



Full wwPDB EM Validation Report ⓘ

Mar 17, 2026 – 11:09 PM UTC

PDB ID : 8BQD / pdb_00008bqd
EMDB ID : EMD-16182
Title : Yeast 80S ribosome in complex with Map1 (conformation 1)
Authors : Knorr, A.G.; Mackens-Kiani, T.; Musial, J.; Berninghausen, O.; Becker, T.;
Beatrix, B.; Beckmann, R.
Deposited on : 2022-11-21
Resolution : 3.90 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

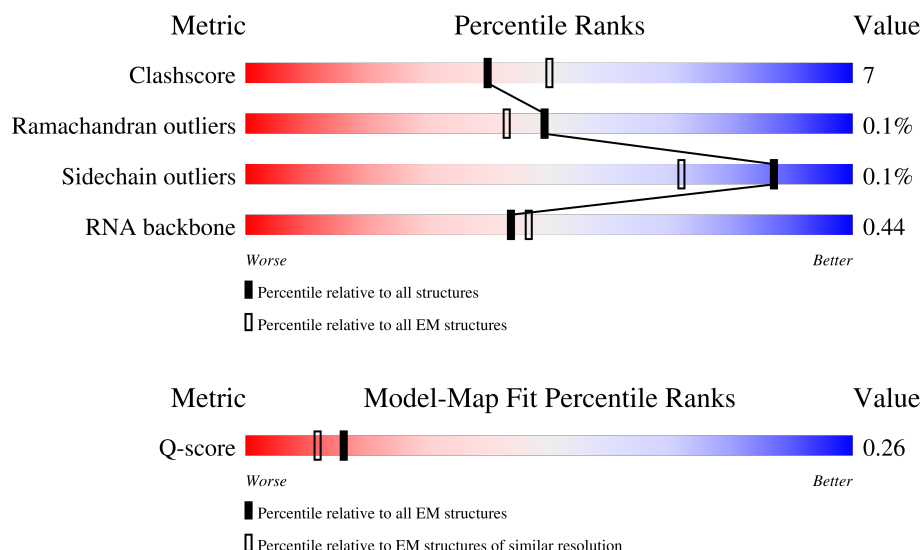
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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	8855 (3.40 - 4.40)

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	B	206	
2	A	222	
3	C	92	

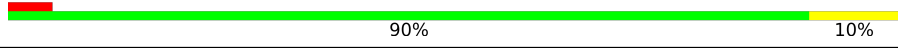
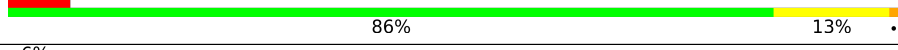
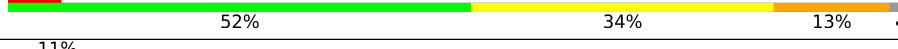
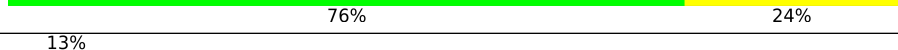
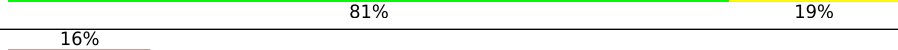
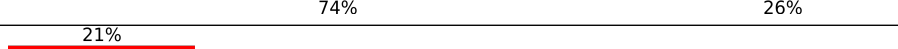
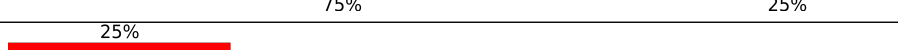
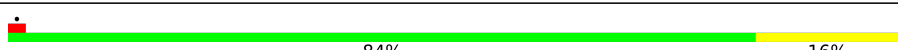
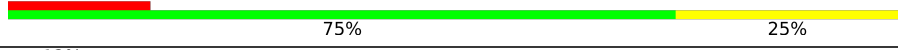
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Mol	Chain	Length	Quality of chain
4	D	121	
5	E	142	
6	F	141	
7	G	125	
8	H	145	
9	I	143	
10	J	100	
11	K	82	
12	L	63	
13	M	53	
14	N	73	
15	O	312	
16	P	206	
17	Q	232	
18	R	216	
19	S	258	
20	T	228	
21	U	184	
22	V	200	
23	W	184	
24	X	142	
25	Y	150	
26	Z	127	
27	AA	233	
28	BA	386	

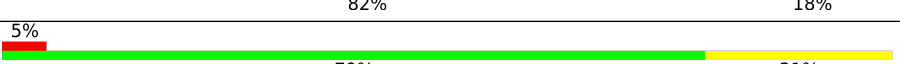
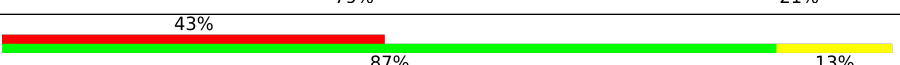
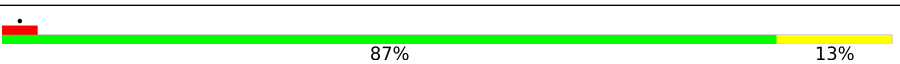
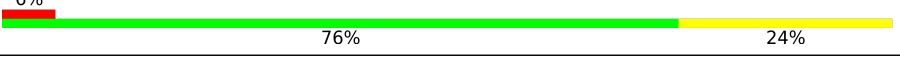
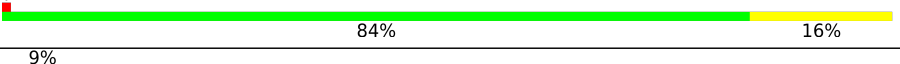
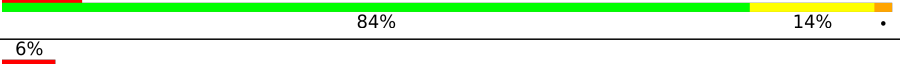
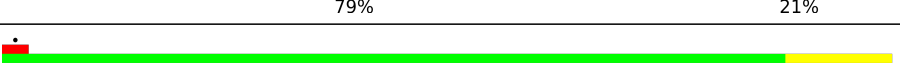
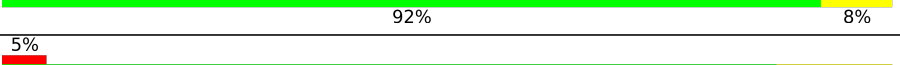
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Mol	Chain	Length	Quality of chain
29	AB	136	
30	BB	185	
31	AC	99	
32	BC	109	
33	2	1798	
34	a	87	
35	b	129	
36	c	144	
37	d	134	
38	e	97	
39	f	81	
40	g	60	
41	BQ	3395	
42	BR	121	
43	BS	158	
44	AW	251	
45	BE	361	
46	BI	294	
47	BM	175	
48	BO	222	
49	AD	191	
50	BD	218	
51	AG	169	
52	AJ	193	
53	AM	136	

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Mol	Chain	Length	Quality of chain
54	AQ	203	
55	AU	197	
56	AX	183	
57	BF	188	
58	BH	171	
59	BJ	159	
60	BL	100	
61	AE	126	
62	AH	121	
63	AK	125	
64	AN	135	
65	AR	148	
66	AV	58	
67	AY	96	
68	BG	127	
69	BK	106	
70	BN	112	
71	BP	119	
72	AF	81	
73	AI	77	
74	AL	50	
75	AO	52	
76	AS	25	
77	AP	103	
78	AT	91	

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Mol	Chain	Length	Quality of chain
79	x	387	92%
			 89%5% • 5%
80	BT	217	92%
			 97%

2 Entry composition [i](#)

There are 81 unique types of molecules in this entry. The entry contains 205800 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Rps5p.

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

- Molecule 2 is a protein called RPS3 isoform 1.

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

- Molecule 3 is a protein called 40S ribosomal protein S10-A.

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

- Molecule 4 is a protein called 40S ribosomal protein S12.

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

- 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 S16-A.

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

- Molecule 7 is a protein called 40S ribosomal protein S17-A.

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

- Molecule 8 is a protein called 40S ribosomal protein S18-A.

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

- Molecule 9 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 10 is a protein called RPS20 isoform 1.

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

- Molecule 11 is a protein called 40S ribosomal protein S25.

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

- Molecule 12 is a protein called RPS28A isoform 1.

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

- Molecule 13 is a protein called RPS29A isoform 1.

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

- Molecule 14 is a protein called 40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	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 15 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

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

- Molecule 16 is a protein called 40S ribosomal protein S0-A.

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

- Molecule 17 is a protein called 40S ribosomal protein S1-A.

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

- Molecule 18 is a protein called RPS2 isoform 1.

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

- Molecule 19 is a protein called 40S ribosomal protein S4-A.

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

- Molecule 20 is a protein called 40S ribosomal protein S6-A.

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

- Molecule 21 is a protein called 40S ribosomal protein S7-A.

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

- Molecule 22 is a protein called 40S ribosomal protein S8-B.

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

- Molecule 23 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 24 is a protein called 40S ribosomal protein S11-A.

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

- Molecule 25 is a protein called 40S ribosomal protein S13.

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

- Molecule 26 is a protein called 40S ribosomal protein S14-B.

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

- Molecule 27 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 28 is a protein called 60S ribosomal protein L3.

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

- Molecule 29 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 30 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 31 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 32 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 33 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	2	1771	Total	C	N	O	P	0	0
			37739	16872	6683	12413	1771		

- Molecule 34 is a protein called 40S ribosomal protein S21-A.

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

- Molecule 35 is a protein called RPS22A isoform 1.

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

- Molecule 36 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 37 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	d	134	Total	C	N	O	S	0	0
			1032	651	195	186			

- Molecule 38 is a protein called RPS26B isoform 1.

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

- Molecule 39 is a protein called 40S ribosomal protein S27-A.

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

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

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

- Molecule 41 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BQ	3299	Total	C	N	O	P	0	0
			70544	31506	12682	23057	3299		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BQ	?	-	G	deletion	GB 1262303
BQ	1962	A	G	conflict	GB 1262303

- Molecule 42 is a RNA chain called 5S rRNA.

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

- Molecule 43 is a RNA chain called 5.8S rRNA.

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

- Molecule 44 is a protein called 60S ribosomal protein L2-A.

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

- Molecule 45 is a protein called RPL4A isoform 1.

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

- Molecule 46 is a protein called RPL5 isoform 1.

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

- Molecule 47 is a protein called 60S ribosomal protein L6-B.

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

- Molecule 48 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 49 is a protein called RPL9A isoform 1.

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

- Molecule 50 is a protein called RPL10 isoform 1.

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

- Molecule 51 is a protein called RPL11B isoform 1.

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

- Molecule 52 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 53 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 54 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 55 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 56 is a protein called 60S ribosomal protein L17-A.

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

- 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 L24-A.

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

- Molecule 62 is a protein called 60S ribosomal protein L25.

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

- Molecule 63 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 64 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 65 is a protein called 60S ribosomal protein L28.

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

- Molecule 66 is a protein called 60S ribosomal protein L29.

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

- Molecule 67 is a protein called 60S ribosomal protein L30.

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

- Molecule 68 is a protein called RPL32 isoform 1.

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

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

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

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

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

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

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

- Molecule 72 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 73 is a protein called RPL38 isoform 1.

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

- Molecule 74 is a protein called 60S ribosomal protein L39.

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

- Molecule 75 is a protein called 60S ribosomal protein L40-A.

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

- Molecule 76 is a protein called 60S ribosomal protein L41.

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

- Molecule 77 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 78 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 79 is a protein called Methionine aminopeptidase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	x	367	Total	C	N	O	S	0	0
			2899	1825	504	549	21		

- Molecule 80 is a protein called 60S ribosomal protein L1-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
80	BT	217	Total	C	N	O	0	0
			1075	641	217	217		

- Molecule 81 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
81	M	1	Total	Zn	0
			1	1	
81	N	1	Total	Zn	0
			1	1	
81	BN	1	Total	Zn	0
			1	1	

Continued on next page...

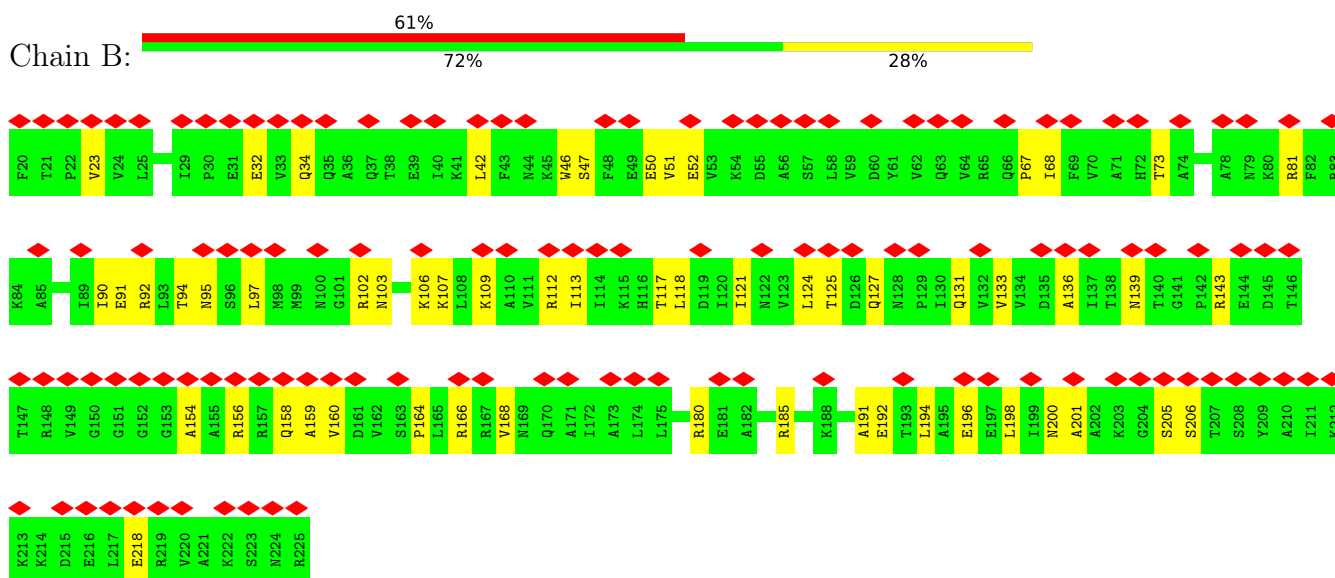
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Mol	Chain	Residues	Atoms		AltConf
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81	AO	1	Total 1	Zn 1	0
81	AP	1	Total 1	Zn 1	0
81	AT	1	Total 1	Zn 1	0

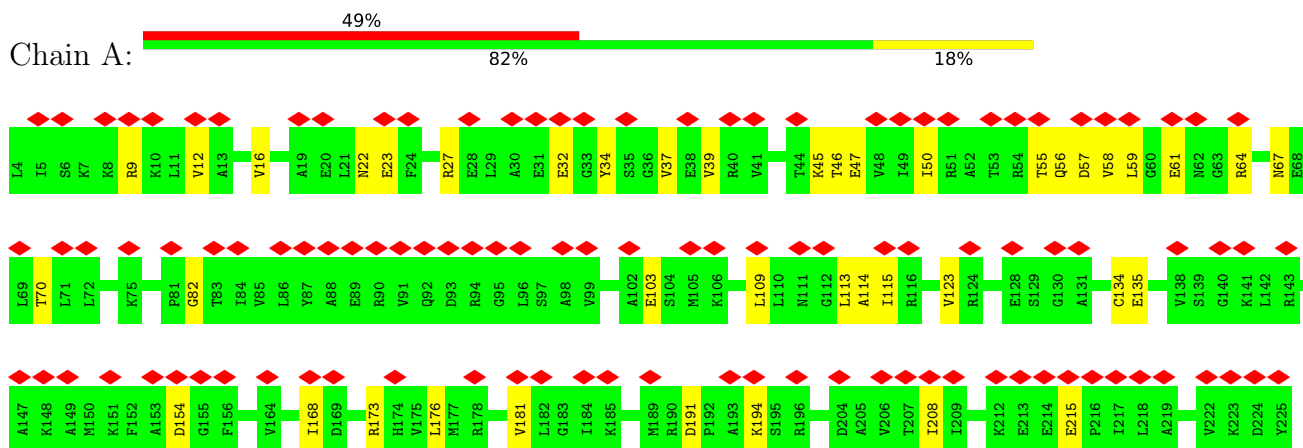
3 Residue-property plots

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.

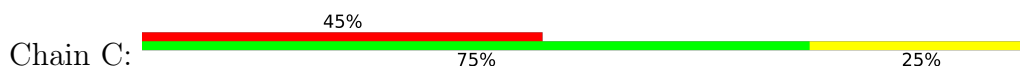
- Molecule 1: Rps5p

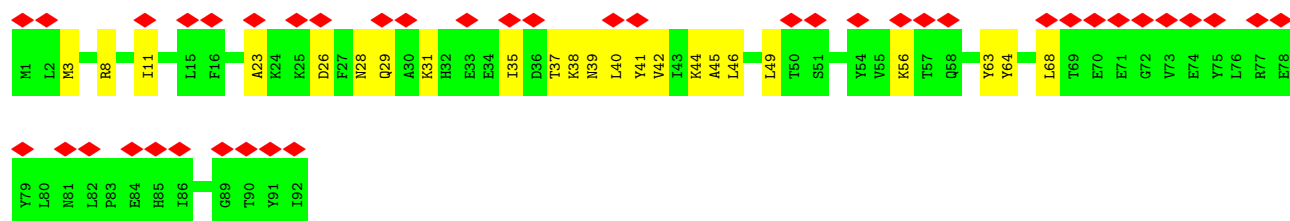


- Molecule 2: RPS3 isoform 1

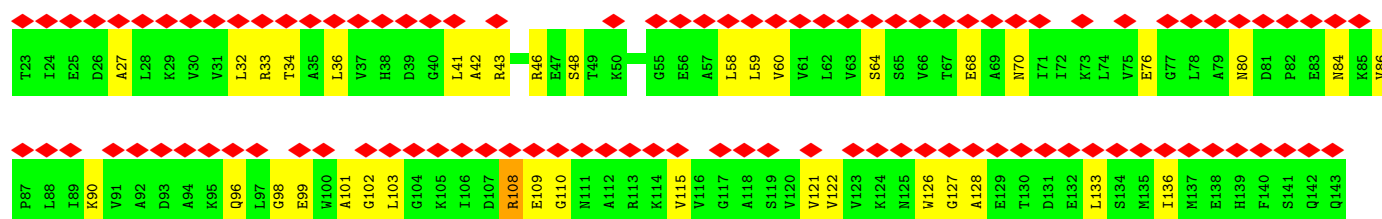
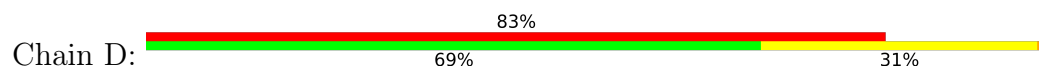


- Molecule 3: 40S ribosomal protein S10-A

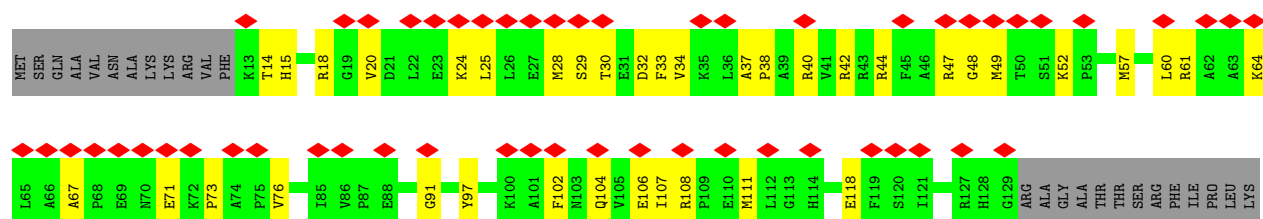




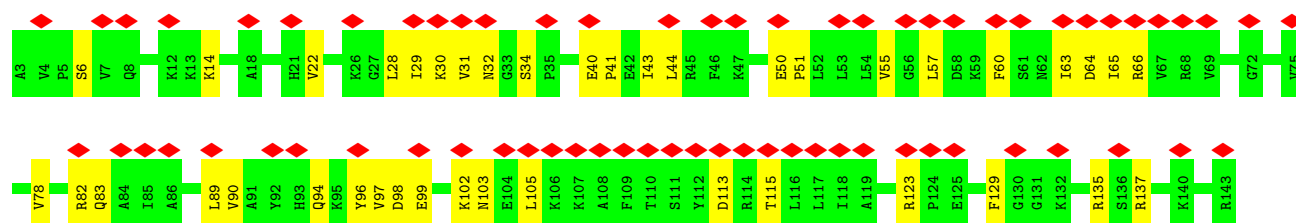
• Molecule 4: 40S ribosomal protein S12



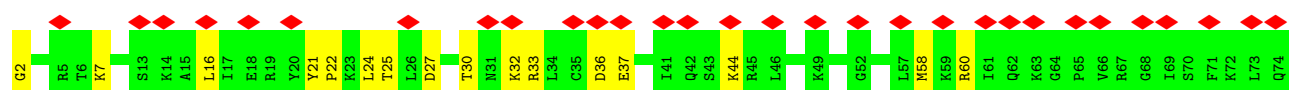
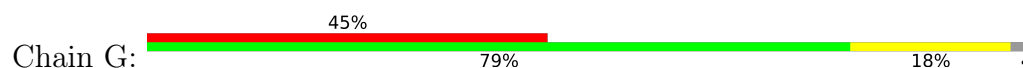
• Molecule 5: 40S ribosomal protein S15

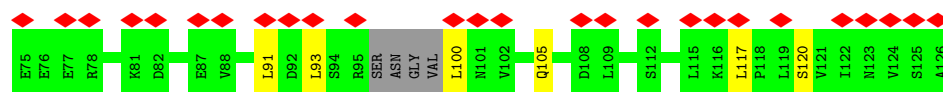


• Molecule 6: 40S ribosomal protein S16-A

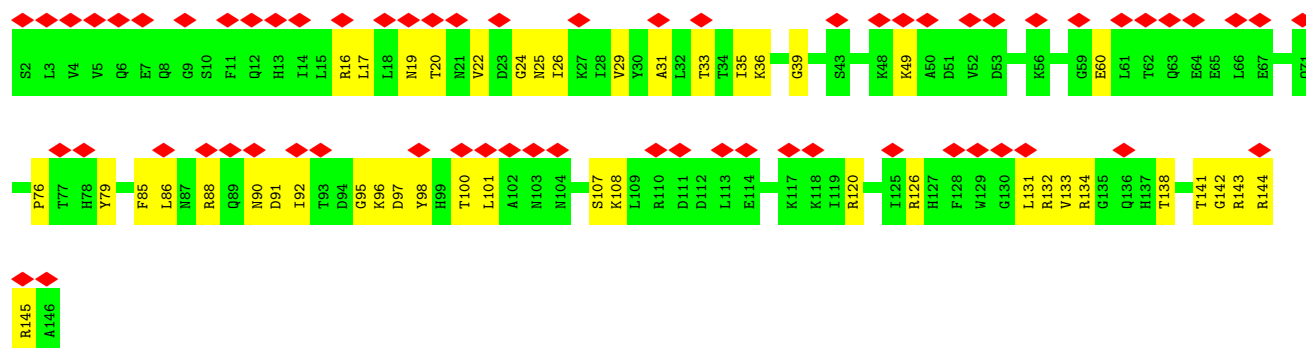
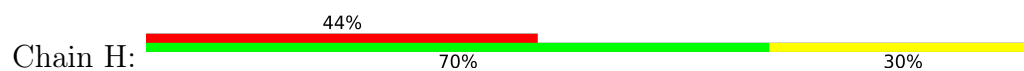


• Molecule 7: 40S ribosomal protein S17-A

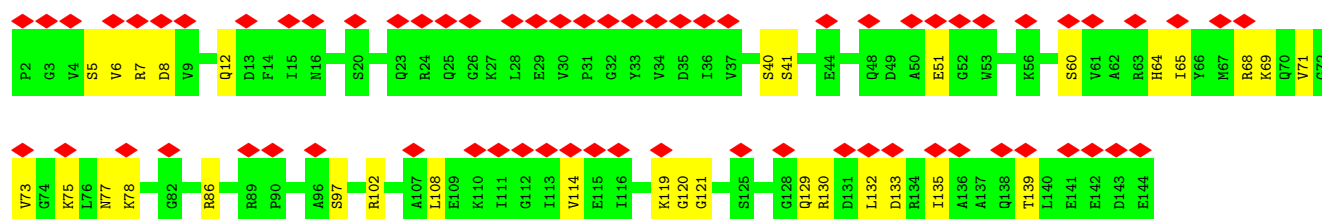
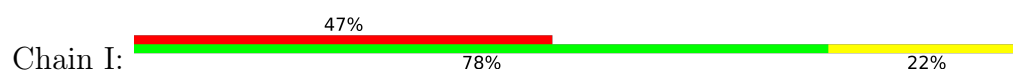




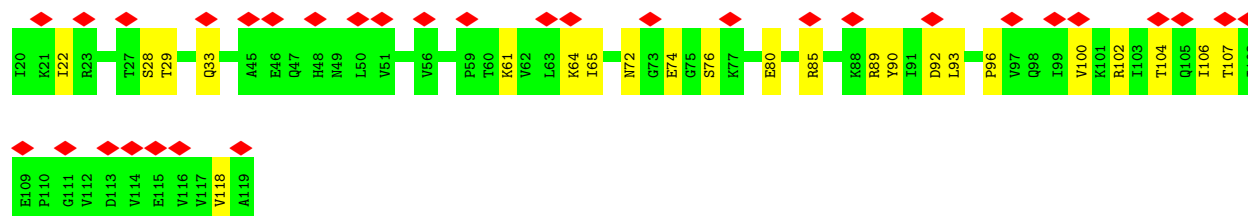
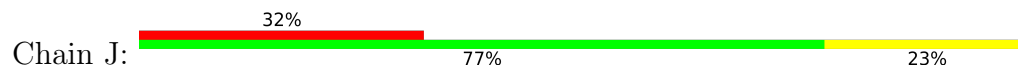
- Molecule 8: 40S ribosomal protein S18-A



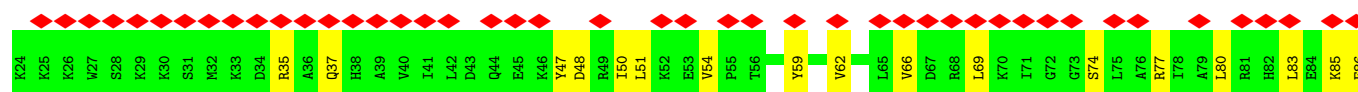
- Molecule 9: 40S ribosomal protein S19-A

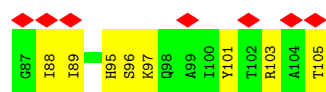


- Molecule 10: RPS20 isoform 1

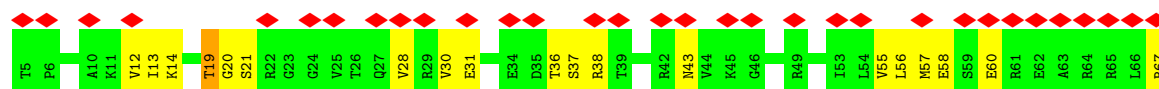


- Molecule 11: 40S ribosomal protein S25

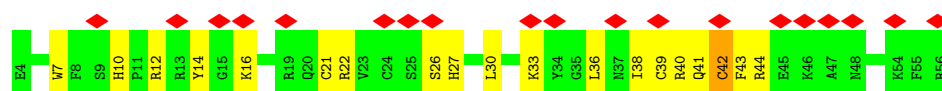




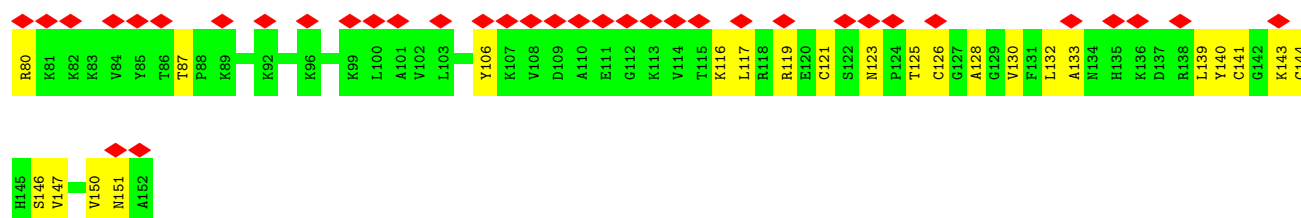
- Molecule 12: RPS28A isoform 1



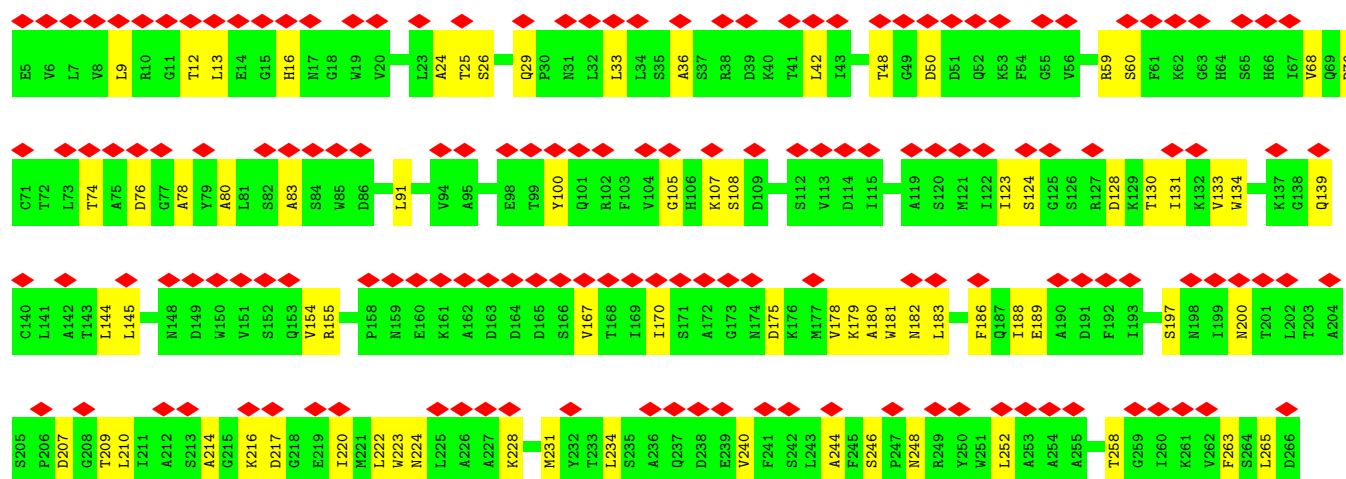
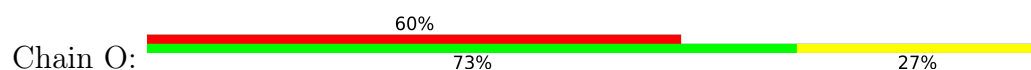
- Molecule 13: RPS29A isoform 1

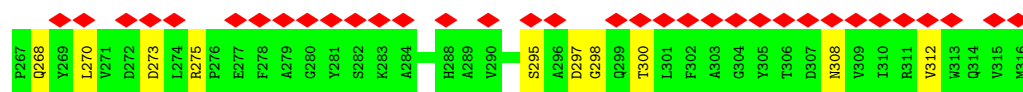


- Molecule 14: 40S ribosomal protein S31

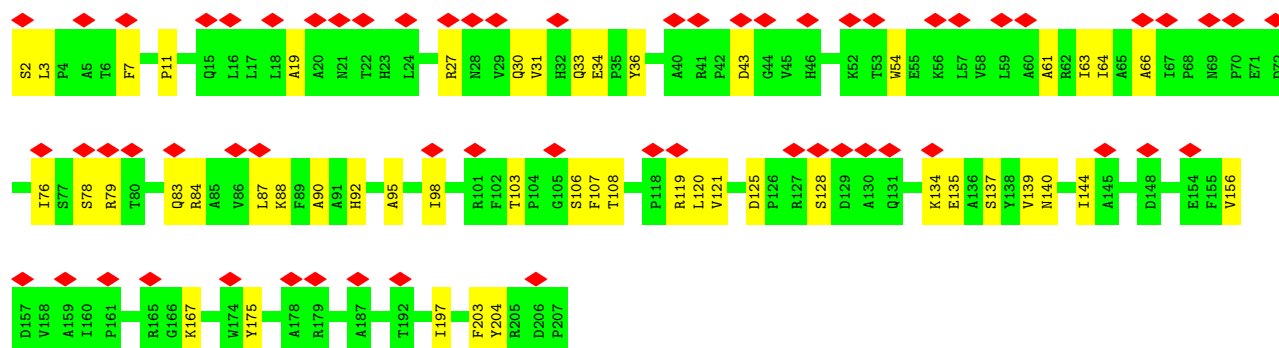
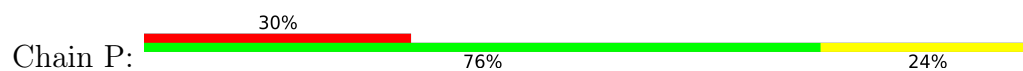


- Molecule 15: Guanine nucleotide-binding protein subunit beta-like protein

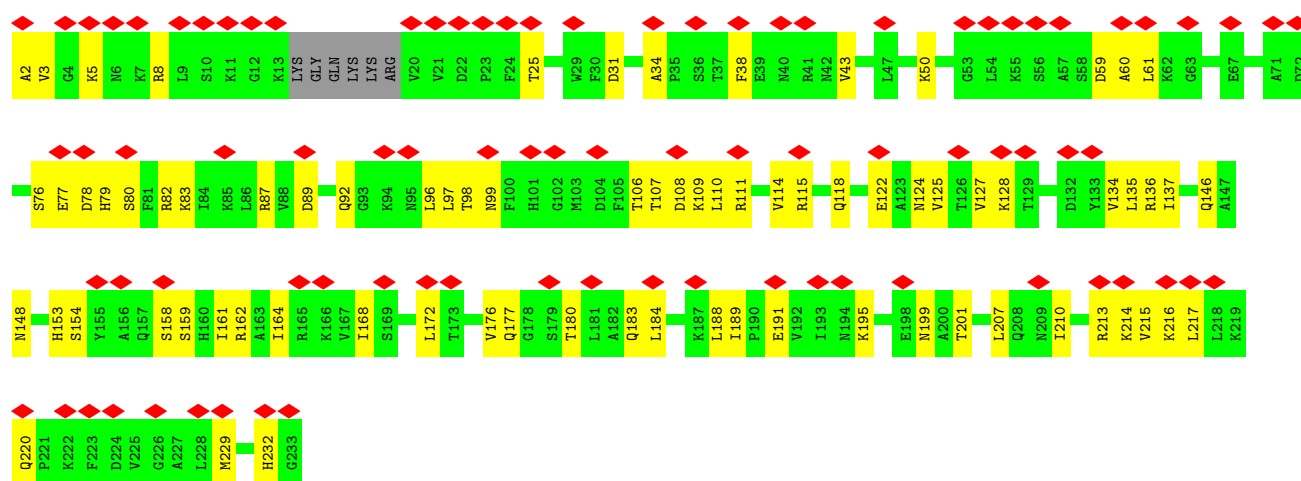
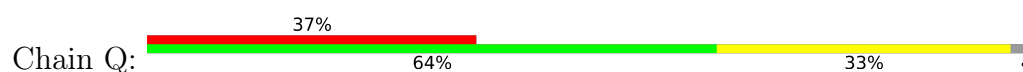




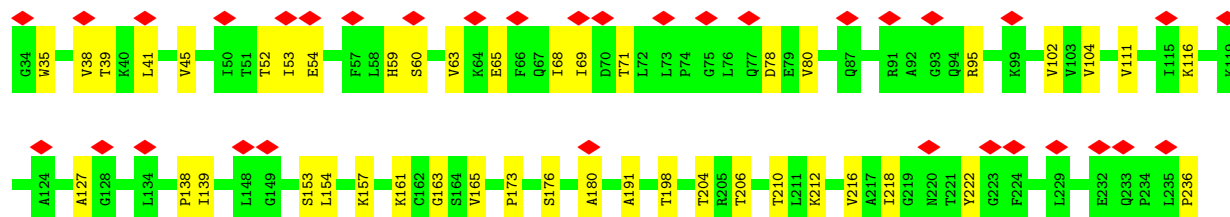
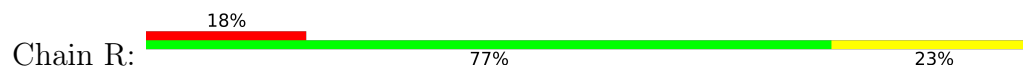
• Molecule 16: 40S ribosomal protein S0-A

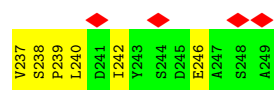


• Molecule 17: 40S ribosomal protein S1-A

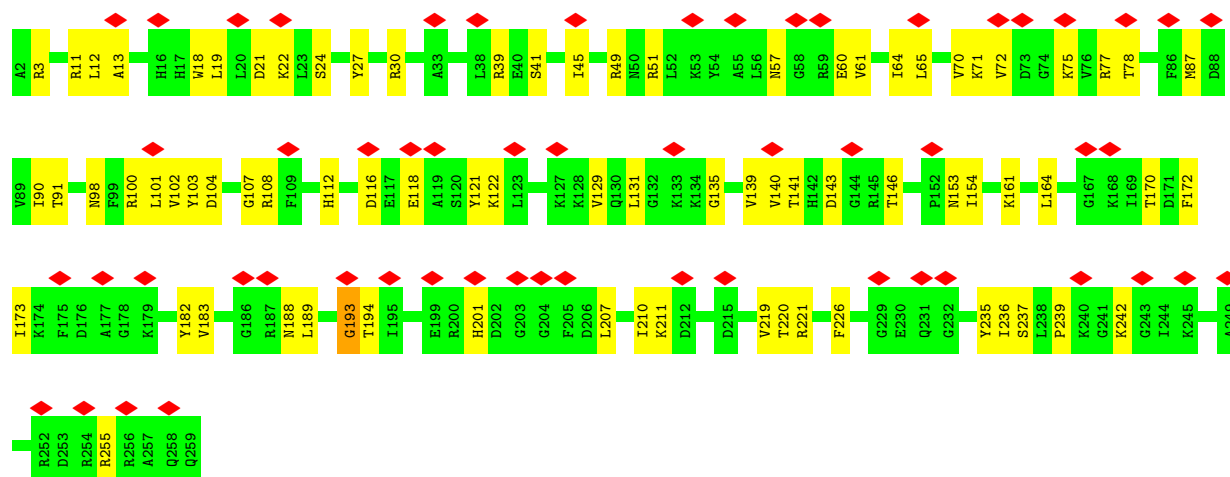


• Molecule 18: RPS2 isoform 1

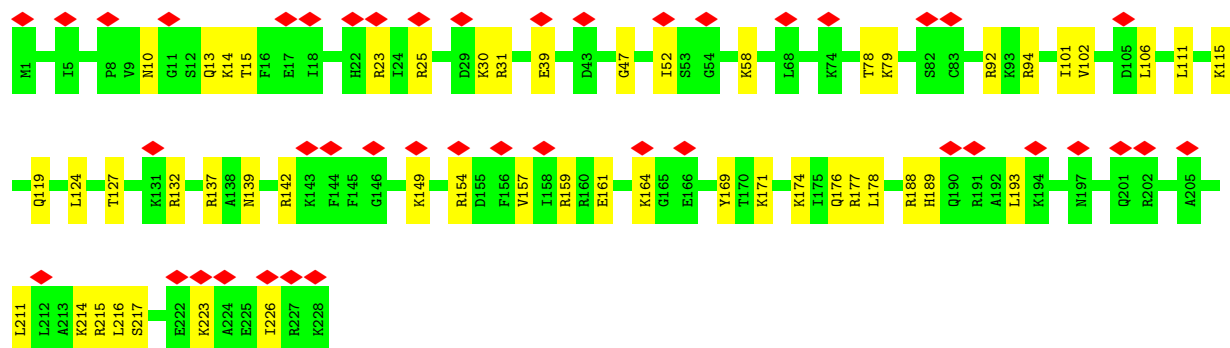
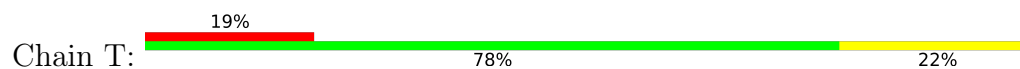




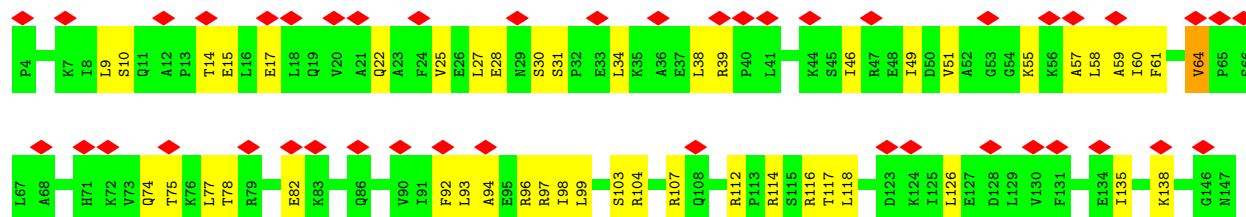
• Molecule 19: 40S ribosomal protein S4-A

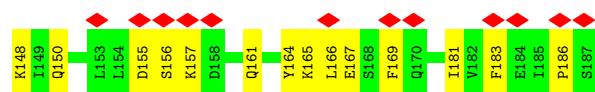


• Molecule 20: 40S ribosomal protein S6-A

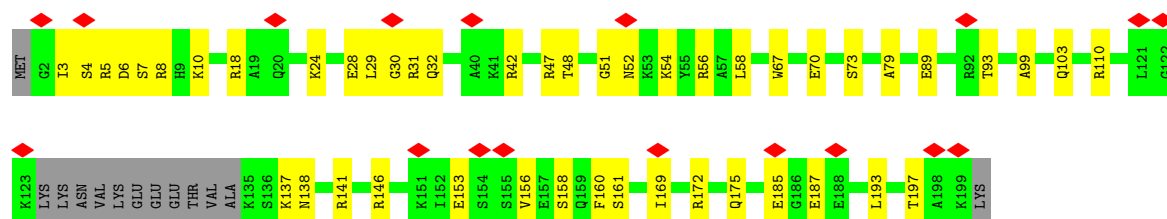


• Molecule 21: 40S ribosomal protein S7-A

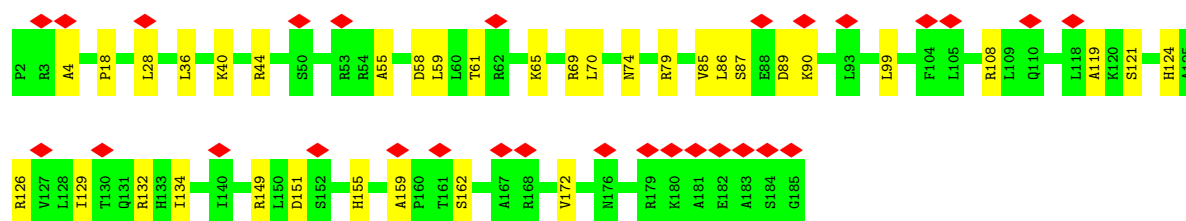
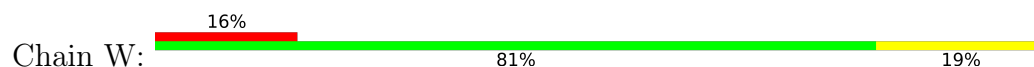




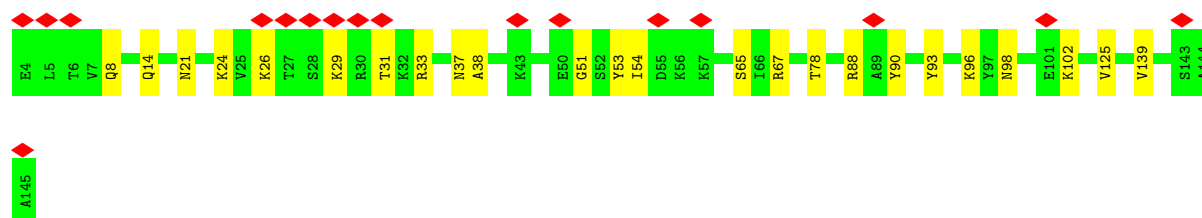
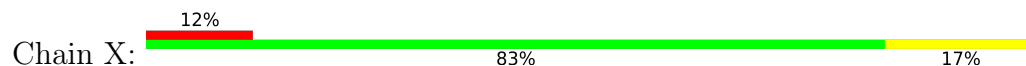
- Molecule 22: 40S ribosomal protein S8-B



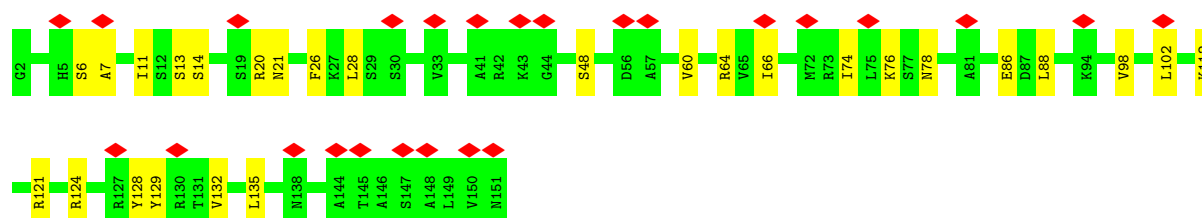
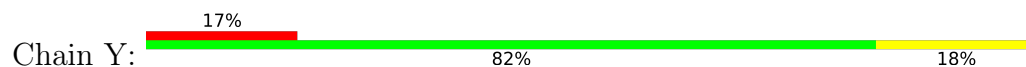
- Molecule 23: 40S ribosomal protein S9-A



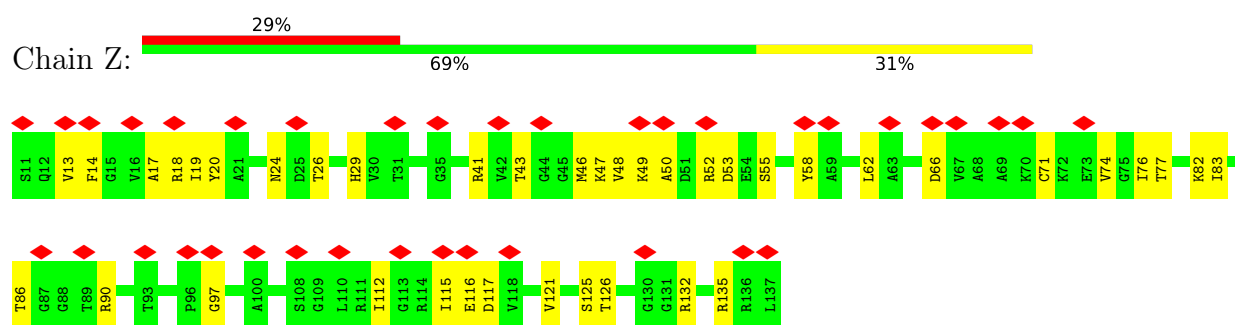
- Molecule 24: 40S ribosomal protein S11-A



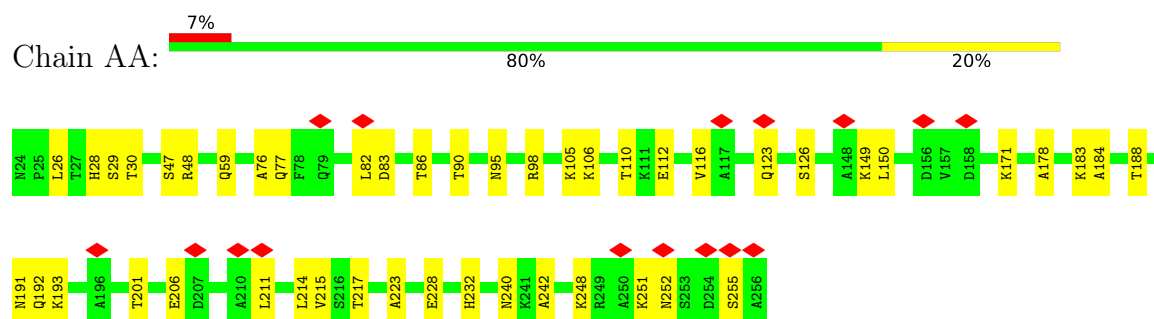
- Molecule 25: 40S ribosomal protein S13



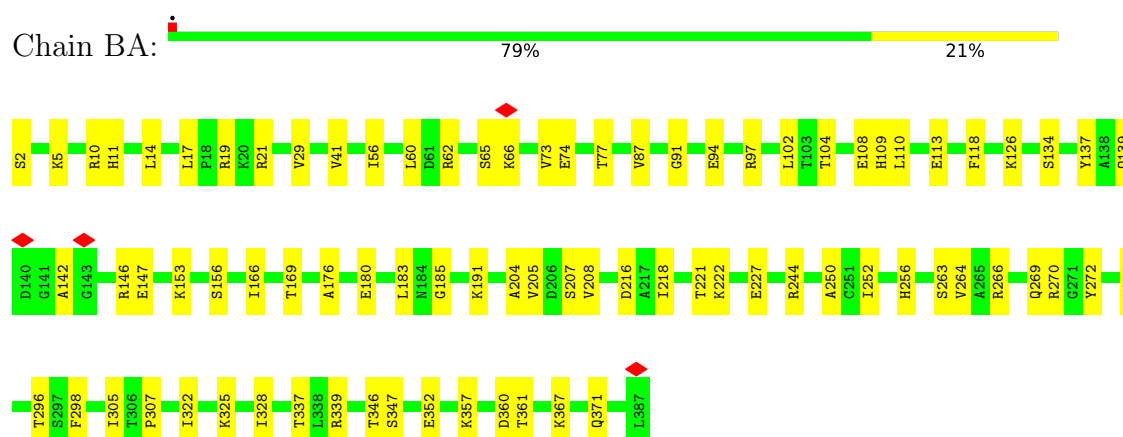
- Molecule 26: 40S ribosomal protein S14-B



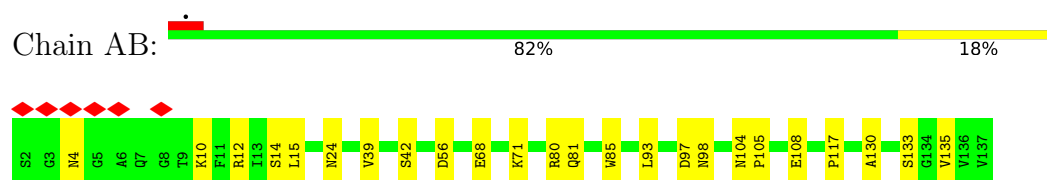
- Molecule 27: 60S ribosomal protein L8-A



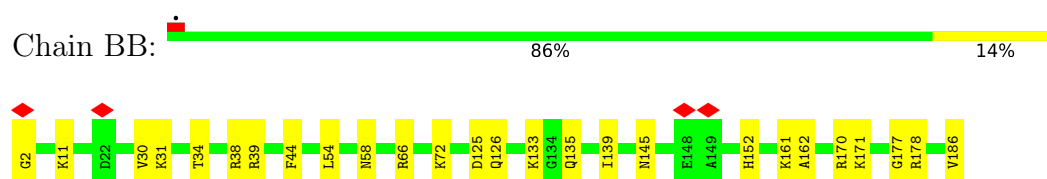
- Molecule 28: 60S ribosomal protein L3



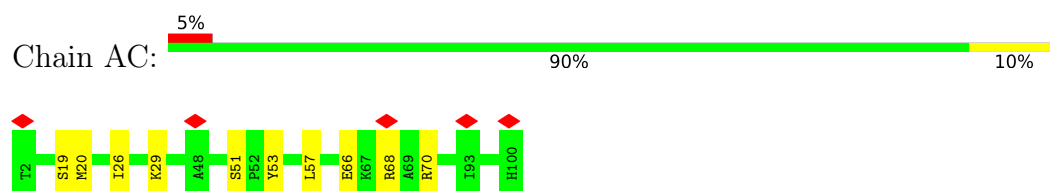
- Molecule 29: 60S ribosomal protein L23-A



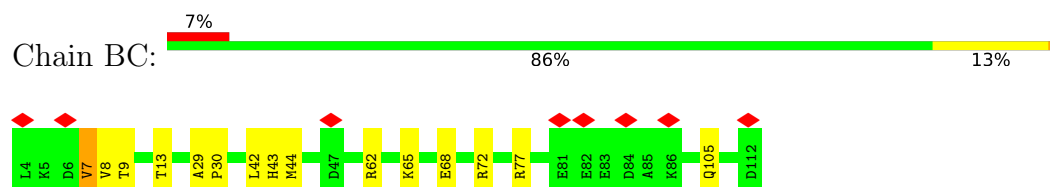
- Molecule 30: 60S ribosomal protein L18-A



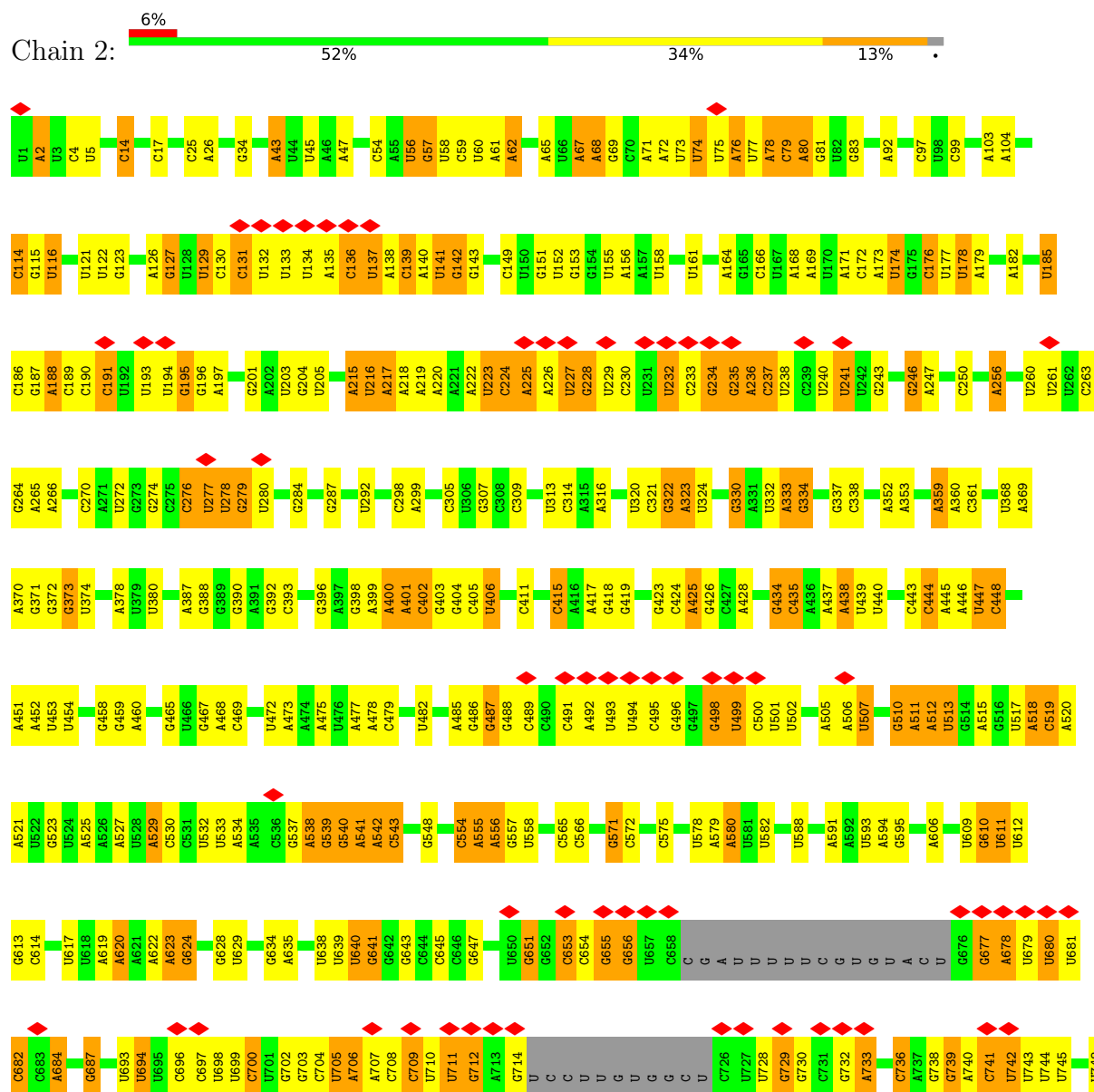
- Molecule 31: 60S ribosomal protein L36-A

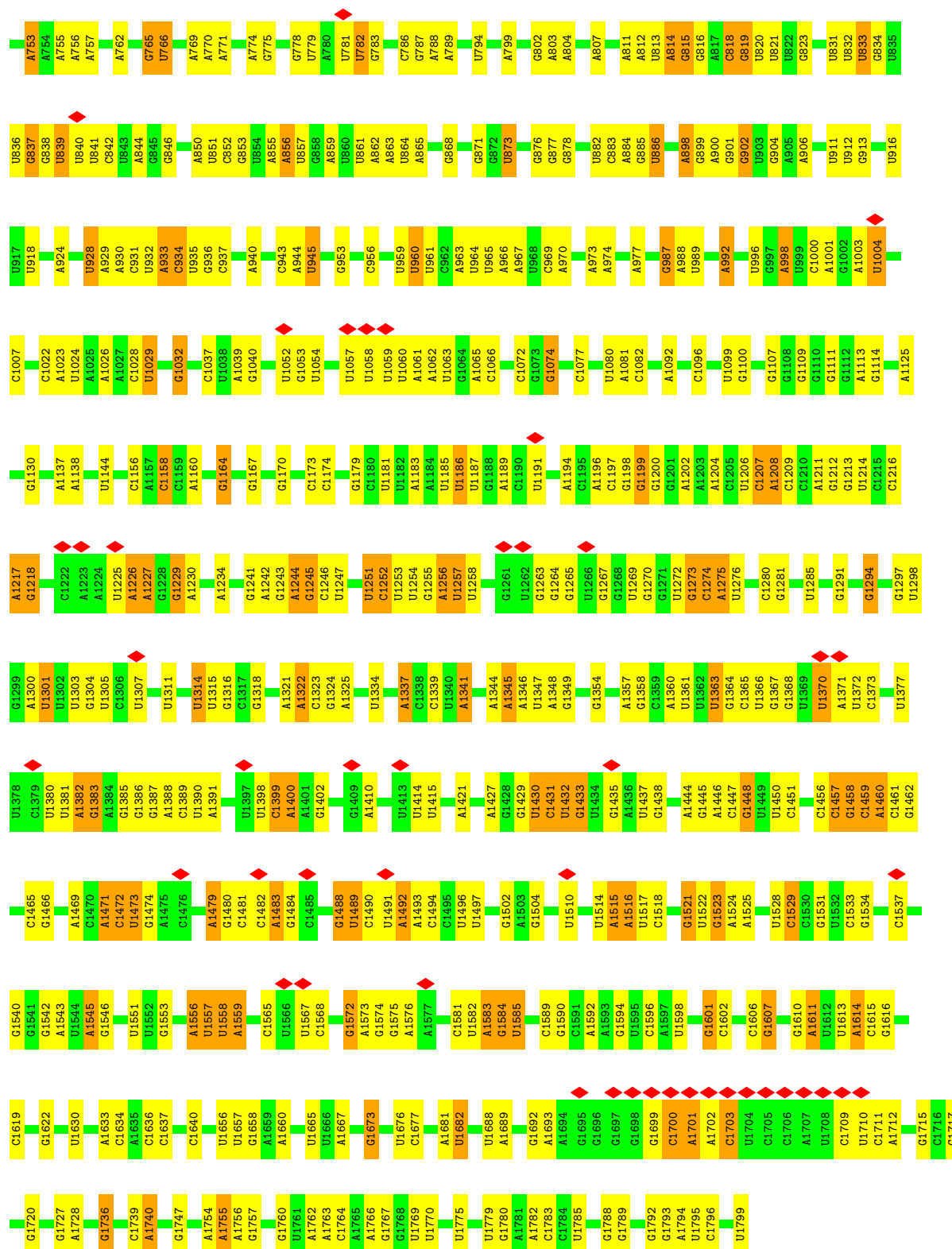


- Molecule 32: 60S ribosomal protein L31-A

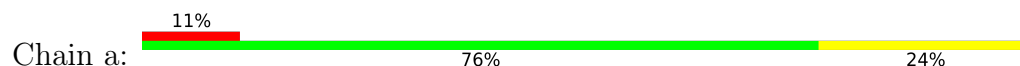


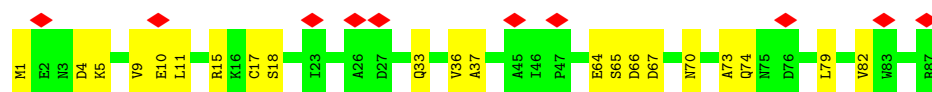
- Molecule 33: 18S rRNA



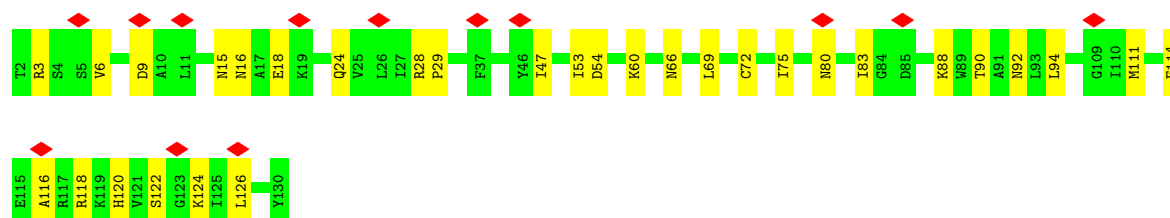
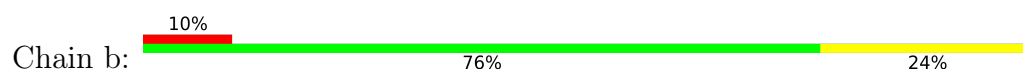


• Molecule 34: 40S ribosomal protein S21-A

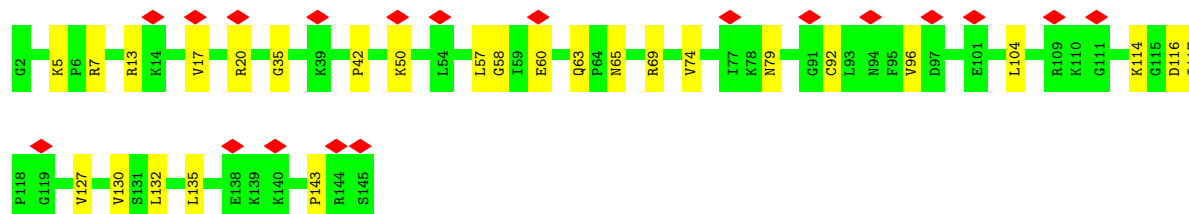
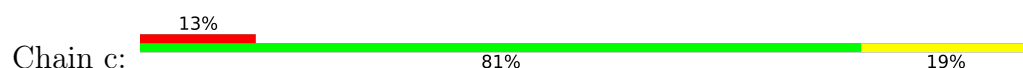




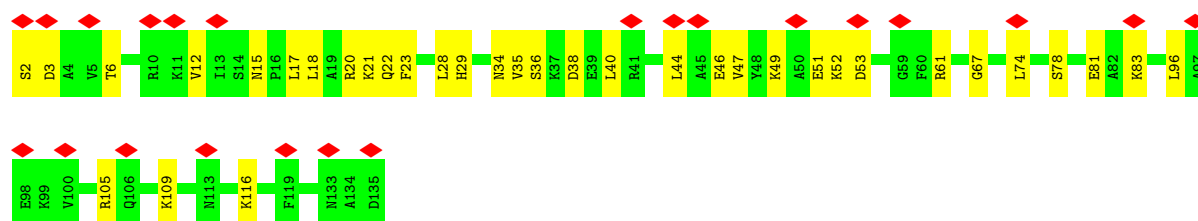
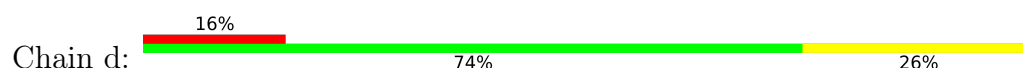
- Molecule 35: RPS22A isoform 1



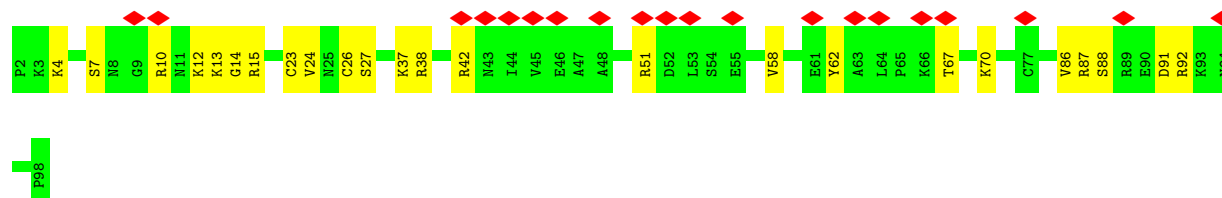
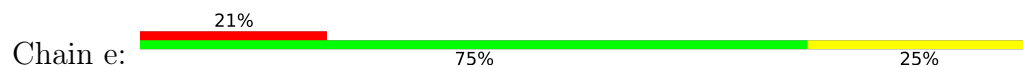
- Molecule 36: 40S ribosomal protein S23-A



- Molecule 37: 40S ribosomal protein S24-A

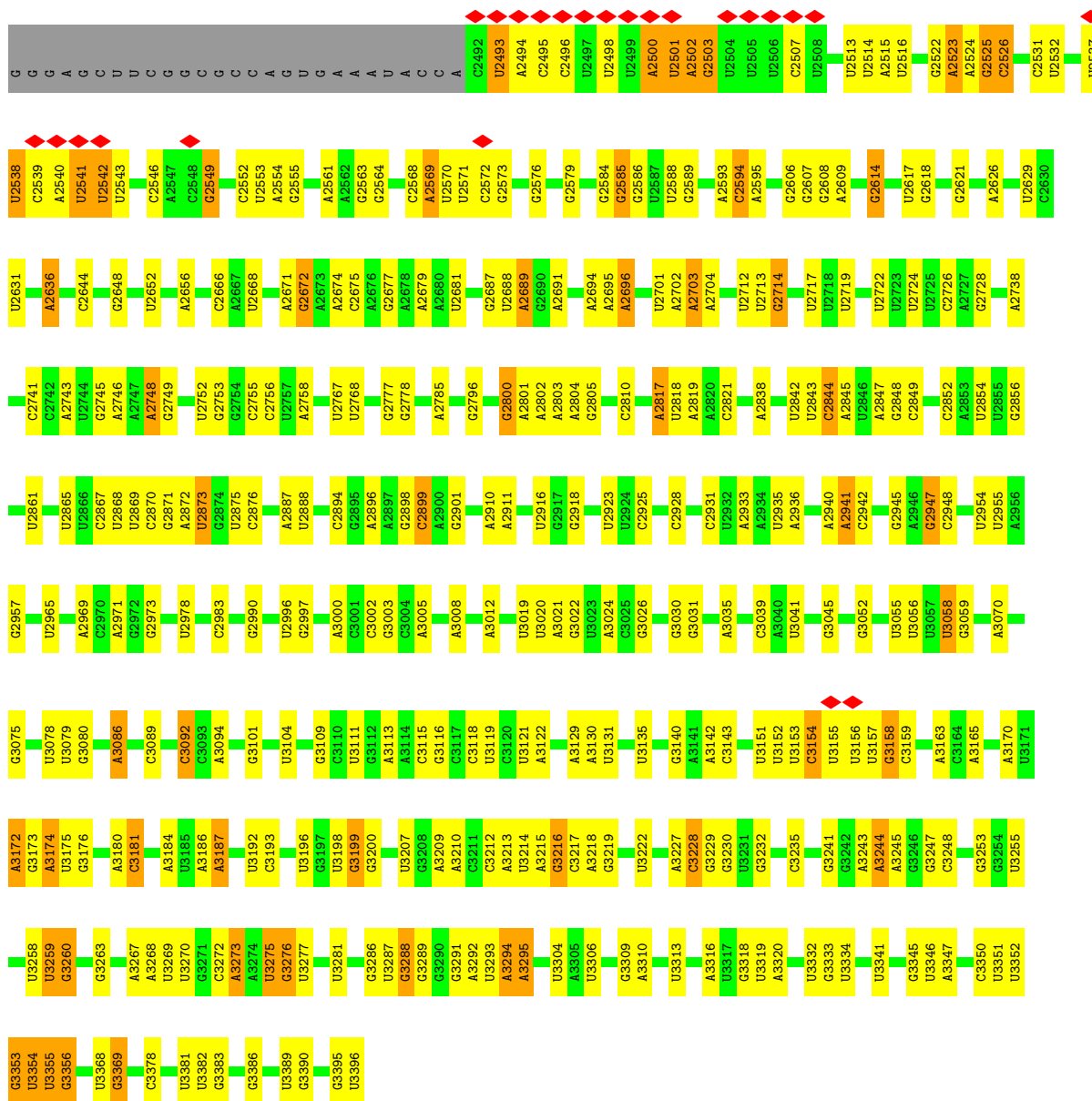


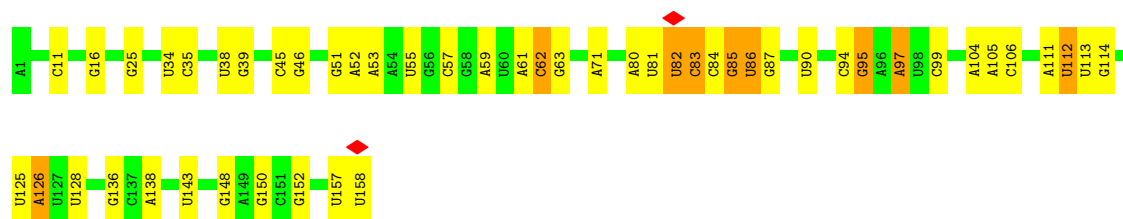
- Molecule 38: RPS26B isoform 1



- Molecule 39: 40S ribosomal protein S27-A

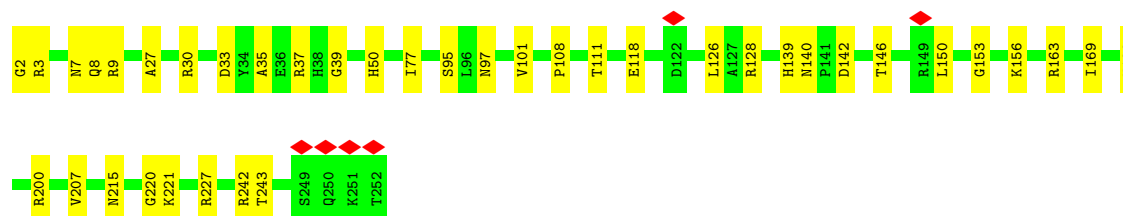
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U1100	C1201	A1271	C1386	A1503	A1602	U1720	G1832	G1969	A2029	G2095	A2251	G2375
G1103	A1202	C1272	A1386	A1508	A1603	U1721	G1833	U1970	U2030	A2096	A2252	G2376
A1104	G1206	A1273	A1390	C1508	G1604	U1722	A1839	C1971	U2031	C2101	A2256	G2377
U1114	G1207	U1276	G1391	U1511	A1605	A1723	U1840	A1972	U2032	U2102	G2261	G2385
G1115	U1208	C1277	G1392	U1517	A1606	U1724	A1841	G1973	G2033	G2111	A2262	U2388
G1116	U1210	C1278	A1399	G1521	U1620	C1725	A1842	A1974	G2034	U2112	C2263	G2392
G1117	G1280	C1279	G1400	U1522	A1613	U1729	A1846	C1975	U2035	A2113	A2270	C2393
C1118	A1217	G1281	G1403	U1523	U1624	G1730	C1849	G1976	G2037	C2118	A2271	G2394
G1126	U1218	G1282	G1404	U1528	A1621	A1760	A1850	C1977	C2038	G2121	G2272	A2397
U1128	C1222	G1285	U1405	U1529	G1624	G1751	A1859	G1978	U2040	G2122	G2273	A2402
G1131	A1223	A1287	A1406	G1533	U1626	C1756	A1866	G1979	U2041	A2131	U2274	A2404
A1135	G1227	U1293	A1407	U1536	U1629	A1761	C1867	G1980	U2043	A2139	A2279	U2411
A1136	C1228	G1295	G1412	G1537	U1630	C1762	A1868	G1981	U2044	U2147	A2280	G2412
U1144	G1230	U1299	C1416	A1558	A1631	U1763	A1874	G1982	U2045	U2148	G2281	A2419
G1145	C1231	U1306	G1417	G1559	A1632	U1764	G1875	U1986	A2047	G2154	G2282	C2422
C1146	C1232	G1307	A1418	G1560	C1633	U1765	U1876	G1987	G2048	G2155	G2283	U2434
G1147	G1233	A1308	A1419	G1561	G1634	G1766	U1880	C1988	A2049	A2158	C2284	G2435
G1148	G1234	U1309	C1420	U1549	U1638	G1767	A1881	U1989	C2050	G2169	U2285	U2436
G1152	U1235	U1312	G1421	U1555	C1639	G1770	A1893	U1992	U2056	U2170	G2286	G2437
A1153	G1236	G1313	U1427	C1556	A1642	C1771	U1896	G1993	U2059	G2185	G2287	A2438
A1154	C1237	U1314	A1428	A1557	A1643	U1772	A1897	G1994	A	U2186	G2288	A2439
C1155	G1238	G1315	G1429	A1558	A1644	G1775	G1897	G1995	G	G2187	U2292	A2440
A1240	C1239	U1316	U1430	G1559	U1645	G1778	G1898	G1996	U	A2188	U2293	C2306
G1157	U1241	C1317	G1431	G1560	G1646	C1779	G1899	U1997	U	C2196	G2294	G2307
A1158	G1242	A1317	G1434	C1562	A1656	U1780	G1906	G1998	U	G2201	A2299	A2303
A1159	G1243	A1318	C1437	C1563	A1657	C1788	C1907	U1999	U	U2205	G2300	C2306
U1167	A1244	U1322	U1442	U1564	G1658	C1793	A1908	U2000	U	G2206	G2301	G2307
A1170	G1245	U1325	U1443	A1566	C1671	U1794	A1930	G2001	G	U2207	A2308	C2308
G1177	U1247	U1326	G1443	U1567	G1677	U1795	G1935	G2002	U	U2208	A2309	A2309
A1179	G1248	A1330	A1446	U1568	U1683	U1796	C1943	G2003	U	A	U2310	U2310
U1180	C1249	G1345	G1447	U1569	U1684	A1797	G1951	U2004	G	U2209	A2313	A2445
U1181	A1251	U1348	U1450	U1570	C1685	A1798	C1952	G2005	A	G2218	U2314	U2446
A1182	C1252	G1349	U1455	A1571	U1686	A1799	G1953	G2006	C	A2223	G2315	A2447
G1186	C1254	U1351	G1473	C1574	U1687	G1808	G1954	G2007	U	U2231	A2207	G2448
C1187	G1255	U1352	A1477	A1575	U1688	U1814	U1955	G2008	C	A2232	A2208	G2450
U1188	U1256	U1353	A1481	G1576	C1693	A1815	A1956	G2009	G	G2237	U2081	G2451
C1189	A1259	G1354	U1482	U1580	A1696	U1816	G1957	U2010	U	A2244	U2082	G2452
A1190	A1260	A1355	U1483	C1581	A1704	G1817	U1958	U2011	U	A2245	G2083	U
U1191	G1261	U1356	U1484	A1583	U1705	U1818	G1959	G2012	U	A2246	U2086	G
C1192	C1262	U1357	G1487	A1587	G1712	U1819	A1960	C2013	A2086	A2247	A2087	A
A1193	A1263	U1361	G1488	A1588	A1715	U1820	G1961	U2014	A2087	A2248	A2088	A
C1196	U1264	A1362	G1489	A1589	G1591	U1821	A1962	U2015	A2088	A2249	A2089	A
A1197	G1265	A1363	U1591	G1590	A1715	C1822	G1963	U2016	U2090	A2250	A2091	A
C1198	U1267	C1364	G1591	A1715	A1715	A1823	C1964	G2017	A2092	A2251	A2092	G
						U1824		G2018				U
								U2019				
								A2020				
								G2021				
								G2022				
								C2023				
								G2024				
								G2025				
								A2026				





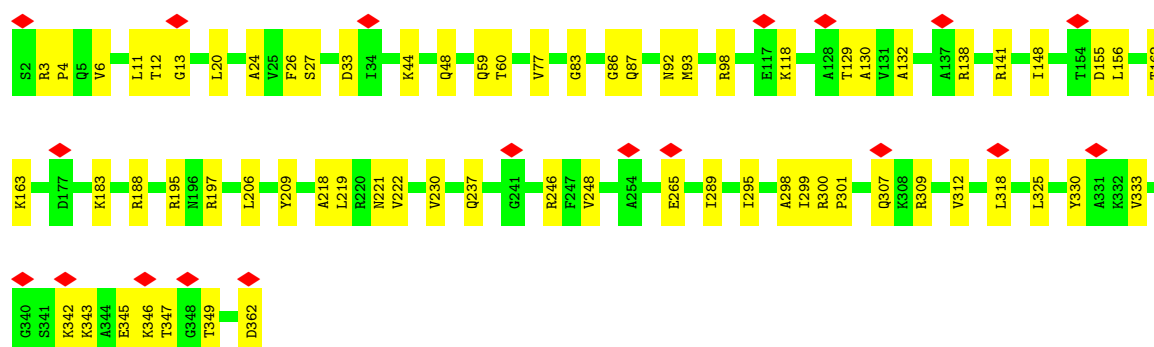
- Molecule 44: 60S ribosomal protein L2-A

Chain AW: 84% 16%



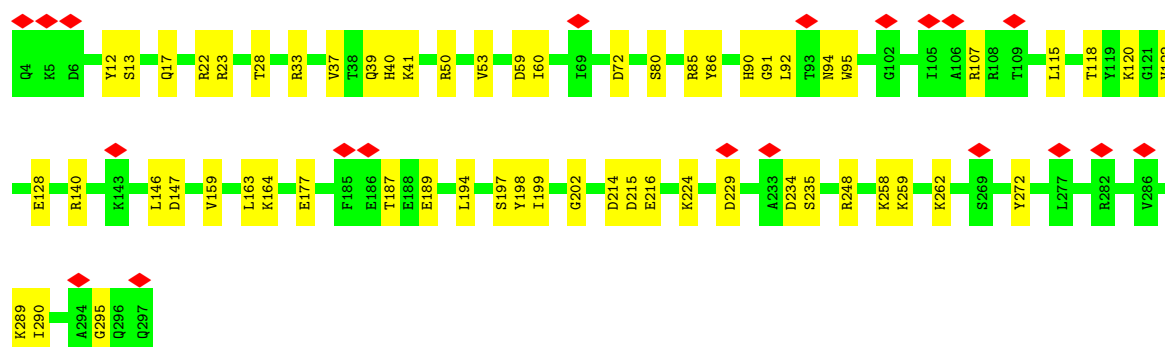
- Molecule 45: RPL4A isoform 1

Chain BE: 5% 81% 19%



- Molecule 46: RPL5 isoform 1

Chain BI: 7% 80% 20%



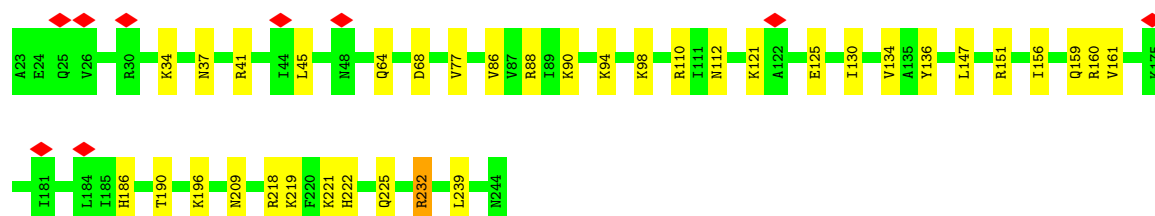
- Molecule 47: 60S ribosomal protein L6-B

Chain BM: 



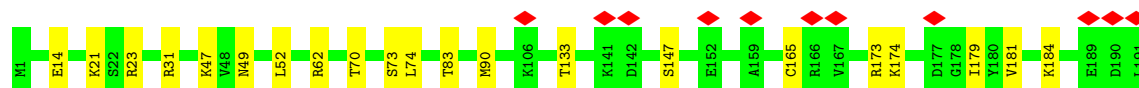
- Molecule 48: 60S ribosomal protein L7-A

Chain BO: 



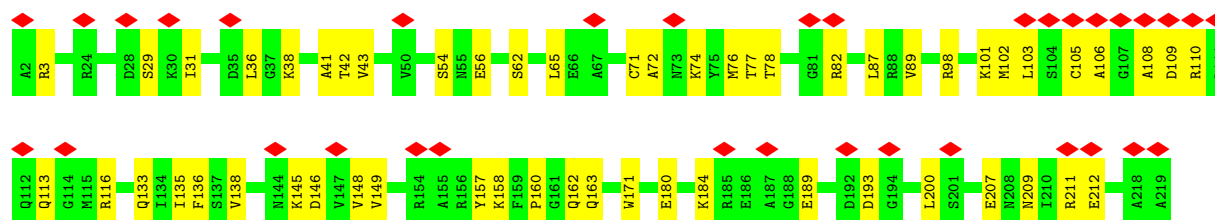
- Molecule 49: RPL9A isoform 1

Chain AD: 



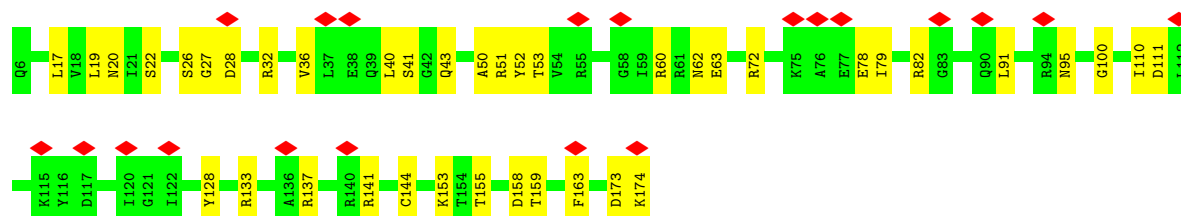
- Molecule 50: RPL10 isoform 1

Chain BD: 

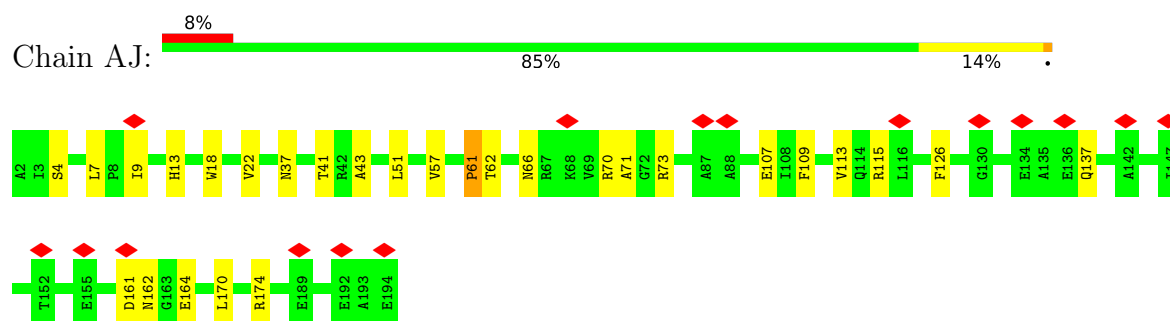


- Molecule 51: RPL11B isoform 1

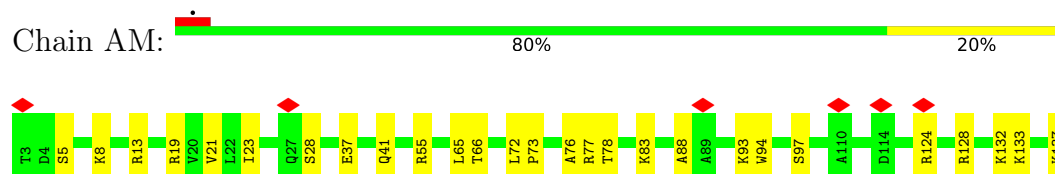
Chain AG: 



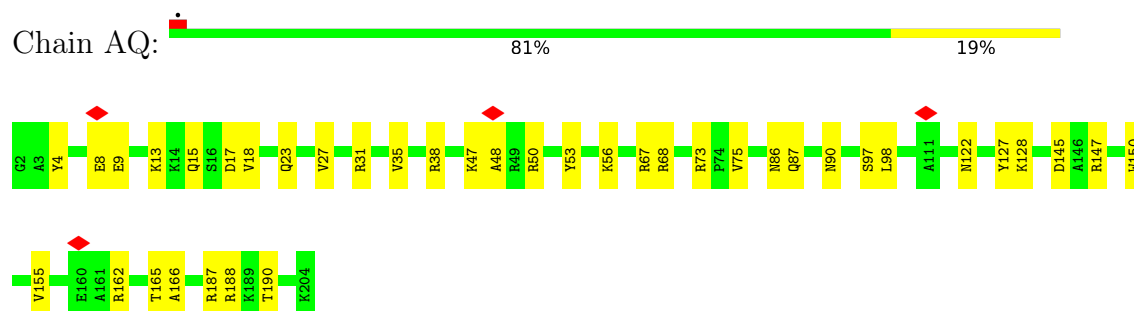
- Molecule 52: 60S ribosomal protein L13-A



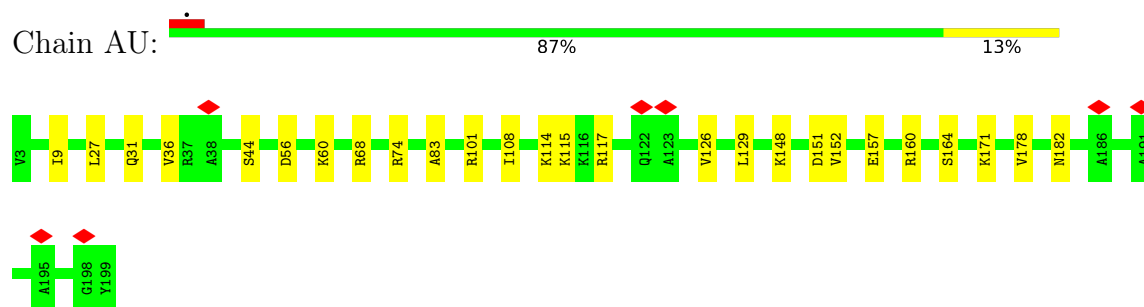
- Molecule 53: 60S ribosomal protein L14-A



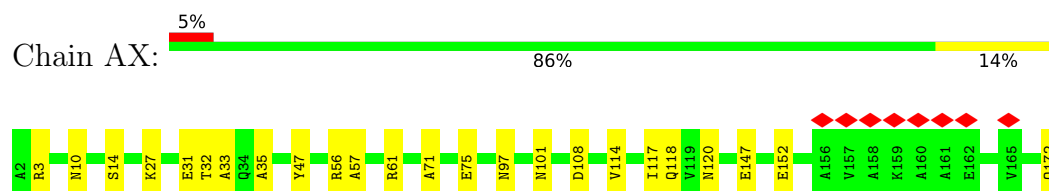
- Molecule 54: 60S ribosomal protein L15-A



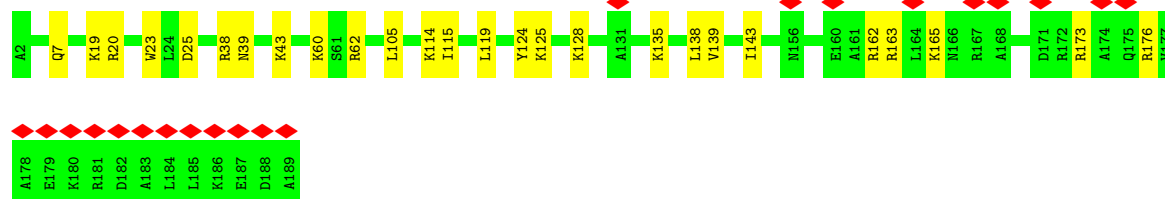
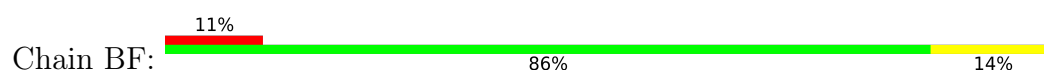
- Molecule 55: 60S ribosomal protein L16-A



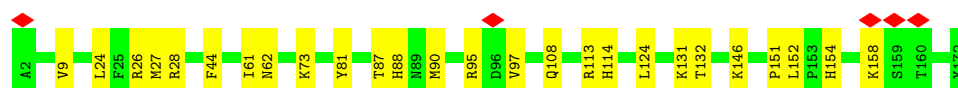
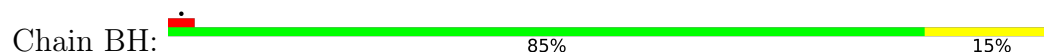
- Molecule 56: 60S ribosomal protein L17-A



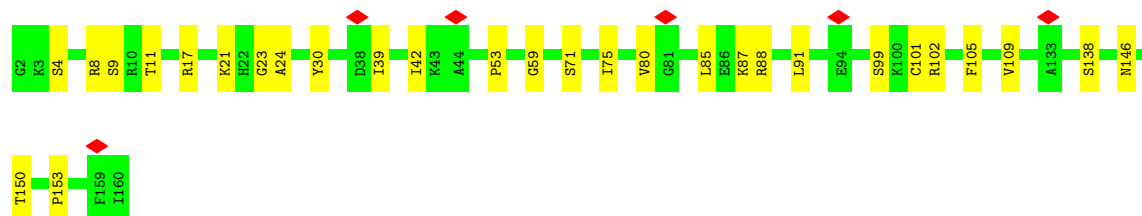
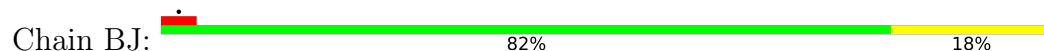
- Molecule 57: 60S ribosomal protein L19-A



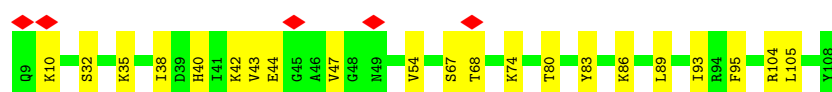
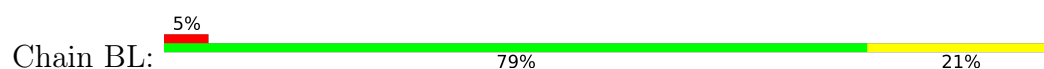
- Molecule 58: 60S ribosomal protein L20-A



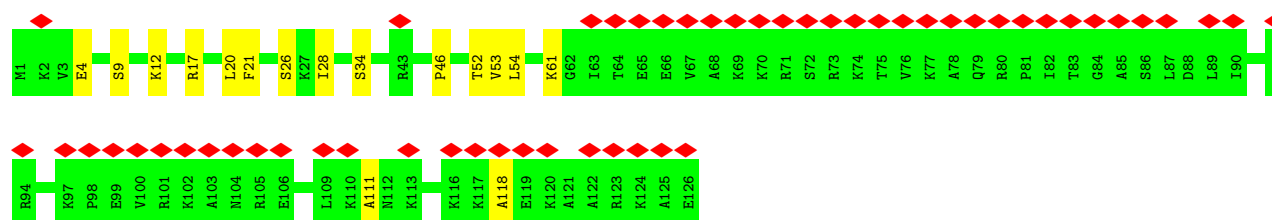
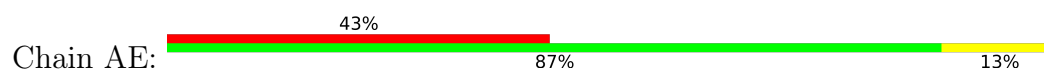
- Molecule 59: 60S ribosomal protein L21-A



- Molecule 60: 60S ribosomal protein L22-A



- Molecule 61: 60S ribosomal protein L24-A



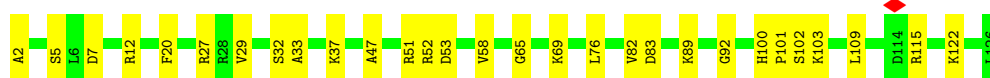
- Molecule 62: 60S ribosomal protein L25





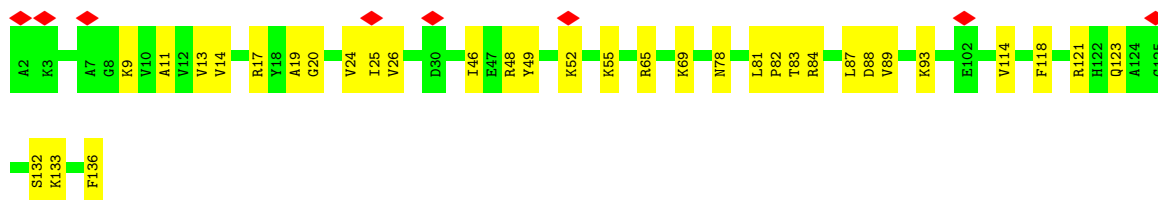
- Molecule 63: 60S ribosomal protein L26-A

Chain AK: 77% 23%



- Molecule 64: 60S ribosomal protein L27-A

Chain AN: 6% 76% 24%



- Molecule 65: 60S ribosomal protein L28

Chain AR: 84% 16%



- Molecule 66: 60S ribosomal protein L29

Chain AV: 9% 84% 14%



- Molecule 67: 60S ribosomal protein L30

Chain AY: 6% 70% 28%

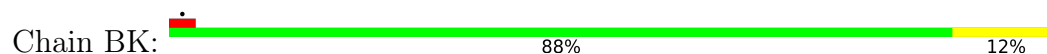


- Molecule 68: RPL32 isoform 1

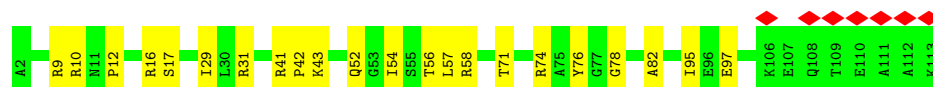
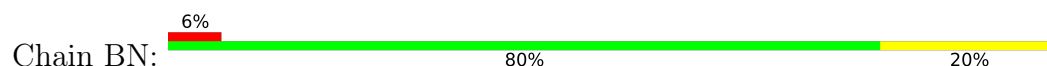
Chain BG: 79% 21%



- Molecule 69: 60S ribosomal protein L33-A



- Molecule 70: 60S ribosomal protein L34-A



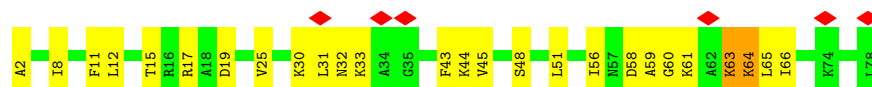
- Molecule 71: 60S ribosomal protein L35-A



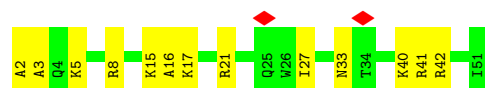
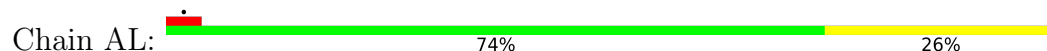
- Molecule 72: 60S ribosomal protein L37-A



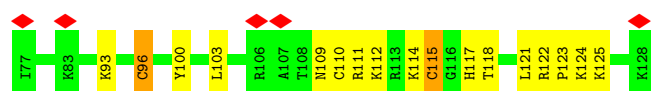
- Molecule 73: RPL38 isoform 1



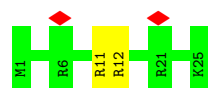
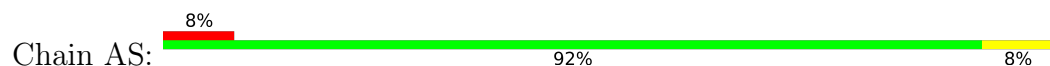
- Molecule 74: 60S ribosomal protein L39



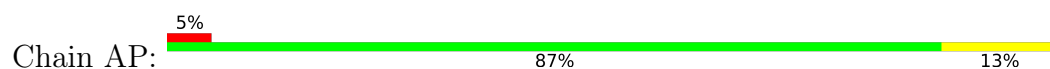
- Molecule 75: 60S ribosomal protein L40-A



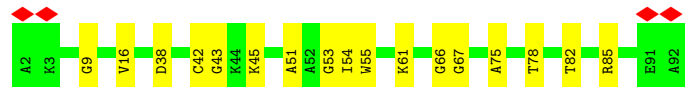
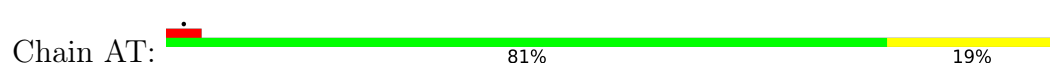
- Molecule 76: 60S ribosomal protein L41



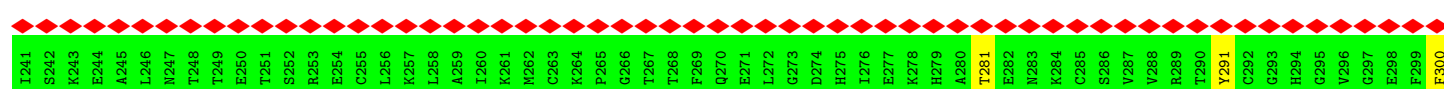
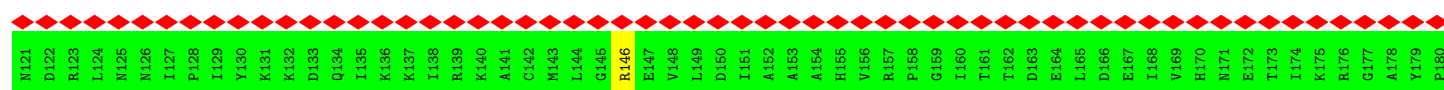
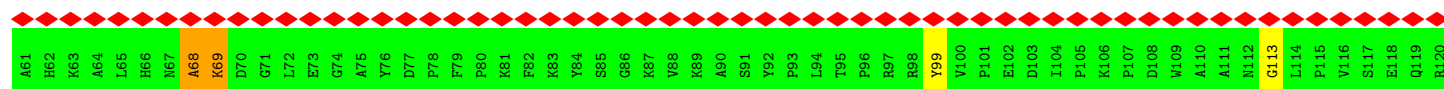
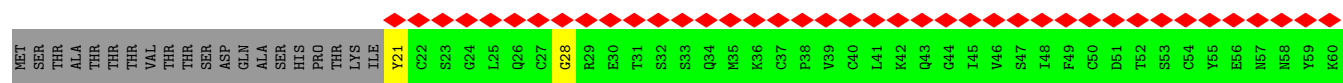
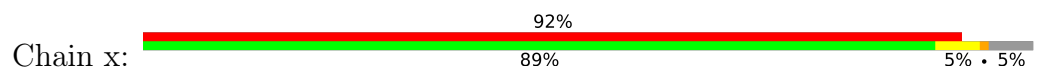
- Molecule 77: 60S ribosomal protein L42-A

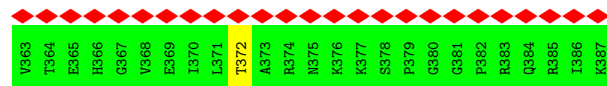
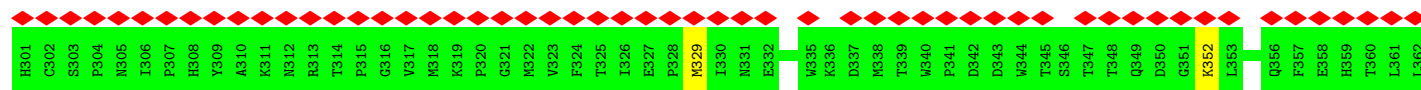


- Molecule 78: 60S ribosomal protein L43-A

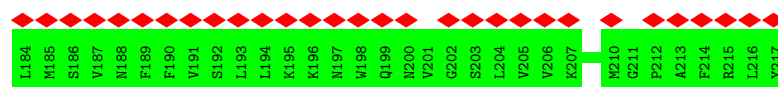
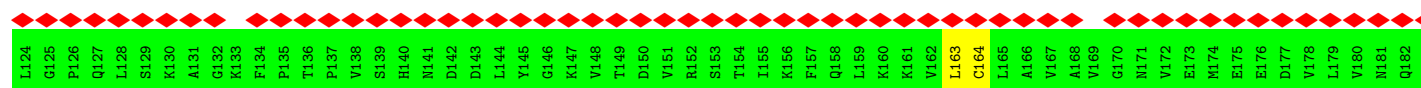
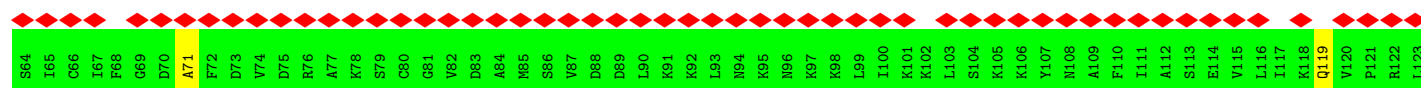


- Molecule 79: Methionine aminopeptidase 1





- Molecule 80: 60S ribosomal protein L1-A



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	11938	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 ($e^-/\text{\AA}^2$)	56.16	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3200	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.094	Depositor
Minimum map value	-0.045	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	455.28, 455.28, 455.28	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	B	0.30	0/1625	0.55	0/2197
2	A	0.33	0/1754	0.53	0/2361
3	C	0.26	0/769	0.50	0/1039
4	D	0.24	0/883	0.61	0/1199
5	E	0.28	0/936	0.57	0/1259
6	F	0.33	0/1125	0.54	0/1510
7	G	0.29	0/957	0.47	0/1283
8	H	0.27	0/1207	0.49	0/1623
9	I	0.31	0/1130	0.54	1/1517 (0.1%)
10	J	0.33	0/807	0.52	0/1091
11	K	0.25	0/661	0.52	0/888
12	L	0.29	0/493	0.60	0/663
13	M	0.40	0/452	0.65	0/600
14	N	0.25	0/567	0.59	0/764
15	O	0.25	0/2436	0.51	0/3318
16	P	0.30	0/1644	0.51	0/2249
17	Q	0.29	0/1823	0.60	2/2447 (0.1%)
18	R	0.38	0/1656	0.55	0/2251
19	S	0.32	0/2097	0.56	0/2823
20	T	0.29	0/1839	0.55	0/2460
21	U	0.36	0/1498	0.65	3/2019 (0.1%)
22	V	0.36	0/1501	0.53	0/2006
23	W	0.31	0/1504	0.57	0/2016
24	X	0.38	0/1168	0.49	0/1575
25	Y	0.36	0/1215	0.58	0/1638
26	Z	0.32	0/934	0.58	0/1257
27	AA	0.43	0/1836	0.56	0/2481
28	BA	0.56	0/3146	0.57	0/4228
29	AB	0.56	0/1018	0.52	0/1369
30	BB	0.54	0/1465	0.57	0/1965
31	AC	0.41	0/772	0.54	0/1026
32	BC	0.55	0/890	0.54	0/1196

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	2	0.33	0/42211	0.44	2/65773 (0.0%)
34	a	0.29	0/682	0.52	0/921
35	b	0.39	0/1038	0.56	1/1395 (0.1%)
36	c	0.42	0/1139	0.59	0/1518
37	d	0.26	0/1046	0.46	0/1401
38	e	0.39	0/778	0.59	0/1042
39	f	0.27	0/620	0.50	0/838
40	g	0.30	0/480	0.53	0/639
41	BQ	0.49	0/78951	0.49	13/123085 (0.0%)
42	BR	0.38	0/2883	0.39	0/4491
43	BS	0.50	0/3746	0.46	0/5832
44	AW	0.64	0/1933	0.62	0/2598
45	BE	0.55	0/2800	0.61	0/3790
46	BI	0.39	0/2400	0.51	0/3239
47	BM	0.44	0/1329	0.57	0/1794
48	BO	0.56	0/1821	0.59	0/2451
49	AD	0.39	0/1529	0.50	0/2060
50	BD	0.44	0/1801	0.56	0/2416
51	AG	0.33	0/1367	0.51	0/1834
52	AJ	0.52	0/1568	0.56	0/2106
53	AM	0.43	0/1068	0.55	0/1438
54	AQ	0.66	0/1757	0.63	0/2354
55	AU	0.58	0/1585	0.53	0/2128
56	AX	0.61	0/1439	0.57	0/1938
57	BF	0.50	0/1532	0.53	0/2043
58	BH	0.50	0/1473	0.56	0/1980
59	BJ	0.51	0/1296	0.53	0/1739
60	BL	0.36	0/812	0.48	0/1099
61	AE	0.42	0/850	0.48	0/1152
62	AH	0.51	0/979	0.54	0/1321
63	AK	0.48	0/995	0.53	0/1329
64	AN	0.42	0/1106	0.53	0/1485
65	AR	0.60	0/1200	0.60	0/1607
66	AV	0.48	0/473	0.58	0/629
67	AY	0.42	0/745	0.67	2/1001 (0.2%)
68	BG	0.60	0/1038	0.56	0/1390
69	BK	0.63	0/868	0.65	0/1168
70	BN	0.57	0/890	0.63	0/1189
71	BP	0.48	0/978	0.53	0/1301
72	AF	0.76	1/660 (0.2%)	0.88	2/875 (0.2%)
73	AI	0.37	0/618	0.51	0/826
74	AL	0.64	0/443	0.58	0/588
75	AO	0.72	1/416 (0.2%)	0.95	2/553 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	AS	0.49	0/230	0.78	0/296
77	AP	0.74	2/836 (0.2%)	0.75	3/1104 (0.3%)
78	AT	0.65	0/701	0.72	0/934
79	x	0.73	0/2970	1.20	2/4023 (0.0%)
80	BT	0.61	0/1074	1.17	2/1496 (0.1%)
All	All	0.45	4/220962 (0.0%)	0.53	35/324527 (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
1	B	0	1
4	D	0	1
6	F	0	1
9	I	0	1
12	L	0	1
14	N	0	1
19	S	0	1
26	Z	0	1
27	AA	0	3
30	BB	0	1
32	BC	0	1
35	b	0	1
45	BE	0	3
48	BO	0	1
65	AR	0	2
66	AV	0	2
71	BP	0	1
All	All	0	23

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
77	AP	14	GLY	C-N	7.24	1.43	1.33
75	AO	103	LEU	C-N	6.36	1.40	1.33
72	AF	39	TYR	C-N	6.08	1.45	1.34
77	AP	79	THR	N-CA	-6.06	1.38	1.46

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
67	AY	48	THR	CA-C-N	8.95	131.03	119.84
67	AY	48	THR	C-N-CA	8.95	131.03	119.84
77	AP	79	THR	N-CA-C	-7.92	96.39	108.67
41	BQ	2093	A	C1'-C2'-O2'	-7.37	97.34	108.40
41	BQ	1986	U	C4'-C3'-O3'	-7.22	102.17	113.00
75	AO	96	CYS	CA-C-N	6.94	129.46	120.44
75	AO	96	CYS	C-N-CA	6.94	129.46	120.44
21	U	64	VAL	CA-C-N	-6.93	112.65	121.04
21	U	64	VAL	C-N-CA	-6.93	112.65	121.04
41	BQ	1963	G	C4'-C3'-O3'	6.90	123.35	113.00
41	BQ	1960	A	C4'-C3'-O3'	6.78	123.17	113.00
41	BQ	1960	A	N9-C1'-C2'	-6.61	102.08	112.00
41	BQ	1985	G	C4'-C3'-O3'	6.61	122.91	113.00
41	BQ	1959	G	P-O3'-C3'	6.24	129.55	120.20
72	AF	22	CYS	CA-C-N	5.98	133.13	121.41
72	AF	22	CYS	C-N-CA	5.98	133.13	121.41
33	2	400	A	C2'-C3'-O3'	5.81	118.21	109.50
77	AP	14	GLY	CA-C-O	-5.78	110.52	120.57
41	BQ	1984	C	C4'-C3'-O3'	5.67	121.50	113.00
17	Q	43	VAL	CA-C-N	-5.59	113.69	120.51
17	Q	43	VAL	C-N-CA	-5.59	113.69	120.51
35	b	28	ARG	C-N-CD	-5.57	108.35	120.60
41	BQ	1961	G	C3'-C2'-O2'	5.43	118.85	110.70
41	BQ	1959	G	C3'-C2'-O2'	5.42	118.83	110.70
80	BT	119	GLN	CA-C-N	5.41	124.66	120.33
80	BT	119	GLN	C-N-CA	5.41	124.66	120.33
41	BQ	1989	U	C1'-C2'-O2'	-5.31	100.44	108.40
79	x	69	LYS	N-CA-C	5.22	118.40	111.30
33	2	400	A	P-O3'-C3'	5.21	128.02	120.20
41	BQ	1959	G	C2'-C3'-O3'	5.15	121.42	113.70
21	U	64	VAL	N-CA-C	5.13	119.96	108.88
77	AP	12	CYS	CA-CB-SG	-5.08	102.71	114.40
79	x	300	PHE	CA-CB-CG	5.08	118.88	113.80
41	BQ	2083	G	O4'-C4'-C3'	5.06	109.06	104.00
9	I	121	GLY	N-CA-C	5.03	116.64	111.56

There are no chirality outliers.

All (23) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
27	AA	30	THR	Peptide
27	AA	76	ALA	Peptide
27	AA	77	GLN	Peptide

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Mol	Chain	Res	Type	Group
65	AR	115	LYS	Peptide
65	AR	14	HIS	Peptide
66	AV	19	ASN	Peptide
66	AV	20	GLY	Peptide
1	B	42	LEU	Peptide
30	BB	161	LYS	Peptide
32	BC	7	VAL	Peptide
45	BE	13	GLY	Peptide
45	BE	3	ARG	Peptide
45	BE	318	LEU	Peptide
48	BO	232	ARG	Peptide
71	BP	83	LYS	Peptide
4	D	108	ARG	Peptide
6	F	40	GLU	Peptide
9	I	120	GLY	Peptide
12	L	19	THR	Peptide
14	N	147	VAL	Peptide
19	S	193	GLY	Peptide
26	Z	90	ARG	Peptide
35	b	54	ASP	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1605	0	1669	46	0
2	A	1729	0	1812	26	0
3	C	752	0	719	17	0
4	D	875	0	878	23	0
5	E	916	0	941	29	0
6	F	1105	0	1166	30	0
7	G	948	0	990	20	0
8	H	1188	0	1218	34	0
9	I	1112	0	1124	25	0
10	J	797	0	863	18	0
11	K	651	0	682	18	0
12	L	491	0	524	13	0
13	M	442	0	428	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	N	556	0	549	24	0
15	O	2383	0	2332	57	0
16	P	1603	0	1610	35	0
17	Q	1798	0	1890	58	0
18	R	1626	0	1715	40	0
19	S	2056	0	2140	68	0
20	T	1815	0	1894	41	0
21	U	1473	0	1554	56	0
22	V	1476	0	1501	35	0
23	W	1479	0	1556	26	0
24	X	1142	0	1209	20	0
25	Y	1192	0	1255	23	0
26	Z	923	0	948	27	0
27	AA	1804	0	1877	32	0
28	BA	3075	0	3142	59	0
29	AB	1003	0	1048	19	0
30	BB	1441	0	1543	20	0
31	AC	766	0	844	7	0
32	BC	876	0	912	9	0
33	2	37739	0	18988	512	0
34	a	673	0	662	17	0
35	b	1021	0	1060	21	0
36	c	1121	0	1196	24	0
37	d	1032	0	1044	32	0
38	e	765	0	814	18	0
39	f	610	0	633	15	0
40	g	472	0	521	11	0
41	BQ	70544	0	35450	620	0
42	BR	2579	0	1304	22	0
43	BS	3353	0	1695	26	0
44	AW	1899	0	1957	30	0
45	BE	2748	0	2859	54	0
46	BI	2351	0	2294	44	0
47	BM	1307	0	1377	22	0
48	BO	1784	0	1862	27	0
49	AD	1508	0	1572	17	0
50	BD	1764	0	1804	37	0
51	AG	1346	0	1370	29	0
52	AJ	1543	0	1608	21	0
53	AM	1053	0	1149	23	0
54	AQ	1720	0	1779	27	0
55	AU	1555	0	1659	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	AX	1416	0	1433	18	0
57	BF	1515	0	1606	29	0
58	BH	1437	0	1475	20	0
59	BJ	1272	0	1312	24	0
60	BL	796	0	812	13	0
61	AE	836	0	706	12	0
62	AH	964	0	1025	13	0
63	AK	984	0	1075	19	0
64	AN	1080	0	1122	23	0
65	AR	1169	0	1211	18	0
66	AV	462	0	491	7	0
67	AY	737	0	792	23	0
68	BG	1017	0	1081	19	0
69	BK	850	0	880	12	0
70	BN	880	0	942	22	0
71	BP	969	0	1078	9	0
72	AF	645	0	645	16	0
73	AI	612	0	682	26	0
74	AL	436	0	475	13	0
75	AO	410	0	442	13	0
76	AS	229	0	273	2	0
77	AP	824	0	890	12	0
78	AT	694	0	734	13	0
79	x	2899	0	2854	16	0
80	BT	1075	0	464	13	0
81	AF	1	0	0	0	0
81	AO	1	0	0	0	0
81	AP	1	0	0	0	0
81	AT	1	0	0	0	0
81	BN	1	0	0	0	0
81	M	1	0	0	0	0
81	N	1	0	0	0	0
All	All	205800	0	151690	2403	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 7.

All (2403) 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)
14:N:123:ASN:ND2	14:N:125:THR:OG1	1.81	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:BQ:2494:A:H4'	80:BT:37:GLY:HA3	1.29	1.07
41:BQ:1977:C:N4	41:BQ:2046:U:O2'	1.88	1.06
41:BQ:1979:G:C6	41:BQ:2045:G:N2	2.26	1.03
21:U:116:ARG:HG3	33:2:856:A:N6	1.74	1.02
78:AT:53:GLY:HA2	78:AT:66:GLY:O	1.61	1.01
41:BQ:2022:G:OP1	79:x:352:LYS:HE3	1.60	1.01
79:x:223:TYR:OH	79:x:226:GLY:HA2	1.61	1.00
41:BQ:2494:A:H4'	80:BT:37:GLY:CA	1.93	0.96
41:BQ:1976:G:N1	41:BQ:2047:A:N3	2.05	0.96
41:BQ:383:G:N2	41:BQ:386:A:N7	2.15	0.94
41:BQ:1979:G:N1	41:BQ:2045:G:N2	2.17	0.93
33:2:219:A:H61	33:2:842:C:H42	1.03	0.93
21:U:116:ARG:HG3	33:2:856:A:H62	1.27	0.92
67:AY:48:THR:CG2	67:AY:49:PRO:HD2	2.00	0.91
41:BQ:1960:A:H2'	41:BQ:1961:G:H4'	1.53	0.90
41:BQ:1977:C:H42	41:BQ:2046:U:C2'	1.84	0.90
33:2:219:A:H61	33:2:842:C:N4	1.70	0.89
78:AT:53:GLY:CA	78:AT:66:GLY:O	2.20	0.89
46:BI:115:LEU:O	46:BI:118:THR:O	1.91	0.89
24:X:65:SER:HG	33:2:114:C:HO2'	1.21	0.89
15:O:167:VAL:HG13	15:O:183:LEU:HD21	1.58	0.86
33:2:219:A:N6	33:2:842:C:H42	1.74	0.85
41:BQ:1238:C:O2	41:BQ:1250:G:N2	2.09	0.85
41:BQ:1977:C:N4	41:BQ:2046:U:C2'	2.40	0.85
2:A:39:VAL:HA	2:A:47:GLU:O	1.76	0.84
41:BQ:3163:A:N6	41:BQ:3288:G:O6	2.10	0.83
14:N:123:ASN:ND2	14:N:144:CYS:SG	2.51	0.83
33:2:959:U:OP2	39:f:20:LYS:NZ	2.12	0.82
41:BQ:1958:U:N3	41:BQ:2083:G:O6	2.12	0.82
33:2:655:G:C2	33:2:678:A:N6	2.47	0.82
41:BQ:1634:G:N7	64:AN:17:ARG:NH1	2.27	0.81
41:BQ:2679:A:O2'	51:AG:52:TYR:OH	1.98	0.81
1:B:121:ILE:O	1:B:124:LEU:O	1.99	0.81
41:BQ:925:A:N6	44:AW:2:GLY:O	2.13	0.81
41:BQ:1977:C:H42	41:BQ:2046:U:H1'	1.44	0.81
41:BQ:1057:A:OP1	48:BO:98:LYS:NZ	2.14	0.81
41:BQ:1977:C:H42	41:BQ:2046:U:C1'	1.93	0.80
41:BQ:1639:C:OP2	70:BN:74:ARG:NH2	2.15	0.80
21:U:116:ARG:NE	33:2:856:A:C6	2.49	0.80
33:2:478:A:N6	33:2:539:G:C2	2.49	0.80
33:2:479:C:O2	33:2:510:G:N2	2.14	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:BQ:3163:A:C6	41:BQ:3288:G:C6	2.69	0.80
33:2:1029:U:OP2	38:e:12:LYS:NZ	2.14	0.80
41:BQ:1876:U:OP2	57:BF:19:LYS:NZ	2.14	0.80
41:BQ:3163:A:N6	41:BQ:3288:G:C6	2.50	0.80
41:BQ:3092:C:O2'	41:BQ:3094:A:OP2	1.99	0.79
17:Q:80:SER:O	17:Q:83:LYS:NZ	2.15	0.79
17:Q:136:ARG:O	17:Q:215:VAL:HA	1.81	0.79
44:AW:27:ALA:O	44:AW:128:ARG:NH2	2.16	0.79
74:AL:27:ILE:O	74:AL:33:ASN:ND2	2.16	0.79
33:2:1229:G:H21	33:2:1256:A:H62	1.29	0.79
21:U:116:ARG:CG	33:2:856:A:N6	2.45	0.79
13:M:7:TRP:O	33:2:1450:U:O2'	2.00	0.79
24:X:37:ASN:O	33:2:247:A:O2'	2.00	0.79
41:BQ:2282:U:OP1	41:BQ:2973:G:O2'	2.01	0.79
26:Z:17:ALA:O	26:Z:29:HIS:O	2.01	0.79
33:2:1230:A:C8	33:2:1255:G:N2	2.49	0.79
41:BQ:1868:G:O2'	41:BQ:2118:C:O2'	2.01	0.78
13:M:10:HIS:O	13:M:12:ARG:NH2	2.15	0.78
9:I:86:ARG:NH1	33:2:1601:G:OP1	2.17	0.78
26:Z:132:ARG:NH2	33:2:1789:G:OP2	2.17	0.78
41:BQ:525:C:O2	41:BQ:568:G:N2	2.17	0.78
33:2:467:G:O2'	33:2:469:C:OP2	2.02	0.78
61:AE:4:GLU:O	61:AE:12:LYS:HA	1.82	0.78
33:2:1339:C:O2'	33:2:1341:A:N7	2.16	0.77
41:BQ:1592:G:OP1	70:BN:58:ARG:NH2	2.17	0.77
41:BQ:2092:A:H2'	41:BQ:2093:A:H4'	1.65	0.77
16:P:103:THR:O	16:P:106:SER:OG	2.03	0.77
33:2:705:U:O2'	33:2:706:A:O5'	2.03	0.77
41:BQ:177:U:O4	41:BQ:239:G:N2	2.17	0.77
33:2:1484:G:N2	33:2:1606:C:O2	2.16	0.77
41:BQ:1899:G:O2'	41:BQ:2334:U:O4	2.02	0.77
3:C:29:GLN:NE2	3:C:31:LYS:O	2.17	0.77
28:BA:10:ARG:NH2	28:BA:11:HIS:O	2.18	0.77
63:AK:29:VAL:O	63:AK:32:SER:OG	2.03	0.77
33:2:458:G:OP2	37:d:105:ARG:NH2	2.18	0.77
33:2:655:G:C2	33:2:678:A:C6	2.73	0.77
42:BR:21:G:HO2'	46:BI:272:TYR:HH	1.22	0.77
30:BB:38:ARG:NH2	41:BQ:1348:U:OP2	2.18	0.77
41:BQ:1363:A:OP1	48:BO:160:ARG:NH1	2.18	0.77
41:BQ:2185:G:O2'	41:BQ:2314:U:OP2	2.03	0.77
41:BQ:2494:A:C4'	80:BT:37:GLY:HA3	2.13	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2:1208:A:O2'	33:2:1270:G:OP2	2.04	0.77
17:Q:25:THR:O	17:Q:50:LYS:NZ	2.18	0.76
17:Q:76:SER:OG	17:Q:78:ASP:OD1	2.02	0.76
41:BQ:1729:A:O4'	67:AY:52:ARG:NH1	2.18	0.76
33:2:61:A:O2'	33:2:62:A:O4'	2.03	0.76
33:2:1198:G:OP1	33:2:1199:G:O2'	2.02	0.76
36:c:42:PRO:O	36:c:79:ASN:ND2	2.18	0.76
41:BQ:269:G:OP1	54:AQ:47:LYS:NZ	2.17	0.76
41:BQ:1977:C:C4	41:BQ:2046:U:O2'	2.37	0.76
41:BQ:2852:C:N3	50:BD:158:LYS:NZ	2.32	0.76
52:AJ:4:SER:O	65:AR:44:ASN:ND2	2.19	0.76
28:BA:10:ARG:NH1	28:BA:263:SER:O	2.19	0.76
41:BQ:1624:G:O6	41:BQ:1819:U:O4	2.02	0.76
21:U:27:LEU:O	21:U:31:SER:OG	2.03	0.76
41:BQ:146:U:O2	41:BQ:148:G:C2	2.39	0.76
41:BQ:2205:U:O4	41:BQ:2237:C:N3	2.19	0.76
50:BD:209:ASN:O	50:BD:212:GLU:O	2.04	0.76
3:C:44:LYS:NZ	33:2:1217:A:O3'	2.19	0.76
41:BQ:1979:G:O6	41:BQ:2045:G:N2	2.18	0.76
47:BM:31:ARG:NH1	69:BK:107:ILE:O	2.19	0.76
51:AG:28:ASP:OD2	80:BT:71:ALA:HB3	1.84	0.76
3:C:11:ILE:HD11	3:C:42:VAL:HG22	1.67	0.75
8:H:138:THR:OG1	33:2:1459:C:OP2	2.04	0.75
33:2:651:G:C6	33:2:684:A:N1	2.54	0.75
41:BQ:593:C:OP2	47:BM:19:LYS:NZ	2.19	0.75
38:e:7:SER:OG	38:e:10:ARG:O	2.03	0.75
38:e:87:ARG:NH1	38:e:91:ASP:O	2.19	0.75
41:BQ:68:C:OP2	41:BQ:301:G:N2	2.19	0.75
44:AW:30:ARG:O	44:AW:163:ARG:NH1	2.20	0.75
11:K:50:ILE:HG22	11:K:69:LEU:HD13	1.68	0.75
18:R:236:PRO:O	34:a:33:GLN:NE2	2.18	0.75
41:BQ:2093:A:C2	57:BF:143:ILE:HD11	2.21	0.75
41:BQ:3212:C:OP2	53:AM:124:ARG:NH2	2.18	0.75
11:K:74:SER:OG	33:2:1534:G:OP2	2.05	0.75
19:S:141:THR:OG1	19:S:143:ASP:OD1	2.03	0.75
33:2:486:G:N2	33:2:501:U:O2'	2.19	0.75
17:Q:5:LYS:NZ	33:2:900:A:N7	2.33	0.75
27:AA:95:ASN:OD1	27:AA:98:ARG:NH2	2.20	0.75
6:F:135:ARG:NH1	33:2:1582:U:OP1	2.20	0.75
22:V:172:ARG:NH1	33:2:330:G:OP2	2.20	0.75
41:BQ:439:C:O2'	41:BQ:440:A:OP1	2.03	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:f:56:CYS:SG	39:f:61:THR:OG1	2.44	0.75
41:BQ:592:A:O2'	47:BM:20:LYS:NZ	2.16	0.75
67:AY:48:THR:HG23	67:AY:49:PRO:HD2	1.69	0.75
29:AB:10:LYS:O	41:BQ:3039:C:O2'	2.04	0.74
33:2:1179:G:H21	33:2:1460:A:H62	1.34	0.74
41:BQ:3163:A:C6	41:BQ:3288:G:N1	2.54	0.74
33:2:67:A:N6	33:2:83:G:O2'	2.20	0.74
33:2:1022:C:O2'	33:2:1125:A:N1	2.19	0.74
41:BQ:3216:G:OP2	69:BK:2:ALA:N	2.19	0.74
44:AW:95:SER:OG	44:AW:97:ASN:ND2	2.21	0.74
17:Q:148:ASN:OD1	33:2:1066:C:O2'	2.05	0.74
33:2:477:A:O2'	40:g:33:ARG:NH2	2.20	0.74
41:BQ:3186:A:O2'	49:AD:23:ARG:NH2	2.20	0.74
1:B:109:LYS:NZ	33:2:1474:G:OP1	2.20	0.74
33:2:17:C:O2'	33:2:1137:A:N1	2.19	0.74
33:2:853:G:OP1	57:BF:176:ARG:NH1	2.21	0.74
41:BQ:1613:A:OP1	73:AI:2:ALA:N	2.20	0.74
41:BQ:2767:U:O2'	77:AP:30:ALA:O	2.05	0.74
41:BQ:3008:A:OP2	55:AU:74[A]:ARG:NH1	2.21	0.74
22:V:31:ARG:NH2	33:2:333:A:OP2	2.20	0.74
41:BQ:533:A:O2'	41:BQ:535:G:OP2	2.06	0.74
41:BQ:1523:U:O4	62:AH:75:LYS:NZ	2.20	0.74
71:BP:76:GLN:O	71:BP:81:ARG:NH2	2.20	0.74
2:A:56:GLN:NE2	2:A:57:ASP:OD1	2.21	0.74
6:F:14:LYS:O	6:F:123:ARG:NH1	2.21	0.74
8:H:144:ARG:NH1	33:2:1461:C:OP1	2.20	0.74
27:AA:193:LYS:NZ	41:BQ:145:G:OP2	2.16	0.74
58:BH:26:ARG:NH1	59:BJ:150:THR:OG1	2.20	0.74
6:F:66:ARG:NH2	33:2:1366:U:OP2	2.21	0.74
30:BB:170:ARG:NH2	41:BQ:89:A:OP2	2.20	0.74
41:BQ:1973:G:H1'	41:BQ:2049:A:H61	1.52	0.74
41:BQ:542:G:C6	41:BQ:550:A:C6	2.76	0.73
24:X:38:ALA:O	33:2:246:G:N2	2.22	0.73
25:Y:121:ARG:NH1	33:2:868:G:OP1	2.21	0.73
41:BQ:213:A:O4'	63:AK:2:ALA:N	2.21	0.73
41:BQ:640:U:OP1	65:AR:21:ARG:NH2	2.22	0.73
47:BM:102:ASN:ND2	47:BM:104:GLU:OE1	2.22	0.73
8:H:22:VAL:HG22	8:H:35:ILE:HD11	1.69	0.73
9:I:119:LYS:NZ	33:2:1370:U:OP1	2.22	0.73
41:BQ:3111:U:OP1	49:AD:184:LYS:NZ	2.21	0.73
3:C:8:ARG:NH2	33:2:1257:U:O2'	2.21	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:20:VAL:HG21	5:E:28:MET:HE1	1.70	0.73
9:I:12:GLN:NE2	33:2:1479:A:N3	2.36	0.73
33:2:74:U:O2'	33:2:76:A:OP2	2.05	0.73
9:I:75:LYS:NZ	33:2:1497:U:O3'	2.22	0.73
14:N:123:ASN:HB3	14:N:126:CYS:SG	2.28	0.73
15:O:214:ALA:HB1	15:O:240:VAL:HG21	1.71	0.73
24:X:102:LYS:O	36:c:13:ARG:NH2	2.20	0.73
41:BQ:815:G:OP2	72:AF:31:LYS:NZ	2.21	0.73
41:BQ:1016:C:N4	41:BQ:2671:A:OP1	2.21	0.73
1:B:121:ILE:O	1:B:124:LEU:C	2.32	0.73
4:D:34:THR:OG1	4:D:127:GLY:O	2.06	0.73
33:2:878:G:OP1	33:2:943:C:O2'	2.05	0.73
41:BQ:1045:C:OP1	50:BD:133:GLN:NE2	2.22	0.73
41:BQ:1345:G:N2	45:BE:307:GLN:OE1	2.21	0.73
41:BQ:1385:C:O2	47:BM:2:THR:N	2.21	0.73
41:BQ:2525:G:O2'	41:BQ:2526:C:OP2	2.06	0.73
46:BI:41:LYS:NZ	59:BJ:30:TYR:O	2.19	0.73
46:BI:122:VAL:O	46:BI:248:ARG:NH1	2.22	0.73
16:P:84:ARG:NH1	16:P:203:PHE:O	2.21	0.73
37:d:78:SER:OG	37:d:81:GLU:OE1	2.07	0.73
41:BQ:284:A:OP2	77:AP:41:ARG:NH1	2.22	0.73
42:BR:64:A:OP2	46:BI:289:LYS:NZ	2.22	0.73
27:AA:149:LYS:NZ	27:AA:201:THR:O	2.20	0.72
41:BQ:1046:A:O2'	41:BQ:1048:A:OP2	2.07	0.72
41:BQ:1778:G:O2'	41:BQ:1780:G:OP2	2.06	0.72
9:I:65:ILE:O	9:I:68:ARG:O	2.07	0.72
21:U:27:LEU:O	21:U:30:SER:O	2.07	0.72
33:2:924:A:O2'	33:2:987:G:OP1	2.06	0.72
4:D:46:ARG:NH2	33:2:1254:U:OP2	2.22	0.72
7:G:60:ARG:NH1	33:2:1400:A:O3'	2.22	0.72
27:AA:251:LYS:O	27:AA:255:SER:OG	2.07	0.72
33:2:653:C:N4	33:2:681:U:C4	2.58	0.72
67:AY:74:ASN:ND2	67:AY:86:ARG:HD3	2.03	0.72
68:BG:101:SER:OG	68:BG:104:ASN:OD1	2.07	0.72
20:T:94:ARG:NH2	33:2:406:U:O2'	2.22	0.72
33:2:371:G:O3'	35:b:88:LYS:NZ	2.22	0.72
33:2:883:C:N3	33:2:945:U:O4	2.22	0.72
41:BQ:1244:A:O2'	41:BQ:1247:U:OP1	2.06	0.72
46:BI:120:LYS:O	46:BI:248:ARG:NH2	2.22	0.72
6:F:66:ARG:NH1	33:2:1365:C:OP1	2.23	0.72
33:2:1273:G:O2'	33:2:1430:U:OP2	2.07	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:AG:155:THR:OG1	51:AG:158:ASP:OD1	2.06	0.72
16:P:27:ARG:NH2	16:P:43:ASP:O	2.22	0.72
33:2:1245:G:O2'	33:2:1247:U:OP2	2.08	0.72
38:e:37:LYS:O	38:e:38:ARG:NH1	2.23	0.72
8:H:17:LEU:O	8:H:20:THR:OG1	2.07	0.72
29:AB:10:LYS:NZ	29:AB:56:ASP:OD1	2.22	0.72
29:AB:71:LYS:NZ	41:BQ:2294:U:OP2	2.21	0.72
1:B:23:VAL:O	1:B:34:GLN:NE2	2.23	0.72
9:I:73:VAL:O	9:I:77:ASN:ND2	2.22	0.72
33:2:936:G:OP1	33:2:1074:G:N2	2.23	0.72
51:AG:60:ARG:N	51:AG:63:GLU:OE1	2.22	0.72
8:H:16:ARG:NH2	51:AG:111:ASP:OD1	2.23	0.72
14:N:123:ASN:HB2	14:N:144:CYS:SG	2.30	0.72
21:U:75:THR:OG1	21:U:161:GLN:OE1	2.08	0.72
33:2:873:U:O4	33:2:953:G:O6	2.08	0.72
41:BQ:2800:G:O6	65:AR:42:ARG:NH2	2.23	0.72
43:BS:52:A:OP1	74:AL:21:ARG:NH1	2.23	0.72
6:F:129:PHE:O	6:F:137:ARG:NH1	2.23	0.71
24:X:65:SER:OG	33:2:114:C:O2'	2.05	0.71
52:AJ:126:PHE:O	71:BP:114:ARG:NH2	2.23	0.71
20:T:137:ARG:NH1	33:2:169:A:OP2	2.23	0.71
22:V:110:ARG:NH1	22:V:160:PHE:O	2.24	0.71
41:BQ:1633:C:OP2	64:AN:69:LYS:NZ	2.24	0.71
8:H:49:LYS:NZ	8:H:79:TYR:O	2.23	0.71
16:P:88:LYS:O	16:P:92:HIS:ND1	2.23	0.71
33:2:1521:G:C5	33:2:1523:G:C2	2.78	0.71
39:f:15:GLU:O	39:f:29:ARG:NH2	2.23	0.71
41:BQ:292:U:OP2	54:AQ:68:ARG:NH1	2.24	0.71
41:BQ:1198:C:OP2	41:BQ:1199:C:O2'	2.08	0.71
41:BQ:3227:A:O3'	53:AM:133:LYS:NZ	2.22	0.71
12:L:13:ILE:O	12:L:14:LYS:NZ	2.22	0.71
20:T:174:LYS:NZ	20:T:176:GLN:OE1	2.23	0.71
28:BA:97:ARG:NH2	41:BQ:3244:A:OP1	2.23	0.71
33:2:472:U:O2'	33:2:769:A:N3	2.23	0.71
41:BQ:1824:U:O3'	73:AI:17:ARG:NH1	2.23	0.71
41:BQ:1958:U:C2	41:BQ:2083:G:O6	2.43	0.71
8:H:120:ARG:NH1	41:BQ:1025:A:O2'	2.24	0.71
33:2:1630:U:HO2'	33:2:1764:C:HO2'	1.35	0.71
41:BQ:1427:U:OP1	45:BE:44:LYS:NZ	2.23	0.71
41:BQ:3052:G:OP1	61:AE:34:SER:OG	2.07	0.71
50:BD:211:ARG:NH1	50:BD:212:GLU:OE2	2.24	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:248:ASN:ND2	15:O:297:ASP:O	2.24	0.71
41:BQ:21:G:OP2	71:BP:86:ARG:NH2	2.23	0.71
41:BQ:2002:G:O2'	79:x:281:THR:HG23	1.91	0.71
41:BQ:3181:C:O2'	55:AU:164[A]:SER:OG	2.07	0.71
33:2:956:C:OP1	33:2:1072:C:O2'	2.08	0.71
41:BQ:1268:G:O2'	41:BQ:1269:U:O2	2.08	0.71
41:BQ:1390:A:N6	41:BQ:1418:A:O2'	2.23	0.71
41:BQ:1631:C:OP2	64:AN:48:ARG:NH2	2.23	0.71
14:N:80:ARG:NH2	33:2:1209:C:OP1	2.22	0.71
14:N:116:LYS:NZ	14:N:128:ALA:O	2.24	0.71
41:BQ:936:A:OP1	65:AR:32:ARG:NH2	2.24	0.71
33:2:1226:A:O2'	33:2:1227:A:O5'	2.08	0.70
5:E:24:LYS:HB3	5:E:28:MET:HE2	1.72	0.70
33:2:229:U:O4	33:2:237:C:N3	2.25	0.70
37:d:36:SER:OG	37:d:38:ASP:OD1	2.07	0.70
41:BQ:1765:U:OP2	57:BF:39:ASN:ND2	2.24	0.70
33:2:415:C:O2	33:2:418:G:O6	2.09	0.70
42:BR:11:A:N6	46:BI:13:SER:O	2.24	0.70
13:M:12:ARG:NH1	33:2:1451:C:OP1	2.24	0.70
23:W:126:ARG:NE	33:2:475:A:OP1	2.24	0.70
41:BQ:221:A:O2'	41:BQ:223:U:OP2	2.07	0.70
41:BQ:1079:A:O2'	46:BI:140:ARG:O	2.08	0.70
28:BA:205:VAL:HG11	28:BA:322:ILE:HD11	1.73	0.70
33:2:1584:G:N2	33:2:1611:A:OP2	2.24	0.70
41:BQ:1693:C:HO2'	41:BQ:1772:U:HO2'	1.38	0.70
46:BI:197:SER:O	46:BI:202:GLY:N	2.25	0.70
58:BH:73:LYS:NZ	58:BH:97:VAL:O	2.25	0.70
5:E:37:ALA:O	5:E:42:ARG:NH1	2.24	0.70
15:O:154:VAL:O	15:O:155:ARG:NH1	2.24	0.70
15:O:295:SER:OG	15:O:297:ASP:OD1	2.09	0.70
18:R:180:ALA:HB2	18:R:198:THR:HG21	1.73	0.70
19:S:19:LEU:HD11	19:S:108:ARG:HD2	1.74	0.70
24:X:29:LYS:NZ	24:X:31:THR:O	2.25	0.70
33:2:651:G:O6	33:2:684:A:C6	2.45	0.70
41:BQ:1671:C:OP1	57:BF:60:LYS:NZ	2.23	0.70
64:AN:78:ASN:OD1	67:AY:35:ARG:NH2	2.25	0.70
16:P:167:LYS:NZ	16:P:204:TYR:O	2.18	0.70
20:T:164:LYS:NZ	33:2:72:A:N7	2.39	0.70
28:BA:137:TYR:O	28:BA:139:GLN:NE2	2.24	0.70
33:2:850:A:OP1	57:BF:165:LYS:NZ	2.16	0.70
41:BQ:3158:G:O6	41:BQ:3292:A:N1	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:AU:56[A]:ASP:OD1	55:AU:60[A]:LYS:NZ	2.23	0.70
33:2:487:G:C2	33:2:501:U:C2	2.80	0.70
33:2:1213:G:O2'	33:2:1244:A:N7	2.25	0.70
41:BQ:3070:A:OP1	57:BF:62:ARG:NH2	2.24	0.70
19:S:30:ARG:NH1	33:2:298:C:O2'	2.24	0.69
21:U:116:ARG:NE	33:2:856:A:N6	2.40	0.69
33:2:322:G:O2'	33:2:323:A:OP2	2.09	0.69
33:2:541:A:O2'	33:2:542:A:OP1	2.09	0.69
47:BM:66:THR:OG1	47:BM:138:GLN:NE2	2.25	0.69
33:2:129:U:O3'	33:2:131:C:N4	2.24	0.69
33:2:227:U:C4	33:2:235:G:O6	2.45	0.69
43:BS:55:U:O4	43:BS:62:C:N3	2.25	0.69
14:N:123:ASN:CB	14:N:144:CYS:SG	2.80	0.69
33:2:1673:G:O6	33:2:1728:A:N1	2.26	0.69
41:BQ:3026:G:OP1	49:AD:174:LYS:NZ	2.23	0.69
46:BI:53:VAL:HG21	46:BI:159:VAL:HG23	1.72	0.69
9:I:69:LYS:NZ	33:2:1368:G:OP1	2.24	0.69
41:BQ:542:G:N1	41:BQ:550:A:C6	2.60	0.69
41:BQ:3215:A:HO2'	41:BQ:3259:U:H3	1.40	0.69
49:AD:133:THR:OG1	49:AD:147:SER:OG	2.10	0.69
56:AX:118:GLN:NE2	56:AX:147:GLU:OE2	2.25	0.69
33:2:540:G:N2	33:2:542:A:H62	1.91	0.69
33:2:1430:U:O2'	33:2:1431:C:OP1	2.08	0.69
13:M:14:TYR:OH	33:2:1553:G:O2'	2.06	0.69
42:BR:72:A:O2'	42:BR:74:C:OP1	2.11	0.69
51:AG:78:GLU:OE2	51:AG:82:ARG:NE	2.26	0.69
28:BA:180:GLU:OE2	41:BQ:3002:C:O2'	2.10	0.69
33:2:188:A:N6	33:2:197:A:O2'	2.25	0.69
33:2:1594:G:OP2	33:2:1596:C:N4	2.25	0.69
2:A:22:ASN:OD1	2:A:34:TYR:OH	2.11	0.69
4:D:96:GLN:NE2	4:D:99:GLU:OE2	2.26	0.69
16:P:78:SER:OG	16:P:128:SER:OG	2.08	0.69
18:R:198:THR:O	33:2:2:A:O2'	2.10	0.69
28:BA:216:ASP:OD2	28:BA:339:ARG:NH2	2.26	0.69
28:BA:222:LYS:NZ	41:BQ:3089:C:OP1	2.25	0.69
33:2:393:C:N4	33:2:401:A:OP2	2.26	0.69
41:BQ:448:U:O2	41:BQ:488:U:O2'	2.10	0.69
41:BQ:515:C:O5'	45:BE:343:LYS:NZ	2.25	0.69
41:BQ:1155:C:O2'	41:BQ:1197:A:N1	2.22	0.69
41:BQ:1562:C:O2'	41:BQ:1563:C:O4'	2.11	0.69
5:E:102:PHE:O	5:E:104:GLN:NE2	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:142:GLY:O	8:H:145:ARG:NH2	2.26	0.69
21:U:116:ARG:CD	33:2:856:A:N6	2.56	0.69
33:2:853:G:OP2	57:BF:173:ARG:NE	2.26	0.69
33:2:1297:G:N2	33:2:1300:A:OP2	2.19	0.69
15:O:108:SER:OG	15:O:128:ASP:N	2.26	0.69
15:O:265:LEU:O	15:O:268:GLN:NE2	2.26	0.69
19:S:11:ARG:NH2	19:S:21:ASP:O	2.25	0.69
19:S:100:ARG:NH2	19:S:121:TYR:O	2.26	0.69
22:V:146:ARG:NH2	33:2:185:U:O5'	2.26	0.69
33:2:487:G:N1	33:2:501:U:C2	2.62	0.69
41:BQ:150:A:OP1	54:AQ:56:LYS:NZ	2.26	0.69
41:BQ:2681:U:O2	51:AG:20:ASN:ND2	2.26	0.69
41:BQ:2209:U:O4	80:BT:45:ARG:CB	2.41	0.68
33:2:588:U:O2	40:g:57:ASN:ND2	2.25	0.68
67:AY:48:THR:HG22	67:AY:49:PRO:HD2	1.73	0.68
41:BQ:524:U:OP1	53:AM:77:ARG:NH2	2.26	0.68
41:BQ:590:G:O2'	45:BE:309:ARG:NH1	2.26	0.68
50:BD:138:VAL:HG21	50:BD:148:VAL:HG21	1.74	0.68
60:BL:10:LYS:O	60:BL:68:THR:OG1	2.10	0.68
19:S:98:ASN:ND2	19:S:116:ASP:OD1	2.27	0.68
22:V:187:GLU:OE2	24:X:21:ASN:ND2	2.26	0.68
33:2:225:A:N6	33:2:837:G:C2	2.62	0.68
33:2:651:G:N1	33:2:684:A:C2	2.62	0.68
41:BQ:804:C:OP1	45:BE:98:ARG:NH1	2.26	0.68
6:F:94:GLN:NE2	15:O:60:SER:O	2.26	0.68
30:BB:2:GLY:N	41:BQ:1159:A:OP1	2.27	0.68
33:2:1558:U:OP2	33:2:1559:A:O2'	2.04	0.68
33:2:1754:A:O2'	36:c:60:GLU:OE2	2.09	0.68
69:BK:39:GLN:OE1	69:BK:39:GLN:N	2.25	0.68
18:R:222:TYR:OH	34:a:11:LEU:O	2.07	0.68
19:S:27:TYR:O	33:2:447:U:O2'	2.11	0.68
25:Y:86:GLU:OE2	33:2:961:U:O2'	2.10	0.68
33:2:57:G:OP2	37:d:116:LYS:NZ	2.26	0.68
41:BQ:520:U:O4	45:BE:349:THR:OG1	2.12	0.68
41:BQ:2154:U:OP1	44:AW:242:ARG:NH1	2.27	0.68
65:AR:96:LYS:NZ	65:AR:142:GLY:O	2.26	0.68
67:AY:22:LYS:NZ	67:AY:94:GLU:OE2	2.26	0.68
41:BQ:1686:U:OP1	60:BL:42:LYS:NZ	2.18	0.68
9:I:60:SER:OG	33:2:1480:G:OP1	2.11	0.68
9:I:133:ASP:OD2	33:2:1358:G:O2'	2.08	0.68
33:2:226:A:O2'	33:2:228:G:OP2	2.10	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2:655:G:N2	33:2:678:A:C6	2.61	0.68
41:BQ:1222:G:N2	41:BQ:1285:G:O2'	2.24	0.68
68:BG:98:HIS:O	68:BG:125:ARG:NH2	2.26	0.68
79:x:223:TYR:CZ	79:x:226:GLY:HA2	2.28	0.68
15:O:48:THR:OG1	15:O:50:ASP:OD2	2.08	0.68
18:R:63:VAL:HG21	18:R:69:ILE:HD11	1.76	0.68
27:AA:171:LYS:NZ	27:AA:223:ALA:O	2.27	0.68
30:BB:39:ARG:NH1	41:BQ:1348:U:OP1	2.26	0.68
41:BQ:2093:A:H2	57:BF:143:ILE:HD11	1.58	0.68
63:AK:20:PHE:O	63:AK:27:ARG:NH2	2.27	0.68
78:AT:75:ALA:O	78:AT:78:THR:OG1	2.11	0.68
41:BQ:1003:A:N1	41:BQ:1049:C:O2'	2.26	0.68
51:AG:141:ARG:NH2	51:AG:144:CYS:O	2.27	0.68
28:BA:142:ALA:O	28:BA:146:ARG:NH1	2.27	0.67
33:2:1202:A:O2'	33:2:1204:A:OP2	2.11	0.67
33:2:1542:G:H1	33:2:1568:C:HO2'	1.38	0.67
41:BQ:449:U:O2'	41:BQ:450:G:N2	2.28	0.67
14:N:146:SER:OG	33:2:1234:A:O2'	2.07	0.67
19:S:255:ARG:NH1	33:2:786:C:O4'	2.27	0.67
29:AB:104:ASN:OD1	29:AB:108:GLU:N	2.27	0.67
35:b:3:ARG:NH1	35:b:9:ASP:OD2	2.27	0.67
41:BQ:3199:G:OP1	49:AD:21:LYS:NZ	2.27	0.67
73:AI:60:GLY:O	73:AI:64:LYS:HG3	1.94	0.67
11:K:96:SER:OG	11:K:97:LYS:NZ	2.20	0.67
34:a:15:ARG:NH1	34:a:33:GLN:OE1	2.27	0.67
41:BQ:2375:G:O2'	41:BQ:2377:G:OP2	2.10	0.67
41:BQ:2843:U:OP2	41:BQ:2844:C:N4	2.25	0.67
45:BE:11:LEU:HD21	45:BE:156:LEU:HB2	1.75	0.67
16:P:79:ARG:O	16:P:83:GLN:NE2	2.27	0.67
41:BQ:173:G:C6	41:BQ:246:U:O2	2.48	0.67
41:BQ:2896:A:O2'	75:AO:122:ARG:NH2	2.28	0.67
9:I:78:LYS:NZ	33:2:1522:U:O3'	2.27	0.67
20:T:47:GLY:O	20:T:115:LYS:NZ	2.26	0.67
41:BQ:1055:A:N3	42:BR:81:U:O2'	2.27	0.67
33:2:518:A:N1	33:2:533:U:C4	2.62	0.67
28:BA:126:LYS:NZ	41:BQ:3294:A:OP2	2.27	0.67
41:BQ:1244:A:N6	41:BQ:1271:A:OP1	2.27	0.67
41:BQ:1712:G:O6	67:AY:28:LYS:NZ	2.27	0.67
41:BQ:3184:A:N3	41:BQ:3187:A:O2'	2.27	0.67
41:BQ:3273:A:OP2	47:BM:77:ARG:NH2	2.28	0.67
48:BO:186:HIS:O	48:BO:190:THR:OG1	2.11	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:AK:5:SER:OG	63:AK:7:ASP:OD1	2.10	0.67
5:E:118:GLU:OE2	33:2:1557:U:O2'	2.11	0.67
11:K:35:ARG:O	11:K:37:GLN:NE2	2.28	0.67
17:Q:159:SER:OG	17:Q:162:ARG:NH2	2.28	0.67
39:f:34:ASP:OD1	39:f:82:LYS:NZ	2.28	0.66
41:BQ:1364:C:OP1	48:BO:110:ARG:NH2	2.28	0.66
41:BQ:1761:C:OP2	79:x:68:ALA:HB1	1.95	0.66
41:BQ:1825:G:OP1	73:AI:48:SER:OG	2.13	0.66
43:BS:53:A:O2'	74:AL:40:LYS:NZ	2.28	0.66
50:BD:56:GLU:OE1	50:BD:162:GLN:N	2.28	0.66
5:E:18:ARG:NH1	8:H:90:ASN:O	2.28	0.66
33:2:139:C:O2'	33:2:177:U:O2	2.07	0.66
33:2:1466:G:O2'	33:2:1602:C:OP1	2.13	0.66
42:BR:6:C:O2'	46:BI:50:ARG:NH2	2.29	0.66
33:2:523:G:O2'	33:2:529:A:N6	2.28	0.66
33:2:1226:A:HO2'	33:2:1227:A:P	2.18	0.66
41:BQ:1976:G:O2'	73:AI:60:GLY:HA3	1.95	0.66
41:BQ:2452:G:O6	41:BQ:2493:U:C4	2.48	0.66
18:R:52:THR:OG1	18:R:54:GLU:OE2	2.14	0.66
33:2:43:A:O2'	33:2:99:C:OP1	2.09	0.66
33:2:415:C:O2	33:2:418:G:C6	2.48	0.66
49:AD:47:LYS:NZ	53:AM:5:SER:O	2.20	0.66
50:BD:209:ASN:O	50:BD:212:GLU:C	2.38	0.66
17:Q:195:LYS:O	17:Q:199:ASN:ND2	2.28	0.66
41:BQ:208:C:OP2	45:BE:163:LYS:NZ	2.28	0.66
41:BQ:1833:G:O2'	74:AL:3:ALA:O	2.14	0.66
46:BI:50:ARG:NH2	46:BI:72:ASP:OD2	2.28	0.66
33:2:220:A:OP2	33:2:831:U:O2'	2.13	0.66
33:2:1218:G:O4'	33:2:1444:A:N6	2.29	0.66
41:BQ:2158:A:OP2	44:AW:156:LYS:NZ	2.29	0.66
50:BD:105:CYS:SG	50:BD:106:ALA:N	2.69	0.66
15:O:224:ASN:O	15:O:228:LYS:N	2.28	0.66
28:BA:153:LYS:NZ	41:BQ:3241:G:OP2	2.28	0.66
9:I:65:ILE:O	9:I:68:ARG:C	2.39	0.66
10:J:74:GLU:OE2	33:2:1189:A:O2'	2.08	0.66
19:S:3:ARG:NH1	33:2:402:C:OP1	2.29	0.66
22:V:7:SER:O	22:V:18:ARG:NH1	2.29	0.66
30:BB:178:ARG:NH2	41:BQ:780:A:OP1	2.28	0.66
31:AC:68:ARG:NH1	41:BQ:2218:G:OP1	2.29	0.66
37:d:46:GLU:O	37:d:49:LYS:NZ	2.27	0.66
41:BQ:2631:U:OP2	59:BJ:4:SER:OG	2.13	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:BI:91:GLY:O	46:BI:94:ASN:ND2	2.29	0.66
47:BM:56:LYS:NZ	47:BM:101:PHE:O	2.28	0.66
56:AX:56:ARG:NH1	56:AX:75:GLU:OE2	2.28	0.66
25:Y:76:LYS:NZ	33:2:859:A:N1	2.43	0.66
41:BQ:542:G:O6	41:BQ:550:A:N6	2.29	0.66
41:BQ:2945:G:O2'	41:BQ:2948:C:OP2	2.11	0.66
41:BQ:3200:G:OP2	53:AM:8:LYS:NZ	2.26	0.66
41:BQ:3291:G:C6	41:BQ:3292:A:N6	2.64	0.66
64:AN:11:ALA:HB2	64:AN:25:ILE:HD11	1.77	0.66
22:V:5:ARG:NH2	33:2:334:G:O6	2.29	0.65
28:BA:244:ARG:NH2	41:BQ:2948:C:OP1	2.28	0.65
37:d:38:ASP:O	37:d:52:LYS:NZ	2.29	0.65
45:BE:77:VAL:O	45:BE:86:GLY:N	2.29	0.65
78:AT:38:ASP:OD1	78:AT:45:LYS:NZ	2.30	0.65
42:BR:1:G:O6	46:BI:262:LYS:NZ	2.17	0.65
59:BJ:71:SER:OG	59:BJ:91:LEU:O	2.08	0.65
73:AI:32:ASN:OD1	73:AI:33:LYS:N	2.29	0.65
9:I:129:GLN:NE2	33:2:1357:A:N3	2.45	0.65
21:U:107:ARG:NH1	33:2:742:U:O2'	2.29	0.65
33:2:623:A:O2'	33:2:624:G:OP1	2.10	0.65
33:2:868:G:O6	33:2:960:U:O4	2.13	0.65
50:BD:101:LYS:NZ	50:BD:102:MET:O	2.20	0.65
53:AM:19:ARG:NH2	53:AM:66:THR:O	2.29	0.65
33:2:1521:G:C8	33:2:1523:G:N2	2.64	0.65
41:BQ:2703:A:N6	46:BI:28:THR:O	2.26	0.65
41:BQ:2965:U:O2	44:AW:221:LYS:NZ	2.15	0.65
54:AQ:23:GLN:NE2	54:AQ:122:ASN:OD1	2.29	0.65
77:AP:45:ARG:O	77:AP:48:SER:OG	2.12	0.65
41:BQ:117:U:O2'	41:BQ:119:U:OP2	2.08	0.65
1:B:133:VAL:HG23	1:B:198:LEU:HD22	1.78	0.65
17:Q:216:LYS:NZ	33:2:886:U:OP2	2.30	0.65
21:U:49:ILE:O	21:U:57:ALA:N	2.28	0.65
41:BQ:1156:C:OP2	48:BO:94:LYS:NZ	2.29	0.65
15:O:91:LEU:O	15:O:100:TYR:N	2.30	0.65
25:Y:124:ARG:NH1	33:2:628:G:OP1	2.29	0.65
33:2:217:A:N1	33:2:844:A:O2'	2.24	0.65
39:f:45:THR:OG1	39:f:82:LYS:NZ	2.30	0.65
3:C:23:ALA:O	3:C:63:TYR:C	2.40	0.65
5:E:57:MET:SD	5:E:61:ARG:NH2	2.70	0.65
11:K:85:LYS:NZ	11:K:86:GLU:OE1	2.30	0.65
20:T:188:ARG:NH1	33:2:284:G:N7	2.44	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BA:205:VAL:HA	28:BA:208:VAL:HG12	1.79	0.65
33:2:1304:G:OP2	33:2:1305:U:O2'	2.07	0.65
35:b:80:ASN:OD1	35:b:124:LYS:NZ	2.28	0.65
41:BQ:2494:A:H1'	80:BT:164:CYS:N	2.12	0.65
43:BS:126:A:O2'	43:BS:128:U:OP2	2.10	0.65
46:BI:39:GLN:OE1	46:BI:40:HIS:N	2.30	0.65
73:AI:61:LYS:HA	73:AI:64:LYS:HZ2	1.61	0.65
1:B:102:ARG:O	1:B:106:LYS:NZ	2.20	0.65
41:BQ:2899:C:O2'	41:BQ:2901:G:OP2	2.07	0.65
47:BM:40:LEU:HD11	47:BM:54:TYR:HB2	1.79	0.65
41:BQ:992:A:H61	41:BQ:1057:A:H61	1.46	0.64
33:2:1114:G:O2'	33:2:1130:G:O6	2.13	0.64
42:BR:85:G:O2'	48:BO:221:LYS:NZ	2.29	0.64
5:E:18:ARG:N	8:H:92:ILE:O	2.29	0.64
6:F:31:VAL:HG12	6:F:32:ASN:HD22	1.62	0.64
27:AA:90:THR:HG22	27:AA:214:LEU:HD21	1.80	0.64
33:2:58:U:O2'	33:2:451:A:N3	2.29	0.64
33:2:444:C:O5'	37:d:105:ARG:NH1	2.30	0.64
34:a:17:CYS:SG	34:a:18:SER:N	2.69	0.64
41:BQ:535:G:OP1	58:BH:146:LYS:NZ	2.22	0.64
10:J:100:VAL:O	10:J:104:THR:HG23	1.98	0.64
41:BQ:1190:A:O2'	41:BQ:1193:A:OP2	2.10	0.64
19:S:140:VAL:HG12	19:S:146:THR:HG22	1.78	0.64
33:2:434:G:N1	33:2:437:A:OP2	2.30	0.64
45:BE:188:ARG:NE	45:BE:197:ARG:O	2.27	0.64
2:A:61:GLU:OE2	2:A:64:ARG:NH1	2.31	0.64
17:Q:122:GLU:OE2	17:Q:213:ARG:NH2	2.30	0.64
19:S:70:VAL:CG2	19:S:90:ILE:HD11	2.28	0.64
20:T:159:ARG:NH1	33:2:78:A:O3'	2.30	0.64
33:2:1229:G:H21	33:2:1256:A:N6	1.95	0.64
45:BE:237:GLN:O	45:BE:246:ARG:NH1	2.31	0.64
41:BQ:2549:G:N2	41:BQ:2549:G:OP2	2.31	0.64
60:BL:32:SER:OG	60:BL:83:TYR:OH	2.09	0.64
62:AH:76:VAL:HG12	62:AH:81:ILE:O	1.97	0.64
1:B:67:PRO:O	1:B:68:ILE:HD13	1.97	0.64
27:AA:183:LYS:NZ	41:BQ:147:U:O4	2.24	0.64
41:BQ:1186:G:O3'	58:BH:113:ARG:NH2	2.30	0.64
1:B:81:ARG:NH2	33:2:1615:C:OP1	2.30	0.64
21:U:156:SER:OG	21:U:186:PRO:O	2.15	0.64
41:BQ:362:U:OP1	72:AF:45:ARG:NH1	2.31	0.64
41:BQ:3369:G:OP2	61:AE:61:LYS:NZ	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:BO:156:ILE:HD12	48:BO:161:VAL:HG21	1.79	0.64
23:W:129:ILE:HD13	23:W:134:ILE:HG21	1.80	0.64
41:BQ:649:A:OP2	41:BQ:2868:U:O2'	2.15	0.64
10:J:22:ILE:HG22	10:J:118:VAL:HG22	1.79	0.63
11:K:103:ARG:NH2	11:K:105:THR:OG1	2.31	0.63
18:R:173:PRO:O	18:R:176:SER:OG	2.13	0.63
41:BQ:2101:C:O2'	41:BQ:2102:U:O5'	2.08	0.63
6:F:90:VAL:HG22	6:F:105:LEU:HD23	1.79	0.63
17:Q:128:LYS:O	17:Q:177:GLN:NE2	2.31	0.63
20:T:10:ASN:ND2	20:T:127:THR:O	2.31	0.63
37:d:12:VAL:HG12	37:d:23:PHE:HB3	1.81	0.63
15:O:9:LEU:HD12	15:O:312:VAL:O	1.99	0.63
33:2:1345:A:N6	33:2:1377:U:O2'	2.31	0.63
41:BQ:2101:C:O2'	41:BQ:2102:U:O4'	2.16	0.63
62:AH:127:THR:OG1	62:AH:129:ASP:OD1	2.11	0.63
22:V:10:LYS:NZ	33:2:323:A:OP2	2.29	0.63
41:BQ:2714:G:OP2	77:AP:8:ARG:NH2	2.32	0.63
44:AW:118:GLU:OE2	44:AW:156:LYS:NZ	2.31	0.63
19:S:13:ALA:O	19:S:39:ARG:NH1	2.31	0.63
43:BS:143:U:OP1	54:AQ:38:ARG:NH2	2.31	0.63
23:W:86:LEU:HD21	23:W:90:LYS:O	1.98	0.63
33:2:59:C:O2'	33:2:60:U:O4'	2.16	0.63
41:BQ:499:G:OP1	69:BK:48:ARG:NH2	2.32	0.63
44:AW:140:ASN:ND2	44:AW:142:ASP:O	2.31	0.63
57:BF:7:GLN:OE1	57:BF:7:GLN:N	2.31	0.63
58:BH:131:LYS:NZ	58:BH:132:THR:O	2.20	0.63
27:AA:29:SER:OG	41:BQ:2563:G:O2'	2.12	0.63
41:BQ:2969:A:N7	44:AW:215:ASN:ND2	2.47	0.63
73:AI:11:PHE:O	73:AI:15:THR:HG23	1.99	0.63
2:A:191:ASP:OD2	2:A:194:LYS:N	2.31	0.63
33:2:222:A:OP2	33:2:833:U:O2'	2.11	0.63
41:BQ:2564:G:OP2	64:AN:55:LYS:NZ	2.28	0.63
49:AD:133:THR:HG1	49:AD:147:SER:HG	1.41	0.63
70:BN:41:ARG:O	70:BN:43:LYS:NZ	2.32	0.63
41:BQ:1793:C:O2	44:AW:188:LYS:NZ	2.29	0.62
41:BQ:3020:U:OP2	41:BQ:3021:A:O2'	2.17	0.62
45:BE:26:PHE:CD1	45:BE:130:ALA:HB2	2.34	0.62
72:AF:37:CYS:O	72:AF:44:THR:HA	1.99	0.62
11:K:80:LEU:HD22	11:K:101:TYR:CE1	2.35	0.62
27:AA:83:ASP:OD1	27:AA:86:THR:OG1	2.09	0.62
41:BQ:1492:G:N7	74:AL:2:ALA:N	2.47	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:BQ:1721:U:OP2	57:BF:124:TYR:OH	2.15	0.62
41:BQ:1382:G:OP2	45:BE:188:ARG:NH1	2.32	0.62
41:BQ:1958:U:O2	41:BQ:2083:G:O6	2.18	0.62
52:AJ:37:ASN:O	52:AJ:41:THR:HG23	1.99	0.62
64:AN:88:ASP:O	64:AN:121:ARG:NH1	2.33	0.62
69:BK:49:ILE:HD11	69:BK:71:VAL:CG2	2.29	0.62
30:BB:145:ASN:ND2	41:BQ:746:A:OP1	2.32	0.62
41:BQ:2307:G:O2'	41:BQ:2310:U:OP2	2.16	0.62
41:BQ:2501:U:O2'	41:BQ:2502:A:OP1	2.15	0.62
10:J:80:GLU:OE1	13:M:44:ARG:NH1	2.32	0.62
22:V:42:ARG:NH1	33:2:1677:C:OP1	2.33	0.62
33:2:540:G:N2	33:2:542:A:N6	2.47	0.62
41:BQ:1979:G:H1	41:BQ:2045:G:N2	1.97	0.62
44:AW:150:LEU:O	44:AW:153:GLY:N	2.32	0.62
33:2:487:G:C6	33:2:501:U:N3	2.67	0.62
22:V:153:GLU:OE2	22:V:156:VAL:HG13	2.00	0.62
33:2:227:U:C4	33:2:235:G:C6	2.87	0.62
41:BQ:1564:U:O2	41:BQ:1576:G:C2	2.53	0.62
5:E:64:LYS:NZ	5:E:91:GLY:O	2.33	0.62
35:b:24:GLN:N	35:b:24:GLN:OE1	2.33	0.62
2:A:45:LYS:NZ	2:A:82:GLY:O	2.30	0.62
12:L:37:SER:O	38:e:51:ARG:NH2	2.33	0.62
17:Q:111:ARG:NH2	33:2:930:A:N3	2.48	0.62
25:Y:124:ARG:NH2	33:2:967:A:OP2	2.33	0.62
29:AB:4:ASN:ND2	29:AB:105:PRO:O	2.32	0.62
33:2:539:G:N3	33:2:540:G:N2	2.48	0.62
51:AG:32:ARG:O	51:AG:36:VAL:HG23	1.99	0.62
20:T:161:GLU:OE1	20:T:169:TYR:N	2.33	0.62
23:W:149:ARG:NH2	33:2:765:G:N7	2.48	0.62
16:P:120:LEU:HD21	16:P:144:ILE:HD13	1.82	0.61
22:V:6:ASP:OD1	22:V:8:ARG:N	2.32	0.61
28:BA:77:THR:HG21	28:BA:328:ILE:HG12	1.80	0.61
47:BM:35:VAL:O	47:BM:38:THR:OG1	2.09	0.61
74:AL:2:ALA:O	74:AL:5:LYS:NZ	2.25	0.61
9:I:102:ARG:NH2	33:2:1502:G:N7	2.47	0.61
23:W:132:ARG:NH2	33:2:532:U:OP1	2.32	0.61
25:Y:74:ILE:O	25:Y:78:ASN:ND2	2.33	0.61
30:BB:72:LYS:NZ	41:BQ:720:A:OP1	2.31	0.61
33:2:512:A:C6	33:2:539:G:O6	2.54	0.61
41:BQ:1481:A:OP2	41:BQ:1859:A:N6	2.32	0.61
54:AQ:8:GLU:OE2	54:AQ:50:ARG:NE	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:143:ARG:NH1	12:L:57:MET:SD	2.73	0.61
8:H:91:ASP:OD1	8:H:95:GLY:N	2.33	0.61
33:2:498:G:O2'	33:2:499:U:O2	2.06	0.61
43:BS:11:C:O3'	56:AX:3:ARG:NH1	2.33	0.61
48:BO:86:VAL:HG22	48:BO:136:TYR:HB3	1.82	0.61
27:AA:47:SER:OG	41:BQ:2585:G:O6	2.10	0.61
27:AA:105:LYS:NZ	41:BQ:123:A:OP1	2.23	0.61
33:2:278:U:O2	33:2:279:G:N1	2.33	0.61
41:BQ:383:G:N2	41:BQ:386:A:C8	2.68	0.61
46:BI:216:GLU:N	46:BI:216:GLU:OE1	2.34	0.61
22:V:137:LYS:NZ	33:2:195:G:N7	2.47	0.61
32:BC:65:LYS:NZ	41:BQ:3058:U:O4	2.20	0.61
41:BQ:1315:U:OP2	55:AU:44[A]:SER:OG	2.09	0.61
52:AJ:107:GLU:OE1	52:AJ:107:GLU:N	2.34	0.61
15:O:170:ILE:HD11	15:O:178:VAL:HG12	1.82	0.61
17:Q:87:ARG:NE	17:Q:89:ASP:OD1	2.34	0.61
41:BQ:1974:A:OP1	41:BQ:2048:G:N2	2.34	0.61
50:BD:77:THR:HG22	50:BD:82:ARG:HA	1.82	0.61
66:AV:16:ALA:O	66:AV:20:GLY:CA	2.49	0.61
19:S:70:VAL:HG22	19:S:90:ILE:HD11	1.83	0.61
41:BQ:424:G:O2'	68:BG:23:ASP:OD2	2.14	0.61
41:BQ:1984:C:N3	41:BQ:2037:G:O6	2.33	0.61
6:F:83:GLN:NE2	6:F:115:THR:O	2.33	0.61
11:K:77:ARG:NH1	33:2:1533:C:OP2	2.33	0.61
15:O:24:ALA:O	15:O:33:LEU:HD12	2.01	0.61
21:U:64:VAL:O	21:U:64:VAL:HG22	2.01	0.61
33:2:1755:A:O2'	33:2:1756:A:O4'	2.14	0.61
41:BQ:105:C:O2'	41:BQ:684:G:O2'	2.19	0.61
41:BQ:733:G:HO2'	41:BQ:735:A:H62	1.49	0.61
41:BQ:951:A:OP1	66:AV:18:ARG:NH2	2.34	0.61
41:BQ:1231:A:N6	41:BQ:1276:U:O5'	2.34	0.61
41:BQ:1257:C:C4	41:BQ:1261:G:N2	2.68	0.61
63:AK:27:ARG:NH1	63:AK:76:LEU:O	2.34	0.61
33:2:126:A:N6	33:2:292:U:C5	2.69	0.61
41:BQ:444:U:C4	41:BQ:491:A:C5	2.89	0.61
41:BQ:2617:U:O2'	50:BD:116:ARG:NH2	2.34	0.61
45:BE:345:GLU:OE1	45:BE:347:THR:OG1	2.17	0.61
17:Q:97:LEU:HD22	17:Q:232:HIS:CD2	2.36	0.61
33:2:620:A:N3	33:2:1107:G:O2'	2.27	0.61
33:2:1000:C:N4	33:2:1003:A:OP2	2.33	0.61
41:BQ:283:G:OP1	77:AP:45:ARG:NH1	2.32	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:BQ:2093:A:C2	57:BF:143:ILE:CG1	2.84	0.61
20:T:23:ARG:NH1	20:T:39:GLU:O	2.34	0.60
21:U:27:LEU:O	21:U:30:SER:C	2.44	0.60
36:c:96:VAL:HG12	36:c:127:VAL:HG21	1.83	0.60
41:BQ:1961:G:O6	41:BQ:2059:U:H3'	2.01	0.60
41:BQ:2713:U:O2'	77:AP:8:ARG:NH1	2.33	0.60
41:BQ:2741:C:O2'	77:AP:20:HIS:ND1	2.28	0.60
53:AM:94:TRP:O	53:AM:97:SER:OG	2.14	0.60
33:2:1656:U:O2'	41:BQ:2292:U:O2'	2.18	0.60
41:BQ:1976:G:N2	41:BQ:2047:A:O2'	2.34	0.60
41:BQ:1977:C:N4	41:BQ:2046:U:H1'	2.13	0.60
41:BQ:2901:G:O2'	41:BQ:3024:A:N1	2.32	0.60
59:BJ:80:VAL:HG21	59:BJ:85:LEU:HD12	1.82	0.60
15:O:182:ASN:O	15:O:186:PHE:N	2.33	0.60
54:AQ:67:ARG:NH2	54:AQ:127:TYR:OH	2.34	0.60
21:U:167:GLU:OE1	21:U:167:GLU:N	2.35	0.60
41:BQ:2516:U:OP1	54:AQ:31:ARG:NH1	2.34	0.60
66:AV:56:ALA:O	66:AV:59:LYS:NZ	2.34	0.60
78:AT:53:GLY:HA3	78:AT:66:GLY:O	2.01	0.60
5:E:44:ARG:O	5:E:47:ARG:C	2.44	0.60
21:U:97:ARG:NH2	33:2:856:A:OP2	2.34	0.60
41:BQ:1517:G:OP2	74:AL:41:ARG:NH2	2.34	0.60
17:Q:82:ARG:NH2	17:Q:188:LEU:O	2.35	0.60
33:2:655:G:N3	33:2:678:A:N1	2.50	0.60
41:BQ:1684:U:OP1	60:BL:86:LYS:NZ	2.26	0.60
43:BS:52:A:H62	74:AL:27:ILE:HD13	1.66	0.60
50:BD:207:GLU:N	50:BD:207:GLU:OE2	2.33	0.60
61:AE:20:LEU:HD23	61:AE:21:PHE:N	2.17	0.60
1:B:73:THR:N	1:B:91:GLU:OE2	2.35	0.60
27:AA:240:ASN:ND2	41:BQ:2584:G:O2'	2.33	0.60
33:2:1399:C:O2'	33:2:1400:A:O5'	2.18	0.60
41:BQ:1010:G:N2	50:BD:193:ASP:OD2	2.29	0.60
41:BQ:2722:U:O2'	59:BJ:88:ARG:O	2.19	0.60
9:I:97:SER:OG	33:2:1504:G:OP1	2.14	0.60
46:BI:214:ASP:OD1	46:BI:215:ASP:N	2.35	0.60
47:BM:100:LYS:NZ	47:BM:137:ASP:OD1	2.28	0.60
20:T:157:VAL:HG11	33:2:78:A:C5'	2.32	0.60
25:Y:20:ARG:NH2	33:2:861:U:O3'	2.35	0.60
33:2:205:U:O2	33:2:263:C:N3	2.34	0.60
41:BQ:1973:G:C2	41:BQ:2048:G:H2'	2.37	0.60
41:BQ:2608:G:OP1	44:AW:2:GLY:N	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:BO:77:VAL:O	59:BJ:138:SER:OG	2.13	0.60
21:U:161:GLN:O	21:U:165:LYS:NZ	2.26	0.60
33:2:223:U:O4	33:2:838:G:O6	2.20	0.60
33:2:396:G:N1	33:2:399:A:OP2	2.34	0.60
14:N:130:VAL:HG23	33:2:1253:U:H5''	1.82	0.59
15:O:222:LEU:O	15:O:231:MET:N	2.34	0.59
17:Q:8:ARG:NH2	33:2:911:U:OP2	2.35	0.59
24:X:93:TYR:OH	24:X:98:ASN:OD1	2.18	0.59
33:2:936:G:N7	38:e:15:ARG:NH2	2.50	0.59
41:BQ:1232:C:N4	41:BQ:1262:G:OP2	2.35	0.59
3:C:26:ASP:O	3:C:39:ASN:ND2	2.35	0.59
58:BH:87:THR:O	58:BH:88:HIS:ND1	2.35	0.59
14:N:106:TYR:O	14:N:117:LEU:N	2.35	0.59
19:S:239:PRO:O	19:S:242:LYS:NZ	2.25	0.59
22:V:48:THR:OG1	22:V:52:ASN:O	2.12	0.59
33:2:538:A:O4'	33:2:543:C:N4	2.33	0.59
56:AX:172:GLN:NE2	69:BK:60:ARG:O	2.34	0.59
62:AH:115:ARG:O	62:AH:118:GLY:N	2.35	0.59
5:E:67:ALA:HB1	5:E:71:GLU:O	2.02	0.59
27:AA:86:THR:O	27:AA:90:THR:HG23	2.02	0.59
15:O:16:HIS:O	15:O:308:ASN:ND2	2.35	0.59
19:S:194:THR:OG1	19:S:211:LYS:O	2.17	0.59
41:BQ:1277:C:O2'	41:BQ:1278:A:O5'	2.18	0.59
66:AV:43:HIS:CE1	66:AV:47:LEU:HD11	2.37	0.59
33:2:554:C:N4	33:2:571:G:O6	2.35	0.59
41:BQ:551:A:O2'	41:BQ:552:G:O4'	2.21	0.59
41:BQ:1764:U:OP2	57:BF:43:LYS:NZ	2.21	0.59
46:BI:146:LEU:HD22	46:BI:163:LEU:CD1	2.32	0.59
73:AI:63:LYS:O	73:AI:66:ILE:HG12	2.03	0.59
37:d:83:LYS:HD3	37:d:96:LEU:HD23	1.84	0.59
1:B:164:PRO:O	1:B:168:VAL:HG23	2.02	0.59
33:2:653:C:C5	33:2:681:U:O4	2.56	0.59
41:BQ:3228:C:OP1	53:AM:137:LYS:NZ	2.36	0.59
45:BE:83:GLY:O	45:BE:87:GLN:NE2	2.36	0.59
46:BI:146:LEU:HD22	46:BI:163:LEU:HD12	1.83	0.59
2:A:67:ASN:O	2:A:70:THR:OG1	2.20	0.59
18:R:206:THR:HG21	33:2:14:C:OP2	2.03	0.59
20:T:92:ARG:O	33:2:405:C:O2'	2.20	0.59
33:2:540:G:C2	33:2:542:A:N6	2.70	0.59
33:2:733:A:H1'	33:2:736:C:H41	1.67	0.59
41:BQ:148:G:OP2	54:AQ:4:TYR:OH	2.14	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:BQ:446:U:O2'	41:BQ:489:U:O2	2.21	0.59
41:BQ:2095:G:H2'	41:BQ:2096:A:H8	1.66	0.59
50:BD:36:LEU:HD13	50:BD:87:LEU:HD22	1.85	0.59
51:AG:100:GLY:O	51:AG:159:THR:HG21	2.03	0.59
42:BR:6:C:OP2	46:BI:22:ARG:NH1	2.35	0.59
64:AN:84:ARG:NH1	70:BN:97:GLU:OE1	2.36	0.59
3:C:64:TYR:OH	33:2:1435:G:O6	2.20	0.58
8:H:134:ARG:NE	33:2:1546:G:OP2	2.35	0.58
9:I:130:ARG:NH1	33:2:1358:G:OP1	2.35	0.58
38:e:88:SER:N	38:e:91:ASP:OD1	2.36	0.58
41:BQ:600:G:O2'	41:BQ:602:A:N6	2.32	0.58
41:BQ:1831:U:O2'	43:BS:114:G:OP1	2.16	0.58
41:BQ:2205:U:O4	41:BQ:2237:C:C4	2.56	0.58
24:X:8:GLN:NE2	24:X:14:GLN:O	2.36	0.58
33:2:687:G:O5'	35:b:118:ARG:NH1	2.36	0.58
41:BQ:494:G:N2	41:BQ:619:A:N1	2.51	0.58
41:BQ:1761:C:O2'	41:BQ:1762:C:O3'	2.20	0.58
41:BQ:2493:U:OP1	80:BT:35:GLN:CB	2.51	0.58
61:AE:46:PRO:HB3	61:AE:52:THR:HG21	1.85	0.58
7:G:105:GLN:OE1	7:G:105:GLN:N	2.36	0.58
18:R:35:TRP:NE1	18:R:65:GLU:OE1	2.36	0.58
19:S:153:ASN:OD1	20:T:215:ARG:NH1	2.36	0.58
37:d:15:ASN:OD1	37:d:18:LEU:N	2.35	0.58
41:BQ:3022:G:O2'	41:BQ:3031:G:O6	2.19	0.58
41:BQ:3163:A:N1	41:BQ:3288:G:C6	2.71	0.58
67:AY:77:LEU:HD23	67:AY:87:VAL:O	2.02	0.58
1:B:154:ALA:O	1:B:156:ARG:NH1	2.37	0.58
5:E:106:GLU:OE2	5:E:108:ARG:NE	2.37	0.58
41:BQ:451:U:O2'	41:BQ:486:A:N3	2.31	0.58
41:BQ:2033:G:O6	41:BQ:2035:G:N1	2.36	0.58
41:BQ:2245:C:O2'	44:AW:220:GLY:O	2.21	0.58
48:BO:121:LYS:NZ	48:BO:125:GLU:OE1	2.37	0.58
58:BH:124:LEU:HD23	59:BJ:153:PRO:HB2	1.85	0.58
1:B:185:ARG:NH1	33:2:1572:G:O2'	2.37	0.58
14:N:133:ALA:HB3	14:N:140:TYR:HB3	1.86	0.58
15:O:25:THR:HG22	15:O:33:LEU:HD13	1.85	0.58
41:BQ:520:U:O2	45:BE:346:LYS:NZ	2.28	0.58
44:AW:242:ARG:NH2	44:AW:243:THR:O	2.36	0.58
19:S:107:GLY:HA2	19:S:189:LEU:HD23	1.86	0.58
22:V:138:ASN:OD1	22:V:141:ARG:NH2	2.37	0.58
27:AA:191:ASN:O	27:AA:192:GLN:NE2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2:1206:U:OP2	33:2:1207:C:O2'	2.16	0.58
41:BQ:1973:G:H1'	41:BQ:2049:A:N6	2.17	0.58
41:BQ:2196:C:O2'	41:BQ:2270:A:N3	2.30	0.58
48:BO:219:LYS:O	48:BO:221:LYS:N	2.37	0.58
54:AQ:73:ARG:NH1	54:AQ:86:ASN:O	2.37	0.58
4:D:33:ARG:NH2	4:D:99:GLU:O	2.37	0.58
10:J:89:ARG:NH2	33:2:1383:G:OP1	2.35	0.58
17:Q:148:ASN:ND2	33:2:1054:U:O2	2.37	0.58
1:B:139:ASN:ND2	1:B:201:ALA:O	2.37	0.58
6:F:94:GLN:O	15:O:59:ARG:NH1	2.35	0.58
6:F:123:ARG:NH2	33:2:1337:A:OP1	2.35	0.58
19:S:100:ARG:NH2	19:S:118:GLU:O	2.36	0.58
41:BQ:1361:U:O2	48:BO:159:GLN:NE2	2.37	0.58
48:BO:64:GLN:NE2	48:BO:68:ASP:OD1	2.35	0.58
26:Z:19:ILE:HB	26:Z:83:ILE:HD13	1.86	0.58
33:2:818:C:N4	33:2:819:G:N7	2.52	0.58
33:2:1699:G:C6	33:2:1703:C:N3	2.72	0.58
36:c:63:GLN:NE2	36:c:65:ASN:O	2.37	0.58
37:d:44:LEU:HA	37:d:47:VAL:HG12	1.85	0.58
41:BQ:560:G:OP1	53:AM:83:LYS:NZ	2.34	0.58
41:BQ:3192:U:C4	41:BQ:3193:C:N4	2.72	0.58
45:BE:265:GLU:N	45:BE:265:GLU:OE1	2.35	0.58
18:R:139:ILE:HD12	18:R:218:ILE:HB	1.86	0.58
33:2:1681:A:N6	33:2:1720:G:O2'	2.36	0.58
36:c:74:VAL:HG11	36:c:104:LEU:HD11	1.86	0.58
50:BD:72:ALA:HB1	50:BD:76:MET:HE1	1.86	0.58
16:P:134:LYS:O	16:P:137:SER:OG	2.19	0.57
36:c:57:LEU:HD22	40:g:4:VAL:CG1	2.34	0.57
41:BQ:348:A:N3	41:BQ:352:A:O2'	2.37	0.57
46:BI:85:ARG:NH2	46:BI:86:TYR:OH	2.37	0.57
67:AY:39:SER:HA	67:AY:93:LEU:HD23	1.86	0.57
41:BQ:952:A:N3	41:BQ:1114:U:O2'	2.36	0.57
74:AL:16:ALA:HB1	74:AL:42:ARG:HH21	1.69	0.57
15:O:220:ILE:HD11	15:O:234:LEU:HD22	1.85	0.57
37:d:20:ARG:HD2	37:d:74:LEU:HD11	1.86	0.57
2:A:154:ASP:N	2:A:154:ASP:OD1	2.37	0.57
4:D:84:ASN:O	4:D:86:VAL:HG23	2.04	0.57
9:I:51:GLU:N	9:I:51:GLU:OE1	2.37	0.57
12:L:19:THR:HG22	12:L:20:GLY:H	1.68	0.57
15:O:200:ASN:ND2	15:O:240:VAL:O	2.38	0.57
18:R:212:LYS:NZ	33:2:1298:U:O3'	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:104:ASP:OD1	19:S:108:ARG:N	2.37	0.57
30:BB:31:LYS:O	30:BB:34:THR:OG1	2.22	0.57
33:2:513:U:C2	33:2:538:A:N6	2.73	0.57
33:2:1471:A:O2'	33:2:1472:C:OP1	2.17	0.57
41:BQ:2093:A:H62	57:BF:114:LYS:HE2	1.70	0.57
41:BQ:2452:G:N2	41:BQ:2494:A:C6	2.72	0.57
41:BQ:2568:C:O2'	41:BQ:2569:A:O4'	2.19	0.57
3:C:28:ASN:OD1	13:M:7:TRP:NE1	2.38	0.57
7:G:117:LEU:HD11	16:P:11:PRO:O	2.03	0.57
14:N:123:ASN:CG	14:N:144:CYS:SG	2.88	0.57
33:2:656:G:C6	33:2:679:U:O2	2.58	0.57
41:BQ:2494:A:C4'	80:BT:37:GLY:CA	2.76	0.57
59:BJ:9:SER:O	59:BJ:11:THR:HG23	2.04	0.57
16:P:120:LEU:HD21	16:P:144:ILE:CD1	2.35	0.57
24:X:88:ARG:NH1	33:2:305:C:O3'	2.37	0.57
33:2:458:G:OP1	37:d:109:LYS:NZ	2.25	0.57
41:BQ:340:C:OP2	45:BE:195:ARG:NH2	2.38	0.57
33:2:232:U:C2	33:2:234:G:O6	2.58	0.57
41:BQ:1977:C:H4'	73:AI:59:ALA:HB1	1.85	0.57
41:BQ:2717:U:O3'	77:AP:13:LYS:NZ	2.37	0.57
1:B:112:ARG:NH2	33:2:1529:C:OP1	2.38	0.57
16:P:30:GLN:OE1	16:P:31:VAL:N	2.37	0.57
19:S:45:ILE:HD12	19:S:61:VAL:HG21	1.86	0.57
19:S:64:ILE:HD11	37:d:18:LEU:CD1	2.35	0.57
22:V:5:ARG:NH1	22:V:29:LEU:O	2.36	0.57
37:d:51:GLU:OE1	37:d:53:ASP:N	2.35	0.57
41:BQ:2033:G:N7	41:BQ:2035:G:C6	2.73	0.57
29:AB:68:GLU:OE1	29:AB:68:GLU:N	2.38	0.57
31:AC:29:LYS:NZ	41:BQ:264:G:O6	2.37	0.57
33:2:540:G:C2	33:2:542:A:C6	2.93	0.57
41:BQ:1412:G:OP1	68:BG:105:ARG:NH2	2.37	0.57
49:AD:173:ARG:NH1	75:AO:125:LYS:O	2.36	0.57
55:AU:178[A]:VAL:O	55:AU:182[A]:ASN:ND2	2.38	0.57
67:AY:25:LEU:O	67:AY:29:SER:OG	2.22	0.57
16:P:175:TYR:OH	16:P:197:ILE:O	2.12	0.57
28:BA:10:ARG:NH1	28:BA:14:LEU:HD21	2.20	0.57
33:2:1229:G:N2	33:2:1256:A:H62	2.02	0.57
35:b:75:ILE:N	35:b:126:LEU:O	2.37	0.57
41:BQ:1152:G:OP2	41:BQ:1152:G:N2	2.29	0.57
43:BS:71:A:N1	43:BS:82:U:O2'	2.38	0.57
53:AM:21:VAL:HG12	53:AM:65:LEU:HD23	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:158:GLN:NE2	1:B:159:ALA:O	2.36	0.56
15:O:29:GLN:NE2	15:O:76:ASP:O	2.38	0.56
15:O:182:ASN:N	15:O:189:GLU:OE1	2.37	0.56
21:U:135:ILE:HD11	21:U:138:LYS:HD3	1.86	0.56
22:V:89:GLU:O	22:V:93:THR:HG22	2.04	0.56
33:2:368:U:O2	33:2:373:G:O6	2.22	0.56
41:BQ:339:C:OP1	45:BE:195:ARG:NH1	2.37	0.56
41:BQ:440:A:OP1	41:BQ:493:U:O2'	2.19	0.56
41:BQ:2768:U:O2	77:AP:82:GLN:NE2	2.38	0.56
41:BQ:3267:A:OP1	41:BQ:3268:A:N6	2.38	0.56
4:D:36:LEU:HD11	4:D:41:LEU:HD22	1.86	0.56
15:O:70:ASP:OD1	15:O:83:ALA:HB3	2.05	0.56
17:Q:3:VAL:HG13	26:Z:48:VAL:O	2.05	0.56
21:U:112:ARG:NH1	21:U:117:THR:OG1	2.37	0.56
33:2:479:C:C2	33:2:510:G:N2	2.73	0.56
33:2:1665:U:O2	33:2:1736:G:O6	2.23	0.56
41:BQ:1564:U:C2	41:BQ:1576:G:N1	2.72	0.56
41:BQ:3181:C:OP2	55:AU:171[A]:LYS:NZ	2.18	0.56
60:BL:43:VAL:HG22	60:BL:44:GLU:OE1	2.04	0.56
5:E:30:THR:O	5:E:34:VAL:HG23	2.06	0.56
5:E:44:ARG:O	5:E:47:ARG:O	2.23	0.56
17:Q:127:VAL:CG1	17:Q:176:VAL:HG11	2.35	0.56
21:U:51:VAL:HG12	21:U:55:LYS:O	2.06	0.56
28:BA:307:PRO:HA	28:BA:361:THR:HG22	1.86	0.56
30:BB:44:PHE:CD1	30:BB:139:ILE:HD11	2.39	0.56
33:2:276:C:H41	61:AE:118:ALA:HB3	1.70	0.56
41:BQ:726:G:N1	41:BQ:743:C:OP2	2.37	0.56
41:BQ:1100:U:OP2	48:BO:196:LYS:NZ	2.34	0.56
41:BQ:2335:G:N2	41:BQ:2339:C:O2	2.37	0.56
41:BQ:2365:C:O2'	55:AU:68[A]:ARG:NH2	2.38	0.56
41:BQ:3172:A:O2'	55:AU:101[A]:ARG:NH2	2.39	0.56
46:BI:90:HIS:NE2	46:BI:229:ASP:OD2	2.38	0.56
51:AG:17:LEU:HD12	51:AG:128:TYR:O	2.05	0.56
53:AM:41:GLN:NE2	53:AM:41:GLN:O	2.37	0.56
16:P:83:GLN:O	16:P:87:LEU:HD23	2.05	0.56
21:U:46:ILE:HD13	21:U:60:ILE:HG13	1.87	0.56
27:AA:26:LEU:HD21	64:AN:123:GLN:HA	1.87	0.56
41:BQ:3153:U:HO2'	41:BQ:3154:C:C4'	2.16	0.56
7:G:100:LEU:O	7:G:120:SER:N	2.39	0.56
8:H:91:ASP:OD1	8:H:96:LYS:N	2.38	0.56
27:AA:206:GLU:OE1	27:AA:206:GLU:N	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2:487:G:N1	33:2:501:U:N3	2.54	0.56
35:b:15:ASN:ND2	35:b:72:CYS:O	2.38	0.56
41:BQ:1271:A:O2'	41:BQ:1272:C:OP1	2.16	0.56
41:BQ:1293:U:O2'	58:BH:88:HIS:NE2	2.39	0.56
16:P:33:GLN:NE2	34:a:64:GLU:OE2	2.39	0.56
27:AA:150:LEU:HD13	27:AA:215:VAL:HG12	1.88	0.56
41:BQ:215:G:OP1	63:AK:12:ARG:NH1	2.39	0.56
51:AG:133:ARG:NH1	51:AG:153:LYS:O	2.38	0.56
52:AJ:70:ARG:NH1	52:AJ:71:ALA:O	2.37	0.56
17:Q:125:VAL:CG2	17:Q:172:LEU:HD12	2.35	0.56
27:AA:48:ARG:NH2	41:BQ:2588:U:OP1	2.38	0.56
27:AA:123:GLN:O	41:BQ:120:G:N2	2.39	0.56
27:AA:184:ALA:O	27:AA:188:THR:HG23	2.06	0.56
28:BA:221:THR:O	28:BA:272:TYR:N	2.39	0.56
33:2:864:U:O4	35:b:60:LYS:NZ	2.23	0.56
73:AI:45:VAL:O	73:AI:51:LEU:HD12	2.06	0.56
2:A:23:GLU:OE2	2:A:27:ARG:NE	2.39	0.56
10:J:85:ARG:NH2	33:2:1334:U:O2'	2.38	0.56
15:O:258:THR:HG22	15:O:275:ARG:HD3	1.88	0.56
20:T:58:LYS:NZ	20:T:106:LEU:O	2.38	0.56
23:W:79:ARG:NH2	33:2:762:A:OP1	2.39	0.56
25:Y:13:SER:OG	25:Y:14:SER:N	2.38	0.56
41:BQ:398:A:N7	56:AX:3:ARG:NH2	2.54	0.56
41:BQ:2666:C:OP2	41:BQ:2687:G:N1	2.38	0.56
41:BQ:2688:U:OP1	46:BI:12:TYR:OH	2.21	0.56
15:O:131:ILE:HG23	15:O:144:LEU:HB2	1.87	0.56
33:2:126:A:N6	33:2:292:U:C4	2.74	0.56
41:BQ:515:C:O2'	45:BE:342:LYS:O	2.24	0.56
41:BQ:542:G:C6	41:BQ:550:A:N6	2.73	0.56
1:B:94:THR:HA	1:B:97:LEU:HD12	1.88	0.56
16:P:156:VAL:O	34:a:65:SER:OG	2.24	0.56
17:Q:82:ARG:NH1	17:Q:191:GLU:OE2	2.39	0.56
20:T:13:GLN:NE2	33:2:151:G:N3	2.54	0.56
28:BA:91:GLY:O	28:BA:102:LEU:HD23	2.06	0.56
33:2:116:U:O2'	33:2:333:A:N3	2.38	0.56
41:BQ:1976:G:H22	41:BQ:2047:A:H1'	1.71	0.56
42:BR:38:U:N3	42:BR:41:G:OP2	2.38	0.56
8:H:85:PHE:O	33:2:1565:C:O2'	2.15	0.55
15:O:175:ASP:OD2	15:O:179:LYS:NZ	2.39	0.55
16:P:7:PHE:O	16:P:54:TRP:NE1	2.38	0.55
17:Q:217:LEU:HD21	17:Q:220:GLN:HB3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:33:ARG:NH2	24:X:51:GLY:O	2.39	0.55
33:2:1747:G:O2'	41:BQ:2303:A:O2'	2.24	0.55
34:a:74:GLN:OE1	34:a:82:VAL:N	2.39	0.55
41:BQ:610:G:N7	45:BE:309:ARG:NH2	2.54	0.55
41:BQ:1603:A:OP1	57:BF:38:ARG:NH2	2.37	0.55
54:AQ:9:GLU:OE2	54:AQ:13:LYS:NZ	2.40	0.55
72:AF:59:THR:HG22	72:AF:64:MET:HE3	1.86	0.55
1:B:117:THR:HG21	1:B:194:LEU:HD23	1.88	0.55
8:H:88:ARG:O	8:H:98:TYR:N	2.39	0.55
19:S:87:MET:N	19:S:101:LEU:O	2.40	0.55
33:2:223:U:O4	33:2:838:G:C6	2.59	0.55
71:BP:8:GLU:O	71:BP:11:THR:OG1	2.23	0.55
5:E:67:ALA:HB2	5:E:73:PRO:HA	1.88	0.55
5:E:97:TYR:OH	33:2:1211:A:N3	2.39	0.55
15:O:123:ILE:HG22	15:O:133:VAL:HG12	1.89	0.55
17:Q:107:THR:OG1	26:Z:117:ASP:O	2.25	0.55
51:AG:50:ALA:HB3	51:AG:62:ASN:H	1.69	0.55
75:AO:122:ARG:NH1	75:AO:123:PRO:O	2.39	0.55
41:BQ:1497:C:O2'	41:BQ:1602:A:N3	2.29	0.55
60:BL:80:THR:HG21	60:BL:95:PHE:HD2	1.71	0.55
62:AH:82:LEU:HD11	62:AH:135:ILE:HD11	1.89	0.55
22:V:32:GLN:NE2	33:2:1727:G:N3	2.54	0.55
28:BA:56:ILE:O	28:BA:73:VAL:HG23	2.06	0.55
33:2:447:U:O2'	33:2:448:C:OP1	2.25	0.55
41:BQ:1874:A:N7	57:BF:20:ARG:NH1	2.54	0.55
41:BQ:2033:G:C8	41:BQ:2033:G:H5''	2.42	0.55
50:BD:62:SER:HA	50:BD:65:LEU:HD12	1.88	0.55
70:BN:71:THR:OG1	70:BN:78:GLY:N	2.40	0.55
11:K:83:LEU:HD12	11:K:88:ILE:CG2	2.35	0.55
15:O:123:ILE:HB	15:O:131:ILE:HD11	1.89	0.55
16:P:63:ILE:CG1	34:a:36:VAL:HG22	2.37	0.55
21:U:181:ILE:HD12	21:U:183:PHE:HE1	1.71	0.55
36:c:58:GLY:HA2	40:g:8:LEU:HD21	1.88	0.55
41:BQ:2848:G:OP1	75:AO:100:TYR:OH	2.17	0.55
61:AE:53:VAL:HG13	61:AE:54:LEU:HD22	1.89	0.55
2:A:215:GLU:N	2:A:215:GLU:OE1	2.40	0.55
9:I:135:ILE:O	9:I:139:THR:HG23	2.06	0.55
19:S:65:LEU:HD13	19:S:70:VAL:HG11	1.88	0.55
19:S:71:LYS:O	19:S:90:ILE:HD12	2.06	0.55
33:2:224:C:O2'	33:2:225:A:OP1	2.25	0.55
33:2:479:C:N3	33:2:510:G:N1	2.55	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:BQ:1750:A:OP1	73:AI:44:LYS:NZ	2.34	0.55
41:BQ:2553:U:C5	70:BN:95:ILE:HG22	2.41	0.55
41:BQ:2701:U:OP1	59:BJ:23:GLY:N	2.39	0.55
67:AY:75:ASN:O	67:AY:79:THR:HG23	2.06	0.55
25:Y:112:LYS:NZ	33:2:974:A:O3'	2.32	0.55
33:2:435:C:O3'	36:c:50:LYS:NZ	2.39	0.55
33:2:629:U:OP2	33:2:969:C:N4	2.38	0.55
33:2:779:U:N3	33:2:782:U:O4	2.38	0.55
37:d:29:HIS:O	37:d:67:GLY:HA2	2.07	0.55
45:BE:24:ALA:O	45:BE:27:SER:OG	2.17	0.55
65:AR:76:ASP:OD1	65:AR:76:ASP:N	2.37	0.55
78:AT:82:THR:OG1	78:AT:85:ARG:NH2	2.40	0.55
15:O:197:SER:OG	15:O:217:ASP:N	2.38	0.55
17:Q:77:GLU:O	17:Q:80:SER:OG	2.23	0.55
18:R:78:ASP:HB3	18:R:104:VAL:HG12	1.88	0.55
19:S:57:ASN:N	19:S:60:GLU:OE1	2.38	0.55
26:Z:55:SER:O	26:Z:55:SER:OG	2.23	0.55
33:2:428:A:N3	33:2:440:U:O2'	2.35	0.55
33:2:1037:C:O2	35:b:16:ASN:ND2	2.39	0.55
43:BS:94:C:OP1	72:AF:76:ASN:ND2	2.40	0.55
45:BE:300:ARG:NH1	45:BE:301:PRO:O	2.38	0.55
69:BK:49:ILE:HD11	69:BK:71:VAL:HG22	1.88	0.55
73:AI:17:ARG:NE	73:AI:19:ASP:OD1	2.38	0.55
7:G:32:LYS:NZ	33:2:1388:A:OP2	2.40	0.55
15:O:128:ASP:OD1	15:O:130:THR:OG1	2.17	0.55
17:Q:158:SER:HA	17:Q:161:ILE:HD12	1.88	0.55
18:R:138:PRO:O	18:R:139:ILE:HD13	2.06	0.55
18:R:180:ALA:HB2	18:R:198:THR:CG2	2.37	0.55
20:T:177:ARG:NH1	33:2:143:G:N7	2.54	0.55
21:U:97:ARG:HH22	33:2:856:A:P	2.30	0.55
26:Z:112:ILE:O	38:e:58:VAL:HG22	2.06	0.55
31:AC:51:SER:OG	54:AQ:15:GLN:OE1	2.25	0.55
41:BQ:396:A:O2'	41:BQ:399:A:OP1	2.20	0.55
44:AW:33:ASP:O	44:AW:37:ARG:NH1	2.40	0.55
63:AK:47:ALA:O	63:AK:122:LYS:NZ	2.40	0.55
78:AT:51:ALA:HB3	78:AT:54:ILE:HD12	1.89	0.55
9:I:6:VAL:HG21	9:I:132:LEU:HD21	1.88	0.54
18:R:95:ARG:NH2	33:2:1291:G:OP1	2.40	0.54
33:2:539:G:O2'	33:2:540:G:OP2	2.17	0.54
41:BQ:1170:A:O3'	48:BO:218:ARG:NH1	2.39	0.54
41:BQ:1976:G:H1	41:BQ:2047:A:H1'	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:65:ILE:HD13	9:I:71:VAL:HG22	1.88	0.54
21:U:61:PHE:HD1	21:U:93:LEU:HD22	1.73	0.54
33:2:1204:A:OP1	33:2:1456:C:N4	2.40	0.54
37:d:81:GLU:OE1	37:d:81:GLU:N	2.40	0.54
41:BQ:681:U:O4	45:BE:118:LYS:NZ	2.39	0.54
2:A:134:CYS:SG	2:A:135:GLU:N	2.80	0.54
4:D:42:ALA:O	4:D:48:SER:OG	2.21	0.54
4:D:64:SER:O	4:D:90:LYS:NZ	2.39	0.54
4:D:76:GLU:O	4:D:80:ASN:ND2	2.40	0.54
8:H:126:ARG:HD2	8:H:131:LEU:HD12	1.90	0.54
33:2:782:U:OP2	37:d:21:LYS:NZ	2.38	0.54
33:2:862:A:O2'	33:2:963:A:N6	2.27	0.54
41:BQ:679:U:O2'	41:BQ:788:C:O2	2.24	0.54
41:BQ:1963:G:OP1	41:BQ:1963:G:H3'	2.07	0.54
9:I:5:SER:N	9:I:8:ASP:OD2	2.40	0.54
14:N:130:VAL:HG21	14:N:143:LYS:HB2	1.89	0.54
17:Q:172:LEU:O	17:Q:176:VAL:HG12	2.08	0.54
29:AB:39:VAL:O	41:BQ:2931:C:O2'	2.26	0.54
33:2:680:U:O4	33:2:682:C:N4	2.40	0.54
41:BQ:209:A:O2'	41:BQ:211:A:OP2	2.24	0.54
41:BQ:763:G:C6	41:BQ:769:G:C2	2.96	0.54
41:BQ:2093:A:C2	57:BF:143:ILE:CD1	2.91	0.54
41:BQ:3019:U:O2	41:BQ:3035:A:N6	2.35	0.54
4:D:108:ARG:O	4:D:110:GLY:N	2.40	0.54
19:S:72:VAL:N	19:S:75:LYS:O	2.41	0.54
35:b:53:ILE:HD11	39:f:8:LEU:HD23	1.89	0.54
41:BQ:68:C:N4	41:BQ:314:U:O2'	2.40	0.54
45:BE:129:THR:HG23	45:BE:246:ARG:O	2.08	0.54
51:AG:40:LEU:HD21	51:AG:79:ILE:HD12	1.88	0.54
79:x:21:TYR:CE1	79:x:99:TYR:CD2	2.96	0.54
47:BM:57:HIS:ND1	47:BM:58:LEU:O	2.40	0.54
1:B:196:GLU:O	1:B:200:ASN:ND2	2.40	0.54
16:P:125:ASP:OD1	16:P:128:SER:N	2.40	0.54
33:2:505:A:O2'	33:2:507:U:OP1	2.11	0.54
33:2:653:C:C4	33:2:681:U:O4	2.61	0.54
33:2:748:U:O3'	35:b:122:SER:OG	2.25	0.54
11:K:62:VAL:O	11:K:66:VAL:HG23	2.08	0.54
26:Z:13:VAL:O	26:Z:77:THR:OG1	2.24	0.54
41:BQ:1206:G:OP1	50:BD:157:TYR:OH	2.12	0.54
41:BQ:1977:C:N3	41:BQ:2046:U:O2'	2.41	0.54
41:BQ:3353:G:O2'	41:BQ:3354:U:O4'	2.15	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:BE:59:GLN:OE1	72:AF:55:ARG:NH2	2.40	0.54
50:BD:160:PRO:O	50:BD:163:GLN:NE2	2.41	0.54
22:V:99:ALA:N	22:V:169:ILE:O	2.41	0.54
29:AB:12:ARG:NH1	41:BQ:3041:U:OP1	2.41	0.54
33:2:1457:C:O2'	33:2:1458:G:O5'	2.21	0.54
41:BQ:1488:G:O2'	70:BN:10:ARG:O	2.25	0.54
43:BS:136:G:OP1	62:AH:48:SER:OG	2.17	0.54
4:D:60:VAL:HG22	4:D:122:VAL:HG13	1.89	0.54
21:U:96:ARG:O	33:2:694:U:N3	2.40	0.54
24:X:24:LYS:O	24:X:26:LYS:NZ	2.38	0.54
41:BQ:1987:G:N3	41:BQ:1987:G:H2'	2.23	0.54
41:BQ:2033:G:O6	41:BQ:2035:G:C2	2.60	0.54
41:BQ:2555:G:N7	70:BN:95:ILE:HD11	2.23	0.54
65:AR:89:GLN:N	65:AR:89:GLN:OE1	2.39	0.54
75:AO:109:ASN:ND2	75:AO:117:HIS:O	2.40	0.54
5:E:24:LYS:CB	5:E:28:MET:HE2	2.37	0.53
18:R:116:LYS:HG2	18:R:127:ALA:HB3	1.90	0.53
32:BC:62:ARG:NH1	32:BC:68:GLU:OE1	2.39	0.53
33:2:651:G:C6	33:2:684:A:C6	2.96	0.53
41:BQ:67:A:O2'	41:BQ:315:C:O2	2.25	0.53
41:BQ:1015:U:O2	41:BQ:1017:C:O2'	2.21	0.53
41:BQ:1135:A:OP1	66:AV:6:ASN:N	2.37	0.53
41:BQ:1982:G:N2	41:BQ:2040:U:H3	2.05	0.53
45:BE:155:ASP:OD1	45:BE:156:LEU:N	2.41	0.53
20:T:25:ARG:NH1	28:BA:298:PHE:O	2.40	0.53
23:W:151:ASP:O	23:W:155:HIS:ND1	2.40	0.53
28:BA:126:LYS:N	41:BQ:3295:A:OP2	2.41	0.53
30:BB:44:PHE:HD1	30:BB:139:ILE:HD11	1.73	0.53
33:2:933:A:H61	33:2:944:A:H61	1.56	0.53
33:2:1272:U:O2	33:2:1438:G:O6	2.26	0.53
41:BQ:2553:U:C4	70:BN:95:ILE:HG22	2.43	0.53
64:AN:114:VAL:O	64:AN:118:PHE:N	2.41	0.53
67:AY:12:GLN:OE1	67:AY:12:GLN:N	2.41	0.53
4:D:32:LEU:O	4:D:36:LEU:HD23	2.08	0.53
7:G:7:LYS:N	33:2:1316:G:OP1	2.41	0.53
17:Q:34:ALA:O	17:Q:232:HIS:NE2	2.40	0.53
19:S:72:VAL:HG22	19:S:90:ILE:HD13	1.91	0.53
33:2:487:G:C2	33:2:501:U:O2	2.61	0.53
41:BQ:3198:U:O2	49:AD:21:LYS:N	2.41	0.53
50:BD:54:SER:HB2	50:BD:135:ILE:HD11	1.89	0.53
50:BD:89:VAL:HG12	50:BD:136:PHE:CE1	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:AY:76:GLU:OE2	67:AY:76:GLU:N	2.41	0.53
27:AA:126:SER:O	41:BQ:120:G:N2	2.41	0.53
41:BQ:1210:U:OP1	49:AD:62:ARG:NE	2.39	0.53
15:O:197:SER:OG	15:O:216:LYS:N	2.41	0.53
22:V:48:THR:OG1	22:V:51:GLY:O	2.27	0.53
22:V:70:GLU:OE1	22:V:70:GLU:N	2.41	0.53
28:BA:367:LYS:NZ	41:BQ:3086:A:OP1	2.42	0.53
33:2:518:A:C6	33:2:533:U:O4	2.62	0.53
33:2:656:G:O6	33:2:679:U:O2	2.25	0.53
41:BQ:1167:U:O2	48:BO:209:ASN:ND2	2.41	0.53
41:BQ:1968:G:C3'	41:BQ:1969:G:H4'	2.39	0.53
58:BH:81:TYR:CE1	58:BH:90:MET:HE3	2.44	0.53
75:AO:96:CYS:HA	75:AO:121:LEU:HD23	1.90	0.53
1:B:91:GLU:O	1:B:95:ASN:ND2	2.41	0.53
6:F:99:GLU:OE2	6:F:102:LYS:NZ	2.27	0.53
28:BA:60:LEU:HD12	28:BA:352:GLU:OE2	2.09	0.53
41:BQ:3258:U:O2'	41:BQ:3260:G:OP1	2.19	0.53
50:BD:71:CYS:SG	50:BD:72:ALA:N	2.81	0.53
11:K:47:TYR:CZ	11:K:51:LEU:HD11	2.43	0.53
15:O:270:LEU:HD21	15:O:273:ASP:HB2	1.89	0.53
19:S:12:LEU:HD11	23:W:4:ALA:HB2	1.91	0.53
21:U:99:LEU:HD13	21:U:116:ARG:HB3	1.91	0.53
22:V:158:SER:O	22:V:161:SER:OG	2.18	0.53
26:Z:47:LYS:NZ	26:Z:66:ASP:OD2	2.31	0.53
28:BA:2:SER:N	41:BQ:2940:A:OP2	2.42	0.53
33:2:540:G:N3	33:2:542:A:C5	2.77	0.53
36:c:58:GLY:N	40:g:4:VAL:O	2.37	0.53
37:d:20:ARG:CD	37:d:74:LEU:HD11	2.39	0.53
41:BQ:242:C:O2'	41:BQ:243:G:OP2	2.26	0.53
47:BM:60:ASP:O	47:BM:62:THR:HG23	2.08	0.53
51:AG:91:LEU:HD12	51:AG:163:PHE:CE2	2.43	0.53
15:O:224:ASN:HB3	15:O:231:MET:HE3	1.91	0.53
26:Z:52:ARG:NH2	33:2:906:A:OP1	2.42	0.53
28:BA:10:ARG:HH11	28:BA:14:LEU:HD21	1.74	0.53
33:2:575:C:N4	36:c:65:ASN:OD1	2.34	0.53
41:BQ:884:A:OP2	41:BQ:2139:A:N6	2.42	0.53
41:BQ:1977:C:H4'	73:AI:59:ALA:CB	2.39	0.53
48:BO:88:ARG:O	48:BO:112:ASN:N	2.41	0.53
1:B:103:ASN:ND2	33:2:1473:U:O2'	2.41	0.53
7:G:36:ASP:OD1	7:G:37:GLU:N	2.42	0.53
25:Y:88:LEU:HD22	25:Y:129:TYR:CD2	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:BN:74:ARG:NH2	70:BN:82:ALA:HB2	2.24	0.53
19:S:19:LEU:HD12	19:S:51:ARG:HH22	1.74	0.53
20:T:132:ARG:O	33:2:68:A:N6	2.40	0.53
21:U:22:GLN:HA	21:U:25:VAL:HG22	1.91	0.53
33:2:1488:G:O2'	33:2:1494:C:O2	2.11	0.53
35:b:53:ILE:HD11	39:f:8:LEU:CD2	2.39	0.53
41:BQ:3216:G:OP1	47:BM:162:SER:N	2.42	0.53
54:AQ:155:VAL:O	54:AQ:162:ARG:NH2	2.40	0.53
15:O:74:THR:OG1	15:O:78:ALA:N	2.42	0.52
15:O:246:SER:OG	15:O:248:ASN:OD1	2.27	0.52
16:P:108:THR:OG1	33:2:1294:G:O2'	2.25	0.52
21:U:155:ASP:OD1	21:U:157:LYS:NZ	2.27	0.52
25:Y:129:TYR:CB	25:Y:135:LEU:HD12	2.40	0.52
41:BQ:2724:U:OP2	59:BJ:87:LYS:NZ	2.26	0.52
41:BQ:2724:U:OP2	41:BQ:2726:C:N4	2.42	0.52
41:BQ:3153:U:OP2	41:BQ:3293:U:O2'	2.14	0.52
14:N:132:LEU:HD13	14:N:139:LEU:HD23	1.90	0.52
22:V:73:SER:OG	33:2:256:A:N3	2.21	0.52
32:BC:105:GLN:OE1	41:BQ:3383:G:N2	2.32	0.52
33:2:452:A:O2'	33:2:453:U:O4'	2.26	0.52
33:2:1489:U:O2'	33:2:1492:A:N3	2.36	0.52
33:2:1779:U:O4	76:AS:12:ARG:NH1	2.42	0.52
8:H:26:ILE:HD11	8:H:31:ALA:HB2	1.90	0.52
20:T:30:LYS:O	20:T:102:VAL:HG23	2.09	0.52
20:T:214:LYS:O	20:T:217:SER:OG	2.19	0.52
27:AA:248:LYS:O	27:AA:252:ASN:ND2	2.43	0.52
33:2:225:A:N6	33:2:837:G:N1	2.56	0.52
33:2:815:G:O2'	57:BF:162:ARG:NH2	2.42	0.52
37:d:21:LYS:O	37:d:74:LEU:HD12	2.09	0.52
64:AN:13:VAL:O	64:AN:20:GLY:N	2.42	0.52
66:AV:16:ALA:O	66:AV:20:GLY:HA3	2.09	0.52
6:F:50:GLU:OE1	6:F:82:ARG:NH2	2.43	0.52
18:R:68:ILE:O	18:R:71:THR:OG1	2.27	0.52
21:U:61:PHE:CD1	21:U:93:LEU:HD22	2.44	0.52
33:2:998:A:N6	33:2:1004:U:OP2	2.43	0.52
36:c:130:VAL:HG21	36:c:143:PRO:HD2	1.90	0.52
43:BS:57:C:OP2	72:AF:68:LYS:NZ	2.42	0.52
51:AG:40:LEU:HD21	51:AG:79:ILE:CD1	2.39	0.52
26:Z:50:ALA:HB3	26:Z:53:ASP:HB2	1.92	0.52
33:2:451:A:N6	33:2:453:U:O2	2.43	0.52
38:e:87:ARG:NH2	38:e:92:ARG:O	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:BQ:1257:C:N3	41:BQ:1261:G:N2	2.57	0.52
17:Q:115:ARG:O	17:Q:118:GLN:NE2	2.42	0.52
19:S:64:ILE:HD11	37:d:18:LEU:HD12	1.91	0.52
41:BQ:66:A:N6	41:BQ:75:G:N2	2.58	0.52
41:BQ:1955:U:H3	41:BQ:2086:A:H61	1.57	0.52
23:W:134:ILE:N	23:W:159:ALA:HB2	2.25	0.52
24:X:96:LYS:NZ	33:2:374:U:OP1	2.32	0.52
41:BQ:1952:G:C5	41:BQ:2095:G:N1	2.77	0.52
17:Q:106:THR:OG1	17:Q:108:ASP:OD1	2.15	0.52
39:f:34:ASP:OD2	39:f:80:ARG:NH1	2.43	0.52
41:BQ:1953:G:H5''	41:BQ:1954:G:H5'	1.92	0.52
41:BQ:2494:A:H1'	80:BT:163:LEU:C	2.35	0.52
7:G:44:LYS:NZ	33:2:1386:G:OP2	2.39	0.52
20:T:15:THR:HG23	33:2:152:U:O2'	2.10	0.52
20:T:31:ARG:HG2	20:T:101:ILE:HD13	1.91	0.52
33:2:97:C:O2	33:2:425:A:O2'	2.27	0.52
33:2:655:G:N3	33:2:678:A:C6	2.77	0.52
41:BQ:1126:G:OP1	50:BD:98:ARG:NH2	2.43	0.52
45:BE:33:ASP:N	45:BE:33:ASP:OD1	2.43	0.52
46:BI:107:ARG:NH1	46:BI:120:LYS:O	2.43	0.52
75:AO:110:CYS:SG	75:AO:111:ARG:N	2.83	0.52
6:F:28:LEU:O	6:F:29:ILE:HD13	2.10	0.52
11:K:48:ASP:HA	11:K:51:LEU:HD12	1.92	0.52
28:BA:218:ILE:HD11	28:BA:339:ARG:NH1	2.25	0.52
34:a:9:VAL:HG22	34:a:10:GLU:H	1.75	0.52
41:BQ:2033:G:H5''	41:BQ:2033:G:H8	1.75	0.52
54:AQ:56:LYS:NZ	54:AQ:145:ASP:OD2	2.43	0.52
68:BG:97:ALA:O	68:BG:105:ARG:NH2	2.43	0.52
17:Q:146:GLN:NE2	33:2:1065:A:N3	2.58	0.51
22:V:4:SER:OG	22:V:6:ASP:OD2	2.28	0.51
28:BA:204:ALA:O	28:BA:207:SER:OG	2.24	0.51
29:AB:130:ALA:O	29:AB:133:SER:OG	2.28	0.51
33:2:1553:G:N1	33:2:1556:A:OP2	2.43	0.51
33:2:1582:U:O2'	33:2:1583:A:OP2	2.24	0.51
41:BQ:1952:G:C4	41:BQ:2095:G:C2	2.98	0.51
41:BQ:2695:A:HO2'	41:BQ:2696:A:P	2.33	0.51
45:BE:219:LEU:HA	45:BE:222:VAL:HG22	1.92	0.51
48:BO:86:VAL:HG22	48:BO:136:TYR:CB	2.40	0.51
48:BO:232:ARG:NH1	48:BO:239:LEU:HD13	2.24	0.51
53:AM:72:LEU:HD12	53:AM:73:PRO:HD2	1.92	0.51
61:AE:20:LEU:HD21	61:AE:28:ILE:HG23	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:41:ARG:NH2	33:2:916:U:O4	2.43	0.51
29:AB:108:GLU:N	29:AB:108:GLU:OE1	2.43	0.51
30:BB:66:ARG:NH2	41:BQ:744:A:OP1	2.43	0.51
39:f:44:THR:HG21	39:f:63:LEU:HD13	1.91	0.51
41:BQ:999:G:N3	41:BQ:1002:A:N6	2.57	0.51
41:BQ:1306:G:O6	41:BQ:2366:C:O2'	2.28	0.51
41:BQ:2696:A:N7	41:BQ:2758:A:N6	2.58	0.51
63:AK:58:VAL:O	63:AK:65:GLY:N	2.44	0.51
68:BG:83:GLU:HA	68:BG:86:THR:HG23	1.92	0.51
4:D:34:THR:HG21	4:D:128:ALA:HB2	1.91	0.51
11:K:50:ILE:O	11:K:54:VAL:HG13	2.10	0.51
17:Q:108:ASP:OD1	17:Q:109:LYS:N	2.44	0.51
23:W:55:ALA:O	23:W:59:LEU:HD23	2.10	0.51
29:AB:14:SER:O	29:AB:81:GLN:NE2	2.44	0.51
41:BQ:836:A:O2'	78:AT:9:GLY:O	2.25	0.51
60:BL:80:THR:HG21	60:BL:95:PHE:CD2	2.46	0.51
10:J:90:TYR:OH	33:2:1347:U:OP1	2.18	0.51
33:2:931:C:OP2	38:e:70:LYS:NZ	2.40	0.51
41:BQ:1386:A:O4'	45:BE:141:ARG:NH1	2.44	0.51
10:J:102:ARG:O	10:J:106:ILE:HG22	2.11	0.51
15:O:144:LEU:C	15:O:145:LEU:HD22	2.35	0.51
17:Q:92:GLN:OE1	17:Q:229:MET:HE1	2.10	0.51
41:BQ:901:G:OP1	72:AF:13:ASN:ND2	2.43	0.51
41:BQ:1405:U:OP2	68:BG:59:SER:OG	2.19	0.51
54:AQ:98:LEU:HD22	54:AQ:128:LYS:HD2	1.93	0.51
63:AK:89:LYS:O	63:AK:92:GLY:N	2.39	0.51
18:R:165:VAL:HG11	18:R:210:THR:HG22	1.92	0.51
25:Y:60:VAL:HG13	25:Y:66:ILE:HD13	1.92	0.51
26:Z:50:ALA:HB1	26:Z:52:ARG:NH2	2.25	0.51
41:BQ:1116:G:N2	41:BQ:2817:A:O4'	2.43	0.51
41:BQ:2672:G:O2'	51:AG:95:ASN:O	2.24	0.51
42:BR:21:G:O2'	46:BI:272:TYR:OH	2.03	0.51
43:BS:85:G:HO2'	43:BS:86:U:P	2.33	0.51
69:BK:49:ILE:HD11	69:BK:71:VAL:HG23	1.92	0.51
79:x:192:LEU:HD12	79:x:219:ASP:O	2.09	0.51
15:O:124:SER:OG	15:O:134:TRP:NE1	2.43	0.51
18:R:212:LYS:O	18:R:216:VAL:HG23	2.10	0.51
23:W:28:LEU:HD21	40:g:40:TYR:HA	1.92	0.51
33:2:443:C:O2'	33:2:445:A:N7	2.39	0.51
41:BQ:1261:G:N2	41:BQ:1261:G:OP2	2.43	0.51
41:BQ:1299:U:O2'	75:AO:114:LYS:O	2.27	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:BQ:1643:A:O2'	41:BQ:1644:C:O4'	2.23	0.51
78:AT:16:VAL:HG12	78:AT:16:VAL:O	2.11	0.51
29:AB:12:ARG:HH22	29:AB:15:LEU:HD12	1.76	0.51
33:2:1229:G:N2	33:2:1255:G:O2'	2.28	0.51
41:BQ:203:G:OP1	45:BE:183:LYS:NZ	2.44	0.51
41:BQ:591:G:O2'	47:BM:17:ALA:O	2.28	0.51
41:BQ:2261:G:H21	41:BQ:2262:A:H62	1.58	0.51
73:AI:61:LYS:O	73:AI:65:LEU:HD23	2.11	0.51
19:S:129:VAL:HG12	19:S:139:VAL:HG12	1.93	0.51
21:U:114:ARG:O	21:U:117:THR:HG22	2.11	0.51
21:U:166:LEU:HD13	21:U:169:PHE:HD2	1.76	0.51
28:BA:60:LEU:HD11	28:BA:62:ARG:NE	2.26	0.51
33:2:699:U:O2'	33:2:700:C:O5'	2.28	0.51
33:2:1488:G:H3'	33:2:1515:A:H61	1.76	0.51
33:2:1775:U:OP1	76:AS:11:ARG:NH1	2.41	0.51
36:c:58:GLY:CA	40:g:8:LEU:HD21	2.41	0.51
41:BQ:450:G:N7	41:BQ:487:U:O2'	2.39	0.51
41:BQ:1638:A:O2'	70:BN:52:GLN:NE2	2.44	0.51
41:BQ:2027:C:O2	41:BQ:2027:C:H2'	2.10	0.51
41:BQ:2093:A:H2	57:BF:143:ILE:CD1	2.22	0.51
45:BE:92:ASN:OD1	45:BE:93:MET:N	2.44	0.51
56:AX:47:TYR:OH	56:AX:57:ALA:O	2.12	0.51
10:J:76:SER:OG	33:2:1281:G:O3'	2.25	0.51
13:M:44:ARG:NH2	33:2:1280:C:OP1	2.44	0.51
24:X:8:GLN:OE1	24:X:14:GLN:N	2.41	0.51
28:BA:266:ARG:NH2	41:BQ:2392:C:O2'	2.41	0.51
33:2:1303:U:O2'	33:2:1322:A:OP2	2.28	0.51
67:AY:17:VAL:HG11	67:AY:92:ILE:HD12	1.93	0.51
18:R:153:SER:OG	18:R:154:LEU:N	2.45	0.50
18:R:239:PRO:HA	18:R:242:ILE:HD12	1.93	0.50
33:2:478:A:N6	33:2:539:G:N1	2.58	0.50
37:d:2:SER:OG	37:d:3:ASP:N	2.44	0.50
41:BQ:1268:G:N2	41:BQ:1269:U:O4	2.45	0.50
41:BQ:1724:U:O2'	41:BQ:1725:C:OP2	2.24	0.50
41:BQ:3153:U:O2'	41:BQ:3154:C:O4'	2.13	0.50
65:AR:22:ILE:H	65:AR:22:ILE:HD12	1.76	0.50
2:A:32:GLU:OE1	2:A:32:GLU:N	2.45	0.50
2:A:103:GLU:OE2	2:A:173:ARG:NE	2.41	0.50
5:E:60:LEU:HD23	5:E:76:VAL:HG21	1.92	0.50
13:M:30:LEU:HD22	13:M:30:LEU:N	2.26	0.50
26:Z:26:THR:HG21	26:Z:97:GLY:HA3	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:BB:152:HIS:ND1	30:BB:162:ALA:O	2.41	0.50
33:2:1181:U:C2	33:2:1458:G:N1	2.79	0.50
55:AU:108[A]:ILE:HD12	55:AU:157[A]:GLU:OE2	2.11	0.50
18:R:161:LYS:NZ	18:R:163:GLY:O	2.24	0.50
21:U:97:ARG:NH2	33:2:856:A:P	2.84	0.50
28:BA:109:HIS:C	28:BA:110:LEU:HD22	2.36	0.50
28:BA:346:THR:OG1	28:BA:347:SER:N	2.42	0.50
33:2:1432:U:O2'	33:2:1433:G:OP2	2.28	0.50
35:b:18:GLU:HG3	35:b:69:LEU:HD23	1.94	0.50
41:BQ:69:C:HO2'	41:BQ:101:G:HO2'	1.54	0.50
41:BQ:1976:G:O2'	73:AI:60:GLY:CA	2.59	0.50
41:BQ:1989:U:O2	41:BQ:1989:U:H2'	2.12	0.50
41:BQ:2035:G:H4'	41:BQ:2035:G:OP1	2.11	0.50
43:BS:82:U:O2'	43:BS:83:C:OP1	2.27	0.50
30:BB:135:GLN:N	30:BB:135:GLN:OE1	2.43	0.50
33:2:898:A:N1	33:2:911:U:O2'	2.35	0.50
34:a:1:MET:N	34:a:10:GLU:OE2	2.44	0.50
39:f:80:ARG:NH2	39:f:81:ARG:O	2.44	0.50
41:BQ:2095:G:H2'	41:BQ:2096:A:C8	2.45	0.50
41:BQ:2746:A:C2	46:BI:146:LEU:HD23	2.47	0.50
21:U:46:ILE:HD12	21:U:59:ALA:O	2.12	0.50
41:BQ:590:G:OP1	68:BG:62:LYS:NZ	2.44	0.50
41:BQ:1657:C:O2	70:BN:16:ARG:NH2	2.44	0.50
41:BQ:2896:A:OP1	75:AO:124:LYS:NZ	2.28	0.50
49:AD:14:GLU:OE1	49:AD:14:GLU:N	2.42	0.50
54:AQ:147:ARG:O	54:AQ:150:TRP:NE1	2.43	0.50
55:AU:115[A]:LYS:O	55:AU:117[A]:ARG:NH1	2.45	0.50
26:Z:20:TYR:OH	26:Z:86:THR:HG22	2.10	0.50
33:2:227:U:O4	33:2:235:G:C6	2.64	0.50
41:BQ:1977:C:N4	41:BQ:2046:U:C1'	2.66	0.50
51:AG:50:ALA:HB3	51:AG:62:ASN:N	2.27	0.50
1:B:51:VAL:HG13	1:B:131:GLN:HA	1.92	0.50
1:B:52:GLU:OE1	1:B:52:GLU:N	2.42	0.50
2:A:9:ARG:HA	2:A:12:VAL:HG22	1.93	0.50
7:G:33:ARG:NH1	33:2:1387:G:OP1	2.44	0.50
18:R:157:LYS:NZ	35:b:92:ASN:O	2.45	0.50
33:2:219:A:N1	33:2:842:C:N3	2.60	0.50
52:AJ:9:ILE:HG23	65:AR:34:MET:HE3	1.93	0.50
71:BP:13:SER:OG	71:BP:15:GLU:OE1	2.28	0.50
72:AF:19:CYS:SG	72:AF:20:ASN:N	2.85	0.50
7:G:2:GLY:N	33:2:1311:U:O3'	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:33:THR:HG22	8:H:39:GLY:C	2.37	0.50
18:R:78:ASP:CB	18:R:104:VAL:HG12	2.42	0.50
21:U:116:ARG:CZ	33:2:856:A:C6	2.94	0.50
41:BQ:542:G:C6	41:BQ:550:A:N1	2.80	0.50
41:BQ:2261:G:H21	41:BQ:2262:A:N6	2.10	0.50
41:BQ:2502:A:O2'	41:BQ:2503:G:OP1	2.26	0.50
63:AK:100:HIS:ND1	63:AK:102:SER:OG	2.27	0.50
78:AT:61:LYS:CE	78:AT:61:LYS:HA	2.42	0.50
18:R:59:HIS:O	34:a:15:ARG:NH2	2.45	0.50
20:T:157:VAL:HG11	33:2:78:A:H5'	1.94	0.50
33:2:76:A:O2'	33:2:80:A:N6	2.44	0.50
33:2:651:G:C6	33:2:684:A:C2	2.99	0.50
41:BQ:2046:U:H2'	41:BQ:2047:A:C4	2.47	0.50
41:BQ:2618:G:OP1	41:BQ:2644:C:O2'	2.28	0.50
60:BL:54:VAL:HG12	60:BL:67:SER:CB	2.42	0.50
1:B:47:SER:OG	1:B:50:GLU:OE2	2.29	0.49
5:E:40:ARG:NH1	33:2:1551:U:O4	2.42	0.49
25:Y:64:ARG:NH2	33:2:861:U:OP1	2.43	0.49
33:2:142:G:H22	33:2:173:A:H2	1.60	0.49
33:2:1251:U:O2'	33:2:1252:C:OP1	2.30	0.49
41:BQ:72:C:O2'	52:AJ:61:PRO:O	2.26	0.49
41:BQ:1953:G:C5'	41:BQ:1954:G:H5'	2.42	0.49
41:BQ:2031:U:H6	41:BQ:2031:U:O5'	1.95	0.49
1:B:23:VAL:CG1	6:F:57:LEU:HD12	2.42	0.49
19:S:182:TYR:N	19:S:226:PHE:O	2.44	0.49
29:AB:135:VAL:HG11	61:AE:26:SER:OG	2.13	0.49
41:BQ:439:C:H1'	41:BQ:494:G:H21	1.77	0.49
41:BQ:2688:U:N3	46:BI:17:GLN:O	2.42	0.49
46:BI:194:LEU:HD11	46:BI:198:TYR:CZ	2.47	0.49
1:B:95:ASN:O	33:2:1611:A:O2'	2.29	0.49
26:Z:24:ASN:ND2	33:2:902:G:N7	2.60	0.49
42:BR:6:C:O2'	46:BI:72:ASP:OD2	2.24	0.49
79:x:231:LEU:HD13	79:x:372:THR:HB	1.93	0.49
3:C:11:ILE:CD1	3:C:42:VAL:HG22	2.40	0.49
11:K:50:ILE:CG2	11:K:69:LEU:HD13	2.39	0.49
28:BA:118:PHE:O	41:BQ:3000:A:O2'	2.30	0.49
28:BA:360:ASP:OD2	61:AE:17:ARG:NH2	2.45	0.49
33:2:1521:G:C5	33:2:1523:G:N2	2.80	0.49
41:BQ:2675:C:N4	51:AG:22:SER:OG	2.38	0.49
47:BM:42:LEU:O	47:BM:49:GLY:N	2.43	0.49
59:BJ:17:ARG:NH1	59:BJ:21:LYS:O	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:32:GLU:OE1	1:B:32:GLU:N	2.44	0.49
1:B:117:THR:HG22	1:B:191:ALA:O	2.13	0.49
5:E:108:ARG:H	5:E:111:MET:HE3	1.75	0.49
8:H:22:VAL:CG2	8:H:35:ILE:HD11	2.39	0.49
11:K:95:HIS:ND1	11:K:96:SER:O	2.42	0.49
21:U:148:LYS:NZ	33:2:641:G:OP1	2.46	0.49
28:BA:166:ILE:O	28:BA:169:THR:OG1	2.30	0.49
33:2:103:A:O2'	33:2:309:C:N4	2.45	0.49
33:2:1158:C:O2'	33:2:1581:C:OP2	2.30	0.49
37:d:22:GLN:HB3	37:d:74:LEU:HD13	1.95	0.49
41:BQ:488:U:O2'	41:BQ:489:U:O4'	2.31	0.49
41:BQ:1963:G:C2'	41:BQ:1964:C:H4'	2.42	0.49
41:BQ:2452:G:N2	41:BQ:2494:A:C5	2.81	0.49
43:BS:83:C:O2	63:AK:51:ARG:NH2	2.45	0.49
45:BE:289:ILE:O	45:BE:295:ILE:HD12	2.12	0.49
46:BI:128:GLU:O	46:BI:164:LYS:NZ	2.23	0.49
77:AP:17:CYS:SG	77:AP:77:CYS:SG	3.10	0.49
21:U:166:LEU:HD13	21:U:169:PHE:CD2	2.48	0.49
35:b:6:VAL:HG23	35:b:29:PRO:HD2	1.93	0.49
38:e:26:CYS:O	38:e:27:SER:OG	2.26	0.49
41:BQ:190:U:OP1	63:AK:37:LYS:NZ	2.33	0.49
63:AK:53:ASP:O	63:AK:69:LYS:NZ	2.46	0.49
15:O:295:SER:OG	15:O:300:THR:OG1	2.30	0.49
19:S:65:LEU:HD12	19:S:78:THR:HA	1.93	0.49
33:2:655:G:N2	33:2:678:A:N6	2.60	0.49
41:BQ:535:G:HO2'	41:BQ:554:A:H61	1.58	0.49
41:BQ:959:C:O2	41:BQ:2614:G:O2'	2.26	0.49
41:BQ:1521:G:O6	74:AL:17:LYS:NZ	2.45	0.49
47:BM:64:LEU:HD12	47:BM:77:ARG:O	2.12	0.49
52:AJ:7:LEU:O	65:AR:49:HIS:NE2	2.42	0.49
57:BF:105:LEU:HD23	57:BF:138:LEU:HD23	1.93	0.49
59:BJ:39:ILE:HD12	59:BJ:102:ARG:HD3	1.93	0.49
8:H:133:VAL:HG12	33:2:1545:A:O5'	2.12	0.49
14:N:133:ALA:HB2	33:2:1252:C:H1'	1.95	0.49
17:Q:214:LYS:NZ	33:2:886:U:OP1	2.39	0.49
26:Z:14:PHE:C	26:Z:76:ILE:HD11	2.37	0.49
36:c:17:VAL:HG12	36:c:20:ARG:NH2	2.28	0.49
41:BQ:70:A:H2	41:BQ:72:C:H42	1.60	0.49
41:BQ:1564:U:C2	41:BQ:1576:G:C2	3.00	0.49
63:AK:33:ALA:HB2	63:AK:101:PRO:HB2	1.95	0.49
65:AR:82:ILE:HD11	65:AR:102:ILE:HD11	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:31:VAL:HG12	6:F:32:ASN:ND2	2.28	0.49
10:J:64:LYS:O	13:M:33:LYS:NZ	2.45	0.49
18:R:80:VAL:HG12	18:R:102:VAL:HG12	1.94	0.49
19:S:193:GLY:O	19:S:211:LYS:N	2.45	0.49
29:AB:24:ASN:ND2	29:AB:97:ASP:OD2	2.45	0.49
33:2:478:A:N1	33:2:511:A:N6	2.61	0.49
41:BQ:912:G:OP2	44:AW:9:ARG:NH1	2.41	0.49
1:B:107:LYS:NZ	33:2:1611:A:OP1	2.44	0.49
2:A:109:LEU:CD2	2:A:115:ILE:HG22	2.42	0.49
8:H:86:LEU:HD12	8:H:97:ASP:HB3	1.95	0.49
21:U:181:ILE:HD12	21:U:183:PHE:CE1	2.46	0.49
23:W:59:LEU:HD12	23:W:69:ARG:HA	1.94	0.49
33:2:518:A:O2'	33:2:519:C:O5'	2.20	0.49
33:2:548:G:C6	33:2:591:A:C6	3.01	0.49
55:AU:27[A]:LEU:HD23	55:AU:31[A]:GLN:O	2.13	0.49
71:BP:84:LYS:O	71:BP:85:THR:HG23	2.12	0.49
2:A:37:VAL:HG12	2:A:50:ILE:HG12	1.94	0.48
13:M:39:CYS:HB2	13:M:42:CYS:SG	2.53	0.48
19:S:19:LEU:HD11	19:S:108:ARG:CD	2.43	0.48
19:S:77:ARG:NH2	33:2:122:U:O3'	2.46	0.48
22:V:5:ARG:N	22:V:28:GLU:O	2.46	0.48
25:Y:129:TYR:HB2	25:Y:135:LEU:HD12	1.94	0.48
32:BC:44:MET:O	32:BC:77:ARG:NH1	2.46	0.48
33:2:1582:U:C2	33:2:1614:A:C6	3.00	0.48
37:d:12:VAL:HG12	37:d:23:PHE:CB	2.43	0.48
41:BQ:2155:G:O2'	44:AW:227:ARG:NH2	2.46	0.48
42:BR:63:A:O2'	42:BR:65:G:O4'	2.30	0.48
45:BE:26:PHE:HD1	45:BE:130:ALA:HB2	1.78	0.48
8:H:133:VAL:HG13	8:H:134:ARG:HG2	1.94	0.48
17:Q:135:LEU:HD13	17:Q:217:LEU:HA	1.94	0.48
31:AC:66:GLU:OE1	31:AC:70:ARG:NH1	2.46	0.48
41:BQ:596:C:OP2	48:BO:34:LYS:NZ	2.33	0.48
41:BQ:1188:U:OP1	41:BQ:1210:U:O2'	2.17	0.48
41:BQ:1543:G:OP1	54:AQ:35:VAL:HG23	2.13	0.48
41:BQ:2703:A:OP2	46:BI:23:ARG:NH2	2.46	0.48
41:BQ:2898:G:O6	75:AO:125:LYS:NZ	2.46	0.48
49:AD:70:THR:O	49:AD:74:LEU:HD23	2.14	0.48
54:AQ:187:ARG:O	54:AQ:190:THR:OG1	2.30	0.48
62:AH:55:ASN:ND2	62:AH:57:LEU:O	2.45	0.48
5:E:48:GLY:O	5:E:52:LYS:NZ	2.28	0.48
10:J:61:LYS:NZ	33:2:1516:A:OP2	2.25	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:83:LEU:HD12	11:K:88:ILE:HG22	1.94	0.48
21:U:77:LEU:HD22	21:U:92:PHE:HZ	1.78	0.48
22:V:193:LEU:O	22:V:197:THR:HG23	2.14	0.48
33:2:149:C:N3	33:2:166:C:N4	2.61	0.48
33:2:505:A:N1	33:2:507:U:C4	2.81	0.48
33:2:699:U:O2	33:2:739:G:N2	2.44	0.48
36:c:130:VAL:HG11	36:c:135:LEU:HD21	1.96	0.48
41:BQ:2320:A:H2	78:AT:16:VAL:HG12	1.78	0.48
57:BF:115:ILE:HG13	57:BF:119:LEU:HD23	1.95	0.48
60:BL:35:LYS:HA	60:BL:38:ILE:HD12	1.95	0.48
3:C:23:ALA:O	3:C:63:TYR:O	2.31	0.48
10:J:92:ASP:C	10:J:93:LEU:HD22	2.39	0.48
28:BA:183:LEU:O	28:BA:191:LYS:NZ	2.47	0.48
33:2:478:A:N6	33:2:539:G:N2	2.60	0.48
34:a:73:ALA:HB3	34:a:79:LEU:HD12	1.95	0.48
41:BQ:2681:U:OP2	51:AG:51:ARG:NE	2.46	0.48
58:BH:90:MET:HE1	58:BH:114:HIS:NE2	2.28	0.48
77:AP:17:CYS:HG	77:AP:77:CYS:HG	1.61	0.48
2:A:123:VAL:HG12	2:A:134:CYS:SG	2.53	0.48
16:P:107:PHE:N	16:P:135:GLU:OE1	2.46	0.48
21:U:9:LEU:HD23	21:U:10:SER:N	2.29	0.48
21:U:14:THR:HG22	21:U:17:GLU:OE2	2.13	0.48
33:2:1382:A:O2'	33:2:1383:G:OP1	2.27	0.48
41:BQ:2007:G:H1	41:BQ:2014:U:H3	1.60	0.48
41:BQ:2609:A:N3	54:AQ:87:GLN:NE2	2.61	0.48
50:BD:42:THR:OG1	50:BD:43:VAL:N	2.46	0.48
56:AX:10:ASN:O	56:AX:14:SER:OG	2.21	0.48
67:AY:74:ASN:HD21	67:AY:86:ARG:HD3	1.77	0.48
75:AO:96:CYS:HA	75:AO:121:LEU:CD2	2.43	0.48
15:O:214:ALA:HB1	15:O:240:VAL:CG2	2.43	0.48
20:T:189:HIS:O	20:T:193:LEU:HD23	2.14	0.48
33:2:76:A:C2'	33:2:80:A:H62	2.27	0.48
36:c:114:LYS:HB3	36:c:117:ILE:HD11	1.95	0.48
42:BR:28:C:OP1	51:AG:137:ARG:NH1	2.41	0.48
1:B:113:ILE:O	1:B:117:THR:HG23	2.14	0.48
14:N:119:ARG:O	14:N:132:LEU:HD12	2.13	0.48
14:N:141:CYS:SG	14:N:144:CYS:N	2.84	0.48
20:T:52:ILE:HA	20:T:111:LEU:HD23	1.94	0.48
25:Y:88:LEU:HD22	25:Y:129:TYR:HD2	1.79	0.48
33:2:279:G:C8	61:AE:111:ALA:HB1	2.48	0.48
41:BQ:1322:U:O2	58:BH:108:GLN:NE2	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:BQ:1988:C:H2'	41:BQ:1989:U:H1'	1.96	0.48
41:BQ:2040:U:H2'	41:BQ:2041:U:C6	2.49	0.48
22:V:67:TRP:NE1	22:V:185:GLU:OE2	2.43	0.48
50:BD:29:SER:OG	50:BD:31:ILE:O	2.25	0.48
55:AU:126[A]:VAL:O	58:BH:154:HIS:NE2	2.45	0.48
17:Q:127:VAL:HG13	17:Q:176:VAL:HG11	1.95	0.48
23:W:134:ILE:H	23:W:159:ALA:HB2	1.77	0.48
25:Y:48:SER:OG	33:2:960:U:O2	2.32	0.48
25:Y:60:VAL:HG13	25:Y:66:ILE:CD1	2.44	0.48
33:2:54:C:O2'	33:2:459:G:N7	2.37	0.48
41:BQ:610:G:C8	45:BE:312:VAL:HG21	2.48	0.48
41:BQ:1724:U:OP1	57:BF:128:LYS:NZ	2.41	0.48
45:BE:132:ALA:HB2	45:BE:148:ILE:HD11	1.95	0.48
45:BE:330:TYR:HA	45:BE:333:VAL:HG22	1.95	0.48
62:AH:115:ARG:HD3	62:AH:119:THR:HG23	1.95	0.48
17:Q:184:LEU:O	17:Q:188:LEU:HD23	2.14	0.48
19:S:22:LYS:NZ	33:2:757:A:O3'	2.45	0.48
20:T:223:LYS:O	20:T:226:ILE:O	2.32	0.48
21:U:107:ARG:NE	33:2:741:C:O2	2.46	0.48
25:Y:11:ILE:HG23	25:Y:11:ILE:O	2.14	0.48
27:AA:214:LEU:O	27:AA:217:THR:OG1	2.24	0.48
33:2:190:C:N4	33:2:191:C:O2	2.47	0.48
41:BQ:217:U:O2	63:AK:103:LYS:NZ	2.29	0.48
41:BQ:3113:A:OP1	49:AD:73:SER:OG	2.21	0.48
44:AW:108:PRO:O	44:AW:111:THR:OG1	2.27	0.48
27:AA:112:GLU:O	27:AA:116:VAL:HG22	2.14	0.47
33:2:656:G:O6	33:2:679:U:C2	2.66	0.47
41:BQ:1477:A:OP1	41:BQ:3075:G:O2'	2.28	0.47
58:BH:151:PRO:O	58:BH:152:LEU:HD23	2.14	0.47
2:A:208:ILE:HD12	7:G:16:LEU:HD21	1.95	0.47
12:L:31:GLU:OE2	12:L:38:ARG:N	2.47	0.47
30:BB:177:GLY:O	30:BB:186:VAL:N	2.46	0.47
41:BQ:114:A:N1	41:BQ:266:A:O2'	2.44	0.47
17:Q:61:LEU:HD21	17:Q:96:LEU:HD13	1.96	0.47
17:Q:134:VAL:C	17:Q:135:LEU:HD22	2.39	0.47
17:Q:137:ILE:HG13	17:Q:172:LEU:HD13	1.95	0.47
19:S:102:VAL:HG22	19:S:103:TYR:H	1.79	0.47
26:Z:71:CYS:HA	26:Z:74:VAL:HG12	1.96	0.47
33:2:478:A:N7	33:2:539:G:N2	2.62	0.47
41:BQ:444:U:C4	41:BQ:491:A:C6	3.02	0.47
3:C:3:MET:HE3	3:C:41:TYR:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:43:ARG:NH2	4:D:102:GLY:O	2.44	0.47
8:H:20:THR:OG1	8:H:35:ILE:HD12	2.15	0.47
8:H:100:THR:C	8:H:101:LEU:HD22	2.39	0.47
41:BQ:98:G:N7	52:AJ:13:HIS:NE2	2.61	0.47
41:BQ:2756:C:O2	59:BJ:8:ARG:NH2	2.47	0.47
43:BS:85:G:HO2'	43:BS:86:U:C5'	2.26	0.47
1:B:205:SER:O	1:B:206:SER:OG	2.26	0.47
19:S:72:VAL:CG2	19:S:90:ILE:HD13	2.45	0.47
28:BA:221:THR:HG21	28:BA:275:ARG:HG3	1.97	0.47
33:2:532:U:O2	37:d:34:ASN:ND2	2.45	0.47
41:BQ:439:C:O2'	41:BQ:494:G:N3	2.47	0.47
41:BQ:1307:G:O2'	41:BQ:1308:A:OP2	2.24	0.47
42:BR:121:U:O5'	46:BI:259:LYS:NZ	2.42	0.47
50:BD:145:LYS:O	50:BD:148:VAL:HG12	2.15	0.47
7:G:7:LYS:NZ	33:2:1316:G:OP2	2.39	0.47
21:U:103:SER:OG	21:U:104:ARG:N	2.46	0.47
29:AB:117:PRO:HA	29:AB:135:VAL:HG13	1.96	0.47
30:BB:54:LEU:HD13	30:BB:58:ASN:O	2.15	0.47
33:2:937:C:N4	38:e:14:GLY:O	2.43	0.47
33:2:1584:G:O2'	33:2:1610:G:N1	2.47	0.47
41:BQ:3355:U:O2'	41:BQ:3356:G:O3'	2.32	0.47
12:L:31:GLU:OE2	12:L:37:SER:N	2.47	0.47
15:O:234:LEU:HD21	15:O:263:PHE:CZ	2.50	0.47
20:T:157:VAL:HG11	33:2:78:A:H5''	1.95	0.47
20:T:171:LYS:NZ	33:2:68:A:OP1	2.27	0.47
20:T:216:LEU:HD21	33:2:241:U:H5'	1.97	0.47
23:W:85:VAL:HG12	23:W:99:LEU:HD13	1.97	0.47
28:BA:14:LEU:HA	28:BA:17:LEU:HD13	1.95	0.47
33:2:612:U:OP1	36:c:7:ARG:NH2	2.44	0.47
34:a:64:GLU:OE1	34:a:64:GLU:N	2.48	0.47
41:BQ:872:U:O2'	41:BQ:1908:A:OP1	2.31	0.47
41:BQ:1606:U:O4	70:BN:9:ARG:NE	2.39	0.47
41:BQ:1980:C:H3'	41:BQ:1981:G:H5''	1.97	0.47
41:BQ:2038:C:H2'	41:BQ:2039:C:C6	2.49	0.47
47:BM:71:VAL:HG11	47:BM:159:LEU:HB2	1.96	0.47
68:BG:100:ILE:O	68:BG:105:ARG:NE	2.44	0.47
73:AI:2:ALA:N	73:AI:51:LEU:O	2.47	0.47
17:Q:137:ILE:HD11	17:Q:172:LEU:HB3	1.97	0.47
18:R:38:VAL:O	18:R:39:THR:OG1	2.27	0.47
28:BA:108:GLU:OE1	28:BA:109:HIS:NE2	2.48	0.47
33:2:653:C:C4	33:2:681:U:C4	3.02	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:BQ:1590:G:OP1	70:BN:17:SER:OG	2.32	0.47
41:BQ:2033:G:N7	41:BQ:2035:G:C5	2.83	0.47
50:BD:180:GLU:OE2	50:BD:184:LYS:NZ	2.46	0.47
53:AM:55:ARG:NH2	53:AM:76:ALA:O	2.47	0.47
1:B:23:VAL:HG13	6:F:57:LEU:HD12	1.96	0.47
18:R:59:HIS:NE2	18:R:237:VAL:O	2.48	0.47
33:2:653:C:C4	33:2:681:U:N3	2.83	0.47
35:b:114:GLU:OE1	35:b:114:GLU:N	2.45	0.47
41:BQ:113:C:OP1	54:AQ:147:ARG:NE	2.37	0.47
41:BQ:2668:U:O4	41:BQ:2687:G:N2	2.48	0.47
60:BL:89:LEU:HB3	60:BL:93:ILE:HD12	1.97	0.47
67:AY:25:LEU:HD23	67:AY:90:VAL:HG23	1.95	0.47
73:AI:17:ARG:NH2	73:AI:19:ASP:OD2	2.47	0.47
2:A:55:THR:O	2:A:59:LEU:HD23	2.15	0.47
9:I:64:HIS:NE2	33:2:1523:G:N7	2.62	0.47
20:T:142:ARG:NH1	20:T:149:LYS:O	2.47	0.47
22:V:56:ARG:O	22:V:58:LEU:HD12	2.15	0.47
26:Z:82:LYS:NZ	26:Z:116:GLU:OE1	2.48	0.47
31:AC:53:TYR:O	31:AC:57:LEU:HD23	2.15	0.47
33:2:56:U:OP1	33:2:403:G:N1	2.45	0.47
33:2:1181:U:O2	33:2:1458:G:C2	2.68	0.47
33:2:1216:C:O2'	33:2:1217:A:O5'	2.25	0.47
33:2:1399:C:HO2'	33:2:1400:A:P	2.37	0.47
41:BQ:2147:A:OP2	44:AW:200:ARG:NH1	2.48	0.47
53:AM:13:ARG:NH1	53:AM:65:LEU:O	2.46	0.47
54:AQ:48:ALA:HB1	54:AQ:53:TYR:HB3	1.97	0.47
55:AU:44[A]:SER:HB3	55:AU:129[A]:LEU:HD21	1.97	0.47
1:B:90:ILE:O	1:B:94:THR:HG23	2.15	0.46
6:F:97:VAL:HG12	6:F:98:ASP:H	1.81	0.46
7:G:27:ASP:HB3	7:G:30:THR:HG22	1.96	0.46
23:W:172:VAL:HG13	33:2:511:A:H5''	1.97	0.46
32:BC:8:VAL:HG22	32:BC:9:THR:H	1.80	0.46
33:2:555:A:O2'	33:2:556:A:O5'	2.28	0.46
36:c:130:VAL:HG21	36:c:143:PRO:CD	2.45	0.46
41:BQ:154:U:OP2	71:BP:103:LYS:NZ	2.32	0.46
41:BQ:2712:U:O2'	41:BQ:2743:A:O2'	2.08	0.46
56:AX:31:GLU:OE2	56:AX:61:ARG:N	2.43	0.46
1:B:109:LYS:HZ1	33:2:1474:G:P	2.36	0.46
8:H:107:SER:OG	8:H:108:LYS:N	2.49	0.46
12:L:55:VAL:C	12:L:56:LEU:HD22	2.40	0.46
20:T:223:LYS:O	20:T:226:ILE:C	2.58	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2:647:G:H22	33:2:687:G:H22	1.62	0.46
41:BQ:1403:C:OP1	68:BG:11:LYS:NZ	2.37	0.46
45:BE:162:THR:HA	45:BE:218:ALA:HB1	1.98	0.46
51:AG:173:ASP:OD1	51:AG:174:LYS:N	2.48	0.46
10:J:96:PRO:O	10:J:100:VAL:HG23	2.15	0.46
19:S:154:ILE:HD11	19:S:172:PHE:HB3	1.98	0.46
26:Z:125:SER:OG	26:Z:126:THR:N	2.46	0.46
33:2:1596:C:O2'	33:2:1598:U:OP2	2.15	0.46
41:BQ:1385:C:OP1	45:BE:141:ARG:NH2	2.46	0.46
46:BI:59:ASP:OD1	46:BI:60:ILE:N	2.48	0.46
52:AJ:18:TRP:O	52:AJ:22:VAL:HG23	2.15	0.46
9:I:7:ARG:NH1	33:2:1366:U:O2'	2.46	0.46
12:L:21:SER:N	12:L:67:ARG:O	2.46	0.46
15:O:210:LEU:HD12	15:O:223:TRP:O	2.15	0.46
16:P:61:ALA:HA	16:P:64:ILE:HD12	1.96	0.46
19:S:49:ARG:NH2	33:2:447:U:O5'	2.49	0.46
26:Z:121:VAL:O	26:Z:121:VAL:HG13	2.15	0.46
26:Z:135:ARG:NH2	33:2:1007:C:O2'	2.48	0.46
33:2:78:A:O2'	33:2:79:C:O4'	2.32	0.46
39:f:55:THR:OG1	39:f:56:CYS:N	2.48	0.46
41:BQ:562:C:OP2	53:AM:77:ARG:NH1	2.47	0.46
43:BS:46:G:O2'	43:BS:61:A:N1	2.41	0.46
1:B:133:VAL:HG23	1:B:198:LEU:CD2	2.45	0.46
1:B:166:ARG:NH2	33:2:1164:G:OP1	2.49	0.46
6:F:64:ASP:OD1	6:F:64:ASP:N	2.49	0.46
8:H:141:THR:HG22	33:2:1173:C:OP2	2.16	0.46
16:P:139:VAL:O	16:P:139:VAL:HG12	2.15	0.46
18:R:45:VAL:HG11	18:R:68:ILE:HG23	1.98	0.46
19:S:221:ARG:NH2	33:2:753:A:O4'	2.48	0.46
22:V:3:ILE:O	22:V:30:GLY:N	2.47	0.46
28:BA:65:SER:OG	28:BA:66:LYS:N	2.48	0.46
33:2:815:G:OP2	57:BF:163:ARG:NH2	2.46	0.46
33:2:1795:U:OP2	38:e:4:LYS:NZ	2.27	0.46
41:BQ:2021:G:H2'	41:BQ:2021:G:N3	2.31	0.46
14:N:121:CYS:HB2	14:N:132:LEU:HD21	1.97	0.46
30:BB:11:LYS:NZ	41:BQ:1104:G:OP1	2.44	0.46
41:BQ:242:C:O2'	41:BQ:243:G:N7	2.49	0.46
41:BQ:1219:C:N4	41:BQ:1287:A:N6	2.63	0.46
41:BQ:1523:U:OP2	41:BQ:1604:G:O2'	2.30	0.46
41:BQ:2093:A:N6	57:BF:114:LYS:HE2	2.30	0.46
46:BI:50:ARG:NH1	46:BI:147:ASP:OD2	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:AN:9:LYS:CB	64:AN:25:ILE:HD12	2.45	0.46
2:A:113:LEU:HD12	2:A:114:ALA:H	1.81	0.46
5:E:25:LEU:HB3	5:E:28:MET:HE3	1.97	0.46
10:J:33:GLN:OE1	10:J:33:GLN:N	2.47	0.46
12:L:12:VAL:HA	12:L:30:VAL:HG22	1.97	0.46
16:P:120:LEU:HD23	16:P:121:VAL:N	2.31	0.46
17:Q:98:THR:OG1	17:Q:99:ASN:N	2.49	0.46
23:W:119:ALA:HB1	23:W:121:SER:O	2.16	0.46
41:BQ:371:G:N1	41:BQ:374:A:OP2	2.44	0.46
41:BQ:2854:U:OP2	50:BD:3:ARG:NH2	2.49	0.46
19:S:18:TRP:NE1	19:S:41:SER:O	2.48	0.46
21:U:14:THR:OG1	21:U:15:GLU:OE2	2.31	0.46
23:W:40:LYS:N	33:2:593:U:OP1	2.47	0.46
33:2:235:G:O2'	33:2:236:A:O5'	2.27	0.46
33:2:548:G:N1	33:2:591:A:C6	2.84	0.46
33:2:1186:U:C4	33:2:1208:A:N6	2.84	0.46
40:g:41:THR:HA	40:g:45:VAL:HG12	1.98	0.46
41:BQ:712:G:OP1	52:AJ:174:ARG:NH1	2.48	0.46
41:BQ:1952:G:C5	41:BQ:2095:G:C6	3.03	0.46
41:BQ:2538:U:O2'	41:BQ:2541:U:N3	2.49	0.46
44:AW:101:VAL:O	44:AW:101:VAL:HG12	2.16	0.46
63:AK:109:LEU:HD22	63:AK:115:ARG:HH21	1.80	0.46
8:H:19:ASN:ND2	51:AG:111:ASP:OD1	2.45	0.46
15:O:12:THR:C	15:O:13:LEU:HD22	2.41	0.46
21:U:93:LEU:HD23	21:U:94:ALA:N	2.30	0.46
22:V:47:ARG:NH2	33:2:398:G:OP2	2.46	0.46
23:W:119:ALA:O	23:W:124:HIS:ND1	2.49	0.46
33:2:1692:G:N1	33:2:1710:U:C2	2.84	0.46
42:BR:38:U:O2'	42:BR:42:A:N6	2.48	0.46
46:BI:95:TRP:HZ3	46:BI:199:ILE:HD13	1.80	0.46
49:AD:31:ARG:NH2	49:AD:83:THR:O	2.48	0.46
3:C:42:VAL:O	3:C:46:LEU:HD23	2.16	0.46
7:G:22:PRO:O	15:O:216:LYS:NZ	2.40	0.46
16:P:66:ALA:HB2	34:a:37:ALA:HB2	1.98	0.46
17:Q:127:VAL:HG11	17:Q:176:VAL:HG11	1.98	0.46
19:S:131:LEU:HD11	19:S:135:GLY:HA2	1.98	0.46
30:BB:125:ASP:OD1	30:BB:126:GLN:N	2.48	0.46
30:BB:133:LYS:NZ	45:BE:298:ALA:O	2.44	0.46
33:2:1630:U:O2'	33:2:1764:C:O2'	2.12	0.46
41:BQ:1147:G:OP1	68:BG:47:ARG:NH1	2.48	0.46
41:BQ:1760:A:H5'	79:x:69:LYS:HD3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:BQ:1795:U:OP2	44:AW:50:HIS:NE2	2.45	0.46
41:BQ:1987:G:P	41:BQ:1988:C:H5''	2.56	0.46
42:BR:40:C:O2	51:AG:72:ARG:NE	2.47	0.46
70:BN:42:PRO:HG2	70:BN:54:ILE:HG21	1.98	0.46
6:F:31:VAL:N	6:F:34:SER:O	2.44	0.45
18:R:204:THR:OG1	33:2:5:U:OP2	2.10	0.45
23:W:36:LEU:HD21	23:W:108:ARG:NH1	2.31	0.45
23:W:44:ARG:NH1	33:2:473:A:OP1	2.45	0.45
28:BA:29:VAL:CG2	28:BA:337:THR:HG21	2.46	0.45
37:d:53:ASP:O	37:d:96:LEU:HD21	2.15	0.45
38:e:13:LYS:O	38:e:15:ARG:NH1	2.47	0.45
41:BQ:519:A:OP1	58:BH:62:ASN:ND2	2.44	0.45
41:BQ:1963:G:H2'	41:BQ:1964:C:H4'	1.97	0.45
41:BQ:2087:C:H2'	41:BQ:2088:A:H2'	1.97	0.45
41:BQ:2785:A:O2'	77:AP:41:ARG:NH2	2.50	0.45
44:AW:35:ALA:O	44:AW:39:GLY:N	2.47	0.45
58:BH:27:MET:HE1	58:BH:44:PHE:CD2	2.51	0.45
2:A:181:VAL:HG23	33:2:1437:U:O2'	2.16	0.45
3:C:45:ALA:O	3:C:49:LEU:HD23	2.16	0.45
8:H:24:GLY:O	8:H:25:ASN:ND2	2.49	0.45
15:O:105:GLY:O	15:O:107:LYS:NZ	2.49	0.45
27:AA:106:LYS:O	27:AA:110:THR:HG23	2.15	0.45
41:BQ:776:U:C4	41:BQ:2738:A:N1	2.84	0.45
41:BQ:1219:C:O2'	41:BQ:1286:A:N1	2.49	0.45
41:BQ:1729:A:N6	78:AT:42:CYS:HA	2.30	0.45
41:BQ:2036:U:H2'	41:BQ:2037:G:H8	1.81	0.45
43:BS:95:G:OP2	72:AF:72:ARG:NH1	2.48	0.45
45:BE:11:LEU:CD2	45:BE:156:LEU:HD12	2.45	0.45
58:BH:9:VAL:HG22	58:BH:61:ILE:HG13	1.98	0.45
20:T:119:GLN:OE1	20:T:119:GLN:N	2.43	0.45
21:U:150:GLN:HB3	21:U:181:ILE:HG22	1.98	0.45
33:2:934:C:N4	33:2:1077:C:O3'	2.50	0.45
41:BQ:1158:A:OP2	48:BO:90:LYS:NZ	2.24	0.45
41:BQ:1977:C:H5'	73:AI:60:GLY:HA2	1.99	0.45
41:BQ:2494:A:O2'	80:BT:163:LEU:CB	2.65	0.45
64:AN:52:LYS:O	64:AN:65:ARG:NH2	2.46	0.45
6:F:44:LEU:HD12	6:F:78:VAL:HG11	1.99	0.45
16:P:76:ILE:CD1	16:P:98:ILE:HD13	2.46	0.45
19:S:129:VAL:HG12	19:S:139:VAL:CG1	2.47	0.45
19:S:173:ILE:HD11	19:S:235:TYR:CZ	2.52	0.45
22:V:175:GLN:NE2	33:2:332:U:OP2	2.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:AA:126:SER:OG	41:BQ:120:G:N2	2.49	0.45
33:2:515:A:N6	33:2:537:G:O2'	2.46	0.45
33:2:518:A:N6	33:2:533:U:O4	2.50	0.45
44:AW:126:LEU:HD12	44:AW:150:LEU:CD2	2.47	0.45
45:BE:6:VAL:O	45:BE:20:LEU:N	2.47	0.45
51:AG:41:SER:OG	51:AG:43:GLN:O	2.33	0.45
68:BG:89:THR:HG22	68:BG:117:ILE:HG12	1.97	0.45
7:G:24:LEU:HD12	7:G:58:MET:HE2	1.98	0.45
20:T:139:ASN:ND2	33:2:142:G:OP1	2.50	0.45
28:BA:113:GLU:HB2	28:BA:176:ALA:HB2	1.98	0.45
28:BA:250:ALA:HB1	41:BQ:2947:G:C2	2.52	0.45
33:2:222:A:N1	33:2:839:U:C4	2.85	0.45
39:f:30:SER:OG	39:f:31:TYR:N	2.50	0.45
41:BQ:597:G:OP2	48:BO:37:ASN:ND2	2.44	0.45
41:BQ:1136:A:O4'	41:BQ:2636:A:N6	2.49	0.45
41:BQ:2494:A:H4'	80:BT:37:GLY:HA2	1.92	0.45
65:AR:79:TRP:CE3	65:AR:82:ILE:HD12	2.51	0.45
1:B:143:ARG:NH2	1:B:218:GLU:OE1	2.49	0.45
31:AC:26:ILE:CG1	41:BQ:155:G:H21	2.29	0.45
33:2:127:G:H21	33:2:178:U:H1'	1.82	0.45
33:2:518:A:C6	33:2:533:U:C4	3.04	0.45
33:2:530:C:O2	37:d:61:ARG:NH2	2.50	0.45
41:BQ:1488:G:H21	70:BN:12:PRO:HG3	1.81	0.45
41:BQ:1729:A:H8	41:BQ:1729:A:OP1	1.99	0.45
41:BQ:2034:C:N4	41:BQ:2035:G:N3	2.64	0.45
41:BQ:3275:U:O2'	41:BQ:3276:G:OP1	2.29	0.45
4:D:126:TRP:CD1	4:D:133:LEU:HD21	2.52	0.45
21:U:74:GLN:O	21:U:78:THR:HG23	2.16	0.45
41:BQ:1114:U:OP1	65:AR:23:GLY:N	2.43	0.45
41:BQ:1620:U:O2'	41:BQ:1825:G:N2	2.45	0.45
50:BD:74:LYS:O	50:BD:78:THR:OG1	2.12	0.45
5:E:29:SER:OG	5:E:32:ASP:OD2	2.32	0.45
8:H:36:LYS:NZ	33:2:1567:U:O3'	2.33	0.45
12:L:58:GLU:OE1	12:L:60:GLU:N	2.50	0.45
13:M:30:LEU:N	13:M:30:LEU:CD2	2.80	0.45
18:R:111:VAL:HG11	18:R:191:ALA:HB2	1.99	0.45
21:U:166:LEU:HD12	21:U:183:PHE:CG	2.52	0.45
33:2:232:U:C2	33:2:234:G:C6	3.04	0.45
37:d:6:THR:HG21	37:d:28:LEU:HD12	1.97	0.45
41:BQ:118:U:N3	41:BQ:122:A:OP2	2.47	0.45
41:BQ:1015:U:O2'	41:BQ:1017:C:OP2	2.35	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:BQ:2285:C:OP2	41:BQ:2286:U:O2'	2.29	0.45
59:BJ:17:ARG:NH2	59:BJ:24:ALA:O	2.49	0.45
5:E:32:ASP:OD1	5:E:33:PHE:N	2.50	0.45
6:F:99:GLU:OE1	6:F:103:ASN:ND2	2.48	0.45
28:BA:74:GLU:OE1	28:BA:325:LYS:NZ	2.44	0.45
33:2:129:U:O4'	33:2:264:G:N1	2.50	0.45
33:2:651:G:C2	33:2:684:A:C2	3.04	0.45
33:2:1274:C:O2'	33:2:1275:A:OP2	2.27	0.45
41:BQ:1677:G:N7	60:BL:74:LYS:NZ	2.63	0.45
45:BE:6:VAL:N	45:BE:20:LEU:O	2.50	0.45
52:AJ:43:ALA:HB2	52:AJ:51:LEU:HD13	1.99	0.45
10:J:72:ASN:ND2	33:2:1429:G:N3	2.65	0.45
27:AA:26:LEU:O	27:AA:28:HIS:ND1	2.50	0.45
33:2:1273:G:H4'	33:2:1274:C:H3'	1.98	0.45
41:BQ:2445:A:O2'	41:BQ:2446:U:OP1	2.34	0.45
42:BR:37:G:N2	42:BR:41:G:N3	2.65	0.45
44:AW:142:ASP:OD1	44:AW:142:ASP:N	2.50	0.45
73:AI:25:VAL:HG12	73:AI:43:PHE:CD2	2.52	0.45
5:E:20:VAL:CG2	5:E:28:MET:HE1	2.45	0.44
6:F:51:PRO:O	6:F:55:VAL:HG22	2.16	0.44
6:F:60:PHE:HA	6:F:63:ILE:HD13	1.98	0.44
10:J:106:ILE:O	10:J:107:THR:OG1	2.29	0.44
19:S:161:LYS:O	19:S:170:THR:N	2.46	0.44
20:T:31:ARG:NH1	33:2:1682:U:OP1	2.45	0.44
33:2:151:G:N1	33:2:164:A:C6	2.85	0.44
33:2:928:U:O2'	33:2:945:U:OP2	2.34	0.44
41:BQ:270:U:O2'	41:BQ:318:A:N3	2.45	0.44
41:BQ:441:U:OP2	41:BQ:490:C:N4	2.50	0.44
41:BQ:1951:C:O2	41:BQ:1951:C:H2'	2.16	0.44
41:BQ:1985:G:H2'	41:BQ:1986:U:H4'	1.98	0.44
41:BQ:3158:G:C6	41:BQ:3292:A:N1	2.85	0.44
48:BO:130:ILE:O	48:BO:134:VAL:HG22	2.16	0.44
54:AQ:165:THR:OG1	54:AQ:166:ALA:N	2.50	0.44
18:R:53:ILE:H	18:R:53:ILE:HD12	1.83	0.44
19:S:201:HIS:NE2	33:2:799:A:O2'	2.49	0.44
20:T:78:THR:HG22	20:T:79:LYS:H	1.81	0.44
33:2:811:A:H2	33:2:814:A:H62	1.65	0.44
41:BQ:212:G:OP2	63:AK:2:ALA:N	2.50	0.44
41:BQ:1814:A:N3	41:BQ:1815:U:N3	2.65	0.44
41:BQ:1965:C:N4	41:BQ:2059:U:O2	2.50	0.44
41:BQ:2494:A:H1'	80:BT:164:CYS:CA	2.46	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:BQ:2516:U:O2	41:BQ:2594:C:N4	2.50	0.44
47:BM:37:GLY:N	47:BM:54:TYR:O	2.49	0.44
59:BJ:42:ILE:O	59:BJ:59:GLY:N	2.47	0.44
62:AH:82:LEU:HD11	62:AH:135:ILE:CD1	2.47	0.44
4:D:27:ALA:HB3	4:D:136:ILE:HG23	2.00	0.44
17:Q:59:ASP:OD1	17:Q:60:ALA:N	2.50	0.44
21:U:126:LEU:HD21	21:U:181:ILE:HD13	1.98	0.44
23:W:86:LEU:HD23	23:W:87:SER:N	2.33	0.44
32:BC:42:LEU:HD23	32:BC:43:HIS:N	2.31	0.44
33:2:612:U:OP2	33:2:613:G:O2'	2.34	0.44
41:BQ:2206:G:N3	41:BQ:2207:A:N6	2.65	0.44
41:BQ:2621:G:O6	50:BD:113:GLN:NE2	2.49	0.44
45:BE:11:LEU:HD21	45:BE:156:LEU:HD12	1.97	0.44
47:BM:72:ASN:OD1	47:BM:73:GLY:N	2.49	0.44
52:AJ:161:ASP:OD1	65:AR:139:ARG:NH1	2.49	0.44
54:AQ:17:ASP:OD1	54:AQ:18:VAL:N	2.51	0.44
6:F:29:ILE:O	6:F:30:LYS:NZ	2.34	0.44
13:M:41:GLN:NE2	33:2:1433:G:O4'	2.51	0.44
24:X:90:TYR:OH	33:2:307:G:OP1	2.31	0.44
28:BA:256:HIS:ND1	41:BQ:2941:A:OP2	2.45	0.44
33:2:1521:G:O2'	33:2:1523:G:OP2	2.35	0.44
41:BQ:209:A:N3	45:BE:221:ASN:ND2	2.65	0.44
41:BQ:1243:G:N2	41:BQ:1270:A:O2'	2.49	0.44
41:BQ:2092:A:N7	41:BQ:2093:A:H1'	2.32	0.44
44:AW:7:ASN:OD1	44:AW:8:GLN:N	2.50	0.44
10:J:28:SER:OG	10:J:29:THR:N	2.51	0.44
33:2:653:C:N4	33:2:681:U:N3	2.66	0.44
33:2:1430:U:HO2'	33:2:1431:C:P	2.34	0.44
38:e:42:ARG:O	38:e:67:THR:HG22	2.17	0.44
41:BQ:1312:C:O2'	55:AU:83[A]:ALA:O	2.35	0.44
41:BQ:1564:U:N3	41:BQ:1576:G:N1	2.65	0.44
41:BQ:1621:A:H62	41:BQ:1820:U:H3	1.65	0.44
41:BQ:1973:G:C1'	41:BQ:2049:A:N6	2.80	0.44
49:AD:90:MET:HE3	49:AD:181:VAL:HB	1.98	0.44
50:BD:138:VAL:HG21	50:BD:148:VAL:CG2	2.43	0.44
52:AJ:170:LEU:HD21	65:AR:147:LEU:HD13	2.00	0.44
53:AM:88:ALA:O	53:AM:93:LYS:NZ	2.33	0.44
55:AU:157[A]:GLU:OE1	55:AU:160[A]:ARG:NH2	2.44	0.44
79:x:223:TYR:CZ	79:x:226:GLY:CA	2.99	0.44
1:B:192:GLU:OE1	11:K:59:TYR:OH	2.33	0.44
15:O:144:LEU:HD23	15:O:181:TRP:CG	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:79:ARG:NH1	16:P:125:ASP:OD2	2.50	0.44
16:P:90:ALA:HA	16:P:95:ALA:HB3	1.98	0.44
17:Q:201:THR:OG1	17:Q:207:LEU:HD23	2.18	0.44
19:S:91:THR:HG23	19:S:98:ASN:ND2	2.33	0.44
22:V:47:ARG:NH2	33:2:396:G:N7	2.65	0.44
24:X:53:TYR:C	24:X:54:ILE:HD13	2.43	0.44
26:Z:58:TYR:O	26:Z:62:LEU:HD13	2.18	0.44
28:BA:361:THR:N	28:BA:371:GLN:OE1	2.46	0.44
33:2:136:C:N4	33:2:137:U:O4	2.51	0.44
33:2:139:C:N3	33:2:176:C:N4	2.65	0.44
41:BQ:412:G:N2	56:AX:118:GLN:OE1	2.43	0.44
41:BQ:1253:U:N3	41:BQ:1264:G:OP1	2.46	0.44
41:BQ:1729:A:OP1	41:BQ:1729:A:C8	2.70	0.44
41:BQ:2523:A:OP1	62:AH:31:THR:HG22	2.17	0.44
15:O:207:ASP:HB2	15:O:209:THR:HG22	2.00	0.44
18:R:246:GLU:OE1	18:R:246:GLU:N	2.51	0.44
19:S:122:LYS:HD2	19:S:164:LEU:HD11	2.00	0.44
21:U:118:LEU:HD21	33:2:640:U:C4	2.53	0.44
26:Z:18:ARG:NH1	33:2:918:U:O3'	2.50	0.44
28:BA:252:ILE:O	28:BA:264:VAL:HG21	2.17	0.44
33:2:623:A:H3'	33:2:624:G:H5''	2.00	0.44
33:2:883:C:C4	33:2:945:U:O4	2.71	0.44
33:2:992:A:O2'	33:2:1785:U:O2	2.23	0.44
33:2:1480:G:OP2	33:2:1481:C:N4	2.50	0.44
39:f:55:THR:OG1	39:f:61:THR:OG1	2.12	0.44
41:BQ:945:C:O2'	41:BQ:1406:A:N3	2.47	0.44
41:BQ:1473:G:O3'	57:BF:23:TRP:NE1	2.45	0.44
41:BQ:1560:G:N1	41:BQ:1561:G:C6	2.86	0.44
43:BS:97:A:O2'	71:BP:59:ASN:OD1	2.35	0.44
59:BJ:75:ILE:HD11	59:BJ:88:ARG:CZ	2.47	0.44
61:AE:9:SER:HA	61:AE:52:THR:HG23	1.98	0.44
64:AN:89:VAL:HG12	64:AN:93:LYS:HB3	1.99	0.44
68:BG:106:VAL:HA	68:BG:109:LEU:HD12	2.00	0.44
13:M:16:LYS:O	13:M:27:HIS:ND1	2.49	0.44
23:W:65:LYS:HA	23:W:70:LEU:HD11	2.00	0.44
23:W:89:ASP:OD1	23:W:89:ASP:N	2.48	0.44
24:X:125:VAL:HG12	24:X:139:VAL:HG12	1.98	0.44
33:2:540:G:C2	33:2:542:A:C5	3.06	0.44
33:2:640:U:O2'	33:2:641:G:OP1	2.34	0.44
33:2:1218:G:H5''	33:2:1444:A:H61	1.83	0.44
33:2:1523:G:N2	33:2:1523:G:OP2	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:BQ:1446:A:O2'	41:BQ:1447:G:OP2	2.32	0.44
41:BQ:1985:G:C5	41:BQ:1986:U:H1'	2.52	0.44
72:AF:21:ARG:HD2	72:AF:37:CYS:SG	2.58	0.44
1:B:160:VAL:HG12	12:L:43:ASN:ND2	2.33	0.44
8:H:29:VAL:O	8:H:33:THR:HG23	2.18	0.44
8:H:76:PRO:O	8:H:79:TYR:N	2.47	0.44
17:Q:180:THR:HG22	17:Q:183:GLN:OE1	2.17	0.44
19:S:193:GLY:O	19:S:210:ILE:HG23	2.18	0.44
41:BQ:798:G:OP1	65:AR:33:GLY:N	2.51	0.44
41:BQ:2819:A:N6	41:BQ:2870:C:O2	2.50	0.44
41:BQ:3310:A:OP1	56:AX:71:ALA:HB2	2.18	0.44
59:BJ:80:VAL:CG2	59:BJ:85:LEU:HD12	2.47	0.44
1:B:180:ARG:NH2	33:2:1473:U:O4	2.51	0.43
3:C:35:ILE:HG22	3:C:37:THR:HG22	2.00	0.43
10:J:65:ILE:HG21	13:M:43:PHE:CE2	2.53	0.43
33:2:372:G:HO2'	33:2:611:U:H3	1.65	0.43
41:BQ:494:G:H1	41:BQ:619:A:H61	1.66	0.43
41:BQ:818:C:N3	41:BQ:920:A:H5'	2.33	0.43
41:BQ:1983:G:C2'	41:BQ:1984:C:H5'	2.48	0.43
44:AW:77:ILE:HG21	44:AW:169:ILE:HD12	2.00	0.43
56:AX:120:ASN:OD1	56:AX:120:ASN:N	2.51	0.43
68:BG:95:GLU:OE1	68:BG:120:THR:OG1	2.16	0.43
17:Q:136:ARG:NH1	33:2:885:G:OP1	2.50	0.43
33:2:1179:G:N2	33:2:1460:A:H62	2.11	0.43
41:BQ:808:A:HO2'	41:BQ:2412:G:HO2'	1.66	0.43
41:BQ:1223:A:OP2	41:BQ:1285:G:N2	2.50	0.43
41:BQ:1564:U:N3	41:BQ:1576:G:C6	2.87	0.43
41:BQ:1751:G:O6	73:AI:44:LYS:NZ	2.49	0.43
41:BQ:3152:U:OP2	41:BQ:3395:G:N2	2.40	0.43
48:BO:147:LEU:O	48:BO:151:ARG:N	2.45	0.43
51:AG:110:ILE:H	51:AG:110:ILE:HD12	1.83	0.43
1:B:136:ALA:HB1	1:B:201:ALA:HB3	2.00	0.43
3:C:40:LEU:HD11	33:2:1217:A:C4	2.53	0.43
7:G:21:TYR:CE1	7:G:58:MET:HE1	2.53	0.43
20:T:164:LYS:NZ	33:2:71:A:N7	2.47	0.43
20:T:171:LYS:HZ1	33:2:67:A:P	2.41	0.43
33:2:655:G:O2'	33:2:677:G:O6	2.31	0.43
33:2:748:U:C2	33:2:802:G:N1	2.86	0.43
33:2:871:G:N2	39:f:68:GLY:O	2.48	0.43
33:2:1144:U:O2'	33:2:1301:U:O2'	2.33	0.43
33:2:1667:A:O2'	41:BQ:1935:G:O2'	2.36	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:BQ:1063:G:O2'	41:BQ:1097:G:N2	2.51	0.43
41:BQ:1219:C:N3	41:BQ:1287:A:C6	2.87	0.43
41:BQ:1348:U:H5''	41:BQ:1355:A:H61	1.83	0.43
68:BG:23:ASP:OD1	68:BG:23:ASP:N	2.50	0.43
2:A:55:THR:O	2:A:58:VAL:HG22	2.17	0.43
2:A:176:LEU:HG	2:A:181:VAL:HG22	1.99	0.43
14:N:87:THR:O	33:2:1445:G:N2	2.44	0.43
15:O:244:ALA:O	15:O:252:LEU:HD12	2.18	0.43
41:BQ:31:C:OP2	54:AQ:188:ARG:NH2	2.46	0.43
41:BQ:148:G:HO2'	41:BQ:149:U:P	2.39	0.43
41:BQ:338:A:OP1	45:BE:48:GLN:N	2.51	0.43
41:BQ:600:G:C2'	41:BQ:602:A:H62	2.31	0.43
49:AD:165:CYS:SG	49:AD:179:ILE:N	2.88	0.43
62:AH:129:ASP:OD1	62:AH:129:ASP:N	2.52	0.43
67:AY:10:ILE:HD13	67:AY:13:LYS:CE	2.48	0.43
70:BN:56:THR:O	70:BN:57:LEU:HD23	2.19	0.43
73:AI:61:LYS:HA	73:AI:64:LYS:NZ	2.31	0.43
16:P:63:ILE:O	16:P:66:ALA:HB3	2.18	0.43
33:2:487:G:O2'	33:2:488:G:O4'	2.35	0.43
41:BQ:1392:G:O2'	41:BQ:1417:G:N1	2.42	0.43
41:BQ:1973:G:N2	41:BQ:2048:G:H2'	2.34	0.43
41:BQ:2745:G:N2	41:BQ:2748:A:OP2	2.44	0.43
46:BI:80:SER:O	46:BI:92:LEU:HD22	2.18	0.43
51:AG:53:THR:HG22	51:AG:60:ARG:HA	2.00	0.43
52:AJ:109:PHE:O	52:AJ:113:VAL:HG23	2.17	0.43
56:AX:108:ASP:N	56:AX:152:GLU:OE2	2.47	0.43
62:AH:117:ASN:OD1	62:AH:119:THR:HG22	2.18	0.43
68:BG:119:VAL:HG12	68:BG:121:ASN:H	1.84	0.43
72:AF:17:THR:OG1	72:AF:18:LEU:N	2.50	0.43
79:x:113:GLY:HA2	79:x:184:ASN:O	2.18	0.43
5:E:14:THR:OG1	5:E:15:HIS:N	2.51	0.43
7:G:25:THR:HG23	7:G:27:ASP:H	1.84	0.43
12:L:36:THR:O	12:L:37:SER:OG	2.27	0.43
28:BA:250:ALA:HB1	41:BQ:2947:G:N3	2.33	0.43
28:BA:305:ILE:O	28:BA:361:THR:HG23	2.19	0.43
33:2:126:A:C6	33:2:292:U:C4	3.06	0.43
41:BQ:95:A:OP1	65:AR:52:TYR:OH	2.24	0.43
41:BQ:364:G:O6	72:AF:56:ARG:NE	2.46	0.43
41:BQ:1281:G:O6	41:BQ:1282:G:O6	2.37	0.43
41:BQ:2617:U:O3'	50:BD:116:ARG:NH2	2.44	0.43
56:AX:97:ASN:OD1	56:AX:101:ASN:ND2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:125:THR:O	1:B:127:GLN:N	2.51	0.43
5:E:37:ALA:HB1	5:E:38:PRO:HD2	2.00	0.43
6:F:6:SER:N	6:F:96:TYR:OH	2.52	0.43
18:R:80:VAL:HG12	18:R:102:VAL:CG1	2.49	0.43
19:S:91:THR:HG23	19:S:98:ASN:HD21	1.83	0.43
33:2:1387:G:H21	33:2:1410:A:H61	1.66	0.43
35:b:111:MET:HE3	35:b:116:ALA:HA	2.00	0.43
41:BQ:1447:G:OP2	56:AX:27:LYS:NZ	2.50	0.43
19:S:70:VAL:HG23	19:S:90:ILE:HD11	2.01	0.43
24:X:67:ARG:NH2	33:2:115:G:N7	2.67	0.43
25:Y:21:ASN:OD1	25:Y:21:ASN:N	2.52	0.43
29:AB:85:TRP:CE2	29:AB:93:LEU:HD21	2.53	0.43
33:2:224:C:O2'	33:2:226:A:N7	2.45	0.43
34:a:66:ASP:OD1	34:a:67:ASP:N	2.49	0.43
43:BS:39:G:O2'	43:BS:105:A:N1	2.51	0.43
46:BI:177:GLU:OE1	46:BI:177:GLU:N	2.45	0.43
52:AJ:57:VAL:HG23	52:AJ:115:ARG:HD2	2.01	0.43
6:F:22:VAL:HG22	6:F:65:ILE:HG12	2.00	0.43
6:F:89:LEU:HG	6:F:105:LEU:HD21	2.01	0.43
7:G:21:TYR:CD1	7:G:58:MET:HE1	2.54	0.43
21:U:31:SER:OG	21:U:34:LEU:HD11	2.19	0.43
27:AA:211:LEU:O	27:AA:215:VAL:HG13	2.18	0.43
33:2:92:A:P	33:2:398:G:H22	2.42	0.43
33:2:359:A:H62	36:c:35:GLY:HA3	1.84	0.43
33:2:610:G:O2'	33:2:613:G:O2'	2.12	0.43
33:2:1483:A:N3	33:2:1607:G:O2'	2.48	0.43
41:BQ:1572:U:O2'	41:BQ:1573:G:O5'	2.28	0.43
41:BQ:1598:G:OP2	70:BN:31:ARG:NH1	2.47	0.43
41:BQ:3232:G:O6	41:BQ:3255:U:C4	2.71	0.43
45:BE:299:ILE:HG22	45:BE:300:ARG:O	2.19	0.43
64:AN:9:LYS:NZ	64:AN:83:THR:O	2.46	0.43
4:D:103:LEU:HB2	4:D:115:VAL:HG22	2.01	0.43
21:U:28:GLU:OE2	21:U:39:ARG:N	2.52	0.43
33:2:227:U:O2	33:2:834:G:N2	2.51	0.43
33:2:1311:U:N3	33:2:1314:U:OP2	2.45	0.43
33:2:1700:C:O2'	33:2:1701:A:O5'	2.27	0.43
34:a:4:ASP:OD1	34:a:5:LYS:N	2.51	0.43
35:b:47:ILE:O	35:b:66:ASN:ND2	2.52	0.43
44:AW:3:ARG:HB3	44:AW:207:VAL:HG22	2.01	0.43
65:AR:6:THR:HG22	65:AR:8:THR:H	1.84	0.43
13:M:36:LEU:HD23	13:M:36:LEU:H	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:112:HIS:NE2	19:S:237:SER:OG	2.50	0.42
19:S:182:TYR:O	19:S:226:PHE:N	2.52	0.42
33:2:513:U:N3	33:2:538:A:N6	2.67	0.42
35:b:120:HIS:O	35:b:120:HIS:ND1	2.52	0.42
41:BQ:364:G:OP1	45:BE:60:THR:HG22	2.19	0.42
41:BQ:1306:G:N2	41:BQ:1307:G:N7	2.67	0.42
41:BQ:1416:C:O2'	41:BQ:1417:G:O4'	2.35	0.42
41:BQ:1572:U:HO2'	41:BQ:1573:G:P	2.42	0.42
41:BQ:1972:A:C6	41:BQ:2049:A:N1	2.87	0.42
45:BE:138:ARG:O	45:BE:138:ARG:NH1	2.47	0.42
50:BD:146:ASP:HA	50:BD:149:VAL:HG22	2.01	0.42
8:H:126:ARG:NE	8:H:132:ARG:O	2.50	0.42
15:O:297:ASP:OD1	15:O:298:GLY:N	2.52	0.42
17:Q:111:ARG:NH2	17:Q:114:VAL:HG21	2.34	0.42
19:S:57:ASN:O	19:S:61:VAL:HG23	2.18	0.42
21:U:57:ALA:C	21:U:58:LEU:HD22	2.44	0.42
41:BQ:763:G:O2'	41:BQ:764:U:OP1	2.37	0.42
41:BQ:2888:U:O4'	41:BQ:2911:A:N6	2.51	0.42
41:BQ:3213:A:H62	53:AM:124:ARG:NH1	2.17	0.42
41:BQ:3291:G:N1	41:BQ:3292:A:C6	2.87	0.42
44:AW:139:HIS:ND1	44:AW:146:THR:HG22	2.34	0.42
50:BD:189:GLU:OE1	50:BD:200:LEU:HD22	2.19	0.42
55:AU:9[A]:ILE:O	55:AU:36[A]:VAL:HG22	2.18	0.42
56:AX:32:THR:O	56:AX:35:ALA:HB3	2.19	0.42
59:BJ:53:PRO:HB3	59:BJ:91:LEU:HD21	2.01	0.42
75:AO:115:CYS:SG	75:AO:118:THR:HG22	2.60	0.42
2:A:39:VAL:CA	2:A:47:GLU:O	2.60	0.42
6:F:113:ASP:CG	6:F:115:THR:HG22	2.44	0.42
28:BA:94:GLU:OE1	28:BA:156:SER:OG	2.27	0.42
33:2:438:A:O2'	33:2:465:G:N2	2.51	0.42
33:2:647:G:N2	33:2:687:G:H22	2.17	0.42
41:BQ:655:C:OP1	68:BG:27:ARG:N	2.52	0.42
41:BQ:1720:U:O4	57:BF:125:LYS:NZ	2.50	0.42
41:BQ:2261:G:O2'	41:BQ:2263:C:N4	2.52	0.42
42:BR:50:U:O2'	46:BI:224:LYS:NZ	2.39	0.42
44:AW:126:LEU:HD12	44:AW:150:LEU:HD22	2.01	0.42
59:BJ:101:CYS:SG	59:BJ:102:ARG:N	2.92	0.42
64:AN:9:LYS:HB2	64:AN:25:ILE:HD12	2.01	0.42
73:AI:32:ASN:O	73:AI:33:LYS:NZ	2.34	0.42
1:B:46:TRP:CE3	1:B:118:LEU:HD23	2.54	0.42
14:N:133:ALA:HB2	33:2:1252:C:C1'	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:111:ARG:HA	17:Q:114:VAL:HG22	2.01	0.42
17:Q:210:ILE:O	17:Q:210:ILE:HG22	2.19	0.42
19:S:24:SER:O	19:S:24:SER:OG	2.36	0.42
23:W:70:LEU:O	23:W:74:ASN:ND2	2.53	0.42
28:BA:147:GLU:OE1	28:BA:147:GLU:N	2.50	0.42
33:2:1525:A:N3	33:2:1589:C:O2'	2.38	0.42
41:BQ:2004:U:H3	41:BQ:2017:G:H1	1.67	0.42
41:BQ:2494:A:C1'	80:BT:164:CYS:CB	2.97	0.42
56:AX:33:ALA:HB1	56:AX:117:ILE:HD13	2.02	0.42
64:AN:81:LEU:HD12	64:AN:82:PRO:HD2	2.00	0.42
1:B:97:LEU:O	1:B:180:ARG:NH2	2.52	0.42
14:N:130:VAL:HG21	14:N:143:LYS:H	1.84	0.42
17:Q:164:ILE:HG22	17:Q:168:ILE:HD12	2.01	0.42
19:S:87:MET:HE1	19:S:236:ILE:HG21	2.00	0.42
19:S:207:LEU:HD22	19:S:219:VAL:CG1	2.49	0.42
20:T:178:LEU:HD13	33:2:78:A:C2	2.55	0.42
28:BA:41:VAL:HG22	28:BA:185:GLY:O	2.20	0.42
30:BB:171:LYS:NZ	41:BQ:89:A:N7	2.68	0.42
33:2:622:A:O2'	33:2:1032:G:OP2	2.31	0.42
41:BQ:2093:A:H2	57:BF:143:ILE:CG1	2.32	0.42
41:BQ:3214:U:OP2	53:AM:128:ARG:NH1	2.52	0.42
46:BI:33:ARG:O	46:BI:37:VAL:HG22	2.19	0.42
46:BI:187:THR:O	46:BI:189:GLU:N	2.53	0.42
52:AJ:164:GLU:OE1	52:AJ:164:GLU:N	2.53	0.42
67:AY:9:SER:OG	67:AY:10:ILE:N	2.44	0.42
67:AY:66:LYS:NZ	67:AY:101:LEU:O	2.53	0.42
3:C:56:LYS:NZ	3:C:68:LEU:O	2.42	0.42
9:I:108:LEU:C	9:I:114:VAL:HG12	2.45	0.42
28:BA:134:SER:O	28:BA:137:TYR:C	2.63	0.42
33:2:647:G:H22	33:2:687:G:H1	1.66	0.42
33:2:711:U:O2'	33:2:712:G:OP2	2.29	0.42
33:2:1521:G:C4	33:2:1523:G:N2	2.87	0.42
41:BQ:28:C:O2'	41:BQ:61:A:N3	2.49	0.42
41:BQ:2424:A:OP1	54:AQ:90:ASN:ND2	2.47	0.42
45:BE:362:ASP:OD1	58:BH:28:ARG:NH2	2.53	0.42
2:A:39:VAL:HG23	2:A:46:THR:OG1	2.20	0.42
12:L:12:VAL:HG23	12:L:28:VAL:HB	2.01	0.42
13:M:40:ARG:NH2	33:2:1198:G:O3'	2.52	0.42
14:N:150:VAL:O	14:N:151:ASN:ND2	2.51	0.42
19:S:194:THR:OG1	19:S:194:THR:O	2.36	0.42
26:Z:43:THR:HG23	26:Z:46:MET:H	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:115:ILE:N	38:e:62:TYR:OH	2.48	0.42
28:BA:296:THR:OG1	28:BA:357:LYS:O	2.37	0.42
33:2:580:A:O2'	33:2:582:U:OP2	2.23	0.42
33:2:1640:C:O2	33:2:1763:A:N6	2.53	0.42
40:g:15:LYS:O	40:g:18:THR:HG22	2.19	0.42
41:BQ:535:G:O2'	41:BQ:554:A:N6	2.28	0.42
41:BQ:1985:G:H2'	41:BQ:1986:U:C4'	2.50	0.42
42:BR:119:U:O5'	46:BI:258:LYS:NZ	2.50	0.42
43:BS:97:A:O5'	71:BP:63:ARG:NE	2.53	0.42
45:BE:209:TYR:O	45:BE:230:VAL:HG23	2.20	0.42
50:BD:38:LYS:HG3	50:BD:41:ALA:HB2	2.02	0.42
60:BL:104:ARG:C	60:BL:105:LEU:HD12	2.45	0.42
6:F:41:PRO:O	6:F:43:ILE:HD12	2.20	0.42
16:P:36:TYR:OH	34:a:70:ASN:ND2	2.46	0.42
17:Q:78:ASP:OD1	17:Q:79:HIS:N	2.52	0.42
33:2:151:G:C2	33:2:164:A:C6	3.08	0.42
33:2:478:A:C5	33:2:539:G:N2	2.88	0.42
33:2:748:U:O2	33:2:802:G:C2	2.72	0.42
33:2:766:U:C2	33:2:770:A:N6	2.87	0.42
33:2:1213:G:C1'	33:2:1242:A:H61	2.32	0.42
37:d:29:HIS:O	37:d:67:GLY:CA	2.67	0.42
41:BQ:524:U:O2'	53:AM:78:THR:HG21	2.19	0.42
41:BQ:3005:A:O2'	41:BQ:3140:G:N2	2.48	0.42
41:BQ:3332:U:H2'	41:BQ:3333:G:O4'	2.20	0.42
5:E:49:MET:HE2	5:E:49:MET:HA	2.02	0.42
16:P:140:ASN:ND2	18:R:60:SER:O	2.53	0.42
18:R:38:VAL:O	18:R:38:VAL:HG13	2.19	0.42
18:R:41:LEU:HD22	18:R:68:ILE:HD13	2.02	0.42
21:U:98:ILE:C	21:U:99:LEU:HD12	2.45	0.42
25:Y:128:TYR:CE1	25:Y:132:VAL:HG11	2.55	0.42
33:2:614:C:OP2	36:c:5:LYS:NZ	2.44	0.42
42:BR:3:U:O2'	42:BR:25:G:N3	2.53	0.42
43:BS:112:U:OP1	74:AL:8:ARG:NH1	2.51	0.42
50:BD:43:VAL:HG12	50:BD:171:TRP:CD1	2.54	0.42
52:AJ:162:ASN:OD1	52:AJ:162:ASN:N	2.53	0.42
53:AM:23:ILE:HG21	53:AM:28:SER:HB2	2.01	0.42
53:AM:72:LEU:HD12	53:AM:73:PRO:CD	2.50	0.42
63:AK:82:VAL:HG12	63:AK:83:ASP:O	2.19	0.42
70:BN:95:ILE:HG21	70:BN:95:ILE:HD13	1.85	0.42
1:B:92:ARG:NH2	33:2:1613:U:OP1	2.47	0.42
15:O:36:ALA:HB2	15:O:42:LEU:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:139:GLN:OE1	15:O:139:GLN:N	2.49	0.42
19:S:75:LYS:NZ	33:2:123:G:OP1	2.46	0.42
20:T:14:LYS:HB3	20:T:124:LEU:HD21	2.02	0.42
22:V:24:LYS:NZ	33:2:392:G:OP1	2.45	0.42
33:2:928:U:O3'	33:2:944:A:O2'	2.37	0.42
37:d:35:VAL:HG11	37:d:40:LEU:HD21	2.01	0.42
41:BQ:1404:G:N2	41:BQ:1407:A:OP2	2.50	0.42
41:BQ:3268:A:OP1	56:AX:181:ARG:NH2	2.53	0.42
58:BH:24:LEU:HD12	59:BJ:146:ASN:CG	2.45	0.42
64:AN:46:ILE:HG21	64:AN:49:TYR:CD1	2.55	0.42
68:BG:78:ASN:HA	68:BG:108:ILE:HD11	2.01	0.42
69:BK:59:VAL:HG23	69:BK:60:ARG:H	1.85	0.42
4:D:68:GLU:OE2	4:D:70:ASN:ND2	2.52	0.41
4:D:98:GLY:O	4:D:101:ALA:C	2.63	0.41
23:W:159:ALA:HB3	23:W:162:SER:HB3	2.01	0.41
32:BC:13:THR:OG1	32:BC:72:ARG:NH1	2.47	0.41
33:2:1267:G:O2'	33:2:1448:G:O2'	2.35	0.41
41:BQ:2022:G:OP1	79:x:352:LYS:CE	2.49	0.41
43:BS:95:G:O2'	72:AF:81:GLY:O	2.37	0.41
47:BM:104:GLU:OE1	47:BM:104:GLU:N	2.47	0.41
54:AQ:97:SER:OG	54:AQ:98:LEU:N	2.52	0.41
59:BJ:99:SER:OG	59:BJ:101:CYS:SG	2.51	0.41
68:BG:69:SER:OG	68:BG:71:HIS:ND1	2.51	0.41
69:BK:72:THR:OG1	69:BK:73:ARG:N	2.53	0.41
15:O:26:SER:OG	15:O:76:ASP:O	2.34	0.41
15:O:68:VAL:HG23	15:O:68:VAL:O	2.20	0.41
15:O:80:ALA:O	15:O:91:LEU:HD12	2.20	0.41
15:O:183:LEU:HD23	15:O:183:LEU:H	1.84	0.41
17:Q:110:LEU:O	17:Q:114:VAL:HG22	2.20	0.41
21:U:82:GLU:OE1	21:U:164:TYR:OH	2.36	0.41
24:X:78:THR:O	24:X:78:THR:HG22	2.19	0.41
27:AA:59:GLN:NE2	43:BS:150:G:H21	2.18	0.41
33:2:371:G:N2	33:2:612:U:O2	2.52	0.41
33:2:478:A:H62	33:2:539:G:N2	2.17	0.41
33:2:512:A:N1	33:2:539:G:C6	2.88	0.41
33:2:566:C:O3'	40:g:10:ARG:NH2	2.53	0.41
33:2:655:G:N2	33:2:678:A:C5	2.87	0.41
36:c:132:LEU:HD23	36:c:135:LEU:HD12	2.01	0.41
41:BQ:110:G:OP2	52:AJ:73:ARG:NH1	2.47	0.41
41:BQ:1222:G:O2'	41:BQ:1285:G:N1	2.50	0.41
4:D:41:LEU:HD12	4:D:121:VAL:HG13	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:41:LEU:HD21	4:D:43:ARG:CZ	2.50	0.41
5:E:91:GLY:N	5:E:107:ILE:O	2.52	0.41
9:I:40:SER:OG	9:I:41:SER:N	2.53	0.41
17:Q:31:ASP:O	17:Q:96:LEU:HD23	2.20	0.41
22:V:79:ALA:N	22:V:103:GLN:O	2.49	0.41
27:AA:228:GLU:O	27:AA:232:HIS:ND1	2.52	0.41
28:BA:19:ARG:NH2	41:BQ:3045:G:OP1	2.53	0.41
28:BA:87:VAL:HG23	28:BA:87:VAL:O	2.21	0.41
33:2:548:G:C6	33:2:591:A:N6	2.88	0.41
33:2:1174:C:H42	33:2:1465:C:H41	1.68	0.41
36:c:69:ARG:NH2	36:c:116:ASP:OD2	2.45	0.41
41:BQ:733:G:HO2'	41:BQ:735:A:N6	2.16	0.41
45:BE:206:LEU:HD23	45:BE:248:VAL:HG22	2.01	0.41
45:BE:325:LEU:O	48:BO:41:ARG:NH2	2.52	0.41
49:AD:49:ASN:OD1	49:AD:52:LEU:N	2.53	0.41
52:AJ:62:THR:O	52:AJ:66:ASN:N	2.53	0.41
57:BF:25:ASP:N	57:BF:25:ASP:OD1	2.53	0.41
64:AN:136:PHE:O	70:BN:76:TYR:OH	2.22	0.41
11:K:88:ILE:HG23	11:K:89:ILE:HG23	2.01	0.41
17:Q:2:ALA:N	26:Z:49:LYS:O	2.54	0.41
19:S:108:ARG:NH1	33:2:788:A:OP2	2.52	0.41
19:S:183:VAL:HG11	19:S:188:ASN:HB2	2.02	0.41
25:Y:26:PHE:CZ	25:Y:28:LEU:HD12	2.56	0.41
27:AA:242:ALA:N	41:BQ:2586:G:O6	2.47	0.41
33:2:540:G:O2'	33:2:541:A:O3'	2.34	0.41
33:2:1272:U:C2	33:2:1438:G:O6	2.73	0.41
41:BQ:1896:A:H61	41:BQ:2339:C:H42	1.68	0.41
41:BQ:3109:G:OP1	75:AO:93:LYS:NZ	2.54	0.41
41:BQ:3248:C:O4'	55:AU:114[A]:LYS:NZ	2.54	0.41
50:BD:103:LEU:HD12	50:BD:108:ALA:HB1	2.02	0.41
19:S:207:LEU:HD22	19:S:219:VAL:HG12	2.02	0.41
32:BC:29:ALA:HB3	32:BC:30:PRO:HD3	2.02	0.41
33:2:151:G:C2	33:2:164:A:N1	2.89	0.41
33:2:174:U:H3	33:2:266:A:H62	1.68	0.41
33:2:541:A:HO2'	33:2:542:A:P	2.38	0.41
39:f:35:VAL:HG23	39:f:79:PHE:HB3	2.02	0.41
41:BQ:1813:A:O2'	41:BQ:1816:A:N3	2.29	0.41
41:BQ:2563:G:O6	41:BQ:2579:G:C2	2.73	0.41
41:BQ:2689:A:N6	41:BQ:2702:A:O2'	2.53	0.41
59:BJ:75:ILE:HD11	59:BJ:88:ARG:NH2	2.35	0.41
3:C:38:LYS:O	3:C:42:VAL:HG23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:140:VAL:CG1	19:S:146:THR:HG22	2.48	0.41
23:W:58:ASP:C	23:W:61:THR:HG22	2.46	0.41
32:BC:7:VAL:O	32:BC:7:VAL:HG13	2.20	0.41
35:b:83:ILE:H	35:b:83:ILE:HD12	1.86	0.41
38:e:23:CYS:SG	38:e:24:VAL:N	2.90	0.41
41:BQ:63:A:N3	41:BQ:78:U:O2'	2.45	0.41
41:BQ:799:G:H2'	41:BQ:801:A:H62	1.85	0.41
41:BQ:1238:C:N4	41:BQ:1245:A:OP2	2.53	0.41
64:AN:26:VAL:HG23	64:AN:89:VAL:HG11	2.03	0.41
66:AV:16:ALA:O	66:AV:20:GLY:HA2	2.20	0.41
79:x:146:ARG:HA	79:x:231:LEU:HD11	2.01	0.41
14:N:139:LEU:HD13	14:N:150:VAL:HG23	2.03	0.41
16:P:2:SER:OG	16:P:3:LEU:N	2.54	0.41
17:Q:78:ASP:OD1	17:Q:79:HIS:ND1	2.45	0.41
29:AB:97:ASP:OD1	29:AB:98:ASN:N	2.49	0.41
30:BB:30:VAL:O	30:BB:34:THR:HG23	2.21	0.41
31:AC:19:SER:OG	31:AC:20:MET:N	2.54	0.41
33:2:141:U:O2'	33:2:142:G:O5'	2.29	0.41
33:2:1251:U:HO2'	33:2:1252:C:P	2.42	0.41
41:BQ:503:C:O2	47:BM:23:LYS:NZ	2.36	0.41
41:BQ:1182:A:O3'	58:BH:158:LYS:NZ	2.52	0.41
41:BQ:1656:A:N6	41:BQ:1799:A:OP2	2.45	0.41
41:BQ:2500:A:O2'	41:BQ:2501:U:OP1	2.31	0.41
41:BQ:3135:U:OP1	55:AU:148[A]:LYS:NZ	2.49	0.41
42:BR:13:A:OP2	42:BR:67:G:N2	2.53	0.41
18:R:138:PRO:C	18:R:139:ILE:HD13	2.46	0.41
19:S:64:ILE:HD12	37:d:17:LEU:HB3	2.02	0.41
19:S:146:THR:OG1	33:2:123:G:N3	2.47	0.41
24:X:67:ARG:NE	33:2:115:G:OP1	2.42	0.41
28:BA:269:GLN:NE2	41:BQ:3306:U:OP1	2.53	0.41
36:c:92:CYS:O	36:c:96:VAL:HG22	2.21	0.41
41:BQ:1279:C:H2'	41:BQ:1280:C:O4'	2.20	0.41
41:BQ:1693:C:O2'	41:BQ:1772:U:O2'	2.14	0.41
41:BQ:3291:G:O6	41:BQ:3292:A:N6	2.54	0.41
51:AG:26:SER:OG	51:AG:27:GLY:N	2.53	0.41
52:AJ:43:ALA:HB1	52:AJ:137:GLN:HE22	1.85	0.41
53:AM:37:GLU:OE1	58:BH:95:ARG:NH2	2.53	0.41
54:AQ:73:ARG:O	54:AQ:75:VAL:N	2.54	0.41
55:AU:151[A]:ASP:OD1	55:AU:152[A]:VAL:N	2.54	0.41
67:AY:13:LYS:CB	67:AY:100:ILE:HD11	2.50	0.41
2:A:16:VAL:HG21	13:M:22:ARG:NH1	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:26:SER:HB3	13:M:39:CYS:SG	2.61	0.41
17:Q:38:PHE:CE1	17:Q:189:ILE:HD11	2.56	0.41
20:T:211:LEU:HD11	20:T:215:ARG:HH21	1.86	0.41
21:U:93:LEU:HD23	21:U:94:ALA:C	2.45	0.41
28:BA:5:LYS:NZ	41:BQ:2925:C:OP2	2.54	0.41
28:BA:21:ARG:NH2	41:BQ:3309:G:O6	2.50	0.41
28:BA:227:GLU:HG2	28:BA:270:ARG:HE	1.86	0.41
29:AB:42:SER:OG	41:BQ:2931:C:O2'	2.39	0.41
33:2:1225:U:O2	33:2:1230:A:O2'	2.17	0.41
33:2:1323:C:H2'	33:2:1324:G:O4'	2.20	0.41
33:2:1584:G:O2'	33:2:1585:U:OP2	2.39	0.41
41:BQ:53:G:OP1	72:AF:48:ASN:N	2.46	0.41
41:BQ:829:U:H3	41:BQ:895:A:H62	1.68	0.41
41:BQ:1995:A:H2'	41:BQ:1996:C:C6	2.56	0.41
41:BQ:2451:G:H21	41:BQ:2495:C:H5	1.68	0.41
41:BQ:2538:U:O2'	41:BQ:2542:U:O2	2.32	0.41
41:BQ:2618:G:O2'	41:BQ:2865:U:OP1	2.31	0.41
45:BE:330:TYR:HD1	48:BO:45:LEU:HD12	1.85	0.41
46:BI:234:ASP:OD1	46:BI:235:SER:N	2.54	0.41
50:BD:109:ASP:OD1	50:BD:110:ARG:N	2.53	0.41
51:AG:17:LEU:HD21	51:AG:19:LEU:HD21	2.03	0.41
59:BJ:105:PHE:O	59:BJ:109:VAL:HG23	2.21	0.41
60:BL:40:HIS:HA	60:BL:47:VAL:HG11	2.03	0.41
67:AY:48:THR:HG22	67:AY:49:PRO:CD	2.45	0.41
73:AI:30:LYS:O	73:AI:31:LEU:HD22	2.21	0.41
79:x:223:TYR:HD1	79:x:228:HIS:CE1	2.38	0.41
79:x:291:TYR:CB	79:x:329:MET:HE1	2.51	0.41
18:R:237:VAL:HG22	18:R:238:SER:H	1.86	0.41
25:Y:6:SER:OG	25:Y:7:ALA:N	2.54	0.41
33:2:566:C:O2'	40:g:10:ARG:NE	2.54	0.41
41:BQ:776:U:C4	41:BQ:2738:A:C6	3.09	0.41
41:BQ:1528:G:OP1	70:BN:9:ARG:NH1	2.53	0.41
41:BQ:1646:G:O2'	41:BQ:1808:G:N2	2.51	0.41
41:BQ:2032:U:C3'	41:BQ:2032:U:C6	3.04	0.41
41:BQ:2042:G:H8	41:BQ:2042:G:O5'	2.04	0.41
41:BQ:2869:U:O2'	41:BQ:2873:U:OP1	2.37	0.41
41:BQ:3159:C:N3	41:BQ:3292:A:N1	2.69	0.41
41:BQ:3235:C:O2	41:BQ:3253:G:N2	2.54	0.41
43:BS:45:C:OP2	74:AL:15:LYS:NZ	2.54	0.41
70:BN:29:ILE:HD11	70:BN:31:ARG:NH2	2.36	0.41
4:D:58:LEU:C	4:D:59:LEU:HD12	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:91:LEU:HD12	16:P:19:ALA:HB3	2.02	0.40
20:T:154:ARG:HG2	20:T:178:LEU:HD11	2.03	0.40
22:V:48:THR:HG21	22:V:54:LYS:HB2	2.03	0.40
36:c:96:VAL:CG1	36:c:132:LEU:HD21	2.52	0.40
57:BF:135:LYS:O	57:BF:139:VAL:HG23	2.21	0.40
62:AH:79:GLY:HA3	62:AH:81:ILE:HD12	2.03	0.40
63:AK:51:ARG:HG2	63:AK:52:ARG:H	1.86	0.40
64:AN:14:VAL:O	64:AN:19:ALA:HB1	2.21	0.40
73:AI:8:ILE:O	73:AI:12:LEU:HD23	2.20	0.40
1:B:81:ARG:NE	33:2:1615:C:OP2	2.52	0.40
4:D:36:LEU:CD1	4:D:41:LEU:HD22	2.50	0.40
8:H:143:ARG:NH1	33:2:1462:G:OP2	2.48	0.40
15:O:180:ALA:O	15:O:188:ILE:HD12	2.20	0.40
27:AA:82:LEU:HD11	27:AA:178:ALA:HB1	2.02	0.40
29:AB:80:ARG:NH1	29:AB:117:PRO:O	2.50	0.40
33:2:276:C:O2'	33:2:277:U:O5'	2.35	0.40
33:2:1213:G:H1'	33:2:1242:A:H61	1.86	0.40
33:2:1795:U:OP1	38:e:86:VAL:HG13	2.20	0.40
41:BQ:1565:G:H21	41:BQ:1566:A:H1'	1.86	0.40
41:BQ:1626:U:O4	41:BQ:1817:G:O6	2.40	0.40
7:G:93:LEU:HD13	7:G:100:LEU:HB3	2.03	0.40
16:P:30:GLN:NE2	16:P:34:GLU:O	2.55	0.40
17:Q:153:HIS:O	17:Q:154:SER:OG	2.32	0.40
21:U:34:LEU:HD13	21:U:38:LEU:HD21	2.03	0.40
33:2:709:C:H41	33:2:729:G:H2'	1.86	0.40
33:2:1363:U:O2'	33:2:1364:G:O4'	2.31	0.40
33:2:1380:U:O2'	33:2:1516:A:N1	2.49	0.40
35:b:90:THR:HA	35:b:94:LEU:HD23	2.02	0.40
41:BQ:1968:G:C4	41:BQ:1969:G:H1'	2.57	0.40
46:BI:290:ILE:O	46:BI:295:GLY:N	2.53	0.40
48:BO:222:HIS:O	48:BO:225:GLN:N	2.51	0.40
56:AX:114:VAL:O	56:AX:114:VAL:HG13	2.21	0.40
64:AN:132:SER:OG	64:AN:133:LYS:N	2.54	0.40
67:AY:47:ASN:HD21	67:AY:74:ASN:H	1.69	0.40
69:BK:11:GLY:O	69:BK:98:VAL:HG12	2.21	0.40
78:AT:55:TRP:NE1	78:AT:67:GLY:O	2.45	0.40
8:H:60:GLU:OE1	8:H:60:GLU:N	2.54	0.40
9:I:78:LYS:HZ3	33:2:1523:G:P	2.43	0.40
13:M:21:CYS:SG	13:M:38:ILE:HA	2.61	0.40
16:P:119:ARG:NE	18:R:240:LEU:HD22	2.36	0.40
17:Q:124:ASN:ND2	33:2:884:A:O2'	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:207:LEU:HD23	19:S:220:THR:O	2.22	0.40
22:V:141:ARG:NH1	33:2:196:G:N7	2.60	0.40
33:2:521:A:O2'	37:d:35:VAL:O	2.39	0.40
33:2:634:G:N1	33:2:965:U:OP2	2.54	0.40
33:2:1186:U:OP2	33:2:1456:C:O2'	2.11	0.40
33:2:1739:C:H2'	33:2:1740:A:O4'	2.21	0.40
41:BQ:664:U:H2'	41:BQ:665:A:C8	2.57	0.40
41:BQ:826:G:OP1	41:BQ:1590:G:O2'	2.32	0.40
41:BQ:2032:U:C6	41:BQ:2032:U:H3'	2.57	0.40
41:BQ:3174:A:OP1	69:BK:97:SER:OG	2.31	0.40
41:BQ:3230:G:H4'	53:AM:132:LYS:HD3	2.04	0.40
43:BS:51:G:C8	74:AL:27:ILE:HD11	2.56	0.40
14:N:130:VAL:HG13	14:N:130:VAL:O	2.21	0.40
15:O:224:ASN:CB	15:O:231:MET:HE3	2.51	0.40
25:Y:98:VAL:O	25:Y:102:LEU:HD23	2.22	0.40
33:2:215:A:O2'	33:2:216:U:OP1	2.37	0.40
33:2:1389:C:N4	33:2:1391:A:O4'	2.55	0.40
41:BQ:800:G:C2	41:BQ:933:A:N6	2.89	0.40
41:BQ:874:U:N3	41:BQ:2978:U:OP1	2.48	0.40
41:BQ:1257:C:N3	41:BQ:1261:G:C2	2.90	0.40
64:AN:24:VAL:HG21	64:AN:87:LEU:HD23	2.03	0.40
72:AF:22:CYS:O	72:AF:22:CYS:SG	2.79	0.40
73:AI:56:ILE:HG22	73:AI:58:ASP:H	1.86	0.40
79:x:223:TYR:CD1	79:x:228:HIS:CE1	3.10	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	204/206 (99%)	190 (93%)	14 (7%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	220/222 (99%)	208 (94%)	12 (6%)	0	100	100
3	C	90/92 (98%)	77 (86%)	13 (14%)	0	100	100
4	D	119/121 (98%)	89 (75%)	29 (24%)	1 (1%)	16	50
5	E	115/142 (81%)	100 (87%)	15 (13%)	0	100	100
6	F	139/141 (99%)	124 (89%)	15 (11%)	0	100	100
7	G	117/125 (94%)	111 (95%)	6 (5%)	0	100	100
8	H	143/145 (99%)	130 (91%)	13 (9%)	0	100	100
9	I	141/143 (99%)	128 (91%)	13 (9%)	0	100	100
10	J	98/100 (98%)	87 (89%)	11 (11%)	0	100	100
11	K	80/82 (98%)	71 (89%)	9 (11%)	0	100	100
12	L	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
13	M	51/53 (96%)	48 (94%)	3 (6%)	0	100	100
14	N	71/73 (97%)	48 (68%)	23 (32%)	0	100	100
15	O	310/312 (99%)	264 (85%)	46 (15%)	0	100	100
16	P	204/206 (99%)	181 (89%)	23 (11%)	0	100	100
17	Q	222/232 (96%)	196 (88%)	26 (12%)	0	100	100
18	R	214/216 (99%)	189 (88%)	25 (12%)	0	100	100
19	S	256/258 (99%)	224 (88%)	32 (12%)	0	100	100
20	T	226/228 (99%)	210 (93%)	16 (7%)	0	100	100
21	U	182/184 (99%)	158 (87%)	24 (13%)	0	100	100
22	V	183/200 (92%)	165 (90%)	18 (10%)	0	100	100
23	W	182/184 (99%)	161 (88%)	20 (11%)	1 (0%)	24	59
24	X	140/142 (99%)	125 (89%)	15 (11%)	0	100	100
25	Y	148/150 (99%)	131 (88%)	17 (12%)	0	100	100
26	Z	125/127 (98%)	108 (86%)	17 (14%)	0	100	100
27	AA	231/233 (99%)	209 (90%)	22 (10%)	0	100	100
28	BA	384/386 (100%)	354 (92%)	30 (8%)	0	100	100
29	AB	134/136 (98%)	127 (95%)	7 (5%)	0	100	100
30	BB	183/185 (99%)	170 (93%)	13 (7%)	0	100	100
31	AC	97/99 (98%)	91 (94%)	6 (6%)	0	100	100
32	BC	107/109 (98%)	92 (86%)	15 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	a	85/87 (98%)	72 (85%)	13 (15%)	0	100	100
35	b	127/129 (98%)	114 (90%)	13 (10%)	0	100	100
36	c	142/144 (99%)	122 (86%)	20 (14%)	0	100	100
37	d	132/134 (98%)	123 (93%)	9 (7%)	0	100	100
38	e	95/97 (98%)	85 (90%)	10 (10%)	0	100	100
39	f	79/81 (98%)	71 (90%)	8 (10%)	0	100	100
40	g	58/60 (97%)	48 (83%)	10 (17%)	0	100	100
44	AW	249/251 (99%)	220 (88%)	29 (12%)	0	100	100
45	BE	359/361 (99%)	321 (89%)	37 (10%)	1 (0%)	36	69
46	BI	292/294 (99%)	268 (92%)	24 (8%)	0	100	100
47	BM	163/175 (93%)	146 (90%)	17 (10%)	0	100	100
48	BO	220/222 (99%)	205 (93%)	15 (7%)	0	100	100
49	AD	189/191 (99%)	172 (91%)	17 (9%)	0	100	100
50	BD	216/218 (99%)	188 (87%)	28 (13%)	0	100	100
51	AG	167/169 (99%)	155 (93%)	12 (7%)	0	100	100
52	AJ	191/193 (99%)	169 (88%)	21 (11%)	1 (0%)	24	59
53	AM	134/136 (98%)	120 (90%)	14 (10%)	0	100	100
54	AQ	201/203 (99%)	181 (90%)	20 (10%)	0	100	100
55	AU	195/197 (99%)	186 (95%)	9 (5%)	0	100	100
56	AX	181/183 (99%)	165 (91%)	16 (9%)	0	100	100
57	BF	186/188 (99%)	178 (96%)	8 (4%)	0	100	100
58	BH	169/171 (99%)	157 (93%)	12 (7%)	0	100	100
59	BJ	157/159 (99%)	142 (90%)	15 (10%)	0	100	100
60	BL	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
61	AE	124/126 (98%)	106 (86%)	18 (14%)	0	100	100
62	AH	119/121 (98%)	109 (92%)	10 (8%)	0	100	100
63	AK	123/125 (98%)	116 (94%)	7 (6%)	0	100	100
64	AN	133/135 (98%)	117 (88%)	16 (12%)	0	100	100
65	AR	146/148 (99%)	128 (88%)	18 (12%)	0	100	100
66	AV	56/58 (97%)	47 (84%)	9 (16%)	0	100	100
67	AY	94/96 (98%)	89 (95%)	4 (4%)	1 (1%)	11	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	BG	125/127 (98%)	114 (91%)	11 (9%)	0	100	100
69	BK	104/106 (98%)	98 (94%)	6 (6%)	0	100	100
70	BN	110/112 (98%)	105 (96%)	5 (4%)	0	100	100
71	BP	117/119 (98%)	109 (93%)	8 (7%)	0	100	100
72	AF	79/81 (98%)	72 (91%)	7 (9%)	0	100	100
73	AI	75/77 (97%)	72 (96%)	3 (4%)	0	100	100
74	AL	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
75	AO	50/52 (96%)	43 (86%)	7 (14%)	0	100	100
76	AS	23/25 (92%)	23 (100%)	0	0	100	100
77	AP	101/103 (98%)	93 (92%)	8 (8%)	0	100	100
78	AT	89/91 (98%)	84 (94%)	4 (4%)	1 (1%)	11	43
79	x	365/387 (94%)	350 (96%)	13 (4%)	2 (0%)	24	59
80	BT	215/217 (99%)	209 (97%)	6 (3%)	0	100	100
All	All	11558/11794 (98%)	10452 (90%)	1098 (10%)	8 (0%)	49	80

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	109	GLU
45	BE	4	PRO
79	x	68	ALA
52	AJ	61	PRO
67	AY	49	PRO
23	W	18	PRO
78	AT	43	GLY
79	x	28	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	172/173 (99%)	172 (100%)	0	100	100
2	A	182/182 (100%)	181 (100%)	1 (0%)	81	82
3	C	77/85 (91%)	77 (100%)	0	100	100
4	D	88/98 (90%)	88 (100%)	0	100	100
5	E	95/118 (80%)	95 (100%)	0	100	100
6	F	117/117 (100%)	117 (100%)	0	100	100
7	G	101/113 (89%)	101 (100%)	0	100	100
8	H	127/128 (99%)	127 (100%)	0	100	100
9	I	115/115 (100%)	115 (100%)	0	100	100
10	J	93/93 (100%)	93 (100%)	0	100	100
11	K	67/73 (92%)	67 (100%)	0	100	100
12	L	55/56 (98%)	55 (100%)	0	100	100
13	M	47/47 (100%)	46 (98%)	1 (2%)	47	65
14	N	56/63 (89%)	56 (100%)	0	100	100
15	O	250/257 (97%)	250 (100%)	0	100	100
16	P	170/173 (98%)	170 (100%)	0	100	100
17	Q	200/205 (98%)	200 (100%)	0	100	100
18	R	175/175 (100%)	175 (100%)	0	100	100
19	S	220/220 (100%)	220 (100%)	0	100	100
20	T	189/195 (97%)	189 (100%)	0	100	100
21	U	163/165 (99%)	163 (100%)	0	100	100
22	V	148/161 (92%)	148 (100%)	0	100	100
23	W	156/157 (99%)	156 (100%)	0	100	100
24	X	126/127 (99%)	126 (100%)	0	100	100
25	Y	127/127 (100%)	127 (100%)	0	100	100
26	Z	90/96 (94%)	90 (100%)	0	100	100
27	AA	187/191 (98%)	187 (100%)	0	100	100
28	BA	318/322 (99%)	317 (100%)	1 (0%)	86	85
29	AB	104/104 (100%)	104 (100%)	0	100	100
30	BB	150/150 (100%)	150 (100%)	0	100	100
31	AC	80/81 (99%)	80 (100%)	0	100	100
32	BC	92/96 (96%)	92 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	a	71/74 (96%)	71 (100%)	0	100	100
35	b	110/110 (100%)	110 (100%)	0	100	100
36	c	119/119 (100%)	119 (100%)	0	100	100
37	d	102/112 (91%)	102 (100%)	0	100	100
38	e	82/83 (99%)	82 (100%)	0	100	100
39	f	70/70 (100%)	70 (100%)	0	100	100
40	g	50/51 (98%)	50 (100%)	0	100	100
44	AW	190/193 (98%)	190 (100%)	0	100	100
45	BE	288/288 (100%)	287 (100%)	1 (0%)	86	85
46	BI	241/243 (99%)	241 (100%)	0	100	100
47	BM	139/154 (90%)	139 (100%)	0	100	100
48	BO	186/186 (100%)	186 (100%)	0	100	100
49	AD	168/171 (98%)	168 (100%)	0	100	100
50	BD	185/185 (100%)	185 (100%)	0	100	100
51	AG	145/147 (99%)	145 (100%)	0	100	100
52	AJ	154/154 (100%)	154 (100%)	0	100	100
53	AM	107/107 (100%)	107 (100%)	0	100	100
54	AQ	175/175 (100%)	174 (99%)	1 (1%)	78	80
55	AU	160/160 (100%)	160 (100%)	0	100	100
56	AX	138/145 (95%)	138 (100%)	0	100	100
57	BF	152/153 (99%)	152 (100%)	0	100	100
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	AE	56/108 (52%)	56 (100%)	0	100	100
62	AH	104/105 (99%)	104 (100%)	0	100	100
63	AK	108/108 (100%)	108 (100%)	0	100	100
64	AN	112/115 (97%)	112 (100%)	0	100	100
65	AR	117/118 (99%)	117 (100%)	0	100	100
66	AV	46/46 (100%)	46 (100%)	0	100	100
67	AY	81/81 (100%)	81 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	BG	108/109 (99%)	108 (100%)	0	100	100
69	BK	90/90 (100%)	90 (100%)	0	100	100
70	BN	95/95 (100%)	95 (100%)	0	100	100
71	BP	104/104 (100%)	104 (100%)	0	100	100
72	AF	67/67 (100%)	65 (97%)	2 (3%)	36	57
73	AI	68/68 (100%)	66 (97%)	2 (3%)	37	58
74	AL	45/45 (100%)	45 (100%)	0	100	100
75	AO	45/47 (96%)	43 (96%)	2 (4%)	25	49
76	AS	22/23 (96%)	22 (100%)	0	100	100
77	AP	87/88 (99%)	87 (100%)	0	100	100
78	AT	71/71 (100%)	71 (100%)	0	100	100
79	x	322/340 (95%)	321 (100%)	1 (0%)	86	85
All	All	9494/9749 (97%)	9482 (100%)	12 (0%)	87	89

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	168	ILE
13	M	42	CYS
28	BA	104	THR
45	BE	12	THR
54	AQ	27	VAL
72	AF	19	CYS
72	AF	22	CYS
73	AI	63	LYS
73	AI	64	LYS
75	AO	112	LYS
75	AO	115	CYS
79	x	221	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (63) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	29	GLN
6	F	32	ASN
8	H	6	GLN
8	H	25	ASN

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Mol	Chain	Res	Type
8	H	71	GLN
8	H	104	ASN
9	I	12	GLN
10	J	49	ASN
14	N	123	ASN
14	N	151	ASN
15	O	106	HIS
16	P	39	ASN
25	Y	58	HIS
27	AA	59	GLN
27	AA	85	ASN
27	AA	192	GLN
27	AA	240	ASN
28	BA	139	GLN
28	BA	279	ASN
30	BB	23	ASN
30	BB	126	GLN
35	b	70	ASN
37	d	34	ASN
44	AW	97	ASN
44	AW	140	ASN
44	AW	144	ASN
44	AW	187	HIS
44	AW	194	ASN
44	AW	205	ASN
45	BE	243	HIS
46	BI	63	GLN
46	BI	296	GLN
48	BO	93	ASN
48	BO	186	HIS
49	AD	64	HIS
49	AD	116	ASN
49	AD	162	GLN
50	BD	55	ASN
52	AJ	160	GLN
53	AM	56	GLN
55	AU	122[A]	GLN
56	AX	34	GLN
56	AX	55	GLN
58	BH	138	GLN
61	AE	59	HIS
64	AN	103	GLN

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Mol	Chain	Res	Type
64	AN	122	HIS
65	AR	11	HIS
66	AV	6	ASN
66	AV	43	HIS
68	BG	35	GLN
68	BG	49	ASN
69	BK	26	ASN
69	BK	88	ASN
69	BK	106	ASN
71	BP	16	GLN
72	AF	12	HIS
72	AF	30	GLN
74	AL	32	ASN
77	AP	23	HIS
79	x	275	HIS
79	x	349	GLN
79	x	356	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
33	2	1768/1798 (98%)	536 (30%)	53 (2%)
41	BQ	3293/3395 (96%)	764 (23%)	53 (1%)
42	BR	120/121 (99%)	15 (12%)	1 (0%)
43	BS	157/158 (99%)	32 (20%)	3 (1%)
All	All	5338/5472 (97%)	1347 (25%)	110 (2%)

All (1347) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
33	2	2	A
33	2	4	C
33	2	14	C
33	2	25	C
33	2	26	A
33	2	34	G
33	2	43	A
33	2	45	U
33	2	47	A
33	2	56	U
33	2	57	G

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Mol	Chain	Res	Type
33	2	62	A
33	2	65	A
33	2	67	A
33	2	68	A
33	2	69	G
33	2	73	U
33	2	74	U
33	2	75	U
33	2	76	A
33	2	78	A
33	2	79	C
33	2	80	A
33	2	81	G
33	2	104	A
33	2	114	C
33	2	116	U
33	2	121	U
33	2	127	G
33	2	129	U
33	2	130	C
33	2	131	C
33	2	132	U
33	2	133	U
33	2	134	U
33	2	135	A
33	2	136	C
33	2	137	U
33	2	138	A
33	2	140	A
33	2	141	U
33	2	142	G
33	2	153	G
33	2	155	U
33	2	156	A
33	2	158	U
33	2	161	U
33	2	168	A
33	2	171	A
33	2	172	C
33	2	174	U
33	2	176	C
33	2	178	U

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Mol	Chain	Res	Type
33	2	179	A
33	2	182	A
33	2	185	U
33	2	186	C
33	2	187	G
33	2	188	A
33	2	189	C
33	2	191	C
33	2	193	U
33	2	194	U
33	2	195	G
33	2	201	G
33	2	203	U
33	2	204	G
33	2	216	U
33	2	217	A
33	2	218	A
33	2	223	U
33	2	224	C
33	2	225	A
33	2	227	U
33	2	228	G
33	2	230	C
33	2	232	U
33	2	233	C
33	2	234	G
33	2	235	G
33	2	236	A
33	2	238	U
33	2	240	U
33	2	241	U
33	2	243	G
33	2	246	G
33	2	250	C
33	2	256	A
33	2	260	U
33	2	261	U
33	2	265	A
33	2	270	C
33	2	272	U
33	2	274	G
33	2	276	C

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Mol	Chain	Res	Type
33	2	277	U
33	2	278	U
33	2	279	G
33	2	280	U
33	2	287	G
33	2	299	A
33	2	313	U
33	2	314	C
33	2	316	A
33	2	320	U
33	2	321	C
33	2	322	G
33	2	323	A
33	2	324	U
33	2	330	G
33	2	333	A
33	2	334	G
33	2	337	G
33	2	338	C
33	2	352	A
33	2	353	A
33	2	359	A
33	2	360	A
33	2	361	C
33	2	369	A
33	2	370	A
33	2	373	G
33	2	378	A
33	2	380	U
33	2	388	G
33	2	390	G
33	2	400	A
33	2	401	A
33	2	402	C
33	2	404	G
33	2	406	U
33	2	411	C
33	2	415	C
33	2	417	A
33	2	419	G
33	2	423	G
33	2	424	C

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Mol	Chain	Res	Type
33	2	425	A
33	2	426	G
33	2	434	G
33	2	435	C
33	2	438	A
33	2	439	U
33	2	444	C
33	2	446	A
33	2	447	U
33	2	448	C
33	2	454	U
33	2	460	A
33	2	468	A
33	2	482	U
33	2	485	A
33	2	487	G
33	2	489	C
33	2	491	C
33	2	492	A
33	2	493	U
33	2	494	U
33	2	495	C
33	2	496	G
33	2	498	G
33	2	499	U
33	2	500	C
33	2	502	U
33	2	506	A
33	2	507	U
33	2	510	G
33	2	511	A
33	2	512	A
33	2	513	U
33	2	517	U
33	2	518	A
33	2	519	C
33	2	520	A
33	2	525	A
33	2	527	A
33	2	529	A
33	2	534	A
33	2	538	A

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Mol	Chain	Res	Type
33	2	539	G
33	2	540	G
33	2	541	A
33	2	542	A
33	2	543	C
33	2	554	C
33	2	555	A
33	2	556	A
33	2	557	G
33	2	558	U
33	2	565	C
33	2	571	G
33	2	572	C
33	2	578	U
33	2	579	A
33	2	580	A
33	2	594	A
33	2	595	G
33	2	606	A
33	2	609	U
33	2	610	G
33	2	611	U
33	2	617	U
33	2	619	A
33	2	620	A
33	2	623	A
33	2	624	G
33	2	635	A
33	2	638	U
33	2	639	U
33	2	640	U
33	2	641	G
33	2	643	G
33	2	645	C
33	2	651	G
33	2	653	C
33	2	654	C
33	2	655	G
33	2	656	G
33	2	677	G
33	2	678	A
33	2	680	U

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Mol	Chain	Res	Type
33	2	682	C
33	2	684	A
33	2	687	G
33	2	693	U
33	2	694	U
33	2	696	C
33	2	697	C
33	2	698	U
33	2	700	C
33	2	702	G
33	2	703	G
33	2	704	C
33	2	705	U
33	2	706	A
33	2	707	A
33	2	708	C
33	2	709	C
33	2	710	U
33	2	711	U
33	2	712	G
33	2	714	G
33	2	728	U
33	2	729	G
33	2	730	G
33	2	732	G
33	2	733	A
33	2	736	C
33	2	738	G
33	2	739	G
33	2	741	C
33	2	742	U
33	2	743	U
33	2	744	U
33	2	745	U
33	2	753	A
33	2	755	A
33	2	756	A
33	2	765	G
33	2	766	U
33	2	771	A
33	2	774	A
33	2	775	G

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Mol	Chain	Res	Type
33	2	778	G
33	2	781	U
33	2	782	U
33	2	783	G
33	2	787	G
33	2	789	A
33	2	794	U
33	2	804	A
33	2	807	A
33	2	812	A
33	2	813	U
33	2	814	A
33	2	815	G
33	2	816	G
33	2	818	C
33	2	819	G
33	2	820	U
33	2	821	U
33	2	823	G
33	2	832	U
33	2	833	U
33	2	836	U
33	2	837	G
33	2	839	U
33	2	840	U
33	2	841	U
33	2	846	G
33	2	851	U
33	2	852	C
33	2	855	A
33	2	856	A
33	2	857	U
33	2	863	A
33	2	865	A
33	2	873	U
33	2	876	G
33	2	877	G
33	2	882	U
33	2	886	U
33	2	898	A
33	2	899	G
33	2	901	G

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Mol	Chain	Res	Type
33	2	902	G
33	2	904	G
33	2	912	U
33	2	913	G
33	2	929	A
33	2	932	U
33	2	933	A
33	2	934	C
33	2	935	U
33	2	940	A
33	2	945	U
33	2	960	U
33	2	964	U
33	2	966	A
33	2	970	A
33	2	973	A
33	2	977	A
33	2	988	A
33	2	989	U
33	2	992	A
33	2	996	U
33	2	998	A
33	2	1001	A
33	2	1004	U
33	2	1024	U
33	2	1026	A
33	2	1028	C
33	2	1029	U
33	2	1032	G
33	2	1039	A
33	2	1040	G
33	2	1052	U
33	2	1053	G
33	2	1057	U
33	2	1058	U
33	2	1059	U
33	2	1060	U
33	2	1061	A
33	2	1062	A
33	2	1063	U
33	2	1074	G
33	2	1080	U

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Mol	Chain	Res	Type
33	2	1081	A
33	2	1082	C
33	2	1092	A
33	2	1096	C
33	2	1099	U
33	2	1100	G
33	2	1109	G
33	2	1111	G
33	2	1113	A
33	2	1138	A
33	2	1156	C
33	2	1158	C
33	2	1160	A
33	2	1164	G
33	2	1167	G
33	2	1170	G
33	2	1183	A
33	2	1185	U
33	2	1186	U
33	2	1187	U
33	2	1191	U
33	2	1194	A
33	2	1196	A
33	2	1197	C
33	2	1199	G
33	2	1200	G
33	2	1208	A
33	2	1212	G
33	2	1214	U
33	2	1217	A
33	2	1218	G
33	2	1227	A
33	2	1229	G
33	2	1241	G
33	2	1243	G
33	2	1244	A
33	2	1245	G
33	2	1246	C
33	2	1251	U
33	2	1252	C
33	2	1256	A
33	2	1257	U

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Mol	Chain	Res	Type
33	2	1258	U
33	2	1263	G
33	2	1264	G
33	2	1265	G
33	2	1269	U
33	2	1273	G
33	2	1274	C
33	2	1275	A
33	2	1276	U
33	2	1285	U
33	2	1294	G
33	2	1301	U
33	2	1307	U
33	2	1314	U
33	2	1315	U
33	2	1318	G
33	2	1321	A
33	2	1322	A
33	2	1325	A
33	2	1337	A
33	2	1341	A
33	2	1344	A
33	2	1345	A
33	2	1346	A
33	2	1348	A
33	2	1349	G
33	2	1354	G
33	2	1360	A
33	2	1361	U
33	2	1363	U
33	2	1367	G
33	2	1370	U
33	2	1371	A
33	2	1372	U
33	2	1373	C
33	2	1381	U
33	2	1382	A
33	2	1383	G
33	2	1385	G
33	2	1390	U
33	2	1398	U
33	2	1399	C

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Mol	Chain	Res	Type
33	2	1400	A
33	2	1402	G
33	2	1414	U
33	2	1415	U
33	2	1421	A
33	2	1427	A
33	2	1431	C
33	2	1432	U
33	2	1433	G
33	2	1446	A
33	2	1447	C
33	2	1448	G
33	2	1457	C
33	2	1458	G
33	2	1459	C
33	2	1460	A
33	2	1469	A
33	2	1472	C
33	2	1473	U
33	2	1479	A
33	2	1482	C
33	2	1483	A
33	2	1488	G
33	2	1489	U
33	2	1490	C
33	2	1491	U
33	2	1492	A
33	2	1493	A
33	2	1496	U
33	2	1510	U
33	2	1514	U
33	2	1515	A
33	2	1516	A
33	2	1517	U
33	2	1518	C
33	2	1521	G
33	2	1523	G
33	2	1524	A
33	2	1528	U
33	2	1529	C
33	2	1531	G
33	2	1537	C

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Mol	Chain	Res	Type
33	2	1540	G
33	2	1543	A
33	2	1545	A
33	2	1556	A
33	2	1557	U
33	2	1558	U
33	2	1559	A
33	2	1572	G
33	2	1573	A
33	2	1574	G
33	2	1575	G
33	2	1576	A
33	2	1583	A
33	2	1584	G
33	2	1585	U
33	2	1590	G
33	2	1592	A
33	2	1601	G
33	2	1607	G
33	2	1611	A
33	2	1614	A
33	2	1616	G
33	2	1619	C
33	2	1622	G
33	2	1634	C
33	2	1637	C
33	2	1657	U
33	2	1658	G
33	2	1660	A
33	2	1673	G
33	2	1676	U
33	2	1682	U
33	2	1688	U
33	2	1689	A
33	2	1693	A
33	2	1700	C
33	2	1701	A
33	2	1702	A
33	2	1703	C
33	2	1709	C
33	2	1711	C
33	2	1712	A

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Mol	Chain	Res	Type
33	2	1715	G
33	2	1717	G
33	2	1736	G
33	2	1740	A
33	2	1755	A
33	2	1757	G
33	2	1760	G
33	2	1762	A
33	2	1766	A
33	2	1767	G
33	2	1769	U
33	2	1770	U
33	2	1780	G
33	2	1782	A
33	2	1783	C
33	2	1788	G
33	2	1792	G
33	2	1793	G
33	2	1794	A
33	2	1796	C
33	2	1799	U
41	BQ	6	A
41	BQ	11	A
41	BQ	14	U
41	BQ	15	C
41	BQ	21	G
41	BQ	22	G
41	BQ	26	A
41	BQ	30	G
41	BQ	40	A
41	BQ	43	A
41	BQ	44	U
41	BQ	48	A
41	BQ	49	A
41	BQ	51	A
41	BQ	57	A
41	BQ	60	A
41	BQ	65	A
41	BQ	66	A
41	BQ	73	C
41	BQ	74	G
41	BQ	76	G

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Mol	Chain	Res	Type
41	BQ	85	A
41	BQ	89	A
41	BQ	92	G
41	BQ	109	A
41	BQ	110	G
41	BQ	111	C
41	BQ	113	C
41	BQ	120	G
41	BQ	121	A
41	BQ	122	A
41	BQ	133	U
41	BQ	136	G
41	BQ	143	G
41	BQ	150	A
41	BQ	156	G
41	BQ	157	A
41	BQ	166	C
41	BQ	173	G
41	BQ	187	A
41	BQ	190	U
41	BQ	191	U
41	BQ	200	C
41	BQ	206	G
41	BQ	210	U
41	BQ	211	A
41	BQ	213	A
41	BQ	218	G
41	BQ	219	A
41	BQ	221	A
41	BQ	231	G
41	BQ	236	G
41	BQ	239	G
41	BQ	240	U
41	BQ	243	G
41	BQ	249	U
41	BQ	252	U
41	BQ	258	G
41	BQ	263	C
41	BQ	269	G
41	BQ	282	G
41	BQ	283	G
41	BQ	286	U

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Mol	Chain	Res	Type
41	BQ	295	A
41	BQ	298	U
41	BQ	315	C
41	BQ	323	A
41	BQ	329	U
41	BQ	330	G
41	BQ	334	A
41	BQ	338	A
41	BQ	339	C
41	BQ	346	C
41	BQ	350	C
41	BQ	351	A
41	BQ	376	G
41	BQ	385	A
41	BQ	390	G
41	BQ	395	A
41	BQ	397	A
41	BQ	399	A
41	BQ	401	U
41	BQ	402	A
41	BQ	403	C
41	BQ	404	G
41	BQ	421	G
41	BQ	422	A
41	BQ	438	A
41	BQ	440	A
41	BQ	441	U
41	BQ	442	G
41	BQ	443	G
41	BQ	445	G
41	BQ	446	U
41	BQ	447	U
41	BQ	448	U
41	BQ	449	U
41	BQ	450	G
41	BQ	487	U
41	BQ	488	U
41	BQ	489	U
41	BQ	490	C
41	BQ	491	A
41	BQ	492	C
41	BQ	494	G

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Mol	Chain	Res	Type
41	BQ	498	A
41	BQ	510	G
41	BQ	515	C
41	BQ	517	G
41	BQ	520	U
41	BQ	521	A
41	BQ	535	G
41	BQ	543	C
41	BQ	544	C
41	BQ	545	U
41	BQ	546	C
41	BQ	547	G
41	BQ	552	G
41	BQ	555	U
41	BQ	557	A
41	BQ	559	A
41	BQ	568	G
41	BQ	578	A
41	BQ	579	G
41	BQ	597	G
41	BQ	600	G
41	BQ	603	A
41	BQ	604	G
41	BQ	609	G
41	BQ	610	G
41	BQ	611	A
41	BQ	612	U
41	BQ	619	A
41	BQ	620	U
41	BQ	621	A
41	BQ	625	G
41	BQ	637	C
41	BQ	638	C
41	BQ	642	U
41	BQ	649	A
41	BQ	650	C
41	BQ	660	A
41	BQ	667	C
41	BQ	677	A
41	BQ	681	U
41	BQ	691	A
41	BQ	699	A

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Mol	Chain	Res	Type
41	BQ	705	A
41	BQ	712	G
41	BQ	716	A
41	BQ	718	G
41	BQ	719	U
41	BQ	720	A
41	BQ	726	G
41	BQ	737	G
41	BQ	742	G
41	BQ	758	C
41	BQ	763	G
41	BQ	764	U
41	BQ	765	C
41	BQ	766	U
41	BQ	767	U
41	BQ	771	A
41	BQ	774	G
41	BQ	776	U
41	BQ	777	U
41	BQ	780	A
41	BQ	781	G
41	BQ	785	G
41	BQ	786	A
41	BQ	806	A
41	BQ	808	A
41	BQ	817	A
41	BQ	830	A
41	BQ	832	G
41	BQ	848	A
41	BQ	849	C
41	BQ	850	U
41	BQ	851	C
41	BQ	861	C
41	BQ	865	U
41	BQ	868	C
41	BQ	871	U
41	BQ	874	U
41	BQ	879	U
41	BQ	894	G
41	BQ	895	A
41	BQ	896	A
41	BQ	899	U

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Mol	Chain	Res	Type
41	BQ	906	A
41	BQ	907	G
41	BQ	908	G
41	BQ	914	A
41	BQ	916	G
41	BQ	917	A
41	BQ	921	A
41	BQ	923	C
41	BQ	932	U
41	BQ	934	G
41	BQ	937	G
41	BQ	944	C
41	BQ	959	C
41	BQ	960	U
41	BQ	971	G
41	BQ	974	G
41	BQ	981	U
41	BQ	982	C
41	BQ	991	G
41	BQ	1002	A
41	BQ	1012	G
41	BQ	1015	U
41	BQ	1018	G
41	BQ	1020	G
41	BQ	1021	G
41	BQ	1024	G
41	BQ	1026	A
41	BQ	1028	U
41	BQ	1029	G
41	BQ	1040	A
41	BQ	1041	U
41	BQ	1045	C
41	BQ	1047	A
41	BQ	1049	C
41	BQ	1064	A
41	BQ	1065	A
41	BQ	1072	G
41	BQ	1081	U
41	BQ	1093	A
41	BQ	1094	U
41	BQ	1095	U
41	BQ	1096	U

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Mol	Chain	Res	Type
41	BQ	1097	G
41	BQ	1098	A
41	BQ	1103	A
41	BQ	1104	G
41	BQ	1117	G
41	BQ	1118	C
41	BQ	1128	U
41	BQ	1131	G
41	BQ	1144	U
41	BQ	1145	G
41	BQ	1148	G
41	BQ	1153	A
41	BQ	1158	A
41	BQ	1159	A
41	BQ	1177	G
41	BQ	1178	G
41	BQ	1180	A
41	BQ	1181	U
41	BQ	1182	A
41	BQ	1190	A
41	BQ	1192	C
41	BQ	1193	A
41	BQ	1196	C
41	BQ	1197	A
41	BQ	1201	C
41	BQ	1202	A
41	BQ	1206	G
41	BQ	1208	U
41	BQ	1217	A
41	BQ	1218	U
41	BQ	1222	G
41	BQ	1223	A
41	BQ	1227	C
41	BQ	1229	G
41	BQ	1234	G
41	BQ	1236	G
41	BQ	1237	G
41	BQ	1238	C
41	BQ	1239	C
41	BQ	1240	A
41	BQ	1241	U
41	BQ	1242	G

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Mol	Chain	Res	Type
41	BQ	1243	G
41	BQ	1244	A
41	BQ	1245	A
41	BQ	1246	G
41	BQ	1248	C
41	BQ	1251	A
41	BQ	1253	U
41	BQ	1258	U
41	BQ	1262	G
41	BQ	1263	A
41	BQ	1264	G
41	BQ	1266	G
41	BQ	1267	U
41	BQ	1269	U
41	BQ	1270	A
41	BQ	1271	A
41	BQ	1272	C
41	BQ	1278	A
41	BQ	1279	C
41	BQ	1280	C
41	BQ	1282	G
41	BQ	1285	G
41	BQ	1286	A
41	BQ	1287	A
41	BQ	1295	G
41	BQ	1307	G
41	BQ	1308	A
41	BQ	1309	U
41	BQ	1313	G
41	BQ	1316	C
41	BQ	1318	A
41	BQ	1325	U
41	BQ	1330	A
41	BQ	1345	G
41	BQ	1348	U
41	BQ	1349	G
41	BQ	1351	U
41	BQ	1352	A
41	BQ	1354	G
41	BQ	1355	A
41	BQ	1356	U
41	BQ	1357	G

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Mol	Chain	Res	Type
41	BQ	1386	A
41	BQ	1392	G
41	BQ	1399	A
41	BQ	1400	G
41	BQ	1418	A
41	BQ	1419	A
41	BQ	1421	G
41	BQ	1429	G
41	BQ	1430	U
41	BQ	1431	G
41	BQ	1434	G
41	BQ	1437	C
41	BQ	1442	U
41	BQ	1443	G
41	BQ	1446	A
41	BQ	1450	G
41	BQ	1455	U
41	BQ	1481	A
41	BQ	1482	A
41	BQ	1483	G
41	BQ	1484	U
41	BQ	1487	G
41	BQ	1488	G
41	BQ	1503	A
41	BQ	1508	C
41	BQ	1511	U
41	BQ	1523	U
41	BQ	1528	G
41	BQ	1533	U
41	BQ	1536	G
41	BQ	1542	G
41	BQ	1549	U
41	BQ	1555	U
41	BQ	1556	C
41	BQ	1557	A
41	BQ	1559	A
41	BQ	1560	G
41	BQ	1562	C
41	BQ	1563	C
41	BQ	1565	G
41	BQ	1566	A
41	BQ	1567	U

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Mol	Chain	Res	Type
41	BQ	1568	U
41	BQ	1569	U
41	BQ	1572	U
41	BQ	1573	G
41	BQ	1574	C
41	BQ	1575	A
41	BQ	1576	G
41	BQ	1580	A
41	BQ	1581	C
41	BQ	1582	C
41	BQ	1583	A
41	BQ	1587	A
41	BQ	1588	A
41	BQ	1589	A
41	BQ	1590	G
41	BQ	1602	A
41	BQ	1605	A
41	BQ	1621	A
41	BQ	1629	U
41	BQ	1632	A
41	BQ	1639	C
41	BQ	1642	A
41	BQ	1643	A
41	BQ	1645	U
41	BQ	1658	G
41	BQ	1677	G
41	BQ	1683	A
41	BQ	1687	U
41	BQ	1688	U
41	BQ	1696	A
41	BQ	1704	A
41	BQ	1705	U
41	BQ	1715	A
41	BQ	1716	U
41	BQ	1717	U
41	BQ	1722	U
41	BQ	1724	U
41	BQ	1725	C
41	BQ	1729	A
41	BQ	1730	G
41	BQ	1750	A
41	BQ	1751	G

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Mol	Chain	Res	Type
41	BQ	1756	C
41	BQ	1760	A
41	BQ	1765	U
41	BQ	1766	G
41	BQ	1770	G
41	BQ	1775	G
41	BQ	1780	G
41	BQ	1788	C
41	BQ	1796	G
41	BQ	1797	A
41	BQ	1814	A
41	BQ	1816	A
41	BQ	1817	G
41	BQ	1819	U
41	BQ	1820	U
41	BQ	1821	U
41	BQ	1822	C
41	BQ	1839	A
41	BQ	1840	U
41	BQ	1841	A
41	BQ	1842	A
41	BQ	1846	C
41	BQ	1849	C
41	BQ	1850	A
41	BQ	1866	C
41	BQ	1867	A
41	BQ	1874	A
41	BQ	1880	U
41	BQ	1881	A
41	BQ	1893	A
41	BQ	1897	G
41	BQ	1906	G
41	BQ	1908	A
41	BQ	1930	A
41	BQ	1935	G
41	BQ	1943	C
41	BQ	1952	G
41	BQ	1953	G
41	BQ	1954	G
41	BQ	1956	A
41	BQ	1957	G
41	BQ	1958	U

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Mol	Chain	Res	Type
41	BQ	1960	A
41	BQ	1961	G
41	BQ	1962	A
41	BQ	1963	G
41	BQ	1964	C
41	BQ	1969	G
41	BQ	1972	A
41	BQ	1973	G
41	BQ	1976	G
41	BQ	1981	G
41	BQ	1984	C
41	BQ	1986	U
41	BQ	1988	C
41	BQ	1989	U
41	BQ	1992	U
41	BQ	1994	G
41	BQ	1998	G
41	BQ	2001	U
41	BQ	2006	G
41	BQ	2010	U
41	BQ	2013	C
41	BQ	2017	G
41	BQ	2020	A
41	BQ	2022	G
41	BQ	2032	U
41	BQ	2035	G
41	BQ	2039	C
41	BQ	2047	A
41	BQ	2048	G
41	BQ	2049	A
41	BQ	2050	C
41	BQ	2059	U
41	BQ	2081	U
41	BQ	2082	U
41	BQ	2087	C
41	BQ	2088	A
41	BQ	2089	A
41	BQ	2093	A
41	BQ	2101	C
41	BQ	2102	U
41	BQ	2111	G
41	BQ	2112	U

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Mol	Chain	Res	Type
41	BQ	2113	A
41	BQ	2121	G
41	BQ	2122	G
41	BQ	2131	A
41	BQ	2139	A
41	BQ	2149	A
41	BQ	2158	A
41	BQ	2169	G
41	BQ	2170	U
41	BQ	2187	G
41	BQ	2188	A
41	BQ	2201	G
41	BQ	2205	U
41	BQ	2206	G
41	BQ	2207	A
41	BQ	2209	U
41	BQ	2223	A
41	BQ	2232	A
41	BQ	2244	A
41	BQ	2249	G
41	BQ	2250	G
41	BQ	2252	A
41	BQ	2256	A
41	BQ	2262	A
41	BQ	2272	G
41	BQ	2273	G
41	BQ	2274	U
41	BQ	2279	A
41	BQ	2280	A
41	BQ	2281	A
41	BQ	2282	U
41	BQ	2284	C
41	BQ	2285	C
41	BQ	2288	G
41	BQ	2299	A
41	BQ	2306	C
41	BQ	2307	G
41	BQ	2308	C
41	BQ	2309	A
41	BQ	2310	U
41	BQ	2313	A
41	BQ	2314	U

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Mol	Chain	Res	Type
41	BQ	2315	G
41	BQ	2335	G
41	BQ	2347	U
41	BQ	2364	G
41	BQ	2372	A
41	BQ	2373	A
41	BQ	2374	C
41	BQ	2375	G
41	BQ	2385	G
41	BQ	2388	U
41	BQ	2393	G
41	BQ	2394	G
41	BQ	2397	A
41	BQ	2402	A
41	BQ	2403	G
41	BQ	2404	A
41	BQ	2411	U
41	BQ	2412	G
41	BQ	2419	A
41	BQ	2422	C
41	BQ	2434	U
41	BQ	2435	G
41	BQ	2437	G
41	BQ	2438	A
41	BQ	2439	A
41	BQ	2440	G
41	BQ	2446	U
41	BQ	2451	G
41	BQ	2452	G
41	BQ	2493	U
41	BQ	2496	C
41	BQ	2498	U
41	BQ	2501	U
41	BQ	2502	A
41	BQ	2503	G
41	BQ	2507	C
41	BQ	2514	U
41	BQ	2515	A
41	BQ	2522	G
41	BQ	2523	A
41	BQ	2524	A
41	BQ	2525	G

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Mol	Chain	Res	Type
41	BQ	2526	C
41	BQ	2531	C
41	BQ	2532	U
41	BQ	2537	U
41	BQ	2538	U
41	BQ	2539	C
41	BQ	2540	A
41	BQ	2541	U
41	BQ	2542	U
41	BQ	2543	U
41	BQ	2546	C
41	BQ	2549	G
41	BQ	2552	C
41	BQ	2554	A
41	BQ	2561	A
41	BQ	2569	A
41	BQ	2570	U
41	BQ	2571	U
41	BQ	2572	C
41	BQ	2573	G
41	BQ	2576	G
41	BQ	2585	G
41	BQ	2589	G
41	BQ	2593	A
41	BQ	2594	C
41	BQ	2595	A
41	BQ	2606	G
41	BQ	2607	G
41	BQ	2614	G
41	BQ	2626	A
41	BQ	2629	U
41	BQ	2636	A
41	BQ	2648	G
41	BQ	2652	U
41	BQ	2656	A
41	BQ	2672	G
41	BQ	2674	A
41	BQ	2677	G
41	BQ	2689	A
41	BQ	2691	A
41	BQ	2694	A
41	BQ	2696	A

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Mol	Chain	Res	Type
41	BQ	2703	A
41	BQ	2704	A
41	BQ	2714	G
41	BQ	2719	U
41	BQ	2728	G
41	BQ	2748	A
41	BQ	2749	G
41	BQ	2752	U
41	BQ	2753	G
41	BQ	2755	C
41	BQ	2777	G
41	BQ	2778	G
41	BQ	2796	G
41	BQ	2800	G
41	BQ	2801	A
41	BQ	2802	A
41	BQ	2803	A
41	BQ	2804	A
41	BQ	2805	G
41	BQ	2810	C
41	BQ	2817	A
41	BQ	2818	U
41	BQ	2821	C
41	BQ	2838	A
41	BQ	2842	U
41	BQ	2844	C
41	BQ	2845	A
41	BQ	2847	A
41	BQ	2849	C
41	BQ	2856	G
41	BQ	2861	U
41	BQ	2867	C
41	BQ	2871	G
41	BQ	2872	A
41	BQ	2873	U
41	BQ	2875	U
41	BQ	2876	C
41	BQ	2887	A
41	BQ	2894	C
41	BQ	2899	C
41	BQ	2910	A
41	BQ	2916	U

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Mol	Chain	Res	Type
41	BQ	2918	G
41	BQ	2923	U
41	BQ	2928	C
41	BQ	2933	A
41	BQ	2935	U
41	BQ	2936	A
41	BQ	2941	A
41	BQ	2942	C
41	BQ	2947	G
41	BQ	2954	U
41	BQ	2955	U
41	BQ	2957	G
41	BQ	2971	A
41	BQ	2983	C
41	BQ	2990	G
41	BQ	2996	U
41	BQ	2997	G
41	BQ	3003	G
41	BQ	3012	A
41	BQ	3030	G
41	BQ	3055	U
41	BQ	3056	U
41	BQ	3058	U
41	BQ	3059	G
41	BQ	3078	U
41	BQ	3079	U
41	BQ	3080	G
41	BQ	3086	A
41	BQ	3092	C
41	BQ	3101	G
41	BQ	3104	U
41	BQ	3115	C
41	BQ	3116	G
41	BQ	3118	C
41	BQ	3119	U
41	BQ	3122	A
41	BQ	3129	A
41	BQ	3130	A
41	BQ	3131	U
41	BQ	3142	A
41	BQ	3143	C
41	BQ	3151	U

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Mol	Chain	Res	Type
41	BQ	3154	C
41	BQ	3155	U
41	BQ	3156	U
41	BQ	3157	U
41	BQ	3158	G
41	BQ	3165	A
41	BQ	3170	A
41	BQ	3172	A
41	BQ	3173	G
41	BQ	3174	A
41	BQ	3175	U
41	BQ	3176	G
41	BQ	3180	A
41	BQ	3181	C
41	BQ	3187	A
41	BQ	3196	U
41	BQ	3199	G
41	BQ	3207	U
41	BQ	3209	A
41	BQ	3210	A
41	BQ	3216	G
41	BQ	3217	C
41	BQ	3218	A
41	BQ	3219	G
41	BQ	3222	U
41	BQ	3229	G
41	BQ	3243	A
41	BQ	3244	A
41	BQ	3245	A
41	BQ	3247	G
41	BQ	3259	U
41	BQ	3260	G
41	BQ	3263	G
41	BQ	3270	U
41	BQ	3272	C
41	BQ	3273	A
41	BQ	3276	G
41	BQ	3277	U
41	BQ	3281	U
41	BQ	3286	G
41	BQ	3287	U
41	BQ	3288	G

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Mol	Chain	Res	Type
41	BQ	3289	G
41	BQ	3294	A
41	BQ	3295	A
41	BQ	3304	U
41	BQ	3313	U
41	BQ	3316	A
41	BQ	3318	G
41	BQ	3319	U
41	BQ	3320	A
41	BQ	3334	U
41	BQ	3341	U
41	BQ	3345	G
41	BQ	3346	U
41	BQ	3347	A
41	BQ	3351	U
41	BQ	3352	U
41	BQ	3353	G
41	BQ	3354	U
41	BQ	3355	U
41	BQ	3356	G
41	BQ	3368	U
41	BQ	3369	G
41	BQ	3378	C
41	BQ	3381	U
41	BQ	3382	U
41	BQ	3386	G
41	BQ	3389	U
41	BQ	3390	G
41	BQ	3396	U
42	BR	7	G
42	BR	10	C
42	BR	17	A
42	BR	22	A
42	BR	35	C
42	BR	52	G
42	BR	53	U
42	BR	54	U
42	BR	65	G
42	BR	74	C
42	BR	76	A
42	BR	99	G
42	BR	102	A

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Mol	Chain	Res	Type
42	BR	112	G
42	BR	121	U
43	BS	16	G
43	BS	25	G
43	BS	34	U
43	BS	35	C
43	BS	38	U
43	BS	59	A
43	BS	62	C
43	BS	63	G
43	BS	80	A
43	BS	81	U
43	BS	82	U
43	BS	83	C
43	BS	84	C
43	BS	85	G
43	BS	86	U
43	BS	87	G
43	BS	90	U
43	BS	95	G
43	BS	97	A
43	BS	99	C
43	BS	104	A
43	BS	106	C
43	BS	111	A
43	BS	112	U
43	BS	113	U
43	BS	125	U
43	BS	126	A
43	BS	138	A
43	BS	148	G
43	BS	152	G
43	BS	157	U
43	BS	158	U

All (110) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
33	2	68	A
33	2	77	U
33	2	139	C
33	2	141	U

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Mol	Chain	Res	Type
33	2	215	A
33	2	224	C
33	2	237	C
33	2	278	U
33	2	313	U
33	2	322	G
33	2	352	A
33	2	387	A
33	2	400	A
33	2	447	U
33	2	511	A
33	2	518	A
33	2	539	G
33	2	541	A
33	2	555	A
33	2	609	U
33	2	639	U
33	2	640	U
33	2	705	U
33	2	711	U
33	2	740	A
33	2	755	A
33	2	803	A
33	2	819	G
33	2	912	U
33	2	928	U
33	2	987	G
33	2	1023	A
33	2	1207	C
33	2	1226	A
33	2	1245	G
33	2	1251	U
33	2	1256	A
33	2	1273	G
33	2	1274	C
33	2	1314	U
33	2	1344	A
33	2	1348	A
33	2	1382	A
33	2	1399	C
33	2	1430	U
33	2	1471	A

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Mol	Chain	Res	Type
33	2	1556	A
33	2	1557	U
33	2	1573	A
33	2	1584	G
33	2	1633	A
33	2	1636	C
33	2	1700	C
41	BQ	13	A
41	BQ	282	G
41	BQ	439	C
41	BQ	637	C
41	BQ	763	G
41	BQ	849	C
41	BQ	873	C
41	BQ	896	A
41	BQ	916	G
41	BQ	993	G
41	BQ	1064	A
41	BQ	1097	G
41	BQ	1271	A
41	BQ	1307	G
41	BQ	1355	A
41	BQ	1562	C
41	BQ	1572	U
41	BQ	1582	C
41	BQ	1716	U
41	BQ	1729	A
41	BQ	1815	U
41	BQ	1820	U
41	BQ	1952	G
41	BQ	1953	G
41	BQ	1956	A
41	BQ	1957	G
41	BQ	1959	G
41	BQ	1961	G
41	BQ	1962	A
41	BQ	1963	G
41	BQ	1964	C
41	BQ	2086	A
41	BQ	2112	U
41	BQ	2231	C
41	BQ	2445	A

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Mol	Chain	Res	Type
41	BQ	2500	A
41	BQ	2501	U
41	BQ	2502	A
41	BQ	2513	U
41	BQ	2514	U
41	BQ	2525	G
41	BQ	2537	U
41	BQ	2538	U
41	BQ	2541	U
41	BQ	3055	U
41	BQ	3078	U
41	BQ	3121	U
41	BQ	3218	A
41	BQ	3228	C
41	BQ	3269	U
41	BQ	3275	U
41	BQ	3319	U
41	BQ	3350	C
42	BR	52	G
43	BS	82	U
43	BS	85	G
43	BS	125	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 7 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

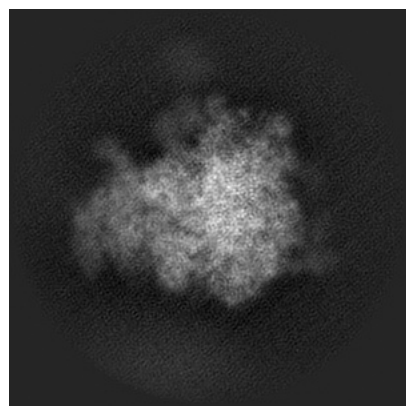
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16182. These allow visual inspection of the internal detail of the map and identification of artifacts.

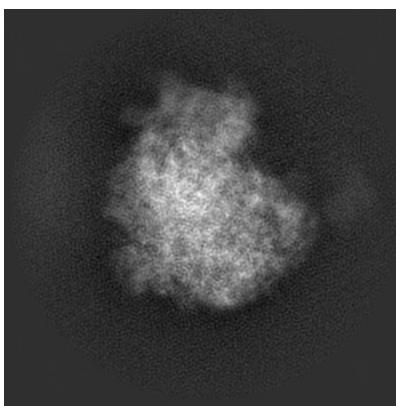
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

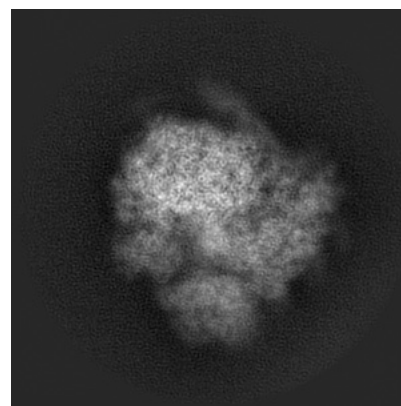
6.1.1 Primary map



X

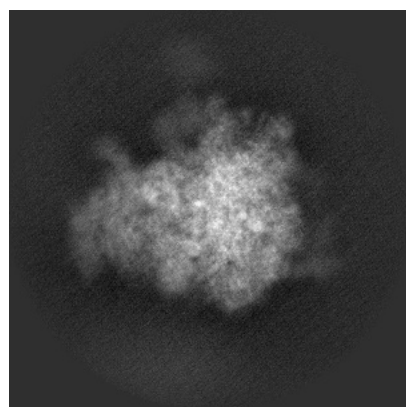


Y

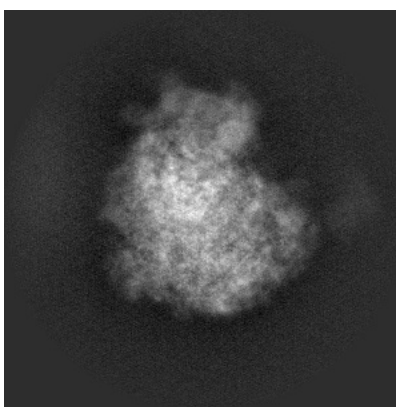


Z

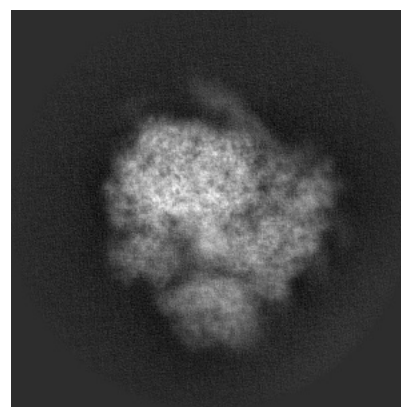
6.1.2 Raw map



X



Y

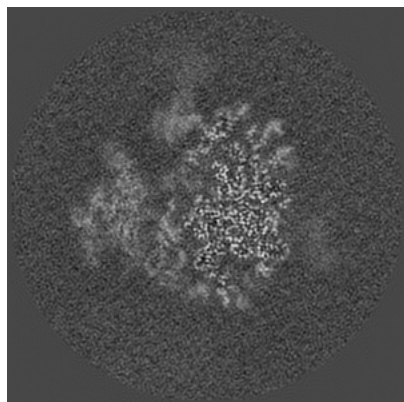


Z

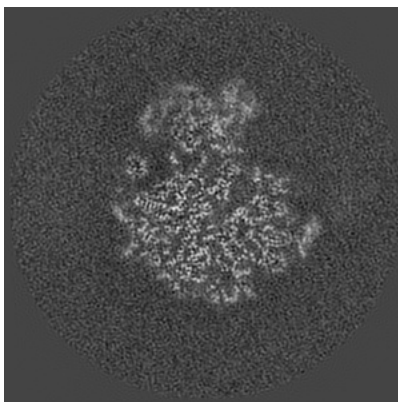
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

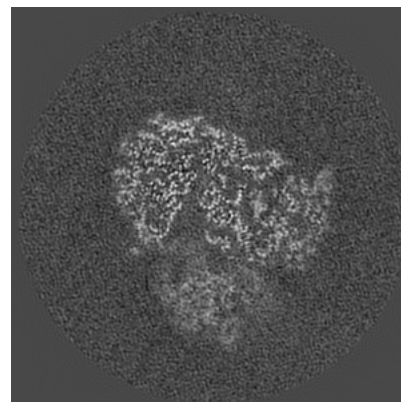
6.2.1 Primary map



X Index: 210

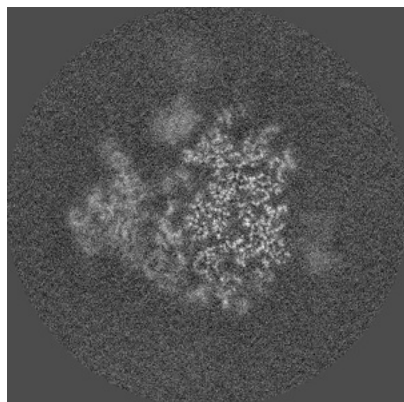


Y Index: 210

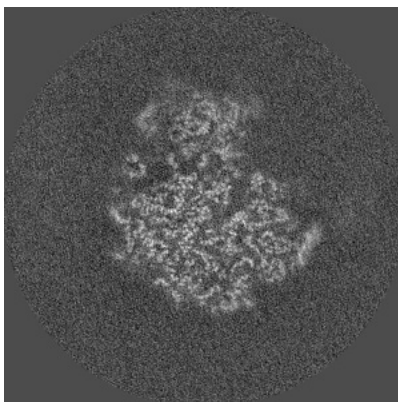


Z Index: 210

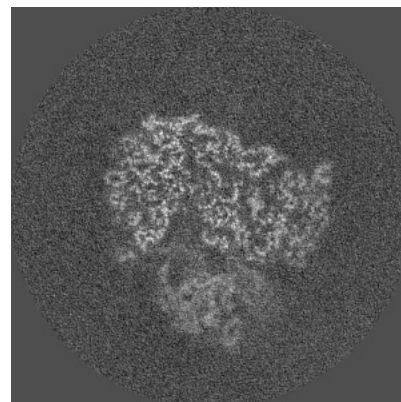
6.2.2 Raw map



X Index: 210



Y Index: 210

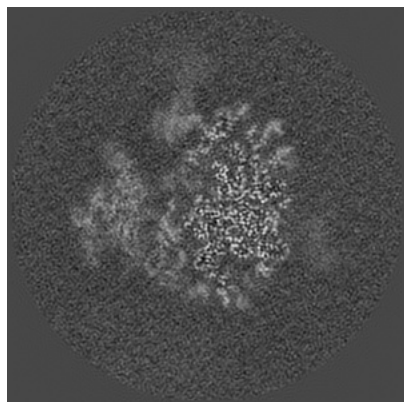


Z Index: 210

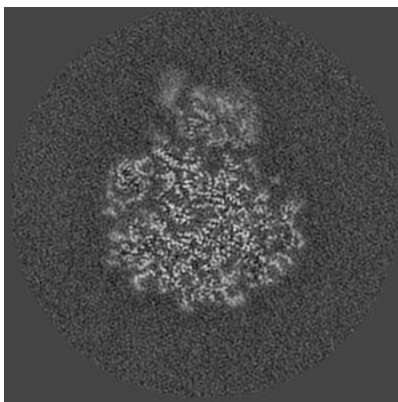
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

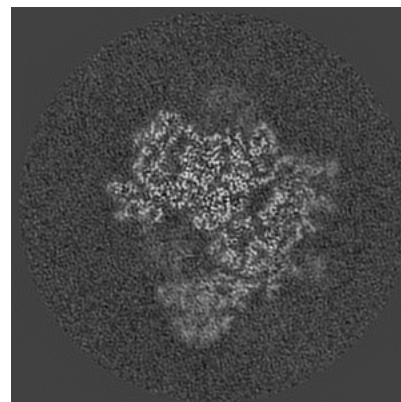
6.3.1 Primary map



X Index: 210

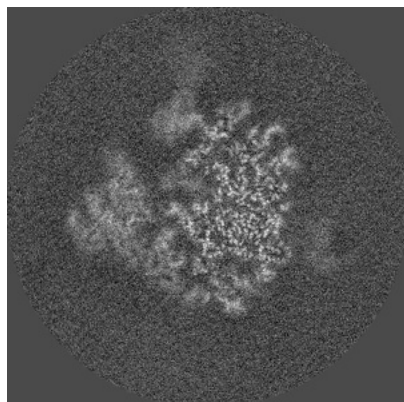


Y Index: 234

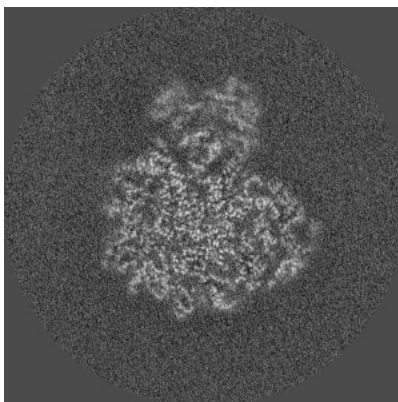


Z Index: 190

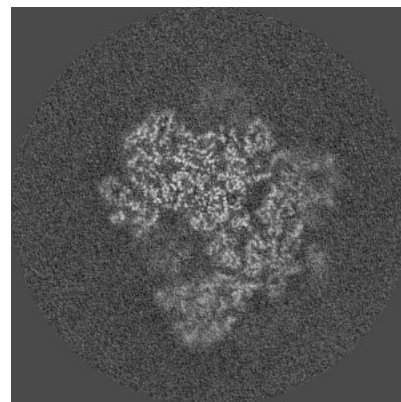
6.3.2 Raw map



X Index: 204



Y Index: 226

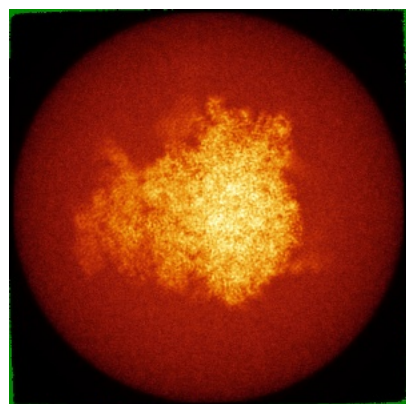


Z Index: 188

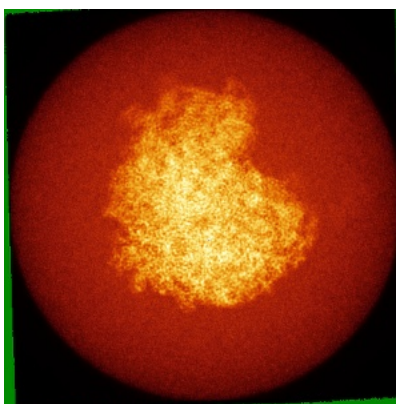
The images above show the largest variance slices of the map in three orthogonal directions.

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

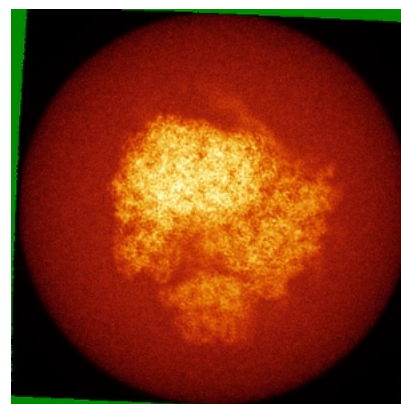
6.4.1 Primary map



X

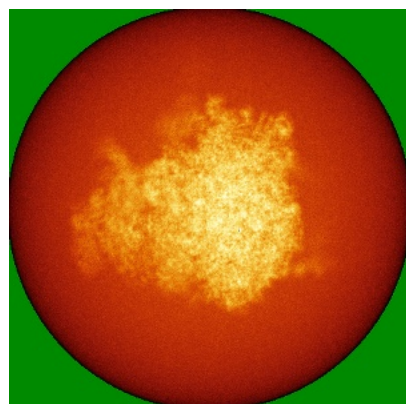


Y

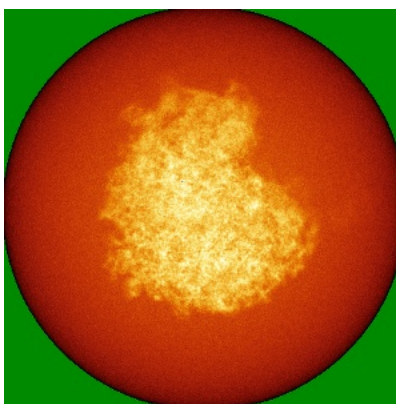


Z

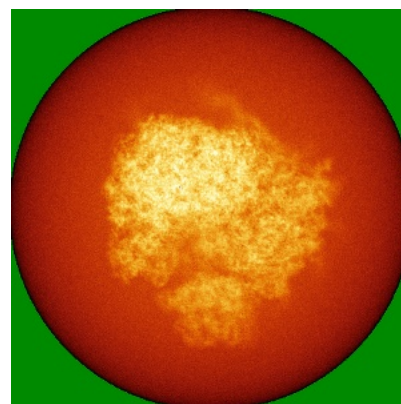
6.4.2 Raw map



X



Y

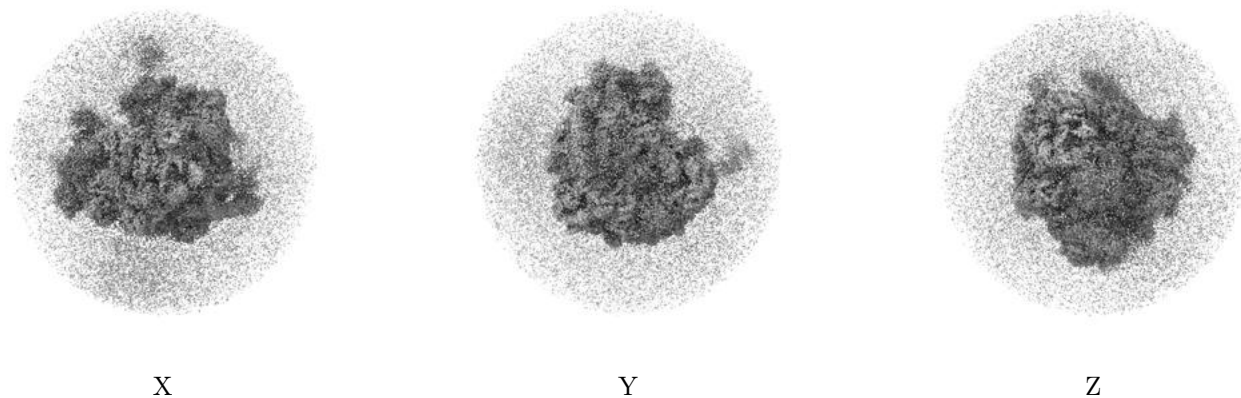


Z

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

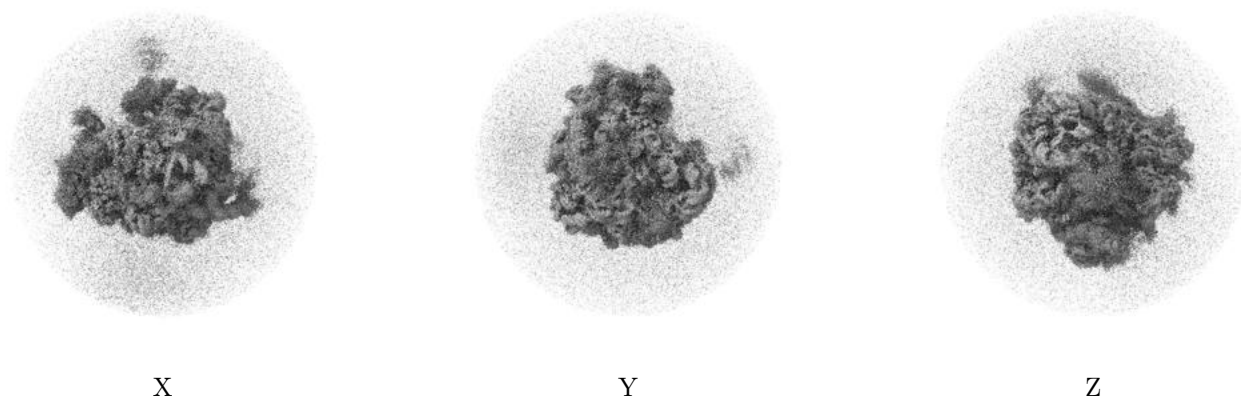
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

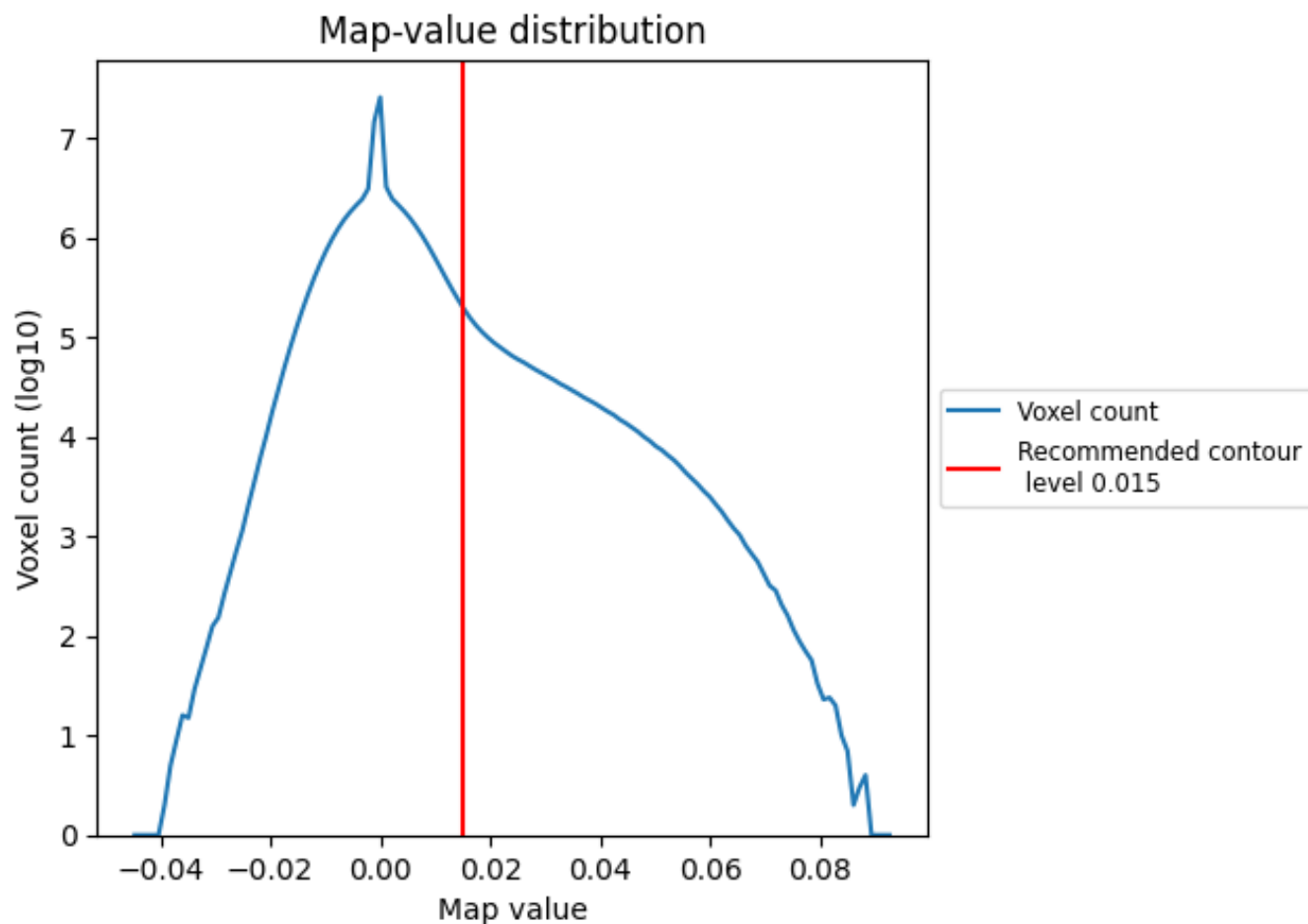
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

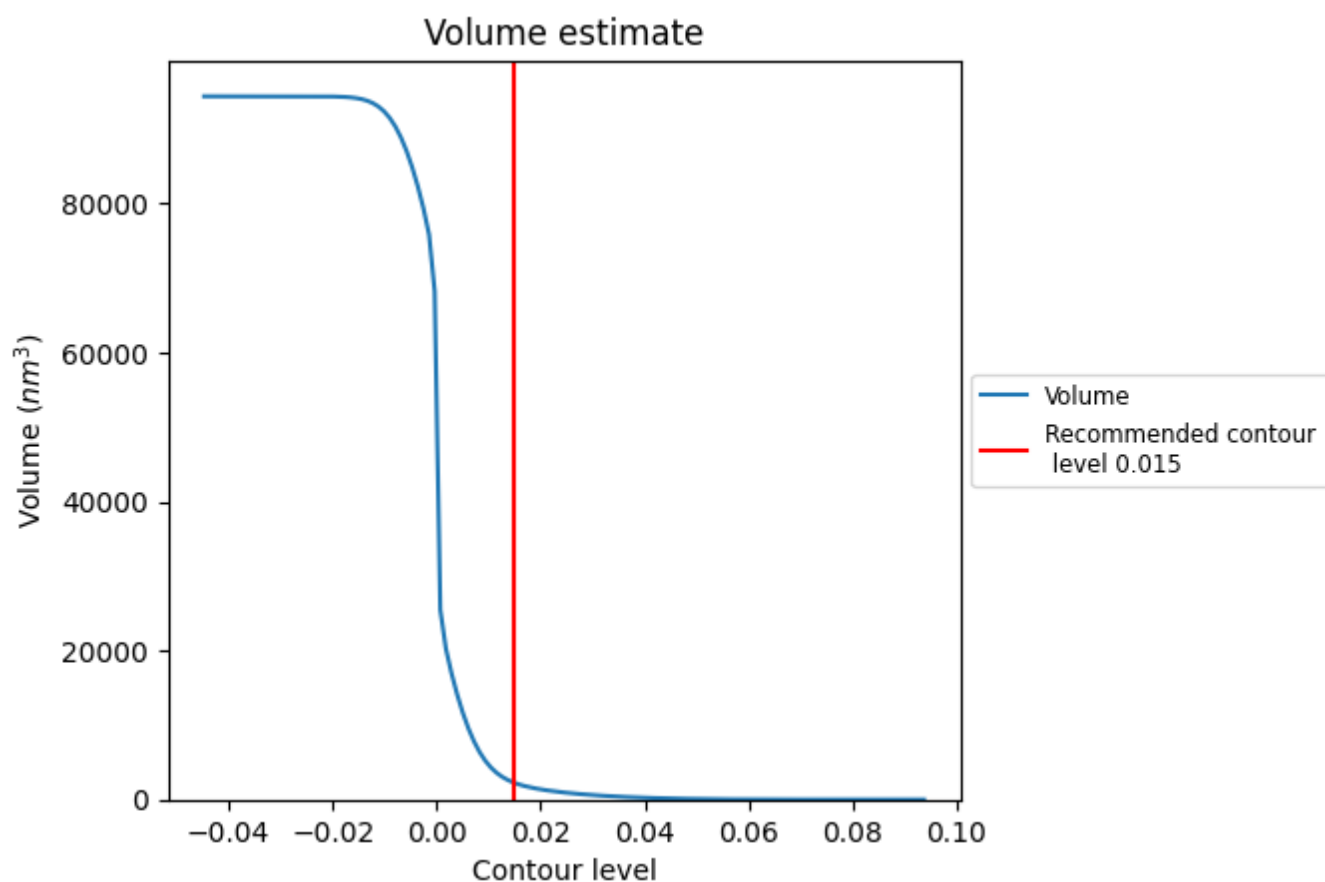
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

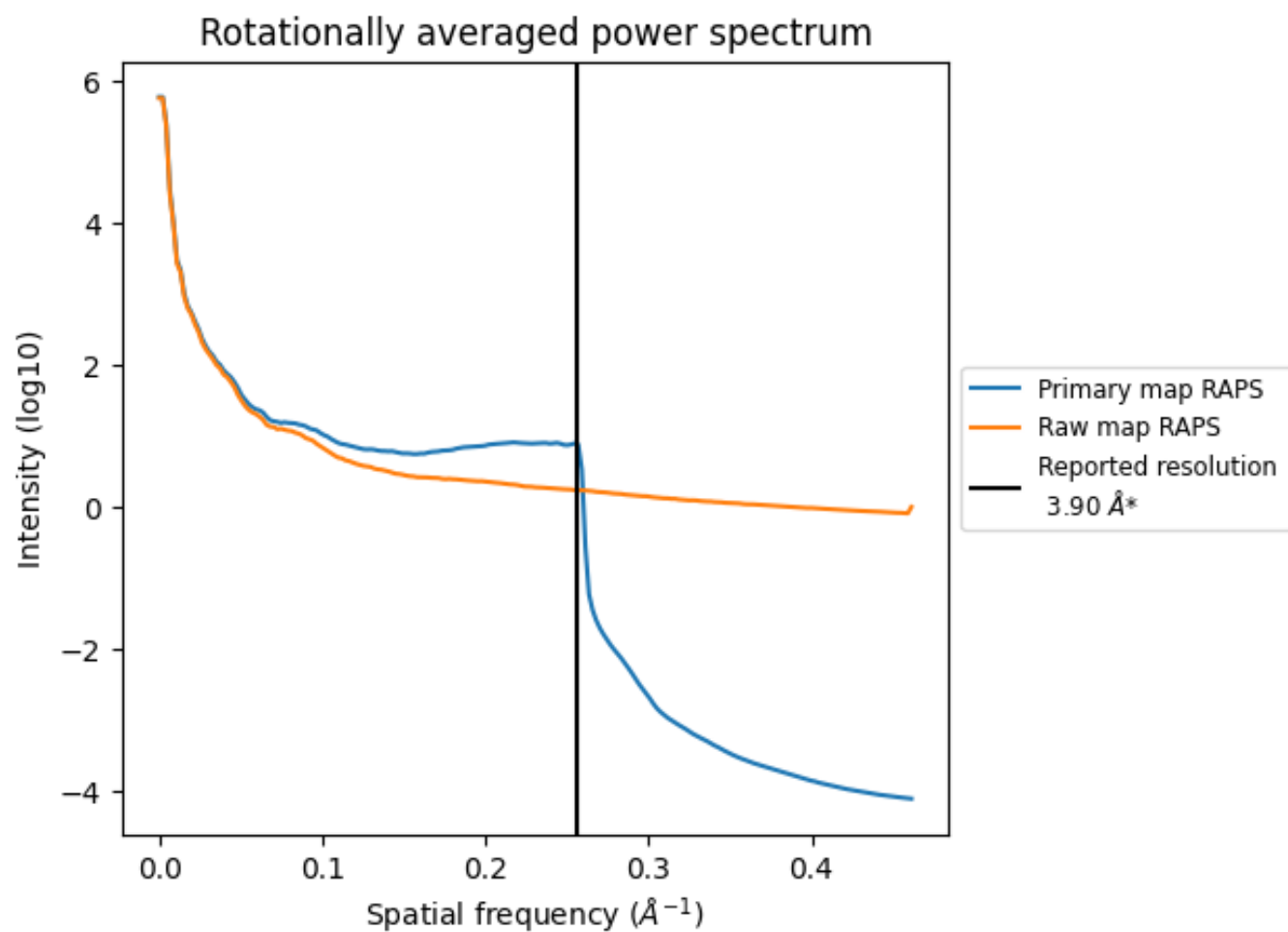
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2238 nm³; this corresponds to an approximate mass of 2022 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 ⓘ

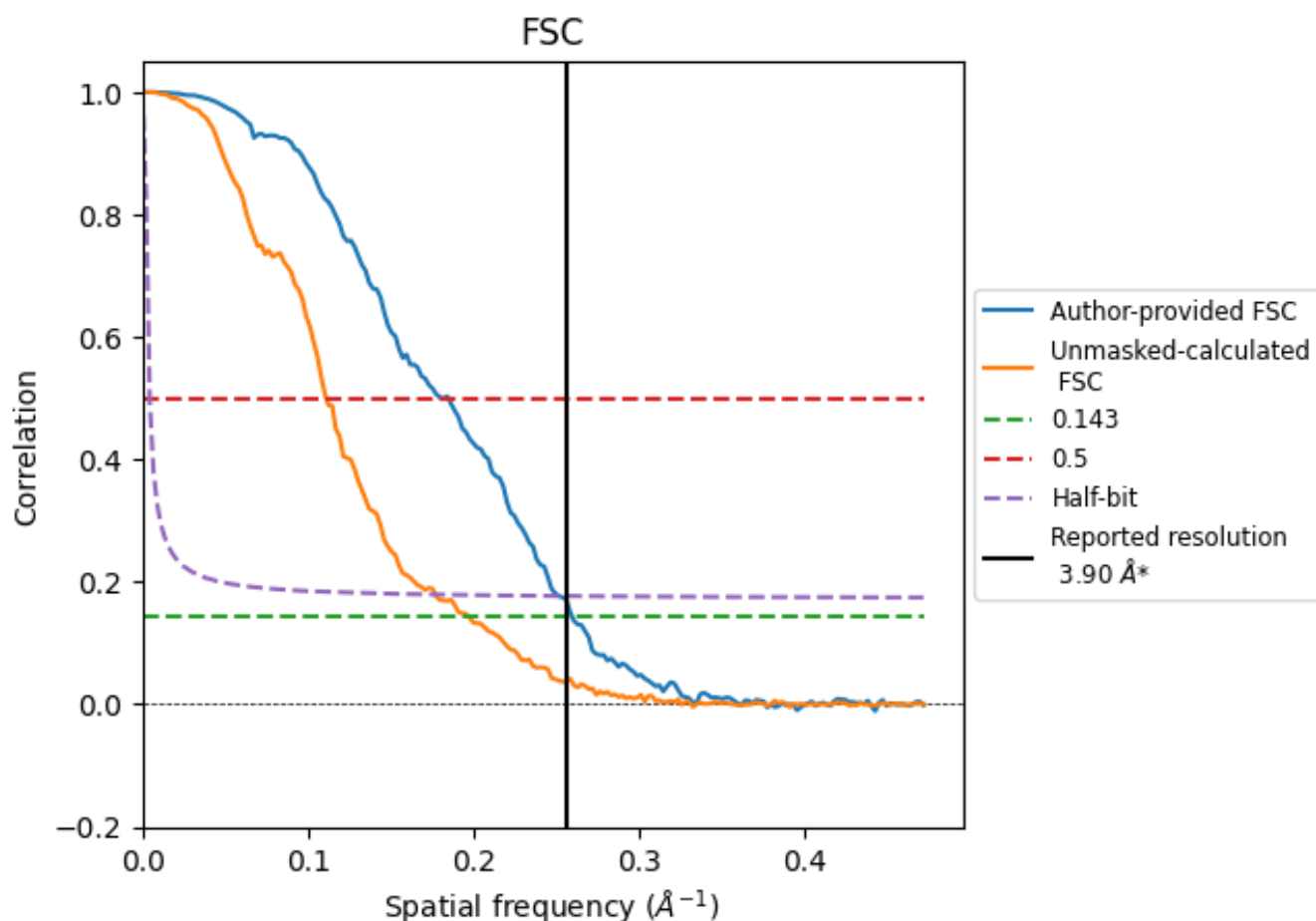


*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

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 0.256 Å⁻¹

8.2 Resolution estimates [i](#)

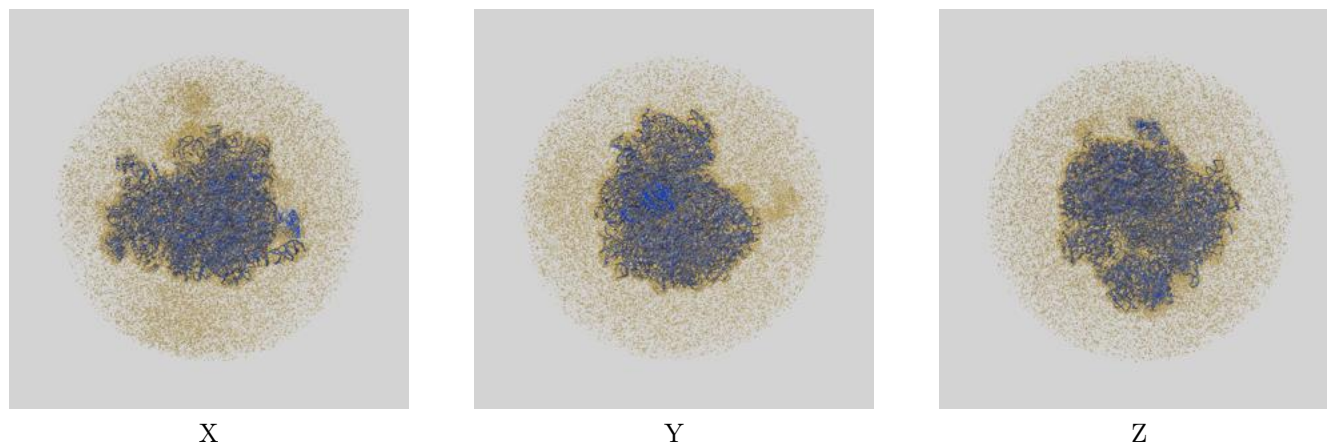
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.85	5.41	3.97
Unmasked-calculated*	5.07	9.00	5.65

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.07 differs from the reported value 3.9 by more than 10 %

9 Map-model fit [i](#)

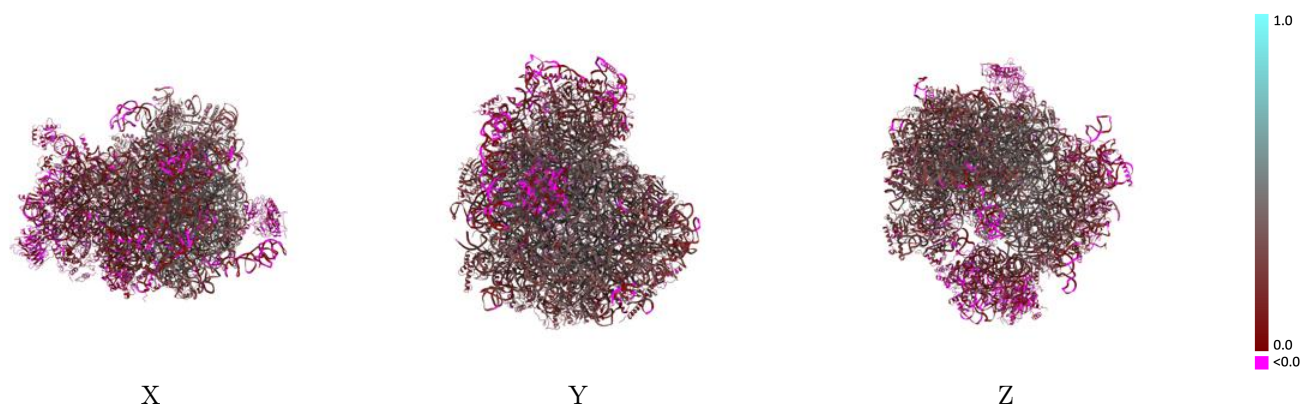
This section contains information regarding the fit between EMDB map EMD-16182 and PDB model 8BQD. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

9.1 Map-model overlay [i](#)



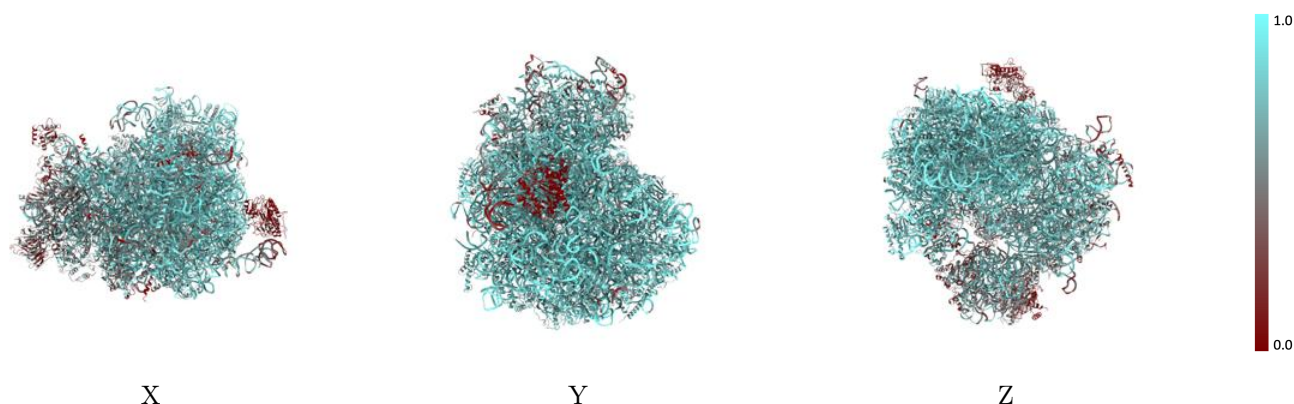
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



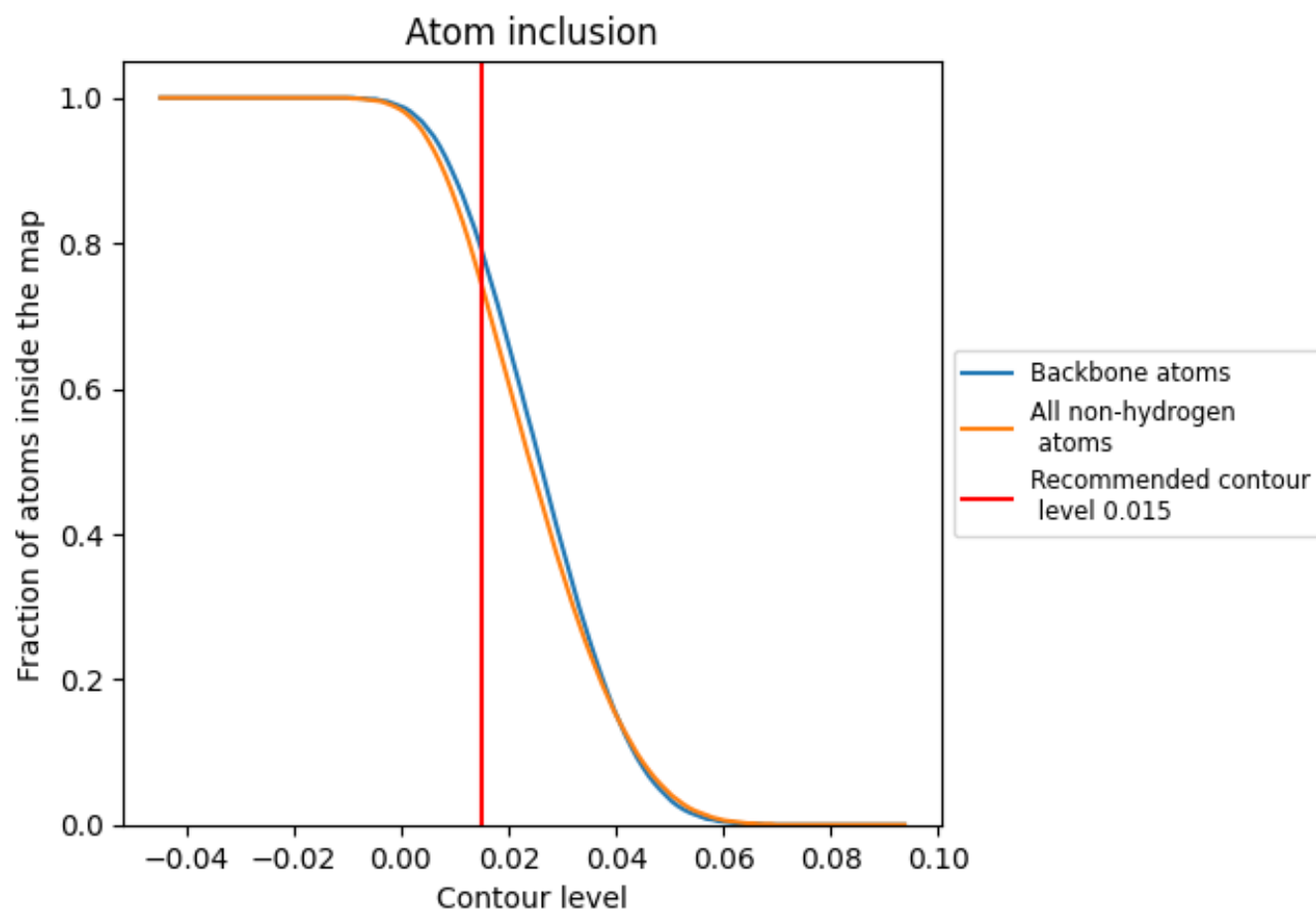
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 74% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7440	 0.2600
2	 0.7670	 0.2040
A	 0.4170	 0.1210
AA	 0.7120	 0.2650
AB	 0.7440	 0.3750
AC	 0.7150	 0.2650
AD	 0.7370	 0.2810
AE	 0.5680	 0.2350
AF	 0.8550	 0.4080
AG	 0.6770	 0.2200
AH	 0.7650	 0.3430
AI	 0.7110	 0.3040
AJ	 0.7340	 0.2860
AK	 0.7790	 0.3130
AL	 0.7710	 0.3550
AM	 0.7430	 0.2710
AN	 0.7090	 0.2730
AO	 0.7580	 0.2840
AP	 0.7490	 0.3520
AQ	 0.7820	 0.3420
AR	 0.7830	 0.3310
AS	 0.6730	 0.2600
AT	 0.7390	 0.3600
AU	 0.7610	 0.3040
AV	 0.7460	 0.3250
AW	 0.7810	 0.3900
AX	 0.7820	 0.3600
AY	 0.7450	 0.3220
B	 0.3660	 0.0380
BA	 0.7810	 0.3370
BB	 0.7730	 0.3240
BC	 0.7510	 0.3530
BD	 0.6430	 0.2270
BE	 0.7550	 0.3080
BF	 0.7290	 0.3190



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Chain	Atom inclusion	Q-score
BG	 0.7710	 0.3430
BH	 0.7690	 0.3200
BI	 0.7250	 0.2450
BJ	 0.7730	 0.3330
BK	 0.7540	 0.3170
BL	 0.7580	 0.2960
BM	 0.7000	 0.2150
BN	 0.7480	 0.3660
BO	 0.7620	 0.3070
BP	 0.7530	 0.3070
BQ	 0.8710	 0.3260
BR	 0.8930	 0.2850
BS	 0.9070	 0.3440
BT	 0.1430	 0.0560
C	 0.4820	 0.1510
D	 0.2020	 0.0520
E	 0.4730	 0.1120
F	 0.4410	 0.0520
G	 0.4540	 0.0960
H	 0.4500	 0.0500
I	 0.4700	 0.0640
J	 0.4920	 0.0910
K	 0.3460	 0.0080
L	 0.3950	 0.0930
M	 0.5280	 0.1000
N	 0.4170	 0.0560
O	 0.3390	 0.0220
P	 0.5450	 0.1210
Q	 0.5020	 0.1420
R	 0.6180	 0.2140
S	 0.6130	 0.2080
T	 0.6090	 0.1620
U	 0.5260	 0.1190
V	 0.6910	 0.2410
W	 0.6420	 0.2120
X	 0.6620	 0.2750
Y	 0.6630	 0.2510
Z	 0.5330	 0.1600
a	 0.6130	 0.1810
b	 0.6300	 0.2330
c	 0.6750	 0.2970
d	 0.6280	 0.1720

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Chain	Atom inclusion	Q-score
e	 0.5840	 0.1750
f	 0.5510	 0.1600
g	 0.5570	 0.1940
x	 0.0510	 0.0080