



Full wwPDB EM Validation Report ⓘ

Mar 28, 2026 – 02:03 AM UTC

PDB ID : 6TB3 / pdb_00006tb3
EMDB ID : EMD-10431
Title : yeast 80S ribosome in complex with the Not5 subunit of the CCR4-NOT complex
Authors : Buschauer, R.; Cheng, J.; Berninghausen, O.; Tesina, P.; Becker, T.; Beckmann, R.
Deposited on : 2019-10-31
Resolution : 2.80 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

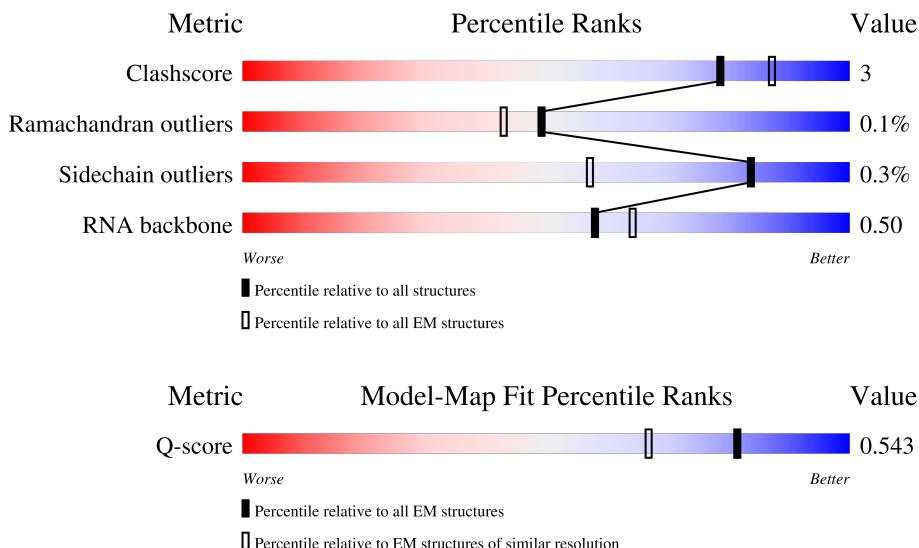
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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	11806 (2.30 - 3.30)

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	1	3	
3	P	206	

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Mol	Chain	Length	Quality of chain
4	Q	232	
5	E	117	
6	R	216	
7	A	222	
8	S	258	
9	B	206	
10	T	228	
11	U	184	
12	V	187	
13	W	184	
14	C	92	
15	X	142	
16	D	121	
17	Y	150	
18	Z	127	
19	F	141	
20	G	125	
21	H	145	
22	I	143	
23	J	100	
24	n	75	
25	a	87	
26	b	129	
27	c	144	
28	d	134	

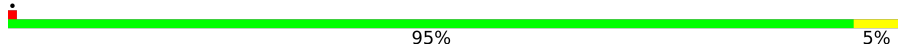
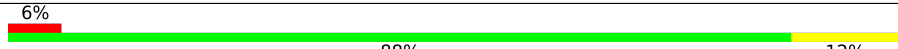
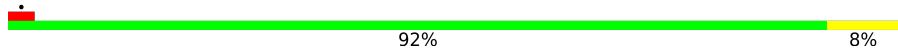
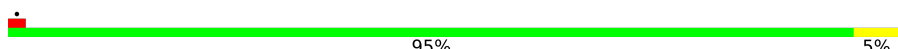
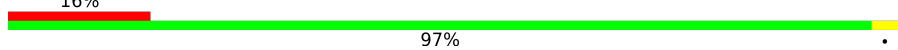
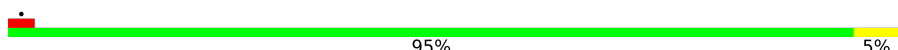
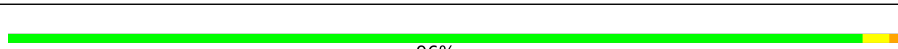
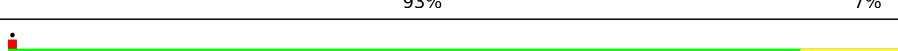
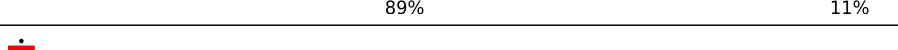
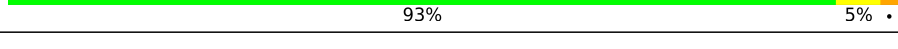
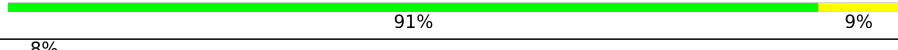
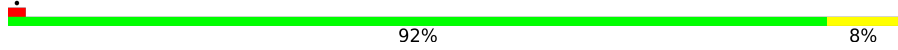
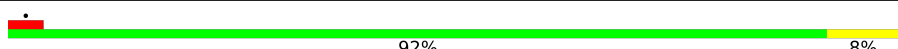
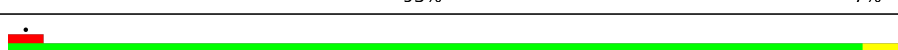
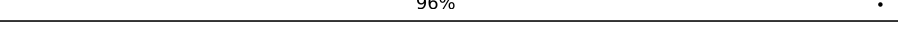
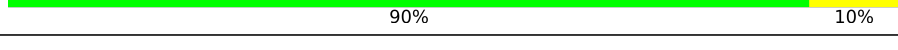
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Mol	Chain	Length	Quality of chain
29	K	82	
30	e	97	
31	f	81	
32	M	53	
33	g	60	
34	N	73	
35	O	312	
36	L	63	
37	BQ	3223	
38	BT	204	
39	BR	121	
40	BS	158	
41	AW	251	
42	BA	386	
43	BE	361	
44	BI	294	
45	BM	175	
46	BO	222	
47	AA	233	
48	AD	191	
49	BD	218	
50	AG	169	
51	AJ	193	
52	AM	136	
53	AQ	203	

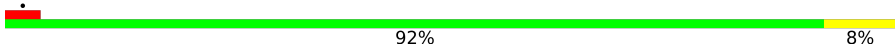
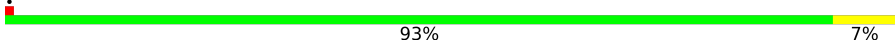
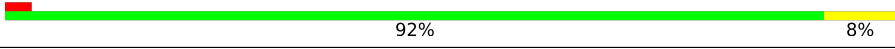
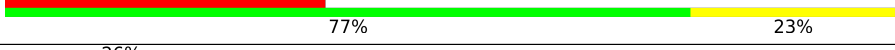
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Mol	Chain	Length	Quality of chain
54	AU	197	
55	AX	183	
56	BB	185	
57	BF	188	
58	BH	171	
59	BJ	159	
60	BL	100	
61	AB	136	
62	AE	126	
63	AH	121	
64	AK	125	
65	AN	135	
66	AR	148	
67	AV	58	
68	AY	96	
69	BC	109	
70	BG	127	
71	BK	106	
72	BN	112	
73	BP	119	
74	AC	99	
75	AF	81	
76	AI	77	
77	AL	50	
78	AO	52	

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Mol	Chain	Length	Quality of chain
79	AS	25	 92%8%
80	AP	103	 93%7%
81	AT	91	 92%8%
82	BV	22	 36%77%23%
83	BW	112	 26%82%16%

2 Entry composition [i](#)

There are 86 unique types of molecules in this entry. The entry contains 205032 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 *Saccharomyces cerevisiae* S288C 18S ribosomal RNA (RDN18-1), rRNA.

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 mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	3	Total	C	N	O	P	0	0
			65	29	12	21	3		

- Molecule 3 is a protein called 40S ribosomal protein S0-A.

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

- Molecule 4 is a protein called 40S ribosomal protein S1-A.

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

- Molecule 5 is a protein called 40S ribosomal protein S15.

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

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

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

- Molecule 7 is a protein called 40S ribosomal protein S3.

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

- Molecule 8 is a protein called 40S ribosomal protein S4-A.

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

- Molecule 9 is a protein called 40S ribosomal protein S5.

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

- Molecule 10 is a protein called 40S ribosomal protein S6-A.

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

- Molecule 11 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	U	184	Total	C	N	O	S	0	0
			1473	946	263	264			

- Molecule 12 is a protein called 40S ribosomal protein S8.

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

- Molecule 13 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 14 is a protein called 40S ribosomal protein S10-A.

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

- Molecule 15 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	X	142	Total	C	N	O	S	0	0
			1142	733	217	189	3		

- Molecule 16 is a protein called 40S ribosomal protein S12.

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

- Molecule 17 is a protein called 40S ribosomal protein S13.

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

- Molecule 18 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Z	127	Total	C	N	O	S	0	0
			923	568	185	167	3		

- Molecule 19 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	F	141	Total	C	N	O	0	0
			1105	708	203	194		

- Molecule 20 is a protein called 40S ribosomal protein S17-B.

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

- Molecule 21 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	H	145	Total	C	N	O	S	0	0
			1188	741	237	208	2		

- Molecule 22 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 23 is a protein called 40S ribosomal protein S20.

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

- Molecule 24 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	n	75	Total	C	N	O	P	0	0
			1624	728	298	523	75		

- Molecule 25 is a protein called 40S ribosomal protein S21-A.

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

- Molecule 26 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 27 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 28 is a protein called 40S ribosomal protein S24-A.

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

- Molecule 29 is a protein called 40S ribosomal protein S25-A.

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

- Molecule 30 is a protein called 40S ribosomal protein S26-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	97	Total	C	N	O	S	0	0
			765	473	160	127	5		

- Molecule 31 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 32 is a protein called 40S ribosomal protein S29-A.

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

- Molecule 33 is a protein called 40S ribosomal protein S30-A.

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

- Molecule 34 is a protein called Ubiquitin-40S ribosomal protein S31.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	97	ALA	LYS	conflict	UNP P05759

- Molecule 35 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

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

- Molecule 36 is a protein called 40S ribosomal protein S28-A.

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

- Molecule 37 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BQ	3223	Total	C	N	O	P	0	0
			68931	30790	12416	22502	3223		

- Molecule 38 is a protein called 60S ribosomal protein L1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BT	204	Total	C	N	O	S	0	0
			1609	1031	279	290	9		

- Molecule 39 is a RNA chain called 5S rRNA.

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

- Molecule 40 is a RNA chain called 5.8S rRNA.

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

- Molecule 41 is a protein called 60S ribosomal protein L2-A.

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

- Molecule 42 is a protein called 60S ribosomal protein L3.

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

- Molecule 43 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 44 is a protein called 60S ribosomal protein L5.

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

- Molecule 45 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	BM	167	Total	C	N	O	0	0
			1307	843	234	230		

- Molecule 46 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 47 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 48 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 49 is a protein called 60S ribosomal protein L10.

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

- Molecule 50 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	AG	169	Total	C	N	O	S	0	0
			1346	843	252	247	4		

- Molecule 51 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 52 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 53 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 54 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 55 is a protein called 60S ribosomal protein L17-A.

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

- Molecule 56 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 57 is a protein called 60S ribosomal protein L19-A.

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

- Molecule 58 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 59 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	BJ	159	Total	C	N	O	S	0	0
			1272	802	245	221	4		

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

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

- Molecule 61 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 62 is a protein called 60S ribosomal protein L24-A.

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

- Molecule 63 is a protein called 60S ribosomal protein L25.

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

- Molecule 64 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 65 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AN	135	Total	C	N	O		0	0
			1080	701	199	180			

- Molecule 66 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AR	148	Total	C	N	O	S	0	0
			1169	747	231	188	3		

- Molecule 67 is a protein called 60S ribosomal protein L29.

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

- Molecule 68 is a protein called 60S ribosomal protein L30.

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

- Molecule 69 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 70 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	BG	127	Total	C	N	O	S	0	0
			1013	642	205	165	1		

- Molecule 71 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 72 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 73 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 74 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 75 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	AF	81	Total	C	N	O	S	0	0
			645	393	141	106	5		

- Molecule 76 is a protein called 60S ribosomal protein L38.

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

- Molecule 77 is a protein called 60S ribosomal protein L39.

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

- Molecule 78 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	AO	52	Total	C	N	O	S	0	0
			410	254	86	65	5		

- Molecule 79 is a protein called 60S ribosomal protein L41-B.

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

- Molecule 80 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 81 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 82 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	BV	22	Total	C	N	O	S	0	0
			207	127	56	23	1		

- Molecule 83 is a protein called General negative regulator of transcription subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	BW	112	Total	C	N	O	S	0	0
			940	585	170	182	3		

- Molecule 84 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
84	2	89	Total	Mg	0
			89	89	
84	S	1	Total	Mg	0
			1	1	
84	B	1	Total	Mg	0
			1	1	
84	n	3	Total	Mg	0
			3	3	
84	BQ	220	Total	Mg	0
			220	220	
84	BR	1	Total	Mg	0
			1	1	
84	AW	2	Total	Mg	0
			2	2	
84	BA	3	Total	Mg	0
			3	3	
84	BO	1	Total	Mg	0
			1	1	
84	AQ	1	Total	Mg	0
			1	1	
84	AX	1	Total	Mg	0
			1	1	
84	BF	1	Total	Mg	0
			1	1	
84	AB	1	Total	Mg	0
			1	1	
84	BG	1	Total	Mg	0
			1	1	
84	BN	1	Total	Mg	0
			1	1	

- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn).

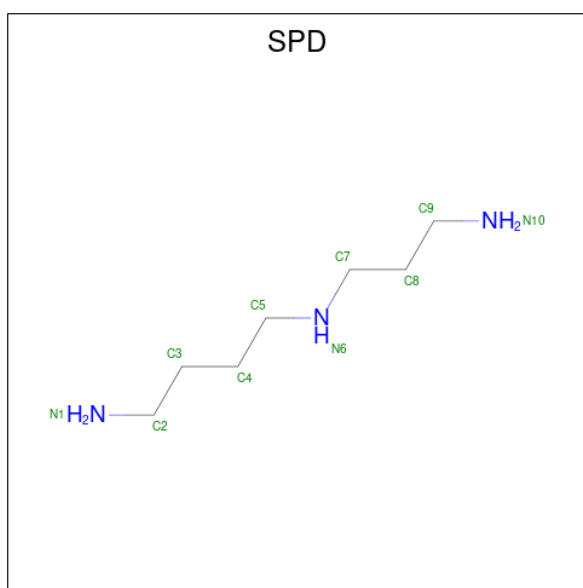
Mol	Chain	Residues	Atoms		AltConf
85	M	1	Total	Zn	0
			1	1	
85	N	1	Total	Zn	0
			1	1	

Continued on next page...

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Mol	Chain	Residues	Atoms		AltConf
85	BN	1	Total	Zn	0
			1	1	
85	AF	1	Total	Zn	0
			1	1	
85	AO	1	Total	Zn	0
			1	1	
85	AP	1	Total	Zn	0
			1	1	
85	AT	1	Total	Zn	0
			1	1	

- Molecule 86 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$).

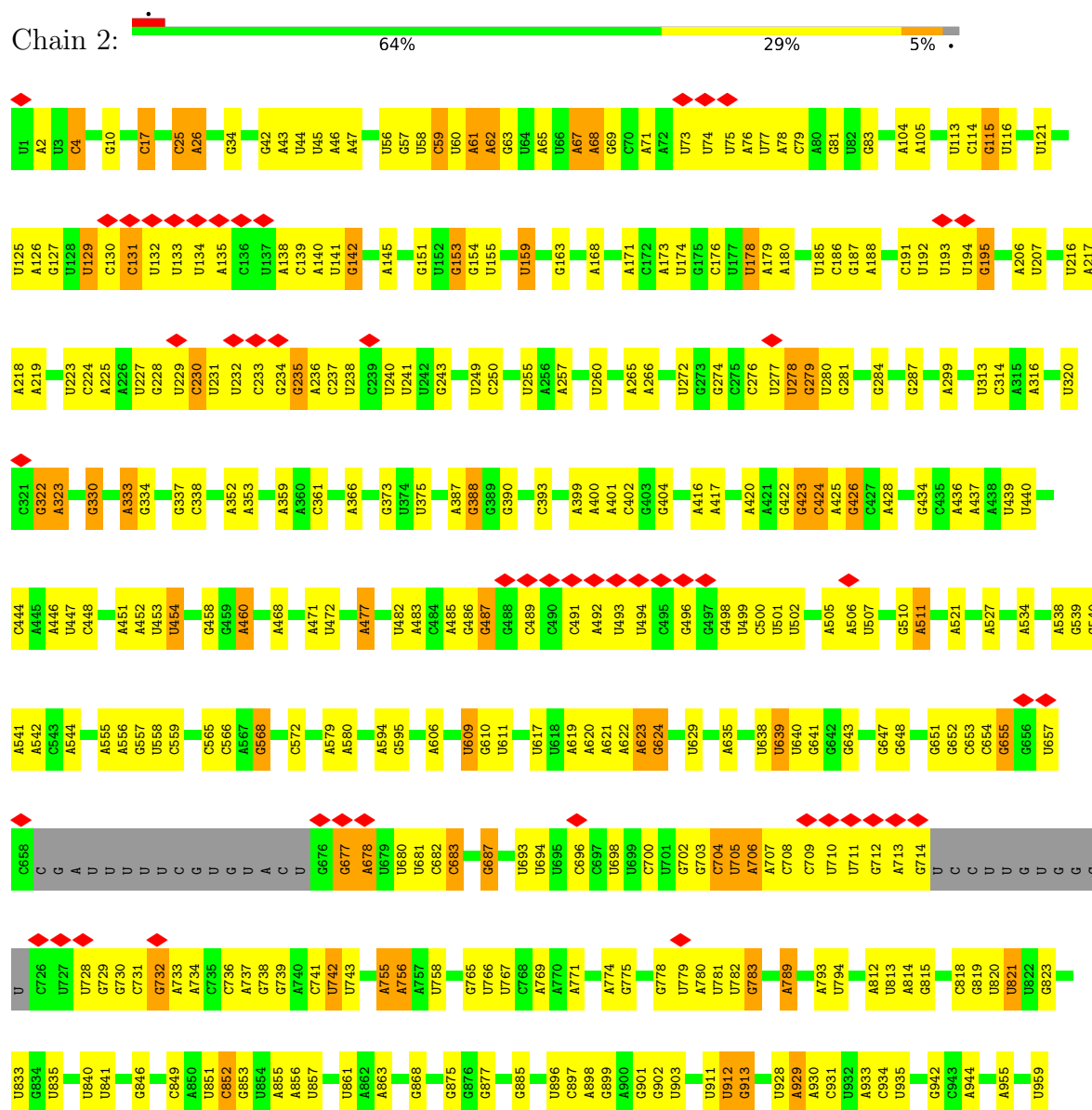


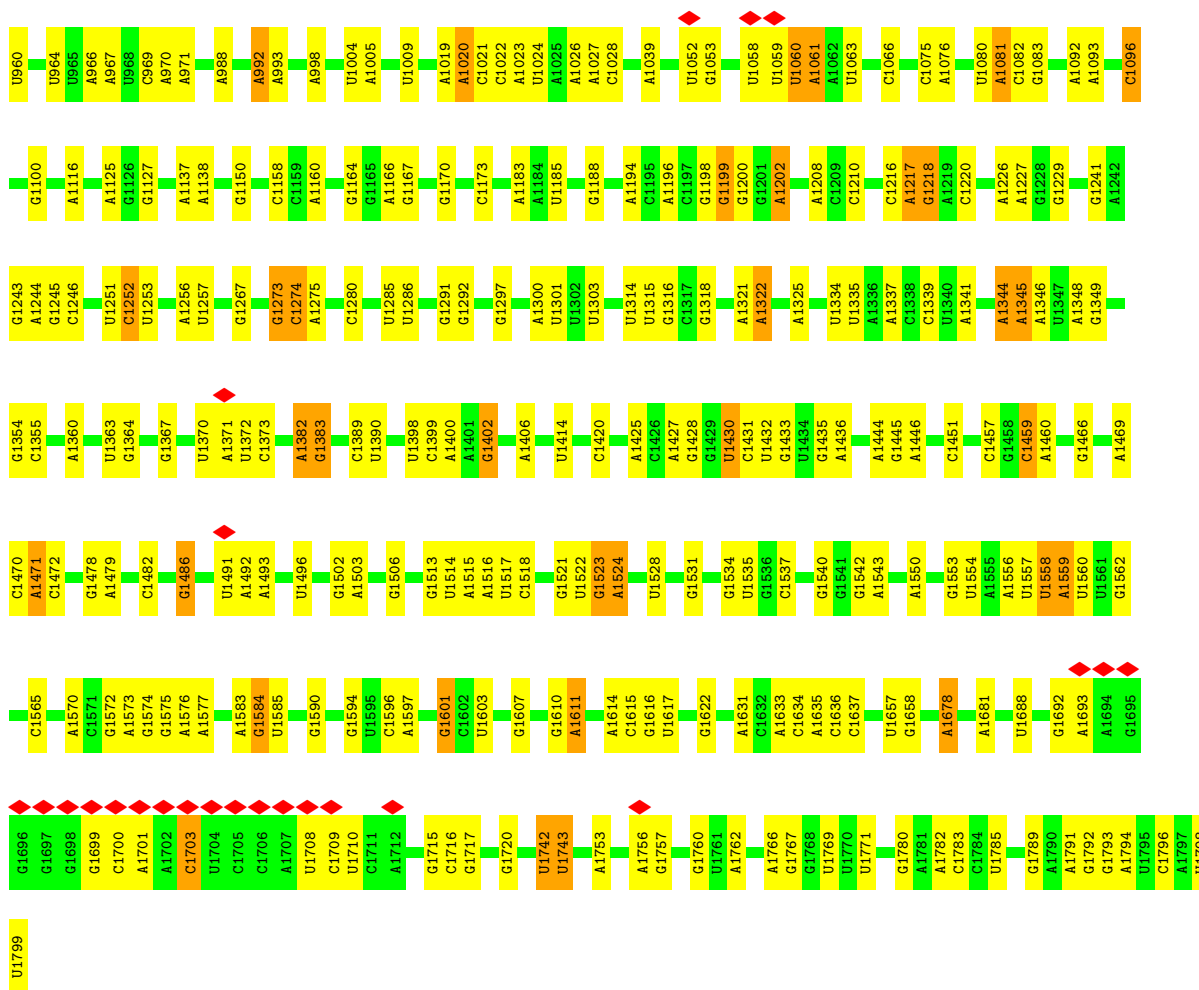
Mol	Chain	Residues	Atoms			AltConf
86	BQ	1	Total	C	N	0
			10	7	3	

3 Residue-property plots

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

- Molecule 1: *Saccharomyces cerevisiae* S288C 18S ribosomal RNA (RDN18-1), rRNA





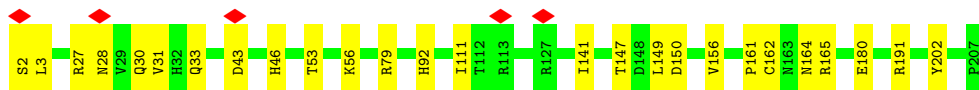
- Molecule 2: mRNA

Chain I: 100%

There are no outlier residues recorded for this chain.

- Molecule 3: 40S ribosomal protein S0-A

Chain P: 87% 13%

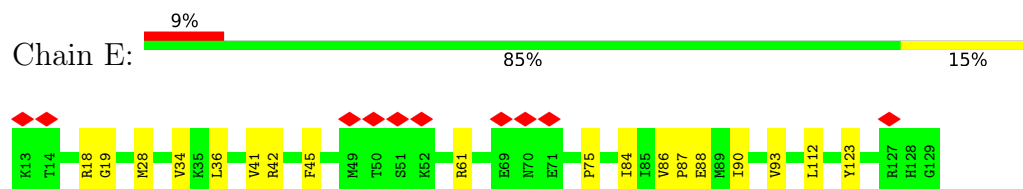


- Molecule 4: 40S ribosomal protein S1-A

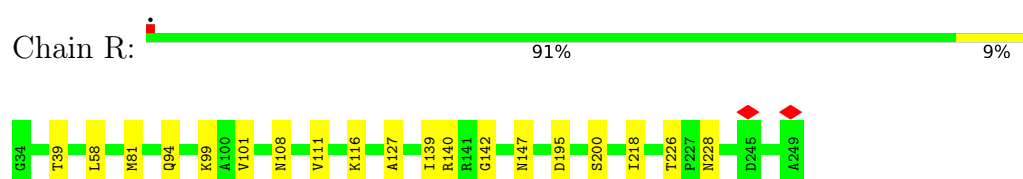
Chain Q: 5% 88% 9%



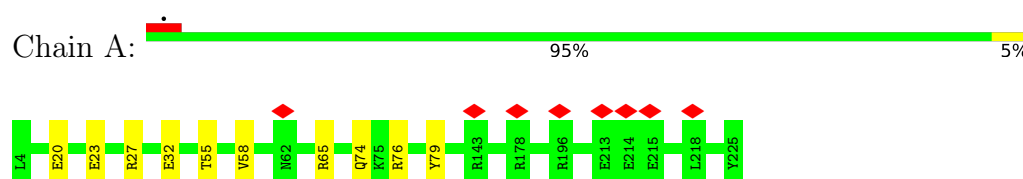
- Molecule 5: 40S ribosomal protein S15



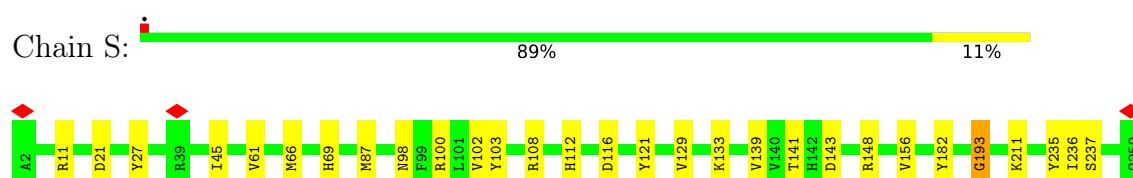
- Molecule 6: 40S ribosomal protein S2



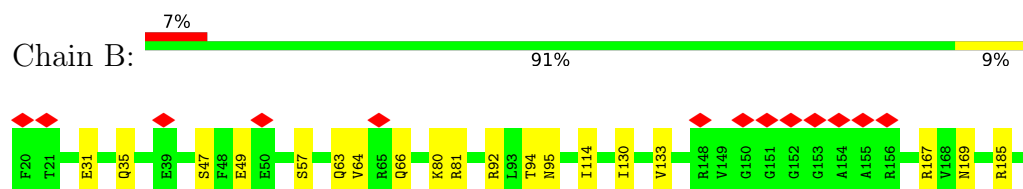
- Molecule 7: 40S ribosomal protein S3



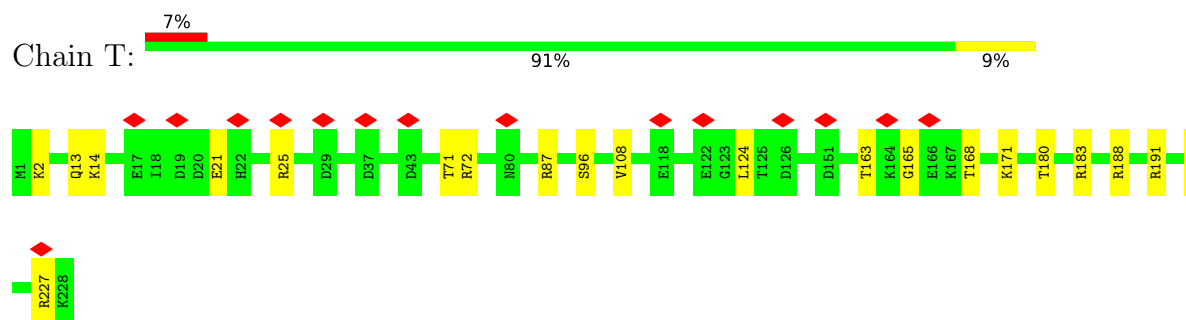
- Molecule 8: 40S ribosomal protein S4-A



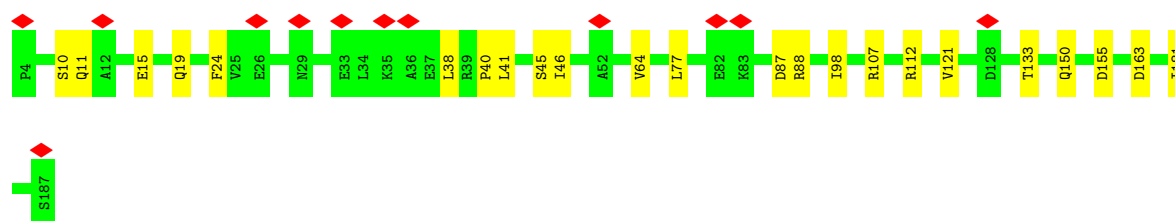
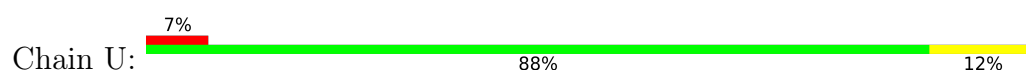
- Molecule 9: 40S ribosomal protein S5



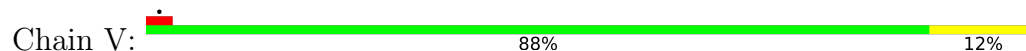
- Molecule 10: 40S ribosomal protein S6-A



- Molecule 11: 40S ribosomal protein S7-A



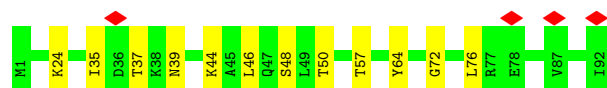
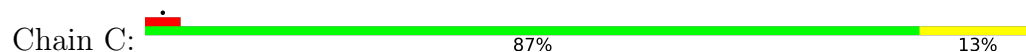
- Molecule 12: 40S ribosomal protein S8



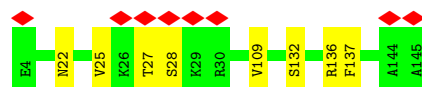
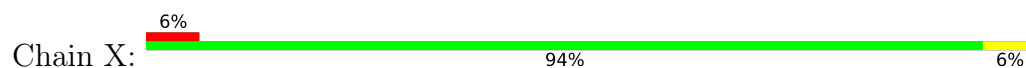
- Molecule 13: 40S ribosomal protein S9-A



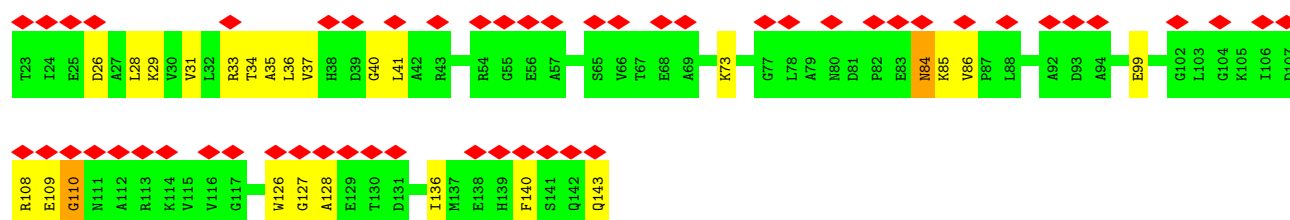
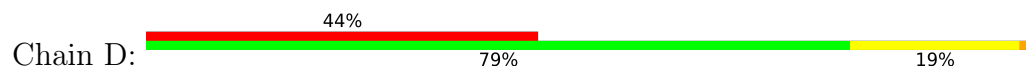
- Molecule 14: 40S ribosomal protein S10-A



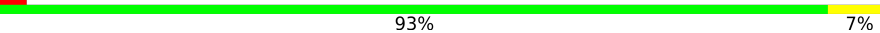
- Molecule 15: 40S ribosomal protein S11-A

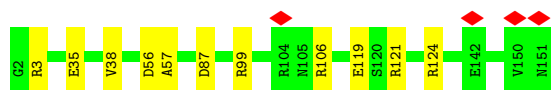


- Molecule 16: 40S ribosomal protein S12



- Molecule 17: 40S ribosomal protein S13

Chain Y:  93% 7%



- Molecule 18: 40S ribosomal protein S14-B

Chain Z:  88% 12%

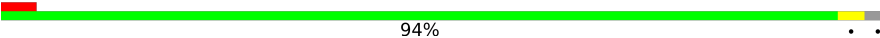


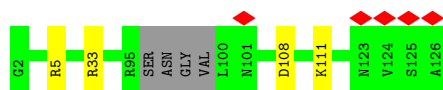
- Molecule 19: 40S ribosomal protein S16-A

Chain F:  91% 9%



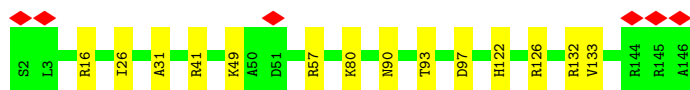
- Molecule 20: 40S ribosomal protein S17-B

Chain G:  94% 6%



- Molecule 21: 40S ribosomal protein S18-A

Chain H:  90% 10%

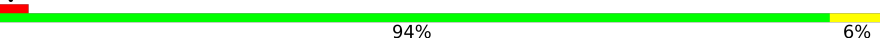


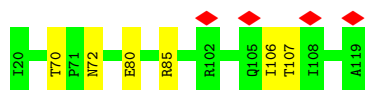
- Molecule 22: 40S ribosomal protein S19-A

Chain I:  85% 15%

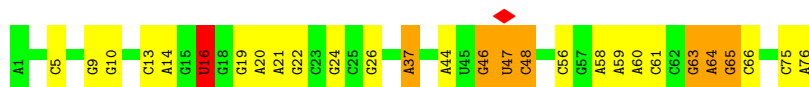


- Molecule 23: 40S ribosomal protein S20

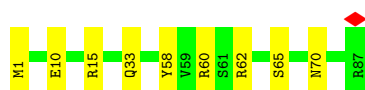
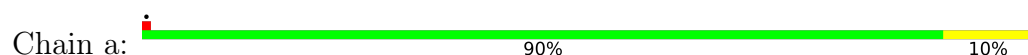
Chain J:  94% 6%



- Molecule 24: tRNA



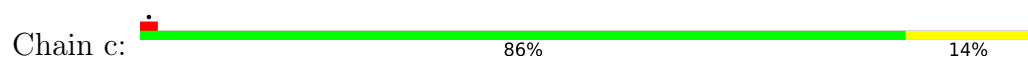
- Molecule 25: 40S ribosomal protein S21-A



- Molecule 26: 40S ribosomal protein S22-A



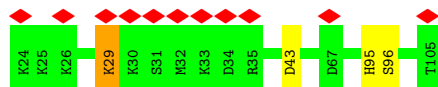
- Molecule 27: 40S ribosomal protein S23-A



- Molecule 28: 40S ribosomal protein S24-A



- Molecule 29: 40S ribosomal protein S25-A



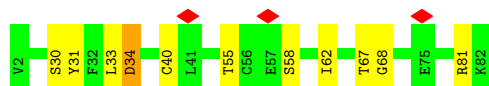
- Molecule 30: 40S ribosomal protein S26-B

Chain e:  90% 10%



- Molecule 31: 40S ribosomal protein S27-A

Chain f:  86% 12%



- Molecule 32: 40S ribosomal protein S29-A

Chain M:  89% 11%



- Molecule 33: 40S ribosomal protein S30-A

Chain g:  22% 93% 7%



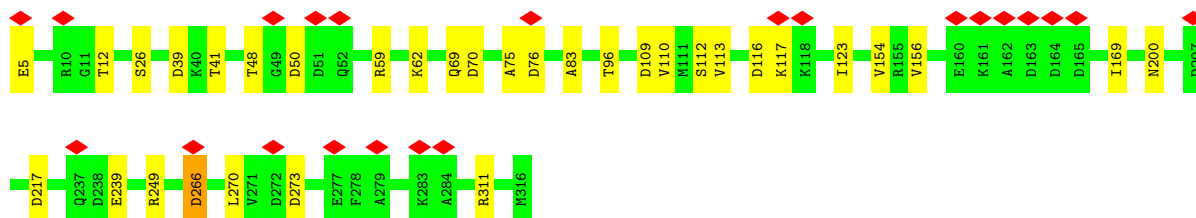
- Molecule 34: Ubiquitin-40S ribosomal protein S31

Chain N:  40% 82% 16%



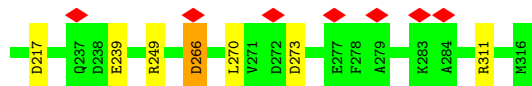
- Molecule 35: Guanine nucleotide-binding protein subunit beta-like protein

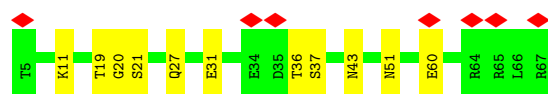
Chain O:  7% 89% 10%



- Molecule 36: 40S ribosomal protein S28-A

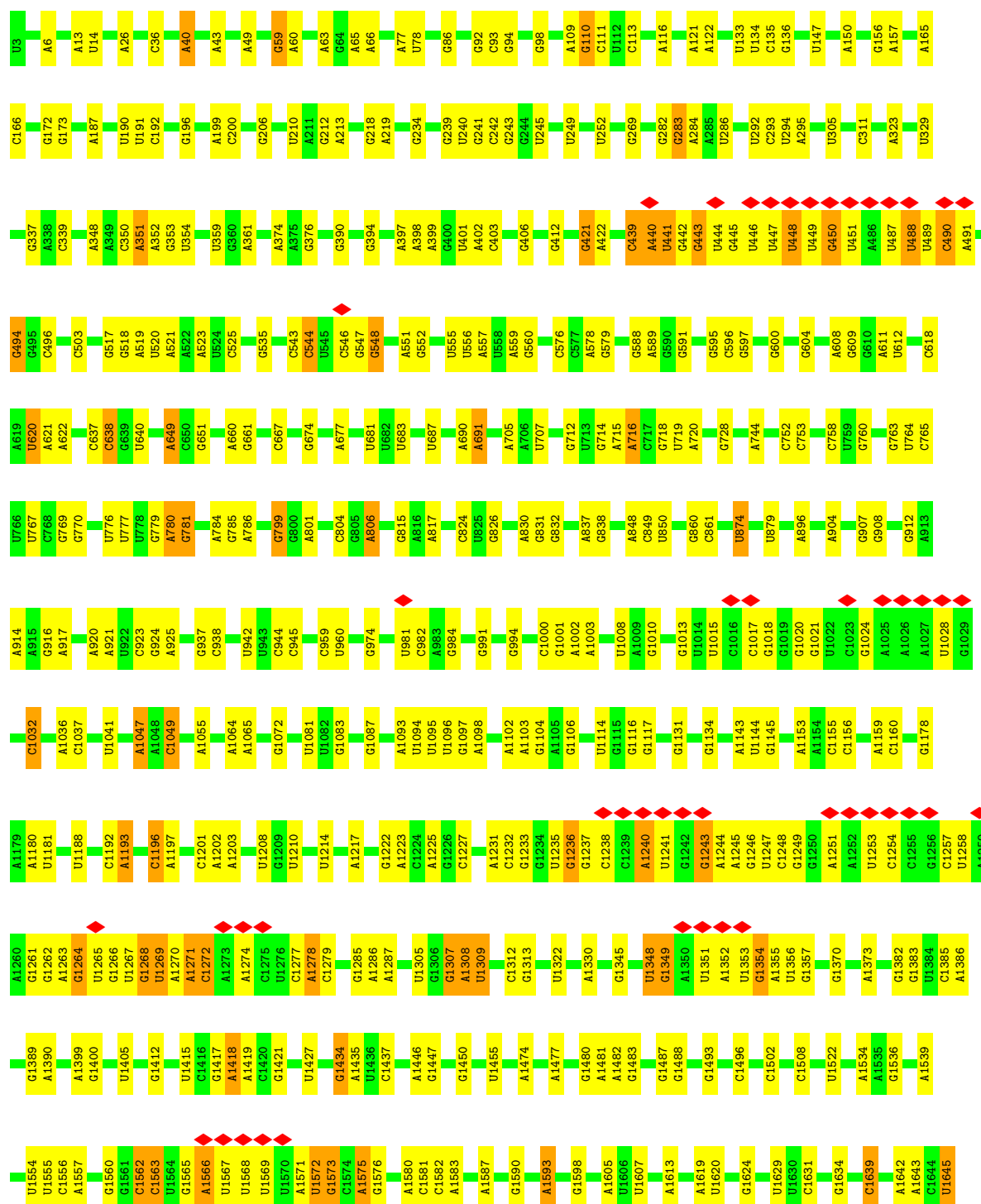
Chain L:  11% 83% 17%

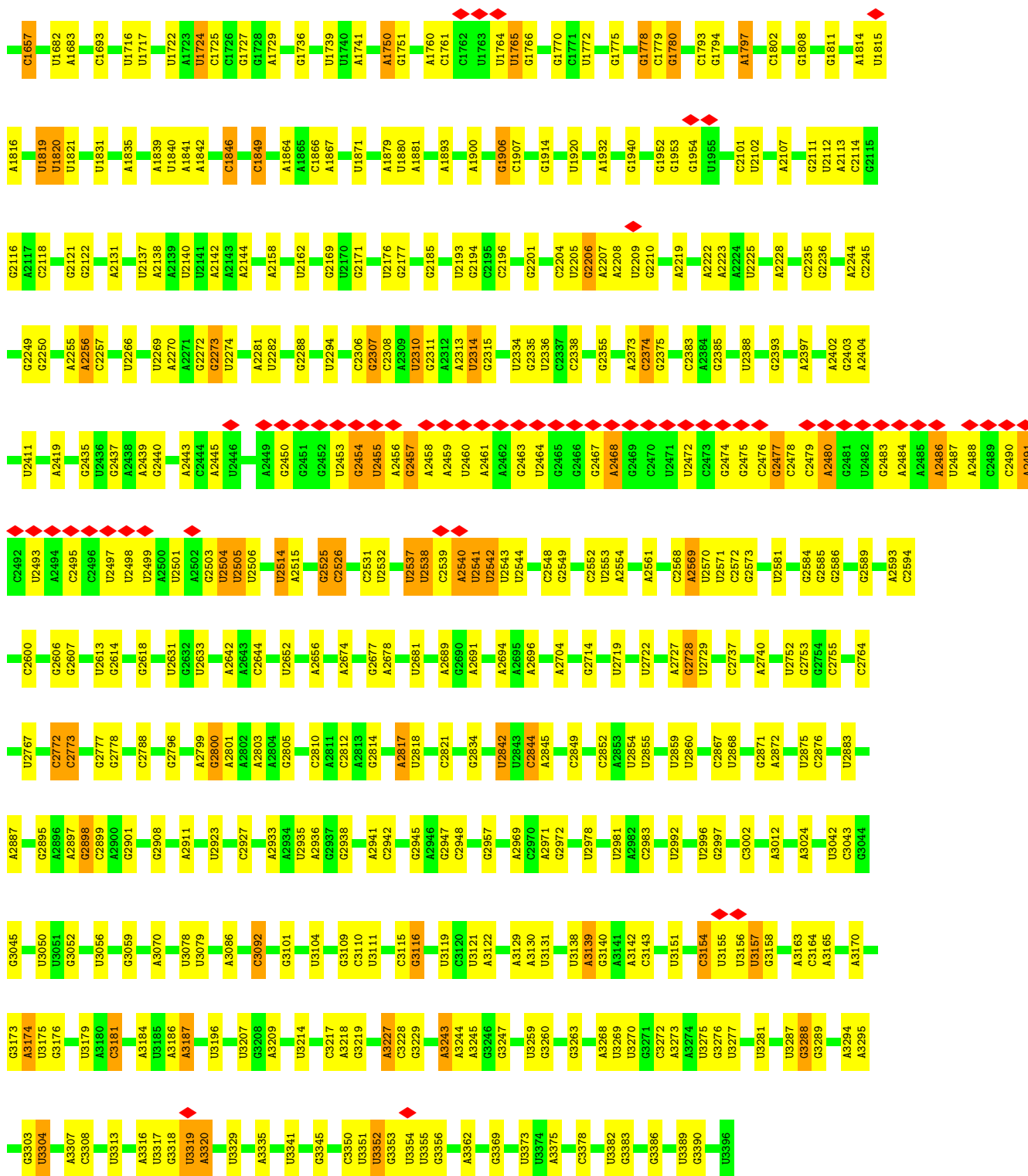




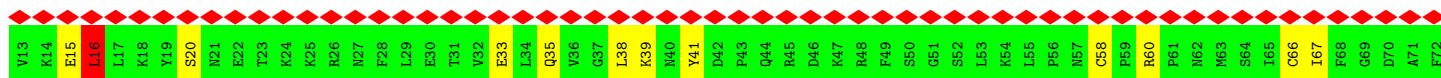
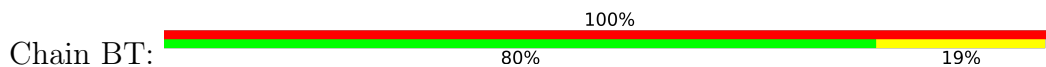
• Molecule 37: 25S rRNA

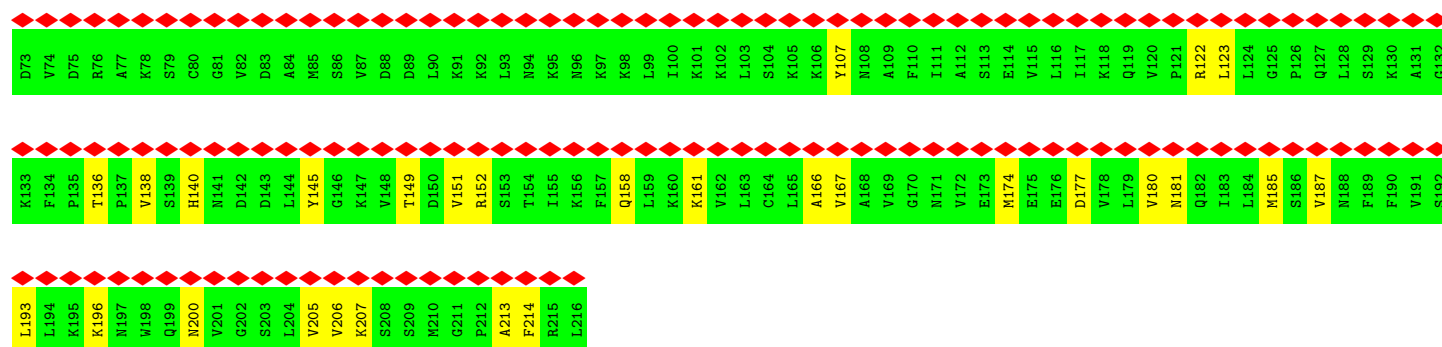
Chain BQ: 72% 24%



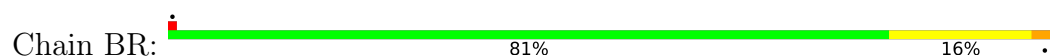


• Molecule 38: 60S ribosomal protein L1-A

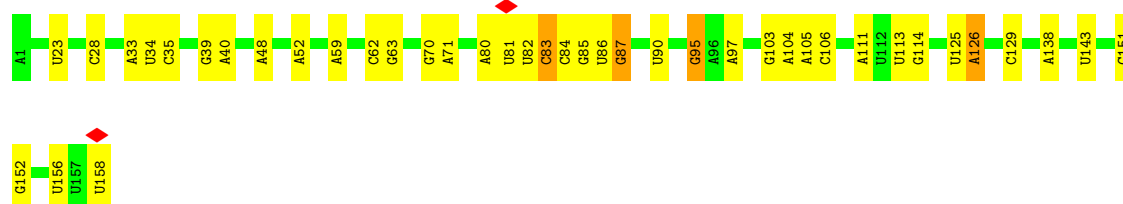
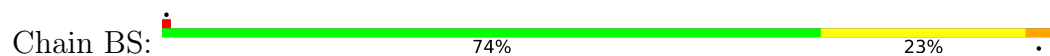




• Molecule 39: 5S rRNA



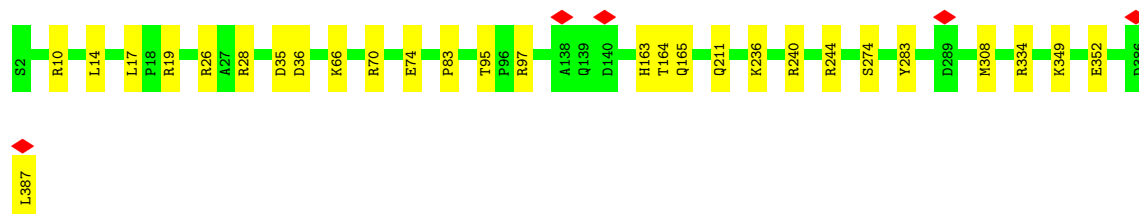
• Molecule 40: 5.8S rRNA



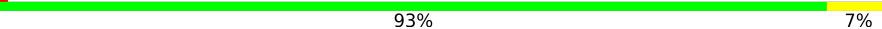
• Molecule 41: 60S ribosomal protein L2-A



• Molecule 42: 60S ribosomal protein L3



• Molecule 43: 60S ribosomal protein L4-A

Chain BE:  93% 7%



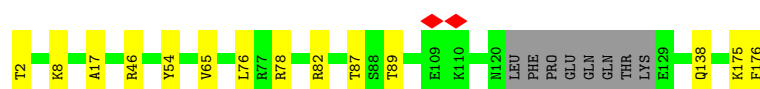
- Molecule 44: 60S ribosomal protein L5

Chain BI:  93% 7%

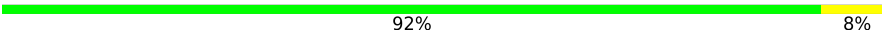


- Molecule 45: 60S ribosomal protein L6-B

Chain BM:  87% 8% 5%

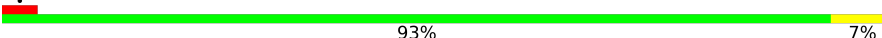


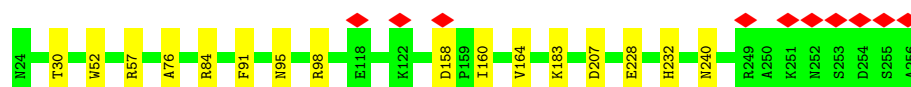
- Molecule 46: 60S ribosomal protein L7-A

Chain BO:  92% 8%

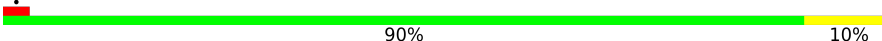


- Molecule 47: 60S ribosomal protein L8-A

Chain AA:  93% 7%



- Molecule 48: 60S ribosomal protein L9-A

Chain AD:  90% 10%



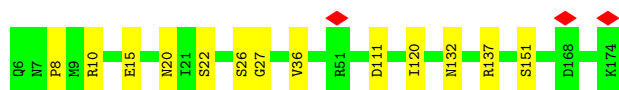
- Molecule 49: 60S ribosomal protein L10

Chain BD:  91% 9%



- Molecule 50: 60S ribosomal protein L11-B

Chain AG:  92% 8%



- Molecule 51: 60S ribosomal protein L13-A

Chain AJ:  93% 7%

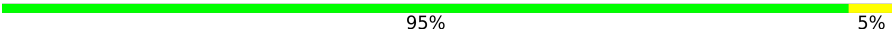


- Molecule 52: 60S ribosomal protein L14-A

Chain AM:  85% 14%

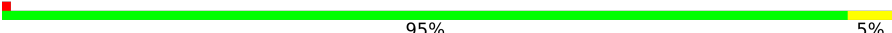


- Molecule 53: 60S ribosomal protein L15-A

Chain AQ:  95% 5%



- Molecule 54: 60S ribosomal protein L16-A

Chain AU:  95% 5%



- Molecule 55: 60S ribosomal protein L17-A

Chain AX:  5% 96%

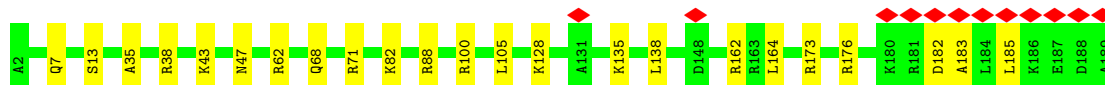
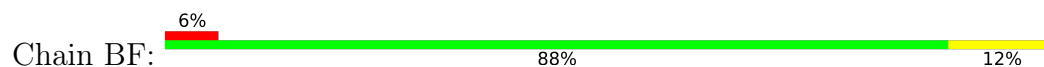


- Molecule 56: 60S ribosomal protein L18-A

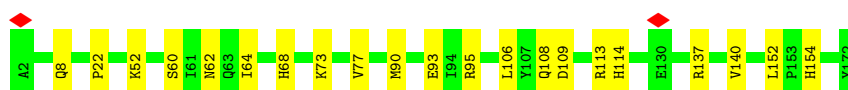
Chain BB:  91% 9%



- Molecule 57: 60S ribosomal protein L19-A



- Molecule 58: 60S ribosomal protein L20-A



- Molecule 59: 60S ribosomal protein L21-A



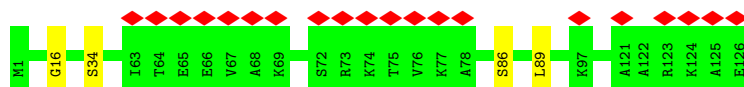
- Molecule 60: 60S ribosomal protein L22-A



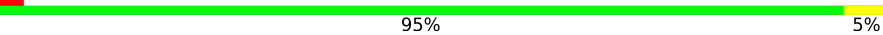
- Molecule 61: 60S ribosomal protein L23-A

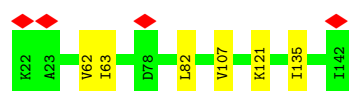


- Molecule 62: 60S ribosomal protein L24-A

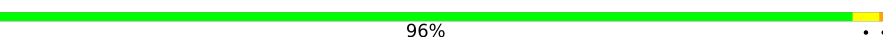


- Molecule 63: 60S ribosomal protein L25

Chain AH:  95% 5%



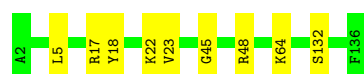
- Molecule 64: 60S ribosomal protein L26-A

Chain AK:  96% ..



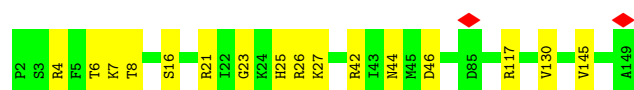
- Molecule 65: 60S ribosomal protein L27-A

Chain AN:  93% 7%

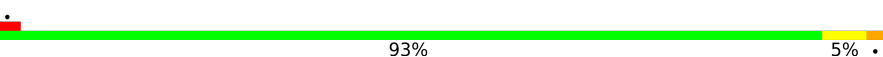


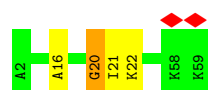
- Molecule 66: 60S ribosomal protein L28

Chain AR:  89% 11%



- Molecule 67: 60S ribosomal protein L29

Chain AV:  93% 5% .



- Molecule 68: 60S ribosomal protein L30

Chain AY:  91% 9%



- Molecule 69: 60S ribosomal protein L31-A

Chain BC:  8% 89% 11%



- Molecule 70: 60S ribosomal protein L32

Chain BG:  92% 8%



- Molecule 71: 60S ribosomal protein L33-A

Chain BK:  90% 10%



- Molecule 72: 60S ribosomal protein L34-A

Chain BN:  92% 8%

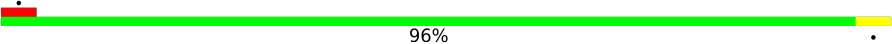


- Molecule 73: 60S ribosomal protein L35-A

Chain BP:  93% 7%



- Molecule 74: 60S ribosomal protein L36-A

Chain AC:  96%



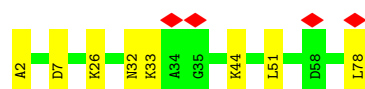
- Molecule 75: 60S ribosomal protein L37-A

Chain AF:  88% 12%



- Molecule 76: 60S ribosomal protein L38

Chain AI:  90% 10%



- Molecule 77: 60S ribosomal protein L39

Chain AL:  82% 18%

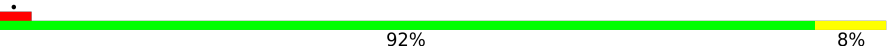


- Molecule 78: Ubiquitin-60S ribosomal protein L40

Chain AO:  90% 10%

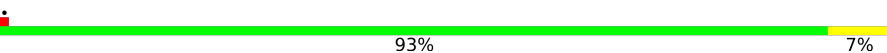


- Molecule 79: 60S ribosomal protein L41-B

Chain AS:  92% 8%



- Molecule 80: 60S ribosomal protein L42-A

Chain AP:  93% 7%



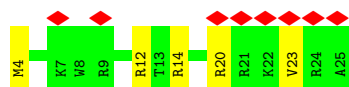
- Molecule 81: 60S ribosomal protein L43-A

Chain AT:  92% 8%



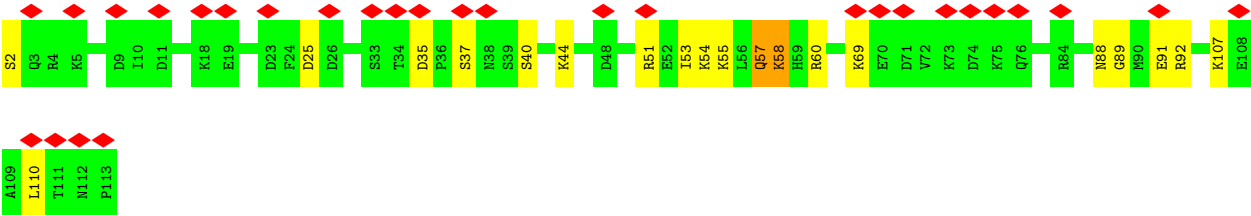
- Molecule 82: 60S ribosomal protein L41-A

Chain BV:  36% 77% 23%



- Molecule 83: General negative regulator of transcription subunit 5

Chain BW:  26% 82% 16%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	176111	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 ($e^-/\text{\AA}^2$)	28	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.361	Depositor
Minimum map value	-0.101	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.038	Depositor
Map size ($\text{\AA}$)	520.32, 520.32, 520.32	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	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: 7MG, ZN, 2MG, T6A, 5MC, M2G, 1MA, MG, SPD, H2U, 1MG

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	0.24	0/42211	0.41	0/65773
2	l	0.24	0/72	0.24	0/110
3	P	0.25	0/1644	0.47	0/2249
4	Q	0.26	0/1823	0.60	0/2447
5	E	0.25	0/936	0.56	0/1259
6	R	0.29	0/1656	0.56	0/2251
7	A	0.25	0/1754	0.55	0/2361
8	S	0.24	0/2097	0.53	1/2823 (0.0%)
9	B	0.25	0/1625	0.53	0/2197
10	T	0.24	0/1839	0.52	0/2460
11	U	0.26	0/1498	0.58	0/2019
12	V	0.26	0/1501	0.51	0/2006
13	W	0.25	0/1504	0.56	0/2016
14	C	0.25	0/769	0.55	0/1039
15	X	0.27	0/1168	0.50	0/1575
16	D	0.28	0/883	0.73	0/1199
17	Y	0.29	0/1215	0.58	0/1638
18	Z	0.27	0/934	0.57	0/1257
19	F	0.27	0/1125	0.59	2/1510 (0.1%)
20	G	0.24	0/957	0.53	0/1283
21	H	0.26	0/1207	0.56	0/1623
22	I	0.28	0/1130	0.53	0/1517
23	J	0.27	0/807	0.58	0/1091
24	n	0.31	1/1577 (0.1%)	0.44	1/2457 (0.0%)
25	a	0.26	0/682	0.51	0/921
26	b	0.30	0/1038	0.53	0/1395
27	c	0.29	0/1139	0.57	0/1518
28	d	0.25	0/1087	0.49	0/1449
29	K	0.28	0/661	0.61	0/888
30	e	0.29	0/778	0.51	0/1042
31	f	0.25	0/620	0.52	0/838
32	M	0.26	0/452	0.55	0/600

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.27	0/480	0.74	1/639 (0.2%)
34	N	0.25	0/567	0.64	0/764
35	O	0.23	0/2436	0.54	0/3318
36	L	0.28	0/493	0.60	0/663
37	BQ	0.27	0/77157	0.39	0/120295
38	BT	0.40	0/1634	0.98	1/2195 (0.0%)
39	BR	0.24	0/2883	0.33	0/4491
40	BS	0.27	0/3746	0.36	0/5832
41	AW	0.33	0/1933	0.51	0/2598
42	BA	0.30	0/3146	0.49	0/4228
43	BE	0.30	0/2800	0.50	0/3790
44	BI	0.27	0/2400	0.49	0/3239
45	BM	0.25	0/1329	0.49	0/1794
46	BO	0.30	0/1821	0.49	0/2451
47	AA	0.27	0/1836	0.50	0/2481
48	AD	0.26	0/1529	0.52	0/2060
49	BD	0.27	0/1801	0.47	0/2416
50	AG	0.26	0/1367	0.54	0/1834
51	AJ	0.31	0/1568	0.55	0/2106
52	AM	0.26	0/1068	0.52	0/1438
53	AQ	0.34	0/1757	0.49	0/2354
54	AU	0.31	0/1585	0.47	0/2128
55	AX	0.29	0/1439	0.52	0/1938
56	BB	0.30	0/1465	0.52	0/1965
57	BF	0.29	0/1532	0.54	0/2043
58	BH	0.28	0/1473	0.49	0/1980
59	BJ	0.28	0/1296	0.47	0/1739
60	BL	0.25	0/812	0.50	0/1099
61	AB	0.27	0/1018	0.47	0/1369
62	AE	0.24	0/850	0.41	0/1152
63	AH	0.28	0/979	0.45	0/1321
64	AK	0.27	0/995	0.45	0/1329
65	AN	0.28	0/1106	0.51	0/1485
66	AR	0.30	0/1200	0.49	0/1607
67	AV	0.28	0/473	0.54	0/629
68	AY	0.25	0/745	0.42	0/1001
69	BC	0.29	0/890	0.51	0/1196
70	BG	0.28	0/1034	0.43	0/1385
71	BK	0.32	0/868	0.48	0/1168
72	BN	0.30	0/890	0.52	0/1189
73	BP	0.26	0/978	0.48	0/1301
74	AC	0.27	0/772	0.51	0/1026
75	AF	0.35	0/660	0.49	0/875

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	AI	0.24	0/618	0.50	0/826
77	AL	0.31	0/443	0.43	0/588
78	AO	0.29	0/416	0.54	0/553
79	AS	0.32	0/230	0.66	0/296
80	AP	0.28	0/836	0.46	0/1104
81	AT	0.30	0/701	0.52	0/934
82	BV	0.30	0/208	0.75	0/267
83	BW	0.33	0/950	0.72	0/1260
All	All	0.27	1/219602 (0.0%)	0.45	6/322550 (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
11	U	0	1
12	V	0	1
16	D	0	2
19	F	0	1
34	N	0	1
35	O	0	2
38	BT	0	1
43	BE	0	2
47	AA	0	2
48	AD	0	1
52	AM	0	1
67	AV	0	1
69	BC	0	1
73	BP	0	1
All	All	0	18

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	n	61	C	O3'-P	5.64	1.69	1.61

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	F	39	VAL	CA-C-N	6.13	136.75	121.80
19	F	39	VAL	C-N-CA	6.13	136.75	121.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	n	61	C	P-O3'-C3'	6.10	129.35	120.20
33	g	3	LYS	CA-CB-CG	6.04	126.18	114.10
8	S	193	GLY	N-CA-C	5.16	125.41	113.18
38	BT	16	LEU	CA-CB-CG	5.16	134.34	116.30

There are no chirality outliers.

All (18) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
47	AA	30	THR	Peptide
47	AA	76	ALA	Peptide
48	AD	21	LYS	Peptide
52	AM	12	TRP	Peptide
67	AV	20	GLY	Peptide
69	BC	83	GLU	Peptide
43	BE	13	GLY	Peptide
43	BE	318	LEU	Peptide
73	BP	83	LYS	Peptide
38	BT	16	LEU	Peptide
16	D	110	GLY	Peptide
16	D	84	ASN	Peptide
19	F	40	GLU	Peptide
34	N	144	CYS	Peptide
35	O	116	ASP	Peptide
35	O	117	LYS	Peptide
11	U	64	VAL	Peptide
12	V	187	GLU	Sidechain

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	183	0
2	1	65	0	33	0	0
3	P	1603	0	1610	15	0
4	Q	1798	0	1890	15	0
5	E	916	0	941	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	R	1626	0	1715	13	0
7	A	1729	0	1812	6	0
8	S	2056	0	2140	20	0
9	B	1605	0	1669	12	0
10	T	1815	0	1894	17	0
11	U	1473	0	1555	13	0
12	V	1476	0	1501	17	0
13	W	1479	0	1556	6	0
14	C	752	0	719	8	0
15	X	1142	0	1209	4	0
16	D	875	0	878	13	0
17	Y	1192	0	1255	9	0
18	Z	923	0	948	14	0
19	F	1105	0	1166	8	0
20	G	948	0	990	3	0
21	H	1188	0	1218	13	0
22	I	1112	0	1124	15	0
23	J	797	0	863	5	0
24	n	1624	0	841	11	0
25	a	673	0	662	8	0
26	b	1021	0	1060	6	0
27	c	1121	0	1196	12	0
28	d	1073	0	1132	11	0
29	K	651	0	682	3	0
30	e	765	0	814	8	0
31	f	610	0	633	7	0
32	M	442	0	428	7	0
33	g	472	0	521	2	0
34	N	556	0	550	8	0
35	O	2383	0	2332	21	0
36	L	491	0	524	7	0
37	BQ	68931	0	34632	286	0
38	BT	1609	0	1701	25	0
39	BR	2579	0	1303	12	0
40	BS	3353	0	1695	15	0
41	AW	1899	0	1957	15	0
42	BA	3075	0	3142	23	0
43	BE	2748	0	2859	16	0
44	BI	2351	0	2294	13	0
45	BM	1307	0	1377	12	0
46	BO	1784	0	1862	13	0
47	AA	1804	0	1877	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
48	AD	1508	0	1572	15	0
49	BD	1764	0	1804	13	0
50	AG	1346	0	1370	9	0
51	AJ	1543	0	1608	10	0
52	AM	1053	0	1149	16	0
53	AQ	1720	0	1779	9	0
54	AU	1555	0	1659	8	0
55	AX	1416	0	1433	7	0
56	BB	1441	0	1543	14	0
57	BF	1515	0	1606	17	0
58	BH	1437	0	1475	15	0
59	BJ	1272	0	1312	9	0
60	BL	796	0	812	3	0
61	AB	1003	0	1048	8	0
62	AE	836	0	706	3	0
63	AH	964	0	1025	3	0
64	AK	984	0	1075	6	0
65	AN	1080	0	1122	7	0
66	AR	1169	0	1211	15	0
67	AV	462	0	491	3	0
68	AY	737	0	792	6	0
69	BC	876	0	912	7	0
70	BG	1013	0	1077	10	0
71	BK	850	0	880	8	0
72	BN	880	0	942	8	0
73	BP	969	0	1078	5	0
74	AC	766	0	844	4	0
75	AF	645	0	645	10	0
76	AI	612	0	682	7	0
77	AL	436	0	475	8	0
78	AO	410	0	442	6	0
79	AS	229	0	273	2	0
80	AP	824	0	888	5	0
81	AT	694	0	734	7	0
82	BV	207	0	250	5	0
83	BW	940	0	973	13	0
84	2	89	0	0	0	0
84	AB	1	0	0	0	0
84	AQ	1	0	0	0	0
84	AW	2	0	0	0	0
84	AX	1	0	0	0	0
84	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
84	BA	3	0	0	0	0
84	BF	1	0	0	0	0
84	BG	1	0	0	0	0
84	BN	1	0	0	0	0
84	BO	1	0	0	0	0
84	BQ	220	0	0	0	0
84	BR	1	0	0	0	0
84	S	1	0	0	0	0
84	n	3	0	0	0	0
85	AF	1	0	0	0	0
85	AO	1	0	0	0	0
85	AP	1	0	0	0	0
85	AT	1	0	0	0	0
85	BN	1	0	0	0	0
85	M	1	0	0	0	0
85	N	1	0	0	0	0
86	BQ	10	0	19	2	0
All	All	205032	0	151454	934	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (934) 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)
83:BW:53:ILE:O	83:BW:57:GLN:HG3	1.69	0.92
24:n:64:A:C8	24:n:64:A:H5''	2.09	0.88
67:AV:16:ALA:O	67:AV:20:GLY:HA3	1.75	0.85
38:BT:60:ARG:NH2	38:BT:166:ALA:O	2.10	0.85
37:BQ:687:U:OP2	51:AJ:36:ARG:NH2	2.13	0.81
37:BQ:2883:U:OP1	42:BA:10:ARG:NH2	2.14	0.80
16:D:34:THR:OG1	16:D:127:GLY:O	1.99	0.80
36:L:27:GLN:OE1	36:L:43:ASN:ND2	2.16	0.78
38:BT:20:SER:OG	38:BT:174:MET:SD	2.39	0.78
1:2:1339:C:O2'	1:2:1341:A:N7	2.18	0.77
37:BQ:2767:U:O2'	80:AP:30:ALA:O	2.03	0.76
38:BT:145:TYR:O	38:BT:149:THR:OG1	2.03	0.76
23:J:106:ILE:HG23	23:J:107:THR:HG23	1.68	0.75
37:BQ:2177:G:OP2	41:AW:128:ARG:NH1	2.20	0.75
37:BQ:1257:C:N4	37:BQ:1261:G:H22	1.85	0.74
37:BQ:2245:C:O2'	41:AW:220:GLY:O	2.05	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BQ:1682:U:O4	60:BL:90:ARG:NH1	2.21	0.74
37:BQ:3181:C:O2'	54:AU:164[A]:SER:OG	2.05	0.74
37:BQ:1722:U:OP1	57:BF:100:ARG:NH1	2.20	0.73
1:2:159:U:O2'	10:T:87:ARG:NH1	2.22	0.73
37:BQ:1243:G:O2'	37:BQ:1271:A:O2'	2.06	0.73
37:BQ:1257:C:H42	37:BQ:1261:G:N2	1.86	0.72
37:BQ:560:G:OP1	52:AM:83:LYS:NZ	2.22	0.72
1:2:278:U:OP2	1:2:279:G:N2	2.23	0.72
23:J:80:GLU:OE1	32:M:44:ARG:NH1	2.22	0.72
1:2:151:G:O6	28:d:124:ARG:NH1	2.23	0.72
37:BQ:1724:U:OP2	57:BF:128:LYS:NZ	2.19	0.72
51:AJ:4:SER:O	66:AR:44:ASN:ND2	2.23	0.72
1:2:1459:C:OP1	21:H:126:ARG:NH2	2.23	0.72
37:BQ:838:G:O6	81:AT:4:ARG:NH2	2.23	0.72
1:2:231:U:O2	1:2:235:G:N2	2.23	0.71
10:T:21:GLU:OE1	10:T:25:ARG:NH2	2.23	0.71
44:BI:206:GLN:NE2	44:BI:210:GLU:OE1	2.22	0.71
37:BQ:804:C:OP1	43:BE:98:ARG:NH1	2.23	0.71
1:2:1009:U:OP2	18:Z:129:LYS:NZ	2.23	0.71
37:BQ:1348:U:OP2	56:BB:38:ARG:NH2	2.23	0.71
8:S:100:ARG:NH2	8:S:121:TYR:O	2.23	0.71
37:BQ:3045:G:OP1	42:BA:19:ARG:NH2	2.25	0.70
24:n:64:A:H5''	24:n:64:A:H8	1.56	0.70
37:BQ:1634:G:N7	65:AN:17:ARG:NH1	2.39	0.70
40:BS:95:G:OP2	75:AF:72:ARG:NH1	2.24	0.70
37:BQ:1106:G:OP1	67:AV:22:LYS:NZ	2.25	0.70
1:2:1502:G:N7	22:I:102:ARG:NH2	2.39	0.69
41:AW:27:ALA:O	41:AW:128:ARG:NH2	2.25	0.69
37:BQ:1778:G:O2'	37:BQ:1780:G:OP2	2.09	0.69
37:BQ:2457:G:N2	37:BQ:2486:A:C2	2.59	0.69
1:2:1435:G:O6	14:C:64:TYR:OH	2.07	0.69
37:BQ:714:G:HO2'	37:BQ:753:C:HO2'	1.40	0.69
49:BD:66:GLU:OE1	49:BD:69:ARG:NH2	2.25	0.69
1:2:153:G:OP2	28:d:131:ARG:NH2	2.25	0.69
24:n:75:C:OP2	49:BD:110:ARG:NH1	2.25	0.69
3:P:156:VAL:O	25:a:65:SER:OG	2.11	0.69
37:BQ:1566:A:N1	37:BQ:1571:A:N6	2.40	0.69
47:AA:52:TRP:O	47:AA:57:ARG:NH1	2.26	0.69
3:P:92:HIS:HD1	3:P:202:TYR:HH	1.41	0.68
37:BQ:2219:A:OP2	74:AC:68:ARG:NH2	2.26	0.68
37:BQ:1846:C:OP1	37:BQ:1849:C:N4	2.24	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BQ:2514:U:OP2	37:BQ:2586:G:N2	2.26	0.68
47:AA:95:ASN:OD1	47:AA:98:ARG:NH2	2.27	0.68
37:BQ:3187:A:OP1	48:AD:23:ARG:NH2	2.27	0.68
44:BI:41:LYS:NZ	59:BJ:30:TYR:O	2.26	0.68
37:BQ:1383:G:O3'	43:BE:138:ARG:NH2	2.25	0.68
37:BQ:1493:G:O6	77:AL:2:ALA:N	2.27	0.68
16:D:140:PHE:O	16:D:143:GLN:NE2	2.27	0.68
37:BQ:2116:G:OP1	37:BQ:2118:C:N4	2.27	0.68
1:2:852:C:OP2	57:BF:173:ARG:NH2	2.28	0.67
37:BQ:1244:A:O2'	37:BQ:1247:U:OP1	2.07	0.67
72:BN:87:GLU:OE1	72:BN:91:ARG:NH1	2.28	0.67
18:Z:111:ARG:NH2	30:e:57:SER:O	2.27	0.67
38:BT:58:CYS:SG	38:BT:152:ARG:NH2	2.68	0.67
13:W:107:ARG:NH2	13:W:153:GLU:OE2	2.28	0.67
37:BQ:860:G:OP1	81:AT:17:ARG:NH1	2.27	0.67
1:2:898:A:N1	1:2:911:U:O2'	2.27	0.67
1:2:1451:C:OP1	32:M:12:ARG:NH2	2.29	0.66
37:BQ:3272:C:OP2	45:BM:78:ARG:NH1	2.28	0.66
44:BI:50:ARG:NH2	44:BI:72:ASP:OD2	2.27	0.66
67:AV:16:ALA:O	67:AV:20:GLY:CA	2.43	0.66
37:BQ:496:C:OP1	70:BG:8:LYS:NZ	2.28	0.66
65:AN:22:LYS:NZ	65:AN:132:SER:O	2.27	0.66
16:D:73:LYS:NZ	34:N:109:ASP:O	2.25	0.66
37:BQ:1196:C:OP1	37:BQ:1309:U:O2'	2.13	0.66
37:BQ:2852:C:N3	49:BD:158:LYS:NZ	2.44	0.66
37:BQ:1348:U:O2	37:BQ:1349:G:N2	2.28	0.66
37:BQ:3214:U:OP2	52:AM:128:ARG:NH1	2.27	0.66
1:2:1584:G:N2	1:2:1611:A:OP2	2.27	0.66
3:P:27:ARG:NH2	3:P:43:ASP:O	2.29	0.66
37:BQ:1474:A:O2'	69:BC:57:GLN:OE1	2.14	0.66
37:BQ:1598:G:OP2	72:BN:31:ARG:NH2	2.29	0.66
1:2:1558:U:OP2	1:2:1559:A:O2'	2.12	0.65
17:Y:99:ARG:NH2	17:Y:119:GLU:OE1	2.29	0.65
66:AR:6:THR:HG22	66:AR:8:THR:H	1.61	0.65
69:BC:4:LEU:O	69:BC:79:ARG:NH2	2.29	0.65
24:n:20:A:N3	24:n:60:A:N6	2.45	0.65
37:BQ:3050:U:O2'	62:AE:16:GLY:O	2.14	0.65
37:BQ:618:C:OP1	55:AX:173:ARG:NH2	2.30	0.65
11:U:133:THR:OG1	11:U:155:ASP:OD1	2.15	0.65
44:BI:120:LYS:O	44:BI:248:ARG:NH2	2.30	0.65
1:2:1482:C:O2'	19:F:72:GLY:O	2.15	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:771:A:OP1	13:W:9:SER:OG	2.14	0.64
37:BQ:2895:G:O2'	78:AO:100:TYR:O	2.15	0.64
57:BF:182:ASP:OD1	57:BF:183:ALA:N	2.30	0.64
1:2:125:U:OP1	10:T:201:GLN:NE2	2.30	0.64
37:BQ:2307:G:O2'	37:BQ:2310:U:OP2	2.16	0.64
54:AU:54[A]:TYR:OH	54:AU:73[A]:PHE:O	2.15	0.64
37:BQ:1565:G:N2	37:BQ:1575:A:C5	2.65	0.64
39:BR:50:U:O3'	44:BI:224:LYS:NZ	2.31	0.64
8:S:129:VAL:HG12	8:S:139:VAL:HG12	1.79	0.64
37:BQ:1693:C:O2'	37:BQ:1772:U:O2'	2.15	0.64
8:S:103:TYR:O	8:S:182:TYR:OH	2.16	0.64
34:N:141:CYS:SG	34:N:142:GLY:N	2.71	0.64
1:2:992:A:O2'	1:2:1785:U:O2	2.16	0.64
11:U:15:GLU:OE1	11:U:19:GLN:NE2	2.30	0.64
39:BR:85:G:O3'	46:BO:218:ARG:NH2	2.31	0.63
9:B:57:SER:OG	9:B:167:ARG:NH2	2.32	0.63
11:U:38:LEU:HA	11:U:41:LEU:HD23	1.80	0.63
61:AB:14:SER:O	61:AB:81:GLN:NE2	2.31	0.63
1:2:944:A:OP2	30:e:19:LYS:NZ	2.25	0.63
61:AB:104:ASN:OD1	61:AB:108:GLU:N	2.32	0.63
1:2:861:U:O2'	26:b:56:HIS:O	2.16	0.63
1:2:868:G:OP1	17:Y:121:ARG:NH1	2.29	0.63
37:BQ:801:A:OP1	66:AR:27:LYS:NZ	2.26	0.63
83:BW:25:ASP:OD1	83:BW:92:ARG:NH1	2.31	0.63
1:2:472:U:O2'	1:2:769:A:N3	2.31	0.63
9:B:63:GLN:NE2	9:B:64:VAL:O	2.31	0.63
1:2:1300:A:OP1	6:R:99:LYS:NZ	2.32	0.63
1:2:237:C:O2'	1:2:238:U:O4'	2.15	0.62
37:BQ:1793:C:OP2	81:AT:49:ARG:NH2	2.32	0.62
37:BQ:283:G:OP1	80:AP:45:ARG:NH1	2.31	0.62
49:BD:61:SER:OG	49:BD:63:GLU:OE1	2.16	0.62
1:2:1562:G:OP1	22:I:89:ARG:NH2	2.33	0.62
18:Z:88:GLY:O	18:Z:92:LYS:NZ	2.29	0.62
39:BR:44:C:OP2	50:AG:137:ARG:NH2	2.33	0.62
9:B:63:GLN:NE2	9:B:66:GLN:OE1	2.32	0.62
27:c:42:PRO:O	27:c:79:ASN:ND2	2.33	0.62
37:BQ:86:G:O2'	37:BQ:98:G:O6	2.16	0.62
4:Q:70:LEU:HD23	4:Q:82:ARG:HE	1.64	0.62
37:BQ:2355:G:OP1	55:AX:141:SER:OG	2.13	0.62
37:BQ:718:G:OP1	66:AR:117:ARG:NH2	2.32	0.62
22:I:16:ASN:OD1	22:I:56:LYS:NZ	2.32	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BQ:649:A:OP2	37:BQ:2868:U:O2'	2.17	0.61
42:BA:74:GLU:OE1	42:BA:283:TYR:OH	2.16	0.61
1:2:219:A:OP1	10:T:227:ARG:NH2	2.33	0.61
1:2:687:G:OP1	26:b:118:ARG:NH1	2.33	0.61
37:BQ:640:U:OP1	66:AR:21:ARG:NH2	2.33	0.61
37:BQ:40:A:OP1	86:BQ:3621:SPD:N10	2.27	0.61
9:B:92:ARG:NH2	9:B:169:ASN:OD1	2.34	0.61
37:BQ:1565:G:C2	37:BQ:1575:A:N6	2.68	0.61
37:BQ:2491:A:OP1	38:BT:207:LYS:NZ	2.22	0.61
37:BQ:2948:C:OP1	42:BA:244:ARG:NH2	2.32	0.61
13:W:18:PRO:O	13:W:23:ARG:NH2	2.34	0.61
37:BQ:443:G:O6	37:BQ:490:C:N4	2.32	0.61
37:BQ:3268:A:OP1	45:BM:46:ARG:NH1	2.32	0.61
1:2:207:U:O2	12:V:178:ARG:NH1	2.33	0.61
1:2:460:A:HO2'	8:S:27:TYR:HH	1.48	0.61
1:2:154:G:OP1	10:T:2:LYS:NZ	2.34	0.61
1:2:789:A:OP1	8:S:108:ARG:NH2	2.34	0.61
37:BQ:3227:A:O3'	52:AM:133:LYS:NZ	2.34	0.61
44:BI:163:LEU:HD21	44:BI:175:HIS:CG	2.36	0.61
76:AI:2:ALA:N	76:AI:51:LEU:O	2.34	0.60
37:BQ:1193:A:OP1	54:AU:49[A]:ARG:NH2	2.34	0.60
37:BQ:3373:U:OP2	69:BC:102:LYS:NZ	2.26	0.60
1:2:897:C:O2	18:Z:41:ARG:NH2	2.35	0.60
62:AE:86:SER:O	62:AE:89:LEU:N	2.34	0.60
1:2:1382:A:O2'	1:2:1383:G:OP1	2.17	0.60
1:2:44:U:OP2	1:2:437:A:N6	2.34	0.60
1:2:1019:A:OP1	17:Y:106:ARG:NH1	2.34	0.60
1:2:1534:G:OP1	21:H:57:ARG:NH2	2.35	0.60
1:2:1594:G:OP2	1:2:1596:C:N4	2.35	0.60
37:BQ:837:A:OP2	81:AT:4:ARG:NH1	2.35	0.60
37:BQ:1811:G:N7	65:AN:64:LYS:NZ	2.48	0.60
1:2:68:A:OP1	10:T:171:LYS:NZ	2.32	0.60
48:AD:137:SER:OG	48:AD:143:GLU:OE1	2.13	0.60
37:BQ:519:A:N7	43:BE:360:LYS:NZ	2.49	0.60
45:BM:82:ARG:NH1	71:BK:106:ASN:OD1	2.35	0.60
24:n:24:G:O2'	37:BQ:2266:U:OP1	2.20	0.59
37:BQ:1231:A:O2'	37:BQ:1261:G:O2'	2.12	0.59
1:2:61:A:O2'	1:2:62:A:O4'	2.19	0.59
37:BQ:1727:G:OP1	81:AT:44:LYS:NZ	2.33	0.59
37:BQ:2898:G:N7	78:AO:125:LYS:NZ	2.50	0.59
37:BQ:3042:U:OP2	37:BQ:3092:C:N4	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:AN:17:ARG:NH2	65:AN:18:TYR:OH	2.36	0.59
37:BQ:1631:C:OP2	65:AN:48:ARG:NH2	2.35	0.59
3:P:79:ARG:NH2	3:P:164:ASN:O	2.35	0.59
37:BQ:2478:C:OP2	37:BQ:2480:A:N6	2.35	0.59
56:BB:36:LEU:O	56:BB:40:THR:OG1	2.20	0.59
73:BP:30:GLU:OE2	73:BP:34:GLN:NE2	2.36	0.59
30:e:32:LYS:O	30:e:37:LYS:NZ	2.30	0.59
37:BQ:1257:C:H42	37:BQ:1261:G:H22	1.41	0.59
29:K:95:HIS:ND1	29:K:96:SER:O	2.36	0.59
38:BT:41:TYR:O	38:BT:200:ASN:ND2	2.36	0.59
27:c:69:ARG:NH2	27:c:116:ASP:OD2	2.33	0.59
30:e:57:SER:OG	30:e:59:TYR:O	2.19	0.59
37:BQ:2800:G:O6	66:AR:42:ARG:NH2	2.35	0.59
39:BR:28:C:OP1	50:AG:137:ARG:NH1	2.36	0.59
1:2:955:A:OP1	17:Y:3:ARG:NE	2.36	0.58
4:Q:175:GLU:O	4:Q:187:LYS:NZ	2.36	0.58
37:BQ:1779:C:N4	57:BF:88:ARG:O	2.36	0.58
8:S:98:ASN:ND2	8:S:116:ASP:OD1	2.36	0.58
3:P:53:THR:HG22	3:P:161:PRO:HG2	1.85	0.58
50:AG:10:ARG:NH2	50:AG:151:SER:O	2.35	0.58
23:J:70:THR:OG1	23:J:72:ASN:OD1	2.22	0.58
29:K:29:LYS:HE2	83:BW:110:LEU:HA	1.84	0.58
1:2:930:A:O2'	4:Q:111:ARG:NH1	2.36	0.58
1:2:1020:A:OP2	17:Y:106:ARG:NH2	2.36	0.58
24:n:63:G:H4'	24:n:63:G:OP1	2.03	0.58
37:BQ:439:C:OP1	70:BG:2:ALA:N	2.36	0.58
1:2:1334:U:O3'	23:J:85:ARG:NH2	2.36	0.58
8:S:141:THR:OG1	8:S:143:ASP:OD1	2.18	0.58
37:BQ:1243:G:N2	37:BQ:1271:A:OP1	2.36	0.58
37:BQ:1619:A:OP1	82:BV:14:ARG:NH1	2.36	0.58
37:BQ:2854:U:OP2	49:BD:3:ARG:NH2	2.36	0.58
31:f:55:THR:HB	31:f:62:ILE:HD13	1.84	0.58
1:2:1116:A:OP1	79:AS:17:ARG:NH2	2.37	0.58
10:T:163:THR:OG1	10:T:165:GLY:O	2.21	0.58
35:O:5:GLU:OE1	35:O:249:ARG:NH1	2.37	0.58
37:BQ:2476:C:N4	37:BQ:2477:G:O6	2.37	0.58
1:2:163:G:OP2	1:2:163:G:N2	2.32	0.57
1:2:1096:C:OP2	26:b:71:LYS:NZ	2.35	0.57
11:U:24:PHE:HE1	11:U:77:LEU:HD11	1.68	0.57
1:2:142:G:H22	1:2:173:A:H2	1.51	0.57
1:2:1681:A:N6	1:2:1720:G:O2'	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:BT:151:VAL:HG21	38:BT:166:ALA:HB3	1.86	0.57
1:2:911:U:OP2	4:Q:8:ARG:NH2	2.36	0.57
21:H:126:ARG:HB3	21:H:133:VAL:HG12	1.86	0.57
37:BQ:2374:C:N4	37:BQ:2941:A:O4'	2.37	0.57
37:BQ:2504:U:O2'	37:BQ:2505:U:OP1	2.13	0.57
37:BQ:2568:C:O2'	37:BQ:2569:A:O4'	2.21	0.57
35:O:48:THR:OG1	35:O:50:ASP:OD1	2.18	0.57
1:2:655:G:C2	1:2:678:A:N6	2.73	0.57
1:2:1220:C:OP1	14:C:48:SER:OG	2.17	0.57
37:BQ:596:C:N3	37:BQ:608:A:O2'	2.36	0.57
37:BQ:3275:U:O2'	71:BK:99:ARG:NH1	2.38	0.57
37:BQ:212:G:OP2	64:AK:2:ALA:N	2.37	0.57
37:BQ:2468:A:O2'	37:BQ:2477:G:N2	2.38	0.57
12:V:4:SER:OG	12:V:6:ASP:OD1	2.23	0.57
1:2:1022:C:O2'	1:2:1125:A:N1	2.36	0.56
6:R:140:ARG:NH2	25:a:10:GLU:OE1	2.36	0.56
38:BT:66:CYS:SG	38:BT:67:ILE:N	2.78	0.56
83:BW:51:ARG:O	83:BW:55:LYS:HG3	2.04	0.56
1:2:885:G:N2	18:Z:123:SER:O	2.38	0.56
5:E:18:ARG:NH1	21:H:90:ASN:O	2.38	0.56
4:Q:129:THR:OG1	4:Q:179:SER:O	2.23	0.56
36:L:31:GLU:OE2	36:L:37:SER:N	2.36	0.56
37:BQ:2455:U:N3	37:BQ:2483:G:O2'	2.38	0.56
1:2:1565:C:OP1	21:H:41:ARG:NH1	2.36	0.56
1:2:388:G:OP1	1:2:423:G:O2'	2.23	0.56
3:P:56:LYS:NZ	25:a:70:ASN:OD1	2.32	0.56
37:BQ:351:A:N6	77:AL:37:TYR:O	2.38	0.56
50:AG:26:SER:OG	50:AG:27:GLY:N	2.36	0.56
48:AD:47:LYS:NZ	52:AM:5:SER:O	2.24	0.56
1:2:195:G:N7	12:V:137:LYS:NZ	2.44	0.56
9:B:47:SER:OG	9:B:49:GLU:OE1	2.23	0.56
37:BQ:2256:A:H3'	37:BQ:2256:A:H8	1.71	0.56
1:2:521:A:N3	28:d:34:ASN:ND2	2.54	0.56
37:BQ:440:A:N7	37:BQ:441:U:O2'	2.35	0.56
37:BQ:1447:G:O2'	37:BQ:2355:G:O6	2.21	0.56
1:2:113:U:O2'	1:2:115:G:O2'	2.21	0.56
6:R:226:THR:OG1	6:R:228:ASN:OD1	2.23	0.55
37:BQ:3184:A:OP2	54:AU:12[A]:LYS:NZ	2.36	0.55
57:BF:105:LEU:HD22	57:BF:135:LYS:HG3	1.88	0.55
14:C:35:ILE:HG22	14:C:37:THR:H	1.71	0.55
37:BQ:2138:A:HO2'	75:AF:2:GLY:N	2.04	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BQ:2269:U:OP1	83:BW:55:LYS:HE3	2.05	0.55
49:BD:21:ARG:O	49:BD:24:ARG:NH2	2.39	0.55
4:Q:207:LEU:O	4:Q:210:ILE:HD11	2.04	0.55
13:W:59:LEU:HD22	13:W:69:ARG:HA	1.87	0.55
37:BQ:1203:A:N3	37:BQ:2855:U:O2'	2.33	0.55
37:BQ:2681:U:O2	50:AG:20:ASN:ND2	2.40	0.55
58:BH:22:PRO:O	59:BJ:146:ASN:ND2	2.37	0.55
1:2:1066:C:O2'	4:Q:148:ASN:OD1	2.17	0.55
37:BQ:595:G:OP2	46:BO:30:ARG:NH2	2.40	0.55
37:BQ:1322:U:O2	58:BH:108:GLN:NE2	2.35	0.55
37:BQ:1940:G:H21	37:BQ:3362:A:H8	1.55	0.55
37:BQ:3308:C:N3	55:AX:69:ARG:NH1	2.54	0.55
1:2:609:U:N3	27:c:22:ASN:O	2.38	0.55
1:2:1075:C:O2'	30:e:13:LYS:O	2.24	0.55
1:2:1173:C:OP1	21:H:132:ARG:NH2	2.40	0.55
6:R:58:LEU:O	25:a:15:ARG:NE	2.40	0.55
37:BQ:1831:U:O2'	40:BS:114:G:OP1	2.13	0.55
3:P:141:ILE:O	25:a:60:ARG:NH1	2.38	0.55
58:BH:93:GLU:OE2	58:BH:137:ARG:N	2.38	0.55
1:2:929:A:OP1	1:2:931:C:N4	2.39	0.55
37:BQ:824:C:O2'	37:BQ:1534:A:N3	2.39	0.55
37:BQ:2185:G:O2'	37:BQ:2314:U:OP2	2.23	0.55
37:BQ:1008:U:O2'	49:BD:35:ASP:OD2	2.25	0.55
37:BQ:2969:A:N7	41:AW:215:ASN:ND2	2.55	0.55
49:BD:140:THR:HG21	49:BD:148:VAL:HG11	1.88	0.55
4:Q:69:CYS:SG	18:Z:114:ARG:NH1	2.80	0.55
28:d:78:SER:OG	28:d:81:GLU:OE1	2.24	0.55
37:BQ:394:G:N1	37:BQ:397:A:OP2	2.40	0.55
37:BQ:1382:G:OP2	43:BE:188:ARG:NH1	2.38	0.55
1:2:129:U:O2'	1:2:131:C:N4	2.39	0.55
1:2:821:U:N3	1:2:852:C:O2	2.39	0.55
21:H:90:ASN:N	21:H:97:ASP:OD1	2.40	0.55
22:I:109:GLU:OE2	22:I:122:ARG:NE	2.40	0.55
37:BQ:3214:U:O4	52:AM:124:ARG:NH1	2.39	0.55
83:BW:54:LYS:O	83:BW:58:LYS:HD3	2.07	0.55
35:O:26:SER:OG	35:O:75:ALA:O	2.24	0.54
43:BE:292:SER:OG	43:BE:294:GLU:OE1	2.25	0.54
1:2:1280:C:OP1	32:M:44:ARG:NH2	2.40	0.54
37:BQ:2525:G:O2'	37:BQ:2526:C:OP2	2.16	0.54
1:2:1198:G:OP1	1:2:1199:G:O2'	2.15	0.54
20:G:33:ARG:NE	35:O:109:ASP:OD2	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BQ:284:A:OP2	80:AP:41:ARG:NH1	2.38	0.54
37:BQ:1114:U:OP1	66:AR:23:GLY:N	2.41	0.54
37:BQ:2613:U:O2'	37:BQ:2805:G:OP2	2.22	0.54
83:BW:53:ILE:O	83:BW:57:GLN:CG	2.50	0.54
5:E:86:VAL:HG22	5:E:87:PRO:HD2	1.89	0.54
11:U:87:ASP:O	11:U:88:ARG:NH1	2.41	0.54
37:BQ:1593:A:OP1	72:BN:60:ARG:NH1	2.41	0.54
71:BK:49:ILE:HD11	71:BK:71:VAL:HG22	1.90	0.54
10:T:163:THR:HB	10:T:168:THR:HG22	1.89	0.54
37:BQ:2901:G:O2'	37:BQ:3024:A:N1	2.38	0.54
43:BE:286:VAL:HG11	56:BB:31:LYS:HE3	1.89	0.54
44:BI:64:ILE:HG13	44:BI:109:THR:HG21	1.90	0.54
11:U:98:ILE:HG12	11:U:121:VAL:HG21	1.90	0.53
37:BQ:544:C:O2	37:BQ:548:G:N2	2.40	0.53
48:AD:9:GLN:HB3	48:AD:52:LEU:HD11	1.89	0.53
25:a:15:ARG:NH1	25:a:33:GLN:OE1	2.40	0.53
37:BQ:113:C:OP1	53:AQ:147:ARG:NE	2.41	0.53
37:BQ:1156:C:OP2	46:BO:94:LYS:NZ	2.37	0.53
52:AM:15:VAL:HG23	52:AM:35:ILE:HD13	1.89	0.53
35:O:41:THR:HG22	35:O:62:LYS:HG2	1.90	0.53
37:BQ:1257:C:N3	37:BQ:1261:G:N1	2.54	0.53
37:BQ:1345:G:N2	43:BE:307:GLN:OE1	2.39	0.53
40:BS:97:A:OP1	73:BP:67:ARG:NH2	2.42	0.53
43:BE:266:THR:HG23	43:BE:267:VAL:HG13	1.89	0.53
1:2:1617:U:O2'	36:L:21:SER:O	2.27	0.53
37:BQ:2256:A:H3'	37:BQ:2256:A:C8	2.43	0.53
11:U:150:GLN:HB3	11:U:181:ILE:HG22	1.89	0.53
37:BQ:2137:U:OP2	37:BQ:2142:A:N6	2.36	0.53
37:BQ:2631:U:OP2	59:BJ:4:SER:OG	2.26	0.53
52:AM:123:LEU:HD22	54:AU:190[A]:VAL:HG23	1.91	0.53
1:2:1360:A:HO2'	22:I:2:PRO:N	2.07	0.53
12:V:11:ARG:NH1	12:V:15:GLY:O	2.41	0.53
27:c:62:LYS:N	27:c:116:ASP:O	2.40	0.53
37:BQ:674:G:O6	56:BB:56:LYS:NZ	2.41	0.53
42:BA:349:LYS:NZ	42:BA:352:GLU:OE1	2.41	0.53
37:BQ:293:C:O2'	74:AC:76:ARG:O	2.26	0.53
46:BO:80:GLN:OE1	59:BJ:136:ARG:NH1	2.40	0.53
19:F:129:PHE:O	19:F:137:ARG:NH1	2.41	0.53
37:BQ:1562:C:O2'	37:BQ:1563:C:O5'	2.26	0.53
37:BQ:2338:C:OP1	42:BA:236:LYS:NZ	2.32	0.53
1:2:1344:A:O2'	1:2:1345:A:OP1	2.22	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BQ:744:A:OP1	56:BB:66:ARG:NH2	2.41	0.53
38:BT:193:LEU:O	38:BT:196:LYS:NZ	2.41	0.53
1:2:59:C:O2'	1:2:60:U:O4'	2.26	0.52
1:2:151:G:N3	10:T:13:GLN:NE2	2.55	0.52
1:2:655:G:N3	1:2:678:A:C6	2.77	0.52
8:S:112:HIS:NE2	8:S:237:SER:OG	2.42	0.52
12:V:138:ASN:OD1	12:V:141:ARG:NH2	2.40	0.52
37:BQ:2468:A:O2'	37:BQ:2478:C:O2	2.24	0.52
1:2:959:U:OP1	31:f:30:SER:OG	2.27	0.52
37:BQ:591:G:O2'	45:BM:17:ALA:O	2.25	0.52
1:2:566:C:OP2	27:c:66:SER:OG	2.28	0.52
37:BQ:1134:G:O2'	37:BQ:2642:A:N3	2.30	0.52
38:BT:107:TYR:OH	38:BT:140:HIS:O	2.27	0.52
47:AA:91:PHE:O	47:AA:95:ASN:ND2	2.43	0.52
8:S:193:GLY:O	8:S:211:LYS:N	2.42	0.52
12:V:48:THR:OG1	12:V:52:ASN:O	2.27	0.52
18:Z:99:GLN:NE2	30:e:44:ILE:O	2.41	0.52
24:n:44:A:OP2	83:BW:107:LYS:NZ	2.35	0.52
37:BQ:1373:A:OP2	66:AR:7:LYS:NZ	2.36	0.52
68:AY:30:THR:HG23	68:AY:91:SER:HB2	1.92	0.52
4:Q:72:ASP:OD1	18:Z:114:ARG:NH2	2.43	0.52
37:BQ:904:A:OP2	75:AF:30:GLN:NE2	2.43	0.52
37:BQ:1565:G:N3	37:BQ:1575:A:N6	2.57	0.52
52:AM:36:VAL:HG11	52:AM:55:ARG:HH21	1.75	0.52
1:2:105:A:O3'	12:V:8:ARG:NH1	2.42	0.52
1:2:1060:U:H3'	1:2:1061:A:H5''	1.92	0.52
47:AA:207:ASP:N	47:AA:207:ASP:OD1	2.43	0.52
1:2:629:U:OP2	1:2:969:C:N4	2.37	0.52
26:b:2:THR:OG1	26:b:3:ARG:N	2.43	0.52
16:D:34:THR:HG21	16:D:128:ALA:HB2	1.92	0.52
37:BQ:1613:A:OP1	76:AI:2:ALA:N	2.42	0.52
37:BQ:2945:G:O2'	37:BQ:2948:C:OP2	2.25	0.52
35:O:12:THR:HG22	35:O:311:ARG:HG2	1.92	0.51
37:BQ:3002:C:OP1	42:BA:26:ARG:NH2	2.42	0.51
58:BH:8:GLN:HB3	58:BH:64:ILE:HD11	1.93	0.51
1:2:333:A:OP2	12:V:31:ARG:NH2	2.38	0.51
37:BQ:945:C:OP1	70:BG:36:LYS:NZ	2.43	0.51
38:BT:181:ASN:O	38:BT:185:MET:N	2.31	0.51
8:S:121:TYR:OH	8:S:235:TYR:O	2.28	0.51
68:AY:9:SER:OG	68:AY:10:ILE:N	2.39	0.51
76:AI:7:ASP:N	76:AI:7:ASP:OD1	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BQ:359:U:HO2'	75:AF:16:HIS:HD1	1.58	0.51
5:E:123:TYR:OH	21:H:122:HIS:NE2	2.29	0.51
37:BQ:3329:U:H5''	42:BA:308:MET:HE2	1.93	0.51
57:BF:105:LEU:HD23	57:BF:138:LEU:HD23	1.92	0.51
1:2:17:C:O2'	1:2:1137:A:N1	2.39	0.51
37:BQ:1370:G:OP1	66:AR:16:SER:OG	2.29	0.51
44:BI:54:ARG:NH1	44:BI:147:ASP:O	2.42	0.51
53:AQ:68:ARG:HA	53:AQ:98:LEU:HD21	1.91	0.51
1:2:967:A:OP2	17:Y:124:ARG:NH2	2.42	0.51
8:S:148:ARG:NH1	10:T:201:GLN:OE1	2.40	0.51
28:d:38:ASP:O	28:d:52:LYS:NZ	2.44	0.51
37:BQ:1565:G:N2	37:BQ:1575:A:N7	2.58	0.51
38:BT:158:GLN:NE2	38:BT:161:LYS:O	2.43	0.51
41:AW:130:SER:OG	41:AW:174:ARG:NH2	2.44	0.51
45:BM:87:THR:HG22	45:BM:89:THR:H	1.76	0.51
37:BQ:2273:G:O2'	37:BQ:2311:G:O6	2.27	0.51
40:BS:156:U:OP2	47:AA:84:ARG:NH2	2.44	0.51
16:D:26:ASP:OD1	16:D:29:LYS:NZ	2.44	0.51
37:BQ:1214:U:OP2	58:BH:137:ARG:NH2	2.44	0.51
37:BQ:1729:A:O4'	68:AY:52:ARG:NH1	2.42	0.51
1:2:322:G:O2'	1:2:323:A:OP2	2.29	0.51
1:2:704:C:N4	1:2:732:G:O2'	2.44	0.51
1:2:849:C:OP1	57:BF:162:ARG:NH1	2.43	0.51
37:BQ:361:A:O3'	75:AF:45:ARG:NH2	2.44	0.51
37:BQ:1645:U:O2'	82:BV:12:ARG:NH2	2.44	0.51
55:AX:126:ARG:NH2	55:AX:140:GLU:OE2	2.44	0.51
70:BG:96:ILE:HG21	70:BG:105:ARG:HG2	1.94	0.51
37:BQ:1021:G:N2	37:BQ:1032:C:O2	2.45	0.50
37:BQ:1210:U:OP1	48:AD:62:ARG:NH1	2.44	0.50
49:BD:76:MET:SD	49:BD:148:VAL:HG12	2.51	0.50
5:E:34:VAL:HG23	5:E:41:VAL:HG12	1.93	0.50
37:BQ:421:G:O6	37:BQ:2383:C:O2'	2.29	0.50
37:BQ:799:G:O2'	51:AJ:18:TRP:NE1	2.40	0.50
51:AJ:126:PHE:O	73:BP:114:ARG:NH2	2.42	0.50
71:BK:35:VAL:HG23	71:BK:40:ASP:HB2	1.93	0.50
1:2:853:G:OP2	57:BF:173:ARG:NH1	2.44	0.50
37:BQ:938:C:OP2	66:AR:26:ARG:NH1	2.43	0.50
37:BQ:1639:C:OP2	72:BN:74:ARG:NH2	2.37	0.50
38:BT:122:ARG:HG3	38:BT:123:LEU:HD12	1.93	0.50
47:AA:228:GLU:O	47:AA:232:HIS:ND1	2.41	0.50
80:AP:77:CYS:SG	80:AP:79:THR:OG1	2.56	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:F:64:ASP:OD1	19:F:64:ASP:N	2.44	0.50
37:BQ:1565:G:C2	37:BQ:1575:A:C6	2.99	0.50
42:BA:211:GLN:NE2	42:BA:283:TYR:O	2.44	0.50
21:H:16:ARG:NH1	50:AG:111:ASP:OD1	2.45	0.50
37:BQ:1624:G:O6	37:BQ:1819:U:O4	2.30	0.50
37:BQ:1385:C:HO2'	45:BM:2:THR:N	2.09	0.50
1:2:852:C:OP1	57:BF:176:ARG:NH2	2.45	0.50
1:2:1556:A:O2'	1:2:1560:U:OP2	2.24	0.50
37:BQ:353:G:O6	75:AF:55:ARG:NH1	2.45	0.50
48:AD:120:ASP:OD2	48:AD:124:ARG:NH2	2.43	0.50
58:BH:60:SER:OG	58:BH:62:ASN:OD1	2.30	0.50
1:2:1303:U:O2'	1:2:1322:A:OP2	2.27	0.50
1:2:1471:A:OP1	9:B:185:ARG:NH2	2.44	0.50
1:2:1596:C:OP1	32:M:16:LYS:NZ	2.41	0.50
37:BQ:348:A:N3	37:BQ:352:A:O2'	2.44	0.50
37:BQ:1145:G:O2'	70:BG:45:ARG:O	2.25	0.50
37:BQ:63:A:N3	37:BQ:78:U:O2'	2.39	0.49
37:BQ:1003:A:N1	37:BQ:1049:C:O2'	2.43	0.49
40:BS:95:G:O2'	75:AF:81:GLY:O	2.29	0.49
1:2:1274:C:OP1	1:2:1428:G:OP2	2.31	0.49
4:Q:82:ARG:NH2	4:Q:188:LEU:O	2.44	0.49
7:A:23:GLU:OE1	7:A:27:ARG:NE	2.46	0.49
37:BQ:412:G:OP1	55:AX:62:ARG:NH1	2.45	0.49
57:BF:13:SER:OG	57:BF:38:ARG:NH2	2.45	0.49
61:AB:10:LYS:NZ	61:AB:56:ASP:OD1	2.28	0.49
64:AK:74:TYR:CZ	64:AK:77:LYS:HE2	2.47	0.49
12:V:57:ALA:HB2	12:V:177:GLY:HA2	1.94	0.49
16:D:33:ARG:NH2	16:D:99:GLU:O	2.42	0.49
34:N:123:ASN:ND2	34:N:144:CYS:SG	2.85	0.49
15:X:109:VAL:HG12	15:X:137:PHE:HB2	1.93	0.49
37:BQ:3260:G:OP2	52:AM:128:ARG:NH2	2.45	0.49
43:BE:35:VAL:HG21	43:BE:244:LEU:HD21	1.94	0.49
1:2:1253:U:H5''	34:N:130:VAL:HG23	1.94	0.49
37:BQ:874:U:N3	37:BQ:2978:U:OP1	2.40	0.49
61:AB:15:LEU:HD23	61:AB:53:SER:HB3	1.94	0.49
1:2:284:G:N7	10:T:188:ARG:NH1	2.61	0.49
1:2:366:A:OP1	1:2:758:U:O2'	2.28	0.49
1:2:1081:A:O2'	1:2:1083:G:N7	2.44	0.49
24:n:64:A:C8	24:n:64:A:C5'	2.92	0.49
37:BQ:2256:A:C8	37:BQ:2256:A:C3'	2.95	0.49
37:BQ:3304:U:O2'	42:BA:334:ARG:NH2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1601:G:OP1	22:I:86:ARG:NH1	2.41	0.49
38:BT:107:TYR:OH	38:BT:138:VAL:HG11	2.13	0.49
69:BC:77:ARG:HD2	69:BC:89:LEU:HD13	1.95	0.49
1:2:655:G:N3	1:2:678:A:N6	2.61	0.49
1:2:912:U:OP1	1:2:913:G:O2'	2.24	0.49
37:BQ:1277:C:O2'	37:BQ:1278:A:O5'	2.30	0.49
56:BB:176:ARG:NH1	66:AR:46:ASP:OD2	2.45	0.49
1:2:330:G:OP2	12:V:172:ARG:NH1	2.46	0.49
35:O:123:ILE:HG21	35:O:169:ILE:HG21	1.95	0.49
52:AM:60:LEU:HD13	58:BH:152:LEU:HD11	1.94	0.49
1:2:4:C:OP2	6:R:200:SER:OG	2.31	0.48
1:2:67:A:N6	1:2:83:G:O2'	2.46	0.48
1:2:896:U:OP1	4:Q:26:ARG:NH2	2.46	0.48
37:BQ:815:G:OP2	75:AF:31:LYS:NZ	2.40	0.48
37:BQ:1907:C:O2	42:BA:240:ARG:NH2	2.45	0.48
37:BQ:3244:A:OP1	42:BA:97:ARG:NH2	2.40	0.48
74:AC:21:THR:O	74:AC:21:THR:OG1	2.30	0.48
1:2:705:U:O2'	1:2:706:A:O5'	2.21	0.48
1:2:1183:A:N3	1:2:1210:C:O2'	2.39	0.48
1:2:1402:G:OP2	20:G:5:ARG:NH1	2.46	0.48
5:E:75:PRO:HA	5:E:93:VAL:HG23	1.94	0.48
8:S:87:MET:HE3	8:S:236:ILE:HD13	1.94	0.48
31:f:67:THR:HG22	31:f:68:GLY:H	1.78	0.48
34:N:102:VAL:O	34:N:105:TYR:OH	2.30	0.48
37:BQ:147:U:O4	47:AA:183:LYS:NZ	2.39	0.48
37:BQ:449:U:O2'	37:BQ:450:G:N2	2.46	0.48
37:BQ:1236:G:N2	37:BQ:1272:C:OP1	2.47	0.48
37:BQ:1240:A:H61	37:BQ:1244:A:H5''	1.78	0.48
37:BQ:3243:A:H4'	42:BA:95:THR:HG22	1.93	0.48
1:2:454:U:H5'	8:S:66:MET:HE3	1.95	0.48
1:2:1603:U:OP2	19:F:132:LYS:NZ	2.46	0.48
7:A:20:GLU:OE2	7:A:76:ARG:NE	2.40	0.48
10:T:180:THR:HG23	10:T:183:ARG:H	1.77	0.48
1:2:1188:G:O2'	1:2:1430:U:OP1	2.26	0.48
1:2:1202:A:N6	1:2:1457:C:O5'	2.46	0.48
16:D:84:ASN:O	16:D:86:VAL:N	2.47	0.48
3:P:180:GLU:OE1	3:P:191:ARG:NH2	2.40	0.48
5:E:61:ARG:NH2	5:E:88:GLU:OE2	2.46	0.48
37:BQ:2538:U:O2	37:BQ:2542:U:N3	2.47	0.48
39:BR:52:G:O2'	39:BR:53:U:OP1	2.27	0.48
59:BJ:68:THR:OG1	59:BJ:71:SER:OG	2.21	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:AK:77:LYS:NZ	77:AL:31:THR:HG21	2.29	0.48
65:AN:23:VAL:HG12	65:AN:45:GLY:HA3	1.95	0.48
76:AI:26:LYS:HD2	76:AI:78:LEU:HD12	1.96	0.48
1:2:511:A:H5''	13:W:172:VAL:HG13	1.95	0.48
3:P:30:GLN:HE22	3:P:149:LEU:HD13	1.78	0.48
37:BQ:912:G:OP2	41:AW:9:ARG:NH1	2.44	0.48
37:BQ:1047:A:N3	37:BQ:2633:U:O2'	2.46	0.48
37:BQ:1900:A:O2'	37:BQ:1906:G:N7	2.47	0.48
37:BQ:3070:A:OP1	57:BF:62:ARG:NH2	2.42	0.48
37:BQ:3319:U:O2'	37:BQ:3320:A:OP1	2.31	0.48
40:BS:83:C:O2	64:AK:51:ARG:NH2	2.47	0.48
59:BJ:17:ARG:NH2	59:BJ:23:GLY:O	2.46	0.48
69:BC:51:LEU:HB3	69:BC:55:LEU:HD23	1.95	0.48
3:P:2:SER:OG	3:P:3:LEU:N	2.47	0.48
35:O:83:ALA:HB1	35:O:110:VAL:HG23	1.94	0.48
37:BQ:2618:G:OP1	37:BQ:2644:C:O2'	2.30	0.48
45:BM:175:LYS:O	52:AM:117:ARG:NH2	2.47	0.48
63:AH:82:LEU:HD11	63:AH:135:ILE:HD11	1.96	0.48
6:R:195:ASP:OD1	6:R:195:ASP:N	2.43	0.47
37:BQ:294:U:H4'	74:AC:77:LEU:HD23	1.94	0.47
37:BQ:831:G:O2'	37:BQ:1864:A:N3	2.42	0.47
37:BQ:1820:U:OP2	82:BV:12:ARG:NE	2.47	0.47
83:BW:88:ASN:OD1	83:BW:89:GLY:N	2.47	0.47
8:S:45:ILE:HA	8:S:61:VAL:HG11	1.96	0.47
37:BQ:94:G:OP1	86:BQ:3621:SPD:N1	2.47	0.47
37:BQ:98:G:N7	51:AJ:13:HIS:NE2	2.62	0.47
37:BQ:1244:A:O2'	37:BQ:1249:G:O6	2.32	0.47
61:AB:10:LYS:NZ	61:AB:53:SER:OG	2.47	0.47
1:2:875:G:O2'	1:2:877:G:OP2	2.26	0.47
28:d:86:GLU:OE1	28:d:90:ARG:NH1	2.47	0.47
34:N:121:CYS:SG	34:N:122:SER:N	2.87	0.47
35:O:112:SER:HB3	35:O:154:VAL:HG22	1.96	0.47
37:BQ:3111:U:OP1	48:AD:184:LYS:NZ	2.44	0.47
42:BA:10:ARG:HH12	42:BA:14:LEU:HD21	1.79	0.47
77:AL:5:LYS:HE2	77:AL:13:MET:HE1	1.97	0.47
16:D:35:ALA:O	16:D:40:GLY:N	2.45	0.47
37:BQ:1657:C:O2'	37:BQ:1797:A:OP2	2.28	0.47
43:BE:59:GLN:OE1	75:AF:55:ARG:NH2	2.47	0.47
81:AT:8:VAL:O	81:AT:11:THR:OG1	2.32	0.47
1:2:652:G:N2	1:2:683:C:OP2	2.48	0.47
33:g:24:THR:O	33:g:26:LYS:NZ	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:BA:83:PRO:O	42:BA:165:GLN:NE2	2.47	0.47
1:2:393:C:OP2	12:V:2:GLY:N	2.48	0.47
24:n:16:H2U:O4'	83:BW:60:ARG:NH1	2.48	0.47
31:f:34:ASP:OD1	31:f:34:ASP:N	2.41	0.47
37:BQ:2193:U:H5'	37:BQ:2194:G:H5'	1.96	0.47
37:BQ:3275:U:N3	37:BQ:3277:U:O4'	2.48	0.47
41:AW:14:SER:OG	41:AW:15:ILE:N	2.47	0.47
35:O:156:VAL:HG12	35:O:169:ILE:HG22	1.97	0.47
35:O:266:ASP:OD1	35:O:266:ASP:N	2.42	0.47
37:BQ:638:C:OP1	70:BG:21:HIS:NE2	2.45	0.47
37:BQ:781:G:OP1	56:BB:151:ARG:NE	2.48	0.47
37:BQ:2842:U:OP1	37:BQ:2844:C:N4	2.42	0.47
37:BQ:3052:G:OP1	62:AE:34:SER:OG	2.31	0.47
48:AD:23:ARG:HE	48:AD:39:LYS:HA	1.79	0.47
14:C:24:LYS:O	14:C:39:ASN:ND2	2.47	0.47
71:BK:15:SER:OG	71:BK:16:TYR:N	2.47	0.47
1:2:655:G:C2	1:2:678:A:C6	3.03	0.47
21:H:41:ARG:NH2	22:I:36:ILE:O	2.48	0.47
37:BQ:292:U:OP2	53:AQ:68:ARG:NH1	2.46	0.47
37:BQ:1750:A:OP1	76:AI:44:LYS:NZ	2.45	0.47
37:BQ:2981:U:OP2	42:BA:244:ARG:NH1	2.48	0.47
40:BS:40:A:OP2	40:BS:103:G:N1	2.44	0.47
40:BS:52:A:OP1	77:AL:21:ARG:NH1	2.46	0.47
46:BO:83:LEU:HD11	46:BO:116:PHE:HB3	1.97	0.47
1:2:783:G:C8	28:d:12:VAL:HG22	2.50	0.47
22:I:13:ASP:OD1	22:I:13:ASP:N	2.46	0.47
22:I:108:LEU:HA	22:I:111:ILE:HG22	1.97	0.47
24:n:65:G:H2'	24:n:66:C:C6	2.50	0.47
37:BQ:1522:U:OP2	63:AH:121:LYS:NZ	2.47	0.47
56:BB:123:THR:OG1	56:BB:125:ASP:OD1	2.30	0.47
1:2:487:G:C6	1:2:501:U:N3	2.82	0.46
20:G:108:ASP:HA	20:G:111:LYS:HG2	1.97	0.46
26:b:15:ASN:ND2	26:b:72:CYS:O	2.48	0.46
37:BQ:1764:U:H3'	37:BQ:1765:U:H4'	1.96	0.46
37:BQ:2538:U:O2'	37:BQ:2541:U:N3	2.47	0.46
37:BQ:683:U:OP1	53:AQ:204:LYS:NZ	2.46	0.46
54:AU:126[A]:VAL:O	58:BH:154:HIS:NE2	2.43	0.46
58:BH:90:MET:HE1	58:BH:114:HIS:NE2	2.29	0.46
1:2:1436:A:OP2	7:A:27:ARG:NH2	2.45	0.46
3:P:31:VAL:HG12	3:P:33:GLN:H	1.79	0.46
4:Q:129:THR:OG1	4:Q:130:SER:N	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:U:10:SER:OG	11:U:11:GLN:N	2.49	0.46
37:BQ:1565:G:N3	37:BQ:1575:A:C6	2.83	0.46
37:BQ:1739:U:HO2'	72:BN:56:THR:HG1	1.52	0.46
1:2:58:U:O2'	1:2:451:A:N3	2.49	0.46
1:2:428:A:N3	1:2:440:U:O2'	2.27	0.46
1:2:1127:G:OP1	79:AS:11:ARG:NH1	2.49	0.46
12:V:20:GLN:NE2	12:V:22:ARG:O	2.48	0.46
31:f:40:CYS:SG	31:f:58:SER:OG	2.54	0.46
37:BQ:196:G:N1	37:BQ:199:A:OP2	2.48	0.46
37:BQ:439:C:O2'	37:BQ:440:A:OP1	2.32	0.46
37:BQ:1354:G:N3	45:BM:8:LYS:NZ	2.63	0.46
37:BQ:2464:U:O2	38:BT:39:LYS:NZ	2.33	0.46
37:BQ:2553:U:C5	72:BN:95:ILE:HG22	2.50	0.46
38:BT:206:VAL:HG12	38:BT:214:PHE:HE1	1.80	0.46
40:BS:103:G:OP2	40:BS:105:A:O2'	2.33	0.46
11:U:45:SER:OG	11:U:46:ILE:N	2.47	0.46
37:BQ:716:A:OP1	37:BQ:752:C:O2'	2.33	0.46
37:BQ:779:G:OP1	56:BB:185:LYS:NZ	2.48	0.46
1:2:477:A:O3'	33:g:33:ARG:NH2	2.48	0.46
37:BQ:1116:G:N2	37:BQ:2817:A:O4'	2.49	0.46
38:BT:206:VAL:HG12	38:BT:214:PHE:CE1	2.51	0.46
41:AW:137:ILE:HD11	41:AW:149:ARG:HB2	1.96	0.46
1:2:1292:G:H21	3:P:111:ILE:HD11	1.79	0.46
1:2:1513:G:O2'	1:2:1515:A:N3	2.43	0.46
22:I:86:ARG:NH1	22:I:90:PRO:O	2.48	0.46
35:O:200:ASN:ND2	35:O:239:GLU:OE2	2.49	0.46
37:BQ:2908:G:O2'	78:AO:114:LYS:NZ	2.44	0.46
58:BH:77:VAL:HG11	58:BH:106:LEU:HD22	1.98	0.46
1:2:1550:A:OP2	5:E:42:ARG:NH2	2.47	0.46
37:BQ:3115:C:OP1	48:AD:62:ARG:NH2	2.49	0.46
40:BS:71:A:O2'	64:AK:52:ARG:NH2	2.49	0.46
46:BO:110:ARG:O	46:BO:113:SER:OG	2.27	0.46
1:2:821:U:O4	1:2:852:C:N3	2.49	0.46
13:W:89:ASP:OD1	13:W:89:ASP:N	2.48	0.46
27:c:97:ASP:OD1	27:c:97:ASP:N	2.49	0.46
48:AD:130:ASP:OD1	48:AD:130:ASP:N	2.49	0.46
6:R:142:GLY:HA2	25:a:1:MET:HE1	1.98	0.45
15:X:22:ASN:HB3	15:X:25:VAL:HG22	1.97	0.45
35:O:270:LEU:HD21	35:O:273:ASP:HB2	1.98	0.45
37:BQ:1188:U:OP1	37:BQ:1210:U:O2'	2.29	0.45
52:AM:3:THR:OG1	52:AM:4:ASP:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BQ:691:A:N1	40:BS:28:C:O2'	2.42	0.45
37:BQ:1572:U:O2'	37:BQ:1573:G:O4'	2.25	0.45
1:2:460:A:O2'	8:S:27:TYR:OH	2.18	0.45
1:2:1610:G:N7	19:F:14:LYS:NZ	2.62	0.45
37:BQ:1412:G:OP1	70:BG:105:ARG:NH1	2.46	0.45
58:BH:95:ARG:HB2	58:BH:140:VAL:HG23	1.98	0.45
1:2:10:G:O2'	6:R:94:GLN:OE1	2.34	0.45
1:2:1335:U:OP1	23:J:85:ARG:NH1	2.50	0.45
5:E:41:VAL:HG22	5:E:84:ILE:HD13	1.99	0.45
37:BQ:110:G:OP2	51:AJ:73:ARG:NH1	2.43	0.45
37:BQ:439:C:O2'	37:BQ:494:G:N2	2.43	0.45
37:BQ:2196:C:O2'	37:BQ:2270:A:N3	2.39	0.45
37:BQ:2537:U:O2'	37:BQ:2538:U:O5'	2.27	0.45
49:BD:47:PRO:O	49:BD:172:GLY:N	2.49	0.45
1:2:1553:G:N1	1:2:1556:A:OP2	2.49	0.45
5:E:34:VAL:HG21	5:E:45:PHE:HB2	1.98	0.45
37:BQ:1390:A:N6	37:BQ:1418:A:O2'	2.49	0.45
38:BT:107:TYR:CZ	38:BT:138:VAL:HG11	2.52	0.45
1:2:451:A:N6	1:2:453:U:O2	2.49	0.45
1:2:458:G:OP1	28:d:109:LYS:NZ	2.38	0.45
16:D:34:THR:HA	16:D:37:VAL:HG22	1.98	0.45
24:n:5:C:OP1	83:BW:69:LYS:NZ	2.44	0.45
41:AW:108:PRO:HG2	81:AT:86:LEU:HD13	1.98	0.45
43:BE:126:ILE:O	43:BE:129:THR:OG1	2.34	0.45
54:AU:189[A]:ASP:OD1	54:AU:189[A]:ASP:N	2.50	0.45
9:B:31:GLU:OE1	9:B:35:GLN:NE2	2.50	0.45
10:T:71:THR:OG1	10:T:72:ARG:N	2.49	0.45
37:BQ:93:C:OP2	37:BQ:2764:C:O2'	2.28	0.45
1:2:623:A:O2'	1:2:624:G:OP1	2.20	0.45
5:E:19:GLY:N	21:H:93:THR:O	2.48	0.45
34:N:133:ALA:HB3	34:N:140:TYR:HB3	1.99	0.45
57:BF:7:GLN:NE2	57:BF:35:ALA:O	2.50	0.45
1:2:793:A:H5''	1:2:794:U:H5'	1.99	0.45
1:2:1742:U:O2'	1:2:1743:U:OP1	2.31	0.45
3:P:147:THR:O	3:P:162:CYS:N	2.46	0.45
8:S:11:ARG:NH2	8:S:21:ASP:O	2.47	0.45
31:f:33:LEU:HD23	31:f:81:ARG:HA	1.99	0.45
37:BQ:2540:A:N3	37:BQ:2541:U:N3	2.65	0.45
40:BS:143:U:OP1	53:AQ:38:ARG:NH2	2.49	0.45
37:BQ:651:G:O2'	37:BQ:1435:A:OP1	2.33	0.45
49:BD:54:SER:OG	49:BD:130:ASP:O	2.34	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:AJ:43:ALA:O	51:AJ:47:ALA:HA	2.17	0.45
60:BL:20:SER:HA	60:BL:23:THR:HG22	1.98	0.45
16:D:31:VAL:HA	16:D:34:THR:HG22	1.99	0.44
17:Y:56:ASP:OD1	17:Y:57:ALA:N	2.50	0.44
37:BQ:1802:C:OP1	82:BV:4:MET:N	2.50	0.44
37:BQ:1920:U:O2'	37:BQ:1932:A:N7	2.45	0.44
46:BO:74:SER:OG	46:BO:75:TYR:N	2.50	0.44
58:BH:68:HIS:O	58:BH:73:LYS:NZ	2.50	0.44
7:A:55:THR:HA	7:A:58:VAL:HG12	1.99	0.44
39:BR:101:G:N7	58:BH:52:LYS:NZ	2.63	0.44
40:BS:126:A:O2'	40:BS:129:C:N4	2.50	0.44
60:BL:56:VAL:HG12	60:BL:65:VAL:HG22	1.99	0.44
1:2:447:U:O2'	8:S:27:TYR:O	2.33	0.44
16:D:28:LEU:HA	16:D:31:VAL:HG22	1.99	0.44
37:BQ:806:A:N3	37:BQ:2812:C:O2'	2.40	0.44
37:BQ:2772:C:H4'	37:BQ:2773:C:H5'	1.99	0.44
39:BR:72:A:O2'	39:BR:74:C:OP1	2.33	0.44
46:BO:47:ARG:NH1	46:BO:183:ASP:OD2	2.49	0.44
70:BG:23:ASP:OD1	70:BG:23:ASP:N	2.50	0.44
1:2:1027:A:OP1	1:2:1789:G:O2'	2.35	0.44
19:F:50:GLU:OE2	19:F:82:ARG:NH2	2.48	0.44
7:A:32:GLU:OE2	7:A:65:ARG:NH2	2.49	0.44
14:C:50:THR:HG21	14:C:57:THR:CG2	2.47	0.44
15:X:27:THR:OG1	15:X:28:SER:N	2.50	0.44
37:BQ:591:G:N2	37:BQ:612:U:OP1	2.48	0.44
42:BA:14:LEU:HA	42:BA:17:LEU:HD13	1.99	0.44
50:AG:22:SER:O	50:AG:22:SER:OG	2.36	0.44
38:BT:33:GLU:OE1	38:BT:35:GLN:NE2	2.47	0.44
75:AF:58:THR:OG1	75:AF:59:THR:N	2.51	0.44
1:2:755:A:O2'	1:2:756:A:OP1	2.34	0.44
3:P:28:ASN:OD1	3:P:46:HIS:NE2	2.48	0.44
27:c:70:LYS:HB3	27:c:93:LEU:HD22	1.99	0.44
37:BQ:760:G:O2'	37:BQ:770:G:N2	2.46	0.44
37:BQ:1493:G:OP2	37:BQ:1493:G:N2	2.48	0.44
1:2:154:G:OP2	28:d:132:ARG:NH2	2.51	0.44
1:2:229:U:OP2	1:2:230:C:N4	2.39	0.44
1:2:323:A:OP2	12:V:10:LYS:NZ	2.39	0.44
1:2:1252:C:OP2	34:N:118:ARG:NE	2.46	0.44
37:BQ:1268:G:O2'	37:BQ:1269:U:O2	2.36	0.44
37:BQ:3154:C:N3	37:BQ:3157:U:O4	2.51	0.44
58:BH:109:ASP:OD2	58:BH:113:ARG:NH1	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Q:5:LYS:NZ	18:Z:51:ASP:OD2	2.51	0.43
4:Q:168:ILE:HG12	4:Q:197:ILE:HD12	2.00	0.43
6:R:108:ASN:OD1	6:R:108:ASN:N	2.49	0.43
22:I:144:GLU:OE2	22:I:144:GLU:N	2.51	0.43
37:BQ:406:G:OP1	37:BQ:1415:U:O2'	2.33	0.43
37:BQ:2584:G:O2'	47:AA:240:ASN:OD1	2.36	0.43
8:S:100:ARG:HG2	8:S:102:VAL:HG13	2.00	0.43
17:Y:35:GLU:HA	17:Y:38:VAL:HG22	2.00	0.43
17:Y:87:ASP:OD1	17:Y:87:ASP:N	2.49	0.43
1:2:647:G:H22	1:2:687:G:H1	1.66	0.43
1:2:1611:A:O2'	9:B:95:ASN:O	2.35	0.43
28:d:38:ASP:OD1	28:d:38:ASP:N	2.52	0.43
37:BQ:2897:A:OP2	78:AO:124:LYS:NZ	2.51	0.43
40:BS:70:G:O2'	40:BS:87:G:N2	2.52	0.43
41:AW:95:SER:O	41:AW:100:ASN:ND2	2.45	0.43
1:2:639:U:OP1	11:U:112:ARG:NH2	2.49	0.43
1:2:1553:G:O2'	32:M:14:TYR:OH	2.26	0.43
1:2:1681:A:H2	1:2:1720:G:H21	1.66	0.43
7:A:74:GLN:NE2	7:A:79:TYR:O	2.45	0.43
18:Z:31:THR:HG22	18:Z:38:THR:HA	1.99	0.43
37:BQ:728:G:H5''	56:BB:43:PRO:HB2	2.01	0.43
37:BQ:3139:A:OP1	42:BA:274:SER:OG	2.29	0.43
44:BI:77:ALA:O	44:BI:108:ARG:NH1	2.49	0.43
64:AK:77:LYS:NZ	77:AL:31:THR:CG2	2.81	0.43
1:2:25:C:H5'	1:2:26:A:H5'	2.01	0.43
37:BQ:620:U:OP1	55:AX:167:ARG:NH2	2.51	0.43
37:BQ:1307:G:O2'	37:BQ:1308:A:OP2	2.25	0.43
37:BQ:2206:G:O2'	37:BQ:2208:A:N6	2.43	0.43
37:BQ:3110:C:O3'	48:AD:155:SER:OG	2.28	0.43
5:E:90:ILE:HD11	5:E:112:LEU:HD21	2.01	0.43
31:f:31:TYR:HE2	31:f:33:LEU:HD21	1.83	0.43
37:BQ:59:G:H2'	40:BS:33:A:H2'	2.01	0.43
42:BA:163:HIS:ND1	42:BA:164:THR:O	2.51	0.43
50:AG:36:VAL:HG22	50:AG:120:ILE:HD12	2.00	0.43
57:BF:68:GLN:OE1	57:BF:71:ARG:NH2	2.49	0.43
58:BH:90:MET:HE1	58:BH:114:HIS:CE1	2.54	0.43
1:2:487:G:N1	1:2:501:U:C2	2.87	0.43
3:P:150:ASP:OD2	3:P:165:ARG:NH2	2.51	0.43
71:BK:16:TYR:OH	71:BK:89:LEU:O	2.33	0.43
83:BW:57:GLN:HE21	83:BW:57:GLN:HB3	1.58	0.43
18:Z:29:HIS:HB3	18:Z:41:ARG:HA	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:O:69:GLN:N	35:O:83:ALA:O	2.47	0.43
37:BQ:1055:A:N3	39:BR:81:U:O2'	2.52	0.43
37:BQ:2162:U:OP1	41:AW:234:LYS:NZ	2.50	0.43
38:BT:185:MET:HA	38:BT:187:VAL:HG13	2.01	0.43
71:BK:37:THR:HG23	71:BK:40:ASP:H	1.82	0.43
37:BQ:661:G:N7	66:AR:25:HIS:ND1	2.64	0.43
37:BQ:769:G:O2'	51:AJ:168:ARG:NH1	2.50	0.43
37:BQ:3116:G:N2	37:BQ:3116:G:OP1	2.52	0.43
37:BQ:3140:G:N7	42:BA:28:ARG:NH2	2.65	0.43
41:AW:142:ASP:OD1	41:AW:142:ASP:N	2.51	0.43
4:Q:110:LEU:O	4:Q:114:VAL:HG12	2.19	0.43
16:D:36:LEU:HB3	16:D:41:LEU:HD13	2.01	0.43
22:I:136:ALA:HA	22:I:139:THR:HG22	2.00	0.43
35:O:76:ASP:OD1	35:O:76:ASP:N	2.51	0.43
37:BQ:1385:C:O2	45:BM:2:THR:N	2.51	0.43
37:BQ:3174:A:OP1	71:BK:97:SER:OG	2.24	0.43
42:BA:10:ARG:NH1	42:BA:14:LEU:HD21	2.33	0.43
21:H:26:ILE:HG13	21:H:31:ALA:HB2	2.00	0.42
27:c:98:GLU:N	27:c:100:ASP:OD1	2.52	0.42
43:BE:237:GLN:O	43:BE:246:ARG:NH1	2.52	0.42
50:AG:15:GLU:OE2	50:AG:132:ASN:ND2	2.51	0.42
80:AP:2:VAL:N	80:AP:90:HIS:O	2.52	0.42
1:2:1678:A:OP1	12:V:59:ARG:NH1	2.52	0.42
35:O:96:THR:O	35:O:96:THR:OG1	2.32	0.42
36:L:11:LYS:NZ	36:L:51:ASN:OD1	2.52	0.42
37:BQ:2294:U:OP2	61:AB:71:LYS:NZ	2.52	0.42
41:AW:114:SER:N	41:AW:165:VAL:O	2.51	0.42
49:BD:182:LEU:HA	49:BD:185:ARG:HG2	2.00	0.42
56:BB:131:ALA:HB1	56:BB:135:GLN:H	1.84	0.42
69:BC:36:ILE:HD12	69:BC:59:ILE:HD11	2.00	0.42
1:2:334:G:O6	12:V:5:ARG:NH2	2.52	0.42
39:BR:7:G:OP1	44:BI:33:ARG:NH1	2.51	0.42
39:BR:29:C:O2'	39:BR:51:A:N1	2.46	0.42
43:BE:328:ASN:OD1	46:BO:48:ASN:ND2	2.52	0.42
44:BI:234:ASP:OD1	44:BI:234:ASP:N	2.52	0.42
49:BD:169:LYS:NZ	59:BJ:158:THR:OG1	2.52	0.42
1:2:1267:G:OP1	1:2:1435:G:N2	2.52	0.42
1:2:1478:G:OP1	22:I:39:THR:OG1	2.38	0.42
28:d:12:VAL:HG12	28:d:23:PHE:HB3	2.01	0.42
37:BQ:1480:G:O2'	37:BQ:1871:U:O4	2.36	0.42
5:E:28:MET:HE1	5:E:36:LEU:HD21	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:C:72:GLY:O	14:C:76:LEU:HD23	2.19	0.42
19:F:95:LYS:O	35:O:59:ARG:NH1	2.48	0.42
46:BO:149:TYR:OH	46:BO:182:ASP:OD1	2.33	0.42
53:AQ:119:TYR:OH	53:AQ:131:GLU:OE1	2.29	0.42
15:X:132:SER:O	15:X:136:ARG:NH1	2.51	0.42
22:I:65:ILE:HG12	22:I:71:VAL:HG22	2.01	0.42
35:O:83:ALA:HB2	35:O:113:VAL:HB	2.00	0.42
37:BQ:1405:U:OP2	70:BG:59:SER:OG	2.35	0.42
37:BQ:2553:U:C4	72:BN:95:ILE:HG22	2.54	0.42
39:BR:53:U:O2'	39:BR:55:A:N7	2.50	0.42
53:AQ:46:ASP:OD1	53:AQ:46:ASP:N	2.53	0.42
73:BP:76:GLN:O	73:BP:81:ARG:NH2	2.47	0.42
1:2:651:G:O6	1:2:652:G:N1	2.52	0.42
1:2:1482:C:N4	1:2:1524:A:OP2	2.45	0.42
9:B:130:ILE:HA	9:B:133:VAL:HG22	2.02	0.42
21:H:49:LYS:NZ	21:H:80:LYS:O	2.52	0.42
30:e:24:VAL:HG11	30:e:71:LEU:HD12	2.02	0.42
43:BE:261:VAL:HG23	43:BE:262:TRP:CD1	2.55	0.42
47:AA:160:ILE:O	47:AA:164:VAL:HG13	2.19	0.42
52:AM:113:THR:OG1	52:AM:114:ASP:N	2.52	0.42
1:2:896:U:O2	18:Z:41:ARG:NH1	2.53	0.42
37:BQ:784:A:OP2	56:BB:69:ARG:NH1	2.52	0.42
38:BT:15:GLU:OE2	38:BT:181:ASN:ND2	2.47	0.42
39:BR:5:G:OP2	44:BI:27:LYS:NZ	2.53	0.42
43:BE:27:SER:O	43:BE:279:HIS:NE2	2.44	0.42
45:BM:54:TYR:HA	45:BM:65:VAL:HG12	2.01	0.42
48:AD:22:SER:OG	48:AD:39:LYS:NZ	2.52	0.42
1:2:742:U:O2	11:U:107:ARG:NH2	2.49	0.42
1:2:1615:C:OP1	9:B:81:ARG:NH2	2.53	0.42
9:B:94:THR:HG22	9:B:114:ILE:HG13	2.01	0.42
30:e:27:SER:O	30:e:27:SER:OG	2.33	0.42
35:O:39:ASP:OD1	35:O:41:THR:OG1	2.38	0.42
36:L:19:THR:HG22	36:L:20:GLY:H	1.84	0.42
42:BA:66:LYS:O	42:BA:70:ARG:NH2	2.53	0.42
48:AD:93:VAL:HG13	78:AO:78:ILE:HG21	2.01	0.42
6:R:139:ILE:HD12	6:R:218:ILE:HB	2.01	0.42
25:a:58:TYR:OH	25:a:62:ARG:NH1	2.53	0.42
35:O:217:ASP:OD1	35:O:217:ASP:N	2.52	0.42
37:BQ:2525:G:O5'	41:AW:37:ARG:NH1	2.52	0.42
42:BA:35:ASP:OD1	42:BA:36:ASP:N	2.53	0.42
52:AM:91:CYS:SG	52:AM:92:GLU:N	2.92	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:BW:35:ASP:O	83:BW:37:SER:N	2.53	0.42
1:2:568:G:N7	27:c:69:ARG:NH1	2.65	0.41
1:2:623:A:H3'	1:2:624:G:H5''	2.02	0.41
10:T:2:LYS:HB3	10:T:108:VAL:HG22	2.02	0.41
37:BQ:1613:A:OP1	76:AI:51:LEU:N	2.45	0.41
48:AD:41:ILE:HD13	48:AD:71:VAL:HB	2.02	0.41
1:2:322:G:O2'	12:V:10:LYS:NZ	2.53	0.41
1:2:424:C:O2'	1:2:426:G:OP1	2.21	0.41
37:BQ:1914:G:O2'	57:BF:82:LYS:O	2.36	0.41
38:BT:174:MET:HB3	38:BT:177:ASP:HB2	2.02	0.41
51:AJ:107:GLU:OE1	51:AJ:107:GLU:N	2.46	0.41
1:2:174:U:H3	1:2:266:A:H62	1.68	0.41
11:U:40:PRO:HB3	57:BF:185:LEU:HD11	2.03	0.41
22:I:37:VAL:HG21	22:I:100:ILE:HD11	2.01	0.41
69:BC:44:MET:O	69:BC:77:ARG:NH1	2.53	0.41
73:BP:102:GLU:OE1	73:BP:102:GLU:N	2.46	0.41
1:2:1406:A:OP2	9:B:80:LYS:NZ	2.54	0.41
6:R:81:MET:HB2	6:R:101:VAL:HG13	2.03	0.41
27:c:59:ILE:HD12	27:c:71:CYS:HB2	2.03	0.41
29:K:43:ASP:OD1	29:K:43:ASP:N	2.52	0.41
36:L:36:THR:OG1	36:L:37:SER:N	2.53	0.41
37:BQ:36:C:OP2	53:AQ:83:LYS:NZ	2.42	0.41
37:BQ:2722:U:O2'	59:BJ:88:ARG:O	2.32	0.41
37:BQ:3043:C:OP1	61:AB:45:ARG:NE	2.54	0.41
38:BT:205:VAL:HG13	38:BT:213:ALA:HA	2.03	0.41
48:AD:173:ARG:NH1	78:AO:125:LYS:O	2.46	0.41
68:AY:12:GLN:OE1	68:AY:12:GLN:N	2.52	0.41
1:2:487:G:N1	1:2:501:U:N3	2.67	0.41
1:2:375:U:OP1	27:c:23:ARG:NH2	2.53	0.41
37:BQ:448:U:O2	37:BQ:488:U:O2'	2.28	0.41
37:BQ:2208:A:H2	37:BQ:2236:G:H22	1.68	0.41
37:BQ:2727:A:OP2	37:BQ:2728:G:N2	2.49	0.41
45:BM:176:PHE:O	52:AM:113:THR:OG1	2.24	0.41
1:2:1523:G:OP2	1:2:1523:G:N2	2.43	0.41
1:2:1597:A:OP2	32:M:32:ARG:NH2	2.54	0.41
6:R:147:ASN:ND2	6:R:147:ASN:O	2.54	0.41
56:BB:27:LYS:HA	56:BB:30:VAL:HG12	2.02	0.41
14:C:46:LEU:O	14:C:50:THR:HG23	2.21	0.41
37:BQ:525:C:OP2	52:AM:77:ARG:NH2	2.49	0.41
41:AW:127:ALA:HB2	41:AW:134:VAL:HG23	2.02	0.41
61:AB:38:ALA:HB3	61:AB:59:MET:HB2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:AH:62:VAL:HG23	63:AH:63:ILE:HG13	2.03	0.41
76:AI:32:ASN:OD1	76:AI:33:LYS:N	2.48	0.41
1:2:178:U:OP1	10:T:191:ARG:NH2	2.49	0.41
1:2:420:A:OP1	10:T:96:SER:OG	2.20	0.41
1:2:657:U:C2	1:2:677:G:C2	3.09	0.41
1:2:1217:A:O3'	14:C:44:LYS:NZ	2.50	0.41
1:2:1218:G:N2	1:2:1444:A:OP2	2.29	0.41
1:2:1692:G:N1	1:2:1710:U:N3	2.68	0.41
6:R:116:LYS:HG2	6:R:127:ALA:HB3	2.03	0.41
8:S:112:HIS:NE2	8:S:237:SER:O	2.54	0.41
11:U:163:ASP:N	11:U:163:ASP:OD1	2.53	0.41
18:Z:16:VAL:HG12	18:Z:80:HIS:HB2	2.03	0.41
18:Z:107:ARG:NH1	36:L:60:GLU:OE2	2.54	0.41
26:b:89:TRP:O	26:b:93:LEU:HD23	2.20	0.41
44:BI:236:LEU:HA	44:BI:239:ILE:HG12	2.03	0.41
51:AJ:162:ASN:OD1	51:AJ:162:ASN:N	2.51	0.41
66:AR:130:VAL:HG11	66:AR:145:VAL:HG11	2.01	0.41
68:AY:17:VAL:HG11	68:AY:92:ILE:HD12	2.03	0.41
82:BV:20:ARG:HA	82:BV:23:VAL:HG12	2.02	0.41
16:D:108:ARG:O	16:D:110:GLY:N	2.54	0.41
37:BQ:576:C:OP1	46:BO:241:LYS:NZ	2.50	0.41
37:BQ:2600:C:OP1	53:AQ:93:LYS:NZ	2.45	0.41
1:2:1585:U:OP1	19:F:125:GLU:N	2.45	0.40
37:BQ:1389:G:OP1	70:BG:104:ASN:ND2	2.48	0.40
37:BQ:3163:A:N6	37:BQ:3288:G:O6	2.54	0.40
57:BF:43:LYS:O	57:BF:47:ASN:ND2	2.54	0.40
1:2:206:A:OP1	8:S:133:LYS:NZ	2.50	0.40
1:2:1486:G:N2	1:2:1522:U:O4	2.55	0.40
1:2:1699:G:C6	1:2:1703:C:N3	2.89	0.40
10:T:14:LYS:HB3	10:T:124:LEU:HD21	2.02	0.40
37:BQ:942:U:OP1	37:BQ:1434:G:C8	2.74	0.40
1:2:1420:C:OP1	32:M:54:LYS:NZ	2.50	0.40
27:c:125:VAL:HG12	27:c:126:LYS:HG3	2.03	0.40
35:O:70:ASP:OD1	35:O:83:ALA:HB3	2.21	0.40
37:BQ:1312:C:O2'	54:AU:83[A]:ALA:O	2.39	0.40
37:BQ:2799:A:O2'	66:AR:42:ARG:NH1	2.54	0.40
43:BE:326:ARG:O	46:BO:41:ARG:NH2	2.52	0.40
77:AL:24:PRO:HD2	77:AL:27:ILE:HD12	2.02	0.40
1:2:322:G:HO2'	1:2:323:A:P	2.45	0.40
1:2:1273:G:H4'	1:2:1274:C:H3'	2.03	0.40
12:V:162:ALA:O	37:BQ:3352:U:O2'	2.34	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BQ:354:U:O2'	77:AL:40:LYS:NZ	2.50	0.40
37:BQ:520:U:OP2	46:BO:70:LYS:NZ	2.49	0.40
37:BQ:707:U:OP1	37:BQ:780:A:O2'	2.24	0.40
38:BT:136:THR:O	38:BT:138:VAL:N	2.54	0.40
45:BM:76:LEU:N	45:BM:138:GLN:OE1	2.54	0.40
59:BJ:91:LEU:HD12	59:BJ:96:ILE:HD11	2.04	0.40
1:2:1297:G:N2	1:2:1300:A:OP2	2.41	0.40
37:BQ:1264:G:N2	37:BQ:1265:U:O4	2.53	0.40
37:BQ:1427:U:OP2	66:AR:4:ARG:NH1	2.46	0.40
37:BQ:1447:G:OP1	55:AX:65:SER:OG	2.29	0.40
37:BQ:2454:G:O5'	37:BQ:2484:A:N6	2.55	0.40
37:BQ:2504:U:HO2'	37:BQ:2505:U:P	2.35	0.40
38:BT:38:LEU:HD21	38:BT:167:VAL:HB	2.03	0.40
56:BB:125:ASP:OD1	56:BB:125:ASP:N	2.54	0.40
65:AN:5:LEU:HD11	68:AY:35:ARG:HD2	2.03	0.40
72:BN:79:SER:OG	72:BN:80:ARG:NH1	2.53	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	
3	P	204/206 (99%)	188 (92%)	16 (8%)	0	100	100
4	Q	222/232 (96%)	202 (91%)	20 (9%)	0	100	100
5	E	115/117 (98%)	107 (93%)	8 (7%)	0	100	100
6	R	214/216 (99%)	195 (91%)	19 (9%)	0	100	100
7	A	220/222 (99%)	209 (95%)	11 (5%)	0	100	100
8	S	256/258 (99%)	237 (93%)	19 (7%)	0	100	100
9	B	204/206 (99%)	186 (91%)	18 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	T	226/228 (99%)	212 (94%)	14 (6%)	0	100	100
11	U	182/184 (99%)	171 (94%)	11 (6%)	0	100	100
12	V	183/187 (98%)	174 (95%)	9 (5%)	0	100	100
13	W	182/184 (99%)	174 (96%)	8 (4%)	0	100	100
14	C	90/92 (98%)	75 (83%)	15 (17%)	0	100	100
15	X	140/142 (99%)	131 (94%)	9 (6%)	0	100	100
16	D	119/121 (98%)	93 (78%)	23 (19%)	3 (2%)	4	16
17	Y	148/150 (99%)	141 (95%)	7 (5%)	0	100	100
18	Z	125/127 (98%)	113 (90%)	12 (10%)	0	100	100
19	F	139/141 (99%)	130 (94%)	8 (6%)	1 (1%)	18	47
20	G	117/125 (94%)	111 (95%)	6 (5%)	0	100	100
21	H	143/145 (99%)	137 (96%)	6 (4%)	0	100	100
22	I	141/143 (99%)	136 (96%)	5 (4%)	0	100	100
23	J	98/100 (98%)	90 (92%)	8 (8%)	0	100	100
25	a	85/87 (98%)	78 (92%)	7 (8%)	0	100	100
26	b	127/129 (98%)	116 (91%)	11 (9%)	0	100	100
27	c	142/144 (99%)	129 (91%)	12 (8%)	1 (1%)	18	47
28	d	132/134 (98%)	127 (96%)	5 (4%)	0	100	100
29	K	80/82 (98%)	72 (90%)	8 (10%)	0	100	100
30	e	95/97 (98%)	89 (94%)	6 (6%)	0	100	100
31	f	79/81 (98%)	72 (91%)	7 (9%)	0	100	100
32	M	51/53 (96%)	51 (100%)	0	0	100	100
33	g	58/60 (97%)	51 (88%)	7 (12%)	0	100	100
34	N	71/73 (97%)	50 (70%)	21 (30%)	0	100	100
35	O	310/312 (99%)	276 (89%)	34 (11%)	0	100	100
36	L	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
38	BT	202/204 (99%)	140 (69%)	62 (31%)	0	100	100
41	AW	249/251 (99%)	234 (94%)	15 (6%)	0	100	100
42	BA	384/386 (100%)	358 (93%)	26 (7%)	0	100	100
43	BE	359/361 (99%)	331 (92%)	27 (8%)	1 (0%)	36	66
44	BI	292/294 (99%)	276 (94%)	16 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	BM	163/175 (93%)	154 (94%)	9 (6%)	0	100	100
46	BO	220/222 (99%)	208 (94%)	12 (6%)	0	100	100
47	AA	231/233 (99%)	218 (94%)	13 (6%)	0	100	100
48	AD	189/191 (99%)	175 (93%)	14 (7%)	0	100	100
49	BD	216/218 (99%)	206 (95%)	10 (5%)	0	100	100
50	AG	167/169 (99%)	156 (93%)	10 (6%)	1 (1%)	21	51
51	AJ	191/193 (99%)	174 (91%)	16 (8%)	1 (0%)	24	55
52	AM	134/136 (98%)	125 (93%)	9 (7%)	0	100	100
53	AQ	201/203 (99%)	188 (94%)	13 (6%)	0	100	100
54	AU	195/197 (99%)	192 (98%)	3 (2%)	0	100	100
55	AX	181/183 (99%)	170 (94%)	11 (6%)	0	100	100
56	BB	183/185 (99%)	171 (93%)	12 (7%)	0	100	100
57	BF	186/188 (99%)	184 (99%)	2 (1%)	0	100	100
58	BH	169/171 (99%)	166 (98%)	3 (2%)	0	100	100
59	BJ	157/159 (99%)	150 (96%)	7 (4%)	0	100	100
60	BL	98/100 (98%)	90 (92%)	8 (8%)	0	100	100
61	AB	134/136 (98%)	130 (97%)	4 (3%)	0	100	100
62	AE	124/126 (98%)	112 (90%)	12 (10%)	0	100	100
63	AH	119/121 (98%)	115 (97%)	4 (3%)	0	100	100
64	AK	123/125 (98%)	119 (97%)	4 (3%)	0	100	100
65	AN	133/135 (98%)	127 (96%)	6 (4%)	0	100	100
66	AR	146/148 (99%)	134 (92%)	12 (8%)	0	100	100
67	AV	56/58 (97%)	49 (88%)	6 (11%)	1 (2%)	6	23
68	AY	94/96 (98%)	94 (100%)	0	0	100	100
69	BC	107/109 (98%)	98 (92%)	9 (8%)	0	100	100
70	BG	125/127 (98%)	123 (98%)	2 (2%)	0	100	100
71	BK	104/106 (98%)	101 (97%)	3 (3%)	0	100	100
72	BN	110/112 (98%)	106 (96%)	4 (4%)	0	100	100
73	BP	117/119 (98%)	112 (96%)	5 (4%)	0	100	100
74	AC	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
75	AF	79/81 (98%)	75 (95%)	4 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
76	AI	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
77	AL	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
78	AO	50/52 (96%)	47 (94%)	3 (6%)	0	100	100
79	AS	23/25 (92%)	23 (100%)	0	0	100	100
80	AP	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
81	AT	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
82	BV	20/22 (91%)	18 (90%)	2 (10%)	0	100	100
83	BW	110/112 (98%)	105 (96%)	5 (4%)	0	100	100
All	All	11310/11490 (98%)	10528 (93%)	773 (7%)	9 (0%)	49	77

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	D	85	LYS
16	D	126	TRP
16	D	109	GLU
43	BE	4	PRO
67	AV	21	ILE
19	F	41	PRO
50	AG	8	PRO
51	AJ	61	PRO
27	c	88	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	
3	P	170/173 (98%)	170 (100%)	0	100	100
4	Q	200/205 (98%)	200 (100%)	0	100	100
5	E	95/98 (97%)	95 (100%)	0	100	100
6	R	175/175 (100%)	173 (99%)	2 (1%)	65	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	A	182/182 (100%)	182 (100%)	0	100	100
8	S	220/220 (100%)	218 (99%)	2 (1%)	70	89
9	B	172/173 (99%)	172 (100%)	0	100	100
10	T	189/195 (97%)	189 (100%)	0	100	100
11	U	163/165 (99%)	163 (100%)	0	100	100
12	V	148/149 (99%)	148 (100%)	0	100	100
13	W	156/157 (99%)	156 (100%)	0	100	100
14	C	77/85 (91%)	77 (100%)	0	100	100
15	X	126/127 (99%)	126 (100%)	0	100	100
16	D	88/98 (90%)	87 (99%)	1 (1%)	65	87
17	Y	127/127 (100%)	127 (100%)	0	100	100
18	Z	90/96 (94%)	90 (100%)	0	100	100
19	F	117/117 (100%)	117 (100%)	0	100	100
20	G	101/113 (89%)	101 (100%)	0	100	100
21	H	127/128 (99%)	127 (100%)	0	100	100
22	I	115/115 (100%)	114 (99%)	1 (1%)	70	89
23	J	93/93 (100%)	93 (100%)	0	100	100
25	a	71/74 (96%)	71 (100%)	0	100	100
26	b	110/110 (100%)	110 (100%)	0	100	100
27	c	119/119 (100%)	117 (98%)	2 (2%)	53	83
28	d	112/112 (100%)	112 (100%)	0	100	100
29	K	67/73 (92%)	66 (98%)	1 (2%)	57	84
30	e	82/83 (99%)	82 (100%)	0	100	100
31	f	70/70 (100%)	69 (99%)	1 (1%)	59	85
32	M	47/47 (100%)	47 (100%)	0	100	100
33	g	50/51 (98%)	50 (100%)	0	100	100
34	N	56/63 (89%)	56 (100%)	0	100	100
35	O	250/257 (97%)	249 (100%)	1 (0%)	84	94
36	L	55/56 (98%)	55 (100%)	0	100	100
38	BT	185/185 (100%)	183 (99%)	2 (1%)	65	87
41	AW	190/193 (98%)	190 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	BA	321/322 (100%)	320 (100%)	1 (0%)	86	95
43	BE	288/288 (100%)	288 (100%)	0	100	100
44	BI	241/243 (99%)	241 (100%)	0	100	100
45	BM	139/154 (90%)	139 (100%)	0	100	100
46	BO	186/186 (100%)	186 (100%)	0	100	100
47	AA	187/191 (98%)	186 (100%)	1 (0%)	81	93
48	AD	168/171 (98%)	168 (100%)	0	100	100
49	BD	185/185 (100%)	185 (100%)	0	100	100
50	AG	145/147 (99%)	145 (100%)	0	100	100
51	AJ	154/154 (100%)	153 (99%)	1 (1%)	78	92
52	AM	107/107 (100%)	106 (99%)	1 (1%)	70	89
53	AQ	175/175 (100%)	175 (100%)	0	100	100
54	AU	160/160 (100%)	160 (100%)	0	100	100
55	AX	138/145 (95%)	138 (100%)	0	100	100
56	BB	150/150 (100%)	150 (100%)	0	100	100
57	BF	152/153 (99%)	151 (99%)	1 (1%)	76	91
58	BH	155/155 (100%)	155 (100%)	0	100	100
59	BJ	135/136 (99%)	135 (100%)	0	100	100
60	BL	87/87 (100%)	87 (100%)	0	100	100
61	AB	104/104 (100%)	103 (99%)	1 (1%)	68	88
62	AE	56/108 (52%)	56 (100%)	0	100	100
63	AH	104/105 (99%)	103 (99%)	1 (1%)	68	88
64	AK	108/108 (100%)	107 (99%)	1 (1%)	70	89
65	AN	112/115 (97%)	112 (100%)	0	100	100
66	AR	117/118 (99%)	117 (100%)	0	100	100
67	AV	46/46 (100%)	46 (100%)	0	100	100
68	AY	81/81 (100%)	81 (100%)	0	100	100
69	BC	92/96 (96%)	92 (100%)	0	100	100
70	BG	107/109 (98%)	107 (100%)	0	100	100
71	BK	90/90 (100%)	90 (100%)	0	100	100
72	BN	95/95 (100%)	95 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
73	BP	104/104 (100%)	104 (100%)	0	100	100
74	AC	80/81 (99%)	80 (100%)	0	100	100
75	AF	67/67 (100%)	67 (100%)	0	100	100
76	AI	68/68 (100%)	68 (100%)	0	100	100
77	AL	45/45 (100%)	45 (100%)	0	100	100
78	AO	45/47 (96%)	45 (100%)	0	100	100
79	AS	22/23 (96%)	22 (100%)	0	100	100
80	AP	87/88 (99%)	87 (100%)	0	100	100
81	AT	71/71 (100%)	71 (100%)	0	100	100
82	BV	20/20 (100%)	20 (100%)	0	100	100
83	BW	109/109 (100%)	103 (94%)	6 (6%)	19	51
All	All	9498/9691 (98%)	9471 (100%)	27 (0%)	84	95

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	R	39	THR
6	R	111	VAL
8	S	69	HIS
8	S	156	VAL
16	D	136	ILE
22	I	140	LEU
27	c	74	VAL
27	c	120	VAL
29	K	29	LYS
31	f	34	ASP
35	O	266	ASP
38	BT	16	LEU
38	BT	180	VAL
42	BA	387	LEU
47	AA	158	ASP
51	AJ	58	VAL
52	AM	15	VAL
57	BF	164	LEU
61	AB	91	VAL
63	AH	107	VAL
64	AK	74	TYR
83	BW	2	SER

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Mol	Chain	Res	Type
83	BW	40	SER
83	BW	44	LYS
83	BW	57	GLN
83	BW	58	LYS
83	BW	91	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (49) such sidechains are listed below:

Mol	Chain	Res	Type
3	P	30	GLN
3	P	69	ASN
3	P	163	ASN
4	Q	199	ASN
8	S	96	ASN
8	S	216	ASN
9	B	63	GLN
9	B	66	GLN
9	B	116	HIS
10	T	176	GLN
10	T	182	GLN
10	T	197	ASN
17	Y	78	ASN
21	H	6	GLN
27	c	63	GLN
29	K	44	GLN
30	e	80	HIS
30	e	94	ASN
31	f	5	GLN
32	M	37	ASN
33	g	17	GLN
35	O	196	ASN
36	L	43	ASN
41	AW	211	HIS
43	BE	196	ASN
46	BO	37	ASN
46	BO	244	ASN
48	AD	125	ASN
49	BD	73	ASN
53	AQ	95	GLN
55	AX	55	GLN
55	AX	133	HIS
57	BF	47	ASN

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Mol	Chain	Res	Type
58	BH	122	HIS
58	BH	138	GLN
59	BJ	127	GLN
59	BJ	134	GLN
64	AK	120	GLN
65	AN	122	HIS
65	AN	127	ASN
66	AR	38	GLN
66	AR	62	HIS
70	BG	49	ASN
72	BN	98	GLN
73	BP	16	GLN
80	AP	102	GLN
83	BW	57	GLN
83	BW	62	GLN
83	BW	104	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1768/1798 (98%)	472 (26%)	39 (2%)
2	l	2/3 (66%)	0	0
24	n	74/75 (98%)	16 (21%)	0
37	BQ	3220/3223 (99%)	654 (20%)	35 (1%)
39	BR	120/121 (99%)	11 (9%)	1 (0%)
40	BS	157/158 (99%)	28 (17%)	1 (0%)
All	All	5341/5378 (99%)	1181 (22%)	76 (1%)

All (1181) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	17	C
1	2	25	C
1	2	26	A
1	2	34	G
1	2	42	G
1	2	43	A
1	2	45	U
1	2	46	A

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Mol	Chain	Res	Type
1	2	47	A
1	2	56	U
1	2	57	G
1	2	59	C
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	71	A
1	2	73	U
1	2	74	U
1	2	75	U
1	2	76	A
1	2	78	A
1	2	79	C
1	2	81	G
1	2	104	A
1	2	114	C
1	2	115	G
1	2	116	U
1	2	121	U
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	133	U
1	2	134	U
1	2	135	A
1	2	138	A
1	2	140	A
1	2	141	U
1	2	142	G
1	2	145	A
1	2	153	G
1	2	155	U
1	2	159	U
1	2	168	A

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Mol	Chain	Res	Type
1	2	171	A
1	2	176	C
1	2	178	U
1	2	179	A
1	2	180	A
1	2	185	U
1	2	186	C
1	2	187	G
1	2	188	A
1	2	191	C
1	2	192	U
1	2	193	U
1	2	194	U
1	2	195	G
1	2	216	U
1	2	217	A
1	2	218	A
1	2	223	U
1	2	224	C
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	235	G
1	2	236	A
1	2	240	U
1	2	241	U
1	2	243	G
1	2	249	U
1	2	250	C
1	2	255	U
1	2	257	A
1	2	260	U
1	2	265	A
1	2	272	U
1	2	274	G
1	2	276	C
1	2	277	U
1	2	278	U

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Mol	Chain	Res	Type
1	2	279	G
1	2	280	U
1	2	281	G
1	2	287	G
1	2	299	A
1	2	313	U
1	2	314	C
1	2	316	A
1	2	320	U
1	2	322	G
1	2	323	A
1	2	330	G
1	2	333	A
1	2	337	G
1	2	338	C
1	2	352	A
1	2	353	A
1	2	359	A
1	2	361	C
1	2	373	G
1	2	388	G
1	2	390	G
1	2	399	A
1	2	400	A
1	2	401	A
1	2	402	C
1	2	404	G
1	2	416	A
1	2	417	A
1	2	422	G
1	2	423	G
1	2	424	C
1	2	425	A
1	2	426	G
1	2	434	G
1	2	436	A
1	2	439	U
1	2	444	C
1	2	446	A
1	2	448	C
1	2	452	A
1	2	454	U

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Mol	Chain	Res	Type
1	2	460	A
1	2	468	A
1	2	471	A
1	2	477	A
1	2	482	U
1	2	483	A
1	2	485	A
1	2	486	G
1	2	487	G
1	2	489	C
1	2	491	C
1	2	492	A
1	2	493	U
1	2	494	U
1	2	496	G
1	2	498	G
1	2	499	U
1	2	500	C
1	2	502	U
1	2	505	A
1	2	506	A
1	2	507	U
1	2	510	G
1	2	511	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	556	A
1	2	557	G
1	2	558	U
1	2	559	C
1	2	565	C
1	2	568	G
1	2	572	C
1	2	579	A
1	2	580	A
1	2	594	A
1	2	595	G

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Mol	Chain	Res	Type
1	2	606	A
1	2	610	G
1	2	611	U
1	2	617	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	635	A
1	2	638	U
1	2	639	U
1	2	640	U
1	2	641	G
1	2	643	G
1	2	648	G
1	2	653	C
1	2	654	C
1	2	655	G
1	2	677	G
1	2	678	A
1	2	680	U
1	2	681	U
1	2	682	C
1	2	683	C
1	2	687	G
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	703	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

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Mol	Chain	Res	Type
1	2	712	G
1	2	713	A
1	2	714	G
1	2	728	U
1	2	729	G
1	2	730	G
1	2	731	C
1	2	732	G
1	2	733	A
1	2	734	A
1	2	736	C
1	2	737	A
1	2	738	G
1	2	739	G
1	2	741	C
1	2	742	U
1	2	743	U
1	2	756	A
1	2	765	G
1	2	766	U
1	2	767	U
1	2	774	A
1	2	775	G
1	2	778	G
1	2	779	U
1	2	780	A
1	2	781	U
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	818	C
1	2	819	G
1	2	820	U
1	2	821	U
1	2	823	G
1	2	833	U
1	2	835	U
1	2	840	U

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Mol	Chain	Res	Type
1	2	841	U
1	2	846	G
1	2	851	U
1	2	852	C
1	2	855	A
1	2	856	A
1	2	857	U
1	2	863	A
1	2	899	G
1	2	901	G
1	2	902	G
1	2	903	U
1	2	912	U
1	2	913	G
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
1	2	993	A
1	2	998	A
1	2	1004	U
1	2	1005	A
1	2	1020	A
1	2	1021	C
1	2	1024	U
1	2	1026	A
1	2	1028	C
1	2	1039	A
1	2	1052	U
1	2	1053	G
1	2	1058	U
1	2	1059	U
1	2	1060	U
1	2	1061	A

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Mol	Chain	Res	Type
1	2	1063	U
1	2	1076	A
1	2	1080	U
1	2	1081	A
1	2	1082	C
1	2	1092	A
1	2	1093	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	1202	A
1	2	1208	A
1	2	1216	C
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
1	2	1246	C
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

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Mol	Chain	Res	Type
1	2	1291	G
1	2	1301	U
1	2	1314	U
1	2	1315	U
1	2	1316	G
1	2	1318	G
1	2	1321	A
1	2	1322	A
1	2	1325	A
1	2	1337	A
1	2	1344	A
1	2	1345	A
1	2	1346	A
1	2	1348	A
1	2	1349	G
1	2	1354	G
1	2	1355	C
1	2	1363	U
1	2	1364	G
1	2	1367	G
1	2	1370	U
1	2	1371	A
1	2	1372	U
1	2	1373	C
1	2	1382	A
1	2	1383	G
1	2	1389	C
1	2	1390	U
1	2	1398	U
1	2	1399	C
1	2	1400	A
1	2	1402	G
1	2	1414	U
1	2	1425	A
1	2	1427	A
1	2	1431	C
1	2	1432	U
1	2	1433	G
1	2	1445	G
1	2	1446	A
1	2	1459	C
1	2	1460	A

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Mol	Chain	Res	Type
1	2	1466	G
1	2	1469	A
1	2	1470	C
1	2	1471	A
1	2	1472	C
1	2	1479	A
1	2	1486	G
1	2	1491	U
1	2	1492	A
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	1531	G
1	2	1535	U
1	2	1537	C
1	2	1540	G
1	2	1542	G
1	2	1543	A
1	2	1554	U
1	2	1557	U
1	2	1558	U
1	2	1559	A
1	2	1570	A
1	2	1572	G
1	2	1573	A
1	2	1574	G
1	2	1575	G
1	2	1576	A
1	2	1577	A
1	2	1583	A
1	2	1584	G
1	2	1590	G
1	2	1601	G

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Mol	Chain	Res	Type
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	1678	A
1	2	1688	U
1	2	1693	A
1	2	1700	C
1	2	1701	A
1	2	1703	C
1	2	1708	U
1	2	1709	C
1	2	1715	G
1	2	1716	C
1	2	1717	G
1	2	1743	U
1	2	1753	A
1	2	1756	A
1	2	1757	G
1	2	1760	G
1	2	1762	A
1	2	1766	A
1	2	1767	G
1	2	1769	U
1	2	1771	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	1796	C
1	2	1798	U
1	2	1799	U

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Mol	Chain	Res	Type
24	n	13	C
24	n	14	A
24	n	16	H2U
24	n	19	G
24	n	21	A
24	n	22	G
24	n	37	T6A
24	n	46	7MG
24	n	47	H2U
24	n	48	5MC
24	n	56	C
24	n	59	A
24	n	63	G
24	n	64	A
24	n	65	G
24	n	76	A
37	BQ	6	A
37	BQ	13	A
37	BQ	14	U
37	BQ	26	A
37	BQ	40	A
37	BQ	43	A
37	BQ	49	A
37	BQ	59	G
37	BQ	60	A
37	BQ	65	A
37	BQ	66	A
37	BQ	77	A
37	BQ	92	G
37	BQ	109	A
37	BQ	110	G
37	BQ	111	C
37	BQ	116	A
37	BQ	121	A
37	BQ	122	A
37	BQ	133	U
37	BQ	134	U
37	BQ	135	C
37	BQ	136	G
37	BQ	150	A
37	BQ	156	G
37	BQ	157	A

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Mol	Chain	Res	Type
37	BQ	165	A
37	BQ	166	C
37	BQ	172	G
37	BQ	173	G
37	BQ	187	A
37	BQ	190	U
37	BQ	191	U
37	BQ	192	C
37	BQ	200	C
37	BQ	206	G
37	BQ	210	U
37	BQ	213	A
37	BQ	218	G
37	BQ	219	A
37	BQ	234	G
37	BQ	240	U
37	BQ	241	G
37	BQ	242	C
37	BQ	243	G
37	BQ	245	U
37	BQ	249	U
37	BQ	252	U
37	BQ	269	G
37	BQ	283	G
37	BQ	286	U
37	BQ	295	A
37	BQ	305	U
37	BQ	311	C
37	BQ	323	A
37	BQ	329	U
37	BQ	337	G
37	BQ	339	C
37	BQ	350	C
37	BQ	351	A
37	BQ	374	A
37	BQ	376	G
37	BQ	390	G
37	BQ	398	A
37	BQ	399	A
37	BQ	401	U
37	BQ	402	A
37	BQ	403	C

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Mol	Chain	Res	Type
37	BQ	421	G
37	BQ	422	A
37	BQ	439	C
37	BQ	440	A
37	BQ	441	U
37	BQ	442	G
37	BQ	443	G
37	BQ	444	U
37	BQ	445	G
37	BQ	446	U
37	BQ	447	U
37	BQ	448	U
37	BQ	450	G
37	BQ	451	U
37	BQ	487	U
37	BQ	488	U
37	BQ	489	U
37	BQ	490	C
37	BQ	491	A
37	BQ	494	G
37	BQ	503	C
37	BQ	517	G
37	BQ	518	G
37	BQ	521	A
37	BQ	523	A
37	BQ	535	G
37	BQ	543	C
37	BQ	544	C
37	BQ	546	C
37	BQ	547	G
37	BQ	548	G
37	BQ	551	A
37	BQ	552	G
37	BQ	555	U
37	BQ	556	U
37	BQ	557	A
37	BQ	559	A
37	BQ	578	A
37	BQ	579	G
37	BQ	589	A
37	BQ	597	G
37	BQ	600	G

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Mol	Chain	Res	Type
37	BQ	604	G
37	BQ	609	G
37	BQ	611	A
37	BQ	620	U
37	BQ	621	A
37	BQ	622	A
37	BQ	637	C
37	BQ	638	C
37	BQ	649	A
37	BQ	660	A
37	BQ	667	C
37	BQ	677	A
37	BQ	681	U
37	BQ	690	A
37	BQ	691	A
37	BQ	705	A
37	BQ	712	G
37	BQ	715	A
37	BQ	716	A
37	BQ	719	U
37	BQ	720	A
37	BQ	758	C
37	BQ	763	G
37	BQ	764	U
37	BQ	765	C
37	BQ	767	U
37	BQ	776	U
37	BQ	777	U
37	BQ	780	A
37	BQ	781	G
37	BQ	785	G
37	BQ	786	A
37	BQ	799	G
37	BQ	806	A
37	BQ	817	A
37	BQ	826	G
37	BQ	830	A
37	BQ	832	G
37	BQ	848	A
37	BQ	849	C
37	BQ	850	U
37	BQ	861	C

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Mol	Chain	Res	Type
37	BQ	874	U
37	BQ	879	U
37	BQ	896	A
37	BQ	907	G
37	BQ	908	G
37	BQ	914	A
37	BQ	916	G
37	BQ	917	A
37	BQ	920	A
37	BQ	921	A
37	BQ	923	C
37	BQ	924	G
37	BQ	925	A
37	BQ	937	G
37	BQ	944	C
37	BQ	959	C
37	BQ	960	U
37	BQ	974	G
37	BQ	981	U
37	BQ	982	C
37	BQ	984	G
37	BQ	991	G
37	BQ	994	G
37	BQ	1000	C
37	BQ	1001	G
37	BQ	1002	A
37	BQ	1010	G
37	BQ	1013	G
37	BQ	1015	U
37	BQ	1017	C
37	BQ	1018	G
37	BQ	1020	G
37	BQ	1024	G
37	BQ	1028	U
37	BQ	1032	C
37	BQ	1036	A
37	BQ	1037	C
37	BQ	1041	U
37	BQ	1047	A
37	BQ	1049	C
37	BQ	1064	A
37	BQ	1065	A

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Mol	Chain	Res	Type
37	BQ	1072	G
37	BQ	1081	U
37	BQ	1083	G
37	BQ	1087	G
37	BQ	1093	A
37	BQ	1094	U
37	BQ	1095	U
37	BQ	1096	U
37	BQ	1097	G
37	BQ	1098	A
37	BQ	1102	A
37	BQ	1103	A
37	BQ	1104	G
37	BQ	1117	G
37	BQ	1131	G
37	BQ	1143	A
37	BQ	1144	U
37	BQ	1153	A
37	BQ	1155	C
37	BQ	1159	A
37	BQ	1160	C
37	BQ	1178	G
37	BQ	1180	A
37	BQ	1181	U
37	BQ	1192	C
37	BQ	1193	A
37	BQ	1196	C
37	BQ	1197	A
37	BQ	1201	C
37	BQ	1202	A
37	BQ	1208	U
37	BQ	1217	A
37	BQ	1222	G
37	BQ	1223	A
37	BQ	1225	A
37	BQ	1227	C
37	BQ	1232	C
37	BQ	1233	G
37	BQ	1235	U
37	BQ	1236	G
37	BQ	1237	G
37	BQ	1238	C

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Mol	Chain	Res	Type
37	BQ	1240	A
37	BQ	1241	U
37	BQ	1243	G
37	BQ	1245	A
37	BQ	1246	G
37	BQ	1248	C
37	BQ	1251	A
37	BQ	1253	U
37	BQ	1254	C
37	BQ	1258	U
37	BQ	1262	G
37	BQ	1263	A
37	BQ	1264	G
37	BQ	1266	G
37	BQ	1267	U
37	BQ	1268	G
37	BQ	1269	U
37	BQ	1270	A
37	BQ	1271	A
37	BQ	1272	C
37	BQ	1274	A
37	BQ	1278	A
37	BQ	1279	C
37	BQ	1285	G
37	BQ	1286	A
37	BQ	1287	A
37	BQ	1305	U
37	BQ	1307	G
37	BQ	1308	A
37	BQ	1309	U
37	BQ	1313	G
37	BQ	1330	A
37	BQ	1348	U
37	BQ	1349	G
37	BQ	1351	U
37	BQ	1352	A
37	BQ	1353	U
37	BQ	1354	G
37	BQ	1356	U
37	BQ	1357	G
37	BQ	1386	A
37	BQ	1399	A

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Mol	Chain	Res	Type
37	BQ	1400	G
37	BQ	1417	G
37	BQ	1418	A
37	BQ	1419	A
37	BQ	1421	G
37	BQ	1434	G
37	BQ	1437	C
37	BQ	1446	A
37	BQ	1450	G
37	BQ	1455	U
37	BQ	1477	A
37	BQ	1481	A
37	BQ	1482	A
37	BQ	1483	G
37	BQ	1487	G
37	BQ	1488	G
37	BQ	1496	C
37	BQ	1502	C
37	BQ	1508	C
37	BQ	1536	G
37	BQ	1539	A
37	BQ	1555	U
37	BQ	1556	C
37	BQ	1557	A
37	BQ	1560	G
37	BQ	1562	C
37	BQ	1563	C
37	BQ	1566	A
37	BQ	1567	U
37	BQ	1568	U
37	BQ	1569	U
37	BQ	1572	U
37	BQ	1573	G
37	BQ	1575	A
37	BQ	1576	G
37	BQ	1580	A
37	BQ	1581	C
37	BQ	1582	C
37	BQ	1583	A
37	BQ	1587	A
37	BQ	1590	G
37	BQ	1593	A

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Mol	Chain	Res	Type
37	BQ	1605	A
37	BQ	1607	U
37	BQ	1620	U
37	BQ	1629	U
37	BQ	1639	C
37	BQ	1642	A
37	BQ	1643	A
37	BQ	1645	U
37	BQ	1657	C
37	BQ	1683	A
37	BQ	1716	U
37	BQ	1717	U
37	BQ	1724	U
37	BQ	1725	C
37	BQ	1736	G
37	BQ	1741	A
37	BQ	1750	A
37	BQ	1751	G
37	BQ	1760	A
37	BQ	1761	C
37	BQ	1765	U
37	BQ	1766	G
37	BQ	1770	G
37	BQ	1775	G
37	BQ	1778	G
37	BQ	1780	G
37	BQ	1794	G
37	BQ	1797	A
37	BQ	1808	G
37	BQ	1814	A
37	BQ	1816	A
37	BQ	1819	U
37	BQ	1820	U
37	BQ	1821	U
37	BQ	1835	A
37	BQ	1839	A
37	BQ	1840	U
37	BQ	1841	A
37	BQ	1842	A
37	BQ	1846	C
37	BQ	1849	C
37	BQ	1866	C

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Mol	Chain	Res	Type
37	BQ	1867	A
37	BQ	1879	A
37	BQ	1880	U
37	BQ	1881	A
37	BQ	1893	A
37	BQ	1906	G
37	BQ	1952	G
37	BQ	1953	G
37	BQ	1954	G
37	BQ	2101	C
37	BQ	2102	U
37	BQ	2107	A
37	BQ	2111	G
37	BQ	2112	U
37	BQ	2113	A
37	BQ	2114	C
37	BQ	2121	G
37	BQ	2122	G
37	BQ	2131	A
37	BQ	2140	U
37	BQ	2144	A
37	BQ	2158	A
37	BQ	2169	G
37	BQ	2171	G
37	BQ	2176	U
37	BQ	2201	G
37	BQ	2204	C
37	BQ	2205	U
37	BQ	2206	G
37	BQ	2207	A
37	BQ	2209	U
37	BQ	2210	G
37	BQ	2222	A
37	BQ	2223	A
37	BQ	2225	U
37	BQ	2228	A
37	BQ	2235	C
37	BQ	2244	A
37	BQ	2249	G
37	BQ	2250	G
37	BQ	2255	A
37	BQ	2256	A

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Mol	Chain	Res	Type
37	BQ	2257	C
37	BQ	2272	G
37	BQ	2273	G
37	BQ	2274	U
37	BQ	2281	A
37	BQ	2282	U
37	BQ	2288	G
37	BQ	2306	C
37	BQ	2307	G
37	BQ	2308	C
37	BQ	2310	U
37	BQ	2313	A
37	BQ	2314	U
37	BQ	2315	G
37	BQ	2334	U
37	BQ	2335	G
37	BQ	2336	U
37	BQ	2373	A
37	BQ	2374	C
37	BQ	2375	G
37	BQ	2385	G
37	BQ	2388	U
37	BQ	2393	G
37	BQ	2397	A
37	BQ	2402	A
37	BQ	2403	G
37	BQ	2404	A
37	BQ	2411	U
37	BQ	2419	A
37	BQ	2435	G
37	BQ	2437	G
37	BQ	2439	A
37	BQ	2440	G
37	BQ	2443	A
37	BQ	2445	A
37	BQ	2450	G
37	BQ	2453	U
37	BQ	2454	G
37	BQ	2455	U
37	BQ	2456	A
37	BQ	2457	G
37	BQ	2458	A

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Mol	Chain	Res	Type
37	BQ	2459	A
37	BQ	2460	U
37	BQ	2461	A
37	BQ	2463	G
37	BQ	2467	G
37	BQ	2468	A
37	BQ	2472	U
37	BQ	2474	G
37	BQ	2475	G
37	BQ	2477	G
37	BQ	2479	C
37	BQ	2480	A
37	BQ	2486	A
37	BQ	2487	U
37	BQ	2488	A
37	BQ	2490	C
37	BQ	2491	A
37	BQ	2493	U
37	BQ	2495	C
37	BQ	2497	U
37	BQ	2498	U
37	BQ	2499	U
37	BQ	2501	U
37	BQ	2503	G
37	BQ	2505	U
37	BQ	2506	U
37	BQ	2514	U
37	BQ	2515	A
37	BQ	2526	C
37	BQ	2531	C
37	BQ	2532	U
37	BQ	2537	U
37	BQ	2538	U
37	BQ	2539	C
37	BQ	2540	A
37	BQ	2541	U
37	BQ	2542	U
37	BQ	2543	U
37	BQ	2544	U
37	BQ	2548	C
37	BQ	2549	G
37	BQ	2552	C

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Mol	Chain	Res	Type
37	BQ	2554	A
37	BQ	2561	A
37	BQ	2569	A
37	BQ	2570	U
37	BQ	2571	U
37	BQ	2572	C
37	BQ	2573	G
37	BQ	2581	U
37	BQ	2585	G
37	BQ	2589	G
37	BQ	2593	A
37	BQ	2594	C
37	BQ	2606	G
37	BQ	2607	G
37	BQ	2614	G
37	BQ	2652	U
37	BQ	2656	A
37	BQ	2674	A
37	BQ	2677	G
37	BQ	2678	A
37	BQ	2689	A
37	BQ	2691	A
37	BQ	2694	A
37	BQ	2696	A
37	BQ	2704	A
37	BQ	2714	G
37	BQ	2719	U
37	BQ	2728	G
37	BQ	2729	U
37	BQ	2737	C
37	BQ	2740	A
37	BQ	2752	U
37	BQ	2753	G
37	BQ	2755	C
37	BQ	2772	C
37	BQ	2773	C
37	BQ	2777	G
37	BQ	2778	G
37	BQ	2788	C
37	BQ	2796	G
37	BQ	2800	G
37	BQ	2801	A

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Mol	Chain	Res	Type
37	BQ	2803	A
37	BQ	2810	C
37	BQ	2814	G
37	BQ	2817	A
37	BQ	2818	U
37	BQ	2821	C
37	BQ	2834	G
37	BQ	2842	U
37	BQ	2844	C
37	BQ	2845	A
37	BQ	2849	C
37	BQ	2859	U
37	BQ	2860	U
37	BQ	2867	C
37	BQ	2871	G
37	BQ	2872	A
37	BQ	2875	U
37	BQ	2876	C
37	BQ	2887	A
37	BQ	2898	G
37	BQ	2899	C
37	BQ	2911	A
37	BQ	2923	U
37	BQ	2927	C
37	BQ	2933	A
37	BQ	2935	U
37	BQ	2936	A
37	BQ	2938	G
37	BQ	2942	C
37	BQ	2947	G
37	BQ	2957	G
37	BQ	2971	A
37	BQ	2972	G
37	BQ	2983	C
37	BQ	2992	U
37	BQ	2996	U
37	BQ	2997	G
37	BQ	3012	A
37	BQ	3056	U
37	BQ	3059	G
37	BQ	3078	U
37	BQ	3079	U

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Mol	Chain	Res	Type
37	BQ	3086	A
37	BQ	3092	C
37	BQ	3101	G
37	BQ	3104	U
37	BQ	3109	G
37	BQ	3116	G
37	BQ	3119	U
37	BQ	3122	A
37	BQ	3129	A
37	BQ	3130	A
37	BQ	3131	U
37	BQ	3138	U
37	BQ	3139	A
37	BQ	3142	A
37	BQ	3143	C
37	BQ	3151	U
37	BQ	3154	C
37	BQ	3155	U
37	BQ	3156	U
37	BQ	3157	U
37	BQ	3158	G
37	BQ	3164	C
37	BQ	3165	A
37	BQ	3170	A
37	BQ	3173	G
37	BQ	3174	A
37	BQ	3175	U
37	BQ	3176	G
37	BQ	3179	U
37	BQ	3181	C
37	BQ	3186	A
37	BQ	3187	A
37	BQ	3196	U
37	BQ	3207	U
37	BQ	3209	A
37	BQ	3217	C
37	BQ	3218	A
37	BQ	3219	G
37	BQ	3227	A
37	BQ	3228	C
37	BQ	3229	G
37	BQ	3243	A

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Mol	Chain	Res	Type
37	BQ	3245	A
37	BQ	3247	G
37	BQ	3259	U
37	BQ	3263	G
37	BQ	3269	U
37	BQ	3270	U
37	BQ	3273	A
37	BQ	3276	G
37	BQ	3281	U
37	BQ	3287	U
37	BQ	3288	G
37	BQ	3289	G
37	BQ	3294	A
37	BQ	3295	A
37	BQ	3303	G
37	BQ	3304	U
37	BQ	3307	A
37	BQ	3313	U
37	BQ	3316	A
37	BQ	3317	U
37	BQ	3318	G
37	BQ	3319	U
37	BQ	3320	A
37	BQ	3335	A
37	BQ	3341	U
37	BQ	3345	G
37	BQ	3351	U
37	BQ	3352	U
37	BQ	3353	G
37	BQ	3354	U
37	BQ	3355	U
37	BQ	3356	G
37	BQ	3369	G
37	BQ	3375	A
37	BQ	3378	C
37	BQ	3382	U
37	BQ	3383	G
37	BQ	3386	G
37	BQ	3389	U
37	BQ	3390	G
39	BR	7	G
39	BR	53	U

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Mol	Chain	Res	Type
39	BR	54	U
39	BR	55	A
39	BR	65	G
39	BR	73	C
39	BR	76	A
39	BR	99	G
39	BR	102	A
39	BR	112	G
39	BR	121	U
40	BS	23	U
40	BS	34	U
40	BS	35	C
40	BS	39	G
40	BS	48	A
40	BS	59	A
40	BS	62	C
40	BS	63	G
40	BS	80	A
40	BS	81	U
40	BS	82	U
40	BS	83	C
40	BS	84	C
40	BS	85	G
40	BS	86	U
40	BS	87	G
40	BS	90	U
40	BS	95	G
40	BS	104	A
40	BS	106	C
40	BS	111	A
40	BS	113	U
40	BS	125	U
40	BS	126	A
40	BS	138	A
40	BS	151	C
40	BS	152	G
40	BS	158	U

All (76) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	68	A

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Mol	Chain	Res	Type
1	2	77	U
1	2	139	C
1	2	141	U
1	2	224	C
1	2	278	U
1	2	280	U
1	2	313	U
1	2	322	G
1	2	352	A
1	2	387	A
1	2	400	A
1	2	539	G
1	2	541	A
1	2	555	A
1	2	609	U
1	2	639	U
1	2	640	U
1	2	705	U
1	2	711	U
1	2	755	A
1	2	765	G
1	2	819	G
1	2	912	U
1	2	928	U
1	2	1023	A
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	1573	A
1	2	1633	A
1	2	1636	C
1	2	1742	U
1	2	1791	A
37	BQ	13	A
37	BQ	239	G
37	BQ	282	G
37	BQ	439	C

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Mol	Chain	Res	Type
37	BQ	588	G
37	BQ	637	C
37	BQ	715	A
37	BQ	763	G
37	BQ	849	C
37	BQ	916	G
37	BQ	1064	A
37	BQ	1097	G
37	BQ	1307	G
37	BQ	1355	A
37	BQ	1554	U
37	BQ	1562	C
37	BQ	1716	U
37	BQ	1815	U
37	BQ	1820	U
37	BQ	2101	C
37	BQ	2112	U
37	BQ	2249	G
37	BQ	2504	U
37	BQ	2505	U
37	BQ	2525	G
37	BQ	2537	U
37	BQ	2541	U
37	BQ	3078	U
37	BQ	3121	U
37	BQ	3218	A
37	BQ	3228	C
37	BQ	3269	U
37	BQ	3316	A
37	BQ	3319	U
37	BQ	3350	C
39	BR	52	G
40	BS	85	G

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

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

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
24	2MG	n	10	24	23,26,27	2.80	8 (34%)	33,38,41	2.07	9 (27%)
24	T6A	n	37	24,84	31,34,35	1.89	8 (25%)	43,49,52	2.24	13 (30%)
24	H2U	n	47	24	18,21,22	3.72	3 (16%)	19,30,33	1.49	4 (21%)
24	5MC	n	48	24	19,22,23	3.79	8 (42%)	26,32,35	0.94	2 (7%)
24	1MA	n	58	24	21,25,26	2.99	5 (23%)	30,37,40	2.66	7 (23%)
24	M2G	n	26	24	24,27,28	2.50	9 (37%)	33,40,43	1.83	9 (27%)
24	H2U	n	16	24	18,21,22	3.61	3 (16%)	19,30,33	1.42	4 (21%)
24	7MG	n	46	24	23,26,27	3.33	10 (43%)	27,39,42	2.08	9 (33%)
24	1MG	n	9	24	23,26,27	2.91	8 (34%)	33,39,42	1.80	9 (27%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	2MG	n	10	24	-	0/9/27/28	0/3/3/3
24	T6A	n	37	24,84	-	3/23/41/42	0/3/3/3
24	H2U	n	47	24	-	6/7/38/39	0/2/2/2
24	5MC	n	48	24	-	2/7/25/26	0/2/2/2
24	1MA	n	58	24	-	0/7/25/26	0/3/3/3
24	M2G	n	26	24	-	0/11/29/30	0/3/3/3
24	H2U	n	16	24	-	0/7/38/39	0/2/2/2
24	7MG	n	46	24	-	0/7/37/38	0/3/3/3
24	1MG	n	9	24	-	2/7/25/26	0/3/3/3

All (62) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	n	47	H2U	C2-N1	12.98	1.53	1.35
24	n	16	H2U	C2-N1	12.46	1.52	1.35
24	n	48	5MC	C6-C5	9.22	1.49	1.34
24	n	58	1MA	C2-N3	8.81	1.46	1.30
24	n	46	7MG	C8-N9	8.15	1.51	1.45
24	n	9	1MG	C2-N3	7.87	1.46	1.33
24	n	58	1MA	C4-N3	7.45	1.50	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	n	10	2MG	C2-N3	7.41	1.46	1.32
24	n	47	H2U	C2-N3	6.72	1.49	1.38
24	n	16	H2U	C2-N3	6.67	1.49	1.38
24	n	48	5MC	C4-N3	6.59	1.44	1.34
24	n	46	7MG	C5-N7	6.58	1.44	1.35
24	n	10	2MG	C4-N3	6.45	1.49	1.34
24	n	48	5MC	C5-C4	6.43	1.49	1.44
24	n	26	M2G	C4-N3	6.36	1.48	1.34
24	n	9	1MG	C4-N3	6.36	1.48	1.34
24	n	9	1MG	C2-N2	6.27	1.45	1.34
24	n	48	5MC	C2-N3	6.07	1.48	1.36
24	n	26	M2G	C2-N3	5.68	1.45	1.32
24	n	26	M2G	C2-N2	5.56	1.45	1.35
24	n	37	T6A	C10-N6	5.52	1.49	1.37
24	n	10	2MG	C2-N2	5.48	1.44	1.33
24	n	46	7MG	C4-N3	5.48	1.46	1.34
24	n	46	7MG	C2-N3	5.45	1.46	1.33
24	n	16	H2U	C4-N3	5.33	1.46	1.37
24	n	47	H2U	C4-N3	5.26	1.46	1.37
24	n	37	T6A	C6-N6	5.17	1.50	1.39
24	n	10	2MG	C2-N1	4.56	1.44	1.36
24	n	48	5MC	C6-N1	4.52	1.45	1.38
24	n	58	1MA	C2-N1	4.52	1.45	1.35
24	n	46	7MG	C2-N2	4.51	1.44	1.34
24	n	48	5MC	C4-N4	4.33	1.45	1.34
24	n	48	5MC	C2-N1	4.30	1.49	1.40
24	n	46	7MG	C4-N9	4.30	1.43	1.37
24	n	9	1MG	C2-N1	4.17	1.44	1.37
24	n	58	1MA	C5-C6	4.12	1.54	1.43
24	n	37	T6A	C10-N11	3.77	1.45	1.35
24	n	46	7MG	C2-N1	3.61	1.46	1.37
24	n	26	M2G	C2-N1	3.29	1.44	1.36
24	n	46	7MG	C5-C6	3.23	1.51	1.43
24	n	9	1MG	C5-N7	-3.13	1.32	1.39
24	n	10	2MG	C5-N7	-3.09	1.32	1.39
24	n	26	M2G	C5-N7	-3.08	1.32	1.39
24	n	46	7MG	C6-N1	3.05	1.44	1.38
24	n	9	1MG	C5-C6	3.00	1.53	1.45
24	n	46	7MG	O6-C6	-2.64	1.18	1.23
24	n	48	5MC	O2-C2	-2.55	1.19	1.23
24	n	10	2MG	O6-C6	-2.53	1.18	1.23
24	n	26	M2G	O6-C6	-2.51	1.18	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	n	58	1MA	C5-N7	-2.48	1.34	1.39
24	n	26	M2G	C5-C6	2.42	1.53	1.44
24	n	26	M2G	C6-N1	2.41	1.43	1.38
24	n	10	2MG	C5-C6	2.36	1.53	1.44
24	n	37	T6A	C5-C4	-2.27	1.35	1.39
24	n	9	1MG	C4-N9	-2.16	1.32	1.38
24	n	37	T6A	C6-N1	-2.15	1.31	1.35
24	n	37	T6A	C5-N7	-2.14	1.35	1.39
24	n	26	M2G	C4-N9	-2.13	1.32	1.38
24	n	10	2MG	C6-N1	2.12	1.42	1.38
24	n	37	T6A	ODB-C13	-2.11	1.23	1.30
24	n	9	1MG	O6-C6	-2.07	1.18	1.23
24	n	37	T6A	O10-C10	-2.05	1.19	1.23

All (66) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	n	58	1MA	C1'-N9-C8	-8.28	103.20	126.73
24	n	58	1MA	C1'-N9-C4	7.29	148.03	126.49
24	n	37	T6A	N6-C10-N11	7.17	123.63	113.77
24	n	10	2MG	C2-N3-C4	6.12	119.65	112.00
24	n	37	T6A	N3-C2-N1	-5.59	120.11	128.58
24	n	10	2MG	C5-C4-N3	-5.23	120.07	128.39
24	n	37	T6A	C5-C4-N3	-5.08	119.73	126.72
24	n	9	1MG	C5-C4-N3	-4.94	120.52	128.39
24	n	26	M2G	C5-C4-N3	-4.94	120.53	128.39
24	n	58	1MA	N1-C2-N3	-4.92	120.16	126.00
24	n	46	7MG	C5-C6-N1	4.65	119.13	110.94
24	n	58	1MA	C5-C4-N3	-4.49	120.66	127.27
24	n	37	T6A	C4-C5-C6	4.24	120.31	116.78
24	n	46	7MG	C2-N3-C4	4.17	119.49	112.30
24	n	10	2MG	C2-N1-C6	-4.15	119.54	124.55
24	n	46	7MG	C4-C5-N7	4.12	110.25	105.38
24	n	26	M2G	C2-N3-C4	4.07	120.03	112.51
24	n	47	H2U	N3-C2-N1	3.92	120.58	116.65
24	n	26	M2G	C1'-N9-C8	-3.82	115.87	126.73
24	n	58	1MA	C2-N3-C4	3.73	119.83	112.53
24	n	46	7MG	C5-C4-N3	-3.72	121.14	128.13
24	n	37	T6A	N9-C8-N7	-3.59	108.84	113.94
24	n	9	1MG	C2-N3-C4	3.45	119.73	111.98
24	n	26	M2G	C1'-N9-C4	3.37	136.44	126.49
24	n	58	1MA	N9-C8-N7	-3.37	107.16	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	n	10	2MG	N1-C2-N2	3.31	119.94	116.56
24	n	37	T6A	C2-N3-C4	3.29	119.87	111.83
24	n	16	H2U	N3-C2-N1	3.27	119.93	116.65
24	n	9	1MG	N2-C2-N1	3.27	121.41	118.79
24	n	46	7MG	C5-C4-N9	3.19	110.42	106.33
24	n	37	T6A	O10-C10-N6	-3.16	118.01	123.64
24	n	9	1MG	N9-C8-N7	-3.15	107.56	113.40
24	n	47	H2U	C5-C6-N1	3.04	120.72	111.52
24	n	46	7MG	O6-C6-C5	-3.00	120.26	127.62
24	n	16	H2U	C5-C4-N3	3.00	119.88	116.69
24	n	10	2MG	N9-C4-N3	2.99	131.93	125.95
24	n	48	5MC	C5-C6-N1	-2.96	120.10	123.31
24	n	37	T6A	N3-C4-N9	2.90	132.10	127.17
24	n	26	M2G	N9-C8-N7	-2.86	108.11	113.40
24	n	9	1MG	N9-C4-N3	2.83	131.60	125.95
24	n	16	H2U	C5-C6-N1	2.79	119.95	111.52
24	n	47	H2U	C5-C4-N3	2.72	119.58	116.69
24	n	37	T6A	C5-N7-C8	2.67	107.64	103.45
24	n	26	M2G	N9-C4-N3	2.57	131.10	125.95
24	n	26	M2G	C5-C6-N1	2.57	119.78	113.25
24	n	10	2MG	C5-C6-N1	2.55	119.74	113.25
24	n	10	2MG	N9-C8-N7	-2.54	108.69	113.40
24	n	16	H2U	O2-C2-N1	-2.54	120.05	123.10
24	n	9	1MG	C5-C6-N1	2.52	119.68	115.02
24	n	46	7MG	C2-N1-C6	-2.48	120.61	125.11
24	n	26	M2G	O6-C6-C5	-2.47	120.02	126.53
24	n	46	7MG	N9-C8-N7	2.41	106.78	103.37
24	n	10	2MG	O6-C6-C5	-2.39	120.22	126.53
24	n	47	H2U	O2-C2-N1	-2.39	120.23	123.10
24	n	37	T6A	N6-C6-N1	2.35	123.62	117.54
24	n	58	1MA	C8-N7-C5	2.33	108.42	104.26
24	n	9	1MG	C8-N7-C5	2.27	108.30	104.26
24	n	37	T6A	C5-C4-N9	2.15	108.16	105.81
24	n	9	1MG	C1'-N9-C4	-2.12	120.23	126.49
24	n	9	1MG	O6-C6-C5	-2.12	119.14	124.59
24	n	10	2MG	CM2-N2-C2	-2.08	119.17	123.65
24	n	26	M2G	C8-N7-C5	2.07	107.95	104.26
24	n	37	T6A	C4-C5-N7	-2.06	108.22	110.58
24	n	46	7MG	N9-C4-N3	2.03	128.44	125.46
24	n	37	T6A	O10-C10-N11	-2.02	118.36	122.67
24	n	48	5MC	CM5-C5-C6	-2.00	120.14	122.85

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	n	47	H2U	O4'-C4'-C5'-O5'
24	n	47	H2U	C3'-C4'-C5'-O5'
24	n	47	H2U	O4'-C1'-N1-C6
24	n	47	H2U	C2'-C1'-N1-C6
24	n	48	5MC	O4'-C4'-C5'-O5'
24	n	47	H2U	O4'-C1'-N1-C2
24	n	47	H2U	C2'-C1'-N1-C2
24	n	48	5MC	C3'-C4'-C5'-O5'
24	n	37	T6A	C3'-C4'-C5'-O5'
24	n	37	T6A	O4'-C4'-C5'-O5'
24	n	9	1MG	C2'-C1'-N9-C4
24	n	9	1MG	C2'-C1'-N9-C8
24	n	37	T6A	N11-C12-C13-ODB

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	n	16	H2U	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 335 ligands modelled in this entry, 334 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
86	SPD	BQ	3621	-	9,9,9	0.29	0	8,8,8	0.60	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
86	SPD	BQ	3621	-	-	6/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
86	BQ	3621	SPD	C3-C4-C5-N6
86	BQ	3621	SPD	N6-C7-C8-C9
86	BQ	3621	SPD	C2-C3-C4-C5
86	BQ	3621	SPD	C4-C5-N6-C7
86	BQ	3621	SPD	C7-C8-C9-N10
86	BQ	3621	SPD	C8-C7-N6-C5

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
86	BQ	3621	SPD	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
37	BQ	2
12	V	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BQ	1955:U	O3'	2093:A	P	26.76
1	V	123:LYS	C	135:LYS	N	21.11
1	BQ	451:U	O3'	486:A	P	9.87

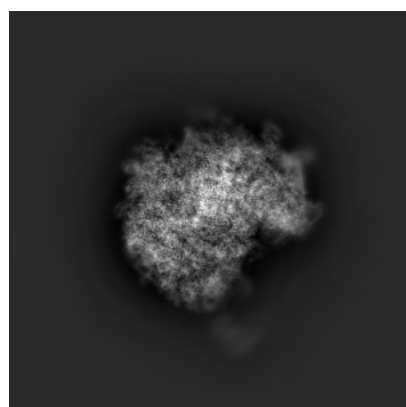
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10431. These allow visual inspection of the internal detail of the map and identification of artifacts.

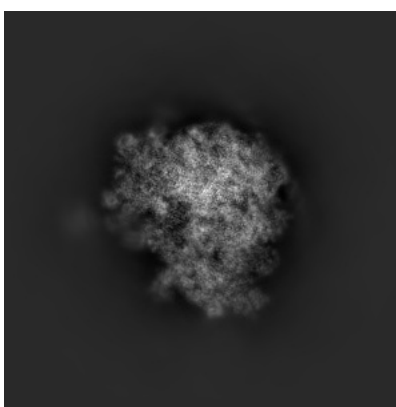
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

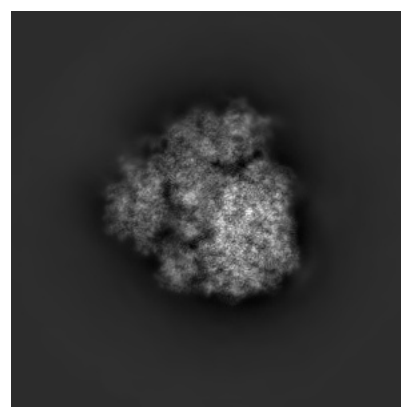
6.1.1 Primary map



X



Y

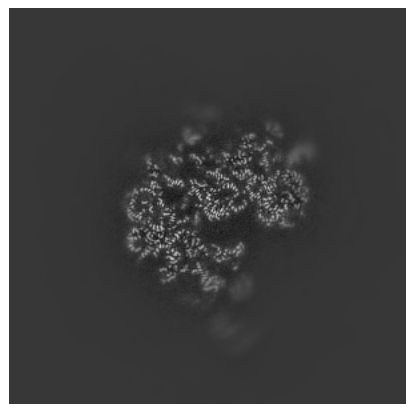


Z

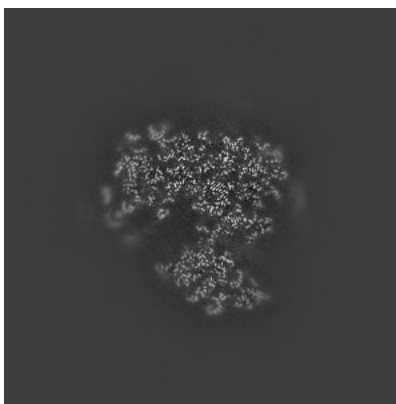
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

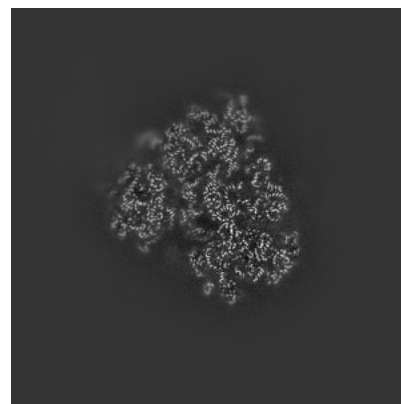
6.2.1 Primary map



X Index: 240



Y Index: 240

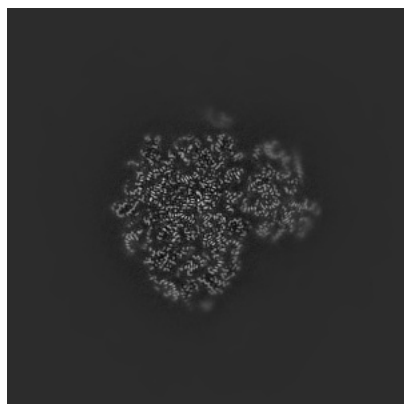


Z Index: 240

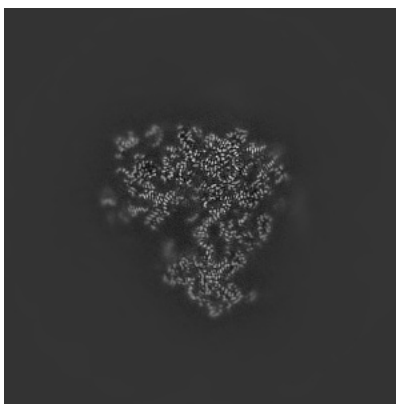
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

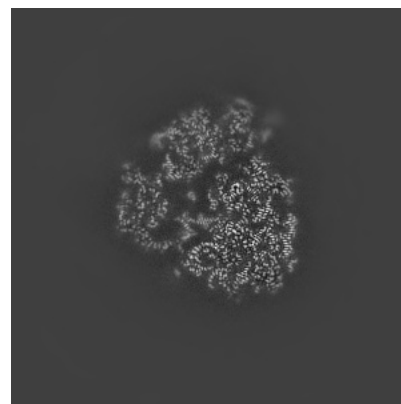
6.3.1 Primary map



X Index: 263



Y Index: 231

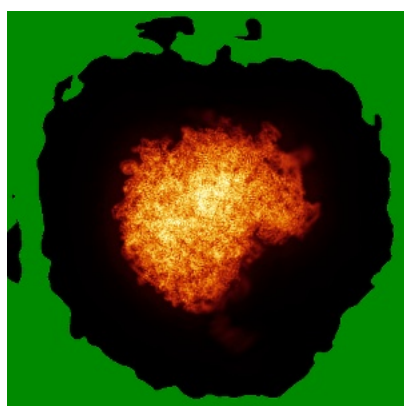


Z Index: 228

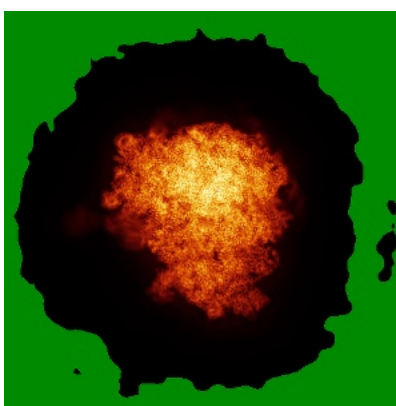
The images above show the largest variance slices of the map in three orthogonal directions.

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

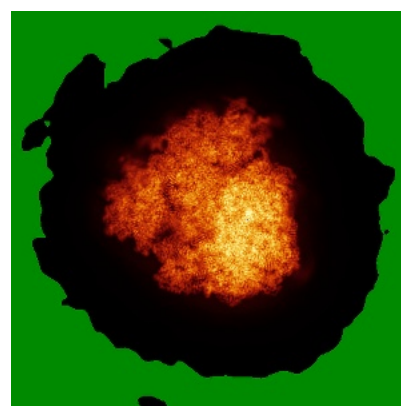
6.4.1 Primary map



X



Y

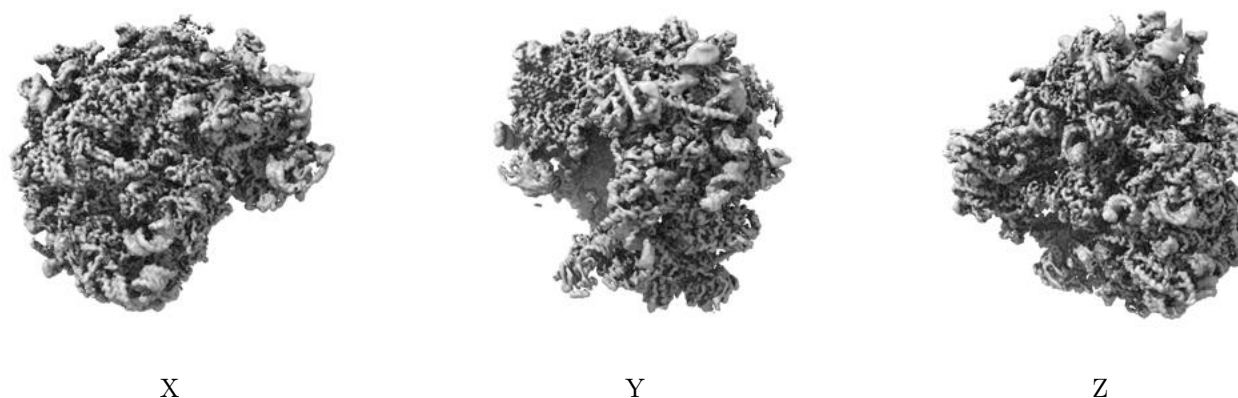


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.038. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

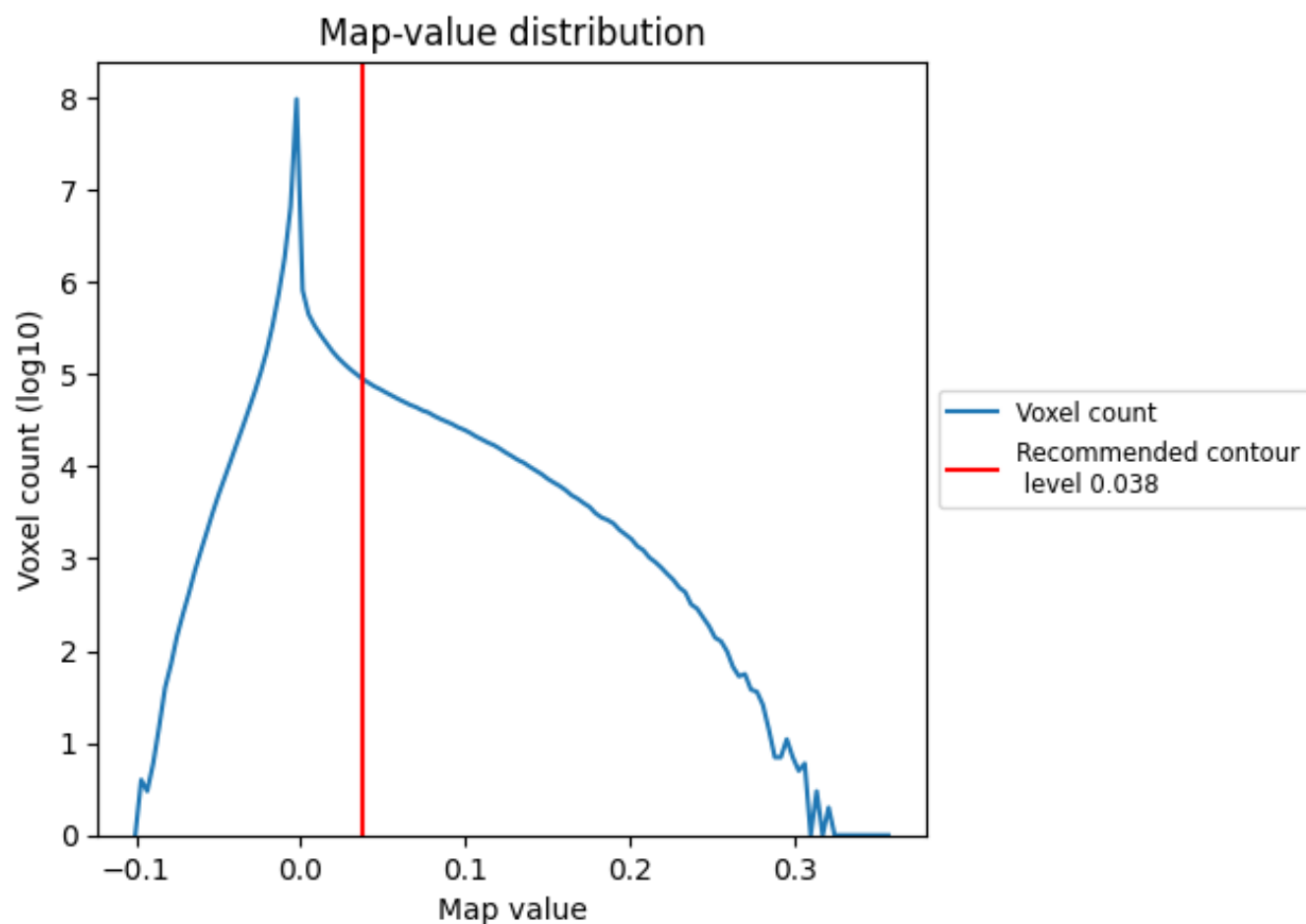
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

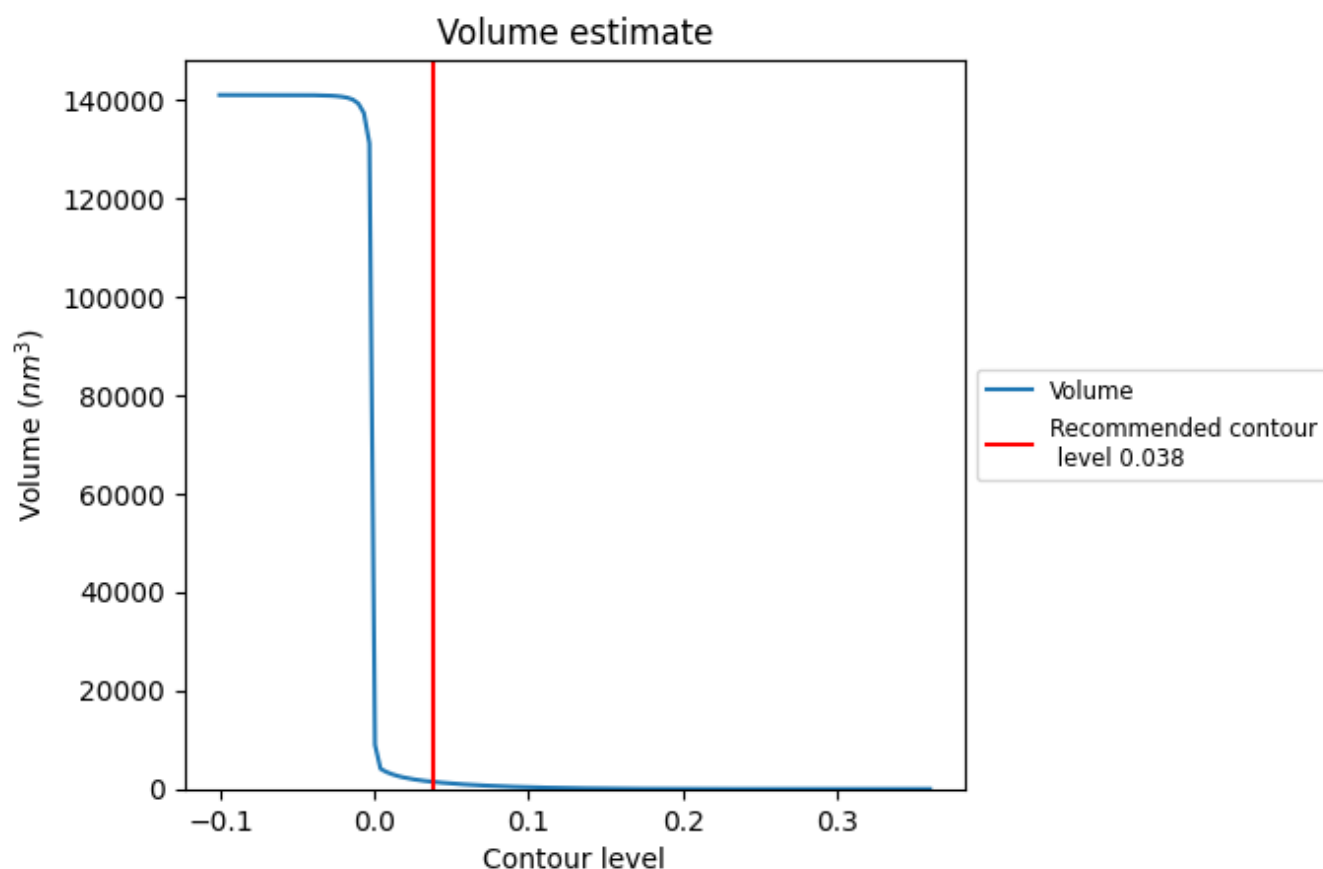
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

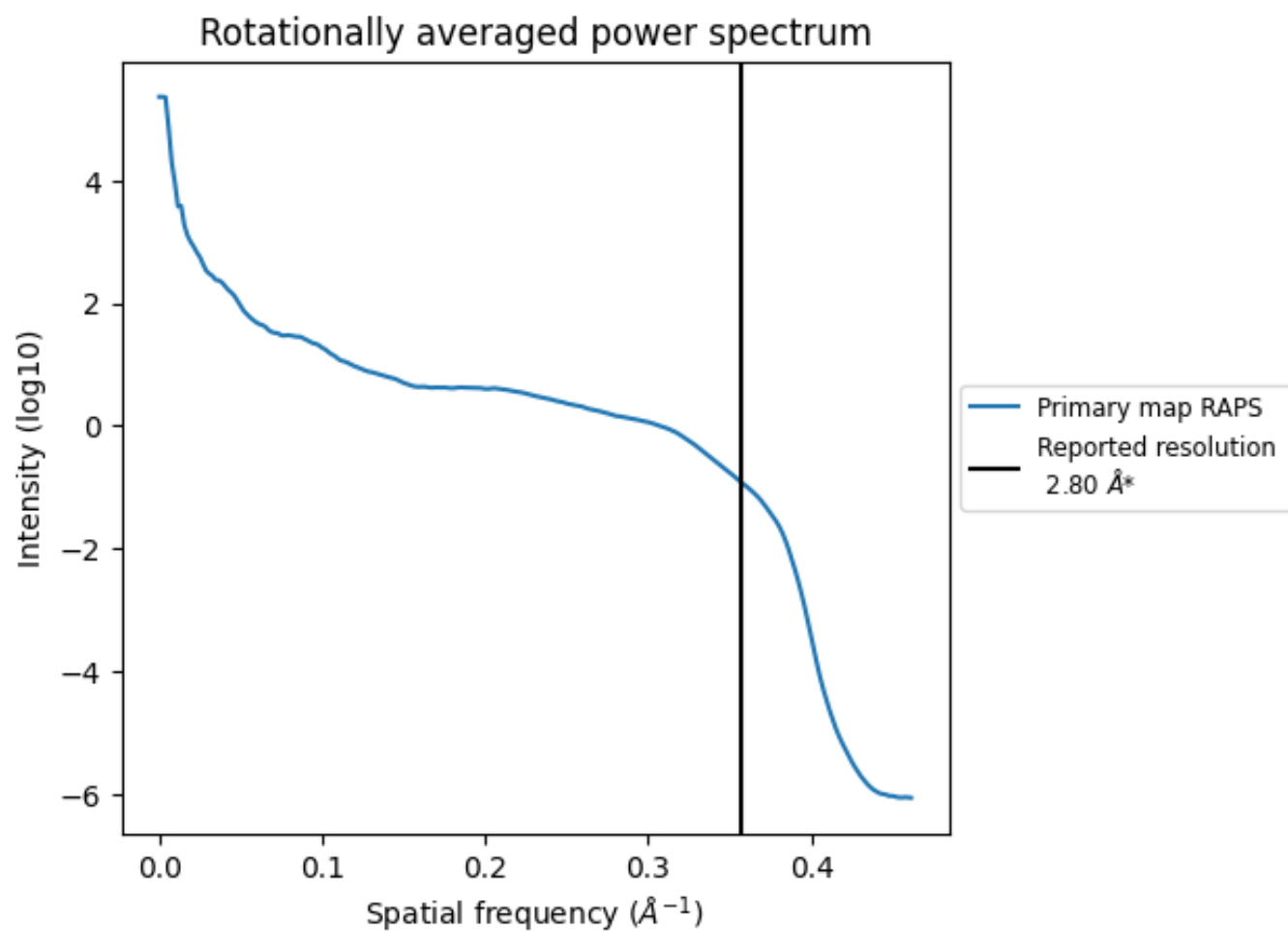
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1447 nm^3 ; this corresponds to an approximate mass of 1307 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 ⓘ

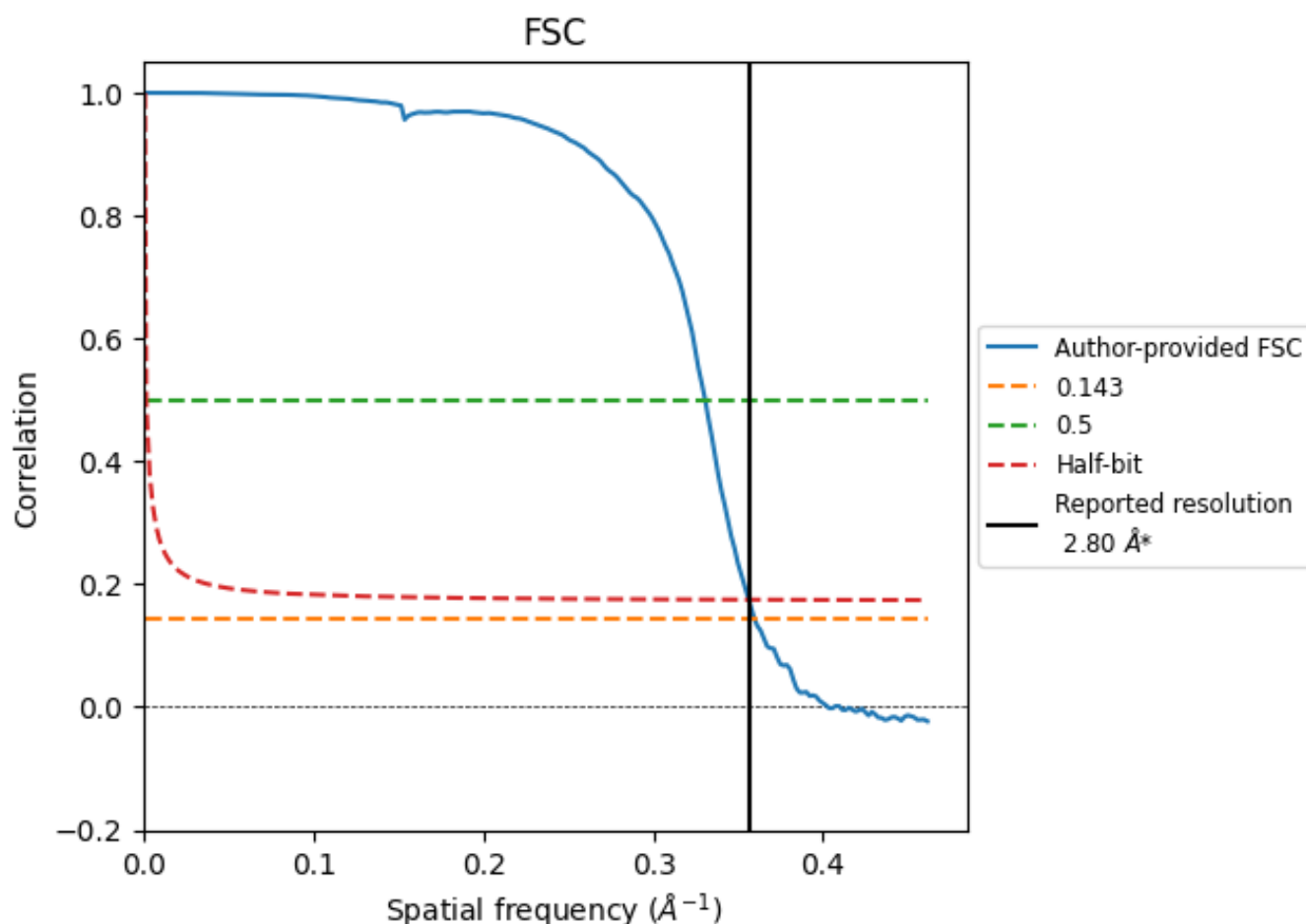


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

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 0.357 Å⁻¹

8.2 Resolution estimates [i](#)

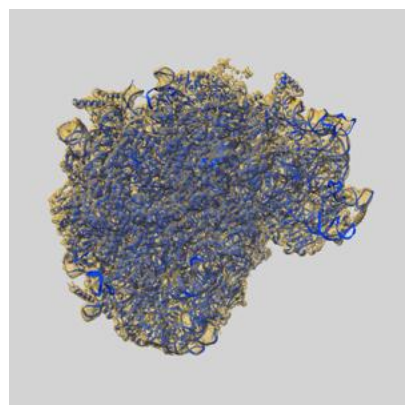
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.78	3.02	2.81
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

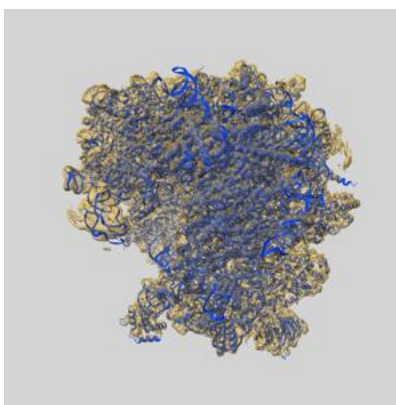
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10431 and PDB model 6TB3. Per-residue inclusion information can be found in section [3](#) on page [21](#).

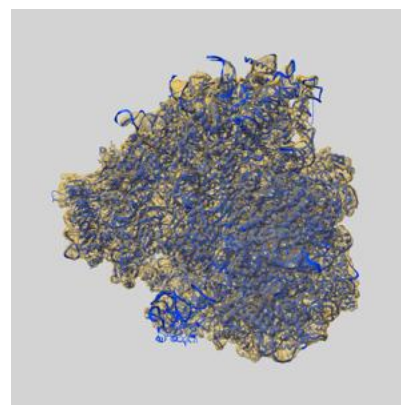
9.1 Map-model overlay [i](#)



X



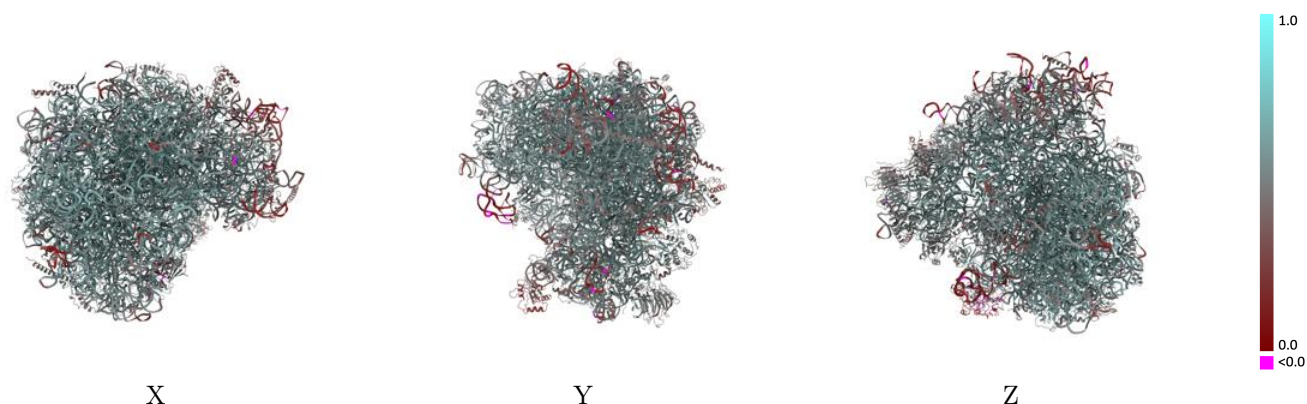
Y



Z

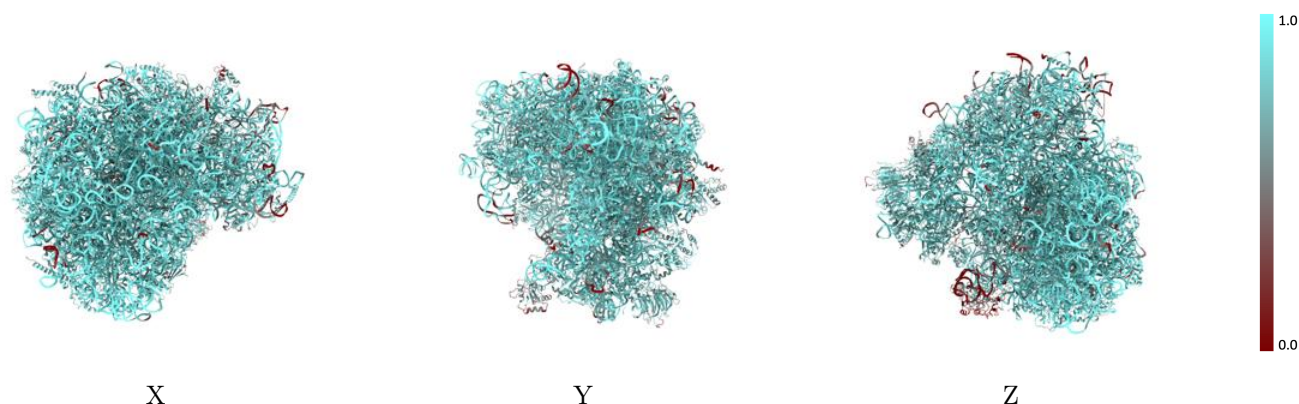
The images above show the 3D surface view of the map at the recommended contour level 0.038 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



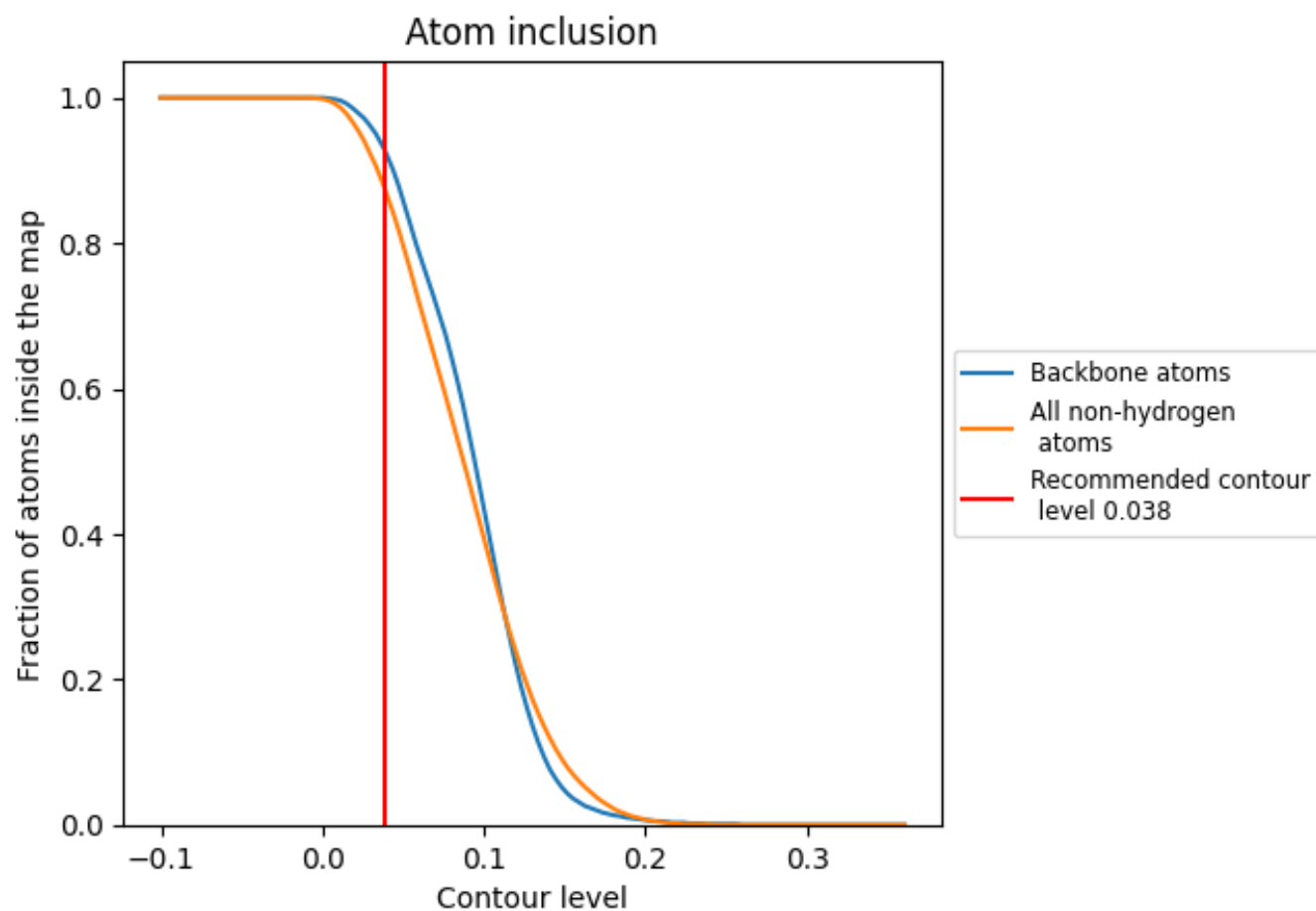
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.038).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 88% 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 (0.038) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8780	 0.5430
2	 0.9210	 0.5320
A	 0.7460	 0.4840
AA	 0.8130	 0.5200
AB	 0.8160	 0.5760
AC	 0.8370	 0.5330
AD	 0.8140	 0.5300
AE	 0.7490	 0.4990
AF	 0.9390	 0.6270
AG	 0.8100	 0.5140
AH	 0.8520	 0.5620
AI	 0.7460	 0.4970
AJ	 0.8720	 0.5570
AK	 0.8590	 0.5590
AL	 0.8840	 0.6100
AM	 0.8580	 0.5310
AN	 0.8630	 0.5410
AO	 0.8540	 0.5590
AP	 0.8410	 0.5870
AQ	 0.9170	 0.6160
AR	 0.9030	 0.5910
AS	 0.7880	 0.5930
AT	 0.8240	 0.5930
AU	 0.8750	 0.5690
AV	 0.8210	 0.5470
AW	 0.8880	 0.6160
AX	 0.8700	 0.5830
AY	 0.8610	 0.5590
B	 0.7330	 0.4850
BA	 0.8800	 0.5720
BB	 0.8840	 0.5830
BC	 0.8180	 0.5560
BD	 0.8030	 0.5390
BE	 0.8790	 0.5660
BF	 0.8060	 0.5320



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Chain	Atom inclusion	Q-score
BG	 0.8830	 0.5890
BH	 0.8570	 0.5670
BI	 0.8390	 0.5080
BJ	 0.8550	 0.5660
BK	 0.9130	 0.6050
BL	 0.7930	 0.4880
BM	 0.8310	 0.5130
BN	 0.8510	 0.5800
BO	 0.8790	 0.5540
BP	 0.8420	 0.5440
BQ	 0.9460	 0.5710
BR	 0.9890	 0.5810
BS	 0.9760	 0.5990
BT	 0.0030	 0.0840
BV	 0.4840	 0.5200
BW	 0.4950	 0.4600
C	 0.7470	 0.4500
D	 0.4370	 0.2870
E	 0.7390	 0.4740
F	 0.8120	 0.5270
G	 0.7660	 0.4850
H	 0.7760	 0.4950
I	 0.8150	 0.5110
J	 0.7440	 0.4730
K	 0.6920	 0.4730
L	 0.7170	 0.5080
M	 0.8910	 0.5600
N	 0.5160	 0.3000
O	 0.7350	 0.4620
P	 0.8270	 0.5190
Q	 0.7480	 0.5090
R	 0.8250	 0.5480
S	 0.8010	 0.5280
T	 0.7570	 0.4530
U	 0.7230	 0.4550
V	 0.8340	 0.5390
W	 0.7650	 0.4970
X	 0.8210	 0.5760
Y	 0.8090	 0.5360
Z	 0.8300	 0.5460
a	 0.8130	 0.5230
b	 0.8600	 0.5680

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Chain	Atom inclusion	Q-score
c	 0.7820	 0.5530
d	 0.7740	 0.4800
e	 0.8600	 0.5720
f	 0.7890	 0.5210
g	 0.6580	 0.4650
l	 0.9850	 0.6020
n	 0.9470	 0.5400