8	2.49	0.48
4:5:3089:C:H2'	4:5:3090:U:O4'	2.13	0.48
9:AD:108:LYS:HD2	9:AD:118:ALA:HB1	1.96	0.48
12:AG:149:LYS:HG3	12:AG:150:GLU:CD	2.39	0.48
13:AH:51:VAL:HG23	13:AH:53:GLY:H	1.78	0.48
18:AM:130:THR:OG1	18:AM:131:ASP:N	2.46	0.48
23:AR:17:ILE:HG12	23:AR:58:MET:HE3	1.96	0.48
61:BW:67:ILE:HD12	61:BW:121:LYS:HG3	1.95	0.48
80:CA:380:LEU:HG	80:CA:397:ILE:HD11	1.96	0.48
80:CA:926:MET:HE2	80:CA:926:MET:HA	1.95	0.48
80:CA:1143:MET:O	80:CA:1324:TYR:OH	2.15	0.48
1:2:85:A:N3	1:2:148:A:O2'	2.42	0.48
1:2:119:A:H1'	1:2:397:A:C5	2.48	0.48
1:2:222:A:H2'	1:2:223:U:C6	2.48	0.48
1:2:453:U:H2'	1:2:454:U:H5''	1.96	0.48
1:2:819:G:H4'	1:2:820:U:O5'	2.12	0.48
1:2:1582:U:O2'	1:2:1583:A:OP2	2.29	0.48
1:2:1732:A:H2'	1:2:1733:C:C6	2.49	0.48
2:3:95:G:O2'	73:Bi:81:GLY:O	2.26	0.48
4:5:75:G:H5''	49:BK:58:VAL:HG22	1.95	0.48
4:5:523:A:O2'	56:BR:69:PRO:HD2	2.14	0.48
4:5:1298:C:H4'	76:Bl:113:ARG:HH21	1.79	0.48
4:5:1660:C:H2'	4:5:1661:G:H8	1.78	0.48
4:5:2696:A:H2'	4:5:2697:A:C8	2.48	0.48
4:5:2768:U:H2'	4:5:2769:A:C8	2.47	0.48
24:AS:15:LEU:H	24:AS:15:LEU:HD23	1.79	0.48
51:BM:10:LEU:HG	51:BM:19:LEU:HD11	1.95	0.48
80:CA:298:VAL:O	80:CA:302:THR:OG1	2.23	0.48
1:2:903:U:H5''	20:AO:135:ARG:NH2	2.29	0.48
1:2:1533:C:OP2	31:AZ:77:ARG:NH2	2.46	0.48
1:2:1584:G:C8	22:AQ:122:ARG:HB3	2.49	0.48
3:4:52:G:O2'	3:4:53:U:OP1	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:1190:A:H5'	4:5:1191:U:OP1	2.14	0.48
4:5:3033:A:H2'	4:5:3034:C:C6	2.49	0.48
4:5:3298:C:C2	4:5:3299:A:C8	3.02	0.48
5:6:63:U:H2'	5:6:64:G:H8	1.79	0.48
12:AG:22:HIS:C	12:AG:25:ARG:NH1	2.72	0.48
53:BO:120:ASN:OD1	53:BO:145:HIS:HB2	2.14	0.48
80:CA:536:MET:O	80:CA:640:ILE:N	2.37	0.48
81:CB:242:PHE:HE1	81:CB:279:VAL:HG22	1.79	0.48
1:2:1208:A:H4'	1:2:1270:G:P	2.53	0.48
3:4:71:G:H2'	3:4:72:A:H8	1.79	0.48
4:5:1274:A:H2'	4:5:1275:C:C6	2.49	0.48
4:5:3047:U:O2'	4:5:3048:A:H5'	2.13	0.48
4:5:3269:U:H4'	4:5:3270:U:O5'	2.14	0.48
10:AE:105:VAL:HG21	10:AE:245:LYS:H	1.79	0.48
21:AP:81:ARG:HH21	21:AP:120:SER:HB3	1.79	0.48
24:AS:127:HIS:CD2	24:AS:133:VAL:HG11	2.48	0.48
54:BP:40:THR:OG1	54:BP:45:ASN:ND2	2.47	0.48
55:BQ:68:GLN:OE1	55:BQ:71:ARG:NH2	2.41	0.48
55:BQ:170:ARG:O	55:BQ:174:ALA:N	2.42	0.48
79:Bo:49:ARG:HB2	79:Bo:55:TRP:CZ3	2.48	0.48
80:CA:606:ASP:OD1	80:CA:607:ARG:N	2.47	0.48
80:CA:1011:VAL:C	80:CA:1012:MET:HE2	2.39	0.48
80:CA:1383:ARG:O	80:CA:1387:LEU:HG	2.13	0.48
1:2:140:A:H1'	12:AG:184:LEU:HD21	1.94	0.47
1:2:332:U:P	14:AI:56:ARG:HH22	2.37	0.47
1:2:406:U:H2'	1:2:407:A:H8	1.77	0.47
4:5:2433:U:H1'	51:BM:125:SER:HB2	1.96	0.47
4:5:3192:U:H2'	4:5:3193:C:C6	2.49	0.47
11:AF:72:HIS:ND1	22:AQ:79:TYR:OH	2.47	0.47
11:AF:125:THR:O	11:AF:127:GLN:N	2.46	0.47
50:BL:23:ILE:HG21	50:BL:28:SER:HB2	1.96	0.47
80:CA:452:GLU:O	80:CA:455:GLN:NE2	2.47	0.47
1:2:622:A:O2'	1:2:1032:G:H5'	2.14	0.47
1:2:849:C:H2'	1:2:850:A:H8	1.79	0.47
4:5:947:G:H2'	4:5:948:C:C6	2.49	0.47
4:5:1257:C:O2	4:5:1261:G:O6	2.32	0.47
4:5:1597:C:H2'	4:5:1598:G:C8	2.48	0.47
4:5:1615:C:H2'	4:5:1616:U:C6	2.49	0.47
4:5:2180:G:H2'	4:5:2181:C:C6	2.49	0.47
4:5:2941:A:H8	4:5:2941:A:OP2	1.97	0.47
4:5:3163:A:N6	4:5:3288:G:O6	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:AP:29:SER:OG	21:AP:31:GLU:OE1	2.28	0.47
26:AU:61:LYS:HB2	26:AU:86:ILE:HB	1.95	0.47
41:BC:304:GLN:NE2	41:BC:306:THR:O	2.43	0.47
49:BK:76:THR:O	49:BK:78:ALA:N	2.47	0.47
80:CA:1057:ARG:HD3	80:CA:1058:ARG:HH12	1.78	0.47
80:CA:1874:LEU:HB3	80:CA:1935:LEU:HB2	1.96	0.47
1:2:1344:A:H2'	1:2:1345:A:C8	2.49	0.47
1:2:1584:G:O3'	22:AQ:124:PRO:HA	2.15	0.47
4:5:792:G:H2'	4:5:793:C:C6	2.49	0.47
4:5:1455:U:H1'	67:Bc:26:LYS:HE3	1.96	0.47
4:5:1798:A:H2'	4:5:1799:A:C8	2.48	0.47
4:5:2376:G:H2'	4:5:2377:G:C8	2.50	0.47
4:5:2423:U:H2'	4:5:2424:A:C8	2.49	0.47
8:AC:194:GLU:N	8:AC:194:GLU:OE2	2.47	0.47
12:AG:130:PRO:HB3	60:BV:81:PRO:HB2	1.95	0.47
21:AP:57:MET:HA	21:AP:60:LEU:HB2	1.95	0.47
22:AQ:58:ASP:OD1	22:AQ:58:ASP:N	2.47	0.47
24:AS:7:GLU:HB2	31:AZ:43:ASP:HA	1.96	0.47
46:BH:48:VAL:HG21	46:BH:52:LEU:HD23	1.96	0.47
47:BI:44:ASP:OD1	47:BI:181:TYR:OH	2.27	0.47
78:Bn:71:ARG:NH2	78:Bn:80:ARG:HH11	2.11	0.47
80:CA:778:LEU:HB3	80:CA:784:ILE:HG12	1.96	0.47
80:CA:1265:MET:HE1	80:CA:1299:LEU:HD12	1.96	0.47
81:CB:55:TYR:O	81:CB:61:ASN:ND2	2.34	0.47
2:3:142:C:H2'	2:3:143:U:H6	1.79	0.47
3:4:19:C:H2'	3:4:20:A:H8	1.79	0.47
4:5:16:A:OP1	61:BW:44:PRO:HB3	2.15	0.47
4:5:517:G:OP1	44:BF:67:ARG:NH2	2.39	0.47
4:5:1046:A:H2'	4:5:1049:C:C5	2.50	0.47
4:5:2106:A:H2'	4:5:2107:A:H8	1.79	0.47
46:BH:9:GLN:CG	46:BH:52:LEU:HD11	2.44	0.47
54:BP:161:LYS:HD3	54:BP:161:LYS:HA	1.71	0.47
62:BX:56:VAL:HG21	62:BX:104:LEU:HD13	1.95	0.47
1:2:495:C:H4'	1:2:496:G:N7	2.29	0.47
1:2:872:G:N2	1:2:1047:G:H4'	2.29	0.47
1:2:1564:U:H2'	1:2:1565:C:C6	2.49	0.47
1:2:1650:U:H2'	1:2:1651:A:C8	2.49	0.47
4:5:127:G:H2'	4:5:128:G:H8	1.78	0.47
4:5:1945:A:H2'	4:5:1946:A:C8	2.49	0.47
14:AI:149:SER:O	17:AL:24:LYS:NZ	2.41	0.47
25:AT:61:VAL:HG21	25:AT:104:VAL:HG11	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:AU:20:ILE:HG22	26:AU:22:ILE:HG12	1.97	0.47
47:BI:36:LEU:HD11	47:BI:69:ARG:HD2	1.95	0.47
59:BU:66:LYS:HG2	59:BU:68:GLU:H	1.78	0.47
80:CA:1187:LYS:HG3	80:CA:1259:ASP:HB3	1.96	0.47
1:2:1012:U:H4'	39:BA:247:ARG:HB3	1.97	0.47
1:2:1171:A:H2'	1:2:1172:G:H8	1.76	0.47
4:5:243:G:H2'	4:5:244:G:C8	2.48	0.47
4:5:716:A:N6	64:BZ:117:ARG:HG3	2.30	0.47
4:5:987:U:H2'	4:5:988:U:C6	2.49	0.47
4:5:1120:A:H2'	4:5:1121:U:H6	1.80	0.47
4:5:2103:U:H5''	55:BQ:85:ARG:HE	1.78	0.47
13:AH:47:ARG:HH12	13:AH:49:ILE:HD11	1.79	0.47
35:Ad:30:LEU:HD21	35:Ad:37:ASN:HA	1.97	0.47
41:BC:14:GLU:HG2	41:BC:15:ALA:H	1.79	0.47
55:BQ:11:ALA:O	55:BQ:15:VAL:HG22	2.14	0.47
72:Bh:5:THR:HG23	72:Bh:12:ASN:HB2	1.95	0.47
73:Bi:66:TYR:OH	73:Bi:73:ARG:NH2	2.48	0.47
80:CA:1331:ARG:NH1	80:CA:1335:LEU:HB2	2.29	0.47
80:CA:1518:VAL:O	80:CA:1520:THR:OG1	2.32	0.47
80:CA:1641:LEU:HD12	80:CA:1644:ARG:HH21	1.78	0.47
1:2:647:G:N2	1:2:687:G:H22	2.11	0.47
1:2:809:A:H2'	1:2:810:G:C8	2.50	0.47
1:2:1079:U:H2'	1:2:1080:U:C6	2.50	0.47
1:2:1396:U:H2'	1:2:1397:U:C6	2.50	0.47
1:2:1672:G:H2'	1:2:1673:G:H8	1.76	0.47
1:2:1738:U:H2'	1:2:1739:C:C6	2.49	0.47
2:3:151:C:C5	61:BW:24:LEU:HD11	2.50	0.47
4:5:248:U:H3'	4:5:249:U:H5''	1.97	0.47
4:5:543:C:O2'	4:5:544:C:O4'	2.25	0.47
4:5:789:A:H2'	4:5:790:U:C6	2.49	0.47
4:5:1014:U:H3	4:5:1036:A:H61	1.61	0.47
4:5:1343:A:H2'	4:5:1344:G:C8	2.50	0.47
4:5:1621:A:H2'	4:5:1622:U:C6	2.49	0.47
4:5:2148:U:H2'	4:5:2149:A:C8	2.50	0.47
4:5:3371:G:H2'	4:5:3372:A:C8	2.49	0.47
8:AC:35:TRP:NE1	8:AC:67:GLN:OE1	2.48	0.47
12:AG:49:VAL:HG12	12:AG:115:LYS:HB3	1.97	0.47
13:AH:64:VAL:HG23	13:AH:67:LEU:HB2	1.95	0.47
15:AJ:100:LYS:HD3	15:AJ:100:LYS:HA	1.68	0.47
30:AY:27:VAL:HG11	30:AY:35:VAL:HG21	1.96	0.47
38:Ag:109:ASP:O	38:Ag:127:ARG:N	2.35	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:Ag:270:LEU:HD21	38:Ag:273:ASP:HB2	1.97	0.47
39:BA:80:GLU:HB2	79:Bo:66:GLY:HA2	1.96	0.47
42:BD:95:TRP:HD1	42:BD:158:ARG:HA	1.78	0.47
48:BJ:110:ILE:HD11	48:BJ:122:ILE:HG22	1.96	0.47
48:BJ:166:LYS:NZ	48:BJ:167:TYR:H	2.12	0.47
56:BR:77:VAL:HG21	56:BR:106:LEU:HD13	1.96	0.47
80:CA:395:GLN:OE1	80:CA:395:GLN:N	2.48	0.47
80:CA:810:GLU:CD	82:CC:377:GLN:HE22	2.21	0.47
80:CA:1248:SER:O	80:CA:1285:ARG:NH1	2.48	0.47
80:CA:1941:ILE:HD12	80:CA:1946:LEU:HD11	1.96	0.47
81:CB:178:ILE:HG21	81:CB:221:LEU:HD21	1.95	0.47
1:2:17:C:H2'	1:2:18:C:C6	2.49	0.47
4:5:2217:U:H2'	4:5:2218:G:H8	1.79	0.47
4:5:2305:G:OP2	4:5:2305:G:N2	2.31	0.47
4:5:2367:A:H2'	4:5:2368:A:C8	2.49	0.47
48:BJ:92:ARG:HA	48:BJ:172:LEU:HG	1.97	0.47
50:BL:67:PRO:HD3	50:BL:99:TRP:HZ3	1.80	0.47
66:Bb:16:LEU:HB3	66:Bb:98:SER:HB3	1.97	0.47
80:CA:1482:PHE:HB3	80:CA:1493:MET:HE2	1.97	0.47
1:2:762:A:OP1	15:AJ:79:ARG:NH2	2.41	0.47
1:2:955:A:H5''	19:AN:10:GLY:HA3	1.96	0.47
1:2:1147:A:H2'	1:2:1148:C:C6	2.50	0.47
1:2:1506:G:H2'	1:2:1507:G:H8	1.80	0.47
1:2:1593:A:H2'	1:2:1594:G:H8	1.80	0.47
4:5:239:G:O2'	4:5:240:U:OP1	2.31	0.47
4:5:434:U:H2'	4:5:435:C:C6	2.50	0.47
4:5:2557:A:OP1	39:BA:69:TYR:OH	2.23	0.47
4:5:2661:G:H2'	4:5:2662:G:C8	2.50	0.47
4:5:3371:G:H2'	4:5:3372:A:H8	1.79	0.47
12:AG:157:VAL:HG11	12:AG:172:ALA:HB1	1.97	0.47
13:AH:150:GLN:O	13:AH:181:ILE:HA	2.14	0.47
22:AQ:82:ARG:HE	22:AQ:116:LEU:HD23	1.79	0.47
26:AU:58:LEU:HD21	26:AU:90:TYR:HE1	1.80	0.47
29:AX:57:LEU:HD22	36:Ae:4:VAL:HB	1.96	0.47
48:BJ:7:ASN:HA	48:BJ:10:ARG:HD2	1.96	0.47
48:BJ:30:LEU:HD11	48:BJ:67:VAL:HG13	1.97	0.47
51:BM:8:GLU:HB2	51:BM:50:ARG:NH2	2.30	0.47
60:BV:47:ARG:NH1	60:BV:47:ARG:HB3	2.30	0.47
67:Bc:10:ARG:HG2	67:Bc:108:VAL:HG22	1.96	0.47
80:CA:354:PRO:HB3	80:CA:431:LEU:HD11	1.96	0.47
80:CA:427:ASP:HA	80:CA:463:LEU:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:CA:911:PHE:HB2	80:CA:926:MET:HG3	1.97	0.47
80:CA:1753:SER:HA	80:CA:1914:LEU:HD23	1.97	0.47
1:2:712:G:O6	1:2:726:C:O2'	2.33	0.47
1:2:1331:A:H5''	23:AR:45:ARG:HH11	1.79	0.47
1:2:1419:G:H2'	1:2:1420:C:O4'	2.14	0.47
1:2:1482:C:O2'	22:AQ:77:GLN:NE2	2.41	0.47
1:2:1553:G:O6	21:AP:43:ARG:NE	2.42	0.47
1:2:1609:U:H2'	1:2:1610:G:O4'	2.15	0.47
1:2:1737:G:H2'	1:2:1738:U:C6	2.50	0.47
4:5:591:G:O2'	43:BE:17:ALA:O	2.33	0.47
4:5:756:U:H2'	4:5:757:C:H6	1.79	0.47
4:5:1279:C:H2'	4:5:1280:C:C6	2.50	0.47
4:5:1656:A:OP2	70:Bf:37:LYS:NZ	2.46	0.47
4:5:1804:A:H2'	4:5:1805:C:C6	2.50	0.47
4:5:2353:G:H5''	53:BO:86:LYS:HB2	1.97	0.47
4:5:3107:U:H2'	4:5:3108:G:C8	2.49	0.47
4:5:3162:C:H2'	4:5:3163:A:C8	2.50	0.47
4:5:3193:C:H2'	4:5:3194:C:C6	2.50	0.47
7:AB:36:SER:HB2	7:AB:231:LEU:O	2.14	0.47
14:AI:7:SER:O	14:AI:18:ARG:NH2	2.48	0.47
20:AO:50:ALA:C	20:AO:52:ARG:H	2.23	0.47
21:AP:48:GLY:O	21:AP:52:LYS:NZ	2.47	0.47
42:BD:41:LYS:HB2	57:BS:68:THR:O	2.15	0.47
80:CA:719:ILE:HG22	80:CA:795:ALA:HB2	1.96	0.47
80:CA:908:ARG:NE	80:CA:934:GLU:OE2	2.42	0.47
81:CB:97:ASN:HB3	81:CB:100:VAL:HG23	1.96	0.47
1:2:10:G:OP1	1:2:1633:A:O2'	2.25	0.46
1:2:885:G:H21	20:AO:123:SER:HB2	1.79	0.46
1:2:1107:G:O2'	1:2:1108:G:H5'	2.15	0.46
1:2:1439:C:H2'	1:2:1440:C:H6	1.81	0.46
1:2:1592:A:H2'	1:2:1593:A:H8	1.79	0.46
5:6:63:U:H2'	5:6:64:G:C8	2.51	0.46
10:AE:79:ASP:HB3	10:AE:82:TYR:HB2	1.96	0.46
10:AE:94:ALA:HB1	30:AY:16:PRO:HG2	1.97	0.46
11:AF:99:MET:HG3	11:AF:100:ASN:N	2.29	0.46
14:AI:34:ALA:HB2	14:AI:56:ARG:HD2	1.98	0.46
25:AT:113:ILE:HG22	25:AT:114:VAL:HG23	1.97	0.46
34:Ac:11:LYS:NZ	34:Ac:12:VAL:O	2.48	0.46
38:Ag:106:HIS:CE1	38:Ag:132:LYS:HD2	2.50	0.46
58:BT:14:THR:HG22	58:BT:66:VAL:HG22	1.97	0.46
80:CA:472:ASP:OD2	80:CA:742:ARG:NH1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:CB:85:ALA:HB1	81:CB:135:LYS:HD2	1.96	0.46
82:CC:185:VAL:HA	82:CC:200:CYS:HA	1.97	0.46
1:2:492:A:H4'	1:2:493:U:H5''	1.97	0.46
1:2:1125:A:OP1	77:Bm:18:ARG:NH2	2.49	0.46
1:2:1166:A:H2'	1:2:1167:G:O4'	2.15	0.46
1:2:1719:A:H2'	1:2:1720:G:O4'	2.15	0.46
2:3:63:G:H22	2:3:97:A:H2	1.63	0.46
4:5:872:U:H2'	4:5:873:C:C6	2.50	0.46
4:5:943:U:H3'	64:BZ:13:GLY:HA2	1.96	0.46
4:5:1596:C:H2'	4:5:1597:C:H6	1.80	0.46
4:5:3204:C:H2'	4:5:3205:G:C8	2.50	0.46
4:5:3296:A:H2'	4:5:3297:U:C6	2.50	0.46
5:6:43:A:H2'	5:6:44:A:C8	2.49	0.46
11:AF:30:PRO:O	11:AF:33:VAL:HG12	2.14	0.46
16:AK:68:LEU:HD23	16:AK:68:LEU:H	1.79	0.46
25:AT:100:ILE:O	25:AT:104:VAL:HG23	2.15	0.46
38:Ag:177:MET:SD	38:Ag:179:LYS:NZ	2.88	0.46
45:BG:78:PHE:C	45:BG:80:TYR:H	2.23	0.46
60:BV:43:ARG:NE	60:BV:43:ARG:HA	2.30	0.46
61:BW:126:LEU:HD11	61:BW:135:ILE:HD11	1.98	0.46
80:CA:1775:TYR:HD2	80:CA:1779:ASP:HB2	1.79	0.46
81:CB:2:LEU:HD23	81:CB:2:LEU:H	1.80	0.46
1:2:1041:G:H2'	1:2:1042:G:H8	1.80	0.46
1:2:1503:A:H3'	1:2:1504:G:H8	1.79	0.46
1:2:1634:C:H5''	1:2:1635:A:C8	2.51	0.46
4:5:845:G:N2	4:5:848:A:OP2	2.48	0.46
4:5:1326:A:O2'	69:Be:77:ASN:OD1	2.24	0.46
4:5:2585:G:H2'	4:5:2585:G:N3	2.30	0.46
4:5:2812:C:H2'	4:5:2813:A:C8	2.51	0.46
10:AE:104:ASP:OD1	10:AE:105:VAL:N	2.48	0.46
13:AH:51:VAL:HG12	13:AH:171:ALA:HB3	1.97	0.46
19:AN:11:ILE:HG13	19:AN:11:ILE:O	2.16	0.46
20:AO:16:VAL:O	20:AO:30:VAL:HA	2.16	0.46
22:AQ:69:VAL:HG21	22:AQ:81:ILE:HG12	1.98	0.46
31:AZ:58:ARG:HA	31:AZ:103:ARG:NH1	2.30	0.46
47:BI:97:LEU:HD11	47:BI:126:ALA:HB2	1.96	0.46
51:BM:165:THR:HG22	51:BM:166:ALA:H	1.80	0.46
55:BQ:139:VAL:O	55:BQ:143:ILE:HG12	2.15	0.46
62:BX:100:HIS:ND1	62:BX:102:SER:OG	2.42	0.46
63:BY:119:GLU:O	63:BY:123:GLN:HG2	2.15	0.46
66:Bb:30:THR:HG23	66:Bb:91:SER:HB2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:CA:257:ASP:N	80:CA:257:ASP:OD1	2.49	0.46
80:CA:586:ASP:HB3	80:CA:590:ILE:HD13	1.96	0.46
1:2:305:C:H2'	1:2:306:U:C6	2.50	0.46
1:2:886:U:H2'	1:2:887:A:H8	1.81	0.46
1:2:888:U:H2'	1:2:889:U:C6	2.50	0.46
1:2:1303:U:H2'	1:2:1304:G:O4'	2.16	0.46
4:5:2106:A:H2'	4:5:2107:A:C8	2.51	0.46
4:5:2711:C:O2'	4:5:2744:U:OP1	2.33	0.46
4:5:2801:A:O2'	4:5:2802:A:H2'	2.16	0.46
25:AT:67:MET:HB2	25:AT:68:ARG:HD2	1.96	0.46
39:BA:21:ARG:HE	39:BA:22:LEU:HG	1.80	0.46
57:BS:12:ARG:O	57:BS:16:GLN:HG3	2.15	0.46
60:BV:23:ARG:HB3	60:BV:25:ASP:OD1	2.16	0.46
64:BZ:72:VAL:HG12	64:BZ:111:LYS:HB3	1.96	0.46
80:CA:238:VAL:HG11	80:CA:242:ARG:HB2	1.95	0.46
80:CA:1431:ILE:HD11	80:CA:1459:ILE:HD12	1.98	0.46
1:2:419:G:H5'	12:AG:72:ARG:HH21	1.81	0.46
1:2:707:A:N7	1:2:731:C:N4	2.59	0.46
1:2:1696:G:H2'	1:2:1697:G:H8	1.80	0.46
4:5:429:U:H2'	4:5:430:U:H6	1.80	0.46
4:5:1306:G:C6	52:BN:62[A]:THR:HA	2.51	0.46
4:5:1687:U:OP2	58:BT:42:LYS:NZ	2.44	0.46
4:5:3000:A:H2'	4:5:3001:C:C6	2.51	0.46
4:5:3322:A:H2'	4:5:3323:A:H8	1.80	0.46
16:AK:14:TYR:CE2	16:AK:18:GLU:HG3	2.50	0.46
19:AN:127:ARG:O	19:AN:131:THR:HG23	2.16	0.46
29:AX:42:PRO:O	29:AX:79:ASN:ND2	2.49	0.46
45:BG:134:TYR:CG	45:BG:190:VAL:HG21	2.49	0.46
49:BK:165:SER:C	49:BK:167:PHE:H	2.23	0.46
58:BT:43:VAL:HB	58:BT:49:ASN:HB3	1.98	0.46
60:BV:46:PRO:HB2	60:BV:54:LEU:HD23	1.97	0.46
80:CA:254:PRO:HD2	80:CA:499:GLN:HB2	1.97	0.46
1:2:420:A:OP1	12:AG:96:SER:OG	2.30	0.46
1:2:1220:C:H2'	1:2:1221:A:H8	1.80	0.46
2:3:126:A:O2'	2:3:129:C:N4	2.49	0.46
2:3:156:U:H2'	2:3:157:U:C6	2.51	0.46
4:5:38:U:H2'	4:5:39:A:O4'	2.15	0.46
4:5:162:G:H2'	4:5:163:C:C6	2.51	0.46
4:5:362:U:O4	73:Bi:24:ARG:NH2	2.48	0.46
4:5:1295:G:H2'	4:5:1296:C:C6	2.51	0.46
4:5:1899:G:O2'	4:5:2334:U:O4	2.23	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:2767:U:H2'	4:5:2768:U:H6	1.80	0.46
20:AO:30:VAL:HG13	20:AO:39:ILE:HB	1.96	0.46
29:AX:90:ASP:O	29:AX:136:TRP:NE1	2.44	0.46
39:BA:143:GLU:O	39:BA:145:LYS:HG2	2.16	0.46
44:BF:88:ARG:HD2	44:BF:103:LEU:HD22	1.98	0.46
45:BG:81:THR:HG22	45:BG:155:ASN:ND2	2.31	0.46
54:BP:170:ARG:HD2	64:BZ:57:GLY:HA3	1.98	0.46
54:BP:175:ALA:C	64:BZ:51:GLY:HA2	2.40	0.46
80:CA:1183:PHE:HD2	80:CA:1186:LYS:HG3	1.81	0.46
80:CA:1217:VAL:HG13	80:CA:1236:ILE:O	2.15	0.46
82:CC:366:SER:HB2	82:CC:368:ARG:CZ	2.46	0.46
1:2:65:A:H2	1:2:84:A:N7	2.14	0.46
1:2:246:G:N2	17:AL:38:ALA:O	2.44	0.46
1:2:602:U:H2'	1:2:603:U:C6	2.51	0.46
2:3:104:A:N3	4:5:22:G:H1'	2.31	0.46
4:5:95:A:H5''	64:BZ:34:MET:HB2	1.98	0.46
4:5:264:G:OP1	72:Bh:34:SER:HB2	2.15	0.46
4:5:1794:G:O2'	4:5:1796:G:N2	2.48	0.46
6:AA:41:ARG:HG3	23:AR:105:GLN:HB2	1.97	0.46
48:BJ:26:SER:HA	48:BJ:30:LEU:HB2	1.96	0.46
80:CA:616:ASP:N	80:CA:616:ASP:OD1	2.48	0.46
1:2:15:U:H2'	1:2:16:G:O4'	2.16	0.46
1:2:68:A:OP1	12:AG:160:ARG:NH2	2.49	0.46
1:2:1433:G:O2'	35:Ad:24:CYS:SG	2.71	0.46
1:2:1498:G:H2'	1:2:1499:G:H8	1.81	0.46
1:2:1542:G:N2	1:2:1568:C:H1'	2.31	0.46
1:2:1649:G:H2'	1:2:1650:U:C6	2.51	0.46
4:5:1119:C:H2'	4:5:1120:A:C8	2.50	0.46
4:5:1274:A:H2'	4:5:1275:C:H6	1.80	0.46
4:5:1569:U:H5''	4:5:1570:U:H6	1.81	0.46
4:5:1757:A:H5''	58:BT:94:ARG:NH2	2.30	0.46
4:5:3049:A:H4'	40:BB:364:LYS:HE3	1.97	0.46
24:AS:101:LEU:O	24:AS:105:VAL:HG23	2.15	0.46
26:AU:70:THR:OG1	26:AU:72:ASN:OD1	2.32	0.46
50:BL:13:ARG:NH1	50:BL:65:LEU:O	2.48	0.46
57:BS:26:HIS:ND1	57:BS:28:SER:OG	2.45	0.46
80:CA:1548:ASP:HA	80:CA:1640:HIS:CD2	2.51	0.46
1:2:324:U:O2'	17:AL:80:MET:HE2	2.16	0.46
1:2:959:U:C6	19:AN:61:THR:HB	2.49	0.46
1:2:1102:G:OP2	29:AX:7:ARG:NH1	2.41	0.46
1:2:1443:U:H4'	1:2:1446:A:H1'	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1499:G:H1	1:2:1508:U:H3	1.63	0.46
1:2:1680:G:H1'	1:2:1721:A:H61	1.81	0.46
4:5:542:G:C2	4:5:550:A:C2	3.04	0.46
4:5:1336:U:H2'	4:5:1337:A:C8	2.50	0.46
4:5:1411:C:OP1	68:Bd:98:HIS:N	2.47	0.46
4:5:1616:U:H2'	4:5:1617:G:C8	2.51	0.46
4:5:2615:G:H2'	4:5:2616:C:C6	2.51	0.46
4:5:2675:C:OP2	4:5:2676:A:O2'	2.26	0.46
4:5:2697:A:H2'	4:5:2698:G:H8	1.79	0.46
4:5:3218:A:H5''	4:5:3219:G:C4	2.51	0.46
6:AA:182:LEU:HB3	6:AA:188:LEU:HD13	1.98	0.46
8:AC:53:ILE:HG13	8:AC:56:ILE:HD12	1.96	0.46
35:Ad:53:ASN:HB2	35:Ad:55:PHE:CE1	2.51	0.46
38:Ag:17:ASN:HA	38:Ag:308:ASN:HD21	1.81	0.46
40:BB:137:TYR:O	40:BB:139:GLN:NE2	2.49	0.46
41:BC:3:ARG:HB3	41:BC:22:LEU:H	1.81	0.46
46:BH:115:ARG:HG2	46:BH:123:ILE:HD12	1.98	0.46
50:BL:16:GLU:HB3	56:BR:149:LYS:HB3	1.98	0.46
53:BO:138:LYS:HD2	53:BO:140:GLU:CD	2.41	0.46
80:CA:1269:HIS:ND1	80:CA:1303:SER:HB2	2.31	0.46
1:2:139:C:H4'	1:2:140:A:O5'	2.16	0.46
1:2:250:C:H2'	1:2:251:A:C8	2.50	0.46
1:2:1572:G:O2'	11:AF:185:ARG:NH2	2.49	0.46
4:5:1079:A:O2'	42:BD:139:PRO:O	2.26	0.46
4:5:1128:U:OP1	47:BI:4:ARG:NH1	2.35	0.46
4:5:1222:G:O2'	4:5:1223:A:OP2	2.32	0.46
4:5:1576:G:H2'	4:5:1577:G:C8	2.51	0.46
4:5:1619:A:H2	4:5:1825:G:H22	1.64	0.46
4:5:2704:A:O2'	4:5:2705:A:O5'	2.33	0.46
4:5:3066:U:H2'	4:5:3067:C:C6	2.51	0.46
7:AB:54:LEU:HD23	7:AB:54:LEU:H	1.81	0.46
7:AB:189:ILE:HB	7:AB:190:PRO:HD3	1.98	0.46
14:AI:184:LEU:HD22	14:AI:188:GLU:HG2	1.98	0.46
25:AT:20:SER:O	25:AT:24:ARG:HG3	2.16	0.46
38:Ag:249:ARG:HB3	38:Ag:251:TRP:HE3	1.81	0.46
50:BL:38:ILE:O	56:BR:95:ARG:NH2	2.48	0.46
55:BQ:122:VAL:O	55:BQ:126:GLU:HG3	2.15	0.46
59:BU:104:ASN:OD1	59:BU:108:GLU:N	2.48	0.46
62:BX:56:VAL:CG2	62:BX:104:LEU:HB3	2.45	0.46
80:CA:370:LEU:HB3	80:CA:375:ILE:HD13	1.98	0.46
80:CA:434:GLU:OE2	80:CA:660:SER:OG	2.32	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:CA:1746:GLN:OE1	80:CA:1919:ARG:NH2	2.49	0.46
1:2:97:C:H2'	1:2:98:U:C6	2.51	0.45
1:2:227:U:H1'	1:2:834:G:H22	1.81	0.45
1:2:835:U:N3	1:2:836:U:O4	2.49	0.45
1:2:850:A:H2'	1:2:851:U:C6	2.51	0.45
1:2:1691:A:H2'	1:2:1692:G:C8	2.49	0.45
4:5:675:C:H2'	4:5:676:G:O4'	2.17	0.45
4:5:798:G:H4'	49:BK:15:ARG:NE	2.28	0.45
4:5:1001:G:H1'	4:5:1041:U:H5'	1.98	0.45
4:5:1660:C:H2'	4:5:1661:G:C8	2.52	0.45
4:5:1863:G:N1	4:5:1866:C:OP2	2.31	0.45
4:5:3166:C:H2'	4:5:3167:A:C8	2.49	0.45
4:5:3348:G:H1	4:5:3357:U:H3	1.64	0.45
6:AA:27:ARG:HG3	6:AA:28:ASN:H	1.81	0.45
25:AT:34:VAL:O	25:AT:36:ILE:HG13	2.16	0.45
25:AT:65:ILE:HG12	25:AT:71:VAL:HB	1.97	0.45
42:BD:82:GLU:O	42:BD:85:ARG:HG2	2.16	0.45
44:BF:121:LYS:HB2	57:BS:133:ALA:HB3	1.97	0.45
47:BI:36:LEU:HD21	47:BI:69:ARG:NH1	2.31	0.45
48:BJ:37:LEU:HD13	48:BJ:69:VAL:HG12	1.97	0.45
50:BL:73:PRO:HG2	50:BL:76:ALA:HB2	1.98	0.45
52:BN:37[A]:ARG:HG2	52:BN:107[A]:GLY:HA2	1.98	0.45
53:BO:115:SER:OG	53:BO:151:THR:OG1	2.22	0.45
80:CA:1348:PHE:O	80:CA:1352:MET:HE2	2.15	0.45
80:CA:1725:LEU:HD13	80:CA:1730:TYR:HB3	1.98	0.45
81:CB:218:LEU:HD22	81:CB:233:ALA:HB1	1.98	0.45
1:2:52:U:H2'	1:2:53:G:C8	2.51	0.45
1:2:200:A:H2'	1:2:201:G:C8	2.52	0.45
1:2:842:C:H2'	1:2:843:U:O4'	2.15	0.45
1:2:1368:G:H5''	25:AT:69:LYS:HG2	1.96	0.45
1:2:1550:A:H2'	1:2:1551:U:C6	2.51	0.45
4:5:616:G:H2'	4:5:617:G:H8	1.81	0.45
4:5:1565:G:H1	4:5:1574:C:N4	2.13	0.45
5:6:19:U:O2'	5:6:21:A:OP1	2.34	0.45
10:AE:182:TYR:HB2	10:AE:228:ILE:HD13	1.99	0.45
16:AK:4:PRO:HG2	16:AK:7:ASP:HB2	1.97	0.45
27:AV:71:ARG:HE	33:Ab:4:VAL:HG11	1.81	0.45
38:Ag:54:PHE:CD2	38:Ag:312:VAL:HG21	2.51	0.45
40:BB:88:GLY:HA2	40:BB:105:VAL:O	2.16	0.45
42:BD:119:TYR:OH	42:BD:140:ARG:N	2.49	0.45
45:BG:161:GLU:CD	51:BM:26:ARG:HH22	2.24	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:Bc:31:ARG:O	67:Bc:35:GLU:HG2	2.17	0.45
78:Bn:8:ARG:HG2	78:Bn:10:THR:HG23	1.98	0.45
80:CA:240:THR:HB	80:CA:254:PRO:HB3	1.98	0.45
80:CA:1387:LEU:HD22	81:CB:94:LEU:HB3	1.99	0.45
1:2:1477:G:H2'	1:2:1478:G:C8	2.49	0.45
3:4:45:A:H2'	3:4:46:A:C8	2.50	0.45
4:5:1566:A:H2'	4:5:1567:U:C5	2.52	0.45
4:5:3296:A:H2'	4:5:3297:U:H6	1.80	0.45
4:5:3387:U:H2'	4:5:3388:C:C6	2.51	0.45
8:AC:232:GLU:N	8:AC:232:GLU:OE1	2.49	0.45
9:AD:195:SER:O	9:AD:196:ARG:HG2	2.15	0.45
10:AE:19:LEU:HB2	10:AE:51:ARG:HH22	1.81	0.45
16:AK:11:ILE:HD11	16:AK:42:VAL:HG22	1.98	0.45
21:AP:108:ARG:NH1	21:AP:110:GLU:HB3	2.32	0.45
22:AQ:46:PHE:HA	22:AQ:49:TYR:HD2	1.80	0.45
41:BC:35:VAL:HG21	41:BC:244:LEU:HD21	1.97	0.45
51:BM:65:ARG:HB2	51:BM:127:TYR:HB3	1.98	0.45
52:BN:113[A]:ASP:OD1	52:BN:114[A]:LYS:N	2.49	0.45
58:BT:19:VAL:O	58:BT:22:PRO:HD2	2.16	0.45
80:CA:696:LEU:O	80:CA:700:GLN:NE2	2.49	0.45
80:CA:1151:LEU:H	80:CA:1151:LEU:HD23	1.80	0.45
80:CA:1483:PHE:HB2	80:CA:1490:TYR:CE2	2.51	0.45
80:CA:1507:ARG:HB2	80:CA:1510:TYR:HB2	1.98	0.45
1:2:183:U:H2'	1:2:184:C:C6	2.52	0.45
1:2:841:U:H2'	1:2:842:C:H6	1.81	0.45
1:2:1359:C:OP1	25:AT:130:ARG:NH1	2.49	0.45
1:2:1534:G:OP2	31:AZ:74:SER:OG	2.18	0.45
3:4:115:G:H2'	3:4:116:C:C6	2.52	0.45
4:5:707:U:OP1	4:5:780:A:O2'	2.21	0.45
4:5:737:G:H2'	4:5:738:A:H8	1.81	0.45
4:5:1097:G:H4'	4:5:1098:A:O5'	2.17	0.45
4:5:1666:G:H2'	4:5:1667:A:H8	1.81	0.45
8:AC:59:HIS:CE1	8:AC:239:PRO:HD3	2.51	0.45
11:AF:37:GLN:HA	22:AQ:53:LEU:HB3	1.97	0.45
15:AJ:59:LEU:HD22	15:AJ:69:ARG:HA	1.99	0.45
23:AR:78:ARG:NH1	23:AR:78:ARG:O	2.49	0.45
26:AU:30:LYS:NZ	26:AU:111:GLY:HA3	2.31	0.45
62:BX:23:PRO:HG2	62:BX:26:GLN:HG3	1.98	0.45
70:Bf:76:TYR:HB3	70:Bf:80:ARG:HB2	1.98	0.45
80:CA:641:ILE:HB	80:CA:683:LEU:HA	1.98	0.45
80:CA:1906:LEU:N	80:CA:1918:LYS:O	2.44	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:103:A:H4'	1:2:105:A:C8	2.52	0.45
1:2:979:A:H5'	1:2:1787:C:H1'	1.98	0.45
1:2:1146:G:H2'	1:2:1147:A:C8	2.52	0.45
1:2:1216:C:HO2'	1:2:1217:A:P	2.40	0.45
1:2:1524:A:N3	1:2:1590:G:O2'	2.37	0.45
4:5:781:G:OP1	54:BP:151:ARG:NH1	2.40	0.45
4:5:798:G:OP1	64:BZ:33:GLY:N	2.45	0.45
4:5:2745:G:N2	4:5:2748:A:OP2	2.44	0.45
4:5:2767:U:H2'	4:5:2768:U:C6	2.52	0.45
8:AC:59:HIS:CD2	8:AC:238:SER:HA	2.52	0.45
30:AY:63:GLN:HG3	30:AY:68:LYS:HB3	1.98	0.45
32:Aa:64:LEU:HD12	32:Aa:64:LEU:HA	1.82	0.45
38:Ag:108:SER:HB3	38:Ag:127:ARG:HB3	1.97	0.45
41:BC:3:ARG:HE	41:BC:22:LEU:HB2	1.82	0.45
50:BL:3:THR:OG1	50:BL:4:ASP:N	2.48	0.45
80:CA:383:ASP:OD1	80:CA:383:ASP:N	2.49	0.45
80:CA:446:ARG:HD3	80:CA:721:LEU:HD21	1.97	0.45
80:CA:493:ARG:HH12	80:CA:497:LEU:HD22	1.80	0.45
80:CA:538:PHE:HD2	80:CA:639:VAL:HG13	1.82	0.45
80:CA:1117:LYS:O	80:CA:1117:LYS:HD3	2.16	0.45
1:2:227:U:H2'	1:2:228:G:C8	2.52	0.45
1:2:844:A:H2'	1:2:845:G:C8	2.52	0.45
1:2:928:U:H4'	1:2:929:A:O5'	2.16	0.45
1:2:1508:U:H2'	1:2:1509:C:C6	2.52	0.45
2:3:26:U:H2'	2:3:27:U:C6	2.51	0.45
4:5:776:U:OP1	65:Ba:41:ARG:NH1	2.43	0.45
4:5:1407:A:O3'	68:Bd:33:ARG:NH2	2.50	0.45
4:5:1597:C:H2'	4:5:1598:G:H8	1.80	0.45
4:5:2961:G:H2'	4:5:2962:U:H6	1.80	0.45
9:AD:222:VAL:HG12	38:Ag:192:PHE:HD1	1.81	0.45
12:AG:27:PHE:HE1	12:AG:36:VAL:HG21	1.82	0.45
24:AS:4:VAL:HG22	31:AZ:82:HIS:CE1	2.52	0.45
38:Ag:107:LYS:HE2	38:Ag:107:LYS:HA	1.98	0.45
39:BA:103:PRO:HA	39:BA:163:ARG:HA	1.98	0.45
40:BB:348:ARG:HG2	40:BB:348:ARG:O	2.16	0.45
50:BL:65:LEU:HG	56:BR:172:TYR:OH	2.16	0.45
56:BR:77:VAL:HG12	56:BR:126:VAL:HG22	1.98	0.45
58:BT:50:LEU:HB2	58:BT:54:VAL:HG22	1.98	0.45
64:BZ:78:LEU:O	64:BZ:78:LEU:HD23	2.16	0.45
80:CA:348:LYS:HE2	80:CA:420:LYS:HE2	1.98	0.45
80:CA:380:LEU:HD22	80:CA:403:LYS:HE2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1:U:H3	15:AJ:50:SER:HG	1.63	0.45
1:2:571:G:H5''	29:AX:114:LYS:HE2	1.97	0.45
1:2:1040:G:H5'	6:AA:32:HIS:CD2	2.48	0.45
1:2:1241:G:H1'	21:AP:79:HIS:H	1.81	0.45
1:2:1480:G:H2'	1:2:1481:C:O4'	2.16	0.45
2:3:27:U:H2'	2:3:28:C:H6	1.82	0.45
4:5:314:U:H2'	4:5:315:C:H6	1.82	0.45
4:5:533:A:O2'	4:5:535:G:OP2	2.32	0.45
4:5:1257:C:N4	4:5:1261:G:N2	2.65	0.45
4:5:2836:C:H5	4:5:2852:C:H42	1.64	0.45
38:Ag:260:ILE:HB	38:Ag:274:LEU:HB2	1.97	0.45
46:BH:112:ILE:HB	46:BH:126:VAL:HG23	1.98	0.45
68:Bd:12:LYS:NZ	68:Bd:58:GLY:O	2.42	0.45
69:Be:20:LYS:HG2	69:Be:21:ARG:HD2	1.99	0.45
80:CA:467:LEU:HD21	80:CA:473:VAL:HG11	1.98	0.45
80:CA:651:LYS:HG2	80:CA:655:ILE:HG21	1.98	0.45
80:CA:1452:LYS:HE2	80:CA:1454:LYS:HD2	1.98	0.45
81:CB:120:LEU:HD11	81:CB:148:LEU:HB3	1.98	0.45
1:2:153:G:H5'	30:AY:131:ARG:NH1	2.32	0.45
1:2:861:U:O2'	28:AW:56:HIS:O	2.35	0.45
1:2:1116:A:OP1	77:Bm:17:ARG:NH2	2.46	0.45
1:2:1290:U:H2'	1:2:1291:G:N3	2.32	0.45
1:2:1488:G:O2'	1:2:1494:C:O2	2.32	0.45
4:5:295:A:H2'	4:5:296:A:C8	2.51	0.45
4:5:632:G:H2'	4:5:633:C:C6	2.52	0.45
4:5:1018:G:O6	4:5:1034:U:O4	2.35	0.45
4:5:1404:G:N2	4:5:1407:A:OP2	2.29	0.45
4:5:2423:U:H2'	4:5:2424:A:H8	1.81	0.45
4:5:3281:U:H2'	4:5:3282:U:C6	2.51	0.45
10:AE:176:ASP:HB2	10:AE:179:LYS:HZ2	1.81	0.45
12:AG:23:ARG:H	12:AG:24:ILE:HD12	1.81	0.45
21:AP:34:VAL:HG11	21:AP:45:PHE:HD2	1.81	0.45
22:AQ:129:PHE:CE2	26:AU:78:THR:HA	2.52	0.45
36:Ae:52:GLY:O	36:Ae:53:LYS:HE2	2.17	0.45
38:Ag:10:ARG:HB2	38:Ag:314:GLN:NE2	2.32	0.45
38:Ag:144:LEU:HD12	38:Ag:181:TRP:CE3	2.51	0.45
41:BC:23:PRO:HD2	41:BC:26:PHE:CD2	2.51	0.45
46:BH:19:SER:OG	46:BH:26:LYS:HE2	2.17	0.45
55:BQ:23:TRP:CE3	55:BQ:51:VAL:HG22	2.52	0.45
73:Bi:29:VAL:O	73:Bi:32:LYS:NZ	2.34	0.45
80:CA:435:ASP:HA	80:CA:706:ARG:HD2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:CA:535:VAL:O	80:CA:536:MET:HE2	2.16	0.45
80:CA:1199:ARG:NH2	80:CA:1203:ASP:OD1	2.50	0.45
81:CB:287:LYS:O	81:CB:294:ASN:ND2	2.45	0.45
1:2:35:U:H2'	1:2:36:C:C6	2.52	0.45
1:2:119:A:H1'	1:2:397:A:C8	2.52	0.45
1:2:125:U:OP1	12:AG:201:GLN:NE2	2.50	0.45
1:2:1414:U:H5'	23:AR:3:ARG:NH2	2.30	0.45
1:2:1592:A:H2'	1:2:1593:A:C8	2.52	0.45
2:3:10:A:H2'	2:3:11:C:C6	2.51	0.45
4:5:976:U:H2'	4:5:977:C:O4'	2.17	0.45
7:AB:157:GLN:C	7:AB:159:SER:H	2.25	0.45
11:AF:57:SER:OG	11:AF:167:ARG:NH2	2.50	0.45
26:AU:22:ILE:N	26:AU:93:LEU:O	2.45	0.45
37:Af:83:LYS:HD2	37:Af:85:TYR:H	1.82	0.45
41:BC:126:ILE:HD11	41:BC:233:LEU:HD13	1.99	0.45
48:BJ:26:SER:HB2	48:BJ:64:LYS:O	2.17	0.45
53:BO:41:LEU:HD13	53:BO:150:VAL:HG11	1.99	0.45
80:CA:457:MET:HE2	80:CA:457:MET:N	2.32	0.45
80:CA:1448:GLN:O	80:CA:1452:LYS:NZ	2.50	0.45
81:CB:250:LEU:HB2	81:CB:289:LYS:HD2	1.98	0.45
1:2:108:A:H2'	1:2:109:G:C8	2.51	0.45
1:2:190:C:C5	1:2:191:C:H1'	2.52	0.45
1:2:407:A:H2'	1:2:408:C:H6	1.82	0.45
1:2:632:U:O2'	1:2:1103:U:OP1	2.35	0.45
1:2:930:A:O2'	7:AB:111:ARG:NH1	2.50	0.45
1:2:996:U:H3	1:2:1008:G:H1	1.65	0.45
1:2:1182:U:H4'	21:AP:124:THR:HB	1.98	0.45
1:2:1281:G:O3'	26:AU:76:SER:OG	2.35	0.45
1:2:1623:C:H2'	1:2:1624:C:H6	1.82	0.45
1:2:1790:A:O2'	1:2:1791:A:H5'	2.17	0.45
1:2:1797:A:N6	32:Aa:84:VAL:HB	2.32	0.45
3:4:16:U:H2'	3:4:17:A:C8	2.52	0.45
4:5:393:U:H2'	4:5:394:G:O4'	2.17	0.45
4:5:674:G:H2'	4:5:675:C:C6	2.52	0.45
4:5:1193:A:OP2	52:BN:49[A]:ARG:NH1	2.49	0.45
4:5:1758:G:H2'	4:5:1759:C:C6	2.52	0.45
4:5:2426:U:H2'	4:5:2427:U:C6	2.52	0.45
15:AJ:83:VAL:HA	15:AJ:149:ARG:HA	1.99	0.45
35:Ad:11:PRO:HB2	35:Ad:13:ARG:HE	1.82	0.45
38:Ag:127:ARG:HD2	38:Ag:150:TRP:CG	2.52	0.45
41:BC:77:VAL:O	41:BC:86:GLY:N	2.35	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:BL:113:THR:OG1	50:BL:116:GLU:HG3	2.17	0.45
80:CA:422:LYS:NZ	80:CA:456:SER:OG	2.48	0.45
80:CA:520:VAL:O	80:CA:524:LYS:NZ	2.49	0.45
80:CA:604:ARG:HA	80:CA:607:ARG:HG2	1.98	0.45
1:2:451:A:N6	1:2:453:U:O2	2.50	0.44
1:2:1025:A:H5'	1:2:1774:G:H4'	1.99	0.44
1:2:1392:U:OP1	23:AR:59:LYS:NZ	2.45	0.44
4:5:45:A:OP2	51:BM:85:THR:HG21	2.18	0.44
4:5:759:U:H2'	4:5:760:G:O4'	2.17	0.44
4:5:821:U:H2'	4:5:822:G:H8	1.82	0.44
4:5:1784:G:H2'	4:5:1785:U:O4'	2.17	0.44
4:5:2549:G:OP2	4:5:2549:G:N2	2.50	0.44
4:5:2991:A:N3	53:BO:69:ARG:NH2	2.65	0.44
4:5:3251:U:H2'	4:5:3252:G:C8	2.52	0.44
6:AA:157:ASP:OD1	27:AV:60:ARG:NH1	2.50	0.44
7:AB:122:GLU:HG2	7:AB:140:ILE:HG13	2.00	0.44
10:AE:87:MET:HE3	10:AE:226:PHE:CE2	2.53	0.44
14:AI:121:LEU:HA	14:AI:121:LEU:HD23	1.85	0.44
19:AN:119:GLU:HG2	19:AN:141:TYR:HE2	1.81	0.44
28:AW:89:TRP:O	28:AW:93:LEU:HD23	2.17	0.44
64:BZ:77:LYS:C	64:BZ:79:TRP:N	2.74	0.44
71:Bg:38:ARG:HH11	71:Bg:38:ARG:HG2	1.82	0.44
80:CA:1373:LEU:HD23	80:CA:1475:VAL:HG12	1.98	0.44
1:2:655:G:H4'	1:2:656:G:C8	2.52	0.44
1:2:824:G:H2'	1:2:825:U:H6	1.82	0.44
1:2:835:U:H2'	1:2:836:U:C5	2.51	0.44
1:2:1287:A:H4'	1:2:1288:G:H5'	1.99	0.44
1:2:1553:G:N2	1:2:1555:A:H3'	2.32	0.44
1:2:1591:C:H2'	1:2:1592:A:C8	2.52	0.44
4:5:129:U:H2'	4:5:130:A:C8	2.52	0.44
4:5:1225:A:C6	4:5:1226:G:C6	3.06	0.44
4:5:2512:C:H2'	4:5:2513:U:C6	2.52	0.44
10:AE:193:GLY:HA3	10:AE:210:ILE:CG2	2.46	0.44
22:AQ:37:THR:O	22:AQ:45:ARG:NH1	2.50	0.44
37:Af:135:HIS:C	37:Af:136:LYS:HD2	2.42	0.44
62:BX:53:ASP:O	62:BX:69:LYS:NZ	2.44	0.44
66:Bb:14:LEU:O	66:Bb:18:ILE:HG12	2.17	0.44
67:Bc:11:GLU:HG2	67:Bc:96:VAL:HG21	1.99	0.44
80:CA:1042:SER:HB2	80:CA:1078:PRO:HD2	2.00	0.44
80:CA:1257:VAL:HG13	80:CA:1257:VAL:O	2.17	0.44
80:CA:1612:ARG:HD2	80:CA:1617:VAL:HG13	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:141:U:O2'	1:2:142:G:H8	2.01	0.44
1:2:886:U:C2	1:2:887:A:C8	3.06	0.44
1:2:1087:A:H2'	1:2:1088:A:C8	2.52	0.44
1:2:1237:G:H2'	1:2:1238:A:H8	1.82	0.44
2:3:114:G:OP1	4:5:1831:U:O2'	2.25	0.44
4:5:59:G:H4'	4:5:60:A:H4'	1.99	0.44
4:5:178:U:H3	4:5:239:G:H22	1.66	0.44
4:5:698:U:H2'	4:5:699:A:O4'	2.17	0.44
4:5:1609:C:H2'	4:5:1610:G:C8	2.52	0.44
4:5:1824:U:C2	4:5:1825:G:C8	3.06	0.44
8:AC:39:THR:HG22	8:AC:41:LEU:H	1.82	0.44
8:AC:139:ILE:HD13	8:AC:218:ILE:HB	1.98	0.44
18:AM:67:THR:HG22	18:AM:68:GLU:HG3	1.98	0.44
20:AO:80:HIS:ND1	20:AO:114:ARG:HB2	2.33	0.44
23:AR:89:SER:O	23:AR:92:ASP:N	2.34	0.44
26:AU:28:SER:HB3	26:AU:112:VAL:HA	1.99	0.44
38:Ag:312:VAL:O	38:Ag:313:TRP:HD1	2.01	0.44
48:BJ:85:LYS:HE2	48:BJ:85:LYS:HB2	1.76	0.44
49:BK:155:GLU:OE2	64:BZ:90:TYR:OH	2.32	0.44
63:BY:25:ILE:HA	63:BY:43:VAL:HG12	1.99	0.44
80:CA:474:ALA:HB3	80:CA:481:ARG:NH2	2.32	0.44
80:CA:1606:SER:O	80:CA:1609:GLU:HG3	2.18	0.44
80:CA:1615:GLN:HE21	80:CA:1647:LEU:HD22	1.82	0.44
1:2:513:U:H2'	1:2:514:G:H8	1.81	0.44
1:2:817:A:H2'	1:2:818:C:C6	2.52	0.44
1:2:1260:U:H2'	1:2:1261:G:C8	2.52	0.44
1:2:1511:U:H2'	1:2:1512:G:C8	2.53	0.44
1:2:1625:C:H2'	1:2:1626:U:H6	1.82	0.44
1:2:1684:U:H2'	1:2:1685:G:H8	1.83	0.44
1:2:1775:U:H2'	1:2:1776:A:C8	2.53	0.44
4:5:12:A:H2'	4:5:13:A:C8	2.52	0.44
4:5:180:C:H2'	4:5:181:U:H6	1.83	0.44
4:5:1497:C:O2'	4:5:1602:A:N3	2.44	0.44
4:5:1801:U:H2'	4:5:1802:C:C6	2.52	0.44
4:5:3272:C:O2	43:BE:80:ASN:ND2	2.38	0.44
4:5:3302:U:H3	4:5:3312:U:H3	1.66	0.44
7:AB:32:ILE:HB	7:AB:43:VAL:HB	1.98	0.44
18:AM:108:ARG:O	18:AM:110:GLY:N	2.50	0.44
22:AQ:77:GLN:O	22:AQ:81:ILE:HG13	2.18	0.44
38:Ag:192:PHE:HE1	38:Ag:228:LYS:HG3	1.83	0.44
42:BD:148:ILE:HG22	42:BD:159:VAL:HG21	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:BD:183:TRP:HD1	42:BD:190:ILE:HB	1.83	0.44
48:BJ:112:LEU:O	48:BJ:114:ILE:HG12	2.17	0.44
67:Bc:20:LEU:HD11	67:Bc:32:ALA:HB2	1.99	0.44
76:Bl:99:CYS:HB2	76:Bl:114:LYS:HD2	1.99	0.44
80:CA:253:ILE:HA	80:CA:499:GLN:O	2.17	0.44
80:CA:742:ARG:HA	80:CA:742:ARG:HD2	1.83	0.44
80:CA:1746:GLN:HA	80:CA:1749:ILE:HD12	2.00	0.44
81:CB:171:GLN:HB2	81:CB:214:TRP:CE3	2.52	0.44
1:2:172:C:H2'	1:2:173:A:C8	2.53	0.44
1:2:448:C:OP1	10:AE:29:PRO:HG3	2.17	0.44
1:2:1086:A:H2'	1:2:1087:A:C8	2.52	0.44
1:2:1226:A:O2'	1:2:1227:A:O5'	2.29	0.44
3:4:19:C:H2'	3:4:20:A:C8	2.53	0.44
4:5:73:C:N3	72:Bh:15:LYS:HD3	2.33	0.44
4:5:307:A:H2'	4:5:308:A:H8	1.82	0.44
4:5:1941:C:H2'	4:5:1942:U:C6	2.51	0.44
4:5:2896:A:OP1	76:Bl:124:LYS:NZ	2.47	0.44
4:5:2947:G:C2	40:BB:250:ALA:HB1	2.53	0.44
19:AN:119:GLU:HA	19:AN:122:ILE:HD12	2.00	0.44
38:Ag:214:ALA:HB1	38:Ag:240:VAL:HG11	1.99	0.44
40:BB:111:SER:O	40:BB:115:LYS:HG2	2.17	0.44
40:BB:343:TYR:CE2	40:BB:345:ASN:HB2	2.51	0.44
47:Bl:170:LYS:HA	47:Bl:177:ASP:HA	1.99	0.44
50:BL:70:PHE:CE2	50:BL:72:LEU:HG	2.52	0.44
80:CA:1520:THR:HG21	80:CA:1528:TYR:HE2	1.81	0.44
80:CA:1685:MET:HE1	80:CA:1730:TYR:HE2	1.82	0.44
81:CB:291:LEU:HD23	81:CB:291:LEU:H	1.82	0.44
1:2:1494:C:H2'	1:2:1495:C:C6	2.53	0.44
1:2:1757:G:OP2	4:5:2256:A:N6	2.51	0.44
2:3:40:A:N1	4:5:22:G:O2'	2.49	0.44
3:4:74:C:H2'	3:4:75:G:C8	2.53	0.44
4:5:117:U:O2'	4:5:119:U:OP2	2.23	0.44
4:5:132:C:H2'	4:5:133:U:H5''	1.99	0.44
4:5:184:U:H2'	4:5:185:C:C6	2.53	0.44
4:5:551:A:O2'	4:5:552:G:H8	2.01	0.44
4:5:926:A:H2'	4:5:927:C:C6	2.52	0.44
4:5:992:A:O2'	4:5:993:G:H5'	2.17	0.44
4:5:1621:A:H2'	4:5:1622:U:H6	1.83	0.44
4:5:1667:A:H2'	4:5:1668:G:H8	1.79	0.44
4:5:2933:A:OP1	4:5:3015:G:H4'	2.18	0.44
6:AA:168:HIS:ND1	6:AA:203:PHE:HE2	2.15	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AB:97:LEU:HD22	7:AB:232:HIS:CG	2.53	0.44
10:AE:94:ALA:O	10:AE:95:THR:OG1	2.29	0.44
13:AH:14:THR:O	13:AH:18:LEU:HG	2.18	0.44
21:AP:108:ARG:HG2	21:AP:109:PRO:HD2	2.00	0.44
32:Aa:58:VAL:HG23	32:Aa:59:TYR:CD2	2.52	0.44
33:Ab:40:CYS:HB2	33:Ab:42:ASN:ND2	2.32	0.44
43:BE:7:PRO:HG2	43:BE:10:TYR:CZ	2.52	0.44
44:BF:175:LYS:HB2	44:BF:175:LYS:HE3	1.75	0.44
47:BI:82:ARG:HE	47:BI:83:ASP:CG	2.26	0.44
63:BY:89:VAL:HG12	63:BY:92:PHE:CZ	2.52	0.44
70:Bf:15:THR:HG22	70:Bf:16:ARG:N	2.33	0.44
80:CA:639:VAL:HG21	80:CA:665:ILE:O	2.17	0.44
80:CA:644:THR:HG21	80:CA:693:TYR:HE2	1.82	0.44
80:CA:1425:LEU:HD23	80:CA:1425:LEU:H	1.83	0.44
1:2:627:C:H2'	1:2:628:G:O4'	2.17	0.44
1:2:890:C:H2'	1:2:891:A:H8	1.83	0.44
1:2:1584:G:O2'	1:2:1585:U:OP2	2.35	0.44
1:2:1647:U:H2'	1:2:1648:A:H8	1.81	0.44
4:5:358:G:N2	4:5:361:A:OP2	2.47	0.44
4:5:1362:G:H2'	4:5:1363:A:C8	2.53	0.44
4:5:1486:G:H21	70:Bf:6:THR:HG22	1.81	0.44
4:5:1804:A:H2'	4:5:1805:C:H6	1.83	0.44
4:5:2668:U:H2'	4:5:2669:G:C8	2.52	0.44
4:5:2927:C:H2'	4:5:2928:C:C6	2.53	0.44
4:5:3335:A:H2'	4:5:3336:A:C8	2.53	0.44
9:AD:42:THR:HB	9:AD:45:LYS:O	2.17	0.44
12:AG:159:ARG:HB3	12:AG:170:THR:HB	2.00	0.44
18:AM:74:LEU:HD21	37:Af:106:TYR:CD2	2.52	0.44
33:Ab:61:THR:O	33:Ab:62:ILE:HG12	2.18	0.44
38:Ag:29:GLN:HG3	38:Ag:32:LEU:HD13	1.99	0.44
46:BH:118:LEU:HD11	46:BH:167:VAL:HG22	1.99	0.44
52:BN:194[A]:LEU:HD22	52:BN:199[A]:TYR:HB2	2.00	0.44
58:BT:19:VAL:O	58:BT:23:THR:HG23	2.17	0.44
64:BZ:27:LYS:HA	64:BZ:27:LYS:HD2	1.73	0.44
80:CA:242:ARG:HA	80:CA:252:ILE:HG23	2.00	0.44
80:CA:467:LEU:HD23	80:CA:473:VAL:HG21	2.00	0.44
80:CA:535:VAL:O	80:CA:621:VAL:HA	2.18	0.44
80:CA:563:ASP:N	80:CA:563:ASP:OD1	2.50	0.44
80:CA:1666:ALA:HB3	80:CA:1669:TYR:HD2	1.81	0.44
1:2:213:A:H2'	1:2:214:G:O4'	2.17	0.44
1:2:252:U:H2'	1:2:253:A:H8	1.80	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1518:C:H2'	1:2:1519:U:C6	2.52	0.44
4:5:113:C:OP1	51:BM:147:ARG:NE	2.40	0.44
4:5:546:C:H5''	4:5:547:G:H5'	2.00	0.44
4:5:1771:C:H2'	4:5:1772:U:O4'	2.18	0.44
7:AB:138:PHE:O	7:AB:212:VAL:HG22	2.18	0.44
7:AB:222:LYS:C	7:AB:222:LYS:HD3	2.43	0.44
8:AC:35:TRP:CE3	8:AC:46:LYS:HD3	2.51	0.44
11:AF:145:ASP:HB2	11:AF:162:VAL:HG22	2.00	0.44
13:AH:8:ILE:O	13:AH:42:GLN:HG3	2.18	0.44
18:AM:129:GLU:OE1	18:AM:130:THR:HG22	2.18	0.44
22:AQ:49:TYR:HD1	22:AQ:52:LEU:HD12	1.83	0.44
25:AT:23:GLN:NE2	25:AT:51:GLU:O	2.51	0.44
58:BT:99:LYS:HB2	58:BT:102:GLU:CD	2.42	0.44
59:BU:38:ALA:HB3	59:BU:59:MET:HB2	1.99	0.44
62:BX:70:ILE:HD12	62:BX:80:VAL:CG1	2.48	0.44
63:BY:105:SER:HG	63:BY:106:GLN:N	2.15	0.44
80:CA:351:TYR:HB3	80:CA:398:VAL:HG22	1.99	0.44
80:CA:488:PHE:HB3	80:CA:492:PHE:HD2	1.82	0.44
80:CA:640:ILE:HG23	80:CA:682:ILE:HD11	2.00	0.44
80:CA:1189:VAL:HG22	80:CA:1237:VAL:HB	1.99	0.44
80:CA:1352:MET:HG3	80:CA:1381:GLN:OE1	2.18	0.44
80:CA:1385:THR:HG22	80:CA:1478:LYS:HE3	2.00	0.44
80:CA:1740:GLN:HG3	80:CA:1743:ARG:HD3	1.98	0.44
1:2:17:C:H2'	1:2:18:C:H6	1.83	0.44
1:2:56:U:H5''	1:2:403:G:H22	1.83	0.44
1:2:404:G:H2'	1:2:405:C:C6	2.53	0.44
1:2:989:U:H2'	1:2:990:C:C6	2.53	0.44
1:2:1004:U:O2'	1:2:1779:U:O2'	2.29	0.44
2:3:141:C:H2'	2:3:142:C:H6	1.83	0.44
4:5:631:U:H2'	4:5:632:G:C8	2.53	0.44
4:5:928:C:H2'	4:5:929:A:C8	2.52	0.44
4:5:929:A:H2'	4:5:930:U:C6	2.53	0.44
4:5:1307:G:H1'	4:5:1308:A:C8	2.53	0.44
4:5:2668:U:H2'	4:5:2669:G:H8	1.83	0.44
4:5:2972:G:H2'	4:5:2973:G:H8	1.82	0.44
4:5:3159:C:H2'	4:5:3160:U:C6	2.53	0.44
11:AF:112:ARG:HD2	11:AF:116:HIS:CE1	2.53	0.44
13:AH:159:VAL:HG12	13:AH:163:ASP:HB3	2.00	0.44
14:AI:194:ARG:HH11	14:AI:194:ARG:HG3	1.83	0.44
27:AV:12:TYR:CG	27:AV:12:TYR:O	2.70	0.44
30:AY:15:ASN:ND2	30:AY:22:GLN:OE1	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Aa:37:LYS:HD3	32:Aa:37:LYS:H	1.83	0.44
39:BA:140:ASN:O	39:BA:144:ASN:HA	2.18	0.44
45:BG:228:GLU:OE1	45:BG:228:GLU:N	2.51	0.44
52:BN:189[A]:ASP:OD1	52:BN:189[A]:ASP:N	2.47	0.44
80:CA:279:CYS:SG	80:CA:300:TYR:OH	2.72	0.44
80:CA:1153:ASN:HD21	82:CC:197:LYS:HE3	1.83	0.44
80:CA:1298:ARG:NH2	80:CA:1299:LEU:O	2.32	0.44
80:CA:1533:ASN:ND2	82:CC:346:THR:OG1	2.45	0.44
80:CA:1773:GLN:HB2	80:CA:1775:TYR:CD1	2.53	0.44
80:CA:1904:TRP:HB3	80:CA:1950:LEU:HD11	2.00	0.44
80:CA:1939:GLU:HA	80:CA:1942:ARG:HG3	1.99	0.44
81:CB:199:SER:HB3	81:CB:201:GLN:HE21	1.83	0.44
1:2:649:U:H2'	1:2:650:U:C6	2.53	0.43
1:2:1430:U:O2'	1:2:1431:C:OP1	2.28	0.43
1:2:1522:U:H4'	1:2:1523:G:OP2	2.18	0.43
4:5:346:C:N4	4:5:349:A:OP2	2.27	0.43
4:5:1665:C:H2'	4:5:1666:G:H8	1.83	0.43
4:5:2366:C:H2'	4:5:2367:A:C8	2.52	0.43
7:AB:79:HIS:O	7:AB:82:ARG:HB2	2.18	0.43
8:AC:188:LEU:HD13	8:AC:196:VAL:HG11	2.00	0.43
15:AJ:90:LYS:HD2	15:AJ:95:TYR:CD1	2.53	0.43
18:AM:62:LEU:HD23	18:AM:63:VAL:O	2.17	0.43
58:BT:38:ILE:HG23	58:BT:50:LEU:HD11	1.99	0.43
62:BX:31:LEU:HB3	62:BX:101:PRO:HG3	1.99	0.43
80:CA:578:SER:HA	80:CA:581:LYS:HE2	2.00	0.43
80:CA:1358:PRO:HA	80:CA:1361:MET:HE2	1.99	0.43
81:CB:169:GLN:HA	81:CB:172:GLN:HE22	1.83	0.43
1:2:189:C:H41	14:AI:137:LYS:HE3	1.83	0.43
1:2:856:A:N6	13:AH:116:ARG:HD2	2.33	0.43
1:2:886:U:H2'	1:2:887:A:C8	2.54	0.43
1:2:1222:C:H2'	1:2:1223:A:H8	1.83	0.43
4:5:80:G:H2'	4:5:81:C:H6	1.84	0.43
4:5:130:A:H2'	4:5:131:C:C6	2.53	0.43
4:5:595:G:N1	4:5:609:G:H5''	2.32	0.43
4:5:1098:A:OP2	57:BS:129:LYS:HA	2.18	0.43
4:5:3006:A:H2'	4:5:3007:U:O4'	2.19	0.43
15:AJ:119:ALA:O	15:AJ:120:LYS:HG2	2.18	0.43
49:BK:154:VAL:HG22	49:BK:155:GLU:H	1.83	0.43
52:BN:126[A]:VAL:O	56:BR:154:HIS:NE2	2.44	0.43
61:BW:69:SER:O	61:BW:73:MET:N	2.48	0.43
64:BZ:91:LEU:HA	64:BZ:121:VAL:HG21	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:Bd:96:ILE:HG21	68:Bd:105:ARG:HG2	2.00	0.43
74:Bj:3:ARG:NH1	74:Bj:4:GLU:OE1	2.51	0.43
80:CA:1475:VAL:HG22	80:CA:1505:ALA:HB2	2.00	0.43
1:2:161:U:OP2	12:AG:87:ARG:NH2	2.51	0.43
1:2:187:G:H3'	14:AI:138:ASN:HD22	1.83	0.43
1:2:196:G:O6	14:AI:137:LYS:NZ	2.52	0.43
1:2:1220:C:H2'	1:2:1221:A:C8	2.53	0.43
1:2:1281:G:H5''	26:AU:78:THR:HG21	2.00	0.43
2:3:128:U:OP1	2:3:129:C:N4	2.31	0.43
4:5:246:U:H2'	4:5:247:C:C6	2.53	0.43
4:5:411:U:H2'	4:5:412:G:H8	1.83	0.43
4:5:426:G:OP1	68:Bd:15:LYS:NZ	2.46	0.43
4:5:1317:A:O2'	4:5:1318:A:H3'	2.18	0.43
4:5:2154:U:H2'	4:5:2155:G:C8	2.53	0.43
4:5:2218:G:H2'	4:5:2219:A:H8	1.82	0.43
4:5:2588:U:OP1	45:BG:241:LYS:NZ	2.50	0.43
6:AA:84:ARG:HH21	6:AA:88:LYS:HZ3	1.66	0.43
8:AC:58:LEU:HA	27:AV:12:TYR:HE1	1.83	0.43
9:AD:40:ARG:HH12	9:AD:49:ILE:HD11	1.83	0.43
15:AJ:99:LEU:O	15:AJ:100:LYS:HB2	2.18	0.43
22:AQ:45:ARG:HG2	22:AQ:49:TYR:HE2	1.82	0.43
39:BA:65:ASP:HB3	39:BA:68:LYS:O	2.18	0.43
39:BA:116:VAL:O	39:BA:125:ALA:HB3	2.17	0.43
40:BB:287:LYS:HD2	40:BB:287:LYS:N	2.32	0.43
48:BJ:110:ILE:H	48:BJ:110:ILE:HD12	1.84	0.43
49:BK:2:ALA:HB1	64:BZ:33:GLY:O	2.19	0.43
50:BL:12:TRP:HB2	56:BR:172:TYR:C	2.44	0.43
57:BS:93:VAL:HA	57:BS:96:ILE:HG22	2.01	0.43
78:Bn:71:ARG:HH21	78:Bn:80:ARG:NH1	2.15	0.43
81:CB:175:LYS:HZ2	81:CB:221:LEU:HB2	1.83	0.43
1:2:186:C:H3'	1:2:187:G:H8	1.83	0.43
1:2:256:A:H2'	1:2:257:A:O4'	2.18	0.43
1:2:693:U:H5''	1:2:694:U:H5'	1.99	0.43
1:2:1564:U:H2'	1:2:1565:C:H6	1.82	0.43
4:5:1214:U:H2'	4:5:1215:U:C6	2.53	0.43
4:5:2495:C:H2'	4:5:2496:C:C5	2.53	0.43
4:5:2508:U:H2'	4:5:2509:U:C6	2.52	0.43
7:AB:205:PHE:CG	7:AB:206:PRO:HD2	2.53	0.43
21:AP:41:VAL:HG13	21:AP:84:ILE:HG21	1.99	0.43
21:AP:86:VAL:HG22	21:AP:87:PRO:HD2	2.00	0.43
25:AT:57:ARG:O	25:AT:61:VAL:HG23	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:Ag:112:SER:HB2	38:Ag:153:GLN:HA	1.99	0.43
50:BL:20:VAL:O	50:BL:66:THR:OG1	2.25	0.43
69:Be:53:TYR:CZ	69:Be:65:ARG:HB2	2.53	0.43
70:Bf:39:ALA:HB3	70:Bf:56:THR:HG22	2.01	0.43
80:CA:502:LEU:HD11	80:CA:524:LYS:HE3	2.01	0.43
80:CA:1011:VAL:O	80:CA:1012:MET:HE2	2.18	0.43
1:2:82:U:H2'	1:2:83:G:O4'	2.18	0.43
1:2:830:U:H2'	1:2:831:U:H6	1.83	0.43
1:2:1633:A:H4'	1:2:1634:C:O5'	2.18	0.43
1:2:1656:U:HO2'	4:5:2292:U:HO2'	1.51	0.43
2:3:28:C:H2'	2:3:29:U:H6	1.84	0.43
2:3:155:A:H5''	45:BG:84:ARG:NH2	2.31	0.43
3:4:16:U:H2'	3:4:17:A:H8	1.83	0.43
4:5:93:C:OP2	4:5:2764:C:O2'	2.27	0.43
4:5:527:A:H2'	4:5:528:U:C6	2.54	0.43
4:5:955:U:H2'	4:5:956:U:C6	2.54	0.43
4:5:2747:A:H5'	42:BD:175:HIS:HA	2.00	0.43
4:5:2923:U:H2'	4:5:2924:U:C6	2.53	0.43
7:AB:61:LEU:HD23	7:AB:88:VAL:HG11	1.99	0.43
9:AD:106:LYS:HG3	9:AD:175:VAL:HG22	1.99	0.43
10:AE:241:GLY:O	10:AE:244:ILE:HG12	2.18	0.43
20:AO:40:ALA:O	20:AO:67:VAL:HG22	2.19	0.43
20:AO:84:ARG:HG2	20:AO:85:ALA:O	2.18	0.43
25:AT:42:GLY:HA2	25:AT:84:LYS:HD2	1.99	0.43
40:BB:41:VAL:HA	40:BB:185:GLY:HA3	2.00	0.43
41:BC:206:LEU:HD23	41:BC:248:VAL:HG22	2.01	0.43
44:BF:40:LYS:O	44:BF:44:ILE:HG12	2.19	0.43
44:BF:86:VAL:O	44:BF:114:GLY:HA2	2.19	0.43
49:BK:157:ARG:HG3	64:BZ:101:VAL:HG21	1.99	0.43
54:BP:64:VAL:HG13	54:BP:88:THR:O	2.19	0.43
63:BY:36:HIS:HB2	63:BY:40:HIS:CE1	2.54	0.43
80:CA:250:GLU:HG3	80:CA:505:ARG:HH12	1.82	0.43
80:CA:348:LYS:HB2	80:CA:421:VAL:HA	2.00	0.43
1:2:207:U:H2'	1:2:208:U:C6	2.54	0.43
3:4:23:A:H2'	3:4:24:A:C8	2.53	0.43
4:5:158:G:H2'	4:5:159:A:H8	1.84	0.43
4:5:1211:U:H2'	4:5:1212:A:C8	2.53	0.43
4:5:2526:C:H2'	4:5:2527:G:H8	1.83	0.43
4:5:2536:A:N3	4:5:2537:U:H5	2.17	0.43
4:5:2655:U:H4'	4:5:2656:A:O4'	2.18	0.43
4:5:3026:G:N2	4:5:3029:A:OP2	2.41	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AA:50:VAL:HG22	23:AR:109:LEU:HD21	2.01	0.43
7:AB:109:LYS:O	7:AB:113:MET:HG3	2.19	0.43
7:AB:180:THR:OG1	7:AB:181:LEU:N	2.51	0.43
10:AE:15:PRO:HG2	10:AE:18:TRP:CE2	2.53	0.43
11:AF:77:TYR:HB3	11:AF:84:LYS:HA	2.00	0.43
13:AH:139:ARG:HB3	28:AW:51:GLU:OE2	2.18	0.43
14:AI:48:THR:OG1	14:AI:52:ASN:O	2.29	0.43
18:AM:74:LEU:HD11	37:Af:106:TYR:H	1.84	0.43
20:AO:31:THR:HG22	20:AO:38:THR:HG22	2.00	0.43
32:Aa:3:LYS:HE3	32:Aa:8:ASN:OD1	2.19	0.43
38:Ag:153:GLN:HB3	38:Ag:202:LEU:HD23	2.01	0.43
48:BJ:65:ILE:HG13	48:BJ:66:ALA:N	2.34	0.43
49:BK:57:VAL:HB	49:BK:147:ILE:HD12	2.01	0.43
1:2:1133:A:N3	1:2:1650:U:O2'	2.51	0.43
1:2:1521:G:N2	1:2:1523:G:O4'	2.51	0.43
1:2:1757:G:HO2'	4:5:2255:A:HO2'	1.65	0.43
3:4:67:G:H2'	3:4:68:C:O4'	2.19	0.43
4:5:70:A:N1	4:5:313:A:O2'	2.51	0.43
4:5:756:U:H2'	4:5:757:C:C6	2.53	0.43
4:5:2093:A:H2'	4:5:2094:C:C6	2.52	0.43
4:5:2829:U:C2	4:5:2830:G:C8	3.07	0.43
4:5:3159:C:H2'	4:5:3160:U:H6	1.82	0.43
10:AE:67:GLN:HB2	10:AE:69:HIS:CD2	2.53	0.43
14:AI:21:PHE:CE2	14:AI:22:ARG:HG3	2.54	0.43
14:AI:37:LYS:HD3	14:AI:37:LYS:HA	1.76	0.43
15:AJ:77:ILE:HG23	15:AJ:86:LEU:HD23	2.00	0.43
19:AN:17:PRO:HG3	33:Ab:28:PRO:HG3	2.01	0.43
24:AS:36:LYS:HB2	24:AS:102:ALA:HA	2.01	0.43
31:AZ:60:VAL:HG13	31:AZ:101:TYR:HB2	2.00	0.43
41:BC:265:GLU:H	41:BC:265:GLU:CD	2.27	0.43
41:BC:361:HIS:ND1	41:BC:362:ASP:O	2.51	0.43
43:BE:20:LYS:HD3	43:BE:20:LYS:HA	1.76	0.43
44:BF:77:VAL:HB	57:BS:139:ARG:HG2	2.00	0.43
61:BW:85:GLN:HG3	61:BW:115:ARG:HH21	1.84	0.43
80:CA:506:GLY:O	80:CA:507:LYS:HG2	2.18	0.43
80:CA:1342:PHE:HB3	80:CA:1351:LEU:HD11	1.99	0.43
80:CA:1615:GLN:HE21	80:CA:1647:LEU:HD13	1.83	0.43
81:CB:230:HIS:CD2	81:CB:231:LYS:HG2	2.54	0.43
1:2:257:A:H1'	14:AI:73:SER:HB2	1.99	0.43
1:2:458:G:OP2	30:AY:105:ARG:NH2	2.51	0.43
1:2:639:U:H1'	1:2:640:U:OP2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1054:U:H2'	1:2:1055:U:H6	1.84	0.43
1:2:1615:C:P	11:AF:81:ARG:HE	2.42	0.43
1:2:1729:C:H2'	1:2:1730:A:O4'	2.19	0.43
4:5:178:U:H2'	4:5:179:C:C6	2.53	0.43
4:5:226:C:H2'	4:5:227:G:O4'	2.19	0.43
4:5:340:C:H2'	4:5:341:G:O4'	2.19	0.43
4:5:901:G:OP1	73:Bi:13:ASN:ND2	2.45	0.43
4:5:1488:G:C2	4:5:1489:A:C8	3.07	0.43
4:5:1861:G:O2'	4:5:3066:U:OP1	2.32	0.43
5:6:2:U:H2'	5:6:3:C:C6	2.54	0.43
33:Ab:46:VAL:HG12	33:Ab:54:VAL:HG11	2.00	0.43
37:Af:115:THR:O	37:Af:116:LYS:HE2	2.18	0.43
48:BJ:26:SER:OG	48:BJ:27:GLY:N	2.51	0.43
50:BL:8:LYS:HA	50:BL:8:LYS:HD3	1.68	0.43
57:BS:122:GLN:HG2	57:BS:124:VAL:HG23	2.01	0.43
66:Bb:9:SER:OG	66:Bb:10:ILE:N	2.51	0.43
66:Bb:36:GLN:HB2	66:Bb:38:LYS:HG3	2.01	0.43
1:2:146:U:H2'	1:2:147:A:H8	1.82	0.43
1:2:333:A:N6	14:AI:27:PHE:HB2	2.34	0.43
1:2:884:A:H2'	1:2:885:G:H8	1.83	0.43
1:2:1115:U:H5''	77:Bm:10:THR:HG21	2.00	0.43
1:2:1560:U:H2'	1:2:1561:U:O4'	2.19	0.43
4:5:20:A:H2'	4:5:21:G:C8	2.54	0.43
4:5:35:A:H2'	4:5:36:C:H6	1.84	0.43
4:5:127:G:H2'	4:5:128:G:C8	2.53	0.43
4:5:297:G:OP2	4:5:297:G:N2	2.26	0.43
4:5:1506:A:H1'	4:5:1848:G:O6	2.19	0.43
4:5:2160:G:H2'	4:5:2161:G:C8	2.54	0.43
4:5:2351:U:H2'	4:5:2352:A:C8	2.53	0.43
4:5:3121:U:OP2	76:Bl:111:ARG:NH2	2.45	0.43
4:5:3243:A:H4'	40:BB:95:THR:HG22	2.01	0.43
7:AB:140:ILE:N	7:AB:212:VAL:O	2.52	0.43
13:AH:70:PHE:O	13:AH:74:GLN:HG3	2.19	0.43
18:AM:32:LEU:HD22	18:AM:100:TRP:O	2.18	0.43
26:AU:57:ARG:HG2	26:AU:89:ARG:HG2	2.01	0.43
26:AU:82:TYR:HB3	35:Ad:52:PHE:HB3	2.01	0.43
36:Ae:13:LYS:O	36:Ae:17:GLN:HG3	2.19	0.43
39:BA:204:MET:SD	39:BA:209:HIS:HB2	2.59	0.43
40:BB:256:HIS:HA	40:BB:257:PRO:C	2.44	0.43
44:BF:165:ASP:OD2	44:BF:166:ASN:N	2.52	0.43
46:BH:38:LEU:HD13	46:BH:71:VAL:HG13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:BP:54:LEU:HD22	54:BP:58:ASN:HB3	2.00	0.43
59:BU:114:ILE:HD12	59:BU:133:SER:HB3	2.00	0.43
60:BV:47:ARG:HG2	60:BV:54:LEU:HG	2.01	0.43
80:CA:913:ILE:HG22	80:CA:917:ARG:HD2	2.00	0.43
80:CA:923:SER:O	80:CA:927:LEU:N	2.41	0.43
80:CA:1187:LYS:HD2	80:CA:1187:LYS:O	2.18	0.43
1:2:156:A:H2'	1:2:157:A:O4'	2.18	0.43
1:2:586:G:H2'	1:2:587:C:C6	2.54	0.43
1:2:823:G:N7	1:2:850:A:C6	2.87	0.43
1:2:1077:C:H2'	1:2:1078:C:H6	1.82	0.43
1:2:1434:U:H4'	35:Ad:24:CYS:HB2	2.01	0.43
1:2:1445:G:N9	37:Af:91:ILE:HD11	2.34	0.43
4:5:1643:A:H2'	4:5:1644:C:C2	2.54	0.43
4:5:2389:C:H1'	53:BO:69:ARG:NH2	2.34	0.43
4:5:2413:A:H2'	4:5:2414:G:H8	1.84	0.43
4:5:2835:U:H2'	4:5:2836:C:O2	2.18	0.43
11:AF:125:THR:HG21	11:AF:199:ILE:HG12	2.01	0.43
17:AL:57:LYS:O	17:AL:138:ASN:ND2	2.45	0.43
21:AP:36:LEU:HD23	21:AP:36:LEU:H	1.84	0.43
21:AP:87:PRO:HA	21:AP:90:ILE:HG13	2.01	0.43
23:AR:31:ASN:ND2	23:AR:55:THR:OG1	2.46	0.43
24:AS:26:ILE:HG13	24:AS:31:ALA:HB2	2.01	0.43
31:AZ:59:TYR:HE1	31:AZ:100:ILE:HG23	1.84	0.43
41:BC:4:PRO:O	41:BC:5:GLN:HG2	2.19	0.43
61:BW:110:VAL:HG22	61:BW:124:VAL:HG22	2.00	0.43
64:BZ:132:LYS:O	64:BZ:136:GLU:HG3	2.18	0.43
74:Bj:56:ILE:HG22	74:Bj:58:ASP:H	1.84	0.43
80:CA:1010:ASN:O	80:CA:1011:VAL:HG13	2.19	0.43
1:2:5:U:H2'	1:2:6:G:H8	1.83	0.42
1:2:180:A:H3'	1:2:181:A:H8	1.84	0.42
1:2:958:U:O2'	19:AN:55:ARG:NH1	2.52	0.42
1:2:1232:U:H2'	1:2:1233:G:H8	1.83	0.42
1:2:1564:U:H5''	25:AT:38:LYS:NZ	2.34	0.42
1:2:1601:G:H22	25:AT:88:VAL:HG22	1.84	0.42
3:4:113:C:H2'	3:4:114:U:O4'	2.19	0.42
4:5:335:G:OP1	62:BX:9:SER:HB2	2.19	0.42
4:5:1609:C:H2'	4:5:1610:G:H8	1.84	0.42
4:5:1635:G:N2	4:5:1638:A:OP2	2.44	0.42
4:5:1925:U:O2'	4:5:1927:G:N7	2.52	0.42
4:5:2416:U:H2'	4:5:2417:U:C6	2.54	0.42
4:5:2631:U:OP1	4:5:2757:U:O2'	2.31	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:2836:C:H2'	4:5:2837:A:O4'	2.18	0.42
4:5:3230:G:H4'	50:BL:132:LYS:HD3	2.01	0.42
4:5:3267:A:H2'	43:BE:69:PHE:CZ	2.54	0.42
9:AD:43:PRO:HD2	26:AU:108:ILE:HG12	2.01	0.42
11:AF:147:THR:HG21	34:Ac:25:VAL:HG21	2.01	0.42
14:AI:87:ASN:HB3	14:AI:90:LEU:HG	2.01	0.42
18:AM:84:ASN:O	18:AM:86:VAL:HG13	2.19	0.42
23:AR:25:THR:OG1	23:AR:26:LEU:N	2.51	0.42
29:AX:69:ARG:HG3	29:AX:117:ILE:HG12	2.01	0.42
31:AZ:82:HIS:O	31:AZ:85:LYS:NZ	2.52	0.42
35:Ad:22:ARG:NH1	35:Ad:36:LEU:O	2.52	0.42
38:Ag:246:SER:HB3	38:Ag:249:ARG:O	2.19	0.42
40:BB:289:ASP:OD1	40:BB:289:ASP:N	2.48	0.42
43:BE:58:LEU:HB2	43:BE:62:THR:HG22	2.01	0.42
46:BH:86:TYR:CD2	46:BH:151:VAL:HB	2.54	0.42
47:BI:54:SER:HB2	47:BI:135:ILE:HD11	1.99	0.42
52:BN:89[A]:SER:O	52:BN:95[A]:GLY:HA3	2.19	0.42
56:BR:90:MET:HE1	56:BR:114:HIS:CE1	2.54	0.42
76:Bl:79:GLU:O	76:Bl:81:SER:N	2.52	0.42
80:CA:354:PRO:HG3	80:CA:428:GLU:HG3	2.01	0.42
80:CA:523:ASP:OD1	80:CA:523:ASP:N	2.51	0.42
80:CA:990:LYS:O	80:CA:994:ARG:HG2	2.19	0.42
1:2:901:G:H3'	1:2:902:G:C8	2.54	0.42
1:2:959:U:OP1	33:Ab:30:SER:OG	2.25	0.42
1:2:1445:G:C4	37:Af:91:ILE:HD11	2.53	0.42
1:2:1787:C:H2'	1:2:1788:G:C8	2.54	0.42
4:5:178:U:H2'	4:5:179:C:H6	1.84	0.42
4:5:190:U:OP1	62:BX:37:LYS:NZ	2.49	0.42
4:5:939:U:O2'	4:5:2402:A:N1	2.49	0.42
4:5:1345:G:N2	41:BC:307:GLN:OE1	2.44	0.42
4:5:1351:U:O2'	4:5:1352:A:H5'	2.19	0.42
4:5:1562:C:HO2'	4:5:1563:C:C5'	2.32	0.42
4:5:1757:A:H2'	4:5:1758:G:H8	1.84	0.42
4:5:2747:A:H2'	4:5:2748:A:C8	2.54	0.42
7:AB:55:LYS:HA	7:AB:55:LYS:HD2	1.71	0.42
7:AB:194:ASN:HD21	7:AB:212:VAL:N	2.17	0.42
10:AE:103:TYR:O	10:AE:182:TYR:OH	2.37	0.42
12:AG:113:ILE:HD11	12:AG:124:LEU:HD13	2.01	0.42
13:AH:15:GLU:HA	13:AH:18:LEU:HD12	2.00	0.42
15:AJ:111:THR:O	15:AJ:115:LYS:HG2	2.19	0.42
17:AL:32:LYS:HE2	17:AL:32:LYS:HB3	1.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AR:41:ILE:HG22	23:AR:43:SER:H	1.83	0.42
40:BB:43:LEU:HB3	40:BB:181:ILE:HG21	2.00	0.42
51:BM:65:ARG:HB3	51:BM:129:TYR:CD2	2.54	0.42
76:Bl:126:LYS:HE2	76:Bl:126:LYS:HB2	1.81	0.42
80:CA:659:ILE:HD11	80:CA:697:ILE:HB	2.01	0.42
80:CA:1482:PHE:HD1	80:CA:1493:MET:HG2	1.85	0.42
80:CA:1576:ARG:O	80:CA:1580:HIS:ND1	2.52	0.42
82:CC:179:GLN:OE1	82:CC:198:VAL:N	2.41	0.42
82:CC:334:ARG:HA	82:CC:337:TYR:HB3	2.01	0.42
1:2:850:A:H5''	55:BQ:165:LYS:CD	2.49	0.42
1:2:1241:G:H5''	21:AP:79:HIS:CE1	2.54	0.42
1:2:1486:G:N1	1:2:1522:U:O4	2.52	0.42
1:2:1776:A:H2'	1:2:1777:G:H8	1.84	0.42
3:4:73:C:H42	56:BR:19:VAL:HG11	1.83	0.42
4:5:80:G:H2'	4:5:81:C:C6	2.54	0.42
4:5:2097:U:H2'	4:5:2098:C:C6	2.55	0.42
4:5:3232:G:C6	4:5:3256:G:C6	3.08	0.42
4:5:3304:U:O2'	40:BB:334:ARG:NH2	2.52	0.42
12:AG:142:ARG:HG3	12:AG:153:VAL:HG11	2.01	0.42
15:AJ:157:ASP:OD1	15:AJ:158:PHE:N	2.49	0.42
21:AP:86:VAL:HG12	21:AP:89:MET:HE1	2.01	0.42
22:AQ:49:TYR:O	22:AQ:53:LEU:HG	2.19	0.42
25:AT:52:GLY:C	25:AT:54:PHE:H	2.28	0.42
28:AW:90:THR:O	28:AW:94:LEU:HB2	2.19	0.42
31:AZ:62:VAL:HG13	31:AZ:76:ALA:HB3	2.02	0.42
32:Aa:79:ILE:HG12	32:Aa:85:ARG:HA	2.01	0.42
35:Ad:12:ARG:HG3	35:Ad:12:ARG:NH1	2.32	0.42
37:Af:135:HIS:O	37:Af:136:LYS:HD2	2.19	0.42
45:BG:33:ASN:ND2	45:BG:38:GLN:HE21	2.17	0.42
49:BK:126:PHE:HZ	49:BK:135:ALA:HB2	1.84	0.42
80:CA:448:LEU:HD22	80:CA:736:TYR:HB3	2.00	0.42
80:CA:721:LEU:HD11	80:CA:723:SER:HB3	2.01	0.42
81:CB:74:ARG:O	81:CB:78:ARG:HG2	2.18	0.42
81:CB:283:LEU:HD22	81:CB:286:LEU:HD23	2.00	0.42
1:2:79:C:O2	12:AG:174:LYS:HG2	2.19	0.42
1:2:280:U:H4'	1:2:281:G:O5'	2.20	0.42
1:2:928:U:O2'	1:2:945:U:OP2	2.33	0.42
1:2:1222:C:H2'	1:2:1223:A:C8	2.54	0.42
1:2:1254:U:OP2	18:AM:46:ARG:NH2	2.52	0.42
4:5:501:A:H2'	4:5:502:U:C6	2.54	0.42
4:5:1146:C:H4'	4:5:1331:U:C4	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:2273:G:N2	4:5:2311:G:H2'	2.34	0.42
4:5:2282:U:O2	4:5:2310:U:H4'	2.19	0.42
4:5:2495:C:O2'	4:5:2496:C:OP1	2.34	0.42
4:5:2904:U:H2'	4:5:2905:U:C6	2.55	0.42
4:5:3256:G:H2'	4:5:3257:C:C6	2.54	0.42
7:AB:131:ASP:CG	7:AB:180:THR:HB	2.44	0.42
11:AF:189:THR:N	11:AF:192:GLU:OE2	2.47	0.42
25:AT:71:VAL:HG13	25:AT:75:LYS:HB2	2.02	0.42
27:AV:80:LYS:O	27:AV:82:VAL:N	2.52	0.42
38:Ag:90:ARG:HG2	38:Ag:102:ARG:HG2	2.01	0.42
47:BI:50:VAL:HG22	47:BI:167:LEU:HD13	2.01	0.42
48:BJ:173:ASP:OD1	48:BJ:173:ASP:N	2.52	0.42
52:BN:37[A]:ARG:HG3	52:BN:108[A]:ILE:HG13	2.01	0.42
56:BR:154:HIS:HA	56:BR:170:THR:HB	2.01	0.42
60:BV:8:PHE:CD1	60:BV:46:PRO:HG3	2.54	0.42
68:Bd:3:SER:HB3	68:Bd:71:HIS:CE1	2.54	0.42
69:Be:43:PHE:HZ	69:Be:107:ILE:HD11	1.84	0.42
71:Bg:13:SER:OG	71:Bg:14:LYS:N	2.52	0.42
80:CA:348:LYS:NZ	80:CA:391:ILE:O	2.53	0.42
81:CB:6:ASN:HB2	81:CB:37:LYS:HZ2	1.84	0.42
81:CB:25:PHE:HE1	81:CB:83:GLU:HG3	1.84	0.42
1:2:153:G:N2	12:AG:56:ASN:HD21	2.15	0.42
1:2:252:U:H2'	1:2:253:A:C8	2.55	0.42
1:2:556:A:H5''	36:Ae:56:MET:SD	2.59	0.42
1:2:799:A:H4'	10:AE:201:HIS:CE1	2.54	0.42
1:2:1525:A:H2'	1:2:1526:A:C8	2.55	0.42
4:5:1348:U:C4	54:BP:31:LYS:HE3	2.54	0.42
4:5:2107:A:H2	4:5:3344:A:H8	1.67	0.42
4:5:2383:C:H2'	4:5:2384:A:O4'	2.20	0.42
6:AA:66:ALA:HB2	27:AV:37:ALA:HB2	2.02	0.42
7:AB:31:ASP:O	7:AB:96:LEU:HG	2.19	0.42
7:AB:40:ASN:ND2	7:AB:72:ASP:O	2.43	0.42
13:AH:76:LYS:H	13:AH:76:LYS:HD2	1.83	0.42
24:AS:6:GLN:NE2	31:AZ:44:GLN:OE1	2.52	0.42
26:AU:28:SER:OG	26:AU:34:LEU:HD13	2.19	0.42
26:AU:58:LEU:HD12	26:AU:88:LYS:HD2	2.00	0.42
33:Ab:36:LYS:HB2	33:Ab:78:SER:HB2	2.02	0.42
38:Ag:70:ASP:OD1	38:Ag:71:CYS:N	2.48	0.42
58:BT:98:THR:O	58:BT:99:LYS:HD2	2.19	0.42
74:Bj:13:GLU:OE1	74:Bj:16:ARG:NH2	2.52	0.42
80:CA:817:GLN:HB2	82:CC:370:ARG:CZ	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:CA:892:LEU:HD23	80:CA:892:LEU:HA	1.90	0.42
1:2:407:A:H2'	1:2:408:C:C6	2.55	0.42
1:2:656:G:N3	1:2:656:G:H2'	2.34	0.42
1:2:852:C:H2'	1:2:853:G:N9	2.34	0.42
1:2:889:U:H2'	1:2:890:C:H6	1.85	0.42
1:2:1142:A:H2'	1:2:1143:A:C8	2.54	0.42
1:2:1177:C:H5''	1:2:1189:A:H61	1.85	0.42
1:2:1308:G:H2'	1:2:1309:C:H6	1.84	0.42
1:2:1566:U:H5''	24:AS:39:GLY:N	2.35	0.42
1:2:1612:U:H2'	1:2:1613:U:O4'	2.19	0.42
1:2:1673:G:N1	1:2:1728:A:C2	2.70	0.42
1:2:1688:U:H2'	1:2:1689:A:O4'	2.19	0.42
1:2:1756:A:H3'	4:5:2256:A:H61	1.83	0.42
4:5:675:C:H5'	41:BC:116:ASN:HD21	1.84	0.42
4:5:839:C:O2'	4:5:1724:U:OP1	2.34	0.42
4:5:2144:A:H1'	4:5:2281:A:N6	2.34	0.42
4:5:2424:A:N1	39:BA:230:VAL:HG11	2.34	0.42
15:AJ:66:ASP:HB3	15:AJ:69:ARG:HB3	2.01	0.42
23:AR:24:LEU:O	23:AR:24:LEU:HD12	2.18	0.42
40:BB:128:LYS:HD3	40:BB:128:LYS:HA	1.78	0.42
44:BF:96:PRO:HB2	44:BF:99:PRO:HD2	2.02	0.42
48:BJ:14:ILE:HG23	48:BJ:129:VAL:HG13	2.02	0.42
59:BU:86:ARG:HB2	59:BU:92:PHE:CZ	2.55	0.42
80:CA:1144:GLN:HB3	80:CA:1147:THR:HB	2.00	0.42
80:CA:1434:HIS:ND1	80:CA:1464:LEU:HD21	2.34	0.42
80:CA:1773:GLN:HB3	80:CA:1784:VAL:HG11	2.02	0.42
80:CA:1843:SER:O	80:CA:1846:THR:OG1	2.35	0.42
1:2:963:A:O2'	1:2:964:U:O5'	2.38	0.42
1:2:963:A:H4'	19:AN:128:TYR:OH	2.20	0.42
1:2:1065:A:H4'	7:AB:205:PHE:CD1	2.54	0.42
1:2:1263:G:H2'	1:2:1264:G:O4'	2.19	0.42
1:2:1352:G:H2'	1:2:1353:U:C6	2.55	0.42
1:2:1727:G:H2'	1:2:1728:A:H8	1.84	0.42
4:5:296:A:N3	4:5:299:G:O2'	2.52	0.42
4:5:2344:U:H2'	4:5:2345:A:C8	2.55	0.42
4:5:2813:A:H2'	4:5:2814:G:O4'	2.19	0.42
4:5:2916:U:H2'	4:5:2917:G:H8	1.85	0.42
4:5:3049:A:O2'	40:BB:55:THR:OG1	2.32	0.42
4:5:3160:U:H2'	4:5:3161:C:H6	1.85	0.42
4:5:3218:A:H4'	4:5:3219:G:O5'	2.19	0.42
6:AA:41:ARG:HG2	6:AA:42:PRO:HD2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AB:205:PHE:CD2	7:AB:206:PRO:HD2	2.55	0.42
22:AQ:31:VAL:HG11	22:AQ:81:ILE:HD13	2.01	0.42
29:AX:51:GLY:HA2	29:AX:77:ILE:HG13	2.01	0.42
32:Aa:12:LYS:HB2	32:Aa:33:ASP:OD2	2.18	0.42
41:BC:302:ALA:HB2	54:BP:39:ARG:CZ	2.50	0.42
44:BF:233:GLU:OE1	44:BF:233:GLU:N	2.51	0.42
45:BG:90:THR:HG23	45:BG:214:LEU:HD21	2.01	0.42
47:BI:170:LYS:NZ	47:BI:175:ASN:O	2.33	0.42
51:BM:162:ARG:HB2	51:BM:164:LEU:HD23	2.01	0.42
58:BT:86:LYS:HE2	58:BT:86:LYS:HB3	1.86	0.42
66:Bb:24:THR:OG1	66:Bb:91:SER:HB3	2.20	0.42
67:Bc:35:GLU:O	67:Bc:39:PHE:N	2.37	0.42
68:Bd:32:TRP:CZ2	68:Bd:53:PRO:HD2	2.54	0.42
80:CA:286:GLU:OE2	80:CA:287:THR:OG1	2.35	0.42
80:CA:363:VAL:HG11	80:CA:379:GLU:HB2	2.01	0.42
80:CA:1159:PHE:CE1	80:CA:1268:ILE:HD11	2.54	0.42
1:2:72:A:H62	12:AG:167:LYS:NZ	2.17	0.42
1:2:1348:A:H2'	1:2:1349:G:O4'	2.19	0.42
4:5:230:U:H2'	4:5:231:G:O4'	2.20	0.42
4:5:250:U:H5''	4:5:251:G:H2'	2.02	0.42
4:5:542:G:C5	4:5:543:C:N3	2.88	0.42
4:5:753:C:H2'	4:5:754:G:H8	1.84	0.42
4:5:945:C:H2'	4:5:946:U:C6	2.55	0.42
4:5:1066:G:H2'	4:5:1067:U:H6	1.85	0.42
4:5:1221:A:H5''	4:5:1222:G:H5''	2.02	0.42
4:5:2510:U:H2'	4:5:2511:A:C8	2.54	0.42
4:5:2881:C:H2'	4:5:2882:U:C6	2.54	0.42
7:AB:126:THR:O	7:AB:126:THR:HG22	2.20	0.42
26:AU:26:LEU:O	26:AU:88:LYS:HA	2.20	0.42
28:AW:81:VAL:O	28:AW:122:SER:OG	2.25	0.42
35:Ad:15:GLY:O	35:Ad:18:SER:OG	2.35	0.42
38:Ag:225:LEU:HD23	38:Ag:225:LEU:H	1.84	0.42
39:BA:20:THR:HG22	39:BA:23:ARG:HD2	2.01	0.42
54:BP:89:ASP:HB2	54:BP:110:ALA:N	2.35	0.42
63:BY:30:ASP:OD1	63:BY:30:ASP:N	2.49	0.42
79:Bo:39:CYS:HB3	79:Bo:42:CYS:SG	2.60	0.42
80:CA:418:VAL:O	80:CA:421:VAL:HG22	2.20	0.42
80:CA:1265:MET:HG2	80:CA:1268:ILE:CG2	2.50	0.42
80:CA:1344:ASP:OD1	80:CA:1521:LYS:HD3	2.20	0.42
1:2:292:U:H2'	1:2:293:U:C6	2.54	0.42
1:2:604:A:H2'	1:2:605:A:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:781:U:OP2	30:AY:9:THR:OG1	2.24	0.42
1:2:876:G:H2'	1:2:936:G:N2	2.34	0.42
1:2:1082:C:H4'	27:AV:58:TYR:HE1	1.85	0.42
1:2:1216:C:O2	1:2:1446:A:N6	2.53	0.42
1:2:1613:U:H2'	1:2:1614:A:H5''	2.02	0.42
1:2:1767:G:OP1	1:2:1770:U:H4'	2.20	0.42
4:5:516:A:H5''	41:BC:344:ALA:HB2	2.02	0.42
4:5:776:U:H5'	4:5:777:U:OP2	2.20	0.42
4:5:958:C:C4	4:5:960:U:H1'	2.55	0.42
4:5:999:G:N3	4:5:1002:A:N6	2.68	0.42
4:5:1452:A:N3	4:5:2346:C:O2'	2.51	0.42
4:5:1715:A:N7	66:Bb:84:LEU:HD12	2.35	0.42
4:5:1896:A:N6	4:5:2339:C:H42	2.15	0.42
4:5:2683:U:H2'	4:5:2684:C:H6	1.84	0.42
4:5:3122:A:C2	4:5:3123:A:C8	3.08	0.42
7:AB:130:SER:HB2	7:AB:180:THR:HG22	2.00	0.42
8:AC:35:TRP:HH2	8:AC:68:ILE:HG13	1.85	0.42
14:AI:6:ASP:HB3	14:AI:28:GLU:CD	2.45	0.42
22:AQ:9:THR:HG21	22:AQ:88:GLY:HA2	2.01	0.42
25:AT:125:SER:O	25:AT:129:GLN:N	2.48	0.42
33:Ab:50:ALA:H	33:Ab:71:ALA:HB2	1.85	0.42
37:Af:102:VAL:HG13	37:Af:105:TYR:OH	2.20	0.42
41:BC:110:ASN:HD22	51:BM:201:ARG:HB3	1.84	0.42
43:BE:112:THR:HG23	43:BE:115:GLU:H	1.84	0.42
48:BJ:93:ASP:HB3	48:BJ:174:LYS:C	2.45	0.42
56:BR:90:MET:HE1	56:BR:114:HIS:NE2	2.34	0.42
62:BX:112:ASP:N	62:BX:112:ASP:OD1	2.53	0.42
63:BY:22:LYS:HD3	63:BY:129:TRP:CZ3	2.55	0.42
80:CA:370:LEU:HB3	80:CA:375:ILE:HB	2.01	0.42
80:CA:1188:ILE:HG23	80:CA:1262:LEU:O	2.19	0.42
1:2:59:C:O2'	1:2:60:U:O4'	2.35	0.42
1:2:121:U:H2'	1:2:122:U:C6	2.55	0.42
1:2:153:G:O6	30:AY:128:LYS:NZ	2.44	0.42
1:2:895:G:H2'	1:2:896:U:C6	2.55	0.42
1:2:1044:U:H2'	1:2:1045:C:C6	2.55	0.42
1:2:1770:U:H2'	1:2:1771:U:C6	2.55	0.42
4:5:180:C:H2'	4:5:181:U:C6	2.55	0.42
4:5:671:U:H5''	54:BP:16:ARG:HH22	1.85	0.42
4:5:1120:A:H2'	4:5:1121:U:C6	2.53	0.42
4:5:3228:C:H1'	4:5:3229:G:OP2	2.19	0.42
4:5:3261:C:OP1	50:BL:126:GLN:NE2	2.42	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AF:27:THR:HG23	22:AQ:28:LEU:HB2	2.01	0.42
11:AF:99:MET:HE2	11:AF:99:MET:HB2	1.94	0.42
18:AM:36:LEU:HD13	18:AM:102:GLY:HA3	2.02	0.42
38:Ag:182:ASN:HB2	38:Ag:189:GLU:OE2	2.20	0.42
40:BB:37:ARG:NH1	40:BB:188:ILE:HG23	2.35	0.42
47:BI:66:GLU:OE2	47:BI:69:ARG:NH2	2.33	0.42
55:BQ:93:VAL:HG12	55:BQ:97:ARG:HE	1.84	0.42
66:Bb:53:LYS:HD2	66:Bb:69:TYR:HE2	1.85	0.42
80:CA:348:LYS:HE3	80:CA:417:LEU:HA	2.01	0.42
81:CB:16:ALA:HB3	81:CB:20:LEU:HA	2.01	0.42
81:CB:280:HIS:O	81:CB:287:LYS:NZ	2.53	0.42
1:2:260:U:O2	14:AI:41:LYS:NZ	2.34	0.41
1:2:828:U:H2'	1:2:829:A:O4'	2.20	0.41
1:2:919:A:OP1	20:AO:18:ARG:NH1	2.53	0.41
2:3:26:U:H2'	2:3:27:U:H6	1.85	0.41
4:5:341:G:C6	41:BC:194:TYR:HE2	2.38	0.41
4:5:1438:U:H2'	4:5:1439:U:C6	2.54	0.41
4:5:1471:U:H2'	4:5:1472:U:C6	2.54	0.41
4:5:1565:G:N3	4:5:1575:A:N6	2.67	0.41
4:5:2759:U:H5''	4:5:2760:C:H5'	2.02	0.41
4:5:2964:G:N2	4:5:2967:A:OP2	2.43	0.41
4:5:3231:U:H2'	4:5:3232:G:H8	1.85	0.41
4:5:3305:A:H2'	4:5:3306:U:O4'	2.19	0.41
7:AB:164:ILE:CD1	7:AB:207:LEU:HD11	2.50	0.41
8:AC:56:ILE:HG23	8:AC:61:LEU:HB2	2.02	0.41
9:AD:44:THR:HG22	9:AD:44:THR:O	2.20	0.41
13:AH:159:VAL:HG11	13:AH:185:ILE:HD13	2.02	0.41
22:AQ:20:ALA:HB2	22:AQ:84:ALA:HB1	2.02	0.41
26:AU:53:LYS:HB3	26:AU:92:ASP:HB2	2.01	0.41
35:Ad:47:ALA:HB1	35:Ad:52:PHE:HB2	2.02	0.41
38:Ag:206:PRO:HD3	38:Ag:245:PHE:HB3	2.01	0.41
40:BB:286:GLY:C	40:BB:287:LYS:HD2	2.45	0.41
42:BD:34:LYS:O	42:BD:38:THR:OG1	2.29	0.41
52:BN:188[A]:SER:O	52:BN:192[A]:LYS:HG2	2.19	0.41
55:BQ:114:LYS:HE3	55:BQ:114:LYS:HB3	1.92	0.41
73:Bi:52:LYS:HG2	73:Bi:55:ARG:NH2	2.34	0.41
80:CA:541:SER:HB3	80:CA:544:GLU:CD	2.45	0.41
80:CA:693:TYR:O	80:CA:697:ILE:HG22	2.20	0.41
80:CA:1315:TRP:CE2	80:CA:1573:PHE:HB2	2.55	0.41
80:CA:1611:LEU:HD21	80:CA:1630:LEU:HD11	2.01	0.41
80:CA:1915:LEU:HD13	80:CA:1941:ILE:HG21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:519:C:C4	1:2:534:A:N7	2.88	0.41
1:2:594:A:P	15:AJ:38:ASN:HD21	2.43	0.41
1:2:768:C:H1'	15:AJ:143:ILE:HG21	2.02	0.41
3:4:119:U:OP2	42:BD:258:LYS:NZ	2.34	0.41
4:5:506:U:H2'	4:5:507:U:O4'	2.19	0.41
4:5:1229:G:H2'	4:5:1230:G:C8	2.55	0.41
4:5:1257:C:C4	4:5:1261:G:N2	2.88	0.41
4:5:1269:U:O2	4:5:1269:U:H2'	2.19	0.41
4:5:1915:A:H2'	4:5:1916:U:C6	2.56	0.41
4:5:1921:A:H2'	4:5:1922:A:C8	2.55	0.41
4:5:2267:C:H2'	4:5:2268:U:O4'	2.20	0.41
4:5:2772:C:H4'	4:5:2773:C:H5'	2.01	0.41
4:5:3146:G:H2'	4:5:3147:G:C8	2.55	0.41
5:6:22:C:H2'	5:6:23:G:O4'	2.20	0.41
5:6:43:A:H2'	5:6:44:A:H8	1.84	0.41
6:AA:139:VAL:HG23	6:AA:141:ILE:HG13	2.02	0.41
8:AC:38:VAL:O	8:AC:39:THR:OG1	2.31	0.41
9:AD:135:GLU:HG3	9:AD:153:ALA:HB2	2.01	0.41
13:AH:160:GLN:HA	13:AH:163:ASP:OD2	2.20	0.41
14:AI:11:ARG:H	14:AI:11:ARG:HG3	1.64	0.41
21:AP:80:MET:SD	21:AP:83:MET:HE3	2.59	0.41
28:AW:30:SER:HB2	28:AW:61:ILE:HG13	2.02	0.41
28:AW:47:ILE:HG13	28:AW:48:GLY:N	2.36	0.41
29:AX:97:ASP:OD1	29:AX:97:ASP:N	2.52	0.41
45:BG:140:VAL:HA	45:BG:143:ILE:HD12	2.02	0.41
56:BR:13:ARG:O	56:BR:22:PRO:HG2	2.20	0.41
74:Bj:24:THR:HG22	74:Bj:76:ASN:OD1	2.21	0.41
74:Bj:54:LEU:HG	74:Bj:56:ILE:HD11	2.02	0.41
80:CA:1104:ILE:H	80:CA:1107:PHE:HD2	1.67	0.41
80:CA:1450:PHE:CD1	80:CA:1458:LEU:HD11	2.55	0.41
81:CB:17:ASP:C	81:CB:19:SER:H	2.27	0.41
1:2:404:G:H2'	1:2:405:C:H6	1.84	0.41
1:2:827:C:H2'	1:2:828:U:H6	1.85	0.41
1:2:1481:C:P	25:AT:63:ARG:HH22	2.43	0.41
1:2:1528:U:OP1	11:AF:109:LYS:HG3	2.20	0.41
1:2:1541:G:H1'	1:2:1570:A:H61	1.84	0.41
2:3:76:C:H2'	2:3:77:A:O4'	2.20	0.41
4:5:291:C:H2'	4:5:292:U:C6	2.55	0.41
4:5:717:C:OP1	4:5:751:A:O2'	2.32	0.41
4:5:763:G:O2'	4:5:764:U:OP1	2.38	0.41
4:5:2228:A:H2'	4:5:2229:A:H8	1.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:2597:U:H2'	4:5:2598:G:H8	1.85	0.41
4:5:3000:A:H2'	4:5:3001:C:H6	1.85	0.41
5:6:5:U:O2	5:6:68:G:N2	2.32	0.41
20:AO:40:ALA:HB2	20:AO:70:LYS:HG2	2.03	0.41
23:AR:93:LEU:HD11	23:AR:100:LEU:HB3	2.02	0.41
26:AU:22:ILE:HG13	26:AU:100:VAL:HG11	2.03	0.41
38:Ag:66:HIS:CG	38:Ag:67:ILE:H	2.38	0.41
46:BH:49:ASN:C	46:BH:51:GLN:H	2.28	0.41
54:BP:175:ALA:HB3	64:BZ:51:GLY:O	2.20	0.41
55:BQ:7:GLN:NE2	55:BQ:35:ALA:O	2.51	0.41
55:BQ:93:VAL:O	55:BQ:97:ARG:HG3	2.21	0.41
80:CA:747:PRO:HG3	80:CA:757:ILE:HD13	2.01	0.41
80:CA:1114:LYS:NZ	80:CA:1143:MET:HA	2.35	0.41
80:CA:1279:LEU:HA	80:CA:1282:ILE:HD12	2.01	0.41
80:CA:1542:LEU:HD21	80:CA:1574:LEU:HB2	2.02	0.41
1:2:205:U:C2	1:2:206:A:C8	3.08	0.41
1:2:1183:A:C5	21:AP:100:LYS:HG2	2.56	0.41
1:2:1350:U:H2'	1:2:1351:G:C8	2.55	0.41
1:2:1636:C:H4'	1:2:1637:C:O5'	2.21	0.41
4:5:594:U:P	4:5:609:G:H1	2.43	0.41
4:5:825:U:OP2	39:BA:21:ARG:NH1	2.53	0.41
4:5:1181:U:O4	52:BN:21[A]:SER:OG	2.33	0.41
4:5:1302:A:N7	4:5:2857:C:O2'	2.54	0.41
4:5:1386:A:O4'	41:BC:141:ARG:NH2	2.53	0.41
4:5:1622:U:H2'	4:5:1623:G:C8	2.55	0.41
4:5:1886:A:O4'	4:5:3307:A:H5'	2.21	0.41
4:5:2861:U:H2'	4:5:2862:U:O4'	2.19	0.41
4:5:3217:C:H6	4:5:3266:G:H21	1.69	0.41
12:AG:25:ARG:HG3	12:AG:28:PHE:CD2	2.56	0.41
19:AN:140:LYS:HA	19:AN:140:LYS:HD2	1.77	0.41
32:Aa:83:ILE:C	32:Aa:85:ARG:H	2.16	0.41
42:BD:129:TYR:CD1	42:BD:177:GLU:HB3	2.55	0.41
48:BJ:110:ILE:HA	48:BJ:114:ILE:HB	2.01	0.41
53:BO:56:ARG:NH2	53:BO:75:GLU:OE2	2.31	0.41
56:BR:10:ILE:HG12	56:BR:26:ARG:HG3	2.03	0.41
61:BW:111:ASN:HB2	61:BW:123:TYR:HB2	2.01	0.41
66:Bb:52:ARG:HG3	66:Bb:52:ARG:NH1	2.34	0.41
73:Bi:27:PHE:HA	73:Bi:34:CYS:HA	2.02	0.41
80:CA:632:VAL:O	80:CA:633:ASN:HB2	2.19	0.41
80:CA:683:LEU:HD21	80:CA:693:TYR:CD2	2.46	0.41
80:CA:1178:HIS:CE1	80:CA:1298:ARG:HG3	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:CA:1554:ILE:HD12	80:CA:1558:SER:HB2	2.03	0.41
80:CA:1634:SER:C	80:CA:1636:TYR:H	2.28	0.41
1:2:1280:C:H4'	26:AU:69:LYS:HB3	2.01	0.41
1:2:1555:A:O2'	21:AP:82:ASN:ND2	2.54	0.41
1:2:1584:G:O2'	1:2:1585:U:P	2.79	0.41
2:3:11:C:H1'	53:BO:6:ALA:HB2	2.03	0.41
2:3:103:G:H4'	73:Bi:21:ARG:HG3	2.01	0.41
3:4:56:A:H4'	48:BJ:152:HIS:HB2	2.01	0.41
4:5:210:U:C2	4:5:230:U:H4'	2.56	0.41
4:5:821:U:H2'	4:5:822:G:C8	2.56	0.41
4:5:1046:A:O2'	4:5:1048:A:OP2	2.27	0.41
4:5:1090:G:H2'	4:5:1091:A:H8	1.85	0.41
4:5:1616:U:H2'	4:5:1617:G:H8	1.85	0.41
4:5:1641:U:O2'	4:5:1642:A:H3'	2.21	0.41
4:5:1766:G:H2'	4:5:1767:C:C6	2.55	0.41
4:5:2615:G:H2'	4:5:2616:C:H6	1.86	0.41
4:5:2882:U:H2'	4:5:2883:U:H6	1.86	0.41
4:5:2947:G:N3	40:BB:250:ALA:HB1	2.36	0.41
4:5:3001:C:H2'	4:5:3002:C:C6	2.55	0.41
5:6:74:C:H3'	47:BI:110:ARG:HH22	1.85	0.41
6:AA:52:LYS:HZ2	27:AV:82:VAL:HA	1.85	0.41
7:AB:108:ASP:OD1	7:AB:109:LYS:N	2.54	0.41
13:AH:171:ALA:O	13:AH:175:LYS:HG2	2.20	0.41
16:AK:15:LEU:HD22	16:AK:46:LEU:HD11	2.02	0.41
19:AN:138:ASN:OD1	19:AN:138:ASN:C	2.64	0.41
23:AR:21:TYR:CD1	23:AR:58:MET:HE1	2.56	0.41
25:AT:116:ILE:HD12	25:AT:116:ILE:HA	1.94	0.41
38:Ag:129:LYS:HG2	38:Ag:149:ASP:C	2.46	0.41
41:BC:64:SER:HA	41:BC:75:PRO:HA	2.02	0.41
44:BF:106:LEU:HD21	44:BF:126:LEU:HD23	2.02	0.41
49:BK:12:ASN:HB3	49:BK:14:PHE:HD2	1.84	0.41
52:BN:46[A]:GLU:HG3	52:BN:49[A]:ARG:H	1.86	0.41
68:Bd:79:VAL:O	68:Bd:83:GLU:HG3	2.20	0.41
80:CA:370:LEU:HD22	80:CA:375:ILE:HD13	2.03	0.41
80:CA:1612:ARG:HD3	80:CA:1619:LEU:HG	2.02	0.41
81:CB:237:ILE:HG23	81:CB:273:MET:HE1	2.02	0.41
1:2:86:A:H2'	1:2:87:C:H6	1.86	0.41
1:2:138:A:H2'	1:2:139:C:C6	2.55	0.41
1:2:153:G:H21	12:AG:56:ASN:ND2	2.15	0.41
1:2:1073:G:H4'	19:AN:10:GLY:HA2	2.02	0.41
1:2:1474:G:P	11:AF:109:LYS:HZ1	2.42	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:156:G:OP2	72:Bh:25:LYS:HB3	2.21	0.41
4:5:507:U:H2'	4:5:508:U:C6	2.56	0.41
4:5:663:C:H2'	4:5:664:U:C6	2.55	0.41
4:5:741:U:H2'	4:5:742:G:O4'	2.20	0.41
4:5:791:A:H2'	4:5:792:G:C8	2.55	0.41
4:5:791:A:H2'	4:5:792:G:H8	1.86	0.41
4:5:1281:G:C6	4:5:1282:G:N7	2.89	0.41
4:5:1856:C:H2'	4:5:1857:C:H6	1.85	0.41
4:5:2836:C:H41	4:5:2852:C:N4	2.18	0.41
4:5:2904:U:H2'	4:5:2905:U:H6	1.85	0.41
4:5:3187:A:H5'	46:BH:22:SER:HB2	2.03	0.41
10:AE:42:LEU:HD12	10:AE:42:LEU:HA	1.81	0.41
10:AE:139:VAL:HG13	10:AE:150:PRO:HG3	2.02	0.41
13:AH:85:PHE:HE2	13:AH:88:ARG:CZ	2.34	0.41
27:AV:1:MET:H3	27:AV:10:GLU:HB3	1.85	0.41
37:Af:147:VAL:HG13	37:Af:147:VAL:O	2.21	0.41
40:BB:292:ALA:HB2	40:BB:302:LYS:HD3	2.03	0.41
42:BD:34:LYS:HA	57:BS:27:LEU:HD21	2.01	0.41
42:BD:184:ASP:OD2	42:BD:187:THR:OG1	2.27	0.41
47:BI:57:LEU:HA	47:BI:130:ASP:HA	2.02	0.41
47:BI:102:MET:HE3	47:BI:112:GLN:NE2	2.34	0.41
51:BM:165:THR:HG22	51:BM:166:ALA:N	2.35	0.41
68:Bd:15:LYS:HB3	68:Bd:15:LYS:HE2	1.72	0.41
74:Bj:17:ARG:HB3	74:Bj:19:ASP:OD1	2.21	0.41
80:CA:531:ARG:HD2	80:CA:533:TYR:CE2	2.55	0.41
80:CA:809:ASN:OD1	80:CA:809:ASN:N	2.53	0.41
80:CA:928:ASN:O	80:CA:932:SER:OG	2.28	0.41
1:2:153:G:H2'	1:2:154:G:C8	2.55	0.41
1:2:293:U:H2'	1:2:294:C:H6	1.85	0.41
1:2:889:U:H2'	1:2:890:C:C6	2.55	0.41
1:2:1135:U:H2'	1:2:1136:U:C6	2.56	0.41
1:2:1159:C:O2'	22:AQ:140:LYS:NZ	2.33	0.41
1:2:1291:G:C8	1:2:1292:G:C8	3.08	0.41
1:2:1330:G:H2'	1:2:1331:A:O4'	2.21	0.41
1:2:1725:U:H2'	1:2:1726:G:H8	1.84	0.41
2:3:28:C:H2'	2:3:29:U:C6	2.56	0.41
4:5:440:A:P	4:5:440:A:H8	2.44	0.41
4:5:1428:A:OP2	64:BZ:2:PRO:HA	2.20	0.41
4:5:1580:A:H5''	4:5:2522:G:C2	2.56	0.41
4:5:1740:U:H1'	4:5:1741:A:H2	1.85	0.41
4:5:3184:A:OP2	52:BN:12[A]:LYS:NZ	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:6:74:C:O5'	47:BI:110:ARG:NH2	2.54	0.41
11:AF:203:LYS:HB2	11:AF:203:LYS:HE2	1.87	0.41
18:AM:67:THR:C	18:AM:68:GLU:HG3	2.46	0.41
18:AM:84:ASN:OD1	18:AM:85:LYS:N	2.50	0.41
26:AU:40:ASN:OD1	26:AU:40:ASN:N	2.53	0.41
38:Ag:192:PHE:CB	38:Ag:223:TRP:HZ3	2.29	0.41
39:BA:36:GLU:HA	39:BA:91:GLY:HA2	2.03	0.41
41:BC:120:TYR:CE1	41:BC:277:PRO:HB3	2.55	0.41
46:BH:67:ALA:O	46:BH:71:VAL:HG23	2.20	0.41
58:BT:78:TYR:O	58:BT:82:LYS:HG2	2.21	0.41
58:BT:101:ASN:HA	58:BT:103:TYR:CZ	2.56	0.41
80:CA:598:HIS:HA	80:CA:602:MET:HE2	2.02	0.41
80:CA:1447:HIS:O	80:CA:1451:GLN:N	2.52	0.41
1:2:44:U:OP2	1:2:437:A:N6	2.41	0.41
1:2:826:U:H2'	1:2:827:C:H6	1.85	0.41
1:2:850:A:H5''	55:BQ:165:LYS:HD2	2.03	0.41
1:2:1514:U:H1'	9:AD:6:SER:HB2	2.03	0.41
2:3:63:G:N3	2:3:63:G:H2'	2.35	0.41
3:4:22:A:H2'	3:4:23:A:C8	2.56	0.41
4:5:1837:U:H2'	4:5:1838:G:O4'	2.19	0.41
4:5:2555:G:N1	70:Bf:96:GLU:OE1	2.51	0.41
4:5:2683:U:H2'	4:5:2684:C:C6	2.55	0.41
4:5:2993:G:H2'	4:5:3142:A:N6	2.35	0.41
11:AF:56:ALA:O	11:AF:57:SER:OG	2.35	0.41
12:AG:120:GLU:OE2	12:AG:125:THR:HB	2.20	0.41
12:AG:152:ASP:OD1	12:AG:154:ARG:HB2	2.21	0.41
14:AI:81:VAL:HG22	14:AI:102:VAL:HG12	2.03	0.41
17:AL:125:VAL:HG12	17:AL:139:VAL:HA	2.02	0.41
26:AU:57:ARG:HA	26:AU:89:ARG:HG3	2.02	0.41
37:Af:89:LYS:NZ	37:Af:91:ILE:HD13	2.36	0.41
39:BA:147:ARG:HG3	39:BA:157:VAL:HG22	2.02	0.41
40:BB:86:VAL:HG22	40:BB:162:VAL:HG12	2.02	0.41
40:BB:306:THR:HG21	40:BB:316:GLU:HG3	2.02	0.41
45:BG:73:PRO:HD3	45:BG:233:TRP:CE2	2.55	0.41
48:BJ:75:LYS:HA	48:BJ:75:LYS:HD2	1.72	0.41
57:BS:8:ARG:HH11	57:BS:52:MET:HE1	1.85	0.41
80:CA:373:PHE:HB2	80:CA:375:ILE:HD11	2.02	0.41
80:CA:417:LEU:O	80:CA:421:VAL:HG13	2.21	0.41
80:CA:481:ARG:NH1	80:CA:485:MET:HG3	2.35	0.41
80:CA:983:LYS:HE2	80:CA:983:LYS:HB2	1.85	0.41
80:CA:1202:VAL:O	80:CA:1206:ARG:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:545:A:H2'	36:Ae:31:LYS:HE2	2.03	0.41
1:2:546:U:H2'	1:2:547:U:C6	2.56	0.41
1:2:859:A:C5	19:AN:73:ARG:HD3	2.56	0.41
1:2:891:A:H2'	1:2:892:A:H8	1.85	0.41
1:2:1010:C:H2'	1:2:1011:G:O4'	2.21	0.41
1:2:1098:U:OP1	8:AC:159:THR:OG1	2.16	0.41
1:2:1236:A:H2'	1:2:1237:G:C8	2.56	0.41
1:2:1241:G:O4'	21:AP:79:HIS:ND1	2.41	0.41
1:2:1260:U:H2'	1:2:1261:G:H8	1.86	0.41
1:2:1320:U:O2'	1:2:1322:A:OP1	2.35	0.41
1:2:1357:A:H2'	1:2:1358:G:C8	2.56	0.41
1:2:1515:A:O2'	1:2:1517:U:OP2	2.26	0.41
1:2:1552:U:O2	1:2:1597:A:H2	2.04	0.41
4:5:293:C:H2'	4:5:294:U:O4'	2.20	0.41
4:5:377:A:H1'	4:5:392:G:N2	2.36	0.41
4:5:594:U:H2'	4:5:609:G:O6	2.20	0.41
4:5:629:U:H2'	4:5:630:A:C8	2.56	0.41
4:5:696:C:OP1	41:BC:272:VAL:HG22	2.20	0.41
4:5:860:G:O2'	4:5:895:A:H4'	2.21	0.41
4:5:968:G:H2'	4:5:969:C:C6	2.56	0.41
4:5:1290:A:H2'	4:5:1291:A:C8	2.56	0.41
4:5:1497:C:H2'	4:5:1498:A:H8	1.85	0.41
4:5:1551:C:H2'	4:5:1552:G:O4'	2.20	0.41
4:5:1583:A:H2'	4:5:1584:U:O4'	2.20	0.41
4:5:1623:G:C4	4:5:1624:G:C8	3.09	0.41
4:5:1659:U:H2'	4:5:1660:C:H6	1.85	0.41
4:5:2130:G:O4'	4:5:2144:A:H4'	2.21	0.41
4:5:2383:C:H5'	52:BN:71[A]:PHE:CE2	2.56	0.41
4:5:2538:U:HO2'	4:5:2541:U:H3	1.59	0.41
4:5:2651:G:H5''	4:5:2652:U:O4'	2.21	0.41
4:5:2981:U:OP2	40:BB:244:ARG:NH1	2.54	0.41
4:5:3041:U:H2'	4:5:3042:U:C6	2.56	0.41
5:6:2:U:H2'	5:6:3:C:H6	1.86	0.41
6:AA:110:TYR:CD1	8:AC:64:LYS:HB3	2.55	0.41
9:AD:11:LEU:HD11	26:AU:27:THR:O	2.21	0.41
10:AE:185:GLY:O	10:AE:224:ASN:ND2	2.54	0.41
13:AH:34:LEU:HB2	13:AH:38:LEU:HD13	2.01	0.41
14:AI:143:TRP:N	14:AI:143:TRP:CD1	2.89	0.41
15:AJ:30:LEU:HD23	15:AJ:30:LEU:HA	1.94	0.41
18:AM:66:VAL:HG23	18:AM:67:THR:H	1.86	0.41
19:AN:53:LEU:HD23	19:AN:53:LEU:HA	1.94	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AR:83:GLN:OE1	23:AR:83:GLN:N	2.53	0.41
23:AR:110:VAL:HG21	23:AR:119:LEU:HD21	2.02	0.41
26:AU:26:LEU:HB3	26:AU:34:LEU:HD11	2.02	0.41
30:AY:45:ALA:O	30:AY:49:LYS:N	2.53	0.41
33:Ab:14:SER:HA	33:Ab:17:ARG:NH1	2.36	0.41
46:BH:47:LYS:NZ	50:BL:5:SER:O	2.37	0.41
47:BI:156:ARG:HG3	47:BI:163:GLN:HB2	2.03	0.41
49:BK:166:ALA:HB3	64:BZ:135:GLU:OE1	2.21	0.41
49:BK:186:ARG:O	49:BK:189:GLU:HG3	2.21	0.41
51:BM:42:PRO:HD3	51:BM:61:ILE:HG13	2.03	0.41
53:BO:126:ARG:HA	53:BO:140:GLU:HG2	2.02	0.41
58:BT:38:ILE:HD11	58:BT:56:VAL:HB	2.03	0.41
62:BX:70:ILE:HD13	62:BX:82:VAL:HG22	2.03	0.41
80:CA:223:SER:O	80:CA:224:THR:OG1	2.24	0.41
80:CA:234:PHE:CG	80:CA:235:THR:N	2.89	0.41
80:CA:246:ASN:ND2	80:CA:249:GLU:OE1	2.54	0.41
80:CA:844:ARG:HB3	80:CA:846:GLU:OE1	2.21	0.41
80:CA:1027:ARG:HG3	80:CA:1028:ILE:HG23	2.02	0.41
80:CA:1083:LYS:HG2	80:CA:1095:THR:HG23	2.02	0.41
80:CA:1160:VAL:HG13	80:CA:1324:TYR:HD2	1.84	0.41
80:CA:1206:ARG:NH1	80:CA:1210:THR:OG1	2.54	0.41
80:CA:1669:TYR:HE1	80:CA:1737:VAL:HA	1.85	0.41
81:CB:168:TYR:O	81:CB:171:GLN:HG2	2.21	0.41
1:2:393:C:N4	1:2:401:A:OP2	2.54	0.41
1:2:802:G:N2	28:AW:107:SER:OG	2.52	0.41
1:2:948:G:H2'	1:2:949:C:C6	2.56	0.41
1:2:1308:G:H2'	1:2:1309:C:C6	2.55	0.41
1:2:1442:U:H2'	1:2:1443:U:O4'	2.21	0.41
1:2:1657:U:H5'	1:2:1658:G:H5''	2.02	0.41
1:2:1667:A:H2'	1:2:1668:G:C8	2.56	0.41
2:3:27:U:H2'	2:3:28:C:C6	2.56	0.41
4:5:195:U:H2'	4:5:196:G:O4'	2.20	0.41
4:5:242:C:HO2'	4:5:243:G:H8	1.69	0.41
4:5:911:C:OP2	39:BA:9:ARG:HD2	2.21	0.41
4:5:1015:U:O2'	4:5:1017:C:OP2	2.36	0.41
4:5:1253:U:C2	4:5:1263:A:H3'	2.55	0.41
4:5:1805:C:H2'	4:5:1806:A:C8	2.54	0.41
4:5:2389:C:H2'	4:5:2390:A:C8	2.56	0.41
4:5:2679:A:HO2'	48:BJ:52:TYR:HH	1.67	0.41
4:5:2741:C:O2	78:Bn:20:HIS:HE1	2.03	0.41
4:5:3272:C:OP2	43:BE:78:ARG:NE	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AC:38:VAL:O	8:AC:38:VAL:HG13	2.21	0.41
9:AD:56:GLN:HG2	9:AD:57:ASP:N	2.36	0.41
11:AF:82:PHE:CE2	34:Ac:49:ARG:HG3	2.56	0.41
11:AF:209:TYR:HA	11:AF:212:LYS:NZ	2.36	0.41
14:AI:48:THR:HG21	14:AI:54:LYS:HE3	2.02	0.41
18:AM:36:LEU:HD23	18:AM:36:LEU:H	1.86	0.41
19:AN:102:LEU:HD23	19:AN:102:LEU:HA	1.88	0.41
25:AT:140:LEU:HD23	25:AT:140:LEU:H	1.85	0.41
28:AW:122:SER:OG	28:AW:123:GLY:N	2.53	0.41
44:BF:232:ARG:O	44:BF:232:ARG:HG3	2.21	0.41
46:BH:168:ARG:HA	46:BH:168:ARG:HD3	1.73	0.41
63:BY:83:THR:HG22	70:Bf:93:PHE:CZ	2.55	0.41
64:BZ:24:LYS:O	64:BZ:25:HIS:C	2.64	0.41
80:CA:1425:LEU:HD11	81:CB:94:LEU:HA	2.02	0.41
80:CA:1608:LEU:HD13	80:CA:1619:LEU:HD11	2.02	0.41
81:CB:160:GLN:NE2	81:CB:163:GLN:HE21	2.19	0.41
1:2:13:C:H4'	1:2:1298:U:O2	2.22	0.40
1:2:397:A:H2'	1:2:398:G:C8	2.56	0.40
1:2:629:U:C6	4:5:846:A:C5	3.09	0.40
1:2:1023:A:H4'	1:2:1024:U:O5'	2.21	0.40
1:2:1410:A:H5''	22:AQ:118:ILE:HD13	2.03	0.40
2:3:62:C:H4'	2:3:63:G:O5'	2.21	0.40
4:5:269:G:OP2	51:BM:44:ARG:NH2	2.51	0.40
4:5:348:A:H4'	4:5:367:A:N6	2.36	0.40
4:5:1225:A:H2'	4:5:1226:G:C8	2.57	0.40
4:5:1412:G:OP1	68:Bd:105:ARG:NH1	2.51	0.40
4:5:1757:A:H2'	4:5:1758:G:C8	2.55	0.40
4:5:2855:U:H2'	4:5:2856:G:O4'	2.21	0.40
16:AK:60:SER:HB2	16:AK:65:TYR:CE1	2.56	0.40
20:AO:40:ALA:HB1	20:AO:67:VAL:HA	2.03	0.40
24:AS:25:ASN:HB2	31:AZ:40:VAL:HG11	2.02	0.40
26:AU:25:THR:C	26:AU:26:LEU:HD12	2.46	0.40
27:AV:69:LEU:HD12	27:AV:69:LEU:HA	1.90	0.40
38:Ag:29:GLN:HG3	38:Ag:32:LEU:HD22	2.04	0.40
40:BB:53:MET:HE2	40:BB:53:MET:HB3	1.90	0.40
42:BD:23:ARG:HD2	42:BD:23:ARG:HA	1.79	0.40
45:BG:99:PRO:HG2	45:BG:190:VAL:HG23	2.03	0.40
49:BK:94:GLY:HA3	71:Bg:116:TYR:OH	2.20	0.40
54:BP:158:HIS:H	54:BP:186:VAL:HG12	1.87	0.40
64:BZ:114:GLY:O	64:BZ:137:LYS:NZ	2.52	0.40
80:CA:685:THR:OG1	80:CA:686:SER:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:CA:990:LYS:O	80:CA:994:ARG:NH1	2.54	0.40
80:CA:1055:LEU:HD23	80:CA:1055:LEU:HA	1.87	0.40
80:CA:1721:SER:HB2	80:CA:1723:VAL:HG23	2.03	0.40
80:CA:1765:ILE:HD12	80:CA:1951:ILE:HD12	2.03	0.40
81:CB:157:ILE:HG22	81:CB:159:THR:HG23	2.03	0.40
1:2:14:C:H2'	1:2:15:U:C6	2.56	0.40
1:2:400:A:H4'	1:2:401:A:O5'	2.21	0.40
1:2:652:G:H1'	1:2:683:C:H42	1.86	0.40
1:2:1321:A:H5''	6:AA:104:PRO:HG2	2.02	0.40
1:2:1600:A:H2'	1:2:1600:A:N3	2.36	0.40
2:3:20:U:O2'	4:5:1419:A:OP1	2.35	0.40
4:5:65:A:H1'	4:5:77:A:H1'	2.04	0.40
4:5:245:U:H2'	4:5:246:U:C6	2.56	0.40
4:5:446:U:H4'	4:5:447:U:H5	1.85	0.40
4:5:664:U:H5'	41:BC:107:ARG:HA	2.03	0.40
4:5:817:A:O2'	73:Bi:11:ARG:HG2	2.21	0.40
4:5:830:A:H2'	4:5:831:G:O4'	2.20	0.40
4:5:1011:A:H2'	4:5:1012:G:C8	2.56	0.40
4:5:1178:G:N3	4:5:1328:C:O2'	2.54	0.40
4:5:1288:U:H2'	4:5:1289:G:H8	1.86	0.40
4:5:1595:U:C2	4:5:1596:C:C5	3.10	0.40
4:5:2150:G:H22	4:5:2313:A:H2	1.69	0.40
7:AB:103:MET:HB3	7:AB:103:MET:HE3	1.93	0.40
12:AG:32:ILE:HG12	12:AG:100:ALA:HB1	2.02	0.40
15:AJ:108:ARG:HH21	15:AJ:145:SER:HB3	1.86	0.40
30:AY:57:VAL:HB	30:AY:60:PHE:CE2	2.51	0.40
42:BD:123:GLU:N	42:BD:123:GLU:OE1	2.54	0.40
56:BR:14:LEU:HD23	56:BR:14:LEU:HA	1.93	0.40
57:BS:124:VAL:O	57:BS:124:VAL:HG12	2.22	0.40
63:BY:78:ASN:HA	66:Bb:35:ARG:HH22	1.85	0.40
80:CA:381:THR:O	80:CA:384:MET:HE1	2.21	0.40
80:CA:620:LYS:O	80:CA:621:VAL:HG12	2.21	0.40
80:CA:1404:ASN:HB2	80:CA:1454:LYS:HA	2.03	0.40
1:2:237:C:O2'	1:2:238:U:O4'	2.36	0.40
1:2:824:G:H2'	1:2:825:U:C6	2.56	0.40
1:2:900:A:OP1	20:AO:43:THR:OG1	2.38	0.40
1:2:968:U:H2'	1:2:969:C:O4'	2.21	0.40
1:2:1471:A:HO2'	1:2:1472:C:P	2.44	0.40
1:2:1542:G:H22	1:2:1568:C:H1'	1.86	0.40
1:2:1561:U:H2'	1:2:1562:G:H8	1.86	0.40
1:2:1669:U:H2'	1:2:1670:G:O4'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:47:C:OP2	4:5:48:A:O2'	2.31	0.40
4:5:985:U:H2'	4:5:986:U:H6	1.85	0.40
4:5:2584:G:H1'	45:BG:240:ASN:ND2	2.37	0.40
14:AI:6:ASP:OD1	14:AI:9:HIS:HD2	2.05	0.40
17:AL:75:VAL:HG21	17:AL:117:VAL:CG1	2.51	0.40
26:AU:30:LYS:HZ1	26:AU:111:GLY:HA3	1.85	0.40
28:AW:41:MET:HG2	28:AW:129:VAL:HG21	2.03	0.40
32:Aa:45:VAL:HG23	32:Aa:46:GLU:N	2.36	0.40
37:Af:123:ASN:HB3	37:Af:126:CYS:SG	2.62	0.40
40:BB:323:MET:HE1	40:BB:359:ILE:HD13	2.03	0.40
42:BD:294:ALA:HB2	47:BI:210:ILE:HD13	2.04	0.40
54:BP:177:GLY:O	54:BP:186:VAL:N	2.47	0.40
63:BY:16:GLY:O	70:Bf:74:ARG:HG3	2.22	0.40
64:BZ:36:GLY:HA2	64:BZ:39:HIS:HB2	2.04	0.40
75:Bk:34:THR:O	75:Bk:36:ARG:NH1	2.54	0.40
1:2:400:A:H4'	1:2:401:A:C5'	2.51	0.40
1:2:463:U:H2'	1:2:464:A:C8	2.56	0.40
1:2:929:A:H8	1:2:929:A:OP2	2.04	0.40
1:2:948:G:H2'	1:2:949:C:H6	1.85	0.40
1:2:1158:C:H6	1:2:1158:C:H2'	1.74	0.40
1:2:1310:U:H2'	1:2:1311:U:C6	2.56	0.40
1:2:1345:A:OP1	26:AU:54:GLY:HA3	2.22	0.40
1:2:1365:C:H5''	22:AQ:66:ARG:NH2	2.34	0.40
1:2:1644:C:O2'	4:5:2255:A:N1	2.54	0.40
1:2:1792:G:H3'	1:2:1792:G:OP2	2.21	0.40
4:5:89:A:OP1	64:BZ:60:TYR:N	2.44	0.40
4:5:179:C:H2'	4:5:180:C:H6	1.86	0.40
4:5:273:A:H2'	4:5:274:G:C8	2.56	0.40
4:5:907:G:H2'	4:5:926:A:H62	1.87	0.40
4:5:916:G:H5'	4:5:917:A:OP1	2.22	0.40
4:5:947:G:H2'	4:5:948:C:H6	1.87	0.40
4:5:2674:A:H1'	48:BJ:107:ASP:OD1	2.21	0.40
9:AD:223:LYS:HB2	38:Ag:191:ASP:OD1	2.22	0.40
10:AE:252:ARG:HD2	10:AE:256:ARG:HH21	1.87	0.40
19:AN:67:THR:HG22	19:AN:68:GLY:N	2.36	0.40
24:AS:134:ARG:HB2	24:AS:136:GLN:OE1	2.22	0.40
31:AZ:91:PRO:HB3	31:AZ:101:TYR:CE2	2.57	0.40
33:Ab:15:GLU:O	33:Ab:29:ARG:NH2	2.55	0.40
35:Ad:31:ILE:HB	35:Ad:36:LEU:HD11	2.02	0.40
41:BC:217:LYS:HE2	41:BC:220:ARG:HH12	1.86	0.40
42:BD:262:LYS:HE3	42:BD:262:LYS:HB3	1.84	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:BK:46:ILE:HD11	49:BK:51:LEU:HD12	2.02	0.40
55:BQ:23:TRP:CZ3	55:BQ:25:ASP:HB2	2.55	0.40
55:BQ:52:LYS:O	55:BQ:53:LYS:HG3	2.20	0.40
56:BR:17:GLU:HG2	56:BR:18:SER:N	2.36	0.40
66:Bb:14:LEU:HD21	66:Bb:43:ILE:HD12	2.04	0.40
66:Bb:18:ILE:HA	66:Bb:23:TYR:CE2	2.56	0.40
73:Bi:69:HIS:O	73:Bi:73:ARG:HG3	2.22	0.40
80:CA:234:PHE:CD2	80:CA:235:THR:HG22	2.56	0.40
80:CA:442:THR:HB	80:CA:446:ARG:NH2	2.37	0.40
80:CA:540:HIS:NE2	80:CA:657:LEU:HD22	2.36	0.40
80:CA:661:ASP:O	80:CA:664:GLN:HG3	2.21	0.40
80:CA:910:LEU:HA	80:CA:913:ILE:HD12	2.02	0.40
81:CB:290:LEU:HD22	81:CB:292:PHE:HE1	1.87	0.40
1:2:78:A:H4'	12:AG:172:ALA:HB3	2.03	0.40
1:2:151:G:C2	1:2:152:U:C4	3.10	0.40
1:2:304:U:H2'	1:2:305:C:H6	1.86	0.40
1:2:555:A:HO2'	1:2:556:A:C5'	2.29	0.40
1:2:990:C:H2'	1:2:991:G:O4'	2.21	0.40
1:2:1426:C:O2'	1:2:1428:G:H8	2.04	0.40
1:2:1451:C:P	35:Ad:12:ARG:HH22	2.45	0.40
1:2:1704:U:H2'	1:2:1705:C:C6	2.57	0.40
2:3:4:C:H2'	2:3:5:U:H6	1.87	0.40
3:4:107:C:H2'	3:4:108:A:H8	1.87	0.40
4:5:511:G:H2'	4:5:512:U:O4'	2.22	0.40
4:5:800:G:H2'	4:5:801:A:N7	2.36	0.40
4:5:1011:A:H2'	4:5:1012:G:H8	1.87	0.40
4:5:1062:A:H4'	57:BS:105:PHE:CE1	2.56	0.40
4:5:2429:G:H2'	4:5:2430:A:C8	2.55	0.40
4:5:2618:G:C8	4:5:2865:U:H5''	2.57	0.40
4:5:2686:A:H2'	4:5:2687:G:O4'	2.22	0.40
4:5:2946:A:H5''	4:5:2947:G:H5'	2.03	0.40
4:5:3069:G:C2	4:5:3070:A:C8	3.09	0.40
4:5:3160:U:H3	4:5:3290:G:H1	1.70	0.40
6:AA:88:LYS:NZ	23:AR:82:ASP:O	2.36	0.40
9:AD:12:VAL:O	9:AD:16:VAL:HG23	2.21	0.40
10:AE:230:GLU:CD	10:AE:231:GLN:H	2.30	0.40
11:AF:133:VAL:HG12	11:AF:198:LEU:HD13	2.03	0.40
13:AH:29:ASN:OD1	13:AH:29:ASN:N	2.53	0.40
16:AK:61:TRP:CE2	35:Ad:23:VAL:HG22	2.55	0.40
18:AM:54:ARG:NH1	37:Af:127:GLY:HA3	2.32	0.40
22:AQ:36:ILE:HD13	22:AQ:52:LEU:HD11	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:AS:27:LYS:HB2	24:AS:30:TYR:HD2	1.86	0.40
25:AT:21:PHE:HE2	25:AT:134:ARG:HH22	1.69	0.40
26:AU:62:VAL:HG12	26:AU:64:LYS:HG2	2.04	0.40
28:AW:50:PHE:HB3	28:AW:63:VAL:HG13	2.04	0.40
31:AZ:86:GLU:HG2	31:AZ:87:GLY:N	2.36	0.40
34:Ac:29:ARG:HA	34:Ac:41:VAL:HA	2.03	0.40
38:Ag:176:LYS:HB3	38:Ag:195:HIS:O	2.21	0.40
38:Ag:301:LEU:O	38:Ag:312:VAL:HA	2.21	0.40
47:BI:52:LEU:HB3	47:BI:136:PHE:HB2	2.03	0.40
47:BI:193:ASP:HB2	47:BI:196:PHE:O	2.21	0.40
57:BS:119:ALA:HB3	57:BS:126:VAL:HG12	2.04	0.40
63:BY:103:GLN:HE21	63:BY:106:GLN:NE2	2.19	0.40
64:BZ:7:LYS:HD3	64:BZ:7:LYS:HA	1.90	0.40
65:Ba:47:LEU:HD23	65:Ba:47:LEU:HA	1.89	0.40
69:Be:12:LYS:NZ	69:Be:95:GLY:O	2.33	0.40
74:Bj:26:LYS:HD3	74:Bj:78:LEU:HD12	2.03	0.40
80:CA:595:PHE:CZ	80:CA:619:ILE:HG22	2.57	0.40
80:CA:753:ASP:OD1	80:CA:753:ASP:N	2.49	0.40
80:CA:1693:VAL:HG13	80:CA:1697:PHE:HD2	1.87	0.40
80:CA:1786:PRO:HG3	80:CA:1892:TYR:CZ	2.56	0.40
81:CB:126:PHE:O	81:CB:129:SER:OG	2.37	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	AA	204/206 (99%)	192 (94%)	12 (6%)	0	100	100
7	AB	222/255 (87%)	211 (95%)	10 (4%)	1 (0%)	24	58
8	AC	214/216 (99%)	205 (96%)	9 (4%)	0	100	100
9	AD	220/222 (99%)	218 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	AE	256/258 (99%)	245 (96%)	10 (4%)	1 (0%)	30	62
11	AF	204/206 (99%)	195 (96%)	9 (4%)	0	100	100
12	AG	226/228 (99%)	211 (93%)	14 (6%)	1 (0%)	30	62
13	AH	182/184 (99%)	172 (94%)	10 (6%)	0	100	100
14	AI	183/200 (92%)	173 (94%)	8 (4%)	2 (1%)	11	42
15	AJ	182/184 (99%)	173 (95%)	9 (5%)	0	100	100
16	AK	90/92 (98%)	85 (94%)	5 (6%)	0	100	100
17	AL	142/144 (99%)	136 (96%)	6 (4%)	0	100	100
18	AM	119/121 (98%)	95 (80%)	22 (18%)	2 (2%)	7	34
19	AN	148/150 (99%)	141 (95%)	7 (5%)	0	100	100
20	AO	125/127 (98%)	119 (95%)	6 (5%)	0	100	100
21	AP	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
22	AQ	139/141 (99%)	131 (94%)	8 (6%)	0	100	100
23	AR	117/136 (86%)	112 (96%)	5 (4%)	0	100	100
24	AS	143/145 (99%)	135 (94%)	8 (6%)	0	100	100
25	AT	141/143 (99%)	134 (95%)	7 (5%)	0	100	100
26	AU	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
27	AV	85/87 (98%)	77 (91%)	8 (9%)	0	100	100
28	AW	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
29	AX	142/144 (99%)	129 (91%)	13 (9%)	0	100	100
30	AY	132/134 (98%)	125 (95%)	7 (5%)	0	100	100
31	AZ	80/82 (98%)	75 (94%)	5 (6%)	0	100	100
32	Aa	95/97 (98%)	81 (85%)	11 (12%)	3 (3%)	3	24
33	Ab	79/81 (98%)	73 (92%)	6 (8%)	0	100	100
34	Ac	61/63 (97%)	60 (98%)	1 (2%)	0	100	100
35	Ad	51/53 (96%)	51 (100%)	0	0	100	100
36	Ae	58/60 (97%)	55 (95%)	3 (5%)	0	100	100
37	Af	71/73 (97%)	63 (89%)	8 (11%)	0	100	100
38	Ag	310/312 (99%)	302 (97%)	8 (3%)	0	100	100
39	BA	249/251 (99%)	238 (96%)	10 (4%)	1 (0%)	30	62
40	BB	384/386 (100%)	371 (97%)	12 (3%)	1 (0%)	36	67

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	BC	359/361 (99%)	347 (97%)	11 (3%)	1 (0%)	36	67
42	BD	292/294 (99%)	283 (97%)	8 (3%)	1 (0%)	36	67
43	BE	163/176 (93%)	158 (97%)	5 (3%)	0	100	100
44	BF	220/222 (99%)	215 (98%)	5 (2%)	0	100	100
45	BG	231/233 (99%)	222 (96%)	9 (4%)	0	100	100
46	BH	189/191 (99%)	186 (98%)	3 (2%)	0	100	100
47	BI	216/218 (99%)	214 (99%)	2 (1%)	0	100	100
48	BJ	167/169 (99%)	158 (95%)	9 (5%)	0	100	100
49	BK	191/193 (99%)	178 (93%)	10 (5%)	3 (2%)	7	36
50	BL	134/136 (98%)	132 (98%)	2 (2%)	0	100	100
51	BM	201/203 (99%)	196 (98%)	5 (2%)	0	100	100
52	BN	195/197 (99%)	189 (97%)	4 (2%)	2 (1%)	12	44
53	BO	181/183 (99%)	175 (97%)	6 (3%)	0	100	100
54	BP	183/185 (99%)	178 (97%)	5 (3%)	0	100	100
55	BQ	186/188 (99%)	184 (99%)	2 (1%)	0	100	100
56	BR	169/171 (99%)	165 (98%)	4 (2%)	0	100	100
57	BS	157/159 (99%)	150 (96%)	7 (4%)	0	100	100
58	BT	98/100 (98%)	98 (100%)	0	0	100	100
59	BU	134/136 (98%)	134 (100%)	0	0	100	100
60	BV	124/126 (98%)	120 (97%)	4 (3%)	0	100	100
61	BW	119/121 (98%)	117 (98%)	1 (1%)	1 (1%)	16	49
62	BX	123/125 (98%)	121 (98%)	2 (2%)	0	100	100
63	BY	133/135 (98%)	131 (98%)	2 (2%)	0	100	100
64	BZ	146/148 (99%)	136 (93%)	8 (6%)	2 (1%)	9	38
65	Ba	56/58 (97%)	49 (88%)	7 (12%)	0	100	100
66	Bb	94/96 (98%)	94 (100%)	0	0	100	100
67	Bc	107/109 (98%)	101 (94%)	6 (6%)	0	100	100
68	Bd	125/127 (98%)	121 (97%)	4 (3%)	0	100	100
69	Be	104/106 (98%)	102 (98%)	2 (2%)	0	100	100
70	Bf	110/112 (98%)	108 (98%)	2 (2%)	0	100	100
71	Bg	117/119 (98%)	115 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
72	Bh	97/99 (98%)	96 (99%)	1 (1%)	0	100	100
73	Bi	83/85 (98%)	83 (100%)	0	0	100	100
74	Bj	75/77 (97%)	75 (100%)	0	0	100	100
75	Bk	48/50 (96%)	48 (100%)	0	0	100	100
76	Bl	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
77	Bm	23/25 (92%)	23 (100%)	0	0	100	100
78	Bn	101/103 (98%)	99 (98%)	2 (2%)	0	100	100
79	Bo	89/91 (98%)	89 (100%)	0	0	100	100
80	CA	1738/1967 (88%)	1664 (96%)	69 (4%)	5 (0%)	36	67
81	CB	295/297 (99%)	292 (99%)	2 (1%)	1 (0%)	36	67
82	CC	110/530 (21%)	106 (96%)	4 (4%)	0	100	100
All	All	13127/14000 (94%)	12615 (96%)	484 (4%)	28 (0%)	44	74

All (28) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	AI	10	LYS
32	Aa	84	VAL
52	BN	111[A]	PRO
80	CA	224	THR
80	CA	621	VAL
80	CA	633	ASN
80	CA	1123	THR
81	CB	9	ILE
49	BK	63	VAL
49	BK	77	LEU
61	BW	44	PRO
64	BZ	78	LEU
80	CA	1148	PHE
7	AB	212	VAL
10	AE	43	PRO
64	BZ	40	HIS
12	AG	173	PRO
14	AI	9	HIS
18	AM	131	ASP
32	Aa	9	GLY
40	BB	128	LYS
42	BD	20	PHE

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Mol	Chain	Res	Type
52	BN	110[A]	PRO
18	AM	109	GLU
32	Aa	62	TYR
39	BA	126	LEU
49	BK	166	ALA
41	BC	4	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	AA	170/173 (98%)	170 (100%)	0	100	100
7	AB	200/224 (89%)	200 (100%)	0	100	100
8	AC	175/175 (100%)	175 (100%)	0	100	100
9	AD	182/182 (100%)	182 (100%)	0	100	100
10	AE	220/220 (100%)	220 (100%)	0	100	100
11	AF	172/173 (99%)	172 (100%)	0	100	100
12	AG	189/195 (97%)	189 (100%)	0	100	100
13	AH	163/165 (99%)	163 (100%)	0	100	100
14	AI	148/161 (92%)	148 (100%)	0	100	100
15	AJ	156/157 (99%)	156 (100%)	0	100	100
16	AK	77/85 (91%)	77 (100%)	0	100	100
17	AL	129/129 (100%)	129 (100%)	0	100	100
18	AM	88/98 (90%)	88 (100%)	0	100	100
19	AN	127/127 (100%)	127 (100%)	0	100	100
20	AO	91/96 (95%)	91 (100%)	0	100	100
21	AP	95/98 (97%)	95 (100%)	0	100	100
22	AQ	117/117 (100%)	117 (100%)	0	100	100
23	AR	101/124 (82%)	101 (100%)	0	100	100
24	AS	128/128 (100%)	128 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	AT	115/115 (100%)	115 (100%)	0	100	100
26	AU	93/93 (100%)	93 (100%)	0	100	100
27	AV	71/74 (96%)	71 (100%)	0	100	100
28	AW	110/110 (100%)	110 (100%)	0	100	100
29	AX	119/119 (100%)	119 (100%)	0	100	100
30	AY	112/112 (100%)	112 (100%)	0	100	100
31	AZ	67/73 (92%)	67 (100%)	0	100	100
32	Aa	83/83 (100%)	83 (100%)	0	100	100
33	Ab	70/70 (100%)	70 (100%)	0	100	100
34	Ac	55/56 (98%)	55 (100%)	0	100	100
35	Ad	47/47 (100%)	47 (100%)	0	100	100
36	Ae	50/51 (98%)	50 (100%)	0	100	100
37	Af	56/64 (88%)	56 (100%)	0	100	100
38	Ag	250/257 (97%)	250 (100%)	0	100	100
39	BA	190/193 (98%)	190 (100%)	0	100	100
40	BB	321/322 (100%)	319 (99%)	2 (1%)	78	79
41	BC	288/288 (100%)	288 (100%)	0	100	100
42	BD	241/243 (99%)	241 (100%)	0	100	100
43	BE	138/155 (89%)	138 (100%)	0	100	100
44	BF	186/186 (100%)	186 (100%)	0	100	100
45	BG	187/191 (98%)	187 (100%)	0	100	100
46	BH	168/171 (98%)	168 (100%)	0	100	100
47	BI	185/185 (100%)	184 (100%)	1 (0%)	81	80
48	BJ	146/147 (99%)	146 (100%)	0	100	100
49	BK	154/154 (100%)	154 (100%)	0	100	100
50	BL	107/107 (100%)	107 (100%)	0	100	100
51	BM	175/175 (100%)	175 (100%)	0	100	100
52	BN	160/160 (100%)	160 (100%)	0	100	100
53	BO	138/145 (95%)	138 (100%)	0	100	100
54	BP	150/150 (100%)	150 (100%)	0	100	100
55	BQ	152/153 (99%)	152 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	BR	155/155 (100%)	155 (100%)	0	100	100
57	BS	136/136 (100%)	136 (100%)	0	100	100
58	BT	87/87 (100%)	87 (100%)	0	100	100
59	BU	104/104 (100%)	104 (100%)	0	100	100
60	BV	56/107 (52%)	56 (100%)	0	100	100
61	BW	104/105 (99%)	104 (100%)	0	100	100
62	BX	108/108 (100%)	108 (100%)	0	100	100
63	BY	115/115 (100%)	115 (100%)	0	100	100
64	BZ	118/118 (100%)	118 (100%)	0	100	100
65	Ba	46/46 (100%)	46 (100%)	0	100	100
66	Bb	81/81 (100%)	81 (100%)	0	100	100
67	Bc	92/96 (96%)	92 (100%)	0	100	100
68	Bd	108/109 (99%)	108 (100%)	0	100	100
69	Be	90/90 (100%)	90 (100%)	0	100	100
70	Bf	95/95 (100%)	95 (100%)	0	100	100
71	Bg	104/104 (100%)	104 (100%)	0	100	100
72	Bh	80/81 (99%)	80 (100%)	0	100	100
73	Bi	69/69 (100%)	69 (100%)	0	100	100
74	Bj	68/68 (100%)	68 (100%)	0	100	100
75	Bk	45/45 (100%)	45 (100%)	0	100	100
76	Bl	47/47 (100%)	47 (100%)	0	100	100
77	Bm	22/23 (96%)	22 (100%)	0	100	100
78	Bn	87/88 (99%)	87 (100%)	0	100	100
79	Bo	71/71 (100%)	71 (100%)	0	100	100
80	CA	1560/1770 (88%)	1560 (100%)	0	100	100
81	CB	266/266 (100%)	266 (100%)	0	100	100
82	CC	97/482 (20%)	97 (100%)	0	100	100
All	All	11123/11942 (93%)	11120 (100%)	3 (0%)	100	100

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

Mol	Chain	Res	Type
40	BB	89	VAL

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Mol	Chain	Res	Type
40	BB	90	VAL
47	BI	55	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (110) such sidechains are listed below:

Mol	Chain	Res	Type
6	AA	28	ASN
6	AA	32	HIS
6	AA	131	GLN
7	AB	74	GLN
7	AB	220	GLN
8	AC	87	GLN
10	AE	98	ASN
10	AE	157	ASN
11	AF	63	GLN
11	AF	139	ASN
11	AF	158	GLN
11	AF	224	ASN
13	AH	74	GLN
13	AH	180	GLN
15	AJ	38	ASN
15	AJ	110	GLN
16	AK	32	HIS
18	AM	143	GLN
20	AO	99	GLN
22	AQ	100	GLN
25	AT	101	ASN
26	AU	87	HIS
27	AV	35	ASN
27	AV	74	GLN
28	AW	12	ASN
28	AW	39	GLN
28	AW	80	ASN
29	AX	27	ASN
30	AY	110	GLN
30	AY	133	ASN
33	Ab	42	ASN
34	Ac	27	GLN
35	Ad	53	ASN
36	Ae	5	HIS
38	Ag	101	GLN
38	Ag	182	ASN

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Mol	Chain	Res	Type
38	Ag	185	GLN
38	Ag	237	GLN
39	BA	205	ASN
40	BB	109	HIS
40	BB	139	GLN
40	BB	211	GLN
41	BC	110	ASN
41	BC	116	ASN
41	BC	175	HIS
41	BC	291	ASN
42	BD	63	GLN
42	BD	296	GLN
43	BE	97	ASN
44	BF	112	ASN
45	BG	38	GLN
45	BG	192	GLN
46	BH	8	GLN
46	BH	9	GLN
46	BH	125	ASN
47	BI	92	HIS
47	BI	123	HIS
47	BI	162	GLN
48	BJ	90	GLN
51	BM	182	ASN
53	BO	54	HIS
54	BP	135	GLN
55	BQ	7	GLN
55	BQ	134	HIS
57	BS	77	ASN
57	BS	103	GLN
57	BS	131	GLN
57	BS	134	GLN
59	BU	24	ASN
59	BU	98	ASN
62	BX	98	ASN
63	BY	103	GLN
66	Bb	11	ASN
67	Bc	57	GLN
68	Bd	49	ASN
69	Be	75	HIS
69	Be	88	ASN
69	Be	106	ASN

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Mol	Chain	Res	Type
71	Bg	20	GLN
71	Bg	59	ASN
71	Bg	113	GLN
74	Bj	10	GLN
74	Bj	57	ASN
75	Bk	43	ASN
75	Bk	50	ASN
76	Bl	120	GLN
78	Bn	27	GLN
80	CA	248	HIS
80	CA	258	GLN
80	CA	261	ASN
80	CA	292	GLN
80	CA	455	GLN
80	CA	759	ASN
80	CA	809	ASN
80	CA	866	GLN
80	CA	924	ASN
80	CA	1287	ASN
80	CA	1398	ASN
80	CA	1404	ASN
80	CA	1412	GLN
80	CA	1456	GLN
80	CA	1615	GLN
80	CA	1653	HIS
80	CA	1670	ASN
81	CB	103	GLN
81	CB	163	GLN
81	CB	173	HIS
81	CB	276	ASN
82	CC	358	ASN
82	CC	377	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1768/1798 (98%)	413 (23%)	36 (2%)
2	3	157/158 (99%)	27 (17%)	1 (0%)
3	4	120/121 (99%)	9 (7%)	1 (0%)
4	5	3180/3396 (93%)	530 (16%)	30 (0%)
5	6	75/76 (98%)	12 (16%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	5300/5549 (95%)	991 (18%)	68 (1%)

All (991) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	25	C
1	2	26	A
1	2	34	G
1	2	43	A
1	2	47	A
1	2	56	U
1	2	57	G
1	2	61	A
1	2	62	A
1	2	63	G
1	2	65	A
1	2	67	A
1	2	68	A
1	2	69	G
1	2	72	A
1	2	74	U
1	2	75	U
1	2	76	A
1	2	78	A
1	2	79	C
1	2	80	A
1	2	81	G
1	2	104	A
1	2	114	C
1	2	126	A
1	2	127	G
1	2	129	U
1	2	130	C
1	2	131	C
1	2	132	U
1	2	134	U
1	2	138	A
1	2	140	A
1	2	141	U
1	2	142	G

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Mol	Chain	Res	Type
1	2	153	G
1	2	155	U
1	2	156	A
1	2	161	U
1	2	166	C
1	2	171	A
1	2	176	C
1	2	178	U
1	2	180	A
1	2	186	C
1	2	187	G
1	2	188	A
1	2	191	C
1	2	193	U
1	2	195	G
1	2	196	G
1	2	198	A
1	2	216	U
1	2	217	A
1	2	218	A
1	2	225	A
1	2	227	U
1	2	228	G
1	2	230	C
1	2	232	U
1	2	233	C
1	2	234	G
1	2	236	A
1	2	240	U
1	2	241	U
1	2	250	C
1	2	257	A
1	2	260	U
1	2	276	C
1	2	278	U
1	2	279	G
1	2	280	U
1	2	281	G
1	2	287	G
1	2	299	A
1	2	314	C
1	2	316	A

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Mol	Chain	Res	Type
1	2	320	U
1	2	322	G
1	2	323	A
1	2	330	G
1	2	335	U
1	2	337	G
1	2	338	C
1	2	352	A
1	2	359	A
1	2	361	C
1	2	388	G
1	2	390	G
1	2	400	A
1	2	401	A
1	2	402	C
1	2	404	G
1	2	415	C
1	2	416	A
1	2	417	A
1	2	419	G
1	2	423	G
1	2	424	C
1	2	425	A
1	2	426	G
1	2	428	A
1	2	434	G
1	2	439	U
1	2	444	C
1	2	452	A
1	2	454	U
1	2	460	A
1	2	461	G
1	2	468	A
1	2	469	C
1	2	477	A
1	2	482	U
1	2	483	A
1	2	485	A
1	2	487	G
1	2	491	C
1	2	493	U
1	2	494	U

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Mol	Chain	Res	Type
1	2	495	C
1	2	496	G
1	2	498	G
1	2	499	U
1	2	500	C
1	2	506	A
1	2	507	U
1	2	510	G
1	2	511	A
1	2	515	A
1	2	527	A
1	2	534	A
1	2	538	A
1	2	540	G
1	2	541	A
1	2	542	A
1	2	544	A
1	2	546	U
1	2	549	G
1	2	555	A
1	2	556	A
1	2	557	G
1	2	558	U
1	2	565	C
1	2	568	G
1	2	572	C
1	2	578	U
1	2	580	A
1	2	582	U
1	2	594	A
1	2	595	G
1	2	606	A
1	2	611	U
1	2	619	A
1	2	620	A
1	2	621	A
1	2	622	A
1	2	623	A
1	2	624	G
1	2	629	U
1	2	630	A
1	2	639	U

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Mol	Chain	Res	Type
1	2	640	U
1	2	641	G
1	2	653	C
1	2	654	C
1	2	655	G
1	2	677	G
1	2	678	A
1	2	679	U
1	2	680	U
1	2	681	U
1	2	693	U
1	2	694	U
1	2	696	C
1	2	698	U
1	2	700	C
1	2	702	G
1	2	704	C
1	2	705	U
1	2	706	A
1	2	707	A
1	2	708	C
1	2	709	C
1	2	710	U
1	2	711	U
1	2	712	G
1	2	728	U
1	2	730	G
1	2	732	G
1	2	733	A
1	2	734	A
1	2	739	G
1	2	741	C
1	2	742	U
1	2	743	U
1	2	753	A
1	2	765	G
1	2	766	U
1	2	774	A
1	2	775	G
1	2	778	G
1	2	780	A
1	2	781	U

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Mol	Chain	Res	Type
1	2	782	U
1	2	783	G
1	2	789	A
1	2	812	A
1	2	813	U
1	2	814	A
1	2	815	G
1	2	816	G
1	2	820	U
1	2	821	U
1	2	823	G
1	2	833	U
1	2	836	U
1	2	837	G
1	2	840	U
1	2	841	U
1	2	846	G
1	2	852	C
1	2	855	A
1	2	856	A
1	2	857	U
1	2	863	A
1	2	876	G
1	2	899	G
1	2	901	G
1	2	902	G
1	2	912	U
1	2	913	G
1	2	915	A
1	2	921	U
1	2	929	A
1	2	933	A
1	2	934	C
1	2	935	U
1	2	942	G
1	2	960	U
1	2	964	U
1	2	966	A
1	2	970	A
1	2	971	A
1	2	988	A
1	2	992	A

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Mol	Chain	Res	Type
1	2	993	A
1	2	1001	A
1	2	1003	A
1	2	1004	U
1	2	1005	A
1	2	1007	C
1	2	1023	A
1	2	1024	U
1	2	1026	A
1	2	1028	C
1	2	1039	A
1	2	1053	G
1	2	1058	U
1	2	1060	U
1	2	1061	A
1	2	1076	A
1	2	1082	C
1	2	1092	A
1	2	1096	C
1	2	1100	G
1	2	1138	A
1	2	1150	G
1	2	1158	C
1	2	1160	A
1	2	1164	G
1	2	1166	A
1	2	1167	G
1	2	1170	G
1	2	1185	U
1	2	1194	A
1	2	1196	A
1	2	1199	G
1	2	1200	G
1	2	1212	G
1	2	1217	A
1	2	1218	G
1	2	1227	A
1	2	1229	G
1	2	1241	G
1	2	1243	G
1	2	1244	A
1	2	1245	G

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Mol	Chain	Res	Type
1	2	1246	C
1	2	1249	U
1	2	1251	U
1	2	1252	C
1	2	1256	A
1	2	1257	U
1	2	1274	C
1	2	1275	A
1	2	1285	U
1	2	1286	U
1	2	1291	G
1	2	1301	U
1	2	1314	U
1	2	1315	U
1	2	1318	G
1	2	1321	A
1	2	1322	A
1	2	1337	A
1	2	1338	C
1	2	1340	U
1	2	1344	A
1	2	1345	A
1	2	1346	A
1	2	1348	A
1	2	1349	G
1	2	1360	A
1	2	1361	U
1	2	1363	U
1	2	1367	G
1	2	1370	U
1	2	1371	A
1	2	1373	C
1	2	1381	U
1	2	1382	A
1	2	1383	G
1	2	1388	A
1	2	1389	C
1	2	1390	U
1	2	1398	U
1	2	1399	C
1	2	1400	A
1	2	1402	G

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Mol	Chain	Res	Type
1	2	1414	U
1	2	1425	A
1	2	1427	A
1	2	1428	G
1	2	1431	C
1	2	1436	A
1	2	1445	G
1	2	1446	A
1	2	1447	C
1	2	1459	C
1	2	1460	A
1	2	1466	G
1	2	1468	U
1	2	1469	A
1	2	1470	C
1	2	1471	A
1	2	1472	C
1	2	1473	U
1	2	1479	A
1	2	1486	G
1	2	1491	U
1	2	1493	A
1	2	1496	U
1	2	1503	A
1	2	1506	G
1	2	1514	U
1	2	1516	A
1	2	1517	U
1	2	1518	C
1	2	1521	G
1	2	1523	G
1	2	1524	A
1	2	1528	U
1	2	1535	U
1	2	1536	G
1	2	1537	C
1	2	1540	G
1	2	1542	G
1	2	1543	A
1	2	1557	U
1	2	1558	U
1	2	1559	A

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Mol	Chain	Res	Type
1	2	1569	A
1	2	1570	A
1	2	1576	A
1	2	1583	A
1	2	1585	U
1	2	1590	G
1	2	1601	G
1	2	1607	G
1	2	1611	A
1	2	1614	A
1	2	1616	G
1	2	1622	G
1	2	1631	A
1	2	1634	C
1	2	1635	A
1	2	1636	C
1	2	1637	C
1	2	1657	U
1	2	1658	G
1	2	1688	U
1	2	1701	A
1	2	1709	C
1	2	1711	C
1	2	1715	G
1	2	1717	G
1	2	1756	A
1	2	1760	G
1	2	1762	A
1	2	1766	A
1	2	1767	G
1	2	1769	U
1	2	1780	G
1	2	1782	A
1	2	1783	C
1	2	1792	G
1	2	1793	G
1	2	1794	A
1	2	1795	U
1	2	1796	C
1	2	1799	U
2	3	23	U
2	3	34	U

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Mol	Chain	Res	Type
2	3	35	C
2	3	52	A
2	3	59	A
2	3	62	C
2	3	63	G
2	3	80	A
2	3	81	U
2	3	82	U
2	3	85	G
2	3	86	U
2	3	87	G
2	3	90	U
2	3	95	G
2	3	104	A
2	3	106	C
2	3	111	A
2	3	112	U
2	3	113	U
2	3	125	U
2	3	126	A
2	3	148	G
2	3	152	G
2	3	155	A
2	3	156	U
2	3	158	U
3	4	7	G
3	4	53	U
3	4	54	U
3	4	65	G
3	4	76	A
3	4	77	G
3	4	102	A
3	4	112	G
3	4	121	U
4	5	6	A
4	5	14	U
4	5	18	G
4	5	22	G
4	5	26	A
4	5	40	A
4	5	43	A
4	5	49	A

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Mol	Chain	Res	Type
4	5	59	G
4	5	60	A
4	5	65	A
4	5	66	A
4	5	67	A
4	5	92	G
4	5	96	G
4	5	99	A
4	5	109	A
4	5	110	G
4	5	111	C
4	5	113	C
4	5	117	U
4	5	121	A
4	5	122	A
4	5	133	U
4	5	136	G
4	5	146	U
4	5	148	G
4	5	156	G
4	5	157	A
4	5	166	C
4	5	187	A
4	5	190	U
4	5	191	U
4	5	192	C
4	5	200	C
4	5	210	U
4	5	213	A
4	5	218	G
4	5	219	A
4	5	240	U
4	5	241	G
4	5	243	G
4	5	245	U
4	5	248	U
4	5	249	U
4	5	252	U
4	5	269	G
4	5	283	G
4	5	286	U
4	5	295	A

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Mol	Chain	Res	Type
4	5	305	U
4	5	323	A
4	5	329	U
4	5	339	C
4	5	342	A
4	5	349	A
4	5	350	C
4	5	351	A
4	5	352	A
4	5	376	G
4	5	398	A
4	5	401	U
4	5	402	A
4	5	403	C
4	5	421	G
4	5	422	A
4	5	440	A
4	5	441	U
4	5	442	G
4	5	443	G
4	5	445	G
4	5	447	U
4	5	448	U
4	5	450	G
4	5	487	U
4	5	488	U
4	5	489	U
4	5	491	A
4	5	493	U
4	5	494	G
4	5	521	A
4	5	523	A
4	5	535	G
4	5	543	C
4	5	546	C
4	5	547	G
4	5	552	G
4	5	555	U
4	5	557	A
4	5	559	A
4	5	579	G
4	5	589	A

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Mol	Chain	Res	Type
4	5	609	G
4	5	611	A
4	5	620	U
4	5	621	A
4	5	637	C
4	5	638	C
4	5	648	C
4	5	649	A
4	5	660	A
4	5	677	A
4	5	681	U
4	5	691	A
4	5	705	A
4	5	712	G
4	5	715	A
4	5	716	A
4	5	719	U
4	5	720	A
4	5	725	G
4	5	758	C
4	5	764	U
4	5	767	U
4	5	776	U
4	5	777	U
4	5	780	A
4	5	781	G
4	5	785	G
4	5	786	A
4	5	806	A
4	5	807	A
4	5	808	A
4	5	817	A
4	5	830	A
4	5	846	A
4	5	847	A
4	5	849	C
4	5	857	G
4	5	861	C
4	5	871	U
4	5	874	U
4	5	875	G
4	5	879	U

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Mol	Chain	Res	Type
4	5	896	A
4	5	897	U
4	5	907	G
4	5	908	G
4	5	914	A
4	5	916	G
4	5	917	A
4	5	921	A
4	5	923	C
4	5	924	G
4	5	925	A
4	5	937	G
4	5	938	C
4	5	944	C
4	5	953	G
4	5	959	C
4	5	960	U
4	5	963	G
4	5	964	G
4	5	991	G
4	5	995	U
4	5	1002	A
4	5	1010	G
4	5	1015	U
4	5	1024	G
4	5	1025	A
4	5	1028	U
4	5	1032	C
4	5	1036	A
4	5	1041	U
4	5	1047	A
4	5	1049	C
4	5	1064	A
4	5	1065	A
4	5	1072	G
4	5	1081	U
4	5	1093	A
4	5	1094	U
4	5	1095	U
4	5	1097	G
4	5	1098	A
4	5	1103	A

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Mol	Chain	Res	Type
4	5	1104	G
4	5	1117	G
4	5	1131	G
4	5	1144	U
4	5	1150	A
4	5	1153	A
4	5	1155	C
4	5	1156	C
4	5	1159	A
4	5	1180	A
4	5	1181	U
4	5	1192	C
4	5	1193	A
4	5	1196	C
4	5	1201	C
4	5	1202	A
4	5	1208	U
4	5	1217	A
4	5	1222	G
4	5	1225	A
4	5	1227	C
4	5	1231	A
4	5	1232	C
4	5	1233	G
4	5	1235	U
4	5	1236	G
4	5	1240	A
4	5	1241	U
4	5	1242	G
4	5	1245	A
4	5	1246	G
4	5	1253	U
4	5	1254	C
4	5	1258	U
4	5	1262	G
4	5	1263	A
4	5	1264	G
4	5	1265	U
4	5	1269	U
4	5	1270	A
4	5	1271	A
4	5	1274	A

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Mol	Chain	Res	Type
4	5	1278	A
4	5	1279	C
4	5	1285	G
4	5	1286	A
4	5	1287	A
4	5	1309	U
4	5	1313	G
4	5	1331	U
4	5	1349	G
4	5	1351	U
4	5	1352	A
4	5	1353	U
4	5	1354	G
4	5	1355	A
4	5	1356	U
4	5	1357	G
4	5	1386	A
4	5	1392	G
4	5	1399	A
4	5	1400	G
4	5	1417	G
4	5	1419	A
4	5	1421	G
4	5	1434	G
4	5	1437	C
4	5	1446	A
4	5	1481	A
4	5	1482	A
4	5	1483	G
4	5	1494	U
4	5	1508	C
4	5	1509	A
4	5	1536	G
4	5	1539	A
4	5	1555	U
4	5	1556	C
4	5	1557	A
4	5	1560	G
4	5	1562	C
4	5	1563	C
4	5	1566	A
4	5	1567	U

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Mol	Chain	Res	Type
4	5	1568	U
4	5	1569	U
4	5	1572	U
4	5	1573	G
4	5	1575	A
4	5	1576	G
4	5	1580	A
4	5	1581	C
4	5	1587	A
4	5	1588	A
4	5	1593	A
4	5	1596	C
4	5	1605	A
4	5	1620	U
4	5	1629	U
4	5	1639	C
4	5	1642	A
4	5	1643	A
4	5	1645	U
4	5	1646	G
4	5	1724	U
4	5	1725	C
4	5	1730	G
4	5	1741	A
4	5	1750	A
4	5	1751	G
4	5	1765	U
4	5	1766	G
4	5	1769	G
4	5	1770	G
4	5	1775	G
4	5	1780	G
4	5	1796	G
4	5	1797	A
4	5	1813	A
4	5	1814	A
4	5	1816	A
4	5	1817	G
4	5	1819	U
4	5	1820	U
4	5	1821	U
4	5	1835	A

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Mol	Chain	Res	Type
4	5	1839	A
4	5	1842	A
4	5	1846	C
4	5	1866	C
4	5	1867	A
4	5	1878	G
4	5	1880	U
4	5	1893	A
4	5	1899	G
4	5	1906	G
4	5	1908	A
4	5	1952	G
4	5	1954	G
4	5	2101	C
4	5	2102	U
4	5	2110	G
4	5	2111	G
4	5	2112	U
4	5	2113	A
4	5	2121	G
4	5	2122	G
4	5	2131	A
4	5	2140	U
4	5	2142	A
4	5	2144	A
4	5	2158	A
4	5	2169	G
4	5	2170	U
4	5	2188	A
4	5	2192	C
4	5	2193	U
4	5	2194	G
4	5	2198	A
4	5	2205	U
4	5	2206	G
4	5	2207	A
4	5	2209	U
4	5	2210	G
4	5	2223	A
4	5	2225	U
4	5	2249	G
4	5	2250	G

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Mol	Chain	Res	Type
4	5	2256	A
4	5	2257	C
4	5	2272	G
4	5	2273	G
4	5	2282	U
4	5	2288	G
4	5	2307	G
4	5	2308	C
4	5	2310	U
4	5	2313	A
4	5	2314	U
4	5	2315	G
4	5	2334	U
4	5	2335	G
4	5	2336	U
4	5	2373	A
4	5	2374	C
4	5	2375	G
4	5	2386	A
4	5	2388	U
4	5	2393	G
4	5	2397	A
4	5	2402	A
4	5	2403	G
4	5	2404	A
4	5	2411	U
4	5	2419	A
4	5	2435	G
4	5	2439	A
4	5	2446	U
4	5	2447	A
4	5	2449	A
4	5	2452	G
4	5	2496	C
4	5	2498	U
4	5	2499	U
4	5	2501	U
4	5	2502	A
4	5	2505	U
4	5	2506	U
4	5	2507	C
4	5	2514	U

Continued on next page...

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Mol	Chain	Res	Type
4	5	2515	A
4	5	2538	U
4	5	2539	C
4	5	2540	A
4	5	2541	U
4	5	2542	U
4	5	2549	G
4	5	2552	C
4	5	2554	A
4	5	2561	A
4	5	2569	A
4	5	2570	U
4	5	2571	U
4	5	2572	C
4	5	2573	G
4	5	2585	G
4	5	2593	A
4	5	2606	G
4	5	2607	G
4	5	2614	G
4	5	2651	G
4	5	2652	U
4	5	2656	A
4	5	2657	A
4	5	2672	G
4	5	2674	A
4	5	2677	G
4	5	2689	A
4	5	2691	A
4	5	2694	A
4	5	2696	A
4	5	2704	A
4	5	2714	G
4	5	2728	G
4	5	2729	U
4	5	2752	U
4	5	2753	G
4	5	2755	C
4	5	2772	C
4	5	2777	G
4	5	2778	G
4	5	2788	C

Continued on next page...

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Mol	Chain	Res	Type
4	5	2796	G
4	5	2799	A
4	5	2800	G
4	5	2801	A
4	5	2803	A
4	5	2810	C
4	5	2814	G
4	5	2817	A
4	5	2821	C
4	5	2842	U
4	5	2844	C
4	5	2845	A
4	5	2849	C
4	5	2856	G
4	5	2860	U
4	5	2867	C
4	5	2871	G
4	5	2872	A
4	5	2875	U
4	5	2887	A
4	5	2888	U
4	5	2889	C
4	5	2898	G
4	5	2911	A
4	5	2923	U
4	5	2935	U
4	5	2936	A
4	5	2938	G
4	5	2942	C
4	5	2947	G
4	5	2951	G
4	5	2971	A
4	5	2983	C
4	5	2996	U
4	5	2997	G
4	5	3012	A
4	5	3056	U
4	5	3059	G
4	5	3078	U
4	5	3079	U
4	5	3086	A
4	5	3092	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	5	3101	G
4	5	3104	U
4	5	3122	A
4	5	3129	A
4	5	3130	A
4	5	3131	U
4	5	3142	A
4	5	3143	C
4	5	3151	U
4	5	3154	C
4	5	3155	U
4	5	3156	U
4	5	3157	U
4	5	3165	A
4	5	3170	A
4	5	3172	A
4	5	3173	G
4	5	3174	A
4	5	3175	U
4	5	3176	G
4	5	3179	U
4	5	3181	C
4	5	3187	A
4	5	3206	C
4	5	3207	U
4	5	3210	A
4	5	3216	G
4	5	3217	C
4	5	3218	A
4	5	3219	G
4	5	3229	G
4	5	3239	G
4	5	3243	A
4	5	3245	A
4	5	3247	G
4	5	3259	U
4	5	3270	U
4	5	3273	A
4	5	3276	G
4	5	3281	U
4	5	3288	G
4	5	3289	G

Continued on next page...

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Mol	Chain	Res	Type
4	5	3294	A
4	5	3304	U
4	5	3313	U
4	5	3316	A
4	5	3318	G
4	5	3319	U
4	5	3320	A
4	5	3335	A
4	5	3341	U
4	5	3345	G
4	5	3351	U
4	5	3352	U
4	5	3353	G
4	5	3354	U
4	5	3369	G
4	5	3375	A
4	5	3378	C
4	5	3396	U
5	6	16	U
5	6	17	G
5	6	18	G
5	6	19	U
5	6	21	A
5	6	22	C
5	6	47	U
5	6	48	U
5	6	58	A
5	6	60	U
5	6	73	G
5	6	76	A

All (68) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	68	A
1	2	77	U
1	2	139	C
1	2	141	U
1	2	224	C
1	2	280	U
1	2	322	G
1	2	387	A

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Mol	Chain	Res	Type
1	2	400	A
1	2	539	G
1	2	541	A
1	2	545	A
1	2	555	A
1	2	639	U
1	2	640	U
1	2	705	U
1	2	711	U
1	2	765	G
1	2	819	G
1	2	912	U
1	2	928	U
1	2	963	A
1	2	1023	A
1	2	1216	C
1	2	1226	A
1	2	1256	A
1	2	1273	G
1	2	1274	C
1	2	1344	A
1	2	1382	A
1	2	1430	U
1	2	1471	A
1	2	1584	G
1	2	1633	A
1	2	1636	C
1	2	1791	A
2	3	85	G
3	4	52	G
4	5	239	G
4	5	282	G
4	5	647	A
4	5	715	A
4	5	763	G
4	5	846	A
4	5	873	C
4	5	916	G
4	5	1064	A
4	5	1097	G
4	5	1355	A
4	5	1562	C

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Mol	Chain	Res	Type
4	5	1815	U
4	5	1816	A
4	5	1820	U
4	5	2101	C
4	5	2112	U
4	5	2446	U
4	5	2495	C
4	5	2500	A
4	5	2537	U
4	5	2541	U
4	5	3121	U
4	5	3218	A
4	5	3228	C
4	5	3269	U
4	5	3319	U
4	5	3350	C
4	5	3351	U
4	5	3353	G

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 95 ligands modelled in this entry, 95 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

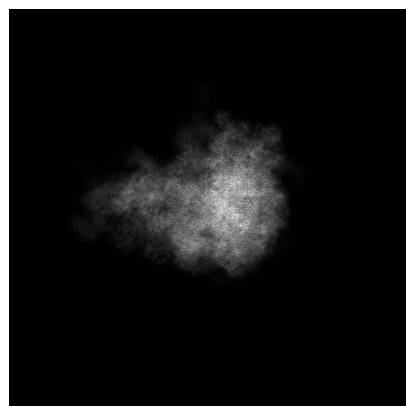
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14861. These allow visual inspection of the internal detail of the map and identification of artifacts.

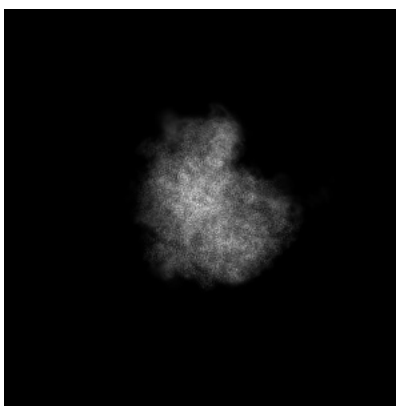
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

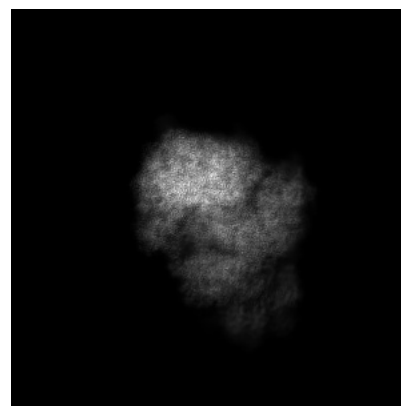
6.1.1 Primary map



X

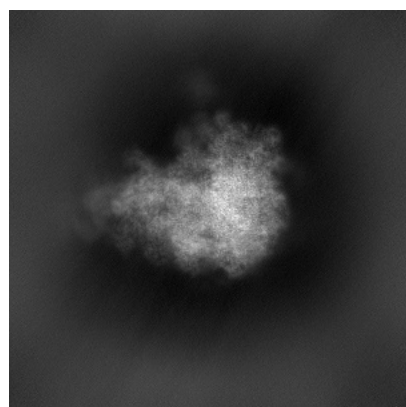


Y

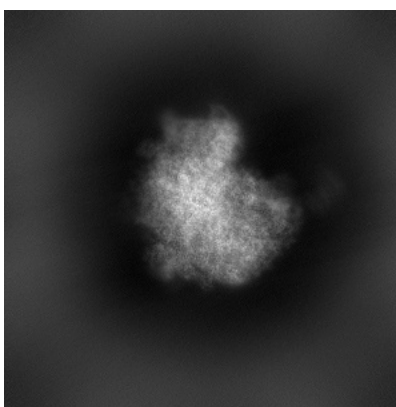


Z

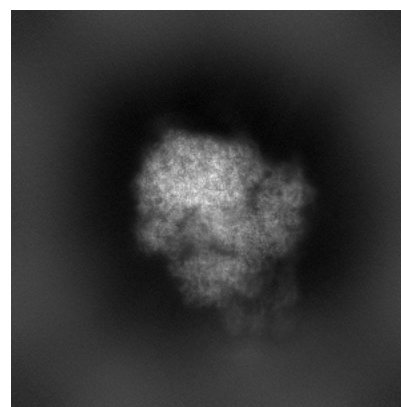
6.1.2 Raw map



X



Y

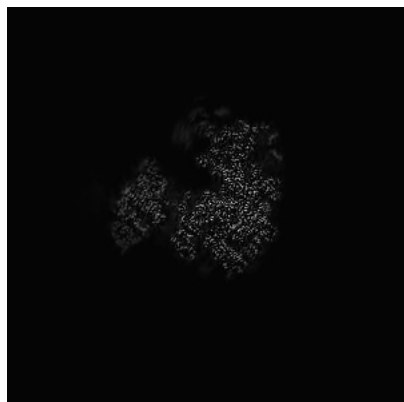


Z

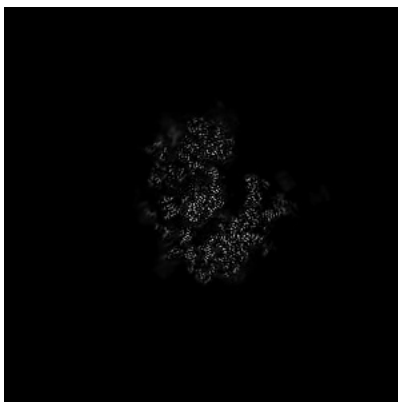
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

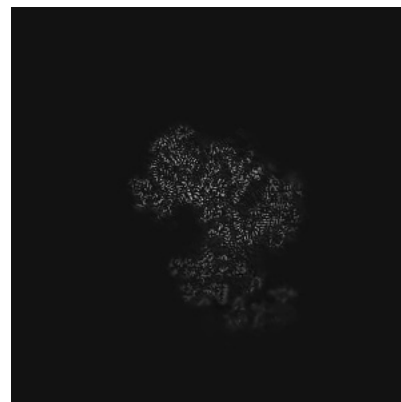
6.2.1 Primary map



X Index: 280

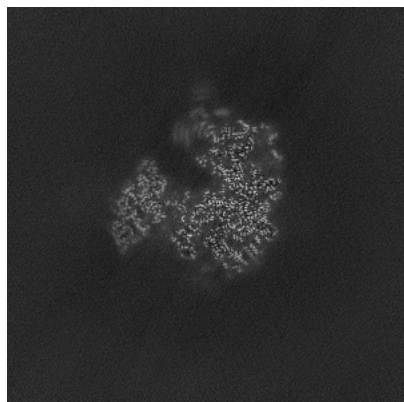


Y Index: 280

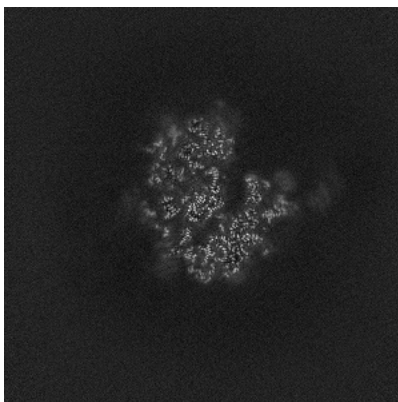


Z Index: 280

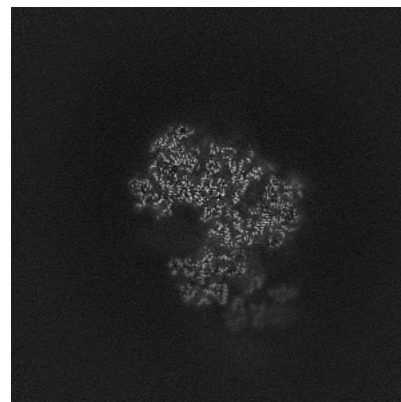
6.2.2 Raw map



X Index: 280



Y Index: 280

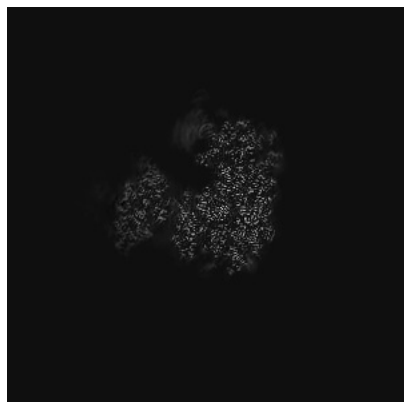


Z Index: 280

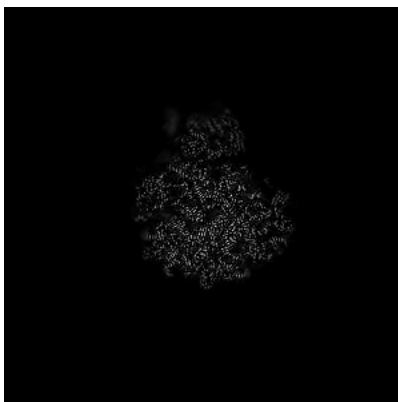
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

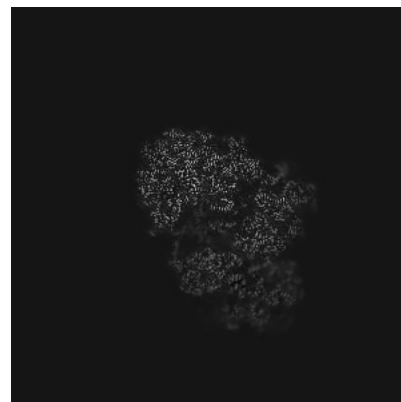
6.3.1 Primary map



X Index: 285

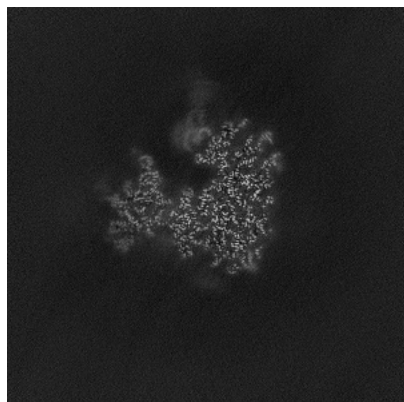


Y Index: 314

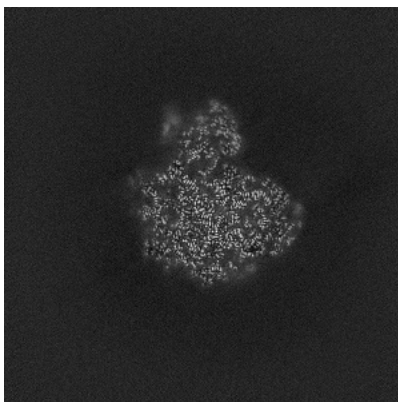


Z Index: 300

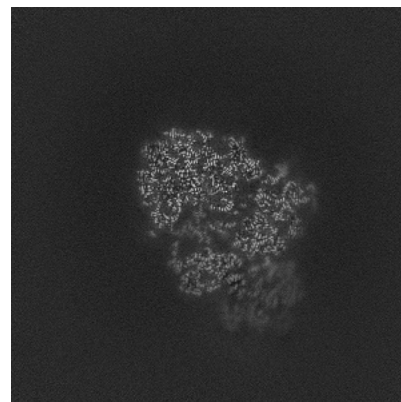
6.3.2 Raw map



X Index: 290



Y Index: 305

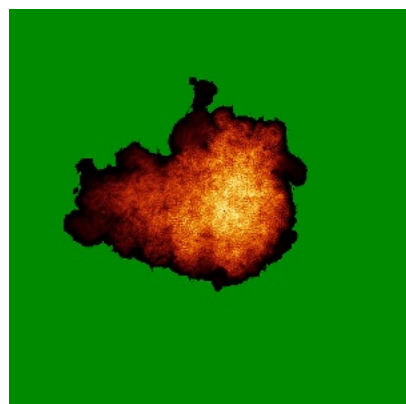


Z Index: 300

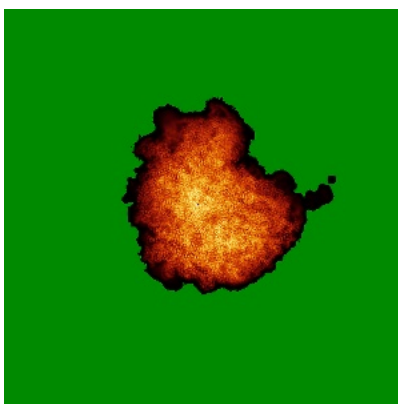
The images above show the largest variance slices of the map in three orthogonal directions.

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

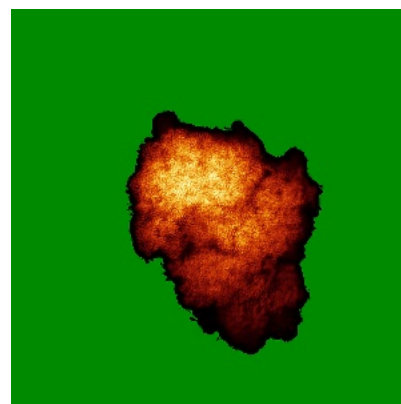
6.4.1 Primary map



X

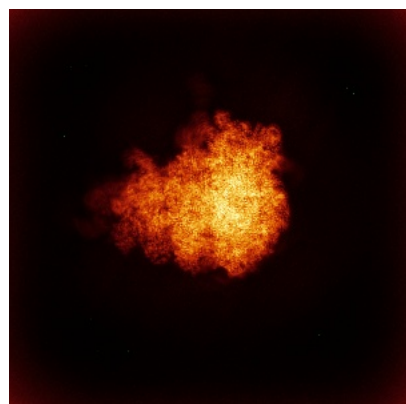


Y

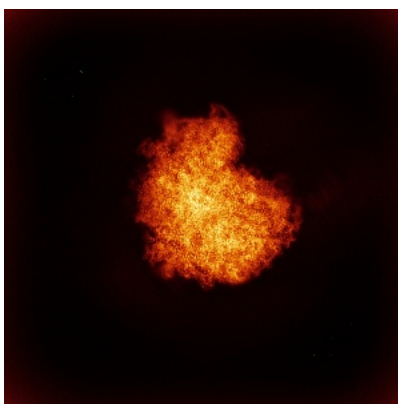


Z

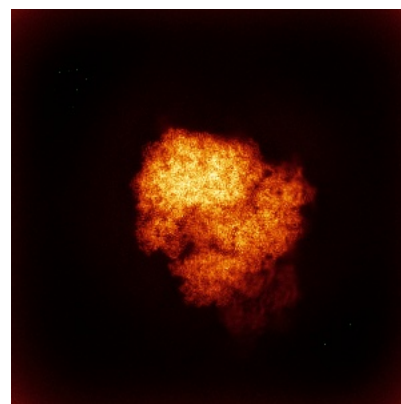
6.4.2 Raw map



X



Y

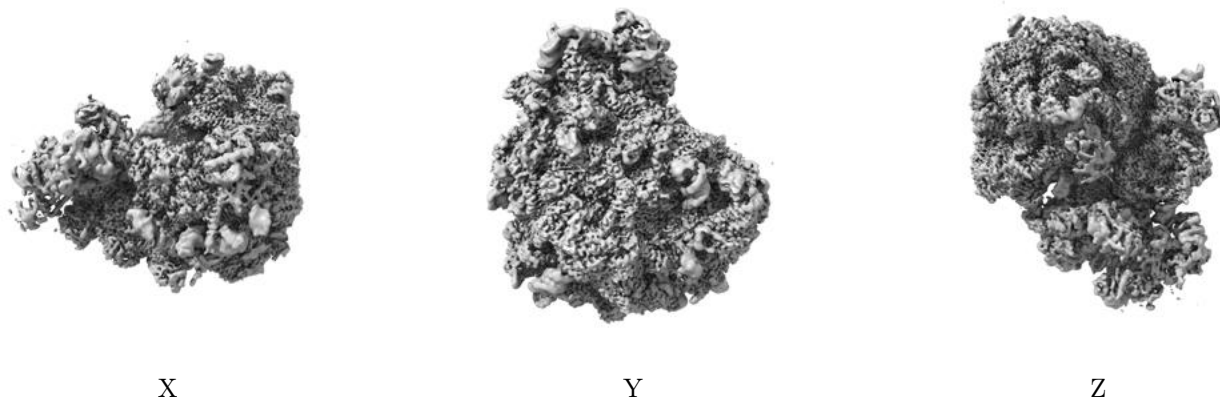


Z

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.

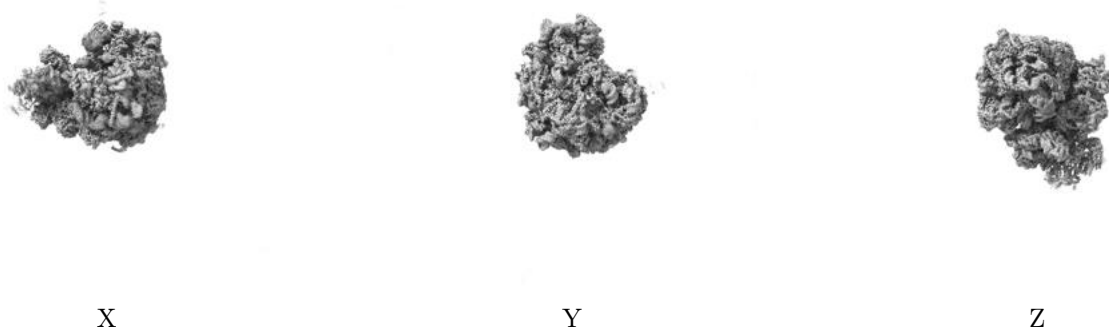
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.4. 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.

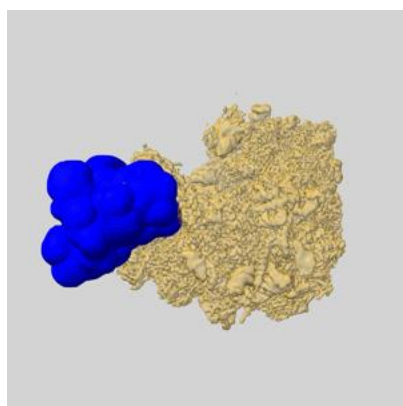
6.6 Mask visualisation [i](#)

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

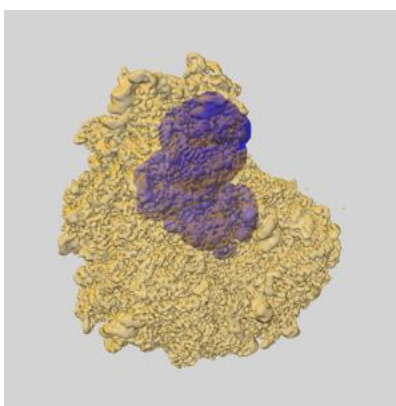
A mask typically either:

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

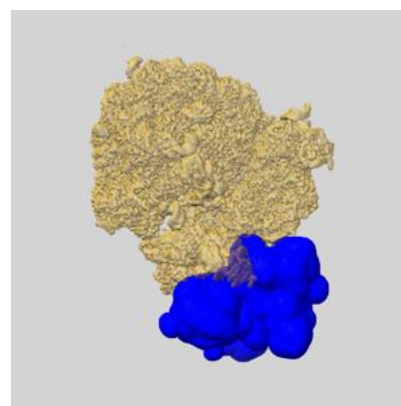
6.6.1 emd_14861_msk_2.map [i](#)



X

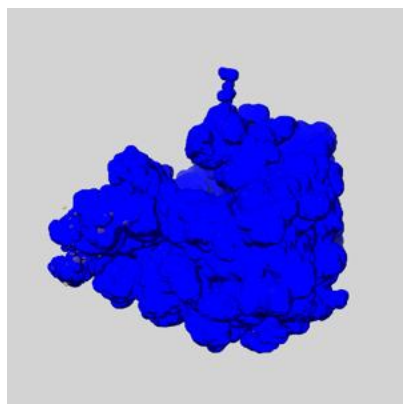


Y

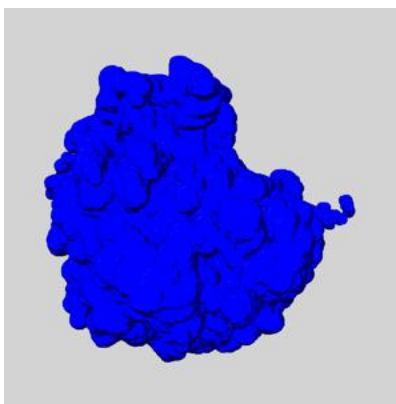


Z

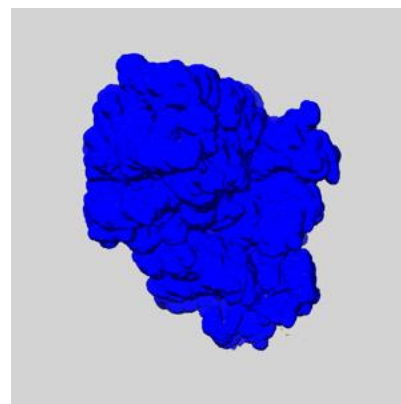
6.6.2 emd_14861_msk_1.map [i](#)



X



Y

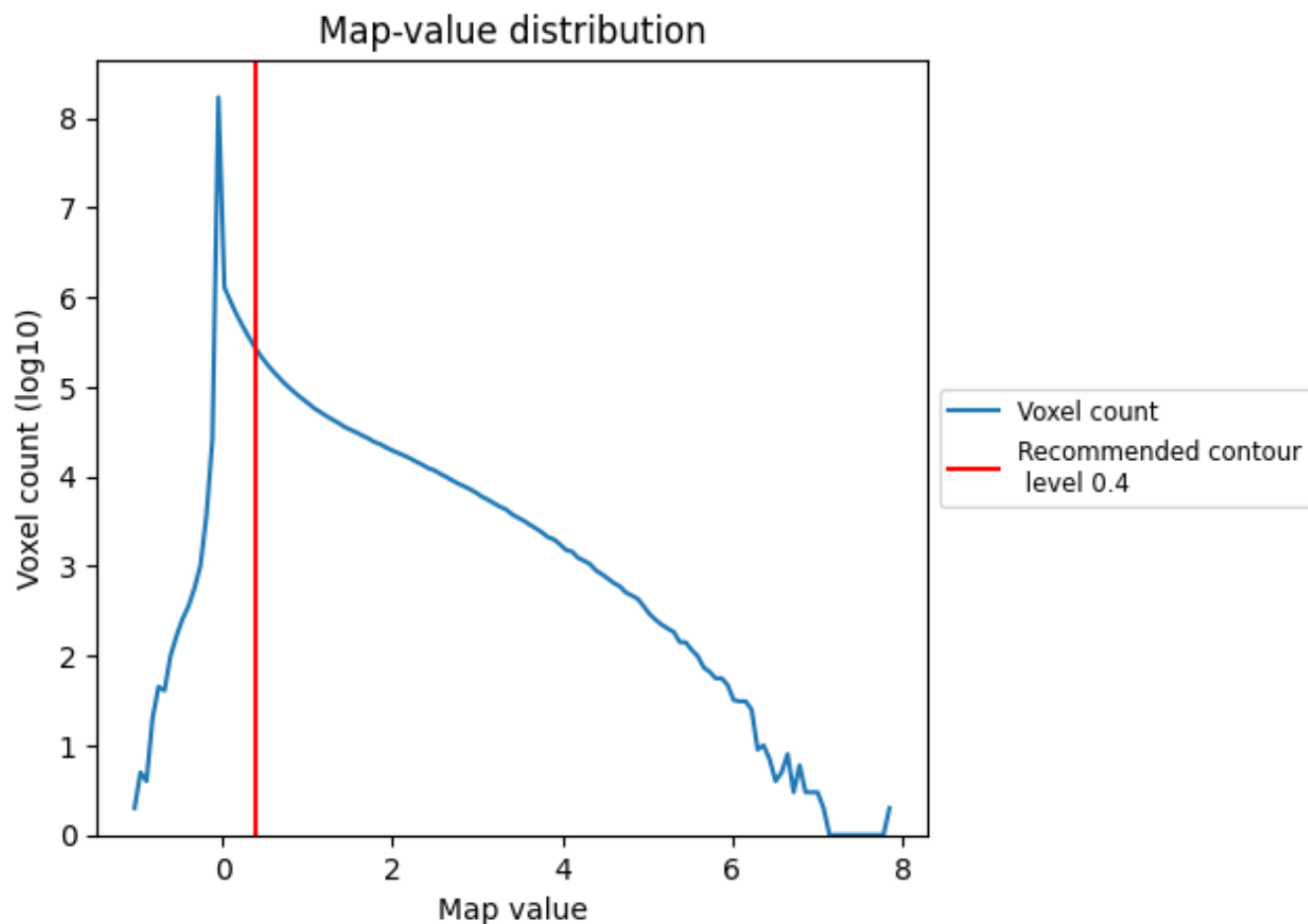


Z

7 Map analysis [i](#)

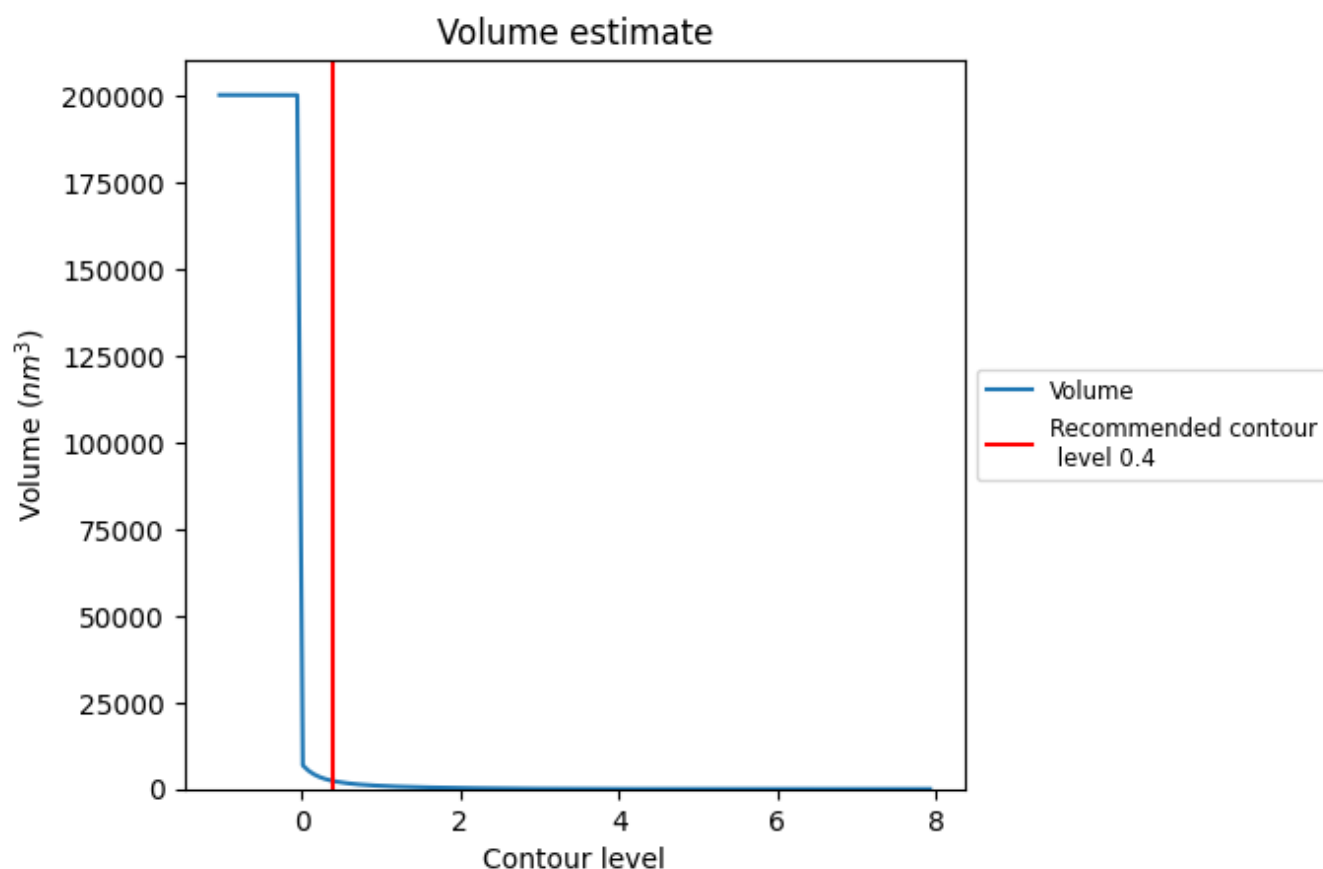
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

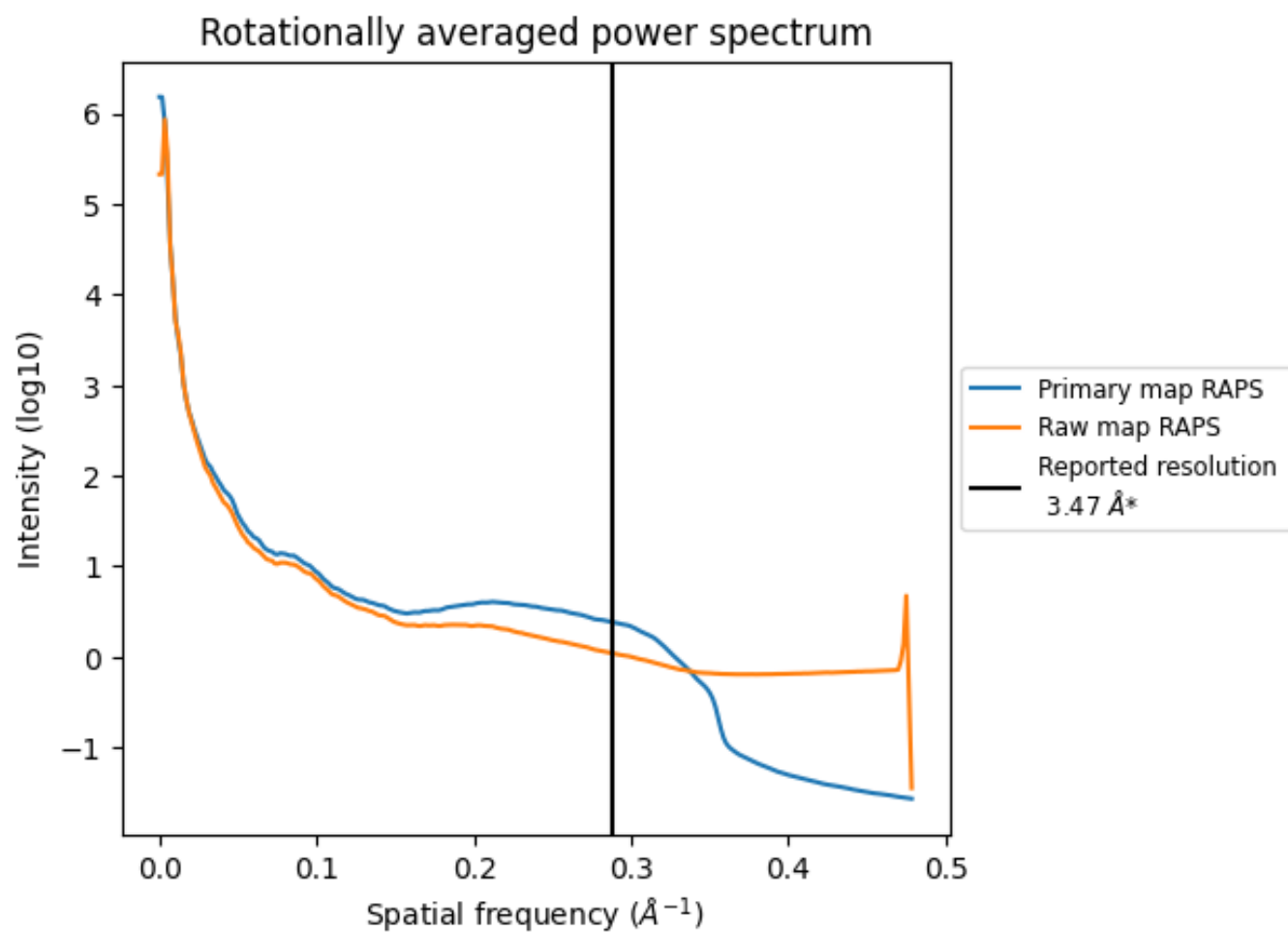
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2315 nm³; this corresponds to an approximate mass of 2091 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 ⓘ

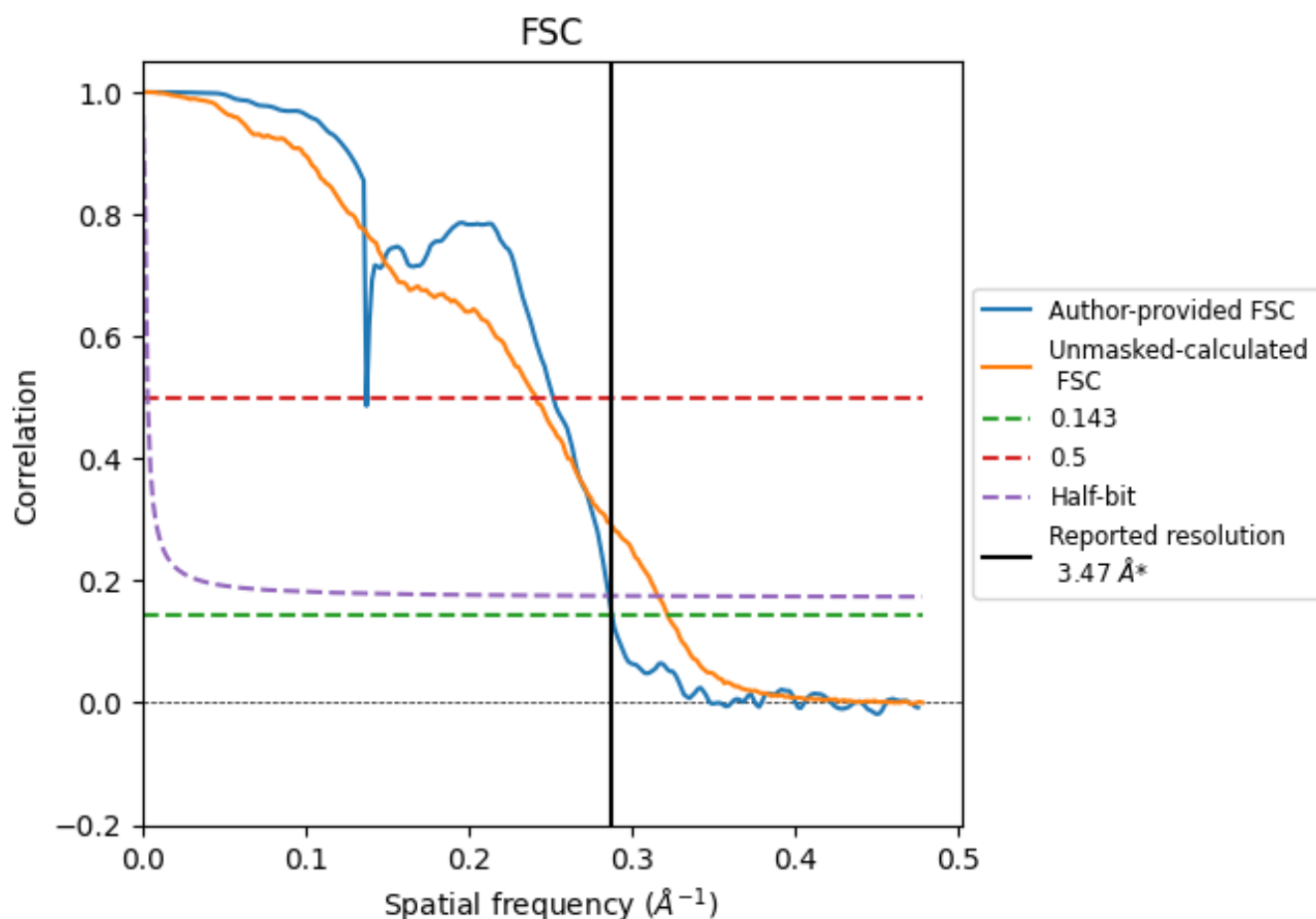


*Reported resolution corresponds to spatial frequency of 0.288 Å⁻¹

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 0.288 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

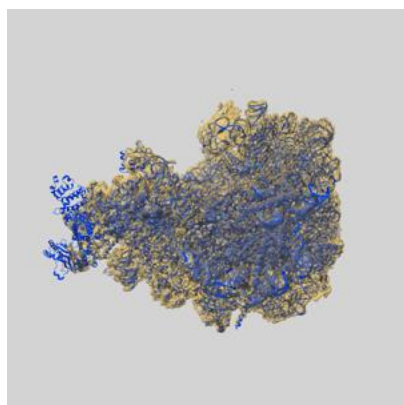
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.47	-	-
Author-provided FSC curve	3.47	7.27	3.49
Unmasked-calculated*	3.10	4.14	3.16

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.10 differs from the reported value 3.47 by more than 10 %

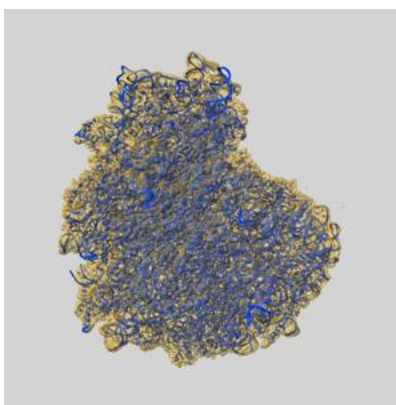
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14861 and PDB model 7ZPQ. Per-residue inclusion information can be found in section 3 on page 21.

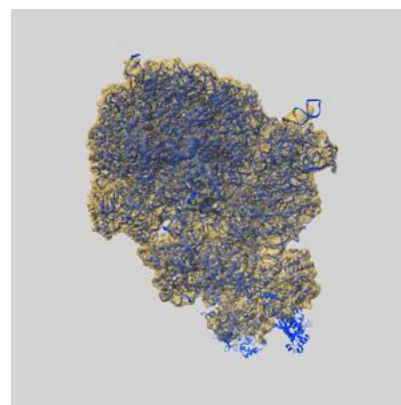
9.1 Map-model overlay [i](#)



X



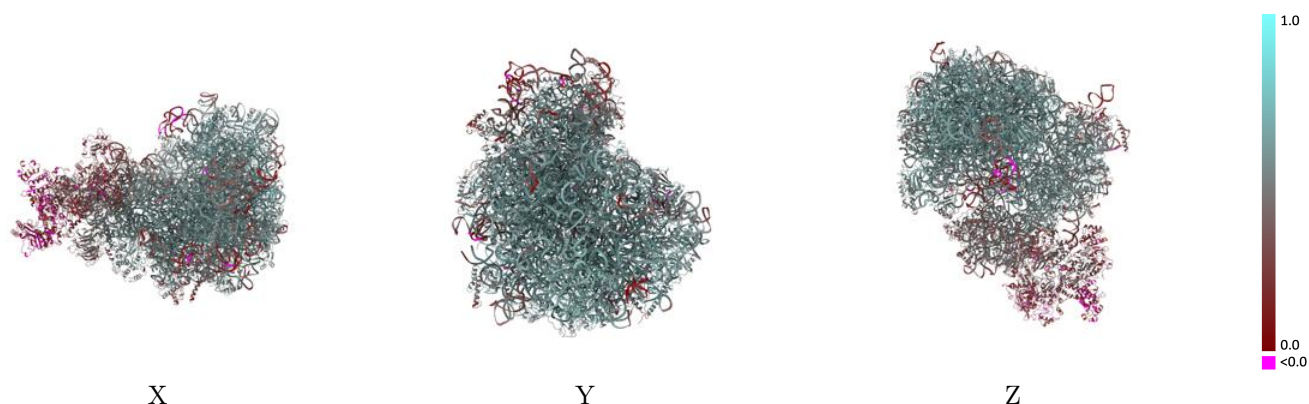
Y



Z

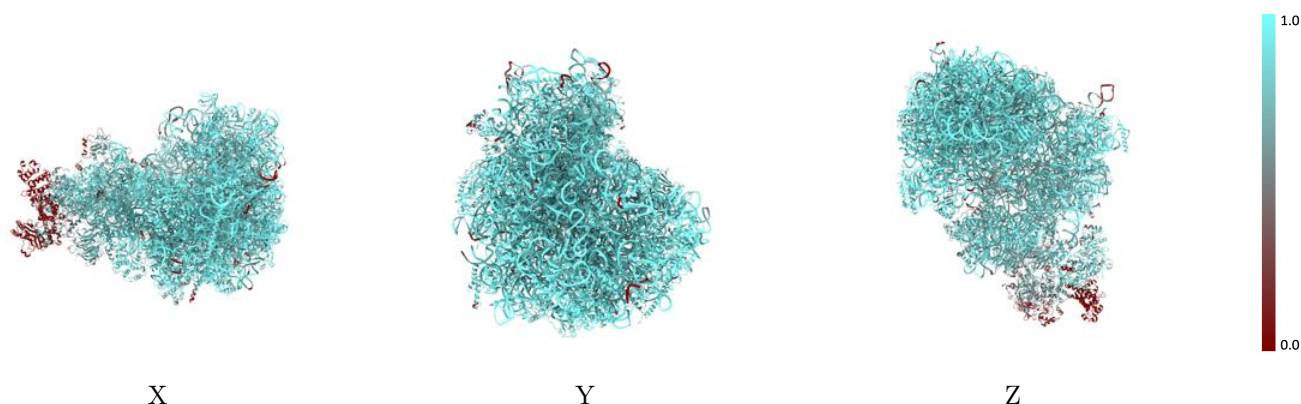
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



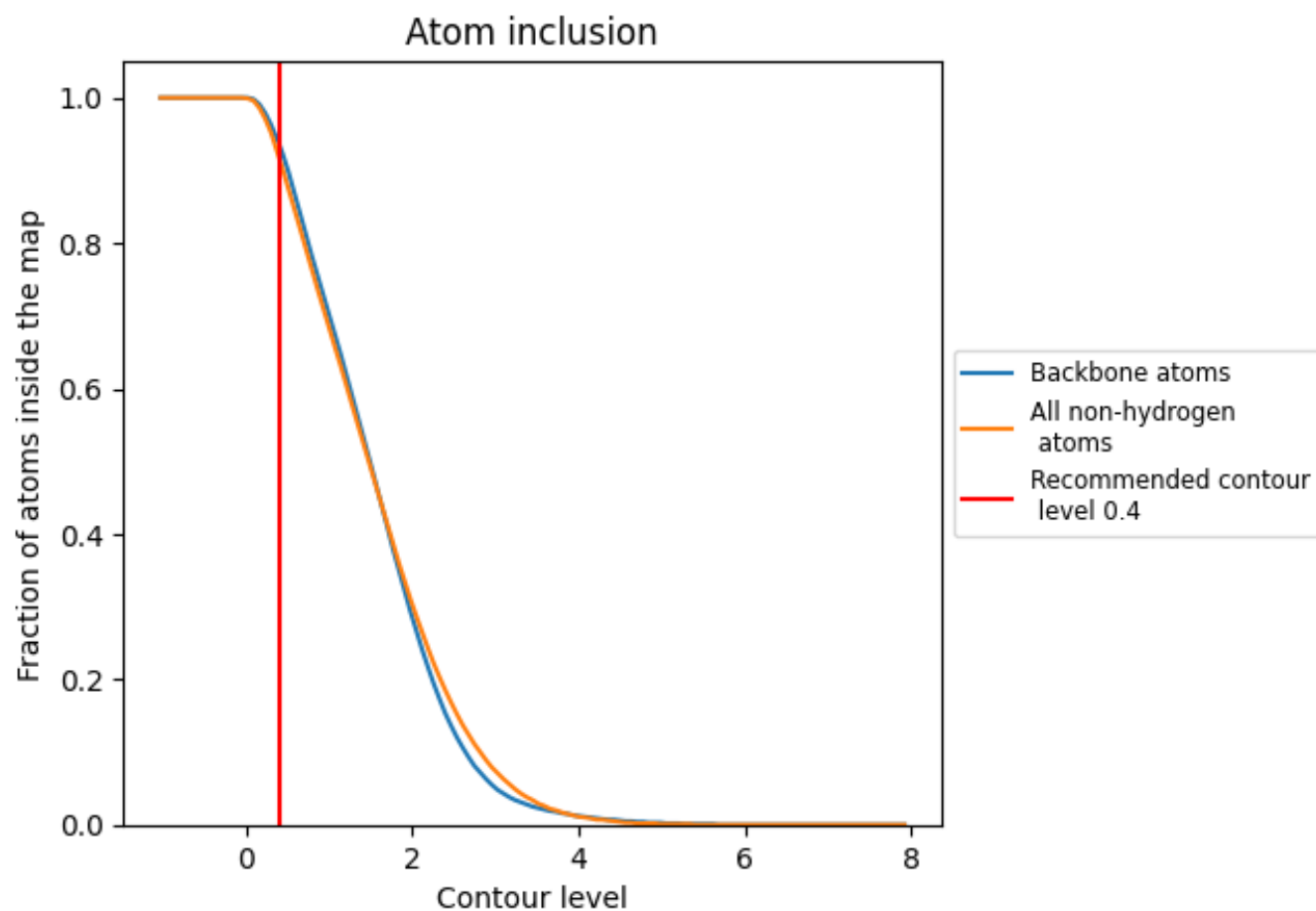
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 92% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9160	 0.5220
2	 0.9550	 0.5070
3	 0.9840	 0.6030
4	 0.9940	 0.5830
5	 0.9730	 0.5810
6	 0.7800	 0.3420
AA	 0.9560	 0.5340
AB	 0.9370	 0.5280
AC	 0.9800	 0.5800
AD	 0.9130	 0.4710
AE	 0.9690	 0.5590
AF	 0.8620	 0.4420
AG	 0.8810	 0.4570
AH	 0.8740	 0.4690
AI	 0.9620	 0.5670
AJ	 0.9360	 0.5350
AK	 0.8360	 0.3770
AL	 0.9500	 0.5850
AM	 0.4240	 0.2170
AN	 0.9510	 0.5690
AO	 0.9750	 0.5550
AP	 0.8030	 0.3460
AQ	 0.8910	 0.4500
AR	 0.9090	 0.4860
AS	 0.8430	 0.3680
AT	 0.8540	 0.3900
AU	 0.8400	 0.4140
AV	 0.9510	 0.5510
AW	 0.9900	 0.6070
AX	 0.9610	 0.5750
AY	 0.9120	 0.4900
AZ	 0.7100	 0.3240
Aa	 0.9530	 0.5480
Ab	 0.9470	 0.5290
Ac	 0.8880	 0.4940



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Chain	Atom inclusion	Q-score
Ad	 0.9600	 0.5120
Ae	 0.9030	 0.5010
Af	 0.5810	 0.2000
Ag	 0.7310	 0.3670
BA	 0.9880	 0.6380
BB	 0.9770	 0.6060
BC	 0.9770	 0.6100
BD	 0.9310	 0.5350
BE	 0.9480	 0.5500
BF	 0.9770	 0.6100
BG	 0.9370	 0.5430
BH	 0.9520	 0.5660
BI	 0.9600	 0.5730
BJ	 0.9170	 0.4780
BK	 0.9600	 0.5890
BL	 0.9700	 0.5780
BM	 0.9960	 0.6420
BN	 0.9820	 0.6130
BO	 0.9580	 0.6080
BP	 0.9890	 0.6210
BQ	 0.9270	 0.5640
BR	 0.9830	 0.6130
BS	 0.9700	 0.5930
BT	 0.9270	 0.5100
BU	 0.9630	 0.6130
BV	 0.9340	 0.5150
BW	 0.9650	 0.5820
BX	 0.9780	 0.5910
BY	 0.9400	 0.5550
BZ	 0.9780	 0.6210
Ba	 0.9450	 0.5620
Bb	 0.9810	 0.5840
Bc	 0.9340	 0.5730
Bd	 0.9860	 0.6270
Be	 0.9930	 0.6410
Bf	 0.9610	 0.5970
Bg	 0.9640	 0.5820
Bh	 0.9600	 0.5670
Bi	 0.9940	 0.6460
Bj	 0.9130	 0.5180
Bk	 0.9880	 0.6270
Bl	 0.9480	 0.5850

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Chain	Atom inclusion	Q-score
Bm	 0.9950	 0.6340
Bn	 0.9720	 0.5940
Bo	 0.9840	 0.6190
CA	 0.6130	 0.2420
CB	 0.0080	 0.1040
CC	 0.3930	 0.1640