



## Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 11:38 AM UTC

PDB ID : 9V21 / pdb\_00009v21  
EMDB ID : EMD-64713  
Title : Cryo- EM structure of 75S ribosome with P- tRNA from Entamoeba histolytica  
Authors : Sharma, S.; Mishra, S.; Gourinath, S.; Kaushal, P.S.  
Deposited on : 2025-05-19  
Resolution : 3.00 Å(reported)  
Based on initial model : 6QZP

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

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

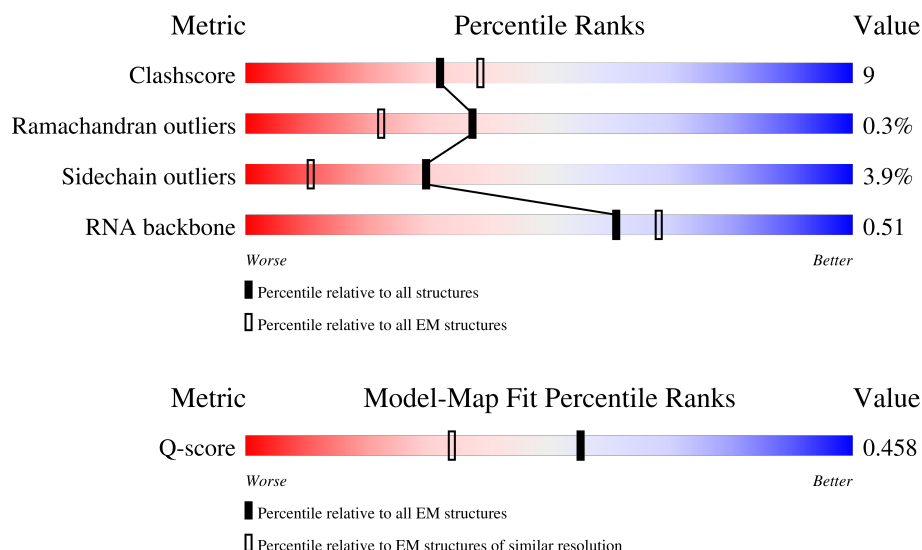
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.00 Å.

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























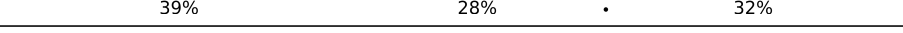




Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 ( 2.50 - 3.50 )

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  $\geq 3$ , 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	1A	3503	
2	1B	155	
3	1C	117	

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Mol	Chain	Length	Quality of chain
4	ID	246	
5	IE	402	
6	IF	431	
7	IG	286	
8	IH	203	
9	II	230	
10	IJ	286	
11	IK	197	
12	IL	210	
13	IM	174	
14	IN	291	
15	IO	204	
16	IP	135	
17	IQ	204	
18	IR	179	
19	IS	167	
20	IT	173	
21	IU	198	
22	IV	165	
23	IW	137	
24	IX	140	
25	IY	121	
26	IZ	163	
27	la	213	
28	lb	139	







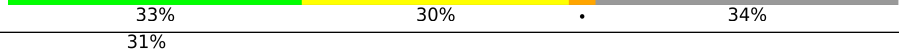
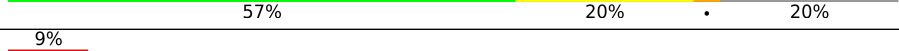
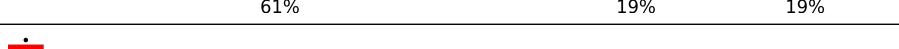
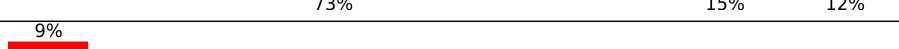
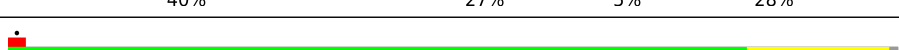

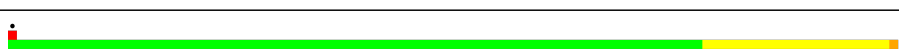

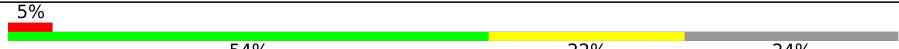





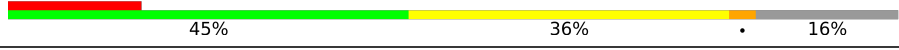
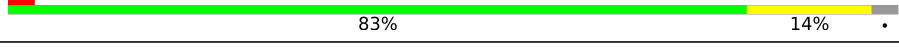



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Mol	Chain	Length	Quality of chain
29	lc	148	
30	ld	64	
31	le	109	
32	lf	150	
33	lg	134	
34	lh	137	
35	li	122	
36	lj	108	
37	lk	104	
38	ll	77	
39	lm	93	
40	ln	88	
41	lo	50	
42	lp	56	
43	lq	98	
44	ls	14	
45	sA	137	
46	sB	144	
47	sC	83	
48	sD	69	
49	sE	55	
50	sG	321	
51	sH	76	
52	sK	6	
53	sa	1947	

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Mol	Chain	Length	Quality of chain
54	sb	254	
55	sc	255	
56	sd	244	
57	se	256	
58	sf	326	
59	sg	206	
60	sh	266	
61	si	201	
62	sj	237	
63	sk	185	
64	sl	127	
65	sm	156	
66	sn	136	
67	so	150	
68	sp	146	
69	sq	144	
70	sr	129	
71	ss	157	
72	st	117	
73	su	155	
74	sv	155	
75	sw	118	
76	sx	86	
77	sy	141	
78	sz	140	

## 2 Entry composition

There are 78 unique types of molecules in this entry. The entry contains 191389 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 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1A	3180	Total	C	N	O	P	0	0
			67965	30470	12340	21975	3180		

- Molecule 2 is a RNA chain called 5.8S.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1B	145	Total	C	N	O	P	0	0
			3097	1390	560	1002	145		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1C	117	Total	C	N	O	P	0	0
			2477	1108	425	827	117		

- Molecule 4 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	1D	246	Total	C	N	O	S	0	0
			1881	1165	382	326	8		

- Molecule 5 is a protein called 60S ribosomal protein L3, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	1E	388	Total	C	N	O	S	0	0
			3085	1961	579	530	15		

- Molecule 6 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	1F	420	Total	C	N	O	S	0	0
			3248	2070	617	547	14		

- Molecule 7 is a protein called 60S ribosomal protein L5, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	lG	282	Total	C	N	O	S	0	0
			2245	1434	405	398	8		

- Molecule 8 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	lH	203	Total	C	N	O	S	0	0
			1608	1054	272	278	4		

- Molecule 9 is a protein called 60S ribosomal protein L7, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	lI	210	Total	C	N	O	S	0	0
			1658	1067	301	282	8		

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	lJ	209	Total	C	N	O	S	0	0
			1697	1097	310	285	5		

- Molecule 11 is a protein called 60S ribosomal protein L9, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	lK	193	Total	C	N	O	S	0	0
			1538	974	279	279	6		

- Molecule 12 is a protein called Ribosomal protein L10, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	lL	201	Total	C	N	O	S	0	0
			1608	1023	306	265	14		

- Molecule 13 is a protein called 60S ribosomal protein L11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	lM	170	Total	C	N	O	S	0	0
			1350	857	243	245	5		

- Molecule 14 is a protein called 60S ribosomal protein L13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	lN	266	Total	C	N	O	S	0	0
			2121	1352	410	351	8		

- Molecule 15 is a protein called 60S ribosomal protein L13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	lO	204	Total	C	N	O	S	0	0
			1616	1030	302	275	9		

- Molecule 16 is a protein called 60S ribosomal protein L14, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	lP	130	Total	C	N	O	S	0	0
			1020	654	188	174	4		

- Molecule 17 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	lQ	204	Total	C	N	O	S	0	0
			1676	1051	356	264	5		

- Molecule 18 is a protein called 60S ribosomal protein L17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	lR	155	Total	C	N	O	S	0	0
			1211	765	234	207	5		

- Molecule 19 is a protein called 60S ribosomal protein L18, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	lS	167	Total	C	N	O	S	0	0
			1321	835	258	219	9		

- Molecule 20 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	lT	173	Total	C	N	O	S	0	0
			1413	910	259	235	9		

- Molecule 21 is a protein called Ribosomal protein L19.



Mol	Chain	Residues	Atoms					AltConf	Trace
21	IU	150	Total	C	N	O	S	0	0
			1235	787	246	197	5		

- Molecule 22 is a protein called 60S ribosomal protein L21, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	IV	165	Total	C	N	O	S	0	0
			1320	846	254	217	3		

- Molecule 23 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	IW	93	Total	C	N	O	S	0	0
			763	493	132	133	5		

- Molecule 24 is a protein called 60S ribosomal protein L23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	IX	133	Total	C	N	O	S	0	0
			1015	629	196	182	8		

- Molecule 25 is a protein called Ribosomal protein L23A, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	IY	116	Total	C	N	O	S	0	0
			926	597	166	159	4		

- Molecule 26 is a protein called 60S ribosomal protein L24, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	IZ	57	Total	C	N	O	S	0	0
			481	318	88	73	2		

- Molecule 27 is a protein called 60S ribosomal protein L26, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	la	210	Total	C	N	O	S	0	0
			1651	1055	304	285	7		

- Molecule 28 is a protein called 60S ribosomal protein L27, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	lb	137	Total	C	N	O	S	0	0
			1094	707	196	187	4		

- Molecule 29 is a protein called Large ribosomal subunit protein uL15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	lc	148	Total	C	N	O	S	0	0
			1192	757	236	194	5		

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	ld	60	Total	C	N	O	S	0	0
			478	297	97	82	2		

- Molecule 31 is a protein called 60S ribosomal protein L30, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	le	103	Total	C	N	O	S	0	0
			768	486	131	149	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	lf	128	Total	C	N	O	S	0	0
			1039	671	193	169	6		

- Molecule 33 is a protein called 60S ribosomal protein L32, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	lg	124	Total	C	N	O	S	0	0
			1019	649	202	163	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
34	lh	105	Total	C	N	O	S	0	0
			820	512	169	133	6		

- Molecule 35 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	li	122	Total	C	N	O	S	0	0
			974	620	188	162	4		

- Molecule 36 is a protein called 60S ribosomal protein L35a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	lj	106	Total	C	N	O	S	0	0
			841	545	158	135	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	lk	89	Total	C	N	O	S	0	0
			712	447	144	116	5		

- Molecule 38 is a protein called 60S ribosomal protein L37-A, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	ll	72	Total	C	N	O	S	0	0
			591	361	132	91	7		

- Molecule 39 is a protein called 60S ribosomal protein L37A, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	lm	90	Total	C	N	O	S	0	0
			688	428	135	119	6		

- Molecule 40 is a protein called 60S ribosomal protein L38, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	ln	73	Total	C	N	O	S	0	0
			584	378	104	100	2		

- Molecule 41 is a protein called Ribosomal protein L39, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	lo	50	Total	C	N	O	S	0	0
			432	275	91	63	3		

- Molecule 42 is a protein called 60S ribosomal protein L40, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	lp	53	Total	C	N	O	S	0	0
			420	259	86	69	6		

- Molecule 43 is a protein called 60S ribosomal protein L44, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	lq	92	Total	C	N	O	S	0	0
			756	480	148	122	6		

- Molecule 44 is a protein called nascent polypeptide (Unk).

Mol	Chain	Residues	Atoms					AltConf	Trace
44	ls	14	Total	C	N	O		0	0
			76	45	17	14			

- Molecule 45 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	sA	72	Total	C	N	O	S	0	0
			568	368	96	100	4		

- Molecule 46 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	sB	98	Total	C	N	O	S	0	0
			787	478	169	134	6		

- Molecule 47 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	sC	83	Total	C	N	O	S	0	0
			641	407	117	111	6		

- Molecule 48 is a protein called 40S ribosomal protein S28, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	sD	60	Total	C	N	O	S	0	0
			468	289	93	84	2		

- Molecule 49 is a protein called Ribosomal protein S29, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	sE	55	Total	C	N	O	S	0	0
			442	273	90	75	4		

- Molecule 50 is a protein called Guanine nucleotide-binding protein subunit beta 2-like 1, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	sG	305	Total	C	N	O	S	0	0
			2347	1488	398	448	13		

- Molecule 51 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	sH	74	Total	C	N	O	P	0	0
			1573	703	276	520	74		

- Molecule 52 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	sK	6	Total	C	N	O	P	0	0
			126	57	21	42	6		

- Molecule 53 is a RNA chain called 17S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	sa	1453	Total	C	N	O	P	0	0
			31080	13913	5653	10061	1453		

- Molecule 54 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	sb	205	Total	C	N	O	S	0	0
			1626	1029	286	296	15		

- Molecule 55 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	sc	215	Total	C	N	O	S	0	0
			1642	1052	291	291	8		

- Molecule 56 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	sd	221	Total	C	N	O	S	0	0
			1708	1080	312	305	11		

- Molecule 57 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	se	212	Total	C	N	O	S	0	0
			1717	1097	305	306	9		

- Molecule 58 is a protein called 40S ribosomal protein S4, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	sf	256	Total	C	N	O	S	0	0
			2031	1297	378	345	11		

- Molecule 59 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	sg	185	Total	C	N	O	S	0	0
			1473	930	267	265	11		

- Molecule 60 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	sh	176	Total	C	N	O	S	0	0
			1395	880	278	230	7		

- Molecule 61 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	si	160	Total	C	N	O	S	0	0
			1246	813	220	209	4		

- Molecule 62 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	sj	192	Total	C	N	O	S	0	0
			1536	970	285	276	5		

- Molecule 63 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	sk	162	Total	C	N	O	S	0	0
			1323	845	251	221	6		

- Molecule 64 is a protein called 40S ribosomal protein S10, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	sl	91	Total	C	N	O	S	0	0
			729	475	122	123	9		

- Molecule 65 is a protein called 40S ribosomal protein S11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	sm	154	Total	C	N	O	S	0	0
			1263	796	243	217	7		

- Molecule 66 is a protein called 40S ribosomal protein S12, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	sn	53	Total	C	N	O	S	0	0
			428	277	77	72	2		

- Molecule 67 is a protein called 40S ribosomal protein S13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	so	150	Total	C	N	O	S	0	0
			1184	756	218	204	6		

- Molecule 68 is a protein called Ribosomal protein S14, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	sp	133	Total	C	N	O	S	0	0
			999	615	192	186	6		

- Molecule 69 is a protein called 40S ribosomal protein S15, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	sq	109	Total	C	N	O	S	0	0
			873	561	155	152	5		

- Molecule 70 is a protein called 40S ribosomal protein S15a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	sr	129	Total	C	N	O	S	0	0
			1022	650	186	181	5		

- Molecule 71 is a protein called 40S ribosomal protein S16, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	ss	141	Total	C	N	O	S	0	0
			1104	713	198	189	4		

- Molecule 72 is a protein called 40S ribosomal protein S17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	st	111	Total	C	N	O	S	0	0
			907	573	169	162	3		

- Molecule 73 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	su	144	Total	C	N	O	S	0	0
			1163	722	233	202	6		

- Molecule 74 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	sv	155	Total	C	N	O	S	0	0
			1245	796	223	217	9		

- Molecule 75 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	sw	99	Total	C	N	O	S	0	0
			774	490	135	144	5		

- Molecule 76 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	sx	83	Total	C	N	O	S	0	0
			651	412	117	119	3		

- Molecule 77 is a protein called 40S ribosomal protein S23, putative.



Mol	Chain	Residues	Atoms					AltConf	Trace
77	sy	130	Total	C	N	O	S	0	0
			1010	637	200	169	4		

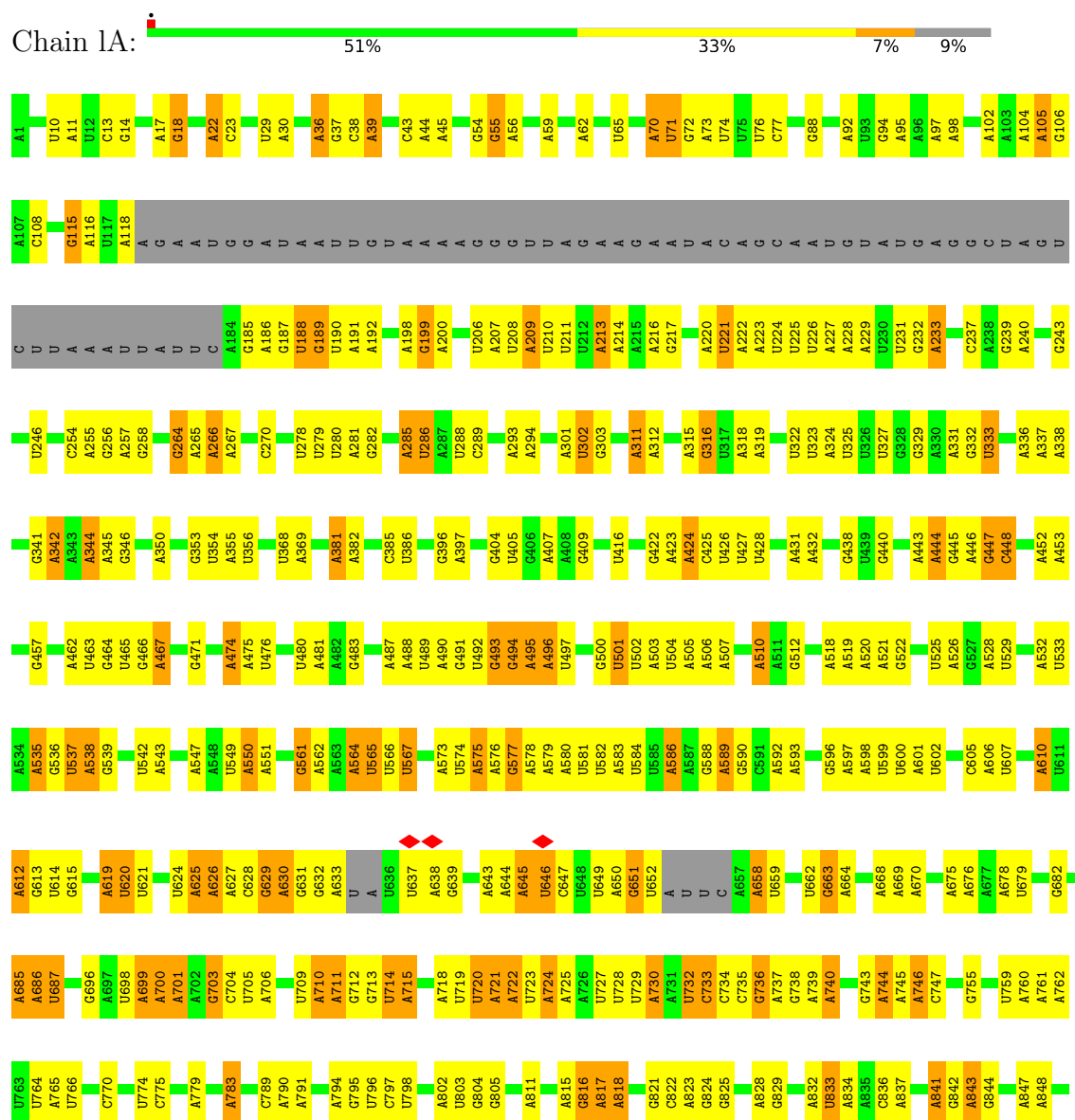
- Molecule 78 is a protein called 40S ribosomal protein S24, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	sz	76	Total	C	N	O	S	0	0
			598	394	103	99	2		

### 3 Residue-property plots

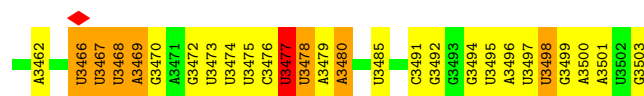
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 25S rRNA



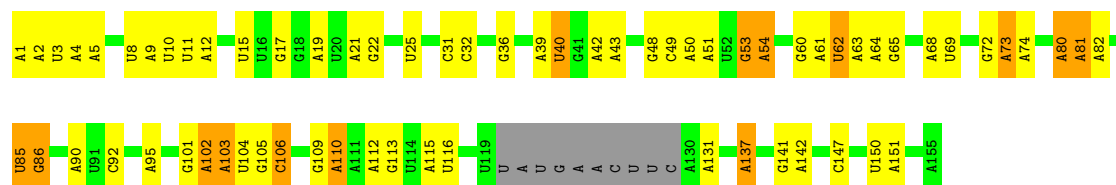
U2056	U1985	A1886	G	G1629	A1513	U1429	G1357	U1248	U1079
G2061	A1887	U	A	A1630	A1516	G1430	G1358	G1252	G1086
A2062	A1888	U	U	A1631	C1517	A1431	C1156	A1157	G1087
A2064	U	A	G1728	G1632	U1432	U1433	G1360	A1255	G960
G2067	C1980	A	G1729	G1633	A1520	A1437	G1361	A1256	A1090
A1981	A1893	U	G1730	G1634	A1521	U	C	A1091	A1091
U1982	C1994	A	U	U1636	G1522	U	C	A1092	A1092
A1983	U	U	A1735	U1639	G1523	A	A	G1093	G975
A1984	U	C	A1736	U1639	A1524	U	U	A1094	G979
U1989	A1898	A	A1737	A1640	A1527	U	G	A1095	A980
A1992	U	A	G1738	A1641	A1527	U	G	U1096	U1097
G1993	A1902	U	G1739	U	A1527	U	A	A1098	U992
U1998	A1903	A	G1740	U1648	U1533	A1450	A1369	A1283	A988
C	U1998	A	A1741	U1649	U1534	A1451	G1370	A1284	G969
U	U	A1809	U	A1451	C1452	U	A	A1284	A970
U	C	A1810	U	C1452	U1535	U	U	A1284	A971
U	A	A1811	U	A1453	A1536	U	A	A1284	A972
U	U	A1906	U	U1652	A1537	U	A	A1284	A973
U	A	A1907	U1812	G1681	G1538	U	G	A1284	A974
G	A	G1813	U	U	U	U	C	A1284	A975
A	U	A1814	U	U	U	U	C	A1284	A976
G	U	G1912	U	U	U	U	C	A1284	A977
C	U	G1913	U	U	U	U	C	A1284	A978
A	U	A1914	U	U	U	U	C	A1284	A979
U	U	A1915	U	U	U	U	C	A1284	A980
U	A	A1817	U	U	U	U	C	A1284	A981
A	U	C1818	U	U	U	U	C	A1284	A982
A	U	U1921	U	U	U	U	C	A1284	A983
U	U	U1922	U	U	U	U	C	A1284	A984
G	U	U1822	U	U	U	U	C	A1284	A985
A	U	C1823	U	U	U	U	C	A1284	A986
U	U	A1925	U	U	U	U	C	A1284	A987
U	U	U1926	U	U	U	U	C	A1284	A988
A	U	U1927	U	U	U	U	C	A1284	A989
A	U	G1928	U	U	U	U	C	A1284	A990
U	U	U1929	U	U	U	U	C	A1284	A991
U	U	A1764	U	U	U	U	C	A1284	A992
A	U	U1765	U	U	U	U	C	A1284	A993
U	U	G1766	U	U	U	U	C	A1284	A994
U	U	A1767	U	U	U	U	C	A1284	A995
A	U	G1768	U	U	U	U	C	A1284	A996
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U	U	A	U	U	U	U	C	A1284	A999
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U	U	A	U	U	U	U	C	A1284	A1001
U	U	A	U	U	U	U	C	A1284	A1002
U	U	A	U	U	U	U	C	A1284	A1003
U	U	A	U	U	U	U	C	A1284	A1004
U	U	A	U	U	U	U	C	A1284	A1005
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U	U	A	U	U	U	U	C	A1284	A1008
U	U	A	U	U	U	U	C	A1284	A1009
U	U	A	U	U	U	U	C	A1284	A1010

C3376	U3289	A3186	C3103	G3006	U2790	G2677	G2595	G	G2466	A2356	G2263	U
U3377	C3290	C3188	G3104	A3007	U2797	G2678	A2598	C	G2469	A2357	A2264	A
C3380	G3299	C3189	U3105	U3008	G2798	U2681	U2601	U	G2470	C2360	U2265	A
A3381	G3299	U3194	C3106	C3009	U2799	U2682	A2606	G	G2471	U2374	U2269	A2173
A3382	U3302	G3195	G3107	G3013	A2806	G2683	A	G	G2472	G2381	C2272	G2176
A3383	A3303	U3196	A3110	G3014	G2815	G2684	A	G	G2473	C2382	C2273	A2177
A3384	C3304	G3200	A3111	A3015	A2818	U2688	U	A	G2478	G2383	A2274	U2178
G3385	G3201	C3201	U3114	C3019	U2819	G2689	G	U	G2479	C2384	A2274	U2179
G3392	A3203	C3202	U3117	U3023	U2822	G2690	U	G	A2480	U2385	C2280	C2184
A3393	C3204	G3202	U3121	U3025	G2823	G2691	A	C	G2481	U2386	U2281	C2185
A3394	G3207	C3207	C3126	U3028	G2825	G2692	U	U	G2482	A2389	G2282	U2186
C3397	A3208	U3209	C3127	A3029	A2832	G2693	U	U	U2483	U2390	A2283	C2186
U3398	U3210	U3210	G3128	A3030	U2833	G2709	C	U	U2484	G2391	A2284	U2190
A3400	A3211	U3212	U3129	U3031	C2835	G2710	A	C	U2485	C2396	U2285	G2193
G3401	U3213	U3213	A3130	C3033	A2838	U2711	U	A	U2486	U2397	G2286	C2194
A3405	U3218	U3218	G3133	C3038	U2841	G2715	A	A	C2398	C2398	A2289	G2197
C3406	A3219	U3220	U3136	U3041	U2842	G2721	U	U	U2410	U2399	A2290	G2198
A3409	U3220	G3223	C3137	G3044	U2843	U2722	U	A	G2411	U2410	A2294	C2205
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U3411	A3228	G3232	U3140	U3048	U2845	A2726	A2628	U	C2415	U2416	U2301	G2207
U3412	G3232	U3232	A3141	A3049	A2847	A2727	A2629	A	U2417	U2417	U2302	C2208
U3413	U3232	U3232	G3142	G3049	A2857	U2730	C2632	U	U2418	U2418	U2303	U2213
A3414	U3232	U3232	A3143	A3054	A2858	G2731	A2634	A	U2419	U2419	U2304	A2214
A3415	U3232	U3232	U3144	G3055	U2859	U2732	U	C	A2428	A2428	A2215	A2216
A3416	U3232	U3232	U3145	G3056	U2860	A2733	A2637	A	U2429	U2429	A2217	U2218
G3417	U3232	U3232	U3146	G3057	U2861	U2734	A2640	C	G2431	G2431	A2218	A2218
C3418	U3232	U3232	A3150	A3061	A2862	U2735	C	C	A2432	A2432	A2223	A2223
A3422	U3232	U3232	A3151	A3062	A2863	G2745	U	A	A2433	A2433	G2324	G2226
C3423	U3232	U3232	A3152	C2967	A2864	A2746	U	C	A2434	A2434	G2325	G2226
U3426	U3232	U3232	A3153	C2968	A2865	G2747	U	A	C2438	C2438	U2330	U2230
U3430	U3232	U3232	A3154	C2971	A2866	U2753	G	A	A2439	A2439	A2331	C2231
U3431	U3232	U3232	U3155	G2977	C2866	G2754	U	A	U2440	U2440	A2332	U2232
A3432	U3232	U3232	U3156	C2978	A2867	C2755	U	A	U2441	U2441	C2333	G2233
U3433	U3232	U3232	G3162	C2979	U2868	A2759	U	A	C2442	C2442	U2334	A2234
A3434	U3232	U3232	A3163	A2869	U2870	G2760	U	A	A2443	A2443	U2335	U2235
G3435	U3232	U3232	G3164	U2871	U2871	A2761	U	U	U2444	U2444	U2336	A2236
A3436	U3232	U3232	U3165	A2881	U2872	A2762	U	C	G2445	G2445	G2337	A2237
G3441	U3232	U3232	G3166	G2882	U2873	U2763	U	U	G2446	G2446	A2338	A2237
A3447	U3232	U3232	A3170	C2985	U2874	U2764	U	A	U2449	U2449	C2341	C2240
G3448	U3232	U3232	A3171	C2986	U2875	U2765	U	U	C2450	C2450	U2342	U2241
A3449	U3232	U3232	C3174	A2988	U2885	A2766	U	U	G2451	G2451	A2245	A2245
U3452	U3232	U3232	A3175	C3084	G2887	G2767	U	G	G2452	G2452	G2246	G2246
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G3454	U3232	U3232	G3086	C2992	G2889	A2769	U	U	U2459	U2459	C2250	C2250
G3455	U3232	U3232	A3089	C2993	A2890	U2770	U	A	U2460	U2460	A2251	A2251
U3456	U3232	U3232	G3090	C2994	G2891	U2771	U	U	G2461	G2461	G2261	G2261
G3457	U3232	U3232	C3091	U3005	A2892	G2772	U	A	G2462	G2462	G2262	U2262
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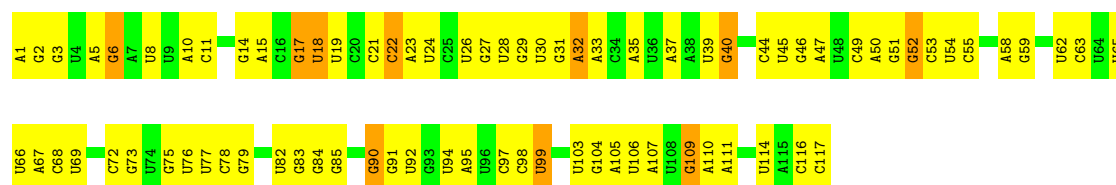
- Molecule 2: 5.8S

Chain 1B: 50% 34% 9% 6%



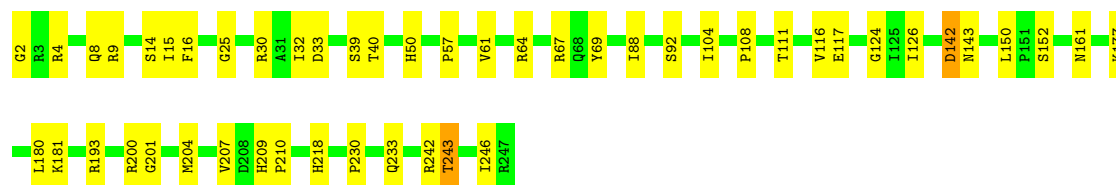
- Molecule 3: 5S rRNA

Chain 1C: 32% 59% 9%



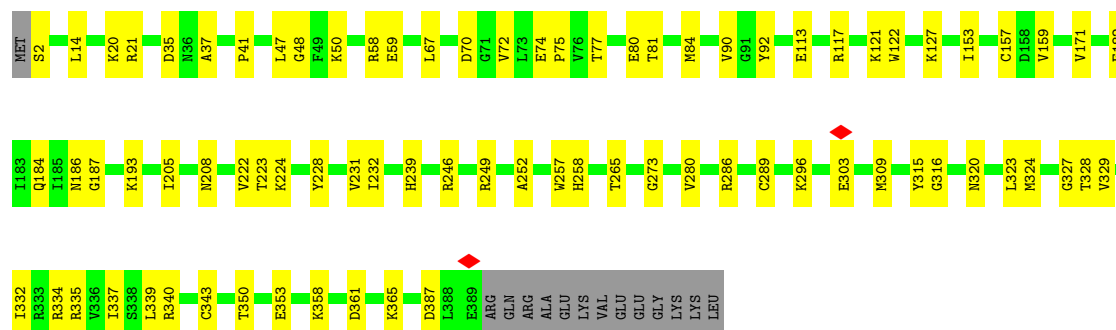
- Molecule 4: Large ribosomal subunit protein uL2

Chain 1D: 80% 19%




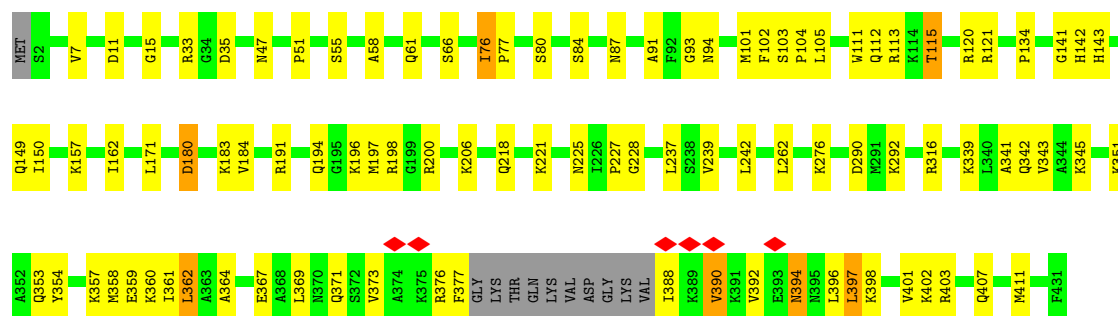
- Molecule 5: 60S ribosomal protein L3, putative

Chain 1E: 77% 20%




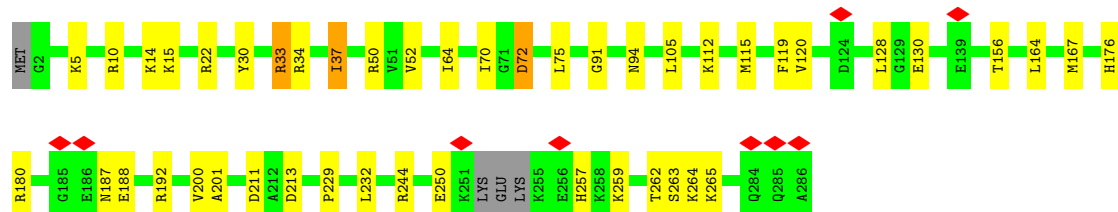
- Molecule 6: Large ribosomal subunit protein uL4

Chain 1F: 




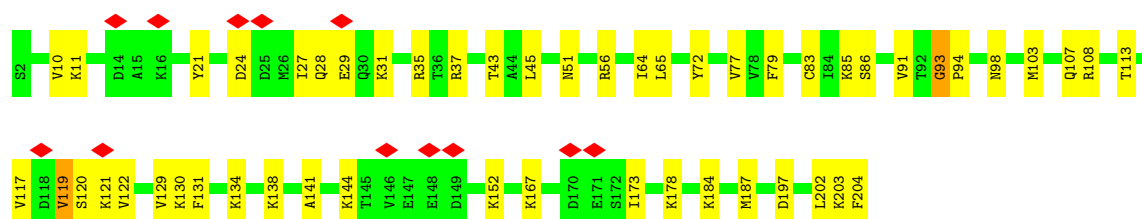
- Molecule 7: 60S ribosomal protein L5, putative

Chain 1G: 




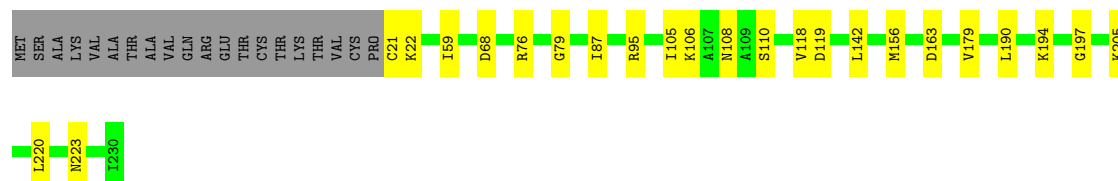
- Molecule 8: Large ribosomal subunit protein eL6

Chain 1H: 



- Molecule 9: 60S ribosomal protein L7, putative

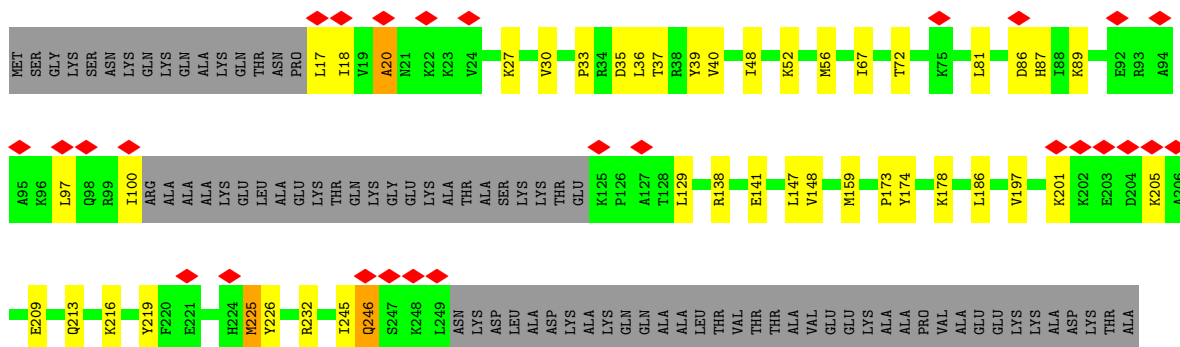
Chain 1I: 



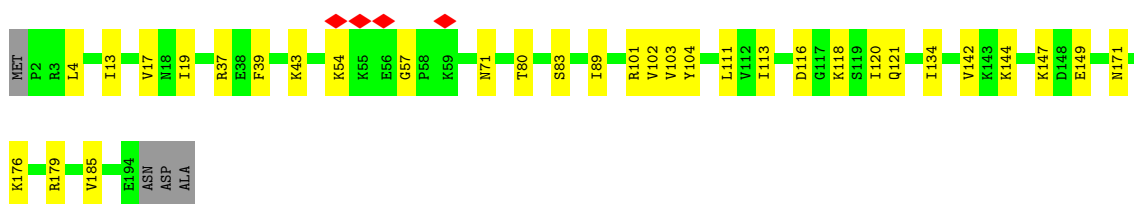
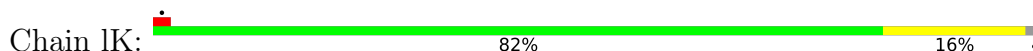
- Molecule 10: 60S ribosomal protein L7a

Chain 1J: 

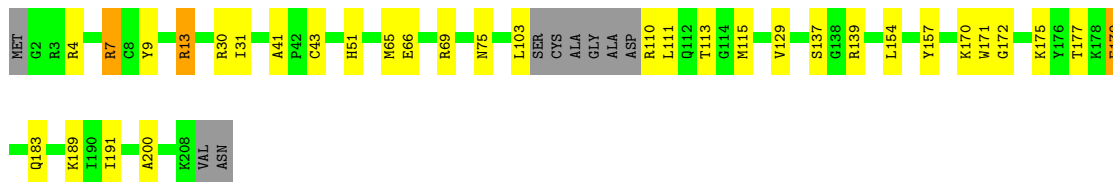
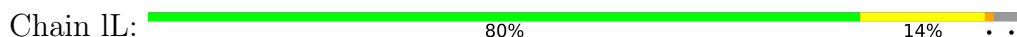




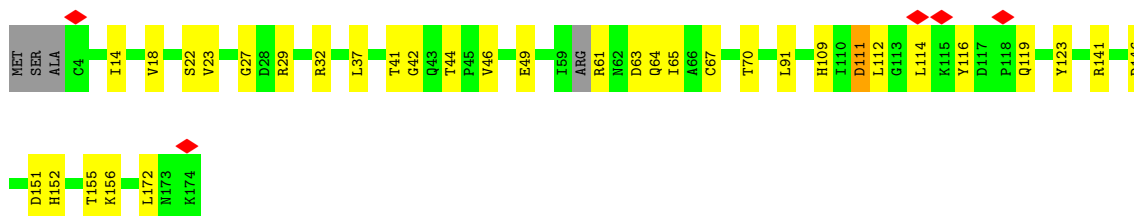
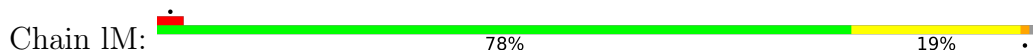
- Molecule 11: 60S ribosomal protein L9, putative



- Molecule 12: Ribosomal protein L10, putative

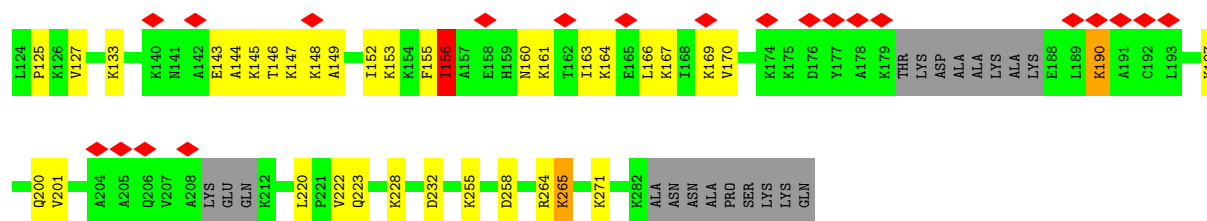


- Molecule 13: 60S ribosomal protein L11, putative



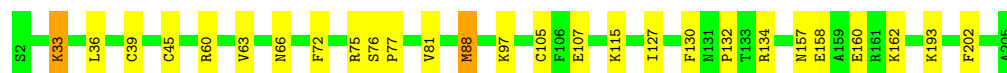
- Molecule 14: 60S ribosomal protein L13, putative





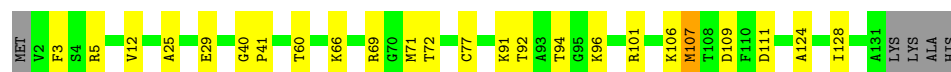
- Molecule 15: 60S ribosomal protein L13, putative

Chain IO: 87% 12%



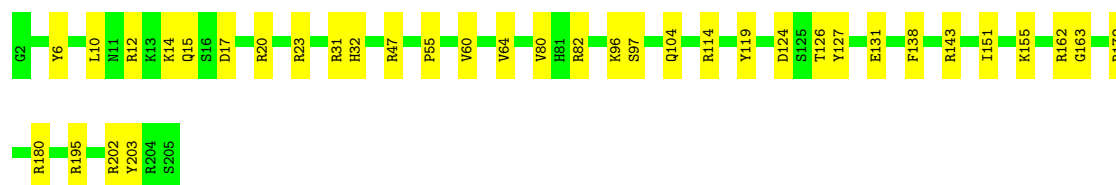
- Molecule 16: 60S ribosomal protein L14, putative

Chain IP: 79% 17%



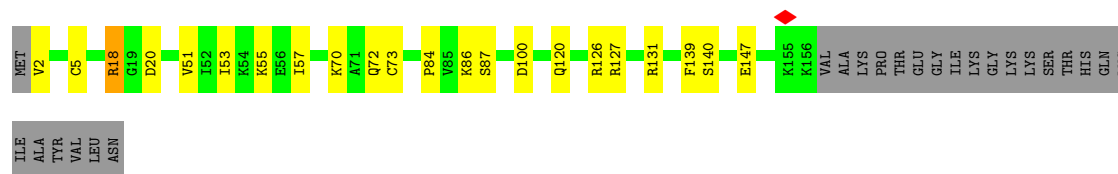
- Molecule 17: Ribosomal protein L15

Chain IQ: 82% 18%



- Molecule 18: 60S ribosomal protein L17, putative

Chain IR: 74% 12% 13%




- Molecule 19: 60S ribosomal protein L18, putative

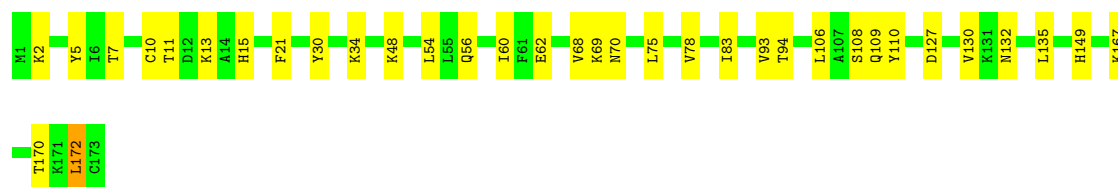
Chain IS: 87% 13%



- Molecule 20: 60S ribosomal protein L18a

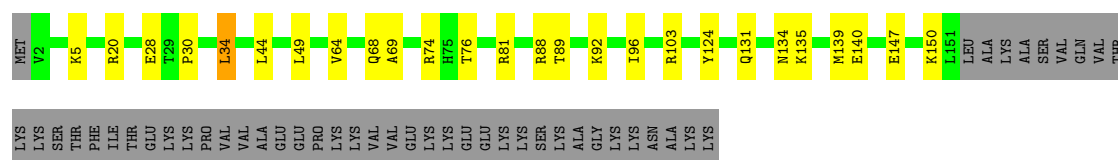


Chain IT: 




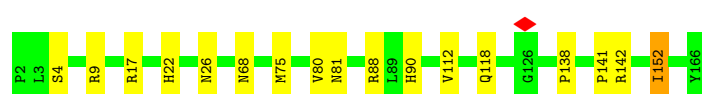
• Molecule 21: Ribosomal protein L19

Chain IU: 



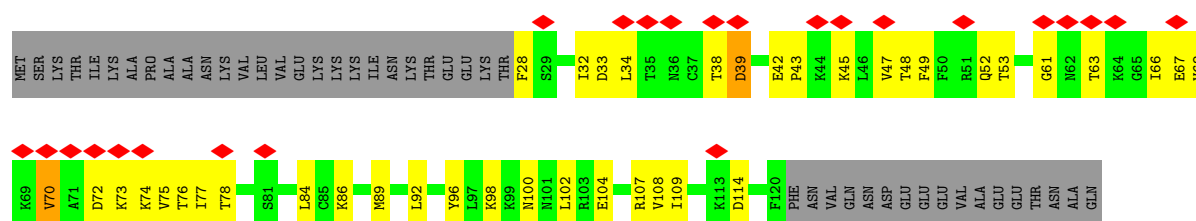
• Molecule 22: 60S ribosomal protein L21, putative

Chain IV: 



• Molecule 23: Large ribosomal subunit protein eL22

Chain IW: 




• Molecule 24: 60S ribosomal protein L23, putative

Chain IX: 

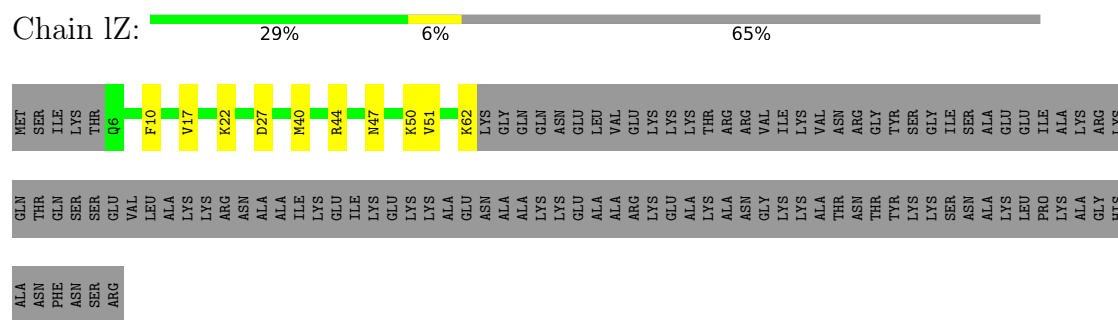


• Molecule 25: Ribosomal protein L23A, putative

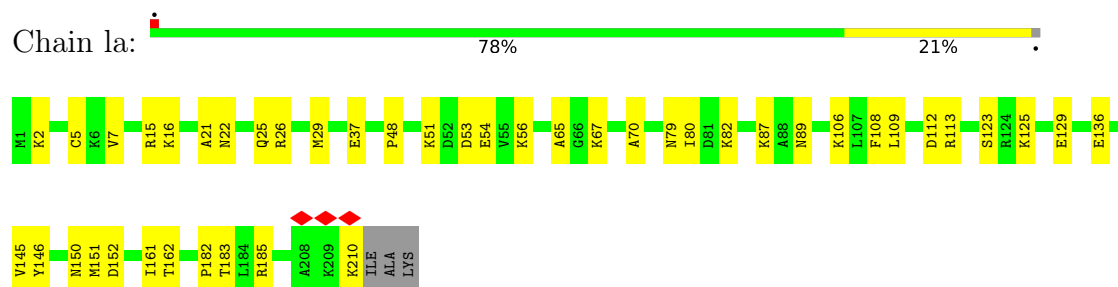
Chain IY: 



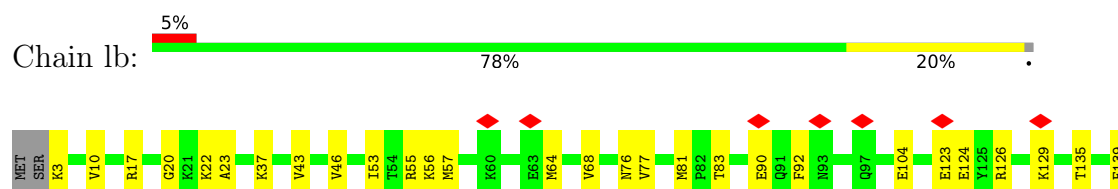
- Molecule 26: 60S ribosomal protein L24, putative



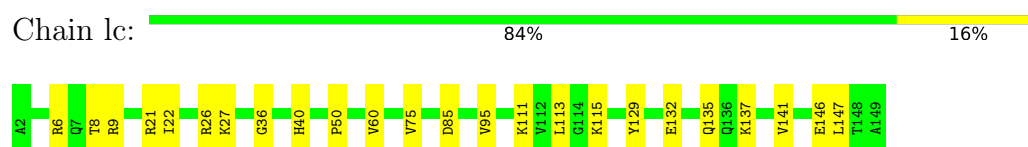
- Molecule 27: 60S ribosomal protein L26, putative



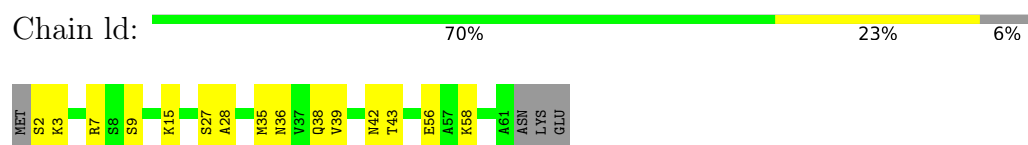
- Molecule 28: 60S ribosomal protein L27, putative



- Molecule 29: Large ribosomal subunit protein uL15A

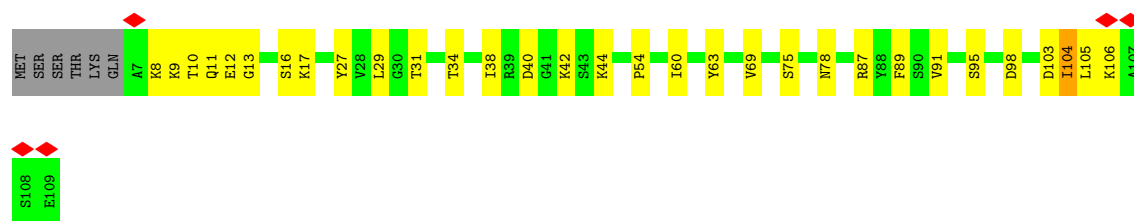


- Molecule 30: 60S ribosomal protein L29

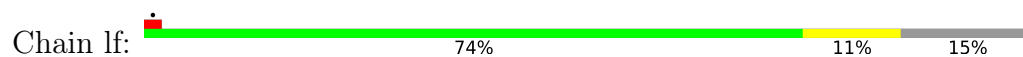


- Molecule 31: 60S ribosomal protein L30, putative

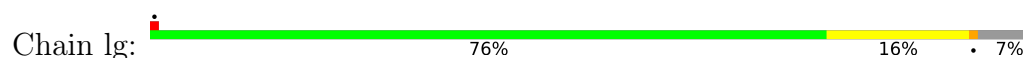




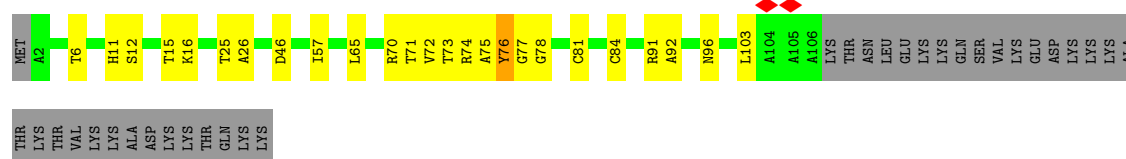
- Molecule 32: 60S ribosomal protein L31, putative



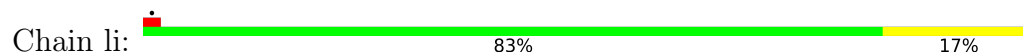
- Molecule 33: 60S ribosomal protein L32, putative



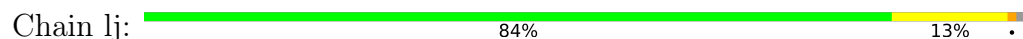
- Molecule 34: 60S ribosomal protein L34, putative



- Molecule 35: uL29



- Molecule 36: 60S ribosomal protein L35a, putative



- Molecule 37: 60S ribosomal protein L36, putative

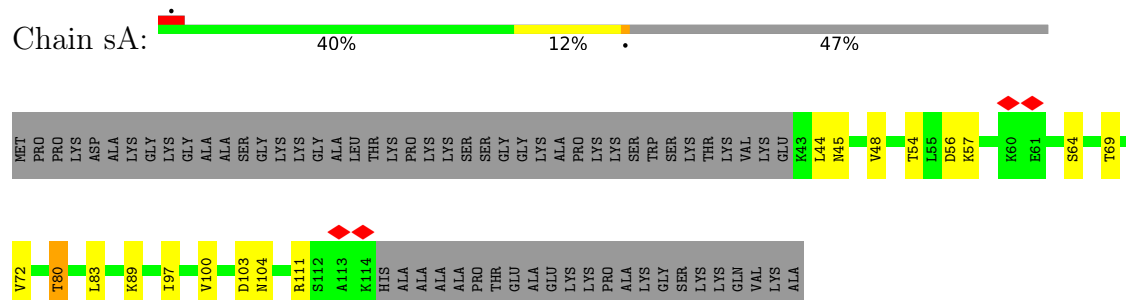




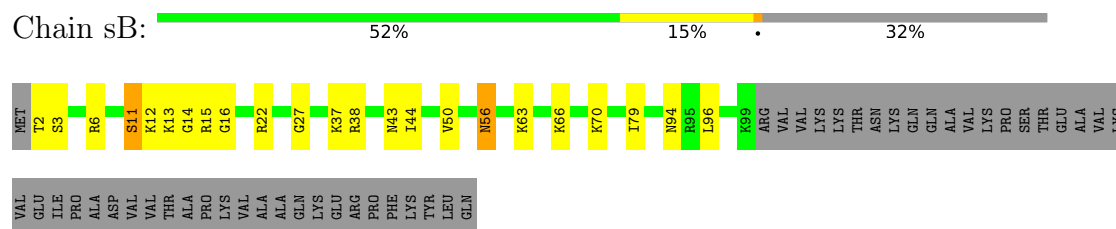
Chain ls:  100%

There are no outlier residues recorded for this chain.

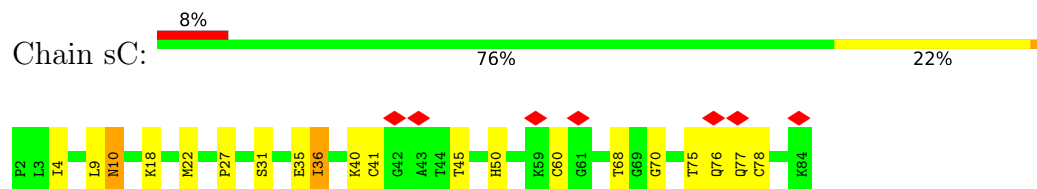
- Molecule 45: 40S ribosomal protein S25



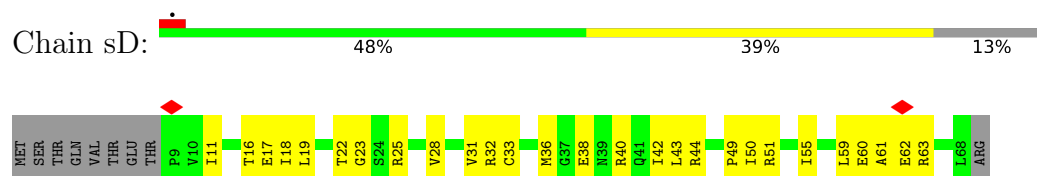
- Molecule 46: 40S ribosomal protein S26



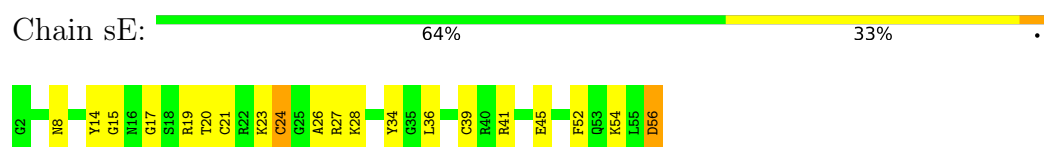
- Molecule 47: Small ribosomal subunit protein eS27



- Molecule 48: 40S ribosomal protein S28, putative



- Molecule 49: Ribosomal protein S29, putative



- Molecule 50: Guanine nucleotide-binding protein subunit beta 2-like 1, putative



- Molecule 51: P-tRNA

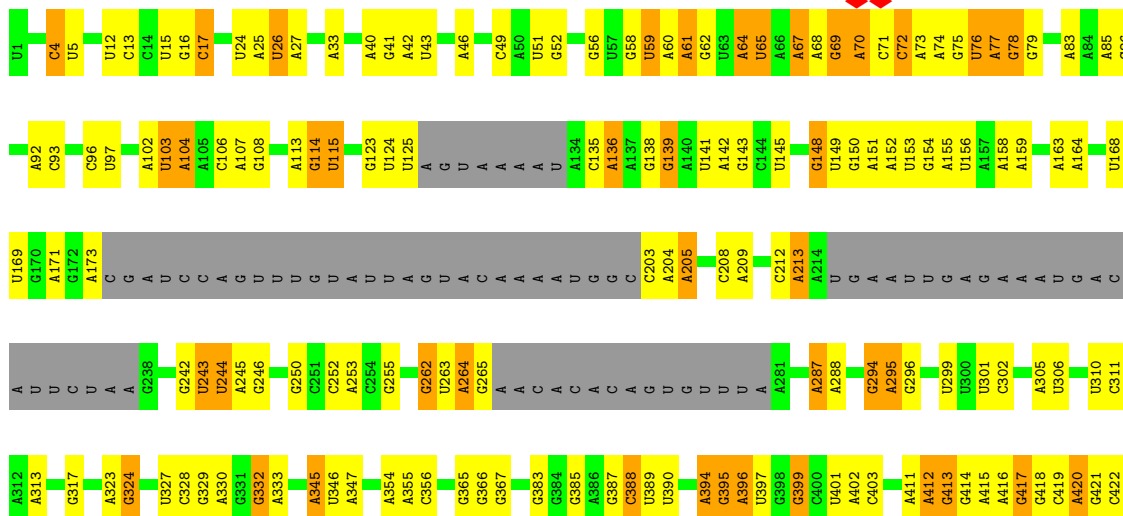


- Molecule 52: mRNA

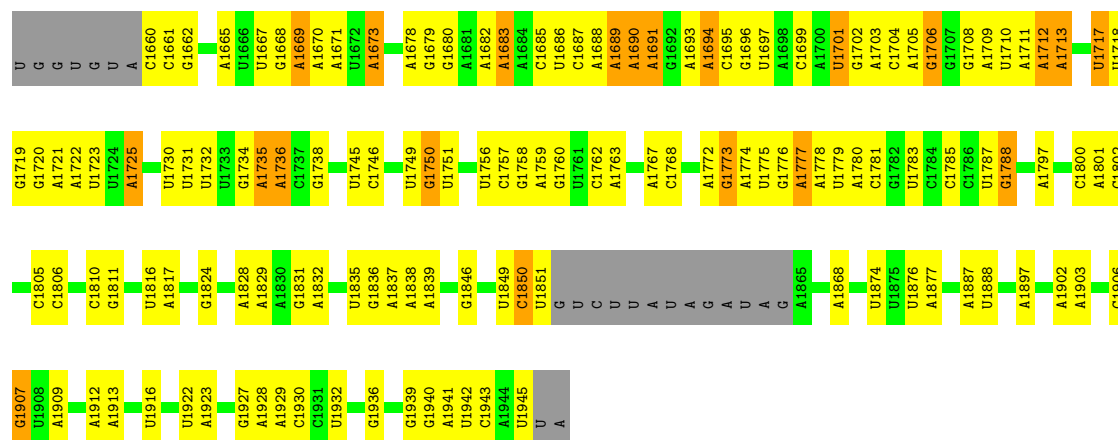


There are no outlier residues recorded for this chain.

- Molecule 53: 17S rRNA

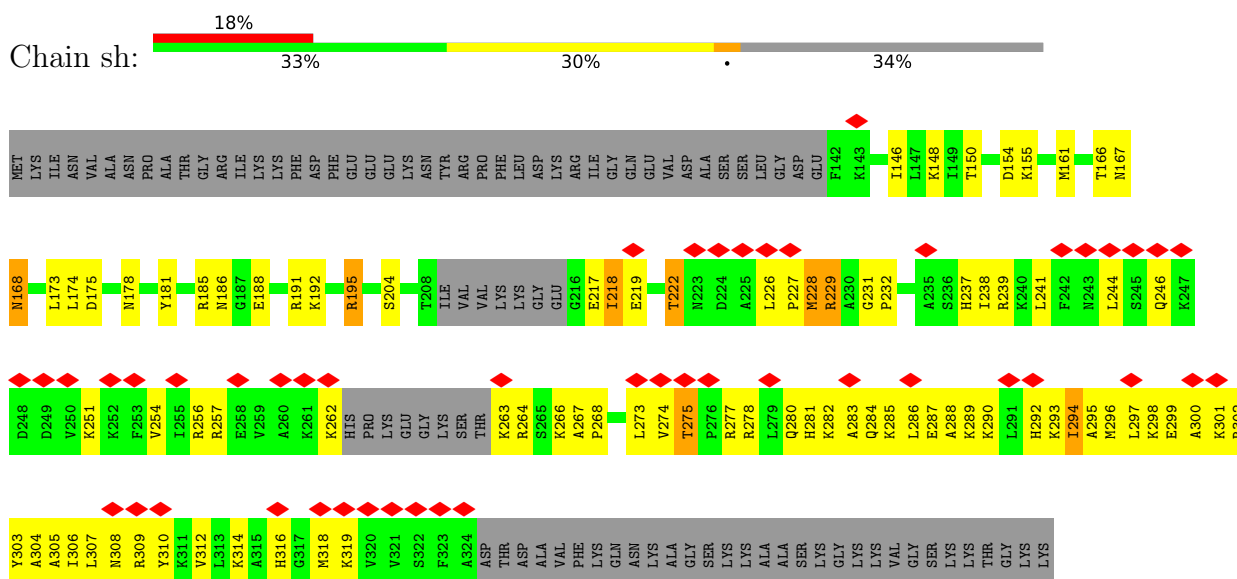


G1593	A1508	C1382	U1284	U1207	U1095	U919	G	A765	A	A	A	C560	U
A1594	G1509	C1383	A1285	U1207	U1096	A919	A	A766	A	A	A	A561	G
U1595	A1510	U1286	A1286	U1207	C1097	A921	G	A767	A	A	A	G562	A
U1596	A1511	U1287	U1287	U1210	A1095	A921	A	A768	A	A	A	C563	A
A1597	A1512	G1288	G1288	U1210	A1106	G923	A	C769	U	U	U	A564	G
U	A1513	U1386	U1386	A1219	A1107	A924	A	A770	C	C	C	G565	G
U	A1514	A1387	U1297	C1220	G1108	U925	A	A771	A	A	A	C566	A
U	G1515	A1388	G1298	A1221	A1111	U926	G	A772	A	A	A	G567	A
U	G1516	A1389	C1299	C1222	A1112	U927	G	U773	A	A	A	U568	U
A	U1519	A1390	A1300	G1223	A1115	U927	A	U774	A	A	A	C569	U
U	G1519	C1391	A1300	G1224	C1115	C930	A	U775	A	A	A	G570	G
C	C1520	A1392	U1308	G1225	U1116	U931	A	U776	A	A	A	U571	U
C	C1520	G1393	G1309	A1226	U1116	C932	A	U777	A	A	A	G572	G
A	A1521	A1394	U1310	A1227	U1117	A933	A	A778	A	A	A	U573	U
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A	A1534	U	U1315	U1232	U1124	U936	A	U782	A	A	A	A579	G
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A	G1536	G1317	G1317	A1239	G1126	U940	A	U784	A	A	A	C581	U
C	U1537	U	U	C1240	U1133	A946	A	U785	A	A	A	G583	A
C	G1540	G1322	U1323	C1241	G1134	U947	A	U786	A	A	A	A585	A
U	U1541	U1324	G1324	A1243	G1135	U948	A	U787	A	A	A	A586	U
U	G1542	A1325	U1325	C1244	U1140	C949	A	A788	A	A	A	U587	U
U	A1543	U1326	U1326	C1245	G1140	A950	A	A789	A	A	A	C588	C
U	U1544	C	U	A1246	U1158	U956	A	U794	A	A	A	U589	U
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U	G1568	U	U	C1260	G1175	C997	A	G	A	A	A	U612	U
A	G1569	U	U	A1261	G1176	C997	A	G	A	A	A	A613	G
A	U1573	C	U	G1262	A1177	U998	A	G	A	A	A	A614	A
U	C1574	U	U	A1263	C1184	U998	A	A746	A	A	A	A615	G
A	A1578	U	U	A1266	A1185	U1002	A	A747	A	A	A	G546	A
U	A1579	U	U	G1267	C1186	A1003	A	A748	A	A	A	G547	G
U	U1580	A	U	A1269	C1187	U1006	A	A749	A	A	A	C617	U
A	G1581	U	U	U1270	A1188	A1007	A	U750	A	A	A	A549	A
G	G1582	U	U	U1271	G1192	C1008	A	A751	A	A	A	C619	A
G	U1585	U	U	U1274	G1195	U1011	A	A752	A	A	A	U620	A
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U	A1587	G	U	U1276	G1197	U1013	A	U757	A	A	A	U623	G
C	G1588	U	U	C1277	U1202	A1020	A	U758	A	A	A	G628	A
U	U1589	A	U	U1281	G1203	A1033	A	A760	A	A	A	A633	U
A	A1590	U	U	A1282	U1281	U1283	A	A761	A	A	A	U	U
A	G1591	U	U	U1283	U1283	U1283	A	A762	A	A	A	G557	U
G	A1592	U	U	U1283	U1283	U1283	A	A762	A	A	A	C559	U
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U	U1594	U	U	U1283	U1283	U1283	A	A762	A	A	A	U	U
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U	U1600	U	U	U1283	U1283	U1283	A	A762	A	A	A	U	U
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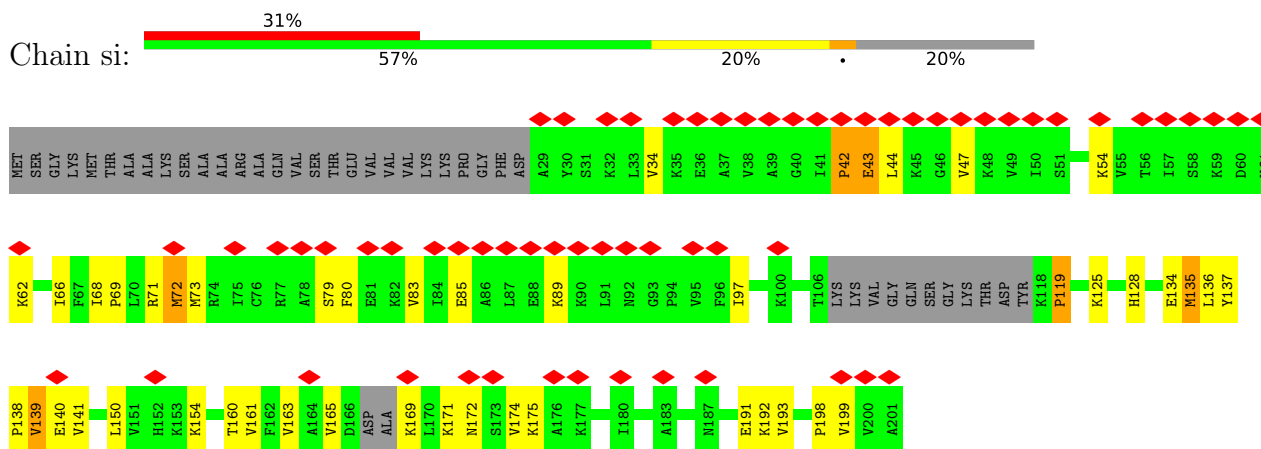




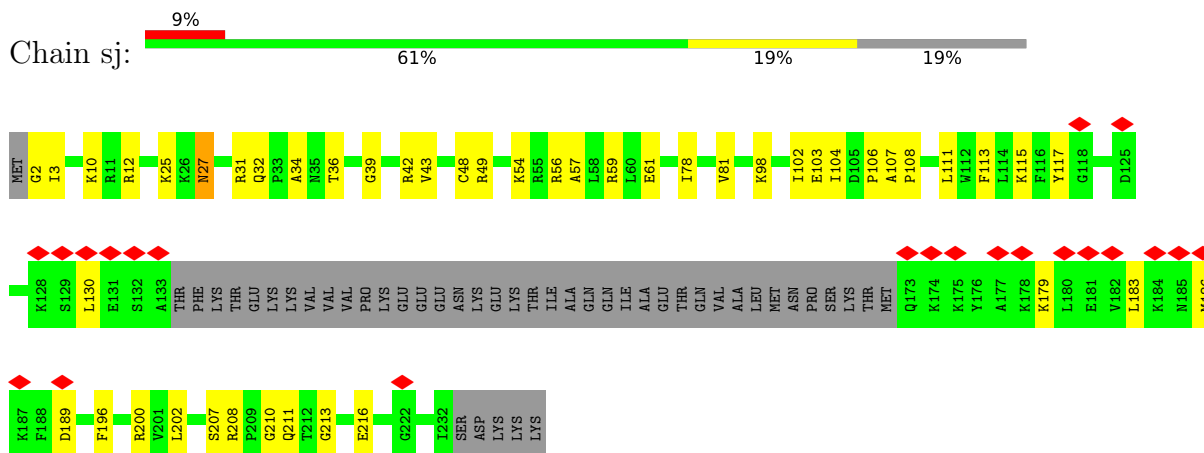




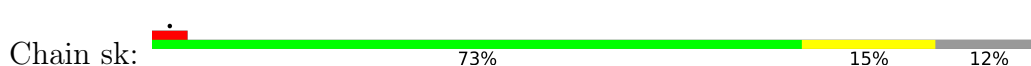
- Molecule 61: 40S ribosomal protein S7

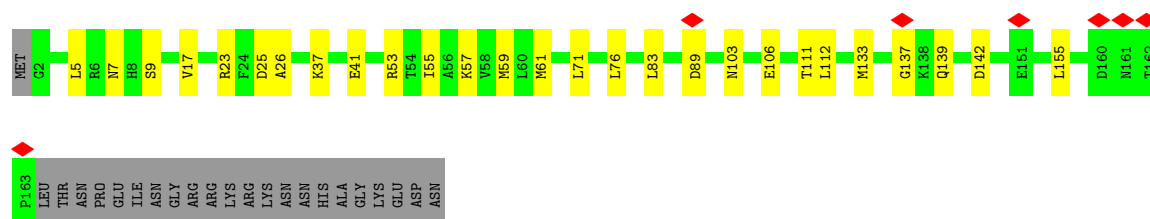


- Molecule 62: 40S ribosomal protein S8

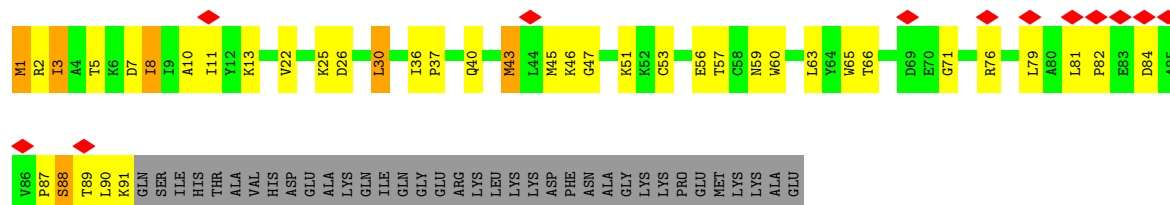
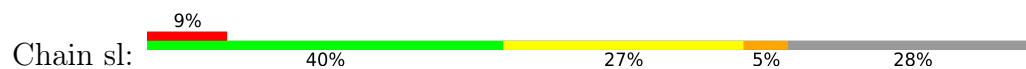


- Molecule 63: Small ribosomal subunit protein uS4

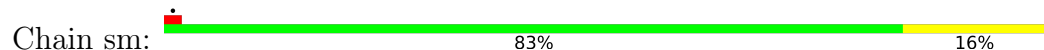




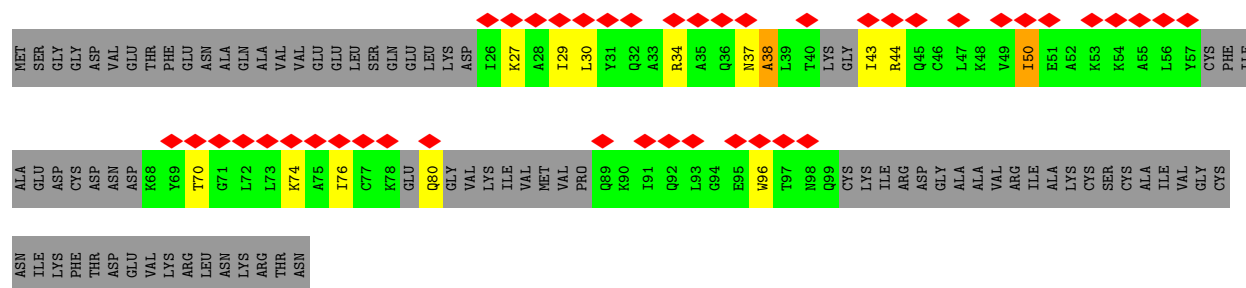
- Molecule 64: 40S ribosomal protein S10, putative



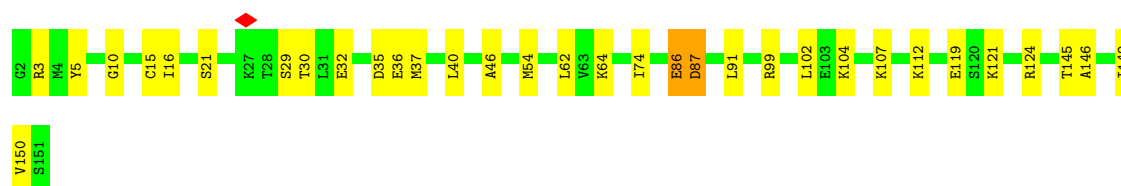
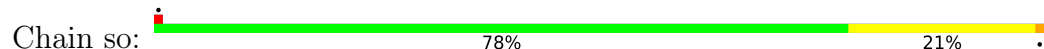
- Molecule 65: 40S ribosomal protein S11, putative



- Molecule 66: 40S ribosomal protein S12, putative

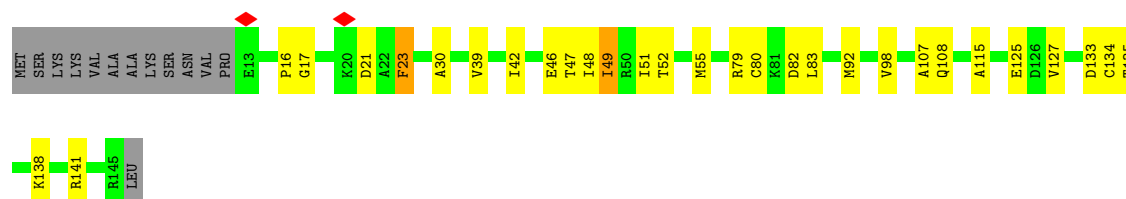


- Molecule 67: 40S ribosomal protein S13, putative



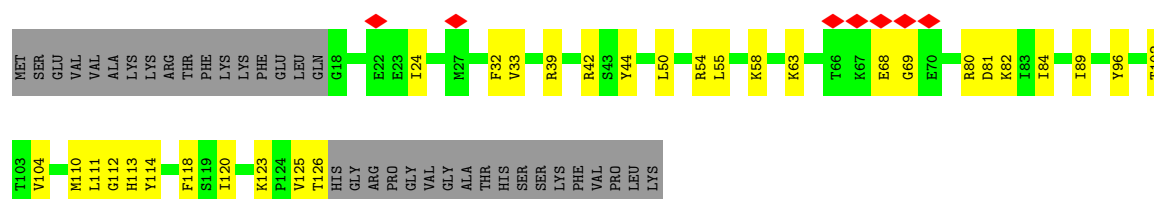
- Molecule 68: Ribosomal protein S14, putative

Chain sp: 




- Molecule 69: 40S ribosomal protein S15, putative

Chain sq: 



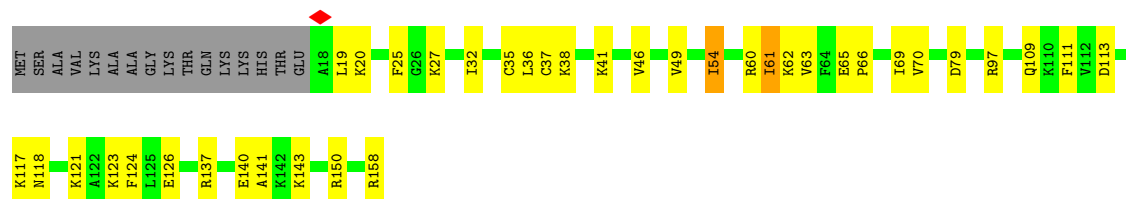
- Molecule 70: 40S ribosomal protein S15a, putative

Chain sr: 



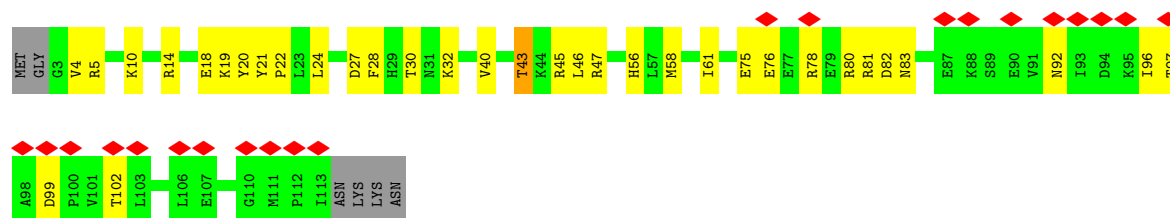
- Molecule 71: 40S ribosomal protein S16, putative

Chain ss: 

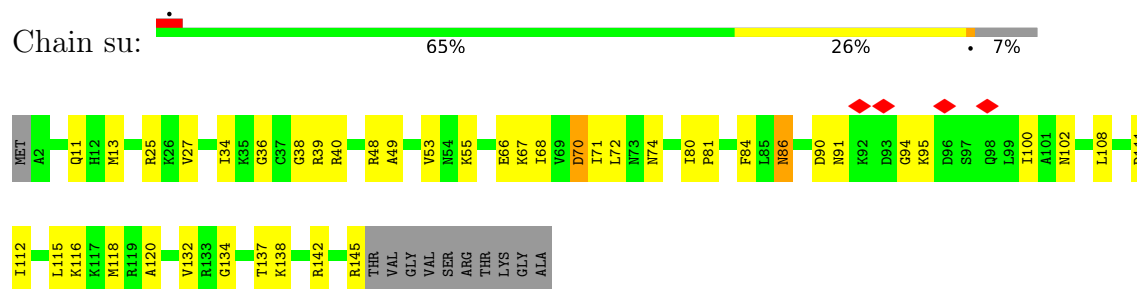


- Molecule 72: 40S ribosomal protein S17, putative

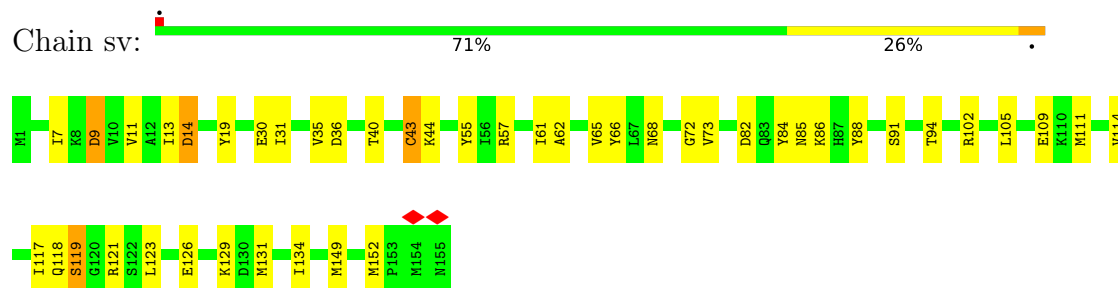
Chain st: 



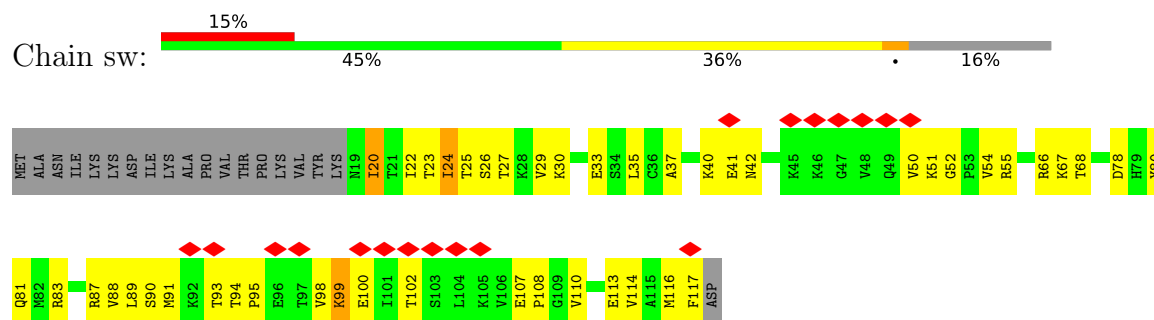
- Molecule 73: Small ribosomal subunit protein uS13



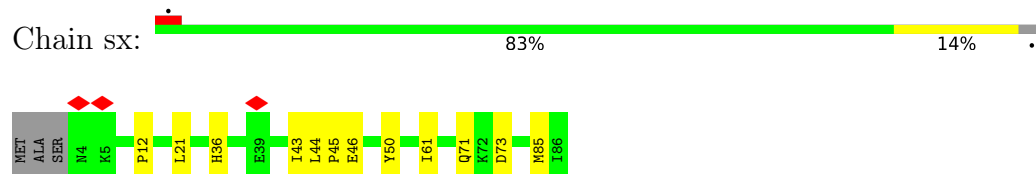
- Molecule 74: Small ribosomal subunit protein eS19



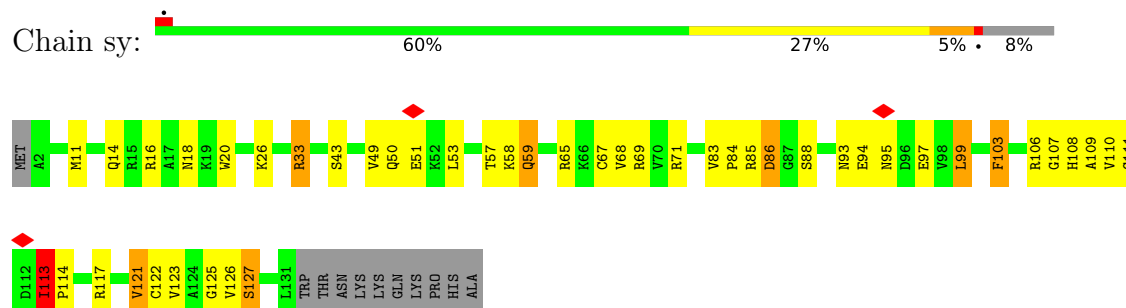
- Molecule 75: Small ribosomal subunit protein uS10



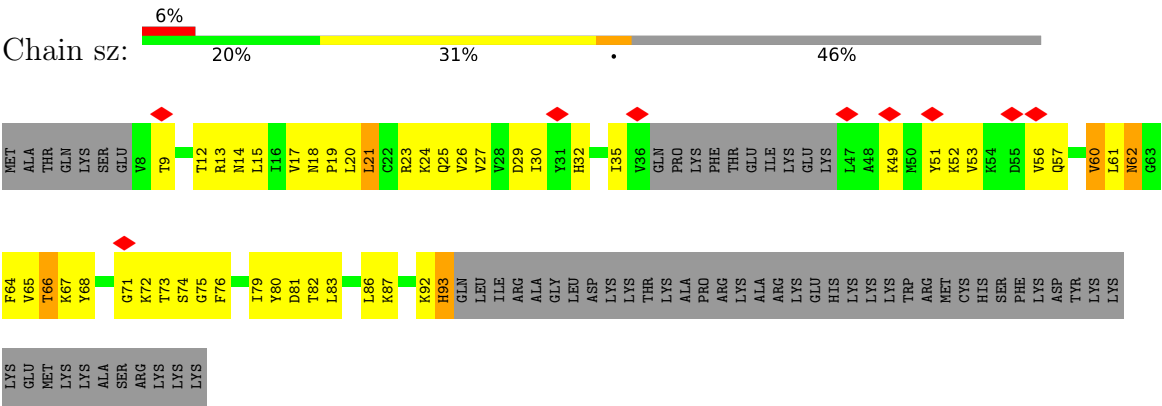
- Molecule 76: 40S ribosomal protein S21



- Molecule 77: 40S ribosomal protein S23, putative



● Molecule 78: 40S ribosomal protein S24, putative



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	53764	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	1.106	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	17.312	Depositor
Minimum map value	-5.684	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.5	Depositor
Map size (Å)	428.00003, 428.00003, 428.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	Depositor

## 5 Model quality

### 5.1 Standard geometry

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	1A	0.20	1/76160 (0.0%)	0.31	1/118640 (0.0%)
2	1B	0.18	0/3470	0.29	0/5401
3	1C	0.21	0/2765	0.38	2/4303 (0.0%)
4	1D	0.18	0/1920	0.29	0/2582
5	1E	0.16	0/3149	0.28	0/4228
6	1F	0.18	0/3306	0.36	1/4437 (0.0%)
7	1G	0.15	0/2284	0.31	0/3059
8	1H	0.14	0/1640	0.30	0/2204
9	1I	0.15	0/1680	0.24	0/2252
10	1J	0.12	0/1727	0.29	0/2320
11	1K	0.14	0/1562	0.24	0/2103
12	1L	0.14	0/1644	0.25	0/2198
13	1M	0.14	0/1369	0.30	0/1834
14	1N	0.15	0/2149	0.29	0/2864
15	1O	0.16	0/1646	0.24	0/2209
16	1P	0.15	0/1032	0.23	0/1388
17	1Q	0.18	0/1707	0.25	0/2276
18	1R	0.16	0/1230	0.23	0/1647
19	1S	0.16	0/1342	0.25	0/1796
20	1T	0.16	0/1445	0.24	0/1946
21	1U	0.16	0/1253	0.22	0/1666
22	1V	0.16	0/1351	0.26	0/1819
23	1W	0.17	0/774	0.38	0/1031
24	1X	0.18	0/1030	0.29	0/1384
25	1Y	0.13	0/941	0.22	0/1262
26	1Z	0.17	0/492	0.25	0/656
27	1a	0.13	0/1673	0.24	0/2236
28	1b	0.14	0/1112	0.25	0/1489
29	1c	0.18	0/1223	0.24	0/1636
30	1d	0.16	0/485	0.24	0/639
31	1e	0.17	0/776	0.38	0/1044
32	1f	0.15	0/1058	0.24	0/1413
33	1g	0.16	0/1036	0.23	0/1381
34	1h	0.16	0/833	0.32	0/1115



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	li	0.12	0/984	0.21	0/1310
36	lj	0.19	0/862	0.29	0/1163
37	lk	0.12	0/721	0.19	0/955
38	ll	0.20	0/602	0.32	0/797
39	lm	0.20	0/696	0.34	0/928
40	ln	0.14	0/592	0.27	0/789
41	lo	0.18	0/444	0.22	0/587
42	lp	0.17	0/425	0.44	2/563 (0.4%)
43	lq	0.16	0/770	0.23	0/1019
44	ls	0.09	0/10	0.27	0/11
45	sA	0.15	0/575	0.39	0/775
46	sB	0.17	0/797	0.30	0/1062
47	sC	0.13	0/654	0.29	0/879
48	sD	0.15	0/470	0.44	0/630
49	sE	0.17	0/449	0.40	0/595
50	sG	0.11	0/2395	0.29	0/3248
51	sH	0.24	0/1755	0.48	3/2727 (0.1%)
52	sK	0.13	0/140	0.17	0/215
53	sa	0.18	0/34809	0.31	7/54226 (0.0%)
54	sb	0.13	0/1659	0.25	0/2243
55	sc	0.15	0/1673	0.29	0/2257
56	sd	0.12	0/1729	0.30	0/2316
57	se	0.15	0/1741	0.28	0/2328
58	sf	0.14	0/2072	0.29	0/2792
59	sg	0.12	0/1495	0.27	0/2009
60	sh	0.19	0/1411	0.50	0/1875
61	si	0.13	0/1265	0.36	0/1698
62	sj	0.16	0/1560	0.28	0/2083
63	sk	0.13	0/1344	0.26	0/1800
64	sl	0.12	0/745	0.32	0/1007
65	sm	0.15	0/1291	0.27	0/1725
66	sn	0.09	0/428	0.39	0/566
67	so	0.14	0/1204	0.26	0/1613
68	sp	0.14	0/1013	0.30	0/1361
69	sq	0.12	0/888	0.35	0/1186
70	sr	0.16	0/1040	0.30	0/1404
71	ss	0.14	0/1121	0.30	0/1503
72	st	0.12	0/919	0.28	0/1234
73	su	0.14	0/1181	0.32	0/1584
74	sv	0.12	0/1271	0.25	0/1708
75	sw	0.13	0/784	0.37	0/1055
76	sx	0.14	0/663	0.26	0/898
77	sy	0.24	0/1027	0.75	1/1376 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
78	sz	0.25	0/608	0.76	0/820
All	All	0.18	1/205546 (0.0%)	0.31	17/301378 (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
5	lE	0	1
8	lH	0	1
34	lh	0	1
38	ll	0	1
49	sE	0	1
70	sr	0	1
77	sy	0	1
All	All	0	7

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	lA	3473	U	O3'-P	-5.31	1.53	1.61

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	lC	62	U	OP1-P-O3'	-8.78	81.66	108.00
3	lC	62	U	OP2-P-O3'	-8.72	81.83	108.00
53	sa	1396	A	C1'-C2'-O2'	-8.07	96.30	108.40
1	lA	3477	U	C2'-C3'-O3'	-7.42	98.36	109.50
53	sa	1425	A	C4'-C3'-O3'	-6.86	102.71	113.00
53	sa	1394	A	C4'-C3'-O3'	-6.75	102.88	113.00
53	sa	1395	A	C2'-C3'-O3'	-6.49	103.97	113.70
53	sa	1425	A	C2'-C3'-O3'	6.35	123.22	113.70
51	sH	19	G	O4'-C4'-C3'	-6.24	99.86	106.10
77	sy	16	ARG	N-CA-C	-6.23	106.90	114.75
6	lF	354	TYR	N-CA-C	-5.93	107.28	114.75
42	lp	35	CYS	CA-CB-SG	5.38	126.78	114.40
53	sa	1427	U	C4'-C3'-O3'	5.31	117.37	109.40
53	sa	1393	G	O4'-C4'-C3'	-5.29	98.70	104.00
42	lp	24	CYS	CA-CB-SG	5.22	126.41	114.40
51	sH	16	U	O4'-C1'-C2'	-5.13	102.47	107.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	sH	16	U	C1'-C2'-O2'	-5.10	100.75	108.40

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	lE	258	HIS	Peptide
8	lH	93	GLY	Peptide
34	lh	76	TYR	Peptide
38	ll	39	TYR	Peptide
49	sE	15	GLY	Peptide
70	sr	76	SER	Peptide
77	sy	59	GLN	Peptide

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	lA	67965	0	34095	930	0
2	lB	3097	0	1552	47	0
3	lC	2477	0	1252	86	0
4	lD	1881	0	1928	32	0
5	lE	3085	0	3215	51	0
6	lF	3248	0	3472	65	0
7	lG	2245	0	2325	32	0
8	lH	1608	0	1728	32	0
9	lI	1658	0	1802	17	0
10	lJ	1697	0	1820	25	0
11	lK	1538	0	1598	21	0
12	lL	1608	0	1667	25	0
13	lM	1350	0	1390	22	0
14	lN	2121	0	2325	52	0
15	lO	1616	0	1700	20	0
16	lP	1020	0	1107	20	0
17	lQ	1676	0	1777	24	0
18	lR	1211	0	1280	17	0
19	lS	1321	0	1427	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	lT	1413	0	1479	22	0
21	lU	1235	0	1369	17	0
22	lV	1320	0	1406	12	0
23	lW	763	0	818	28	0
24	lX	1015	0	1054	17	0
25	lY	926	0	997	13	0
26	lZ	481	0	518	4	0
27	la	1651	0	1822	29	0
28	lb	1094	0	1174	20	0
29	lc	1192	0	1205	18	0
30	ld	478	0	507	10	0
31	le	768	0	810	21	0
32	lf	1039	0	1121	11	0
33	lg	1019	0	1104	17	0
34	lh	820	0	864	15	0
35	li	974	0	1093	13	0
36	lj	841	0	878	11	0
37	lk	712	0	755	12	0
38	ll	591	0	617	10	0
39	lm	688	0	728	14	0
40	ln	584	0	643	16	0
41	lo	432	0	444	8	0
42	lp	420	0	450	10	0
43	lq	756	0	821	12	0
44	ls	76	0	34	0	0
45	sA	568	0	627	14	0
46	sB	787	0	831	19	0
47	sC	641	0	681	14	0
48	sD	468	0	500	20	0
49	sE	442	0	443	19	0
50	sG	2347	0	2325	73	0
51	sH	1573	0	797	31	0
52	sK	126	0	64	0	0
53	sa	31080	0	15618	475	0
54	sb	1626	0	1627	23	0
55	sc	1642	0	1721	38	0
56	sd	1708	0	1809	43	0
57	se	1717	0	1822	26	0
58	sf	2031	0	2145	51	0
59	sg	1473	0	1533	38	0
60	sh	1395	0	1518	82	0
61	si	1246	0	1370	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	sj	1536	0	1588	37	0
63	sk	1323	0	1420	17	0
64	sl	729	0	760	28	0
65	sm	1263	0	1279	16	0
66	sn	428	0	466	7	0
67	so	1184	0	1272	22	0
68	sp	999	0	1024	22	0
69	sq	873	0	942	18	0
70	sr	1022	0	1051	17	0
71	ss	1104	0	1185	29	0
72	st	907	0	962	24	0
73	su	1163	0	1202	30	0
74	sv	1245	0	1285	36	0
75	sw	774	0	835	31	0
76	sx	651	0	668	8	0
77	sy	1010	0	1067	35	0
78	sz	598	0	650	39	0
All	All	191389	0	143258	2840	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (2840) 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)
1:1A:3454:G:N1	1:1A:3501:A:C2	2.19	1.11
1:1A:3454:G:N1	1:1A:3501:A:H2	1.49	1.08
3:1C:27:G:H1	3:1C:50:A:N6	1.60	0.98
53:sa:1441:C:HO2'	53:sa:1442:A:H8	0.97	0.97
1:1A:631:G:H1	1:1A:659:U:H3	0.96	0.95
3:1C:84:G:H1	3:1C:91:G:H22	1.12	0.92
3:1C:27:G:H1	3:1C:50:A:H61	0.93	0.92
3:1C:79:G:H1	3:1C:95:A:H2	1.15	0.92
1:1A:3431:U:H3	1:1A:3441:G:H1	1.18	0.91
3:1C:79:G:N1	3:1C:95:A:C2	2.37	0.91
1:1A:1605:A:H2	1:1A:3430:U:H3	1.22	0.88
3:1C:26:U:H3	3:1C:51:G:H22	1.22	0.88
51:sH:15:G:H2'	51:sH:16:U:O4'	1.75	0.87
69:sq:68:GLU:HG2	69:sq:69:GLY:H	1.39	0.87
77:sy:113:ILE:HB	77:sy:114:PRO:HD3	1.53	0.87
19:lS:73:HIS:HB3	19:lS:76:GLU:HG3	1.55	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:sa:1378:U:H3	53:sa:1394:A:H61	1.23	0.86
53:sa:1383:C:H5	53:sa:1389:G:H1	1.24	0.85
1:lA:869:G:H21	1:lA:872:A:N6	1.75	0.85
53:sa:103:U:OP2	53:sa:305:A:N6	2.11	0.84
3:lC:27:G:N2	3:lC:50:A:N1	2.26	0.83
53:sa:1394:A:C8	53:sa:1394:A:H5''	2.14	0.83
35:li:-7:LEU:HD22	35:li:42:ASP:HB3	1.59	0.83
3:lC:52:G:N2	3:lC:54:U:O4	2.11	0.83
1:lA:869:G:N2	1:lA:872:A:N6	2.26	0.82
1:lA:3457:G:H1	1:lA:3495:U:H3	1.27	0.82
1:lA:631:G:N2	1:lA:659:U:O2	2.13	0.82
1:lA:3475:U:H3	1:lA:3479:A:H62	1.24	0.82
78:sz:24:LYS:HB2	78:sz:79:ILE:HB	1.61	0.82
1:lA:869:G:N2	1:lA:872:A:C5	2.47	0.81
51:sH:21:A:N6	51:sH:46:G:H2'	1.95	0.81
1:lA:737:A:H3'	1:lA:738:G:H21	1.46	0.81
1:lA:869:G:N2	1:lA:872:A:C6	2.49	0.81
1:lA:493:G:H21	1:lA:580:A:H61	1.29	0.80
3:lC:69:U:H3	3:lC:104:G:H1	1.28	0.80
53:sa:770:A:H3'	53:sa:772:U:H5''	1.64	0.80
3:lC:59:G:H5'	7:lG:265:LYS:HG2	1.64	0.79
53:sa:956:G:H1	53:sa:1003:A:HO2'	1.31	0.79
1:lA:2269:U:H5'	1:lA:2270:G:H5'	1.65	0.79
1:lA:682:G:H5'	20:IT:2:LYS:HD3	1.65	0.78
51:sH:26:A:H61	51:sH:44:G:H1	1.28	0.78
1:lA:3329:U:H4'	1:lA:3411:U:H4'	1.66	0.78
51:sH:16:U:N3	51:sH:59:U:O2	2.16	0.78
1:lA:1818:C:OP2	34:lh:74:ARG:NH2	2.16	0.78
53:sa:1253:G:OP2	66:sn:43:ILE:N	2.16	0.78
6:lF:101:MET:HE3	6:lF:104:PRO:HA	1.66	0.77
8:lH:98:ASN:ND2	8:lH:187:MET:O	2.16	0.77
1:lA:668:A:H2'	1:lA:669:A:H8	1.48	0.77
3:lC:75:G:H1	3:lC:99:U:H5	1.28	0.77
53:sa:1661:C:H2'	53:sa:1662:G:H8	1.48	0.77
1:lA:3454:G:O6	1:lA:3501:A:N1	2.18	0.77
1:lA:3452:U:H3	1:lA:3503:G:H22	1.28	0.76
53:sa:1378:U:H3	53:sa:1394:A:N6	1.83	0.76
55:sc:80:GLU:HB2	55:sc:131:MET:HE1	1.66	0.76
46:sB:2:THR:HG21	53:sa:612:U:H1'	1.66	0.76
40:ln:8:PHE:HE2	40:ln:52:LYS:HB3	1.51	0.76
58:sf:181:MET:N	58:sf:181:MET:SD	2.58	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:sa:114:G:H5'	65:sm:129:ARG:HD2	1.66	0.75
62:sj:130:LEU:HD21	62:sj:183:LEU:HD12	1.67	0.75
60:sh:308:ASN:HA	60:sh:312:VAL:HG12	1.67	0.75
54:sb:75:ASN:OD1	54:sb:193:GLN:NE2	2.20	0.75
1:lA:1093:G:OP1	19:lS:19:ARG:NH2	2.20	0.75
1:lA:1118:A:H2	1:lA:1165:A:H62	1.34	0.75
53:sa:104:A:N6	53:sa:305:A:C2	2.53	0.75
74:sv:117:ILE:HG22	74:sv:119:SER:H	1.52	0.75
3:lC:79:G:N1	3:lC:95:A:H2	1.79	0.74
57:se:31:TRP:NE1	68:sp:17:GLY:O	2.20	0.74
1:lA:1648:U:OP2	1:lA:2081:A:O2'	2.05	0.74
1:lA:344:A:N1	1:lA:2877:U:O2'	2.21	0.74
22:IV:80:VAL:HG12	22:IV:81:ASN:H	1.53	0.73
58:sf:58:GLU:OE1	78:sz:23:ARG:NH1	2.18	0.73
1:lA:98:A:H4'	14:lN:59:MET:HE2	1.69	0.73
1:lA:1661:G:O2'	1:lA:1751:A:N6	2.21	0.73
77:sy:106:ARG:HD3	77:sy:107:GLY:H	1.52	0.73
1:lA:774:U:OP1	29:lc:21:ARG:NH2	2.22	0.73
66:sn:30:LEU:HD23	66:sn:96:TRP:HB3	1.71	0.73
1:lA:1086:G:H1	1:lA:1240:C:H5	1.37	0.73
53:sa:866:G:N2	68:sp:133:ASP:OD1	2.22	0.73
47:sC:50:HIS:ND1	47:sC:70:GLY:O	2.22	0.73
46:sB:15:ARG:NH2	53:sa:916:G:N7	2.33	0.72
1:lA:920:A:OP1	29:lc:27:LYS:NZ	2.20	0.72
1:lA:1186:G:H21	1:lA:1220:A:H61	1.37	0.72
1:lA:3146:U:H4'	1:lA:3147:U:H5''	1.71	0.72
58:sf:71:ASP:OD2	58:sf:143:ARG:NH2	2.23	0.72
1:lA:3038:C:O2'	42:lp:25:TYR:O	2.07	0.72
56:sd:54:ARG:HB3	75:sw:108:PRO:HG3	1.70	0.72
1:lA:896:A:O2'	1:lA:2790:U:OP1	2.08	0.72
53:sa:389:U:H3	53:sa:396:A:H62	1.37	0.72
53:sa:1364:C:O2'	53:sa:1366:A:N7	2.23	0.71
1:lA:409:G:OP2	38:ll:56:ARG:NH2	2.23	0.71
53:sa:972:A:O2'	53:sa:1932:U:O2	2.07	0.71
1:lA:2721:G:H1	1:lA:2941:C:H5	1.37	0.71
34:lh:92:ALA:O	34:lh:96:ASN:ND2	2.23	0.71
53:sa:866:G:H2'	53:sa:867:A:C8	2.25	0.71
59:sg:55:ALA:O	71:ss:137:ARG:NH2	2.23	0.71
72:st:43:THR:HG22	72:st:46:LEU:H	1.55	0.71
3:lC:6:G:H1	3:lC:111:A:H2	1.38	0.71
18:lR:18:ARG:NH1	18:lR:20:ASP:OD1	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:sE:14:TYR:HB3	53:sa:1763:A:C8	2.25	0.71
69:sq:68:GLU:HG2	69:sq:69:GLY:N	2.05	0.71
75:sw:50:VAL:HG12	75:sw:91:MET:HE1	1.73	0.71
14:lN:264:ARG:NH1	29:lc:132:GLU:OE2	2.24	0.71
53:sa:1581:G:H2'	53:sa:1582:G:C8	2.26	0.71
59:sg:20:LEU:O	59:sg:22:ASN:N	2.23	0.70
12:lL:177:THR:OG1	12:lL:179:GLU:OE1	2.09	0.70
49:sE:52:PHE:HB3	75:sw:80:TYR:HB3	1.71	0.70
53:sa:1750:G:N2	53:sa:1776:G:O2'	2.25	0.70
62:sj:42:ARG:HE	62:sj:59:ARG:HH21	1.40	0.70
36:lj:5:ARG:NH1	36:lj:7:HIS:O	2.25	0.70
67:so:99:ARG:NH2	67:so:119:GLU:OE2	2.23	0.70
73:su:36:GLY:HA3	73:su:100:ILE:HA	1.72	0.70
1:lA:886:A:H4'	30:ld:27:SER:HB2	1.73	0.70
53:sa:1581:G:H2'	53:sa:1582:G:H8	1.57	0.70
1:lA:213:A:H5''	14:lN:133:LYS:H	1.57	0.70
49:sE:17:GLY:HA2	49:sE:27:ARG:HE	1.55	0.70
53:sa:1569:G:N7	73:su:142:ARG:NH2	2.39	0.70
5:lE:70:ASP:O	5:lE:358:LYS:NZ	2.25	0.69
1:lA:538:A:OP2	14:lN:167:LYS:NZ	2.24	0.69
1:lA:2062:A:O2'	1:lA:3220:U:OP1	2.09	0.69
3:lC:22:C:H2'	3:lC:23:A:H8	1.57	0.69
58:sf:98:ARG:HB2	58:sf:112:LEU:HD11	1.75	0.69
1:lA:3367:U:H2'	1:lA:3368:G:C8	2.27	0.69
1:lA:3454:G:H1	1:lA:3501:A:H2	0.74	0.69
53:sa:394:A:OP1	62:sj:49:ARG:NH2	2.26	0.69
1:lA:2178:A:HO2'	1:lA:2179:U:H6	1.41	0.69
1:lA:3150:A:H2'	1:lA:3151:A:H8	1.58	0.69
1:lA:341:G:OP2	17:lQ:15:GLN:NE2	2.26	0.69
1:lA:2282:G:O2'	53:sa:893:U:O2	2.10	0.69
50:sG:227:LEU:HA	50:sG:234:TYR:HA	1.74	0.69
23:lW:70:VAL:HG22	23:lW:72:ASP:H	1.57	0.69
53:sa:1712:A:H2'	53:sa:1713:A:C8	2.27	0.69
60:sh:282:LYS:HA	60:sh:286:LEU:HB2	1.75	0.69
1:lA:1502:A:N6	19:lS:15:SER:OG	2.27	0.68
55:sc:152:GLU:O	55:sc:176:ARG:NH2	2.26	0.68
1:lA:908:A:H2'	1:lA:909:A:C8	2.29	0.68
40:ln:30:GLU:N	40:ln:30:GLU:OE2	2.26	0.68
50:sG:256:GLU:OE1	50:sG:257:GLN:N	2.24	0.68
1:lA:721:A:H2'	1:lA:722:A:H8	1.58	0.68
8:lH:56:ARG:NH2	8:lH:107:GLN:O	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:sf:163:GLU:HG2	58:sf:164:THR:HG23	1.76	0.68
53:sa:395:G:H5''	62:sj:25:LYS:HA	1.76	0.68
53:sa:1281:A:H4'	53:sa:1282:U:H5'	1.76	0.68
53:sa:797:G:OP2	53:sa:797:G:N2	2.24	0.68
53:sa:1437:G:OP1	72:st:32:LYS:NZ	2.26	0.68
53:sa:1776:G:OP1	59:sg:53:HIS:NE2	2.25	0.68
55:sc:169:VAL:HG22	55:sc:202:THR:HG22	1.75	0.68
71:ss:62:LYS:HG3	71:ss:97:ARG:HD2	1.76	0.68
53:sa:865:A:H2'	53:sa:866:G:C8	2.28	0.68
1:lA:626:A:OP1	1:lA:664:A:N6	2.27	0.68
1:lA:639:G:H1	1:lA:650:A:H2	1.41	0.68
1:lA:3458:U:H3	1:lA:3494:G:H1	1.42	0.68
53:sa:104:A:H62	53:sa:305:A:H2	1.38	0.68
53:sa:783:A:N7	53:sa:784:U:O2'	2.25	0.68
61:si:42:PRO:O	61:si:44:LEU:N	2.27	0.68
61:si:169:LYS:HD2	61:si:171:LYS:HB2	1.76	0.68
1:lA:2213:U:OP2	1:lA:2218:A:N6	2.25	0.67
1:lA:3091:C:OP1	5:lE:246:ARG:NH1	2.27	0.67
7:lG:50:ARG:NH2	7:lG:72:ASP:OD2	2.26	0.67
16:lP:25:ALA:HA	16:lP:40:GLY:HA3	1.76	0.67
1:lA:2416:U:OP2	5:lE:239:HIS:ND1	2.25	0.67
1:lA:457:G:N2	18:lR:5:CYS:SG	2.67	0.67
53:sa:64:A:H2	53:sa:83:A:H62	1.42	0.67
1:lA:2991:G:OP1	42:lp:25:TYR:OH	2.11	0.67
3:lC:85:G:H1	3:lC:90:G:H22	1.42	0.67
50:sG:257:GLN:HG2	50:sG:272:LYS:HD2	1.76	0.67
57:se:29:LYS:NZ	68:sp:46:GLU:OE1	2.27	0.67
1:lA:225:U:H3	1:lA:282:G:H1	1.40	0.67
53:sa:295:A:N7	58:sf:37:LYS:NZ	2.42	0.67
1:lA:2897:A:O2'	1:lA:2898:A:OP1	2.12	0.67
1:lA:2979:C:H5	1:lA:2995:C:H42	1.41	0.67
57:se:173:LEU:HD21	57:se:198:GLU:HG2	1.77	0.67
60:sh:161:MET:HE1	60:sh:178:ASN:HD22	1.59	0.67
64:sl:11:ILE:H	64:sl:11:ILE:HD12	1.60	0.67
71:ss:65:GLU:HG2	71:ss:66:PRO:HD3	1.76	0.67
1:lA:2865:A:O2'	1:lA:2866:C:O4'	2.10	0.67
2:lB:101:G:OP2	2:lB:103:A:O2'	2.12	0.67
6:lF:367:GLU:N	6:lF:367:GLU:OE1	2.27	0.67
53:sa:294:G:H4'	53:sa:295:A:H5''	1.77	0.67
60:sh:167:ASN:O	60:sh:195:ARG:NH1	2.28	0.67
48:sD:44:ARG:HH12	48:sD:63:ARG:HB2	1.60	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:sz:62:ASN:OD1	78:sz:62:ASN:N	2.28	0.67
16:IP:69:ARG:NH2	20:IT:127:ASP:OD2	2.24	0.66
17:IQ:143:ARG:NH2	35:li:82:ARG:O	2.28	0.66
37:lk:2:ALA:O	37:lk:4:GLY:N	2.28	0.66
53:sa:60:A:O2'	53:sa:262:G:O2'	2.13	0.66
32:lf:16:GLU:OE1	32:lf:16:GLU:N	2.28	0.66
48:sD:51:ARG:HH22	59:sg:66:ILE:HD13	1.61	0.66
49:sE:21:CYS:SG	49:sE:24:CYS:N	2.66	0.66
60:sh:174:LEU:HD12	60:sh:192:LYS:HB2	1.78	0.66
1:lA:586:A:N6	8:IH:43:THR:O	2.28	0.66
48:sD:60:GLU:OE2	48:sD:62:GLU:N	2.28	0.66
53:sa:138:G:H2'	53:sa:139:G:C8	2.31	0.66
1:lA:869:G:N2	1:lA:872:A:H62	1.91	0.66
1:lA:3476:C:H41	1:lA:3478:U:H1'	1.60	0.66
3:lC:3:G:H1	3:lC:114:U:H3	1.43	0.66
8:IH:56:ARG:NH1	36:lj:108:ILE:O	2.29	0.66
63:sk:25:ASP:OD1	63:sk:26:ALA:N	2.28	0.66
66:sn:76:ILE:O	66:sn:80:GLN:N	2.28	0.66
74:sv:43:CYS:SG	74:sv:94:THR:OG1	2.54	0.66
46:sB:56:ASN:ND2	68:sp:115:ALA:O	2.28	0.66
53:sa:104:A:N7	53:sa:305:A:N1	2.42	0.66
53:sa:295:A:N6	58:sf:38:GLU:OE1	2.28	0.66
1:lA:3454:G:C6	1:lA:3501:A:N1	2.64	0.66
47:sC:75:THR:OG1	47:sC:78:CYS:SG	2.53	0.66
2:lB:60:G:O6	38:ll:63:ARG:NH2	2.29	0.66
51:sH:21:A:H61	51:sH:46:G:H2'	1.59	0.66
53:sa:1124:A:OP1	55:sc:161:THR:OG1	2.13	0.66
53:sa:1267:A:OP1	69:sq:58:LYS:NZ	2.27	0.66
53:sa:1839:A:OP1	60:sh:191:ARG:NH2	2.29	0.66
78:sz:29:ASP:HA	78:sz:74:SER:HA	1.78	0.66
1:lA:493:G:O2'	1:lA:578:A:N6	2.29	0.66
1:lA:3349:G:OP2	16:IP:5:ARG:NH2	2.28	0.66
53:sa:1284:U:O4	53:sa:1285:A:N6	2.28	0.66
60:sh:232:PRO:HG3	60:sh:241:LEU:HD21	1.77	0.66
1:lA:491:G:O6	1:lA:581:U:O2	2.13	0.66
53:sa:1308:U:OP2	53:sa:1309:C:O2'	2.13	0.66
71:ss:141:ALA:O	71:ss:143:LYS:NZ	2.29	0.66
75:sw:95:PRO:HG3	75:sw:116:MET:HE1	1.78	0.66
1:lA:495:A:N7	1:lA:577:G:O2'	2.28	0.65
1:lA:502:U:H2'	1:lA:503:A:H8	1.61	0.65
53:sa:399:G:OP1	60:sh:185:ARG:NH2	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:sa:1542:G:N7	64:sl:25:LYS:NZ	2.45	0.65
34:lh:76:TYR:O	34:lh:78:GLY:N	2.26	0.65
48:sD:44:ARG:NH1	48:sD:63:ARG:O	2.28	0.65
53:sa:1679:G:H21	53:sa:1685:C:H1'	1.61	0.65
58:sf:17:MET:HE1	58:sf:106:ARG:HE	1.60	0.65
1:lA:1728:A:N7	1:lA:1729:G:N2	2.44	0.65
53:sa:866:G:H2'	53:sa:867:A:H8	1.60	0.65
77:sy:99:LEU:HB2	77:sy:122:CYS:HB2	1.77	0.65
1:lA:2261:G:O2'	1:lA:2390:U:OP2	2.14	0.65
34:lh:81:CYS:SG	34:lh:84:CYS:N	2.68	0.65
1:lA:1813:G:N7	28:lb:17:ARG:NH2	2.44	0.65
1:lA:3349:G:H5''	16:lP:94:THR:HB	1.78	0.65
6:lF:373:VAL:HA	6:lF:377:PHE:HB2	1.77	0.65
51:sH:26:A:N6	51:sH:44:G:H1	1.95	0.65
53:sa:345:A:H5''	53:sa:346:U:H3'	1.79	0.65
1:lA:220:A:H2'	1:lA:221:U:C6	2.32	0.65
1:lA:1639:U:H2'	1:lA:1640:A:H8	1.62	0.65
2:lB:11:U:H2'	2:lB:12:A:H8	1.62	0.65
50:sG:194:ILE:HD12	50:sG:225:TRP:HZ3	1.62	0.65
69:sq:33:VAL:HG21	69:sq:44:TYR:HD2	1.61	0.65
1:lA:1858:A:OP1	23:lW:86:LYS:NZ	2.26	0.65
3:lC:21:C:N4	3:lC:52:G:O2'	2.30	0.65
9:lI:95:ARG:NH2	9:lI:190:LEU:O	2.30	0.65
14:lN:155:PHE:O	14:lN:156:ILE:HG12	1.96	0.65
53:sa:549:A:N3	53:sa:584:C:O2'	2.28	0.65
39:lm:8:VAL:HG13	39:lm:11:VAL:HG23	1.78	0.64
64:sl:10:ALA:HA	64:sl:13:LYS:HE2	1.78	0.64
71:ss:69:ILE:HG23	71:ss:70:VAL:HG13	1.79	0.64
78:sz:92:LYS:O	78:sz:93:HIS:ND1	2.25	0.64
1:lA:1763:C:H2'	1:lA:1764:A:C8	2.32	0.64
1:lA:2131:A:H4'	1:lA:2397:C:H5'	1.79	0.64
37:lk:29:LYS:O	37:lk:32:HIS:ND1	2.30	0.64
53:sa:76:U:O2	60:sh:256:ARG:NH1	2.30	0.64
3:lC:94:U:H2'	3:lC:95:A:C8	2.33	0.64
5:lE:361:ASP:OD2	5:lE:365:LYS:NZ	2.30	0.64
53:sa:1760:G:OP2	53:sa:1762:C:N4	2.30	0.64
61:si:47:VAL:HB	61:si:72:MET:HE3	1.79	0.64
73:su:72:LEU:HD22	73:su:100:ILE:HG21	1.80	0.64
1:lA:2981:A:N6	1:lA:2993:G:O2'	2.30	0.64
1:lA:3475:U:H3	1:lA:3479:A:N6	1.96	0.64
49:sE:41:ARG:NH2	53:sa:1224:G:OP2	2.29	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1744:A:H2'	1:1A:1745:A:C8	2.33	0.64
12:1L:170:LYS:HA	12:1L:177:THR:HA	1.80	0.64
32:1f:49:GLU:HG2	32:1f:112:ARG:HB2	1.77	0.64
35:1i:59:ARG:HG3	35:1i:72:LEU:HD22	1.79	0.64
50:sG:258:TYR:HB3	50:sG:272:LYS:HA	1.79	0.64
53:sa:746:A:H2'	53:sa:747:A:C8	2.33	0.64
1:1A:2629:A:H8	31:1e:54:PRO:HB3	1.62	0.64
2:1B:49:C:O2'	2:1B:63:A:O2'	2.15	0.64
3:1C:14:G:H2'	3:1C:15:A:H8	1.63	0.64
1:1A:331:A:OP2	43:lq:39:ARG:NH1	2.30	0.64
1:1A:789:C:H2'	1:1A:790:A:H8	1.63	0.64
1:1A:1841:G:H22	1:1A:1975:G:H1	1.46	0.64
22:1V:88:ARG:NH2	30:1d:28:ALA:O	2.23	0.64
53:sa:1718:U:O2'	53:sa:1763:A:N3	2.31	0.64
1:1A:2152:U:H2'	1:1A:2153:U:H4'	1.80	0.64
3:1C:85:G:H22	3:1C:90:G:N2	1.96	0.64
4:1D:126:ILE:HG21	4:1D:150:LEU:HD22	1.80	0.64
57:se:26:PHE:HA	57:se:29:LYS:HG3	1.80	0.64
1:1A:705:U:H2'	1:1A:706:A:H8	1.63	0.64
6:1F:143:HIS:N	6:1F:180:ASP:OD1	2.24	0.64
8:1H:64:ILE:O	8:1H:113:THR:OG1	2.16	0.64
53:sa:1298:G:H4'	53:sa:1299:C:H5'	1.80	0.64
1:1A:1883:A:H62	1:1A:1931:U:H3	1.45	0.63
27:1a:21:ALA:O	27:1a:26:ARG:NH1	2.31	0.63
53:sa:746:A:H2'	53:sa:747:A:H8	1.62	0.63
1:1A:2335:A:N6	53:sa:1811:G:O2'	2.31	0.63
9:1I:21:CYS:SG	9:1I:22:LYS:N	2.67	0.63
36:1j:34:VAL:HG13	36:1j:39:ASP:HB2	1.80	0.63
45:sA:103:ASP:OD1	45:sA:104:ASN:N	2.24	0.63
1:1A:2381:G:OP2	1:1A:2381:G:N2	2.30	0.63
50:sG:212:ILE:HD11	50:sG:224:MET:HB2	1.79	0.63
54:sb:75:ASN:ND2	76:sx:43:ILE:HD11	2.13	0.63
1:1A:1431:G:OP2	15:1O:60:ARG:NH1	2.32	0.63
53:sa:1441:C:O2'	53:sa:1442:A:O5'	2.16	0.63
60:sh:280:GLN:HG2	60:sh:283:ALA:HB3	1.81	0.63
1:1A:698:U:O2'	1:1A:699:A:N3	2.32	0.63
1:1A:1293:U:O4	1:1A:1454:G:O2'	2.16	0.63
35:1i:34:SER:HA	35:1i:37:ARG:HD3	1.81	0.63
53:sa:4:C:OP1	55:sc:202:THR:OG1	2.15	0.63
67:so:16:ILE:HD12	67:so:62:LEU:HD11	1.80	0.63
1:1A:643:A:OP1	16:1P:91:LYS:NZ	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:sh:262:LYS:O	60:sh:263:LYS:NZ	2.32	0.63
2:lB:73:A:H4'	2:lB:74:A:H5'	1.79	0.63
7:lG:91:GLY:O	7:lG:94:ASN:ND2	2.32	0.63
10:lJ:17:LEU:N	28:lB:126:ARG:O	2.32	0.63
47:sC:31:SER:HB3	47:sC:50:HIS:CD2	2.34	0.63
53:sa:1388:A:H2'	53:sa:1389:G:O4'	1.99	0.63
1:lA:1303:A:N3	1:lA:1453:U:O2'	2.31	0.63
1:lA:2075:A:OP2	21:lU:20:ARG:NH1	2.30	0.63
53:sa:1232:U:H3	53:sa:1563:C:H5	1.46	0.63
53:sa:1717:U:OP2	69:sq:42:ARG:NH1	2.31	0.63
67:so:35:ASP:OD1	67:so:36:GLU:N	2.32	0.63
50:sG:179:VAL:HB	50:sG:194:ILE:HB	1.81	0.62
58:sf:212:LYS:HE2	58:sf:242:ILE:HD13	1.80	0.62
1:lA:500:G:O6	1:lA:573:A:N6	2.32	0.62
1:lA:1523:U:OP1	33:lg:105:LYS:NZ	2.33	0.62
70:sr:80:ASN:OD1	70:sr:124:ARG:NH1	2.32	0.62
62:sj:103:GLU:HG2	62:sj:200:ARG:HB3	1.80	0.62
1:lA:65:U:O2'	1:lA:97:A:O2'	2.09	0.62
1:lA:1177:A:H2'	1:lA:1178:A:C8	2.35	0.62
1:lA:3454:G:C2	1:lA:3501:A:H2	2.17	0.62
53:sa:875:G:H21	68:sp:47:THR:HG21	1.63	0.62
58:sf:84:PHE:O	58:sf:86:ASP:N	2.32	0.62
60:sh:275:THR:OG1	60:sh:278:ARG:NH2	2.30	0.62
73:su:49:ALA:HB1	73:su:67:LYS:HG2	1.82	0.62
74:sv:109:GLU:HG3	74:sv:114:VAL:HG23	1.80	0.62
1:lA:1071:A:H4'	1:lA:1087:G:N2	2.14	0.62
33:lg:36:PRO:HG2	33:lg:44:ARG:HB3	1.81	0.62
48:sD:18:ILE:HG12	48:sD:31:VAL:HG12	1.81	0.62
1:lA:1186:G:H21	1:lA:1220:A:N6	1.95	0.62
1:lA:1763:C:H2'	1:lA:1764:A:H8	1.64	0.62
3:lC:29:G:O6	3:lC:46:G:O6	2.17	0.62
58:sf:33:PRO:HD2	58:sf:81:PRO:HG2	1.80	0.62
73:su:86:ASN:N	73:su:86:ASN:OD1	2.31	0.62
59:sg:184:LYS:HG2	59:sg:185:SER:H	1.63	0.62
1:lA:590:G:OP1	8:lH:37:ARG:NH1	2.33	0.62
1:lA:1358:G:H3'	1:lA:1359:U:H2'	1.81	0.62
1:lA:3474:U:H3	1:lA:3480:A:H62	1.46	0.62
28:lB:53:ILE:HA	28:lB:57:MET:HE1	1.82	0.62
1:lA:452:A:C2	2:lB:19:A:H1'	2.35	0.62
1:lA:669:A:N3	6:lF:394:ASN:ND2	2.48	0.62
1:lA:1270:G:OP1	33:lg:45:ARG:NH1	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:lA:3456:U:H3	1:lA:3496:A:H2	1.46	0.62
10:lJ:27:LYS:HE2	10:lJ:33:PRO:HD2	1.82	0.62
10:lJ:174:TYR:HH	10:lJ:226:TYR:HH	1.43	0.62
58:sf:120:LYS:NZ	58:sf:141:ASP:OD2	2.33	0.62
3:lC:6:G:O3'	7:lG:33:ARG:NH1	2.33	0.62
61:si:43:GLU:OE2	61:si:79:SER:OG	2.17	0.62
1:lA:816:G:N2	1:lA:829:G:OP2	2.32	0.61
1:lA:1209:U:OP1	1:lA:1211:A:O2'	2.18	0.61
6:lF:61:GLN:OE1	38:ll:55:ARG:NH2	2.30	0.61
10:lJ:18:ILE:O	10:lJ:20:ALA:N	2.31	0.61
24:lX:96:LEU:HD13	26:lZ:22:LYS:HD2	1.82	0.61
53:sa:366:G:N2	53:sa:606:U:O2	2.33	0.61
53:sa:1259:A:OP2	53:sa:1270:G:O2'	2.16	0.61
53:sa:1579:A:H4'	53:sa:1580:U:H5'	1.81	0.61
1:lA:1640:A:H2'	1:lA:1641:A:H8	1.65	0.61
1:lA:3477:U:H6	1:lA:3477:U:O5'	1.83	0.61
3:lC:78:C:H2'	3:lC:79:G:H8	1.65	0.61
24:lX:22:ASN:ND2	24:lX:40:ILE:O	2.30	0.61
49:sE:19:ARG:NH2	53:sa:1763:A:OP1	2.34	0.61
1:lA:1553:A:OP1	2:lB:22:G:O2'	2.17	0.61
53:sa:1693:A:H2'	53:sa:1694:A:H8	1.65	0.61
53:sa:1811:G:H22	53:sa:1902:A:H2	1.48	0.61
55:sc:218:ASP:OD1	55:sc:221:ARG:NH1	2.33	0.61
1:lA:2678:G:OP1	4:lD:2:GLY:N	2.34	0.61
10:lJ:72:THR:HG21	10:lJ:178:LYS:HG3	1.83	0.61
53:sa:1394:A:H5''	53:sa:1394:A:H8	1.63	0.61
58:sf:58:GLU:HB3	78:sz:21:LEU:HD11	1.82	0.61
24:lX:83:ARG:NH2	24:lX:118:THR:O	2.33	0.61
54:sb:92:ARG:NH2	72:st:82:ASP:O	2.34	0.61
1:lA:386:U:OP2	6:lF:198:ARG:NH2	2.24	0.61
3:lC:6:G:OP1	7:lG:33:ARG:NE	2.33	0.61
8:lH:94:PRO:HG3	8:lH:173:ILE:HD12	1.83	0.61
53:sa:947:A:OP2	67:so:124:ARG:NH2	2.33	0.61
1:lA:764:U:H2'	1:lA:765:A:H8	1.65	0.61
2:lB:8:U:H2'	2:lB:9:A:H8	1.65	0.61
3:lC:28:U:H3'	3:lC:29:G:H21	1.66	0.61
5:lE:50:LYS:HB2	5:lE:337:ILE:HD11	1.83	0.61
53:sa:1439:C:H2'	53:sa:1440:A:H4'	1.83	0.61
1:lA:255:A:N3	6:lF:225:ASN:ND2	2.49	0.61
1:lA:2114:U:N3	1:lA:2198:G:OP2	2.33	0.61
7:lG:156:THR:OG1	7:lG:180:ARG:NH1	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:lQ:163:GLY:O	17:lQ:172:ARG:NH1	2.30	0.61
51:sH:33:U:OP2	71:ss:158:ARG:NH2	2.34	0.61
53:sa:204:A:H3'	53:sa:205:A:H8	1.65	0.61
53:sa:332:G:O2'	62:sj:10:LYS:NZ	2.32	0.61
58:sf:210:ASP:OD1	58:sf:211:ALA:N	2.31	0.61
73:su:70:ASP:N	73:su:70:ASP:OD1	2.30	0.61
1:lA:72:G:O2'	14:lN:98:ARG:NH1	2.32	0.61
1:lA:225:U:O2	1:lA:282:G:N2	2.31	0.61
1:lA:3254:U:H4'	1:lA:3255:G:H5'	1.82	0.61
45:sA:56:ASP:OD1	45:sA:57:LYS:N	2.34	0.61
53:sa:387:G:OP1	53:sa:1876:U:O2'	2.18	0.61
53:sa:887:A:H2'	53:sa:888:A:H8	1.65	0.61
3:lC:79:G:O6	3:lC:95:A:N1	2.34	0.60
34:lh:25:THR:HG22	34:lh:26:ALA:H	1.66	0.60
53:sa:785:A:H2'	53:sa:786:U:O4'	2.01	0.60
53:sa:1567:A:OP2	73:su:145:ARG:NH2	2.29	0.60
29:lc:85:ASP:OD1	29:lc:85:ASP:N	2.34	0.60
40:ln:8:PHE:HE1	40:ln:12:LEU:HD21	1.65	0.60
62:sj:78:ILE:HA	62:sj:104:ILE:HG22	1.82	0.60
63:sk:137:GLY:N	63:sk:155:LEU:O	2.33	0.60
1:lA:3088:G:O2'	1:lA:3091:C:OP2	2.16	0.60
6:lF:33:ARG:NH2	6:lF:35:ASP:OD2	2.32	0.60
47:sC:31:SER:HB3	47:sC:50:HIS:HD2	1.67	0.60
60:sh:289:LYS:O	60:sh:293:LYS:N	2.30	0.60
1:lA:1277:G:N2	1:lA:1277:G:OP2	2.34	0.60
23:lW:63:THR:HB	23:lW:66:ILE:HG13	1.83	0.60
49:sE:54:LYS:HE2	75:sw:78:ASP:HB2	1.83	0.60
50:sG:136:LEU:HB3	50:sG:145:ALA:HB3	1.84	0.60
56:sd:76:LYS:HG2	56:sd:77:GLY:H	1.67	0.60
1:lA:3044:G:O2'	1:lA:3178:A:N1	2.34	0.60
49:sE:20:THR:HG22	49:sE:27:ARG:HD3	1.83	0.60
53:sa:1731:U:OP1	73:su:40:ARG:NH1	2.34	0.60
7:lG:33:ARG:CZ	7:lG:37:ILE:HD11	2.31	0.60
20:lT:78:VAL:HG22	20:lT:83:ILE:HG12	1.83	0.60
39:lm:39:CYS:HB2	39:lm:47:VAL:HG23	1.83	0.60
50:sG:168:ASN:HB3	50:sG:184:LEU:HD13	1.82	0.60
53:sa:1838:A:H2'	53:sa:1839:A:C8	2.36	0.60
61:si:68:ILE:HD12	61:si:72:MET:HE1	1.83	0.60
73:su:81:PRO:HG2	73:su:84:PHE:HB2	1.82	0.60
1:lA:3368:G:H2'	1:lA:3369:U:C6	2.37	0.60
6:lF:77:PRO:HB2	6:lF:91:ALA:HB3	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1F:141:GLY:O	6:1F:183:LYS:NZ	2.34	0.60
17:1Q:155:LYS:O	17:1Q:162:ARG:NH2	2.34	0.60
40:1n:49:ASP:HB3	40:1n:52:LYS:HG3	1.81	0.60
53:sa:328:C:C5	62:sj:49:ARG:HD2	2.37	0.60
78:sz:64:PHE:HA	78:sz:74:SER:O	2.02	0.60
1:1A:721:A:H2'	1:1A:722:A:C8	2.37	0.60
27:1a:152:ASP:OD1	27:1a:152:ASP:N	2.31	0.60
74:sv:118:GLN:OE1	74:sv:118:GLN:N	2.33	0.60
74:sv:126:GLU:CD	74:sv:126:GLU:H	2.08	0.60
1:1A:760:A:H2'	1:1A:761:A:H8	1.66	0.60
1:1A:1476:G:O2'	1:1A:1477:A:H5'	2.01	0.60
12:1L:171:TRP:CD1	12:1L:172:GLY:H	2.20	0.60
27:1a:80:ILE:HG22	27:1a:82:LYS:H	1.66	0.60
64:sl:76:ARG:HG3	64:sl:81:LEU:HB2	1.83	0.60
74:sv:11:VAL:HG12	74:sv:14:ASP:H	1.67	0.60
1:1A:1511:G:OP1	6:1F:200:ARG:NH1	2.34	0.60
1:1A:2898:A:C2	1:1A:2899:G:H1'	2.37	0.60
1:1A:3170:A:H2'	1:1A:3171:A:H8	1.67	0.60
9:1I:68:ASP:HB2	22:1V:141:PRO:HB3	1.83	0.60
55:sc:51:LYS:HB3	55:sc:245:TYR:HE2	1.67	0.60
1:1A:1430:G:O6	1:1A:2442:C:O2'	2.19	0.59
1:1A:2283:A:H2'	1:1A:2284:A:C8	2.37	0.59
6:1F:371:GLN:O	6:1F:371:GLN:HG2	2.00	0.59
31:1e:34:THR:HG23	31:1e:95:SER:OG	2.02	0.59
53:sa:1590:A:N3	53:sa:1773:G:O2'	2.30	0.59
60:sh:232:PRO:HG2	60:sh:238:ILE:HD13	1.82	0.59
60:sh:306:ILE:HD11	60:sh:310:TYR:CE2	2.37	0.59
1:1A:804:G:H2'	1:1A:805:G:C8	2.37	0.59
12:1L:41:ALA:O	12:1L:139:ARG:NH2	2.34	0.59
64:sl:45:MET:HG2	64:sl:65:TRP:CD2	2.37	0.59
1:1A:1393:U:H3	1:1A:1395:A:H3'	1.67	0.59
1:1A:2780:A:H2'	1:1A:2781:U:C6	2.37	0.59
50:sG:92:LEU:HB2	50:sG:106:PHE:HB2	1.85	0.59
53:sa:388:C:OP2	62:sj:2:GLY:N	2.35	0.59
53:sa:769:C:H2'	53:sa:770:A:C8	2.38	0.59
58:sf:93:THR:HG22	78:sz:19:PRO:HG2	1.82	0.59
1:1A:191:A:H2'	1:1A:192:A:H8	1.67	0.59
62:sj:57:ALA:HB2	62:sj:213:GLY:HA2	1.85	0.59
1:1A:1401:C:H2'	1:1A:1402:A:H8	1.67	0.59
12:1L:66:GLU:OE1	12:1L:69:ARG:NH2	2.35	0.59
14:1N:144:ALA:HA	14:1N:147:LYS:HD2	1.82	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:lQ:17:ASP:OD1	17:lQ:20:ARG:NH2	2.35	0.59
59:sg:94:VAL:HG11	59:sg:171:LEU:HD23	1.84	0.59
1:lA:535:A:H5'	14:lN:152:ILE:HD12	1.85	0.59
1:lA:668:A:H2'	1:lA:669:A:C8	2.34	0.59
6:lF:80:SER:O	6:lF:87:ASN:ND2	2.35	0.59
50:sG:272:LYS:HD3	50:sG:277:LYS:HD2	1.84	0.59
53:sa:158:A:H4'	60:sh:150:THR:HG23	1.85	0.59
53:sa:773:A:H5'	53:sa:774:U:C5	2.37	0.59
56:sd:21:ARG:HA	56:sd:21:ARG:HH11	1.68	0.59
5:lE:223:THR:OG1	5:lE:273:GLY:O	2.21	0.59
11:lK:103:VAL:HG22	42:lp:7:LEU:HD13	1.85	0.59
69:sq:111:LEU:O	69:sq:113:HIS:N	2.36	0.59
75:sw:20:ILE:HG12	75:sw:91:MET:HB2	1.84	0.59
1:lA:871:A:H2'	1:lA:872:A:C8	2.37	0.59
1:lA:1313:U:N3	1:lA:1440:A:OP2	2.35	0.59
2:lB:25:U:OP2	27:la:15:ARG:NH1	2.36	0.59
3:lC:17:G:H1	3:lC:59:G:H22	1.50	0.59
10:lJ:89:LYS:HE2	10:lJ:186:LEU:HA	1.85	0.59
38:ll:51:TYR:HA	38:ll:54:LEU:HD12	1.84	0.59
53:sa:243:U:OP1	65:sm:33:TYR:OH	2.17	0.59
68:sp:30:ALA:HB3	68:sp:107:ALA:HB2	1.84	0.59
1:lA:333:U:O2'	17:lQ:180:ARG:O	2.21	0.59
1:lA:1166:A:N3	1:lA:2703:U:O2'	2.36	0.59
1:lA:1459:U:H5''	9:ll:194:LYS:HB3	1.83	0.59
1:lA:3456:U:H5''	5:lE:309:MET:HE3	1.83	0.59
28:lb:90:GLU:OE2	28:lb:90:GLU:N	2.36	0.59
31:le:8:LYS:HG3	31:le:9:LYS:H	1.66	0.59
50:sG:111:GLY:H	50:sG:131:ASP:HB3	1.66	0.59
53:sa:104:A:N6	53:sa:305:A:H2	1.97	0.59
53:sa:948:U:OP1	53:sa:1013:U:O2'	2.20	0.59
53:sa:1227:A:N6	53:sa:1564:C:O5'	2.35	0.59
60:sh:168:ASN:OD1	60:sh:168:ASN:N	2.36	0.59
72:st:99:ASP:OD1	72:st:102:THR:OG1	2.13	0.59
1:lA:732:U:O2'	1:lA:733:C:O5'	2.16	0.59
2:lB:11:U:H2'	2:lB:12:A:C8	2.37	0.59
53:sa:998:U:OP1	67:so:107:LYS:NZ	2.32	0.59
53:sa:1591:G:H21	53:sa:1772:A:H1'	1.68	0.59
77:sy:106:ARG:HD3	77:sy:107:GLY:N	2.18	0.59
1:lA:404:G:N2	1:lA:407:A:OP2	2.30	0.58
14:lN:258:ASP:OD1	29:lc:135:GLN:NE2	2.33	0.58
47:sC:40:LYS:HE2	47:sC:60:CYS:HB2	1.83	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:sy:83:VAL:HG12	77:sy:88:SER:HB2	1.84	0.58
2:IB:62:U:OP1	25:IY:33:ARG:NH2	2.33	0.58
6:IF:237:LEU:HD22	6:IF:242:LEU:HD21	1.86	0.58
49:sE:21:CYS:HB3	49:sE:26:ALA:H	1.68	0.58
50:sG:13:LEU:HB2	50:sG:306:ILE:HB	1.84	0.58
53:sa:1441:C:OP2	72:st:5:ARG:NH2	2.36	0.58
56:sd:80:ILE:HD11	56:sd:102:VAL:HG23	1.84	0.58
78:sz:49:LYS:HD3	78:sz:49:LYS:N	2.17	0.58
1:lA:893:U:H3	1:lA:897:A:H2	1.50	0.58
1:lA:1087:G:N3	30:ld:15:LYS:NZ	2.51	0.58
74:sv:19:TYR:HD1	74:sv:134:ILE:HD12	1.69	0.58
1:lA:1154:A:H3'	1:lA:1155:A:H8	1.68	0.58
1:lA:2098:A:H61	1:lA:2415:C:H42	1.51	0.58
1:lA:2730:U:H2'	1:lA:2731:G:H8	1.67	0.58
1:lA:3315:U:O2'	1:lA:3418:C:OP2	2.21	0.58
1:lA:3368:G:H2'	1:lA:3369:U:H6	1.68	0.58
19:lS:152:VAL:HA	19:lS:159:ALA:H	1.68	0.58
43:lq:72:CYS:SG	43:lq:75:CYS:N	2.76	0.58
58:sf:250:VAL:O	58:sf:254:ILE:HG12	2.03	0.58
53:sa:1661:C:H2'	53:sa:1662:G:C8	2.34	0.58
53:sa:1717:U:O4	69:sq:39:ARG:NH2	2.37	0.58
59:sg:54:THR:OG1	59:sg:72:GLU:OE1	2.21	0.58
1:lA:381:A:H2'	1:lA:382:A:H8	1.68	0.58
1:lA:3149:A:H2'	1:lA:3150:A:C8	2.37	0.58
3:lC:79:G:C6	3:lC:95:A:N1	2.72	0.58
4:lD:201:GLY:HA2	4:lD:204:MET:HG3	1.85	0.58
53:sa:1699:C:H4'	53:sa:1705:A:N6	2.18	0.58
56:sd:34:GLU:OE1	64:sl:59:ASN:ND2	2.37	0.58
1:lA:118:A:N6	1:lA:189:G:O2'	2.34	0.58
1:lA:804:G:H22	1:lA:911:U:H3	1.49	0.58
3:lC:22:C:H2'	3:lC:23:A:C8	2.39	0.58
35:li:-6:LYS:O	35:li:-3:ALA:N	2.33	0.58
47:sC:76:GLN:HG2	47:sC:77:GLN:HG2	1.86	0.58
59:sg:127:SER:OG	59:sg:138:ARG:NH1	2.36	0.58
73:su:70:ASP:O	73:su:74:ASN:ND2	2.36	0.58
1:lA:220:A:H2'	1:lA:221:U:H6	1.68	0.58
1:lA:3336:G:O2'	15:lO:115:LYS:O	2.21	0.58
77:sy:57:THR:HG23	77:sy:113:ILE:HG13	1.84	0.58
77:sy:99:LEU:HB3	77:sy:121:VAL:HG22	1.86	0.58
1:lA:979:G:C5	4:lD:181:LYS:HB3	2.38	0.58
1:lA:1370:G:H21	1:lA:1389:U:H3'	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:IB:141:G:H5''	17:IQ:60:VAL:HG11	1.84	0.58
6:IF:142:HIS:ND1	6:IF:180:ASP:OD2	2.32	0.58
23:IW:100:ASN:HB2	23:IW:102:LEU:CD2	2.34	0.58
53:sa:1172:G:H2'	53:sa:1173:A:C8	2.39	0.58
1:IA:493:G:N2	1:IA:580:A:H61	1.98	0.58
1:IA:2186:U:O2'	1:IA:3485:U:O2'	2.20	0.58
33:lg:41:ASN:HB3	33:lg:44:ARG:HG2	1.85	0.58
50:sG:25:VAL:HG22	50:sG:33:LEU:HD13	1.86	0.58
53:sa:1161:U:OP2	77:sy:117:ARG:NH2	2.37	0.58
53:sa:1204:G:H21	53:sa:1567:A:H62	1.51	0.58
56:sd:94:PRO:HG2	56:sd:97:LYS:HD3	1.85	0.58
56:sd:99:GLU:HG3	56:sd:101:TYR:HE1	1.68	0.58
60:sh:298:LYS:HG3	60:sh:302:ARG:HH21	1.68	0.58
64:sl:3:ILE:HG12	64:sl:40:GLN:HB3	1.86	0.58
71:ss:25:PHE:HE2	71:ss:27:LYS:HE2	1.69	0.58
1:IA:822:C:H2'	1:IA:823:A:C8	2.39	0.57
20:IT:69:LYS:NZ	20:IT:93:VAL:O	2.37	0.57
53:sa:1251:A:O2'	53:sa:1281:A:N6	2.28	0.57
1:IA:709:U:O2'	1:IA:710:A:OP1	2.22	0.57
3:IC:1:A:H61	3:IC:116:C:H42	1.52	0.57
30:ld:38:GLN:NE2	30:ld:42:ASN:OD1	2.37	0.57
53:sa:1369:A:H4'	75:sw:52:GLY:HA3	1.86	0.57
23:IW:39:ASP:OD1	23:IW:39:ASP:N	2.36	0.57
53:sa:1188:A:N3	53:sa:1779:U:O2'	2.26	0.57
58:sf:102:ASN:HD21	58:sf:106:ARG:HB3	1.69	0.57
1:IA:1292:A:O2'	9:II:197:GLY:O	2.14	0.57
1:IA:3211:A:H2	1:IA:3239:G:H21	1.52	0.57
56:sd:142:ASP:N	56:sd:142:ASP:OD1	2.37	0.57
1:IA:502:U:H2'	1:IA:503:A:C8	2.40	0.57
1:IA:1639:U:H2'	1:IA:1640:A:C8	2.40	0.57
11:IK:43:LYS:HE3	15:IO:132:PRO:HG2	1.86	0.57
37:lk:1:MET:HE3	37:lk:2:ALA:H	1.69	0.57
48:sD:36:MET:N	48:sD:36:MET:SD	2.71	0.57
55:sc:122:GLU:OE2	56:sd:130:ARG:NH1	2.37	0.57
57:se:38:LYS:HE3	57:se:233:GLN:HA	1.85	0.57
1:IA:720:U:H2'	1:IA:721:A:C8	2.39	0.57
28:lb:104:GLU:OE1	28:lb:104:GLU:N	2.26	0.57
50:sG:37:SER:OG	50:sG:38:ARG:N	2.37	0.57
53:sa:401:U:H2'	53:sa:402:A:H8	1.69	0.57
53:sa:1508:A:OP1	72:st:56:HIS:NE2	2.30	0.57
74:sv:105:LEU:HD13	74:sv:121:ARG:HH11	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:239:G:H2'	1:1A:240:A:C8	2.39	0.57
1:1A:2079:A:H2'	1:1A:2080:A:O4'	2.04	0.57
27:1a:54:GLU:OE2	27:1a:67:LYS:NZ	2.31	0.57
61:si:135:MET:HG2	61:si:136:LEU:HD12	1.86	0.57
1:1A:685:A:O4'	1:1A:1450:A:N6	2.37	0.57
4:1D:30:ARG:NH2	4:1D:33:ASP:OD2	2.37	0.57
46:sB:11:SER:O	46:sB:11:SER:OG	2.22	0.57
50:sG:124:LYS:HE2	50:sG:184:LEU:HD11	1.86	0.57
53:sa:1751:U:H3	53:sa:1777:A:H2	1.53	0.57
1:1A:115:G:N7	10:1J:138:ARG:NH1	2.49	0.57
2:1B:21:A:H2'	2:1B:22:G:H8	1.70	0.57
7:1G:64:ILE:HG13	7:1G:105:LEU:HD21	1.86	0.57
78:sz:18:ASN:HD22	78:sz:21:LEU:HB2	1.70	0.57
1:1A:1252:G:N2	1:1A:1255:A:OP2	2.37	0.57
3:1C:2:G:O2'	3:1C:24:U:O2	2.23	0.57
3:1C:84:G:H22	3:1C:91:G:N2	2.03	0.57
17:1Q:31:ARG:NH1	17:1Q:124:ASP:OD2	2.36	0.57
20:1T:7:THR:OG1	20:1T:56:GLN:OE1	2.20	0.57
53:sa:125:U:O2'	53:sa:203:C:O2	2.19	0.57
76:sx:50:TYR:OH	76:sx:73:ASP:OD2	2.17	0.57
1:1A:1073:A:H62	1:1A:1086:G:H21	1.52	0.56
1:1A:1892:C:H2'	1:1A:1893:A:H8	1.69	0.56
1:1A:2064:G:N1	1:1A:2067:A:OP2	2.38	0.56
1:1A:2893:C:H2'	1:1A:2894:C:C6	2.39	0.56
8:1H:178:LYS:HD3	8:1H:184:LYS:HG3	1.86	0.56
1:1A:1086:G:H2'	1:1A:1087:G:H8	1.69	0.56
1:1A:1912:A:H61	39:lm:42:CYS:HA	1.70	0.56
1:1A:2331:A:H5'	1:1A:2337:G:H22	1.69	0.56
1:1A:2944:A:O2'	1:1A:2945:A:H2'	2.05	0.56
7:1G:10:ARG:HH21	7:1G:14:LYS:HE3	1.71	0.56
50:sG:303:ASP:OD2	50:sG:305:LYS:NZ	2.39	0.56
60:sh:278:ARG:HA	60:sh:281:HIS:CD2	2.40	0.56
1:1A:497:U:H3	1:1A:576:A:H2	1.52	0.56
1:1A:501:U:H2'	1:1A:502:U:C6	2.40	0.56
1:1A:501:U:H2'	1:1A:502:U:H6	1.69	0.56
1:1A:605:C:H2'	1:1A:606:A:H8	1.70	0.56
1:1A:700:A:H5''	1:1A:745:A:H62	1.69	0.56
1:1A:1814:G:N2	1:1A:1817:A:OP2	2.38	0.56
1:1A:1904:U:OP2	21:1U:124:TYR:OH	2.21	0.56
4:1D:108:PRO:O	4:1D:111:THR:OG1	2.16	0.56
18:1R:126:ARG:NH1	18:1R:140:SER:OG	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:sG:138:ASN:HD21	50:sG:140:VAL:HG12	1.70	0.56
53:sa:208:C:H2'	53:sa:209:A:H8	1.71	0.56
53:sa:324:G:H5''	62:sj:98:LYS:HB3	1.87	0.56
53:sa:389:U:O4	53:sa:396:A:N7	2.38	0.56
60:sh:292:HIS:HA	60:sh:296:MET:HB2	1.87	0.56
73:su:118:MET:HE2	73:su:120:ALA:HB2	1.86	0.56
76:sx:36:HIS:O	76:sx:44:LEU:N	2.38	0.56
77:sy:20:TRP:HE3	77:sy:26:LYS:HG3	1.69	0.56
77:sy:106:ARG:HB2	77:sy:110:VAL:HG22	1.86	0.56
1:lA:43:C:H5''	14:lN:14:LYS:HG3	1.88	0.56
1:lA:639:G:N1	1:lA:651:G:O6	2.39	0.56
1:lA:720:U:H2'	1:lA:721:A:H8	1.71	0.56
1:lA:1197:G:H2'	1:lA:1198:U:H6	1.71	0.56
1:lA:1640:A:H2'	1:lA:1641:A:C8	2.40	0.56
1:lA:1840:A:H2'	1:lA:1841:G:C8	2.41	0.56
43:lq:8:ARG:O	43:lq:21:HIS:N	2.34	0.56
45:sA:104:ASN:ND2	53:sa:1696:G:OP2	2.35	0.56
67:so:87:ASP:OD1	67:so:87:ASP:N	2.28	0.56
1:lA:662:U:H2'	1:lA:663:G:O4'	2.05	0.56
1:lA:729:U:O4	1:lA:730:A:N6	2.38	0.56
1:lA:828:A:OP1	17:lQ:202:ARG:NH2	2.39	0.56
1:lA:1370:G:N2	1:lA:1389:U:H3'	2.20	0.56
10:lJ:87:HIS:HB3	10:lJ:201:LYS:HD2	1.88	0.56
25:lY:26:PRO:HD2	35:li:69:PRO:HG3	1.88	0.56
51:sH:14:A:H1'	51:sH:22:G:N2	2.21	0.56
53:sa:367:G:O2'	53:sa:605:C:N3	2.38	0.56
3:lC:84:G:H1	3:lC:91:G:N2	1.94	0.56
8:lH:138:LYS:O	8:lH:152:LYS:NZ	2.39	0.56
53:sa:1721:A:O2'	69:sq:81:ASP:OD2	2.16	0.56
1:lA:597:A:N3	8:lH:51:ASN:ND2	2.51	0.56
1:lA:765:A:N3	36:lj:92:PRO:HG2	2.21	0.56
1:lA:2857:A:H1'	1:lA:2858:A:H5''	1.87	0.56
53:sa:561:A:H62	53:sa:570:G:H21	1.54	0.56
58:sf:112:LEU:HD23	58:sf:235:ASN:HD21	1.70	0.56
1:lA:444:A:O2'	1:lA:448:C:O2'	2.21	0.56
6:lF:388:ILE:HG23	6:lF:390:VAL:HB	1.87	0.56
8:lH:43:THR:OG1	8:lH:85:LYS:NZ	2.39	0.56
19:lS:6:ASP:OD1	19:lS:6:ASP:N	2.39	0.56
23:lW:33:ASP:OD1	23:lW:74:LYS:NZ	2.34	0.56
53:sa:1207:U:OP1	69:sq:123:LYS:NZ	2.39	0.56
53:sa:1223:G:OP1	53:sa:1224:G:O2'	2.19	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:sb:188:GLU:OE1	54:sb:198:ARG:NH2	2.38	0.56
1:lA:467:A:N1	1:lA:2438:C:O2'	2.31	0.56
1:lA:732:U:O2'	1:lA:733:C:H6	1.87	0.56
3:lC:10:A:N1	3:lC:65:U:O2'	2.35	0.56
9:II:87:ILE:HG23	9:II:118:VAL:HG12	1.87	0.56
45:sA:69:THR:HG22	45:sA:72:VAL:HG12	1.88	0.56
56:sd:43:LEU:HD11	56:sd:83:LEU:HD11	1.86	0.56
59:sg:53:HIS:HB2	59:sg:92:MET:SD	2.45	0.56
1:lA:105:A:N1	1:lA:368:U:O2'	2.37	0.56
1:lA:199:G:N1	1:lA:311:A:OP2	2.33	0.56
1:lA:764:U:H2'	1:lA:765:A:C8	2.40	0.56
1:lA:817:A:H2'	1:lA:818:A:C8	2.41	0.56
1:lA:3426:U:O4	5:IE:121:LYS:NZ	2.39	0.56
13:IM:141:ARG:NH2	13:IM:146:ASP:OD2	2.39	0.56
24:IX:60:MET:SD	24:IX:78:THR:HG22	2.46	0.56
50:sG:211:SER:HA	50:sG:227:LEU:HD22	1.88	0.56
53:sa:762:A:H5'	63:sk:7:ASN:HB2	1.88	0.56
53:sa:872:A:H2'	53:sa:873:A:C8	2.41	0.56
53:sa:1580:U:O2'	59:sg:84:ASN:OD1	2.21	0.56
67:so:29:SER:OG	67:so:32:GLU:OE1	2.20	0.56
6:lF:339:LYS:O	6:lF:343:VAL:HG23	2.07	0.55
53:sa:1224:G:H8	75:sw:66:ARG:HG3	1.71	0.55
68:sp:52:THR:HG23	68:sp:55:MET:HE3	1.89	0.55
1:lA:1992:A:H2'	1:lA:1993:G:H8	1.71	0.55
32:lf:84:THR:HG1	32:lf:127:THR:HG1	1.51	0.55
53:sa:5:U:OP2	55:sc:206:THR:OG1	2.24	0.55
53:sa:586:A:O2'	53:sa:590:U:OP1	2.23	0.55
53:sa:1566:C:OP2	73:su:137:THR:OG1	2.24	0.55
57:se:88:PHE:HB3	57:se:100:MET:HB3	1.88	0.55
1:lA:700:A:O2'	1:lA:701:A:OP1	2.24	0.55
1:lA:816:G:H22	1:lA:829:G:P	2.30	0.55
1:lA:1206:A:H2'	1:lA:1207:C:C6	2.41	0.55
1:lA:2499:U:H2'	1:lA:2500:A:C8	2.41	0.55
9:II:76:ARG:NH2	9:II:79:GLY:O	2.39	0.55
11:IK:101:ARG:NH1	11:IK:149:GLU:OE1	2.39	0.55
14:IN:166:LEU:HA	14:IN:169:LYS:HE3	1.86	0.55
53:sa:1268:G:H8	69:sq:54:ARG:HH11	1.54	0.55
57:se:30:GLU:OE2	57:se:96:LYS:NZ	2.39	0.55
60:sh:274:VAL:O	60:sh:274:VAL:HG12	2.07	0.55
60:sh:306:ILE:HD12	60:sh:309:ARG:HB2	1.87	0.55
68:sp:49:ILE:HD11	68:sp:51:ILE:HD11	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:lA:13:C:P	25:lY:27:ARG:HH22	2.29	0.55
1:lA:95:A:OP1	17:lQ:195:ARG:NH1	2.36	0.55
1:lA:760:A:H2'	1:lA:761:A:C8	2.41	0.55
1:lA:3357:U:H4'	1:lA:3358:A:H5'	1.88	0.55
6:lF:115:THR:HB	6:lF:120:ARG:HD2	1.89	0.55
23:lW:84:LEU:HD22	23:lW:89:MET:HE1	1.87	0.55
46:sB:12:LYS:HE3	46:sB:16:GLY:HA2	1.87	0.55
78:sz:32:HIS:O	78:sz:71:GLY:HA2	2.06	0.55
1:lA:1225:A:H5''	9:lI:95:ARG:HD2	1.88	0.55
1:lA:1864:C:OP1	23:lW:98:LYS:NZ	2.33	0.55
1:lA:2341:C:N4	1:lA:2342:U:O4	2.40	0.55
1:lA:2753:U:H2'	1:lA:2754:C:C6	2.41	0.55
53:sa:1662:G:O2'	53:sa:1687:C:N4	2.39	0.55
56:sd:122:LYS:NZ	56:sd:135:SER:OG	2.39	0.55
58:sf:250:VAL:HG21	63:sk:71:LEU:HD11	1.89	0.55
1:lA:233:A:N3	1:lA:254:C:O2'	2.37	0.55
1:lA:789:C:H2'	1:lA:790:A:C8	2.42	0.55
31:le:31:THR:HG23	31:le:60:ILE:HD11	1.87	0.55
57:se:36:VAL:O	57:se:43:ARG:NH1	2.40	0.55
1:lA:316:G:OP1	17:lQ:47:ARG:NE	2.40	0.55
1:lA:619:A:O2'	1:lA:620:U:O5'	2.23	0.55
1:lA:3008:U:HO2'	1:lA:3009:C:P	2.29	0.55
5:lE:59:GLU:HG3	5:lE:358:LYS:HD2	1.88	0.55
8:lH:141:ALA:HB3	8:lH:144:LYS:HG3	1.89	0.55
28:lb:20:GLY:HA3	28:lb:139:PHE:HZ	1.72	0.55
53:sa:40:A:O2'	53:sa:432:A:O2'	2.18	0.55
53:sa:1357:C:OP2	72:st:45:ARG:NH1	2.40	0.55
60:sh:256:ARG:HD3	60:sh:267:ALA:HB2	1.89	0.55
53:sa:622:G:N1	53:sa:950:A:OP2	2.27	0.55
53:sa:1243:A:O4'	53:sa:1551:A:N6	2.39	0.55
53:sa:1394:A:H4'	53:sa:1394:A:OP1	2.07	0.55
54:sb:84:VAL:HG22	54:sb:131:VAL:HG12	1.88	0.55
60:sh:273:LEU:HG	60:sh:274:VAL:H	1.70	0.55
1:lA:1220:A:H2'	1:lA:1220:A:N3	2.22	0.55
1:lA:1313:U:O2'	1:lA:1315:A:N7	2.38	0.55
1:lA:2466:G:N2	5:lE:228:TYR:OH	2.30	0.55
1:lA:2582:U:H2'	1:lA:2583:U:C6	2.41	0.55
6:lF:353:GLN:HG2	6:lF:353:GLN:O	2.07	0.55
51:sH:18:G:N2	51:sH:58:A:C4	2.75	0.55
53:sa:564:A:N6	77:sy:111:GLY:O	2.39	0.55
53:sa:1704:C:O3'	73:su:25:ARG:NH2	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:sr:44:HIS:NE2	70:sr:112:ASP:OD2	2.33	0.55
75:sw:99:LYS:HG3	75:sw:102:THR:HA	1.88	0.55
77:sy:85:ARG:HG3	77:sy:86:ASP:N	2.22	0.55
1:lA:1841:G:N2	1:lA:1975:G:H22	2.05	0.55
1:lA:3372:U:O2'	1:lA:3374:C:OP2	2.20	0.55
3:lC:104:G:H2'	3:lC:105:A:H8	1.72	0.55
53:sa:545:G:H2'	53:sa:546:G:H8	1.72	0.55
59:sg:33:ILE:HG22	59:sg:36:LYS:HD3	1.89	0.55
1:lA:38:C:O2'	1:lA:39:A:H5'	2.06	0.54
1:lA:2272:C:O2'	1:lA:2346:A:N3	2.35	0.54
1:lA:3329:U:O2'	1:lA:3411:U:O2'	2.25	0.54
5:lE:47:LEU:HB3	5:lE:84:MET:HE3	1.89	0.54
15:lO:63:VAL:HG12	15:lO:66:ASN:H	1.72	0.54
46:sB:6:ARG:NH2	53:sa:1116:U:OP2	2.39	0.54
53:sa:104:A:OP1	62:sj:12:ARG:NE	2.40	0.54
53:sa:1545:G:H5'	56:sd:190:LEU:HD11	1.89	0.54
55:sc:239:GLN:HG2	55:sc:244:LYS:HB3	1.89	0.54
65:sm:61:SER:OG	65:sm:62:ASP:N	2.40	0.54
1:lA:227:A:H2'	1:lA:228:A:C8	2.42	0.54
1:lA:504:U:H2'	1:lA:505:A:H8	1.72	0.54
1:lA:2732:A:H2'	1:lA:2733:A:H8	1.72	0.54
1:lA:2767:A:H2'	1:lA:2768:G:C8	2.42	0.54
1:lA:3033:C:O2'	1:lA:3076:A:N3	2.36	0.54
8:lH:203:LYS:HE2	16:lP:106:LYS:HA	1.88	0.54
27:la:87:LYS:O	27:la:89:ASN:N	2.39	0.54
53:sa:1196:A:H2'	53:sa:1197:G:C8	2.42	0.54
56:sd:59:LYS:HA	56:sd:97:LYS:HB2	1.88	0.54
56:sd:219:PRO:O	72:st:20:TYR:OH	2.23	0.54
63:sk:37:LYS:N	63:sk:41:GLU:OE1	2.40	0.54
1:lA:342:A:H1'	37:lk:76:ARG:HD3	1.88	0.54
6:lF:194:GLN:HG3	6:lF:197:MET:HE3	1.89	0.54
53:sa:887:A:H2'	53:sa:888:A:C8	2.42	0.54
53:sa:1573:G:O2'	53:sa:1768:C:OP1	2.25	0.54
57:se:57:ARG:NH1	57:se:62:GLN:OE1	2.34	0.54
58:sf:90:ILE:HG21	78:sz:20:LEU:HD11	1.88	0.54
1:lA:92:A:N6	19:lS:166:GLN:OE1	2.41	0.54
1:lA:2415:C:OP1	24:IX:54:ARG:NH2	2.41	0.54
1:lA:2688:G:O2'	1:lA:3008:U:OP1	2.20	0.54
3:lC:45:U:H2'	3:lC:46:G:H8	1.73	0.54
62:sj:43:VAL:HG12	62:sj:57:ALA:HA	1.90	0.54
1:lA:2798:G:OP1	19:lS:151:LYS:NZ	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:lA:3203:A:H4'	5:lE:365:LYS:HD2	1.90	0.54
3:lC:103:U:H2'	3:lC:104:G:H8	1.72	0.54
5:lE:184:GLN:NE2	5:lE:186:ASN:OD1	2.32	0.54
51:sH:15:G:N2	51:sH:48:C:H42	2.04	0.54
53:sa:867:A:H2	68:sp:135:THR:HG23	1.73	0.54
53:sa:1261:A:H2'	53:sa:1262:G:H8	1.72	0.54
53:sa:1287:U:H2'	53:sa:1288:G:C8	2.42	0.54
53:sa:1586:U:OP1	74:sv:57:ARG:NE	2.34	0.54
71:ss:140:GLU:OE2	71:ss:150:ARG:NH2	2.40	0.54
3:lC:8:U:OP1	22:lV:26:ASN:HB3	2.06	0.54
53:sa:327:U:H5''	62:sj:31:ARG:HH11	1.72	0.54
53:sa:619:C:H2'	53:sa:620:U:C6	2.43	0.54
53:sa:1245:C:H2'	53:sa:1246:A:H8	1.72	0.54
53:sa:1775:U:O2'	59:sg:86:GLY:O	2.18	0.54
1:lA:1115:A:O2'	3:lC:76:U:O2	2.24	0.54
9:lI:142:LEU:HD12	9:lI:156:MET:HE2	1.89	0.54
31:le:11:GLN:OE1	31:le:75:SER:OG	2.25	0.54
45:sA:104:ASN:OD1	53:sa:1696:G:N2	2.37	0.54
4:lD:61:VAL:HG11	4:lD:88:ILE:HD11	1.89	0.54
46:sB:37:LYS:O	46:sB:38:ARG:NH1	2.41	0.54
53:sa:543:G:O2'	53:sa:550:A:N1	2.35	0.54
53:sa:1432:A:H1'	75:sw:55:ARG:HD2	1.88	0.54
1:lA:487:A:H2'	1:lA:488:A:H8	1.73	0.54
1:lA:1312:A:H62	1:lA:1441:U:H3	1.54	0.54
1:lA:1876:U:H2'	1:lA:1936:A:H61	1.71	0.54
1:lA:2241:U:OP1	4:lD:4:ARG:NH2	2.31	0.54
50:sG:62:LYS:HG2	50:sG:100:MET:HE3	1.89	0.54
53:sa:776:U:H5''	53:sa:777:U:H2'	1.90	0.54
63:sk:139:GLN:HE22	78:sz:67:LYS:HE3	1.73	0.54
75:sw:22:ILE:HG12	75:sw:114:VAL:HG22	1.90	0.54
1:lA:790:A:H2'	1:lA:791:A:C8	2.43	0.54
7:lG:75:LEU:O	7:lG:112:LYS:NZ	2.41	0.54
11:lK:101:ARG:HE	42:lp:7:LEU:HD21	1.72	0.54
48:sD:49:PRO:HG2	59:sg:146:LEU:HD23	1.90	0.54
60:sh:290:LYS:HZ3	60:sh:290:LYS:N	2.06	0.54
1:lA:73:A:N7	14:lN:71:ARG:NH2	2.56	0.53
1:lA:869:G:C5	1:lA:870:A:H1'	2.43	0.53
1:lA:2753:U:H2'	1:lA:2754:C:H6	1.73	0.53
53:sa:17:C:O2'	53:sa:1163:A:N1	2.33	0.53
55:sc:172:VAL:HB	55:sc:199:PHE:HB2	1.88	0.53
72:st:5:ARG:HB2	72:st:10:LYS:HE3	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:su:111:ASP:O	73:su:115:LEU:N	2.33	0.53
1:lA:625:A:O2'	1:lA:626:A:OP1	2.27	0.53
1:lA:3083:A:N7	5:lE:2:SER:N	2.57	0.53
4:lD:117:GLU:HG2	4:lD:124:GLY:H	1.73	0.53
54:sb:139:GLN:NE2	54:sb:143:GLU:OE2	2.32	0.53
1:lA:1310:A:H2'	1:lA:1311:C:C6	2.44	0.53
1:lA:3136:U:H2'	1:lA:3137:C:C6	2.43	0.53
20:lT:70:ASN:HD22	20:lT:130:VAL:HG21	1.73	0.53
32:lF:48:ARG:NH1	32:lF:144:THR:OG1	2.41	0.53
48:sD:40:ARG:HH22	48:sD:61:ALA:HB1	1.72	0.53
53:sa:1346:A:H4'	53:sa:1347:A:O5'	2.07	0.53
61:si:44:LEU:O	61:si:47:VAL:HG22	2.08	0.53
3:lC:3:G:H22	3:lC:114:U:H3	1.57	0.53
53:sa:767:A:O2'	53:sa:768:A:OP1	2.19	0.53
58:sf:195:LYS:HB3	58:sf:207:HIS:HB2	1.90	0.53
3:lC:106:U:H2'	3:lC:107:A:H8	1.73	0.53
10:lJ:40:VAL:HG21	25:lY:6:ARG:HD3	1.91	0.53
46:sB:13:LYS:O	46:sB:15:ARG:N	2.42	0.53
53:sa:1595:G:O2'	53:sa:1661:C:O2	2.23	0.53
59:sg:143:VAL:HG13	59:sg:147:ARG:HG2	1.90	0.53
1:lA:221:U:H2'	1:lA:222:A:H8	1.74	0.53
1:lA:506:A:H2'	1:lA:507:A:C8	2.42	0.53
2:lB:10:U:H2'	2:lB:11:U:C6	2.43	0.53
53:sa:1323:U:H5	53:sa:1324:G:C4	2.27	0.53
1:lA:258:G:C8	6:lF:227:PRO:HG3	2.43	0.53
1:lA:491:G:C5	1:lA:492:U:C4	2.96	0.53
1:lA:1846:A:H2'	1:lA:1847:A:C8	2.44	0.53
1:lA:3138:G:O2'	2:lB:2:A:N3	2.36	0.53
6:lF:134:PRO:HD3	6:lF:150:ILE:HG21	1.90	0.53
53:sa:467:C:O2'	53:sa:760:A:N3	2.37	0.53
53:sa:1341:C:O2'	72:st:10:LYS:NZ	2.40	0.53
1:lA:424:A:O2'	1:lA:425:C:OP2	2.26	0.53
1:lA:1019:G:H1'	1:lA:1737:A:N6	2.23	0.53
1:lA:1173:A:H5''	1:lA:2707:A:H61	1.74	0.53
1:lA:3393:A:H2'	1:lA:3394:A:C8	2.44	0.53
53:sa:555:G:H2'	53:sa:556:G:H8	1.73	0.53
53:sa:1248:U:H2'	53:sa:1249:A:H8	1.74	0.53
53:sa:1749:U:OP1	71:ss:150:ARG:NH1	2.34	0.53
78:sz:66:THR:HG22	78:sz:67:LYS:H	1.73	0.53
1:lA:59:A:N3	1:lA:74:U:O2'	2.37	0.53
1:lA:804:G:H2'	1:lA:805:G:H8	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:IE:208:ASN:ND2	5:IE:289:CYS:SG	2.80	0.53
6:IF:184:VAL:HG11	6:IF:228:GLY:HA3	1.91	0.53
23:IW:100:ASN:HB2	23:IW:102:LEU:HD22	1.89	0.53
31:IE:87:ARG:HG2	31:IE:89:PHE:CZ	2.43	0.53
34:IH:65:LEU:O	34:IH:70:ARG:NH2	2.38	0.53
48:SD:16:THR:OG1	48:SD:32:ARG:O	2.22	0.53
55:SC:43:LEU:HD11	55:SC:58:ILE:HG12	1.91	0.53
55:SC:244:LYS:HG3	55:SC:245:TYR:CD1	2.44	0.53
57:SE:125:THR:HG22	57:SE:141:CYS:HB3	1.89	0.53
1:IA:1558:C:H4'	27:IA:182:PRO:HG2	1.91	0.53
1:IA:3150:A:H2'	1:IA:3151:A:C8	2.43	0.53
1:IA:3476:C:O2	1:IA:3476:C:O4'	2.27	0.53
5:IE:286:ARG:H	5:IE:324:MET:HB3	1.72	0.53
12:IL:31:ILE:HG21	12:IL:65:MET:HE2	1.91	0.53
14:IN:105:GLU:OE1	14:IN:105:GLU:N	2.41	0.53
53:SA:65:U:H2'	60:SH:257:ARG:HH21	1.74	0.53
53:SA:956:G:N1	53:SA:1003:A:O2'	2.35	0.53
55:SC:139:VAL:HG22	55:SC:140:PRO:HD2	1.91	0.53
59:SG:120:ASN:ND2	59:SG:183:SER:O	2.42	0.53
1:IA:700:A:H2'	1:IA:701:A:H8	1.74	0.52
1:IA:735:C:H2'	1:IA:736:G:O4'	2.10	0.52
2:IB:15:U:H5'	18:IR:2:VAL:HG13	1.90	0.52
4:ID:33:ASP:OD2	4:ID:67:ARG:NH2	2.42	0.52
5:IE:58:ARG:NH1	5:IE:353:GLU:OE2	2.41	0.52
13:IM:116:TYR:CE2	73:SU:13:MET:HE2	2.44	0.52
53:SA:43:U:OP2	53:SA:432:A:N6	2.40	0.52
77:SY:113:ILE:HB	77:SY:114:PRO:CD	2.32	0.52
1:IA:504:U:H2'	1:IA:505:A:C8	2.44	0.52
1:IA:582:U:H2'	1:IA:583:A:C8	2.45	0.52
1:IA:1105:U:H2'	1:IA:1106:U:C6	2.43	0.52
1:IA:1121:A:N1	1:IA:1168:C:O2'	2.41	0.52
3:IC:58:A:O2'	7:IG:262:THR:OG1	2.24	0.52
20:IT:106:LEU:HD13	20:IT:110:TYR:HD2	1.75	0.52
24:IX:60:MET:HE2	24:IX:129:TRP:CH2	2.44	0.52
58:SF:46:LEU:HD12	58:SF:59:VAL:HG13	1.89	0.52
59:SG:20:LEU:HD22	59:SG:111:ILE:HD11	1.91	0.52
3:IC:75:G:N1	3:IC:99:U:H5	2.04	0.52
12:IL:191:ILE:HD11	12:IL:200:ALA:HB2	1.92	0.52
28:IB:23:ALA:HB1	28:IB:43:VAL:HB	1.91	0.52
53:SA:623:U:OP2	53:SA:949:C:N4	2.36	0.52
53:SA:1115:C:N4	53:SA:1116:U:O4	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:sb:45:GLU:OE2	54:sb:46:ARG:N	2.43	0.52
78:sz:18:ASN:ND2	78:sz:21:LEU:HB2	2.24	0.52
1:lA:1633:G:H1'	1:lA:2044:C:H5''	1.91	0.52
1:lA:3163:G:O2'	5:lE:14:LEU:O	2.25	0.52
6:lF:47:ASN:HA	6:lF:112:GLN:HG3	1.91	0.52
56:sd:10:LEU:HD12	56:sd:90:ARG:HD2	1.90	0.52
1:lA:1476:G:H2'	1:lA:1476:G:N3	2.24	0.52
1:lA:2033:C:OP1	25:IY:67:GLN:NE2	2.43	0.52
3:lC:54:U:H4'	13:lM:152:HIS:HB2	1.91	0.52
7:lG:201:ALA:HB2	7:lG:232:LEU:HD12	1.90	0.52
14:lN:163:ILE:HD12	14:lN:164:LYS:N	2.25	0.52
35:li:48:THR:O	35:li:52:THR:OG1	2.23	0.52
53:sa:781:G:H4'	53:sa:782:A:H4'	1.91	0.52
53:sa:1196:A:H2'	53:sa:1197:G:H8	1.74	0.52
60:sh:282:LYS:O	60:sh:287:GLU:N	2.31	0.52
68:sp:125:GLU:HG2	68:sp:127:VAL:HG13	1.90	0.52
1:lA:725:A:N6	9:lI:59:ILE:HG13	2.24	0.52
1:lA:2303:U:H2'	1:lA:2304:A:C8	2.44	0.52
3:lC:26:U:O2	3:lC:52:G:N2	2.36	0.52
60:sh:306:ILE:HD11	60:sh:310:TYR:CZ	2.44	0.52
75:sw:67:LYS:HE3	75:sw:78:ASP:HB3	1.90	0.52
1:lA:1112:G:O2'	1:lA:1172:G:O6	2.23	0.52
12:lL:110:ARG:O	12:lL:113:THR:OG1	2.28	0.52
51:sH:27:C:H2'	51:sH:28:G:H8	1.74	0.52
53:sa:1745:U:H2'	53:sa:1746:C:C6	2.45	0.52
59:sg:16:PHE:CE2	59:sg:18:PRO:HG3	2.44	0.52
1:lA:1342:U:H2'	1:lA:1343:A:H4'	1.91	0.52
1:lA:1502:A:N7	19:lS:19:ARG:NH2	2.57	0.52
1:lA:3302:U:H2'	1:lA:3303:A:H8	1.75	0.52
3:lC:17:G:H1	3:lC:59:G:H1	1.58	0.52
6:lF:290:ASP:OD1	6:lF:292:LYS:N	2.41	0.52
51:sH:28:G:H2'	51:sH:29:G:H8	1.73	0.52
53:sa:1331:C:N3	53:sa:1344:G:N2	2.58	0.52
1:lA:43:C:OP2	1:lA:44:A:O2'	2.20	0.52
1:lA:1117:G:N3	1:lA:1120:A:N6	2.58	0.52
1:lA:2178:A:O2'	1:lA:2179:U:H6	1.92	0.52
1:lA:3476:C:H41	1:lA:3478:U:C1'	2.23	0.52
17:lQ:114:ARG:NH1	17:lQ:151:ILE:O	2.43	0.52
38:ll:64:MET:HE3	38:ll:67:LEU:HD23	1.92	0.52
53:sa:390:U:O2'	60:sh:186:ASN:OD1	2.27	0.52
53:sa:839:A:C8	61:si:119:PRO:HA	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:sc:51:LYS:HB3	55:sc:245:TYR:CE2	2.45	0.52
74:sv:126:GLU:OE1	74:sv:126:GLU:N	2.38	0.52
77:sy:85:ARG:HG3	77:sy:86:ASP:H	1.74	0.52
3:lc:17:G:H22	3:lc:59:G:N2	2.08	0.52
6:lf:407:GLN:O	6:lf:411:MET:HG2	2.10	0.52
46:sb:79:ILE:HD11	53:sa:1942:U:H5'	1.91	0.52
55:sc:100:LEU:HD13	55:sc:123:VAL:HG22	1.91	0.52
55:sc:161:THR:O	55:sc:222:GLN:NE2	2.43	0.52
69:sq:80:ARG:NH1	69:sq:96:TYR:O	2.43	0.52
72:st:58:MET:HA	72:st:61:ILE:HB	1.92	0.52
74:sv:119:SER:O	74:sv:119:SER:OG	2.20	0.52
1:la:1239:U:H5''	29:lc:22:ILE:HD12	1.92	0.51
1:la:2591:U:H2'	1:la:2592:U:H6	1.74	0.51
4:ld:39:SER:OG	4:ld:40:THR:N	2.44	0.51
10:lj:67:ILE:HG12	10:lj:225:MET:HE2	1.92	0.51
14:ln:46:PRO:HA	14:ln:49:ILE:HB	1.91	0.51
16:lp:29:GLU:HG2	20:lt:68:VAL:HG21	1.92	0.51
53:sa:443:U:H2'	53:sa:444:U:C6	2.46	0.51
53:sa:783:A:H3'	53:sa:784:U:H4'	1.92	0.51
55:sc:139:VAL:HG21	55:sc:221:ARG:HG3	1.91	0.51
1:la:790:A:H2'	1:la:791:A:H8	1.75	0.51
1:la:2331:A:N1	53:sa:1810:C:O2'	2.36	0.51
1:la:2357:A:H8	1:la:3117:U:H1'	1.74	0.51
1:la:2589:C:OP2	1:la:2656:G:N2	2.44	0.51
1:la:2640:A:OP2	28:lb:55:ARG:NH1	2.43	0.51
1:la:2745:C:N4	13:lm:22:SER:OG	2.43	0.51
23:lw:28:PHE:HE2	23:lw:84:LEU:HB2	1.75	0.51
53:sa:1173:A:O2'	53:sa:1802:C:OP2	2.28	0.51
58:sf:190:VAL:HG23	58:sf:241:GLY:HA3	1.92	0.51
1:la:948:C:O2'	1:la:949:G:N7	2.43	0.51
1:la:3466:U:O2'	1:la:3467:U:OP1	2.24	0.51
1:la:487:A:H2'	1:la:488:A:C8	2.44	0.51
1:la:663:G:OP2	16:lp:72:THR:OG1	2.17	0.51
1:la:739:A:H2'	1:la:740:A:H8	1.75	0.51
1:la:1370:G:H2'	1:la:1371:U:C6	2.46	0.51
1:la:1512:G:OP2	6:lf:191:ARG:NH1	2.39	0.51
1:la:3104:G:H2'	1:la:3105:U:C6	2.45	0.51
16:lp:12:VAL:O	16:lp:60:THR:OG1	2.22	0.51
27:la:2:LYS:HD3	27:la:7:VAL:HG23	1.92	0.51
31:le:13:GLY:O	31:le:16:SER:N	2.43	0.51
51:sH:26:A:N1	51:sH:44:G:N2	2.52	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:sa:1868:A:H4'	60:sh:178:ASN:HD21	1.75	0.51
77:sy:58:LYS:H	77:sy:113:ILE:HG21	1.74	0.51
1:lA:17:A:H2	2:lB:137:A:H61	1.57	0.51
1:lA:566:U:H2'	1:lA:567:U:C6	2.46	0.51
1:lA:700:A:H5''	1:lA:745:A:N6	2.25	0.51
45:sA:80:THR:HG22	45:sA:83:LEU:HB2	1.92	0.51
53:sa:1690:A:O2'	53:sa:1691:A:H8	1.93	0.51
75:sw:91:MET:HB3	75:sw:93:THR:HG23	1.93	0.51
78:sz:24:LYS:O	78:sz:79:ILE:N	2.42	0.51
1:lA:1744:A:H2'	1:lA:1745:A:H8	1.74	0.51
1:lA:2505:A:H2'	1:lA:2506:U:C6	2.46	0.51
13:lM:151:ASP:N	13:lM:151:ASP:OD1	2.42	0.51
31:le:103:ASP:HB2	31:le:106:LYS:HD2	1.91	0.51
50:sG:94:LEU:HB3	50:sG:104:ARG:HB2	1.92	0.51
50:sG:159:VAL:O	50:sG:160:ARG:HD3	2.11	0.51
53:sa:107:A:H2'	53:sa:108:G:C8	2.46	0.51
56:sd:88:ILE:HD11	56:sd:98:ILE:HG21	1.92	0.51
72:st:27:ASP:OD2	72:st:30:THR:OG1	2.22	0.51
1:lA:14:G:OP1	35:li:73:ARG:NH2	2.41	0.51
1:lA:97:A:H2'	1:lA:98:A:O4'	2.11	0.51
1:lA:926:A:N1	1:lA:2487:U:O2'	2.41	0.51
1:lA:1461:G:H2'	1:lA:1462:A:H8	1.75	0.51
27:la:56:LYS:HD2	27:la:65:ALA:HB2	1.93	0.51
53:sa:1596:U:O2'	53:sa:1660:C:O2	2.23	0.51
60:sh:239:ARG:HA	60:sh:244:LEU:HB2	1.92	0.51
74:sv:35:VAL:HG13	74:sv:36:ASP:OD1	2.11	0.51
1:lA:324:A:H2'	1:lA:325:U:C6	2.46	0.51
1:lA:3139:G:H1'	2:lB:1:A:H2	1.75	0.51
7:lG:187:ASN:OD1	7:lG:187:ASN:N	2.43	0.51
45:sA:64:SER:O	45:sA:111:ARG:NH2	2.41	0.51
53:sa:301:U:O2	65:sm:68:ARG:NH2	2.41	0.51
53:sa:934:A:H2'	53:sa:935:C:C6	2.45	0.51
53:sa:936:U:OP1	53:sa:1097:C:O2'	2.26	0.51
53:sa:1245:C:H2'	53:sa:1246:A:C8	2.45	0.51
53:sa:1734:G:H4'	53:sa:1735:A:O5'	2.11	0.51
53:sa:1816:U:H2'	53:sa:1817:A:C8	2.45	0.51
70:sr:52:VAL:HG22	70:sr:61:ILE:HG12	1.92	0.51
1:lA:564:A:H4'	1:lA:565:U:O5'	2.10	0.51
1:lA:832:A:O2'	1:lA:833:U:OP1	2.26	0.51
1:lA:1090:A:H2'	1:lA:1091:A:C8	2.46	0.51
1:lA:1982:U:H2'	4:lD:50:HIS:CD2	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:3103:C:H2'	1:1A:3104:G:H8	1.74	0.51
1:1A:3474:U:H3	1:1A:3480:A:N6	2.09	0.51
8:1H:65:LEU:HD11	8:1H:79:PHE:HB2	1.93	0.51
50:sG:233:LEU:HD23	50:sG:233:LEU:H	1.76	0.51
64:sl:43:MET:HA	64:sl:46:LYS:HG2	1.93	0.51
1:1A:739:A:H2'	1:1A:740:A:C8	2.46	0.51
1:1A:1086:G:H2'	1:1A:1087:G:C8	2.45	0.51
1:1A:1200:A:H1'	7:1G:115:MET:HE1	1.93	0.51
14:1N:49:ILE:O	14:1N:232:ASP:HA	2.11	0.51
18:1R:18:ARG:NH2	18:1R:147:GLU:HG2	2.26	0.51
23:1W:86:LYS:HD2	23:1W:114:ASP:HA	1.93	0.51
28:1b:10:VAL:O	28:1b:83:THR:OG1	2.26	0.51
53:sa:1322:G:N2	53:sa:1325:A:OP2	2.38	0.51
57:se:68:VAL:HG13	68:sp:42:ILE:HG22	1.93	0.51
61:si:71:ARG:HD2	61:si:71:ARG:H	1.75	0.51
64:sl:87:PRO:HG2	64:sl:91:LYS:HD2	1.93	0.51
1:1A:699:A:H5''	1:1A:746:A:H62	1.75	0.50
1:1A:1649:U:O2'	1:1A:2429:G:O2'	2.27	0.50
2:1B:10:U:H2'	2:1B:11:U:H6	1.76	0.50
10:1J:37:THR:C	10:1J:39:TYR:H	2.19	0.50
13:1M:61:ARG:NH2	51:sH:56:C:O4'	2.45	0.50
24:1X:31:ASN:OD1	24:1X:31:ASN:N	2.44	0.50
30:1d:7:ARG:NH2	30:1d:9:SER:OG	2.44	0.50
50:sG:90:HIS:ND1	50:sG:110:GLU:O	2.44	0.50
50:sG:223:ALA:HB1	50:sG:225:TRP:NE1	2.26	0.50
53:sa:442:U:H2'	53:sa:443:U:O4'	2.11	0.50
53:sa:1126:G:H1'	70:sr:76:SER:OG	2.11	0.50
59:sg:52:PRO:HG2	59:sg:92:MET:HG2	1.93	0.50
1:1A:670:A:H2	6:1F:397:LEU:HD23	1.75	0.50
1:1A:1634:G:O6	41:1o:2:THR:N	2.44	0.50
3:1C:103:U:H2'	3:1C:104:G:C8	2.46	0.50
28:1b:46:VAL:HG13	28:1b:68:VAL:HG13	1.92	0.50
53:sa:150:G:N2	53:sa:153:U:OP2	2.33	0.50
53:sa:765:A:OP2	53:sa:781:G:N1	2.43	0.50
53:sa:780:U:H2'	53:sa:781:G:C8	2.46	0.50
53:sa:1442:A:H2'	53:sa:1443:U:C6	2.46	0.50
53:sa:1585:U:OP1	74:sv:40:THR:OG1	2.25	0.50
1:1A:222:A:H2'	1:1A:223:A:H8	1.76	0.50
1:1A:685:A:H5''	1:1A:1450:A:H61	1.76	0.50
1:1A:802:A:H2'	1:1A:803:U:C6	2.46	0.50
1:1A:2499:U:H2'	1:1A:2500:A:H8	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2978:C:H2'	1:1A:2979:C:O2	2.11	0.50
1:1A:3090:G:N3	5:1E:252:ALA:HB1	2.27	0.50
7:1G:164:LEU:HD21	7:1G:176:HIS:CD2	2.47	0.50
19:1S:36:ALA:HB1	19:1S:45:LYS:HG2	1.92	0.50
35:1I:79:LYS:O	35:1I:83:GLN:HG2	2.12	0.50
53:sa:442:U:OP1	58:sf:47:ARG:NH1	2.45	0.50
53:sa:841:U:O2'	53:sa:842:A:O4'	2.30	0.50
59:sg:177:ASP:HA	59:sg:180:VAL:HG22	1.92	0.50
61:si:43:GLU:OE1	61:si:43:GLU:N	2.45	0.50
63:sk:17:VAL:O	63:sk:23:ARG:NH1	2.32	0.50
74:sv:30:GLU:OE1	74:sv:30:GLU:N	2.44	0.50
1:1A:227:A:H2'	1:1A:228:A:H8	1.76	0.50
1:1A:2838:A:O2'	43:lq:69:LYS:NZ	2.43	0.50
3:1C:17:G:N2	3:1C:59:G:H22	2.09	0.50
25:1Y:6:ARG:HH21	25:1Y:8:THR:HG23	1.74	0.50
29:lc:6:ARG:HB3	29:lc:8:THR:HG22	1.94	0.50
53:sa:841:U:O2'	53:sa:842:A:O5'	2.30	0.50
53:sa:1835:U:H2'	53:sa:1836:G:O4'	2.12	0.50
61:si:69:PRO:HG2	61:si:72:MET:SD	2.51	0.50
62:sj:103:GLU:HG3	62:sj:202:LEU:HD23	1.93	0.50
1:1A:897:A:O2'	1:1A:899:A:N1	2.39	0.50
1:1A:1533:U:H2'	1:1A:1534:U:C6	2.47	0.50
4:1D:209:HIS:CD2	4:1D:210:PRO:HD2	2.46	0.50
31:le:98:ASP:N	31:le:98:ASP:OD1	2.44	0.50
33:lg:95:ALA:HB3	33:lg:120:VAL:HG22	1.93	0.50
53:sa:287:A:H2'	53:sa:288:A:C8	2.46	0.50
75:sw:24:ILE:HD13	75:sw:35:LEU:HD12	1.93	0.50
1:1A:1330:G:OP1	12:1L:157:TYR:OH	2.30	0.50
1:1A:1537:A:O2'	33:lg:66:ASN:OD1	2.30	0.50
1:1A:2841:A:H5''	1:1A:2842:U:H5''	1.92	0.50
1:1A:3139:G:H1'	2:1B:1:A:C2	2.46	0.50
1:1A:3204:C:O2	24:1X:89:ARG:NH1	2.35	0.50
3:1C:2:G:H2'	3:1C:3:G:H8	1.75	0.50
5:1E:67:LEU:HD22	5:1E:72:VAL:HG11	1.94	0.50
50:sG:96:ASP:OD1	50:sG:96:ASP:N	2.44	0.50
53:sa:866:G:OP1	57:se:216:LYS:NZ	2.45	0.50
55:sc:41:THR:OG1	55:sc:67:GLU:OE1	2.28	0.50
65:sm:56:LYS:HD3	65:sm:131:LEU:HB3	1.94	0.50
67:so:91:LEU:HD21	67:so:121:LYS:HB3	1.94	0.50
71:ss:35:CYS:SG	71:ss:36:LEU:N	2.84	0.50
78:sz:66:THR:HG23	78:sz:73:THR:HB	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:lA:1027:G:H4'	1:lA:1028:G:O5'	2.10	0.50
1:lA:2492:U:H2'	1:lA:2493:U:C6	2.46	0.50
1:lA:3008:U:O2'	1:lA:3009:C:OP1	2.22	0.50
2:lB:21:A:H2'	2:lB:22:G:C8	2.47	0.50
60:sh:181:TYR:OH	60:sh:188:GLU:OE2	2.29	0.50
1:lA:222:A:H2'	1:lA:223:A:C8	2.47	0.50
1:lA:1538:G:N2	1:lA:1541:A:OP2	2.42	0.50
1:lA:1912:A:H62	31:le:78:ASN:ND2	2.10	0.50
1:lA:3156:U:O2'	5:le:182:GLU:OE2	2.26	0.50
2:lB:1:A:H2'	2:lB:2:A:C8	2.47	0.50
4:lD:177:LYS:HA	39:lm:29:ILE:HD13	1.92	0.50
50:sG:4:GLY:N	50:sG:277:LYS:O	2.45	0.50
53:sa:1376:U:H2'	53:sa:1377:U:C6	2.47	0.50
53:sa:1667:U:OP1	74:sv:121:ARG:NH2	2.44	0.50
1:lA:550:A:H2'	1:lA:551:A:C8	2.47	0.50
1:lA:836:C:H2'	1:lA:837:A:C8	2.47	0.50
1:lA:1520:A:H4'	1:lA:1521:A:O5'	2.12	0.50
1:lA:2303:U:H2'	1:lA:2304:A:H8	1.77	0.50
12:IL:189:LYS:HA	12:IL:200:ALA:HB3	1.93	0.50
31:le:103:ASP:N	31:le:103:ASP:OD1	2.44	0.50
53:sa:585:A:H2'	53:sa:586:A:C8	2.47	0.50
60:sh:239:ARG:HH12	60:sh:246:GLN:HE21	1.60	0.50
1:lA:255:A:H4'	1:lA:257:A:N7	2.27	0.49
1:lA:700:A:H2'	1:lA:701:A:C8	2.47	0.49
1:lA:1157:A:H4'	7:lG:5:LYS:H	1.76	0.49
1:lA:2767:A:H2'	1:lA:2768:G:H8	1.77	0.49
6:lF:369:LEU:O	6:lF:373:VAL:HG22	2.12	0.49
8:lH:10:VAL:O	8:lH:21:TYR:OH	2.20	0.49
53:sa:1245:C:H5''	64:sl:51:LYS:NZ	2.26	0.49
59:sg:51:LEU:HD22	59:sg:92:MET:HE3	1.94	0.49
64:sl:30:LEU:HD23	64:sl:37:PRO:HD3	1.94	0.49
74:sv:19:TYR:CD1	74:sv:134:ILE:HD12	2.46	0.49
75:sw:40:LYS:HA	75:sw:50:VAL:HG11	1.93	0.49
1:lA:1358:G:OP2	1:lA:1359:U:O2'	2.29	0.49
27:la:54:GLU:HG3	27:la:106:LYS:HB3	1.93	0.49
47:sC:18:LYS:HE2	53:sa:1095:U:H4'	1.93	0.49
55:sc:47:VAL:HG21	55:sc:70:ILE:HG12	1.94	0.49
59:sg:158:MET:SD	59:sg:161:ARG:NH1	2.84	0.49
77:sy:20:TRP:CE3	77:sy:26:LYS:HG3	2.48	0.49
1:lA:208:U:H2'	1:lA:209:A:C8	2.47	0.49
1:lA:239:G:H2'	1:lA:240:A:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:lA:444:A:HO2'	1:lA:448:C:HO2'	1.51	0.49
1:lA:852:A:OP1	29:lc:137:LYS:NZ	2.41	0.49
1:lA:2445:G:H2'	1:lA:2446:G:C8	2.47	0.49
1:lA:3456:U:N3	1:lA:3496:A:H2	2.10	0.49
34:lh:71:THR:OG1	34:lh:72:VAL:N	2.46	0.49
49:sE:23:LYS:HB3	64:sl:60:TRP:CD2	2.48	0.49
53:sa:242:G:O2'	53:sa:243:U:OP1	2.24	0.49
54:sb:77:THR:O	54:sb:77:THR:OG1	2.29	0.49
72:st:28:PHE:CZ	72:st:32:LYS:HD3	2.47	0.49
1:lA:336:A:H5''	17:lQ:97:SER:HB3	1.94	0.49
1:lA:381:A:H2'	1:lA:382:A:C8	2.47	0.49
1:lA:761:A:H2'	1:lA:762:A:C8	2.48	0.49
1:lA:1177:A:H4'	1:lA:2708:A:C4	2.46	0.49
1:lA:1874:C:O2'	1:lA:1960:U:O2'	2.20	0.49
1:lA:3149:A:H2'	1:lA:3150:A:H8	1.77	0.49
1:lA:3312:U:H2'	1:lA:3313:U:C6	2.47	0.49
1:lA:3362:U:H2'	1:lA:3363:C:C6	2.47	0.49
8:lH:11:LYS:HD2	8:lH:29:GLU:HG2	1.93	0.49
17:lQ:14:LYS:O	17:lQ:23:ARG:NH2	2.45	0.49
53:sa:209:A:N6	53:sa:250:G:O6	2.45	0.49
53:sa:243:U:H4'	53:sa:244:U:OP2	2.12	0.49
62:sj:111:LEU:HD11	62:sj:115:LYS:HE3	1.94	0.49
1:lA:191:A:H2'	1:lA:192:A:C8	2.46	0.49
1:lA:462:A:H2'	1:lA:463:U:C6	2.48	0.49
1:lA:1107:G:H2'	1:lA:1108:A:C8	2.47	0.49
1:lA:1615:A:O2'	32:lf:95:GLN:OE1	2.30	0.49
1:lA:1846:A:H2'	1:lA:1847:A:H8	1.76	0.49
1:lA:1905:C:OP2	21:lU:103:ARG:NH1	2.46	0.49
1:lA:2865:A:O2'	1:lA:2866:C:OP1	2.30	0.49
1:lA:3478:U:H3'	1:lA:3478:U:O2	2.12	0.49
2:lB:8:U:H2'	2:lB:9:A:C8	2.47	0.49
3:lC:17:G:H22	3:lC:59:G:H22	1.60	0.49
13:lM:46:VAL:O	13:lM:67:CYS:HA	2.12	0.49
40:ln:8:PHE:CE1	40:ln:12:LEU:HD21	2.47	0.49
40:ln:31:ASN:OD1	40:ln:31:ASN:N	2.45	0.49
50:sG:207:SER:OG	50:sG:209:ASP:OD1	2.25	0.49
58:sf:69:LYS:NZ	58:sf:72:GLY:O	2.42	0.49
61:si:44:LEU:HD11	61:si:83:VAL:HG13	1.93	0.49
74:sv:31:ILE:HD11	74:sv:55:TYR:HE1	1.77	0.49
75:sw:81:GLN:OE1	75:sw:83:ARG:NH2	2.37	0.49
77:sy:49:VAL:HG13	77:sy:68:VAL:HB	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:327:U:O2'	1:1A:329:G:N7	2.41	0.49
1:1A:405:U:OP1	38:1L:11:ARG:NH2	2.45	0.49
1:1A:836:C:H2'	1:1A:837:A:H8	1.77	0.49
1:1A:1502:A:H3'	1:1A:1502:A:N3	2.28	0.49
1:1A:3268:A:OP1	11:1K:83:SER:OG	2.30	0.49
2:1B:90:A:H5'	27:1a:22:ASN:HD22	1.78	0.49
5:1E:232:ILE:HG13	5:1E:249:ARG:HB3	1.93	0.49
6:1F:11:ASP:OD1	27:1a:146:TYR:OH	2.30	0.49
28:1b:22:LYS:NZ	28:1b:135:THR:O	2.33	0.49
50:sG:229:ASN:N	50:sG:229:ASN:OD1	2.45	0.49
53:sa:78:G:OP2	60:sh:256:ARG:NH1	2.45	0.49
59:sg:32:ASP:OD1	59:sg:34:SER:OG	2.27	0.49
1:1A:474:A:H2'	1:1A:475:A:H8	1.77	0.49
1:1A:2101:G:O2'	1:1A:2410:U:O4	2.22	0.49
1:1A:2226:G:O2'	1:1A:2265:U:OP1	2.29	0.49
1:1A:3084:A:H8	1:1A:3084:A:OP2	1.95	0.49
3:1C:85:G:H1	3:1C:90:G:N2	2.09	0.49
12:1L:110:ARG:HD2	12:1L:111:LEU:H	1.78	0.49
14:1N:169:LYS:HZ1	14:1N:170:VAL:HG23	1.76	0.49
48:sD:19:LEU:HD11	48:sD:43:LEU:HD11	1.95	0.49
53:sa:1185:A:H2'	53:sa:1186:C:C6	2.46	0.49
58:sf:119:PHE:HD2	58:sf:159:LYS:HG3	1.77	0.49
73:su:34:ILE:HG22	73:su:36:GLY:H	1.78	0.49
76:sx:44:LEU:HD13	76:sx:45:PRO:HD2	1.94	0.49
1:1A:70:A:OP2	14:1N:103:SER:OG	2.24	0.49
1:1A:425:C:H2'	1:1A:426:U:H6	1.77	0.49
2:1B:141:G:H2'	2:1B:142:A:C8	2.48	0.49
14:1N:116:GLU:OE2	14:1N:120:ARG:NH2	2.30	0.49
16:1P:3:PHE:CD1	20:1T:172:LEU:HD11	2.47	0.49
56:sd:207:ASP:HB3	56:sd:208:PRO:HD3	1.95	0.49
63:sk:55:ILE:HG22	63:sk:76:LEU:HD22	1.93	0.49
68:sp:79:ARG:HD2	68:sp:83:LEU:HD13	1.94	0.49
71:ss:70:VAL:HG12	71:ss:123:LYS:HD2	1.94	0.49
77:sy:67:CYS:HA	77:sy:83:VAL:HG23	1.95	0.49
1:1A:312:A:OP2	37:1k:28:THR:OG1	2.22	0.49
1:1A:575:A:H2'	1:1A:576:A:O4'	2.13	0.49
1:1A:2236:A:H2'	1:1A:2237:A:C8	2.47	0.49
3:1C:79:G:C2	3:1C:95:A:H2	2.31	0.49
51:sH:15:G:H22	51:sH:48:C:N4	2.11	0.49
53:sa:67:A:OP1	60:sh:257:ARG:NH2	2.46	0.49
53:sa:554:U:O2'	53:sa:555:G:H8	1.96	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:sa:865:A:OP1	57:se:218:LYS:NZ	2.27	0.49
55:sc:208:THR:HG22	55:sc:211:ASN:H	1.77	0.49
65:sm:56:LYS:NZ	65:sm:131:LEU:O	2.43	0.49
70:sr:94:LEU:HD12	70:sr:100:GLY:HA3	1.95	0.49
1:lA:94:G:N7	14:lN:11:HIS:HE1	2.11	0.49
1:lA:796:U:H2'	1:lA:797:C:C6	2.48	0.49
1:lA:1524:A:O2'	1:lA:1552:A:N1	2.43	0.49
1:lA:2230:U:H2'	1:lA:2231:C:C6	2.48	0.49
1:lA:2308:A:H2'	1:lA:2309:A:C8	2.48	0.49
1:lA:3377:U:H5''	32:lf:13:LYS:HE2	1.94	0.49
1:lA:3497:U:H4'	1:lA:3498:U:H5'	1.94	0.49
2:lB:50:A:O2'	2:lB:53:G:N2	2.46	0.49
3:lC:14:G:H2'	3:lC:15:A:C8	2.45	0.49
23:lW:43:PRO:O	23:lW:47:VAL:HG23	2.13	0.49
38:ll:19:CYS:SG	38:ll:20:LYS:N	2.86	0.49
50:sG:272:LYS:HG2	50:sG:273:ASP:OD1	2.12	0.49
53:sa:327:U:H5''	62:sj:31:ARG:NH1	2.28	0.49
53:sa:1381:G:H2'	53:sa:1382:C:C6	2.48	0.49
1:lA:104:A:N6	14:lN:53:LYS:HE2	2.27	0.48
1:lA:231:U:H4'	27:la:123:SER:HB3	1.95	0.48
1:lA:774:U:H2'	1:lA:775:C:C6	2.48	0.48
1:lA:993:U:OP2	1:lA:2109:C:O2'	2.23	0.48
1:lA:1737:A:OP2	34:lh:11:HIS:ND1	2.37	0.48
1:lA:1816:A:N3	1:lA:1892:C:O2'	2.43	0.48
1:lA:2112:C:C2	1:lA:2113:A:C8	3.01	0.48
1:lA:3352:G:H4'	1:lA:3353:U:H5''	1.95	0.48
50:sG:216:ALA:HB2	50:sG:222:ILE:HG23	1.96	0.48
53:sa:389:U:H2'	53:sa:390:U:C6	2.48	0.48
53:sa:1282:U:O2'	64:sl:1:MET:O	2.27	0.48
1:lA:1306:A:H2'	1:lA:1307:G:H8	1.78	0.48
1:lA:1535:A:H2'	1:lA:1536:A:H8	1.78	0.48
1:lA:2432:A:H61	1:lA:3126:C:H5	1.57	0.48
1:lA:2482:C:H2'	1:lA:2483:C:H6	1.78	0.48
8:lH:79:PHE:HA	8:lH:91:VAL:HG12	1.93	0.48
21:lU:92:LYS:O	21:lU:96:ILE:HG13	2.13	0.48
53:sa:563:C:OP1	77:sy:85:ARG:HA	2.13	0.48
61:si:163:VAL:HA	61:si:198:PRO:HD3	1.95	0.48
61:si:172:ASN:H	61:si:175:LYS:HG3	1.79	0.48
70:sr:36:GLU:HB2	70:sr:110:ILE:HD12	1.94	0.48
1:lA:2098:A:H61	1:lA:2415:C:N4	2.12	0.48
1:lA:2745:C:OP2	1:lA:2746:A:O2'	2.24	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2899:G:H5'	1:1A:2900:G:OP2	2.13	0.48
4:1D:161:ASN:OD1	4:1D:161:ASN:N	2.45	0.48
13:1M:109:HIS:CE1	13:1M:123:TYR:H	2.31	0.48
40:1n:14:LEU:HD21	40:1n:38:CYS:SG	2.53	0.48
47:sC:40:LYS:NZ	47:sC:41:CYS:SG	2.86	0.48
1:1A:1356:C:H2'	1:1A:1357:G:C8	2.48	0.48
1:1A:2205:C:H2'	1:1A:2206:G:H8	1.77	0.48
50:sG:258:TYR:H	50:sG:272:LYS:HG3	1.79	0.48
53:sa:51:U:H2'	53:sa:52:G:H8	1.78	0.48
53:sa:762:A:OP1	63:sk:9:SER:OG	2.30	0.48
53:sa:1002:U:O4	53:sa:1003:A:N6	2.46	0.48
53:sa:1244:A:O2'	64:sl:47:GLY:HA2	2.12	0.48
53:sa:1297:U:O2'	53:sa:1300:A:OP2	2.24	0.48
65:sm:74:VAL:HG22	65:sm:83:ILE:HD12	1.95	0.48
1:1A:525:U:H2'	1:1A:526:A:C8	2.47	0.48
1:1A:862:G:C6	1:1A:880:A:C2	3.02	0.48
1:1A:926:A:H62	1:1A:1053:G:H1	1.61	0.48
1:1A:1095:A:H2	1:1A:1099:A:H2	1.60	0.48
1:1A:1524:A:H5''	33:lg:102:SER:HB3	1.93	0.48
1:1A:2660:U:H2'	1:1A:2661:U:C6	2.48	0.48
1:1A:2841:A:O2'	1:1A:2842:U:OP2	2.29	0.48
1:1A:2981:A:H2'	1:1A:2982:G:O4'	2.13	0.48
4:1D:142:ASP:N	4:1D:142:ASP:OD1	2.46	0.48
7:1G:130:GLU:HB3	7:1G:188:GLU:HG2	1.94	0.48
8:1H:45:LEU:HD11	8:1H:130:LYS:HD2	1.96	0.48
22:IV:75:MET:SD	22:IV:88:ARG:NH1	2.85	0.48
24:IX:51:ARG:HH21	24:IX:54:ARG:HH12	1.62	0.48
46:sB:44:ILE:O	68:sp:108:GLN:NE2	2.41	0.48
56:sd:133:VAL:HG11	56:sd:166:PHE:CG	2.48	0.48
58:sf:126:LYS:HE2	58:sf:138:VAL:HG21	1.94	0.48
63:sk:57:LYS:HB2	63:sk:57:LYS:HE3	1.60	0.48
1:1A:630:A:C4	1:1A:631:G:C8	3.01	0.48
1:1A:1207:C:H2'	1:1A:1208:U:O4'	2.13	0.48
1:1A:1509:A:H2'	1:1A:1510:A:C8	2.47	0.48
1:1A:1608:A:H2	1:1A:2083:A:N3	2.12	0.48
1:1A:1729:G:O2'	1:1A:1730:G:O4'	2.21	0.48
1:1A:2730:U:H2'	1:1A:2731:G:C8	2.47	0.48
1:1A:3477:U:O5'	1:1A:3477:U:C6	2.66	0.48
8:1H:120:SER:O	8:1H:121:LYS:HG2	2.14	0.48
53:sa:751:A:H2'	53:sa:752:A:O4'	2.13	0.48
53:sa:1443:U:H3	53:sa:1512:A:N6	2.11	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:sc:244:LYS:HE2	55:sc:245:TYR:CE1	2.49	0.48
55:sc:244:LYS:HE2	55:sc:245:TYR:HE1	1.78	0.48
57:se:210:ASP:OD1	57:se:211:ASN:N	2.45	0.48
1:lA:476:U:OP1	36:lj:66:ARG:NH1	2.46	0.48
1:lA:1513:A:OP1	6:lF:206:LYS:HE2	2.14	0.48
1:lA:1649:U:OP1	18:lR:127:ARG:NH2	2.46	0.48
1:lA:1841:G:H22	1:lA:1975:G:H22	1.61	0.48
3:lC:85:G:N2	3:lC:90:G:H22	2.11	0.48
17:lQ:138:PHE:HA	17:lQ:143:ARG:HH11	1.79	0.48
25:lY:38:GLU:O	25:lY:81:ARG:NH1	2.46	0.48
53:sa:327:U:OP1	62:sj:56:ARG:NH2	2.39	0.48
56:sd:49:SER:OG	56:sd:111:CYS:SG	2.64	0.48
58:sf:192:VAL:HG21	58:sf:230:THR:HG22	1.95	0.48
1:lA:22:A:H2'	1:lA:23:C:H6	1.78	0.48
3:lC:5:A:OP2	7:lG:22:ARG:NH2	2.46	0.48
33:lg:128:LYS:HD3	33:lg:128:LYS:HA	1.70	0.48
39:lm:16:THR:O	39:lm:16:THR:OG1	2.24	0.48
53:sa:287:A:H2'	53:sa:288:A:H8	1.79	0.48
66:sn:50:ILE:HD13	66:sn:76:ILE:HG21	1.94	0.48
1:lA:494:G:H4'	1:lA:495:A:OP1	2.14	0.48
1:lA:765:A:H2'	1:lA:766:U:C6	2.49	0.48
1:lA:880:A:H2'	1:lA:881:G:O4'	2.14	0.48
1:lA:1126:U:H2'	1:lA:1127:A:O4'	2.13	0.48
2:lB:85:U:H3'	2:lB:86:G:H5'	1.96	0.48
6:lF:157:LYS:HE3	27:la:145:VAL:HG12	1.96	0.48
6:lF:358:MET:O	6:lF:362:LEU:HB2	2.13	0.48
12:lL:43:CYS:HA	12:lL:139:ARG:HH12	1.78	0.48
30:ld:36:ASN:HB3	30:ld:39:VAL:HB	1.96	0.48
50:sG:92:LEU:HD11	50:sG:113:VAL:HG11	1.95	0.48
50:sG:114:MET:HG2	50:sG:129:GLY:HA2	1.94	0.48
53:sa:540:U:H2'	53:sa:541:U:C6	2.48	0.48
53:sa:1274:U:H2'	53:sa:1275:U:C6	2.48	0.48
54:sb:92:ARG:HH21	54:sb:208:LEU:HD12	1.78	0.48
56:sd:149:GLU:CB	56:sd:171:MET:HE1	2.44	0.48
58:sf:183:GLY:HA3	58:sf:222:ASN:CG	2.38	0.48
1:lA:265:A:H1'	1:lA:266:A:H2	1.78	0.48
1:lA:1057:C:OP2	29:lc:26:ARG:NH1	2.46	0.48
1:lA:1757:C:H2'	1:lA:1758:U:C6	2.49	0.48
1:lA:2056:U:O2'	34:lh:12:SER:O	2.26	0.48
3:lC:11:C:OP2	3:lC:66:U:O2'	2.28	0.48
5:lE:84:MET:HB2	5:lE:205:ILE:HG13	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:IE:92:TYR:HB2	5:IE:159:VAL:HB	1.95	0.48
10:IJ:205:LYS:O	10:IJ:209:GLU:HG3	2.14	0.48
13:IM:63:ASP:OD1	13:IM:63:ASP:N	2.45	0.48
50:sG:169:LYS:HE3	50:sG:183:THR:HG23	1.96	0.48
53:sa:213:A:H2	53:sa:245:A:N1	2.11	0.48
53:sa:401:U:H2'	53:sa:402:A:C8	2.49	0.48
53:sa:1712:A:H2'	53:sa:1713:A:H8	1.77	0.48
55:sc:177:GLY:HA3	63:sk:53:ARG:NE	2.29	0.48
58:sf:137:ILE:HG23	58:sf:148:PRO:HG3	1.96	0.48
59:sg:20:LEU:HD12	59:sg:20:LEU:HA	1.70	0.48
71:ss:20:LYS:HB3	71:ss:111:PHE:CZ	2.49	0.48
73:su:27:VAL:HG23	73:su:55:LYS:O	2.13	0.48
1:lA:525:U:H2'	1:lA:526:A:H8	1.79	0.47
1:lA:2186:U:HO2'	1:lA:3485:U:HO2'	1.62	0.47
1:lA:3103:C:H2'	1:lA:3104:G:C8	2.48	0.47
6:lF:84:SER:OG	6:lF:87:ASN:OD1	2.28	0.47
14:lN:148:LYS:O	14:lN:152:ILE:HG12	2.14	0.47
24:lX:22:ASN:HB2	24:lX:53:PRO:HD2	1.96	0.47
31:le:17:LYS:HB3	31:le:104:ILE:HG23	1.96	0.47
33:lg:88:MET:SD	33:lg:88:MET:N	2.84	0.47
53:sa:1383:C:H2'	53:sa:1384:U:C6	2.48	0.47
53:sa:1709:A:H2'	53:sa:1710:U:O4'	2.14	0.47
59:sg:16:PHE:CD2	71:ss:69:ILE:HD12	2.49	0.47
67:so:5:TYR:HE2	67:so:121:LYS:HG3	1.79	0.47
69:sq:24:ILE:HD11	69:sq:32:PHE:CD1	2.48	0.47
75:sw:107:GLU:CD	75:sw:107:GLU:H	2.22	0.47
1:lA:2442:C:H2'	1:lA:2443:A:H8	1.79	0.47
1:lA:3309:U:H2'	1:lA:3310:C:C6	2.49	0.47
10:IJ:141:GLU:OE2	17:lQ:6:TYR:OH	2.32	0.47
48:sD:22:THR:OG1	48:sD:28:VAL:HB	2.14	0.47
53:sa:555:G:H2'	53:sa:556:G:C8	2.49	0.47
59:sg:169:LYS:HG2	59:sg:173:GLU:HG2	1.96	0.47
61:si:161:VAL:HG23	61:si:193:VAL:HG11	1.96	0.47
64:sl:7:ASP:O	64:sl:11:ILE:HD12	2.13	0.47
74:sv:62:ALA:HB1	74:sv:131:MET:HE1	1.95	0.47
1:lA:36:A:O2'	1:lA:1056:G:O6	2.29	0.47
1:lA:243:G:O2'	1:lA:264:G:N2	2.47	0.47
1:lA:589:A:OP1	8:lH:35:ARG:NH1	2.41	0.47
1:lA:858:A:O2'	1:lA:1185:A:N7	2.47	0.47
1:lA:1327:A:H2'	1:lA:1328:A:C8	2.49	0.47
1:lA:1473:G:O6	19:lS:37:ARG:NH2	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1887:A:H2'	1:1A:1888:A:C8	2.49	0.47
1:1A:2505:A:H2'	1:1A:2506:U:H6	1.80	0.47
1:1A:2939:G:N7	43:lq:61:LYS:NZ	2.62	0.47
1:1A:3177:U:H2'	1:1A:3178:A:H8	1.80	0.47
1:1A:3332:A:H1'	1:1A:3375:U:O2'	2.14	0.47
3:1C:66:U:H2'	3:1C:67:A:H8	1.79	0.47
7:1G:257:HIS:HE1	7:1G:259:LYS:HG3	1.78	0.47
53:sa:412:A:H4'	53:sa:413:G:O5'	2.14	0.47
53:sa:1536:G:H2'	53:sa:1537:U:C6	2.50	0.47
60:sh:290:LYS:HZ3	60:sh:290:LYS:H	1.62	0.47
62:sj:208:ARG:HH11	62:sj:211:GLN:HG3	1.80	0.47
78:sz:23:ARG:HB3	78:sz:80:TYR:CE1	2.50	0.47
1:1A:223:A:H2'	1:1A:224:U:C6	2.49	0.47
1:1A:1310:A:N3	20:1T:108:SER:OG	2.43	0.47
1:1A:1555:U:H2'	1:1A:1556:G:C8	2.50	0.47
1:1A:1892:C:H2'	1:1A:1893:A:C8	2.48	0.47
1:1A:2701:U:H2'	1:1A:2702:G:H8	1.79	0.47
1:1A:3448:G:H2'	1:1A:3449:A:C8	2.49	0.47
25:1Y:89:VAL:HG22	25:1Y:103:VAL:HG22	1.95	0.47
53:sa:69:G:N7	60:sh:266:LYS:NZ	2.43	0.47
53:sa:803:G:H2'	53:sa:804:C:C6	2.50	0.47
53:sa:1756:U:H2'	53:sa:1757:C:H6	1.79	0.47
75:sw:23:THR:HB	75:sw:113:GLU:OE1	2.15	0.47
1:1A:520:A:H2'	1:1A:521:A:C8	2.50	0.47
1:1A:713:G:H3'	1:1A:714:U:C5'	2.45	0.47
45:sA:97:ILE:HD12	45:sA:97:ILE:O	2.14	0.47
53:sa:455:A:H3'	53:sa:456:G:H8	1.79	0.47
53:sa:1668:G:O6	53:sa:1669:A:N6	2.48	0.47
56:sd:220:ASP:OD1	56:sd:221:VAL:N	2.48	0.47
58:sf:9:ARG:HE	58:sf:18:LEU:HB3	1.79	0.47
63:sk:142:ASP:OD1	63:sk:142:ASP:N	2.47	0.47
67:so:102:LEU:HD21	67:so:112:LYS:HG2	1.96	0.47
77:sy:103:PHE:CZ	77:sy:111:GLY:HA3	2.49	0.47
1:1A:355:A:H2'	1:1A:356:U:C6	2.50	0.47
1:1A:495:A:H1'	1:1A:496:A:C8	2.50	0.47
1:1A:505:A:H2'	1:1A:506:A:C8	2.49	0.47
1:1A:1073:A:H62	1:1A:1086:G:N2	2.13	0.47
1:1A:2262:U:OP2	4:1D:200:ARG:HD2	2.14	0.47
1:1A:2429:G:H5''	18:1R:86:LYS:HB2	1.96	0.47
1:1A:3243:C:OP1	5:1E:224:LYS:NZ	2.40	0.47
2:1B:2:A:H2'	2:1B:3:U:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:lC:85:G:H22	3:lC:90:G:H22	1.61	0.47
27:la:2:LYS:HE3	27:la:2:LYS:HB3	1.60	0.47
27:la:70:ALA:HB3	27:la:79:ASN:HB2	1.96	0.47
49:sE:23:LYS:HA	64:sl:60:TRP:HA	1.96	0.47
53:sa:442:U:O2'	58:sf:25:PHE:O	2.32	0.47
53:sa:851:A:H2'	53:sa:852:A:C8	2.49	0.47
53:sa:960:G:H4'	53:sa:1923:A:H4'	1.95	0.47
53:sa:1588:C:H2'	53:sa:1589:U:C6	2.50	0.47
59:sg:14:HIS:ND1	59:sg:15:THR:HG22	2.29	0.47
62:sj:81:VAL:HG22	62:sj:102:ILE:HG22	1.97	0.47
78:sz:13:ARG:O	78:sz:13:ARG:HG2	2.14	0.47
1:lA:489:U:H2'	1:lA:490:A:C8	2.50	0.47
1:lA:868:A:H2'	1:lA:869:G:C8	2.48	0.47
1:lA:1631:A:O2'	38:ll:12:HIS:O	2.30	0.47
1:lA:2440:G:H22	1:lA:2472:G:H1'	1.80	0.47
1:lA:2452:G:H2'	1:lA:2453:G:C8	2.50	0.47
1:lA:2766:A:H2'	1:lA:2767:A:C8	2.50	0.47
1:lA:2806:A:O2'	22:IV:68:ASN:ND2	2.46	0.47
1:lA:3170:A:H2'	1:lA:3171:A:C8	2.49	0.47
1:lA:3331:C:O2'	32:lf:6:THR:HA	2.14	0.47
1:lA:3469:A:H2'	1:lA:3470:G:O4'	2.15	0.47
3:lC:30:U:H2'	3:lC:31:G:C8	2.50	0.47
3:lC:76:U:H2'	3:lC:77:U:O4'	2.15	0.47
12:lL:51:HIS:ND1	12:lL:137:SER:OG	2.37	0.47
14:lN:197:LYS:O	14:lN:201:VAL:HG23	2.15	0.47
15:lO:202:PHE:CZ	16:lP:111:ASP:HB3	2.49	0.47
16:lP:124:ALA:O	16:lP:128:ILE:HG12	2.14	0.47
19:lS:155:LYS:HE3	19:lS:155:LYS:HB2	1.65	0.47
29:lc:147:LEU:HD13	37:lk:5:ILE:HG13	1.97	0.47
40:ln:7:GLU:N	40:ln:7:GLU:OE2	2.48	0.47
43:lq:72:CYS:HB3	43:lq:77:TYR:H	1.79	0.47
45:sA:44:LEU:HD12	53:sa:1701:U:H5'	1.96	0.47
50:sG:116:VAL:HG12	50:sG:127:SER:HB3	1.97	0.47
51:sH:28:G:H2'	51:sH:29:G:C8	2.49	0.47
51:sH:56:C:H2'	51:sH:57:G:C8	2.49	0.47
53:sa:65:U:C6	60:sh:268:PRO:HG3	2.49	0.47
53:sa:580:G:H2'	53:sa:581:C:C6	2.50	0.47
53:sa:864:C:H2'	53:sa:865:A:C8	2.49	0.47
53:sa:926:U:O2'	53:sa:927:U:H6	1.98	0.47
53:sa:1174:C:O2'	53:sa:1912:A:N1	2.41	0.47
56:sd:76:LYS:HE2	56:sd:78:ARG:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:sr:75:ILE:HG22	70:sr:76:SER:O	2.14	0.47
71:ss:63:VAL:O	71:ss:66:PRO:HD2	2.14	0.47
71:ss:113:ASP:C	71:ss:113:ASP:OD1	2.58	0.47
1:lA:13:C:OP2	25:lY:27:ARG:NH2	2.46	0.47
1:lA:1071:A:H4'	1:lA:1087:G:H22	1.79	0.47
1:lA:1467:U:H2'	1:lA:1468:A:C8	2.50	0.47
1:lA:1508:U:H2'	1:lA:1509:A:C8	2.50	0.47
1:lA:1581:G:O2'	1:lA:2431:G:O6	2.29	0.47
1:lA:1841:G:H22	1:lA:1975:G:N2	2.13	0.47
7:lG:201:ALA:HB1	7:lG:229:PRO:O	2.15	0.47
53:sa:1510:A:H2'	53:sa:1511:A:H8	1.79	0.47
54:sb:15:PRO:HB3	54:sb:60:TRP:CD2	2.50	0.47
67:so:37:MET:HE1	67:so:74:ILE:HD13	1.96	0.47
1:lA:1475:A:H1'	27:la:185:ARG:HH22	1.79	0.47
1:lA:1855:G:H2'	1:lA:1856:G:O4'	2.15	0.47
1:lA:2979:C:H2'	1:lA:2980:A:O4'	2.14	0.47
1:lA:3498:U:H5''	32:lf:56:ALA:HB1	1.97	0.47
5:lE:296:LYS:NZ	5:lE:303:GLU:HG3	2.30	0.47
21:lU:147:GLU:HG3	21:lU:150:LYS:HE3	1.97	0.47
24:lX:13:LYS:HB2	24:lX:128:LEU:HD21	1.97	0.47
24:lX:123:LYS:HG2	24:lX:139:ILE:HG22	1.95	0.47
50:sG:28:THR:HG21	50:sG:79:ASP:HA	1.97	0.47
50:sG:185:ASP:OD1	50:sG:185:ASP:N	2.45	0.47
53:sa:933:A:H2'	53:sa:934:A:C8	2.49	0.47
62:sj:107:ALA:HB3	62:sj:108:PRO:HD3	1.97	0.47
1:lA:996:C:O2'	1:lA:999:G:O2'	2.26	0.47
1:lA:1877:A:H2'	1:lA:1878:A:C8	2.50	0.47
1:lA:2732:A:H2'	1:lA:2733:A:C8	2.48	0.47
7:lG:156:THR:O	7:lG:156:THR:HG22	2.15	0.47
12:lL:43:CYS:O	12:lL:171:TRP:NE1	2.43	0.47
16:lP:92:THR:O	16:lP:96:LYS:HG3	2.15	0.47
24:lX:32:THR:HG21	24:lX:113:LYS:HG2	1.96	0.47
24:lX:82:ILE:HG13	24:lX:83:ARG:HG2	1.97	0.47
27:la:53:ASP:OD1	27:la:108:PHE:N	2.48	0.47
39:lm:92:SER:O	39:lm:92:SER:OG	2.33	0.47
42:lp:21:CYS:HB2	42:lp:28:LEU:HD11	1.96	0.47
51:sH:4:C:H2'	51:sH:5:U:C6	2.50	0.47
53:sa:773:A:N3	53:sa:773:A:H2'	2.30	0.47
56:sd:49:SER:OG	56:sd:49:SER:O	2.31	0.47
57:se:174:ILE:HG13	57:se:195:LEU:HD21	1.96	0.47
58:sf:159:LYS:N	58:sf:169:ASP:O	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:st:82:ASP:OD1	72:st:83:ASN:N	2.48	0.47
1:lA:353:G:H2'	1:lA:354:U:C6	2.50	0.46
1:lA:493:G:H21	1:lA:580:A:N6	2.06	0.46
1:lA:564:A:H1'	1:lA:565:U:OP2	2.15	0.46
1:lA:732:U:O2'	1:lA:733:C:O4'	2.32	0.46
1:lA:1219:A:H4'	1:lA:1220:A:H5'	1.97	0.46
1:lA:1921:A:H2'	1:lA:1922:U:O2	2.15	0.46
1:lA:2427:U:H2'	1:lA:2428:A:H8	1.80	0.46
1:lA:3134:U:OP1	5:lE:21:ARG:HG2	2.15	0.46
1:lA:3340:A:N7	20:lT:167:LYS:NZ	2.63	0.46
20:lT:132:ASN:HB3	20:lT:135:LEU:HB3	1.97	0.46
31:lE:29:LEU:HD11	31:lE:87:ARG:HE	1.80	0.46
37:lK:68:LYS:HD3	37:lK:74:HIS:HA	1.97	0.46
40:lN:13:LYS:O	40:lN:17:SER:OG	2.24	0.46
53:sA:148:G:H2'	53:sA:149:U:H6	1.81	0.46
53:sA:1172:G:H2'	53:sA:1173:A:H8	1.79	0.46
56:sD:149:GLU:HB3	56:sD:171:MET:HE1	1.97	0.46
61:sI:54:LYS:HD2	61:sI:62:LYS:HD3	1.97	0.46
62:sJ:207:SER:HB3	62:sJ:216:GLU:HB2	1.96	0.46
1:lA:723:U:O2'	1:lA:724:A:H5'	2.15	0.46
1:lA:908:A:H2'	1:lA:909:A:H8	1.75	0.46
1:lA:2207:A:C8	1:lA:2264:A:C8	3.03	0.46
1:lA:2240:C:OP1	4:lD:8:GLN:NE2	2.42	0.46
4:lD:180:LEU:HD22	39:lM:18:TYR:HB3	1.98	0.46
5:lE:224:LYS:HB2	5:lE:332:ILE:HG23	1.98	0.46
6:lF:402:LYS:HD3	6:lF:403:ARG:H	1.80	0.46
11:lK:13:ILE:HG12	11:lK:19:ILE:HD12	1.96	0.46
15:lO:77:PRO:O	15:lO:81:VAL:HG23	2.15	0.46
19:lS:70:MET:HE3	19:lS:136:ILE:HD11	1.97	0.46
23:lW:49:PHE:CE2	23:lW:96:TYR:HB2	2.51	0.46
36:lJ:89:ASN:OD1	36:lJ:89:ASN:N	2.48	0.46
47:sC:4:ILE:HG22	76:sX:61:ILE:HD11	1.97	0.46
50:sG:14:GLU:O	50:sG:60:PRO:HD3	2.16	0.46
50:sG:49:THR:HG21	50:sG:291:SER:HB2	1.97	0.46
50:sG:272:LYS:HB3	50:sG:277:LYS:HD2	1.96	0.46
60:sh:148:LYS:HD2	60:sh:148:LYS:HA	1.76	0.46
1:lA:1524:A:OP1	33:lG:102:SER:OG	2.24	0.46
1:lA:2100:G:O2'	24:lX:24:SER:OG	2.30	0.46
1:lA:2759:A:OP2	7:lG:15:LYS:NZ	2.49	0.46
23:lW:48:THR:O	23:lW:52:GLN:HG3	2.15	0.46
23:lW:52:GLN:NE2	23:lW:53:THR:HG23	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:sG:132:LYS:HG2	50:sG:154:GLU:C	2.41	0.46
50:sG:183:THR:O	50:sG:188:CYS:HA	2.14	0.46
53:sa:96:C:O2	53:sa:420:A:O2'	2.32	0.46
53:sa:1007:A:OP1	53:sa:1936:G:O2'	2.24	0.46
53:sa:1936:G:OP2	68:sp:141:ARG:NH2	2.48	0.46
1:lA:424:A:OP2	1:lA:438:G:H1'	2.15	0.46
1:lA:975:G:OP1	21:lU:92:LYS:NZ	2.40	0.46
1:lA:1105:U:H2'	1:lA:1106:U:H6	1.79	0.46
1:lA:1299:G:N2	15:lO:88:MET:SD	2.89	0.46
1:lA:2971:G:OP2	12:lL:7:ARG:NH1	2.45	0.46
1:lA:3467:U:O2'	1:lA:3468:U:OP1	2.28	0.46
3:lC:104:G:H2'	3:lC:105:A:C8	2.49	0.46
21:lU:44:LEU:HD22	21:lU:49:LEU:HD12	1.97	0.46
33:lg:50:THR:O	33:lg:50:THR:OG1	2.28	0.46
53:sa:115:U:O2'	53:sa:328:C:O2	2.32	0.46
53:sa:264:A:H2'	53:sa:265:G:C8	2.50	0.46
53:sa:1133:A:O2'	53:sa:1134:G:H5'	2.14	0.46
60:sh:301:LYS:HA	60:sh:304:ALA:HB3	1.96	0.46
60:sh:303:TYR:HA	60:sh:309:ARG:HH22	1.80	0.46
67:so:3:ARG:NH1	67:so:10:GLY:H	2.14	0.46
78:sz:60:VAL:O	78:sz:61:LEU:HD23	2.16	0.46
1:lA:537:U:C2	14:lN:200:GLN:HG2	2.51	0.46
1:lA:1356:C:H2'	1:lA:1357:G:H8	1.81	0.46
1:lA:1661:G:H5''	25:lY:48:THR:HG21	1.97	0.46
1:lA:2504:U:H2'	1:lA:2505:A:H8	1.81	0.46
1:lA:2688:G:H2'	12:lL:115:MET:O	2.16	0.46
1:lA:3187:A:H2'	1:lA:3188:C:H6	1.81	0.46
6:lF:341:ALA:O	6:lF:345:LYS:HG2	2.16	0.46
7:lG:257:HIS:CE1	7:lG:259:LYS:HG3	2.50	0.46
17:lQ:80:VAL:HB	17:lQ:82:ARG:HD2	1.97	0.46
25:lY:69:ALA:O	25:lY:99:LYS:NZ	2.38	0.46
50:sG:64:LEU:HD21	50:sG:100:MET:HG3	1.96	0.46
50:sG:89:ASP:OD1	50:sG:89:ASP:N	2.47	0.46
53:sa:16:G:H2'	53:sa:17:C:C6	2.50	0.46
53:sa:245:A:C8	58:sf:129:LEU:HB2	2.51	0.46
53:sa:1158:A:H2'	53:sa:1159:A:H8	1.81	0.46
53:sa:1195:G:C2	53:sa:1196:A:C8	3.04	0.46
53:sa:1338:A:H62	72:st:4:VAL:HG23	1.81	0.46
53:sa:1392:A:O2'	53:sa:1393:G:H5'	2.15	0.46
55:sc:181:VAL:O	55:sc:200:THR:OG1	2.28	0.46
58:sf:106:ARG:HG2	58:sf:107:PHE:N	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:sg:180:VAL:O	59:sg:183:SER:OG	2.23	0.46
1:lA:1902:A:H4'	1:lA:1915:A:H4'	1.96	0.46
1:lA:2289:A:H2'	1:lA:2290:A:C8	2.50	0.46
5:lE:77:THR:OG1	5:lE:327:GLY:O	2.33	0.46
7:lG:262:THR:OG1	7:lG:263:SER:N	2.49	0.46
9:lI:220:LEU:O	9:lI:223:ASN:ND2	2.48	0.46
50:sG:87:SER:HB3	50:sG:89:ASP:OD1	2.15	0.46
51:sH:18:G:N1	51:sH:55:U:O2'	2.48	0.46
53:sa:584:C:H2'	53:sa:585:A:C8	2.50	0.46
53:sa:1253:G:O2'	53:sa:1254:G:OP1	2.28	0.46
53:sa:1680:G:H1'	53:sa:1685:C:O2	2.16	0.46
57:se:156:SER:O	57:se:156:SER:OG	2.32	0.46
58:sf:112:LEU:HB3	58:sf:116:GLN:HG3	1.98	0.46
60:sh:305:ALA:O	60:sh:309:ARG:HG3	2.16	0.46
73:su:112:ILE:HG22	73:su:116:LYS:HD2	1.97	0.46
1:lA:960:G:O2'	21:lU:131:GLN:OE1	2.34	0.46
1:lA:1555:U:H2'	1:lA:1556:G:H8	1.78	0.46
1:lA:1664:G:OP2	1:lA:1752:U:O2'	2.33	0.46
1:lA:3397:C:OP2	1:lA:3398:U:O2'	2.31	0.46
6:lF:55:SER:HB3	6:lF:58:ALA:HB2	1.96	0.46
11:lK:19:ILE:HD11	11:lK:89:ILE:HD11	1.98	0.46
14:lN:74:THR:HG22	14:lN:99:ARG:HB3	1.98	0.46
28:lb:20:GLY:HA3	28:lb:139:PHE:CZ	2.50	0.46
50:sG:297:ILE:HG13	50:sG:309:TRP:HB2	1.98	0.46
53:sa:402:A:H2'	53:sa:403:C:H6	1.80	0.46
53:sa:867:A:N1	53:sa:906:A:H2	2.13	0.46
53:sa:1107:A:H2'	53:sa:1108:G:H8	1.81	0.46
53:sa:1393:G:C6	53:sa:1394:A:N7	2.84	0.46
53:sa:1693:A:H2'	53:sa:1694:A:C8	2.47	0.46
59:sg:83:LYS:HB2	59:sg:83:LYS:HE3	1.70	0.46
1:lA:542:U:H2'	1:lA:543:A:H8	1.80	0.46
1:lA:676:A:H5''	6:lF:351:LYS:HD3	1.96	0.46
1:lA:993:U:N3	1:lA:3121:U:OP1	2.37	0.46
1:lA:1103:U:H2'	1:lA:1104:A:H8	1.80	0.46
1:lA:1513:A:H5'	6:lF:206:LYS:HG2	1.96	0.46
1:lA:2295:A:H2'	1:lA:2296:U:C6	2.51	0.46
1:lA:2324:C:H2'	1:lA:2349:G:H5''	1.97	0.46
1:lA:2815:G:N2	1:lA:2818:A:OP2	2.41	0.46
1:lA:3218:U:H2'	1:lA:3219:A:H8	1.79	0.46
3:lC:45:U:H2'	3:lC:46:G:C8	2.49	0.46
6:lF:162:ILE:HD11	6:lF:171:LEU:HD13	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:IH:72:TYR:HD2	8:IH:103:MET:HE1	1.81	0.46
8:IH:204:PHE:HD1	16:IP:109:ASP:HB2	1.80	0.46
14:IN:72:GLY:HA3	14:IN:96:ASP:HB2	1.97	0.46
27:la:125:LYS:O	27:la:129:GLU:HG2	2.16	0.46
43:lq:2:VAL:O	43:lq:90:GLU:N	2.39	0.46
49:sE:34:TYR:OH	53:sa:1594:A:OP1	2.26	0.46
49:sE:45:GLU:OE2	53:sa:1540:G:N2	2.32	0.46
49:sE:56:ASP:OD1	49:sE:56:ASP:N	2.48	0.46
51:sH:53:G:H2'	51:sH:54:U:C6	2.51	0.46
53:sa:212:C:H2'	53:sa:213:A:O4'	2.16	0.46
53:sa:841:U:OP1	67:so:64:LYS:NZ	2.37	0.46
54:sb:33:THR:O	54:sb:46:ARG:NH1	2.40	0.46
78:sz:30:ILE:N	78:sz:73:THR:O	2.48	0.46
1:lA:1848:A:H2'	1:lA:1849:A:H8	1.81	0.46
1:lA:2632:A:O2'	28:lb:139:PHE:O	2.19	0.46
1:lA:3194:U:H2'	1:lA:3195:G:H8	1.81	0.46
1:lA:3287:U:H2'	1:lA:3288:U:C6	2.50	0.46
1:lA:3496:A:OP2	32:lf:108:ARG:NH2	2.49	0.46
8:IH:24:ASP:HA	8:IH:27:ILE:HB	1.97	0.46
13:lM:114:LEU:HD12	73:su:11:GLN:HG2	1.97	0.46
46:sB:13:LYS:HD3	46:sB:13:LYS:HA	1.51	0.46
49:sE:14:TYR:OH	53:sa:1719:G:O3'	2.33	0.46
53:sa:415:A:O2'	53:sa:416:A:H5'	2.16	0.46
53:sa:604:G:O2'	53:sa:607:G:O2'	2.24	0.46
53:sa:1887:A:H2'	53:sa:1888:U:C6	2.51	0.46
58:sf:255:LYS:HB2	58:sf:255:LYS:HE3	1.75	0.46
69:sq:55:LEU:HD23	69:sq:82:LYS:HG3	1.97	0.46
74:sv:117:ILE:HG23	74:sv:118:GLN:OE1	2.16	0.46
75:sw:51:LYS:HA	75:sw:51:LYS:HD2	1.75	0.46
1:lA:445:G:H5''	1:lA:448:C:H1'	1.96	0.46
1:lA:711:A:H2'	1:lA:712:G:O4'	2.16	0.46
1:lA:1844:U:H2'	1:lA:1845:G:H8	1.81	0.46
1:lA:2205:C:H2'	1:lA:2206:G:C8	2.51	0.46
1:lA:2897:A:HO2'	1:lA:2898:A:P	2.39	0.46
1:lA:3174:C:H2'	1:lA:3187:A:N6	2.30	0.46
3:lC:18:U:H3	3:lC:58:A:H61	1.63	0.46
35:li:85:THR:HG22	35:li:87:ALA:H	1.81	0.46
46:sB:2:THR:OG1	46:sB:3:SER:N	2.38	0.46
50:sG:114:MET:HE1	50:sG:130:ARG:CZ	2.46	0.46
53:sa:1595:G:H3'	53:sa:1682:A:H61	1.81	0.46
68:sp:92:MET:HE1	68:sp:107:ALA:HB1	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:sz:86:LEU:O	78:sz:86:LEU:HD13	2.16	0.46
1:lA:315:A:C5	17:lQ:12:ARG:HD3	2.50	0.45
1:lA:624:U:H2'	1:lA:625:A:O4'	2.17	0.45
1:lA:645:A:O2'	1:lA:646:U:H5''	2.16	0.45
1:lA:1629:G:C2	1:lA:1630:A:C8	3.04	0.45
1:lA:1738:G:C2	1:lA:1739:G:C8	3.04	0.45
1:lA:1886:A:H2'	1:lA:1887:A:C8	2.50	0.45
1:lA:1933:U:H2'	1:lA:1934:G:H8	1.80	0.45
1:lA:2250:C:OP1	4:lD:193:ARG:NH2	2.42	0.45
2:lB:74:A:OP2	27:la:51:LYS:HB2	2.17	0.45
3:lC:33:A:N1	3:lC:45:U:O2'	2.45	0.45
3:lC:97:C:OP2	20:lT:48:LYS:NZ	2.42	0.45
10:lJ:97:LEU:HA	10:lJ:100:ILE:HG22	1.97	0.45
13:lM:155:THR:HG22	13:lM:156:LYS:H	1.80	0.45
53:sa:72:C:H2'	53:sa:73:A:C8	2.50	0.45
53:sa:1281:A:OP1	64:sl:5:THR:OG1	2.22	0.45
57:se:195:LEU:HB3	57:se:196:PRO:HD3	1.98	0.45
57:se:200:VAL:O	57:se:204:SER:OG	2.26	0.45
58:sf:123:LYS:HB2	58:sf:224:PHE:CE2	2.52	0.45
58:sf:150:PRO:HB2	60:sh:314:LYS:HE3	1.97	0.45
61:si:150:LEU:HD23	61:si:150:LEU:HA	1.86	0.45
75:sw:107:GLU:OE1	75:sw:107:GLU:N	2.46	0.45
1:lA:428:U:O2'	18:lR:100:ASP:OD2	2.27	0.45
1:lA:528:A:H2'	1:lA:529:U:H6	1.81	0.45
1:lA:996:C:HO2'	1:lA:999:G:HO2'	1.57	0.45
1:lA:2383:G:O2'	1:lA:2386:U:OP2	2.33	0.45
1:lA:2647:U:H2'	1:lA:2648:U:C6	2.51	0.45
1:lA:2890:A:H2'	1:lA:2891:G:C8	2.51	0.45
3:lC:17:G:H1	3:lC:59:G:N2	2.12	0.45
20:lT:10:CYS:SG	20:lT:15:HIS:ND1	2.89	0.45
23:lW:67:GLU:HB2	23:lW:78:THR:HG23	1.98	0.45
27:la:37:GLU:OE1	27:la:37:GLU:N	2.49	0.45
53:sa:58:G:H4'	53:sa:448:A:H5'	1.98	0.45
53:sa:1850:C:H2'	53:sa:1851:U:C6	2.52	0.45
54:sb:148:ASN:ND2	55:sc:62:GLY:O	2.49	0.45
55:sc:142:ARG:HG2	55:sc:157:PRO:HG3	1.97	0.45
60:sh:219:GLU:OE2	60:sh:226:LEU:HD22	2.15	0.45
65:sm:151:LYS:HE2	65:sm:151:LYS:HB2	1.76	0.45
74:sv:61:ILE:O	74:sv:65:VAL:HG23	2.16	0.45
1:lA:463:U:O2'	1:lA:464:G:H5'	2.16	0.45
1:lA:598:A:H2'	1:lA:599:U:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:lA:1090:A:H2'	1:lA:1091:A:H8	1.80	0.45
1:lA:1811:A:C8	1:lA:1824:A:H2'	2.52	0.45
1:lA:2482:C:H2'	1:lA:2483:C:C6	2.51	0.45
2:lB:25:U:H4'	27:la:16:LYS:HB2	1.98	0.45
6:lF:357:LYS:O	6:lF:361:ILE:HG13	2.16	0.45
12:lL:75:ASN:ND2	12:lL:154:LEU:HD12	2.32	0.45
31:le:29:LEU:HD13	31:le:91:VAL:HG21	1.98	0.45
46:sB:43:ASN:HA	46:sB:66:LYS:HA	1.99	0.45
50:sG:23:ILE:HD11	50:sG:306:ILE:HG12	1.98	0.45
53:sa:1712:A:HO2'	53:sa:1713:A:P	2.39	0.45
54:sb:152:ILE:HG12	54:sb:166:ILE:HB	1.98	0.45
55:sc:155:THR:OG1	55:sc:197:ASP:O	2.23	0.45
61:si:154:LYS:HD3	61:si:154:LYS:HA	1.66	0.45
77:sy:14:GLN:O	77:sy:18:ASN:HB2	2.16	0.45
78:sz:14:ASN:OD1	78:sz:27:VAL:N	2.44	0.45
1:lA:612:A:H62	1:lA:715:A:H2'	1.82	0.45
1:lA:844:G:N2	1:lA:847:A:OP2	2.42	0.45
1:lA:1247:G:H1	3:lC:92:U:H5	1.64	0.45
1:lA:1482:U:H2'	1:lA:1483:U:C6	2.51	0.45
1:lA:1545:A:H4'	33:lg:122:ASN:HD21	1.81	0.45
1:lA:1569:A:H5''	1:lA:1570:U:O5'	2.17	0.45
1:lA:1675:A:H2'	1:lA:1676:A:C8	2.51	0.45
1:lA:2236:A:H2'	1:lA:2237:A:H8	1.80	0.45
23:lW:96:TYR:CE1	23:lW:100:ASN:ND2	2.84	0.45
31:le:40:ASP:HB3	31:le:42:LYS:HE2	1.99	0.45
43:lq:63:THR:O	43:lq:85:ARG:NH1	2.47	0.45
53:sa:12:U:H2'	53:sa:13:C:C6	2.51	0.45
53:sa:67:A:P	60:sh:257:ARG:HH22	2.39	0.45
53:sa:959:A:N3	53:sa:1922:U:O2'	2.49	0.45
53:sa:1196:A:O2'	53:sa:1736:A:N3	2.40	0.45
59:sg:61:LYS:HG3	59:sg:64:ARG:HH21	1.81	0.45
62:sj:106:PRO:HB2	62:sj:196:PHE:CE1	2.51	0.45
78:sz:56:VAL:HG12	78:sz:57:GLN:N	2.32	0.45
1:lA:2647:U:H2'	1:lA:2648:U:H6	1.82	0.45
1:lA:3343:A:OP1	20:lT:149:HIS:ND1	2.37	0.45
4:lD:230:PRO:HD2	4:lD:233:GLN:HG2	1.99	0.45
7:lG:5:LYS:HD2	7:lG:5:LYS:HA	1.72	0.45
13:lM:18:VAL:HG13	13:lM:70:THR:HG22	1.97	0.45
31:le:38:ILE:HG21	31:le:63:TYR:HB3	1.98	0.45
50:sG:106:PHE:CE2	50:sG:141:GLY:HA2	2.52	0.45
53:sa:775:G:C8	53:sa:776:U:C5	3.04	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:sa:788:C:N4	53:sa:789:A:H62	2.15	0.45
58:sf:197:GLU:H	58:sf:197:GLU:HG2	1.67	0.45
64:sl:82:PRO:HB2	64:sl:84:ASP:OD1	2.16	0.45
72:st:32:LYS:HD2	72:st:47:ARG:HH11	1.82	0.45
1:lA:510:A:N6	1:lA:561:G:O2'	2.45	0.45
1:lA:765:A:C2	36:lj:92:PRO:HG2	2.52	0.45
1:lA:909:A:H2'	1:lA:910:A:H8	1.81	0.45
1:lA:1188:A:H2'	1:lA:1189:U:C6	2.51	0.45
1:lA:1627:G:H21	34:lh:6:THR:HG22	1.81	0.45
1:lA:3201:C:OP1	5:lE:224:LYS:N	2.44	0.45
1:lA:3478:U:C5	62:sj:200:ARG:NH2	2.78	0.45
3:lC:44:C:H2'	3:lC:45:U:C6	2.52	0.45
3:lC:94:U:H2'	3:lC:95:A:H8	1.81	0.45
8:lH:83:CYS:SG	8:lH:86:SER:OG	2.72	0.45
21:lU:28:GLU:OE1	21:lU:28:GLU:HA	2.17	0.45
33:lg:64:THR:HA	33:lg:67:MET:HE3	1.99	0.45
50:sG:176:ASP:HB2	50:sG:178:GLN:HB2	1.99	0.45
50:sG:212:ILE:HG13	50:sG:251:PHE:CZ	2.52	0.45
53:sa:777:U:C4	53:sa:779:A:H1'	2.51	0.45
55:sc:159:LYS:HE3	70:sr:95:PRO:HA	1.99	0.45
1:lA:76:U:H2'	1:lA:77:C:H6	1.81	0.45
1:lA:919:G:H22	6:lF:103:SER:HA	1.82	0.45
1:lA:1154:A:H3'	1:lA:1155:A:C8	2.49	0.45
1:lA:1414:A:H2'	1:lA:1415:A:H8	1.82	0.45
1:lA:3351:U:O4	16:lP:101:ARG:NE	2.41	0.45
15:lO:36:LEU:HB2	15:lO:39:CYS:SG	2.57	0.45
53:sa:60:A:C6	53:sa:265:G:H1'	2.52	0.45
53:sa:783:A:H2'	53:sa:785:A:OP1	2.16	0.45
53:sa:1393:G:N2	53:sa:1394:A:H1'	2.32	0.45
53:sa:1441:C:C2	53:sa:1442:A:C8	3.04	0.45
60:sh:251:LYS:HA	60:sh:254:VAL:HG23	1.99	0.45
1:lA:280:U:H2'	1:lA:281:A:H8	1.81	0.45
1:lA:301:A:H2'	1:lA:302:U:C6	2.52	0.45
1:lA:1035:G:H5'	1:lA:1036:A:OP1	2.16	0.45
1:lA:1205:C:H2'	1:lA:1206:A:H8	1.81	0.45
1:lA:1208:U:H4'	30:ld:43:THR:HG23	1.99	0.45
1:lA:1360:G:N2	1:lA:1369:A:N7	2.64	0.45
1:lA:3148:C:H2'	1:lA:3149:A:H8	1.82	0.45
8:lH:197:ASP:HB3	8:lH:202:LEU:HD21	1.97	0.45
14:lN:143:GLU:O	14:lN:146:THR:OG1	2.32	0.45
18:lR:127:ARG:HB2	18:lR:139:PHE:HB3	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:lk:51:MET:HE2	37:lk:84:ILE:HG13	1.98	0.45
42:lp:4:GLU:OE1	42:lp:4:GLU:N	2.44	0.45
53:sa:155:A:H2'	53:sa:156:U:O4'	2.17	0.45
53:sa:1731:U:OP1	73:su:40:ARG:HD3	2.17	0.45
71:ss:109:GLN:HG3	71:ss:117:LYS:NZ	2.32	0.45
1:lA:1219:A:H4'	1:lA:1220:A:OP2	2.17	0.45
1:lA:1823:C:H2'	1:lA:1824:A:C4	2.52	0.45
1:lA:2495:A:H2'	1:lA:2496:C:C6	2.52	0.45
1:lA:3435:G:H2'	1:lA:3436:A:H5''	1.99	0.45
5:lE:48:GLY:HA3	5:lE:81:THR:HG22	1.99	0.45
11:lK:171:ASN:HD22	11:lK:185:VAL:HG23	1.82	0.45
17:lQ:119:TYR:OH	17:lQ:131:GLU:OE1	2.22	0.45
53:sa:383:G:OP2	53:sa:418:G:O2'	2.34	0.45
53:sa:1096:U:H2'	53:sa:1097:C:H6	1.82	0.45
53:sa:1695:C:O2'	53:sa:1696:G:H5'	2.17	0.45
53:sa:1758:G:H2'	53:sa:1759:A:H8	1.82	0.45
53:sa:1774:A:H2'	53:sa:1775:U:H6	1.82	0.45
53:sa:1907:G:H1'	53:sa:1928:A:H2	1.82	0.45
56:sd:205:ASP:O	56:sd:208:PRO:HD2	2.17	0.45
1:lA:71:U:O5'	14:lN:56:VAL:HB	2.17	0.45
1:lA:1290:A:OP1	36:lj:85:ARG:NH2	2.38	0.45
1:lA:2034:G:O2'	41:lo:3:GLY:O	2.33	0.45
1:lA:2485:G:H3'	1:lA:2486:U:H4'	1.99	0.45
1:lA:2844:U:H2'	1:lA:2845:U:C6	2.52	0.45
1:lA:2898:A:H2'	1:lA:2899:G:H4'	1.98	0.45
2:lB:32:C:OP1	14:lN:32:ARG:NH2	2.49	0.45
10:lJ:219:TYR:HD1	10:lJ:225:MET:HE1	1.80	0.45
48:sD:23:GLY:O	48:sD:25:ARG:N	2.50	0.45
48:sD:49:PRO:HB3	53:sa:1781:C:P	2.57	0.45
53:sa:444:U:H2'	53:sa:445:C:H6	1.82	0.45
53:sa:1376:U:H2'	53:sa:1377:U:H6	1.82	0.45
53:sa:1389:G:H2'	53:sa:1390:A:H8	1.82	0.45
56:sd:86:LEU:HD12	56:sd:86:LEU:HA	1.85	0.45
60:sh:166:THR:OG1	60:sh:167:ASN:N	2.50	0.45
65:sm:46:GLU:HG2	65:sm:113:ALA:HA	1.98	0.45
68:sp:23:PHE:HB3	68:sp:42:ILE:HD11	1.98	0.45
75:sw:26:SER:HB3	75:sw:110:VAL:HG13	1.99	0.45
1:lA:221:U:H2'	1:lA:222:A:C8	2.51	0.44
1:lA:492:U:H2'	1:lA:493:G:C5	2.52	0.44
1:lA:761:A:H2'	1:lA:762:A:H8	1.82	0.44
1:lA:1869:U:H2'	1:lA:1870:U:C6	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2230:U:H2'	1:1A:2231:C:H6	1.81	0.44
1:1A:2432:A:H2	18:1R:131:ARG:HH22	1.65	0.44
1:1A:3447:A:H2'	1:1A:3448:G:O4'	2.17	0.44
2:1B:39:A:OP1	2:1B:40:U:O2'	2.26	0.44
3:1C:32:A:H2'	3:1C:33:A:C8	2.53	0.44
5:1E:153:ILE:O	5:1E:157:CYS:HB2	2.16	0.44
12:1L:103:LEU:HB2	12:1L:113:THR:HG22	1.99	0.44
20:1T:7:THR:HA	20:1T:21:PHE:O	2.17	0.44
34:1h:15:THR:HG22	34:1h:16:LYS:N	2.32	0.44
46:sB:94:ASN:HD21	46:sB:96:LEU:HB2	1.81	0.44
47:sC:22:MET:HA	47:sC:27:PRO:HB3	1.99	0.44
48:sD:60:GLU:OE2	48:sD:61:ALA:N	2.51	0.44
53:sa:748:A:C5	53:sa:749:A:C8	3.04	0.44
53:sa:898:G:H2'	53:sa:899:C:C6	2.53	0.44
53:sa:1170:U:H2'	53:sa:1171:U:C6	2.53	0.44
58:sf:104:LYS:HD2	58:sf:106:ARG:HH12	1.82	0.44
60:sh:219:GLU:HG2	60:sh:226:LEU:HB3	1.99	0.44
1:1A:474:A:H2'	1:1A:475:A:C8	2.52	0.44
4:1D:242:ARG:NH2	4:1D:246:ILE:HG12	2.32	0.44
5:1E:41:PRO:HA	5:1E:187:GLY:HA3	1.98	0.44
6:1F:121:ARG:HG2	6:1F:276:LYS:HD3	2.00	0.44
7:1G:167:MET:HE2	7:1G:167:MET:HB3	1.80	0.44
11:1K:17:VAL:HG11	11:1K:89:ILE:HG12	1.99	0.44
11:1K:147:LYS:HD2	11:1K:147:LYS:HA	1.75	0.44
50:sG:154:GLU:HG2	50:sG:176:ASP:CG	2.43	0.44
51:sH:15:G:H22	51:sH:48:C:H42	1.63	0.44
53:sa:26:U:H2'	53:sa:27:A:H8	1.81	0.44
53:sa:1689:A:N6	53:sa:1774:A:O4'	2.51	0.44
53:sa:1778:A:H2'	53:sa:1779:U:O4'	2.17	0.44
57:se:87:LYS:HB2	57:se:87:LYS:HE3	1.80	0.44
60:sh:283:ALA:HA	60:sh:287:GLU:HB3	1.99	0.44
70:sr:94:LEU:HD21	70:sr:102:LEU:HG	1.99	0.44
1:1A:440:G:N1	1:1A:443:A:OP2	2.46	0.44
1:1A:1745:A:H2'	1:1A:1746:G:C8	2.52	0.44
1:1A:2746:A:H5'	1:1A:2747:G:C8	2.52	0.44
1:1A:3024:C:H2'	1:1A:3025:U:C6	2.52	0.44
5:1E:35:ASP:OD2	5:1E:193:LYS:NZ	2.51	0.44
11:1K:71:ASN:OD1	11:1K:71:ASN:N	2.50	0.44
12:1L:75:ASN:HD21	12:1L:154:LEU:HD12	1.83	0.44
15:1O:127:ILE:HD12	20:1T:170:THR:HG23	1.98	0.44
16:1P:41:PRO:HB3	16:1P:77:CYS:SG	2.57	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:sC:10:ASN:OD1	47:sC:10:ASN:N	2.51	0.44
53:sa:5:U:O2'	53:sa:547:G:H4'	2.18	0.44
53:sa:579:A:H2'	53:sa:580:G:H8	1.81	0.44
53:sa:767:A:O2'	53:sa:768:A:H8	2.01	0.44
53:sa:774:U:H4'	53:sa:775:G:H2'	1.98	0.44
53:sa:1285:A:H2'	53:sa:1286:U:O4'	2.17	0.44
60:sh:277:ARG:O	60:sh:281:HIS:ND1	2.50	0.44
62:sj:48:CYS:SG	62:sj:54:LYS:HB2	2.58	0.44
71:ss:19:LEU:HD23	71:ss:19:LEU:HA	1.84	0.44
74:sv:129:LYS:HB2	74:sv:129:LYS:HE2	1.79	0.44
75:sw:22:ILE:HB	75:sw:89:LEU:HB2	2.00	0.44
75:sw:54:VAL:HB	75:sw:88:VAL:HB	1.99	0.44
1:lA:619:A:H2'	1:lA:619:A:N3	2.32	0.44
1:lA:851:A:OP2	29:lc:113:LEU:HB3	2.17	0.44
1:lA:1495:A:H2'	1:lA:1496:A:H8	1.82	0.44
1:lA:2137:G:H2'	1:lA:2138:A:H8	1.81	0.44
1:lA:2433:A:H2'	1:lA:2434:A:H8	1.82	0.44
1:lA:2485:G:O2'	1:lA:2487:U:H5''	2.17	0.44
1:lA:2661:U:H2'	1:lA:2662:G:O4'	2.17	0.44
1:lA:3312:U:H2'	1:lA:3313:U:H6	1.82	0.44
2:lB:31:C:H2'	2:lB:32:C:H6	1.82	0.44
3:lC:28:U:C2	3:lC:29:G:C2	3.06	0.44
3:lC:82:U:O2'	3:lC:83:G:H5''	2.17	0.44
3:lC:106:U:C2	3:lC:107:A:C8	3.06	0.44
12:lL:30:ARG:HD2	12:lL:30:ARG:HA	1.84	0.44
13:lM:18:VAL:HG22	13:lM:70:THR:HG22	1.98	0.44
16:lP:66:LYS:HE3	16:lP:66:LYS:HB2	1.82	0.44
16:lP:107:MET:HG2	16:lP:111:ASP:HB2	1.98	0.44
53:sa:1593:G:O6	53:sa:1594:A:N6	2.50	0.44
63:sk:55:ILE:O	63:sk:59:MET:HG2	2.18	0.44
71:ss:25:PHE:CE2	71:ss:27:LYS:HE2	2.52	0.44
76:sx:61:ILE:HD12	76:sx:61:ILE:HA	1.82	0.44
1:lA:37:G:N2	1:lA:2946:A:H62	2.15	0.44
1:lA:189:G:H5'	17:lQ:55:PRO:HG3	1.98	0.44
1:lA:216:A:H2'	1:lA:217:G:O4'	2.17	0.44
1:lA:992:U:H3'	1:lA:993:U:H4'	2.00	0.44
1:lA:1452:C:H2'	1:lA:1453:U:H6	1.81	0.44
1:lA:1741:A:N3	1:lA:1763:C:O2'	2.44	0.44
1:lA:2233:G:N7	4:lD:152:SER:OG	2.44	0.44
1:lA:2905:U:H5''	14:lN:265:LYS:HD2	1.99	0.44
1:lA:3207:G:H2'	1:lA:3208:A:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:lA:3335:U:H3'	1:lA:3336:G:H5''	2.00	0.44
23:lW:38:THR:HG21	23:lW:73:LYS:NZ	2.32	0.44
31:le:40:ASP:N	31:le:40:ASP:OD1	2.50	0.44
46:sB:63:LYS:HE2	46:sB:63:LYS:HB2	1.75	0.44
48:sD:11:ILE:HD11	48:sD:61:ALA:HB2	1.99	0.44
49:sE:17:GLY:N	53:sa:1230:C:O2	2.50	0.44
53:sa:1690:A:N1	53:sa:1774:A:H1'	2.33	0.44
54:sb:56:LEU:HD23	54:sb:56:LEU:HA	1.85	0.44
55:sc:46:LEU:HD22	55:sc:245:TYR:HD2	1.83	0.44
56:sd:72:ILE:HA	56:sd:75:ASP:HB2	1.99	0.44
69:sq:84:ILE:HD11	69:sq:118:PHE:HE2	1.82	0.44
69:sq:123:LYS:HE2	69:sq:123:LYS:HB3	1.62	0.44
77:sy:50:GLN:HG2	77:sy:69:ARG:HG2	1.98	0.44
1:lA:223:A:H2'	1:lA:224:U:H6	1.82	0.44
1:lA:285:A:H4'	1:lA:286:U:C5'	2.47	0.44
1:lA:710:A:O2'	1:lA:736:G:N2	2.42	0.44
1:lA:1624:G:C8	1:lA:1626:G:C8	3.06	0.44
1:lA:2308:A:H2'	1:lA:2309:A:H8	1.82	0.44
1:lA:3041:G:OP2	11:lK:179:ARG:NH2	2.49	0.44
6:lF:51:PRO:HA	6:lF:111:TRP:CE2	2.53	0.44
19:lS:81:VAL:HG22	19:lS:120:PHE:CZ	2.53	0.44
53:sa:906:A:H2'	53:sa:907:U:O4'	2.17	0.44
53:sa:908:G:O2'	53:sa:925:U:H5'	2.18	0.44
53:sa:1705:A:H4'	73:su:39:ARG:CZ	2.48	0.44
54:sb:141:LEU:HD23	54:sb:151:THR:HG21	1.98	0.44
59:sg:16:PHE:CE2	71:ss:69:ILE:HD12	2.53	0.44
59:sg:120:ASN:ND2	59:sg:184:LYS:O	2.50	0.44
60:sh:154:ASP:HB2	60:sh:195:ARG:HG3	1.99	0.44
60:sh:300:ALA:O	60:sh:304:ALA:N	2.50	0.44
61:si:34:VAL:HG11	61:si:66:ILE:HG21	1.99	0.44
62:sj:34:ALA:HB3	62:sj:56:ARG:HD2	2.00	0.44
67:so:54:MET:HE3	67:so:54:MET:HB3	1.86	0.44
77:sy:94:GLU:HG2	77:sy:95:ASN:OD1	2.17	0.44
1:lA:10:U:H2'	1:lA:11:A:H8	1.82	0.44
1:lA:55:G:OP2	35:li:79:LYS:NZ	2.47	0.44
1:lA:187:G:H4'	1:lA:188:U:H5''	2.00	0.44
1:lA:937:C:O2'	1:lA:2214:A:N1	2.42	0.44
1:lA:3048:U:H2'	1:lA:3049:G:H8	1.83	0.44
1:lA:3303:A:H2'	1:lA:3304:C:C6	2.53	0.44
1:lA:3432:A:N6	1:lA:3434:A:N3	2.66	0.44
1:lA:3432:A:HO2'	1:lA:3433:U:P	2.40	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1F:113:ARG:HD3	6:1F:113:ARG:HA	1.78	0.44
10:1J:35:ASP:OD1	10:1J:36:LEU:N	2.51	0.44
14:1N:83:ILE:HG12	14:1N:118:MET:HE2	2.00	0.44
14:1N:228:LYS:HD3	14:1N:228:LYS:HA	1.78	0.44
37:1k:44:PHE:HB3	37:1k:48:GLU:HB2	1.99	0.44
53:sa:758:U:O4'	78:sz:68:TYR:OH	2.36	0.44
54:sb:82:VAL:HG23	54:sb:126:PRO:HB3	2.00	0.44
56:sd:137:MET:HA	56:sd:140:ILE:HD12	1.98	0.44
57:se:27:SER:HA	68:sp:16:PRO:HB2	1.99	0.44
70:sr:124:ARG:H	70:sr:124:ARG:HG2	1.54	0.44
1:1A:542:U:H2'	1:1A:543:A:C8	2.52	0.44
1:1A:718:A:H2'	1:1A:719:U:C6	2.53	0.44
1:1A:1848:A:H2'	1:1A:1849:A:C8	2.53	0.44
37:1k:88:LEU:HD23	37:1k:88:LEU:HA	1.84	0.44
53:sa:208:C:H2'	53:sa:209:A:C8	2.53	0.44
53:sa:618:G:H2'	53:sa:619:C:C6	2.53	0.44
53:sa:772:U:H2'	53:sa:772:U:O2	2.17	0.44
53:sa:1204:G:N2	53:sa:1567:A:H62	2.15	0.44
53:sa:1828:A:H2'	53:sa:1829:A:C8	2.53	0.44
54:sb:174:SER:O	54:sb:178:ILE:HG13	2.17	0.44
56:sd:16:LYS:NZ	56:sd:18:ASN:O	2.48	0.44
57:se:205:LYS:HD2	57:se:205:LYS:HA	1.58	0.44
60:sh:273:LEU:HD23	60:sh:275:THR:HG23	2.00	0.44
72:st:82:ASP:OD1	72:st:83:ASN:ND2	2.43	0.44
1:1A:1636:U:H5	1:1A:2036:A:N1	2.16	0.44
1:1A:1934:G:O3'	40:1n:44:THR:HG21	2.17	0.44
1:1A:2128:A:H2'	39:1m:7:LYS:HE2	2.00	0.44
1:1A:2632:A:C8	34:1h:91:ARG:HD2	2.53	0.44
1:1A:3129:U:C2	1:1A:3130:A:C8	3.06	0.44
3:1C:2:G:H2'	3:1C:3:G:C8	2.51	0.44
6:1F:390:VAL:O	6:1F:392:VAL:HG23	2.18	0.44
8:1H:45:LEU:HD21	8:1H:130:LYS:HG3	1.98	0.44
29:1c:111:LYS:HG3	29:1c:129:TYR:HB2	1.99	0.44
51:sH:21:A:H2'	51:sH:46:G:O6	2.18	0.44
53:sa:593:A:H2'	53:sa:594:U:C6	2.53	0.44
53:sa:1310:U:C2	53:sa:1311:U:H5	2.36	0.44
58:sf:181:MET:HB2	58:sf:186:GLY:O	2.18	0.44
71:ss:61:ILE:HD12	71:ss:62:LYS:N	2.33	0.44
78:sz:27:VAL:HG13	78:sz:75:GLY:O	2.17	0.44
1:1A:2488:G:H2'	1:1A:2489:A:C8	2.53	0.43
1:1A:2504:U:H2'	1:1A:2505:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:lA:2835:C:O3'	43:lq:37:GLY:HA3	2.18	0.43
1:lA:3107:G:N2	1:lA:3110:A:OP2	2.46	0.43
4:lD:57:PRO:HB3	39:lm:54:ILE:HG12	2.00	0.43
23:lW:52:GLN:HA	23:lW:61:GLY:HA2	1.99	0.43
27:la:53:ASP:CG	27:la:113:ARG:HH12	2.24	0.43
30:ld:2:SER:O	30:ld:2:SER:OG	2.28	0.43
46:sB:37:LYS:HG2	46:sB:70:LYS:HE3	2.00	0.43
51:sH:19:G:C8	51:sH:19:G:H5'	2.53	0.43
53:sa:1241:C:HO2'	53:sa:1551:A:H62	1.59	0.43
53:sa:1706:G:OP1	73:su:39:ARG:NH2	2.47	0.43
53:sa:1725:A:H5''	73:su:134:GLY:HA3	2.00	0.43
53:sa:1874:U:O2	62:sj:32:GLN:NE2	2.40	0.43
60:sh:312:VAL:HG22	60:sh:316:HIS:NE2	2.32	0.43
67:so:91:LEU:HA	67:so:91:LEU:HD12	1.83	0.43
1:lA:658:A:H1'	1:lA:659:U:C6	2.53	0.43
1:lA:718:A:H2'	1:lA:719:U:H6	1.82	0.43
1:lA:1078:C:O2'	1:lA:2486:U:O4	2.36	0.43
1:lA:1107:G:H2'	1:lA:1108:A:H8	1.83	0.43
1:lA:1764:A:H2'	1:lA:1765:A:C8	2.53	0.43
1:lA:3237:G:H2'	1:lA:3238:A:C8	2.53	0.43
1:lA:3466:U:O2'	1:lA:3467:U:P	2.76	0.43
2:lB:54:A:H5'	41:lo:21:ARG:HD3	1.99	0.43
5:lE:340:ARG:HH21	5:lE:343:CYS:HB2	1.82	0.43
11:lK:111:LEU:HD13	11:lK:144:LYS:HE2	2.00	0.43
23:lW:42:GLU:OE2	23:lW:45:LYS:HB2	2.18	0.43
28:lb:3:LYS:HA	28:lb:3:LYS:HD2	1.84	0.43
40:ln:69:ILE:HG23	40:ln:74:PRO:HD3	2.00	0.43
48:sD:22:THR:HG1	48:sD:28:VAL:HB	1.83	0.43
53:sa:443:U:H2'	53:sa:444:U:H6	1.82	0.43
56:sd:128:PRO:HG2	56:sd:131:ARG:HD3	2.00	0.43
56:sd:217:ARG:HG3	72:st:40:VAL:HG13	2.00	0.43
70:sr:14:ILE:HG23	70:sr:65:LEU:HD21	1.98	0.43
75:sw:116:MET:HG2	75:sw:117:PHE:H	1.82	0.43
78:sz:67:LYS:HD3	78:sz:72:LYS:HB3	2.00	0.43
1:lA:592:A:H2'	1:lA:593:A:C8	2.53	0.43
1:lA:843:A:N3	1:lA:893:U:O2'	2.51	0.43
1:lA:1752:U:H4'	1:lA:2036:A:H4'	2.01	0.43
1:lA:1904:U:O2'	1:lA:1906:A:N7	2.38	0.43
1:lA:2294:A:H2'	1:lA:2295:A:H8	1.81	0.43
1:lA:2895:G:O6	14:lN:190:LYS:NZ	2.44	0.43
6:lF:371:GLN:O	6:lF:371:GLN:CG	2.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:lF:398:LYS:HA	6:lF:398:LYS:HE3	2.00	0.43
13:lM:32:ARG:HG2	13:lM:119:GLN:O	2.18	0.43
17:lQ:96:LYS:NZ	17:lQ:104:GLN:OE1	2.51	0.43
47:sC:31:SER:OG	53:sa:939:G:OP1	2.33	0.43
48:sD:17:GLU:OE1	48:sD:18:ILE:N	2.51	0.43
53:sa:327:U:P	62:sj:56:ARG:HH22	2.41	0.43
53:sa:1902:A:OP1	77:sy:59:GLN:HG3	2.18	0.43
65:sm:150:LYS:HE3	65:sm:152:GLN:HE21	1.83	0.43
70:sr:90:GLU:OE2	70:sr:113:ASN:ND2	2.51	0.43
72:st:14:ARG:O	72:st:18:GLU:HG3	2.18	0.43
1:lA:471:G:OP1	33:lg:19:LYS:NZ	2.41	0.43
1:lA:631:G:H2'	1:lA:631:G:N3	2.33	0.43
1:lA:759:U:H2'	1:lA:760:A:H8	1.84	0.43
1:lA:2286:G:H8	1:lA:2286:G:OP1	2.02	0.43
1:lA:2332:A:H61	53:sa:1902:A:H2'	1.84	0.43
1:lA:2489:A:H2'	1:lA:2490:G:H8	1.83	0.43
1:lA:3154:A:H2'	1:lA:3155:U:C6	2.54	0.43
1:lA:3453:C:H2'	1:lA:3454:G:C8	2.53	0.43
6:lF:112:GLN:HB3	17:lQ:203:TYR:CE2	2.52	0.43
11:lK:116:ASP:OD1	11:lK:116:ASP:N	2.40	0.43
14:lN:123:VAL:O	14:lN:222:VAL:HA	2.18	0.43
50:sG:214:ALA:HA	50:sG:224:MET:HA	2.01	0.43
53:sa:584:C:H2'	53:sa:585:A:H8	1.82	0.43
53:sa:1394:A:C8	53:sa:1394:A:C5'	2.93	0.43
53:sa:1730:U:C4	53:sa:1731:U:O4	2.71	0.43
53:sa:1787:U:H2'	53:sa:1788:G:O4'	2.18	0.43
57:se:167:ARG:O	57:se:171:ASN:HB2	2.18	0.43
58:sf:169:ASP:OD1	58:sf:170:PHE:N	2.51	0.43
61:si:140:GLU:OE2	67:so:21:SER:OG	2.31	0.43
65:sm:38:GLY:O	65:sm:40:GLY:N	2.51	0.43
75:sw:37:ALA:O	75:sw:41:GLU:HG2	2.18	0.43
1:lA:190:U:C2	1:lA:191:A:C8	3.07	0.43
1:lA:322:U:H2'	1:lA:323:U:C6	2.52	0.43
1:lA:1688:A:H2'	1:lA:1689:A:C8	2.54	0.43
1:lA:2128:A:H5''	39:lm:8:VAL:HG21	2.00	0.43
3:lC:35:A:H8	3:lC:35:A:O5'	2.01	0.43
5:lE:329:VAL:HG21	5:lE:337:ILE:HD13	2.00	0.43
28:lb:56:LYS:HB3	28:lb:56:LYS:HE2	1.80	0.43
42:lp:18:LYS:HD3	42:lp:27:ARG:HG2	2.00	0.43
50:sG:40:LYS:HB3	50:sG:67:HIS:O	2.19	0.43
50:sG:224:MET:C	50:sG:225:TRP:HD1	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:sa:402:A:O2'	53:sa:1837:A:N3	2.38	0.43
53:sa:444:U:H2'	53:sa:445:C:C6	2.54	0.43
53:sa:919:A:H2'	53:sa:920:A:C8	2.54	0.43
53:sa:1134:G:OP2	53:sa:1134:G:N2	2.41	0.43
53:sa:1510:A:H2'	53:sa:1511:A:C8	2.53	0.43
53:sa:1732:U:H5''	73:su:38:GLY:N	2.33	0.43
55:sc:151:GLY:HA2	55:sc:152:GLU:HA	1.69	0.43
56:sd:12:VAL:HG22	56:sd:14:VAL:H	1.83	0.43
70:sr:57:ARG:O	70:sr:58:SER:OG	2.33	0.43
1:lA:703:G:O6	1:lA:744:A:C6	2.72	0.43
1:lA:880:A:H4'	19:lS:73:HIS:NE2	2.33	0.43
1:lA:1003:A:OP1	38:ll:5:THR:OG1	2.28	0.43
1:lA:1168:C:H2'	1:lA:1169:U:C6	2.53	0.43
1:lA:2150:G:C4	1:lA:2176:G:N2	2.87	0.43
1:lA:2418:U:OP1	1:lA:3243:C:O2'	2.31	0.43
6:lF:218:GLN:O	6:lF:221:LYS:HE3	2.18	0.43
8:lH:131:PHE:HA	8:lH:134:LYS:HE3	1.99	0.43
15:lO:157:ASN:O	15:lO:160:GLU:HG2	2.19	0.43
21:lU:30:PRO:O	21:lU:34:LEU:HD22	2.19	0.43
27:la:210:LYS:HE2	27:la:210:LYS:HB2	1.84	0.43
34:lh:15:THR:HG22	34:lh:16:LYS:H	1.83	0.43
50:sG:202:ASN:HB2	50:sG:217:GLY:HA2	2.00	0.43
53:sa:1516:G:N2	53:sa:1519:G:OP2	2.50	0.43
53:sa:1774:A:C4	53:sa:1775:U:C5	3.07	0.43
58:sf:118:LYS:HE2	58:sf:118:LYS:HB3	1.76	0.43
60:sh:217:GLU:HG2	60:sh:218:ILE:H	1.83	0.43
61:si:128:HIS:ND1	61:si:191:GLU:OE2	2.40	0.43
64:sl:56:GLU:HG3	64:sl:65:TRP:HE1	1.83	0.43
74:sv:123:LEU:HD23	74:sv:123:LEU:HA	1.91	0.43
74:sv:131:MET:HE2	74:sv:131:MET:HB2	1.91	0.43
76:sx:71:GLN:HG2	76:sx:85:MET:HE2	1.99	0.43
77:sy:93:ASN:O	77:sy:94:GLU:HB2	2.17	0.43
1:lA:1283:A:OP1	9:ll:205:LYS:NZ	2.50	0.43
1:lA:1757:C:C2	1:lA:1758:U:C5	3.07	0.43
1:lA:2129:G:C8	39:lm:16:THR:HB	2.53	0.43
2:lB:2:A:H2'	2:lB:3:U:H6	1.82	0.43
2:lB:68:A:H2'	2:lB:69:U:C6	2.53	0.43
6:lF:360:LYS:O	6:lF:364:ALA:N	2.52	0.43
18:lR:57:ILE:HB	18:lR:72:GLN:HB2	2.01	0.43
18:lR:70:LYS:HD3	18:lR:70:LYS:HA	1.74	0.43
21:lU:20:ARG:H	21:lU:20:ARG:HG2	1.60	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:IW:49:PHE:HA	23:IW:52:GLN:HE21	1.83	0.43
45:sA:80:THR:HG23	45:sA:83:LEU:H	1.83	0.43
53:sa:301:U:H2'	53:sa:302:C:C6	2.54	0.43
53:sa:329:G:H2'	53:sa:330:A:H8	1.83	0.43
53:sa:558:G:N1	53:sa:574:A:OP2	2.52	0.43
53:sa:581:C:H2'	53:sa:582:U:C6	2.54	0.43
53:sa:1011:U:H4'	53:sa:1012:G:OP2	2.17	0.43
60:sh:289:LYS:HE2	60:sh:289:LYS:HB2	1.88	0.43
60:sh:294:ILE:HG13	60:sh:295:ALA:N	2.32	0.43
62:sj:27:ASN:OD1	62:sj:27:ASN:N	2.51	0.43
62:sj:117:TYR:HD1	62:sj:179:LYS:HD2	1.84	0.43
77:sy:51:GLU:HG3	77:sy:53:LEU:HG	2.01	0.43
1:lA:226:U:H2'	1:lA:227:A:C8	2.54	0.43
1:lA:1220:A:H2'	1:lA:1220:A:OP2	2.19	0.43
1:lA:1484:A:H2'	1:lA:1485:A:C8	2.53	0.43
1:lA:1502:A:O2'	1:lA:1503:U:OP2	2.31	0.43
1:lA:1533:U:HO2'	1:lA:1534:U:P	2.40	0.43
3:lC:106:U:H2'	3:lC:107:A:C8	2.52	0.43
7:lG:120:VAL:O	7:lG:244:ARG:NH2	2.37	0.43
10:lJ:173:PRO:HG3	10:lJ:216:LYS:HE3	2.00	0.43
12:lL:175:LYS:HA	12:lL:175:LYS:HD2	1.73	0.43
28:lb:123:GLU:HG3	28:lb:124:GLU:N	2.33	0.43
33:lg:33:TRP:CH2	33:lg:53:LEU:HD23	2.54	0.43
42:lp:35:CYS:HB2	42:lp:43:SER:N	2.34	0.43
53:sa:15:U:H2'	53:sa:16:G:O4'	2.18	0.43
57:se:66:ARG:HH12	68:sp:46:GLU:HG2	1.83	0.43
1:lA:532:A:H2'	1:lA:533:U:C6	2.54	0.43
1:lA:663:G:H5'	16:lP:72:THR:HG23	2.00	0.43
1:lA:1244:C:H2'	1:lA:1245:A:H8	1.84	0.43
1:lA:2251:A:N3	4:lD:25:GLY:HA2	2.34	0.43
1:lA:2710:A:H2'	1:lA:2711:U:O4'	2.18	0.43
2:lB:9:A:H2'	2:lB:10:U:C6	2.54	0.43
9:lI:108:ASN:HB2	22:lV:138:PRO:HB2	2.01	0.43
10:lJ:245:ILE:O	10:lJ:246:GLN:HB2	2.19	0.43
48:sD:50:ILE:HD12	59:sg:144:SER:HB2	2.00	0.43
50:sG:258:TYR:HB3	50:sG:272:LYS:HG3	2.00	0.43
53:sa:742:G:H2'	53:sa:743:A:H8	1.84	0.43
53:sa:1111:A:H2'	53:sa:1112:A:C8	2.54	0.43
53:sa:1574:C:O2'	74:sv:88:TYR:O	2.32	0.43
53:sa:1693:A:O2'	53:sa:1694:A:OP1	2.32	0.43
58:sf:145:ILE:HD13	58:sf:167:ILE:HD11	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:sh:319:LYS:HD2	60:sh:319:LYS:HA	1.76	0.43
62:sj:113:PHE:CE1	62:sj:117:TYR:HD2	2.37	0.43
71:ss:38:LYS:HB2	71:ss:38:LYS:HE3	1.74	0.43
75:sw:26:SER:HB3	75:sw:110:VAL:HA	2.00	0.43
1:lA:905:A:C8	19:lS:60:ILE:HD11	2.54	0.43
1:lA:1606:A:H5''	18:lR:53:ILE:HB	2.00	0.43
1:lA:1992:A:H2'	1:lA:1993:G:C8	2.53	0.43
1:lA:2634:A:OP1	4:lD:69:TYR:OH	2.30	0.43
1:lA:3162:A:OP2	15:lO:75:ARG:NH2	2.48	0.43
2:lB:105:G:O2'	2:lB:106:C:OP1	2.36	0.43
5:lE:122:TRP:CZ2	5:lE:127:LYS:HG2	2.54	0.43
6:lF:101:MET:HE1	6:lF:105:LEU:HG	2.00	0.43
7:lG:128:LEU:HB2	7:lG:192:ARG:HG3	2.01	0.43
20:lT:62:GLU:HG2	20:lT:94:THR:HG22	2.00	0.43
23:lW:68:VAL:HA	23:lW:76:THR:O	2.19	0.43
35:li:9:ALA:HB1	35:li:45:ARG:HH12	1.84	0.43
40:ln:57:LYS:HA	40:ln:60:ILE:HD12	2.01	0.43
50:sG:93:ARG:CZ	50:sG:105:ARG:HD3	2.48	0.43
50:sG:264:THR:OG1	50:sG:265:GLU:N	2.52	0.43
51:sH:60:U:H5''	51:sH:61:C:H5	1.82	0.43
53:sa:163:A:OP1	60:sh:237:HIS:ND1	2.52	0.43
53:sa:1158:A:H2'	53:sa:1159:A:C8	2.54	0.43
53:sa:1805:C:H2'	53:sa:1806:C:O4'	2.17	0.43
60:sh:278:ARG:HA	60:sh:281:HIS:CG	2.53	0.43
75:sw:33:GLU:OE2	75:sw:87:ARG:NE	2.36	0.43
78:sz:15:LEU:HD12	78:sz:15:LEU:HA	1.90	0.43
1:lA:705:U:N3	1:lA:743:G:N7	2.67	0.42
1:lA:1565:G:N7	29:lc:9:ARG:NH2	2.67	0.42
1:lA:1930:C:H2'	1:lA:1931:U:H6	1.83	0.42
1:lA:2670:U:H2'	1:lA:2671:A:H8	1.84	0.42
1:lA:2887:G:H2'	1:lA:2888:U:O4'	2.19	0.42
1:lA:3207:G:H2'	1:lA:3208:A:H8	1.84	0.42
10:lJ:48:ILE:HD11	17:lQ:32:HIS:HB2	2.00	0.42
10:lJ:159:MET:HE2	10:lJ:159:MET:HB3	1.73	0.42
13:lM:112:LEU:HD23	13:lM:112:LEU:O	2.19	0.42
23:lW:52:GLN:CD	23:lW:53:THR:HG23	2.44	0.42
29:lc:146:GLU:HB3	37:lk:1:MET:HE1	2.02	0.42
53:sa:59:U:C6	53:sa:61:A:H5'	2.54	0.42
53:sa:136:A:H62	60:sh:286:LEU:HG	1.84	0.42
53:sa:796:G:O2'	70:sr:107:SER:HB3	2.19	0.42
53:sa:1241:C:H1'	53:sa:1242:G:H3'	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:sa:1543:A:OP2	56:sd:41:ARG:NH2	2.39	0.42
56:sd:76:LYS:HG3	64:sl:89:THR:HG21	2.01	0.42
56:sd:119:ILE:HG12	56:sd:136:VAL:HG11	2.01	0.42
64:sl:53:CYS:SG	64:sl:71:GLY:HA2	2.59	0.42
77:sy:123:VAL:C	77:sy:125:GLY:H	2.27	0.42
78:sz:25:GLN:HB2	78:sz:76:PHE:CE1	2.54	0.42
1:lA:207:A:H2'	1:lA:208:U:C6	2.54	0.42
1:lA:228:A:H2'	1:lA:229:A:C8	2.54	0.42
1:lA:576:A:H62	1:lA:577:G:H21	1.67	0.42
1:lA:605:C:H2'	1:lA:606:A:C8	2.52	0.42
1:lA:1006:A:H2'	1:lA:1007:C:C6	2.54	0.42
1:lA:1351:U:N3	1:lA:1352:A:N7	2.66	0.42
1:lA:1893:A:H2'	1:lA:1894:C:C6	2.53	0.42
1:lA:2583:U:H2'	1:lA:2584:U:C6	2.54	0.42
1:lA:3141:A:H1'	1:lA:3142:G:C8	2.54	0.42
1:lA:3203:A:C6	5:lE:75:PRO:HB3	2.54	0.42
6:lF:262:LEU:HD23	6:lF:262:LEU:HA	1.91	0.42
12:lL:110:ARG:HD2	12:lL:111:LEU:N	2.34	0.42
14:lN:197:LYS:HE2	14:lN:197:LYS:HB3	1.75	0.42
15:lO:33:LYS:HE2	15:lO:33:LYS:HB3	1.88	0.42
21:lU:5:LYS:HE3	21:lU:5:LYS:HB3	1.85	0.42
29:lc:75:VAL:HG22	29:lc:115:LYS:H	1.84	0.42
50:sG:212:ILE:HG13	50:sG:251:PHE:HZ	1.84	0.42
53:sa:1374:G:H2'	53:sa:1375:U:C6	2.53	0.42
53:sa:1662:G:H21	53:sa:1686:U:H1'	1.85	0.42
65:sm:58:PRO:HA	65:sm:63:VAL:HG23	2.00	0.42
70:sr:66:ASN:OD1	70:sr:66:ASN:N	2.52	0.42
1:lA:686:A:H2'	1:lA:687:U:C6	2.54	0.42
1:lA:1635:U:C6	41:lo:17:ILE:HD11	2.55	0.42
1:lA:2273:C:H4'	1:lA:2274:A:O5'	2.19	0.42
1:lA:2512:G:OP1	10:lJ:232:ARG:NH1	2.53	0.42
1:lA:2725:A:H4'	1:lA:2726:A:O4'	2.18	0.42
1:lA:3069:A:H2'	1:lA:3070:C:C6	2.54	0.42
1:lA:3371:U:H2'	1:lA:3372:U:C6	2.54	0.42
1:lA:3422:A:H2'	1:lA:3423:C:O4'	2.18	0.42
1:lA:3477:U:O2	1:lA:3478:U:C5	2.73	0.42
4:lD:143:ASN:OD1	4:lD:143:ASN:N	2.49	0.42
5:lE:117:ARG:HE	5:lE:117:ARG:HB3	1.70	0.42
26:lZ:10:PHE:HZ	26:lZ:51:VAL:HG21	1.84	0.42
30:ld:56:GLU:HA	30:ld:56:GLU:OE1	2.18	0.42
50:sG:125:ILE:O	50:sG:137:TRP:N	2.36	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:sa:65:U:O4	60:sh:231:GLY:N	2.50	0.42
53:sa:203:C:H5	53:sa:255:G:H21	1.66	0.42
53:sa:1261:A:H2'	53:sa:1262:G:C8	2.52	0.42
53:sa:1831:G:H2'	53:sa:1832:A:H8	1.83	0.42
54:sb:88:GLU:HA	54:sb:91:HIS:CE1	2.54	0.42
61:si:171:LYS:HD3	61:si:175:LYS:HE2	2.02	0.42
62:sj:56:ARG:NH1	62:sj:210:GLY:O	2.41	0.42
67:so:146:ALA:HA	67:so:149:ILE:HG12	2.01	0.42
1:lA:336:A:H2'	1:lA:337:A:C8	2.54	0.42
1:lA:628:C:H2'	1:lA:629:G:C8	2.54	0.42
1:lA:2483:C:H2'	1:lA:2484:U:H6	1.84	0.42
1:lA:3278:A:N1	11:lK:80:THR:OG1	2.41	0.42
5:lE:14:LEU:HD11	5:lE:265:THR:HG22	2.01	0.42
6:lF:15:GLY:HA2	27:la:161:ILE:HD11	2.02	0.42
6:lF:403:ARG:HB2	6:lF:407:GLN:OE1	2.19	0.42
7:lG:115:MET:HE2	7:lG:119:PHE:CE2	2.54	0.42
11:lK:37:ARG:HD3	11:lK:39:PHE:CE1	2.55	0.42
13:lM:111:ASP:HB3	13:lM:112:LEU:H	1.51	0.42
14:lN:160:ASN:HB2	14:lN:163:ILE:HD11	2.01	0.42
22:IV:118:GLN:OE1	22:IV:118:GLN:HA	2.19	0.42
22:IV:152:ILE:HD13	22:IV:152:ILE:HA	1.84	0.42
29:lc:36:GLY:HA3	29:lc:40:HIS:CE1	2.55	0.42
50:sG:21:THR:O	50:sG:287:SER:HB3	2.18	0.42
53:sa:102:A:H4'	53:sa:103:U:O5'	2.19	0.42
53:sa:151:A:H2'	53:sa:152:A:O4'	2.19	0.42
53:sa:1267:A:O2'	53:sa:1269:A:OP1	2.25	0.42
54:sb:141:LEU:HD23	54:sb:141:LEU:HA	1.90	0.42
61:si:137:TYR:CD1	61:si:138:PRO:HA	2.53	0.42
61:si:139:VAL:HG21	61:si:174:VAL:HG11	2.01	0.42
74:sv:84:TYR:CE2	74:sv:86:LYS:HG3	2.54	0.42
1:lA:18:G:H1'	2:lB:102:A:N3	2.35	0.42
1:lA:208:U:H2'	1:lA:209:A:H8	1.85	0.42
1:lA:213:A:H2'	14:lN:127:VAL:HG21	2.02	0.42
1:lA:583:A:H2'	1:lA:584:U:C6	2.54	0.42
1:lA:821:G:OP1	14:lN:37:ARG:NE	2.52	0.42
1:lA:1197:G:H2'	1:lA:1198:U:C6	2.53	0.42
1:lA:1408:C:N4	1:lA:1409:G:O6	2.52	0.42
1:lA:3061:G:C2	1:lA:3062:A:N7	2.88	0.42
1:lA:3176:G:O2'	1:lA:3185:G:O6	2.33	0.42
1:lA:3434:A:H2'	1:lA:3435:G:O4'	2.20	0.42
9:II:68:ASP:OD1	22:IV:142:ARG:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:IK:120:ILE:HG12	11:IK:121:GLN:H	1.85	0.42
26:IZ:47:ASN:HB3	26:IZ:50:LYS:HG2	2.01	0.42
51:sH:16:U:C6	51:sH:16:U:H5''	2.54	0.42
51:sH:33:U:P	71:ss:158:ARG:HH22	2.41	0.42
53:sa:606:U:OP2	53:sa:607:G:O2'	2.37	0.42
53:sa:853:U:H2'	53:sa:854:U:C6	2.55	0.42
53:sa:869:A:H2'	53:sa:870:A:H8	1.84	0.42
53:sa:1371:U:H5	53:sa:1683:A:N7	2.18	0.42
53:sa:1756:U:H2'	53:sa:1757:C:C6	2.54	0.42
53:sa:1906:C:H2'	53:sa:1907:G:O4'	2.20	0.42
60:sh:166:THR:OG1	60:sh:168:ASN:OD1	2.35	0.42
66:sn:44:ARG:HD2	66:sn:44:ARG:HA	1.70	0.42
67:so:104:LYS:H	67:so:104:LYS:HG2	1.67	0.42
75:sw:30:LYS:HB3	75:sw:30:LYS:HE2	1.70	0.42
78:sz:72:LYS:HB2	78:sz:72:LYS:HE3	1.78	0.42
1:lA:279:U:H2'	1:lA:280:U:H6	1.84	0.42
1:lA:425:C:H2'	1:lA:426:U:C6	2.54	0.42
1:lA:1297:G:O2'	1:lA:1304:A:N1	2.49	0.42
1:lA:1412:U:H2'	1:lA:1413:G:H8	1.85	0.42
1:lA:1460:C:O3'	6:lF:316:ARG:NH2	2.53	0.42
1:lA:1847:A:H2'	1:lA:1848:A:C8	2.54	0.42
1:lA:2747:G:H2'	1:lA:2747:G:N3	2.34	0.42
3:lC:39:U:H5''	3:lC:40:G:OP2	2.20	0.42
3:lC:84:G:H22	3:lC:91:G:H21	1.66	0.42
12:IL:13:ARG:HE	12:IL:13:ARG:HB3	1.47	0.42
46:sB:22:ARG:NH1	46:sB:27:GLY:O	2.52	0.42
49:sE:8:ASN:ND2	53:sa:1557:C:H5''	2.34	0.42
49:sE:28:LYS:HE3	53:sa:1224:G:OP2	2.19	0.42
53:sa:138:G:H2'	53:sa:139:G:H8	1.78	0.42
53:sa:402:A:OP1	60:sh:191:ARG:HD2	2.19	0.42
53:sa:1248:U:H2'	53:sa:1249:A:C8	2.54	0.42
70:sr:87:ASP:OD1	70:sr:117:ARG:NH2	2.48	0.42
74:sv:7:ILE:HG23	74:sv:66:TYR:CZ	2.55	0.42
74:sv:9:ASP:N	74:sv:9:ASP:OD1	2.53	0.42
74:sv:123:LEU:HD11	74:sv:131:MET:HE3	2.01	0.42
1:lA:210:U:H2'	1:lA:211:U:C6	2.55	0.42
1:lA:465:U:O4	15:lO:97:LYS:HE3	2.20	0.42
1:lA:779:A:O2'	1:lA:783:A:N6	2.52	0.42
1:lA:842:G:H2'	1:lA:843:A:C8	2.55	0.42
1:lA:1634:G:OP2	1:lA:1634:G:N2	2.47	0.42
1:lA:2294:A:H2'	1:lA:2295:A:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2598:A:H5'	25:1Y:9:THR:HG21	2.01	0.42
1:1A:3227:A:H2'	1:1A:3228:A:O4'	2.19	0.42
6:1F:339:LYS:O	6:1F:342:GLN:HG2	2.19	0.42
6:1F:369:LEU:C	6:1F:371:GLN:H	2.26	0.42
13:1M:91:LEU:HD23	13:1M:91:LEU:HA	1.83	0.42
22:1V:17:ARG:HB2	22:1V:22:HIS:CE1	2.54	0.42
27:1a:29:MET:HB2	27:1a:29:MET:HE2	1.75	0.42
36:1j:90:LEU:HD11	36:1j:99:LEU:HD21	2.01	0.42
46:sB:37:LYS:HB2	46:sB:37:LYS:HE2	1.71	0.42
51:sH:22:G:H3'	51:sH:23:A:H5''	2.01	0.42
53:sa:69:G:O2'	53:sa:70:A:OP1	2.36	0.42
53:sa:1202:C:N4	73:su:138:LYS:HE2	2.35	0.42
53:sa:1356:A:H61	56:sd:175:GLY:HA3	1.84	0.42
55:sc:84:THR:HB	55:sc:209:LEU:HD13	2.02	0.42
56:sd:2:PHE:HB3	56:sd:4:LEU:HG	2.01	0.42
62:sj:117:TYR:OH	62:sj:183:LEU:HG	2.19	0.42
67:so:46:ALA:HB1	67:so:86:GLU:HG3	2.01	0.42
68:sp:138:LYS:HB3	68:sp:138:LYS:HE3	1.90	0.42
74:sv:73:VAL:HG21	74:sv:102:ARG:HG3	2.01	0.42
77:sy:33:ARG:H	77:sy:33:ARG:HG3	1.35	0.42
77:sy:71:ARG:HB3	77:sy:71:ARG:CZ	2.48	0.42
77:sy:126:VAL:O	77:sy:127:SER:HB2	2.18	0.42
1:1A:592:A:H2'	1:1A:593:A:H8	1.85	0.42
1:1A:1509:A:H2'	1:1A:1510:A:H8	1.85	0.42
1:1A:2027:U:H2'	1:1A:2028:U:C6	2.55	0.42
1:1A:2459:U:H5'	15:1O:72:PHE:CE2	2.55	0.42
1:1A:3090:G:C2	5:1E:252:ALA:HB1	2.55	0.42
2:1B:9:A:H2'	2:1B:10:U:H6	1.85	0.42
3:1C:85:G:H1	3:1C:90:G:H1	1.67	0.42
4:1D:242:ARG:NH1	4:1D:243:THR:O	2.53	0.42
8:1H:31:LYS:HD2	8:1H:31:LYS:HA	1.77	0.42
8:1H:77:VAL:HG12	8:1H:93:GLY:HA3	2.02	0.42
14:1N:9:ASN:HB2	19:1S:165:LYS:HB2	2.02	0.42
23:1W:45:LYS:HB2	23:1W:45:LYS:HE3	1.65	0.42
31:1e:8:LYS:HD2	31:1e:8:LYS:HA	1.81	0.42
53:sa:1669:A:N6	53:sa:1673:A:H61	2.17	0.42
55:sc:230:ASP:OD1	55:sc:231:LEU:HG	2.20	0.42
58:sf:127:ARG:NH2	58:sf:150:PRO:O	2.53	0.42
68:sp:98:VAL:HG12	68:sp:134:CYS:HB2	2.01	0.42
72:st:76:GLU:O	72:st:80:ARG:HG2	2.20	0.42
78:sz:30:ILE:HD11	78:sz:64:PHE:HE2	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:sz:32:HIS:CD2	78:sz:32:HIS:H	2.38	0.42
1:lA:491:G:C6	1:lA:492:U:C4	3.08	0.42
1:lA:518:A:H2'	1:lA:519:A:O4'	2.20	0.42
1:lA:1877:A:H2'	1:lA:1878:A:H8	1.85	0.42
1:lA:2282:G:H8	1:lA:2282:G:OP2	2.03	0.42
1:lA:2492:U:H2'	1:lA:2493:U:H6	1.85	0.42
4:lD:14:SER:O	4:lD:16:PHE:N	2.52	0.42
5:lE:37:ALA:HA	5:lE:187:GLY:O	2.20	0.42
6:lF:76:ILE:HD11	6:lF:93:GLY:HA3	2.01	0.42
13:lM:49:GLU:HA	13:lM:64:GLN:HA	2.01	0.42
18:lR:53:ILE:HG13	18:lR:55:LYS:HG2	2.02	0.42
21:lU:135:LYS:O	21:lU:139:MET:HG3	2.20	0.42
23:lW:102:LEU:HD23	23:lW:102:LEU:H	1.84	0.42
32:lf:5:LYS:HD3	32:lf:5:LYS:HA	1.95	0.42
40:ln:72:LYS:HE2	40:ln:72:LYS:HB2	1.69	0.42
50:sG:11:SER:HB3	50:sG:308:MET:HE2	2.02	0.42
50:sG:281:LYS:HE2	50:sG:281:LYS:HB2	1.76	0.42
53:sa:416:A:O2'	53:sa:417:G:H8	2.03	0.42
53:sa:580:G:H2'	53:sa:581:C:H6	1.85	0.42
53:sa:594:U:H2'	53:sa:595:A:H8	1.85	0.42
53:sa:996:C:H2'	53:sa:997:C:H6	1.84	0.42
53:sa:1432:A:O2'	53:sa:1433:A:H8	2.03	0.42
53:sa:1522:U:H2'	53:sa:1523:U:C6	2.55	0.42
53:sa:1868:A:O2'	60:sh:178:ASN:ND2	2.52	0.42
58:sf:43:ILE:HA	58:sf:59:VAL:HG11	2.02	0.42
58:sf:228:LYS:HB3	58:sf:228:LYS:HE3	1.84	0.42
60:sh:284:GLN:C	60:sh:285:LYS:HD3	2.45	0.42
61:si:44:LEU:HG	61:si:83:VAL:HG22	2.00	0.42
64:sl:3:ILE:HB	64:sl:8:ILE:HD11	2.00	0.42
73:su:94:GLY:O	73:su:95:LYS:HD2	2.19	0.42
73:su:102:ASN:C	73:su:102:ASN:OD1	2.62	0.42
77:sy:126:VAL:O	77:sy:126:VAL:HG22	2.19	0.42
78:sz:87:LYS:HD3	78:sz:87:LYS:HA	1.77	0.42
1:lA:207:A:H2'	1:lA:208:U:H6	1.84	0.42
1:lA:280:U:H2'	1:lA:281:A:C8	2.54	0.42
1:lA:823:A:H2'	1:lA:824:G:H2'	2.02	0.42
1:lA:1188:A:H2'	1:lA:1189:U:H6	1.84	0.42
1:lA:2864:A:C4	1:lA:2865:A:C2	3.08	0.42
1:lA:2877:U:H4'	37:lk:32:HIS:CD2	2.55	0.42
1:lA:3467:U:H2'	1:lA:3468:U:C5	2.55	0.42
3:lC:85:G:N2	3:lC:90:G:N2	2.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:IH:117:VAL:O	8:IH:119:VAL:HG23	2.20	0.42
21:IU:64:VAL:O	21:IU:68:GLN:HG2	2.20	0.42
22:IV:4:SER:O	22:IV:9:ARG:HD3	2.20	0.42
47:sC:36:ILE:HD12	47:sC:45:THR:O	2.19	0.42
53:sa:136:A:H61	60:sh:282:LYS:N	2.18	0.42
53:sa:789:A:H5''	65:sm:92:TYR:HD2	1.84	0.42
53:sa:1246:A:H2'	53:sa:1247:G:H8	1.85	0.42
53:sa:1379:C:H2'	53:sa:1380:U:C6	2.54	0.42
71:ss:41:LYS:H	71:ss:41:LYS:HD3	1.85	0.42
74:sv:31:ILE:HD11	74:sv:55:TYR:CE1	2.54	0.42
1:lA:431:A:H2'	1:lA:432:A:C8	2.55	0.41
1:lA:496:A:H2'	1:lA:497:U:O4'	2.20	0.41
1:lA:686:A:C8	1:lA:687:U:H5	2.37	0.41
1:lA:1306:A:H2'	1:lA:1307:G:C8	2.55	0.41
1:lA:1627:G:N2	34:lh:6:THR:HG22	2.35	0.41
1:lA:2216:U:O2'	1:lA:3121:U:H5'	2.19	0.41
7:lG:30:TYR:O	7:lG:34:ARG:HG3	2.20	0.41
10:lJ:174:TYR:OH	10:lJ:226:TYR:OH	2.18	0.41
13:lM:23:VAL:O	13:lM:65:ILE:HG23	2.20	0.41
19:lS:152:VAL:HG13	29:lc:50:PRO:HD3	2.02	0.41
21:IU:76:THR:O	21:IU:76:THR:OG1	2.36	0.41
25:IY:46:LEU:HD13	25:IY:64:LEU:HD11	2.01	0.41
28:lb:92:PHE:CZ	28:lb:124:GLU:HG2	2.55	0.41
53:sa:65:U:C5	60:sh:268:PRO:HG3	2.55	0.41
53:sa:168:U:H2'	53:sa:169:U:C6	2.55	0.41
53:sa:966:G:H2'	53:sa:967:G:O4'	2.20	0.41
53:sa:1758:G:H2'	53:sa:1759:A:C8	2.55	0.41
56:sd:218:ILE:HD12	72:st:19:LYS:HD2	2.01	0.41
66:sn:70:THR:O	66:sn:74:LYS:HG2	2.20	0.41
1:lA:397:A:N6	41:lo:35:ILE:HG23	2.35	0.41
1:lA:610:A:H8	1:lA:610:A:O5'	2.02	0.41
1:lA:678:A:H2'	1:lA:679:U:C6	2.55	0.41
1:lA:1876:U:H2'	1:lA:1936:A:N6	2.35	0.41
1:lA:2503:U:H2'	1:lA:2504:U:C6	2.55	0.41
1:lA:2633:C:H2'	1:lA:2634:A:O4'	2.19	0.41
1:lA:3054:A:H4'	1:lA:3055:A:C8	2.55	0.41
1:lA:3194:U:H2'	1:lA:3195:G:C8	2.54	0.41
2:lB:110:A:N6	41:lo:51:MET:O	2.53	0.41
2:lB:112:A:OP1	41:lo:8:SER:OG	2.30	0.41
3:lC:6:G:N1	3:lC:111:A:H2	2.13	0.41
3:lC:97:C:H2'	3:lC:98:C:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:IN:255:LYS:HE3	29:lc:95:VAL:HG22	2.02	0.41
15:IO:45:CYS:HB2	15:IO:130:PHE:HZ	1.84	0.41
53:sa:70:A:H4'	53:sa:71:C:H3'	2.02	0.41
53:sa:158:A:H2'	53:sa:159:A:H8	1.85	0.41
53:sa:323:A:H2'	53:sa:324:G:O4'	2.20	0.41
53:sa:773:A:OP1	53:sa:774:U:H3'	2.19	0.41
53:sa:1722:A:OP1	69:sq:114:TYR:OH	2.37	0.41
54:sb:11:ASP:HA	54:sb:14:LYS:NZ	2.35	0.41
60:sh:175:ASP:OD1	60:sh:175:ASP:N	2.53	0.41
60:sh:318:MET:HE3	60:sh:318:MET:HB2	1.85	0.41
61:si:125:LYS:HE2	61:si:125:LYS:HB3	1.90	0.41
1:IA:841:A:H4'	1:IA:842:G:H5'	2.02	0.41
1:IA:1736:A:C6	41:lo:4:HIS:HB3	2.55	0.41
1:IA:2514:A:H2'	1:IA:2515:A:C8	2.56	0.41
1:IA:2846:U:H2'	1:IA:2847:A:C8	2.55	0.41
1:IA:3028:C:O2'	1:IA:3029:U:H5'	2.20	0.41
11:IK:54:LYS:HB3	11:IK:57:GLY:HA3	2.02	0.41
13:IM:37:LEU:HD23	13:IM:37:LEU:HA	1.91	0.41
14:IN:161:LYS:HD3	14:IN:161:LYS:HA	1.88	0.41
27:la:48:PRO:O	27:la:113:ARG:NH2	2.53	0.41
40:ln:31:ASN:HD22	40:ln:46:ILE:HG23	1.84	0.41
50:sG:132:LYS:HE2	50:sG:132:LYS:HB2	1.89	0.41
53:sa:145:U:H4'	60:sh:229:ARG:HH12	1.83	0.41
53:sa:402:A:H2'	53:sa:403:C:C6	2.55	0.41
53:sa:1257:U:O2'	64:sl:2:ARG:NH1	2.42	0.41
59:sg:80:GLN:HG3	59:sg:81:HIS:H	1.86	0.41
71:ss:118:ASN:HA	71:ss:121:LYS:HG2	2.02	0.41
77:sy:103:PHE:CE2	77:sy:111:GLY:HA3	2.56	0.41
1:IA:278:U:H2'	1:IA:279:U:C6	2.56	0.41
1:IA:279:U:H2'	1:IA:280:U:C6	2.55	0.41
1:IA:526:A:H5''	1:IA:538:A:N1	2.35	0.41
1:IA:720:U:HO2'	1:IA:721:A:P	2.42	0.41
1:IA:873:U:H2'	1:IA:874:A:C8	2.56	0.41
1:IA:1048:A:H2'	1:IA:1049:U:C6	2.56	0.41
1:IA:1104:A:N3	9:II:110:SER:OG	2.51	0.41
1:IA:1569:A:H4'	1:IA:1570:U:OP2	2.21	0.41
1:IA:3412:U:H3'	1:IA:3413:U:C5'	2.50	0.41
3:IC:109:G:H2'	3:IC:110:A:C8	2.55	0.41
5:IE:296:LYS:HZ3	5:IE:303:GLU:HG3	1.85	0.41
8:IH:167:LYS:HA	8:IH:167:LYS:HD2	1.79	0.41
23:IW:73:LYS:HA	23:IW:73:LYS:HD2	1.80	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:sA:45:ASN:O	45:sA:45:ASN:CG	2.63	0.41
50:sG:169:LYS:HD3	50:sG:183:THR:HA	2.02	0.41
51:sH:1:G:H2'	51:sH:2:A:H8	1.85	0.41
53:sa:142:A:H2'	53:sa:143:G:C8	2.55	0.41
53:sa:422:C:H1'	53:sa:454:G:H1'	2.02	0.41
64:sl:25:LYS:HD3	64:sl:63:LEU:HD11	2.01	0.41
71:ss:41:LYS:N	71:ss:79:ASP:OD1	2.52	0.41
71:ss:69:ILE:HG21	71:ss:124:PHE:CE1	2.55	0.41
74:sv:149:MET:HB2	74:sv:149:MET:HE3	1.71	0.41
1:lA:574:U:H2'	1:lA:575:A:C8	2.55	0.41
1:lA:1335:U:O2	20:IT:109:GLN:NE2	2.46	0.41
1:lA:1353:G:H2'	1:lA:1354:G:H8	1.85	0.41
1:lA:1440:A:OP2	15:lO:134:ARG:HD3	2.20	0.41
2:lB:115:A:H2'	2:lB:116:U:C6	2.56	0.41
9:lI:87:ILE:HD12	9:lI:118:VAL:HG12	2.02	0.41
14:lN:220:LEU:HD23	14:lN:220:LEU:HA	1.95	0.41
19:lS:25:MET:HE3	19:lS:25:MET:HB3	1.81	0.41
30:ld:58:LYS:HB3	30:ld:58:LYS:HE2	1.86	0.41
31:le:10:THR:C	31:le:12:GLU:H	2.29	0.41
33:lg:75:PHE:HZ	33:lg:85:MET:HE2	1.86	0.41
48:sD:33:CYS:O	48:sD:42:ILE:N	2.52	0.41
53:sa:26:U:H2'	53:sa:27:A:C8	2.55	0.41
53:sa:124:U:H2'	53:sa:125:U:C6	2.56	0.41
53:sa:766:A:H2'	53:sa:767:A:O4'	2.20	0.41
53:sa:1383:C:H2'	53:sa:1384:U:H6	1.85	0.41
55:sc:164:CYS:HB2	55:sc:215:ALA:HB2	2.03	0.41
61:si:68:ILE:HD11	61:si:73:MET:SD	2.61	0.41
63:sk:5:LEU:HA	63:sk:5:LEU:HD23	1.85	0.41
64:sl:43:MET:HA	64:sl:46:LYS:CG	2.51	0.41
1:lA:102:A:H1'	14:lN:33:ARG:HH21	1.86	0.41
1:lA:426:U:H2'	1:lA:427:U:C6	2.55	0.41
1:lA:699:A:H5''	1:lA:746:A:N6	2.36	0.41
1:lA:1940:A:H2'	1:lA:1941:A:H8	1.85	0.41
1:lA:2433:A:H2'	1:lA:2434:A:C8	2.55	0.41
1:lA:3013:C:H6	1:lA:3013:C:H2'	1.68	0.41
1:lA:3212:U:OP2	32:lf:66:ARG:NH2	2.49	0.41
2:lB:48:G:N3	2:lB:63:A:H2	2.18	0.41
2:lB:80:A:O2'	2:lB:81:A:OP1	2.34	0.41
11:lK:113:ILE:HG12	11:lK:120:ILE:HG13	2.02	0.41
12:lL:4:ARG:NH1	12:lL:9:TYR:OH	2.50	0.41
26:lZ:40:MET:O	26:lZ:44:ARG:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:lq:12:CYS:HB2	43:lq:21:HIS:CE1	2.55	0.41
45:sA:100:VAL:HG21	59:sg:104:LEU:HD11	2.02	0.41
46:sB:12:LYS:HG3	46:sB:15:ARG:HG3	2.03	0.41
53:sa:469:C:H2'	53:sa:470:A:H5''	2.02	0.41
53:sa:601:G:N1	53:sa:607:G:H5'	2.35	0.41
53:sa:801:A:H2'	53:sa:802:U:C6	2.55	0.41
53:sa:1346:A:OP2	54:sb:109:ARG:NH2	2.42	0.41
53:sa:1665:A:H5''	74:sv:72:GLY:HA3	2.03	0.41
55:sc:184:PRO:O	55:sc:188:LYS:HG3	2.19	0.41
55:sc:185:THR:HB	55:sc:186:PRO:HD3	2.03	0.41
56:sd:84:THR:O	56:sd:88:ILE:HG12	2.20	0.41
61:si:80:PHE:CE1	61:si:97:ILE:HD11	2.54	0.41
62:sj:36:THR:OG1	62:sj:57:ALA:O	2.28	0.41
67:so:35:ASP:OD1	67:so:35:ASP:C	2.64	0.41
78:sz:32:HIS:NE2	78:sz:73:THR:HB	2.35	0.41
1:lA:231:U:H2'	1:lA:232:G:O4'	2.20	0.41
1:lA:897:A:H4'	1:lA:898:U:OP1	2.21	0.41
1:lA:1030:C:OP2	4:lD:9:ARG:HD2	2.21	0.41
1:lA:1345:U:H4'	1:lA:1346:G:H5'	2.02	0.41
1:lA:1841:G:H2'	1:lA:1842:U:C6	2.55	0.41
1:lA:2052:G:O2'	38:ll:6:SER:OG	2.34	0.41
1:lA:2304:A:H2'	1:lA:2305:C:C6	2.56	0.41
1:lA:2759:A:N3	1:lA:2759:A:H2'	2.35	0.41
1:lA:3289:U:H2'	1:lA:3290:C:H6	1.86	0.41
1:lA:3380:C:H2'	1:lA:3381:A:O4'	2.21	0.41
8:lH:134:LYS:HE3	8:lH:134:LYS:HB2	1.90	0.41
10:lJ:129:LEU:HD23	10:lJ:129:LEU:HA	1.95	0.41
42:lp:13:LYS:HE2	42:lp:13:LYS:HB3	1.89	0.41
45:sA:69:THR:CG2	45:sA:72:VAL:HG12	2.50	0.41
47:sC:27:PRO:HB2	67:so:15:CYS:SG	2.61	0.41
53:sa:106:C:H2'	53:sa:107:A:H8	1.85	0.41
53:sa:768:A:H2'	53:sa:769:C:C2	2.56	0.41
53:sa:1202:C:H41	73:su:138:LYS:HE2	1.85	0.41
53:sa:1315:U:H2'	53:sa:1316:G:N3	2.36	0.41
59:sg:80:GLN:O	59:sg:84:ASN:ND2	2.44	0.41
74:sv:85:ASN:HB3	74:sv:91:SER:HB3	2.01	0.41
1:lA:337:A:H2'	1:lA:338:A:H8	1.85	0.41
1:lA:490:A:N1	1:lA:583:A:N6	2.69	0.41
1:lA:941:A:H2'	1:lA:942:C:C6	2.56	0.41
1:lA:1392:G:H2'	1:lA:1393:U:C6	2.55	0.41
1:lA:2681:U:H2'	1:lA:2682:U:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:3155:U:H2'	1:1A:3156:U:C6	2.56	0.41
1:1A:3302:U:H2'	1:1A:3303:A:C8	2.56	0.41
6:1F:102:PHE:O	6:1F:103:SER:C	2.63	0.41
7:1G:211:ASP:OD1	7:1G:213:ASP:N	2.49	0.41
10:1J:147:LEU:O	10:1J:197:VAL:N	2.51	0.41
19:1S:156:LYS:HA	19:1S:156:LYS:HD2	1.86	0.41
23:1W:32:ILE:HD12	23:1W:75:VAL:HB	2.03	0.41
48:sD:63:ARG:NH1	59:sg:206:ARG:HB3	2.35	0.41
50:sG:147:VAL:HG11	50:sG:182:TRP:CZ3	2.56	0.41
53:sa:60:A:C3'	53:sa:61:A:H5''	2.51	0.41
53:sa:570:G:H5'	53:sa:571:G:OP2	2.21	0.41
53:sa:1245:C:H5''	64:sl:51:LYS:HZ2	1.86	0.41
56:sd:70:THR:HA	56:sd:73:ILE:HG13	2.03	0.41
58:sf:102:ASN:HD22	58:sf:108:CYS:HB2	1.85	0.41
60:sh:296:MET:HA	60:sh:299:GLU:HG2	2.02	0.41
60:sh:306:ILE:HD13	60:sh:309:ARG:NH1	2.36	0.41
64:sl:79:LEU:CD2	64:sl:81:LEU:HG	2.51	0.41
65:sm:18:SER:HB3	65:sm:31:LYS:HG2	2.02	0.41
77:sy:50:GLN:OE1	77:sy:71:ARG:HG3	2.21	0.41
78:sz:35:ILE:HD12	78:sz:35:ILE:HA	1.99	0.41
1:1A:318:A:H2'	1:1A:319:A:O4'	2.21	0.41
1:1A:573:A:H2'	1:1A:574:U:C6	2.55	0.41
1:1A:601:A:H2'	1:1A:602:U:C6	2.56	0.41
1:1A:795:G:H4'	1:1A:796:U:C6	2.56	0.41
1:1A:815:A:H4'	1:1A:817:A:OP1	2.21	0.41
1:1A:939:A:H2'	1:1A:940:U:C6	2.56	0.41
1:1A:1850:U:O2'	1:1A:2061:G:OP1	2.28	0.41
1:1A:1980:C:OP2	39:lm:49:ARG:NH2	2.36	0.41
1:1A:2442:C:H2'	1:1A:2443:A:C8	2.56	0.41
1:1A:2443:A:H2'	1:1A:2444:A:C8	2.56	0.41
1:1A:2486:U:H5	1:1A:2944:A:N1	2.18	0.41
1:1A:2591:U:H2'	1:1A:2592:U:C6	2.54	0.41
1:1A:2967:G:H2'	1:1A:2968:C:H6	1.84	0.41
1:1A:3005:U:H2'	1:1A:3006:G:O4'	2.21	0.41
1:1A:3128:C:H2'	1:1A:3129:U:C6	2.56	0.41
1:1A:3195:G:H2'	1:1A:3196:U:C6	2.55	0.41
1:1A:3452:U:H3	1:1A:3503:G:N2	2.07	0.41
3:1C:5:A:H4'	7:1G:52:VAL:HG11	2.01	0.41
5:1E:113:GLU:H	5:1E:113:GLU:HG3	1.62	0.41
10:1J:209:GLU:O	10:1J:213:GLN:HG2	2.20	0.41
11:1K:4:LEU:HD12	11:1K:4:LEU:HA	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:IM:27:GLY:O	13:IM:29:ARG:N	2.54	0.41
14:IN:44:VAL:HG23	14:IN:44:VAL:O	2.20	0.41
17:IQ:126:THR:HB	17:IQ:127:TYR:CD1	2.56	0.41
18:IR:55:LYS:HA	18:IR:55:LYS:HD3	1.81	0.41
24:IX:48:ARG:HD2	24:IX:51:ARG:NH1	2.35	0.41
28:lb:81:MET:SD	31:le:63:TYR:HE1	2.44	0.41
31:le:44:LYS:HB3	31:le:105:LEU:HD22	2.03	0.41
49:sE:17:GLY:HA2	49:sE:27:ARG:NE	2.28	0.41
50:sG:88:TRP:HA	50:sG:112:ASP:HB3	2.03	0.41
51:sH:18:G:H4'	51:sH:19:G:OP1	2.20	0.41
53:sa:77:A:O2'	53:sa:78:G:OP1	2.33	0.41
53:sa:1096:U:H2'	53:sa:1097:C:C6	2.56	0.41
53:sa:1522:U:H2'	53:sa:1523:U:H6	1.86	0.41
53:sa:1586:U:P	74:sv:57:ARG:HH21	2.44	0.41
53:sa:1738:G:H2'	53:sa:1738:G:N3	2.36	0.41
53:sa:1802:C:O2	53:sa:1912:A:N6	2.54	0.41
53:sa:1831:G:H2'	53:sa:1832:A:C8	2.55	0.41
59:sg:51:LEU:HD23	59:sg:51:LEU:HA	1.95	0.41
60:sh:282:LYS:HD2	60:sh:286:LEU:HB3	2.03	0.41
63:sk:106:GLU:HA	63:sk:111:THR:HG21	2.03	0.41
66:sn:37:ASN:OD1	66:sn:38:ALA:N	2.51	0.41
69:sq:33:VAL:HG11	69:sq:44:TYR:CD2	2.55	0.41
71:ss:27:LYS:HG2	71:ss:32:ILE:HG12	2.03	0.41
72:st:75:GLU:HB3	72:st:78:ARG:HH21	1.84	0.41
73:su:111:ASP:C	73:su:111:ASP:OD1	2.63	0.41
75:sw:42:ASN:OD1	75:sw:99:LYS:HE2	2.21	0.41
77:sy:11:MET:HB3	77:sy:11:MET:HE3	1.84	0.41
1:lA:280:U:C2	1:lA:281:A:C8	3.09	0.41
1:lA:453:A:N3	1:lA:789:C:O2'	2.46	0.41
1:lA:480:U:H2'	1:lA:481:A:O4'	2.20	0.41
1:lA:766:U:O2	36:lj:22:GLN:NE2	2.46	0.41
1:lA:943:U:O2'	1:lA:1675:A:N3	2.42	0.41
1:lA:1181:A:H5''	1:lA:1182:A:H5'	2.03	0.41
1:lA:1198:U:H3	1:lA:1204:A:H62	1.68	0.41
1:lA:1359:U:H4'	1:lA:1360:G:H3'	2.02	0.41
1:lA:1758:U:H2'	1:lA:1759:U:C6	2.55	0.41
1:lA:1847:A:H2'	1:lA:1848:A:H8	1.85	0.41
1:lA:2634:A:OP2	4:ID:64:ARG:NH2	2.54	0.41
1:lA:3287:U:H2'	1:lA:3288:U:H6	1.86	0.41
1:lA:3373:A:H1'	1:lA:3385:G:C4	2.55	0.41
3:lC:90:G:H2'	3:lC:91:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:II:105:ILE:HG22	9:II:106:LYS:O	2.21	0.41
14:IN:72:GLY:HA2	14:IN:94:ALA:C	2.46	0.41
18:IR:57:ILE:HG12	18:IR:73:CYS:SG	2.61	0.41
28:lb:76:ASN:OD1	28:lb:77:VAL:N	2.53	0.41
40:ln:54:GLU:O	40:ln:58:LYS:HG2	2.21	0.41
50:sG:69:HIS:HB3	50:sG:88:TRP:HB2	2.03	0.41
53:sa:96:C:H2'	53:sa:97:U:H6	1.86	0.41
53:sa:1173:A:H2'	53:sa:1174:C:C6	2.56	0.41
54:sb:11:ASP:OD1	54:sb:11:ASP:N	2.54	0.41
54:sb:159:ASN:HD22	54:sb:159:ASN:HA	1.66	0.41
60:sh:292:HIS:O	60:sh:297:LEU:HB2	2.20	0.41
71:ss:54:ILE:N	71:ss:60:ARG:HE	2.19	0.41
76:sx:12:PRO:HG2	76:sx:21:LEU:HD22	2.02	0.41
1:lA:493:G:H1'	1:lA:579:A:N6	2.36	0.40
1:lA:528:A:H2'	1:lA:529:U:C6	2.56	0.40
1:lA:606:A:H2'	1:lA:607:U:C6	2.55	0.40
1:lA:1270:G:O2'	33:lg:46:LYS:O	2.29	0.40
1:lA:1554:C:OP2	6:lF:196:LYS:NZ	2.43	0.40
1:lA:1681:C:C2	1:lA:1682:A:C8	3.09	0.40
1:lA:2096:U:O2	1:lA:3208:A:H4'	2.22	0.40
1:lA:2207:A:N6	39:lm:17:ARG:O	2.48	0.40
4:ID:104:ILE:HD12	4:ID:104:ILE:HA	1.90	0.40
5:IE:257:TRP:CD1	5:IE:257:TRP:C	2.99	0.40
14:IN:125:PRO:HD3	14:IN:223:GLN:O	2.21	0.40
15:IO:76:SER:OG	15:IO:107:GLU:OE2	2.38	0.40
21:IU:81:ARG:HG2	21:IU:88:ARG:CZ	2.51	0.40
50:sG:238:TYR:CD2	50:sG:274:LYS:HG3	2.57	0.40
51:sH:16:U:C2	51:sH:59:U:O2	2.74	0.40
53:sa:85:A:H2'	53:sa:86:C:H6	1.85	0.40
53:sa:92:A:H5'	53:sa:93:C:H5	1.85	0.40
53:sa:906:A:OP1	53:sa:996:C:O2'	2.31	0.40
53:sa:1262:G:C6	53:sa:1263:A:C5	3.10	0.40
53:sa:1356:A:H61	56:sd:175:GLY:CA	2.33	0.40
53:sa:1772:A:H2'	53:sa:1773:G:C8	2.57	0.40
57:se:95:GLY:O	57:se:96:LYS:HB2	2.22	0.40
57:se:99:LEU:HB2	57:se:230:LEU:HD21	2.03	0.40
59:sg:167:ASN:OD1	59:sg:168:SER:N	2.54	0.40
60:sh:155:LYS:HA	60:sh:204:SER:HB3	2.03	0.40
60:sh:273:LEU:H	60:sh:278:ARG:NE	2.19	0.40
61:si:192:LYS:H	61:si:192:LYS:HG2	1.55	0.40
62:sj:3:ILE:H	62:sj:3:ILE:HG13	1.73	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:sj:39:GLY:O	62:sj:61:GLU:HB2	2.21	0.40
64:sl:88:SER:C	64:sl:90:LEU:H	2.29	0.40
65:sm:74:VAL:HG12	65:sm:119:GLU:HA	2.03	0.40
72:st:21:TYR:N	72:st:22:PRO:HD2	2.36	0.40
72:st:24:LEU:HB2	72:st:58:MET:SD	2.61	0.40
74:sv:44:LYS:H	74:sv:44:LYS:HG2	1.63	0.40
77:sy:106:ARG:HD2	77:sy:109:ALA:O	2.21	0.40
1:lA:71:U:H1'	14:lN:59:MET:SD	2.61	0.40
1:lA:549:U:HO2'	1:lA:550:A:H8	1.64	0.40
13:lM:41:THR:OG1	13:lM:42:GLY:N	2.55	0.40
16:lP:3:PHE:HD1	20:lT:172:LEU:HD11	1.86	0.40
20:lT:30:TYR:HD2	20:lT:34:LYS:HE3	1.85	0.40
21:lU:69:ALA:HB1	21:lU:74:ARG:HB2	2.03	0.40
24:lX:33:GLY:O	24:lX:69:LYS:HG2	2.21	0.40
40:ln:9:LYS:HE2	40:ln:9:LYS:HB2	1.85	0.40
50:sG:263:ALA:HB2	50:sG:288:ILE:HB	2.02	0.40
53:sa:204:A:H3'	53:sa:205:A:C8	2.52	0.40
53:sa:440:A:OP2	58:sf:57:ARG:NH2	2.52	0.40
53:sa:1565:G:H5''	53:sa:1566:C:OP2	2.20	0.40
60:sh:298:LYS:O	60:sh:302:ARG:HB2	2.21	0.40
63:sk:103:ASN:N	63:sk:103:ASN:OD1	2.54	0.40
63:sk:139:GLN:HE22	78:sz:67:LYS:CE	2.34	0.40
67:so:40:LEU:HD23	67:so:40:LEU:HA	1.96	0.40
1:lA:447:G:N2	2:lB:17:G:OP2	2.54	0.40
1:lA:467:A:C2	1:lA:2439:A:H4'	2.56	0.40
1:lA:535:A:H1'	14:lN:155:PHE:CD2	2.56	0.40
1:lA:597:A:H2'	1:lA:598:A:H8	1.86	0.40
1:lA:797:C:H2'	1:lA:798:U:C6	2.56	0.40
1:lA:848:A:H5'	14:lN:271:LYS:NZ	2.37	0.40
1:lA:873:U:H2'	1:lA:874:A:H8	1.87	0.40
1:lA:1047:U:H2'	1:lA:1048:A:C8	2.57	0.40
1:lA:1194:A:O2'	1:lA:1195:G:H5'	2.21	0.40
1:lA:1423:U:H2'	1:lA:1424:G:O4'	2.21	0.40
1:lA:1471:A:H2'	1:lA:1472:U:C6	2.56	0.40
1:lA:1483:U:H2'	1:lA:1484:A:C8	2.56	0.40
1:lA:2025:C:H2'	1:lA:2026:U:C6	2.56	0.40
1:lA:2701:U:H2'	1:lA:2702:G:C8	2.56	0.40
1:lA:2869:A:N3	1:lA:2869:A:H2'	2.36	0.40
1:lA:2876:U:O2'	1:lA:2877:U:O4'	2.37	0.40
1:lA:2959:G:N7	1:lA:3013:C:H5'	2.37	0.40
1:lA:3023:U:O2	5:lE:252:ALA:HB3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:lA:3337:A:C5	15:lO:115:LYS:HG2	2.56	0.40
5:lE:20:LYS:HE3	5:lE:20:LYS:HB3	1.84	0.40
5:lE:222:VAL:O	5:lE:335:ARG:NH1	2.54	0.40
6:lF:7:VAL:HG13	6:lF:149:GLN:HE22	1.86	0.40
6:lF:376:ARG:HG2	6:lF:392:VAL:HG22	2.03	0.40
12:lL:171:TRP:CG	12:lL:172:GLY:H	2.39	0.40
15:lO:36:LEU:O	15:lO:105:CYS:HA	2.20	0.40
27:la:22:ASN:OD1	27:la:25:GLN:NE2	2.28	0.40
34:lh:74:ARG:HG2	34:lh:75:ALA:H	1.85	0.40
36:lj:9:ASN:HD22	36:lj:9:ASN:HA	1.52	0.40
39:lm:14:TYR:HB3	39:lm:18:TYR:HD2	1.86	0.40
45:sA:89:LYS:HA	45:sA:89:LYS:HD2	1.91	0.40
53:sa:1513:A:H2'	53:sa:1514:A:H8	1.87	0.40
53:sa:1591:G:N2	53:sa:1772:A:N3	2.69	0.40
53:sa:1597:A:N3	53:sa:1597:A:H2'	2.36	0.40
53:sa:1673:A:H8	53:sa:1673:A:O5'	2.04	0.40
55:sc:53:LYS:HE3	55:sc:53:LYS:HB3	1.75	0.40
55:sc:183:ALA:O	55:sc:186:PRO:HD2	2.21	0.40
56:sd:205:ASP:OD1	56:sd:206:THR:N	2.46	0.40
58:sf:169:ASP:OD1	58:sf:169:ASP:C	2.64	0.40
60:sh:282:LYS:C	60:sh:287:GLU:H	2.24	0.40
65:sm:3:GLU:CD	65:sm:3:GLU:H	2.29	0.40
71:ss:46:VAL:O	71:ss:49:VAL:HG22	2.21	0.40
75:sw:99:LYS:HA	75:sw:99:LYS:HD2	1.77	0.40
78:sz:12:THR:HA	78:sz:27:VAL:O	2.21	0.40
1:lA:210:U:H2'	1:lA:211:U:H6	1.87	0.40
1:lA:228:A:H2'	1:lA:229:A:H8	1.86	0.40
1:lA:2205:C:N4	1:lA:2395:C:H41	2.19	0.40
1:lA:2209:U:O4	1:lA:2223:A:H2	2.05	0.40
1:lA:2280:C:H2'	1:lA:2282:G:C8	2.56	0.40
1:lA:3031:U:C2	1:lA:3054:A:N6	2.90	0.40
1:lA:3501:A:H4'	5:lE:316:GLY:HA2	2.03	0.40
5:lE:80:GLU:OE1	5:lE:315:TYR:OH	2.26	0.40
5:lE:80:GLU:OE2	5:lE:320:ASN:ND2	2.32	0.40
11:lK:118:LYS:HE3	11:lK:118:LYS:HB3	1.84	0.40
14:lN:145:LYS:HE3	14:lN:149:ALA:HB2	2.04	0.40
15:lO:158:GLU:O	15:lO:162:LYS:HG2	2.21	0.40
20:IT:5:TYR:HB2	20:IT:60:ILE:HD11	2.02	0.40
35:li:70:LYS:HG2	35:li:73:ARG:NH1	2.36	0.40
42:lp:24:CYS:HB3	42:lp:40:CYS:HB3	1.16	0.40
43:lq:86:CYS:SG	43:lq:89:PHE:HB2	2.61	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:sH:68:A:H2'	51:sH:69:G:O4'	2.20	0.40
53:sa:860:G:H2'	53:sa:861:A:C8	2.56	0.40
53:sa:864:C:H2'	53:sa:865:A:H8	1.85	0.40
53:sa:1377:U:H2'	53:sa:1378:U:C6	2.56	0.40
60:sh:173:LEU:HD12	60:sh:173:LEU:HA	1.93	0.40
60:sh:287:GLU:HG2	60:sh:288:ALA:H	1.86	0.40
62:sj:56:ARG:HD3	62:sj:210:GLY:O	2.22	0.40
68:sp:39:VAL:HG21	68:sp:80:CYS:SG	2.61	0.40
69:sq:63:LYS:HB2	69:sq:63:LYS:HE2	1.88	0.40
70:sr:88:LYS:HB2	70:sr:88:LYS:HE3	1.90	0.40
73:su:48:ARG:HG3	73:su:80:ILE:HD11	2.02	0.40
74:sv:13:ILE:HD12	74:sv:13:ILE:HA	1.91	0.40
78:sz:64:PHE:CD1	78:sz:75:GLY:HA3	2.56	0.40
78:sz:81:ASP:O	78:sz:82:THR:C	2.64	0.40
1:lA:466:G:O2'	1:lA:2441:U:OP2	2.29	0.40
1:lA:1026:G:H4'	1:lA:1027:G:H5''	2.02	0.40
1:lA:2857:A:H2	1:lA:2901:U:O4	2.05	0.40
1:lA:3057:G:N3	1:lA:3077:A:H2	2.19	0.40
2:lB:42:A:H2'	2:lB:43:A:C8	2.57	0.40
6:lF:102:PHE:CG	6:lF:103:SER:N	2.89	0.40
14:lN:152:ILE:HG12	14:lN:152:ILE:H	1.72	0.40
14:lN:153:LYS:HD2	14:lN:153:LYS:HA	1.63	0.40
18:lR:84:PRO:HB2	18:lR:87:SER:OG	2.22	0.40
23:lW:107:ARG:CZ	23:lW:109:ILE:HD11	2.52	0.40
27:la:150:ASN:OD1	27:la:151:MET:N	2.52	0.40
28:lb:129:LYS:H	28:lb:129:LYS:HG2	1.59	0.40
43:lq:11:TYR:HB2	43:lq:18:HIS:CE1	2.56	0.40
50:sG:138:ASN:ND2	50:sG:140:VAL:HG12	2.36	0.40
53:sa:601:G:H4'	53:sa:604:G:N2	2.37	0.40
53:sa:794:U:H2'	53:sa:795:G:C8	2.57	0.40
53:sa:1774:A:H2'	53:sa:1775:U:C6	2.57	0.40
56:sd:21:ARG:HD2	75:sw:25:THR:HG21	2.04	0.40
57:se:30:GLU:OE1	57:se:52:LYS:HG2	2.21	0.40
60:sh:296:MET:O	60:sh:298:LYS:N	2.54	0.40
61:si:89:LYS:H	61:si:89:LYS:HG2	1.78	0.40
68:sp:39:VAL:HG23	68:sp:48:ILE:HB	2.02	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	1D	244/246 (99%)	232 (95%)	11 (4%)	1 (0%)	30	65
5	1E	386/402 (96%)	370 (96%)	16 (4%)	0	100	100
6	1F	416/431 (96%)	391 (94%)	25 (6%)	0	100	100
7	1G	278/286 (97%)	255 (92%)	22 (8%)	1 (0%)	30	65
8	1H	201/203 (99%)	183 (91%)	17 (8%)	1 (0%)	24	60
9	1I	208/230 (90%)	198 (95%)	9 (4%)	1 (0%)	24	60
10	1J	205/286 (72%)	191 (93%)	12 (6%)	2 (1%)	12	45
11	1K	191/197 (97%)	182 (95%)	8 (4%)	1 (0%)	24	60
12	1L	197/210 (94%)	190 (96%)	7 (4%)	0	100	100
13	1M	166/174 (95%)	161 (97%)	4 (2%)	1 (1%)	21	56
14	1N	260/291 (89%)	247 (95%)	12 (5%)	1 (0%)	30	65
15	1O	202/204 (99%)	196 (97%)	6 (3%)	0	100	100
16	1P	128/135 (95%)	126 (98%)	2 (2%)	0	100	100
17	1Q	202/204 (99%)	194 (96%)	8 (4%)	0	100	100
18	1R	153/179 (86%)	152 (99%)	1 (1%)	0	100	100
19	1S	165/167 (99%)	153 (93%)	12 (7%)	0	100	100
20	1T	171/173 (99%)	162 (95%)	9 (5%)	0	100	100
21	1U	148/198 (75%)	146 (99%)	2 (1%)	0	100	100
22	1V	163/165 (99%)	160 (98%)	3 (2%)	0	100	100
23	1W	91/137 (66%)	87 (96%)	4 (4%)	0	100	100
24	1X	131/140 (94%)	125 (95%)	6 (5%)	0	100	100
25	1Y	114/121 (94%)	112 (98%)	2 (2%)	0	100	100
26	1Z	55/163 (34%)	53 (96%)	2 (4%)	0	100	100
27	1a	208/213 (98%)	202 (97%)	6 (3%)	0	100	100
28	1b	135/139 (97%)	133 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	lc	146/148 (99%)	138 (94%)	8 (6%)	0	100	100
30	ld	58/64 (91%)	56 (97%)	2 (3%)	0	100	100
31	le	101/109 (93%)	94 (93%)	7 (7%)	0	100	100
32	lf	124/150 (83%)	123 (99%)	1 (1%)	0	100	100
33	lg	122/134 (91%)	119 (98%)	3 (2%)	0	100	100
34	lh	103/137 (75%)	96 (93%)	6 (6%)	1 (1%)	12	45
35	li	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
36	lj	104/108 (96%)	102 (98%)	2 (2%)	0	100	100
37	lk	83/104 (80%)	83 (100%)	0	0	100	100
38	ll	70/77 (91%)	65 (93%)	4 (6%)	1 (1%)	9	36
39	lm	88/93 (95%)	81 (92%)	7 (8%)	0	100	100
40	ln	71/88 (81%)	69 (97%)	2 (3%)	0	100	100
41	lo	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
42	lp	51/56 (91%)	51 (100%)	0	0	100	100
43	lq	90/98 (92%)	87 (97%)	3 (3%)	0	100	100
44	ls	1/14 (7%)	1 (100%)	0	0	100	100
45	sA	70/137 (51%)	65 (93%)	4 (6%)	1 (1%)	9	36
46	sB	96/144 (67%)	89 (93%)	6 (6%)	1 (1%)	12	45
47	sC	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
48	sD	58/69 (84%)	54 (93%)	4 (7%)	0	100	100
49	sE	53/55 (96%)	45 (85%)	8 (15%)	0	100	100
50	sG	299/321 (93%)	280 (94%)	19 (6%)	0	100	100
54	sb	203/254 (80%)	199 (98%)	4 (2%)	0	100	100
55	sc	213/255 (84%)	203 (95%)	9 (4%)	1 (0%)	24	60
56	sd	219/244 (90%)	195 (89%)	23 (10%)	1 (0%)	24	60
57	se	210/256 (82%)	203 (97%)	7 (3%)	0	100	100
58	sf	254/326 (78%)	239 (94%)	14 (6%)	1 (0%)	30	65
59	sg	181/206 (88%)	171 (94%)	10 (6%)	0	100	100
60	sh	170/266 (64%)	144 (85%)	21 (12%)	5 (3%)	3	20
61	si	154/201 (77%)	141 (92%)	10 (6%)	3 (2%)	6	30
62	sj	188/237 (79%)	181 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	sk	160/185 (86%)	157 (98%)	3 (2%)	0	100	100
64	sl	89/127 (70%)	81 (91%)	7 (8%)	1 (1%)	11	43
65	sm	152/156 (97%)	145 (95%)	7 (5%)	0	100	100
66	sn	44/136 (32%)	36 (82%)	7 (16%)	1 (2%)	5	25
67	so	148/150 (99%)	144 (97%)	4 (3%)	0	100	100
68	sp	131/146 (90%)	124 (95%)	7 (5%)	0	100	100
69	sq	107/144 (74%)	97 (91%)	9 (8%)	1 (1%)	14	48
70	sr	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
71	ss	139/157 (88%)	132 (95%)	7 (5%)	0	100	100
72	st	109/117 (93%)	104 (95%)	3 (3%)	2 (2%)	6	31
73	su	142/155 (92%)	131 (92%)	11 (8%)	0	100	100
74	sv	153/155 (99%)	148 (97%)	5 (3%)	0	100	100
75	sw	97/118 (82%)	90 (93%)	6 (6%)	1 (1%)	12	45
76	sx	81/86 (94%)	79 (98%)	2 (2%)	0	100	100
77	sy	128/141 (91%)	100 (78%)	25 (20%)	3 (2%)	5	25
78	sz	72/140 (51%)	52 (72%)	18 (25%)	2 (3%)	4	21
All	All	10526/12142 (87%)	9954 (95%)	537 (5%)	35 (0%)	37	70

All (35) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	lJ	246	GLN
34	lh	77	GLY
38	ll	40	PRO
60	sh	222	THR
60	sh	227	PRO
60	sh	228	MET
60	sh	229	ARG
61	si	43	GLU
61	si	119	PRO
66	sn	38	ALA
77	sy	84	PRO
77	sy	113	ILE
77	sy	127	SER
78	sz	53	VAL
13	lM	111	ASP

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Mol	Chain	Res	Type
45	sA	48	VAL
46	sB	14	GLY
56	sd	76	LYS
58	sf	85	MET
69	sq	112	GLY
75	sw	98	VAL
7	lG	264	LYS
60	sh	264	ARG
61	si	42	PRO
72	st	96	ILE
72	st	97	THR
8	lH	119	VAL
10	lJ	20	ALA
11	lK	134	ILE
64	sl	88	SER
78	sz	17	VAL
14	lN	156	ILE
4	lD	15	ILE
9	lI	179	VAL
55	sc	165	GLY

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	lD	195/195 (100%)	188 (96%)	7 (4%)	31	65
5	lE	331/343 (96%)	320 (97%)	11 (3%)	33	67
6	lF	336/345 (97%)	323 (96%)	13 (4%)	28	62
7	lG	227/231 (98%)	221 (97%)	6 (3%)	40	72
8	lH	172/172 (100%)	168 (98%)	4 (2%)	44	74
9	lI	178/195 (91%)	176 (99%)	2 (1%)	65	83
10	lJ	184/242 (76%)	177 (96%)	7 (4%)	29	63
11	lK	171/174 (98%)	167 (98%)	4 (2%)	44	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	IL	170/176 (97%)	165 (97%)	5 (3%)	37	70
13	IM	144/147 (98%)	141 (98%)	3 (2%)	47	75
14	IN	223/243 (92%)	217 (97%)	6 (3%)	39	71
15	IO	167/167 (100%)	164 (98%)	3 (2%)	51	77
16	IP	113/117 (97%)	111 (98%)	2 (2%)	51	77
17	IQ	171/171 (100%)	169 (99%)	2 (1%)	63	82
18	IR	127/147 (86%)	124 (98%)	3 (2%)	43	73
19	IS	142/142 (100%)	142 (100%)	0	100	100
20	IT	156/156 (100%)	151 (97%)	5 (3%)	34	67
21	IU	132/174 (76%)	128 (97%)	4 (3%)	36	69
22	IV	144/144 (100%)	141 (98%)	3 (2%)	47	75
23	IW	86/125 (69%)	79 (92%)	7 (8%)	11	38
24	IX	109/113 (96%)	104 (95%)	5 (5%)	24	58
25	IY	99/102 (97%)	97 (98%)	2 (2%)	48	76
26	IZ	52/137 (38%)	49 (94%)	3 (6%)	18	51
27	la	177/179 (99%)	171 (97%)	6 (3%)	32	66
28	lb	121/123 (98%)	119 (98%)	2 (2%)	53	78
29	lc	120/120 (100%)	118 (98%)	2 (2%)	53	78
30	ld	50/54 (93%)	48 (96%)	2 (4%)	28	62
31	le	86/92 (94%)	83 (96%)	3 (4%)	32	65
32	lf	110/128 (86%)	107 (97%)	3 (3%)	39	71
33	lg	108/116 (93%)	106 (98%)	2 (2%)	50	76
34	lh	86/116 (74%)	82 (95%)	4 (5%)	23	58
35	li	103/103 (100%)	102 (99%)	1 (1%)	68	84
36	lj	89/91 (98%)	86 (97%)	3 (3%)	32	66
37	lk	71/82 (87%)	70 (99%)	1 (1%)	59	80
38	ll	60/64 (94%)	57 (95%)	3 (5%)	22	56
39	lm	72/74 (97%)	71 (99%)	1 (1%)	59	80
40	ln	63/76 (83%)	60 (95%)	3 (5%)	23	57
41	lo	44/44 (100%)	42 (96%)	2 (4%)	24	59
42	lp	45/48 (94%)	44 (98%)	1 (2%)	45	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	lq	85/91 (93%)	85 (100%)	0	100	100
44	ls	1/1 (100%)	1 (100%)	0	100	100
45	sA	66/112 (59%)	64 (97%)	2 (3%)	36	69
46	sB	87/127 (68%)	84 (97%)	3 (3%)	32	66
47	sC	72/72 (100%)	67 (93%)	5 (7%)	14	45
48	sD	50/59 (85%)	47 (94%)	3 (6%)	17	50
49	sE	45/45 (100%)	41 (91%)	4 (9%)	9	34
50	sG	260/272 (96%)	243 (94%)	17 (6%)	15	47
54	sb	178/218 (82%)	173 (97%)	5 (3%)	38	70
55	sc	172/199 (86%)	160 (93%)	12 (7%)	14	44
56	sd	184/206 (89%)	168 (91%)	16 (9%)	9	35
57	se	193/227 (85%)	188 (97%)	5 (3%)	40	72
58	sf	223/283 (79%)	211 (95%)	12 (5%)	20	53
59	sg	165/178 (93%)	161 (98%)	4 (2%)	43	73
60	sh	146/220 (66%)	137 (94%)	9 (6%)	16	49
61	si	136/167 (81%)	127 (93%)	9 (7%)	15	46
62	sj	163/205 (80%)	160 (98%)	3 (2%)	51	77
63	sk	144/164 (88%)	139 (96%)	5 (4%)	32	65
64	sl	81/111 (73%)	71 (88%)	10 (12%)	4	21
65	sm	136/138 (99%)	134 (98%)	2 (2%)	57	80
66	sn	44/114 (39%)	40 (91%)	4 (9%)	9	33
67	so	128/128 (100%)	123 (96%)	5 (4%)	28	62
68	sp	103/114 (90%)	99 (96%)	4 (4%)	28	62
69	sq	97/127 (76%)	89 (92%)	8 (8%)	10	37
70	sr	112/112 (100%)	107 (96%)	5 (4%)	24	59
71	ss	114/126 (90%)	110 (96%)	4 (4%)	32	65
72	st	101/106 (95%)	98 (97%)	3 (3%)	36	69
73	su	122/130 (94%)	112 (92%)	10 (8%)	10	37
74	sv	132/132 (100%)	124 (94%)	8 (6%)	17	49
75	sw	90/107 (84%)	81 (90%)	9 (10%)	7	29
76	sX	75/77 (97%)	74 (99%)	1 (1%)	61	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
77	sy	104/114 (91%)	94 (90%)	10 (10%)	8	31
78	sz	67/125 (54%)	56 (84%)	11 (16%)	2	12
All	All	9110/10275 (89%)	8756 (96%)	354 (4%)	30	62

All (354) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	ID	32	ILE
4	ID	92	SER
4	ID	116	VAL
4	ID	142	ASP
4	ID	207	VAL
4	ID	218	HIS
4	ID	243	THR
5	IE	74	GLU
5	IE	90	VAL
5	IE	171	VAL
5	IE	231	VAL
5	IE	280	VAL
5	IE	323	LEU
5	IE	328	THR
5	IE	334	ARG
5	IE	339	LEU
5	IE	350	THR
5	IE	387	ASP
6	IF	66	SER
6	IF	76	ILE
6	IF	94	ASN
6	IF	115	THR
6	IF	180	ASP
6	IF	239	VAL
6	IF	359	GLU
6	IF	362	LEU
6	IF	390	VAL
6	IF	394	ASN
6	IF	396	LEU
6	IF	397	LEU
6	IF	401	VAL
7	IG	33	ARG
7	IG	37	ILE
7	IG	70	ILE

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Mol	Chain	Res	Type
7	IG	72	ASP
7	IG	200	VAL
7	IG	250	GLU
8	IH	28	GLN
8	IH	108	ARG
8	IH	122	VAL
8	IH	129	VAL
9	II	119	ASP
9	II	163	ASP
10	IJ	30	VAL
10	IJ	52	LYS
10	IJ	56	MET
10	IJ	81	LEU
10	IJ	86	ASP
10	IJ	148	VAL
10	IJ	225	MET
11	IK	102	VAL
11	IK	104	TYR
11	IK	142	VAL
11	IK	176	LYS
12	IL	7	ARG
12	IL	13	ARG
12	IL	129	VAL
12	IL	179	GLU
12	IL	183	GLN
13	IM	14	ILE
13	IM	44	THR
13	IM	172	LEU
14	IN	22	THR
14	IN	49	ILE
14	IN	61	GLN
14	IN	156	ILE
14	IN	190	LYS
14	IN	265	LYS
15	IO	33	LYS
15	IO	88	MET
15	IO	193	LYS
16	IP	71	MET
16	IP	107	MET
17	IQ	10	LEU
17	IQ	64	VAL
18	IR	18	ARG

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Mol	Chain	Res	Type
18	lR	51	VAL
18	lR	120	GLN
20	lT	11	THR
20	lT	13	LYS
20	lT	54	LEU
20	lT	75	LEU
20	lT	172	LEU
21	lU	34	LEU
21	lU	89	THR
21	lU	134	ASN
21	lU	140	GLU
22	lV	90	HIS
22	lV	112	VAL
22	lV	152	ILE
23	lW	34	LEU
23	lW	39	ASP
23	lW	70	VAL
23	lW	77	ILE
23	lW	92	LEU
23	lW	104	GLU
23	lW	108	VAL
24	lX	31	ASN
24	lX	92	ASP
24	lX	95	THR
24	lX	118	THR
24	lX	127	ASP
25	lY	57	ASP
25	lY	114	VAL
26	lZ	17	VAL
26	lZ	27	ASP
26	lZ	62	LYS
27	la	5	CYS
27	la	109	LEU
27	la	112	ASP
27	la	136	GLU
27	la	162	THR
27	la	183	THR
28	lb	37	LYS
28	lb	64	MET
29	lc	60	VAL
29	lc	141	VAL
30	ld	3	LYS

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Mol	Chain	Res	Type
30	ld	35	MET
31	le	27	TYR
31	le	69	VAL
31	le	104	ILE
32	lf	19	LYS
32	lf	50	MET
32	lf	111	VAL
33	lg	15	THR
33	lg	88	MET
34	lh	46	ASP
34	lh	57	ILE
34	lh	73	THR
34	lh	103	LEU
35	li	-5	ILE
36	lj	9	ASN
36	lj	56	VAL
36	lj	78	ASN
37	lk	20	THR
38	ll	7	CYS
38	ll	68	LYS
38	ll	72	LYS
39	lm	16	THR
40	ln	11	ILE
40	ln	24	ARG
40	ln	72	LYS
41	lo	42	ARG
41	lo	51	MET
42	lp	35	CYS
45	sA	54	THR
45	sA	80	THR
46	sB	11	SER
46	sB	50	VAL
46	sB	56	ASN
47	sC	9	LEU
47	sC	10	ASN
47	sC	35	GLU
47	sC	36	ILE
47	sC	68	THR
48	sD	38	GLU
48	sD	55	ILE
48	sD	59	LEU
49	sE	24	CYS

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Mol	Chain	Res	Type
49	sE	36	LEU
49	sE	39	CYS
49	sE	56	ASP
50	sG	5	LEU
50	sG	81	GLN
50	sG	95	TRP
50	sG	109	HIS
50	sG	112	ASP
50	sG	118	PHE
50	sG	121	ASP
50	sG	134	ILE
50	sG	197	HIS
50	sG	224	MET
50	sG	229	ASN
50	sG	245	GLN
50	sG	256	GLU
50	sG	286	MET
50	sG	290	LEU
50	sG	296	VAL
50	sG	302	VAL
54	sb	84	VAL
54	sb	124	MET
54	sb	143	GLU
54	sb	161	LEU
54	sb	204	VAL
55	sc	80	GLU
55	sc	100	LEU
55	sc	122	GLU
55	sc	131	MET
55	sc	139	VAL
55	sc	143	ARG
55	sc	197	ASP
55	sc	198	VAL
55	sc	207	LYS
55	sc	213	VAL
55	sc	220	VAL
55	sc	238	LYS
56	sd	12	VAL
56	sd	13	ASP
56	sd	17	THR
56	sd	34	GLU
56	sd	51	VAL

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Mol	Chain	Res	Type
56	sd	67	THR
56	sd	72	ILE
56	sd	76	LYS
56	sd	80	ILE
56	sd	105	VAL
56	sd	113	VAL
56	sd	133	VAL
56	sd	159	GLN
56	sd	182	TYR
56	sd	193	MET
56	sd	203	MET
57	se	63	LEU
57	se	105	LEU
57	se	171	ASN
57	se	181	ARG
57	se	231	LEU
58	sf	9	ARG
58	sf	43	ILE
58	sf	74	ILE
58	sf	76	THR
58	sf	84	PHE
58	sf	87	VAL
58	sf	181	MET
58	sf	198	VAL
58	sf	204	GLU
58	sf	217	THR
58	sf	226	ILE
58	sf	246	LEU
59	sg	15	THR
59	sg	33	ILE
59	sg	54	THR
59	sg	95	VAL
60	sh	146	ILE
60	sh	168	ASN
60	sh	195	ARG
60	sh	218	ILE
60	sh	222	THR
60	sh	228	MET
60	sh	275	THR
60	sh	294	ILE
60	sh	307	LEU
61	si	72	MET

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Mol	Chain	Res	Type
61	si	85	GLU
61	si	134	GLU
61	si	135	MET
61	si	139	VAL
61	si	141	VAL
61	si	160	THR
61	si	165	VAL
61	si	199	VAL
62	sj	27	ASN
62	sj	186	MET
62	sj	189	ASP
63	sk	61	MET
63	sk	83	LEU
63	sk	89	ASP
63	sk	112	LEU
63	sk	133	MET
64	sl	1	MET
64	sl	3	ILE
64	sl	8	ILE
64	sl	22	VAL
64	sl	26	ASP
64	sl	30	LEU
64	sl	36	ILE
64	sl	43	MET
64	sl	57	THR
64	sl	66	THR
65	sm	66	ARG
65	sm	108	VAL
66	sn	27	LYS
66	sn	29	ILE
66	sn	34	ARG
66	sn	50	ILE
67	so	30	THR
67	so	86	GLU
67	so	87	ASP
67	so	145	THR
67	so	150	VAL
68	sp	21	ASP
68	sp	23	PHE
68	sp	49	ILE
68	sp	82	ASP
69	sq	50	LEU

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Mol	Chain	Res	Type
69	sq	89	ILE
69	sq	102	THR
69	sq	104	VAL
69	sq	110	MET
69	sq	120	ILE
69	sq	125	VAL
69	sq	126	THR
70	sr	51	THR
70	sr	53	VAL
70	sr	80	ASN
70	sr	83	LEU
70	sr	98	HIS
71	ss	37	CYS
71	ss	54	ILE
71	ss	61	ILE
71	ss	126	GLU
72	st	43	THR
72	st	81	ARG
72	st	92	ASN
73	su	53	VAL
73	su	66	GLU
73	su	68	ILE
73	su	70	ASP
73	su	71	ILE
73	su	86	ASN
73	su	90	ASP
73	su	91	ASN
73	su	108	LEU
73	su	132	VAL
74	sv	9	ASP
74	sv	14	ASP
74	sv	43	CYS
74	sv	68	ASN
74	sv	82	ASP
74	sv	111	MET
74	sv	119	SER
74	sv	152	MET
75	sw	20	ILE
75	sw	24	ILE
75	sw	27	THR
75	sw	29	VAL
75	sw	68	THR

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Mol	Chain	Res	Type
75	sw	90	SER
75	sw	94	THR
75	sw	99	LYS
75	sw	100	GLU
76	sx	46	GLU
77	sy	33	ARG
77	sy	43	SER
77	sy	65	ARG
77	sy	86	ASP
77	sy	97	GLU
77	sy	99	LEU
77	sy	103	PHE
77	sy	108	HIS
77	sy	113	ILE
77	sy	121	VAL
78	sz	9	THR
78	sz	21	LEU
78	sz	26	VAL
78	sz	51	TYR
78	sz	52	LYS
78	sz	60	VAL
78	sz	62	ASN
78	sz	65	VAL
78	sz	66	THR
78	sz	83	LEU
78	sz	93	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (78) such sidechains are listed below:

Mol	Chain	Res	Type
4	lD	22	HIS
4	lD	68	GLN
4	lD	221	HIS
5	lE	42	HIS
5	lE	175	GLN
6	lF	149	GLN
6	lF	194	GLN
6	lF	269	GLN
6	lF	285	GLN
6	lF	371	GLN
7	lG	94	ASN
7	lG	118	GLN

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Mol	Chain	Res	Type
7	lG	176	HIS
7	lG	276	GLN
9	lI	81	ASN
9	lI	174	HIS
9	lI	182	HIS
10	lJ	77	ASN
10	lJ	144	GLN
10	lJ	171	GLN
10	lJ	188	HIS
10	lJ	214	ASN
11	lK	10	HIS
11	lK	25	ASN
11	lK	97	GLN
14	lN	119	ASN
14	lN	224	GLN
14	lN	234	ASN
16	lP	34	ASN
18	lR	97	ASN
20	lT	70	ASN
20	lT	72	GLN
20	lT	101	GLN
20	lT	136	HIS
22	lV	45	ASN
22	lV	58	HIS
23	lW	52	GLN
25	lY	90	ASN
27	la	10	ASN
27	la	62	GLN
29	lc	87	GLN
30	ld	38	GLN
30	ld	42	ASN
31	le	70	GLN
33	lg	117	ASN
34	lh	40	ASN
36	lj	9	ASN
38	ll	30	GLN
38	ll	66	HIS
43	lq	21	HIS
46	sB	94	ASN
50	sG	178	GLN
50	sG	202	ASN
54	sb	49	ASN

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Mol	Chain	Res	Type
55	sc	91	GLN
56	sd	40	GLN
57	se	185	GLN
58	sf	15	HIS
58	sf	96	ASN
59	sg	80	GLN
60	sh	178	ASN
62	sj	94	ASN
63	sk	139	GLN
64	sl	17	ASN
64	sl	38	ASN
65	sm	10	GLN
65	sm	97	GLN
65	sm	116	GLN
67	so	101	HIS
69	sq	52	HIS
70	sr	20	GLN
70	sr	24	GLN
70	sr	56	HIS
70	sr	64	ASN
72	st	29	HIS
74	sv	69	ASN
74	sv	87	HIS
78	sz	18	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	lA	3165/3503 (90%)	588 (18%)	0
2	lB	143/155 (92%)	32 (22%)	0
3	lC	116/117 (99%)	21 (18%)	0
51	sH	72/76 (94%)	22 (30%)	0
52	sK	5/6 (83%)	0	0
53	sa	1440/1947 (73%)	314 (21%)	0
All	All	4941/5804 (85%)	977 (19%)	0

All (977) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	lA	18	G
1	lA	22	A

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Mol	Chain	Res	Type
1	lA	29	U
1	lA	30	A
1	lA	36	A
1	lA	39	A
1	lA	45	A
1	lA	54	G
1	lA	55	G
1	lA	56	A
1	lA	62	A
1	lA	70	A
1	lA	71	U
1	lA	88	G
1	lA	105	A
1	lA	106	G
1	lA	108	C
1	lA	115	G
1	lA	116	A
1	lA	185	G
1	lA	186	A
1	lA	188	U
1	lA	189	G
1	lA	198	A
1	lA	199	G
1	lA	200	A
1	lA	206	U
1	lA	209	A
1	lA	213	A
1	lA	214	A
1	lA	221	U
1	lA	233	A
1	lA	237	C
1	lA	246	U
1	lA	256	G
1	lA	264	G
1	lA	266	A
1	lA	267	A
1	lA	270	C
1	lA	285	A
1	lA	286	U
1	lA	288	U
1	lA	289	C
1	lA	293	A

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Mol	Chain	Res	Type
1	lA	294	A
1	lA	302	U
1	lA	303	G
1	lA	311	A
1	lA	316	G
1	lA	332	G
1	lA	333	U
1	lA	342	A
1	lA	344	A
1	lA	345	A
1	lA	346	G
1	lA	350	A
1	lA	369	A
1	lA	381	A
1	lA	385	C
1	lA	396	G
1	lA	416	U
1	lA	422	G
1	lA	423	A
1	lA	424	A
1	lA	444	A
1	lA	446	A
1	lA	447	G
1	lA	448	C
1	lA	467	A
1	lA	474	A
1	lA	483	G
1	lA	493	G
1	lA	494	G
1	lA	495	A
1	lA	496	A
1	lA	501	U
1	lA	510	A
1	lA	512	G
1	lA	522	G
1	lA	535	A
1	lA	536	G
1	lA	537	U
1	lA	538	A
1	lA	539	G
1	lA	547	A
1	lA	550	A

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Mol	Chain	Res	Type
1	lA	561	G
1	lA	562	A
1	lA	564	A
1	lA	565	U
1	lA	567	U
1	lA	575	A
1	lA	577	G
1	lA	586	A
1	lA	588	G
1	lA	589	A
1	lA	596	G
1	lA	600	U
1	lA	610	A
1	lA	612	A
1	lA	613	G
1	lA	614	U
1	lA	615	G
1	lA	619	A
1	lA	620	U
1	lA	621	U
1	lA	625	A
1	lA	626	A
1	lA	627	A
1	lA	629	G
1	lA	630	A
1	lA	632	G
1	lA	633	A
1	lA	637	U
1	lA	638	A
1	lA	644	A
1	lA	645	A
1	lA	646	U
1	lA	647	C
1	lA	649	U
1	lA	651	G
1	lA	652	U
1	lA	658	A
1	lA	663	G
1	lA	675	A
1	lA	685	A
1	lA	686	A
1	lA	687	U

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Mol	Chain	Res	Type
1	lA	696	G
1	lA	699	A
1	lA	700	A
1	lA	701	A
1	lA	703	G
1	lA	704	C
1	lA	710	A
1	lA	711	A
1	lA	714	U
1	lA	715	A
1	lA	720	U
1	lA	721	A
1	lA	722	A
1	lA	724	A
1	lA	727	U
1	lA	728	U
1	lA	730	A
1	lA	732	U
1	lA	733	C
1	lA	734	C
1	lA	736	G
1	lA	740	A
1	lA	744	A
1	lA	746	A
1	lA	747	C
1	lA	755	G
1	lA	770	C
1	lA	783	A
1	lA	794	A
1	lA	811	A
1	lA	816	G
1	lA	817	A
1	lA	818	A
1	lA	825	G
1	lA	833	U
1	lA	834	A
1	lA	841	A
1	lA	843	A
1	lA	851	A
1	lA	853	A
1	lA	855	A
1	lA	864	G

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Mol	Chain	Res	Type
1	lA	865	U
1	lA	872	A
1	lA	873	U
1	lA	874	A
1	lA	881	G
1	lA	889	A
1	lA	898	U
1	lA	904	A
1	lA	905	A
1	lA	911	U
1	lA	918	G
1	lA	925	A
1	lA	934	G
1	lA	936	A
1	lA	968	C
1	lA	980	A
1	lA	993	U
1	lA	994	A
1	lA	998	U
1	lA	999	G
1	lA	1016	U
1	lA	1026	G
1	lA	1028	G
1	lA	1033	A
1	lA	1035	G
1	lA	1036	A
1	lA	1043	G
1	lA	1056	G
1	lA	1063	C
1	lA	1073	A
1	lA	1078	C
1	lA	1079	U
1	lA	1096	U
1	lA	1097	U
1	lA	1098	A
1	lA	1099	A
1	lA	1112	G
1	lA	1119	U
1	lA	1120	A
1	lA	1123	G
1	lA	1127	A
1	lA	1154	A

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Mol	Chain	Res	Type
1	lA	1166	A
1	lA	1168	C
1	lA	1183	G
1	lA	1184	A
1	lA	1210	C
1	lA	1211	A
1	lA	1219	A
1	lA	1220	A
1	lA	1221	A
1	lA	1222	U
1	lA	1242	G
1	lA	1248	U
1	lA	1256	G
1	lA	1275	A
1	lA	1284	A
1	lA	1291	G
1	lA	1292	A
1	lA	1306	A
1	lA	1312	A
1	lA	1314	A
1	lA	1315	A
1	lA	1316	C
1	lA	1325	C
1	lA	1343	A
1	lA	1344	U
1	lA	1345	U
1	lA	1360	G
1	lA	1361	G
1	lA	1370	G
1	lA	1388	A
1	lA	1389	U
1	lA	1410	A
1	lA	1411	A
1	lA	1417	G
1	lA	1429	U
1	lA	1431	G
1	lA	1433	U
1	lA	1437	A
1	lA	1440	A
1	lA	1441	U
1	lA	1447	C
1	lA	1450	A

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Mol	Chain	Res	Type
1	lA	1455	A
1	lA	1474	A
1	lA	1475	A
1	lA	1476	G
1	lA	1477	A
1	lA	1478	C
1	lA	1480	U
1	lA	1495	A
1	lA	1499	G
1	lA	1500	A
1	lA	1502	A
1	lA	1503	U
1	lA	1505	G
1	lA	1516	A
1	lA	1517	C
1	lA	1521	A
1	lA	1527	A
1	lA	1534	U
1	lA	1553	A
1	lA	1568	G
1	lA	1570	U
1	lA	1571	C
1	lA	1580	A
1	lA	1584	G
1	lA	1603	A
1	lA	1604	A
1	lA	1605	A
1	lA	1606	A
1	lA	1607	A
1	lA	1622	A
1	lA	1624	G
1	lA	1649	U
1	lA	1652	U
1	lA	1674	U
1	lA	1677	A
1	lA	1690	A
1	lA	1698	G
1	lA	1729	G
1	lA	1735	A
1	lA	1737	A
1	lA	1738	G
1	lA	1753	A

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Mol	Chain	Res	Type
1	lA	1754	G
1	lA	1767	A
1	lA	1810	A
1	lA	1818	C
1	lA	1821	A
1	lA	1822	U
1	lA	1823	C
1	lA	1864	C
1	lA	1865	U
1	lA	1897	A
1	lA	1898	A
1	lA	1907	A
1	lA	1913	G
1	lA	1914	A
1	lA	1925	A
1	lA	1926	U
1	lA	1928	G
1	lA	1936	A
1	lA	1937	A
1	lA	1938	G
1	lA	1958	A
1	lA	1959	U
1	lA	1960	U
1	lA	1961	G
1	lA	1965	U
1	lA	1975	G
1	lA	1983	A
1	lA	1984	A
1	lA	2040	A
1	lA	2043	A
1	lA	2044	C
1	lA	2050	C
1	lA	2051	A
1	lA	2067	A
1	lA	2079	A
1	lA	2080	A
1	lA	2081	A
1	lA	2083	A
1	lA	2095	G
1	lA	2098	A
1	lA	2108	G
1	lA	2109	C

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Mol	Chain	Res	Type
1	lA	2132	A
1	lA	2153	U
1	lA	2178	A
1	lA	2179	U
1	lA	2184	A
1	lA	2190	A
1	lA	2193	G
1	lA	2197	G
1	lA	2198	G
1	lA	2207	A
1	lA	2210	G
1	lA	2218	A
1	lA	2233	G
1	lA	2234	A
1	lA	2245	A
1	lA	2246	G
1	lA	2250	C
1	lA	2263	G
1	lA	2274	A
1	lA	2281	U
1	lA	2285	U
1	lA	2286	G
1	lA	2299	A
1	lA	2301	U
1	lA	2308	A
1	lA	2325	G
1	lA	2330	U
1	lA	2331	A
1	lA	2332	A
1	lA	2333	C
1	lA	2335	A
1	lA	2336	U
1	lA	2338	A
1	lA	2342	U
1	lA	2343	C
1	lA	2348	G
1	lA	2349	G
1	lA	2355	A
1	lA	2356	A
1	lA	2360	C
1	lA	2374	U
1	lA	2383	G

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Mol	Chain	Res	Type
1	lA	2384	C
1	lA	2386	U
1	lA	2389	A
1	lA	2390	U
1	lA	2391	G
1	lA	2395	C
1	lA	2397	C
1	lA	2410	U
1	lA	2411	G
1	lA	2412	U
1	lA	2439	A
1	lA	2440	G
1	lA	2441	U
1	lA	2449	A
1	lA	2450	C
1	lA	2451	G
1	lA	2461	G
1	lA	2462	G
1	lA	2469	G
1	lA	2470	G
1	lA	2473	A
1	lA	2478	A
1	lA	2479	G
1	lA	2480	A
1	lA	2487	U
1	lA	2494	G
1	lA	2509	U
1	lA	2513	A
1	lA	2514	A
1	lA	2515	A
1	lA	2589	C
1	lA	2594	C
1	lA	2595	G
1	lA	2598	A
1	lA	2601	U
1	lA	2629	A
1	lA	2637	A
1	lA	2651	A
1	lA	2655	G
1	lA	2656	G
1	lA	2663	A
1	lA	2676	G

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Mol	Chain	Res	Type
1	lA	2677	G
1	lA	2684	G
1	lA	2689	G
1	lA	2696	A
1	lA	2715	G
1	lA	2722	U
1	lA	2726	A
1	lA	2727	A
1	lA	2744	A
1	lA	2747	G
1	lA	2759	A
1	lA	2761	A
1	lA	2764	A
1	lA	2766	A
1	lA	2784	G
1	lA	2797	A
1	lA	2798	G
1	lA	2799	U
1	lA	2819	U
1	lA	2822	U
1	lA	2823	G
1	lA	2825	C
1	lA	2832	A
1	lA	2842	U
1	lA	2843	U
1	lA	2844	U
1	lA	2858	A
1	lA	2859	U
1	lA	2860	U
1	lA	2861	U
1	lA	2862	A
1	lA	2864	A
1	lA	2865	A
1	lA	2866	C
1	lA	2867	A
1	lA	2868	U
1	lA	2870	U
1	lA	2876	U
1	lA	2885	G
1	lA	2887	G
1	lA	2889	G
1	lA	2890	A

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Mol	Chain	Res	Type
1	lA	2891	G
1	lA	2895	G
1	lA	2897	A
1	lA	2898	A
1	lA	2899	G
1	lA	2900	G
1	lA	2901	U
1	lA	2902	G
1	lA	2903	A
1	lA	2904	U
1	lA	2905	U
1	lA	2916	C
1	lA	2920	U
1	lA	2925	A
1	lA	2926	U
1	lA	2931	C
1	lA	2939	G
1	lA	2943	G
1	lA	2944	A
1	lA	2945	A
1	lA	2946	A
1	lA	2951	A
1	lA	2953	C
1	lA	2959	G
1	lA	2960	A
1	lA	2977	G
1	lA	2985	C
1	lA	2988	A
1	lA	3009	C
1	lA	3015	A
1	lA	3019	C
1	lA	3030	A
1	lA	3041	G
1	lA	3047	U
1	lA	3066	U
1	lA	3073	U
1	lA	3078	U
1	lA	3079	A
1	lA	3084	A
1	lA	3085	C
1	lA	3090	G
1	lA	3114	A

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Mol	Chain	Res	Type
1	lA	3126	C
1	lA	3133	G
1	lA	3141	A
1	lA	3142	G
1	lA	3143	A
1	lA	3144	U
1	lA	3145	U
1	lA	3146	U
1	lA	3147	U
1	lA	3148	C
1	lA	3151	A
1	lA	3166	G
1	lA	3175	A
1	lA	3200	G
1	lA	3210	U
1	lA	3212	U
1	lA	3213	U
1	lA	3223	G
1	lA	3232	G
1	lA	3240	A
1	lA	3246	A
1	lA	3247	C
1	lA	3254	U
1	lA	3256	A
1	lA	3259	U
1	lA	3271	G
1	lA	3277	C
1	lA	3278	A
1	lA	3285	A
1	lA	3286	A
1	lA	3287	U
1	lA	3299	G
1	lA	3327	A
1	lA	3332	A
1	lA	3334	U
1	lA	3335	U
1	lA	3336	G
1	lA	3337	A
1	lA	3338	A
1	lA	3344	U
1	lA	3345	A
1	lA	3351	U

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Mol	Chain	Res	Type
1	lA	3353	U
1	lA	3354	A
1	lA	3359	U
1	lA	3360	U
1	lA	3361	A
1	lA	3383	A
1	lA	3384	A
1	lA	3385	G
1	lA	3392	G
1	lA	3398	U
1	lA	3399	G
1	lA	3401	G
1	lA	3405	A
1	lA	3406	C
1	lA	3409	A
1	lA	3410	A
1	lA	3411	U
1	lA	3412	U
1	lA	3413	U
1	lA	3415	A
1	lA	3416	A
1	lA	3423	C
1	lA	3430	U
1	lA	3431	U
1	lA	3433	U
1	lA	3447	A
1	lA	3462	A
1	lA	3466	U
1	lA	3467	U
1	lA	3468	U
1	lA	3469	A
1	lA	3472	G
1	lA	3477	U
1	lA	3478	U
1	lA	3480	A
1	lA	3491	C
1	lA	3492	G
1	lA	3498	U
1	lA	3499	G
1	lA	3500	A
2	lB	4	A
2	lB	5	A

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Mol	Chain	Res	Type
2	lB	36	G
2	lB	40	U
2	lB	51	A
2	lB	53	G
2	lB	54	A
2	lB	61	A
2	lB	62	U
2	lB	64	A
2	lB	65	G
2	lB	72	G
2	lB	73	A
2	lB	80	A
2	lB	81	A
2	lB	82	A
2	lB	85	U
2	lB	86	G
2	lB	92	C
2	lB	95	A
2	lB	102	A
2	lB	103	A
2	lB	104	U
2	lB	106	C
2	lB	109	G
2	lB	110	A
2	lB	113	G
2	lB	131	A
2	lB	137	A
2	lB	147	C
2	lB	150	U
2	lB	151	A
3	lC	6	G
3	lC	17	G
3	lC	18	U
3	lC	19	U
3	lC	22	C
3	lC	32	A
3	lC	37	A
3	lC	40	G
3	lC	47	A
3	lC	49	C
3	lC	52	G
3	lC	53	C

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Mol	Chain	Res	Type
3	lC	55	C
3	lC	63	C
3	lC	68	C
3	lC	72	C
3	lC	73	G
3	lC	90	G
3	lC	99	U
3	lC	109	G
3	lC	117	C
51	sH	2	A
51	sH	3	C
51	sH	10	G
51	sH	12	U
51	sH	14	A
51	sH	18	G
51	sH	19	G
51	sH	22	G
51	sH	23	A
51	sH	45	U
51	sH	46	G
51	sH	47	U
51	sH	48	C
51	sH	49	A
51	sH	50	U
51	sH	55	U
51	sH	56	C
51	sH	57	G
51	sH	59	U
51	sH	67	A
51	sH	69	G
51	sH	76	A
53	sa	4	C
53	sa	17	C
53	sa	24	U
53	sa	25	A
53	sa	26	U
53	sa	33	A
53	sa	41	G
53	sa	42	A
53	sa	46	A
53	sa	49	C
53	sa	56	G

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Mol	Chain	Res	Type
53	sa	59	U
53	sa	61	A
53	sa	62	G
53	sa	64	A
53	sa	65	U
53	sa	67	A
53	sa	68	A
53	sa	69	G
53	sa	70	A
53	sa	72	C
53	sa	74	A
53	sa	75	G
53	sa	76	U
53	sa	77	A
53	sa	78	G
53	sa	79	G
53	sa	103	U
53	sa	104	A
53	sa	113	A
53	sa	114	G
53	sa	115	U
53	sa	123	G
53	sa	135	C
53	sa	136	A
53	sa	139	G
53	sa	141	U
53	sa	148	G
53	sa	154	G
53	sa	164	A
53	sa	171	A
53	sa	173	A
53	sa	205	A
53	sa	213	A
53	sa	243	U
53	sa	244	U
53	sa	246	G
53	sa	252	C
53	sa	253	A
53	sa	262	G
53	sa	263	U
53	sa	264	A
53	sa	287	A

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Mol	Chain	Res	Type
53	sa	294	G
53	sa	295	A
53	sa	296	G
53	sa	299	U
53	sa	306	U
53	sa	310	U
53	sa	311	C
53	sa	313	A
53	sa	317	G
53	sa	324	G
53	sa	332	G
53	sa	333	A
53	sa	345	A
53	sa	347	A
53	sa	354	A
53	sa	355	A
53	sa	356	C
53	sa	365	G
53	sa	385	G
53	sa	388	C
53	sa	394	A
53	sa	395	G
53	sa	396	A
53	sa	397	U
53	sa	399	G
53	sa	411	A
53	sa	412	A
53	sa	413	G
53	sa	414	G
53	sa	417	G
53	sa	419	C
53	sa	420	A
53	sa	421	G
53	sa	430	U
53	sa	434	U
53	sa	439	C
53	sa	448	A
53	sa	449	U
53	sa	451	G
53	sa	452	A
53	sa	456	G
53	sa	463	A

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Mol	Chain	Res	Type
53	sa	470	A
53	sa	551	G
53	sa	553	C
53	sa	555	G
53	sa	559	C
53	sa	561	A
53	sa	562	G
53	sa	566	C
53	sa	568	G
53	sa	571	G
53	sa	572	U
53	sa	576	U
53	sa	579	A
53	sa	584	C
53	sa	588	A
53	sa	589	G
53	sa	602	U
53	sa	604	G
53	sa	605	C
53	sa	613	A
53	sa	614	A
53	sa	616	A
53	sa	617	C
53	sa	618	G
53	sa	628	G
53	sa	742	G
53	sa	746	A
53	sa	756	G
53	sa	757	U
53	sa	765	A
53	sa	767	A
53	sa	768	A
53	sa	769	C
53	sa	771	U
53	sa	772	U
53	sa	773	A
53	sa	774	U
53	sa	775	G
53	sa	776	U
53	sa	777	U
53	sa	781	G
53	sa	782	A

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Mol	Chain	Res	Type
53	sa	783	A
53	sa	784	U
53	sa	785	A
53	sa	786	U
53	sa	803	G
53	sa	804	C
53	sa	840	U
53	sa	842	A
53	sa	843	A
53	sa	845	A
53	sa	852	A
53	sa	853	U
53	sa	856	G
53	sa	902	U
53	sa	911	C
53	sa	913	A
53	sa	915	A
53	sa	922	G
53	sa	924	A
53	sa	927	U
53	sa	930	C
53	sa	932	C
53	sa	939	G
53	sa	940	U
53	sa	946	A
53	sa	972	A
53	sa	973	A
53	sa	984	U
53	sa	985	A
53	sa	1006	A
53	sa	1008	C
53	sa	1012	G
53	sa	1020	A
53	sa	1033	A
53	sa	1091	C
53	sa	1094	G
53	sa	1106	A
53	sa	1117	U
53	sa	1118	G
53	sa	1122	U
53	sa	1123	U
53	sa	1134	G

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Mol	Chain	Res	Type
53	sa	1135	G
53	sa	1140	G
53	sa	1163	A
53	sa	1164	A
53	sa	1176	G
53	sa	1177	A
53	sa	1184	C
53	sa	1185	A
53	sa	1192	G
53	sa	1210	U
53	sa	1219	A
53	sa	1221	A
53	sa	1224	G
53	sa	1225	G
53	sa	1227	A
53	sa	1232	U
53	sa	1239	A
53	sa	1242	G
53	sa	1243	A
53	sa	1253	G
53	sa	1254	G
53	sa	1255	A
53	sa	1266	A
53	sa	1269	A
53	sa	1270	G
53	sa	1271	U
53	sa	1276	U
53	sa	1277	C
53	sa	1281	A
53	sa	1282	U
53	sa	1283	U
53	sa	1284	U
53	sa	1287	U
53	sa	1298	G
53	sa	1299	C
53	sa	1310	U
53	sa	1311	U
53	sa	1312	A
53	sa	1316	G
53	sa	1317	G
53	sa	1326	U
53	sa	1331	C

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Mol	Chain	Res	Type
53	sa	1332	A
53	sa	1339	U
53	sa	1340	U
53	sa	1343	G
53	sa	1346	A
53	sa	1365	U
53	sa	1370	A
53	sa	1371	U
53	sa	1379	C
53	sa	1386	U
53	sa	1389	G
53	sa	1393	G
53	sa	1394	A
53	sa	1395	A
53	sa	1396	A
53	sa	1426	C
53	sa	1427	U
53	sa	1428	U
53	sa	1438	A
53	sa	1439	C
53	sa	1440	A
53	sa	1442	A
53	sa	1520	C
53	sa	1522	U
53	sa	1534	A
53	sa	1535	G
53	sa	1540	G
53	sa	1551	A
53	sa	1552	G
53	sa	1554	C
53	sa	1566	C
53	sa	1567	A
53	sa	1578	A
53	sa	1580	U
53	sa	1581	G
53	sa	1588	C
53	sa	1593	G
53	sa	1669	A
53	sa	1670	A
53	sa	1671	A
53	sa	1673	A
53	sa	1678	A

*Continued on next page...*

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Mol	Chain	Res	Type
53	sa	1683	A
53	sa	1688	A
53	sa	1689	A
53	sa	1690	A
53	sa	1691	A
53	sa	1694	A
53	sa	1697	U
53	sa	1701	U
53	sa	1702	G
53	sa	1703	A
53	sa	1706	G
53	sa	1708	G
53	sa	1711	A
53	sa	1712	A
53	sa	1713	A
53	sa	1717	U
53	sa	1720	G
53	sa	1723	U
53	sa	1725	A
53	sa	1735	A
53	sa	1736	A
53	sa	1750	G
53	sa	1767	A
53	sa	1773	G
53	sa	1777	A
53	sa	1780	A
53	sa	1783	U
53	sa	1785	C
53	sa	1788	G
53	sa	1797	A
53	sa	1800	C
53	sa	1801	A
53	sa	1824	G
53	sa	1846	G
53	sa	1849	U
53	sa	1850	C
53	sa	1877	A
53	sa	1897	A
53	sa	1903	A
53	sa	1907	G
53	sa	1909	A
53	sa	1913	A

*Continued on next page...*

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Mol	Chain	Res	Type
53	sa	1916	U
53	sa	1927	G
53	sa	1929	A
53	sa	1930	C
53	sa	1939	G
53	sa	1940	G
53	sa	1941	A
53	sa	1943	C
53	sa	1945	U

There are no RNA pucker outliers to report.

## 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](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

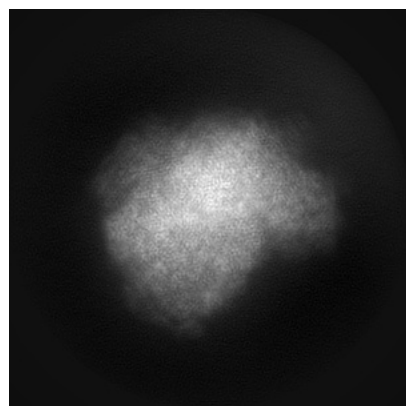
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64713. These allow visual inspection of the internal detail of the map and identification of artifacts.

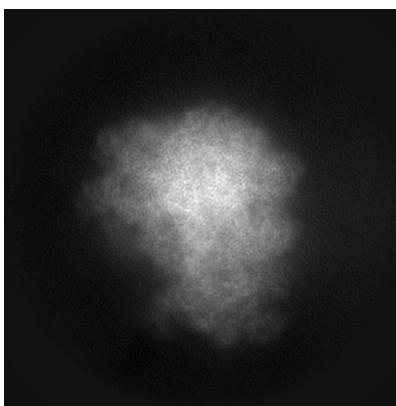
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

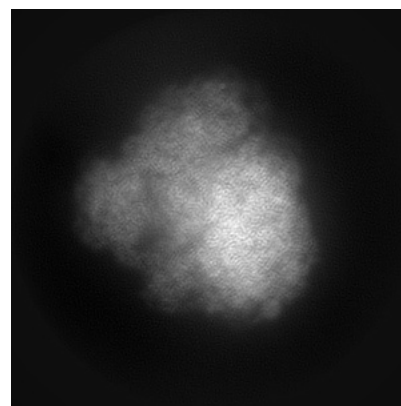
#### 6.1.1 Primary map



X

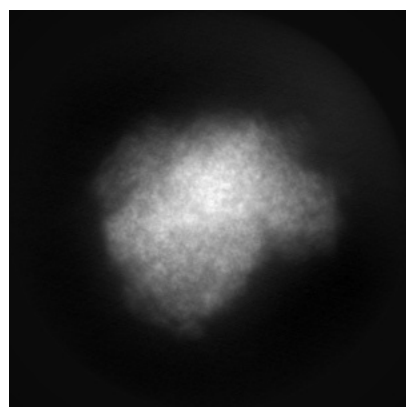


Y

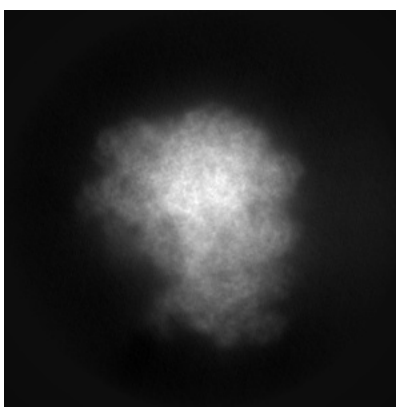


Z

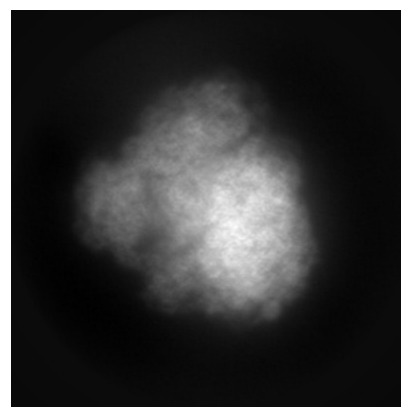
#### 6.1.2 Raw map



X



Y

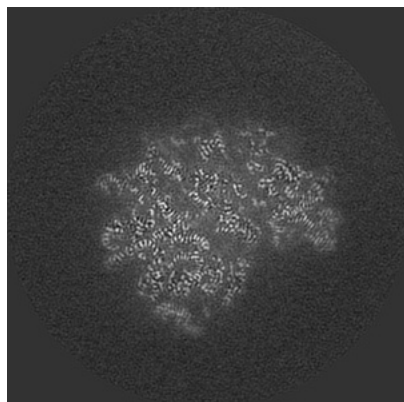


Z

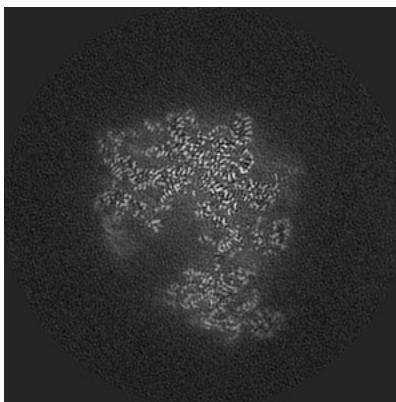
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

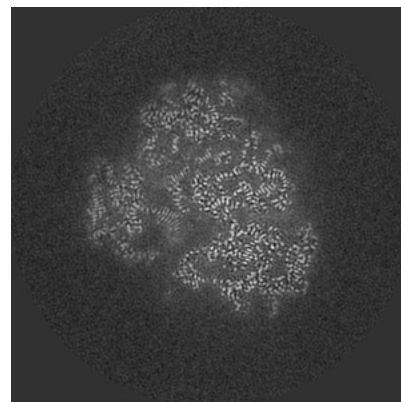
### 6.2.1 Primary map



X Index: 200

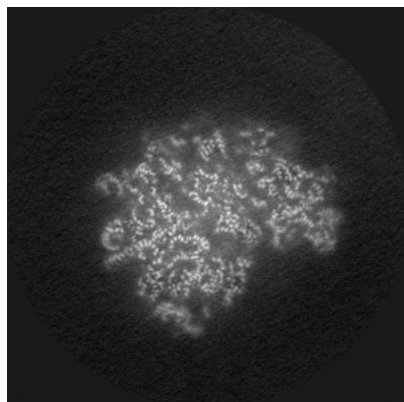


Y Index: 200

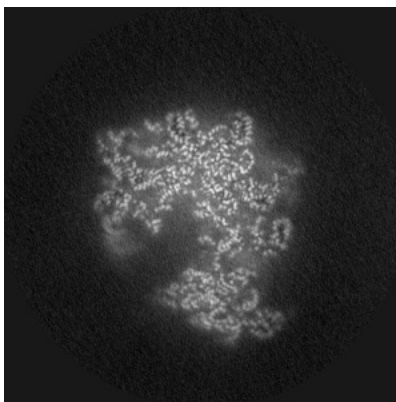


Z Index: 200

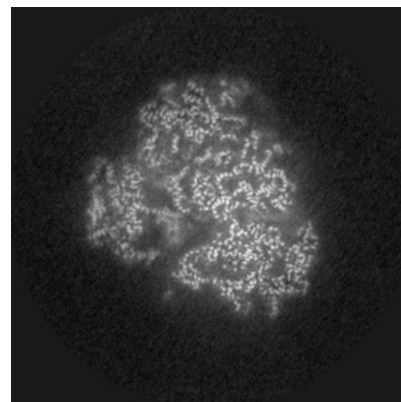
### 6.2.2 Raw map



X Index: 200



Y Index: 200

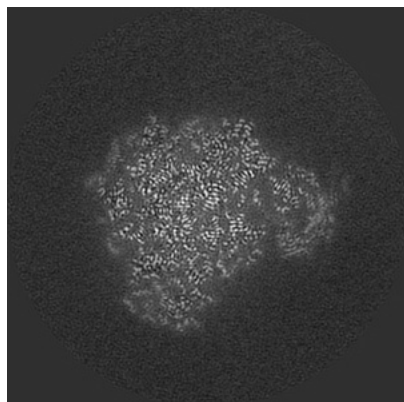


Z Index: 200

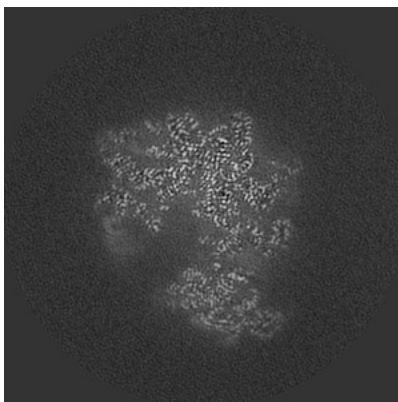
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

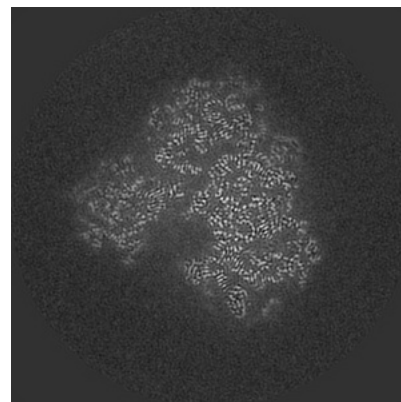
### 6.3.1 Primary map



X Index: 221

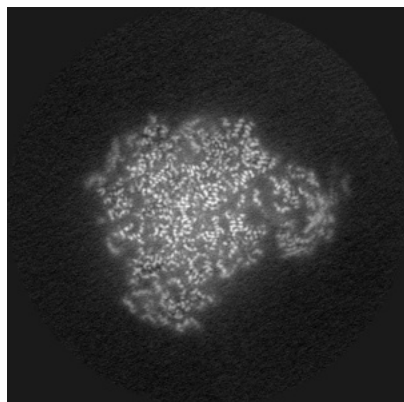


Y Index: 201

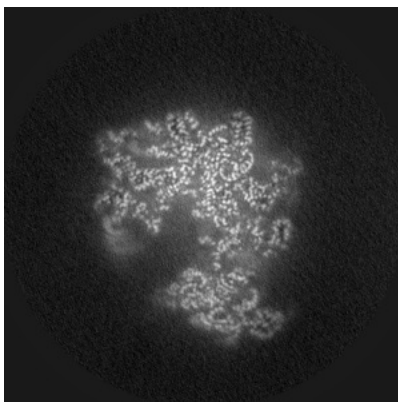


Z Index: 212

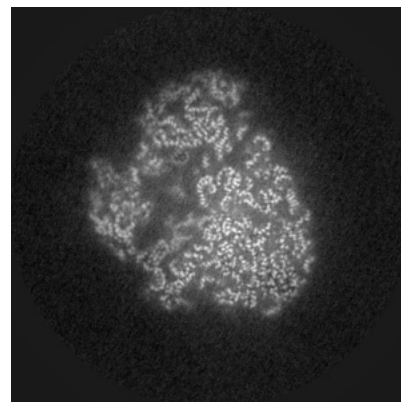
### 6.3.2 Raw map



X Index: 221



Y Index: 201



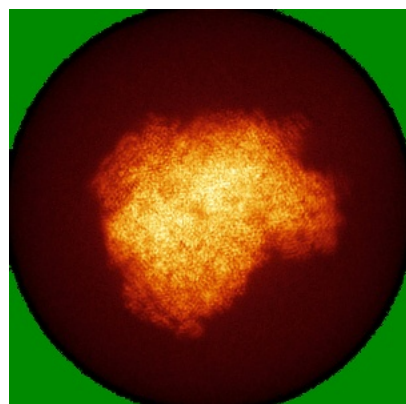
Z Index: 191

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

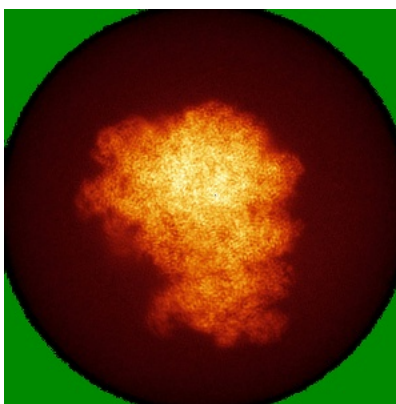


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

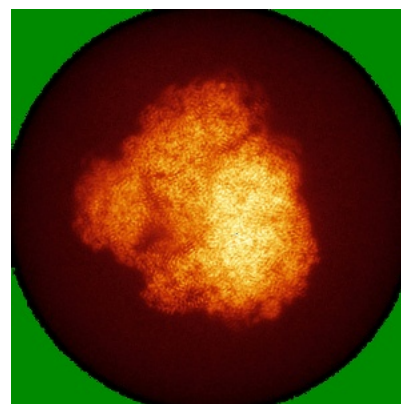
### 6.4.1 Primary map



X

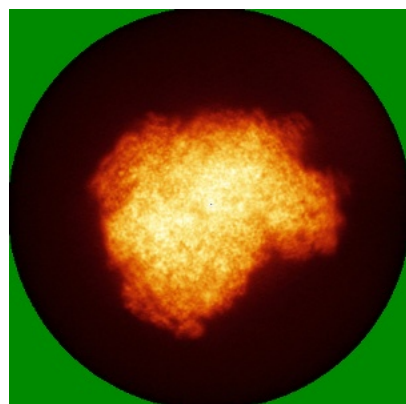


Y

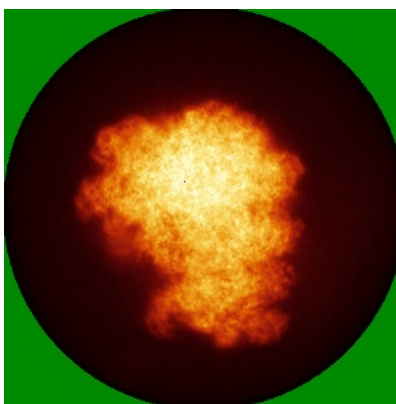


Z

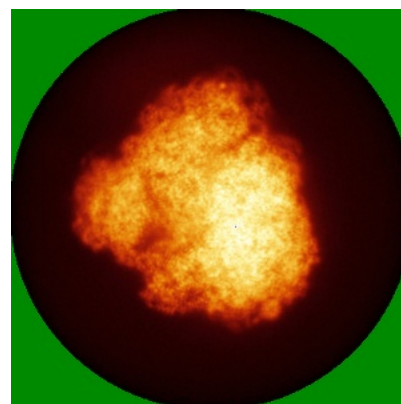
### 6.4.2 Raw map



X



Y

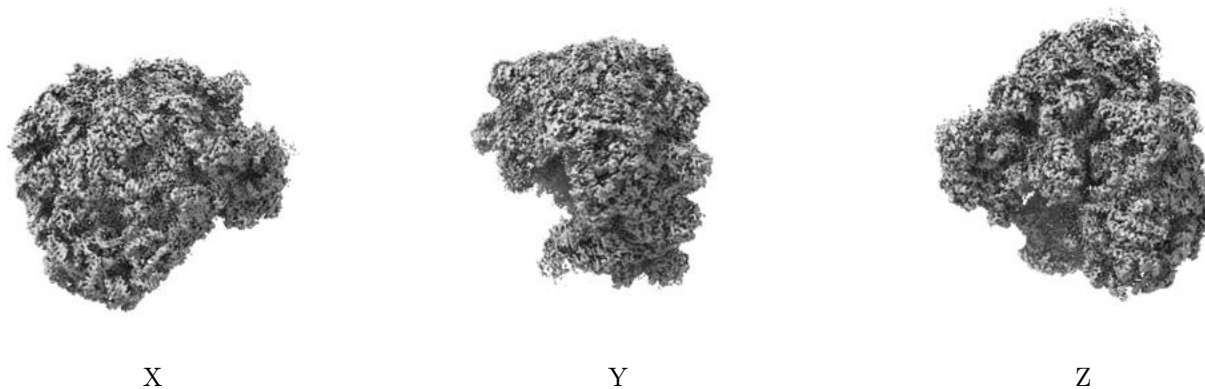


Z

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

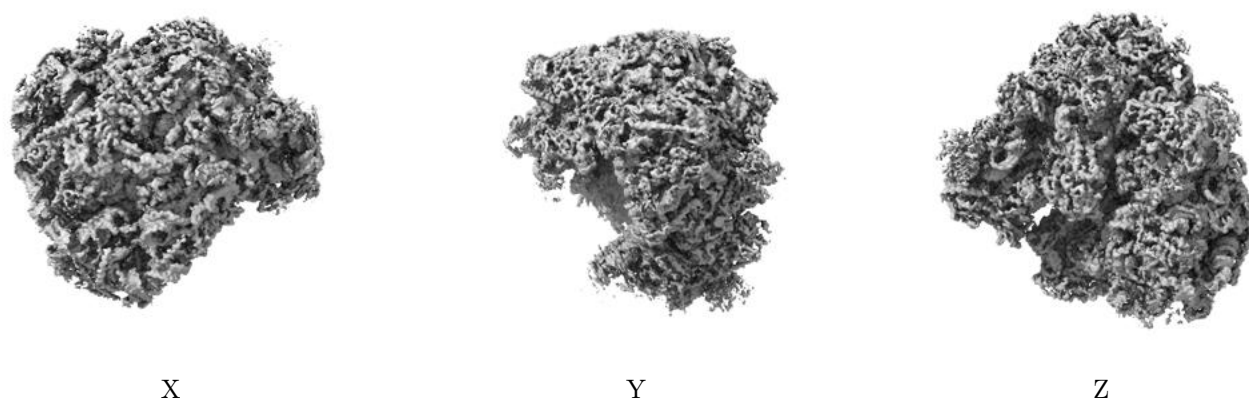
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



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

## 6.6 Mask visualisation [i](#)

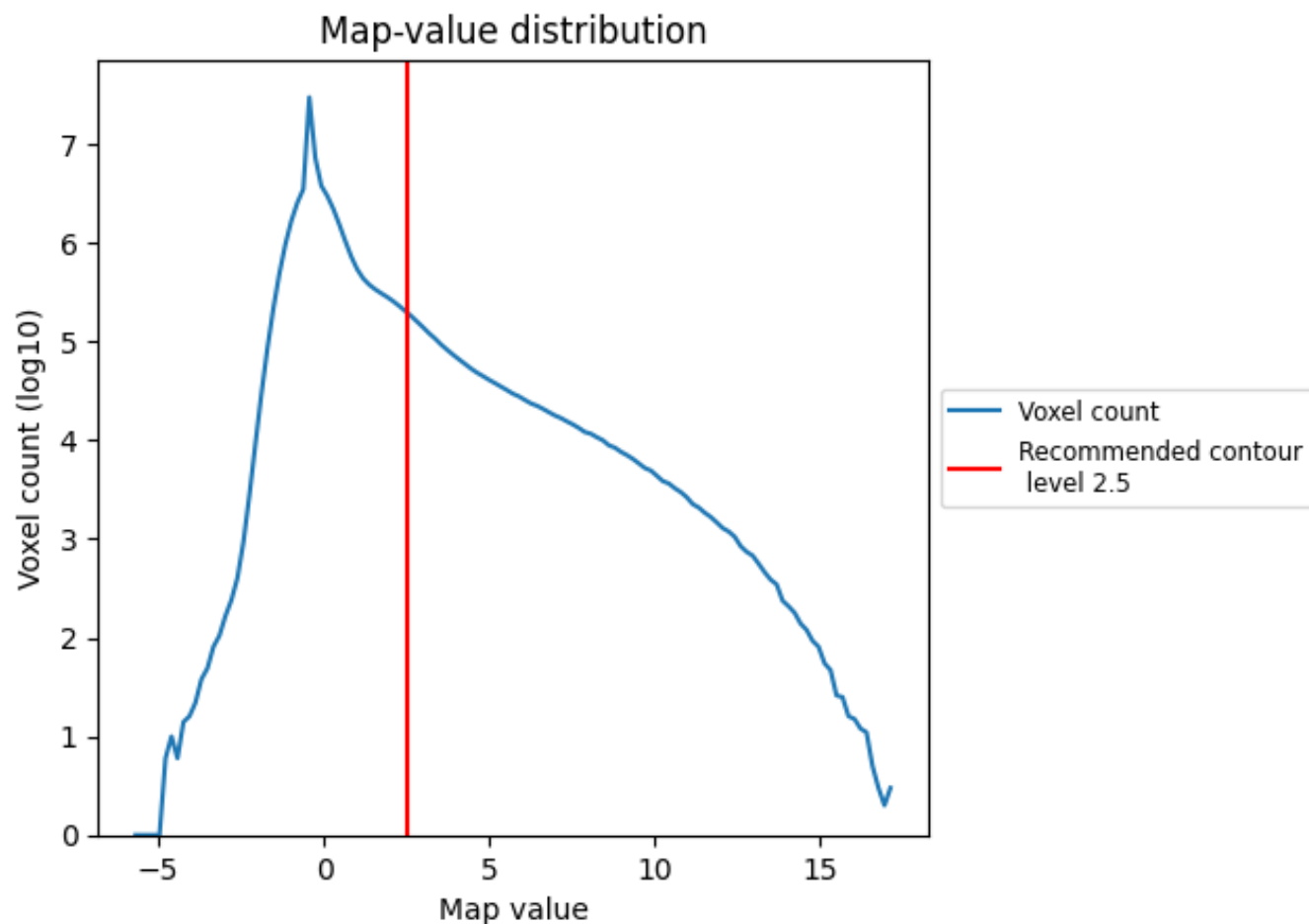
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

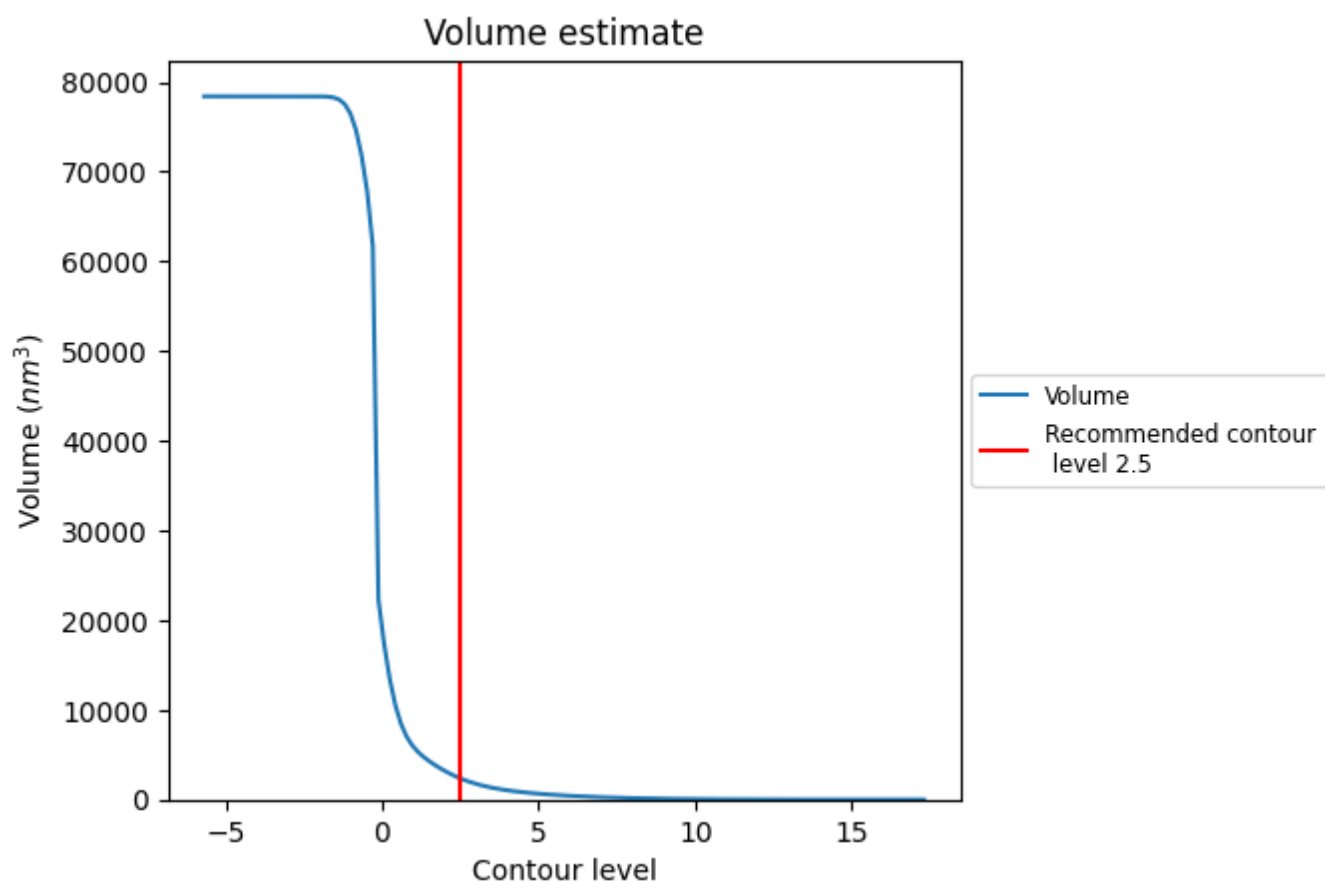
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

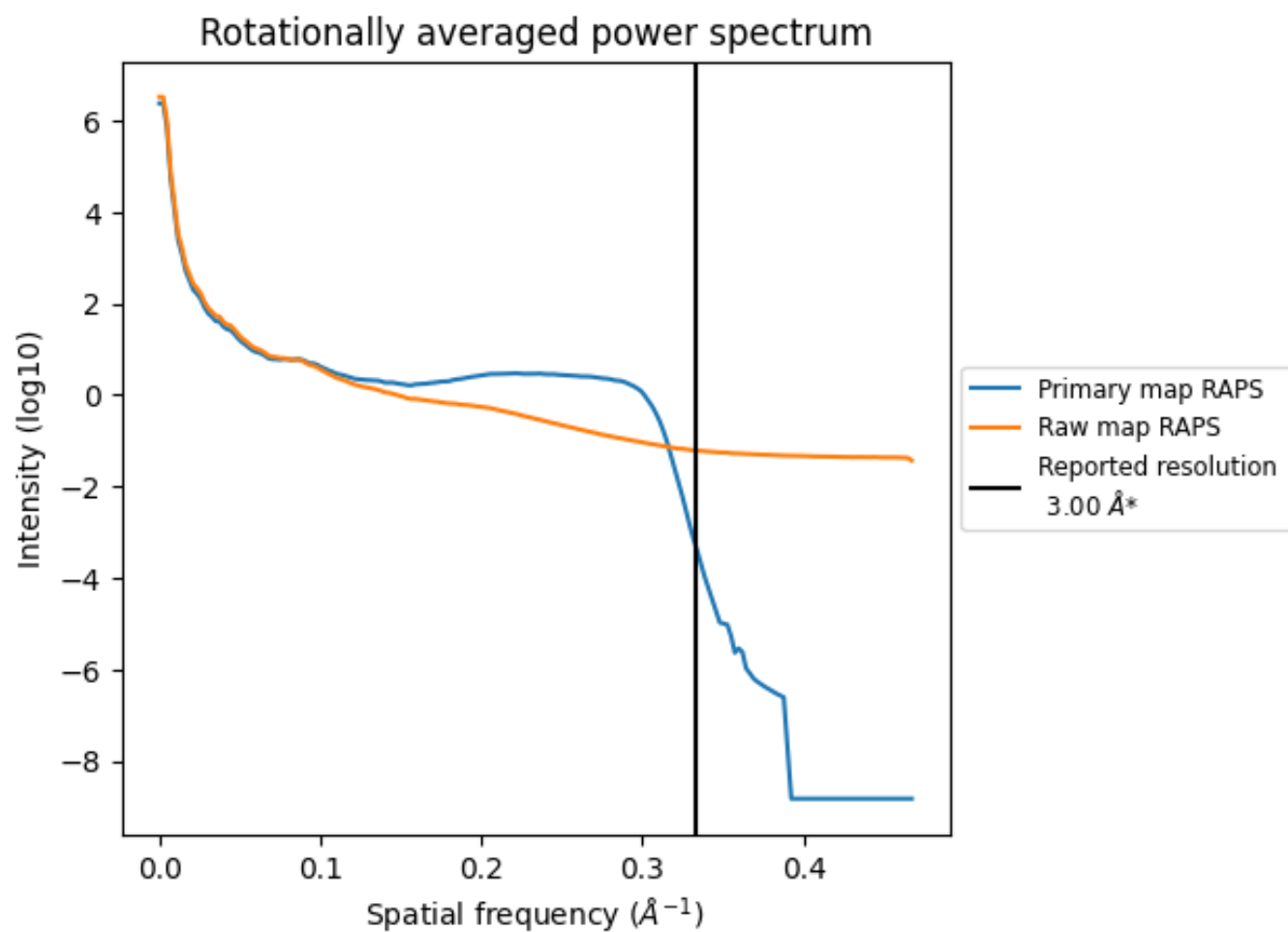
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2367 nm<sup>3</sup>; this corresponds to an approximate mass of 2138 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 ⓘ

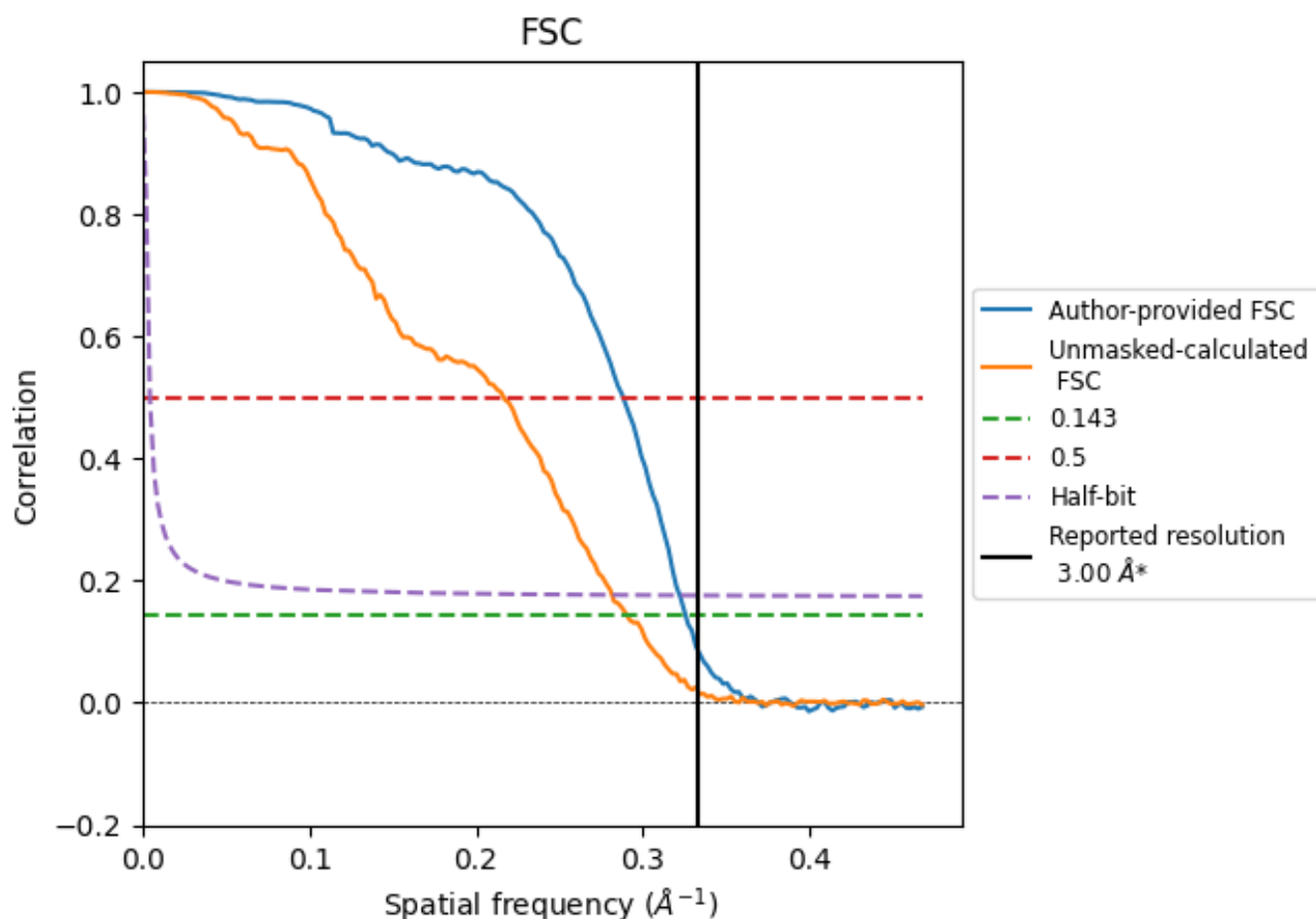


\*Reported resolution corresponds to spatial frequency of 0.333 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.333  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

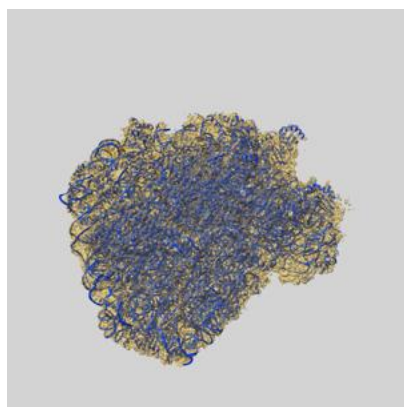
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.07	3.47	3.10
Unmasked-calculated*	3.44	4.62	3.55

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.44 differs from the reported value 3.0 by more than 10 %

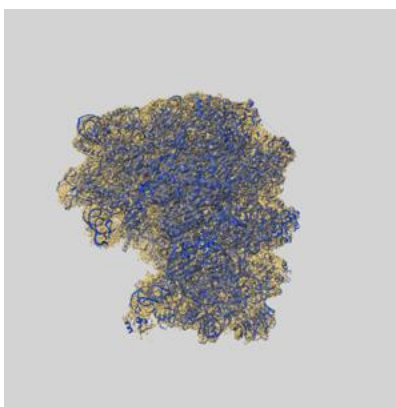
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-64713 and PDB model 9V21. Per-residue inclusion information can be found in [section 3](#) on [page 18](#).

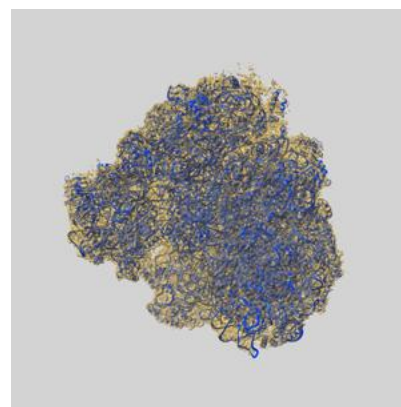
### 9.1 Map-model overlay [i](#)



X



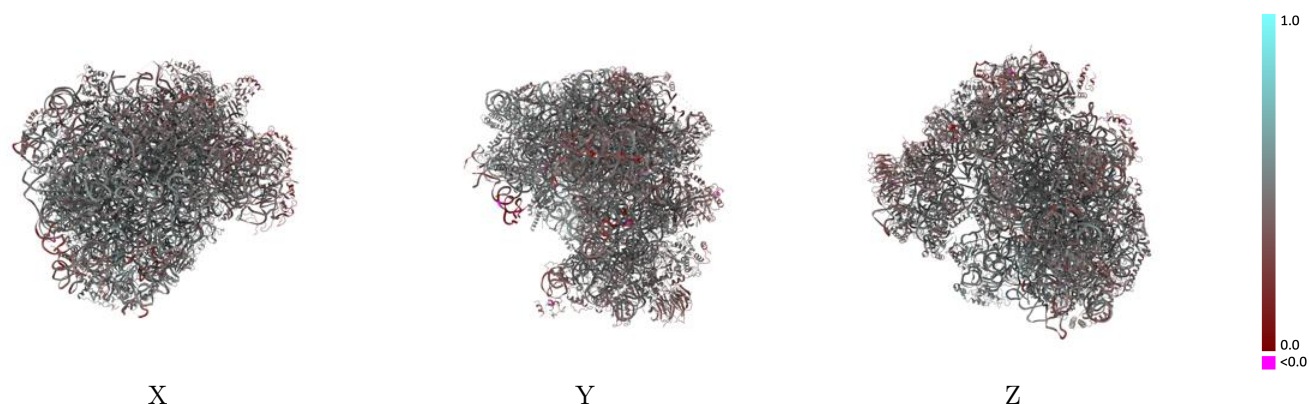
Y



Z

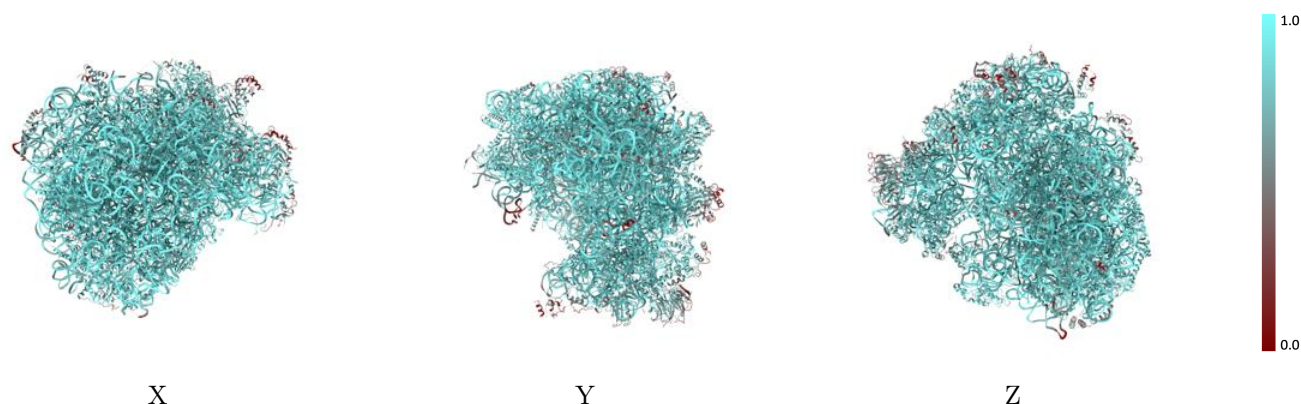
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



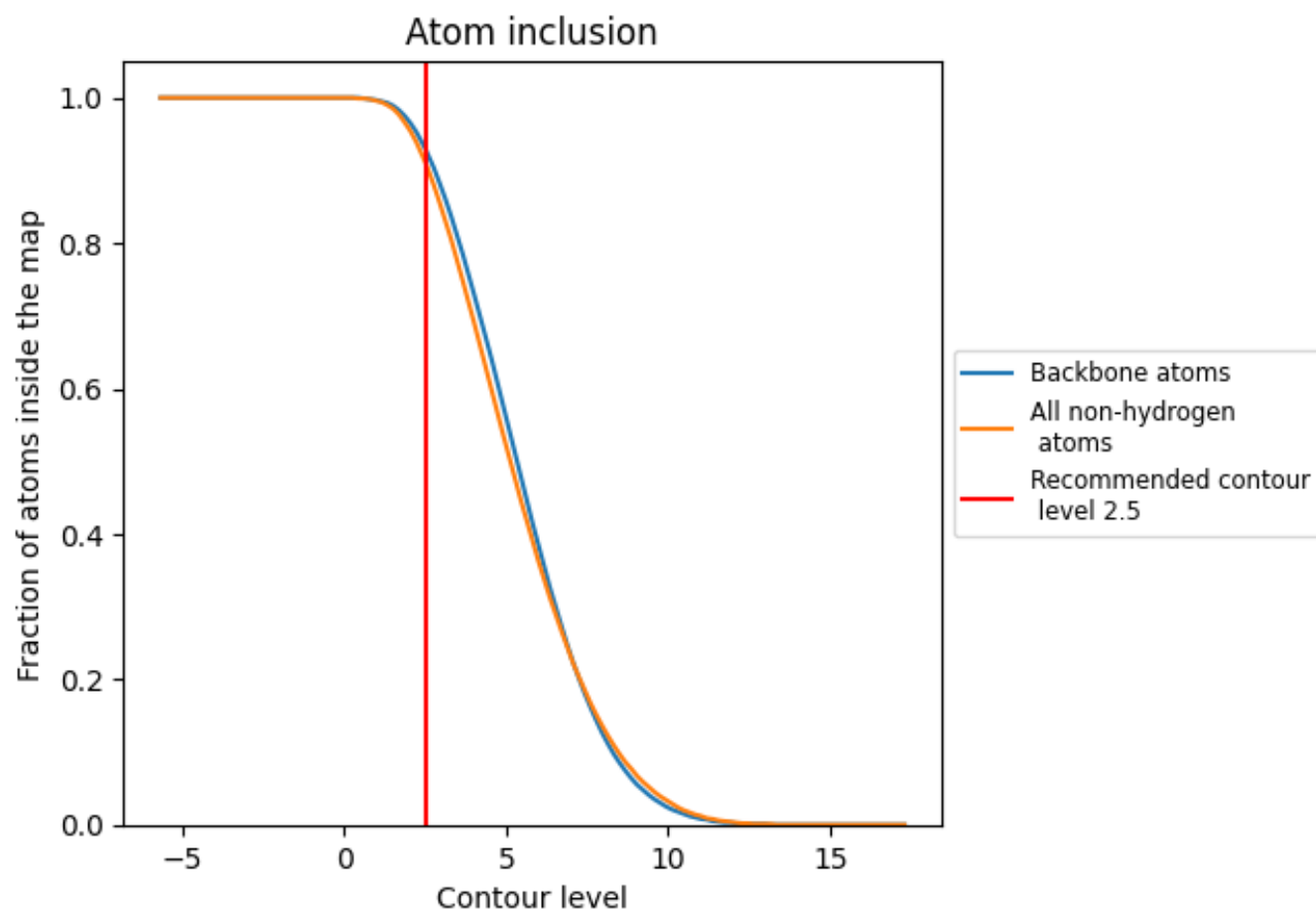
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2.5).

## 9.4 Atom inclusion [i](#)






































At the recommended contour level, 93% of all backbone atoms, 91% 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 (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9110	 0.4580
1A	 0.9560	 0.4660
1B	 0.9730	 0.4670
1C	 0.9780	 0.4740
1D	 0.9680	 0.4800
1E	 0.9350	 0.4840
1F	 0.9140	 0.4890
1G	 0.8720	 0.5020
1H	 0.7950	 0.4520
1I	 0.9500	 0.5050
1J	 0.7410	 0.4250
1K	 0.8660	 0.4730
1L	 0.9630	 0.4890
1M	 0.8610	 0.4670
1N	 0.7900	 0.4470
1O	 0.9370	 0.4960
1P	 0.9130	 0.5010
1Q	 0.9730	 0.4920
1R	 0.9540	 0.4730
1S	 0.9710	 0.5040
1T	 0.9640	 0.5110
1U	 0.9190	 0.4440
1V	 0.9510	 0.5150
1W	 0.5700	 0.3230
1X	 0.9630	 0.4730
1Y	 0.8680	 0.4300
1Z	 0.9440	 0.4680
1a	 0.8720	 0.4580
1b	 0.7650	 0.4120
1c	 0.9580	 0.5120
1d	 0.9700	 0.5060
1e	 0.8160	 0.4350
1f	 0.8770	 0.4480
1g	 0.9560	 0.4880
1h	 0.9310	 0.4420







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Chain	Atom inclusion	Q-score
li	 0.8660	 0.4390
lj	 0.9560	 0.5040
lk	 0.9050	 0.4760
ll	 0.9910	 0.4900
lm	 0.9610	 0.4620
ln	 0.6570	 0.3740
lo	 0.9860	 0.4740
lp	 0.9360	 0.4900
lq	 0.9650	 0.5010
ls	 1.0000	 0.4080
sA	 0.7400	 0.4520
sB	 0.9300	 0.4760
sC	 0.7760	 0.4200
sD	 0.8350	 0.4170
sE	 0.9260	 0.4610
sG	 0.5630	 0.3670
sH	 0.9890	 0.4410
sK	 1.0000	 0.4930
sa	 0.9630	 0.4520
sb	 0.8280	 0.4380
sc	 0.8810	 0.4680
sd	 0.7700	 0.4310
se	 0.8440	 0.4410
sf	 0.8050	 0.4300
sg	 0.8650	 0.4610
sh	 0.6160	 0.3070
si	 0.4910	 0.3530
sj	 0.7700	 0.3930
sk	 0.8070	 0.4430
sl	 0.6620	 0.4140
sm	 0.8940	 0.4400
sn	 0.2170	 0.3190
so	 0.8680	 0.4270
sp	 0.9170	 0.4720
sq	 0.7640	 0.4360
sr	 0.9160	 0.4570
ss	 0.8530	 0.4680
st	 0.6810	 0.3580
su	 0.8500	 0.4500
sv	 0.8230	 0.4580
sw	 0.6830	 0.4090
sx	 0.8150	 0.4440

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Chain	Atom inclusion	Q-score
sy	 0.8520	 0.4310
sz	 0.6220	 0.3850