



Full wwPDB EM Validation Report ⓘ

Jun 11, 2025 – 02:32 AM JST

PDB ID : 9J9H / pdb_00009j9h
EMDB ID : EMD-61272
Title : High-resolution cryo-EM structure of the Plasmodium falciparum 80S ribosome bound to RACK1 and E-tRNA
Authors : Yan, X.F.; Gao, Y.G.
Deposited on : 2024-08-22
Resolution : 2.45 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.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

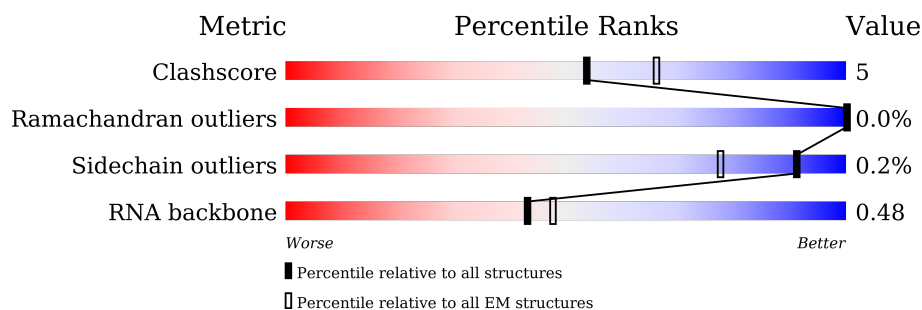
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.45 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	A	3788	
2	0	162	
3	q	306	
4	AQ	74	
5	B	119	
6	1	146	
7	r	195	

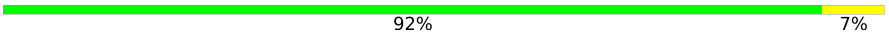




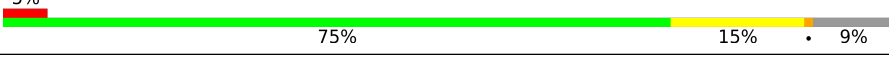

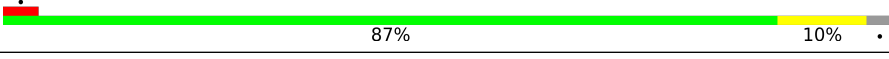
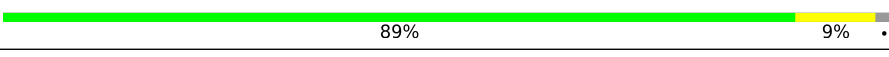


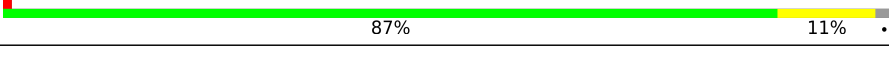
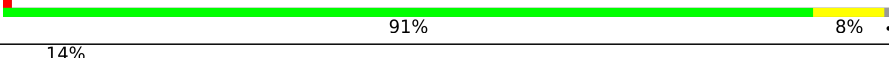
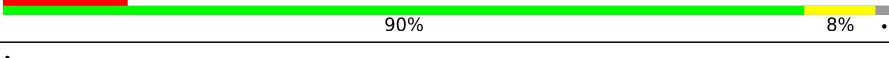

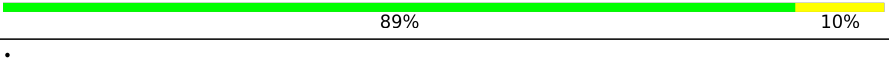



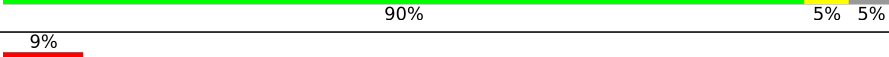
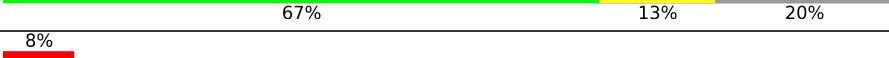
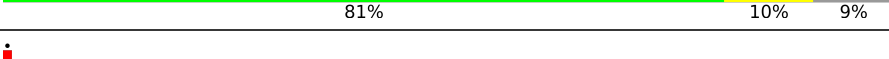

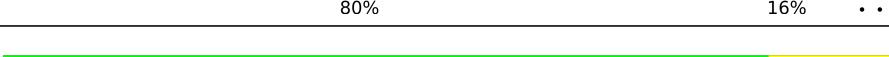

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Mol	Chain	Length	Quality of chain
8	AR	323	
9	C	159	
10	2	127	
11	s	194	
12	D	260	
13	3	124	
14	t	130	
15	E	386	
16	4	67	
17	u	218	
18	F	411	
19	5	257	
20	v	144	
21	G	173	
22	6	108	
23	w	118	
24	H	190	
25	7	120	
26	x	137	
27	I	221	
28	8	131	
29	y	151	
30	J	283	
31	9	140	
32	z	145	











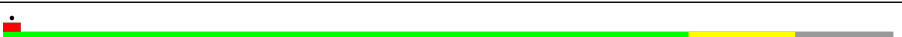


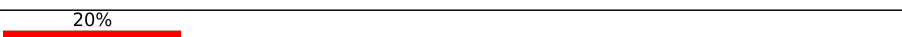
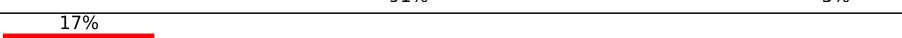
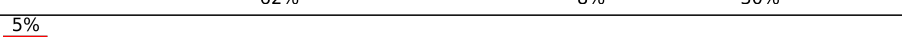

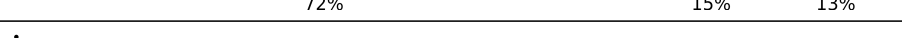
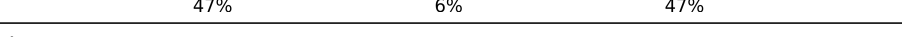
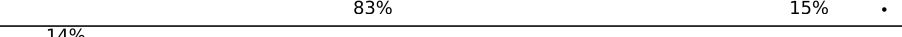



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Mol	Chain	Length	Quality of chain
33	K	202	
34	a	150	
35	AA	141	
36	L	215	
37	b	112	
38	AB	156	
39	M	139	
40	c	92	
41	AC	54	
42	N	165	
43	d	87	
44	AD	151	
45	O	148	
46	e	51	
47	AE	161	
48	P	205	
49	f	128	
50	AF	137	
51	Q	219	
52	g	39	
53	AG	145	
54	R	294	
55	h	96	
56	AH	170	
57	S	187	

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Mol	Chain	Length	Quality of chain
58	i	104	
59	AI	82	
60	T	182	
61	j	2092	
62	AJ	133	
63	U	184	
64	k	262	
65	AK	105	
66	V	161	
67	l	263	
68	AL	107	
69	W	203	
70	m	221	
71	AM	82	
72	X	139	
73	n	189	
74	AN	67	
75	Y	190	
76	o	261	
77	AO	58	
78	Z	126	
79	p	272	
80	AP	149	

2 Entry composition [i](#)

There are 82 unique types of molecules in this entry. The entry contains 200146 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3203	Total	C	N	O	P	0	0
			68120	30541	12090	22310	3179		

- Molecule 2 is a protein called 60S ribosomal protein L24, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	0	62	Total	C	N	O	S	0	0
			521	336	97	87	1		

- Molecule 3 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	q	213	Total	C	N	O	S	0	0
			1717	1087	329	295	6		

- Molecule 4 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AQ	74	Total	C	N	O	P	0	0
			1571	702	275	521	73		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	118	Total	C	N	O	P	0	0
			2525	1128	461	818	118		

- Molecule 6 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	1	145	Total	C	N	O	S	0	0
			1171	758	212	198	3		

- Molecule 7 is a protein called 40S ribosomal protein S5, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	r	189	Total	C	N	O	S	0	0
			1487	931	278	268	10		

- Molecule 8 is a protein called Receptor for activated c kinase.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AR	323	Total	C	N	O	S	0	0
			2509	1583	426	488	12		

- Molecule 9 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	152	Total	C	N	O	P	0	0
			3246	1454	594	1046	152		

- Molecule 10 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	2	121	Total	C	N	O	S	0	0
			960	607	173	177	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	s	188	Total	C	N	O	S	0	0
			1528	982	264	278	4		

- Molecule 12 is a protein called 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D	247	Total	C	N	O	S	0	0
			1866	1166	374	317	9		

- Molecule 13 is a protein called 60S ribosomal protein L35, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	3	122	Total	C	N	O	S	0	0
			1022	652	200	168	2		

- Molecule 14 is a protein called 40S ribosomal protein S15A, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	t	129	Total	C	N	O	S	0	0
			1037	665	189	178	5		

- Molecule 15 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	E	380	Total	C	N	O	S	0	0
			3061	1948	575	521	17		

- Molecule 16 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	4	66	Total	C	N	O	S	0	0
			555	347	116	90	2		

- Molecule 17 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	u	168	Total	C	N	O	S	0	0
			1352	854	257	237	4		

- Molecule 18 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	F	390	Total	C	N	O	S	0	0
			3094	1962	594	527	11		

- Molecule 19 is a protein called 60S ribosomal protein L7, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	5	223	Total	C	N	O	S	0	0
			1879	1211	357	306	5		

- Molecule 20 is a protein called 40S ribosomal protein S16, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	v	138	Total	C	N	O	S	0	0
			1098	704	200	193	1		

- Molecule 21 is a protein called 60S ribosomal protein L11a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	G	165	Total	C	N	O	S	0	0
			1352	858	253	235	6		

- Molecule 22 is a protein called 60S ribosomal protein L30e, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	6	98	Total	C	N	O	S	0	0
			740	462	132	139	7		

- Molecule 23 is a protein called 40S ribosomal protein S20e, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	w	102	Total	C	N	O	S	0	0
			813	508	148	152	5		

- Molecule 24 is a protein called 60S ribosomal protein L6, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	H	186	Total	C	N	O	S	0	0
			1468	943	262	256	7		

- Molecule 25 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	7	97	Total	C	N	O	S	0	0
			802	514	153	130	5		

- Molecule 26 is a protein called 40S ribosomal protein S10, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	x	98	Total	C	N	O	S	0	0
			839	555	142	140	2		

- Molecule 27 is a protein called 60S ribosomal protein L6, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	I	207	Total	C	N	O	S	0	0
			1684	1096	298	285	5		

- Molecule 28 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	8	125	Total	C	N	O	S	0	0
			1036	660	206	163	7		

- Molecule 29 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	y	133	Total	C	N	O	S	0	0
			998	619	192	184	3		

- Molecule 30 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	J	229	Total	C	N	O	S	0	0
			1873	1210	337	319	7		

- Molecule 31 is a protein called 60S ribosomal protein L35ae, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	9	105	Total	C	N	O	S	0	0
			858	550	166	139	3		

- Molecule 32 is a protein called 40S ribosomal protein S23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	z	144	Total	C	N	O	S	0	0
			1129	712	222	193	2		

- Molecule 33 is a protein called 60S ribosomal protein L13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	K	201	Total	C	N	O	S	0	0
			1666	1070	311	277	8		

- Molecule 34 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	a	106	Total	C	N	O	S	0	0
			858	530	184	138	6		

- Molecule 35 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AA	117	Total	C	N	O	S	0	0
			903	573	152	174	4		

- Molecule 36 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	L	211	Total	C	N	O	S	0	0
			1761	1119	349	290	3		

- Molecule 37 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	b	95	Total	C	N	O	S	0	0
			756	477	150	129			

- Molecule 38 is a protein called 40S ribosomal protein S18, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	AB	142	Total	C	N	O	S	0	0
			1161	726	228	203	4		

- Molecule 39 is a protein called 60S ribosomal protein L23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	M	132	Total	C	N	O	S	0	0
			996	631	179	178	8		

- Molecule 40 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	c	89	Total	C	N	O	S	0	0
			705	439	150	111	5		

- Molecule 41 is a protein called 40S ribosomal protein S29, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AC	53	Total	C	N	O	S	0	0
			438	273	91	69	5		

- Molecule 42 is a protein called 60S ribosomal protein L14, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	N	146	Total	C	N	O	S	0	0
			1203	782	211	204	6		

- Molecule 43 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	d	76	Total	C	N	O	S	0	0
			636	415	114	105	2		

- Molecule 44 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AD	148	Total	C	N	O	S	0	0
			1196	766	219	208	3		

- Molecule 45 is a protein called 60S ribosomal protein L27a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	O	147	Total	C	N	O	S	0	0
			1172	747	232	189	4		

- Molecule 46 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	e	50	Total	C	N	O	S	0	0
			452	284	104	63	1		

- Molecule 47 is a protein called 40S ribosomal protein S11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	AE	147	Total	C	N	O	S	0	0
			1214	778	228	201	7		

- Molecule 48 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	P	204	Total	C	N	O	S	0	0
			1697	1075	351	267	4		

- Molecule 49 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	f	51	Total	C	N	O	S	0	0
			413	255	87	66	5		

- Molecule 50 is a protein called 40S ribosomal protein S17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	AF	118	Total	C	N	O	S	0	0
			963	612	179	168	4		

- Molecule 51 is a protein called 60S ribosomal protein L10, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Q	192	Total	C	N	O	S	0	0
			1567	997	297	264	9		

- Molecule 52 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	g	37	Total	C	N	O	S	0	0
			342	210	86	44	2		

- Molecule 53 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	AG	116	Total	C	N	O	S	0	0
			945	602	175	164	4		

- Molecule 54 is a protein called 60S ribosomal protein L5, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	R	267	Total	C	N	O	S	0	0
			2171	1376	406	383	6		

- Molecule 55 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	h	85	Total	C	N	O	S	0	0
			658	417	127	107	7		

- Molecule 56 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	AH	165	Total	C	N	O	S	0	0
			1353	866	253	232	2		

- Molecule 57 is a protein called 60S ribosomal protein L18-2, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	S	186	Total	C	N	O	S	0	0
			1502	958	299	240	5		

- Molecule 58 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	i	96	Total	C	N	O	S	0	0
			787	496	154	128	9		

- Molecule 59 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AI	81	Total	C	N	O	S	0	0
			631	395	113	118	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	T	181	Total	C	N	O	S	0	0
			1505	949	308	244	4		

- Molecule 61 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	j	1644	Total	C	N	O	P	0	0
			35005	15689	6240	11443	1633		

- Molecule 62 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AJ	121	Total	C	N	O	S	0	0
			994	637	190	165	2		

- Molecule 63 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	U	180	Total	C	N	O	S	0	0
			1496	946	289	254	7		

- Molecule 64 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	k	210	Total	C	N	O	S	0	0
			1713	1097	301	303	12		

- Molecule 65 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AK	72	Total	C	N	O	S	0	0
			565	361	100	101	3		

- Molecule 66 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	V	156	Total	C	N	O	S	0	0
			1279	816	242	215	6		

- Molecule 67 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	l	195	Total	C	N	O	S	0	0
			1538	990	266	273	9		

- Molecule 68 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	AL	95	Total	C	N	O	S	0	0
			781	478	169	128	6		

- Molecule 69 is a protein called 60S ribosomal protein L17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	W	172	Total	C	N	O	S	0	0
			1336	836	270	223	7		

- Molecule 70 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	m	213	Total	C	N	O	S	0	0
			1667	1047	315	298	7		

- Molecule 71 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	AM	79	Total	C	N	O	S	0	0
			610	384	105	112	9		

- Molecule 72 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	X	97	Total	C	N	O	S	0	0
			824	548	135	139	2		

- Molecule 73 is a protein called 40S ribosomal protein S9, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	n	185	Total	C	N	O	S	0	0
			1528	971	295	260	2		

- Molecule 74 is a protein called 40S ribosomal protein S28e, putative.

Mol	Chain	Residues	Atoms				AltConf	Trace
74	AN	58	Total	C	N	O	0	0
			451	282	90	79		

- Molecule 75 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Y	101	Total	C	N	O	S	0	0
			796	502	144	144	6		

- Molecule 76 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	o	257	Total	C	N	O	S	0	0
			2061	1320	377	356	8		

- Molecule 77 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms				AltConf	Trace
77	AO	43	Total	C	N	O	0	0
			345	213	75	57		

- Molecule 78 is a protein called 60S ribosomal protein L26, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Z	122	Total	C	N	O	S	0	0
			1005	629	207	166	3		

- Molecule 79 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	p	224	Total	C	N	O	S	0	0
			1757	1132	307	309	9		

- Molecule 80 is a protein called Ribosomal protein S27a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	AP	70	Total	C	N	O	S	0	0
			573	368	109	90	6		

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

Mol	Chain	Residues	Atoms		AltConf
81	A	172	Total	Mg	0
			172	172	
81	0	1	Total	Mg	0
			1	1	
81	B	3	Total	Mg	0
			3	3	
81	C	8	Total	Mg	0
			8	8	
81	8	1	Total	Mg	0
			1	1	
81	a	1	Total	Mg	0
			1	1	
81	M	1	Total	Mg	0
			1	1	
81	c	1	Total	Mg	0
			1	1	
81	Q	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
81	AH	1	Total 1	Mg 1	0
81	j	59	Total 59	Mg 59	0
81	k	1	Total 1	Mg 1	0
81	V	1	Total 1	Mg 1	0
81	W	1	Total 1	Mg 1	0
81	X	1	Total 1	Mg 1	0
81	o	1	Total 1	Mg 1	0

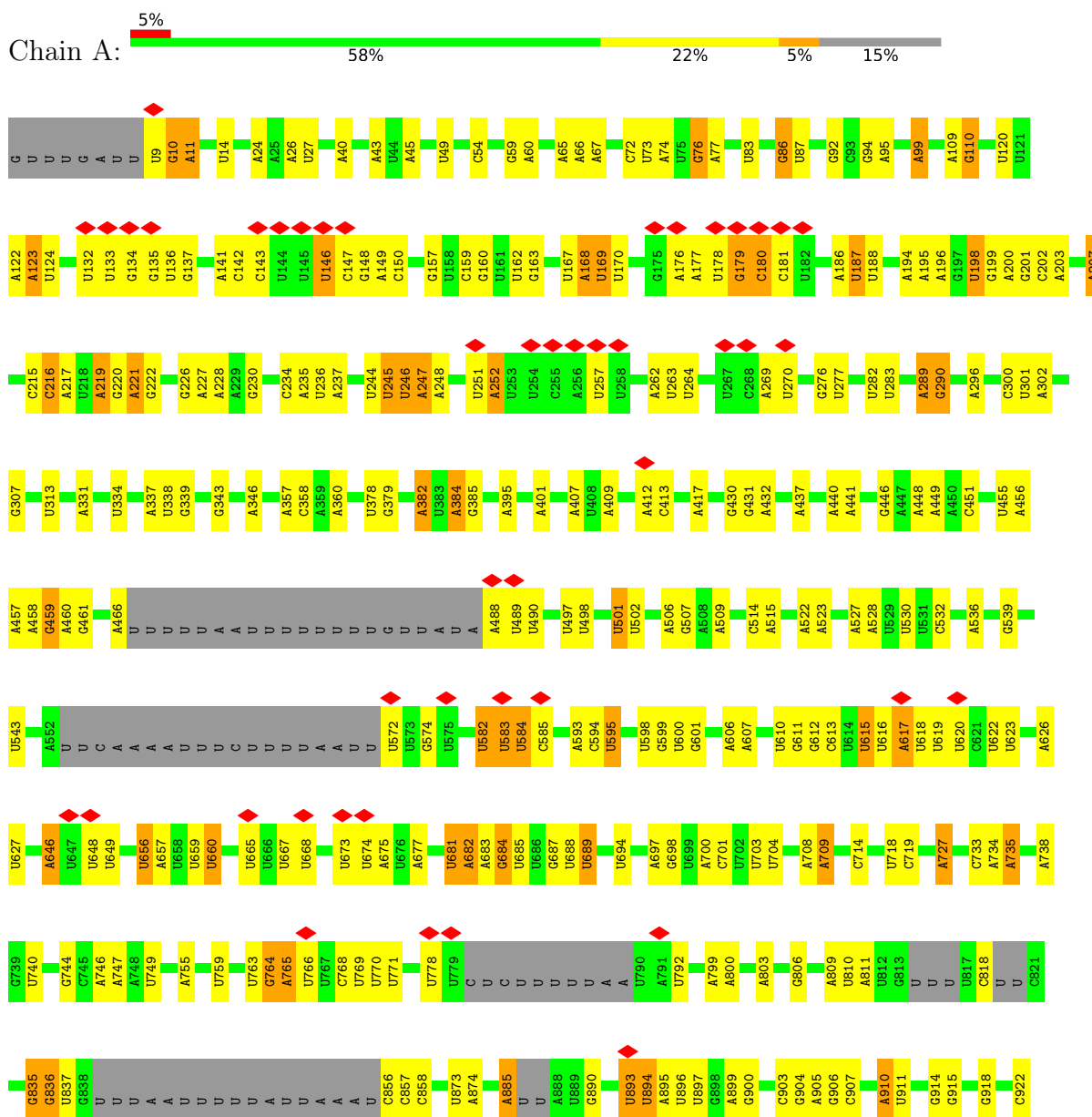
- Molecule 82 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
82	a	1	Total 1	Zn 1	0
82	c	1	Total 1	Zn 1	0
82	AC	1	Total 1	Zn 1	0
82	f	1	Total 1	Zn 1	0
82	h	1	Total 1	Zn 1	0
82	i	1	Total 1	Zn 1	0

3 Residue-property plots

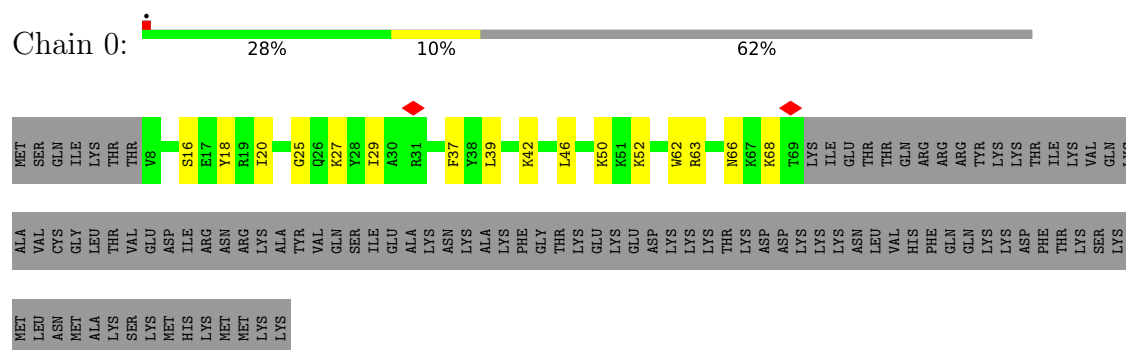
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 28S ribosomal RNA

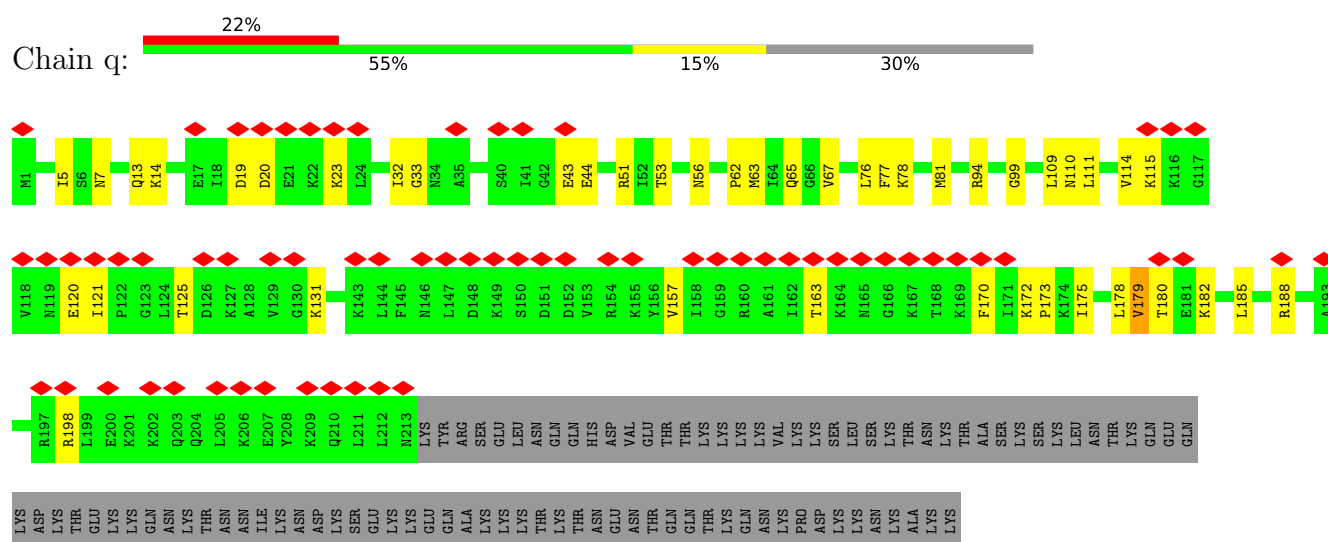




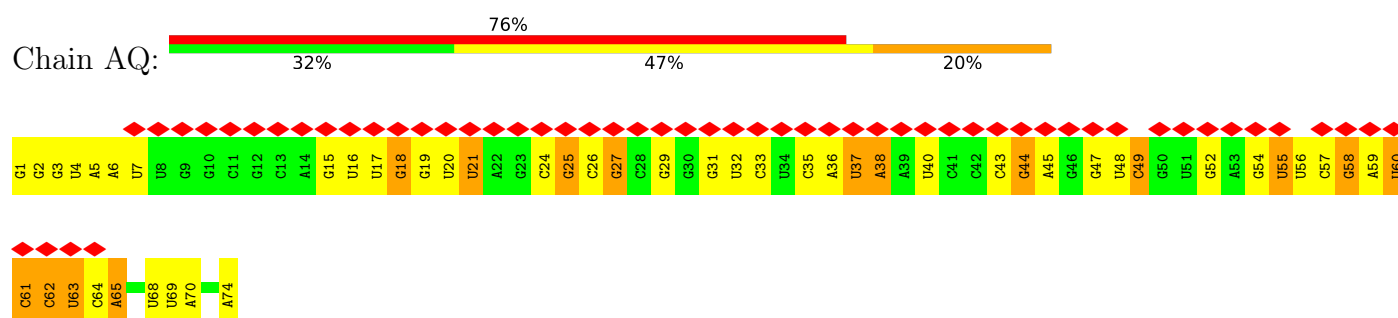




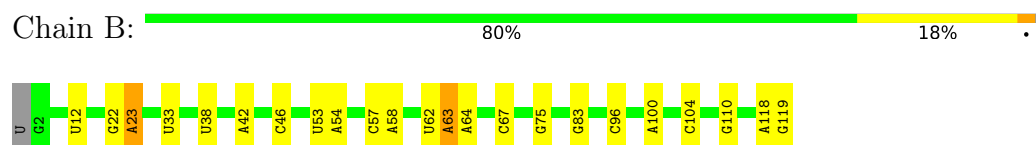
• Molecule 3: 40S ribosomal protein S6



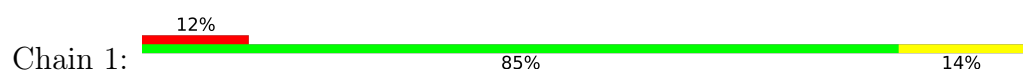
• Molecule 4: tRNA

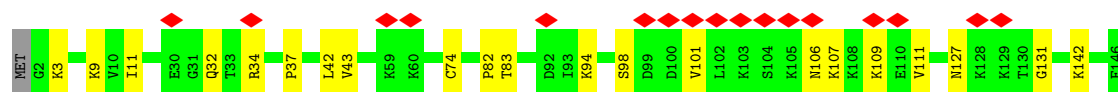


• Molecule 5: 5S ribosomal RNA

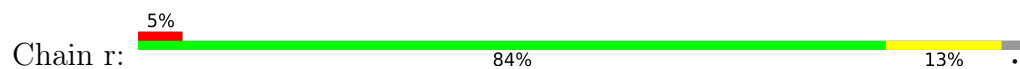


• Molecule 6: 60S ribosomal protein L27

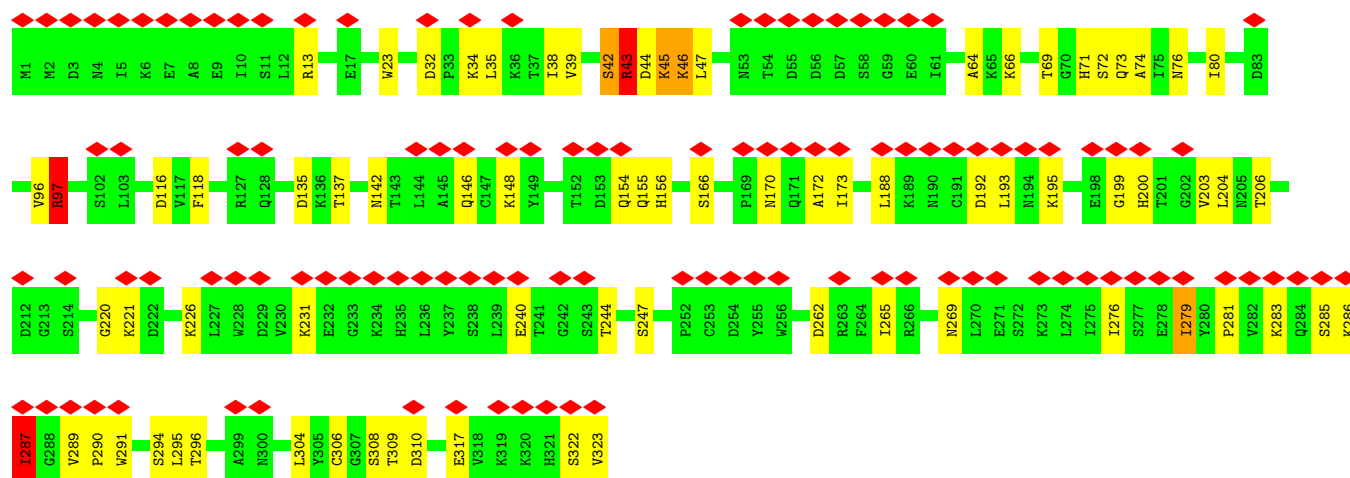
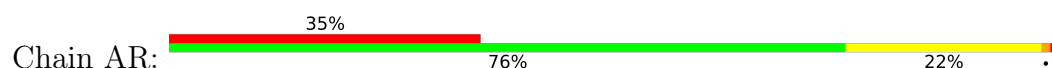




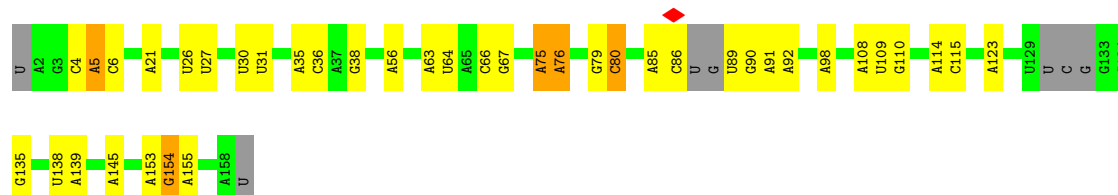
- Molecule 7: 40S ribosomal protein S5, putative



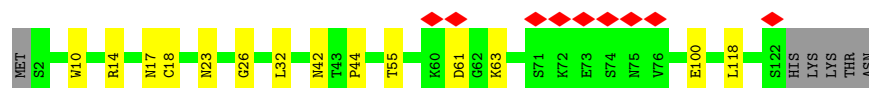
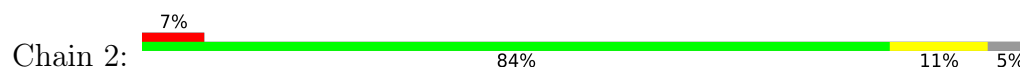
- Molecule 8: Receptor for activated c kinase



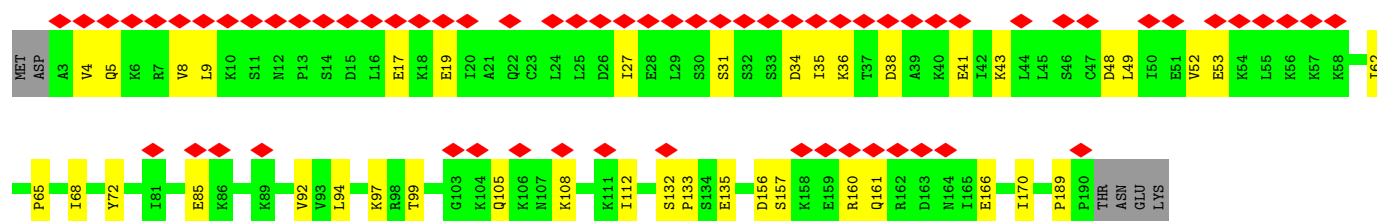
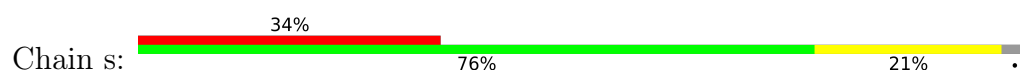
- Molecule 9: 5.8S ribosomal RNA



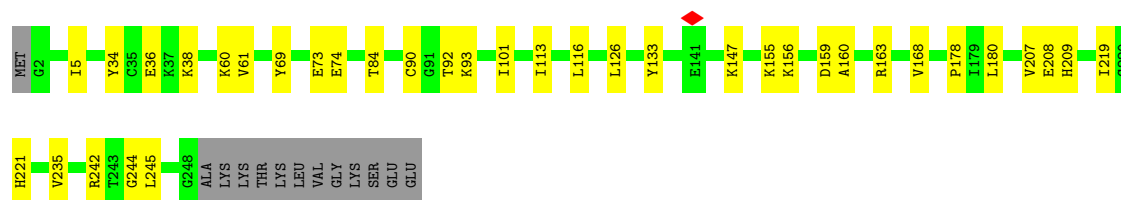
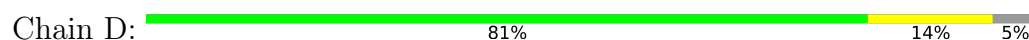
- Molecule 10: 60S ribosomal protein L28



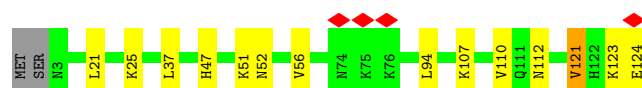
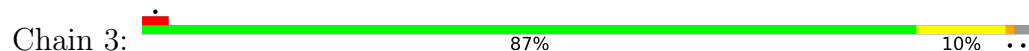
- Molecule 11: 40S ribosomal protein S7



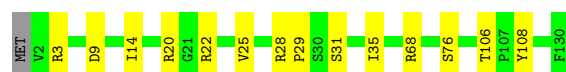
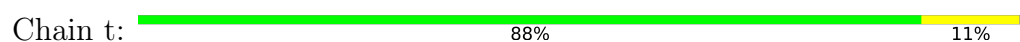
- Molecule 12: 60S ribosomal protein L2



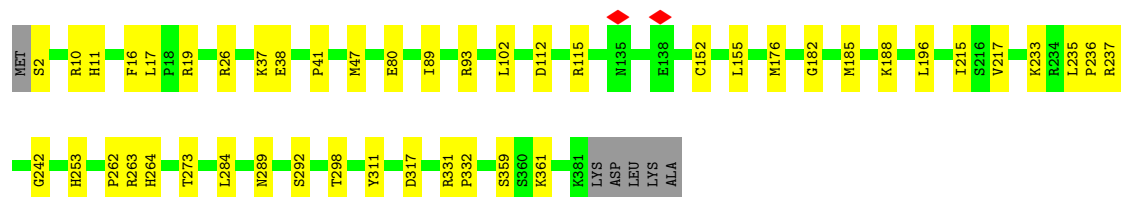
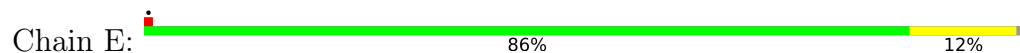
- Molecule 13: 60S ribosomal protein L35, putative



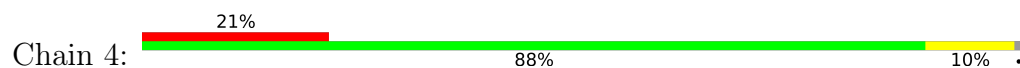
- Molecule 14: 40S ribosomal protein S15A, putative



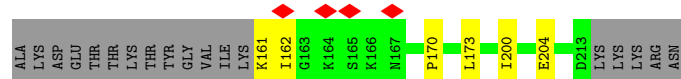
- Molecule 15: 60S ribosomal protein L3



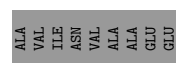
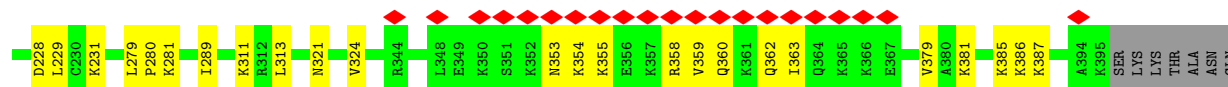
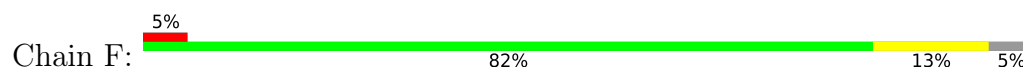
- Molecule 16: 60S ribosomal protein L29



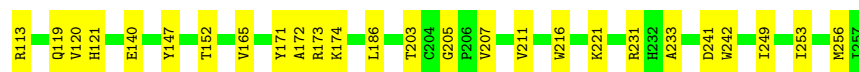
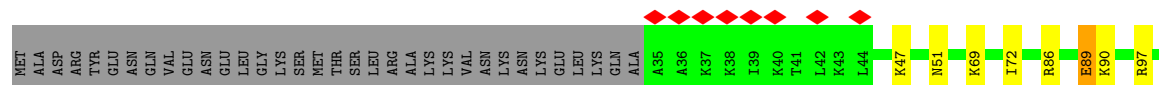
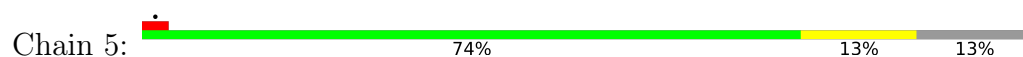
- Molecule 17: 40S ribosomal protein S8



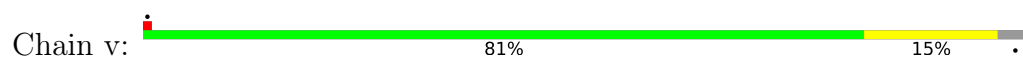
- Molecule 18: 60S ribosomal protein L4



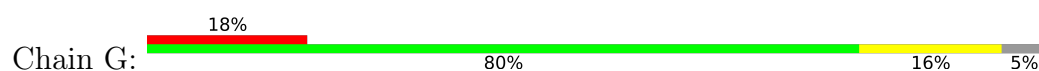
- Molecule 19: 60S ribosomal protein L7, putative



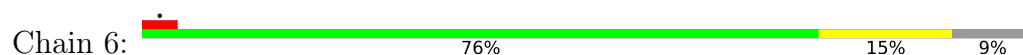
- Molecule 20: 40S ribosomal protein S16, putative



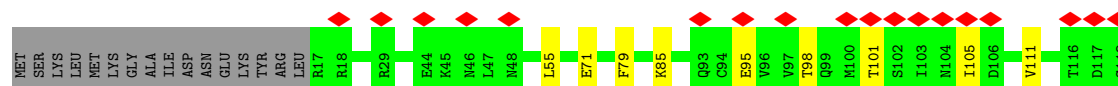
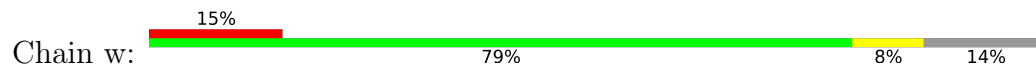
- Molecule 21: 60S ribosomal protein L11a, putative



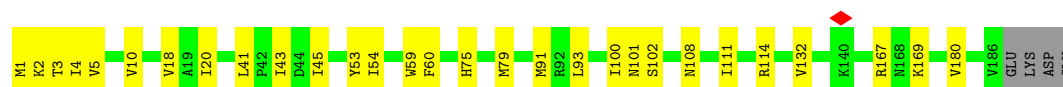
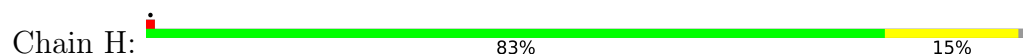
- Molecule 22: 60S ribosomal protein L30e, putative



- Molecule 23: 40S ribosomal protein S20e, putative



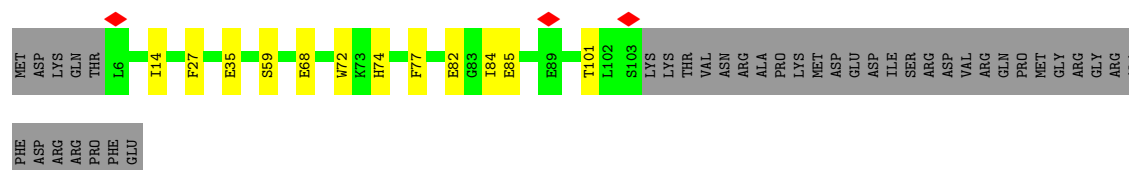
- Molecule 24: 60S ribosomal protein L6, putative



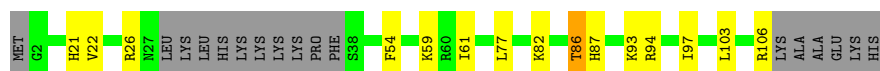
- Molecule 25: 60S ribosomal protein L31



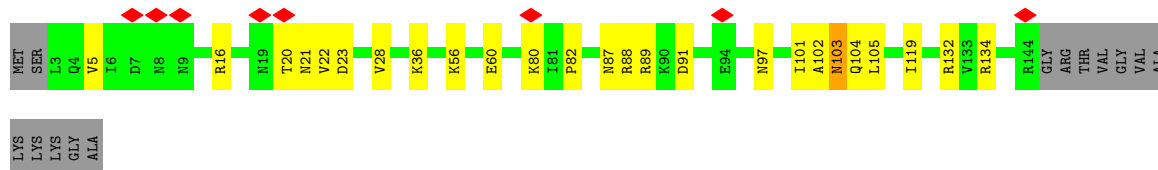
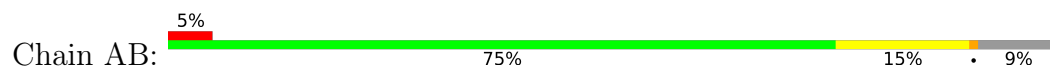
- Molecule 26: 40S ribosomal protein S10, putative



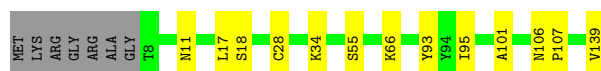
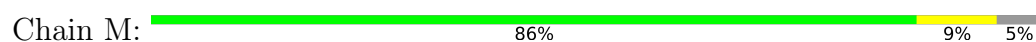
- Molecule 27: 60S ribosomal protein L6, putative



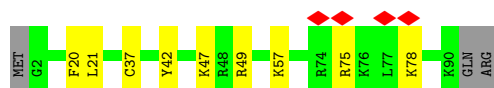
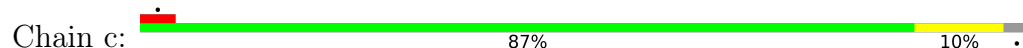
- Molecule 38: 40S ribosomal protein S18, putative



- Molecule 39: 60S ribosomal protein L23, putative



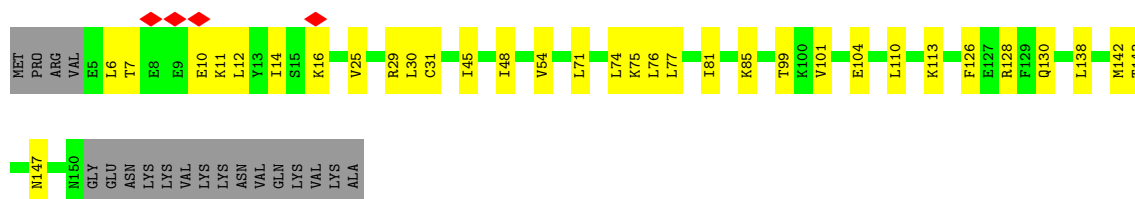
- Molecule 40: Ribosomal protein L37



- Molecule 41: 40S ribosomal protein S29, putative



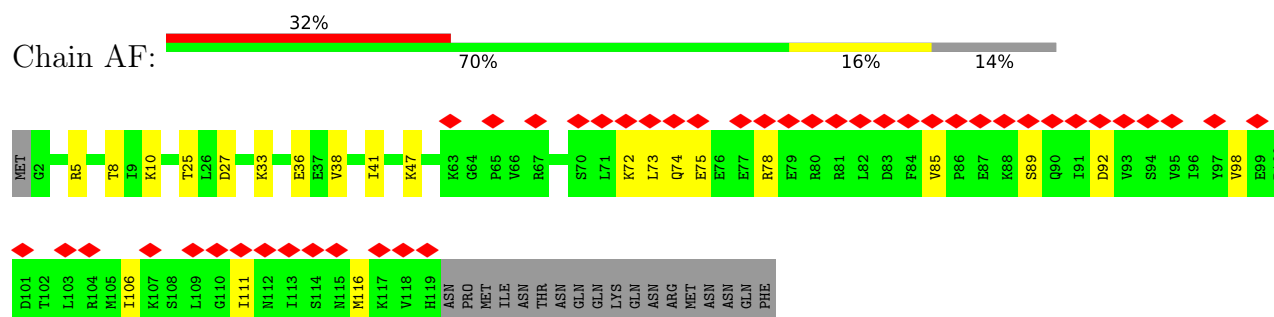
- Molecule 42: 60S ribosomal protein L14, putative



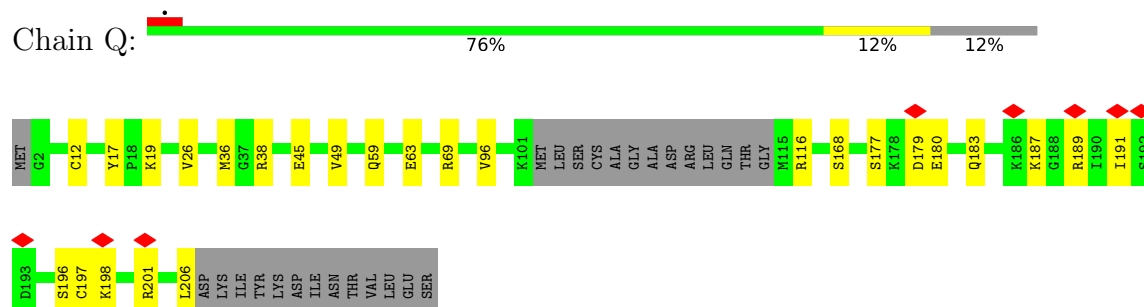
- Molecule 43: 60S ribosomal protein L38



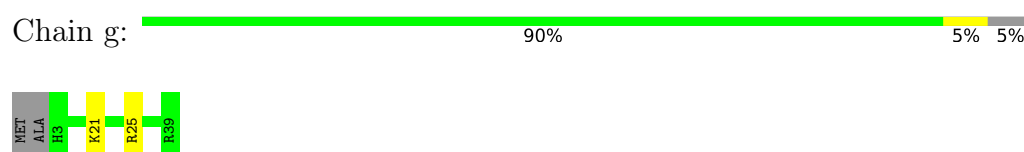
- Molecule 50: 40S ribosomal protein S17, putative



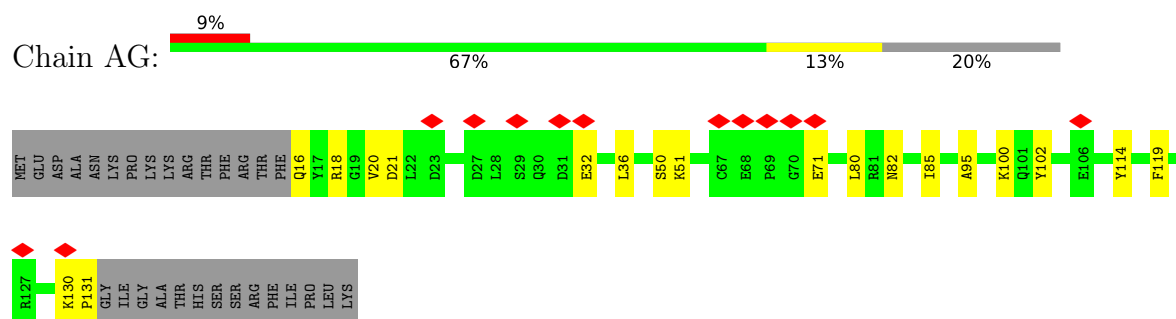
- Molecule 51: 60S ribosomal protein L10, putative



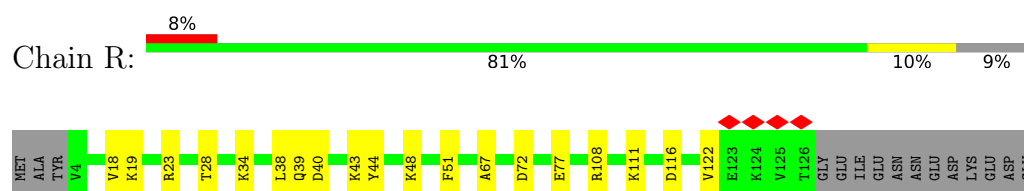
- Molecule 52: 60S ribosomal protein L41

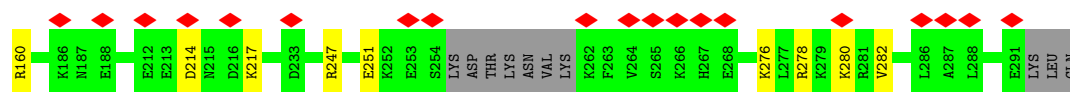


- Molecule 53: 40S ribosomal protein S19

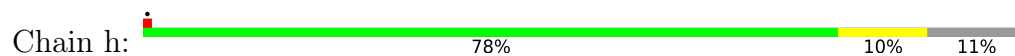


- Molecule 54: 60S ribosomal protein L5, putative

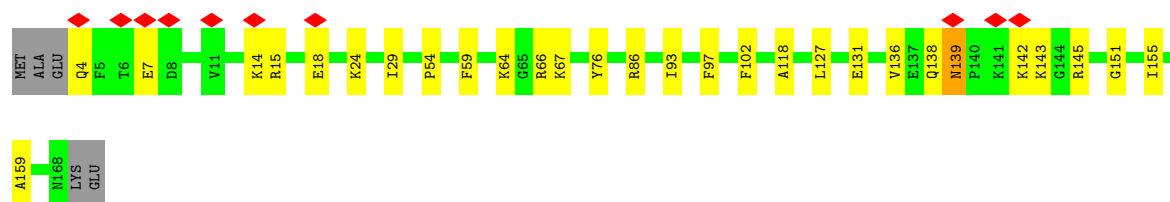
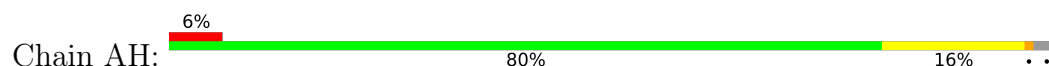




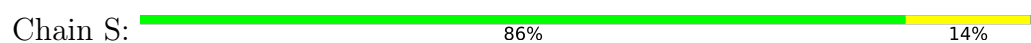
- Molecule 55: Large ribosomal subunit protein eL43



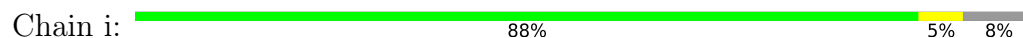
- Molecule 56: 40S ribosomal protein S19



- Molecule 57: 60S ribosomal protein L18-2, putative



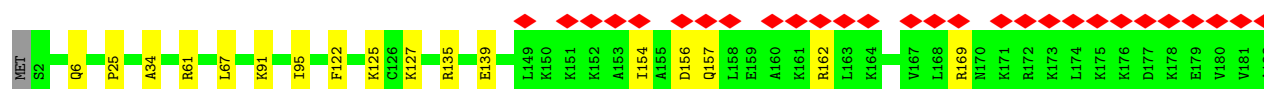
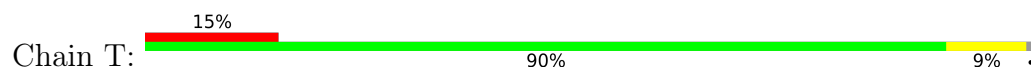
- Molecule 58: Large ribosomal subunit protein eL42



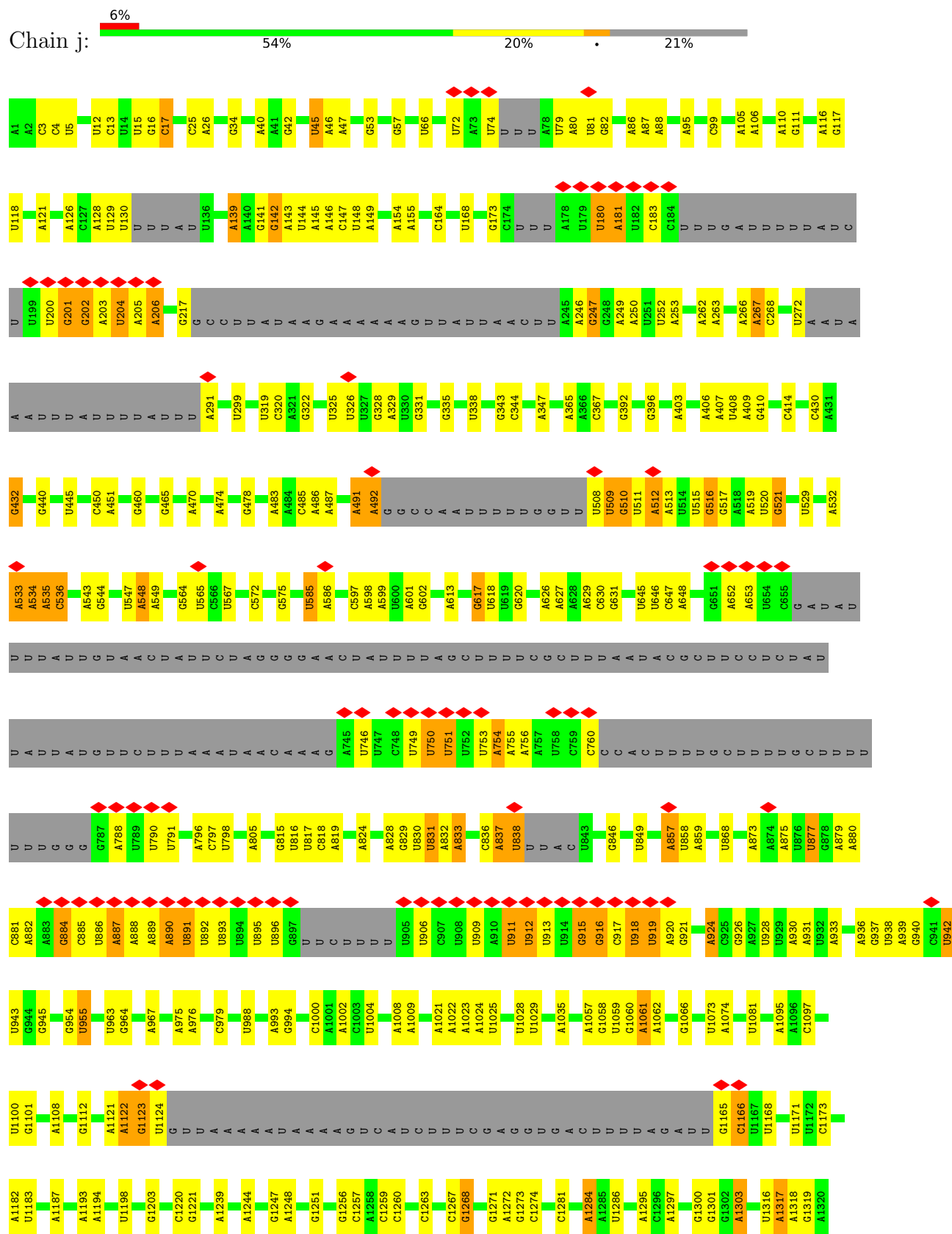
- Molecule 59: 40S ribosomal protein S21

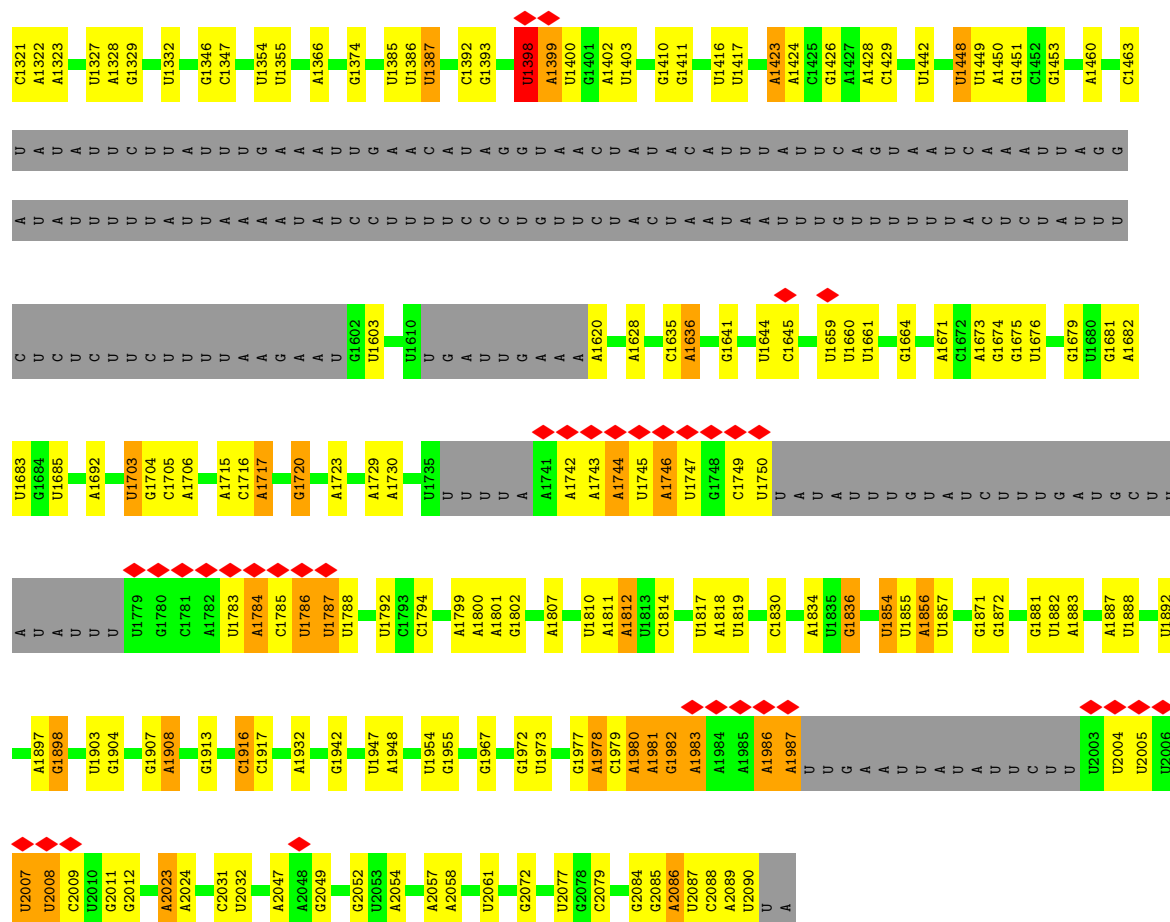


- Molecule 60: 60S ribosomal protein L19

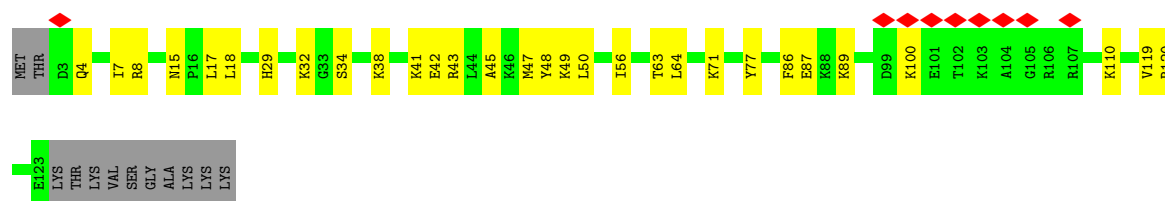


• Molecule 61: 18S ribosomal RNA

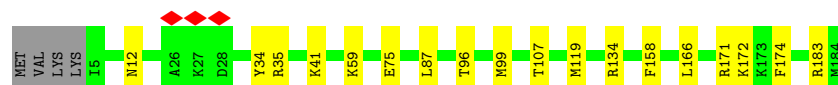
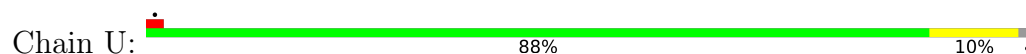




• Molecule 62: 40S ribosomal protein S24

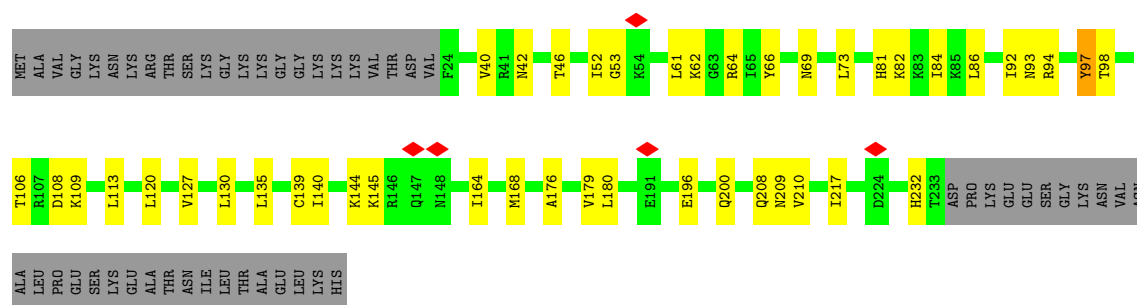


• Molecule 63: 60S ribosomal protein L18a

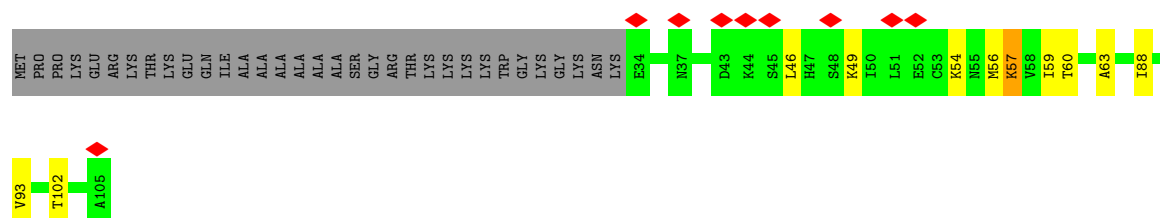


• Molecule 64: Small ribosomal subunit protein eS1

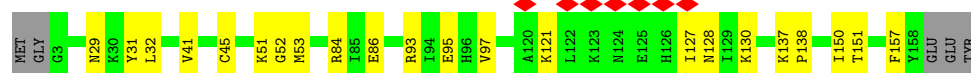
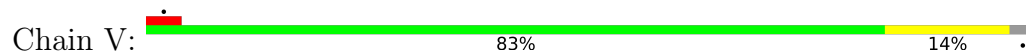




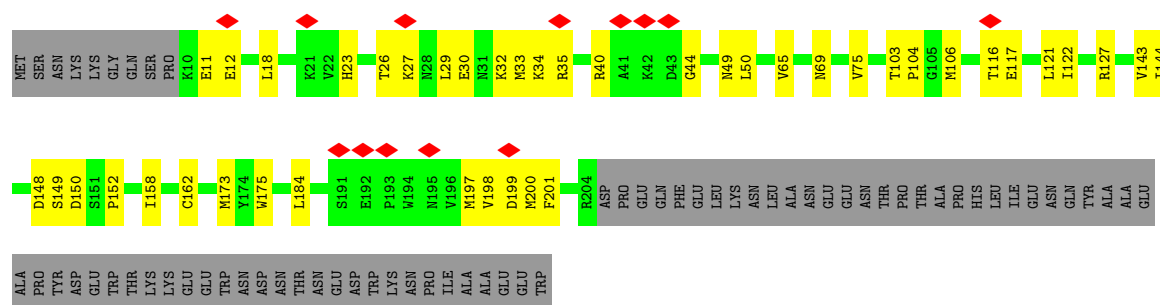
• Molecule 65: 40S ribosomal protein S25



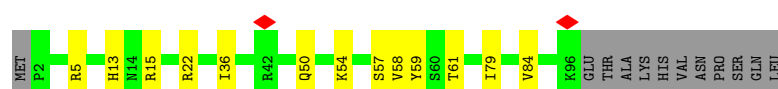
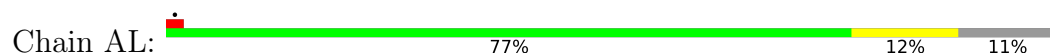
• Molecule 66: 60S ribosomal protein L21




• Molecule 67: Small ribosomal subunit protein uS2

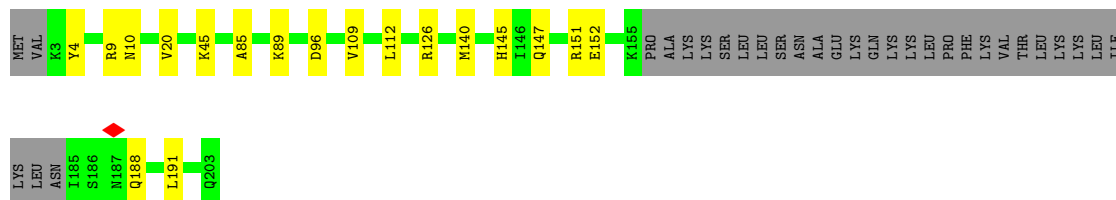


• Molecule 68: 40S ribosomal protein S26




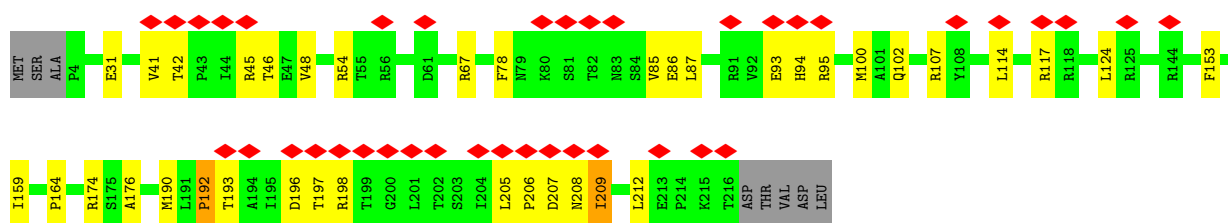
- Molecule 69: 60S ribosomal protein L17, putative

Chain W:  76% 9% 15%



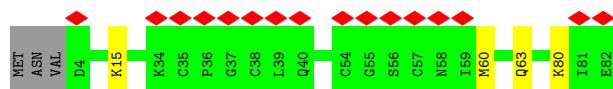
- Molecule 70: 40S ribosomal protein S3

Chain m:  18% 79% 16% . .



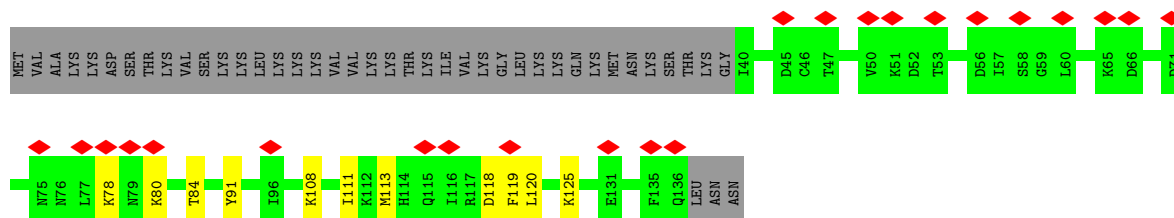
- Molecule 71: 40S ribosomal protein S27

Chain AM:  20% 91% 5% .




- Molecule 72: Large ribosomal subunit protein eL22

Chain X:  17% 62% 8% 30%

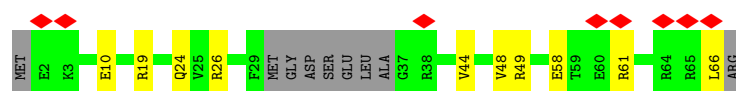
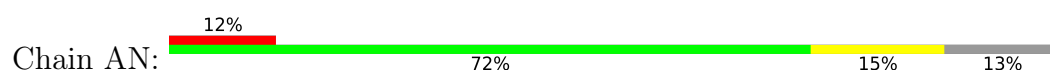


- Molecule 73: 40S ribosomal protein S9, putative

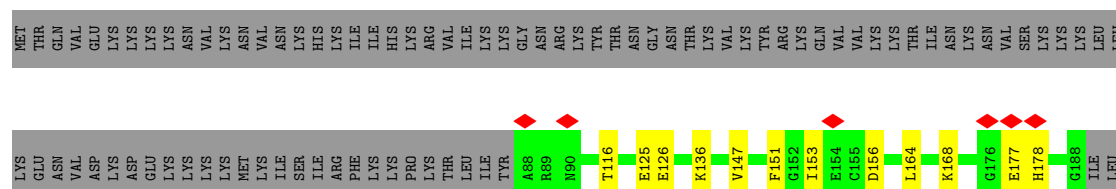
Chain n:  5% 86% 12% .



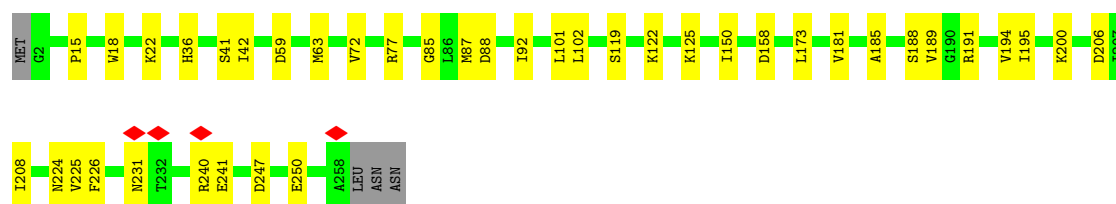
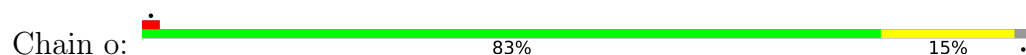
- Molecule 74: 40S ribosomal protein S28e, putative



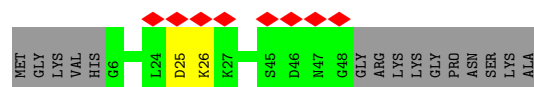
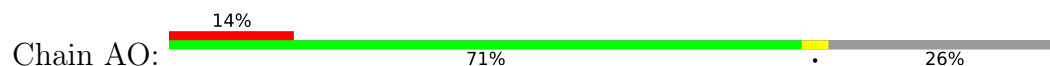
• Molecule 75: 60S ribosomal protein L23



• Molecule 76: 40S ribosomal protein S4



• Molecule 77: Small ribosomal subunit protein eS30



• Molecule 78: 60S ribosomal protein L26, putative



• Molecule 79: 40S ribosomal protein S5





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	98057	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.038	Depositor
Minimum map value	-0.005	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.003	Depositor
Map size (\AA)	465.6, 465.6, 465.6	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.97, 0.97, 0.97	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, MG

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	A	0.28	2/76208 (0.0%)	0.39	2/118656 (0.0%)
2	0	0.23	0/533	0.46	0/711
3	q	0.20	0/1735	0.45	0/2304
4	AQ	0.16	0/1754	0.30	0/2732
5	B	0.25	0/2826	0.33	0/4404
6	1	0.22	0/1189	0.42	0/1582
7	r	0.29	0/1507	0.51	0/2023
8	AR	0.55	4/2565 (0.2%)	0.78	12/3488 (0.3%)
9	C	0.28	0/3633	0.36	0/5654
10	2	0.23	0/973	0.44	0/1298
11	s	0.18	0/1544	0.38	0/2064
12	D	0.27	0/1901	0.48	0/2544
13	3	0.27	0/1033	0.49	0/1367
14	t	0.24	0/1054	0.45	0/1411
15	E	0.25	0/3129	0.47	0/4195
16	4	0.25	0/564	0.46	0/737
17	u	0.25	0/1376	0.48	1/1840 (0.1%)
18	F	0.26	0/3144	0.46	0/4205
19	5	0.27	0/1917	0.50	0/2562
20	v	0.30	0/1113	0.53	0/1487
21	G	0.22	0/1373	0.45	0/1830
22	6	0.26	0/748	0.50	0/1001
23	w	0.28	0/821	0.52	0/1106
24	H	0.25	0/1493	0.49	0/2019
25	7	0.26	0/814	0.48	0/1085
26	x	0.30	0/867	0.60	1/1174 (0.1%)
27	I	0.23	0/1707	0.45	0/2274
28	8	0.27	0/1053	0.51	0/1399
29	y	0.23	0/1012	0.51	0/1358
30	J	0.21	0/1901	0.45	0/2537
31	9	0.28	0/878	0.54	0/1179
32	z	0.22	0/1149	0.43	0/1532

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	K	0.26	0/1697	0.45	0/2271
34	a	0.26	0/871	0.47	0/1161
35	AA	0.20	0/916	0.41	0/1233
36	L	0.26	0/1793	0.49	0/2387
37	b	0.25	0/762	0.45	0/1008
38	AB	0.32	0/1178	0.64	2/1582 (0.1%)
39	M	0.22	0/1012	0.43	0/1363
40	c	0.29	0/718	0.57	0/946
41	AC	0.31	0/445	0.53	0/590
42	N	0.26	0/1219	0.47	0/1622
43	d	0.25	0/645	0.52	0/858
44	AD	0.23	0/1217	0.41	0/1627
45	O	0.28	0/1199	0.54	0/1597
46	e	0.23	0/462	0.40	0/610
47	AE	0.23	0/1241	0.43	0/1656
48	P	0.30	0/1735	0.54	0/2320
49	f	0.25	0/418	0.49	0/556
50	AF	0.23	0/974	0.41	0/1301
51	Q	0.23	0/1602	0.43	0/2142
52	g	0.26	0/347	0.48	0/448
53	AG	0.31	0/963	0.60	2/1287 (0.2%)
54	R	0.24	0/2204	0.44	0/2946
55	h	0.26	0/667	0.48	0/887
56	AH	0.31	0/1382	0.55	0/1861
57	S	0.27	0/1530	0.52	0/2040
58	i	0.26	0/797	0.47	0/1043
59	AI	0.20	0/640	0.38	0/860
60	T	0.24	0/1521	0.47	0/2012
61	j	0.27	1/39168 (0.0%)	0.36	0/60989
62	AJ	0.23	0/1007	0.54	0/1333
63	U	0.27	0/1526	0.46	0/2043
64	k	0.23	0/1737	0.54	0/2321
65	AK	0.38	0/572	0.54	0/767
66	V	0.24	0/1304	0.40	0/1737
67	l	0.21	0/1569	0.43	0/2129
68	AL	0.25	0/793	0.47	0/1055
69	W	0.26	0/1356	0.51	0/1815
70	m	0.27	0/1686	0.52	0/2258
71	AM	0.22	0/621	0.37	0/834
72	X	0.18	0/841	0.41	0/1125
73	n	0.24	0/1552	0.47	0/2070
74	AN	0.30	0/452	0.50	0/599
75	Y	0.25	0/805	0.44	0/1074

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	o	0.24	0/2097	0.49	0/2819
77	AO	0.22	0/348	0.53	0/458
78	Z	0.27	0/1017	0.54	0/1346
79	p	0.23	0/1799	0.40	0/2429
80	AP	0.21	0/583	0.50	0/767
All	All	0.27	7/214502 (0.0%)	0.42	20/313940 (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
8	AR	0	1
13	3	0	1
15	E	0	2
19	5	0	2
27	I	0	2
32	z	0	1
57	S	0	1
62	AJ	0	1
64	k	0	1
All	All	0	12

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	AR	279	ILE	C-N	14.93	1.53	1.33
8	AR	97	ARG	C-N	11.76	1.49	1.33
8	AR	96	VAL	C-N	-10.44	1.20	1.33
1	A	3566	C	C1'-N1	7.42	1.59	1.48
8	AR	38	ILE	C-N	7.36	1.44	1.33
61	j	1398	U	C1'-N1	6.05	1.56	1.47
1	A	3599	U	C1'-N1	5.40	1.56	1.48

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	AR	287	ILE	N-CA-C	14.55	139.61	109.34
8	AR	96	VAL	O-C-N	-14.47	107.93	122.98
8	AR	96	VAL	CA-C-N	12.96	142.58	121.58
8	AR	96	VAL	C-N-CA	12.96	142.58	121.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	AR	97	ARG	O-C-N	7.89	133.04	123.26
53	AG	71	GLU	CA-C-N	7.09	131.45	120.68
53	AG	71	GLU	C-N-CA	7.09	131.45	120.68
8	AR	47	LEU	O-C-N	-6.87	115.13	123.30
8	AR	287	ILE	CB-CA-C	-6.72	100.26	111.29
38	AB	80	LYS	CA-C-N	-6.39	117.99	122.59
38	AB	80	LYS	C-N-CA	-6.39	117.99	122.59
1	A	709	A	C4-N9-C1'	6.17	144.80	126.30
1	A	709	A	C8-N9-C1'	-6.09	109.42	127.70
8	AR	42	SER	N-CA-C	5.86	117.04	108.14
8	AR	38	ILE	CA-C-N	-5.71	115.74	123.10
8	AR	38	ILE	C-N-CA	-5.71	115.74	123.10
8	AR	43	ARG	N-CA-CB	5.35	119.67	109.93
17	u	91	VAL	N-CA-C	-5.33	105.76	113.07
8	AR	38	ILE	O-C-N	5.23	128.60	123.00
26	x	72	TRP	CA-CB-CG	5.20	123.48	113.60

There are no chirality outliers.

All (12) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
13	3	121	VAL	Peptide
19	5	241	ASP	Peptide
19	5	89	GLU	Peptide
62	AJ	49	LYS	Peptide
8	AR	97	ARG	Mainchain
15	E	16	PHE	Peptide
15	E	253	HIS	Peptide
27	I	214	MET	Peptide
27	I	33	TYR	Peptide
57	S	7	ASN	Peptide
64	k	97	TYR	Peptide
32	z	109	ARG	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	A	68120	0	34331	512	0
2	0	521	0	539	10	0
3	q	1717	0	1886	31	0
4	AQ	1571	0	797	32	0
5	B	2525	0	1274	14	0
6	l	1171	0	1288	13	0
7	r	1487	0	1543	18	0
8	AR	2509	0	2472	59	0
9	C	3246	0	1641	12	0
10	2	960	0	1016	8	0
11	s	1528	0	1680	30	0
12	D	1866	0	1964	25	0
13	3	1022	0	1147	10	0
14	t	1037	0	1099	9	0
15	E	3061	0	3205	29	0
16	4	555	0	599	5	0
17	u	1352	0	1409	17	0
18	F	3094	0	3333	40	0
19	5	1879	0	2005	28	0
20	v	1098	0	1183	13	0
21	G	1352	0	1412	18	0
22	6	740	0	763	13	0
23	w	813	0	863	7	0
24	H	1468	0	1544	17	0
25	7	802	0	881	9	0
26	x	839	0	852	8	0
27	I	1684	0	1849	19	0
28	8	1036	0	1139	6	0
29	y	998	0	1042	18	0
30	J	1873	0	2055	30	0
31	9	858	0	897	10	0
32	z	1129	0	1196	7	0
33	K	1666	0	1789	10	0
34	a	858	0	908	8	0
35	AA	903	0	912	13	0
36	L	1761	0	1896	22	0
37	b	756	0	842	10	0
38	AB	1161	0	1212	18	0
39	M	996	0	1044	10	0
40	c	705	0	753	7	0
41	AC	438	0	451	4	0
42	N	1203	0	1320	25	0
43	d	636	0	726	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	AD	1196	0	1294	11	0
45	O	1172	0	1230	14	0
46	e	452	0	492	4	0
47	AE	1214	0	1250	10	0
48	P	1697	0	1802	16	0
49	f	413	0	448	7	0
50	AF	963	0	1045	23	0
51	Q	1567	0	1607	17	0
52	g	342	0	388	1	0
53	AG	945	0	1000	10	0
54	R	2171	0	2257	23	0
55	h	658	0	723	8	0
56	AH	1353	0	1401	22	0
57	S	1502	0	1636	18	0
58	i	787	0	870	4	0
59	AI	631	0	637	6	0
60	T	1505	0	1671	12	0
61	j	35005	0	17635	238	0
62	AJ	994	0	1082	28	0
63	U	1496	0	1556	14	0
64	k	1713	0	1838	32	0
65	AK	565	0	607	5	0
66	V	1279	0	1358	17	0
67	l	1538	0	1600	33	0
68	AL	781	0	818	10	0
69	W	1336	0	1345	13	0
70	m	1667	0	1764	30	0
71	AM	610	0	630	4	0
72	X	824	0	882	7	0
73	n	1528	0	1638	14	0
74	AN	451	0	485	8	0
75	Y	796	0	850	10	0
76	o	2061	0	2199	25	0
77	AO	345	0	381	1	0
78	Z	1005	0	1104	25	0
79	p	1757	0	1811	25	0
80	AP	573	0	624	9	0
81	0	1	0	0	0	0
81	8	1	0	0	0	0
81	A	172	0	0	0	0
81	AH	1	0	0	0	0
81	B	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
81	C	8	0	0	0	0
81	M	1	0	0	0	0
81	Q	1	0	0	0	0
81	V	1	0	0	0	0
81	W	1	0	0	0	0
81	X	1	0	0	0	0
81	a	1	0	0	0	0
81	c	1	0	0	0	0
81	j	59	0	0	0	0
81	k	1	0	0	0	0
81	o	1	0	0	0	0
82	AC	1	0	0	0	0
82	a	1	0	0	0	0
82	c	1	0	0	0	0
82	f	1	0	0	0	0
82	h	1	0	0	0	0
82	i	1	0	0	0	0
All	All	200146	0	150715	1729	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 5.

All (1729) 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)
8:AR:322:SER:O	8:AR:323:VAL:CG2	1.75	1.34
70:m:205:LEU:HD12	70:m:206:PRO:HD2	1.34	1.08
1:A:3747:U:H2'	1:A:3748:U:O4'	1.59	1.03
8:AR:322:SER:O	8:AR:323:VAL:HG23	0.83	1.00
70:m:164:PRO:HG3	70:m:206:PRO:HG3	1.45	0.98
1:A:1195:A:N1	1:A:1212:U:C5	2.32	0.98
1:A:1195:A:N1	1:A:1212:U:H5	1.61	0.97
1:A:1978:U:O4	1:A:1990:A:C6	2.16	0.97
70:m:164:PRO:CG	70:m:206:PRO:HG3	1.96	0.95
1:A:3747:U:H2'	1:A:3748:U:C6	2.01	0.95
1:A:1762:A:HO2'	1:A:1763:G:H8	0.98	0.93
1:A:458:A:N1	1:A:497:U:C4	2.37	0.93
1:A:3747:U:O2'	1:A:3748:U:H5'	1.68	0.92
1:A:3636:U:H3	1:A:3649:G:H1	1.07	0.92
36:L:61:THR:HG22	36:L:63:ARG:H	1.35	0.92
8:AR:322:SER:C	8:AR:323:VAL:HG23	1.93	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3747:U:C2'	1:A:3748:U:O4'	2.19	0.90
1:A:2735:G:H1	1:A:2814:U:H3	1.15	0.90
1:A:3409:U:C4	1:A:3418:A:C6	2.61	0.89
1:A:1484:A:N1	1:A:1496:U:C5	2.41	0.89
1:A:458:A:N1	1:A:497:U:O4	2.05	0.88
38:AB:89:ARG:O	38:AB:97:ASN:ND2	2.07	0.87
61:j:877:U:H3	61:j:926:G:H1	0.91	0.87
1:A:1102:U:H3	1:A:1231:A:H2	1.23	0.86
1:A:1474:A:N1	1:A:1507:U:C5	2.44	0.86
70:m:207:ASP:O	70:m:208:ASN:OD1	1.93	0.86
61:j:1061:A:H2	61:j:1081:U:H3	1.24	0.85
1:A:9:U:H2'	1:A:10:G:C8	2.12	0.84
1:A:1195:A:C2	1:A:1212:U:H5	1.94	0.84
61:j:88:A:H5'	62:AJ:120:ARG:HG2	1.57	0.84
1:A:3599:U:C5	1:A:3606:G:C2	2.65	0.83
1:A:3116:A:C6	45:O:60:HIS:CE1	2.67	0.83
61:j:492:A:H62	61:j:508:U:H3	1.25	0.83
1:A:684:G:H22	18:F:311:LYS:HE3	1.44	0.82
64:k:196:GLU:OE2	64:k:200:GLN:NE2	2.10	0.82
1:A:3747:U:H2'	1:A:3748:U:H6	1.41	0.82
43:d:23:VAL:HG11	43:d:67:LEU:HD21	1.62	0.82
1:A:1484:A:C2	1:A:1496:U:H5	1.98	0.82
1:A:1976:A:N1	1:A:1992:U:C5	2.47	0.82
1:A:3596:A:N1	1:A:3608:U:C5	2.48	0.82
1:A:1978:U:O4	1:A:1990:A:N1	2.13	0.81
61:j:886:U:C2	61:j:916:G:N1	2.49	0.81
1:A:1474:A:C2	1:A:1507:U:H5	2.00	0.80
1:A:1531:G:H1	1:A:1573:C:H5	1.29	0.80
61:j:1981:A:N6	61:j:2008:U:O4	2.15	0.80
1:A:1084:A:H5''	36:L:3:ALA:HB2	1.62	0.80
4:AQ:27:G:O6	4:AQ:45:A:N1	2.14	0.80
1:A:593:A:C5	42:N:6:LEU:HD21	2.16	0.80
14:t:106:THR:HG22	14:t:108:TYR:H	1.45	0.80
1:A:1143:G:N2	1:A:1154:C:O2	2.16	0.79
34:a:20:VAL:HG13	34:a:32:ILE:HG23	1.63	0.79
1:A:2738:U:C4	1:A:2811:A:C6	2.71	0.79
1:A:1474:A:N1	1:A:1507:U:H5	1.80	0.78
5:B:62:U:OP2	54:R:278:ARG:NH1	2.15	0.78
30:J:102:PRO:HG2	30:J:105:GLN:HE21	1.48	0.78
50:AF:41:ILE:HG12	70:m:209:ILE:HG22	1.65	0.78
61:j:886:U:N3	61:j:916:G:N1	2.32	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2830:U:H3	1:A:2832:A:H8	1.31	0.78
61:j:886:U:C4	61:j:916:G:O6	2.37	0.78
61:j:1882:U:H3	61:j:1908:A:H2	1.32	0.78
61:j:890:A:N6	61:j:912:U:C4	2.52	0.78
49:f:18:LEU:HD13	49:f:29:PRO:HA	1.67	0.77
76:o:194:VAL:O	76:o:195:ILE:HG13	1.84	0.77
1:A:458:A:C6	1:A:497:U:O4	2.38	0.77
1:A:24:A:OP1	40:c:49:ARG:NH1	2.17	0.76
61:j:886:U:C4	61:j:916:G:C6	2.73	0.76
4:AQ:15:G:H22	4:AQ:48:U:H3	1.34	0.76
1:A:3407:G:N1	1:A:3418:A:N7	2.34	0.76
1:A:3596:A:N1	1:A:3608:U:C4	2.53	0.75
61:j:829:G:N7	62:AJ:8:ARG:NH1	2.34	0.75
43:d:27:LYS:H	43:d:77:PRO:HG3	1.50	0.75
61:j:796:A:N1	61:j:868:U:C4	2.54	0.75
61:j:491:A:H3'	61:j:492:A:H5''	1.68	0.75
1:A:3747:U:O2'	1:A:3748:U:C5'	2.35	0.75
7:r:120:GLY:HA2	7:r:125:VAL:HG12	1.67	0.75
8:AR:39:VAL:HG23	8:AR:80:ILE:HD12	1.68	0.75
61:j:886:U:N3	61:j:915:G:O6	2.19	0.74
1:A:3736:A:H2	1:A:3753:G:H21	1.32	0.74
61:j:1982:G:N1	61:j:2007:U:O4	2.16	0.74
1:A:1980:G:N2	1:A:1989:A:N7	2.37	0.73
27:I:31:LYS:HB3	27:I:34:PHE:O	1.88	0.73
35:AA:43:ARG:NH2	61:j:1354:U:OP1	2.21	0.73
61:j:877:U:O2	61:j:926:G:N2	2.18	0.73
1:A:3409:U:H5	1:A:3410:A:N7	1.86	0.73
7:r:195:ARG:NH1	74:AN:58:GLU:OE1	2.22	0.73
54:R:111:LYS:NZ	54:R:251:GLU:OE2	2.18	0.73
61:j:886:U:N3	61:j:916:G:C6	2.57	0.73
56:AH:14:LYS:O	56:AH:15:ARG:HG2	1.88	0.72
38:AB:101:ILE:HG22	38:AB:102:ALA:H	1.53	0.72
1:A:1122:A:H2	1:A:1169:A:H62	1.36	0.72
10:2:23:ASN:ND2	10:2:26:GLY:O	2.22	0.72
51:Q:38:ARG:NH2	51:Q:45:GLU:OE2	2.23	0.72
53:AG:130:LYS:HD2	53:AG:131:PRO:HD2	1.71	0.72
61:j:796:A:N1	61:j:868:U:O4	2.23	0.72
74:AN:24:GLN:HG3	74:AN:66:LEU:HD13	1.72	0.72
1:A:1484:A:N1	1:A:1496:U:C4	2.58	0.72
1:A:3409:U:N3	1:A:3418:A:N6	2.38	0.72
3:q:13:GLN:NE2	61:j:149:A:N3	2.37	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:j:1983:A:N1	61:j:2007:U:C4	2.58	0.71
1:A:2738:U:N3	1:A:2811:A:C6	2.58	0.71
1:A:221:A:OP1	78:Z:2:LYS:NZ	2.23	0.71
69:W:20:VAL:O	69:W:145:HIS:ND1	2.18	0.71
28:8:70:ASN:O	28:8:70:ASN:ND2	2.23	0.71
1:A:3636:U:O2	1:A:3649:G:N2	2.19	0.70
38:AB:82:PRO:HG3	56:AH:59:PHE:CE1	2.26	0.70
1:A:187:U:H5	1:A:244:U:H3	1.38	0.70
1:A:2810:A:H1'	1:A:2811:A:H5''	1.73	0.70
1:A:3566:C:OP1	69:W:10:ASN:ND2	2.21	0.70
4:AQ:3:G:N2	4:AQ:68:U:O2	2.16	0.70
1:A:3549:U:H3	1:A:3680:A:H2	1.38	0.70
1:A:1912:A:H62	1:A:1957:U:H3	1.40	0.70
61:j:1982:G:C6	61:j:2008:U:C4	2.79	0.70
74:AN:10:GLU:OE2	74:AN:26:ARG:NE	2.23	0.70
1:A:528:A:H4'	19:5:72:ILE:HD11	1.74	0.69
1:A:1335:G:H21	49:f:41:ARG:HH22	1.40	0.69
1:A:1484:A:N1	1:A:1496:U:H5	1.82	0.69
1:A:1995:C:H5''	1:A:1996:C:H5'	1.74	0.69
61:j:1980:A:O2'	61:j:1981:A:O5'	2.09	0.69
61:j:2008:U:H6	61:j:2009:C:H5	1.40	0.69
18:F:387:LYS:HG3	63:U:134:ARG:HD3	1.73	0.69
1:A:2208:G:H21	1:A:3754:A:H8	1.39	0.69
8:AR:206:THR:HG21	8:AR:247:SER:HA	1.73	0.69
61:j:890:A:O2'	61:j:891:U:O5'	2.10	0.69
62:AJ:119:VAL:HG22	62:AJ:120:ARG:H	1.57	0.69
42:N:143:THR:O	42:N:147:ASN:ND2	2.26	0.69
1:A:3409:U:C5	1:A:3418:A:N1	2.61	0.69
1:A:3747:U:O2'	1:A:3748:U:O4'	2.10	0.69
18:F:360:GLN:HG3	18:F:363:ILE:HD12	1.75	0.69
32:z:16:ARG:NH2	47:AE:104:GLU:OE1	2.25	0.69
61:j:1123:G:N2	61:j:1165:G:O5'	2.24	0.69
1:A:1209:U:H4'	54:R:44:TYR:HE1	1.56	0.69
1:A:1976:A:N1	1:A:1992:U:C4	2.61	0.69
1:A:2470:A:O2'	12:D:126:LEU:O	2.10	0.68
70:m:117:ARG:NH2	79:p:132:GLU:OE1	2.26	0.68
30:J:238:ASN:O	30:J:242:ASN:ND2	2.22	0.68
62:AJ:4:GLN:O	62:AJ:32:LYS:NZ	2.26	0.68
1:A:2835:G:OP2	30:J:68:TYR:OH	2.10	0.68
1:A:2738:U:C4	1:A:2811:A:N1	2.61	0.68
30:J:245:LEU:HA	30:J:248:LYS:HZ3	1.59	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:p:99:GLN:HG2	79:p:108:THR:HG22	1.75	0.68
15:E:155:LEU:HD12	15:E:188:LYS:HB3	1.74	0.68
56:AH:143:LYS:HE2	61:j:1794:C:H1'	1.75	0.68
1:A:135:G:N2	1:A:143:C:C2	2.62	0.68
8:AR:32:ASP:HB3	8:AR:35:LEU:HD23	1.76	0.68
61:j:180:U:H2'	61:j:181:A:H8	1.58	0.68
64:k:144:LYS:HG3	64:k:208:GLN:HG3	1.76	0.68
18:F:281:LYS:NZ	57:S:106:GLU:OE2	2.26	0.68
25:7:96:LYS:HG3	25:7:97:MET:HG2	1.75	0.68
4:AQ:24:C:H2'	4:AQ:25:G:C8	2.29	0.68
48:P:177:VAL:HG23	48:P:182:SER:HB2	1.76	0.67
8:AR:39:VAL:CG2	8:AR:80:ILE:HD12	2.23	0.67
10:2:118:LEU:HB3	28:8:111:ARG:HH22	1.57	0.67
70:m:45:ARG:NH1	70:m:86:GLU:OE2	2.27	0.67
29:y:34:PHE:HB3	29:y:41:PHE:HB2	1.76	0.67
1:A:1474:A:N1	1:A:1507:U:C4	2.63	0.67
1:A:1484:A:C2	1:A:1496:U:C5	2.83	0.67
3:q:131:LYS:NZ	61:j:164:C:OP1	2.27	0.67
30:J:163:LYS:NZ	30:J:190:LYS:O	2.27	0.67
32:z:103:LEU:HD12	32:z:126:LYS:HD3	1.76	0.67
1:A:3736:A:O2'	1:A:3737:G:O4'	2.09	0.66
22:6:77:ASN:HB3	22:6:89:ARG:HB2	1.77	0.66
1:A:2742:G:N2	1:A:2807:U:OP1	2.29	0.66
1:A:3409:U:C5	1:A:3410:A:N7	2.63	0.66
2:0:62:TRP:O	2:0:66:ASN:ND2	2.27	0.66
1:A:437:A:OP2	28:8:15:LYS:NZ	2.27	0.66
17:u:200:ILE:HG23	17:u:204:GLU:HG3	1.75	0.66
61:j:1303:A:N6	61:j:1703:U:OP1	2.28	0.66
1:A:3441:A:H2	1:A:3471:A:H62	1.40	0.66
1:A:1195:A:N1	1:A:1212:U:C4	2.64	0.66
73:n:5:TYR:O	76:o:22:LYS:NZ	2.29	0.66
50:AF:89:SER:HB3	67:l:197:MET:HE3	1.76	0.66
8:AR:295:LEU:HD23	8:AR:306:CYS:HB3	1.78	0.66
1:A:382:A:C8	1:A:385:G:H5'	2.31	0.65
1:A:1976:A:C2	1:A:1992:U:H5	2.12	0.65
1:A:3737:G:O3'	17:u:92:ARG:NH2	2.30	0.65
61:j:205:A:H3'	61:j:206:A:H4'	1.77	0.65
1:A:684:G:H5''	18:F:313:LEU:HD12	1.78	0.65
78:Z:82:GLU:OE2	78:Z:83:ARG:NH2	2.30	0.65
70:m:164:PRO:HG2	70:m:206:PRO:HG3	1.76	0.65
24:H:4:ILE:HG22	24:H:5:VAL:HG13	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1978:U:C5	1:A:1990:A:N6	2.66	0.64
1:A:146:U:O2'	1:A:147:C:O4'	2.16	0.64
69:W:126:ARG:HG3	69:W:140:MET:HE1	1.78	0.64
42:N:31:CYS:SG	42:N:76:LEU:HD23	2.38	0.64
1:A:1978:U:C4	1:A:1990:A:C6	2.86	0.64
1:A:1906:A:H2'	1:A:1907:A:C8	2.33	0.64
30:J:100:THR:HG22	30:J:196:ILE:HG22	1.80	0.64
61:j:886:U:H2'	61:j:887:A:H8	1.62	0.64
70:m:48:VAL:HB	70:m:87:LEU:HD22	1.79	0.64
1:A:2386:A:H5''	1:A:2387:A:H8	1.63	0.63
30:J:266:ASP:OD1	30:J:267:LYS:N	2.31	0.63
61:j:491:A:H62	61:j:509:U:H3	1.45	0.63
69:W:151:ARG:NH1	69:W:152:GLU:O	2.29	0.63
76:o:208:ILE:HD11	76:o:225:VAL:HG21	1.80	0.63
1:A:382:A:H8	1:A:384:A:H3'	1.62	0.63
18:F:12:SER:OG	18:F:14:ASN:OD1	2.15	0.63
30:J:188:ARG:NH1	30:J:194:TYR:OH	2.31	0.63
54:R:214:ASP:HB3	54:R:217:LYS:HB3	1.80	0.63
61:j:1745:U:H2'	61:j:1746:A:H8	1.62	0.63
8:AR:45:LYS:HG2	8:AR:73:GLN:C	2.23	0.63
12:D:36:GLU:OE1	12:D:163:ARG:NH2	2.32	0.63
1:A:574:G:OP2	18:F:381:LYS:NZ	2.30	0.63
1:A:1711:G:H2'	1:A:1712:G:C8	2.33	0.63
1:A:3596:A:C2	1:A:3608:U:H5	2.15	0.63
15:E:37:LYS:NZ	15:E:38:GLU:OE2	2.31	0.63
76:o:188:SER:HB2	76:o:191:ARG:HG3	1.80	0.63
1:A:656:U:H5	1:A:677:A:N1	1.94	0.63
1:A:3013:A:H5''	21:G:105:GLY:HA3	1.81	0.63
31:9:46:ILE:HG22	31:9:63:ILE:HD12	1.81	0.63
1:A:466:A:N1	1:A:489:U:C4	2.66	0.63
24:H:102:SER:HB2	24:H:111:ILE:HD11	1.81	0.63
43:d:40:LYS:HG2	43:d:53:VAL:HG22	1.79	0.63
61:j:1786:U:O4	61:j:1787:U:N3	2.30	0.63
1:A:740:U:O2	18:F:103:ASN:ND2	2.32	0.62
1:A:1096:G:H21	1:A:1231:A:H8	1.46	0.62
8:AR:308:SER:OG	8:AR:310:ASP:OD1	2.10	0.62
11:s:8:VAL:HA	11:s:43:LYS:HG2	1.81	0.62
36:L:61:THR:HG21	45:O:66:ASN:HB3	1.81	0.62
2:0:50:LYS:O	2:0:52:LYS:NZ	2.32	0.62
30:J:260:LEU:HD13	30:J:263:LYS:HE3	1.80	0.62
1:A:922:C:H5'	18:F:102:PHE:HE1	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:N:48:ILE:HG22	42:N:54:VAL:HG22	1.81	0.62
45:O:76:ASP:HB3	57:S:90:ARG:HG2	1.82	0.62
1:A:3106:U:O2'	58:i:29:LYS:O	2.15	0.62
1:A:1910:C:N4	1:A:1960:U:O2	2.30	0.62
61:j:617:G:HO2'	61:j:620:G:HO2'	1.46	0.62
7:r:16:TYR:HB3	7:r:100:LEU:HD23	1.82	0.62
42:N:31:CYS:SG	42:N:45:ILE:HD11	2.40	0.62
56:AH:127:LEU:HD22	56:AH:145:ARG:HD2	1.81	0.62
61:j:1892:U:H3	61:j:1897:A:H2	1.48	0.62
1:A:3409:U:C2	1:A:3418:A:N6	2.68	0.62
7:r:10:LEU:HB2	7:r:16:TYR:HE2	1.64	0.62
1:A:2506:A:H2'	1:A:2507:A:C8	2.35	0.61
61:j:1171:U:O2'	71:AM:15:LYS:NZ	2.32	0.61
1:A:506:A:H2'	1:A:507:G:H8	1.64	0.61
1:A:3116:A:N1	45:O:60:HIS:CE1	2.68	0.61
8:AR:199:GLY:O	8:AR:226:LYS:NZ	2.33	0.61
17:u:26:LYS:HD2	17:u:29:LEU:HD21	1.81	0.61
20:v:38:ASP:OD2	56:AH:24:LYS:NZ	2.21	0.61
60:T:162:ARG:NH2	61:j:877:U:OP1	2.32	0.61
2:O:29:ILE:HG12	39:M:139:VAL:HG11	1.83	0.61
7:r:21:ILE:HD12	7:r:30:ILE:HD11	1.80	0.61
56:AH:131:GLU:HG3	56:AH:136:VAL:HG23	1.80	0.61
8:AR:142:ASN:HD22	8:AR:148:LYS:HE3	1.66	0.61
1:A:803:A:H8	45:O:58:MET:HE2	1.65	0.61
1:A:1976:A:N1	1:A:1992:U:H5	1.97	0.61
1:A:3738:U:P	17:u:92:ARG:HH21	2.23	0.61
7:r:64:VAL:HG12	7:r:84:VAL:HG21	1.82	0.61
39:M:28:CYS:HB2	39:M:101:ALA:HB1	1.82	0.61
71:AM:60:MET:SD	71:AM:63:GLN:NE2	2.73	0.61
31:9:53:GLN:HG2	31:9:54:ARG:HG3	1.83	0.61
35:AA:50:GLU:OE2	80:AP:127:GLY:HA3	2.01	0.61
1:A:506:A:H2'	1:A:507:G:C8	2.36	0.61
1:A:3596:A:N1	1:A:3608:U:H5	1.99	0.61
18:F:101:MET:HE1	18:F:105:THR:HG23	1.83	0.61
1:A:993:U:OP2	15:E:238:LYS:HE2	2.01	0.60
1:A:3453:U:OP2	60:T:61:ARG:NH2	2.32	0.60
61:j:886:U:O2	61:j:916:G:N2	2.33	0.60
1:A:379:G:H22	1:A:382:A:H5''	1.65	0.60
1:A:1221:A:H5''	1:A:1222:U:H1'	1.84	0.60
1:A:2832:A:C5	30:J:70:LYS:HE2	2.36	0.60
3:q:114:VAL:HG12	3:q:115:LYS:HG2	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:j:887:A:C6	61:j:915:G:C6	2.89	0.60
61:j:1316:U:H2'	61:j:1317:A:C8	2.36	0.60
61:j:1385:U:H4'	61:j:1386:U:H5'	1.82	0.60
1:A:2738:U:N3	1:A:2811:A:N6	2.49	0.60
1:A:3319:C:H2'	1:A:3320:G:C8	2.36	0.60
26:x:101:THR:O	70:m:67:ARG:NH1	2.34	0.60
79:p:256:SER:O	79:p:260:GLU:HG3	2.01	0.60
8:AR:71:HIS:CE1	8:AR:97:ARG:HD2	2.36	0.60
47:AE:113:HIS:HB3	47:AE:141:ASN:HB3	1.84	0.60
44:AD:14:SER:HB2	61:j:1028:U:H5''	1.83	0.60
1:A:3407:G:C5	1:A:3418:A:N6	2.70	0.60
76:o:59:ASP:O	76:o:63:MET:HG3	2.01	0.60
54:R:122:VAL:O	54:R:247:ARG:NH2	2.35	0.60
70:m:42:THR:OG1	70:m:45:ARG:O	2.17	0.60
1:A:3131:A:O2'	1:A:3133:U:OP2	2.19	0.60
80:AP:121:CYS:SG	80:AP:122:ASP:N	2.69	0.60
4:AQ:18:G:N1	4:AQ:55:U:O2	2.30	0.60
27:I:211:ARG:H	27:I:214:MET:HE2	1.67	0.60
1:A:458:A:O2'	1:A:459:G:O5'	2.13	0.60
1:A:3302:G:OP2	15:E:2:SER:OG	2.17	0.60
5:B:23:A:H2	5:B:118:A:HO2'	1.50	0.60
1:A:195:A:H8	1:A:216:C:O2'	1.85	0.59
61:j:180:U:H2'	61:j:181:A:C8	2.36	0.59
61:j:272:U:O4	61:j:291:A:N6	2.34	0.59
1:A:3606:G:H2'	1:A:3607:G:H8	1.67	0.59
60:T:91:LYS:O	60:T:95:ILE:HG12	2.02	0.59
61:j:993:A:H2'	61:j:994:G:C8	2.38	0.59
1:A:1170:A:H8	1:A:2972:U:O2'	1.85	0.59
8:AR:45:LYS:HG2	8:AR:73:GLN:O	2.02	0.59
45:O:51:GLY:HA2	57:S:177:ARG:O	2.01	0.59
61:j:1745:U:H2'	61:j:1746:A:C8	2.37	0.59
6:1:127:ASN:O	6:1:131:GLY:N	2.34	0.59
12:D:242:ARG:NH2	12:D:244:GLY:O	2.35	0.59
69:W:109:VAL:HA	69:W:112:LEU:HD13	1.83	0.59
47:AE:119:ASP:O	47:AE:147:LYS:NZ	2.36	0.59
61:j:828:A:O2'	61:j:832:A:N6	2.35	0.59
61:j:1453:G:O2'	61:j:1620:A:N6	2.35	0.59
3:q:120:GLU:O	3:q:125:THR:OG1	2.19	0.59
13:3:112:ASN:O	13:3:112:ASN:ND2	2.35	0.59
73:n:157:ASP:OD1	73:n:158:PHE:N	2.35	0.59
1:A:3747:U:O2'	1:A:3748:U:C4'	2.51	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1:106:ASN:HB3	6:1:109:LYS:HE3	1.84	0.59
27:I:210:LEU:HA	27:I:214:MET:HE2	1.84	0.59
42:N:6:LEU:HD22	42:N:10:GLU:OE1	2.03	0.59
17:u:56:ARG:NH2	61:j:338:U:OP1	2.29	0.59
1:A:681:U:O2'	1:A:682:A:OP1	2.20	0.58
6:1:11:ILE:HD11	6:1:43:VAL:HG11	1.84	0.58
8:AR:116:ASP:OD2	50:AF:33:LYS:NZ	2.25	0.58
70:m:31:GLU:O	70:m:54:ARG:NH2	2.26	0.58
1:A:76:G:H3'	36:L:72:LYS:HD3	1.84	0.58
5:B:104:C:O3'	51:Q:201:ARG:NH2	2.36	0.58
42:N:29:ARG:HB3	42:N:45:ILE:HD13	1.85	0.58
67:l:32:LYS:O	67:l:35:ARG:NH2	2.37	0.58
1:A:2737:C:N4	1:A:2810:A:H62	2.01	0.58
1:A:3658:G:HO2'	1:A:3659:C:H6	1.49	0.58
2:O:16:SER:O	2:O:18:TYR:N	2.35	0.58
4:AQ:5:A:H2'	4:AQ:6:A:C8	2.38	0.58
20:v:13:LYS:HG2	20:v:18:VAL:HG22	1.84	0.58
62:AJ:77:TYR:OH	62:AJ:87:GLU:OE1	2.13	0.58
1:A:593:A:C6	42:N:6:LEU:HD21	2.38	0.58
30:J:102:PRO:HG2	30:J:105:GLN:NE2	2.17	0.58
48:P:68:ARG:NH1	48:P:125:ASP:O	2.34	0.58
50:AF:38:VAL:O	70:m:212:LEU:HG	2.04	0.58
61:j:519:A:H61	61:j:548:A:H2	1.52	0.58
64:k:86:LEU:HB3	64:k:98:THR:HG23	1.85	0.58
1:A:1788:C:OP2	34:a:74:ARG:NH1	2.36	0.58
15:E:235:LEU:HD12	15:E:236:PRO:HD2	1.84	0.58
61:j:148:U:H2'	61:j:149:A:C8	2.38	0.58
1:A:1851:A:H62	1:A:1969:A:H2	1.49	0.58
7:r:19:ILE:HD11	7:r:32:VAL:HG21	1.84	0.58
18:F:321:ASN:HB3	18:F:324:VAL:HG22	1.85	0.58
59:AI:2:PHE:O	79:p:159:LYS:NZ	2.24	0.58
60:T:156:ASP:OD1	60:T:157:GLN:N	2.37	0.58
1:A:3566:C:N4	69:W:9:ARG:CZ	2.67	0.58
1:A:3571:A:H8	1:A:3677:A:O2'	1.86	0.58
17:u:161:LYS:HG3	17:u:162:ILE:HG12	1.85	0.58
67:l:75:VAL:HG12	67:l:122:ILE:HB	1.85	0.58
1:A:1113:C:H2'	1:A:1114:A:C8	2.39	0.58
54:R:39:GLN:HG3	54:R:48:LYS:HE3	1.85	0.58
61:j:796:A:C2	61:j:868:U:C5	2.91	0.58
76:o:158:ASP:HB2	76:o:173:LEU:O	2.04	0.58
47:AE:77:MET:HE1	47:AE:157:GLN:HG3	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:k:52:ILE:HG22	64:k:53:GLY:H	1.69	0.58
1:A:3116:A:N1	45:O:60:HIS:HE1	2.01	0.58
17:u:81:VAL:HG12	17:u:102:VAL:HG12	1.86	0.58
26:x:82:GLU:OE2	26:x:82:GLU:N	2.31	0.58
29:y:34:PHE:HD1	29:y:98:ARG:HD3	1.68	0.58
38:AB:132:ARG:NH2	61:j:1274:C:OP1	2.35	0.58
39:M:34:LYS:HB2	39:M:66:LYS:HG3	1.84	0.58
61:j:492:A:OP1	61:j:492:A:H4'	2.04	0.58
1:A:749:U:C2	1:A:910:A:N6	2.72	0.57
43:d:68:LEU:HD23	43:d:70:SER:H	1.69	0.57
1:A:617:A:O2'	1:A:618:U:OP2	2.19	0.57
3:q:185:LEU:HD23	3:q:188:ARG:HD3	1.86	0.57
1:A:1266:U:OP1	16:4:13:ASN:ND2	2.32	0.57
1:A:1736:A:H8	1:A:1758:C:HO2'	1.52	0.57
1:A:3577:A:H3'	1:A:3581:A:H61	1.69	0.57
12:D:92:THR:HG23	12:D:93:LYS:HG3	1.84	0.57
15:E:155:LEU:HG	15:E:185:MET:HE1	1.86	0.57
24:H:10:VAL:O	24:H:53:TYR:HA	2.04	0.57
38:AB:20:THR:O	38:AB:21:ASN:ND2	2.38	0.57
64:k:69:ASN:O	64:k:69:ASN:ND2	2.38	0.57
70:m:207:ASP:O	70:m:208:ASN:CG	2.46	0.57
7:r:92:HIS:HB2	7:r:99:PRO:HG3	1.86	0.57
11:s:166:GLU:O	11:s:170:ILE:HG12	2.05	0.57
26:x:68:GLU:HB3	26:x:77:PHE:CD1	2.39	0.57
27:l:31:LYS:HE2	27:l:37:LYS:HD3	1.87	0.57
61:j:585:U:H4'	61:j:586:A:H3'	1.86	0.57
67:l:175:TRP:HA	67:l:201:PHE:HE2	1.68	0.57
4:AQ:18:G:N2	4:AQ:57:C:OP2	2.38	0.57
70:m:124:LEU:HD11	70:m:153:PHE:HB3	1.86	0.57
1:A:3256:C:H5''	49:f:49:LYS:HG3	1.87	0.57
61:j:145:A:H3'	61:j:146:A:H8	1.70	0.57
1:A:202:C:H2'	1:A:203:A:C8	2.39	0.57
2:0:27:LYS:HB2	39:M:95:ILE:HD13	1.85	0.57
9:C:79:G:H2'	9:C:80:C:C6	2.40	0.57
12:D:147:LYS:HE2	12:D:155:LYS:HD3	1.87	0.57
1:A:1083:G:H2'	1:A:1084:A:C8	2.40	0.57
1:A:3596:A:N1	1:A:3608:U:O4	2.38	0.57
76:o:240:ARG:HG3	76:o:241:GLU:HG2	1.87	0.57
34:a:5:VAL:HG21	34:a:32:ILE:HD11	1.87	0.56
69:W:188:GLN:O	69:W:191:LEU:N	2.37	0.56
1:A:446:G:H1	1:A:701:C:H5	1.51	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:j:796:A:C6	61:j:868:U:O4	2.57	0.56
1:A:1976:A:C2	1:A:1992:U:C5	2.90	0.56
14:t:28:ARG:HB3	14:t:29:PRO:HD3	1.87	0.56
23:w:101:THR:O	23:w:105:ILE:HD11	2.05	0.56
4:AQ:18:G:O2'	4:AQ:56:U:N3	2.28	0.56
15:E:217:VAL:O	15:E:331:ARG:NH1	2.38	0.56
20:v:67:ARG:NH2	61:j:1603:U:OP1	2.38	0.56
50:AF:89:SER:HB3	67:l:197:MET:CE	2.35	0.56
67:l:40:ARG:HE	67:l:44:GLY:HA2	1.70	0.56
61:j:80:A:H2'	61:j:81:U:C6	2.40	0.56
61:j:1272:A:H2'	61:j:1273:G:C8	2.41	0.56
61:j:1742:A:H2'	61:j:1743:A:C8	2.41	0.56
79:p:46:LYS:HG2	79:p:259:LEU:HD21	1.88	0.56
1:A:3256:C:H2'	1:A:3258:C:H5'	1.87	0.56
1:A:3409:U:C5	1:A:3418:A:C6	2.94	0.56
9:C:30:U:H2'	9:C:31:U:C6	2.41	0.56
17:u:170:PRO:O	17:u:173:LEU:N	2.39	0.56
42:N:29:ARG:HG2	42:N:76:LEU:HD22	1.88	0.56
1:A:222:G:H21	78:Z:14:MET:CE	2.19	0.56
1:A:1821:U:H2'	1:A:1822:A:C8	2.41	0.56
3:q:32:ILE:HD11	3:q:65:GLN:HB2	1.88	0.56
1:A:194:A:OP2	78:Z:121:LYS:NZ	2.35	0.55
1:A:1996:C:O2'	1:A:1997:G:N2	2.36	0.55
1:A:3738:U:OP1	17:u:92:ARG:NH2	2.39	0.55
8:AR:64:ALA:HB1	20:v:100:GLU:OE2	2.05	0.55
61:j:796:A:N1	61:j:868:U:C5	2.75	0.55
61:j:886:U:H2'	61:j:887:A:C8	2.39	0.55
1:A:1978:U:C4	1:A:1990:A:N1	2.74	0.55
8:AR:142:ASN:ND2	8:AR:146:GLN:HB2	2.20	0.55
17:u:79:ILE:HB	17:u:103:VAL:HG13	1.88	0.55
61:j:1983:A:C6	61:j:2007:U:O4	2.59	0.55
1:A:26:A:H2'	1:A:27:U:H6	1.72	0.55
1:A:2176:A:H1'	15:E:237:ARG:NH2	2.21	0.55
15:E:80:GLU:OE1	15:E:311:TYR:OH	2.13	0.55
29:y:41:PHE:HA	29:y:57:THR:HA	1.88	0.55
47:AE:125:ILE:HD12	47:AE:161:PHE:HZ	1.71	0.55
11:s:105:GLN:NE2	61:j:754:A:N7	2.53	0.55
61:j:141:G:O2'	61:j:142:G:H5'	2.06	0.55
61:j:890:A:N6	61:j:912:U:N3	2.55	0.55
1:A:764:G:H2'	1:A:765:A:C8	2.41	0.55
40:c:49:ARG:NH2	40:c:57:LYS:HG2	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:c:75:ARG:HG2	40:c:78:LYS:NZ	2.22	0.55
67:l:65:VAL:HG11	67:l:184:LEU:HD23	1.88	0.55
1:A:179:G:O2'	1:A:180:C:OP1	2.24	0.55
31:9:136:TYR:HB2	31:9:137:PRO:HD3	1.88	0.55
61:j:1008:A:H2'	61:j:1009:A:C8	2.42	0.55
1:A:763:U:OP1	36:L:38:ARG:NH2	2.39	0.55
1:A:3409:U:C4	1:A:3418:A:N6	2.75	0.55
1:A:3596:A:C2	1:A:3608:U:C5	2.91	0.55
3:q:65:GLN:HG3	61:j:1978:A:H8	1.71	0.55
11:s:4:VAL:HG12	11:s:5:GLN:HG3	1.89	0.55
30:J:173:ASP:OD1	30:J:173:ASP:N	2.38	0.55
61:j:890:A:C6	61:j:912:U:N3	2.75	0.55
61:j:918:U:H2'	61:j:919:U:C6	2.42	0.55
61:j:954:G:H2'	61:j:955:U:C6	2.42	0.55
1:A:217:A:O2'	1:A:219:A:OP2	2.24	0.55
1:A:1540:G:H8	1:A:1566:A:H62	1.55	0.55
3:q:67:VAL:HG23	3:q:99:GLY:HA2	1.89	0.55
10:2:55:THR:OG1	10:2:100:GLU:OE2	2.25	0.55
22:6:80:LEU:HD21	22:6:93:LEU:HD23	1.89	0.55
1:A:236:U:O2'	78:Z:2:LYS:HB2	2.07	0.55
1:A:1958:U:N3	1:A:1959:G:O6	2.40	0.55
1:A:3748:U:H2'	1:A:3749:U:H6	1.71	0.55
3:q:157:VAL:HG23	3:q:172:LYS:HD3	1.88	0.55
4:AQ:44:G:H2'	4:AQ:45:A:C8	2.42	0.55
11:s:108:LYS:NZ	61:j:880:A:O2'	2.37	0.55
50:AF:5:ARG:HB2	50:AF:10:LYS:HE3	1.87	0.55
80:AP:87:LYS:HD3	80:AP:88:PRO:HD2	1.89	0.55
1:A:528:A:C4'	19:5:72:ILE:HD11	2.37	0.54
1:A:94:G:H2'	1:A:95:A:C8	2.42	0.54
1:A:2157:G:H5''	15:E:242:GLY:HA3	1.88	0.54
1:A:3402:A:H2'	1:A:3403:A:C8	2.43	0.54
1:A:3655:U:H2'	1:A:3656:A:C8	2.43	0.54
4:AQ:24:C:H2'	4:AQ:25:G:H8	1.70	0.54
22:6:77:ASN:HD22	22:6:91:SER:HB2	1.72	0.54
51:Q:206:LEU:HD11	54:R:282:VAL:HG13	1.89	0.54
53:AG:82:ASN:HB3	61:j:1854:U:O4	2.06	0.54
64:k:93:ASN:OD1	64:k:94:ARG:N	2.40	0.54
4:AQ:18:G:HO2'	4:AQ:56:U:H3	1.51	0.54
11:s:52:VAL:HG22	11:s:53:GLU:H	1.71	0.54
36:L:86:PRO:O	36:L:90:GLN:HG2	2.07	0.54
38:AB:102:ALA:O	38:AB:104:GLN:N	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:AF:89:SER:OG	50:AF:92:ASP:OD1	2.22	0.54
76:o:247:ASP:OD1	76:o:250:GLU:HG2	2.07	0.54
1:A:159:C:H2'	1:A:160:G:H8	1.73	0.54
1:A:2649:A:H61	1:A:3342:C:H5	1.54	0.54
64:k:127:VAL:HG21	64:k:176:ALA:HB3	1.87	0.54
64:k:179:VAL:HG23	64:k:180:LEU:H	1.72	0.54
1:A:3658:G:O2'	1:A:3659:C:O5'	2.26	0.54
8:AR:269:ASN:HB2	8:AR:276:ILE:HD11	1.89	0.54
58:i:36:SER:O	58:i:40:ARG:HG3	2.07	0.54
1:A:1248:A:H2'	1:A:1249:U:C6	2.42	0.54
9:C:75:A:H2	9:C:89:U:H3	1.54	0.54
24:H:20:ILE:HG21	24:H:45:ILE:HD11	1.89	0.54
51:Q:179:ASP:O	51:Q:183:GLN:HG2	2.08	0.54
73:n:88:GLU:OE1	73:n:88:GLU:N	2.40	0.54
79:p:238:THR:OG1	79:p:240:ASP:OD1	2.22	0.54
1:A:252:A:OP1	36:L:130:ASN:ND2	2.40	0.54
1:A:456:A:H2'	1:A:457:A:H8	1.73	0.54
18:F:353:ASN:C	18:F:355:LYS:H	2.14	0.54
1:A:289:A:O2'	1:A:290:G:OP2	2.20	0.54
1:A:1821:U:H2'	1:A:1822:A:H8	1.73	0.54
11:s:112:ILE:HD11	61:j:873:A:H2'	1.89	0.54
50:AF:25:THR:HG23	50:AF:27:ASP:H	1.73	0.54
54:R:34:LYS:HD3	66:V:31:TYR:HE2	1.72	0.54
73:n:137:GLY:O	73:n:138:LYS:HG3	2.07	0.54
1:A:168:A:H2'	1:A:169:U:C6	2.43	0.54
30:J:264:MET:SD	30:J:269:ARG:NH2	2.73	0.54
1:A:3348:U:O2'	15:E:264:HIS:O	2.26	0.53
9:C:153:A:H2'	9:C:154:G:C8	2.42	0.53
21:G:83:GLY:HA3	21:G:127:PHE:HE2	1.72	0.53
61:j:491:A:N6	61:j:509:U:H3	2.07	0.53
79:p:248:ASP:OD1	79:p:249:LYS:N	2.38	0.53
1:A:856:C:H2'	1:A:857:C:O2	2.08	0.53
35:AA:63:CYS:HB2	35:AA:69:LYS:HE3	1.90	0.53
42:N:30:LEU:HB3	42:N:77:LEU:HB2	1.90	0.53
61:j:148:U:H2'	61:j:149:A:H8	1.72	0.53
1:A:198:U:O2'	78:Z:59:ARG:NH1	2.42	0.53
1:A:893:U:H1'	1:A:894:U:H5'	1.90	0.53
1:A:3425:G:O2'	39:M:11:ASN:O	2.26	0.53
1:A:3716:C:H4'	25:7:21:THR:HG23	1.90	0.53
8:AR:43:ARG:HA	8:AR:74:ALA:HB1	1.90	0.53
8:AR:322:SER:O	8:AR:323:VAL:CB	2.53	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:AI:16:LYS:NZ	79:p:243:LYS:O	2.39	0.53
67:l:148:ASP:OD1	67:l:149:SER:N	2.34	0.53
69:W:45:LYS:NZ	69:W:96:ASP:OD1	2.42	0.53
1:A:770:U:OP2	1:A:771:U:O2'	2.24	0.53
3:q:33:GLY:O	3:q:51:ARG:NH2	2.41	0.53
19:5:173:ARG:HB2	19:5:216:TRP:CE3	2.43	0.53
27:I:135:SER:HA	27:I:175:LYS:HD2	1.89	0.53
56:AH:29:ILE:HG22	56:AH:159:ALA:HB2	1.91	0.53
61:j:598:A:H2'	61:j:599:A:C8	2.43	0.53
61:j:836:C:O2'	61:j:837:A:H8	1.91	0.53
1:A:3748:U:H2'	1:A:3749:U:C6	2.43	0.53
4:AQ:20:U:H2'	4:AQ:21:U:H4'	1.90	0.53
18:F:38:GLN:O	18:F:42:THR:HG23	2.08	0.53
19:5:69:LYS:O	19:5:72:ILE:HG22	2.08	0.53
31:9:130:ARG:HH12	33:K:2:TYR:HD2	1.56	0.53
44:AD:98:MET:HE1	44:AD:114:ARG:HB2	1.91	0.53
78:Z:117:ILE:HG23	78:Z:120:ARG:HH21	1.72	0.53
1:A:2113:C:OP1	1:A:2116:C:N4	2.39	0.53
1:A:2699:C:H2'	1:A:2700:C:C6	2.43	0.53
5:B:12:U:OP2	5:B:67:C:O2'	2.26	0.53
1:A:2478:G:O2'	1:A:2607:U:OP2	2.21	0.53
1:A:3319:C:H2'	1:A:3320:G:H8	1.72	0.53
27:I:28:THR:HG22	27:I:38:VAL:HG12	1.90	0.53
37:b:54:PHE:O	37:b:59:LYS:NZ	2.42	0.53
62:AJ:43:ARG:HG3	62:AJ:47:MET:HE3	1.91	0.53
78:Z:44:THR:HG23	78:Z:121:LYS:HD2	1.91	0.53
24:H:3:THR:O	24:H:60:PHE:HA	2.08	0.53
38:AB:134:ARG:HG2	61:j:1856:A:C5	2.43	0.53
76:o:88:ASP:OD1	76:o:122:LYS:NZ	2.40	0.53
1:A:3566:C:P	69:W:10:ASN:HD22	2.32	0.53
4:AQ:62:C:O2'	4:AQ:63:U:OP1	2.26	0.53
8:AR:142:ASN:HD21	8:AR:146:GLN:HB2	1.73	0.53
33:K:181:LYS:HA	42:N:142:MET:HE1	1.91	0.53
61:j:486:A:H2'	61:j:487:A:H8	1.74	0.53
15:E:112:ASP:OD1	15:E:115:ARG:NH1	2.41	0.53
23:w:105:ILE:HD12	23:w:105:ILE:H	1.74	0.53
36:L:39:GLU:OE2	36:L:42:ARG:NH1	2.42	0.53
1:A:222:G:H21	78:Z:14:MET:HE1	1.74	0.52
1:A:1482:A:C2	27:I:35:GLY:HA3	2.44	0.52
35:AA:100:PHE:HB3	35:AA:111:ILE:HG23	1.91	0.52
1:A:2500:A:H5'	1:A:2501:A:H2	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:f:40:GLY:C	49:f:41:ARG:HD3	2.34	0.52
61:j:1263:C:H4'	74:AN:19:ARG:HD3	1.90	0.52
78:Z:11:ARG:O	78:Z:15:ARG:HB3	2.09	0.52
1:A:764:G:O2'	1:A:765:A:OP1	2.27	0.52
1:A:2738:U:O2'	1:A:2739:U:O4'	2.27	0.52
1:A:3042:A:N6	54:R:28:THR:O	2.39	0.52
5:B:57:C:H2'	5:B:58:A:H8	1.74	0.52
8:AR:283:LYS:C	8:AR:285:SER:N	2.65	0.52
30:J:227:LYS:HE3	30:J:231:PHE:HE2	1.74	0.52
56:AH:29:ILE:HG21	56:AH:155:ILE:HG22	1.91	0.52
61:j:110:A:H2'	61:j:111:G:C8	2.44	0.52
62:AJ:15:ASN:HD21	62:AJ:18:LEU:HD23	1.74	0.52
1:A:1195:A:O2'	1:A:1196:A:OP1	2.28	0.52
10:2:61:ASP:O	10:2:63:LYS:N	2.39	0.52
29:y:46:ASP:OD2	64:k:46:THR:OG1	2.24	0.52
42:N:12:LEU:O	42:N:16:LYS:HG2	2.10	0.52
1:A:1895:U:H2'	1:A:1896:C:C6	2.44	0.52
1:A:3709:U:H5''	1:A:3710:U:H5'	1.92	0.52
10:2:10:TRP:O	10:2:14:ARG:HG3	2.10	0.52
18:F:218:LYS:O	18:F:222:ARG:HG3	2.10	0.52
50:AF:85:VAL:HG12	67:l:200:MET:HE2	1.89	0.52
64:k:108:ASP:OD1	64:k:109:LYS:N	2.43	0.52
75:Y:147:VAL:HG12	75:Y:153:ILE:HB	1.92	0.52
1:A:2386:A:H5''	1:A:2387:A:C8	2.43	0.52
1:A:2525:A:H2'	1:A:2526:A:C8	2.44	0.52
1:A:2884:G:O6	34:a:99:LYS:NZ	2.42	0.52
1:A:3001:A:H2'	1:A:3002:G:C8	2.45	0.52
15:E:102:LEU:HD12	15:E:152:CYS:SG	2.50	0.52
61:j:829:G:O4'	61:j:832:A:N6	2.43	0.52
64:k:139:CYS:SG	64:k:140:ILE:N	2.83	0.52
1:A:2574:A:H8	1:A:3333:U:H1'	1.73	0.52
8:AR:172:ALA:HB1	8:AR:188:LEU:HB3	1.92	0.52
11:s:34:ASP:OD1	11:s:35:ILE:N	2.39	0.52
27:I:98:ARG:NH1	27:I:133:ASP:OD1	2.43	0.52
61:j:1122:A:H61	61:j:1166:C:H5	1.56	0.52
78:Z:56:LEU:HD13	78:Z:66:GLU:HG2	1.91	0.52
1:A:2957:G:H5'	51:Q:116:ARG:HH21	1.75	0.52
36:L:20:HIS:HD2	48:P:198:LEU:HA	1.75	0.52
42:N:110:LEU:HD12	42:N:113:LYS:HD3	1.92	0.52
72:X:78:LYS:HD2	72:X:80:LYS:HZ1	1.75	0.52
1:A:1959:G:C6	1:A:1960:U:C2	2.98	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3241:U:H2'	1:A:3242:U:C6	2.44	0.52
1:A:3407:G:C4	1:A:3418:A:N6	2.77	0.52
11:s:31:SER:HA	11:s:36:LYS:HZ1	1.75	0.52
26:x:27:PHE:HE1	26:x:84:ILE:HG23	1.75	0.52
61:j:516:G:HO2'	61:j:517:G:H8	1.56	0.52
1:A:2451:A:OP2	12:D:156:LYS:NZ	2.34	0.52
3:q:20:ASP:OD2	3:q:23:LYS:N	2.37	0.52
8:AR:42:SER:HB3	8:AR:44:ASP:OD1	2.09	0.52
8:AR:195:LYS:NZ	8:AR:231:LYS:O	2.43	0.52
61:j:1122:A:N6	61:j:1166:C:H41	2.08	0.52
61:j:1784:A:C4	61:j:1786:U:C4	2.98	0.52
64:k:92:ILE:HG22	64:k:93:ASN:H	1.75	0.52
1:A:727:A:OP2	1:A:3227:U:O2'	2.27	0.51
7:r:118:ARG:HE	7:r:127:ARG:HD3	1.75	0.51
12:D:34:TYR:CE1	12:D:38:LYS:HG3	2.44	0.51
12:D:60:LYS:HG3	12:D:73:GLU:OE2	2.11	0.51
38:AB:16:ARG:NE	38:AB:21:ASN:O	2.43	0.51
64:k:97:TYR:O	64:k:232:HIS:NE2	2.43	0.51
1:A:1707:A:O2'	1:A:1710:G:H8	1.93	0.51
8:AR:13:ARG:HH21	8:AR:317:GLU:HG2	1.74	0.51
12:D:242:ARG:NH1	12:D:245:LEU:O	2.24	0.51
49:f:17:LYS:HD3	49:f:26:ARG:HG2	1.92	0.51
62:AJ:38:LYS:NZ	62:AJ:42:GLU:OE2	2.40	0.51
1:A:1220:U:H3'	1:A:1221:A:C2	2.46	0.51
9:C:154:G:H2'	9:C:155:A:C8	2.45	0.51
10:2:32:LEU:HD12	10:2:42:ASN:HA	1.92	0.51
13:3:37:LEU:HD21	75:Y:116:THR:HG21	1.91	0.51
76:o:36:HIS:CD2	76:o:85:GLY:HA3	2.44	0.51
1:A:1649:G:H2'	1:A:1650:U:O4'	2.09	0.51
4:AQ:3:G:O6	4:AQ:68:U:O4	2.27	0.51
13:3:123:LYS:HB3	13:3:124:GLU:OE1	2.10	0.51
15:E:331:ARG:HD3	15:E:332:PRO:HD2	1.91	0.51
42:N:81:ILE:HD12	42:N:99:THR:HG21	1.91	0.51
44:AD:99:ARG:NH2	44:AD:119:GLU:OE2	2.43	0.51
56:AH:7:GLU:OE2	56:AH:7:GLU:N	2.39	0.51
57:S:184:ALA:O	57:S:185:TYR:HB3	2.11	0.51
14:t:3:ARG:NH2	14:t:9:ASP:OD2	2.42	0.51
61:j:534:A:O3'	61:j:535:A:H8	1.94	0.51
1:A:1881:C:OP2	60:T:127:LYS:NZ	2.41	0.51
9:C:154:G:H2'	9:C:155:A:H8	1.76	0.51
44:AD:30:PRO:HB3	44:AD:67:THR:HG22	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:j:12:U:H2'	61:j:13:C:C6	2.44	0.51
61:j:121:A:H1'	61:j:403:A:C5	2.46	0.51
62:AJ:45:ALA:HA	62:AJ:50:LEU:HD12	1.92	0.51
76:o:185:ALA:HB3	76:o:224:ASN:HD22	1.74	0.51
1:A:646:A:N7	27:I:33:TYR:HE1	2.09	0.51
1:A:1822:A:N1	1:A:2004:U:H5	2.09	0.51
1:A:3090:G:OP1	66:V:51:LYS:NZ	2.44	0.51
6:1:11:ILE:HG22	6:1:82:PRO:HA	1.92	0.51
50:AF:106:ILE:HD11	67:l:18:LEU:HD21	1.92	0.51
1:A:746:A:H2'	1:A:747:A:C8	2.46	0.51
1:A:2164:A:H61	1:A:2632:C:H42	1.58	0.51
3:q:179:VAL:HG12	61:j:139:A:C2	2.46	0.51
56:AH:66:ARG:O	61:j:1723:A:OP1	2.29	0.51
57:S:51:ARG:HA	57:S:54:MET:HE2	1.91	0.51
1:A:1214:C:H2'	1:A:1215:A:H8	1.75	0.51
18:F:144:ILE:HB	18:F:147:LEU:HD12	1.93	0.51
27:I:212:ASN:C	27:I:212:ASN:HD22	2.19	0.51
53:AG:32:GLU:OE1	53:AG:32:GLU:N	2.43	0.51
1:A:1978:U:C4	1:A:1990:A:N6	2.79	0.51
40:c:75:ARG:HG2	40:c:78:LYS:HZ2	1.76	0.51
61:j:942:U:H2'	61:j:943:U:C6	2.46	0.51
1:A:1739:C:H2'	1:A:1740:A:C8	2.46	0.50
1:A:2401:C:H1'	1:A:3736:A:C8	2.46	0.50
1:A:3010:A:O2'	21:G:98:ASP:OD1	2.17	0.50
1:A:3362:A:P	15:E:93:ARG:HH22	2.33	0.50
17:u:56:ARG:HH22	61:j:338:U:P	2.33	0.50
51:Q:49:VAL:HG13	51:Q:168:SER:HB3	1.92	0.50
1:A:3747:U:HO2'	1:A:3748:U:C4'	2.23	0.50
5:B:75:G:C4	63:U:59:LYS:HE3	2.46	0.50
8:AR:32:ASP:OD1	8:AR:34:LYS:HG2	2.12	0.50
8:AR:265:ILE:HG12	8:AR:291:TRP:CZ3	2.46	0.50
8:AR:283:LYS:C	8:AR:285:SER:H	2.19	0.50
25:7:17:THR:OG1	25:7:84:GLU:OE2	2.28	0.50
44:AD:15:THR:O	61:j:1028:U:H5'	2.12	0.50
61:j:45:U:O2'	61:j:46:A:H2'	2.11	0.50
61:j:325:U:H4'	61:j:329:A:C8	2.46	0.50
1:A:1736:A:H8	1:A:1758:C:O2'	1.94	0.50
1:A:1770:G:H21	1:A:1798:A:H8	1.58	0.50
8:AR:240:GLU:OE1	8:AR:240:GLU:N	2.44	0.50
24:H:18:VAL:HG11	24:H:54:ILE:HD11	1.93	0.50
25:7:87:ARG:HA	25:7:97:MET:SD	2.51	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:O:75:VAL:HB	45:O:116:LEU:HD21	1.93	0.50
60:T:135:ARG:O	60:T:139:GLU:HG3	2.12	0.50
61:j:796:A:C2	61:j:868:U:H5	2.29	0.50
61:j:940:G:H2'	61:j:942:U:H5''	1.94	0.50
62:AJ:89:LYS:HD3	62:AJ:100:LYS:HD3	1.93	0.50
1:A:455:U:H2'	1:A:456:A:H8	1.76	0.50
1:A:2088:A:H2'	1:A:2089:C:C6	2.47	0.50
7:r:86:TYR:OH	65:AK:93:VAL:O	2.28	0.50
37:b:61:ILE:HG22	37:b:97:ILE:HG21	1.94	0.50
61:j:1836:G:H5''	61:j:1836:G:H8	1.77	0.50
70:m:100:MET:HE3	70:m:174:ARG:HH22	1.76	0.50
1:A:1511:U:H2'	1:A:1512:A:C8	2.46	0.50
1:A:1816:G:H2'	1:A:1817:G:C8	2.46	0.50
1:A:2669:G:H2'	1:A:2670:G:C8	2.47	0.50
8:AR:221:LYS:HA	8:AR:244:THR:HG23	1.93	0.50
9:C:26:U:OP1	78:Z:11:ARG:NH2	2.38	0.50
73:n:169:PRO:HB2	73:n:173:LYS:HB2	1.94	0.50
1:A:1158:G:C2	1:A:1159:A:H1'	2.46	0.50
4:AQ:60:U:H2'	4:AQ:61:C:C6	2.47	0.50
12:D:116:LEU:HD22	12:D:126:LEU:HD12	1.94	0.50
29:y:64:ALA:C	29:y:66:ARG:H	2.19	0.50
35:AA:112:ILE:HD11	61:j:1327:U:C4	2.47	0.50
50:AF:74:GLN:HB3	50:AF:78:ARG:NH1	2.26	0.50
65:AK:54:LYS:HA	65:AK:88:ILE:HD11	1.93	0.50
1:A:703:U:H2'	1:A:704:U:C6	2.47	0.50
1:A:1247:C:H2'	1:A:1248:A:H8	1.77	0.50
1:A:1827:C:H42	1:A:1998:A:H61	1.60	0.50
2:O:25:GLY:HA3	2:O:37:PHE:CE1	2.46	0.50
11:s:132:SER:OG	11:s:133:PRO:HD3	2.12	0.50
42:N:25:VAL:HG22	63:U:158:PHE:O	2.12	0.50
61:j:515:U:H2'	61:j:516:G:H5'	1.93	0.50
61:j:1729:A:H2'	61:j:1730:A:C8	2.47	0.50
70:m:164:PRO:HG2	70:m:206:PRO:CG	2.42	0.50
1:A:497:U:C4	1:A:498:U:C4	2.99	0.50
1:A:1712:G:H2'	1:A:1713:G:H8	1.77	0.50
1:A:3599:U:C5	1:A:3606:G:N1	2.79	0.50
4:AQ:58:G:OP2	4:AQ:59:A:N6	2.45	0.50
17:u:25:ARG:NH2	61:j:392:G:OP2	2.44	0.50
26:x:14:ILE:HD12	26:x:14:ILE:H	1.77	0.50
29:y:34:PHE:CD1	29:y:98:ARG:HD3	2.47	0.50
51:Q:17:TYR:O	51:Q:96:VAL:HG22	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:Q:179:ASP:OD1	51:Q:180:GLU:N	2.45	0.50
62:AJ:18:LEU:HD12	62:AJ:86:PHE:CD1	2.46	0.50
64:k:135:LEU:HD23	64:k:217:ILE:HA	1.93	0.50
6:1:98:SER:O	6:1:101:VAL:HG12	2.12	0.50
8:AR:23:TRP:CH2	8:AR:290:PRO:HG3	2.47	0.50
68:AL:57:SER:OG	68:AL:58:VAL:O	2.29	0.50
1:A:142:C:H2'	1:A:143:C:C6	2.47	0.49
1:A:1568:C:OP2	18:F:195:LYS:NZ	2.45	0.49
30:J:50:LYS:HE3	30:J:51:ARG:HH12	1.77	0.49
1:A:615:U:C4	1:A:616:U:O4	2.65	0.49
1:A:1195:A:C2	1:A:1212:U:C5	2.86	0.49
3:q:78:LYS:H	3:q:81:MET:HE3	1.76	0.49
18:F:379:VAL:HG22	63:U:35:ARG:HH22	1.77	0.49
61:j:1061:A:O2'	61:j:2077:U:O2	2.30	0.49
78:Z:32:SER:HB2	78:Z:105:LEU:HD22	1.93	0.49
1:A:9:U:H2'	1:A:10:G:H8	1.69	0.49
1:A:417:A:C2	9:C:21:A:H1'	2.47	0.49
1:A:1101:A:H2'	1:A:1102:U:C6	2.47	0.49
1:A:1801:G:O2'	1:A:2031:A:N6	2.45	0.49
18:F:358:ARG:O	18:F:362:GLN:HG2	2.11	0.49
73:n:16:LYS:HG3	73:n:16:LYS:O	2.11	0.49
1:A:766:U:O2'	18:F:231:LYS:NZ	2.45	0.49
1:A:2180:U:O2'	1:A:2181:A:OP1	2.27	0.49
8:AR:135:ASP:OD1	8:AR:137:THR:OG1	2.23	0.49
26:x:59:SER:OG	61:j:1321:C:OP1	2.30	0.49
41:AC:31:LYS:O	41:AC:34:ILE:HG12	2.12	0.49
61:j:838:U:OP1	61:j:838:U:H4'	2.12	0.49
1:A:237:A:H5'	78:Z:2:LYS:HB3	1.94	0.49
61:j:857:A:N7	61:j:859:A:C8	2.80	0.49
61:j:1386:U:H4'	61:j:1387:U:O5'	2.11	0.49
1:A:1979:C:H5	1:A:1980:G:C5	2.30	0.49
1:A:2015:C:OP2	55:h:49:ARG:NH1	2.44	0.49
15:E:41:PRO:HA	15:E:182:GLY:HA3	1.95	0.49
62:AJ:48:TYR:HB2	62:AJ:50:LEU:HG	1.95	0.49
62:AJ:77:TYR:HE1	62:AJ:86:PHE:CE1	2.30	0.49
1:A:1683:A:H2'	1:A:1684:A:C8	2.48	0.49
1:A:3021:C:H2'	1:A:3022:U:O2	2.13	0.49
42:N:126:PHE:O	42:N:130:GLN:HG3	2.13	0.49
47:AE:137:THR:OG1	61:j:331:G:OP1	2.21	0.49
54:R:276:LYS:HG2	54:R:280:LYS:HZ1	1.78	0.49
61:j:87:A:H8	61:j:146:A:O2'	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:j:1247:G:H2'	61:j:1248:A:C8	2.47	0.49
61:j:1717:A:H2	61:j:1720:G:N3	2.11	0.49
61:j:1799:A:H2'	61:j:1800:A:O4'	2.12	0.49
1:A:109:A:H4'	1:A:110:G:OP1	2.12	0.49
1:A:885:A:C2	1:A:3111:U:H5	2.31	0.49
1:A:1331:A:H2'	1:A:1332:A:C8	2.48	0.49
1:A:2735:G:O6	1:A:2814:U:O4	2.30	0.49
17:u:87:ASN:OD1	17:u:90:LEU:HD13	2.13	0.49
31:9:74:ALA:HB2	31:9:112:GLY:HA2	1.95	0.49
38:AB:36:LYS:HB3	38:AB:102:ALA:HA	1.95	0.49
49:f:34:CYS:O	49:f:35:ARG:HG2	2.12	0.49
61:j:141:G:H2'	61:j:142:G:C8	2.48	0.49
61:j:485:C:H2'	61:j:486:A:H8	1.77	0.49
79:p:182:VAL:HG22	79:p:209:PHE:HB2	1.95	0.49
3:q:5:ILE:HA	3:q:111:LEU:O	2.13	0.49
6:1:32:GLN:HG3	6:1:37:PRO:HA	1.94	0.49
14:t:20:ARG:NH1	61:j:1108:A:O5'	2.45	0.49
21:G:141:ARG:O	21:G:145:ARG:HB3	2.13	0.49
27:I:86:VAL:HB	27:I:96:LEU:HD23	1.95	0.49
34:a:38:LYS:O	34:a:58:ARG:NH2	2.40	0.49
35:AA:76:CYS:SG	35:AA:83:LEU:HD21	2.53	0.49
39:M:93:TYR:CE1	39:M:95:ILE:HD11	2.47	0.49
61:j:146:A:H5''	61:j:147:C:OP2	2.13	0.49
61:j:510:G:O2'	61:j:511:U:H5'	2.12	0.49
61:j:755:A:H2'	61:j:756:A:C8	2.47	0.49
1:A:220:G:H2'	18:F:223:ASN:OD1	2.13	0.49
1:A:1248:A:H2'	1:A:1249:U:H6	1.77	0.49
5:B:46:C:OP1	54:R:160:ARG:HG3	2.12	0.49
22:6:77:ASN:ND2	22:6:91:SER:HB2	2.27	0.49
25:7:87:ARG:O	25:7:87:ARG:HD2	2.12	0.49
32:z:63:GLN:NE2	61:j:2047:A:OP1	2.45	0.49
54:R:67:ALA:HA	54:R:72:ASP:HB3	1.95	0.49
61:j:1744:A:H2	61:j:1788:U:H5	1.61	0.49
62:AJ:41:LYS:NZ	62:AJ:56:ILE:O	2.45	0.49
75:Y:136:LYS:HA	75:Y:168:LYS:HG3	1.94	0.49
1:A:1064:U:H2'	1:A:1065:U:C6	2.48	0.48
1:A:1462:C:H2'	1:A:1463:A:H8	1.78	0.48
1:A:3323:G:N2	1:A:3326:A:OP2	2.41	0.48
3:q:53:THR:OG1	3:q:110:ASN:O	2.29	0.48
18:F:353:ASN:O	18:F:354:LYS:HG2	2.13	0.48
22:6:50:ASN:O	22:6:50:ASN:ND2	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:U:166:LEU:O	63:U:171:ARG:NH2	2.43	0.48
80:AP:130:MET:SD	80:AP:137:ASP:HB3	2.53	0.48
1:A:1484:A:N1	1:A:1496:U:O4	2.46	0.48
1:A:1704:U:O2'	1:A:1705:A:OP1	2.24	0.48
1:A:2738:U:O4	1:A:2811:A:N1	2.46	0.48
1:A:2743:A:H2'	1:A:2744:G:O4'	2.13	0.48
1:A:2812:G:H2'	1:A:2813:U:C6	2.48	0.48
1:A:3133:U:OP1	36:L:206:LYS:HE2	2.13	0.48
20:v:47:THR:O	20:v:51:GLU:HG3	2.12	0.48
48:P:5:LYS:O	48:P:9:GLU:HG2	2.13	0.48
61:j:154:A:H2'	61:j:155:A:O4'	2.13	0.48
30:J:272:GLU:O	30:J:275:LYS:HG3	2.14	0.48
78:Z:50:ARG:NH1	78:Z:111:ASP:OD2	2.46	0.48
1:A:2669:G:O2'	1:A:2670:G:H5'	2.13	0.48
1:A:3655:U:H2'	1:A:3656:A:H8	1.77	0.48
3:q:56:ASN:HB3	3:q:62:PRO:HA	1.96	0.48
32:z:137:LYS:C	32:z:139:LYS:H	2.21	0.48
61:j:857:A:C8	61:j:858:U:H2'	2.49	0.48
67:l:11:GLU:HG2	67:l:12:GLU:N	2.28	0.48
1:A:914:G:H2'	1:A:915:G:C8	2.48	0.48
1:A:2083:U:H2'	1:A:2084:U:C6	2.48	0.48
1:A:2549:A:N6	61:j:2047:A:N3	2.62	0.48
5:B:83:G:H4'	19:5:231:ARG:HG2	1.96	0.48
7:r:13:LYS:NZ	7:r:89:GLU:OE1	2.39	0.48
33:K:6:TYR:CD1	63:U:174:PHE:CE2	3.01	0.48
48:P:202:ARG:O	48:P:205:ARG:HG3	2.14	0.48
49:f:9:LEU:O	49:f:12:LYS:HG2	2.13	0.48
61:j:1855:U:H3'	61:j:1856:A:H4'	1.96	0.48
70:m:197:THR:HG22	70:m:198:ARG:N	2.29	0.48
1:A:733:C:H2'	1:A:734:A:H8	1.79	0.48
1:A:3020:U:OP2	21:G:51:ARG:NH2	2.46	0.48
4:AQ:37:U:H3'	4:AQ:38:A:H5''	1.95	0.48
11:s:62:ILE:HB	11:s:94:LEU:HD23	1.96	0.48
18:F:381:LYS:O	18:F:385:LYS:HG2	2.13	0.48
38:AB:5:VAL:O	38:AB:5:VAL:HG12	2.13	0.48
45:O:134:GLU:OE2	45:O:138:LYS:HD2	2.14	0.48
1:A:1656:G:H2'	1:A:2147:A:H1'	1.95	0.48
3:q:43:GLU:HG2	3:q:44:GLU:N	2.29	0.48
11:s:19:GLU:OE1	11:s:19:GLU:N	2.41	0.48
11:s:27:ILE:O	11:s:36:LYS:NZ	2.47	0.48
27:I:221:PHE:HB3	42:N:128:ARG:HH22	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:J:172:ASN:HB2	30:J:197:VAL:O	2.13	0.48
50:AF:106:ILE:HD13	67:l:18:LEU:HD11	1.96	0.48
67:l:69:ASN:HB3	79:p:260:GLU:OE2	2.13	0.48
1:A:3409:U:H5	1:A:3410:A:C5	2.32	0.48
15:E:89:ILE:HD11	15:E:196:LEU:HD21	1.96	0.48
29:y:45:THR:HG22	29:y:52:THR:HA	1.95	0.48
70:m:95:ARG:O	70:m:102:GLN:NE2	2.47	0.48
1:A:1820:U:H2'	1:A:1821:U:C6	2.49	0.48
1:A:3433:C:O2'	1:A:3434:A:H5'	2.14	0.48
4:AQ:1:G:H22	4:AQ:70:A:H2	1.60	0.48
5:B:119:G:H8	5:B:119:G:O5'	1.96	0.48
6:l:9:LYS:NZ	6:l:83:THR:O	2.45	0.48
7:r:16:TYR:HA	7:r:19:ILE:HG23	1.95	0.48
7:r:195:ARG:HH22	74:AN:61:ARG:CB	2.27	0.48
15:E:26:ARG:HD2	15:E:47:MET:HE1	1.95	0.48
47:AE:135:SER:OG	47:AE:138:VAL:HG12	2.14	0.48
61:j:911:U:H3'	61:j:912:U:H6	1.78	0.48
1:A:1006:G:H2'	1:A:1007:U:C6	2.49	0.48
4:AQ:52:G:O6	4:AQ:60:U:C2	2.67	0.48
11:s:65:PRO:HG2	11:s:68:ILE:HD13	1.96	0.48
20:v:61:LEU:HD12	20:v:64:LEU:HD12	1.96	0.48
1:A:123:A:O2'	1:A:124:U:H5'	2.14	0.47
1:A:440:A:H2'	1:A:441:A:C8	2.48	0.47
1:A:803:A:C8	45:O:58:MET:HE2	2.47	0.47
1:A:1207:U:H2'	1:A:1208:G:O4'	2.14	0.47
1:A:2020:A:H2'	1:A:2021:A:C8	2.49	0.47
4:AQ:57:C:H3'	4:AQ:59:A:N6	2.29	0.47
11:s:48:ASP:OD1	11:s:49:LEU:N	2.47	0.47
20:v:48:LYS:HB3	20:v:83:ARG:HD2	1.95	0.47
20:v:70:VAL:HG21	20:v:82:ILE:HD11	1.96	0.47
36:L:3:ALA:O	36:L:4:HIS:CG	2.67	0.47
61:j:1715:A:H2'	61:j:1716:C:C6	2.49	0.47
61:j:1986:A:N6	61:j:2004:U:H1'	2.29	0.47
1:A:136:U:H5	1:A:141:A:N1	2.12	0.47
1:A:1646:C:H2'	1:A:1647:U:C6	2.49	0.47
22:6:12:ASN:O	22:6:16:LYS:HG3	2.14	0.47
68:AL:13:HIS:O	68:AL:15:ARG:NH1	2.48	0.47
76:o:125:LYS:HB3	76:o:226:PHE:CE2	2.48	0.47
1:A:296:A:H2	48:P:93:LYS:HD3	1.80	0.47
1:A:836:G:H2'	1:A:837:U:C6	2.50	0.47
1:A:1322:G:H2'	1:A:1323:A:C8	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3588:A:OP2	33:K:11:LYS:NZ	2.47	0.47
35:AA:21:ASN:OD1	35:AA:135:GLN:NE2	2.47	0.47
61:j:831:U:O4	62:AJ:43:ARG:NH1	2.47	0.47
67:l:117:GLU:O	67:l:117:GLU:HG2	2.15	0.47
1:A:1482:A:N3	27:I:35:GLY:HA3	2.29	0.47
19:5:172:ALA:O	19:5:174:LYS:HG2	2.14	0.47
22:6:56:ARG:O	22:6:60:GLU:HG3	2.14	0.47
36:L:105:GLU:OE1	37:b:26:ARG:HG3	2.14	0.47
43:d:23:VAL:HG12	43:d:43:LEU:HD23	1.95	0.47
53:AG:95:ALA:HB1	53:AG:102:TYR:HB3	1.95	0.47
60:T:6:GLN:NE2	60:T:34:ALA:O	2.45	0.47
61:j:203:A:C5	61:j:204:U:H1'	2.49	0.47
61:j:911:U:H3'	61:j:912:U:C6	2.49	0.47
64:k:86:LEU:HB3	64:k:98:THR:CG2	2.44	0.47
4:AQ:26:C:H3'	4:AQ:27:G:H5''	1.97	0.47
8:AR:46:LYS:HD3	8:AR:69:THR:HG22	1.96	0.47
35:AA:124:GLU:N	35:AA:124:GLU:OE1	2.48	0.47
38:AB:101:ILE:O	38:AB:105:LEU:HB2	2.14	0.47
53:AG:80:LEU:O	53:AG:80:LEU:HD12	2.15	0.47
55:h:21:SER:O	55:h:25:GLN:HG3	2.14	0.47
56:AH:66:ARG:O	56:AH:67:LYS:HG2	2.13	0.47
61:j:857:A:H2'	61:j:858:U:C6	2.49	0.47
64:k:81:HIS:CD2	64:k:82:LYS:HG3	2.49	0.47
64:k:120:LEU:HD23	64:k:120:LEU:H	1.79	0.47
65:AK:46:LEU:HD12	65:AK:49:LYS:HB2	1.97	0.47
80:AP:82:LYS:HD2	80:AP:83:LYS:O	2.13	0.47
1:A:1113:C:H2'	1:A:1114:A:H8	1.77	0.47
1:A:1841:U:O2'	1:A:1842:U:OP1	2.25	0.47
3:q:14:LYS:HE2	3:q:121:ILE:HD11	1.96	0.47
3:q:19:ASP:OD1	3:q:19:ASP:N	2.48	0.47
8:AR:154:GLN:HG2	8:AR:193:LEU:HD13	1.97	0.47
11:s:35:ILE:HG13	11:s:38:ASP:OD2	2.15	0.47
62:AJ:7:ILE:HB	62:AJ:47:MET:HE1	1.97	0.47
75:Y:177:GLU:HG3	75:Y:178:HIS:ND1	2.29	0.47
79:p:160:ILE:HG12	79:p:161:GLY:H	1.79	0.47
1:A:459:G:H2'	1:A:460:A:H8	1.79	0.47
1:A:2152:A:H2'	1:A:2153:A:O4'	2.14	0.47
1:A:3000:A:H2'	1:A:3001:A:C8	2.50	0.47
5:B:23:A:H2	5:B:118:A:O2'	1.97	0.47
6:1:34:ARG:HB3	6:1:34:ARG:NH1	2.30	0.47
12:D:133:TYR:HB3	12:D:168:VAL:HG12	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:5:90:LYS:HG3	19:5:147:TYR:CG	2.50	0.47
29:y:138:ASP:HB2	61:j:955:U:H3	1.80	0.47
54:R:276:LYS:HG2	54:R:280:LYS:NZ	2.29	0.47
59:AI:25:PRO:HD2	59:AI:28:GLU:OE1	2.15	0.47
61:j:478:G:O2'	61:j:819:A:N3	2.45	0.47
61:j:533:A:H2'	61:j:533:A:N3	2.29	0.47
64:k:40:VAL:HG12	64:k:42:ASN:H	1.79	0.47
64:k:73:LEU:HD12	64:k:84:ILE:HG21	1.97	0.47
76:o:181:VAL:CG1	76:o:225:VAL:HG13	2.43	0.47
1:A:203:A:H2	1:A:207:A:C2	2.32	0.47
1:A:1507:U:H2'	1:A:1508:U:O2	2.15	0.47
1:A:1959:G:C2	1:A:1960:U:H1'	2.50	0.47
1:A:3780:A:H2'	1:A:3781:A:H8	1.80	0.47
3:q:180:THR:HG22	3:q:182:LYS:H	1.80	0.47
7:r:52:PHE:CE2	74:AN:49:ARG:HG3	2.50	0.47
8:AR:296:THR:O	8:AR:304:LEU:HD12	2.14	0.47
50:AF:98:VAL:HG11	50:AF:116:MET:HE3	1.97	0.47
62:AJ:18:LEU:HD12	62:AJ:86:PHE:CE1	2.50	0.47
76:o:72:VAL:HG22	76:o:77:ARG:HG3	1.96	0.47
1:A:2500:A:H5'	1:A:2501:A:C2	2.50	0.47
5:B:57:C:H2'	5:B:58:A:C8	2.48	0.47
8:AR:310:ASP:OD1	8:AR:310:ASP:N	2.47	0.47
15:E:10:ARG:HG2	15:E:11:HIS:N	2.30	0.47
24:H:41:LEU:HD12	24:H:43:ILE:HG12	1.95	0.47
24:H:93:LEU:HD12	24:H:100:ILE:HB	1.97	0.47
61:j:146:A:H5'	62:AJ:120:ARG:HD3	1.97	0.47
1:A:2886:A:OP2	12:D:69:TYR:OH	2.25	0.47
1:A:3729:A:H2'	1:A:3730:C:C6	2.49	0.47
19:5:86:ARG:NH1	66:V:138:PRO:O	2.48	0.47
23:w:101:THR:HG23	23:w:111:VAL:HG11	1.97	0.47
29:y:67:ASP:O	29:y:70:SER:OG	2.23	0.47
61:j:246:A:H2'	61:j:247:G:C8	2.50	0.47
76:o:119:SER:O	76:o:119:SER:OG	2.29	0.47
1:A:1019:A:H2'	1:A:1020:C:C6	2.50	0.46
1:A:2473:A:H2'	1:A:2474:C:C6	2.50	0.46
1:A:2590:U:O2	1:A:2590:U:H2'	2.14	0.46
8:AR:285:SER:O	8:AR:286:LYS:C	2.58	0.46
11:s:85:GLU:HG3	11:s:92:VAL:HG22	1.96	0.46
18:F:110:ARG:HA	48:P:205:ARG:HH12	1.80	0.46
29:y:146:ARG:HG2	61:j:2079:C:OP2	2.15	0.46
51:Q:63:GLU:OE1	51:Q:63:GLU:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:j:1398:U:H4'	61:j:1399:A:H2'	1.97	0.46
65:AK:57:LYS:O	65:AK:102:THR:HA	2.15	0.46
70:m:41:VAL:HA	70:m:46:THR:HG23	1.96	0.46
76:o:101:LEU:O	76:o:102:LEU:HD22	2.15	0.46
1:A:1230:A:OP1	19:5:113:ARG:NH2	2.48	0.46
1:A:2548:A:O2'	1:A:2549:A:OP1	2.34	0.46
1:A:3442:C:H5	25:7:32:CYS:HB2	1.80	0.46
8:AR:154:GLN:NE2	8:AR:193:LEU:HD22	2.30	0.46
9:C:75:A:H8	9:C:76:A:H1'	1.79	0.46
24:H:91:MET:HG2	24:H:180:VAL:HA	1.97	0.46
26:x:85:GLU:OE1	26:x:85:GLU:HA	2.16	0.46
29:y:149:ARG:NH2	29:y:151:LEU:HD21	2.30	0.46
1:A:1613:G:N2	1:A:1616:A:OP2	2.45	0.46
1:A:1909:U:O2'	1:A:1910:C:H5	1.99	0.46
11:s:135:GLU:OE2	44:AD:21:LYS:NZ	2.35	0.46
54:R:77:GLU:O	54:R:108:ARG:NH1	2.47	0.46
61:j:88:A:C5'	62:AJ:120:ARG:HG2	2.39	0.46
61:j:1448:U:H5	61:j:1812:A:N7	2.14	0.46
67:l:23:HIS:HB3	67:l:50:LEU:HD11	1.97	0.46
1:A:906:G:H2'	1:A:907:C:C6	2.51	0.46
1:A:1232:U:H5	57:S:6:LYS:O	1.98	0.46
1:A:3320:G:H2'	1:A:3321:U:C6	2.49	0.46
21:G:117:ASP:HB3	21:G:120:THR:OG1	2.15	0.46
61:j:2089:A:N6	68:AL:84:VAL:HG13	2.30	0.46
75:Y:126:GLU:OE1	75:Y:126:GLU:N	2.40	0.46
78:Z:86:ARG:HG3	78:Z:87:GLU:N	2.29	0.46
1:A:2211:C:O2'	17:u:92:ARG:NH1	2.48	0.46
3:q:170:PHE:O	3:q:172:LYS:HG3	2.16	0.46
4:AQ:27:G:C6	4:AQ:45:A:N1	2.83	0.46
8:AR:166:SER:HB2	8:AR:173:ILE:HG12	1.96	0.46
51:Q:201:ARG:HA	51:Q:201:ARG:HD2	1.74	0.46
61:j:536:C:H4'	61:j:536:C:OP1	2.14	0.46
72:X:84:THR:HG23	72:X:91:TYR:HB2	1.98	0.46
76:o:181:VAL:HG11	76:o:225:VAL:HG13	1.97	0.46
79:p:101:GLN:HA	79:p:106:GLN:HA	1.97	0.46
1:A:1142:G:H2'	1:A:1143:G:H4'	1.96	0.46
1:A:1473:A:N1	1:A:1508:U:H5	2.14	0.46
1:A:3599:U:O4	1:A:3606:G:C6	2.68	0.46
1:A:3658:G:O2'	1:A:3659:C:H6	1.98	0.46
1:A:3741:A:N6	1:A:3748:U:H3	2.14	0.46
1:A:3767:U:O2'	1:A:3770:C:OP2	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:G:71:VAL:C	21:G:72:ARG:HD2	2.40	0.46
57:S:3:ILE:HG12	57:S:5:LEU:HD23	1.97	0.46
57:S:40:THR:O	57:S:40:THR:OG1	2.32	0.46
61:j:1947:U:H2'	61:j:1948:A:C8	2.50	0.46
1:A:466:A:C6	1:A:489:U:O4	2.69	0.46
1:A:3740:A:O2'	1:A:3741:A:H5''	2.16	0.46
44:AD:101:HIS:NE2	44:AD:108:ASP:OD2	2.41	0.46
61:j:173:G:H22	61:j:267:A:H5'	1.81	0.46
61:j:1244:A:H8	61:j:1402:A:H2	1.64	0.46
64:k:179:VAL:HG23	64:k:180:LEU:N	2.31	0.46
1:A:458:A:C2	1:A:497:U:C4	3.03	0.46
1:A:3598:C:H2'	1:A:3599:U:O4'	2.16	0.46
1:A:3599:U:H5	1:A:3606:G:C2	2.29	0.46
22:6:50:ASN:OD1	22:6:77:ASN:OD1	2.34	0.46
29:y:47:LEU:HD12	64:k:66:TYR:HD2	1.80	0.46
35:AA:25:ILE:O	35:AA:29:ILE:HG12	2.15	0.46
48:P:89:VAL:O	48:P:90:HIS:HB2	2.15	0.46
53:AG:100:LYS:HG3	61:j:1284:A:C5	2.51	0.46
57:S:171:ARG:HA	57:S:175:LYS:HD3	1.98	0.46
63:U:12:ASN:O	63:U:41:LYS:HA	2.16	0.46
1:A:135:G:C2	1:A:143:C:C2	3.03	0.46
1:A:343:G:OP1	78:Z:8:SER:OG	2.31	0.46
1:A:734:A:H2'	1:A:735:A:C8	2.51	0.46
1:A:1539:U:H4'	1:A:1540:G:OP2	2.16	0.46
18:F:150:VAL:CG1	18:F:151:PRO:HD3	2.46	0.46
25:7:98:TYR:HE2	25:7:100:ILE:HD11	1.81	0.46
28:8:67:LEU:HB3	28:8:68:PRO:HD2	1.98	0.46
41:AC:13:GLY:O	41:AC:17:ARG:NH1	2.48	0.46
57:S:51:ARG:HG2	57:S:54:MET:HE2	1.97	0.46
61:j:911:U:H5''	61:j:912:U:H5	1.81	0.46
61:j:2008:U:C6	61:j:2009:C:H5	2.26	0.46
62:AJ:32:LYS:HE3	62:AJ:32:LYS:HB2	1.64	0.46
1:A:246:U:O2'	1:A:247:A:OP2	2.29	0.46
1:A:2157:G:H2'	1:A:2158:U:C6	2.50	0.46
1:A:2738:U:H2'	1:A:2810:A:H2	1.80	0.46
19:5:90:LYS:HD3	19:5:90:LYS:HA	1.70	0.46
21:G:108:GLU:HG2	21:G:122:ILE:CG2	2.46	0.46
22:6:80:LEU:HD22	22:6:90:ILE:HB	1.97	0.46
23:w:95:GLU:HA	23:w:98:THR:HG22	1.97	0.46
27:I:176:VAL:O	27:I:180:GLU:HG2	2.16	0.46
30:J:268:ALA:O	30:J:272:GLU:HG3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:b:21:HIS:CD2	37:b:22:VAL:H	2.34	0.46
62:AJ:45:ALA:HA	62:AJ:50:LEU:HB2	1.98	0.46
64:k:164:ILE:O	64:k:168:MET:HG3	2.16	0.46
67:l:29:LEU:HD21	67:l:34:LYS:HG2	1.98	0.46
1:A:1629:G:O2'	1:A:2138:U:O4	2.29	0.45
1:A:2089:C:H2'	1:A:2090:U:C6	2.51	0.45
1:A:3401:C:H2'	1:A:3402:A:H8	1.81	0.45
12:D:90:CYS:SG	12:D:101:ILE:HD12	2.56	0.45
16:4:39:PHE:O	16:4:43:GLN:HG2	2.16	0.45
27:I:78:LEU:HB2	27:I:82:LEU:O	2.16	0.45
42:N:71:LEU:HD12	42:N:74:LEU:HD12	1.97	0.45
46:e:8:ARG:HA	46:e:8:ARG:HD3	1.70	0.45
61:j:1322:A:H2'	61:j:1323:A:H8	1.81	0.45
61:j:2008:U:H6	61:j:2009:C:C5	2.25	0.45
79:p:100:LYS:HD2	79:p:107:ARG:NH2	2.31	0.45
79:p:109:ARG:HB2	79:p:130:ALA:O	2.16	0.45
61:j:1980:A:O2'	61:j:1981:A:H8	1.99	0.45
64:k:92:ILE:HG12	64:k:97:TYR:HE2	1.82	0.45
67:l:144:ILE:HG13	67:l:158:ILE:HB	1.98	0.45
5:B:96:C:O2'	19:5:140:GLU:OE1	2.34	0.45
35:AA:41:GLY:HA2	61:j:1329:G:OP2	2.15	0.45
51:Q:19:LYS:HD3	51:Q:26:VAL:CG2	2.47	0.45
61:j:217:G:H21	61:j:253:A:H2	1.63	0.45
73:n:150:VAL:O	73:n:153:GLU:HG2	2.17	0.45
1:A:338:U:H2'	1:A:339:G:H8	1.81	0.45
1:A:488:A:O2'	1:A:489:U:O2	2.35	0.45
1:A:1958:U:H2'	1:A:1959:G:C8	2.52	0.45
15:E:17:LEU:O	15:E:19:ARG:N	2.49	0.45
18:F:9:ASN:ND2	18:F:149:GLU:OE2	2.50	0.45
19:5:47:LYS:O	19:5:51:ASN:ND2	2.50	0.45
32:z:135:LEU:HD11	32:z:143:PRO:HD3	1.98	0.45
67:l:121:LEU:HD22	67:l:143:VAL:HG22	1.98	0.45
78:Z:7:LYS:HB2	78:Z:7:LYS:HE3	1.73	0.45
1:A:458:A:C2	1:A:497:U:C5	3.05	0.45
1:A:1812:C:O2'	1:A:2019:A:OP2	2.24	0.45
6:1:107:LYS:O	6:1:111:VAL:HG23	2.17	0.45
8:AR:23:TRP:NE1	8:AR:309:THR:HG23	2.32	0.45
61:j:884:G:H2'	61:j:884:G:N3	2.30	0.45
1:A:10:G:H2'	1:A:11:A:O4'	2.16	0.45
1:A:584:U:H5'	42:N:85:LYS:HG2	1.98	0.45
1:A:612:G:H2'	1:A:613:C:H6	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AR:45:LYS:HB2	8:AR:45:LYS:HE3	1.42	0.45
15:E:215:ILE:HG13	15:E:273:THR:HG23	1.97	0.45
18:F:150:VAL:HG12	18:F:151:PRO:HD3	1.99	0.45
38:AB:28:VAL:HG23	38:AB:56:LYS:O	2.16	0.45
50:AF:72:LYS:O	50:AF:75:GLU:N	2.50	0.45
61:j:750:U:H2'	61:j:751:U:H5'	1.97	0.45
1:A:509:A:H5''	31:9:119:LYS:HE2	1.98	0.45
1:A:2181:A:N3	1:A:2413:A:H2'	2.31	0.45
1:A:2829:U:H2'	1:A:2830:U:C6	2.51	0.45
1:A:3301:C:OP1	1:A:3301:C:H3'	2.17	0.45
1:A:3577:A:H3'	1:A:3581:A:N6	2.29	0.45
1:A:3747:U:O3'	1:A:3747:U:OP2	2.35	0.45
4:AQ:63:U:H2'	4:AQ:64:C:C6	2.51	0.45
8:AR:45:LYS:NZ	8:AR:71:HIS:O	2.36	0.45
29:y:75:MET:HG2	29:y:76:MET:HE2	1.98	0.45
30:J:89:LYS:HB3	30:J:252:GLN:HG3	1.99	0.45
33:K:59:LEU:HD12	33:K:69:PRO:HG2	1.99	0.45
34:a:20:VAL:CG1	34:a:32:ILE:HD12	2.47	0.45
54:R:116:ASP:OD1	54:R:116:ASP:N	2.50	0.45
61:j:414:C:H1'	61:j:2023:A:H8	1.81	0.45
70:m:164:PRO:CG	70:m:206:PRO:CG	2.83	0.45
70:m:205:LEU:HG	70:m:207:ASP:H	1.81	0.45
1:A:3571:A:O2'	1:A:3572:A:N3	2.47	0.45
11:s:35:ILE:O	11:s:36:LYS:HE2	2.17	0.45
12:D:84:THR:O	55:h:62:ARG:NH1	2.49	0.45
64:k:144:LYS:HG2	64:k:145:LYS:H	1.81	0.45
68:AL:50:GLN:O	68:AL:54:LYS:HG2	2.17	0.45
1:A:282:U:H2'	1:A:283:U:C6	2.51	0.45
1:A:1454:A:H2'	1:A:1455:C:O4'	2.17	0.45
1:A:1494:U:O2	1:A:1494:U:H2'	2.16	0.45
1:A:1690:A:H2'	1:A:1691:G:O4'	2.17	0.45
1:A:2662:G:H2'	1:A:2663:G:C8	2.52	0.45
4:AQ:62:C:H2'	4:AQ:63:U:C6	2.52	0.45
18:F:289:ILE:HG23	57:S:32:LEU:HD13	1.98	0.45
21:G:163:PHE:CE2	21:G:169:GLY:HA3	2.51	0.45
56:AH:102:PHE:O	56:AH:118:ALA:HB2	2.17	0.45
1:A:157:G:OP2	48:P:4:TYR:OH	2.33	0.45
12:D:61:VAL:HG13	12:D:74:GLU:HB2	1.98	0.45
19:5:207:VAL:HG12	19:5:211:VAL:HG23	1.98	0.45
61:j:886:U:C2	61:j:916:G:C2	3.05	0.45
61:j:890:A:N7	61:j:912:U:H2'	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:U:99:MET:HE1	63:U:119:MET:HE1	1.99	0.45
79:p:169:LYS:HG2	79:p:182:VAL:HG12	1.99	0.45
1:A:606:A:H2'	1:A:607:A:C8	2.52	0.44
1:A:1622:G:H4'	60:T:25:PRO:HG3	1.99	0.44
1:A:3738:U:P	17:u:92:ARG:NH2	2.88	0.44
1:A:3747:U:C2'	1:A:3748:U:C5'	2.95	0.44
6:1:42:LEU:HA	6:1:74:CYS:HA	1.99	0.44
18:F:110:ARG:HA	48:P:205:ARG:NH1	2.32	0.44
23:w:55:LEU:HD12	23:w:85:LYS:HD3	1.98	0.44
30:J:129:LEU:HD23	30:J:129:LEU:HA	1.85	0.44
30:J:260:LEU:O	30:J:264:MET:HG2	2.17	0.44
42:N:138:LEU:HD11	42:N:142:MET:HE2	1.99	0.44
51:Q:191:ILE:HD11	51:Q:198:LYS:HD2	1.99	0.44
76:o:15:PRO:HG2	76:o:18:TRP:CE2	2.52	0.44
80:AP:110:ASP:O	80:AP:113:LYS:NZ	2.34	0.44
1:A:688:U:H2'	1:A:689:U:C6	2.53	0.44
1:A:2169:A:O2'	1:A:3277:G:OP1	2.30	0.44
16:4:61:ALA:O	16:4:65:LYS:HG3	2.18	0.44
24:H:101:ASN:HB2	24:H:114:ARG:HB2	1.99	0.44
46:e:17:ARG:CZ	75:Y:164:LEU:HD23	2.47	0.44
61:j:146:A:H5'	62:AJ:120:ARG:CD	2.47	0.44
61:j:508:U:H2'	61:j:509:U:O4'	2.18	0.44
64:k:113:LEU:HD22	64:k:209:ASN:HD21	1.82	0.44
67:l:26:THR:OG1	67:l:27:LYS:N	2.50	0.44
70:m:78:PHE:CD1	70:m:85:VAL:HG21	2.52	0.44
70:m:159:ILE:HG13	70:m:190:MET:HE1	1.99	0.44
1:A:86:G:N2	1:A:99:A:OP2	2.40	0.44
1:A:244:U:O2'	1:A:245:U:H5'	2.17	0.44
1:A:378:U:H3	1:A:382:A:H2	1.63	0.44
1:A:873:U:H2'	1:A:874:A:C8	2.52	0.44
1:A:1506:C:H2'	1:A:1507:U:O2	2.17	0.44
2:0:20:ILE:HG12	2:0:39:LEU:HB3	2.00	0.44
4:AQ:2:G:H1	4:AQ:69:U:H3	1.65	0.44
9:C:4:C:H2'	9:C:5:A:H5''	1.99	0.44
50:AF:92:ASP:OD1	50:AF:92:ASP:N	2.46	0.44
53:AG:50:SER:OG	53:AG:51:LYS:N	2.49	0.44
61:j:396:G:H8	61:j:2023:A:O2'	2.00	0.44
76:o:87:MET:HE3	76:o:226:PHE:CE1	2.53	0.44
78:Z:33:LYS:O	78:Z:105:LEU:HD23	2.18	0.44
79:p:80:GLN:O	79:p:84:CYS:HB3	2.16	0.44
79:p:131:LYS:HB2	79:p:131:LYS:HE3	1.74	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2742:G:H2'	1:A:2743:A:C8	2.52	0.44
3:q:78:LYS:N	3:q:81:MET:HE3	2.33	0.44
8:AR:290:PRO:HG2	8:AR:309:THR:OG1	2.17	0.44
15:E:359:SER:O	15:E:361:LYS:NZ	2.48	0.44
17:u:81:VAL:HG21	17:u:94:LYS:HA	1.99	0.44
54:R:18:VAL:HG12	54:R:19:LYS:O	2.18	0.44
61:j:509:U:H3'	61:j:510:G:H8	1.82	0.44
61:j:1322:A:H2'	61:j:1323:A:C8	2.53	0.44
61:j:2086:A:N3	68:AL:79:ILE:HD11	2.31	0.44
72:X:119:PHE:C	72:X:120:LEU:HD22	2.42	0.44
1:A:142:C:H2'	1:A:143:C:H6	1.82	0.44
1:A:2180:U:HO2'	1:A:2181:A:P	2.40	0.44
8:AR:170:ASN:OD1	8:AR:170:ASN:N	2.50	0.44
11:s:105:GLN:HE22	61:j:754:A:H62	1.64	0.44
19:5:152:THR:HG21	19:5:253:ILE:HD11	1.98	0.44
21:G:38:GLU:HG2	21:G:45:PRO:HD3	2.00	0.44
68:AL:79:ILE:HG22	68:AL:84:VAL:HB	1.99	0.44
1:A:1765:A:H2'	1:A:1766:U:C6	2.53	0.44
1:A:1976:A:N1	1:A:1992:U:O4	2.50	0.44
1:A:3593:U:H2'	1:A:3594:G:H8	1.82	0.44
4:AQ:15:G:N2	4:AQ:48:U:H3	2.08	0.44
24:H:93:LEU:HD23	24:H:93:LEU:H	1.83	0.44
30:J:170:ILE:HD12	30:J:183:LEU:HD13	2.00	0.44
34:a:30:LEU:HA	34:a:30:LEU:HD23	1.86	0.44
42:N:101:VAL:O	42:N:104:GLU:HG3	2.18	0.44
47:AE:53:GLU:OE1	47:AE:53:GLU:N	2.50	0.44
61:j:1967:G:H21	61:j:2023:A:H2	1.65	0.44
63:U:34:TYR:CE1	66:V:150:ILE:HD11	2.52	0.44
1:A:195:A:C8	1:A:216:C:O2'	2.68	0.44
1:A:1083:G:H2'	1:A:1084:A:H8	1.81	0.44
1:A:1681:C:H2'	1:A:1682:U:C6	2.52	0.44
8:AR:295:LEU:HD22	8:AR:304:LEU:HD11	1.99	0.44
12:D:219:ILE:HG22	12:D:221:HIS:H	1.83	0.44
16:4:37:PRO:C	16:4:39:PHE:H	2.25	0.44
18:F:228:ASP:OD1	18:F:229:LEU:N	2.49	0.44
24:H:53:TYR:O	24:H:53:TYR:CD1	2.70	0.44
31:9:46:ILE:HG22	31:9:63:ILE:CD1	2.46	0.44
38:AB:56:LYS:HB2	38:AB:60:GLU:OE2	2.18	0.44
40:c:37:CYS:HB3	40:c:42:TYR:H	1.82	0.44
43:d:10:LYS:O	43:d:14:ILE:HG12	2.17	0.44
51:Q:187:LYS:HB2	51:Q:189:ARG:HG2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:j:884:G:O6	61:j:917:C:N4	2.50	0.44
61:j:911:U:H5''	61:j:912:U:C5	2.53	0.44
61:j:1428:A:H2'	61:j:1429:C:H6	1.82	0.44
68:AL:59:TYR:C	68:AL:61:THR:H	2.26	0.44
1:A:149:A:H2'	1:A:150:C:C6	2.53	0.44
1:A:1474:A:N1	1:A:1507:U:O4	2.50	0.44
1:A:1912:A:H8	1:A:1913:A:C8	2.35	0.44
1:A:3358:U:H2'	1:A:3359:A:C8	2.52	0.44
1:A:3566:C:C4	69:W:9:ARG:CZ	3.01	0.44
18:F:218:LYS:HA	18:F:229:LEU:HD13	1.99	0.44
20:v:101:SER:O	20:v:105:GLU:HG3	2.16	0.44
21:G:108:GLU:HG2	21:G:122:ILE:HG21	1.99	0.44
29:y:19:PRO:HB2	29:y:20:GLN:H	1.66	0.44
30:J:102:PRO:O	30:J:106:THR:HG23	2.17	0.44
44:AD:114:ARG:O	44:AD:118:THR:HG23	2.18	0.44
59:AI:4:ASP:OD1	59:AI:5:GLN:N	2.51	0.44
64:k:130:LEU:HD23	64:k:130:LEU:HA	1.87	0.44
70:m:192:PRO:O	70:m:193:THR:C	2.59	0.44
79:p:82:ASN:O	79:p:83:GLU:HG2	2.18	0.44
1:A:459:G:H2'	1:A:460:A:C8	2.53	0.44
1:A:656:U:H2'	1:A:657:A:C8	2.53	0.44
1:A:1155:C:H2'	1:A:1156:U:H5''	1.99	0.44
1:A:2165:G:H1'	39:M:18:SER:HB3	1.99	0.44
4:AQ:62:C:O2'	4:AQ:63:U:P	2.76	0.44
22:6:39:THR:HB	22:6:41:LYS:HG2	2.00	0.44
31:9:99:CYS:SG	31:9:100:ILE:N	2.91	0.44
50:AF:36:GLU:HG3	50:AF:47:LYS:HD2	2.00	0.44
54:R:39:GLN:HG2	54:R:40:ASP:H	1.83	0.44
59:AI:15:ARG:HH11	59:AI:33:GLN:HE21	1.65	0.44
61:j:486:A:H2'	61:j:487:A:C8	2.51	0.44
61:j:1059:U:H2'	61:j:1060:G:O4'	2.18	0.44
78:Z:51:LYS:O	78:Z:69:VAL:HB	2.18	0.44
1:A:1141:G:N2	1:A:1157:U:O4	2.51	0.43
3:q:198:ARG:NH2	61:j:180:U:O3'	2.29	0.43
8:AR:281:PRO:HB3	8:AR:291:TRP:NE1	2.33	0.43
12:D:113:ILE:HD12	12:D:116:LEU:HD12	2.00	0.43
33:K:42:ILE:HG22	33:K:43:SER:H	1.83	0.43
36:L:77:GLU:OE1	37:b:26:ARG:NH1	2.47	0.43
50:AF:116:MET:HE2	50:AF:116:MET:HB3	1.84	0.43
61:j:512:A:OP2	61:j:512:A:H3'	2.18	0.43
61:j:1675:G:H2'	61:j:1676:U:C6	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:j:1836:G:H5''	61:j:1836:G:C8	2.53	0.43
70:m:197:THR:HG22	70:m:198:ARG:H	1.83	0.43
72:X:108:LYS:HA	72:X:111:ILE:HG12	1.99	0.43
75:Y:125:GLU:OE1	75:Y:125:GLU:N	2.51	0.43
76:o:185:ALA:O	76:o:189:VAL:HG22	2.17	0.43
80:AP:92:LYS:HG3	80:AP:93:HIS:H	1.82	0.43
1:A:600:U:H2'	1:A:601:G:H8	1.83	0.43
1:A:718:U:H2'	1:A:719:C:C6	2.54	0.43
1:A:2008:G:H2'	1:A:2009:A:C8	2.53	0.43
13:3:107:LYS:HA	13:3:110:VAL:HG12	2.00	0.43
14:t:14:ILE:HD13	14:t:25:VAL:HG11	1.99	0.43
18:F:386:LYS:HD3	66:V:151:THR:O	2.19	0.43
21:G:24:GLY:HA2	21:G:65:ILE:HG23	2.00	0.43
38:AB:119:ILE:HG22	53:AG:119:PHE:HE1	1.84	0.43
40:c:47:LYS:HZ2	40:c:49:ARG:HD2	1.82	0.43
42:N:75:LYS:HG3	63:U:183:ARG:HH21	1.83	0.43
59:AI:24:ILE:H	59:AI:24:ILE:HD12	1.83	0.43
61:j:1271:G:C2	61:j:1272:A:C8	3.06	0.43
61:j:2011:G:H2'	61:j:2012:G:O4'	2.18	0.43
19:5:233:ALA:HB2	19:5:242:TRP:CE2	2.53	0.43
29:y:36:SER:C	29:y:38:ASN:H	2.27	0.43
56:AH:4:GLN:O	56:AH:4:GLN:NE2	2.49	0.43
62:AJ:29:HIS:CE1	62:AJ:34:SER:H	2.36	0.43
1:A:87:U:H5	1:A:99:A:N7	2.16	0.43
1:A:626:A:H2'	1:A:627:U:C6	2.53	0.43
1:A:1109:U:H2'	1:A:1110:U:C6	2.53	0.43
14:t:31:SER:O	14:t:35:ILE:HG12	2.18	0.43
24:H:75:HIS:O	24:H:79:MET:HG2	2.18	0.43
27:I:87:GLY:O	27:I:88:PRO:C	2.61	0.43
44:AD:99:ARG:O	44:AD:103:GLU:HG2	2.19	0.43
61:j:1916:C:H2'	61:j:1917:C:H6	1.82	0.43
76:o:200:LYS:HA	76:o:206:ASP:CG	2.44	0.43
1:A:167:U:H3	1:A:264:U:H3	1.65	0.43
1:A:2460:A:H2'	1:A:2461:A:C8	2.54	0.43
1:A:3384:G:H2'	1:A:3385:U:C6	2.54	0.43
4:AQ:60:U:C6	4:AQ:61:C:H5	2.35	0.43
42:N:25:VAL:HG12	42:N:76:LEU:HD21	2.00	0.43
57:S:98:LYS:HG2	57:S:118:GLU:HG2	1.99	0.43
58:i:92:MET:HE2	58:i:92:MET:HB2	1.78	0.43
61:j:963:U:H2'	61:j:964:G:C8	2.54	0.43
61:j:1025:U:OP1	61:j:1173:C:O2'	2.35	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:j:1273:G:H2'	61:j:1274:C:O4'	2.19	0.43
67:l:198:VAL:HG12	67:l:199:ASP:H	1.83	0.43
1:A:169:U:H2'	1:A:170:U:O4'	2.19	0.43
1:A:660:U:O2	1:A:660:U:H2'	2.18	0.43
1:A:1156:U:H2'	1:A:1157:U:O4'	2.18	0.43
1:A:2708:C:H5''	12:D:207:VAL:HG12	2.01	0.43
8:AR:155:GLN:HG3	8:AR:156:HIS:H	1.83	0.43
32:z:70:LYS:HG2	32:z:93:LEU:HD22	2.01	0.43
33:K:192:GLN:HA	33:K:195:VAL:HG12	2.00	0.43
36:L:28:ASN:HA	36:L:31:LYS:HG2	2.01	0.43
38:AB:88:ARG:HB3	38:AB:91:ASP:OD1	2.18	0.43
51:Q:36:MET:HE2	51:Q:69:ARG:HH11	1.83	0.43
67:l:127:ARG:NH2	67:l:152:PRO:HD3	2.34	0.43
78:Z:31:SER:HA	78:Z:48:PRO:HA	2.00	0.43
6:1:94:LYS:HB2	6:1:94:LYS:HE3	1.73	0.43
21:G:60:ARG:HB3	21:G:63:GLU:HG3	2.00	0.43
24:H:167:ARG:O	24:H:169:LYS:N	2.50	0.43
30:J:224:ASP:N	30:J:224:ASP:OD1	2.51	0.43
43:d:34:LYS:O	43:d:35:ASN:C	2.59	0.43
66:V:41:VAL:HG21	66:V:97:VAL:HG13	2.00	0.43
78:Z:30:MET:HE3	78:Z:77:TYR:HA	2.01	0.43
1:A:179:G:HO2'	1:A:180:C:P	2.42	0.43
2:0:63:ARG:HB2	2:0:68:LYS:HB3	2.01	0.43
5:B:42:A:C1'	21:G:72:ARG:HH12	2.31	0.43
8:AR:265:ILE:HB	8:AR:279:ILE:HB	2.01	0.43
11:s:156:ASP:OD1	11:s:156:ASP:N	2.49	0.43
11:s:157:SER:OG	11:s:189:PRO:HG2	2.19	0.43
13:3:47:HIS:O	13:3:51:LYS:HG2	2.18	0.43
20:v:128:LYS:HG2	61:j:1903:U:OP2	2.18	0.43
36:L:45:ASN:HB3	36:L:48:THR:HG23	2.01	0.43
55:h:80:LYS:O	55:h:84:ILE:HG12	2.18	0.43
78:Z:77:TYR:O	78:Z:78:LYS:HG3	2.18	0.43
1:A:1035:G:H5'	1:A:1036:A:OP1	2.19	0.43
1:A:1990:A:H5'	1:A:1991:U:OP2	2.18	0.43
1:A:3036:A:H2'	1:A:3037:G:C8	2.54	0.43
9:C:79:G:N7	46:e:30:LYS:HE2	2.33	0.43
12:D:180:LEU:HD13	55:h:26:ILE:HG13	2.00	0.43
14:t:76:SER:OG	61:j:1203:G:OP1	2.24	0.43
15:E:47:MET:HE3	15:E:176:MET:SD	2.59	0.43
20:v:116:SER:HA	20:v:119:VAL:O	2.18	0.43
21:G:102:PHE:CE2	21:G:129:VAL:HG21	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:z:107:PHE:CE2	32:z:114:VAL:HB	2.54	0.43
52:g:21:LYS:HE2	52:g:25:ARG:HH21	1.84	0.43
57:S:19:LEU:HD11	57:S:30:VAL:HG21	2.01	0.43
61:j:831:U:C4	62:AJ:47:MET:HE2	2.54	0.43
67:l:49:ASN:C	67:l:49:ASN:HD22	2.25	0.43
72:X:113:MET:HE3	72:X:113:MET:HB2	1.84	0.43
73:n:92:LYS:HD3	73:n:95:TYR:HE2	1.84	0.43
1:A:455:U:H2'	1:A:456:A:C8	2.54	0.43
1:A:1225:A:H5'	66:V:130:LYS:HB2	1.99	0.43
1:A:1961:U:O2'	1:A:1962:U:OP2	2.28	0.43
1:A:3566:C:N4	69:W:9:ARG:NH2	2.67	0.43
3:q:109:LEU:HB3	3:q:111:LEU:HD22	2.01	0.43
6:1:3:LYS:HE2	22:6:39:THR:HG22	2.01	0.43
12:D:178:PRO:HD2	55:h:26:ILE:HD13	2.00	0.43
19:5:89:GLU:H	19:5:89:GLU:HG2	1.66	0.43
29:y:85:LEU:HD23	29:y:85:LEU:HA	1.87	0.43
44:AD:33:ILE:HD12	44:AD:66:VAL:HG11	2.01	0.43
75:Y:156:ASP:OD1	75:Y:156:ASP:N	2.52	0.43
1:A:456:A:H2'	1:A:457:A:C8	2.51	0.42
18:F:70:GLY:C	18:F:72:ALA:H	2.27	0.42
18:F:114:LYS:HE2	18:F:114:LYS:HB2	1.80	0.42
33:K:174:LEU:HD23	33:K:174:LEU:HA	1.87	0.42
37:b:86:THR:O	37:b:87:HIS:C	2.62	0.42
55:h:14:TYR:HE2	55:h:26:ILE:HG21	1.83	0.42
56:AH:131:GLU:OE1	56:AH:145:ARG:NH1	2.51	0.42
61:j:890:A:N7	61:j:912:U:C2	2.87	0.42
61:j:1122:A:H61	61:j:1166:C:H41	1.65	0.42
64:k:98:THR:O	64:k:98:THR:HG22	2.19	0.42
79:p:132:GLU:HB2	79:p:135:THR:HG22	2.00	0.42
1:A:1247:C:H2'	1:A:1248:A:C8	2.55	0.42
1:A:2538:C:H4'	12:D:221:HIS:O	2.19	0.42
3:q:7:ASN:C	3:q:7:ASN:HD22	2.26	0.42
3:q:63:MET:HG2	3:q:99:GLY:O	2.19	0.42
7:r:35:LYS:HB2	7:r:35:LYS:HE3	1.88	0.42
19:5:97:ARG:HD3	19:5:119:GLN:O	2.19	0.42
19:5:203:THR:O	19:5:205:GLY:N	2.52	0.42
50:AF:106:ILE:CD1	67:l:18:LEU:HD11	2.49	0.42
57:S:82:VAL:O	57:S:82:VAL:HG12	2.19	0.42
60:T:169:ARG:HH22	61:j:877:U:H5''	1.85	0.42
61:j:201:G:H2'	61:j:202:G:C8	2.54	0.42
61:j:1423:A:H4'	61:j:1424:A:O5'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:V:45:CYS:SG	66:V:53:MET:HE3	2.59	0.42
67:l:30:GLU:HG3	67:l:30:GLU:O	2.19	0.42
1:A:3028:A:N3	1:A:3028:A:H2'	2.34	0.42
1:A:3524:G:H2'	1:A:3525:A:O4'	2.18	0.42
6:l:142:LYS:HB2	6:l:142:LYS:HE2	1.78	0.42
7:r:69:MET:HG2	7:r:70:HIS:H	1.84	0.42
12:D:159:ASP:OD1	12:D:160:ALA:N	2.53	0.42
17:u:112:TRP:O	17:u:115:ASN:ND2	2.51	0.42
19:5:186:LEU:HD21	19:5:211:VAL:HG22	2.01	0.42
19:5:221:LYS:O	19:5:256:MET:HB2	2.19	0.42
22:6:76:ASP:H	22:6:79:ASP:HB2	1.83	0.42
30:J:174:VAL:HG21	30:J:180:VAL:HG22	2.01	0.42
36:L:106:GLU:OE2	36:L:106:GLU:N	2.48	0.42
38:AB:22:VAL:HG23	38:AB:23:ASP:H	1.84	0.42
53:AG:85:ILE:HG12	53:AG:114:TYR:O	2.20	0.42
57:S:42:ALA:C	57:S:44:PHE:H	2.27	0.42
61:j:1022:A:H2'	61:j:1023:A:O4'	2.19	0.42
70:m:114:LEU:HD12	70:m:114:LEU:HA	1.90	0.42
1:A:709:A:H8	1:A:709:A:H2'	1.58	0.42
1:A:1762:A:O2'	1:A:1763:G:H8	1.79	0.42
1:A:1906:A:H2'	1:A:1907:A:H8	1.80	0.42
1:A:3375:A:H2'	1:A:3376:U:C6	2.54	0.42
4:AQ:65:A:H2'	4:AQ:65:A:N3	2.33	0.42
5:B:63:A:H2'	5:B:63:A:N3	2.34	0.42
8:AR:200:HIS:CE1	8:AR:204:LEU:CD2	3.03	0.42
29:y:142:LYS:HB3	68:AL:22:ARG:NE	2.35	0.42
57:S:30:VAL:HG22	57:S:52:LEU:CD1	2.49	0.42
61:j:585:U:O2'	61:j:1685:U:O2'	2.37	0.42
61:j:1267:C:H2'	61:j:1268:G:O4'	2.20	0.42
64:k:81:HIS:HA	64:k:106:THR:HG21	2.00	0.42
72:X:118:ASP:OD1	72:X:118:ASP:O	2.37	0.42
1:A:610:U:C2	1:A:611:G:C8	3.07	0.42
1:A:896:U:H2'	1:A:897:U:C6	2.54	0.42
1:A:2832:A:H4'	1:A:2833:U:OP2	2.20	0.42
1:A:2832:A:C6	30:J:70:LYS:HE2	2.55	0.42
1:A:3609:A:H2'	1:A:3610:C:C6	2.55	0.42
2:O:27:LYS:HB2	39:M:95:ILE:CD1	2.50	0.42
13:3:21:LEU:HD11	13:3:25:LYS:HE3	2.00	0.42
19:5:90:LYS:HG3	19:5:147:TYR:CD1	2.54	0.42
21:G:34:ALA:O	21:G:38:GLU:HG3	2.19	0.42
39:M:106:ASN:OD1	39:M:107:PRO:HD2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:e:41:ARG:HA	46:e:41:ARG:HD2	1.87	0.42
62:AJ:64:LEU:HD21	62:AJ:71:LYS:HE3	2.01	0.42
66:V:84:ARG:NH1	66:V:86:GLU:OE2	2.52	0.42
70:m:93:GLU:HG2	70:m:94:HIS:N	2.35	0.42
73:n:63:ASP:OD1	73:n:64:GLU:N	2.53	0.42
78:Z:113:ASN:O	78:Z:117:ILE:HG12	2.20	0.42
1:A:744:G:N2	1:A:915:G:N2	2.68	0.42
1:A:1642:G:OP2	1:A:1642:G:N2	2.41	0.42
1:A:1981:U:H3	1:A:1989:A:H61	1.67	0.42
1:A:3645:A:N7	1:A:3646:G:H1'	2.34	0.42
37:b:103:LEU:HD12	37:b:106:ARG:NH2	2.34	0.42
44:AD:25:TRP:CD2	71:AM:80:LYS:HD3	2.55	0.42
61:j:1986:A:H5'	61:j:1987:A:OP2	2.20	0.42
64:k:62:LYS:HB2	64:k:62:LYS:HE3	1.81	0.42
67:l:33:MET:HE3	67:l:33:MET:HB3	1.86	0.42
67:l:116:THR:HG23	67:l:116:THR:O	2.20	0.42
67:l:150:ASP:OD1	67:l:150:ASP:N	2.50	0.42
79:p:182:VAL:CG2	79:p:209:PHE:HB2	2.49	0.42
80:AP:121:CYS:HA	80:AP:130:MET:CE	2.50	0.42
1:A:300:C:H2'	1:A:301:U:O4'	2.20	0.42
1:A:615:U:H2'	1:A:616:U:C6	2.54	0.42
1:A:681:U:HO2'	1:A:682:A:P	2.39	0.42
1:A:1534:U:O2'	1:A:1535:G:OP2	2.32	0.42
4:AQ:7:U:O2'	4:AQ:49:C:H5''	2.19	0.42
11:s:41:GLU:HG3	11:s:72:TYR:CE2	2.54	0.42
61:j:16:G:H2'	61:j:17:C:C6	2.54	0.42
61:j:818:C:C2	73:n:143:ILE:HD13	2.54	0.42
61:j:1744:A:H8	61:j:1744:A:OP2	2.02	0.42
62:AJ:63:THR:O	62:AJ:63:THR:HG22	2.20	0.42
69:W:85:ALA:O	69:W:89:LYS:HG3	2.20	0.42
73:n:182:GLU:HA	73:n:185:GLU:HG3	2.02	0.42
79:p:173:LYS:HG3	79:p:178:ARG:NH2	2.35	0.42
1:A:234:C:H2'	1:A:235:A:O4'	2.19	0.42
1:A:583:U:HO2'	1:A:584:U:H6	1.62	0.42
1:A:3713:C:H2'	1:A:3714:C:C6	2.55	0.42
8:AR:42:SER:C	8:AR:44:ASP:H	2.28	0.42
14:t:22:ARG:HA	14:t:22:ARG:HD3	1.86	0.42
19:5:120:VAL:HG12	19:5:121:HIS:CD2	2.55	0.42
27:I:58:LYS:HB2	27:I:74:ILE:HD11	2.02	0.42
31:9:50:LYS:O	31:9:57:ASP:HB3	2.20	0.42
33:K:31:ARG:HD3	33:K:100:LYS:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:L:92:ILE:O	36:L:94:ILE:N	2.51	0.42
48:P:114:LEU:HB3	48:P:135:LEU:HD12	2.00	0.42
76:o:41:SER:OG	76:o:42:ILE:N	2.53	0.42
79:p:196:THR:HG22	79:p:226:ILE:HD11	2.02	0.42
1:A:857:C:H2'	1:A:858:C:C6	2.55	0.42
1:A:3035:A:H2'	1:A:3036:A:C8	2.55	0.42
1:A:3490:A:H2'	1:A:3491:U:O4'	2.20	0.42
3:q:175:ILE:HD11	3:q:178:LEU:HD12	2.01	0.42
10:2:17:ASN:OD1	10:2:18:CYS:N	2.53	0.42
13:3:52:ASN:O	13:3:56:VAL:HG23	2.20	0.42
14:t:68:ARG:HD3	79:p:242:TRP:CZ2	2.55	0.42
24:H:59:TRP:O	24:H:60:PHE:C	2.63	0.42
26:x:35:GLU:OE1	26:x:74:HIS:NE2	2.53	0.42
30:J:223:GLU:OE2	30:J:223:GLU:N	2.53	0.42
39:M:17:LEU:HD23	39:M:55:SER:HB3	2.02	0.42
42:N:11:LYS:HA	42:N:14:ILE:HD12	2.01	0.42
61:j:597:C:H2'	61:j:598:A:C8	2.55	0.42
64:k:208:GLN:O	64:k:210:VAL:HG23	2.20	0.42
66:V:52:GLY:HA3	66:V:93:ARG:HB2	2.00	0.42
74:AN:10:GLU:HG3	74:AN:26:ARG:O	2.20	0.42
78:Z:51:LYS:HA	78:Z:72:ILE:HD11	2.01	0.42
1:A:835:G:HO2'	1:A:836:G:P	2.42	0.42
1:A:1828:G:H22	1:A:1997:G:H8	1.66	0.42
1:A:2699:C:H2'	1:A:2700:C:H6	1.84	0.42
1:A:3599:U:H5	1:A:3606:G:C4	2.37	0.42
3:q:173:PRO:HB3	61:j:66:U:O2	2.20	0.42
30:J:114:LYS:HE2	30:J:114:LYS:HB2	1.71	0.42
36:L:135:GLY:HA3	36:L:139:ILE:O	2.19	0.42
45:O:61:LEU:HD23	45:O:61:LEU:HA	1.80	0.42
61:j:1744:A:C2	61:j:1788:U:H5	2.37	0.42
66:V:29:ASN:HD22	66:V:32:LEU:HD12	1.85	0.42
1:A:857:C:H2'	1:A:858:C:H6	1.85	0.41
1:A:2738:U:H3	1:A:2811:A:N6	2.17	0.41
1:A:3120:U:OP1	1:A:3140:U:H5	2.03	0.41
1:A:3402:A:H2'	1:A:3403:A:H8	1.82	0.41
10:2:10:TRP:CZ2	10:2:44:PRO:HD3	2.54	0.41
23:w:71:GLU:HG2	61:j:1675:G:H1'	2.02	0.41
40:c:20:PHE:CG	40:c:21:LEU:N	2.88	0.41
50:AF:111:ILE:HD11	67:l:11:GLU:HA	2.01	0.41
53:AG:36:LEU:HD23	53:AG:36:LEU:HA	1.87	0.41
61:j:1220:C:H2'	61:j:1221:G:H8	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:j:1972:G:H2'	61:j:1973:U:C6	2.55	0.41
61:j:2031:C:H2'	61:j:2032:U:C6	2.55	0.41
1:A:501:U:H2'	1:A:502:U:C6	2.55	0.41
1:A:594:C:H5'	1:A:595:U:OP2	2.20	0.41
1:A:687:G:H2'	1:A:688:U:C6	2.54	0.41
1:A:993:U:OP1	1:A:994:G:H5'	2.19	0.41
1:A:1540:G:OP1	28:8:125:ARG:NH1	2.53	0.41
1:A:1914:A:H2'	1:A:1915:A:H4'	2.02	0.41
1:A:1968:C:H2'	1:A:1969:A:C2	2.54	0.41
1:A:3606:G:H2'	1:A:3607:G:C8	2.49	0.41
1:A:3713:C:H2'	1:A:3714:C:H6	1.84	0.41
3:q:77:PHE:HA	3:q:81:MET:HE3	2.01	0.41
4:AQ:4:U:H2'	4:AQ:5:A:C8	2.55	0.41
8:AR:45:LYS:NZ	8:AR:72:SER:HA	2.35	0.41
8:AR:287:ILE:H	8:AR:287:ILE:HG12	1.42	0.41
11:s:9:LEU:HD11	11:s:17:GLU:CG	2.50	0.41
11:s:68:ILE:H	11:s:68:ILE:HD12	1.85	0.41
30:J:255:SER:O	30:J:259:MET:HG2	2.19	0.41
33:K:93:LYS:HA	33:K:96:LEU:HD12	2.01	0.41
57:S:89:LYS:HA	57:S:89:LYS:HD2	1.93	0.41
60:T:122:PHE:HA	60:T:125:LYS:HB2	2.02	0.41
65:AK:60:THR:HG23	65:AK:63:ALA:H	1.84	0.41
1:A:296:A:C2	48:P:93:LYS:HD3	2.55	0.41
1:A:953:U:H2'	1:A:954:G:O4'	2.20	0.41
1:A:2441:U:H2'	1:A:2442:A:C8	2.56	0.41
1:A:2740:A:H2'	1:A:2741:A:O4'	2.20	0.41
1:A:3379:A:H2'	1:A:3380:U:C6	2.56	0.41
9:C:138:U:H2'	9:C:139:A:H5''	2.02	0.41
34:a:20:VAL:HG11	34:a:32:ILE:HD12	2.01	0.41
36:L:45:ASN:HB3	36:L:48:THR:CG2	2.50	0.41
37:b:82:LYS:HD2	37:b:82:LYS:HA	1.81	0.41
47:AE:40:LYS:HB2	47:AE:40:LYS:HE2	1.95	0.41
48:P:85:LYS:HA	58:i:49:PHE:O	2.20	0.41
57:S:145:ARG:HE	57:S:147:ALA:HB3	1.85	0.41
60:T:67:LEU:HD23	60:T:67:LEU:HA	1.96	0.41
61:j:53:G:H4'	62:AJ:110:LYS:NZ	2.35	0.41
61:j:1744:A:H2'	61:j:1745:U:C5	2.54	0.41
61:j:1830:C:H4'	61:j:1836:G:C6	2.56	0.41
1:A:582:U:O2'	1:A:583:U:H5''	2.19	0.41
1:A:893:U:O2'	1:A:894:U:O4'	2.38	0.41
1:A:1536:U:O4	18:F:188:LYS:HE2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1739:C:H2'	1:A:1740:A:H8	1.84	0.41
1:A:3418:A:H2'	1:A:3419:U:O2	2.21	0.41
13:3:94:LEU:HD21	48:P:153:CYS:SG	2.60	0.41
18:F:359:VAL:O	18:F:363:ILE:HG13	2.20	0.41
19:5:89:GLU:OE2	66:V:137:LYS:N	2.52	0.41
37:b:77:LEU:HB2	37:b:94:ARG:NH2	2.35	0.41
54:R:38:LEU:HD13	66:V:31:TYR:HB3	2.03	0.41
54:R:67:ALA:H	54:R:72:ASP:HB2	1.85	0.41
61:j:485:C:H2'	61:j:486:A:C8	2.55	0.41
61:j:520:U:H2'	61:j:521:G:C8	2.56	0.41
61:j:1392:C:H2'	61:j:1393:G:H8	1.84	0.41
63:U:87:LEU:HD12	63:U:99:MET:O	2.20	0.41
63:U:96:THR:HG23	66:V:157:PHE:CD2	2.56	0.41
68:AL:36:ILE:O	68:AL:36:ILE:HG13	2.20	0.41
80:AP:118:LYS:HB2	80:AP:129:LEU:HD23	2.02	0.41
1:A:527:A:H2'	1:A:528:A:H8	1.86	0.41
1:A:873:U:H2'	1:A:874:A:H8	1.84	0.41
11:s:9:LEU:HD11	11:s:17:GLU:HG2	2.02	0.41
15:E:289:ASN:HB2	15:E:292:SER:OG	2.20	0.41
16:4:13:ASN:HA	16:4:16:ALA:HB3	2.02	0.41
20:v:115:ARG:C	20:v:117:LEU:H	2.29	0.41
21:G:23:VAL:HG12	21:G:25:GLU:HG2	2.03	0.41
25:7:27:LEU:HD22	25:7:43:GLU:OE1	2.20	0.41
38:AB:103:ASN:O	38:AB:104:GLN:C	2.62	0.41
61:j:880:A:H2'	61:j:881:C:O4'	2.20	0.41
61:j:1942:G:H22	61:j:2047:A:H2	1.67	0.41
62:AJ:17:LEU:HD11	76:o:92:ILE:HG21	2.02	0.41
1:A:203:A:C2	1:A:207:A:C2	3.09	0.41
1:A:939:A:H2'	1:A:940:A:C8	2.56	0.41
1:A:3116:A:N6	45:O:60:HIS:ND1	2.68	0.41
24:H:1:MET:HG2	24:H:2:LYS:N	2.36	0.41
24:H:108:ASN:HB3	24:H:132:VAL:HG23	2.01	0.41
27:I:137:ILE:O	27:I:175:LYS:NZ	2.32	0.41
29:y:61:LYS:HE2	29:y:76:MET:HB3	2.03	0.41
30:J:263:LYS:HB2	30:J:267:LYS:HD3	2.01	0.41
35:AA:76:CYS:HB2	35:AA:83:LEU:HD11	2.01	0.41
35:AA:112:ILE:HD13	35:AA:112:ILE:HA	1.88	0.41
43:d:59:LYS:O	43:d:63:ILE:HG12	2.20	0.41
54:R:51:PHE:N	54:R:147:PHE:O	2.41	0.41
54:R:111:LYS:HA	54:R:111:LYS:HD2	1.92	0.41
56:AH:64:LYS:HE2	56:AH:64:LYS:HB3	1.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:j:937:G:H2'	61:j:938:U:C6	2.55	0.41
61:j:1321:C:H2'	61:j:1322:A:H8	1.86	0.41
67:l:148:ASP:HA	67:l:162:CYS:O	2.21	0.41
1:A:203:A:H2	1:A:207:A:N1	2.19	0.41
1:A:1462:C:H2'	1:A:1463:A:C8	2.55	0.41
1:A:1992:U:C5	1:A:1993:A:C5	3.09	0.41
1:A:3001:A:H2'	1:A:3002:G:H8	1.85	0.41
1:A:3379:A:H2'	1:A:3380:U:H6	1.85	0.41
8:AR:262:ASP:HB2	8:AR:290:PRO:HA	2.03	0.41
23:w:79:PHE:HB3	41:AC:50:PHE:HB3	2.01	0.41
43:d:42:LYS:HA	43:d:50:TYR:O	2.21	0.41
56:AH:54:PRO:HD3	56:AH:76:TYR:CE2	2.55	0.41
61:j:543:A:H2'	61:j:544:G:O4'	2.21	0.41
61:j:1000:C:O2	64:k:120:LEU:HD21	2.21	0.41
61:j:1171:U:H4'	71:AM:15:LYS:HZ2	1.85	0.41
1:A:134:G:H2'	1:A:135:G:C8	2.56	0.41
1:A:622:U:H2'	1:A:623:U:C6	2.55	0.41
15:E:155:LEU:HG	15:E:185:MET:CE	2.51	0.41
18:F:279:LEU:HD12	18:F:280:PRO:HD2	2.02	0.41
55:h:51:CYS:SG	55:h:52:VAL:N	2.92	0.41
66:V:127:ILE:HD12	66:V:128:ASN:H	1.86	0.41
79:p:71:GLU:HB2	79:p:74:ILE:CD1	2.51	0.41
1:A:514:C:H2'	1:A:515:A:H8	1.86	0.41
1:A:617:A:H1'	1:A:618:U:O4'	2.21	0.41
1:A:2095:U:HO2'	1:A:2096:G:H8	1.66	0.41
1:A:2588:A:O2'	1:A:2589:A:O4'	2.38	0.41
1:A:3023:C:O2'	21:G:99:THR:HG21	2.21	0.41
1:A:3101:A:H2'	1:A:3102:U:H6	1.85	0.41
1:A:3717:A:H2'	1:A:3718:G:C8	2.56	0.41
3:q:76:LEU:HD23	3:q:94:ARG:NH2	2.36	0.41
4:AQ:15:G:N2	4:AQ:58:G:H22	2.19	0.41
7:r:16:TYR:HE1	7:r:37:CYS:HG	1.68	0.41
7:r:129:ALA:H	7:r:195:ARG:CB	2.33	0.41
11:s:38:ASP:HA	11:s:41:GLU:OE2	2.20	0.41
11:s:99:THR:HG22	61:j:924:A:N7	2.36	0.41
13:3:121:VAL:C	36:L:157:LEU:HD22	2.46	0.41
19:5:86:ARG:O	19:5:86:ARG:HG3	2.20	0.41
19:5:165:VAL:N	19:5:171:TYR:O	2.48	0.41
27:I:78:LEU:HD23	27:I:78:LEU:HA	1.90	0.41
28:8:32:TRP:HH2	28:8:52:MET:HG2	1.86	0.41
38:AB:87:ASN:O	38:AB:88:ARG:C	2.64	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:P:80:VAL:HG11	48:P:86:HIS:O	2.20	0.41
51:Q:177:SER:HB3	51:Q:180:GLU:HB3	2.02	0.41
51:Q:196:SER:OG	51:Q:197:CYS:N	2.54	0.41
56:AH:139:ASN:ND2	56:AH:142:LYS:H	2.19	0.41
61:j:509:U:H2'	61:j:510:G:O4'	2.20	0.41
61:j:652:A:C2	61:j:749:U:H1'	2.56	0.41
61:j:1332:U:H5	61:j:1355:U:O2	2.04	0.41
61:j:1784:A:N3	61:j:1786:U:N3	2.69	0.41
67:l:122:ILE:HG13	67:l:144:ILE:CG2	2.50	0.41
73:n:15:PRO:O	73:n:16:LYS:HB3	2.21	0.41
79:p:41:TRP:CE2	79:p:73:GLN:HB3	2.56	0.41
1:A:1098:U:H5'	1:A:1099:U:H2'	2.03	0.41
1:A:1539:U:H5''	1:A:1540:G:N2	2.36	0.41
1:A:1843:U:H2'	1:A:1844:G:C8	2.56	0.41
1:A:2709:U:H2'	1:A:2710:U:C6	2.55	0.41
15:E:262:PRO:O	15:E:263:ARG:HD2	2.21	0.41
20:v:43:TYR:OH	56:AH:18:GLU:OE2	2.31	0.41
47:AE:49:LYS:NZ	47:AE:53:GLU:OE2	2.53	0.41
51:Q:12:CYS:SG	51:Q:59:GLN:HG3	2.61	0.41
54:R:40:ASP:HB2	54:R:43:LYS:HB2	2.02	0.41
56:AH:93:ILE:HD12	56:AH:97:PHE:CG	2.56	0.41
56:AH:93:ILE:HG23	56:AH:97:PHE:HB3	2.02	0.41
60:T:154:ILE:O	60:T:157:GLN:HG3	2.21	0.41
61:j:976:A:H8	61:j:1066:G:O2'	2.04	0.41
66:V:95:GLU:OE1	66:V:95:GLU:N	2.54	0.41
67:l:103:THR:HB	67:l:106:MET:HG3	2.03	0.41
72:X:125:LYS:HA	72:X:125:LYS:HE2	2.03	0.41
1:A:1845:C:H2'	1:A:1846:A:H8	1.86	0.40
1:A:1964:G:O2'	1:A:1965:U:H4'	2.22	0.40
1:A:2631:C:OP1	15:E:233:LYS:NZ	2.49	0.40
1:A:2672:U:H2'	1:A:2673:U:C6	2.55	0.40
1:A:3250:U:H2'	1:A:3251:U:H5'	2.02	0.40
15:E:292:SER:HB3	15:E:298:THR:O	2.20	0.40
18:F:24:ILE:HA	18:F:25:PRO:HD3	1.98	0.40
19:5:97:ARG:HB3	19:5:120:VAL:O	2.21	0.40
19:5:173:ARG:HB2	19:5:216:TRP:CZ3	2.56	0.40
25:7:14:LYS:HB2	25:7:15:PRO:HD2	2.02	0.40
37:b:93:LYS:HA	37:b:93:LYS:HD3	1.92	0.40
45:O:100:ILE:HD12	45:O:122:ILE:HD11	2.02	0.40
50:AF:8:THR:HB	70:m:209:ILE:HD11	2.03	0.40
50:AF:72:LYS:HD2	50:AF:73:LEU:N	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:j:832:A:O2'	61:j:833:A:H5''	2.21	0.40
64:k:61:LEU:O	64:k:64:ARG:HG3	2.20	0.40
67:l:103:THR:HA	67:l:104:PRO:HD3	1.97	0.40
73:n:110:GLN:NE2	73:n:126:ARG:HB2	2.35	0.40
75:Y:151:PHE:HB2	75:Y:153:ILE:HG13	2.03	0.40
76:o:150:ILE:HD12	76:o:150:ILE:HA	1.99	0.40
1:A:1710:G:H2'	1:A:1711:G:O4'	2.21	0.40
1:A:2738:U:H2'	1:A:2810:A:C2	2.55	0.40
1:A:3116:A:C2	45:O:60:HIS:HE1	2.39	0.40
1:A:3399:U:H2'	1:A:3400:C:C6	2.56	0.40
1:A:3401:C:H2'	1:A:3402:A:C8	2.56	0.40
8:AR:66:LYS:HA	8:AR:66:LYS:HD2	1.68	0.40
8:AR:76:ASN:HD22	8:AR:118:PHE:HD1	1.69	0.40
8:AR:192:ASP:OD1	8:AR:192:ASP:N	2.54	0.40
13:3:37:LEU:CD2	75:Y:116:THR:HG21	2.50	0.40
18:F:177:LYS:O	18:F:180:VAL:HG12	2.21	0.40
18:F:182:ARG:O	18:F:186:SER:HB3	2.21	0.40
19:5:249:ILE:O	19:5:253:ILE:HG12	2.21	0.40
42:N:31:CYS:HA	42:N:75:LYS:O	2.21	0.40
50:AF:72:LYS:HA	50:AF:75:GLU:HG3	2.02	0.40
56:AH:151:GLY:O	56:AH:155:ILE:HG12	2.21	0.40
73:n:57:ARG:O	73:n:61:THR:HG23	2.21	0.40
1:A:1221:A:H3'	1:A:1221:A:N3	2.37	0.40
1:A:1819:U:H2'	1:A:1820:U:C6	2.56	0.40
1:A:2145:A:H2'	1:A:2146:A:O4'	2.20	0.40
1:A:3617:A:O2'	63:U:172:LYS:HE2	2.21	0.40
2:0:42:LYS:O	2:0:46:LEU:HD13	2.21	0.40
12:D:5:ILE:HD12	12:D:208:GLU:O	2.21	0.40
36:L:72:LYS:HE2	36:L:72:LYS:HB2	1.78	0.40
48:P:66:VAL:HG21	48:P:102:ALA:HB2	2.04	0.40
56:AH:86:ARG:HA	56:AH:86:ARG:HD3	1.91	0.40
61:j:1635:C:H2'	61:j:1636:A:H4'	2.02	0.40
63:U:75:GLU:HG3	63:U:107:THR:HG23	2.02	0.40
69:W:4:TYR:HA	69:W:147:GLN:NE2	2.37	0.40
76:o:231:ASN:OD1	76:o:231:ASN:N	2.53	0.40
77:AO:25:ASP:OD1	77:AO:26:LYS:N	2.48	0.40
1:A:262:A:H2'	1:A:263:U:C6	2.56	0.40
1:A:572:U:P	1:A:572:U:H6	2.45	0.40
1:A:885:A:N1	1:A:3111:U:H5	2.18	0.40
1:A:1140:A:N6	1:A:1158:G:O6	2.55	0.40
1:A:1538:U:H5''	1:A:1540:G:O4'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2399:A:H2'	1:A:2400:A:C8	2.56	0.40
1:A:3407:G:C2	1:A:3418:A:N7	2.89	0.40
3:q:163:THR:HG22	3:q:163:THR:O	2.21	0.40
8:AR:294:SER:O	8:AR:306:CYS:HA	2.21	0.40
11:s:97:LYS:HE2	11:s:97:LYS:HB2	1.90	0.40
15:E:284:LEU:HA	15:E:317:ASP:HB3	2.03	0.40
35:AA:112:ILE:HG21	61:j:1328:A:C8	2.56	0.40
36:L:92:ILE:HG22	36:L:93:GLY:N	2.36	0.40
61:j:99:C:H1'	61:j:432:G:H5'	2.02	0.40
61:j:797:C:H2'	61:j:798:U:C6	2.56	0.40
61:j:886:U:O2	61:j:916:G:C2	2.73	0.40
61:j:939:A:H2'	61:j:940:G:C8	2.56	0.40
61:j:1897:A:H4'	61:j:1898:G:OP1	2.21	0.40
61:j:2087:U:H3'	68:AL:5:ARG:NH2	2.36	0.40
67:l:162:CYS:SG	67:l:173:MET:HE2	2.61	0.40
70:m:107:ARG:HG3	70:m:176:ALA:HB2	2.04	0.40
1:A:1219:A:OP1	66:V:121:LYS:NZ	2.39	0.40
1:A:1977:U:H2'	1:A:1978:U:H4'	2.03	0.40
1:A:3469:C:H2'	1:A:3470:G:O4'	2.21	0.40
1:A:3737:G:H2'	1:A:3738:U:O4'	2.21	0.40
8:AR:203:VAL:O	8:AR:220:GLY:HA3	2.21	0.40
11:s:160:ARG:HG2	11:s:161:GLN:H	1.86	0.40
12:D:126:LEU:HD23	12:D:126:LEU:HA	1.74	0.40
12:D:209:HIS:CE1	12:D:235:VAL:HG21	2.56	0.40
18:F:192:GLY:O	18:F:195:LYS:HE2	2.21	0.40
22:6:71:HIS:O	22:6:71:HIS:ND1	2.53	0.40
31:9:136:TYR:O	31:9:138:SER:N	2.54	0.40
41:AC:17:ARG:HD3	41:AC:17:ARG:H	1.87	0.40
50:AF:47:LYS:HE2	50:AF:47:LYS:HB3	1.80	0.40
54:R:23:ARG:O	54:R:23:ARG:NH1	2.55	0.40
61:j:1410:G:H2'	61:j:1411:G:C8	2.57	0.40
74:AN:44:VAL:HG11	74:AN:48:VAL:HG11	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

entries.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	0	60/162 (37%)	57 (95%)	3 (5%)	0	100	100
3	q	211/306 (69%)	194 (92%)	17 (8%)	0	100	100
6	1	143/146 (98%)	134 (94%)	9 (6%)	0	100	100
7	r	187/195 (96%)	172 (92%)	15 (8%)	0	100	100
8	AR	321/323 (99%)	290 (90%)	31 (10%)	0	100	100
10	2	119/127 (94%)	105 (88%)	14 (12%)	0	100	100
11	s	186/194 (96%)	174 (94%)	12 (6%)	0	100	100
12	D	245/260 (94%)	230 (94%)	15 (6%)	0	100	100
13	3	120/124 (97%)	109 (91%)	11 (9%)	0	100	100
14	t	127/130 (98%)	116 (91%)	11 (9%)	0	100	100
15	E	378/386 (98%)	360 (95%)	18 (5%)	0	100	100
16	4	64/67 (96%)	58 (91%)	6 (9%)	0	100	100
17	u	164/218 (75%)	151 (92%)	13 (8%)	0	100	100
18	F	388/411 (94%)	365 (94%)	23 (6%)	0	100	100
19	5	221/257 (86%)	205 (93%)	16 (7%)	0	100	100
20	v	136/144 (94%)	128 (94%)	8 (6%)	0	100	100
21	G	163/173 (94%)	155 (95%)	8 (5%)	0	100	100
22	6	96/108 (89%)	87 (91%)	9 (9%)	0	100	100
23	w	100/118 (85%)	90 (90%)	10 (10%)	0	100	100
24	H	184/190 (97%)	164 (89%)	20 (11%)	0	100	100
25	7	93/120 (78%)	91 (98%)	2 (2%)	0	100	100
26	x	96/137 (70%)	83 (86%)	13 (14%)	0	100	100
27	I	203/221 (92%)	185 (91%)	18 (9%)	0	100	100
28	8	123/131 (94%)	115 (94%)	8 (6%)	0	100	100
29	y	131/151 (87%)	111 (85%)	20 (15%)	0	100	100
30	J	225/283 (80%)	213 (95%)	12 (5%)	0	100	100
31	9	103/140 (74%)	89 (86%)	14 (14%)	0	100	100
32	z	142/145 (98%)	135 (95%)	7 (5%)	0	100	100
33	K	199/202 (98%)	191 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	a	104/150 (69%)	101 (97%)	3 (3%)	0	100	100
35	AA	115/141 (82%)	107 (93%)	8 (7%)	0	100	100
36	L	209/215 (97%)	198 (95%)	11 (5%)	0	100	100
37	b	91/112 (81%)	82 (90%)	8 (9%)	1 (1%)	12	13
38	AB	140/156 (90%)	116 (83%)	23 (16%)	1 (1%)	19	24
39	M	130/139 (94%)	118 (91%)	12 (9%)	0	100	100
40	c	87/92 (95%)	78 (90%)	9 (10%)	0	100	100
41	AC	51/54 (94%)	48 (94%)	3 (6%)	0	100	100
42	N	144/165 (87%)	132 (92%)	12 (8%)	0	100	100
43	d	74/87 (85%)	69 (93%)	5 (7%)	0	100	100
44	AD	146/151 (97%)	140 (96%)	6 (4%)	0	100	100
45	O	145/148 (98%)	134 (92%)	11 (8%)	0	100	100
46	e	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
47	AE	143/161 (89%)	137 (96%)	6 (4%)	0	100	100
48	P	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
49	f	49/128 (38%)	47 (96%)	2 (4%)	0	100	100
50	AF	116/137 (85%)	114 (98%)	2 (2%)	0	100	100
51	Q	188/219 (86%)	169 (90%)	19 (10%)	0	100	100
52	g	35/39 (90%)	32 (91%)	3 (9%)	0	100	100
53	AG	114/145 (79%)	110 (96%)	4 (4%)	0	100	100
54	R	261/294 (89%)	243 (93%)	18 (7%)	0	100	100
55	h	83/96 (86%)	78 (94%)	5 (6%)	0	100	100
56	AH	163/170 (96%)	150 (92%)	13 (8%)	0	100	100
57	S	184/187 (98%)	170 (92%)	14 (8%)	0	100	100
58	i	94/104 (90%)	84 (89%)	10 (11%)	0	100	100
59	AI	79/82 (96%)	75 (95%)	4 (5%)	0	100	100
60	T	179/182 (98%)	177 (99%)	2 (1%)	0	100	100
62	AJ	119/133 (90%)	104 (87%)	15 (13%)	0	100	100
63	U	178/184 (97%)	170 (96%)	8 (4%)	0	100	100
64	k	208/262 (79%)	176 (85%)	32 (15%)	0	100	100
65	AK	70/105 (67%)	64 (91%)	6 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
66	V	154/161 (96%)	146 (95%)	8 (5%)	0	100	100
67	l	193/263 (73%)	170 (88%)	23 (12%)	0	100	100
68	AL	93/107 (87%)	86 (92%)	7 (8%)	0	100	100
69	W	168/203 (83%)	156 (93%)	12 (7%)	0	100	100
70	m	211/221 (96%)	189 (90%)	21 (10%)	1 (0%)	25	32
71	AM	77/82 (94%)	73 (95%)	4 (5%)	0	100	100
72	X	95/139 (68%)	87 (92%)	8 (8%)	0	100	100
73	n	183/189 (97%)	171 (93%)	12 (7%)	0	100	100
74	AN	54/67 (81%)	54 (100%)	0	0	100	100
75	Y	99/190 (52%)	95 (96%)	4 (4%)	0	100	100
76	o	255/261 (98%)	227 (89%)	28 (11%)	0	100	100
77	AO	41/58 (71%)	37 (90%)	4 (10%)	0	100	100
78	Z	120/126 (95%)	116 (97%)	4 (3%)	0	100	100
79	p	222/272 (82%)	210 (95%)	12 (5%)	0	100	100
80	AP	68/149 (46%)	64 (94%)	4 (6%)	0	100	100
All	All	10910/12551 (87%)	10100 (93%)	807 (7%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
37	b	86	THR
38	AB	103	ASN
70	m	192	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	0	53/146 (36%)	53 (100%)	0	100	100
3	q	189/279 (68%)	188 (100%)	1 (0%)	86	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	1	131/132 (99%)	131 (100%)	0	100	100
7	r	160/165 (97%)	160 (100%)	0	100	100
8	AR	287/287 (100%)	282 (98%)	5 (2%)	56	70
10	2	112/118 (95%)	112 (100%)	0	100	100
11	s	177/183 (97%)	177 (100%)	0	100	100
12	D	191/202 (95%)	191 (100%)	0	100	100
13	3	113/115 (98%)	113 (100%)	0	100	100
14	t	115/116 (99%)	115 (100%)	0	100	100
15	E	335/340 (98%)	335 (100%)	0	100	100
16	4	60/61 (98%)	60 (100%)	0	100	100
17	u	148/193 (77%)	148 (100%)	0	100	100
18	F	336/352 (96%)	336 (100%)	0	100	100
19	5	201/231 (87%)	201 (100%)	0	100	100
20	v	116/122 (95%)	116 (100%)	0	100	100
21	G	147/155 (95%)	147 (100%)	0	100	100
22	6	83/92 (90%)	83 (100%)	0	100	100
23	w	95/109 (87%)	95 (100%)	0	100	100
24	H	165/173 (95%)	165 (100%)	0	100	100
25	7	91/112 (81%)	91 (100%)	0	100	100
26	x	94/129 (73%)	94 (100%)	0	100	100
27	I	189/203 (93%)	188 (100%)	1 (0%)	86	92
28	8	114/120 (95%)	113 (99%)	1 (1%)	75	86
29	y	104/119 (87%)	104 (100%)	0	100	100
30	J	211/260 (81%)	211 (100%)	0	100	100
31	9	92/127 (72%)	92 (100%)	0	100	100
32	z	120/121 (99%)	120 (100%)	0	100	100
33	K	182/182 (100%)	182 (100%)	0	100	100
34	a	89/128 (70%)	89 (100%)	0	100	100
35	AA	100/121 (83%)	100 (100%)	0	100	100
36	L	190/194 (98%)	190 (100%)	0	100	100
37	b	82/97 (84%)	82 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	AB	127/136 (93%)	127 (100%)	0	100	100
39	M	106/110 (96%)	106 (100%)	0	100	100
40	c	73/77 (95%)	73 (100%)	0	100	100
41	AC	47/48 (98%)	47 (100%)	0	100	100
42	N	135/152 (89%)	134 (99%)	1 (1%)	81	89
43	d	73/83 (88%)	72 (99%)	1 (1%)	62	76
44	AD	132/133 (99%)	132 (100%)	0	100	100
45	O	121/122 (99%)	121 (100%)	0	100	100
46	e	47/48 (98%)	47 (100%)	0	100	100
47	AE	132/144 (92%)	132 (100%)	0	100	100
48	P	179/180 (99%)	179 (100%)	0	100	100
49	f	45/114 (40%)	45 (100%)	0	100	100
50	AF	108/127 (85%)	108 (100%)	0	100	100
51	Q	167/190 (88%)	167 (100%)	0	100	100
52	g	34/35 (97%)	34 (100%)	0	100	100
53	AG	105/130 (81%)	101 (96%)	4 (4%)	28	41
54	R	229/254 (90%)	229 (100%)	0	100	100
55	h	70/80 (88%)	70 (100%)	0	100	100
56	AH	147/151 (97%)	145 (99%)	2 (1%)	62	76
57	S	158/159 (99%)	158 (100%)	0	100	100
58	i	88/93 (95%)	88 (100%)	0	100	100
59	AI	69/70 (99%)	69 (100%)	0	100	100
60	T	161/163 (99%)	161 (100%)	0	100	100
62	AJ	105/115 (91%)	105 (100%)	0	100	100
63	U	162/166 (98%)	162 (100%)	0	100	100
64	k	195/238 (82%)	195 (100%)	0	100	100
65	AK	64/88 (73%)	61 (95%)	3 (5%)	22	32
66	V	140/144 (97%)	140 (100%)	0	100	100
67	l	167/227 (74%)	167 (100%)	0	100	100
68	AL	87/98 (89%)	87 (100%)	0	100	100
69	W	130/178 (73%)	130 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
70	m	179/188 (95%)	177 (99%)	2 (1%)	70	81
71	AM	73/76 (96%)	73 (100%)	0	100	100
72	X	92/131 (70%)	92 (100%)	0	100	100
73	n	164/167 (98%)	164 (100%)	0	100	100
74	AN	46/54 (85%)	46 (100%)	0	100	100
75	Y	90/177 (51%)	90 (100%)	0	100	100
76	o	233/237 (98%)	233 (100%)	0	100	100
77	AO	36/47 (77%)	36 (100%)	0	100	100
78	Z	111/115 (96%)	111 (100%)	0	100	100
79	p	191/222 (86%)	191 (100%)	0	100	100
80	AP	62/135 (46%)	62 (100%)	0	100	100
All	All	9752/11086 (88%)	9731 (100%)	21 (0%)	91	95

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	q	179	VAL
8	AR	43	ARG
8	AR	45	LYS
8	AR	46	LYS
8	AR	287	ILE
8	AR	289	VAL
27	I	212	ASN
28	8	70	ASN
42	N	7	THR
43	d	36	THR
53	AG	16	GLN
53	AG	18	ARG
53	AG	20	VAL
53	AG	21	ASP
56	AH	138	GLN
56	AH	139	ASN
65	AK	56	MET
65	AK	57	LYS
65	AK	59	ILE
70	m	196	ASP
70	m	209	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (86) such sidechains are listed below:

Mol	Chain	Res	Type
3	q	213	ASN
6	1	15	ASN
7	r	73	ASN
7	r	108	GLN
8	AR	51	ASN
8	AR	71	HIS
8	AR	128	GLN
8	AR	154	GLN
8	AR	200	HIS
11	s	164	ASN
12	D	22	HIS
12	D	31	HIS
12	D	205	ASN
13	3	74	ASN
13	3	106	GLN
14	t	56	HIS
15	E	179	GLN
15	E	181	ASN
17	u	42	GLN
18	F	29	GLN
18	F	50	HIS
18	F	353	ASN
19	5	248	HIS
21	G	15	ASN
21	G	164	GLN
22	6	50	ASN
24	H	97	HIS
26	x	50	ASN
27	I	126	ASN
29	y	94	HIS
29	y	113	GLN
30	J	99	HIS
30	J	107	GLN
30	J	111	ASN
31	9	92	HIS
32	z	33	HIS
33	K	89	HIS
34	a	103	GLN
35	AA	33	HIS
38	AB	137	HIS
39	M	77	ASN

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Mol	Chain	Res	Type
41	AC	18	GLN
45	O	60	HIS
46	e	11	GLN
47	AE	9	HIS
47	AE	14	GLN
47	AE	23	ASN
48	P	86	HIS
49	f	44	GLN
50	AF	74	GLN
50	AF	112	ASN
51	Q	44	ASN
53	AG	16	GLN
53	AG	41	GLN
53	AG	66	ASN
54	R	17	GLN
54	R	221	HIS
56	AH	139	ASN
57	S	7	ASN
58	i	14	ASN
59	AI	35	ASN
59	AI	60	GLN
60	T	19	ASN
60	T	57	HIS
60	T	85	ASN
62	AJ	31	ASN
63	U	42	ASN
63	U	58	ASN
64	k	69	ASN
65	AK	38	HIS
66	V	29	ASN
66	V	49	GLN
67	l	23	HIS
67	l	155	HIS
67	l	179	GLN
68	AL	40	ASN
68	AL	71	GLN
69	W	97	ASN
69	W	147	GLN
70	m	94	HIS
72	X	95	HIS
73	n	26	GLN
75	Y	165	ASN

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Mol	Chain	Res	Type
76	o	142	HIS
76	o	157	ASN
77	AO	16	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3171/3788 (83%)	588 (18%)	24 (0%)
4	AQ	73/74 (98%)	28 (38%)	1 (1%)
5	B	117/119 (98%)	9 (7%)	1 (0%)
61	j	1626/2092 (77%)	334 (20%)	0
9	C	149/159 (93%)	28 (18%)	1 (0%)
All	All	5136/6232 (82%)	987 (19%)	27 (0%)

All (987) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	11	A
1	A	14	U
1	A	40	A
1	A	43	A
1	A	45	A
1	A	49	U
1	A	54	C
1	A	59	G
1	A	60	A
1	A	65	A
1	A	66	A
1	A	67	A
1	A	72	C
1	A	73	U
1	A	74	A
1	A	76	G
1	A	77	A
1	A	83	U
1	A	86	G
1	A	92	G
1	A	99	A
1	A	110	G
1	A	120	U
1	A	122	A

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Mol	Chain	Res	Type
1	A	123	A
1	A	132	U
1	A	133	U
1	A	137	G
1	A	146	U
1	A	148	G
1	A	163	G
1	A	168	A
1	A	169	U
1	A	177	A
1	A	178	U
1	A	180	C
1	A	181	C
1	A	186	A
1	A	187	U
1	A	188	U
1	A	196	A
1	A	198	U
1	A	199	G
1	A	200	A
1	A	201	G
1	A	207	A
1	A	216	C
1	A	219	A
1	A	221	A
1	A	226	G
1	A	227	A
1	A	228	A
1	A	230	G
1	A	245	U
1	A	246	U
1	A	247	A
1	A	248	A
1	A	251	U
1	A	252	A
1	A	257	U
1	A	269	A
1	A	270	U
1	A	276	G
1	A	277	U
1	A	290	G
1	A	302	A

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Mol	Chain	Res	Type
1	A	307	G
1	A	313	U
1	A	331	A
1	A	334	U
1	A	337	A
1	A	346	A
1	A	357	A
1	A	358	C
1	A	360	A
1	A	382	A
1	A	384	A
1	A	395	A
1	A	401	A
1	A	407	A
1	A	409	A
1	A	412	A
1	A	413	C
1	A	430	G
1	A	431	G
1	A	432	A
1	A	448	A
1	A	449	A
1	A	451	C
1	A	459	G
1	A	461	G
1	A	490	U
1	A	501	U
1	A	522	A
1	A	523	A
1	A	530	U
1	A	532	C
1	A	536	A
1	A	539	G
1	A	543	U
1	A	582	U
1	A	583	U
1	A	584	U
1	A	585	C
1	A	595	U
1	A	598	U
1	A	599	G
1	A	615	U

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Mol	Chain	Res	Type
1	A	617	A
1	A	619	U
1	A	620	U
1	A	646	A
1	A	648	U
1	A	649	U
1	A	656	U
1	A	659	U
1	A	660	U
1	A	665	U
1	A	667	U
1	A	668	U
1	A	673	U
1	A	674	U
1	A	675	A
1	A	681	U
1	A	682	A
1	A	683	A
1	A	684	G
1	A	685	U
1	A	689	U
1	A	694	U
1	A	698	G
1	A	700	A
1	A	708	A
1	A	714	C
1	A	727	A
1	A	735	A
1	A	738	A
1	A	755	A
1	A	759	U
1	A	765	A
1	A	768	C
1	A	769	U
1	A	778	U
1	A	792	U
1	A	799	A
1	A	800	A
1	A	806	G
1	A	809	A
1	A	810	U
1	A	811	A

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Mol	Chain	Res	Type
1	A	818	C
1	A	835	G
1	A	836	G
1	A	885	A
1	A	890	G
1	A	893	U
1	A	894	U
1	A	895	A
1	A	899	A
1	A	900	G
1	A	903	C
1	A	904	G
1	A	905	A
1	A	910	A
1	A	911	U
1	A	918	G
1	A	925	A
1	A	936	A
1	A	945	G
1	A	948	G
1	A	951	A
1	A	973	A
1	A	978	G
1	A	980	A
1	A	985	G
1	A	990	U
1	A	993	U
1	A	994	G
1	A	998	U
1	A	999	G
1	A	1004	U
1	A	1015	A
1	A	1016	A
1	A	1019	A
1	A	1020	C
1	A	1026	G
1	A	1033	A
1	A	1035	G
1	A	1036	A
1	A	1040	A
1	A	1043	G
1	A	1044	A

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Mol	Chain	Res	Type
1	A	1052	A
1	A	1056	G
1	A	1063	A
1	A	1070	A
1	A	1078	C
1	A	1082	G
1	A	1099	U
1	A	1100	A
1	A	1102	U
1	A	1116	G
1	A	1123	U
1	A	1124	A
1	A	1132	G
1	A	1140	A
1	A	1142	G
1	A	1143	G
1	A	1155	C
1	A	1156	U
1	A	1170	A
1	A	1172	C
1	A	1187	A
1	A	1188	A
1	A	1195	A
1	A	1196	A
1	A	1199	A
1	A	1205	U
1	A	1206	U
1	A	1207	U
1	A	1210	A
1	A	1219	A
1	A	1221	A
1	A	1222	U
1	A	1223	U
1	A	1225	A
1	A	1229	A
1	A	1230	A
1	A	1233	A
1	A	1245	G
1	A	1259	G
1	A	1270	G
1	A	1271	A
1	A	1272	U

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Mol	Chain	Res	Type
1	A	1287	A
1	A	1306	A
1	A	1309	U
1	A	1310	A
1	A	1317	C
1	A	1320	G
1	A	1324	U
1	A	1325	C
1	A	1329	U
1	A	1337	G
1	A	1340	G
1	A	1346	U
1	A	1423	G
1	A	1428	G
1	A	1435	G
1	A	1437	U
1	A	1441	G
1	A	1444	A
1	A	1445	A
1	A	1457	G
1	A	1459	U
1	A	1460	A
1	A	1474	A
1	A	1476	A
1	A	1477	A
1	A	1481	A
1	A	1487	U
1	A	1494	U
1	A	1495	U
1	A	1503	A
1	A	1505	U
1	A	1506	C
1	A	1535	G
1	A	1539	U
1	A	1550	A
1	A	1565	G
1	A	1566	A
1	A	1567	A
1	A	1572	U
1	A	1581	C
1	A	1583	G
1	A	1586	C

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Mol	Chain	Res	Type
1	A	1595	A
1	A	1601	A
1	A	1602	A
1	A	1619	U
1	A	1630	A
1	A	1632	G
1	A	1634	G
1	A	1660	U
1	A	1696	A
1	A	1702	U
1	A	1703	U
1	A	1704	U
1	A	1705	A
1	A	1707	A
1	A	1714	U
1	A	1722	C
1	A	1725	U
1	A	1731	A
1	A	1732	A
1	A	1736	A
1	A	1748	A
1	A	1751	C
1	A	1763	G
1	A	1774	U
1	A	1800	U
1	A	1812	C
1	A	1817	G
1	A	1822	A
1	A	1842	U
1	A	1844	G
1	A	1852	C
1	A	1856	U
1	A	1881	C
1	A	1902	A
1	A	1903	C
1	A	1904	U
1	A	1905	C
1	A	1907	A
1	A	1909	U
1	A	1914	A
1	A	1915	A
1	A	1959	G

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Mol	Chain	Res	Type
1	A	1961	U
1	A	1962	U
1	A	1964	G
1	A	1968	C
1	A	1969	A
1	A	1970	A
1	A	1971	U
1	A	1978	U
1	A	1979	C
1	A	1981	U
1	A	1990	A
1	A	1991	U
1	A	1996	C
1	A	1997	G
1	A	1999	A
1	A	2003	G
1	A	2015	C
1	A	2018	G
1	A	2019	A
1	A	2034	G
1	A	2037	U
1	A	2038	U
1	A	2039	U
1	A	2040	G
1	A	2075	U
1	A	2091	U
1	A	2093	U
1	A	2094	A
1	A	2095	U
1	A	2096	G
1	A	2097	A
1	A	2107	C
1	A	2108	A
1	A	2109	A
1	A	2110	C
1	A	2113	C
1	A	2116	C
1	A	2117	A
1	A	2133	C
1	A	2138	U
1	A	2143	U
1	A	2145	A

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Mol	Chain	Res	Type
1	A	2146	A
1	A	2147	A
1	A	2154	A
1	A	2174	G
1	A	2178	A
1	A	2181	A
1	A	2207	G
1	A	2211	C
1	A	2220	U
1	A	2221	U
1	A	2387	A
1	A	2395	U
1	A	2404	A
1	A	2405	A
1	A	2411	C
1	A	2415	G
1	A	2424	A
1	A	2433	U
1	A	2435	A
1	A	2437	A
1	A	2450	G
1	A	2451	A
1	A	2453	A
1	A	2461	A
1	A	2481	A
1	A	2494	G
1	A	2500	A
1	A	2506	A
1	A	2524	C
1	A	2537	A
1	A	2542	G
1	A	2549	A
1	A	2565	G
1	A	2566	G
1	A	2573	A
1	A	2582	U
1	A	2591	U
1	A	2600	G
1	A	2603	U
1	A	2606	A
1	A	2607	U
1	A	2608	G

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Mol	Chain	Res	Type
1	A	2627	U
1	A	2629	U
1	A	2666	A
1	A	2667	C
1	A	2668	G
1	A	2670	G
1	A	2686	G
1	A	2690	A
1	A	2694	A
1	A	2695	A
1	A	2696	G
1	A	2697	A
1	A	2704	U
1	A	2715	C
1	A	2719	U
1	A	2731	A
1	A	2736	A
1	A	2737	C
1	A	2738	U
1	A	2739	U
1	A	2740	A
1	A	2741	A
1	A	2742	G
1	A	2744	G
1	A	2746	U
1	A	2807	U
1	A	2808	U
1	A	2809	A
1	A	2810	A
1	A	2811	A
1	A	2812	G
1	A	2816	U
1	A	2823	U
1	A	2824	A
1	A	2835	G
1	A	2884	G
1	A	2886	A
1	A	2919	A
1	A	2932	A
1	A	2945	G
1	A	2946	G
1	A	2953	G

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Mol	Chain	Res	Type
1	A	2965	A
1	A	2980	U
1	A	2987	G
1	A	2991	U
1	A	2994	A
1	A	2995	A
1	A	3013	A
1	A	3014	C
1	A	3016	G
1	A	3025	U
1	A	3027	U
1	A	3028	A
1	A	3029	G
1	A	3030	A
1	A	3042	A
1	A	3043	A
1	A	3053	G
1	A	3061	U
1	A	3067	G
1	A	3068	A
1	A	3092	G
1	A	3094	C
1	A	3101	A
1	A	3112	U
1	A	3116	A
1	A	3123	C
1	A	3124	G
1	A	3130	U
1	A	3131	A
1	A	3133	U
1	A	3141	G
1	A	3155	G
1	A	3158	U
1	A	3159	G
1	A	3160	A
1	A	3161	A
1	A	3163	A
1	A	3169	C
1	A	3176	A
1	A	3203	C
1	A	3204	C
1	A	3220	U

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Mol	Chain	Res	Type
1	A	3226	C
1	A	3230	G
1	A	3231	A
1	A	3246	A
1	A	3251	U
1	A	3252	G
1	A	3257	G
1	A	3258	C
1	A	3259	A
1	A	3270	A
1	A	3275	C
1	A	3292	A
1	A	3294	U
1	A	3295	A
1	A	3300	A
1	A	3301	C
1	A	3302	G
1	A	3306	G
1	A	3310	G
1	A	3327	G
1	A	3330	A
1	A	3331	G
1	A	3338	U
1	A	3342	C
1	A	3349	G
1	A	3353	A
1	A	3357	U
1	A	3362	A
1	A	3365	U
1	A	3382	U
1	A	3398	A
1	A	3414	G
1	A	3418	A
1	A	3425	G
1	A	3442	C
1	A	3443	A
1	A	3463	G
1	A	3471	A
1	A	3477	A
1	A	3483	U
1	A	3485	G
1	A	3507	A

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Mol	Chain	Res	Type
1	A	3515	A
1	A	3516	A
1	A	3526	U
1	A	3527	U
1	A	3528	A
1	A	3546	C
1	A	3547	U
1	A	3548	U
1	A	3549	U
1	A	3550	U
1	A	3551	U
1	A	3567	U
1	A	3571	A
1	A	3572	A
1	A	3573	U
1	A	3576	A
1	A	3577	A
1	A	3581	A
1	A	3582	G
1	A	3585	A
1	A	3586	U
1	A	3591	U
1	A	3599	U
1	A	3615	A
1	A	3616	U
1	A	3617	A
1	A	3618	A
1	A	3626	A
1	A	3633	U
1	A	3635	G
1	A	3636	U
1	A	3637	G
1	A	3638	A
1	A	3639	G
1	A	3645	A
1	A	3646	G
1	A	3655	U
1	A	3659	C
1	A	3664	G
1	A	3668	U
1	A	3670	U
1	A	3683	G

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Mol	Chain	Res	Type
1	A	3684	A
1	A	3693	A
1	A	3698	U
1	A	3712	G
1	A	3732	U
1	A	3736	A
1	A	3737	G
1	A	3739	A
1	A	3740	A
1	A	3741	A
1	A	3753	G
1	A	3761	G
1	A	3770	C
1	A	3774	A
1	A	3775	G
1	A	3776	U
1	A	3777	G
1	A	3778	G
4	AQ	16	U
4	AQ	17	U
4	AQ	18	G
4	AQ	19	G
4	AQ	21	U
4	AQ	25	G
4	AQ	27	G
4	AQ	29	G
4	AQ	31	G
4	AQ	32	U
4	AQ	33	C
4	AQ	35	C
4	AQ	36	A
4	AQ	37	U
4	AQ	38	A
4	AQ	40	U
4	AQ	43	C
4	AQ	44	G
4	AQ	47	G
4	AQ	49	C
4	AQ	54	G
4	AQ	55	U
4	AQ	58	G
4	AQ	60	U

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Mol	Chain	Res	Type
4	AQ	61	C
4	AQ	63	U
4	AQ	65	A
4	AQ	74	A
5	B	23	A
5	B	33	U
5	B	38	U
5	B	53	U
5	B	54	A
5	B	63	A
5	B	64	A
5	B	100	A
5	B	110	G
9	C	5	A
9	C	6	C
9	C	27	U
9	C	36	C
9	C	38	G
9	C	56	A
9	C	63	A
9	C	64	U
9	C	66	C
9	C	67	G
9	C	75	A
9	C	76	A
9	C	80	C
9	C	85	A
9	C	86	C
9	C	90	G
9	C	91	A
9	C	92	A
9	C	98	A
9	C	108	A
9	C	109	U
9	C	110	G
9	C	114	A
9	C	115	C
9	C	123	A
9	C	135	G
9	C	145	A
9	C	154	G
61	j	3	C

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Mol	Chain	Res	Type
61	j	4	C
61	j	5	U
61	j	15	U
61	j	17	C
61	j	25	C
61	j	26	A
61	j	34	G
61	j	40	A
61	j	42	G
61	j	45	U
61	j	47	A
61	j	57	G
61	j	72	U
61	j	74	U
61	j	79	U
61	j	82	G
61	j	86	A
61	j	95	A
61	j	105	A
61	j	106	A
61	j	116	A
61	j	117	G
61	j	118	U
61	j	126	A
61	j	128	A
61	j	129	U
61	j	130	U
61	j	139	A
61	j	142	G
61	j	143	A
61	j	144	U
61	j	168	U
61	j	180	U
61	j	181	A
61	j	183	C
61	j	200	U
61	j	201	G
61	j	202	G
61	j	204	U
61	j	206	A
61	j	247	G
61	j	249	A

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Mol	Chain	Res	Type
61	j	250	A
61	j	252	U
61	j	262	A
61	j	263	A
61	j	266	A
61	j	267	A
61	j	268	C
61	j	299	U
61	j	319	U
61	j	320	C
61	j	322	G
61	j	326	U
61	j	328	G
61	j	335	G
61	j	343	G
61	j	344	C
61	j	347	A
61	j	365	A
61	j	367	C
61	j	406	A
61	j	407	A
61	j	408	U
61	j	409	A
61	j	410	G
61	j	430	C
61	j	432	G
61	j	440	G
61	j	445	U
61	j	450	C
61	j	451	A
61	j	460	G
61	j	465	G
61	j	470	A
61	j	474	A
61	j	483	A
61	j	491	A
61	j	492	A
61	j	509	U
61	j	510	G
61	j	512	A
61	j	513	A
61	j	516	G

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Mol	Chain	Res	Type
61	j	521	G
61	j	529	U
61	j	532	A
61	j	533	A
61	j	534	A
61	j	535	A
61	j	536	C
61	j	547	U
61	j	548	A
61	j	549	A
61	j	564	G
61	j	565	U
61	j	567	U
61	j	572	C
61	j	575	G
61	j	585	U
61	j	601	A
61	j	602	G
61	j	613	A
61	j	617	G
61	j	618	U
61	j	626	A
61	j	627	A
61	j	629	A
61	j	630	C
61	j	631	G
61	j	645	U
61	j	646	U
61	j	647	C
61	j	648	A
61	j	653	A
61	j	746	U
61	j	750	U
61	j	751	U
61	j	753	U
61	j	754	A
61	j	760	C
61	j	788	A
61	j	790	U
61	j	791	U
61	j	805	A
61	j	815	G

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Mol	Chain	Res	Type
61	j	816	U
61	j	817	U
61	j	824	A
61	j	830	U
61	j	831	U
61	j	833	A
61	j	837	A
61	j	838	U
61	j	846	G
61	j	849	U
61	j	857	A
61	j	875	A
61	j	877	U
61	j	879	A
61	j	882	A
61	j	884	G
61	j	885	C
61	j	887	A
61	j	888	A
61	j	889	A
61	j	890	A
61	j	891	U
61	j	892	U
61	j	893	U
61	j	895	U
61	j	896	U
61	j	906	U
61	j	909	U
61	j	911	U
61	j	912	U
61	j	913	U
61	j	915	G
61	j	916	G
61	j	918	U
61	j	919	U
61	j	920	A
61	j	921	G
61	j	924	A
61	j	928	U
61	j	930	A
61	j	931	A
61	j	933	A

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Mol	Chain	Res	Type
61	j	936	A
61	j	942	U
61	j	945	G
61	j	955	U
61	j	967	A
61	j	975	A
61	j	979	C
61	j	988	U
61	j	1002	A
61	j	1004	U
61	j	1021	A
61	j	1024	A
61	j	1029	U
61	j	1035	A
61	j	1057	A
61	j	1058	G
61	j	1061	A
61	j	1062	A
61	j	1073	U
61	j	1074	A
61	j	1095	A
61	j	1097	C
61	j	1100	U
61	j	1101	G
61	j	1112	G
61	j	1121	A
61	j	1122	A
61	j	1123	G
61	j	1124	U
61	j	1166	C
61	j	1168	U
61	j	1182	A
61	j	1183	U
61	j	1187	A
61	j	1193	A
61	j	1194	A
61	j	1198	U
61	j	1239	A
61	j	1251	G
61	j	1256	G
61	j	1257	C
61	j	1259	C

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Mol	Chain	Res	Type
61	j	1260	C
61	j	1268	G
61	j	1281	C
61	j	1284	A
61	j	1286	U
61	j	1295	A
61	j	1297	A
61	j	1300	G
61	j	1301	G
61	j	1303	A
61	j	1317	A
61	j	1318	A
61	j	1319	G
61	j	1346	G
61	j	1347	C
61	j	1366	A
61	j	1374	G
61	j	1387	U
61	j	1398	U
61	j	1399	A
61	j	1400	U
61	j	1403	U
61	j	1416	U
61	j	1417	U
61	j	1423	A
61	j	1426	G
61	j	1442	U
61	j	1448	U
61	j	1449	U
61	j	1450	A
61	j	1451	G
61	j	1460	A
61	j	1463	C
61	j	1628	A
61	j	1636	A
61	j	1641	G
61	j	1644	U
61	j	1645	C
61	j	1659	U
61	j	1660	U
61	j	1661	U
61	j	1664	G

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Mol	Chain	Res	Type
61	j	1671	A
61	j	1673	A
61	j	1674	G
61	j	1679	G
61	j	1681	G
61	j	1682	A
61	j	1683	U
61	j	1692	A
61	j	1703	U
61	j	1704	G
61	j	1705	C
61	j	1706	A
61	j	1717	A
61	j	1720	G
61	j	1744	A
61	j	1746	A
61	j	1747	U
61	j	1749	C
61	j	1750	U
61	j	1783	U
61	j	1784	A
61	j	1785	C
61	j	1786	U
61	j	1787	U
61	j	1792	U
61	j	1801	A
61	j	1802	G
61	j	1807	A
61	j	1810	U
61	j	1811	A
61	j	1812	A
61	j	1814	C
61	j	1817	U
61	j	1818	A
61	j	1819	U
61	j	1834	A
61	j	1836	G
61	j	1854	U
61	j	1856	A
61	j	1857	U
61	j	1871	G
61	j	1872	G

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Mol	Chain	Res	Type
61	j	1881	G
61	j	1883	A
61	j	1887	A
61	j	1888	U
61	j	1898	G
61	j	1904	G
61	j	1907	G
61	j	1908	A
61	j	1913	G
61	j	1916	C
61	j	1932	A
61	j	1954	U
61	j	1955	G
61	j	1977	G
61	j	1978	A
61	j	1979	C
61	j	1980	A
61	j	1981	A
61	j	1982	G
61	j	1983	A
61	j	1986	A
61	j	1987	A
61	j	2005	U
61	j	2007	U
61	j	2008	U
61	j	2023	A
61	j	2024	A
61	j	2049	G
61	j	2052	G
61	j	2054	A
61	j	2057	A
61	j	2058	A
61	j	2061	U
61	j	2072	G
61	j	2084	G
61	j	2085	G
61	j	2086	A
61	j	2088	C
61	j	2090	U

All (27) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	10	G
1	A	162	U
1	A	168	A
1	A	176	A
1	A	179	G
1	A	215	C
1	A	289	A
1	A	681	U
1	A	697	A
1	A	764	G
1	A	799	A
1	A	835	G
1	A	1035	G
1	A	1195	A
1	A	1538	U
1	A	1704	U
1	A	1841	U
1	A	1961	U
1	A	2180	U
1	A	2548	A
1	A	2738	U
1	A	2885	A
1	A	3160	A
1	A	3667	C
4	AQ	62	C
5	B	22	G
9	C	35	A

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 260 ligands modelled in this entry, 260 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.

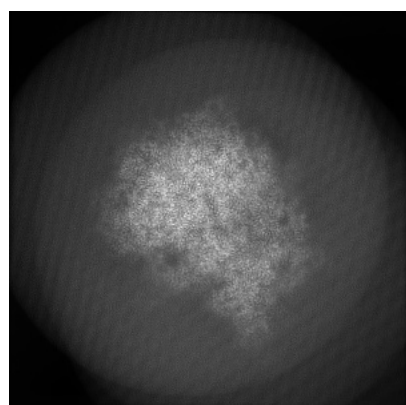
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61272. These allow visual inspection of the internal detail of the map and identification of artifacts.

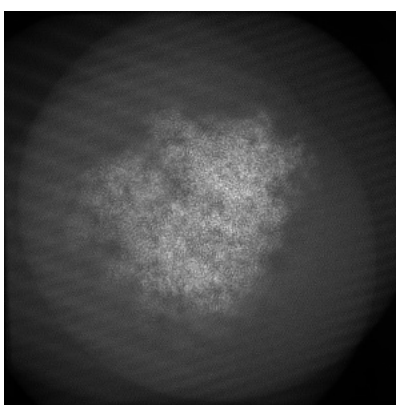
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

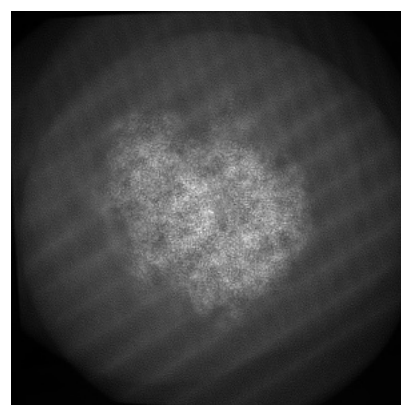
6.1.1 Primary map



X



Y

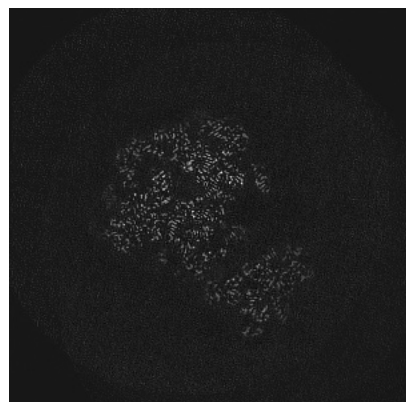


Z

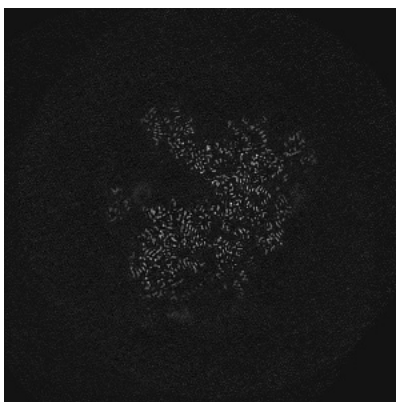
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

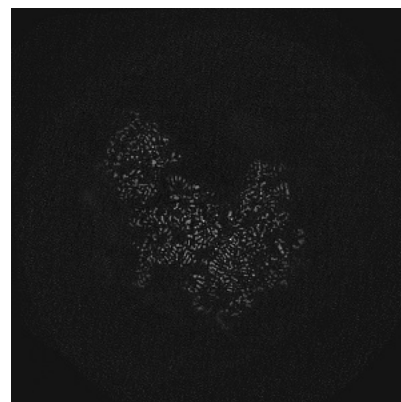
6.2.1 Primary map



X Index: 240



Y Index: 240

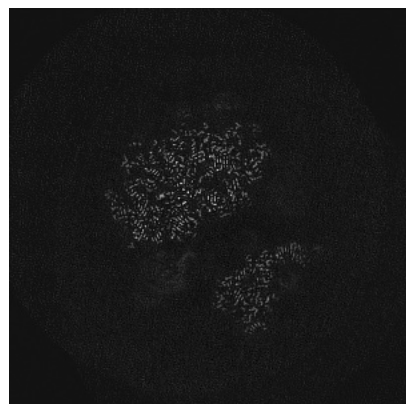


Z Index: 240

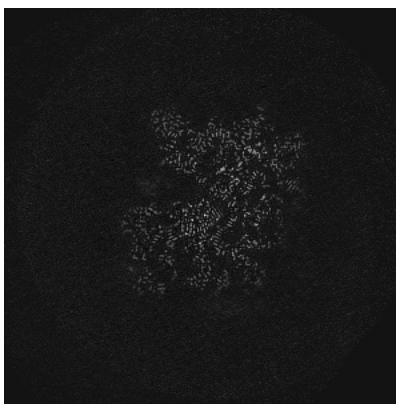
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

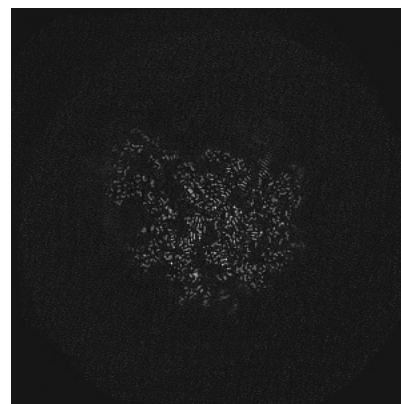
6.3.1 Primary map



X Index: 282



Y Index: 224

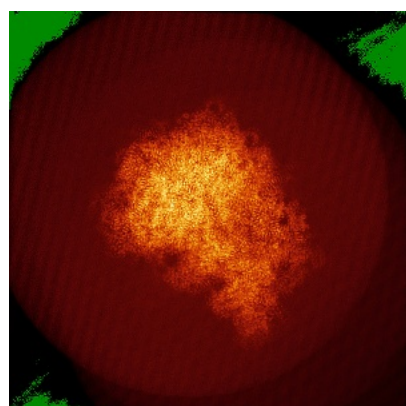


Z Index: 272

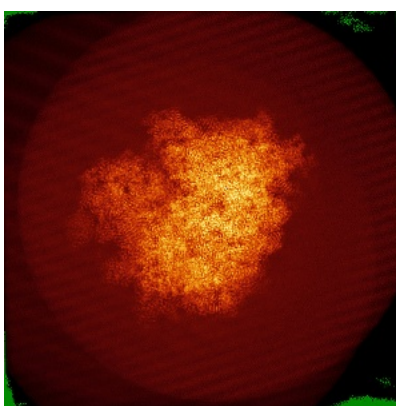
The images above show the largest variance slices of the map in three orthogonal directions.

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

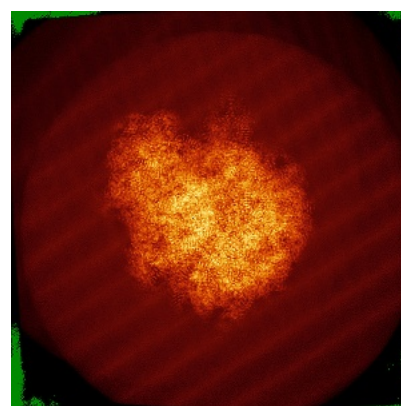
6.4.1 Primary map



X



Y

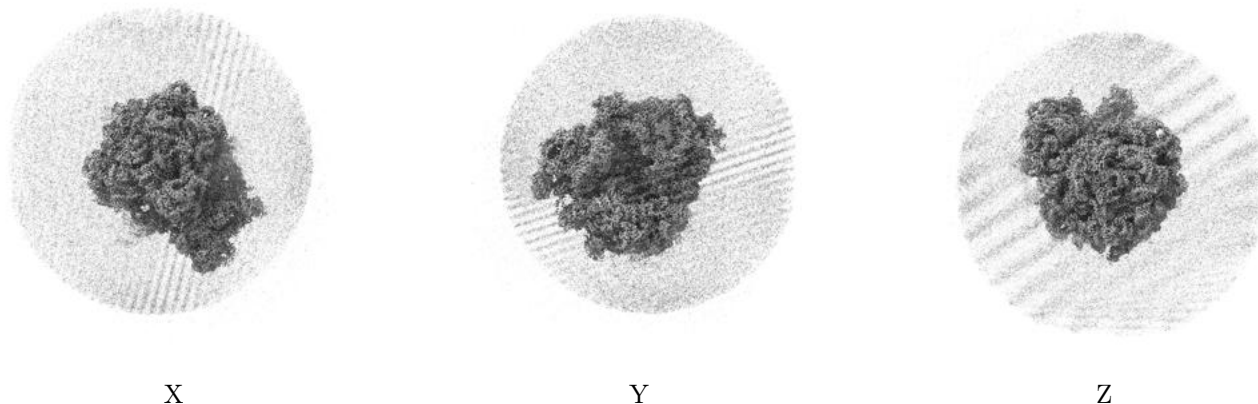


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.003. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

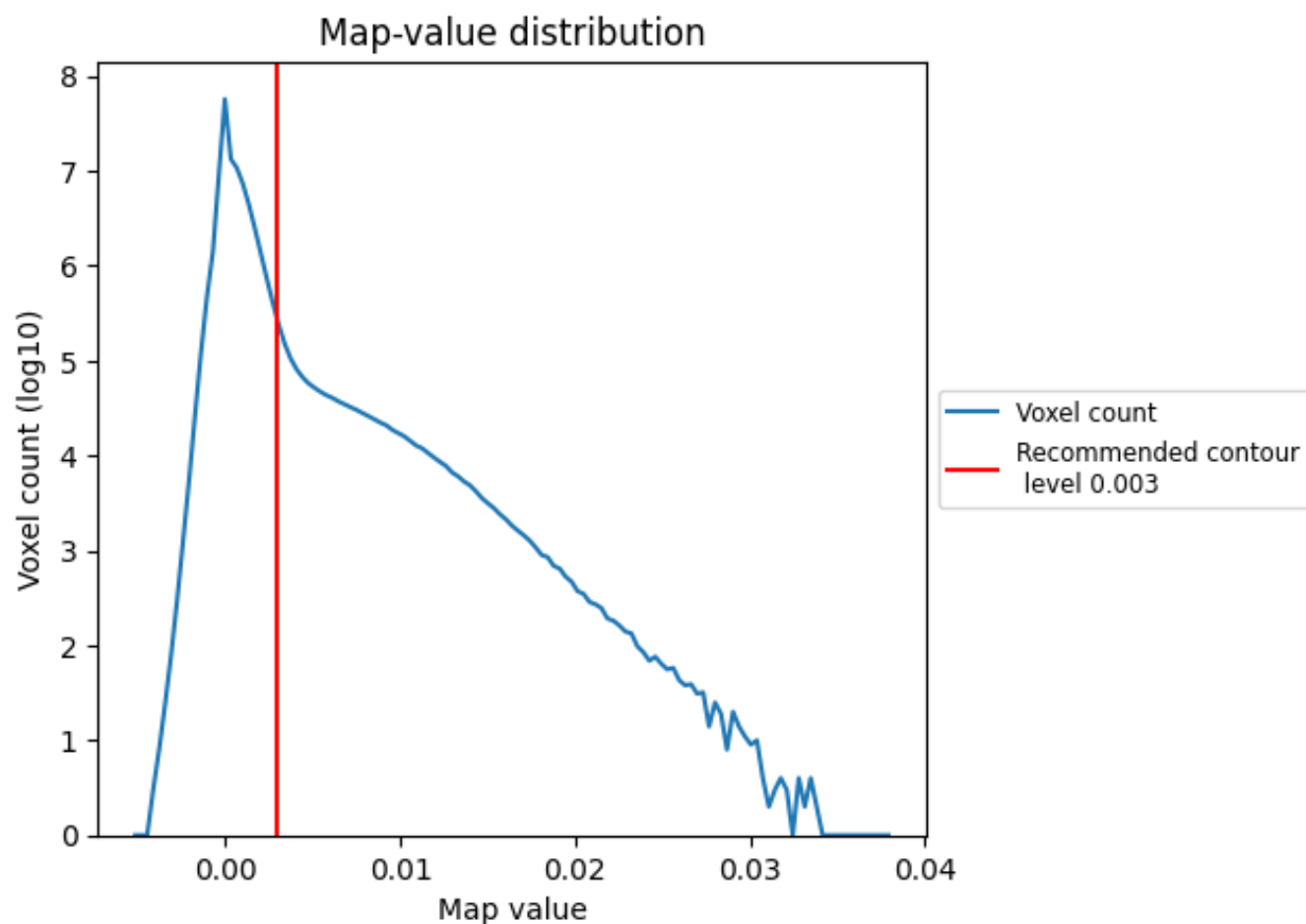
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

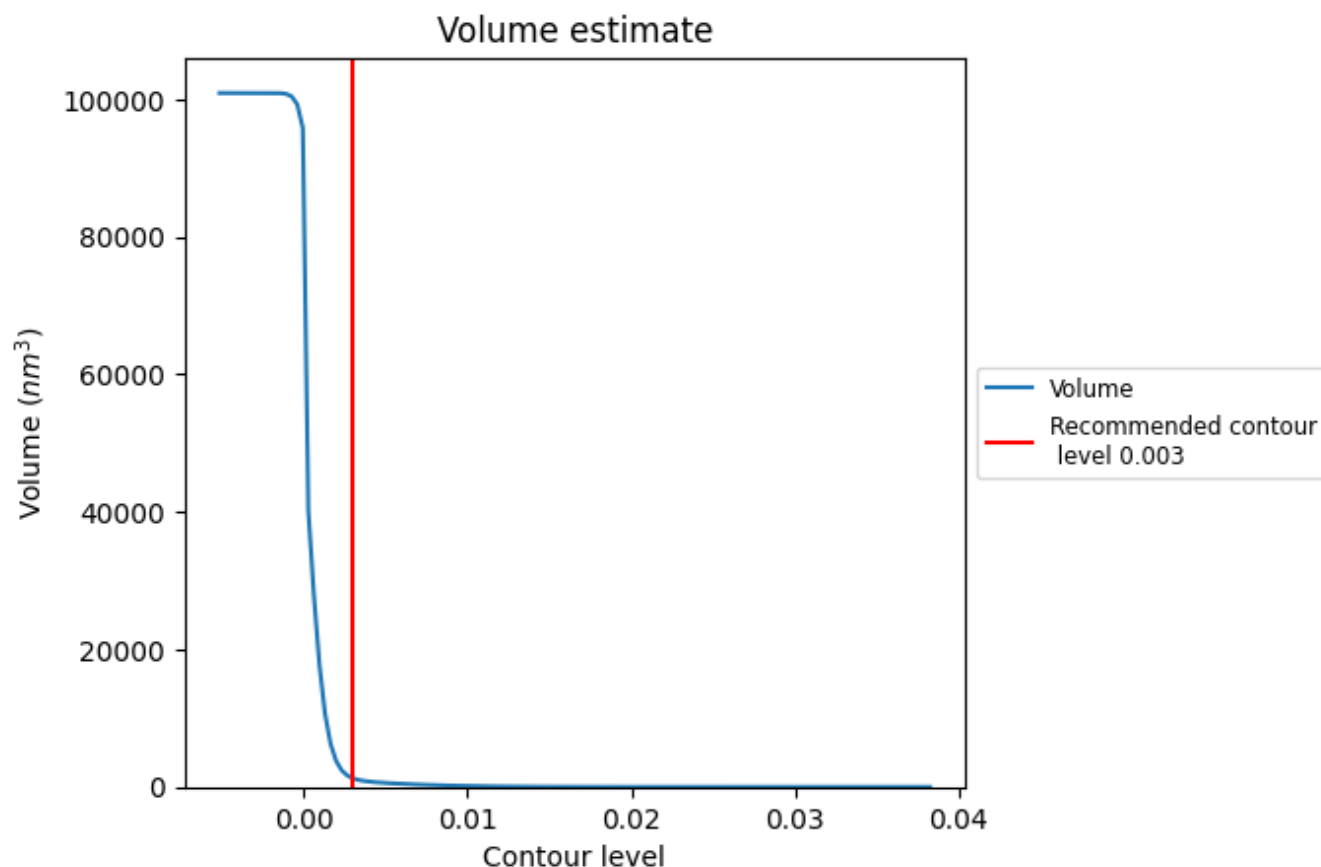
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

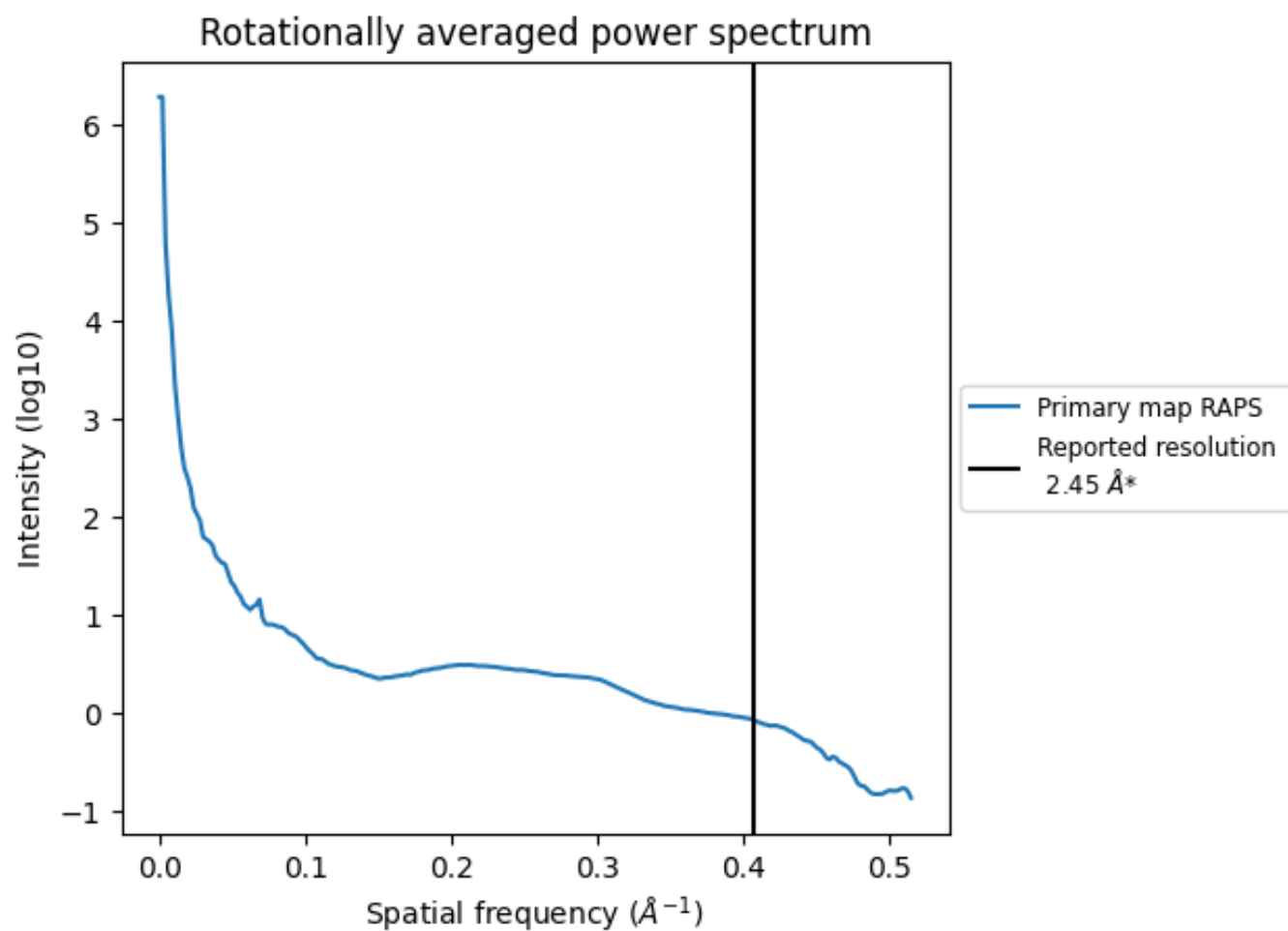
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1259 nm³; this corresponds to an approximate mass of 1137 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 0.408 Å⁻¹

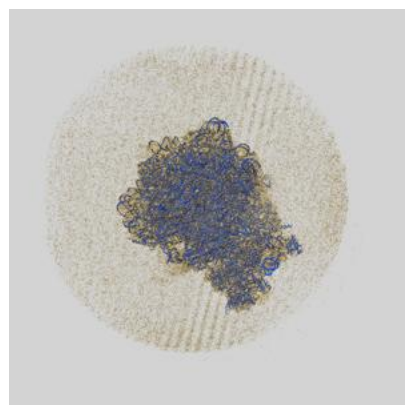
8 Fourier-Shell correlation

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

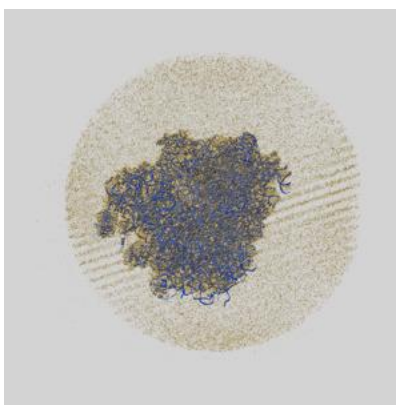
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-61272 and PDB model 9J9H. Per-residue inclusion information can be found in [section 3](#) on [page 19](#).

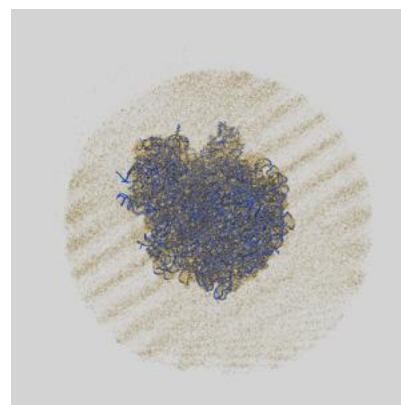
9.1 Map-model overlay [i](#)



X



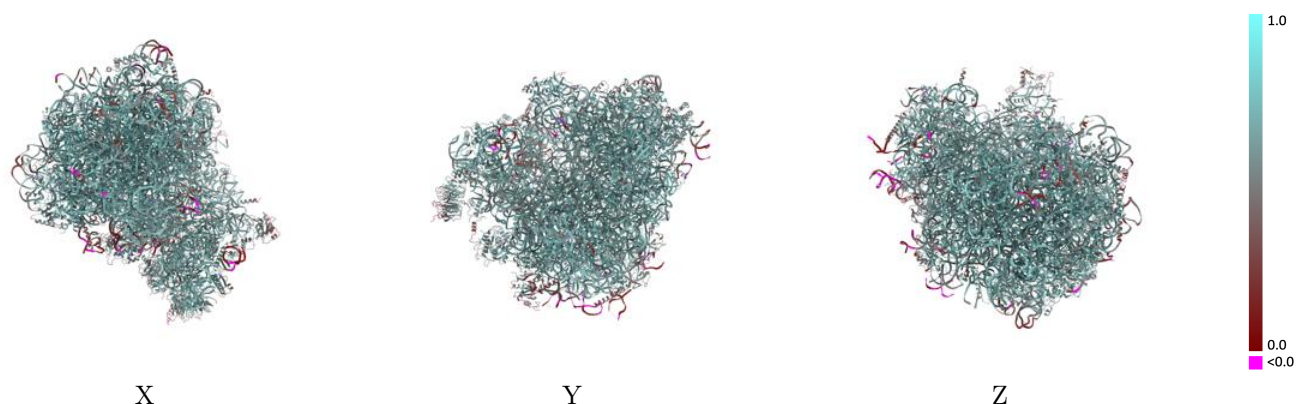
Y



Z

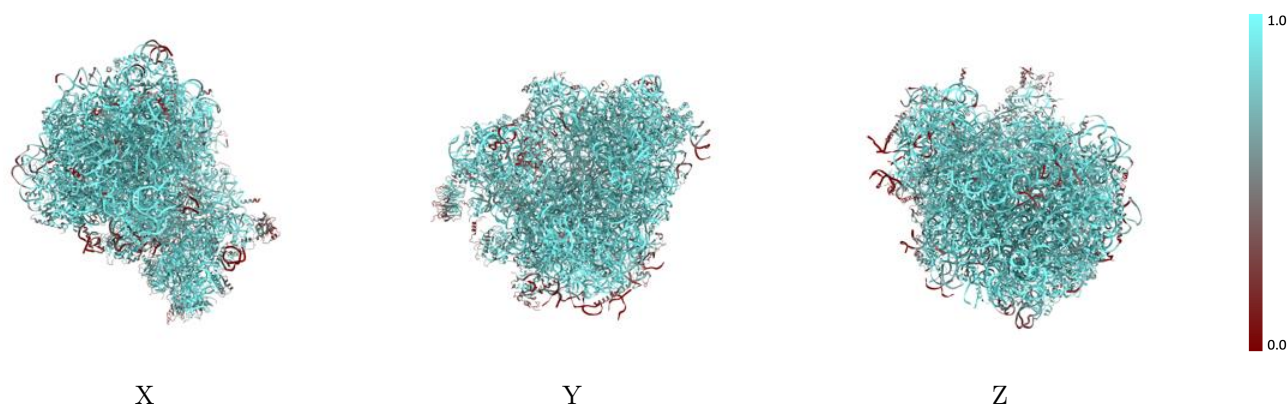
The images above show the 3D surface view of the map at the recommended contour level 0.003 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



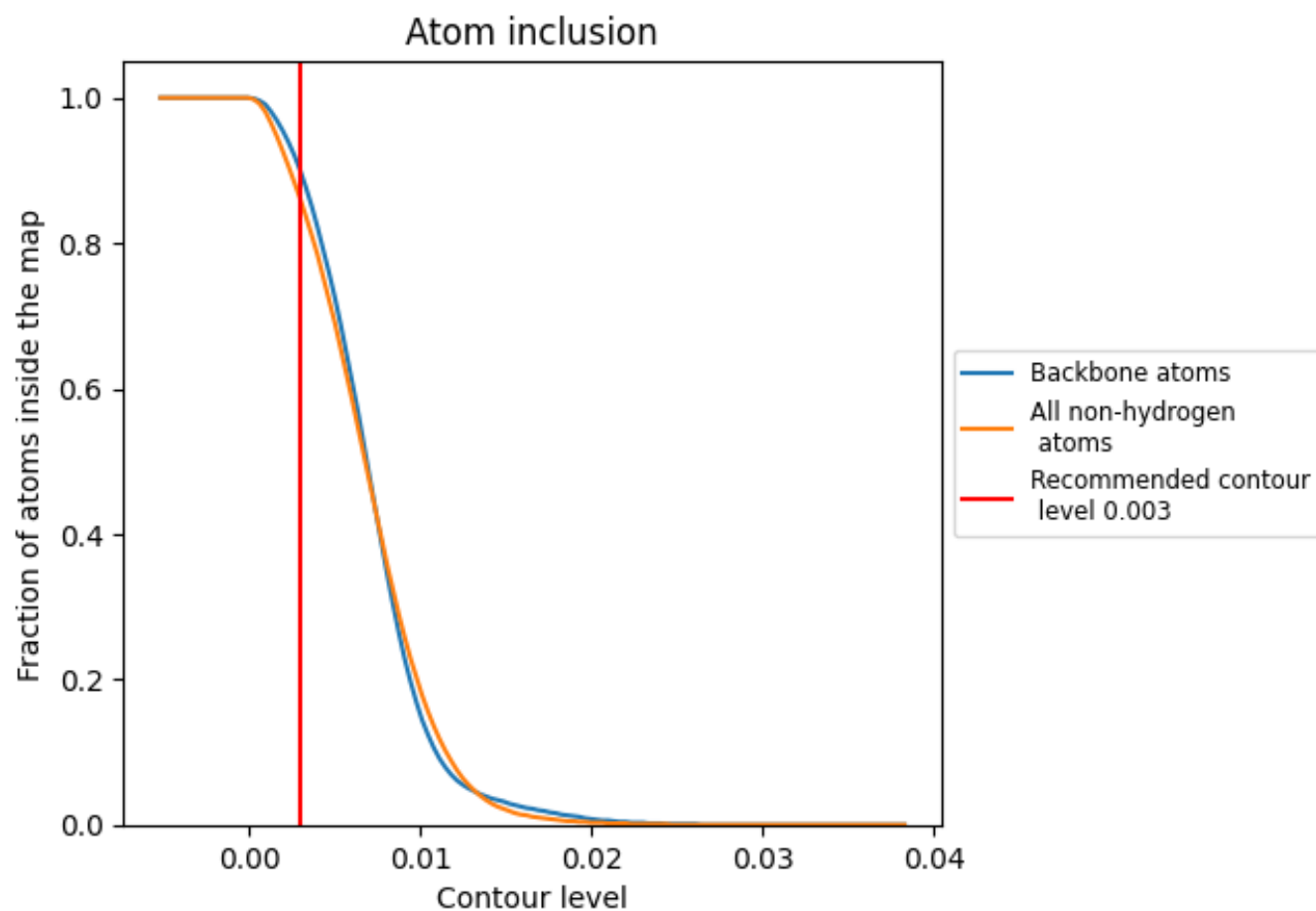
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.003).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 86% 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 (0.003) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8610	 0.6200
0	 0.8830	 0.6190
1	 0.7390	 0.5490
2	 0.8070	 0.6020
3	 0.8410	 0.6140
4	 0.7210	 0.5290
5	 0.8920	 0.6450
6	 0.8270	 0.5930
7	 0.8920	 0.6430
8	 0.8990	 0.6710
9	 0.9210	 0.6690
A	 0.9120	 0.6450
AA	 0.3460	 0.3950
AB	 0.7890	 0.5690
AC	 0.9150	 0.6710
AD	 0.8560	 0.6270
AE	 0.9110	 0.6700
AF	 0.5510	 0.4900
AG	 0.7830	 0.5890
AH	 0.8450	 0.6060
AI	 0.8110	 0.6070
AJ	 0.7780	 0.5780
AK	 0.7020	 0.5310
AL	 0.8590	 0.6270
AM	 0.6960	 0.5580
AN	 0.7010	 0.5000
AO	 0.7020	 0.5290
AP	 0.5000	 0.4450
AQ	 0.3000	 0.2700
AR	 0.5130	 0.4660
B	 0.9740	 0.6680
C	 0.9500	 0.6650
D	 0.9470	 0.6870
E	 0.9130	 0.6560
F	 0.8660	 0.6390






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Chain	Atom inclusion	Q-score
G	 0.6390	 0.4850
H	 0.8890	 0.6320
I	 0.7960	 0.5700
J	 0.6730	 0.5370
K	 0.9170	 0.6730
L	 0.8900	 0.6540
M	 0.9170	 0.6640
N	 0.8430	 0.5990
O	 0.9400	 0.6880
P	 0.9690	 0.7080
Q	 0.8460	 0.6280
R	 0.7870	 0.5840
S	 0.9280	 0.6820
T	 0.7760	 0.5840
U	 0.9220	 0.6650
V	 0.8730	 0.6570
W	 0.9230	 0.6670
X	 0.5860	 0.4770
Y	 0.8360	 0.6010
Z	 0.8360	 0.5930
a	 0.8640	 0.6300
b	 0.8380	 0.6060
c	 0.9160	 0.6670
d	 0.7180	 0.5280
e	 0.8040	 0.6030
f	 0.8970	 0.6450
g	 0.9050	 0.6470
h	 0.9390	 0.6830
i	 0.9100	 0.6700
j	 0.8960	 0.6260
k	 0.7990	 0.5900
l	 0.7480	 0.5710
m	 0.6540	 0.5270
n	 0.8300	 0.6150
o	 0.8680	 0.6270
p	 0.8660	 0.6270
q	 0.5740	 0.4890
r	 0.8290	 0.5880
s	 0.5420	 0.4740
t	 0.9220	 0.6580
u	 0.8850	 0.6230
v	 0.8530	 0.6250

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Chain	Atom inclusion	Q-score
w	 0.7000	 0.5530
x	 0.8070	 0.5780
y	 0.8590	 0.6120
z	 0.8680	 0.6310