



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 08:05 AM UTC

PDB ID : 7OHQ / pdb_00007ohq
EMDB ID : EMD-12905
Title : Nog1-TAP associated immature ribosomal particle population C from *S. cerevisiae*
Authors : Milkereit, P.; Poell, G.
Deposited on : 2021-05-11
Resolution : 3.10 Å(reported)
Based on initial model : 3JCT

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

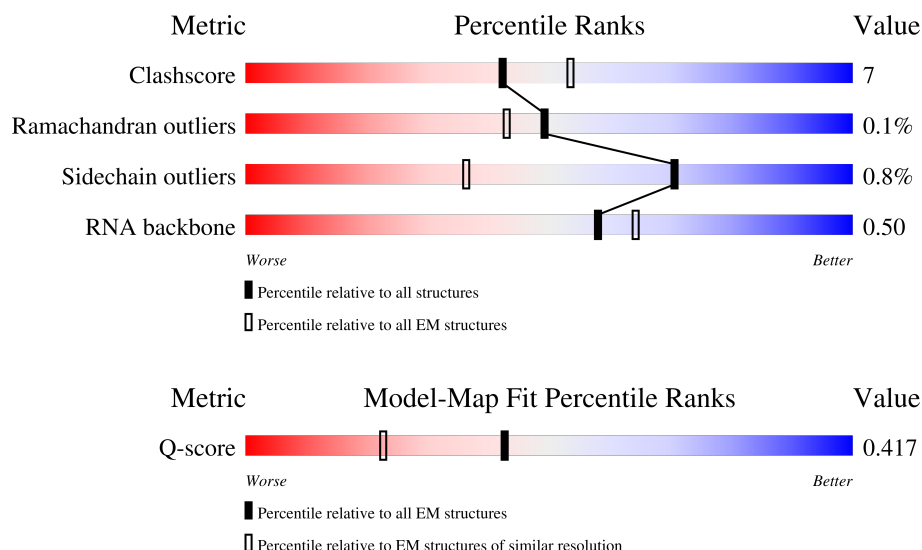
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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	14724 (2.60 - 3.60)

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	1	3396	
2	2	158	
3	3	121	

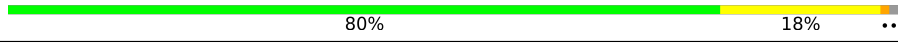
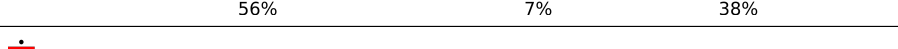
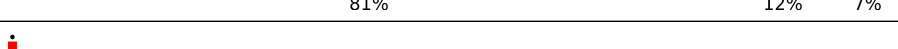
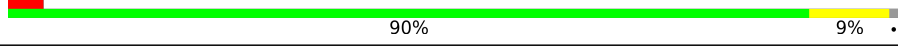
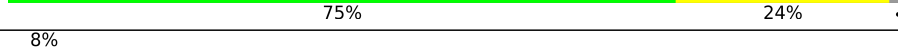
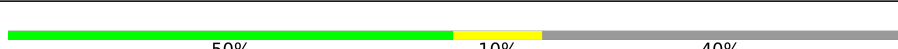
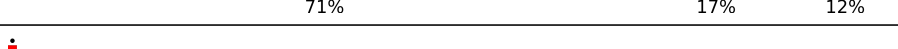
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Mol	Chain	Length	Quality of chain
4	5	120	
5	6	232	
6	A	254	
7	B	387	
8	C	362	
9	D	297	
10	E	176	
11	F	244	
12	G	256	
13	H	191	
14	J	174	
15	K	376	
16	L	199	
17	M	138	
18	N	204	
19	O	199	
20	P	184	
21	Q	186	
22	R	189	
23	S	172	
24	T	160	
25	U	121	
26	V	137	
27	W	236	
28	X	142	

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Mol	Chain	Length	Quality of chain
29	Y	127	
30	Z	136	
31	a	149	
32	b	647	
33	c	105	
34	d	113	
35	e	130	
36	f	107	
37	g	121	
38	h	120	
39	i	100	
40	j	88	
41	k	78	
42	l	51	
43	m	486	
44	n	605	
45	o	220	
46	p	92	
47	q	455	
48	r	261	
49	s	520	
50	t	322	
51	u	199	
52	v	344	
53	w	203	

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Mol	Chain	Length	Quality of chain
54	x	515	10%67%13%20%
55	y	245	79%20%
56	z	106	7%37%7%57%

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 264865 atoms, of which 115934 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	1	3053	Total	C	H	N	O	P	0	0
			98146	29178	32819	11796	21300	3053		

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	2	158	Total	C	H	N	O	P	0	0
			5048	1500	1695	586	1109	158		

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

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

- Molecule 4 is a protein called rRNA-processing protein CGR1.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	5	51	Total	C	H	N	O	S	0	0
			927	280	475	86	85	1		

- Molecule 5 is a RNA chain called ITS2.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	6	65	Total	C	H	N	O	P	0	0
			2061	614	691	228	463	65		

- Molecule 6 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	A	212	Total	C	H	N	O	S	0	0
			3314	1021	1684	325	283	1		

- Molecule 7 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	B	386	Total	C	H	N	O	S	0	0
			6247	1956	3166	584	533	8		

- Molecule 8 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	C	361	Total	C	H	N	O	S	0	0
			5613	1730	2864	522	494	3		

- Molecule 9 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	D	261	Total	C	H	N	O	S	0	0
			4178	1335	2066	372	403	2		

- Molecule 10 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	E	156	Total	C	H	N	O	S	0	0
			2567	800	1328	222	216	1		

- Molecule 11 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	F	222	Total	C	H	N	O	S	0	0
			3647	1151	1863	324	308	1		

- Molecule 12 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	G	233	Total	C	H	N	O	S	0	0
			3726	1159	1909	326	329	3		

- Molecule 13 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 14 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	J	169	Total	C	H	N	O	S	0	0
			2737	847	1384	253	249	4		

- Molecule 15 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	K	252	Total	C	H	N	O	S	0	0
			4153	1312	2121	336	381	3		

- Molecule 16 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	L	187	Total	C	H	N	O	S	0	0
			3057	934	1558	307	258			

- Molecule 17 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	M	137	Total	C	H	N	O	S	0	0
			2214	678	1155	200	179	2		

- Molecule 18 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	N	203	Total	C	H	N	O	S	0	0
			3500	1077	1780	361	281	1		

- Molecule 19 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	O	197	Total	C	H	N	O	S	0	0
			3215	1003	1660	289	262	1		

- Molecule 20 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	P	177	Total	C	H	N	O	S	0	0
			2845	871	1443	280	251			

- Molecule 21 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	Q	134	Total	C	H	N	O	S	0	0
			2151	659	1116	196	179	1		

- Molecule 22 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	R	156	Total	C	H	N	O		0	0
			2601	781	1343	265	212			

- Molecule 23 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	S	171	Total	C	H	N	O	S	0	0
			2913	925	1476	266	243	3		

- Molecule 24 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	T	116	Total	C	H	N	O	S	0	0
			1902	584	978	176	161	3		

- Molecule 25 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	U	101	Total	C	H	N	O		0	0
			1617	519	816	131	151			

- Molecule 26 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	V	136	Total	C	H	N	O	S	0	0
			2052	628	1049	189	179	7		

- Molecule 27 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	W	234	Total	C	H	N	O	S	0	0
			3806	1194	1921	323	362	6		

- Molecule 28 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	X	141	Total	C	H	N	O	S	0	0
			2288	705	1188	196	197	2		

- Molecule 29 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	Y	126	Total	C	H	N	O		0	0
			2075	625	1082	192	176			

- Molecule 30 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	Z	135	Total	C	H	N	O		0	0
			2248	710	1156	202	180			

- Molecule 31 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	a	93	Total	C	H	N	O	S	0	0
			1512	479	777	130	125	1		

- Molecule 32 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	b	537	Total	C	H	N	O	S	0	0
			8784	2760	4427	763	811	23		

- Molecule 33 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	c	97	Total	C	H	N	O	S	0	0
			1541	479	798	124	139	1		

- Molecule 34 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	d	105	Total	C	H	N	O	S	0	0
			1761	544	905	163	148	1		

- Molecule 35 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	e	127	Total	C	H	N	O	S	0	0
			2112	647	1092	205	167	1		

- Molecule 36 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	f	106	Total	C	H	N	O	S	0	0
			1731	540	881	165	144	1		

- Molecule 37 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	g	112	Total	C	H	N	O	S	0	0
			1831	546	950	179	152	4		

- Molecule 38 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	h	119	Total	C	H	N	O	S	0	0
			2048	615	1079	186	167	1		

- Molecule 39 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	i	99	Total	C	H	N	O	S	0	0
			1621	481	850	156	132	2		

- Molecule 40 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	j	85	Total	C	H	N	O	S	0	0
			1348	408	678	146	111	5		

- Molecule 41 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	k	77	Total	C	H	N	O		0	0
			1295	391	683	115	106			

- Molecule 42 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	l	50	Total	C	H	N	O	S	0	0
			912	272	476	97	65	2		

- Molecule 43 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	m	461	Total	C	H	N	O	S	0	0
			7508	2350	3788	675	686	9		

- Molecule 44 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	n	371	Total	C	H	N	O	S	0	0
			6139	1963	3109	523	534	10		

- Molecule 45 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	o	133	Total	C	H	N	O	S	0	0
			2267	716	1160	198	189	4		

- Molecule 46 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	p	91	Total	C	H	N	O	S	0	0
			1434	429	740	138	121	6		

- Molecule 47 is a protein called Ribosome biogenesis protein NOP53.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	q	147	Total	C	H	N	O	S	0	0
			2501	778	1268	222	232	1		

- Molecule 48 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	r	230	Total	C	H	N	O	S	0	0
			3827	1177	1967	352	324	7		

- Molecule 49 is a protein called Nuclear GTP-binding protein NUG1.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	s	53	Total	C	H	N	O	S	0	0
			935	274	499	90	70	2		

- Molecule 50 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	t	287	Total	C	H	N	O	S	0	0
			4762	1459	2456	427	417	3		

- Molecule 51 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	u	150	Total	C	H	N	O	S	0	0
			2582	793	1317	253	210	9		

- Molecule 52 is a protein called Ribosome biogenesis protein RPF2.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	v	287	Total	C	H	N	O	S	0	0
			4718	1482	2400	408	412	16		

- Molecule 53 is a protein called Regulator of ribosome biosynthesis.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	w	182	Total	C	H	N	O	S	0	0
			2960	911	1512	261	271	5		

- Molecule 54 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	x	413	Total	C	H	N	O	S	0	0
			6438	2030	3207	583	598	20		

- Molecule 55 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	y	244	Total	C	H	N	O	S	0	0
			3685	1146	1836	319	377	7		

- Molecule 56 is a protein called UPF0642 protein YBL028C.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	z	46	Total	C	H	N	O	0	0
			772	228	402	75	67		

- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	b	1	Total	Mg	0
			1	1	
57	m	1	Total	Mg	0
			1	1	

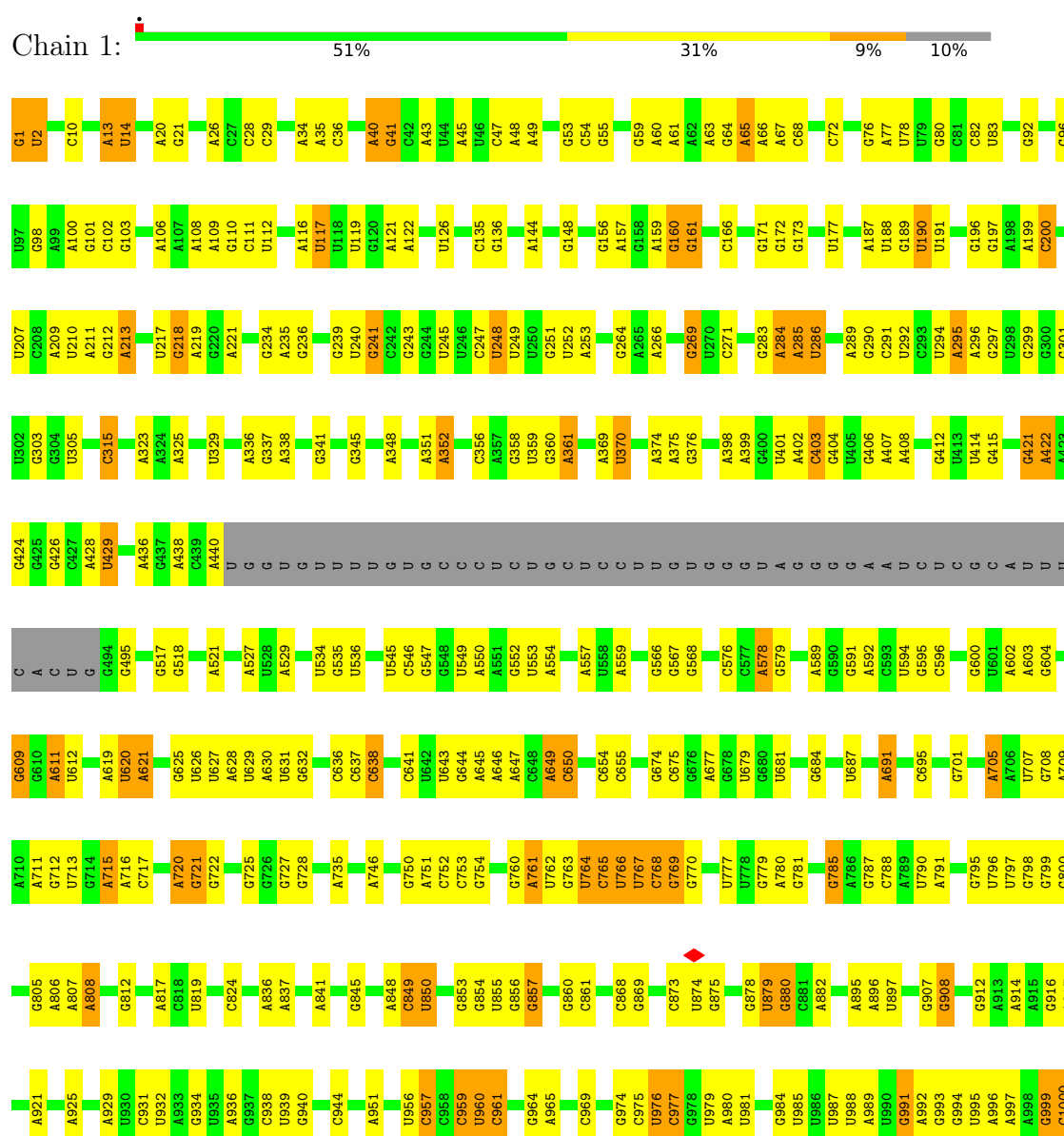
- Molecule 58 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
58	j	1	Total	Zn	0
			1	1	
58	p	1	Total	Zn	0
			1	1	
58	u	1	Total	Zn	0
			1	1	

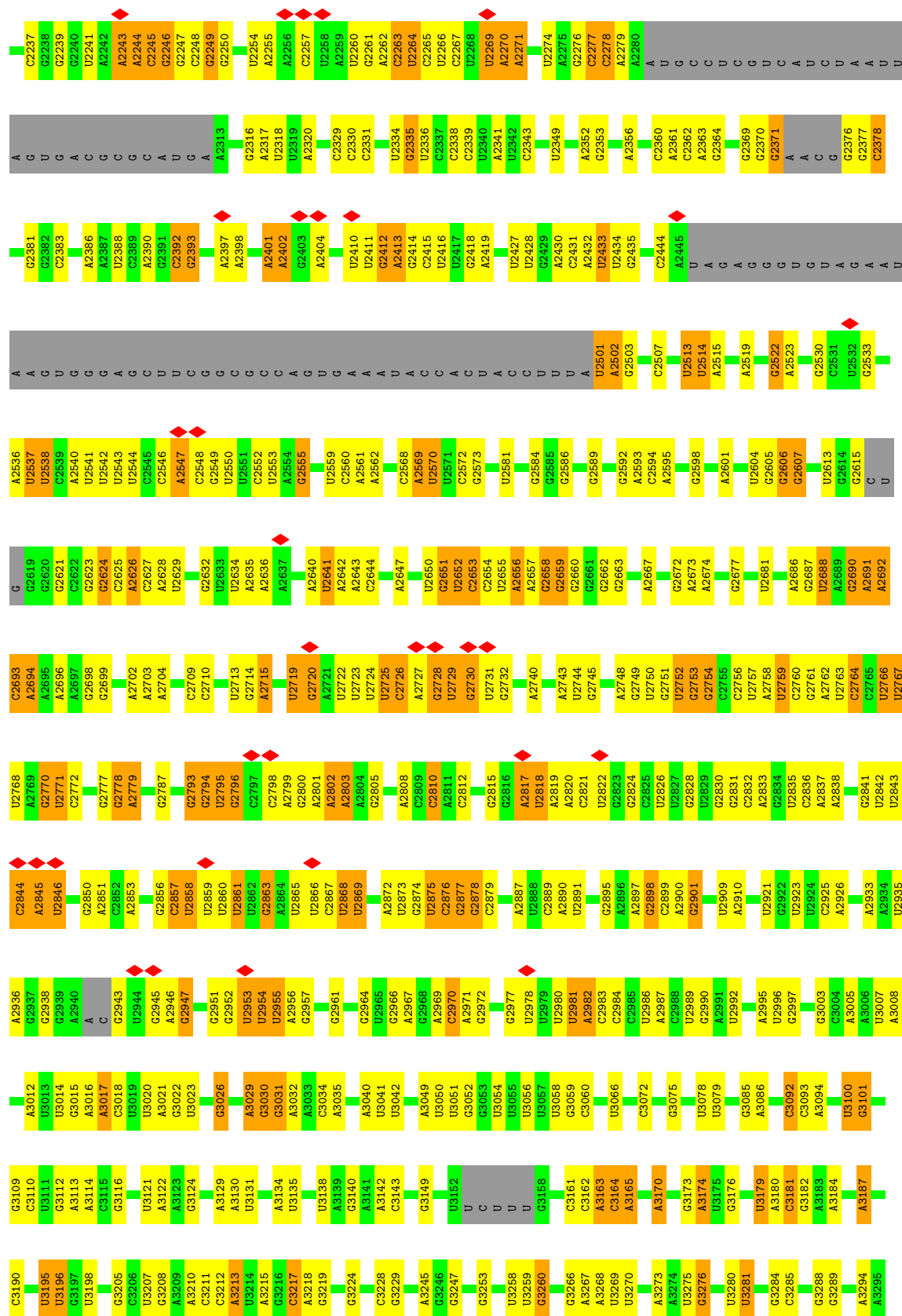
3 Residue-property plots [i](#)

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

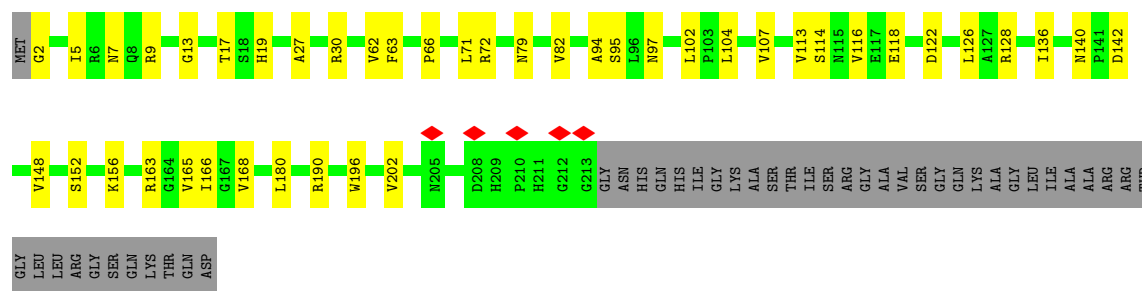
• Molecule 1: 25S rRNA





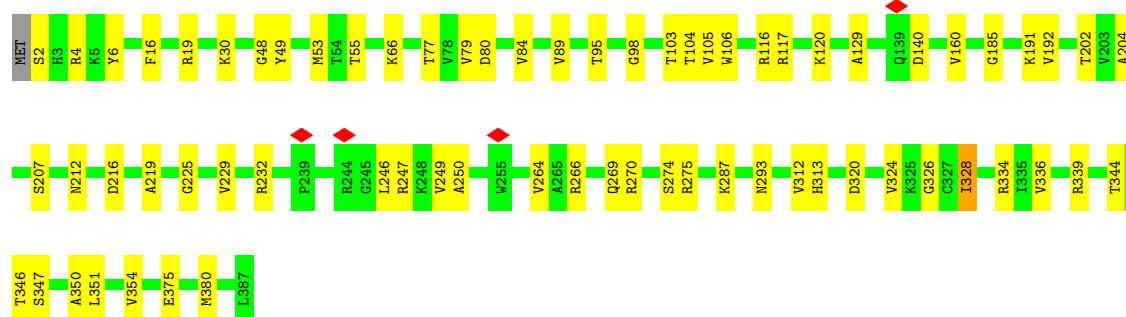


Chain A: 



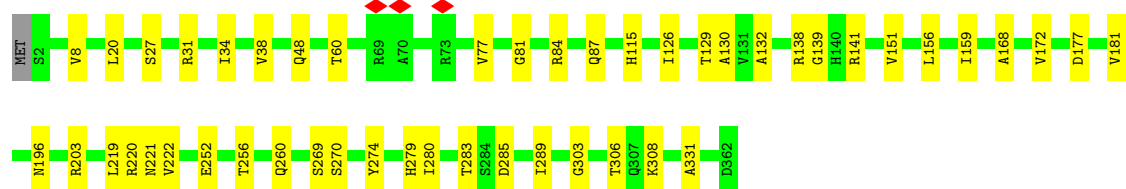
• Molecule 7: 60S ribosomal protein L3

Chain B: 



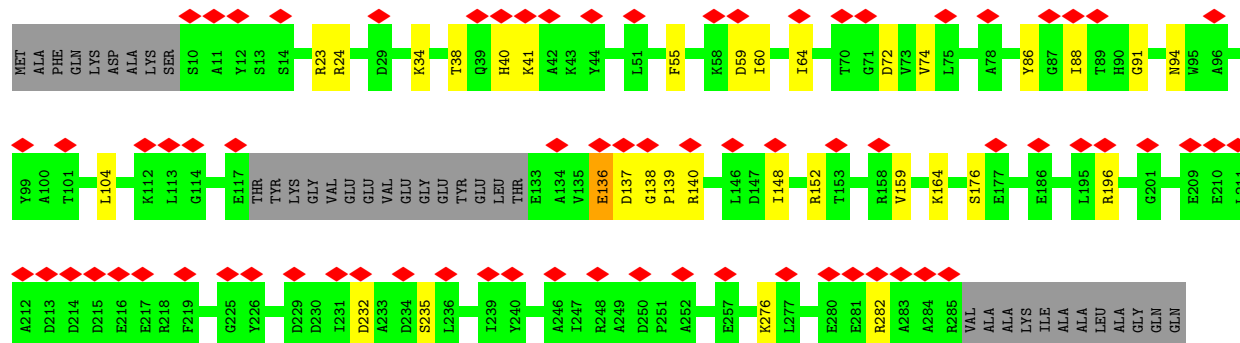
• Molecule 8: 60S ribosomal protein L4-A

Chain C: 



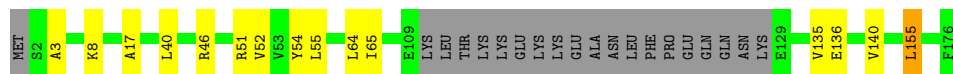
• Molecule 9: 60S ribosomal protein L5

Chain D: 



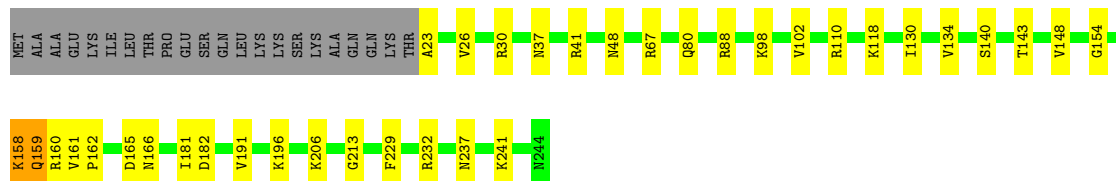
- Molecule 10: 60S ribosomal protein L6-A

Chain E:  80% 8% 11%



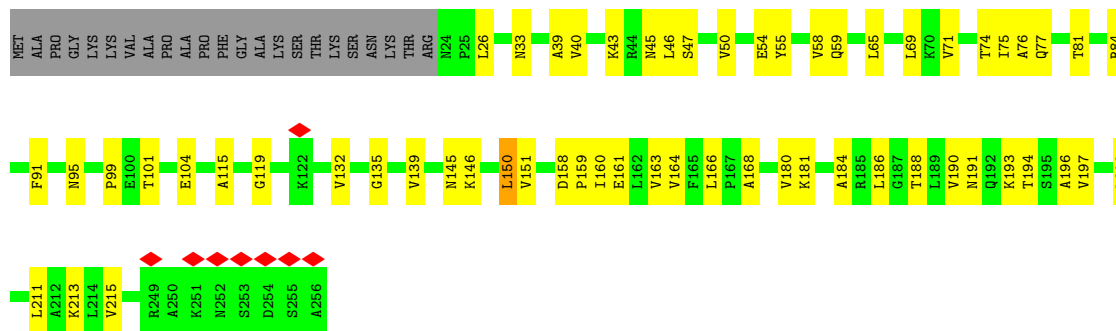
- Molecule 11: 60S ribosomal protein L7-A

Chain F:  76% 14% 9%



- Molecule 12: 60S ribosomal protein L8-A

Chain G:  68% 23% 9%



- Molecule 13: 60S ribosomal protein L9-A

Chain H:  77% 23% 0%

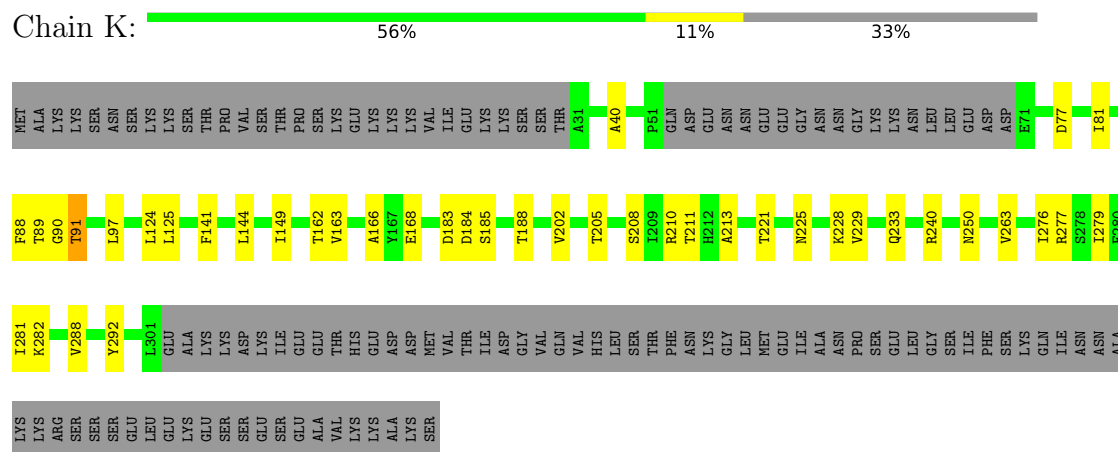


- Molecule 14: 60S ribosomal protein L11-A

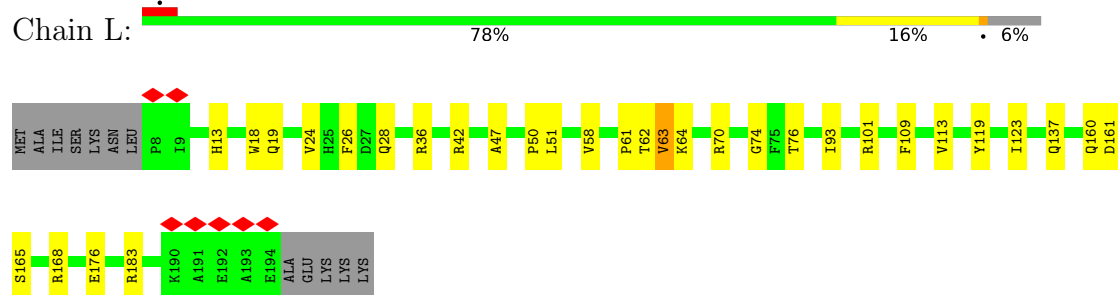
Chain J:  83% 14% 0%



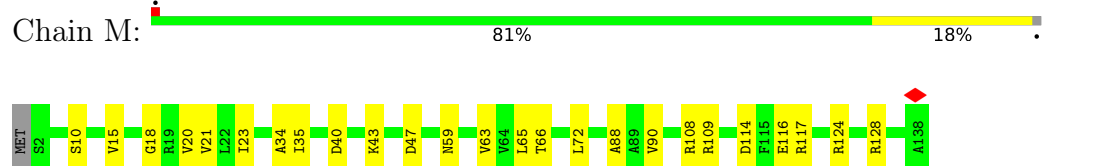
- Molecule 15: Proteasome-interacting protein CIC1



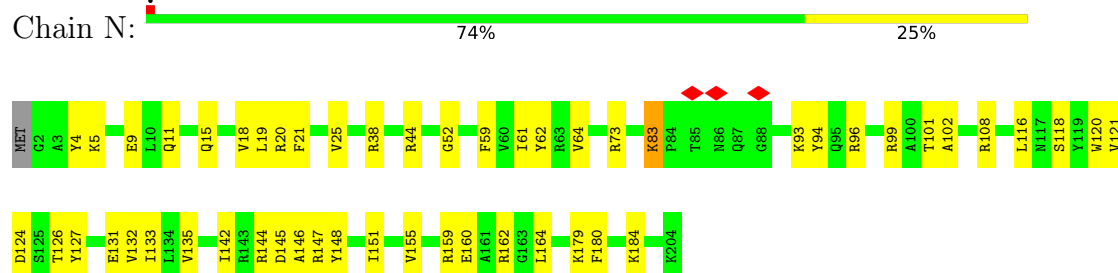
- Molecule 16: 60S ribosomal protein L13-A



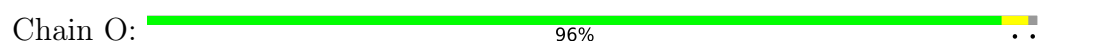
- Molecule 17: 60S ribosomal protein L14-A

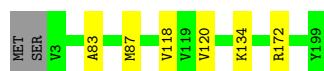


- Molecule 18: 60S ribosomal protein L15-A

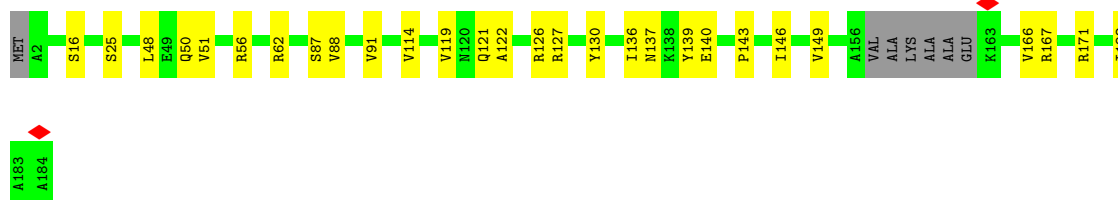
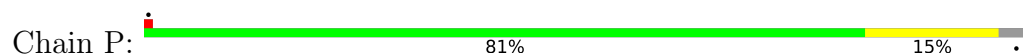


- Molecule 19: 60S ribosomal protein L16-A

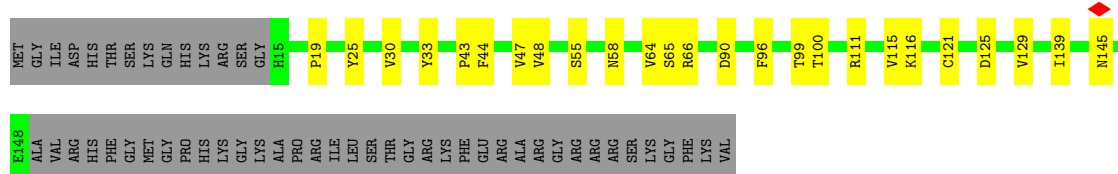




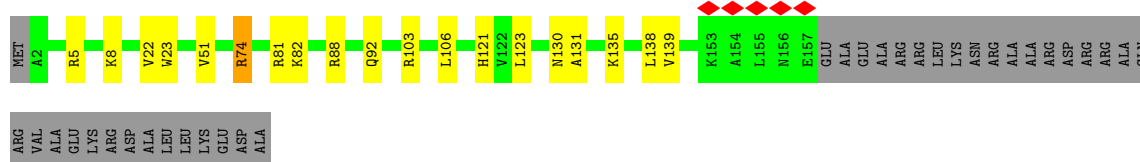
- Molecule 20: 60S ribosomal protein L17-A



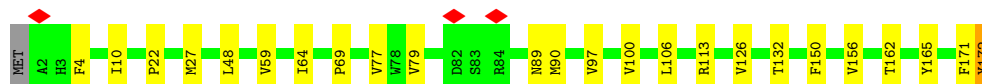
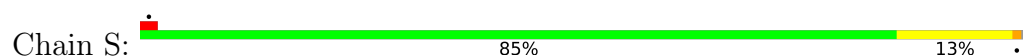
- Molecule 21: 60S ribosomal protein L18-A



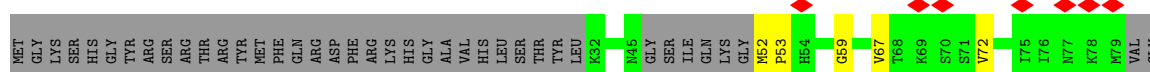
- Molecule 22: 60S ribosomal protein L19-A

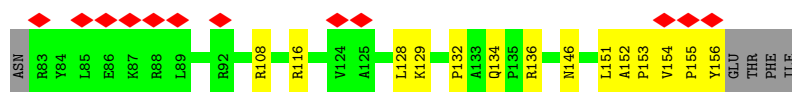


- Molecule 23: 60S ribosomal protein L20-A



- Molecule 24: 60S ribosomal protein L21-A

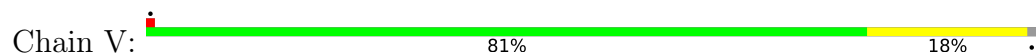




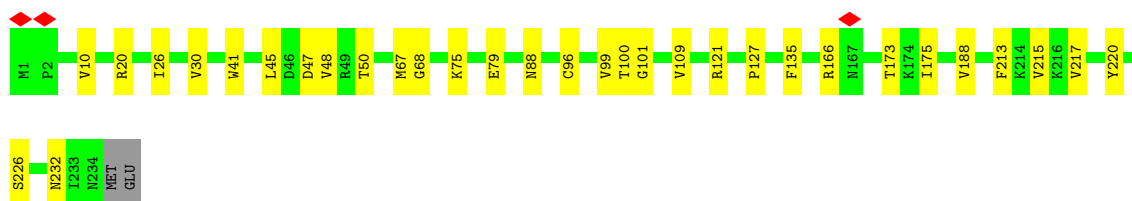
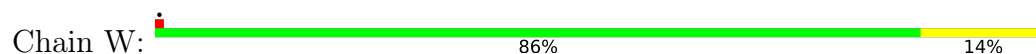
- Molecule 25: 60S ribosomal protein L22-A

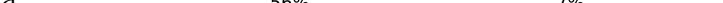


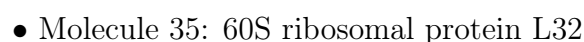
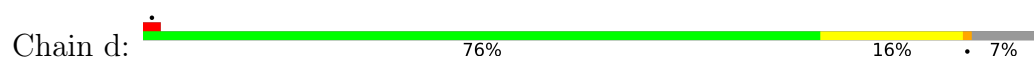
- Molecule 26: 60S ribosomal protein L23-A



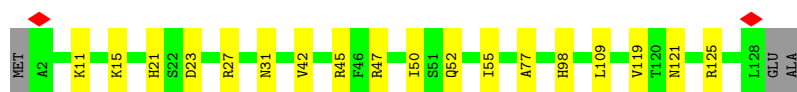
- Molecule 27: Ribosome assembly factor MRT4



- Chain a: 

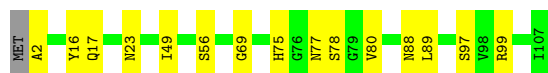


Chain e:  84% 14%



- Molecule 36: 60S ribosomal protein L33-A

Chain f:  85% 14%



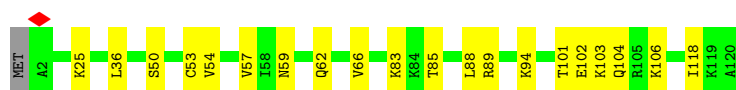
- Molecule 37: 60S ribosomal protein L34-A

Chain g:  81% 12% 7%



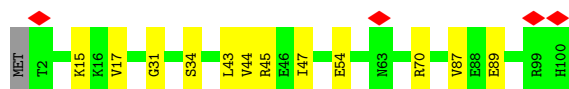
- Molecule 38: 60S ribosomal protein L35-A

Chain h:  82% 17%



- Molecule 39: 60S ribosomal protein L36-A

Chain i:  87% 12%



- Molecule 40: 60S ribosomal protein L37-A

Chain j:  75% 20%



- Molecule 41: 60S ribosomal protein L38

Chain k:  90% 9%



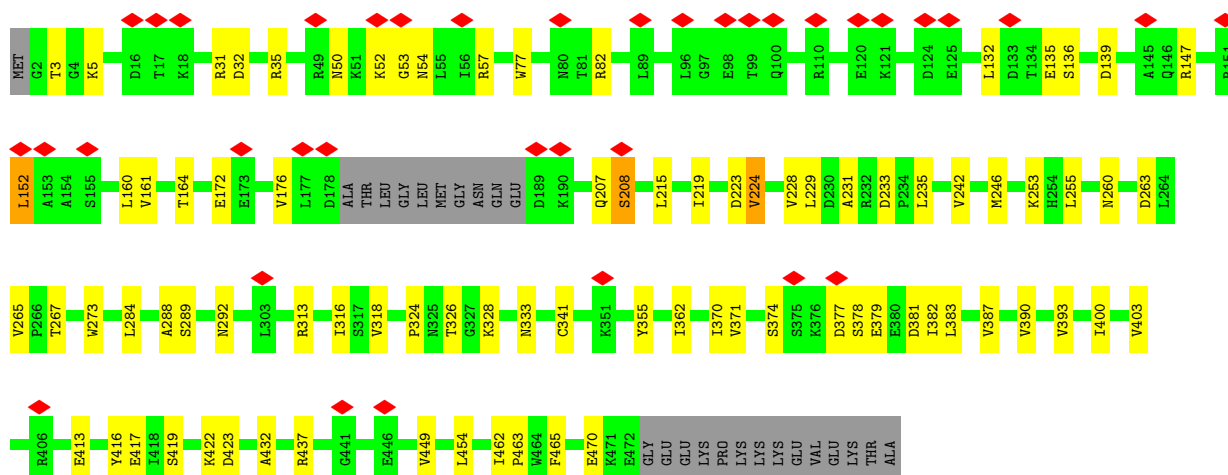
- Molecule 42: 60S ribosomal protein L39

Chain l:  75% 24%



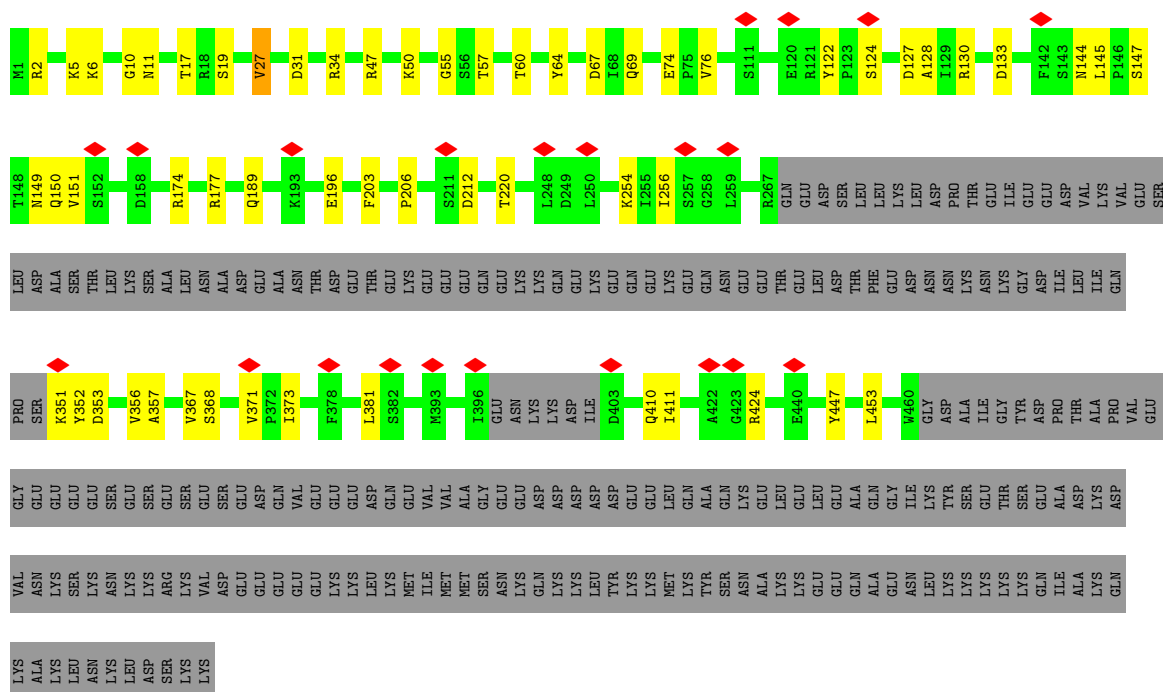
- Molecule 43: Nucleolar GTP-binding protein 2

Chain m:  8% 77% 17% 5%

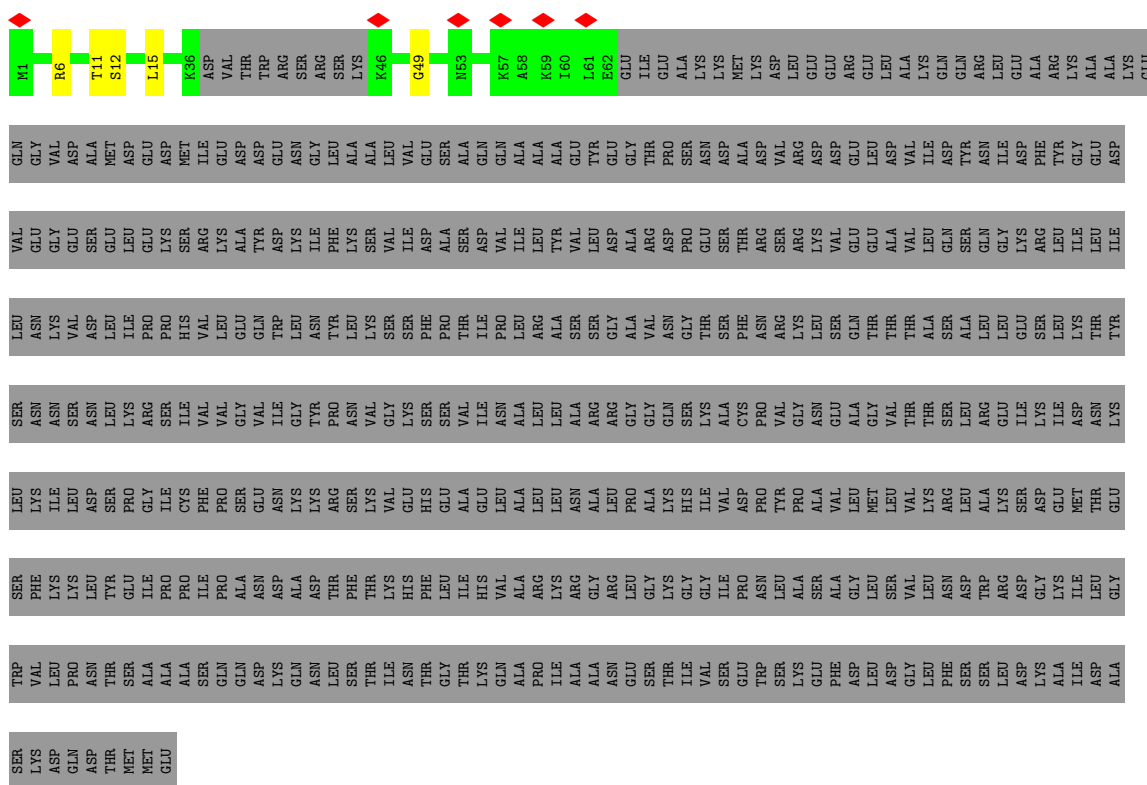


- Molecule 44: Pescadillo homolog

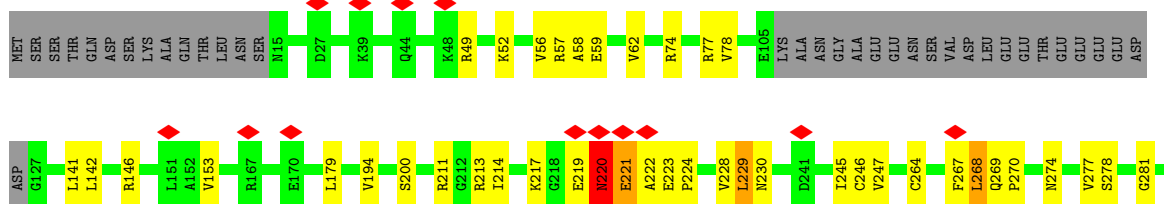
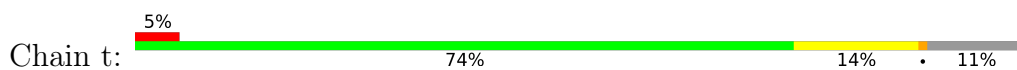
Chain n:  52% 9% 39%



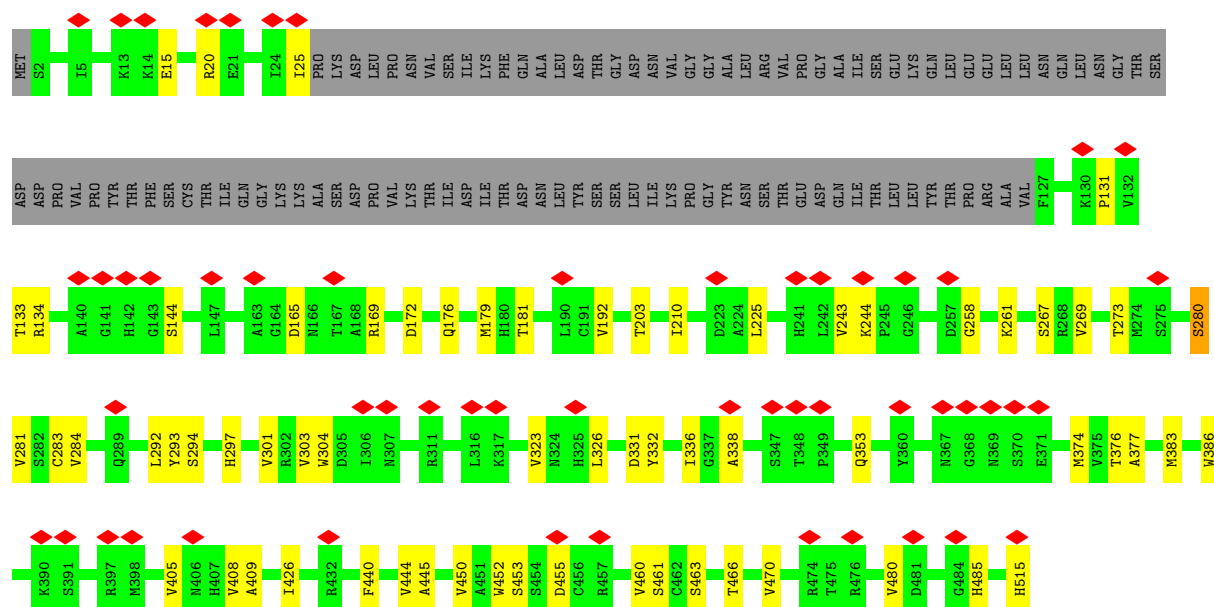
- Molecule 49: Nuclear GTP-binding protein NUG1



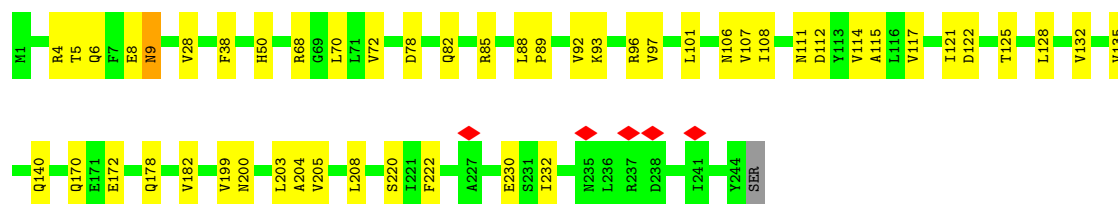
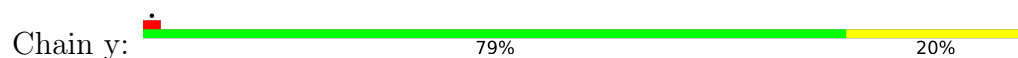
- Molecule 50: Ribosome biogenesis protein RLP7



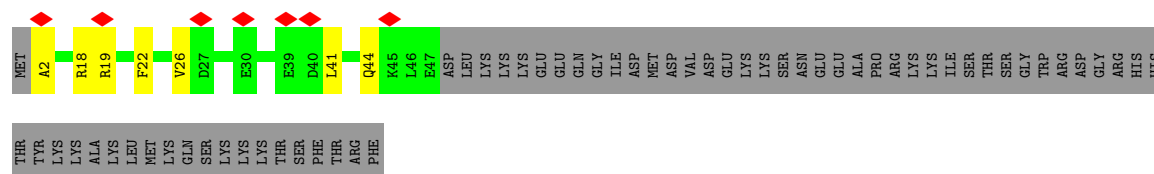
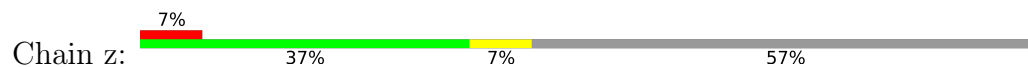




- Molecule 55: Eukaryotic translation initiation factor 6



- Molecule 56: UPF0642 protein YBL028C



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	34162	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 ($e^-/\text{\AA}^2$)	84.67	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.165	Depositor
Minimum map value	-0.045	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.021	Depositor
Map size (Å)	425.40002, 425.40002, 425.40002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0635, 1.0635, 1.0635	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 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	1	0.08	0/73123	0.23	0/113993
2	2	0.08	0/3746	0.22	0/5832
3	3	0.07	0/2883	0.21	0/4491
4	5	0.13	0/455	0.25	0/596
5	6	0.09	0/1527	0.31	0/2371
6	A	0.13	0/1662	0.31	0/2236
7	B	0.11	0/3152	0.30	0/4239
8	C	0.10	0/2801	0.28	0/3792
9	D	0.10	0/2158	0.28	0/2910
10	E	0.11	0/1260	0.25	0/1694
11	F	0.11	0/1821	0.33	0/2451
12	G	0.12	0/1849	0.30	0/2495
13	H	0.10	0/1539	0.30	0/2073
14	J	0.12	0/1374	0.30	0/1842
15	K	0.11	0/2066	0.30	0/2789
16	L	0.12	0/1524	0.32	0/2046
17	M	0.11	0/1074	0.27	0/1446
18	N	0.16	0/1757	0.31	0/2354
19	O	0.11	0/1585	0.24	0/2128
20	P	0.11	0/1424	0.28	0/1911
21	Q	0.11	0/1050	0.25	0/1419
22	R	0.12	0/1275	0.29	0/1702
23	S	0.11	0/1473	0.29	0/1980
24	T	0.14	0/937	0.34	0/1256
25	U	0.10	0/817	0.27	0/1108
26	V	0.11	0/1018	0.28	0/1369
27	W	0.11	0/1918	0.30	0/2586
28	X	0.10	0/1116	0.27	0/1503
29	Y	0.11	0/1004	0.26	0/1341
30	Z	0.14	0/1118	0.30	0/1497
31	a	0.12	0/751	0.23	0/1013
32	b	0.12	0/4435	0.30	0/5971

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.11	0/751	0.24	0/1008
34	d	0.12	0/870	0.26	0/1168
35	e	0.12	0/1041	0.27	0/1394
36	f	0.12	0/868	0.28	0/1168
37	g	0.12	0/891	0.27	0/1191
38	h	0.11	0/978	0.25	0/1301
39	i	0.13	0/778	0.29	0/1034
40	j	0.14	0/685	0.27	0/908
41	k	0.13	0/618	0.27	0/826
42	l	0.14	0/443	0.29	0/588
43	m	0.13	0/3794	0.34	0/5108
44	n	0.11	0/3101	0.34	1/4187 (0.0%)
45	o	0.10	0/1129	0.26	0/1502
46	p	0.14	0/701	0.32	0/934
47	q	0.12	0/1254	0.33	0/1675
48	r	0.11	0/1892	0.34	0/2528
49	s	0.10	0/440	0.30	0/573
50	t	0.12	0/2333	0.35	0/3128
51	u	0.12	0/1287	0.32	0/1711
52	v	0.10	0/2361	0.25	0/3153
53	w	0.11	0/1471	0.29	0/1980
54	x	0.09	0/3313	0.25	0/4490
55	y	0.10	0/1872	0.28	0/2548
56	z	0.12	0/371	0.26	0/489
All	All	0.10	0/158934	0.26	1/231026 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
11	F	0	1
30	Z	0	1
32	b	0	1
43	m	0	1
50	t	0	2
All	All	0	6

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	n	151	VAL	N-CA-C	-5.54	107.24	111.62

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	F	158	LYS	Peptide
30	Z	104	PRO	Peptide
32	b	369	ARG	Peptide
43	m	77	TRP	Peptide
50	t	220	ASN	Peptide
50	t	221	GLU	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	1	65327	32819	32829	831	0
2	2	3353	1695	1695	70	0
3	3	2579	1304	1304	26	0
4	5	452	475	474	0	0
5	6	1370	691	692	29	0
6	A	1630	1684	1682	33	0
7	B	3081	3166	3165	50	0
8	C	2749	2864	2863	36	0
9	D	2112	2066	2064	27	0
10	E	1239	1328	1326	14	0
11	F	1784	1863	1862	27	0
12	G	1817	1909	1908	44	0
13	H	1518	1587	1587	33	0
14	J	1353	1384	1383	16	0
15	K	2032	2121	2119	28	0
16	L	1499	1558	1558	28	0
17	M	1059	1155	1154	20	0
18	N	1720	1780	1779	39	0
19	O	1555	1660	1659	6	0
20	P	1402	1443	1441	20	0
21	Q	1035	1116	1115	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	R	1258	1343	1342	14	0
23	S	1437	1476	1475	19	0
24	T	924	978	975	17	0
25	U	801	816	815	9	0
26	V	1003	1049	1048	19	0
27	W	1885	1921	1921	24	0
28	X	1100	1188	1187	17	0
29	Y	993	1082	1081	11	0
30	Z	1092	1156	1155	18	0
31	a	735	777	776	8	0
32	b	4357	4427	4425	69	0
33	c	743	798	797	9	0
34	d	856	905	904	11	0
35	e	1020	1092	1090	15	0
36	f	850	881	880	13	0
37	g	881	950	949	12	0
38	h	969	1079	1078	18	0
39	i	771	850	849	9	0
40	j	670	678	673	18	0
41	k	612	683	682	5	0
42	l	436	476	475	10	0
43	m	3720	3788	3786	63	0
44	n	3030	3109	3107	38	0
45	o	1107	1160	1159	20	0
46	p	694	740	734	13	0
47	q	1233	1268	1266	11	0
48	r	1860	1967	1965	34	0
49	s	436	499	498	4	0
50	t	2306	2456	2454	33	0
51	u	1265	1317	1314	22	0
52	v	2318	2400	2398	22	0
53	w	1448	1512	1510	21	0
54	x	3231	3207	3202	43	0
55	y	1849	1836	1836	34	0
56	z	370	402	401	7	0
57	b	1	0	0	0	0
57	m	1	0	0	0	0
58	j	1	0	0	0	0
58	p	1	0	0	0	0
58	u	1	0	0	0	0
All	All	148931	115934	115866	1722	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 (1722) 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)
2:2:13:A:O2'	20:P:121:GLN:O	1.82	0.96
1:1:960:U:O2'	1:1:961:C:O2	1.83	0.95
1:1:2868:U:O2'	1:1:2869:U:OP2	1.84	0.95
50:t:229:LEU:HD11	50:t:247:VAL:HG21	1.48	0.95
1:1:408:A:N3	1:1:655:C:O2'	2.01	0.93
1:1:2100:A:O2'	1:1:2101:C:O4'	1.89	0.91
1:1:1477:A:OP1	1:1:3075:G:O2'	1.90	0.90
1:1:2673:A:OP1	14:J:95:ASN:ND2	2.05	0.89
11:F:158:LYS:O	11:F:160:ARG:N	2.06	0.89
1:1:1482:A:O2'	1:1:1483:G:OP2	1.89	0.88
1:1:3094:A:OP1	26:V:14:SER:OG	1.91	0.88
3:3:97:A:O2'	3:3:98:C:O4'	1.92	0.87
1:1:2964:G:O2'	43:m:31:ARG:NH2	2.08	0.87
1:1:2624:G:O2'	1:1:2656:A:N1	2.07	0.86
1:1:1105:A:O2'	1:1:1106:G:O4'	1.92	0.86
1:1:1712:G:N2	1:1:1733:G:O6	2.08	0.86
1:1:1152:G:N2	1:1:1152:G:OP2	2.07	0.86
1:1:1353:U:O2'	10:E:8:LYS:O	1.93	0.86
1:1:2416:U:O2	1:1:2966:G:N2	2.09	0.86
1:1:3149:G:O2'	7:B:129:ALA:O	1.92	0.85
1:1:2753:G:O2'	1:1:2754:G:OP2	1.94	0.85
5:6:16:U:O2'	5:6:17:G:OP2	1.93	0.85
1:1:3350:C:O2'	1:1:3351:U:OP1	1.94	0.85
1:1:649:A:O2'	1:1:650:C:OP1	1.95	0.84
7:B:53:MET:SD	7:B:77:THR:OG1	2.35	0.84
1:1:879:U:O2'	1:1:880:G:OP1	1.96	0.84
1:1:2501:U:O2'	1:1:2502:A:OP1	1.96	0.84
1:1:2857:C:O2'	1:1:2858:U:OP1	1.96	0.83
36:f:16:TYR:OH	36:f:89:LEU:O	1.96	0.83
1:1:297:G:OP2	1:1:297:G:N2	2.11	0.83
1:1:2276:G:N2	43:m:267:THR:OG1	2.11	0.83
1:1:2808:A:O2'	1:1:2969:A:OP1	1.96	0.83
1:1:3305:A:O2'	1:1:3306:U:O4'	1.95	0.83
1:1:2890:A:O2'	1:1:2933:A:N3	2.12	0.83
1:1:1:G:O2'	1:1:2:U:OP2	1.96	0.82
1:1:2628:A:N6	1:1:2650:U:C2	2.47	0.82
1:1:2757:U:OP1	53:w:198:ASN:ND2	2.13	0.82
1:1:3367:C:OP2	1:1:3368:U:O2'	1.97	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:960:U:O2'	1:1:961:C:O5'	1.99	0.81
1:1:3015:G:OP2	56:z:2:ALA:N	2.14	0.81
1:1:1229:G:O2'	27:W:47:ASP:OD1	1.98	0.81
5:6:232:A:OP1	50:t:52:LYS:NZ	2.14	0.80
1:1:422:A:N6	1:1:2362:C:O2	2.14	0.80
54:x:466:THR:OG1	54:x:485:HIS:O	1.99	0.80
1:1:289:A:O2'	18:N:93:LYS:O	1.99	0.80
1:1:2634:U:O2	1:1:2642:A:N6	2.15	0.80
2:2:128:U:O2	44:n:11:ASN:ND2	2.15	0.80
45:o:121:ARG:NH2	45:o:175:LYS:O	2.13	0.80
1:1:1566:A:N6	44:n:212:ASP:O	2.13	0.80
1:1:2349:U:O2'	1:1:3307:A:N3	2.14	0.80
1:1:117:U:O2'	1:1:119:U:OP2	2.00	0.80
1:1:2377:G:OP1	1:1:2378:C:N4	2.14	0.80
1:1:399:A:O2'	1:1:403:C:O2'	2.00	0.79
1:1:2830:G:N2	48:r:254:CYS:SG	2.54	0.79
1:1:1364:C:OP1	11:F:110:ARG:NH1	2.15	0.79
1:1:2215:A:O2'	1:1:2430:A:O2'	2.00	0.79
1:1:2626:A:O2'	1:1:2627:C:O4'	2.01	0.79
32:b:352:SER:O	32:b:355:ASN:ND2	2.15	0.79
1:1:1844:C:O2'	40:j:8:PHE:O	2.01	0.79
1:1:2643:A:HO2'	1:1:2694:A:HO2'	1.30	0.79
1:1:2764:C:N4	1:1:2795:U:C4	2.50	0.79
1:1:102:C:O2'	16:L:62:THR:OG1	2.00	0.79
1:1:3353:G:O2'	1:1:3354:U:OP1	2.01	0.78
2:2:103:G:OP2	2:2:105:A:O2'	2.00	0.78
1:1:2513:U:O2'	1:1:2514:U:O5'	2.01	0.78
1:1:1722:U:OP2	22:R:103:ARG:NH2	2.17	0.78
1:1:356:C:O2'	8:C:81:GLY:O	2.00	0.78
1:1:1115:G:OP2	1:1:1115:G:N2	2.16	0.78
1:1:3341:U:O2'	1:1:3342:A:OP2	2.00	0.78
5:6:27:G:OP1	45:o:130:ASN:ND2	2.17	0.78
1:1:68:C:OP2	1:1:301:G:N2	2.17	0.78
1:1:764:U:O2'	1:1:765:C:OP1	2.00	0.78
1:1:1117:G:O6	1:1:1142:G:N2	2.17	0.78
1:1:1329:U:O2'	1:1:1330:A:OP1	2.02	0.78
1:1:1222:G:O2'	1:1:1223:A:OP2	2.01	0.78
1:1:518:G:N2	1:1:518:G:OP2	2.16	0.77
1:1:806:A:O2'	1:1:2812:C:O2'	2.02	0.77
1:1:1543:G:O2'	1:1:2168:A:O2'	2.01	0.77
1:1:1063:G:N3	1:1:1066:G:O2'	2.17	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1117:G:O2'	1:1:1118:C:OP2	2.01	0.77
1:1:1942:U:OP2	22:R:74:ARG:NH1	2.16	0.77
5:6:39:U:O4	45:o:191:LYS:NZ	2.18	0.77
1:1:63:A:N3	1:1:78:U:O2'	2.16	0.77
1:1:2802:A:O2'	1:1:2803:A:OP1	2.01	0.77
1:1:1794:G:O2'	1:1:1796:G:N2	2.16	0.77
1:1:929:A:O2'	40:j:49:TRP:O	2.02	0.77
8:C:139:GLY:O	8:C:141:ARG:NH1	2.18	0.77
1:1:188:U:O2'	1:1:207:U:O2	2.01	0.77
1:1:211:A:OP1	8:C:220:ARG:NH1	2.17	0.77
1:1:1394:A:N6	1:1:1416:C:O2	2.17	0.77
32:b:70:ASN:ND2	32:b:72:ASN:OD1	2.18	0.77
1:1:2165:G:N2	1:1:2168:A:OP2	2.18	0.77
1:1:2343:C:O2'	1:1:3056:U:OP1	2.01	0.77
1:1:2992:U:OP1	1:1:3310:A:O2'	2.03	0.77
2:2:110:C:O2'	2:2:112:U:OP2	2.01	0.77
5:6:38:U:O2	5:6:42:G:O6	2.02	0.77
1:1:67:A:O2'	1:1:315:C:O2	2.01	0.77
32:b:11:VAL:HG12	32:b:64:ILE:HD12	1.67	0.77
32:b:177:ASN:ND2	32:b:196:PRO:O	2.18	0.76
16:L:76:THR:HG22	16:L:101:ARG:HB3	1.67	0.76
1:1:59:G:O5'	2:2:33:A:O2'	2.03	0.76
1:1:422:A:N1	1:1:2362:C:O2'	2.18	0.76
1:1:2112:U:OP1	51:u:44:ARG:NH2	2.19	0.76
1:1:3170:A:O5'	36:f:56:SER:OG	2.01	0.76
1:1:1474:A:O2'	34:d:57:GLN:NE2	2.19	0.76
1:1:3110:C:O2'	13:H:155:SER:OG	2.01	0.76
43:m:50:ASN:OD1	43:m:54:ASN:N	2.18	0.76
1:1:10:C:O2	1:1:1558:A:N6	2.18	0.76
1:1:1312:C:O2'	19:O:83:ALA:O	2.03	0.76
1:1:1493:G:N2	1:1:1493:G:OP2	2.19	0.76
1:1:1508:C:HO2'	1:1:2353:G:HO2'	0.76	0.76
1:1:2693:C:O2'	52:v:11:ARG:NH1	2.19	0.76
1:1:1419:A:OP1	2:2:20:U:O2'	2.02	0.76
1:1:2964:G:N2	1:1:2967:A:OP2	2.16	0.76
1:1:1176:C:OP2	1:1:1177:G:O2'	2.03	0.75
1:1:3030:G:O2'	1:1:3031:G:OP1	2.02	0.75
1:1:3018:C:OP1	55:y:9:ASN:ND2	2.19	0.75
23:S:22:PRO:O	24:T:146:ASN:ND2	2.20	0.75
1:1:239:G:OP1	38:h:94:LYS:NZ	2.19	0.75
1:1:1580:A:OP2	1:1:2522:G:N1	2.20	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2416:U:O2'	1:1:2966:G:N3	2.20	0.75
1:1:2726:C:O2'	1:1:2728:G:OP1	2.04	0.75
27:W:45:LEU:HD12	27:W:48:VAL:HG21	1.68	0.75
48:r:203:ASN:OD1	48:r:219:THR:OG1	2.03	0.75
1:1:2215:A:HO2'	1:1:2430:A:HO2'	1.28	0.75
12:G:132:VAL:HG12	12:G:200:LEU:HD11	1.68	0.75
1:1:412:G:OP1	20:P:62:ARG:NH1	2.20	0.74
1:1:717:C:OP1	1:1:751:A:O2'	2.03	0.74
38:h:83:LYS:O	40:j:73:ARG:NH1	2.20	0.74
1:1:3020:U:OP2	1:1:3021:A:O2'	2.02	0.74
1:1:2970:C:O2'	1:1:2972:G:OP2	2.04	0.74
1:1:3375:A:O2'	1:1:3378:C:OP2	2.05	0.74
1:1:2605:G:O2'	1:1:2607:G:N7	2.21	0.74
32:b:243:ILE:O	32:b:281:LYS:NZ	2.17	0.74
43:m:215:LEU:HD22	43:m:370:ILE:HG12	1.70	0.74
1:1:951:A:O2'	1:1:969:C:O2'	2.03	0.74
1:1:429:U:O2'	36:f:88:ASN:O	2.04	0.74
32:b:398:LEU:O	32:b:401:ASP:N	2.21	0.74
48:r:215:LEU:O	48:r:219:THR:OG1	2.05	0.74
12:G:81:THR:HG21	12:G:181:LYS:HD2	1.70	0.73
23:S:89:ASN:ND2	49:s:49:GLY:O	2.21	0.73
1:1:1693:C:O2'	1:1:1772:U:O3'	2.06	0.73
1:1:1805:C:OP1	37:g:71:THR:OG1	2.03	0.73
1:1:209:A:O2'	1:1:211:A:OP2	2.06	0.73
1:1:762:U:O4	1:1:769:G:N2	2.20	0.73
1:1:1390:A:N6	1:1:1418:A:O2'	2.21	0.73
15:K:184:ASP:OD2	15:K:208:SER:OG	2.05	0.73
5:6:58:G:OP1	5:6:58:G:N2	2.20	0.73
51:u:2:ARG:NH1	55:y:78:ASP:OD1	2.21	0.73
1:1:200:C:N4	1:1:218:G:OP1	2.21	0.72
1:1:1404:G:N2	1:1:1407:A:OP2	2.21	0.72
16:L:61:PRO:O	16:L:62:THR:OG1	2.07	0.72
1:1:1304:A:N1	1:1:2938:G:O2'	2.20	0.72
1:1:3190:C:OP1	19:O:172:ARG:NH1	2.22	0.72
1:1:3060:C:O2	1:1:3332:U:O2'	2.06	0.72
1:1:3026:G:N2	1:1:3029:A:OP2	2.22	0.72
18:N:124:ASP:OD1	18:N:127:TYR:N	2.22	0.72
1:1:687:U:OP2	16:L:36:ARG:NH2	2.22	0.72
1:1:3116:G:OP1	1:1:3116:G:N2	2.18	0.72
1:1:3268:A:OP1	10:E:46:ARG:NH1	2.22	0.72
1:1:117:U:O4	12:G:145:ASN:ND2	2.21	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:D:91:GLY:O	9:D:94:ASN:ND2	2.22	0.72
55:y:85:ARG:NH1	55:y:89:PRO:O	2.23	0.72
1:1:348:A:N3	1:1:352:A:O2'	2.23	0.71
1:1:991:G:N2	24:T:59:GLY:O	2.22	0.71
8:C:126:ILE:O	8:C:129:THR:OG1	2.07	0.71
43:m:260:ASN:ND2	43:m:326:THR:O	2.23	0.71
1:1:1:G:N1	5:6:232:A:OP2	2.23	0.71
1:1:2243:A:O2'	1:1:2244:A:OP1	2.06	0.71
1:1:3020:U:OP1	32:b:400:ARG:NH2	2.23	0.71
1:1:54:C:O2'	1:1:1547:G:O2'	2.01	0.71
1:1:1488:G:O2'	37:g:10:ARG:O	2.07	0.71
1:1:2764:C:N4	1:1:2795:U:N3	2.39	0.71
1:1:47:C:OP2	1:1:48:A:O2'	2.04	0.71
1:1:2555:G:N2	30:Z:135:ARG:O	2.24	0.71
6:A:180:LEU:HD11	46:p:26:VAL:HG21	1.72	0.71
18:N:94:TYR:OH	18:N:101:THR:OG1	2.09	0.71
5:6:7:C:O2'	5:6:8:A:OP2	2.09	0.70
1:1:2393:G:O2'	1:1:2982:A:N6	2.23	0.70
55:y:101:LEU:HB3	55:y:107:VAL:HG21	1.73	0.70
1:1:421:G:O6	1:1:2383:C:O2'	2.07	0.70
1:1:436:A:OP2	1:1:621:A:N6	2.25	0.70
51:u:25:ASP:OD2	51:u:27:LYS:NZ	2.25	0.70
1:1:297:G:O2'	39:i:31:GLY:O	2.07	0.70
35:e:42:VAL:O	35:e:52:GLN:NE2	2.25	0.70
1:1:1188:U:OP1	1:1:1210:U:O2'	2.09	0.70
1:1:1282:G:H5'	27:W:99:VAL:HG22	1.74	0.70
32:b:210:ASP:OD1	32:b:215:ARG:NH1	2.23	0.70
43:m:377:ASP:HB3	43:m:382:ILE:HD11	1.72	0.70
52:v:279:LYS:NZ	52:v:281:ASP:OD1	2.25	0.70
1:1:807:A:O2'	1:1:808:A:O5'	2.05	0.70
1:1:1063:G:O2'	1:1:1097:G:N2	2.24	0.70
1:1:3100:U:O2'	1:1:3101:G:OP2	2.07	0.70
27:W:88:ASN:ND2	27:W:226:SER:O	2.24	0.70
35:e:98:HIS:O	35:e:125:ARG:NH2	2.25	0.70
1:1:1361:U:O2'	11:F:159:GLN:OE1	2.09	0.69
1:1:1686:U:O2	1:1:1688:U:O2'	2.04	0.69
1:1:2129:U:O2'	1:1:2144:A:O4'	2.08	0.69
1:1:53:G:OP2	40:j:48:ASN:ND2	2.25	0.69
1:1:600:G:N2	1:1:603:A:OP2	2.21	0.69
1:1:2969:A:O2'	1:1:2970:C:O5'	2.11	0.69
1:1:2245:C:O2'	1:1:2246:G:O5'	2.05	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:G:160:ILE:O	12:G:164:VAL:HG13	1.92	0.69
1:1:34:A:OP2	18:N:73:ARG:NH2	2.25	0.69
1:1:800:G:OP1	16:L:19:GLN:NE2	2.26	0.69
48:r:224:ASN:ND2	48:r:226:SER:OG	2.26	0.69
1:1:2767:U:O2'	1:1:2768:U:O4'	2.11	0.69
1:1:3041:U:OP1	26:V:12:ARG:NH1	2.25	0.69
1:1:1174:G:N2	19:O:87:MET:SD	2.66	0.69
1:1:1713:G:O2'	1:1:1730:G:N2	2.26	0.69
1:1:3092:C:O2'	1:1:3094:A:OP2	2.10	0.69
2:2:149:A:N3	12:G:55:TYR:OH	2.23	0.69
55:y:200:ASN:OD1	55:y:203:LEU:N	2.25	0.69
1:1:98:G:N7	16:L:13:HIS:NE2	2.41	0.68
1:1:1064:A:O2'	1:1:1065:A:OP2	2.08	0.68
1:1:1405:U:H3	35:e:55:ILE:HD12	1.58	0.68
1:1:1326:A:O2'	36:f:77:ASN:OD1	2.09	0.68
45:o:153:ASN:OD1	45:o:165:ARG:NH1	2.26	0.68
47:q:214:VAL:HG12	47:q:215:LYS:H	1.57	0.68
54:x:283:CYS:SG	54:x:326:LEU:N	2.65	0.68
1:1:126:U:OP1	18:N:144:ARG:NH1	2.26	0.68
1:1:2415:C:OP1	6:A:2:GLY:N	2.27	0.68
1:1:294:U:OP2	18:N:15:GLN:NE2	2.27	0.68
1:1:856:G:OP1	22:R:92:GLN:NE2	2.27	0.68
1:1:1447:G:N2	1:1:2356:A:OP2	2.25	0.68
1:1:517:G:OP1	11:F:67:ARG:NH2	2.26	0.68
44:n:50:LYS:O	44:n:55:GLY:N	2.27	0.68
1:1:1219:C:O2'	1:1:1286:A:N1	2.26	0.68
43:m:223:ASP:OD1	43:m:313:ARG:NH1	2.27	0.68
28:X:20:GLY:O	47:q:448:LYS:N	2.27	0.67
1:1:2124:G:O3'	43:m:437:ARG:NH2	2.26	0.67
1:1:2568:C:OP2	1:1:2569:A:N6	2.27	0.67
1:1:2263:C:O2'	1:1:2264:U:OP1	2.13	0.67
1:1:1757:A:O2'	25:U:104:ARG:NH2	2.27	0.67
28:X:58:ASP:OD1	38:h:25:LYS:NZ	2.28	0.67
44:n:67:ASP:OD1	47:q:206:THR:OG1	2.12	0.67
54:x:284:VAL:HG23	54:x:294:SER:HB3	1.77	0.67
1:1:760:G:O2'	1:1:761:A:OP2	2.13	0.67
1:1:1729:A:N6	46:p:41:PHE:O	2.27	0.67
9:D:34:LYS:O	9:D:38:THR:OG1	2.12	0.67
1:1:746:A:OP1	21:Q:145:ASN:ND2	2.29	0.66
1:1:2793:G:O2'	1:1:2794:G:O4'	2.13	0.66
3:3:44:C:OP2	14:J:137:ARG:NH2	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:6:51:U:O2'	5:6:54:A:N7	2.28	0.66
1:1:2891:U:O2'	1:1:3014:U:OP1	2.13	0.66
50:t:74:ARG:NH2	50:t:303:ASN:OD1	2.27	0.66
1:1:2966:G:O6	43:m:31:ARG:NH2	2.29	0.66
14:J:58:GLY:O	14:J:60:ARG:NH1	2.28	0.66
7:B:274:SER:O	7:B:275:ARG:NE	2.29	0.66
1:1:72:C:H4'	16:L:63:VAL:HG22	1.77	0.66
16:L:176:GLU:OE1	16:L:183:ARG:NH1	2.28	0.66
43:m:263:ASP:O	52:v:287:THR:OG1	2.13	0.66
1:1:1776:G:O2'	1:1:1777:U:O4'	2.11	0.66
5:6:1:C:O2'	5:6:2:C:OP2	2.12	0.66
1:1:1057:A:O2'	1:1:1058:U:O5'	2.14	0.66
1:1:1142:G:OP2	1:1:1143:A:O2'	2.05	0.66
1:1:2569:A:O2'	1:1:2570:U:OP2	2.11	0.66
43:m:378:SER:OG	43:m:381:ASP:OD2	2.10	0.66
2:2:150:G:O2'	12:G:59:GLN:NE2	2.28	0.66
1:1:36:C:O2'	1:1:934:G:N3	2.29	0.65
19:O:120:VAL:HG13	23:S:162:THR:O	1.95	0.65
27:W:75:LYS:NZ	27:W:79:GLU:OE1	2.30	0.65
33:c:60:ALA:O	33:c:64:LYS:N	2.29	0.65
45:o:92:ILE:HG23	45:o:167:LEU:HB2	1.78	0.65
7:B:269:GLN:NE2	7:B:270:ARG:O	2.29	0.65
30:Z:22:LYS:NZ	30:Z:129:TRP:O	2.27	0.65
32:b:169:THR:O	32:b:248:SER:OG	2.10	0.65
1:1:527:A:N6	1:1:566:G:O6	2.29	0.65
1:1:1746:U:O2'	41:k:4:GLU:OE2	2.15	0.65
1:1:2895:G:OP1	13:H:166:ARG:NH1	2.29	0.65
1:1:358:G:N2	1:1:361:A:OP2	2.28	0.65
1:1:2643:A:O2'	1:1:2694:A:O2'	2.07	0.65
32:b:247:ARG:O	32:b:248:SER:OG	2.15	0.65
1:1:3184:A:N3	1:1:3187:A:O2'	2.28	0.65
1:1:3284:G:O2'	1:1:3285:C:O4'	2.13	0.64
26:V:81:GLN:O	26:V:98:ASN:ND2	2.31	0.64
28:X:115:ARG:NE	28:X:119:THR:OG1	2.30	0.64
1:1:1447:G:N7	20:P:25:SER:OG	2.31	0.64
32:b:359:ASN:OD1	55:y:170:GLN:NE2	2.31	0.64
1:1:1097:G:O2'	1:1:1098:A:OP2	2.08	0.64
1:1:2810:C:OP2	1:1:2955:U:O2'	2.06	0.64
7:B:287:LYS:O	7:B:293:ASN:ND2	2.31	0.64
8:C:168:ALA:O	8:C:172:VAL:HG23	1.97	0.64
8:C:269:SER:OG	8:C:274:TYR:O	2.10	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:N:142:ILE:HG21	18:N:151:ILE:HD11	1.78	0.64
26:V:86:ARG:O	26:V:88:ARG:NH1	2.30	0.64
1:1:1122:U:O2'	1:1:1123:U:O5'	2.08	0.64
1:1:2719:U:O2'	1:1:2720:G:O4'	2.12	0.64
13:H:23:ARG:NH2	13:H:39:LYS:O	2.30	0.64
1:1:1:G:OP2	1:1:1:G:N2	2.31	0.64
1:1:1411:C:OP1	35:e:98:HIS:ND1	2.31	0.64
26:V:91:VAL:HG21	51:u:30:ARG:HH12	1.62	0.64
34:d:88:PRO:O	34:d:89:LEU:HD12	1.98	0.64
6:A:180:LEU:CD1	46:p:26:VAL:HG21	2.28	0.64
18:N:9:GLU:HB3	39:i:44:VAL:HG21	1.80	0.64
1:1:160:G:HO2'	1:1:161:G:P	2.20	0.64
1:1:2851:A:N3	48:r:55:TYR:OH	2.27	0.64
1:1:3060:C:O3'	1:1:3371:G:N2	2.31	0.64
1:1:849:C:O2'	1:1:850:U:OP1	2.13	0.64
53:w:76:SER:O	54:x:134:ARG:NH1	2.30	0.64
1:1:1254:C:O2'	1:1:1255:C:O4'	2.11	0.64
1:1:3050:U:O2'	51:u:16:GLY:O	2.14	0.64
32:b:368:ALA:O	55:y:178:GLN:NE2	2.31	0.64
54:x:15:GLU:O	54:x:20:ARG:NH1	2.31	0.64
1:1:3113:A:OP1	13:H:69:ARG:NH1	2.31	0.63
23:S:48:LEU:HD12	24:T:151:LEU:HD12	1.80	0.63
2:2:95:G:OP1	40:j:76:ASN:ND2	2.31	0.63
5:6:231:A:O2'	5:6:232:A:N3	2.25	0.63
1:1:769:G:O2'	1:1:770:G:O4'	2.16	0.63
50:t:229:LEU:HD13	50:t:229:LEU:O	1.97	0.63
1:1:172:G:O6	1:1:247:C:N4	2.31	0.63
1:1:675:C:O2'	1:1:679:U:OP1	2.15	0.63
1:1:936:A:O2'	1:1:938:C:N4	2.31	0.63
2:2:156:U:OP1	12:G:84:ARG:NH2	2.31	0.63
1:1:1194:G:O2'	1:1:1319:G:O2'	2.16	0.63
5:6:56:U:O2'	5:6:57:U:OP2	2.10	0.63
1:1:2432:A:N6	1:1:2598:G:O6	2.31	0.63
3:3:28:C:OP1	14:J:137:ARG:NH1	2.31	0.63
6:A:19:HIS:ND1	6:A:190:ARG:O	2.30	0.63
34:d:98:VAL:HG21	34:d:104:LEU:HD11	1.80	0.63
48:r:151:ILE:HG22	48:r:153:LYS:H	1.63	0.63
20:P:126:ARG:NE	20:P:140:GLU:OE1	2.31	0.63
5:6:38:U:O2	5:6:42:G:C6	2.52	0.63
1:1:596:C:OP1	11:F:37:ASN:ND2	2.32	0.62
1:1:1241:U:N3	1:1:1244:A:OP1	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:n:124:SER:O	44:n:127:ASP:N	2.30	0.62
2:2:52:A:H62	42:l:27:ILE:HD13	1.64	0.62
33:c:66:LYS:NZ	33:c:101:LEU:O	2.32	0.62
1:1:286:U:O2'	18:N:179:LYS:O	2.16	0.62
1:1:959:C:O2'	1:1:960:U:O2	2.15	0.62
1:1:2501:U:HO2'	1:1:2502:A:P	2.22	0.62
50:t:245:ILE:HG22	50:t:246:CYS:H	1.64	0.62
1:1:1884:A:N6	1:1:2349:U:O4	2.33	0.62
8:C:283:THR:HG22	8:C:285:ASP:H	1.63	0.62
1:1:3179:U:O4	1:1:3208:G:N2	2.32	0.62
11:F:140:SER:N	11:F:237:ASN:OD1	2.33	0.62
15:K:279:ILE:HD13	15:K:292:TYR:HD1	1.65	0.62
53:w:161:GLU:O	53:w:162:VAL:HG13	2.00	0.62
9:D:196:ARG:NH2	54:x:179:MET:SD	2.73	0.62
15:K:124:LEU:HD23	15:K:125:LEU:N	2.15	0.62
21:Q:125:ASP:O	21:Q:129:VAL:HG23	2.00	0.62
1:1:351:A:N6	42:l:37:TYR:O	2.33	0.62
1:1:1655:G:N2	1:1:1801:U:O4	2.32	0.62
1:1:2249:G:N7	52:v:262:ASN:ND2	2.47	0.62
15:K:279:ILE:HD13	15:K:292:TYR:CD1	2.35	0.62
11:F:154:GLY:N	11:F:161:VAL:O	2.27	0.62
54:x:301:VAL:HG23	54:x:323:VAL:HG21	1.80	0.62
1:1:2537:U:O2'	1:1:2538:U:O5'	2.17	0.62
26:V:85:TRP:NE1	26:V:121:GLU:OE2	2.32	0.62
43:m:378:SER:O	43:m:381:ASP:N	2.32	0.62
1:1:65:A:N1	1:1:109:A:O2'	2.30	0.61
1:1:715:A:N1	1:1:781:G:O2'	2.31	0.61
54:x:169:ARG:NH1	54:x:181:THR:OG1	2.33	0.61
1:1:1102:A:O2'	1:1:1104:G:O6	2.18	0.61
1:1:1579:C:H4'	1:1:1580:A:OP1	2.01	0.61
8:C:8:VAL:HG22	8:C:151:VAL:HG11	1.82	0.61
12:G:184:ALA:O	12:G:188:THR:HG23	2.01	0.61
13:H:55:VAL:HG23	13:H:68:LEU:HD11	1.82	0.61
27:W:67:MET:SD	27:W:68:GLY:N	2.73	0.61
1:1:629:U:O2	1:1:630:A:N7	2.34	0.61
1:1:1699:A:N6	1:1:1747:G:O6	2.34	0.61
1:1:632:G:N3	36:f:23:ASN:ND2	2.48	0.61
35:e:109:LEU:HD23	35:e:119:VAL:HG21	1.83	0.61
54:x:453:SER:OG	54:x:455:ASP:OD1	2.17	0.61
55:y:4:ARG:HB3	55:y:208:LEU:HD23	1.83	0.61
1:1:3109:G:N2	13:H:156:GLN:OE1	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:13:A:C2	2:2:14:C:C5	2.89	0.61
15:K:229:VAL:HG22	15:K:233:GLN:OE1	2.01	0.61
48:r:184:VAL:HG21	48:r:223:VAL:HG21	1.83	0.61
50:t:318:LEU:O	50:t:322:ASN:N	2.34	0.61
1:1:1719:G:OP2	22:R:121:HIS:ND1	2.34	0.60
1:1:406:G:O2'	1:1:407:A:OP2	2.19	0.60
1:1:3268:A:N1	10:E:135:VAL:HG22	2.16	0.60
13:H:80:THR:OG1	13:H:86:TYR:OH	2.19	0.60
32:b:324:LEU:O	32:b:324:LEU:HD12	2.00	0.60
1:1:2715:A:OP1	53:w:131:LYS:NZ	2.34	0.60
1:1:2770:G:O2'	1:1:2771:U:OP1	2.16	0.60
3:3:115:G:N2	9:D:72:ASP:O	2.32	0.60
17:M:23:ILE:HA	17:M:63:VAL:HG23	1.82	0.60
43:m:160:LEU:O	43:m:164:THR:HG23	2.01	0.60
1:1:684:G:OP2	16:L:28:GLN:NE2	2.35	0.60
1:1:1097:G:O6	24:T:116:ARG:NH2	2.34	0.60
1:1:336:A:O2'	8:C:48:GLN:NE2	2.35	0.60
27:W:26:ILE:O	27:W:30:VAL:HG23	2.02	0.60
50:t:213:ARG:O	50:t:214:ILE:HD13	2.00	0.60
1:1:799:G:O2'	16:L:18:TRP:NE1	2.34	0.60
1:1:1482:A:N6	1:1:1866:C:O2	2.35	0.60
17:M:34:ALA:N	17:M:47:ASP:O	2.33	0.60
50:t:146:ARG:HA	50:t:194:VAL:HG12	1.84	0.60
1:1:415:G:O6	2:2:9:A:N6	2.34	0.60
1:1:3163:A:N6	1:1:3288:G:O6	2.34	0.60
15:K:97:LEU:HD21	15:K:205:THR:HG21	1.84	0.60
1:1:549:U:O4	1:1:550:A:N6	2.34	0.59
12:G:213:LYS:NZ	45:o:159:GLY:O	2.34	0.59
26:V:130:ALA:O	55:y:106:ASN:ND2	2.35	0.59
1:1:1282:G:C5'	27:W:99:VAL:HG22	2.32	0.59
32:b:363:VAL:HG23	55:y:182:VAL:HG23	1.84	0.59
1:1:845:G:N2	1:1:848:A:OP2	2.30	0.59
7:B:219:ALA:HB2	7:B:336:VAL:HG12	1.84	0.59
2:2:157:U:OP1	50:t:57:ARG:NH1	2.35	0.59
31:a:84:GLU:OE2	31:a:87:ARG:NH2	2.36	0.59
32:b:312:VAL:HG13	32:b:315:VAL:HG13	1.85	0.59
3:3:89:G:N2	3:3:92:A:OP2	2.36	0.59
37:g:62:TYR:O	37:g:65:VAL:HG22	2.02	0.59
1:1:707:U:O2'	1:1:754:G:N3	2.35	0.59
1:1:985:U:O2'	11:F:102:VAL:HG22	2.03	0.59
1:1:1306:G:N2	1:1:1307:G:N7	2.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2207:A:O2'	1:1:2237:C:O2	2.15	0.59
43:m:52:LYS:N	43:m:53:GLY:HA2	2.18	0.59
1:1:1205:A:O2'	1:1:1206:G:O5'	2.19	0.59
1:1:1482:A:HO2'	1:1:1483:G:P	2.25	0.59
1:1:2276:G:O6	52:v:287:THR:HG22	2.02	0.59
1:1:2955:U:OP1	1:1:2977:G:N2	2.33	0.59
1:1:2964:G:OP1	43:m:35:ARG:NH2	2.36	0.59
1:1:1863:G:N1	1:1:1865:A:O5'	2.36	0.59
2:2:75:G:OP2	29:Y:74:TYR:OH	2.21	0.59
17:M:40:ASP:OD2	17:M:43:LYS:NZ	2.29	0.59
1:1:807:A:HO2'	1:1:808:A:P	2.25	0.58
1:1:2692:A:O2'	1:1:2693:C:OP2	2.19	0.58
18:N:44:ARG:NH1	18:N:120:TRP:O	2.35	0.58
45:o:92:ILE:HD12	45:o:173:ILE:HG13	1.83	0.58
1:1:785:G:OP2	21:Q:66:ARG:NH1	2.36	0.58
1:1:1221:A:N7	27:W:20:ARG:NH2	2.50	0.58
1:1:1643:A:O2'	1:1:1644:C:O4'	2.20	0.58
51:u:62:GLU:O	51:u:63:LEU:HD23	2.03	0.58
40:j:54:LYS:O	40:j:58:THR:HG23	2.03	0.58
1:1:64:G:HO2'	1:1:77:A:HO2'	1.47	0.58
1:1:595:G:OP2	11:F:30:ARG:NH2	2.36	0.58
1:1:2947:G:C2	7:B:250:ALA:HB1	2.38	0.58
12:G:168:ALA:HB3	39:i:47:ILE:HD11	1.86	0.58
1:1:1300:G:OP1	48:r:44:GLY:N	2.36	0.58
1:1:1801:U:O2'	37:g:60:ARG:NH1	2.37	0.58
1:1:1920:U:O2'	1:1:1932:A:N7	2.35	0.58
7:B:204:ALA:O	7:B:207:SER:OG	2.20	0.58
14:J:59:ILE:HD13	14:J:65:ILE:HD12	1.84	0.58
43:m:152:LEU:O	43:m:152:LEU:HD13	2.03	0.58
43:m:390:VAL:HG21	43:m:454:LEU:CB	2.34	0.58
51:u:79:VAL:O	55:y:82:GLN:NE2	2.36	0.58
13:H:71:VAL:O	13:H:75:VAL:HG23	2.02	0.58
14:J:134:PRO:O	14:J:152:HIS:NE2	2.36	0.58
17:M:15:VAL:HG22	23:S:150:PHE:O	2.03	0.58
25:U:80:THR:HG21	25:U:95:PHE:CE2	2.39	0.58
43:m:371:VAL:HG21	43:m:387:VAL:HG11	1.84	0.58
1:1:2099:A:N1	1:1:2100:A:N6	2.51	0.58
1:1:2149:A:OP1	6:A:196:TRP:NE1	2.33	0.58
52:v:187:GLN:OE1	53:w:46:ARG:NH2	2.36	0.58
1:1:908:G:N2	1:1:925:A:N7	2.52	0.58
1:1:1678:G:O2'	1:1:1756:C:OP1	2.21	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3049:A:O2'	7:B:55:THR:N	2.36	0.58
18:N:155:VAL:O	18:N:162:ARG:NH2	2.36	0.58
32:b:363:VAL:HG21	55:y:230:GLU:OE2	2.03	0.58
34:d:10:ARG:HD3	34:d:108:VAL:HG22	1.85	0.58
51:u:62:GLU:C	51:u:63:LEU:HD23	2.29	0.58
1:1:80:G:O6	1:1:106:A:N6	2.36	0.58
1:1:1180:A:OP1	36:f:78:SER:N	2.37	0.58
47:q:392:GLU:OE1	47:q:393:ARG:N	2.36	0.58
1:1:2116:G:OP1	1:1:2118:C:N4	2.36	0.58
52:v:39:ASN:OD1	52:v:42:LEU:N	2.34	0.58
1:1:55:G:OP1	40:j:43:LYS:NZ	2.36	0.57
1:1:1240:A:H61	1:1:1244:A:P	2.27	0.57
1:1:3124:G:OP1	19:O:134:LYS:NZ	2.34	0.57
1:1:2245:C:HO2'	1:1:2246:G:P	2.27	0.57
1:1:2828:G:N2	32:b:19:ASP:OD1	2.37	0.57
7:B:66:LYS:NZ	26:V:124:ASP:OD2	2.31	0.57
32:b:446:ASP:O	32:b:449:ILE:HG23	2.04	0.57
8:C:252:GLU:OE1	8:C:252:GLU:N	2.36	0.57
48:r:218:GLY:H	48:r:245:VAL:HG23	1.68	0.57
1:1:1861:G:O2'	1:1:3066:U:OP1	2.14	0.57
6:A:95:SER:OG	6:A:97:ASN:OD1	2.21	0.57
8:C:156:LEU:HD22	8:C:159:ILE:HD12	1.87	0.57
44:n:74:GLU:OE2	44:n:76:VAL:HG23	2.04	0.57
2:2:95:G:OP2	40:j:72:ARG:NH1	2.37	0.57
5:6:31:G:N2	5:6:32:A:N7	2.50	0.57
7:B:344:THR:HG23	56:z:26:VAL:HG21	1.87	0.57
17:M:20:VAL:HG23	17:M:66:THR:OG1	2.05	0.57
32:b:227:ARG:NE	32:b:231:GLU:O	2.37	0.57
55:y:122:ASP:OD2	55:y:125:THR:OG1	2.18	0.57
18:N:116:LEU:HB3	18:N:133:ILE:HD11	1.87	0.57
43:m:255:LEU:O	43:m:255:LEU:HD13	2.05	0.57
43:m:416:TYR:N	43:m:417:GLU:HA	2.19	0.57
1:1:638:C:HO2'	1:1:1434:G:H1	1.51	0.57
1:1:1951:C:N4	1:1:1952:G:O6	2.37	0.57
12:G:115:ALA:O	12:G:119:GLY:N	2.35	0.57
50:t:281:GLY:O	50:t:285:ARG:N	2.36	0.57
54:x:292:LEU:N	54:x:304:TRP:O	2.37	0.57
17:M:34:ALA:O	17:M:47:ASP:N	2.36	0.57
27:W:175:ILE:HG23	27:W:175:ILE:O	2.04	0.57
48:r:206:SER:O	48:r:206:SER:OG	2.22	0.57
54:x:210:ILE:O	54:x:225:LEU:N	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:576:C:OP1	11:F:241:LYS:NZ	2.32	0.56
1:1:1805:C:O2	1:1:1806:A:N7	2.38	0.56
1:1:2185:G:OP1	6:A:202:VAL:HG23	2.04	0.56
6:A:113:VAL:HG12	6:A:166:ILE:HD13	1.87	0.56
13:H:27:VAL:O	13:H:33:THR:OG1	2.13	0.56
28:X:50:ALA:O	38:h:66:VAL:HG21	2.05	0.56
52:v:181:VAL:HG11	53:w:58:VAL:HG21	1.86	0.56
54:x:377:ALA:HB2	54:x:408:VAL:CG2	2.34	0.56
11:F:80:GLN:OE1	24:T:136:ARG:NH1	2.38	0.56
1:1:160:G:O2'	1:1:161:G:OP1	2.17	0.56
1:1:1940:G:H21	1:1:3362:A:H8	1.53	0.56
1:1:2390:A:O4'	1:1:3307:A:N6	2.38	0.56
1:1:2877:G:O2'	1:1:2878:G:OP2	2.23	0.56
11:F:23:ALA:O	11:F:26:VAL:HG22	2.03	0.56
29:Y:58:VAL:HG22	29:Y:104:LEU:HD22	1.86	0.56
32:b:220:ASP:OD2	32:b:221:THR:N	2.38	0.56
55:y:111:ASN:OD1	55:y:114:VAL:N	2.36	0.56
1:1:1128:U:O2'	1:1:1130:A:OP2	2.21	0.56
1:1:2338:C:OP2	1:1:2339:C:O2'	2.13	0.56
6:A:79:ASN:ND2	6:A:166:ILE:O	2.38	0.56
1:1:103:G:OP1	16:L:70:ARG:NE	2.39	0.56
1:1:1468:A:H61	1:1:1881:A:HO2'	1.51	0.56
6:A:94:ALA:O	6:A:102:LEU:HD21	2.06	0.56
9:D:164:LYS:NZ	54:x:176:GLN:OE1	2.36	0.56
15:K:91:THR:O	15:K:240:ARG:NE	2.39	0.56
20:P:114:VAL:O	20:P:114:VAL:HG13	2.05	0.56
1:1:1309:U:OP2	49:s:6:ARG:NH1	2.39	0.56
7:B:351:LEU:O	7:B:351:LEU:HD13	2.05	0.56
11:F:98:LYS:O	11:F:102:VAL:HG23	2.06	0.56
51:u:75:ARG:HB3	51:u:77:VAL:HG22	1.88	0.56
1:1:196:G:N1	1:1:199:A:OP2	2.37	0.56
1:1:2990:G:OP1	7:B:19:ARG:N	2.35	0.56
7:B:89:VAL:HG12	7:B:160:VAL:HG12	1.87	0.56
1:1:701:G:N2	1:1:788:C:O3'	2.39	0.56
1:1:1889:G:OP1	7:B:246:LEU:N	2.34	0.56
23:S:77:VAL:HG22	23:S:126:VAL:HG13	1.88	0.56
1:1:1184:A:N6	1:1:1323:G:O6	2.39	0.56
1:1:1395:G:O2'	2:2:18:U:O2	2.21	0.56
1:1:1563:C:N4	1:1:1577:G:O6	2.39	0.56
1:1:2191:U:O2'	43:m:292:ASN:OD1	2.19	0.56
1:1:2615:G:O6	43:m:57:ARG:NH1	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2874:G:OP2	48:r:143:ARG:NH1	2.38	0.56
3:3:5:G:O6	3:3:117:A:N6	2.39	0.56
21:Q:111:ARG:NE	21:Q:121:CYS:SG	2.78	0.56
39:i:45:ARG:NH2	39:i:54:GLU:OE2	2.39	0.56
1:1:2433:U:OP2	1:1:2434:U:O2'	2.16	0.55
1:1:3030:G:HO2'	1:1:3031:G:P	2.27	0.55
54:x:383:MET:SD	54:x:405:VAL:HG11	2.46	0.55
1:1:2802:A:HO2'	1:1:2803:A:P	2.28	0.55
1:1:2832:C:O4'	48:r:256:ASN:ND2	2.39	0.55
23:S:79:VAL:O	23:S:90:MET:N	2.38	0.55
43:m:379:GLU:HA	43:m:382:ILE:HD12	1.88	0.55
1:1:269:G:OP2	18:N:44:ARG:NH2	2.40	0.55
1:1:2691:A:O2'	1:1:2692:A:O4'	2.24	0.55
20:P:48:LEU:HD22	20:P:88:VAL:HG13	1.87	0.55
27:W:41:TRP:HE3	27:W:217:VAL:HG21	1.71	0.55
1:1:35:A:OP1	18:N:83:LYS:HD3	2.07	0.55
3:3:6:C:O2'	9:D:72:ASP:OD2	2.23	0.55
13:H:99:ILE:CG2	13:H:101:VAL:HG23	2.36	0.55
26:V:28:ASN:ND2	26:V:112:SER:OG	2.39	0.55
44:n:64:TYR:O	44:n:67:ASP:N	2.37	0.55
1:1:2745:G:N2	1:1:2748:A:OP2	2.33	0.55
12:G:50:VAL:HG21	28:X:27:ARG:HD3	1.89	0.55
12:G:196:ALA:O	12:G:197:VAL:HG13	2.07	0.55
1:1:1334:U:OP1	11:F:206:LYS:NZ	2.27	0.55
3:3:52:G:HO2'	3:3:53:U:P	2.30	0.55
1:1:1547:G:OP1	18:N:108:ARG:NH2	2.40	0.55
1:1:1579:C:OP1	12:G:43:LYS:NZ	2.30	0.55
2:2:129:C:OP1	44:n:10:GLY:N	2.40	0.55
14:J:104:PHE:O	14:J:127:PHE:N	2.40	0.55
26:V:58:VAL:O	26:V:76:ALA:N	2.39	0.55
1:1:406:G:OP1	1:1:1415:U:O2'	2.15	0.55
1:1:878:G:O2'	1:1:880:G:N2	2.39	0.55
1:1:2876:C:HO2'	1:1:2877:G:C5'	2.19	0.55
1:1:2900:A:OP1	48:r:6:TYR:OH	2.23	0.55
32:b:263:THR:HG23	32:b:266:ALA:H	1.72	0.55
2:2:71:A:H62	2:2:87:G:N2	2.05	0.55
10:E:51:ARG:NH1	17:M:114:ASP:OD2	2.40	0.55
32:b:290:THR:O	32:b:294:ARG:N	2.40	0.55
50:t:211:ARG:NH1	50:t:274:ASN:OD1	2.40	0.55
1:1:1146:C:OP1	35:e:47:ARG:N	2.39	0.55
1:1:2863:G:C6	32:b:95:LEU:HD13	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:m:219:ILE:O	43:m:253:LYS:NZ	2.34	0.55
48:r:151:ILE:HD11	48:r:212:LEU:HD23	1.88	0.55
1:1:2201:G:O6	1:1:2241:U:O2	2.25	0.54
9:D:148:ILE:HG22	9:D:159:VAL:HG11	1.88	0.54
13:H:101:VAL:HG22	13:H:114:VAL:HG22	1.89	0.54
21:Q:116:LYS:NZ	31:a:88:ASP:OD2	2.23	0.54
43:m:228:VAL:C	43:m:229:LEU:HD12	2.31	0.54
44:n:17:THR:HG23	44:n:60:THR:HG23	1.89	0.54
54:x:409:ALA:O	54:x:452:TRP:NE1	2.37	0.54
12:G:75:ILE:HD11	18:N:18:VAL:HG23	1.88	0.54
15:K:183:ASP:OD1	15:K:211:THR:OG1	2.12	0.54
43:m:400:ILE:O	43:m:403:VAL:HG22	2.07	0.54
1:1:2743:A:N6	1:1:2751:G:O6	2.41	0.54
18:N:121:VAL:HG21	18:N:131:GLU:HG3	1.88	0.54
18:N:180:PHE:O	18:N:184:LYS:N	2.40	0.54
32:b:246:LEU:O	32:b:281:LYS:NZ	2.39	0.54
50:t:264:CYS:O	50:t:268:LEU:HD23	2.07	0.54
1:1:1194:G:HO2'	1:1:1319:G:HO2'	1.55	0.54
28:X:68:THR:HG21	38:h:36:LEU:HD13	1.89	0.54
44:n:368:SER:O	44:n:371:VAL:HG22	2.08	0.54
55:y:85:ARG:NH2	55:y:92:VAL:O	2.41	0.54
1:1:912:G:OP2	6:A:9:ARG:NH1	2.40	0.54
1:1:112:U:OP1	38:h:103:LYS:NZ	2.40	0.54
1:1:2157:G:N7	6:A:152:SER:OG	2.33	0.54
30:Z:103:GLN:CG	30:Z:103:GLN:O	2.55	0.54
32:b:268:VAL:HG21	32:b:305:LEU:HB3	1.88	0.54
1:1:849:C:O2'	1:1:850:U:P	2.66	0.54
1:1:1899:G:O2'	1:1:2334:U:O4	2.21	0.54
10:E:64:LEU:HD23	10:E:65:ILE:N	2.23	0.54
43:m:316:ILE:O	43:m:316:ILE:HG23	2.07	0.54
1:1:1779:C:N4	22:R:88:ARG:O	2.36	0.54
1:1:3138:U:O2'	7:B:16:PHE:O	2.26	0.54
23:S:27:MET:HG3	24:T:151:LEU:HD21	1.89	0.54
1:1:637:C:O2'	1:1:638:C:OP2	2.21	0.54
1:1:1816:A:O2'	1:1:1817:G:OP1	2.23	0.54
6:A:27:ALA:O	6:A:128:ARG:NH2	2.37	0.54
15:K:124:LEU:HD23	15:K:125:LEU:H	1.72	0.54
1:1:609:G:O6	8:C:308:LYS:NZ	2.41	0.53
1:1:2698:G:O2'	1:1:2699:G:O4'	2.26	0.53
3:3:52:G:O2'	3:3:53:U:OP1	2.23	0.53
1:1:591:G:O2'	10:E:17:ALA:O	2.17	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:J:7:ASN:OD1	14:J:10:ARG:NH2	2.41	0.53
1:1:406:G:N2	2:2:16:G:O2'	2.40	0.53
1:1:1393:A:N3	1:1:1419:A:O2'	2.41	0.53
1:1:2125:A:OP1	43:m:437:ARG:NH1	2.42	0.53
1:1:2626:A:O2'	1:1:2627:C:O5'	2.25	0.53
1:1:3275:U:O2'	36:f:99:ARG:NH1	2.41	0.53
50:t:219:GLU:O	50:t:220:ASN:O	2.27	0.53
1:1:1057:A:HO2'	1:1:1058:U:C5'	2.22	0.53
1:1:940:G:O2'	1:1:1435:A:O2'	2.24	0.53
1:1:3305:A:OP1	7:B:334:ARG:NH2	2.42	0.53
20:P:16:SER:HB3	20:P:149:VAL:HG22	1.89	0.53
1:1:631:U:O2	1:1:632:G:N7	2.41	0.53
1:1:1239:C:O2	1:1:1239:C:H2'	2.08	0.53
1:1:2254:U:N3	1:1:2264:U:O2	2.41	0.53
32:b:241:TYR:O	32:b:245:HIS:ND1	2.29	0.53
55:y:115:ALA:HB2	55:y:135:VAL:HG21	1.91	0.53
1:1:2876:C:O2'	1:1:2877:G:O5'	2.20	0.53
11:F:140:SER:O	11:F:143:THR:OG1	2.23	0.53
52:v:140:MET:O	52:v:182:ILE:N	2.41	0.53
1:1:2833:A:N6	1:1:2856:G:O6	2.41	0.53
1:1:3213:A:N7	17:M:124:ARG:NH2	2.54	0.53
54:x:192:VAL:HG12	54:x:203:THR:HG22	1.91	0.53
1:1:709:A:N3	1:1:2787:G:O2'	2.38	0.53
1:1:1145:G:N2	1:1:1331:U:O2'	2.41	0.53
1:1:2401:A:H3'	1:1:2402:A:C5'	2.39	0.53
1:1:2857:C:O2'	1:1:2858:U:P	2.67	0.53
5:6:7:C:O2'	5:6:7:C:O2	2.27	0.53
6:A:79:ASN:O	6:A:82:VAL:HG22	2.09	0.53
32:b:1:MET:O	32:b:5:TRP:NE1	2.40	0.53
32:b:388:TYR:OH	32:b:398:LEU:HD11	2.09	0.53
55:y:108:ILE:HG12	55:y:117:VAL:HG12	1.90	0.53
2:2:56:G:N2	2:2:62:C:O4'	2.42	0.52
8:C:280:ILE:HD11	21:Q:25:TYR:HB2	1.90	0.52
21:Q:55:SER:OG	21:Q:58:ASN:ND2	2.42	0.52
30:Z:110:ALA:O	30:Z:114:VAL:HG23	2.09	0.52
9:D:86:TYR:CE1	9:D:104:LEU:HD11	2.44	0.52
10:E:64:LEU:HD23	10:E:65:ILE:H	1.74	0.52
1:1:1235:U:N3	1:1:1237:G:O4'	2.42	0.52
1:1:3350:C:O2'	1:1:3351:U:P	2.67	0.52
3:3:52:G:O2'	3:3:53:U:P	2.66	0.52
54:x:336:ILE:HD12	54:x:338:ALA:N	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:428:A:O3'	36:f:88:ASN:ND2	2.42	0.52
1:1:591:G:N2	1:1:612:U:OP1	2.35	0.52
1:1:940:G:HO2'	1:1:1435:A:HO2'	1.56	0.52
1:1:2604:U:OP2	43:m:3:THR:N	2.37	0.52
15:K:90:GLY:O	15:K:91:THR:HG22	2.09	0.52
26:V:91:VAL:HG21	51:u:30:ARG:NH1	2.25	0.52
43:m:390:VAL:O	43:m:393:VAL:HG22	2.09	0.52
54:x:376:THR:OG1	54:x:386:TRP:NE1	2.41	0.52
1:1:594:U:OP1	1:1:609:G:N1	2.41	0.52
18:N:64:VAL:HG11	18:N:102:ALA:HB1	1.92	0.52
1:1:1490:A:OP2	42:l:2:ALA:N	2.43	0.52
1:1:1753:G:O6	1:1:1772:U:O2	2.27	0.52
1:1:3092:C:O2	26:V:12:ARG:NE	2.42	0.52
1:1:3174:A:OP1	36:f:97:SER:OG	2.23	0.52
1:1:3258:U:O2'	1:1:3260:G:OP1	2.27	0.52
2:2:123:G:O2'	2:2:124:G:P	2.67	0.52
18:N:52:GLY:O	18:N:148:TYR:OH	2.21	0.52
50:t:277:VAL:HG22	50:t:278:SER:O	2.10	0.52
1:1:1405:U:H4'	1:1:1406:A:OP1	2.09	0.52
1:1:1635:G:N2	1:1:1638:A:OP2	2.42	0.52
1:1:2729:U:O2'	1:1:2730:G:O5'	2.27	0.52
1:1:2837:A:O2'	1:1:2850:G:N2	2.41	0.52
2:2:34:U:O2'	2:2:35:C:OP2	2.26	0.52
12:G:71:VAL:HG11	12:G:76:ALA:HB2	1.92	0.52
43:m:82:ARG:O	48:r:239:TRP:NE1	2.42	0.52
6:A:30:ARG:O	6:A:163:ARG:NH1	2.40	0.52
51:u:6:CYS:N	51:u:11:SER:O	2.40	0.52
53:w:39:LEU:O	53:w:46:ARG:NE	2.39	0.52
54:x:377:ALA:HB1	54:x:405:VAL:CG2	2.39	0.52
1:1:3212:C:C2'	1:1:3213:A:O5'	2.58	0.52
6:A:104:LEU:O	6:A:107:VAL:HG22	2.10	0.52
15:K:225:ASN:O	15:K:229:VAL:HG23	2.10	0.52
32:b:309:VAL:O	32:b:315:VAL:HG21	2.10	0.52
44:n:147:SER:OG	50:t:211:ARG:NH1	2.43	0.52
48:r:146:SER:O	48:r:148:LYS:N	2.43	0.52
1:1:234:G:C2	1:1:235:A:C8	2.98	0.52
1:1:1102:A:O2'	1:1:1103:A:P	2.68	0.52
1:1:3215:A:OP1	36:f:2:ALA:N	2.43	0.52
12:G:91:PHE:CE1	12:G:180:VAL:HG21	2.45	0.52
17:M:40:ASP:OD1	17:M:43:LYS:N	2.43	0.52
23:S:69:PRO:O	23:S:97:VAL:HG22	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:y:199:VAL:HG23	55:y:204:ALA:HB2	1.91	0.52
2:2:125:U:O2'	2:2:126:A:OP1	2.21	0.51
7:B:185:GLY:O	7:B:191:LYS:NZ	2.31	0.51
17:M:114:ASP:OD1	17:M:117:ARG:NH1	2.39	0.51
1:1:1205:A:O2'	1:1:1206:G:P	2.67	0.51
1:1:2435:G:P	18:N:20:ARG:HH12	2.32	0.51
1:1:2835:U:H2'	1:1:2836:C:O2	2.10	0.51
2:2:95:G:O2'	40:j:81:GLY:O	2.28	0.51
13:H:100:ASN:OD1	13:H:102:ASN:ND2	2.43	0.51
32:b:4:SER:O	32:b:4:SER:OG	2.27	0.51
32:b:483:ALA:O	32:b:486:VAL:HG12	2.10	0.51
48:r:259:LEU:HD23	48:r:260:LEU:N	2.25	0.51
1:1:1347:U:OP1	8:C:303:GLY:N	2.42	0.51
1:1:1534:A:OP2	1:1:1586:G:N1	2.40	0.51
37:g:81:CYS:O	37:g:85:VAL:HG23	2.10	0.51
1:1:426:G:OP1	35:e:15:LYS:NZ	2.38	0.51
1:1:1307:G:O2'	1:1:1308:A:OP2	2.22	0.51
1:1:1383:G:OP1	8:C:203:ARG:NE	2.43	0.51
1:1:2513:U:HO2'	1:1:2514:U:P	2.32	0.51
11:F:118:LYS:HE3	11:F:191:VAL:HG11	1.92	0.51
1:1:271:C:C2	1:1:295:A:N6	2.78	0.51
1:1:878:G:HO2'	1:1:880:G:N2	2.08	0.51
1:1:1141:C:H2'	1:1:1142:G:O4'	2.09	0.51
1:1:1349:G:H22	1:1:1355:A:H62	1.57	0.51
1:1:1914:G:N2	22:R:81:ARG:O	2.40	0.51
17:M:108:ARG:NH1	17:M:116:GLU:OE2	2.43	0.51
20:P:119:VAL:HG12	20:P:146:ILE:HG23	1.93	0.51
1:1:2795:U:H4'	1:1:2796:G:O5'	2.11	0.51
10:E:55:LEU:HD12	10:E:64:LEU:HD22	1.93	0.51
48:r:215:LEU:HB3	48:r:245:VAL:HG21	1.92	0.51
55:y:72:VAL:HG23	55:y:96:ARG:HG2	1.92	0.51
6:A:114:SER:O	6:A:165:VAL:HG12	2.11	0.51
1:1:1914:G:O2'	22:R:82:LYS:O	2.26	0.51
1:1:3100:U:OP1	56:z:18:ARG:NH2	2.44	0.51
26:V:104:ASN:OD1	26:V:108:GLU:N	2.44	0.51
45:o:93:ILE:HG23	45:o:164:VAL:HG23	1.92	0.51
54:x:243:VAL:O	54:x:353:GLN:NE2	2.44	0.51
1:1:2386:A:O2'	2:2:3:A:N1	2.27	0.51
7:B:202:THR:N	56:z:44:GLN:OE1	2.43	0.51
9:D:138:GLY:N	9:D:139:PRO:CD	2.74	0.51
15:K:202:VAL:O	15:K:205:THR:HG22	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:i:43:LEU:HD13	39:i:47:ILE:HD12	1.93	0.51
1:1:1392:G:N2	1:1:1417:G:O2'	2.44	0.51
1:1:3007:U:O4	1:1:3008:A:N6	2.43	0.51
1:1:3212:C:O2'	1:1:3213:A:O5'	2.28	0.51
8:C:156:LEU:CD2	8:C:159:ILE:HD12	2.41	0.51
25:U:52:ASN:C	25:U:52:ASN:OD1	2.54	0.51
32:b:173:CYS:N	32:b:251:LEU:O	2.44	0.51
48:r:186:HIS:CE1	48:r:261:VAL:HG22	2.46	0.51
54:x:377:ALA:HB1	54:x:405:VAL:HG23	1.92	0.51
1:1:1596:C:O2'	1:1:1696:A:N3	2.37	0.50
1:1:2652:U:H4'	1:1:2653:C:OP1	2.12	0.50
7:B:324:VAL:HG11	7:B:328:ILE:HD11	1.92	0.50
14:J:12:LEU:HD13	14:J:13:LYS:N	2.25	0.50
26:V:58:VAL:N	26:V:76:ALA:O	2.41	0.50
7:B:79:VAL:HG13	7:B:79:VAL:O	2.12	0.50
23:S:4:PHE:O	23:S:100:VAL:HG21	2.10	0.50
43:m:383:LEU:HD11	43:m:393:VAL:HG11	1.93	0.50
1:1:1154:A:N7	1:1:2371:G:N1	2.60	0.50
1:1:2877:G:O2'	1:1:2878:G:P	2.69	0.50
1:1:3040:A:C2	1:1:3041:U:C5	2.99	0.50
1:1:3314:A:OP1	7:B:116:ARG:NH1	2.45	0.50
54:x:267:SER:O	54:x:269:VAL:HG23	2.11	0.50
1:1:625:G:N2	1:1:1401:A:OP1	2.31	0.50
1:1:649:A:HO2'	1:1:650:C:P	2.32	0.50
2:2:63:G:H22	2:2:97:A:H2	1.59	0.50
8:C:20:LEU:HD13	8:C:256:THR:HG23	1.92	0.50
30:Z:14:VAL:O	30:Z:14:VAL:HG12	2.11	0.50
32:b:154:ARG:HA	32:b:157:ILE:HG22	1.93	0.50
48:r:151:ILE:HD12	48:r:173:ARG:HG3	1.93	0.50
1:1:849:C:HO2'	1:1:850:U:P	2.35	0.50
7:B:312:VAL:HG12	7:B:313:HIS:ND1	2.26	0.50
24:T:152:ALA:O	24:T:153:PRO:C	2.55	0.50
30:Z:76:ASN:OD1	30:Z:77:TYR:N	2.44	0.50
1:1:303:G:O2'	1:1:2778:G:OP2	2.28	0.50
1:1:1190:A:O2'	1:1:1193:A:OP2	2.19	0.50
1:1:1831:U:C2	1:1:1832:C:C5	3.00	0.50
1:1:2662:G:O2'	9:D:152:ARG:NH2	2.44	0.50
1:1:2699:G:N2	52:v:81:LYS:O	2.32	0.50
53:w:54:THR:O	53:w:58:VAL:HG23	2.12	0.50
1:1:534:U:OP1	23:S:132:THR:OG1	2.23	0.50
1:1:2861:U:O2	1:1:2861:U:H2'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3208:G:O4'	1:1:3210:A:C8	2.64	0.50
1:1:3213:A:H62	17:M:124:ARG:NH2	2.10	0.50
8:C:260:GLN:O	8:C:270:SER:OG	2.29	0.50
12:G:193:LYS:O	12:G:194:THR:HG23	2.12	0.50
22:R:8:LYS:HD2	22:R:22:VAL:HG23	1.94	0.50
39:i:45:ARG:NH1	39:i:89:GLU:OE2	2.45	0.50
44:n:447:TYR:CD2	44:n:453:LEU:HD12	2.47	0.50
54:x:192:VAL:HG12	54:x:203:THR:CG2	2.42	0.50
55:y:88:LEU:CD2	55:y:92:VAL:HG11	2.41	0.50
1:1:713:U:O2'	1:1:754:G:OP1	2.29	0.50
1:1:991:G:O6	1:1:1058:U:O2	2.30	0.50
1:1:1224:C:O4'	1:1:1288:U:O2'	2.30	0.50
1:1:1894:U:O2'	1:1:3054:U:OP1	2.27	0.50
1:1:2723:U:N3	1:1:2724:U:O4	2.45	0.50
1:1:1455:U:OP1	1:1:1879:A:N6	2.45	0.50
1:1:1807:G:O3'	1:1:1808:G:O4'	2.30	0.50
1:1:2246:G:N2	1:1:2246:G:OP2	2.45	0.50
1:1:2954:U:O2'	1:1:2977:G:O6	2.28	0.50
24:T:132:PRO:O	24:T:134:GLN:NE2	2.44	0.50
26:V:118:VAL:HG21	26:V:133:SER:OG	2.12	0.50
50:t:228:VAL:HG23	50:t:230:ASN:OD1	2.11	0.50
1:1:289:A:C2	1:1:290:G:N7	2.80	0.49
1:1:2435:G:OP1	18:N:20:ARG:NH1	2.39	0.49
1:1:2836:C:H2'	1:1:2837:A:O4'	2.12	0.49
2:2:12:A:N6	2:2:13:A:H62	2.10	0.49
5:6:231:A:O2'	5:6:232:A:O5'	2.28	0.49
7:B:264:VAL:HG23	7:B:266:ARG:HG2	1.93	0.49
38:h:53:CYS:O	38:h:57:VAL:HG23	2.12	0.49
43:m:413:GLU:OE1	43:m:419:SER:OG	2.23	0.49
55:y:121:ILE:HD11	55:y:125:THR:HG21	1.94	0.49
2:2:36:G:OP2	38:h:85:THR:OG1	2.23	0.49
18:N:99:ARG:NH2	18:N:118:SER:O	2.46	0.49
38:h:102:GLU:OE1	38:h:106:LYS:NZ	2.38	0.49
44:n:27:VAL:HG22	44:n:31:ASP:HB2	1.94	0.49
55:y:38:PHE:CE1	55:y:205:VAL:HG21	2.46	0.49
55:y:140:GLN:NE2	55:y:172:GLU:OE1	2.42	0.49
1:1:1230:G:HO2'	27:W:50:THR:HG1	1.60	0.49
20:P:122:ALA:N	20:P:143:PRO:O	2.42	0.49
32:b:32:VAL:O	32:b:33:ILE:HG23	2.12	0.49
49:s:12:SER:O	49:s:15:LEU:N	2.44	0.49
1:1:649:A:O2'	1:1:650:C:P	2.69	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1204:A:N6	1:1:1300:G:O2'	2.27	0.49
1:1:1230:G:O2'	27:W:50:THR:OG1	2.25	0.49
1:1:2263:C:HO2'	1:1:2264:U:P	2.36	0.49
34:d:7:VAL:O	34:d:8:VAL:HG23	2.12	0.49
1:1:2642:A:O2'	1:1:2643:A:O4'	2.29	0.49
1:1:3113:A:OP1	13:H:73:SER:OG	2.28	0.49
5:6:227:C:N4	50:t:153:VAL:O	2.45	0.49
12:G:132:VAL:HG12	12:G:200:LEU:CD1	2.37	0.49
13:H:93:VAL:HG21	48:r:18:LEU:HD11	1.94	0.49
13:H:190:ASP:OD1	13:H:190:ASP:N	2.38	0.49
16:L:93:ILE:HG22	16:L:93:ILE:O	2.13	0.49
43:m:231:ALA:HB1	43:m:265:VAL:HG21	1.95	0.49
32:b:57:PHE:CE1	32:b:140:VAL:HG21	2.48	0.49
1:1:217:U:O2	29:Y:103:LYS:NZ	2.45	0.49
1:1:1123:U:O2'	1:1:1124:U:O4'	2.25	0.49
9:D:55:PHE:CE1	9:D:159:VAL:HG22	2.48	0.49
12:G:186:LEU:O	12:G:190:VAL:HG23	2.13	0.49
18:N:118:SER:HB3	18:N:132:VAL:HG22	1.95	0.49
24:T:154:VAL:HB	24:T:156:TYR:N	2.27	0.49
25:U:76:LEU:O	25:U:80:THR:HG23	2.12	0.49
1:1:284:A:O2'	1:1:285:A:OP2	2.22	0.49
15:K:40:ALA:HB1	15:K:281:ILE:HD11	1.95	0.49
43:m:172:GLU:O	43:m:176:VAL:HG23	2.11	0.49
1:1:177:U:O2	1:1:241:G:O6	2.30	0.49
2:2:19:C:C2	2:2:20:U:C5	3.00	0.49
10:E:40:LEU:N	10:E:52:VAL:O	2.43	0.49
13:H:86:TYR:CE2	13:H:151:VAL:HG13	2.48	0.49
16:L:109:PHE:O	16:L:113:VAL:HG23	2.12	0.49
20:P:127:ARG:O	20:P:139:TYR:N	2.44	0.49
33:c:78:GLY:HA2	33:c:81:VAL:HG22	1.95	0.49
54:x:293:TYR:HD1	54:x:303:VAL:HG22	1.77	0.49
54:x:331:ASP:OD1	54:x:332:TYR:N	2.45	0.49
1:1:171:G:N2	1:1:248:U:O2	2.46	0.49
1:1:1329:U:OP1	36:f:17:GLN:NE2	2.46	0.49
1:1:2875:U:O2'	1:1:2951:G:N2	2.46	0.49
2:2:52:A:N6	42:l:27:ILE:HD13	2.27	0.49
11:F:88:ARG:HA	11:F:134:VAL:HG12	1.95	0.49
27:W:135:PHE:O	27:W:188:VAL:HG22	2.12	0.49
46:p:53:GLY:O	46:p:66:GLY:N	2.46	0.49
1:1:28:C:O2'	1:1:61:A:N3	2.46	0.48
1:1:611:A:O2'	1:1:612:U:OP2	2.25	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:993:G:N7	1:1:994:G:N1	2.61	0.48
1:1:1620:U:OP1	44:n:47:ARG:NE	2.43	0.48
1:1:2360:C:O2'	1:1:2362:C:OP2	2.21	0.48
26:V:33:ASN:OD1	26:V:64:LYS:N	2.46	0.48
43:m:423:ASP:C	43:m:423:ASP:OD1	2.55	0.48
1:1:2981:U:O2'	1:1:2982:A:OP2	2.22	0.48
12:G:74:THR:O	12:G:77:GLN:NE2	2.43	0.48
13:H:48:VAL:HG13	13:H:49:ASN:H	1.78	0.48
43:m:371:VAL:HG21	43:m:387:VAL:CG1	2.43	0.48
44:n:410:GLN:OE1	44:n:424:ARG:NH2	2.41	0.48
50:t:214:ILE:HD12	50:t:267:PHE:CE2	2.48	0.48
54:x:131:PRO:O	54:x:515:HIS:ND1	2.44	0.48
1:1:1101:G:OP2	11:F:196:LYS:NZ	2.43	0.48
1:1:1225:A:H61	1:1:1284:C:H42	1.61	0.48
1:1:1810:A:N3	44:n:57:THR:OG1	2.43	0.48
1:1:2760:C:OP2	53:w:190:LYS:NZ	2.46	0.48
27:W:121:ARG:O	27:W:213:PHE:N	2.45	0.48
28:X:133:LEU:O	28:X:133:LEU:HD13	2.13	0.48
44:n:206:PRO:O	50:t:230:ASN:ND2	2.45	0.48
48:r:154:HIS:ND1	48:r:179:GLN:OE1	2.46	0.48
1:1:2412:G:H2'	1:1:2413:A:O4'	2.14	0.48
1:1:2703:A:OP2	9:D:23:ARG:NH2	2.41	0.48
2:2:85:G:O6	29:Y:114:ASP:N	2.41	0.48
40:j:14:LYS:HE2	42:l:51:ILE:HD11	1.95	0.48
53:w:160:VAL:O	53:w:162:VAL:HG22	2.14	0.48
1:1:708:G:N2	1:1:711:A:OP2	2.41	0.48
1:1:3085:G:OP1	51:u:34:SER:OG	2.28	0.48
1:1:3195:U:O2'	1:1:3196:U:OP1	2.26	0.48
1:1:3333:G:N2	1:1:3369:G:O2'	2.46	0.48
2:2:71:A:H4'	2:2:72:A:O5'	2.13	0.48
7:B:229:VAL:HG21	7:B:249:VAL:HG23	1.95	0.48
44:n:447:TYR:HD2	44:n:453:LEU:HD12	1.79	0.48
1:1:691:A:N1	2:2:28:C:O2'	2.37	0.48
1:1:1928:G:N2	1:1:2320:A:O2'	2.42	0.48
6:A:66:PRO:O	12:G:40:VAL:HG13	2.13	0.48
6:A:118:GLU:OE2	6:A:156:LYS:NZ	2.47	0.48
9:D:23:ARG:O	9:D:23:ARG:NH1	2.37	0.48
12:G:161:GLU:OE2	18:N:11:GLN:NE2	2.45	0.48
13:H:48:VAL:HG13	13:H:49:ASN:N	2.28	0.48
16:L:24:VAL:HG11	16:L:26:PHE:CZ	2.47	0.48
1:1:2943:G:OP2	7:B:2:SER:OG	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3341:U:HO2'	1:1:3342:A:P	2.28	0.48
12:G:190:VAL:O	12:G:190:VAL:HG12	2.14	0.48
16:L:119:TYR:O	16:L:123:ILE:HG23	2.13	0.48
1:1:1471:U:OP1	22:R:5:ARG:NH2	2.46	0.48
1:1:2830:G:H2'	1:1:2831:G:C8	2.49	0.48
3:3:83:U:H2'	3:3:84:A:C8	2.49	0.48
10:E:40:LEU:O	10:E:52:VAL:N	2.43	0.48
13:H:80:THR:HG1	13:H:86:TYR:HH	1.52	0.48
28:X:95:ILE:O	28:X:99:VAL:HG23	2.13	0.48
1:1:805:G:N1	1:1:939:U:O4	2.47	0.48
1:1:1579:C:O2'	1:1:1580:A:O4'	2.32	0.48
1:1:3138:U:OP2	7:B:30:LYS:NZ	2.36	0.48
50:t:222:ALA:HB1	50:t:224:PRO:HD2	1.96	0.48
1:1:2751:G:C2	1:1:2752:U:C4	3.01	0.48
1:1:2868:U:C2'	1:1:2869:U:OP2	2.61	0.48
12:G:26:LEU:HB3	30:Z:53:VAL:HG11	1.96	0.48
54:x:336:ILE:HD12	54:x:338:ALA:H	1.79	0.48
54:x:450:VAL:HG12	54:x:461:SER:CB	2.43	0.48
1:1:197:G:O2'	1:1:218:G:N2	2.47	0.47
1:1:1242:G:N3	1:1:1242:G:H2'	2.28	0.47
1:1:2163:C:N3	1:1:2172:A:N6	2.62	0.47
1:1:2392:C:O2'	7:B:266:ARG:NH1	2.42	0.47
1:1:2709:C:C2	1:1:2710:C:C5	3.01	0.47
1:1:3313:U:OP1	7:B:117:ARG:NH1	2.47	0.47
2:2:141:C:O3'	18:N:62:TYR:OH	2.29	0.47
11:F:130:ILE:O	11:F:134:VAL:HG22	2.13	0.47
15:K:213:ALA:HB2	15:K:221:THR:HG21	1.95	0.47
20:P:51:VAL:HG11	20:P:88:VAL:HG21	1.96	0.47
21:Q:111:ARG:O	21:Q:115:VAL:HG23	2.14	0.47
25:U:43:VAL:HG21	25:U:50:LEU:HA	1.96	0.47
32:b:98:ILE:HD13	32:b:143:LEU:HD21	1.95	0.47
43:m:333:ASN:OD1	43:m:341:CYS:N	2.47	0.47
43:m:390:VAL:HG21	43:m:454:LEU:HB2	1.96	0.47
1:1:213:A:OP1	29:Y:2:ALA:N	2.47	0.47
1:1:578:A:H1'	8:C:331:ALA:HB1	1.96	0.47
1:1:695:C:OP2	8:C:115:HIS:NE2	2.45	0.47
1:1:1792:C:HO2'	1:1:1794:G:H8	1.62	0.47
1:1:1833:G:OP1	42:l:10:LYS:NZ	2.41	0.47
8:C:289:ILE:HG23	21:Q:129:VAL:HG22	1.95	0.47
46:p:73:THR:HG23	46:p:76:ALA:H	1.79	0.47
47:q:219:GLU:OE1	47:q:422:LYS:NZ	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:r:151:ILE:HD12	48:r:173:ARG:CG	2.44	0.47
1:1:1097:G:H1'	1:1:1098:A:OP2	2.14	0.47
1:1:1656:A:OP2	37:g:16:ARG:NH1	2.47	0.47
1:1:2513:U:O2'	1:1:2514:U:P	2.71	0.47
10:E:136:GLU:O	10:E:140:VAL:HG23	2.14	0.47
44:n:149:ASN:ND2	44:n:150:GLN:OE1	2.47	0.47
1:1:853:G:C6	1:1:854:G:N7	2.82	0.47
1:1:1619:A:H2'	1:1:1620:U:O4'	2.14	0.47
1:1:2897:A:OP2	1:1:2899:C:N4	2.41	0.47
6:A:116:VAL:HG13	6:A:126:LEU:HD12	1.96	0.47
9:D:139:PRO:O	9:D:140:ARG:C	2.57	0.47
28:X:67:ILE:HD12	28:X:83:VAL:HG12	1.96	0.47
37:g:51:LEU:HD23	37:g:51:LEU:H	1.78	0.47
42:l:24:PRO:HD2	42:l:27:ILE:HD12	1.95	0.47
52:v:172:LEU:HD23	53:w:89:LEU:HD12	1.96	0.47
1:1:1786:G:H2'	1:1:1787:A:C8	2.50	0.47
5:6:229:U:OP2	50:t:49:ARG:NH1	2.47	0.47
13:H:140:VAL:HG11	13:H:143:GLU:OE2	2.15	0.47
20:P:166:VAL:HG13	20:P:166:VAL:O	2.13	0.47
22:R:130:ASN:O	22:R:131:ALA:HB3	2.14	0.47
28:X:75:LYS:O	28:X:79:GLY:N	2.48	0.47
43:m:324:PRO:HD2	43:m:387:VAL:HG22	1.96	0.47
1:1:35:A:H5''	18:N:83:LYS:HD2	1.96	0.47
1:1:765:C:H1'	1:1:766:U:OP1	2.15	0.47
1:1:1122:U:C2'	1:1:1123:U:O5'	2.62	0.47
1:1:1277:C:O2	1:1:1278:A:C8	2.67	0.47
1:1:2628:A:C6	1:1:2650:U:C2	3.02	0.47
7:B:49:TYR:O	7:B:80:ASP:N	2.47	0.47
8:C:27:SER:O	8:C:279:HIS:NE2	2.39	0.47
10:E:155:LEU:O	10:E:155:LEU:HD13	2.14	0.47
14:J:97:SER:N	14:J:101:ASN:O	2.44	0.47
24:T:151:LEU:HD23	24:T:151:LEU:H	1.79	0.47
34:d:29:ALA:HB3	34:d:30:PRO:HD3	1.96	0.47
50:t:74:ARG:O	50:t:78:VAL:HG23	2.14	0.47
1:1:144:A:OP1	12:G:193:LYS:NZ	2.33	0.47
1:1:679:U:HO2'	1:1:788:C:C2'	2.24	0.47
1:1:763:G:O6	1:1:769:G:N1	2.48	0.47
1:1:1413:G:C2	1:1:1414:G:N7	2.83	0.47
1:1:2213:A:N3	1:1:2601:A:O2'	2.47	0.47
1:1:2255:A:H62	1:1:2261:G:H22	1.62	0.47
1:1:2277:C:H3'	1:1:2278:C:C5'	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:140:ASN:ND2	6:A:142:ASP:O	2.48	0.47
8:C:219:LEU:O	8:C:222:VAL:HG12	2.15	0.47
15:K:210:ARG:O	15:K:221:THR:HG22	2.14	0.47
29:Y:49:PRO:O	29:Y:115:ARG:NH2	2.46	0.47
30:Z:11:ALA:O	30:Z:23:VAL:N	2.40	0.47
32:b:54:GLY:O	32:b:58:VAL:HG23	2.15	0.47
32:b:86:TYR:O	32:b:149:TYR:OH	2.31	0.47
48:r:55:TYR:O	48:r:59:VAL:HG23	2.14	0.47
53:w:175:ASP:O	53:w:178:THR:OG1	2.32	0.47
1:1:1249:G:H2'	1:1:1249:G:N3	2.30	0.47
1:1:2961:G:O2'	43:m:355:TYR:O	2.32	0.47
2:2:71:A:OP1	29:Y:28:ARG:NE	2.40	0.47
3:3:58:C:C2	3:3:59:U:C5	3.02	0.47
12:G:211:LEU:O	12:G:215:VAL:HG23	2.15	0.47
13:H:99:ILE:HG22	13:H:101:VAL:HG23	1.97	0.47
22:R:106:LEU:HD21	22:R:123:LEU:CB	2.44	0.47
38:h:101:THR:HG23	38:h:104:GLN:H	1.78	0.47
54:x:258:GLY:HA2	54:x:281:VAL:HG23	1.97	0.47
2:2:123:G:O2'	2:2:124:G:OP1	2.33	0.47
1:1:29:C:O2'	18:N:162:ARG:O	2.27	0.47
1:1:921:A:N6	1:1:1846:C:OP2	2.48	0.47
1:1:2522:G:H2'	1:1:2522:G:N3	2.30	0.47
2:2:4:C:C2	2:2:5:U:C5	3.03	0.47
6:A:180:LEU:CG	46:p:26:VAL:HG21	2.45	0.47
9:D:136:GLU:O	9:D:137:ASP:C	2.58	0.47
30:Z:75:VAL:HG11	30:Z:80:LEU:HD21	1.95	0.47
32:b:277:LEU:HD13	43:m:161:VAL:HG22	1.95	0.47
1:1:988:U:O4	1:1:989:A:N6	2.48	0.46
1:1:1225:A:H61	1:1:1284:C:N4	2.13	0.46
1:1:1593:A:H61	44:n:2:ARG:HA	1.79	0.46
1:1:1613:A:OP1	41:k:2:ALA:N	2.49	0.46
1:1:2244:A:O2'	1:1:2245:C:O4'	2.31	0.46
43:m:32:ASP:O	43:m:35:ARG:N	2.48	0.46
44:n:177:ARG:HA	44:n:356:VAL:HG11	1.97	0.46
1:1:59:G:C5'	2:2:33:A:HO2'	2.29	0.46
1:1:247:C:H2'	1:1:248:U:C6	2.51	0.46
1:1:1098:A:OP2	24:T:108:ARG:NH2	2.48	0.46
12:G:91:PHE:O	12:G:95:ASN:ND2	2.48	0.46
13:H:107:ASP:OD2	56:z:19:ARG:NH2	2.47	0.46
21:Q:44:PHE:O	21:Q:48:VAL:HG23	2.15	0.46
30:Z:83:THR:HG23	37:g:93:PHE:HZ	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:v:172:LEU:HD12	53:w:91:GLN:HA	1.95	0.46
1:1:2856:G:H21	48:r:192:THR:HG21	1.80	0.46
1:1:2986:U:C2	1:1:2987:A:C8	3.02	0.46
1:1:3042:U:OP2	1:1:3092:C:N4	2.48	0.46
1:1:3351:U:O4	1:1:3356:G:N2	2.45	0.46
2:2:42:G:OP1	40:j:62:GLY:N	2.47	0.46
27:W:41:TRP:CE3	27:W:217:VAL:HG21	2.49	0.46
45:o:92:ILE:HG23	45:o:167:LEU:CB	2.45	0.46
53:w:158:TRP:CE2	53:w:159:LEU:HD23	2.49	0.46
1:1:291:C:HO2'	1:1:2598:G:H21	1.61	0.46
1:1:654:C:OP1	35:e:27:ARG:NH2	2.48	0.46
1:1:3369:G:N1	7:B:380:MET:O	2.49	0.46
8:C:84:ARG:NH1	8:C:87:GLN:OE1	2.43	0.46
1:1:2432:A:N6	1:1:2598:G:C6	2.84	0.46
1:1:3267:A:OP1	1:1:3268:A:N6	2.48	0.46
32:b:443:ASP:O	51:u:75:ARG:NH2	2.49	0.46
38:h:62:GLN:O	38:h:66:VAL:HG23	2.15	0.46
43:m:462:ILE:HD12	43:m:463:PRO:HD2	1.96	0.46
55:y:88:LEU:HD23	55:y:92:VAL:HG11	1.96	0.46
1:1:1224:C:C2	1:1:1225:A:C8	3.04	0.46
1:1:1416:C:O3'	1:1:1417:G:O4'	2.34	0.46
1:1:2690:G:O2'	1:1:2691:A:P	2.73	0.46
1:1:2874:G:O2'	1:1:2876:C:OP1	2.26	0.46
8:C:289:ILE:HG23	21:Q:129:VAL:CG2	2.46	0.46
45:o:92:ILE:HD12	45:o:173:ILE:CG1	2.45	0.46
1:1:108:A:OP1	16:L:42:ARG:NE	2.49	0.46
1:1:1049:C:O2'	1:1:1050:U:C6	2.69	0.46
1:1:1102:A:O2'	1:1:1103:A:O5'	2.34	0.46
1:1:1390:A:O4'	1:1:1418:A:N6	2.49	0.46
1:1:2692:A:O2'	1:1:2693:C:P	2.74	0.46
1:1:3296:A:OP1	7:B:120:LYS:N	2.49	0.46
12:G:47:SER:O	12:G:50:VAL:HG12	2.15	0.46
13:H:52:LEU:HD23	13:H:53:ILE:N	2.30	0.46
37:g:20:ILE:HD11	37:g:34:HIS:CE1	2.51	0.46
43:m:470:GLU:OE1	43:m:470:GLU:N	2.47	0.46
44:n:189:GLN:NE2	44:n:196:GLU:OE1	2.47	0.46
53:w:70:MET:N	53:w:70:MET:SD	2.88	0.46
1:1:961:C:O2	1:1:961:C:O4'	2.33	0.46
1:1:1339:C:O2'	1:1:1405:U:O4	2.33	0.46
1:1:2624:G:OP1	53:w:151:ASN:ND2	2.49	0.46
1:1:2860:U:OP2	32:b:100:ARG:NE	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:q:384:GLY:O	47:q:385:THR:HG22	2.15	0.46
1:1:2898:G:C2	48:r:7:ILE:HG22	2.51	0.46
1:1:3164:C:HO2'	1:1:3165:A:H8	1.64	0.46
2:2:142:C:OP1	18:N:38:ARG:NH1	2.46	0.46
5:6:1:C:C2'	5:6:2:C:OP2	2.64	0.46
5:6:230:A:O4'	50:t:292:ARG:NH2	2.49	0.46
6:A:62:VAL:HG21	6:A:71:LEU:HD23	1.98	0.46
18:N:160:GLU:OE1	18:N:160:GLU:N	2.46	0.46
44:n:367:VAL:HG12	44:n:411:ILE:HD12	1.98	0.46
54:x:426:ILE:O	54:x:440:PHE:N	2.48	0.46
1:1:1384:U:OP1	8:C:138:ARG:NH1	2.44	0.46
1:1:3276:G:O6	20:P:171:ARG:NH1	2.44	0.46
2:2:71:A:H62	2:2:87:G:H21	1.63	0.46
18:N:21:PHE:O	18:N:25:VAL:HG23	2.16	0.46
27:W:166:ARG:NH1	48:r:18:LEU:O	2.48	0.46
34:d:80:ASN:ND2	34:d:86:LYS:O	2.46	0.46
39:i:15:LYS:HG2	39:i:17:VAL:HG23	1.98	0.46
41:k:75:VAL:O	41:k:77:ARG:NH1	2.48	0.46
43:m:265:VAL:HG12	43:m:465:PHE:HB3	1.98	0.46
1:1:824:C:O2'	1:1:1534:A:N3	2.40	0.45
1:1:1863:G:H22	1:1:1865:A:H3'	1.81	0.45
1:1:2111:G:N2	1:1:2114:C:OP2	2.49	0.45
1:1:2190:U:H2'	1:1:2191:U:H5'	1.97	0.45
2:2:14:C:H3'	2:2:15:G:C8	2.52	0.45
6:A:136:ILE:HG13	6:A:148:VAL:HG12	1.98	0.45
13:H:113:GLU:OE1	13:H:115:ARG:NE	2.46	0.45
53:w:86:VAL:HG13	54:x:133:THR:HG21	1.98	0.45
1:1:959:C:C2'	1:1:960:U:O2	2.64	0.45
1:1:1097:G:C8	24:T:128:LEU:HD13	2.52	0.45
1:1:1367:G:OP1	35:e:45:ARG:NH2	2.43	0.45
1:1:1566:A:OP1	47:q:432:ARG:NH2	2.49	0.45
1:1:2863:G:C5	32:b:95:LEU:HD13	2.52	0.45
2:2:97:A:O3'	38:h:59:ASN:ND2	2.50	0.45
3:3:30:G:N1	3:3:48:U:O4	2.49	0.45
16:L:62:THR:O	16:L:64:LYS:N	2.49	0.45
21:Q:65:SER:OG	21:Q:90:ASP:OD2	2.23	0.45
32:b:150:LEU:HA	32:b:153:VAL:HG22	1.97	0.45
1:1:931:C:OP2	1:1:932:U:O2'	2.19	0.45
1:1:1404:G:OP2	35:e:11:LYS:NZ	2.49	0.45
1:1:1805:C:O2	1:1:1805:C:H2'	2.16	0.45
1:1:1816:A:HO2'	1:1:1817:G:P	2.39	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2743:A:H2'	1:1:2744:U:O4'	2.17	0.45
1:1:2756:C:O3'	53:w:195:GLN:NE2	2.49	0.45
2:2:36:G:O2'	2:2:104:A:N1	2.45	0.45
2:2:83:C:O2	2:2:83:C:H2'	2.15	0.45
9:D:148:ILE:HG22	9:D:159:VAL:CG1	2.46	0.45
18:N:18:VAL:HG13	18:N:19:LEU:H	1.82	0.45
27:W:217:VAL:O	27:W:232:ASN:ND2	2.44	0.45
1:1:1480:G:O4'	1:1:1483:G:N2	2.38	0.45
1:1:1517:G:OP1	42:l:41:ARG:NH1	2.46	0.45
1:1:2155:G:O6	1:1:2182:A:N6	2.49	0.45
7:B:202:THR:O	56:z:44:GLN:NE2	2.48	0.45
7:B:324:VAL:HG11	7:B:328:ILE:CD1	2.47	0.45
45:o:92:ILE:HD13	45:o:171:ALA:HB3	1.99	0.45
48:r:247:ASN:OD1	48:r:256:ASN:N	2.47	0.45
50:t:142:LEU:HD11	50:t:179:LEU:HD22	1.98	0.45
51:u:63:LEU:O	51:u:63:LEU:HG	2.16	0.45
54:x:280:SER:O	54:x:297:HIS:N	2.47	0.45
1:1:1408:G:OP2	35:e:31:ASN:ND2	2.49	0.45
1:1:1825:G:OP1	41:k:17:ARG:NH2	2.49	0.45
1:1:2843:U:O2'	1:1:2844:C:O4'	2.34	0.45
6:A:63:PHE:O	6:A:72:ARG:N	2.44	0.45
7:B:48:GLY:N	7:B:336:VAL:O	2.49	0.45
16:L:119:TYR:CE2	38:h:118:ILE:HD11	2.52	0.45
43:m:374:SER:N	43:m:377:ASP:OD1	2.47	0.45
44:n:174:ARG:NH2	44:n:381:LEU:O	2.49	0.45
48:r:207:PRO:O	48:r:210:THR:HG22	2.17	0.45
1:1:1389:G:O2'	1:1:1418:A:N1	2.46	0.45
1:1:1689:U:C2	1:1:1690:C:C5	3.05	0.45
1:1:2778:G:C2	1:1:2779:A:N7	2.85	0.45
12:G:158:ASP:HB3	12:G:159:PRO:HD3	1.99	0.45
15:K:40:ALA:CB	15:K:281:ILE:HD11	2.47	0.45
33:c:34:LEU:HD11	33:c:42:ILE:HG21	1.98	0.45
1:1:424:G:O2'	35:e:23:ASP:OD2	2.27	0.45
1:1:1503:A:C2	1:1:1504:A:C8	3.05	0.45
1:1:3121:U:H4'	1:1:3122:A:OP1	2.16	0.45
21:Q:43:PRO:O	21:Q:47:VAL:HG23	2.16	0.45
54:x:460:VAL:HA	54:x:470:VAL:HG23	1.98	0.45
1:1:291:C:H2'	1:1:292:U:O2	2.17	0.45
1:1:341:G:N1	2:2:24:G:O6	2.50	0.45
1:1:369:A:O2'	1:1:370:U:H5''	2.17	0.45
1:1:1333:C:O2	1:1:1334:U:C5	2.70	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:77:THR:OG1	7:B:326:GLY:O	2.28	0.45
1:1:1671:C:H2'	1:1:1672:U:O4'	2.16	0.45
1:1:2530:G:N2	1:1:2581:U:O2	2.50	0.45
1:1:2687:G:O2'	1:1:2688:U:OP2	2.26	0.45
1:1:3113:A:N1	1:1:3122:A:C8	2.85	0.45
1:1:3213:A:OP2	17:M:128:ARG:NH2	2.50	0.45
15:K:162:THR:HG23	15:K:163:VAL:N	2.32	0.45
34:d:77:ARG:HD2	34:d:89:LEU:HD23	1.99	0.45
1:1:795:G:C2	1:1:796:U:C5	3.05	0.45
1:1:999:G:H4'	1:1:1000:C:O5'	2.16	0.45
1:1:2146:C:C2	1:1:2147:A:C8	3.05	0.45
1:1:2752:U:H2'	1:1:2753:G:O4'	2.17	0.45
1:1:3051:U:C2	1:1:3052:G:C8	3.05	0.45
11:F:48:ASN:ND2	11:F:182:ASP:OD1	2.50	0.45
12:G:135:GLY:O	12:G:139:VAL:HG23	2.17	0.45
43:m:235:LEU:HD13	43:m:273:TRP:CZ3	2.52	0.45
1:1:627:U:H2'	1:1:628:A:H8	1.81	0.44
1:1:752:C:C2	1:1:753:C:C5	3.05	0.44
1:1:2270:A:H62	52:v:279:LYS:HE2	1.82	0.44
1:1:2376:G:O2'	1:1:2377:G:O4'	2.32	0.44
1:1:2584:G:OP1	47:q:452:LYS:NZ	2.24	0.44
1:1:2650:U:O2'	1:1:2651:G:O4'	2.28	0.44
12:G:99:PRO:O	12:G:191:ASN:ND2	2.49	0.44
1:1:100:A:H3'	1:1:101:G:H21	1.82	0.44
1:1:1329:U:HO2'	1:1:1330:A:P	2.33	0.44
1:1:1710:C:C2	1:1:1711:C:C5	3.05	0.44
7:B:95:THR:OG1	7:B:98:GLY:O	2.30	0.44
15:K:88:PHE:O	15:K:89:THR:HG22	2.17	0.44
15:K:282:LYS:HD3	15:K:288:VAL:HG12	2.00	0.44
35:e:121:ASN:OD1	35:e:121:ASN:N	2.50	0.44
36:f:75:HIS:N	36:f:80:VAL:O	2.42	0.44
1:1:619:A:OP1	20:P:167:ARG:NE	2.46	0.44
1:1:855:U:C4	1:1:856:G:C6	3.06	0.44
1:1:1608:C:C2	1:1:1609:C:C5	3.06	0.44
6:A:113:VAL:HG12	6:A:166:ILE:CD1	2.46	0.44
9:D:40:HIS:N	9:D:41:LYS:HA	2.32	0.44
22:R:23:TRP:HB3	22:R:51:VAL:HG22	1.99	0.44
42:l:25:GLN:OE1	42:l:28:ARG:NH1	2.45	0.44
43:m:377:ASP:O	43:m:378:SER:C	2.60	0.44
1:1:841:A:C6	1:1:853:G:C6	3.05	0.44
1:1:1690:C:C2	1:1:1691:U:C5	3.05	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:157:U:O2	2:2:157:U:O4'	2.34	0.44
5:6:28:A:OP1	45:o:125:ASN:ND2	2.47	0.44
8:C:130:ALA:O	8:C:132:ALA:N	2.51	0.44
12:G:150:LEU:HD23	12:G:151:VAL:N	2.33	0.44
47:q:214:VAL:O	47:q:215:LYS:C	2.61	0.44
1:1:880:G:N3	1:1:882:A:N6	2.65	0.44
1:1:1107:C:N4	1:1:1108:U:O4	2.50	0.44
1:1:3210:A:OP1	17:M:109:ARG:NH1	2.50	0.44
2:2:119:C:OP1	44:n:69:GLN:NE2	2.48	0.44
9:D:64:ILE:O	9:D:74:VAL:HG13	2.18	0.44
12:G:45:ASN:O	12:G:46:LEU:HD23	2.17	0.44
12:G:75:ILE:HG22	12:G:76:ALA:N	2.33	0.44
13:H:41:ILE:CG2	13:H:43:VAL:HG22	2.47	0.44
16:L:161:ASP:OD1	31:a:139:ARG:NH1	2.43	0.44
32:b:71:ILE:HG23	32:b:72:ASN:N	2.32	0.44
33:c:10:ILE:HD11	33:c:100:ILE:HD11	1.99	0.44
42:l:9:ILE:HG22	42:l:13:MET:HE3	1.99	0.44
43:m:139:ASP:OD2	43:m:139:ASP:N	2.50	0.44
46:p:50:GLY:HA3	46:p:54:ILE:HB	1.99	0.44
54:x:377:ALA:HB2	54:x:408:VAL:HG21	1.98	0.44
2:2:83:C:O2	2:2:83:C:C2'	2.65	0.44
13:H:41:ILE:HG23	13:H:43:VAL:HG22	2.00	0.44
32:b:171:LEU:O	32:b:251:LEU:N	2.40	0.44
32:b:441:VAL:HG22	51:u:93:MET:HE1	2.00	0.44
48:r:132:GLU:C	48:r:134:PHE:H	2.26	0.44
51:u:4:TYR:O	51:u:13:CYS:N	2.49	0.44
55:y:5:THR:HG22	55:y:6:GLN:N	2.33	0.44
1:1:338:A:OP1	8:C:48:GLN:N	2.40	0.44
1:1:873:C:H3'	1:1:874:U:C5'	2.48	0.44
1:1:1299:U:O2	1:1:1299:U:O4'	2.36	0.44
1:1:2519:A:N6	1:1:2589:G:O6	2.51	0.44
1:1:2836:C:O2	1:1:2836:C:O4'	2.34	0.44
1:1:3211:C:C2	1:1:3212:C:C5	3.05	0.44
13:H:126:VAL:HG22	13:H:164:ILE:HG13	1.98	0.44
16:L:50:PRO:HG2	38:h:118:ILE:HD12	2.00	0.44
27:W:109:VAL:HG21	27:W:220:TYR:CE1	2.53	0.44
32:b:453:LEU:HD11	51:u:92:ALA:HB2	2.00	0.44
33:c:30:THR:HG22	33:c:91:SER:HB3	2.00	0.44
44:n:351:LYS:HG2	44:n:352:TYR:N	2.32	0.44
52:v:181:VAL:HG21	53:w:58:VAL:HG22	1.98	0.44
1:1:856:G:O3'	1:1:857:G:O4'	2.36	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:959:C:H2'	1:1:960:U:O2	2.17	0.44
1:1:1467:A:N3	1:1:1469:C:OP1	2.51	0.44
1:1:1776:G:H2'	1:1:1777:U:C6	2.53	0.44
1:1:1847:A:O4'	20:P:130:TYR:OH	2.24	0.44
1:1:3113:A:H2'	1:1:3114:A:O4'	2.18	0.44
5:6:7:C:O2'	5:6:8:A:P	2.76	0.44
11:F:229:PHE:CD2	11:F:229:PHE:C	2.96	0.44
20:P:87:SER:O	20:P:91:VAL:HG23	2.17	0.44
27:W:10:VAL:O	27:W:10:VAL:HG13	2.18	0.44
32:b:525:THR:O	32:b:525:THR:HG23	2.17	0.44
1:1:1508:C:H2'	1:1:1509:A:O4'	2.18	0.44
1:1:1807:G:O2'	1:1:2559:U:O4	2.36	0.44
8:C:34:ILE:O	8:C:38:VAL:HG23	2.18	0.44
12:G:54:GLU:O	12:G:58:VAL:HG23	2.18	0.44
44:n:144:ASN:ND2	44:n:203:PHE:O	2.51	0.44
54:x:445:ALA:O	54:x:463:SER:OG	2.31	0.44
1:1:21:G:OP1	2:2:36:G:N1	2.45	0.43
1:1:553:U:H2'	1:1:554:A:O4'	2.18	0.43
1:1:602:A:O2'	1:1:603:A:O4'	2.29	0.43
1:1:797:U:O2	1:1:798:G:C8	2.71	0.43
1:1:1048:A:H2'	1:1:1048:A:N3	2.32	0.43
1:1:1117:G:O2'	1:1:1118:C:P	2.76	0.43
1:1:1362:G:H4'	11:F:160:ARG:HB3	2.00	0.43
1:1:1561:G:O2'	1:1:1562:C:P	2.76	0.43
1:1:1661:G:H2'	1:1:1662:G:C8	2.53	0.43
1:1:1699:A:C6	1:1:1747:G:C6	3.06	0.43
1:1:2724:U:O2'	1:1:2725:U:P	2.76	0.43
1:1:3023:U:O2	1:1:3023:U:O4'	2.35	0.43
15:K:81:ILE:HD12	15:K:263:VAL:HG13	2.00	0.43
21:Q:64:VAL:HG22	21:Q:96:PHE:CE2	2.53	0.43
43:m:390:VAL:HG21	43:m:454:LEU:HB3	1.99	0.43
44:n:254:LYS:O	50:t:200:SER:OG	2.34	0.43
45:o:172:LYS:O	45:o:173:ILE:C	2.60	0.43
47:q:215:LYS:O	47:q:425:SER:OG	2.24	0.43
51:u:63:LEU:HD22	51:u:104:GLU:HA	1.99	0.43
54:x:133:THR:HG22	54:x:480:VAL:HG11	2.00	0.43
1:1:705:A:N7	31:a:74:ASN:ND2	2.64	0.43
1:1:790:U:O2	1:1:791:A:C8	2.71	0.43
1:1:819:U:OP1	40:j:10:LYS:NZ	2.47	0.43
1:1:874:U:OP2	1:1:1907:C:O2'	2.35	0.43
1:1:1836:C:O2'	1:1:1842:A:N1	2.30	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2752:U:O2'	1:1:2753:G:O4'	2.34	0.43
1:1:2868:U:HO2'	1:1:2869:U:P	2.26	0.43
2:2:99:C:OP1	28:X:53:HIS:NE2	2.47	0.43
3:3:77:G:O6	52:v:95:LYS:N	2.52	0.43
10:E:40:LEU:HD11	10:E:54:TYR:HB2	2.00	0.43
14:J:54:VAL:HG21	14:J:59:ILE:HD11	2.00	0.43
30:Z:8:GLY:N	30:Z:25:ILE:O	2.48	0.43
43:m:378:SER:O	43:m:379:GLU:C	2.60	0.43
44:n:453:LEU:H	44:n:453:LEU:HD22	1.83	0.43
45:o:122:LEU:HD21	45:o:131:SER:HB2	2.00	0.43
48:r:148:LYS:O	48:r:149:ARG:NH2	2.47	0.43
48:r:214:VAL:CG1	48:r:216:THR:HG23	2.48	0.43
1:1:189:G:O2'	1:1:190:U:O4'	2.36	0.43
1:1:796:U:C2	1:1:797:U:C5	3.06	0.43
1:1:1310:G:H21	1:1:2381:G:P	2.41	0.43
1:1:1679:A:H4'	32:b:520:PRO:HB3	2.00	0.43
1:1:2188:A:N3	1:1:2188:A:H2'	2.34	0.43
16:L:47:ALA:O	16:L:137:GLN:NE2	2.52	0.43
20:P:50:GLN:OE1	20:P:56:ARG:NH2	2.50	0.43
23:S:171:PHE:HA	23:S:172:TYR:CD1	2.53	0.43
24:T:67:VAL:HG13	24:T:72:VAL:HG12	1.99	0.43
32:b:90:HIS:NE2	43:m:135:GLU:O	2.50	0.43
1:1:53:G:OP1	40:j:48:ASN:N	2.45	0.43
1:1:359:U:H2'	1:1:360:G:O4'	2.18	0.43
1:1:712:G:N2	1:1:754:G:O3'	2.50	0.43
1:1:1437:C:O2	1:1:1437:C:H2'	2.19	0.43
1:1:1803:C:C2	1:1:1804:A:C8	3.06	0.43
1:1:2513:U:H4'	1:1:2514:U:OP1	2.18	0.43
1:1:3181:C:O2	1:1:3181:C:O4'	2.34	0.43
2:2:56:G:OP1	40:j:68:LYS:NZ	2.46	0.43
11:F:148:VAL:HG12	11:F:181:ILE:HD11	2.00	0.43
16:L:74:GLY:O	16:L:101:ARG:NH1	2.51	0.43
18:N:159:ARG:HG2	18:N:164:LEU:HD12	1.99	0.43
27:W:109:VAL:HG21	27:W:220:TYR:CZ	2.53	0.43
46:p:59:CYS:O	46:p:60:CYS:SG	2.77	0.43
1:1:750:G:C2	1:1:751:A:C8	3.06	0.43
1:1:2260:U:O2'	1:1:2262:A:N6	2.51	0.43
1:1:2794:G:O2'	1:1:2795:U:OP2	2.23	0.43
1:1:2909:U:H2'	1:1:2910:A:O4'	2.18	0.43
1:1:3280:U:HO2'	1:1:3281:U:H6	1.65	0.43
13:H:128:VAL:HG22	13:H:134:ILE:HD13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:J:12:LEU:HD11	14:J:131:MET:HB3	2.00	0.43
15:K:166:ALA:O	15:K:168:GLU:N	2.51	0.43
31:a:71:PRO:O	31:a:110:GLY:N	2.47	0.43
41:k:11:PHE:O	41:k:15:THR:HG23	2.18	0.43
44:n:122:TYR:HB3	44:n:128:ALA:HB2	2.01	0.43
48:r:186:HIS:HE1	48:r:261:VAL:HG22	1.83	0.43
1:1:637:C:N4	1:1:2361:A:N7	2.66	0.43
1:1:1833:G:H2'	1:1:1834:U:O4'	2.18	0.43
1:1:2660:G:H4'	1:1:2750:U:O2	2.19	0.43
6:A:13:GLY:O	6:A:17:THR:HG23	2.18	0.43
7:B:103:THR:HG22	7:B:104:THR:N	2.33	0.43
12:G:150:LEU:HD12	12:G:215:VAL:HG22	1.99	0.43
28:X:2:ALA:O	45:o:141:ASN:ND2	2.51	0.43
50:t:269:GLN:O	50:t:270:PRO:C	2.61	0.43
1:1:80:G:C6	1:1:106:A:C6	3.07	0.43
1:1:2330:C:C2	1:1:2331:C:C5	3.07	0.43
1:1:2857:C:HO2'	1:1:2858:U:P	2.32	0.43
3:3:9:C:OP2	3:3:10:C:N4	2.52	0.43
3:3:37:G:O2'	3:3:38:U:O4'	2.33	0.43
12:G:145:ASN:H	12:G:146:LYS:HA	1.83	0.43
15:K:144:LEU:HD22	15:K:149:ILE:HD11	2.00	0.43
16:L:42:ARG:NH1	16:L:51:LEU:O	2.41	0.43
22:R:135:LYS:O	22:R:139:VAL:HG23	2.18	0.43
38:h:50:SER:O	38:h:54:VAL:HG23	2.19	0.43
44:n:353:ASP:H	44:n:357:ALA:HB3	1.83	0.43
1:1:13:A:H4'	1:1:14:U:OP1	2.19	0.43
1:1:1412:G:C2	1:1:1413:G:C8	3.07	0.43
1:1:1494:U:O2'	1:1:1496:C:N4	2.52	0.43
1:1:1791:C:OP1	46:p:34:HIS:NE2	2.52	0.43
1:1:1912:U:N3	1:1:2122:G:O4'	2.51	0.43
1:1:2753:G:H4'	1:1:2754:G:O5'	2.19	0.43
1:1:2759:U:O2	1:1:2759:U:O4'	2.36	0.43
1:1:3049:A:C8	7:B:53:MET:HE3	2.53	0.43
3:3:25:G:C2	3:3:26:C:C6	3.07	0.43
14:J:69:VAL:O	14:J:69:VAL:HG13	2.18	0.43
32:b:260:CYS:O	32:b:262:PHE:N	2.47	0.43
1:1:159:A:C2	1:1:160:G:N7	2.86	0.43
1:1:212:G:OP2	29:Y:2:ALA:N	2.51	0.43
1:1:728:G:H5'	21:Q:47:VAL:HG21	1.99	0.43
1:1:1258:U:O2	1:1:1261:G:N1	2.52	0.43
1:1:1615:C:C2	1:1:1616:U:C5	3.07	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1618:G:H2'	1:1:1619:A:C8	2.53	0.43
1:1:1704:A:HO2'	1:1:1705:U:H6	1.64	0.43
1:1:2989:U:O2'	7:B:232:ARG:NH2	2.47	0.43
2:2:57:C:O2	2:2:61:A:O2'	2.30	0.43
8:C:177:ASP:O	8:C:181:VAL:HG23	2.19	0.43
18:N:4:TYR:CG	18:N:5:LYS:N	2.87	0.43
22:R:106:LEU:HD21	22:R:123:LEU:HB3	2.01	0.43
31:a:144:VAL:HG23	31:a:144:VAL:O	2.19	0.43
36:f:49:ILE:O	36:f:69:GLY:N	2.48	0.43
44:n:17:THR:HG23	44:n:60:THR:CG2	2.49	0.43
45:o:157:LEU:HD23	50:t:59:GLU:CG	2.48	0.43
1:1:40:A:O2'	1:1:41:G:N2	2.51	0.43
1:1:1204:A:H2'	1:1:1205:A:O4'	2.19	0.43
1:1:2766:U:H2'	1:1:2767:U:O4'	2.19	0.43
1:1:2845:A:H3'	1:1:2846:U:H5'	2.01	0.43
1:1:3005:A:N1	1:1:3140:G:O2'	2.50	0.43
1:1:3217:C:N3	20:P:182:ILE:HG23	2.33	0.43
2:2:155:A:H2'	2:2:156:U:O4'	2.19	0.43
5:6:1:C:O2'	5:6:2:C:P	2.77	0.43
8:C:172:VAL:O	8:C:172:VAL:HG12	2.19	0.43
9:D:59:ASP:OD1	9:D:60:ILE:N	2.51	0.43
13:H:44:THR:HG23	17:M:10:SER:OG	2.18	0.43
18:N:145:ASP:O	18:N:147:ARG:N	2.52	0.43
50:t:217:LYS:O	50:t:219:GLU:HG2	2.19	0.43
55:y:199:VAL:HG11	55:y:222:PHE:CZ	2.54	0.43
1:1:1480:G:H4'	1:1:1481:A:C5'	2.49	0.42
1:1:2341:A:OP2	7:B:247:ARG:NH2	2.52	0.42
1:1:2432:A:C6	1:1:2598:G:C6	3.07	0.42
1:1:3306:U:OP1	7:B:225:GLY:N	2.50	0.42
2:2:132:G:OP1	28:X:91:ASN:ND2	2.45	0.42
5:6:18:U:OP1	15:K:228:LYS:NZ	2.29	0.42
7:B:347:SER:O	7:B:350:ALA:N	2.52	0.42
9:D:232:ASP:N	9:D:232:ASP:OD1	2.51	0.42
16:L:160:GLN:O	31:a:144:VAL:HG21	2.19	0.42
18:N:61:ILE:HD12	18:N:133:ILE:HG22	2.00	0.42
27:W:45:LEU:HB3	27:W:215:VAL:HG23	2.01	0.42
27:W:100:THR:HA	27:W:101:GLY:HA3	1.83	0.42
32:b:11:VAL:HG12	32:b:64:ILE:CD1	2.42	0.42
32:b:68:PHE:CZ	32:b:150:LEU:HD22	2.54	0.42
44:n:17:THR:HG22	44:n:19:SER:H	1.83	0.42
44:n:256:ILE:HD11	44:n:373:ILE:HG21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:296:A:N3	1:1:299:G:O2'	2.52	0.42
1:1:995:U:H3'	1:1:996:A:H5'	2.00	0.42
7:B:347:SER:O	7:B:351:LEU:N	2.42	0.42
15:K:185:SER:O	15:K:188:THR:HG22	2.19	0.42
23:S:156:VAL:HG23	23:S:156:VAL:O	2.19	0.42
30:Z:11:ALA:N	30:Z:23:VAL:O	2.49	0.42
43:m:224:VAL:O	43:m:318:VAL:HG23	2.18	0.42
45:o:185:VAL:O	45:o:185:VAL:HG13	2.19	0.42
52:v:266:ASP:N	52:v:270:ASP:O	2.52	0.42
1:1:406:G:HO2'	1:1:407:A:P	2.42	0.42
1:1:1649:U:C4	1:1:1807:G:N2	2.87	0.42
1:1:2148:U:H2'	1:1:2149:A:C8	2.54	0.42
3:3:100:C:OP1	52:v:96:ARG:NH1	2.49	0.42
32:b:312:VAL:O	32:b:315:VAL:HG22	2.19	0.42
43:m:132:LEU:HD13	43:m:136:SER:HA	2.02	0.42
50:t:141:LEU:HD22	50:t:142:LEU:H	1.83	0.42
1:1:1110:U:O2'	1:1:1111:U:OP2	2.30	0.42
1:1:1497:C:H2'	1:1:1498:A:H8	1.84	0.42
1:1:1592:G:H3'	1:1:1593:A:H5''	2.01	0.42
1:1:2752:U:H2'	1:1:2753:G:C8	2.54	0.42
1:1:2841:G:N1	1:1:2845:A:O2'	2.53	0.42
1:1:3058:U:OP1	34:d:28:ARG:NH1	2.49	0.42
2:2:142:C:C2	2:2:143:U:C5	3.08	0.42
25:U:91:ASP:OD1	32:b:521:ARG:NE	2.41	0.42
48:r:173:ARG:O	48:r:178:ARG:NE	2.48	0.42
1:1:868:C:N4	1:1:869:G:O6	2.52	0.42
1:1:956:U:O2'	1:1:957:C:O5'	2.36	0.42
1:1:1353:U:O5'	1:1:1354:G:N2	2.52	0.42
1:1:1749:A:O4'	1:1:1750:A:C4	2.73	0.42
1:1:1881:A:C6	1:1:2352:A:N6	2.87	0.42
1:1:1927:G:C8	46:p:16:VAL:HG22	2.54	0.42
1:1:3351:U:O2'	1:1:3352:U:OP1	2.31	0.42
12:G:101:THR:HG23	12:G:104:GLU:H	1.85	0.42
13:H:55:VAL:HB	13:H:68:LEU:HD21	2.01	0.42
25:U:18:ASP:OD1	25:U:19:VAL:N	2.53	0.42
27:W:41:TRP:CZ2	27:W:109:VAL:HG23	2.55	0.42
33:c:26:GLY:O	33:c:30:THR:HG23	2.20	0.42
40:j:39:TYR:O	40:j:39:TYR:CG	2.72	0.42
44:n:5:LYS:O	44:n:6:LYS:C	2.62	0.42
52:v:214:GLY:HA3	53:w:11:VAL:HG22	2.02	0.42
54:x:261:LYS:HG2	54:x:273:THR:HG23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:977:C:N3	1:1:1105:A:N6	2.68	0.42
1:1:2112:U:O2	1:1:2112:U:H2'	2.19	0.42
1:1:2428:U:O2	1:1:2428:U:O4'	2.38	0.42
1:1:2836:C:N4	1:1:2853:A:C6	2.87	0.42
1:1:3112:G:OP1	13:H:77:ASN:ND2	2.52	0.42
1:1:3164:C:C2	1:1:3165:A:N7	2.87	0.42
1:1:3332:U:H2'	1:1:3333:G:O4'	2.19	0.42
7:B:140:ASP:OD1	7:B:140:ASP:N	2.53	0.42
11:F:165:ASP:OD1	11:F:166:ASN:N	2.53	0.42
16:L:76:THR:HG22	16:L:101:ARG:CB	2.42	0.42
23:S:48:LEU:CD1	24:T:151:LEU:HD12	2.46	0.42
29:Y:126:LEU:HD12	29:Y:127:GLU:N	2.34	0.42
32:b:136:MET:O	32:b:140:VAL:HG23	2.19	0.42
43:m:288:ALA:O	43:m:289:SER:OG	2.34	0.42
55:y:70:LEU:N	55:y:93:LYS:O	2.53	0.42
1:1:812:G:O6	1:1:929:A:N6	2.52	0.42
1:1:1115:G:H21	1:1:1115:G:P	2.38	0.42
1:1:3205:G:HO2'	23:S:171:PHE:HZ	1.63	0.42
2:2:3:A:C4	2:2:4:C:C6	3.08	0.42
6:A:5:ILE:HD12	6:A:7:ASN:HD21	1.85	0.42
7:B:105:VAL:HG12	7:B:106:TRP:N	2.34	0.42
7:B:212:ASN:OD1	7:B:354:VAL:HG12	2.20	0.42
10:E:3:ALA:HB2	35:e:77:ALA:HB2	2.02	0.42
13:H:67:ALA:O	13:H:71:VAL:HG23	2.19	0.42
17:M:21:VAL:HG12	17:M:65:LEU:HA	2.02	0.42
29:Y:110:HIS:O	29:Y:115:ARG:NH1	2.53	0.42
30:Z:83:THR:HG23	37:g:93:PHE:CZ	2.55	0.42
31:a:76:ASP:OD1	31:a:77:LYS:N	2.52	0.42
32:b:173:CYS:O	32:b:253:PHE:N	2.40	0.42
50:t:219:GLU:C	50:t:220:ASN:O	2.63	0.42
55:y:8:GLU:O	55:y:9:ASN:ND2	2.53	0.42
1:1:720:A:C4'	1:1:721:G:OP2	2.68	0.42
1:1:1190:A:N3	1:1:1190:A:H2'	2.34	0.42
1:1:2329:C:C2	1:1:2330:C:C5	3.07	0.42
1:1:2640:A:HO2'	1:1:2641:U:H6	1.66	0.42
1:1:3306:U:H2'	1:1:3307:A:H5''	2.01	0.42
12:G:39:ALA:O	12:G:40:VAL:C	2.61	0.42
20:P:136:ILE:O	20:P:137:ASN:ND2	2.53	0.42
45:o:113:GLN:OE1	50:t:56:VAL:HG23	2.20	0.42
1:1:414:U:N3	1:1:415:G:N7	2.68	0.42
1:1:628:A:H2'	1:1:629:U:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:674:G:OP1	8:C:31:ARG:NH1	2.53	0.42
1:1:1140:G:H2'	1:1:1141:C:O4'	2.20	0.42
1:1:1392:G:O2'	1:1:1393:A:OP2	2.28	0.42
1:1:1416:C:H2'	1:1:1417:G:C4	2.55	0.42
1:1:1764:U:H3'	1:1:1765:U:H5''	2.02	0.42
1:1:2212:C:O2'	1:1:2231:C:N3	2.42	0.42
1:1:3072:C:H4'	1:1:3336:A:H4'	2.00	0.42
1:1:3181:C:C6	1:1:3182:G:C8	3.08	0.42
2:2:117:C:N3	2:2:118:C:C5	2.87	0.42
5:6:16:U:C2'	5:6:17:G:OP2	2.66	0.42
14:J:110:ILE:HG21	14:J:116:TYR:HD1	1.84	0.42
15:K:183:ASP:OD2	15:K:184:ASP:N	2.52	0.42
16:L:123:ILE:HG22	38:h:118:ILE:HG12	2.00	0.42
19:O:118:VAL:HG12	23:S:165:TYR:CD2	2.54	0.42
21:Q:33:TYR:CZ	21:Q:48:VAL:HG11	2.55	0.42
24:T:128:LEU:HD12	24:T:129:LYS:N	2.34	0.42
28:X:85:GLN:OE1	28:X:115:ARG:NH2	2.53	0.42
32:b:145:ASP:HB2	32:b:146:PRO:HD3	2.01	0.42
45:o:191:LYS:NZ	45:o:195:GLN:OE1	2.50	0.42
50:t:58:ALA:O	50:t:62:VAL:HG23	2.20	0.42
55:y:28:VAL:HG12	55:y:50:HIS:HB3	2.01	0.42
1:1:760:G:N2	1:1:770:G:O2'	2.48	0.42
1:1:1105:A:H2'	1:1:1106:G:C8	2.55	0.42
1:1:1567:U:H1'	1:1:1568:U:OP2	2.20	0.42
1:1:1650:G:C2	1:1:1806:A:N6	2.88	0.42
1:1:2876:C:HO2'	1:1:2877:G:P	2.40	0.42
3:3:62:U:OP1	9:D:282:ARG:NH1	2.53	0.42
3:3:93:C:C2	3:3:94:C:C5	3.08	0.42
26:V:10:LYS:NZ	26:V:56:ASP:OD2	2.44	0.42
1:1:337:G:OP2	8:C:196:ASN:ND2	2.52	0.41
1:1:407:A:H5'	1:1:1396:C:O2'	2.20	0.41
1:1:1242:G:C2	1:1:1243:G:N7	2.87	0.41
1:1:1896:A:H61	1:1:2339:C:H42	1.67	0.41
1:1:2752:U:C2'	1:1:2753:G:O4'	2.68	0.41
1:1:3161:C:C2	1:1:3162:C:C5	3.08	0.41
1:1:3163:A:O2'	1:1:3164:C:H5'	2.20	0.41
2:2:143:U:C2	2:2:144:G:C8	3.08	0.41
6:A:104:LEU:HD13	6:A:116:VAL:HG23	2.02	0.41
23:S:77:VAL:HG11	23:S:106:LEU:CD2	2.50	0.41
24:T:155:PRO:O	24:T:156:TYR:C	2.62	0.41
37:g:20:ILE:HD12	37:g:32:ALA:HB1	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:x:144:SER:OG	54:x:165:ASP:N	2.49	0.41
1:1:626:U:H2'	1:1:627:U:O4'	2.19	0.41
1:1:1150:A:H61	1:1:2369:G:H1'	1.85	0.41
1:1:1186:G:O3'	23:S:113:ARG:NH2	2.53	0.41
1:1:1560:G:O2'	1:1:1561:G:P	2.77	0.41
1:1:2623:G:N1	1:1:2756:C:O2	2.53	0.41
1:1:2632:G:O6	1:1:2647:A:N6	2.53	0.41
1:1:2868:U:OP2	1:1:2869:U:N3	2.52	0.41
1:1:2900:A:H3'	1:1:2901:G:H5''	2.01	0.41
1:1:3030:G:O2'	1:1:3031:G:P	2.77	0.41
11:F:161:VAL:HG12	11:F:162:PRO:O	2.19	0.41
24:T:52:MET:N	24:T:53:PRO:HD2	2.35	0.41
32:b:294:ARG:O	32:b:296:GLU:N	2.53	0.41
43:m:207:GLN:O	43:m:208:SER:CB	2.67	0.41
44:n:34:ARG:HG2	44:n:220:THR:HG21	2.02	0.41
1:1:426:G:H5'	35:e:50:ILE:HG22	2.01	0.41
1:1:1187:C:O2'	1:1:1295:G:N2	2.50	0.41
1:1:1338:C:O2	1:1:1339:C:C5	2.74	0.41
1:1:1480:G:H4'	1:1:1481:A:H5''	2.01	0.41
1:1:3050:U:C2	1:1:3051:U:C5	3.07	0.41
2:2:9:A:C2	2:2:10:A:C5	3.08	0.41
2:2:67:U:OP1	40:j:85:LYS:NZ	2.45	0.41
2:2:104:A:OP1	40:j:21:ARG:NH2	2.49	0.41
3:3:48:U:HO2'	3:3:49:G:C5'	2.33	0.41
3:3:61:G:OP1	9:D:276:LYS:NZ	2.39	0.41
21:Q:19:PRO:HG3	21:Q:30:VAL:HG21	2.01	0.41
21:Q:99:THR:HG22	21:Q:100:THR:O	2.20	0.41
43:m:233:ASP:N	43:m:233:ASP:OD1	2.53	0.41
1:1:212:G:O2'	8:C:221:ASN:O	2.38	0.41
1:1:767:U:O2	1:1:768:C:C5	2.74	0.41
1:1:960:U:O2'	1:1:961:C:P	2.78	0.41
1:1:1185:C:OP1	17:M:59:ASN:ND2	2.52	0.41
15:K:77:ASP:OD2	15:K:250:ASN:ND2	2.54	0.41
28:X:11:LYS:NZ	45:o:150:GLU:OE1	2.34	0.41
29:Y:106:ILE:HG21	29:Y:109:LEU:HG	2.02	0.41
30:Z:26:VAL:HA	30:Z:89:VAL:HG21	2.01	0.41
30:Z:68:ILE:HG22	30:Z:69:LYS:N	2.35	0.41
43:m:432:ALA:HB2	43:m:449:VAL:HG21	2.02	0.41
49:s:11:THR:O	49:s:12:SER:OG	2.35	0.41
51:u:78:PRO:O	51:u:79:VAL:C	2.62	0.41
1:1:160:G:O2'	1:1:161:G:P	2.74	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:727:G:H22	21:Q:139:ILE:HB	1.84	0.41
1:1:987:U:H2'	1:1:988:U:C6	2.56	0.41
1:1:1281:G:C2	1:1:1282:G:C8	3.08	0.41
1:1:1463:U:H3	1:1:1467:A:H62	1.68	0.41
1:1:1486:G:H3'	1:1:1487:G:H5''	2.03	0.41
1:1:1794:G:HO2'	1:1:1796:G:N2	2.17	0.41
1:1:1907:C:C2	1:1:1908:A:C8	3.09	0.41
1:1:2515:A:N6	1:1:2592:G:O2'	2.52	0.41
1:1:2722:U:O2	1:1:2722:U:O4'	2.38	0.41
5:6:16:U:C2'	15:K:221:THR:HG1	2.26	0.41
5:6:38:U:C2	5:6:42:G:O6	2.73	0.41
20:P:16:SER:CB	20:P:149:VAL:HG22	2.50	0.41
32:b:64:ILE:N	32:b:64:ILE:HD13	2.35	0.41
47:q:386:LYS:O	47:q:386:LYS:HG2	2.20	0.41
1:1:1330:A:C5	1:1:1332:A:C8	3.08	0.41
1:1:1482:A:H4'	1:1:1483:G:O5'	2.20	0.41
1:1:1551:C:H2'	1:1:1552:G:O4'	2.20	0.41
1:1:2363:A:H2'	1:1:2364:G:C8	2.56	0.41
1:1:2658:G:HO2'	1:1:2659:G:C5'	2.32	0.41
1:1:2876:C:O2'	1:1:2877:G:P	2.79	0.41
2:2:69:U:H2'	2:2:70:G:O4'	2.21	0.41
9:D:140:ARG:NH2	52:v:174:ASP:OD2	2.47	0.41
12:G:65:LEU:HD13	12:G:69:LEU:HD13	2.03	0.41
16:L:62:THR:O	16:L:63:VAL:C	2.64	0.41
17:M:88:ALA:HB3	17:M:90:VAL:HG13	2.02	0.41
25:U:39:ASP:OD1	25:U:40:HIS:N	2.53	0.41
38:h:85:THR:HG23	38:h:88:LEU:H	1.84	0.41
51:u:81:TYR:CE1	51:u:86:VAL:HG21	2.54	0.41
1:1:975:C:HO2'	1:1:976:U:H5	1.65	0.41
1:1:1302:A:C4'	1:1:1303:A:OP1	2.69	0.41
1:1:2431:C:C2	1:1:2432:A:N7	2.89	0.41
1:1:2690:G:H4'	1:1:2691:A:OP2	2.21	0.41
1:1:2703:A:H2'	1:1:2703:A:N3	2.36	0.41
1:1:2728:G:H1'	1:1:2729:U:OP2	2.20	0.41
1:1:3016:A:C2	1:1:3017:A:N7	2.88	0.41
1:1:3134:A:C6	1:1:3135:U:C5	3.09	0.41
30:Z:90:GLU:OE2	30:Z:90:GLU:N	2.52	0.41
32:b:104:LEU:O	32:b:108:VAL:HG23	2.20	0.41
55:y:112:ASP:O	55:y:135:VAL:HG12	2.21	0.41
1:1:708:G:H5'	1:1:754:G:H21	1.86	0.41
1:1:951:A:H2	1:1:1113:G:H21	1.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1239:C:N3	1:1:1240:A:N7	2.68	0.41
1:1:1263:A:H2'	1:1:1263:A:N3	2.35	0.41
1:1:1339:C:H2'	1:1:1340:G:H8	1.84	0.41
1:1:2207:A:H3'	1:1:2208:A:H5'	2.02	0.41
1:1:2269:U:H1'	1:1:2270:A:OP1	2.21	0.41
1:1:2553:U:O2	1:1:2553:U:C2'	2.68	0.41
1:1:2606:G:OP1	43:m:5:LYS:NZ	2.54	0.41
1:1:2933:A:N7	1:1:3014:U:O2'	2.54	0.41
5:6:5:C:N3	50:t:77:ARG:NH2	2.68	0.41
12:G:163:VAL:HG12	12:G:166:LEU:HD12	2.03	0.41
23:S:10:ILE:O	23:S:59:VAL:N	2.50	0.41
33:c:27:TYR:CZ	33:c:31:VAL:HG21	2.56	0.41
55:y:199:VAL:HG11	55:y:222:PHE:CE1	2.56	0.41
55:y:220:SER:OG	55:y:232:ILE:HD11	2.20	0.41
1:1:495:G:N2	1:1:620:U:O4	2.46	0.41
1:1:715:A:O2'	1:1:752:C:O2	2.33	0.41
1:1:860:G:N3	1:1:860:G:H3'	2.36	0.41
1:1:1168:U:OP1	11:F:213:GLY:N	2.54	0.41
1:1:1340:G:H2'	1:1:1341:U:C6	2.55	0.41
1:1:1614:C:C2	1:1:1615:C:C5	3.09	0.41
1:1:1778:G:O2'	1:1:1780:G:OP2	2.38	0.41
1:1:1929:G:OP2	1:1:1930:A:O2'	2.34	0.41
1:1:2257:C:O2	1:1:2257:C:H2'	2.21	0.41
1:1:2613:U:O2'	1:1:2805:G:OP2	2.15	0.41
1:1:3170:A:C2	1:1:3281:U:C4	3.09	0.41
2:2:48:A:O2'	2:2:50:C:OP2	2.37	0.41
2:2:117:C:O2	2:2:118:C:C6	2.74	0.41
3:3:13:A:O2'	9:D:24:ARG:NH1	2.54	0.41
3:3:48:U:O2'	3:3:49:G:O5'	2.36	0.41
5:6:37:C:OP1	15:K:277:ARG:NH2	2.47	0.41
6:A:104:LEU:CD2	6:A:148:VAL:HG11	2.50	0.41
7:B:4:ARG:NH1	7:B:6:TYR:O	2.53	0.41
8:C:130:ALA:C	8:C:132:ALA:N	2.79	0.41
14:J:173:ASP:O	14:J:174:LYS:C	2.64	0.41
17:M:21:VAL:HG11	17:M:35:ILE:HD11	2.03	0.41
18:N:118:SER:CB	18:N:132:VAL:HG22	2.51	0.41
26:V:90:GLY:O	51:u:16:GLY:N	2.42	0.41
32:b:87:GLU:O	32:b:90:HIS:N	2.54	0.41
32:b:275:LYS:N	32:b:276:PRO:HD2	2.35	0.41
32:b:441:VAL:HG13	51:u:93:MET:HE1	2.03	0.41
43:m:215:LEU:HD13	43:m:370:ILE:HD11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:m:228:VAL:HG21	43:m:328:LYS:HG2	2.02	0.41
44:n:31:ASP:OD1	44:n:34:ARG:NH2	2.54	0.41
52:v:215:GLY:HA2	54:x:25:ILE:HD11	2.03	0.41
53:w:9:LEU:N	53:w:10:PRO:CD	2.84	0.41
54:x:301:VAL:CG2	54:x:323:VAL:HG21	2.49	0.41
54:x:374:MET:O	54:x:386:TRP:N	2.52	0.41
55:y:128:LEU:O	55:y:132:VAL:HG23	2.21	0.41
1:1:1152:G:C8	1:1:2370:G:H4'	2.56	0.41
1:1:1804:A:C4	1:1:1805:C:C5	3.09	0.41
1:1:2128:C:C4	1:1:2129:U:C4	3.09	0.41
1:1:2817:A:H1'	1:1:2818:U:P	2.61	0.41
1:1:3034:C:C2	1:1:3035:A:C8	3.09	0.41
1:1:3284:G:H2'	1:1:3285:C:C6	2.56	0.41
3:3:12:U:C4'	3:3:110:G:H21	2.34	0.41
13:H:188:THR:HA	13:H:189:GLU:C	2.45	0.41
28:X:15:VAL:O	28:X:15:VAL:HG12	2.19	0.41
30:Z:104:PRO:CB	30:Z:105:SER:HA	2.50	0.41
34:d:76:SER:N	34:d:92:TYR:O	2.43	0.41
39:i:70:ARG:CG	39:i:87:VAL:HG21	2.51	0.41
52:v:118:VAL:HG13	52:v:230:LEU:HD22	2.03	0.41
1:1:82:C:C4	1:1:83:U:C4	3.09	0.40
1:1:1636:U:O2'	30:Z:79:HIS:ND1	2.51	0.40
1:1:2547:A:N3	1:1:2547:A:H2'	2.36	0.40
1:1:2830:G:O4'	32:b:134:GLY:HA3	2.21	0.40
1:1:2953:U:O2	1:1:2953:U:H2'	2.21	0.40
7:B:346:THR:HG21	56:z:22:PHE:O	2.21	0.40
9:D:88:ILE:O	9:D:88:ILE:HG22	2.21	0.40
18:N:59:PHE:CD1	18:N:135:VAL:HG22	2.56	0.40
32:b:369:ARG:O	32:b:370:ASP:C	2.64	0.40
44:n:145:LEU:HD12	44:n:145:LEU:O	2.21	0.40
1:1:117:U:HO2'	1:1:119:U:P	2.31	0.40
1:1:235:A:C2	1:1:236:G:N7	2.90	0.40
1:1:1106:G:O2'	1:1:1107:C:O4'	2.39	0.40
1:1:1232:C:N4	1:1:1233:G:O6	2.54	0.40
1:1:1376:C:C2	1:1:1377:G:C8	3.09	0.40
1:1:1832:C:O2	1:1:1833:G:C8	2.74	0.40
1:1:1897:G:H21	26:V:18:PRO:CG	2.34	0.40
1:1:2271:A:N6	52:v:280:GLN:O	2.52	0.40
1:1:2427:U:H2'	1:1:2428:U:O2	2.21	0.40
1:1:2868:U:O2'	1:1:2869:U:P	2.77	0.40
2:2:126:A:O2'	2:2:128:U:OP1	2.32	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:L:165:SER:O	16:L:168:ARG:N	2.53	0.40
1:1:20:A:C6	2:2:140:G:C6	3.10	0.40
1:1:567:G:H2'	1:1:568:G:C8	2.57	0.40
1:1:837:A:OP2	46:p:4:ARG:NH1	2.54	0.40
1:1:1238:C:H2'	1:1:1238:C:O2	2.20	0.40
1:1:1458:U:O2	34:d:56:ASN:ND2	2.49	0.40
1:1:1637:A:H5''	1:1:1638:A:OP1	2.22	0.40
1:1:2335:G:N2	1:1:2339:C:O2'	2.55	0.40
8:C:60:THR:CG2	8:C:77:VAL:HG22	2.52	0.40
9:D:40:HIS:HB3	9:D:41:LYS:HA	2.04	0.40
9:D:232:ASP:OD1	9:D:235:SER:OG	2.31	0.40
12:G:33:ASN:O	12:G:39:ALA:HB3	2.22	0.40
17:M:18:GLY:HA2	17:M:72:LEU:HD12	2.03	0.40
25:U:39:ASP:OD1	25:U:40:HIS:ND1	2.44	0.40
32:b:78:HIS:HE1	32:b:163:ILE:HG23	1.86	0.40
33:c:74:ASN:OD1	33:c:75:ASN:N	2.55	0.40
55:y:68:ARG:NH1	55:y:112:ASP:O	2.52	0.40
1:1:264:G:OP1	39:i:34:SER:OG	2.34	0.40
1:1:345:G:O2'	2:2:25:G:N3	2.54	0.40
1:1:764:U:H3'	1:1:765:C:C5'	2.52	0.40
1:1:766:U:H4'	1:1:767:U:O5'	2.21	0.40
1:1:854:G:C2	1:1:855:U:C5	3.10	0.40
1:1:2188:A:C6	1:1:2189:U:C5	3.10	0.40
1:1:2190:U:C2'	1:1:2191:U:H5'	2.52	0.40
1:1:2572:C:O2	1:1:2572:C:H2'	2.21	0.40
1:1:2660:G:O2'	1:1:2744:U:H1'	2.22	0.40
2:2:37:A:OP1	38:h:89:ARG:NH2	2.52	0.40
3:3:99:G:C6	3:3:100:C:C4	3.10	0.40
6:A:118:GLU:N	6:A:122:ASP:OD2	2.54	0.40
6:A:168:VAL:CG1	46:p:79:VAL:HG21	2.51	0.40
7:B:216:ASP:N	7:B:339:ARG:O	2.52	0.40
14:J:110:ILE:HD13	14:J:116:TYR:CD1	2.57	0.40
32:b:47:MET:CG	32:b:116:LEU:HD23	2.51	0.40
32:b:312:VAL:CG1	32:b:315:VAL:HG13	2.51	0.40
40:j:5:THR:HG23	40:j:6:PRO:HD3	2.04	0.40
54:x:172:ASP:O	54:x:176:GLN:N	2.54	0.40
54:x:243:VAL:HG12	54:x:244:LYS:O	2.22	0.40
1:1:1644:C:H41	37:g:68:THR:CG2	2.34	0.40
1:1:2257:C:O2	1:1:2257:C:C2'	2.69	0.40
6:A:180:LEU:HG	46:p:26:VAL:HG21	2.04	0.40
11:F:159:GLN:HB3	11:F:161:VAL:HG22	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:G:46:LEU:HD12	28:X:28:THR:O	2.21	0.40
18:N:126:THR:O	18:N:126:THR:HG22	2.21	0.40
43:m:242:VAL:HG12	43:m:246:MET:HE2	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	5	49/120 (41%)	49 (100%)	0	0	100	100
6	A	210/254 (83%)	199 (95%)	11 (5%)	0	100	100
7	B	384/387 (99%)	358 (93%)	26 (7%)	0	100	100
8	C	359/362 (99%)	336 (94%)	23 (6%)	0	100	100
9	D	257/297 (86%)	246 (96%)	11 (4%)	0	100	100
10	E	152/176 (86%)	145 (95%)	7 (5%)	0	100	100
11	F	220/244 (90%)	210 (96%)	9 (4%)	1 (0%)	24	57
12	G	231/256 (90%)	212 (92%)	19 (8%)	0	100	100
13	H	189/191 (99%)	177 (94%)	12 (6%)	0	100	100
14	J	167/174 (96%)	152 (91%)	15 (9%)	0	100	100
15	K	248/376 (66%)	231 (93%)	17 (7%)	0	100	100
16	L	185/199 (93%)	174 (94%)	10 (5%)	1 (0%)	24	57
17	M	135/138 (98%)	132 (98%)	3 (2%)	0	100	100
18	N	201/204 (98%)	187 (93%)	13 (6%)	1 (0%)	24	57
19	O	195/199 (98%)	194 (100%)	1 (0%)	0	100	100
20	P	173/184 (94%)	168 (97%)	5 (3%)	0	100	100
21	Q	132/186 (71%)	131 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	R	154/189 (82%)	147 (96%)	7 (4%)	0	100	100
23	S	169/172 (98%)	160 (95%)	9 (5%)	0	100	100
24	T	110/160 (69%)	98 (89%)	12 (11%)	0	100	100
25	U	99/121 (82%)	95 (96%)	4 (4%)	0	100	100
26	V	134/137 (98%)	129 (96%)	5 (4%)	0	100	100
27	W	232/236 (98%)	219 (94%)	12 (5%)	1 (0%)	30	61
28	X	139/142 (98%)	133 (96%)	6 (4%)	0	100	100
29	Y	124/127 (98%)	122 (98%)	2 (2%)	0	100	100
30	Z	133/136 (98%)	123 (92%)	10 (8%)	0	100	100
31	a	91/149 (61%)	86 (94%)	5 (6%)	0	100	100
32	b	533/647 (82%)	490 (92%)	43 (8%)	0	100	100
33	c	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
34	d	103/113 (91%)	97 (94%)	6 (6%)	0	100	100
35	e	125/130 (96%)	120 (96%)	5 (4%)	0	100	100
36	f	104/107 (97%)	95 (91%)	9 (9%)	0	100	100
37	g	110/121 (91%)	108 (98%)	2 (2%)	0	100	100
38	h	117/120 (98%)	112 (96%)	5 (4%)	0	100	100
39	i	97/100 (97%)	91 (94%)	6 (6%)	0	100	100
40	j	83/88 (94%)	78 (94%)	5 (6%)	0	100	100
41	k	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
42	l	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
43	m	457/486 (94%)	420 (92%)	36 (8%)	1 (0%)	43	73
44	n	365/605 (60%)	340 (93%)	25 (7%)	0	100	100
45	o	131/220 (60%)	123 (94%)	8 (6%)	0	100	100
46	p	89/92 (97%)	80 (90%)	9 (10%)	0	100	100
47	q	143/455 (31%)	130 (91%)	13 (9%)	0	100	100
48	r	224/261 (86%)	199 (89%)	25 (11%)	0	100	100
49	s	49/520 (9%)	46 (94%)	3 (6%)	0	100	100
50	t	283/322 (88%)	261 (92%)	20 (7%)	2 (1%)	18	49
51	u	148/199 (74%)	143 (97%)	5 (3%)	0	100	100
52	v	283/344 (82%)	270 (95%)	13 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	w	178/203 (88%)	174 (98%)	4 (2%)	0	100	100
54	x	409/515 (79%)	391 (96%)	18 (4%)	0	100	100
55	y	242/245 (99%)	229 (95%)	13 (5%)	0	100	100
56	z	44/106 (42%)	44 (100%)	0	0	100	100
All	All	9407/11749 (80%)	8864 (94%)	536 (6%)	7 (0%)	49	78

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	F	159	GLN
50	t	220	ASN
50	t	221	GLU
18	N	146	ALA
43	m	208	SER
16	L	63	VAL
27	W	127	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	5	48/106 (45%)	48 (100%)	0	100	100
6	A	166/196 (85%)	166 (100%)	0	100	100
7	B	322/323 (100%)	317 (98%)	5 (2%)	55	75
8	C	288/289 (100%)	286 (99%)	2 (1%)	76	82
9	D	219/245 (89%)	217 (99%)	2 (1%)	70	80
10	E	134/153 (88%)	133 (99%)	1 (1%)	76	82
11	F	186/205 (91%)	184 (99%)	2 (1%)	65	78
12	G	191/208 (92%)	190 (100%)	1 (0%)	81	85
13	H	171/171 (100%)	169 (99%)	2 (1%)	63	78
14	J	147/150 (98%)	145 (99%)	2 (1%)	59	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	K	233/346 (67%)	230 (99%)	3 (1%)	61	77
16	L	149/159 (94%)	148 (99%)	1 (1%)	76	82
17	M	108/109 (99%)	108 (100%)	0	100	100
18	N	175/176 (99%)	173 (99%)	2 (1%)	65	78
19	O	160/162 (99%)	160 (100%)	0	100	100
20	P	142/146 (97%)	142 (100%)	0	100	100
21	Q	110/151 (73%)	110 (100%)	0	100	100
22	R	129/154 (84%)	127 (98%)	2 (2%)	55	75
23	S	155/156 (99%)	153 (99%)	2 (1%)	61	77
24	T	100/137 (73%)	100 (100%)	0	100	100
25	U	88/107 (82%)	87 (99%)	1 (1%)	65	78
26	V	104/105 (99%)	104 (100%)	0	100	100
27	W	211/213 (99%)	209 (99%)	2 (1%)	70	80
28	X	117/118 (99%)	116 (99%)	1 (1%)	70	80
29	Y	109/110 (99%)	109 (100%)	0	100	100
30	Z	115/116 (99%)	114 (99%)	1 (1%)	70	80
31	a	76/119 (64%)	76 (100%)	0	100	100
32	b	482/573 (84%)	478 (99%)	4 (1%)	73	81
33	c	81/88 (92%)	79 (98%)	2 (2%)	42	69
34	d	92/97 (95%)	90 (98%)	2 (2%)	45	71
35	e	109/111 (98%)	108 (99%)	1 (1%)	70	80
36	f	90/91 (99%)	90 (100%)	0	100	100
37	g	95/103 (92%)	95 (100%)	0	100	100
38	h	104/105 (99%)	104 (100%)	0	100	100
39	i	81/82 (99%)	81 (100%)	0	100	100
40	j	69/71 (97%)	68 (99%)	1 (1%)	59	76
41	k	68/69 (99%)	68 (100%)	0	100	100
42	l	45/46 (98%)	44 (98%)	1 (2%)	45	71
43	m	408/428 (95%)	402 (98%)	6 (2%)	57	75
44	n	334/548 (61%)	331 (99%)	3 (1%)	70	80
45	o	118/199 (59%)	116 (98%)	2 (2%)	53	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	p	71/72 (99%)	71 (100%)	0	100	100
47	q	137/420 (33%)	137 (100%)	0	100	100
48	r	203/229 (89%)	199 (98%)	4 (2%)	48	72
49	s	47/445 (11%)	47 (100%)	0	100	100
50	t	256/287 (89%)	252 (98%)	4 (2%)	55	75
51	u	133/180 (74%)	133 (100%)	0	100	100
52	v	258/309 (84%)	257 (100%)	1 (0%)	84	86
53	w	161/179 (90%)	160 (99%)	1 (1%)	78	83
54	x	361/451 (80%)	359 (99%)	2 (1%)	78	83
55	y	210/211 (100%)	208 (99%)	2 (1%)	68	79
56	z	40/95 (42%)	39 (98%)	1 (2%)	42	69
All	All	8206/10119 (81%)	8137 (99%)	69 (1%)	70	81

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	B	84	VAL
7	B	192	VAL
7	B	320	ASP
7	B	328	ILE
7	B	375	GLU
8	C	182	LEU
8	C	306	THR
9	D	136	GLU
9	D	176	SER
10	E	155	LEU
11	F	41	ARG
11	F	232	ARG
12	G	150	LEU
13	H	73	SER
13	H	157	ASN
14	J	112	LEU
14	J	130	VAL
15	K	91	THR
15	K	141	PHE
15	K	276	ILE
16	L	58	VAL
18	N	83	LYS

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Mol	Chain	Res	Type
18	N	96	ARG
22	R	74	ARG
22	R	138	LEU
23	S	64	ILE
23	S	172	TYR
25	U	52	ASN
27	W	96	CYS
27	W	173	THR
28	X	133	LEU
30	Z	67	LYS
32	b	180	LYS
32	b	280	ASN
32	b	324	LEU
32	b	432	MET
33	c	11	ASN
33	c	102	THR
34	d	89	LEU
34	d	96	VAL
35	e	21	HIS
40	j	58	THR
42	l	21	ARG
43	m	147	ARG
43	m	152	LEU
43	m	224	VAL
43	m	284	LEU
43	m	362	ILE
43	m	422	LYS
44	n	27	VAL
44	n	130	ARG
44	n	133	ASP
45	o	157	LEU
45	o	220	TRP
48	r	17	ARG
48	r	133	MET
48	r	162	THR
48	r	210	THR
50	t	223	GLU
50	t	229	LEU
50	t	268	LEU
50	t	314	ILE
52	v	206	LEU
53	w	162	VAL

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Mol	Chain	Res	Type
54	x	280	SER
54	x	444	VAL
55	y	9	ASN
55	y	97	VAL
56	z	41	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (80) such sidechains are listed below:

Mol	Chain	Res	Type
6	A	140	ASN
6	A	209	HIS
7	B	198	HIS
7	B	273	HIS
8	C	48	GLN
8	C	58	HIS
8	C	304	GLN
8	C	307	GLN
9	D	57	ASN
10	E	167	ASN
11	F	93	ASN
12	G	59	GLN
12	G	85	ASN
12	G	240	ASN
13	H	58	HIS
13	H	96	HIS
13	H	163	GLN
14	J	109	HIS
15	K	247	HIS
15	K	262	ASN
16	L	137	GLN
17	M	105	GLN
18	N	37	HIS
18	N	95	GLN
19	O	122	GLN
20	P	55	GLN
20	P	133	HIS
21	Q	58	ASN
22	R	92	GLN
22	R	141	HIS
23	S	63	GLN
23	S	74	ASN
23	S	108	GLN

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Mol	Chain	Res	Type
25	U	88	GLN
27	W	22	ASN
28	X	19	ASN
28	X	137	ASN
31	a	62	HIS
31	a	120	ASN
32	b	70	ASN
32	b	72	ASN
32	b	78	HIS
32	b	152	GLN
32	b	177	ASN
32	b	356	ASN
34	d	57	GLN
37	g	34	HIS
38	h	59	ASN
38	h	99	GLN
39	i	100	HIS
40	j	12	HIS
41	k	40	GLN
42	l	33	ASN
43	m	213	ASN
43	m	305	GLN
44	n	53	ASN
44	n	165	GLN
45	o	130	ASN
47	q	228	ASN
47	q	381	HIS
48	r	33	HIS
48	r	68	HIS
48	r	224	ASN
48	r	256	ASN
49	s	7	GLN
50	t	25	ASN
50	t	238	GLN
50	t	322	ASN
51	u	130	ASN
52	v	67	HIS
52	v	82	ASN
52	v	144	GLN
53	w	64	GLN
53	w	151	ASN
53	w	198	ASN

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Mol	Chain	Res	Type
54	x	314	ASN
54	x	321	HIS
54	x	407	HIS
55	y	79	GLN
55	y	187	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3044/3396 (89%)	615 (20%)	78 (2%)
2	2	157/158 (99%)	27 (17%)	2 (1%)
3	3	120/121 (99%)	16 (13%)	2 (1%)
5	6	64/232 (27%)	21 (32%)	5 (7%)
All	All	3385/3907 (86%)	679 (20%)	87 (2%)

All (679) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	U
1	1	13	A
1	1	14	U
1	1	26	A
1	1	40	A
1	1	41	G
1	1	43	A
1	1	45	A
1	1	49	A
1	1	60	A
1	1	65	A
1	1	66	A
1	1	76	G
1	1	92	G
1	1	96	G
1	1	110	G
1	1	111	C
1	1	116	A
1	1	117	U
1	1	121	A
1	1	122	A
1	1	135	C
1	1	136	G

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Mol	Chain	Res	Type
1	1	148	G
1	1	156	G
1	1	157	A
1	1	161	G
1	1	166	C
1	1	173	G
1	1	187	A
1	1	190	U
1	1	191	U
1	1	200	C
1	1	210	U
1	1	213	A
1	1	218	G
1	1	219	A
1	1	221	A
1	1	240	U
1	1	241	G
1	1	243	G
1	1	245	U
1	1	248	U
1	1	249	U
1	1	251	G
1	1	252	U
1	1	253	A
1	1	266	A
1	1	269	G
1	1	283	G
1	1	284	A
1	1	285	A
1	1	286	U
1	1	295	A
1	1	305	U
1	1	315	C
1	1	323	A
1	1	325	A
1	1	329	U
1	1	352	A
1	1	361	A
1	1	370	U
1	1	374	A
1	1	375	A
1	1	376	G

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Mol	Chain	Res	Type
1	1	398	A
1	1	401	U
1	1	402	A
1	1	403	C
1	1	404	G
1	1	421	G
1	1	422	A
1	1	429	U
1	1	438	A
1	1	440	A
1	1	521	A
1	1	529	A
1	1	535	G
1	1	536	U
1	1	546	C
1	1	547	G
1	1	552	G
1	1	557	A
1	1	559	A
1	1	578	A
1	1	579	G
1	1	589	A
1	1	592	A
1	1	604	G
1	1	609	G
1	1	611	A
1	1	620	U
1	1	621	A
1	1	636	C
1	1	638	C
1	1	641	C
1	1	643	U
1	1	644	G
1	1	645	A
1	1	646	A
1	1	647	A
1	1	649	A
1	1	650	C
1	1	677	A
1	1	681	U
1	1	691	A
1	1	705	A

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Mol	Chain	Res	Type
1	1	715	A
1	1	716	A
1	1	720	A
1	1	721	G
1	1	722	G
1	1	725	G
1	1	735	A
1	1	761	A
1	1	764	U
1	1	765	C
1	1	766	U
1	1	767	U
1	1	768	C
1	1	769	G
1	1	777	U
1	1	779	G
1	1	780	A
1	1	785	G
1	1	787	G
1	1	808	A
1	1	817	A
1	1	836	A
1	1	850	U
1	1	857	G
1	1	861	C
1	1	875	G
1	1	879	U
1	1	880	G
1	1	895	A
1	1	896	A
1	1	897	U
1	1	907	G
1	1	908	G
1	1	914	A
1	1	916	G
1	1	917	A
1	1	944	C
1	1	957	C
1	1	959	C
1	1	960	U
1	1	961	C
1	1	964	G

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Mol	Chain	Res	Type
1	1	965	A
1	1	974	G
1	1	976	U
1	1	977	C
1	1	979	U
1	1	980	A
1	1	981	U
1	1	984	G
1	1	991	G
1	1	992	A
1	1	997	A
1	1	999	G
1	1	1000	C
1	1	1003	A
1	1	1048	A
1	1	1050	U
1	1	1051	U
1	1	1057	A
1	1	1058	U
1	1	1063	G
1	1	1064	A
1	1	1065	A
1	1	1066	G
1	1	1072	G
1	1	1074	U
1	1	1087	G
1	1	1093	A
1	1	1094	U
1	1	1095	U
1	1	1097	G
1	1	1098	A
1	1	1103	A
1	1	1104	G
1	1	1111	U
1	1	1116	G
1	1	1117	G
1	1	1118	C
1	1	1123	U
1	1	1127	G
1	1	1129	A
1	1	1132	C
1	1	1153	A

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Mol	Chain	Res	Type
1	1	1155	C
1	1	1180	A
1	1	1181	U
1	1	1189	C
1	1	1190	A
1	1	1191	U
1	1	1192	C
1	1	1193	A
1	1	1196	C
1	1	1198	C
1	1	1199	C
1	1	1200	A
1	1	1201	C
1	1	1203	A
1	1	1206	G
1	1	1207	G
1	1	1222	G
1	1	1234	G
1	1	1241	U
1	1	1242	G
1	1	1243	G
1	1	1244	A
1	1	1245	A
1	1	1246	G
1	1	1251	A
1	1	1252	A
1	1	1253	U
1	1	1259	A
1	1	1263	A
1	1	1270	A
1	1	1272	C
1	1	1278	A
1	1	1286	A
1	1	1287	A
1	1	1303	A
1	1	1304	A
1	1	1307	G
1	1	1308	A
1	1	1325	U
1	1	1330	A
1	1	1348	U
1	1	1349	G

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Mol	Chain	Res	Type
1	1	1351	U
1	1	1352	A
1	1	1353	U
1	1	1354	G
1	1	1356	U
1	1	1357	G
1	1	1386	A
1	1	1392	G
1	1	1399	A
1	1	1400	G
1	1	1406	A
1	1	1408	G
1	1	1417	G
1	1	1419	A
1	1	1434	G
1	1	1436	U
1	1	1437	C
1	1	1455	U
1	1	1481	A
1	1	1483	G
1	1	1487	G
1	1	1496	C
1	1	1508	C
1	1	1555	U
1	1	1560	G
1	1	1561	G
1	1	1562	C
1	1	1567	U
1	1	1568	U
1	1	1569	U
1	1	1571	A
1	1	1572	U
1	1	1573	G
1	1	1575	A
1	1	1580	A
1	1	1581	C
1	1	1582	C
1	1	1583	A
1	1	1588	A
1	1	1589	A
1	1	1593	A
1	1	1607	U

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Mol	Chain	Res	Type
1	1	1613	A
1	1	1620	U
1	1	1629	U
1	1	1638	A
1	1	1639	C
1	1	1643	A
1	1	1647	A
1	1	1683	A
1	1	1687	U
1	1	1688	U
1	1	1694	U
1	1	1713	G
1	1	1716	U
1	1	1717	U
1	1	1724	U
1	1	1725	C
1	1	1741	A
1	1	1750	A
1	1	1751	G
1	1	1760	A
1	1	1763	U
1	1	1765	U
1	1	1770	G
1	1	1775	G
1	1	1780	G
1	1	1796	G
1	1	1797	A
1	1	1808	G
1	1	1812	G
1	1	1813	A
1	1	1816	A
1	1	1817	G
1	1	1820	U
1	1	1821	U
1	1	1839	A
1	1	1841	A
1	1	1849	C
1	1	1851	G
1	1	1863	G
1	1	1866	C
1	1	1878	G
1	1	1906	G

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Mol	Chain	Res	Type
1	1	1909	A
1	1	1952	G
1	1	2094	C
1	1	2100	A
1	1	2102	U
1	1	2114	C
1	1	2121	G
1	1	2122	G
1	1	2131	A
1	1	2158	A
1	1	2163	C
1	1	2167	A
1	1	2169	G
1	1	2188	A
1	1	2191	U
1	1	2192	C
1	1	2193	U
1	1	2194	G
1	1	2195	C
1	1	2205	U
1	1	2207	A
1	1	2208	A
1	1	2210	G
1	1	2223	A
1	1	2239	G
1	1	2243	A
1	1	2244	A
1	1	2246	G
1	1	2247	G
1	1	2248	C
1	1	2249	G
1	1	2250	G
1	1	2264	U
1	1	2265	C
1	1	2266	U
1	1	2267	C
1	1	2270	A
1	1	2271	A
1	1	2274	U
1	1	2277	C
1	1	2278	C
1	1	2279	A

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Mol	Chain	Res	Type
1	1	2316	G
1	1	2318	U
1	1	2335	G
1	1	2336	U
1	1	2371	G
1	1	2378	C
1	1	2388	U
1	1	2393	G
1	1	2397	A
1	1	2398	A
1	1	2401	A
1	1	2402	A
1	1	2404	A
1	1	2410	U
1	1	2411	U
1	1	2412	G
1	1	2413	A
1	1	2414	G
1	1	2418	G
1	1	2419	A
1	1	2433	U
1	1	2444	C
1	1	2502	A
1	1	2503	G
1	1	2507	C
1	1	2514	U
1	1	2522	G
1	1	2523	A
1	1	2533	G
1	1	2536	A
1	1	2538	U
1	1	2540	A
1	1	2541	U
1	1	2542	U
1	1	2543	U
1	1	2544	U
1	1	2546	C
1	1	2547	A
1	1	2548	C
1	1	2549	G
1	1	2550	U
1	1	2552	C

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Mol	Chain	Res	Type
1	1	2555	G
1	1	2560	C
1	1	2561	A
1	1	2562	A
1	1	2570	U
1	1	2573	G
1	1	2586	G
1	1	2593	A
1	1	2594	C
1	1	2595	A
1	1	2606	G
1	1	2607	G
1	1	2621	G
1	1	2625	C
1	1	2626	A
1	1	2629	U
1	1	2635	A
1	1	2636	A
1	1	2641	U
1	1	2644	C
1	1	2651	G
1	1	2652	U
1	1	2653	C
1	1	2654	C
1	1	2655	U
1	1	2656	A
1	1	2657	A
1	1	2659	G
1	1	2663	G
1	1	2667	A
1	1	2672	G
1	1	2674	A
1	1	2677	G
1	1	2681	U
1	1	2686	A
1	1	2688	U
1	1	2690	G
1	1	2691	A
1	1	2692	A
1	1	2693	C
1	1	2694	A
1	1	2696	A

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Mol	Chain	Res	Type
1	1	2702	A
1	1	2704	A
1	1	2713	U
1	1	2714	G
1	1	2715	A
1	1	2719	U
1	1	2720	G
1	1	2725	U
1	1	2726	C
1	1	2727	A
1	1	2728	G
1	1	2729	U
1	1	2730	G
1	1	2731	U
1	1	2732	G
1	1	2740	A
1	1	2749	G
1	1	2752	U
1	1	2754	G
1	1	2758	A
1	1	2759	U
1	1	2762	A
1	1	2763	U
1	1	2764	C
1	1	2766	U
1	1	2767	U
1	1	2770	G
1	1	2771	U
1	1	2772	C
1	1	2777	G
1	1	2778	G
1	1	2779	A
1	1	2793	G
1	1	2794	G
1	1	2795	U
1	1	2796	G
1	1	2798	C
1	1	2799	A
1	1	2800	G
1	1	2801	A
1	1	2802	A
1	1	2803	A

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Mol	Chain	Res	Type
1	1	2810	C
1	1	2815	G
1	1	2817	A
1	1	2818	U
1	1	2819	A
1	1	2820	A
1	1	2821	C
1	1	2822	U
1	1	2824	G
1	1	2826	U
1	1	2838	A
1	1	2842	U
1	1	2844	C
1	1	2845	A
1	1	2846	U
1	1	2858	U
1	1	2859	U
1	1	2861	U
1	1	2863	G
1	1	2865	U
1	1	2866	U
1	1	2867	C
1	1	2868	U
1	1	2869	U
1	1	2872	A
1	1	2873	U
1	1	2875	U
1	1	2876	C
1	1	2877	G
1	1	2878	G
1	1	2879	C
1	1	2887	A
1	1	2889	C
1	1	2898	G
1	1	2901	G
1	1	2921	U
1	1	2923	U
1	1	2925	C
1	1	2926	A
1	1	2935	U
1	1	2936	A
1	1	2945	G

Continued on next page...

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Mol	Chain	Res	Type
1	1	2947	G
1	1	2952	G
1	1	2953	U
1	1	2954	U
1	1	2955	U
1	1	2956	A
1	1	2957	G
1	1	2970	C
1	1	2971	A
1	1	2978	U
1	1	2980	U
1	1	2981	U
1	1	2982	A
1	1	2983	C
1	1	2984	C
1	1	2995	A
1	1	2996	U
1	1	2997	G
1	1	3003	G
1	1	3012	A
1	1	3017	A
1	1	3022	G
1	1	3026	G
1	1	3029	A
1	1	3030	G
1	1	3031	G
1	1	3032	A
1	1	3059	G
1	1	3078	U
1	1	3079	U
1	1	3086	A
1	1	3092	C
1	1	3093	C
1	1	3100	U
1	1	3101	G
1	1	3129	A
1	1	3130	A
1	1	3131	U
1	1	3142	A
1	1	3143	C
1	1	3163	A
1	1	3164	C

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Mol	Chain	Res	Type
1	1	3165	A
1	1	3170	A
1	1	3173	G
1	1	3174	A
1	1	3176	G
1	1	3179	U
1	1	3180	A
1	1	3181	C
1	1	3187	A
1	1	3196	U
1	1	3198	U
1	1	3207	U
1	1	3213	A
1	1	3217	C
1	1	3218	A
1	1	3219	G
1	1	3224	G
1	1	3229	G
1	1	3245	A
1	1	3247	G
1	1	3253	G
1	1	3259	U
1	1	3260	G
1	1	3266	G
1	1	3270	U
1	1	3273	A
1	1	3276	G
1	1	3281	U
1	1	3289	G
1	1	3294	A
1	1	3304	U
1	1	3307	A
1	1	3316	A
1	1	3319	U
1	1	3334	U
1	1	3335	A
1	1	3341	U
1	1	3342	A
1	1	3350	C
1	1	3351	U
1	1	3352	U
1	1	3354	U

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Mol	Chain	Res	Type
1	1	3355	U
1	1	3369	G
1	1	3378	C
1	1	3389	U
2	2	16	G
2	2	34	U
2	2	35	C
2	2	39	G
2	2	59	A
2	2	62	C
2	2	63	G
2	2	71	A
2	2	72	A
2	2	80	A
2	2	81	U
2	2	82	U
2	2	83	C
2	2	84	C
2	2	86	U
2	2	90	U
2	2	95	G
2	2	100	U
2	2	104	A
2	2	106	C
2	2	111	A
2	2	113	U
2	2	116	G
2	2	124	G
2	2	125	U
2	2	126	A
2	2	151	C
3	3	7	G
3	3	22	A
3	3	27	A
3	3	49	G
3	3	53	U
3	3	54	U
3	3	65	G
3	3	72	A
3	3	74	C
3	3	76	A
3	3	87	G

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Mol	Chain	Res	Type
3	3	95	A
3	3	102	A
3	3	112	G
3	3	113	C
3	3	121	U
5	6	2	C
5	6	5	C
5	6	6	U
5	6	7	C
5	6	8	A
5	6	14	U
5	6	16	U
5	6	17	G
5	6	24	A
5	6	34	A
5	6	37	C
5	6	40	U
5	6	41	G
5	6	52	G
5	6	53	A
5	6	54	A
5	6	56	U
5	6	57	U
5	6	59	C
5	6	231	A
5	6	232	A

All (87) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1	G
1	1	13	A
1	1	40	A
1	1	116	A
1	1	160	G
1	1	284	A
1	1	545	U
1	1	645	A
1	1	649	A
1	1	720	A
1	1	765	C
1	1	849	C

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Mol	Chain	Res	Type
1	1	916	G
1	1	960	U
1	1	999	G
1	1	1057	A
1	1	1064	A
1	1	1097	G
1	1	1102	A
1	1	1103	A
1	1	1128	U
1	1	1205	A
1	1	1241	U
1	1	1302	A
1	1	1307	G
1	1	1329	U
1	1	1355	A
1	1	1405	U
1	1	1482	A
1	1	1567	U
1	1	1568	U
1	1	1570	U
1	1	1579	C
1	1	1581	C
1	1	1716	U
1	1	1816	A
1	1	2101	C
1	1	2166	A
1	1	2209	U
1	1	2243	A
1	1	2245	C
1	1	2263	C
1	1	2269	U
1	1	2317	A
1	1	2392	C
1	1	2501	U
1	1	2513	U
1	1	2537	U
1	1	2541	U
1	1	2569	A
1	1	2593	A
1	1	2624	G
1	1	2625	C
1	1	2651	G

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Mol	Chain	Res	Type
1	1	2652	U
1	1	2658	G
1	1	2690	G
1	1	2728	G
1	1	2753	G
1	1	2761	G
1	1	2770	G
1	1	2795	U
1	1	2802	A
1	1	2817	A
1	1	2857	C
1	1	2868	U
1	1	2875	U
1	1	2946	A
1	1	2954	U
1	1	3030	G
1	1	3078	U
1	1	3195	U
1	1	3218	A
1	1	3228	C
1	1	3269	U
1	1	3350	C
1	1	3351	U
1	1	3353	G
2	2	123	G
2	2	125	U
3	3	52	G
3	3	86	U
5	6	1	C
5	6	5	C
5	6	16	U
5	6	23	U
5	6	56	U

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 5 ligands modelled in this entry, 5 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.

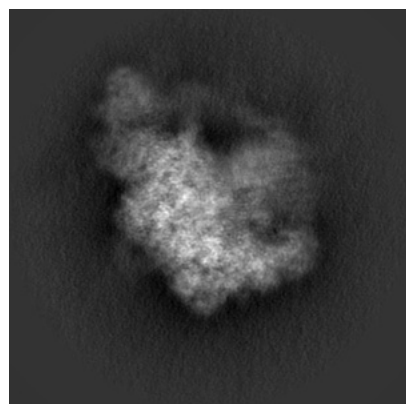
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12905. These allow visual inspection of the internal detail of the map and identification of artifacts.

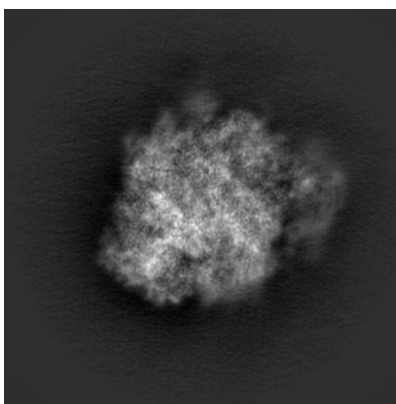
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

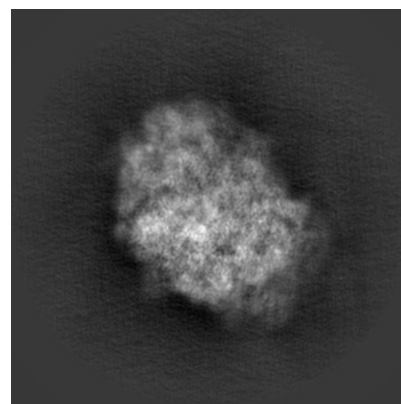
6.1.1 Primary map



X

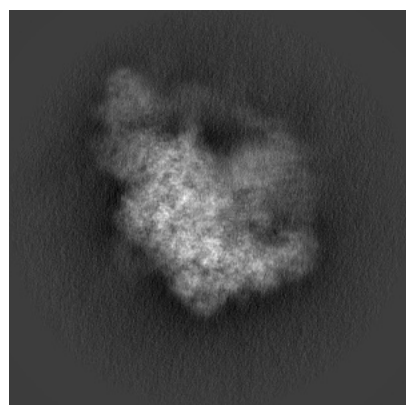


Y

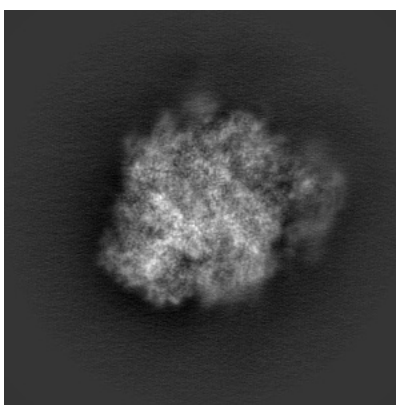


Z

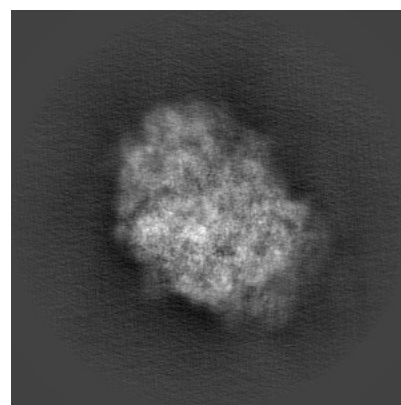
6.1.2 Raw map



X



Y

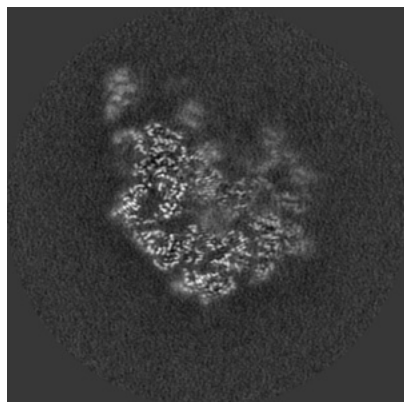


Z

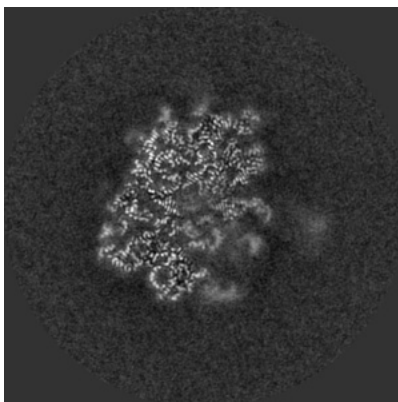
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

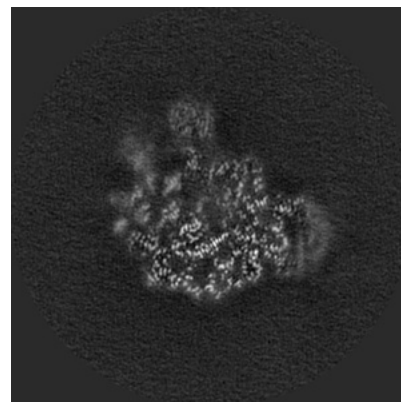
6.2.1 Primary map



X Index: 200

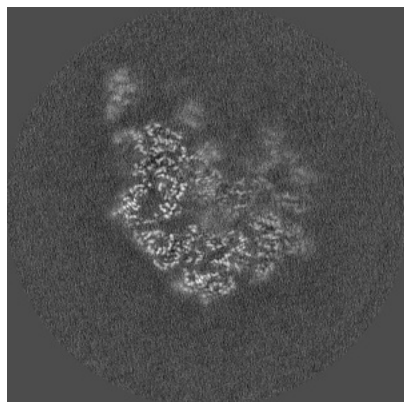


Y Index: 200

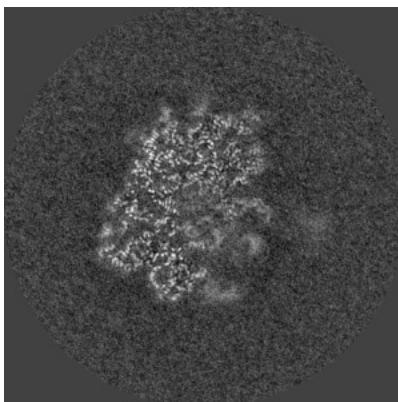


Z Index: 200

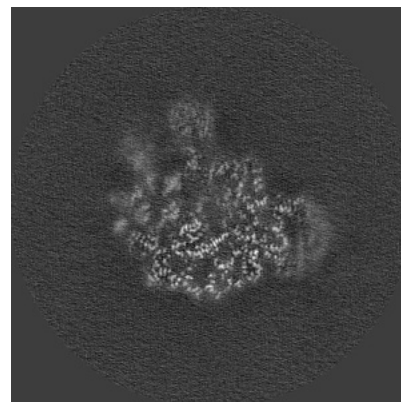
6.2.2 Raw map



X Index: 200



Y Index: 200

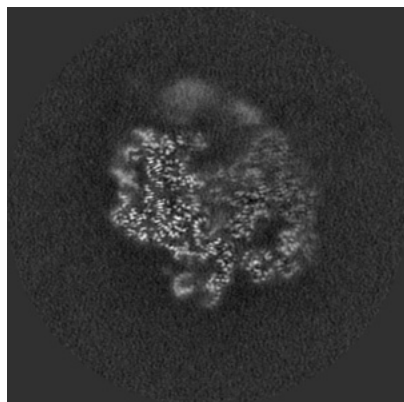


Z Index: 200

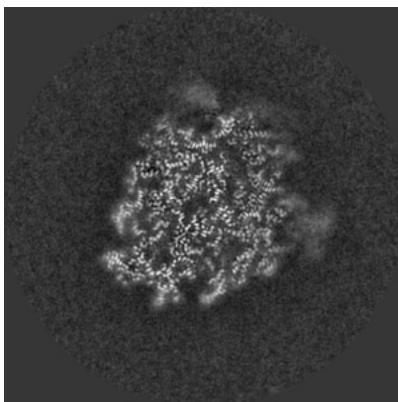
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

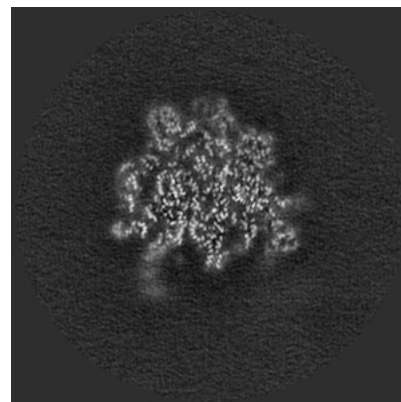
6.3.1 Primary map



X Index: 183

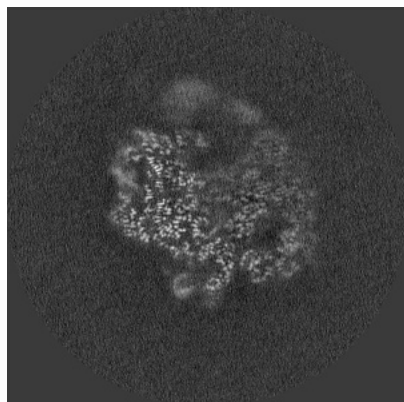


Y Index: 178

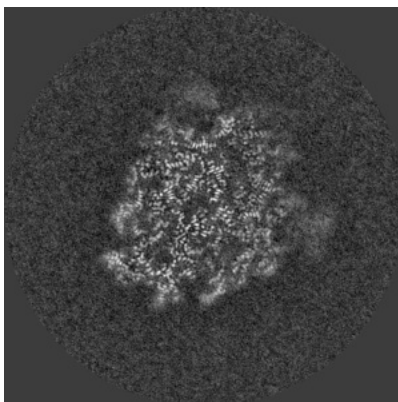


Z Index: 153

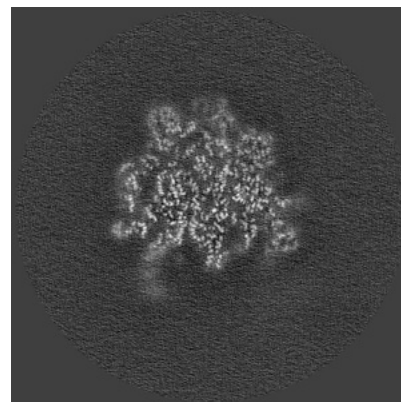
6.3.2 Raw map



X Index: 184



Y Index: 178

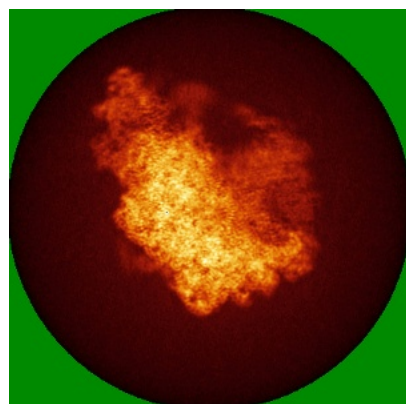


Z Index: 153

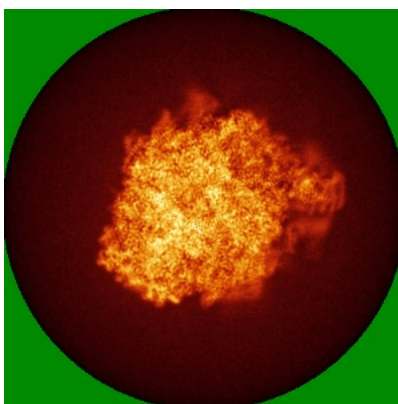
The images above show the largest variance slices of the map in three orthogonal directions.

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

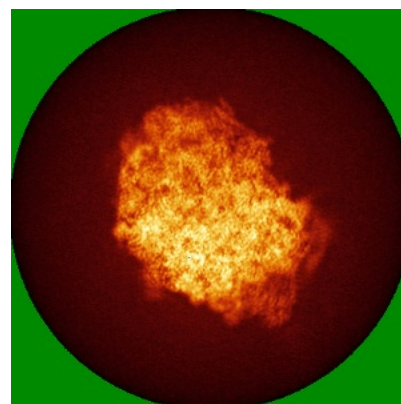
6.4.1 Primary map



X

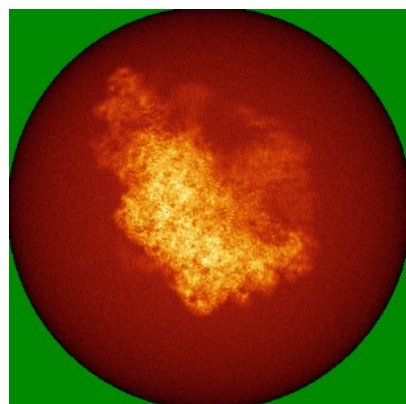


Y

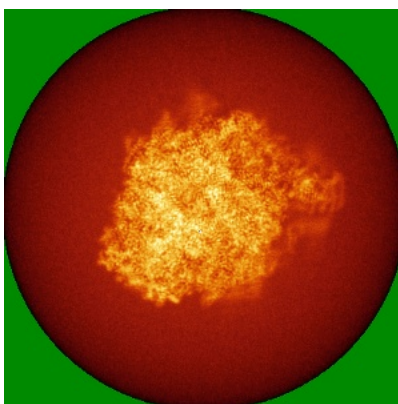


Z

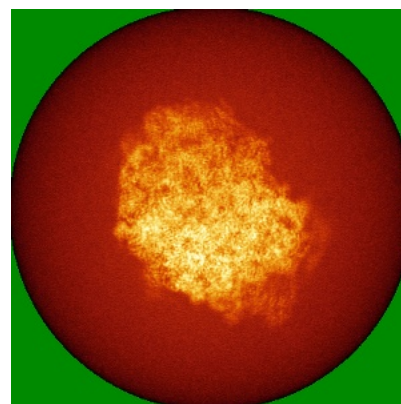
6.4.2 Raw map



X



Y



Z

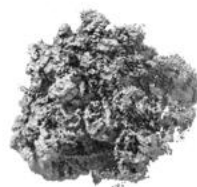
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

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 0.021. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

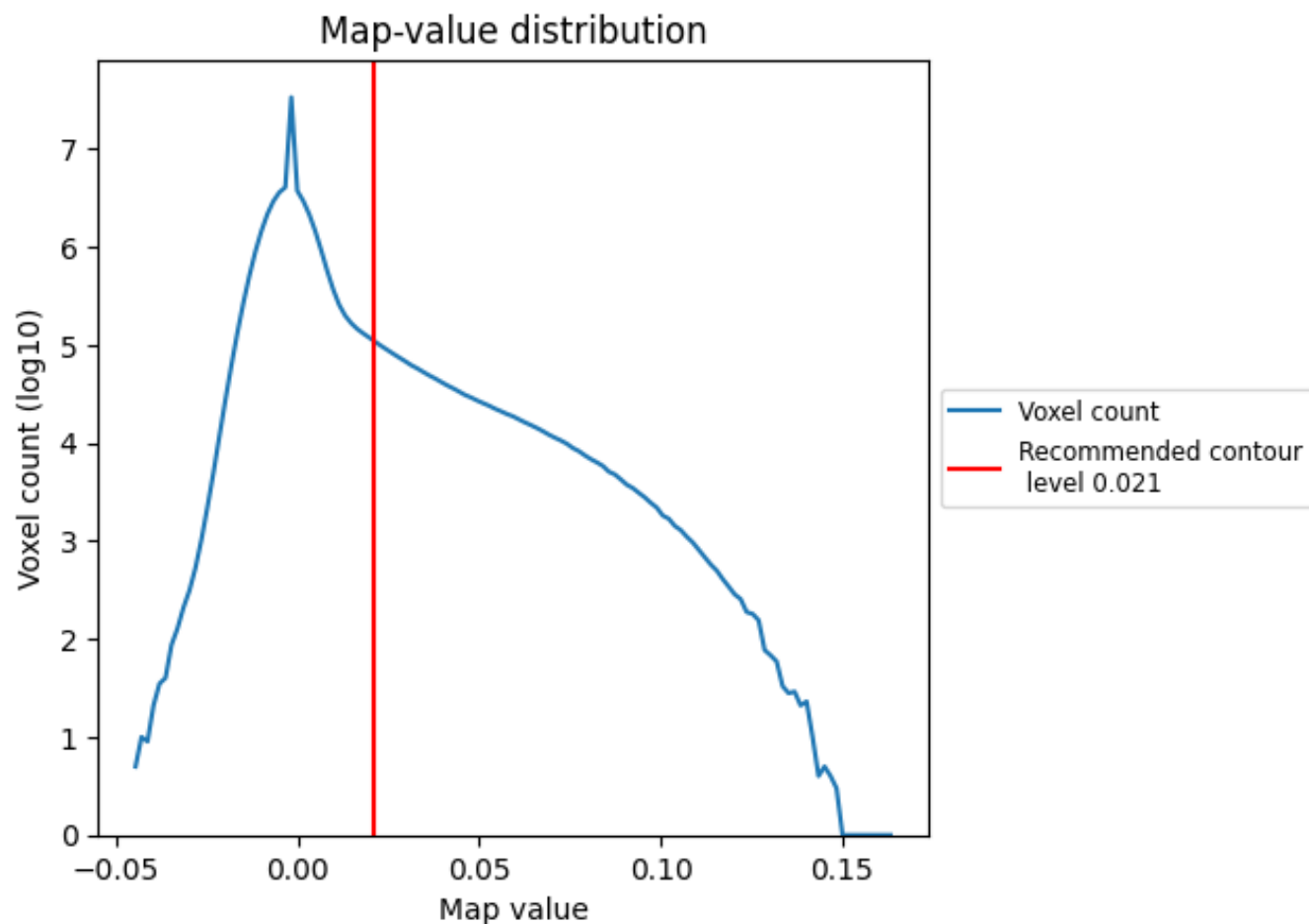
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

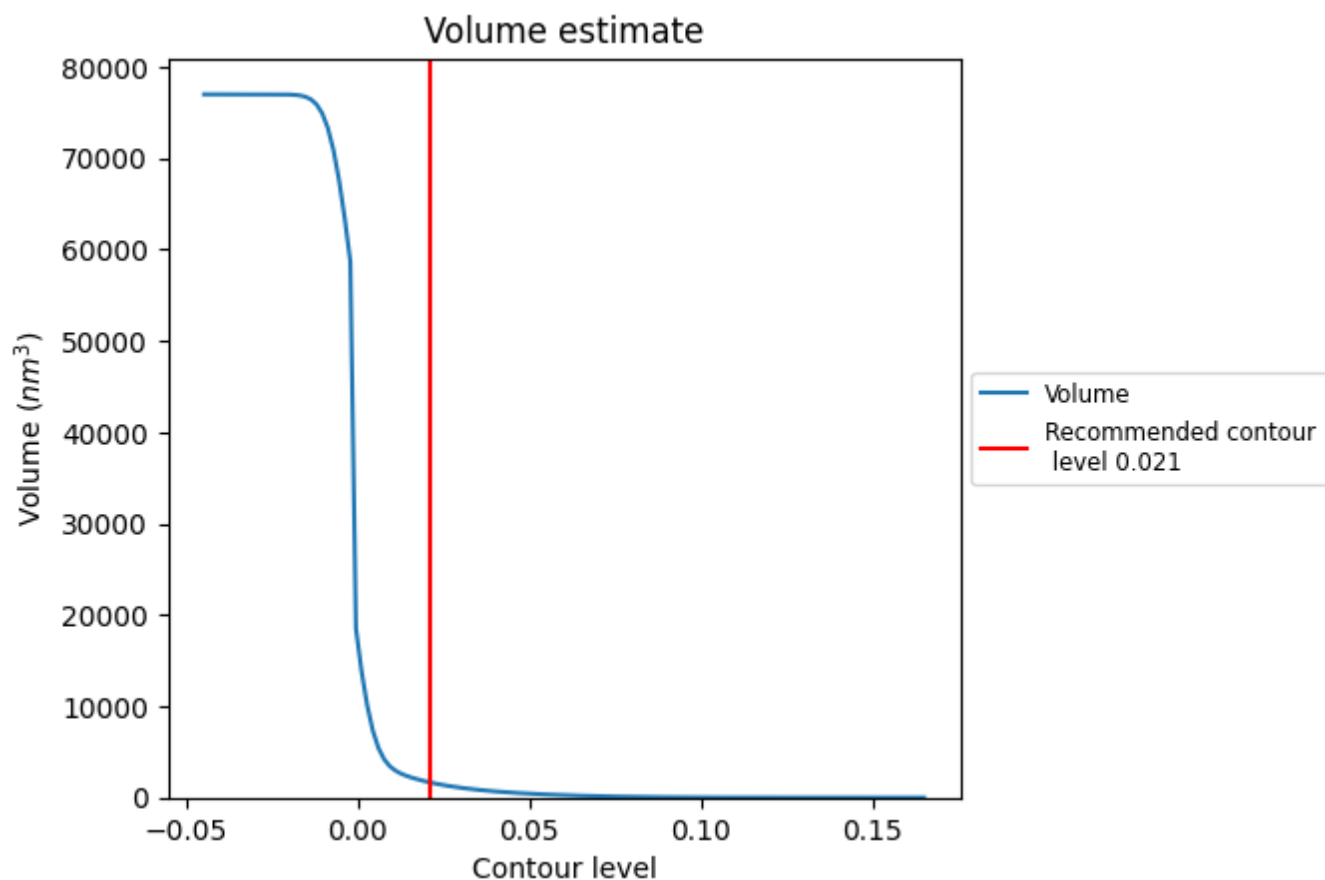
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

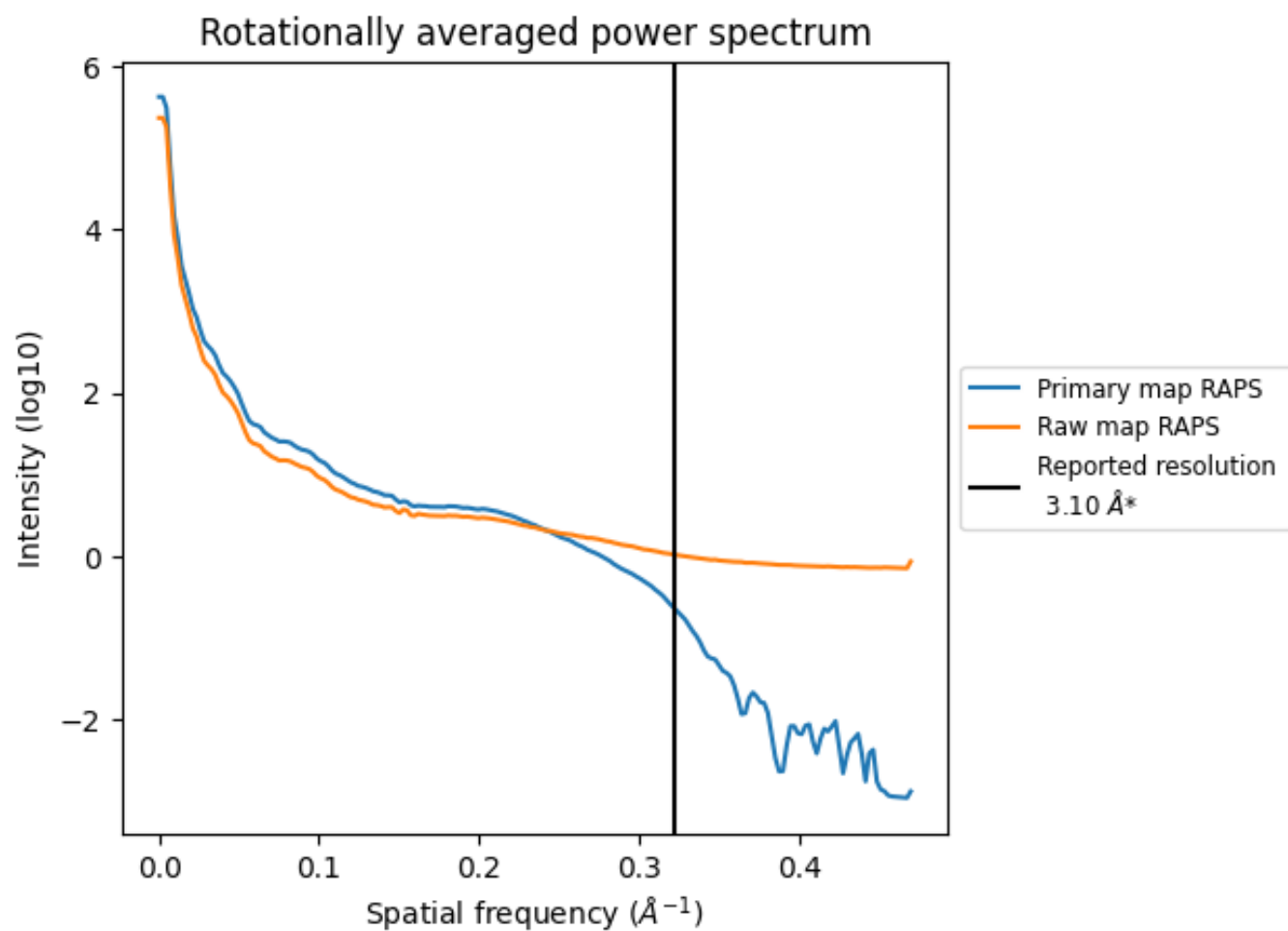
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1666 nm³; this corresponds to an approximate mass of 1505 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 ⓘ

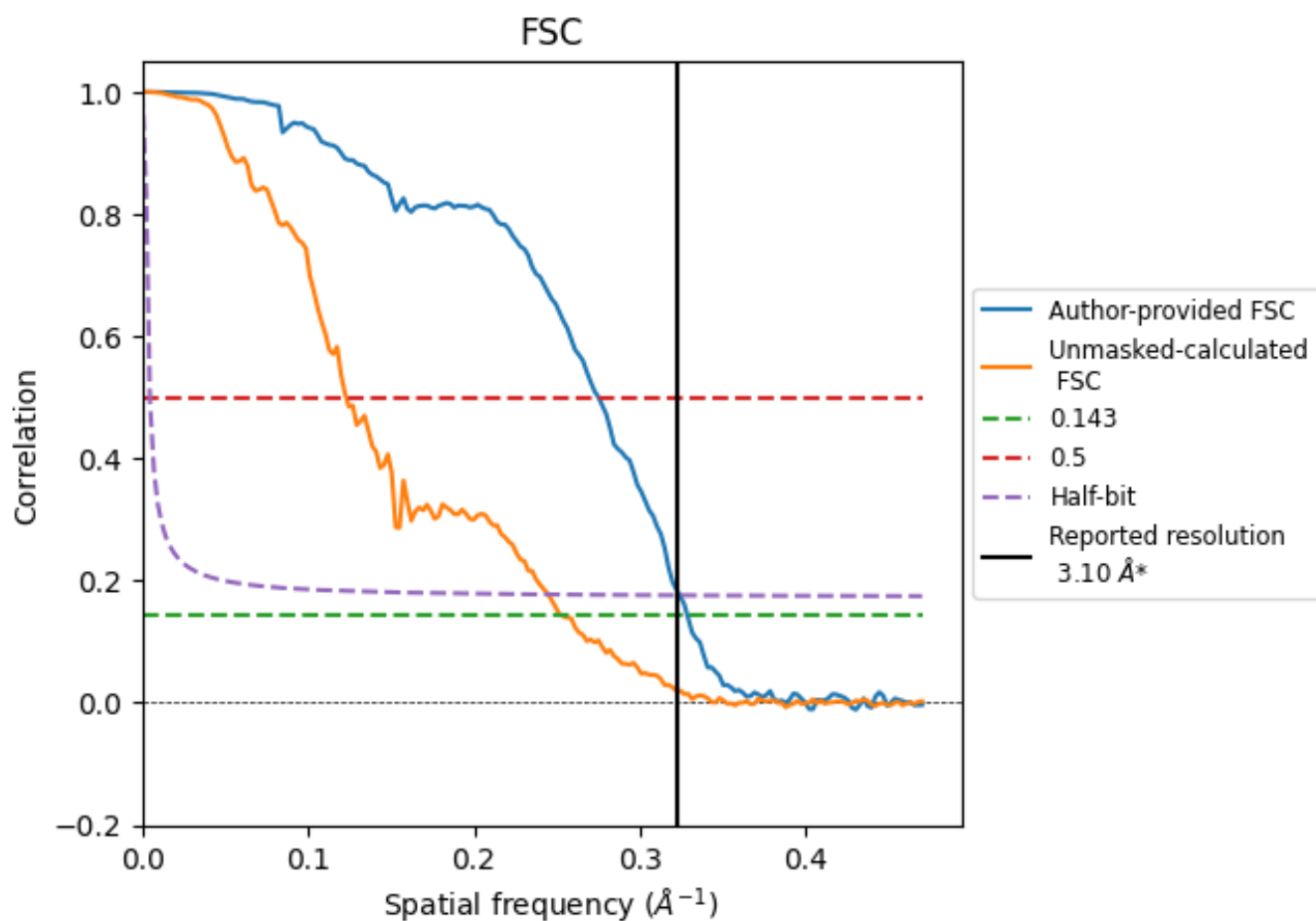


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.323 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

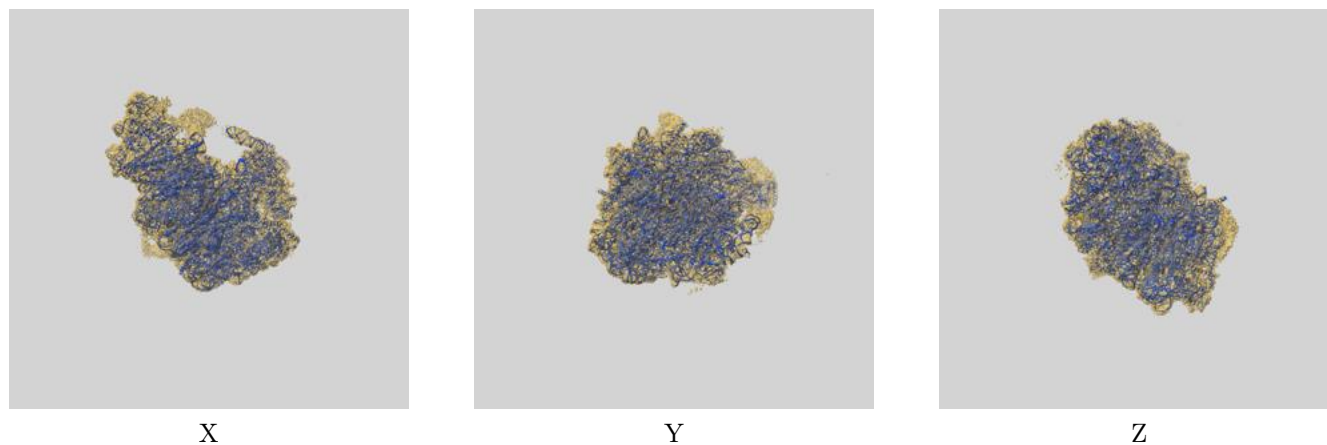
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.04	3.64	3.09
Unmasked-calculated*	3.96	8.13	4.08

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.96 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

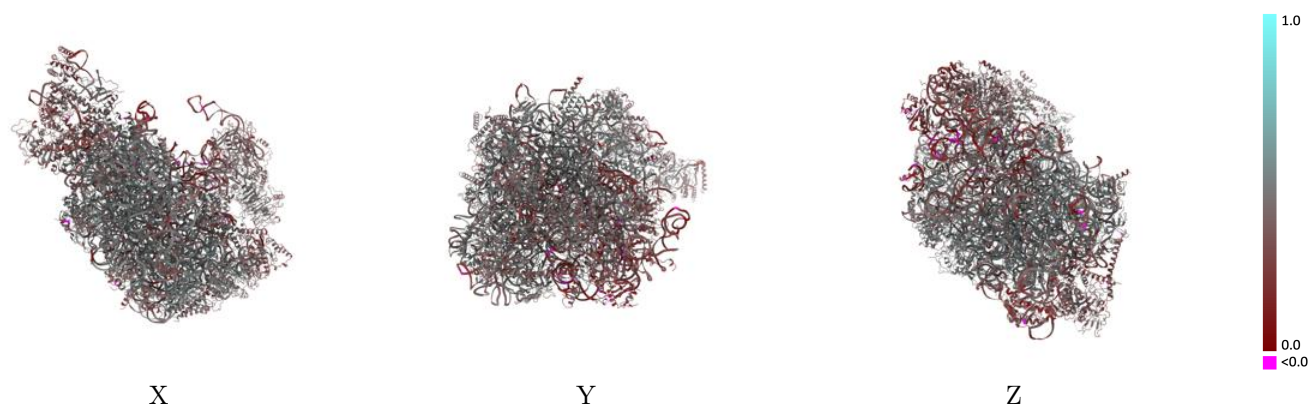
This section contains information regarding the fit between EMDB map EMD-12905 and PDB model 7OHQ. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.021 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](#)

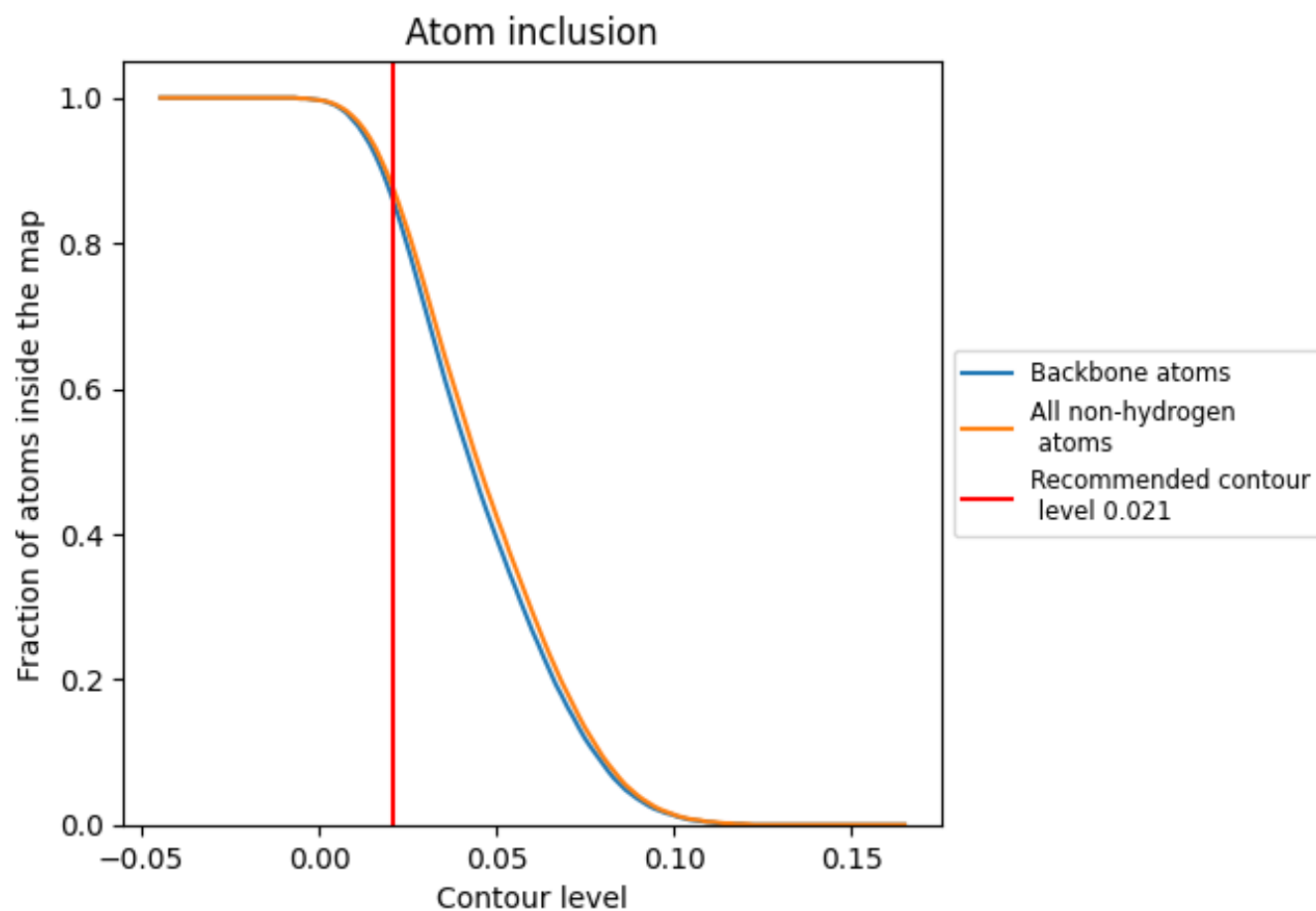


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion ⓘ



At the recommended contour level, 86% of all backbone atoms, 87% 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 (0.021) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8740	 0.4170
1	 0.9350	 0.4130
2	 0.9650	 0.4520
3	 0.8170	 0.2760
5	 0.4060	 0.3030
6	 0.9490	 0.3430
A	 0.8330	 0.4950
B	 0.9060	 0.4830
C	 0.9010	 0.4850
D	 0.5710	 0.3230
E	 0.9200	 0.4710
F	 0.8970	 0.4610
G	 0.8210	 0.4330
H	 0.8650	 0.4550
J	 0.8020	 0.2580
K	 0.8690	 0.3340
L	 0.8770	 0.4590
M	 0.9020	 0.4760
N	 0.8720	 0.4900
O	 0.9130	 0.4980
P	 0.8920	 0.4910
Q	 0.8920	 0.4770
R	 0.8630	 0.4700
S	 0.8710	 0.4460
T	 0.6870	 0.3660
U	 0.8840	 0.4050
V	 0.8920	 0.4860
W	 0.8530	 0.3920
X	 0.8780	 0.4840
Y	 0.9220	 0.4890
Z	 0.8890	 0.4450
a	 0.8780	 0.4650
b	 0.7950	 0.3960
c	 0.9060	 0.4650
d	 0.8660	 0.4800



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Chain	Atom inclusion	Q-score
e	 0.8850	 0.5040
f	 0.9240	 0.5200
g	 0.8560	 0.4790
h	 0.9070	 0.4650
i	 0.8230	 0.4390
j	 0.9260	 0.5020
k	 0.7750	 0.4200
l	 0.8770	 0.4790
m	 0.7340	 0.4130
n	 0.7430	 0.3810
o	 0.8580	 0.3770
p	 0.8580	 0.4650
q	 0.6570	 0.3280
r	 0.7600	 0.4280
s	 0.6480	 0.4110
t	 0.7300	 0.3400
u	 0.8420	 0.4370
v	 0.5730	 0.3560
w	 0.5790	 0.3370
x	 0.6480	 0.3860
y	 0.8930	 0.4510
z	 0.5940	 0.4060