



Full wwPDB EM Validation Report ⓘ

Jun 15, 2026 – 04:50 PM EDT

PDB ID : 9Y79 / pdb_00009y79
EMDB ID : EMD-72646
Title : Escherichia coli transcription-translation loosely coupled complex (TTC-LC[^]walked) containing mRNA with a 39 nt long spacer, NusG, NusA, and fMet-tRNAs in E-site and P-site
Authors : Shandilya, S.; Wang, C.; Molodtsov, V.; Ebright, R.H.
Deposited on : 2025-09-09
Resolution : 3.20 Å (reported)
Based on initial model : 8VOQ

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

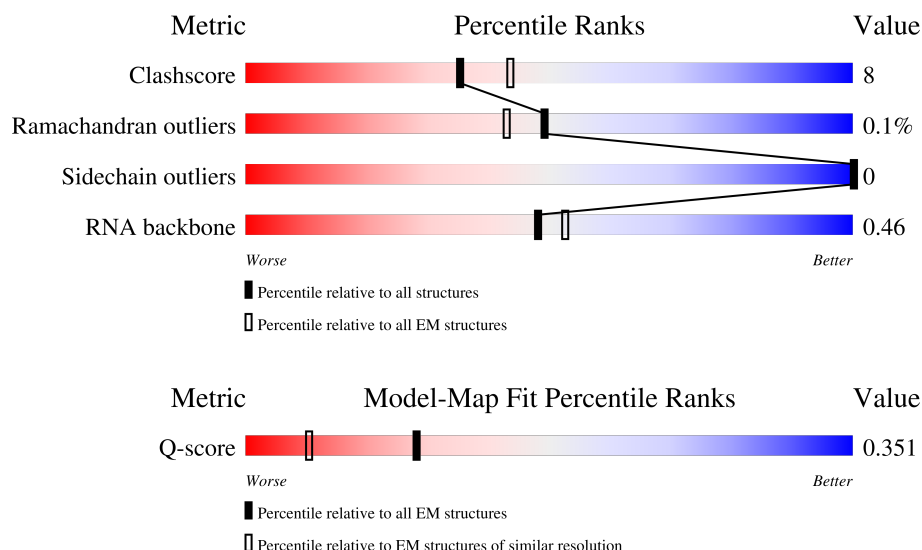
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 Å.

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



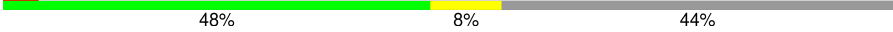
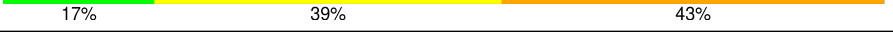
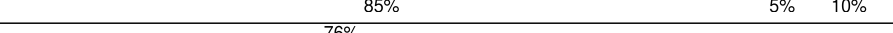
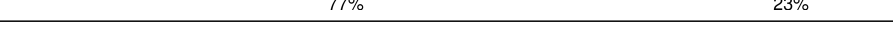
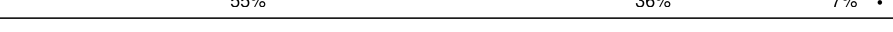
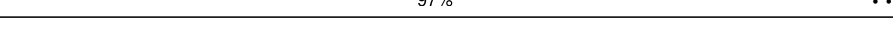
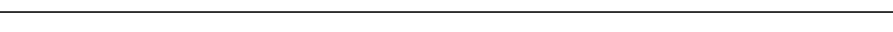
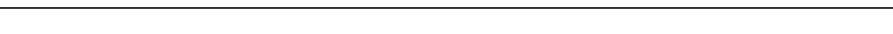
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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

Mol	Chain	Length	Quality of chain
1	0	103	 85% 15%
2	1	110	 95% 5%
3	2	100	 82% 12% 6%

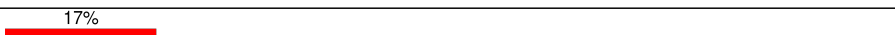
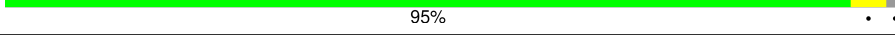
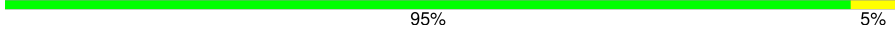
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Mol	Chain	Length	Quality of chain
4	3	104	
5	4	94	
6	5	50	
7	6	50	
8	7	56	
9	9	165	
10	A	76	
10	B	76	
11	AA	1342	
12	AC	329	
12	AD	329	
13	AE	1407	
14	AF	91	
15	AG	495	
16	C	75	
17	D	1542	
18	E	87	
19	F	71	
20	G	241	
21	H	557	
22	I	233	
23	J	206	
24	K	167	
25	L	135	
26	M	179	

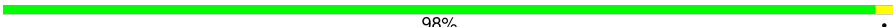
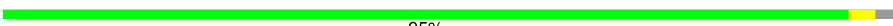
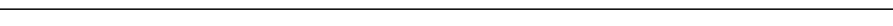
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Mol	Chain	Length	Quality of chain
27	N	130	
28	NG	181	
29	O	130	
30	P	103	
31	Q	129	
32	R	124	
33	S	101	
34	T	89	
35	U	82	
36	V	84	
37	W	92	
38	X	118	
39	Y	142	
40	Z	121	
41	a	2904	
42	b	85	
43	c	78	
44	d	120	
45	e	63	
46	f	59	
47	g	70	
48	h	273	
49	i	57	
50	j	209	
51	k	55	

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Mol	Chain	Length	Quality of chain
52	l	201	 90% 10%
53	m	46	 98% .
54	n	179	 84% 15% .
55	o	65	 95% . .
56	p	177	 85% 14% .
57	q	38	 89% 11%
58	r	149	 6% 77% 23%
59	s	142	 87% 13%
60	t	123	 85% 15%
61	u	144	 . 94% 6%
62	v	136	 93% 7%
63	w	127	 90% . 6%
64	x	117	 84% 15% .
65	y	115	 90% 9% .
66	z	118	 92% 7% .

2 Entry composition [i](#)

There are 68 unique types of molecules in this entry. The entry contains 313173 atoms, of which 131874 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Ribosomal protein L21.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	0	103	Total	C	H	N	O	S	0	0
			1655	516	839	153	145	2		

- Molecule 2 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	1	110	Total	C	H	N	O	S	0	0
			1779	532	922	166	156	3		

- Molecule 3 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	2	94	Total	C	H	N	O	S	0	0
			1557	470	811	140	134	2		

- Molecule 4 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	3	103	Total	C	H	N	O		0	0
			1633	498	845	148	142			

- Molecule 5 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	4	94	Total	C	H	N	O	S	0	0
			1533	479	780	137	134	3		

- Molecule 6 is a DNA chain called NT DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	5	23	Total	C	H	N	O	P	0	0
			734	225	260	84	142	23		

- Molecule 7 is a DNA chain called T DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	6	28	Total	C	H	N	O	P	0	0
			884	271	312	110	163	28		

- Molecule 8 is a RNA chain called mRNA with 39 nt long spacer.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	7	31	Total	C	H	N	O	P	0	0
			955	285	318	82	239	31		

- Molecule 9 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	9	148	Total	C	H	N	O	S	0	0
			2272	705	1155	196	209	7		

- Molecule 10 is a RNA chain called E-site and P-site tRNA (fMet).

Mol	Chain	Residues	Atoms						AltConf	Trace
10	A	76	Total	C	H	N	O	P	0	0
			2445	723	825	295	527	75		
10	B	76	Total	C	H	N	O	P	0	0
			2445	723	825	295	527	75		

- Molecule 11 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	AA	1340	Total	C	H	N	O	S	0	0
			21153	6631	10586	1841	2052	43		

- Molecule 12 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	AC	220	Total	C	H	N	O	S	0	0
			3406	1056	1716	298	330	6		
12	AD	298	Total	C	H	N	O	S	0	0
			3965	1284	1892	377	406	6		

- Molecule 13 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	AE	1335	Total	C	H	N	O	S	0	0
			21006	6526	10618	1854	1958	50		

- Molecule 14 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	AF	82	Total	C	H	N	O	S	0	0
			1309	396	659	122	131	1		

- Molecule 15 is a protein called Transcription termination/antitermination protein NusA.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	AG	495	Total	C	H	N	O	S	0	0
			7687	2396	3835	669	774	13		

- Molecule 16 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	C	66	Total	C	H	N	O	S	0	0
			1105	344	561	102	97	1		

- Molecule 17 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	D	1524	Total	C	H	N	O	P	0	0
			49154	14585	16451	6003	10591	1524		

- Molecule 18 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	E	86	Total	C	H	N	O	S	0	0
			1389	414	720	138	114	3		

- Molecule 19 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	F	70	Total	C	H	N	O	S	0	0
			1219	366	630	125	97	1		

- Molecule 20 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	G	225	Total	C	H	N	O	S	0	0
			3548	1113	1788	316	323	8		

- Molecule 21 is a protein called Small ribosomal subunit protein bS1.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	H	259	Total	C	H	N	O	S	0	0
			3187	1073	1457	305	349	3		

- Molecule 22 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	I	208	Total	C	H	N	O	S	0	0
			3347	1036	1711	307	290	3		

- Molecule 23 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	J	205	Total	C	H	N	O	S	0	0
			3351	1026	1708	315	298	4		

- Molecule 24 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	K	156	Total	C	H	N	O	S	0	0
			2349	717	1197	217	212	6		

- Molecule 25 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	L	104	Total	C	H	N	O	S	0	0
			1694	536	846	153	152	7		

- Molecule 26 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	M	151	Total	C	H	N	O	S	0	0
			2420	735	1239	227	215	4		

- Molecule 27 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	N	129	Total	C	H	N	O	S	0	0
			2011	616	1032	173	184	6		

- Molecule 28 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	NG	162	Total	C	H	N	O	S	0	0
			1752	824	459	223	239	7		

- Molecule 29 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	O	127	Total	C	H	N	O	S	0	0
			2093	634	1071	206	179	3		

- Molecule 30 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	P	99	Total	C	H	N	O	S	0	0
			1622	495	832	151	143	1		

- Molecule 31 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	Q	117	Total	C	H	N	O	S	0	0
			1765	540	888	174	160	3		

- Molecule 32 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	R	121	Total	C	H	N	O	S	0	0
			1941	580	1002	194	161	4		

- Molecule 33 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	S	100	Total	C	H	N	O	S	0	0
			1650	499	845	164	139	3		

- Molecule 34 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	T	88	Total	C	H	N	O	S	0	0
			1449	439	735	144	130	1		

- Molecule 35 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	U	82	Total	C	H	N	O	S	0	0
			1315	406	666	128	114	1		

- Molecule 36 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	V	80	Total	C	H	N	O	S	0	0
			1340	411	692	121	113	3		

- Molecule 37 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	W	83	Total	C	H	N	O	S	0	0
			1352	424	689	126	111	2		

- Molecule 38 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	X	116	Total	C	H	N	O	S	0	0
			1866	558	966	181	158	3		

- Molecule 39 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	Y	141	Total	C	H	N	O	S	0	0
			2118	651	1086	179	196	6		

- Molecule 40 is a protein called Large ribosomal subunit protein bL12.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	Z	30	Total	C	H	N	O	S	0	0
			462	144	235	33	47	3		

- Molecule 41 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	a	2880	Total	C	H	N	O	P	0	0
			92945	27587	31104	11398	19976	2880		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	887	A	U	conflict	GB 937521852

- Molecule 42 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	b	76	Total	C	H	N	O	S	0	0
			1182	360	600	117	104	1		

- Molecule 43 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	c	77	Total	C	H	N	O	S	0	0
			1278	388	653	129	106	2		

- Molecule 44 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	d	120	Total	C	H	N	O	P	0	0
			3869	1144	1300	468	837	120		

- Molecule 45 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	e	62	Total	C	H	N	O	S	0	0
			1033	308	532	98	94	1		

- Molecule 46 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	f	58	Total	C	H	N	O	S	0	0
			937	281	489	87	78	2		

- Molecule 47 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	g	66	Total	C	H	N	O	S	0	0
			1042	323	520	99	94	6		

- Molecule 48 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	h	271	Total	C	H	N	O	S	0	0
			4237	1288	2155	423	364	7		

- Molecule 49 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	i	56	Total	C	H	N	O	S	0	0
			903	269	459	94	80	1		

- Molecule 50 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	j	209	Total	C	H	N	O	S	0	0
			3181	979	1616	288	294	4		

- Molecule 51 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	k	52	Total	C	H	N	O		0	0
			891	275	465	78	73			

- Molecule 52 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	l	201	Total	C	H	N	O	S	0	0
			3171	974	1619	283	290	5		

- Molecule 53 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	m	46	Total	C	H	N	O	S	0	0
			795	228	418	90	57	2		

- Molecule 54 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	n	177	Total	C	H	N	O	S	0	0
			2855	899	1445	249	256	6		

- Molecule 55 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	o	64	Total	C	H	N	O	S	0	0
			1077	323	573	105	74	2		

- Molecule 56 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	p	175	Total	C	H	N	O	S	0	0
			2672	826	1359	241	244	2		

- Molecule 57 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	q	38	Total	C	H	N	O	S	0	0
			645	185	343	65	48	4		

- Molecule 58 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	r	149	Total	C	H	N	O	S	0	0
			2259	699	1148	197	214	1		

- Molecule 59 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	s	142	Total	C	H	N	O	S	0	0
			2291	714	1162	212	199	4		

- Molecule 60 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms						AltConf	Trace
60	t	123	Total	C	H	N	O	S	0	0
			1969	593	1023	181	166	6		

- Molecule 61 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms						AltConf	Trace
61	u	144	Total	C	H	N	O	S	0	0
			2182	654	1129	207	190	2		

- Molecule 62 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms						AltConf	Trace
62	v	136	Total	C	H	N	O	S	0	0
			2231	686	1157	205	177	6		

- Molecule 63 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms						AltConf	Trace
63	w	119	Total	C	H	N	O	S	0	0
			1945	588	994	195	163	5		

- Molecule 64 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms						AltConf	Trace
64	x	116	Total	C	H	N	O		0	0
			1816	552	924	178	162			

- Molecule 65 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms						AltConf	Trace
65	y	114	Total	C	H	N	O	S	0	0
			1880	574	963	179	163	1		

- Molecule 66 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms						AltConf	Trace
66	z	117	Total	C	H	N	O		0	0
			1967	604	1020	192	151			

- Molecule 67 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
67	AE	1	Total	Mg	0
			1	1	

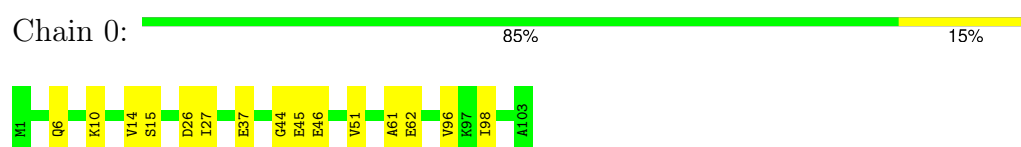
- Molecule 68 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
68	AE	2	Total	Zn	0
			2	2	

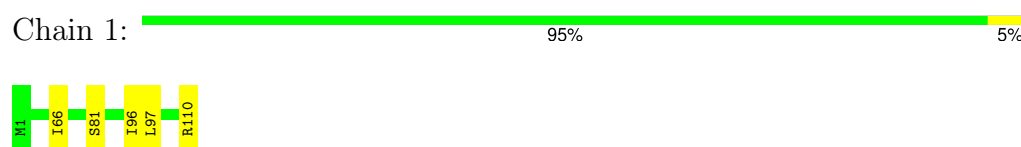
3 Residue-property plots [i](#)

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.

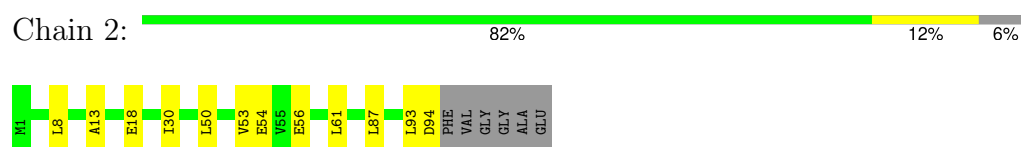
- Molecule 1: Ribosomal protein L21



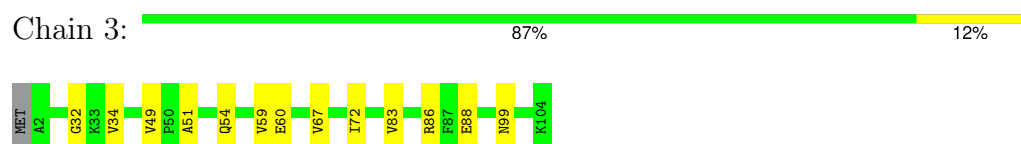
- Molecule 2: 50S ribosomal protein L22



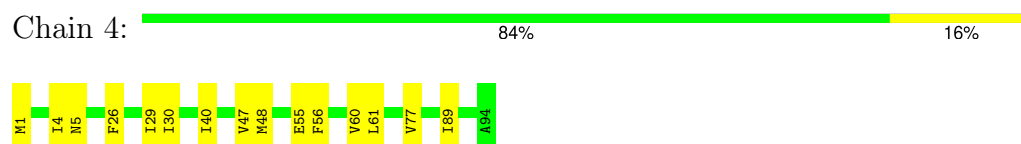
- Molecule 3: 50S ribosomal protein L23



- Molecule 4: 50S ribosomal protein L24

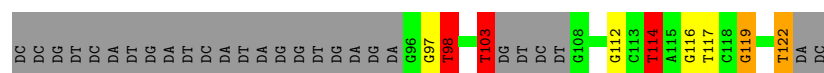


- Molecule 5: Large ribosomal subunit protein bL25

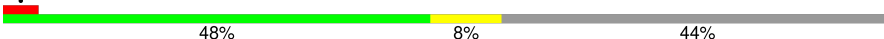


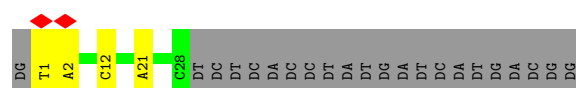
- Molecule 6: NT DNA

Chain 5: 

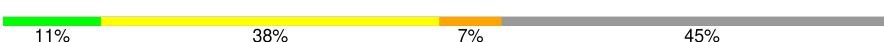


• Molecule 7: T DNA

Chain 6: 



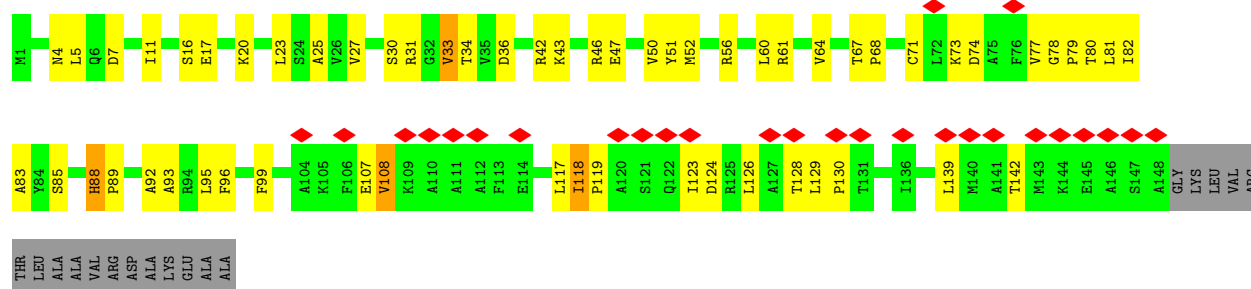
• Molecule 8: mRNA with 39 nt long spacer

Chain 7: 



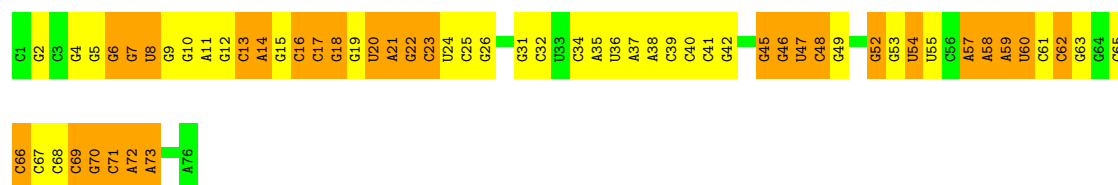
• Molecule 9: 50S ribosomal protein L10

Chain 9: 



• Molecule 10: E-site and P-site tRNA (fMet)

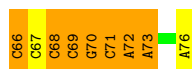
Chain A: 



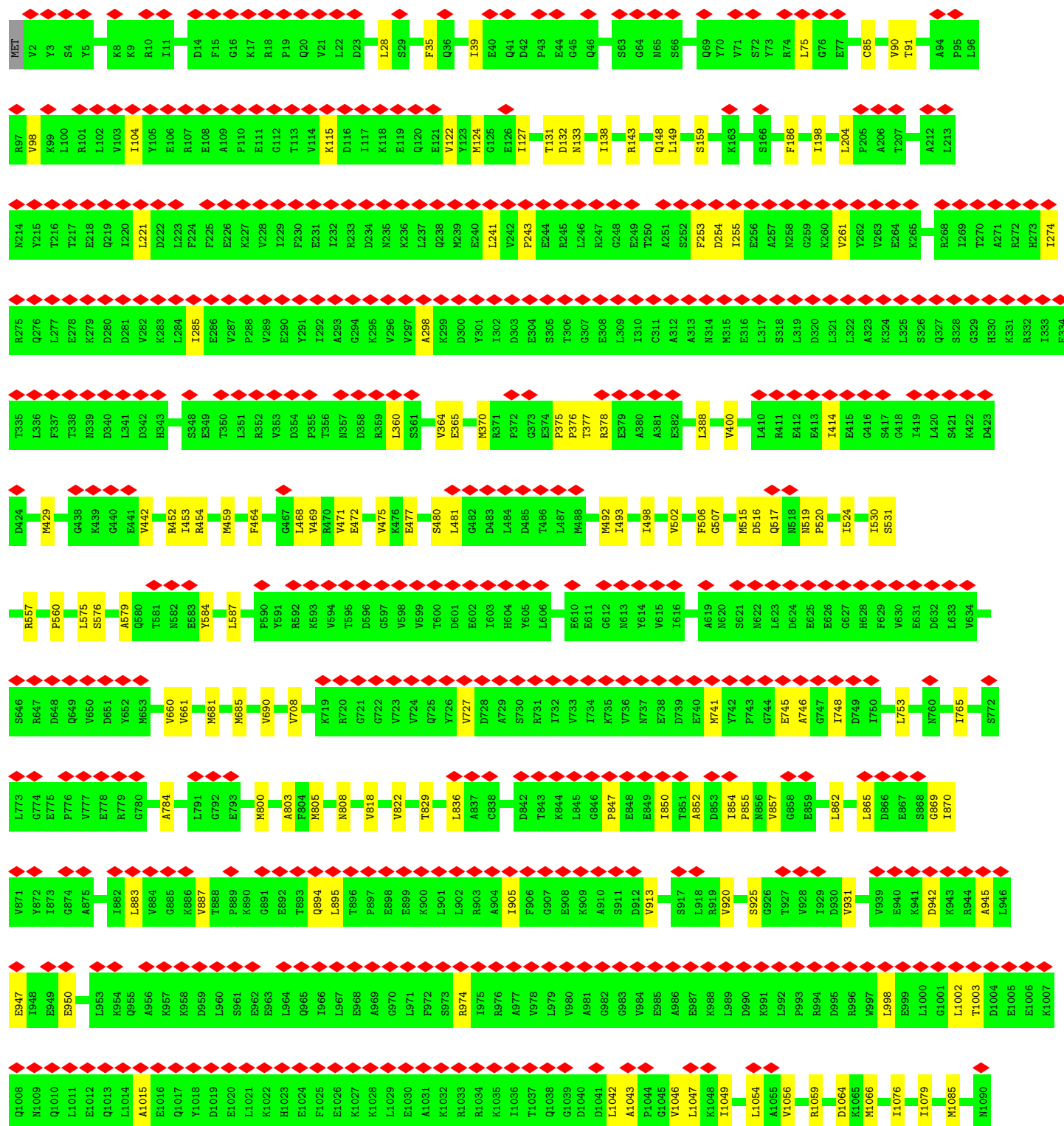
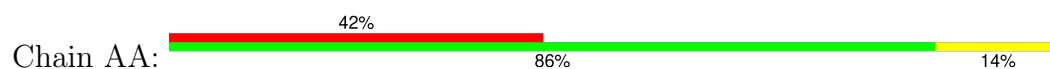
• Molecule 10: E-site and P-site tRNA (fMet)

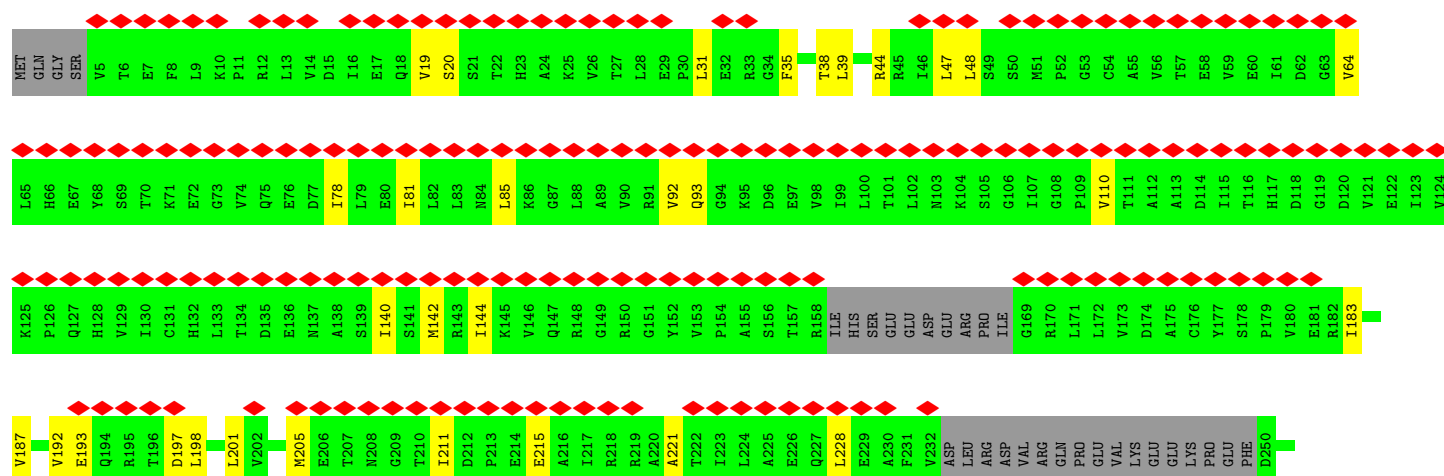
Chain B: 

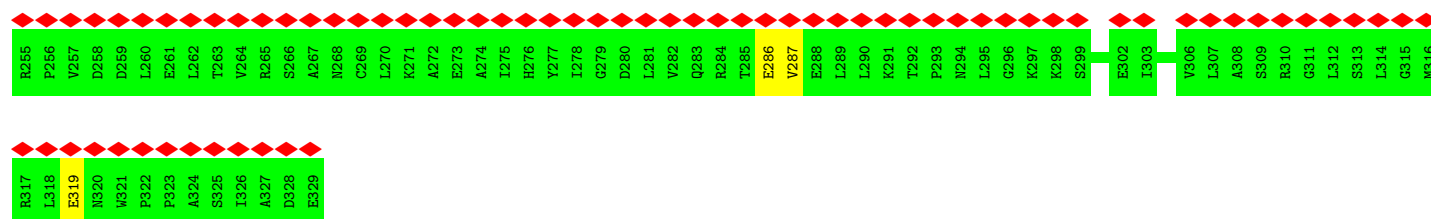




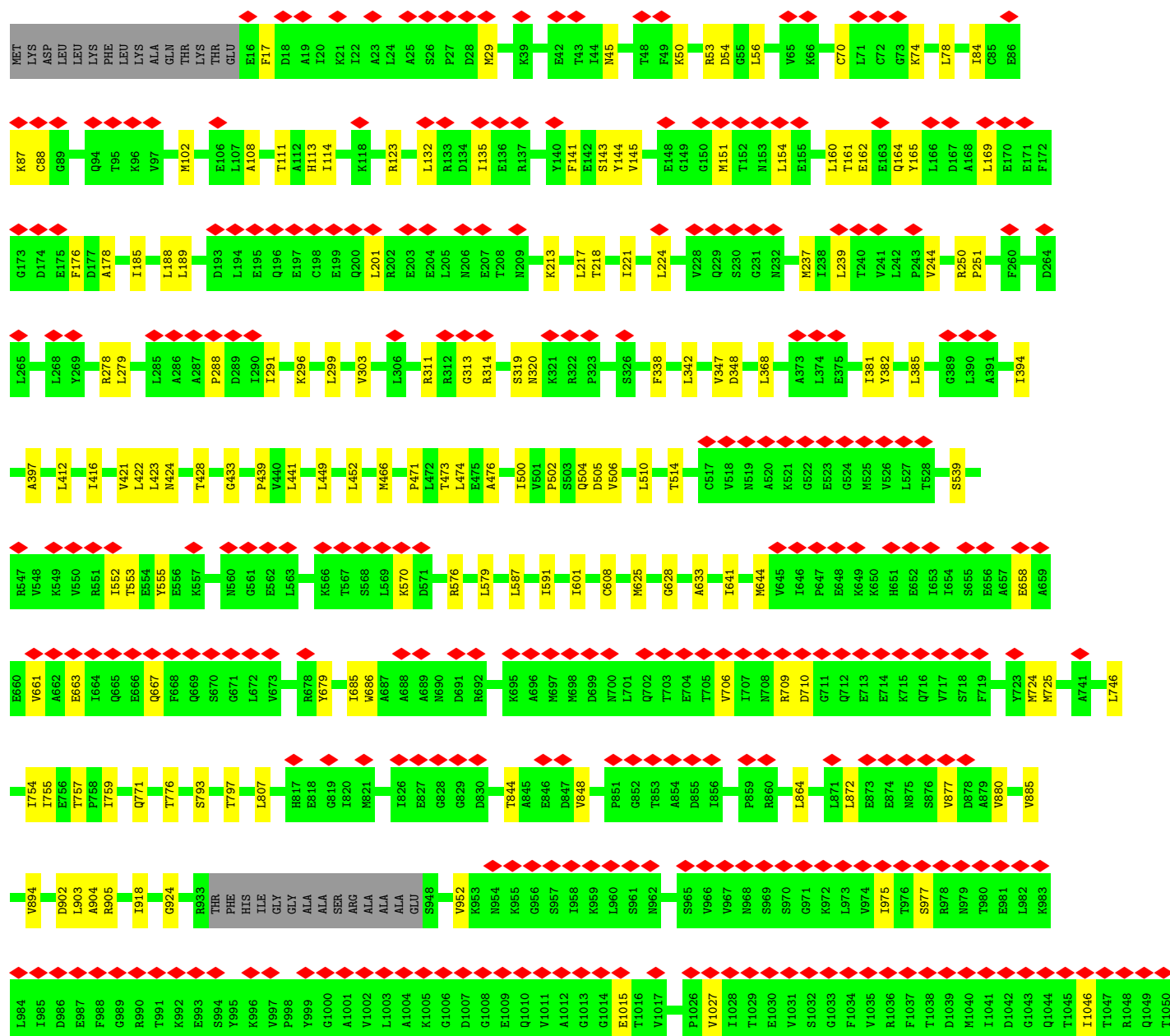
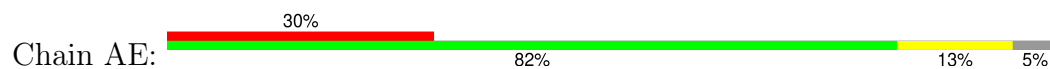
● Molecule 11: DNA-directed RNA polymerase subunit beta

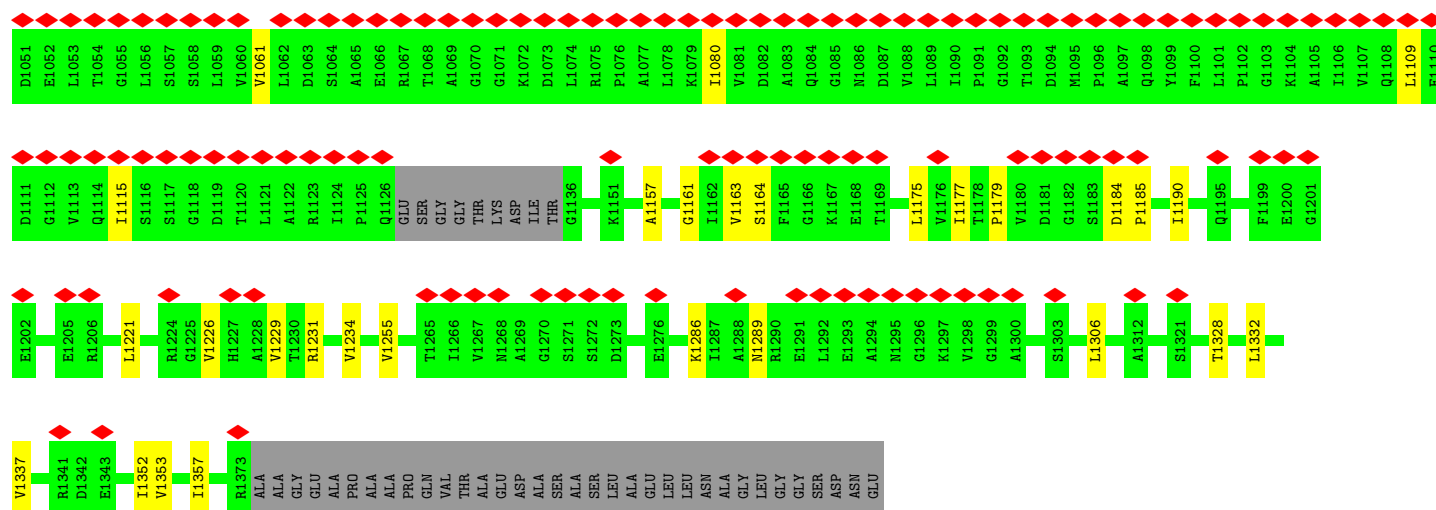




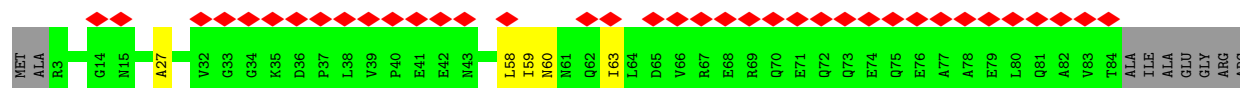
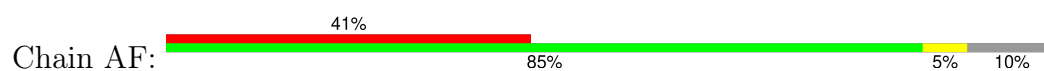


• Molecule 13: DNA-directed RNA polymerase subunit beta'

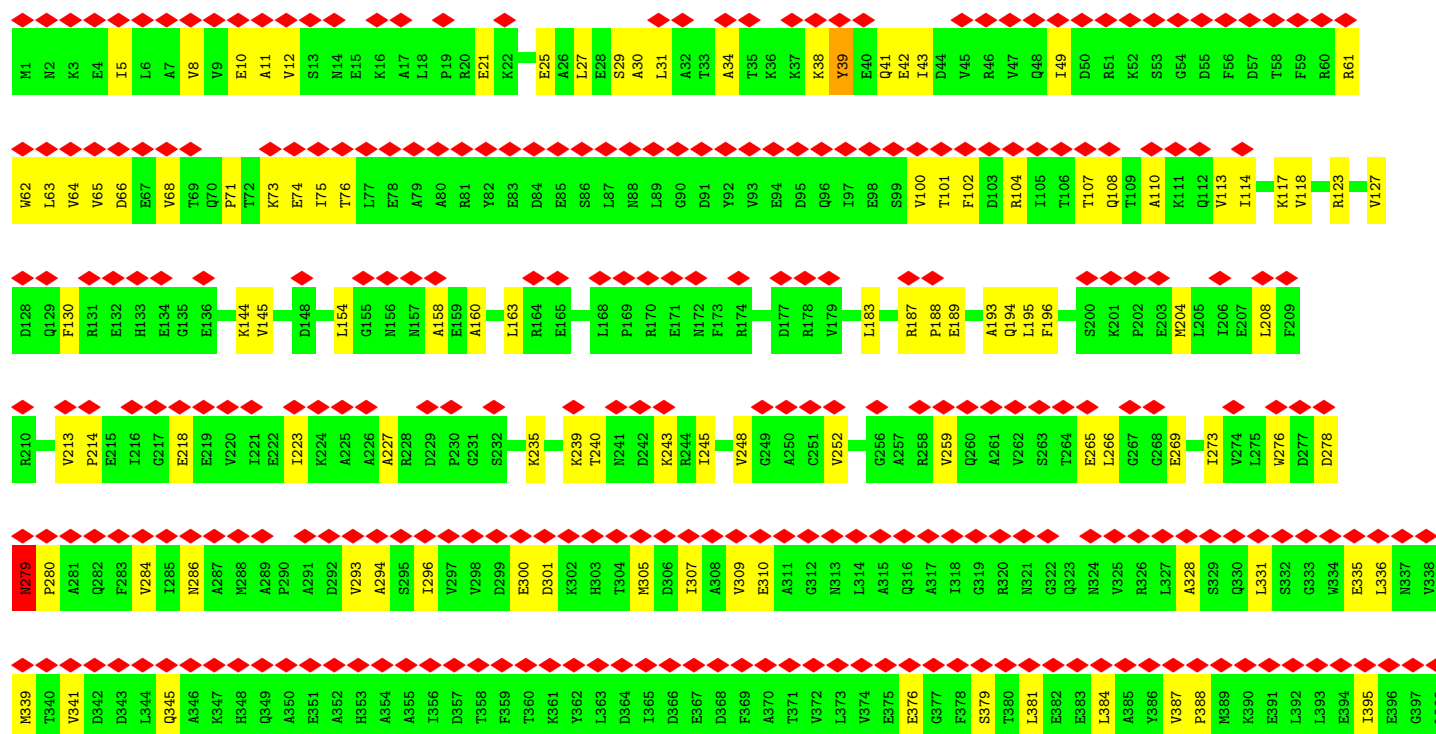
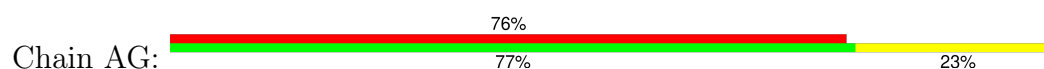




- Molecule 14: DNA-directed RNA polymerase subunit omega



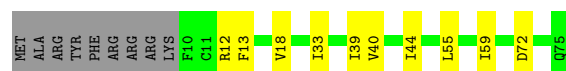
- Molecule 15: Transcription termination/antitermination protein NusA





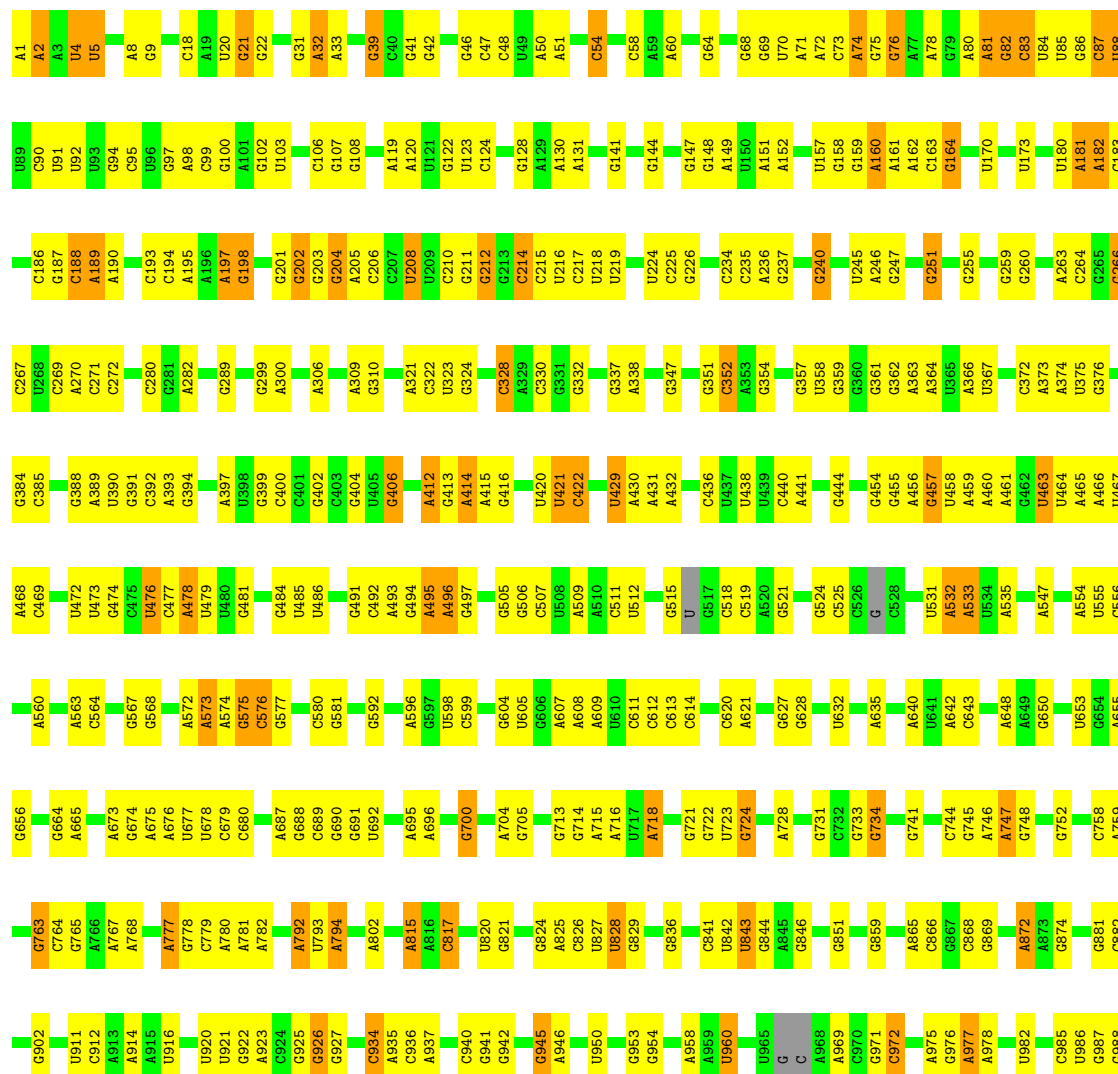
• Molecule 16: Small ribosomal subunit protein bS18

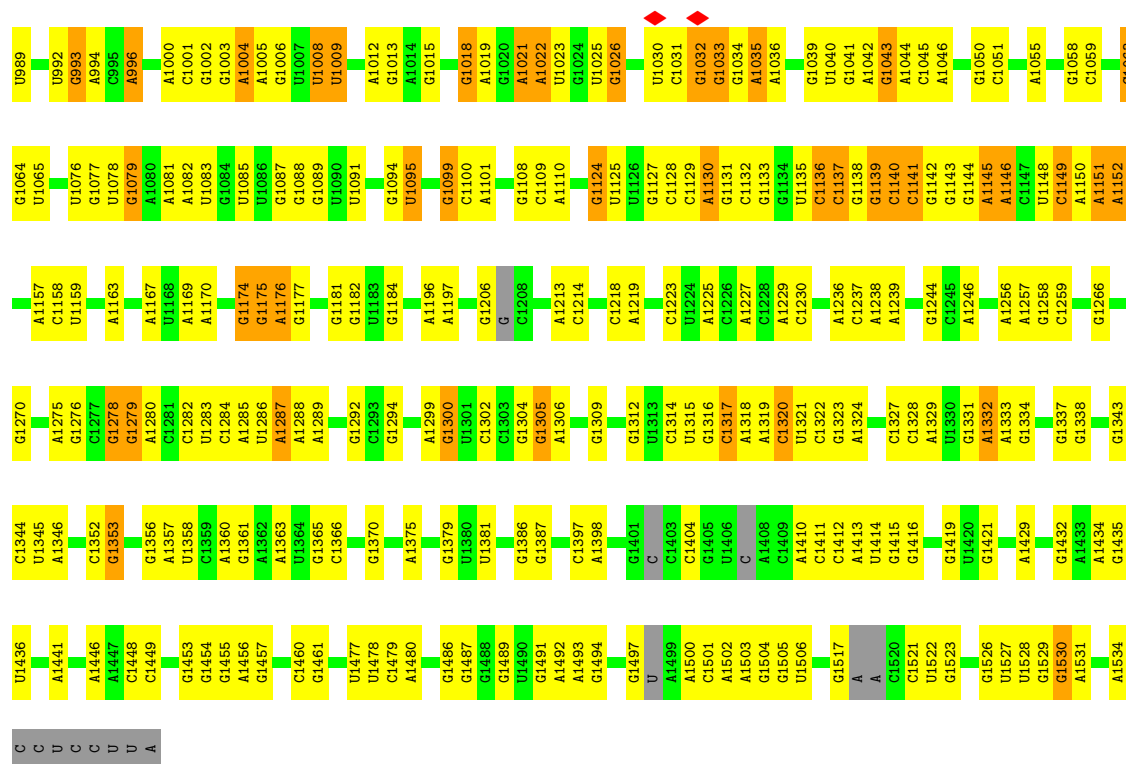
Chain C: 75% 13% 12%



• Molecule 17: 16S rRNA

Chain D: 55% 36% 7%





- Molecule 18: Small ribosomal subunit protein bS20

Chain E: 97%



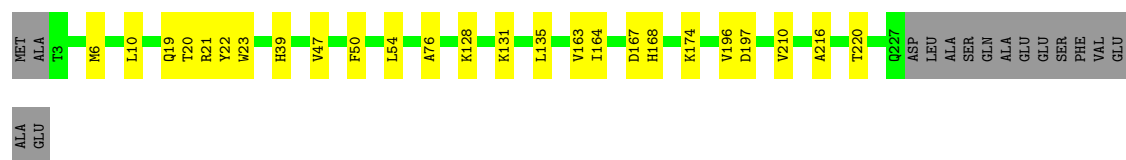
- Molecule 19: Small ribosomal subunit protein bS21

Chain F: 87%



- Molecule 20: 30S ribosomal protein S2

Chain G: 83%

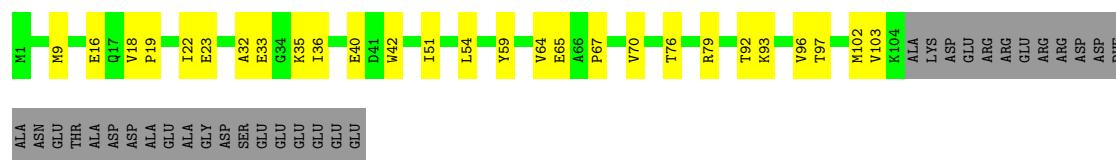


- Molecule 21: Small ribosomal subunit protein bS1

Chain H: 17%



Chain L:  57% 20% 23%



- Molecule 26: Small ribosomal subunit protein uS7

Chain M:  77% 7% 16%



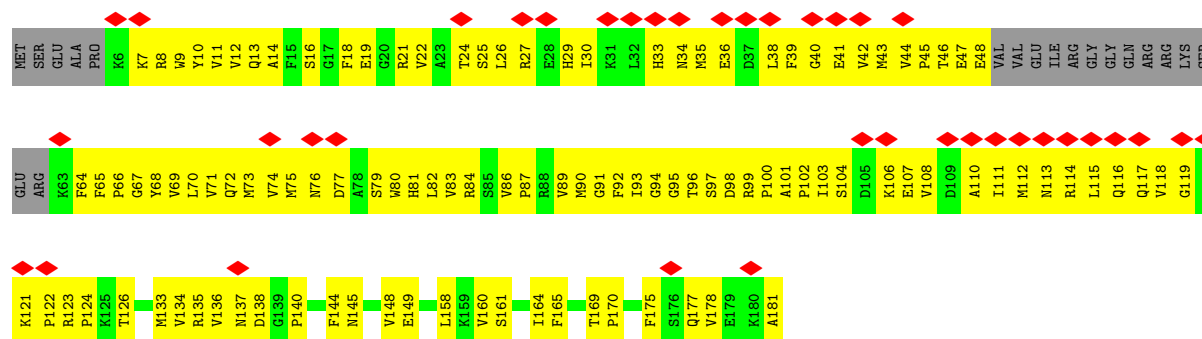
- Molecule 27: Small ribosomal subunit protein uS8

Chain N:  89% 10%



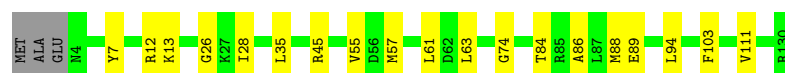
- Molecule 28: Transcription termination/antitermination protein NusG

Chain NG:  21% 28% 62% 10%



- Molecule 29: Small ribosomal subunit protein uS9

Chain O:  83% 15%



- Molecule 30: Small ribosomal subunit protein uS10

Chain P:  71% 24%



- Molecule 31: 30S ribosomal protein S11

Chain Q:  81% 10% 9%



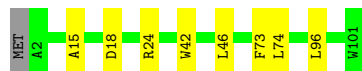
- Molecule 32: 30S ribosomal protein S12

Chain R:  92% 6%



- Molecule 33: Small ribosomal subunit protein uS14

Chain S:  91% 8%



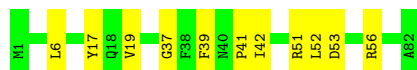
- Molecule 34: Small ribosomal subunit protein uS15

Chain T:  88% 11%



- Molecule 35: Small ribosomal subunit protein bS16

Chain U:  87% 13%



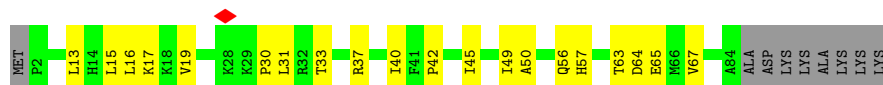
- Molecule 36: Small ribosomal subunit protein uS17

Chain V:  82% 13% 5%

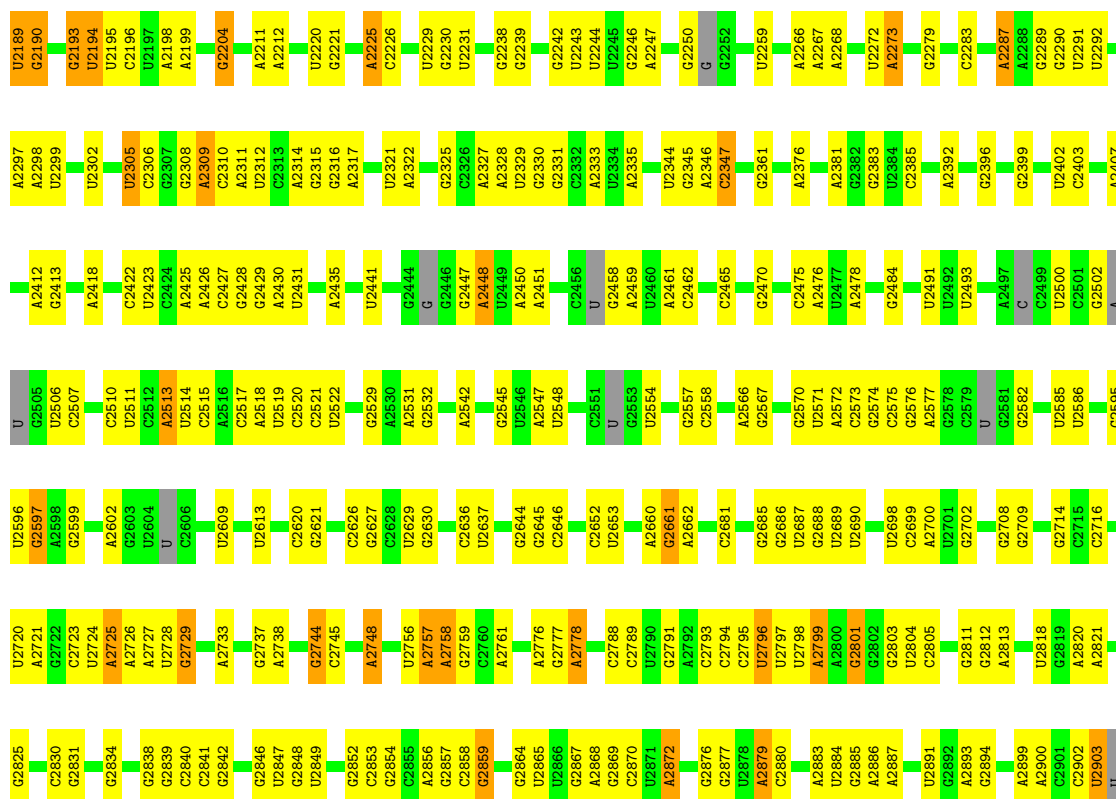


- Molecule 37: Small ribosomal subunit protein uS19

Chain W:  68% 22% 10%

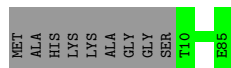


U2118	U2119	U2120	G2121	G2122	G2123	G2124	G2125	A2126	G2127	G2128	U2131	U2132	G2133	G2134	U2139	G2140	G2141	G2142	G2143	G2144	G2145	G2146	A2147	G2148	G2149	U2151	G2152	G2157	A2158	G2159	G2160	G2161	G2162	A2163	G2164	G2165	U2166	U2167	G2168	A2171	U2172	A2173	G2174	G2175	A2176	G2177	U2182	A2183	A2184	U2185	G2186	U2187	U2188
U2022	C2023	G2027	U2028	G2029	A	A2031	G2032	A2033	G2038	U2039	G2040	C2043	G2048	G2049	A2052	C2055	G2056	A2060	G2061	A2062	U2068	G	A2070	A2071	C2072	C2073	U	U2075	G2093	A2097	U2098	U2099	G2100	A2101	G2102	C2104	G2107	A2108	U2109	G2110	U2111	C2112	U2113	A2114	U2185	G2186	U2187	U2188					
G1831	C1832	C1833	U1834	G	G1836	C1837	G1840	U1841	G1842	G1843	G1844	G1845	G1846	A1847	G1848	G1849	A1853	A1854	U1855	U1856	G1857	A1858	U1859	G1869	C1870	A1871	A1872	A1876	A1877	U1880	C1881	G1884	A1885	U1886	C1887	G1888	A1889	G1896	G1897	U1898	A1899	G1904	C1905	G1906	G1907	U1908	G2018	A2019	A2020	C2021			
A1913	C1914	U	A1916	U	A1918	G1921	G1922	U1923	C1924	C1925	G1929	G1930	A1936	A1937	A1938	U	U1940	C1941	C1942	G1945	U1946	C1947	G1948	U1955	G1959	A1960	C1961	U1963	G1964	C1967	A1970	U1971	G1972	G1973	C1974	G1975	A1987	U1991	G1992	U1993	C1996	C1997	U1998	G2018	A2019	A2020	C2021						
U1714	G1715	U1720	A1721	A1722	U1729	C1730	G1731	G1732	G1733	G1734	A1735	U1736	U1737	G1738	G1739	G1740	U1751	C1752	G1756	A1757	U1758	C1760	G1764	U1765	G1766	A1773	C1774	U1784	A1789	C1790	U1791	G1792	G1795	U1796	C1800	A1801	A1802	A1803	A1808	C1905	G1906	G1907	U1908	G1910	U	A1912							
U1509	A1510	G1511	A1515	G1516	G1517	C1518	G1519	U1520	G1521	G1524	A1528	G1529	A1532	C1533	U1534	A1535	C1536	G1537	U1538	G1540	C1541	U1542	A1544	A1551	A1552	A1553	U1554	G1560	C1561	U1562	U1563	C1564	C1565	A1566	A1569	C1575	U1576	C1577	U1578	A1579	C1582	U1583	U1584	C1585	A1586	G1587	U1588						
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A1509	A1510	G1511	A1515	G1516	G1517	C1518	G1519	U1520	G1521	G1524	A1528	G1529	A1532	C1533	U1534	A1535	C1536	G1537	U1538	G1540	C1541	U1542	A1544	A1551	A1552	A1553	U1554	G1560	C1561	U1562	U1563	C1564	C1565	A1566	A1569	C1575	U1576	C1577	U1578	A1579	C1582	U1583	U1584	C1585	A1586	G1587	U1588						
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A1284	A1285	A1286	G1287	G1288	C1289	C1290	C1291	A1292	C1293	U1294	U1295	G1296	C1297	C1298	G1299	G1300	A1301	A1302	A1303	C1309	C1319	A1321	A1322	C1323	U1329	C1345	G1346	U1352	A1353	A1354	G1355	G1356	C1357	G1358	A1359	A1365	A1378	U1379	C1385	A1386	A1387	C1270	G1271	A1272	U1273	A1395	G1401						
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C817	G818	A819	A825	U826	U827	U828	A833	G834	U839	A845	U846	U847	C848	A849	U850	G856	G857	G858	G859	U860	G862	U868	U869	G870	U871	U872	G873	G874	G875	C876	A877	G878	G879	G880	G881	G882	U883	U884	C885	C886	A887	C888	C889	A890	G891	A892	C893	U894	A895	A896	C897		
A699	G707	G708	U709	U710	G711	U714	A715	U716	C717	A721	G728	G729	A730	G733	A734	G738	U744	G	U	U	G748	A752	U868	U869	U870	U871	U872	G873	G874	G875	C876	A877	G878	G879	G880	G881	G882	U883	U884	C885	C886	A887	C888	C889	A890	G891	A892	C893	U894	A895	A896	C897	



• Molecule 42: 50S ribosomal protein L27

Chain b: 89% 11%



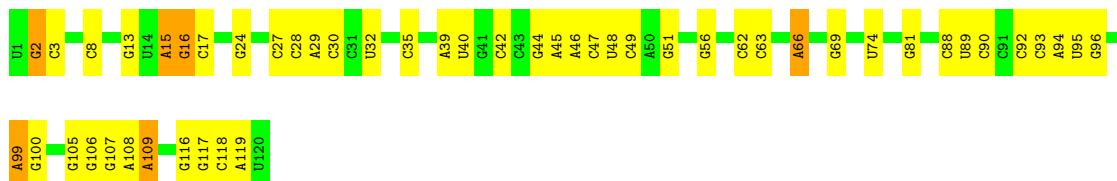
• Molecule 43: 50S ribosomal protein L28

Chain c: 88% 10%



• Molecule 44: 5S rRNA

Chain d: 58% 37% 5%



• Molecule 45: Large ribosomal subunit protein uL29

Chain e:  86% 13%



- Molecule 46: 50S ribosomal protein L30

Chain f:  80% 19%



- Molecule 47: 50S ribosomal protein L31

Chain g:  69% 26% 6%

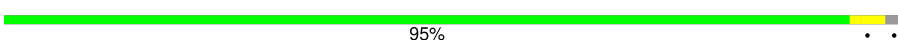


- Molecule 48: 50S ribosomal protein L2

Chain h:  89% 10%

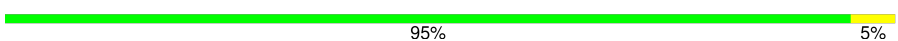


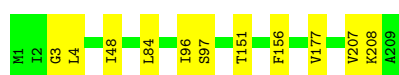
- Molecule 49: 50S ribosomal protein L32

Chain i:  95%



- Molecule 50: 50S ribosomal protein L3

Chain j:  95% 5%



- Molecule 51: 50S ribosomal protein L33

Chain k:  82% 13% 5%

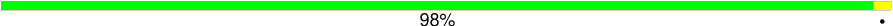


- Molecule 52: Large ribosomal subunit protein uL4

Chain l:  90% 10%



- Molecule 53: 50S ribosomal protein L34

Chain m:  98%



- Molecule 54: Large ribosomal subunit protein uL5

Chain n:  84% 15%



- Molecule 55: 50S ribosomal protein L35

Chain o:  95%



- Molecule 56: Large ribosomal subunit protein uL6

Chain p:  85% 14%



- Molecule 57: 50S ribosomal protein L36

Chain q:  89% 11%



- Molecule 58: Large ribosomal subunit protein bL9

Chain r:  6% 77% 23%





- Molecule 59: Large ribosomal subunit protein uL13

Chain s: 87% 13%



- Molecule 60: Large ribosomal subunit protein uL14

Chain t: 85% 15%



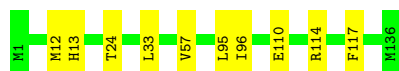
- Molecule 61: Large ribosomal subunit protein uL15

Chain u: 94% 6%



- Molecule 62: 50S ribosomal protein L16

Chain v: 93% 7%



- Molecule 63: Large ribosomal subunit protein bL17

Chain w: 90% 6%



- Molecule 64: Large ribosomal subunit protein uL18

Chain x: 84% 15%

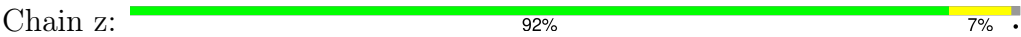


- Molecule 65: Large ribosomal subunit protein bL19

Chain y: 90% 9%



- Molecule 66: 50S ribosomal protein L20



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	31000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.076	Depositor
Minimum map value	-0.092	Depositor
Average map value	0.010	Depositor
Map value standard deviation	0.044	Depositor
Recommended contour level	0.15	Depositor
Map size ($\text{\AA}$)	666.624, 666.624, 666.624	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.302, 1.302, 1.302	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	0	0.30	0/829	0.37	0/1107
2	1	0.28	0/864	0.33	0/1156
3	2	0.27	0/752	0.32	0/1005
4	3	0.25	0/796	0.37	0/1062
5	4	0.24	0/766	0.33	0/1025
6	5	3.89	22/529 (4.2%)	3.65	39/813 (4.8%)
7	6	0.19	0/642	0.39	0/987
8	7	0.41	0/703	0.61	0/1086
9	9	0.20	0/1131	0.48	0/1524
10	A	0.19	0/1810	0.36	0/2821
10	B	0.22	0/1810	0.39	0/2821
11	AA	0.13	0/10736	0.31	0/14487
12	AC	0.12	0/1710	0.27	0/2317
12	AD	0.11	0/2091	0.29	0/2847
13	AE	0.12	0/10545	0.31	0/14236
14	AF	0.12	0/652	0.27	0/879
15	AG	0.15	0/3897	0.39	1/5273 (0.0%)
16	C	0.26	0/553	0.34	0/743
17	D	0.28	0/36610	0.29	0/57091
18	E	0.26	0/675	0.39	0/895
19	F	0.22	0/597	0.33	0/792
20	G	0.21	0/1791	0.35	0/2413
21	H	0.18	0/1746	0.47	0/2382
22	I	0.24	0/1663	0.34	0/2241
23	J	0.22	0/1665	0.30	0/2227
24	K	0.26	0/1165	0.35	0/1568
25	L	0.24	0/867	0.39	0/1171
26	M	0.20	0/1195	0.31	0/1602
27	N	0.26	0/989	0.31	0/1326
28	NG	0.24	0/1322	0.55	0/1782
29	O	0.22	0/1034	0.36	0/1375
30	P	0.25	0/800	0.42	0/1082

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	Q	0.25	0/893	0.31	0/1205
32	R	0.23	0/952	0.29	0/1274
33	S	0.22	0/817	0.31	0/1088
34	T	0.25	0/722	0.41	0/964
35	U	0.24	0/659	0.34	0/884
36	V	0.26	0/657	0.39	0/881
37	W	0.20	0/680	0.30	0/915
38	X	0.22	0/909	0.36	0/1215
39	Y	0.16	0/1046	0.39	0/1410
40	Z	0.17	0/227	0.47	0/304
41	a	0.32	0/69247	0.31	0/107985
42	b	0.28	0/589	0.32	0/779
43	c	0.30	0/635	0.33	0/848
44	d	0.28	0/2872	0.26	0/4478
45	e	0.26	0/502	0.32	0/667
46	f	0.31	0/452	0.39	0/605
47	g	0.20	0/531	0.39	0/709
48	h	0.29	0/2121	0.35	0/2852
49	i	0.28	0/450	0.30	0/599
50	j	0.29	0/1586	0.33	0/2134
51	k	0.27	0/433	0.29	0/576
52	l	0.26	0/1571	0.32	0/2113
53	m	0.29	0/380	0.33	0/498
54	n	0.22	0/1434	0.35	0/1926
55	o	0.28	0/513	0.32	0/676
56	p	0.22	0/1333	0.31	0/1805
57	q	0.26	0/303	0.33	0/397
58	r	0.18	0/1122	0.35	0/1515
59	s	0.31	0/1152	0.35	0/1551
60	t	0.28	0/955	0.35	0/1279
61	u	0.27	0/1062	0.35	0/1413
62	v	0.25	0/1093	0.32	0/1460
63	w	0.30	0/964	0.40	0/1289
64	x	0.25	0/902	0.32	0/1209
65	y	0.27	0/929	0.30	0/1242
66	z	0.33	0/960	0.36	0/1278
All	All	0.34	22/194588 (0.0%)	0.38	40/286159 (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
6	5	0	5
12	AD	0	1
21	H	0	1
28	NG	0	1
30	P	0	1
All	All	0	9

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	5	114	DT	C4-C5	-38.15	0.68	1.44
6	5	122	DT	C4-C5	-35.41	0.73	1.44
6	5	98	DT	N1-C2	-34.02	0.70	1.38
6	5	103	DT	N1-C2	-33.99	0.70	1.38
6	5	119	DG	C5-C4	-29.97	0.78	1.38
6	5	98	DT	C1'-N1	15.82	1.97	1.49
6	5	103	DT	C1'-N1	15.65	1.96	1.49
6	5	114	DT	C5-C6	14.31	1.62	1.34
6	5	122	DT	N3-C4	13.15	1.65	1.38
6	5	114	DT	N3-C4	12.75	1.64	1.38
6	5	114	DT	N1-C2	-11.35	1.15	1.38
6	5	103	DT	C2-N3	10.99	1.59	1.37
6	5	98	DT	C2-N3	10.91	1.59	1.37
6	5	119	DG	N9-C8	-10.81	1.16	1.37
6	5	122	DT	C5-C7	8.77	1.68	1.50
6	5	119	DG	N3-C4	8.39	1.52	1.35
6	5	119	DG	N7-C5	7.46	1.54	1.39
6	5	98	DT	C4-C5	-6.93	1.30	1.44
6	5	103	DT	C4-C5	-6.82	1.30	1.44
6	5	122	DT	N1-C2	-6.18	1.25	1.38
6	5	103	DT	N1-C6	5.30	1.49	1.38
6	5	98	DT	N1-C6	5.13	1.48	1.38

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	5	103	DT	C2-N1-C1'	-32.82	70.12	119.35
6	5	98	DT	C2-N1-C1'	-32.68	70.34	119.35
6	5	122	DT	C4-C5-C7	-32.52	73.62	122.40
6	5	119	DG	C4-C5-N7	-31.16	64.06	110.80
6	5	114	DT	C4-C5-C6	-28.40	76.60	119.20
6	5	114	DT	N3-C4-C5	-21.64	82.34	114.80
6	5	98	DT	N1-C2-N3	-17.93	87.90	114.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	5	114	DT	C5-C4-O4	-17.50	96.35	122.60
6	5	114	DT	C4-C5-C7	-17.32	96.43	122.40
6	5	122	DT	C5-C4-O4	-17.03	97.05	122.60
6	5	122	DT	N3-C4-C5	-16.98	89.33	114.80
6	5	103	DT	N1-C2-N3	-16.88	89.48	114.80
6	5	119	DG	N3-C4-C5	-16.39	103.81	128.40
6	5	103	DT	C6-N1-C1'	16.37	143.91	119.35
6	5	103	DT	N1-C2-O2	-16.32	98.73	123.20
6	5	98	DT	C6-N1-C1'	16.20	143.64	119.35
6	5	98	DT	N1-C2-O2	-15.58	99.83	123.20
6	5	114	DT	C6-C5-C7	14.73	146.09	124.00
6	5	103	DT	C6-N1-C2	-13.45	101.12	121.30
6	5	122	DT	C6-C5-C7	13.29	143.94	124.00
6	5	98	DT	C6-N1-C2	-13.05	101.73	121.30
6	5	119	DG	N7-C8-N9	-12.61	94.58	113.50
6	5	122	DT	C4-C5-C6	-11.15	102.47	119.20
6	5	119	DG	N9-C4-C5	-10.13	90.41	105.60
6	5	119	DG	C8-N9-C4	-9.30	92.05	106.00
6	5	114	DT	N1-C2-N3	-8.88	101.49	114.80
6	5	114	DT	N3-C4-O4	8.77	135.76	122.60
6	5	119	DG	C4-C5-C6	-8.51	106.33	119.10
6	5	114	DT	C6-N1-C2	-7.90	109.45	121.30
6	5	98	DT	C4-C5-C6	-7.10	108.55	119.20
6	5	103	DT	C4-C5-C6	-6.88	108.89	119.20
6	5	122	DT	N1-C2-N3	-6.22	105.47	114.80
6	5	119	DG	C6-C5-N7	6.15	139.33	130.10
6	5	122	DT	C6-N1-C2	-6.08	112.18	121.30
6	5	103	DT	N3-C4-C5	-5.89	105.97	114.80
6	5	98	DT	N3-C4-C5	-5.83	106.05	114.80
15	AG	279	ASN	CB-CA-C	5.68	121.37	110.17
6	5	122	DT	N3-C4-O4	5.59	130.98	122.60
6	5	119	DG	C6-N1-C2	-5.53	116.61	124.90
6	5	119	DG	N1-C2-N3	-5.41	115.89	124.00

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	5	103	DT	Sidechain
6	5	114	DT	Sidechain
6	5	119	DG	Sidechain
6	5	122	DT	Sidechain

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Mol	Chain	Res	Type	Group
6	5	98	DT	Sidechain
12	AD	319	GLU	Peptide
21	H	274	TYR	Peptide
28	NG	126	THR	Peptide
30	P	86	ALA	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	816	839	839	12	0
2	1	857	922	922	4	0
3	2	746	811	811	13	0
4	3	788	845	844	8	0
5	4	753	780	780	10	0
6	5	474	260	261	28	0
7	6	572	312	313	4	0
8	7	637	318	319	15	0
9	9	1117	1155	1155	65	0
10	A	1620	825	827	48	0
10	B	1620	825	827	58	0
11	AA	10567	10586	10585	168	0
12	AC	1690	1716	1714	14	0
12	AD	2073	1892	1889	26	0
13	AE	10388	10618	10610	137	0
14	AF	650	659	658	5	0
15	AG	3852	3835	3835	115	0
16	C	544	561	560	11	0
17	D	32703	16451	16460	380	0
18	E	669	720	719	1	0
19	F	589	630	629	8	0
20	G	1760	1788	1787	22	0
21	H	1730	1457	1455	60	0
22	I	1636	1711	1710	12	0
23	J	1643	1708	1707	9	0
24	K	1152	1197	1196	17	0
25	L	848	846	846	18	0
26	M	1181	1239	1238	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	N	979	1032	1031	9	0
28	NG	1293	459	1278	240	0
29	O	1022	1071	1070	15	0
30	P	790	832	831	27	0
31	Q	877	888	887	17	0
32	R	939	1002	1001	4	0
33	S	805	845	844	7	0
34	T	714	735	734	7	0
35	U	649	666	666	6	0
36	V	648	692	691	7	0
37	W	663	689	688	14	0
38	X	900	966	965	21	0
39	Y	1032	1086	1088	25	0
40	Z	227	235	237	7	0
41	a	61841	31104	31125	667	0
42	b	582	600	599	0	0
43	c	625	653	652	4	0
44	d	2569	1300	1301	31	0
45	e	501	532	531	7	0
46	f	448	489	488	8	0
47	g	522	520	520	23	0
48	h	2082	2155	2154	24	0
49	i	444	459	458	3	0
50	j	1565	1616	1616	8	0
51	k	426	465	464	4	0
52	l	1552	1619	1619	12	0
53	m	377	418	418	1	0
54	n	1410	1445	1444	18	0
55	o	504	573	572	1	0
56	p	1313	1359	1358	16	0
57	q	302	343	343	2	0
58	r	1111	1148	1148	26	0
59	s	1129	1162	1162	16	0
60	t	946	1023	1023	12	0
61	u	1053	1129	1129	7	0
62	v	1074	1157	1157	8	0
63	w	951	994	994	4	0
64	x	892	924	923	15	0
65	y	917	963	962	6	0
66	z	947	1020	1019	6	0
67	AE	1	0	0	0	0
68	AE	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	181299	131874	132686	2452	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 8.

All (2452) 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)
6:5:103:DT:C2	6:5:103:DT:C1'	1.84	1.59
6:5:98:DT:C2	6:5:98:DT:C1'	1.85	1.57
6:5:98:DT:C1'	6:5:98:DT:O2	1.68	1.36
6:5:103:DT:C1'	6:5:103:DT:O2	1.64	1.34
6:5:98:DT:C1'	6:5:98:DT:N3	1.91	1.31
6:5:103:DT:C1'	6:5:103:DT:N3	1.93	1.31
6:5:98:DT:C1'	6:5:98:DT:N1	1.96	1.24
6:5:103:DT:C1'	6:5:103:DT:N1	1.96	1.24
28:NG:30:ILE:HA	28:NG:82:LEU:HD21	1.19	1.17
28:NG:94:GLY:HA3	28:NG:101:ALA:HB2	1.25	1.17
6:5:98:DT:O2	6:5:98:DT:H1'	1.50	1.08
28:NG:42:VAL:HG23	28:NG:71:VAL:HG22	1.39	1.04
28:NG:70:LEU:HD13	28:NG:111:ILE:HD13	1.35	1.03
6:5:114:DT:N3	6:5:114:DT:C7	2.05	1.02
15:AG:27:LEU:HD22	15:AG:114:ILE:HG23	1.44	1.00
28:NG:19:GLU:HG3	28:NG:69:VAL:HG22	1.44	0.99
28:NG:108:VAL:HG12	28:NG:112:MET:HE1	0.99	0.99
24:K:96:MET:HE1	24:K:115:LEU:HD11	1.45	0.98
6:5:103:DT:C2	6:5:103:DT:H1'	1.98	0.98
28:NG:45:PRO:HA	28:NG:115:LEU:HD13	1.45	0.98
6:5:103:DT:C1'	6:5:103:DT:H3	1.68	0.97
6:5:98:DT:C1'	6:5:98:DT:H3	1.66	0.97
28:NG:73:MET:HE1	28:NG:83:VAL:HG21	1.47	0.97
28:NG:108:VAL:CG1	28:NG:112:MET:HE1	1.95	0.96
28:NG:13:GLN:HG3	28:NG:90:MET:HB3	1.47	0.96
6:5:103:DT:O2	6:5:103:DT:O4'	1.84	0.96
6:5:103:DT:N3	6:5:103:DT:H1'	1.79	0.95
28:NG:30:ILE:HA	28:NG:82:LEU:CD2	1.98	0.94
11:AA:375:PRO:HB2	28:NG:98:ASP:HB2	1.50	0.94
28:NG:108:VAL:HG12	28:NG:112:MET:CE	1.95	0.93
28:NG:26:LEU:HD22	28:NG:83:VAL:HG13	1.51	0.92
41:a:2139:U:O2	41:a:2152:G:O6	1.86	0.92
6:5:103:DT:H1'	6:5:103:DT:H3	1.34	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:NG:8:ARG:HH12	28:NG:102:PRO:HB2	1.33	0.91
28:NG:94:GLY:HA3	28:NG:101:ALA:CB	2.00	0.90
28:NG:14:ALA:HB1	28:NG:22:VAL:HG21	1.55	0.89
41:a:285:G:O6	41:a:355:U:O2	1.91	0.89
28:NG:26:LEU:HD13	28:NG:83:VAL:HA	1.53	0.88
21:H:321:VAL:HG13	21:H:322:VAL:HG23	1.55	0.88
28:NG:12:VAL:HA	28:NG:92:PHE:HA	1.56	0.88
28:NG:30:ILE:CA	28:NG:82:LEU:HD21	2.03	0.88
28:NG:13:GLN:HG2	28:NG:91:GLY:O	1.75	0.86
17:D:157:U:O2	17:D:164:G:O6	1.94	0.86
28:NG:84:ARG:HD3	28:NG:91:GLY:HA2	1.57	0.85
6:5:114:DT:N3	6:5:114:DT:H71	1.92	0.83
11:AA:1286:THR:HG22	11:AA:1290:MET:HE1	1.57	0.83
47:g:16:CYS:CB	47:g:37:CYS:HB3	2.09	0.83
11:AA:481:LEU:HD21	28:NG:21:ARG:HH21	1.44	0.83
28:NG:94:GLY:CA	28:NG:101:ALA:HB2	2.07	0.82
47:g:16:CYS:HB2	47:g:37:CYS:HB3	1.62	0.82
21:H:49:PRO:HD2	21:H:84:LEU:HD11	1.62	0.82
28:NG:75:MET:HE3	28:NG:100:PRO:HG3	1.63	0.80
28:NG:9:TRP:CZ3	28:NG:72:GLN:HB2	2.18	0.79
28:NG:83:VAL:HB	28:NG:92:PHE:HE2	1.47	0.78
13:AE:78:LEU:HD12	13:AE:78:LEU:O	1.83	0.78
19:F:3:VAL:HG22	31:Q:111:THR:HG23	1.66	0.78
28:NG:99:ARG:HH22	28:NG:102:PRO:HG3	1.49	0.77
41:a:2297:A:N1	41:a:2321:U:C4	2.52	0.77
15:AG:11:ALA:HB3	15:AG:12:VAL:HA	1.66	0.77
28:NG:96:THR:HG22	28:NG:99:ARG:HB3	1.65	0.77
28:NG:10:TYR:CD1	28:NG:100:PRO:HG2	2.19	0.77
41:a:2756:U:C4	41:a:2759:G:O6	2.38	0.77
11:AA:375:PRO:CB	28:NG:98:ASP:HB2	2.15	0.76
34:T:21:ASP:O	34:T:22:THR:HG22	1.85	0.76
41:a:1529:G:O6	41:a:1542:U:O2	2.03	0.76
28:NG:92:PHE:HB3	28:NG:100:PRO:HB3	1.66	0.76
28:NG:22:VAL:HG13	28:NG:89:VAL:HG22	1.67	0.76
21:H:60:LEU:HD21	21:H:62:ILE:O	1.85	0.76
28:NG:12:VAL:HB	28:NG:69:VAL:O	1.85	0.76
28:NG:103:ILE:HA	28:NG:107:GLU:OE2	1.85	0.75
28:NG:113:ASN:O	28:NG:116:GLN:HG3	1.86	0.75
6:5:98:DT:N3	6:5:98:DT:O4'	2.20	0.75
26:M:69:VAL:HG23	26:M:100:ALA:HB1	1.66	0.75
12:AD:85:LEU:HD11	12:AD:142:MET:HE1	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:NG:29:HIS:CE1	28:NG:86:VAL:HA	2.22	0.74
28:NG:38:LEU:HA	28:NG:74:VAL:HG12	1.68	0.74
15:AG:279:ASN:OD1	15:AG:280:PRO:HD2	1.87	0.74
28:NG:104:SER:O	28:NG:108:VAL:HG23	1.88	0.74
11:AA:375:PRO:HD2	28:NG:97:SER:HB2	1.70	0.74
28:NG:8:ARG:NH1	28:NG:102:PRO:HB2	2.03	0.73
15:AG:280:PRO:O	15:AG:284:VAL:HG23	1.89	0.73
28:NG:10:TYR:HB3	28:NG:100:PRO:HG2	1.71	0.73
28:NG:83:VAL:HB	28:NG:92:PHE:CE2	2.24	0.73
28:NG:11:VAL:HB	28:NG:101:ALA:HB3	1.71	0.73
47:g:18:CYS:CB	47:g:40:CYS:CB	2.67	0.72
6:5:98:DT:C2	6:5:98:DT:O4'	2.43	0.71
24:K:115:LEU:HD12	24:K:120:VAL:HG21	1.71	0.71
28:NG:96:THR:CG2	28:NG:99:ARG:HB3	2.19	0.71
31:Q:88:GLY:H	31:Q:114:THR:HG22	1.55	0.71
17:D:1006:G:O6	17:D:1023:U:O2	2.08	0.71
21:H:70:VAL:HG12	21:H:83:LEU:O	1.90	0.71
40:Z:2:ILE:HG22	40:Z:4:LYS:H	1.55	0.71
28:NG:136:VAL:HG22	28:NG:178:VAL:HG12	1.72	0.71
28:NG:46:THR:O	28:NG:119:GLY:HA2	1.90	0.71
6:5:103:DT:N3	6:5:103:DT:C2'	2.54	0.71
10:B:23:C:H2'	10:B:24:U:C6	2.26	0.71
17:D:1006:G:O6	17:D:1023:U:C2	2.44	0.71
28:NG:35:MET:CE	28:NG:38:LEU:HB2	2.21	0.70
11:AA:360:LEU:O	11:AA:364:VAL:HG23	1.91	0.70
9:9:77:VAL:HG12	9:9:82:ILE:HG21	1.71	0.70
28:NG:134:VAL:HG21	28:NG:160:VAL:HG21	1.72	0.70
21:H:74:ALA:HB3	21:H:83:LEU:CD2	2.21	0.70
13:AE:506:VAL:HG23	13:AE:628:GLY:HA3	1.72	0.70
15:AG:31:LEU:HD23	15:AG:110:ALA:HB1	1.74	0.70
28:NG:26:LEU:HD11	28:NG:83:VAL:HG22	1.73	0.70
8:7:47:G:P	11:AA:1259:LEU:HD21	2.32	0.69
28:NG:26:LEU:HA	28:NG:86:VAL:CG2	2.22	0.69
13:AE:368:LEU:HD12	13:AE:439:PRO:HB3	1.75	0.69
28:NG:7:LYS:HG2	28:NG:74:VAL:HB	1.73	0.69
60:t:113:MET:SD	60:t:116:ILE:HD11	2.33	0.69
11:AA:905:ILE:HD11	15:AG:5:ILE:HD13	1.75	0.69
17:D:412:A:H62	17:D:431:A:H61	1.41	0.69
6:5:98:DT:N3	6:5:98:DT:C2'	2.55	0.69
48:h:157:SER:O	48:h:195:VAL:HG11	1.93	0.68
15:AG:62:TRP:HB3	15:AG:75:ILE:HD11	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:x:58:ILE:HD11	64:x:73:ALA:HB1	1.74	0.68
21:H:333:LEU:HD12	21:H:345:GLY:HA3	1.74	0.68
22:I:142:MET:HE2	22:I:142:MET:HA	1.76	0.68
28:NG:26:LEU:HA	28:NG:86:VAL:HG22	1.74	0.68
28:NG:47:GLU:HA	28:NG:118:VAL:HG12	1.74	0.68
11:AA:1151:LEU:O	11:AA:1151:LEU:HD23	1.94	0.68
47:g:18:CYS:CB	47:g:40:CYS:HB3	2.24	0.68
9:9:16:SER:O	9:9:20:LYS:HG2	1.94	0.68
21:H:74:ALA:HB3	21:H:83:LEU:HD21	1.76	0.68
13:AE:797:THR:HG22	13:AE:924:GLY:HA3	1.74	0.68
13:AE:123:ARG:HG2	13:AE:1337:VAL:HG11	1.76	0.68
11:AA:159:SER:HB2	11:AA:442:VAL:HG11	1.75	0.67
12:AC:51:MET:HA	12:AC:51:MET:HE3	1.77	0.67
9:9:7:ASP:O	9:9:11:ILE:HD12	1.94	0.67
13:AE:288:PRO:CG	28:NG:110:ALA:HB2	2.25	0.67
9:9:142:THR:HG21	40:Z:7:ILE:HD13	1.76	0.67
28:NG:64:PHE:HB2	28:NG:65:PHE:HD1	1.57	0.67
31:Q:88:GLY:N	31:Q:114:THR:HG22	2.09	0.67
6:5:98:DT:H3	6:5:98:DT:C2'	2.07	0.67
17:D:151:A:N7	17:D:170:U:O2	2.28	0.67
28:NG:103:ILE:HG22	28:NG:108:VAL:HG23	1.76	0.67
11:AA:1287:LEU:HD13	13:AE:1357:ILE:HD11	1.77	0.67
17:D:180:U:O2	17:D:195:A:N7	2.27	0.67
21:H:308:GLU:HG2	21:H:309:MET:H	1.60	0.67
28:NG:45:PRO:CA	28:NG:115:LEU:HD13	2.24	0.67
11:AA:364:VAL:HG13	11:AA:376:PRO:CG	2.25	0.66
41:a:2756:U:C4	41:a:2759:G:C6	2.83	0.66
17:D:673:A:H2'	17:D:674:G:C8	2.30	0.66
28:NG:64:PHE:HZ	28:NG:114:ARG:HB3	1.61	0.66
58:r:6:LEU:HD11	58:r:37:VAL:HG23	1.77	0.66
1:0:44:GLY:O	1:0:45:GLU:HG3	1.96	0.66
6:5:103:DT:H3	6:5:103:DT:C2'	2.07	0.66
11:AA:1042:LEU:HD22	11:AA:1049:ILE:HD12	1.78	0.66
28:NG:19:GLU:HG3	28:NG:69:VAL:CG2	2.23	0.66
29:O:57:MET:HE2	29:O:61:LEU:HD11	1.76	0.66
28:NG:75:MET:HE3	28:NG:100:PRO:CG	2.26	0.66
28:NG:80:TRP:CZ2	28:NG:84:ARG:HG3	2.31	0.66
13:AE:759:ILE:HG23	13:AE:771:GLN:HB3	1.76	0.65
47:g:18:CYS:HB3	47:g:40:CYS:CB	2.26	0.65
29:O:84:THR:HG21	29:O:103:PHE:HB3	1.78	0.65
28:NG:99:ARG:NH2	28:NG:102:PRO:HG3	2.10	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:905:ILE:HD12	15:AG:8:VAL:HG11	1.78	0.65
28:NG:35:MET:HE2	28:NG:38:LEU:HB2	1.78	0.65
12:AC:231:PHE:CE2	12:AD:221:ALA:HB2	2.31	0.65
25:L:32:ALA:O	25:L:33:GLU:HG3	1.97	0.65
28:NG:99:ARG:O	28:NG:99:ARG:HD3	1.95	0.65
11:AA:375:PRO:HD2	28:NG:98:ASP:H	1.61	0.65
28:NG:22:VAL:HG13	28:NG:89:VAL:CG2	2.26	0.65
28:NG:43:MET:HE3	28:NG:111:ILE:HD13	1.79	0.65
11:AA:186:PHE:CG	11:AA:429:MET:HE1	2.31	0.65
28:NG:9:TRP:CH2	28:NG:72:GLN:HB2	2.32	0.65
13:AE:165:TYR:CE1	13:AE:178:ALA:HB3	2.32	0.64
9:9:95:LEU:HD12	9:9:99:PHE:CE2	2.32	0.64
13:AE:1328:THR:HG22	13:AE:1332:LEU:HD13	1.79	0.64
28:NG:29:HIS:CB	28:NG:82:LEU:HD11	2.27	0.64
11:AA:800:MET:HE1	11:AA:822:VAL:HG13	1.80	0.64
28:NG:103:ILE:HG22	28:NG:108:VAL:CG2	2.28	0.64
41:a:2756:U:O4	41:a:2759:G:C6	2.51	0.64
11:AA:887:VAL:CG2	11:AA:913:VAL:HG13	2.27	0.63
28:NG:73:MET:HE1	28:NG:92:PHE:HZ	1.63	0.63
59:s:84:ILE:HG23	59:s:84:ILE:O	1.98	0.63
28:NG:38:LEU:HD22	28:NG:76:ASN:OD1	1.98	0.63
11:AA:818:VAL:HG13	11:AA:822:VAL:HG21	1.79	0.63
47:g:36:VAL:O	47:g:36:VAL:HG13	1.98	0.63
47:g:16:CYS:CB	47:g:37:CYS:CB	2.77	0.63
4:3:34:VAL:HG13	4:3:67:VAL:HG22	1.81	0.63
28:NG:41:GLU:N	28:NG:72:GLN:HB3	2.14	0.63
28:NG:135:ARG:HG3	28:NG:181:ALA:HB2	1.81	0.63
28:NG:13:GLN:HB3	28:NG:93:ILE:CG1	2.29	0.62
21:H:273:ARG:HG2	21:H:280:LEU:HD21	1.79	0.62
28:NG:96:THR:H	28:NG:100:PRO:HA	1.63	0.62
15:AG:27:LEU:HD21	15:AG:118:VAL:HG23	1.81	0.62
28:NG:9:TRP:NE1	28:NG:108:VAL:HG11	2.14	0.62
48:h:17:VAL:HB	48:h:204:VAL:HG12	1.82	0.62
60:t:108:ARG:HB2	60:t:116:ILE:HD13	1.82	0.62
9:9:81:LEU:HD21	41:a:1107:G:O2'	2.00	0.62
11:AA:575:LEU:HD23	11:AA:576:SER:O	2.00	0.62
11:AA:515:MET:SD	11:AA:517:GLN:HB2	2.40	0.62
13:AE:165:TYR:HE1	13:AE:178:ALA:HB3	1.64	0.62
52:l:149:ILE:HD11	52:l:188:MET:HE2	1.81	0.62
4:3:32:GLY:O	4:3:67:VAL:HG23	1.99	0.62
41:a:284:U:O2	41:a:356:G:N2	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:s:31:GLU:HG2	59:s:142:ILE:HG23	1.81	0.62
28:NG:86:VAL:HB	28:NG:89:VAL:HG21	1.81	0.61
28:NG:92:PHE:HB3	28:NG:100:PRO:CB	2.30	0.61
9:9:43:LYS:HE2	9:9:95:LEU:HD13	1.80	0.61
28:NG:11:VAL:HG23	28:NG:103:ILE:HG12	1.82	0.61
11:AA:375:PRO:HG2	28:NG:98:ASP:H	1.63	0.61
11:AA:454:ARG:CG	11:AA:459:MET:HE3	2.31	0.61
11:AA:905:ILE:HD12	15:AG:8:VAL:HG21	1.80	0.61
13:AE:201:LEU:HD12	13:AE:224:LEU:HD12	1.82	0.61
28:NG:24:THR:HA	28:NG:27:ARG:NH1	2.15	0.61
11:AA:400:VAL:HG21	11:AA:452:ARG:HE	1.65	0.61
28:NG:11:VAL:HB	28:NG:93:ILE:O	2.02	0.60
23:J:101:VAL:HG12	23:J:105:MET:HE1	1.83	0.60
58:r:143:ILE:HG23	58:r:143:ILE:O	2.00	0.60
28:NG:22:VAL:CG1	28:NG:89:VAL:HG22	2.30	0.60
28:NG:94:GLY:HA3	28:NG:101:ALA:CA	2.30	0.60
28:NG:96:THR:O	28:NG:100:PRO:HA	2.01	0.60
66:z:83:LEU:HD22	66:z:113:ALA:HB2	1.83	0.60
10:B:15:G:H22	10:B:20:U:H3	1.48	0.60
36:V:46:VAL:HG21	36:V:61:ILE:HD13	1.82	0.60
21:H:270:ILE:HG23	21:H:270:ILE:O	2.01	0.60
23:J:4:TYR:C	23:J:5:LEU:HD12	2.27	0.60
41:a:548:G:H3'	41:a:549:G:O4'	2.01	0.60
41:a:2139:U:C2	41:a:2152:G:O6	2.55	0.60
15:AG:123:ARG:O	15:AG:127:VAL:HG23	2.02	0.60
41:a:2392:A:C2	61:u:55:MET:HE3	2.37	0.60
9:9:36:ASP:OD2	9:9:108:VAL:HG23	2.02	0.60
11:AA:241:LEU:HD22	11:AA:285:ILE:HD13	1.83	0.60
50:j:151:THR:HG23	50:j:151:THR:O	2.02	0.60
1:0:51:VAL:O	1:0:51:VAL:HG13	2.02	0.60
11:AA:1079:ILE:HG23	11:AA:1079:ILE:O	2.01	0.60
31:Q:112:ASP:OD1	31:Q:114:THR:HG23	2.01	0.60
11:AA:1223:ARG:HH12	13:AE:724:MET:HE1	1.66	0.59
17:D:664:G:H22	17:D:741:G:H1	1.50	0.59
41:a:2298:A:C4	41:a:2321:U:C5	2.89	0.59
11:AA:149:LEU:HB2	11:AA:530:ILE:HG22	1.83	0.59
17:D:675:A:H1'	31:Q:118:HIS:HD2	1.67	0.59
17:D:842:U:H3'	17:D:843:U:C5'	2.32	0.59
41:a:2796:U:H3	41:a:2799:A:H61	1.49	0.59
11:AA:198:ILE:HG21	11:AA:370:MET:HE1	1.84	0.59
15:AG:208:LEU:HD22	15:AG:265:GLU:OE2	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:H:297:GLU:O	21:H:300:VAL:HG13	2.02	0.59
22:I:130:PHE:HD2	22:I:134:MET:HE2	1.67	0.59
52:I:131:THR:HG22	52:I:160:ALA:O	2.02	0.59
8:7:12:U:H4'	24:K:56:VAL:HG11	1.82	0.59
10:B:22:G:H2'	10:B:23:C:C6	2.38	0.59
9:9:56:ARG:NH2	41:a:1084:A:C4	2.70	0.59
64:x:53:THR:HG23	64:x:74:VAL:HG21	1.84	0.59
11:AA:454:ARG:CD	11:AA:459:MET:HE3	2.32	0.59
41:a:2447:G:H2'	41:a:2500:U:OP2	2.01	0.59
11:AA:1101:LEU:HD12	13:AE:505:ASP:OD1	2.02	0.59
28:NG:25:SER:HB2	28:NG:86:VAL:HG13	1.85	0.59
1:0:61:ALA:HB1	1:0:96:VAL:HG22	1.85	0.58
11:AA:1286:THR:HG22	11:AA:1290:MET:CE	2.30	0.58
17:D:362:G:H5''	32:R:58:THR:HG21	1.85	0.58
38:X:52:GLN:O	38:X:56:LEU:HD23	2.02	0.58
64:x:70:ALA:O	64:x:74:VAL:HG23	2.02	0.58
9:9:129:LEU:HD12	9:9:129:LEU:O	2.03	0.58
28:NG:9:TRP:CD1	28:NG:108:VAL:HG21	2.38	0.58
41:a:2187:U:H2'	41:a:2188:U:O4'	2.02	0.58
54:n:34:ILE:HD12	54:n:96:MET:HG2	1.83	0.58
64:x:26:LEU:HD12	64:x:38:GLN:O	2.04	0.58
9:9:52:MET:HE1	9:9:85:SER:C	2.29	0.58
13:AE:506:VAL:HG21	13:AE:625:MET:HA	1.85	0.58
15:AG:376:GLU:OE1	15:AG:395:ILE:HG23	2.04	0.58
28:NG:29:HIS:C	28:NG:82:LEU:HD11	2.28	0.58
41:a:1844:C:C2	41:a:1897:G:N2	2.72	0.58
9:9:81:LEU:HD21	41:a:1107:G:H4'	1.85	0.58
11:AA:375:PRO:CG	28:NG:98:ASP:H	2.16	0.58
11:AA:870:ILE:HG21	11:AA:931:VAL:HG11	1.85	0.58
11:AA:39:ILE:HG23	11:AA:39:ILE:O	2.04	0.58
25:L:19:PRO:O	25:L:23:GLU:OE1	2.22	0.58
28:NG:95:GLY:H	28:NG:101:ALA:HA	1.68	0.58
28:NG:107:GLU:O	28:NG:111:ILE:HG13	2.02	0.58
39:Y:20:SER:HB3	39:Y:21:PRO:HD3	1.85	0.58
11:AA:375:PRO:CD	28:NG:98:ASP:H	2.16	0.58
15:AG:107:THR:HA	15:AG:110:ALA:HB3	1.84	0.58
28:NG:73:MET:CE	28:NG:83:VAL:HG21	2.28	0.58
12:AD:48:LEU:HB2	12:AD:183:ILE:HD11	1.86	0.58
15:AG:62:TRP:CB	15:AG:75:ILE:HD11	2.34	0.58
17:D:203:G:N2	17:D:205:A:H61	2.01	0.58
13:AE:1163:VAL:HG22	13:AE:1175:LEU:HD11	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:M:15:ASP:OD2	26:M:23:LEU:HD23	2.03	0.57
41:a:2204:G:O6	41:a:2220:U:O2	2.21	0.57
11:AA:727:VAL:O	12:AC:134:THR:HG21	2.03	0.57
45:e:18:LEU:HD11	45:e:54:LYS:HE3	1.86	0.57
10:A:68:C:H2'	10:A:69:C:O4'	2.05	0.57
11:AA:364:VAL:HG13	11:AA:376:PRO:HG3	1.85	0.57
13:AE:84:ILE:O	13:AE:84:ILE:HG13	2.02	0.57
15:AG:204:MET:HE1	15:AG:208:LEU:HD11	1.84	0.57
28:NG:29:HIS:HE1	28:NG:87:PRO:HD2	1.69	0.57
41:a:1176:U:H4'	41:a:1177:G:O4'	2.04	0.57
12:AD:286:GLU:O	15:AG:68:VAL:HG11	2.04	0.57
15:AG:130:PHE:HB3	15:AG:195:LEU:HD21	1.87	0.57
14:AF:60:ASN:OD1	14:AF:63:ILE:HG22	2.05	0.57
28:NG:33:HIS:ND1	28:NG:82:LEU:HD13	2.20	0.57
28:NG:158:LEU:HD21	28:NG:175:PHE:CE1	2.40	0.57
41:a:2189:U:OP1	41:a:2189:U:O4'	2.22	0.57
13:AE:288:PRO:HG3	28:NG:106:LYS:HE3	1.87	0.57
28:NG:103:ILE:CG2	28:NG:107:GLU:HG3	2.35	0.57
41:a:1353:A:C8	41:a:1354:A:N7	2.73	0.57
48:h:141:VAL:HG11	48:h:190:ALA:HB1	1.86	0.57
11:AA:39:ILE:HD11	11:AA:75:LEU:HD22	1.85	0.57
21:H:316:ILE:HD11	21:H:321:VAL:HG11	1.85	0.57
29:O:86:ALA:O	29:O:89:GLU:HG2	2.05	0.57
41:a:668:A:H2'	41:a:670:A:H62	1.70	0.57
20:G:20:THR:O	20:G:23:TRP:CD1	2.58	0.57
28:NG:117:GLN:HG3	28:NG:118:VAL:N	2.20	0.57
29:O:35:LEU:HD21	29:O:45:ARG:HG2	1.87	0.57
59:s:31:GLU:HG3	59:s:142:ILE:HD12	1.87	0.57
41:a:2102:G:O6	41:a:2187:U:O4	2.23	0.57
8:7:4:U:C4	17:D:1500:A:C2	2.93	0.56
9:9:77:VAL:HG12	9:9:77:VAL:O	2.04	0.56
9:9:88:HIS:HB2	9:9:89:PRO:HD3	1.86	0.56
15:AG:130:PHE:CD1	15:AG:195:LEU:HD11	2.40	0.56
15:AG:145:VAL:HG13	15:AG:145:VAL:O	2.05	0.56
15:AG:183:LEU:HD13	15:AG:195:LEU:HD22	1.86	0.56
17:D:157:U:O2	17:D:164:G:C6	2.58	0.56
20:G:128:LYS:HD2	20:G:128:LYS:O	2.05	0.56
28:NG:99:ARG:HH12	28:NG:102:PRO:HB3	1.69	0.56
28:NG:148:VAL:O	28:NG:148:VAL:HG13	2.05	0.56
56:p:98:VAL:O	56:p:99:LYS:HE2	2.04	0.56
13:AE:514:THR:HG22	13:AE:576:ARG:HA	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:v:24:THR:O	62:v:24:THR:HG22	2.04	0.56
5:4:60:VAL:C	5:4:61:LEU:HD12	2.30	0.56
9:9:33:VAL:HG12	9:9:34:THR:H	1.71	0.56
17:D:1125:U:C2	17:D:1127:G:C8	2.93	0.56
28:NG:26:LEU:CD1	28:NG:83:VAL:HG22	2.35	0.56
41:a:1085:A:H2'	41:a:1086:A:C4	2.41	0.56
41:a:2297:A:C2	41:a:2321:U:C5	2.94	0.56
54:n:25:VAL:O	54:n:28:VAL:HG12	2.05	0.56
11:AA:375:PRO:HD3	28:NG:96:THR:OG1	2.05	0.56
28:NG:75:MET:HE1	28:NG:80:TRP:HD1	1.70	0.56
41:a:2841:C:C2	41:a:2877:G:N2	2.74	0.56
54:n:16:LEU:HD23	54:n:19:GLU:OE2	2.05	0.56
54:n:17:MET:HE1	54:n:22:TYR:O	2.05	0.56
66:z:79:PHE:CE1	66:z:83:LEU:HD21	2.40	0.56
41:a:927:A:H2'	41:a:928:A:C8	2.41	0.56
17:D:988:G:H1'	17:D:1015:G:H22	1.71	0.56
21:H:19:ARG:CG	21:H:20:PRO:HD3	2.36	0.56
24:K:18:VAL:HG23	24:K:18:VAL:O	2.06	0.56
3:2:8:LEU:HD23	3:2:50:LEU:HD21	1.87	0.56
9:9:88:HIS:CB	9:9:89:PRO:HD3	2.35	0.56
41:a:856:G:H2'	41:a:857:G:C8	2.41	0.56
28:NG:13:GLN:OE1	28:NG:93:ILE:HD11	2.06	0.56
41:a:1039:A:H2	41:a:1116:G:H22	1.54	0.56
41:a:1153:C:H2'	41:a:1154:G:O4'	2.06	0.56
41:a:2514:U:H2'	41:a:2515:C:C6	2.41	0.56
46:f:36:VAL:HG22	46:f:37:GLU:H	1.70	0.56
28:NG:13:GLN:HB3	28:NG:93:ILE:HG13	1.88	0.56
13:AE:422:LEU:HD13	13:AE:471:PRO:HG3	1.88	0.56
16:C:44:ILE:HG21	21:H:341:ARG:HB2	1.88	0.56
17:D:1004:A:H2'	17:D:1005:A:O4'	2.06	0.55
17:D:1356:G:H2'	17:D:1357:A:C8	2.40	0.55
25:L:36:ILE:HG23	25:L:36:ILE:O	2.06	0.55
28:NG:19:GLU:OE2	28:NG:44:VAL:HG13	2.05	0.55
41:a:1141:U:H4'	41:a:1142:A:O4'	2.06	0.55
41:a:2150:C:H2'	41:a:2151:U:O4'	2.05	0.55
11:AA:870:ILE:CG2	11:AA:931:VAL:HG11	2.36	0.55
13:AE:111:THR:HG21	13:AE:303:VAL:HB	1.88	0.55
13:AE:288:PRO:HG2	28:NG:110:ALA:HB2	1.88	0.55
17:D:820:U:H4'	17:D:821:G:OP2	2.06	0.55
24:K:134:ILE:HD12	24:K:134:ILE:H	1.71	0.55
28:NG:48:GLU:HG2	28:NG:121:LYS:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:NG:9:TRP:CE2	28:NG:108:VAL:HG11	2.41	0.55
41:a:1922:G:C2'	41:a:1923:U:H5'	2.36	0.55
41:a:2102:G:O6	41:a:2187:U:C4	2.59	0.55
25:L:102:MET:SD	25:L:103:VAL:HG23	2.46	0.55
28:NG:27:ARG:HA	28:NG:30:ILE:HD12	1.87	0.55
28:NG:42:VAL:HA	28:NG:71:VAL:HA	1.87	0.55
41:a:1529:G:O6	41:a:1542:U:C2	2.59	0.55
10:A:72:A:H2'	10:A:73:A:O4'	2.06	0.55
17:D:393:A:C2	17:D:394:G:C8	2.95	0.55
41:a:360:U:O3'	41:a:361:G:O4'	2.25	0.55
41:a:1071:G:H2'	41:a:1072:C:N1	2.22	0.55
41:a:1320:C:H2'	41:a:1329:U:OP1	2.07	0.55
46:f:10:THR:HG22	46:f:54:MET:O	2.06	0.55
21:H:31:ILE:CD1	21:H:36:VAL:HG22	2.37	0.55
28:NG:65:PHE:HB2	28:NG:68:TYR:HB2	1.87	0.55
13:AE:1175:LEU:HD22	13:AE:1190:ILE:CD1	2.37	0.55
17:D:713:G:H2'	17:D:714:G:C8	2.41	0.55
41:a:280:U:H2'	41:a:281:C:O4'	2.07	0.55
41:a:2723:C:H2'	41:a:2724:U:O4'	2.07	0.55
13:AE:449:LEU:HD22	13:AE:466:MET:HE1	1.89	0.55
15:AG:266:LEU:HD23	15:AG:266:LEU:H	1.72	0.55
19:F:3:VAL:HG22	31:Q:111:THR:CG2	2.36	0.55
17:D:718:A:C6	31:Q:118:HIS:CE1	2.95	0.55
28:NG:19:GLU:CG	28:NG:69:VAL:HG22	2.27	0.55
41:a:2143:C:H2'	41:a:2144:G:O4'	2.07	0.55
44:d:118:C:N3	44:d:119:A:C8	2.75	0.55
3:2:53:VAL:HG21	3:2:87:LEU:HD23	1.88	0.55
17:D:714:G:H2'	17:D:715:A:C8	2.42	0.55
28:NG:35:MET:HE2	28:NG:38:LEU:HD12	1.88	0.55
41:a:1510:G:H2'	41:a:1511:G:O4'	2.07	0.55
45:e:18:LEU:HD11	45:e:54:LYS:CE	2.36	0.55
17:D:1175:G:N3	17:D:1176:A:C8	2.75	0.54
15:AG:284:VAL:HG11	15:AG:296:ILE:HD13	1.90	0.54
41:a:1069:A:H4'	41:a:1070:A:C8	2.43	0.54
47:g:16:CYS:HB2	47:g:37:CYS:CB	2.35	0.54
12:AC:100:LEU:HD23	12:AC:115:ILE:HG21	1.89	0.54
15:AG:284:VAL:HG22	15:AG:305:MET:CE	2.37	0.54
28:NG:38:LEU:HA	28:NG:74:VAL:CG1	2.37	0.54
28:NG:80:TRP:CZ2	28:NG:97:SER:HB3	2.41	0.54
41:a:1109:C:H2'	41:a:1110:G:C4	2.43	0.54
60:t:35:VAL:HG11	60:t:69:VAL:HG11	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:NG:35:MET:HE1	28:NG:38:LEU:HB2	1.88	0.54
28:NG:41:GLU:H	28:NG:72:GLN:HB3	1.70	0.54
41:a:1664:A:H61	41:a:1996:C:H42	1.55	0.54
45:e:17:GLU:HA	45:e:17:GLU:OE2	2.08	0.54
8:7:4:U:O4	17:D:1501:C:C6	2.61	0.54
9:9:71:CYS:CB	9:9:117:LEU:HD13	2.38	0.54
13:AE:1175:LEU:HD22	13:AE:1190:ILE:HD11	1.89	0.54
15:AG:127:VAL:HG22	15:AG:193:ALA:CB	2.37	0.54
30:P:57:VAL:HG13	30:P:57:VAL:O	2.07	0.54
47:g:18:CYS:HB2	47:g:40:CYS:HB3	1.90	0.54
28:NG:11:VAL:HG23	28:NG:103:ILE:CG1	2.37	0.54
9:9:126:LEU:HD11	9:9:129:LEU:HD23	1.89	0.54
10:A:5:G:H2'	10:A:6:G:H5'	1.90	0.54
28:NG:26:LEU:CD2	28:NG:71:VAL:HG21	2.38	0.54
11:AA:765:ILE:HG23	11:AA:765:ILE:O	2.07	0.54
15:AG:467:LEU:HD12	15:AG:482:ILE:HD11	1.90	0.54
10:B:23:C:H2'	10:B:24:U:H6	1.73	0.54
28:NG:10:TYR:CE1	28:NG:102:PRO:HA	2.43	0.54
28:NG:99:ARG:HH12	28:NG:102:PRO:CG	2.21	0.54
28:NG:148:VAL:HB	28:NG:160:VAL:HG22	1.88	0.54
44:d:81:G:O6	44:d:95:U:O2	2.25	0.54
56:p:121:ILE:HD13	56:p:144:VAL:HG21	1.90	0.54
11:AA:454:ARG:HD3	11:AA:459:MET:HE3	1.89	0.54
11:AA:681:MET:CE	11:AA:685:MET:HE3	2.38	0.54
13:AE:903:LEU:O	13:AE:904:ALA:HB3	2.07	0.54
15:AG:65:VAL:HG12	15:AG:66:ASP:N	2.22	0.54
15:AG:335:GLU:O	15:AG:336:LEU:HD12	2.08	0.54
20:G:19:GLN:HE21	21:H:75:VAL:HG13	1.72	0.54
41:a:1169:A:H62	41:a:1180:U:H3	1.56	0.54
62:v:95:LEU:O	62:v:96:ILE:HD13	2.07	0.54
9:9:139:LEU:HD11	40:Z:11:VAL:HG23	1.90	0.53
11:AA:1002:LEU:HD23	11:AA:1003:THR:O	2.09	0.53
13:AE:113:HIS:CD2	13:AE:239:LEU:HD11	2.43	0.53
13:AE:474:LEU:HD21	14:AF:27:ALA:CB	2.38	0.53
13:AE:165:TYR:CE2	13:AE:169:LEU:HD11	2.42	0.53
41:a:2328:A:H2'	41:a:2329:U:C6	2.43	0.53
48:h:107:PRO:HD2	48:h:110:LEU:HD22	1.89	0.53
21:H:31:ILE:HG23	21:H:31:ILE:O	2.08	0.53
28:NG:99:ARG:HH12	28:NG:102:PRO:CB	2.21	0.53
41:a:306:U:H2'	41:a:307:G:O4'	2.09	0.53
41:a:2189:U:O4'	41:a:2189:U:P	2.66	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:f:7:ILE:HD13	46:f:48:ILE:HD11	1.90	0.53
58:r:84:ALA:CB	58:r:90:LEU:HD12	2.38	0.53
20:G:163:VAL:HG12	20:G:164:ILE:H	1.73	0.53
11:AA:481:LEU:CD2	28:NG:21:ARG:HH21	2.20	0.53
11:AA:836:LEU:HD13	11:AA:1054:LEU:HD13	1.91	0.53
15:AG:453:VAL:HG11	15:AG:459:LEU:CD2	2.39	0.53
10:B:52:G:H2'	10:B:53:G:O4'	2.08	0.53
20:G:50:PHE:HE1	20:G:54:LEU:HD11	1.73	0.53
30:P:65:TYR:HB2	33:S:96:LEU:HD11	1.91	0.53
28:NG:10:TYR:CG	28:NG:100:PRO:HG2	2.43	0.53
28:NG:103:ILE:HG23	28:NG:107:GLU:HG3	1.91	0.53
56:p:76:VAL:O	56:p:80:THR:HG22	2.08	0.53
58:r:132:PHE:HB2	58:r:140:ALA:HB3	1.90	0.53
11:AA:1064:ASP:O	11:AA:1076:ILE:HD12	2.09	0.53
28:NG:13:GLN:NE2	28:NG:90:MET:HG2	2.24	0.53
28:NG:117:GLN:HG3	28:NG:118:VAL:H	1.73	0.53
41:a:2297:A:C6	41:a:2321:U:O4	2.61	0.53
58:r:1:MET:CE	58:r:26:ALA:HB3	2.39	0.53
10:B:72:A:H2'	10:B:73:A:O4'	2.09	0.53
41:a:1056:G:H22	41:a:1102:C:H3'	1.73	0.53
50:j:3:GLY:C	50:j:4:LEU:HD12	2.34	0.53
17:D:147:G:H2'	17:D:148:G:C8	2.43	0.53
17:D:673:A:C6	17:D:734:G:C6	2.97	0.53
26:M:79:ARG:O	26:M:79:ARG:HD2	2.09	0.53
41:a:1921:G:H2'	41:a:1922:G:H8	1.74	0.53
1:0:44:GLY:C	1:0:45:GLU:HG3	2.33	0.53
10:A:38:A:H2'	10:A:39:C:O4'	2.09	0.53
21:H:19:ARG:HG2	21:H:20:PRO:HD3	1.91	0.53
21:H:305:HIS:CG	21:H:306:VAL:H	2.27	0.53
41:a:2458:G:H21	41:a:2459:A:N6	2.06	0.53
9:9:67:THR:HG21	9:9:74:ASP:HB2	1.91	0.52
12:AD:287:VAL:HA	15:AG:68:VAL:HG21	1.90	0.52
15:AG:284:VAL:HG22	15:AG:305:MET:SD	2.48	0.52
16:C:72:ASP:OD2	19:F:3:VAL:HG23	2.09	0.52
17:D:157:U:C2	17:D:164:G:O6	2.62	0.52
21:H:308:GLU:O	21:H:310:ASP:N	2.42	0.52
28:NG:13:GLN:HB3	28:NG:93:ILE:HG12	1.89	0.52
41:a:1068:G:H21	41:a:1095:A:H1'	1.73	0.52
41:a:1857:G:C2	41:a:1884:G:N3	2.77	0.52
48:h:146:MET:CE	48:h:154:LEU:HD21	2.39	0.52
17:D:492:C:H2'	17:D:493:A:C8	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:D:1360:A:C4	17:D:1361:G:C8	2.97	0.52
20:G:163:VAL:HG12	20:G:164:ILE:N	2.24	0.52
28:NG:38:LEU:CA	28:NG:74:VAL:HG12	2.39	0.52
41:a:885:C:C2	41:a:892:A:N1	2.77	0.52
9:9:67:THR:N	9:9:68:PRO:CD	2.72	0.52
11:AA:375:PRO:HG2	28:NG:98:ASP:N	2.24	0.52
13:AE:793:SER:O	13:AE:797:THR:HG23	2.10	0.52
10:B:44:A:H2'	10:B:45:G:O4'	2.10	0.52
28:NG:10:TYR:CB	28:NG:100:PRO:HG2	2.38	0.52
41:a:1936:A:N7	41:a:1945:G:C8	2.78	0.52
41:a:2287:A:N7	41:a:2289:G:C8	2.77	0.52
9:9:33:VAL:HG12	9:9:34:THR:N	2.25	0.52
11:AA:905:ILE:CG1	15:AG:8:VAL:HG21	2.40	0.52
13:AE:1027:VAL:O	13:AE:1027:VAL:HG12	2.09	0.52
15:AG:248:VAL:O	15:AG:252:VAL:HG23	2.09	0.52
17:D:206:C:H42	17:D:214:C:H1'	1.74	0.52
17:D:1125:U:N3	17:D:1127:G:C8	2.77	0.52
3:2:30:ILE:HG21	3:2:93:LEU:HD23	1.92	0.52
11:AA:375:PRO:HB2	28:NG:98:ASP:CB	2.30	0.52
15:AG:278:ASP:C	15:AG:279:ASN:O	2.50	0.52
10:B:11:A:H2'	10:B:12:G:C1'	2.39	0.52
17:D:392:C:C2	17:D:393:A:C8	2.98	0.52
17:D:1157:A:C2	17:D:1181:G:C4	2.97	0.52
41:a:447:A:C4	41:a:473:G:N7	2.78	0.52
1:0:46:GLU:OE1	1:0:46:GLU:O	2.28	0.52
9:9:71:CYS:HB3	9:9:117:LEU:HD13	1.92	0.52
10:B:48:C:O2	10:B:48:C:H2'	2.10	0.52
17:D:459:A:C6	17:D:474:G:C6	2.97	0.52
17:D:1304:G:O3'	17:D:1305:G:O4'	2.27	0.52
28:NG:26:LEU:O	28:NG:30:ILE:HG13	2.09	0.52
41:a:285:G:O6	41:a:355:U:C2	2.63	0.52
41:a:382:A:C2	41:a:393:C:C2	2.98	0.52
41:a:1433:A:H2'	41:a:1434:A:O4'	2.09	0.52
41:a:2140:G:H2'	41:a:2141:G:O4'	2.09	0.52
12:AD:35:PHE:HA	12:AD:38:THR:HG22	1.92	0.52
10:B:49:G:C2	10:B:66:C:C2	2.97	0.52
17:D:218:U:H2'	17:D:219:U:O4'	2.10	0.52
15:AG:34:ALA:HB2	15:AG:113:VAL:HG21	1.91	0.52
17:D:718:A:N1	31:Q:118:HIS:CE1	2.78	0.52
17:D:1055:A:C2	17:D:1206:G:N3	2.78	0.52
25:L:67:PRO:O	25:L:70:VAL:HG22	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:585:G:H2'	41:a:1251:C:H42	1.75	0.52
47:g:10:GLU:O	47:g:12:ILE:HD12	2.09	0.52
11:AA:480:SER:C	11:AA:481:LEU:HD12	2.35	0.52
13:AE:279:LEU:HD11	13:AE:296:LYS:HG2	1.91	0.52
13:AE:975:ILE:HG22	13:AE:977:SER:H	1.75	0.52
19:F:32:VAL:HG11	31:Q:89:PRO:HG3	1.91	0.52
28:NG:43:MET:HG3	28:NG:70:LEU:HB2	1.91	0.52
41:a:886:A:H2'	41:a:887:A:O4'	2.10	0.52
44:d:39:A:H2'	44:d:40:U:C6	2.45	0.52
4:3:99:ASN:C	4:3:99:ASN:OD1	2.53	0.51
12:AD:44:ARG:HA	12:AD:183:ILE:HD12	1.92	0.51
13:AE:151:MET:SD	13:AE:151:MET:O	2.69	0.51
17:D:1230:C:H41	38:X:104:THR:HG21	1.75	0.51
31:Q:19:GLY:O	31:Q:82:LEU:HD12	2.10	0.51
41:a:760:G:H2'	41:a:761:A:O4'	2.09	0.51
10:A:22:G:O2'	10:A:23:C:P	2.69	0.51
15:AG:38:LYS:O	15:AG:39:TYR:C	2.53	0.51
28:NG:22:VAL:CG1	28:NG:69:VAL:HG21	2.40	0.51
17:D:1033:G:H2'	17:D:1034:G:O4'	2.10	0.51
17:D:1287:A:H2'	17:D:1288:A:C8	2.45	0.51
17:D:1375:A:H5''	26:M:25:LYS:HZ2	1.74	0.51
21:H:74:ALA:HB3	21:H:83:LEU:HD23	1.90	0.51
28:NG:35:MET:O	28:NG:35:MET:SD	2.69	0.51
30:P:82:LYS:O	30:P:85:ASP:OD1	2.28	0.51
41:a:983:A:N6	41:a:984:A:H62	2.08	0.51
41:a:2109:U:H2'	41:a:2110:G:C8	2.44	0.51
50:j:156:PHE:CE1	59:s:81:ILE:HD13	2.44	0.51
63:w:2:ARG:HD2	63:w:2:ARG:O	2.10	0.51
21:H:24:VAL:HG23	21:H:24:VAL:O	2.10	0.51
41:a:623:C:C2	41:a:624:C:C5	2.99	0.51
41:a:2652:C:H2'	41:a:2653:U:O4'	2.10	0.51
11:AA:847:PRO:HB3	11:AA:1047:LEU:HD11	1.91	0.51
27:N:52:GLU:N	27:N:52:GLU:OE2	2.44	0.51
41:a:285:G:C6	41:a:355:U:O2	2.62	0.51
41:a:543:G:H1	41:a:550:C:H42	1.56	0.51
11:AA:90:VAL:HG12	11:AA:91:THR:N	2.24	0.51
13:AE:279:LEU:HD13	13:AE:299:LEU:HD13	1.92	0.51
15:AG:284:VAL:CG1	15:AG:296:ILE:HG21	2.41	0.51
10:B:22:G:H2'	10:B:23:C:C5	2.45	0.51
41:a:393:C:C2	41:a:394:C:C5	2.99	0.51
41:a:1353:A:C2	41:a:1378:A:C2	2.99	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:1473:G:C6	41:a:1519:G:C6	2.98	0.51
48:h:146:MET:HE1	48:h:154:LEU:HD21	1.91	0.51
65:y:51:ARG:HE	65:y:53:ARG:HG3	1.76	0.51
2:1:110:ARG:C	2:1:110:ARG:HE	2.19	0.51
11:AA:519:ASN:OD1	11:AA:520:PRO:HD2	2.10	0.51
13:AE:145:VAL:CG2	13:AE:188:LEU:HD11	2.40	0.51
17:D:1218:C:H2'	17:D:1219:A:H8	1.75	0.51
12:AD:19:VAL:HG12	12:AD:20:SER:H	1.75	0.51
28:NG:83:VAL:O	28:NG:86:VAL:HB	2.10	0.51
30:P:78:GLU:O	30:P:78:GLU:CD	2.54	0.51
41:a:1183:U:H2'	41:a:1184:U:C6	2.46	0.51
28:NG:26:LEU:CD2	28:NG:83:VAL:HG13	2.35	0.51
41:a:967:U:H2'	41:a:968:C:C6	2.46	0.51
41:a:2521:C:C2	41:a:2545:G:N2	2.79	0.51
10:A:9:G:H4'	10:A:10:G:OP2	2.11	0.51
12:AD:187:VAL:HG22	12:AD:201:LEU:HA	1.92	0.51
13:AE:473:THR:HG23	13:AE:476:ALA:H	1.75	0.51
15:AG:68:VAL:HG13	15:AG:74:GLU:OE1	2.11	0.51
15:AG:235:LYS:HE2	15:AG:331:LEU:HD11	1.92	0.51
17:D:444:G:C6	17:D:491:G:C6	2.99	0.51
28:NG:64:PHE:HB2	28:NG:65:PHE:CD1	2.43	0.51
9:9:71:CYS:HA	9:9:117:LEU:HD22	1.93	0.50
11:AA:138:ILE:HD12	11:AA:506:PHE:HB3	1.93	0.50
15:AG:387:VAL:HB	15:AG:388:PRO:HD2	1.92	0.50
17:D:972:C:O2'	30:P:57:VAL:HG23	2.11	0.50
41:a:1040:A:H2'	41:a:1041:G:O4'	2.10	0.50
41:a:1528:A:C4	41:a:1544:A:C6	3.00	0.50
58:r:8:LYS:HD2	58:r:8:LYS:C	2.36	0.50
11:AA:998:LEU:HD21	11:AA:1015:ALA:HB2	1.93	0.50
13:AE:145:VAL:HG21	13:AE:188:LEU:HD11	1.93	0.50
10:B:13:C:O4'	10:B:13:C:OP1	2.29	0.50
27:N:11:LEU:HD22	27:N:75:ILE:HD11	1.93	0.50
28:NG:26:LEU:HD21	28:NG:71:VAL:HG11	1.93	0.50
30:P:57:VAL:O	30:P:58:ASN:CG	2.54	0.50
37:W:16:LEU:O	37:W:19:VAL:HG12	2.12	0.50
39:Y:32:VAL:HG22	39:Y:58:ILE:HG21	1.93	0.50
9:9:129:LEU:N	9:9:130:PRO:HD3	2.26	0.50
11:AA:454:ARG:HG2	11:AA:459:MET:HE3	1.92	0.50
17:D:18:C:H5''	24:K:132:ASN:ND2	2.26	0.50
20:G:6:MET:HG3	20:G:47:VAL:HG21	1.93	0.50
21:H:265:ASP:HB2	21:H:266:PRO:HD3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:NG:164:ILE:O	28:NG:165:PHE:HB2	2.12	0.50
41:a:1922:G:H2'	41:a:1923:U:H5'	1.93	0.50
47:g:18:CYS:HB3	47:g:40:CYS:HB2	1.92	0.50
11:AA:850:ILE:O	11:AA:850:ILE:HG22	2.10	0.50
12:AD:19:VAL:HG12	12:AD:20:SER:N	2.26	0.50
13:AE:56:LEU:HD21	13:AE:250:ARG:CZ	2.41	0.50
15:AG:154:LEU:HB2	15:AG:158:ALA:HB3	1.93	0.50
41:a:1433:A:H2'	41:a:1434:A:C1'	2.42	0.50
41:a:2812:G:H2'	41:a:2813:A:O4'	2.11	0.50
13:AE:213:LYS:O	13:AE:217:LEU:HD13	2.10	0.50
15:AG:213:VAL:HG13	15:AG:213:VAL:O	2.11	0.50
39:Y:16:MET:O	39:Y:16:MET:SD	2.69	0.50
41:a:404:A:H1'	41:a:405:U:OP2	2.12	0.50
13:AE:87:LYS:HG3	13:AE:88:CYS:SG	2.51	0.50
10:B:70:G:H2'	10:B:71:C:O4'	2.11	0.50
17:D:204:G:C6	17:D:465:A:C5	3.00	0.50
17:D:1006:G:C6	17:D:1023:U:O2	2.64	0.50
17:D:1317:C:H5''	33:S:24:ARG:HH22	1.76	0.50
41:a:1050:A:H2'	41:a:1051:G:O4'	2.12	0.50
10:A:8:U:H3	10:A:14:A:H62	1.57	0.50
13:AE:347:VAL:HG12	13:AE:348:ASP:O	2.12	0.50
13:AE:474:LEU:HD21	14:AF:27:ALA:HB1	1.93	0.50
17:D:555:U:H2'	17:D:556:C:C6	2.46	0.50
17:D:779:C:H2'	17:D:780:A:O4'	2.12	0.50
28:NG:26:LEU:HA	28:NG:86:VAL:HG21	1.94	0.50
41:a:287:G:H2'	41:a:288:U:C6	2.47	0.50
41:a:464:U:C2'	41:a:465:G:O5'	2.59	0.50
41:a:543:G:C6	41:a:544:C:N4	2.80	0.50
41:a:848:C:H2'	41:a:849:A:H8	1.75	0.50
54:n:31:VAL:HG23	54:n:96:MET:HE1	1.94	0.50
11:AA:1280:ALA:HB1	13:AE:918:ILE:HG22	1.94	0.50
15:AG:227:ALA:HB3	15:AG:331:LEU:HD23	1.93	0.50
17:D:119:A:C2	17:D:240:G:C8	2.99	0.50
17:D:373:A:C2	17:D:374:A:C8	3.00	0.50
17:D:704:A:C4	17:D:705:G:C8	2.99	0.50
24:K:114:VAL:HG13	24:K:115:LEU:HD22	1.94	0.50
28:NG:9:TRP:CD1	28:NG:108:VAL:HG11	2.47	0.50
28:NG:14:ALA:HB2	28:NG:22:VAL:HG11	1.94	0.50
39:Y:27:LEU:HD11	39:Y:34:ILE:HD13	1.92	0.50
40:Z:14:MET:HE2	40:Z:17:MET:SD	2.52	0.50
41:a:2114:A:H2'	41:a:2167:U:H5'	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:g:12:ILE:HG22	47:g:13:THR:N	2.26	0.50
10:A:22:G:H2'	10:A:23:C:C6	2.47	0.50
11:AA:1275:VAL:HG13	11:AA:1287:LEU:HD11	1.93	0.50
17:D:81:A:N1	17:D:88:U:O4	2.44	0.50
21:H:331:MET:HE3	21:H:333:LEU:HG	1.94	0.50
28:NG:82:LEU:O	28:NG:86:VAL:HG23	2.12	0.50
41:a:1169:A:H3'	41:a:1170:C:O4'	2.11	0.50
41:a:2141:G:H2'	41:a:2142:A:O4'	2.11	0.50
56:p:11:VAL:HG13	56:p:11:VAL:O	2.11	0.50
9:9:50:VAL:HG13	9:9:50:VAL:O	2.12	0.49
10:B:12:G:H2'	10:B:13:C:OP1	2.12	0.49
41:a:1582:C:H2'	41:a:1583:A:O4'	2.12	0.49
11:AA:803:ALA:HB1	11:AA:805:MET:HE1	1.93	0.49
11:AA:1274:GLU:HG3	13:AE:424:ASN:HD21	1.77	0.49
15:AG:434:LEU:HD22	15:AG:459:LEU:HD12	1.93	0.49
29:O:28:ILE:HG12	29:O:63:LEU:HD21	1.93	0.49
37:W:64:ASP:O	37:W:67:VAL:HG23	2.12	0.49
41:a:356:G:H2'	41:a:357:C:C6	2.48	0.49
41:a:1418:G:H2'	41:a:1579:A:H62	1.77	0.49
41:a:2744:G:C6	41:a:2761:A:C6	3.00	0.49
3:2:93:LEU:HD12	3:2:94:ASP:H	1.78	0.49
9:9:25:ALA:HB3	9:9:99:PHE:CD2	2.47	0.49
10:A:35:A:H2'	10:A:36:U:C6	2.47	0.49
10:A:48:C:H2'	10:A:48:C:O2	2.12	0.49
15:AG:30:ALA:HB1	15:AG:113:VAL:C	2.36	0.49
22:I:130:PHE:CD2	22:I:134:MET:HE2	2.47	0.49
22:I:156:ARG:O	22:I:156:ARG:HG3	2.12	0.49
28:NG:48:GLU:C	28:NG:122:PRO:HB3	2.38	0.49
41:a:728:G:H3'	41:a:729:G:H5'	1.94	0.49
41:a:1071:G:H8	41:a:1071:G:O5'	1.94	0.49
41:a:1167:C:C2	41:a:1168:G:C8	3.00	0.49
41:a:1415:U:C2	41:a:1588:G:N1	2.80	0.49
41:a:1590:A:H2'	41:a:1591:A:C8	2.47	0.49
48:h:94:VAL:HG21	48:h:116:ILE:HD11	1.94	0.49
58:r:109:GLU:O	58:r:109:GLU:HG2	2.11	0.49
10:A:48:C:C5	10:A:59:A:C8	3.01	0.49
12:AC:149:GLY:HA3	12:AC:177:TYR:CD2	2.47	0.49
15:AG:284:VAL:HG11	15:AG:296:ILE:HG21	1.94	0.49
25:L:33:GLU:OE1	25:L:33:GLU:O	2.30	0.49
28:NG:123:ARG:O	28:NG:124:PRO:C	2.55	0.49
41:a:1107:G:C2	41:a:1108:U:C5	3.00	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:1042:LEU:HD22	11:AA:1049:ILE:CD1	2.41	0.49
17:D:1460:C:C2	17:D:1461:G:C8	3.01	0.49
28:NG:25:SER:CB	28:NG:86:VAL:HG13	2.41	0.49
28:NG:80:TRP:HE1	28:NG:92:PHE:HB2	1.78	0.49
41:a:273:G:C2	41:a:365:U:C2	3.00	0.49
41:a:464:U:H2'	41:a:465:G:O5'	2.13	0.49
41:a:880:G:C2	41:a:881:G:C8	3.00	0.49
49:i:43:ILE:HD11	63:w:98:LEU:HB3	1.94	0.49
62:v:57:VAL:O	62:v:57:VAL:HG22	2.12	0.49
15:AG:160:ALA:HA	15:AG:195:LEU:HB2	1.93	0.49
17:D:1218:C:H2'	17:D:1219:A:C8	2.48	0.49
17:D:1477:U:H2'	17:D:1478:U:C6	2.48	0.49
41:a:2570:G:H2'	41:a:2571:U:O4'	2.13	0.49
41:a:2708:G:C2	41:a:2709:G:C8	3.00	0.49
10:A:10:G:H2'	10:A:11:A:C8	2.48	0.49
11:AA:464:PHE:CE2	11:AA:468:LEU:HD11	2.48	0.49
13:AE:452:LEU:HB3	13:AE:500:ILE:HG22	1.94	0.49
15:AG:240:THR:HG21	15:AG:245:ILE:HG21	1.94	0.49
15:AG:252:VAL:HA	15:AG:259:VAL:HG23	1.95	0.49
15:AG:307:ILE:HG22	15:AG:309:VAL:HG23	1.94	0.49
28:NG:12:VAL:HG22	28:NG:92:PHE:CG	2.47	0.49
28:NG:79:SER:O	28:NG:83:VAL:HG23	2.13	0.49
38:X:104:THR:O	38:X:104:THR:HG22	2.11	0.49
41:a:884:U:O2'	41:a:885:C:O4'	2.26	0.49
41:a:1707:G:C8	41:a:1756:G:C5	3.00	0.49
47:g:16:CYS:HB3	47:g:37:CYS:HB3	1.91	0.49
58:r:83:LYS:C	58:r:83:LYS:HD3	2.38	0.49
15:AG:12:VAL:O	15:AG:12:VAL:HG12	2.13	0.49
20:G:20:THR:O	20:G:23:TRP:HD1	1.96	0.49
21:H:71:ALA:O	21:H:72:LEU:HD12	2.13	0.49
28:NG:10:TYR:CD1	28:NG:102:PRO:HA	2.47	0.49
41:a:784:G:H5'	41:a:785:G:OP1	2.13	0.49
41:a:1115:G:N3	41:a:1116:G:C8	2.80	0.49
41:a:1462:C:C2	41:a:1463:C:C5	3.01	0.49
41:a:2120:G:C6	41:a:2121:G:C6	3.01	0.49
52:l:9:GLN:OE1	52:l:9:GLN:N	2.45	0.49
54:n:122:PHE:HB3	54:n:163:ASP:OD1	2.12	0.49
58:r:37:VAL:HG13	58:r:38:PRO:HD2	1.94	0.49
11:AA:1232:MET:C	11:AA:1233:LEU:HD12	2.37	0.49
10:B:60:U:P	10:B:61:C:H41	2.35	0.49
20:G:19:GLN:HG3	21:H:76:GLU:HB3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:NG:138:ASP:HB3	28:NG:177:GLN:HG3	1.93	0.49
34:T:64:ARG:NE	34:T:64:ARG:HA	2.28	0.49
41:a:1100:C:H2'	41:a:1101:U:O4'	2.13	0.49
41:a:1103:A:H3'	41:a:1104:C:C6	2.48	0.49
45:e:17:GLU:O	45:e:21:LEU:HD23	2.13	0.49
46:f:6:LYS:HD3	46:f:37:GLU:HB2	1.95	0.49
2:1:66:ILE:HD12	2:1:66:ILE:H	1.78	0.49
10:A:31:G:H2'	10:A:32:C:C6	2.48	0.49
21:H:264:GLU:O	21:H:268:VAL:HG23	2.13	0.49
28:NG:83:VAL:HG21	28:NG:92:PHE:HZ	1.77	0.49
41:a:1720:U:H2'	41:a:1721:G:O4'	2.12	0.49
41:a:2101:A:H2'	41:a:2102:G:O4'	2.13	0.49
41:a:2220:U:H4'	58:r:97:ARG:NH2	2.28	0.49
3:2:50:LEU:HD23	45:e:26:PHE:CZ	2.47	0.48
12:AD:192:VAL:HG12	12:AD:193:GLU:N	2.27	0.48
15:AG:183:LEU:HD11	15:AG:195:LEU:HD13	1.95	0.48
10:B:24:U:H2'	10:B:25:C:N1	2.28	0.48
17:D:604:G:H2'	17:D:605:U:O4'	2.13	0.48
33:S:42:TRP:O	33:S:46:LEU:HD23	2.13	0.48
41:a:1107:G:C2	41:a:1108:U:C6	3.00	0.48
41:a:1593:A:H2'	41:a:1594:U:C6	2.48	0.48
41:a:2737:G:H2'	41:a:2738:A:C8	2.48	0.48
44:d:106:G:H2'	44:d:107:G:O4'	2.13	0.48
48:h:132:MET:HE3	48:h:188:CYS:O	2.13	0.48
54:n:130:MET:C	54:n:130:MET:SD	2.96	0.48
17:D:75:G:H2'	17:D:76:G:O4'	2.12	0.48
17:D:1148:U:H2'	17:D:1149:C:O4'	2.13	0.48
21:H:71:ALA:HB3	21:H:83:LEU:O	2.12	0.48
24:K:15:LEU:HD12	24:K:15:LEU:O	2.13	0.48
29:O:84:THR:O	29:O:88:MET:HG2	2.12	0.48
38:X:102:THR:O	38:X:103:LYS:C	2.55	0.48
39:Y:14:ALA:CB	39:Y:54:ILE:HD12	2.43	0.48
41:a:2899:A:H2'	41:a:2900:A:C8	2.48	0.48
44:d:8:C:O2'	64:x:40:ILE:HD13	2.13	0.48
54:n:57:LEU:HD12	54:n:87:CYS:SG	2.52	0.48
59:s:34:ARG:HG3	59:s:39:LYS:HB2	1.96	0.48
64:x:21:LEU:HD23	64:x:21:LEU:C	2.38	0.48
10:A:16:C:H3'	10:A:17:C:H5'	1.94	0.48
13:AE:382:TYR:CD1	13:AE:397:ALA:HB1	2.48	0.48
17:D:721:G:H4'	17:D:722:G:O4'	2.13	0.48
17:D:792:A:H1'	17:D:794:A:N7	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:D:1021:A:N1	17:D:1022:A:C6	2.82	0.48
17:D:1322:C:O2	17:D:1322:C:O4'	2.31	0.48
21:H:337:GLU:OE2	21:H:338:GLU:OE2	2.32	0.48
25:L:9:MET:SD	25:L:59:TYR:CZ	3.06	0.48
29:O:88:MET:HE1	29:O:94:LEU:HB2	1.93	0.48
41:a:359:G:C5	41:a:360:U:C4	3.01	0.48
41:a:419:U:H2'	41:a:420:C:C6	2.48	0.48
54:n:35:THR:C	54:n:36:LEU:HD12	2.38	0.48
54:n:40:VAL:HG23	54:n:40:VAL:O	2.13	0.48
8:7:3:G:C6	10:B:35:A:C5	3.02	0.48
11:AA:28:LEU:HD13	11:AA:133:ASN:O	2.13	0.48
13:AE:1164:SER:O	13:AE:1175:LEU:HD12	2.13	0.48
10:B:22:G:O2'	10:B:23:C:P	2.71	0.48
17:D:1087:G:C6	17:D:1099:G:N1	2.81	0.48
17:D:1319:A:C8	17:D:1323:G:C5	3.02	0.48
41:a:543:G:C6	41:a:551:G:C6	3.01	0.48
41:a:871:U:H2'	41:a:872:U:C6	2.49	0.48
41:a:1064:C:H2'	41:a:1065:U:C6	2.49	0.48
56:p:159:GLY:HA2	56:p:169:VAL:HG11	1.96	0.48
11:AA:254:ASP:OD2	11:AA:261:VAL:HG13	2.14	0.48
11:AA:1212:LEU:HD11	11:AA:1227:VAL:HG11	1.95	0.48
17:D:204:G:H3'	17:D:205:A:C8	2.48	0.48
17:D:1278:G:HO2'	17:D:1279:G:P	2.35	0.48
20:G:10:LEU:CD2	21:H:9:PHE:HB3	2.43	0.48
28:NG:14:ALA:HB3	28:NG:69:VAL:HG23	1.95	0.48
34:T:55:GLY:O	34:T:59:MET:HG3	2.13	0.48
41:a:1858:A:H2'	41:a:1859:U:O4'	2.13	0.48
41:a:2290:G:H2'	41:a:2291:U:O4'	2.13	0.48
41:a:2557:G:H2'	41:a:2558:C:C6	2.48	0.48
48:h:76:ALA:HB1	48:h:94:VAL:HG22	1.95	0.48
58:r:84:ALA:HB2	58:r:90:LEU:HD12	1.95	0.48
11:AA:660:VAL:HG13	11:AA:661:VAL:HG13	1.95	0.48
11:AA:1287:LEU:HD22	13:AE:1357:ILE:HD11	1.95	0.48
14:AF:58:LEU:HD12	14:AF:59:ILE:HG12	1.95	0.48
21:H:274:TYR:HA	21:H:335:ILE:CD1	2.42	0.48
28:NG:164:ILE:HG13	30:P:88:MET:HB2	1.95	0.48
29:O:12:ARG:HD2	29:O:74:GLY:HA2	1.96	0.48
38:X:81:MET:HB3	41:a:888:C:N4	2.29	0.48
41:a:984:A:N3	41:a:984:A:H2'	2.29	0.48
41:a:1012:U:O4	59:s:30:THR:HG21	2.13	0.48
41:a:1278:C:H2'	41:a:1279:G:H8	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:g:28:VAL:HG11	47:g:32:LEU:HD21	1.95	0.48
60:t:108:ARG:CB	60:t:116:ILE:HD13	2.42	0.48
10:A:12:G:C2'	10:A:13:C:OP1	2.62	0.48
11:AA:852:ALA:HA	11:AA:869:GLY:HA2	1.95	0.48
17:D:160:A:H2'	17:D:161:A:O4'	2.14	0.48
28:NG:43:MET:HE3	28:NG:70:LEU:HD13	1.95	0.48
30:P:17:LEU:HD21	30:P:93:ALA:HB3	1.94	0.48
37:W:13:LEU:HD11	37:W:17:LYS:HD3	1.96	0.48
41:a:217:A:C4	41:a:218:A:C8	3.01	0.48
41:a:1528:A:N6	41:a:1529:G:C2	2.81	0.48
9:9:60:LEU:HD23	9:9:64:VAL:HG21	1.94	0.48
11:AA:745:GLU:O	11:AA:746:ALA:C	2.55	0.48
13:AE:144:TYR:HB2	13:AE:160:LEU:HB2	1.95	0.48
13:AE:1184:ASP:N	13:AE:1185:PRO:CD	2.77	0.48
10:B:22:G:P	10:B:22:G:H8	2.37	0.48
17:D:80:A:C2	17:D:81:A:C8	3.02	0.48
17:D:718:A:C5	31:Q:118:HIS:ND1	2.82	0.48
17:D:920:U:H2'	17:D:921:U:C6	2.47	0.48
17:D:1002:G:H2'	17:D:1003:G:O4'	2.13	0.48
17:D:1244:G:C6	17:D:1294:G:C6	3.02	0.48
17:D:1527:U:H2'	17:D:1528:U:C6	2.49	0.48
41:a:291:G:C6	41:a:350:G:C6	3.02	0.48
41:a:1474:U:O2	41:a:1517:G:O6	2.32	0.48
41:a:2847:U:H2'	41:a:2848:G:O4'	2.14	0.48
64:x:21:LEU:HD23	64:x:21:LEU:O	2.14	0.48
1:0:14:VAL:HG21	1:0:98:ILE:HG13	1.95	0.48
10:A:71:C:H3'	10:A:72:A:C8	2.49	0.48
11:AA:253:PHE:CE2	11:AA:255:ILE:HA	2.49	0.48
13:AE:686:TRP:HB3	13:AE:746:LEU:HD11	1.95	0.48
15:AG:440:VAL:CG2	15:AG:481:LEU:HD22	2.44	0.48
17:D:828:U:C4	17:D:859:G:C4	3.01	0.48
17:D:1129:C:C2	17:D:1144:G:N2	2.81	0.48
21:H:332:VAL:HG12	21:H:334:ASP:H	1.78	0.48
28:NG:9:TRP:CB	28:NG:103:ILE:HB	2.44	0.48
28:NG:16:SER:HA	28:NG:67:GLY:HA3	1.95	0.48
30:P:18:ILE:O	30:P:22:THR:HG23	2.14	0.48
37:W:65:GLU:HB2	38:X:83:LEU:HD21	1.95	0.48
41:a:1291:C:C2	41:a:1292:G:C8	3.02	0.48
11:AA:375:PRO:CG	28:NG:98:ASP:HB2	2.44	0.48
13:AE:123:ARG:CG	13:AE:1337:VAL:HG11	2.43	0.48
17:D:1:A:O2'	17:D:2:A:O5'	2.30	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:D:75:G:C4	17:D:76:G:C8	3.01	0.48
17:D:181:A:H1'	17:D:182:A:C8	2.49	0.48
17:D:399:G:H2'	17:D:400:C:C6	2.49	0.48
28:NG:134:VAL:CG2	28:NG:160:VAL:HG11	2.44	0.48
29:O:7:TYR:O	29:O:89:GLU:OE2	2.31	0.48
41:a:2794:C:C2	41:a:2803:G:C2	3.02	0.48
63:w:114:GLU:OE1	63:w:115:LEU:O	2.32	0.48
10:A:70:G:C6	10:A:71:C:C4	3.02	0.47
13:AE:500:ILE:HG22	13:AE:500:ILE:O	2.14	0.47
15:AG:21:GLU:HB3	15:AG:49:ILE:HD12	1.94	0.47
15:AG:31:LEU:CD2	15:AG:110:ALA:HB1	2.43	0.47
17:D:1375:A:C5'	26:M:25:LYS:HZ2	2.27	0.47
28:NG:30:ILE:HG12	28:NG:39:PHE:CE2	2.49	0.47
28:NG:140:PRO:HG3	30:P:79:PRO:HB3	1.95	0.47
41:a:471:A:H2'	41:a:472:A:O4'	2.14	0.47
41:a:1069:A:C8	41:a:1073:A:N6	2.82	0.47
41:a:1071:G:H2'	41:a:1072:C:C6	2.49	0.47
41:a:1319:C:O2'	41:a:1320:C:H5'	2.13	0.47
41:a:1551:A:H2'	41:a:1552:A:O4'	2.14	0.47
41:a:1831:G:C4	41:a:1975:G:N2	2.82	0.47
44:d:94:A:H2'	44:d:95:U:O4'	2.13	0.47
9:9:52:MET:HE1	9:9:85:SER:CA	2.44	0.47
9:9:56:ARG:O	9:9:56:ARG:HG2	2.13	0.47
10:A:15:G:H3'	10:A:15:G:N3	2.29	0.47
11:AA:1066:MET:HG2	11:AA:1076:ILE:HD11	1.95	0.47
17:D:563:A:C2	17:D:567:G:C5	3.02	0.47
17:D:744:C:H2'	17:D:745:G:C8	2.49	0.47
21:H:267:TRP:HZ3	21:H:342:ILE:HD11	1.78	0.47
27:N:120:GLY:C	27:N:121:LEU:HD12	2.39	0.47
28:NG:74:VAL:HG13	28:NG:74:VAL:O	2.14	0.47
41:a:1039:A:H2'	41:a:1040:A:O4'	2.14	0.47
41:a:2720:U:C2	41:a:2721:A:C8	3.02	0.47
10:A:5:G:C2'	10:A:6:G:H5'	2.45	0.47
10:A:23:C:H2'	10:A:24:U:C6	2.49	0.47
11:AA:883:LEU:HD11	11:AA:920:VAL:HG22	1.96	0.47
11:AA:905:ILE:CD1	15:AG:8:VAL:HG21	2.43	0.47
11:AA:1120:ALA:HB1	11:AA:1198:LEU:HG	1.96	0.47
12:AC:61:ILE:HD13	12:AC:78:ILE:HG23	1.96	0.47
13:AE:382:TYR:CD2	13:AE:394:ILE:HD11	2.48	0.47
15:AG:11:ALA:H	15:AG:12:VAL:HG22	1.79	0.47
15:AG:453:VAL:HG11	15:AG:459:LEU:HG	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:D:234:C:H2'	17:D:235:C:H6	1.80	0.47
17:D:465:A:H2'	17:D:466:A:O4'	2.14	0.47
28:NG:133:MET:C	28:NG:181:ALA:HB3	2.39	0.47
41:a:1913:A:H1'	41:a:1914:C:OP1	2.13	0.47
48:h:120:VAL:HG22	48:h:131:PRO:CD	2.44	0.47
52:l:188:MET:SD	52:l:193:VAL:HG22	2.54	0.47
9:9:61:ARG:CZ	41:a:1047:G:N7	2.77	0.47
11:AA:685:MET:SD	11:AA:1235:LEU:HD13	2.54	0.47
11:AA:803:ALA:HB2	11:AA:1227:VAL:HG12	1.96	0.47
13:AE:218:THR:HA	13:AE:221:ILE:HG22	1.96	0.47
10:B:21:A:H4'	10:B:21:A:OP1	2.14	0.47
10:B:24:U:H2'	10:B:25:C:C6	2.49	0.47
17:D:1139:G:N2	17:D:1143:G:C6	2.82	0.47
30:P:44:THR:HG22	30:P:45:ARG:N	2.30	0.47
41:a:221:A:C4	41:a:266:G:N7	2.83	0.47
41:a:489:G:C6	41:a:491:G:C2	3.02	0.47
41:a:874:G:C6	41:a:904:G:C6	3.01	0.47
41:a:1353:A:N7	41:a:1354:A:N7	2.63	0.47
41:a:2297:A:N1	41:a:2321:U:O4	2.47	0.47
41:a:2854:G:C6	41:a:2864:G:C6	3.02	0.47
49:i:43:ILE:HD12	63:w:99:LYS:O	2.14	0.47
11:AA:1085:MET:HE2	11:AA:1085:MET:N	2.29	0.47
11:AA:1101:LEU:HD13	13:AE:504:GLN:HG3	1.97	0.47
15:AG:75:ILE:HG22	15:AG:76:THR:N	2.30	0.47
17:D:1315:U:H2'	17:D:1316:G:O4'	2.14	0.47
28:NG:12:VAL:HG22	28:NG:92:PHE:CD1	2.49	0.47
28:NG:18:PHE:O	28:NG:22:VAL:HG23	2.15	0.47
41:a:301:G:C6	41:a:317:G:C5	3.03	0.47
41:a:538:A:H2'	41:a:539:G:O4'	2.14	0.47
41:a:1059:G:C6	41:a:1080:A:C6	3.03	0.47
41:a:2661:G:H2'	41:a:2662:A:O4'	2.15	0.47
41:a:2681:C:C2	41:a:2724:U:O4	2.68	0.47
3:2:61:LEU:C	3:2:61:LEU:HD12	2.39	0.47
8:7:12:U:C4'	24:K:56:VAL:HG11	2.45	0.47
13:AE:706:VAL:HG23	13:AE:706:VAL:O	2.15	0.47
17:D:323:U:H2'	17:D:324:G:O4'	2.13	0.47
17:D:868:C:H2'	17:D:869:G:O4'	2.14	0.47
17:D:1139:G:C2	17:D:1141:C:N4	2.83	0.47
28:NG:29:HIS:HE1	28:NG:86:VAL:HA	1.73	0.47
39:Y:48:ILE:HG13	39:Y:49:GLU:N	2.30	0.47
41:a:1051:G:C5	41:a:1052:C:C5	3.03	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:1415:U:O2	41:a:1588:G:C2	2.67	0.47
41:a:1722:A:C2	41:a:1739:A:H1'	2.49	0.47
41:a:2127:G:H2'	41:a:2128:G:C8	2.50	0.47
7:6:1:DT:H4'	7:6:2:DA:O5'	2.15	0.47
11:AA:370:MET:HE3	11:AA:388:LEU:HD11	1.97	0.47
11:AA:905:ILE:HD11	15:AG:5:ILE:CD1	2.41	0.47
11:AA:913:VAL:HG21	15:AG:108:GLN:CD	2.40	0.47
11:AA:1151:LEU:HD12	11:AA:1201:LEU:HD22	1.96	0.47
11:AA:1286:THR:O	11:AA:1290:MET:SD	2.73	0.47
15:AG:25:GLU:HG3	15:AG:49:ILE:HD11	1.96	0.47
15:AG:278:ASP:O	15:AG:279:ASN:O	2.33	0.47
15:AG:339:MET:HA	15:AG:339:MET:HE3	1.96	0.47
17:D:4:U:H2'	17:D:5:U:H2'	1.97	0.47
17:D:936:C:C4	17:D:937:A:N7	2.83	0.47
17:D:1063:C:C4	17:D:1064:G:C5	3.02	0.47
17:D:1087:G:C6	17:D:1099:G:C6	3.02	0.47
17:D:1309:G:C6	17:D:1329:A:N1	2.83	0.47
20:G:50:PHE:CE1	20:G:54:LEU:HD11	2.49	0.47
41:a:572:A:C2	41:a:2033:A:C2	3.02	0.47
41:a:1159:U:C2	41:a:1160:G:C8	3.03	0.47
41:a:1378:A:N3	41:a:1380:G:C8	2.83	0.47
41:a:1584:U:H4'	41:a:1585:C:O5'	2.15	0.47
41:a:2139:U:O2	41:a:2152:G:C6	2.64	0.47
44:d:15:A:O4'	44:d:109:A:C8	2.67	0.47
11:AA:481:LEU:HD21	28:NG:21:ARG:NH2	2.20	0.47
12:AD:192:VAL:HG12	12:AD:193:GLU:H	1.80	0.47
10:B:13:C:H4'	41:a:1924:C:O2'	2.14	0.47
10:B:52:G:C6	10:B:63:G:O6	2.68	0.47
16:C:55:LEU:HD11	16:C:59:ILE:HD11	1.95	0.47
17:D:1124:G:O2'	17:D:1145:A:N6	2.48	0.47
17:D:1327:C:C2	17:D:1328:C:C5	3.03	0.47
23:J:102:VAL:HA	23:J:105:MET:HE2	1.97	0.47
24:K:96:MET:CB	24:K:125:ALA:HB2	2.45	0.47
27:N:75:ILE:HG23	27:N:75:ILE:O	2.15	0.47
33:S:15:ALA:HA	33:S:18:ASP:OD1	2.15	0.47
41:a:690:G:H2'	41:a:691:C:O4'	2.15	0.47
41:a:817:C:H2'	41:a:818:G:O4'	2.15	0.47
41:a:2189:U:O2'	41:a:2190:G:H8	1.98	0.47
44:d:116:G:H2'	44:d:117:G:H8	1.79	0.47
50:j:48:ILE:HG23	50:j:84:LEU:HD11	1.96	0.47
17:D:421:U:O2	17:D:421:U:O4'	2.33	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:D:836:G:C5	17:D:851:G:C6	3.03	0.47
17:D:1501:C:N4	17:D:1504:G:C2	2.83	0.47
20:G:216:ALA:O	20:G:220:THR:HG23	2.14	0.47
38:X:29:ARG:O	38:X:33:ILE:HG12	2.15	0.47
41:a:271:G:C2	41:a:272:A:C5	3.03	0.47
41:a:1165:A:H2'	41:a:1166:G:H8	1.79	0.47
41:a:1506:U:H2'	41:a:1507:C:C5	2.50	0.47
41:a:2698:U:H2'	41:a:2699:C:C6	2.50	0.47
48:h:133:ARG:HG3	58:r:123:ARG:NH2	2.29	0.47
58:r:94:ILE:O	58:r:94:ILE:HG13	2.15	0.47
9:9:56:ARG:H	9:9:56:ARG:HD3	1.79	0.47
10:B:24:U:H2'	10:B:25:C:C1'	2.44	0.47
41:a:1157:G:O2'	46:f:32:ILE:HD11	2.14	0.47
41:a:1664:A:H61	41:a:1996:C:N4	2.12	0.47
44:d:44:G:OP1	47:g:1:MET:SD	2.73	0.47
10:A:21:A:H4'	10:A:21:A:OP1	2.15	0.46
17:D:80:A:C2	17:D:81:A:N7	2.83	0.46
17:D:337:G:H2'	17:D:338:A:C8	2.50	0.46
17:D:455:G:C2	17:D:478:A:N1	2.83	0.46
17:D:1076:U:P	20:G:174:LYS:HZ1	2.38	0.46
28:NG:148:VAL:CA	28:NG:160:VAL:HG22	2.45	0.46
41:a:348:A:H2'	41:a:349:U:O4'	2.15	0.46
41:a:1073:A:C6	41:a:1074:G:C5	3.03	0.46
41:a:1141:U:H4'	41:a:1142:A:O5'	2.15	0.46
41:a:2038:G:H2'	41:a:2039:U:O4'	2.15	0.46
44:d:45:A:C4	44:d:46:A:C8	3.02	0.46
58:r:78:VAL:HG21	58:r:103:VAL:HG22	1.97	0.46
58:r:79:THR:HG23	58:r:145:ASN:ND2	2.30	0.46
58:r:93:SER:OG	58:r:121:VAL:HG13	2.15	0.46
60:t:114:LYS:O	60:t:118:LEU:HD23	2.15	0.46
1:0:10:LYS:HE2	41:a:994:C:O2'	2.14	0.46
11:AA:243:PRO:HB2	11:AA:274:ILE:HG23	1.96	0.46
11:AA:468:LEU:HA	11:AA:471:VAL:HG12	1.97	0.46
13:AE:661:VAL:HG12	13:AE:685:ILE:HD11	1.98	0.46
10:B:15:G:H3'	10:B:15:G:N3	2.30	0.46
16:C:33:ILE:HG23	16:C:33:ILE:O	2.15	0.46
17:D:1000:A:N1	17:D:1041:G:C6	2.83	0.46
21:H:302:GLY:HA2	21:H:342:ILE:O	2.15	0.46
22:I:140:ASN:O	22:I:144:LEU:HD23	2.14	0.46
29:O:111:VAL:O	29:O:111:VAL:HG23	2.14	0.46
41:a:445:C:H2'	41:a:446:G:O4'	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:1678:A:C4	41:a:1679:A:C8	3.03	0.46
44:d:92:C:C2	44:d:93:C:C5	3.03	0.46
10:A:58:A:C2	10:A:61:C:C6	3.03	0.46
15:AG:187:ARG:CB	15:AG:188:PRO:CD	2.94	0.46
16:C:12:ARG:NH2	21:H:268:VAL:HG22	2.30	0.46
17:D:950:U:OP2	38:X:101:ARG:HD2	2.16	0.46
21:H:274:TYR:HA	21:H:335:ILE:HD12	1.98	0.46
30:P:11:LYS:HG2	30:P:71:LEU:HD23	1.97	0.46
41:a:64:A:H2'	41:a:65:U:C6	2.50	0.46
41:a:1196:C:H2'	41:a:1197:G:O4'	2.16	0.46
41:a:1355:G:C2	41:a:1356:G:C8	3.03	0.46
41:a:1422:G:C6	41:a:1577:C:N3	2.84	0.46
41:a:1593:A:H2'	41:a:1594:U:O4'	2.16	0.46
41:a:2125:G:H21	41:a:2174:C:N4	2.14	0.46
41:a:2184:A:H2'	41:a:2185:U:C6	2.51	0.46
41:a:2788:C:H2'	41:a:2789:C:C6	2.50	0.46
65:y:84:ILE:HG22	65:y:85:SER:N	2.30	0.46
1:0:62:GLU:O	1:0:96:VAL:HG23	2.16	0.46
10:A:53:G:C2	10:A:54:U:C5	3.04	0.46
15:AG:341:VAL:HG12	15:AG:345:GLN:OE1	2.16	0.46
17:D:216:U:H2'	17:D:217:C:C6	2.51	0.46
17:D:613:C:H2'	17:D:614:C:C6	2.50	0.46
17:D:865:A:H2'	17:D:866:C:C6	2.50	0.46
17:D:1136:C:O2	17:D:1136:C:O4'	2.33	0.46
20:G:131:LYS:O	20:G:135:LEU:HD23	2.16	0.46
30:P:56:HIS:ND1	30:P:57:VAL:HG12	2.31	0.46
41:a:38:A:H2'	41:a:39:G:O4'	2.16	0.46
41:a:464:U:C4	41:a:788:A:C5	3.02	0.46
41:a:967:U:H2'	41:a:968:C:H6	1.81	0.46
41:a:1831:G:C6	41:a:1832:C:C4	3.03	0.46
48:h:195:VAL:HG22	48:h:196:GLY:H	1.80	0.46
6:5:116:DG:H2''	6:5:117:DT:O2	2.16	0.46
11:AA:131:THR:HG22	11:AA:132:ASP:N	2.31	0.46
11:AA:1287:LEU:HD13	13:AE:1357:ILE:CD1	2.45	0.46
20:G:76:ALA:HB1	20:G:210:VAL:HG11	1.97	0.46
21:H:342:ILE:H	21:H:342:ILE:HD12	1.79	0.46
28:NG:96:THR:HG22	28:NG:99:ARG:O	2.15	0.46
41:a:479:A:H4'	41:a:480:A:OP1	2.15	0.46
44:d:16:G:N2	44:d:69:G:H1'	2.31	0.46
48:h:183:LYS:O	48:h:184:VAL:HG23	2.15	0.46
10:A:13:C:OP1	10:A:13:C:O4'	2.34	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:148:GLN:O	11:AA:453:ILE:HA	2.16	0.46
11:AA:524:ILE:HG21	11:AA:708:VAL:HG13	1.97	0.46
11:AA:1043:ALA:O	11:AA:1046:VAL:HG12	2.16	0.46
13:AE:56:LEU:C	13:AE:56:LEU:HD23	2.40	0.46
17:D:1003:G:H2'	17:D:1003:G:N3	2.31	0.46
28:NG:136:VAL:HG23	28:NG:144:PHE:O	2.16	0.46
30:P:11:LYS:CG	30:P:71:LEU:HD23	2.46	0.46
35:U:6:LEU:HD23	35:U:17:TYR:HB3	1.98	0.46
41:a:849:A:N6	41:a:928:A:H61	2.14	0.46
41:a:1041:G:C6	41:a:1042:G:N7	2.84	0.46
41:a:1510:G:C2	41:a:1511:G:C4	3.04	0.46
41:a:2311:A:N1	54:n:41:GLY:HA3	2.30	0.46
59:s:17:VAL:HG23	59:s:137:PRO:HB2	1.98	0.46
60:t:35:VAL:HG22	60:t:36:GLY:N	2.30	0.46
12:AD:78:ILE:O	12:AD:81:ILE:HG22	2.16	0.46
15:AG:163:LEU:HD21	15:AG:196:PHE:CE1	2.51	0.46
17:D:81:A:C2	17:D:82:G:N7	2.84	0.46
17:D:440:C:C4	17:D:441:A:N7	2.84	0.46
28:NG:29:HIS:HB3	28:NG:82:LEU:HD11	1.98	0.46
28:NG:40:GLY:O	28:NG:41:GLU:HG3	2.16	0.46
28:NG:169:THR:HG22	28:NG:169:THR:O	2.14	0.46
52:l:60:TRP:CD1	52:l:65:THR:HG21	2.51	0.46
58:r:73:ASN:HB2	58:r:108:VAL:HG23	1.97	0.46
1:0:61:ALA:HB2	1:0:98:ILE:HD13	1.97	0.46
10:A:70:G:H2'	10:A:71:C:O4'	2.16	0.46
11:AA:122:VAL:HG21	11:AA:493:ILE:CG2	2.46	0.46
11:AA:204:LEU:HD11	11:AA:365:GLU:HG3	1.98	0.46
13:AE:160:LEU:O	13:AE:165:TYR:HB2	2.16	0.46
17:D:98:A:H2'	17:D:99:C:C6	2.51	0.46
17:D:251:G:C6	17:D:266:G:O6	2.68	0.46
17:D:357:G:C2	17:D:358:U:C5	3.04	0.46
17:D:715:A:H2'	17:D:716:A:C8	2.51	0.46
17:D:1304:G:N2	17:D:1334:G:C6	2.83	0.46
23:J:155:VAL:HG11	23:J:178:MET:CE	2.46	0.46
41:a:1028:A:H2'	41:a:1029:A:C8	2.50	0.46
41:a:1142:A:C4	41:a:1144:A:N7	2.84	0.46
41:a:1385:A:H1'	41:a:1386:C:C6	2.51	0.46
41:a:2596:U:C2'	41:a:2597:G:O5'	2.64	0.46
43:c:6:GLN:O	43:c:71:LEU:HD21	2.16	0.46
50:j:156:PHE:CD1	59:s:81:ILE:HD13	2.51	0.46
11:AA:375:PRO:HG2	28:NG:98:ASP:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:414:ILE:HD12	11:AA:584:TYR:OH	2.16	0.46
13:AE:848:VAL:HG21	13:AE:880:VAL:HG13	1.98	0.46
17:D:1109:C:C2	17:D:1110:A:C8	3.04	0.46
17:D:1415:G:C6	17:D:1486:G:C6	3.04	0.46
28:NG:42:VAL:O	28:NG:42:VAL:HG13	2.15	0.46
36:V:9:GLN:OE1	36:V:58:VAL:HG12	2.16	0.46
41:a:365:U:H2'	41:a:366:C:O4'	2.15	0.46
41:a:1173:U:H4'	41:a:1174:U:OP1	2.15	0.46
41:a:2104:C:N4	41:a:2186:G:C2	2.84	0.46
41:a:2175:C:H2'	41:a:2176:A:C8	2.51	0.46
41:a:2757:A:C6	41:a:2758:A:N7	2.84	0.46
13:AE:502:PRO:HB3	13:AE:506:VAL:CG1	2.46	0.46
13:AE:807:LEU:HD13	13:AE:1255:VAL:CG2	2.46	0.46
15:AG:127:VAL:HG22	15:AG:193:ALA:N	2.31	0.46
15:AG:328:ALA:HA	15:AG:331:LEU:HD12	1.97	0.46
10:B:32:C:O2	10:B:32:C:H2'	2.16	0.46
17:D:39:G:C4	17:D:404:G:N2	2.84	0.46
17:D:80:A:N3	17:D:81:A:C8	2.84	0.46
17:D:1008:U:O2	17:D:1008:U:H2'	2.15	0.46
32:R:86:ARG:HA	32:R:94:ARG:HA	1.98	0.46
41:a:1297:C:H2'	41:a:1298:C:H6	1.81	0.46
47:g:4:ASP:OD1	47:g:5:ILE:N	2.49	0.46
61:u:124:GLY:C	61:u:125:LEU:HD12	2.41	0.46
15:AG:61:ARG:HG3	15:AG:73:LYS:HG2	1.97	0.45
10:B:51:C:N3	10:B:64:G:C6	2.84	0.45
17:D:20:U:H2'	17:D:21:G:C5'	2.46	0.45
17:D:215:C:H2'	17:D:216:U:C6	2.51	0.45
17:D:532:A:H3'	17:D:533:A:C5'	2.46	0.45
18:E:35:VAL:HG22	18:E:50:ALA:CB	2.45	0.45
39:Y:31:GLY:O	39:Y:60:VAL:HG21	2.15	0.45
41:a:510:C:H2'	41:a:511:U:O4'	2.16	0.45
41:a:639:U:H2'	41:a:640:C:C6	2.51	0.45
41:a:752:A:OP1	53:m:1:MET:HE1	2.16	0.45
41:a:1411:U:O2	41:a:1591:A:N1	2.49	0.45
41:a:1792:G:H5''	48:h:204:VAL:HG23	1.98	0.45
41:a:1897:G:H2'	41:a:1898:U:O4'	2.16	0.45
46:f:36:VAL:HG22	46:f:37:GLU:N	2.31	0.45
55:o:34:THR:HG23	55:o:35:LYS:N	2.31	0.45
13:AE:1080:ILE:CD1	13:AE:1115:ILE:HD11	2.47	0.45
15:AG:104:ARG:H	15:AG:104:ARG:HD2	1.80	0.45
17:D:186:C:H2'	17:D:187:G:O4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:D:1130:A:C8	17:D:1146:A:N1	2.84	0.45
17:D:1530:G:H2'	17:D:1531:A:C8	2.51	0.45
21:H:36:VAL:HG12	21:H:37:LEU:N	2.32	0.45
28:NG:13:GLN:CD	28:NG:93:ILE:HD11	2.41	0.45
39:Y:78:LEU:HD12	39:Y:112:LYS:HZ2	1.81	0.45
41:a:150:U:H2'	41:a:151:C:C6	2.51	0.45
41:a:221:A:C2	41:a:266:G:C8	3.05	0.45
41:a:328:U:O2'	41:a:329:G:P	2.74	0.45
41:a:329:G:C2	41:a:477:A:N1	2.84	0.45
41:a:910:A:H62	62:v:12:MET:HA	1.81	0.45
41:a:2229:U:H2'	41:a:2230:G:H8	1.81	0.45
44:d:118:C:C2	44:d:119:A:C8	3.04	0.45
59:s:124:VAL:HG22	59:s:125:TYR:N	2.31	0.45
9:9:4:ASN:O	9:9:7:ASP:OD1	2.34	0.45
11:AA:741:MET:HE2	11:AA:746:ALA:O	2.16	0.45
13:AE:160:LEU:HD11	13:AE:176:PHE:HZ	1.82	0.45
10:B:10:G:H2'	10:B:11:A:C8	2.51	0.45
10:B:68:C:H2'	10:B:69:C:O4'	2.15	0.45
17:D:204:G:C5	17:D:465:A:C6	3.04	0.45
17:D:763:G:H2'	17:D:764:C:C6	2.51	0.45
17:D:934:C:N4	17:D:1345:U:C4	2.84	0.45
28:NG:10:TYR:HA	28:NG:103:ILE:HG13	1.97	0.45
28:NG:140:PRO:HG2	30:P:84:VAL:HG21	1.98	0.45
39:Y:79:LEU:O	39:Y:79:LEU:HD23	2.16	0.45
39:Y:121:ILE:HA	39:Y:124:MET:HE2	1.97	0.45
41:a:80:G:C6	41:a:107:G:C6	3.05	0.45
41:a:303:G:C6	41:a:315:G:C6	3.03	0.45
41:a:323:C:H2'	52:l:163:ASN:OD1	2.15	0.45
41:a:604:G:C6	41:a:625:G:N1	2.84	0.45
41:a:1054:A:C6	41:a:1106:G:C6	3.04	0.45
41:a:1065:U:O2'	41:a:1066:U:P	2.75	0.45
41:a:1594:U:H2'	41:a:1595:C:C6	2.51	0.45
41:a:1856:U:H2'	41:a:1857:G:O4'	2.17	0.45
41:a:2519:U:C4	41:a:2542:A:C5	3.04	0.45
5:4:4:ILE:HG22	5:4:5:ASN:N	2.32	0.45
9:9:77:VAL:O	9:9:82:ILE:HG13	2.16	0.45
10:A:18:G:H21	10:A:57:A:H3'	1.80	0.45
10:A:26:G:N1	10:A:45:G:N2	2.64	0.45
12:AC:79:LEU:HD23	12:AC:83:LEU:HD13	1.99	0.45
17:D:1140:C:HO2'	17:D:1141:C:H6	1.64	0.45
17:D:1145:A:HO2'	17:D:1146:A:P	2.39	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:H:297:GLU:O	21:H:297:GLU:HG2	2.16	0.45
27:N:25:VAL:HG12	27:N:26:THR:N	2.31	0.45
28:NG:11:VAL:CB	28:NG:101:ALA:HB3	2.41	0.45
28:NG:12:VAL:HG22	28:NG:92:PHE:CD2	2.51	0.45
28:NG:114:ARG:HA	28:NG:117:GLN:HG2	1.99	0.45
41:a:620:G:H4'	41:a:621:A:O5'	2.15	0.45
41:a:1013:C:C2	41:a:1014:A:C8	3.04	0.45
41:a:1328:A:O2'	41:a:1329:U:P	2.74	0.45
41:a:1677:A:C4	41:a:1678:A:C8	3.05	0.45
41:a:2176:A:H2'	41:a:2177:C:C6	2.51	0.45
58:r:58:LEU:O	58:r:61:VAL:HG22	2.16	0.45
15:AG:63:LEU:HD12	15:AG:73:LYS:HB3	1.98	0.45
17:D:201:G:H2'	17:D:202:G:C1'	2.46	0.45
28:NG:26:LEU:HB2	28:NG:86:VAL:HG21	1.98	0.45
39:Y:106:GLN:OE1	39:Y:125:THR:HG21	2.17	0.45
41:a:667:U:H2'	41:a:668:A:O4'	2.16	0.45
41:a:1036:G:C5	41:a:1120:G:C6	3.04	0.45
41:a:1169:A:N3	41:a:1169:A:O4'	2.49	0.45
51:k:47:VAL:HG12	51:k:48:ILE:N	2.30	0.45
5:4:1:MET:HE1	5:4:60:VAL:O	2.16	0.45
11:AA:852:ALA:O	11:AA:862:LEU:HD21	2.17	0.45
13:AE:53:ARG:CZ	28:NG:135:ARG:HH21	2.30	0.45
15:AG:61:ARG:HD2	15:AG:63:LEU:HD11	1.98	0.45
15:AG:453:VAL:HG11	15:AG:459:LEU:HD23	1.99	0.45
17:D:580:C:H2'	17:D:581:G:O4'	2.16	0.45
17:D:1176:A:H2'	17:D:1177:G:O4'	2.17	0.45
22:I:15:VAL:HG23	22:I:16:LYS:N	2.32	0.45
28:NG:26:LEU:HD22	28:NG:83:VAL:CG1	2.35	0.45
41:a:280:U:O4	41:a:361:G:N2	2.50	0.45
41:a:563:A:C6	41:a:2018:G:C4	3.05	0.45
41:a:711:G:C6	41:a:721:A:C6	3.05	0.45
41:a:756:A:H2'	41:a:757:G:O4'	2.17	0.45
41:a:825:A:H2'	41:a:826:U:O4'	2.16	0.45
54:n:7:TYR:O	54:n:10:ASP:OD1	2.35	0.45
8:7:3:G:O6	10:B:34:C:N3	2.50	0.45
9:9:123:ILE:O	9:9:123:ILE:HG23	2.16	0.45
11:AA:854:ILE:HG23	11:AA:857:VAL:HG11	1.98	0.45
12:AD:110:VAL:HG13	12:AD:110:VAL:O	2.16	0.45
17:D:41:G:C6	17:D:402:G:C6	3.05	0.45
17:D:106:C:H2'	17:D:107:G:O4'	2.17	0.45
17:D:555:U:H2'	17:D:556:C:H6	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:D:993:G:O2'	17:D:994:A:N7	2.50	0.45
17:D:1032:G:H3'	17:D:1032:G:N3	2.32	0.45
17:D:1316:G:H22	17:D:1319:A:C5'	2.30	0.45
27:N:104:VAL:HG23	27:N:124:GLU:O	2.17	0.45
28:NG:140:PRO:HD3	30:P:79:PRO:HB2	1.99	0.45
30:P:28:THR:HG23	30:P:31:ARG:NH2	2.30	0.45
38:X:46:SER:C	38:X:47:GLU:HG3	2.41	0.45
39:Y:78:LEU:HD12	39:Y:112:LYS:NZ	2.32	0.45
41:a:305:C:H2'	41:a:306:U:C6	2.52	0.45
41:a:2107:G:C6	41:a:2183:A:C6	3.04	0.45
50:j:96:ILE:HG22	50:j:97:SER:N	2.32	0.45
51:k:9:ILE:HD13	51:k:25:LYS:HD2	1.98	0.45
11:AA:377:THR:HG22	11:AA:378:ARG:N	2.32	0.45
11:AA:1066:MET:CG	11:AA:1076:ILE:HD11	2.46	0.45
13:AE:709:ARG:HG2	13:AE:710:ASP:N	2.31	0.45
17:D:235:C:H2'	17:D:236:A:C8	2.51	0.45
17:D:456:A:C6	17:D:457:G:C5	3.04	0.45
17:D:1025:U:H4'	17:D:1026:G:C8	2.51	0.45
17:D:1058:G:H2'	17:D:1059:C:O4'	2.17	0.45
17:D:1278:G:O2'	17:D:1279:G:P	2.74	0.45
17:D:1486:G:H2'	17:D:1487:G:O4'	2.17	0.45
41:a:278:A:O5'	41:a:279:A:P	2.75	0.45
41:a:707:G:C4	41:a:708:G:C8	3.05	0.45
41:a:879:G:C6	41:a:899:A:C2	3.05	0.45
41:a:893:C:C4	41:a:894:U:O4	2.69	0.45
41:a:1000:A:H2'	41:a:1001:A:C8	2.52	0.45
41:a:1416:G:C6	41:a:1583:A:N1	2.84	0.45
41:a:1563:U:H2'	41:a:1564:C:C6	2.52	0.45
41:a:2193:G:O2'	41:a:2194:U:P	2.75	0.45
41:a:2450:A:C2	41:a:2451:A:C4	3.05	0.45
56:p:11:VAL:O	56:p:48:ASN:OD1	2.35	0.45
65:y:26:VAL:HG22	65:y:27:GLU:N	2.31	0.45
1:0:26:ASP:O	1:0:27:ILE:HD13	2.16	0.45
3:2:93:LEU:HD12	3:2:94:ASP:OD1	2.17	0.45
11:AA:498:ILE:H	11:AA:498:ILE:HD12	1.82	0.45
13:AE:844:THR:CG2	13:AE:864:LEU:HD11	2.47	0.45
13:AE:1109:LEU:HD22	13:AE:1115:ILE:HG22	1.99	0.45
15:AG:30:ALA:HB2	15:AG:117:LYS:HG3	1.99	0.45
15:AG:100:VAL:HG12	15:AG:101:THR:N	2.32	0.45
15:AG:187:ARG:HB2	15:AG:188:PRO:CD	2.47	0.45
10:B:48:C:O5'	10:B:59:A:O4'	2.34	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:C:40:VAL:HG11	21:H:339:ARG:CA	2.46	0.45
17:D:688:G:C5	17:D:700:G:C2	3.05	0.45
17:D:690:G:C6	17:D:691:G:C6	3.04	0.45
17:D:718:A:N1	31:Q:118:HIS:HE1	2.14	0.45
19:F:12:PHE:CE2	19:F:16:LEU:HD11	2.51	0.45
28:NG:136:VAL:N	28:NG:144:PHE:O	2.50	0.45
39:Y:14:ALA:HB2	39:Y:54:ILE:HD12	1.99	0.45
39:Y:130:GLY:HA3	41:a:1081:U:H4'	1.99	0.45
41:a:75:G:N3	41:a:75:G:H2'	2.32	0.45
41:a:1186:G:H2'	41:a:1187:G:O4'	2.17	0.45
41:a:1577:C:H2'	41:a:1578:U:C1'	2.46	0.45
41:a:2048:G:C4	41:a:2049:G:C8	3.05	0.45
41:a:2291:U:H2'	41:a:2292:U:C6	2.51	0.45
41:a:2838:G:C4	41:a:2839:G:C8	3.05	0.45
44:d:39:A:C2	44:d:44:G:C2	3.05	0.45
48:h:120:VAL:HG22	48:h:131:PRO:HD2	1.99	0.45
58:r:1:MET:HE3	58:r:26:ALA:HB3	1.97	0.45
64:x:53:THR:O	64:x:59:ALA:HB2	2.17	0.45
11:AA:1119:MET:HB2	11:AA:1228:GLY:HA2	1.99	0.45
12:AC:192:VAL:O	12:AC:193:GLU:CB	2.64	0.45
15:AG:309:VAL:HG12	15:AG:310:GLU:N	2.32	0.45
17:D:1:A:C2'	17:D:2:A:O5'	2.64	0.45
17:D:235:C:H2'	17:D:236:A:H8	1.82	0.45
21:H:284:VAL:HA	21:H:294:VAL:HA	1.99	0.45
30:P:85:ASP:OD1	30:P:85:ASP:C	2.59	0.45
41:a:151:C:H2'	41:a:152:A:H8	1.81	0.45
41:a:545:U:O2'	41:a:546:U:H4'	2.17	0.45
41:a:1084:A:H1'	41:a:1105:U:O2'	2.17	0.45
41:a:1520:U:H2'	41:a:1521:G:O4'	2.17	0.45
41:a:1858:A:C2	41:a:1885:A:O4'	2.70	0.45
41:a:2758:A:C2	41:a:2759:G:N9	2.85	0.45
9:9:73:LYS:HG2	9:9:117:LEU:HD21	1.98	0.44
9:9:78:GLY:N	9:9:79:PRO:HD2	2.33	0.44
11:AA:855:PRO:HG3	11:AA:913:VAL:HG11	1.99	0.44
11:AA:1096:ILE:HG22	11:AA:1098:LEU:HD12	1.99	0.44
12:AC:224:LEU:HD22	12:AD:228:LEU:HD11	1.99	0.44
13:AE:342:LEU:HD23	13:AE:1352:ILE:HG23	1.99	0.44
13:AE:514:THR:HG21	13:AE:579:LEU:HD23	1.99	0.44
15:AG:41:GLN:HG3	15:AG:42:GLU:N	2.32	0.44
10:B:9:G:N3	10:B:46:G:OP1	2.50	0.44
17:D:438:U:C4	17:D:494:G:C5	3.05	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:D:767:A:C4	17:D:768:A:C8	3.06	0.44
23:J:139:PRO:HA	23:J:182:PHE:O	2.16	0.44
27:N:96:MET:CE	27:N:130:ALA:HB1	2.47	0.44
38:X:16:VAL:HG23	38:X:17:ILE:HD12	1.98	0.44
41:a:136:G:C6	41:a:137:U:C4	3.05	0.44
41:a:1432:G:H2'	41:a:1433:A:C8	2.52	0.44
41:a:2189:U:O2'	41:a:2190:G:C5'	2.65	0.44
47:g:59:ARG:O	47:g:62:LYS:HG2	2.18	0.44
9:9:27:VAL:HG23	9:9:83:ALA:HB3	2.00	0.44
12:AD:48:LEU:HD21	13:AE:539:SER:HB3	1.99	0.44
13:AE:160:LEU:HD23	13:AE:164:GLN:HB3	1.98	0.44
13:AE:903:LEU:O	13:AE:904:ALA:CB	2.65	0.44
13:AE:1046:ILE:HG22	13:AE:1061:VAL:HA	1.98	0.44
17:D:74:A:C2	17:D:75:G:C4	3.06	0.44
17:D:151:A:C5	17:D:152:A:C8	3.05	0.44
17:D:592:G:C6	17:D:648:A:C6	3.05	0.44
17:D:745:G:H2'	17:D:746:A:H8	1.81	0.44
17:D:746:A:H2'	17:D:747:A:C1'	2.47	0.44
17:D:978:A:C5	17:D:1319:A:C2	3.05	0.44
17:D:1352:C:H2'	17:D:1353:G:O4'	2.18	0.44
24:K:85:VAL:HG22	24:K:86:LYS:N	2.32	0.44
25:L:42:TRP:CE2	25:L:102:MET:SD	3.10	0.44
28:NG:170:PRO:HG2	30:P:99:GLN:OE1	2.18	0.44
41:a:5:A:H2'	41:a:6:A:H8	1.82	0.44
41:a:1378:A:C2	41:a:1380:G:C8	3.05	0.44
41:a:1386:C:H2'	41:a:1387:A:C8	2.53	0.44
41:a:1789:A:H2'	41:a:1790:C:O4'	2.17	0.44
41:a:2517:C:C2	41:a:2542:A:N6	2.85	0.44
44:d:66:A:H61	44:d:107:G:H3'	1.83	0.44
56:p:24:ILE:HD11	56:p:43:VAL:HG11	1.99	0.44
56:p:133:LEU:HD23	56:p:133:LEU:H	1.82	0.44
3:2:93:LEU:HD12	3:2:94:ASP:N	2.32	0.44
9:9:36:ASP:OD1	9:9:107:GLU:HB3	2.17	0.44
10:A:53:G:C2	10:A:62:C:C2	3.04	0.44
13:AE:510:LEU:HD22	13:AE:601:ILE:HD12	1.99	0.44
15:AG:10:GLU:HA	15:AG:12:VAL:HG22	2.00	0.44
15:AG:63:LEU:O	15:AG:65:VAL:HG23	2.17	0.44
15:AG:239:LYS:O	15:AG:240:THR:HG23	2.18	0.44
17:D:41:G:H2'	17:D:42:G:H8	1.82	0.44
17:D:1306:A:C5	17:D:1332:A:C2	3.06	0.44
17:D:1526:G:C2	17:D:1527:U:C4	3.05	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:NG:26:LEU:HD13	28:NG:83:VAL:CA	2.37	0.44
28:NG:103:ILE:HG23	28:NG:107:GLU:CD	2.42	0.44
41:a:894:U:C4'	41:a:895:U:OP1	2.66	0.44
41:a:1075:C:H2'	41:a:1076:C:C6	2.52	0.44
41:a:1096:A:O2'	41:a:1097:U:O5'	2.32	0.44
41:a:1510:G:H2'	41:a:1511:G:C8	2.52	0.44
54:n:35:THR:O	54:n:36:LEU:HD12	2.18	0.44
60:t:115:ILE:HD12	60:t:115:ILE:H	1.83	0.44
65:y:13:MET:HE2	65:y:55:LEU:N	2.32	0.44
10:A:52:G:N1	10:A:63:G:C6	2.86	0.44
11:AA:253:PHE:CD2	11:AA:254:ASP:O	2.71	0.44
11:AA:557:ARG:HB3	11:AA:587:LEU:HD13	2.00	0.44
13:AE:29:MET:SD	13:AE:29:MET:C	3.01	0.44
13:AE:428:THR:HG23	13:AE:433:GLY:HA3	1.99	0.44
15:AG:248:VAL:HG22	15:AG:273:ILE:HG22	1.99	0.44
17:D:322:C:H2'	17:D:323:U:C6	2.53	0.44
17:D:1127:G:C4	17:D:1128:C:C5	3.05	0.44
21:H:19:ARG:O	21:H:72:LEU:HB2	2.18	0.44
21:H:43:LYS:HZ1	21:H:76:GLU:HB2	1.81	0.44
28:NG:164:ILE:HG13	30:P:88:MET:CA	2.47	0.44
40:Z:20:VAL:O	40:Z:20:VAL:HG12	2.16	0.44
41:a:1045:C:H41	41:a:1111:A:H2'	1.81	0.44
41:a:1619:G:C2	41:a:1620:G:C8	3.05	0.44
41:a:2097:A:N1	41:a:2193:G:C6	2.85	0.44
41:a:2147:A:H3'	41:a:2148:G:O4'	2.17	0.44
41:a:2148:G:H2'	41:a:2149:U:C6	2.53	0.44
6:5:98:DT:N3	6:5:98:DT:H2'	2.30	0.44
9:9:92:ALA:CB	9:9:129:LEU:HD22	2.48	0.44
9:9:92:ALA:O	9:9:95:LEU:HD23	2.17	0.44
11:AA:1076:ILE:HD12	11:AA:1076:ILE:H	1.82	0.44
12:AD:64:VAL:HG11	12:AD:78:ILE:HD13	1.98	0.44
17:D:1099:G:H2'	17:D:1100:C:O4'	2.18	0.44
17:D:1276:G:O2'	17:D:1282:C:O4'	2.36	0.44
26:M:50:LEU:HD22	26:M:124:LEU:HB3	1.99	0.44
28:NG:11:VAL:CG2	28:NG:101:ALA:HB3	2.46	0.44
28:NG:149:GLU:OE2	28:NG:161:SER:HB2	2.18	0.44
34:T:21:ASP:O	34:T:22:THR:CG2	2.61	0.44
37:W:49:ILE:HG23	37:W:49:ILE:O	2.17	0.44
40:Z:6:GLN:O	40:Z:10:ALA:HB3	2.17	0.44
41:a:278:A:H2'	41:a:362:A:H1'	1.99	0.44
41:a:281:C:H2'	41:a:282:A:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:1087:G:C6	41:a:1089:A:C2	3.06	0.44
41:a:1413:A:H2'	41:a:1414:C:O4'	2.17	0.44
41:a:1461:C:H2'	41:a:1462:C:H6	1.82	0.44
41:a:2302:U:O2	54:n:123:ASP:OD1	2.35	0.44
41:a:2687:U:H2'	41:a:2688:G:O4'	2.18	0.44
41:a:2834:G:H2'	41:a:2879:A:H61	1.81	0.44
54:n:130:MET:HE1	54:n:132:VAL:HG23	1.99	0.44
8:7:4:U:N3	17:D:1501:C:C4	2.86	0.44
13:AE:952:VAL:HG12	13:AE:1015:GLU:O	2.18	0.44
15:AG:65:VAL:O	15:AG:75:ILE:O	2.36	0.44
17:D:188:C:H2'	17:D:189:A:O4'	2.17	0.44
17:D:1522:U:H2'	17:D:1523:G:H8	1.82	0.44
21:H:76:GLU:C	21:H:78:GLY:H	2.26	0.44
41:a:282:A:N6	41:a:359:G:O6	2.50	0.44
41:a:584:C:N4	41:a:585:G:O6	2.50	0.44
41:a:846:U:H6	41:a:848:C:H41	1.65	0.44
41:a:1073:A:H2'	41:a:1074:G:O4'	2.17	0.44
41:a:1321:A:C4	41:a:1322:A:C8	3.05	0.44
41:a:2308:G:O6	41:a:2311:A:N7	2.50	0.44
47:g:59:ARG:HH12	47:g:63:ARG:HD2	1.81	0.44
61:u:76:GLU:HB2	61:u:111:ILE:HD13	1.99	0.44
10:A:41:C:H2'	10:A:42:G:C8	2.52	0.44
13:AE:78:LEU:HD11	15:AG:144:LYS:HE2	2.00	0.44
13:AE:135:ILE:CD1	13:AE:185:ILE:HD12	2.47	0.44
28:NG:29:HIS:HB2	28:NG:82:LEU:HD11	1.99	0.44
32:R:24:LEU:HD12	32:R:27:CYS:O	2.18	0.44
38:X:22:ILE:O	38:X:25:VAL:HG12	2.17	0.44
39:Y:16:MET:HE1	39:Y:18:ASN:O	2.17	0.44
41:a:81:G:H2'	41:a:82:U:O4'	2.17	0.44
41:a:282:A:H2'	41:a:283:G:C8	2.53	0.44
41:a:819:A:C4	41:a:1189:A:C2	3.05	0.44
41:a:1095:A:O2'	41:a:1096:A:C8	2.69	0.44
41:a:1196:C:C2	41:a:1197:G:C8	3.05	0.44
41:a:1289:C:H2'	41:a:1290:C:H6	1.82	0.44
41:a:1356:G:C6	41:a:1357:C:C4	3.06	0.44
41:a:1591:A:C6	41:a:1592:C:C4	3.06	0.44
41:a:2346:A:H4'	41:a:2347:C:OP2	2.18	0.44
48:h:141:VAL:CG1	48:h:190:ALA:HB1	2.48	0.44
51:k:43:VAL:O	51:k:43:VAL:HG12	2.16	0.44
58:r:8:LYS:HD2	58:r:9:VAL:N	2.33	0.44
5:4:77:VAL:HG13	5:4:77:VAL:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:24:U:H2'	10:A:25:C:C6	2.52	0.44
11:AA:1064:ASP:HB2	11:AA:1076:ILE:HD13	1.99	0.44
12:AD:47:LEU:CD1	12:AD:205:MET:HE1	2.48	0.44
13:AE:423:LEU:HD23	13:AE:466:MET:SD	2.58	0.44
15:AG:31:LEU:HD21	15:AG:114:ILE:HD11	2.00	0.44
15:AG:379:SER:OG	15:AG:384:LEU:HD11	2.18	0.44
17:D:32:A:H2'	17:D:33:A:C8	2.52	0.44
17:D:189:A:H2'	17:D:190:A:O4'	2.17	0.44
17:D:598:U:C2	17:D:599:C:C5	3.06	0.44
17:D:674:G:O2'	17:D:675:A:H5'	2.17	0.44
17:D:815:A:H4'	17:D:817:C:C5	2.53	0.44
17:D:953:G:C6	17:D:1229:A:C6	3.06	0.44
21:H:72:LEU:O	21:H:73:ASP:HB2	2.18	0.44
22:I:131:ARG:HA	22:I:134:MET:HE3	2.00	0.44
25:L:51:ILE:O	25:L:54:LEU:HD23	2.18	0.44
37:W:64:ASP:OD1	37:W:65:GLU:N	2.51	0.44
41:a:263:G:H2'	41:a:264:C:O4'	2.18	0.44
41:a:299:A:N1	41:a:322:A:C4	2.86	0.44
41:a:1036:G:C6	41:a:1120:G:C6	3.06	0.44
41:a:2531:A:C4	41:a:2532:G:C8	3.05	0.44
51:k:54:ILE:HG23	51:k:55:LYS:N	2.32	0.44
11:AA:925:SER:O	11:AA:1056:VAL:HG22	2.18	0.44
12:AC:78:ILE:HD13	12:AC:81:ILE:HD12	2.00	0.44
12:AD:140:ILE:HG23	12:AD:140:ILE:O	2.17	0.44
13:AE:587:LEU:HD11	13:AE:608:CYS:HA	1.99	0.44
10:B:12:G:C2'	10:B:13:C:OP1	2.65	0.44
10:B:71:C:O3'	10:B:72:A:O4'	2.34	0.44
17:D:148:G:H2'	17:D:149:A:O4'	2.17	0.44
17:D:389:A:H3'	17:D:390:U:H6	1.83	0.44
17:D:524:G:C2	17:D:525:C:C4	3.05	0.44
17:D:611:C:C2	17:D:612:C:C6	3.06	0.44
20:G:54:LEU:HD22	20:G:220:THR:HG21	2.00	0.44
39:Y:124:MET:O	39:Y:128:ILE:HG12	2.18	0.44
41:a:418:C:H2'	41:a:419:U:C6	2.52	0.44
41:a:2109:U:O3'	41:a:2110:G:O4'	2.34	0.44
41:a:2220:U:H2'	41:a:2221:G:C8	2.52	0.44
9:9:31:ARG:NE	41:a:1053:C:O3'	2.51	0.43
10:A:31:G:H2'	10:A:32:C:O4'	2.18	0.43
11:AA:805:MET:SD	11:AA:1225:VAL:HG21	2.58	0.43
11:AA:847:PRO:CB	11:AA:1047:LEU:HD11	2.47	0.43
11:AA:1253:LEU:HD22	13:AE:251:PRO:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AE:1080:ILE:HD12	13:AE:1115:ILE:HD11	1.99	0.43
13:AE:1231:ARG:HA	13:AE:1234:VAL:HG22	2.00	0.43
17:D:151:A:N7	17:D:170:U:C2	2.86	0.43
17:D:269:C:H2'	17:D:270:A:C8	2.53	0.43
17:D:363:A:C2'	17:D:364:A:O5'	2.66	0.43
17:D:459:A:H2'	17:D:460:A:O4'	2.19	0.43
17:D:642:A:C6	17:D:643:C:C4	3.06	0.43
20:G:20:THR:O	20:G:22:TYR:N	2.51	0.43
22:I:73:PRO:HB3	22:I:103:ILE:HG21	2.00	0.43
28:NG:33:HIS:O	28:NG:34:ASN:OD1	2.36	0.43
28:NG:75:MET:CE	28:NG:100:PRO:HG3	2.41	0.43
28:NG:144:PHE:HZ	30:P:85:ASP:HB3	1.82	0.43
39:Y:45:THR:O	39:Y:45:THR:HG22	2.17	0.43
41:a:25:U:C2'	41:a:26:G:O5'	2.66	0.43
41:a:1588:G:C6	41:a:1589:U:O4	2.71	0.43
41:a:2842:G:C6	41:a:2876:G:C6	3.06	0.43
44:d:28:C:C2	44:d:29:A:C8	3.06	0.43
56:p:117:LEU:HD21	56:p:123:ALA:HB2	1.99	0.43
56:p:121:ILE:CD1	56:p:144:VAL:HG21	2.47	0.43
60:t:53:LYS:HD2	60:t:54:LYS:O	2.18	0.43
64:x:83:LEU:HD23	64:x:83:LEU:C	2.43	0.43
11:AA:400:VAL:HG11	11:AA:452:ARG:HD2	2.00	0.43
12:AD:31:LEU:HD21	12:AD:39:LEU:HD12	2.00	0.43
13:AE:291:ILE:HD12	28:NG:65:PHE:CZ	2.53	0.43
15:AG:300:GLU:O	15:AG:301:ASP:C	2.62	0.43
17:D:309:A:H2'	17:D:310:G:H8	1.83	0.43
17:D:678:U:H2'	17:D:679:C:O4'	2.17	0.43
17:D:1002:G:C6	17:D:1039:G:C6	3.06	0.43
25:L:40:GLU:CD	25:L:103:VAL:HG21	2.43	0.43
28:NG:43:MET:HE3	28:NG:111:ILE:CD1	2.47	0.43
28:NG:144:PHE:CZ	30:P:85:ASP:HB3	2.53	0.43
37:W:50:ALA:HB1	37:W:57:HIS:HB3	2.01	0.43
38:X:22:ILE:HB	38:X:25:VAL:HG11	2.00	0.43
41:a:289:G:H2'	41:a:290:U:O4'	2.18	0.43
41:a:396:G:C6	41:a:397:U:C4	3.05	0.43
41:a:1096:A:C2'	41:a:1097:U:O4'	2.66	0.43
41:a:1670:C:H2'	41:a:1671:U:O4'	2.17	0.43
41:a:1845:G:C6	41:a:1896:G:C6	3.06	0.43
41:a:2259:U:C6	41:a:2427:C:C4	3.06	0.43
41:a:2513:A:C5	41:a:2574:G:N1	2.85	0.43
41:a:2799:A:C2	41:a:2801:G:C4	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:d:2:G:C6	44:d:119:A:C6	3.07	0.43
47:g:59:ARG:HA	47:g:62:LYS:HE3	2.00	0.43
54:n:7:TYR:CE1	54:n:11:GLU:OE1	2.71	0.43
61:u:111:ILE:HG22	61:u:112:LEU:N	2.33	0.43
11:AA:748:ILE:HG13	11:AA:748:ILE:O	2.17	0.43
12:AC:99:ILE:HG23	12:AC:99:ILE:O	2.19	0.43
13:AE:755:ILE:HG22	13:AE:757:THR:H	1.84	0.43
10:B:38:A:C4	10:B:39:C:C6	3.06	0.43
17:D:255:G:C2	17:D:272:C:C2	3.06	0.43
17:D:1320:C:H41	37:W:37:ARG:HB3	1.83	0.43
23:J:129:VAL:O	23:J:129:VAL:HG13	2.19	0.43
28:NG:47:GLU:OE1	28:NG:118:VAL:HG11	2.18	0.43
30:P:67:ILE:O	30:P:67:ILE:HG13	2.18	0.43
37:W:42:PRO:O	37:W:45:ILE:HG12	2.19	0.43
41:a:1175:A:OP1	41:a:1177:G:H1'	2.18	0.43
41:a:1532:A:C6	41:a:1540:G:C6	3.06	0.43
41:a:1589:U:HO2'	41:a:1590:A:P	2.41	0.43
41:a:1972:G:C2	41:a:1973:G:N7	2.86	0.43
41:a:2852:G:H2'	41:a:2853:C:O4'	2.18	0.43
44:d:95:U:H2'	44:d:96:G:C8	2.53	0.43
59:s:73:VAL:HG12	59:s:74:TYR:N	2.32	0.43
2:1:81:SER:HB3	2:1:97:LEU:HD12	2.00	0.43
6:5:97:DG:H2''	6:5:98:DT:O5'	2.18	0.43
15:AG:214:PRO:O	15:AG:218:GLU:OE1	2.35	0.43
17:D:361:G:H2'	17:D:362:G:O4'	2.18	0.43
17:D:363:A:O2'	17:D:364:A:H5'	2.19	0.43
17:D:472:U:H2'	17:D:473:U:C6	2.53	0.43
17:D:1009:U:O2	17:D:1021:A:C2	2.71	0.43
17:D:1288:A:H2'	17:D:1289:A:O4'	2.18	0.43
22:I:66:VAL:HG12	22:I:67:THR:N	2.32	0.43
41:a:36:G:C6	41:a:37:C:C4	3.06	0.43
41:a:553:G:C5	41:a:554:U:C5	3.07	0.43
41:a:2039:U:H2'	41:a:2040:G:H8	1.84	0.43
41:a:2799:A:C4	41:a:2801:G:C8	3.07	0.43
44:d:29:A:H2'	44:d:30:C:O4'	2.19	0.43
48:h:175:ARG:HG3	48:h:181:MET:HE1	2.00	0.43
58:r:99:ILE:O	58:r:103:VAL:HG23	2.19	0.43
8:7:4:U:N3	17:D:1500:A:C6	2.87	0.43
10:A:7:G:H4'	10:A:8:U:OP2	2.18	0.43
11:AA:127:ILE:O	11:AA:127:ILE:HG13	2.19	0.43
11:AA:148:GLN:HA	11:AA:531:SER:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:753:LEU:HD21	11:AA:784:ALA:HB1	2.00	0.43
13:AE:313:GLY:O	13:AE:314:ARG:C	2.62	0.43
10:B:6:G:C4	10:B:7:G:C8	3.06	0.43
17:D:691:G:H2'	17:D:692:U:C6	2.54	0.43
17:D:826:C:H2'	17:D:827:U:C6	2.54	0.43
17:D:926:G:C6	17:D:1505:G:C6	3.06	0.43
17:D:1035:A:C2	17:D:1036:A:C8	3.06	0.43
17:D:1140:C:O2'	17:D:1141:C:O5'	2.37	0.43
28:NG:16:SER:HA	28:NG:67:GLY:CA	2.48	0.43
37:W:40:ILE:H	37:W:40:ILE:HD12	1.82	0.43
39:Y:58:ILE:HG23	39:Y:66:PHE:CD2	2.53	0.43
41:a:582:A:C4	41:a:583:G:C8	3.07	0.43
41:a:767:U:H2'	41:a:768:G:H8	1.83	0.43
41:a:947:A:H2'	41:a:948:C:C6	2.54	0.43
41:a:1056:G:C2	41:a:1104:C:N4	2.87	0.43
41:a:2720:U:C6	41:a:2872:A:N6	2.86	0.43
41:a:2748:A:C2	41:a:2757:A:C6	3.07	0.43
41:a:2789:C:N4	41:a:2893:A:C2	2.86	0.43
61:u:120:VAL:HG12	61:u:121:THR:N	2.33	0.43
4:3:86:ARG:HG3	4:3:88:GLU:HG2	2.00	0.43
9:9:129:LEU:N	9:9:130:PRO:CD	2.82	0.43
11:AA:808:ASN:H	13:AE:633:ALA:HB2	1.84	0.43
13:AE:553:THR:HG22	13:AE:555:TYR:HE1	1.84	0.43
17:D:74:A:N1	17:D:97:G:C6	2.86	0.43
17:D:158:G:C6	17:D:164:G:C5	3.06	0.43
17:D:722:G:C6	17:D:724:G:C4	3.06	0.43
17:D:728:A:C8	34:T:54:ARG:CZ	3.01	0.43
17:D:1082:A:C6	17:D:1083:U:C4	3.06	0.43
17:D:1149:C:O5'	17:D:1149:C:H6	2.02	0.43
21:H:304:VAL:HG22	21:H:344:LEU:C	2.43	0.43
28:NG:39:PHE:CE2	28:NG:82:LEU:HD23	2.54	0.43
35:U:42:ILE:O	35:U:42:ILE:HG22	2.19	0.43
38:X:55:THR:O	38:X:59:GLU:OE1	2.36	0.43
41:a:858:G:C4	41:a:2268:A:C2	3.07	0.43
41:a:881:G:C6	41:a:882:G:C5	3.07	0.43
41:a:1087:G:N1	41:a:1090:A:N6	2.67	0.43
41:a:1792:G:C5'	48:h:204:VAL:HG23	2.48	0.43
41:a:2186:G:H2'	41:a:2187:U:C6	2.53	0.43
41:a:2514:U:H2'	41:a:2515:C:H6	1.83	0.43
41:a:2748:A:C2	41:a:2757:A:C5	3.07	0.43
58:r:133:GLN:HG3	58:r:133:GLN:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:71:C:H3'	10:A:72:A:H8	1.83	0.43
11:AA:35:PHE:O	11:AA:39:ILE:HG22	2.19	0.43
11:AA:127:ILE:HG22	11:AA:502:VAL:HG21	2.00	0.43
11:AA:575:LEU:HD21	11:AA:579:ALA:O	2.19	0.43
13:AE:1161:GLY:HA3	13:AE:1179:PRO:HA	2.00	0.43
10:B:47:U:O3'	10:B:48:C:H4'	2.19	0.43
10:B:56:C:OP1	10:B:56:C:H6	2.02	0.43
17:D:83:C:O2'	17:D:86:G:O6	2.36	0.43
17:D:376:G:C2	17:D:389:A:C2	3.06	0.43
17:D:506:G:H2'	17:D:507:C:O4'	2.18	0.43
17:D:695:A:H2'	17:D:696:A:O4'	2.18	0.43
17:D:1000:A:H2'	17:D:1001:C:O4'	2.19	0.43
17:D:1328:C:O2'	17:D:1329:A:H5'	2.19	0.43
17:D:1412:C:C2	17:D:1489:G:N2	2.87	0.43
20:G:23:TRP:CD1	20:G:39:HIS:HE1	2.37	0.43
21:H:324:VAL:HG23	21:H:324:VAL:O	2.19	0.43
24:K:138:ARG:O	24:K:141:ILE:HG22	2.18	0.43
25:L:18:VAL:HG12	25:L:22:ILE:CD1	2.49	0.43
28:NG:9:TRP:CG	28:NG:108:VAL:HG21	2.54	0.43
39:Y:10:LEU:HD21	39:Y:23:VAL:CG2	2.49	0.43
41:a:627:A:H4'	41:a:628:G:OP1	2.18	0.43
41:a:947:A:C6	41:a:971:G:N1	2.87	0.43
41:a:1048:A:H2'	41:a:1048:A:N3	2.33	0.43
41:a:1289:C:C2	41:a:1290:C:C5	3.07	0.43
41:a:1737:G:O3'	41:a:1738:G:O4'	2.36	0.43
41:a:2134:A:N6	41:a:2157:G:O2'	2.51	0.43
41:a:2794:C:O2	41:a:2794:C:H2'	2.19	0.43
15:AG:29:SER:HA	15:AG:43:ILE:HD12	2.00	0.43
15:AG:38:LYS:O	15:AG:39:TYR:O	2.37	0.43
17:D:58:C:O2	17:D:58:C:H2'	2.19	0.43
17:D:162:A:H2'	17:D:163:C:O4'	2.19	0.43
17:D:455:G:N1	17:D:456:A:C5	2.86	0.43
17:D:524:G:H2'	17:D:525:C:C6	2.53	0.43
17:D:690:G:H2'	17:D:691:G:C8	2.54	0.43
17:D:1012:A:H2'	17:D:1013:G:O4'	2.17	0.43
17:D:1077:G:N1	17:D:1081:A:C6	2.87	0.43
17:D:1258:G:H2'	17:D:1259:C:C6	2.53	0.43
17:D:1357:A:H2'	17:D:1358:U:O4'	2.19	0.43
21:H:62:ILE:O	21:H:62:ILE:HG13	2.18	0.43
23:J:50:ASP:O	23:J:53:VAL:HG22	2.18	0.43
25:L:16:GLU:O	25:L:19:PRO:HD2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:NG:21:ARG:NH2	28:NG:87:PRO:HG2	2.34	0.43
29:O:55:VAL:HG13	29:O:55:VAL:O	2.17	0.43
41:a:1048:A:C2	41:a:1049:C:C5	3.06	0.43
41:a:1198:U:H2'	41:a:1199:U:C6	2.54	0.43
41:a:1387:A:C6	41:a:1401:G:N1	2.87	0.43
41:a:1582:C:O5'	41:a:1583:A:OP2	2.37	0.43
41:a:1774:C:O2	41:a:1774:C:H2'	2.17	0.43
41:a:2804:U:H2'	41:a:2805:C:H6	1.84	0.43
11:AA:1223:ARG:O	11:AA:1224:PRO:C	2.62	0.43
13:AE:102:MET:HB2	13:AE:244:VAL:O	2.19	0.43
13:AE:108:ALA:HB3	13:AE:279:LEU:HD22	2.01	0.43
13:AE:114:ILE:HD11	13:AE:311:ARG:HB3	2.01	0.43
13:AE:663:GLU:O	13:AE:667:GLN:HG3	2.19	0.43
10:B:38:A:C5	10:B:39:C:C5	3.06	0.43
16:C:13:PHE:HB3	16:C:18:VAL:HG12	2.01	0.43
17:D:94:G:N1	17:D:98:A:C2	2.87	0.43
17:D:309:A:C2	17:D:310:G:N7	2.87	0.43
17:D:575:G:H4'	17:D:576:C:H5''	2.01	0.43
17:D:689:C:C2	17:D:690:G:C8	3.07	0.43
17:D:718:A:C2	31:Q:118:HIS:CE1	3.07	0.43
17:D:872:A:C2	17:D:874:G:C6	3.07	0.43
17:D:925:G:C2	17:D:927:G:C8	3.06	0.43
17:D:1088:G:H2'	17:D:1089:G:O4'	2.19	0.43
17:D:1129:C:C2	17:D:1139:G:C6	3.06	0.43
17:D:1163:A:C6	17:D:1174:G:C6	3.07	0.43
17:D:1316:G:H22	17:D:1319:A:H5''	1.83	0.43
17:D:1386:G:C2	17:D:1387:G:C8	3.06	0.43
17:D:1435:G:H2'	17:D:1436:U:C6	2.54	0.43
21:H:61:GLU:HG2	21:H:62:ILE:HG23	2.01	0.43
24:K:133:PRO:HA	24:K:136:VAL:HG12	2.01	0.43
28:NG:80:TRP:CD1	28:NG:92:PHE:CD2	3.07	0.43
30:P:65:TYR:CB	33:S:96:LEU:HD11	2.48	0.43
37:W:15:LEU:HD21	37:W:33:THR:OG1	2.19	0.43
41:a:329:G:C2	41:a:477:A:C2	3.07	0.43
41:a:545:U:O2'	41:a:547:A:C5'	2.67	0.43
41:a:1066:U:H2'	41:a:1067:A:H2'	1.99	0.43
41:a:1108:U:C2'	41:a:1109:C:O5'	2.67	0.43
41:a:1141:U:P	59:s:65:THR:HG21	2.59	0.43
41:a:1459:G:C2	41:a:1461:C:C2	3.07	0.43
41:a:1921:G:C2	41:a:1922:G:N7	2.87	0.43
52:l:4:VAL:HG22	52:l:5:LEU:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:30:ILE:HG21	3:2:93:LEU:CD2	2.49	0.43
8:7:53:C:O2	8:7:53:C:O5'	2.37	0.43
9:9:73:LYS:CG	9:9:117:LEU:HD21	2.48	0.43
11:AA:1119:MET:HG3	11:AA:1204:LEU:HD13	2.01	0.43
11:AA:1157:GLN:HG3	11:AA:1159:VAL:HG13	2.01	0.43
13:AE:143:SER:HA	13:AE:161:THR:HA	2.00	0.43
13:AE:368:LEU:HD11	13:AE:421:VAL:HG21	2.01	0.43
15:AG:130:PHE:HE1	15:AG:158:ALA:HB1	1.84	0.43
17:D:71:A:C6	17:D:100:G:C8	3.07	0.43
17:D:945:G:C2	17:D:946:A:C8	3.07	0.43
17:D:958:A:H1'	17:D:985:C:O2'	2.19	0.43
28:NG:45:PRO:HG3	28:NG:111:ILE:HG23	2.00	0.43
30:P:32:THR:HG21	30:P:86:ALA:HB2	2.01	0.43
41:a:75:G:C2	41:a:76:C:C5	3.07	0.43
41:a:607:U:O2	41:a:608:A:C8	2.72	0.43
41:a:1790:C:O3'	41:a:1791:A:C8	2.72	0.43
41:a:2124:G:C2	41:a:2125:G:H1'	2.54	0.43
41:a:2744:G:C6	41:a:2745:C:N4	2.87	0.43
56:p:76:VAL:HA	56:p:79:VAL:HG22	2.01	0.43
56:p:83:PHE:HB2	56:p:141:ILE:HD13	1.99	0.43
9:9:80:THR:HA	41:a:1108:U:C5'	2.49	0.42
12:AC:149:GLY:HA3	12:AC:177:TYR:CE2	2.54	0.42
13:AE:885:VAL:HG13	13:AE:894:VAL:HG21	2.00	0.42
13:AE:1328:THR:CG2	13:AE:1332:LEU:HD13	2.47	0.42
16:C:39:ILE:H	16:C:39:ILE:HD12	1.83	0.42
17:D:80:A:C2	17:D:90:C:N3	2.87	0.42
17:D:123:U:C2	17:D:124:C:C5	3.08	0.42
17:D:573:A:H2'	17:D:574:A:O4'	2.19	0.42
17:D:1283:U:H2'	17:D:1284:C:O4'	2.19	0.42
17:D:1333:A:H2'	17:D:1334:G:O4'	2.19	0.42
21:H:336:ASP:O	21:H:340:ARG:N	2.52	0.42
41:a:26:G:H2'	41:a:27:G:O4'	2.19	0.42
41:a:983:A:N6	41:a:984:A:N6	2.67	0.42
41:a:1042:G:C5	41:a:1043:C:C5	3.07	0.42
41:a:1087:G:C6	41:a:1103:A:N6	2.87	0.42
41:a:1096:A:H2'	41:a:1097:U:O4'	2.19	0.42
41:a:1257:C:C2	41:a:1258:U:C5	3.07	0.42
41:a:1406:U:C2	41:a:1407:G:C8	3.07	0.42
41:a:1533:C:C2'	41:a:1534:U:O5'	2.67	0.42
41:a:2133:G:O2'	41:a:2157:G:N2	2.52	0.42
41:a:2199:A:C4	41:a:2225:A:C2	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:2685:G:H2'	41:a:2686:G:H8	1.84	0.42
41:a:2803:G:C2	41:a:2804:U:C4	3.07	0.42
41:a:2811:G:H2'	41:a:2812:G:O4'	2.18	0.42
44:d:27:C:C4	44:d:28:C:C4	3.07	0.42
9:9:118:ILE:HB	9:9:119:PRO:HD3	2.00	0.42
10:A:20:U:H3'	10:A:21:A:H5''	2.00	0.42
11:AA:253:PHE:CZ	11:AA:255:ILE:HG12	2.53	0.42
11:AA:1109:ILE:HD11	13:AE:644:MET:HE3	2.01	0.42
11:AA:1243:MET:SD	11:AA:1243:MET:C	3.02	0.42
13:AE:45:ASN:HB2	13:AE:50:LYS:HG3	2.02	0.42
15:AG:11:ALA:N	15:AG:12:VAL:HG22	2.34	0.42
15:AG:49:ILE:O	15:AG:49:ILE:HG22	2.17	0.42
17:D:459:A:H2'	17:D:460:A:C8	2.54	0.42
17:D:496:A:O2'	17:D:497:G:N7	2.52	0.42
17:D:676:A:H2'	17:D:677:U:H6	1.83	0.42
17:D:718:A:C2	31:Q:118:HIS:HE1	2.37	0.42
17:D:1151:A:O2'	17:D:1152:A:H8	2.02	0.42
17:D:1365:G:C6	17:D:1366:C:C4	3.08	0.42
19:F:58:LYS:O	19:F:62:ARG:HG3	2.20	0.42
28:NG:29:HIS:CE1	28:NG:87:PRO:HD2	2.52	0.42
28:NG:35:MET:CE	28:NG:38:LEU:HD12	2.50	0.42
28:NG:35:MET:SD	28:NG:39:PHE:HE2	2.41	0.42
28:NG:77:ASP:OD1	28:NG:81:HIS:HE1	2.02	0.42
28:NG:103:ILE:CG2	28:NG:108:VAL:HG22	2.48	0.42
29:O:28:ILE:HG21	29:O:35:LEU:HD12	2.00	0.42
39:Y:60:VAL:HB	39:Y:66:PHE:HB3	2.01	0.42
41:a:271:G:C6	41:a:367:G:C6	3.07	0.42
41:a:398:C:H2'	41:a:399:U:O5'	2.19	0.42
41:a:960:A:C8	41:a:962:G:C8	3.07	0.42
41:a:1064:C:N4	41:a:1069:A:O2'	2.52	0.42
41:a:1090:A:N1	41:a:1102:C:C2	2.87	0.42
41:a:1268:A:H2'	41:a:1269:A:O4'	2.19	0.42
41:a:1473:G:C6	41:a:1519:G:N1	2.87	0.42
41:a:2412:A:H2'	41:a:2413:G:O4'	2.19	0.42
41:a:2513:A:C6	41:a:2574:G:C6	3.07	0.42
41:a:2839:G:H2'	41:a:2840:C:H6	1.84	0.42
43:c:33:LEU:O	43:c:34:HIS:CG	2.73	0.42
47:g:5:ILE:HG13	47:g:6:HIS:N	2.34	0.42
50:j:177:VAL:O	50:j:177:VAL:HG13	2.18	0.42
64:x:26:LEU:HD13	64:x:39:VAL:HG22	2.01	0.42
9:9:126:LEU:HD13	9:9:128:THR:OG1	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:143:ARG:NH1	11:AA:507:GLY:O	2.53	0.42
11:AA:477:GLU:O	11:AA:481:LEU:HD13	2.20	0.42
13:AE:161:THR:O	13:AE:164:GLN:N	2.52	0.42
10:B:76:A:H2'	10:B:76:A:N3	2.35	0.42
17:D:1149:C:H2'	17:D:1150:A:H8	1.84	0.42
17:D:1246:A:C6	17:D:1292:G:C6	3.08	0.42
27:N:11:LEU:HD12	27:N:77:ARG:CD	2.49	0.42
28:NG:103:ILE:HG22	28:NG:107:GLU:HG3	2.00	0.42
34:T:7:ALA:O	34:T:11:ILE:HG12	2.19	0.42
41:a:156:A:H2'	41:a:157:C:O4'	2.19	0.42
41:a:839:U:O2'	41:a:1191:G:H1'	2.19	0.42
41:a:1082:U:O5'	41:a:1082:U:H6	2.02	0.42
41:a:1106:G:C4	41:a:1107:G:C8	3.07	0.42
41:a:1485:U:C2	41:a:1505:A:C2	3.07	0.42
41:a:1590:A:C2	41:a:1591:A:C6	3.07	0.42
41:a:2174:C:C2	41:a:2175:C:C6	3.07	0.42
41:a:2858:C:C2'	41:a:2859:G:O5'	2.68	0.42
43:c:68:LEU:HD22	43:c:78:TYR:CE1	2.54	0.42
48:h:204:VAL:O	48:h:204:VAL:HG13	2.20	0.42
64:x:40:ILE:HG22	64:x:41:ALA:O	2.20	0.42
66:z:58:ARG:O	66:z:62:ILE:HG12	2.19	0.42
3:2:56:GLU:OE1	3:2:56:GLU:C	2.63	0.42
15:AG:183:LEU:HD21	15:AG:195:LEU:HB3	2.01	0.42
16:C:40:VAL:HG11	21:H:339:ARG:HA	2.02	0.42
17:D:74:A:C4	17:D:75:G:C8	3.08	0.42
17:D:197:A:H1'	17:D:198:G:OP2	2.20	0.42
17:D:406:G:C5	17:D:495:A:C5	3.07	0.42
17:D:496:A:C2'	17:D:496:A:N3	2.81	0.42
17:D:1320:C:C4	17:D:1321:U:C4	3.08	0.42
17:D:1410:A:N6	17:D:1491:G:O6	2.52	0.42
20:G:19:GLN:OE1	20:G:22:TYR:CE2	2.72	0.42
21:H:305:HIS:CG	21:H:306:VAL:N	2.88	0.42
21:H:341:ARG:O	21:H:341:ARG:HG2	2.19	0.42
25:L:35:LYS:HD3	25:L:35:LYS:N	2.34	0.42
25:L:76:THR:HA	25:L:79:ARG:HG2	2.00	0.42
41:a:607:U:C5	41:a:620:G:C8	3.08	0.42
41:a:967:U:C2	41:a:968:C:C5	3.07	0.42
41:a:1386:C:H2'	41:a:1387:A:H8	1.83	0.42
41:a:1414:C:O2'	41:a:1415:U:H5'	2.19	0.42
41:a:1584:U:H5'	41:a:1585:C:O4'	2.20	0.42
41:a:1837:C:C4	41:a:1899:A:C5	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:1841:U:C2	41:a:1842:G:C8	3.08	0.42
41:a:1948:G:C6	41:a:1959:G:C6	3.07	0.42
62:v:33:LEU:HD12	62:v:33:LEU:HA	1.94	0.42
66:z:91:ASP:OD1	66:z:91:ASP:C	2.61	0.42
10:A:65:C:H2'	10:A:66:C:C6	2.54	0.42
11:AA:1101:LEU:HD23	13:AE:725:MET:SD	2.60	0.42
11:AA:1323:PHE:O	11:AA:1327:LEU:HD13	2.20	0.42
12:AD:92:VAL:HG12	12:AD:93:GLN:N	2.34	0.42
13:AE:141:PHE:CZ	13:AE:296:LYS:HB3	2.54	0.42
13:AE:552:ILE:HD11	13:AE:570:LYS:HG3	2.01	0.42
15:AG:243:LYS:CG	15:AG:243:LYS:O	2.67	0.42
10:B:8:U:O4	10:B:14:A:N7	2.51	0.42
17:D:259:G:C4	17:D:260:G:C8	3.08	0.42
17:D:477:C:H2'	17:D:478:A:C8	2.54	0.42
17:D:1040:U:H2'	17:D:1041:G:C8	2.54	0.42
17:D:1091:U:C2	17:D:1095:U:C4	3.07	0.42
28:NG:145:ASN:OD1	28:NG:145:ASN:C	2.61	0.42
37:W:63:THR:HG22	37:W:64:ASP:N	2.34	0.42
41:a:184:C:C2	41:a:213:A:N1	2.87	0.42
41:a:428:A:C2'	41:a:429:A:O5'	2.67	0.42
41:a:522:A:H2'	41:a:523:C:C6	2.54	0.42
41:a:1069:A:O2'	41:a:1073:A:N6	2.51	0.42
41:a:1094:U:O2	41:a:1096:A:H3'	2.20	0.42
41:a:2796:U:H3	41:a:2799:A:N6	2.15	0.42
9:9:78:GLY:N	9:9:79:PRO:CD	2.81	0.42
10:A:37:A:C6	10:A:38:A:C5	3.08	0.42
13:AE:381:ILE:O	13:AE:385:LEU:HD23	2.19	0.42
15:AG:183:LEU:CD1	15:AG:195:LEU:HD13	2.49	0.42
10:B:36:U:H2'	10:B:37:A:C5'	2.49	0.42
17:D:193:C:H2'	17:D:194:C:C6	2.54	0.42
17:D:390:U:H2'	17:D:391:G:H8	1.85	0.42
17:D:420:U:C2	17:D:422:C:N3	2.87	0.42
28:NG:9:TRP:HB2	28:NG:103:ILE:HB	2.00	0.42
30:P:15:HIS:HA	30:P:18:ILE:HG22	2.02	0.42
35:U:39:PHE:CD2	35:U:41:PRO:HD3	2.55	0.42
35:U:53:ASP:OD2	35:U:56:ARG:HG2	2.20	0.42
41:a:146:A:H2'	41:a:147:C:C6	2.55	0.42
41:a:1070:A:O2'	41:a:1097:U:H4'	2.19	0.42
41:a:1150:C:C2	41:a:1151:A:C8	3.08	0.42
41:a:1407:G:C2	41:a:1596:A:C2	3.08	0.42
41:a:1416:G:C4	41:a:1417:C:C5	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:1759:A:C4	41:a:1760:C:C5	3.08	0.42
41:a:1853:A:H2'	41:a:1854:A:C8	2.54	0.42
41:a:1889:A:H2'	41:a:1890:A:O4'	2.19	0.42
41:a:2630:G:C5	41:a:2894:G:C6	3.08	0.42
41:a:2725:A:C4	41:a:2727:A:C8	3.08	0.42
44:d:117:G:C5	44:d:118:C:C5	3.08	0.42
56:p:45:HIS:HA	56:p:50:LEU:HD23	2.02	0.42
64:x:62:LEU:C	64:x:62:LEU:HD12	2.45	0.42
64:x:100:HIS:CG	64:x:101:GLY:N	2.87	0.42
5:4:26:PHE:CE2	5:4:89:ILE:HD12	2.53	0.42
5:4:55:GLU:O	5:4:56:PHE:C	2.63	0.42
8:7:52:U:O2	8:7:52:U:O5'	2.38	0.42
13:AE:679:TYR:CE1	13:AE:754:ILE:HG22	2.54	0.42
15:AG:27:LEU:CD2	15:AG:114:ILE:HG23	2.31	0.42
15:AG:293:VAL:HG22	15:AG:294:ALA:N	2.34	0.42
10:B:76:A:C2	41:a:2493:U:H5''	2.55	0.42
17:D:87:C:H2'	17:D:88:U:C5	2.55	0.42
17:D:299:G:H2'	17:D:300:A:C8	2.54	0.42
17:D:1130:A:H61	17:D:1144:G:H1'	1.85	0.42
17:D:1415:G:C4	17:D:1416:G:C8	3.08	0.42
29:O:26:GLY:HA2	29:O:61:LEU:O	2.20	0.42
38:X:22:ILE:HB	38:X:25:VAL:CG1	2.50	0.42
38:X:34:LEU:HD21	38:X:41:GLU:HA	2.01	0.42
41:a:940:G:H2'	41:a:941:A:O4'	2.19	0.42
41:a:1419:A:N7	41:a:1579:A:N7	2.67	0.42
41:a:1443:U:C2	41:a:1444:G:C8	3.08	0.42
41:a:1490:A:O2'	41:a:1491:G:H5'	2.20	0.42
41:a:1590:A:C2	41:a:1591:A:C5	3.07	0.42
41:a:1751:U:H2'	41:a:1752:C:C6	2.54	0.42
41:a:1840:G:C6	41:a:1841:U:C4	3.08	0.42
41:a:2098:U:H2'	41:a:2099:U:C1'	2.50	0.42
41:a:2183:A:H2'	41:a:2184:A:C8	2.54	0.42
41:a:2194:U:H2'	41:a:2195:U:H6	1.85	0.42
41:a:2547:A:H2'	41:a:2548:U:C6	2.54	0.42
41:a:2574:G:H2'	41:a:2575:C:O4'	2.20	0.42
41:a:2776:A:C2	41:a:2778:A:C4	3.08	0.42
5:4:30:ILE:HD11	5:4:40:ILE:HD13	2.01	0.42
9:9:43:LYS:CE	9:9:95:LEU:HD13	2.50	0.42
11:AA:104:ILE:O	11:AA:104:ILE:HG13	2.19	0.42
11:AA:681:MET:HE3	11:AA:685:MET:HE3	2.01	0.42
11:AA:947:GLU:HA	11:AA:950:GLU:HG2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AE:154:LEU:CD2	13:AE:160:LEU:HD11	2.50	0.42
15:AG:421:GLN:O	15:AG:425:LEU:HB2	2.20	0.42
10:B:26:G:N1	10:B:45:G:N2	2.67	0.42
17:D:246:A:C2	17:D:282:A:C5	3.08	0.42
17:D:374:A:C4	17:D:375:U:C5	3.07	0.42
17:D:655:A:C6	17:D:656:G:C5	3.08	0.42
22:I:156:ARG:HD3	22:I:160:ALA:O	2.19	0.42
28:NG:24:THR:O	28:NG:27:ARG:HG2	2.19	0.42
28:NG:148:VAL:CB	28:NG:160:VAL:HG22	2.48	0.42
41:a:464:U:C4	41:a:788:A:C4	3.08	0.42
41:a:827:U:H4'	41:a:828:U:C5	2.55	0.42
41:a:833:A:H2'	41:a:834:G:C8	2.55	0.42
41:a:1108:U:H3'	41:a:1109:C:C5	2.55	0.42
41:a:1258:U:C2	41:a:1259:G:C8	3.08	0.42
41:a:1766:G:C6	41:a:1987:A:C6	3.08	0.42
41:a:1923:U:HO2'	41:a:1924:C:H5	1.62	0.42
41:a:2902:C:H2'	41:a:2903:U:H5'	2.02	0.42
52:l:1:MET:HE3	52:l:19:PHE:O	2.19	0.42
4:3:49:VAL:HG22	4:3:54:GLN:HB2	2.00	0.42
9:9:23:LEU:HD11	9:9:96:PHE:CE2	2.55	0.42
9:9:119:PRO:HG3	9:9:124:ASP:OD2	2.20	0.42
10:A:35:A:H2'	10:A:36:U:O4'	2.20	0.42
11:AA:515:MET:SD	11:AA:517:GLN:CB	3.07	0.42
13:AE:1226:VAL:O	13:AE:1229:VAL:HG12	2.20	0.42
10:B:1:C:C4	10:B:2:G:C5	3.08	0.42
16:C:12:ARG:HA	21:H:264:GLU:CB	2.49	0.42
17:D:374:A:C6	17:D:375:U:C4	3.08	0.42
17:D:384:G:H2'	17:D:385:C:C6	2.54	0.42
17:D:457:G:N2	17:D:476:U:C2	2.88	0.42
17:D:554:A:H2'	17:D:555:U:C6	2.54	0.42
17:D:1282:C:H2'	17:D:1283:U:C6	2.54	0.42
20:G:196:VAL:HG12	20:G:197:ASP:N	2.34	0.42
21:H:295:GLU:HB2	21:H:300:VAL:O	2.20	0.42
22:I:14:ILE:HG22	22:I:15:VAL:HG13	2.01	0.42
28:NG:21:ARG:NH1	28:NG:87:PRO:HG2	2.35	0.42
30:P:10:LEU:HD12	30:P:22:THR:HG22	2.01	0.42
36:V:32:PRO:HB2	36:V:33:ILE:HD12	2.02	0.42
41:a:250:G:H2'	41:a:251:A:O4'	2.20	0.42
41:a:261:G:C2	41:a:262:A:C8	3.08	0.42
41:a:284:U:O2	41:a:356:G:C2	2.73	0.42
41:a:1087:G:H2'	41:a:1089:A:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:1094:U:C2	41:a:1097:U:OP2	2.73	0.42
41:a:1296:G:C4	41:a:1645:G:N2	2.88	0.42
41:a:1802:A:H2'	41:a:1803:A:C8	2.55	0.42
44:d:28:C:H2'	44:d:29:A:O4'	2.20	0.42
48:h:141:VAL:HG12	48:h:142:HIS:N	2.34	0.42
59:s:57:LEU:C	59:s:57:LEU:HD12	2.44	0.42
7:6:21:DA:N1	8:7:51:G:O6	2.52	0.42
9:9:5:LEU:H	9:9:5:LEU:HD23	1.85	0.42
11:AA:1286:THR:HA	11:AA:1289:GLU:HG2	2.01	0.42
13:AE:412:LEU:CD2	13:AE:441:LEU:HD21	2.50	0.42
15:AG:266:LEU:HD21	15:AG:269:GLU:CD	2.45	0.42
17:D:236:A:C4	17:D:237:G:C8	3.08	0.42
17:D:328:C:O2	17:D:328:C:H2'	2.18	0.42
17:D:406:G:C4	17:D:495:A:C6	3.08	0.42
17:D:463:U:O2	17:D:463:U:H2'	2.20	0.42
17:D:1492:A:C5	41:a:1913:A:C6	3.08	0.42
22:I:87:LEU:O	22:I:91:VAL:HG23	2.20	0.42
39:Y:48:ILE:HG13	39:Y:49:GLU:H	1.84	0.42
39:Y:134:SER:HB3	41:a:1059:G:H1'	2.01	0.42
41:a:273:G:C6	41:a:274:C:C4	3.08	0.42
41:a:357:C:H2'	41:a:358:U:O4'	2.19	0.42
41:a:807:U:OP2	61:u:41:ARG:NH2	2.53	0.42
41:a:849:A:H61	41:a:928:A:N6	2.17	0.42
41:a:850:U:O2'	46:f:23:THR:HA	2.20	0.42
41:a:957:C:N4	41:a:959:A:C2	2.88	0.42
41:a:1418:G:O2'	41:a:1580:A:N6	2.53	0.42
41:a:1452:G:C2	41:a:2702:G:C5	3.08	0.42
41:a:2230:G:H2'	41:a:2231:U:C6	2.54	0.42
41:a:2298:A:C2	41:a:2299:U:H1'	2.55	0.42
41:a:2316:G:C2	41:a:2317:A:C8	3.08	0.42
41:a:2856:A:H2'	41:a:2857:G:O4'	2.19	0.42
1:0:14:VAL:HG22	1:0:15:SER:N	2.35	0.41
3:2:13:ALA:HB1	45:e:33:ALA:CB	2.50	0.41
9:9:126:LEU:C	9:9:126:LEU:HD12	2.44	0.41
10:A:58:A:O2'	10:A:59:A:H3'	2.20	0.41
10:A:66:C:H2'	10:A:67:C:H6	1.85	0.41
11:AA:471:VAL:O	11:AA:475:VAL:HG23	2.20	0.41
11:AA:894:GLN:HG3	11:AA:895:LEU:HD23	2.02	0.41
11:AA:942:ASP:OD1	11:AA:945:ALA:HB2	2.20	0.41
12:AC:231:PHE:O	12:AC:232:VAL:C	2.62	0.41
13:AE:1221:LEU:HD22	13:AE:1306:LEU:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AG:381:LEU:HA	15:AG:384:LEU:HD12	2.01	0.41
10:B:50:U:O2	10:B:65:C:N3	2.53	0.41
17:D:73:C:N4	17:D:74:A:N6	2.68	0.41
17:D:80:A:H2'	17:D:81:A:H8	1.85	0.41
17:D:953:G:C6	17:D:954:G:C5	3.08	0.41
17:D:986:U:H2'	17:D:987:G:O4'	2.20	0.41
17:D:1132:C:O2	17:D:1132:C:H2'	2.19	0.41
17:D:1137:C:O2	17:D:1138:G:N1	2.53	0.41
26:M:87:VAL:O	26:M:87:VAL:HG23	2.20	0.41
41:a:227:A:C2	41:a:2407:A:H1'	2.55	0.41
41:a:1137:G:H2'	41:a:1138:G:O4'	2.20	0.41
41:a:1284:A:H2'	41:a:1285:A:O4'	2.19	0.41
41:a:1922:G:N1	41:a:1923:U:C4	2.88	0.41
41:a:2020:A:C2	41:a:2022:U:O4'	2.73	0.41
41:a:2107:G:C6	41:a:2108:A:C5	3.08	0.41
41:a:2188:U:H2'	41:a:2189:U:OP1	2.20	0.41
41:a:2660:A:H2'	41:a:2661:G:C8	2.55	0.41
48:h:132:MET:HE1	48:h:188:CYS:HB2	2.02	0.41
64:x:106:LEU:HD23	64:x:106:LEU:C	2.45	0.41
9:9:51:TYR:HB2	9:9:88:HIS:HB2	2.01	0.41
9:9:81:LEU:HD23	9:9:81:LEU:HA	1.88	0.41
10:A:58:A:O2'	10:A:60:U:OP2	2.38	0.41
13:AE:319:SER:HA	13:AE:320:ASN:HA	1.81	0.41
13:AE:902:ASP:HB3	13:AE:905:ARG:HB2	2.02	0.41
15:AG:71:PRO:HA	15:AG:74:GLU:CD	2.45	0.41
15:AG:130:PHE:CE1	15:AG:158:ALA:HB1	2.55	0.41
15:AG:204:MET:CE	15:AG:266:LEU:HD13	2.50	0.41
10:B:9:G:H21	10:B:45:G:H3'	1.85	0.41
17:D:215:C:H2'	17:D:216:U:H6	1.85	0.41
17:D:454:G:C4	17:D:455:G:C8	3.08	0.41
17:D:560:A:C5	24:K:128:TYR:CE1	3.09	0.41
17:D:607:A:H2'	17:D:608:A:O4'	2.20	0.41
17:D:977:A:H1'	17:D:982:U:O4	2.19	0.41
17:D:1130:A:C4	17:D:1131:G:C8	3.08	0.41
17:D:1236:A:H2'	17:D:1237:C:C6	2.55	0.41
17:D:1454:G:C2	17:D:1455:G:C8	3.09	0.41
28:NG:106:LYS:HD2	28:NG:106:LYS:O	2.20	0.41
29:O:12:ARG:HD3	29:O:13:LYS:HG3	2.02	0.41
36:V:80:GLU:OE1	36:V:80:GLU:O	2.38	0.41
39:Y:77:VAL:HA	39:Y:80:LYS:HG2	2.02	0.41
41:a:24:G:H2'	41:a:25:U:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:804:A:H2'	41:a:806:C:C4	2.55	0.41
41:a:1042:G:C4	41:a:1043:C:C6	3.09	0.41
41:a:1509:A:O2'	41:a:1510:G:P	2.79	0.41
41:a:1560:G:C5	41:a:1561:C:C5	3.08	0.41
41:a:1876:A:C4	41:a:1877:A:C8	3.07	0.41
41:a:2309:A:O2'	41:a:2310:C:H5'	2.20	0.41
41:a:2510:C:C4	41:a:2511:U:C4	3.08	0.41
41:a:2515:C:C2	41:a:2570:G:C2	3.08	0.41
41:a:2636:C:H2'	41:a:2637:U:H6	1.85	0.41
41:a:2699:C:C2	41:a:2700:A:C8	3.08	0.41
41:a:2854:G:C6	41:a:2864:G:O6	2.73	0.41
43:c:56:MET:O	43:c:59:ILE:HG22	2.21	0.41
57:q:10:LEU:HD23	57:q:33:HIS:CD2	2.56	0.41
59:s:31:GLU:CG	59:s:142:ILE:HG23	2.50	0.41
66:z:62:ILE:HD12	66:z:76:TYR:OH	2.20	0.41
10:A:39:C:C2	10:A:40:C:C5	3.09	0.41
13:AE:144:TYR:CE2	13:AE:165:TYR:CD2	3.08	0.41
13:AE:161:THR:O	13:AE:162:GLU:C	2.62	0.41
15:AG:64:VAL:HG22	15:AG:75:ILE:HD13	2.02	0.41
17:D:505:G:C6	17:D:535:A:C2	3.08	0.41
17:D:533:A:HO2'	17:D:535:A:P	2.43	0.41
17:D:554:A:C2	17:D:555:U:C4	3.08	0.41
17:D:573:A:O2'	17:D:574:A:H5'	2.20	0.41
24:K:134:ILE:O	24:K:137:VAL:HG12	2.20	0.41
24:K:141:ILE:HD12	24:K:141:ILE:HA	1.93	0.41
26:M:22:LEU:HD12	26:M:101:MET:HE1	2.01	0.41
36:V:41:THR:HG22	36:V:42:THR:N	2.35	0.41
41:a:303:G:C6	41:a:315:G:N1	2.89	0.41
41:a:551:G:C6	41:a:552:U:C4	3.08	0.41
41:a:861:A:H2'	41:a:862:G:O4'	2.21	0.41
41:a:1011:G:C4	41:a:1013:C:C6	3.08	0.41
41:a:1065:U:H1'	41:a:1066:U:O4'	2.20	0.41
41:a:1880:U:H2'	41:a:1881:C:C6	2.55	0.41
41:a:1906:G:H2'	41:a:1907:G:O4'	2.20	0.41
41:a:1945:G:C4	41:a:1946:U:C5	3.08	0.41
41:a:2146:C:H4'	41:a:2147:A:O5'	2.20	0.41
41:a:2595:G:N1	41:a:2599:G:C6	2.88	0.41
45:e:8:GLU:O	45:e:9:LYS:HD3	2.20	0.41
58:r:4:ILE:HD12	58:r:17:ASP:O	2.20	0.41
58:r:143:ILE:O	58:r:143:ILE:CG2	2.67	0.41
60:t:24:VAL:HG11	60:t:30:ARG:HG2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:v:33:LEU:HD13	62:v:117:PHE:HB3	2.02	0.41
1:0:6:GLN:O	1:0:37:GLU:OE2	2.38	0.41
17:D:70:U:H2'	17:D:94:G:N7	2.35	0.41
17:D:608:A:C2	17:D:609:A:H1'	2.55	0.41
17:D:620:C:H2'	17:D:621:A:O4'	2.20	0.41
17:D:764:C:H2'	17:D:765:G:O4'	2.20	0.41
17:D:777:A:C6	17:D:778:G:C5	3.09	0.41
17:D:792:A:N3	17:D:794:A:C5	2.88	0.41
17:D:960:U:O2'	17:D:1223:C:H4'	2.20	0.41
17:D:1501:C:C5	17:D:1504:G:C4	3.08	0.41
21:H:33:LYS:HA	21:H:34:ASP:HA	1.78	0.41
28:NG:95:GLY:H	28:NG:101:ALA:CA	2.34	0.41
28:NG:103:ILE:HG23	28:NG:107:GLU:CG	2.49	0.41
35:U:19:VAL:HG12	35:U:37:GLY:C	2.45	0.41
41:a:301:G:C4	41:a:302:C:C5	3.08	0.41
41:a:545:U:OP2	41:a:545:U:O2	2.38	0.41
41:a:910:A:C6	62:v:13:HIS:CE1	3.08	0.41
41:a:1106:G:C6	41:a:1107:G:N7	2.88	0.41
41:a:1542:U:H2'	41:a:1543:G:O4'	2.20	0.41
41:a:1581:G:C4	41:a:1582:C:C5	3.08	0.41
41:a:1857:G:N2	41:a:1884:G:H1'	2.35	0.41
41:a:1924:C:H2'	41:a:1925:C:C6	2.56	0.41
41:a:2127:G:H21	41:a:2173:A:C1'	2.34	0.41
41:a:2287:A:C8	41:a:2289:G:C8	3.08	0.41
44:d:46:A:C5	44:d:47:C:C5	3.09	0.41
44:d:99:A:C4	44:d:100:G:C8	3.08	0.41
3:2:18:GLU:CD	41:a:1392:A:H62	2.29	0.41
4:3:49:VAL:HG23	4:3:51:ALA:O	2.21	0.41
11:AA:375:PRO:HA	11:AA:376:PRO:HD3	1.97	0.41
13:AE:1286:LYS:O	13:AE:1289:ASN:OD1	2.39	0.41
17:D:224:U:H2'	17:D:225:C:C6	2.56	0.41
17:D:1266:G:N1	17:D:1270:G:C6	2.89	0.41
17:D:1323:G:H2'	17:D:1324:A:C8	2.55	0.41
17:D:1421:G:C6	17:D:1480:A:C6	3.08	0.41
17:D:1448:C:C2	17:D:1449:C:C5	3.09	0.41
17:D:1456:A:H2'	17:D:1457:G:O4'	2.20	0.41
19:F:4:ILE:CD1	19:F:19:PHE:HA	2.50	0.41
20:G:167:ASP:OD1	20:G:168:HIS:N	2.54	0.41
28:NG:43:MET:HE1	28:NG:111:ILE:HD12	2.02	0.41
28:NG:86:VAL:HB	28:NG:89:VAL:CG2	2.47	0.41
31:Q:61:PHE:O	31:Q:64:GLN:HG2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:S:73:PHE:O	33:S:74:LEU:HD22	2.20	0.41
38:X:3:ARG:O	38:X:4:ILE:HD13	2.20	0.41
39:Y:79:LEU:HD21	39:Y:137:LEU:CD2	2.49	0.41
41:a:521:U:H2'	41:a:522:A:H8	1.86	0.41
41:a:900:A:C6	41:a:901:C:C5	3.08	0.41
41:a:945:A:C5	41:a:2448:A:C2	3.09	0.41
41:a:1168:G:H3'	41:a:1169:A:H5''	2.01	0.41
41:a:1199:U:H2'	41:a:1200:C:O4'	2.20	0.41
41:a:1405:U:H2'	41:a:1406:U:C6	2.54	0.41
41:a:2100:G:C6	41:a:2101:A:C5	3.08	0.41
41:a:2461:A:C6	41:a:2462:C:C4	3.09	0.41
41:a:2521:C:H2'	41:a:2522:U:O4'	2.21	0.41
59:s:28:LEU:HD12	59:s:142:ILE:HG21	2.01	0.41
60:t:4:GLU:O	60:t:5:GLN:HB2	2.20	0.41
10:A:21:A:C2	10:A:46:G:C2	3.09	0.41
11:AA:1113:LEU:CD1	13:AE:641:ILE:HD13	2.51	0.41
17:D:309:A:C2	17:D:310:G:C5	3.08	0.41
17:D:632:U:O2	17:D:632:U:H2'	2.21	0.41
17:D:1410:A:H2'	17:D:1411:C:C6	2.55	0.41
23:J:138:SER:OG	23:J:139:PRO:HD2	2.20	0.41
23:J:173:VAL:HG22	23:J:174:ASP:N	2.35	0.41
35:U:51:ARG:C	35:U:52:LEU:HD12	2.45	0.41
41:a:64:A:H2'	41:a:65:U:H6	1.85	0.41
41:a:492:A:H2'	41:a:493:G:O4'	2.20	0.41
41:a:1107:G:N1	41:a:1108:U:C5	2.89	0.41
41:a:1721:G:H2'	41:a:1738:G:H22	1.86	0.41
41:a:2330:G:C6	41:a:2331:G:C5	3.08	0.41
41:a:2345:G:N3	41:a:2381:A:H2'	2.35	0.41
41:a:2644:G:O2'	41:a:2645:G:H5'	2.20	0.41
47:g:24:ILE:HG12	54:n:102:ARG:HG3	2.03	0.41
52:l:24:ASN:OD1	52:l:24:ASN:C	2.63	0.41
9:9:30:SER:HA	9:9:81:LEU:CD1	2.51	0.41
9:9:42:ARG:O	9:9:46:ARG:HG3	2.20	0.41
10:A:18:G:N2	10:A:57:A:H3'	2.34	0.41
10:A:39:C:H2'	10:A:40:C:H6	1.83	0.41
13:AE:848:VAL:CG2	13:AE:880:VAL:HG13	2.50	0.41
10:B:18:G:H21	10:B:57:A:H3'	1.86	0.41
10:B:66:C:C2	10:B:67:C:C6	3.09	0.41
17:D:208:U:O4'	17:D:212:G:N2	2.52	0.41
17:D:216:U:H2'	17:D:217:C:H6	1.86	0.41
17:D:251:G:N1	17:D:266:G:C6	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:D:412:A:N6	17:D:431:A:H61	2.14	0.41
17:D:414:A:C4	17:D:415:A:C8	3.09	0.41
17:D:911:U:H2'	17:D:912:C:C6	2.56	0.41
17:D:1501:C:C5	17:D:1504:G:C5	3.08	0.41
17:D:1502:A:C5	17:D:1504:G:C6	3.09	0.41
21:H:272:LYS:HG3	21:H:273:ARG:HD2	2.02	0.41
24:K:25:VAL:HG11	24:K:30:ILE:HD12	2.01	0.41
28:NG:116:GLN:NE2	28:NG:117:GLN:HB3	2.36	0.41
37:W:30:PRO:C	37:W:31:LEU:HD12	2.46	0.41
41:a:594:U:H2'	41:a:595:C:C6	2.55	0.41
41:a:607:U:H5	41:a:620:G:C4	2.39	0.41
41:a:1171:G:C6	41:a:1172:C:C4	3.09	0.41
41:a:1199:U:C2	41:a:1200:C:C6	3.09	0.41
41:a:1408:G:N3	41:a:1408:G:H2'	2.35	0.41
41:a:2056:G:C6	41:a:2577:A:C4	3.08	0.41
41:a:2246:G:H2'	41:a:2247:A:H8	1.85	0.41
41:a:2316:G:C4	41:a:2317:A:C8	3.08	0.41
41:a:2854:G:N1	41:a:2864:G:C6	2.89	0.41
41:a:2868:A:C6	41:a:2869:G:C6	3.09	0.41
52:l:85:PHE:O	52:l:86:ALA:C	2.63	0.41
58:r:70:GLU:OE2	58:r:140:ALA:HB2	2.20	0.41
3:2:53:VAL:HG22	3:2:54:GLU:N	2.36	0.41
4:3:72:ILE:HG21	4:3:83:VAL:CG2	2.50	0.41
8:7:2:U:C4	10:B:35:A:N6	2.88	0.41
10:A:19:G:C2	41:a:2112:G:O4'	2.73	0.41
11:AA:469:VAL:O	11:AA:472:GLU:HG2	2.21	0.41
11:AA:690:VAL:HG12	11:AA:1234:LYS:O	2.21	0.41
13:AE:1163:VAL:CG2	13:AE:1175:LEU:HD11	2.51	0.41
10:B:38:A:N3	10:B:38:A:H2'	2.34	0.41
16:C:44:ILE:O	21:H:340:ARG:HB2	2.20	0.41
17:D:460:A:H2'	17:D:461:A:C8	2.56	0.41
17:D:604:G:C6	17:D:635:A:C6	3.08	0.41
17:D:679:C:C2	17:D:680:C:C5	3.09	0.41
17:D:1004:A:C8	17:D:1025:U:O4'	2.74	0.41
17:D:1314:C:H2'	17:D:1315:U:C6	2.56	0.41
17:D:1478:U:H2'	17:D:1479:C:C6	2.54	0.41
17:D:1500:A:OP1	17:D:1505:G:OP1	2.39	0.41
21:H:308:GLU:HG2	21:H:309:MET:N	2.33	0.41
26:M:105:VAL:O	26:M:109:ARG:HG2	2.21	0.41
28:NG:30:ILE:HG22	28:NG:36:GLU:OE1	2.21	0.41
41:a:84:A:N1	41:a:103:A:C5	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:215:G:H4'	41:a:216:A:OP1	2.21	0.41
41:a:280:U:H2'	41:a:281:C:C6	2.55	0.41
41:a:1070:A:C8	41:a:1096:A:O2'	2.73	0.41
41:a:1107:G:N3	41:a:1107:G:H2'	2.35	0.41
41:a:1174:U:H4'	41:a:1177:G:N2	2.35	0.41
41:a:1419:A:N3	41:a:1421:G:C8	2.88	0.41
41:a:1482:G:C2	41:a:1508:A:C8	3.09	0.41
41:a:1795:C:H2'	41:a:1796:U:O4'	2.21	0.41
41:a:1857:G:H22	41:a:1884:G:H1'	1.86	0.41
41:a:2061:G:H3'	41:a:2061:G:P	2.61	0.41
41:a:2795:C:H2'	41:a:2796:U:C6	2.56	0.41
52:l:101:TYR:CE2	52:l:105:LEU:HD11	2.55	0.41
57:q:16:ILE:HG22	57:q:25:VAL:HG22	2.02	0.41
60:t:24:VAL:HG13	60:t:33:ALA:HB2	2.03	0.41
60:t:38:ILE:HD11	60:t:112:PHE:HZ	1.85	0.41
62:v:110:GLU:OE2	62:v:114:ARG:HD2	2.21	0.41
6:5:112:DG:H1	7:6:12:DC:H42	1.68	0.41
9:9:17:GLU:HG2	9:9:88:HIS:NE2	2.36	0.41
9:9:92:ALA:HB1	9:9:129:LEU:HD22	2.03	0.41
11:AA:829:THR:HG23	11:AA:1059:ARG:HG2	2.02	0.41
11:AA:862:LEU:HG	11:AA:865:LEU:HD12	2.02	0.41
11:AA:1287:LEU:HA	11:AA:1290:MET:HE2	2.02	0.41
13:AE:412:LEU:HD23	13:AE:441:LEU:HD21	2.03	0.41
14:AF:60:ASN:H	14:AF:63:ILE:HG22	1.85	0.41
15:AG:68:VAL:O	15:AG:68:VAL:HG12	2.21	0.41
15:AG:189:GLU:HB2	15:AG:194:GLN:H	1.85	0.41
10:B:26:G:C4	10:B:27:U:C5	3.09	0.41
10:B:56:C:C4	10:B:57:A:C8	3.09	0.41
10:B:58:A:O2'	10:B:59:A:H3'	2.21	0.41
17:D:102:G:C2	17:D:103:U:C6	3.09	0.41
17:D:158:G:H2'	17:D:159:G:O4'	2.21	0.41
17:D:270:A:H2'	17:D:271:C:C6	2.56	0.41
17:D:627:G:H2'	17:D:628:G:O4'	2.21	0.41
17:D:767:A:H2'	17:D:768:A:O4'	2.20	0.41
17:D:825:A:H2'	17:D:826:C:C6	2.55	0.41
17:D:881:G:H2'	17:D:882:C:O4'	2.21	0.41
17:D:922:G:H2'	17:D:923:A:C8	2.55	0.41
17:D:1343:G:H2'	17:D:1344:C:C6	2.56	0.41
25:L:97:THR:O	25:L:97:THR:HG22	2.21	0.41
25:L:102:MET:SD	25:L:102:MET:C	3.04	0.41
36:V:23:VAL:HG21	36:V:61:ILE:HD11	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:V:75:LEU:C	36:V:75:LEU:HD12	2.46	0.41
37:W:56:GLN:OE1	37:W:56:GLN:N	2.54	0.41
38:X:11:ASP:HA	38:X:45:ILE:HB	2.01	0.41
38:X:34:LEU:CD2	38:X:41:GLU:HA	2.51	0.41
41:a:2:G:H2'	41:a:3:U:C6	2.55	0.41
41:a:5:A:H2'	41:a:6:A:C8	2.55	0.41
41:a:44:A:H2'	41:a:45:G:O4'	2.21	0.41
41:a:110:G:C4	41:a:111:A:C8	3.09	0.41
41:a:289:G:C6	41:a:352:A:N1	2.88	0.41
41:a:317:G:C6	41:a:318:C:C4	3.09	0.41
41:a:357:C:H2'	41:a:358:U:C6	2.56	0.41
41:a:733:G:O6	41:a:761:A:C8	2.74	0.41
41:a:785:G:C6	41:a:786:C:C4	3.09	0.41
41:a:868:U:H2'	41:a:869:G:O4'	2.21	0.41
41:a:875:G:H2'	41:a:876:C:O4'	2.21	0.41
41:a:1022:G:C6	41:a:1141:U:C5	3.08	0.41
41:a:1022:G:C6	41:a:1140:C:C4	3.08	0.41
41:a:1028:A:H2'	41:a:1029:A:H8	1.85	0.41
41:a:1062:G:H2'	41:a:1063:G:O4'	2.21	0.41
41:a:1072:C:OP2	41:a:1097:U:OP1	2.39	0.41
41:a:1076:C:H2'	41:a:1077:A:C8	2.55	0.41
41:a:1179:G:C6	41:a:1180:U:C4	3.09	0.41
41:a:1322:A:C5	41:a:1323:C:C5	3.09	0.41
41:a:1417:C:C4	41:a:1418:G:C5	3.09	0.41
41:a:1418:G:H2'	41:a:1579:A:N6	2.36	0.41
41:a:1528:A:H3'	41:a:1529:G:O4'	2.21	0.41
41:a:1613:G:H3'	41:a:1614:A:C5'	2.51	0.41
41:a:1691:C:N4	41:a:1697:G:N2	2.68	0.41
41:a:1739:A:H2'	41:a:1740:G:O4'	2.21	0.41
41:a:1837:C:C2	41:a:1904:G:C2	3.09	0.41
41:a:1855:U:C4	41:a:1856:U:C4	3.09	0.41
41:a:2305:U:H2'	41:a:2306:C:C6	2.56	0.41
41:a:2447:G:C2'	41:a:2500:U:OP2	2.67	0.41
41:a:2465:C:O2	41:a:2465:C:H2'	2.21	0.41
41:a:2620:C:C4	41:a:2621:G:N7	2.88	0.41
41:a:2645:G:H3'	41:a:2646:C:H5'	2.02	0.41
41:a:2708:G:N3	41:a:2709:G:C8	2.89	0.41
41:a:2869:G:H2'	41:a:2870:C:C6	2.56	0.41
44:d:2:G:C6	44:d:3:C:C4	3.09	0.41
44:d:39:A:C2	44:d:44:G:N3	2.89	0.41
50:j:207:VAL:HG13	50:j:208:LYS:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:p:87:LEU:HD12	56:p:87:LEU:N	2.35	0.41
56:p:124:GLU:CD	56:p:124:GLU:C	2.88	0.41
56:p:127:THR:HG22	56:p:128:GLN:N	2.36	0.41
59:s:140:LEU:HD12	59:s:141:ASP:N	2.35	0.41
64:x:47:VAL:HG13	64:x:47:VAL:O	2.20	0.41
65:y:46:VAL:HG12	65:y:47:VAL:N	2.35	0.41
6:5:103:DT:H3	6:5:103:DT:H2''	1.83	0.41
11:AA:85:CYS:SG	11:AA:90:VAL:O	2.79	0.41
11:AA:91:THR:HG22	11:AA:138:ILE:O	2.21	0.41
11:AA:515:MET:HG2	11:AA:516:ASP:C	2.45	0.41
11:AA:855:PRO:CG	11:AA:913:VAL:HG11	2.51	0.41
11:AA:1326:LEU:HD21	13:AE:338:PHE:CZ	2.56	0.41
13:AE:17:PHE:HZ	13:AE:1353:VAL:HG13	1.86	0.41
13:AE:70:CYS:CB	13:AE:74:LYS:HG2	2.51	0.41
15:AG:11:ALA:HB3	15:AG:12:VAL:CA	2.44	0.41
17:D:358:U:C2	17:D:359:G:C8	3.09	0.41
17:D:431:A:C4	17:D:432:A:C8	3.09	0.41
17:D:1042:A:H2'	17:D:1043:G:C1'	2.50	0.41
17:D:1050:G:C2	17:D:1051:C:C5	3.09	0.41
20:G:19:GLN:OE1	20:G:21:ARG:HG2	2.21	0.41
21:H:274:TYR:O	21:H:275:PRO:C	2.64	0.41
33:S:73:PHE:C	33:S:74:LEU:HD22	2.46	0.41
38:X:47:GLU:O	38:X:47:GLU:OE1	2.39	0.41
41:a:394:C:O2'	41:a:395:U:H5'	2.21	0.41
41:a:538:A:N1	41:a:556:A:C8	2.89	0.41
41:a:892:A:H2'	41:a:893:C:O4'	2.20	0.41
41:a:1509:A:N3	41:a:1510:G:C8	2.89	0.41
41:a:1564:C:H2'	41:a:1565:C:C6	2.55	0.41
41:a:1737:G:H2'	41:a:1738:G:H1'	2.03	0.41
41:a:1887:C:H2'	41:a:1888:G:O4'	2.21	0.41
41:a:2125:G:H21	41:a:2174:C:H41	1.68	0.41
41:a:2242:G:C2'	41:a:2243:U:O5'	2.69	0.41
41:a:2311:A:O2'	41:a:2312:U:O4'	2.36	0.41
41:a:2315:G:C2	41:a:2316:G:C8	3.09	0.41
41:a:2728:U:C2	41:a:2729:G:N7	2.89	0.41
44:d:32:U:C4	44:d:51:G:N1	2.89	0.41
58:r:138:VAL:HG12	58:r:139:PHE:O	2.21	0.41
5:4:47:VAL:O	5:4:48:MET:C	2.64	0.40
8:7:4:U:C4	17:D:1500:A:N1	2.89	0.40
9:9:23:LEU:HA	9:9:118:ILE:HG13	2.02	0.40
9:9:30:SER:HA	9:9:81:LEU:HD12	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:98:VAL:HB	11:AA:124:MET:HE3	2.04	0.40
11:AA:221:LEU:HD12	11:AA:298:ALA:O	2.21	0.40
11:AA:370:MET:HE3	11:AA:388:LEU:CD1	2.51	0.40
11:AA:481:LEU:HD21	28:NG:21:ARG:HE	1.86	0.40
11:AA:560:PRO:HB2	13:AE:776:THR:HG21	2.03	0.40
12:AC:64:VAL:HG13	12:AC:69:SER:OG	2.21	0.40
12:AD:85:LEU:CD1	12:AD:142:MET:HE1	2.45	0.40
13:AE:189:LEU:HD13	13:AE:237:MET:SD	2.60	0.40
13:AE:1157:ALA:HB1	13:AE:1177:ILE:HD13	2.04	0.40
15:AG:223:ILE:O	15:AG:223:ILE:HG23	2.20	0.40
17:D:46:G:C6	17:D:366:A:C2	3.08	0.40
17:D:54:C:H2'	17:D:352:C:H41	1.86	0.40
17:D:263:A:H2'	17:D:264:C:C6	2.57	0.40
17:D:415:A:C4	17:D:416:G:C8	3.10	0.40
17:D:781:A:C8	17:D:782:A:C8	3.09	0.40
17:D:1078:U:C2'	17:D:1079:G:O5'	2.69	0.40
17:D:1169:A:H2'	17:D:1170:A:O4'	2.21	0.40
17:D:1181:G:H1'	17:D:1182:G:C5	2.56	0.40
17:D:1413:A:H2'	17:D:1414:U:O4'	2.22	0.40
28:NG:29:HIS:O	28:NG:82:LEU:HD11	2.20	0.40
28:NG:96:THR:O	28:NG:100:PRO:CA	2.67	0.40
28:NG:102:PRO:O	28:NG:103:ILE:C	2.64	0.40
31:Q:84:VAL:HG23	31:Q:107:ILE:CD1	2.51	0.40
40:Z:2:ILE:O	40:Z:6:GLN:OE1	2.39	0.40
41:a:78:U:H2'	41:a:79:C:C6	2.56	0.40
41:a:141:G:N2	41:a:142:A:C8	2.89	0.40
41:a:289:G:C6	41:a:352:A:C6	3.10	0.40
41:a:1301:A:H2'	41:a:1301:A:N3	2.36	0.40
41:a:1848:A:C4	41:a:1849:G:C8	3.09	0.40
41:a:2272:U:H5''	41:a:2273:A:OP1	2.21	0.40
41:a:2290:G:H2'	41:a:2291:U:C6	2.56	0.40
41:a:2626:C:H2'	41:a:2627:G:O4'	2.21	0.40
41:a:2727:A:O2'	41:a:2728:U:H5'	2.22	0.40
41:a:2886:A:C4	41:a:2887:A:C8	3.10	0.40
48:h:168:ASP:O	48:h:168:ASP:OD1	2.39	0.40
48:h:195:VAL:HG22	48:h:196:GLY:N	2.37	0.40
66:z:3:ARG:O	66:z:3:ARG:HG3	2.21	0.40
2:1:96:ILE:O	2:1:96:ILE:HG13	2.20	0.40
5:4:61:LEU:HD12	5:4:61:LEU:N	2.36	0.40
9:9:47:GLU:HB3	9:9:51:TYR:OH	2.21	0.40
9:9:56:ARG:NH2	41:a:1084:A:N9	2.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:9:80:THR:HA	41:a:1108:U:H5'	2.03	0.40
9:9:93:ALA:O	9:9:129:LEU:O	2.39	0.40
11:AA:475:VAL:HA	11:AA:492:MET:HE3	2.03	0.40
11:AA:746:ALA:HA	11:AA:974:ARG:HE	1.86	0.40
11:AA:1150:ASP:O	11:AA:1151:LEU:C	2.64	0.40
12:AD:85:LEU:HD22	12:AD:144:ILE:HD12	2.04	0.40
13:AE:132:LEU:O	13:AE:135:ILE:HG22	2.20	0.40
13:AE:658:GLU:HA	13:AE:661:VAL:HG22	2.03	0.40
13:AE:872:LEU:CD2	13:AE:877:VAL:HG21	2.51	0.40
15:AG:243:LYS:O	15:AG:243:LYS:HG3	2.20	0.40
10:B:39:C:N3	10:B:40:C:C5	2.89	0.40
17:D:375:U:C2	17:D:376:G:C8	3.09	0.40
17:D:716:A:N3	31:Q:119:ASN:O	2.54	0.40
17:D:824:G:H2'	17:D:825:A:H8	1.87	0.40
17:D:1130:A:N7	17:D:1146:A:C6	2.89	0.40
17:D:1305:G:C5	17:D:1331:G:C2	3.08	0.40
28:NG:123:ARG:NE	28:NG:123:ARG:HA	2.36	0.40
34:T:70:LEU:O	34:T:74:ASP:O	2.40	0.40
41:a:116:C:H2'	41:a:117:G:O4'	2.21	0.40
41:a:144:A:H2'	41:a:145:C:C6	2.56	0.40
41:a:324:A:H2'	41:a:325:G:O4'	2.21	0.40
41:a:563:A:N6	41:a:2018:G:C5	2.90	0.40
41:a:714:U:C2	41:a:716:A:OP2	2.74	0.40
41:a:1346:G:C6	41:a:1601:G:C6	3.09	0.40
41:a:1411:U:H3'	41:a:1412:U:C6	2.56	0.40
41:a:1506:U:H2'	41:a:1507:C:C6	2.56	0.40
41:a:1575:C:C4	41:a:1576:U:C4	3.10	0.40
41:a:2864:G:C5	41:a:2865:U:C4	3.09	0.40
59:s:73:VAL:HG11	59:s:75:TYR:CZ	2.57	0.40
65:y:26:VAL:HG22	65:y:27:GLU:H	1.87	0.40
4:3:59:VAL:HG12	4:3:60:GLU:N	2.37	0.40
10:A:46:G:O2'	10:A:47:U:C6	2.72	0.40
11:AA:1304:MET:SD	11:AA:1304:MET:C	3.05	0.40
12:AD:19:VAL:O	12:AD:20:SER:C	2.64	0.40
15:AG:65:VAL:HG12	15:AG:66:ASP:H	1.86	0.40
10:B:44:A:H2'	10:B:45:G:C8	2.57	0.40
17:D:429:U:O2	17:D:430:A:C8	2.75	0.40
17:D:996:A:H61	17:D:1045:C:H2'	1.86	0.40
17:D:1312:G:P	47:g:63:ARG:CZ	3.09	0.40
17:D:1329:A:H4'	38:X:24:GLY:O	2.21	0.40
17:D:1434:A:H2'	17:D:1435:G:O4'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:D:1521:C:H2'	17:D:1522:U:C6	2.55	0.40
25:L:64:VAL:HG12	25:L:65:GLU:N	2.36	0.40
25:L:92:THR:HG22	25:L:93:LYS:N	2.36	0.40
28:NG:136:VAL:O	28:NG:137:ASN:OD1	2.40	0.40
29:O:63:LEU:HD23	29:O:63:LEU:N	2.36	0.40
32:R:74:LEU:HD11	32:R:80:ILE:CG2	2.51	0.40
41:a:271:G:C4	41:a:272:A:N7	2.89	0.40
41:a:323:C:C4	41:a:333:G:C8	3.08	0.40
41:a:1055:G:C6	41:a:1056:G:C5	3.09	0.40
41:a:1059:G:H2'	41:a:1060:U:C5	2.56	0.40
41:a:1301:A:C4	41:a:1303:G:N7	2.89	0.40
41:a:1379:U:O2'	41:a:1380:G:P	2.79	0.40
41:a:2266:A:H4'	41:a:2267:A:N3	2.36	0.40
41:a:2399:G:C6	41:a:2418:A:C6	3.08	0.40
41:a:2830:C:O2'	41:a:2831:G:H5'	2.21	0.40
41:a:2846:G:H2'	41:a:2847:U:O4'	2.21	0.40
44:d:48:U:H2'	44:d:49:C:C6	2.56	0.40
44:d:95:U:H2'	44:d:96:G:H8	1.86	0.40
47:g:12:ILE:HG21	47:g:32:LEU:HD23	2.03	0.40
7:6:21:DA:N1	8:7:51:G:C6	2.90	0.40
10:A:18:G:O4'	10:A:18:G:OP1	2.39	0.40
11:AA:104:ILE:HD12	11:AA:115:LYS:HE2	2.02	0.40
13:AE:53:ARG:HA	13:AE:54:ASP:HA	1.85	0.40
13:AE:416:ILE:O	13:AE:416:ILE:HG22	2.21	0.40
15:AG:130:PHE:CD2	15:AG:195:LEU:HG	2.57	0.40
15:AG:276:TRP:HA	15:AG:286:ASN:ND2	2.36	0.40
10:B:55:U:O2	10:B:58:A:N7	2.54	0.40
10:B:56:C:H2'	10:B:57:A:C4'	2.52	0.40
17:D:632:U:O2	17:D:632:U:C2'	2.70	0.40
17:D:704:A:C6	17:D:705:G:C5	3.10	0.40
17:D:940:C:H2'	17:D:941:G:O4'	2.22	0.40
17:D:1360:A:C6	17:D:1361:G:C5	3.10	0.40
28:NG:43:MET:O	28:NG:70:LEU:HB2	2.21	0.40
28:NG:92:PHE:CD1	28:NG:100:PRO:HG3	2.56	0.40
41:a:1178:C:H2'	41:a:1179:G:O4'	2.21	0.40
41:a:1412:U:N3	41:a:1413:A:N7	2.69	0.40
41:a:1630:A:C6	41:a:1637:A:N6	2.90	0.40
41:a:1845:G:N1	41:a:1846:G:C5	2.89	0.40
41:a:1846:G:C6	41:a:1847:A:C6	3.10	0.40
41:a:2142:A:H2'	41:a:2143:C:C6	2.57	0.40
41:a:2186:G:H2'	41:a:2187:U:O4'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:2195:U:C2	41:a:2196:C:C6	3.10	0.40
46:f:51:VAL:O	46:f:55:VAL:HG22	2.21	0.40
52:l:146:VAL:HG22	52:l:147:LEU:N	2.37	0.40
61:u:55:MET:HE2	61:u:55:MET:HB2	2.01	0.40
5:4:29:ILE:HD13	44:d:74:U:O2	2.22	0.40
11:AA:1113:LEU:HD11	13:AE:641:ILE:HD13	2.03	0.40
12:AD:197:ASP:C	12:AD:198:LEU:HD12	2.47	0.40
12:AD:211:ILE:HD11	12:AD:215:GLU:OE1	2.21	0.40
13:AE:278:ARG:NH2	28:NG:66:PRO:HG3	2.37	0.40
13:AE:587:LEU:HD23	13:AE:591:ILE:HG21	2.02	0.40
15:AG:453:VAL:HG13	15:AG:458:ASP:HB2	2.02	0.40
17:D:81:A:N7	17:D:83:C:N4	2.70	0.40
17:D:640:A:O2'	27:N:107:SER:HB3	2.22	0.40
17:D:1018:G:H2'	17:D:1019:A:O4'	2.22	0.40
17:D:1300:G:C4	17:D:1334:G:C6	3.09	0.40
19:F:4:ILE:HD12	19:F:19:PHE:HA	2.04	0.40
38:X:101:ARG:HG3	38:X:101:ARG:O	2.21	0.40
39:Y:93:ASN:HB2	39:Y:135:MET:SD	2.60	0.40
41:a:65:U:C2	41:a:66:C:C6	3.10	0.40
41:a:190:A:N6	41:a:207:A:H1'	2.36	0.40
41:a:230:G:C2	41:a:231:A:C8	3.10	0.40
41:a:287:G:C6	41:a:354:A:C6	3.09	0.40
41:a:327:G:H2'	41:a:328:U:C6	2.56	0.40
41:a:367:G:C6	41:a:368:A:C6	3.10	0.40
41:a:699:A:N7	41:a:734:A:C5	2.90	0.40
41:a:802:A:C4	41:a:803:U:C5	3.09	0.40
41:a:901:C:C2	41:a:902:C:C6	3.10	0.40
41:a:1108:U:H2'	41:a:1109:C:C6	2.57	0.40
41:a:1179:G:O4'	41:a:1179:G:N3	2.54	0.40
41:a:1199:U:H2'	41:a:1200:C:H6	1.87	0.40
41:a:1212:G:N2	41:a:1236:G:H1'	2.37	0.40
41:a:1223:G:C6	41:a:1227:G:C6	3.09	0.40
41:a:1287:A:O2'	41:a:1288:G:H5'	2.21	0.40
41:a:1294:U:C4	41:a:1295:C:C5	3.08	0.40
41:a:1321:A:C5	41:a:1322:A:C8	3.09	0.40
41:a:2097:A:C2	41:a:2098:U:C2	3.09	0.40
41:a:2243:U:H2'	41:a:2244:U:C6	2.57	0.40
44:d:62:C:H2'	44:d:63:C:H6	1.86	0.40
48:h:165:VAL:HG23	48:h:166:ALA:N	2.35	0.40
49:i:46:ASP:OD1	49:i:46:ASP:C	2.64	0.40
54:n:4:LEU:HD11	54:n:101:GLU:HA	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	101/103 (98%)	92 (91%)	9 (9%)	0	100	100
2	1	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	2	92/100 (92%)	88 (96%)	4 (4%)	0	100	100
4	3	101/104 (97%)	95 (94%)	6 (6%)	0	100	100
5	4	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
9	9	146/165 (88%)	114 (78%)	28 (19%)	4 (3%)	4	25
11	AA	1338/1342 (100%)	1265 (94%)	73 (6%)	0	100	100
12	AC	216/329 (66%)	208 (96%)	8 (4%)	0	100	100
12	AD	292/329 (89%)	275 (94%)	17 (6%)	0	100	100
13	AE	1329/1407 (94%)	1259 (95%)	70 (5%)	0	100	100
14	AF	80/91 (88%)	78 (98%)	2 (2%)	0	100	100
15	AG	493/495 (100%)	432 (88%)	58 (12%)	3 (1%)	21	56
16	C	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
18	E	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
19	F	68/71 (96%)	67 (98%)	1 (2%)	0	100	100
20	G	223/241 (92%)	212 (95%)	11 (5%)	0	100	100
21	H	255/557 (46%)	201 (79%)	53 (21%)	1 (0%)	30	62
22	I	206/233 (88%)	196 (95%)	10 (5%)	0	100	100
23	J	203/206 (98%)	201 (99%)	2 (1%)	0	100	100
24	K	154/167 (92%)	147 (96%)	7 (4%)	0	100	100
25	L	102/135 (76%)	98 (96%)	3 (3%)	1 (1%)	12	45
26	M	149/179 (83%)	143 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	N	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
28	NG	158/181 (87%)	141 (89%)	17 (11%)	0	100	100
29	O	125/130 (96%)	113 (90%)	12 (10%)	0	100	100
30	P	97/103 (94%)	86 (89%)	11 (11%)	0	100	100
31	Q	115/129 (89%)	109 (95%)	6 (5%)	0	100	100
32	R	117/124 (94%)	108 (92%)	9 (8%)	0	100	100
33	S	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
34	T	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
35	U	80/82 (98%)	74 (92%)	6 (8%)	0	100	100
36	V	78/84 (93%)	70 (90%)	8 (10%)	0	100	100
37	W	81/92 (88%)	77 (95%)	4 (5%)	0	100	100
38	X	114/118 (97%)	104 (91%)	9 (8%)	1 (1%)	14	47
39	Y	139/142 (98%)	126 (91%)	12 (9%)	1 (1%)	18	52
40	Z	28/121 (23%)	25 (89%)	3 (11%)	0	100	100
42	b	74/85 (87%)	70 (95%)	4 (5%)	0	100	100
43	c	75/78 (96%)	69 (92%)	6 (8%)	0	100	100
45	e	60/63 (95%)	59 (98%)	1 (2%)	0	100	100
46	f	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
47	g	64/70 (91%)	61 (95%)	3 (5%)	0	100	100
48	h	269/273 (98%)	248 (92%)	21 (8%)	0	100	100
49	i	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
50	j	207/209 (99%)	194 (94%)	13 (6%)	0	100	100
51	k	50/55 (91%)	47 (94%)	3 (6%)	0	100	100
52	l	199/201 (99%)	193 (97%)	6 (3%)	0	100	100
53	m	44/46 (96%)	44 (100%)	0	0	100	100
54	n	175/179 (98%)	162 (93%)	13 (7%)	0	100	100
55	o	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
56	p	173/177 (98%)	165 (95%)	8 (5%)	0	100	100
57	q	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
58	r	147/149 (99%)	138 (94%)	9 (6%)	0	100	100
59	s	140/142 (99%)	132 (94%)	8 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
60	t	121/123 (98%)	108 (89%)	13 (11%)	0	100	100
61	u	142/144 (99%)	136 (96%)	6 (4%)	0	100	100
62	v	134/136 (98%)	127 (95%)	7 (5%)	0	100	100
63	w	117/127 (92%)	107 (92%)	10 (8%)	0	100	100
64	x	114/117 (97%)	105 (92%)	9 (8%)	0	100	100
65	y	112/115 (97%)	106 (95%)	6 (5%)	0	100	100
66	z	115/118 (98%)	110 (96%)	5 (4%)	0	100	100
All	All	10079/11072 (91%)	9423 (94%)	645 (6%)	11 (0%)	49	79

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	9	88	HIS
15	AG	39	TYR
21	H	309	MET
38	X	103	LYS
9	9	33	VAL
9	9	108	VAL
15	AG	102	PHE
9	9	118	ILE
39	Y	20	SER
15	AG	279	ASN
25	L	96	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	84/84 (100%)	84 (100%)	0	100	100
2	1	93/93 (100%)	93 (100%)	0	100	100
3	2	81/84 (96%)	81 (100%)	0	100	100
4	3	84/85 (99%)	84 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	4	78/78 (100%)	78 (100%)	0	100	100
9	9	112/123 (91%)	112 (100%)	0	100	100
11	AA	1155/1157 (100%)	1155 (100%)	0	100	100
12	AC	185/286 (65%)	185 (100%)	0	100	100
12	AD	185/286 (65%)	185 (100%)	0	100	100
13	AE	1120/1168 (96%)	1120 (100%)	0	100	100
14	AF	70/75 (93%)	70 (100%)	0	100	100
15	AG	409/409 (100%)	409 (100%)	0	100	100
16	C	57/65 (88%)	57 (100%)	0	100	100
18	E	65/66 (98%)	65 (100%)	0	100	100
19	F	60/61 (98%)	60 (100%)	0	100	100
20	G	187/199 (94%)	187 (100%)	0	100	100
21	H	137/461 (30%)	137 (100%)	0	100	100
22	I	171/190 (90%)	171 (100%)	0	100	100
23	J	172/173 (99%)	172 (100%)	0	100	100
24	K	119/126 (94%)	119 (100%)	0	100	100
25	L	91/116 (78%)	91 (100%)	0	100	100
26	M	124/147 (84%)	124 (100%)	0	100	100
27	N	104/105 (99%)	104 (100%)	0	100	100
28	NG	142/158 (90%)	142 (100%)	0	100	100
29	O	105/107 (98%)	105 (100%)	0	100	100
30	P	86/90 (96%)	86 (100%)	0	100	100
31	Q	90/99 (91%)	90 (100%)	0	100	100
32	R	101/104 (97%)	101 (100%)	0	100	100
33	S	83/84 (99%)	83 (100%)	0	100	100
34	T	76/77 (99%)	76 (100%)	0	100	100
35	U	65/65 (100%)	65 (100%)	0	100	100
36	V	74/78 (95%)	74 (100%)	0	100	100
37	W	72/79 (91%)	72 (100%)	0	100	100
38	X	94/96 (98%)	94 (100%)	0	100	100
39	Y	109/110 (99%)	109 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	Z	26/85 (31%)	26 (100%)	0	100	100
42	b	58/63 (92%)	58 (100%)	0	100	100
43	c	67/68 (98%)	67 (100%)	0	100	100
45	e	54/55 (98%)	54 (100%)	0	100	100
46	f	48/49 (98%)	48 (100%)	0	100	100
47	g	59/62 (95%)	59 (100%)	0	100	100
48	h	216/218 (99%)	216 (100%)	0	100	100
49	i	47/48 (98%)	47 (100%)	0	100	100
50	j	164/164 (100%)	164 (100%)	0	100	100
51	k	47/49 (96%)	47 (100%)	0	100	100
52	l	165/165 (100%)	165 (100%)	0	100	100
53	m	38/38 (100%)	38 (100%)	0	100	100
54	n	148/150 (99%)	148 (100%)	0	100	100
55	o	51/52 (98%)	51 (100%)	0	100	100
56	p	136/138 (99%)	136 (100%)	0	100	100
57	q	34/34 (100%)	34 (100%)	0	100	100
58	r	114/114 (100%)	114 (100%)	0	100	100
59	s	116/116 (100%)	116 (100%)	0	100	100
60	t	104/104 (100%)	104 (100%)	0	100	100
61	u	103/103 (100%)	103 (100%)	0	100	100
62	v	109/109 (100%)	109 (100%)	0	100	100
63	w	99/103 (96%)	99 (100%)	0	100	100
64	x	86/87 (99%)	86 (100%)	0	100	100
65	y	99/100 (99%)	99 (100%)	0	100	100
66	z	89/90 (99%)	89 (100%)	0	100	100
All	All	8317/9148 (91%)	8317 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (56) such sidechains are listed below:

Mol	Chain	Res	Type
4	3	46	GLN

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Mol	Chain	Res	Type
5	4	80	HIS
5	4	87	GLN
11	AA	120	GLN
11	AA	330	HIS
11	AA	573	ASN
11	AA	628	HIS
11	AA	808	ASN
11	AA	1099	ASN
11	AA	1268	GLN
12	AD	41	ASN
12	AD	84	ASN
12	AD	117	HIS
12	AD	128	HIS
12	AD	227	GLN
13	AE	448	GLN
13	AE	875	ASN
13	AE	1238	GLN
13	AE	1366	HIS
14	AF	29	GLN
15	AG	194	GLN
18	E	3	ASN
20	G	39	HIS
20	G	170	HIS
22	I	102	ASN
23	J	41	HIS
23	J	116	GLN
24	K	70	ASN
24	K	121	HIS
25	L	3	HIS
29	O	4	ASN
30	P	15	HIS
31	Q	24	HIS
35	U	9	HIS
35	U	59	HIS
36	V	47	HIS
39	Y	33	ASN
45	e	36	GLN
48	h	53	HIS
49	i	19	HIS
51	k	46	HIS
52	l	29	HIS
52	l	41	GLN

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Mol	Chain	Res	Type
52	l	115	GLN
53	m	16	HIS
54	n	127	ASN
55	o	28	ASN
55	o	43	HIS
56	p	38	ASN
56	p	73	ASN
57	q	13	ASN
59	s	130	HIS
61	u	54	GLN
63	w	31	HIS
64	x	19	GLN
65	y	52	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	75/76 (98%)	34 (45%)	3 (4%)
10	B	75/76 (98%)	38 (50%)	5 (6%)
17	D	1513/1542 (98%)	268 (17%)	5 (0%)
41	a	2859/2904 (98%)	494 (17%)	0
44	d	119/120 (99%)	17 (14%)	0
8	7	30/56 (53%)	20 (66%)	3 (10%)
All	All	4671/4774 (97%)	871 (18%)	16 (0%)

All (871) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	3	G
8	7	4	U
8	7	5	U
8	7	6	U
8	7	7	U
8	7	8	U
8	7	9	U
8	7	10	U
8	7	11	U
8	7	13	U
8	7	14	U
8	7	15	U
8	7	16	U

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Mol	Chain	Res	Type
8	7	17	U
8	7	18	U
8	7	19	U
8	7	20	U
8	7	48	U
8	7	49	C
8	7	52	U
10	A	2	G
10	A	4	G
10	A	6	G
10	A	7	G
10	A	8	U
10	A	13	C
10	A	14	A
10	A	16	C
10	A	17	C
10	A	18	G
10	A	20	U
10	A	21	A
10	A	22	G
10	A	23	C
10	A	34	C
10	A	45	G
10	A	46	G
10	A	47	U
10	A	48	C
10	A	49	G
10	A	52	G
10	A	54	U
10	A	55	U
10	A	57	A
10	A	58	A
10	A	59	A
10	A	60	U
10	A	62	C
10	A	66	C
10	A	69	C
10	A	70	G
10	A	71	C
10	A	72	A
10	A	73	A
10	B	2	G

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Mol	Chain	Res	Type
10	B	4	G
10	B	5	G
10	B	6	G
10	B	7	G
10	B	8	U
10	B	10	G
10	B	12	G
10	B	13	C
10	B	16	C
10	B	17	C
10	B	18	G
10	B	19	G
10	B	20	U
10	B	21	A
10	B	22	G
10	B	23	C
10	B	36	U
10	B	37	A
10	B	38	A
10	B	46	G
10	B	47	U
10	B	48	C
10	B	56	C
10	B	57	A
10	B	58	A
10	B	59	A
10	B	60	U
10	B	61	C
10	B	64	G
10	B	65	C
10	B	66	C
10	B	68	C
10	B	69	C
10	B	70	G
10	B	71	C
10	B	72	A
10	B	73	A
17	D	2	A
17	D	4	U
17	D	5	U
17	D	8	A
17	D	9	G

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Mol	Chain	Res	Type
17	D	21	G
17	D	22	G
17	D	31	G
17	D	32	A
17	D	39	G
17	D	47	C
17	D	48	C
17	D	50	A
17	D	51	A
17	D	54	C
17	D	60	A
17	D	64	G
17	D	68	G
17	D	69	G
17	D	72	A
17	D	74	A
17	D	76	G
17	D	78	A
17	D	81	A
17	D	82	G
17	D	83	C
17	D	84	U
17	D	85	U
17	D	87	C
17	D	88	U
17	D	91	U
17	D	92	U
17	D	95	C
17	D	108	G
17	D	120	A
17	D	122	G
17	D	128	G
17	D	130	A
17	D	131	A
17	D	141	G
17	D	144	G
17	D	160	A
17	D	164	G
17	D	173	U
17	D	181	A
17	D	182	A
17	D	183	C

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Mol	Chain	Res	Type
17	D	188	C
17	D	189	A
17	D	197	A
17	D	198	G
17	D	202	G
17	D	204	G
17	D	208	U
17	D	210	C
17	D	211	G
17	D	212	G
17	D	214	C
17	D	226	G
17	D	240	G
17	D	245	U
17	D	247	G
17	D	251	G
17	D	266	G
17	D	267	C
17	D	280	C
17	D	289	G
17	D	306	A
17	D	321	A
17	D	328	C
17	D	330	C
17	D	332	G
17	D	347	G
17	D	351	G
17	D	352	C
17	D	354	G
17	D	367	U
17	D	372	C
17	D	388	G
17	D	397	A
17	D	406	G
17	D	412	A
17	D	413	G
17	D	414	A
17	D	421	U
17	D	422	C
17	D	429	U
17	D	436	C
17	D	457	G

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Mol	Chain	Res	Type
17	D	458	U
17	D	463	U
17	D	464	U
17	D	467	U
17	D	468	A
17	D	469	C
17	D	476	U
17	D	478	A
17	D	479	U
17	D	481	G
17	D	484	G
17	D	485	U
17	D	486	U
17	D	495	A
17	D	496	A
17	D	509	A
17	D	511	C
17	D	512	U
17	D	515	G
17	D	518	C
17	D	519	C
17	D	521	G
17	D	531	U
17	D	532	A
17	D	533	A
17	D	547	A
17	D	564	C
17	D	568	G
17	D	572	A
17	D	573	A
17	D	575	G
17	D	576	C
17	D	577	G
17	D	596	A
17	D	650	G
17	D	653	U
17	D	665	A
17	D	687	A
17	D	700	G
17	D	718	A
17	D	723	U
17	D	724	G

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Mol	Chain	Res	Type
17	D	731	G
17	D	733	G
17	D	734	G
17	D	747	A
17	D	748	G
17	D	752	G
17	D	759	A
17	D	763	G
17	D	777	A
17	D	792	A
17	D	793	U
17	D	794	A
17	D	802	A
17	D	815	A
17	D	817	C
17	D	828	U
17	D	829	G
17	D	841	C
17	D	843	U
17	D	844	G
17	D	846	G
17	D	872	A
17	D	902	G
17	D	914	A
17	D	916	U
17	D	926	G
17	D	934	C
17	D	935	A
17	D	942	G
17	D	945	G
17	D	960	U
17	D	969	A
17	D	971	G
17	D	972	C
17	D	975	A
17	D	976	G
17	D	977	A
17	D	989	U
17	D	992	U
17	D	993	G
17	D	996	A
17	D	1004	A

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Mol	Chain	Res	Type
17	D	1008	U
17	D	1009	U
17	D	1018	G
17	D	1021	A
17	D	1022	A
17	D	1026	G
17	D	1030	U
17	D	1031	C
17	D	1032	G
17	D	1033	G
17	D	1035	A
17	D	1043	G
17	D	1044	A
17	D	1046	A
17	D	1063	C
17	D	1065	U
17	D	1079	G
17	D	1085	U
17	D	1094	G
17	D	1095	U
17	D	1099	G
17	D	1101	A
17	D	1108	G
17	D	1124	G
17	D	1130	A
17	D	1133	G
17	D	1135	U
17	D	1136	C
17	D	1137	C
17	D	1139	G
17	D	1140	C
17	D	1141	C
17	D	1142	G
17	D	1145	A
17	D	1146	A
17	D	1149	C
17	D	1151	A
17	D	1152	A
17	D	1158	C
17	D	1159	U
17	D	1167	A
17	D	1174	G

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Mol	Chain	Res	Type
17	D	1175	G
17	D	1176	A
17	D	1184	G
17	D	1196	A
17	D	1197	A
17	D	1213	A
17	D	1214	C
17	D	1225	A
17	D	1227	A
17	D	1238	A
17	D	1239	A
17	D	1256	A
17	D	1257	A
17	D	1275	A
17	D	1278	G
17	D	1279	G
17	D	1280	A
17	D	1285	A
17	D	1286	U
17	D	1287	A
17	D	1299	A
17	D	1300	G
17	D	1302	C
17	D	1305	G
17	D	1317	C
17	D	1318	A
17	D	1320	C
17	D	1332	A
17	D	1338	G
17	D	1346	A
17	D	1353	G
17	D	1363	A
17	D	1370	G
17	D	1379	G
17	D	1381	U
17	D	1397	C
17	D	1398	A
17	D	1404	C
17	D	1419	G
17	D	1429	A
17	D	1432	G
17	D	1441	A

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Mol	Chain	Res	Type
17	D	1446	A
17	D	1453	G
17	D	1493	A
17	D	1494	G
17	D	1497	G
17	D	1503	A
17	D	1506	U
17	D	1517	G
17	D	1529	G
17	D	1530	G
17	D	1534	A
41	a	10	A
41	a	26	G
41	a	27	G
41	a	34	U
41	a	46	G
41	a	51	G
41	a	60	G
41	a	63	A
41	a	71	A
41	a	74	A
41	a	75	G
41	a	80	G
41	a	85	G
41	a	101	A
41	a	102	U
41	a	103	A
41	a	118	A
41	a	120	U
41	a	137	U
41	a	139	U
41	a	140	C
41	a	149	A
41	a	163	C
41	a	165	A
41	a	171	U
41	a	181	A
41	a	196	A
41	a	199	A
41	a	215	G
41	a	216	A
41	a	222	A

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Mol	Chain	Res	Type
41	a	248	G
41	a	249	C
41	a	264	C
41	a	265	A
41	a	266	G
41	a	275	C
41	a	278	A
41	a	279	A
41	a	285	G
41	a	296	U
41	a	311	A
41	a	329	G
41	a	330	A
41	a	335	C
41	a	352	A
41	a	353	C
41	a	361	G
41	a	362	A
41	a	367	G
41	a	370	G
41	a	371	A
41	a	372	G
41	a	386	G
41	a	396	G
41	a	404	A
41	a	405	U
41	a	406	G
41	a	411	G
41	a	412	A
41	a	421	C
41	a	424	G
41	a	429	A
41	a	456	C
41	a	457	A
41	a	465	G
41	a	473	G
41	a	475	C
41	a	479	A
41	a	481	G
41	a	491	G
41	a	501	A
41	a	505	A

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Mol	Chain	Res	Type
41	a	508	A
41	a	509	C
41	a	510	C
41	a	530	G
41	a	532	A
41	a	533	G
41	a	543	G
41	a	544	C
41	a	546	U
41	a	547	A
41	a	548	G
41	a	549	G
41	a	551	G
41	a	563	A
41	a	572	A
41	a	573	U
41	a	574	A
41	a	575	A
41	a	588	U
41	a	603	A
41	a	613	A
41	a	614	A
41	a	615	U
41	a	627	A
41	a	637	A
41	a	645	C
41	a	647	G
41	a	654	A
41	a	686	U
41	a	710	U
41	a	717	C
41	a	730	A
41	a	738	G
41	a	775	G
41	a	776	G
41	a	782	A
41	a	784	G
41	a	785	G
41	a	805	G
41	a	812	C
41	a	819	A
41	a	827	U

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Mol	Chain	Res	Type
41	a	828	U
41	a	845	A
41	a	846	U
41	a	847	U
41	a	858	G
41	a	859	G
41	a	869	G
41	a	877	A
41	a	878	A
41	a	883	G
41	a	884	U
41	a	885	C
41	a	886	A
41	a	888	C
41	a	889	C
41	a	891	G
41	a	893	C
41	a	895	U
41	a	896	A
41	a	897	C
41	a	910	A
41	a	914	G
41	a	915	C
41	a	941	A
41	a	945	A
41	a	946	C
41	a	953	G
41	a	961	C
41	a	974	G
41	a	983	A
41	a	995	C
41	a	996	A
41	a	999	U
41	a	1012	U
41	a	1013	C
41	a	1022	G
41	a	1023	U
41	a	1033	U
41	a	1034	G
41	a	1043	C
41	a	1045	C
41	a	1046	A

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Mol	Chain	Res	Type
41	a	1047	G
41	a	1049	C
41	a	1054	A
41	a	1062	G
41	a	1064	C
41	a	1065	U
41	a	1066	U
41	a	1067	A
41	a	1070	A
41	a	1071	G
41	a	1073	A
41	a	1075	C
41	a	1083	U
41	a	1084	A
41	a	1087	G
41	a	1088	A
41	a	1101	U
41	a	1109	C
41	a	1110	G
41	a	1111	A
41	a	1112	G
41	a	1119	U
41	a	1128	G
41	a	1129	A
41	a	1132	U
41	a	1133	A
41	a	1134	A
41	a	1135	C
41	a	1136	G
41	a	1142	A
41	a	1151	A
41	a	1169	A
41	a	1170	C
41	a	1171	G
41	a	1173	U
41	a	1174	U
41	a	1175	A
41	a	1176	U
41	a	1177	G
41	a	1178	C
41	a	1179	G
41	a	1186	G

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Mol	Chain	Res	Type
41	a	1227	G
41	a	1235	G
41	a	1236	G
41	a	1238	G
41	a	1248	G
41	a	1249	U
41	a	1253	A
41	a	1256	G
41	a	1266	G
41	a	1271	G
41	a	1272	A
41	a	1273	U
41	a	1300	G
41	a	1301	A
41	a	1302	A
41	a	1321	A
41	a	1329	U
41	a	1345	C
41	a	1352	U
41	a	1359	A
41	a	1365	A
41	a	1379	U
41	a	1380	G
41	a	1383	A
41	a	1395	A
41	a	1408	G
41	a	1410	G
41	a	1411	U
41	a	1416	G
41	a	1417	C
41	a	1427	A
41	a	1428	C
41	a	1452	G
41	a	1453	A
41	a	1454	C
41	a	1482	G
41	a	1490	A
41	a	1493	C
41	a	1497	U
41	a	1503	A
41	a	1508	A
41	a	1510	G

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Mol	Chain	Res	Type
41	a	1515	A
41	a	1524	G
41	a	1529	G
41	a	1532	A
41	a	1533	C
41	a	1534	U
41	a	1535	A
41	a	1536	C
41	a	1537	G
41	a	1538	G
41	a	1554	U
41	a	1566	A
41	a	1569	A
41	a	1578	U
41	a	1580	A
41	a	1582	C
41	a	1583	A
41	a	1584	U
41	a	1585	C
41	a	1586	A
41	a	1587	G
41	a	1589	U
41	a	1590	A
41	a	1608	A
41	a	1610	A
41	a	1616	A
41	a	1622	G
41	a	1646	C
41	a	1647	U
41	a	1648	U
41	a	1649	G
41	a	1651	G
41	a	1673	G
41	a	1674	G
41	a	1675	C
41	a	1698	A
41	a	1703	G
41	a	1714	U
41	a	1715	G
41	a	1722	A
41	a	1729	U
41	a	1730	C

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Mol	Chain	Res	Type
41	a	1732	C
41	a	1733	G
41	a	1735	A
41	a	1738	G
41	a	1756	G
41	a	1758	U
41	a	1764	C
41	a	1773	A
41	a	1784	A
41	a	1791	A
41	a	1800	C
41	a	1802	A
41	a	1808	A
41	a	1811	G
41	a	1816	C
41	a	1817	G
41	a	1829	A
41	a	1833	C
41	a	1848	A
41	a	1858	A
41	a	1869	G
41	a	1870	C
41	a	1872	A
41	a	1884	G
41	a	1906	G
41	a	1907	G
41	a	1909	C
41	a	1910	G
41	a	1913	A
41	a	1914	C
41	a	1922	G
41	a	1923	U
41	a	1925	C
41	a	1929	G
41	a	1930	G
41	a	1936	A
41	a	1938	A
41	a	1942	C
41	a	1955	U
41	a	1964	G
41	a	1967	C
41	a	1970	A

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Mol	Chain	Res	Type
41	a	1971	U
41	a	1972	G
41	a	1991	U
41	a	1992	G
41	a	1993	U
41	a	1997	C
41	a	2022	U
41	a	2023	C
41	a	2027	G
41	a	2032	G
41	a	2033	A
41	a	2043	C
41	a	2052	A
41	a	2055	C
41	a	2056	G
41	a	2060	A
41	a	2061	G
41	a	2062	A
41	a	2072	C
41	a	2093	G
41	a	2097	A
41	a	2099	U
41	a	2110	G
41	a	2111	U
41	a	2112	G
41	a	2113	U
41	a	2115	G
41	a	2116	G
41	a	2117	A
41	a	2118	U
41	a	2121	G
41	a	2122	U
41	a	2124	G
41	a	2125	G
41	a	2126	A
41	a	2127	G
41	a	2128	G
41	a	2131	U
41	a	2132	U
41	a	2133	G
41	a	2134	A
41	a	2142	A

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Mol	Chain	Res	Type
41	a	2147	A
41	a	2148	G
41	a	2157	G
41	a	2158	A
41	a	2159	G
41	a	2161	C
41	a	2163	A
41	a	2164	C
41	a	2165	C
41	a	2168	G
41	a	2171	A
41	a	2172	U
41	a	2173	A
41	a	2176	A
41	a	2182	U
41	a	2183	A
41	a	2185	U
41	a	2186	G
41	a	2189	U
41	a	2190	G
41	a	2193	G
41	a	2194	U
41	a	2198	A
41	a	2204	G
41	a	2211	A
41	a	2212	A
41	a	2225	A
41	a	2226	C
41	a	2238	G
41	a	2239	G
41	a	2250	G
41	a	2273	A
41	a	2279	G
41	a	2283	C
41	a	2287	A
41	a	2305	U
41	a	2309	A
41	a	2314	A
41	a	2322	A
41	a	2325	G
41	a	2327	A
41	a	2333	A

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Mol	Chain	Res	Type
41	a	2335	A
41	a	2344	U
41	a	2347	C
41	a	2361	G
41	a	2376	A
41	a	2383	G
41	a	2385	C
41	a	2396	G
41	a	2402	U
41	a	2403	C
41	a	2422	C
41	a	2423	U
41	a	2425	A
41	a	2426	A
41	a	2428	G
41	a	2429	G
41	a	2430	A
41	a	2431	U
41	a	2435	A
41	a	2441	U
41	a	2448	A
41	a	2470	G
41	a	2475	C
41	a	2476	A
41	a	2478	A
41	a	2484	G
41	a	2491	U
41	a	2502	G
41	a	2506	U
41	a	2507	C
41	a	2513	A
41	a	2518	A
41	a	2520	C
41	a	2529	G
41	a	2554	U
41	a	2566	A
41	a	2567	G
41	a	2572	A
41	a	2573	C
41	a	2576	G
41	a	2582	G
41	a	2585	U

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Mol	Chain	Res	Type
41	a	2586	U
41	a	2597	G
41	a	2602	A
41	a	2609	U
41	a	2613	U
41	a	2629	U
41	a	2661	G
41	a	2689	U
41	a	2690	U
41	a	2714	G
41	a	2716	C
41	a	2725	A
41	a	2726	A
41	a	2729	G
41	a	2733	A
41	a	2744	G
41	a	2748	A
41	a	2757	A
41	a	2758	A
41	a	2777	G
41	a	2778	A
41	a	2791	G
41	a	2793	C
41	a	2796	U
41	a	2797	U
41	a	2798	U
41	a	2799	A
41	a	2801	G
41	a	2818	U
41	a	2820	A
41	a	2821	A
41	a	2825	G
41	a	2849	U
41	a	2859	G
41	a	2867	G
41	a	2872	A
41	a	2879	A
41	a	2880	C
41	a	2883	A
41	a	2884	U
41	a	2885	G
41	a	2891	U

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Mol	Chain	Res	Type
41	a	2903	U
44	d	2	G
44	d	13	G
44	d	15	A
44	d	16	G
44	d	17	C
44	d	24	G
44	d	35	C
44	d	42	C
44	d	56	G
44	d	66	A
44	d	88	C
44	d	89	U
44	d	90	C
44	d	99	A
44	d	105	G
44	d	108	A
44	d	109	A

All (16) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	7	8	U
8	7	10	U
8	7	47	G
10	A	6	G
10	A	21	A
10	A	22	G
10	B	6	G
10	B	21	A
10	B	22	G
10	B	46	G
10	B	58	A
17	D	197	A
17	D	758	C
17	D	1145	A
17	D	1337	G
17	D	1493	A

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

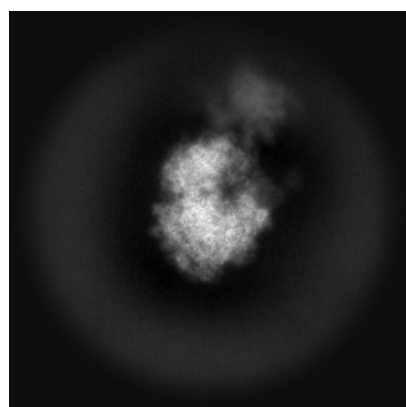
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72646. These allow visual inspection of the internal detail of the map and identification of artifacts.

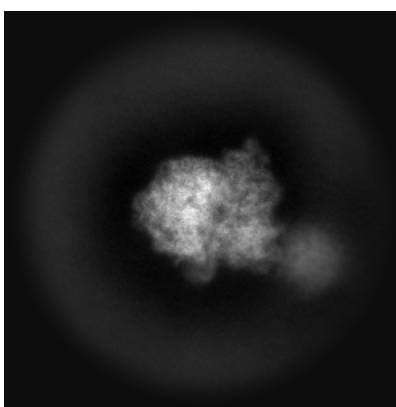
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

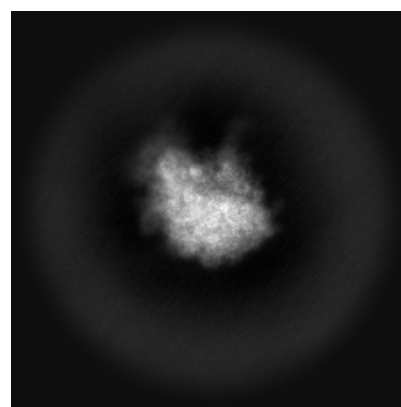
6.1.1 Primary map



X



Y

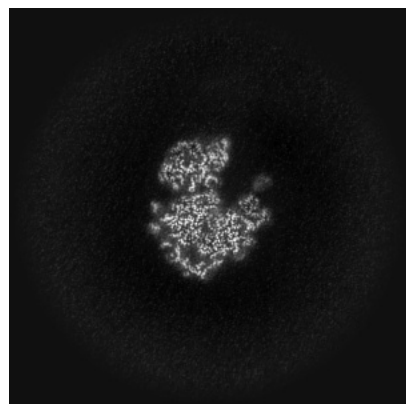


Z

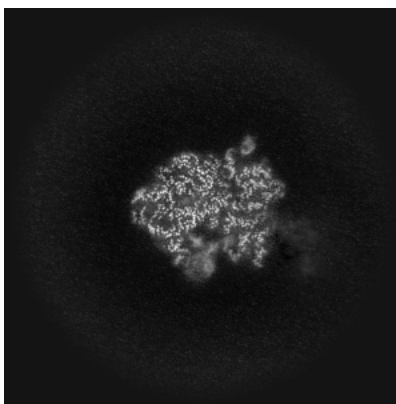
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

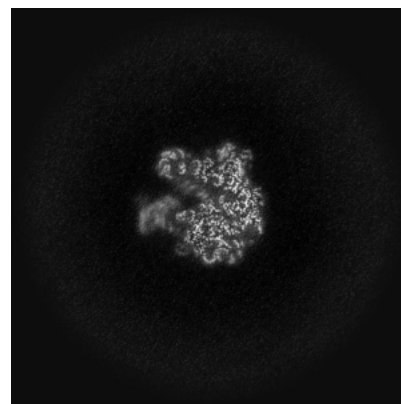
6.2.1 Primary map



X Index: 256



Y Index: 256

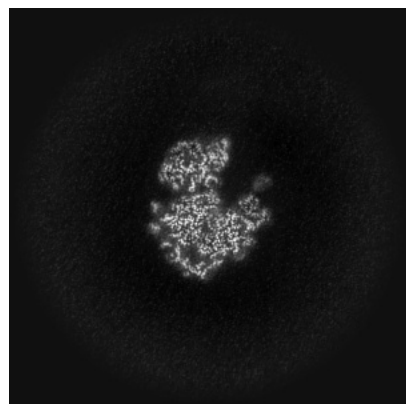


Z Index: 256

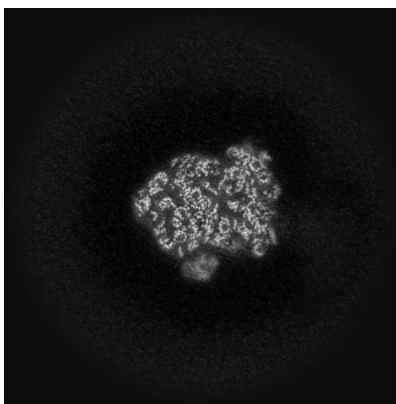
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

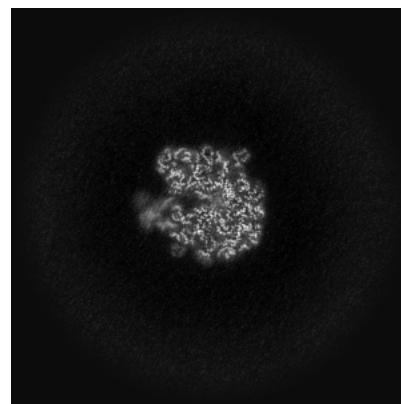
6.3.1 Primary map



X Index: 256



Y Index: 244

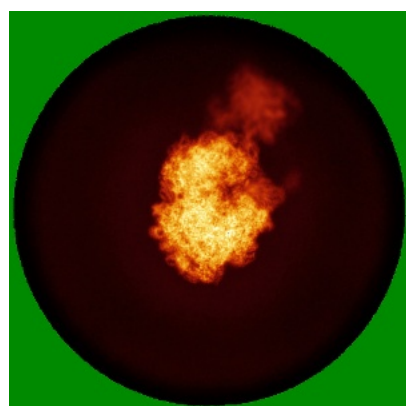


Z Index: 247

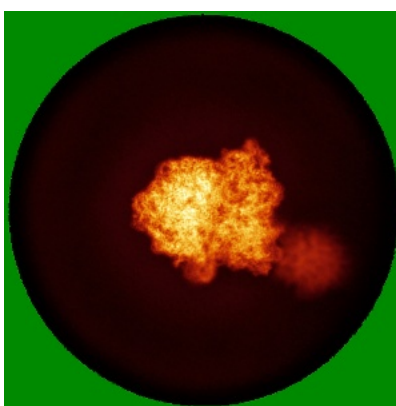
The images above show the largest variance slices of the map in three orthogonal directions.

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

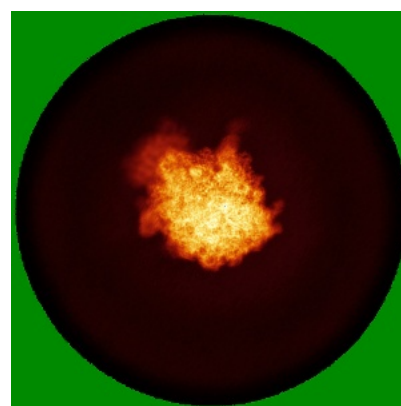
6.4.1 Primary map



X



Y

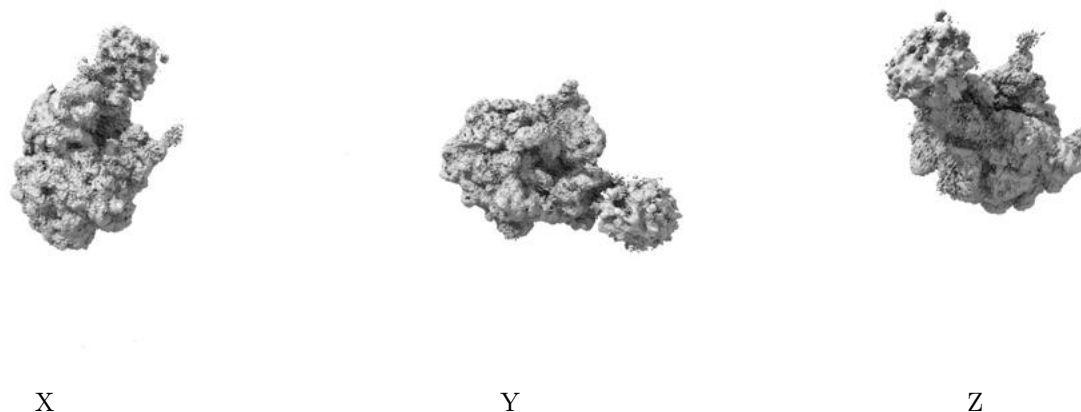


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

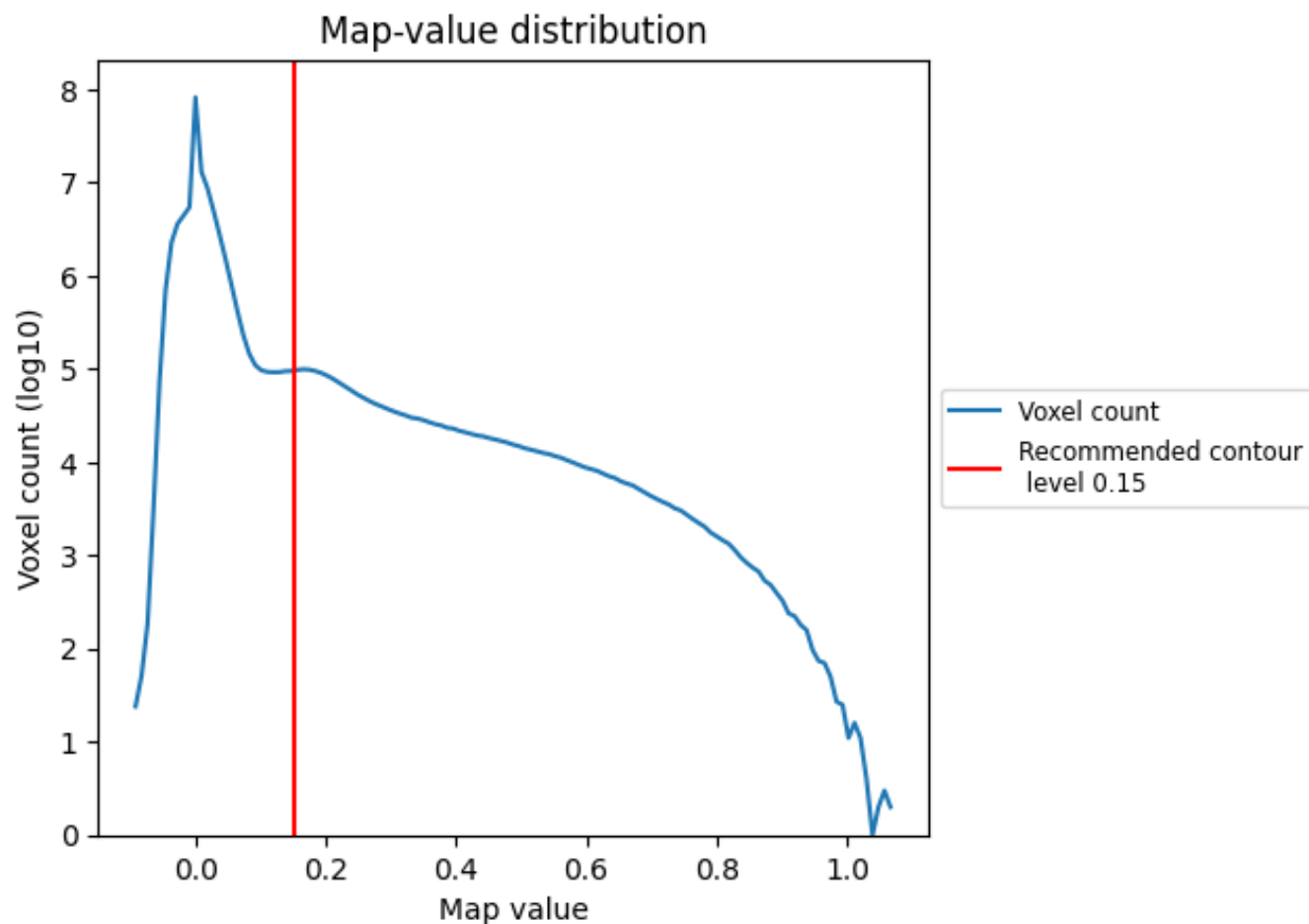
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

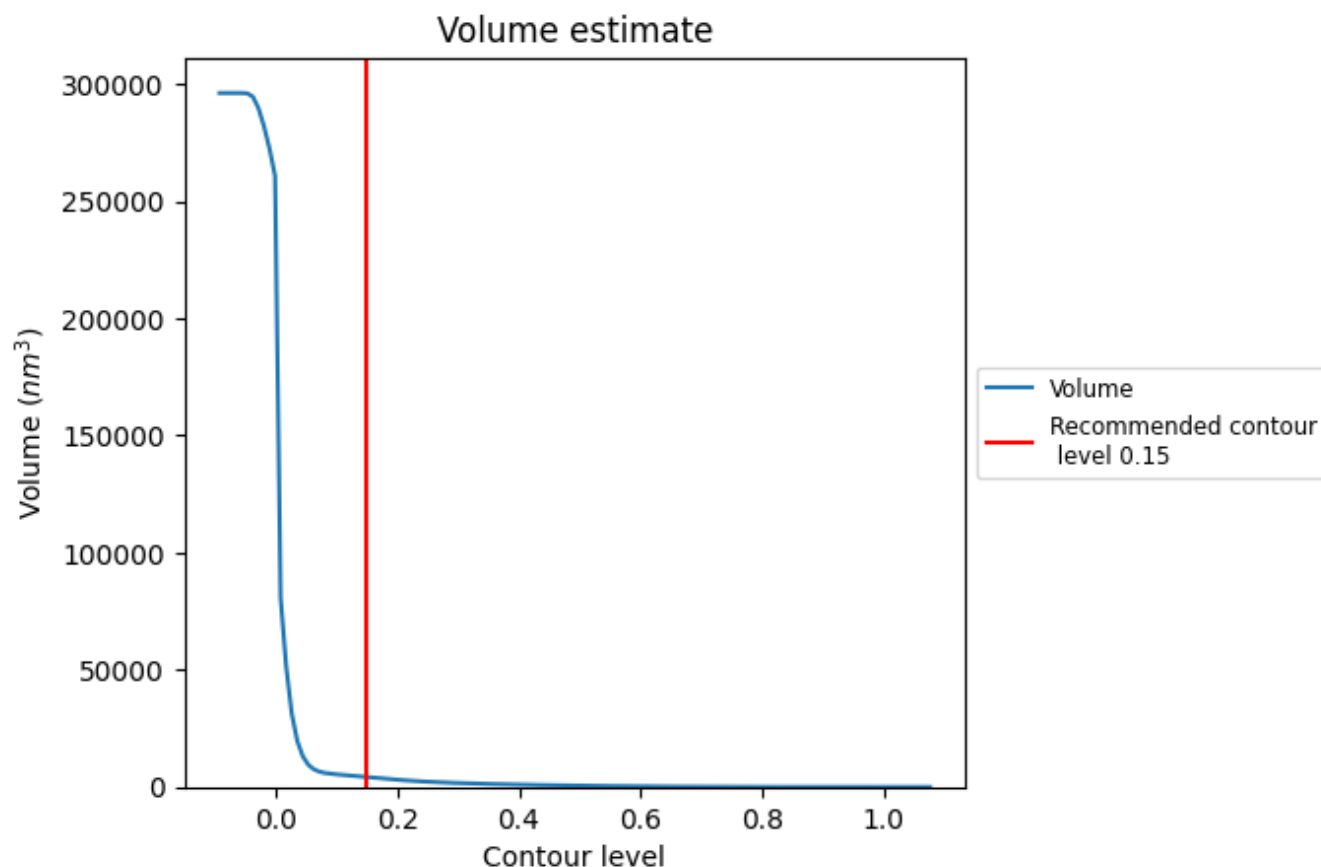
This section contains the results of statistical analysis of the map.

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.

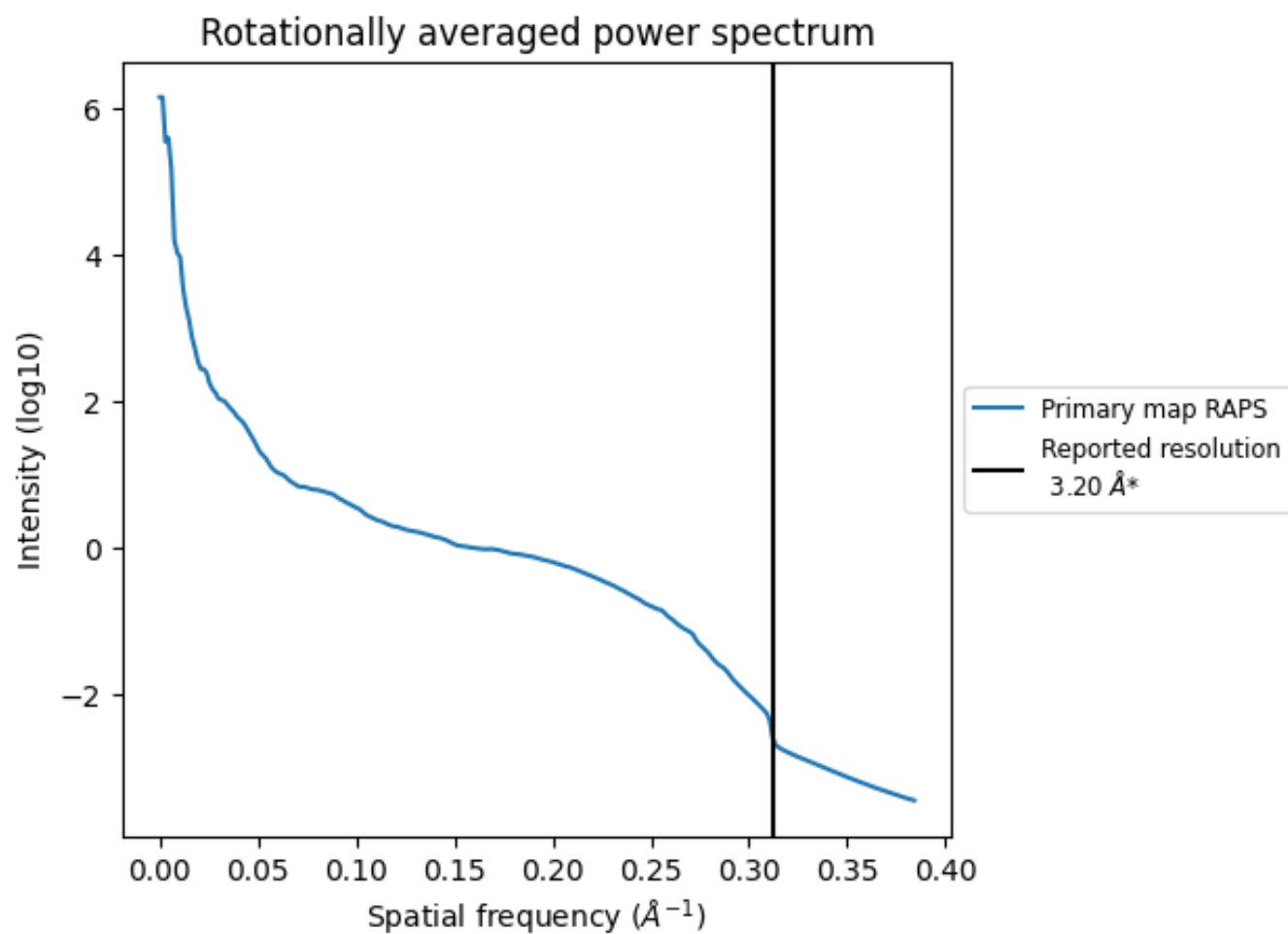
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4241 nm^3 ; this corresponds to an approximate mass of 3831 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 0.312 Å⁻¹

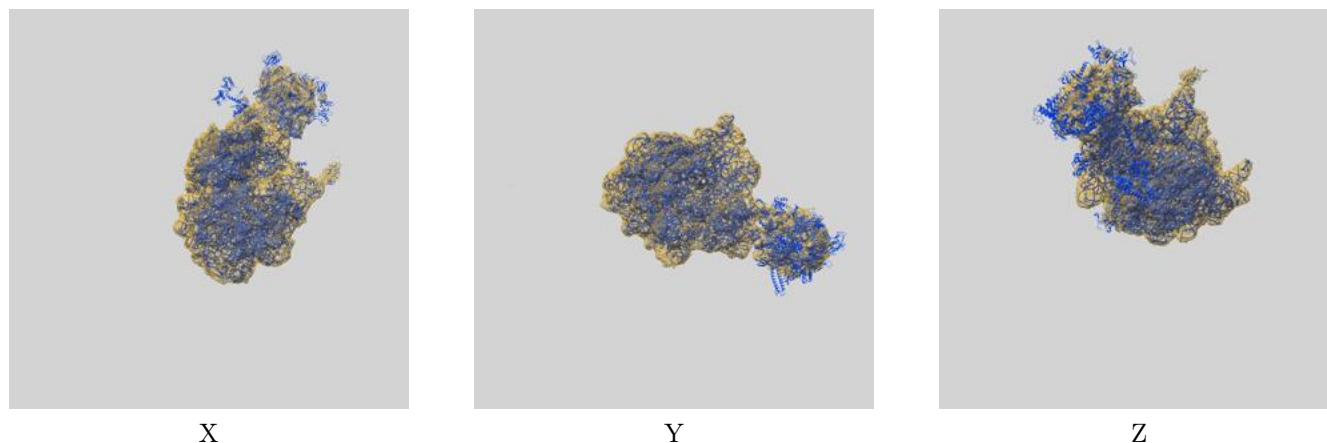
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

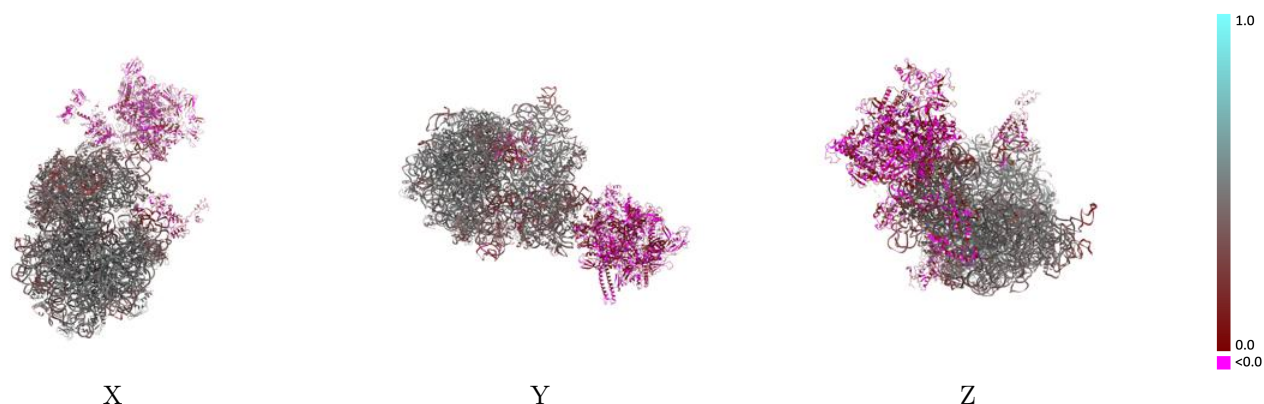
This section contains information regarding the fit between EMDB map EMD-72646 and PDB model 9Y79. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



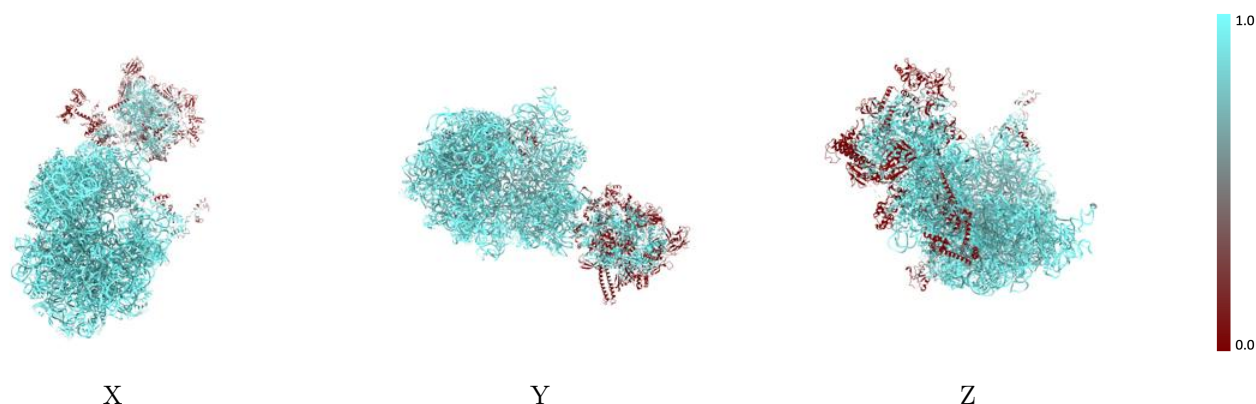
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



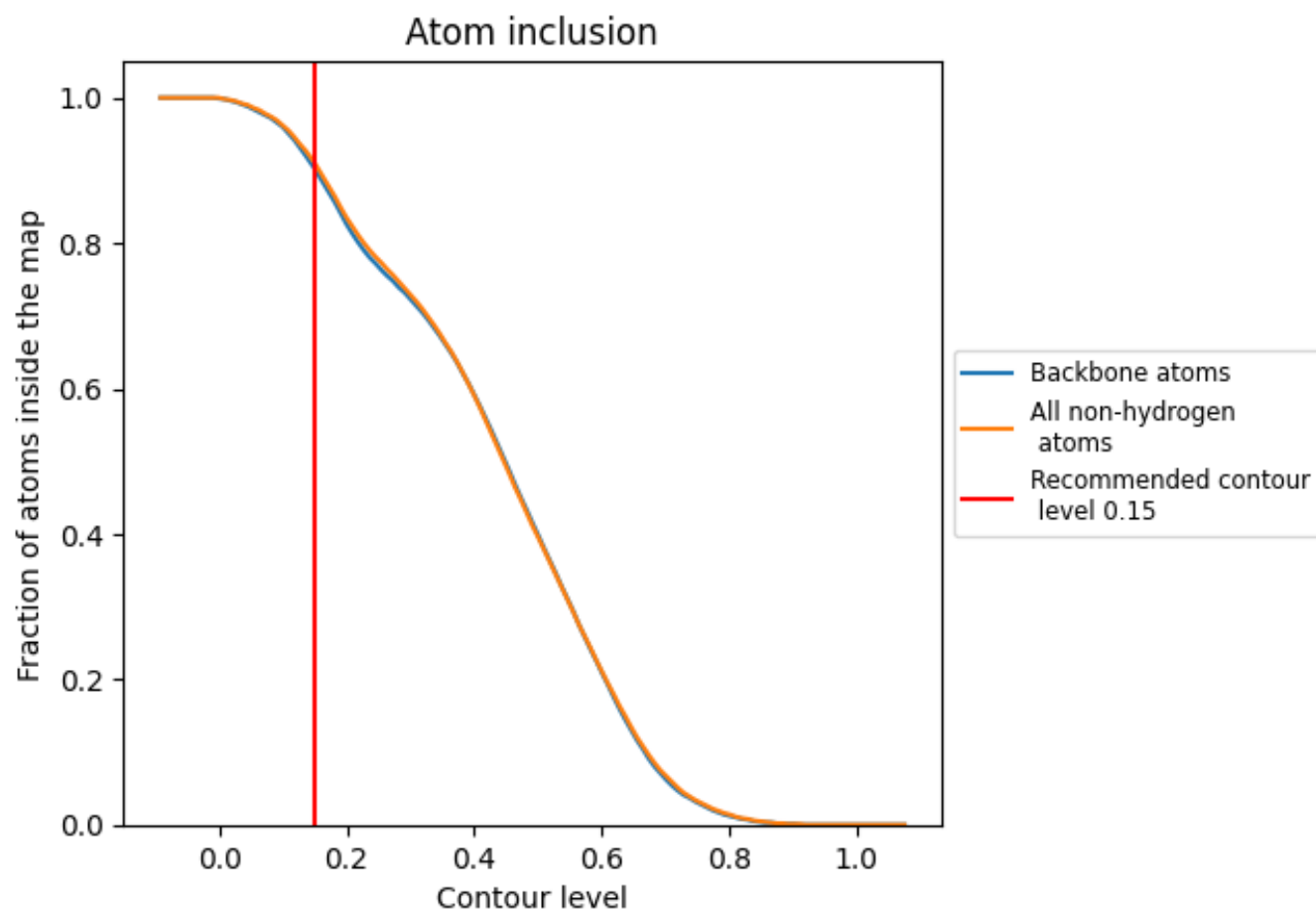
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 91% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9100	 0.3510
0	 0.9940	 0.4760
1	 0.9960	 0.4760
2	 0.9990	 0.4540
3	 0.9870	 0.4520
4	 0.9820	 0.4400
5	 0.9620	 0.1240
6	 0.9110	 0.0990
7	 0.9480	 0.0990
9	 0.7720	 0.1230
A	 0.9990	 0.2240
AA	 0.5500	 0.0360
AC	 0.3630	 0.0540
AD	 0.1610	 0.0300
AE	 0.6610	 0.0470
AF	 0.5270	 0.0500
AG	 0.2180	 0.0360
B	 0.9830	 0.2330
C	 0.9980	 0.4200
D	 0.9970	 0.4220
E	 0.9990	 0.3870
F	 0.9890	 0.3560
G	 0.9690	 0.3750
H	 0.6330	 0.1120
I	 0.9870	 0.4170
J	 0.9910	 0.4180
K	 0.9990	 0.4420
L	 0.9950	 0.4120
M	 0.9860	 0.3740
N	 0.9950	 0.4440
NG	 0.6940	 0.1100
O	 0.9850	 0.3940
P	 0.9920	 0.3670
Q	 0.9980	 0.4360
R	 0.9910	 0.4490



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Chain	Atom inclusion	Q-score
S	 0.9960	 0.4110
T	 0.9970	 0.3980
U	 0.9870	 0.4490
V	 0.9920	 0.4180
W	 0.9740	 0.3660
X	 0.9990	 0.3560
Y	 0.6020	 0.0990
Z	 0.2470	 0.1670
a	 0.9990	 0.4340
b	 0.9970	 0.4770
c	 1.0000	 0.4650
d	 1.0000	 0.4240
e	 0.9760	 0.3950
f	 0.9930	 0.4680
g	 0.9550	 0.2960
h	 1.0000	 0.4820
i	 0.9910	 0.4730
j	 0.9940	 0.4850
k	 1.0000	 0.4550
l	 0.9840	 0.4360
m	 1.0000	 0.4820
n	 0.9930	 0.3640
o	 0.9980	 0.4970
p	 0.9890	 0.4010
q	 1.0000	 0.4660
r	 0.8360	 0.2660
s	 0.9960	 0.4750
t	 0.9990	 0.4650
u	 0.9900	 0.4680
v	 1.0000	 0.4650
w	 1.0000	 0.4810
x	 0.9950	 0.4130
y	 0.9980	 0.4780
z	 0.9990	 0.4730