



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 09:23 PM UTC

PDB ID : 6XIQ / pdb_00006xiq
EMDB ID : EMD-22196
Title : Cryo-EM Structure of K63R Ubiquitin Mutant Ribosome under Oxidative Stress
Authors : Zhou, Y.; Bartesaghi, A.; Silva, G.M.
Deposited on : 2020-06-21
Resolution : 4.20 Å(reported)
Based on initial model : 6GQ1

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

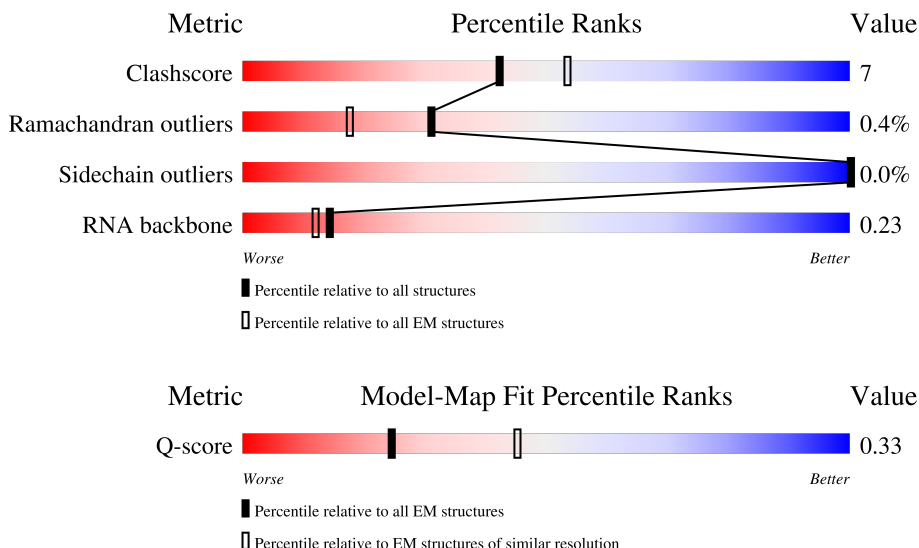
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 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.



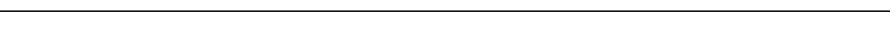
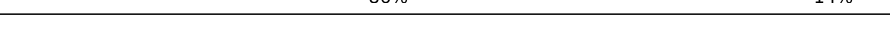
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5410 (3.70 - 4.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	254	
2	B	387	
3	C	362	

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Mol	Chain	Length	Quality of chain
4	D	297	
5	E	176	
6	F	244	
7	G	256	
8	H	191	
9	I	221	
10	J	174	
11	L	199	
12	M	138	
13	N	204	
14	O	199	
15	P	184	
16	Q	186	
17	R	189	
18	S	172	
19	T	160	
20	U	121	
21	V	137	
22	W	155	
23	X	142	
24	Y	127	
25	Z	136	
26	AA	105	
27	AB	156	
28	1	3395	

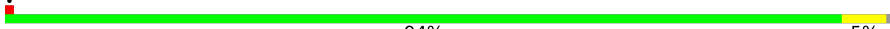
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Mol	Chain	Length	Quality of chain
29	3	121	
30	4	158	
31	P0	312	
32	P2	165	
33	a	149	
34	b	59	
35	c	105	
36	d	113	
37	e	130	
38	f	107	
39	g	121	
40	h	120	
41	i	100	
42	j	88	
43	k	78	
44	l	51	
45	m	128	
46	n	25	
47	o	106	
48	p	92	
49	2	1800	
50	q	252	
51	r	255	
52	s	254	
53	t	240	

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Mol	Chain	Length	Quality of chain
54	u	261	
55	v	225	
56	w	236	
57	x	190	
58	y	200	
59	z	197	
60	AD	151	
61	AE	138	
62	AF	142	
63	AG	143	
64	AH	136	
65	AI	146	
66	AJ	144	
67	AK	121	
68	AL	87	
69	AM	130	
70	AN	145	
71	AO	135	
72	AP	108	
73	AQ	119	
74	AR	82	
75	AS	67	
76	AT	56	
77	AU	63	
78	AV	319	

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Mol	Chain	Length	Quality of chain
79	AX	76	28% 49% 24%
79	AZ	76	39% 51% 9%
80	AY	8	25% 75%
81	L1	217	9% 84% 9% 6%

2 Entry composition

There are 82 unique types of molecules in this entry. The entry contains 356903 atoms, of which 151628 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	252	Total	C	H	N	O	S	0	0
			3895	1191	1981	388	334	1		

- Molecule 2 is a protein called RPL3 isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	386	Total	C	H	N	O	S	0	0
			6217	1950	3142	584	533	8		

- Molecule 3 is a protein called RPL4A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	C	361	Total	C	H	N	O	S	0	0
			5607	1729	2859	522	494	3		

- Molecule 4 is a protein called RPL5 isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	296	Total	C	H	N	O	S	0	0
			4701	1501	2326	414	458	2		

- Molecule 5 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	156	Total	C	H	N	O	S	0	0
			2565	800	1326	222	216	1		

- Molecule 6 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	F	222	Total	C	H	N	O	S	0	0
			3646	1151	1862	324	308	1		

- Molecule 7 is a protein called RPL8A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	G	233	Total	C	H	N	O	S	0	0
			3681	1151	1877	323	327	3		

- Molecule 8 is a protein called RPL9A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	H	191	Total	C	H	N	O	S	0	0
			3105	963	1587	274	277	4		

- Molecule 9 is a protein called RPL10 isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	I	211	Total	C	H	N	O	S	0	0
			3441	1083	1736	322	294	6		

- Molecule 10 is a protein called RPL11B isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	J	169	Total	C	H	N	O	S	0	0
			2736	847	1383	253	249	4		

- Molecule 11 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	193	Total	C	H	N	O	0	0
			3151	962	1608	315	266		

- Molecule 12 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	M	136	Total	C	H	N	O	S	0	0
			2202	675	1149	199	177	2		

- Molecule 13 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	N	203	Total	C	H	N	O	S	0	0
			3499	1077	1779	361	281	1		

- Molecule 14 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	O	197	Total	C	H	N	O	S	0	0
			3214	1003	1659	289	262	1		

- Molecule 15 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	P	183	Total	C	H	N	O		0	0
			2857	882	1437	281	257			

- Molecule 16 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	Q	185	Total	C	H	N	O	S	0	0
			2984	908	1543	290	241	2		

- Molecule 17 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	R	188	Total	C	H	N	O		0	0
			3138	935	1617	326	260			

- Molecule 18 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	S	172	Total	C	H	N	O	S	0	0
			2932	930	1487	267	244	4		

- Molecule 19 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	T	159	Total	C	H	N	O	S	0	0
			2599	805	1323	246	221	4		

- Molecule 20 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	U	100	Total	C	H	N	O		0	0
			1608	516	812	131	149			

- Molecule 21 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	V	136	Total	C	H	N	O	S	0	0
			2051	628	1048	189	179	7		

- Molecule 22 is a protein called RPL24A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	W	63	Total	C	H	N	O	S	0	0
			1072	336	551	102	82	1		

- Molecule 23 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	X	121	Total	C	H	N	O	S	0	0
			1989	620	1025	169	173	2		

- Molecule 24 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	Y	126	Total	C	H	N	O		0	0
			2074	625	1081	192	176			

- Molecule 25 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	Z	135	Total	C	H	N	O		0	0
			2247	710	1155	202	180			

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

Mol	Chain	Residues	Atoms						AltConf	Trace
26	AA	96	Total	C	H	N	O	S	0	0
			1499	499	727	126	145	2		

- Molecule 27 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	AB	153	Total	C	H	N	O	S	0	0
			2502	780	1282	231	206	3		

- Molecule 28 is a RNA chain called 35S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	1	3223	Total	C	H	N	O	P	0	0
			103566	30790	34635	12416	22502	3223		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	?	-	G	deletion	GB 380294104

- Molecule 29 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	3	121	Total	C	H	N	O	P	0	0
			3883	1152	1304	461	845	121		

- Molecule 30 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	4	158	Total	C	H	N	O	P	0	0
			5048	1500	1695	586	1109	158		

- Molecule 31 is a protein called RPP0 isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	P0	189	Total	C	H	N	O	S	0	0
			2987	942	1514	257	270	4		

- Molecule 32 is a protein called RPL12A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	P2	94	Total	C	H	N	O	S	0	0
			1497	448	774	138	135	2		

- Molecule 33 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	a	148	Total	C	H	N	O	S	0	0
			2388	749	1215	231	190	3		

- Molecule 34 is a protein called RPL29 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	b	58	Total	C	H	N	O	0	0
			953	289	491	100	73		

- Molecule 35 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	c	97	Total	C	H	N	O	S	0	0
			1540	479	797	124	139	1		

- Molecule 36 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	d	109	Total	C	H	N	O	S	0	0
			1801	559	918	167	156	1		

- Molecule 37 is a protein called RPL32 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
37	e	127	Total	C	H	N	O	S	0	0
			2110	647	1090	205	167	1		

- Molecule 38 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	f	106	Total	C	H	N	O	S	0	0
			1730	540	880	165	144	1		

- Molecule 39 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	g	112	Total	C	H	N	O	S	0	0
			1821	545	941	179	152	4		

- Molecule 40 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
40	h	119	Total	C	H	N	O	S	0	0
			2047	615	1078	186	167	1		

- Molecule 41 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	i	99	Total	C	H	N	O	S	
			1620	481	849	156	132	2	
								0	0

- Molecule 42 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	j	87	Total	C	H	N	O	S	
			1364	414	683	148	114	5	
								0	0

- Molecule 43 is a protein called RPL38 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	k	77	Total	C	H	N	O		
			1294	391	682	115	106		
								0	0

- Molecule 44 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	l	50	Total	C	H	N	O	S	
			911	272	475	97	65	2	
								0	0

- Molecule 45 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	m	52	Total	C	H	N	O	S	
			873	259	456	86	67	5	
								0	0

- Molecule 46 is a protein called RPL41A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	n	25	Total	C	H	N	O	S	
			500	139	273	60	27	1	
								0	0

- Molecule 47 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	o	105	Total	C	H	N	O	S	
			1762	534	915	170	138	5	
								0	0

- Molecule 48 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	p	91	Total	C	H	N	O	S	0	0
			1428	429	734	138	121	6		

- Molecule 49 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	2	1743	Total	C	H	N	O	P	0	0
			55827	16603	18686	6578	12217	1743		

- Molecule 50 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	q	206	Total	C	H	N	O	S	0	0
			3144	1014	1567	278	283	2		

- Molecule 51 is a protein called RPS1A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	r	214	Total	C	H	N	O	S	0	0
			3493	1084	1784	310	311	4		

- Molecule 52 is a protein called RPS2 isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	s	217	Total	C	H	N	O	S	0	0
			3358	1047	1723	289	297	2		

- Molecule 53 is a protein called RPS3 isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	t	223	Total	C	H	N	O	S	0	0
			3551	1101	1817	313	314	6		

- Molecule 54 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	u	260	Total	C	H	N	O	S	0	0
			4222	1316	2154	389	360	3		

- Molecule 55 is a protein called Rps5p.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	v	206	Total	C	H	N	O	S	0	0
			3284	1007	1675	300	299	3		

- Molecule 56 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	w	223	Total	C	H	N	O	S	0	0
			3671	1123	1881	346	318	3		

- Molecule 57 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	x	184	Total	C	H	N	O	S	0	0
			3053	951	1572	265	265			

- Molecule 58 is a protein called RPS8A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	y	188	Total	C	H	N	O	S	0	0
			3014	925	1525	298	264	2		

- Molecule 59 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	z	185	Total	C	H	N	O	S	0	0
			3067	943	1573	289	261	1		

- Molecule 60 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms						AltConf	Trace
60	AD	150	Total	C	H	N	O	S	0	0
			2447	759	1255	224	207	2		

- Molecule 61 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms						AltConf	Trace
61	AE	127	Total	C	H	N	O	S	0	0
			1774	545	883	182	163	1		

- Molecule 62 is a protein called RPS15 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AF	124	Total	C	H	N	O	S	
			1979	622	1002	182	166	7	
								0	0

- Molecule 63 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AG	141	Total	C	H	N	O		
			2271	708	1166	203	194		
								0	0

- Molecule 64 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AH	120	Total	C	H	N	O	S	
			1856	577	930	177	170	2	
								0	0

- Molecule 65 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AI	145	Total	C	H	N	O	S	
			2414	743	1222	237	210	2	
								0	0

- Molecule 66 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AJ	143	Total	C	H	N	O	S	
			2236	694	1124	208	208	2	
								0	0

- Molecule 67 is a protein called RPS20 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	AK	107	Total	C	H	N	O	S	
			1772	539	917	156	159	1	
								0	0

- Molecule 68 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	AL	87	Total	C	H	N	O	S	
			1356	420	672	125	137	2	
								0	0

- Molecule 69 is a protein called RPS22A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
69	AM	129	Total	C	H	N	O	S	0	0
			2081	650	1060	188	180	3		

- Molecule 70 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
70	AN	144	Total	C	H	N	O	S	0	0
			2317	708	1196	220	191	2		

- Molecule 71 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
71	AO	134	Total	C	H	N	O		0	0
			2205	676	1132	208	189			

- Molecule 72 is a protein called RPS25A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
72	AP	70	Total	C	H	N	O		0	0
			1166	360	603	104	99			

- Molecule 73 is a protein called RPS26B isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
73	AQ	97	Total	C	H	N	O	S	0	0
			1583	475	814	160	129	5		

- Molecule 74 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
74	AR	81	Total	C	H	N	O	S	0	0
			1242	382	632	110	113	5		

- Molecule 75 is a protein called RPS28A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
75	AS	63	Total	C	H	N	O	S	0	0
			1032	306	535	99	91	1		

- Molecule 76 is a protein called RPS29A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
76	AT	53	Total	C	H	N	O	S	0	0
			873	274	431	92	72	4		

- Molecule 77 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
77	AU	60	Total	C	H	N	O	S	0	0
			1000	299	525	98	77	1		

- Molecule 78 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
78	AV	318	Total	C	H	N	O	S	0	0
			4823	1541	2386	418	470	8		

- Molecule 79 is a RNA chain called Transfer RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
79	AX	76	Total	C	H	N	O	P	0	0
			2446	725	820	293	532	76		
79	AZ	76	Total	C	H	N	O	P	0	0
			2446	725	820	293	532	76		

- Molecule 80 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
80	AY	8	Total	C	H	N	O	P	0	0
			248	74	84	23	59	8		

- Molecule 81 is a protein called RPL1A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
81	L1	204	Total	C	H	N	O	S	0	0
			3310	1031	1701	279	290	9		

- Molecule 82 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
82	j	1	Total	Zn	0
			1	1	
82	m	1	Total	Zn	0
			1	1	

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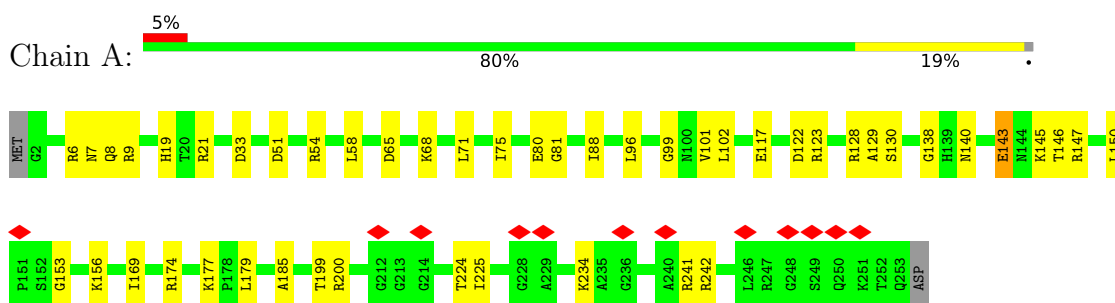
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Mol	Chain	Residues	Atoms		AltConf
82	o	1	Total 1	Zn 1	0
82	p	1	Total 1	Zn 1	0
82	AQ	1	Total 1	Zn 1	0
82	AR	1	Total 1	Zn 1	0
82	AT	1	Total 1	Zn 1	0

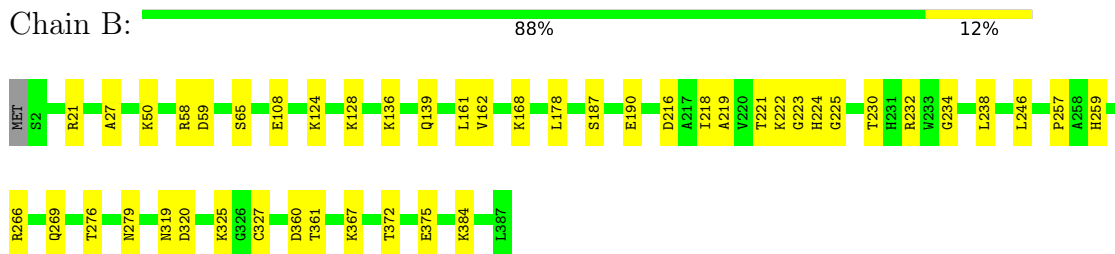
3 Residue-property plots

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

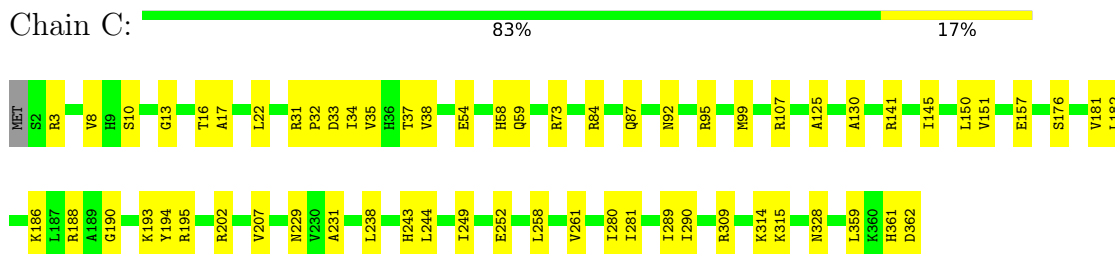
- Molecule 1: 60S ribosomal protein L2-A



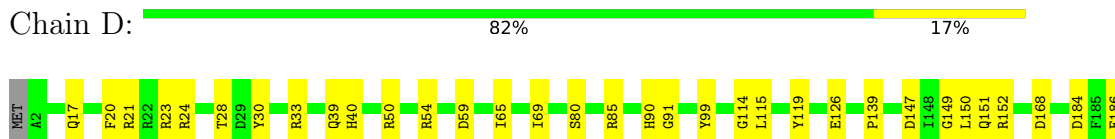
- Molecule 2: RPL3 isoform 1



- Molecule 3: RPL4A isoform 1



- Molecule 4: RPL5 isoform 1





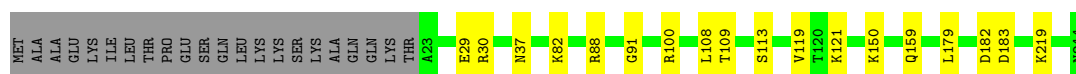
- Molecule 5: 60S ribosomal protein L6-A

Chain E: 80% 9% 11%



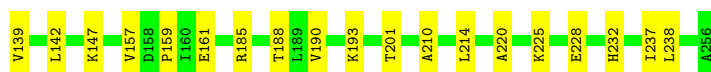
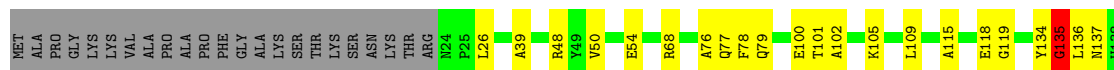
- Molecule 6: 60S ribosomal protein L7-A

Chain F: 84% 7% 9%



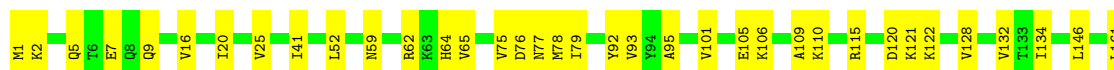
- Molecule 7: RPL8A isoform 1

Chain G: 75% 16% 9%



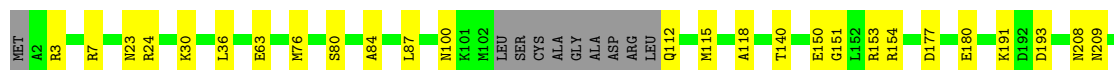
- Molecule 8: RPL9A isoform 1

Chain H: 77% 23%



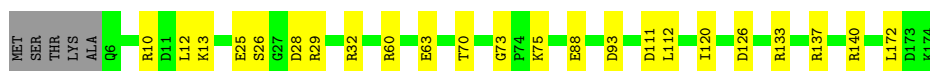
- Molecule 9: RPL10 isoform 1

Chain I: 84% 12% 5%



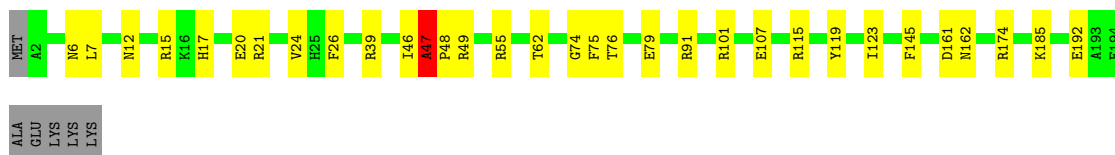
- Molecule 10: RPL11B isoform 1

Chain J: 84% 13% 3%



- Molecule 11: 60S ribosomal protein L13-A

Chain L: 81% 16% ..



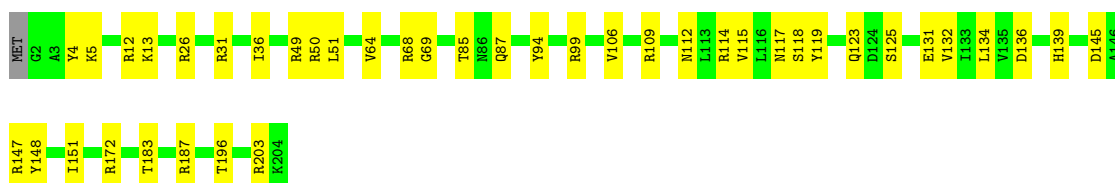
- Molecule 12: 60S ribosomal protein L14-A

Chain M: 83% 15% .



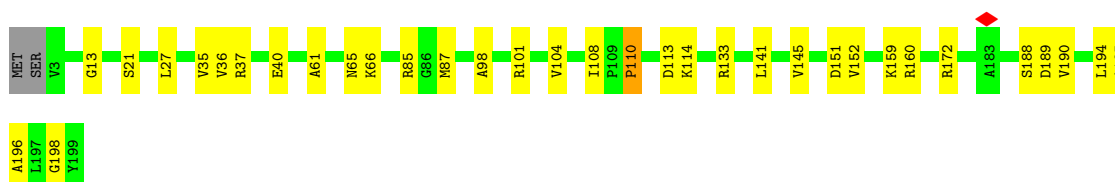
- Molecule 13: 60S ribosomal protein L15-A

Chain N: 79% 20%



- Molecule 14: 60S ribosomal protein L16-A

Chain O: 82% 17% ..



- Molecule 15: 60S ribosomal protein L17-A

Chain P: 86% 13% .



- Molecule 16: 60S ribosomal protein L18-A

MT1	G2	I3	D4	R16	L29	F35	L36	N45	S65	R66	I67	V81	R92	R111	V115	T123	Q126	V129	Q135	S146	R147	E148	H152	A162	F163	R164	R170	R179	V196
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|-----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|
| MET | A2 | T6 | Q7 | A11 | V15 | G16 | V17 | R20 | K21 | E31 | K53 | R62 | Y78 | T84 | L99 | R100 | R103 | R110 | D116 | K117 | H118 | L119 | Y120 | R172 | R173 | A189 |
|-----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|

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|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|-----|------|------|------|------|------|------|------|------|------|------|------|
| M1 | V9 | E34 | Q46 | V51 | I61 | I64 | NG5 | T70 | K71 | V72 | K73 | DS2 | SS3 | T87 | H88 | A112 | R113 | H14 | R115 | A116 | I121 | E130 | K131 | T132 | A133 | D134 | R137 | K161 | V172 |
|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|-----|------|------|------|------|------|------|------|------|------|------|------|

- | MET | G2 | R8 | S9 | R10 | T11 | Q16 | R17 | D18 | F19 | R20 | K21 | H22 | L31 | K50 | G51 | K55 | T68 | K69 | M79 | V80 | R88 | H95 | Q103 | K110 | R116 | K120 | E137 | S142 | T143 | T160 |
|-----|----|----|----|------|------|------|------|------|------|------|------|
|-----|----|----|----|------|------|------|------|------|------|------|------|

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|-----|-----|-----|-----|-----|-----|-----|-----|----|-----|-----|-----|-----|-----|-----|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MET | ALA | PRO | ASN | THR | SER | ARG | LYS | Q9 | Y33 | L37 | K70 | Y83 | N87 | I93 | A106 | F107 | Y108 | GLN | VAL | THR | PRO | GLU | GLU | ASP | GLU | GLU | GLU | ASP | GLU | GLU |
|-----|-----|-----|-----|-----|-----|-----|-----|----|-----|-----|-----|-----|-----|-----|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

- | | | | | | | | | | | | | | | | | | | | | | | |
|-----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|
| ME1 | S2 | G3 | C25 | A26 | D27 | N28 | S29 | R32 | I37 | R48 | E68 | D97 | N98 | N104 | P105 | G107 | K106 | E108 | M109 | S112 | V136 | V137 |
|-----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|

- [illegible]

- Molecule 23: 60S ribosomal protein L25

Chain X:  71% 14% 15%



- Molecule 24: 60S ribosomal protein L26-A

Chain Y:  84% 15%



- Molecule 25: 60S ribosomal protein L27-A

Chain Z:  82% 17%



- Molecule 26: 40S ribosomal protein S10-A

Chain AA:  83% 9% 9%

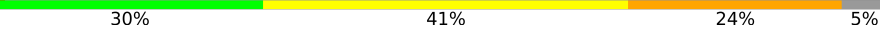


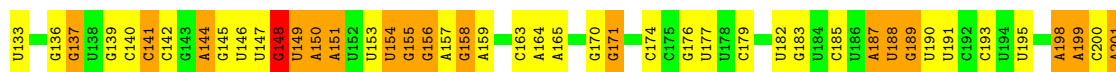
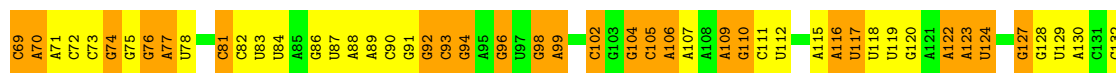
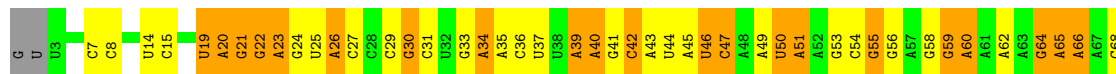
- Molecule 27: 40S ribosomal protein S11-A

Chain AB:  88% 10%



- Molecule 28: 35S ribosomal RNA

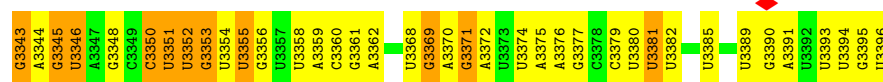
Chain 1:  30% 41% 24% 5%



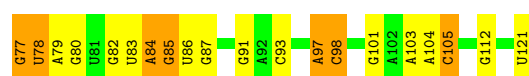
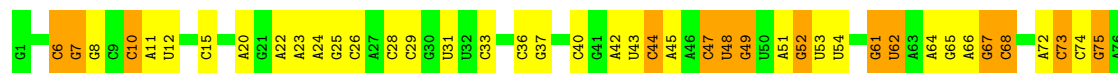


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U2205	U2137	A	A1883	G1817	C1738	C1665	A1594	U1530	U1399	A1330	A1260
C2206	C2138	C	A1884	U1818	U1739	G1666	U1595	C1531	G1465	U1331	A1269
A2207	A2139	C	U1885	U1819	U1740	A1667	C1596	U1532	A1467	A1332	G1261
U2208	U2140	G	A1886	U1820	U1741	G1668	C1597	U1533	A1468	C1333	G1262
U2209	U2141	U	A1887	U1821	U1742	C1669	G1598	A1534	C1469	U1334	A1263
C2210	C2142	C	U1888	U1822	U1743	C1670	A1599	A1535	U1470	G1335	G1264
A2211	A2143	G	U1889	U1823	U1744	C1671	U1600	U1536	U1405	U1336	U1265
C2212	C2144	C	G1829	G1829	G1745	C1672	A1601	A1537	A1406	G1339	U1266
U2213	U2145	U	G1830	G1830	A1749	U1672	A1602	U1538	U1407	U1340	U1267
A2214	A2146	U	U1831	U1831	G1750	G1675	G1603	G1541	G1408	U1341	U1268
U2215	U2147	C	G1832	G1832	G1751	A1676	G1604	U1542	G1409	A1342	U1269
C2216	C2148	C	G1833	G1833	A1752	G1677	A1605	G1543	U1410	A1343	A1270
U2217	U2149	U	U1834	U1834	G1753	G1678	U1606	G1544	C1411	G1344	A1271
C2218	C2150	A	A1835	A1835	G1754	U1679	G1607	U1545	G1412	U1345	A1272
A2219	A2151	C	G1836	G1836	U1755	A1679	U1608	A1546	G1413	U1348	A1273
U2220	U2152	U	U1837	U1837	A1757	G1680	C1609	U1547	G1414	U1349	A1274
C2221	C2153	A	G1838	G1838	U1758	U1681	G1610	G1548	U1415	A1350	C1275
U2223	U2154	U	A1839	A1839	A1760	U1682	G1611	U1549	C1416	U1351	U1276
A2224	A2155	U	U1840	U1840	C1761	A1683	A1612	C1551	G1417	A1352	C1277
U2225	U2156	C	A1841	A1841	U1762	U1687	G1618	G1552	A1418	U1353	A1278
C2226	C2157	G	U1842	U1842	U1763	U1688	A1619	G1553	A1489	G1354	C1279
U2227	U2158	A	C1843	C1843	U1764	U1689	U1620	U1554	A1490	A1355	C1280
A2229	A2159	C	U1844	U1844	U1765	U1693	U1626	U1555	A1491	U1356	G1281
C2230	C2160	U	G1845	G1845	U1772	C1693	U1627	A1556	G1492	G1357	G1282
U2231	U2161	C	C1846	C1846	U1773	U1694	A1628	A1557	U1493	U1361	C1283
C2232	C2162	C	A1847	A1847	C1773	U1695	C1629	A1558	U1494	G1364	G1284
A2233	A2163	U	G1848	G1848	U1774	U1696	U1630	A1559	C1495	U1365	G1285
U2234	U2164	C	C1849	C1849	U1775	A1697	G1631	G1560	C1497	G1366	G1295
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A2237	A2167	C	U1852	U1852	U1780	U1702	U1634	U1563	U1501	A1369	A1302
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C2239	C2169	U	G1854	G1854	U1782	C1708	U1636	A1565	A1503	A1371	A1304
U2240	U2170	C	U1855	U1855	U1783	U1709	A1637	U1566	A1504	C1372	U1305
A2241	A2171	G	C1856	C1856	U1784	C1709	U1638	U1569	C1505	A1373	G1306
U2242	U2172	U	G1857	G1857	U1785	U1710	G1639	U1570	U1506	G1374	G1307
C2243	C2173	C	U1858	U1858	U1786	G1713	G1640	A1571	G1507	G1375	A1308
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C2245	C2175	U	G1860	G1860	U1788	U1715	A1642	U1442	U1441	G1378	G1310
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C2247	C2177	G	G1862	G1862	U1790	U1717	C1644	U1576	G1444	G1379	C1312
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C2249	C2179	C	U1864	U1864	U1792	U1720	G1646	U1578	G1513	A1381	G1314
U2250	U2180	A	G1865	G1865	U1793	U1721	U1649	C1579	G1514	G1382	U1315
A2251	A2181	U	A1866	A1866	U1794	U1722	U1650	A1580	A1515	G1383	C1316
C2252	C2182	C	U1867	U1867	G1795	U1723	U1651	C1581	C1516	U1384	C1317
U2253	U2183	U	G1868	G1868	U1796	U1724	U1652	A1583	G1448	A1386	A1317
C2254	C2184	C	U1869	U1869	U1797	C1725	A1654	C1584	U1449	G1387	A1318
A2255	A2185	U	A1870	A1870	U1798	U1726	U1655	U1585	C1451	U1388	G1320
U2256	U2186	C	C1871	C1871	U1799	C1727	G1656	G1586	A1452	G1389	C1321
C2257	C2187	G	U1872	U1872	U1800	U1728	A1657	U1587	A1453	U1390	G1322
U2258	U2188	A	G1873	G1873	U1801	U1729	G1658	A1588	A1454	G1391	G1323
A2259	A2189	U	U1874	U1874	U1802	U1730	U1659	A1589	U1455	U1324	U1324
C2260	C2190	C	U1875	U1875	U1803	U1731	U1660	G1590	U1456	G1392	U1325
U2261	U2191	U	G1876	G1876	U1804	U1732	U1661	U1591	U1457	A1393	A1326
A2262	A2192	C	U1877	U1877	U1805	U1733	U1662	U1592	C1527	A1394	G1327
U2263	U2193	G	U1878	U1878	U1806	U1734	U1663	G1520			
C2264	C2194	C	G1879	G1879	U1807	C1725	A1654	U1584			
U2265	U2195	U	U1880	U1880	G1807	C1726	U1655	C1585			
A2266	A2196	C	A1881	A1881	U1808	U1727	G1656	G1586			
C2267	C2197	G	U1882	U1882	U1809	U1728	A1657	U1587			
U2268	U2198	U	G1883	G1883	U1810	U1729	G1658	A1588			
A2269	A2199	C	U1884	U1884	U1811	U1730	U1659	A1589			
C2270	C2200	C	U1885	U1885	U1812	U1731	U1660	G1590			
U2271	U2201	U	G1886	G1886	U1813	U1732	U1661	U1591			
A2272	A2202	C	U1887	U1887	U1814	U1733					
C2273	C2203	G	U1888	U1888							
U2274	U2204	U									
A2275	A2205	C									
C2276	C2206	U									

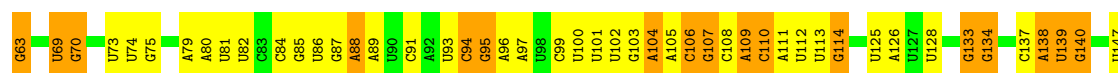
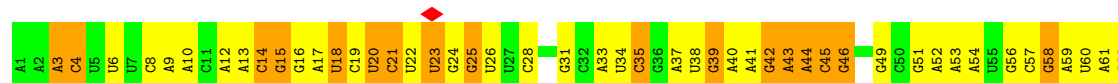
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U3198	C3119	A3049	G2973	G2834	A2768	A2694	C2616	G2550	A2488	U2421	C2354	A2279
G3199	U3119	U3050	U2974	U2835	A2769	A2695	G2617	U2551	C2489	C2422	G2355	A2280
C3206	C3120	U3051	U2975	G2836	C2772	A2696	G2618	C2552	C2490	A2423	A2356	U2281
U3207	U3121	G3052	A2976	A2837	C2773	G2697	G2619	U2553	A2491	A2424	A2357	U2282
G3208	A3122	G3053	G2977	A2838	C2774	G2698	G2620	A2554	C2492	G2425	A2358	G2283
A3209	U3125	U3054	U2978	G2841	C2775	G2699	G2621	G2555	U2493	U2426	C2359	C2287
G3208	C3126	U3055	U2979	G2842	C2776	G2700	G2622	G2556	A2494	U2427	C2360	C2288
A3210	A3127	U3056	U2980	C2844	G2777	U2701	C2627	A2557	C2495	U2428	A2361	G2289
C3211	A3128	U3057	G2912	G2845	G2778	A2703	A2628	U2558	C2496	G2429	A2362	U2289
G3212	C3128	A2982	C2913	U2846	A2779	A2704	U2629	U2559	U2497	A2430	A2363	C2290
A3213	U3129	C2983	G2914	U2847	A2780	U2705	G2632	C2560	U2498	C2431	A2364	A2291
U3214	A3130	C2984	U2916	A2847	A2781	U2713	G2633	A2561	U2499	A2432	C2365	U2292
A3215	U3131	G2990	G2917	G2848	U2782	G2714	G2634	A2562	A2500	U2433	G2370	C2293
G3216	C3132	U3064	U2918	C2849	U2783	G2715	U2634	G2563	U2501	U2434	A2371	U2294
C3217	C3133	A2993	U2919	G2850	G2784	U2716	A2635	G2564	A2502	G2435	A2295	A2296
A3218	G3136	U3066	U2920	A2851	A2785	U2717	A2636	U2565	G2503	U2436	A2372	A2297
G3219	C3137	C3067	U2923	C2852	G2786	U2720	A2637	C2568	U2504	G2440	A2373	U2298
G3220	U3138	G2997	U2924	A2853	G2787	U2721	G2640	A2569	U2505	A2441	G2374	U2299
G3224	A3139	A3005	A2925	U2854	C2788	U2722	U2641	U2570	C2507	G2442	G2376	G2302
C3225	G3140	A3006	A2926	U2855	U2789	U2723	A2642	U2571	U2508	U2446	G2377	A2303
A3226	C3141	U3007	C2927	G2856	U2790	U2724	A2643	C2572	U2509	A2447	G2378	C2304
G3227	A3142	C3072	C2928	U2860	G2794	C2726	A2644	U2578	U2510	G2450	C2379	G2305
C3228	C3143	A3073	C2929	G2863	U2795	A2727	G2645	G2579	A2511	G2451	C2383	C2306
G3229	G3144	G3074	A2930	U2864	G2796	U2728	C2646	A2580	C2512	G2452	A2384	G2307
G3230	C3145	G3075	C2931	A2865	C2797	U2729	A2647	U2581	U2513	U2453	G2385	U2310
A3234	A3150	A3076	U2932	U2866	A2798	U2730	G2648	C2582	U2514	U2454	A2386	G2311
G3235	U3151	A3077	A2933	U2867	G2800	U2731	A2649	C2583	U2515	U2455	A2387	U2310
C3236	C3152	U3078	A2934	G2868	A2801	U2732	U2650	G2584	U2516	A2456	U2388	G2311
U3237	U3153	U3079	U2935	U2869	A2802	A2734	G2651	G2585	U2517	A2457	C2389	U2314
G3238	C3154	G3080	A2936	U2870	A2803	U2735	U2652	G2586	C2518	A2458	A2390	G2315
C3239	U3155	C2871	C2870	G2871	A2804	U2736	C2653	U2587	A2519	U2459	G2391	G2322
G3240	U3157	G2939	G2939	G2872	G2805	C2737	C2654	U2588	U2520	U2460	C2392	G2323
A3241	C3165	A2940	A2940	G2873	U2806	C2741	A2655	G2589	U2521	A2461	G2393	G2324
G3242	U3169	A3021	C2942	U2874	U2807	C2742	A2656	A2591	A2523	A2462	G2394	A2325
U3251	A3170	G3022	G2943	U2875	C2808	U2743	A2657	G2592	A2524	G2463	G2395	G2326
G3252	U3171	C3023	G2944	C2876	C2809	G2745	G2658	A2593	G2525	U2464	G2396	A2327
U3255	A3172	A3024	G2945	U2877	A2810	U2746	A2667	C2594	C2526	G2465	A2397	U2328
G3256	C3173	A3025	G2946	G2878	A2811	A2747	U2668	C2594	G2527	G2466	C2399	G2329
C3257	U3174	G3026	U2947	U2879	C2812	U2748	U2669	A2595	G2530	G2467	G2400	C2330
U3258	A3175	A3027	G2948	U2880	A2813	G2749	A2674	U2596	C2531	A2468	A2401	G2335
G3259	C3176	C3028	G2949	U2881	G2814	U2750	C2675	U2597	U2532	G2469	A2402	U2336
C3260	U3177	A3029	G2950	U2882	G2815	G2751	A2676	U2598	G2533	C2470	G2403	G2336
G3261	A3178	C3030	G2951	U2883	G2816	U2752	A2677	U2599	A2534	U2471	A2404	C2339
U3262	U3179	U3031	G2952	A2887	A2817	G2753	A2678	C2600	G2535	U2472	C2405	C2340
C3263	A3180	G3032	U2953	U2888	A2818	G2754	A2679	A2601	A2536	C2473	C2406	U2340
G3264	C3181	A3033	A2954	G2889	A2819	C2755	C2682	G2602	U2537	G2474	C2407	U2341
C3265	U3182	C2959	A2955	U2890	C2820	C2756	C2683	U2603	U2538	G2475	U2408	U2342
G3266	A3183	C2960	G2956	U2891	U2822	U2757	C2684	G2604	C2539	C2476	G2409	U2343
A3267	C3184	G2957	G2957	U2892	G2823	G2760	C2685	G2605	A2540	C2477	U2410	U2344
G3268	U3185	U3041	U2958	U2893	G2824	U2761	A2686	G2606	U2541	G2478	G2414	C2345
C3269	A3186	U3042	U2959	U2894	G2825	A2762	G2687	G2607	U2542	C2479	C2415	U2346
U3270	C3187	C3043	G2960	U2895	U2826	U2763	U2688	G2608	U2543	G2480	U2416	U2347
G3271	A3188	G3044	U2961	U2896	U2827	U2764	A2689	G2609	C2545	U2481	U2417	U2348
C3272	U3189	A3045	G2962	U2897	G2828	C2765	A2691	U2611	C2546	U2482	G2418	U2349
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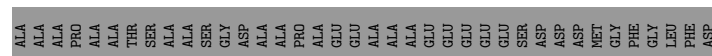
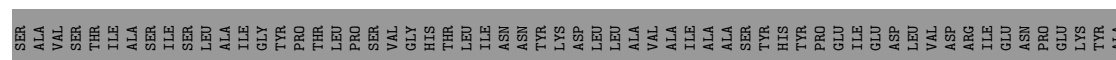
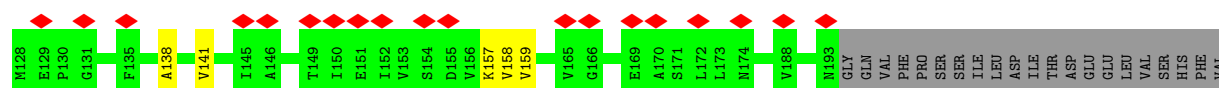
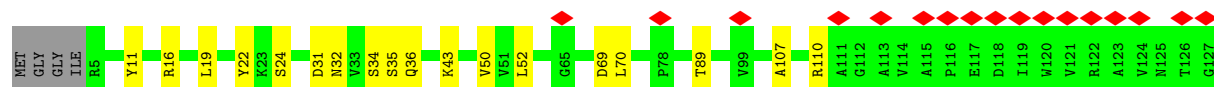
• Molecule 29: 5S ribosomal RNA



• Molecule 30: 5.8S ribosomal RNA

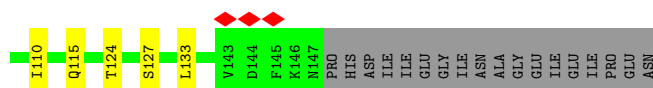
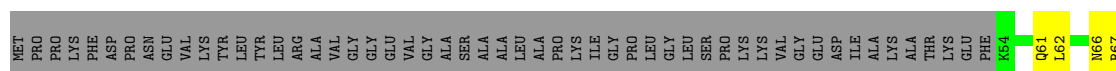


• Molecule 31: RPP0 isoform 1



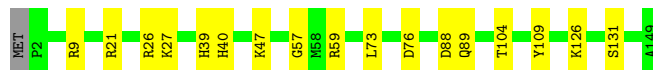
• Molecule 32: RPL12A isoform 1





- Molecule 33: 60S ribosomal protein L28

Chain a: 88% 11% .



- Molecule 34: RPL29 isoform 1

Chain b: 88% 10% .



- Molecule 35: 60S ribosomal protein L30

Chain c: 79% 13% 8% .



- Molecule 36: 60S ribosomal protein L31-A

Chain d: 82% 14% .



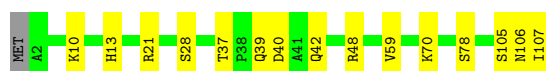
- Molecule 37: RPL32 isoform 1

Chain e: 92% 6% .



- Molecule 38: 60S ribosomal protein L33-A

Chain f: 85% 14% .



- Molecule 39: 60S ribosomal protein L34-A

Chain g:  81% 12% 7%



- Molecule 40: 60S ribosomal protein L35-A

Chain h:  88% 11% .



- Molecule 41: 60S ribosomal protein L36-A

Chain i:  87% 12% .



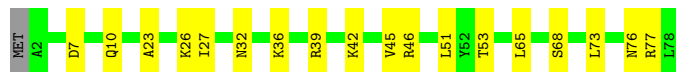
- Molecule 42: 60S ribosomal protein L37-A

Chain j:  80% 18% ..



- Molecule 43: RPL38 isoform 1

Chain k:  76% 23% .



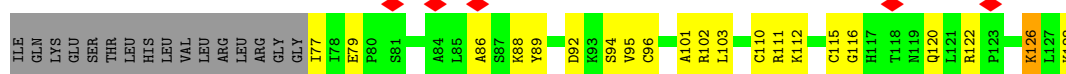
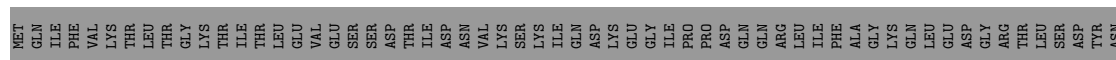
- Molecule 44: 60S ribosomal protein L39

Chain l:  80% 18% .

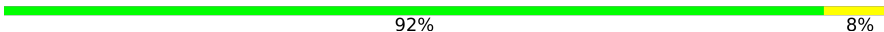


- Molecule 45: 60S ribosomal protein L40

Chain m:  24% 16% . 59%



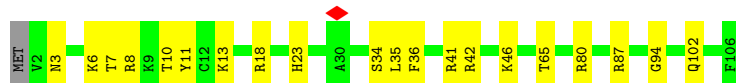
- Molecule 46: RPL41A isoform 1

Chain n:  92% 8%



- Molecule 47: 60S ribosomal protein L42-A

Chain o:  80% 19%



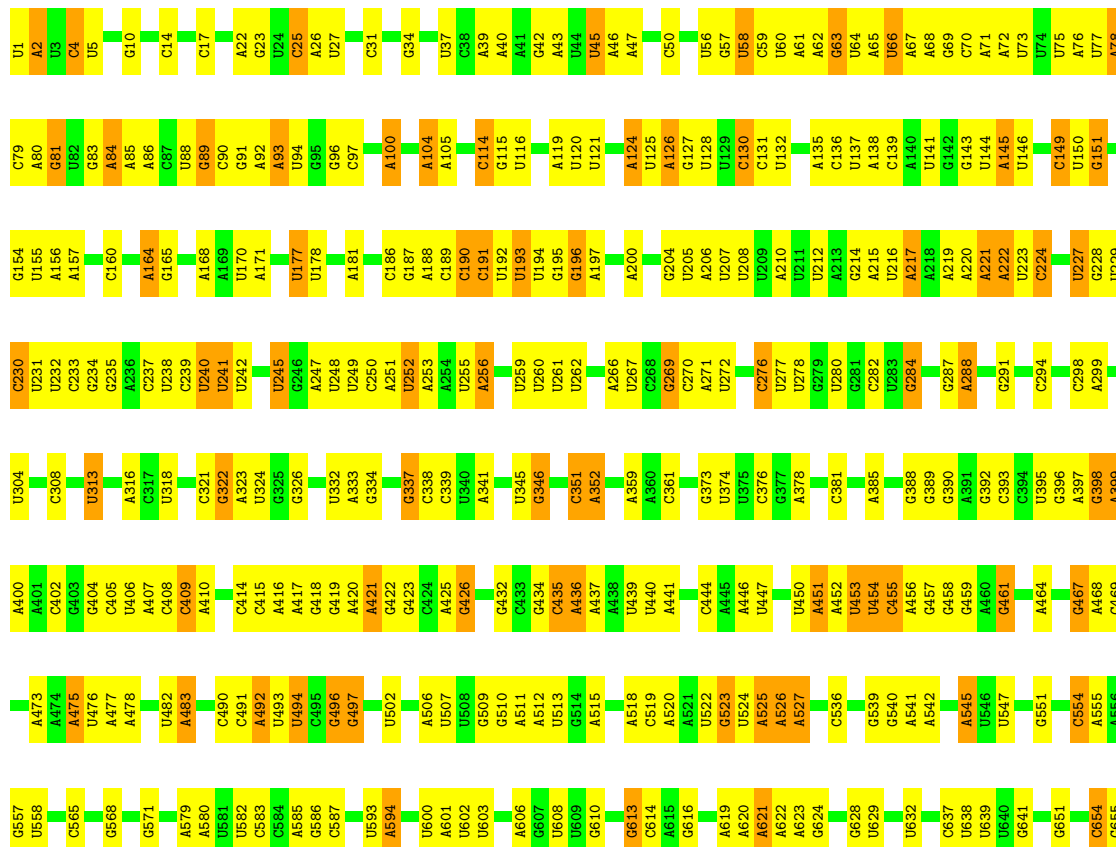
- Molecule 48: 60S ribosomal protein L43-A

Chain p:  89% 10%



- Molecule 49: 18S ribosomal RNA

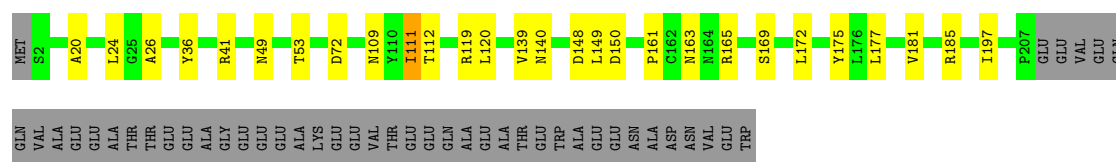
Chain 2:  46% 40% 11%



G1796	U1710	G1540	G1474	A1384	G1308	U	G1064	A966	A799	G722	G656
A1797	C1711	G1541	A1475	G1387	C1309	U	A1065	A969	G802	G723	U657
U1798	A1712	G1542	G1476	A1388	G1310	G	C1066	C967	G802	G724	C658
A	G1713	A1547	G1477	U1311	A1165	A	C1072	A970	A804	U725	G
	G1715	A1548	G1478	A1312	A1166	C	G972	A971	U805	U726	A
	G1716	A1550	A1479	A1313	G1167	A	A1076	A973	U806	U727	U
	G1717	A1551	G1480	U1314	U1168	G	A1081	G976	A807	U728	U
	G1718	G1553	C1481	U1315	G1169	A	C1082	G977	U808	G729	U
	A1719	U1554	G1482	A1321	A1171	U	G985	C883	A809	G730	U
	G1720	A1555	A1483	G1330	U1174	G	A988	A884	G810	C731	U
	A1721	U1556	G1484	U1335	G1175	A	U989	G885	A811	G732	U
	U1723	U1557	C1485	U1336	G1176	G	A1091	U886	A812	A733	C
	U1724	U1558	U1489	U1337	U1177	A	C990	A891	U813	C734	G
	A1725	U1559	G1490	A1338	C1180	C	A1092	A892	G815	C735	U
	U1726	U1560	U1491	C1339	U1181	G	A992	U893	U820	C736	U
	U1727	U1561	A1402	C1340	U1182	C	A993	U894	U821	A740	U
	A1728	U1562	C1403	U1341	A1183	U	A1001	U895	G819	G738	A
	G1729	A1569	G1404	U1342	A1184	U	G1002	U896	U822	G739	C
	A1730	U1570	U1407	U1343	U1185	U	G1003	A898	G823	U743	U
	U1731	G1572	A1410	A1344	C1190	C	U1004	U903	U826	U744	U
	G1734	A1575	G1412	A1345	U1191	U	A1005	A906	A752	A753	U
	U1735	U1576	U1413	A1346	G1192	G	G1011	U912	A754	C883	U
	G1736	A1577	U1414	U1347	A1193	A	U1012	U913	A755	A884	U
	G1745	U1582	U1415	A1348	C1194	U	C1016	G914	A756	A885	U
	A1746	A1583	G1416	G1349	C1195	U	U1017	U917	A757	C886	U
	G1747	U1584	A1417	A1350	U1200	U	U1018	U918	U758	U694	U
	G1748	U1585	G1427	G1351	G1201	G	U1019	U919	U759	U695	U
	A1755	G1507	U1428	U1352	A1202	C	A1020	U920	A760	C696	U
	U1756	U1508	G1431	U1353	A1203	U	C1021	U921	A762	C697	U
	G1757	C1509	U1432	U1354	G1204	U	A1025	G925	G655	C698	U
	U1758	U1510	U1433	U1355	U1264	U	A1026	A926	U766	U699	U
	C1759	U1511	U1434	U1356	C1205	U	A1027	C927	A770	C700	U
	A1762	U1512	G1441	A1357	U1206	U	C1028	A928	A771	G702	U
	U1763	G1513	A1444	G1358	C1207	U	A1029	U928	G703	G703	U
	G1764	U1514	G1445	U1359	A1211	U	U1030	A929	A772	C704	U
	A1765	U1515	U1446	U1360	G1212	U	U1031	A930	C773	U705	U
	G1766	U1516	C1447	U1361	U1213	U	G1032	C931	A774	A706	U
	U1767	U1517	G1447	G1362	U1214	U	A1039	U932	A777	A707	U
	A1693	U1522	U1457	U1363	C1215	U	C1045	A933	G778	C708	U
	A1694	G1523	G1458	U1364	C1216	U	U1052	C934	U779	C709	U
	G1695	A1524	C1459	A1371	G1217	U	U1053	U935	A780	U710	U
	G1696	G1527	A1460	U1372	A1219	U	U1054	A944	U781	U711	U
	G1697	U1530	G1464	C1373	A1221	U	U1055	U945	G782	G712	U
	G1698	G1531	C1465	A1374	C1222	U	U1056	A951	G783	A713	U
	A1782	U1615	G1466	C1375	C1223	U	G1149	A952	C784	G714	U
	C1783	U1616	C1467	U1376	A1224	U	U1150	A953	U785	G715	U
	G1786	C1617	G1468	U1377	A1225	U	A1151	C956	G786	U716	U
	A1791	C1618	U1469	C1378	U1226	U	U	U	G787	C717	U
	G1792	C1619	A1469	U1379	A1227	U	U	U	A788	C718	U
	C1793	C1620	C1470	C1380	A1228	U	U	U	A789	U719	U
	U1794	U1621	A1471	U1381	G1304	U	A1062	A969	U794	G720	U
	A1795	G1622	C1472	A1382	U1305	G	U1063	U961		U721	U
		G1629	U1473	G1383	U1307	A					

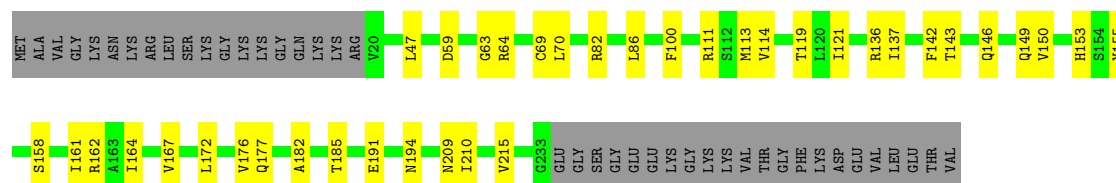
- Molecule 50: 40S ribosomal protein S0-A

Chain q:  71% 11% 18%



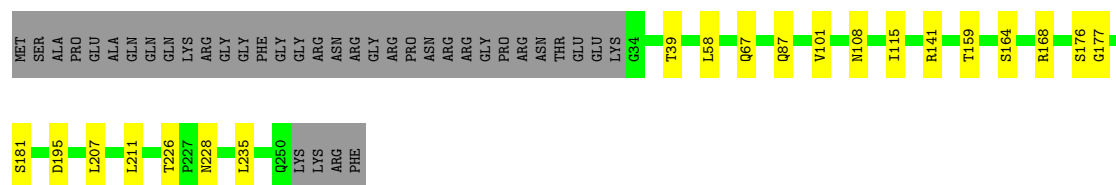
- Molecule 51: RPS1A isoform 1

Chain r:  69% 15% 16%



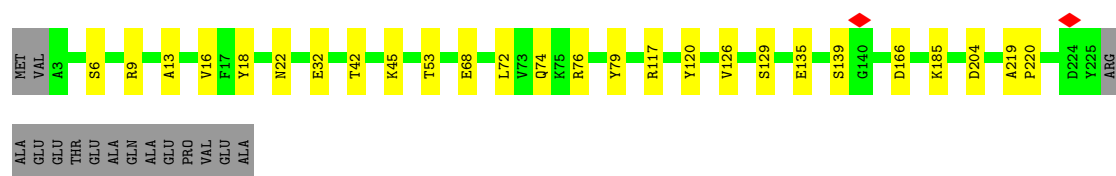
- Molecule 52: RPS2 isoform 1

Chain s:  78% 8% 15%



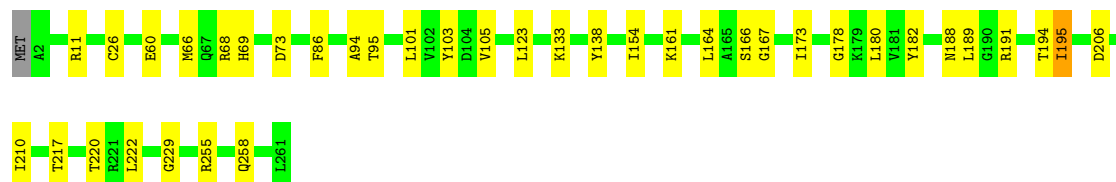
- Molecule 53: RPS3 isoform 1

Chain t:  82% 11% 7%



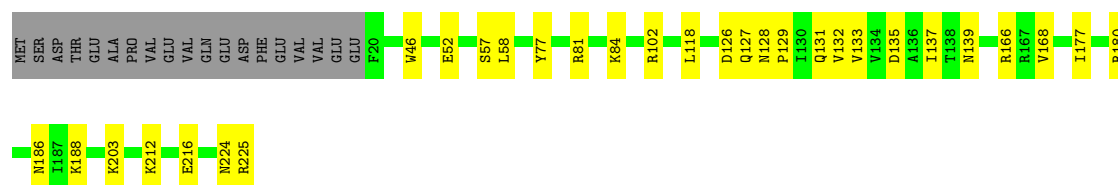
- Molecule 54: 40S ribosomal protein S4-A

Chain u:  85% 14%



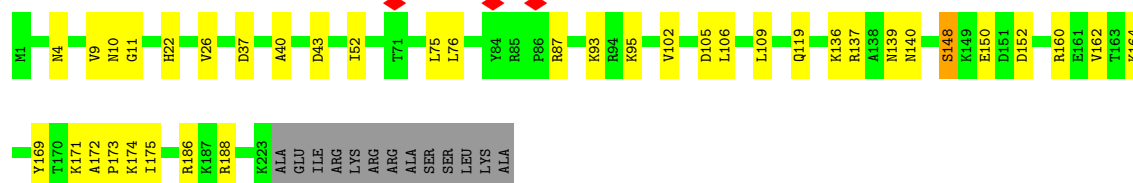
- Molecule 55: Rps5p

Chain v: 



- Molecule 56: 40S ribosomal protein S6-A

Chain w: 



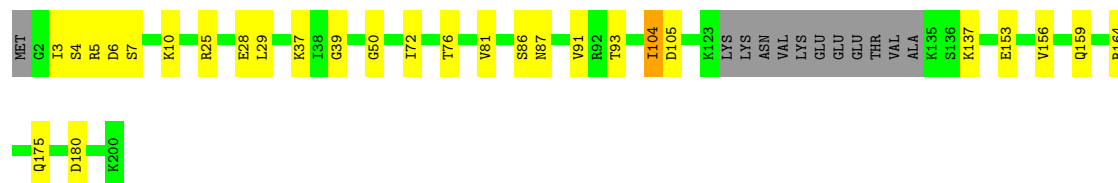
- Molecule 57: 40S ribosomal protein S7-A

Chain x: 



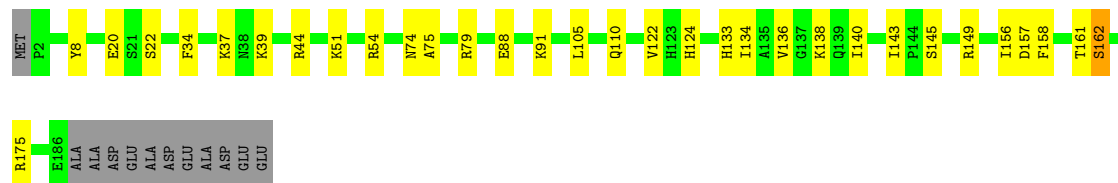
- Molecule 58: RPS8A isoform 1

Chain y: 



- Molecule 59: 40S ribosomal protein S9-A

Chain z: 



- Molecule 60: 40S ribosomal protein S13

Chain AD: 



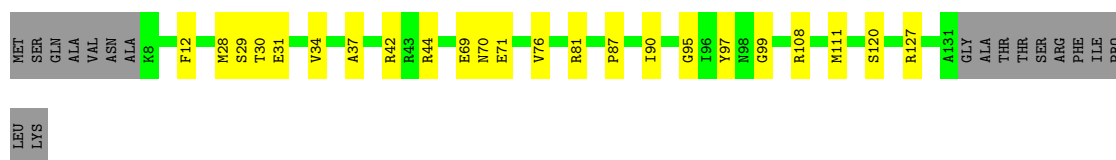
- Molecule 61: 40S ribosomal protein S14-B

Chain AE: 85% 7% 8%



- Molecule 62: RPS15 isoform 1

Chain AF: 71% 16% 13%



- Molecule 63: 40S ribosomal protein S16-A

Chain AG: 87% 12% .



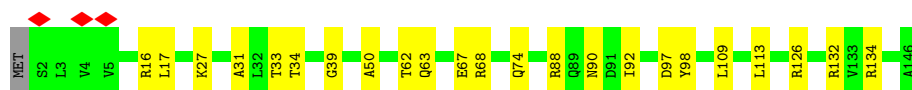
- Molecule 64: 40S ribosomal protein S17-B

Chain AH: 79% 9% 12%



- Molecule 65: 40S ribosomal protein S18-A

Chain AI: 84% 16% .



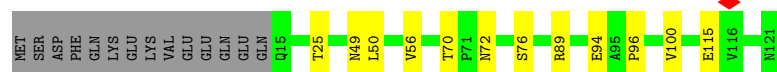
- Molecule 66: 40S ribosomal protein S19-A

Chain AJ: 88% 12% .



- Molecule 67: RPS20 isoform 1

Chain AK:  79% 10% 12%



- Molecule 68: 40S ribosomal protein S21-A

Chain AL:  90% 9%



- Molecule 69: RPS22A isoform 1

Chain AM:  82% 17%



- Molecule 70: 40S ribosomal protein S23-A

Chain AN:  84% 15%



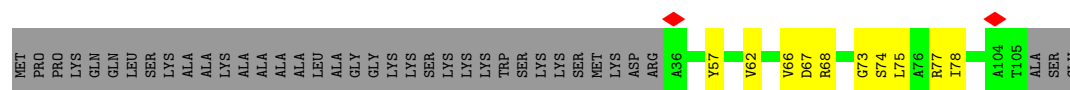
- Molecule 71: 40S ribosomal protein S24-A

Chain AO:  80% 19%



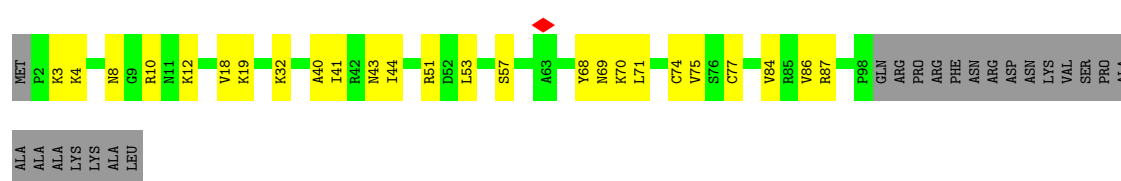
- Molecule 72: RPS25A isoform 1

Chain AP:  56% 9% 35%

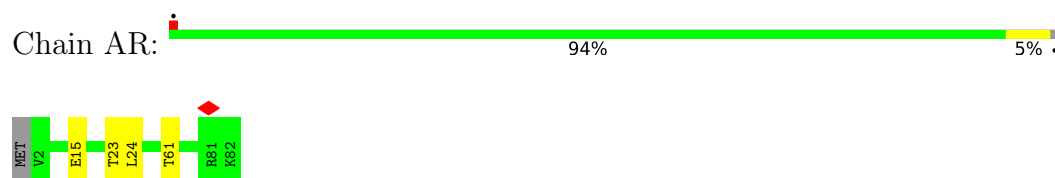


- Molecule 73: RPS26B isoform 1

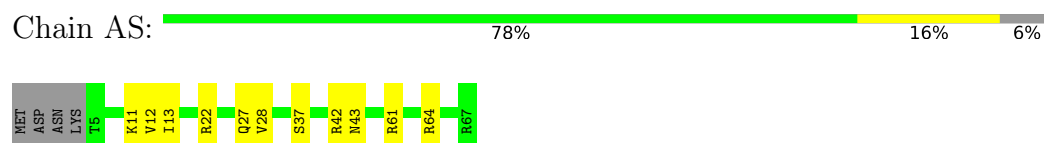
Chain AQ:  61% 21% 18%



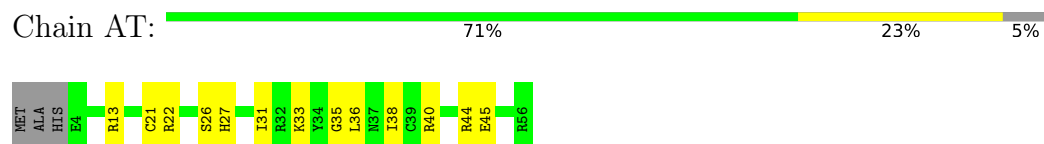
- Molecule 74: 40S ribosomal protein S27-A



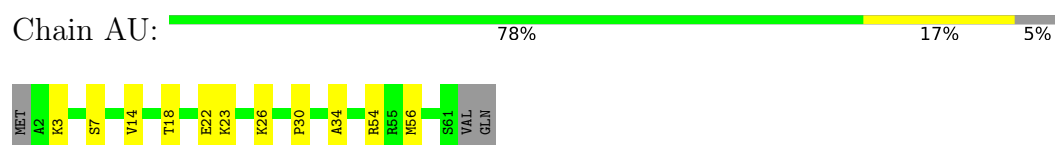
- Molecule 75: RPS28A isoform 1



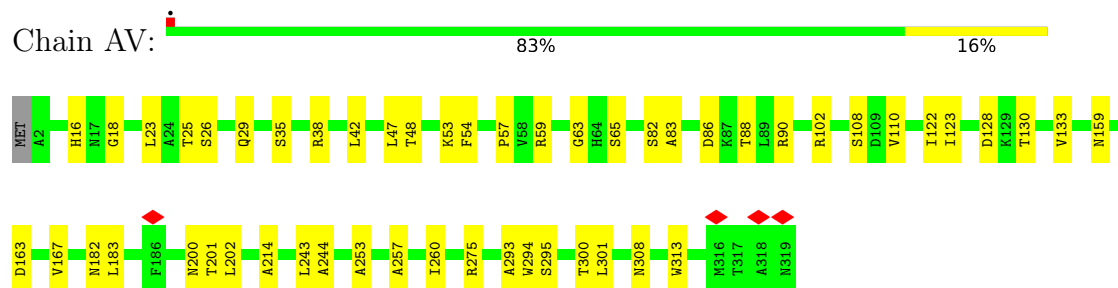
- Molecule 76: RPS29A isoform 1



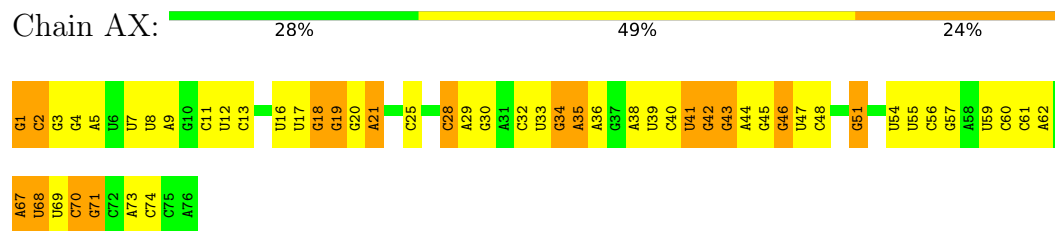
- Molecule 77: 40S ribosomal protein S30-A



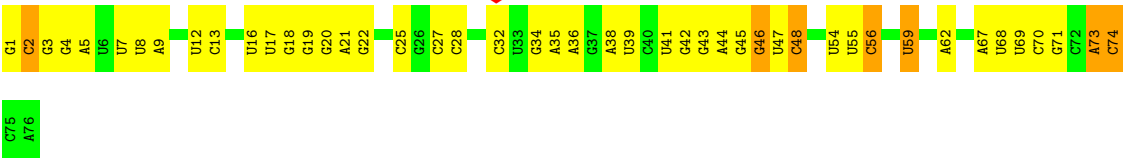
- Molecule 78: Guanine nucleotide-binding protein subunit beta-like protein



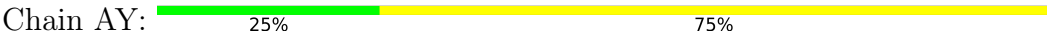
- Molecule 79: Transfer RNA



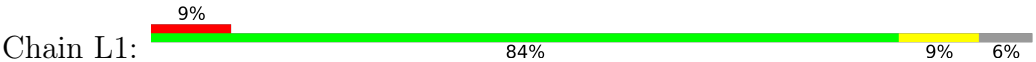
- Molecule 79: Transfer RNA



• Molecule 80: mRNA



• Molecule 81: RPL1A isoform 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	9629	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	27.135	Depositor
Minimum map value	-15.154	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	545.792, 545.792, 545.792	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.066, 1.066, 1.066	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.20	0/1948	0.44	0/2617
2	B	0.19	0/3146	0.41	0/4228
3	C	0.19	0/2800	0.43	0/3790
4	D	0.18	0/2425	0.38	0/3271
5	E	0.18	0/1260	0.36	0/1694
6	F	0.20	0/1821	0.44	0/2451
7	G	0.85	2/1836 (0.1%)	0.49	2/2481 (0.1%)
8	H	0.20	0/1539	0.43	0/2073
9	I	0.18	0/1741	0.40	0/2335
10	J	0.20	0/1374	0.46	0/1842
11	L	0.21	0/1568	0.47	0/2106
12	M	0.19	0/1068	0.36	0/1438
13	N	0.20	0/1757	0.42	0/2354
14	O	0.21	0/1585	0.41	0/2128
15	P	0.18	0/1443	0.40	0/1944
16	Q	0.18	0/1465	0.39	0/1965
17	R	0.19	0/1538	0.40	0/2050
18	S	0.19	0/1481	0.42	0/1990
19	T	0.20	0/1300	0.41	0/1743
20	U	0.19	0/812	0.40	0/1099
21	V	0.19	0/1018	0.41	0/1369
22	W	0.18	0/533	0.33	0/707
23	X	0.16	0/979	0.39	0/1321
24	Y	0.17	0/1004	0.41	0/1341
25	Z	0.18	0/1118	0.40	0/1497
26	AA	0.20	0/789	0.44	0/1067
27	AB	0.18	0/1247	0.41	0/1681
28	1	0.59	12/77157 (0.0%)	0.41	4/120295 (0.0%)
29	3	0.17	0/2883	0.37	0/4491
30	4	1.82	6/3746 (0.2%)	0.44	1/5832 (0.0%)
31	P0	0.23	0/1498	0.47	0/2025
32	P2	0.25	0/728	0.44	0/975

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	a	0.19	0/1204	0.42	0/1612
34	b	0.18	0/473	0.36	0/629
35	c	0.17	0/751	0.37	0/1008
36	d	0.19	0/897	0.39	0/1205
37	e	0.17	0/1041	0.37	0/1394
38	f	0.20	0/868	0.43	0/1168
39	g	0.21	0/890	0.41	0/1189
40	h	0.18	0/978	0.43	0/1301
41	i	0.19	0/778	0.38	0/1034
42	j	2.27	1/696 (0.1%)	0.75	2/923 (0.2%)
43	k	0.17	0/618	0.41	0/826
44	l	0.24	0/443	0.53	0/588
45	m	0.26	0/423	0.49	0/562
46	n	0.19	0/228	0.39	0/293
47	o	0.19	0/860	0.45	0/1136
48	p	0.19	0/701	0.44	0/934
49	2	0.39	4/41539 (0.0%)	0.34	9/64723 (0.0%)
50	q	0.20	0/1617	0.41	0/2215
51	r	0.19	0/1735	0.47	0/2335
52	s	0.18	0/1665	0.42	0/2263
53	t	0.21	0/1759	0.45	0/2368
54	u	0.20	0/2109	0.50	0/2839
55	v	0.21	0/1629	0.47	0/2202
56	w	0.22	0/1814	0.53	0/2425
57	x	0.19	0/1506	0.44	0/2028
58	y	0.22	0/1514	0.52	0/2021
59	z	0.19	0/1519	0.46	0/2035
60	AD	0.19	0/1215	0.48	0/1638
61	AE	0.20	0/901	0.43	0/1217
62	AF	0.22	0/998	0.49	0/1341
63	AG	0.23	0/1125	0.50	0/1510
64	AH	0.19	0/935	0.46	0/1254
65	AI	0.19	0/1211	0.45	0/1628
66	AJ	0.21	0/1130	0.44	0/1517
67	AK	0.21	0/865	0.44	0/1169
68	AL	0.20	0/693	0.49	0/935
69	AM	0.18	0/1038	0.40	0/1395
70	AN	0.20	0/1139	0.47	0/1518
71	AO	0.18	0/1087	0.42	0/1449
72	AP	0.21	0/571	0.44	0/768
73	AQ	0.23	0/782	0.48	0/1047
74	AR	0.17	0/620	0.42	0/838
75	AS	0.21	0/499	0.41	0/670

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	AT	0.20	0/452	0.38	0/600
77	AU	0.20	0/483	0.39	0/643
78	AV	0.18	0/2490	0.39	0/3389
79	AX	0.13	0/1818	0.30	0/2831
79	AZ	0.13	0/1818	0.31	0/2831
80	AY	0.17	0/181	0.40	0/278
81	L1	0.20	0/1634	0.42	0/2195
All	All	0.50	25/220547 (0.0%)	0.41	18/324117 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
3	C	0	1
7	G	0	1
11	L	0	1
14	O	0	1
39	g	0	1
45	m	0	1
54	u	0	1
55	v	0	1
81	L1	0	1
All	All	0	10

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	2	1759	C	C1'-N1	69.46	2.52	1.48
42	j	81	GLY	CA-C	59.37	2.35	1.51
28	1	148	G	C6-N1	53.78	2.47	1.39
28	1	148	G	N1-C2	52.97	2.43	1.37
28	1	148	G	C2-N3	52.07	2.36	1.32
28	1	148	G	N3-C4	50.51	2.36	1.35
30	4	95	G	N3-C4	48.64	2.32	1.35
30	4	95	G	C2-N3	48.03	2.28	1.32
30	4	95	G	C6-N1	47.66	2.34	1.39
30	4	95	G	N1-C2	46.03	2.29	1.37
28	1	2262	A	N1-C2	43.52	2.21	1.34
28	1	148	G	C5-C6	43.35	2.29	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	1	2262	A	C2-N3	42.54	2.18	1.33
30	4	95	G	C5-C6	41.86	2.26	1.42
28	1	2262	A	C6-N1	41.30	2.18	1.35
28	1	2262	A	N3-C4	40.39	2.15	1.34
28	1	148	G	C5-C4	38.76	2.15	1.38
28	1	2262	A	C5-C6	38.71	2.18	1.41
30	4	95	G	C5-C4	37.35	2.13	1.38
7	G	135	GLY	CA-C	35.11	2.01	1.51
28	1	2262	A	C5-C4	34.46	2.07	1.38
49	2	1759	C	N1-C2	15.61	1.71	1.40
49	2	1759	C	N1-C6	13.08	1.63	1.37
7	G	135	GLY	N-CA	5.88	1.53	1.45
49	2	1759	C	C2'-C1'	5.50	1.61	1.53

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	2	1759	C	C6-N1-C2	-16.88	69.58	120.20
42	j	81	GLY	O-C-N	-15.86	102.09	122.70
49	2	1759	C	N1-C1'-C2'	12.29	130.44	112.00
49	2	1759	C	C5-C6-N1	11.53	155.57	121.00
7	G	135	GLY	N-CA-C	9.12	134.81	113.18
49	2	1759	C	N3-C2-O2	-9.02	94.86	121.90
49	2	1759	C	C2-N1-C1'	8.56	144.48	118.80
49	2	1759	C	O4'-C1'-N1	8.46	121.19	108.50
49	2	1759	C	C6-N1-C1'	8.38	145.93	120.80
49	2	1759	C	N1-C2-N3	8.12	143.57	119.20
7	G	135	GLY	O-C-N	-7.60	112.82	122.70
49	2	1759	C	O4'-C1'-C2'	-6.34	101.26	107.60
42	j	81	GLY	N-CA-C	6.30	128.11	113.18
28	1	2262	A	N1-C2-N3	-5.94	111.49	129.30
30	4	95	G	N3-C4-N9	5.76	143.28	126.00
28	1	2291	A	O5'-C5'-C4'	5.63	119.95	111.50
28	1	148	G	N3-C4-N9	5.34	142.02	126.00
28	1	148	G	C4-C5-N7	-5.08	95.56	110.80

There are no chirality outliers.

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	150	LEU	Peptide
3	C	182	LEU	Peptide

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Mol	Chain	Res	Type	Group
7	G	135	GLY	Mainchain
11	L	47	ALA	Peptide
81	L1	120	VAL	Peptide
14	O	110	PRO	Peptide
39	g	80	ARG	Peptide
45	m	126	LYS	Peptide
54	u	195	ILE	Peptide
55	v	127	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	A	1914	1981	1981	40	0
2	B	3075	3142	3142	34	0
3	C	2748	2859	2859	47	0
4	D	2375	2326	2325	36	0
5	E	1239	1326	1326	15	0
6	F	1784	1862	1862	14	0
7	G	1804	1877	1877	48	0
8	H	1518	1587	1587	33	0
9	I	1705	1736	1736	20	0
10	J	1353	1383	1383	16	0
11	L	1543	1608	1608	25	0
12	M	1053	1149	1149	17	0
13	N	1720	1779	1779	34	0
14	O	1555	1659	1659	23	0
15	P	1420	1437	1437	18	0
16	Q	1441	1543	1543	24	0
17	R	1521	1617	1617	20	0
18	S	1445	1487	1487	20	0
19	T	1276	1323	1323	21	0
20	U	796	812	812	4	0
21	V	1003	1048	1048	14	0
22	W	521	551	551	2	0
23	X	964	1025	1025	12	0
24	Y	993	1081	1081	14	0
25	Z	1092	1155	1155	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	AA	772	727	727	4	0
27	AB	1220	1282	1281	11	0
28	1	68931	34635	34637	1006	0
29	3	2579	1304	1304	31	0
30	4	3353	1695	1695	82	0
31	P0	1473	1514	1514	20	0
32	P2	723	774	774	8	0
33	a	1173	1215	1215	13	0
34	b	462	491	491	5	0
35	c	743	797	797	8	0
36	d	883	918	918	12	0
37	e	1020	1090	1090	6	0
38	f	850	880	880	12	0
39	g	880	941	941	10	0
40	h	969	1078	1078	14	0
41	i	771	849	849	7	0
42	j	681	683	683	39	0
43	k	612	682	682	11	0
44	l	436	475	475	7	0
45	m	417	456	456	18	0
46	n	227	273	273	2	0
47	o	847	915	915	15	0
48	p	694	734	734	9	0
49	2	37141	18686	18690	398	0
50	q	1577	1567	1567	19	0
51	r	1709	1784	1784	25	0
52	s	1635	1723	1723	14	0
53	t	1734	1817	1817	16	0
54	u	2068	2154	2154	25	0
55	v	1609	1675	1675	16	0
56	w	1790	1881	1881	27	0
57	x	1481	1572	1572	19	0
58	y	1489	1525	1525	22	0
59	z	1494	1573	1573	22	0
60	AD	1192	1255	1255	18	0
61	AE	891	883	883	8	0
62	AF	977	1002	1002	14	0
63	AG	1105	1166	1166	13	0
64	AH	926	930	930	11	0
65	AI	1192	1222	1222	13	0
66	AJ	1112	1124	1124	14	0
67	AK	855	917	917	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
68	AL	684	672	672	7	0
69	AM	1021	1060	1060	14	0
70	AN	1121	1196	1196	16	0
71	AO	1073	1132	1132	22	0
72	AP	563	603	603	9	0
73	AQ	769	814	814	20	0
74	AR	610	632	632	2	0
75	AS	497	535	535	7	0
76	AT	442	431	431	9	0
77	AU	475	525	525	8	0
78	AV	2437	2386	2386	37	0
79	AX	1626	820	820	16	0
79	AZ	1626	820	820	10	0
80	AY	164	84	84	0	0
81	L1	1609	1701	1701	14	0
82	AQ	1	0	0	0	0
82	AR	1	0	0	0	0
82	AT	1	0	0	0	0
82	j	1	0	0	0	0
82	m	1	0	0	0	0
82	o	1	0	0	0	0
82	p	1	0	0	0	0
All	All	205275	151628	151632	2244	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (2244) 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)
49:2:1759:C:C2	49:2:1759:C:N1	1.71	1.56
30:4:95:G:C4	30:4:95:G:C5	2.13	1.34
28:1:2262:A:C4	28:1:2262:A:C5	2.07	1.33
7:G:135:GLY:CA	7:G:135:GLY:C	2.01	1.33
28:1:148:G:C4	28:1:148:G:C5	2.15	1.32
28:1:2262:A:C5	28:1:2262:A:C6	2.18	1.32
30:4:95:G:C5	30:4:95:G:C6	2.26	1.24
49:2:1759:C:C2	49:2:1759:C:C6	1.91	1.23
28:1:148:G:C5	28:1:148:G:C6	2.29	1.21
28:1:2262:A:N3	49:2:1759:C:H1'	1.60	1.16
28:1:2262:A:C4	28:1:2262:A:N3	2.15	1.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:2262:A:C6	28:1:2262:A:N1	2.18	1.10
28:1:2262:A:N3	28:1:2262:A:C2	2.18	1.10
28:1:2262:A:N1	28:1:2262:A:C2	2.21	1.08
7:G:135:GLY:O	28:1:148:G:N1	1.89	1.06
30:4:95:G:C2	30:4:95:G:N3	2.28	1.02
42:j:81:GLY:CA	42:j:81:GLY:C	2.35	1.00
30:4:95:G:C2	30:4:95:G:N1	2.29	0.99
28:1:2838:A:H62	28:1:2850:G:H21	1.07	0.99
56:w:52:ILE:HD11	56:w:109:LEU:HD11	1.46	0.98
49:2:1116:A:H62	49:2:1130:G:H21	1.07	0.98
28:1:1918:C:C2	28:1:1934:G:N2	2.33	0.97
30:4:95:G:C4	30:4:95:G:N3	2.32	0.97
7:G:135:GLY:HA3	28:1:148:G:N3	1.80	0.96
30:4:95:G:C6	30:4:95:G:N1	2.34	0.95
7:G:135:GLY:HA2	28:1:148:G:C5	2.00	0.95
49:2:1311:U:HO2'	64:AH:2:GLY:N	1.65	0.94
28:1:148:G:N3	28:1:148:G:C2	2.36	0.94
28:1:148:G:C4	28:1:148:G:N3	2.36	0.93
30:4:95:G:N1	42:j:81:GLY:HA2	1.83	0.93
7:G:136:LEU:N	28:1:148:G:N3	2.16	0.93
30:4:95:G:C5	42:j:81:GLY:HA3	2.04	0.92
49:2:1673:G:N1	49:2:1728:A:C2	2.37	0.91
30:4:95:G:C2	42:j:81:GLY:CA	2.54	0.89
7:G:135:GLY:C	28:1:148:G:C2	2.51	0.89
7:G:135:GLY:CA	28:1:148:G:C2	2.55	0.89
28:1:2262:A:C2	49:2:1759:C:N1	2.40	0.89
30:4:95:G:N3	42:j:81:GLY:N	2.22	0.87
49:2:1116:A:H62	49:2:1130:G:N2	1.72	0.87
45:m:110:CYS:O	45:m:115:CYS:SG	2.32	0.86
28:1:148:G:N1	28:1:148:G:C2	2.43	0.86
30:4:95:G:C4	42:j:81:GLY:CA	2.58	0.86
30:4:95:G:C6	42:j:81:GLY:CA	2.59	0.85
28:1:1918:C:O2	28:1:1934:G:C2	2.29	0.85
28:1:2262:A:C2	49:2:1759:C:H1'	2.11	0.85
30:4:95:G:N3	42:j:81:GLY:CA	2.40	0.85
7:G:135:GLY:CA	28:1:148:G:C4	2.60	0.85
28:1:2262:A:C4	49:2:1759:C:N1	2.45	0.85
7:G:135:GLY:HA2	28:1:148:G:C4	2.12	0.84
49:2:1116:A:N6	49:2:1130:G:H21	1.76	0.84
28:1:2262:A:N1	49:2:1759:C:N1	2.26	0.84
28:1:2262:A:C2	49:2:1759:C:C1'	2.60	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:148:G:C6	28:1:148:G:N1	2.47	0.83
30:4:95:G:C2	42:j:81:GLY:C	2.56	0.83
79:AX:1:G:H21	79:AX:73:A:N6	1.76	0.83
78:AV:295:SER:HG	78:AV:300:THR:HG1	1.26	0.82
28:1:2262:A:C6	49:2:1759:C:C1'	2.62	0.82
7:G:135:GLY:C	28:1:148:G:N1	2.36	0.82
30:4:95:G:N1	42:j:81:GLY:CA	2.42	0.81
28:1:2302:G:N2	49:2:1746:A:O2'	2.13	0.81
7:G:135:GLY:CA	28:1:148:G:C6	2.63	0.81
49:2:124:A:O2'	49:2:125:U:O4'	1.98	0.81
49:2:435:C:O2'	49:2:436:A:O4'	2.00	0.80
28:1:1384:U:O2'	28:1:1385:C:O4'	1.99	0.80
28:1:1259:A:H61	31:P0:50:VAL:HG11	1.46	0.80
7:G:135:GLY:CA	28:1:148:G:N3	2.44	0.79
28:1:2262:A:C5	49:2:1759:C:N1	2.51	0.79
28:1:2838:A:H62	28:1:2850:G:N2	1.79	0.79
7:G:135:GLY:CA	28:1:148:G:N1	2.45	0.79
28:1:2766:U:O2'	28:1:2768:U:OP2	2.01	0.79
28:1:307:A:N6	28:1:308:A:N6	2.31	0.79
28:1:1130:A:O2'	28:1:2825:C:N4	2.16	0.79
28:1:343:U:O2'	28:1:1429:G:N2	2.16	0.78
28:1:2959:C:O2'	28:1:2960:C:OP1	2.02	0.78
28:1:547:G:O2'	28:1:548:G:O4'	2.01	0.78
28:1:971:G:O6	28:1:1110:U:O4	2.02	0.78
30:4:95:G:C5	42:j:81:GLY:CA	2.66	0.78
28:1:301:G:O2'	28:1:317:A:OP1	2.02	0.78
28:1:70:A:N6	28:1:314:U:O2'	2.16	0.78
49:2:898:A:H62	49:2:914:G:N2	1.81	0.78
28:1:2236:G:O2'	79:AX:70:C:O2	2.00	0.78
7:G:135:GLY:C	28:1:148:G:C6	2.62	0.77
28:1:2262:A:C4	49:2:1759:C:C1'	2.67	0.77
28:1:2262:A:C6	49:2:1759:C:N1	2.52	0.77
79:AX:42:G:O2'	79:AX:43:G:O4'	2.01	0.77
49:2:1181:U:O2'	49:2:1182:U:OP1	2.01	0.77
4:D:23:ARG:NH2	4:D:28:THR:O	2.18	0.77
28:1:2563:G:O6	28:1:2578:U:O2	2.03	0.77
28:1:2713:U:O2'	28:1:2715:A:OP1	2.03	0.77
29:3:47:C:O2'	29:3:48:U:OP1	2.03	0.77
28:1:1918:C:O2	28:1:1934:G:N2	2.17	0.77
28:1:2292:U:OP2	49:2:1745:G:O2'	2.03	0.77
28:1:3104:U:OP2	28:1:3127:A:N6	2.18	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:40:A:N6	28:1:937:G:OP2	2.19	0.76
28:1:105:C:N4	28:1:683:U:O2'	2.19	0.76
28:1:1797:A:O2'	28:1:1798:A:O4'	2.02	0.76
49:2:1211:A:O2'	62:AF:99:GLY:O	2.03	0.76
28:1:2514:U:O2'	28:1:2515:A:N7	2.18	0.76
28:1:344:A:N6	28:1:348:A:OP2	2.18	0.76
28:1:392:G:N2	28:1:397:A:OP2	2.19	0.76
28:1:342:A:N1	28:1:349:A:O2'	2.16	0.76
28:1:2434:U:O2'	28:1:2593:A:N3	2.16	0.76
49:2:114:C:N4	49:2:247:A:N6	2.34	0.76
52:s:226:THR:OG1	52:s:228:ASN:OD1	2.03	0.76
10:J:137:ARG:NH2	29:3:44:C:OP2	2.18	0.76
49:2:1275:A:N7	49:2:1431:C:N4	2.34	0.76
28:1:2262:A:N3	49:2:1759:C:N1	2.34	0.76
28:1:207:U:O2	28:1:209:A:N6	2.18	0.75
6:F:37:ASN:ND2	28:1:597:G:OP2	2.20	0.75
7:G:135:GLY:CA	28:1:148:G:C5	2.68	0.75
28:1:2293:C:N4	28:1:2297:U:OP2	2.20	0.75
28:1:1187:C:O2'	28:1:1188:U:O5'	2.04	0.75
49:2:187:G:N2	49:2:197:A:N7	2.35	0.75
28:1:1393:A:N6	28:1:1418:A:OP1	2.20	0.75
28:1:1141:C:OP2	28:1:1144:U:O2'	2.05	0.75
28:1:1410:U:O2'	28:1:1411:C:OP1	2.03	0.75
30:4:95:G:C4	42:j:81:GLY:C	2.65	0.75
49:2:1135:U:OP2	70:AN:121:ARG:NH2	2.20	0.75
28:1:1654:A:N6	28:1:1800:A:OP2	2.20	0.75
3:C:10:SER:OG	3:C:13:GLY:O	2.05	0.75
10:J:60:ARG:NH1	10:J:63:GLU:OE2	2.19	0.75
28:1:69:C:O5'	28:1:302:U:O2'	2.05	0.75
53:t:42:THR:OG1	53:t:45:LYS:O	2.05	0.75
28:1:2520:A:O2'	28:1:2521:U:OP1	2.05	0.74
49:2:903:U:O2	49:2:906:A:N7	2.20	0.74
7:G:135:GLY:C	28:1:148:G:N3	2.45	0.74
13:N:31:ARG:NH1	28:1:2515:A:O2'	2.20	0.74
28:1:92:G:O5'	47:o:46:LYS:NZ	2.20	0.74
28:1:170:G:O2'	28:1:171:G:N7	2.19	0.74
28:1:341:G:O2'	28:1:342:A:O5'	2.05	0.74
28:1:2140:U:O2'	28:1:2141:U:OP1	2.04	0.74
28:1:3352:U:OP1	28:1:3353:G:N2	2.19	0.74
28:1:934:G:OP2	28:1:934:G:N2	2.20	0.74
28:1:1451:C:O2'	28:1:1880:U:OP1	2.05	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2:68:A:N7	56:w:160:ARG:NH2	2.36	0.74
28:1:2699:G:O2'	28:1:2700:G:OP1	2.05	0.74
28:1:3128:G:O2'	45:m:88:LYS:NZ	2.20	0.74
49:2:593:U:O2'	49:2:594:A:O4'	2.06	0.74
28:1:35:A:O2'	28:1:36:C:O4'	2.03	0.74
28:1:494:G:O2'	28:1:496:C:OP2	2.06	0.74
28:1:2262:A:N1	49:2:1759:C:C1'	2.50	0.74
27:AB:69:LYS:NZ	49:2:304:U:O2	2.21	0.74
11:L:39:ARG:NH2	28:1:685:G:OP1	2.21	0.74
16:Q:179:ARG:NH2	28:1:2789:U:OP1	2.21	0.74
28:1:2728:G:N2	28:1:2728:G:OP2	2.20	0.74
49:2:810:G:O6	57:x:111:LYS:NZ	2.21	0.74
28:1:998:A:O2'	29:3:103:A:O2'	2.05	0.73
49:2:207:U:O2'	58:y:180:ASP:OD2	2.06	0.73
49:2:610:G:HO2'	49:2:613:G:HO2'	1.30	0.73
28:1:1501:U:O2'	28:1:1502:C:OP1	2.06	0.73
28:1:3138:U:O2'	28:1:3139:A:O5'	2.04	0.73
29:3:66:A:H62	29:3:67:G:H21	1.36	0.73
11:L:174:ARG:NH2	28:1:713:U:OP1	2.22	0.73
30:4:101:U:O2'	30:4:102:U:O4'	2.04	0.73
28:1:104:G:N2	28:1:683:U:O2'	2.22	0.73
28:1:848:A:N1	49:2:973:A:O2'	2.21	0.73
28:1:2755:C:O2'	28:1:2756:C:O4'	2.07	0.73
30:4:95:G:C6	42:j:81:GLY:C	2.67	0.73
28:1:994:G:OP1	28:1:2637:A:O2'	2.07	0.73
30:4:95:G:C5	42:j:81:GLY:C	2.67	0.73
49:2:1759:C:N1	49:2:1759:C:C1'	2.52	0.73
1:A:51:ASP:OD2	1:A:54:ARG:NH1	2.21	0.73
28:1:117:U:OP2	28:1:123:A:N6	2.22	0.73
28:1:2838:A:N6	28:1:2850:G:H21	1.83	0.73
28:1:1047:A:O2'	28:1:2634:U:OP2	2.05	0.72
28:1:1377:G:O6	28:1:1428:A:N6	2.21	0.72
28:1:1649:U:O4	28:1:1807:G:N2	2.22	0.72
28:1:2290:C:O2	49:2:1746:A:O2'	2.07	0.72
49:2:410:A:N1	49:2:423:G:O6	2.21	0.72
2:B:50:LYS:NZ	28:1:3047:U:OP2	2.22	0.72
58:y:37:LYS:NZ	58:y:93:THR:O	2.22	0.72
7:G:135:GLY:C	28:1:148:G:C5	2.67	0.72
28:1:30:G:N2	28:1:1546:A:N7	2.36	0.72
28:1:999:G:O2'	28:1:1000:C:O5'	2.04	0.72
28:1:1525:G:O2'	28:1:1526:U:OP1	2.07	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:4:3:A:O2'	30:4:4:C:OP1	2.07	0.72
40:h:83:LYS:NZ	42:j:66:TYR:OH	2.22	0.72
49:2:522:U:O2'	71:AO:59:GLY:O	2.06	0.72
28:1:509:U:O2'	28:1:510:G:OP1	2.07	0.72
28:1:1110:U:O2'	28:1:1111:U:O5'	2.06	0.72
49:2:1304:G:OP2	49:2:1305:U:O2'	2.06	0.72
49:2:1681:A:N6	49:2:1721:A:OP2	2.22	0.72
28:1:1231:A:N6	31:P0:36:GLN:OE1	2.23	0.72
28:1:1847:A:O2'	28:1:1848:G:O5'	2.08	0.72
28:1:1929:G:OP2	28:1:1930:A:O2'	2.06	0.72
30:4:95:G:N1	42:j:81:GLY:C	2.48	0.72
49:2:1346:A:OP2	49:2:1376:C:N4	2.22	0.72
6:F:121:LYS:NZ	28:1:987:U:OP1	2.22	0.72
28:1:251:G:O2'	28:1:252:U:OP2	2.06	0.72
28:1:350:C:O2'	28:1:352:A:OP1	2.06	0.72
28:1:632:G:O2'	38:f:21:ARG:O	2.07	0.72
28:1:2342:U:OP1	28:1:3089:C:O2'	2.07	0.72
12:M:55:ARG:NH1	18:S:70:THR:OG1	2.23	0.72
28:1:347:G:N2	28:1:366:A:OP2	2.23	0.72
28:1:2714:G:OP1	28:1:2742:C:O2'	2.05	0.72
28:1:340:C:OP1	30:4:25:G:N2	2.21	0.72
28:1:344:A:O2'	28:1:1429:G:O6	2.06	0.72
28:1:2359:C:O2	28:1:2360:C:N4	2.21	0.72
50:q:111:ILE:HG22	50:q:112:THR:HG23	1.71	0.72
28:1:635:G:N2	28:1:637:C:OP1	2.18	0.72
28:1:1084:A:O2'	28:1:1085:A:OP1	2.06	0.72
49:2:318:U:O2	49:2:346:G:O6	2.07	0.72
57:x:11:GLN:NE2	57:x:44:LYS:O	2.22	0.72
28:1:931:C:OP2	28:1:932:U:O2'	2.02	0.71
28:1:1172:G:O2'	28:1:1173:U:O5'	2.06	0.71
28:1:1179:A:O2'	28:1:1326:A:O2'	2.08	0.71
28:1:1669:C:O2'	28:1:1858:A:OP1	2.07	0.71
28:1:1807:G:O2'	28:1:2559:U:O4	2.07	0.71
28:1:1918:C:C2	28:1:1934:G:C2	2.78	0.71
28:1:493:U:O2'	28:1:494:G:O4'	2.08	0.71
79:AX:67:A:O2'	79:AX:68:U:OP1	2.07	0.71
28:1:66:A:H62	28:1:76:G:N2	1.88	0.71
28:1:362:U:OP2	42:j:45:ARG:NH1	2.22	0.71
49:2:385:A:OP1	58:y:25:ARG:NH2	2.23	0.71
28:1:310:U:OP1	41:i:84:LYS:NZ	2.23	0.71
28:1:409:A:O2'	28:1:653:A:N1	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:710:A:O3'	28:1:2777:G:N2	2.24	0.71
28:1:762:U:O2	28:1:769:G:O6	2.07	0.71
30:4:106:C:N4	30:4:138:A:OP2	2.22	0.71
49:2:50:C:OP1	49:2:423:G:N2	2.23	0.71
49:2:97:C:O2	49:2:425:A:O2'	2.08	0.71
28:1:106:A:OP1	28:1:107:A:O2'	2.07	0.71
28:1:678:G:N2	28:1:788:C:OP1	2.24	0.71
28:1:1751:G:O2'	28:1:1752:A:O5'	2.08	0.71
28:1:3150:A:O2'	28:1:3294:A:OP1	2.08	0.71
49:2:1497:U:O2'	49:2:1498:G:OP1	2.08	0.71
28:1:187:A:O2'	28:1:188:U:OP1	2.06	0.71
28:1:424:G:N2	28:1:2363:A:OP1	2.24	0.71
30:4:133:G:O2'	30:4:134:G:OP1	2.08	0.71
49:2:1786:G:OP2	61:AE:133:ARG:NH1	2.24	0.71
28:1:198:A:O2'	28:1:199:A:OP1	2.08	0.71
28:1:656:A:N6	28:1:1440:G:O6	2.24	0.71
4:D:33:ARG:NH1	29:3:7:G:OP1	2.24	0.71
28:1:2262:A:N3	49:2:1759:C:C1'	2.50	0.71
28:1:436:A:O4'	28:1:1400:G:O2'	2.08	0.71
45:m:103:LEU:O	45:m:120:GLN:NE2	2.23	0.71
56:w:43:ASP:O	56:w:119:GLN:NE2	2.24	0.71
79:AZ:1:G:H21	79:AZ:73:A:N6	1.89	0.71
7:G:135:GLY:HA3	28:1:148:G:C2	2.26	0.71
8:H:77:ASN:ND2	28:1:3112:G:OP1	2.24	0.71
28:1:818:C:O4'	28:1:920:A:N6	2.23	0.71
28:1:2678:A:N1	79:AZ:56:C:O2'	2.22	0.71
28:1:397:A:O2'	28:1:400:G:N7	2.24	0.70
28:1:1379:G:O6	28:1:1427:U:O2	2.09	0.70
28:1:3229:G:O2'	28:1:3230:G:O5'	2.07	0.70
50:q:36:TYR:O	50:q:49:ASN:ND2	2.23	0.70
79:AX:28:C:N4	79:AX:41:U:O4	2.24	0.70
17:R:20:ARG:NH1	28:1:1874:A:N7	2.38	0.70
28:1:1529:A:O2'	28:1:1530:U:OP1	2.07	0.70
28:1:1585:C:OP1	30:4:109:A:O2'	2.07	0.70
30:4:95:G:N3	42:j:81:GLY:C	2.49	0.70
49:2:868:G:OP1	60:AD:121:ARG:NH1	2.24	0.70
7:G:135:GLY:C	28:1:148:G:C4	2.69	0.70
23:X:109:LYS:NZ	28:1:1523:U:O2	2.23	0.70
28:1:830:A:N1	28:1:1865:A:O2'	2.22	0.70
49:2:1396:U:O2	49:2:1402:G:O6	2.09	0.70
17:R:21:LYS:NZ	28:1:1874:A:OP2	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:177:U:O2	28:1:241:G:C6	2.43	0.70
28:1:2494:A:O2'	28:1:2496:C:N4	2.24	0.70
49:2:545:A:N6	49:2:594:A:OP2	2.23	0.70
79:AX:21:A:N6	79:AX:46:G:O2'	2.25	0.70
28:1:679:U:O2	28:1:701:G:O6	2.09	0.70
28:1:818:C:O5'	28:1:920:A:N6	2.25	0.70
28:1:1526:U:O2	28:1:1594:A:O2'	2.07	0.70
28:1:2416:U:O4'	28:1:2805:G:N2	2.25	0.70
28:1:3325:G:O6	28:1:3381:U:O2	2.09	0.70
28:1:2469:G:OP1	28:1:2477:G:N2	2.24	0.70
28:1:3042:U:OP2	28:1:3092:C:N4	2.24	0.70
1:A:241:ARG:NH1	28:1:2202:C:O3'	2.24	0.70
28:1:940:G:O2'	28:1:941:G:OP1	2.07	0.70
28:1:945:C:O2	28:1:1374:G:N2	2.25	0.70
28:1:1480:G:N2	28:1:1871:U:OP2	2.25	0.70
49:2:473:A:OP1	59:z:44:ARG:NH1	2.24	0.70
49:2:1102:G:OP2	70:AN:7:ARG:NH2	2.25	0.70
12:M:105:GLN:NE2	14:O:198:GLY:O	2.25	0.70
77:AU:54:ARG:NH2	77:AU:56:MET:SD	2.65	0.70
17:R:6:THR:OG1	17:R:7:GLN:OE1	2.09	0.70
28:1:21:G:N2	30:4:139:U:O2	2.24	0.70
28:1:50:U:O2'	28:1:51:A:OP1	2.08	0.70
28:1:1626:U:O2	28:1:1817:G:O6	2.10	0.70
28:1:2262:A:H62	49:2:1758:U:H3'	1.57	0.70
28:1:2423:U:O2	28:1:2424:A:N6	2.24	0.70
49:2:885:G:O2'	49:2:886:U:O4'	2.10	0.70
49:2:1108:G:N2	70:AN:22:ASN:OD1	2.25	0.70
14:O:159:LYS:NZ	28:1:3242:G:OP1	2.19	0.70
28:1:971:G:O3'	28:1:1371:G:N2	2.23	0.70
28:1:1065:A:OP1	34:b:27:TYR:OH	2.08	0.70
28:1:1111:U:O2'	28:1:1370:G:OP2	2.08	0.70
28:1:1308:A:O2'	28:1:1309:U:OP2	2.09	0.70
28:1:1840:U:O2'	28:1:1848:G:N2	2.25	0.70
28:1:2262:A:C5	49:2:1759:C:C1'	2.75	0.70
28:1:2378:C:O2'	28:1:2379:U:OP1	2.08	0.70
59:z:88:GLU:O	59:z:91:LYS:NZ	2.24	0.70
2:B:384:LYS:NZ	28:1:3369:G:O2'	2.24	0.69
28:1:93:C:N4	28:1:2764:C:O5'	2.25	0.69
28:1:1165:A:O2'	28:1:1166:G:OP1	2.11	0.69
28:1:1919:G:N2	28:1:1932:A:OP1	2.25	0.69
28:1:2908:G:O2'	28:1:3106:A:OP1	2.10	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:U:70:LYS:NZ	28:1:1687:U:O4	2.24	0.69
25:Z:15:ARG:NH1	28:1:1709:C:OP1	2.25	0.69
28:1:1368:U:OP1	33:a:21:ARG:NH2	2.25	0.69
49:2:628:G:OP1	60:AD:124:ARG:NH1	2.25	0.69
11:L:91:ARG:NH1	28:1:110:G:OP2	2.25	0.69
13:N:125:SER:OG	28:1:2432:A:N7	2.23	0.69
25:Z:33:SER:OG	25:Z:35:SER:O	2.08	0.69
28:1:1279:C:OP1	28:1:1280:C:N4	2.26	0.69
5:E:77:ARG:NH2	28:1:3273:A:OP1	2.25	0.69
28:1:681:U:O2'	28:1:682:U:O4'	2.05	0.69
38:f:37:THR:OG1	38:f:40:ASP:OD1	2.08	0.69
49:2:1122:G:N2	49:2:1125:A:OP2	2.25	0.69
11:L:185:LYS:NZ	28:1:2780:A:O3'	2.24	0.69
28:1:1440:G:O2'	30:4:16:G:O5'	2.10	0.69
28:1:2257:C:O2	77:AU:3:LYS:NZ	2.24	0.69
28:1:2298:U:O2'	28:1:2920:U:O3'	2.11	0.69
49:2:1171:A:HO2'	49:2:1570:A:HO2'	1.34	0.69
23:X:96:LYS:NZ	23:X:107:VAL:O	2.25	0.69
28:1:396:A:O3'	28:1:398:A:O2'	2.05	0.69
28:1:322:U:O2'	28:1:323:A:OP1	2.08	0.69
28:1:667:C:N4	28:1:794:U:O4	2.26	0.69
28:1:778:U:O2'	28:1:779:G:OP1	2.11	0.69
28:1:1489:A:N6	28:1:1839:A:N1	2.39	0.69
29:3:73:C:O2'	29:3:75:G:N7	2.22	0.69
30:4:58:G:O2'	30:4:100:U:OP1	2.10	0.69
70:AN:65:ASN:ND2	70:AN:116:ASP:OD2	2.26	0.69
1:A:156:LYS:NZ	28:1:2158:A:OP2	2.19	0.69
17:R:172:ARG:NH2	49:2:851:U:OP1	2.25	0.69
17:R:172:ARG:NH1	49:2:852:C:OP2	2.25	0.69
28:1:34:A:O2'	28:1:810:A:OP1	2.09	0.69
28:1:336:A:O2'	28:1:337:G:OP1	2.09	0.69
28:1:950:G:N2	28:1:1143:A:N1	2.40	0.69
28:1:1375:G:N2	28:1:1407:A:O2'	2.25	0.69
28:1:2400:G:OP1	28:1:2871:G:O2'	2.10	0.69
49:2:170:U:OP1	49:2:267:U:O2'	2.09	0.69
49:2:1192:C:N4	49:2:1285:U:OP2	2.26	0.69
49:2:1341:A:OP1	78:AV:102:ARG:NH2	2.26	0.69
60:AD:104:ARG:O	60:AD:106:ARG:N	2.26	0.69
6:F:88:ARG:NH2	6:F:91:GLY:O	2.25	0.69
8:H:20:ILE:O	12:M:8:LYS:NZ	2.26	0.69
11:L:20:GLU:N	11:L:20:GLU:OE1	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R:78:TYR:O	28:1:1914:G:N2	2.26	0.69
27:AB:132:SER:O	27:AB:136:ARG:NH2	2.25	0.69
28:1:2360:C:O2'	28:1:2361:A:O5'	2.07	0.69
28:1:3235:C:N4	28:1:3251:U:O4	2.25	0.69
49:2:1614:A:O4'	55:v:166:ARG:NH2	2.26	0.69
54:u:188:ASN:OD1	54:u:220:THR:OG1	2.11	0.69
4:D:278:SER:OG	4:D:280:GLU:OE1	2.10	0.69
13:N:49:ARG:NH2	28:1:149:U:OP1	2.25	0.69
29:3:84:A:N1	29:3:97:A:N6	2.41	0.69
49:2:4:C:OP1	52:s:181:SER:OG	2.11	0.69
9:I:177:ASP:N	9:I:180:GLU:OE2	2.25	0.68
16:Q:66:ARG:NH2	28:1:784:A:O2'	2.27	0.68
49:2:524:U:O2'	49:2:527:A:N6	2.26	0.68
73:AQ:74:CYS:N	73:AQ:77:CYS:SG	2.65	0.68
7:G:136:LEU:N	28:1:148:G:C4	2.62	0.68
13:N:5:LYS:NZ	28:1:267:G:OP2	2.27	0.68
1:A:123:ARG:NH2	28:1:2521:U:OP2	2.27	0.68
10:J:137:ARG:NH1	29:3:43:U:OP1	2.26	0.68
28:1:109:A:O2'	28:1:110:G:O5'	2.10	0.68
28:1:2525:G:OP1	28:1:2586:G:N2	2.24	0.68
49:2:326:G:O6	49:2:337:G:O6	2.11	0.68
49:2:1684:U:O2	49:2:1718:G:O6	2.12	0.68
3:C:84:ARG:NH1	28:1:366:A:OP1	2.27	0.68
28:1:124:U:O2'	28:1:150:A:N7	2.24	0.68
28:1:856:G:O2'	28:1:857:G:O5'	2.10	0.68
28:1:1188:U:N3	28:1:1317:A:OP1	2.26	0.68
32:P2:124:THR:OG1	32:P2:127:SER:OG	2.08	0.68
76:AT:22:ARG:NE	76:AT:36:LEU:O	2.27	0.68
4:D:20:PHE:O	4:D:24:ARG:NH2	2.26	0.68
11:L:55:ARG:NH1	28:1:107:A:O2'	2.26	0.68
25:Z:107:ARG:NH1	28:1:1634:G:OP1	2.26	0.68
28:1:41:G:OP2	28:1:959:C:O2'	2.06	0.68
28:1:872:U:OP2	28:1:2141:U:O2'	2.08	0.68
28:1:969:C:OP1	34:b:19:ASN:ND2	2.26	0.68
28:1:1612:A:OP2	43:k:46:ARG:NH1	2.26	0.68
28:1:2133:U:OP1	28:1:2322:C:O2'	2.11	0.68
49:2:56:U:O3'	49:2:457:G:O2'	2.10	0.68
49:2:114:C:C4	49:2:247:A:N6	2.60	0.68
49:2:1554:U:OP1	76:AT:13:ARG:NH1	2.26	0.68
51:r:182:ALA:O	51:r:185:THR:OG1	2.12	0.68
4:D:273:ARG:NH1	4:D:274:GLN:O	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:21:G:O2'	28:1:22:G:O4'	2.11	0.68
28:1:696:C:O2'	28:1:697:A:OP1	2.12	0.68
28:1:3229:G:N2	28:1:3258:U:O2'	2.27	0.68
49:2:1353:U:OP1	49:2:1363:U:O2'	2.12	0.68
79:AZ:1:G:N2	79:AZ:73:A:H62	1.92	0.68
6:F:159:GLN:NE2	28:1:1361:U:O2	2.27	0.68
21:V:25:CYS:SG	21:V:26:ALA:N	2.67	0.68
49:2:1719:A:H62	49:2:1720:G:H21	1.42	0.68
55:v:186:ASN:ND2	55:v:188:LYS:O	2.26	0.68
28:1:49:A:N6	28:1:279:U:O2'	2.26	0.68
28:1:983:A:N6	28:1:1100:U:O4	2.26	0.68
28:1:1139:G:OP2	34:b:14:ARG:NH2	2.27	0.68
28:1:1276:U:OP1	31:P0:35:SER:OG	2.11	0.68
49:2:1358:G:O2'	49:2:1359:C:OP1	2.10	0.68
1:A:71:LEU:N	28:1:1651:U:OP2	2.26	0.67
13:N:50:ARG:NH1	28:1:267:G:O4'	2.27	0.67
13:N:68:ARG:NE	28:1:290:G:OP2	2.27	0.67
28:1:371:G:N2	44:l:31:THR:O	2.27	0.67
28:1:1875:G:O2'	28:1:1876:U:O5'	2.11	0.67
49:2:339:C:OP2	58:y:10:LYS:NZ	2.26	0.67
63:AG:98:ASP:O	63:AG:101:SER:OG	2.09	0.67
72:AP:73:GLY:O	72:AP:77:ARG:NH1	2.27	0.67
78:AV:257:ALA:O	78:AV:275:ARG:NH1	2.27	0.67
7:G:137:ASN:ND2	28:1:116:A:OP2	2.27	0.67
13:N:50:ARG:NH1	28:1:267:G:N3	2.41	0.67
17:R:62:ARG:NH2	28:1:3068:U:OP2	2.28	0.67
28:1:1871:U:OP1	28:1:3076:C:O2'	2.11	0.67
49:2:1758:U:O2'	49:2:1759:C:OP1	2.12	0.67
78:AV:25:THR:HG23	78:AV:293:ALA:HB1	1.76	0.67
1:A:179:LEU:HD23	1:A:185:ALA:HB2	1.76	0.67
4:D:184:ASP:OD2	4:D:187:THR:OG1	2.12	0.67
28:1:894:G:O2'	28:1:1660:C:OP2	2.12	0.67
28:1:3153:U:O2'	28:1:3154:C:O4'	2.11	0.67
49:2:523:G:O2'	49:2:524:U:O4'	2.08	0.67
49:2:779:U:O2'	49:2:781:U:OP1	2.11	0.67
12:M:59:ASN:ND2	28:1:1184:A:OP2	2.27	0.67
21:V:68:GLU:OE1	21:V:68:GLU:N	2.27	0.67
28:1:1693:C:O2'	28:1:1772:U:O2	2.09	0.67
28:1:3108:G:O2'	45:m:92:ASP:OD1	2.06	0.67
49:2:587:C:OP2	77:AU:23:LYS:NZ	2.28	0.67
55:v:212:LYS:NZ	55:v:216:GLU:OE1	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:325:LYS:NZ	28:1:3096:C:O3'	2.25	0.67
2:B:367:LYS:NZ	28:1:3050:U:OP2	2.25	0.67
14:O:172:ARG:NH1	28:1:3190:C:OP1	2.27	0.67
28:1:2592:G:O2'	28:1:2594:C:O2	2.10	0.67
28:1:3108:G:OP2	28:1:3120:C:N4	2.27	0.67
42:j:19:CYS:O	42:j:23:GLY:N	2.28	0.67
49:2:826:U:O2	49:2:846:G:O6	2.11	0.67
50:q:24:LEU:O	50:q:163:ASN:ND2	2.27	0.67
3:C:195:ARG:NH2	30:4:20:U:OP1	2.28	0.67
28:1:630:A:O2'	28:1:631:U:OP1	2.13	0.67
4:D:99:TYR:OH	4:D:168:ASP:OD2	2.12	0.67
28:1:600:G:N2	28:1:603:A:C6	2.62	0.67
28:1:1750:A:OP2	43:k:42:LYS:NZ	2.27	0.67
28:1:3324:C:OP1	36:d:70:ARG:NH2	2.28	0.67
49:2:39:A:O2'	49:2:40:A:N7	2.27	0.67
62:AF:37:ALA:O	62:AF:42:ARG:NH1	2.27	0.67
67:AK:56:VAL:O	67:AK:89:ARG:NH2	2.27	0.67
2:B:221:THR:OG1	28:1:3046:A:OP1	2.13	0.67
28:1:829:U:O2'	28:1:893:C:N4	2.28	0.67
28:1:3266:G:OP1	28:1:3268:A:N6	2.27	0.67
28:1:1760:A:OP2	28:1:1761:C:N4	2.27	0.67
28:1:2291:A:O2'	49:2:1654:G:N2	2.26	0.67
28:1:2450:G:O2'	28:1:2451:G:O4'	2.10	0.67
28:1:2469:G:O2'	28:1:2470:C:O5'	2.10	0.67
43:k:32:ASN:ND2	43:k:36:LYS:O	2.27	0.67
28:1:2837:A:O2'	28:1:2838:A:O5'	2.13	0.67
49:2:898:A:N6	49:2:914:G:H21	1.93	0.67
49:2:1162:C:OP1	75:AS:22:ARG:NH1	2.28	0.67
56:w:102:VAL:HG21	56:w:106:LEU:HD13	1.76	0.67
28:1:1749:A:OP2	43:k:53:THR:OG1	2.08	0.66
28:1:2165:G:N2	28:1:2167:A:N7	2.43	0.66
28:1:2854:U:O2'	28:1:2855:U:OP1	2.13	0.66
49:2:154:G:O2'	49:2:155:U:O4'	2.05	0.66
49:2:1513:G:O2'	49:2:1514:U:O5'	2.08	0.66
2:B:58:ARG:NH1	2:B:59:ASP:O	2.29	0.66
49:2:704:C:OP2	49:2:732:G:N2	2.28	0.66
25:Z:88:ASP:O	25:Z:121:ARG:NH2	2.28	0.66
28:1:91:G:OP2	47:o:42:ARG:NE	2.27	0.66
28:1:769:G:N2	28:1:770:G:O4'	2.27	0.66
49:2:332:U:OP2	58:y:175:GLN:NE2	2.29	0.66
49:2:1470:C:O2'	49:2:1572:G:N3	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:65:SER:OG	28:1:3038:U:O3'	2.12	0.66
28:1:1354:G:N2	28:1:1424:C:OP1	2.29	0.66
45:m:94:SER:O	45:m:102:ARG:NH1	2.28	0.66
49:2:616:G:N7	70:AN:3:LYS:NZ	2.38	0.66
49:2:1279:C:O3'	76:AT:44:ARG:NH2	2.29	0.66
1:A:117:GLU:OE2	1:A:122:ASP:N	2.29	0.66
28:1:383:G:N2	28:1:386:A:OP2	2.28	0.66
28:1:802:C:O4'	33:a:27:LYS:NZ	2.24	0.66
28:1:1668:G:O2'	28:1:1669:C:OP1	2.13	0.66
28:1:2255:A:N7	28:1:2260:U:O2	2.28	0.66
28:1:2262:A:C6	49:2:1759:C:C6	2.84	0.66
30:4:43:A:O2'	42:j:22:CYS:O	2.13	0.66
49:2:632:U:O3'	70:AN:11:SER:OG	2.13	0.66
67:AK:25:THR:OG1	67:AK:115:GLU:OE1	2.13	0.66
73:AQ:53:LEU:O	73:AQ:57:SER:OG	2.10	0.66
14:O:21:SER:HG	28:1:1174:G:HO2'	1.44	0.66
28:1:66:A:N6	28:1:76:G:H21	1.93	0.66
28:1:1592:G:O2'	28:1:1593:A:N7	2.28	0.66
28:1:1596:C:O2'	28:1:1597:C:O5'	2.13	0.66
28:1:1655:G:OP1	39:g:40:THR:OG1	2.07	0.66
71:AO:106:GLN:OE1	71:AO:110:GLN:NE2	2.28	0.66
28:1:913:A:O2'	28:1:2135:U:O2	2.13	0.66
28:1:1538:G:N1	28:1:1552:G:N7	2.43	0.66
28:1:2802:A:O2'	28:1:2803:A:O4'	2.12	0.66
33:a:57:GLY:O	33:a:59:ARG:NH1	2.28	0.66
45:m:110:CYS:O	45:m:116:GLY:N	2.29	0.66
49:2:447:U:O2'	54:u:11:ARG:NH1	2.29	0.66
49:2:491:C:N4	49:2:497:G:O6	2.28	0.66
21:V:48:ARG:NH1	28:1:2339:C:OP2	2.28	0.66
28:1:349:A:O2'	28:1:350:C:OP1	2.13	0.66
28:1:3035:A:O2'	45:m:77:ILE:O	2.13	0.66
49:2:1555:A:O3'	62:AF:44:ARG:NH2	2.29	0.66
49:2:1655:A:H62	49:2:1745:G:H21	1.43	0.66
78:AV:26:SER:OG	78:AV:29:GLN:O	2.06	0.66
3:C:73:ARG:NH2	28:1:804:C:O2	2.29	0.66
18:S:83:SER:OG	28:1:1295:G:OP1	2.13	0.66
21:V:37:ILE:HD13	28:1:2295:A:H62	1.61	0.66
28:1:3315:G:O2'	28:1:3316:A:OP1	2.11	0.66
54:u:255:ARG:NH2	54:u:258:GLN:OE1	2.28	0.66
12:M:106:ARG:NH2	28:1:3208:G:OP2	2.29	0.65
28:1:393:U:O4	28:1:397:A:N6	2.27	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:1907:C:O2'	28:1:1908:A:N7	2.24	0.65
28:1:2874:G:N2	28:1:2945:G:O4'	2.28	0.65
30:4:12:A:O2'	30:4:13:A:O4'	2.08	0.65
49:2:114:C:N4	49:2:247:A:H62	1.92	0.65
28:1:2292:U:OP2	49:2:1655:A:N6	2.28	0.65
28:1:3395:G:N2	28:1:3395:G:OP2	2.27	0.65
30:4:95:G:C6	42:j:81:GLY:HA3	2.30	0.65
49:2:410:A:C2	49:2:423:G:N1	2.64	0.65
49:2:490:C:OP2	49:2:492:A:N6	2.29	0.65
49:2:1747:G:O2'	49:2:1748:G:O5'	2.15	0.65
3:C:92:ASN:ND2	28:1:659:G:O2'	2.29	0.65
5:E:17:ALA:O	28:1:591:G:O2'	2.14	0.65
28:1:1496:C:OP1	28:1:1514:G:N2	2.30	0.65
49:2:410:A:N1	49:2:423:G:C6	2.65	0.65
49:2:1311:U:O2'	64:AH:2:GLY:N	2.29	0.65
24:Y:3:LYS:NZ	28:1:337:G:OP2	2.29	0.65
28:1:708:G:N7	28:1:710:A:N6	2.45	0.65
28:1:860:G:O2'	48:p:18:TYR:OH	2.13	0.65
28:1:886:C:N4	28:1:887:G:O6	2.30	0.65
28:1:1123:U:O2'	28:1:2635:A:OP2	2.15	0.65
35:c:13:LYS:NZ	35:c:99:ASP:O	2.30	0.65
15:P:23:ARG:NH1	15:P:125:GLN:OE1	2.29	0.65
18:S:71:LYS:O	18:S:73:LYS:NZ	2.29	0.65
36:d:15:ASN:O	36:d:19:ARG:NH1	2.29	0.65
49:2:224:C:N4	49:2:836:U:O4	2.30	0.65
64:AH:27:ASP:OD2	78:AV:38:ARG:NH2	2.29	0.65
2:B:225:GLY:O	2:B:269:GLN:NE2	2.29	0.65
4:D:85:ARG:NH2	4:D:250:ASP:OD2	2.29	0.65
25:Z:25:ILE:HA	25:Z:43:VAL:HG12	1.78	0.65
25:Z:25:ILE:HD13	25:Z:41:ALA:HB1	1.78	0.65
28:1:384:A:N7	28:1:1465:A:N6	2.43	0.65
28:1:997:A:O2'	29:3:103:A:N7	2.28	0.65
14:O:85:ARG:NH2	28:1:2383:C:OP2	2.30	0.65
16:Q:65:SER:OG	28:1:784:A:N6	2.29	0.65
19:T:110:LYS:NZ	28:1:1067:U:OP1	2.24	0.65
30:4:14:C:O2'	30:4:16:G:OP2	2.09	0.65
1:A:6:ARG:NH1	28:1:2184:U:OP2	2.30	0.65
13:N:112:ASN:ND2	28:1:20:A:N3	2.45	0.65
28:1:1435:A:O2'	28:1:1436:U:OP1	2.12	0.65
28:1:2211:U:O2'	79:AX:71:G:N2	2.29	0.65
30:4:73:U:O2	30:4:89:A:O2'	2.09	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:407:A:N6	28:1:656:A:O4'	2.29	0.65
79:AZ:42:G:O2'	79:AZ:43:G:O4'	2.10	0.65
5:E:83:TYR:OH	28:1:499:G:O3'	2.11	0.65
28:1:346:C:O2'	28:1:366:A:OP2	2.14	0.65
30:4:106:C:O2'	30:4:107:G:O5'	2.15	0.65
35:c:26:GLY:O	35:c:30:THR:OG1	2.15	0.65
79:AX:1:G:N2	79:AX:73:A:N6	2.45	0.65
28:1:58:G:N2	28:1:60:A:O2'	2.30	0.64
28:1:1428:A:N7	33:a:9:ARG:NH2	2.45	0.64
28:1:1535:A:O2'	28:1:1536:G:OP1	2.12	0.64
47:o:102:GLN:OE1	47:o:102:GLN:N	2.30	0.64
3:C:309:ARG:NH2	28:1:610:G:O6	2.30	0.64
28:1:518:G:N2	28:1:518:G:OP2	2.31	0.64
28:1:2953:U:N3	28:1:2978:U:OP2	2.30	0.64
30:4:69:U:O2'	30:4:70:G:O4'	2.16	0.64
49:2:765:G:O4'	59:z:149:ARG:NH2	2.31	0.64
49:2:1338:C:O2'	49:2:1339:C:O5'	2.15	0.64
5:E:20:LYS:NZ	28:1:592:A:O2'	2.29	0.64
8:H:168:ARG:NH2	45:m:86:ALA:O	2.30	0.64
28:1:212:G:OP1	28:1:227:G:O2'	2.12	0.64
49:2:1357:A:N6	49:2:1367:G:O6	2.29	0.64
52:s:176:SER:N	52:s:195:ASP:OD1	2.29	0.64
49:2:526:A:OP2	71:AO:93:ARG:NH2	2.31	0.64
4:D:33:ARG:NH2	29:3:7:G:O3'	2.30	0.64
6:F:88:ARG:NH1	6:F:109:THR:O	2.29	0.64
28:1:87:U:C2	28:1:99:A:N6	2.65	0.64
41:i:57:LEU:HD11	41:i:90:MET:SD	2.38	0.64
7:G:220:ALA:O	7:G:225:LYS:NZ	2.27	0.64
8:H:169:ASN:ND2	45:m:86:ALA:O	2.31	0.64
24:Y:121:ARG:NH1	28:1:185:C:O2'	2.31	0.64
28:1:2262:A:C5	49:2:1759:C:O4'	2.50	0.64
28:1:3302:U:OP2	28:1:3305:A:N6	2.30	0.64
28:1:1483:G:O2'	28:1:1485:G:O6	2.14	0.64
28:1:1727:G:N2	28:1:1728:G:O6	2.31	0.64
28:1:2207:A:N6	28:1:2210:G:N7	2.46	0.64
49:2:104:A:O4'	49:2:308:C:N4	2.30	0.64
54:u:189:LEU:O	54:u:191:ARG:NH1	2.30	0.64
1:A:225:ILE:O	1:A:241:ARG:NH1	2.31	0.64
7:G:77:GLN:OE1	7:G:77:GLN:N	2.31	0.64
28:1:1180:A:N6	28:1:1325:U:O4	2.31	0.64
28:1:1410:U:O2	28:1:1411:C:N4	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2:96:G:N2	49:2:426:G:O5'	2.31	0.64
49:2:240:U:O2'	49:2:241:U:OP1	2.13	0.64
49:2:1309:C:O2'	49:2:1401:A:N6	2.30	0.64
49:2:1684:U:O2'	49:2:1685:G:OP1	2.13	0.64
79:AZ:48:C:O2'	79:AZ:59:U:O2'	2.13	0.64
13:N:147:ARG:NH2	28:1:151:A:OP2	2.31	0.64
28:1:1906:G:O6	28:1:2330:C:N4	2.31	0.64
1:A:6:ARG:NH2	1:A:199:THR:O	2.31	0.63
4:D:152:ARG:NH2	29:3:44:C:O3'	2.31	0.63
9:I:84:ALA:O	9:I:140:THR:OG1	2.14	0.63
19:T:50:LYS:NZ	28:1:2756:C:OP1	2.25	0.63
49:2:66:U:O2	56:w:171:LYS:NZ	2.32	0.63
49:2:898:A:H62	49:2:914:G:H21	1.44	0.63
28:1:418:A:O2'	28:1:419:G:OP1	2.12	0.63
30:4:42:G:O2'	30:4:43:A:O4'	2.08	0.63
49:2:739:G:OP2	49:2:741:C:N4	2.31	0.63
75:AS:27:GLN:NE2	75:AS:64:ARG:O	2.32	0.63
1:A:80:GLU:OE1	1:A:81:GLY:N	2.31	0.63
7:G:147:LYS:O	7:G:201:THR:OG1	2.15	0.63
14:O:87:MET:HE3	28:1:1174:G:H21	1.63	0.63
28:1:835:G:O2'	28:1:836:A:N7	2.31	0.63
28:1:964:G:O2'	28:1:965:A:OP1	2.13	0.63
28:1:1591:G:O3'	39:g:37:LYS:NZ	2.31	0.63
54:u:66:MET:O	54:u:68:ARG:NH1	2.32	0.63
28:1:1232:C:N4	28:1:1257:C:N3	2.47	0.63
28:1:1274:A:OP1	32:P2:61:GLN:NE2	2.31	0.63
28:1:2466:G:OP1	81:L1:102:LYS:NZ	2.30	0.63
28:1:2480:A:O2'	72:AP:57:TYR:OH	2.10	0.63
30:4:97:A:OP1	40:h:63:ARG:NE	2.31	0.63
15:P:30:ARG:NH2	28:1:413:U:OP1	2.31	0.63
28:1:940:G:OP2	33:a:26:ARG:NH2	2.31	0.63
28:1:2414:G:O2'	28:1:2967:A:O2'	2.17	0.63
9:I:112:GLN:N	79:AZ:74:C:OP1	2.31	0.63
10:J:140:ARG:O	29:3:43:U:O2'	2.14	0.63
13:N:4:TYR:OH	28:1:148:G:OP2	2.17	0.63
28:1:1204:A:N3	28:1:2834:G:N2	2.43	0.63
28:1:1260:A:N1	31:P0:43:LYS:NZ	2.42	0.63
28:1:1532:C:N4	28:1:1534:A:N7	2.46	0.63
28:1:2467:G:O2'	28:1:2468:A:OP1	2.16	0.63
28:1:2554:A:OP1	39:g:91:ARG:NE	2.30	0.63
42:j:26:SER:OG	42:j:34:CYS:SG	2.56	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2:1002:G:O6	49:2:1003:A:N6	2.32	0.63
28:1:679:U:C2	28:1:701:G:O6	2.51	0.63
28:1:3175:U:OP2	38:f:10:LYS:NZ	2.23	0.63
7:G:135:GLY:O	28:1:148:G:C6	2.51	0.63
45:m:95:VAL:O	45:m:122:ARG:NH2	2.32	0.63
49:2:1466:G:O2'	49:2:1602:C:OP1	2.16	0.63
54:u:69:HIS:NE2	71:AO:17:LEU:O	2.31	0.63
5:E:19:LYS:NZ	28:1:593:C:OP2	2.32	0.62
27:AB:122:ILE:O	27:AB:143:SER:OG	2.16	0.62
28:1:1920:U:O2'	28:1:1930:A:N6	2.20	0.62
11:L:47:ALA:O	11:L:49:ARG:N	2.31	0.62
28:1:698:U:O4	28:1:699:A:N6	2.33	0.62
28:1:1847:A:N7	28:1:1849:C:N4	2.48	0.62
7:G:54:GLU:N	7:G:54:GLU:OE2	2.32	0.62
21:V:109:MET:N	21:V:109:MET:SD	2.72	0.62
28:1:872:U:O2'	28:1:873:C:O4'	2.16	0.62
49:2:1484:G:N7	49:2:1522:U:O2'	2.31	0.62
53:t:135:GLU:N	53:t:135:GLU:OE1	2.33	0.62
1:A:174:ARG:NH2	28:1:2180:G:OP1	2.32	0.62
28:1:3024:A:O2'	31:P0:138:ALA:O	2.17	0.62
49:2:1613:U:O2'	49:2:1615:C:N4	2.28	0.62
30:4:43:A:O2'	30:4:44:A:OP1	2.16	0.62
49:2:628:G:H21	49:2:971:A:H62	1.47	0.62
49:2:1389:C:O2'	49:2:1391:A:OP1	2.14	0.62
79:AX:1:G:O2'	79:AX:2:C:OP1	2.16	0.62
8:H:122:LYS:NZ	45:m:79:GLU:OE1	2.28	0.62
9:I:193:ASP:OD2	28:1:1010:G:N2	2.33	0.62
26:AA:26:ASP:O	26:AA:39:ASN:ND2	2.32	0.62
28:1:66:A:N6	28:1:76:G:N2	2.46	0.62
28:1:273:A:O2'	28:1:274:G:O4'	2.18	0.62
28:1:957:C:O2'	33:a:39:HIS:O	2.10	0.62
28:1:3165:A:N6	28:1:3285:C:N3	2.47	0.62
45:m:111:ARG:NH1	45:m:111:ARG:O	2.33	0.62
49:2:58:U:O2'	49:2:451:A:O2'	2.07	0.62
70:AN:130:VAL:HG11	70:AN:135:LEU:HD11	1.80	0.62
28:1:3005:A:N6	28:1:3140:G:N7	2.47	0.62
49:2:708:C:N4	49:2:726:C:OP2	2.32	0.62
28:1:177:U:O2	28:1:241:G:O6	2.16	0.62
28:1:3057:U:O2'	28:1:3058:U:O4'	2.17	0.62
73:AQ:51:ARG:NH2	75:AS:37:SER:O	2.33	0.62
4:D:30:TYR:OH	29:3:8:G:OP2	2.16	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:180:GLU:N	9:I:180:GLU:OE1	2.33	0.62
28:1:720:A:O2'	28:1:721:G:OP2	2.16	0.62
28:1:2230:C:O2'	28:1:2231:C:O4'	2.17	0.62
30:4:20:U:O2'	30:4:21:C:OP1	2.17	0.62
49:2:1615:C:OP1	55:v:81:ARG:NH1	2.32	0.62
78:AV:202:LEU:HB2	78:AV:243:LEU:HD12	1.81	0.62
7:G:135:GLY:N	28:1:148:G:N1	2.47	0.61
15:P:155:GLU:N	15:P:155:GLU:OE1	2.32	0.61
25:Z:67:LYS:NZ	28:1:1630:U:OP1	2.31	0.61
28:1:2469:G:HO2'	28:1:2470:C:P	2.22	0.61
28:1:2714:G:O2'	28:1:2752:U:O4	2.09	0.61
28:1:2785:A:O2'	47:o:36:PHE:O	2.16	0.61
37:e:2:ALA:O	37:e:71:HIS:NE2	2.33	0.61
17:R:120:TYR:OH	28:1:1721:U:OP2	2.17	0.61
28:1:971:G:N1	28:1:1110:U:C4	2.68	0.61
28:1:1672:U:OP2	28:1:1859:A:O2'	2.19	0.61
49:2:610:G:O2'	49:2:613:G:O2'	2.06	0.61
49:2:927:C:O2'	49:2:928:U:O4'	2.15	0.61
49:2:990:C:O2'	61:AE:127:ARG:NH1	2.33	0.61
49:2:1502:G:OP2	66:AJ:102:ARG:NH2	2.33	0.61
19:T:88:ARG:N	28:1:2723:U:OP1	2.33	0.61
28:1:2394:G:OP2	28:1:2946:A:N6	2.32	0.61
28:1:2425:G:N2	28:1:2604:U:O4'	2.33	0.61
49:2:14:C:OP1	52:s:164:SER:OG	2.15	0.61
49:2:1680:G:N3	49:2:1681:A:N6	2.48	0.61
18:S:113:ARG:NH1	28:1:1211:U:O2'	2.33	0.61
21:V:136:VAL:HG12	21:V:137:VAL:HG23	1.81	0.61
28:1:2950:G:O2'	28:1:2953:U:O2	2.18	0.61
41:i:5:THR:O	41:i:13:LYS:NZ	2.32	0.61
28:1:365:A:OP2	42:j:52:LYS:NZ	2.32	0.61
28:1:936:A:N6	28:1:2409:G:O3'	2.33	0.61
28:1:1202:A:N6	28:1:1301:A:O4'	2.33	0.61
49:2:154:G:N7	71:AO:132:ARG:NH1	2.48	0.61
25:Z:17:ARG:NH1	28:1:1634:G:N7	2.49	0.61
28:1:1188:U:O2'	28:1:1190:A:N6	2.32	0.61
74:AR:15:GLU:OE2	74:AR:23:THR:OG1	2.18	0.61
28:1:23:A:N6	30:4:35:C:N3	2.40	0.61
28:1:709:A:N3	28:1:2787:G:O2'	2.32	0.61
28:1:1850:A:O2'	28:1:1851:G:O5'	2.11	0.61
28:1:2117:A:N7	28:1:2118:C:O2'	2.33	0.61
28:1:3022:G:O2'	28:1:3023:U:OP2	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2:932:U:OP1	51:r:155:TYR:OH	2.09	0.61
43:k:7:ASP:OD1	43:k:10:GLN:NE2	2.34	0.61
44:l:30:ARG:O	44:l:32:ASN:ND2	2.34	0.61
49:2:475:A:O5'	59:z:37:LYS:NZ	2.34	0.61
69:AM:27:ILE:HD11	69:AM:61:ILE:HD11	1.81	0.61
24:Y:16:ARG:NH1	28:1:216:G:OP1	2.33	0.61
28:1:693:A:O2'	28:1:694:C:OP1	2.16	0.61
28:1:1161:G:O2'	37:e:54:LYS:NZ	2.23	0.61
28:1:1852:G:O2'	28:1:1853:U:O5'	2.11	0.61
28:1:2213:A:N6	28:1:2230:C:O4'	2.34	0.61
66:AJ:38:LYS:NZ	66:AJ:43:ASN:O	2.26	0.61
8:H:95:ALA:O	31:P0:157:LYS:NZ	2.34	0.61
28:1:660:A:OP2	28:1:1432:C:N4	2.34	0.61
28:1:999:G:HO2'	28:1:1000:C:P	2.24	0.61
28:1:1947:G:O2'	28:1:2099:A:N6	2.34	0.61
28:1:2808:A:HO2'	28:1:2968:G:HO2'	1.32	0.61
28:1:2844:C:O2'	28:1:2845:A:OP1	2.14	0.61
28:1:2846:U:O2'	28:1:2848:G:N7	2.34	0.61
49:2:1216:C:O2'	49:2:1444:A:N6	2.25	0.61
49:2:1547:A:O4'	65:AI:88:ARG:NH2	2.33	0.61
27:AB:127:GLN:NE2	49:2:304:U:O4'	2.34	0.60
28:1:2236:G:O3'	79:AX:70:C:O2'	2.12	0.60
28:1:3229:G:O2'	28:1:3230:G:O4'	2.18	0.60
71:AO:36:SER:OG	71:AO:37:LYS:N	2.33	0.60
28:1:1902:G:N2	28:1:1905:G:O5'	2.33	0.60
28:1:2498:U:O2'	28:1:2499:U:OP2	2.18	0.60
33:a:73:LEU:HD22	33:a:109:TYR:CD2	2.35	0.60
49:2:1559:A:N7	65:AI:134:ARG:NH1	2.49	0.60
8:H:173:ARG:NH1	28:1:2897:A:OP2	2.34	0.60
19:T:116:ARG:NH1	28:1:1094:U:OP1	2.34	0.60
25:Z:41:ALA:HB2	25:Z:77:TYR:HE1	1.66	0.60
28:1:1513:G:N2	28:1:1514:G:O2'	2.35	0.60
28:1:1852:G:HO2'	28:1:1853:U:P	2.24	0.60
58:y:159:GLN:NE2	58:y:164:ARG:O	2.34	0.60
28:1:74:G:O2'	28:1:75:G:O4'	2.17	0.60
28:1:2606:G:N2	28:1:2609:A:N7	2.50	0.60
65:AI:74:GLN:OE1	65:AI:98:TYR:OH	2.12	0.60
79:AZ:1:G:N2	79:AZ:73:A:N6	2.49	0.60
51:r:137:ILE:HG21	51:r:172:LEU:HD21	1.82	0.60
62:AF:81:ARG:NH1	62:AF:120:SER:OG	2.34	0.60
28:1:1325:U:O2'	28:1:1326:A:O5'	2.20	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:2538:U:O2'	28:1:2541:U:OP2	2.19	0.60
28:1:3343:G:O2'	28:1:3344:A:N7	2.33	0.60
49:2:130:C:N4	49:2:177:U:OP2	2.28	0.60
56:w:93:LYS:O	56:w:95:LYS:NZ	2.34	0.60
63:AG:21:HIS:ND1	63:AG:66:ARG:O	2.35	0.60
28:1:93:C:O2'	28:1:94:G:OP1	2.13	0.60
28:1:141:C:O2'	28:1:144:A:O4'	2.19	0.60
28:1:3006:A:O2'	28:1:3007:U:OP1	2.19	0.60
49:2:334:G:O6	58:y:5:ARG:NH2	2.34	0.60
49:2:554:C:N4	49:2:571:G:O6	2.33	0.60
57:x:8:ILE:HG23	57:x:9:LEU:HD22	1.83	0.60
29:3:84:A:O2'	29:3:85:G:OP1	2.15	0.60
49:2:1427:A:O2'	49:2:1428:G:OP1	2.13	0.60
51:r:47:LEU:O	51:r:64:ARG:NH1	2.35	0.60
73:AQ:18:VAL:HG23	73:AQ:19:LYS:H	1.65	0.60
1:A:200:ARG:NH2	28:1:2186:U:OP2	2.34	0.60
10:J:32:ARG:NE	10:J:120:ILE:O	2.35	0.60
19:T:8:ARG:O	19:T:11:THR:OG1	2.19	0.60
28:1:323:A:O2'	28:1:324:A:OP1	2.19	0.60
28:1:947:G:N2	28:1:1371:G:N7	2.50	0.60
28:1:1390:A:O2'	28:1:1391:C:OP2	2.16	0.60
28:1:1880:U:O4	28:1:1881:A:N6	2.35	0.60
28:1:3101:G:O2'	28:1:3102:G:OP1	2.19	0.60
49:2:1433:G:N2	76:AT:45:GLU:OE1	2.35	0.60
21:V:32:ARG:NH1	49:2:1734:U:OP1	2.35	0.60
28:1:1469:C:N4	28:1:1878:G:O3'	2.35	0.60
28:1:2357:A:N7	28:1:2983:C:N4	2.50	0.60
17:R:53:LYS:NZ	28:1:1473:G:OP1	2.35	0.59
28:1:1230:G:OP1	28:1:1277:C:N4	2.34	0.59
28:1:1597:C:O2'	28:1:1598:G:O5'	2.19	0.59
28:1:2974:U:HO2'	28:1:2976:A:H62	1.47	0.59
30:4:44:A:O2'	30:4:45:C:OP1	2.15	0.59
49:2:220:A:N6	49:2:830:U:O4	2.35	0.59
3:C:258:LEU:HA	3:C:261:VAL:HG12	1.84	0.59
24:Y:17:LYS:O	24:Y:21:THR:HG22	2.02	0.59
28:1:153:U:O2'	28:1:154:U:O4'	2.18	0.59
28:1:3345:G:O2'	28:1:3346:U:OP1	2.19	0.59
56:w:172:ALA:O	56:w:174:LYS:NZ	2.32	0.59
2:B:223:GLY:O	2:B:224:HIS:ND1	2.35	0.59
24:Y:72:SER:OG	24:Y:81:GLN:NE2	2.35	0.59
28:1:1629:U:OP2	28:1:1814:A:N6	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:2745:G:N2	28:1:2748:A:OP2	2.32	0.59
1:A:242:ARG:NH1	28:1:2241:U:O4'	2.35	0.59
3:C:107:ARG:NH1	28:1:1427:U:O2'	2.36	0.59
7:G:48:ARG:NH2	28:1:2586:G:O2'	2.36	0.59
28:1:1630:U:O2'	28:1:1812:G:N2	2.35	0.59
28:1:1870:C:O2'	28:1:3066:U:O2'	2.05	0.59
30:4:95:G:N3	42:j:81:GLY:O	2.35	0.59
51:r:82:ARG:NH1	51:r:191:GLU:OE1	2.35	0.59
60:AD:46:THR:HG21	60:AD:90:TYR:HE2	1.68	0.59
24:Y:17:LYS:NZ	30:4:23:U:OP1	2.28	0.59
28:1:2204:C:O2'	28:1:2205:U:OP2	2.17	0.59
30:4:60:U:O4	30:4:97:A:O2'	2.09	0.59
49:2:151:G:OP2	71:AO:123:LYS:NZ	2.35	0.59
15:P:125:GLN:N	15:P:140:GLU:OE1	2.35	0.59
24:Y:62:SER:OG	28:1:218:G:O6	2.14	0.59
28:1:1591:G:O5'	28:1:1655:G:O2'	2.20	0.59
36:d:13:THR:OG1	36:d:72:ARG:NH1	2.35	0.59
49:2:884:A:O2'	49:2:885:G:O5'	2.15	0.59
4:D:91:GLY:N	29:3:49:G:OP2	2.35	0.59
28:1:272:G:O6	28:1:273:A:N6	2.36	0.59
28:1:1367:G:N2	28:1:1368:U:O4	2.36	0.59
28:1:1434:G:OP1	28:1:1437:C:N4	2.35	0.59
49:2:1149:G:N3	49:2:1765:A:O2'	2.35	0.59
21:V:37:ILE:HD13	28:1:2295:A:N6	2.18	0.59
28:1:2568:C:O2'	28:1:2569:A:O5'	2.19	0.59
49:2:1686:C:N4	49:2:1687:U:O2	2.30	0.59
77:AU:14:VAL:O	77:AU:18:THR:HG23	2.03	0.59
5:E:52:VAL:HG23	5:E:65:ILE:HD11	1.83	0.59
49:2:883:C:N3	49:2:945:U:O4	2.36	0.59
3:C:195:ARG:NH2	28:1:341:G:N7	2.50	0.59
28:1:21:G:O2'	28:1:22:G:O5'	2.21	0.59
28:1:644:G:O6	28:1:2868:U:O2'	2.09	0.59
28:1:1469:C:O2'	28:1:1470:U:OP2	2.18	0.59
28:1:3009:G:O2'	28:1:3011:A:N7	2.33	0.59
29:3:61:G:O2'	29:3:62:U:OP1	2.21	0.59
49:2:494:U:O2'	49:2:496:G:N7	2.29	0.59
49:2:1576:A:O2'	79:AX:40:C:O2'	2.16	0.59
30:4:69:U:O2'	30:4:70:G:O5'	2.21	0.58
49:2:214:G:N2	49:2:252:U:O4	2.36	0.58
49:2:1534:G:OP2	72:AP:74:SER:OG	2.11	0.58
49:2:1717:G:N1	49:2:1718:G:O6	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:u:94:ALA:O	54:u:95:THR:OG1	2.21	0.58
3:C:315:LYS:NZ	28:1:608:A:O3'	2.35	0.58
14:O:27:LEU:HD21	14:O:98:ALA:O	2.01	0.58
28:1:961:C:O2'	28:1:2616:C:OP1	2.21	0.58
29:3:75:G:N2	29:3:105:C:O2	2.36	0.58
49:2:780:A:N7	71:AO:10:ARG:NE	2.50	0.58
49:2:1098:U:OP1	52:s:159:THR:OG1	2.21	0.58
72:AP:62:VAL:O	72:AP:66:VAL:HG13	2.03	0.58
78:AV:48:THR:OG1	78:AV:53:LYS:O	2.21	0.58
1:A:147:ARG:NH1	49:2:891:A:O2'	2.37	0.58
16:Q:92:ARG:NE	33:a:76:ASP:OD2	2.35	0.58
28:1:2580:A:O2'	28:1:2582:C:OP1	2.06	0.58
67:AK:50:LEU:HD21	67:AK:94:GLU:O	2.03	0.58
28:1:2808:A:O2'	28:1:2968:G:O2'	2.04	0.58
65:AI:126:ARG:NH1	65:AI:132:ARG:O	2.36	0.58
3:C:186:LYS:NZ	28:1:1387:G:N7	2.52	0.58
28:1:848:A:N7	28:1:849:C:O2'	2.35	0.58
28:1:1087:G:OP1	34:b:28:LYS:NZ	2.36	0.58
11:L:76:THR:OG1	11:L:79:GLU:OE2	2.20	0.58
28:1:2714:G:N2	28:1:2752:U:OP2	2.34	0.58
71:AO:106:GLN:NE2	71:AO:107:GLN:OE1	2.36	0.58
11:L:123:ILE:HD11	40:h:116:TYR:CD2	2.38	0.58
16:Q:170:ARG:NH2	33:a:57:GLY:O	2.37	0.58
24:Y:24:SER:O	24:Y:75:ARG:NH1	2.36	0.58
28:1:268:A:N6	28:1:295:A:OP2	2.35	0.58
28:1:1902:G:O2'	28:1:1903:U:OP1	2.20	0.58
71:AO:91:LEU:HD23	71:AO:96:LEU:HD21	1.85	0.58
9:I:36:LEU:HD21	9:I:87:LEU:HD23	1.86	0.58
11:L:17:HIS:O	11:L:21:ARG:NH1	2.36	0.58
12:M:108:ARG:NH1	14:O:195:ALA:O	2.36	0.58
28:1:584:G:O3'	38:f:70:LYS:NZ	2.37	0.58
28:1:1204:A:O4'	28:1:1300:G:N2	2.36	0.58
28:1:2325:G:O2'	28:1:2326:A:OP1	2.17	0.58
49:2:1066:C:O3'	51:r:149:GLN:NE2	2.37	0.58
54:u:210:ILE:O	54:u:217:THR:OG1	2.10	0.58
71:AO:7:ILE:HD12	71:AO:27:VAL:HG13	1.86	0.58
28:1:518:G:N2	28:1:520:U:O3'	2.36	0.58
28:1:1593:A:O2'	28:1:1594:A:N7	2.32	0.58
46:n:9:ARG:NH2	49:2:1782:A:OP1	2.37	0.58
47:o:13:LYS:O	47:o:18:ARG:NH2	2.37	0.58
49:2:1330:G:N2	53:t:204:ASP:OD1	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:y:4:SER:OG	58:y:6:ASP:OD1	2.21	0.58
10:J:88:GLU:OE1	62:AF:12:PHE:N	2.36	0.58
28:1:733:G:N2	28:1:736:A:OP2	2.29	0.58
49:2:245:U:N3	49:2:248:U:OP2	2.37	0.58
49:2:1045:C:OP1	51:r:153:HIS:NE2	2.36	0.58
65:AI:67:GLU:N	65:AI:67:GLU:OE2	2.37	0.57
1:A:19:HIS:NE2	28:1:822:G:O2'	2.37	0.57
9:I:3:ARG:NH1	9:I:63:GLU:OE2	2.37	0.57
13:N:85:THR:OG1	28:1:44:U:OP1	2.20	0.57
24:Y:10:SER:OG	28:1:337:G:O5'	2.20	0.57
28:1:283:G:O2'	47:o:41:ARG:NH1	2.37	0.57
28:1:646:A:O2'	28:1:647:A:OP1	2.21	0.57
36:d:12:TYR:CD2	36:d:75:ILE:HD12	2.39	0.57
54:u:194:THR:HG23	54:u:195:ILE:HG22	1.85	0.57
23:X:131:ASP:OD1	23:X:132:ALA:N	2.37	0.57
28:1:1521:G:N2	28:1:1835:A:N3	2.52	0.57
28:1:1829:G:O2'	28:1:1830:G:OP1	2.15	0.57
28:1:2470:C:N3	28:1:2488:A:O2'	2.35	0.57
49:2:482:U:O4	49:2:483:A:N6	2.37	0.57
49:2:918:U:O3'	61:AE:18:ARG:NH1	2.38	0.57
49:2:1553:G:N1	49:2:1556:A:OP2	2.37	0.57
54:u:60:GLU:OE2	71:AO:20:ARG:NH1	2.37	0.57
15:P:72:GLN:NE2	28:1:3297:U:O3'	2.37	0.57
28:1:2262:A:C4	49:2:1759:C:H1'	2.39	0.57
28:1:2262:A:C6	49:2:1759:C:H6	2.21	0.57
49:2:151:G:O6	49:2:164:A:N6	2.38	0.57
49:2:459:G:OP2	71:AO:105:ARG:NH2	2.38	0.57
71:AO:56:SER:OG	71:AO:76:TYR:OH	2.10	0.57
28:1:688:G:H21	28:1:692:A:N6	2.01	0.57
30:4:39:G:O2'	30:4:103:G:N1	2.37	0.57
2:B:360:ASP:OD1	2:B:361:THR:N	2.37	0.57
9:I:30:LYS:NZ	28:1:2853:A:OP1	2.38	0.57
13:N:12:ARG:NH2	28:1:318:A:N7	2.52	0.57
14:O:108:ILE:HD13	14:O:160:ARG:HE	1.68	0.57
28:1:3353:G:O2'	28:1:3355:U:O5'	2.23	0.57
1:A:96:LEU:O	48:p:87:ARG:NE	2.36	0.57
28:1:968:G:N7	28:1:969:C:N4	2.52	0.57
28:1:2271:A:O2'	28:1:2272:G:O5'	2.23	0.57
28:1:2361:A:O2'	28:1:2362:C:OP1	2.17	0.57
42:j:22:CYS:SG	42:j:23:GLY:N	2.77	0.57
49:2:351:C:O2'	49:2:352:A:OP1	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2:374:U:O2'	49:2:603:U:OP1	2.22	0.57
52:s:58:LEU:O	68:AL:15:ARG:NE	2.35	0.57
6:F:179:LEU:N	6:F:183:ASP:OD2	2.36	0.57
28:1:1112:A:O2'	28:1:1113:G:OP1	2.18	0.57
28:1:2769:A:O2'	47:o:80:ARG:O	2.12	0.57
28:1:2901:G:N2	28:1:3031:G:O2'	2.37	0.57
40:h:8:GLU:OE1	40:h:8:GLU:N	2.38	0.57
54:u:105:VAL:O	54:u:191:ARG:NH2	2.38	0.57
23:X:103:TYR:O	23:X:105:VAL:HG23	2.04	0.57
28:1:55:G:OP1	28:1:1546:A:N6	2.37	0.57
28:1:289:A:O2'	28:1:290:G:OP1	2.23	0.57
28:1:407:A:O3'	30:4:13:A:N6	2.37	0.57
28:1:1259:A:N1	31:P0:52:LEU:HD21	2.20	0.57
28:1:1910:A:O2'	28:1:1911:A:O4'	2.23	0.57
41:i:34:SER:OG	41:i:37:THR:OG1	2.10	0.57
67:AK:70:THR:OG1	67:AK:72:ASN:O	2.22	0.57
28:1:2457:G:OP1	55:v:203:LYS:NZ	2.38	0.57
28:1:2819:A:H61	28:1:2870:C:H42	1.52	0.57
81:L1:106:LYS:HB2	81:L1:128:LEU:HD23	1.87	0.57
1:A:88:ILE:HD11	1:A:99:GLY:C	2.30	0.56
17:R:110:ARG:NH2	28:1:1720:U:OP1	2.38	0.56
26:AA:1:MET:O	26:AA:5:LYS:NZ	2.34	0.56
28:1:1410:U:HO2'	28:1:1411:C:P	2.26	0.56
30:4:95:G:C6	42:j:82:SER:N	2.73	0.56
49:2:454:U:O2'	49:2:455:C:O5'	2.23	0.56
49:2:654:C:O2'	49:2:656:G:N2	2.36	0.56
49:2:884:A:OP1	51:r:136:ARG:NH2	2.38	0.56
49:2:956:C:OP1	49:2:1072:C:O2'	2.22	0.56
49:2:1601:G:N7	66:AJ:89:ARG:NH2	2.53	0.56
62:AF:30:THR:O	62:AF:34:VAL:HG23	2.05	0.56
10:J:111:ASP:OD1	10:J:112:LEU:N	2.37	0.56
17:R:7:GLN:OE1	17:R:7:GLN:N	2.38	0.56
28:1:42:C:OP2	28:1:2410:U:O2'	2.23	0.56
28:1:2598:G:O2'	28:1:2599:U:O5'	2.15	0.56
49:2:867:G:OP2	60:AD:3:ARG:NH2	2.38	0.56
1:A:7:ASN:OD1	1:A:8:GLN:N	2.39	0.56
28:1:345:G:O2'	28:1:346:C:O5'	2.19	0.56
28:1:952:A:H5''	28:1:968:G:H22	1.70	0.56
28:1:1720:U:O2'	28:1:1721:U:O4'	2.20	0.56
28:1:1842:A:O2'	28:1:1843:C:OP1	2.21	0.56
40:h:95:PHE:O	40:h:98:SER:OG	2.24	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:AO:83:LYS:HD2	71:AO:91:LEU:HD21	1.86	0.56
79:AZ:48:C:HO2'	79:AZ:59:U:HO2'	1.52	0.56
28:1:704:U:O4	28:1:715:A:N6	2.26	0.56
28:1:1603:A:N1	28:1:1604:G:N2	2.53	0.56
49:2:253:A:OP1	54:u:133:LYS:NZ	2.23	0.56
49:2:1665:U:O2	49:2:1736:G:O6	2.24	0.56
4:D:151:GLN:N	4:D:151:GLN:OE1	2.37	0.56
28:1:2295:A:OP1	28:1:2296:A:N6	2.23	0.56
47:o:65:THR:O	47:o:87:ARG:NH1	2.39	0.56
50:q:185:ARG:O	68:AL:44:ARG:NH2	2.39	0.56
3:C:252:GLU:OE1	3:C:252:GLU:N	2.38	0.56
9:I:76:MET:O	9:I:80:SER:OG	2.23	0.56
28:1:406:G:N1	30:4:17:A:C6	2.74	0.56
28:1:600:G:C2	28:1:603:A:C6	2.93	0.56
28:1:860:G:HO2'	48:p:18:TYR:HH	1.45	0.56
49:2:1196:A:OP2	49:2:1464:G:N2	2.27	0.56
76:AT:26:SER:OG	76:AT:27:HIS:N	2.39	0.56
81:L1:44:GLN:NE2	81:L1:160:LYS:O	2.39	0.56
8:H:115:ARG:NH2	8:H:122:LYS:O	2.38	0.56
11:L:21:ARG:O	13:N:196:THR:OG1	2.23	0.56
16:Q:126:GLN:OE1	16:Q:126:GLN:N	2.39	0.56
19:T:16:GLN:OE1	28:1:2698:G:O2'	2.20	0.56
28:1:2391:G:O2'	28:1:2393:G:N7	2.32	0.56
49:2:221:A:N1	49:2:222:A:N6	2.54	0.56
81:L1:120:VAL:HG12	81:L1:121:PRO:HD3	1.88	0.56
12:M:116:GLU:OE1	12:M:116:GLU:N	2.39	0.56
13:N:51:LEU:HD21	13:N:117:ASN:HB3	1.88	0.56
18:S:134:ASP:OD1	18:S:134:ASP:N	2.37	0.56
49:2:1277:G:O3'	53:t:139:SER:OG	2.20	0.56
56:w:26:VAL:HG21	56:w:40:ALA:HB1	1.88	0.56
1:A:117:GLU:OE2	1:A:123:ARG:N	2.38	0.56
11:L:12:ASN:ND2	28:1:797:U:O2	2.38	0.56
21:V:108:GLU:OE1	21:V:108:GLU:N	2.39	0.56
28:1:908:G:N2	28:1:2610:G:O5'	2.39	0.56
28:1:2262:A:N3	49:2:1759:C:C2	2.74	0.56
28:1:2618:G:N1	28:1:2644:C:OP1	2.38	0.56
49:2:227:U:O2	49:2:230:C:N4	2.38	0.56
49:2:1655:A:H62	49:2:1745:G:N2	2.03	0.56
3:C:54:GLU:OE1	3:C:54:GLU:N	2.39	0.56
6:F:108:LEU:HD11	6:F:113:SER:O	2.06	0.56
28:1:2198:A:N7	28:1:2270:A:N6	2.54	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2:1353:U:O2'	49:2:1369:U:O4	2.12	0.56
69:AM:12:ASN:OD1	69:AM:16:ASN:ND2	2.39	0.56
4:D:39:GLN:OE1	4:D:40:HIS:N	2.40	0.55
12:M:20:VAL:O	12:M:66:THR:OG1	2.23	0.55
28:1:1172:G:HO2'	28:1:1173:U:P	2.29	0.55
36:d:54:GLU:N	36:d:54:GLU:OE1	2.40	0.55
49:2:1082:C:O2	68:AL:62:ARG:NH2	2.39	0.55
49:2:1472:C:OP2	49:2:1473:U:O2'	2.17	0.55
63:AG:99:GLU:OE1	78:AV:59:ARG:NH1	2.38	0.55
28:1:375:A:N1	28:1:394:G:N2	2.55	0.55
28:1:760:G:O2'	28:1:770:G:N2	2.38	0.55
28:1:2509:U:O2'	28:1:2510:U:O4'	2.05	0.55
28:1:2563:G:C6	28:1:2578:U:O2	2.59	0.55
30:4:95:G:C4	42:j:81:GLY:O	2.59	0.55
55:v:52:GLU:O	55:v:131:GLN:NE2	2.36	0.55
57:x:112:ARG:NH2	57:x:117:THR:OG1	2.40	0.55
81:L1:44:GLN:O	81:L1:45:ARG:NE	2.39	0.55
15:P:62:ARG:NE	30:4:4:C:OP2	2.38	0.55
28:1:969:C:O2'	28:1:970:A:O4'	2.24	0.55
49:2:959:U:C2	60:AD:61:THR:HG22	2.41	0.55
4:D:119:TYR:OH	4:D:139:PRO:O	2.23	0.55
28:1:2409:G:O2'	28:1:2410:U:OP1	2.22	0.55
38:f:42:GLN:N	38:f:42:GLN:OE1	2.38	0.55
75:AS:27:GLN:NE2	75:AS:43:ASN:OD1	2.40	0.55
5:E:78:ARG:NH1	28:1:3272:C:OP2	2.40	0.55
6:F:30:ARG:NH1	28:1:595:G:OP1	2.39	0.55
28:1:433:A:N1	28:1:625:G:N2	2.54	0.55
28:1:1188:U:N3	28:1:1317:A:C8	2.75	0.55
28:1:1401:A:O2'	28:1:1402:C:O5'	2.20	0.55
48:p:58:SER:OG	48:p:59:CYS:N	2.37	0.55
49:2:1475:A:O2'	49:2:1539:G:N3	2.34	0.55
79:AX:42:G:O2'	79:AX:43:G:O5'	2.23	0.55
2:B:168:LYS:O	2:B:319:ASN:ND2	2.40	0.55
14:O:61:ALA:O	28:1:1307:G:N1	2.39	0.55
25:Z:25:ILE:CD1	25:Z:41:ALA:HB1	2.36	0.55
28:1:885:U:O2'	28:1:886:C:OP1	2.24	0.55
49:2:10:G:O2'	52:s:87:GLN:OE1	2.23	0.55
54:u:103:TYR:O	54:u:182:TYR:OH	2.25	0.55
62:AF:81:ARG:NH2	62:AF:97:TYR:O	2.40	0.55
2:B:187:SER:OG	2:B:190:GLU:OE2	2.24	0.55
5:E:82:ARG:O	38:f:105:SER:N	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:23:ASN:OD1	9:I:24:ARG:N	2.39	0.55
21:V:27:ASP:OD2	21:V:29:SER:N	2.40	0.55
28:1:74:G:H21	28:1:102:C:H5'	1.71	0.55
28:1:201:A:O2'	28:1:202:G:OP1	2.21	0.55
28:1:1715:A:OP1	33:a:131:SER:OG	2.14	0.55
28:1:1947:G:O2'	28:1:1948:G:N7	2.38	0.55
29:3:103:A:OP2	29:3:105:C:N4	2.36	0.55
4:D:17:GLN:NE2	19:T:22:HIS:O	2.38	0.55
14:O:190:VAL:O	14:O:194:LEU:HD23	2.07	0.55
28:1:327:A:O2'	28:1:328:U:O5'	2.20	0.55
28:1:2434:U:H1'	28:1:2515:A:H61	1.72	0.55
28:1:2473:C:OP1	28:1:2474:G:N1	2.40	0.55
51:r:137:ILE:HG21	51:r:172:LEU:CD2	2.37	0.55
78:AV:244:ALA:HB1	78:AV:294:TRP:HZ2	1.72	0.55
28:1:64:G:H1	28:1:323:A:H62	1.55	0.55
28:1:1565:G:O2'	28:1:1566:A:OP1	2.21	0.55
28:1:2597:U:N3	28:1:2598:G:O6	2.40	0.55
38:f:106:ASN:CG	38:f:107:ILE:HD12	2.32	0.55
49:2:1532:U:OP2	72:AP:77:ARG:NE	2.33	0.55
50:q:150:ASP:OD2	50:q:165:ARG:NH2	2.39	0.55
59:z:34:PHE:CD2	59:z:105:LEU:HD12	2.41	0.55
1:A:21:ARG:NH1	28:1:825:U:OP2	2.40	0.55
27:AB:90:TYR:OH	27:AB:105:LYS:NZ	2.40	0.55
28:1:384:A:N6	28:1:1467:A:OP1	2.40	0.55
28:1:1173:U:O2'	28:1:1179:A:N7	2.35	0.55
78:AV:244:ALA:HB1	78:AV:294:TRP:CZ2	2.42	0.55
2:B:136:LYS:O	2:B:139:GLN:NE2	2.40	0.54
8:H:167:VAL:O	45:m:128:LYS:NZ	2.40	0.54
28:1:109:A:N7	28:1:323:A:N6	2.55	0.54
28:1:441:U:O2	37:e:2:ALA:N	2.40	0.54
31:P0:11:TYR:OH	31:P0:16:ARG:NH2	2.41	0.54
43:k:23:ALA:HB3	43:k:73:LEU:HD21	1.89	0.54
78:AV:122:ILE:O	78:AV:123:ILE:HD13	2.06	0.54
16:Q:16:ARG:NH2	28:1:671:U:OP1	2.41	0.54
28:1:1187:C:N4	28:1:1317:A:N7	2.56	0.54
28:1:3010:U:O2	28:1:3136:G:O6	2.25	0.54
45:m:112:LYS:O	45:m:116:GLY:N	2.40	0.54
49:2:1098:U:OP2	52:s:168:ARG:NH2	2.39	0.54
7:G:100:GLU:OE1	7:G:100:GLU:N	2.40	0.54
7:G:118:GLU:N	7:G:118:GLU:OE1	2.41	0.54
28:1:86:G:O2'	28:1:98:G:O6	2.20	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:1307:G:O2'	28:1:1308:A:OP2	2.24	0.54
49:2:686:C:O2'	69:AM:118:ARG:NH1	2.40	0.54
49:2:1489:U:N3	49:2:1492:A:N3	2.55	0.54
56:w:9:VAL:O	56:w:11:GLY:N	2.40	0.54
63:AG:100:GLN:NE2	78:AV:57:PRO:O	2.40	0.54
11:L:192:GLU:N	11:L:192:GLU:OE2	2.40	0.54
49:2:1116:A:N1	49:2:1131:A:N6	2.49	0.54
49:2:1150:G:O2'	49:2:1151:A:OP1	2.21	0.54
49:2:1593:A:O2'	76:AT:33:LYS:NZ	2.41	0.54
57:x:134:GLU:OE1	57:x:134:GLU:N	2.40	0.54
57:x:180:GLN:OE1	57:x:180:GLN:N	2.40	0.54
2:B:27:ALA:HB1	2:B:218:ILE:HG22	1.89	0.54
9:I:115:MET:HE2	9:I:118:ALA:HB2	1.89	0.54
15:P:121:GLN:OE1	28:1:410:U:O2'	2.25	0.54
65:AI:31:ALA:O	65:AI:34:THR:OG1	2.25	0.54
3:C:207:VAL:HG12	3:C:249:ILE:HD11	1.89	0.54
9:I:76:MET:HE3	9:I:151:GLY:HA3	1.88	0.54
28:1:1305:U:O4	28:1:2374:C:N4	2.41	0.54
28:1:1400:G:N2	28:1:1412:G:OP1	2.37	0.54
49:2:1218:G:O2'	49:2:1219:A:N7	2.37	0.54
2:B:124:LYS:NZ	28:1:3296:A:N7	2.56	0.54
28:1:1580:A:O2'	28:1:1581:C:OP1	2.21	0.54
28:1:1904:C:N4	28:1:2951:G:O6	2.41	0.54
28:1:2303:A:O2'	28:1:2304:C:OP1	2.20	0.54
49:2:787:G:O2'	49:2:788:A:O4'	2.12	0.54
1:A:140:ASN:ND2	1:A:143:GLU:OE2	2.41	0.54
11:L:107:GLU:OE1	11:L:107:GLU:N	2.41	0.54
28:1:2262:A:N1	49:2:1759:C:C2'	2.71	0.54
51:r:69:CYS:SG	51:r:70:LEU:N	2.81	0.54
3:C:281:ILE:HD11	16:Q:29:LEU:HG	1.89	0.54
57:x:87:ASP:O	57:x:88:ARG:NH1	2.41	0.54
2:B:232:ARG:NH1	2:B:266:ARG:O	2.40	0.53
4:D:50:ARG:NH1	4:D:65:ILE:HD11	2.23	0.53
12:M:124:ARG:NH1	28:1:3212:C:OP2	2.41	0.53
13:N:109:ARG:NH2	30:4:140:G:OP1	2.39	0.53
13:N:119:TYR:OH	13:N:131:GLU:OE2	2.17	0.53
15:P:120:ASN:ND2	30:4:12:A:O4'	2.41	0.53
28:1:69:C:C5'	28:1:302:U:HO2'	2.19	0.53
28:1:1306:G:N2	28:1:1307:G:N7	2.56	0.53
28:1:1595:U:H3	28:1:1606:U:HO2'	1.57	0.53
62:AF:31:GLU:OE1	62:AF:31:GLU:N	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:AO:7:ILE:CD1	71:AO:27:VAL:HG13	2.38	0.53
8:H:9:GLN:CD	8:H:52:LEU:HD22	2.32	0.53
27:AB:102:LYS:NZ	49:2:632:U:OP1	2.36	0.53
28:1:2287:C:O2'	28:1:2288:G:O5'	2.21	0.53
30:4:95:G:N1	42:j:82:SER:N	2.56	0.53
33:a:104:THR:OG1	33:a:126:LYS:O	2.20	0.53
60:AD:63:ALA:O	60:AD:67:THR:OG1	2.10	0.53
5:E:2:SER:N	28:1:1387:G:HO2'	2.05	0.53
5:E:94:GLU:OE1	5:E:94:GLU:N	2.41	0.53
16:Q:152:HIS:ND1	16:Q:162:ALA:O	2.42	0.53
18:S:137:ARG:NH2	28:1:1214:U:OP2	2.41	0.53
49:2:1351:G:O2'	63:AG:66:ARG:NH2	2.41	0.53
54:u:180:LEU:N	54:u:229:GLY:O	2.41	0.53
28:1:136:G:O2'	28:1:137:G:O5'	2.22	0.53
28:1:2372:A:O2'	28:1:2373:A:OP1	2.21	0.53
28:1:3022:G:N3	28:1:3024:A:N6	2.54	0.53
28:1:3212:C:O2'	28:1:3213:A:O5'	2.24	0.53
40:h:15:GLU:OE1	40:h:15:GLU:N	2.40	0.53
28:1:431:U:O2'	28:1:432:G:OP1	2.24	0.53
28:1:2846:U:N3	28:1:2850:G:O6	2.42	0.53
49:2:221:A:N6	49:2:833:U:O4	2.40	0.53
49:2:861:U:O2'	69:AM:56:HIS:O	2.27	0.53
49:2:903:U:C2	49:2:906:A:N7	2.77	0.53
49:2:1583:A:N6	49:2:1611:A:OP2	2.42	0.53
49:2:1758:U:HO2'	49:2:1759:C:P	2.29	0.53
7:G:139:VAL:HA	7:G:142:LEU:HD12	1.89	0.53
28:1:2765:C:O2'	28:1:2766:U:OP1	2.22	0.53
35:c:44:ILE:HG22	35:c:89:VAL:HG12	1.89	0.53
49:2:476:U:OP1	49:2:477:A:O2'	2.14	0.53
50:q:53:THR:HG22	50:q:161:PRO:HG2	1.90	0.53
57:x:133:THR:OG1	57:x:134:GLU:N	2.41	0.53
3:C:31:ARG:NH2	28:1:672:A:O3'	2.41	0.53
28:1:822:G:O6	28:1:903:U:C4	2.61	0.53
28:1:1618:G:O2'	28:1:1619:A:O4'	2.26	0.53
28:1:2537:U:O4	28:1:2542:U:N3	2.42	0.53
49:2:105:A:N6	49:2:308:C:O2	2.42	0.53
15:P:130:TYR:O	28:1:1507:G:N2	2.41	0.53
28:1:816:A:N6	28:1:910:G:H21	2.07	0.53
28:1:1161:G:H21	37:e:56:GLY:HA2	1.73	0.53
28:1:3136:G:O2'	28:1:3137:C:OP1	2.23	0.53
28:1:3184:A:O2'	28:1:3187:A:O2'	2.27	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2:593:U:OP1	59:z:39:LYS:N	2.41	0.53
18:S:46:GLN:NE2	18:S:51:VAL:O	2.42	0.53
28:1:373:A:N6	28:1:394:G:O2'	2.26	0.53
49:2:441:A:N6	49:2:464:A:N6	2.57	0.53
53:t:76:ARG:NH1	53:t:76:ARG:O	2.42	0.53
65:AI:90:ASN:N	65:AI:97:ASP:OD2	2.41	0.53
72:AP:75:LEU:HD12	72:AP:78:ILE:HB	1.90	0.53
81:L1:62:ASN:HD21	81:L1:154:THR:HG23	1.73	0.53
19:T:68:THR:HG22	19:T:69:LYS:H	1.74	0.53
28:1:3019:U:O4	28:1:3021:A:N6	2.42	0.53
28:1:3181:C:N4	28:1:3182:G:O6	2.42	0.53
28:1:3210:A:O2'	28:1:3211:C:OP1	2.24	0.53
32:P2:110:ILE:HD13	32:P2:133:LEU:HD21	1.91	0.53
8:H:105:GLU:OE2	8:H:106:LYS:N	2.41	0.52
18:S:161:LYS:NZ	28:1:3209:A:OP1	2.38	0.52
28:1:22:G:H22	40:h:86:ARG:HE	1.56	0.52
28:1:392:G:O2'	28:1:396:A:OP2	2.23	0.52
28:1:1490:A:H62	28:1:1838:G:H21	1.55	0.52
50:q:72:ASP:OD2	50:q:119:ARG:N	2.42	0.52
8:H:168:ARG:NH1	8:H:169:ASN:OD1	2.42	0.52
28:1:499:G:OP1	38:f:48:ARG:NH2	2.41	0.52
28:1:1305:U:OP2	28:1:2939:G:N2	2.42	0.52
28:1:3029:A:H61	28:1:3032:A:N6	2.07	0.52
50:q:148:ASP:OD1	50:q:149:LEU:N	2.41	0.52
28:1:946:U:N3	28:1:1373:A:N7	2.57	0.52
49:2:326:G:O6	49:2:337:G:C6	2.63	0.52
49:2:927:C:O2	61:AE:125:SER:OG	2.26	0.52
51:r:158:SER:O	51:r:162:ARG:NH1	2.43	0.52
51:r:194:ASN:ND2	51:r:210:ILE:O	2.42	0.52
58:y:5:ARG:NH1	58:y:29:LEU:O	2.43	0.52
3:C:59:GLN:O	42:j:52:LYS:NZ	2.31	0.52
15:P:131:ARG:NE	28:1:2356:A:N1	2.58	0.52
16:Q:67:ILE:HD12	16:Q:81:VAL:HG21	1.90	0.52
28:1:815:G:O6	28:1:906:A:O2'	2.19	0.52
28:1:1949:G:O2'	28:1:1950:U:OP1	2.23	0.52
28:1:2262:A:C2	49:2:1759:C:C2	2.96	0.52
28:1:3021:A:O2'	28:1:3022:G:OP2	2.23	0.52
49:2:313:U:O4'	49:2:1118:G:N2	2.42	0.52
49:2:446:A:N1	49:2:461:G:O2'	2.38	0.52
79:AX:1:G:N2	79:AX:73:A:H62	2.06	0.52
28:1:492:C:OP2	28:1:494:G:N2	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:1148:G:O2'	28:1:1149:G:O4'	2.24	0.52
28:1:2996:U:O2'	28:1:2997:G:O5'	2.24	0.52
28:1:3184:A:HO2'	28:1:3187:A:HO2'	1.57	0.52
30:4:95:G:C2	42:j:81:GLY:HA2	2.44	0.52
36:d:51:LEU:HD12	36:d:55:LEU:HD23	1.91	0.52
49:2:525:A:OP1	49:2:526:A:N6	2.43	0.52
51:r:59:ASP:N	51:r:59:ASP:OD2	2.40	0.52
62:AF:70:ASN:OD1	62:AF:71:GLU:N	2.43	0.52
76:AT:21:CYS:SG	76:AT:22:ARG:N	2.82	0.52
28:1:359:U:OP2	28:1:920:A:O2'	2.13	0.52
28:1:971:G:N1	28:1:1110:U:N3	2.58	0.52
28:1:3251:U:N3	28:1:3252:G:O6	2.42	0.52
47:o:6:LYS:O	47:o:8:ARG:N	2.43	0.52
49:2:269:G:N7	56:w:186:ARG:NH2	2.58	0.52
68:AL:9:VAL:HG22	68:AL:10:GLU:H	1.74	0.52
79:AX:51:G:O6	79:AX:64:A:N6	2.42	0.52
28:1:2124:G:O2'	49:2:1657:U:O2	2.28	0.52
28:1:2131:A:H61	48:p:18:TYR:HA	1.74	0.52
28:1:2144:A:O2'	28:1:2145:A:OP1	2.20	0.52
28:1:2293:C:N4	28:1:2296:A:O2'	2.43	0.52
28:1:3027:A:O2'	31:P0:141:VAL:HG23	2.09	0.52
29:3:67:G:O2'	29:3:68:C:OP1	2.26	0.52
78:AV:128:ASP:OD2	78:AV:130:THR:OG1	2.17	0.52
1:A:179:LEU:HD22	28:1:2149:A:OP1	2.10	0.52
28:1:932:U:O2'	28:1:933:A:OP2	2.27	0.52
49:2:1181:U:N3	49:2:1458:G:C6	2.77	0.52
21:V:97:ASP:OD2	21:V:98:ASN:N	2.43	0.52
28:1:554:A:H2'	28:1:557:A:H61	1.75	0.52
28:1:2609:A:O2'	28:1:2610:G:OP1	2.26	0.52
37:e:60:ASN:OD1	37:e:61:LYS:N	2.42	0.52
49:2:862:A:O2'	49:2:863:A:OP2	2.28	0.52
81:L1:36:VAL:HG21	81:L1:166:ALA:HA	1.92	0.52
28:1:266:A:O2'	28:1:267:G:N7	2.43	0.51
28:1:2262:A:H62	49:2:1758:U:C3'	2.23	0.51
64:AH:29:GLN:OE1	64:AH:29:GLN:N	2.42	0.51
78:AV:63:GLY:O	78:AV:90:ARG:NH1	2.41	0.51
28:1:60:A:OP2	28:1:326:U:N3	2.41	0.51
28:1:69:C:P	28:1:302:U:HO2'	2.30	0.51
28:1:1531:C:O2'	28:1:1800:A:N3	2.31	0.51
28:1:2158:A:N1	28:1:2174:G:N1	2.58	0.51
28:1:2271:A:O2'	28:1:2272:G:O4'	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:c:11:ASN:OD1	35:c:12:GLN:N	2.44	0.51
47:o:3:ASN:ND2	47:o:94:GLY:O	2.43	0.51
64:AH:25:THR:O	64:AH:31:ASN:ND2	2.38	0.51
28:1:961:C:N4	28:1:2627:C:N3	2.58	0.51
28:1:1448:U:O2'	28:1:1449:A:OP1	2.24	0.51
30:4:82:U:N3	30:4:88:A:O2'	2.44	0.51
49:2:930:A:OP2	49:2:931:C:N4	2.34	0.51
49:2:1161:C:O2'	49:2:1162:C:O5'	2.21	0.51
53:t:18:TYR:O	53:t:22:ASN:ND2	2.43	0.51
4:D:59:ASP:OD1	4:D:80:SER:OG	2.28	0.51
28:1:46:U:O2'	28:1:47:C:OP1	2.24	0.51
28:1:81:C:O2'	28:1:683:U:O5'	2.27	0.51
28:1:1820:U:OP1	28:1:1821:U:O2'	2.15	0.51
39:g:46:ASP:N	39:g:46:ASP:OD1	2.44	0.51
49:2:1692:G:N2	49:2:1710:U:OP1	2.44	0.51
3:C:32:PRO:HA	3:C:35:VAL:HG12	1.92	0.51
4:D:114:GLY:C	4:D:115:LEU:HD12	2.36	0.51
4:D:188:GLU:OE1	4:D:188:GLU:N	2.43	0.51
28:1:644:G:O4'	28:1:1153:A:N6	2.44	0.51
28:1:2491:A:O2'	28:1:2492:C:OP1	2.25	0.51
31:P0:19:LEU:HD11	32:P2:115:GLN:HG3	1.93	0.51
49:2:339:C:P	58:y:10:LYS:HZ1	2.34	0.51
60:AD:91:LEU:CB	60:AD:122:ILE:HD11	2.40	0.51
60:AD:118:ILE:HG22	60:AD:121:ARG:HH21	1.76	0.51
78:AV:167:VAL:HG12	78:AV:183:LEU:HD12	1.91	0.51
3:C:280:ILE:O	16:Q:123:THR:OG1	2.29	0.51
28:1:351:A:N6	44:l:37:TYR:O	2.44	0.51
28:1:1230:G:N2	28:1:1260:A:O2'	2.29	0.51
46:n:21:ARG:NH2	49:2:1653:C:O3'	2.43	0.51
65:AI:27:LYS:NZ	72:AP:74:SER:OG	2.36	0.51
30:4:110:C:OP1	30:4:114:G:N2	2.25	0.51
49:2:318:U:C2	49:2:346:G:O6	2.64	0.51
49:2:991:G:N1	49:2:1012:U:OP2	2.43	0.51
49:2:1335:U:O2'	49:2:1336:A:O5'	2.28	0.51
50:q:41:ARG:HH12	64:AH:106:THR:HG23	1.76	0.51
70:AN:66:SER:OG	70:AN:67:ALA:N	2.43	0.51
77:AU:30:PRO:HB2	77:AU:34:ALA:HB3	1.92	0.51
79:AZ:22:G:O6	79:AZ:46:G:N2	2.43	0.51
13:N:136:ASP:OD1	13:N:139:HIS:N	2.44	0.51
29:3:77:G:O2'	29:3:78:U:OP2	2.25	0.51
66:AJ:39:THR:OG1	66:AJ:43:ASN:OD1	2.27	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:143:GLU:O	1:A:145:LYS:N	2.44	0.51
4:D:50:ARG:HH11	4:D:65:ILE:HD11	1.75	0.51
5:E:59:GLU:N	5:E:59:GLU:OE1	2.44	0.51
8:H:41:ILE:HD11	8:H:64:HIS:CE1	2.46	0.51
13:N:12:ARG:HG3	28:1:268:A:H62	1.75	0.51
49:2:1640:C:H2'	49:2:1762:A:H61	1.76	0.51
81:L1:188:ASN:O	81:L1:200:ASN:ND2	2.43	0.51
19:T:55:LYS:NZ	28:1:2640:A:OP1	2.39	0.51
28:1:402:A:O2'	28:1:403:C:O5'	2.22	0.51
28:1:996:A:N1	29:3:101:G:N2	2.59	0.51
49:2:992:A:OP2	49:2:1011:G:N1	2.44	0.51
49:2:1029:U:OP2	73:AQ:12:LYS:NZ	2.43	0.51
78:AV:47:LEU:HD22	78:AV:54:PHE:CZ	2.46	0.51
11:L:39:ARG:NH2	28:1:106:A:O2'	2.43	0.50
11:L:46:ILE:HG23	11:L:46:ILE:O	2.11	0.50
28:1:155:G:O2'	28:1:156:G:OP2	2.26	0.50
28:1:212:G:O2'	28:1:213:A:OP2	2.24	0.50
28:1:2262:A:C2	49:2:1759:C:C2'	2.93	0.50
36:d:75:ILE:HG12	36:d:93:VAL:HG12	1.92	0.50
49:2:256:A:O2'	58:y:72:ILE:O	2.22	0.50
49:2:1279:C:OP2	53:t:185:LYS:NZ	2.34	0.50
54:u:11:ARG:NE	54:u:26:CYS:SG	2.84	0.50
1:A:130:SER:O	28:1:2179:C:O2'	2.19	0.50
28:1:533:A:N6	28:1:556:U:O4	2.44	0.50
28:1:762:U:C2	28:1:769:G:O6	2.64	0.50
30:4:94:C:O2'	42:j:79:GLN:O	2.25	0.50
49:2:628:G:N1	49:2:970:A:OP2	2.43	0.50
53:t:219:ALA:HB1	53:t:220:PRO:HD2	1.91	0.50
3:C:361:HIS:ND1	3:C:362:ASP:O	2.44	0.50
8:H:95:ALA:N	8:H:177:ASP:OD2	2.44	0.50
13:N:99:ARG:NH2	13:N:118:SER:O	2.44	0.50
28:1:303:G:O3'	28:1:304:G:N2	2.44	0.50
28:1:678:G:H4'	28:1:787:G:H21	1.77	0.50
55:v:137:ILE:HG21	55:v:168:VAL:HG23	1.93	0.50
28:1:1318:A:O2'	28:1:1319:G:OP1	2.27	0.50
28:1:2325:G:N2	28:1:2976:A:OP1	2.38	0.50
39:g:44:CYS:SG	39:g:45:GLY:N	2.85	0.50
43:k:26:LYS:NZ	43:k:27:ILE:O	2.32	0.50
49:2:706:A:O2'	49:2:733:A:OP1	2.28	0.50
55:v:177:ILE:HG22	55:v:180:ARG:NH2	2.27	0.50
65:AI:109:LEU:O	65:AI:113:LEU:HD23	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:AM:103:ILE:C	69:AM:104:LEU:HD12	2.37	0.50
3:C:141:ARG:O	3:C:176:SER:OG	2.10	0.50
9:I:150:GLU:OE2	9:I:153:ARG:NH2	2.44	0.50
13:N:87:GLN:NE2	28:1:2421:U:O2	2.44	0.50
28:1:2401:A:N7	28:1:2954:U:O2'	2.41	0.50
49:2:72:A:N6	56:w:169:TYR:OH	2.44	0.50
49:2:93:A:O2'	49:2:398:G:N2	2.45	0.50
49:2:144:U:O4	56:w:137:ARG:NH2	2.45	0.50
49:2:1315:U:O2'	64:AH:5:ARG:O	2.29	0.50
7:G:193:LYS:NZ	28:1:8:C:OP1	2.45	0.50
10:J:70:THR:OG1	29:3:40:C:O2	2.27	0.50
28:1:688:G:N2	28:1:692:A:H62	2.09	0.50
28:1:1490:A:O2'	42:j:12:HIS:O	2.27	0.50
28:1:1626:U:O2	28:1:1817:G:C6	2.64	0.50
39:g:52:GLN:OE1	39:g:53:GLY:N	2.44	0.50
49:2:196:G:O2'	49:2:197:A:O4'	2.27	0.50
49:2:785:U:O4	71:AO:11:LYS:NZ	2.44	0.50
49:2:1687:U:N3	49:2:1714:A:C6	2.80	0.50
53:t:6:SER:OG	53:t:9:ARG:NH2	2.45	0.50
23:X:91:ASN:N	23:X:94:GLN:OE1	2.44	0.50
25:Z:108:GLU:N	25:Z:108:GLU:OE1	2.44	0.50
28:1:1874:A:N6	28:1:1875:G:O6	2.45	0.50
28:1:2283:G:O6	28:1:2288:G:N1	2.44	0.50
49:2:744:U:N3	49:2:808:U:O2	2.45	0.50
49:2:819:G:O6	49:2:852:C:N4	2.45	0.50
49:2:1066:C:O4'	51:r:146:GLN:NE2	2.45	0.50
2:B:27:ALA:HB2	2:B:219:ALA:HA	1.92	0.50
4:D:21:ARG:NH2	29:3:8:G:O6	2.45	0.50
8:H:92:TYR:CE1	8:H:101:VAL:HG11	2.47	0.50
28:1:1230:G:O2'	28:1:1261:G:O5'	2.30	0.50
28:1:2974:U:O2'	28:1:2976:A:N6	2.33	0.50
28:1:3113:A:O2'	28:1:3114:A:OP1	2.30	0.50
49:2:168:A:OP1	56:w:140:ASN:ND2	2.44	0.50
49:2:1673:G:C6	49:2:1728:A:C2	2.99	0.50
1:A:224:THR:O	28:1:2201:G:O2'	2.30	0.50
16:Q:135:GLN:OE1	16:Q:135:GLN:N	2.45	0.50
28:1:2291:A:N6	28:1:2302:G:O3'	2.45	0.50
28:1:2461:A:O2'	28:1:2463:G:OP1	2.30	0.50
51:r:176:VAL:HG12	51:r:177:GLN:H	1.76	0.50
25:Z:55:LYS:NZ	28:1:2564:G:OP2	2.44	0.49
27:AB:92:HIS:O	27:AB:101:GLU:N	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:211:A:O2'	28:1:212:G:N2	2.45	0.49
28:1:3055:U:OP2	28:1:3088:G:N2	2.44	0.49
49:2:84:A:O2'	71:AO:121:THR:HG22	2.12	0.49
49:2:961:U:OP2	60:AD:62:GLN:NE2	2.42	0.49
49:2:1180:C:O4'	49:2:1460:A:N6	2.45	0.49
49:2:1474:G:N2	49:2:1539:G:O2'	2.45	0.49
72:AP:67:ASP:OD2	72:AP:68:ARG:NH1	2.45	0.49
78:AV:108:SER:OG	78:AV:128:ASP:N	2.44	0.49
2:B:108:GLU:N	2:B:108:GLU:OE1	2.45	0.49
13:N:183:THR:HG22	13:N:187:ARG:HG3	1.94	0.49
19:T:103:GLN:OE1	19:T:103:GLN:N	2.45	0.49
49:2:1310:U:O2'	49:2:1402:G:O2'	2.30	0.49
49:2:1417:A:O3'	63:AG:128:LYS:NZ	2.41	0.49
52:s:101:VAL:HG22	52:s:115:ILE:HG22	1.93	0.49
54:u:161:LYS:NZ	54:u:173:ILE:HD11	2.26	0.49
6:F:29:GLU:N	6:F:29:GLU:OE1	2.43	0.49
14:O:36:VAL:HG22	14:O:37:ARG:H	1.77	0.49
19:T:22:HIS:ND1	28:1:2700:G:OP2	2.45	0.49
28:1:1148:G:H21	28:1:1199:C:H41	1.59	0.49
28:1:3057:U:O2'	28:1:3058:U:OP2	2.28	0.49
28:1:3325:G:C6	28:1:3381:U:O2	2.64	0.49
49:2:151:G:N2	56:w:4:ASN:OD1	2.44	0.49
78:AV:244:ALA:HB3	78:AV:253:ALA:HB3	1.94	0.49
4:D:17:GLN:NE2	19:T:20:ARG:O	2.45	0.49
7:G:78:PHE:O	7:G:79:GLN:NE2	2.45	0.49
17:R:11:ALA:O	17:R:15:VAL:HG22	2.11	0.49
17:R:84:THR:N	28:1:1864:A:OP2	2.42	0.49
28:1:500:C:O2'	28:1:501:A:OP1	2.27	0.49
28:1:1303:A:O2'	28:1:1304:A:OP2	2.23	0.49
49:2:78:A:N1	56:w:175:ILE:HD13	2.27	0.49
49:2:114:C:N4	49:2:247:A:C6	2.80	0.49
49:2:1102:G:OP1	69:AM:76:SER:OG	2.16	0.49
61:AE:92:LYS:O	73:AQ:69:ASN:ND2	2.46	0.49
5:E:23:LYS:NZ	28:1:502:U:O2	2.29	0.49
8:H:62:ARG:HA	8:H:65:VAL:HG12	1.95	0.49
28:1:1884:A:OP1	36:d:31:ARG:NH2	2.46	0.49
28:1:2959:C:O2'	28:1:2973:G:N2	2.46	0.49
49:2:287:G:O2'	49:2:288:A:O5'	2.29	0.49
57:x:134:GLU:OE2	57:x:155:ASP:N	2.45	0.49
65:AI:50:ALA:O	65:AI:68:ARG:NH2	2.42	0.49
70:AN:70:LYS:NZ	77:AU:7:SER:O	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:L1:19:TYR:OH	81:L1:169:VAL:O	2.21	0.49
3:C:95:ARG:NH2	28:1:367:A:OP1	2.46	0.49
3:C:188:ARG:NH1	28:1:1383:G:OP2	2.46	0.49
4:D:186:GLU:OE1	4:D:186:GLU:N	2.45	0.49
5:E:80:ASN:OD1	5:E:81:ALA:N	2.46	0.49
8:H:173:ARG:O	8:H:176:LEU:HD11	2.11	0.49
11:L:75:PHE:O	11:L:76:THR:OG1	2.24	0.49
11:L:119:TYR:CZ	11:L:123:ILE:HD12	2.48	0.49
12:M:112:LEU:HD23	12:M:116:GLU:HB3	1.95	0.49
14:O:113:ASP:OD1	14:O:114:LYS:N	2.45	0.49
49:2:762:A:OP1	59:z:79:ARG:NH1	2.45	0.49
8:H:75:VAL:HG23	8:H:78:MET:HE2	1.94	0.49
11:L:74:GLY:O	11:L:101:ARG:NH2	2.45	0.49
17:R:173:ARG:NH1	49:2:853:G:OP2	2.44	0.49
18:S:132:THR:OG1	28:1:534:U:OP1	2.20	0.49
19:T:120:LYS:NZ	28:1:1093:A:OP2	2.46	0.49
28:1:1901:A:O2'	28:1:2917:G:O2'	2.27	0.49
39:g:11:ASN:O	39:g:18:ASN:ND2	2.45	0.49
69:AM:10:ALA:HB1	69:AM:27:ILE:HD13	1.95	0.49
73:AQ:40:ALA:O	73:AQ:41:ILE:HD13	2.12	0.49
2:B:21:ARG:NH1	28:1:3310:A:N1	2.61	0.49
28:1:547:G:O2'	28:1:548:G:O5'	2.30	0.49
43:k:65:LEU:HD12	43:k:68:SER:OG	2.13	0.49
45:m:115:CYS:SG	45:m:116:GLY:N	2.85	0.49
59:z:136:VAL:HG23	59:z:156:ILE:HD13	1.95	0.49
60:AD:137:PRO:O	60:AD:139:TRP:N	2.45	0.49
13:N:68:ARG:NH1	28:1:291:C:OP1	2.45	0.49
25:Z:9:LYS:O	25:Z:25:ILE:HG22	2.13	0.49
28:1:1729:A:O5'	35:c:52:ARG:NH1	2.46	0.49
28:1:1918:C:N3	28:1:1934:G:N1	2.61	0.49
28:1:3215:A:O2'	28:1:3259:U:N3	2.41	0.49
42:j:18:LEU:HD11	44:l:51:ILE:HG21	1.95	0.49
49:2:1655:A:N6	49:2:1745:G:H21	2.08	0.49
77:AU:22:GLU:OE1	77:AU:23:LYS:N	2.45	0.49
1:A:54:ARG:NH2	28:1:2175:U:O2	2.46	0.49
28:1:1492:G:O6	44:l:2:ALA:N	2.45	0.49
28:1:3050:U:O2'	28:1:3051:U:O5'	2.28	0.49
49:2:638:U:O2'	57:x:112:ARG:NH1	2.46	0.49
53:t:74:GLN:OE1	53:t:79:TYR:N	2.45	0.49
78:AV:25:THR:HG23	78:AV:293:ALA:CB	2.42	0.49
1:A:7:ASN:ND2	1:A:234:LYS:O	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:7:ARG:NH2	28:1:2828:G:OP1	2.45	0.48
28:1:1530:U:O2'	28:1:1531:C:OP1	2.25	0.48
28:1:3228:C:O2'	28:1:3229:G:O5'	2.27	0.48
41:i:8:ALA:HB3	41:i:9:ILE:HD12	1.95	0.48
51:r:70:LEU:HD12	51:r:82:ARG:HG3	1.95	0.48
58:y:76:THR:HG21	58:y:104:ILE:HD12	1.94	0.48
64:AH:50:ILE:O	64:AH:54:THR:HG23	2.13	0.48
12:M:108:ARG:NH2	14:O:196:ALA:O	2.46	0.48
21:V:2:SER:OG	21:V:3:GLY:N	2.46	0.48
28:1:19:U:O2'	28:1:20:A:OP1	2.22	0.48
28:1:2876:C:N4	28:1:2950:G:N3	2.61	0.48
28:1:2878:G:O2'	28:1:2879:C:OP2	2.23	0.48
47:o:11:TYR:OH	47:o:18:ARG:NH1	2.47	0.48
49:2:985:G:N1	49:2:1017:U:C2	2.81	0.48
50:q:49:ASN:O	50:q:53:THR:HG23	2.13	0.48
1:A:101:VAL:C	1:A:102:LEU:HD12	2.38	0.48
2:B:279:ASN:ND2	28:1:3098:G:OP1	2.46	0.48
13:N:148:TYR:O	13:N:151:ILE:HG22	2.12	0.48
25:Z:20:GLY:HA2	39:g:89:ILE:HD11	1.96	0.48
25:Z:107:ARG:NH2	28:1:1635:G:OP1	2.45	0.48
28:1:2151:C:O2'	28:1:2243:A:N1	2.45	0.48
49:2:510:G:OP2	59:z:175:ARG:NH2	2.46	0.48
49:2:601:A:O2'	49:2:602:U:O4'	2.12	0.48
70:AN:26:GLU:N	70:AN:26:GLU:OE1	2.46	0.48
3:C:157:GLU:N	3:C:157:GLU:OE1	2.46	0.48
13:N:123:GLN:OE1	13:N:123:GLN:N	2.46	0.48
16:Q:36:LEU:HD23	16:Q:45:ASN:ND2	2.28	0.48
28:1:1281:G:H21	31:P0:52:LEU:HA	1.78	0.48
28:1:3107:U:O2'	28:1:3108:G:O5'	2.31	0.48
30:4:95:G:C4	42:j:81:GLY:HA3	2.47	0.48
49:2:149:C:OP1	71:AO:121:THR:HG23	2.14	0.48
73:AQ:41:ILE:HD12	73:AQ:68:TYR:CD1	2.47	0.48
13:N:51:LEU:HD21	13:N:117:ASN:CB	2.42	0.48
28:1:406:G:C6	30:4:17:A:C6	3.01	0.48
9:I:36:LEU:CD2	9:I:87:LEU:HD23	2.44	0.48
28:1:122:A:N6	28:1:149:U:O4	2.46	0.48
28:1:2217:U:OP2	41:i:75:LYS:NZ	2.47	0.48
49:2:193:U:O2	58:y:137:LYS:NZ	2.46	0.48
49:2:1030:A:OP1	73:AQ:3:LYS:NZ	2.40	0.48
49:2:1539:G:H21	66:AJ:44:GLU:HB3	1.79	0.48
59:z:134:ILE:HG21	59:z:158:PHE:CD1	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:128:LYS:NZ	28:1:3292:A:O3'	2.46	0.48
14:O:101:ARG:NH1	28:1:3173:G:OP2	2.44	0.48
3:C:107:ARG:O	13:N:203:ARG:NH2	2.47	0.48
8:H:20:ILE:HD12	8:H:25:VAL:HG12	1.96	0.48
28:1:1484:U:O2'	28:1:1485:G:O5'	2.21	0.48
49:2:757:A:O2'	49:2:758:U:OP1	2.24	0.48
49:2:1796:C:OP1	73:AQ:87:ARG:NH2	2.46	0.48
57:x:9:LEU:O	57:x:10:SER:OG	2.27	0.48
62:AF:76:VAL:O	62:AF:95:GLY:N	2.47	0.48
68:AL:38:LYS:O	68:AL:46:ILE:HD12	2.13	0.48
70:AN:100:ASP:N	70:AN:100:ASP:OD1	2.46	0.48
78:AV:293:ALA:O	78:AV:301:LEU:HD12	2.14	0.48
1:A:147:ARG:NH2	49:2:892:A:O4'	2.46	0.48
7:G:157:VAL:HG23	7:G:159:PRO:HD2	1.96	0.48
12:M:37:GLU:HB2	12:M:45:LEU:HD21	1.95	0.48
18:S:87:THR:O	18:S:88:HIS:ND1	2.47	0.48
23:X:110:VAL:HG23	23:X:124:VAL:HG12	1.95	0.48
28:1:22:G:H1'	30:4:104:A:H62	1.79	0.48
28:1:373:A:H62	28:1:394:G:HO2'	1.56	0.48
28:1:678:G:H21	28:1:788:C:P	2.36	0.48
28:1:1902:G:N7	28:1:1907:C:N4	2.62	0.48
59:z:110:GLN:NE2	59:z:122:VAL:O	2.46	0.48
3:C:99:MET:HE3	28:1:1429:G:O4'	2.14	0.48
7:G:210:ALA:O	7:G:214:LEU:HD13	2.14	0.48
28:1:1381:A:N1	28:1:1426:C:N4	2.62	0.48
28:1:2213:A:OP2	28:1:2231:C:N4	2.47	0.48
60:AD:30:SER:HA	60:AD:33:VAL:HG12	1.95	0.48
70:AN:57:LEU:O	70:AN:71:CYS:N	2.47	0.48
1:A:65:ASP:OD1	1:A:68:LYS:N	2.44	0.47
5:E:52:VAL:CG2	5:E:65:ILE:HD11	2.44	0.47
8:H:1:MET:SD	8:H:2:LYS:N	2.87	0.47
28:1:1679:A:OP1	28:1:1757:A:O2'	2.32	0.47
48:p:38:ASP:OD1	48:p:38:ASP:N	2.46	0.47
49:2:217:A:N1	49:2:844:A:O2'	2.47	0.47
50:q:20:ALA:HB2	50:q:172:LEU:HD13	1.95	0.47
70:AN:40:SER:O	70:AN:41:SER:OG	2.31	0.47
79:AZ:2:C:O2'	79:AZ:3:G:N7	2.37	0.47
27:AB:132:SER:OG	27:AB:133:LYS:N	2.46	0.47
28:1:213:A:N6	28:1:227:G:O4'	2.47	0.47
28:1:362:U:O2'	28:1:363:G:O4'	2.20	0.47
28:1:2362:C:O2	28:1:2377:G:N2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:2752:U:O2'	28:1:2753:G:OP2	2.25	0.47
60:AD:83:GLU:OE1	60:AD:83:GLU:N	2.44	0.47
28:1:990:U:H2'	28:1:992:A:H62	1.79	0.47
28:1:1860:G:N2	28:1:3066:U:O5'	2.47	0.47
28:1:2158:A:N6	28:1:2176:U:C2	2.82	0.47
28:1:2262:A:C5	49:2:1759:C:C6	3.02	0.47
49:2:1:U:O2'	49:2:2:A:OP2	2.29	0.47
50:q:26:ALA:N	50:q:148:ASP:OD2	2.44	0.47
52:s:177:GLY:N	52:s:195:ASP:OD1	2.45	0.47
63:AG:13:LYS:N	63:AG:16:ALA:O	2.46	0.47
67:AK:49:ASN:O	67:AK:49:ASN:ND2	2.47	0.47
3:C:328:ASN:ND2	6:F:182:ASP:OD2	2.47	0.47
8:H:161:LEU:HD21	8:H:179:ILE:HD13	1.96	0.47
19:T:21:LYS:O	29:3:10:C:N4	2.47	0.47
28:1:1149:G:O6	28:1:1152:G:N1	2.48	0.47
28:1:2417:U:O3'	28:1:2418:G:N2	2.48	0.47
28:1:2699:G:HO2'	28:1:2700:G:P	2.34	0.47
28:1:3219:G:O2'	28:1:3220:G:OP2	2.32	0.47
49:2:1205:C:O2'	49:2:1206:U:OP1	2.26	0.47
59:z:133:HIS:O	59:z:140:ILE:HG23	2.14	0.47
59:z:138:LYS:NZ	71:AO:63:GLN:OE1	2.43	0.47
62:AF:87:PRO:O	62:AF:90:ILE:HG23	2.14	0.47
4:D:54:ARG:NE	29:3:6:C:OP1	2.46	0.47
11:L:15:ARG:NH2	28:1:96:G:O3'	2.47	0.47
28:1:207:U:O2'	28:1:208:C:OP1	2.22	0.47
28:1:437:G:O2'	28:1:438:A:OP1	2.31	0.47
28:1:2958:A:O2'	28:1:2975:U:N3	2.44	0.47
31:P0:69:ASP:C	31:P0:70:LEU:HD12	2.39	0.47
40:h:113:GLN:NE2	40:h:114:ARG:O	2.47	0.47
49:2:522:U:O2'	49:2:523:G:OP1	2.33	0.47
49:2:628:G:N2	49:2:971:A:H62	2.13	0.47
50:q:175:TYR:OH	50:q:197:ILE:O	2.19	0.47
3:C:8:VAL:HG23	3:C:151:VAL:HG23	1.96	0.47
28:1:2262:A:N3	49:2:1759:C:O2	2.47	0.47
31:P0:24:SER:OG	31:P0:89:THR:O	2.25	0.47
42:j:59:THR:HG22	42:j:64:MET:HE1	1.97	0.47
49:2:1695:G:N7	49:2:1696:G:N2	2.63	0.47
56:w:22:HIS:O	56:w:26:VAL:HG22	2.15	0.47
58:y:86:SER:OG	58:y:87:ASN:OD1	2.31	0.47
78:AV:16:HIS:O	78:AV:308:ASN:ND2	2.48	0.47
7:G:185:ARG:HA	7:G:188:THR:HG22	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:L:6:ASN:O	11:L:7:LEU:HD12	2.13	0.47
14:O:188:SER:OG	14:O:189:ASP:N	2.47	0.47
16:Q:2:GLY:N	28:1:1160:C:OP2	2.48	0.47
25:Z:52:LYS:O	25:Z:65:ARG:NH2	2.47	0.47
25:Z:89:VAL:O	25:Z:89:VAL:HG12	2.15	0.47
28:1:816:A:H61	28:1:910:G:N2	2.13	0.47
28:1:971:G:C3'	28:1:1371:G:H21	2.24	0.47
28:1:2302:G:H21	49:2:1746:A:H1'	1.80	0.47
28:1:2361:A:HO2'	28:1:2362:C:P	2.34	0.47
28:1:2596:U:O2'	28:1:2597:U:O4'	2.33	0.47
28:1:2904:U:O2'	28:1:2905:U:OP1	2.24	0.47
30:4:106:C:N4	30:4:138:A:O4'	2.48	0.47
45:m:96:CYS:SG	45:m:101:ALA:N	2.88	0.47
49:2:818:C:N3	49:2:819:G:N2	2.63	0.47
49:2:1414:U:O2'	49:2:1416:G:OP2	2.23	0.47
53:t:126:VAL:O	53:t:129:SER:OG	2.19	0.47
2:B:232:ARG:NH2	2:B:269:GLN:O	2.46	0.47
8:H:93:VAL:HG22	45:m:126:LYS:HE3	1.95	0.47
13:N:36:ILE:CD1	13:N:64:VAL:HG23	2.45	0.47
14:O:13:GLY:N	14:O:40:GLU:OE1	2.48	0.47
14:O:21:SER:OG	28:1:1174:G:O2'	2.19	0.47
28:1:59:G:O2'	28:1:60:A:OP2	2.24	0.47
53:t:117:ARG:NH1	53:t:120:TYR:OH	2.47	0.47
55:v:77:TYR:O	55:v:84:LYS:NZ	2.31	0.47
69:AM:60:LYS:NZ	74:AR:24:LEU:O	2.35	0.47
3:C:290:ILE:HD11	16:Q:35:PHE:CD2	2.50	0.47
8:H:168:ARG:NH2	28:1:2893:C:OP1	2.41	0.47
10:J:28:ASP:OD1	10:J:29:ARG:N	2.47	0.47
18:S:116:ALA:CB	18:S:121:ILE:HD11	2.45	0.47
28:1:1516:C:N4	28:1:1517:G:O6	2.47	0.47
28:1:1638:A:N3	28:1:1708:C:O2'	2.42	0.47
28:1:2928:C:O2'	28:1:2929:C:OP1	2.31	0.47
28:1:3350:C:O2'	28:1:3351:U:OP2	2.26	0.47
49:2:1089:U:O2'	49:2:1093:A:N1	2.40	0.47
54:u:178:GLY:N	54:u:195:ILE:HG21	2.30	0.47
63:AG:43:ILE:O	63:AG:44:LEU:HD22	2.14	0.47
78:AV:123:ILE:HD12	78:AV:133:VAL:HG22	1.95	0.47
8:H:92:TYR:HE1	8:H:101:VAL:HG11	1.80	0.47
27:AB:93:TYR:OH	27:AB:98:ASN:OD1	2.32	0.47
28:1:1147:G:O2'	28:1:1148:G:OP1	2.29	0.47
28:1:1165:A:HO2'	28:1:1166:G:P	2.35	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:2522:G:O2'	28:1:2523:A:O5'	2.31	0.47
49:2:733:A:O2'	49:2:735:C:N4	2.48	0.47
49:2:1183:A:O2'	49:2:1184:A:O4'	2.13	0.47
64:AH:77:GLU:OE1	64:AH:77:GLU:N	2.46	0.47
71:AO:36:SER:OG	71:AO:38:ASP:OD1	2.32	0.47
6:F:100:ARG:NH2	16:Q:4:ASP:OD1	2.48	0.46
10:J:126:ASP:N	10:J:126:ASP:OD1	2.45	0.46
28:1:21:G:OP2	40:h:86:ARG:NH2	2.47	0.46
28:1:373:A:N6	28:1:394:G:O3'	2.48	0.46
28:1:374:A:OP2	28:1:375:A:N6	2.49	0.46
28:1:831:G:O2'	28:1:832:G:OP1	2.27	0.46
28:1:1726:C:OP2	48:p:44:LYS:NZ	2.48	0.46
30:4:63:G:O2'	40:h:49:LYS:NZ	2.48	0.46
49:2:701:U:O4	49:2:737:A:N6	2.49	0.46
7:G:115:ALA:O	7:G:119:GLY:N	2.45	0.46
14:O:65:ASN:OD1	14:O:66:LYS:N	2.48	0.46
15:P:133:HIS:ND1	28:1:880:G:O6	2.47	0.46
18:S:34:GLU:OE1	18:S:34:GLU:N	2.46	0.46
22:W:2:LYS:O	22:W:12:LYS:NZ	2.49	0.46
49:2:656:G:N2	49:2:679:U:OP2	2.48	0.46
50:q:119:ARG:O	50:q:120:LEU:HD22	2.14	0.46
53:t:68:GLU:O	53:t:72:LEU:HD23	2.16	0.46
57:x:141:ARG:HE	57:x:149:ILE:HD11	1.80	0.46
4:D:99:TYR:OH	4:D:126:GLU:OE2	2.30	0.46
4:D:197:SER:O	4:D:202:GLY:N	2.46	0.46
7:G:76:ALA:O	7:G:79:GLN:NE2	2.48	0.46
10:J:73:GLY:O	10:J:75:LYS:N	2.48	0.46
28:1:595:G:O2'	28:1:596:C:OP1	2.31	0.46
28:1:2270:A:O2'	28:1:2271:A:O5'	2.24	0.46
49:2:1199:G:N2	49:2:1594:G:O2'	2.48	0.46
59:z:20:GLU:OE1	59:z:22:SER:N	2.49	0.46
78:AV:23:LEU:HD23	78:AV:35:SER:HB3	1.96	0.46
29:3:51:A:H61	29:3:52:G:H21	1.62	0.46
37:e:12:LYS:NZ	37:e:58:GLY:O	2.29	0.46
49:2:823:G:O6	49:2:850:A:N6	2.48	0.46
49:2:1150:G:HO2'	49:2:1151:A:P	2.38	0.46
49:2:1684:U:O2	49:2:1718:G:C6	2.68	0.46
64:AH:32:LYS:NZ	64:AH:48:ASN:OD1	2.33	0.46
28:1:404:G:N1	30:4:20:U:C2	2.83	0.46
28:1:964:G:H21	33:a:40:HIS:HB2	1.80	0.46
32:P2:66:ASN:OD1	32:P2:67:ARG:N	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:d:51:LEU:CD1	36:d:55:LEU:HD23	2.46	0.46
73:AQ:43:ASN:OD1	73:AQ:44:ILE:N	2.48	0.46
76:AT:22:ARG:NH2	76:AT:35:GLY:O	2.48	0.46
4:D:196:ARG:NH2	4:D:237:GLU:OE2	2.45	0.46
28:1:127:G:O2'	28:1:128:G:O4'	2.28	0.46
28:1:754:G:N2	28:1:778:U:O2'	2.47	0.46
28:1:971:G:C6	28:1:1110:U:O4	2.68	0.46
28:1:1306:G:OP2	28:1:2939:G:N2	2.48	0.46
49:2:1550:A:OP2	62:AF:42:ARG:NH2	2.47	0.46
49:2:1746:A:O2'	49:2:1747:G:OP1	2.34	0.46
49:2:1793:G:N1	73:AQ:75:VAL:HG11	2.31	0.46
75:AS:11:LYS:O	75:AS:13:ILE:HG23	2.15	0.46
28:1:20:A:O2'	28:1:21:G:O5'	2.25	0.46
28:1:719:U:O2'	28:1:720:A:OP1	2.28	0.46
28:1:2596:U:O2'	28:1:2597:U:O5'	2.32	0.46
49:2:761:G:OP1	59:z:51:LYS:NZ	2.48	0.46
49:2:1472:C:OP2	55:v:102:ARG:NE	2.48	0.46
49:2:1679:G:N7	49:2:1680:G:N2	2.63	0.46
54:u:73:ASP:OD1	54:u:164:LEU:HD11	2.16	0.46
78:AV:18:GLY:O	78:AV:308:ASN:ND2	2.46	0.46
28:1:688:G:H21	28:1:692:A:H62	1.64	0.46
28:1:1066:G:O2'	28:1:1067:U:OP1	2.29	0.46
28:1:1379:G:O6	28:1:1427:U:C2	2.68	0.46
28:1:3353:G:N1	28:1:3356:G:O6	2.49	0.46
32:P2:61:GLN:OE1	32:P2:61:GLN:N	2.48	0.46
49:2:1176:G:O2'	49:2:1195:C:O2'	2.16	0.46
50:q:177:LEU:O	50:q:181:VAL:HG13	2.16	0.46
56:w:75:LEU:O	56:w:76:LEU:HD22	2.15	0.46
69:AM:98:GLN:OE1	69:AM:98:GLN:N	2.49	0.46
18:S:113:ARG:NH2	28:1:1185:C:O2'	2.46	0.46
28:1:2103:U:O2'	28:1:2104:A:OP1	2.27	0.46
49:2:1478:G:OP1	66:AJ:57:ARG:NH1	2.48	0.46
17:R:20:ARG:NH1	28:1:1875:G:N7	2.62	0.46
27:AB:133:LYS:NZ	58:y:7:SER:OG	2.25	0.46
28:1:407:A:H4'	30:4:13:A:H62	1.81	0.46
28:1:988:U:O4	28:1:989:A:N6	2.49	0.46
49:2:1629:G:OP1	73:AQ:4:LYS:NZ	2.34	0.46
50:q:140:ASN:ND2	68:AL:31:SER:O	2.44	0.46
55:v:57:SER:OG	55:v:58:LEU:N	2.46	0.46
56:w:172:ALA:HB1	56:w:173:PRO:HD2	1.97	0.46
1:A:128:ARG:NH2	28:1:2174:G:OP1	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:82:LYS:C	6:F:119:VAL:HG12	2.41	0.45
28:1:644:G:O5'	28:1:1153:A:N6	2.49	0.45
28:1:971:G:C6	28:1:1110:U:C4	3.04	0.45
28:1:971:G:O2'	28:1:1371:G:N2	2.49	0.45
28:1:1806:A:O2'	28:1:2557:A:O5'	2.33	0.45
62:AF:108:ARG:H	62:AF:111:MET:HE1	1.81	0.45
2:B:161:LEU:HD12	2:B:178:LEU:HD11	1.97	0.45
4:D:90:HIS:NE2	4:D:229:ASP:OD2	2.49	0.45
15:P:85:ALA:HA	15:P:88:VAL:HG22	1.97	0.45
19:T:142:SER:OG	19:T:143:THR:N	2.49	0.45
28:1:431:U:HO2'	28:1:432:G:P	2.39	0.45
28:1:650:C:N4	28:1:651:G:N7	2.64	0.45
28:1:768:C:O2'	28:1:769:G:O4'	2.28	0.45
28:1:2720:G:N7	28:1:2736:A:N6	2.64	0.45
28:1:2818:U:O2'	28:1:2819:A:O5'	2.34	0.45
28:1:2974:U:HO2'	28:1:2976:A:N6	2.10	0.45
49:2:1716:C:O2'	49:2:1717:G:O5'	2.35	0.45
2:B:327:CYS:SG	28:1:3045:G:N2	2.90	0.45
9:I:76:MET:HE2	9:I:76:MET:HA	1.98	0.45
12:M:71:ALA:O	12:M:72:LEU:HD22	2.17	0.45
28:1:846:A:N1	49:2:628:G:O2'	2.50	0.45
28:1:1066:G:HO2'	28:1:1067:U:P	2.39	0.45
28:1:1797:A:O2'	28:1:1798:A:O5'	2.32	0.45
28:1:2467:G:O2'	28:1:2488:A:N6	2.48	0.45
54:u:123:LEU:HD11	54:u:173:ILE:HD13	1.98	0.45
58:y:3:ILE:O	58:y:29:LEU:HD13	2.16	0.45
59:z:74:ASN:OD1	59:z:75:ALA:N	2.50	0.45
28:1:158:G:O6	28:1:264:G:N2	2.50	0.45
28:1:1895:A:N6	28:1:2335:G:O2'	2.49	0.45
28:1:2431:C:O2	28:1:2432:A:N6	2.46	0.45
30:4:49:G:H5'	40:h:44:ILE:HD11	1.98	0.45
52:s:108:ASN:O	52:s:141:ARG:NH1	2.50	0.45
59:z:143:ILE:HG22	59:z:145:SER:H	1.81	0.45
7:G:101:THR:OG1	7:G:102:ALA:N	2.49	0.45
19:T:137:GLU:N	19:T:137:GLU:OE1	2.49	0.45
20:U:93:ILE:HD12	20:U:106:ALA:O	2.17	0.45
28:1:1885:U:N3	28:1:2344:U:OP1	2.48	0.45
28:1:2685:C:O2'	28:1:2686:A:OP1	2.31	0.45
28:1:2944:U:O2'	28:1:2946:A:OP2	2.16	0.45
17:R:31:GLU:OE1	17:R:31:GLU:N	2.49	0.45
28:1:26:A:OP1	28:1:330:G:N1	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:754:G:H22	28:1:778:U:C2'	2.29	0.45
28:1:1230:G:H21	28:1:1260:A:HO2'	1.60	0.45
28:1:1728:G:N2	35:c:86:ARG:O	2.50	0.45
49:2:25:C:N4	59:z:8:TYR:O	2.49	0.45
49:2:884:A:HO2'	49:2:885:G:C5'	2.24	0.45
49:2:1533:C:OP2	72:AP:77:ARG:NH2	2.50	0.45
78:AV:214:ALA:C	78:AV:243:LEU:HD11	2.42	0.45
22:W:34:SER:OG	28:1:3052:G:N7	2.46	0.45
28:1:1259:A:C2	31:P0:52:LEU:HD21	2.51	0.45
28:1:2261:G:O2'	28:1:2263:C:N4	2.50	0.45
28:1:3153:U:O2'	28:1:3154:C:O5'	2.33	0.45
49:2:621:A:HO2'	49:2:1106:U:HO2'	1.58	0.45
51:r:121:ILE:HD11	51:r:161:ILE:HG22	1.99	0.45
54:u:166:SER:OG	54:u:167:GLY:N	2.48	0.45
60:AD:91:LEU:HB3	60:AD:122:ILE:HD11	1.97	0.45
78:AV:260:ILE:HD13	78:AV:313:TRP:HH2	1.82	0.45
28:1:1557:A:O2'	28:1:1558:A:OP2	2.29	0.45
28:1:1646:G:H21	28:1:1809:A:H62	1.63	0.45
28:1:2836:C:OP2	28:1:2851:A:N6	2.49	0.45
29:3:82:G:H22	29:3:98:C:H2'	1.82	0.45
30:4:45:C:O2'	30:4:46:G:O5'	2.28	0.45
36:d:88:PRO:C	36:d:89:LEU:HD22	2.42	0.45
40:h:44:ILE:HA	40:h:47:VAL:HG12	1.99	0.45
56:w:148:SER:O	56:w:150:GLU:N	2.43	0.45
2:B:257:PRO:O	2:B:259:HIS:N	2.48	0.45
9:I:100:ASN:ND2	28:1:1127:G:OP1	2.50	0.45
13:N:172:ARG:NH2	28:1:62:A:OP1	2.43	0.45
14:O:133:ARG:HH11	28:1:1189:C:H41	1.64	0.45
16:Q:148:GLU:N	16:Q:148:GLU:OE1	2.50	0.45
28:1:2262:A:N1	49:2:1759:C:H2'	2.31	0.45
49:2:40:A:H62	49:2:467:G:N2	2.14	0.45
49:2:1683:C:N4	49:2:1719:A:H61	2.15	0.45
7:G:50:VAL:HG23	23:X:30:ALA:O	2.16	0.45
8:H:132:VAL:HG21	8:H:146:LEU:HD12	1.99	0.45
13:N:106:VAL:HG11	13:N:132:VAL:HG11	1.99	0.45
18:S:82:ASP:CG	18:S:87:THR:HG22	2.41	0.45
25:Z:67:LYS:O	25:Z:68:ILE:HD13	2.17	0.45
28:1:88:A:N6	28:1:281:G:O2'	2.50	0.45
28:1:284:A:N6	28:1:306:A:N3	2.56	0.45
28:1:343:U:N3	30:4:18:U:OP1	2.43	0.45
28:1:2855:U:O2'	28:1:2856:G:O5'	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2:126:A:H61	49:2:291:G:C2'	2.30	0.45
49:2:143:G:OP2	56:w:139:ASN:ND2	2.50	0.45
49:2:875:G:O2'	49:2:877:G:OP2	2.32	0.45
49:2:1673:G:C2	49:2:1728:A:C2	3.02	0.45
62:AF:28:MET:O	62:AF:29:SER:OG	2.28	0.45
1:A:33:ASP:N	1:A:33:ASP:OD1	2.48	0.44
7:G:26:LEU:H	7:G:26:LEU:HD23	1.83	0.44
10:J:93:ASP:CG	10:J:172:LEU:HD12	2.42	0.44
28:1:297:G:OP2	28:1:297:G:N2	2.45	0.44
28:1:1177:G:O2'	28:1:1178:G:OP2	2.33	0.44
28:1:1284:C:H41	28:1:1285:G:N2	2.15	0.44
28:1:2291:A:H5'	49:2:1746:A:H3'	2.00	0.44
28:1:2888:U:O2'	28:1:2908:G:N7	2.36	0.44
29:3:72:A:O2'	29:3:73:C:O5'	2.30	0.44
43:k:45:VAL:O	43:k:51:LEU:HD12	2.17	0.44
3:C:3:ARG:NH1	3:C:22:LEU:O	2.50	0.44
16:Q:164:ARG:NH2	28:1:668:G:O2'	2.49	0.44
25:Z:136:PHE:HA	28:1:2555:G:H21	1.81	0.44
28:1:39:A:N1	28:1:45:A:N6	2.64	0.44
28:1:895:A:O2'	28:1:896:A:OP1	2.25	0.44
28:1:1320:C:N4	28:1:1321:G:O6	2.50	0.44
28:1:2909:U:N3	28:1:3106:A:N1	2.65	0.44
49:2:1388:A:N3	49:2:1411:A:N6	2.65	0.44
50:q:139:VAL:O	50:q:139:VAL:HG12	2.17	0.44
78:AV:65:SER:OG	78:AV:86:ASP:OD2	2.32	0.44
3:C:84:ARG:NE	3:C:87:GLN:OE1	2.49	0.44
28:1:65:A:N3	28:1:77:A:N6	2.58	0.44
28:1:718:G:O2'	28:1:719:U:OP2	2.29	0.44
28:1:1695:U:O2'	28:1:1748:G:O6	2.29	0.44
28:1:2346:C:OP1	36:d:27:LYS:NZ	2.49	0.44
28:1:2434:U:C1'	28:1:2515:A:H61	2.29	0.44
28:1:2801:A:O2'	28:1:2802:A:OP1	2.32	0.44
49:2:896:U:O2	61:AE:41:ARG:NH2	2.50	0.44
49:2:1174:C:H42	49:2:1465:C:H41	1.65	0.44
55:v:135:ASP:OD2	55:v:139:ASN:ND2	2.47	0.44
9:I:150:GLU:OE1	9:I:154:ARG:NH1	2.51	0.44
28:1:584:G:O2'	28:1:585:A:O5'	2.33	0.44
28:1:859:G:O2'	28:1:861:C:OP1	2.35	0.44
49:2:294:C:O2'	54:u:138:TYR:OH	2.27	0.44
1:A:58:LEU:HD13	1:A:75:ILE:HG23	1.98	0.44
1:A:177:LYS:NZ	28:1:1793:C:OP1	2.40	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:134:TYR:CG	7:G:190:VAL:HG21	2.51	0.44
8:H:110:LYS:O	8:H:128:VAL:HG12	2.17	0.44
16:Q:66:ARG:NH1	28:1:784:A:N3	2.64	0.44
28:1:1002:A:O2'	28:1:1003:A:OP1	2.31	0.44
28:1:1778:G:O2'	28:1:1779:C:O3'	2.35	0.44
49:2:23:G:N1	49:2:603:U:C2	2.86	0.44
49:2:518:A:O2'	49:2:519:C:O5'	2.29	0.44
51:r:164:ILE:HA	51:r:167:VAL:HG12	2.00	0.44
66:AJ:34:VAL:O	66:AJ:36:ILE:HD12	2.17	0.44
78:AV:86:ASP:OD1	78:AV:88:THR:OG1	2.35	0.44
2:B:372:THR:HG23	2:B:375:GLU:H	1.83	0.44
11:L:161:ASP:OD1	11:L:162:ASN:N	2.50	0.44
19:T:10:ARG:NH2	28:1:2641:U:OP2	2.51	0.44
28:1:315:C:O2'	28:1:316:U:O4'	2.29	0.44
28:1:600:G:N2	28:1:603:A:N1	2.64	0.44
28:1:3021:A:N6	28:1:3033:A:OP1	2.45	0.44
33:a:88:ASP:OD1	33:a:89:GLN:N	2.50	0.44
38:f:105:SER:OG	38:f:106:ASN:N	2.51	0.44
2:B:221:THR:OG1	2:B:222:LYS:N	2.51	0.44
2:B:320:ASP:OD1	2:B:320:ASP:N	2.51	0.44
7:G:185:ARG:NH1	30:4:153:U:O2'	2.51	0.44
28:1:226:C:O2'	28:1:227:G:O5'	2.35	0.44
28:1:1596:C:N4	28:1:1612:A:N3	2.66	0.44
49:2:126:A:H61	49:2:291:G:H2'	1.83	0.44
13:N:13:LYS:NZ	28:1:296:A:OP2	2.51	0.44
17:R:116:ASP:OD2	17:R:118:HIS:N	2.51	0.44
24:Y:53:ASP:OD1	24:Y:53:ASP:N	2.51	0.44
28:1:410:U:N3	30:4:15:G:N3	2.66	0.44
28:1:2302:G:N7	28:1:2304:C:N4	2.66	0.44
49:2:22:A:N1	49:2:23:G:C6	2.85	0.44
49:2:1351:G:OP1	63:AG:68:ARG:NH2	2.51	0.44
49:2:1684:U:C2	49:2:1718:G:O6	2.70	0.44
66:AJ:3:GLY:N	66:AJ:138:GLN:OE1	2.51	0.44
66:AJ:48:GLN:OE1	66:AJ:48:GLN:N	2.47	0.44
16:Q:111:ARG:O	16:Q:115:VAL:HG22	2.17	0.44
23:X:78:ASP:OD1	23:X:79:GLY:N	2.48	0.44
28:1:1259:A:N6	31:P0:50:VAL:HG11	2.23	0.44
31:P0:19:LEU:HD13	31:P0:22:TYR:OH	2.18	0.44
31:P0:31:ASP:OD1	31:P0:32:ASN:N	2.47	0.44
50:q:20:ALA:HB1	50:q:169:SER:HA	1.99	0.44
55:v:129:PRO:O	55:v:133:VAL:HG22	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:v:224:ASN:OD1	55:v:225:ARG:N	2.50	0.44
58:y:153:GLU:HB3	58:y:156:VAL:HG12	1.98	0.44
70:AN:65:ASN:N	70:AN:65:ASN:OD1	2.51	0.44
78:AV:83:ALA:HB1	78:AV:110:VAL:HG11	2.00	0.44
4:D:65:ILE:HD13	29:3:6:C:O2'	2.18	0.43
8:H:134:ILE:CG2	8:H:146:LEU:HD13	2.48	0.43
17:R:100:ARG:NH2	28:1:1665:C:OP1	2.51	0.43
23:X:72:ALA:O	23:X:76:VAL:HG23	2.17	0.43
28:1:644:G:N2	28:1:2372:A:OP1	2.51	0.43
28:1:1235:U:HO2'	28:1:1246:G:H21	1.65	0.43
28:1:2617:U:N3	28:1:2620:G:OP2	2.51	0.43
28:1:2777:G:H4'	28:1:2778:G:OP1	2.17	0.43
49:2:1793:G:N2	49:2:1794:A:N7	2.59	0.43
53:t:32:GLU:OE2	53:t:53:THR:N	2.48	0.43
16:Q:36:LEU:HD23	16:Q:45:ASN:HD21	1.81	0.43
17:R:15:VAL:HG23	17:R:17:VAL:H	1.84	0.43
19:T:110:LYS:NZ	28:1:1066:G:O2'	2.51	0.43
27:AB:55:ASP:OD1	27:AB:82:ARG:NH1	2.47	0.43
28:1:1236:G:OP1	28:1:1246:G:N2	2.49	0.43
28:1:1868:G:O2'	28:1:1869:C:OP1	2.29	0.43
28:1:2403:G:O2'	28:1:2870:C:O2	2.18	0.43
28:1:3332:U:O2'	28:1:3371:G:N2	2.51	0.43
49:2:60:U:N3	49:2:63:G:OP1	2.47	0.43
65:AI:62:THR:HG22	65:AI:63:GLN:H	1.83	0.43
78:AV:122:ILE:C	78:AV:123:ILE:HD13	2.43	0.43
3:C:194:TYR:O	3:C:195:ARG:NH1	2.50	0.43
3:C:243:HIS:C	3:C:244:LEU:HD22	2.43	0.43
12:M:128:ARG:NH2	28:1:3213:A:OP1	2.50	0.43
28:1:816:A:H61	28:1:910:G:H21	1.65	0.43
28:1:1545:A:N6	28:1:1548:C:OP2	2.45	0.43
28:1:1914:G:OP1	28:1:2115:G:N2	2.50	0.43
51:r:113:MET:HE2	51:r:142:PHE:CD2	2.54	0.43
78:AV:42:LEU:HD11	78:AV:82:SER:HB2	1.99	0.43
9:I:191:LYS:NZ	9:I:193:ASP:OD1	2.51	0.43
24:Y:22:ALA:O	24:Y:27:ARG:NH2	2.51	0.43
5:E:46:ARG:NH2	28:1:3267:A:O2'	2.48	0.43
24:Y:32:SER:OG	24:Y:33:ALA:N	2.51	0.43
28:1:404:G:C2	30:4:20:U:O2	2.71	0.43
28:1:422:A:N6	28:1:2365:C:OP2	2.52	0.43
48:p:85:ARG:NH2	49:2:883:C:OP2	2.49	0.43
49:2:145:A:N6	49:2:171:A:H61	2.16	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2:1174:C:H42	49:2:1465:C:N4	2.16	0.43
49:2:1281:G:O3'	67:AK:76:SER:OG	2.36	0.43
52:s:235:LEU:HD11	68:AL:54:ALA:HB2	2.00	0.43
59:z:161:THR:O	59:z:162:SER:OG	2.33	0.43
75:AS:12:VAL:HG13	75:AS:28:VAL:HG21	2.00	0.43
18:S:65:ASN:O	28:1:519:A:N6	2.51	0.43
28:1:70:A:N6	28:1:315:C:OP1	2.51	0.43
28:1:420:G:N2	28:1:2384:A:N7	2.65	0.43
28:1:767:U:O2	28:1:768:C:N4	2.46	0.43
28:1:891:G:O4'	28:1:2142:A:N6	2.50	0.43
28:1:1442:U:N3	28:1:2357:A:OP2	2.51	0.43
28:1:1714:A:N6	28:1:1730:G:H21	2.17	0.43
49:2:441:A:H61	49:2:464:A:N6	2.16	0.43
49:2:932:U:O2	73:AQ:32:LYS:NZ	2.51	0.43
78:AV:295:SER:OG	78:AV:300:THR:OG1	2.07	0.43
2:B:128:LYS:NZ	28:1:3151:U:OP1	2.50	0.43
10:J:93:ASP:OD2	10:J:172:LEU:HD12	2.18	0.43
19:T:79:MET:SD	19:T:80:VAL:N	2.91	0.43
28:1:129:U:O4	28:1:130:A:N6	2.51	0.43
47:o:34:SER:OG	47:o:35:LEU:N	2.49	0.43
49:2:322:G:N2	49:2:324:U:O4	2.52	0.43
49:2:1746:A:HO2'	49:2:1747:G:P	2.41	0.43
78:AV:200:ASN:OD1	78:AV:201:THR:N	2.51	0.43
8:H:76:ASP:HA	8:H:79:ILE:HG22	2.01	0.43
10:J:25:GLU:OE1	10:J:26:SER:N	2.52	0.43
12:M:18:GLY:HA2	12:M:72:LEU:HD23	2.01	0.43
17:R:99:LEU:HD21	17:R:103:ARG:NH2	2.34	0.43
26:AA:22:VAL:HG12	26:AA:65:TYR:HD1	1.84	0.43
28:1:369:A:N1	30:4:21:C:N4	2.67	0.43
28:1:590:G:N2	28:1:610:G:OP2	2.34	0.43
28:1:907:G:O2'	28:1:908:G:OP2	2.23	0.43
49:2:284:G:OP1	56:w:188:ARG:NH2	2.52	0.43
51:r:113:MET:HE1	51:r:209:ASN:HB2	2.01	0.43
58:y:25:ARG:N	58:y:28:GLU:OE2	2.51	0.43
78:AV:167:VAL:HG12	78:AV:183:LEU:CD1	2.49	0.43
2:B:162:VAL:O	2:B:178:LEU:HD12	2.19	0.43
7:G:105:LYS:O	7:G:109:LEU:HD23	2.19	0.43
8:H:175:PHE:C	8:H:176:LEU:HD12	2.43	0.43
13:N:114:ARG:NH1	13:N:151:ILE:O	2.52	0.43
28:1:3011:A:H3'	28:1:3099:C:H41	1.84	0.43
30:4:63:G:O3'	40:h:49:LYS:NZ	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2:478:A:N1	49:2:510:G:O6	2.52	0.43
49:2:1163:A:N7	49:2:1612:U:O2'	2.51	0.43
49:2:1719:A:H62	49:2:1720:G:N2	2.14	0.43
52:s:67:GLN:OE1	52:s:67:GLN:N	2.49	0.43
54:u:206:ASP:HB2	54:u:222:LEU:HD12	2.01	0.43
11:L:115:ARG:NH2	11:L:145:PHE:O	2.52	0.43
18:S:9:VAL:HG22	18:S:61:ILE:CD1	2.48	0.43
28:1:33:G:H21	28:1:51:A:H62	1.67	0.43
28:1:375:A:H61	28:1:399:A:H62	1.67	0.43
28:1:535:G:O2'	28:1:536:U:OP2	2.33	0.43
28:1:1531:C:H41	28:1:1532:C:N4	2.17	0.43
28:1:2841:G:N2	28:1:2846:U:OP1	2.47	0.43
38:f:39:GLN:O	38:f:42:GLN:NE2	2.46	0.43
49:2:89:G:N2	49:2:450:U:O2'	2.52	0.43
49:2:1096:C:O2'	49:2:1097:U:OP2	2.27	0.43
56:w:37:ASP:OD1	56:w:40:ALA:N	2.52	0.43
57:x:131:PHE:O	57:x:133:THR:N	2.51	0.43
78:AV:182:ASN:N	78:AV:182:ASN:OD1	2.52	0.43
79:AX:18:G:O2'	79:AX:19:G:N7	2.40	0.43
9:I:208:ASN:OD1	9:I:209:ASN:N	2.51	0.42
28:1:706:A:H2	28:1:714:G:H22	1.68	0.42
49:2:587:C:OP1	77:AU:26:LYS:NZ	2.39	0.42
58:y:81:VAL:HG22	58:y:91:VAL:HG12	2.00	0.42
3:C:359:LEU:HD11	18:S:64:ILE:HG22	2.02	0.42
18:S:112:ALA:O	18:S:115:ARG:NH1	2.52	0.42
28:1:322:U:HO2'	28:1:323:A:P	2.36	0.42
28:1:646:A:HO2'	28:1:647:A:P	2.39	0.42
28:1:2819:A:N6	28:1:2870:C:H42	2.15	0.42
28:1:3215:A:N6	28:1:3260:G:OP1	2.52	0.42
54:u:206:ASP:OD1	54:u:206:ASP:N	2.50	0.42
81:L1:181:ASN:OD1	81:L1:182:GLN:N	2.53	0.42
1:A:129:ALA:O	1:A:169:ILE:HG21	2.19	0.42
3:C:58:HIS:ND1	28:1:933:A:OP1	2.51	0.42
14:O:141:LEU:O	14:O:145:VAL:HG12	2.19	0.42
15:P:51:VAL:HG23	15:P:57:ALA:HA	2.02	0.42
15:P:80:LYS:NZ	28:1:2387:A:O2'	2.27	0.42
28:1:643:U:OP2	28:1:1116:G:O2'	2.37	0.42
28:1:2358:A:O2'	28:1:2398:A:N7	2.50	0.42
28:1:2585:G:O2'	28:1:2587:U:OP1	2.14	0.42
49:2:1469:A:O2'	49:2:1540:G:N2	2.53	0.42
51:r:137:ILE:CD1	51:r:215:VAL:HG12	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:307:A:N6	28:1:308:A:H62	2.16	0.42
28:1:338:A:N6	28:1:1380:G:N3	2.67	0.42
28:1:424:G:N2	28:1:2362:C:O2'	2.52	0.42
28:1:986:U:OP1	28:1:1057:A:N6	2.52	0.42
28:1:1484:U:HO2'	28:1:1485:G:P	2.40	0.42
28:1:1857:C:O2	39:g:4:ARG:NH1	2.52	0.42
28:1:1938:U:O2'	28:1:2115:G:OP2	2.26	0.42
28:1:2297:U:N3	28:1:2920:U:OP1	2.52	0.42
28:1:2722:U:O2'	28:1:2723:U:O5'	2.37	0.42
30:4:46:G:N2	30:4:57:C:N3	2.68	0.42
32:P2:110:ILE:CD1	32:P2:133:LEU:HD21	2.50	0.42
44:l:28:ARG:NH1	44:l:36:ARG:O	2.51	0.42
49:2:114:C:N3	49:2:247:A:N7	2.67	0.42
63:AG:5:PRO:C	63:AG:6:SER:HG	2.27	0.42
3:C:229:ASN:OD1	3:C:231:ALA:N	2.50	0.42
12:M:78:THR:HA	12:M:81:VAL:HG12	2.02	0.42
24:Y:5:SER:OG	24:Y:6:LEU:N	2.53	0.42
28:1:1488:G:N2	28:1:1489:A:N7	2.68	0.42
28:1:2409:G:HO2'	28:1:2410:U:P	2.39	0.42
28:1:2611:U:O2	28:1:2803:A:N6	2.52	0.42
28:1:2836:C:H4'	28:1:2845:A:H61	1.85	0.42
28:1:2892:A:H61	28:1:2909:U:H3	1.67	0.42
28:1:2930:A:O2'	28:1:2931:C:OP1	2.36	0.42
28:1:3213:A:O2'	28:1:3214:U:O4'	2.35	0.42
49:2:156:A:N3	49:2:414:C:O2'	2.40	0.42
53:t:13:ALA:HA	53:t:16:VAL:HG12	2.02	0.42
60:AD:91:LEU:HB2	60:AD:122:ILE:HD11	2.00	0.42
1:A:138:GLY:O	1:A:146:THR:OG1	2.36	0.42
1:A:200:ARG:NH1	28:1:2145:A:O3'	2.53	0.42
4:D:50:ARG:NH2	4:D:147:ASP:OD1	2.52	0.42
11:L:6:ASN:O	16:Q:164:ARG:NH1	2.53	0.42
12:M:136:ALA:HB2	28:1:3229:G:OP1	2.17	0.42
24:Y:9:SER:OG	24:Y:10:SER:N	2.53	0.42
25:Z:135:ARG:O	28:1:2555:G:N2	2.52	0.42
28:1:2847:A:OP2	45:m:111:ARG:NH2	2.52	0.42
49:2:45:U:O2'	49:2:46:A:O5'	2.27	0.42
51:r:111:ARG:HA	51:r:114:VAL:HG12	2.01	0.42
28:1:307:A:H61	28:1:308:A:N6	2.14	0.42
28:1:834:U:O2'	28:1:835:G:O4'	2.35	0.42
28:1:1525:G:HO2'	28:1:1526:U:P	2.34	0.42
28:1:2158:A:O2'	28:1:2160:G:N2	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:j:75:LYS:NZ	42:j:76:ASN:OD1	2.50	0.42
49:2:227:U:O2'	49:2:229:U:O4	2.37	0.42
49:2:395:U:O4	49:2:399:A:N7	2.53	0.42
49:2:398:G:OP1	58:y:50:GLY:N	2.48	0.42
49:2:1018:U:O4	49:2:1019:A:N6	2.52	0.42
49:2:1594:G:OP2	49:2:1596:C:N4	2.51	0.42
67:AK:96:PRO:O	67:AK:100:VAL:HG23	2.19	0.42
2:B:218:ILE:CG1	2:B:276:THR:HG23	2.50	0.42
7:G:228:GLU:O	7:G:232:HIS:ND1	2.52	0.42
18:S:71:LYS:NZ	28:1:562:C:O3'	2.45	0.42
28:1:1668:G:HO2'	28:1:1669:C:P	2.38	0.42
28:1:2360:C:O2'	28:1:2361:A:O3'	2.38	0.42
49:2:190:C:O2'	49:2:191:C:OP2	2.36	0.42
49:2:610:G:H21	70:AN:19:ARG:HH22	1.65	0.42
59:z:157:ASP:N	59:z:157:ASP:OD1	2.50	0.42
70:AN:28:ASN:OD1	70:AN:29:TYR:N	2.49	0.42
81:L1:62:ASN:ND2	81:L1:154:THR:HG23	2.34	0.42
1:A:9:ARG:NH1	28:1:911:C:OP2	2.51	0.42
2:B:216:ASP:OD1	2:B:216:ASP:N	2.51	0.42
8:H:105:GLU:OE2	8:H:109:ALA:N	2.47	0.42
19:T:51:GLY:O	19:T:95:HIS:NE2	2.53	0.42
28:1:153:U:O4	28:1:159:A:O2'	2.30	0.42
28:1:2978:U:HO2'	28:1:2979:U:P	2.42	0.42
28:1:3240:C:N4	28:1:3241:G:O6	2.53	0.42
29:3:72:A:HO2'	29:3:73:C:C4'	2.32	0.42
49:2:694:U:C2	57:x:98:ILE:HG22	2.55	0.42
49:2:1586:A:OP1	63:AG:135:ARG:N	2.53	0.42
49:2:1791:A:OP1	73:AQ:8:ASN:ND2	2.53	0.42
50:q:41:ARG:NH1	64:AH:106:THR:HG23	2.34	0.42
58:y:87:ASN:OD1	58:y:87:ASN:N	2.50	0.42
66:AJ:38:LYS:O	66:AJ:39:THR:OG1	2.36	0.42
66:AJ:40:SER:HG	66:AJ:43:ASN:CG	2.22	0.42
76:AT:31:ILE:HD11	76:AT:40:ARG:HB3	2.01	0.42
7:G:237:ILE:C	7:G:238:LEU:HD12	2.45	0.42
23:X:127:THR:OG1	23:X:129:ASP:OD1	2.34	0.42
28:1:307:A:O2'	28:1:308:A:OP1	2.29	0.42
28:1:1264:G:OP2	28:1:1264:G:N2	2.50	0.42
31:P0:34:SER:OG	31:P0:110:ARG:NH1	2.52	0.42
49:2:898:A:N6	49:2:914:G:N2	2.52	0.42
57:x:9:LEU:HD11	57:x:43:PHE:CE1	2.55	0.42
69:AM:42:GLN:NE2	69:AM:49:GLU:OE2	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:31:ARG:NH1	28:1:673:U:O5'	2.53	0.41
8:H:16:VAL:HG21	8:H:79:ILE:HD11	2.02	0.41
28:1:1053:A:O2'	28:1:1054:A:O4'	2.33	0.41
28:1:1627:U:H3	28:1:1816:A:H61	1.68	0.41
28:1:3029:A:N7	28:1:3030:G:N2	2.67	0.41
49:2:1030:A:P	73:AQ:3:LYS:HZ1	2.43	0.41
51:r:119:THR:OG1	51:r:143:THR:OG1	2.29	0.41
54:u:86:PHE:HA	54:u:101:LEU:HD22	2.02	0.41
60:AD:65:VAL:HG13	60:AD:66:ILE:HG23	2.02	0.41
69:AM:106:THR:OG1	69:AM:107:SER:N	2.53	0.41
4:D:69:ILE:HG23	19:T:31:LEU:HD23	2.02	0.41
15:P:29:THR:HA	15:P:32:THR:HG22	2.02	0.41
20:U:83:TYR:O	20:U:87:ASN:ND2	2.52	0.41
21:V:28:ASN:ND2	21:V:112:SER:OG	2.46	0.41
28:1:37:U:O2'	28:1:800:G:OP2	2.36	0.41
28:1:177:U:C2	28:1:241:G:O6	2.72	0.41
28:1:836:A:O2'	28:1:837:A:O5'	2.38	0.41
28:1:2196:C:O2'	28:1:2270:A:N3	2.45	0.41
31:P0:158:VAL:HG13	31:P0:159:VAL:HG12	2.02	0.41
47:o:7:THR:O	47:o:23:HIS:N	2.45	0.41
49:2:100:A:H61	49:2:385:A:H1'	1.84	0.41
49:2:1611:A:O2'	49:2:1612:U:OP1	2.34	0.41
66:AJ:81:GLY:CA	66:AJ:94:ILE:O	2.68	0.41
71:AO:29:HIS:ND1	71:AO:32:ARG:O	2.46	0.41
75:AS:42:ARG:NH1	75:AS:61:ARG:O	2.53	0.41
3:C:145:ILE:HD12	3:C:150:LEU:HD21	2.02	0.41
4:D:149:GLY:C	4:D:150:LEU:HD22	2.44	0.41
28:1:202:G:O2'	28:1:203:G:OP1	2.30	0.41
28:1:1506:A:H5''	28:1:1508:C:H41	1.85	0.41
35:c:30:THR:O	35:c:34:LEU:HD23	2.20	0.41
49:2:46:A:O2'	49:2:432:G:N2	2.52	0.41
73:AQ:69:ASN:OD1	73:AQ:70:LYS:N	2.54	0.41
21:V:107:GLY:N	21:V:108:GLU:OE1	2.54	0.41
28:1:2806:U:O2'	28:1:2807:U:O5'	2.33	0.41
28:1:2901:G:OP1	28:1:2903:A:N6	2.54	0.41
34:b:36:ASP:OD1	34:b:38:LYS:N	2.50	0.41
49:2:373:G:N2	49:2:603:U:O3'	2.54	0.41
55:v:129:PRO:HA	55:v:132:VAL:HG12	2.03	0.41
58:y:105:ASP:OD1	58:y:105:ASP:N	2.53	0.41
3:C:33:ASP:OD2	3:C:33:ASP:N	2.53	0.41
10:J:10:ARG:O	10:J:133:ARG:NH1	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:585:A:N6	28:1:1166:G:OP1	2.51	0.41
28:1:921:A:O2'	28:1:922:U:O5'	2.30	0.41
28:1:997:A:O2'	29:3:79:A:N6	2.53	0.41
28:1:1139:G:O2'	28:1:1158:A:OP2	2.37	0.41
30:4:95:G:C6	42:j:81:GLY:HA2	2.51	0.41
49:2:276:C:O2'	49:2:277:U:OP2	2.26	0.41
49:2:420:A:N7	49:2:421:A:N6	2.68	0.41
49:2:812:A:O2'	49:2:813:U:OP2	2.29	0.41
60:AD:13:SER:OG	60:AD:14:SER:N	2.53	0.41
61:AE:81:VAL:HG11	61:AE:102:LEU:HD11	2.02	0.41
63:AG:115:THR:HG22	63:AG:115:THR:O	2.20	0.41
69:AM:36:LYS:HD2	69:AM:110:ILE:HD13	2.02	0.41
14:O:151:ASP:OD1	14:O:152:VAL:N	2.54	0.41
15:P:82:ARG:NH2	28:1:2352:A:OP2	2.53	0.41
15:P:108:ASP:OD2	15:P:110:THR:OG1	2.30	0.41
15:P:118:GLN:NE2	15:P:147:GLU:OE2	2.53	0.41
23:X:107:VAL:HG23	23:X:126:LEU:HD23	2.01	0.41
28:1:1675:G:H2'	28:1:1676:A:C8	2.55	0.41
28:1:2281:A:O2'	28:1:2282:U:OP1	2.36	0.41
28:1:3026:G:O2'	28:1:3029:A:O4'	2.28	0.41
30:4:49:G:C5'	40:h:44:ILE:HD11	2.51	0.41
31:P0:107:ALA:HB3	32:P2:62:LEU:HD12	2.02	0.41
43:k:76:ASN:OD1	43:k:77:ARG:N	2.50	0.41
49:2:81:G:N1	56:w:169:TYR:OH	2.52	0.41
3:C:314:LYS:NZ	6:F:150:LYS:O	2.49	0.41
28:1:1375:G:O2'	28:1:1376:C:OP1	2.35	0.41
28:1:1763:U:OP2	28:1:1765:U:N3	2.53	0.41
28:1:2551:U:OP1	39:g:102:LYS:NZ	2.45	0.41
49:2:31:C:O2'	49:2:547:U:OP1	2.36	0.41
49:2:214:G:O2'	49:2:251:A:N6	2.52	0.41
49:2:766:U:O4	49:2:770:A:N7	2.53	0.41
73:AQ:84:VAL:O	73:AQ:86:VAL:N	2.52	0.41
1:A:224:THR:HG21	28:1:2201:G:H21	1.84	0.41
3:C:34:ILE:O	3:C:38:VAL:HG12	2.20	0.41
13:N:115:VAL:HG12	13:N:134:LEU:HD11	2.03	0.41
18:S:130:GLU:N	18:S:130:GLU:OE1	2.54	0.41
28:1:2615:G:H21	28:1:2627:C:H41	1.68	0.41
30:4:82:U:H3	30:4:88:A:HO2'	1.67	0.41
35:c:70:PHE:CD2	35:c:77:LEU:HD13	2.56	0.41
41:i:61:ILE:HD11	41:i:87:VAL:HG23	2.02	0.41
48:p:15:GLY:O	48:p:23:ARG:NH1	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2:388:G:N2	49:2:409:C:O2	2.54	0.41
49:2:1791:A:OP2	73:AQ:10:ARG:NH2	2.54	0.41
56:w:136:LYS:NZ	56:w:174:LYS:O	2.49	0.41
2:B:230:THR:O	2:B:234:GLY:N	2.45	0.41
6:F:219:LYS:HZ2	28:1:1168:U:H4'	1.86	0.41
28:1:70:A:OP1	28:1:304:G:N2	2.52	0.41
28:1:149:U:O2'	28:1:150:A:O5'	2.33	0.41
28:1:498:A:O2'	28:1:3273:A:N1	2.35	0.41
28:1:1180:A:OP2	38:f:78:SER:N	2.54	0.41
28:1:1235:U:O2'	28:1:1246:G:N2	2.48	0.41
28:1:2117:A:O2'	28:1:3081:C:O3'	2.35	0.41
28:1:2520:A:HO2'	28:1:2521:U:P	2.37	0.41
28:1:2727:A:HO2'	28:1:2728:G:C5'	2.32	0.41
28:1:3051:U:N3	28:1:3091:A:N1	2.69	0.41
49:2:478:A:HO2'	59:z:124:HIS:CG	2.29	0.41
49:2:637:C:O2	57:x:114:ARG:NH1	2.54	0.41
49:2:826:U:O2	49:2:846:G:C6	2.73	0.41
49:2:1169:G:N2	49:2:1575:G:OP2	2.45	0.41
49:2:1484:G:H21	49:2:1606:C:C2'	2.33	0.41
63:AG:98:ASP:OD2	63:AG:101:SER:N	2.51	0.41
65:AI:16:ARG:O	65:AI:17:LEU:HD22	2.21	0.41
69:AM:5:SER:OG	69:AM:6:VAL:N	2.54	0.41
69:AM:11:LEU:HD13	69:AM:14:ILE:HD11	2.02	0.41
73:AQ:70:LYS:C	73:AQ:71:LEU:HD22	2.46	0.41
78:AV:159:ASN:ND2	78:AV:163:ASP:OD1	2.49	0.41
3:C:181:VAL:HG12	3:C:202:ARG:O	2.20	0.41
4:D:214:ASP:OD1	4:D:215:ASP:N	2.54	0.41
8:H:120:ASP:OD1	8:H:121:LYS:N	2.52	0.41
13:N:69:GLY:O	28:1:289:A:O2'	2.39	0.41
26:AA:46:LEU:HD11	26:AA:55:VAL:HG21	2.02	0.41
28:1:2310:U:O2'	28:1:2311:G:O5'	2.39	0.41
28:1:2465:G:H21	81:L1:35:GLN:HB2	1.85	0.41
28:1:3303:G:HO2'	28:1:3304:U:C5'	2.32	0.41
36:d:7:VAL:HG13	36:d:7:VAL:O	2.21	0.41
47:o:7:THR:OG1	47:o:8:ARG:N	2.53	0.41
49:2:628:G:H21	49:2:971:A:N6	2.15	0.41
65:AI:33:THR:HG23	65:AI:39:GLY:C	2.46	0.41
66:AJ:52:GLY:O	66:AJ:54:PHE:N	2.51	0.41
2:B:238:LEU:O	2:B:246:LEU:HD11	2.20	0.40
3:C:34:ILE:HA	3:C:37:THR:HG22	2.02	0.40
4:D:257:GLU:O	4:D:259:LYS:N	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:5:GLN:NE2	8:H:7:GLU:OE1	2.53	0.40
14:O:35:VAL:CG1	14:O:104:VAL:HG23	2.51	0.40
16:Q:146:SER:O	16:Q:146:SER:OG	2.35	0.40
28:1:150:A:OP2	28:1:151:A:N6	2.55	0.40
28:1:187:A:HO2'	28:1:188:U:P	2.37	0.40
28:1:189:G:P	28:1:206:G:H22	2.43	0.40
28:1:591:G:H22	28:1:612:U:P	2.44	0.40
49:2:453:U:O4	54:u:68:ARG:NH1	2.54	0.40
49:2:1264:G:OP2	49:2:1264:G:N2	2.40	0.40
49:2:1476:C:O2	66:AJ:48:GLN:NE2	2.51	0.40
60:AD:87:ASP:OD1	60:AD:88:LEU:N	2.54	0.40
61:AE:29:HIS:ND1	61:AE:29:HIS:O	2.54	0.40
81:L1:98:LYS:NZ	81:L1:120:VAL:O	2.51	0.40
7:G:68:ARG:NH1	28:1:2514:U:OP1	2.54	0.40
28:1:355:A:O5'	44:l:40:LYS:NZ	2.53	0.40
28:1:3058:U:O2'	28:1:3059:G:N7	2.54	0.40
38:f:13:HIS:NE2	38:f:28:SER:OG	2.46	0.40
53:t:166:ASP:N	53:t:166:ASP:OD1	2.52	0.40
56:w:162:VAL:O	56:w:164:LYS:N	2.54	0.40
57:x:50:ASP:OD1	57:x:51:VAL:N	2.54	0.40
23:X:111:ASN:OD1	23:X:111:ASN:N	2.53	0.40
28:1:358:G:N2	28:1:927:C:O2'	2.53	0.40
28:1:659:G:O6	28:1:1432:C:O2'	2.34	0.40
28:1:1260:A:P	28:1:1279:C:H41	2.44	0.40
28:1:1636:U:O2'	28:1:1637:A:O5'	2.34	0.40
28:1:2374:C:O2'	28:1:2375:G:OP2	2.39	0.40
43:k:27:ILE:HD11	43:k:39:ARG:HB3	2.04	0.40
57:x:172:VAL:O	57:x:176:LEU:HD23	2.22	0.40
3:C:16:THR:OG1	3:C:17:ALA:N	2.55	0.40
3:C:125:ALA:HB1	3:C:238:LEU:HD22	2.04	0.40
10:J:12:LEU:HD23	10:J:13:LYS:N	2.37	0.40
20:U:33:TYR:O	20:U:37:LEU:HD23	2.22	0.40
28:1:1054:A:H5''	28:1:2637:A:H61	1.87	0.40
28:1:1308:A:HO2'	28:1:1309:U:P	2.37	0.40
28:1:1448:U:HO2'	28:1:1449:A:P	2.40	0.40
28:1:1595:U:N3	28:1:1606:U:O2'	2.47	0.40
30:4:95:G:C2	42:j:81:GLY:N	2.90	0.40
47:o:10:THR:HG22	47:o:11:TYR:H	1.86	0.40
49:2:1:U:H2'	59:z:54:ARG:HE	1.86	0.40
49:2:629:U:OP2	49:2:969:C:N4	2.53	0.40
49:2:1114:G:N2	49:2:1131:A:OP2	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:r:86:LEU:HD13	51:r:100:PHE:HA	2.03	0.40
51:r:149:GLN:OE1	51:r:150:VAL:N	2.48	0.40
52:s:207:LEU:O	52:s:211:LEU:HD23	2.22	0.40
57:x:185:ILE:HG23	57:x:185:ILE:O	2.22	0.40
81:L1:31:THR:HG22	81:L1:31:THR:O	2.20	0.40
3:C:190:GLY:O	3:C:193:LYS:NZ	2.48	0.40
3:C:289:ILE:HD11	16:Q:129:VAL:HG11	2.04	0.40
4:D:236:LEU:HA	4:D:239:ILE:HD12	2.03	0.40
7:G:161:GLU:OE2	13:N:26:ARG:NH2	2.55	0.40
11:L:24:VAL:HG21	11:L:26:PHE:CZ	2.57	0.40
28:1:711:A:P	28:1:2777:G:H21	2.44	0.40
28:1:1536:G:O6	28:1:1586:G:N2	2.54	0.40
28:1:2614:G:N2	28:1:2797:C:O4'	2.55	0.40
30:4:95:G:C4	42:j:81:GLY:N	2.90	0.40
49:2:86:A:OP1	56:w:87:ARG:NH2	2.55	0.40
49:2:812:A:O2'	49:2:859:A:N1	2.55	0.40
55:v:46:TRP:NE1	55:v:118:LEU:HD11	2.36	0.40
56:w:105:ASP:OD1	56:w:105:ASP:N	2.55	0.40
79:AX:34:G:N2	79:AX:35:A:O3'	2.54	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	
1	A	250/254 (98%)	215 (86%)	33 (13%)	2 (1%)	16	52
2	B	384/387 (99%)	339 (88%)	45 (12%)	0	100	100
3	C	359/362 (99%)	314 (88%)	44 (12%)	1 (0%)	36	71
4	D	294/297 (99%)	263 (90%)	31 (10%)	0	100	100
5	E	152/176 (86%)	134 (88%)	18 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	F	220/244 (90%)	198 (90%)	22 (10%)	0	100	100
7	G	231/256 (90%)	208 (90%)	22 (10%)	1 (0%)	30	66
8	H	189/191 (99%)	167 (88%)	21 (11%)	1 (0%)	24	62
9	I	207/221 (94%)	185 (89%)	22 (11%)	0	100	100
10	J	167/174 (96%)	139 (83%)	28 (17%)	0	100	100
11	L	191/199 (96%)	154 (81%)	34 (18%)	3 (2%)	7	37
12	M	134/138 (97%)	122 (91%)	11 (8%)	1 (1%)	18	54
13	N	201/204 (98%)	176 (88%)	23 (11%)	2 (1%)	12	47
14	O	195/199 (98%)	177 (91%)	17 (9%)	1 (0%)	24	62
15	P	181/184 (98%)	169 (93%)	12 (7%)	0	100	100
16	Q	183/186 (98%)	168 (92%)	15 (8%)	0	100	100
17	R	186/189 (98%)	175 (94%)	11 (6%)	0	100	100
18	S	170/172 (99%)	148 (87%)	22 (13%)	0	100	100
19	T	157/160 (98%)	139 (88%)	17 (11%)	1 (1%)	21	58
20	U	98/121 (81%)	93 (95%)	5 (5%)	0	100	100
21	V	134/137 (98%)	114 (85%)	18 (13%)	2 (2%)	8	38
22	W	61/155 (39%)	57 (93%)	4 (7%)	0	100	100
23	X	119/142 (84%)	107 (90%)	12 (10%)	0	100	100
24	Y	124/127 (98%)	117 (94%)	7 (6%)	0	100	100
25	Z	133/136 (98%)	117 (88%)	15 (11%)	1 (1%)	16	52
26	AA	94/105 (90%)	81 (86%)	12 (13%)	1 (1%)	11	45
27	AB	151/156 (97%)	129 (85%)	22 (15%)	0	100	100
31	P0	187/312 (60%)	143 (76%)	44 (24%)	0	100	100
32	P2	92/165 (56%)	70 (76%)	22 (24%)	0	100	100
33	a	146/149 (98%)	122 (84%)	23 (16%)	1 (1%)	18	54
34	b	56/59 (95%)	46 (82%)	10 (18%)	0	100	100
35	c	95/105 (90%)	87 (92%)	7 (7%)	1 (1%)	11	45
36	d	107/113 (95%)	96 (90%)	11 (10%)	0	100	100
37	e	125/130 (96%)	111 (89%)	14 (11%)	0	100	100
38	f	104/107 (97%)	89 (86%)	14 (14%)	1 (1%)	12	47
39	g	110/121 (91%)	98 (89%)	12 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	h	117/120 (98%)	105 (90%)	12 (10%)	0	100	100
41	i	97/100 (97%)	82 (84%)	15 (16%)	0	100	100
42	j	85/88 (97%)	74 (87%)	11 (13%)	0	100	100
43	k	75/78 (96%)	69 (92%)	6 (8%)	0	100	100
44	l	48/51 (94%)	41 (85%)	7 (15%)	0	100	100
45	m	50/128 (39%)	37 (74%)	12 (24%)	1 (2%)	6	32
46	n	23/25 (92%)	21 (91%)	2 (9%)	0	100	100
47	o	103/106 (97%)	84 (82%)	19 (18%)	0	100	100
48	p	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
50	q	204/252 (81%)	173 (85%)	29 (14%)	2 (1%)	12	47
51	r	212/255 (83%)	177 (84%)	34 (16%)	1 (0%)	24	62
52	s	215/254 (85%)	195 (91%)	19 (9%)	1 (0%)	24	62
53	t	221/240 (92%)	187 (85%)	34 (15%)	0	100	100
54	u	258/261 (99%)	210 (81%)	47 (18%)	1 (0%)	30	66
55	v	204/225 (91%)	172 (84%)	30 (15%)	2 (1%)	12	47
56	w	221/236 (94%)	171 (77%)	47 (21%)	3 (1%)	9	39
57	x	182/190 (96%)	156 (86%)	26 (14%)	0	100	100
58	y	184/200 (92%)	154 (84%)	28 (15%)	2 (1%)	11	45
59	z	183/197 (93%)	159 (87%)	23 (13%)	1 (0%)	24	62
60	AD	148/151 (98%)	131 (88%)	15 (10%)	2 (1%)	9	39
61	AE	125/138 (91%)	107 (86%)	17 (14%)	1 (1%)	16	52
62	AF	122/142 (86%)	98 (80%)	22 (18%)	2 (2%)	7	37
63	AG	139/143 (97%)	109 (78%)	29 (21%)	1 (1%)	18	54
64	AH	116/136 (85%)	105 (90%)	11 (10%)	0	100	100
65	AI	143/146 (98%)	125 (87%)	17 (12%)	1 (1%)	18	54
66	AJ	141/144 (98%)	123 (87%)	18 (13%)	0	100	100
67	AK	105/121 (87%)	84 (80%)	21 (20%)	0	100	100
68	AL	85/87 (98%)	68 (80%)	16 (19%)	1 (1%)	10	42
69	AM	127/130 (98%)	114 (90%)	13 (10%)	0	100	100
70	AN	142/145 (98%)	113 (80%)	28 (20%)	1 (1%)	18	54
71	AO	132/135 (98%)	119 (90%)	13 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
72	AP	68/108 (63%)	53 (78%)	15 (22%)	0	100	100
73	AQ	95/119 (80%)	69 (73%)	26 (27%)	0	100	100
74	AR	79/82 (96%)	65 (82%)	13 (16%)	1 (1%)	9	41
75	AS	61/67 (91%)	52 (85%)	9 (15%)	0	100	100
76	AT	51/56 (91%)	46 (90%)	5 (10%)	0	100	100
77	AU	58/63 (92%)	51 (88%)	7 (12%)	0	100	100
78	AV	316/319 (99%)	269 (85%)	47 (15%)	0	100	100
81	L1	202/217 (93%)	155 (77%)	46 (23%)	1 (0%)	24	62
All	All	11213/12280 (91%)	9675 (86%)	1493 (13%)	45 (0%)	31	66

All (45) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	L	47	ALA
11	L	48	PRO
11	L	62	THR
14	O	110	PRO
50	q	111	ILE
52	s	39	THR
54	u	154	ILE
56	w	10	ASN
60	AD	105	ASN
62	AF	127	ARG
3	C	130	ALA
19	T	18	ASP
21	V	105	PRO
60	AD	85	PRO
45	m	89	TYR
81	L1	120	VAL
25	Z	102	GLU
26	AA	32	HIS
33	a	47	LYS
58	y	104	ILE
38	f	59	VAL
56	w	148	SER
62	AF	69	GLU
1	A	143	GLU
7	G	39	ALA
8	H	59	ASN

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Mol	Chain	Res	Type
12	M	9	ALA
13	N	94	TYR
13	N	145	ASP
35	c	41	LEU
50	q	109	ASN
55	v	126	ASP
56	w	152	ASP
61	AE	126	THR
70	AN	112	LYS
74	AR	61	THR
55	v	128	ASN
58	y	39	GLY
65	AI	92	ILE
1	A	153	GLY
21	V	104	ASN
51	r	63	GLY
59	z	162	SER
63	AG	33	GLY
68	AL	46	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	193/196 (98%)	193 (100%)	0	100	100
2	B	319/323 (99%)	319 (100%)	0	100	100
3	C	288/289 (100%)	288 (100%)	0	100	100
4	D	244/245 (100%)	244 (100%)	0	100	100
5	E	134/153 (88%)	134 (100%)	0	100	100
6	F	186/205 (91%)	186 (100%)	0	100	100
7	G	187/208 (90%)	187 (100%)	0	100	100
8	H	171/171 (100%)	171 (100%)	0	100	100
9	I	177/187 (95%)	177 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	J	147/151 (97%)	147 (100%)	0	100	100
11	L	154/159 (97%)	154 (100%)	0	100	100
12	M	107/109 (98%)	107 (100%)	0	100	100
13	N	175/176 (99%)	175 (100%)	0	100	100
14	O	160/162 (99%)	160 (100%)	0	100	100
15	P	140/146 (96%)	140 (100%)	0	100	100
16	Q	150/151 (99%)	150 (100%)	0	100	100
17	R	153/154 (99%)	153 (100%)	0	100	100
18	S	156/156 (100%)	156 (100%)	0	100	100
19	T	136/137 (99%)	136 (100%)	0	100	100
20	U	87/107 (81%)	87 (100%)	0	100	100
21	V	104/105 (99%)	104 (100%)	0	100	100
22	W	55/129 (43%)	55 (100%)	0	100	100
23	X	104/118 (88%)	104 (100%)	0	100	100
24	Y	109/110 (99%)	109 (100%)	0	100	100
25	Z	115/116 (99%)	115 (100%)	0	100	100
26	AA	77/98 (79%)	77 (100%)	0	100	100
27	AB	133/137 (97%)	133 (100%)	0	100	100
31	P0	160/254 (63%)	160 (100%)	0	100	100
32	P2	81/136 (60%)	81 (100%)	0	100	100
33	a	118/119 (99%)	118 (100%)	0	100	100
34	b	46/47 (98%)	46 (100%)	0	100	100
35	c	81/88 (92%)	81 (100%)	0	100	100
36	d	94/97 (97%)	94 (100%)	0	100	100
37	e	109/111 (98%)	109 (100%)	0	100	100
38	f	90/91 (99%)	90 (100%)	0	100	100
39	g	95/103 (92%)	95 (100%)	0	100	100
40	h	104/105 (99%)	104 (100%)	0	100	100
41	i	81/82 (99%)	81 (100%)	0	100	100
42	j	70/71 (99%)	70 (100%)	0	100	100
43	k	68/69 (99%)	68 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	l	45/46 (98%)	45 (100%)	0	100	100
45	m	47/116 (40%)	47 (100%)	0	100	100
46	n	22/23 (96%)	22 (100%)	0	100	100
47	o	90/91 (99%)	90 (100%)	0	100	100
48	p	71/72 (99%)	71 (100%)	0	100	100
50	q	164/210 (78%)	164 (100%)	0	100	100
51	r	191/224 (85%)	191 (100%)	0	100	100
52	s	176/205 (86%)	176 (100%)	0	100	100
53	t	182/195 (93%)	182 (100%)	0	100	100
54	u	221/222 (100%)	221 (100%)	0	100	100
55	v	173/191 (91%)	173 (100%)	0	100	100
56	w	189/201 (94%)	189 (100%)	0	100	100
57	x	165/170 (97%)	165 (100%)	0	100	100
58	y	150/161 (93%)	150 (100%)	0	100	100
59	z	158/166 (95%)	158 (100%)	0	100	100
60	AD	127/128 (99%)	127 (100%)	0	100	100
61	AE	81/105 (77%)	81 (100%)	0	100	100
62	AF	101/118 (86%)	101 (100%)	0	100	100
63	AG	117/119 (98%)	117 (100%)	0	100	100
64	AH	94/124 (76%)	94 (100%)	0	100	100
65	AI	128/129 (99%)	128 (100%)	0	100	100
66	AJ	115/116 (99%)	115 (100%)	0	100	100
67	AK	100/114 (88%)	100 (100%)	0	100	100
68	AL	74/74 (100%)	74 (100%)	0	100	100
69	AM	110/111 (99%)	110 (100%)	0	100	100
70	AN	119/120 (99%)	119 (100%)	0	100	100
71	AO	112/113 (99%)	112 (100%)	0	100	100
72	AP	61/89 (68%)	61 (100%)	0	100	100
73	AQ	83/100 (83%)	83 (100%)	0	100	100
74	AR	70/71 (99%)	70 (100%)	0	100	100
75	AS	56/60 (93%)	56 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
76	AT	47/49 (96%)	46 (98%)	1 (2%)	47	65
77	AU	51/54 (94%)	51 (100%)	0	100	100
78	AV	259/262 (99%)	259 (100%)	0	100	100
81	L1	185/198 (93%)	185 (100%)	0	100	100
All	All	9492/10318 (92%)	9491 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
76	AT	38	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	291	ASN
6	F	64	GLN
8	H	9	GLN
8	H	100	ASN
9	I	73	ASN
9	I	92	HIS
10	J	20	ASN
10	J	95	ASN
11	L	37	ASN
12	M	126	GLN
13	N	70	ASN
15	P	118	GLN
16	Q	158	HIS
17	R	66	HIS
18	S	154	HIS
19	T	112	ASN
19	T	146	ASN
21	V	47	ASN
22	W	33	ASN
24	Y	42	GLN
24	Y	81	GLN
32	P2	97	ASN
34	b	19	ASN
36	d	43	HIS
41	i	100	HIS
47	o	20	HIS

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Mol	Chain	Res	Type
47	o	47	GLN
47	o	82	GLN
50	q	30	GLN
51	r	95	ASN
51	r	220	GLN
56	w	22	HIS
58	y	88	ASN
59	z	38	ASN
62	AF	128	HIS
63	AG	100	GLN
65	AI	44	ASN
65	AI	55	HIS
66	AJ	127	ASN
70	AN	99	ASN
71	AO	106	GLN
71	AO	107	GLN
71	AO	110	GLN
72	AP	82	HIS
73	AQ	94	ASN
78	AV	288	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
28	1	3220/3395 (94%)	1864 (57%)	158 (4%)
29	3	120/121 (99%)	49 (40%)	5 (4%)
30	4	157/158 (99%)	86 (54%)	9 (5%)
49	2	1739/1800 (96%)	675 (38%)	20 (1%)
79	AX	76/76 (100%)	51 (67%)	3 (3%)
79	AZ	75/76 (98%)	40 (53%)	1 (1%)
80	AY	7/8 (87%)	6 (85%)	0
All	All	5394/5634 (95%)	2771 (51%)	196 (3%)

All (2771) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
28	1	7	C
28	1	14	U
28	1	15	C
28	1	19	U
28	1	20	A

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Mol	Chain	Res	Type
28	1	21	G
28	1	22	G
28	1	23	A
28	1	24	G
28	1	25	U
28	1	26	A
28	1	27	C
28	1	29	C
28	1	30	G
28	1	31	C
28	1	34	A
28	1	39	A
28	1	40	A
28	1	42	C
28	1	43	A
28	1	47	C
28	1	50	U
28	1	51	A
28	1	53	G
28	1	54	C
28	1	55	G
28	1	56	G
28	1	60	A
28	1	64	G
28	1	65	A
28	1	66	A
28	1	68	C
28	1	69	C
28	1	70	A
28	1	71	A
28	1	72	C
28	1	73	C
28	1	74	G
28	1	76	G
28	1	77	A
28	1	78	U
28	1	81	C
28	1	82	C
28	1	83	U
28	1	84	U
28	1	89	A
28	1	90	C

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Mol	Chain	Res	Type
28	1	92	G
28	1	93	C
28	1	94	G
28	1	96	G
28	1	98	G
28	1	99	A
28	1	102	C
28	1	104	G
28	1	105	C
28	1	106	A
28	1	109	A
28	1	110	G
28	1	111	C
28	1	112	U
28	1	115	A
28	1	116	A
28	1	117	U
28	1	118	U
28	1	119	U
28	1	120	G
28	1	122	A
28	1	123	A
28	1	124	U
28	1	127	G
28	1	132	C
28	1	133	U
28	1	137	G
28	1	139	G
28	1	140	C
28	1	141	C
28	1	142	C
28	1	144	A
28	1	145	G
28	1	146	U
28	1	147	U
28	1	148	G
28	1	149	U
28	1	150	A
28	1	151	A
28	1	154	U
28	1	155	G
28	1	156	G

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Mol	Chain	Res	Type
28	1	157	A
28	1	158	G
28	1	163	C
28	1	164	A
28	1	165	A
28	1	171	G
28	1	174	C
28	1	176	G
28	1	179	C
28	1	182	U
28	1	183	G
28	1	187	A
28	1	188	U
28	1	189	G
28	1	190	U
28	1	191	U
28	1	193	C
28	1	195	U
28	1	198	A
28	1	199	A
28	1	200	C
28	1	201	A
28	1	202	G
28	1	203	G
28	1	204	A
28	1	205	C
28	1	206	G
28	1	208	C
28	1	210	U
28	1	211	A
28	1	212	G
28	1	216	G
28	1	218	G
28	1	219	A
28	1	221	A
28	1	222	A
28	1	225	C
28	1	226	C
28	1	227	G
28	1	229	G
28	1	234	G
28	1	237	G

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Mol	Chain	Res	Type
28	1	239	G
28	1	240	U
28	1	243	G
28	1	244	G
28	1	246	U
28	1	247	C
28	1	248	U
28	1	249	U
28	1	251	G
28	1	252	U
28	1	253	A
28	1	263	C
28	1	264	G
28	1	265	A
28	1	266	A
28	1	267	G
28	1	268	A
28	1	269	G
28	1	272	G
28	1	273	A
28	1	274	G
28	1	275	U
28	1	276	U
28	1	277	G
28	1	278	U
28	1	280	U
28	1	281	G
28	1	282	G
28	1	283	G
28	1	284	A
28	1	285	A
28	1	286	U
28	1	288	C
28	1	289	A
28	1	290	G
28	1	292	U
28	1	293	C
28	1	294	U
28	1	296	A
28	1	298	U
28	1	304	G
28	1	305	U

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Mol	Chain	Res	Type
28	1	306	A
28	1	308	A
28	1	309	U
28	1	314	U
28	1	315	C
28	1	316	U
28	1	318	A
28	1	319	A
28	1	323	A
28	1	324	A
28	1	325	A
28	1	326	U
28	1	327	A
28	1	328	U
28	1	329	U
28	1	330	G
28	1	331	G
28	1	337	G
28	1	338	A
28	1	339	C
28	1	340	C
28	1	341	G
28	1	342	A
28	1	343	U
28	1	344	A
28	1	345	G
28	1	346	C
28	1	347	G
28	1	348	A
28	1	349	A
28	1	350	C
28	1	352	A
28	1	353	G
28	1	354	U
28	1	355	A
28	1	359	U
28	1	360	G
28	1	361	A
28	1	362	U
28	1	365	A
28	1	368	G
28	1	370	U

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Mol	Chain	Res	Type
28	1	371	G
28	1	372	A
28	1	374	A
28	1	375	A
28	1	376	G
28	1	377	A
28	1	378	A
28	1	379	C
28	1	380	U
28	1	381	U
28	1	382	U
28	1	383	G
28	1	384	A
28	1	385	A
28	1	386	A
28	1	387	A
28	1	389	A
28	1	390	G
28	1	391	A
28	1	392	G
28	1	393	U
28	1	394	G
28	1	396	A
28	1	397	A
28	1	398	A
28	1	399	A
28	1	400	G
28	1	401	U
28	1	402	A
28	1	403	C
28	1	404	G
28	1	405	U
28	1	406	G
28	1	407	A
28	1	408	A
28	1	409	A
28	1	410	U
28	1	411	U
28	1	412	G
28	1	413	U
28	1	415	G
28	1	416	A

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Mol	Chain	Res	Type
28	1	419	G
28	1	421	G
28	1	423	A
28	1	430	U
28	1	431	U
28	1	432	G
28	1	433	A
28	1	434	U
28	1	437	G
28	1	438	A
28	1	440	A
28	1	441	U
28	1	442	G
28	1	443	G
28	1	444	U
28	1	446	U
28	1	448	U
28	1	449	U
28	1	488	U
28	1	489	U
28	1	492	C
28	1	493	U
28	1	494	G
28	1	495	G
28	1	500	C
28	1	501	A
28	1	506	U
28	1	507	U
28	1	508	U
28	1	509	U
28	1	510	G
28	1	519	A
28	1	521	A
28	1	523	A
28	1	533	A
28	1	534	U
28	1	535	G
28	1	536	U
28	1	541	U
28	1	542	G
28	1	544	C
28	1	545	U

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Mol	Chain	Res	Type
28	1	546	C
28	1	547	G
28	1	548	G
28	1	549	U
28	1	550	A
28	1	557	A
28	1	558	U
28	1	559	A
28	1	560	G
28	1	565	U
28	1	566	G
28	1	578	A
28	1	579	G
28	1	580	C
28	1	586	C
28	1	587	U
28	1	589	A
28	1	590	G
28	1	592	A
28	1	593	C
28	1	594	U
28	1	595	G
28	1	596	C
28	1	597	G
28	1	601	U
28	1	602	A
28	1	603	A
28	1	608	A
28	1	611	A
28	1	619	A
28	1	621	A
28	1	622	A
28	1	623	U
28	1	625	G
28	1	631	U
28	1	634	C
28	1	636	C
28	1	637	C
28	1	638	C
28	1	639	G
28	1	642	U
28	1	643	U

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Mol	Chain	Res	Type
28	1	644	G
28	1	645	A
28	1	646	A
28	1	647	A
28	1	648	C
28	1	649	A
28	1	650	C
28	1	653	A
28	1	655	C
28	1	656	A
28	1	660	A
28	1	661	G
28	1	662	U
28	1	663	C
28	1	664	U
28	1	665	A
28	1	667	C
28	1	669	U
28	1	671	U
28	1	673	U
28	1	674	G
28	1	675	C
28	1	676	G
28	1	677	A
28	1	678	G
28	1	679	U
28	1	680	G
28	1	681	U
28	1	682	U
28	1	683	U
28	1	684	G
28	1	685	G
28	1	688	G
28	1	689	U
28	1	690	A
28	1	691	A
28	1	692	A
28	1	694	C
28	1	695	C
28	1	696	C
28	1	697	A
28	1	700	C

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Mol	Chain	Res	Type
28	1	702	C
28	1	703	G
28	1	704	U
28	1	705	A
28	1	706	A
28	1	707	U
28	1	708	G
28	1	709	A
28	1	710	A
28	1	711	A
28	1	712	G
28	1	713	U
28	1	715	A
28	1	716	A
28	1	717	C
28	1	718	G
28	1	719	U
28	1	720	A
28	1	721	G
28	1	725	G
28	1	727	G
28	1	728	G
28	1	734	C
28	1	735	A
28	1	736	A
28	1	737	G
28	1	743	C
28	1	747	A
28	1	752	C
28	1	756	U
28	1	760	G
28	1	761	A
28	1	762	U
28	1	763	G
28	1	764	U
28	1	765	C
28	1	766	U
28	1	767	U
28	1	768	C
28	1	769	G
28	1	771	A
28	1	772	U

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Mol	Chain	Res	Type
28	1	773	G
28	1	774	G
28	1	775	A
28	1	776	U
28	1	779	G
28	1	780	A
28	1	781	G
28	1	782	U
28	1	784	A
28	1	785	G
28	1	786	A
28	1	787	G
28	1	789	A
28	1	790	U
28	1	792	G
28	1	794	U
28	1	795	G
28	1	797	U
28	1	798	G
28	1	801	A
28	1	802	C
28	1	803	C
28	1	806	A
28	1	807	A
28	1	808	A
28	1	809	G
28	1	810	A
28	1	811	U
28	1	812	G
28	1	813	G
28	1	814	U
28	1	815	G
28	1	816	A
28	1	817	A
28	1	818	C
28	1	820	A
28	1	821	U
28	1	825	U
28	1	826	G
28	1	829	U
28	1	830	A
28	1	831	G

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Mol	Chain	Res	Type
28	1	832	G
28	1	833	G
28	1	834	U
28	1	845	G
28	1	846	A
28	1	847	A
28	1	849	C
28	1	850	U
28	1	851	C
28	1	857	G
28	1	858	A
28	1	860	G
28	1	861	C
28	1	862	U
28	1	864	G
28	1	865	U
28	1	870	G
28	1	872	U
28	1	874	U
28	1	875	G
28	1	876	A
28	1	878	G
28	1	879	U
28	1	880	G
28	1	881	C
28	1	882	A
28	1	883	A
28	1	884	A
28	1	885	U
28	1	886	C
28	1	893	C
28	1	894	G
28	1	895	A
28	1	896	A
28	1	897	U
28	1	901	G
28	1	902	G
28	1	903	U
28	1	904	A
28	1	905	U
28	1	906	A
28	1	907	G

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Mol	Chain	Res	Type
28	1	908	G
28	1	909	G
28	1	913	A
28	1	914	A
28	1	915	A
28	1	916	G
28	1	917	A
28	1	920	A
28	1	921	A
28	1	922	U
28	1	924	G
28	1	933	A
28	1	934	G
28	1	935	U
28	1	936	A
28	1	937	G
28	1	938	C
28	1	939	U
28	1	940	G
28	1	941	G
28	1	942	U
28	1	943	U
28	1	944	C
28	1	946	U
28	1	947	G
28	1	948	C
28	1	949	C
28	1	951	A
28	1	953	G
28	1	954	U
28	1	958	C
28	1	959	C
28	1	962	A
28	1	963	G
28	1	965	A
28	1	966	U
28	1	967	A
28	1	970	A
28	1	971	G
28	1	974	G
28	1	975	C
28	1	977	C

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Mol	Chain	Res	Type
28	1	979	U
28	1	980	A
28	1	981	U
28	1	984	G
28	1	985	U
28	1	987	U
28	1	991	G
28	1	992	A
28	1	993	G
28	1	994	G
28	1	995	U
28	1	997	A
28	1	999	G
28	1	1000	C
28	1	1001	G
28	1	1002	A
28	1	1003	A
28	1	1006	A
28	1	1007	U
28	1	1008	U
28	1	1010	G
28	1	1014	U
28	1	1016	C
28	1	1018	G
28	1	1020	G
28	1	1023	C
28	1	1024	G
28	1	1025	A
28	1	1029	G
28	1	1031	C
28	1	1034	U
28	1	1035	G
28	1	1038	C
28	1	1043	C
28	1	1047	A
28	1	1049	C
28	1	1057	A
28	1	1058	U
28	1	1063	G
28	1	1064	A
28	1	1066	G
28	1	1067	U

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Mol	Chain	Res	Type
28	1	1069	C
28	1	1071	U
28	1	1072	G
28	1	1073	U
28	1	1075	A
28	1	1076	C
28	1	1081	U
28	1	1082	U
28	1	1085	A
28	1	1087	G
28	1	1089	G
28	1	1090	G
28	1	1093	A
28	1	1094	U
28	1	1096	U
28	1	1097	G
28	1	1098	A
28	1	1099	A
28	1	1100	U
28	1	1101	G
28	1	1104	G
28	1	1105	A
28	1	1110	U
28	1	1111	U
28	1	1112	A
28	1	1113	G
28	1	1114	U
28	1	1115	G
28	1	1117	G
28	1	1118	C
28	1	1119	C
28	1	1120	A
28	1	1124	U
28	1	1127	G
28	1	1128	U
28	1	1129	A
28	1	1131	G
28	1	1133	A
28	1	1134	G
28	1	1138	U
28	1	1140	G
28	1	1141	C

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Mol	Chain	Res	Type
28	1	1142	G
28	1	1143	A
28	1	1144	U
28	1	1145	G
28	1	1146	C
28	1	1147	G
28	1	1148	G
28	1	1150	A
28	1	1151	U
28	1	1152	G
28	1	1153	A
28	1	1154	A
28	1	1155	C
28	1	1156	C
28	1	1157	G
28	1	1161	G
28	1	1162	U
28	1	1163	A
28	1	1164	G
28	1	1165	A
28	1	1166	G
28	1	1167	U
28	1	1168	U
28	1	1170	A
28	1	1171	G
28	1	1173	U
28	1	1174	G
28	1	1175	C
28	1	1176	C
28	1	1177	G
28	1	1178	G
28	1	1180	A
28	1	1181	U
28	1	1182	A
28	1	1183	C
28	1	1184	A
28	1	1188	U
28	1	1189	C
28	1	1190	A
28	1	1192	C
28	1	1196	C
28	1	1197	A

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Mol	Chain	Res	Type
28	1	1199	C
28	1	1200	A
28	1	1203	A
28	1	1204	A
28	1	1205	A
28	1	1206	G
28	1	1207	G
28	1	1208	U
28	1	1211	U
28	1	1217	A
28	1	1219	C
28	1	1220	U
28	1	1221	A
28	1	1225	A
28	1	1226	G
28	1	1227	C
28	1	1228	C
28	1	1229	G
28	1	1231	A
28	1	1232	C
28	1	1233	G
28	1	1234	G
28	1	1236	G
28	1	1238	C
28	1	1240	A
28	1	1241	U
28	1	1242	G
28	1	1243	G
28	1	1244	A
28	1	1245	A
28	1	1247	U
28	1	1248	C
28	1	1249	G
28	1	1250	G
28	1	1253	U
28	1	1254	C
28	1	1257	C
28	1	1258	U
28	1	1259	A
28	1	1260	A
28	1	1261	G
28	1	1262	G

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Mol	Chain	Res	Type
28	1	1263	A
28	1	1264	G
28	1	1265	U
28	1	1266	G
28	1	1268	G
28	1	1269	U
28	1	1271	A
28	1	1272	C
28	1	1274	A
28	1	1277	C
28	1	1279	C
28	1	1280	C
28	1	1282	G
28	1	1283	C
28	1	1284	C
28	1	1295	G
28	1	1300	G
28	1	1301	A
28	1	1304	A
28	1	1305	U
28	1	1306	G
28	1	1307	G
28	1	1308	A
28	1	1309	U
28	1	1310	G
28	1	1311	G
28	1	1312	C
28	1	1313	G
28	1	1315	U
28	1	1316	C
28	1	1317	A
28	1	1318	A
28	1	1319	G
28	1	1323	G
28	1	1324	U
28	1	1325	U
28	1	1326	A
28	1	1327	C
28	1	1328	C
28	1	1330	A
28	1	1331	U
28	1	1332	A

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Mol	Chain	Res	Type
28	1	1334	U
28	1	1335	C
28	1	1336	U
28	1	1339	C
28	1	1341	U
28	1	1342	C
28	1	1343	A
28	1	1348	U
28	1	1349	G
28	1	1350	A
28	1	1351	U
28	1	1352	A
28	1	1353	U
28	1	1354	G
28	1	1355	A
28	1	1357	G
28	1	1364	C
28	1	1366	A
28	1	1367	G
28	1	1368	U
28	1	1369	A
28	1	1370	G
28	1	1371	G
28	1	1372	C
28	1	1373	A
28	1	1374	G
28	1	1375	G
28	1	1376	C
28	1	1377	G
28	1	1378	U
28	1	1379	G
28	1	1380	G
28	1	1381	A
28	1	1386	A
28	1	1387	G
28	1	1389	G
28	1	1390	A
28	1	1391	C
28	1	1392	G
28	1	1393	A
28	1	1394	A
28	1	1395	G

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Mol	Chain	Res	Type
28	1	1396	C
28	1	1399	A
28	1	1400	G
28	1	1401	A
28	1	1402	C
28	1	1405	U
28	1	1406	A
28	1	1407	A
28	1	1408	G
28	1	1409	G
28	1	1410	U
28	1	1411	C
28	1	1412	G
28	1	1413	G
28	1	1414	G
28	1	1416	C
28	1	1418	A
28	1	1419	A
28	1	1420	C
28	1	1423	C
28	1	1426	C
28	1	1427	U
28	1	1428	A
28	1	1429	G
28	1	1430	U
28	1	1431	G
28	1	1432	C
28	1	1433	A
28	1	1435	A
28	1	1436	U
28	1	1437	C
28	1	1440	G
28	1	1441	G
28	1	1442	U
28	1	1444	G
28	1	1445	U
28	1	1446	A
28	1	1447	G
28	1	1448	U
28	1	1449	A
28	1	1450	G
28	1	1453	A

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Mol	Chain	Res	Type
28	1	1454	A
28	1	1455	U
28	1	1456	A
28	1	1457	U
28	1	1458	U
28	1	1464	G
28	1	1465	A
28	1	1466	G
28	1	1467	A
28	1	1468	A
28	1	1469	C
28	1	1470	U
28	1	1476	G
28	1	1480	G
28	1	1481	A
28	1	1482	A
28	1	1483	G
28	1	1484	U
28	1	1485	G
28	1	1486	G
28	1	1494	U
28	1	1497	C
28	1	1498	A
28	1	1499	C
28	1	1500	G
28	1	1502	C
28	1	1504	A
28	1	1506	A
28	1	1507	G
28	1	1508	C
28	1	1509	A
28	1	1510	G
28	1	1511	U
28	1	1512	U
28	1	1514	G
28	1	1516	C
28	1	1517	G
28	1	1520	G
28	1	1521	G
28	1	1522	U
28	1	1523	U
28	1	1524	A

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Mol	Chain	Res	Type
28	1	1525	G
28	1	1526	U
28	1	1528	G
28	1	1529	A
28	1	1530	U
28	1	1531	C
28	1	1532	C
28	1	1533	U
28	1	1534	A
28	1	1535	A
28	1	1536	G
28	1	1541	G
28	1	1542	G
28	1	1543	G
28	1	1544	G
28	1	1546	A
28	1	1547	G
28	1	1548	C
28	1	1551	C
28	1	1553	U
28	1	1554	U
28	1	1556	C
28	1	1557	A
28	1	1558	A
28	1	1559	A
28	1	1560	G
28	1	1562	C
28	1	1563	C
28	1	1564	U
28	1	1565	G
28	1	1566	A
28	1	1569	U
28	1	1570	U
28	1	1571	A
28	1	1574	C
28	1	1575	A
28	1	1577	G
28	1	1578	C
28	1	1580	A
28	1	1581	C
28	1	1582	C
28	1	1584	U

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Mol	Chain	Res	Type
28	1	1585	C
28	1	1586	G
28	1	1587	A
28	1	1588	A
28	1	1589	A
28	1	1590	G
28	1	1591	G
28	1	1592	G
28	1	1593	A
28	1	1595	U
28	1	1596	C
28	1	1597	C
28	1	1598	G
28	1	1600	U
28	1	1601	U
28	1	1603	A
28	1	1604	G
28	1	1605	A
28	1	1607	U
28	1	1608	C
28	1	1609	C
28	1	1610	G
28	1	1611	G
28	1	1619	A
28	1	1620	U
28	1	1627	U
28	1	1628	C
28	1	1629	U
28	1	1631	C
28	1	1632	A
28	1	1635	G
28	1	1640	G
28	1	1641	U
28	1	1642	A
28	1	1643	A
28	1	1644	C
28	1	1645	U
28	1	1646	G
28	1	1651	U
28	1	1655	G
28	1	1656	A
28	1	1657	C

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Mol	Chain	Res	Type
28	1	1659	U
28	1	1660	C
28	1	1661	G
28	1	1663	C
28	1	1664	G
28	1	1665	C
28	1	1666	G
28	1	1667	A
28	1	1669	C
28	1	1670	C
28	1	1672	U
28	1	1675	G
28	1	1676	A
28	1	1679	A
28	1	1680	G
28	1	1681	U
28	1	1682	U
28	1	1683	A
28	1	1688	U
28	1	1689	U
28	1	1693	C
28	1	1694	U
28	1	1696	A
28	1	1698	C
28	1	1699	A
28	1	1702	U
28	1	1703	U
28	1	1709	C
28	1	1713	G
28	1	1714	A
28	1	1715	A
28	1	1716	U
28	1	1719	G
28	1	1720	U
28	1	1721	U
28	1	1722	U
28	1	1724	U
28	1	1725	C
28	1	1726	C
28	1	1727	G
28	1	1728	G
28	1	1729	A

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Mol	Chain	Res	Type
28	1	1730	G
28	1	1731	A
28	1	1733	G
28	1	1734	G
28	1	1737	U
28	1	1738	C
28	1	1740	U
28	1	1746	U
28	1	1748	G
28	1	1749	A
28	1	1750	A
28	1	1751	G
28	1	1752	A
28	1	1753	G
28	1	1754	G
28	1	1757	A
28	1	1760	A
28	1	1761	C
28	1	1762	C
28	1	1764	U
28	1	1765	U
28	1	1772	U
28	1	1773	C
28	1	1777	U
28	1	1778	G
28	1	1780	G
28	1	1781	C
28	1	1785	U
28	1	1786	G
28	1	1787	A
28	1	1788	C
28	1	1790	G
28	1	1793	C
28	1	1794	G
28	1	1795	U
28	1	1797	A
28	1	1798	A
28	1	1799	A
28	1	1801	U
28	1	1807	G
28	1	1808	G
28	1	1809	A

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Mol	Chain	Res	Type
28	1	1813	A
28	1	1814	A
28	1	1819	U
28	1	1821	U
28	1	1822	C
28	1	1830	G
28	1	1832	C
28	1	1833	G
28	1	1835	A
28	1	1836	C
28	1	1838	G
28	1	1839	A
28	1	1840	U
28	1	1842	A
28	1	1843	C
28	1	1844	C
28	1	1846	C
28	1	1848	G
28	1	1849	C
28	1	1850	A
28	1	1851	G
28	1	1852	G
28	1	1853	U
28	1	1856	C
28	1	1857	C
28	1	1858	A
28	1	1859	A
28	1	1863	G
28	1	1864	A
28	1	1866	C
28	1	1867	A
28	1	1869	C
28	1	1871	U
28	1	1872	C
28	1	1873	U
28	1	1874	A
28	1	1875	G
28	1	1876	U
28	1	1877	U
28	1	1879	A
28	1	1880	U
28	1	1882	G

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Mol	Chain	Res	Type
28	1	1883	A
28	1	1884	A
28	1	1886	A
28	1	1887	A
28	1	1888	U
28	1	1894	U
28	1	1897	G
28	1	1900	A
28	1	1901	A
28	1	1902	G
28	1	1903	U
28	1	1905	G
28	1	1906	G
28	1	1908	A
28	1	1909	A
28	1	1910	A
28	1	1911	A
28	1	1912	U
28	1	1913	A
28	1	1914	G
28	1	1915	A
28	1	1920	U
28	1	1922	A
28	1	1924	U
28	1	1927	G
28	1	1932	A
28	1	1938	U
28	1	1939	G
28	1	1940	G
28	1	1941	C
28	1	1942	U
28	1	1946	A
28	1	1947	G
28	1	1948	G
28	1	1950	U
28	1	1951	C
28	1	1952	G
28	1	1953	G
28	1	1954	G
28	1	1955	U
28	1	2095	G
28	1	2098	C

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Mol	Chain	Res	Type
28	1	2100	A
28	1	2101	C
28	1	2103	U
28	1	2104	A
28	1	2105	G
28	1	2110	G
28	1	2111	G
28	1	2112	U
28	1	2114	C
28	1	2115	G
28	1	2116	G
28	1	2117	A
28	1	2118	C
28	1	2119	A
28	1	2120	A
28	1	2121	G
28	1	2122	G
28	1	2126	A
28	1	2127	U
28	1	2129	U
28	1	2131	A
28	1	2132	C
28	1	2133	U
28	1	2134	G
28	1	2136	C
28	1	2137	U
28	1	2138	A
28	1	2139	A
28	1	2140	U
28	1	2141	U
28	1	2142	A
28	1	2143	A
28	1	2144	A
28	1	2145	A
28	1	2146	C
28	1	2147	A
28	1	2152	A
28	1	2154	U
28	1	2155	G
28	1	2156	C
28	1	2157	G
28	1	2159	U

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Mol	Chain	Res	Type
28	1	2160	G
28	1	2163	C
28	1	2165	G
28	1	2167	A
28	1	2170	U
28	1	2173	U
28	1	2174	G
28	1	2175	U
28	1	2176	U
28	1	2177	G
28	1	2178	A
28	1	2179	C
28	1	2188	A
28	1	2192	C
28	1	2194	G
28	1	2197	C
28	1	2198	A
28	1	2201	G
28	1	2202	C
28	1	2203	U
28	1	2204	C
28	1	2205	U
28	1	2206	G
28	1	2208	A
28	1	2209	U
28	1	2210	G
28	1	2213	A
28	1	2214	A
28	1	2215	A
28	1	2218	G
28	1	2220	A
28	1	2224	A
28	1	2225	U
28	1	2226	U
28	1	2229	A
28	1	2230	C
28	1	2231	C
28	1	2234	G
28	1	2242	A
28	1	2243	A
28	1	2244	A
28	1	2246	G

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Mol	Chain	Res	Type
28	1	2248	C
28	1	2249	G
28	1	2254	U
28	1	2255	A
28	1	2261	G
28	1	2262	A
28	1	2263	C
28	1	2269	U
28	1	2270	A
28	1	2271	A
28	1	2273	G
28	1	2274	U
28	1	2276	G
28	1	2278	C
28	1	2280	A
28	1	2282	U
28	1	2283	G
28	1	2288	G
28	1	2289	U
28	1	2290	C
28	1	2291	A
28	1	2292	U
28	1	2293	C
28	1	2294	U
28	1	2296	A
28	1	2297	U
28	1	2299	A
28	1	2302	G
28	1	2303	A
28	1	2304	C
28	1	2305	G
28	1	2306	C
28	1	2307	G
28	1	2311	G
28	1	2314	U
28	1	2315	G
28	1	2324	A
28	1	2325	G
28	1	2326	A
28	1	2328	U
28	1	2336	U
28	1	2340	U

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Mol	Chain	Res	Type
28	1	2342	U
28	1	2348	A
28	1	2349	U
28	1	2352	A
28	1	2354	C
28	1	2355	G
28	1	2356	A
28	1	2357	A
28	1	2358	A
28	1	2359	C
28	1	2360	C
28	1	2361	A
28	1	2362	C
28	1	2363	A
28	1	2364	G
28	1	2365	C
28	1	2370	G
28	1	2371	G
28	1	2372	A
28	1	2373	A
28	1	2374	C
28	1	2375	G
28	1	2378	C
28	1	2379	U
28	1	2383	C
28	1	2385	G
28	1	2386	A
28	1	2387	A
28	1	2389	C
28	1	2390	A
28	1	2391	G
28	1	2392	C
28	1	2394	G
28	1	2396	G
28	1	2397	A
28	1	2398	A
28	1	2399	A
28	1	2400	G
28	1	2401	A
28	1	2402	A
28	1	2403	G
28	1	2404	A

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Mol	Chain	Res	Type
28	1	2406	C
28	1	2409	G
28	1	2410	U
28	1	2415	C
28	1	2416	U
28	1	2417	U
28	1	2419	A
28	1	2420	C
28	1	2423	U
28	1	2425	G
28	1	2427	U
28	1	2429	G
28	1	2432	A
28	1	2433	U
28	1	2434	U
28	1	2435	G
28	1	2436	U
28	1	2440	G
28	1	2441	A
28	1	2442	G
28	1	2446	U
28	1	2447	A
28	1	2450	G
28	1	2452	G
28	1	2455	U
28	1	2458	A
28	1	2459	A
28	1	2460	U
28	1	2462	A
28	1	2463	G
28	1	2464	U
28	1	2468	A
28	1	2469	G
28	1	2470	C
28	1	2471	U
28	1	2473	C
28	1	2477	G
28	1	2479	C
28	1	2480	A
28	1	2481	G
28	1	2482	U
28	1	2485	A

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Mol	Chain	Res	Type
28	1	2487	U
28	1	2490	C
28	1	2491	A
28	1	2492	C
28	1	2493	U
28	1	2494	A
28	1	2496	C
28	1	2498	U
28	1	2499	U
28	1	2500	A
28	1	2501	U
28	1	2503	G
28	1	2504	U
28	1	2505	U
28	1	2506	U
28	1	2508	U
28	1	2509	U
28	1	2511	A
28	1	2513	U
28	1	2514	U
28	1	2515	A
28	1	2516	U
28	1	2517	U
28	1	2518	C
28	1	2521	U
28	1	2523	A
28	1	2525	G
28	1	2526	C
28	1	2530	G
28	1	2531	C
28	1	2532	U
28	1	2534	G
28	1	2536	A
28	1	2537	U
28	1	2539	C
28	1	2540	A
28	1	2542	U
28	1	2543	U
28	1	2544	U
28	1	2545	C
28	1	2546	C
28	1	2547	A

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Mol	Chain	Res	Type
28	1	2549	G
28	1	2550	U
28	1	2551	U
28	1	2553	U
28	1	2554	A
28	1	2555	G
28	1	2557	A
28	1	2558	U
28	1	2560	C
28	1	2562	A
28	1	2565	U
28	1	2569	A
28	1	2570	U
28	1	2571	U
28	1	2572	C
28	1	2580	A
28	1	2581	U
28	1	2582	C
28	1	2583	C
28	1	2585	G
28	1	2586	G
28	1	2587	U
28	1	2588	U
28	1	2589	G
28	1	2591	A
28	1	2592	G
28	1	2593	A
28	1	2594	C
28	1	2597	U
28	1	2598	G
28	1	2599	U
28	1	2600	C
28	1	2601	A
28	1	2603	G
28	1	2604	U
28	1	2605	G
28	1	2606	G
28	1	2607	G
28	1	2608	G
28	1	2610	G
28	1	2611	U
28	1	2614	G

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Mol	Chain	Res	Type
28	1	2615	G
28	1	2617	U
28	1	2618	G
28	1	2619	G
28	1	2620	G
28	1	2622	C
28	1	2627	C
28	1	2628	A
28	1	2629	U
28	1	2632	G
28	1	2634	U
28	1	2635	A
28	1	2636	A
28	1	2637	A
28	1	2642	A
28	1	2644	C
28	1	2645	G
28	1	2647	A
28	1	2648	G
28	1	2649	A
28	1	2650	U
28	1	2651	G
28	1	2652	U
28	1	2653	C
28	1	2655	U
28	1	2656	A
28	1	2658	G
28	1	2667	A
28	1	2668	U
28	1	2674	A
28	1	2675	C
28	1	2676	A
28	1	2677	G
28	1	2678	A
28	1	2679	A
28	1	2682	C
28	1	2686	A
28	1	2688	U
28	1	2689	A
28	1	2690	G
28	1	2692	A
28	1	2694	A

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Mol	Chain	Res	Type
28	1	2696	A
28	1	2697	A
28	1	2698	G
28	1	2699	G
28	1	2700	G
28	1	2702	A
28	1	2703	A
28	1	2704	A
28	1	2713	U
28	1	2715	A
28	1	2716	U
28	1	2717	U
28	1	2720	G
28	1	2722	U
28	1	2723	U
28	1	2726	C
28	1	2728	G
28	1	2729	U
28	1	2731	U
28	1	2735	U
28	1	2736	A
28	1	2737	C
28	1	2741	C
28	1	2742	C
28	1	2747	A
28	1	2748	A
28	1	2749	G
28	1	2750	U
28	1	2753	G
28	1	2755	C
28	1	2756	C
28	1	2757	U
28	1	2760	C
28	1	2762	A
28	1	2763	U
28	1	2764	C
28	1	2765	C
28	1	2766	U
28	1	2767	U
28	1	2768	U
28	1	2772	C
28	1	2773	C

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Mol	Chain	Res	Type
28	1	2774	C
28	1	2775	U
28	1	2776	C
28	1	2778	G
28	1	2779	A
28	1	2781	U
28	1	2783	U
28	1	2784	G
28	1	2785	A
28	1	2786	G
28	1	2787	G
28	1	2788	C
28	1	2794	G
28	1	2795	U
28	1	2796	G
28	1	2798	C
28	1	2799	A
28	1	2800	G
28	1	2801	A
28	1	2802	A
28	1	2803	A
28	1	2805	G
28	1	2806	U
28	1	2807	U
28	1	2808	A
28	1	2809	C
28	1	2810	C
28	1	2811	A
28	1	2813	A
28	1	2814	G
28	1	2815	G
28	1	2816	G
28	1	2817	A
28	1	2819	A
28	1	2820	A
28	1	2821	C
28	1	2823	G
28	1	2824	G
28	1	2826	U
28	1	2827	U
28	1	2833	A
28	1	2835	U

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Mol	Chain	Res	Type
28	1	2837	A
28	1	2838	A
28	1	2844	C
28	1	2845	A
28	1	2846	U
28	1	2847	A
28	1	2850	G
28	1	2855	U
28	1	2856	G
28	1	2860	U
28	1	2863	G
28	1	2865	U
28	1	2866	U
28	1	2867	C
28	1	2868	U
28	1	2869	U
28	1	2870	C
28	1	2871	G
28	1	2874	G
28	1	2875	U
28	1	2877	G
28	1	2878	G
28	1	2879	C
28	1	2880	U
28	1	2881	C
28	1	2882	U
28	1	2883	U
28	1	2887	A
28	1	2893	C
28	1	2894	C
28	1	2895	G
28	1	2896	A
28	1	2898	G
28	1	2899	C
28	1	2900	A
28	1	2901	G
28	1	2902	A
28	1	2903	A
28	1	2905	U
28	1	2906	C
28	1	2908	G
28	1	2909	U

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Mol	Chain	Res	Type
28	1	2910	A
28	1	2911	A
28	1	2913	C
28	1	2916	U
28	1	2919	A
28	1	2920	U
28	1	2923	U
28	1	2924	U
28	1	2926	A
28	1	2928	C
28	1	2929	C
28	1	2930	A
28	1	2931	C
28	1	2932	U
28	1	2933	A
28	1	2935	U
28	1	2936	A
28	1	2941	A
28	1	2942	C
28	1	2943	G
28	1	2944	U
28	1	2945	G
28	1	2946	A
28	1	2947	G
28	1	2950	G
28	1	2951	G
28	1	2952	G
28	1	2953	U
28	1	2959	C
28	1	2960	C
28	1	2964	G
28	1	2965	U
28	1	2966	G
28	1	2968	G
28	1	2971	A
28	1	2972	G
28	1	2973	G
28	1	2974	U
28	1	2975	U
28	1	2976	A
28	1	2977	G
28	1	2978	U

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Mol	Chain	Res	Type
28	1	2979	U
28	1	2982	A
28	1	2983	C
28	1	2984	C
28	1	2990	G
28	1	2993	G
28	1	2997	G
28	1	3005	A
28	1	3006	A
28	1	3007	U
28	1	3010	U
28	1	3011	A
28	1	3012	A
28	1	3018	C
28	1	3019	U
28	1	3021	A
28	1	3022	G
28	1	3023	U
28	1	3024	A
28	1	3025	C
28	1	3026	G
28	1	3027	A
28	1	3028	G
28	1	3029	A
28	1	3032	A
28	1	3034	C
28	1	3035	A
28	1	3036	G
28	1	3040	A
28	1	3043	C
28	1	3044	G
28	1	3045	G
28	1	3047	U
28	1	3049	A
28	1	3051	U
28	1	3052	G
28	1	3053	G
28	1	3055	U
28	1	3056	U
28	1	3057	U
28	1	3058	U
28	1	3059	G

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Mol	Chain	Res	Type
28	1	3062	G
28	1	3064	U
28	1	3065	G
28	1	3067	C
28	1	3070	A
28	1	3071	U
28	1	3073	A
28	1	3074	G
28	1	3075	G
28	1	3076	C
28	1	3077	A
28	1	3078	U
28	1	3080	G
28	1	3081	C
28	1	3087	A
28	1	3088	G
28	1	3090	U
28	1	3092	C
28	1	3093	C
28	1	3099	C
28	1	3100	U
28	1	3101	G
28	1	3102	G
28	1	3103	A
28	1	3105	U
28	1	3106	A
28	1	3107	U
28	1	3112	G
28	1	3114	A
28	1	3115	C
28	1	3118	C
28	1	3120	C
28	1	3122	A
28	1	3125	U
28	1	3126	C
28	1	3130	A
28	1	3131	U
28	1	3132	C
28	1	3133	C
28	1	3137	C
28	1	3138	U
28	1	3139	A

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Mol	Chain	Res	Type
28	1	3142	A
28	1	3143	C
28	1	3144	G
28	1	3151	U
28	1	3152	U
28	1	3153	U
28	1	3154	C
28	1	3155	U
28	1	3156	U
28	1	3157	U
28	1	3169	U
28	1	3170	A
28	1	3171	U
28	1	3172	A
28	1	3173	G
28	1	3174	A
28	1	3176	G
28	1	3179	U
28	1	3180	A
28	1	3181	C
28	1	3182	G
28	1	3185	U
28	1	3186	A
28	1	3187	A
28	1	3196	U
28	1	3198	U
28	1	3199	G
28	1	3206	C
28	1	3207	U
28	1	3209	A
28	1	3211	C
28	1	3212	C
28	1	3213	A
28	1	3216	G
28	1	3217	C
28	1	3218	A
28	1	3219	G
28	1	3220	G
28	1	3224	G
28	1	3226	A
28	1	3228	C
28	1	3229	G

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Mol	Chain	Res	Type
28	1	3230	G
28	1	3234	A
28	1	3235	C
28	1	3236	U
28	1	3237	U
28	1	3238	G
28	1	3242	G
28	1	3251	U
28	1	3252	G
28	1	3255	U
28	1	3256	G
28	1	3258	U
28	1	3259	U
28	1	3260	G
28	1	3261	C
28	1	3262	U
28	1	3265	C
28	1	3267	A
28	1	3270	U
28	1	3271	G
28	1	3273	A
28	1	3275	U
28	1	3277	U
28	1	3278	C
28	1	3279	A
28	1	3281	U
28	1	3289	G
28	1	3290	G
28	1	3292	A
28	1	3293	U
28	1	3294	A
28	1	3298	C
28	1	3299	A
28	1	3301	U
28	1	3303	G
28	1	3304	U
28	1	3305	A
28	1	3306	U
28	1	3307	A
28	1	3308	C
28	1	3309	G
28	1	3310	A

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Mol	Chain	Res	Type
28	1	3311	C
28	1	3312	U
28	1	3313	U
28	1	3316	A
28	1	3317	U
28	1	3318	G
28	1	3319	U
28	1	3320	A
28	1	3326	G
28	1	3331	U
28	1	3332	U
28	1	3333	G
28	1	3335	A
28	1	3336	A
28	1	3337	G
28	1	3339	A
28	1	3341	U
28	1	3342	A
28	1	3343	G
28	1	3345	G
28	1	3346	U
28	1	3348	G
28	1	3350	C
28	1	3351	U
28	1	3352	U
28	1	3353	G
28	1	3354	U
28	1	3355	U
28	1	3358	U
28	1	3359	A
28	1	3360	C
28	1	3361	G
28	1	3362	A
28	1	3368	U
28	1	3369	G
28	1	3370	A
28	1	3371	G
28	1	3372	A
28	1	3374	U
28	1	3375	A
28	1	3376	A
28	1	3377	G

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Mol	Chain	Res	Type
28	1	3379	C
28	1	3380	U
28	1	3381	U
28	1	3382	U
28	1	3385	U
28	1	3389	U
28	1	3390	G
28	1	3391	A
28	1	3393	U
28	1	3394	U
28	1	3396	U
29	3	6	C
29	3	7	G
29	3	10	C
29	3	11	A
29	3	12	U
29	3	15	C
29	3	20	A
29	3	22	A
29	3	23	A
29	3	24	A
29	3	25	G
29	3	26	C
29	3	28	C
29	3	29	C
29	3	31	U
29	3	33	C
29	3	36	C
29	3	37	G
29	3	42	A
29	3	44	C
29	3	45	A
29	3	47	C
29	3	48	U
29	3	49	G
29	3	52	G
29	3	53	U
29	3	54	U
29	3	62	U
29	3	64	A
29	3	65	G
29	3	68	C

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Mol	Chain	Res	Type
29	3	73	C
29	3	74	C
29	3	75	G
29	3	77	G
29	3	78	U
29	3	80	G
29	3	83	U
29	3	85	G
29	3	86	U
29	3	87	G
29	3	91	G
29	3	93	C
29	3	97	A
29	3	98	C
29	3	104	A
29	3	105	C
29	3	112	G
29	3	121	U
30	4	3	A
30	4	4	C
30	4	6	U
30	4	8	C
30	4	9	A
30	4	10	A
30	4	14	C
30	4	15	G
30	4	18	U
30	4	19	C
30	4	20	U
30	4	21	C
30	4	22	U
30	4	23	U
30	4	24	G
30	4	25	G
30	4	26	U
30	4	28	C
30	4	31	G
30	4	33	A
30	4	34	U
30	4	35	C
30	4	37	A
30	4	38	U

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Mol	Chain	Res	Type
30	4	39	G
30	4	40	A
30	4	41	A
30	4	42	G
30	4	43	A
30	4	44	A
30	4	45	C
30	4	46	G
30	4	51	G
30	4	52	A
30	4	53	A
30	4	54	A
30	4	56	G
30	4	58	G
30	4	59	A
30	4	61	A
30	4	62	C
30	4	63	G
30	4	70	G
30	4	74	U
30	4	75	G
30	4	79	A
30	4	80	A
30	4	81	U
30	4	84	C
30	4	85	G
30	4	86	U
30	4	87	G
30	4	88	A
30	4	91	C
30	4	93	U
30	4	94	C
30	4	96	A
30	4	99	C
30	4	104	A
30	4	105	A
30	4	106	C
30	4	107	G
30	4	108	C
30	4	109	A
30	4	110	C
30	4	111	A

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Mol	Chain	Res	Type
30	4	112	U
30	4	113	U
30	4	114	G
30	4	125	U
30	4	126	A
30	4	128	U
30	4	133	G
30	4	134	G
30	4	137	C
30	4	138	A
30	4	139	U
30	4	140	G
30	4	147	U
30	4	151	C
30	4	152	G
30	4	153	U
30	4	155	A
30	4	156	U
30	4	157	U
30	4	158	U
49	2	2	A
49	2	4	C
49	2	5	U
49	2	17	C
49	2	25	C
49	2	26	A
49	2	27	U
49	2	34	G
49	2	37	U
49	2	42	G
49	2	43	A
49	2	45	U
49	2	47	A
49	2	57	G
49	2	58	U
49	2	59	C
49	2	61	A
49	2	62	A
49	2	63	G
49	2	64	U
49	2	65	A
49	2	66	U

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Mol	Chain	Res	Type
49	2	67	A
49	2	69	G
49	2	70	C
49	2	71	A
49	2	73	U
49	2	75	U
49	2	76	A
49	2	77	U
49	2	78	A
49	2	79	C
49	2	80	A
49	2	81	G
49	2	83	G
49	2	84	A
49	2	85	A
49	2	88	U
49	2	89	G
49	2	90	C
49	2	91	G
49	2	92	A
49	2	93	A
49	2	94	U
49	2	100	A
49	2	104	A
49	2	114	C
49	2	115	G
49	2	116	U
49	2	119	A
49	2	120	U
49	2	121	U
49	2	124	A
49	2	126	A
49	2	127	G
49	2	128	U
49	2	130	C
49	2	131	C
49	2	132	U
49	2	135	A
49	2	136	C
49	2	137	U
49	2	138	A
49	2	139	C

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Mol	Chain	Res	Type
49	2	141	U
49	2	145	A
49	2	146	U
49	2	149	C
49	2	150	U
49	2	151	G
49	2	157	A
49	2	160	C
49	2	164	A
49	2	165	G
49	2	177	U
49	2	178	U
49	2	181	A
49	2	186	C
49	2	188	A
49	2	189	C
49	2	190	C
49	2	191	C
49	2	192	U
49	2	193	U
49	2	194	U
49	2	195	G
49	2	196	G
49	2	200	A
49	2	204	G
49	2	205	U
49	2	206	A
49	2	208	U
49	2	210	A
49	2	212	U
49	2	215	A
49	2	216	U
49	2	217	A
49	2	219	A
49	2	221	A
49	2	222	A
49	2	223	U
49	2	224	C
49	2	227	U
49	2	228	G
49	2	230	C
49	2	231	U

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Mol	Chain	Res	Type
49	2	232	U
49	2	233	C
49	2	234	G
49	2	235	G
49	2	237	C
49	2	238	U
49	2	239	C
49	2	240	U
49	2	241	U
49	2	242	U
49	2	245	U
49	2	249	U
49	2	250	C
49	2	252	U
49	2	255	U
49	2	256	A
49	2	259	U
49	2	260	U
49	2	261	U
49	2	262	U
49	2	266	A
49	2	269	G
49	2	270	C
49	2	271	A
49	2	272	U
49	2	276	C
49	2	278	U
49	2	280	U
49	2	282	C
49	2	284	G
49	2	288	A
49	2	298	C
49	2	299	A
49	2	313	U
49	2	316	A
49	2	321	C
49	2	322	G
49	2	323	A
49	2	333	A
49	2	337	G
49	2	338	C
49	2	341	A

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Mol	Chain	Res	Type
49	2	345	U
49	2	346	G
49	2	351	C
49	2	352	A
49	2	359	A
49	2	361	C
49	2	376	C
49	2	378	A
49	2	381	C
49	2	389	G
49	2	390	G
49	2	392	G
49	2	393	C
49	2	396	G
49	2	397	A
49	2	398	G
49	2	399	A
49	2	400	A
49	2	402	C
49	2	404	G
49	2	405	C
49	2	406	U
49	2	407	A
49	2	408	C
49	2	409	C
49	2	415	C
49	2	416	A
49	2	417	A
49	2	418	G
49	2	419	G
49	2	421	A
49	2	422	G
49	2	426	G
49	2	434	G
49	2	435	C
49	2	436	A
49	2	437	A
49	2	439	U
49	2	440	U
49	2	444	C
49	2	451	A
49	2	452	A

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Mol	Chain	Res	Type
49	2	453	U
49	2	454	U
49	2	455	C
49	2	456	A
49	2	458	G
49	2	461	G
49	2	467	G
49	2	468	A
49	2	469	C
49	2	475	A
49	2	483	A
49	2	492	A
49	2	493	U
49	2	494	U
49	2	496	G
49	2	497	G
49	2	502	U
49	2	506	A
49	2	507	U
49	2	509	G
49	2	511	A
49	2	512	A
49	2	513	U
49	2	515	A
49	2	520	A
49	2	523	G
49	2	525	A
49	2	526	A
49	2	527	A
49	2	536	C
49	2	539	G
49	2	540	G
49	2	541	A
49	2	542	A
49	2	545	A
49	2	551	G
49	2	554	C
49	2	555	A
49	2	557	G
49	2	558	U
49	2	565	C
49	2	568	G

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Mol	Chain	Res	Type
49	2	579	A
49	2	580	A
49	2	582	U
49	2	583	C
49	2	585	A
49	2	586	G
49	2	594	A
49	2	600	U
49	2	606	A
49	2	608	U
49	2	613	G
49	2	614	C
49	2	619	A
49	2	620	A
49	2	621	A
49	2	622	A
49	2	623	A
49	2	624	G
49	2	639	U
49	2	641	G
49	2	651	G
49	2	654	C
49	2	655	G
49	2	656	G
49	2	657	U
49	2	658	C
49	2	677	G
49	2	678	A
49	2	679	U
49	2	680	U
49	2	682	C
49	2	684	A
49	2	686	C
49	2	695	U
49	2	696	C
49	2	698	U
49	2	699	U
49	2	702	G
49	2	705	U
49	2	706	A
49	2	707	A
49	2	708	C

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Mol	Chain	Res	Type
49	2	709	C
49	2	711	U
49	2	713	A
49	2	716	C
49	2	717	C
49	2	718	U
49	2	719	U
49	2	721	U
49	2	722	G
49	2	728	U
49	2	729	G
49	2	730	G
49	2	731	C
49	2	732	G
49	2	733	A
49	2	734	A
49	2	735	C
49	2	738	G
49	2	740	A
49	2	741	C
49	2	742	U
49	2	743	U
49	2	744	U
49	2	752	A
49	2	753	A
49	2	755	A
49	2	757	A
49	2	758	U
49	2	759	U
49	2	765	G
49	2	766	U
49	2	771	A
49	2	773	C
49	2	774	A
49	2	778	G
49	2	779	U
49	2	780	A
49	2	783	G
49	2	784	C
49	2	789	A
49	2	794	U
49	2	799	A

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Mol	Chain	Res	Type
49	2	802	G
49	2	803	A
49	2	804	A
49	2	806	A
49	2	807	A
49	2	810	G
49	2	811	A
49	2	812	A
49	2	813	U
49	2	814	A
49	2	815	G
49	2	820	U
49	2	821	U
49	2	829	A
49	2	831	U
49	2	832	U
49	2	833	U
49	2	834	G
49	2	836	U
49	2	840	U
49	2	841	U
49	2	843	U
49	2	845	G
49	2	847	A
49	2	848	C
49	2	850	A
49	2	851	U
49	2	852	C
49	2	853	G
49	2	855	A
49	2	857	U
49	2	862	A
49	2	863	A
49	2	864	U
49	2	865	A
49	2	884	A
49	2	894	U
49	2	895	G
49	2	897	C
49	2	898	A
49	2	903	U
49	2	912	U

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Mol	Chain	Res	Type
49	2	914	G
49	2	917	U
49	2	919	A
49	2	921	U
49	2	925	G
49	2	926	A
49	2	929	A
49	2	931	C
49	2	932	U
49	2	933	A
49	2	935	U
49	2	944	A
49	2	951	A
49	2	960	U
49	2	966	A
49	2	970	A
49	2	973	A
49	2	976	G
49	2	988	A
49	2	992	A
49	2	993	A
49	2	1001	A
49	2	1004	U
49	2	1005	A
49	2	1016	C
49	2	1021	C
49	2	1025	A
49	2	1026	A
49	2	1028	C
49	2	1029	U
49	2	1031	U
49	2	1032	G
49	2	1039	A
49	2	1052	U
49	2	1053	G
49	2	1055	U
49	2	1056	U
49	2	1064	G
49	2	1076	A
49	2	1081	A
49	2	1091	A
49	2	1092	A

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Mol	Chain	Res	Type
49	2	1097	U
49	2	1098	U
49	2	1099	U
49	2	1100	G
49	2	1101	G
49	2	1113	A
49	2	1118	G
49	2	1124	A
49	2	1126	G
49	2	1131	A
49	2	1132	A
49	2	1135	U
49	2	1137	A
49	2	1138	A
49	2	1139	A
49	2	1150	G
49	2	1158	C
49	2	1159	C
49	2	1162	C
49	2	1163	A
49	2	1164	G
49	2	1165	G
49	2	1166	A
49	2	1167	G
49	2	1174	C
49	2	1182	U
49	2	1183	A
49	2	1184	A
49	2	1185	U
49	2	1190	C
49	2	1191	U
49	2	1192	C
49	2	1193	A
49	2	1194	A
49	2	1199	G
49	2	1200	G
49	2	1202	A
49	2	1203	A
49	2	1205	C
49	2	1206	U
49	2	1207	C
49	2	1212	G

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Mol	Chain	Res	Type
49	2	1213	G
49	2	1214	U
49	2	1215	C
49	2	1217	A
49	2	1219	A
49	2	1221	A
49	2	1222	C
49	2	1259	U
49	2	1262	U
49	2	1268	G
49	2	1269	U
49	2	1274	C
49	2	1275	A
49	2	1276	U
49	2	1278	G
49	2	1284	C
49	2	1285	U
49	2	1288	G
49	2	1298	U
49	2	1299	G
49	2	1301	U
49	2	1307	U
49	2	1308	G
49	2	1309	C
49	2	1313	A
49	2	1314	U
49	2	1315	U
49	2	1321	A
49	2	1336	A
49	2	1338	C
49	2	1339	C
49	2	1340	U
49	2	1341	A
49	2	1342	C
49	2	1343	U
49	2	1344	A
49	2	1345	A
49	2	1346	A
49	2	1347	U
49	2	1348	A
49	2	1349	G
49	2	1351	G

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Mol	Chain	Res	Type
49	2	1352	G
49	2	1353	U
49	2	1356	U
49	2	1357	A
49	2	1358	G
49	2	1359	C
49	2	1360	A
49	2	1361	U
49	2	1362	U
49	2	1363	U
49	2	1366	U
49	2	1367	G
49	2	1371	A
49	2	1372	U
49	2	1374	C
49	2	1376	C
49	2	1377	U
49	2	1378	U
49	2	1380	U
49	2	1382	A
49	2	1383	G
49	2	1384	A
49	2	1387	G
49	2	1388	A
49	2	1389	C
49	2	1390	U
49	2	1391	A
49	2	1392	U
49	2	1397	U
49	2	1398	U
49	2	1399	C
49	2	1400	A
49	2	1401	A
49	2	1404	C
49	2	1407	U
49	2	1410	A
49	2	1412	G
49	2	1413	U
49	2	1414	U
49	2	1415	U
49	2	1427	A
49	2	1428	G

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Mol	Chain	Res	Type
49	2	1432	U
49	2	1433	G
49	2	1434	U
49	2	1441	C
49	2	1445	G
49	2	1446	A
49	2	1447	C
49	2	1457	C
49	2	1458	G
49	2	1460	A
49	2	1467	C
49	2	1471	A
49	2	1472	C
49	2	1473	U
49	2	1474	G
49	2	1479	A
49	2	1481	C
49	2	1482	C
49	2	1485	C
49	2	1489	U
49	2	1490	C
49	2	1492	A
49	2	1493	A
49	2	1494	C
49	2	1496	U
49	2	1498	G
49	2	1501	C
49	2	1503	A
49	2	1504	G
49	2	1507	G
49	2	1509	C
49	2	1511	U
49	2	1512	G
49	2	1514	U
49	2	1515	A
49	2	1516	A
49	2	1518	C
49	2	1520	U
49	2	1521	G
49	2	1522	U
49	2	1523	G
49	2	1524	A

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Mol	Chain	Res	Type
49	2	1527	C
49	2	1530	C
49	2	1531	G
49	2	1533	C
49	2	1534	G
49	2	1535	U
49	2	1536	G
49	2	1537	C
49	2	1538	U
49	2	1539	G
49	2	1540	G
49	2	1541	G
49	2	1542	G
49	2	1550	A
49	2	1557	U
49	2	1559	A
49	2	1561	U
49	2	1569	A
49	2	1575	G
49	2	1582	U
49	2	1583	A
49	2	1584	G
49	2	1587	A
49	2	1590	G
49	2	1596	C
49	2	1600	A
49	2	1611	A
49	2	1612	U
49	2	1613	U
49	2	1615	C
49	2	1616	G
49	2	1618	C
49	2	1619	C
49	2	1620	C
49	2	1622	G
49	2	1631	A
49	2	1634	C
49	2	1635	A
49	2	1636	C
49	2	1637	C
49	2	1638	G
49	2	1651	A

Continued on next page...

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Mol	Chain	Res	Type
49	2	1656	U
49	2	1657	U
49	2	1658	G
49	2	1664	C
49	2	1670	G
49	2	1672	G
49	2	1673	G
49	2	1677	C
49	2	1678	A
49	2	1679	G
49	2	1680	G
49	2	1682	U
49	2	1683	C
49	2	1685	G
49	2	1689	A
49	2	1693	A
49	2	1694	A
49	2	1695	G
49	2	1697	G
49	2	1698	G
49	2	1699	G
49	2	1700	C
49	2	1703	C
49	2	1704	U
49	2	1705	C
49	2	1706	C
49	2	1707	A
49	2	1708	U
49	2	1710	U
49	2	1711	C
49	2	1712	A
49	2	1713	G
49	2	1714	A
49	2	1715	G
49	2	1716	C
49	2	1717	G
49	2	1719	A
49	2	1720	G
49	2	1721	A
49	2	1722	A
49	2	1723	U
49	2	1725	U

Continued on next page...

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Mol	Chain	Res	Type
49	2	1730	A
49	2	1731	A
49	2	1745	G
49	2	1746	A
49	2	1747	G
49	2	1755	A
49	2	1757	G
49	2	1758	U
49	2	1759	C
49	2	1763	A
49	2	1766	A
49	2	1768	G
49	2	1769	U
49	2	1770	U
49	2	1779	U
49	2	1780	G
49	2	1782	A
49	2	1783	C
49	2	1792	G
49	2	1794	A
49	2	1795	U
49	2	1796	C
49	2	1797	A
79	AX	2	C
79	AX	3	G
79	AX	4	G
79	AX	5	A
79	AX	7	U
79	AX	8	U
79	AX	9	A
79	AX	11	C
79	AX	12	U
79	AX	13	C
79	AX	16	U
79	AX	17	U
79	AX	18	G
79	AX	19	G
79	AX	20	G
79	AX	21	A
79	AX	25	C
79	AX	28	C
79	AX	29	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
79	AX	30	G
79	AX	32	C
79	AX	33	U
79	AX	34	G
79	AX	35	A
79	AX	36	A
79	AX	38	A
79	AX	39	U
79	AX	41	U
79	AX	42	G
79	AX	43	G
79	AX	44	A
79	AX	45	G
79	AX	46	G
79	AX	47	U
79	AX	48	C
79	AX	51	G
79	AX	54	U
79	AX	55	U
79	AX	56	C
79	AX	57	G
79	AX	59	U
79	AX	60	C
79	AX	61	C
79	AX	62	A
79	AX	64	A
79	AX	66	A
79	AX	68	U
79	AX	69	U
79	AX	70	C
79	AX	71	G
79	AX	74	C
80	AY	44	A
80	AY	45	A
80	AY	46	U
80	AY	48	U
80	AY	49	U
80	AY	50	U
79	AZ	2	C
79	AZ	4	G
79	AZ	5	A
79	AZ	7	U

Continued on next page...

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Mol	Chain	Res	Type
79	AZ	8	U
79	AZ	9	A
79	AZ	12	U
79	AZ	13	C
79	AZ	16	U
79	AZ	17	U
79	AZ	18	G
79	AZ	19	G
79	AZ	20	G
79	AZ	21	A
79	AZ	25	C
79	AZ	27	C
79	AZ	28	C
79	AZ	32	C
79	AZ	34	G
79	AZ	35	A
79	AZ	36	A
79	AZ	38	A
79	AZ	39	U
79	AZ	41	U
79	AZ	44	A
79	AZ	45	G
79	AZ	46	G
79	AZ	47	U
79	AZ	48	C
79	AZ	54	U
79	AZ	55	U
79	AZ	56	C
79	AZ	59	U
79	AZ	62	A
79	AZ	68	U
79	AZ	69	U
79	AZ	70	C
79	AZ	71	G
79	AZ	73	A
79	AZ	74	C

All (196) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
28	1	19	U
28	1	46	U

Continued on next page...

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Mol	Chain	Res	Type
28	1	50	U
28	1	53	G
28	1	55	G
28	1	59	G
28	1	141	C
28	1	149	U
28	1	187	A
28	1	198	A
28	1	201	A
28	1	202	G
28	1	207	U
28	1	251	G
28	1	265	A
28	1	267	G
28	1	283	G
28	1	289	A
28	1	307	A
28	1	318	A
28	1	322	U
28	1	323	A
28	1	336	A
28	1	345	G
28	1	391	A
28	1	418	A
28	1	431	U
28	1	443	G
28	1	500	C
28	1	509	U
28	1	547	G
28	1	578	A
28	1	595	G
28	1	630	A
28	1	646	A
28	1	693	A
28	1	696	C
28	1	707	U
28	1	778	U
28	1	831	G
28	1	846	A
28	1	856	G
28	1	885	U
28	1	900	G

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Mol	Chain	Res	Type
28	1	902	G
28	1	932	U
28	1	935	U
28	1	940	G
28	1	964	G
28	1	998	A
28	1	999	G
28	1	1002	A
28	1	1042	U
28	1	1066	G
28	1	1084	A
28	1	1110	U
28	1	1112	A
28	1	1113	G
28	1	1128	U
28	1	1147	G
28	1	1165	A
28	1	1166	G
28	1	1300	G
28	1	1325	U
28	1	1375	G
28	1	1389	G
28	1	1390	A
28	1	1410	U
28	1	1435	A
28	1	1448	U
28	1	1501	U
28	1	1525	G
28	1	1529	A
28	1	1535	A
28	1	1565	G
28	1	1574	C
28	1	1597	C
28	1	1639	C
28	1	1640	G
28	1	1650	G
28	1	1664	G
28	1	1665	C
28	1	1668	G
28	1	1678	G
28	1	1829	G
28	1	1837	U

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Mol	Chain	Res	Type
28	1	1852	G
28	1	1855	U
28	1	1868	G
28	1	1875	G
28	1	1902	G
28	1	1926	C
28	1	1949	G
28	1	2103	U
28	1	2140	U
28	1	2155	G
28	1	2177	G
28	1	2223	A
28	1	2247	G
28	1	2260	U
28	1	2270	A
28	1	2290	C
28	1	2303	A
28	1	2325	G
28	1	2353	G
28	1	2360	C
28	1	2361	A
28	1	2378	C
28	1	2391	G
28	1	2467	G
28	1	2469	G
28	1	2480	A
28	1	2491	A
28	1	2498	U
28	1	2517	U
28	1	2520	A
28	1	2541	U
28	1	2545	C
28	1	2609	A
28	1	2633	U
28	1	2635	A
28	1	2655	U
28	1	2685	C
28	1	2696	A
28	1	2699	G
28	1	2734	A
28	1	2749	G
28	1	2765	C

Continued on next page...

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Mol	Chain	Res	Type
28	1	2777	G
28	1	2801	A
28	1	2816	G
28	1	2823	G
28	1	2832	C
28	1	2836	C
28	1	2837	A
28	1	2844	C
28	1	2854	U
28	1	2855	U
28	1	2894	C
28	1	2904	U
28	1	2928	C
28	1	2930	A
28	1	2959	C
28	1	2981	U
28	1	3006	A
28	1	3021	A
28	1	3046	A
28	1	3050	U
28	1	3052	G
28	1	3101	G
28	1	3113	A
28	1	3136	G
28	1	3138	U
28	1	3143	C
28	1	3210	A
28	1	3229	G
28	1	3305	A
28	1	3315	G
29	3	25	G
29	3	47	C
29	3	61	G
29	3	67	G
29	3	84	A
30	4	3	A
30	4	14	C
30	4	20	U
30	4	43	A
30	4	44	A
30	4	53	A
30	4	69	U

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Mol	Chain	Res	Type
30	4	86	U
30	4	133	G
49	2	88	U
49	2	240	U
49	2	706	A
49	2	757	A
49	2	1123	C
49	2	1138	A
49	2	1164	G
49	2	1181	U
49	2	1190	C
49	2	1205	C
49	2	1298	U
49	2	1358	G
49	2	1379	C
49	2	1497	U
49	2	1513	G
49	2	1541	G
49	2	1684	U
49	2	1715	G
49	2	1746	A
49	2	1758	U
79	AX	1	G
79	AX	42	G
79	AX	67	A
79	AZ	67	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

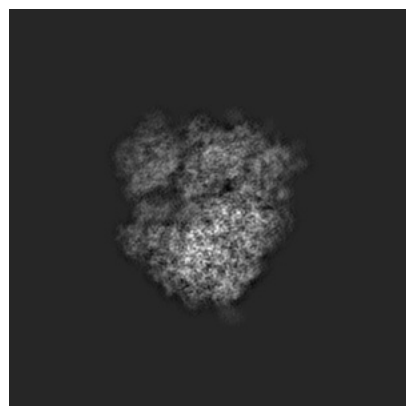
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22196. These allow visual inspection of the internal detail of the map and identification of artifacts.

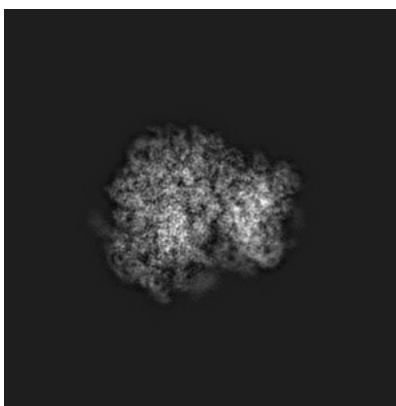
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

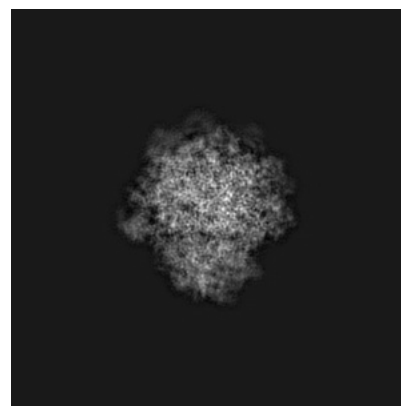
6.1.1 Primary map



X

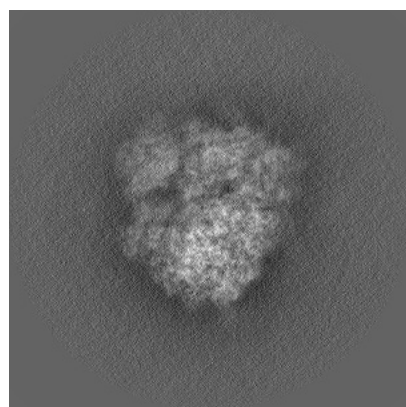


Y

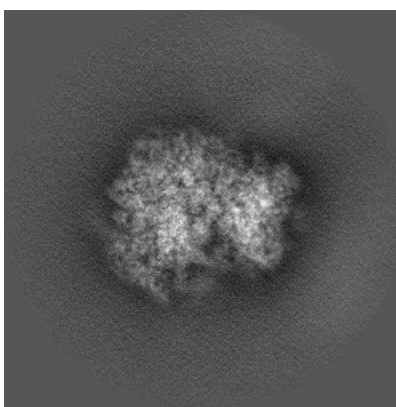


Z

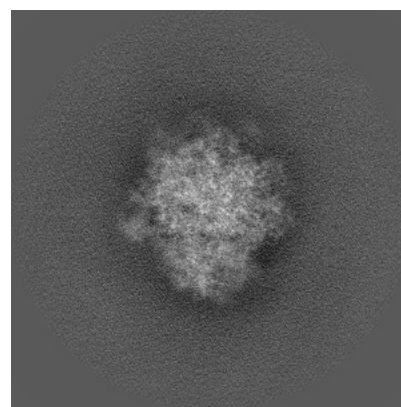
6.1.2 Raw map



X



Y

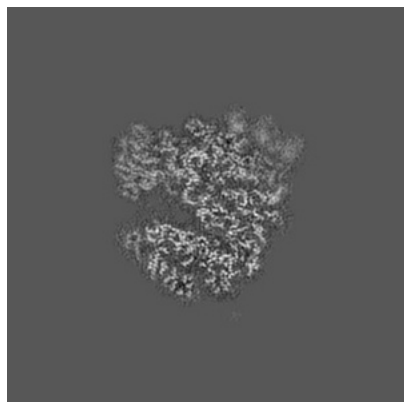


Z

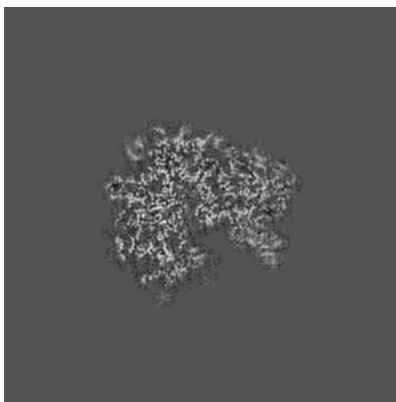
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

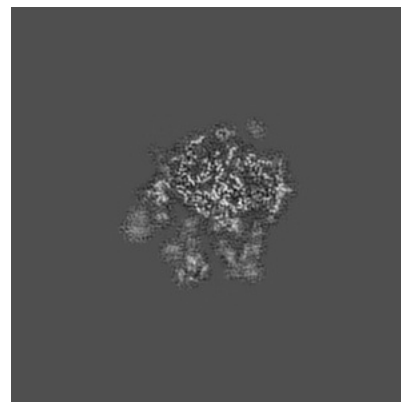
6.2.1 Primary map



X Index: 256

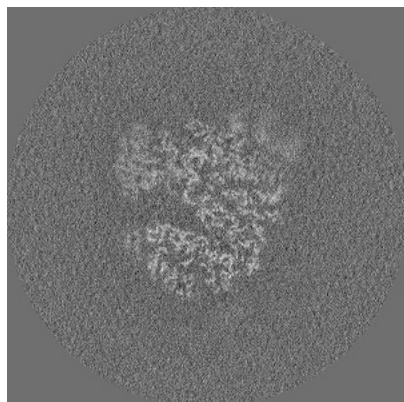


Y Index: 256

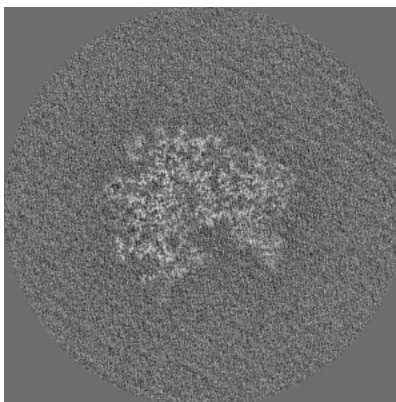


Z Index: 256

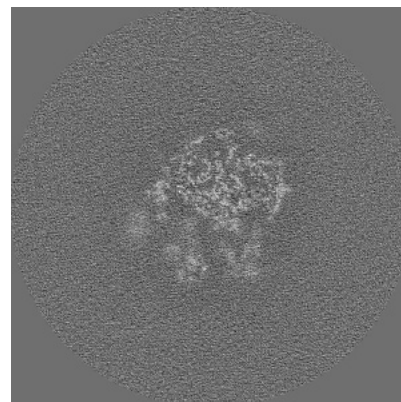
6.2.2 Raw map



X Index: 256



Y Index: 256

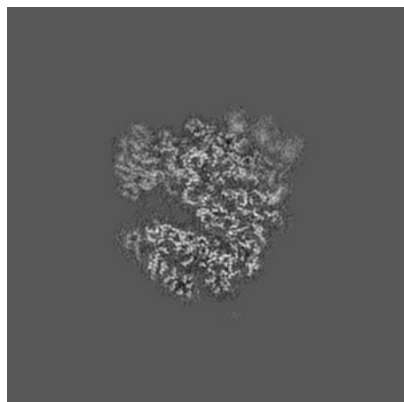


Z Index: 256

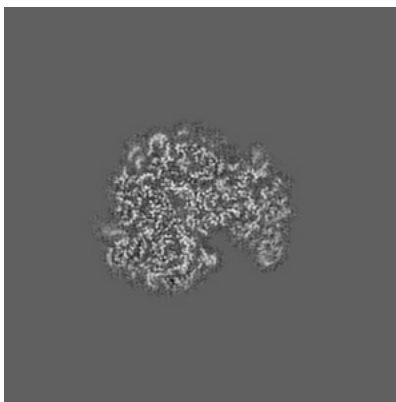
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

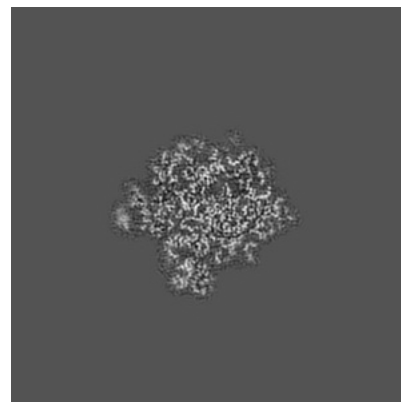
6.3.1 Primary map



X Index: 256

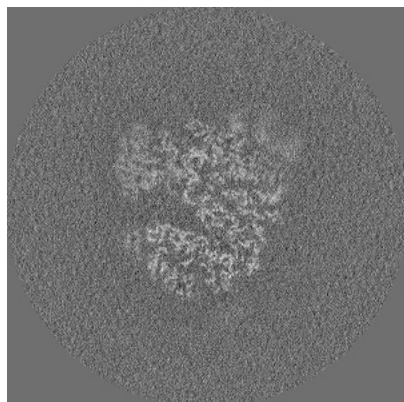


Y Index: 266

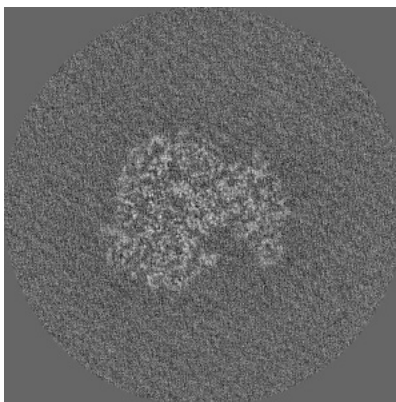


Z Index: 206

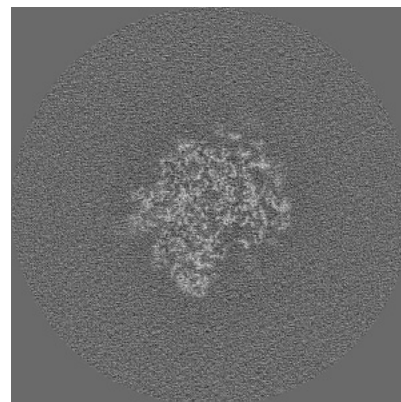
6.3.2 Raw map



X Index: 256



Y Index: 267

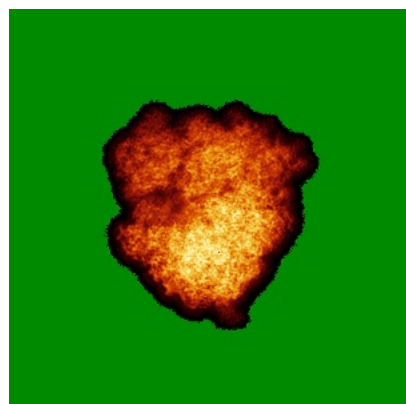


Z Index: 227

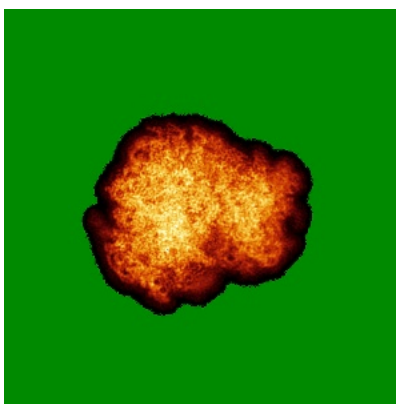
The images above show the largest variance slices of the map in three orthogonal directions.

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

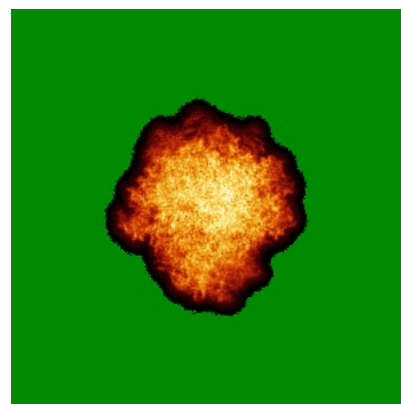
6.4.1 Primary map



X

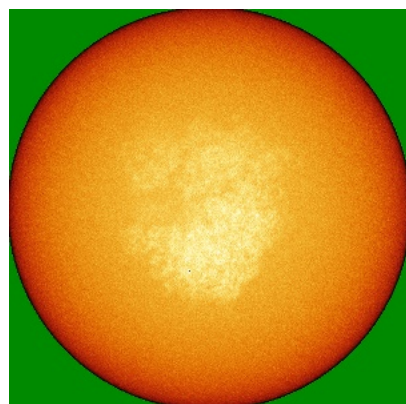


Y

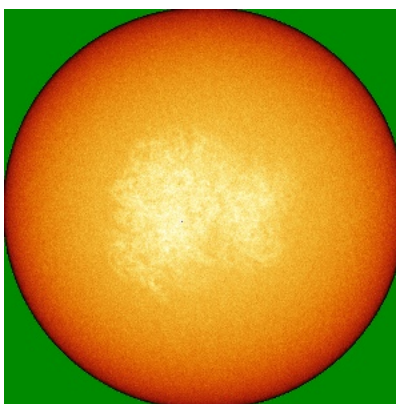


Z

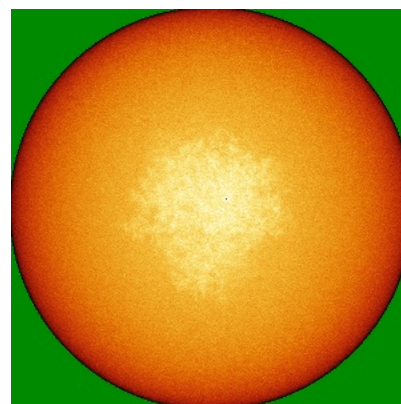
6.4.2 Raw map



X



Y

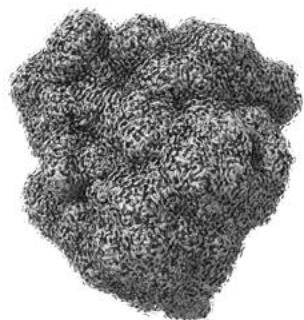


Z

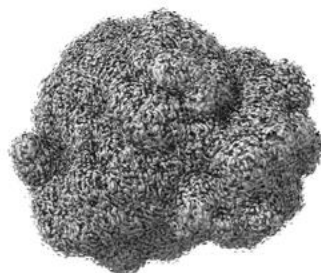
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



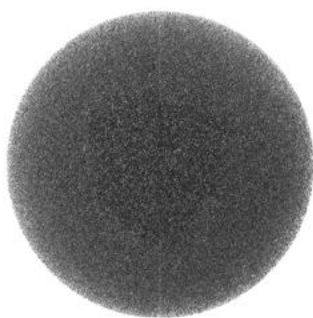
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

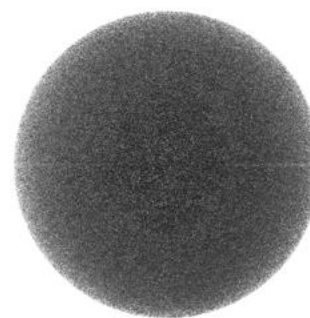
6.5.2 Raw map



X



Y



Z

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

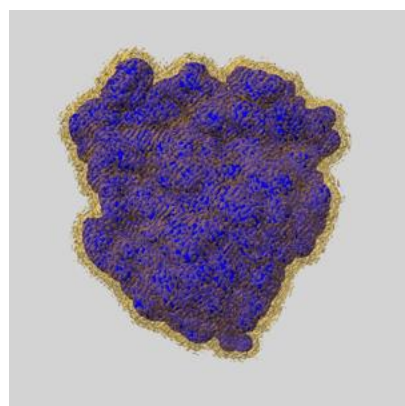
6.6 Mask visualisation [i](#)

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

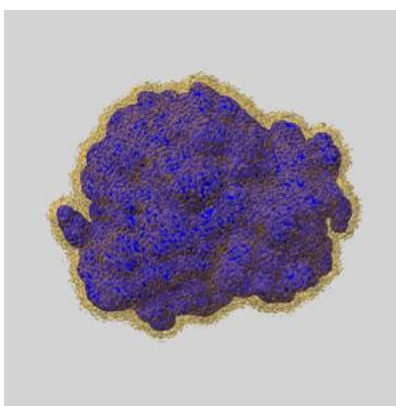
A mask typically either:

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

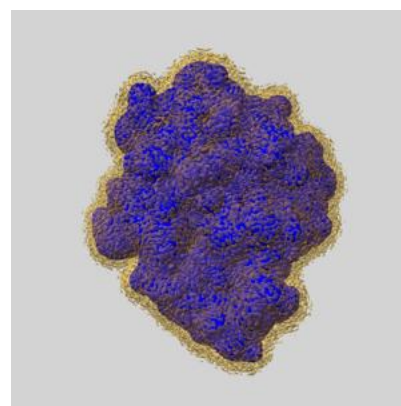
6.6.1 emd_22196_msk_1.map [i](#)



X



Y

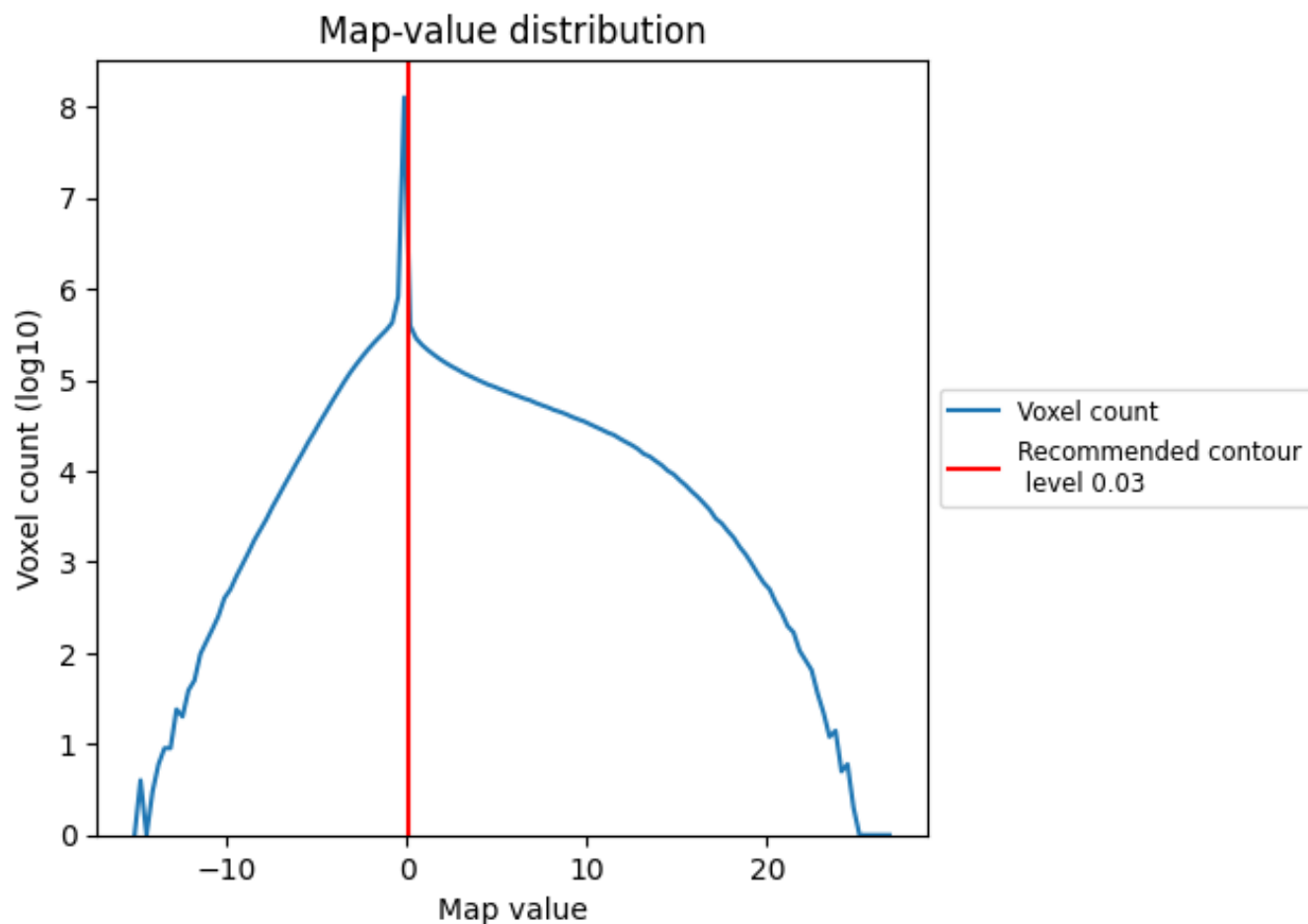


Z

7 Map analysis [i](#)

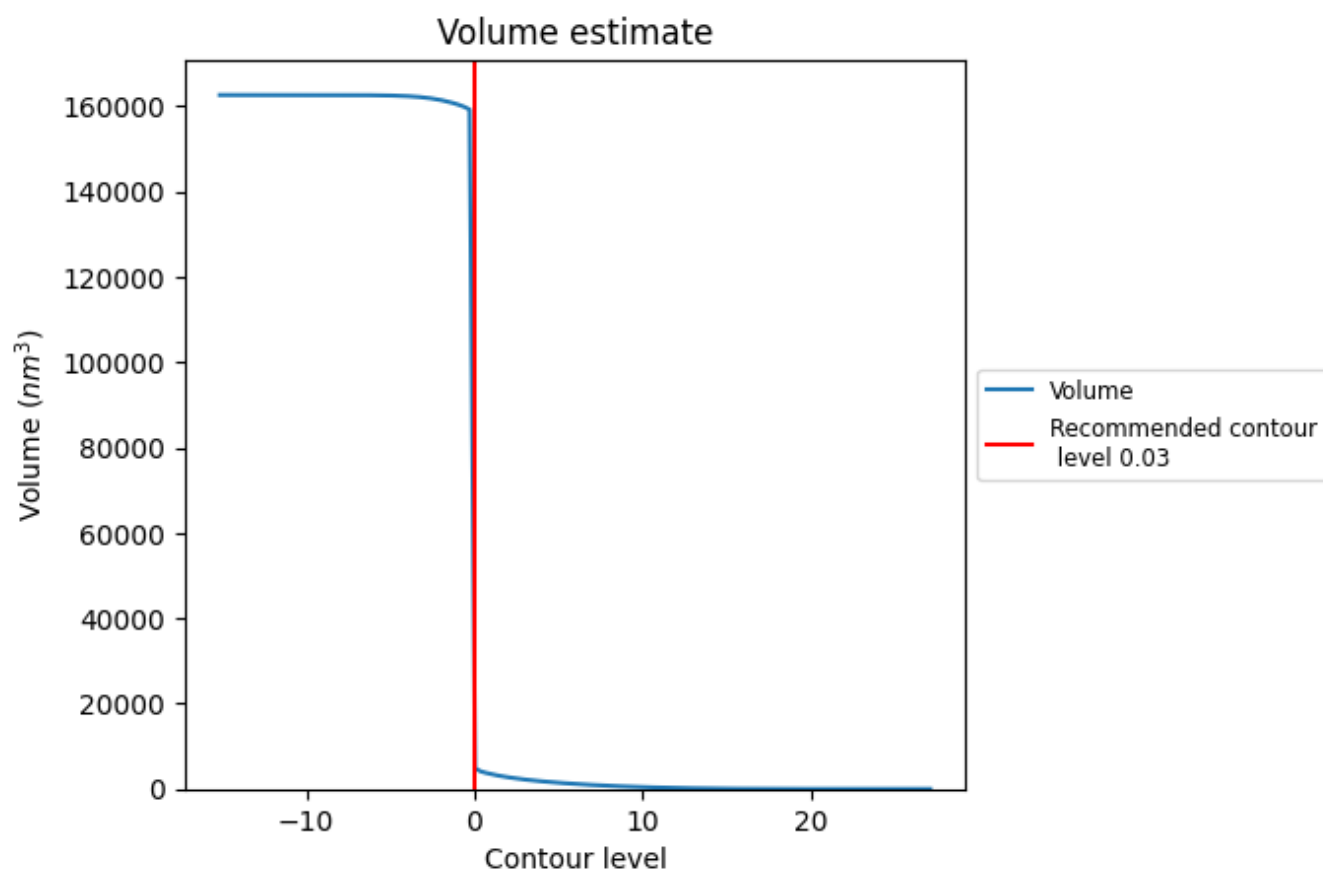
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

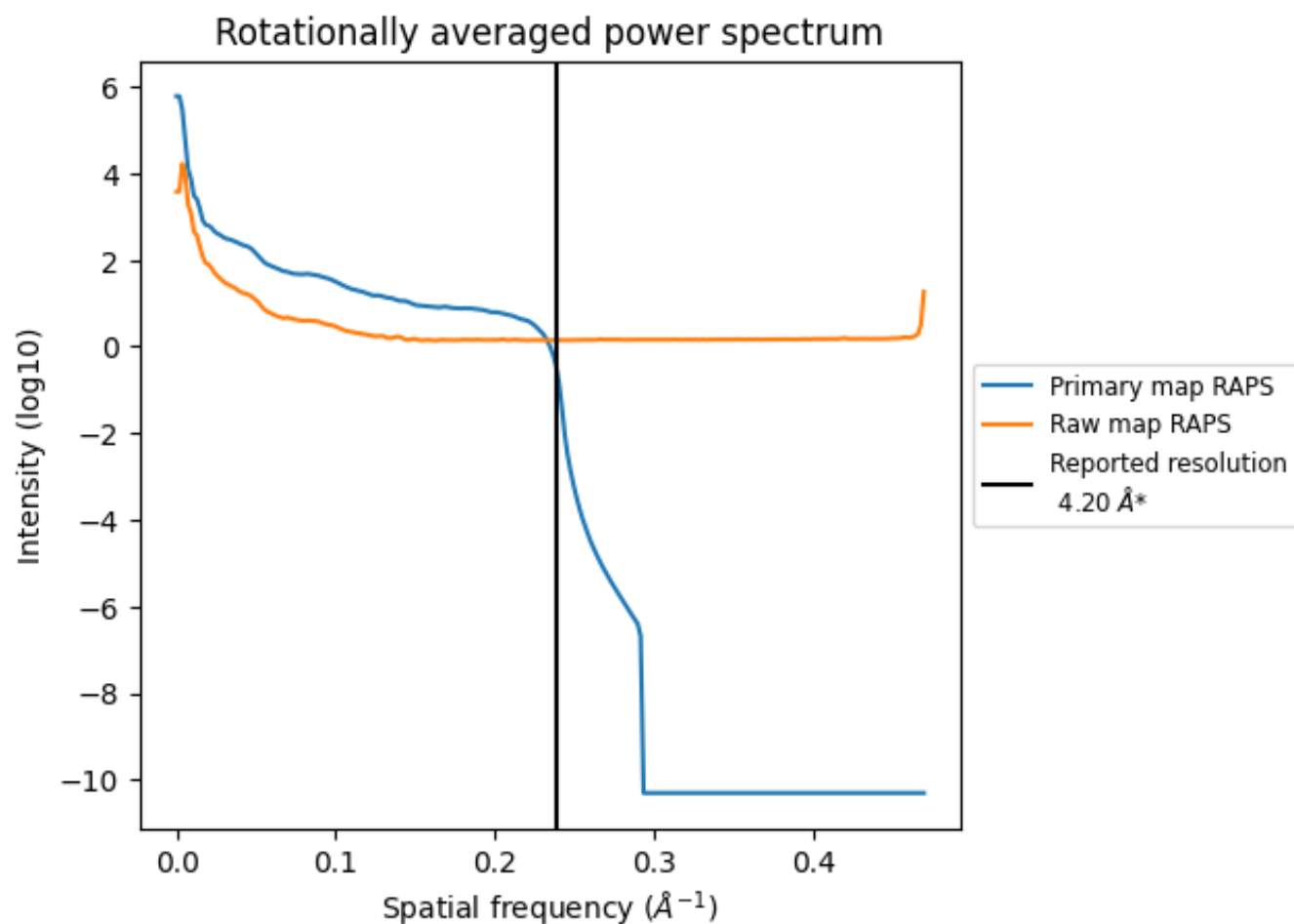
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 11315 nm^3 ; this corresponds to an approximate mass of 10221 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 ⓘ

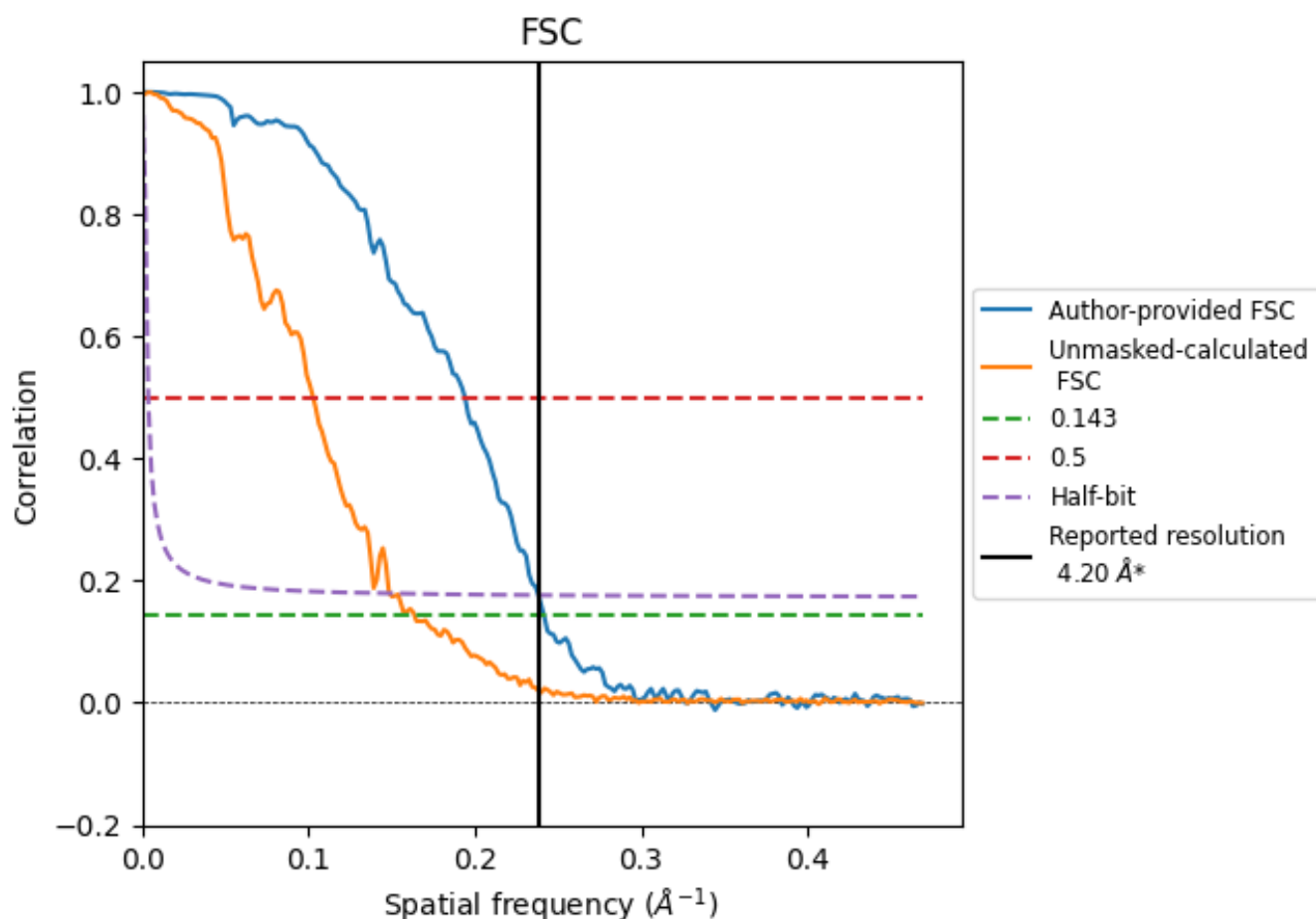


*Reported resolution corresponds to spatial frequency of 0.238 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.238 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

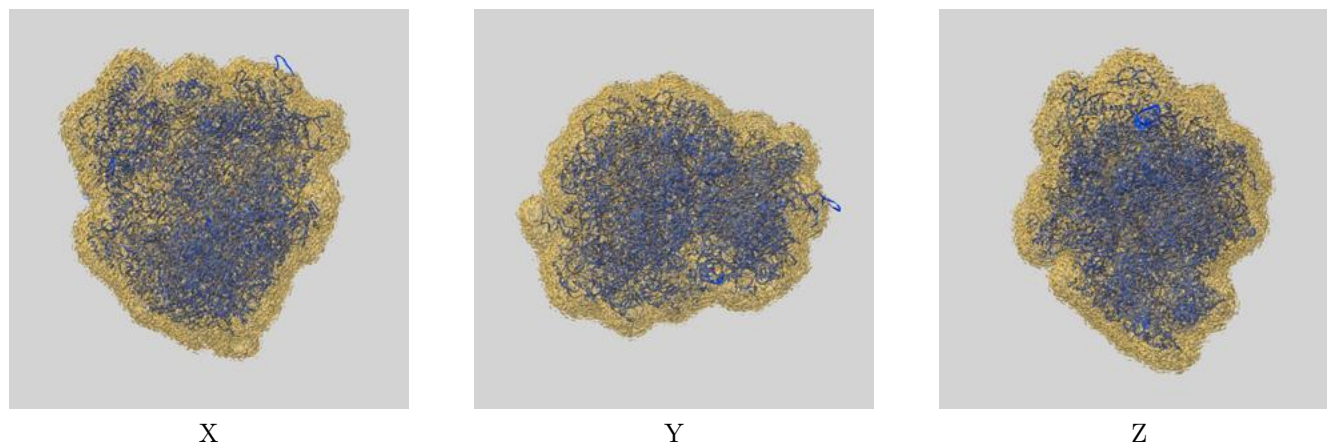
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	4.14	5.15	4.20
Unmasked-calculated*	6.11	9.73	6.72

*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 6.11 differs from the reported value 4.2 by more than 10 %

9 Map-model fit [i](#)

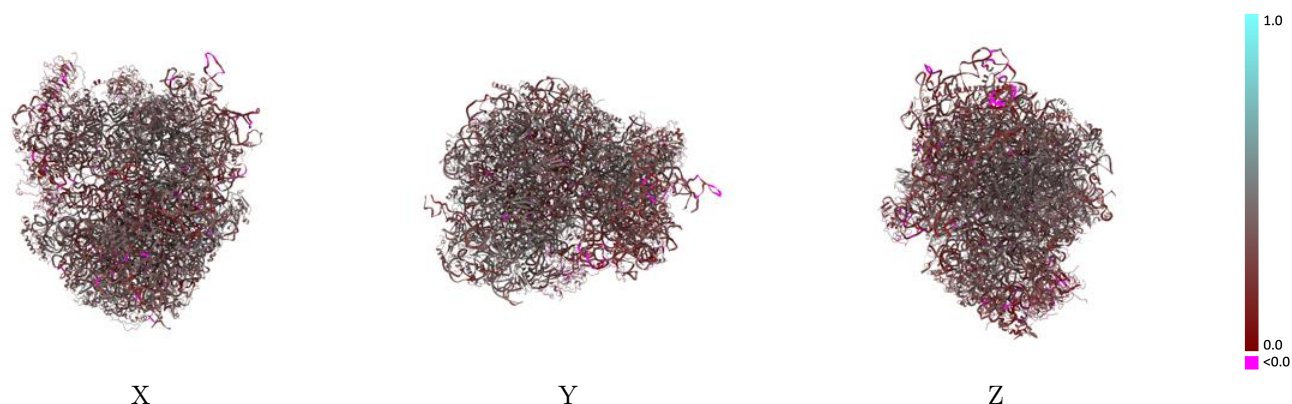
This section contains information regarding the fit between EMDB map EMD-22196 and PDB model 6XIQ. Per-residue inclusion information can be found in section [3](#) on page [20](#).

9.1 Map-model overlay [i](#)



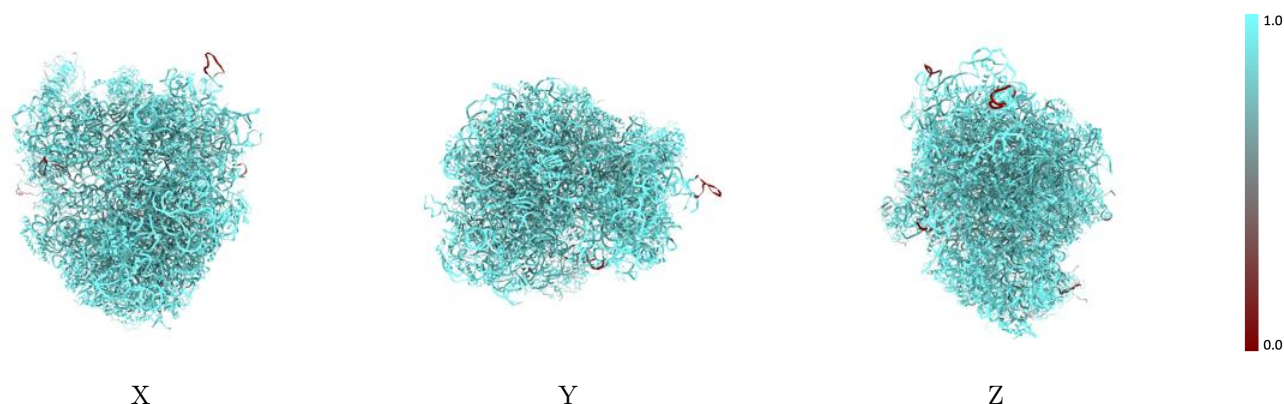
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



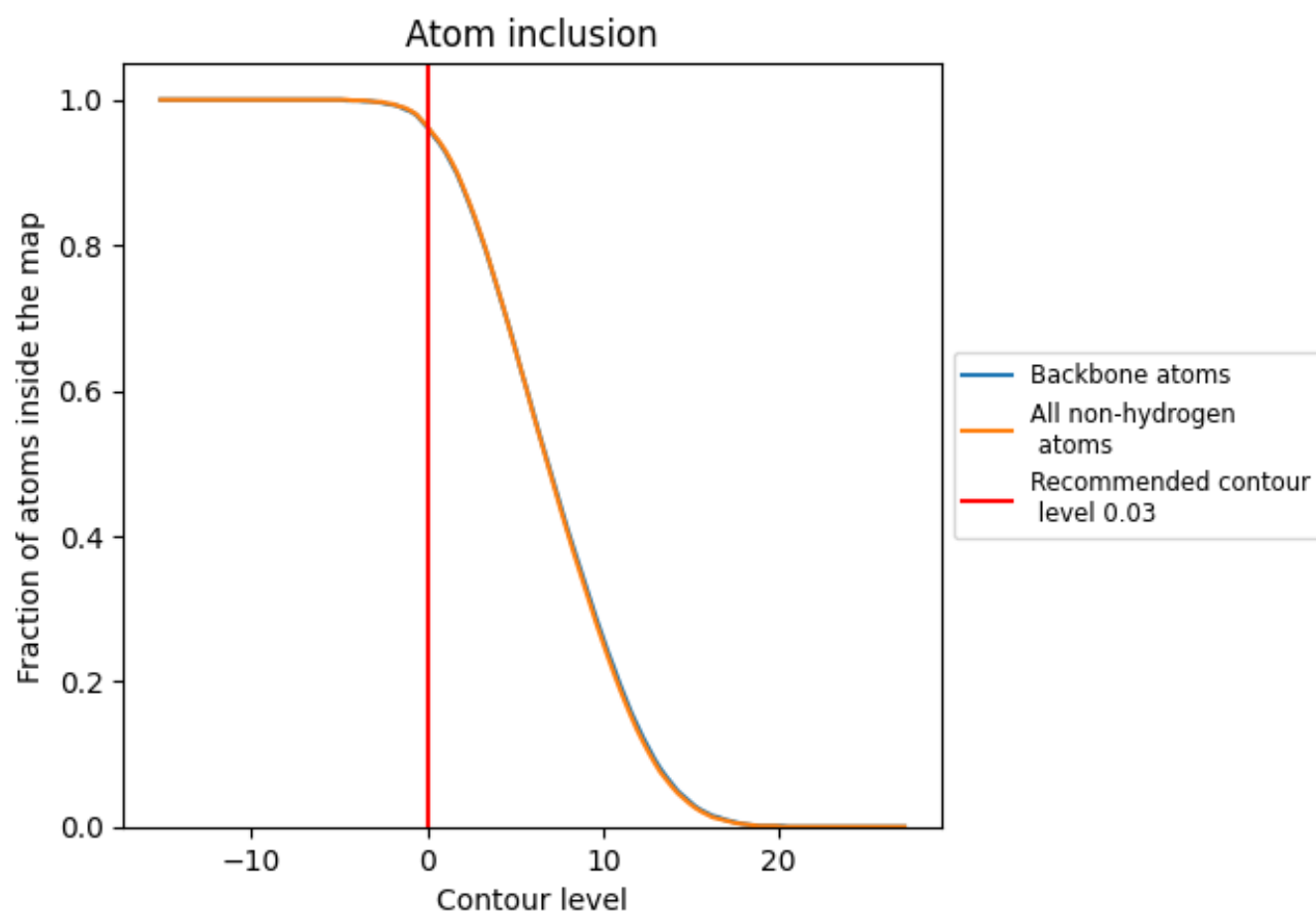
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 96% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9630	 0.3300
1	 0.9460	 0.3020
2	 0.9800	 0.3130
3	 0.9850	 0.3560
4	 0.9370	 0.3160
A	 0.9130	 0.3910
AA	 0.9880	 0.2740
AB	 0.9730	 0.3670
AD	 0.9730	 0.3810
AE	 0.9760	 0.3990
AF	 0.9810	 0.3200
AG	 0.9620	 0.2480
AH	 0.9760	 0.3200
AI	 0.9730	 0.3100
AJ	 0.9880	 0.2840
AK	 0.9320	 0.2860
AL	 0.9850	 0.3640
AM	 0.9800	 0.4010
AN	 0.9830	 0.3760
AO	 0.9910	 0.2670
AP	 0.9450	 0.2230
AQ	 0.9550	 0.3660
AR	 0.9750	 0.3550
AS	 0.9870	 0.3590
AT	 0.9510	 0.3260
AU	 0.9800	 0.3360
AV	 0.9560	 0.2660
AX	 0.9320	 0.2360
AY	 0.9080	 0.2590
AZ	 0.9100	 0.1690
B	 0.9850	 0.4250
C	 0.9860	 0.4240
D	 0.9860	 0.3640
E	 0.9880	 0.4020
F	 0.9850	 0.4110



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Chain	Atom inclusion	Q-score
G	 0.9780	 0.3790
H	 0.9790	 0.3860
I	 0.9820	 0.4020
J	 0.9850	 0.3620
L	 0.9830	 0.4090
L1	 0.8370	 0.1930
M	 0.9890	 0.3960
N	 0.9790	 0.4210
O	 0.9790	 0.4110
P	 0.9690	 0.4140
P0	 0.7510	 0.2000
P2	 0.8960	 0.2190
Q	 0.9850	 0.4280
R	 0.9820	 0.3940
S	 0.9880	 0.4210
T	 0.9850	 0.4200
U	 0.9940	 0.3910
V	 0.9650	 0.4290
W	 0.9940	 0.4230
X	 0.9930	 0.4360
Y	 0.9930	 0.4230
Z	 0.9850	 0.4050
a	 0.9720	 0.4170
b	 0.9800	 0.3850
c	 0.9810	 0.3940
d	 0.9880	 0.4270
e	 0.9860	 0.4440
f	 0.9830	 0.4430
g	 0.9810	 0.4180
h	 0.9820	 0.3880
i	 0.9790	 0.3870
j	 0.9850	 0.4250
k	 0.9920	 0.3930
l	 0.9610	 0.3970
m	 0.7720	 0.1770
n	 0.9860	 0.4250
o	 0.9720	 0.4050
p	 0.9700	 0.4120
q	 0.9740	 0.3570
r	 0.9760	 0.3740
s	 0.9800	 0.3910
t	 0.9670	 0.3370

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Chain	Atom inclusion	Q-score
u	 0.9800	 0.3090
v	 0.9800	 0.3140
w	 0.9590	 0.2640
x	 0.9810	 0.3390
y	 0.9830	 0.3340
z	 0.9750	 0.2930