



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 06:17 AM UTC

PDB ID : 8ESQ / pdb_00008esq
EMDB ID : EMD-24411
Title : Ytm1 associated nascent 60S ribosome State 2
Authors : Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.
Deposited on : 2022-10-14
Resolution : 2.80 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

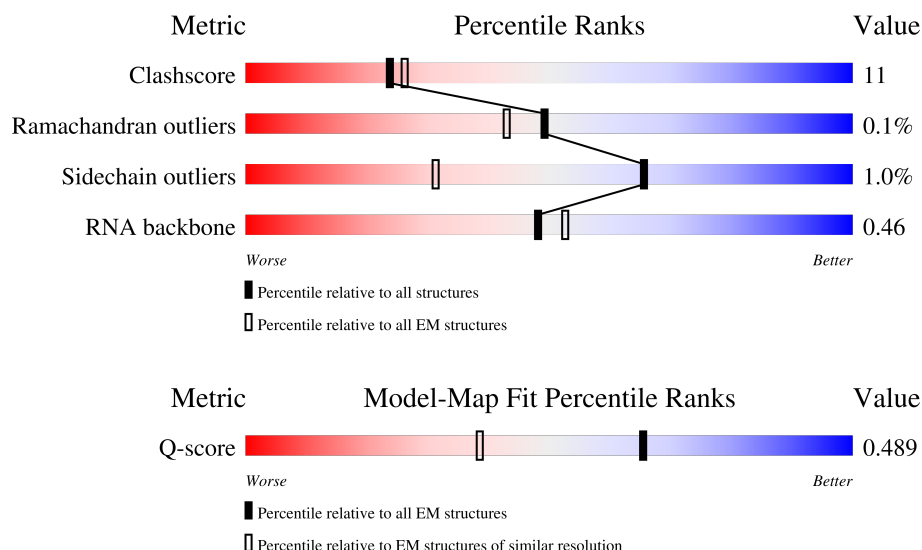
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 2.80 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.



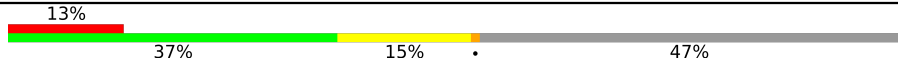
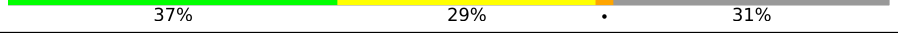
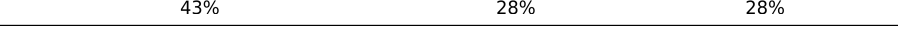
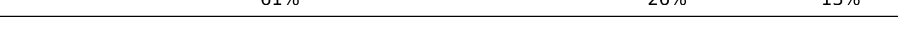
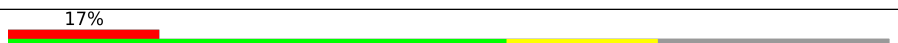
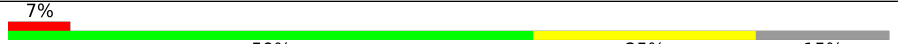
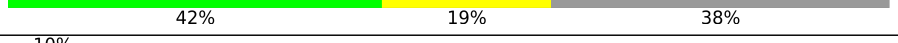
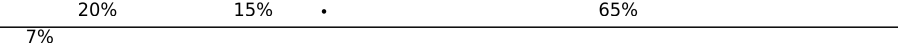
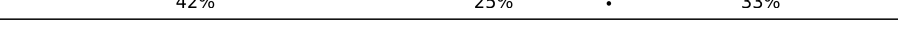
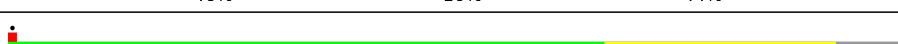
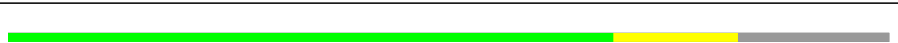
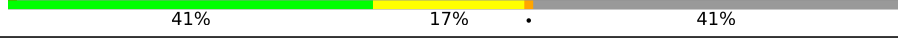
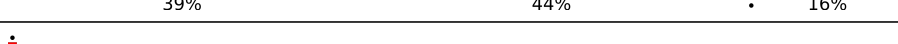
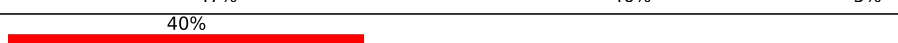
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11806 (2.30 - 3.30)

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	7	707	
2	1	3497	
3	2	165	

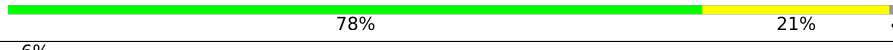
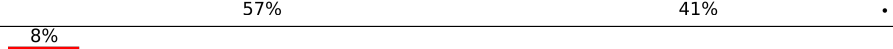
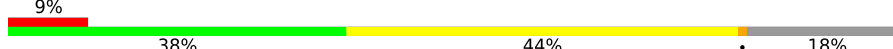
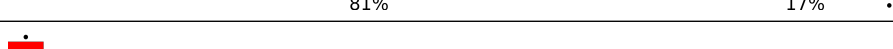
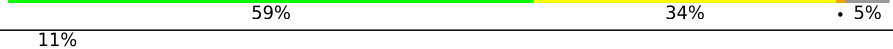
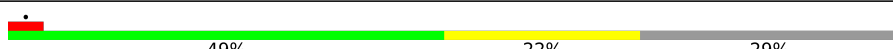
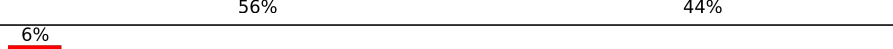
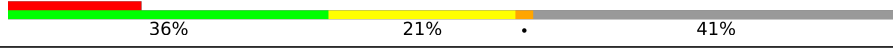
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Mol	Chain	Length	Quality of chain
4	3	302	
5	6	300	
6	8	51	
7	A	295	
8	B	388	
9	C	363	
10	D	578	
11	E	195	
12	F	250	
13	G	259	
14	H	190	
15	I	747	
16	J	333	
17	K	373	
18	L	208	
19	M	134	
20	N	201	
21	O	197	
22	P	187	
23	Q	187	
24	R	193	
25	S	176	
26	U	117	
27	V	139	
28	W	241	

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Mol	Chain	Length	Quality of chain
29	X	141	
30	Y	126	
31	Z	136	
32	a	148	
33	b	642	
34	c	117	
35	d	113	
36	e	127	
37	f	108	
38	g	112	
39	h	122	
40	i	99	
41	j	91	
42	k	74	
43	l	180	
44	m	740	
45	n	607	
46	o	276	
47	p	440	
48	q	608	
49	r	260	
50	s	470	
51	t	249	
52	u	192	
53	v	209	

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Mol	Chain	Length	Quality of chain
54	w	802	36%44%19%37%
55	x	306	5%11%85%
56	y	244	5%57%34%8%
57	z	117	10%17%70%
58	T	160	8%12%8%79%

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 130409 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Noc2.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	7	245	Total	C	N	O	0	0
			1218	728	245	245		

- Molecule 2 is a RNA chain called RNA (2231-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	2230	Total	C	N	O	P	0	0
			47746	21325	8659	15532	2230		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	1746	C	U	conflict	GB 157310483

- Molecule 3 is a RNA chain called RNA (150-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	150	Total	C	N	O	P	0	0
			3189	1427	564	1048	150		

- Molecule 4 is a protein called Protein mak16.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	160	Total	C	N	O	S	0	0
			1336	845	257	228	6		

- Molecule 5 is a RNA chain called RNA (81-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	6	81	Total	C	N	O	P	0	0
			1717	770	296	570	81		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
6	137	C	U	conflict	GB 157310483
6	146	G	U	conflict	GB 157310483

- Molecule 6 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	8	35	Total	C	N	O	0	0
			291	182	64	45		

- Molecule 7 is a protein called Ribosome biogenesis protein brx1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	211	Total	C	N	O	S	0	0
			1686	1079	301	299	7		

- Molecule 8 is a protein called 60S ribosomal protein L3-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	339	Total	C	N	O	S	0	0
			2687	1701	499	478	9		

- Molecule 9 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	359	Total	C	N	O	S	0	0
			2795	1765	536	491	3		

- Molecule 10 is a protein called ATP-dependent RNA helicase has1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	427	Total	C	N	O	S	0	0
			3396	2190	581	614	11		

- Molecule 11 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	165	Total	C	N	O	S	0	0
			1283	822	237	221	3		

- Molecule 12 is a protein called 60S ribosomal protein L7-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	237	Total	C	N	O	S	0	0
			1925	1238	353	331	3		

- Molecule 13 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	206	Total	C	N	O	S	1	0
			1615	1034	295	283	3		

- Molecule 14 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	183	Total	C	N	O	S	0	0
			1451	914	266	265	6		

- Molecule 15 is a protein called Nucleolar complex-associated protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	I	460	Total	C	N	O	S	1	0
			3725	2412	620	682	11		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	607	LYS	LEU	conflict	UNP O94288

- Molecule 16 is a protein called Probable rRNA-processing protein ebp2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J	118	Total	C	N	O	S	0	0
			959	607	166	184	2		

- Molecule 17 is a protein called Putative ribosome biogenesis protein C8F11.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	K	251	Total	C	N	O	S	0	0
			1973	1262	338	367	6		

- Molecule 18 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L	116	Total	C	N	O	S	0	0
			942	592	198	151	1		

- Molecule 19 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	M	125	Total	C	N	O	S	0	0
			1007	644	191	168	4		

- Molecule 20 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	N	166	Total	C	N	O	S	0	0
			1406	883	291	229	3		

- Molecule 21 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	O	196	Total	C	N	O	S	0	0
			1557	999	297	257	4		

- Molecule 22 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P	159	Total	C	N	O	S	0	0
			1248	794	233	218	3		

- Molecule 23 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Q	133	Total	C	N	O	S	0	0
			1032	650	199	182	1		

- Molecule 24 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	R	114	Total	C	N	O	S	0	0
			949	596	195	153	5		

- Molecule 25 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S	168	Total	C	N	O	S	0	0
			1408	909	263	231	5		

- Molecule 26 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	U	98	Total	C	N	O		0	0
			791	513	137	141			

- Molecule 27 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	V	132	Total	C	N	O	S	0	0
			991	625	182	176	8		

- Molecule 28 is a protein called Ribosome assembly factor mrt4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	W	215	Total	C	N	O		0	0
			1057	627	215	215			

- Molecule 29 is a protein called 60S ribosomal protein L25-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	X	132	Total	C	N	O	S	0	0
			1044	664	194	185	1		

- Molecule 30 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Y	125	Total	C	N	O	S	0	0
			998	622	201	173	2		

- Molecule 31 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	134	Total	C	N	O	S	0	0
			1072	693	199	178	2		

- Molecule 32 is a protein called 60S ribosomal protein L28-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	a	80	Total	C	N	O	0	0
			634	404	116	114		

- Molecule 33 is a protein called Probable nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	b	403	Total	C	N	O	0	0
			1999	1193	403	403		

- Molecule 34 is a protein called 60S ribosomal protein L30-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	96	Total	C	N	O	S	0	0
			720	457	125	134	4		

- Molecule 35 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	97	Total	C	N	O	S	0	0
			810	512	159	136	3		

- Molecule 36 is a protein called 60S ribosomal protein L32-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	121	Total	C	N	O	S	0	0
			971	608	198	160	5		

- Molecule 37 is a protein called 60S ribosomal protein L33-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	106	Total	C	N	O	S	0	0
			839	534	162	140	3		

- Molecule 38 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	g	106	Total	C	N	O	S	0	0
			861	540	177	142	2		

- Molecule 39 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	h	121	Total	C	N	O		
			999	629	194	176	0	0

- Molecule 40 is a protein called 60S ribosomal protein L36-B.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	i	85	Total	C	N	O	S	
			696	431	148	116	1	0

- Molecule 41 is a protein called 60S ribosomal protein L37-B.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	j	71	Total	C	N	O	S	
			563	346	121	90	6	0

- Molecule 42 is a protein called 60S ribosomal protein L38-1.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	k	70	Total	C	N	O	S	
			564	357	104	102	1	0

- Molecule 43 is a protein called 60S ribosome subunit biogenesis protein nip7.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	l	174	Total	C	N	O	S	
			1418	906	254	250	8	0

- Molecule 44 is a protein called Ribosome biogenesis protein erb1.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	m	572	Total	C	N	O	S	
			4536	2891	790	843	12	0

- Molecule 45 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	n	433	Total	C	N	O	S	
			3526	2268	608	638	12	0

- Molecule 46 is a protein called Uncharacterized RNA-binding protein C1827.05c.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	o	137	Total	C	N	O	S	0	0
			1138	732	213	187	6		

- Molecule 47 is a protein called Ribosome biogenesis protein ytm1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	p	290	Total	C	N	O		0	0
			1431	851	290	290			

- Molecule 48 is a protein called 25S rRNA (cytosine-C(5))-methyltransferase nop2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	q	341	Total	C	N	O		0	0
			1684	1002	341	341			

- Molecule 49 is a protein called Ribosome biogenesis protein nsa2.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	r	166	Total	C	N	O	S	0	0
			1357	850	259	243	5		

- Molecule 50 is a protein called GTPase grn1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	s	32	Total	C	N	O		0	0
			269	163	63	43			

- Molecule 51 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	t	235	Total	C	N	O	S	0	0
			1948	1242	367	334	5		

- Molecule 52 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	u	114	Total	C	N	O	S	0	0
			944	598	190	147	9		

- Molecule 53 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	v	161	Total	C	N	O	S	0	0
			1299	818	243	235	3		

- Molecule 54 is a protein called AdoMet-dependent rRNA methyltransferase spb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	w	504	Total	C	N	O	S	1	0
			4067	2573	723	753	18		

- Molecule 55 is a protein called Brix domain-containing protein C4F8.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	x	45	Total	C	N	O	S	0	0
			383	236	80	66	1		

- Molecule 56 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	y	225	Total	C	N	O	S	0	0
			1697	1058	293	341	5		

- Molecule 57 is a protein called UPF0642 protein C32H8.05.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	z	35	Total	C	N	O	0	0
			292	183	63	46		

- Molecule 58 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	T	34	Total	C	N	O	S	0	0
			269	168	50	50	1		

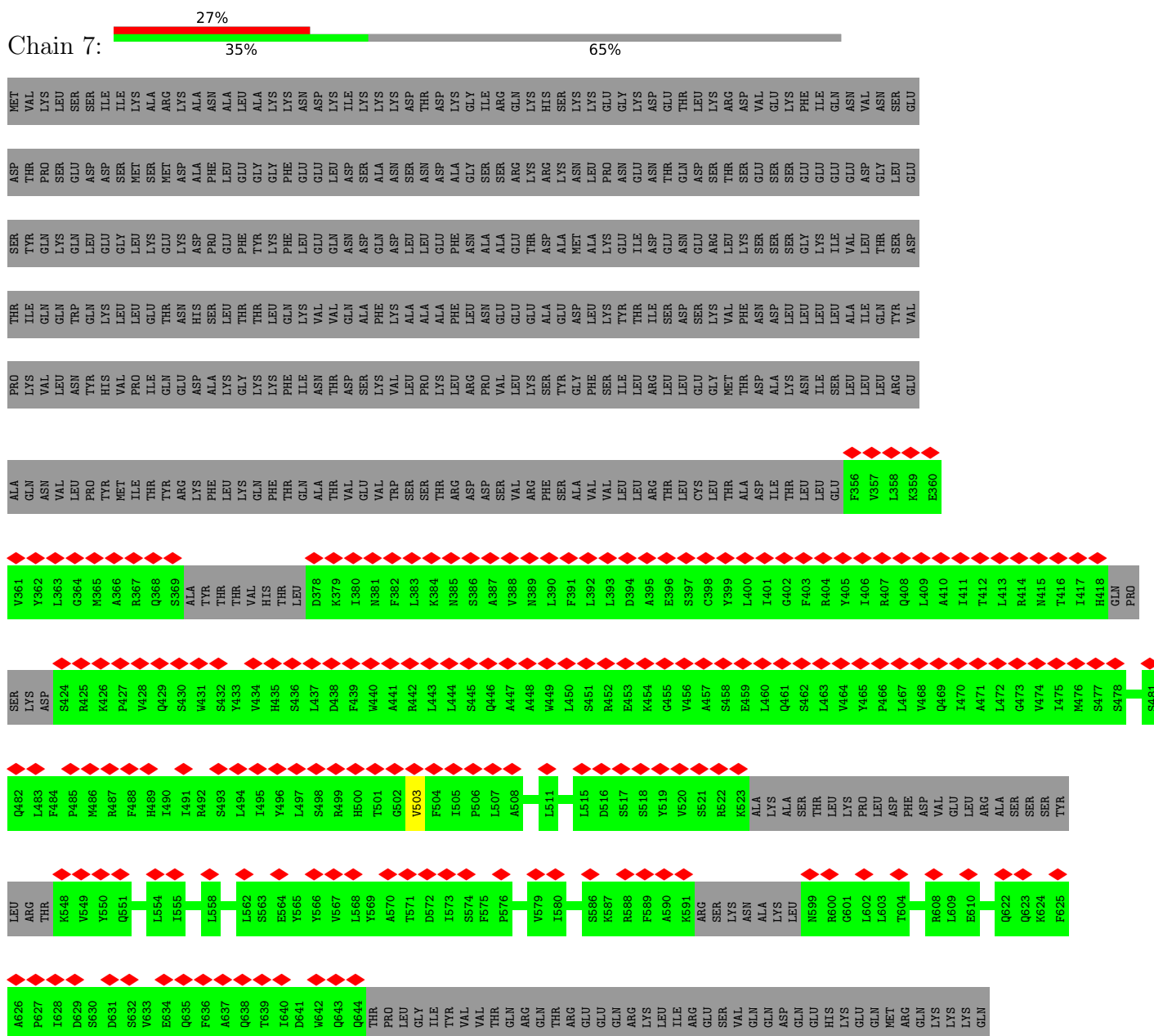
- Molecule 59 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
59	j	1	Total	Zn	0
			1	1	

3 Residue-property plots

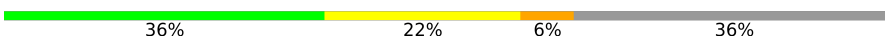
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

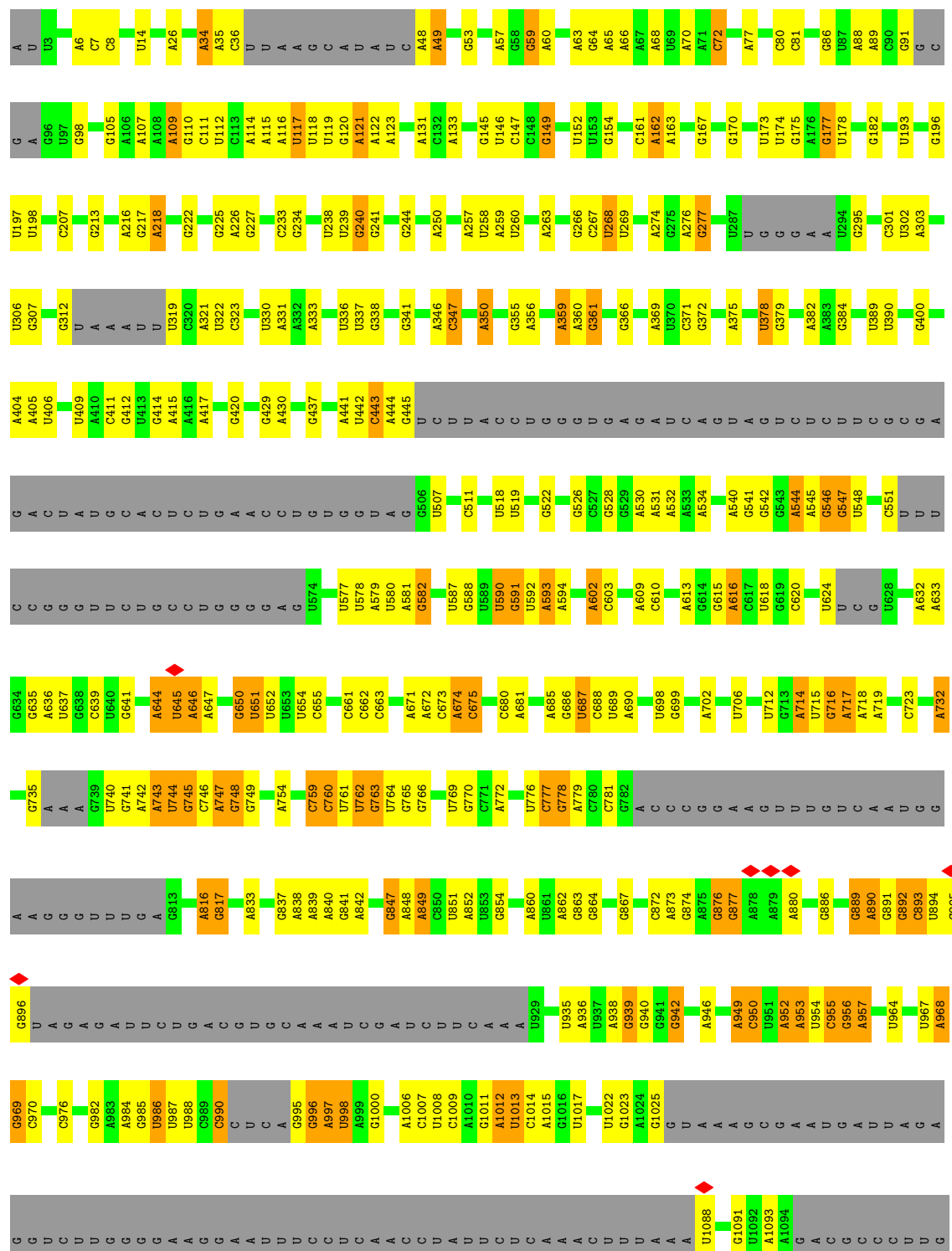
• Molecule 1: Noc2



ALA
LEU
LYS
SER
ASP
ASP
TLE
GLU
LEU
ASP
ASP
SER
GLU
GLU
GLU
ALA
GLU
ASP
TLE
ASP
GLU

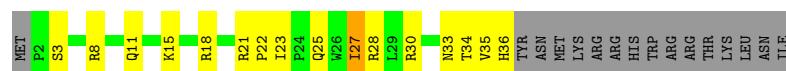
• Molecule 2: RNA (2231-MER)

Chain 1: 

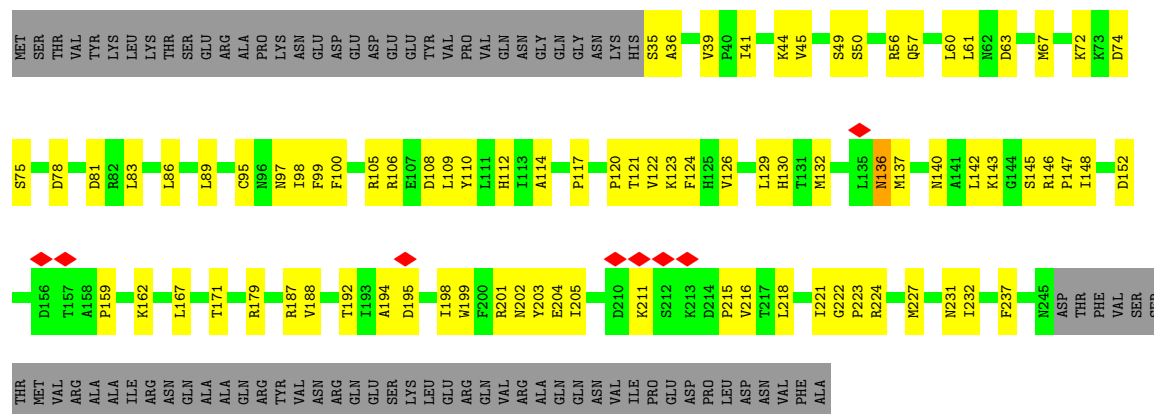




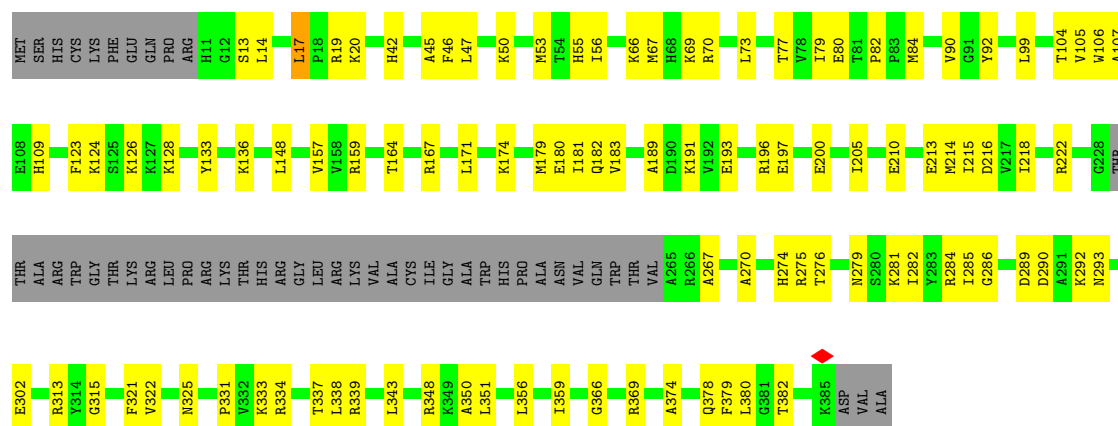




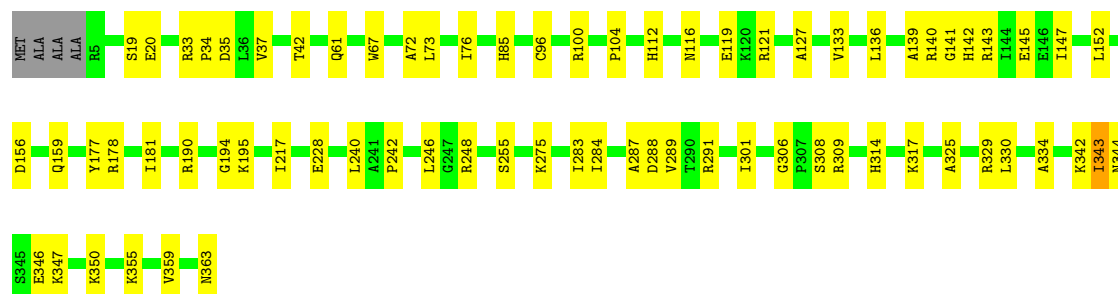
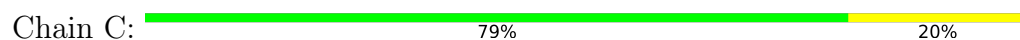
• Molecule 7: Ribosome biogenesis protein brx1



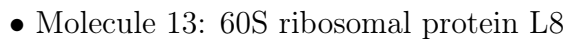
• Molecule 8: 60S ribosomal protein L3-A



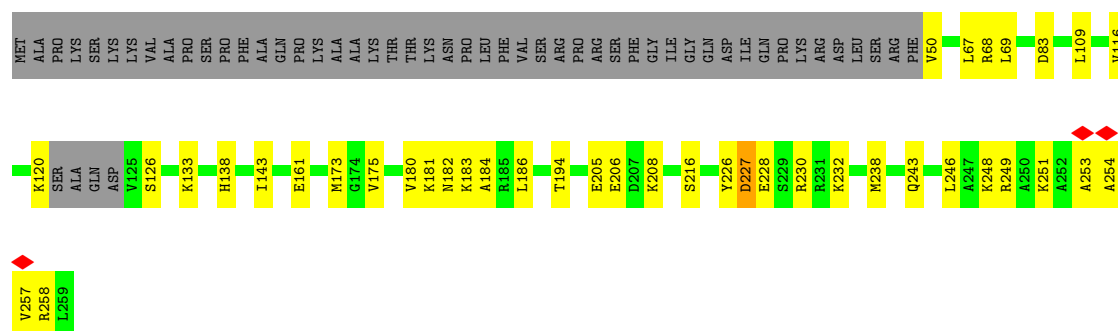
• Molecule 9: 60S ribosomal protein L4-B



- Chain D:

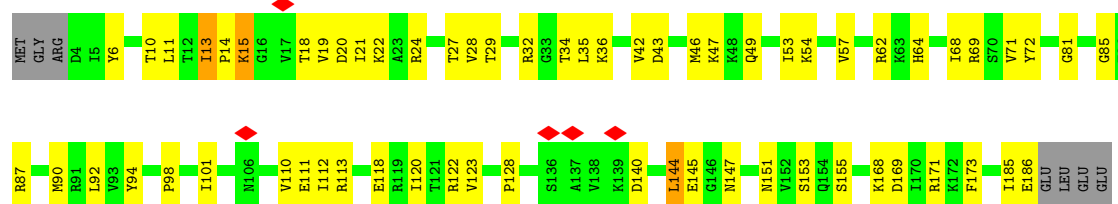


Chain G:  64% 15% 20%

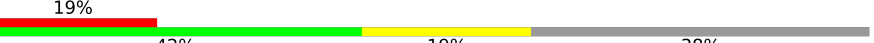


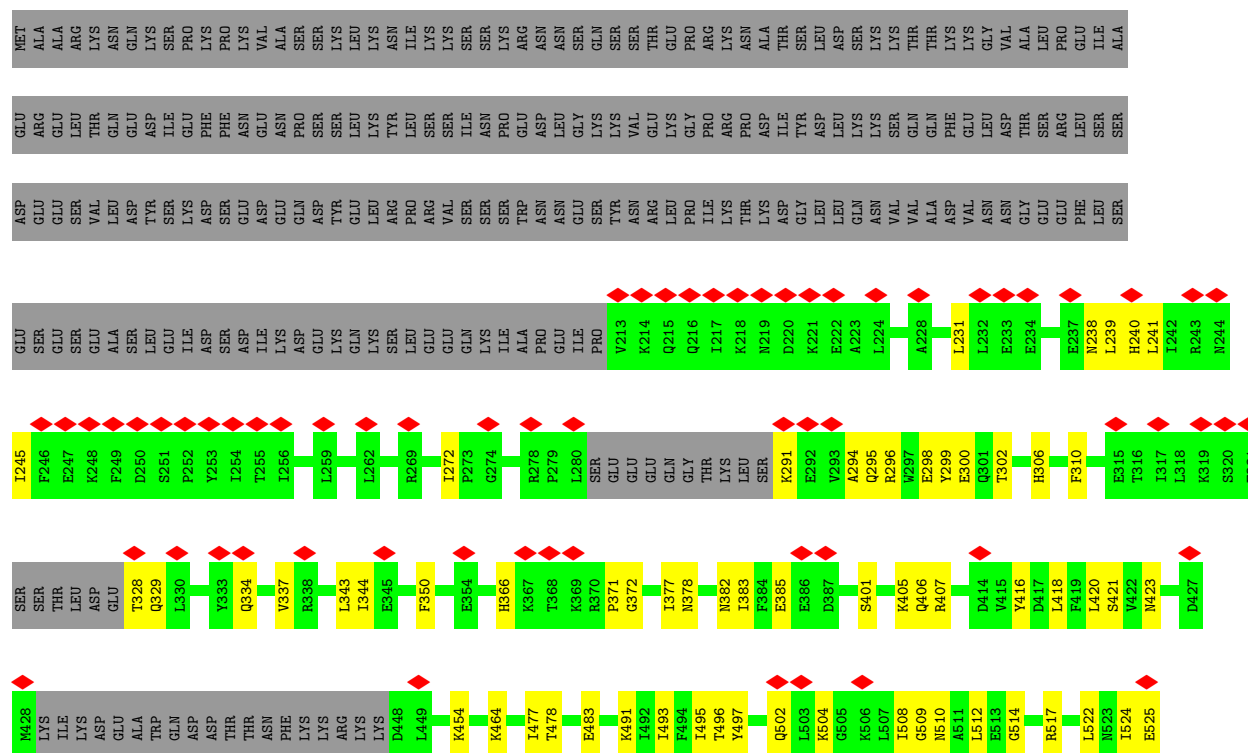
- Molecule 14: 60S ribosomal protein L9-A

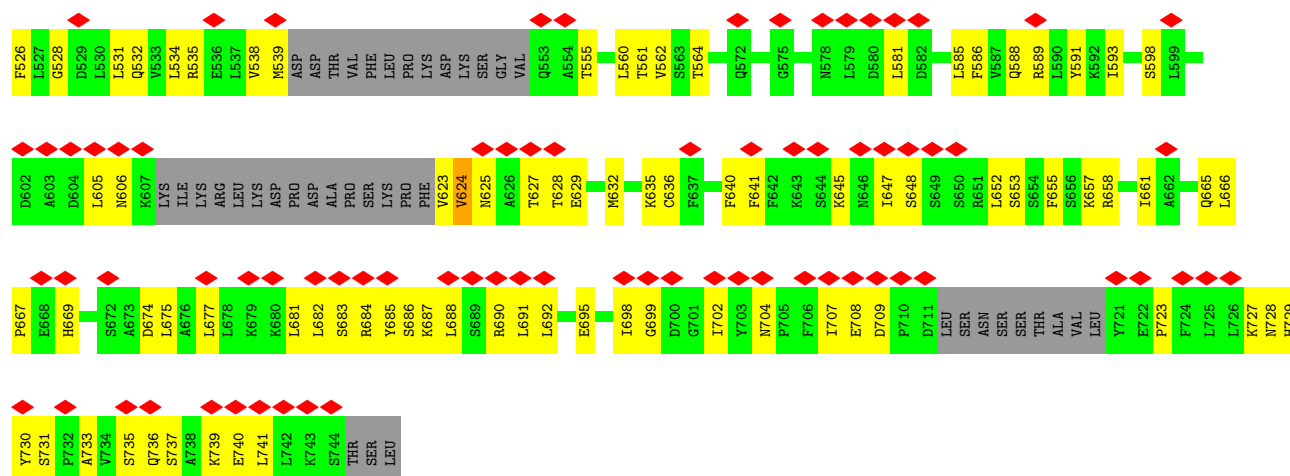
Chain H:  63% 32% . .



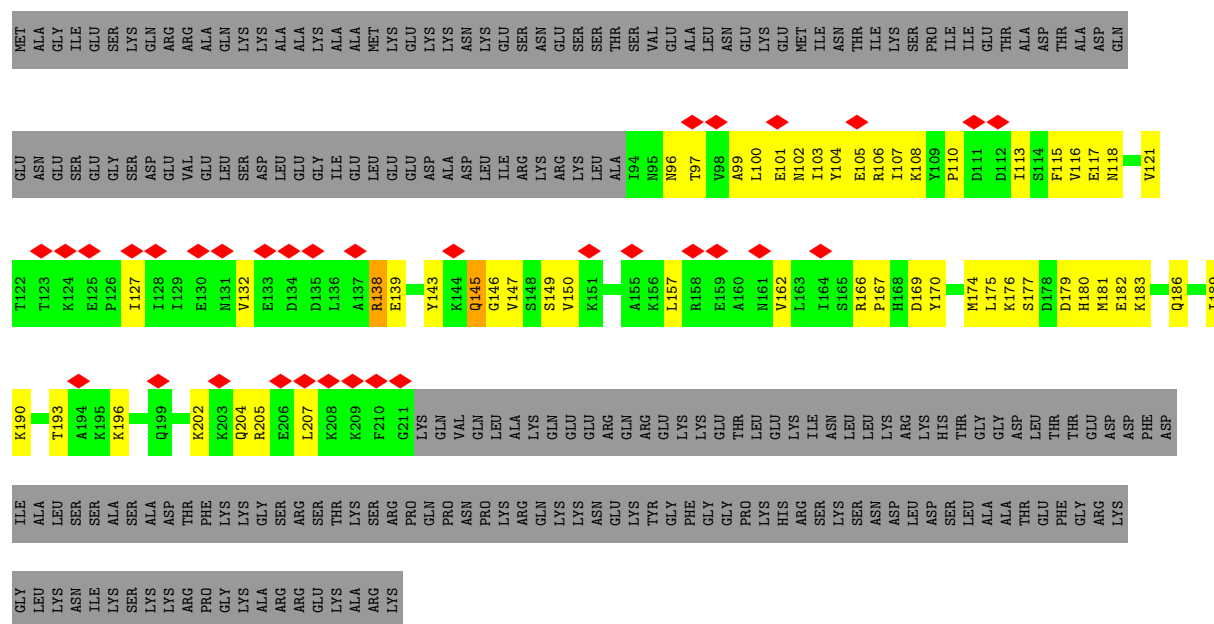
- Molecule 15: Nucleolar complex-associated protein 3

Chain I:  19% 42% 19% 38%

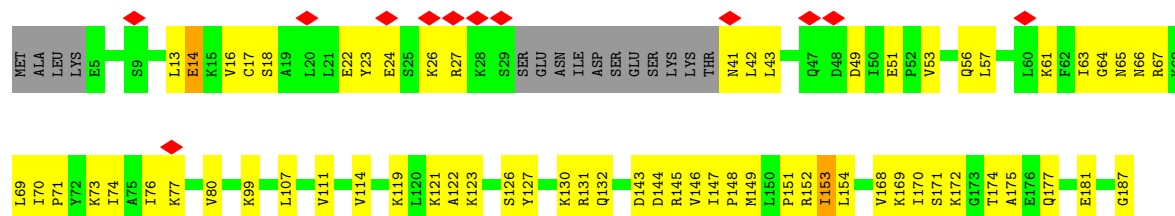


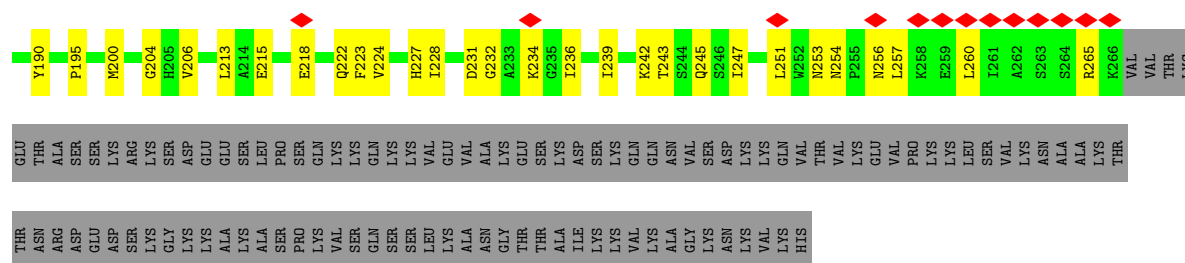


• Molecule 16: Probable rRNA-processing protein ebp2

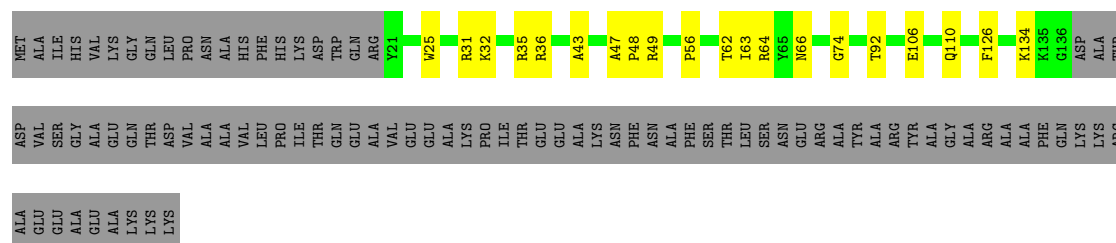


• Molecule 17: Putative ribosome biogenesis protein C8F11.04

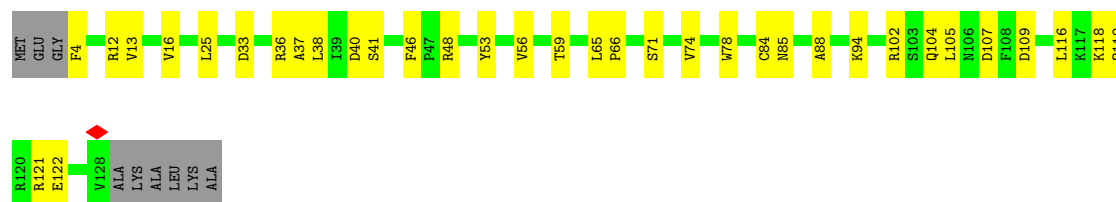




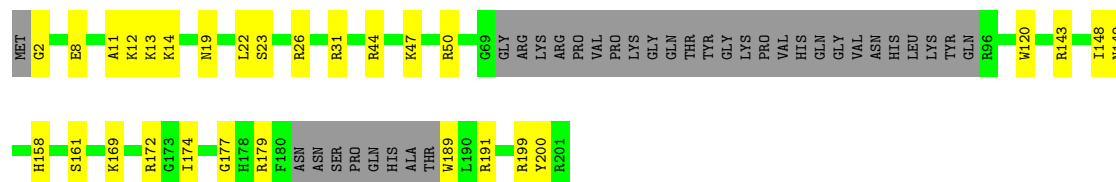
• Molecule 18: 60S ribosomal protein L13



• Molecule 19: 60S ribosomal protein L14

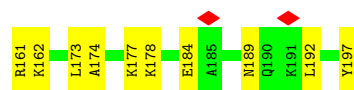


• Molecule 20: 60S ribosomal protein L15-A

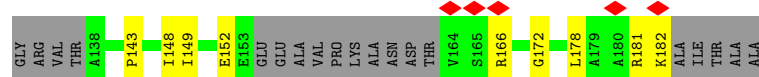
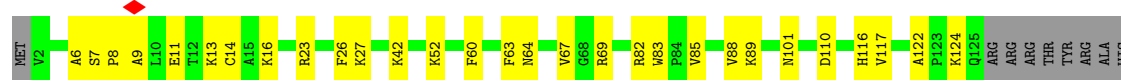


• Molecule 21: 60S ribosomal protein L16-B

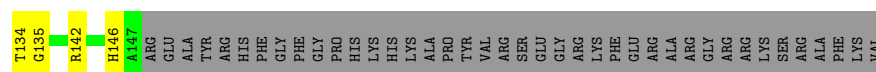




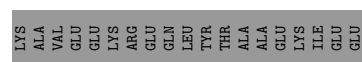
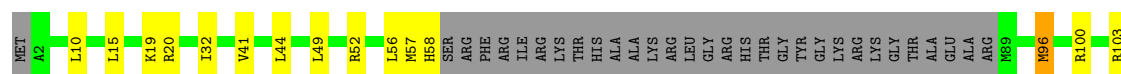
- Molecule 22: 60S ribosomal protein L17-A



- Molecule 23: 60S ribosomal protein L18-A



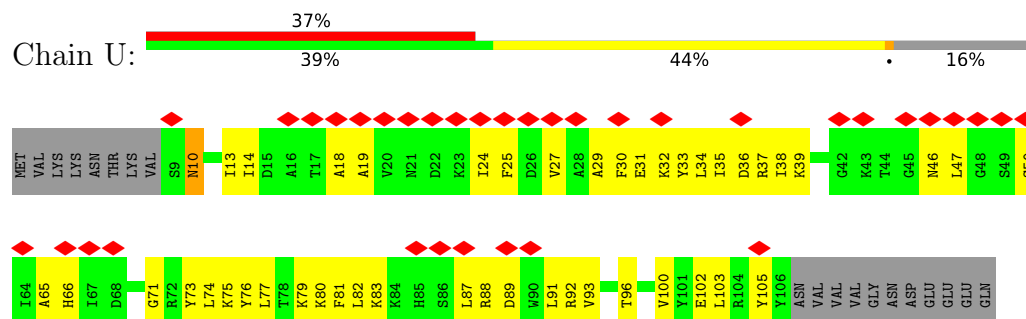
- Molecule 24: 60S ribosomal protein L19-A



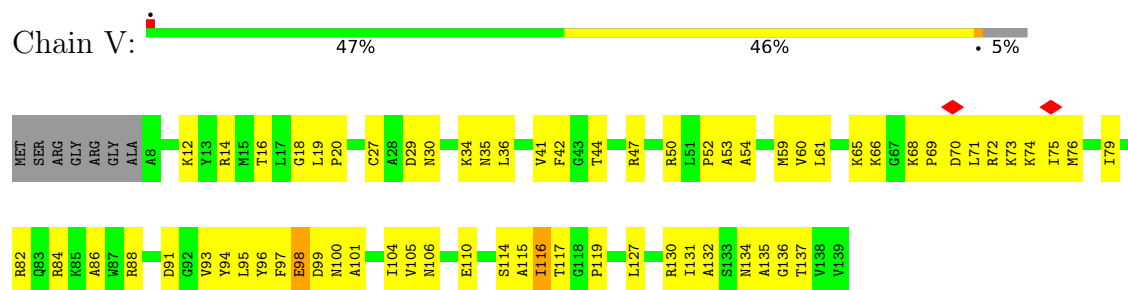
- Molecule 25: 60S ribosomal protein L20-A



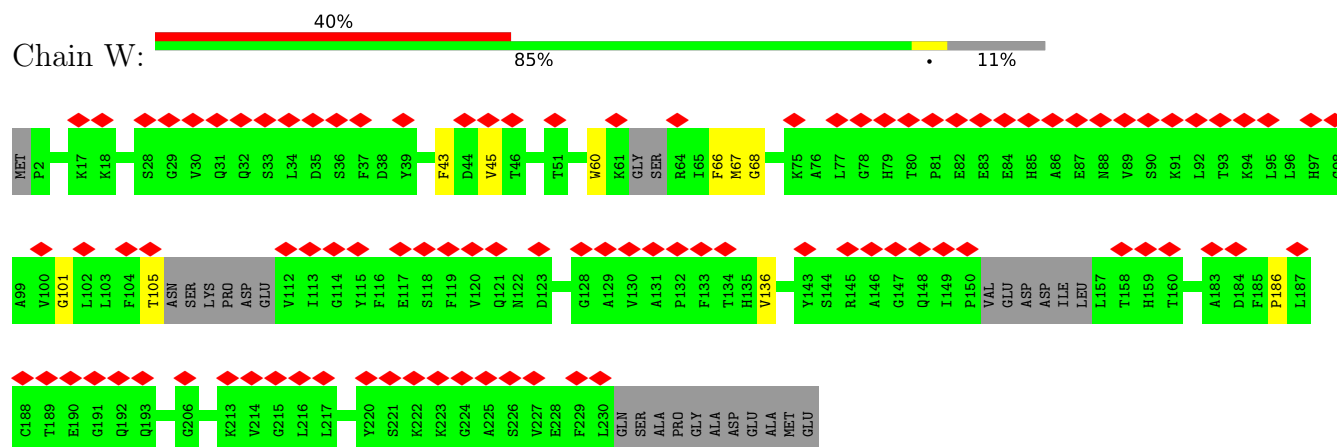
- Molecule 26: 60S ribosomal protein L22



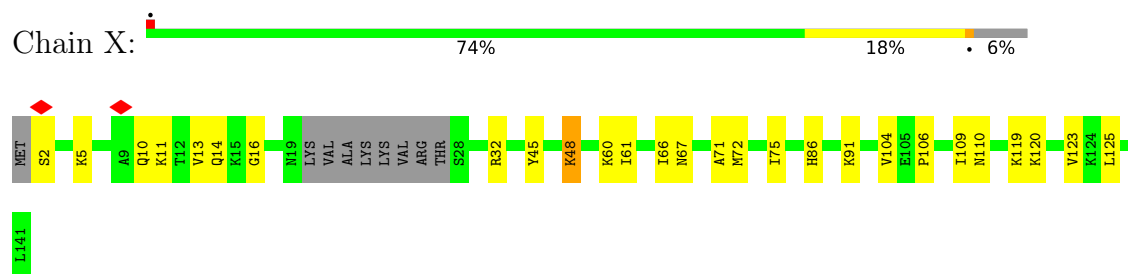
- Molecule 27: 60S ribosomal protein L23-A



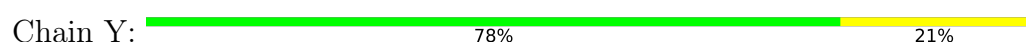
- Molecule 28: Ribosome assembly factor mrt4

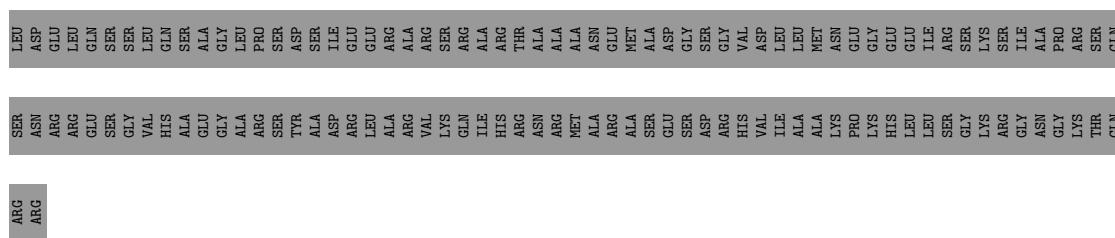


- Molecule 29: 60S ribosomal protein L25-A

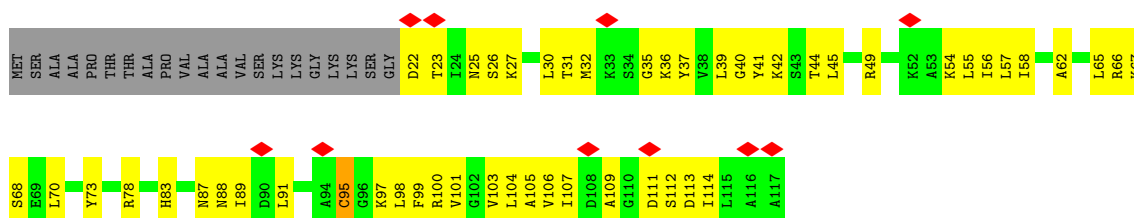


- Molecule 30: 60S ribosomal protein L26

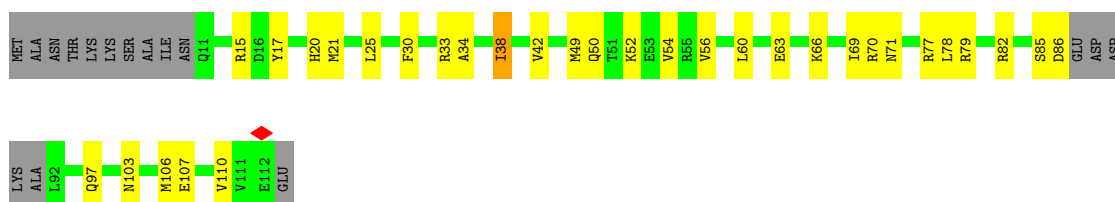




• Molecule 34: 60S ribosomal protein L30-2



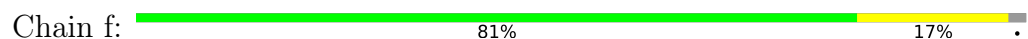
• Molecule 35: 60S ribosomal protein L31



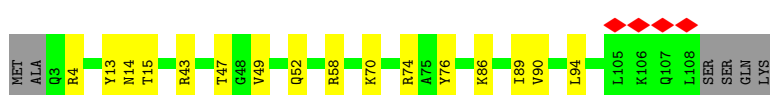
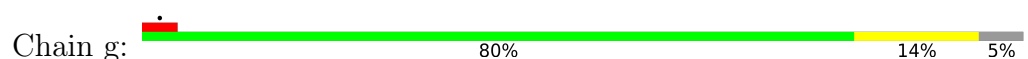
• Molecule 36: 60S ribosomal protein L32-A



• Molecule 37: 60S ribosomal protein L33-B



• Molecule 38: 60S ribosomal protein L34-A



- Molecule 39: 60S ribosomal protein L35

Chain h: 



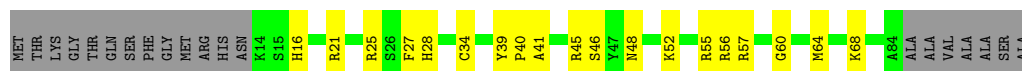
- Molecule 40: 60S ribosomal protein L36-B

Chain i: 



- Molecule 41: 60S ribosomal protein L37-B

Chain j: 



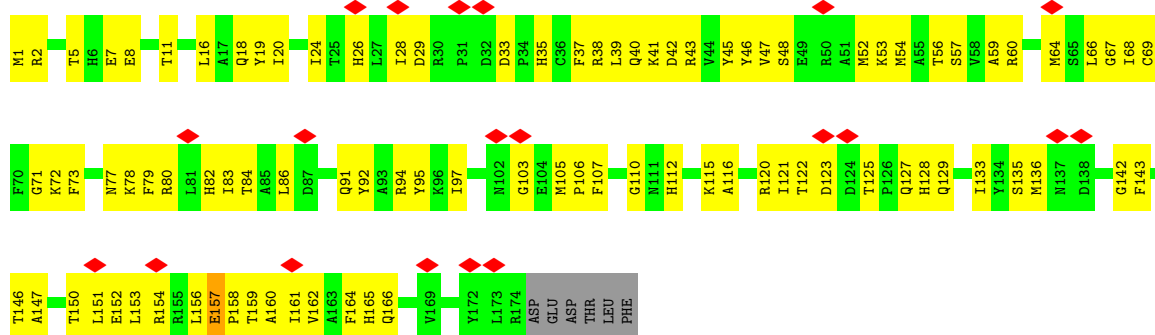
- Molecule 42: 60S ribosomal protein L38-1

Chain k: 



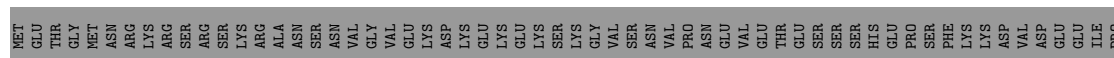
- Molecule 43: 60S ribosome subunit biogenesis protein nip7

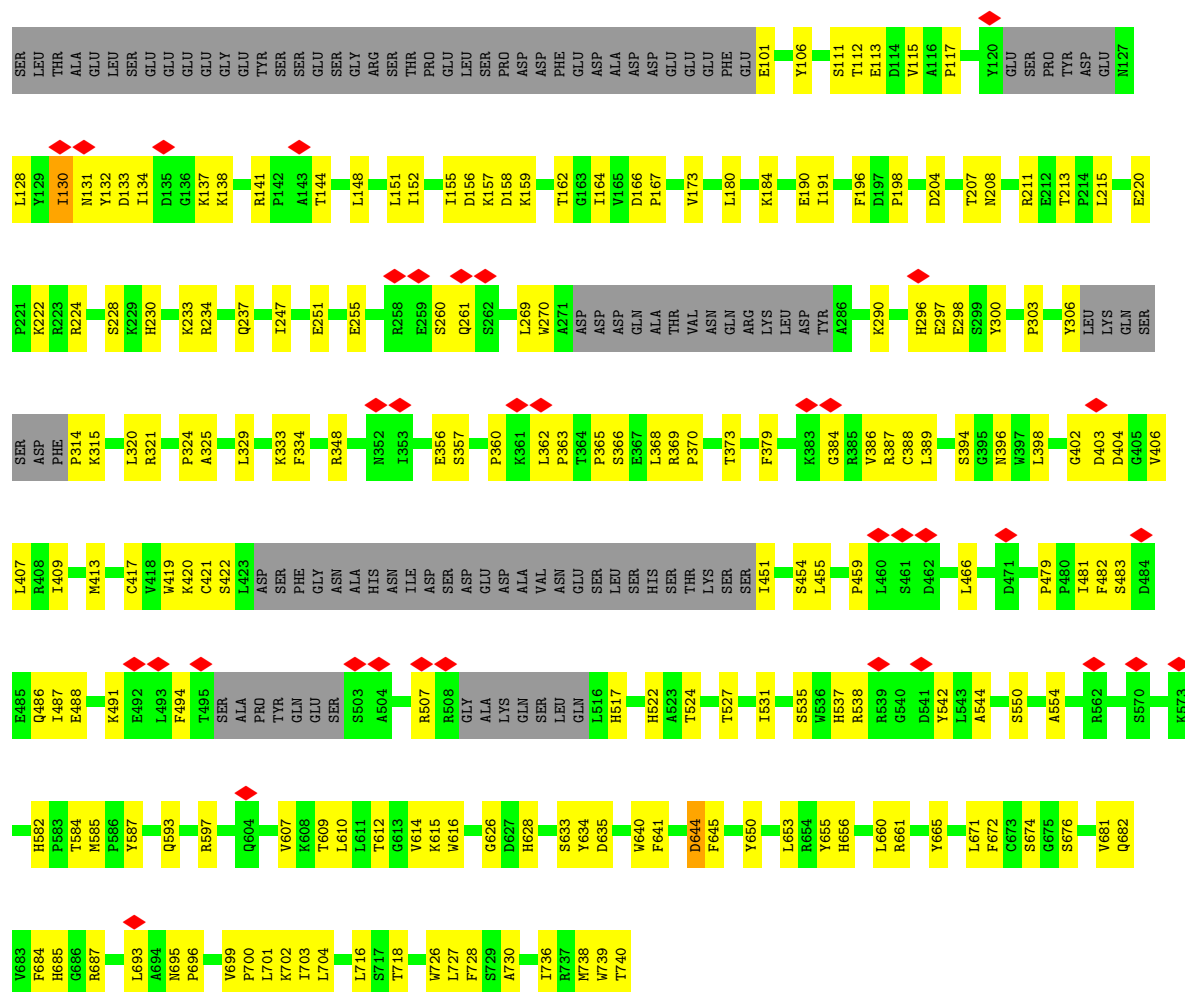
Chain l: 



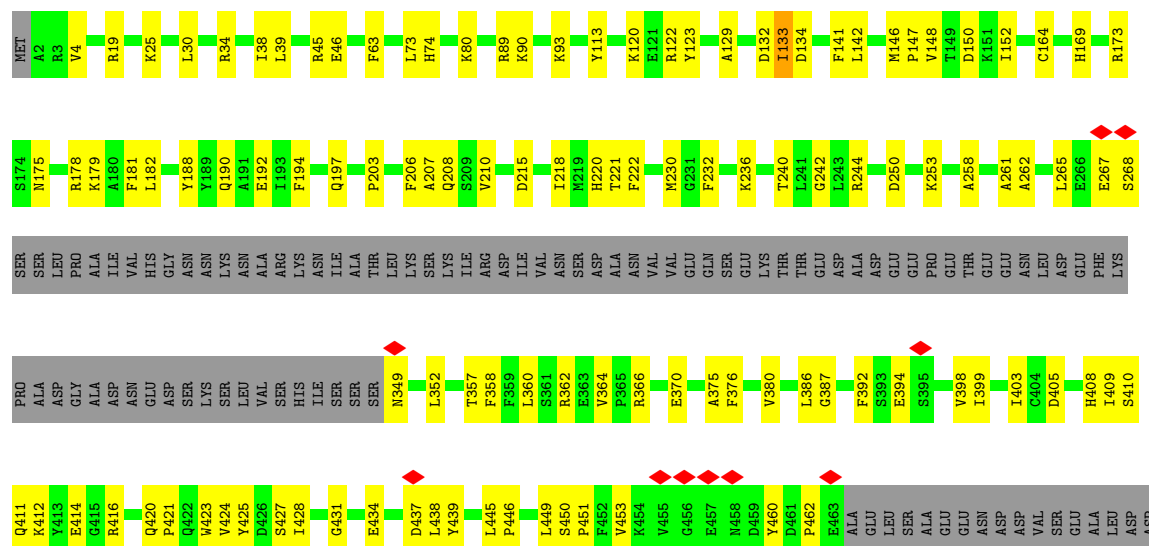
- Molecule 44: Ribosome biogenesis protein erbl

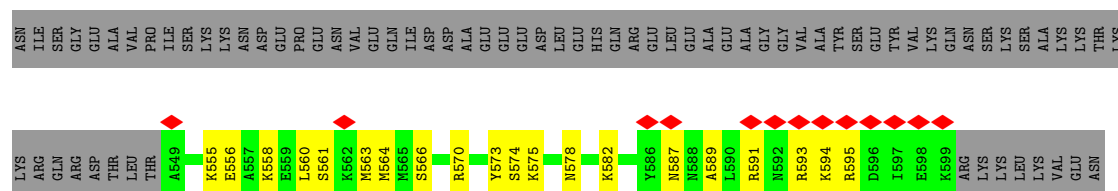
Chain m: 



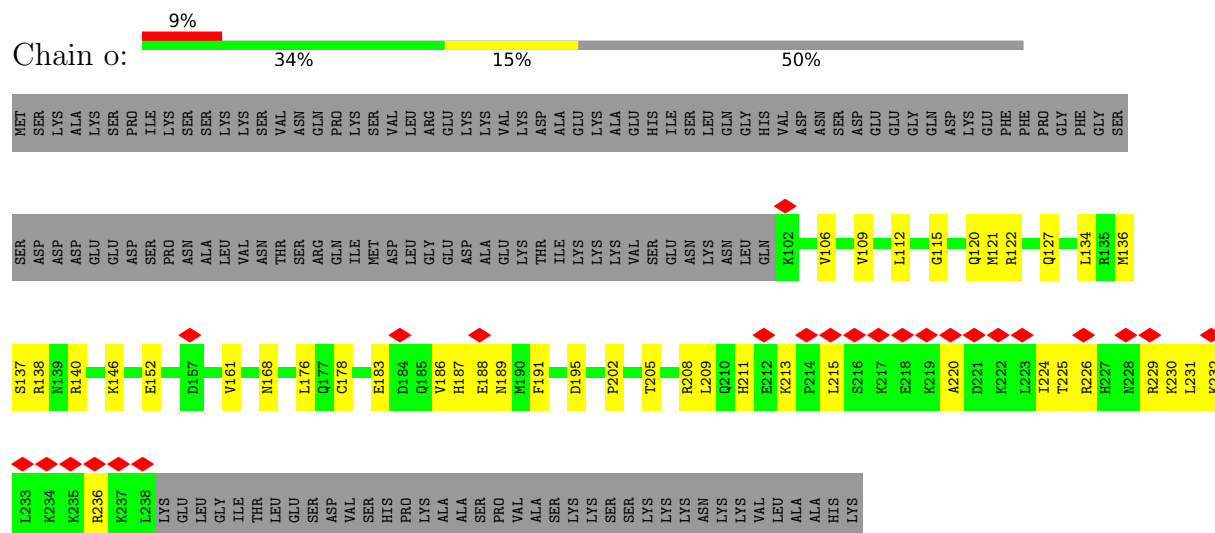


• Molecule 45: Pescadillo homolog

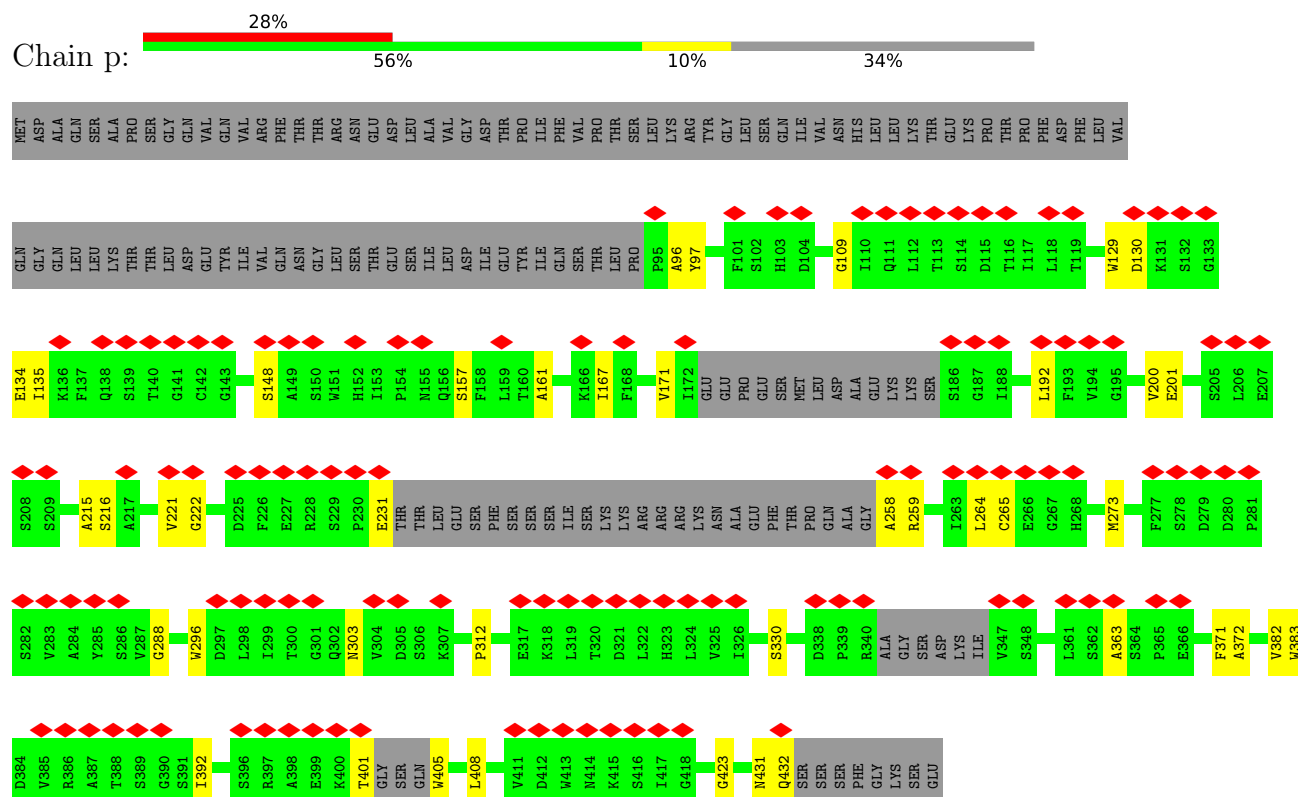




• Molecule 46: Uncharacterized RNA-binding protein C1827.05c

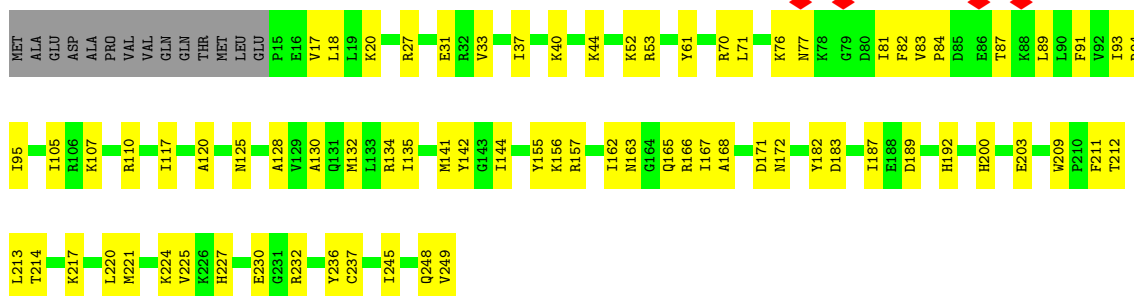


• Molecule 47: Ribosome biogenesis protein ytm1

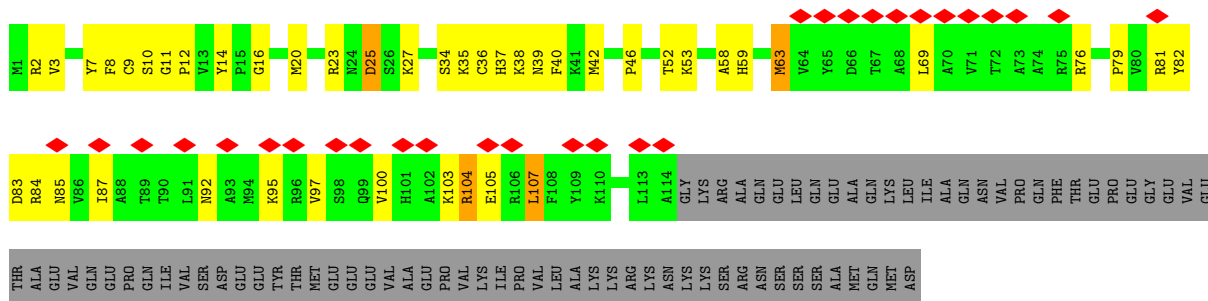
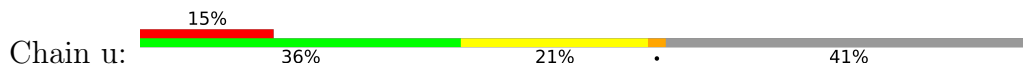


• Molecule 48: 25S rRNA (cytosine-C(5))-methyltransferase nop2

- Molecule 51: 60S ribosomal protein L7-A



- Molecule 52: Ribosome biogenesis protein rlp24



- Molecule 53: Nucleolar protein 16



Chain w:

Category	Percentage
Red	36%
Green	44%
Yellow	19%
Grey	37%







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	172500	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.806	Depositor
Minimum map value	-0.343	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	7	0.05	0/1213	0.17	0/1686
2	1	0.16	0/53422	0.26	0/83211
3	2	0.22	0/3563	0.27	0/5543
4	3	0.15	0/1363	0.37	0/1832
5	6	0.12	0/1916	0.26	0/2973
6	8	0.19	0/298	0.52	0/399
7	A	0.14	0/1722	0.36	0/2325
8	B	0.14	0/2740	0.34	0/3680
9	C	0.18	0/2848	0.34	0/3842
10	D	0.13	0/3458	0.28	0/4662
11	E	0.17	0/1308	0.40	0/1763
12	F	0.15	0/1963	0.30	0/2632
13	G	0.21	0/1637	0.34	0/2203
14	H	0.15	0/1470	0.38	0/1982
15	I	0.11	0/3782	0.30	0/5087
16	J	0.17	0/972	0.40	0/1304
17	K	0.16	0/2008	0.40	0/2713
18	L	0.20	0/960	0.36	0/1288
19	M	0.15	0/1024	0.36	0/1375
20	N	0.22	0/1436	0.32	0/1920
21	O	0.15	0/1588	0.30	0/2128
22	P	0.13	0/1269	0.28	0/1699
23	Q	0.16	0/1043	0.32	0/1401
24	R	0.19	0/963	0.50	0/1284
25	S	0.14	0/1444	0.33	0/1939
26	U	0.17	0/805	0.48	0/1080
27	V	0.16	0/1007	0.42	0/1357
28	W	0.09	0/1053	0.33	0/1457
29	X	0.18	0/1060	0.35	0/1422
30	Y	0.17	0/1008	0.36	0/1341
31	Z	0.14	0/1095	0.34	0/1467
32	a	0.13	0/645	0.27	0/874

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	b	0.07	0/1994	0.23	0/2774
34	c	0.19	0/729	0.50	0/980
35	d	0.14	0/824	0.33	0/1106
36	e	0.16	0/985	0.29	0/1313
37	f	0.16	0/859	0.26	0/1152
38	g	0.13	0/873	0.33	0/1170
39	h	0.19	0/1008	0.32	0/1340
40	i	0.17	0/703	0.27	0/931
41	j	0.19	0/575	0.32	0/761
42	k	0.17	0/570	0.43	0/762
43	l	0.22	0/1452	0.58	0/1961
44	m	0.17	1/4655 (0.0%)	0.34	0/6327
45	n	0.17	0/3607	0.35	0/4856
46	o	0.17	0/1163	0.35	0/1552
47	p	0.07	0/1426	0.22	0/1977
48	q	0.07	0/1682	0.20	0/2339
49	r	0.13	0/1373	0.38	0/1827
50	s	0.10	0/268	0.29	0/346
51	t	0.15	0/1979	0.32	0/2645
52	u	0.14	0/966	0.35	0/1292
53	v	0.18	0/1319	0.33	0/1769
54	w	0.12	0/4139	0.30	0/5567
55	x	0.08	0/384	0.25	0/505
56	y	0.14	0/1720	0.34	0/2345
57	z	0.21	0/297	0.40	0/388
58	T	0.16	0/276	0.36	0/375
All	All	0.16	1/137909 (0.0%)	0.31	0/198229

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	m	156	ASP	CA-CB	5.40	1.62	1.53

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	7	1218	0	528	1	0
2	1	47746	0	24028	588	0
3	2	3189	0	1613	39	0
4	3	1336	0	1375	37	0
5	6	1717	0	866	20	0
6	8	291	0	309	28	0
7	A	1686	0	1704	78	0
8	B	2687	0	2768	83	0
9	C	2795	0	2918	60	0
10	D	3396	0	3509	67	0
11	E	1283	0	1365	36	0
12	F	1925	0	2014	22	0
13	G	1615	0	1739	29	0
14	H	1451	0	1511	44	0
15	I	3725	0	3886	102	0
16	J	959	0	977	58	0
17	K	1973	0	2055	86	0
18	L	942	0	1012	17	0
19	M	1007	0	1072	26	0
20	N	1406	0	1441	27	0
21	O	1557	0	1652	37	0
22	P	1248	0	1290	28	0
23	Q	1032	0	1129	22	0
24	R	949	0	1017	28	0
25	S	1408	0	1462	45	0
26	U	791	0	825	56	0
27	V	991	0	1039	65	0
28	W	1057	0	487	8	0
29	X	1044	0	1112	22	0
30	Y	998	0	1090	16	0
31	Z	1072	0	1145	50	0
32	a	634	0	666	22	0
33	b	1999	0	894	10	0
34	c	720	0	758	53	0
35	d	810	0	852	24	0
36	e	971	0	1040	23	0
37	f	839	0	866	15	0
38	g	861	0	930	16	0
39	h	999	0	1092	18	0
40	i	696	0	763	10	0
41	j	563	0	578	16	0

Continued on next page...

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	k	564	0	611	32	0
43	l	1418	0	1423	95	0
44	m	4536	0	4506	163	0
45	n	3526	0	3557	120	0
46	o	1138	0	1196	41	0
47	p	1431	0	633	21	0
48	q	1684	0	765	2	0
49	r	1357	0	1429	63	0
50	s	269	0	318	17	0
51	t	1948	0	2066	53	0
52	u	944	0	983	42	0
53	v	1299	0	1347	30	0
54	w	4067	0	4147	133	0
55	x	383	0	417	13	0
56	y	1697	0	1679	65	0
57	z	292	0	317	22	0
58	T	269	0	258	14	0
59	j	1	0	0	0	0
All	All	130409	0	103029	2446	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 11.

All (2446) 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)
26:U:91:LEU:HD21	26:U:103:LEU:HB2	1.40	1.03
55:x:7:LYS:HA	55:x:10:ARG:HE	1.32	0.94
8:B:331:PRO:HD2	8:B:334:ARG:HE	1.31	0.93
2:1:873:A:H4'	24:R:126:GLU:HA	1.53	0.89
2:1:3336:G:H1	2:1:3351:U:H3	1.21	0.88
45:n:179:LYS:HD2	45:n:451:PRO:HB2	1.56	0.87
27:V:69:PRO:HD2	54:w:215:ARG:HD2	1.55	0.87
3:2:132:G:H1	3:2:137:A:H61	1.18	0.86
7:A:188:VAL:HG23	7:A:205:ILE:HD11	1.57	0.86
2:1:2458:G:N2	2:1:2463:G:N7	2.23	0.85
6:8:34:THR:HA	55:x:9:VAL:HG11	1.56	0.85
25:S:22:LYS:HA	58:T:146:ASN:HD21	1.42	0.84
56:y:99:GLU:HG3	56:y:101:LEU:H	1.42	0.84
44:m:117:PRO:HB3	44:m:166:ASP:HA	1.58	0.84
2:1:847:G:H1	2:1:957:A:H61	1.23	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:S:12:LYS:HA	25:S:55:GLY:HA2	1.58	0.83
43:l:64:MET:H	43:l:64:MET:HE3	1.44	0.83
5:6:102:G:H21	5:6:184:C:H41	1.25	0.82
31:Z:42:VAL:HG11	31:Z:96:ILE:HG12	1.63	0.81
43:l:116:ALA:HB2	43:l:158:PRO:HB3	1.61	0.81
2:1:1423:G:H5''	36:e:98:SER:HB3	1.63	0.81
2:1:680:C:H5'	36:e:23:LYS:HE2	1.63	0.81
25:S:11:ARG:HD2	25:S:21:PRO:HG2	1.63	0.80
1:7:503:VAL:HA	15:I:728:ASN:HB3	1.64	0.78
6:8:33:ASN:H	55:x:4:ILE:HG12	1.49	0.78
43:l:68:ILE:HD11	48:q:390:ARG:HA	1.66	0.78
54:w:627:MET:HB3	54:w:681:ALA:HB1	1.66	0.77
2:1:2925:G:H5'	33:b:135:GLY:HA3	1.67	0.76
15:I:302:THR:HG22	15:I:306:HIS:HE1	1.51	0.76
44:m:413:MET:H	44:m:413:MET:HE2	1.51	0.76
7:A:126:VAL:HG22	7:A:227:MET:HE1	1.67	0.76
15:I:627:THR:HG23	15:I:628:THR:HG23	1.67	0.75
2:1:3092:U:H3'	2:1:3093:G:H5'	1.67	0.75
8:B:67:MET:HA	8:B:70:ARG:HE	1.51	0.75
30:Y:37:GLU:N	30:Y:37:GLU:OE2	2.19	0.75
39:h:98:GLU:HA	39:h:101:ARG:HG2	1.67	0.75
44:m:597:ARG:HG2	44:m:609:THR:HG22	1.69	0.75
2:1:2993:G:H22	49:r:7:ILE:H	1.33	0.75
42:k:56:LYS:HA	42:k:59:GLN:HE22	1.52	0.75
15:I:632:MET:HA	15:I:635:LYS:HE2	1.69	0.75
34:c:91:LEU:HD21	34:c:104:LEU:HD23	1.67	0.74
7:A:198:ILE:HB	7:A:227:MET:HB3	1.68	0.74
18:L:110:GLN:HB3	53:v:120:LEU:HD13	1.68	0.74
2:1:2931:C:H3'	2:1:2932:A:H8	1.52	0.73
2:1:277:G:H5''	20:N:14:LYS:HE3	1.70	0.73
7:A:148:ILE:HB	7:A:188:VAL:HG22	1.69	0.73
2:1:1763:A:OP2	24:R:103:ARG:NH1	2.20	0.73
21:O:184:GLU:N	21:O:184:GLU:OE2	2.21	0.72
12:F:128:LYS:HA	12:F:128:LYS:HE2	1.70	0.72
15:I:641:PHE:HA	15:I:647:ILE:HD11	1.70	0.72
56:y:21:ASN:HB2	56:y:67:ARG:HB3	1.69	0.72
8:B:193:GLU:OE1	8:B:196:ARG:NH2	2.22	0.72
27:V:82:ARG:HD3	27:V:119:PRO:HG2	1.71	0.72
13:G:173:MET:HE1	44:m:211:ARG:HD3	1.70	0.72
26:U:37:ARG:HA	26:U:37:ARG:NH1	2.03	0.72
2:1:2461:A:H2'	2:1:2462:C:H4'	1.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Z:7:PRO:HA	31:Z:25:ILE:HG22	1.72	0.72
7:A:203:TYR:HB3	7:A:218:LEU:HB2	1.72	0.71
56:y:170:GLN:NE2	56:y:181:LEU:O	2.22	0.71
2:1:3332:U:H3	2:1:3355:G:H1	1.35	0.71
17:K:61:LYS:HA	46:o:211:HIS:HD2	1.55	0.71
43:l:47:VAL:HG12	43:l:67:GLY:HA3	1.72	0.71
54:w:628:THR:HG22	54:w:678:THR:HG22	1.72	0.71
31:Z:4:ILE:HD11	34:c:49:ARG:HA	1.73	0.71
10:D:483:ASN:HB3	10:D:486:LEU:HB2	1.72	0.71
22:P:122:ALA:HB3	22:P:143:PRO:HB2	1.71	0.71
36:e:39:VAL:HG13	36:e:46:THR:HB	1.71	0.71
54:w:49:ILE:HD11	54:w:116:LEU:HG	1.72	0.71
15:I:674:ASP:HA	15:I:677:LEU:HD12	1.72	0.71
49:r:248:PRO:HB3	49:r:254:VAL:HG12	1.72	0.71
2:1:63:A:OP1	20:N:172:ARG:NH2	2.24	0.70
43:l:43:ARG:NH1	43:l:45:TYR:OH	2.24	0.70
7:A:137:MET:HG3	7:A:222:GLY:HA2	1.72	0.70
23:Q:16:SER:O	23:Q:33:ARG:NH2	2.23	0.70
2:1:3375:U:H5'	37:f:67:VAL:HG21	1.73	0.70
4:3:114:ARG:HH21	11:E:31:TYR:HD1	1.39	0.70
10:D:261:MET:HE1	10:D:269:ARG:HH12	1.56	0.70
2:1:1338:G:OP1	21:O:60:ARG:NH1	2.23	0.70
15:I:598:SER:O	15:I:665:GLN:NE2	2.25	0.70
15:I:605:LEU:HD23	15:I:606:ASN:H	1.56	0.70
51:t:84:PRO:O	51:t:125:ASN:ND2	2.21	0.70
54:w:255:THR:HB	54:w:278:VAL:HB	1.73	0.70
56:y:221:ILE:O	56:y:223:LYS:NZ	2.25	0.70
2:1:675:C:H1'	54:w:788:LYS:HD2	1.72	0.70
54:w:180:GLU:HB2	54:w:197:VAL:HB	1.72	0.70
2:1:1674:C:OP2	38:g:74:ARG:NH2	2.24	0.70
2:1:53:G:OP2	41:j:48:ASN:ND2	2.25	0.69
3:2:64:G:H5''	53:v:14:LYS:HE2	1.74	0.69
56:y:66:ASN:HD22	56:y:112:ASP:HA	1.56	0.69
19:M:104:GLN:OE1	19:M:104:GLN:N	2.26	0.69
45:n:190:GLN:HE22	45:n:197:GLN:HB3	1.57	0.69
32:a:72:THR:HG22	32:a:110:LYS:HB3	1.73	0.69
2:1:3184:G:OP1	8:B:313:ARG:NH2	2.26	0.69
2:1:849:A:N6	2:1:939:G:O6	2.26	0.69
2:1:2465:G:H5'	2:1:2466:C:H5	1.58	0.69
3:2:132:G:N2	3:2:137:A:N1	2.34	0.69
4:3:10:VAL:HG22	9:C:34:PRO:HG3	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:92:TYR:HB3	8:B:99:LEU:HD12	1.75	0.69
14:H:118:GLU:OE1	14:H:122:ARG:NH2	2.25	0.69
43:l:1:MET:N	43:l:40:GLN:OE1	2.26	0.69
57:z:109:ASN:HA	57:z:112:LYS:HG3	1.72	0.69
2:1:1224:A:OP2	21:O:50:ARG:NH1	2.23	0.69
54:w:228:VAL:HA	54:w:231:LYS:HE2	1.75	0.69
15:I:688:LEU:H	15:I:688:LEU:HD12	1.58	0.68
56:y:111:ASN:HD21	56:y:114:VAL:HG13	1.58	0.68
2:1:2972:G:H1	2:1:3044:U:H3	1.42	0.68
15:I:509:GLY:O	15:I:623:VAL:N	2.27	0.68
2:1:650:G:N2	2:1:1435:G:OP1	2.22	0.68
2:1:1663:C:H42	2:1:1870:U:H3	1.41	0.68
15:I:561:THR:OG1	15:I:589:ARG:NH2	2.27	0.68
21:O:122:PRO:HA	21:O:125:LEU:HD12	1.76	0.68
34:c:54:LYS:HA	34:c:54:LYS:HE3	1.75	0.68
44:m:455:LEU:HD12	44:m:466:LEU:HD21	1.76	0.68
2:1:257:A:N7	18:L:134:LYS:NZ	2.41	0.68
15:I:675:LEU:HD13	15:I:741:LEU:HD11	1.74	0.68
2:1:312:G:H1	2:1:319:U:H3	1.42	0.68
27:V:20:PRO:HA	27:V:53:ALA:HA	1.76	0.68
41:j:46:SER:HB3	41:j:57:ARG:HH21	1.59	0.68
43:l:80:ARG:HD3	43:l:166:GLN:HB3	1.75	0.68
14:H:145:GLU:N	14:H:145:GLU:OE2	2.26	0.68
23:Q:21:GLU:OE1	23:Q:21:GLU:N	2.18	0.68
34:c:62:ALA:O	34:c:67:LYS:NZ	2.25	0.68
11:E:93:ILE:HD11	11:E:153:ARG:HD2	1.75	0.67
43:l:40:GLN:NE2	43:l:60:ARG:O	2.27	0.67
54:w:669:THR:HG23	54:w:670:VAL:HG23	1.76	0.67
2:1:3013:G:H21	54:w:124:GLY:HA2	1.58	0.67
54:w:167:ASN:ND2	54:w:217:VAL:O	2.24	0.67
2:1:3491:A:HO2'	2:1:3492:G:H8	1.40	0.67
7:A:140:ASN:HB2	16:J:181:MET:HE1	1.75	0.67
25:S:151:LEU:HB3	25:S:154:ARG:HE	1.60	0.67
37:f:53:VAL:HG22	37:f:67:VAL:HG22	1.76	0.67
42:k:69:GLU:HG2	42:k:70:VAL:H	1.59	0.67
35:d:107:GLU:OE1	35:d:107:GLU:N	2.26	0.67
2:1:781:C:OP1	32:a:132:ARG:NH2	2.28	0.67
2:1:1692:C:H5	2:1:1838:A:C8	2.13	0.67
19:M:78:TRP:NE1	19:M:84:CYS:SG	2.63	0.67
44:m:220:GLU:OE2	44:m:224:ARG:NH1	2.28	0.67
49:r:166:LYS:HE2	49:r:168:GLU:HB2	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1758:G:OP2	24:R:121:HIS:ND1	2.26	0.67
26:U:34:LEU:HB2	26:U:55:ARG:HH21	1.60	0.67
56:y:151:TYR:HE1	56:y:192:VAL:HG22	1.60	0.67
2:1:3081:U:H2'	2:1:3082:A:H8	1.60	0.67
26:U:71:GLY:HA2	26:U:74:LEU:HD23	1.77	0.67
27:V:130:ARG:NH2	56:y:12:GLU:OE2	2.28	0.67
2:1:816:A:N3	23:Q:64:SER:OG	2.27	0.66
2:1:1385:U:OP2	9:C:309:ARG:NH1	2.27	0.66
2:1:3111:C:OP2	57:z:83:THR:N	2.29	0.66
56:y:66:ASN:HD21	56:y:68:LYS:HE3	1.60	0.66
2:1:1146:G:N2	2:1:1146:G:OP2	2.26	0.66
2:1:1417:G:O2'	9:C:140:ARG:NH1	2.26	0.66
10:D:339:VAL:HB	10:D:389:ILE:HG13	1.77	0.66
14:H:92:LEU:HB2	14:H:140:ASP:HB2	1.75	0.66
25:S:79:ARG:HE	25:S:121:ARG:HH21	1.42	0.66
2:1:955:C:OP2	2:1:957:A:N6	2.26	0.66
2:1:1639:U:H4'	2:1:1890:A:H4'	1.77	0.66
2:1:2947:C:H1'	49:r:59:ILE:HG21	1.77	0.66
2:1:3314:U:OP2	19:M:121:ARG:NH2	2.29	0.66
30:Y:49:VAL:HG21	30:Y:79:LEU:HD21	1.77	0.66
51:t:71:LEU:HD21	51:t:105:ILE:HD11	1.78	0.66
2:1:531:A:OP2	12:F:77:ARG:NH1	2.29	0.66
10:D:461:GLU:OE1	17:K:41:ASN:ND2	2.28	0.66
34:c:100:ARG:HH11	34:c:100:ARG:HG3	1.61	0.66
45:n:250:ASP:HB3	45:n:253:LYS:HG2	1.76	0.66
45:n:370:GLU:HG2	45:n:380:VAL:HG11	1.76	0.66
6:8:8:ARG:H	6:8:8:ARG:HD3	1.60	0.66
2:1:400:G:OP1	55:x:55:ILE:N	2.28	0.66
15:I:378:ASN:O	15:I:382:ASN:ND2	2.27	0.66
7:A:159:PRO:HB2	16:J:100:LEU:HB3	1.78	0.66
8:B:285:ILE:HG22	8:B:322:VAL:HG22	1.78	0.66
10:D:198:GLY:O	10:D:499:GLN:NE2	2.28	0.66
21:O:76:ALA:HB3	21:O:79:ARG:HG2	1.78	0.66
2:1:997:A:O2'	2:1:998:U:O4'	2.14	0.66
4:3:133:LEU:HB3	36:e:123:VAL:HG22	1.77	0.66
15:I:420:LEU:HD22	15:I:517:ARG:HD3	1.77	0.66
17:K:265:ARG:HE	46:o:215:LEU:HD13	1.61	0.65
36:e:120:GLY:O	36:e:124:ARG:NH1	2.25	0.65
44:m:134:ILE:O	44:m:137:LYS:NZ	2.29	0.65
56:y:200:ASN:OD1	56:y:203:CYS:N	2.29	0.65
3:2:60:A:N1	6:8:33:ASN:HB3	2.11	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:74:ASP:OD1	7:A:75:SER:N	2.29	0.65
10:D:133:ALA:HB3	10:D:139:LYS:HD3	1.79	0.65
10:D:316:VAL:HG23	10:D:438:LEU:HD11	1.78	0.65
10:D:346:CYS:SG	10:D:367:HIS:ND1	2.67	0.65
13:G:238:MET:HG2	13:G:243:GLN:HB3	1.79	0.65
56:y:107:ILE:HB	56:y:118:HIS:HB2	1.78	0.65
17:K:172:LYS:HD3	17:K:172:LYS:H	1.61	0.65
44:m:738:MET:HA	44:m:738:MET:HE3	1.78	0.65
51:t:156:LYS:HD2	51:t:249:VAL:HG22	1.78	0.65
17:K:57:LEU:HD13	17:K:239:ILE:HG12	1.79	0.65
21:O:11:ASP:OD2	25:S:171:ARG:NH2	2.29	0.65
27:V:34:LYS:HE2	54:w:244:GLY:HA3	1.78	0.65
49:r:178:GLN:OE1	49:r:180:LYS:N	2.30	0.65
19:M:65:LEU:HD11	19:M:74:VAL:HG22	1.77	0.65
2:1:369:A:O3'	41:j:45:ARG:NH2	2.27	0.65
10:D:366:LEU:HD21	10:D:379:PHE:HB2	1.78	0.65
31:Z:53:VAL:HG13	31:Z:62:ILE:HD12	1.79	0.65
9:C:100:ARG:HH21	9:C:104:PRO:HD3	1.61	0.65
13:G:258:ARG:HH21	44:m:184:LYS:HD3	1.61	0.65
14:H:171:ARG:HA	49:r:16:ARG:HH22	1.62	0.65
43:l:72:LYS:HG3	43:l:82:HIS:NE2	2.12	0.65
2:1:2933:A:N6	2:1:2945:G:O2'	2.29	0.65
2:1:2996:G:O2'	2:1:3120:A:N1	2.30	0.65
7:A:57:GLN:HG2	7:A:109:LEU:HD22	1.77	0.65
45:n:574:SER:O	45:n:578:ASN:ND2	2.29	0.64
2:1:732:A:N6	2:1:742:A:OP2	2.31	0.64
2:1:3281:A:H5'	25:S:175:PHE:HE1	1.63	0.64
10:D:204:GLU:OE1	10:D:221:ARG:NH1	2.29	0.64
16:J:202:LYS:HA	16:J:205:ARG:HE	1.61	0.64
43:l:157:GLU:HG3	43:l:160:ALA:HB2	1.78	0.64
8:B:222:ARG:HB3	8:B:331:PRO:HD3	1.79	0.64
43:l:136:MET:N	43:l:136:MET:SD	2.70	0.64
47:p:372:ALA:HA	47:p:382:VAL:HA	1.80	0.64
2:1:117:U:OP2	20:N:2:GLY:N	2.31	0.64
17:K:234:LYS:H	17:K:234:LYS:HE2	1.61	0.64
43:l:43:ARG:HG2	43:l:72:LYS:HG2	1.79	0.64
56:y:76:THR:O	56:y:96:ARG:NH2	2.31	0.64
2:1:3288:G:H1	2:1:3299:U:H3	1.46	0.64
3:2:61:A:N6	6:8:33:ASN:OD1	2.31	0.64
32:a:70:ARG:HH11	32:a:110:LYS:HD2	1.63	0.64
42:k:34:LYS:HG2	42:k:47:VAL:HG22	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:l:37:PHE:O	43:l:38:ARG:NE	2.27	0.64
43:l:107:PHE:CZ	43:l:133:ILE:HD13	2.33	0.64
15:I:478:THR:OG1	54:w:483:ARG:NH1	2.30	0.64
45:n:560:LEU:O	45:n:564:MET:HG2	1.98	0.64
52:u:10:SER:HB2	52:u:53:LYS:HB2	1.78	0.64
57:z:114:LEU:HA	57:z:117:LYS:HD3	1.80	0.64
2:l:1887:C:OP1	29:X:119:LYS:NZ	2.30	0.63
7:A:122:VAL:HG13	7:A:232:ILE:HG12	1.80	0.63
15:I:647:ILE:HD12	15:I:652:LEU:HD12	1.79	0.63
27:V:84:ARG:NH1	27:V:84:ARG:O	2.30	0.63
43:l:121:ILE:HG13	43:l:123:ASP:H	1.63	0.63
2:l:2458:G:H5''	2:l:2459:G:H5'	1.81	0.63
7:A:188:VAL:HG21	16:J:150:VAL:HG22	1.80	0.63
2:l:839:A:H61	2:l:967:U:H3	1.47	0.63
2:l:1417:G:O3'	9:C:140:ARG:NH2	2.29	0.63
7:A:204:GLU:HB2	7:A:221:ILE:HD11	1.79	0.63
8:B:50:LYS:HA	8:B:79:ILE:HG22	1.78	0.63
36:e:103:VAL:HG12	36:e:123:VAL:HG23	1.80	0.63
46:o:187:HIS:NE2	46:o:189:ASN:HB3	2.13	0.63
2:l:1012:A:O2'	2:l:1013:U:O4'	2.15	0.63
2:l:3434:G:N7	52:u:35:LYS:NZ	2.46	0.63
11:E:85:PRO:HD2	11:E:178:LEU:HD23	1.80	0.63
31:Z:42:VAL:HG22	31:Z:74:VAL:HG22	1.81	0.63
31:Z:68:VAL:O	31:Z:115:LYS:NZ	2.28	0.63
46:o:225:THR:OG1	46:o:226:ARG:N	2.30	0.63
54:w:100:ARG:HA	54:w:103:LEU:HD12	1.81	0.63
56:y:54:GLY:N	56:y:80:GLU:OE1	2.31	0.63
2:l:1242:U:O2'	25:S:112:ARG:NH1	2.31	0.63
20:N:172:ARG:HG3	20:N:174:ILE:HG12	1.81	0.63
2:l:379:G:N1	2:l:382:A:OP2	2.32	0.63
9:C:363:ASN:HD22	58:T:150:THR:HG21	1.64	0.63
15:I:666[B]:LEU:HG	15:I:667:PRO:HD2	1.81	0.63
32:a:75:LEU:HA	32:a:78:LEU:HD23	1.78	0.63
44:m:628:HIS:HE1	44:m:696:PRO:HG3	1.64	0.63
51:t:94:ARG:HG2	51:t:117:ILE:HA	1.80	0.63
2:l:743:A:OP1	32:a:136:LYS:NZ	2.31	0.63
2:l:2947:C:N3	49:r:63:LYS:NZ	2.44	0.63
9:C:145:GLU:OE1	9:C:178:ARG:NH1	2.32	0.63
2:l:3082:A:H5'	21:O:69:ARG:HH12	1.63	0.63
24:R:105:LEU:HD11	24:R:138:LEU:HD23	1.80	0.63
36:e:116:VAL:HB	36:e:119:ALA:HB2	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:m:387:ARG:H	44:m:402:GLY:HA2	1.63	0.63
54:w:134:GLN:NE2	54:w:158:LYS:O	2.29	0.63
2:1:1274:G:N2	2:1:1301:A:O2'	2.32	0.63
10:D:287:ARG:HH12	10:D:288:ILE:HB	1.63	0.63
21:O:50:ARG:HG2	21:O:54:LYS:HE3	1.79	0.62
54:w:696:PRO:HD2	54:w:699:LYS:HB2	1.80	0.62
56:y:188:ARG:NH1	56:y:209:ASP:OD1	2.31	0.62
2:1:2423:G:N2	2:1:2427:C:O2'	2.32	0.62
26:U:24:ILE:HG23	26:U:87:LEU:HD22	1.81	0.62
27:V:68:LYS:HB2	27:V:71:LEU:HD22	1.81	0.62
2:1:167:G:H5'	44:m:222:LYS:HD2	1.80	0.62
17:K:65:ASN:O	46:o:208:ARG:NH2	2.30	0.62
27:V:106:ASN:HD21	27:V:110:GLU:HB3	1.65	0.62
33:b:445:VAL:H	52:u:76:ARG:HH22	1.47	0.62
2:1:1348:A:OP1	25:S:155:ARG:NH1	2.24	0.62
14:H:111:GLU:HG2	14:H:123:VAL:HG22	1.80	0.62
31:Z:89:LEU:HD12	31:Z:92:LEU:HG	1.81	0.62
34:c:44:THR:HG22	34:c:105:ALA:HB2	1.81	0.62
46:o:225:THR:OG1	46:o:230:LYS:NZ	2.32	0.62
2:1:1836:U:OP1	15:I:464:LYS:NZ	2.31	0.62
54:w:458:ASP:O	54:w:462:MET:HG3	2.00	0.62
56:y:45:VAL:HG12	56:y:46:VAL:HG13	1.81	0.62
56:y:107:ILE:HG13	56:y:108:VAL:HG23	1.81	0.62
22:P:67:VAL:HG13	22:P:82:ARG:HG3	1.82	0.62
30:Y:2:LYS:HD3	30:Y:7:VAL:HG23	1.80	0.62
49:r:174:MET:N	49:r:174:MET:SD	2.73	0.62
13:G:248:LYS:HG3	13:G:251:LYS:HE3	1.81	0.61
25:S:137:ASN:OD1	25:S:138:TYR:N	2.32	0.61
42:k:58:ARG:NH1	42:k:58:ARG:HB2	2.15	0.61
46:o:229:ARG:HG3	46:o:232:LYS:HE3	1.82	0.61
54:w:33:LEU:HD23	54:w:62:VAL:HB	1.82	0.61
2:1:3195:C:N3	2:1:3232:G:O2'	2.32	0.61
15:I:691:LEU:HD11	15:I:709:ASP:HB3	1.80	0.61
34:c:39:LEU:HD23	34:c:101:VAL:HG21	1.82	0.61
45:n:460:TYR:HD2	45:n:587:ASN:HB2	1.65	0.61
2:1:112:U:OP1	39:h:109:LYS:NZ	2.32	0.61
2:1:3195:C:H1'	8:B:343:LEU:HD21	1.83	0.61
11:E:52:LEU:HD13	11:E:80:LEU:HD11	1.81	0.61
15:I:729:HIS:CE1	15:I:731:SER:H	2.17	0.61
31:Z:23:VAL:HG12	31:Z:45:GLY:HA3	1.82	0.61
23:Q:91:ASP:O	23:Q:114:ARG:NH2	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:6:100:U:H4'	46:o:140:ARG:HH21	1.64	0.61
13:G:183:LYS:HB2	13:G:194:THR:HG23	1.82	0.61
15:I:624:VAL:HB	15:I:635:LYS:HZ1	1.64	0.61
26:U:55:ARG:HG2	26:U:61:ILE:HA	1.83	0.61
44:m:389:LEU:HD12	44:m:398:LEU:HD21	1.83	0.61
54:w:16:TRP:NE1	54:w:186:SER:HA	2.16	0.61
2:1:1389:A:OP1	4:3:13:HIS:NE2	2.27	0.61
16:J:110:PRO:O	16:J:113:ILE:HG12	2.01	0.61
17:K:56:GLN:HG2	17:K:200:MET:HG3	1.81	0.61
2:1:609:A:O2'	37:f:85:ARG:NH2	2.34	0.61
5:6:97:C:N3	5:6:98:G:N2	2.49	0.61
15:I:688:LEU:HA	15:I:692:LEU:HD12	1.83	0.61
32:a:99:PRO:HG2	32:a:122:VAL:HG23	1.83	0.61
45:n:376:PHE:CZ	45:n:428:ILE:HG23	2.36	0.61
47:p:200:VAL:HA	47:p:216:SER:HA	1.81	0.61
51:t:120:ALA:HB3	51:t:211:PHE:HB2	1.82	0.61
2:1:838:A:H2'	2:1:839:A:C4	2.35	0.61
17:K:80:VAL:HG12	17:K:204:GLY:HA2	1.82	0.61
2:1:3131:C:H4'	14:H:120:ILE:HD13	1.81	0.60
2:1:3281:A:H5'	25:S:175:PHE:CE1	2.36	0.60
22:P:166:ARG:CZ	37:f:61:ARG:HH12	2.13	0.60
25:S:11:ARG:HH12	25:S:14:PRO:HD3	1.66	0.60
26:U:10:ASN:HD21	26:U:65:ALA:HB3	1.66	0.60
27:V:82:ARG:NH1	27:V:119:PRO:O	2.30	0.60
34:c:32:MET:HE1	34:c:95:CYS:HA	1.82	0.60
43:l:105:MET:HG3	43:l:106:PRO:HD3	1.83	0.60
54:w:628:THR:HG21	54:w:677:ILE:HA	1.83	0.60
10:D:501:TYR:HA	10:D:504:TYR:CD2	2.36	0.60
14:H:145:GLU:HB2	14:H:185:ILE:HD11	1.84	0.60
15:I:483:GLU:OE2	54:w:699:LYS:NZ	2.26	0.60
44:m:356:GLU:HB2	45:n:573:TYR:CE2	2.36	0.60
47:p:222:GLY:HA2	47:p:264:LEU:HA	1.83	0.60
2:1:1332:A:H1'	49:r:44:GLY:HA2	1.83	0.60
45:n:173:ARG:NH1	45:n:267:GLU:OE2	2.34	0.60
17:K:67:ARG:HG2	17:K:195:PRO:HD2	1.82	0.60
26:U:82:LEU:HG	26:U:88:ARG:HG2	1.83	0.60
34:c:57:LEU:HB2	34:c:104:LEU:HG	1.83	0.60
44:m:356:GLU:HB3	45:n:570:ARG:HA	1.83	0.60
54:w:32:LYS:HB3	54:w:195:PHE:HE2	1.65	0.60
7:A:140:ASN:O	7:A:204:GLU:HG3	2.01	0.60
8:B:14:LEU:HG	8:B:17:LEU:HG	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:I:531:LEU:HB2	15:I:581:LEU:HD21	1.83	0.60
11:E:154:ILE:HD12	11:E:154:ILE:H	1.67	0.60
8:B:148:LEU:HD23	8:B:196:ARG:HH11	1.67	0.60
17:K:224:VAL:HA	17:K:228:ILE:HD13	1.82	0.60
49:r:200:LYS:HB3	49:r:219:VAL:HG13	1.82	0.60
52:u:12:PRO:HB2	52:u:14:TYR:CE1	2.37	0.60
2:1:777:C:H3'	2:1:778:G:H5''	1.82	0.60
2:1:3308:G:N7	25:S:170:HIS:NE2	2.49	0.60
11:E:83:THR:HB	11:E:93:ILE:HA	1.83	0.60
44:m:157:LYS:NZ	54:w:687:GLU:OE1	2.35	0.60
2:1:714:A:H4'	53:v:25:LYS:NZ	2.17	0.60
33:b:421:ILE:O	52:u:81:ARG:NH2	2.34	0.60
45:n:591:ARG:HA	45:n:594:LYS:HE3	1.83	0.60
50:s:11:ARG:HG2	50:s:15:LEU:HD22	1.83	0.60
2:1:2925:G:H2'	2:1:2926:G:H8	1.67	0.60
10:D:270:GLN:HE21	10:D:272:LEU:HD11	1.67	0.60
15:I:401:SER:OG	15:I:405:LYS:NZ	2.33	0.60
2:1:2928:A:H1'	49:r:184:THR:HG21	1.82	0.59
15:I:495:ILE:HD11	44:m:152:ILE:HG23	1.83	0.59
29:X:66:ILE:HD12	29:X:120:LYS:HG3	1.82	0.59
32:a:125:GLN:HB3	32:a:147:ILE:HD11	1.84	0.59
43:l:123:ASP:HA	43:l:150:THR:HG21	1.84	0.59
49:r:174:MET:SD	49:r:177:ARG:NH2	2.74	0.59
2:1:6:A:H5'	45:n:93:LYS:HG3	1.84	0.59
2:1:1648:A:OP1	42:k:43:LEU:N	2.34	0.59
44:m:386:VAL:HG21	44:m:736:ILE:HD11	1.84	0.59
2:1:1438:G:N2	2:1:1441:A:OP2	2.31	0.59
11:E:117:GLU:OE2	11:E:117:GLU:N	2.28	0.59
14:H:10:THR:HG22	14:H:54:LYS:HG2	1.83	0.59
34:c:27:LYS:HE3	34:c:114:ILE:HG13	1.82	0.59
8:B:215:ILE:HD12	8:B:338:LEU:HB3	1.85	0.59
31:Z:15:ARG:HH11	38:g:86:LYS:HE2	1.66	0.59
44:m:612:THR:HA	44:m:641:PHE:HZ	1.66	0.59
44:m:614:VAL:HG11	44:m:633:SER:HB2	1.85	0.59
57:z:102:GLY:HA2	57:z:105:ALA:HB3	1.84	0.59
2:1:1312:U:H2'	2:1:1313:G:H8	1.68	0.59
2:1:3194:G:OP1	8:B:279:ASN:ND2	2.33	0.59
11:E:57:VAL:O	11:E:104:THR:OG1	2.20	0.59
11:E:134:LYS:HG2	11:E:135:LYS:H	1.67	0.59
45:n:449:LEU:HD11	45:n:462:PRO:HG2	1.84	0.59
2:1:1665:A:OP2	31:Z:67:ARG:NH1	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:I:691:LEU:HD13	15:I:707:ILE:HD12	1.83	0.59
26:U:27:VAL:HA	26:U:30:PHE:CD2	2.37	0.59
44:m:616:TRP:HB3	44:m:634:TYR:HB2	1.85	0.59
52:u:79:PRO:HG2	56:y:85:ARG:HH11	1.68	0.59
10:D:107:MET:HE2	10:D:109:PHE:HE2	1.67	0.59
43:l:42:ASP:O	43:l:73:PHE:N	2.34	0.59
46:o:122:ARG:NH2	46:o:195:ASP:OD1	2.25	0.59
49:r:247:ASN:HD22	49:r:250:LEU:HD12	1.68	0.59
2:1:1780:G:N2	2:1:1781:G:O6	2.36	0.59
15:I:681:LEU:HG	15:I:683:SER:H	1.68	0.59
16:J:204:GLN:HA	16:J:207:LEU:HB2	1.84	0.59
27:V:19:LEU:HD21	27:V:100:ASN:HD22	1.67	0.59
49:r:17:ARG:HB3	49:r:20:HIS:HB2	1.85	0.59
54:w:111:LYS:HB3	54:w:150:VAL:HB	1.84	0.59
2:1:3039:U:H2'	2:1:3042:G:N7	2.18	0.59
4:3:5:GLU:OE1	4:3:5:GLU:N	2.36	0.59
17:K:254:ASN:HB3	17:K:257:LEU:HB3	1.84	0.59
44:m:701:LEU:O	45:n:555:LYS:NZ	2.35	0.59
52:u:69:LEU:HD23	52:u:97:VAL:HA	1.85	0.59
54:w:26:ARG:HH11	54:w:57:GLY:HA3	1.68	0.59
54:w:698:LYS:O	54:w:702:GLU:HG3	2.03	0.59
2:1:1806:U:O2'	2:1:1807:G:O5'	2.19	0.58
2:1:2458:G:H2'	2:1:2462:C:H5	1.68	0.58
2:1:3278:A:OP1	21:O:162:LYS:NZ	2.35	0.58
17:K:23:TYR:HA	17:K:26:LYS:HE3	1.85	0.58
42:k:56:LYS:HA	42:k:59:GLN:NE2	2.18	0.58
43:l:2:ARG:N	43:l:39:LEU:O	2.33	0.58
44:m:681:VAL:HG11	44:m:727:LEU:HD21	1.84	0.58
13:G:249:ARG:NH1	54:w:661:ASP:OD1	2.36	0.58
34:c:70:LEU:HD13	34:c:103:VAL:HG21	1.85	0.58
44:m:373:THR:N	44:m:740:THR:O	2.35	0.58
57:z:97:LYS:HA	57:z:100:LYS:HG2	1.84	0.58
10:D:492:ASP:OD1	10:D:495:ARG:NH2	2.34	0.58
55:x:4:ILE:HD13	55:x:9:VAL:HG12	1.85	0.58
2:1:2702:G:OP1	43:l:60:ARG:NH1	2.36	0.58
2:1:3004:U:O2'	2:1:3201:A:N3	2.29	0.58
2:1:3146:U:O2'	52:u:16:GLY:O	2.21	0.58
15:I:296:ARG:NH1	15:I:300:GLU:OE1	2.31	0.58
17:K:65:ASN:OD1	46:o:208:ARG:NH1	2.36	0.58
18:L:62:THR:HG23	18:L:64:ARG:H	1.69	0.58
27:V:35:ASN:HB2	27:V:65:LYS:HB3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:n:349:ASN:ND2	45:n:431:GLY:O	2.36	0.58
25:S:41:TRP:HB3	25:S:52:LYS:HD2	1.85	0.58
2:1:64:G:OP2	20:N:169:LYS:NZ	2.36	0.58
2:1:1275:A:OP1	2:1:1302:A:O2'	2.20	0.58
56:y:21:ASN:ND2	56:y:156:ASN:OD1	2.36	0.58
2:1:222:G:H5''	30:Y:11:ARG:HG3	1.84	0.58
14:H:42:VAL:HG21	14:H:71:VAL:HG21	1.84	0.58
39:h:94:LEU:HD22	39:h:98:GLU:HG3	1.86	0.58
42:k:61:LEU:HD12	42:k:65:LEU:HD23	1.85	0.58
43:l:42:ASP:OD1	43:l:42:ASP:N	2.36	0.58
43:l:71:GLY:HA2	43:l:82:HIS:HD2	1.68	0.58
56:y:15:VAL:HA	56:y:61:ARG:HG2	1.86	0.58
24:R:57:MET:SD	24:R:58:HIS:N	2.77	0.58
25:S:130:LYS:HB2	25:S:133:ASP:OD2	2.04	0.58
43:l:95:TYR:HE2	43:l:125:THR:HA	1.68	0.58
44:m:379:PHE:HB2	44:m:736:ILE:HB	1.86	0.58
44:m:660:LEU:HD11	44:m:674:SER:HB2	1.86	0.58
46:o:215:LEU:HD21	46:o:220:ALA:HB2	1.84	0.58
51:t:182:TYR:HB3	51:t:200:HIS:CG	2.39	0.58
2:1:1382:C:O2'	2:1:1384:U:OP1	2.21	0.57
2:1:1529:U:H5	2:1:1890:A:N1	2.01	0.57
8:B:80:GLU:HG2	8:B:82:PRO:HD3	1.86	0.57
15:I:532:GLN:OE1	15:I:535:ARG:NH1	2.37	0.57
27:V:119:PRO:HA	27:V:137:THR:HG23	1.85	0.57
45:n:230:MET:HA	45:n:230:MET:HE3	1.86	0.57
45:n:366:ARG:NH1	45:n:386:LEU:O	2.35	0.57
7:A:216:VAL:HG21	16:J:147:VAL:HA	1.86	0.57
18:L:63:ILE:HD12	18:L:66:ASN:HD21	1.69	0.57
30:Y:55:ILE:HD11	30:Y:81:ILE:HG12	1.86	0.57
44:m:665:TYR:CD1	44:m:672:PHE:HB3	2.40	0.57
52:u:69:LEU:HB2	52:u:97:VAL:HG22	1.86	0.57
2:1:955:C:H5''	2:1:956:G:N7	2.19	0.57
2:1:1474:G:OP1	9:C:85:HIS:NE2	2.37	0.57
28:W:43:PHE:H	28:W:101:GLY:H	1.51	0.57
30:Y:108:LEU:HD22	30:Y:114:ARG:HE	1.67	0.57
41:j:46:SER:HB3	41:j:57:ARG:NH2	2.19	0.57
7:A:124:PHE:CB	7:A:227:MET:HE2	2.34	0.57
8:B:53:MET:HB3	8:B:77:THR:HA	1.84	0.57
10:D:128:ASP:HB3	10:D:290:LEU:HD12	1.87	0.57
45:n:428:ILE:H	45:n:428:ILE:HD12	1.69	0.57
51:t:87:THR:HG22	51:t:89:LEU:H	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1627:G:OP1	38:g:58:ARG:NH2	2.36	0.57
17:K:265:ARG:HB3	46:o:215:LEU:HB3	1.87	0.57
22:P:85:VAL:O	22:P:89:LYS:HG2	2.05	0.57
27:V:95:LEU:HD21	52:u:20:MET:HG2	1.87	0.57
43:l:47:VAL:HG11	43:l:66:LEU:HG	1.86	0.57
13:G:143:ILE:HG23	13:G:175:VAL:HG21	1.86	0.57
17:K:265:ARG:HH21	46:o:215:LEU:HD12	1.68	0.57
26:U:13:ILE:HD11	26:U:60:LYS:HD3	1.86	0.57
43:l:38:ARG:HG3	43:l:52:MET:HG2	1.86	0.57
44:m:527:THR:HG21	44:m:531:ILE:HD11	1.86	0.57
45:n:591:ARG:HH21	45:n:595:ARG:HH12	1.52	0.57
56:y:93:LYS:HE2	56:y:93:LYS:H	1.69	0.57
2:1:847:G:H1	2:1:957:A:N6	1.99	0.57
2:1:1527:G:N2	2:1:1527:G:OP2	2.38	0.57
2:1:1670:G:N2	2:1:1673:A:OP2	2.38	0.57
45:n:358:PHE:HD1	45:n:403:ILE:HD11	1.68	0.57
47:p:109:GLY:HA3	47:p:148:SER:HA	1.87	0.57
49:r:178:GLN:OE1	49:r:179:LYS:N	2.36	0.57
50:s:8:SER:OG	50:s:10:ARG:O	2.22	0.57
14:H:19:VAL:HG13	14:H:28:VAL:HG22	1.87	0.57
24:R:44:LEU:HD22	24:R:49:LEU:HD22	1.87	0.57
43:l:161:ILE:HD12	43:l:162:VAL:H	1.69	0.57
2:1:371:C:OP2	41:j:56:ARG:NH2	2.35	0.57
2:1:990:C:H3'	16:J:205:ARG:HH12	1.70	0.57
2:1:1790:A:OP2	42:k:34:LYS:NZ	2.28	0.57
2:1:2481:G:H1	2:1:3081:U:H3	1.53	0.57
10:D:405:VAL:O	10:D:435:GLY:N	2.38	0.57
12:F:113:LEU:O	12:F:122:ILE:HD13	2.04	0.57
44:m:117:PRO:HG2	54:w:635:SER:HA	1.86	0.57
49:r:199:VAL:HG11	49:r:212:GLY:HA2	1.86	0.57
2:1:699:G:OP1	9:C:33:ARG:NH1	2.32	0.57
2:1:712:U:OP2	18:L:36:ARG:NH2	2.38	0.57
2:1:1169:U:H2'	2:1:1170:G:H8	1.70	0.57
24:R:105:LEU:HB2	24:R:109:TYR:HE1	1.69	0.57
51:t:81:ILE:HG12	51:t:130:ALA:HB1	1.86	0.57
26:U:37:ARG:HH12	26:U:39:LYS:HE3	1.70	0.56
54:w:33:LEU:HA	54:w:36:LEU:HD12	1.87	0.56
55:x:4:ILE:HD12	55:x:10:ARG:HA	1.86	0.56
2:1:1555:G:N2	2:1:1890:A:N3	2.54	0.56
2:1:1606:U:H3	45:n:221:THR:HG22	1.71	0.56
2:1:1758:G:N2	2:1:1771:C:O2'	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:3190:A:OP1	27:V:16:THR:OG1	2.20	0.56
10:D:258:ARG:HH12	10:D:259:GLN:HG2	1.70	0.56
2:1:639:C:O3'	11:E:121:LYS:NZ	2.33	0.56
2:1:955:C:H3'	2:1:956:G:C8	2.40	0.56
2:1:1739:A:N6	2:1:1780:G:O4'	2.39	0.56
2:1:3117:A:N6	2:1:3129:A:OP2	2.34	0.56
4:3:156:LYS:HE2	22:P:11:GLU:HB2	1.87	0.56
10:D:313:GLN:NE2	10:D:420:TYR:OH	2.38	0.56
15:I:310:PHE:HE2	15:I:343:LEU:HD11	1.69	0.56
20:N:44:ARG:NH1	20:N:120:TRP:O	2.39	0.56
30:Y:99:ASP:OD2	30:Y:101:SER:OG	2.23	0.56
32:a:76:ASP:OD1	32:a:76:ASP:N	2.33	0.56
53:v:136:GLU:H	53:v:136:GLU:CD	2.14	0.56
54:w:228:VAL:HB	54:w:272:GLY:HA3	1.86	0.56
2:1:2993:G:C2	49:r:7:ILE:HG12	2.39	0.56
7:A:81:ASP:N	7:A:81:ASP:OD1	2.36	0.56
27:V:41:VAL:HG13	27:V:60:VAL:HG12	1.86	0.56
43:l:1:MET:CE	43:l:38:ARG:HD3	2.35	0.56
2:1:1777:U:O2	38:g:52:GLN:NE2	2.38	0.56
3:2:114:C:H4'	3:2:115:G:H5''	1.87	0.56
4:3:44:PRO:O	4:3:65:LYS:NZ	2.25	0.56
25:S:81:ASP:HB3	25:S:119:SER:HB2	1.87	0.56
49:r:185:HIS:HD2	49:r:227:LEU:HD11	1.70	0.56
54:w:137:LEU:HA	54:w:140:MET:HG3	1.88	0.56
2:1:3315:A:OP2	19:M:118:LYS:NZ	2.39	0.56
7:A:179:ARG:HD3	44:m:113:GLU:HA	1.86	0.56
25:S:11:ARG:HH21	58:T:141:VAL:HG22	1.70	0.56
45:n:439:TYR:CE1	45:n:446:PRO:HD2	2.41	0.56
45:n:582:LYS:HE2	45:n:582:LYS:HA	1.88	0.56
50:s:16:ARG:HA	50:s:19:ILE:HD12	1.87	0.56
54:w:264:ALA:O	54:w:321:ARG:NH2	2.39	0.56
2:1:34:A:N3	2:1:842:A:O2'	2.39	0.56
2:1:72:C:H5'	18:L:63:ILE:HD13	1.87	0.56
2:1:1142:U:O2'	2:1:1143:A:O5'	2.22	0.56
2:1:1273:G:H3'	2:1:1274:G:C8	2.41	0.56
2:1:1746:C:H2'	2:1:1747:A:C8	2.41	0.56
2:1:3109:U:OP2	57:z:86:PRO:HD3	2.06	0.56
16:J:202:LYS:HG2	16:J:205:ARG:HH21	1.71	0.56
28:W:60:TRP:HA	28:W:105:THR:HA	1.87	0.56
45:n:399:ILE:HB	45:n:416:ARG:HD3	1.88	0.56
45:n:589:ALA:O	45:n:593:ARG:HG3	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:p:296:TRP:HA	47:p:303:ASN:HA	1.87	0.56
54:w:666:GLU:HA	54:w:669:THR:HG22	1.87	0.56
2:1:216:A:H4'	2:1:218:A:N7	2.20	0.56
2:1:366:G:N2	2:1:369:A:OP2	2.33	0.56
2:1:1929:A:N7	24:R:20:ARG:NH1	2.54	0.56
2:1:2699:U:H1'	43:l:56:THR:O	2.05	0.56
7:A:152:ASP:HB2	7:A:192:THR:HA	1.88	0.56
19:M:88:ALA:O	19:M:94:LYS:NZ	2.39	0.56
34:c:23:THR:HG22	34:c:27:LYS:HD2	1.87	0.56
34:c:65:LEU:HD11	38:g:90:VAL:HG23	1.88	0.56
2:1:3367:A:H2'	11:E:86:TYR:OH	2.06	0.56
11:E:140:PHE:HE2	22:P:172:GLY:HA3	1.71	0.56
15:I:704:ASN:HB3	15:I:707:ILE:HD13	1.88	0.56
27:V:68:LYS:HG3	54:w:215:ARG:NE	2.21	0.56
37:f:60:VAL:HG12	37:f:61:ARG:HG3	1.88	0.56
45:n:563:MET:HE2	45:n:563:MET:O	2.06	0.56
47:p:401:THR:O	47:p:405:TRP:N	2.39	0.56
56:y:119:PRO:HG2	56:y:146:VAL:HG12	1.86	0.56
56:y:187:ASN:HB2	56:y:190:SER:HB3	1.88	0.56
2:1:1381:G:O2'	4:3:103:ARG:NH1	2.40	0.55
2:1:2699:U:H4'	43:l:59:ALA:HA	1.88	0.55
3:2:60:A:OP2	6:8:18:ARG:NH2	2.39	0.55
13:G:227[A]:ASP:O	13:G:230:ARG:HG2	2.06	0.55
17:K:107:LEU:O	17:K:111:VAL:N	2.32	0.55
56:y:157:GLN:HE22	56:y:201:ASP:HA	1.71	0.55
44:m:222:LYS:HE2	53:v:192:LEU:HB3	1.89	0.55
45:n:434:GLU:HG2	45:n:439:TYR:HE2	1.72	0.55
46:o:226:ARG:HG3	46:o:229:ARG:HE	1.71	0.55
2:1:3123:A:H1'	33:b:208:GLY:HA2	1.89	0.55
7:A:124:PHE:HB2	7:A:227:MET:HE2	1.87	0.55
15:I:502:GLN:HB2	44:m:148:LEU:HD21	1.87	0.55
15:I:657:LYS:NZ	15:I:702:ILE:O	2.39	0.55
21:O:57:ALA:O	21:O:61:LYS:NZ	2.40	0.55
52:u:92:ASN:HA	52:u:95:LYS:HE3	1.88	0.55
2:1:1290:A:OP1	28:W:67:MET:N	2.40	0.55
2:1:1806:U:O2'	2:1:1807:G:O4'	2.25	0.55
14:H:87:ARG:NH2	14:H:185:ILE:HG23	2.22	0.55
15:I:658:ARG:NH1	15:I:699:GLY:O	2.40	0.55
31:Z:14:THR:HG23	31:Z:15:ARG:HG2	1.87	0.55
44:m:320:LEU:HD23	45:n:421:PRO:HG2	1.88	0.55
44:m:718:THR:HB	44:m:727:LEU:HD11	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:u:46:PRO:O	52:u:52:THR:OG1	2.20	0.55
56:y:126:GLU:HG3	56:y:137:VAL:HG11	1.89	0.55
2:1:2925:G:H2'	2:1:2926:G:C8	2.42	0.55
2:1:3415:U:H5''	8:B:174:LYS:HE2	1.89	0.55
9:C:141:GLY:O	9:C:143:ARG:NH1	2.40	0.55
13:G:226:TYR:O	13:G:228:GLU:N	2.38	0.55
16:J:176:LYS:HB2	16:J:181:MET:HE2	1.87	0.55
26:U:47:LEU:HD13	26:U:53:VAL:HG12	1.87	0.55
30:Y:73:TYR:CD1	30:Y:76:LYS:HG3	2.41	0.55
44:m:413:MET:H	44:m:413:MET:CE	2.19	0.55
2:1:26:A:N3	2:1:336:U:O2'	2.38	0.55
2:1:949:A:O2'	2:1:950:C:OP1	2.22	0.55
2:1:2515:U:H3	2:1:2697:G:H1	1.54	0.55
26:U:102:GLU:OE2	26:U:103:LEU:N	2.40	0.55
43:l:97:ILE:HD12	43:l:133:ILE:HA	1.88	0.55
45:n:46:GLU:OE2	51:t:20:LYS:HG3	2.06	0.55
3:2:60:A:H2	6:8:34:THR:O	1.88	0.55
8:B:42:HIS:HB3	57:z:115:LYS:HG3	1.89	0.55
9:C:140:ARG:NH2	9:C:242:PRO:HG2	2.22	0.55
14:H:15:LYS:HZ3	14:H:15:LYS:H	1.55	0.55
15:I:477:ILE:HD13	54:w:480:LYS:HE3	1.89	0.55
16:J:182:GLU:HG3	16:J:186:GLN:NE2	2.22	0.55
36:e:94:ALA:HB3	36:e:97:VAL:HG23	1.87	0.55
43:l:26:HIS:HB2	43:l:92:TYR:HE2	1.72	0.55
49:r:192:MET:N	49:r:192:MET:HE3	2.22	0.55
20:N:143:ARG:O	20:N:149:ASN:ND2	2.34	0.55
27:V:74:LYS:HB3	27:V:76:MET:HG3	1.89	0.55
55:x:4:ILE:HB	55:x:10:ARG:HB3	1.88	0.55
2:1:717:A:C2	53:v:25:LYS:HG2	2.42	0.55
2:1:2993:G:N2	49:r:7:ILE:H	2.02	0.55
17:K:243:THR:HG23	17:K:245:GLN:H	1.72	0.55
47:p:273:MET:H	47:p:288:GLY:HA2	1.71	0.55
54:w:261:PHE:CZ	54:w:321:ARG:HD2	2.42	0.55
11:E:140:PHE:CE2	22:P:172:GLY:HA3	2.43	0.55
14:H:11:LEU:HD23	14:H:72:TYR:HE1	1.70	0.55
27:V:99:ASP:OD1	54:w:245:TYR:OH	2.24	0.55
27:V:115:ALA:HA	27:V:134:ASN:HD21	1.72	0.55
31:Z:90:ASP:OD1	31:Z:90:ASP:N	2.37	0.55
48:q:505:ARG:N	48:q:525:ARG:O	2.35	0.55
53:v:130:ILE:HG13	53:v:131:ALA:H	1.72	0.55
2:1:35:A:HO2'	2:1:841:G:HO2'	1.56	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:149:G:OP1	45:n:90:LYS:NZ	2.40	0.54
2:1:3188:U:O2'	27:V:14:ARG:NH2	2.41	0.54
8:B:66:LYS:O	8:B:70:ARG:NH2	2.40	0.54
8:B:218:ILE:HG12	8:B:337:THR:HB	1.89	0.54
10:D:209:VAL:HG11	40:i:21:PRO:HB3	1.89	0.54
19:M:12:ARG:NH1	19:M:59:THR:O	2.40	0.54
20:N:11:ALA:O	20:N:14:LYS:NZ	2.38	0.54
45:n:175:ASN:ND2	45:n:375:ALA:O	2.30	0.54
45:n:589:ALA:HB3	45:n:593:ARG:HH21	1.70	0.54
51:t:87:THR:HG21	51:t:144:ILE:HG23	1.88	0.54
2:1:1952:G:O2'	27:V:18:GLY:O	2.23	0.54
2:1:2953:U:O4'	49:r:182:ASN:ND2	2.41	0.54
7:A:45:VAL:HG22	7:A:97:ASN:HB2	1.88	0.54
8:B:56:ILE:HD12	8:B:356:LEU:HD22	1.88	0.54
10:D:419:ASP:OD1	10:D:423:ARG:NH2	2.33	0.54
17:K:168:VAL:HG13	17:K:181:GLU:HB3	1.90	0.54
34:c:55:LEU:C	34:c:56:ILE:HD13	2.32	0.54
49:r:192:MET:HE3	49:r:192:MET:H	1.73	0.54
2:1:301:C:O2'	40:i:74:ARG:O	2.24	0.54
2:1:817:G:OP2	23:Q:93:ARG:NH2	2.40	0.54
2:1:867:G:O2'	2:1:889:G:N1	2.38	0.54
2:1:1227:C:H42	50:s:9:LYS:HB3	1.73	0.54
2:1:1380:A:C8	12:F:22:LYS:HG3	2.42	0.54
2:1:1672:A:OP1	31:Z:73:LYS:NZ	2.41	0.54
19:M:119:GLN:O	19:M:122:GLU:HG3	2.06	0.54
26:U:31:GLU:O	26:U:35:ILE:HG12	2.06	0.54
35:d:15:ARG:HG2	35:d:110:VAL:HA	1.89	0.54
40:i:49:ALA:HB3	40:i:52:GLU:HG3	1.89	0.54
45:n:258:ALA:HB1	45:n:261:ALA:HB3	1.89	0.54
2:1:1025:G:H22	2:1:1088:U:H3	1.55	0.54
2:1:1290:A:H5'	28:W:68:GLY:HA2	1.89	0.54
2:1:3081:U:H2'	2:1:3082:A:C8	2.41	0.54
8:B:189:ALA:O	8:B:193:GLU:HG2	2.08	0.54
15:I:562:VAL:HG23	15:I:586:PHE:HB3	1.89	0.54
15:I:657:LYS:HZ2	15:I:702:ILE:HG13	1.71	0.54
24:R:15:LEU:HD22	24:R:52:ARG:HB2	1.90	0.54
54:w:292:LEU:HD13	54:w:324:ILE:HD12	1.90	0.54
3:2:143:G:H5''	29:X:48:LYS:HE2	1.89	0.54
7:A:114:ALA:HB2	7:A:121:THR:HG23	1.88	0.54
15:I:707:ILE:HG13	15:I:708:GLU:H	1.72	0.54
16:J:103:ILE:HG13	16:J:106:ARG:HE	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:m:270:TRP:CD1	45:n:236:LYS:HD2	2.43	0.54
45:n:558:LYS:HD2	45:n:558:LYS:C	2.33	0.54
51:t:220:LEU:HG	51:t:224:LYS:HE2	1.90	0.54
56:y:185:THR:HA	56:y:193:ILE:HD11	1.90	0.54
2:1:741:G:O2'	2:1:781:C:O2'	2.21	0.54
2:1:886:G:H1'	24:R:130:ASN:HD22	1.73	0.54
2:1:1338:G:H4'	2:1:1339:A:H5'	1.89	0.54
2:1:3132:G:H5''	57:z:98:HIS:CE1	2.43	0.54
8:B:123:PHE:CE2	8:B:124:LYS:HG3	2.42	0.54
43:l:83:ILE:HD11	43:l:86:LEU:HD22	1.90	0.54
54:w:289:LEU:HD13	54:w:292:LEU:HD12	1.89	0.54
2:1:34:A:H3'	2:1:48:A:H61	1.73	0.54
8:B:216:ASP:HB2	8:B:339:ARG:HG2	1.89	0.54
15:I:645:LYS:HE3	43:l:120:ARG:HH12	1.72	0.54
27:V:73:LYS:HZ1	54:w:136:GLN:HG2	1.73	0.54
31:Z:103:GLU:OE1	44:m:661:ARG:NH1	2.40	0.54
54:w:149:LEU:HD12	54:w:153:GLY:HA3	1.88	0.54
2:1:1833:C:O2	2:1:1837:G:N2	2.40	0.54
3:2:133:U:H5''	3:2:134:U:OP1	2.08	0.54
10:D:150:MET:HE3	10:D:239:SER:HB2	1.90	0.54
43:l:103:GLY:C	43:l:106:PRO:HD2	2.33	0.54
44:m:363:PRO:HG2	44:m:365:PRO:HD3	1.90	0.54
54:w:181:ALA:HA	54:w:196:VAL:HA	1.89	0.54
2:1:196:G:OP2	30:Y:45:ARG:NH2	2.38	0.54
2:1:545:A:N6	2:1:547:G:N3	2.56	0.54
2:1:3140:A:H4'	8:B:13:SER:HB2	1.90	0.54
8:B:282:ILE:HG21	8:B:285:ILE:HG23	1.90	0.54
19:M:40:ASP:OD1	19:M:41:SER:N	2.41	0.54
21:O:86:ARG:HG2	21:O:100:LEU:HD11	1.89	0.54
26:U:37:ARG:HA	26:U:37:ARG:HH11	1.73	0.54
45:n:358:PHE:CD1	45:n:403:ILE:HD11	2.43	0.54
2:1:741:G:OP1	32:a:131:ARG:HG3	2.07	0.53
10:D:408:ILE:HG23	10:D:437:SER:HA	1.89	0.53
16:J:183:LYS:HA	16:J:186:GLN:OE1	2.07	0.53
18:L:106:GLU:HB3	53:v:120:LEU:HD22	1.90	0.53
26:U:82:LEU:HD11	26:U:88:ARG:HA	1.88	0.53
29:X:2:SER:HB3	29:X:5:LYS:HB2	1.90	0.53
54:w:279:PHE:HB3	54:w:290:TYR:HE1	1.71	0.53
2:1:341:G:OP2	53:v:9:LYS:NZ	2.39	0.53
43:l:115:LYS:HE3	43:l:156:LEU:HB2	1.88	0.53
45:n:148:VAL:O	51:t:157:ARG:NH2	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:r:246:ASN:ND2	49:r:255:ASN:HD22	2.05	0.53
2:1:1312:U:H2'	2:1:1313:G:C8	2.43	0.53
2:1:1663:C:N4	2:1:1870:U:H3	2.06	0.53
8:B:284:ARG:NH1	8:B:293:ASN:O	2.41	0.53
15:I:377:ILE:HG13	15:I:418:LEU:HD21	1.90	0.53
27:V:44:THR:HG21	27:V:52:PRO:HB3	1.90	0.53
42:k:30:ASN:OD1	42:k:32:ASP:HB2	2.09	0.53
44:m:685:HIS:CE1	44:m:687:ARG:HB2	2.44	0.53
10:D:127:ARG:HH11	10:D:295:LEU:HB2	1.73	0.53
43:l:54:MET:HE2	43:l:54:MET:N	2.23	0.53
44:m:700:PRO:HG2	45:n:560:LEU:HA	1.90	0.53
45:n:253:LYS:HD3	45:n:253:LYS:N	2.23	0.53
2:1:3209:A:O2'	14:H:69:ARG:HB3	2.07	0.53
9:C:37:VAL:HG21	9:C:246:LEU:HD21	1.89	0.53
15:I:531:LEU:HA	15:I:534:LEU:HD12	1.89	0.53
27:V:106:ASN:ND2	27:V:110:GLU:OE2	2.42	0.53
39:h:58:THR:O	39:h:62:GLU:HG2	2.08	0.53
42:k:26:LYS:HD2	42:k:70:VAL:HG23	1.91	0.53
44:m:656:HIS:CD2	44:m:660:LEU:HD13	2.44	0.53
2:1:1253:G:HO2'	2:1:1316:G:H1	1.54	0.53
2:1:3185:C:OP1	8:B:222:ARG:NH1	2.42	0.53
10:D:518:ALA:HA	10:D:529:PRO:HG3	1.89	0.53
10:D:529:PRO:HB2	44:m:213:THR:HG22	1.90	0.53
17:K:77:LYS:NZ	17:K:218:GLU:OE2	2.41	0.53
2:1:182:G:H1	2:1:250:A:H61	1.57	0.53
2:1:355:G:OP1	9:C:61:GLN:NE2	2.42	0.53
2:1:952:A:C5	2:1:953:A:H1'	2.43	0.53
5:6:181:C:OP2	46:o:138:ARG:NH2	2.31	0.53
7:A:201:ARG:HH12	16:J:139:GLU:HA	1.74	0.53
14:H:32:ARG:NH2	14:H:186:GLU:OE2	2.41	0.53
15:I:272:ILE:HD11	15:I:350:PHE:CG	2.44	0.53
15:I:625:ASN:OD1	15:I:635:LYS:NZ	2.26	0.53
17:K:172:LYS:H	17:K:172:LYS:CD	2.22	0.53
34:c:31:THR:O	34:c:35:GLY:N	2.42	0.53
47:p:97:TYR:HA	47:p:431:ASN:HA	1.91	0.53
55:x:25:LYS:HD2	55:x:28:ARG:HH12	1.73	0.53
2:1:1749:C:H5''	31:Z:15:ARG:HH22	1.74	0.53
8:B:14:LEU:HA	8:B:17:LEU:HD23	1.90	0.53
8:B:19:ARG:HH22	8:B:270:ALA:HA	1.73	0.53
44:m:409:ILE:HB	44:m:419:TRP:HB3	1.91	0.53
51:t:40:LYS:O	51:t:44:LYS:HD3	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:716:G:H4'	2:1:717:A:O5'	2.09	0.53
2:1:1381:G:O2'	2:1:1387:A:N7	2.36	0.53
2:1:1932:U:H5''	2:1:1933:G:O4'	2.08	0.53
2:1:3409:C:N3	22:P:69:ARG:NH2	2.57	0.53
24:R:32:ILE:HD13	24:R:44:LEU:HD13	1.90	0.53
27:V:82:ARG:HB2	27:V:101:ALA:HB3	1.90	0.53
30:Y:83:ARG:CZ	30:Y:83:ARG:HB2	2.39	0.53
35:d:56:VAL:HG13	35:d:60:LEU:HD23	1.90	0.53
43:l:64:MET:H	43:l:64:MET:CE	2.17	0.53
45:n:424:VAL:O	45:n:428:ILE:HD12	2.09	0.53
56:y:19:LEU:HD21	56:y:200:ASN:HD22	1.74	0.53
2:1:35:A:O2'	2:1:841:G:O2'	2.27	0.53
8:B:369:ARG:HH21	52:u:11:GLY:HA3	1.74	0.53
14:H:128:PRO:O	14:H:151:ASN:ND2	2.42	0.53
27:V:98:GLU:OE1	52:u:23:ARG:HA	2.09	0.53
44:m:582:HIS:NE2	44:m:626:GLY:O	2.40	0.53
47:p:192:LEU:O	47:p:258:ALA:N	2.42	0.53
51:t:142:TYR:CZ	51:t:236:TYR:HB2	2.44	0.53
53:v:3:ASN:HB2	53:v:6:GLN:HG2	1.91	0.53
4:3:41:GLN:HE22	4:3:103:ARG:CZ	2.23	0.52
7:A:159:PRO:HG3	16:J:97:THR:HG23	1.90	0.52
9:C:20:GLU:OE1	9:C:20:GLU:N	2.43	0.52
24:R:135:LYS:HG2	24:R:139:ILE:HD11	1.91	0.52
44:m:251:GLU:O	44:m:255:GLU:HG3	2.09	0.52
44:m:479:PRO:HB2	44:m:481:ILE:HG12	1.91	0.52
51:t:155:TYR:HE1	51:t:187:ILE:HD12	1.74	0.52
2:1:689:U:H2'	2:1:690:A:C8	2.44	0.52
2:1:1424:A:N6	2:1:1452:A:O2'	2.42	0.52
3:2:74:A:OP1	39:h:9:ARG:NH2	2.41	0.52
7:A:72:LYS:NZ	44:m:111:SER:OG	2.42	0.52
7:A:146:ARG:NH1	16:J:116:VAL:O	2.23	0.52
26:U:83:LYS:HB2	26:U:88:ARG:HH11	1.74	0.52
56:y:89:PRO:HB2	56:y:91:PRO:HD2	1.91	0.52
25:S:15:THR:HG23	25:S:18:GLU:H	1.74	0.52
27:V:117:THR:HG22	54:w:250:TYR:HA	1.91	0.52
34:c:67:LYS:HE2	34:c:83:HIS:NE2	2.24	0.52
42:k:18:LYS:H	42:k:18:LYS:HD2	1.73	0.52
52:u:12:PRO:HB2	52:u:14:TYR:HE1	1.73	0.52
56:y:21:ASN:ND2	56:y:112:ASP:OD2	2.42	0.52
2:1:984:A:N3	2:1:1145:U:O2'	2.38	0.52
2:1:1190:A:OP2	12:F:98:GLY:HA3	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:3217:U:H1'	2:1:3218:A:H5''	1.92	0.52
8:B:55:HIS:CD2	8:B:73:LEU:HD11	2.45	0.52
10:D:247:ARG:O	10:D:251:ILE:HG12	2.09	0.52
27:V:27:CYS:HB2	27:V:36:LEU:HG	1.90	0.52
27:V:30:ASN:ND2	27:V:114:SER:OG	2.34	0.52
31:Z:3:LYS:HD2	34:c:78:ARG:HH22	1.73	0.52
44:m:158:ASP:OD1	44:m:159:LYS:N	2.42	0.52
44:m:655:TYR:HB2	44:m:682:GLN:NE2	2.24	0.52
53:v:39:ASN:O	53:v:52:ARG:NH2	2.28	0.52
2:1:723:C:OP2	9:C:121:ARG:NH2	2.37	0.52
2:1:848:A:OP2	41:j:28:HIS:NE2	2.34	0.52
2:1:1242:U:OP2	14:H:62:ARG:NH2	2.42	0.52
2:1:1538:A:OP1	22:P:23:ARG:NH1	2.42	0.52
7:A:142:LEU:HD23	16:J:174:MET:HE1	1.89	0.52
7:A:147:PRO:HB3	7:A:187:ARG:HG3	1.91	0.52
10:D:152:TYR:HD2	10:D:188:HIS:CE1	2.28	0.52
17:K:18:SER:O	17:K:22:GLU:HG2	2.09	0.52
18:L:32:LYS:O	18:L:36:ARG:HG3	2.09	0.52
27:V:12:LYS:HD2	27:V:127:LEU:HD22	1.91	0.52
39:h:23:LEU:HD12	39:h:56:ILE:HD12	1.92	0.52
46:o:106:VAL:HG21	46:o:186:VAL:HG11	1.92	0.52
54:w:210:ARG:HG3	54:w:216:THR:HB	1.91	0.52
2:1:3098:C:O2'	8:B:180:GLU:OE2	2.22	0.52
26:U:60:LYS:C	26:U:61:ILE:HD12	2.34	0.52
34:c:36:LYS:HZ3	34:c:107:ILE:HD13	1.73	0.52
47:p:363:ALA:HA	47:p:371:PHE:HA	1.92	0.52
7:A:60:LEU:HD22	7:A:129:LEU:HD11	1.92	0.52
7:A:143:LYS:HA	16:J:175:LEU:HG	1.92	0.52
9:C:156:ASP:OD2	9:C:255:SER:OG	2.26	0.52
11:E:97:ASN:HB3	11:E:100:TYR:HD1	1.75	0.52
13:G:133:LYS:HD2	13:G:138:HIS:HE1	1.75	0.52
25:S:142:LEU:HD13	25:S:147:LEU:HD21	1.92	0.52
36:e:79:VAL:HG12	36:e:112:LEU:HD12	1.90	0.52
43:l:121:ILE:HD12	43:l:122:THR:H	1.75	0.52
51:t:27:ARG:O	51:t:31:GLU:HG2	2.10	0.52
51:t:82:PHE:CZ	51:t:84:PRO:HG3	2.43	0.52
56:y:24:ALA:HB3	56:y:48:VAL:HG22	1.90	0.52
11:E:93:ILE:HD12	11:E:93:ILE:O	2.10	0.52
15:I:528:GLY:HA2	15:I:581:LEU:HD22	1.92	0.52
19:M:38:LEU:HD11	19:M:48:ARG:HG2	1.91	0.52
44:m:130:ILE:HG12	44:m:141:ARG:HG2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:o:187:HIS:ND1	46:o:188:GLU:N	2.58	0.52
2:1:754:A:N6	2:1:770:G:O2'	2.43	0.52
3:2:121:U:H5'	6:8:8:ARG:NH1	2.25	0.52
15:I:727:LYS:O	15:I:735:SER:OG	2.26	0.52
23:Q:72:ARG:HH11	23:Q:73:LYS:H	1.58	0.52
45:n:194:PHE:HZ	45:n:240:THR:HG21	1.73	0.52
49:r:156:VAL:HG11	49:r:177:ARG:HH11	1.75	0.52
56:y:4:ARG:HG3	56:y:215:LEU:HD11	1.92	0.52
56:y:26:VAL:HG21	56:y:35:TYR:HD2	1.75	0.52
2:1:969:G:N2	2:1:995:G:OP1	2.43	0.52
2:1:2994:C:O2'	2:1:2996:G:OP2	2.28	0.52
2:1:3035:A:H5''	2:1:3036:A:H5''	1.92	0.52
17:K:63:ILE:HD12	17:K:64:GLY:N	2.25	0.52
17:K:143:ASP:OD2	17:K:145:ARG:NH1	2.43	0.52
45:n:34:ARG:O	45:n:38:ILE:HG12	2.10	0.52
45:n:242:GLY:O	45:n:268:SER:OG	2.24	0.52
2:1:1207:C:H2'	2:1:1208:G:N2	2.25	0.51
2:1:1696:G:H2'	2:1:1697:G:C8	2.44	0.51
2:1:1728:U:O2'	2:1:1813:U:O2'	2.27	0.51
2:1:2506:G:H4'	2:1:2507:A:H5'	1.92	0.51
2:1:3284:G:H2'	2:1:3285:G:O4'	2.11	0.51
25:S:25:ARG:HH22	25:S:27:ARG:HD2	1.75	0.51
31:Z:115:LYS:O	31:Z:119:GLU:HG2	2.09	0.51
43:l:80:ARG:O	43:l:80:ARG:HD2	2.10	0.51
44:m:269:LEU:HD22	45:n:120:LYS:HG3	1.91	0.51
49:r:150:ILE:HG22	49:r:152:LYS:H	1.75	0.51
57:z:88:ASP:OD1	57:z:91:ARG:N	2.36	0.51
3:2:59:G:C8	6:8:27:ILE:HD11	2.45	0.51
6:8:21:ARG:HD3	6:8:22:PRO:O	2.10	0.51
7:A:56:ARG:HD3	7:A:129:LEU:HB2	1.91	0.51
8:B:69:LYS:HB2	56:y:28:LEU:HD21	1.92	0.51
24:R:105:LEU:O	24:R:108:LYS:HG2	2.09	0.51
44:m:324:PRO:HB3	51:t:171:ASP:HB3	1.91	0.51
47:p:231:GLU:HA	47:p:259:ARG:HA	1.91	0.51
2:1:1692:C:H5	2:1:1838:A:H8	1.57	0.51
2:1:1734:A:H4'	42:k:3:ARG:HH12	1.75	0.51
4:3:82:LEU:HD13	4:3:112:LEU:HD13	1.91	0.51
10:D:272:LEU:HD23	10:D:274:PHE:HE1	1.75	0.51
25:S:65:GLU:OE2	25:S:72:LYS:NZ	2.41	0.51
2:1:1012:A:O2'	2:1:1013:U:O5'	2.29	0.51
2:1:1319:U:H2'	2:1:1320:G:H8	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:2993:G:N1	49:r:7:ILE:HG12	2.24	0.51
2:1:3013:G:H1	2:1:3023:C:H42	1.57	0.51
8:B:218:ILE:HG22	8:B:276:THR:HG23	1.91	0.51
24:R:139:ILE:HG22	24:R:143:GLN:NE2	2.26	0.51
27:V:70:ASP:OD1	27:V:71:LEU:N	2.44	0.51
34:c:87:ASN:OD1	34:c:89:ILE:HG22	2.10	0.51
45:n:357:THR:OG1	45:n:398:VAL:O	2.28	0.51
54:w:143:LYS:HZ1	54:w:211:PHE:C	2.18	0.51
2:1:2440:A:H5''	22:P:83:TRP:O	2.11	0.51
4:3:54:ARG:HB2	4:3:63:TYR:HE2	1.75	0.51
8:B:109:HIS:ND1	8:B:200:GLU:OE2	2.31	0.51
10:D:366:LEU:HB2	10:D:392:CYS:HB3	1.93	0.51
12:F:95:ARG:NH1	12:F:115:LEU:O	2.42	0.51
12:F:157:LYS:NZ	12:F:250:LEU:O	2.30	0.51
15:I:538:VAL:HG23	15:I:539:MET:SD	2.50	0.51
17:K:265:ARG:NH1	46:o:211:HIS:O	2.41	0.51
22:P:42:LYS:HZ2	22:P:110:ASP:HA	1.75	0.51
38:g:47:THR:OG1	38:g:49:VAL:HG12	2.11	0.51
39:h:84:GLN:OE1	39:h:86:LYS:NZ	2.41	0.51
42:k:53:LYS:HA	42:k:56:LYS:HG2	1.91	0.51
47:p:312:PRO:O	47:p:330:SER:N	2.42	0.51
4:3:5:GLU:O	4:3:9:GLN:HG2	2.10	0.51
7:A:179:ARG:NH1	44:m:112:THR:O	2.41	0.51
10:D:341:VAL:HB	10:D:391:LEU:HD23	1.93	0.51
15:I:239:LEU:HD21	15:I:299:TYR:HE1	1.76	0.51
22:P:13:LYS:HB3	22:P:152:GLU:HB2	1.92	0.51
26:U:91:LEU:HD22	26:U:92:ARG:N	2.26	0.51
2:1:1382:C:OP1	4:3:103:ARG:NH1	2.43	0.51
2:1:3487:C:H4'	35:d:15:ARG:NH1	2.26	0.51
3:2:59:G:H1'	3:2:60:A:N7	2.26	0.51
14:H:27:THR:HG22	14:H:36:LYS:HG3	1.92	0.51
15:I:686:SER:O	15:I:690:ARG:NH2	2.43	0.51
27:V:132:ALA:O	56:y:106:ASN:ND2	2.42	0.51
33:b:374:ARG:HA	56:y:113:TYR:HD2	1.75	0.51
45:n:25:LYS:HE3	45:n:73:LEU:HD11	1.93	0.51
51:t:166:ARG:HD2	51:t:209:TRP:CD1	2.45	0.51
2:1:312:G:H5''	7:A:105:ARG:HH21	1.76	0.51
2:1:1188:G:O2'	2:1:1200:A:N3	2.37	0.51
2:1:3431:A:H4'	8:B:366:GLY:HA3	1.91	0.51
7:A:120:PRO:HG2	7:A:167:LEU:HD22	1.93	0.51
26:U:27:VAL:HA	26:U:30:PHE:HD2	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:U:33:TYR:CE2	26:U:37:ARG:HG3	2.46	0.51
54:w:287:GLN:HA	54:w:290:TYR:CD2	2.46	0.51
2:1:260:U:H1'	53:v:191:LYS:NZ	2.26	0.51
2:1:675:C:H5''	54:w:784:SER:O	2.11	0.51
2:1:759:C:O2'	2:1:760:C:OP1	2.28	0.51
2:1:1701:G:H2'	2:1:1702:A:C8	2.46	0.51
2:1:1871:U:H5'	45:n:575:LYS:HZ1	1.76	0.51
2:1:2926:G:N2	49:r:255:ASN:OD1	2.44	0.51
2:1:3099:G:HO2'	8:B:92:TYR:HH	1.57	0.51
3:2:156:G:OP2	45:n:89:ARG:NH2	2.38	0.51
7:A:201:ARG:HH21	16:J:138:ARG:NH1	2.08	0.51
9:C:112:HIS:HB3	20:N:200:TYR:CE1	2.46	0.51
21:O:48:PHE:HE1	21:O:142:LEU:HA	1.76	0.51
44:m:162:THR:HG21	54:w:634:ALA:HB3	1.92	0.51
46:o:183:GLU:OE2	46:o:183:GLU:N	2.38	0.51
52:u:27:LYS:HE3	56:y:100:ARG:HH21	1.75	0.51
2:1:526:G:OP1	9:C:342:LYS:NZ	2.41	0.50
2:1:1844:C:H2'	2:1:1845:A:H8	1.76	0.50
7:A:203:TYR:CG	7:A:218:LEU:HD13	2.46	0.50
19:M:33:ASP:OD1	19:M:36:ARG:N	2.44	0.50
34:c:25:ASN:OD1	34:c:26:SER:N	2.44	0.50
39:h:4:LYS:HB2	39:h:7:GLU:HG2	1.92	0.50
43:l:80:ARG:NH1	43:l:166:GLN:O	2.44	0.50
2:1:1396:G:H2'	2:1:1397:A:C8	2.46	0.50
2:1:1720:C:OP1	26:U:37:ARG:NH2	2.44	0.50
2:1:1790:A:H4'	42:k:26:LYS:NZ	2.26	0.50
2:1:2902:U:O2'	2:1:2904:C:OP1	2.24	0.50
2:1:3084:U:O2'	8:B:267:ALA:O	2.28	0.50
9:C:19:SER:OG	9:C:20:GLU:OE1	2.27	0.50
13:G:253:ALA:HA	13:G:257:VAL:HB	1.91	0.50
16:J:146:GLY:O	16:J:150:VAL:HG23	2.11	0.50
21:O:2:SER:HB2	25:S:165:LYS:HA	1.92	0.50
29:X:104:VAL:HG21	29:X:125:LEU:HD13	1.93	0.50
30:Y:4:SER:HB3	30:Y:7:VAL:HG22	1.92	0.50
44:m:260:SER:OG	44:m:261:GLN:N	2.44	0.50
49:r:52:GLU:OE2	49:r:55:ARG:NH2	2.44	0.50
54:w:141:SER:O	54:w:144:LEU:HG	2.11	0.50
2:1:1159:U:O2'	2:1:1160:A:O3'	2.28	0.50
4:3:52:THR:HG22	4:3:63:TYR:HB2	1.92	0.50
27:V:54:ALA:HB2	27:V:60:VAL:HG11	1.92	0.50
43:l:35:HIS:ND1	43:l:35:HIS:O	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:t:93:ILE:HD12	51:t:213:LEU:HD12	1.93	0.50
52:u:104:ARG:HA	52:u:107:LEU:HG	1.93	0.50
56:y:106:ASN:OD1	56:y:150:SER:OG	2.28	0.50
2:1:3280:U:C5	21:O:127:VAL:HG11	2.46	0.50
8:B:210:GLU:HB2	57:z:114:LEU:HD23	1.94	0.50
10:D:355:LEU:HD21	10:D:476:LEU:HD11	1.92	0.50
15:I:591:TYR:HD1	15:I:655:PHE:HD1	1.58	0.50
26:U:14:ILE:HB	26:U:61:ILE:HB	1.93	0.50
34:c:27:LYS:O	34:c:31:THR:OG1	2.28	0.50
45:n:420:GLN:OE1	45:n:445:LEU:HD21	2.10	0.50
54:w:77:ASP:OD1	54:w:78:LEU:N	2.45	0.50
2:1:644:A:H5'	2:1:645:U:H5	1.77	0.50
2:1:1339:A:O5'	50:s:8:SER:HB2	2.12	0.50
9:C:159:GLN:HA	9:C:217:ILE:HB	1.92	0.50
13:G:69:LEU:HG	54:w:659:LEU:HD11	1.93	0.50
19:M:16:VAL:HA	19:M:56:VAL:HG12	1.93	0.50
21:O:155:ALA:O	21:O:159:GLU:HG2	2.12	0.50
35:d:103:ASN:O	35:d:106:MET:HE1	2.11	0.50
47:p:129:TRP:HA	47:p:135:ILE:HA	1.94	0.50
49:r:47:ALA:O	49:r:51:GLN:HG2	2.12	0.50
51:t:83:VAL:O	51:t:83:VAL:HG12	2.12	0.50
2:1:2931:C:H3'	2:1:2932:A:C8	2.40	0.50
15:I:658:ARG:NH1	15:I:695:GLU:OE2	2.44	0.50
17:K:73:LYS:HG2	17:K:190:TYR:HE1	1.76	0.50
17:K:168:VAL:HG12	17:K:170:ILE:HG23	1.94	0.50
26:U:36:ASP:O	26:U:37:ARG:HD2	2.10	0.50
31:Z:3:LYS:O	31:Z:6:LYS:NZ	2.43	0.50
54:w:213:ASP:OD1	54:w:215:ARG:HB3	2.12	0.50
2:1:1224:A:P	21:O:50:ARG:HH12	2.33	0.50
2:1:3182:G:N2	2:1:3477:A:H62	2.10	0.50
17:K:130:LYS:HE2	17:K:153:ILE:O	2.12	0.50
22:P:6:ALA:HB1	22:P:8:PRO:HD2	1.94	0.50
27:V:73:LYS:HE2	54:w:133:GLY:HA2	1.94	0.50
31:Z:75:VAL:HB	31:Z:80:LEU:HD21	1.93	0.50
41:j:39:TYR:CD1	41:j:40:PRO:HA	2.46	0.50
43:l:128:HIS:H	43:l:147:ALA:HA	1.77	0.50
45:n:250:ASP:HB2	45:n:262:ALA:HA	1.94	0.50
45:n:555:LYS:NZ	45:n:556:GLU:OE2	2.45	0.50
46:o:109:VAL:HG12	46:o:178:CYS:SG	2.52	0.50
50:s:29:LYS:HA	50:s:33:ALA:HB3	1.93	0.50
54:w:59:TRP:NE1	54:w:118:ASP:OD2	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:718:A:N1	3:2:36:C:O2'	2.42	0.50
7:A:49:SER:HB3	7:A:61:LEU:HD13	1.93	0.50
8:B:193:GLU:O	8:B:197:GLU:HG3	2.11	0.50
44:m:615:LYS:N	44:m:635:ASP:OD2	2.38	0.50
45:n:352:LEU:HD21	45:n:427:SER:HB3	1.93	0.50
2:1:952:A:C6	2:1:953:A:H1'	2.47	0.50
2:1:1959:C:N4	2:1:1960:G:O6	2.45	0.50
14:H:20:ASP:OD1	14:H:22:LYS:N	2.41	0.50
17:K:144:ASP:OD1	17:K:145:ARG:N	2.45	0.50
42:k:10:GLN:OE1	42:k:10:GLN:HA	2.12	0.50
44:m:593:GLN:HG3	44:m:616:TRP:CD1	2.47	0.50
52:u:83:ASP:OD1	52:u:85:ASN:N	2.45	0.50
56:y:177:LEU:HB3	56:y:179:VAL:HG12	1.93	0.50
2:1:1734:A:O2'	42:k:3:ARG:NH1	2.45	0.49
3:2:111:G:OP2	3:2:113:A:O2'	2.29	0.49
10:D:286:ALA:O	10:D:290:LEU:HB2	2.12	0.49
15:I:291:LYS:HE2	15:I:295:GLN:HG2	1.93	0.49
17:K:71:PRO:HB2	17:K:190:TYR:HB3	1.93	0.49
22:P:60:PHE:O	22:P:64:ASN:HB3	2.12	0.49
26:U:35:ILE:CD1	26:U:55:ARG:HH22	2.25	0.49
32:a:71:PRO:O	32:a:109:GLY:N	2.44	0.49
34:c:98:LEU:H	34:c:98:LEU:HD23	1.77	0.49
41:j:25:ARG:HG2	41:j:25:ARG:HH11	1.77	0.49
44:m:535:SER:HB3	44:m:544:ALA:HB3	1.94	0.49
45:n:244:ARG:HB2	45:n:268:SER:HB3	1.94	0.49
2:1:1235:A:N1	2:1:1331:G:O2'	2.43	0.49
2:1:3288:G:H22	2:1:3299:U:H3	1.60	0.49
2:1:3491:A:O2'	2:1:3492:G:H8	1.94	0.49
15:I:416:TYR:HD2	15:I:510:ASN:HB2	1.77	0.49
15:I:555:THR:O	15:I:593:ILE:HD11	2.12	0.49
22:P:16:LYS:O	22:P:101:ASN:ND2	2.42	0.49
22:P:117:VAL:HG23	22:P:148:ILE:HG12	1.94	0.49
26:U:73:TYR:CE1	26:U:77:LEU:HD21	2.47	0.49
45:n:150:ASP:OD1	51:t:217:LYS:N	2.38	0.49
2:1:145:G:H5''	44:m:247:ILE:HG13	1.95	0.49
2:1:717:A:C5	53:v:25:LYS:HE3	2.47	0.49
2:1:1658:G:OP1	45:n:566:SER:OG	2.30	0.49
2:1:1690:G:O6	15:I:454:LYS:NZ	2.45	0.49
8:B:167:ARG:HH12	8:B:174:LYS:HD3	1.77	0.49
22:P:178:LEU:O	22:P:182:LYS:HG2	2.12	0.49
36:e:17:HIS:ND1	36:e:47:ILE:HD11	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:m:303:PRO:HA	44:m:306:TYR:HE2	1.77	0.49
2:1:2461:A:H3'	2:1:2461:A:N3	2.26	0.49
2:1:2514:U:H3	2:1:2698:G:H1	1.60	0.49
5:6:44:A:OP1	17:K:227:HIS:ND1	2.39	0.49
7:A:227:MET:HA	7:A:227:MET:HE3	1.94	0.49
15:I:328:THR:OG1	15:I:329:GLN:N	2.45	0.49
16:J:118:ASN:C	16:J:118:ASN:OD1	2.54	0.49
45:n:45:ARG:O	45:n:63:PHE:HB2	2.12	0.49
2:1:942:G:OP1	54:w:714:ARG:NH1	2.40	0.49
2:1:1886:U:O2'	3:2:122:G:OP1	2.28	0.49
6:8:15:LYS:HA	6:8:18:ARG:HG2	1.95	0.49
7:A:100:PHE:HB3	7:A:112:HIS:HB2	1.93	0.49
11:E:58:CYS:HB3	11:E:101:VAL:HG13	1.94	0.49
16:J:167:PRO:HG2	44:m:132:TYR:CZ	2.46	0.49
42:k:9:LYS:HG3	44:m:644:ASP:HB2	1.93	0.49
54:w:16:TRP:CD1	54:w:186:SER:HA	2.47	0.49
2:1:847:G:N2	2:1:957:A:N1	2.46	0.49
2:1:2927:C:H42	2:1:2951:G:H1	1.60	0.49
2:1:2933:A:H5''	49:r:66:LYS:NZ	2.28	0.49
5:6:57:A:O2'	5:6:58:A:H5''	2.12	0.49
6:8:25:GLN:HE21	6:8:25:GLN:HA	1.77	0.49
15:I:653:SER:HB2	15:I:692:LEU:HD11	1.94	0.49
23:Q:92:GLU:OE1	23:Q:92:GLU:N	2.37	0.49
31:Z:103:GLU:CD	44:m:661:ARG:HH12	2.20	0.49
34:c:36:LYS:NZ	34:c:107:ILE:HD13	2.28	0.49
54:w:93:ASP:HB3	54:w:96:SER:HB2	1.94	0.49
54:w:246:ALA:HB3	54:w:249:ASP:HB3	1.94	0.49
56:y:109:ALA:HB2	56:y:149:GLY:HA2	1.93	0.49
57:z:99:LEU:O	57:z:104:ARG:HB3	2.13	0.49
2:1:114:A:N1	2:1:274:A:O2'	2.43	0.49
2:1:267:C:OP2	10:D:210:LYS:NZ	2.35	0.49
2:1:1347:U:OP1	21:O:134:ARG:HG3	2.12	0.49
2:1:3117:A:H2	2:1:3129:A:H62	1.61	0.49
2:1:3206:C:O3'	14:H:153:SER:OG	2.28	0.49
7:A:146:ARG:NH2	16:J:117:GLU:O	2.45	0.49
10:D:182:LYS:HG2	10:D:192:PHE:CE2	2.48	0.49
15:I:239:LEU:HD21	15:I:299:TYR:CE1	2.48	0.49
24:R:134:HIS:CE1	24:R:137:ALA:HB2	2.48	0.49
25:S:105:MET:HE1	25:S:120:ILE:HG21	1.94	0.49
26:U:55:ARG:HD3	26:U:61:ILE:HG13	1.94	0.49
28:W:136:VAL:HA	28:W:186:PRO:HA	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Z:67:ARG:HA	31:Z:119:GLU:OE2	2.12	0.49
43:l:5:THR:OG1	43:l:8:GLU:OE1	2.30	0.49
46:o:232:LYS:O	46:o:236:ARG:HG2	2.13	0.49
2:1:49:A:H5'	20:N:189:TRP:NE1	2.27	0.49
2:1:350:A:OP2	3:2:29:C:N4	2.45	0.49
2:1:1388:G:N7	4:3:26:ASN:ND2	2.53	0.49
2:1:1517:G:H2'	2:1:1519:G:C8	2.48	0.49
2:1:2933:A:H5''	49:r:66:LYS:HZ2	1.78	0.49
2:1:3275:A:O2'	21:O:118:ARG:NH2	2.46	0.49
2:1:3341:G:N2	2:1:3346:U:OP1	2.36	0.49
11:E:115:SER:OG	11:E:117:GLU:OE2	2.26	0.49
13:G:254:ALA:HA	13:G:258:ARG:HD3	1.95	0.49
25:S:97:THR:HG22	25:S:99:VAL:H	1.78	0.49
26:U:82:LEU:HD13	26:U:91:LEU:HD12	1.94	0.49
29:X:45:TYR:CD1	39:h:77:TYR:HB3	2.46	0.49
42:k:58:ARG:HB2	42:k:58:ARG:HH11	1.77	0.49
43:l:94:ARG:C	43:l:95:TYR:HD1	2.21	0.49
44:m:180:LEU:HD13	54:w:619:VAL:HG12	1.95	0.49
44:m:296:HIS:CE1	44:m:298:GLU:HB2	2.47	0.49
45:n:132:ASP:O	45:n:133:ILE:HD13	2.12	0.49
52:u:25:ASP:OD1	52:u:27:LYS:HB2	2.13	0.49
2:1:88:A:H2'	2:1:89:A:O4'	2.13	0.49
2:1:744:U:H3'	2:1:745:G:C8	2.48	0.49
2:1:1692:C:H2'	2:1:1692:C:O2	2.12	0.49
3:2:131:G:H2'	3:2:132:G:C8	2.48	0.49
6:8:23:ILE:HG22	6:8:27:ILE:HG21	1.95	0.49
7:A:130:HIS:HB2	7:A:224:ARG:HB3	1.94	0.49
8:B:331:PRO:HD2	8:B:334:ARG:NE	2.14	0.49
13:G:50:VAL:HB	54:w:462:MET:HE3	1.95	0.49
13:G:68:ARG:HH21	13:G:246:LEU:HD11	1.78	0.49
14:H:47:LYS:HG2	14:H:49:GLN:OE1	2.12	0.49
16:J:115:PHE:HE2	16:J:121:VAL:HG12	1.78	0.49
16:J:127:ILE:HG13	16:J:127:ILE:O	2.12	0.49
26:U:25:PHE:CZ	26:U:81:PHE:HB2	2.48	0.49
34:c:32:MET:HG2	34:c:37:TYR:CD2	2.48	0.49
34:c:62:ALA:HB3	34:c:67:LYS:HE3	1.95	0.49
34:c:107:ILE:H	34:c:107:ILE:HD12	1.77	0.49
43:l:78:LYS:C	43:l:79:PHE:HD1	2.20	0.49
44:m:368:LEU:HD12	44:m:368:LEU:O	2.12	0.49
46:o:121:MET:HB3	46:o:134:LEU:HD11	1.94	0.49
49:r:16:ARG:NE	49:r:17:ARG:H	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:w:36:LEU:HD11	54:w:195:PHE:CD2	2.48	0.49
54:w:50:ILE:HB	54:w:115:VAL:HG22	1.95	0.49
54:w:277:ILE:HG13	54:w:306:LEU:HD11	1.95	0.49
2:l:3480:C:H4'	8:B:315:GLY:HA2	1.92	0.49
4:3:31:GLU:O	4:3:54:ARG:HD3	2.13	0.49
5:6:47:U:O2	17:K:66:ASN:ND2	2.46	0.49
10:D:450:ARG:HH11	10:D:454:THR:HG23	1.77	0.49
17:K:234:LYS:H	17:K:234:LYS:CE	2.26	0.49
34:c:111:ASP:OD1	34:c:112:SER:N	2.46	0.49
35:d:50:GLN:OE1	35:d:82:ARG:NH2	2.46	0.49
44:m:726:TRP:HB3	44:m:738:MET:HE2	1.93	0.49
51:t:162:ILE:HG22	51:t:163:ASN:OD1	2.12	0.49
56:y:200:ASN:HD21	56:y:203:CYS:HB3	1.78	0.49
2:l:876:G:H3'	2:l:877:G:H8	1.78	0.48
2:l:1173:G:H8	2:l:1173:G:OP2	1.95	0.48
10:D:327:LEU:O	10:D:331:LEU:HG	2.13	0.48
11:E:177:TYR:OH	19:M:107:ASP:OD2	2.26	0.48
17:K:76:ILE:HG22	17:K:187:GLY:O	2.12	0.48
27:V:42:PHE:CD2	27:V:59:MET:HG2	2.46	0.48
27:V:96:TYR:OH	52:u:37:HIS:NE2	2.43	0.48
54:w:451:GLU:HA	54:w:454:ARG:HG2	1.95	0.48
2:l:946:A:OP1	54:w:706:ARG:NH2	2.42	0.48
2:l:2516:U:H2'	2:l:2517:G:C8	2.48	0.48
5:6:93:A:C2	17:K:126:SER:HA	2.48	0.48
10:D:473:GLN:O	10:D:477:GLU:HG3	2.12	0.48
15:I:385:GLU:HA	15:I:423:ASN:HB2	1.95	0.48
16:J:143:TYR:O	16:J:147:VAL:HG13	2.13	0.48
23:Q:76:SER:HA	23:Q:78:GLN:NE2	2.28	0.48
31:Z:136:PHE:OXT	38:g:76:TYR:OH	2.21	0.48
43:l:40:GLN:NE2	43:l:41:LYS:HG3	2.29	0.48
45:n:366:ARG:HE	45:n:370:GLU:CD	2.22	0.48
51:t:155:TYR:CE1	51:t:187:ILE:HD12	2.49	0.48
52:u:100:VAL:HA	52:u:103:LYS:HD2	1.96	0.48
54:w:111:LYS:NZ	54:w:149:LEU:O	2.46	0.48
54:w:468:LYS:O	54:w:472:GLU:HG2	2.13	0.48
2:l:80:C:H5''	20:N:191:ARG:HH21	1.77	0.48
2:l:177:G:H5'	2:l:178:U:OP2	2.14	0.48
7:A:35:SER:OG	7:A:36:ALA:N	2.44	0.48
17:K:27:ARG:O	17:K:27:ARG:HG2	2.13	0.48
27:V:88:ARG:HB2	27:V:94:TYR:CE2	2.48	0.48
43:l:7:GLU:OE2	43:l:7:GLU:N	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:r:2:PRO:HB2	49:r:6:TYR:CG	2.47	0.48
2:1:635:G:N1	2:1:1368:A:OP1	2.29	0.48
2:1:863:G:H2'	2:1:864:G:H8	1.78	0.48
7:A:194:ALA:HB3	7:A:199:TRP:NE1	2.29	0.48
13:G:109:LEU:HD23	44:m:234:ARG:HG2	1.94	0.48
17:K:121:LYS:HE2	17:K:153:ILE:HD11	1.94	0.48
20:N:13:LYS:O	20:N:19:ASN:ND2	2.36	0.48
28:W:43:PHE:N	28:W:101:GLY:H	2.11	0.48
33:b:374:ARG:HA	56:y:113:TYR:CD2	2.48	0.48
44:m:164:ILE:O	44:m:173:VAL:N	2.33	0.48
45:n:169:HIS:HB3	45:n:265:LEU:HD11	1.95	0.48
54:w:696:PRO:HD2	54:w:699:LYS:HD2	1.96	0.48
2:1:295:G:H5'	20:N:179:ARG:HB3	1.96	0.48
2:1:1755:A:C8	34:c:98:LEU:HD21	2.47	0.48
8:B:214:MET:SD	8:B:350:ALA:HA	2.54	0.48
11:E:71:VAL:HG23	11:E:178:LEU:HD21	1.96	0.48
20:N:19:ASN:O	20:N:23:SER:OG	2.30	0.48
34:c:22:ASP:OD1	34:c:23:THR:N	2.46	0.48
34:c:30:LEU:HB2	34:c:112:SER:HB2	1.96	0.48
35:d:21:MET:HE3	35:d:25:LEU:HG	1.95	0.48
39:h:80:LEU:HA	39:h:83:ARG:HD2	1.96	0.48
43:l:128:HIS:N	43:l:146:THR:O	2.46	0.48
44:m:459:PRO:HG3	44:m:537:HIS:O	2.13	0.48
2:1:109:A:N1	2:1:330:U:O2'	2.41	0.48
2:1:161:C:H5''	2:1:162:A:H2'	1.95	0.48
6:8:25:GLN:HE22	55:x:17:ALA:HB2	1.78	0.48
7:A:221:ILE:HG22	7:A:223:PRO:HD3	1.95	0.48
8:B:50:LYS:O	8:B:333:LYS:N	2.41	0.48
15:I:632:MET:HA	15:I:635:LYS:HB3	1.96	0.48
20:N:31:ARG:HD3	54:w:670:VAL:HG11	1.95	0.48
27:V:115:ALA:HA	27:V:134:ASN:ND2	2.29	0.48
45:n:80:LYS:HG3	45:n:113:TYR:HB3	1.96	0.48
54:w:26:ARG:NH1	54:w:57:GLY:HA3	2.27	0.48
2:1:2210:G:H2'	2:1:2211:G:H8	1.79	0.48
2:1:2512:A:H3'	2:1:2513:G:H8	1.79	0.48
2:1:3186:U:H2'	2:1:3187:A:C8	2.48	0.48
2:1:3475:U:OP1	35:d:20:HIS:NE2	2.41	0.48
17:K:265:ARG:NH1	46:o:213:LYS:H	2.11	0.48
22:P:52:LYS:HE3	22:P:88:VAL:HG12	1.96	0.48
23:Q:20:SER:HB3	23:Q:25:LEU:HD23	1.96	0.48
26:U:13:ILE:HG23	26:U:100:VAL:HG13	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:m:117:PRO:HA	44:m:167:PRO:HD3	1.96	0.48
45:n:362:ARG:HH21	51:t:192:HIS:HB3	1.78	0.48
47:p:383:TRP:HA	47:p:392:ILE:H	1.78	0.48
54:w:95:THR:O	54:w:100:ARG:NH1	2.47	0.48
54:w:320:TRP:O	54:w:324:ILE:HG12	2.14	0.48
2:l:765:G:H2'	2:l:766:G:H8	1.78	0.48
2:l:1721:U:N3	26:U:76:TYR:OH	2.46	0.48
26:U:33:TYR:CD2	26:U:81:PHE:HD2	2.31	0.48
34:c:31:THR:HG23	34:c:109:ALA:HA	1.95	0.48
44:m:196:PHE:O	44:m:198:PRO:HD3	2.14	0.48
49:r:221:GLU:HA	49:r:241:TYR:HA	1.96	0.48
51:t:230:GLU:OE1	51:t:232:ARG:NH1	2.47	0.48
54:w:95:THR:HB	54:w:140:MET:HE1	1.95	0.48
2:l:175:G:H5''	39:h:111:ARG:HD2	1.94	0.48
2:l:1423:G:OP2	36:e:101:LYS:HE2	2.14	0.48
2:l:2513:G:H1	2:l:2699:U:H3	1.62	0.48
2:l:3059:G:O2'	43:l:128:HIS:NE2	2.46	0.48
10:D:136:GLY:HA3	10:D:399:GLY:HA3	1.95	0.48
10:D:261:MET:O	10:D:261:MET:HE3	2.13	0.48
10:D:287:ARG:HG2	10:D:287:ARG:HH11	1.78	0.48
17:K:57:LEU:HD11	17:K:236:ILE:HG23	1.95	0.48
27:V:116:ILE:HD11	27:V:136:GLY:H	1.78	0.48
45:n:366:ARG:NE	45:n:370:GLU:OE2	2.47	0.48
2:l:762:U:H3'	2:l:763:G:H8	1.78	0.48
2:l:1885:G:H5''	29:X:91:LYS:HD2	1.96	0.48
2:l:2702:G:OP2	43:l:2:ARG:HG2	2.14	0.48
2:l:3332:U:H2'	2:l:3333:G:H8	1.79	0.48
8:B:106:TRP:HB2	8:B:133:TYR:CE2	2.48	0.48
9:C:35:ASP:HB2	23:Q:21:GLU:HG2	1.96	0.48
16:J:182:GLU:HG3	16:J:186:GLN:HE21	1.79	0.48
19:M:102:ARG:HD3	21:O:197:TYR:CZ	2.48	0.48
23:Q:146:HIS:ND1	23:Q:146:HIS:O	2.46	0.48
49:r:178:GLN:NE2	49:r:180:LYS:O	2.47	0.48
57:z:86:PRO:HA	57:z:91:ARG:NH1	2.28	0.48
58:T:99:SER:OG	58:T:101:CYS:SG	2.71	0.48
2:l:1303:C:H3'	2:l:1304:A:H8	1.78	0.47
7:A:108:ASP:HB3	7:A:110:TYR:CE1	2.48	0.47
8:B:105:VAL:HG21	8:B:148:LEU:HD12	1.94	0.47
10:D:89:GLU:N	10:D:93:ASP:OD2	2.46	0.47
15:I:406:GLN:NE2	54:w:611:ASP:OD1	2.47	0.47
46:o:137:SER:OG	46:o:146:LYS:HD2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1007:C:N4	2:1:1008:U:O4	2.47	0.47
2:1:1416:G:P	9:C:190:ARG:HH12	2.37	0.47
2:1:1844:C:H2'	2:1:1845:A:C8	2.49	0.47
2:1:3337:A:O2'	2:1:3338:A:OP1	2.24	0.47
9:C:140:ARG:HG2	9:C:142:HIS:CD2	2.49	0.47
11:E:156:ASP:O	11:E:160:VAL:HG23	2.14	0.47
43:l:35:HIS:HE1	43:l:46:TYR:CD2	2.32	0.47
44:m:357:SER:C	44:m:360:PRO:HD2	2.39	0.47
46:o:202:PRO:HB2	46:o:205:THR:HB	1.96	0.47
53:v:169:ARG:HD2	53:v:188:LEU:HD22	1.95	0.47
2:1:1378:U:H2'	2:1:1389:A:H61	1.79	0.47
2:1:1753:A:N6	34:c:42:LYS:HD2	2.29	0.47
2:1:3172:C:P	35:d:71:ASN:HD22	2.37	0.47
3:2:132:G:H1	3:2:137:A:N6	1.99	0.47
8:B:214:MET:CE	8:B:279:ASN:HB3	2.44	0.47
26:U:56:GLU:OE1	26:U:56:GLU:N	2.46	0.47
34:c:27:LYS:HE3	34:c:114:ILE:HA	1.95	0.47
43:l:7:GLU:H	43:l:7:GLU:CD	2.17	0.47
43:l:28:ILE:HD12	43:l:29:ASP:N	2.29	0.47
43:l:95:TYR:CE2	43:l:125:THR:HA	2.47	0.47
44:m:702:LYS:HD2	45:n:555:LYS:HZ3	1.78	0.47
45:n:215:ASP:HB3	45:n:218:ILE:HD12	1.95	0.47
54:w:37:ASN:HB2	54:w:43:LEU:HD12	1.95	0.47
2:1:995:G:H2'	2:1:996:G:C8	2.50	0.47
2:1:1542:C:H5''	2:1:2442:C:H1'	1.95	0.47
9:C:363:ASN:HD21	58:T:152:HIS:CE1	2.33	0.47
15:I:524:ILE:HD11	54:w:697:ILE:HA	1.96	0.47
16:J:104:TYR:HE2	16:J:108:LYS:HZ3	1.60	0.47
21:O:184:GLU:HA	21:O:189:ASN:ND2	2.29	0.47
24:R:96:MET:HE1	24:R:100:ARG:HE	1.79	0.47
42:k:8:ILE:HD12	42:k:8:ILE:H	1.79	0.47
44:m:133:ASP:OD1	44:m:134:ILE:N	2.44	0.47
52:u:7:TYR:CE2	52:u:40:PHE:HD2	2.32	0.47
2:1:1093:A:O2'	58:T:102:ARG:NH1	2.47	0.47
2:1:2926:G:H2'	2:1:2927:C:C6	2.49	0.47
2:1:3026:C:HO2'	27:V:44:THR:HG1	1.62	0.47
10:D:128:ASP:HB3	10:D:290:LEU:CD1	2.45	0.47
15:I:648:SER:HB2	15:I:683:SER:HB2	1.95	0.47
21:O:54:LYS:HA	50:s:4:LEU:HD21	1.96	0.47
22:P:9:ALA:HA	22:P:14:CYS:HB2	1.96	0.47
27:V:82:ARG:NH2	54:w:245:TYR:OH	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:j:68:LYS:HD3	53:v:14:LYS:NZ	2.29	0.47
44:m:191:ILE:HG21	44:m:196:PHE:HD2	1.80	0.47
44:m:628:HIS:CE1	44:m:696:PRO:HG3	2.48	0.47
45:n:362:ARG:NH2	51:t:189:ASP:OD1	2.47	0.47
58:T:102:ARG:HH22	58:T:105:PHE:HD2	1.61	0.47
2:1:847:G:H2'	2:1:848:A:O4'	2.15	0.47
2:1:1601:G:C4	45:n:30:LEU:HD22	2.49	0.47
2:1:2952:C:O2'	2:1:2953:U:H5'	2.14	0.47
3:2:28:U:H2'	3:2:29:C:O4'	2.13	0.47
17:K:148:PRO:O	17:K:151:PRO:HD2	2.14	0.47
19:M:13:VAL:O	19:M:59:THR:OG1	2.25	0.47
36:e:98:SER:O	36:e:102:ARG:HG3	2.15	0.47
43:l:127:GLN:HG3	43:l:147:ALA:O	2.15	0.47
45:n:437:ASP:OD1	45:n:438:LEU:N	2.47	0.47
47:p:96:ALA:O	47:p:432:GLN:N	2.45	0.47
51:t:76:LYS:HD3	51:t:77:ASN:N	2.30	0.47
2:1:590:U:H3'	2:1:591:G:H5''	1.97	0.47
2:1:747:A:O2'	2:1:816:A:OP2	2.33	0.47
2:1:1295:G:N2	2:1:1296:U:O4	2.42	0.47
2:1:1537:A:H3'	2:1:1538:A:C8	2.50	0.47
2:1:1702:A:H2'	2:1:1703:G:C8	2.50	0.47
2:1:1845:A:H2'	2:1:1846:A:H8	1.79	0.47
2:1:2898:A:H2'	2:1:2899:A:C8	2.49	0.47
2:1:3013:G:N2	54:w:124:GLY:HA2	2.26	0.47
2:1:3174:A:H5'	35:d:70:ARG:HH12	1.78	0.47
5:6:59:A:C1'	17:K:56:GLN:HE22	2.28	0.47
7:A:142:LEU:HB2	7:A:145:SER:HB3	1.96	0.47
11:E:114:VAL:HA	11:E:163:LYS:HD3	1.95	0.47
12:F:214:LEU:HB3	12:F:249:MET:HB3	1.96	0.47
15:I:629:GLU:HA	15:I:632:MET:SD	2.54	0.47
16:J:121:VAL:HG21	16:J:149:SER:HB2	1.97	0.47
16:J:186:GLN:O	16:J:190:LYS:HG2	2.14	0.47
17:K:231:ASP:O	17:K:234:LYS:HE2	2.14	0.47
25:S:78:ILE:HG21	25:S:105:MET:HE2	1.97	0.47
32:a:129:VAL:HG11	32:a:144:VAL:HG11	1.96	0.47
34:c:37:TYR:CD1	34:c:37:TYR:C	2.93	0.47
36:e:31:LYS:HD2	36:e:32:PRO:HD2	1.96	0.47
39:h:23:LEU:HD22	39:h:49:THR:HG23	1.95	0.47
42:k:69:GLU:HG2	42:k:70:VAL:N	2.28	0.47
43:l:7:GLU:O	43:l:11:THR:OG1	2.20	0.47
54:w:678:THR:HG23	54:w:681:ALA:H	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:y:68:LYS:NZ	56:y:134:ASP:HB2	2.30	0.47
2:1:378:U:H4'	2:1:412:G:H5'	1.97	0.47
2:1:3369:A:H4'	2:1:3370:U:H3'	1.97	0.47
6:8:27:ILE:HD13	6:8:27:ILE:HA	1.72	0.47
7:A:201:ARG:HH12	16:J:139:GLU:HG3	1.80	0.47
10:D:107:MET:HE1	10:D:180:VAL:HG13	1.96	0.47
10:D:371:LYS:O	10:D:375:ARG:HG3	2.15	0.47
15:I:657:LYS:O	15:I:661:ILE:HG13	2.15	0.47
25:S:123:LEU:HD22	58:T:153:PRO:HG2	1.96	0.47
26:U:83:LYS:HB2	26:U:88:ARG:HD2	1.96	0.47
30:Y:65:ARG:HD3	30:Y:84:VAL:HG22	1.96	0.47
43:l:53:LYS:O	43:l:56:THR:OG1	2.32	0.47
44:m:704:LEU:HD22	44:m:739:TRP:CE3	2.50	0.47
49:r:41:LYS:HD3	49:r:41:LYS:HA	1.71	0.47
2:1:593:A:H2'	2:1:594:A:O4'	2.15	0.47
2:1:1022:U:H3	2:1:1091:G:H1	1.63	0.47
2:1:2432:U:H2'	2:1:2433:A:C8	2.50	0.47
2:1:3070:U:O2'	2:1:3071:A:OP1	2.28	0.47
2:1:3182:G:H3'	2:1:3183:A:H8	1.79	0.47
5:6:1:A:OP2	51:t:227:HIS:NE2	2.44	0.47
9:C:355:LYS:O	9:C:359:VAL:HG12	2.15	0.47
13:G:116:VAL:HA	13:G:120:LYS:HD2	1.97	0.47
15:I:294:ALA:O	15:I:298:GLU:HG2	2.15	0.47
20:N:8:GLU:OE2	20:N:12:LYS:NZ	2.44	0.47
26:U:50:SER:O	26:U:66:HIS:N	2.47	0.47
29:X:109:ILE:HG12	29:X:123:VAL:HG22	1.97	0.47
31:Z:77:TYR:HB3	34:c:49:ARG:HD3	1.97	0.47
32:a:132:ARG:HA	32:a:135:GLU:HG2	1.96	0.47
33:b:435:LEU:HA	33:b:440:ASN:HA	1.96	0.47
43:l:52:MET:O	43:l:56:THR:N	2.47	0.47
44:m:582:HIS:HB3	44:m:585:MET:O	2.15	0.47
45:n:182:LEU:HD11	45:n:425:TYR:CD2	2.50	0.47
2:1:359:A:H1'	6:8:35:VAL:O	2.15	0.47
2:1:420:G:H5'	22:P:26:PHE:HZ	1.79	0.47
2:1:1400:A:C2	2:1:1401:G:H1'	2.50	0.47
4:3:70:ALA:HA	4:3:76:LEU:HD23	1.96	0.47
8:B:90:VAL:HG22	8:B:104:THR:HG23	1.96	0.47
9:C:140:ARG:HH21	9:C:242:PRO:HG2	1.80	0.47
10:D:416:ASP:OD1	10:D:416:ASP:N	2.48	0.47
14:H:24:ARG:HG2	14:H:46:MET:HE1	1.97	0.47
17:K:143:ASP:HB3	17:K:146:VAL:HG22	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Q:116:LEU:HD11	23:Q:122:VAL:HG22	1.96	0.47
26:U:46:ASN:O	26:U:46:ASN:ND2	2.42	0.47
47:p:408:LEU:HA	47:p:423:GLY:HA3	1.96	0.47
51:t:162:ILE:HD13	51:t:167:ILE:HB	1.97	0.47
2:1:742:A:OP2	32:a:112:LEU:HB3	2.14	0.46
2:1:1022:U:H3	2:1:1091:G:H22	1.62	0.46
2:1:1701:G:H2'	2:1:1702:A:H8	1.80	0.46
2:1:3368:A:H5''	11:E:145:PRO:HB3	1.98	0.46
7:A:86:LEU:HB3	7:A:98:ILE:HD13	1.96	0.46
8:B:281:LYS:N	8:B:325:ASN:OD1	2.49	0.46
31:Z:63:ALA:O	31:Z:67:ARG:HG3	2.15	0.46
45:n:360:LEU:HD12	45:n:364:VAL:HG21	1.97	0.46
49:r:10:SER:O	49:r:14:HIS:N	2.43	0.46
52:u:38:LYS:O	52:u:42:MET:HE2	2.15	0.46
2:1:719:A:OP1	20:N:199:ARG:NH2	2.45	0.46
2:1:1460:C:H4'	9:C:42:THR:HG23	1.96	0.46
4:3:145:ALA:O	4:3:149:ARG:HG3	2.15	0.46
5:6:48:G:O6	17:K:69:LEU:N	2.39	0.46
9:C:289:VAL:HG21	23:Q:27:LEU:HB3	1.96	0.46
43:l:64:MET:HE3	43:l:64:MET:N	2.22	0.46
43:l:97:ILE:HD12	43:l:97:ILE:O	2.15	0.46
45:n:39:LEU:O	45:n:122:ARG:NH1	2.47	0.46
45:n:563:MET:HE2	45:n:563:MET:C	2.40	0.46
50:s:18:ARG:O	50:s:22:LYS:HG2	2.16	0.46
2:1:68:A:O3'	20:N:177:GLY:HA2	2.14	0.46
2:1:238:U:H5'	2:1:240:G:H5''	1.97	0.46
2:1:359:A:H8	6:8:35:VAL:H	1.63	0.46
2:1:680:C:H2'	2:1:681:A:C8	2.51	0.46
2:1:1336:U:C6	21:O:64:ARG:HG2	2.50	0.46
4:3:53:VAL:O	4:3:111:ARG:NE	2.38	0.46
6:8:23:ILE:HB	55:x:13:GLN:OE1	2.14	0.46
8:B:46:PHE:CD2	8:B:205:ILE:HD12	2.50	0.46
10:D:343:MET:HE3	10:D:352:MET:HE3	1.97	0.46
31:Z:29:ILE:HD12	31:Z:40:HIS:CD2	2.50	0.46
34:c:42:LYS:HA	34:c:45:LEU:HD12	1.96	0.46
38:g:86:LYS:O	38:g:90:VAL:HG13	2.15	0.46
44:m:695:ASN:OD1	44:m:696:PRO:HD2	2.14	0.46
46:o:120:GLN:OE1	46:o:120:GLN:N	2.45	0.46
54:w:210:ARG:O	54:w:216:THR:OG1	2.27	0.46
57:z:105:ALA:C	57:z:107:ASN:N	2.73	0.46
2:1:372:G:OP2	41:j:52:LYS:NZ	2.34	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:53:C:O2'	6:8:11:GLN:OE1	2.28	0.46
16:J:127:ILE:HG21	16:J:145:GLN:HB3	1.98	0.46
27:V:79:ILE:HG13	27:V:105:VAL:HG11	1.97	0.46
31:Z:92:LEU:HD21	31:Z:117:THR:HG21	1.97	0.46
31:Z:109:ALA:O	31:Z:113:THR:HG23	2.16	0.46
43:l:161:ILE:HD12	43:l:162:VAL:N	2.30	0.46
44:m:290:LYS:HD2	51:t:17:VAL:O	2.15	0.46
54:w:95:THR:HG22	54:w:100:ARG:HH11	1.81	0.46
2:1:7:C:H2'	2:1:8:C:C6	2.50	0.46
2:1:2458:G:OP1	50:s:12:THR:HB	2.14	0.46
2:1:3024:C:H1'	54:w:124:GLY:HA3	1.97	0.46
6:8:35:VAL:HG12	6:8:36:HIS:N	2.30	0.46
8:B:183:VAL:O	8:B:191:LYS:NZ	2.35	0.46
10:D:342:PHE:CE2	10:D:408:ILE:HD11	2.51	0.46
11:E:99:ARG:O	37:f:106:SER:N	2.34	0.46
22:P:116:HIS:HB3	22:P:149:ILE:HB	1.97	0.46
26:U:34:LEU:CB	26:U:55:ARG:HH21	2.27	0.46
27:V:47:ARG:HD3	27:V:50:ARG:HG2	1.96	0.46
27:V:116:ILE:HD11	27:V:135:ALA:HA	1.98	0.46
40:i:43:ARG:NH2	40:i:47:GLY:O	2.49	0.46
51:t:70:ARG:NH2	51:t:135:ILE:O	2.39	0.46
54:w:156:VAL:HG22	54:w:197:VAL:HG13	1.97	0.46
2:1:587:U:H2'	2:1:588:G:H8	1.79	0.46
10:D:415:ASP:OD1	10:D:415:ASP:N	2.48	0.46
15:I:735:SER:O	15:I:739:LYS:HG2	2.15	0.46
19:M:116:LEU:HD11	21:O:192:LEU:HD23	1.97	0.46
27:V:137:THR:HB	56:y:101:LEU:HA	1.96	0.46
34:c:89:ILE:HD12	34:c:100:ARG:HG2	1.97	0.46
35:d:34:ALA:HB3	35:d:69:ILE:HG13	1.98	0.46
39:h:27:LEU:O	39:h:31:ARG:HG3	2.15	0.46
2:1:673:C:H3'	2:1:674:A:H8	1.81	0.46
15:I:512:LEU:HD12	15:I:564:THR:HG21	1.97	0.46
20:N:47:LYS:HD2	20:N:50:ARG:HH11	1.80	0.46
27:V:93:VAL:HG21	52:u:20:MET:HE2	1.98	0.46
38:g:13:TYR:O	38:g:15:THR:HG23	2.15	0.46
49:r:38:TYR:CZ	49:r:42:THR:HG21	2.51	0.46
53:v:33:ASN:HD22	53:v:36:ILE:HG12	1.80	0.46
54:w:278:VAL:HG13	54:w:280:PRO:HD3	1.97	0.46
2:1:1806:U:HO2'	2:1:1807:G:P	2.39	0.46
2:1:2926:G:O2'	49:r:251:ASP:OD2	2.24	0.46
2:1:2971:C:O2'	2:1:2972:G:H5'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:I:241:LEU:O	15:I:245:ILE:HG13	2.15	0.46
15:I:337:VAL:HG11	15:I:372:GLY:HA3	1.96	0.46
17:K:53:VAL:HG21	17:K:213:LEU:HD12	1.98	0.46
44:m:537:HIS:HB2	44:m:542:TYR:HB2	1.98	0.46
45:n:570:ARG:NH1	45:n:573:TYR:HB2	2.30	0.46
54:w:49:ILE:HD12	54:w:114:VAL:O	2.16	0.46
54:w:320:TRP:HA	54:w:323:LYS:HE2	1.98	0.46
2:1:872:C:H2'	2:1:873:A:H8	1.81	0.46
7:A:99:PHE:CZ	7:A:171:THR:HG21	2.51	0.46
16:J:106:ARG:HD2	16:J:107:ILE:HG23	1.97	0.46
17:K:99:LYS:HG2	17:K:114:VAL:HB	1.96	0.46
21:O:141:ARG:O	21:O:145:GLU:HG3	2.16	0.46
43:l:33:ASP:OD2	43:l:35:HIS:HB2	2.16	0.46
44:m:494:PHE:CE1	44:m:522:HIS:HB3	2.51	0.46
51:t:183:ASP:CG	51:t:183:ASP:O	2.59	0.46
54:w:107:LEU:HG	54:w:110:TRP:O	2.16	0.46
56:y:199:VAL:HG22	56:y:200:ASN:O	2.16	0.46
2:1:216:A:O2'	2:1:218:A:H8	1.98	0.46
2:1:645:U:H5''	2:1:646:A:OP2	2.15	0.46
2:1:747:A:OP1	2:1:816:A:N6	2.34	0.46
2:1:1539:C:H1'	2:1:1547:G:N2	2.31	0.46
2:1:1567:U:O2'	2:1:1839:A:N3	2.36	0.46
2:1:1666:C:OP2	31:Z:48:ARG:NH1	2.34	0.46
6:8:28:ARG:NH2	55:x:10:ARG:HB2	2.31	0.46
10:D:246:ASP:OD1	10:D:247:ARG:N	2.49	0.46
15:I:733:ALA:O	15:I:736:GLN:NE2	2.49	0.46
17:K:77:LYS:NZ	17:K:215:GLU:HB3	2.31	0.46
17:K:119:LYS:HD3	17:K:123:LYS:NZ	2.31	0.46
27:V:72:ARG:HG2	27:V:73:LYS:N	2.30	0.46
45:n:169:HIS:HB3	45:n:265:LEU:HD21	1.97	0.46
51:t:33:VAL:O	51:t:37:ILE:HG13	2.16	0.46
54:w:624:ALA:O	54:w:628:THR:HG23	2.16	0.46
2:1:1365:C:OP1	12:F:213:LYS:HD3	2.16	0.45
5:6:93:A:H2	17:K:127:TYR:H	1.64	0.45
8:B:214:MET:HG2	8:B:281:LYS:HB2	1.97	0.45
9:C:343:ILE:HG13	9:C:344:ASN:N	2.30	0.45
10:D:135:THR:HB	10:D:398:ARG:HG2	1.98	0.45
10:D:172:GLU:HG3	10:D:395:VAL:HG21	1.98	0.45
15:I:524:ILE:HG13	54:w:700:VAL:HG11	1.98	0.45
17:K:61:LYS:HA	46:o:211:HIS:CD2	2.44	0.45
22:P:42:LYS:NZ	22:P:110:ASP:HA	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:c:27:LYS:NZ	34:c:113:ASP:O	2.49	0.45
34:c:40:GLY:O	34:c:44:THR:OG1	2.34	0.45
44:m:704:LEU:HD13	44:m:739:TRP:CG	2.51	0.45
45:n:423:TRP:HD1	45:n:439:TYR:HD2	1.63	0.45
49:r:184:THR:OG1	49:r:191:THR:HG22	2.17	0.45
2:1:379:G:H4'	2:1:404:A:N1	2.31	0.45
2:1:1529:U:C5	2:1:1890:A:N1	2.84	0.45
2:1:1913:A:N3	38:g:4:ARG:NH1	2.64	0.45
2:1:2898:A:H2'	2:1:2899:A:H8	1.81	0.45
3:2:143:G:H5''	29:X:48:LYS:HD3	1.98	0.45
14:H:90:MET:HE3	14:H:144:LEU:HD11	1.98	0.45
14:H:111:GLU:OE1	14:H:113:ARG:NH2	2.49	0.45
19:M:102:ARG:O	19:M:105:LEU:HB2	2.16	0.45
25:S:70:LYS:O	25:S:72:LYS:HE2	2.16	0.45
31:Z:96:ILE:HD12	31:Z:100:THR:OG1	2.16	0.45
39:h:20:LEU:HB2	39:h:56:ILE:HG21	1.97	0.45
43:l:16:LEU:HB3	43:l:20:ILE:HD11	1.99	0.45
54:w:90:PHE:CE2	54:w:102:GLN:HB3	2.51	0.45
54:w:161:ARG:HH21	54:w:194:ILE:HD13	1.79	0.45
54:w:629:LEU:O	54:w:633:ILE:HG13	2.16	0.45
57:z:105:ALA:O	57:z:106:LYS:C	2.59	0.45
2:1:847:G:H5'	41:j:16:HIS:CE1	2.51	0.45
2:1:1290:A:H61	28:W:45:VAL:CB	2.29	0.45
2:1:2415:U:O2'	54:w:189:ASN:O	2.34	0.45
2:1:3123:A:H2'	2:1:3124:G:O4'	2.16	0.45
2:1:3185:C:H2'	2:1:3186:U:O4'	2.16	0.45
7:A:136:ASN:OD1	7:A:136:ASN:N	2.49	0.45
8:B:374:ALA:O	8:B:378:GLN:HG2	2.17	0.45
9:C:228:GLU:OE1	9:C:248:ARG:NH1	2.33	0.45
21:O:117:LYS:NZ	25:S:169:PRO:O	2.49	0.45
21:O:184:GLU:HA	21:O:189:ASN:HD21	1.81	0.45
32:a:82:LEU:HD13	32:a:86:ALA:HB1	1.98	0.45
49:r:45:ILE:O	49:r:49:LEU:HG	2.15	0.45
2:1:257:A:H62	18:L:134:LYS:NZ	2.14	0.45
2:1:769:U:H5''	23:Q:74:SER:OG	2.15	0.45
7:A:78:ASP:OD1	7:A:78:ASP:N	2.42	0.45
9:C:314:HIS:CE1	9:C:317:LYS:HA	2.52	0.45
12:F:227:LYS:HB2	12:F:233:GLY:HA3	1.98	0.45
15:I:366:HIS:HA	15:I:407:ARG:HH21	1.82	0.45
26:U:47:LEU:HD12	26:U:52:VAL:HA	1.98	0.45
27:V:110:GLU:HA	27:V:130:ARG:HG2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:d:17:TYR:O	35:d:77:ARG:HD2	2.16	0.45
37:f:38:SER:OG	37:f:41:GLU:HG3	2.17	0.45
44:m:479:PRO:HD2	44:m:482:PHE:HE2	1.80	0.45
44:m:538:ARG:NH2	44:m:584:THR:O	2.50	0.45
49:r:16:ARG:HE	49:r:17:ARG:H	1.62	0.45
54:w:99:CYS:O	54:w:103:LEU:HG	2.17	0.45
54:w:208:ASP:O	54:w:212:THR:HG23	2.16	0.45
2:1:268:U:H5'	10:D:207:LYS:HD3	1.98	0.45
2:1:544:A:H2	2:1:582:G:H22	1.64	0.45
2:1:1692:C:N4	2:1:1839:A:OP2	2.49	0.45
4:3:35:THR:O	36:e:85:HIS:NE2	2.50	0.45
4:3:114:ARG:HD3	4:3:114:ARG:N	2.31	0.45
8:B:379:PHE:CZ	52:u:11:GLY:HA2	2.50	0.45
9:C:73:LEU:HD11	54:w:767:GLY:HA2	1.97	0.45
9:C:284:ILE:HD13	9:C:287:ALA:HA	1.99	0.45
9:C:288:ASP:CG	9:C:291:ARG:HG2	2.42	0.45
10:D:352:MET:HE2	10:D:352:MET:HB2	1.80	0.45
11:E:60:LEU:HD11	11:E:96:VAL:HG21	1.98	0.45
16:J:189:ILE:O	16:J:193:THR:HG22	2.17	0.45
17:K:17:CYS:CB	17:K:213:LEU:HD22	2.46	0.45
26:U:96:THR:HG23	26:U:102:GLU:HG2	1.98	0.45
42:k:27:LYS:HD2	42:k:33:VAL:HG22	1.98	0.45
43:l:1:MET:SD	43:l:2:ARG:N	2.90	0.45
49:r:56:LYS:O	49:r:60:GLN:HG2	2.15	0.45
54:w:54:ALA:H	54:w:77:ASP:HB2	1.80	0.45
55:x:21:LYS:O	55:x:25:LYS:HG2	2.16	0.45
2:1:443:C:H2'	2:1:444:A:C8	2.52	0.45
2:1:591:G:H1'	2:1:593:A:H5'	1.97	0.45
2:1:1319:U:H2'	2:1:1320:G:C8	2.50	0.45
2:1:1446:G:H5''	36:e:121:ALA:CB	2.46	0.45
2:1:2697:G:H2'	2:1:2698:G:H8	1.82	0.45
2:1:2928:A:H4'	49:r:257:LEU:HD13	1.97	0.45
7:A:44:LYS:HB3	7:A:95:CYS:HA	1.98	0.45
9:C:283:ILE:HD11	23:Q:106:ARG:NH1	2.31	0.45
13:G:161:GLU:CD	20:N:26:ARG:HH22	2.24	0.45
25:S:47:ILE:HG22	25:S:48:ASN:OD1	2.16	0.45
26:U:35:ILE:HD13	26:U:55:ARG:HH22	1.82	0.45
27:V:69:PRO:HG2	54:w:215:ARG:HA	1.97	0.45
31:Z:97:THR:HG22	31:Z:100:THR:HG23	1.98	0.45
34:c:41:TYR:CZ	34:c:66:ARG:HG3	2.51	0.45
37:f:51:CYS:SG	37:f:100:ARG:HB2	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:h:72:TYR:HB3	39:h:78:ILE:HG22	1.98	0.45
43:l:71:GLY:HA2	43:l:82:HIS:CD2	2.50	0.45
44:m:587:TYR:CZ	44:m:607:VAL:HG21	2.52	0.45
52:u:63:MET:HE1	52:u:105:GLU:HA	1.99	0.45
54:w:447:ASP:O	54:w:451:GLU:HG2	2.16	0.45
2:1:592:U:N3	9:C:346:GLU:O	2.49	0.45
2:1:748:G:P	2:1:748:G:H8	2.40	0.45
2:1:984:A:C2	2:1:1145:U:H4'	2.52	0.45
2:1:3181:G:OP1	52:u:34:SER:OG	2.30	0.45
7:A:57:GLN:NE2	7:A:109:LEU:HB2	2.31	0.45
9:C:76:ILE:HG12	9:C:96:CYS:SG	2.57	0.45
15:I:418:LEU:O	15:I:421:SER:OG	2.33	0.45
17:K:24:GLU:HG2	17:K:206:VAL:HG21	1.97	0.45
17:K:174:THR:H	17:K:177:GLN:NE2	2.15	0.45
31:Z:49:TYR:CD2	31:Z:133:PRO:HB3	2.52	0.45
32:a:90:TYR:CD2	32:a:99:PRO:HD3	2.52	0.45
36:e:102:ARG:NH2	36:e:121:ALA:HB3	2.32	0.45
45:n:152:ILE:HD12	45:n:220:HIS:CD2	2.51	0.45
46:o:152:GLU:HB2	46:o:191:PHE:CZ	2.52	0.45
50:s:21:LYS:O	50:s:25:GLU:HG3	2.17	0.45
50:s:24:ALA:O	50:s:28:ARG:HG2	2.17	0.45
2:1:528:G:OP1	12:F:74:ARG:NH2	2.38	0.45
2:1:714:A:H4'	53:v:25:LYS:HZ3	1.82	0.45
2:1:872:C:H2'	2:1:873:A:C8	2.52	0.45
8:B:92:TYR:HB2	8:B:157:VAL:HB	1.97	0.45
8:B:289:ASP:OD1	8:B:290:ASP:N	2.50	0.45
11:E:72:VAL:HA	11:E:82:VAL:HG12	1.99	0.45
15:I:522:LEU:HD11	54:w:692:LEU:HD23	1.99	0.45
26:U:73:TYR:HE1	26:U:77:LEU:HD21	1.82	0.45
37:f:53:VAL:HG21	37:f:100:ARG:NH2	2.31	0.45
40:i:34:ARG:HG3	44:m:215:LEU:HD21	1.99	0.45
52:u:8:PHE:CZ	52:u:39:ASN:HB3	2.52	0.45
54:w:613:ASP:OD1	54:w:613:ASP:N	2.50	0.45
2:1:414:G:N3	3:2:24:G:C2	2.85	0.45
2:1:1833:C:H3'	2:1:1834:C:H5''	1.98	0.45
14:H:18:THR:HG22	14:H:20:ASP:H	1.82	0.45
16:J:170:TYR:HA	44:m:131:ASN:CG	2.42	0.45
17:K:51:GLU:O	17:K:206:VAL:HG23	2.17	0.45
17:K:242:LYS:HG2	17:K:243:THR:O	2.16	0.45
33:b:445:VAL:O	52:u:76:ARG:NH2	2.49	0.45
45:n:403:ILE:HD12	45:n:403:ILE:H	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:r:223:ASN:OD1	49:r:225:SER:N	2.42	0.45
52:u:42:MET:HE3	52:u:42:MET:HB2	1.85	0.45
52:u:104:ARG:HA	52:u:107:LEU:CG	2.47	0.45
56:y:66:ASN:ND2	56:y:68:LYS:HE3	2.30	0.45
2:1:372:G:O6	41:j:56:ARG:HD3	2.16	0.45
2:1:1628:A:C5	45:n:4:VAL:HG22	2.52	0.45
2:1:1778:A:H2'	2:1:1779:U:C6	2.52	0.45
4:3:156:LYS:HA	22:P:11:GLU:OE1	2.16	0.45
5:6:59:A:H2'	5:6:60:U:O4'	2.16	0.45
7:A:117:PRO:HG3	44:m:101:GLU:HA	1.99	0.45
7:A:146:ARG:HH22	16:J:117:GLU:C	2.25	0.45
7:A:194:ALA:HB3	7:A:199:TRP:CD1	2.52	0.45
15:I:723:PRO:O	15:I:727:LYS:HG3	2.17	0.45
15:I:729:HIS:HE1	15:I:731:SER:HB2	1.81	0.45
17:K:242:LYS:NZ	17:K:243:THR:O	2.43	0.45
42:k:9:LYS:HB2	44:m:645:PHE:HA	1.98	0.45
44:m:417:CYS:HB3	44:m:420:LYS:HE3	1.99	0.45
44:m:421:CYS:SG	44:m:517:HIS:HB3	2.57	0.45
44:m:550:SER:HB3	44:m:554:ALA:HA	1.99	0.45
45:n:357:THR:HB	45:n:392:PHE:HE2	1.82	0.45
51:t:141:MET:HE2	51:t:237:CYS:SG	2.56	0.45
54:w:294:VAL:HG12	54:w:320:TRP:HD1	1.82	0.45
58:T:100:LYS:H	58:T:100:LYS:HD3	1.82	0.45
2:1:1266:U:O4'	2:1:1268:G:H5'	2.16	0.44
3:2:44:G:O2'	3:2:112:A:N1	2.46	0.44
6:8:21:ARG:HG2	6:8:22:PRO:HD2	1.98	0.44
40:i:93:GLN:O	40:i:97:LEU:HG	2.17	0.44
45:n:38:ILE:HD12	45:n:222:PHE:CE2	2.51	0.44
45:n:190:GLN:NE2	45:n:197:GLN:HB3	2.28	0.44
54:w:279:PHE:HB3	54:w:290:TYR:CE1	2.51	0.44
54:w:775:VAL:C	54:w:776:LYS:HD2	2.42	0.44
2:1:7:C:OP2	45:n:93:LYS:NZ	2.44	0.44
2:1:511:C:H5''	11:E:99:ARG:HG3	1.98	0.44
2:1:2996:G:O3'	14:H:168:LYS:NZ	2.49	0.44
5:6:93:A:OP2	17:K:131:ARG:NH2	2.50	0.44
6:8:25:GLN:HA	6:8:25:GLN:NE2	2.32	0.44
14:H:29:THR:HG22	14:H:34:THR:HG23	1.99	0.44
15:I:493:ILE:O	15:I:496:THR:OG1	2.33	0.44
15:I:585:LEU:O	15:I:588:GLN:HG3	2.18	0.44
19:M:25:LEU:HD12	19:M:25:LEU:HA	1.83	0.44
27:V:69:PRO:HB3	54:w:132:TYR:OH	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:c:32:MET:HG2	34:c:37:TYR:CE2	2.52	0.44
39:h:14:GLU:N	39:h:14:GLU:OE2	2.50	0.44
45:n:560:LEU:HG	45:n:561:SER:N	2.32	0.44
49:r:2:PRO:HB2	49:r:6:TYR:CD1	2.53	0.44
49:r:156:VAL:HG12	49:r:172:ARG:HH11	1.83	0.44
51:t:221:MET:O	51:t:225:VAL:HG13	2.17	0.44
2:1:347:C:OP1	2:1:1414:G:O2'	2.34	0.44
2:1:644:A:H5'	2:1:645:U:C5	2.52	0.44
2:1:714:A:H4'	53:v:25:LYS:HZ1	1.82	0.44
2:1:1584:C:H2'	2:1:1585:C:C6	2.52	0.44
2:1:1601:G:OP2	45:n:19:ARG:NH2	2.37	0.44
3:2:60:A:N6	6:8:27:ILE:HG13	2.32	0.44
3:2:132:G:H2'	3:2:134:U:OP2	2.17	0.44
5:6:58:A:OP1	17:K:247:ILE:HD13	2.17	0.44
7:A:167:LEU:HD12	7:A:167:LEU:HA	1.89	0.44
7:A:203:TYR:CD1	7:A:218:LEU:HD13	2.53	0.44
8:B:47:LEU:HD12	8:B:47:LEU:HA	1.85	0.44
11:E:92:PRO:HA	11:E:157:GLN:OE1	2.18	0.44
16:J:105:GLU:HA	16:J:108:LYS:HB2	1.99	0.44
17:K:66:ASN:OD1	17:K:67:ARG:N	2.50	0.44
25:S:164:LYS:HA	25:S:164:LYS:HD3	1.81	0.44
26:U:18:ALA:HB1	26:U:105:TYR:CE2	2.53	0.44
31:Z:81:MET:HE2	31:Z:81:MET:HB3	1.77	0.44
36:e:100:ARG:O	36:e:103:VAL:HG22	2.17	0.44
38:g:90:VAL:O	38:g:94:LEU:HG	2.17	0.44
45:n:409:ILE:HB	45:n:412:LYS:HE2	1.98	0.44
49:r:149:MET:HA	49:r:171:ILE:H	1.83	0.44
2:1:414:G:H1'	3:2:24:G:N2	2.31	0.44
2:1:633:A:H5'	9:C:325:ALA:HB3	2.00	0.44
2:1:3180:C:O2'	2:1:3433:U:OP1	2.26	0.44
7:A:41:ILE:HD13	44:m:106:TYR:CE1	2.52	0.44
7:A:63:ASP:OD2	7:A:132:MET:HG2	2.18	0.44
12:F:105:LYS:HE2	12:F:136:VAL:HG11	1.98	0.44
15:I:509:GLY:HA2	15:I:560:LEU:CD2	2.47	0.44
15:I:737:SER:O	15:I:740:GLU:HG2	2.17	0.44
20:N:158:HIS:HB3	20:N:161:SER:HB3	2.00	0.44
21:O:4:PHE:HZ	37:f:11:LYS:HB3	1.83	0.44
28:W:66:PHE:O	28:W:101:GLY:HA3	2.18	0.44
32:a:75:LEU:HD22	32:a:117:LEU:HD12	1.98	0.44
35:d:79:ARG:HB3	35:d:97:GLN:HG2	1.99	0.44
43:l:153:LEU:HA	43:l:156:LEU:HG	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:m:726:TRP:HD1	44:m:740:THR:HA	1.82	0.44
49:r:154:THR:HG22	49:r:213:VAL:HG22	1.99	0.44
2:1:260:U:H1'	53:v:191:LYS:HZ3	1.81	0.44
2:1:1825:U:H2'	2:1:1826:C:C6	2.53	0.44
2:1:2920:C:O2'	2:1:2921:U:O4'	2.33	0.44
2:1:3144:C:H5'	8:B:53:MET:HE2	2.00	0.44
11:E:69:ARG:HD3	11:E:177:TYR:CE2	2.52	0.44
16:J:96:ASN:O	16:J:100:LEU:HB2	2.17	0.44
16:J:145:GLN:HG3	16:J:146:GLY:N	2.31	0.44
17:K:23:TYR:HA	17:K:26:LYS:HG2	2.00	0.44
17:K:144:ASP:OD2	17:K:169:LYS:HG3	2.16	0.44
21:O:66:ASN:O	21:O:69:ARG:N	2.33	0.44
30:Y:36:LYS:O	30:Y:40:GLU:HG2	2.18	0.44
35:d:42:VAL:HG23	35:d:54:VAL:HB	2.00	0.44
37:f:43:GLN:HA	37:f:46:LEU:HG	2.00	0.44
42:k:60:SER:HB2	44:m:693:LEU:HD23	1.99	0.44
49:r:180:LYS:HG3	49:r:193:GLN:HG2	1.99	0.44
52:u:82:TYR:HD1	56:y:86:ASN:HD21	1.65	0.44
54:w:52:LEU:HD13	54:w:141:SER:HB2	1.98	0.44
2:1:1157:G:H2'	2:1:1158:G:H1'	1.99	0.44
2:1:1253:G:H4'	2:1:1254:A:H5'	1.99	0.44
2:1:3059:G:N2	2:1:3062:A:O2'	2.51	0.44
6:8:27:ILE:HD12	6:8:30:ARG:HH21	1.83	0.44
7:A:137:MET:N	7:A:137:MET:SD	2.91	0.44
8:B:159:ARG:HG2	8:B:182:GLN:HA	2.00	0.44
14:H:11:LEU:HD23	14:H:72:TYR:CE1	2.51	0.44
20:N:22:LEU:O	20:N:26:ARG:HG3	2.18	0.44
23:Q:50:ARG:CZ	23:Q:142:ARG:HD2	2.48	0.44
26:U:19:ALA:N	26:U:103:LEU:HD11	2.32	0.44
26:U:31:GLU:HA	26:U:55:ARG:CZ	2.47	0.44
31:Z:74:VAL:HG23	31:Z:101:PHE:CE2	2.53	0.44
34:c:57:LEU:HD12	34:c:104:LEU:HD21	1.99	0.44
41:j:60:GLY:HA2	41:j:64:MET:SD	2.58	0.44
43:l:28:ILE:HD12	43:l:29:ASP:H	1.81	0.44
44:m:269:LEU:HD11	45:n:232:PHE:CD2	2.52	0.44
44:m:300:TYR:CZ	45:n:182:LEU:HB3	2.53	0.44
51:t:182:TYR:CZ	51:t:203:GLU:HG2	2.53	0.44
2:1:107:A:H1'	2:1:333:A:N3	2.32	0.44
2:1:616:A:H5'	11:E:35:VAL:O	2.18	0.44
7:A:63:ASP:O	7:A:67:MET:HG3	2.17	0.44
7:A:204:GLU:O	7:A:218:LEU:HA	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:H:101:ILE:HG23	14:H:110:VAL:HG13	2.00	0.44
17:K:70:ILE:HG12	17:K:147:ILE:HG21	2.00	0.44
17:K:152:ARG:C	17:K:154:LEU:H	2.25	0.44
27:V:73:LYS:O	27:V:74:LYS:HD3	2.18	0.44
29:X:14:GLN:HA	51:t:53:ARG:HH12	1.81	0.44
31:Z:42:VAL:HG11	31:Z:96:ILE:CG1	2.42	0.44
32:a:77:ARG:O	32:a:80:THR:OG1	2.36	0.44
56:y:222:PHE:HB3	56:y:224:LEU:HG	1.98	0.44
2:1:322:U:H2'	2:1:323:C:C6	2.53	0.44
2:1:3112:A:O2'	2:1:3113:A:H8	1.99	0.44
2:1:3317:A:C5	22:P:181:ARG:HD3	2.53	0.44
4:3:112:LEU:O	4:3:116:THR:OG1	2.34	0.44
7:A:126:VAL:CG2	7:A:227:MET:HE1	2.43	0.44
13:G:182:ASN:ND2	13:G:184:ALA:HB3	2.33	0.44
26:U:79:LYS:HB3	26:U:88:ARG:HH12	1.83	0.44
31:Z:53:VAL:HG13	31:Z:62:ILE:CD1	2.47	0.44
31:Z:89:LEU:HD13	31:Z:91:ASN:N	2.33	0.44
43:l:80:ARG:CD	43:l:166:GLN:HB3	2.46	0.44
45:n:141:PHE:CE1	45:n:164:CYS:HB3	2.53	0.44
53:v:171:ILE:HD11	53:v:202:TYR:HD1	1.82	0.44
54:w:51:ASP:HB3	54:w:75:GLY:HA2	1.99	0.44
2:1:63:A:OP1	20:N:169:LYS:HE2	2.18	0.44
2:1:216:A:O2'	2:1:218:A:OP2	2.32	0.44
2:1:1395:A:H2'	2:1:1396:G:C8	2.53	0.44
4:3:156:LYS:HD2	4:3:159:LYS:HD3	1.98	0.44
12:F:183:TYR:CZ	12:F:204:GLN:HG2	2.51	0.44
14:H:94:TYR:CD2	14:H:98:PRO:HA	2.53	0.44
15:I:504:LYS:HA	15:I:508:ILE:HD11	1.98	0.44
18:L:126:PHE:HB2	39:h:117:LYS:HB2	2.00	0.44
31:Z:89:LEU:HD13	31:Z:91:ASN:H	1.83	0.44
33:b:404:ALA:HA	33:b:408:GLY:HA2	1.99	0.44
43:l:67:GLY:C	43:l:68:ILE:HD13	2.43	0.44
44:m:297:GLU:HA	45:n:450:SER:HB2	1.99	0.44
44:m:348:ARG:HH21	51:t:18:LEU:HD21	1.82	0.44
2:1:1234:A:C2	2:1:1331:G:H2'	2.53	0.43
2:1:2951:G:O2'	49:r:191:THR:N	2.41	0.43
2:1:3235:A:H4'	8:B:20:LYS:HD3	2.00	0.43
16:J:196:LYS:HE2	16:J:196:LYS:HB3	1.74	0.43
17:K:61:LYS:NZ	17:K:231:ASP:OD1	2.51	0.43
19:M:33:ASP:HA	25:S:142:LEU:HD11	2.00	0.43
21:O:110:PRO:HB2	21:O:112:PRO:HD2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:U:89:ASP:O	26:U:92:ARG:NH1	2.51	0.43
27:V:34:LYS:HB2	27:V:66:LYS:HB2	2.00	0.43
29:X:11:LYS:HD2	46:o:161:VAL:HG13	2.00	0.43
30:Y:30:MET:SD	30:Y:77:PHE:HA	2.58	0.43
31:Z:25:ILE:HD12	31:Z:43:VAL:HG12	2.00	0.43
45:n:152:ILE:HD12	45:n:220:HIS:HD2	1.81	0.43
52:u:23:ARG:HB3	52:u:25:ASP:OD1	2.18	0.43
52:u:25:ASP:C	52:u:27:LYS:H	2.26	0.43
54:w:638:LYS:HG3	54:w:643:LEU:HG	2.00	0.43
56:y:103:ALA:HB1	56:y:106:ASN:HB2	1.99	0.43
2:1:117:U:O2	2:1:119:U:H2'	2.18	0.43
2:1:541:G:H2'	2:1:542:G:H8	1.83	0.43
2:1:1639:U:H2'	2:1:1640:A:H5''	2.00	0.43
2:1:2445:A:H2'	2:1:2446:A:C8	2.53	0.43
10:D:284:ASP:O	10:D:288:ILE:HG22	2.18	0.43
19:M:37:ALA:HB2	19:M:53:TYR:CE1	2.53	0.43
22:P:27:LYS:HE2	22:P:63:PHE:CE1	2.54	0.43
25:S:89:MET:HB3	25:S:89:MET:HE2	1.84	0.43
26:U:55:ARG:HB3	26:U:60:LYS:O	2.17	0.43
44:m:702:LYS:HD2	44:m:702:LYS:HA	1.85	0.43
54:w:766:LYS:HE2	54:w:766:LYS:HB2	1.74	0.43
2:1:295:G:C5'	20:N:179:ARG:HB3	2.48	0.43
2:1:712:U:O4	18:L:32:LYS:HE3	2.19	0.43
2:1:1542:C:H2'	2:1:1543:A:O4'	2.18	0.43
2:1:1602:A:C6	44:m:334:PHE:HE2	2.36	0.43
2:1:1688:G:H2'	2:1:1689:A:H8	1.83	0.43
7:A:124:PHE:HB3	7:A:227:MET:HE2	1.99	0.43
10:D:410:GLN:HG2	10:D:439:MET:HE3	1.98	0.43
14:H:43:ASP:H	14:H:64:HIS:HE1	1.66	0.43
16:J:116:VAL:HG21	16:J:162:VAL:HG21	2.01	0.43
17:K:13:LEU:HG	17:K:14:GLU:H	1.82	0.43
21:O:48:PHE:CE1	21:O:142:LEU:HA	2.52	0.43
31:Z:54:THR:O	31:Z:62:ILE:HD11	2.18	0.43
38:g:14:ASN:OD1	38:g:14:ASN:N	2.49	0.43
43:l:110:GLY:HA2	43:l:165:HIS:CD2	2.54	0.43
44:m:386:VAL:HB	44:m:730:ALA:HB1	2.00	0.43
44:m:407:LEU:H	44:m:422:SER:HA	1.83	0.43
44:m:702:LYS:NZ	44:m:703:ILE:O	2.51	0.43
53:v:142:GLU:O	53:v:146:VAL:HG23	2.18	0.43
56:y:157:GLN:NE2	56:y:157:GLN:H	2.16	0.43
58:T:105:PHE:O	58:T:105:PHE:HD1	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1584:C:H2'	2:1:1585:C:H6	1.83	0.43
2:1:2695:C:H2'	2:1:2696:A:C8	2.53	0.43
2:1:2926:G:H21	49:r:255:ASN:HB3	1.83	0.43
5:6:94:A:H62	17:K:131:ARG:HH12	1.65	0.43
11:E:171:ILE:HG13	11:E:172:PRO:HD2	1.99	0.43
11:E:171:ILE:HG23	11:E:174:MET:HG2	2.01	0.43
14:H:20:ASP:OD1	14:H:21:ILE:N	2.51	0.43
17:K:253:ASN:ND2	46:o:231:LEU:HD11	2.33	0.43
19:M:109:ASP:OD1	19:M:109:ASP:N	2.50	0.43
26:U:75:LYS:NZ	26:U:93:VAL:O	2.51	0.43
29:X:10:GLN:HG2	46:o:127:GLN:O	2.19	0.43
34:c:55:LEU:HB3	34:c:106:VAL:CG2	2.48	0.43
35:d:33:ARG:HB2	35:d:69:ILE:O	2.17	0.43
42:k:8:ILE:HD12	42:k:8:ILE:N	2.32	0.43
50:s:24:ALA:HA	50:s:27:LYS:HE3	2.00	0.43
52:u:9:CYS:HB2	52:u:36:CYS:SG	2.58	0.43
56:y:99:GLU:OE1	56:y:125:THR:OG1	2.32	0.43
2:1:301:C:H2'	2:1:302:U:O4'	2.19	0.43
2:1:763:G:H3'	2:1:764:U:H6	1.83	0.43
2:1:2515:U:H2'	2:1:2516:U:C6	2.54	0.43
2:1:2903:A:C8	49:r:206:PRO:HG2	2.53	0.43
2:1:3028:A:OP1	2:1:3111:C:H4'	2.18	0.43
7:A:99:PHE:CE1	7:A:171:THR:HG21	2.53	0.43
7:A:121:THR:HG21	7:A:237:PHE:HA	2.00	0.43
18:L:31:ARG:O	18:L:35:ARG:HG3	2.17	0.43
26:U:29:ALA:O	26:U:32:LYS:HG3	2.19	0.43
29:X:71:ALA:O	29:X:75:ILE:HG13	2.19	0.43
35:d:63:GLU:O	35:d:66:LYS:HD2	2.19	0.43
36:e:78:ASP:OD1	36:e:78:ASP:N	2.51	0.43
37:f:7:ARG:HG3	37:f:9:TYR:CZ	2.54	0.43
43:l:107:PHE:CE1	43:l:165:HIS:HD2	2.36	0.43
43:l:152:GLU:O	43:l:156:LEU:HG	2.18	0.43
51:t:91:PHE:CD2	51:t:245:ILE:HD11	2.53	0.43
2:1:1695:C:H2'	2:1:1696:G:C8	2.53	0.43
5:6:184:C:C2	46:o:209:LEU:HD11	2.53	0.43
8:B:133:TYR:HA	8:B:136:LYS:HG2	2.00	0.43
9:C:67:TRP:CE2	54:w:769:LYS:HG3	2.53	0.43
15:I:635:LYS:HE2	15:I:635:LYS:HB3	1.86	0.43
17:K:232:GLY:O	17:K:236:ILE:HG13	2.19	0.43
27:V:84:ARG:HA	27:V:97:PHE:O	2.19	0.43
31:Z:51:LEU:HB3	31:Z:65:ARG:NH2	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:k:10:GLN:HB2	44:m:645:PHE:O	2.18	0.43
44:m:159:LYS:HG2	44:m:180:LEU:HD11	2.01	0.43
44:m:661:ARG:HG2	44:m:676:SER:HA	2.00	0.43
47:p:157:SER:HA	47:p:171:VAL:HA	2.01	0.43
49:r:223:ASN:OD1	49:r:223:ASN:C	2.62	0.43
51:t:212:THR:HG22	51:t:214:THR:HG23	1.99	0.43
52:u:104:ARG:H	52:u:104:ARG:HG2	1.61	0.43
56:y:65:GLY:HA2	56:y:133:LEU:HD11	2.00	0.43
2:1:1155:U:H2'	2:1:1156:U:H6	1.84	0.43
2:1:1669:G:P	31:Z:111:ARG:HH22	2.41	0.43
2:1:2465:G:H5'	2:1:2466:C:C5	2.47	0.43
2:1:3470:G:C6	8:B:380:LEU:HD13	2.54	0.43
8:B:70:ARG:HH11	56:y:55:GLY:HA2	1.84	0.43
10:D:94:LEU:HD13	10:D:120:ILE:HG21	2.00	0.43
14:H:13:ILE:HD13	14:H:53:ILE:HG13	2.00	0.43
21:O:109:ILE:HD12	21:O:161:ARG:CZ	2.48	0.43
31:Z:82:PRO:HD2	34:c:73:TYR:HE1	1.84	0.43
35:d:30:PHE:HB3	35:d:70:ARG:HG2	2.00	0.43
44:m:321:ARG:HG3	51:t:172:ASN:HD22	1.83	0.43
45:n:178:ARG:NH2	45:n:192:GLU:OE2	2.52	0.43
45:n:179:LYS:HE3	45:n:190:GLN:HG2	2.00	0.43
45:n:392:PHE:CD1	45:n:392:PHE:N	2.85	0.43
45:n:414:GLU:OE1	45:n:414:GLU:N	2.51	0.43
53:v:164:HIS:O	53:v:168:GLN:HB2	2.18	0.43
2:1:698:U:H2'	2:1:699:G:C8	2.53	0.43
2:1:742:A:N7	32:a:114:LYS:HD2	2.34	0.43
2:1:892:G:OP1	2:1:893:C:H4'	2.18	0.43
2:1:1163:C:H2'	2:1:1164:A:H8	1.83	0.43
2:1:1311:C:H2'	2:1:1312:U:C6	2.54	0.43
2:1:3083:C:OP2	21:O:69:ARG:NH2	2.52	0.43
8:B:126:LYS:HB2	8:B:128:LYS:HG2	2.00	0.43
10:D:285:LEU:HD12	10:D:285:LEU:HA	1.84	0.43
12:F:93:VAL:O	12:F:121:GLY:HA2	2.18	0.43
15:I:525:GLU:OE2	54:w:695:ARG:NH2	2.52	0.43
15:I:665:GLN:HG3	15:I:666[A]:LEU:HG	2.00	0.43
21:O:65:TYR:O	21:O:65:TYR:CG	2.72	0.43
23:Q:68:ALA:O	23:Q:72:ARG:HB2	2.19	0.43
24:R:10:LEU:HB3	24:R:41:VAL:HG21	2.00	0.43
27:V:19:LEU:O	27:V:54:ALA:N	2.49	0.43
27:V:95:LEU:CD2	52:u:20:MET:HG2	2.49	0.43
27:V:131:ILE:HD13	27:V:131:ILE:HA	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Z:87:LEU:HD11	31:Z:121:LYS:HE3	2.01	0.43
37:f:51:CYS:HB3	37:f:69:TRP:CZ3	2.53	0.43
43:l:73:PHE:CZ	43:l:77:ASN:HB3	2.53	0.43
54:w:60:LEU:HD11	54:w:75:GLY:HA3	2.01	0.43
2:1:114:A:H2'	2:1:115:A:O4'	2.19	0.43
2:1:120:G:H22	13:G:126:SER:HB3	1.84	0.43
2:1:121:A:OP2	44:m:228:SER:HB2	2.19	0.43
2:1:763:G:H3'	2:1:764:U:C6	2.54	0.43
2:1:984:A:H2'	2:1:985:G:O4'	2.18	0.43
2:1:1765:C:H2'	2:1:1766:C:C6	2.54	0.43
2:1:3044:U:H2'	2:1:3045:G:C8	2.54	0.43
2:1:3300:A:H3'	2:1:3301:C:H5''	2.00	0.43
2:1:3367:A:H3'	2:1:3368:A:C8	2.54	0.43
4:3:45:LEU:HD13	9:C:139:ALA:HB2	1.99	0.43
5:6:97:C:O2'	5:6:98:G:O4'	2.37	0.43
7:A:194:ALA:C	7:A:195:ASP:OD1	2.61	0.43
9:C:275:LYS:HE3	9:C:275:LYS:HB3	1.81	0.43
9:C:343:ILE:HD13	12:F:67:ARG:HD2	2.01	0.43
15:I:231:LEU:HD23	15:I:238:ASN:HB2	2.01	0.43
15:I:707:ILE:HG13	15:I:708:GLU:N	2.33	0.43
17:K:57:LEU:CD2	17:K:224:VAL:HG11	2.49	0.43
17:K:174:THR:O	17:K:177:GLN:HG3	2.18	0.43
25:S:15:THR:OG1	25:S:16:GLU:OE1	2.35	0.43
34:c:58:ILE:HA	34:c:103:VAL:HG22	2.00	0.43
43:l:35:HIS:CE1	43:l:46:TYR:CZ	3.07	0.43
44:m:684:PHE:CD1	44:m:700:PRO:HA	2.53	0.43
2:1:1760:U:H5''	24:R:107:ARG:HH22	1.84	0.43
2:1:2210:G:H2'	2:1:2211:G:C8	2.54	0.43
2:1:2440:A:O3'	22:P:85:VAL:HG22	2.19	0.43
8:B:274:HIS:O	8:B:275:ARG:HD3	2.18	0.43
15:I:495:ILE:HD12	15:I:495:ILE:HA	1.91	0.43
15:I:632:MET:O	15:I:636:CYS:N	2.37	0.43
23:Q:43:PHE:CD2	23:Q:135:GLY:HA3	2.54	0.43
23:Q:46:ALA:O	23:Q:50:ARG:HG3	2.19	0.43
25:S:95:ASP:OD2	25:S:101:ALA:N	2.52	0.43
31:Z:12:LEU:HD21	38:g:89:ILE:CG2	2.49	0.43
32:a:82:LEU:HD23	32:a:82:LEU:HA	1.86	0.43
35:d:77:ARG:C	35:d:78:LEU:HD23	2.43	0.43
43:l:8:GLU:HB2	43:l:73:PHE:CZ	2.54	0.43
44:m:180:LEU:HD23	44:m:180:LEU:HA	1.81	0.43
49:r:184:THR:O	49:r:257:LEU:HD12	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:r:192:MET:HG2	49:r:194:LEU:HD21	2.01	0.43
56:y:199:VAL:HG21	56:y:222:PHE:CE2	2.53	0.43
2:1:361:G:O6	41:j:55:ARG:NH1	2.52	0.42
2:1:1614:U:O2	29:X:32:ARG:NH1	2.52	0.42
2:1:1669:G:OP1	31:Z:111:ARG:NH2	2.51	0.42
2:1:1833:C:H2'	2:1:1834:C:C6	2.54	0.42
2:1:3398:U:O4	8:B:124:LYS:NZ	2.52	0.42
2:1:3494:U:H2'	2:1:3495:U:C6	2.54	0.42
7:A:202:ASN:HB3	7:A:223:PRO:HD2	2.02	0.42
8:B:84:MET:HG2	8:B:164:THR:HA	2.00	0.42
9:C:147:ILE:HG23	9:C:152:LEU:HD22	2.01	0.42
13:G:206:GLU:HG2	17:K:122:ALA:HB1	2.01	0.42
19:M:85:ASN:HA	19:M:88:ALA:HB3	2.00	0.42
29:X:5:LYS:O	29:X:10:GLN:HB2	2.19	0.42
35:d:38:ILE:O	35:d:42:VAL:HG12	2.18	0.42
43:l:20:ILE:HG22	43:l:92:TYR:O	2.19	0.42
43:l:133:ILE:HD12	43:l:142:GLY:O	2.19	0.42
44:m:356:GLU:HB2	45:n:573:TYR:CD2	2.54	0.42
51:t:165:GLN:OE1	51:t:165:GLN:N	2.52	0.42
54:w:145:ALA:O	54:w:149:LEU:N	2.51	0.42
54:w:242:ARG:HG3	54:w:242:ARG:O	2.17	0.42
57:z:106:LYS:HG3	57:z:107:ASN:N	2.28	0.42
2:1:546:G:N7	25:S:143:LEU:HD13	2.34	0.42
2:1:1954:G:OP2	54:w:242:ARG:NH2	2.52	0.42
2:1:2499:U:H2'	2:1:2500:G:C8	2.55	0.42
2:1:2698:G:O2'	43:l:57:SER:O	2.34	0.42
2:1:3174:A:C5'	35:d:70:ARG:HH12	2.31	0.42
2:1:3375:U:OP2	37:f:69:TRP:NE1	2.52	0.42
8:B:382:THR:HB	52:u:105:GLU:HG3	2.01	0.42
9:C:133:VAL:HB	9:C:136:LEU:HD12	2.01	0.42
9:C:301:ILE:HD13	23:Q:134:THR:HG23	2.00	0.42
10:D:159:ARG:HH12	53:v:121:ASP:HB3	1.85	0.42
14:H:6:TYR:H	25:S:141:GLN:HE22	1.67	0.42
14:H:57:VAL:HB	14:H:68:ILE:HD11	2.01	0.42
17:K:174:THR:H	17:K:177:GLN:CD	2.26	0.42
17:K:222:GLN:C	17:K:222:GLN:OE1	2.62	0.42
18:L:48:PRO:HD3	53:v:33:ASN:HB2	2.01	0.42
25:S:137:ASN:OD1	25:S:137:ASN:C	2.62	0.42
34:c:88:ASN:OD1	34:c:88:ASN:C	2.61	0.42
44:m:233:LYS:O	44:m:237:GLN:HG3	2.20	0.42
47:p:221:VAL:O	47:p:265:CYS:N	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:v:203:ILE:HA	53:v:206:LYS:HE2	2.01	0.42
2:l:620:C:O2	9:C:329:ARG:HD3	2.18	0.42
2:l:837:G:H2'	2:l:968:A:H61	1.84	0.42
2:l:1650:C:H2'	2:l:1651:A:C8	2.54	0.42
2:l:1766:C:H2'	2:l:1767:G:C8	2.54	0.42
3:2:29:C:OP1	9:C:195:LYS:NZ	2.42	0.42
4:3:31:GLU:O	4:3:31:GLU:HG3	2.19	0.42
7:A:211:LYS:HA	7:A:215:PRO:HB3	2.00	0.42
9:C:308:SER:O	9:C:309:ARG:C	2.62	0.42
10:D:257:MET:HE2	10:D:285:LEU:HD21	2.02	0.42
10:D:501:TYR:HA	10:D:504:TYR:HD2	1.82	0.42
12:F:54:ARG:NH1	12:F:184:SER:O	2.49	0.42
14:H:18:THR:O	14:H:28:VAL:HA	2.19	0.42
14:H:101:ILE:HG12	14:H:112:ILE:HG12	2.01	0.42
27:V:29:ASP:HA	27:V:116:ILE:HA	2.00	0.42
29:X:13:VAL:HA	29:X:16:GLY:O	2.20	0.42
30:Y:30:MET:O	30:Y:49:VAL:HG22	2.18	0.42
43:l:2:ARG:O	43:l:39:LEU:HB3	2.19	0.42
44:m:610:LEU:HB3	44:m:641:PHE:CE2	2.54	0.42
47:p:201:GLU:N	47:p:215:ALA:O	2.53	0.42
56:y:79:ASN:O	56:y:82:GLN:HG3	2.19	0.42
57:z:104:ARG:O	57:z:107:ASN:HB2	2.19	0.42
2:l:70:A:N1	2:l:321:A:O2'	2.50	0.42
2:l:986:U:O4	2:l:1000:G:N1	2.53	0.42
2:l:1384:U:H4'	2:l:1385:U:O4'	2.19	0.42
2:l:1819:G:O2'	2:l:1821:G:OP2	2.37	0.42
7:A:162:LYS:HB3	16:J:104:TYR:CE1	2.54	0.42
10:D:438:LEU:HD12	10:D:438:LEU:HA	1.84	0.42
13:G:180:VAL:HG21	13:G:186:LEU:HD21	2.01	0.42
18:L:56:PRO:HG3	18:L:74:GLY:O	2.20	0.42
44:m:128:LEU:HG	44:m:130:ILE:HG13	2.01	0.42
44:m:419:TRP:CE2	44:m:421:CYS:HB3	2.54	0.42
45:n:364:VAL:HG11	45:n:403:ILE:HG22	2.01	0.42
51:t:128:ALA:O	51:t:132:MET:HG3	2.19	0.42
51:t:248:GLN:HE21	51:t:248:GLN:HB3	1.65	0.42
8:B:45:ALA:HB3	8:B:181:ILE:HD12	2.02	0.42
8:B:292:LYS:HD3	8:B:302:GLU:HG3	2.01	0.42
9:C:116:ASN:HB2	9:C:119:GLU:HG3	2.02	0.42
10:D:340:ILE:HD11	10:D:392:CYS:SG	2.59	0.42
10:D:361:LEU:O	10:D:363:VAL:HG13	2.19	0.42
13:G:205:GLU:HA	13:G:208:LYS:HG2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:J:166:ARG:NH2	16:J:170:TYR:O	2.52	0.42
16:J:169:ASP:O	44:m:131:ASN:ND2	2.44	0.42
16:J:177:SER:HB3	16:J:180:HIS:HD2	1.84	0.42
25:S:151:LEU:HB3	25:S:154:ARG:NE	2.30	0.42
26:U:33:TYR:HE2	26:U:80:LYS:HB2	1.85	0.42
29:X:60:LYS:O	29:X:86:HIS:HB2	2.20	0.42
34:c:32:MET:HE1	34:c:95:CYS:HB2	2.01	0.42
36:e:102:ARG:HD3	36:e:122:LYS:HB2	2.01	0.42
37:f:15:LEU:HD11	37:f:32:LYS:HB2	2.00	0.42
40:i:44:GLU:OE2	44:m:207:THR:OG1	2.30	0.42
42:k:26:LYS:HB3	42:k:34:LYS:HB2	2.00	0.42
43:l:35:HIS:HA	43:l:48:SER:HA	2.00	0.42
46:o:121:MET:HE1	46:o:136:MET:HB2	2.02	0.42
56:y:38:PHE:HE1	56:y:205:PHE:CG	2.38	0.42
56:y:138:PHE:N	56:y:138:PHE:CD1	2.87	0.42
2:1:63:A:P	20:N:172:ARG:HH22	2.43	0.42
2:1:772:A:H1'	23:Q:142:ARG:NH2	2.34	0.42
2:1:982:G:N1	2:1:1402:U:OP2	2.33	0.42
2:1:1396:G:H1'	12:F:166:GLN:HG2	2.01	0.42
2:1:1883:U:H2'	2:1:1884:G:C8	2.54	0.42
2:1:1950:A:N6	2:1:2423:G:O2'	2.52	0.42
2:1:3091:G:H1'	3:2:8:A:C8	2.54	0.42
2:1:3359:U:H5''	2:1:3361:U:H5	1.84	0.42
4:3:61:TYR:CD1	4:3:79:ARG:HD3	2.54	0.42
9:C:127:ALA:HB1	9:C:240:LEU:HB3	2.00	0.42
14:H:13:ILE:H	14:H:13:ILE:HG12	1.65	0.42
14:H:186:GLU:OE2	14:H:186:GLU:N	2.53	0.42
18:L:92:THR:HB	39:h:116:ARG:HG2	2.02	0.42
24:R:123:LEU:HA	24:R:126:GLU:OE1	2.20	0.42
43:l:1:MET:HE2	43:l:38:ARG:HD3	2.02	0.42
43:l:115:LYS:HB3	43:l:158:PRO:O	2.19	0.42
44:m:320:LEU:HB3	45:n:405:ASP:OD2	2.19	0.42
44:m:384:GLY:N	44:m:404:ASP:OD2	2.52	0.42
44:m:394:SER:OG	44:m:396:ASN:OD1	2.28	0.42
46:o:183:GLU:H	46:o:183:GLU:CD	2.25	0.42
54:w:178:LYS:HE2	54:w:199:ARG:HG3	2.02	0.42
56:y:28:LEU:HD23	56:y:52:THR:HG22	2.02	0.42
58:T:143:THR:OG1	58:T:148:PRO:HD3	2.20	0.42
2:1:86:G:O2'	2:1:98:G:O6	2.34	0.42
2:1:1155:U:H2'	2:1:1156:U:C6	2.54	0.42
3:2:115:G:H4'	3:2:146:A:H5'	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:123:LYS:HB3	7:A:231:ASN:OD1	2.19	0.42
16:J:127:ILE:HD13	16:J:145:GLN:HB3	2.02	0.42
25:S:22:LYS:HA	58:T:146:ASN:ND2	2.22	0.42
27:V:74:LYS:O	27:V:76:MET:HG3	2.20	0.42
27:V:91:ASP:C	27:V:91:ASP:OD1	2.62	0.42
27:V:116:ILE:HD11	27:V:136:GLY:N	2.34	0.42
44:m:403:ASP:HA	44:m:451:ILE:HG22	2.01	0.42
44:m:653:LEU:HG	45:n:563:MET:CE	2.49	0.42
50:s:13:THR:HA	50:s:16:ARG:HG2	2.01	0.42
52:u:58:ALA:O	52:u:59:HIS:ND1	2.46	0.42
52:u:83:ASP:OD1	52:u:83:ASP:C	2.62	0.42
2:1:687:U:H2'	2:1:688:C:C6	2.54	0.42
2:1:1746:C:H5'	2:1:1828:A:H4'	2.01	0.42
2:1:1757:C:H2'	2:1:1758:G:H8	1.83	0.42
2:1:3131:C:H5''	57:z:94:TRP:CD1	2.55	0.42
4:3:25:GLN:OE1	4:3:37:LEU:HD22	2.20	0.42
4:3:63:TYR:CE1	4:3:79:ARG:HG3	2.55	0.42
12:F:68:GLU:O	12:F:72:LEU:HD23	2.20	0.42
15:I:344:ILE:O	15:I:383:ILE:HD11	2.20	0.42
15:I:497:TYR:CE2	15:I:514:GLY:HA3	2.55	0.42
15:I:509:GLY:HA2	15:I:560:LEU:HD21	2.01	0.42
16:J:102:ASN:OD1	16:J:102:ASN:C	2.63	0.42
33:b:377:CYS:N	56:y:201:ASP:OD2	2.53	0.42
35:d:85:SER:OG	35:d:86:ASP:N	2.53	0.42
41:j:21:ARG:NH1	41:j:41:ALA:O	2.49	0.42
44:m:298:GLU:HG3	44:m:314:PRO:HG3	2.01	0.42
45:n:123:TYR:OH	45:n:132:ASP:OD2	2.32	0.42
51:t:91:PHE:CZ	51:t:120:ALA:HB1	2.55	0.42
54:w:180:GLU:HG3	54:w:199:ARG:HH21	1.85	0.42
56:y:18:ASN:HB3	56:y:25:LEU:HD12	2.02	0.42
2:1:518:U:H2'	2:1:519:U:C6	2.54	0.42
2:1:602:A:H1'	9:C:334:ALA:HB1	2.00	0.42
2:1:1158:G:N2	2:1:1163:C:O2	2.53	0.42
2:1:1763:A:OP1	24:R:103:ARG:NH2	2.53	0.42
2:1:1790:A:OP1	42:k:36:LYS:NZ	2.42	0.42
2:1:1844:C:O3'	38:g:70:LYS:HE3	2.19	0.42
2:1:2695:C:H2'	2:1:2696:A:H8	1.85	0.42
3:2:162:C:OP1	13:G:181:LYS:NZ	2.41	0.42
4:3:8:TRP:HB2	4:3:46:ALA:HB1	2.02	0.42
8:B:56:ILE:HG22	8:B:359:ILE:HA	2.02	0.42
9:C:177:TYR:CE2	9:C:181:ILE:HD11	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:E:60:LEU:HD12	11:E:60:LEU:HA	1.94	0.42
15:I:682:LEU:O	15:I:684:ARG:NH1	2.53	0.42
16:J:96:ASN:OD1	16:J:96:ASN:C	2.63	0.42
16:J:132:VAL:HA	16:J:138:ARG:HD3	2.01	0.42
16:J:179:ASP:OD1	16:J:179:ASP:C	2.63	0.42
18:L:43:ALA:O	18:L:47:ALA:HA	2.19	0.42
23:Q:53:GLN:O	23:Q:58:ARG:NH1	2.52	0.42
42:k:53:LYS:HD3	42:k:56:LYS:HD3	2.02	0.42
42:k:58:ARG:HH11	42:k:58:ARG:CB	2.33	0.42
43:l:24:ILE:H	43:l:24:ILE:HG13	1.61	0.42
45:n:129:ALA:O	45:n:133:ILE:HG12	2.20	0.42
45:n:206:PHE:HB2	45:n:208:GLN:NE2	2.34	0.42
45:n:366:ARG:NH1	45:n:387:GLY:HA3	2.34	0.42
45:n:408:HIS:HE1	45:n:410:SER:HB3	1.84	0.42
56:y:85:ARG:HD2	56:y:85:ARG:HA	1.77	0.42
57:z:98:HIS:O	57:z:101:LYS:HG2	2.19	0.42
2:1:1227:C:H42	50:s:9:LYS:CB	2.33	0.42
2:1:1778:A:H2'	2:1:1779:U:H6	1.85	0.42
2:1:2978:U:H3	2:1:3034:G:H1	1.68	0.42
9:C:177:TYR:O	9:C:181:ILE:HG12	2.20	0.42
12:F:150:THR:HG23	12:F:246:VAL:HG11	2.00	0.42
16:J:115:PHE:CD1	16:J:115:PHE:C	2.98	0.42
21:O:173:LEU:O	21:O:177:LYS:HG2	2.20	0.42
27:V:59:MET:HE3	27:V:59:MET:HB2	1.83	0.42
31:Z:64:ARG:HE	31:Z:64:ARG:HB2	1.72	0.42
43:l:35:HIS:HE1	43:l:46:TYR:CE2	2.38	0.42
44:m:113:GLU:OE1	44:m:113:GLU:N	2.53	0.42
44:m:329:LEU:HD23	45:n:203:PRO:HB3	2.02	0.42
44:m:362:LEU:HD23	44:m:362:LEU:H	1.84	0.42
44:m:413:MET:N	44:m:413:MET:SD	2.93	0.42
44:m:488:GLU:HG3	44:m:491:LYS:NZ	2.35	0.42
2:1:672:A:H4'	2:1:2461:A:C8	2.54	0.41
2:1:1320:G:H2'	2:1:1321:A:H8	1.85	0.41
2:1:2949:U:H2'	2:1:2950:U:C6	2.55	0.41
3:2:131:G:H4'	3:2:132:G:OP1	2.20	0.41
5:6:61:U:H4'	46:o:211:HIS:ND1	2.34	0.41
19:M:4:PHE:HB3	25:S:176:TYR:HE2	1.85	0.41
24:R:134:HIS:CE1	24:R:136:ARG:HG2	2.55	0.41
43:l:2:ARG:HE	43:l:60:ARG:NH1	2.18	0.41
45:n:182:LEU:HD21	45:n:425:TYR:CZ	2.55	0.41
46:o:127:GLN:HE22	51:t:52:LYS:HB2	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:w:16:TRP:CE3	54:w:16:TRP:HA	2.55	0.41
54:w:697:ILE:HG13	54:w:698:LYS:N	2.35	0.41
2:1:651:U:H2'	2:1:652:U:C6	2.54	0.41
2:1:1689:A:OP1	38:g:43:ARG:NH1	2.48	0.41
7:A:89:LEU:HG	40:i:78:LEU:HD22	2.02	0.41
11:E:165:LEU:HD13	11:E:168:ILE:HD11	2.01	0.41
13:G:67:LEU:HD13	54:w:452:ARG:HD2	2.01	0.41
13:G:68:ARG:NH2	13:G:246:LEU:HD11	2.35	0.41
15:I:535:ARG:HB3	15:I:586:PHE:CZ	2.56	0.41
15:I:685:TYR:CE2	15:I:687:LYS:HB2	2.55	0.41
17:K:265:ARG:NH1	46:o:213:LYS:HG2	2.35	0.41
25:S:79:ARG:HH22	25:S:86:THR:HA	1.85	0.41
30:Y:31:SER:HA	30:Y:48:PRO:HA	2.01	0.41
32:a:74:ASN:OD1	32:a:112:LEU:HB2	2.20	0.41
43:l:69:CYS:O	43:l:84:THR:OG1	2.37	0.41
44:m:314:PRO:HB2	44:m:315:LYS:H	1.62	0.41
44:m:653:LEU:HG	45:n:563:MET:HE3	2.02	0.41
45:n:146:MET:HE3	45:n:146:MET:HB3	1.74	0.41
49:r:220:ILE:O	49:r:242:ALA:N	2.51	0.41
51:t:81:ILE:HD13	51:t:134:ARG:HB2	2.02	0.41
54:w:35:GLN:HE22	54:w:186:SER:HB3	1.84	0.41
2:1:80:C:H2'	2:1:81:C:C6	2.55	0.41
2:1:890:A:H2'	2:1:891:G:C8	2.55	0.41
2:1:2903:A:N7	49:r:205:SER:OG	2.50	0.41
2:1:3196:C:H41	57:z:87:ARG:HG2	1.86	0.41
4:3:6:VAL:HG23	9:C:287:ALA:HB1	2.01	0.41
5:6:6:C:C4	17:K:152:ARG:HD2	2.55	0.41
14:H:81:GLY:HA2	14:H:85:GLY:HA2	2.02	0.41
15:I:334:GLN:HG2	15:I:371:PRO:HB2	2.01	0.41
26:U:31:GLU:OE1	26:U:55:ARG:NH1	2.54	0.41
27:V:61:LEU:HD13	27:V:75:ILE:HG22	2.02	0.41
36:e:121:ALA:C	36:e:123:VAL:H	2.28	0.41
43:l:151:LEU:HA	43:l:154:ARG:HE	1.85	0.41
44:m:333:LYS:HG3	45:n:142:LEU:HD22	2.01	0.41
44:m:366:SER:HA	44:m:369:ARG:HH21	1.85	0.41
44:m:370:PRO:HB2	44:m:671:LEU:HD11	2.02	0.41
45:n:181:PHE:HB3	45:n:188:TYR:HB2	2.02	0.41
45:n:207:ALA:O	51:t:168:ALA:HB1	2.20	0.41
52:u:84:ARG:O	52:u:87:ILE:HG22	2.20	0.41
56:y:197:LEU:HD12	56:y:205:PHE:O	2.20	0.41
2:1:1707:U:H2'	2:1:1708:G:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1711:A:H2'	2:1:1712:A:H8	1.84	0.41
2:1:1726:U:H2'	2:1:1727:U:C6	2.55	0.41
2:1:3134:U:OP1	8:B:348:ARG:HB2	2.21	0.41
3:2:150:C:H2'	3:2:151:U:C6	2.55	0.41
6:8:23:ILE:CG2	6:8:27:ILE:HG21	2.51	0.41
9:C:346:GLU:CD	9:C:347:LYS:H	2.28	0.41
17:K:16:VAL:HG11	17:K:251:LEU:HD13	2.03	0.41
29:X:61:ILE:O	29:X:86:HIS:N	2.50	0.41
44:m:507:ARG:HB3	44:m:524:THR:OG1	2.20	0.41
44:m:726:TRP:CD1	44:m:740:THR:HA	2.55	0.41
45:n:360:LEU:HD13	45:n:403:ILE:HB	2.03	0.41
45:n:366:ARG:HB3	45:n:386:LEU:HD12	2.03	0.41
50:s:13:THR:HA	50:s:16:ARG:HE	1.84	0.41
54:w:16:TRP:HE1	54:w:186:SER:HA	1.84	0.41
54:w:709:MET:HE3	54:w:710:ARG:N	2.35	0.41
2:1:531:A:H2'	9:C:350:LYS:HD2	2.03	0.41
2:1:1716:U:H2'	2:1:1717:U:H6	1.84	0.41
10:D:316:VAL:HG22	10:D:462:PHE:HB2	2.02	0.41
16:J:179:ASP:OD1	16:J:183:LYS:HE3	2.21	0.41
17:K:42:LEU:HD12	17:K:43:LEU:O	2.21	0.41
17:K:153:ILE:O	17:K:154:LEU:HD23	2.21	0.41
24:R:56:LEU:HD23	24:R:56:LEU:H	1.86	0.41
43:l:112:HIS:HB3	43:l:164:PHE:HA	2.02	0.41
52:u:2:ARG:HE	52:u:3:VAL:N	2.18	0.41
53:v:130:ILE:HG23	53:v:131:ALA:N	2.35	0.41
2:1:146:U:H2'	2:1:147:C:C6	2.55	0.41
2:1:417:A:H61	3:2:23:G:H1'	1.85	0.41
2:1:862:A:H61	2:1:896:G:H1	1.68	0.41
2:1:864:G:H1	2:1:894:U:H3	1.69	0.41
2:1:895:C:H2'	2:1:896:G:C8	2.56	0.41
2:1:1761:U:O2'	2:1:1763:A:N7	2.45	0.41
2:1:1911:C:H2'	2:1:1912:C:C6	2.55	0.41
2:1:2457:G:H5''	50:s:12:THR:HG22	2.02	0.41
3:2:128:U:P	45:n:74:HIS:HE2	2.44	0.41
4:3:80:ILE:HD13	4:3:96:GLN:HG3	2.01	0.41
8:B:351:LEU:HD11	57:z:106:LYS:HD3	2.02	0.41
13:G:206:GLU:H	13:G:206:GLU:HG3	1.72	0.41
17:K:145:ARG:NH1	17:K:171:SER:HA	2.35	0.41
17:K:147:ILE:H	17:K:147:ILE:HG12	1.74	0.41
17:K:169:LYS:O	17:K:181:GLU:HG3	2.21	0.41
19:M:65:LEU:HD23	19:M:66:PRO:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:N:148:ILE:HG13	20:N:148:ILE:O	2.20	0.41
26:U:34:LEU:O	26:U:38:ILE:HG12	2.21	0.41
29:X:10:GLN:HG2	46:o:127:GLN:C	2.45	0.41
34:c:41:TYR:CE1	34:c:70:LEU:HD11	2.55	0.41
40:i:48:PHE:HB3	40:i:52:GLU:HB2	2.02	0.41
41:j:27:PHE:HA	41:j:34:CYS:HA	2.02	0.41
43:l:116:ALA:HB2	43:l:158:PRO:CB	2.42	0.41
44:m:655:TYR:CZ	45:n:563:MET:SD	3.14	0.41
49:r:254:VAL:HG23	49:r:254:VAL:O	2.20	0.41
53:v:122:ASP:OD1	53:v:123:VAL:N	2.53	0.41
2:1:644:A:H1'	2:1:646:A:C6	2.56	0.41
2:1:732:A:N7	32:a:74:ASN:ND2	2.52	0.41
2:1:1643:C:H5''	29:X:110:ASN:HD22	1.85	0.41
6:8:35:VAL:CG1	6:8:36:HIS:N	2.83	0.41
7:A:106:ARG:HA	7:A:106:ARG:HD3	1.95	0.41
9:C:72:ALA:HB3	54:w:766:LYS:HG3	2.02	0.41
15:I:522:LEU:HG	15:I:526:PHE:HD2	1.86	0.41
21:O:174:ALA:O	21:O:178:LYS:HG3	2.21	0.41
22:P:124:LYS:HE2	22:P:124:LYS:HB3	1.79	0.41
36:e:93:ILE:HG12	36:e:105:ILE:HG21	2.03	0.41
54:w:229:ASP:OD1	54:w:230:ALA:N	2.53	0.41
57:z:105:ALA:O	57:z:108:SER:N	2.52	0.41
2:1:302:U:H4'	40:i:75:LEU:HD23	2.03	0.41
2:1:441:A:H2'	2:1:442:U:O4'	2.21	0.41
2:1:546:G:C6	25:S:143:LEU:HD22	2.55	0.41
2:1:717:A:H5''	2:1:719:A:C5	2.55	0.41
2:1:1700:G:H1	2:1:1825:U:H3	1.67	0.41
2:1:3361:U:OP1	19:M:119:GLN:NE2	2.24	0.41
4:3:10:VAL:O	4:3:14:GLU:HB2	2.21	0.41
7:A:67:MET:HA	16:J:175:LEU:HD21	2.01	0.41
8:B:55:HIS:HD2	8:B:73:LEU:HD11	1.86	0.41
8:B:213:GLU:HB3	57:z:110:PHE:CE2	2.56	0.41
8:B:286:GLY:HA3	8:B:321:PHE:CZ	2.55	0.41
12:F:67:ARG:O	12:F:71:GLU:HG2	2.21	0.41
12:F:98:GLY:O	12:F:102:ILE:HD11	2.21	0.41
15:I:636:CYS:O	15:I:640:PHE:HB2	2.21	0.41
15:I:667:PRO:HB2	15:I:669:HIS:HD1	1.86	0.41
15:I:729:HIS:CG	15:I:730:TYR:N	2.89	0.41
16:J:99:ALA:O	16:J:103:ILE:HG22	2.21	0.41
17:K:56:GLN:HE21	17:K:56:GLN:HB3	1.65	0.41
25:S:37:LYS:HE3	25:S:57:ILE:HG21	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:e:102:ARG:NE	36:e:121:ALA:O	2.54	0.41
43:l:73:PHE:CE2	43:l:77:ASN:HB3	2.55	0.41
44:m:132:TYR:CE1	44:m:138:LYS:HG3	2.56	0.41
44:m:325:ALA:HB2	45:n:206:PHE:CD2	2.55	0.41
44:m:685:HIS:HB3	44:m:699:VAL:HG23	2.01	0.41
46:o:112:LEU:HD23	46:o:176:LEU:HD11	2.02	0.41
49:r:219:VAL:HG21	49:r:259:LEU:HD11	2.03	0.41
51:t:95:ILE:CG1	51:t:141:MET:HB2	2.51	0.41
56:y:129:ILE:O	56:y:133:LEU:HB2	2.21	0.41
2:1:609:A:H2'	2:1:610:C:C6	2.56	0.41
2:1:613:A:H1'	2:1:1368:A:H5''	2.02	0.41
2:1:644:A:O2'	2:1:646:A:N7	2.53	0.41
2:1:740:U:H2'	2:1:741:G:O4'	2.21	0.41
2:1:873:A:H5''	24:R:125:LEU:HD23	2.03	0.41
2:1:1163:C:H2'	2:1:1164:A:C8	2.55	0.41
2:1:1629:A:H1'	2:1:1650:C:H1'	2.03	0.41
2:1:1695:C:H2'	2:1:1696:G:H8	1.86	0.41
2:1:1713:G:H2'	2:1:1714:A:C8	2.56	0.41
2:1:1827:G:H2'	2:1:1828:A:C8	2.56	0.41
2:1:2972:G:O2'	2:1:2973:G:OP2	2.33	0.41
2:1:3415:U:H2'	2:1:3416:A:C8	2.56	0.41
4:3:32:TYR:HD1	4:3:52:THR:HG21	1.86	0.41
7:A:50:SER:HB3	7:A:100:PHE:CZ	2.55	0.41
8:B:47:LEU:HD22	8:B:179:MET:SD	2.60	0.41
8:B:171:LEU:HD21	8:B:333:LYS:HB2	2.01	0.41
10:D:296:TYR:OH	10:D:298:ASN:OD1	2.23	0.41
11:E:57:VAL:HG11	11:E:177:TYR:HE2	1.85	0.41
11:E:169:LYS:NZ	11:E:175:LYS:HG3	2.36	0.41
15:I:502:GLN:HB2	44:m:148:LEU:CD2	2.51	0.41
16:J:110:PRO:HB2	16:J:113:ILE:HG23	2.03	0.41
16:J:176:LYS:HD2	16:J:180:HIS:CE1	2.55	0.41
17:K:74:ILE:HG12	17:K:223:PHE:CD1	2.56	0.41
17:K:174:THR:HG22	17:K:175:ALA:N	2.36	0.41
17:K:256:ASN:O	17:K:260:LEU:HG	2.21	0.41
19:M:41:SER:HB3	19:M:46:PHE:HB3	2.01	0.41
21:O:66:ASN:C	21:O:68:SER:N	2.78	0.41
26:U:89:ASP:OD1	26:U:89:ASP:C	2.64	0.41
34:c:68:SER:HB2	38:g:94:LEU:HD13	2.03	0.41
34:c:88:ASN:OD1	34:c:89:ILE:N	2.54	0.41
34:c:97:LYS:HB3	34:c:99:PHE:CE1	2.56	0.41
42:k:25:ILE:HG23	42:k:33:VAL:HG13	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:m:298:GLU:CG	44:m:314:PRO:HG3	2.51	0.41
44:m:482:PHE:HB3	44:m:486:GLN:OE1	2.21	0.41
44:m:587:TYR:CE1	44:m:607:VAL:HG21	2.55	0.41
45:n:591:ARG:HA	45:n:594:LYS:HG2	2.02	0.41
47:p:130:ASP:N	47:p:134:GLU:O	2.50	0.41
49:r:241:TYR:HB2	49:r:259:LEU:HD12	2.02	0.41
50:s:15:LEU:O	50:s:18:ARG:HG2	2.21	0.41
56:y:17:SER:HB3	56:y:34:PHE:HE2	1.86	0.41
56:y:18:ASN:HB3	56:y:25:LEU:HB2	2.02	0.41
2:1:233:C:H2'	2:1:234:G:O4'	2.21	0.41
2:1:1950:A:O2'	2:1:3149:G:H4'	2.21	0.41
2:1:2416:U:O2'	54:w:161:ARG:HD2	2.21	0.41
6:8:35:VAL:HG23	55:x:9:VAL:HG13	2.02	0.41
7:A:39:VAL:O	7:A:41:ILE:HD12	2.21	0.41
8:B:325:ASN:OD1	8:B:325:ASN:N	2.52	0.41
10:D:323:ARG:HG2	10:D:411:TYR:CE1	2.56	0.41
24:R:57:MET:HE1	24:R:58:HIS:CD2	2.56	0.41
25:S:151:LEU:H	25:S:154:ARG:HH21	1.69	0.41
29:X:67:ASN:HB2	29:X:72:MET:HE3	2.01	0.41
31:Z:15:ARG:HG3	31:Z:79:HIS:CD2	2.56	0.41
31:Z:95:LEU:HD23	31:Z:96:ILE:N	2.35	0.41
42:k:9:LYS:HB3	42:k:9:LYS:HE2	1.73	0.41
42:k:13:GLU:OE1	42:k:13:GLU:HA	2.20	0.41
44:m:389:LEU:HD11	44:m:728:PHE:HB3	2.02	0.41
44:m:421:CYS:HB2	44:m:517:HIS:ND1	2.36	0.41
46:o:115:GLY:HA2	51:t:61:TYR:CD1	2.56	0.41
54:w:95:THR:HG22	54:w:100:ARG:NH1	2.36	0.41
54:w:240:ARG:HD2	54:w:240:ARG:N	2.36	0.41
2:1:356:A:H4'	2:1:375:A:N6	2.36	0.40
2:1:1416:G:OP2	9:C:190:ARG:NH1	2.54	0.40
2:1:1531:C:H2'	2:1:1532:A:C8	2.56	0.40
2:1:1711:A:H2'	2:1:1712:A:C8	2.56	0.40
2:1:1851:A:H4'	2:1:1852:G:OP1	2.20	0.40
2:1:2995:A:H5''	14:H:169:ASP:OD2	2.22	0.40
2:1:3416:A:C5	8:B:123:PHE:CE1	3.09	0.40
8:B:292:LYS:HA	8:B:292:LYS:HD2	1.91	0.40
11:E:160:VAL:O	11:E:164:LEU:HD23	2.20	0.40
12:F:210:TRP:CD1	12:F:211:PRO:HD2	2.56	0.40
24:R:136:ARG:HA	24:R:139:ILE:HG13	2.02	0.40
31:Z:61:ARG:HA	31:Z:64:ARG:NE	2.36	0.40
32:a:75:LEU:HA	32:a:75:LEU:HD23	1.89	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:c:100:ARG:HG3	34:c:100:ARG:NH1	2.34	0.40
43:l:19:TYR:CE2	43:l:143:PHE:HB3	2.56	0.40
43:l:164:PHE:CD1	43:l:164:PHE:N	2.87	0.40
44:m:357:SER:O	44:m:360:PRO:HD2	2.21	0.40
44:m:650:TYR:OH	44:m:695:ASN:ND2	2.54	0.40
44:m:716:LEU:HD23	44:m:716:LEU:HA	1.93	0.40
45:n:134:ASP:OD1	45:n:134:ASP:N	2.55	0.40
45:n:147:PRO:HB2	51:t:157:ARG:NH2	2.36	0.40
45:n:394:GLU:O	45:n:416:ARG:NH1	2.35	0.40
49:r:167:TYR:CD2	49:r:168:GLU:HG3	2.56	0.40
54:w:143:LYS:HA	54:w:143:LYS:HD3	1.79	0.40
2:1:686:G:H4'	2:1:687:U:C6	2.56	0.40
2:1:839:A:N6	2:1:967:U:H3	2.15	0.40
2:1:1378:U:OP1	9:C:306:GLY:N	2.50	0.40
2:1:1528:U:H4'	2:1:1529:U:O5'	2.21	0.40
2:1:1540:A:O2'	2:1:1541:G:OP1	2.29	0.40
2:1:1572:G:H2'	2:1:1573:A:C8	2.56	0.40
2:1:1692:C:C5	2:1:1838:A:H8	2.38	0.40
2:1:1769:A:H5'	34:c:41:TYR:HB2	2.04	0.40
2:1:2517:G:H2'	2:1:2518:A:H8	1.85	0.40
2:1:3096:G:H2'	2:1:3097:U:C6	2.56	0.40
4:3:7:ILE:O	4:3:11:VAL:HG22	2.21	0.40
4:3:33:ASN:ND2	4:3:42:SER:O	2.54	0.40
8:B:107:ALA:HB1	8:B:200:GLU:HG3	2.01	0.40
18:L:25:TRP:O	20:N:199:ARG:HD2	2.21	0.40
27:V:76:MET:HE1	27:V:104:ILE:HG23	2.03	0.40
27:V:86:ALA:HA	27:V:96:TYR:HB3	2.03	0.40
35:d:49:MET:O	35:d:82:ARG:NH2	2.54	0.40
35:d:106:MET:HE3	35:d:106:MET:HB3	1.81	0.40
44:m:388:CYS:HB3	44:m:454:SER:HA	2.04	0.40
44:m:389:LEU:HD22	44:m:730:ALA:HB2	2.02	0.40
44:m:483:SER:O	44:m:487:ILE:HD12	2.22	0.40
49:r:172:ARG:HH21	49:r:211:LEU:HD23	1.86	0.40
58:T:102:ARG:NH1	58:T:102:ARG:HA	2.36	0.40
2:1:389:U:H2'	2:1:390:U:C6	2.56	0.40
2:1:654:U:H2'	2:1:655:C:C6	2.56	0.40
2:1:1494:A:H5'	35:d:56:VAL:O	2.22	0.40
2:1:2905:C:H2'	2:1:2906:A:H8	1.86	0.40
7:A:83:LEU:HD11	7:A:100:PHE:CE2	2.56	0.40
17:K:49:ASP:OD1	17:K:49:ASP:N	2.53	0.40
25:S:79:ARG:HH22	25:S:86:THR:HG23	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:U:10:ASN:O	26:U:10:ASN:ND2	2.54	0.40
26:U:25:PHE:HB3	26:U:30:PHE:CE1	2.56	0.40
29:X:106:PRO:HB3	29:X:123:VAL:HG13	2.03	0.40
43:l:33:ASP:O	43:l:35:HIS:N	2.53	0.40
44:m:660:LEU:HA	44:m:676:SER:HB2	2.04	0.40
46:o:168:ASN:N	46:o:176:LEU:O	2.53	0.40
47:p:161:ALA:HA	47:p:167:ILE:HA	2.02	0.40
51:t:107:LYS:O	51:t:110:ARG:HG2	2.21	0.40
53:v:72:ASP:HA	53:v:73:PRO:HD3	1.93	0.40
54:w:16:TRP:HA	54:w:16:TRP:HE3	1.86	0.40
54:w:299:ILE:HD13	54:w:320:TRP:CD1	2.55	0.40
2:1:59:G:H2'	3:2:41:A:O2'	2.20	0.40
2:1:123:A:H1'	44:m:230:HIS:HB3	2.04	0.40
2:1:942:G:OP2	2:1:942:G:H8	2.05	0.40
2:1:949:A:O2'	2:1:950:C:H5'	2.22	0.40
2:1:1422:U:OP1	36:e:101:LYS:HE3	2.21	0.40
2:1:1930:G:OP1	24:R:19:LYS:HG3	2.21	0.40
2:1:3026:C:H2'	2:1:3027:U:O4'	2.22	0.40
9:C:190:ARG:HD2	9:C:194:GLY:HA3	2.03	0.40
13:G:183:LYS:HD3	13:G:194:THR:CG2	2.51	0.40
14:H:151:ASN:O	14:H:155:SER:OG	2.32	0.40
14:H:168:LYS:HB3	14:H:173:PHE:CD2	2.56	0.40
16:J:186:GLN:O	16:J:189:ILE:HG12	2.21	0.40
21:O:55:TYR:CE2	21:O:59:LEU:HD21	2.56	0.40
26:U:39:LYS:HB2	26:U:73:TYR:OH	2.21	0.40
31:Z:120:GLU:C	31:Z:120:GLU:OE1	2.65	0.40
43:l:18:GLN:O	43:l:129:GLN:NE2	2.55	0.40
43:l:91:GLN:HG3	43:l:92:TYR:CE1	2.57	0.40
44:m:166:ASP:OD1	44:m:166:ASP:N	2.55	0.40
44:m:297:GLU:HB2	45:n:453:VAL:HG21	2.03	0.40
44:m:640:TRP:O	44:m:650:TYR:N	2.51	0.40
53:v:168:GLN:HG2	53:v:205:MET:HE1	2.02	0.40
54:w:95:THR:HG23	54:w:144:LEU:HB3	2.04	0.40
56:y:26:VAL:HG21	56:y:35:TYR:CD2	2.56	0.40
56:y:215:LEU:HD23	56:y:215:LEU:HA	1.86	0.40
2:1:674:A:H2'	2:1:675:C:C6	2.56	0.40
2:1:3182:G:H22	2:1:3477:A:H62	1.69	0.40
2:1:3269:A:H4'	2:1:3272:U:O2	2.22	0.40
3:2:70:C:H4'	3:2:71:G:O5'	2.21	0.40
4:3:128:LYS:O	4:3:130:GLN:NE2	2.55	0.40
13:G:228:GLU:OE2	13:G:232:LYS:NZ	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:H:35:LEU:HD21	14:H:147:ASN:CB	2.51	0.40
15:I:491:LYS:HE3	44:m:155:ILE:O	2.22	0.40
16:J:115:PHE:HD1	16:J:157:LEU:HD21	1.87	0.40
22:P:7:SER:N	22:P:8:PRO:HD2	2.37	0.40
24:R:115:ILE:HG23	24:R:119:LEU:HD23	2.03	0.40
24:R:119:LEU:HD12	24:R:122:THR:OG1	2.21	0.40
27:V:29:ASP:N	27:V:29:ASP:OD1	2.49	0.40
44:m:204:ASP:O	44:m:208:ASN:ND2	2.52	0.40
44:m:406:VAL:HA	44:m:422:SER:HB2	2.03	0.40
44:m:419:TRP:NE1	44:m:421:CYS:HB3	2.37	0.40
53:v:121:ASP:OD1	53:v:121:ASP:N	2.53	0.40
58:T:103:GLN:HE21	58:T:107:ASP:CG	2.28	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	7	235/707 (33%)	234 (100%)	1 (0%)	0	100	100
4	3	158/302 (52%)	150 (95%)	8 (5%)	0	100	100
6	8	33/51 (65%)	31 (94%)	2 (6%)	0	100	100
7	A	209/295 (71%)	197 (94%)	12 (6%)	0	100	100
8	B	335/388 (86%)	323 (96%)	12 (4%)	0	100	100
9	C	357/363 (98%)	334 (94%)	23 (6%)	0	100	100
10	D	421/578 (73%)	412 (98%)	9 (2%)	0	100	100
11	E	163/195 (84%)	150 (92%)	13 (8%)	0	100	100
12	F	235/250 (94%)	227 (97%)	8 (3%)	0	100	100
13	G	203/259 (78%)	193 (95%)	8 (4%)	2 (1%)	12	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	H	181/190 (95%)	172 (95%)	8 (4%)	1 (1%)	21	51
15	I	447/747 (60%)	422 (94%)	23 (5%)	2 (0%)	30	60
16	J	116/333 (35%)	111 (96%)	5 (4%)	0	100	100
17	K	247/373 (66%)	227 (92%)	18 (7%)	2 (1%)	16	44
18	L	114/208 (55%)	110 (96%)	4 (4%)	0	100	100
19	M	123/134 (92%)	117 (95%)	6 (5%)	0	100	100
20	N	160/201 (80%)	158 (99%)	2 (1%)	0	100	100
21	O	194/197 (98%)	190 (98%)	4 (2%)	0	100	100
22	P	153/187 (82%)	147 (96%)	6 (4%)	0	100	100
23	Q	131/187 (70%)	127 (97%)	4 (3%)	0	100	100
24	R	110/193 (57%)	109 (99%)	1 (1%)	0	100	100
25	S	164/176 (93%)	156 (95%)	8 (5%)	0	100	100
26	U	96/117 (82%)	89 (93%)	7 (7%)	0	100	100
27	V	130/139 (94%)	126 (97%)	4 (3%)	0	100	100
28	W	207/241 (86%)	194 (94%)	13 (6%)	0	100	100
29	X	128/141 (91%)	125 (98%)	3 (2%)	0	100	100
30	Y	123/126 (98%)	119 (97%)	4 (3%)	0	100	100
31	Z	132/136 (97%)	128 (97%)	4 (3%)	0	100	100
32	a	78/148 (53%)	77 (99%)	1 (1%)	0	100	100
33	b	393/642 (61%)	382 (97%)	11 (3%)	0	100	100
34	c	94/117 (80%)	93 (99%)	1 (1%)	0	100	100
35	d	93/113 (82%)	91 (98%)	2 (2%)	0	100	100
36	e	119/127 (94%)	117 (98%)	2 (2%)	0	100	100
37	f	104/108 (96%)	96 (92%)	8 (8%)	0	100	100
38	g	104/112 (93%)	101 (97%)	3 (3%)	0	100	100
39	h	119/122 (98%)	117 (98%)	2 (2%)	0	100	100
40	i	83/99 (84%)	83 (100%)	0	0	100	100
41	j	69/91 (76%)	67 (97%)	2 (3%)	0	100	100
42	k	68/74 (92%)	67 (98%)	1 (2%)	0	100	100
43	l	172/180 (96%)	163 (95%)	9 (5%)	0	100	100
44	m	558/740 (75%)	527 (94%)	30 (5%)	1 (0%)	43	72

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	n	427/607 (70%)	404 (95%)	23 (5%)	0	100	100
46	o	135/276 (49%)	130 (96%)	5 (4%)	0	100	100
47	p	280/440 (64%)	271 (97%)	9 (3%)	0	100	100
48	q	337/608 (55%)	332 (98%)	5 (2%)	0	100	100
49	r	158/260 (61%)	158 (100%)	0	0	100	100
50	s	30/470 (6%)	29 (97%)	1 (3%)	0	100	100
51	t	233/249 (94%)	220 (94%)	13 (6%)	0	100	100
52	u	112/192 (58%)	105 (94%)	7 (6%)	0	100	100
53	v	157/209 (75%)	150 (96%)	6 (4%)	1 (1%)	21	51
54	w	495/802 (62%)	476 (96%)	19 (4%)	0	100	100
55	x	41/306 (13%)	41 (100%)	0	0	100	100
56	y	223/244 (91%)	215 (96%)	8 (4%)	0	100	100
57	z	33/117 (28%)	31 (94%)	2 (6%)	0	100	100
58	T	30/160 (19%)	30 (100%)	0	0	100	100
All	All	10050/15027 (67%)	9651 (96%)	390 (4%)	9 (0%)	49	77

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	I	698	ILE
17	K	153	ILE
13	G	227[A]	ASP
13	G	227[B]	ASP
15	I	624	VAL
53	v	130	ILE
17	K	14	GLU
44	m	115	VAL
14	H	14	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	3	141/271 (52%)	133 (94%)	8 (6%)	18	49
6	8	31/47 (66%)	29 (94%)	2 (6%)	15	43
7	A	184/266 (69%)	183 (100%)	1 (0%)	81	93
8	B	285/326 (87%)	284 (100%)	1 (0%)	84	94
9	C	296/297 (100%)	294 (99%)	2 (1%)	76	91
10	D	371/505 (74%)	370 (100%)	1 (0%)	86	95
11	E	135/155 (87%)	132 (98%)	3 (2%)	45	78
12	F	199/210 (95%)	198 (100%)	1 (0%)	81	93
13	G	168/212 (79%)	166 (99%)	2 (1%)	63	87
14	H	164/170 (96%)	161 (98%)	3 (2%)	51	82
15	I	418/685 (61%)	417 (100%)	1 (0%)	87	96
16	J	104/288 (36%)	101 (97%)	3 (3%)	37	73
17	K	224/333 (67%)	222 (99%)	2 (1%)	70	89
18	L	97/167 (58%)	96 (99%)	1 (1%)	68	88
19	M	108/113 (96%)	107 (99%)	1 (1%)	70	89
20	N	146/176 (83%)	146 (100%)	0	100	100
21	O	161/162 (99%)	161 (100%)	0	100	100
22	P	128/149 (86%)	128 (100%)	0	100	100
23	Q	114/159 (72%)	114 (100%)	0	100	100
24	R	102/162 (63%)	101 (99%)	1 (1%)	68	88
25	S	150/154 (97%)	147 (98%)	3 (2%)	48	80
26	U	85/103 (82%)	84 (99%)	1 (1%)	63	87
27	V	103/107 (96%)	101 (98%)	2 (2%)	50	81
29	X	114/122 (93%)	113 (99%)	1 (1%)	70	89
30	Y	110/111 (99%)	108 (98%)	2 (2%)	51	82
31	Z	113/115 (98%)	112 (99%)	1 (1%)	70	89
32	a	68/122 (56%)	67 (98%)	1 (2%)	57	84
34	c	77/91 (85%)	76 (99%)	1 (1%)	61	86
35	d	89/102 (87%)	87 (98%)	2 (2%)	45	78
36	e	103/107 (96%)	102 (99%)	1 (1%)	68	88
37	f	89/91 (98%)	89 (100%)	0	100	100
38	g	92/97 (95%)	92 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	h	106/107 (99%)	105 (99%)	1 (1%)	70	89
40	i	74/84 (88%)	74 (100%)	0	100	100
41	j	58/71 (82%)	58 (100%)	0	100	100
42	k	63/66 (96%)	61 (97%)	2 (3%)	34	70
43	l	152/158 (96%)	149 (98%)	3 (2%)	48	80
44	m	506/659 (77%)	501 (99%)	5 (1%)	68	88
45	n	379/532 (71%)	376 (99%)	3 (1%)	73	90
46	o	123/246 (50%)	122 (99%)	1 (1%)	73	90
49	r	146/224 (65%)	144 (99%)	2 (1%)	59	85
50	s	29/409 (7%)	29 (100%)	0	100	100
51	t	211/223 (95%)	211 (100%)	0	100	100
52	u	99/168 (59%)	95 (96%)	4 (4%)	28	63
53	v	138/181 (76%)	138 (100%)	0	100	100
54	w	444/697 (64%)	442 (100%)	2 (0%)	81	93
55	x	42/273 (15%)	42 (100%)	0	100	100
56	y	189/206 (92%)	187 (99%)	2 (1%)	65	87
57	z	31/107 (29%)	28 (90%)	3 (10%)	8	25
58	T	31/139 (22%)	29 (94%)	2 (6%)	15	43
All	All	7590/10725 (71%)	7512 (99%)	78 (1%)	65	88

All (78) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	3	23	GLU
4	3	31	GLU
4	3	35	THR
4	3	43	CYS
4	3	76	LEU
4	3	114	ARG
4	3	134	ILE
4	3	136	ILE
6	8	3	SER
6	8	27	ILE
7	A	136	ASN
8	B	17	LEU
9	C	330	LEU

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Mol	Chain	Res	Type
9	C	343	ILE
10	D	261	MET
11	E	110	ASP
11	E	111	VAL
11	E	173	ASN
12	F	87	GLU
13	G	83	ASP
13	G	216	SER
14	H	13	ILE
14	H	15	LYS
14	H	144	LEU
15	I	240	HIS
16	J	101	GLU
16	J	138	ARG
16	J	145	GLN
17	K	132	GLN
17	K	149	MET
18	L	49	ARG
19	M	71	SER
24	R	96	MET
25	S	123	LEU
25	S	143	LEU
25	S	144	ASN
26	U	10	ASN
27	V	98	GLU
27	V	116	ILE
29	X	48	LYS
30	Y	44	ILE
30	Y	66	GLU
31	Z	66	SER
32	a	126	THR
34	c	95	CYS
35	d	38	ILE
35	d	52	LYS
36	e	5	ASN
39	h	110	GLU
42	k	60	SER
42	k	68	THR
43	l	135	SER
43	l	157	GLU
43	l	159	THR
44	m	130	ILE

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Mol	Chain	Res	Type
44	m	144	THR
44	m	151	LEU
44	m	190	GLU
44	m	644	ASP
45	n	133	ILE
45	n	210	VAL
45	n	411	GLN
46	o	224	ILE
49	r	10	SER
49	r	225	SER
52	u	25	ASP
52	u	63	MET
52	u	104	ARG
52	u	107	LEU
54	w	243[A]	GLU
54	w	243[B]	GLU
56	y	50	HIS
56	y	52	THR
57	z	104	ARG
57	z	106	LYS
57	z	108	SER
58	T	103	GLN
58	T	150	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (69) such sidechains are listed below:

Mol	Chain	Res	Type
4	3	41	GLN
4	3	92	GLN
6	8	25	GLN
8	B	165	GLN
9	C	61	GLN
9	C	112	HIS
9	C	314	HIS
9	C	363	ASN
10	D	99	ASN
10	D	270	GLN
10	D	513	ASN
12	F	45	GLN
12	F	86	HIS
13	G	89	GLN
14	H	59	HIS

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Mol	Chain	Res	Type
15	I	227	GLN
15	I	351	ASN
15	I	366	HIS
15	I	406	GLN
15	I	729	HIS
16	J	145	GLN
16	J	180	HIS
17	K	56	GLN
17	K	256	ASN
19	M	125	ASN
21	O	27	GLN
26	U	10	ASN
26	U	85	HIS
29	X	110	ASN
31	Z	123	GLN
35	d	71	ASN
38	g	18	ASN
39	h	25	GLN
39	h	33	GLN
39	h	61	ASN
40	i	63	GLN
42	k	28	ASN
42	k	59	GLN
43	l	35	HIS
43	l	77	ASN
43	l	129	GLN
43	l	165	HIS
44	m	232	GLN
44	m	237	GLN
44	m	352	ASN
44	m	377	ASN
44	m	682	GLN
44	m	685	HIS
44	m	695	ASN
44	m	706	ASN
45	n	79	GLN
45	n	190	GLN
45	n	197	GLN
45	n	239	ASN
45	n	349	ASN
45	n	580	ASN
49	r	68	HIS

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Mol	Chain	Res	Type
49	r	182	ASN
49	r	246	ASN
51	t	200	HIS
53	v	43	HIS
54	w	674	ASN
56	y	6	GLN
56	y	66	ASN
56	y	86	ASN
56	y	157	GLN
57	z	107	ASN
58	T	103	GLN
58	T	146	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	1	2191/3497 (62%)	555 (25%)	21 (0%)
3	2	147/165 (89%)	27 (18%)	1 (0%)
5	6	77/300 (25%)	31 (40%)	0
All	All	2415/3962 (60%)	613 (25%)	22 (0%)

All (613) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	1	14	U
2	1	34	A
2	1	36	C
2	1	49	A
2	1	57	A
2	1	59	G
2	1	60	A
2	1	65	A
2	1	66	A
2	1	72	C
2	1	77	A
2	1	91	G
2	1	105	G
2	1	109	A
2	1	110	G
2	1	111	C
2	1	116	A

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Mol	Chain	Res	Type
2	1	117	U
2	1	118	U
2	1	121	A
2	1	122	A
2	1	131	A
2	1	133	A
2	1	149	G
2	1	152	U
2	1	154	G
2	1	162	A
2	1	163	A
2	1	170	G
2	1	173	U
2	1	174	U
2	1	177	G
2	1	193	U
2	1	197	U
2	1	198	U
2	1	207	C
2	1	213	G
2	1	217	G
2	1	218	A
2	1	225	G
2	1	226	A
2	1	227	G
2	1	239	U
2	1	240	G
2	1	241	G
2	1	244	G
2	1	258	U
2	1	259	A
2	1	263	A
2	1	266	G
2	1	268	U
2	1	269	U
2	1	276	A
2	1	277	G
2	1	303	A
2	1	306	U
2	1	307	G
2	1	331	A
2	1	337	U

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Mol	Chain	Res	Type
2	1	338	G
2	1	346	A
2	1	347	C
2	1	350	A
2	1	359	A
2	1	360	A
2	1	361	G
2	1	378	U
2	1	384	G
2	1	405	A
2	1	406	U
2	1	409	U
2	1	411	C
2	1	415	A
2	1	429	G
2	1	430	A
2	1	437	G
2	1	443	C
2	1	445	G
2	1	507	U
2	1	522	G
2	1	530	A
2	1	532	A
2	1	534	A
2	1	540	A
2	1	544	A
2	1	546	G
2	1	547	G
2	1	548	U
2	1	551	C
2	1	577	U
2	1	578	U
2	1	579	A
2	1	580	U
2	1	581	A
2	1	582	G
2	1	590	U
2	1	591	G
2	1	593	A
2	1	602	A
2	1	603	C
2	1	615	G

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Mol	Chain	Res	Type
2	1	616	A
2	1	618	U
2	1	624	U
2	1	632	A
2	1	636	A
2	1	637	U
2	1	641	G
2	1	644	A
2	1	645	U
2	1	646	A
2	1	647	A
2	1	650	G
2	1	651	U
2	1	661	C
2	1	662	C
2	1	663	C
2	1	671	A
2	1	674	A
2	1	675	C
2	1	685	A
2	1	687	U
2	1	702	A
2	1	706	U
2	1	714	A
2	1	715	U
2	1	716	G
2	1	717	A
2	1	732	A
2	1	735	G
2	1	743	A
2	1	744	U
2	1	745	G
2	1	746	C
2	1	747	A
2	1	748	G
2	1	749	G
2	1	760	C
2	1	761	U
2	1	762	U
2	1	763	G
2	1	776	U
2	1	777	C

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Mol	Chain	Res	Type
2	1	778	G
2	1	779	A
2	1	816	A
2	1	817	G
2	1	833	A
2	1	840	A
2	1	847	G
2	1	849	A
2	1	851	U
2	1	852	A
2	1	854	G
2	1	860	A
2	1	874	G
2	1	876	G
2	1	877	G
2	1	880	A
2	1	889	G
2	1	890	A
2	1	892	G
2	1	893	C
2	1	935	U
2	1	936	A
2	1	938	A
2	1	939	G
2	1	940	G
2	1	942	G
2	1	950	C
2	1	952	A
2	1	953	A
2	1	954	U
2	1	955	C
2	1	956	G
2	1	957	A
2	1	964	U
2	1	968	A
2	1	969	G
2	1	970	C
2	1	976	C
2	1	986	U
2	1	987	U
2	1	988	U
2	1	990	C

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Mol	Chain	Res	Type
2	1	996	G
2	1	997	A
2	1	998	U
2	1	1006	A
2	1	1009	C
2	1	1011	G
2	1	1012	A
2	1	1013	U
2	1	1014	C
2	1	1015	A
2	1	1017	U
2	1	1023	G
2	1	1135	G
2	1	1138	U
2	1	1139	U
2	1	1141	C
2	1	1142	U
2	1	1143	A
2	1	1147	G
2	1	1148	G
2	1	1157	G
2	1	1158	G
2	1	1159	U
2	1	1160	A
2	1	1161	A
2	1	1163	C
2	1	1167	A
2	1	1168	C
2	1	1171	G
2	1	1172	C
2	1	1173	G
2	1	1184	A
2	1	1185	A
2	1	1186	C
2	1	1191	C
2	1	1205	G
2	1	1210	A
2	1	1211	A
2	1	1212	U
2	1	1223	C
2	1	1227	C
2	1	1234	A

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Mol	Chain	Res	Type
2	1	1235	A
2	1	1239	U
2	1	1241	U
2	1	1244	G
2	1	1245	U
2	1	1249	U
2	1	1251	U
2	1	1253	G
2	1	1255	C
2	1	1260	G
2	1	1263	C
2	1	1266	U
2	1	1269	C
2	1	1272	U
2	1	1273	G
2	1	1274	G
2	1	1275	A
2	1	1276	A
2	1	1277	G
2	1	1279	C
2	1	1282	A
2	1	1286	C
2	1	1289	U
2	1	1290	A
2	1	1291	A
2	1	1293	G
2	1	1295	G
2	1	1296	U
2	1	1297	G
2	1	1303	C
2	1	1308	C
2	1	1309	A
2	1	1312	U
2	1	1316	G
2	1	1317	A
2	1	1318	A
2	1	1332	A
2	1	1333	A
2	1	1334	A
2	1	1335	A
2	1	1336	U
2	1	1337	G

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Mol	Chain	Res	Type
2	1	1338	G
2	1	1340	U
2	1	1347	U
2	1	1348	A
2	1	1361	A
2	1	1363	A
2	1	1379	U
2	1	1380	A
2	1	1381	G
2	1	1382	C
2	1	1383	U
2	1	1384	U
2	1	1387	A
2	1	1388	G
2	1	1389	A
2	1	1390	A
2	1	1420	U
2	1	1421	G
2	1	1426	G
2	1	1433	U
2	1	1451	G
2	1	1452	A
2	1	1453	A
2	1	1459	U
2	1	1465	G
2	1	1468	G
2	1	1471	C
2	1	1484	G
2	1	1502	A
2	1	1515	A
2	1	1517	G
2	1	1518	U
2	1	1519	G
2	1	1521	G
2	1	1528	U
2	1	1529	U
2	1	1537	A
2	1	1538	A
2	1	1539	C
2	1	1541	G
2	1	1542	C
2	1	1546	U

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Mol	Chain	Res	Type
2	1	1548	G
2	1	1568	A
2	1	1570	G
2	1	1588	A
2	1	1589	U
2	1	1590	G
2	1	1591	A
2	1	1594	G
2	1	1603	U
2	1	1604	U
2	1	1605	U
2	1	1607	U
2	1	1608	C
2	1	1622	A
2	1	1623	A
2	1	1624	A
2	1	1628	A
2	1	1640	A
2	1	1643	C
2	1	1654	A
2	1	1655	G
2	1	1663	C
2	1	1664	A
2	1	1665	A
2	1	1674	C
2	1	1677	A
2	1	1678	A
2	1	1686	U
2	1	1691	A
2	1	1709	G
2	1	1715	G
2	1	1718	C
2	1	1731	A
2	1	1736	A
2	1	1737	C
2	1	1753	A
2	1	1754	A
2	1	1764	U
2	1	1780	G
2	1	1782	U
2	1	1790	A
2	1	1791	G

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Mol	Chain	Res	Type
2	1	1797	A
2	1	1798	G
2	1	1806	U
2	1	1807	G
2	1	1811	A
2	1	1814	C
2	1	1816	G
2	1	1818	U
2	1	1819	G
2	1	1820	C
2	1	1821	G
2	1	1829	C
2	1	1833	C
2	1	1834	C
2	1	1835	U
2	1	1836	U
2	1	1838	A
2	1	1849	G
2	1	1852	G
2	1	1871	U
2	1	1872	G
2	1	1873	U
2	1	1874	U
2	1	1876	U
2	1	1917	U
2	1	1935	U
2	1	1936	A
2	1	1940	C
2	1	1941	A
2	1	1961	G
2	1	2423	G
2	1	2424	U
2	1	2451	A
2	1	2452	G
2	1	2455	U
2	1	2456	G
2	1	2458	G
2	1	2459	G
2	1	2461	A
2	1	2462	C
2	1	2463	G
2	1	2464	G

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Mol	Chain	Res	Type
2	1	2465	G
2	1	2466	C
2	1	2473	A
2	1	2476	U
2	1	2480	C
2	1	2481	G
2	1	2498	U
2	1	2499	U
2	1	2505	U
2	1	2506	G
2	1	2507	A
2	1	2521	U
2	1	2700	G
2	1	2701	G
2	1	2702	G
2	1	2706	U
2	1	2898	A
2	1	2902	U
2	1	2905	C
2	1	2906	A
2	1	2907	C
2	1	2908	A
2	1	2921	U
2	1	2925	G
2	1	2929	G
2	1	2931	C
2	1	2932	A
2	1	2946	A
2	1	2952	C
2	1	2953	U
2	1	2971	C
2	1	2972	G
2	1	2973	G
2	1	2978	U
2	1	2982	A
2	1	2984	C
2	1	2993	G
2	1	3009	G
2	1	3011	U
2	1	3014	A
2	1	3023	C
2	1	3024	C

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Mol	Chain	Res	Type
2	1	3025	A
2	1	3030	U
2	1	3031	A
2	1	3036	A
2	1	3037	C
2	1	3038	G
2	1	3040	G
2	1	3042	G
2	1	3044	U
2	1	3046	G
2	1	3057	U
2	1	3059	G
2	1	3060	U
2	1	3061	G
2	1	3062	A
2	1	3063	G
2	1	3064	A
2	1	3065	C
2	1	3071	A
2	1	3072	G
2	1	3073	U
2	1	3082	A
2	1	3085	G
2	1	3087	U
2	1	3093	G
2	1	3107	A
2	1	3108	A
2	1	3113	A
2	1	3117	A
2	1	3118	G
2	1	3119	U
2	1	3125	A
2	1	3126	G
2	1	3128	A
2	1	3151	A
2	1	3155	G
2	1	3168	A
2	1	3170	G
2	1	3172	C
2	1	3173	A
2	1	3174	A
2	1	3176	G

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Mol	Chain	Res	Type
2	1	3182	G
2	1	3188	U
2	1	3189	C
2	1	3192	C
2	1	3195	C
2	1	3198	G
2	1	3200	U
2	1	3218	A
2	1	3225	A
2	1	3226	A
2	1	3227	U
2	1	3237	A
2	1	3238	A
2	1	3239	A
2	1	3248	U
2	1	3272	U
2	1	3273	A
2	1	3275	A
2	1	3276	A
2	1	3282	G
2	1	3288	G
2	1	3301	C
2	1	3307	U
2	1	3309	U
2	1	3315	A
2	1	3316	G
2	1	3317	A
2	1	3318	A
2	1	3319	G
2	1	3327	A
2	1	3337	A
2	1	3338	A
2	1	3339	A
2	1	3343	A
2	1	3344	A
2	1	3345	G
2	1	3346	U
2	1	3349	U
2	1	3351	U
2	1	3353	U
2	1	3354	U
2	1	3357	C

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Mol	Chain	Res	Type
2	1	3359	U
2	1	3360	G
2	1	3362	C
2	1	3367	A
2	1	3368	A
2	1	3370	U
2	1	3372	C
2	1	3373	C
2	1	3374	A
2	1	3375	U
2	1	3404	G
2	1	3405	C
2	1	3414	U
2	1	3417	A
2	1	3418	U
2	1	3419	G
2	1	3420	U
2	1	3421	G
2	1	3424	A
2	1	3425	C
2	1	3430	U
2	1	3431	A
2	1	3435	U
2	1	3436	A
2	1	3469	U
2	1	3470	G
2	1	3476	A
2	1	3479	C
2	1	3483	U
2	1	3490	A
2	1	3491	A
2	1	3492	G
2	1	3493	A
2	1	3495	U
3	2	9	A
3	2	24	G
3	2	29	C
3	2	42	U
3	2	43	C
3	2	46	U
3	2	60	A
3	2	67	A

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Mol	Chain	Res	Type
3	2	70	C
3	2	71	G
3	2	79	A
3	2	87	A
3	2	98	U
3	2	103	G
3	2	112	A
3	2	114	C
3	2	115	G
3	2	124	G
3	2	132	G
3	2	133	U
3	2	134	U
3	2	136	U
3	2	137	A
3	2	156	G
3	2	159	U
3	2	160	G
3	2	162	C
5	6	2	C
5	6	5	U
5	6	6	C
5	6	8	U
5	6	9	C
5	6	47	U
5	6	56	A
5	6	57	A
5	6	60	U
5	6	82	A
5	6	83	A
5	6	86	U
5	6	89	U
5	6	92	G
5	6	93	A
5	6	94	A
5	6	96	U
5	6	97	C
5	6	99	A
5	6	101	U
5	6	102	G
5	6	105	G
5	6	106	A

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Mol	Chain	Res	Type
5	6	108	A
5	6	178	U
5	6	181	C
5	6	182	C
5	6	184	C
5	6	186	U
5	6	187	U
5	6	188	G

All (22) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	1	674	A
2	1	759	C
2	1	761	U
2	1	816	A
2	1	949	A
2	1	996	G
2	1	1159	U
2	1	1272	U
2	1	1333	A
2	1	1380	A
2	1	1389	A
2	1	1540	A
2	1	1806	U
2	1	1851	A
2	1	1916	G
2	1	3024	C
2	1	3070	U
2	1	3081	U
2	1	3217	U
2	1	3337	A
2	1	3367	A
3	2	131	G

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 1 ligands modelled in this entry, 1 is 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.

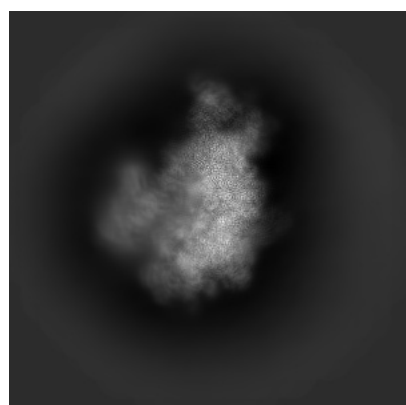
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24411. These allow visual inspection of the internal detail of the map and identification of artifacts.

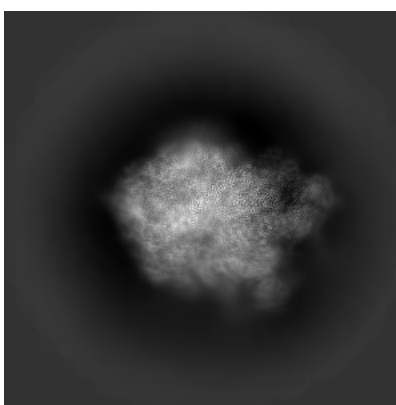
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

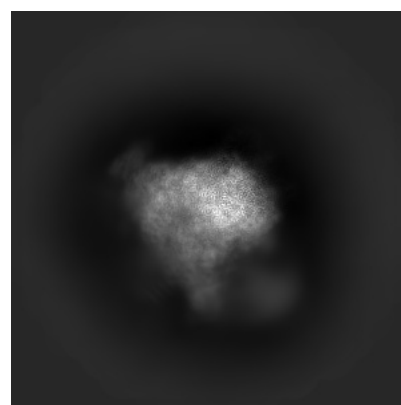
6.1.1 Primary map



X



Y

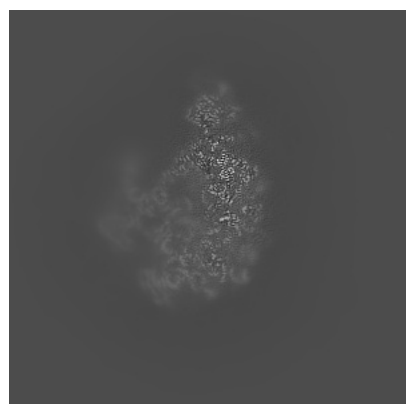


Z

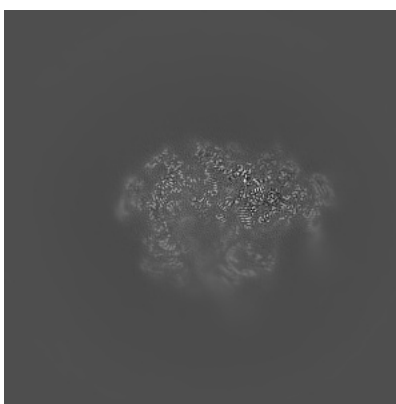
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

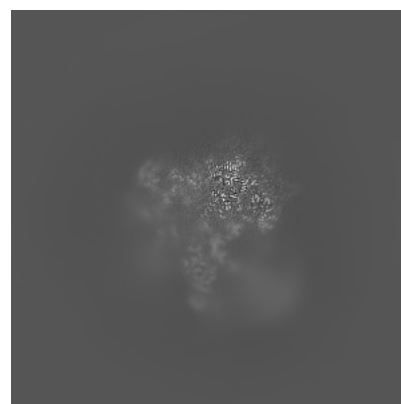
6.2.1 Primary map



X Index: 256



Y Index: 256

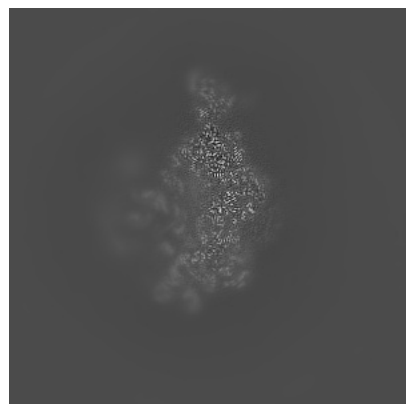


Z Index: 256

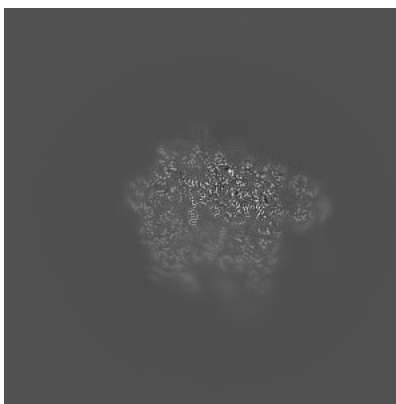
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

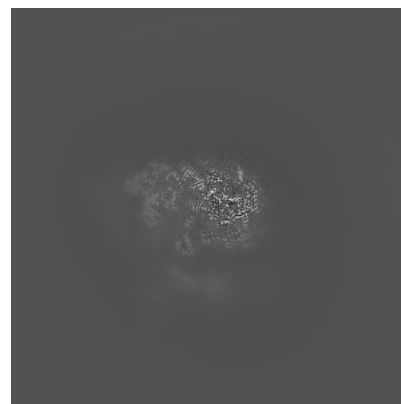
6.3.1 Primary map



X Index: 271



Y Index: 274

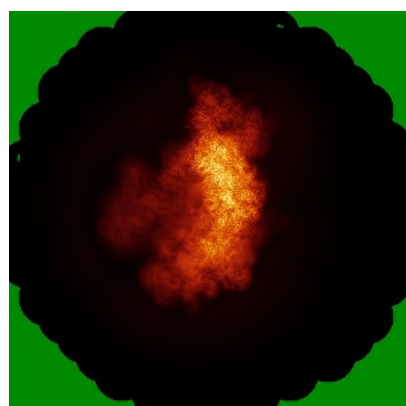


Z Index: 314

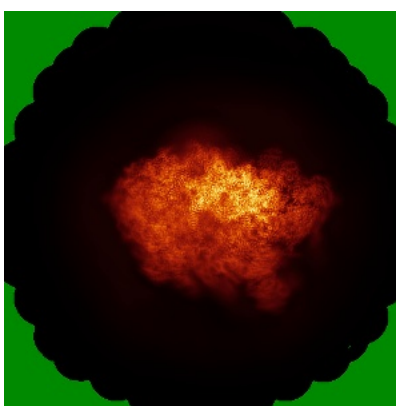
The images above show the largest variance slices of the map in three orthogonal directions.

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

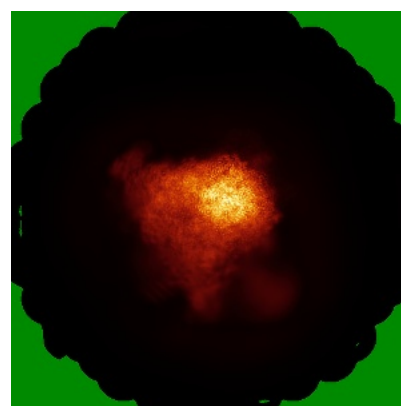
6.4.1 Primary map



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

This section was not generated.

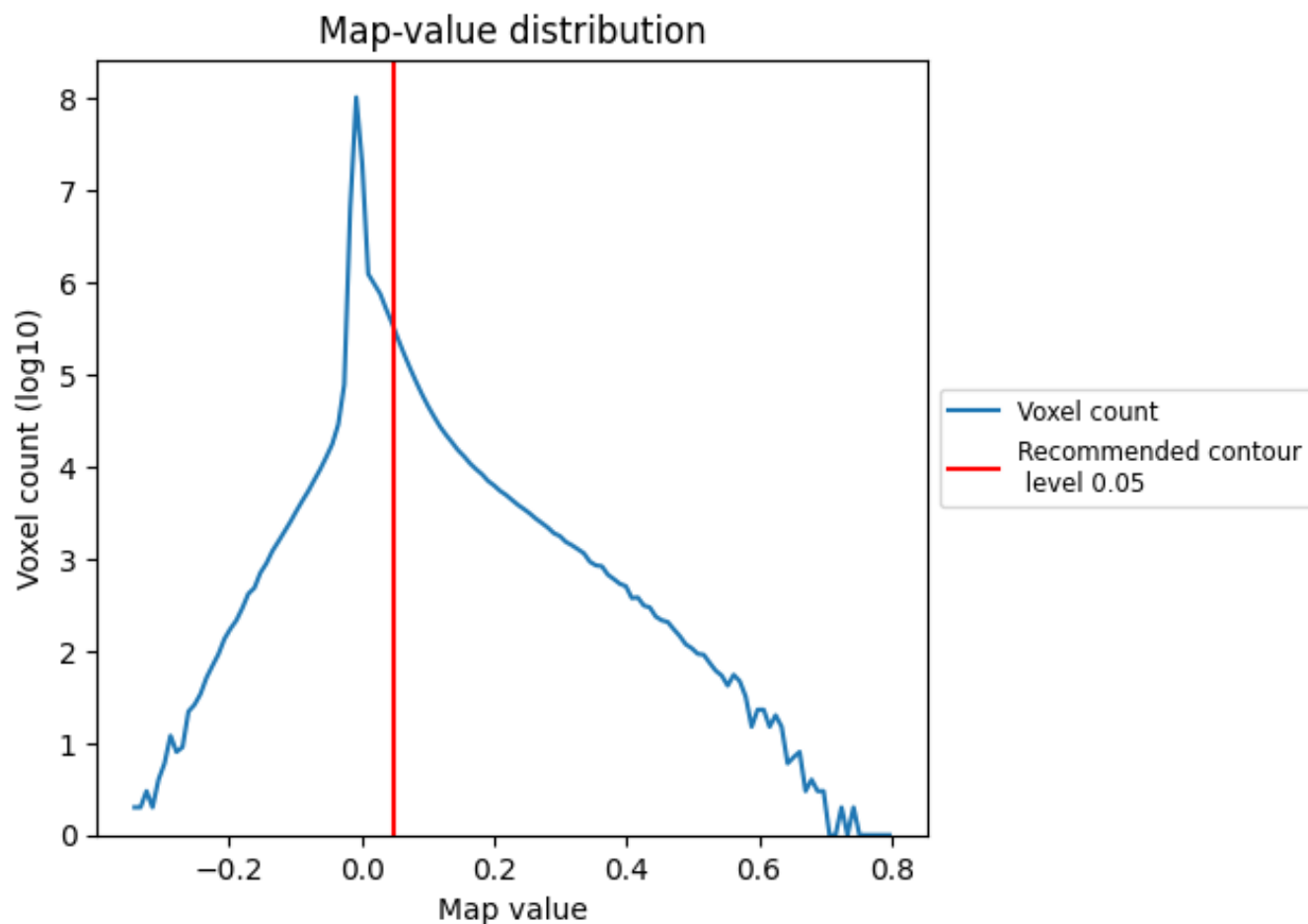
6.6 Mask visualisation

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

7 Map analysis [i](#)

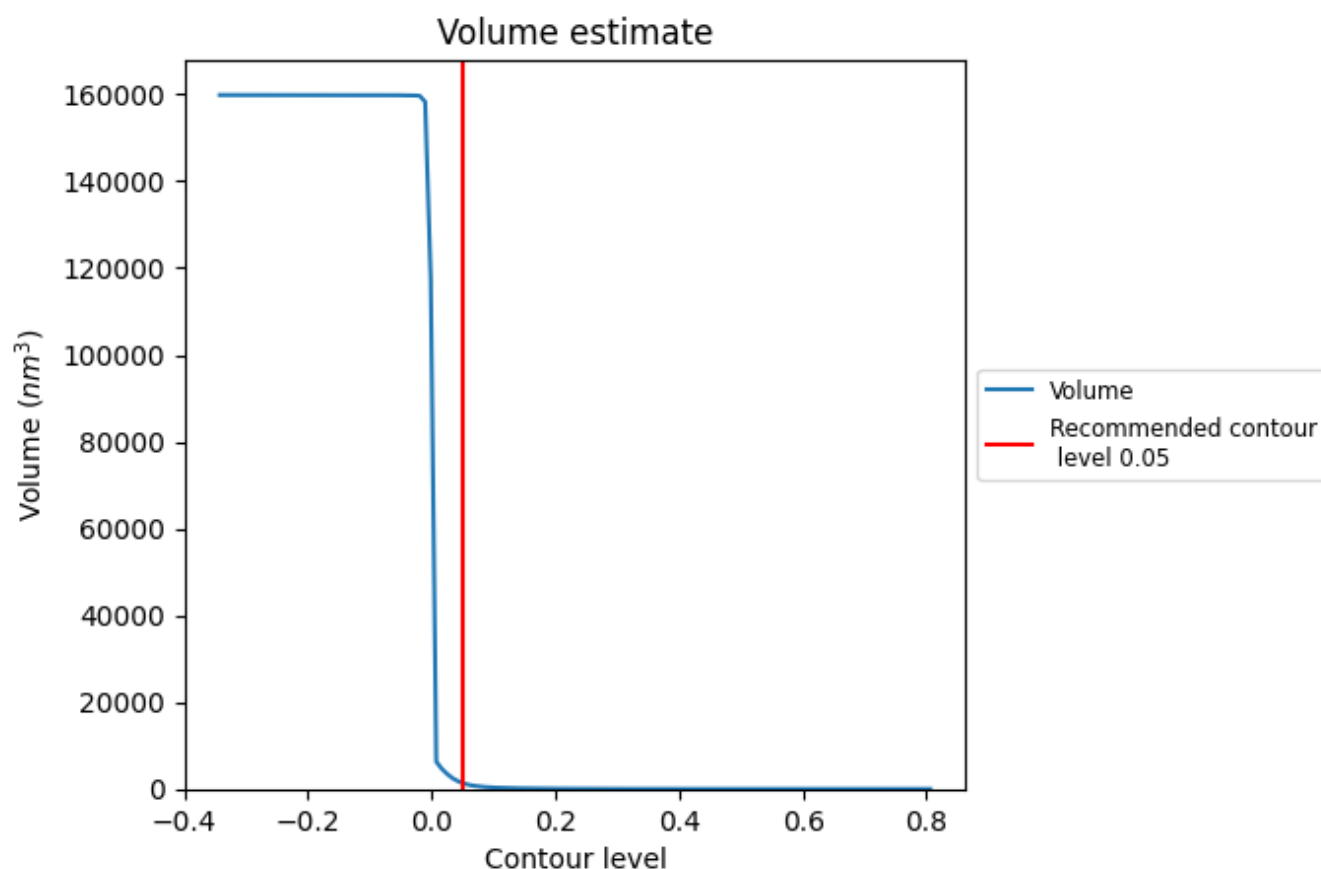
This section contains the results of statistical analysis of the map.

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.

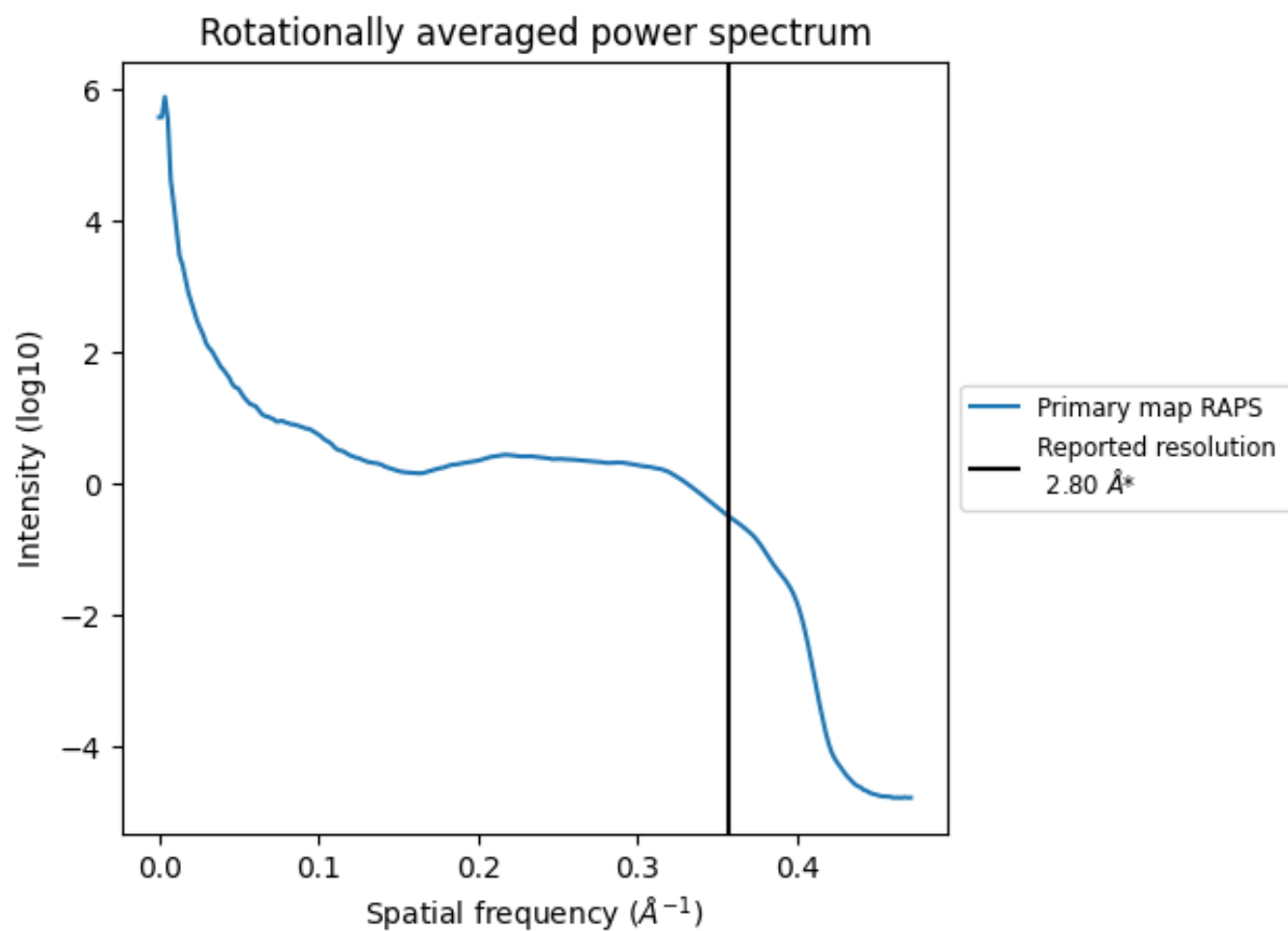
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1366 nm^3 ; this corresponds to an approximate mass of 1234 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 0.357 Å⁻¹

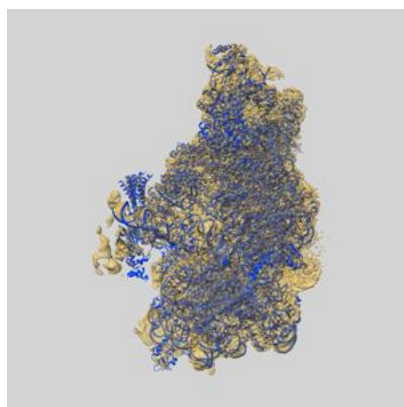
8 Fourier-Shell correlation ⓘ

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

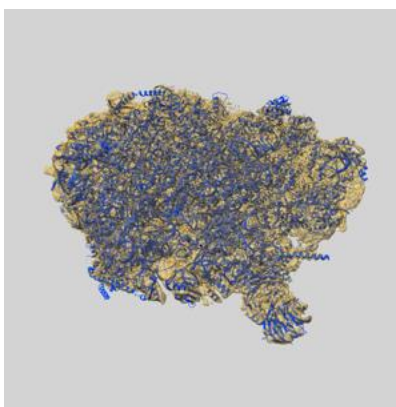
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-24411 and PDB model 8ESQ. Per-residue inclusion information can be found in section [3](#) on page [15](#).

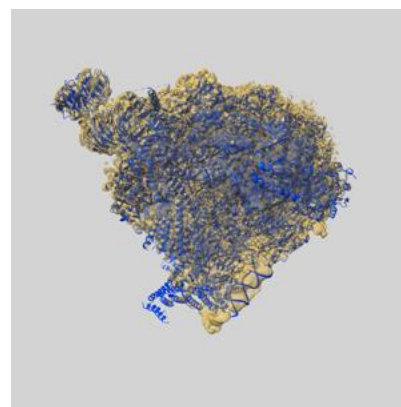
9.1 Map-model overlay [i](#)



X



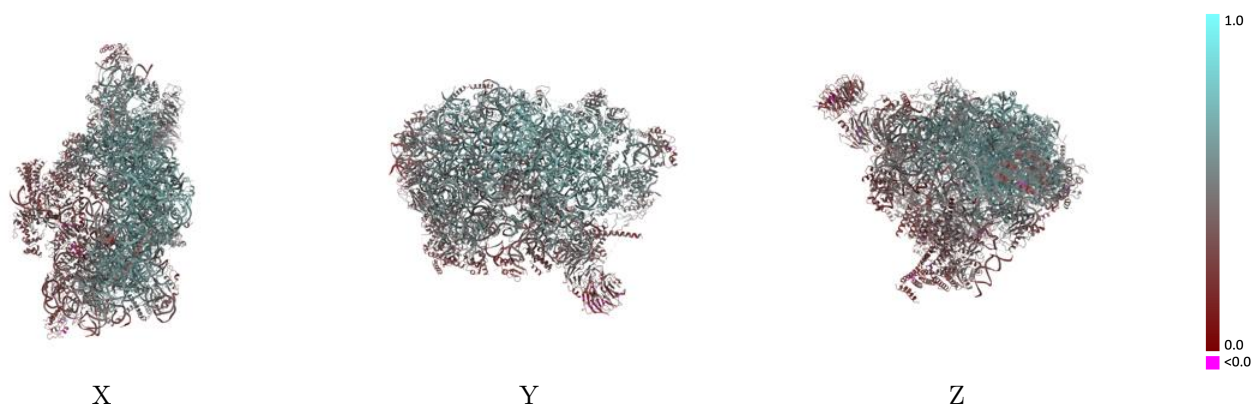
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

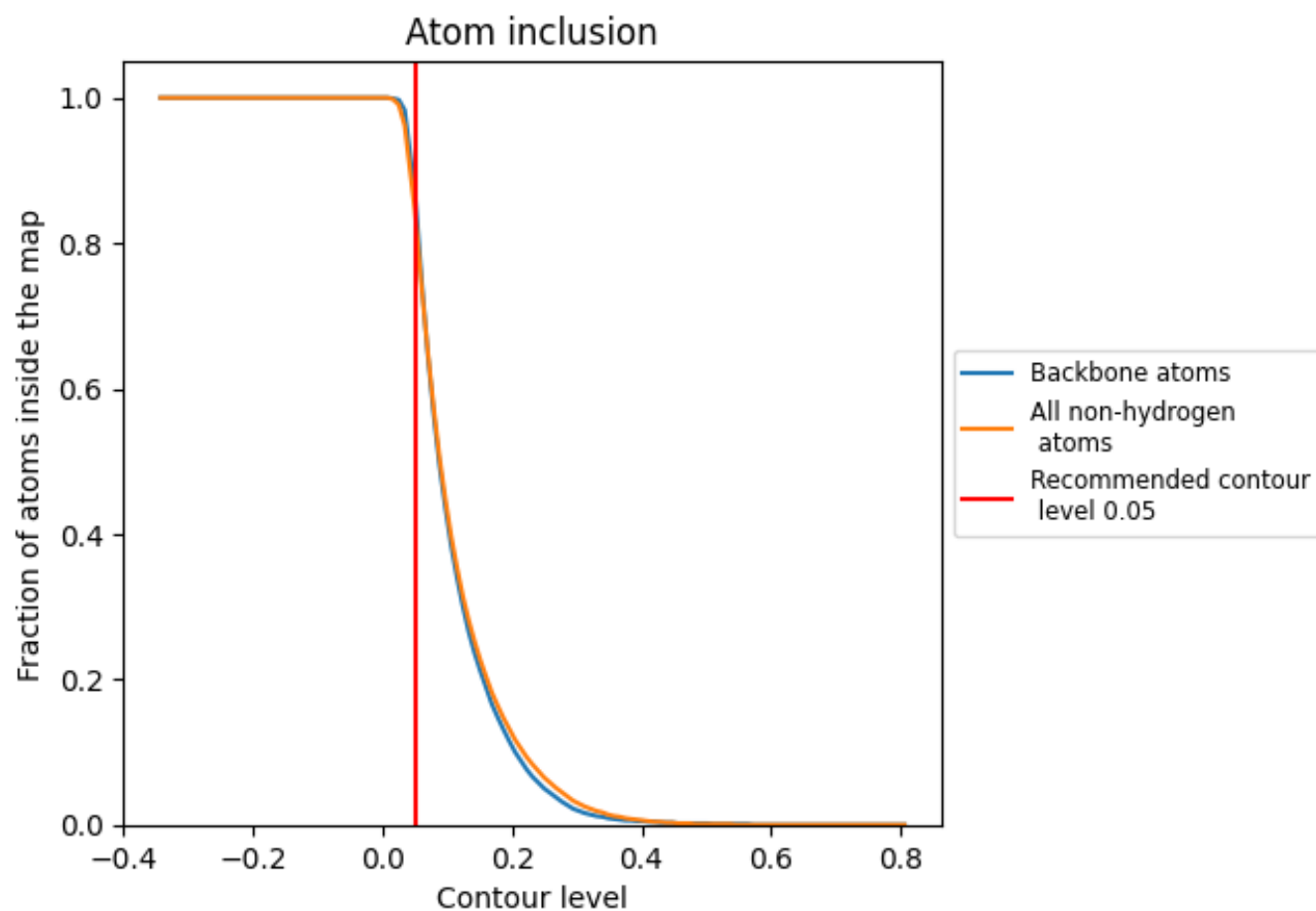


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 84% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8450	 0.4890
1	 0.9670	 0.5130
2	 0.9890	 0.6270
3	 0.6620	 0.5250
6	 0.9450	 0.5020
7	 0.2230	 0.2600
8	 0.8680	 0.4260
A	 0.8410	 0.4450
B	 0.9270	 0.5150
C	 0.9720	 0.6220
D	 0.6480	 0.5090
E	 0.8220	 0.4660
F	 0.8430	 0.5430
G	 0.9500	 0.6220
H	 0.8770	 0.4450
I	 0.5250	 0.3430
J	 0.5650	 0.3300
K	 0.7440	 0.4620
L	 0.9790	 0.6500
M	 0.9590	 0.4900
N	 0.9960	 0.6690
O	 0.9560	 0.5490
P	 0.9130	 0.5590
Q	 0.9420	 0.5830
R	 0.8460	 0.4080
S	 0.8860	 0.4800
T	 0.5360	 0.2880
U	 0.4860	 0.2730
V	 0.8560	 0.4610
W	 0.4890	 0.3040
X	 0.9490	 0.5960
Y	 0.9620	 0.6190
Z	 0.8060	 0.4220
a	 0.7200	 0.5210
b	 0.5980	 0.3670



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Chain	Atom inclusion	Q-score
c	 0.7190	 0.3420
d	 0.9100	 0.5160
e	 0.9670	 0.6030
f	 0.9870	 0.6030
g	 0.9060	 0.5000
h	 0.9660	 0.6270
i	 0.9560	 0.6130
j	 0.9960	 0.6580
k	 0.7930	 0.4590
l	 0.6390	 0.3410
m	 0.7770	 0.4360
n	 0.8550	 0.5060
o	 0.7530	 0.5000
p	 0.5330	 0.2850
q	 0.4790	 0.3460
r	 0.7240	 0.3690
s	 0.6470	 0.3240
t	 0.8780	 0.5260
u	 0.6920	 0.3860
v	 0.9140	 0.5820
w	 0.3880	 0.3550
x	 0.5320	 0.4510
y	 0.7380	 0.3610
z	 0.6210	 0.3470