



Full wwPDB EM Validation Report ⓘ

Mar 7, 2026 – 01:46 AM UTC

PDB ID : 4V8T / pdb_00004v8t
EMDB ID : EMD-2169
Title : Cryo-EM Structure of the 60S Ribosomal Subunit in Complex with Arx1 and Rei1
Authors : Greber, B.J.; Boehringer, D.; Montellese, C.; Ban, N.
Deposited on : 2012-08-07
Resolution : 8.10 Å (reported)
Based on initial models : 3U5I, 3U5H

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

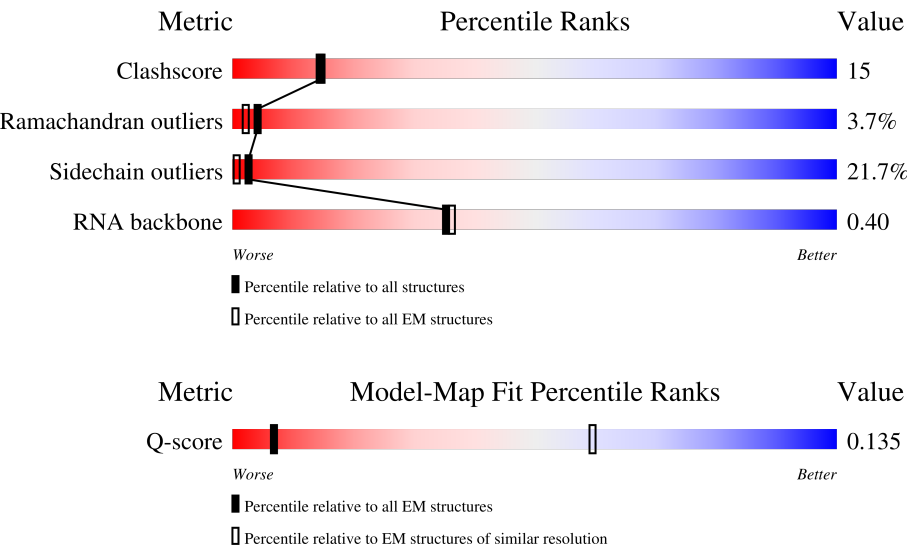
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 8.10 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	342 (7.60 - 8.60)

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

Mol	Chain	Length	Quality of chain
1	A	254	37% 54%32%11%..
2	B	387	17% 52%34%11%.
3	C	362	17% 51%31%15%.

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Mol	Chain	Length	Quality of chain
4	D	297	
5	E	176	
6	F	244	
7	G	256	
8	H	191	
9	I	221	
10	J	174	
11	K	155	
12	L	199	
13	M	138	
14	N	204	
15	O	219	
16	P	184	
17	Q	186	
18	R	189	
19	S	172	
20	T	160	
21	U	121	
22	V	137	
23	W	155	
24	X	142	
25	Y	127	
26	Z	136	
27	a	149	
28	b	59	

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Mol	Chain	Length	Quality of chain
29	c	105	
30	d	113	
31	e	130	
32	f	107	
33	g	121	
34	h	120	
35	i	100	
36	j	88	
37	k	78	
38	l	51	
39	m	128	
40	n	25	
41	o	106	
42	p	92	
43	q	312	
44	r	153	
45	s	46	
46	t	614	
47	1	114	
48	5	3396	
49	7	121	
50	8	158	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
51	ZN	o	501	-	-	X	-

2 Entry composition

There are 51 unique types of molecules in this entry. The entry contains 130050 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 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	252	Total	C	N	O	S	0	0
			1912	1190	388	333	1		

- Molecule 2 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 3 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 4 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	294	Total	C	N	O	S	0	0
			2359	1489	412	456	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	157	Total	C	N	O	S	0	0
			1248	806	224	217	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	223	Total	C	N	O	S	0	0
			1791	1155	325	310	1		

- Molecule 7 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	231	Total	C	N	O	S	0	0
			1763	1130	316	314	3		

- Molecule 8 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 9 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	213	Total	C	N	O	S	0	0
			1722	1094	325	297	6		

- Molecule 10 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 11 is a protein called 60S RIBOSOMAL PROTEIN L12.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	K	150	Total	C	N	O	0	0
			750	450	150	150		

- Molecule 12 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	L	194	Total	C	N	O	0	0
			1548	965	316	267		

- Molecule 13 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	137	Total	C	N	O	S	0	0
			1059	678	200	179	2		

- Molecule 14 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 15 is a protein called Large ribosomal subunit protein uL13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	197	Total	C	N	O	S	197	0
			3119	2008	581	528	2		

- Molecule 16 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	155	Total	C	N	O	S	0	0
			1227	764	238	225			

- Molecule 17 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 18 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	188	Total	C	N	O	S	0	0
			1521	935	326	260			

- Molecule 19 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 20 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 21 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	U	98	Total	C	N	O	0	0
			778	505	127	146		

- Molecule 22 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 23 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	135	Total	C	N	O	S	0	0
			1038	651	206	180	1		

- Molecule 24 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	120	Total	C	N	O	S	0	0
			959	617	168	172	2		

- Molecule 25 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	Y	126	Total	C	N	O	0	0
			993	625	192	176		

- Molecule 26 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	Z	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 27 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 28 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	b	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 29 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	100	Total	C	N	O	S	0	0
			767	492	128	146	1		

- Molecule 30 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	109	Total	C	N	O	S	0	0
			883	559	167	156	1		

- Molecule 31 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 32 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 33 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 34 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	119	Total	C	N	O	S	0	0
			965	612	185	167	1		

- Molecule 35 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	99	Total	C	N	O	S	0	0
			770	481	156	131	2		

- Molecule 36 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	j	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 37 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	k	77	Total	C	N	O	S	0	0
			608	388	114	106			

- Molecule 38 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	l	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 39 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	m	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 40 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	n	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 41 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	o	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 42 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	p	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 43 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	q	143	Total	C	N	O	S	0	0
			1077	687	192	195	3		

- Molecule 44 is a protein called RIBOSOMAL PROTEIN P1 ALPHA, Large ribosomal subunit protein P1A.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	r	47	Total	C	N	O	0	0
			235	141	47	47		

- Molecule 45 is a protein called RIBOSOMAL PROTEIN P2 BETA.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	s	46	Total	C	N	O	0	0
			230	138	46	46		

- Molecule 46 is a protein called Probable metalloprotease ARX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	t	380	Total	C	N	O	S	0	0
			2938	1853	511	563	11		

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
t	-20	HIS	-	expression tag	UNP Q03862
t	-19	HIS	-	expression tag	UNP Q03862
t	-18	HIS	-	expression tag	UNP Q03862
t	-17	HIS	-	expression tag	UNP Q03862
t	-16	HIS	-	expression tag	UNP Q03862
t	-15	HIS	-	expression tag	UNP Q03862
t	-14	ASP	-	expression tag	UNP Q03862
t	-13	TYR	-	expression tag	UNP Q03862
t	-12	ASP	-	expression tag	UNP Q03862
t	-11	ILE	-	expression tag	UNP Q03862
t	-10	PRO	-	expression tag	UNP Q03862

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Chain	Residue	Modelled	Actual	Comment	Reference
t	-9	THR	-	expression tag	UNP Q03862
t	-8	THR	-	expression tag	UNP Q03862
t	-7	GLU	-	expression tag	UNP Q03862
t	-6	ASN	-	expression tag	UNP Q03862
t	-5	LEU	-	expression tag	UNP Q03862
t	-4	TYR	-	expression tag	UNP Q03862
t	-3	PHE	-	expression tag	UNP Q03862
t	-2	GLN	-	expression tag	UNP Q03862
t	-1	GLY	-	expression tag	UNP Q03862
t	0	ALA	-	expression tag	UNP Q03862

- Molecule 47 is a RNA chain called ES27 OF THE 25S RRNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
47	1	114	Total	P	0	114
			114	114		

- Molecule 48 is a RNA chain called 25S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	5	3150	Total	C	N	O	P	0	0
			67376	30095	12145	21987	3149		

- Molecule 49 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	7	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 50 is a RNA chain called 5.8S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	8	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 51 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

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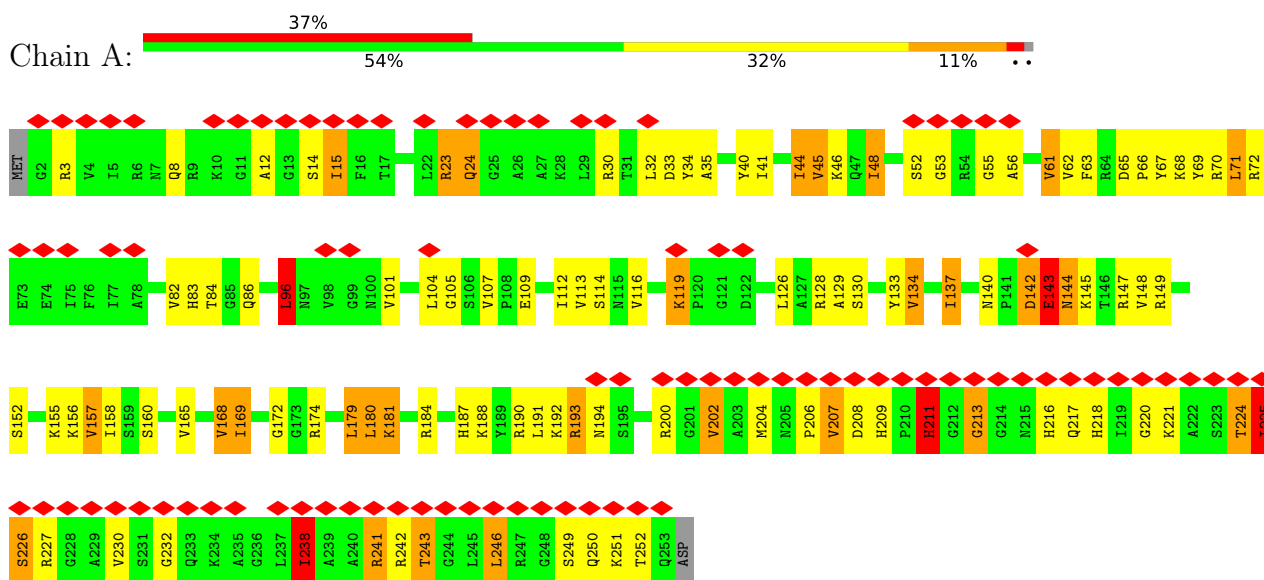
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Mol	Chain	Residues	Atoms		AltConf
51	o	1	Total 1	Zn 1	0
51	p	1	Total 1	Zn 1	0

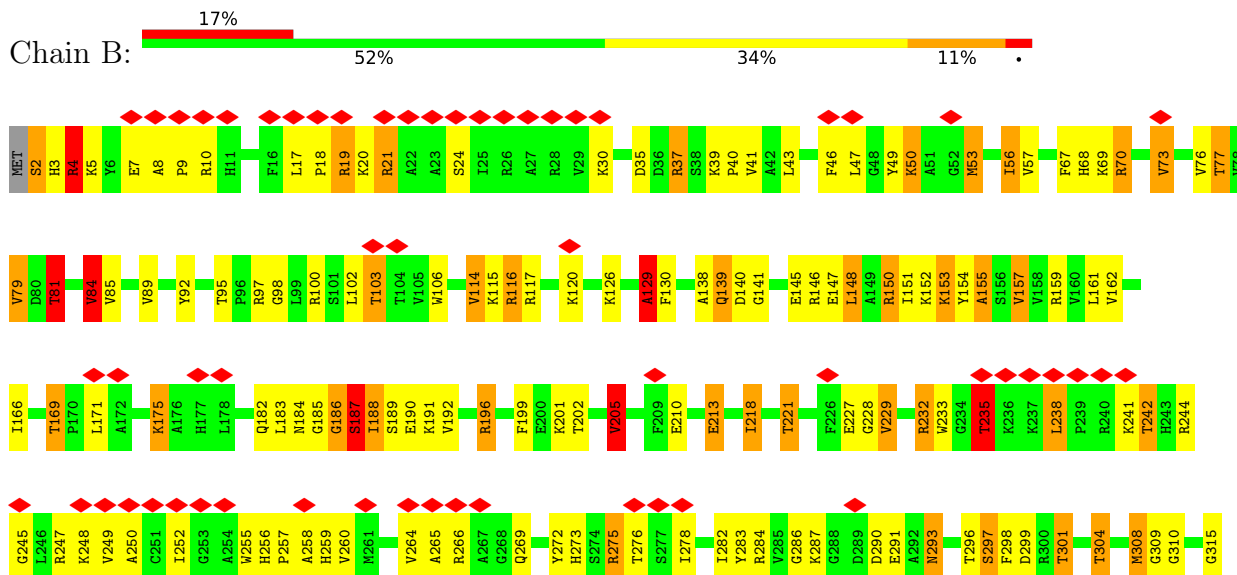
3 Residue-property plots

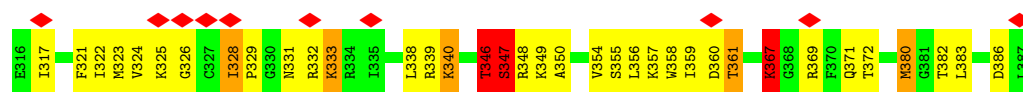
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 60S ribosomal protein L2-A

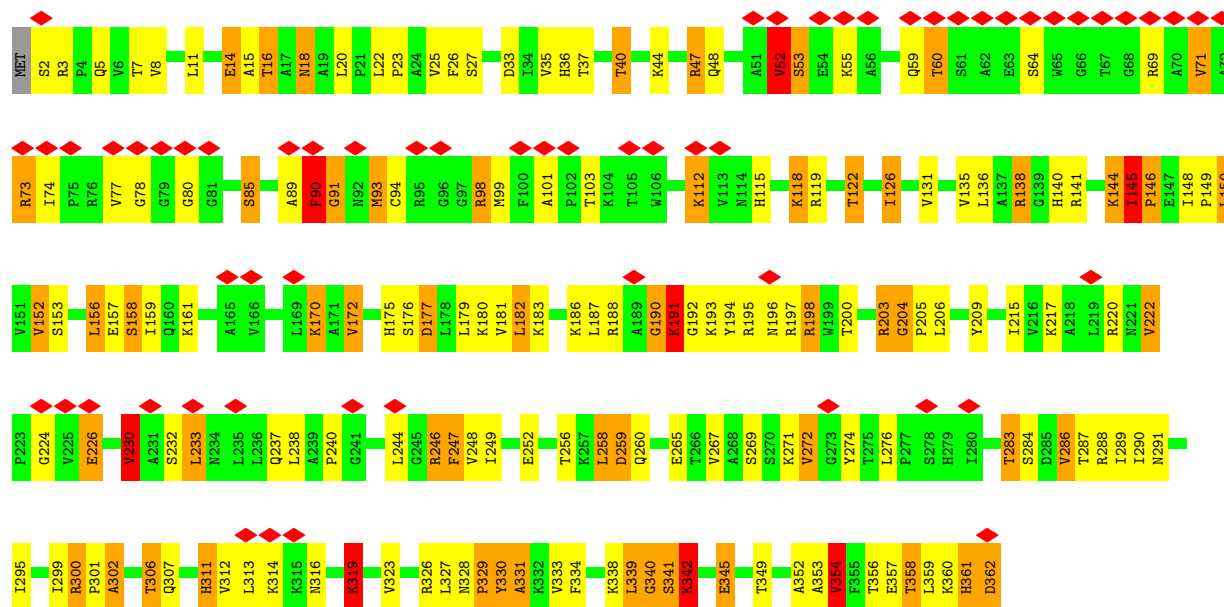


• Molecule 2: 60S ribosomal protein L3

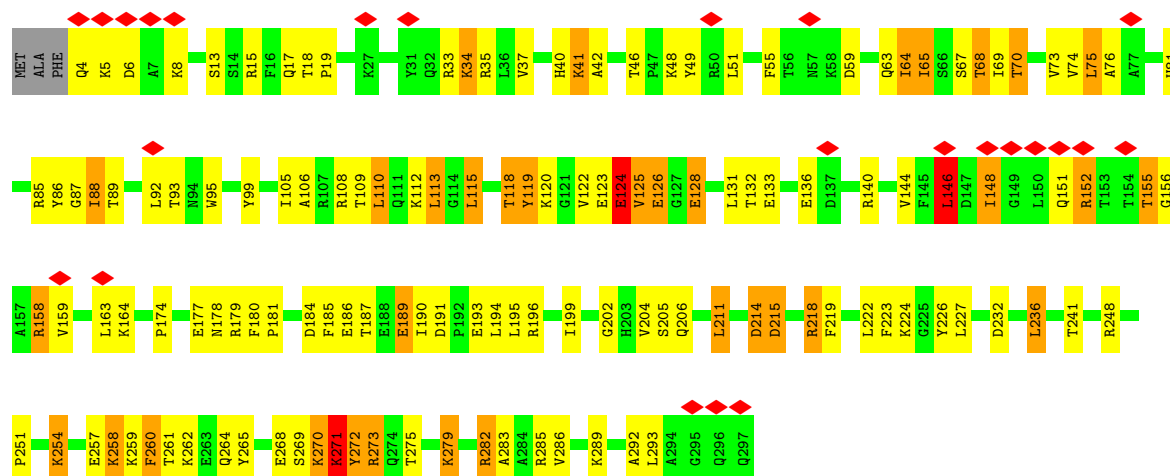




• Molecule 3: 60S ribosomal protein L4-A



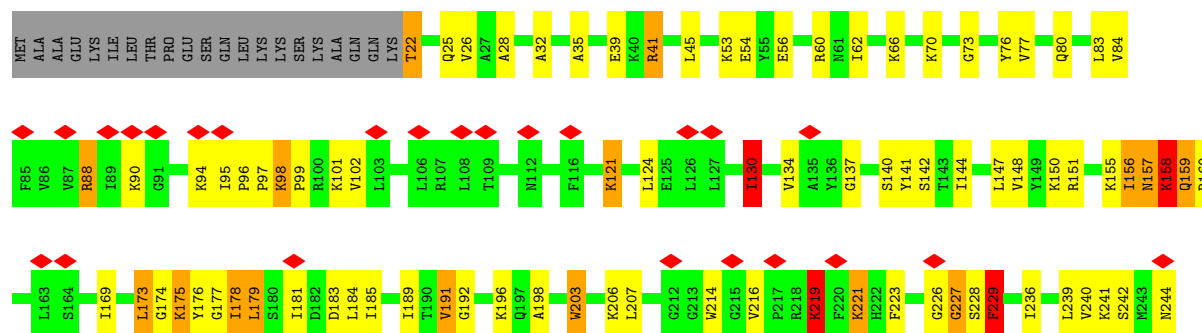
• Molecule 4: 60S ribosomal protein L5



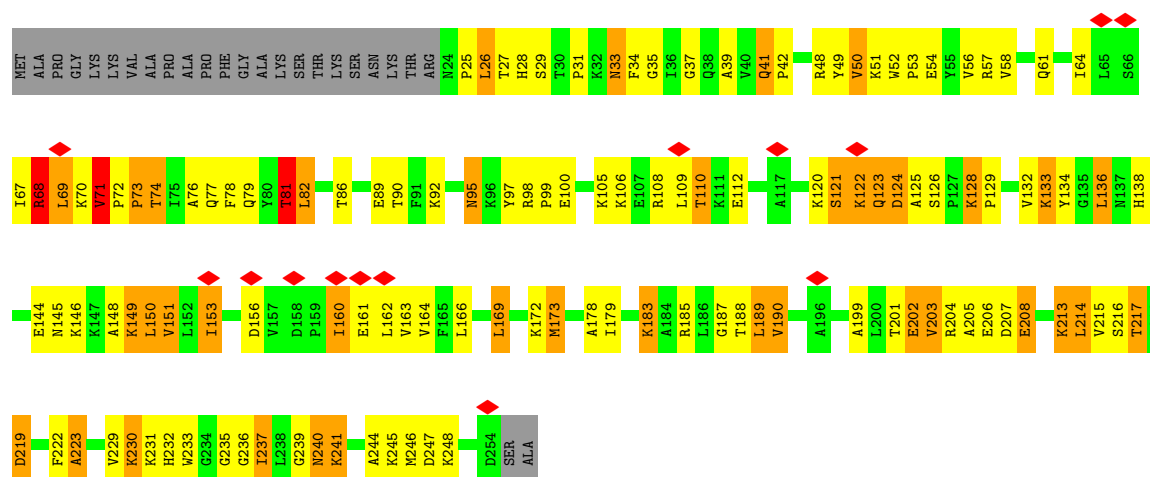
• Molecule 5: 60S ribosomal protein L6-A



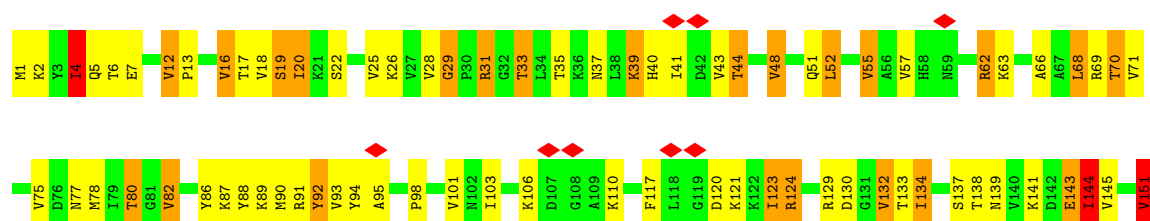
- Molecule 6: 60S ribosomal protein L7-A

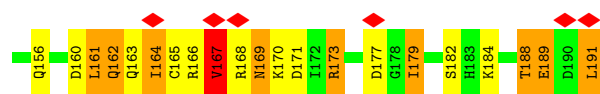


- Molecule 7: 60S ribosomal protein L8-A

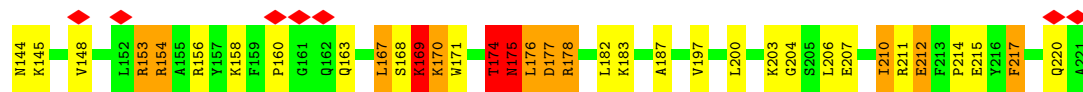
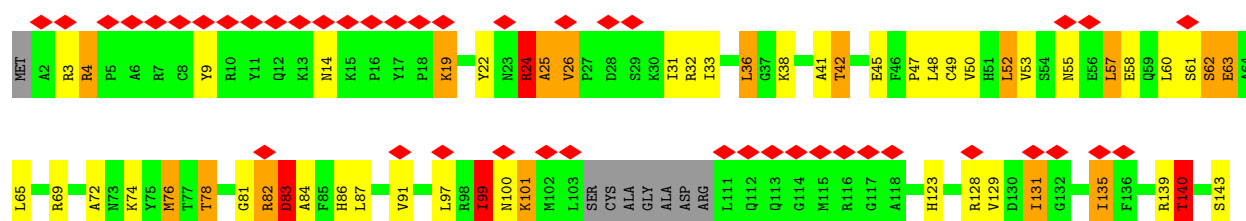


- Molecule 8: 60S ribosomal protein L9-A

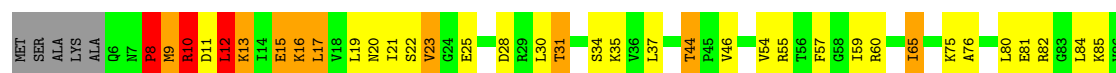




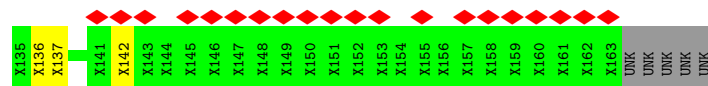
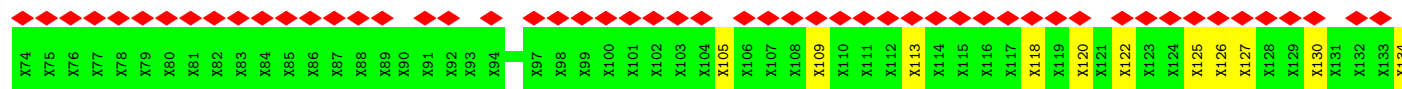
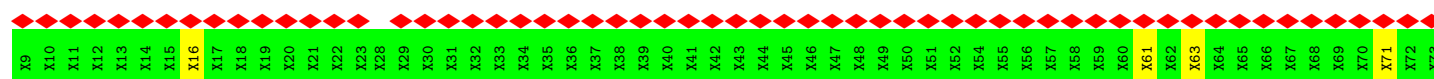
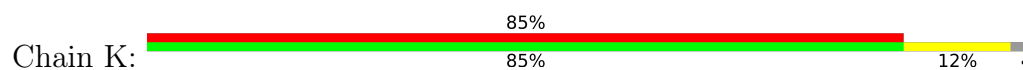
• Molecule 9: 60S ribosomal protein L10



• Molecule 10: 60S ribosomal protein L11-A

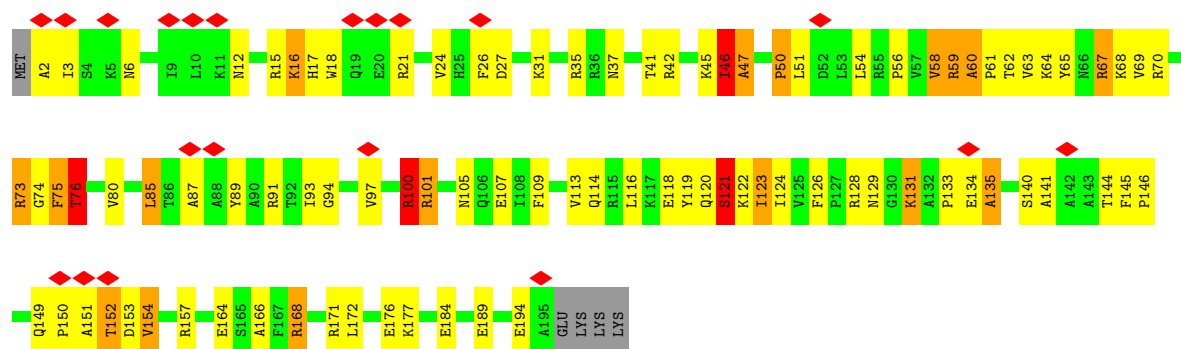


• Molecule 11: 60S RIBOSOMAL PROTEIN L12

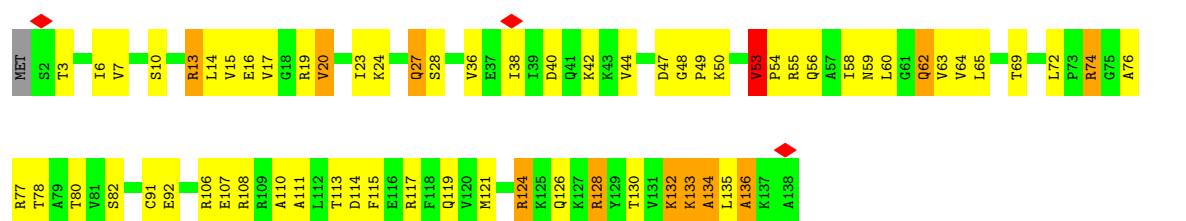


• Molecule 12: 60S ribosomal protein L13-A

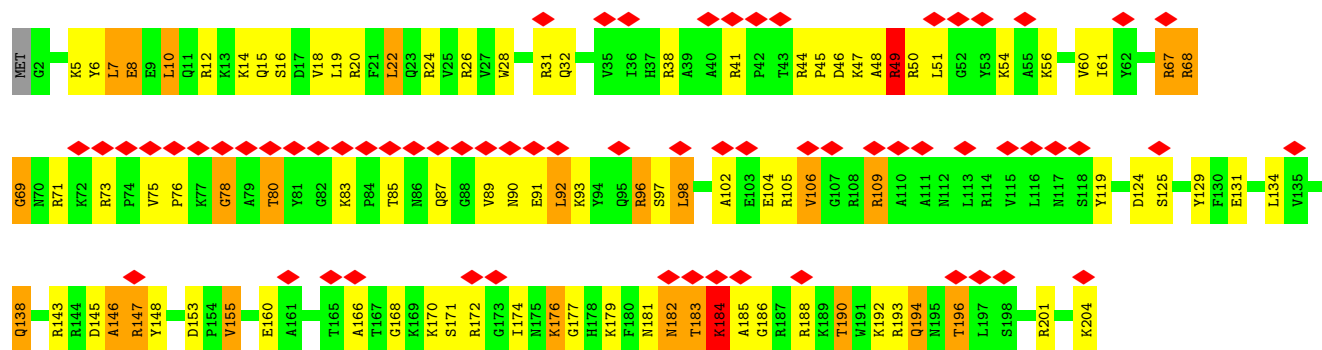




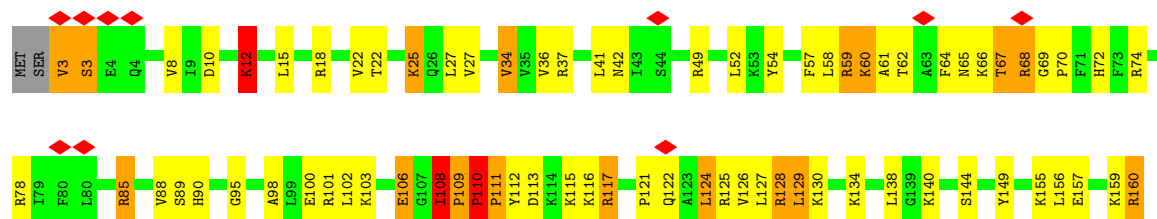
• Molecule 13: 60S ribosomal protein L14-A

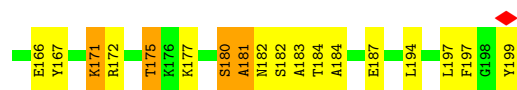


• Molecule 14: 60S ribosomal protein L15-A

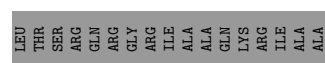


• Molecule 15: Large ribosomal subunit protein uL13A

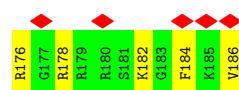
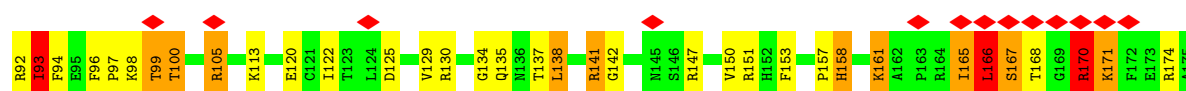
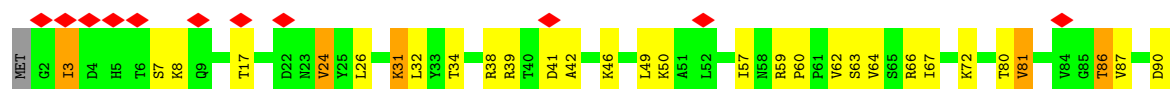




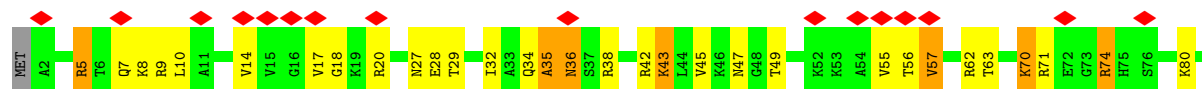
• Molecule 16: 60S ribosomal protein L17-A



• Molecule 17: 60S ribosomal protein L18-A

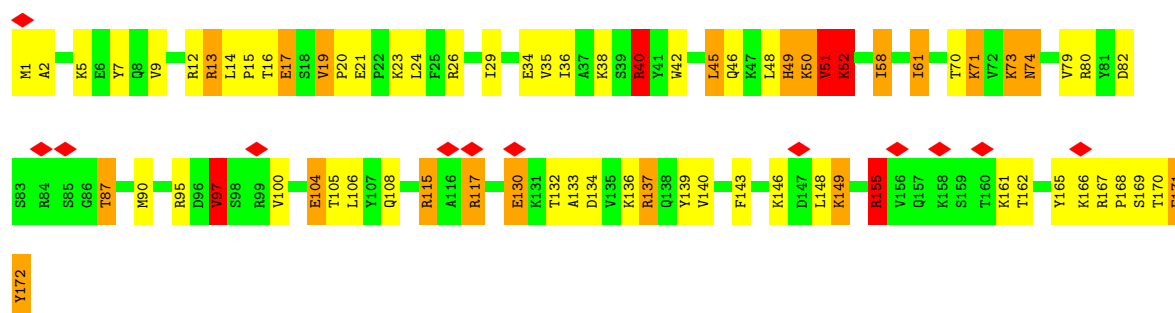


• Molecule 18: 60S ribosomal protein L19-A

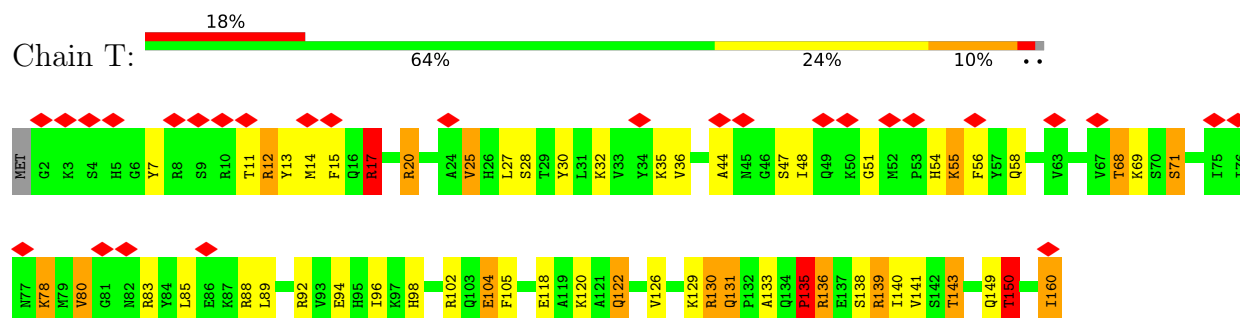


• Molecule 19: 60S ribosomal protein L20-A

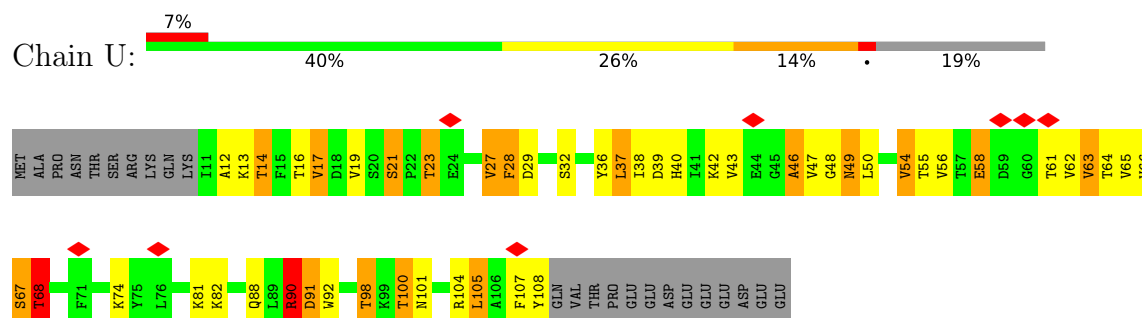




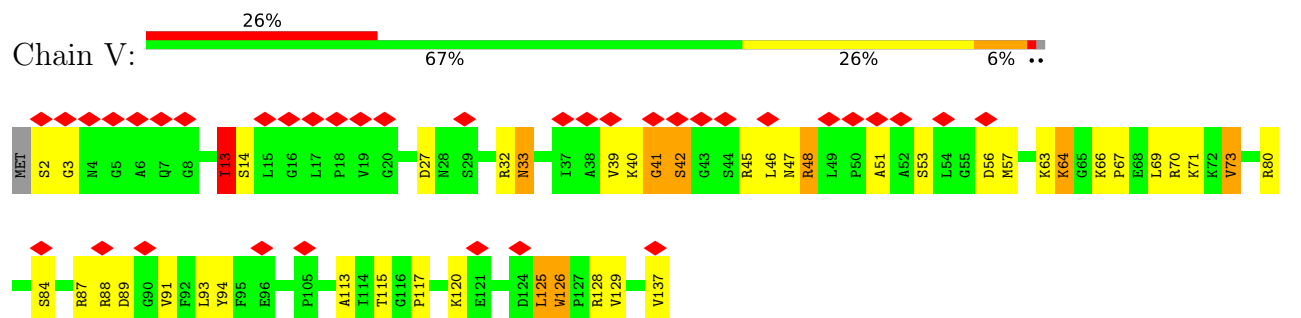
- Molecule 20: 60S ribosomal protein L21-A



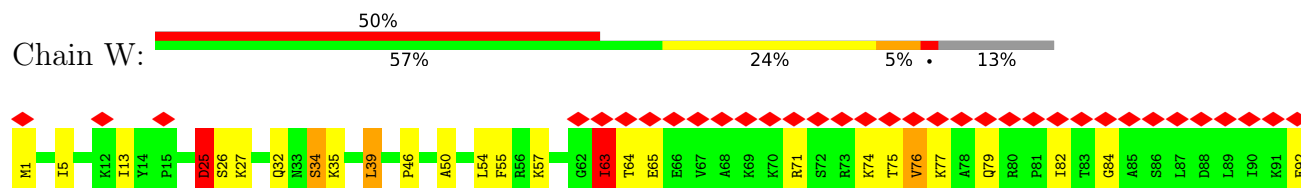
- Molecule 21: 60S ribosomal protein L22-A



- Molecule 22: 60S ribosomal protein L23-A

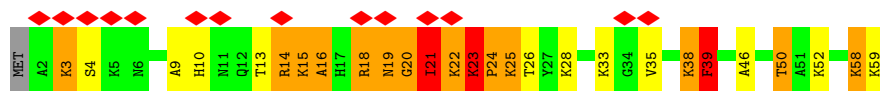


- Molecule 23: 60S ribosomal protein L24-A

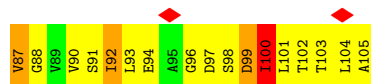
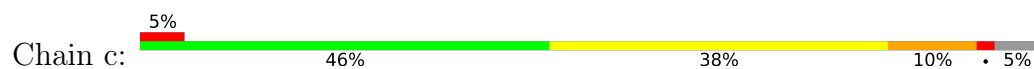




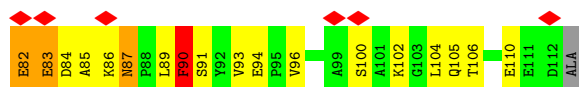
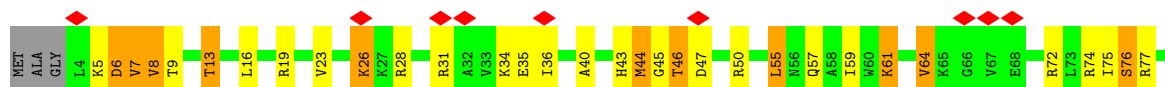
- Molecule 28: 60S ribosomal protein L29



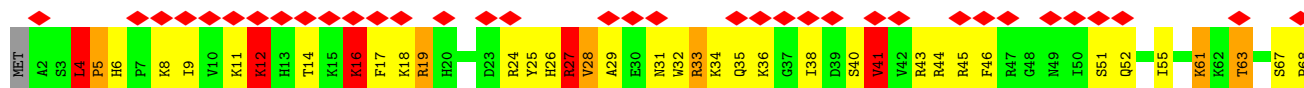
- Molecule 29: 60S ribosomal protein L30



- Molecule 30: 60S ribosomal protein L31-A

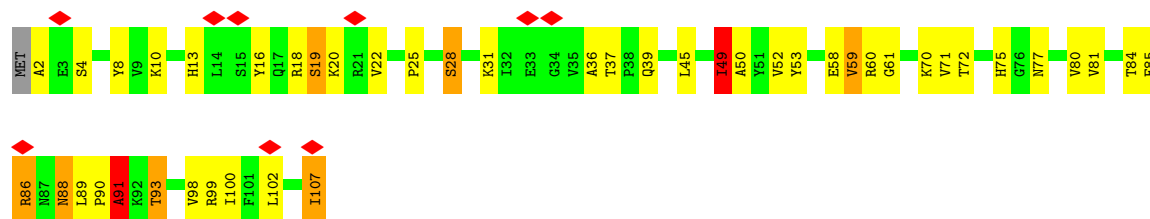


- Molecule 31: 60S ribosomal protein L32

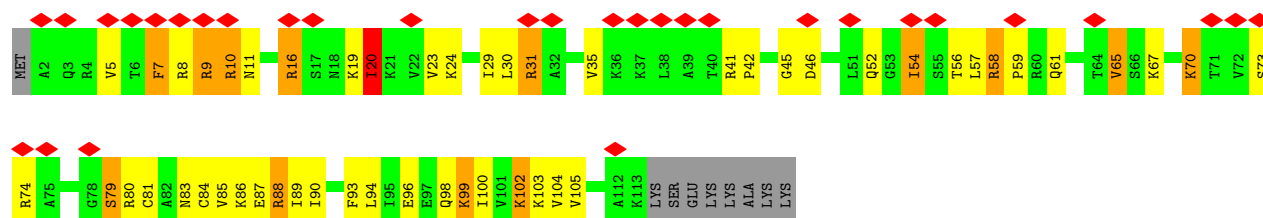


- Molecule 32: 60S ribosomal protein L33-A

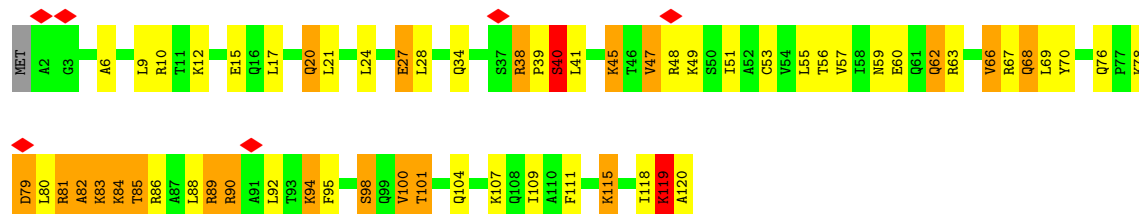




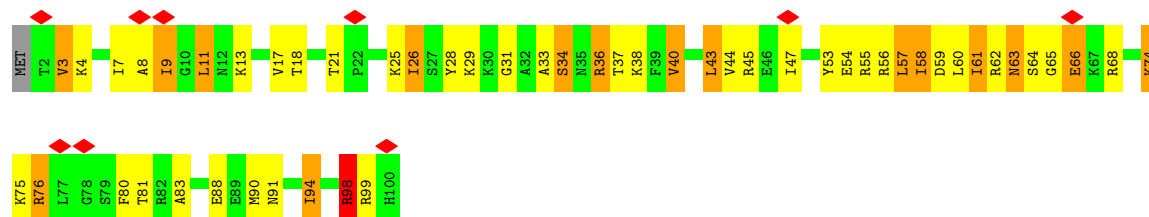
- Molecule 33: 60S ribosomal protein L34-A



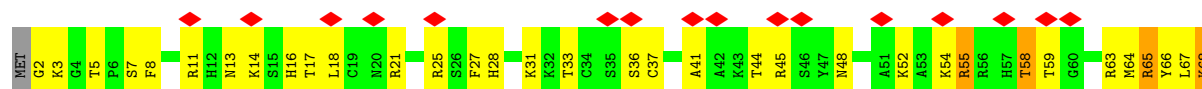
- Molecule 34: 60S ribosomal protein L35-A



- Molecule 35: 60S ribosomal protein L36-A



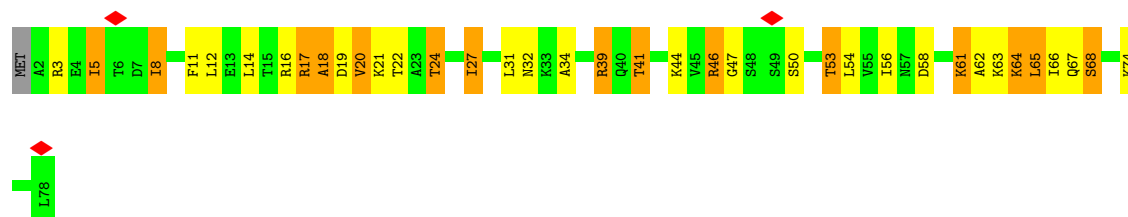
- Molecule 36: 60S ribosomal protein L37-A





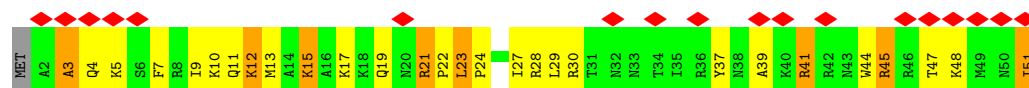
- Molecule 37: 60S ribosomal protein L38

Chain k: 51% 28% 19%



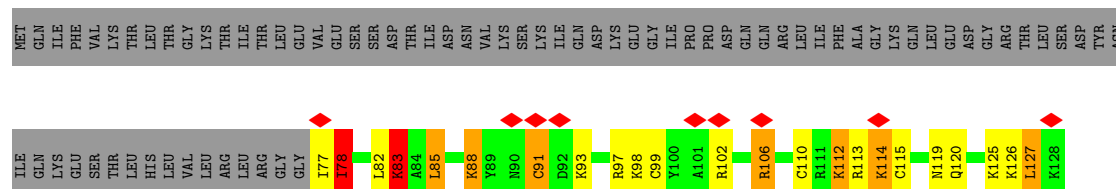
- Molecule 38: 60S ribosomal protein L39

Chain l: 35% 43% 39% 16%



- Molecule 39: Ubiquitin-60S ribosomal protein L40

Chain m: 7% 23% 11% 5% 59%



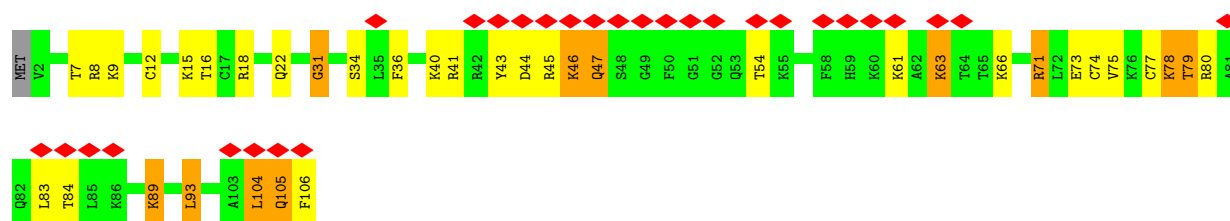
- Molecule 40: 60S ribosomal protein L41-A

Chain n: 100% 44% 24% 32%



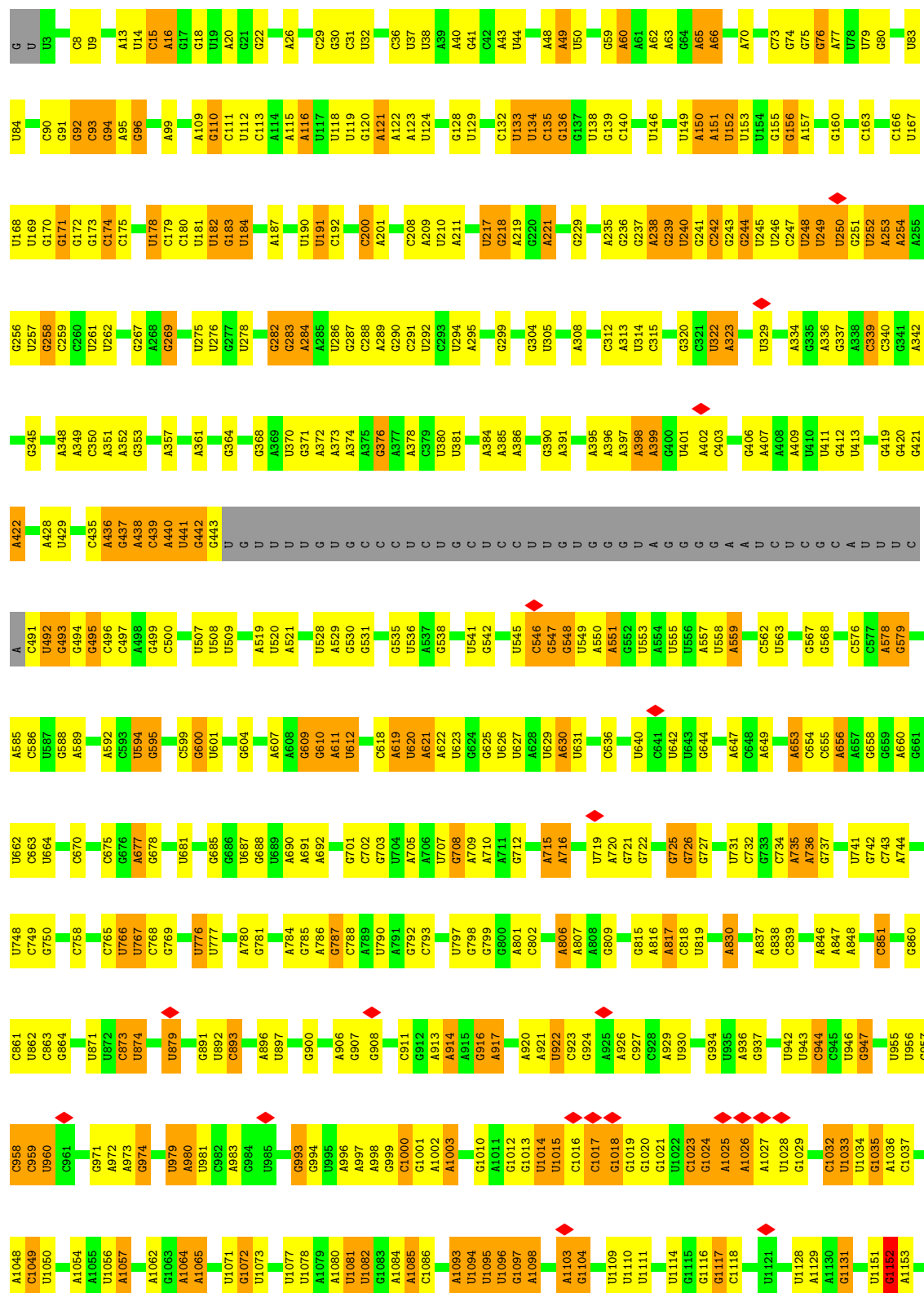
- Molecule 41: 60S ribosomal protein L42-A

Chain o: 27% 64% 25% 10%

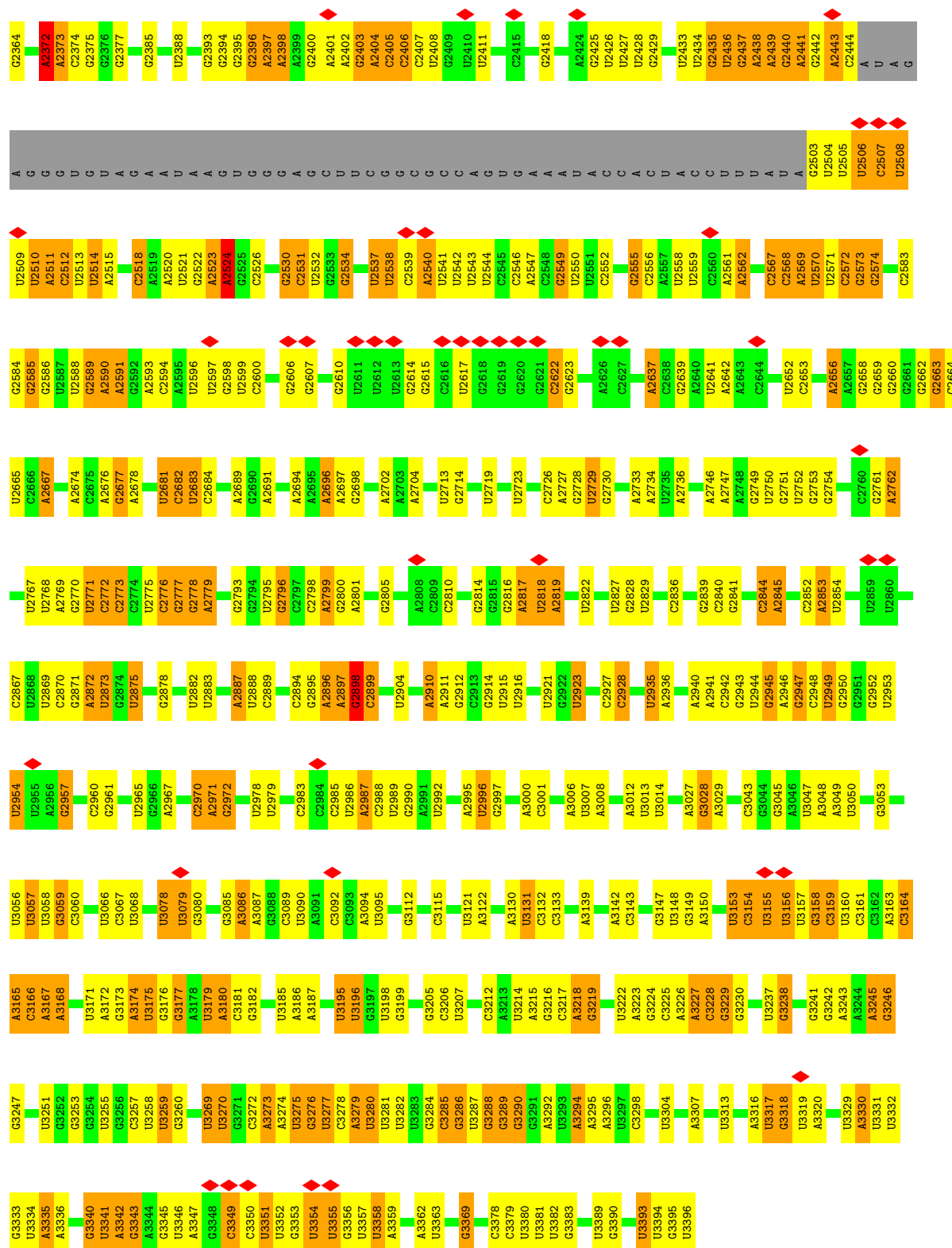


● Molecule 48: 25S RIBOSOMAL RNA

Chain 5:





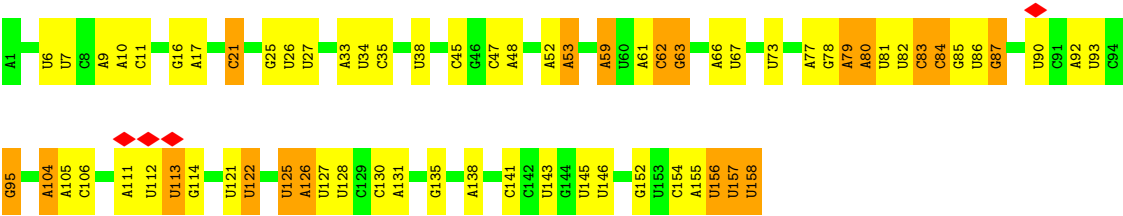


• Molecule 49: 5S RIBOSOMAL RNA

Chain 7: 57% 40%



• Molecule 50: 5.8S RIBOSOMAL RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	84113	Depositor
Resolution determination method	Not provided	
CTF correction method	PER FRAME	Depositor
Microscope	FEI TECNAI 20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	83000	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor
Maximum map value	425.313	Depositor
Minimum map value	-221.732	Depositor
Average map value	-13.190	Depositor
Map value standard deviation	29.801	Depositor
Recommended contour level	35	Depositor
Map size ($\text{\AA}$)	405.44, 405.44, 405.44	wwPDB
Map dimensions	224, 224, 224	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.81, 1.81, 1.81	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	1.11	4/1946 (0.2%)	1.43	18/2614 (0.7%)
2	B	1.23	4/3146 (0.1%)	1.44	26/4228 (0.6%)
3	C	1.12	6/2800 (0.2%)	1.43	34/3790 (0.9%)
4	D	1.02	1/2408 (0.0%)	1.27	21/3248 (0.6%)
5	E	1.07	0/1269	1.37	11/1705 (0.6%)
6	F	1.17	2/1828 (0.1%)	1.43	26/2461 (1.1%)
7	G	0.78	0/1795	1.18	14/2429 (0.6%)
8	H	1.17	0/1539	1.45	13/2073 (0.6%)
9	I	1.11	0/1758	1.38	12/2358 (0.5%)
10	J	0.99	1/1374 (0.1%)	1.36	17/1842 (0.9%)
12	L	1.06	3/1573 (0.2%)	1.40	19/2113 (0.9%)
13	M	1.18	0/1074	1.36	9/1446 (0.6%)
14	N	0.99	2/1757 (0.1%)	1.30	14/2354 (0.6%)
15	O	0.64	0/3159	0.95	14/4205 (0.3%)
16	P	1.34	3/1250 (0.2%)	1.41	6/1683 (0.4%)
17	Q	1.08	1/1465 (0.1%)	1.42	10/1965 (0.5%)
18	R	0.94	0/1538	1.21	5/2050 (0.2%)
19	S	1.20	3/1481 (0.2%)	1.43	17/1990 (0.9%)
20	T	1.16	2/1300 (0.2%)	1.35	6/1743 (0.3%)
21	U	0.67	0/794	1.20	8/1076 (0.7%)
22	V	1.25	2/1018 (0.2%)	1.42	6/1369 (0.4%)
23	W	0.99	0/1052	1.22	7/1398 (0.5%)
24	X	0.87	0/974	1.25	7/1314 (0.5%)
25	Y	0.94	0/1004	1.31	6/1341 (0.4%)
26	Z	0.65	0/1118	1.18	9/1497 (0.6%)
27	a	1.20	6/1204 (0.5%)	1.59	29/1612 (1.8%)
28	b	1.20	2/473 (0.4%)	1.61	10/629 (1.6%)
29	c	0.72	0/775	1.11	3/1040 (0.3%)
30	d	1.11	1/897 (0.1%)	1.32	8/1205 (0.7%)
31	e	1.23	4/1041 (0.4%)	1.58	9/1394 (0.6%)
32	f	1.34	6/868 (0.7%)	1.40	6/1168 (0.5%)
33	g	0.87	0/890	1.26	3/1189 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	h	0.81	0/974	1.15	2/1297 (0.2%)
35	i	0.84	0/777	1.17	2/1033 (0.2%)
36	j	1.02	0/696	1.35	4/923 (0.4%)
37	k	0.66	0/614	1.07	1/822 (0.1%)
38	l	1.03	0/443	1.28	0/588
39	m	1.29	0/423	1.42	5/562 (0.9%)
40	n	1.05	0/234	1.25	2/300 (0.7%)
41	o	0.95	0/860	1.24	0/1136
42	p	1.01	1/701 (0.1%)	1.39	8/934 (0.9%)
43	q	0.62	0/1092	1.11	5/1474 (0.3%)
46	t	5.60	20/2985 (0.7%)	4.28	206/4053 (5.1%)
48	5	0.82	25/75414 (0.0%)	0.66	13/117575 (0.0%)
49	7	0.78	0/2883	0.63	0/4491
50	8	0.66	0/3746	0.61	0/5832
All	All	1.22	99/138410 (0.1%)	1.12	651/203549 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
3	C	0	1
4	D	0	1
5	E	0	1
6	F	0	2
15	O	0	2
19	S	0	1
22	V	0	1
25	Y	0	1
26	Z	0	1
27	a	0	3
28	b	0	1
46	t	0	6
48	5	0	1
All	All	0	24

All (99) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	t	168	PRO	N-CD	120.82	3.16	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	t	545	PRO	N-CD	120.55	3.16	1.47
46	t	162	PRO	N-CD	120.19	3.16	1.47
46	t	172	PRO	N-CD	118.17	3.13	1.47
46	t	520	PRO	N-CD	117.30	3.12	1.47
46	t	175	PRO	N-CD	55.92	2.26	1.47
46	t	62	PRO	N-CD	54.00	2.23	1.47
46	t	135	PRO	N-CD	53.69	2.23	1.47
46	t	240	PRO	N-CD	53.01	2.21	1.47
46	t	357	PRO	N-CD	52.69	2.21	1.47
46	t	436	PRO	N-CD	51.42	2.19	1.47
46	t	305	PRO	N-CD	47.63	2.14	1.47
1	A	211	HIS	C-O	12.12	1.38	1.24
46	t	510	CYS	CB-SG	-11.80	1.42	1.81
46	t	105	CYS	CB-SG	-11.77	1.42	1.81
46	t	504	CYS	CB-SG	-11.77	1.42	1.81
46	t	432	CYS	CB-SG	-11.76	1.42	1.81
46	t	532	CYS	CB-SG	-11.75	1.42	1.81
16	P	66	SER	C-O	8.89	1.35	1.24
32	f	91	ALA	N-CA	7.92	1.56	1.46
48	5	2914	G	P-OP2	-7.71	1.33	1.49
3	C	101	ALA	C-O	7.67	1.27	1.23
27	a	15	VAL	C-O	7.42	1.33	1.24
48	5	1178	G	P-OP2	-6.94	1.35	1.49
31	e	28	VAL	CA-CB	6.88	1.62	1.53
1	A	157	VAL	CA-CB	6.83	1.62	1.54
27	a	15	VAL	CA-CB	-6.81	1.47	1.54
48	5	2817	A	P-OP1	-6.80	1.35	1.49
12	L	46	ILE	CA-CB	6.80	1.62	1.54
12	L	76	THR	CA-CB	6.53	1.64	1.53
48	5	41	G	P-OP1	-6.53	1.35	1.49
48	5	934	G	P-OP1	-6.30	1.36	1.49
30	d	7	VAL	CA-CB	6.30	1.63	1.54
14	N	183	THR	CA-CB	6.28	1.64	1.53
27	a	28	HIS	N-CA	6.28	1.54	1.46
46	t	85	ASN	C-N	-6.26	1.24	1.33
48	5	1902	G	P-OP1	-6.24	1.36	1.49
46	t	21	GLN	C-N	-6.22	1.25	1.33
17	Q	171	LYS	CE-NZ	6.15	1.67	1.49
48	5	2141	U	P-OP2	-6.09	1.36	1.49
48	5	2949	U	P-OP1	-6.09	1.36	1.49
28	b	16	ALA	CA-CB	-6.07	1.42	1.53
48	5	1430	U	P-OP1	-6.05	1.36	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	145	ILE	CA-CB	6.00	1.61	1.54
3	C	354	VAL	C-O	-5.97	1.17	1.24
32	f	22	VAL	CA-CB	-5.93	1.46	1.54
48	5	2887	A	P-OP2	-5.92	1.37	1.49
48	5	1152	G	N9-C4	-5.91	1.26	1.38
1	A	225	ILE	C-O	-5.90	1.17	1.24
48	5	340	C	P-OP1	-5.85	1.37	1.49
19	S	29	ILE	CA-CB	-5.84	1.47	1.54
19	S	36	ILE	CA-CB	-5.78	1.47	1.54
3	C	101	ALA	CA-CB	-5.77	1.48	1.52
16	P	137	ASN	CA-C	-5.74	1.45	1.52
48	5	1449	A	P-OP2	-5.73	1.37	1.49
22	V	73	VAL	CA-CB	5.71	1.61	1.54
6	F	227	GLY	C-O	-5.60	1.18	1.23
48	5	942	U	P-OP1	-5.52	1.38	1.49
46	t	551	GLN	C-N	5.45	1.41	1.33
42	p	54	ILE	CA-CB	5.41	1.60	1.54
2	B	227	GLU	CA-C	-5.38	1.46	1.52
48	5	1307	G	C3'-O3'	5.37	1.51	1.43
31	e	77	ALA	CA-CB	-5.37	1.44	1.53
20	T	150	THR	CA-CB	5.36	1.61	1.53
32	f	36	ALA	CA-CB	-5.36	1.45	1.54
48	5	1152	G	C2-N3	-5.33	1.22	1.32
16	P	88	VAL	CA-CB	-5.33	1.48	1.54
32	f	50	ALA	CA-CB	-5.31	1.43	1.53
27	a	8	THR	N-CA	-5.29	1.39	1.46
48	5	2754	G	P-OP1	-5.29	1.38	1.49
3	C	358	THR	CA-CB	5.26	1.61	1.53
48	5	1152	G	N9-C8	5.26	1.48	1.37
48	5	1835	A	P-OP1	-5.25	1.38	1.49
20	T	44	ALA	CA-CB	-5.24	1.45	1.53
48	5	1369	A	P-OP2	-5.23	1.38	1.49
10	J	8	PRO	CB-CG	5.23	1.75	1.49
27	a	22	ILE	CA-CB	-5.22	1.47	1.54
19	S	35	VAL	CA-CB	-5.22	1.48	1.54
32	f	52	VAL	CA-CB	5.21	1.60	1.54
3	C	52	VAL	CA-CB	-5.20	1.49	1.54
1	A	12	ALA	CA-CB	-5.19	1.44	1.53
6	F	130	ILE	CA-CB	-5.18	1.48	1.54
27	a	47	LYS	N-CA	5.16	1.52	1.46
48	5	2945	G	P-O5'	-5.15	1.52	1.59
22	V	13	ILE	CA-CB	5.12	1.61	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	f	91	ALA	CA-CB	5.12	1.62	1.53
2	B	260	VAL	CA-CB	-5.12	1.49	1.54
31	e	12	LYS	N-CA	5.12	1.52	1.46
4	D	119	TYR	N-CA	5.11	1.52	1.46
48	5	2214	A	P-OP2	-5.10	1.38	1.49
28	b	15	LYS	C-O	-5.07	1.18	1.24
48	5	348	A	P-OP1	-5.07	1.38	1.49
2	B	53	MET	SD-CE	-5.07	1.66	1.79
31	e	29	ALA	CA-CB	-5.06	1.45	1.53
2	B	367	LYS	CE-NZ	5.05	1.64	1.49
48	5	1837	U	P-OP2	-5.05	1.38	1.49
14	N	183	THR	N-CA	5.04	1.52	1.46
48	5	922	U	P-OP2	-5.02	1.39	1.49
12	L	152	THR	CA-CB	5.00	1.61	1.53

All (651) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	t	81	LYS	O-C-N	-96.20	4.54	122.87
46	t	544	ASN	O-C-N	-71.67	32.42	121.29
46	t	520	PRO	N-CA-CB	51.27	148.48	103.36
46	t	15	LYS	O-C-N	-50.72	41.85	123.00
46	t	168	PRO	N-CA-CB	50.42	148.65	103.27
46	t	172	PRO	N-CA-CB	43.21	148.62	103.25
46	t	545	PRO	N-CA-CB	43.12	148.52	103.25
46	t	516	THR	N-CA-CB	35.32	154.44	114.17
46	t	162	PRO	N-CA-CB	34.31	148.71	103.42
46	t	162	PRO	CA-N-CD	-33.05	65.72	112.00
46	t	168	PRO	CA-N-CD	-33.01	65.78	112.00
46	t	545	PRO	CA-N-CD	-32.99	65.81	112.00
46	t	172	PRO	CA-N-CD	-32.67	66.26	112.00
46	t	520	PRO	CA-N-CD	-32.61	66.34	112.00
46	t	520	PRO	CB-CA-C	-30.30	74.79	111.46
46	t	526	THR	N-CA-CB	29.48	155.98	110.28
46	t	166	THR	N-CA-CB	29.45	155.66	110.30
46	t	168	PRO	CB-CA-C	-28.73	75.45	111.64
46	t	60	THR	N-CA-CB	28.53	156.29	111.22
46	t	517	THR	N-CA-CB	28.46	155.25	110.57
46	t	531	THR	N-CA-CB	27.87	155.38	110.23
46	t	55	THR	N-CA-CB	27.76	155.33	110.92
46	t	54	THR	N-CA-CB	26.89	156.03	110.32
46	t	516	THR	CB-CA-C	-25.49	73.36	110.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	t	163	VAL	N-CA-CB	24.06	142.37	110.13
46	t	162	PRO	CB-CA-C	-23.17	76.24	111.22
46	t	61	VAL	N-CA-CB	22.38	142.54	111.21
46	t	545	PRO	CB-CA-C	-22.27	74.81	111.56
46	t	55	THR	CB-CA-C	-22.02	75.57	111.02
46	t	172	PRO	CB-CA-C	-21.70	75.75	111.56
46	t	514	VAL	N-CA-CB	21.36	142.71	111.52
46	t	387	VAL	CB-CA-C	-20.68	82.74	111.28
46	t	531	THR	CB-CA-C	-20.24	76.13	109.53
46	t	517	THR	CB-CA-C	-19.88	75.34	109.72
46	t	246	ARG	NH1-CZ-NH2	19.46	144.60	119.30
46	t	29	ARG	NH1-CZ-NH2	19.44	144.58	119.30
46	t	75	ARG	NH1-CZ-NH2	19.43	144.56	119.30
46	t	57	ARG	NH1-CZ-NH2	19.42	144.55	119.30
46	t	243	ARG	NH1-CZ-NH2	19.41	144.53	119.30
46	t	519	ARG	NH1-CZ-NH2	19.41	144.53	119.30
46	t	441	ARG	NH1-CZ-NH2	19.41	144.53	119.30
46	t	502	ARG	NH1-CZ-NH2	19.40	144.53	119.30
46	t	134	ARG	NH1-CZ-NH2	19.39	144.51	119.30
46	t	245	ARG	NH1-CZ-NH2	19.37	144.47	119.30
46	t	249	ARG	NH1-CZ-NH2	19.35	144.46	119.30
46	t	248	ARG	NH1-CZ-NH2	19.34	144.44	119.30
46	t	87	ARG	NH1-CZ-NH2	19.34	144.44	119.30
46	t	224	ARG	NH1-CZ-NH2	19.33	144.43	119.30
46	t	232	ARG	NH1-CZ-NH2	19.31	144.40	119.30
46	t	84	VAL	N-CA-CB	19.06	142.69	111.23
46	t	550	VAL	N-CA-CB	18.54	141.82	111.23
31	e	4	LEU	CA-C-N	-17.04	98.54	119.84
31	e	4	LEU	C-N-CA	-17.04	98.54	119.84
46	t	514	VAL	CB-CA-C	-17.03	85.47	110.33
46	t	526	THR	CB-CA-C	-17.01	78.01	110.67
46	t	550	VAL	CB-CA-C	-16.93	83.53	111.29
46	t	166	THR	CB-CA-C	-16.63	76.45	110.38
46	t	163	VAL	CB-CA-C	-16.40	84.86	111.59
46	t	387	VAL	N-CA-CB	15.90	141.45	110.45
46	t	84	VAL	CB-CA-C	-15.68	85.57	111.29
46	t	60	THR	CB-CA-C	-15.44	78.69	111.11
46	t	54	THR	CB-CA-C	-15.38	77.86	110.32
46	t	61	VAL	CB-CA-C	-14.51	84.95	111.36
46	t	246	ARG	NE-CZ-NH1	-13.82	107.68	121.50
46	t	441	ARG	NE-CZ-NH1	-13.81	107.69	121.50
46	t	75	ARG	NE-CZ-NH1	-13.80	107.70	121.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	t	243	ARG	NE-CZ-NH1	-13.78	107.72	121.50
46	t	29	ARG	NE-CZ-NH1	-13.77	107.73	121.50
46	t	19	ILE	CB-CA-C	-13.76	91.96	112.05
46	t	502	ARG	NE-CZ-NH1	-13.76	107.74	121.50
46	t	248	ARG	NE-CZ-NH1	-13.76	107.74	121.50
46	t	57	ARG	NE-CZ-NH1	-13.75	107.75	121.50
46	t	224	ARG	NE-CZ-NH1	-13.71	107.78	121.50
46	t	87	ARG	NE-CZ-NH1	-13.71	107.79	121.50
46	t	519	ARG	NE-CZ-NH1	-13.71	107.79	121.50
46	t	134	ARG	NE-CZ-NH1	-13.70	107.80	121.50
46	t	249	ARG	NE-CZ-NH1	-13.70	107.81	121.50
46	t	245	ARG	NE-CZ-NH1	-13.68	107.82	121.50
46	t	232	ARG	NE-CZ-NH1	-13.67	107.83	121.50
46	t	19	ILE	N-CA-CB	13.16	131.20	110.54
46	t	519	ARG	NE-CZ-NH2	-12.80	107.68	119.20
46	t	134	ARG	NE-CZ-NH2	-12.79	107.69	119.20
46	t	29	ARG	NE-CZ-NH2	-12.79	107.69	119.20
46	t	57	ARG	NE-CZ-NH2	-12.78	107.70	119.20
46	t	245	ARG	NE-CZ-NH2	-12.78	107.70	119.20
46	t	246	ARG	NE-CZ-NH2	-12.77	107.71	119.20
46	t	169	ILE	CB-CA-C	-12.75	90.38	111.29
46	t	75	ARG	NE-CZ-NH2	-12.74	107.74	119.20
46	t	502	ARG	NE-CZ-NH2	-12.74	107.74	119.20
46	t	249	ARG	NE-CZ-NH2	-12.73	107.74	119.20
46	t	243	ARG	NE-CZ-NH2	-12.72	107.75	119.20
46	t	232	ARG	NE-CZ-NH2	-12.70	107.77	119.20
46	t	87	ARG	NE-CZ-NH2	-12.69	107.78	119.20
46	t	441	ARG	NE-CZ-NH2	-12.69	107.78	119.20
46	t	224	ARG	NE-CZ-NH2	-12.68	107.79	119.20
46	t	248	ARG	NE-CZ-NH2	-12.65	107.81	119.20
12	L	47	ALA	CA-C-N	-12.28	106.94	120.94
12	L	47	ALA	C-N-CA	-12.28	106.94	120.94
46	t	52	SER	N-CA-CB	11.87	127.58	110.12
46	t	515	SER	CB-CA-C	-11.66	95.33	111.89
46	t	544	ASN	C-N-CD	11.58	172.48	125.00
46	t	169	ILE	N-CA-CB	11.53	130.25	111.23
46	t	49	SER	N-CA-CB	11.53	127.22	110.16
12	L	46	ILE	N-CA-C	-11.33	102.02	112.90
46	t	512	SER	N-CA-CB	10.93	127.70	110.55
46	t	548	SER	N-CA-CB	10.85	127.29	110.14
46	t	513	SER	N-CA-CB	10.83	128.24	110.37
19	S	134	ASP	N-CA-C	-10.75	99.74	113.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	t	171	GLN	C-N-CD	10.69	168.81	125.00
46	t	529	SER	N-CA-CB	10.45	126.32	110.22
46	t	50	TYR	N-CA-CB	10.39	125.54	110.16
46	t	515	SER	N-CA-CB	10.37	127.05	111.70
42	p	16	VAL	CB-CA-C	9.93	120.53	110.70
17	Q	59	ARG	CA-C-N	-9.83	110.25	120.38
17	Q	59	ARG	C-N-CA	-9.83	110.25	120.38
46	t	519	ARG	C-N-CD	9.79	165.13	125.00
46	t	168	PRO	N-CD-CG	-9.74	88.59	103.20
46	t	388	TYR	N-CA-CB	9.68	125.44	110.43
46	t	545	PRO	N-CD-CG	-9.66	88.70	103.20
26	Z	27	LYS	CA-C-N	9.51	130.50	119.47
26	Z	27	LYS	C-N-CA	9.51	130.50	119.47
15	O	109[A]	PRO	O-C-N	9.49	125.61	121.15
15	O	109[B]	PRO	O-C-N	9.49	125.61	121.15
46	t	510	CYS	CB-CA-C	-9.48	94.51	110.43
46	t	167	LYS	C-N-CD	9.47	163.81	125.00
24	X	65	GLN	CA-C-N	-9.39	111.19	120.21
24	X	65	GLN	C-N-CA	-9.39	111.19	120.21
46	t	532	CYS	N-CA-CB	9.37	127.10	111.08
42	p	15	GLY	CA-C-N	-9.34	111.52	122.36
42	p	15	GLY	C-N-CA	-9.34	111.52	122.36
36	j	5	THR	CA-C-N	-9.33	109.30	119.19
36	j	5	THR	C-N-CA	-9.33	109.30	119.19
46	t	510	CYS	N-CA-CB	9.33	125.74	111.56
46	t	162	PRO	N-CD-CG	-9.29	89.26	103.20
46	t	56	GLN	CB-CA-C	-9.21	97.11	111.39
46	t	172	PRO	N-CD-CG	-9.04	89.64	103.20
17	Q	170	ARG	N-CA-C	-9.03	98.08	110.35
2	B	114	VAL	CB-CA-C	-9.01	100.17	112.24
46	t	357	PRO	N-CA-CB	9.00	111.28	103.36
46	t	175	PRO	CA-N-CD	-8.99	99.42	112.00
46	t	49	SER	CB-CA-C	-8.97	95.60	110.85
27	a	46	ASP	N-CA-C	-8.92	95.81	110.17
6	F	94	LYS	CA-C-N	-8.87	113.67	123.43
6	F	94	LYS	C-N-CA	-8.87	113.67	123.43
46	t	529	SER	CB-CA-C	-8.86	94.23	110.63
2	B	2	SER	N-CA-C	-8.84	86.25	111.00
30	d	46	THR	N-CA-C	8.83	120.67	111.14
46	t	52	SER	CB-CA-C	-8.81	96.16	110.79
27	a	15	VAL	N-CA-C	-8.81	96.88	110.09
27	a	67	HIS	N-CA-C	-8.77	101.64	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	H	151	VAL	CB-CA-C	-8.74	100.59	112.04
21	U	46	ALA	N-CA-C	8.67	119.38	108.45
10	J	9	MET	N-CA-C	-8.64	92.40	110.80
46	t	520	PRO	N-CD-CG	-8.61	90.28	103.20
28	b	39	PHE	N-CA-CB	8.60	125.02	110.49
46	t	383	ASP	O-C-N	-8.59	111.00	122.43
46	t	62	PRO	CA-N-CD	-8.55	100.04	112.00
4	D	271	LYS	N-CA-C	-8.52	101.02	112.26
46	t	546	GLN	N-CA-CB	8.47	122.69	110.16
46	t	512	SER	CB-CA-C	-8.45	96.33	110.19
28	b	23	LYS	CA-C-N	-8.44	109.29	119.84
28	b	23	LYS	C-N-CA	-8.44	109.29	119.84
46	t	17	LYS	N-CA-CB	8.43	123.79	110.65
1	A	55	GLY	N-CA-C	-8.40	102.27	111.93
27	a	28	HIS	N-CA-C	8.33	128.21	109.81
46	t	551	GLN	N-CA-CB	8.29	123.83	110.16
46	t	513	SER	CB-CA-C	-8.26	97.56	110.78
1	A	238	ILE	CA-C-N	-8.25	109.30	123.25
1	A	238	ILE	C-N-CA	-8.25	109.30	123.25
46	t	167	LYS	CB-CA-C	-8.24	100.42	111.21
48	5	1152	G	C8-N9-C1'	8.23	151.68	127.00
46	t	385	GLN	N-CA-CB	8.14	122.36	110.06
46	t	171	GLN	N-CA-CB	8.14	123.04	110.43
30	d	6	ASP	N-CA-C	8.13	120.66	109.11
46	t	50	TYR	CB-CA-C	-8.04	97.17	110.85
46	t	135	PRO	N-CD-CG	-8.04	91.15	103.20
10	J	151	SER	N-CA-C	-8.01	99.96	110.53
46	t	357	PRO	CA-N-CD	-7.97	100.84	112.00
9	I	169	LYS	N-CA-C	-7.97	98.23	110.10
27	a	15	VAL	CA-C-N	-7.97	110.92	125.66
27	a	15	VAL	C-N-CA	-7.97	110.92	125.66
32	f	49	ILE	CB-CA-C	-7.94	98.59	110.82
2	B	205	VAL	CB-CA-C	-7.93	99.86	112.16
46	t	388	TYR	CB-CA-C	-7.93	96.90	112.05
15	O	3[B]	SER	CA-C-N	7.92	141.14	121.80
15	O	3[B]	SER	C-N-CA	7.92	141.14	121.80
14	N	182	ASN	N-CA-C	-7.91	98.61	110.24
2	B	129	ALA	CA-C-N	-7.90	109.83	122.95
2	B	129	ALA	C-N-CA	-7.90	109.83	122.95
28	b	38	LYS	N-CA-C	-7.89	98.59	110.28
46	t	161	TYR	C-N-CD	7.88	157.30	125.00
46	t	161	TYR	N-CA-CB	7.88	125.36	111.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	232	GLY	N-CA-C	-7.86	104.59	113.79
46	t	175	PRO	N-CA-CB	7.86	111.50	103.25
19	S	19	VAL	CA-C-N	-7.85	112.75	120.52
19	S	19	VAL	C-N-CA	-7.85	112.75	120.52
46	t	549	ILE	CB-CA-C	-7.83	88.25	111.05
46	t	240	PRO	N-CA-CB	7.81	110.30	103.27
46	t	240	PRO	N-CD-CG	-7.79	91.51	103.20
46	t	62	PRO	N-CA-CB	7.78	111.42	103.25
27	a	14	HIS	N-CA-C	-7.77	97.02	109.76
10	J	133	ARG	CA-C-N	-7.74	112.02	119.76
10	J	133	ARG	C-N-CA	-7.74	112.02	119.76
3	C	319	LYS	N-CA-C	-7.72	98.80	110.14
12	L	100	ARG	N-CA-C	-7.71	100.35	110.53
4	D	6	ASP	N-CA-C	-7.70	103.87	112.57
46	t	436	PRO	N-CD-CG	-7.70	91.65	103.20
6	F	191	VAL	CA-C-N	-7.68	109.81	121.87
6	F	191	VAL	C-N-CA	-7.68	109.81	121.87
14	N	185	ALA	N-CA-C	-7.65	103.94	113.20
17	Q	99	THR	N-CA-C	7.64	127.08	110.80
46	t	170	LEU	N-CA-CB	7.64	121.15	110.07
46	t	240	PRO	CA-N-CD	-7.54	101.44	112.00
27	a	101	VAL	N-CA-C	-7.54	101.84	110.05
46	t	548	SER	CB-CA-C	-7.52	95.86	110.46
46	t	549	ILE	N-CA-CB	7.51	128.96	111.23
46	t	53	LYS	N-CA-CB	7.50	121.15	110.12
46	t	305	PRO	N-CA-CB	7.48	110.42	103.46
46	t	509	LEU	N-CA-CB	7.45	122.30	110.23
33	g	7	PHE	N-CA-C	-7.45	100.00	110.50
14	N	67	ARG	N-CA-C	7.44	120.45	111.82
15	O	108[A]	ILE	CA-C-N	7.43	125.09	119.66
15	O	108[A]	ILE	C-N-CA	7.43	125.09	119.66
15	O	108[B]	ILE	CA-C-N	7.43	125.09	119.66
15	O	108[B]	ILE	C-N-CA	7.43	125.09	119.66
46	t	161	TYR	CB-CA-C	-7.42	96.67	108.91
46	t	170	LEU	CB-CA-C	-7.42	99.18	110.90
3	C	340	GLY	N-CA-C	-7.42	104.09	115.66
4	D	126	GLU	N-CA-C	-7.41	101.98	113.02
46	t	135	PRO	CA-N-CD	-7.41	101.62	112.00
19	S	52	LYS	N-CA-C	-7.41	98.15	109.85
42	p	71	VAL	CB-CA-C	-7.37	102.26	111.70
12	L	50	PRO	CA-C-O	-7.36	110.29	118.68
46	t	135	PRO	N-CA-CB	7.31	109.77	103.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	t	388	TYR	CA-C-N	-7.30	110.71	119.84
46	t	388	TYR	C-N-CA	-7.30	110.71	119.84
48	5	1152	G	C4-N9-C1'	-7.30	104.59	126.50
3	C	341	SER	N-CA-C	-7.30	101.74	108.75
14	N	61	ILE	N-CA-C	7.29	118.39	107.75
46	t	546	GLN	CB-CA-C	-7.28	98.47	110.85
23	W	75	THR	N-CA-C	7.27	120.25	108.76
48	5	1307	G	C2'-C3'-O3'	7.27	120.41	109.50
4	D	37	VAL	N-CA-C	7.27	117.36	110.53
6	F	130	ILE	N-CA-CB	-7.26	103.69	112.33
46	t	175	PRO	N-CD-CG	-7.25	92.32	103.20
13	M	53	VAL	CA-C-N	7.25	128.39	119.98
13	M	53	VAL	C-N-CA	7.25	128.39	119.98
46	t	51	HIS	N-CA-CB	7.25	120.77	110.12
46	t	305	PRO	N-CD-CG	-7.18	92.42	103.20
3	C	230	VAL	CB-CA-C	-7.18	101.56	112.05
21	U	90	ARG	N-CA-C	-7.17	99.83	110.23
42	p	16	VAL	N-CA-C	-7.16	106.33	113.20
34	h	41	LEU	CA-C-N	7.16	126.78	119.19
34	h	41	LEU	C-N-CA	7.16	126.78	119.19
46	t	59	LEU	N-CA-CB	7.14	121.79	110.65
3	C	204	GLY	CA-C-N	-7.14	113.31	120.31
3	C	204	GLY	C-N-CA	-7.14	113.31	120.31
15	O	109[A]	PRO	CA-C-O	-7.14	115.09	120.73
15	O	109[B]	PRO	CA-C-O	-7.14	115.09	120.73
1	A	207	VAL	CB-CA-C	-7.11	101.14	112.16
10	J	65	ILE	CB-CA-C	-7.09	104.82	111.06
46	t	58	GLN	N-CA-CB	7.09	123.83	111.00
46	t	384	LYS	N-CA-CB	7.09	121.59	110.46
7	G	72	PRO	CA-C-N	7.07	128.68	119.84
7	G	72	PRO	C-N-CA	7.07	128.68	119.84
28	b	19	ASN	CA-C-N	-7.05	115.75	122.66
28	b	19	ASN	C-N-CA	-7.05	115.75	122.66
46	t	62	PRO	N-CD-CG	-7.03	92.65	103.20
12	L	75	PHE	N-CA-C	7.01	122.09	112.90
14	N	76	PRO	CA-C-N	-7.01	111.41	123.25
14	N	76	PRO	C-N-CA	-7.01	111.41	123.25
14	N	90	ASN	CA-C-N	-7.00	111.42	123.25
14	N	90	ASN	C-N-CA	-7.00	111.42	123.25
1	A	14	SER	CB-CA-C	-6.99	108.50	116.54
46	t	436	PRO	N-CA-CB	6.96	109.81	103.33
46	t	385	GLN	CB-CA-C	-6.96	97.78	109.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	t	167	LYS	N-CA-CB	6.94	121.64	110.75
19	S	5	LYS	N-CA-C	-6.93	98.78	109.52
16	P	51	VAL	N-CA-C	-6.89	102.20	111.44
46	t	171	GLN	CB-CA-C	-6.88	98.91	112.05
6	F	95	ILE	CA-C-N	6.87	127.45	120.38
6	F	95	ILE	C-N-CA	6.87	127.45	120.38
2	B	81	THR	CA-C-N	-6.86	113.32	120.38
2	B	81	THR	C-N-CA	-6.86	113.32	120.38
3	C	90	PHE	CA-C-N	-6.85	107.98	121.41
3	C	90	PHE	C-N-CA	-6.85	107.98	121.41
8	H	143	GLU	N-CA-C	6.85	122.18	113.55
46	t	357	PRO	N-CD-CG	-6.80	93.00	103.20
23	W	79	GLN	N-CA-C	6.80	120.48	109.40
46	t	549	ILE	N-CA-C	6.80	121.84	113.00
46	t	53	LYS	CB-CA-C	-6.79	99.51	110.79
32	f	86	ARG	N-CA-C	-6.79	103.88	111.28
30	d	90	PHE	CB-CA-C	-6.78	97.49	110.24
6	F	177	GLY	N-CA-C	-6.78	100.42	112.22
46	t	522	LEU	N-CA-CB	6.76	121.57	110.69
26	Z	90	GLU	N-CA-C	6.75	119.26	111.02
31	e	16	LYS	N-CA-C	6.74	118.42	111.14
7	G	128	LYS	CA-C-N	6.73	126.91	120.31
7	G	128	LYS	C-N-CA	6.73	126.91	120.31
46	t	436	PRO	CA-N-CD	-6.72	102.59	112.00
20	T	11	THR	N-CA-C	6.71	121.17	112.92
30	d	40	ALA	N-CA-C	-6.71	103.89	111.07
9	I	153	ARG	N-CA-C	-6.69	104.14	112.90
21	U	68	THR	N-CA-C	-6.68	103.59	113.61
8	H	169	ASN	N-CA-C	6.68	120.38	111.30
2	B	241	LYS	CA-C-N	-6.67	111.88	121.42
2	B	241	LYS	C-N-CA	-6.67	111.88	121.42
27	a	72	VAL	N-CA-C	6.67	119.00	108.87
18	R	45	VAL	N-CA-C	-6.66	103.74	111.00
31	e	45	ARG	CB-CA-C	-6.65	103.30	111.82
6	F	76	TYR	CA-C-N	-6.65	114.25	123.10
6	F	76	TYR	C-N-CA	-6.65	114.25	123.10
15	O	110[A]	PRO	CA-C-O	-6.65	110.92	120.56
15	O	110[B]	PRO	CA-C-O	-6.65	110.92	120.56
8	H	4	ILE	N-CA-CB	6.63	119.56	110.54
46	t	83	LYS	N-CA-CB	6.63	121.36	110.69
7	G	71	VAL	CA-C-N	-6.62	113.56	120.38
7	G	71	VAL	C-N-CA	-6.62	113.56	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	t	57	ARG	N-CA-CB	6.61	122.33	111.62
35	i	66	GLU	N-CA-C	-6.60	104.86	113.17
4	D	272	TYR	N-CA-C	-6.57	103.59	112.26
16	P	24	VAL	CB-CA-C	-6.57	100.56	110.55
46	t	85	ASN	CA-C-N	6.57	132.80	122.94
46	t	85	ASN	C-N-CA	6.57	132.80	122.94
9	I	140	THR	CB-CA-C	-6.54	100.31	114.10
9	I	99	ILE	CB-CA-C	-6.53	101.10	110.83
46	t	305	PRO	CA-N-CD	-6.52	102.87	112.00
39	m	83	LYS	N-CA-C	-6.51	104.11	111.14
26	Z	28	PRO	N-CA-C	6.51	123.25	113.81
9	I	24	ARG	N-CA-C	-6.49	100.91	110.52
24	X	56	ARG	N-CA-C	-6.49	101.34	110.50
27	a	42	ARG	N-CA-C	6.47	119.33	111.82
3	C	248	VAL	N-CA-C	6.46	117.22	108.17
3	C	192	GLY	N-CA-C	-6.46	106.34	114.16
43	q	84	VAL	N-CA-C	6.46	118.02	108.65
10	J	44	THR	CB-CA-C	6.45	117.08	109.47
25	Y	100	HIS	CA-C-N	-6.45	113.16	119.87
25	Y	100	HIS	C-N-CA	-6.45	113.16	119.87
46	t	51	HIS	CB-CA-C	-6.45	100.09	110.79
12	L	151	ALA	N-CA-C	6.44	119.26	111.40
2	B	286	GLY	N-CA-C	6.44	120.29	111.54
43	q	91	GLU	CA-C-N	-6.43	111.80	119.84
43	q	91	GLU	C-N-CA	-6.43	111.80	119.84
9	I	62	SER	N-CA-C	-6.43	104.27	111.28
46	t	532	CYS	CB-CA-C	-6.43	96.66	109.33
6	F	221	LYS	N-CA-C	-6.43	99.80	108.86
7	G	68	ARG	N-CA-C	-6.42	102.02	110.43
12	L	76	THR	N-CA-CB	6.40	121.31	110.49
27	a	8	THR	CB-CA-C	6.39	121.71	110.85
22	V	42	SER	N-CA-C	6.37	124.36	110.80
19	S	40	ARG	CG-CD-NE	6.35	125.96	112.00
46	t	554	PHE	CA-CB-CG	-6.35	107.45	113.80
46	t	298	PHE	CA-CB-CG	-6.34	107.46	113.80
2	B	228	GLY	N-CA-C	6.33	119.29	112.33
9	I	4	ARG	CB-CA-C	6.32	118.59	109.11
32	f	19	SER	N-CA-C	-6.31	100.03	109.94
48	5	1152	G	N3-C4-N9	-6.31	107.06	126.00
9	I	154	ARG	N-CA-C	-6.31	104.28	112.23
39	m	119	ASN	N-CA-C	-6.30	104.90	112.59
48	5	1152	G	N3-C2-N2	-6.30	101.00	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	t	364	PHE	CA-CB-CG	-6.30	107.50	113.80
46	t	250	PHE	CA-CB-CG	-6.30	107.50	113.80
1	A	148	VAL	N-CA-C	6.29	117.89	108.96
25	Y	56	VAL	N-CA-C	6.29	116.65	108.35
46	t	419	PHE	CA-CB-CG	-6.28	107.52	113.80
3	C	222	VAL	CA-C-N	6.27	127.68	119.84
3	C	222	VAL	C-N-CA	6.27	127.68	119.84
5	E	30	LEU	N-CA-C	6.27	119.12	110.35
23	W	76	VAL	N-CA-C	6.27	122.38	109.34
19	S	171	PHE	N-CA-C	6.26	120.66	112.89
46	t	309	PHE	CA-CB-CG	-6.26	107.54	113.80
46	t	71	PHE	CA-CB-CG	-6.25	107.55	113.80
3	C	115	HIS	N-CA-C	-6.24	104.56	111.36
6	F	174	GLY	N-CA-C	-6.24	105.01	113.37
8	H	151	VAL	N-CA-CB	6.22	118.25	110.47
26	Z	35	SER	N-CA-C	-6.22	100.63	109.96
6	F	98	LYS	CA-C-N	-6.20	112.47	119.28
6	F	98	LYS	C-N-CA	-6.20	112.47	119.28
35	i	47	ILE	CB-CA-C	-6.19	104.14	111.94
46	t	21	GLN	N-CA-CB	6.19	123.04	111.53
46	t	530	LYS	CB-CA-C	-6.18	97.85	109.72
46	t	56	GLN	N-CA-CB	6.14	121.80	112.47
21	U	21	SER	CA-C-N	-6.13	112.69	119.19
21	U	21	SER	C-N-CA	-6.13	112.69	119.19
5	E	94	GLU	N-CA-C	6.12	118.49	111.02
16	P	79	THR	N-CA-C	-6.12	106.45	114.04
18	R	57	VAL	N-CA-C	6.09	116.93	108.89
46	t	519	ARG	N-CA-CB	6.07	122.12	111.19
39	m	88	LYS	N-CA-C	-6.05	105.16	112.54
2	B	81	THR	CB-CA-C	6.05	119.13	111.21
46	t	20	LEU	N-CA-CB	6.04	121.69	110.99
46	t	59	LEU	CB-CA-C	-6.04	100.14	110.16
14	N	78	GLY	N-CA-C	-6.03	107.33	115.36
20	T	122	GLN	N-CA-C	-6.03	105.47	114.64
3	C	73	ARG	CB-CG-CD	-6.03	97.44	111.30
42	p	53	GLY	CA-C-N	-6.02	115.72	123.19
42	p	53	GLY	C-N-CA	-6.02	115.72	123.19
28	b	18	ARG	N-CA-C	-6.02	104.35	111.03
48	5	282	G	C2'-C3'-O3'	5.99	122.69	113.70
1	A	107	VAL	CA-C-N	5.99	125.96	120.03
1	A	107	VAL	C-N-CA	5.99	125.96	120.03
1	A	216	HIS	N-CA-C	-5.99	99.59	108.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	S	14	LEU	CA-C-N	5.98	125.94	119.78
19	S	14	LEU	C-N-CA	5.98	125.94	119.78
46	t	530	LYS	N-CA-CB	5.96	119.82	110.46
3	C	191	LYS	N-CA-C	-5.96	105.84	114.12
23	W	27	LYS	N-CA-C	-5.96	101.22	110.10
22	V	126	TRP	CA-C-N	5.94	125.42	119.24
22	V	126	TRP	C-N-CA	5.94	125.42	119.24
29	c	97	ASP	N-CA-C	-5.93	106.09	113.15
21	U	28	PHE	N-CA-C	5.93	118.13	108.76
3	C	276	LEU	CA-C-N	5.93	125.95	119.90
3	C	276	LEU	C-N-CA	5.93	125.95	119.90
7	G	246	MET	N-CA-C	-5.93	106.17	113.41
46	t	551	GLN	CB-CA-C	-5.92	100.09	109.80
20	T	131	GLN	CA-C-N	-5.92	114.66	120.52
20	T	131	GLN	C-N-CA	-5.92	114.66	120.52
17	Q	166	LEU	CB-CA-C	-5.90	101.52	111.02
12	L	16	LYS	N-CA-C	5.89	122.47	112.99
5	E	66	SER	CA-C-N	-5.89	112.63	121.87
5	E	66	SER	C-N-CA	-5.89	112.63	121.87
10	J	17	LEU	CA-C-N	-5.89	115.24	123.13
10	J	17	LEU	C-N-CA	-5.89	115.24	123.13
16	P	64	ASN	CA-C-N	-5.88	114.37	122.30
16	P	64	ASN	C-N-CA	-5.88	114.37	122.30
17	Q	24	VAL	CB-CA-C	-5.87	104.35	112.04
2	B	84	VAL	N-CA-C	-5.86	100.05	108.48
6	F	130	ILE	N-CA-C	-5.85	107.56	113.47
27	a	10	LYS	N-CA-C	-5.85	105.64	112.89
19	S	49	HIS	N-CA-C	-5.84	99.53	108.76
7	G	82	LEU	N-CA-C	-5.83	98.38	110.80
12	L	42	ARG	N-CA-C	-5.82	104.85	111.14
14	N	177	GLY	N-CA-C	5.80	119.12	111.70
2	B	310	GLY	N-CA-C	-5.79	104.41	112.18
3	C	260	GLN	N-CA-C	-5.79	105.10	111.82
24	X	107	VAL	N-CA-C	5.79	116.21	108.11
10	J	127	PHE	CA-C-N	-5.78	114.85	123.00
10	J	127	PHE	C-N-CA	-5.78	114.85	123.00
4	D	88	ILE	CB-CA-C	-5.78	102.99	110.84
13	M	28	SER	N-CA-C	-5.78	106.14	112.72
7	G	151	VAL	N-CA-C	5.77	116.43	108.12
3	C	284	SER	N-CA-C	-5.76	106.11	114.12
13	M	134	ALA	N-CA-C	-5.75	104.93	111.14
3	C	269	SER	N-CA-C	5.75	118.49	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	N	96	ARG	N-CA-C	-5.74	101.53	110.42
37	k	20	VAL	N-CA-C	5.73	112.34	106.21
3	C	118	LYS	N-CA-C	-5.71	104.25	111.11
31	e	41	VAL	CB-CA-C	-5.71	103.01	112.26
9	I	131	ILE	N-CA-CB	5.70	116.93	110.72
19	S	20	PRO	N-CA-C	-5.70	102.64	111.13
5	E	102	ASN	N-CA-C	5.70	116.09	108.23
27	a	19	LYS	N-CA-C	5.70	119.93	112.92
46	t	519	ARG	CB-CA-C	-5.69	99.52	108.91
30	d	87	ASN	CA-C-N	5.68	125.78	119.87
30	d	87	ASN	C-N-CA	5.68	125.78	119.87
22	V	33	ASN	CB-CA-C	-5.68	98.64	109.66
36	j	84	SER	N-CA-C	5.67	118.32	111.40
3	C	64	SER	N-CA-C	-5.67	102.09	110.48
6	F	242	SER	N-CA-C	-5.67	106.37	113.28
26	Z	103	GLN	CA-C-N	5.67	126.92	119.84
26	Z	103	GLN	C-N-CA	5.67	126.92	119.84
2	B	186	GLY	N-CA-C	5.65	120.52	111.64
8	H	55	VAL	CB-CA-C	-5.64	102.10	110.33
10	J	113	GLY	N-CA-C	-5.63	102.42	112.22
8	H	12	VAL	N-CA-C	5.63	112.68	107.56
4	D	204	VAL	CB-CA-C	-5.62	104.46	112.22
32	f	93	THR	N-CA-C	-5.61	105.64	112.88
12	L	46	ILE	CB-CA-C	5.60	118.14	111.20
48	5	1152	G	N3-C4-C5	5.60	145.39	128.60
30	d	64	VAL	CB-CA-C	-5.58	102.13	111.29
24	X	43	ALA	CA-C-N	5.58	126.82	119.84
24	X	43	ALA	C-N-CA	5.58	126.82	119.84
31	e	63	THR	N-CA-C	-5.57	106.31	114.39
8	H	101	VAL	N-CA-C	5.57	115.88	107.75
17	Q	151	ARG	NE-CZ-NH1	-5.57	115.93	121.50
13	M	23	ILE	N-CA-C	5.56	115.57	108.12
4	D	67	SER	N-CA-C	5.56	118.61	109.72
2	B	115	LYS	N-CA-C	-5.55	105.33	111.71
13	M	20	VAL	N-CA-C	5.55	116.29	108.36
17	Q	3	ILE	CB-CA-C	-5.54	101.52	110.28
4	D	46	THR	CB-CA-C	-5.54	100.93	109.85
27	a	138	ILE	N-CA-C	-5.53	105.11	110.42
19	S	97	VAL	N-CA-C	-5.53	106.95	113.42
2	B	235	THR	N-CA-CB	-5.53	101.15	110.49
48	5	2372	A	C4'-C3'-O3'	5.52	117.68	109.40
19	S	51	VAL	CB-CA-C	-5.51	102.25	111.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	t	20	LEU	CB-CA-C	-5.51	99.93	109.86
3	C	190	GLY	N-CA-C	5.51	126.24	113.18
24	X	69	SER	N-CA-C	-5.51	103.42	110.53
1	A	213	GLY	CA-C-N	-5.49	117.93	122.16
1	A	213	GLY	C-N-CA	-5.49	117.93	122.16
6	F	147	LEU	N-CA-C	-5.49	105.38	111.36
2	B	309	GLY	N-CA-C	-5.49	107.37	113.79
18	R	132	PHE	CA-C-N	5.49	127.63	120.28
18	R	132	PHE	C-N-CA	5.49	127.63	120.28
2	B	98	GLY	N-CA-C	5.48	117.61	112.08
27	a	65	GLN	CA-C-N	-5.48	115.38	125.02
27	a	65	GLN	C-N-CA	-5.48	115.38	125.02
32	f	53	TYR	N-CA-C	5.48	117.73	109.41
39	m	91	CYS	N-CA-C	5.48	121.65	114.75
5	E	173	MET	CB-CG-SD	-5.47	96.28	112.70
6	F	203	TRP	CA-C-N	-5.47	113.92	119.83
6	F	203	TRP	C-N-CA	-5.47	113.92	119.83
8	H	48	VAL	N-CA-C	-5.47	106.36	111.45
43	q	213	PHE	N-CA-C	-5.47	106.78	113.50
4	D	75	LEU	N-CA-C	-5.46	104.17	112.04
4	D	254	LYS	CA-C-N	5.46	125.93	120.14
4	D	254	LYS	C-N-CA	5.46	125.93	120.14
27	a	15	VAL	CB-CA-C	-5.46	104.20	111.13
48	5	2372	A	P-O3'-C3'	5.45	128.38	120.20
15	O	110[A]	PRO	CB-CA-C	5.45	117.57	110.92
15	O	110[B]	PRO	CB-CA-C	5.45	117.57	110.92
48	5	2524	A	C3'-C2'-C1'	-5.45	96.05	101.50
12	L	26	PHE	N-CA-C	-5.45	106.47	113.01
40	n	24	SER	N-CA-C	-5.43	105.46	113.61
18	R	70	LYS	N-CA-C	-5.42	105.45	111.36
19	S	155	ARG	CG-CD-NE	5.42	123.93	112.00
8	H	29	GLY	CA-C-N	5.41	125.49	119.32
8	H	29	GLY	C-N-CA	5.41	125.49	119.32
4	D	87	GLY	N-CA-C	5.40	121.12	114.69
5	E	37	GLY	N-CA-C	-5.40	107.65	115.27
1	A	168	VAL	CB-CA-C	-5.40	103.47	111.19
27	a	120	ASN	N-CA-C	5.40	120.28	111.37
27	a	28	HIS	CB-CA-C	-5.39	99.56	110.17
40	n	20	VAL	CB-CA-C	-5.39	104.87	112.14
6	F	219	LYS	CA-C-N	-5.38	114.02	122.08
6	F	219	LYS	C-N-CA	-5.38	114.02	122.08
23	W	84	GLY	N-CA-C	-5.38	107.85	115.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	a	118	ILE	CA-C-N	-5.37	114.71	120.03
27	a	118	ILE	C-N-CA	-5.37	114.71	120.03
48	5	2249	G	C3'-C2'-C1'	-5.36	95.94	101.30
27	a	34	MET	N-CA-C	5.35	118.64	112.97
13	M	110	ALA	N-CA-C	-5.35	106.26	112.89
26	Z	14	VAL	CB-CA-C	5.35	118.64	111.85
46	t	17	LYS	N-CA-C	-5.35	99.69	108.41
19	S	17	GLU	N-CA-C	-5.35	105.62	111.82
10	J	76	ALA	N-CA-C	-5.34	105.50	112.23
2	B	278	ILE	N-CA-C	5.34	117.40	109.17
3	C	101	ALA	CA-C-N	5.33	126.51	119.84
3	C	101	ALA	C-N-CA	5.33	126.51	119.84
19	S	130	GLU	N-CA-C	5.33	116.78	110.97
10	J	166	LYS	N-CA-C	-5.33	101.60	109.86
26	Z	24	VAL	CB-CA-C	-5.33	103.21	110.77
10	J	15	GLU	N-CA-C	-5.32	104.37	111.24
13	M	27	GLN	N-CA-C	-5.32	106.95	113.50
43	q	80	VAL	CB-CA-C	5.32	118.74	111.88
46	t	165	GLU	N-CA-CB	5.31	118.52	110.28
17	Q	158	HIS	N-CA-C	5.31	119.34	112.86
25	Y	112	ASP	N-CA-C	-5.31	99.49	110.80
2	B	245	GLY	N-CA-C	5.31	119.37	112.68
10	J	10	ARG	N-CA-C	5.31	122.11	110.80
3	C	14	GLU	N-CA-C	5.31	122.11	110.80
22	V	129	VAL	N-CA-C	-5.31	105.67	110.82
30	d	8	VAL	CB-CA-C	-5.30	102.59	111.29
46	t	522	LEU	CB-CA-C	-5.30	99.83	109.38
3	C	60	THR	CB-CA-C	-5.30	97.80	109.56
28	b	13	THR	N-CA-CB	5.30	118.49	110.28
46	t	509	LEU	CB-CA-C	-5.29	100.79	109.53
46	t	83	LYS	CB-CA-C	-5.29	99.85	109.38
12	L	24	VAL	CB-CA-C	-5.29	103.73	110.98
6	F	160	ARG	CA-C-N	-5.29	118.25	122.85
6	F	160	ARG	C-N-CA	-5.29	118.25	122.85
21	U	88	GLN	N-CA-C	5.28	118.99	111.92
5	E	75	PRO	CA-C-O	-5.26	115.49	121.96
23	W	97	LYS	CA-C-N	5.26	126.41	119.84
23	W	97	LYS	C-N-CA	5.26	126.41	119.84
29	c	44	ILE	N-CA-C	5.25	116.14	108.58
20	T	135	PRO	CA-C-O	-5.25	111.76	120.05
28	b	28	LYS	N-CA-C	-5.25	101.91	110.20
2	B	8	ALA	N-CA-C	5.24	114.33	108.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	F	198	ALA	CA-C-N	5.24	127.56	120.38
6	F	198	ALA	C-N-CA	5.24	127.56	120.38
7	G	49	TYR	CA-C-N	-5.24	112.94	122.43
7	G	49	TYR	C-N-CA	-5.24	112.94	122.43
22	V	14	SER	N-CA-C	5.24	117.63	110.24
14	N	183	THR	N-CA-C	5.24	121.97	110.80
1	A	119	LYS	CA-C-N	-5.24	114.17	119.83
1	A	119	LYS	C-N-CA	-5.24	114.17	119.83
9	I	49	CYS	N-CA-C	5.24	116.95	108.41
2	B	290	ASP	N-CA-C	5.23	117.28	109.59
36	j	58	THR	CB-CA-C	-5.23	99.63	111.30
32	f	72	THR	N-CA-C	5.23	119.79	113.41
7	G	64	ILE	CB-CA-C	-5.23	105.28	111.97
39	m	85	LEU	N-CA-C	-5.23	105.47	111.07
8	H	167	VAL	N-CA-CB	5.22	119.85	111.23
3	C	198	ARG	N-CA-C	5.22	121.92	110.80
33	g	89	ILE	CB-CA-C	-5.22	105.18	112.02
8	H	123	ILE	N-CA-C	5.22	115.82	108.36
5	E	65	ILE	CA-C-N	-5.22	114.13	122.17
5	E	65	ILE	C-N-CA	-5.22	114.13	122.17
1	A	14	SER	N-CA-C	5.21	116.23	108.31
16	P	31	GLU	N-CA-C	-5.21	105.77	111.82
28	b	20	GLY	O-C-N	5.21	129.06	123.18
1	A	225	ILE	N-CA-C	5.20	116.07	108.53
4	D	146	LEU	N-CA-C	5.20	118.10	110.30
27	a	22	ILE	CB-CA-C	-5.20	105.22	112.04
27	a	144	VAL	CB-CA-C	-5.20	104.05	111.34
2	B	9	PRO	CA-C-O	-5.20	115.33	121.67
4	D	180	PHE	CA-C-N	-5.20	114.41	119.76
4	D	180	PHE	C-N-CA	-5.20	114.41	119.76
25	Y	82	VAL	N-CA-C	5.19	115.05	107.37
3	C	126	ILE	N-CA-C	-5.19	105.79	110.82
48	5	1607	U	C4'-C3'-O3'	5.19	117.18	109.40
4	D	293	LEU	N-CA-C	5.18	117.83	111.82
25	Y	80	VAL	N-CA-C	-5.18	100.78	108.45
2	B	4	ARG	CB-CA-C	5.18	117.97	109.90
10	J	120	ILE	CB-CA-C	-5.18	105.69	111.80
42	p	15	GLY	O-C-N	-5.18	115.97	122.70
27	a	125	VAL	N-CA-C	5.17	115.21	107.51
46	t	172	PRO	CA-C-N	-5.16	111.68	121.54
46	t	172	PRO	C-N-CA	-5.16	111.68	121.54
14	N	69	GLY	N-CA-C	5.16	121.00	112.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	G	33	ASN	N-CA-C	5.15	119.84	113.50
33	g	20	ILE	N-CA-C	5.15	117.16	108.81
3	C	145	ILE	CA-C-N	5.15	126.28	119.84
3	C	145	ILE	C-N-CA	5.15	126.28	119.84
4	D	214	ASP	CB-CA-C	-5.15	101.78	110.64
29	c	92	ILE	CB-CA-C	-5.15	104.46	111.15
4	D	128	GLU	N-CA-C	-5.14	102.18	110.14
3	C	226	GLU	N-CA-C	5.13	117.48	109.52
12	L	149	GLN	CA-C-N	5.13	126.26	119.84
12	L	149	GLN	C-N-CA	5.13	126.26	119.84
27	a	6	THR	CB-CA-C	5.13	119.17	109.37
1	A	211	HIS	CA-C-O	5.12	126.03	120.55
27	a	124	ILE	CB-CA-C	-5.12	104.15	111.31
5	E	89	THR	CB-CA-C	5.11	117.97	109.53
21	U	67	SER	N-CA-C	5.11	117.49	108.75
13	M	36	VAL	CB-CA-C	-5.10	105.68	111.55
48	5	1481	A	P-O3'-C3'	5.10	127.85	120.20
10	J	23	VAL	N-CA-C	5.09	115.24	110.30
19	S	165	TYR	N-CA-C	-5.09	106.38	112.59
14	N	182	ASN	CA-C-O	-5.09	115.41	120.96
9	I	131	ILE	CB-CA-C	-5.09	104.60	110.91
9	I	175	ASN	N-CA-C	-5.09	99.97	110.80
31	e	43	ARG	NE-CZ-NH1	5.09	126.59	121.50
4	D	118	THR	N-CA-C	-5.08	102.35	109.96
20	T	17	ARG	CA-CB-CG	-5.07	103.97	114.10
12	L	50	PRO	N-CA-C	5.06	120.94	114.92
27	a	121	VAL	N-CA-C	5.06	119.80	108.88
6	F	84	VAL	N-CA-C	5.05	117.29	108.95
12	L	123	ILE	CA-C-N	-5.05	115.80	122.98
12	L	123	ILE	C-N-CA	-5.05	115.80	122.98
31	e	52	GLN	CA-C-N	5.05	124.97	119.76
31	e	52	GLN	C-N-CA	5.05	124.97	119.76
17	Q	93	ILE	CB-CA-C	-5.05	104.16	111.68
27	a	25	HIS	N-CA-C	-5.03	99.60	108.20
12	L	21	ARG	NE-CZ-NH1	-5.03	116.47	121.50
4	D	174	PRO	CA-C-O	-5.00	115.87	121.23
2	B	346	THR	CB-CA-C	5.00	117.85	109.80
3	C	247	PHE	CA-C-N	-5.00	116.99	123.19
3	C	247	PHE	C-N-CA	-5.00	116.99	123.19

There are no chirality outliers.

All (24) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
48	5	2898	G	Sidechain
1	A	143	GLU	Peptide
1	A	211	HIS	Peptide
3	C	91	GLY	Peptide
4	D	271	LYS	Peptide
5	E	129	GLU	Peptide
6	F	192	GLY	Peptide
6	F	226	GLY	Peptide
15	O	110[A]	PRO	Peptide
15	O	68[B]	ARG	Peptide
19	S	133	ALA	Peptide
22	V	41	GLY	Peptide
25	Y	111	LEU	Peptide
26	Z	101	PHE	Peptide
27	a	26	ARG	Peptide
27	a	66	ALA	Peptide
27	a	75	LEU	Peptide
28	b	19	ASN	Peptide
46	t	15	LYS	Mainchain
46	t	160	ILE	Mainchain
46	t	383	ASP	Mainchain
46	t	48	ASP	Mainchain
46	t	544	ASN	Mainchain
46	t	81	LYS	Mainchain

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	A	1912	0	1976	87	0
2	B	3075	0	3142	122	0
3	C	2748	0	2859	102	0
4	D	2359	0	2311	91	0
5	E	1248	0	1339	38	0
6	F	1791	0	1869	48	0
7	G	1763	0	1819	76	0
8	H	1518	0	1587	67	0
9	I	1722	0	1755	55	0
10	J	1353	0	1383	56	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	K	750	0	185	11	0
12	L	1548	0	1613	61	0
13	M	1059	0	1154	38	0
14	N	1720	0	1779	67	0
15	O	3119	0	3302	96	0
16	P	1227	0	1236	33	0
17	Q	1441	0	1543	48	0
18	R	1521	0	1617	44	0
19	S	1445	0	1487	51	0
20	T	1276	0	1323	53	0
21	U	778	0	791	25	0
22	V	1003	0	1048	28	0
23	W	1038	0	1071	23	0
24	X	959	0	1020	77	0
25	Y	993	0	1081	30	0
26	Z	1092	0	1155	59	0
27	a	1173	0	1215	57	0
28	b	462	0	491	16	0
29	c	767	0	816	36	0
30	d	883	0	918	28	0
31	e	1020	0	1090	41	0
32	f	850	0	880	30	0
33	g	880	0	945	36	0
34	h	965	0	1067	45	0
35	i	770	0	846	26	0
36	j	681	0	683	24	0
37	k	608	0	671	25	0
38	l	436	0	475	22	0
39	m	417	0	455	17	0
40	n	233	0	284	8	0
41	o	847	0	915	31	0
42	p	694	0	734	26	0
43	q	1077	0	1041	34	0
44	r	235	0	50	5	0
45	s	230	0	49	0	0
46	t	2938	0	2995	639	0
47	1	114	0	0	10	0
48	5	67376	0	33833	1170	0
49	7	2579	0	1303	38	0
50	8	3353	0	1695	49	0
51	j	1	0	0	0	0
51	m	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	o	1	0	0	2	0
51	p	1	0	0	0	0
All	All	130050	0	94896	3381	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 15.

All (3381) 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)
17:Q:171:LYS:NZ	17:Q:171:LYS:CE	1.67	1.55
46:t:82:ASN:HD21	47:1:2029:A:P	1.32	1.52
46:t:198:LEU:HD13	46:t:319:ILE:CD1	1.43	1.49
10:J:8:PRO:CB	10:J:8:PRO:CG	1.75	1.49
24:X:137:ASN:CG	46:t:420:ARG:NH2	1.69	1.49
46:t:39:LEU:CD2	46:t:529:SER:HB2	1.43	1.49
46:t:61:VAL:CG1	46:t:106:PRO:HG3	1.41	1.46
46:t:378:LEU:CD1	46:t:422:GLY:HA3	1.44	1.46
46:t:39:LEU:HD23	46:t:529:SER:CB	1.46	1.45
24:X:137:ASN:HB3	46:t:417:LYS:CE	1.49	1.42
46:t:193:THR:HG21	46:t:226:ILE:CG2	1.48	1.42
46:t:198:LEU:CD1	46:t:319:ILE:CD1	1.98	1.42
46:t:43:THR:HG23	46:t:158:MET:SD	1.58	1.41
46:t:161:TYR:CD2	46:t:162:PRO:O	1.76	1.39
24:X:137:ASN:HB3	46:t:417:LYS:CD	1.53	1.39
46:t:361:VAL:CG2	46:t:388:TYR:HB3	1.53	1.38
24:X:137:ASN:CB	46:t:417:LYS:HD2	1.54	1.36
24:X:137:ASN:CB	46:t:420:ARG:NH2	1.86	1.36
46:t:193:THR:CG2	46:t:226:ILE:HG21	1.57	1.34
46:t:517:THR:CG2	46:t:518:ASP:N	1.68	1.33
46:t:48:ASP:CG	46:t:135:PRO:HD3	1.56	1.30
46:t:353:LEU:O	46:t:354:ILE:HG12	1.19	1.30
46:t:60:THR:HB	46:t:131:GLY:O	1.15	1.30
24:X:137:ASN:HB3	46:t:417:LYS:NZ	1.48	1.28
46:t:361:VAL:HG23	46:t:388:TYR:O	1.25	1.26
46:t:82:ASN:ND2	47:1:2029:A:P	2.06	1.25
46:t:161:TYR:HD2	46:t:162:PRO:O	0.94	1.24
46:t:154:VAL:CG2	46:t:526:THR:HG21	1.67	1.23
46:t:191:MET:HG3	46:t:530:LYS:CE	1.69	1.23
46:t:198:LEU:CD1	46:t:319:ILE:HD12	1.63	1.22
24:X:141:TYR:O	46:t:417:LYS:NZ	1.72	1.22

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:142:ILE:HD13	46:t:417:LYS:O	1.37	1.22
46:t:507:ILE:HD12	46:t:522:LEU:CD2	1.70	1.21
46:t:162:PRO:CD	46:t:167:LYS:HD2	1.71	1.21
24:X:70:GLU:OE1	46:t:372:LEU:HD21	1.39	1.20
46:t:387:VAL:HG22	46:t:388:TYR:N	1.26	1.19
24:X:137:ASN:HB2	46:t:420:ARG:NH2	1.45	1.18
46:t:311:VAL:CG1	46:t:509:LEU:CD1	2.21	1.18
46:t:505:ASN:HB3	46:t:530:LYS:HD2	1.20	1.17
24:X:133:LEU:HD22	46:t:417:LYS:HG2	1.23	1.17
46:t:61:VAL:CG1	46:t:106:PRO:CG	2.23	1.16
46:t:517:THR:HG22	46:t:518:ASP:CA	1.74	1.16
46:t:353:LEU:O	46:t:354:ILE:CG1	1.93	1.15
46:t:68:THR:CG2	46:t:93:THR:OG1	1.94	1.15
46:t:311:VAL:HG11	46:t:509:LEU:CD1	1.76	1.15
46:t:378:LEU:HD12	46:t:422:GLY:CA	1.75	1.14
24:X:137:ASN:CG	46:t:417:LYS:HD2	1.52	1.14
46:t:194:VAL:HG11	46:t:319:ILE:CG2	1.75	1.14
46:t:361:VAL:HG23	46:t:388:TYR:C	1.72	1.14
46:t:533:GLN:NE2	46:t:536:TRP:HE1	1.32	1.14
46:t:105:CYS:SG	46:t:391:LYS:HD3	1.89	1.13
46:t:154:VAL:HG23	46:t:526:THR:CG2	1.78	1.13
24:X:142:ILE:CD1	46:t:417:LYS:O	1.95	1.13
46:t:194:VAL:HG11	46:t:319:ILE:HG21	1.15	1.12
46:t:198:LEU:HD11	46:t:319:ILE:HD12	1.30	1.13
46:t:29:ARG:CZ	47:1:1998:G:P	2.37	1.12
46:t:153:GLU:CB	46:t:318:LEU:CD2	2.27	1.12
46:t:153:GLU:HB2	46:t:318:LEU:CD1	1.79	1.11
46:t:380:THR:O	46:t:383:ASP:OD1	1.67	1.11
46:t:244:VAL:HG13	46:t:318:LEU:O	1.51	1.11
46:t:45:LEU:O	46:t:59:LEU:HD11	1.48	1.11
46:t:154:VAL:HG21	46:t:529:SER:OG	1.50	1.11
46:t:231:ALA:HB2	46:t:323:MET:HE2	1.17	1.10
46:t:45:LEU:O	46:t:59:LEU:CD1	2.00	1.10
46:t:361:VAL:HG21	46:t:388:TYR:CB	1.80	1.10
46:t:326:LEU:HD13	46:t:441:ARG:HB2	1.32	1.09
46:t:387:VAL:CG2	46:t:388:TYR:H	1.57	1.09
18:R:34:GLN:NE2	46:t:369:ILE:HD13	1.67	1.09
46:t:61:VAL:O	46:t:61:VAL:HG22	1.53	1.09
46:t:61:VAL:HG13	46:t:106:PRO:CG	1.80	1.08
46:t:162:PRO:HD3	46:t:167:LYS:CD	1.83	1.08
46:t:388:TYR:HB2	46:t:389:PRO:HD3	1.25	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:t:227:VAL:HG12	46:t:238:VAL:HG21	1.19	1.08
46:t:305:PRO:CD	46:t:305:PRO:N	2.14	1.08
46:t:61:VAL:HG13	46:t:106:PRO:HG3	1.32	1.07
24:X:137:ASN:CB	46:t:417:LYS:NZ	2.16	1.07
46:t:36:GLN:HG2	46:t:529:SER:H	1.16	1.07
46:t:361:VAL:CG2	46:t:388:TYR:O	2.02	1.07
46:t:387:VAL:CG2	46:t:388:TYR:N	2.01	1.06
24:X:137:ASN:CB	46:t:417:LYS:HZ2	1.65	1.06
46:t:46:ILE:HD11	46:t:141:ILE:HD11	1.11	1.06
46:t:159:VAL:HG21	46:t:176:LEU:HD22	1.35	1.06
2:B:296:THR:HG22	2:B:298:PHE:H	1.18	1.06
46:t:29:ARG:NH1	47:1:1998:G:P	2.28	1.06
46:t:153:GLU:HB2	46:t:318:LEU:HD13	1.36	1.06
18:R:34:GLN:HE21	46:t:369:ILE:HD13	0.92	1.06
46:t:378:LEU:CD1	46:t:422:GLY:CA	2.31	1.06
46:t:250:PHE:O	46:t:388:TYR:CE2	2.08	1.05
46:t:387:VAL:HG21	46:t:389:PRO:HD2	1.36	1.05
46:t:378:LEU:HD13	46:t:422:GLY:HA3	1.34	1.05
46:t:436:PRO:N	46:t:436:PRO:CD	2.19	1.05
24:X:137:ASN:OD1	46:t:420:ARG:NH2	1.87	1.05
46:t:180:LYS:HG2	46:t:466:LEU:HD13	1.36	1.05
46:t:216:SER:H	46:t:520:PRO:HG3	1.18	1.05
46:t:392:LEU:HD11	46:t:423:MET:SD	1.97	1.04
46:t:514:VAL:HG12	46:t:515:SER:N	1.70	1.04
46:t:48:ASP:OD1	46:t:135:PRO:HD3	1.58	1.04
46:t:227:VAL:CG1	46:t:238:VAL:HG21	1.85	1.04
46:t:387:VAL:HG11	46:t:389:PRO:O	1.58	1.04
46:t:507:ILE:CD1	46:t:522:LEU:HD23	1.86	1.04
46:t:240:PRO:CD	46:t:240:PRO:N	2.22	1.03
46:t:353:LEU:HD12	46:t:439:ILE:CD1	1.87	1.03
46:t:29:ARG:HH12	47:1:1998:G:P	1.79	1.03
46:t:517:THR:HG22	46:t:518:ASP:N	0.88	1.03
46:t:231:ALA:HB2	46:t:323:MET:CE	1.87	1.03
18:R:34:GLN:NE2	46:t:369:ILE:CD1	2.22	1.03
9:I:76:MET:HE1	9:I:148:VAL:HA	1.38	1.03
46:t:137:ASP:HB2	46:t:160:ILE:HD12	1.41	1.02
46:t:357:PRO:N	46:t:357:PRO:CD	2.21	1.02
46:t:163:VAL:HG22	46:t:164:ASP:N	1.74	1.02
13:M:19:ARG:HA	13:M:69:THR:HG22	1.41	1.02
46:t:60:THR:OG1	46:t:61:VAL:N	1.68	1.02
46:t:378:LEU:HD12	46:t:422:GLY:HA3	1.03	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:34:GLN:HE21	46:t:369:ILE:CD1	1.70	1.02
46:t:62:PRO:N	46:t:62:PRO:CD	2.23	1.02
24:X:137:ASN:CB	46:t:417:LYS:CE	2.37	1.01
46:t:162:PRO:HD3	46:t:167:LYS:HD2	1.04	1.01
46:t:194:VAL:CG1	46:t:319:ILE:HG21	1.89	1.01
46:t:198:LEU:O	46:t:522:LEU:CD2	2.09	1.01
46:t:191:MET:N	46:t:321:LEU:CD1	2.23	1.00
46:t:244:VAL:CG1	46:t:319:ILE:HA	1.91	1.00
46:t:43:THR:CG2	46:t:158:MET:SD	2.48	1.00
46:t:191:MET:HA	46:t:321:LEU:HD11	1.42	1.00
46:t:533:GLN:NE2	46:t:536:TRP:NE1	1.83	1.00
2:B:41:VAL:HA	2:B:185:GLY:HA3	1.39	1.00
46:t:189:ILE:HG21	46:t:543:LEU:HD11	1.44	1.00
46:t:353:LEU:HD12	46:t:439:ILE:HD12	1.41	1.00
46:t:387:VAL:CG1	46:t:389:PRO:O	2.09	1.00
46:t:249:ARG:NH1	46:t:250:PHE:CE2	2.30	0.99
46:t:533:GLN:HE22	46:t:536:TRP:HE1	1.04	0.99
8:H:166:ARG:HH11	8:H:168:ARG:HH22	1.08	0.99
46:t:186:ALA:HB1	46:t:323:MET:SD	2.03	0.99
46:t:250:PHE:O	46:t:388:TYR:CZ	2.16	0.99
46:t:60:THR:CB	46:t:131:GLY:O	2.09	0.99
46:t:61:VAL:HG11	46:t:106:PRO:HG3	1.40	0.99
24:X:133:LEU:HD22	46:t:417:LYS:CG	1.90	0.99
46:t:191:MET:CG	46:t:530:LYS:HE2	1.92	0.99
46:t:46:ILE:HG23	46:t:133:LEU:CD1	1.93	0.98
46:t:244:VAL:HG11	46:t:319:ILE:HA	1.40	0.98
46:t:153:GLU:HB2	46:t:318:LEU:CD2	1.94	0.98
24:X:142:ILE:HG21	46:t:421:LEU:N	1.78	0.98
46:t:135:PRO:N	46:t:135:PRO:CD	2.22	0.97
46:t:175:PRO:CD	46:t:175:PRO:N	2.26	0.97
2:B:53:MET:HE3	48:5:3048:A:H5'	1.45	0.97
28:b:50:THR:HG22	48:5:1073:U:H1'	1.42	0.97
48:5:437:G:H22	48:5:622:A:H61	1.01	0.97
46:t:311:VAL:CG1	46:t:509:LEU:HD13	1.92	0.97
46:t:191:MET:HG3	46:t:530:LYS:HE2	0.98	0.96
46:t:61:VAL:O	46:t:61:VAL:HG13	1.59	0.96
46:t:505:ASN:HB3	46:t:530:LYS:CD	1.96	0.96
46:t:19:ILE:O	46:t:19:ILE:HG22	1.66	0.96
46:t:191:MET:HG2	46:t:530:LYS:NZ	1.81	0.95
46:t:198:LEU:CD1	46:t:319:ILE:HD11	1.79	0.95
46:t:361:VAL:CG2	46:t:388:TYR:CB	2.40	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:188:ARG:NH2	48:5:31:C:OP2	1.99	0.95
46:t:163:VAL:HG13	46:t:166:THR:H	1.27	0.95
46:t:133:LEU:HB3	46:t:160:ILE:HD13	1.47	0.95
46:t:353:LEU:HD12	46:t:439:ILE:CB	1.97	0.94
24:X:133:LEU:CD2	46:t:417:LYS:HG2	1.96	0.94
46:t:197:LEU:HB2	46:t:223:ILE:CD1	1.98	0.94
46:t:198:LEU:O	46:t:522:LEU:HD21	1.66	0.94
46:t:194:VAL:CG1	46:t:198:LEU:CD1	2.45	0.93
46:t:194:VAL:HG13	46:t:198:LEU:CD1	1.99	0.93
46:t:105:CYS:O	46:t:391:LYS:HD2	1.67	0.93
46:t:48:ASP:OD1	46:t:135:PRO:CD	2.17	0.93
46:t:191:MET:CA	46:t:321:LEU:CD1	2.46	0.93
46:t:531:THR:HG21	46:t:532:CYS:O	1.69	0.93
46:t:191:MET:CG	46:t:530:LYS:NZ	2.32	0.93
46:t:550:VAL:HG23	46:t:550:VAL:O	1.68	0.93
24:X:70:GLU:OE1	46:t:372:LEU:CD2	2.17	0.93
24:X:137:ASN:CB	46:t:417:LYS:CD	2.23	0.93
13:M:128:ARG:NH2	48:5:3214:U:OP2	2.03	0.92
46:t:163:VAL:CG1	46:t:166:THR:H	1.82	0.92
46:t:309:PHE:CE2	46:t:310:VAL:O	2.22	0.92
46:t:216:SER:N	46:t:520:PRO:HG3	1.82	0.92
46:t:186:ALA:CB	46:t:323:MET:SD	2.56	0.92
2:B:53:MET:HE3	48:5:3048:A:C5'	1.99	0.92
48:5:1877:U:H5''	48:5:1878:G:H5'	1.50	0.92
13:M:55:ARG:NH2	13:M:76:ALA:O	2.03	0.92
46:t:180:LYS:CG	46:t:466:LEU:HD13	1.99	0.92
46:t:231:ALA:CB	46:t:323:MET:HE2	1.98	0.92
14:N:31:ARG:NH1	14:N:124:ASP:OD2	2.03	0.91
46:t:49:SER:HB3	46:t:132:THR:CG2	2.00	0.91
46:t:198:LEU:CD2	46:t:223:ILE:HG13	2.00	0.91
46:t:238:VAL:CG1	46:t:260:ALA:HB1	2.00	0.91
46:t:439:ILE:HG22	46:t:440:ALA:O	1.70	0.91
48:5:3343:G:H21	48:5:3362:A:H2	1.17	0.91
32:f:19:SER:HB3	48:5:1330:A:OP1	1.71	0.91
48:5:2836:C:H5	48:5:2852:C:H42	1.07	0.91
46:t:76:LEU:HD11	46:t:145:VAL:HG13	1.52	0.90
34:h:81:ARG:NH2	48:5:18:G:OP1	2.05	0.90
46:t:216:SER:HB3	46:t:520:PRO:HD3	1.53	0.90
46:t:105:CYS:SG	46:t:391:LYS:CD	2.60	0.90
14:N:8:GLU:HG3	14:N:50:ARG:HH12	1.35	0.90
46:t:198:LEU:HD13	46:t:319:ILE:HD11	0.90	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:t:507:ILE:HD12	46:t:522:LEU:HD23	0.90	0.90
48:5:1235:U:H4'	48:5:1236:G:H5'	1.53	0.90
46:t:311:VAL:CG1	46:t:509:LEU:HD12	2.02	0.89
46:t:426:ILE:HG22	46:t:432:CYS:SG	2.11	0.89
46:t:46:ILE:HG23	46:t:133:LEU:HD13	1.53	0.89
10:J:94:ARG:O	10:J:96:PHE:N	2.05	0.89
14:N:146:ALA:O	14:N:148:TYR:N	2.05	0.89
46:t:251:LEU:HA	46:t:388:TYR:CE2	2.08	0.89
46:t:244:VAL:HG22	46:t:320:ASP:H	1.35	0.89
1:A:213:GLY:HA3	48:5:2967:A:H5''	1.52	0.89
5:E:31:ARG:NH1	32:f:107:ILE:HG22	1.88	0.89
46:t:68:THR:HG21	46:t:93:THR:OG1	1.72	0.89
46:t:62:PRO:HD3	46:t:130:THR:HB	1.55	0.89
46:t:238:VAL:HG12	46:t:260:ALA:HB1	1.55	0.88
46:t:353:LEU:HD12	46:t:439:ILE:HB	1.54	0.88
46:t:29:ARG:NH2	47:1:1998:G:P	2.46	0.88
46:t:227:VAL:HG12	46:t:238:VAL:CG2	2.03	0.88
46:t:353:LEU:CD1	46:t:439:ILE:HD12	2.02	0.88
46:t:426:ILE:CG2	46:t:432:CYS:SG	2.62	0.88
46:t:140:LYS:HD2	46:t:502:ARG:HD3	1.55	0.88
46:t:193:THR:HG21	46:t:226:ILE:HG21	0.88	0.88
46:t:197:LEU:HD11	46:t:226:ILE:HG13	1.54	0.87
35:i:63:ASN:O	35:i:65:GLY:N	2.06	0.87
46:t:198:LEU:HD12	46:t:319:ILE:HG13	1.56	0.87
48:5:2818:U:H5'	48:5:2818:U:H6	1.37	0.87
46:t:153:GLU:HB3	46:t:318:LEU:HD21	1.54	0.87
24:X:137:ASN:HB2	46:t:420:ARG:CZ	2.03	0.87
41:o:77:CYS:SG	41:o:79:THR:HG23	2.14	0.87
27:a:21:ARG:NH2	48:5:640:U:OP1	2.06	0.87
1:A:70:ARG:NH2	48:5:2522:G:O6	2.08	0.87
46:t:360:TYR:CE1	46:t:423:MET:SD	2.67	0.87
48:5:1759:C:N4	48:5:1766:G:O6	2.06	0.87
46:t:61:VAL:HG12	46:t:106:PRO:HG3	1.55	0.87
33:g:74:ARG:NH2	48:5:1639:C:OP2	2.08	0.87
46:t:246:ARG:HG2	46:t:248:ARG:NH1	1.90	0.87
46:t:246:ARG:CG	46:t:248:ARG:HH12	1.88	0.87
46:t:76:LEU:HD12	46:t:88:GLY:HA2	1.54	0.86
20:T:135:PRO:O	20:T:136:ARG:HB2	1.73	0.86
48:5:2512:C:H6	48:5:2512:C:H5'	1.38	0.86
46:t:311:VAL:HG11	46:t:509:LEU:HD13	1.47	0.86
46:t:191:MET:HA	46:t:321:LEU:CD1	2.06	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:t:191:MET:HG2	46:t:530:LYS:HZ1	1.40	0.86
46:t:251:LEU:HA	46:t:388:TYR:HE2	1.37	0.86
46:t:193:THR:HG21	46:t:226:ILE:HG22	1.53	0.86
46:t:191:MET:CA	46:t:321:LEU:HD11	2.06	0.86
46:t:426:ILE:HG23	46:t:431:LEU:HB2	1.58	0.85
48:5:726:G:H5'	48:5:726:G:H8	1.41	0.85
46:t:311:VAL:HG13	46:t:509:LEU:HD12	1.56	0.85
46:t:530:LYS:O	46:t:530:LYS:HG2	1.74	0.85
48:5:1555:U:O4	48:5:1557:A:N6	2.08	0.85
46:t:194:VAL:HG13	46:t:198:LEU:HD11	1.57	0.85
46:t:48:ASP:CG	46:t:135:PRO:CD	2.47	0.85
46:t:188:HIS:NE2	46:t:191:MET:CE	2.38	0.85
18:R:34:GLN:NE2	46:t:369:ILE:HG21	1.91	0.85
28:b:23:LYS:HB3	28:b:24:PRO:HD3	1.57	0.85
46:t:216:SER:HB3	46:t:520:PRO:CD	2.07	0.85
2:B:76:VAL:HG11	2:B:323:MET:HE3	1.59	0.85
48:5:3278:C:O2'	48:5:3279:A:OP2	1.95	0.85
15:O:160[A]:ARG:NH2	48:5:3182:G:OP1	2.09	0.84
9:I:84:ALA:O	9:I:140:THR:HG22	1.77	0.84
46:t:387:VAL:HG22	46:t:388:TYR:H	0.94	0.84
9:I:175:ASN:OD1	9:I:176:LEU:N	2.08	0.84
3:C:60:THR:HG23	48:5:364:G:OP1	1.77	0.84
46:t:36:GLN:HG2	46:t:529:SER:N	1.90	0.84
41:o:77:CYS:O	41:o:79:THR:N	2.10	0.84
46:t:531:THR:CG2	46:t:532:CYS:O	2.25	0.84
46:t:198:LEU:HD21	46:t:223:ILE:HG13	1.60	0.84
46:t:46:ILE:CD1	46:t:141:ILE:HD11	2.03	0.84
46:t:176:LEU:HD21	46:t:180:LYS:HB3	1.58	0.84
46:t:259:VAL:CG1	46:t:298:PHE:CE1	2.33	0.84
48:5:1025:A:H3'	48:5:1026:A:H4'	1.60	0.83
46:t:42:VAL:CG1	46:t:141:ILE:HD13	2.07	0.83
48:5:1231:A:H5''	48:5:1232:C:H5'	1.61	0.83
43:q:36:GLN:NE2	48:5:1232:C:O2'	2.11	0.83
46:t:188:HIS:CE1	46:t:191:MET:CE	2.61	0.83
4:D:95:TRP:CH2	4:D:181:PRO:HD3	2.13	0.83
46:t:76:LEU:HD13	46:t:88:GLY:N	1.93	0.83
46:t:191:MET:CG	46:t:530:LYS:CE	2.49	0.82
46:t:387:VAL:HG22	46:t:388:TYR:CA	2.09	0.82
46:t:388:TYR:CB	46:t:389:PRO:HD3	2.02	0.82
2:B:169:THR:HG22	2:B:171:LEU:H	1.45	0.82
46:t:514:VAL:CG1	46:t:515:SER:N	2.40	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:t:51:HIS:CD2	46:t:163:VAL:N	2.39	0.82
18:R:62:ARG:NH2	48:5:3068:U:OP2	2.13	0.82
46:t:387:VAL:CG2	46:t:389:PRO:HD2	2.08	0.82
46:t:463:THR:O	46:t:464:SER:OG	1.97	0.82
3:C:204:GLY:O	3:C:246:ARG:NH1	2.12	0.82
33:g:52:GLN:HG2	48:5:1639:C:H5'	1.59	0.81
46:t:361:VAL:HG21	46:t:388:TYR:HB3	0.83	0.81
48:5:851:C:H6	48:5:851:C:H5''	1.44	0.81
3:C:329:PRO:O	3:C:331:ALA:N	2.14	0.81
20:T:28:SER:OG	49:7:9:C:OP1	1.97	0.81
42:p:73:THR:HG22	42:p:76:ALA:H	1.43	0.81
46:t:68:THR:HG22	46:t:93:THR:OG1	1.78	0.81
48:5:1815:U:O2'	48:5:1816:A:OP2	1.98	0.81
48:5:1015:U:O2'	48:5:1017:C:OP1	1.99	0.81
3:C:300:ARG:O	17:Q:39:ARG:NH1	2.13	0.81
16:P:25:SER:O	16:P:29:THR:HG23	1.80	0.81
46:t:168:PRO:O	46:t:169:ILE:HG12	1.79	0.81
46:t:250:PHE:O	46:t:388:TYR:OH	1.97	0.81
39:m:106:ARG:HH11	39:m:106:ARG:HB2	1.46	0.81
46:t:61:VAL:O	46:t:61:VAL:CG2	2.17	0.81
10:J:11:ASP:O	10:J:12:LEU:HB2	1.81	0.80
1:A:193:ARG:NH2	48:5:2181:C:OP1	2.13	0.80
24:X:115:ARG:NH1	24:X:119:THR:OG1	2.14	0.80
46:t:180:LYS:CG	46:t:466:LEU:CD1	2.58	0.80
48:5:776:U:H5	48:5:2719:U:O2	1.64	0.80
8:H:28:VAL:HG22	8:H:33:THR:HB	1.64	0.80
1:A:172:GLY:HA3	42:p:68:ALA:H	1.44	0.80
24:X:137:ASN:HB3	46:t:417:LYS:HZ2	1.18	0.80
46:t:246:ARG:CG	46:t:248:ARG:NH1	2.40	0.80
48:5:766:U:H4'	48:5:767:U:O5'	1.81	0.80
15:O:110[B]:PRO:O	15:O:112[B]:TYR:N	2.15	0.80
46:t:159:VAL:HG21	46:t:176:LEU:CD2	2.11	0.80
48:5:1804:A:H2'	48:5:1805:C:C6	2.16	0.80
48:5:2440:G:H5'	48:5:2440:G:H8	1.46	0.80
46:t:194:VAL:CG1	46:t:198:LEU:HD11	2.11	0.80
8:H:44:THR:HG22	48:5:3186:A:N3	1.97	0.80
46:t:49:SER:HB3	46:t:132:THR:HG21	1.62	0.80
46:t:193:THR:HG23	46:t:556:LEU:HD21	1.64	0.80
46:t:197:LEU:CD1	46:t:226:ILE:HG13	2.12	0.80
46:t:163:VAL:HG13	46:t:163:VAL:O	1.81	0.79
46:t:198:LEU:O	46:t:522:LEU:HD22	1.83	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:120:UNK:O	11:K:122:UNK:N	2.15	0.79
23:W:46:PRO:HB2	23:W:54:LEU:HD23	1.64	0.79
4:D:120:LYS:O	4:D:248:ARG:NH2	2.15	0.79
46:t:153:GLU:HB2	46:t:318:LEU:HD22	1.54	0.79
48:5:2255:A:H5'	48:5:2261:G:H22	1.47	0.79
46:t:36:GLN:HA	46:t:529:SER:HB3	1.65	0.79
46:t:45:LEU:O	46:t:59:LEU:HD13	1.81	0.79
17:Q:38:ARG:NH2	48:5:1348:U:OP2	2.15	0.79
38:l:23:LEU:HD22	38:l:24:PRO:HD2	1.64	0.79
46:t:42:VAL:HG12	46:t:141:ILE:HD13	1.64	0.79
46:t:154:VAL:HG21	46:t:529:SER:HG	1.44	0.79
46:t:180:LYS:HG3	46:t:466:LEU:CD1	2.13	0.79
46:t:191:MET:N	46:t:321:LEU:HD13	1.97	0.79
46:t:361:VAL:CG2	46:t:388:TYR:C	2.50	0.79
46:t:198:LEU:CD1	46:t:319:ILE:CG1	2.61	0.78
48:5:2227:C:H2'	48:5:2228:A:H5''	1.65	0.78
11:K:126:UNK:O	11:K:130:UNK:N	2.16	0.78
46:t:188:HIS:CE1	46:t:191:MET:HE1	2.18	0.78
48:5:1952:G:H1	48:5:2094:C:H42	1.32	0.78
4:D:40:HIS:HD2	4:D:42:ALA:H	1.32	0.78
46:t:194:VAL:HG22	46:t:223:ILE:HG23	1.63	0.78
48:5:437:G:N2	48:5:622:A:H61	1.80	0.78
46:t:76:LEU:HD12	46:t:88:GLY:CA	2.12	0.78
46:t:387:VAL:CG2	46:t:389:PRO:CD	2.61	0.78
24:X:137:ASN:CA	46:t:417:LYS:HZ2	1.97	0.78
8:H:20:ILE:HD13	8:H:25:VAL:HG22	1.65	0.77
46:t:154:VAL:CG2	46:t:526:THR:CG2	2.51	0.77
46:t:19:ILE:O	46:t:19:ILE:CG2	2.31	0.77
46:t:194:VAL:CG1	46:t:198:LEU:HD12	2.14	0.77
24:X:56:ARG:NH2	50:8:135:G:OP2	2.16	0.77
46:t:60:THR:OG1	46:t:62:PRO:N	2.17	0.77
48:5:15:C:H6	48:5:15:C:H5'	1.49	0.77
2:B:37:ARG:HG2	2:B:187:SER:H	1.49	0.77
2:B:188:ILE:HD12	2:B:188:ILE:H	1.50	0.77
46:t:197:LEU:CB	46:t:223:ILE:CD1	2.62	0.77
46:t:244:VAL:CG2	46:t:320:ASP:H	1.98	0.77
48:5:2511:A:H2'	48:5:2512:C:H5''	1.66	0.77
46:t:29:ARG:HH22	47:1:1998:G:P	2.05	0.77
46:t:246:ARG:HB3	46:t:254:GLN:HG2	1.67	0.77
46:t:353:LEU:CD1	46:t:439:ILE:HB	2.14	0.77
48:5:150:A:H2'	48:5:151:A:H5'	1.66	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:5:2444:C:H42	48:5:2503:G:H1	1.31	0.77
46:t:387:VAL:HG21	46:t:389:PRO:CD	2.15	0.77
10:J:109:HIS:HD2	10:J:123:PHE:H	1.32	0.77
46:t:353:LEU:C	46:t:354:ILE:HG12	2.10	0.77
46:t:140:LYS:HD2	46:t:502:ARG:CD	2.14	0.76
46:t:311:VAL:HG11	46:t:509:LEU:HD11	1.66	0.76
46:t:60:THR:HG21	46:t:130:THR:HB	1.68	0.76
46:t:197:LEU:HB2	46:t:223:ILE:HD11	1.67	0.76
46:t:238:VAL:HB	46:t:261:GLU:CG	2.14	0.76
46:t:361:VAL:HG23	46:t:388:TYR:CA	2.14	0.76
48:5:3049:A:H5'	48:5:3049:A:H8	1.50	0.76
6:F:88:ARG:HD2	6:F:90:LYS:O	1.86	0.76
14:N:49:ARG:NH2	48:5:149:U:OP2	2.18	0.76
17:Q:178:ARG:HD3	27:a:50:PRO:HB2	1.66	0.76
5:E:31:ARG:HH11	32:f:107:ILE:HG22	1.47	0.76
46:t:55:THR:O	46:t:55:THR:OG1	1.79	0.76
46:t:105:CYS:CB	46:t:391:LYS:HD3	2.15	0.76
46:t:159:VAL:CG2	46:t:176:LEU:HD22	2.15	0.76
1:A:114:SER:HB2	1:A:169:ILE:HD12	1.67	0.76
46:t:550:VAL:O	46:t:550:VAL:CG2	2.20	0.76
26:Z:83:THR:HG23	26:Z:85:TYR:H	1.50	0.76
2:B:247:ARG:HD3	48:5:1888:U:OP1	1.85	0.76
8:H:77:ASN:HA	8:H:80:THR:HG23	1.66	0.76
25:Y:45:ILE:HD12	25:Y:119:ILE:HG23	1.66	0.76
24:X:133:LEU:CD2	46:t:417:LYS:CG	2.60	0.76
6:F:216:VAL:HG11	6:F:227:GLY:HA3	1.67	0.76
32:f:18:ARG:HD3	48:5:1178:G:H5''	1.68	0.76
35:i:58:ILE:HG22	35:i:90:MET:HG3	1.68	0.76
46:t:387:VAL:HG13	46:t:389:PRO:N	2.01	0.76
48:5:2509:U:H2'	48:5:2510:U:H5''	1.68	0.76
48:5:437:G:H22	48:5:622:A:N6	1.81	0.75
46:t:153:GLU:CB	46:t:318:LEU:HD21	2.06	0.75
46:t:197:LEU:CB	46:t:223:ILE:HD11	2.16	0.75
4:D:269:SER:OG	49:7:1:G:N3	2.19	0.75
9:I:57:LEU:HD12	49:7:93:C:H5'	1.67	0.75
2:B:129:ALA:O	48:5:3150:A:H5'	1.85	0.75
6:F:158:LYS:HD2	6:F:159:GLN:HA	1.66	0.75
46:t:259:VAL:HG11	46:t:298:PHE:CE1	2.19	0.75
27:a:6:THR:HG23	27:a:8:THR:HG23	1.68	0.75
46:t:231:ALA:CB	46:t:323:MET:CE	2.62	0.75
46:t:61:VAL:CG1	46:t:61:VAL:O	2.21	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:130:ARG:HD3	48:5:1098:A:OP2	1.87	0.74
20:T:68:THR:HG22	20:T:71:SER:H	1.51	0.74
48:5:3289:G:H2'	48:5:3290:G:C8	2.23	0.74
4:D:226:TYR:HE2	4:D:236:LEU:HD11	1.51	0.74
48:5:2875:U:H3	48:5:2952:G:H1	1.35	0.74
46:t:191:MET:HB2	46:t:321:LEU:HD12	1.67	0.74
22:V:2:SER:HA	22:V:56:ASP:HA	1.69	0.74
41:o:71:ARG:HH21	41:o:80:ARG:NH1	1.86	0.74
46:t:353:LEU:HB2	46:t:439:ILE:HD12	1.69	0.74
30:d:13:THR:HG22	30:d:72:ARG:HH11	1.51	0.74
46:t:361:VAL:CB	46:t:388:TYR:O	2.34	0.74
46:t:251:LEU:HD23	46:t:254:GLN:OE1	1.88	0.74
46:t:105:CYS:HB2	46:t:391:LYS:HD3	1.70	0.73
12:L:128:ARG:NH2	34:h:109:ILE:O	2.20	0.73
46:t:133:LEU:HD22	46:t:160:ILE:HD11	1.70	0.73
46:t:154:VAL:HG23	46:t:526:THR:HG21	0.83	0.73
46:t:326:LEU:CD1	46:t:441:ARG:HB2	2.14	0.73
48:5:1724:U:H4'	48:5:1725:C:OP1	1.87	0.73
2:B:347:SER:HB3	2:B:350:ALA:H	1.52	0.73
48:5:1308:A:OP2	48:5:1308:A:C8	2.40	0.73
48:5:2211:U:H5	48:5:2234:G:O6	1.71	0.73
5:E:78:ARG:HG3	5:E:78:ARG:HH11	1.53	0.73
15:O:110[A]:PRO:O	15:O:113[A]:ASP:N	2.20	0.73
46:t:251:LEU:CD2	46:t:254:GLN:OE1	2.35	0.73
14:N:172:ARG:HB3	14:N:174:ILE:HD13	1.70	0.73
25:Y:36:SER:HB2	25:Y:37:LYS:HE2	1.71	0.73
46:t:197:LEU:HD22	46:t:222:LEU:CD2	2.19	0.73
36:j:48:ASN:OD1	36:j:54:LYS:NZ	2.20	0.73
3:C:60:THR:HG21	3:C:77:VAL:HG22	1.71	0.73
16:P:69:ARG:HG2	16:P:79:THR:HG23	1.71	0.73
8:H:171:ASP:OD1	8:H:173:ARG:HD3	1.89	0.73
18:R:34:GLN:NE2	46:t:369:ILE:HD12	2.04	0.73
9:I:3:ARG:NH2	48:5:2854:U:OP2	2.22	0.73
48:5:1781:C:H2'	48:5:1782:U:H6	1.54	0.73
14:N:73:ARG:HG2	14:N:75:VAL:HG13	1.70	0.72
46:t:191:MET:CA	46:t:321:LEU:HD12	2.20	0.72
46:t:246:ARG:HD3	46:t:254:GLN:HG2	1.70	0.72
9:I:63:GLU:HB2	48:5:2853:A:H5'	1.70	0.72
46:t:42:VAL:HG12	46:t:141:ILE:CD1	2.19	0.72
10:J:92:ARG:HG2	10:J:92:ARG:HH11	1.51	0.72
31:e:11:LYS:O	31:e:12:LYS:HB2	1.90	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:t:36:GLN:CG	46:t:529:SER:H	1.97	0.72
46:t:96:ASP:OD1	46:t:104:TRP:CB	2.38	0.72
46:t:198:LEU:HD23	46:t:223:ILE:HG13	1.71	0.72
48:5:2397:A:OP1	48:5:2398:A:H5''	1.88	0.72
19:S:108:GLN:NE2	48:5:1322:U:O2	2.22	0.72
46:t:83:LYS:HE2	47:1:2027:C:P	2.29	0.72
48:5:595:G:H1	48:5:609:G:H5''	1.53	0.72
48:5:2434:U:H4'	48:5:2435:G:H5''	1.70	0.72
46:t:51:HIS:CD2	46:t:163:VAL:H	2.07	0.72
46:t:68:THR:CB	46:t:93:THR:OG1	2.37	0.72
46:t:378:LEU:HD11	46:t:418:SER:O	1.88	0.72
10:J:59:ILE:HD12	10:J:65:ILE:HD11	1.72	0.72
46:t:46:ILE:HD11	46:t:141:ILE:CD1	2.06	0.72
46:t:194:VAL:HG11	46:t:319:ILE:HG23	1.72	0.72
2:B:103:THR:HG21	2:B:147:GLU:OE1	1.90	0.72
19:S:90:MET:CG	48:5:1213:G:H4'	2.18	0.72
46:t:186:ALA:HB3	46:t:323:MET:SD	2.29	0.72
16:P:138:LYS:HG3	16:P:140:GLU:HG3	1.72	0.72
18:R:114:LYS:HD3	48:5:2093:A:H61	1.55	0.72
48:5:2372:A:H5''	48:5:2373:A:H5'	1.70	0.71
8:H:166:ARG:NH1	8:H:168:ARG:HH22	1.85	0.71
17:Q:158:HIS:H	17:Q:186:VAL:HG12	1.54	0.71
46:t:180:LYS:HG3	46:t:466:LEU:HD11	1.71	0.71
48:5:2836:C:H5	48:5:2852:C:N4	1.85	0.71
16:P:29:THR:HG22	16:P:87:SER:OG	1.90	0.71
18:R:34:GLN:HE21	46:t:369:ILE:HG21	1.55	0.71
46:t:238:VAL:HB	46:t:261:GLU:HG3	1.70	0.71
46:t:426:ILE:HG21	46:t:432:CYS:SG	2.30	0.71
48:5:2572:C:O2'	48:5:2573:G:OP2	2.08	0.71
48:5:2818:U:H5'	48:5:2818:U:C6	2.23	0.71
21:U:98:THR:HG23	21:U:104:ARG:HH21	1.55	0.71
48:5:1024:G:H2'	48:5:1026:A:H8	1.55	0.71
46:t:545:PRO:HA	46:t:550:VAL:O	1.90	0.71
48:5:1875:G:H2'	48:5:1876:U:H5''	1.73	0.71
46:t:215:SER:HA	46:t:522:LEU:HD11	1.73	0.71
46:t:324:ALA:HB3	46:t:328:HIS:ND1	2.06	0.71
48:5:2437:G:H5'	48:5:2437:G:H8	1.55	0.71
35:i:62:ARG:O	35:i:63:ASN:ND2	2.22	0.71
46:t:76:LEU:CD1	46:t:88:GLY:CA	2.69	0.71
46:t:224:ARG:HD2	46:t:298:PHE:HD2	1.56	0.71
46:t:360:TYR:CZ	46:t:423:MET:SD	2.84	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128:ARG:NH1	48:5:2177:G:OP2	2.23	0.70
27:a:77:LYS:O	27:a:79:TRP:N	2.24	0.70
46:t:194:VAL:HG12	46:t:198:LEU:HD12	1.73	0.70
46:t:246:ARG:HB3	46:t:254:GLN:HB3	1.73	0.70
48:5:595:G:N1	48:5:609:G:H5''	2.06	0.70
48:5:1781:C:H2'	48:5:1782:U:C6	2.26	0.70
3:C:193:LYS:NZ	50:8:21:C:OP1	2.24	0.70
7:G:68:ARG:O	7:G:69:LEU:HB2	1.89	0.70
17:Q:170:ARG:HA	17:Q:174:ARG:HD2	1.71	0.70
46:t:353:LEU:HD12	46:t:439:ILE:CG1	2.20	0.70
19:S:13:ARG:HH11	19:S:13:ARG:HG3	1.55	0.70
46:t:48:ASP:OD1	46:t:134:ARG:HA	1.91	0.70
46:t:193:THR:HG23	46:t:556:LEU:CD2	2.20	0.70
3:C:197:ARG:NH1	48:5:1381:A:OP1	2.24	0.70
4:D:105:ILE:O	4:D:109:THR:HG23	1.92	0.70
41:o:74:CYS:HG	51:o:501:ZN:ZN	1.02	0.70
46:t:198:LEU:HD12	46:t:319:ILE:CG1	2.18	0.70
13:M:17:VAL:HG21	13:M:74:ARG:HB2	1.72	0.70
46:t:61:VAL:HG11	46:t:106:PRO:CG	2.08	0.70
46:t:76:LEU:HD13	46:t:88:GLY:H	1.57	0.70
48:5:2439:A:H2'	48:5:2440:G:H5''	1.72	0.70
26:Z:5:LEU:HD22	26:Z:77:TYR:CE1	2.27	0.70
31:e:55:ILE:HB	48:5:947:G:H5'	1.74	0.70
2:B:56:ILE:HD11	2:B:359:ILE:HG12	1.74	0.70
46:t:227:VAL:CG1	46:t:238:VAL:CG2	2.66	0.70
46:t:240:PRO:HD3	46:t:328:HIS:CB	2.21	0.70
46:t:387:VAL:CG1	46:t:389:PRO:N	2.55	0.70
46:t:513:SER:HB2	46:t:518:ASP:OD1	1.92	0.70
48:5:549:U:H2'	48:5:550:A:C8	2.27	0.70
16:P:33:ALA:HB1	16:P:117:ILE:HG12	1.74	0.70
25:Y:3:LYS:HD2	25:Y:8:VAL:HG23	1.72	0.70
46:t:133:LEU:HB3	46:t:160:ILE:CD1	2.22	0.70
28:b:16:ALA:O	28:b:20:GLY:HA3	1.92	0.69
26:Z:16:GLY:O	26:Z:18:TYR:N	2.25	0.69
48:5:2407:C:H2'	48:5:2408:U:H6	1.56	0.69
7:G:90:THR:HA	7:G:214:LEU:HD21	1.75	0.69
7:G:95:ASN:OD1	7:G:98:ARG:NH1	2.23	0.69
24:X:142:ILE:CG2	46:t:421:LEU:N	2.50	0.69
29:c:22:LYS:HD3	29:c:94:GLU:HG3	1.75	0.69
48:5:1631:C:H5''	48:5:1632:A:H5''	1.73	0.69
48:5:1765:U:H4'	48:5:1765:U:OP1	1.91	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:73:ARG:NH2	48:5:2814:G:OP1	2.25	0.69
31:e:91:THR:HG22	31:e:92:TYR:HD1	1.54	0.69
46:t:198:LEU:HD22	46:t:258:ILE:HD11	1.74	0.69
46:t:517:THR:HG22	46:t:518:ASP:C	2.17	0.69
48:5:155:G:H5'	48:5:156:G:C8	2.27	0.69
10:J:23:VAL:HG12	10:J:25:GLU:H	1.56	0.69
30:d:75:ILE:HG12	30:d:93:VAL:HG13	1.73	0.69
24:X:51:VAL:HG21	34:h:62:GLN:HB3	1.75	0.69
46:t:230:ILE:HD11	46:t:553:ILE:HG23	1.74	0.69
46:t:244:VAL:HG11	46:t:319:ILE:HD13	1.73	0.69
46:t:163:VAL:CG2	46:t:164:ASP:N	2.46	0.69
46:t:224:ARG:CD	46:t:298:PHE:HD2	2.04	0.69
48:5:1355:A:H4'	48:5:1356:U:O5'	1.93	0.69
15:O:62[A]:THR:H	15:O:69[A]:GLY:HA3	1.57	0.69
19:S:9:VAL:HG22	19:S:61:ILE:HD13	1.74	0.69
29:c:9:SER:OG	29:c:10:ILE:N	2.22	0.69
46:t:161:TYR:CE2	46:t:162:PRO:O	2.43	0.69
46:t:176:LEU:HB3	46:t:537:ILE:HD13	1.75	0.69
46:t:230:ILE:HD11	46:t:553:ILE:CG2	2.23	0.69
48:5:2667:A:H5'	48:5:2667:A:H8	1.56	0.69
48:5:3317:U:H4'	48:5:3318:G:O5'	1.92	0.69
2:B:41:VAL:CA	2:B:185:GLY:HA3	2.19	0.69
48:5:3228:C:O2'	48:5:3229:G:OP2	2.11	0.69
3:C:300:ARG:HG2	3:C:300:ARG:HH11	1.58	0.69
8:H:166:ARG:HH11	8:H:168:ARG:NH2	1.87	0.69
26:Z:102:GLU:OE1	26:Z:103:GLN:N	2.25	0.69
41:o:41:ARG:NH1	48:5:284:A:OP2	2.24	0.69
46:t:251:LEU:CA	46:t:388:TYR:HE2	2.05	0.69
48:5:173:G:HO2'	48:5:174:C:H6	1.41	0.69
48:5:439:C:H4'	48:5:440:A:H5'	1.74	0.69
18:R:43:LYS:O	18:R:47:ASN:HB2	1.91	0.68
46:t:42:VAL:O	46:t:46:ILE:HG13	1.92	0.68
2:B:53:MET:CE	48:5:3048:A:H5'	2.22	0.68
15:O:68[B]:ARG:NH1	48:5:2988:C:OP1	2.26	0.68
29:c:26:GLY:O	29:c:30:THR:HG23	1.93	0.68
48:5:2507:C:O2'	48:5:2508:U:OP1	2.10	0.68
1:A:204:MET:HE2	1:A:209:HIS:HB2	1.75	0.68
15:O:121[B]:PRO:HA	15:O:124[B]:LEU:HD22	1.76	0.68
46:t:327:GLU:O	46:t:328:HIS:HB2	1.93	0.68
13:M:133:LYS:NZ	48:5:3227:A:O2'	2.18	0.68
48:5:1239:C:H42	48:5:1249:G:H1	1.41	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:150:ARG:HH11	2:B:150:ARG:HG2	1.58	0.68
3:C:36:HIS:O	3:C:40:THR:HG23	1.94	0.68
7:G:86:THR:O	7:G:90:THR:HG23	1.94	0.68
21:U:19:VAL:O	21:U:23:THR:OG1	2.11	0.68
32:f:2:ALA:HB2	48:5:3216:G:OP2	1.93	0.68
48:5:2872:A:H4'	48:5:2872:A:OP1	1.94	0.68
1:A:68:LYS:NZ	48:5:1579:C:H5''	2.08	0.68
2:B:139:GLN:O	2:B:141:GLY:N	2.27	0.68
6:F:134:VAL:O	6:F:229:PHE:HA	1.94	0.68
15:O:110[A]:PRO:O	15:O:112[A]:TYR:N	2.26	0.68
46:t:39:LEU:HD21	46:t:529:SER:O	1.94	0.68
48:5:1013:G:H2'	48:5:1014:U:O4'	1.94	0.68
7:G:148:ALA:HA	7:G:201:THR:HG22	1.76	0.68
8:H:95:ALA:O	39:m:77:ILE:HG12	1.93	0.68
14:N:109:ARG:NH1	50:8:141:C:OP1	2.26	0.68
34:h:76:GLN:O	34:h:81:ARG:NH1	2.27	0.68
34:h:78:LYS:HA	34:h:81:ARG:HD3	1.76	0.68
46:t:162:PRO:HD2	46:t:167:LYS:HD2	1.72	0.68
48:5:3289:G:H2'	48:5:3290:G:H8	1.59	0.68
1:A:243:THR:OG1	48:5:2244:A:H5''	1.94	0.68
2:B:117:ARG:CZ	2:B:175:LYS:HD2	2.23	0.68
46:t:61:VAL:CG1	46:t:106:PRO:CD	2.72	0.68
46:t:246:ARG:HB3	46:t:254:GLN:CG	2.24	0.68
48:5:420:G:O5'	48:5:420:G:OP2	2.12	0.68
35:i:54:GLU:HG2	35:i:90:MET:HE1	1.76	0.67
48:5:3155:U:H4'	48:5:3156:U:OP2	1.93	0.67
2:B:221:THR:HG22	2:B:273:HIS:H	1.60	0.67
1:A:224:THR:HG21	48:5:2201:G:H21	1.59	0.67
46:t:361:VAL:HG23	46:t:388:TYR:HB3	1.68	0.67
48:5:2403:G:N2	48:5:2404:A:H62	1.91	0.67
2:B:299:ASP:OD1	2:B:301:THR:HG23	1.94	0.67
4:D:40:HIS:CD2	4:D:42:ALA:H	2.11	0.67
4:D:187:THR:HG22	4:D:189:GLU:HB2	1.76	0.67
7:G:241:LYS:HB2	48:5:2586:G:N7	2.08	0.67
9:I:99:ILE:HG13	9:I:123:HIS:HB2	1.76	0.67
19:S:90:MET:HG2	48:5:1213:G:H4'	1.74	0.67
46:t:198:LEU:HD21	46:t:258:ILE:HD13	1.75	0.67
48:5:3295:A:H2'	48:5:3296:A:C8	2.29	0.67
2:B:41:VAL:HA	2:B:185:GLY:CA	2.22	0.67
19:S:13:ARG:HG3	19:S:13:ARG:NH1	2.08	0.67
32:f:86:ARG:NH2	48:5:497:C:O3'	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:5:2957:G:H5'	48:5:2957:G:H8	1.59	0.67
48:5:2996:U:H4'	48:5:2996:U:OP1	1.95	0.67
8:H:188:THR:HG22	8:H:189:GLU:HG2	1.75	0.67
13:M:121:MET:HE1	48:5:3215:A:O5'	1.94	0.67
46:t:153:GLU:CB	46:t:318:LEU:HD22	1.78	0.67
4:D:265:TYR:OH	49:7:121:U:OP2	2.13	0.67
2:B:283:TYR:HB3	2:B:323:MET:HE2	1.76	0.67
4:D:76:ALA:HB3	4:D:109:THR:HG22	1.76	0.67
19:S:50:LYS:NZ	49:7:76:A:O2'	2.19	0.67
48:5:252:U:H4'	48:5:253:A:C5'	2.25	0.67
31:e:40:SER:O	31:e:44:ARG:HG3	1.94	0.67
46:t:216:SER:O	46:t:520:PRO:HD3	1.94	0.67
17:Q:134:GLY:O	17:Q:137:THR:OG1	2.11	0.67
19:S:137:ARG:HG2	19:S:139:TYR:CE2	2.30	0.67
33:g:41:ARG:HG2	33:g:56:THR:HG21	1.76	0.67
48:5:3330:A:H5''	48:5:3330:A:H8	1.58	0.67
15:O:160[B]:ARG:NH2	48:5:3182:G:OP1	2.27	0.66
46:t:92:PRO:O	46:t:94:THR:HG23	1.93	0.66
20:T:51:GLY:HA3	20:T:92:ARG:HG3	1.76	0.66
31:e:91:THR:HG22	31:e:92:TYR:CD1	2.29	0.66
48:5:1560:G:O2'	48:5:1561:G:OP1	2.12	0.66
2:B:126:LYS:NZ	48:5:3294:A:OP2	2.29	0.66
2:B:308:MET:HE2	2:B:372:THR:C	2.20	0.66
12:L:59:ARG:HD3	48:5:73:C:C2	2.31	0.66
43:q:102:SER:OG	43:q:103:ASN:N	2.25	0.66
46:t:161:TYR:CD2	46:t:161:TYR:C	2.72	0.66
48:5:304:G:N3	48:5:304:G:H5'	2.10	0.66
48:5:2204:C:H4'	48:5:2205:U:OP1	1.95	0.66
49:7:91:G:H2'	49:7:92:A:C8	2.30	0.66
18:R:74:ARG:NH1	48:5:1942:U:OP2	2.27	0.66
46:t:47:ASN:H	46:t:59:LEU:HD12	1.60	0.66
46:t:378:LEU:HD13	46:t:422:GLY:CA	2.16	0.66
48:5:1481:A:O4'	48:5:1481:A:OP1	2.12	0.66
5:E:78:ARG:NH1	48:5:3272:C:OP2	2.28	0.66
46:t:37:THR:HG22	46:t:41:TYR:CE2	2.29	0.66
3:C:20:LEU:HD13	3:C:256:THR:HG23	1.76	0.66
9:I:86:HIS:HB3	9:I:139:ARG:HG2	1.77	0.66
41:o:74:CYS:SG	51:o:501:ZN:ZN	1.83	0.66
46:t:230:ILE:CD1	46:t:553:ILE:CG2	2.73	0.66
46:t:387:VAL:HG22	46:t:389:PRO:CD	2.26	0.66
6:F:178:ILE:HA	6:F:183:ASP:HB3	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:9:MET:O	10:J:11:ASP:N	2.29	0.66
20:T:129:LYS:HB3	48:5:1097:G:H4'	1.78	0.66
40:n:9:ARG:HH11	40:n:9:ARG:HG3	1.61	0.66
46:t:20:LEU:HG	46:t:21:GLN:N	2.09	0.66
46:t:153:GLU:CB	46:t:318:LEU:CD1	2.67	0.66
28:b:23:LYS:HB3	28:b:24:PRO:CD	2.25	0.66
46:t:249:ARG:HH12	46:t:250:PHE:HE2	1.39	0.66
14:N:182:ASN:O	14:N:183:THR:HG22	1.96	0.66
46:t:238:VAL:HG11	46:t:260:ALA:HB1	1.78	0.66
46:t:324:ALA:H	46:t:328:HIS:CE1	2.14	0.66
48:5:2549:G:C8	48:5:2549:G:H5'	2.31	0.66
18:R:35:ALA:O	18:R:36:ASN:ND2	2.29	0.66
46:t:230:ILE:HD13	46:t:553:ILE:HG21	1.78	0.66
50:8:79:A:H3'	50:8:80:A:C8	2.31	0.66
34:h:90:ARG:NH1	48:5:20:A:OP2	2.29	0.65
2:B:120:LYS:NZ	48:5:3001:C:OP1	2.28	0.65
18:R:84:THR:O	18:R:88:ARG:HG2	1.96	0.65
26:Z:3:LYS:HE3	26:Z:5:LEU:HD12	1.78	0.65
34:h:62:GLN:O	34:h:66:VAL:HG23	1.97	0.65
46:t:233:SER:CB	46:t:543:LEU:HD23	2.26	0.65
48:5:118:U:O2	48:5:121:A:H5'	1.97	0.65
48:5:618:C:H2'	48:5:619:A:C8	2.31	0.65
48:5:2667:A:H5'	48:5:2667:A:C8	2.30	0.65
48:5:2777:G:C8	48:5:2777:G:H5''	2.31	0.65
1:A:70:ARG:HH22	48:5:2522:G:H1	1.44	0.65
4:D:270:LYS:O	4:D:273:ARG:HB3	1.96	0.65
48:5:15:C:H5'	48:5:15:C:C6	2.31	0.65
48:5:1655:G:C5'	48:5:1655:G:H8	2.08	0.65
3:C:20:LEU:HD11	3:C:252:GLU:HG3	1.78	0.65
18:R:102:LEU:HD13	18:R:127:SER:HB2	1.77	0.65
25:Y:35:LEU:HD13	25:Y:39:LEU:HB3	1.77	0.65
37:k:46:ARG:NH1	37:k:47:GLY:O	2.30	0.65
46:t:197:LEU:HD22	46:t:222:LEU:HD21	1.78	0.65
50:8:77:A:H2'	50:8:78:G:O4'	1.96	0.65
21:U:47:VAL:O	21:U:49:ASN:N	2.29	0.65
27:a:3:SER:O	27:a:6:THR:HB	1.97	0.65
36:j:72:ARG:NH1	50:8:95:G:OP2	2.28	0.65
37:k:46:ARG:NH2	48:5:1613:A:OP2	2.30	0.65
46:t:39:LEU:CD2	46:t:529:SER:O	2.45	0.65
4:D:140:ARG:HD3	48:5:1080:A:OP1	1.97	0.65
14:N:125:SER:HB3	48:5:2433:U:H1'	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:88[A]:VAL:O	15:O:90[A]:HIS:N	2.30	0.65
38:l:10:LYS:HA	38:l:13:MET:HE3	1.79	0.65
48:5:249:U:O2'	48:5:250:U:H5''	1.95	0.65
32:f:49:ILE:HG23	32:f:100:ILE:HG13	1.78	0.65
46:t:176:LEU:HD11	46:t:180:LYS:HE3	1.78	0.65
1:A:116:VAL:HG13	1:A:126:LEU:HB2	1.76	0.65
19:S:137:ARG:HG2	19:S:139:TYR:CZ	2.32	0.65
24:X:142:ILE:CD1	46:t:417:LYS:C	2.69	0.65
38:l:5:LYS:HD3	38:l:13:MET:HE1	1.79	0.65
46:t:162:PRO:CD	46:t:167:LYS:CD	2.55	0.65
48:5:2103:U:H2'	48:5:2104:A:C8	2.31	0.65
13:M:48:GLY:HA3	13:M:53:VAL:HG13	1.78	0.65
29:c:99:ASP:OD1	29:c:99:ASP:N	2.27	0.65
46:t:311:VAL:HG13	46:t:509:LEU:CD1	2.14	0.65
46:t:545:PRO:HB2	46:t:551:GLN:HA	1.77	0.65
48:5:2569:A:H4'	48:5:2570:U:H5'	1.78	0.65
2:B:117:ARG:HA	2:B:175:LYS:HD3	1.78	0.65
4:D:106:ALA:O	4:D:110:LEU:HD22	1.98	0.65
18:R:114:LYS:HD3	48:5:2093:A:N6	2.12	0.65
34:h:39:PRO:O	34:h:40:SER:HB3	1.96	0.65
48:5:900:G:H1'	48:5:1589:A:N6	2.12	0.65
48:5:1659:U:H2'	48:5:1660:C:C6	2.32	0.65
7:G:100:GLU:OE2	7:G:108:ARG:NH1	2.30	0.64
8:H:90:MET:HB2	8:H:144:ILE:HG22	1.80	0.64
25:Y:52:ARG:HA	25:Y:70:ILE:HG22	1.77	0.64
46:t:244:VAL:HG13	46:t:319:ILE:HA	1.73	0.64
46:t:246:ARG:HG2	46:t:248:ARG:HH12	1.54	0.64
48:5:892:U:C2'	48:5:893:C:H5'	2.26	0.64
48:5:1818:U:H2'	48:5:1819:U:C6	2.32	0.64
48:5:2436:U:H3	48:5:2511:A:H62	1.45	0.64
26:Z:25:ILE:HA	26:Z:43:VAL:HG12	1.78	0.64
3:C:339:LEU:HA	3:C:342:LYS:HB3	1.79	0.64
10:J:87:LYS:HD2	10:J:104:PHE:CD2	2.32	0.64
42:p:4:ARG:NH2	48:5:838:G:O6	2.31	0.64
48:5:2436:U:H3	48:5:2511:A:N6	1.95	0.64
8:H:12:VAL:HG13	8:H:16:VAL:HG22	1.79	0.64
46:t:61:VAL:HG11	46:t:106:PRO:CD	2.27	0.64
46:t:191:MET:CB	46:t:321:LEU:HD12	2.26	0.64
46:t:246:ARG:HB3	46:t:254:GLN:CB	2.26	0.64
25:Y:112:ASP:HB3	25:Y:115:ARG:HB2	1.80	0.64
46:t:39:LEU:HD23	46:t:529:SER:CA	2.24	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:t:163:VAL:HG22	46:t:164:ASP:H	1.61	0.64
15:O:12[B]:LYS:O	19:S:167:ARG:NH2	2.28	0.64
46:t:197:LEU:HB2	46:t:223:ILE:HD13	1.79	0.64
48:5:830:A:O2'	48:5:1866:C:H2'	1.98	0.64
48:5:1818:U:H2'	48:5:1819:U:H6	1.62	0.64
33:g:16:ARG:HG3	33:g:16:ARG:HH11	1.63	0.64
12:L:58:VAL:HG13	48:5:75:G:H5''	1.78	0.64
14:N:68:ARG:HA	14:N:98:LEU:HD21	1.80	0.64
15:O:110[A]:PRO:O	15:O:111[A]:PRO:C	2.41	0.64
18:R:173:ARG:HH21	18:R:177:VAL:HG21	1.62	0.64
27:a:64:GLN:HE22	48:5:70:A:H5'	1.61	0.64
48:5:247:C:C2	48:5:248:U:H1'	2.33	0.64
4:D:265:TYR:HE1	49:7:121:U:H5''	1.63	0.64
48:5:3174:A:N6	48:5:3278:C:N3	2.46	0.64
33:g:65:VAL:HG12	33:g:70:LYS:HE2	1.80	0.64
48:5:528:U:H2'	48:5:529:A:C8	2.33	0.64
7:G:121:SER:O	7:G:123:GLN:N	2.31	0.63
12:L:93:ILE:HG22	12:L:94:GLY:H	1.64	0.63
14:N:80:THR:HG21	14:N:87:GLN:HA	1.78	0.63
14:N:143:ARG:HH21	34:h:92:LEU:HA	1.61	0.63
33:g:58:ARG:HG3	33:g:59:PRO:HD2	1.80	0.63
48:5:2403:G:N7	48:5:2870:C:H4'	2.12	0.63
34:h:85:THR:HG22	34:h:88:LEU:H	1.62	0.63
46:t:164:ASP:O	46:t:168:PRO:HA	1.98	0.63
12:L:56:PRO:HG3	12:L:74:GLY:O	1.98	0.63
27:a:18:GLY:O	48:5:1370:G:H5''	1.99	0.63
46:t:42:VAL:HG21	46:t:68:THR:OG1	1.99	0.63
46:t:68:THR:HB	46:t:93:THR:OG1	1.98	0.63
46:t:94:THR:OG1	46:t:142:THR:HB	1.98	0.63
46:t:149:GLY:HA3	46:t:250:PHE:CE1	2.33	0.63
46:t:197:LEU:CB	46:t:223:ILE:HD13	2.28	0.63
48:5:541:U:H2'	48:5:542:G:C8	2.34	0.63
48:5:1085:A:C5'	48:5:1085:A:H8	2.10	0.63
48:5:1241:U:O2'	48:5:1242:G:O5'	2.14	0.63
2:B:293:ASN:HB2	2:B:304:THR:HA	1.80	0.63
4:D:270:LYS:HB3	49:7:1:G:O2'	1.99	0.63
10:J:109:HIS:CD2	10:J:123:PHE:H	2.15	0.63
46:t:42:VAL:HG11	46:t:141:ILE:HD13	1.80	0.63
2:B:238:LEU:HB3	2:B:242:THR:HG21	1.81	0.63
37:k:22:THR:HG22	37:k:74:LYS:HB3	1.80	0.63
39:m:78:ILE:HD11	39:m:83:LYS:HA	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:t:190:ALA:C	46:t:321:LEU:CD1	2.71	0.63
1:A:224:THR:HG23	48:5:2202:C:O4'	1.97	0.63
19:S:26:ARG:HH11	20:T:150:THR:HG21	1.61	0.63
48:5:2970:C:O2'	48:5:2971:A:OP2	2.16	0.63
10:J:60:ARG:NH2	41:o:104:LEU:O	2.27	0.63
16:P:31:GLU:HG3	16:P:60:PHE:HA	1.80	0.63
46:t:361:VAL:HG23	46:t:388:TYR:CB	2.23	0.63
46:t:545:PRO:CB	46:t:551:GLN:HA	2.28	0.63
48:5:2440:G:H2'	48:5:2441:A:C8	2.34	0.63
34:h:101:THR:HG22	34:h:104:GLN:HB2	1.81	0.63
41:o:105:GLN:HB2	41:o:106:PHE:CD2	2.33	0.63
48:5:150:A:C2'	48:5:151:A:H5'	2.29	0.63
1:A:204:MET:CE	1:A:209:HIS:HB2	2.29	0.63
7:G:48:ARG:NH2	48:5:2588:U:OP1	2.29	0.63
7:G:161:GLU:HA	7:G:164:VAL:HG22	1.80	0.63
26:Z:50:PRO:HD3	26:Z:68:ILE:HG12	1.81	0.63
1:A:209:HIS:HD2	1:A:211:HIS:H	1.47	0.62
24:X:142:ILE:HG12	46:t:421:LEU:CD1	2.29	0.62
46:t:324:ALA:O	46:t:328:HIS:CE1	2.51	0.62
48:5:1094:U:O2'	48:5:1095:U:H3'	1.99	0.62
48:5:3049:A:H5'	48:5:3049:A:C8	2.34	0.62
14:N:183:THR:O	14:N:184:LYS:HB3	1.98	0.62
22:V:33:ASN:HD22	22:V:63:LYS:HB2	1.63	0.62
44:r:34:UNK:O	44:r:36:UNK:N	2.32	0.62
48:5:1564:U:H2'	48:5:1565:G:C8	2.34	0.62
48:5:3195:U:O2'	48:5:3196:U:H5'	1.99	0.62
7:G:151:VAL:HG22	7:G:199:ALA:HB1	1.81	0.62
46:t:198:LEU:O	46:t:509:LEU:HD21	1.98	0.62
46:t:244:VAL:HG22	46:t:320:ASP:N	2.10	0.62
2:B:2:SER:HA	48:5:2940:A:N7	2.14	0.62
16:P:62:ARG:NH1	48:5:412:G:OP1	2.32	0.62
17:Q:165:ILE:HD12	17:Q:167:SER:O	1.99	0.62
19:S:73:LYS:NZ	19:S:97:VAL:O	2.32	0.62
46:t:62:PRO:HG3	46:t:130:THR:CG2	2.29	0.62
46:t:530:LYS:O	46:t:530:LYS:CG	2.46	0.62
48:5:734:C:H2'	48:5:735:A:H5''	1.81	0.62
48:5:1023:C:H5''	48:5:1024:G:OP2	1.99	0.62
28:b:20:GLY:O	28:b:21:ILE:HB	1.98	0.62
46:t:230:ILE:HD12	46:t:543:LEU:HD11	1.82	0.62
46:t:246:ARG:O	46:t:254:GLN:CB	2.48	0.62
2:B:296:THR:HG22	2:B:298:PHE:N	2.03	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:g:42:PRO:HD3	33:g:56:THR:HG22	1.80	0.62
48:5:2818:U:H6	48:5:2818:U:C5'	2.10	0.62
4:D:211:LEU:HD13	4:D:219:PHE:HA	1.80	0.62
46:t:188:HIS:CE1	46:t:191:MET:HE3	2.34	0.62
46:t:190:ALA:C	46:t:321:LEU:HD13	2.24	0.62
2:B:221:THR:HB	2:B:273:HIS:O	2.00	0.62
7:G:33:ASN:O	7:G:35:GLY:N	2.33	0.62
9:I:14:ASN:O	9:I:128:ARG:NH2	2.33	0.62
9:I:174:THR:HG23	9:I:175:ASN:H	1.63	0.62
32:f:2:ALA:HB1	48:5:3219:G:N7	2.14	0.62
48:5:979:U:H1'	48:5:980:A:C4	2.34	0.62
48:5:1566:A:H2'	48:5:1567:U:H5'	1.81	0.62
15:O:72[A]:HIS:HD2	48:5:3008:A:OP1	1.83	0.61
20:T:14:MET:HE3	20:T:58:GLN:HB2	1.81	0.61
26:Z:115:LYS:NZ	26:Z:119:GLU:OE1	2.32	0.61
48:5:3358:U:H2'	48:5:3359:A:H8	1.65	0.61
1:A:181:LYS:NZ	48:5:860:G:O5'	2.31	0.61
25:Y:37:LYS:H	25:Y:37:LYS:CD	2.13	0.61
43:q:81:LYS:HD3	48:5:1283:C:OP1	2.00	0.61
46:t:39:LEU:HD23	46:t:529:SER:C	2.25	0.61
48:5:2407:C:H2'	48:5:2408:U:C6	2.35	0.61
13:M:124:ARG:NH2	48:5:3212:C:OP2	2.33	0.61
24:X:133:LEU:HD22	46:t:417:LYS:CD	2.31	0.61
46:t:240:PRO:HD2	46:t:349:LYS:HA	1.82	0.61
48:5:3165:A:H2'	48:5:3166:C:H6	1.65	0.61
2:B:151:ILE:O	2:B:155:ALA:HB3	2.01	0.61
15:O:180[B]:SER:OG	15:O:181[B]:ALA:N	2.29	0.61
46:t:230:ILE:HD12	46:t:543:LEU:CD1	2.30	0.61
48:5:725:G:H2'	48:5:726:G:H5''	1.81	0.61
48:5:817:A:OP2	48:5:817:A:H4'	1.98	0.61
48:5:3227:A:H2'	48:5:3228:C:H5'	1.82	0.61
29:c:40:LYS:HD3	29:c:93:LEU:O	2.00	0.61
32:f:59:VAL:HG23	32:f:60:ARG:H	1.66	0.61
48:5:132:C:H2'	48:5:133:U:H5''	1.82	0.61
15:O:85[A]:ARG:HD3	15:O:90[A]:HIS:CG	2.36	0.61
46:t:61:VAL:N	46:t:131:GLY:O	2.33	0.61
46:t:318:LEU:HD13	46:t:506:THR:OG1	2.01	0.61
48:5:3269:U:H4'	48:5:3270:U:O5'	2.00	0.61
3:C:330:TYR:O	3:C:334:PHE:N	2.31	0.61
46:t:198:LEU:CD2	46:t:258:ILE:HD11	2.30	0.61
9:I:61:SER:HB2	9:I:63:GLU:HG2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:86:THR:HB	17:Q:105:ARG:HB3	1.81	0.61
48:5:1567:U:H1'	48:5:1570:U:H5	1.66	0.61
48:5:1804:A:H2'	48:5:1805:C:H6	1.63	0.61
48:5:2537:U:O2'	48:5:2538:U:P	2.59	0.61
48:5:3195:U:H1'	48:5:3196:U:OP1	2.01	0.61
26:Z:33:SER:HB3	26:Z:36:HIS:HB2	1.83	0.61
46:t:153:GLU:HB2	46:t:318:LEU:CG	2.30	0.61
2:B:53:MET:HE1	48:5:3047:U:O2'	2.00	0.61
2:B:152:LYS:HD3	2:B:189:SER:HA	1.83	0.61
11:K:109:UNK:O	11:K:113:UNK:N	2.34	0.61
46:t:162:PRO:HG2	46:t:163:VAL:O	2.01	0.61
48:5:920:A:OP1	48:5:922:U:H5	1.84	0.61
2:B:147:GLU:OE2	2:B:150:ARG:NH2	2.34	0.60
4:D:41:LYS:HB2	20:T:68:THR:O	2.01	0.60
5:E:40:LEU:HB3	5:E:84:VAL:HG13	1.82	0.60
12:L:177:LYS:HA	35:i:11:LEU:HD22	1.82	0.60
16:P:125:GLN:HB2	16:P:141:SER:HB2	1.83	0.60
32:f:13:HIS:HE2	32:f:28:SER:HG	1.49	0.60
46:t:191:MET:CG	46:t:530:LYS:HZ1	2.06	0.60
1:A:204:MET:HE3	1:A:208:ASP:HB3	1.82	0.60
3:C:232:SER:O	3:C:233:LEU:HB2	2.01	0.60
5:E:109:GLU:CD	5:E:109:GLU:H	2.07	0.60
8:H:70:THR:HG21	48:5:3122:A:N1	2.16	0.60
15:O:68[B]:ARG:NH1	48:5:2988:C:P	2.75	0.60
48:5:2895:G:H2'	48:5:2896:A:H5''	1.82	0.60
14:N:172:ARG:NH1	48:5:29:C:O3'	2.33	0.60
15:O:110[B]:PRO:O	15:O:111[B]:PRO:C	2.44	0.60
38:l:9:ILE:HG22	38:l:13:MET:HE2	1.82	0.60
48:5:1235:U:C4'	48:5:1236:G:H5'	2.29	0.60
2:B:188:ILE:H	2:B:188:ILE:CD1	2.14	0.60
31:e:41:VAL:HG12	31:e:46:PHE:CD2	2.37	0.60
46:t:96:ASP:OD1	46:t:104:TRP:HB3	2.01	0.60
48:5:3341:U:H5''	48:5:3342:A:OP2	2.01	0.60
16:P:59:PRO:HG3	16:P:76:PHE:CD2	2.35	0.60
24:X:57:LEU:HD23	24:X:61:LYS:HG2	1.82	0.60
31:e:105:ARG:NH2	48:5:1412:G:OP1	2.33	0.60
46:t:238:VAL:HB	46:t:261:GLU:HG2	1.82	0.60
3:C:144:LYS:HG2	3:C:145:ILE:H	1.65	0.60
7:G:132:VAL:HG21	7:G:190:VAL:HG22	1.83	0.60
46:t:215:SER:HB2	46:t:520:PRO:HG2	1.84	0.60
46:t:216:SER:HB3	46:t:520:PRO:CG	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:5:385:A:H2'	48:5:386:A:C8	2.36	0.60
48:5:2537:U:H2'	48:5:2538:U:O4'	2.02	0.60
50:8:78:G:H2'	50:8:79:A:O4'	2.02	0.60
9:I:158:LYS:NZ	48:5:2852:C:N3	2.49	0.60
36:j:65:ARG:HH11	36:j:65:ARG:HG3	1.67	0.60
46:t:163:VAL:CG1	46:t:163:VAL:O	2.43	0.60
48:5:1500:G:H2'	48:5:1501:U:O4'	2.01	0.60
7:G:27:THR:O	7:G:28:HIS:ND1	2.34	0.60
7:G:213:LYS:O	7:G:217:THR:HG22	2.02	0.60
8:H:62:ARG:NH2	48:5:3115:C:OP1	2.34	0.60
21:U:82:LYS:NZ	48:5:1686:U:O4	2.33	0.60
46:t:198:LEU:HD21	46:t:258:ILE:CD1	2.32	0.60
9:I:177:ASP:N	9:I:177:ASP:OD1	2.35	0.60
30:d:44:MET:HB3	30:d:77:ARG:NH1	2.17	0.60
46:t:533:GLN:NE2	46:t:536:TRP:CD1	2.67	0.60
48:5:22:G:H1'	50:8:104:A:N3	2.16	0.60
48:5:1764:U:H3'	48:5:1765:U:H5''	1.84	0.60
48:5:2372:A:H4'	48:5:2373:A:OP2	2.02	0.60
16:P:74:LYS:NZ	48:5:3298:C:OP1	2.35	0.59
26:Z:83:THR:HG23	26:Z:85:TYR:N	2.15	0.59
30:d:50:ARG:CZ	30:d:90:PHE:CZ	2.85	0.59
33:g:7:PHE:CD1	33:g:20:ILE:HD12	2.36	0.59
46:t:244:VAL:CG1	46:t:318:LEU:O	2.39	0.59
4:D:64:ILE:HG13	4:D:109:THR:HG21	1.83	0.59
4:D:152:ARG:HH11	4:D:152:ARG:HG3	1.66	0.59
37:k:32:ASN:HD21	37:k:34:ALA:HB3	1.67	0.59
46:t:353:LEU:CD1	46:t:439:ILE:CD1	2.66	0.59
48:5:1329:U:H4'	48:5:1330:A:OP1	2.02	0.59
48:5:2103:U:H2'	48:5:2104:A:H8	1.66	0.59
1:A:105:GLY:HA3	1:A:160:SER:HB3	1.83	0.59
2:B:232:ARG:NH2	48:5:2989:U:O2'	2.36	0.59
13:M:113:THR:HG22	13:M:115:PHE:H	1.66	0.59
27:a:8:THR:HG21	48:5:662:U:OP1	2.02	0.59
35:i:58:ILE:HA	35:i:61:ILE:HG13	1.84	0.59
41:o:45:ARG:NH2	48:5:283:G:OP1	2.34	0.59
43:q:97:LYS:O	43:q:101:VAL:HG23	2.02	0.59
1:A:206:PRO:HD3	1:A:213:GLY:HA2	1.84	0.59
26:Z:46:ILE:HG12	26:Z:49:TYR:CE1	2.37	0.59
35:i:40:VAL:O	35:i:44:VAL:HG23	2.02	0.59
46:t:353:LEU:CB	46:t:439:ILE:HD12	2.31	0.59
12:L:15:ARG:NH2	48:5:96:G:OP1	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:120:GLN:NE2	25:Y:126:LEU:HA	2.17	0.59
38:l:19:GLN:NE2	50:8:53:A:OP1	2.34	0.59
48:5:851:C:H5''	48:5:851:C:C6	2.34	0.59
48:5:1308:A:OP2	48:5:1308:A:H8	1.85	0.59
10:J:166:LYS:O	10:J:168:ASP:N	2.34	0.59
11:K:134:UNK:O	11:K:137:UNK:N	2.35	0.59
12:L:93:ILE:HG22	12:L:94:GLY:N	2.17	0.59
25:Y:82:VAL:O	25:Y:84:LYS:N	2.35	0.59
26:Z:54:THR:H	26:Z:57:HIS:CD2	2.20	0.59
27:a:120:ASN:O	27:a:141:ALA:HB1	2.03	0.59
40:n:16:LYS:O	40:n:20:VAL:HG23	2.02	0.59
46:t:391:LYS:HE3	46:t:393:SER:HB2	1.85	0.59
48:5:1605:A:O2'	48:5:1607:U:OP2	2.12	0.59
48:5:3155:U:H3'	48:5:3156:U:H5''	1.85	0.59
4:D:85:ARG:HD3	4:D:86:TYR:CE1	2.38	0.59
4:D:184:ASP:HB3	4:D:187:THR:HB	1.84	0.59
4:D:261:THR:OG1	4:D:264:GLN:HG3	2.02	0.59
33:g:41:ARG:HA	33:g:56:THR:HG22	1.83	0.59
42:p:6:LYS:HD3	42:p:7:LYS:HE3	1.84	0.59
46:t:62:PRO:CD	46:t:130:THR:HB	2.31	0.59
9:I:72:ALA:O	9:I:76:MET:HG2	2.02	0.59
15:O:36[B]:VAL:HB	15:O:108[B]:ILE:HB	1.85	0.59
35:i:25:LYS:HB2	35:i:28:TYR:HD2	1.67	0.59
46:t:90:ALA:HA	46:t:387:VAL:HB	1.85	0.59
8:H:26:LYS:HG3	8:H:35:THR:HG22	1.85	0.59
48:5:2511:A:C2'	48:5:2512:C:H5''	2.32	0.59
28:b:46:ALA:O	28:b:50:THR:HG23	2.03	0.58
37:k:44:LYS:HG2	37:k:53:THR:HB	1.85	0.58
46:t:189:ILE:HG21	46:t:543:LEU:CD1	2.28	0.58
48:5:208:C:C2'	48:5:209:A:H5'	2.33	0.58
48:5:955:U:H2'	48:5:956:U:C6	2.37	0.58
48:5:2512:C:H5'	48:5:2512:C:C6	2.30	0.58
3:C:16:THR:HG23	3:C:18:ASN:H	1.68	0.58
4:D:226:TYR:CE2	4:D:236:LEU:HD11	2.35	0.58
20:T:17:ARG:NH1	20:T:17:ARG:HG2	2.17	0.58
46:t:61:VAL:HG11	46:t:106:PRO:HD3	1.85	0.58
46:t:161:TYR:HD2	46:t:162:PRO:C	1.98	0.58
46:t:216:SER:CB	46:t:520:PRO:HD3	2.30	0.58
27:a:76:ASP:HB2	27:a:115:LYS:O	2.02	0.58
38:l:7:PHE:HB3	50:8:113:U:H5''	1.84	0.58
48:5:1879:A:H4'	48:5:1880:U:OP2	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:5:2897:A:H2'	48:5:2899:C:C5'	2.32	0.58
48:5:3228:C:H4'	48:5:3229:G:O5'	2.03	0.58
50:8:156:U:O2'	50:8:157:U:OP1	2.17	0.58
3:C:300:ARG:HH11	3:C:300:ARG:CG	2.15	0.58
12:L:3:ILE:HG12	27:a:34:MET:HE2	1.86	0.58
19:S:115:ARG:NH2	48:5:1320:C:O2	2.36	0.58
19:S:155:ARG:HD3	19:S:172:TYR:CG	2.39	0.58
20:T:12:ARG:HD3	20:T:13:TYR:CZ	2.38	0.58
46:t:90:ALA:O	46:t:387:VAL:HG21	2.03	0.58
48:5:438:A:H2'	48:5:494:G:H21	1.68	0.58
48:5:3078:U:H4'	48:5:3079:U:O5'	2.03	0.58
41:o:89:LYS:HB2	48:5:2653:C:OP1	2.04	0.58
48:5:1816:A:O2'	48:5:1817:G:OP1	2.15	0.58
48:5:1949:G:H1	48:5:2097:U:H3	1.50	0.58
2:B:187:SER:HB3	2:B:190:GLU:OE1	2.04	0.58
14:N:119:TYR:OH	14:N:131:GLU:OE1	2.16	0.58
46:t:302:SER:CA	46:t:305:PRO:HD2	2.31	0.58
48:5:547:G:H2'	48:5:548:G:O4'	2.03	0.58
4:D:258:LYS:O	4:D:258:LYS:HG2	2.02	0.58
12:L:153:ASP:OD2	12:L:157:ARG:NH1	2.36	0.58
24:X:77:GLU:CD	46:t:374:THR:HG21	2.28	0.58
24:X:103:TYR:O	24:X:105:VAL:HG23	2.03	0.58
24:X:142:ILE:HD11	46:t:417:LYS:C	2.29	0.58
34:h:10:ARG:NH1	34:h:60:GLU:OE1	2.36	0.58
48:5:171:G:N2	48:5:248:U:O2	2.35	0.58
48:5:2510:U:O2'	48:5:2511:A:H5''	2.03	0.58
2:B:256:HIS:HA	2:B:257:PRO:C	2.29	0.58
3:C:138:ARG:NH2	3:C:240:PRO:HB2	2.18	0.58
14:N:172:ARG:HH11	48:5:30:G:P	2.27	0.58
20:T:14:MET:HE1	20:T:55:LYS:HB2	1.85	0.58
22:V:87:ARG:HH22	22:V:137:VAL:HG22	1.68	0.58
48:5:1574:C:O2'	48:5:1575:A:OP1	2.22	0.58
48:5:3280:U:O2'	48:5:3281:U:H5''	2.03	0.58
1:A:52:SER:HB3	1:A:191:LEU:HD12	1.85	0.58
2:B:46:PHE:CE2	2:B:205:VAL:HG13	2.39	0.58
3:C:259:ASP:OD1	3:C:259:ASP:N	2.35	0.58
9:I:86:HIS:HB3	9:I:139:ARG:CG	2.34	0.58
15:O:10[A]:ASP:OD2	15:O:37[A]:ARG:NH2	2.31	0.58
16:P:67:ILE:HD12	16:P:82:ARG:CZ	2.34	0.58
46:t:249:ARG:NH1	46:t:250:PHE:CD2	2.72	0.58
48:5:243:G:H2'	48:5:244:G:C8	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:5:1579:C:H2'	48:5:1580:A:H5'	1.86	0.58
48:5:2434:U:C4'	48:5:2435:G:H5''	2.33	0.58
2:B:53:MET:HE3	48:5:3048:A:H5''	1.83	0.58
6:F:151:ARG:HD2	6:F:244:ASN:OD1	2.04	0.58
22:V:48:ARG:NH2	48:5:3043:C:OP2	2.36	0.58
24:X:137:ASN:HA	46:t:417:LYS:HZ2	1.67	0.58
46:t:194:VAL:HG13	46:t:198:LEU:CG	2.34	0.58
48:5:2897:A:H2'	48:5:2899:C:H5''	1.86	0.58
3:C:18:ASN:OD1	3:C:18:ASN:N	2.37	0.57
3:C:170:LYS:HG3	3:C:175:HIS:HB2	1.85	0.57
7:G:108:ARG:O	7:G:112:GLU:N	2.31	0.57
9:I:168:SER:HB2	20:T:160:ILE:O	2.03	0.57
12:L:73:ARG:NH1	48:5:110:G:OP2	2.37	0.57
21:U:19:VAL:HG12	21:U:105:LEU:HD22	1.85	0.57
46:t:76:LEU:CD1	46:t:88:GLY:N	2.66	0.57
46:t:259:VAL:O	46:t:298:PHE:CE2	2.49	0.57
48:5:1081:U:HO2'	48:5:1082:U:C5'	2.16	0.57
48:5:2207:A:H62	48:5:2236:G:H1	1.52	0.57
48:5:2211:U:H5	48:5:2234:G:C6	2.22	0.57
49:7:91:G:H2'	49:7:92:A:H8	1.69	0.57
3:C:144:LYS:CG	3:C:145:ILE:H	2.18	0.57
3:C:283:THR:HG21	3:C:288:ARG:HH22	1.69	0.57
4:D:285:ARG:NH1	49:7:62:U:O3'	2.37	0.57
8:H:120:ASP:OD2	8:H:124:ARG:NH2	2.37	0.57
14:N:176:LYS:HE2	48:5:66:A:N3	2.19	0.57
14:N:201:ARG:NH2	48:5:692:A:OP1	2.31	0.57
16:P:30:ARG:HA	16:P:119:VAL:CG1	2.34	0.57
34:h:67:ARG:HG3	34:h:80:LEU:HD22	1.87	0.57
42:p:53:GLY:HA2	42:p:67:GLY:O	2.04	0.57
48:5:2112:U:H4'	48:5:2113:A:H5'	1.86	0.57
48:5:2440:G:O2'	48:5:2441:A:OP1	2.18	0.57
3:C:361:HIS:CG	3:C:362:ASP:H	2.21	0.57
10:J:137:ARG:HG2	49:7:28:C:H5''	1.84	0.57
14:N:67:ARG:O	14:N:68:ARG:HB3	2.04	0.57
21:U:47:VAL:C	21:U:49:ASN:H	2.13	0.57
46:t:191:MET:HG2	46:t:530:LYS:HZ3	1.67	0.57
46:t:246:ARG:O	46:t:254:GLN:HB3	2.04	0.57
46:t:391:LYS:HG2	46:t:393:SER:H	1.69	0.57
48:5:2546:C:H2'	48:5:2547:A:H8	1.68	0.57
2:B:166:ILE:O	2:B:169:THR:HB	2.05	0.57
3:C:59:GLN:OE1	36:j:55:ARG:NH2	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:176:PHE:H	13:M:117:ARG:HH22	1.51	0.57
8:H:91:ARG:NH2	8:H:141:LYS:O	2.37	0.57
15:O:110[B]:PRO:O	15:O:113[B]:ASP:N	2.27	0.57
36:j:45:ARG:NH2	48:5:361:A:O3'	2.35	0.57
46:t:31:ALA:HB2	46:t:147:ILE:HG13	1.86	0.57
46:t:244:VAL:HG13	46:t:318:LEU:C	2.28	0.57
8:H:22:SER:HB2	8:H:39:LYS:NZ	2.19	0.57
11:K:118:UNK:O	11:K:120:UNK:N	2.37	0.57
33:g:8:ARG:HH21	33:g:31:ARG:HD2	1.70	0.57
43:q:25:LEU:HB3	43:q:191:TYR:HD2	1.68	0.57
43:q:97:LYS:HG3	43:q:98:ASN:N	2.20	0.57
7:G:90:THR:HG22	7:G:214:LEU:HG	1.87	0.57
20:T:56:PHE:CZ	20:T:78:LYS:HD3	2.39	0.57
29:c:99:ASP:O	29:c:101:LEU:N	2.37	0.57
46:t:193:THR:HG22	46:t:197:LEU:HD12	1.86	0.57
46:t:194:VAL:HG22	46:t:223:ILE:CG2	2.31	0.57
48:5:708:G:H5''	48:5:708:G:H8	1.70	0.57
48:5:979:U:H4'	48:5:980:A:OP1	2.04	0.57
8:H:86:TYR:CD1	8:H:151:VAL:HG13	2.40	0.57
20:T:7:TYR:OH	20:T:54:HIS:HB2	2.04	0.57
28:b:24:PRO:HD2	28:b:25:LYS:H	1.69	0.57
37:k:65:LEU:HD23	37:k:68:SER:HB2	1.87	0.57
48:5:1093:A:OP1	48:5:1093:A:H4'	2.05	0.57
48:5:1573:G:C6	48:5:1574:C:H1'	2.40	0.57
48:5:2439:A:N6	48:5:2508:U:H3	2.01	0.57
48:5:2442:G:H22	48:5:2506:U:H3	1.53	0.57
9:I:81:GLY:O	9:I:83:ASP:N	2.36	0.57
30:d:44:MET:O	30:d:46:THR:N	2.37	0.57
37:k:58:ASP:HB3	37:k:61:LYS:HG3	1.86	0.57
48:5:3343:G:N2	48:5:3362:A:H2	1.97	0.57
2:B:265:ALA:C	2:B:266:ARG:HG2	2.30	0.57
15:O:159[A]:LYS:NZ	48:5:3243:A:OP1	2.37	0.57
28:b:14:ARG:NH2	28:b:18:ARG:HH11	2.02	0.57
30:d:74:ARG:HB3	30:d:94:GLU:HG2	1.86	0.57
46:t:140:LYS:HD2	46:t:502:ARG:CG	2.35	0.57
46:t:513:SER:CB	46:t:518:ASP:OD1	2.52	0.57
48:5:3358:U:H2'	48:5:3359:A:C8	2.39	0.57
23:W:120:LYS:HA	23:W:123:ARG:HH11	1.69	0.57
48:5:1064:A:H4'	48:5:1065:A:O5'	2.04	0.57
48:5:2537:U:O2'	48:5:2538:U:O5'	2.22	0.57
3:C:288:ARG:O	3:C:291:ASN:N	2.31	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:16:SER:O	14:N:20:ARG:HG2	2.05	0.56
14:N:168:GLY:O	14:N:172:ARG:HB2	2.04	0.56
15:O:65[A]:ASN:OD1	15:O:67[A]:THR:HB	2.04	0.56
46:t:76:LEU:HD21	46:t:145:VAL:CG1	2.35	0.56
46:t:505:ASN:C	46:t:505:ASN:OD1	2.47	0.56
48:5:701:G:H2'	48:5:702:C:C6	2.40	0.56
48:5:1085:A:C5'	48:5:1085:A:C8	2.88	0.56
48:5:2101:C:O2'	48:5:2102:U:OP1	2.22	0.56
15:O:15[A]:LEU:HD21	15:O:125[A]:ARG:HG3	1.86	0.56
38:l:45:ARG:NH2	48:5:1841:A:N3	2.54	0.56
48:5:240:U:O2'	48:5:241:G:O5'	2.19	0.56
48:5:2971:A:OP2	48:5:2971:A:H3'	2.04	0.56
4:D:270:LYS:HG2	49:7:2:G:H5'	1.86	0.56
8:H:86:TYR:CE2	8:H:151:VAL:HG22	2.39	0.56
25:Y:51:ARG:HG2	25:Y:115:ARG:NH2	2.20	0.56
26:Z:36:HIS:CD2	26:Z:74:VAL:HG11	2.41	0.56
31:e:19:ARG:HD2	31:e:28:VAL:HG13	1.87	0.56
31:e:123:LYS:HA	31:e:126:LEU:HG	1.87	0.56
42:p:18:TYR:H	48:5:2131:A:H61	1.52	0.56
46:t:96:ASP:OD1	46:t:104:TRP:HB2	2.05	0.56
48:5:550:A:H2'	48:5:551:A:C8	2.40	0.56
48:5:1032:C:H5'	48:5:1033:U:OP2	2.06	0.56
48:5:1272:C:H2'	48:5:1273:A:H5'	1.88	0.56
48:5:1835:A:H5''	48:5:1836:C:OP2	2.05	0.56
2:B:218:ILE:HG13	2:B:276:THR:HG23	1.88	0.56
13:M:113:THR:HG22	13:M:115:PHE:N	2.20	0.56
14:N:49:ARG:NH1	48:5:115:A:OP1	2.38	0.56
20:T:14:MET:HE3	20:T:58:GLN:CB	2.36	0.56
46:t:163:VAL:HG22	46:t:165:GLU:H	1.70	0.56
46:t:198:LEU:CD2	46:t:258:ILE:CD1	2.84	0.56
48:5:725:G:C3'	48:5:726:G:H5''	2.36	0.56
4:D:191:ASP:OD1	4:D:193:GLU:HB2	2.04	0.56
7:G:133:LYS:HB2	7:G:199:ALA:O	2.04	0.56
14:N:172:ARG:NH1	48:5:30:G:P	2.79	0.56
17:Q:100:THR:HG22	17:Q:120:GLU:HB3	1.86	0.56
48:5:776:U:C5	48:5:2719:U:O2	2.52	0.56
48:5:1157:G:H2'	48:5:1158:A:O4'	2.06	0.56
48:5:2436:U:H2'	48:5:2437:G:H5''	1.88	0.56
2:B:7:GLU:HG2	48:5:2915:U:C5	2.41	0.56
48:5:892:U:O2'	48:5:893:C:H5'	2.04	0.56
48:5:1581:C:OP2	48:5:1581:C:H4'	2.03	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:5:2659:G:H4'	48:5:2751:G:O2'	2.05	0.56
3:C:144:LYS:NZ	3:C:144:LYS:H	2.03	0.56
4:D:146:LEU:HB3	48:5:2746:A:H2	1.71	0.56
5:E:176:PHE:H	13:M:117:ARG:NH2	2.04	0.56
13:M:132:LYS:HD3	48:5:3230:G:H4'	1.87	0.56
15:O:180[B]:SER:O	15:O:183[B]:ALA:N	2.39	0.56
48:5:252:U:H4'	48:5:253:A:H5''	1.86	0.56
48:5:1238:C:H2'	48:5:1239:C:H5''	1.87	0.56
48:5:2946:A:H5''	48:5:2947:G:H5'	1.86	0.56
4:D:152:ARG:HG3	4:D:152:ARG:NH1	2.19	0.56
8:H:70:THR:HB	48:5:3112:G:O2'	2.06	0.56
26:Z:111:LYS:HD3	48:5:1629:U:O4	2.05	0.56
28:b:4:SER:HB2	48:5:1117:G:OP1	2.06	0.56
35:i:26:ILE:HD13	48:5:155:G:H1'	1.87	0.56
38:l:9:ILE:HG22	38:l:13:MET:CE	2.36	0.56
46:t:361:VAL:HA	46:t:388:TYR:O	2.06	0.56
48:5:1688:U:H2'	48:5:1689:U:C6	2.41	0.56
50:8:126:A:O2'	50:8:128:U:OP2	2.16	0.56
7:G:151:VAL:HG13	7:G:199:ALA:HB2	1.87	0.56
19:S:155:ARG:HH11	19:S:172:TYR:H	1.54	0.56
25:Y:55:GLU:HB2	25:Y:108:LYS:HB2	1.87	0.56
30:d:13:THR:CG2	30:d:72:ARG:HH11	2.17	0.56
46:t:149:GLY:HA3	46:t:250:PHE:CD1	2.41	0.56
24:X:142:ILE:HG12	46:t:421:LEU:HD11	1.88	0.56
26:Z:135:ARG:HB3	26:Z:135:ARG:HH11	1.71	0.56
46:t:46:ILE:CG2	46:t:133:LEU:HD13	2.32	0.56
46:t:105:CYS:HB2	46:t:391:LYS:HZ3	1.71	0.56
46:t:168:PRO:O	46:t:169:ILE:CG1	2.50	0.56
48:5:726:G:H5'	48:5:726:G:C8	2.31	0.56
48:5:2676:A:H4'	48:5:2677:G:O5'	2.05	0.56
4:D:270:LYS:HG3	4:D:273:ARG:CB	2.36	0.55
5:E:18:LEU:H	5:E:18:LEU:HD12	1.71	0.55
22:V:3:GLY:HA2	22:V:40:LYS:HB3	1.87	0.55
34:h:85:THR:CG2	34:h:88:LEU:H	2.20	0.55
35:i:91:ASN:O	35:i:94:ILE:HG22	2.06	0.55
48:5:599:C:H2'	48:5:600:G:O4'	2.06	0.55
48:5:1572:U:HO2'	48:5:1573:G:H8	1.50	0.55
48:5:2440:G:HO2'	48:5:2441:A:P	2.29	0.55
48:5:2726:C:O2'	48:5:2727:A:H2'	2.04	0.55
48:5:3160:U:H2'	48:5:3161:C:C6	2.41	0.55
1:A:193:ARG:NH1	48:5:2174:G:OP2	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:316:ASN:O	3:C:319:LYS:O	2.24	0.55
10:J:166:LYS:C	10:J:168:ASP:H	2.13	0.55
30:d:46:THR:HG23	30:d:47:ASP:N	2.19	0.55
33:g:96:GLU:OE2	48:5:2555:G:N1	2.34	0.55
33:g:99:LYS:O	33:g:103:LYS:HG2	2.06	0.55
46:t:259:VAL:O	46:t:298:PHE:HE2	1.87	0.55
48:5:420:G:OP2	48:5:420:G:OP1	2.24	0.55
48:5:541:U:H2'	48:5:542:G:H8	1.70	0.55
48:5:1568:U:H4'	48:5:1569:U:OP1	2.06	0.55
1:A:45:VAL:HG22	1:A:84:THR:HA	1.88	0.55
2:B:21:ARG:HD3	2:B:269:GLN:OE1	2.06	0.55
9:I:74:LYS:O	9:I:78:THR:HG23	2.06	0.55
15:O:64[A]:PHE:HE2	15:O:68[A]:ARG:HH11	1.54	0.55
17:Q:122:ILE:HD11	17:Q:130:ARG:NH1	2.22	0.55
17:Q:153:PHE:O	17:Q:161:LYS:HG2	2.06	0.55
21:U:42:LYS:HG2	21:U:46:ALA:HA	1.88	0.55
48:5:209:A:H4'	48:5:211:A:C8	2.42	0.55
48:5:585:A:H2'	48:5:586:C:C6	2.41	0.55
48:5:1240:A:H2'	48:5:1241:U:H5'	1.87	0.55
48:5:1541:G:H2'	48:5:1542:G:O5'	2.06	0.55
48:5:1716:U:H6	48:5:1716:U:H5'	1.71	0.55
48:5:2530:G:H2'	48:5:2531:C:H5'	1.87	0.55
48:5:3285:C:H2'	48:5:3286:G:H5''	1.88	0.55
1:A:156:LYS:NZ	48:5:2158:A:OP2	2.37	0.55
3:C:361:HIS:CG	3:C:362:ASP:N	2.74	0.55
5:E:3:ALA:HB2	31:e:77:ALA:HB2	1.89	0.55
8:H:20:ILE:HG23	8:H:25:VAL:HG22	1.87	0.55
10:J:90:GLN:HG2	10:J:170:ASP:HB2	1.88	0.55
14:N:14:LYS:HE2	48:5:269:G:H5''	1.88	0.55
25:Y:60:ARG:NH1	48:5:200:C:OP1	2.39	0.55
26:Z:135:ARG:O	48:5:2555:G:N2	2.39	0.55
46:t:76:LEU:CD1	46:t:88:GLY:HA2	2.29	0.55
48:5:8:C:H2'	48:5:9:U:O4'	2.07	0.55
9:I:82:ARG:HG2	9:I:82:ARG:O	2.07	0.55
9:I:210:ILE:HA	9:I:217:PHE:CE1	2.41	0.55
14:N:8:GLU:HG3	14:N:50:ARG:NH1	2.16	0.55
15:O:18[B]:ARG:NH2	48:5:1318:A:OP1	2.39	0.55
23:W:25:ASP:N	23:W:25:ASP:OD1	2.36	0.55
27:a:122:PRO:HB3	27:a:142:GLY:O	2.06	0.55
35:i:56:ARG:HH22	35:i:76:ARG:NH1	2.05	0.55
46:t:161:TYR:CD2	46:t:162:PRO:C	2.76	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:5:59:G:H4'	48:5:60:A:H4'	1.88	0.55
48:5:173:G:H22	48:5:246:U:H1'	1.71	0.55
48:5:1579:C:C2'	48:5:1580:A:H5'	2.37	0.55
5:E:40:LEU:HD11	5:E:54:TYR:HB2	1.87	0.55
12:L:157:ARG:HH22	27:a:146:GLU:CD	2.15	0.55
13:M:16:GLU:HB3	19:S:149:LYS:HB3	1.89	0.55
41:o:77:CYS:SG	41:o:77:CYS:O	2.64	0.55
48:5:1110:U:H2'	48:5:1111:U:C6	2.42	0.55
48:5:1724:U:H1'	48:5:1725:C:C6	2.42	0.55
5:E:50:LYS:HG2	5:E:74:VAL:CG2	2.36	0.55
8:H:12:VAL:N	8:H:51:GLN:O	2.35	0.55
10:J:82:ARG:HD2	10:J:112:LEU:HB2	1.89	0.55
12:L:35:ARG:NH1	48:5:685:G:OP2	2.40	0.55
14:N:46:ASP:N	14:N:46:ASP:OD1	2.38	0.55
14:N:184:LYS:C	14:N:186:GLY:H	2.13	0.55
20:T:54:HIS:CE1	20:T:55:LYS:HD3	2.41	0.55
29:c:78:GLY:HA2	29:c:87:VAL:HG13	1.89	0.55
43:q:37:GLN:HE22	43:q:184:GLY:HA2	1.72	0.55
48:5:1811:G:H2'	48:5:1812:G:O4'	2.07	0.55
48:5:2971:A:H5''	48:5:2972:G:C5'	2.37	0.55
5:E:50:LYS:HG2	5:E:74:VAL:HG21	1.89	0.55
6:F:175:LYS:HD3	6:F:176:TYR:CZ	2.42	0.55
46:t:46:ILE:HG23	46:t:133:LEU:HD11	1.86	0.55
46:t:324:ALA:HB3	46:t:328:HIS:CE1	2.42	0.55
48:5:2403:G:H22	48:5:2404:A:H62	1.55	0.55
48:5:2440:G:H5'	48:5:2440:G:C8	2.35	0.55
10:J:155:THR:O	10:J:159:THR:HG23	2.07	0.55
15:O:172[A]:ARG:HA	15:O:175[A]:THR:HG23	1.89	0.55
16:P:108:ASP:N	16:P:152:GLU:OE2	2.31	0.55
19:S:52:LYS:NZ	49:7:100:C:OP2	2.37	0.55
48:5:1247:U:O5'	48:5:1247:U:H6	1.90	0.55
48:5:3334:U:H4'	48:5:3335:A:H5''	1.88	0.55
2:B:275:ARG:NH1	48:5:3045:G:O3'	2.40	0.55
2:B:367:LYS:HZ1	23:W:34:SER:H	1.54	0.55
10:J:28:ASP:HA	10:J:31:THR:HG23	1.89	0.55
16:P:138:LYS:NZ	48:5:2356:A:OP1	2.39	0.55
33:g:84:CYS:O	33:g:88:ARG:HB2	2.07	0.55
37:k:16:ARG:O	37:k:18:ALA:N	2.39	0.55
46:t:62:PRO:HG3	46:t:130:THR:HG22	1.88	0.55
4:D:279:LYS:HD3	4:D:282:ARG:NH2	2.22	0.54
11:K:63:UNK:HA	11:K:71:UNK:O	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:147:ARG:NH2	48:5:670:C:OP1	2.40	0.54
20:T:130:ARG:O	48:5:1098:A:O2'	2.20	0.54
33:g:80:ARG:HG3	33:g:88:ARG:HH21	1.72	0.54
46:t:245:ARG:HG2	46:t:253:GLY:HA2	1.89	0.54
46:t:314:GLY:H	46:t:510:CYS:HA	1.71	0.54
48:5:3288:G:C4	48:5:3289:G:C8	2.95	0.54
8:H:88:TYR:CZ	8:H:184:LYS:HD3	2.42	0.54
12:L:18:TRP:CD1	12:L:18:TRP:H	2.26	0.54
19:S:90:MET:HG3	48:5:1213:G:H4'	1.88	0.54
24:X:105:VAL:HG11	24:X:126:LEU:HD13	1.89	0.54
30:d:43:HIS:O	30:d:44:MET:HE2	2.07	0.54
39:m:97:ARG:HB2	39:m:120:GLN:O	2.07	0.54
46:t:353:LEU:C	46:t:354:ILE:CG1	2.74	0.54
48:5:2589:G:C2'	48:5:2590:A:H5'	2.37	0.54
10:J:137:ARG:NH2	49:7:44:C:OP2	2.40	0.54
12:L:15:ARG:CZ	48:5:96:G:H5'	2.38	0.54
12:L:75:PHE:H	12:L:97:VAL:HA	1.72	0.54
31:e:27:ARG:NH2	48:5:654:C:OP1	2.40	0.54
42:p:56:THR:HG22	42:p:63:THR:HG23	1.89	0.54
1:A:116:VAL:HG11	1:A:134:VAL:HG11	1.89	0.54
5:E:31:ARG:NH2	5:E:81:ALA:O	2.40	0.54
14:N:183:THR:O	14:N:183:THR:HG23	2.07	0.54
18:R:105:LEU:HG	18:R:138:LEU:HD12	1.89	0.54
32:f:8:TYR:CE2	32:f:99:ARG:HG2	2.43	0.54
44:r:38:UNK:O	44:r:42:UNK:N	2.40	0.54
48:5:3198:U:H4'	48:5:3199:G:OP2	2.08	0.54
48:5:3279:A:C2'	48:5:3280:U:H5'	2.36	0.54
19:S:170:THR:HG1	48:5:3185:U:HO2'	1.55	0.54
23:W:50:ALA:HA	23:W:55:PHE:CG	2.43	0.54
24:X:142:ILE:HA	46:t:421:LEU:HD11	1.88	0.54
29:c:75:ASN:HA	29:c:86:ARG:HB2	1.89	0.54
41:o:22:GLN:O	41:o:75:VAL:HG22	2.07	0.54
48:5:913:A:H2	48:5:2134:G:N3	2.04	0.54
48:5:1566:A:C2'	48:5:1567:U:H5'	2.38	0.54
3:C:326:ARG:O	6:F:41:ARG:NH2	2.40	0.54
5:E:78:ARG:HG3	5:E:78:ARG:NH1	2.19	0.54
12:L:101:ARG:HB2	48:5:76:G:N7	2.22	0.54
14:N:71:ARG:NH2	48:5:32:U:O3'	2.41	0.54
21:U:74:LYS:HE3	48:5:1677:G:N7	2.22	0.54
46:t:37:THR:CG2	46:t:41:TYR:CE2	2.90	0.54
9:I:52:LEU:HD22	9:I:163:GLN:HB2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:92:ARG:O	10:J:95:ASN:HB2	2.07	0.54
13:M:49:PRO:HG3	13:M:78:THR:HG23	1.90	0.54
46:t:246:ARG:HG3	46:t:248:ARG:HH12	1.71	0.54
48:5:252:U:H4'	48:5:253:A:O5'	2.08	0.54
2:B:50:LYS:HE2	2:B:328:ILE:HG22	1.88	0.54
12:L:50:PRO:O	12:L:51:LEU:HB2	2.06	0.54
19:S:12:ARG:HB3	19:S:24:LEU:HD23	1.87	0.54
38:l:15:LYS:O	38:l:19:GLN:HG3	2.07	0.54
46:t:61:VAL:HG13	46:t:106:PRO:CD	2.33	0.54
13:M:55:ARG:HD3	19:S:70:THR:OG1	2.08	0.54
17:Q:178:ARG:HG2	27:a:51:GLY:HA3	1.90	0.54
18:R:128:LYS:HG2	18:R:128:LYS:O	2.08	0.54
20:T:12:ARG:HD3	20:T:13:TYR:CE1	2.43	0.54
28:b:58:LYS:HA	28:b:58:LYS:NZ	2.23	0.54
33:g:8:ARG:NH2	33:g:31:ARG:HD2	2.23	0.54
48:5:916:G:H5'	48:5:917:A:OP1	2.08	0.54
48:5:1085:A:H8	48:5:1085:A:H5'	1.72	0.54
48:5:1654:A:H2'	48:5:1655:G:H5''	1.89	0.54
48:5:2439:A:OP1	48:5:2439:A:H4'	2.07	0.54
2:B:283:TYR:CB	2:B:323:MET:HE2	2.38	0.54
3:C:35:VAL:HG21	3:C:244:LEU:HD21	1.89	0.54
29:c:9:SER:HG	29:c:12:GLN:HB3	1.73	0.54
32:f:91:ALA:C	32:f:93:THR:H	2.16	0.54
36:j:28:HIS:CE1	36:j:31:LYS:HG3	2.43	0.54
38:l:37:TYR:CE1	38:l:39:ALA:HA	2.42	0.54
46:t:391:LYS:HE3	46:t:393:SER:CB	2.37	0.54
48:5:495:G:H2'	48:5:496:C:O4'	2.07	0.54
6:F:155:LYS:C	6:F:156:ILE:HG12	2.32	0.53
7:G:41:GLN:HG3	7:G:42:PRO:HD2	1.90	0.53
8:H:162:GLN:HB2	8:H:179:ILE:O	2.08	0.53
9:I:38:LYS:CG	9:I:41:ALA:HB2	2.38	0.53
12:L:61:PRO:HD2	12:L:70:ARG:HH21	1.72	0.53
33:g:7:PHE:HD1	33:g:20:ILE:HD12	1.70	0.53
48:5:600:G:H8	48:5:600:G:H5''	1.72	0.53
48:5:3153:U:H4'	48:5:3154:C:H5'	1.90	0.53
2:B:37:ARG:CG	2:B:187:SER:H	2.19	0.53
4:D:202:GLY:O	4:D:206:GLN:HG3	2.08	0.53
26:Z:110:ALA:O	26:Z:114:VAL:HG23	2.08	0.53
31:e:19:ARG:HH22	48:5:1433:A:P	2.30	0.53
43:q:10:GLU:O	43:q:13:ALA:HB3	2.08	0.53
48:5:595:G:C8	48:5:609:G:C6	2.96	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:5:2425:G:H2'	48:5:2426:U:O4'	2.08	0.53
48:5:2943:G:H2'	48:5:2944:U:O4'	2.09	0.53
2:B:84:VAL:HG13	2:B:162:VAL:HB	1.91	0.53
9:I:171:TRP:O	9:I:174:THR:HG22	2.07	0.53
37:k:18:ALA:C	37:k:20:VAL:H	2.15	0.53
43:q:4:ILE:H	43:q:4:ILE:HD13	1.73	0.53
46:t:191:MET:CG	46:t:530:LYS:HZ3	2.20	0.53
46:t:505:ASN:OD1	46:t:505:ASN:O	2.25	0.53
2:B:35:ASP:OD2	2:B:37:ARG:HD2	2.09	0.53
3:C:138:ARG:HH21	3:C:240:PRO:HB2	1.72	0.53
15:O:64[A]:PHE:HE2	15:O:68[A]:ARG:NH1	2.05	0.53
34:h:59:ASN:O	34:h:63:ARG:HG2	2.07	0.53
35:i:4:LYS:HD2	35:i:13:LYS:O	2.07	0.53
46:t:513:SER:HA	46:t:518:ASP:OD1	2.08	0.53
48:5:1655:G:H8	48:5:1655:G:H5''	1.73	0.53
1:A:149:ARG:NH2	1:A:252:THR:O	2.42	0.53
4:D:152:ARG:HD3	48:5:2663:G:H5'	1.91	0.53
7:G:78:PHE:CD2	7:G:179:ILE:HD13	2.43	0.53
21:U:54:VAL:HG13	21:U:67:SER:HB2	1.90	0.53
24:X:44:PRO:O	24:X:45:LYS:HB2	2.08	0.53
27:a:65:GLN:O	27:a:66:ALA:HB3	2.07	0.53
48:5:929:A:H2'	48:5:930:U:C6	2.44	0.53
48:5:1716:U:H5'	48:5:1716:U:C6	2.44	0.53
48:5:2257:C:H2'	48:5:2258:U:O4'	2.09	0.53
48:5:3057:U:O2'	48:5:3059:G:OP1	2.27	0.53
48:5:3273:A:C2'	48:5:3274:A:H5'	2.38	0.53
2:B:53:MET:HB2	48:5:3049:A:H5''	1.90	0.53
4:D:260:PHE:CE2	49:7:121:U:H5'	2.44	0.53
5:E:78:ARG:HH11	5:E:78:ARG:CG	2.21	0.53
14:N:31:ARG:HG3	14:N:129:TYR:OH	2.09	0.53
22:V:13:ILE:HD13	22:V:53:SER:HB2	1.89	0.53
34:h:34:GLN:HB3	34:h:38:ARG:NH1	2.24	0.53
35:i:36:ARG:NH1	48:5:116:A:OP1	2.39	0.53
48:5:3330:A:H5''	48:5:3330:A:C8	2.42	0.53
2:B:332:ARG:NH1	2:B:333:LYS:HD2	2.24	0.53
3:C:91:GLY:O	3:C:94:CYS:HB2	2.09	0.53
6:F:70:LYS:NZ	48:5:519:A:OP2	2.40	0.53
25:Y:52:ARG:HA	25:Y:70:ILE:CG2	2.39	0.53
29:c:29:SER:HA	29:c:32:LYS:HD3	1.91	0.53
36:j:8:PHE:HA	36:j:11:ARG:HD3	1.91	0.53
48:5:1307:G:C2	48:5:1308:A:C2	2.96	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:5:1481:A:O2'	48:5:1858:A:C2	2.56	0.53
48:5:2541:U:H4'	48:5:2542:U:OP1	2.09	0.53
48:5:2995:A:H5''	48:5:2996:U:OP2	2.08	0.53
48:5:3354:U:H4'	48:5:3355:U:H5''	1.91	0.53
3:C:183:LYS:HE3	48:5:1386:A:N7	2.24	0.53
19:S:46:GLN:HG2	19:S:51:VAL:O	2.09	0.53
24:X:39:LYS:HG3	48:5:13:A:H4'	1.89	0.53
24:X:133:LEU:HD22	46:t:417:LYS:HD3	1.91	0.53
33:g:9:ARG:O	33:g:11:ASN:N	2.42	0.53
46:t:33:GLN:HE22	47:1:1997:U:P	2.31	0.53
46:t:83:LYS:CE	47:1:2027:C:P	2.96	0.53
46:t:163:VAL:CG1	46:t:166:THR:N	2.64	0.53
46:t:309:PHE:CZ	46:t:310:VAL:O	2.62	0.53
48:5:558:U:H4'	48:5:559:A:OP2	2.09	0.53
48:5:3242:G:H5''	48:5:3245:A:H8	1.74	0.53
2:B:159:ARG:HG2	2:B:182:GLN:HA	1.91	0.53
2:B:210:GLU:O	2:B:213:GLU:HB2	2.09	0.53
8:H:163:GLN:HB3	8:H:166:ARG:HH21	1.74	0.53
15:O:110[B]:PRO:HB2	15:O:111[B]:PRO:HD2	1.91	0.53
20:T:104:GLU:HG3	20:T:105:PHE:N	2.24	0.53
35:i:74:LYS:HG3	35:i:80:PHE:HA	1.90	0.53
46:t:311:VAL:HG12	46:t:509:LEU:HD13	1.85	0.53
48:5:172:G:H2'	48:5:173:G:H5''	1.91	0.53
48:5:1915:A:H2'	48:5:1916:U:C6	2.43	0.53
48:5:2403:G:N2	48:5:2404:A:N7	2.55	0.53
48:5:2438:A:C6	48:5:2510:U:N3	2.77	0.53
48:5:3058:U:H5'	48:5:3059:G:OP1	2.09	0.53
48:5:3165:A:H2'	48:5:3166:C:C6	2.43	0.53
15:O:68[A]:ARG:HH12	48:5:2987:A:H5''	1.74	0.53
24:X:63:ILE:HD13	24:X:63:ILE:C	2.34	0.53
33:g:8:ARG:NH2	48:5:1597:C:OP1	2.42	0.53
41:o:40:LYS:HE3	41:o:44:ASP:OD2	2.08	0.53
46:t:463:THR:O	46:t:464:SER:CB	2.56	0.53
48:5:2778:G:C2'	48:5:2779:A:H5'	2.38	0.53
48:5:2844:C:H5''	48:5:2845:A:OP2	2.09	0.53
3:C:119:ARG:HA	3:C:122:THR:HG23	1.91	0.52
6:F:96:PRO:O	6:F:99:PRO:HD2	2.09	0.52
14:N:45:PRO:O	14:N:49:ARG:HB2	2.10	0.52
31:e:27:ARG:HB3	48:5:655:C:OP1	2.09	0.52
46:t:222:LEU:O	46:t:226:ILE:HG12	2.10	0.52
48:5:2364:G:H22	48:5:2396:G:H1'	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:5:2733:A:H2'	48:5:2734:A:O4'	2.09	0.52
48:5:2778:G:H2'	48:5:2779:A:H5'	1.90	0.52
48:5:3218:A:H5''	48:5:3219:G:C5	2.44	0.52
9:I:50:VAL:HG13	9:I:167:LEU:HA	1.91	0.52
19:S:155:ARG:NH1	19:S:172:TYR:H	2.06	0.52
43:q:19:LEU:HD22	43:q:73:PHE:CZ	2.44	0.52
48:5:1192:C:H41	48:5:1302:A:P	2.31	0.52
48:5:1554:U:H4'	48:5:1555:U:OP1	2.08	0.52
48:5:2568:C:N4	48:5:2574:G:O6	2.42	0.52
49:7:49:G:H4'	49:7:50:U:O5'	2.08	0.52
49:7:64:A:H5'	49:7:65:G:H5''	1.92	0.52
2:B:116:ARG:HG2	2:B:175:LYS:HA	1.92	0.52
3:C:191:LYS:HG3	3:C:194:TYR:CZ	2.44	0.52
21:U:58:GLU:HB2	21:U:63:VAL:HA	1.90	0.52
26:Z:17:ARG:HB2	48:5:1635:G:O6	2.08	0.52
40:n:9:ARG:HG3	40:n:9:ARG:NH1	2.25	0.52
46:t:240:PRO:HD3	46:t:328:HIS:HB3	1.90	0.52
48:5:420:G:O5'	48:5:420:G:OP1	2.26	0.52
48:5:741:U:H2'	48:5:742:G:O4'	2.09	0.52
48:5:1214:U:H2'	48:5:1215:U:C6	2.43	0.52
48:5:1940:G:H21	48:5:3362:A:H8	1.55	0.52
48:5:3380:U:O2'	48:5:3381:U:H5'	2.09	0.52
3:C:271:LYS:HB2	3:C:274:TYR:HB3	1.91	0.52
27:a:4:ARG:NH2	48:5:1427:U:OP2	2.42	0.52
27:a:91:LEU:HD12	27:a:121:VAL:HG21	1.90	0.52
31:e:24:ARG:HD3	31:e:25:TYR:CZ	2.45	0.52
46:t:163:VAL:HG13	46:t:166:THR:N	2.11	0.52
48:5:374:A:N3	48:5:376:G:H5''	2.25	0.52
50:8:66:A:H2'	50:8:67:U:C6	2.45	0.52
2:B:323:MET:HE1	2:B:356:LEU:HD11	1.92	0.52
3:C:157:GLU:HG2	3:C:209:TYR:HB2	1.91	0.52
15:O:72[A]:HIS:CD2	48:5:3008:A:OP1	2.63	0.52
18:R:163:ARG:O	18:R:167:ARG:HG2	2.09	0.52
19:S:79:VAL:HG21	19:S:106:LEU:HD21	1.90	0.52
26:Z:4:PHE:O	26:Z:5:LEU:HG	2.10	0.52
37:k:64:LYS:HG3	37:k:65:LEU:N	2.24	0.52
46:t:250:PHE:O	46:t:388:TYR:HE2	1.81	0.52
48:5:152:U:H5''	48:5:153:U:OP2	2.09	0.52
48:5:996:A:H2'	48:5:997:A:O4'	2.09	0.52
48:5:1017:C:P	48:5:1017:C:H2'	2.50	0.52
7:G:105:LYS:HG3	7:G:109:LEU:HD23	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:129:PRO:HB3	48:5:121:A:C2	2.45	0.52
8:H:48:VAL:HG21	8:H:52:LEU:HD13	1.92	0.52
17:Q:66:ARG:NH2	48:5:744:A:OP1	2.42	0.52
24:X:50:ALA:N	34:h:79:ASP:OD2	2.37	0.52
27:a:73:LEU:HD23	27:a:109:TYR:CZ	2.45	0.52
38:l:21:ARG:HD3	38:l:22:PRO:O	2.09	0.52
48:5:644:G:H2'	48:5:2372:A:N7	2.24	0.52
48:5:725:G:C2'	48:5:726:G:H5''	2.39	0.52
48:5:1878:G:O2'	48:5:1879:A:OP1	2.25	0.52
48:5:2590:A:H2'	48:5:2591:A:O5'	2.09	0.52
12:L:64:LYS:HD3	12:L:65:TYR:CE2	2.45	0.52
23:W:63:ILE:O	23:W:65:GLU:N	2.36	0.52
36:j:55:ARG:HD3	48:5:353:G:N7	2.25	0.52
37:k:3:ARG:NH2	48:5:1824:U:OP1	2.42	0.52
46:t:162:PRO:HD3	46:t:167:LYS:CE	2.37	0.52
46:t:388:TYR:CB	46:t:389:PRO:CD	2.83	0.52
1:A:193:ARG:NH2	48:5:2181:C:H5''	2.25	0.52
3:C:112:LYS:HG2	48:5:790:U:H4'	1.91	0.52
12:L:76:THR:O	12:L:80:VAL:HG23	2.10	0.52
39:m:99:CYS:HB2	39:m:114:LYS:HD3	1.92	0.52
46:t:434:GLU:HG3	46:t:436:PRO:HD3	1.91	0.52
48:5:1655:G:C5'	48:5:1655:G:C8	2.91	0.52
48:5:2209:U:H4'	48:5:2210:G:OP1	2.08	0.52
1:A:143:GLU:O	1:A:145:LYS:N	2.42	0.52
1:A:187:HIS:ND1	1:A:190:ARG:NH1	2.58	0.52
2:B:147:GLU:OE1	2:B:150:ARG:NH2	2.42	0.52
8:H:137:SER:HB2	8:H:143:GLU:HB3	1.91	0.52
32:f:75:HIS:HB3	32:f:80:VAL:HG12	1.91	0.52
34:h:45:LYS:O	34:h:49:LYS:HG2	2.09	0.52
36:j:66:TYR:OH	36:j:73:ARG:NH2	2.43	0.52
48:5:419:G:O3'	48:5:420:G:OP2	2.24	0.52
48:5:428:A:H2'	48:5:429:U:C6	2.45	0.52
48:5:1251:A:H2'	48:5:1252:A:O4'	2.10	0.52
7:G:144:GLU:OE2	35:i:36:ARG:NH2	2.43	0.52
27:a:126:LYS:HB3	27:a:148:ILE:HG21	1.91	0.52
36:j:52:LYS:HA	36:j:55:ARG:HD2	1.92	0.52
46:t:138:LEU:C	46:t:138:LEU:HD23	2.35	0.52
48:5:1876:U:H5''	48:5:1876:U:H6	1.75	0.52
20:T:14:MET:CE	20:T:55:LYS:HB2	2.40	0.51
46:t:324:ALA:H	46:t:328:HIS:HE1	1.57	0.51
48:5:2896:A:H5''	48:5:2896:A:H8	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:162:GLN:HG3	8:H:163:GLN:N	2.25	0.51
12:L:37:ASN:O	12:L:41:THR:HG23	2.09	0.51
14:N:73:ARG:O	14:N:75:VAL:N	2.38	0.51
15:O:15[A]:LEU:HD11	15:O:129[A]:LEU:HD13	1.92	0.51
29:c:45:ALA:O	29:c:48:THR:HG23	2.10	0.51
29:c:99:ASP:O	29:c:102:THR:N	2.40	0.51
36:j:21:ARG:NH2	36:j:41:ALA:O	2.37	0.51
46:t:68:THR:CB	46:t:93:THR:HG21	2.41	0.51
48:5:409:A:H2	48:5:1441:G:N3	2.08	0.51
48:5:621:A:H2'	48:5:622:A:C8	2.45	0.51
6:F:151:ARG:NH1	6:F:244:ASN:O	2.43	0.51
17:Q:178:ARG:CD	27:a:50:PRO:HB2	2.37	0.51
26:Z:46:ILE:HD11	26:Z:49:TYR:CD2	2.45	0.51
35:i:58:ILE:HG22	35:i:90:MET:CG	2.38	0.51
41:o:77:CYS:SG	41:o:79:THR:CG2	2.94	0.51
43:q:95:GLU:O	43:q:99:VAL:HG23	2.10	0.51
46:t:105:CYS:SG	46:t:105:CYS:O	2.68	0.51
48:5:2523:A:H4'	48:5:2524:A:OP2	2.09	0.51
7:G:156:ASP:N	7:G:156:ASP:OD1	2.43	0.51
32:f:8:TYR:CD2	32:f:99:ARG:HG2	2.46	0.51
48:5:385:A:O2'	48:5:386:A:H5'	2.10	0.51
48:5:847:A:H2'	48:5:848:A:C8	2.45	0.51
48:5:2622:C:H5''	48:5:2623:G:OP2	2.10	0.51
5:E:68:PRO:HG2	5:E:71:VAL:CG2	2.40	0.51
16:P:67:ILE:HD11	48:5:1447:G:H3'	1.91	0.51
48:5:65:A:H2'	48:5:110:G:N7	2.25	0.51
3:C:311:HIS:NE2	3:C:314:LYS:HA	2.24	0.51
8:H:44:THR:HG22	48:5:3186:A:C2	2.45	0.51
13:M:13:ARG:NH1	13:M:65:LEU:O	2.43	0.51
14:N:47:LYS:HE3	14:N:51:LEU:HD11	1.90	0.51
31:e:4:LEU:HB3	31:e:5:PRO:CD	2.40	0.51
46:t:60:THR:HG21	46:t:130:THR:CB	2.39	0.51
48:5:1875:G:C2'	48:5:1876:U:H5''	2.40	0.51
48:5:2573:G:H2'	48:5:2574:G:O4'	2.09	0.51
8:H:1:MET:O	8:H:2:LYS:HB2	2.11	0.51
12:L:122:LYS:HA	34:h:120:ALA:HA	1.92	0.51
24:X:73:MET:HE1	24:X:141:TYR:HE2	1.75	0.51
46:t:224:ARG:CD	46:t:298:PHE:CD2	2.92	0.51
48:5:243:G:O2'	48:5:244:G:H5'	2.10	0.51
48:5:2660:G:O3'	48:5:2749:G:N2	2.44	0.51
1:A:140:ASN:OD1	1:A:142:ASP:HB3	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:55:PHE:CZ	4:D:158:ARG:HB3	2.45	0.51
7:G:215:VAL:O	7:G:219:ASP:HB2	2.10	0.51
18:R:151:ARG:O	18:R:155:LEU:HG	2.11	0.51
27:a:82:ILE:HG22	27:a:87:ARG:HG3	1.92	0.51
48:5:435:C:H2'	48:5:436:A:O4'	2.11	0.51
48:5:508:U:H2'	48:5:509:U:C6	2.46	0.51
48:5:2546:C:H2'	48:5:2547:A:C8	2.46	0.51
48:5:3273:A:O2'	48:5:3274:A:H5'	2.11	0.51
2:B:380:MET:HE3	48:5:3369:G:C6	2.46	0.51
5:E:21:THR:HB	48:5:612:U:OP1	2.11	0.51
7:G:205:ALA:C	7:G:207:ASP:H	2.19	0.51
26:Z:88:ASP:O	26:Z:121:ARG:NH2	2.44	0.51
26:Z:95:VAL:HG11	26:Z:110:ALA:HA	1.93	0.51
30:d:19:ARG:HD3	30:d:35:GLU:CG	2.40	0.51
42:p:42:CYS:SG	42:p:44:LYS:HG3	2.51	0.51
48:5:839:C:H1'	48:5:1724:U:OP1	2.11	0.51
48:5:1595:U:C2	48:5:1596:C:C5	2.99	0.51
48:5:3000:A:H2'	48:5:3001:C:C6	2.45	0.51
49:7:3:U:H2'	49:7:4:U:H6	1.75	0.51
2:B:153:LYS:HG2	2:B:154:TYR:CZ	2.46	0.51
6:F:158:LYS:HD2	6:F:159:GLN:CA	2.36	0.51
9:I:60:LEU:HD11	9:I:135:ILE:HD13	1.93	0.51
10:J:13:LYS:HE2	10:J:132:ASN:HD21	1.76	0.51
13:M:47:ASP:C	13:M:49:PRO:HD3	2.36	0.51
16:P:29:THR:HA	16:P:32:THR:HG23	1.93	0.51
16:P:71:ALA:O	16:P:74:LYS:HB2	2.10	0.51
17:Q:166:LEU:O	17:Q:167:SER:HB2	2.11	0.51
24:X:132:ALA:O	24:X:136:ALA:N	2.33	0.51
31:e:26:HIS:O	31:e:28:VAL:N	2.44	0.51
42:p:17:ARG:NH1	48:5:860:G:OP1	2.43	0.51
48:5:2555:G:H5'	48:5:2556:C:OP2	2.10	0.51
2:B:39:LYS:HB2	2:B:40:PRO:CD	2.41	0.50
3:C:286:VAL:HG11	17:Q:31:LYS:HD2	1.93	0.50
5:E:98:VAL:HA	5:E:101:PHE:CD2	2.45	0.50
15:O:36[A]:VAL:HB	15:O:108[A]:ILE:HB	1.92	0.50
17:Q:176:ARG:HD2	48:5:2762:A:O2'	2.12	0.50
24:X:82:LEU:HD11	24:X:135:ILE:HD12	1.92	0.50
32:f:88:ASN:HB2	48:5:429:U:H4'	1.92	0.50
41:o:77:CYS:O	41:o:79:THR:CG2	2.59	0.50
48:5:1258:U:O2	48:5:1260:A:H8	1.92	0.50
3:C:126:ILE:HG13	3:C:238:LEU:HD13	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:181:VAL:HG21	3:C:224:GLY:HA3	1.92	0.50
4:D:17:GLN:HB2	20:T:20:ARG:HG2	1.93	0.50
6:F:223:PHE:HA	6:F:227:GLY:HA2	1.93	0.50
12:L:3:ILE:HG21	27:a:45:MET:HE3	1.91	0.50
15:O:127[A]:LEU:HD11	19:S:168:PRO:HG3	1.94	0.50
17:Q:122:ILE:HD11	17:Q:130:ARG:CZ	2.41	0.50
17:Q:178:ARG:HG2	27:a:51:GLY:CA	2.41	0.50
21:U:92:TRP:O	21:U:108:TYR:N	2.44	0.50
26:Z:65:ARG:HH11	26:Z:65:ARG:HG3	1.76	0.50
32:f:60:ARG:HD2	48:5:3275:U:C4	2.45	0.50
46:t:153:GLU:HB2	46:t:318:LEU:HD11	1.86	0.50
46:t:246:ARG:O	46:t:254:GLN:HB2	2.11	0.50
48:5:787:G:H2'	48:5:788:C:C6	2.46	0.50
48:5:2263:C:C2'	48:5:2264:U:H5'	2.42	0.50
48:5:2439:A:C2'	48:5:2440:G:H5''	2.40	0.50
1:A:44:ILE:HD12	1:A:44:ILE:H	1.76	0.50
3:C:188:ARG:NH1	48:5:1382:G:OP2	2.44	0.50
15:O:61[A]:ALA:HB1	15:O:66[A]:LYS:HG3	1.92	0.50
17:Q:46:LYS:O	17:Q:50:LYS:HG3	2.12	0.50
17:Q:184:PHE:CG	48:5:2730:G:H4'	2.46	0.50
19:S:26:ARG:NH1	20:T:150:THR:HG21	2.26	0.50
20:T:32:LYS:HE3	20:T:98:HIS:HD2	1.75	0.50
23:W:105:ARG:HG2	23:W:109:LEU:HD11	1.93	0.50
43:q:25:LEU:HD13	43:q:88:PHE:CE1	2.47	0.50
48:5:715:A:H4'	48:5:716:A:OP1	2.10	0.50
48:5:1810:A:H2'	48:5:1811:G:C8	2.46	0.50
48:5:2836:C:C5	48:5:2852:C:N4	2.71	0.50
48:5:3241:G:H2'	48:5:3245:A:H8	1.76	0.50
48:5:3274:A:H3'	48:5:3275:U:H5''	1.94	0.50
48:5:3288:G:HO2'	48:5:3289:G:H8	1.55	0.50
1:A:152:SER:HB3	48:5:2157:G:O6	2.11	0.50
2:B:169:THR:CG2	2:B:171:LEU:H	2.18	0.50
3:C:93:MET:HB2	48:5:658:G:N2	2.26	0.50
5:E:47:PHE:O	5:E:50:LYS:HB2	2.11	0.50
6:F:157:ASN:O	6:F:159:GLN:N	2.39	0.50
7:G:29:SER:O	7:G:31:PRO:HD3	2.11	0.50
10:J:143:ARG:NH2	49:7:5:G:OP1	2.45	0.50
21:U:90:ARG:O	21:U:91:ASP:HB2	2.10	0.50
24:X:133:LEU:HD13	46:t:417:LYS:HG2	1.93	0.50
42:p:4:ARG:NH1	48:5:837:A:OP2	2.35	0.50
46:t:76:LEU:CD1	46:t:88:GLY:O	2.59	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:5:209:A:H4'	48:5:211:A:N7	2.25	0.50
48:5:1876:U:H6	48:5:1876:U:C5'	2.24	0.50
3:C:283:THR:HG21	3:C:288:ARG:NH2	2.26	0.50
15:O:116[A]:LYS:HG3	15:O:117[A]:ARG:N	2.26	0.50
18:R:167:ARG:HB3	18:R:167:ARG:HH11	1.74	0.50
19:S:38:LYS:HD2	19:S:58:ILE:HD13	1.94	0.50
37:k:8:ILE:HD12	37:k:8:ILE:H	1.76	0.50
46:t:327:GLU:O	46:t:328:HIS:CB	2.59	0.50
48:5:407:A:C2	50:8:17:A:H1'	2.47	0.50
48:5:1176:C:H2'	48:5:1177:G:N2	2.26	0.50
48:5:1295:G:H2'	48:5:1296:C:C6	2.47	0.50
48:5:1576:G:H5'	48:5:1577:G:OP2	2.12	0.50
48:5:1638:A:H5''	48:5:1639:C:OP2	2.10	0.50
1:A:220:GLY:O	1:A:221:LYS:HG3	2.11	0.50
5:E:89:THR:HG21	13:M:115:PHE:HB2	1.94	0.50
10:J:139:THR:HG22	10:J:146:GLY:O	2.12	0.50
13:M:134:ALA:O	13:M:136:ALA:N	2.44	0.50
14:N:190:THR:O	14:N:194:GLN:HG2	2.11	0.50
15:O:61[A]:ALA:HA	15:O:70[A]:PRO:HD2	1.94	0.50
26:Z:80:LEU:O	26:Z:82:PRO:HD3	2.11	0.50
27:a:27:LYS:NZ	48:5:801:A:OP1	2.29	0.50
46:t:215:SER:HB2	46:t:520:PRO:CG	2.41	0.50
48:5:249:U:OP2	48:5:249:U:H2'	2.11	0.50
48:5:308:A:H5'	48:5:2223:A:O2'	2.11	0.50
48:5:736:A:H2'	48:5:737:G:O4'	2.12	0.50
48:5:1312:C:H5''	48:5:1313:G:OP2	2.11	0.50
48:5:2927:C:H2'	48:5:2928:C:C6	2.47	0.50
2:B:315:GLY:HA2	48:5:3379:C:H4'	1.93	0.50
10:J:104:PHE:O	10:J:127:PHE:HB2	2.11	0.50
24:X:38:LEU:O	24:X:39:LYS:HB2	2.11	0.50
24:X:142:ILE:CA	46:t:421:LEU:HD11	2.41	0.50
26:Z:124:ALA:O	26:Z:126:LYS:N	2.45	0.50
48:5:200:C:H5'	48:5:221:A:C2	2.46	0.50
48:5:1200:A:H5'	48:5:1201:C:O5'	2.10	0.50
48:5:3227:A:C2'	48:5:3228:C:H5'	2.41	0.50
1:A:70:ARG:NH2	48:5:2522:G:C6	2.78	0.50
8:H:168:ARG:HD2	48:5:2894:C:OP1	2.12	0.50
15:O:27[A]:LEU:O	15:O:101[A]:ARG:NH1	2.45	0.50
15:O:59[A]:ARG:NH1	48:5:1307:G:OP2	2.45	0.50
19:S:71:LYS:NZ	48:5:563:U:OP1	2.45	0.50
20:T:17:ARG:HG2	20:T:17:ARG:HH11	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:5:920:A:OP1	48:5:922:U:C5	2.63	0.50
1:A:225:ILE:O	1:A:238:ILE:O	2.29	0.50
3:C:237:GLN:O	3:C:246:ARG:HG3	2.12	0.50
5:E:55:LEU:HD12	5:E:64:LEU:HD13	1.94	0.50
6:F:80:GLN:HG3	20:T:136:ARG:CB	2.41	0.50
10:J:54:VAL:HG23	10:J:57:PHE:HB2	1.93	0.50
12:L:153:ASP:OD1	12:L:157:ARG:HD3	2.12	0.50
30:d:64:VAL:HG13	48:5:1456:A:N1	2.26	0.50
32:f:20:LYS:HE3	48:5:1178:G:O6	2.12	0.50
38:l:44:TRP:CH2	38:l:45:ARG:HG3	2.47	0.50
43:q:19:LEU:HD22	43:q:73:PHE:CE1	2.46	0.50
46:t:47:ASN:H	46:t:59:LEU:CD1	2.24	0.50
46:t:251:LEU:HD21	46:t:254:GLN:OE1	2.12	0.50
46:t:392:LEU:CD1	46:t:419:PHE:CE2	2.72	0.50
48:5:59:G:H2'	50:8:33:A:O2'	2.12	0.50
48:5:94:G:H2'	48:5:95:A:C8	2.47	0.50
48:5:398:A:O2'	48:5:1416:C:OP1	2.20	0.50
48:5:707:U:H2'	48:5:708:G:H5''	1.93	0.50
2:B:250:ALA:HB1	48:5:2947:G:N3	2.27	0.49
3:C:48:GLN:NE2	48:5:336:A:O2'	2.44	0.49
3:C:302:ALA:HB2	17:Q:39:ARG:NH1	2.26	0.49
7:G:161:GLU:OE1	14:N:26:ARG:NH2	2.32	0.49
33:g:45:GLY:HA3	48:5:1652:G:O2'	2.11	0.49
46:t:197:LEU:HB3	46:t:223:ILE:CD1	2.40	0.49
48:5:662:U:H2'	48:5:663:C:C6	2.47	0.49
48:5:1238:C:O2'	48:5:1239:C:OP1	2.09	0.49
48:5:1717:U:H2'	48:5:1718:G:C8	2.47	0.49
48:5:2970:C:HO2'	48:5:2971:A:P	2.34	0.49
2:B:150:ARG:HG2	2:B:150:ARG:NH1	2.26	0.49
3:C:98:ARG:HD2	3:C:99:MET:O	2.13	0.49
10:J:15:GLU:HB3	10:J:130:VAL:HG22	1.93	0.49
12:L:154:VAL:HG23	12:L:157:ARG:HG2	1.94	0.49
15:O:65[A]:ASN:HB3	15:O:68[A]:ARG:HD2	1.94	0.49
16:P:109:ALA:HA	16:P:112:LEU:HD22	1.94	0.49
24:X:142:ILE:HG21	46:t:420:ARG:C	2.35	0.49
36:j:21:ARG:HD2	36:j:37:CYS:SG	2.52	0.49
46:t:353:LEU:CD1	46:t:439:ILE:CB	2.76	0.49
48:5:2249:G:C8	48:5:2249:G:H3'	2.46	0.49
50:8:145:U:H2'	50:8:146:U:C6	2.47	0.49
2:B:339:ARG:HG2	2:B:340:LYS:O	2.12	0.49
3:C:48:GLN:HG3	48:5:337:G:H4'	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:4:ARG:HH21	48:5:2828:G:HO2'	1.58	0.49
15:O:37[A]:ARG:HG3	15:O:108[A]:ILE:HG22	1.94	0.49
22:V:45:ARG:O	22:V:46:LEU:C	2.55	0.49
25:Y:32:SER:HA	25:Y:49:PRO:HA	1.93	0.49
27:a:42:ARG:HH21	48:5:2799:A:H1'	1.77	0.49
48:5:439:C:H4'	48:5:440:A:OP1	2.12	0.49
48:5:959:C:OP2	48:5:960:U:H5	1.95	0.49
48:5:1944:U:H2'	48:5:1945:A:C8	2.47	0.49
48:5:2397:A:OP1	48:5:2398:A:C5'	2.60	0.49
4:D:152:ARG:HH11	4:D:152:ARG:CG	2.25	0.49
7:G:37:GLY:HA3	48:5:2550:U:C6	2.48	0.49
12:L:101:ARG:HA	48:5:76:G:O6	2.13	0.49
22:V:57:MET:HE3	22:V:126:TRP:CH2	2.47	0.49
27:a:46:ASP:O	27:a:47:LYS:HB3	2.12	0.49
41:o:77:CYS:O	41:o:79:THR:HG23	2.13	0.49
48:5:1018:G:H2'	48:5:1019:G:O4'	2.13	0.49
48:5:1131:G:C4	48:5:2373:A:C2	3.00	0.49
48:5:1243:G:OP2	48:5:1243:G:H8	1.95	0.49
2:B:18:PRO:HG2	2:B:20:LYS:HD2	1.95	0.49
7:G:150:LEU:HD22	7:G:151:VAL:H	1.77	0.49
15:O:171[A]:LYS:O	15:O:175[A]:THR:HG22	2.12	0.49
23:W:82:ILE:HG22	23:W:82:ILE:O	2.13	0.49
24:X:142:ILE:HD12	46:t:420:ARG:HB2	1.94	0.49
30:d:55:LEU:O	30:d:59:ILE:HG13	2.12	0.49
41:o:93:LEU:H	41:o:93:LEU:HD12	1.77	0.49
46:t:181:ALA:HA	46:t:537:ILE:HG23	1.94	0.49
48:5:132:C:C4	48:5:134:U:H5	2.30	0.49
48:5:135:C:H4'	48:5:136:G:OP2	2.12	0.49
48:5:2211:U:C5	48:5:2234:G:O6	2.59	0.49
48:5:2960:C:H2'	48:5:2961:G:C8	2.48	0.49
48:5:3259:U:C6	48:5:3259:U:H5'	2.48	0.49
50:8:26:U:H2'	50:8:27:U:C6	2.47	0.49
50:8:27:U:O5'	50:8:27:U:H6	1.95	0.49
2:B:255:TRP:CD1	48:5:2395:G:H5''	2.47	0.49
2:B:361:THR:HG22	2:B:371:GLN:HB3	1.94	0.49
3:C:148:ILE:HA	3:C:149:PRO:C	2.37	0.49
5:E:40:LEU:HD13	5:E:84:VAL:HG11	1.94	0.49
10:J:10:ARG:HA	10:J:134:PRO:HD2	1.94	0.49
12:L:168:ARG:NH2	48:5:769:G:O2'	2.45	0.49
15:O:62[B]:THR:HG21	15:O:68[B]:ARG:HG3	1.95	0.49
29:c:25:LEU:HD22	29:c:90:VAL:HG22	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:c:39:SER:C	29:c:40:LYS:HD2	2.38	0.49
46:t:52:SER:OG	46:t:59:LEU:HG	2.13	0.49
46:t:68:THR:HB	46:t:93:THR:CB	2.42	0.49
46:t:188:HIS:NE2	46:t:191:MET:HE2	2.27	0.49
48:5:256:G:H2'	48:5:257:U:C6	2.47	0.49
1:A:48:ILE:HD13	42:p:65:ALA:HB2	1.95	0.49
10:J:16:LYS:NZ	48:5:2684:C:OP1	2.45	0.49
18:R:80:LYS:HE2	48:5:1940:G:OP1	2.13	0.49
22:V:80:ARG:HD3	22:V:117:PRO:O	2.13	0.49
31:e:33:ARG:HH11	48:5:944:C:H4'	1.78	0.49
34:h:118:ILE:O	34:h:119:LYS:HB2	2.12	0.49
36:j:76:ASN:O	36:j:79:GLN:HG3	2.12	0.49
43:q:40:GLU:HB2	43:q:104:ARG:HG3	1.94	0.49
48:5:36:C:H2'	48:5:37:U:H5'	1.94	0.49
48:5:217:U:H2'	48:5:218:G:OP1	2.13	0.49
48:5:1085:A:H8	48:5:1085:A:H5''	1.78	0.49
48:5:1643:A:H4'	48:5:1822:C:H5'	1.95	0.49
50:8:79:A:OP1	50:8:79:A:H4'	2.11	0.49
4:D:218:ARG:NH1	49:7:31:U:H4'	2.27	0.49
16:P:139:TYR:CE2	48:5:2355:G:H5'	2.47	0.49
28:b:39:PHE:CD1	28:b:39:PHE:C	2.90	0.49
39:m:106:ARG:HB2	39:m:106:ARG:NH1	2.23	0.49
40:n:9:ARG:HH11	40:n:9:ARG:CG	2.24	0.49
48:5:2206:G:O2'	48:5:2207:A:H5'	2.13	0.49
48:5:3346:U:H2'	48:5:3347:A:O4'	2.13	0.49
49:7:23:A:H2'	49:7:24:A:C8	2.47	0.49
7:G:204:ARG:O	7:G:207:ASP:HB2	2.12	0.49
8:H:19:SER:HB3	13:M:6:ILE:H	1.78	0.49
10:J:152:HIS:O	10:J:153:LYS:HB3	2.11	0.49
15:O:60[B]:LYS:NZ	48:5:1307:G:H5''	2.28	0.49
23:W:35:LYS:O	23:W:39:LEU:HD22	2.13	0.49
29:c:30:THR:HB	29:c:91:SER:HB2	1.95	0.49
46:t:361:VAL:CA	46:t:388:TYR:O	2.61	0.49
48:5:873:C:H4'	48:5:874:U:OP2	2.12	0.49
48:5:1036:A:H2'	48:5:1037:C:O4'	2.13	0.49
3:C:141:ARG:CZ	3:C:180:LYS:HD3	2.43	0.49
6:F:22:THR:HA	6:F:25:GLN:HG2	1.94	0.49
10:J:81:GLU:HA	10:J:84:LEU:HD12	1.95	0.49
15:O:108[A]:ILE:HD11	15:O:113[A]:ASP:HA	1.95	0.49
16:P:122:ALA:HB3	16:P:143:PRO:HB2	1.94	0.49
19:S:155:ARG:NH1	19:S:172:TYR:N	2.61	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:92:LYS:HG3	48:5:1831:U:P	2.53	0.49
48:5:1724:U:O2	48:5:1725:C:C2	2.66	0.49
48:5:2702:A:H5'	48:5:2704:A:O4'	2.13	0.49
48:5:3013:U:H2'	48:5:3014:U:C6	2.48	0.49
1:A:202:VAL:HG23	1:A:211:HIS:HB3	1.95	0.48
2:B:296:THR:HG21	2:B:357:LYS:HA	1.95	0.48
7:G:57:ARG:O	7:G:61:GLN:HG3	2.13	0.48
9:I:100:ASN:O	9:I:101:LYS:HB3	2.12	0.48
20:T:69:LYS:HE3	48:5:2750:U:OP2	2.13	0.48
20:T:92:ARG:NH1	48:5:2736:A:OP1	2.42	0.48
23:W:105:ARG:HG2	23:W:105:ARG:HH11	1.78	0.48
31:e:16:LYS:O	31:e:17:PHE:HB2	2.13	0.48
38:l:23:LEU:CD2	38:l:24:PRO:HD2	2.41	0.48
48:5:1567:U:H1'	48:5:1570:U:C5	2.45	0.48
3:C:312:VAL:HG21	48:5:610:G:C8	2.47	0.48
9:I:22:TYR:CZ	48:5:1048:A:H2'	2.48	0.48
12:L:16:LYS:O	12:L:17:HIS:HB2	2.13	0.48
22:V:13:ILE:CD1	22:V:53:SER:HB2	2.42	0.48
25:Y:39:LEU:HD21	25:Y:107:THR:O	2.13	0.48
41:o:31:GLY:HA3	48:5:2767:U:O3'	2.12	0.48
46:t:374:THR:O	46:t:378:LEU:HG	2.13	0.48
48:5:528:U:H2'	48:5:529:A:H8	1.78	0.48
48:5:690:A:H4'	48:5:691:A:OP1	2.13	0.48
48:5:1819:U:H2'	48:5:1820:U:H5'	1.93	0.48
48:5:2228:A:H5''	48:5:2228:A:H8	1.78	0.48
5:E:3:ALA:HB1	31:e:75:LEU:HD13	1.95	0.48
7:G:97:TYR:O	7:G:132:VAL:HG13	2.13	0.48
9:I:38:LYS:HG3	9:I:41:ALA:HB2	1.95	0.48
12:L:131:LYS:HD3	12:L:131:LYS:H	1.77	0.48
23:W:120:LYS:HA	23:W:123:ARG:HD2	1.93	0.48
46:t:224:ARG:HD3	46:t:298:PHE:CD2	2.48	0.48
48:5:547:G:C5	48:5:548:G:H1'	2.48	0.48
48:5:1017:C:OP1	48:5:1017:C:H2'	2.13	0.48
48:5:1097:G:H4'	48:5:1098:A:O5'	2.12	0.48
48:5:1307:G:H1'	48:5:1308:A:N7	2.28	0.48
2:B:37:ARG:HA	2:B:186:GLY:HA2	1.94	0.48
6:F:229:PHE:CD1	6:F:229:PHE:C	2.91	0.48
15:O:65[A]:ASN:C	15:O:67[A]:THR:H	2.21	0.48
22:V:2:SER:O	22:V:57:MET:N	2.42	0.48
26:Z:53:VAL:HA	26:Z:57:HIS:HD2	1.76	0.48
32:f:58:GLU:OE1	32:f:61:GLY:HA2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:m:125:LYS:HD2	48:5:2897:A:H5''	1.96	0.48
46:t:197:LEU:HD22	46:t:222:LEU:HD23	1.94	0.48
48:5:998:A:O2'	48:5:999:G:H5'	2.12	0.48
48:5:1470:U:H2'	48:5:1471:U:C6	2.49	0.48
48:5:3335:A:H5'	48:5:3335:A:H8	1.78	0.48
4:D:15:ARG:CZ	48:5:1003:A:H1'	2.43	0.48
8:H:103:ILE:HD11	8:H:134:ILE:CG2	2.44	0.48
8:H:171:ASP:HA	48:5:2899:C:C5	2.48	0.48
9:I:9:TYR:CG	9:I:97:LEU:HD13	2.48	0.48
12:L:100:ARG:O	12:L:101:ARG:HB3	2.14	0.48
20:T:129:LYS:HE3	48:5:1097:G:H5'	1.94	0.48
20:T:138:SER:C	20:T:139:ARG:HG3	2.38	0.48
24:X:73:MET:HE1	24:X:141:TYR:CE2	2.49	0.48
26:Z:54:THR:HG22	26:Z:57:HIS:CE1	2.48	0.48
34:h:85:THR:HG22	34:h:88:LEU:N	2.28	0.48
46:t:62:PRO:HD3	46:t:130:THR:CB	2.38	0.48
48:5:629:U:H2'	48:5:630:A:C8	2.48	0.48
48:5:1222:G:H8	48:5:1222:G:OP2	1.97	0.48
1:A:242:ARG:NH1	1:A:246:LEU:HD12	2.28	0.48
2:B:39:LYS:HB2	2:B:40:PRO:HD2	1.96	0.48
14:N:93:LYS:NZ	48:5:2600:C:OP1	2.47	0.48
20:T:7:TYR:CZ	20:T:54:HIS:HB2	2.49	0.48
38:l:12:LYS:HE3	50:8:45:C:OP1	2.14	0.48
48:5:996:A:C2	48:5:1054:A:C4	3.01	0.48
48:5:3245:A:H2	48:5:3246:G:N1	2.12	0.48
50:8:156:U:HO2'	50:8:157:U:P	2.33	0.48
1:A:204:MET:HG2	48:5:914:A:C2	2.49	0.48
4:D:265:TYR:O	4:D:269:SER:HB3	2.13	0.48
15:O:42[B]:ASN:OD1	15:O:125[B]:ARG:HD3	2.13	0.48
17:Q:100:THR:CG2	17:Q:120:GLU:HB3	2.43	0.48
18:R:154:ALA:O	18:R:158:GLU:HG2	2.13	0.48
18:R:167:ARG:HB3	18:R:167:ARG:NH1	2.28	0.48
20:T:17:ARG:HD2	20:T:47:SER:HB3	1.96	0.48
32:f:88:ASN:HB2	48:5:429:U:H5'	1.95	0.48
33:g:99:LYS:C	33:g:103:LYS:HG2	2.39	0.48
48:5:2263:C:H2'	48:5:2264:U:H5'	1.96	0.48
50:8:66:A:H2'	50:8:67:U:H6	1.78	0.48
4:D:140:ARG:NH1	48:5:1080:A:OP2	2.46	0.48
4:D:289:LYS:O	4:D:292:ALA:HB3	2.14	0.48
6:F:214:TRP:CZ2	6:F:219:LYS:HE3	2.49	0.48
10:J:92:ARG:HH11	10:J:92:ARG:CG	2.25	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:100:GLY:O	10:J:159:THR:HG21	2.13	0.48
14:N:10:LEU:HD23	14:N:10:LEU:HA	1.71	0.48
15:O:110[A]:PRO:HA	15:O:113[A]:ASP:OD1	2.14	0.48
24:X:64:GLU:OE2	24:X:87:SER:HA	2.14	0.48
24:X:142:ILE:HD11	46:t:417:LYS:CA	2.44	0.48
26:Z:121:ARG:HH11	26:Z:121:ARG:CG	2.27	0.48
27:a:115:LYS:HG3	48:5:715:A:H8	1.78	0.48
33:g:42:PRO:HG2	33:g:54:ILE:HG22	1.94	0.48
46:t:392:LEU:CD1	46:t:419:PHE:HE2	1.86	0.48
48:5:112:U:O2'	48:5:113:C:OP2	2.24	0.48
48:5:508:U:H2'	48:5:509:U:H6	1.79	0.48
48:5:653:A:H5'	48:5:2361:A:H5''	1.95	0.48
48:5:1081:U:O2'	48:5:1082:U:O5'	2.29	0.48
4:D:283:ALA:O	4:D:286:VAL:HB	2.14	0.48
5:E:54:TYR:HA	5:E:65:ILE:CD1	2.44	0.48
17:Q:96:PHE:CG	17:Q:97:PRO:HD2	2.49	0.48
24:X:135:ILE:C	24:X:135:ILE:HD13	2.39	0.48
31:e:33:ARG:NH1	48:5:944:C:H4'	2.29	0.48
34:h:86:ARG:O	34:h:90:ARG:HG2	2.14	0.48
46:t:193:THR:CG2	46:t:226:ILE:CG2	2.39	0.48
48:5:217:U:C2'	48:5:218:G:OP1	2.62	0.48
48:5:677:A:H4'	48:5:678:G:O5'	2.14	0.48
4:D:110:LEU:HA	4:D:113:LEU:HB2	1.96	0.48
4:D:148:ILE:HG23	4:D:151:GLN:HB3	1.96	0.48
10:J:16:LYS:HG3	10:J:130:VAL:HG13	1.96	0.48
15:O:65[B]:ASN:O	15:O:68[B]:ARG:HG2	2.14	0.48
23:W:126:GLU:OE2	23:W:129:LYS:NZ	2.47	0.48
26:Z:65:ARG:HH11	26:Z:65:ARG:CG	2.27	0.48
27:a:48:TYR:O	27:a:49:HIS:CD2	2.67	0.48
40:n:4:LYS:O	40:n:7:LYS:HB3	2.13	0.48
48:5:181:U:H2'	48:5:182:U:O4'	2.14	0.48
48:5:1573:G:C5	48:5:1574:C:H1'	2.48	0.48
50:8:130:C:H2'	50:8:131:A:C8	2.49	0.48
9:I:19:LYS:HG3	9:I:26:VAL:HG22	1.96	0.47
9:I:174:THR:O	9:I:175:ASN:HB2	2.13	0.47
13:M:54:PRO:O	13:M:56:GLN:NE2	2.36	0.47
20:T:120:LYS:C	20:T:122:GLN:H	2.22	0.47
21:U:23:THR:HA	21:U:28:PHE:HB3	1.95	0.47
28:b:21:ILE:O	28:b:22:LYS:C	2.55	0.47
34:h:47:VAL:O	34:h:51:ILE:HG13	2.14	0.47
34:h:53:CYS:O	34:h:56:THR:HB	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:k:21:LYS:HA	37:k:21:LYS:HD3	1.69	0.47
42:p:18:TYR:H	48:5:2131:A:N6	2.12	0.47
46:t:68:THR:OG1	46:t:93:THR:HG21	2.14	0.47
48:5:726:G:H8	48:5:726:G:C5'	2.21	0.47
3:C:300:ARG:HG2	3:C:300:ARG:NH1	2.24	0.47
6:F:80:GLN:HG3	20:T:136:ARG:HB3	1.95	0.47
9:I:3:ARG:CZ	9:I:63:GLU:HG3	2.44	0.47
12:L:27:ASP:CG	12:L:31:LYS:HD2	2.38	0.47
15:O:159[B]:LYS:NZ	48:5:3243:A:OP1	2.46	0.47
15:O:167[B]:TYR:CD1	15:O:167[B]:TYR:C	2.92	0.47
17:Q:62:VAL:O	17:Q:87:VAL:HA	2.14	0.47
23:W:127:LYS:O	23:W:131:ALA:N	2.45	0.47
40:n:6:ARG:O	40:n:10:THR:HG23	2.15	0.47
46:t:83:LYS:HB2	46:t:85:ASN:ND2	2.29	0.47
48:5:2641:U:H5''	48:5:2642:A:OP1	2.14	0.47
2:B:35:ASP:OD1	2:B:184:ASN:O	2.32	0.47
3:C:44:LYS:HB3	3:C:47:ARG:NH1	2.28	0.47
3:C:295:ILE:O	3:C:299:ILE:HG12	2.14	0.47
4:D:270:LYS:HG3	4:D:273:ARG:HB2	1.96	0.47
7:G:230:LYS:O	7:G:230:LYS:HG3	2.14	0.47
20:T:14:MET:HE2	20:T:15:PHE:CE1	2.50	0.47
24:X:137:ASN:HB2	46:t:417:LYS:NZ	2.20	0.47
38:l:41:ARG:NH1	48:5:1517:G:OP1	2.39	0.47
46:t:198:LEU:O	46:t:522:LEU:CD1	2.62	0.47
48:5:687:U:O2'	48:5:688:G:H5'	2.14	0.47
2:B:247:ARG:HG3	48:5:1889:G:OP1	2.14	0.47
14:N:138:GLN:HA	14:N:143:ARG:HD2	1.95	0.47
18:R:95:TRP:CZ2	18:R:99:LEU:HG	2.49	0.47
19:S:52:LYS:NZ	49:7:100:C:P	2.87	0.47
20:T:32:LYS:HE3	20:T:98:HIS:CD2	2.49	0.47
31:e:33:ARG:HH22	48:5:1408:G:P	2.37	0.47
31:e:105:ARG:HE	31:e:124:GLY:HA3	1.78	0.47
46:t:172:PRO:C	46:t:174:GLY:H	2.22	0.47
46:t:307:ASP:OD1	46:t:308:ASP:O	2.32	0.47
46:t:514:VAL:CG1	46:t:515:SER:H	2.27	0.47
48:5:725:G:H3'	48:5:726:G:H5''	1.96	0.47
48:5:731:U:H2'	48:5:732:C:H6	1.79	0.47
48:5:1204:A:C2'	48:5:1205:A:H5'	2.45	0.47
48:5:1256:G:H2'	48:5:1257:C:C6	2.49	0.47
50:8:82:U:H1'	50:8:87:G:H5'	1.95	0.47
1:A:209:HIS:CD2	1:A:211:HIS:H	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:92:TYR:HB2	2:B:157:VAL:HG22	1.95	0.47
2:B:147:GLU:CD	2:B:150:ARG:NH2	2.73	0.47
2:B:153:LYS:HG2	2:B:154:TYR:CE2	2.49	0.47
9:I:81:GLY:C	9:I:83:ASP:H	2.21	0.47
13:M:13:ARG:NH2	48:5:3206:C:N3	2.61	0.47
16:P:105:LYS:HB3	16:P:107:LEU:HD13	1.97	0.47
19:S:171:PHE:O	19:S:172:TYR:C	2.56	0.47
24:X:67:ILE:HB	24:X:83:VAL:HG12	1.97	0.47
31:e:33:ARG:NH2	48:5:1407:A:O3'	2.47	0.47
33:g:46:ASP:CG	33:g:80:ARG:HD2	2.39	0.47
36:j:64:MET:HB2	36:j:68:LYS:HB3	1.96	0.47
46:t:32:GLY:HA2	46:t:152:SER:OG	2.13	0.47
46:t:181:ALA:CB	46:t:537:ILE:HG23	2.43	0.47
46:t:244:VAL:HG13	46:t:319:ILE:CA	2.40	0.47
48:5:191:U:H2'	48:5:192:C:C6	2.49	0.47
48:5:253:A:O2'	48:5:254:A:H8	1.97	0.47
48:5:1765:U:H2'	48:5:1766:G:O4'	2.15	0.47
48:5:3177:G:O2'	48:5:3179:U:OP1	2.22	0.47
4:D:68:THR:HG22	4:D:70:THR:N	2.30	0.47
7:G:169:LEU:HD22	7:G:173:MET:HG2	1.97	0.47
12:L:87:ALA:O	12:L:91:ARG:HG3	2.14	0.47
16:P:30:ARG:HA	16:P:119:VAL:HG11	1.96	0.47
22:V:67:PRO:C	22:V:69:LEU:H	2.22	0.47
24:X:131:ASP:O	24:X:135:ILE:HG22	2.15	0.47
48:5:735:A:O2'	48:5:736:A:OP1	2.30	0.47
48:5:1481:A:C2'	48:5:1858:A:N3	2.78	0.47
48:5:1879:A:H2'	48:5:1879:A:N3	2.29	0.47
49:7:106:U:H2'	49:7:107:C:C6	2.50	0.47
1:A:242:ARG:O	48:5:2154:U:H5''	2.14	0.47
1:A:243:THR:HG1	48:5:2244:A:H5''	1.80	0.47
2:B:53:MET:HG2	2:B:77:THR:HB	1.97	0.47
3:C:329:PRO:HB2	3:C:330:TYR:H	1.39	0.47
4:D:148:ILE:HG13	4:D:159:VAL:HG11	1.96	0.47
7:G:244:ALA:HA	7:G:247:ASP:HB2	1.95	0.47
12:L:89:TYR:HB2	34:h:111:PHE:HE1	1.79	0.47
18:R:121:HIS:HE1	48:5:1719:G:N7	2.13	0.47
19:S:16:THR:HG1	19:S:19:VAL:H	1.61	0.47
19:S:42:TRP:O	19:S:46:GLN:HG3	2.15	0.47
21:U:56:VAL:HG22	21:U:65:VAL:HG22	1.96	0.47
26:Z:23:VAL:HG12	26:Z:45:GLY:HA3	1.96	0.47
27:a:10:LYS:HE2	48:5:1374:G:O6	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:a:73:LEU:HB2	27:a:109:TYR:CD1	2.49	0.47
30:d:13:THR:HG22	30:d:72:ARG:CD	2.44	0.47
31:e:61:LYS:HD3	48:5:1339:C:OP1	2.13	0.47
33:g:88:ARG:NH1	48:5:2556:C:OP1	2.48	0.47
34:h:9:LEU:HD23	34:h:12:LYS:HE3	1.97	0.47
35:i:74:LYS:HA	35:i:83:ALA:HB2	1.95	0.47
41:o:46:LYS:HD3	41:o:54:THR:HB	1.97	0.47
46:t:307:ASP:OD1	46:t:307:ASP:C	2.57	0.47
46:t:387:VAL:CG1	46:t:389:PRO:C	2.84	0.47
48:5:173:G:O2'	48:5:174:C:H6	1.96	0.47
48:5:663:C:H2'	48:5:664:U:C6	2.50	0.47
48:5:1481:A:H2'	48:5:1858:A:N3	2.30	0.47
48:5:1816:A:O2'	48:5:1817:G:H5''	2.14	0.47
48:5:2257:C:O5'	48:5:2257:C:H6	1.98	0.47
48:5:2664:C:O2'	48:5:2665:U:H5'	2.15	0.47
48:5:3241:G:H2'	48:5:3245:A:C8	2.49	0.47
48:5:3242:G:H5''	48:5:3245:A:C8	2.50	0.47
3:C:33:ASP:O	3:C:37:THR:HG23	2.14	0.47
4:D:122:VAL:HG23	4:D:123:GLU:N	2.30	0.47
10:J:106:ILE:CD1	10:J:125:MET:HG2	2.45	0.47
11:K:125:UNK:O	11:K:126:UNK:C	2.62	0.47
14:N:145:ASP:OD1	14:N:147:ARG:HB2	2.15	0.47
15:O:65[B]:ASN:HB3	15:O:68[B]:ARG:HD3	1.97	0.47
24:X:24:LEU:HB3	24:X:25:LYS:H	1.46	0.47
26:Z:4:PHE:HE1	29:c:63:SER:HB3	1.79	0.47
29:c:17:VAL:HG11	29:c:92:ILE:HD12	1.97	0.47
35:i:53:TYR:O	35:i:57:LEU:HB2	2.14	0.47
35:i:59:ASP:O	35:i:63:ASN:HB2	2.14	0.47
46:t:163:VAL:HG13	46:t:165:GLU:N	2.29	0.47
46:t:246:ARG:CB	46:t:254:GLN:HG2	2.41	0.47
48:5:1541:G:C2'	48:5:1542:G:O5'	2.63	0.47
48:5:1561:G:O2'	48:5:1562:C:OP2	2.26	0.47
48:5:1701:C:H2'	48:5:1702:U:O4'	2.15	0.47
48:5:3121:U:H1'	48:5:3122:A:H5''	1.96	0.47
48:5:3242:G:N2	48:5:3245:A:H5''	2.30	0.47
2:B:347:SER:HB3	2:B:350:ALA:N	2.26	0.47
3:C:78:GLY:O	3:C:85:SER:HB3	2.15	0.47
7:G:71:VAL:HG13	7:G:235:GLY:N	2.30	0.47
14:N:50:ARG:HH11	48:5:267:G:H4'	1.80	0.47
23:W:122:ALA:O	23:W:125:ALA:HB3	2.15	0.47
24:X:133:LEU:CD1	46:t:417:LYS:HG2	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:j:16:HIS:HA	36:j:27:PHE:O	2.15	0.47
38:l:4:GLN:HE21	48:5:1833:G:H21	1.63	0.47
46:t:105:CYS:SG	46:t:391:LYS:HD2	2.53	0.47
46:t:233:SER:HB2	46:t:543:LEU:HD23	1.97	0.47
48:5:128:G:H2'	48:5:129:U:O4'	2.14	0.47
48:5:1565:G:N2	48:5:1566:A:H1'	2.30	0.47
48:5:1621:A:H2'	48:5:1622:U:C6	2.50	0.47
48:5:1658:G:H2'	48:5:1659:U:C6	2.50	0.47
48:5:1750:A:H4'	48:5:1751:G:H5'	1.95	0.47
48:5:2111:G:H4'	48:5:2112:U:OP2	2.15	0.47
48:5:2520:A:H2'	48:5:2521:U:C6	2.50	0.47
48:5:2805:G:N3	48:5:2967:A:H2	2.13	0.47
48:5:3288:G:O2'	48:5:3289:G:H8	1.97	0.47
1:A:72:ARG:HG3	1:A:72:ARG:HH11	1.80	0.47
3:C:150:LEU:HD13	3:C:249:ILE:HG12	1.96	0.47
6:F:219:LYS:HA	6:F:228:SER:HB2	1.97	0.47
7:G:106:LYS:O	7:G:110:THR:HG23	2.15	0.47
7:G:150:LEU:HD22	7:G:151:VAL:N	2.29	0.47
29:c:99:ASP:HB2	29:c:103:THR:HG23	1.97	0.47
46:t:68:THR:CG2	46:t:143:LEU:HD22	2.45	0.47
46:t:154:VAL:CB	46:t:526:THR:HG21	2.42	0.47
48:5:322:U:H5''	48:5:323:A:OP1	2.14	0.47
48:5:380:U:H2'	48:5:381:U:C6	2.50	0.47
48:5:792:G:H2'	48:5:793:C:C6	2.50	0.47
48:5:1246:G:O2'	48:5:1264:G:OP2	2.31	0.47
48:5:1355:A:H1'	48:5:1356:U:OP2	2.14	0.47
48:5:2102:U:H2'	48:5:2103:U:C6	2.50	0.47
48:5:2440:G:O2'	48:5:2441:A:P	2.73	0.47
48:5:2537:U:HO2'	48:5:2538:U:P	2.36	0.47
48:5:2816:G:C8	48:5:2869:U:H3'	2.50	0.47
48:5:2898:G:OP2	48:5:2899:C:H5'	2.15	0.47
48:5:2946:A:C5'	48:5:2947:G:H5'	2.45	0.47
50:8:84:C:H5'	50:8:85:G:H5'	1.97	0.47
1:A:204:MET:HE3	1:A:208:ASP:CB	2.45	0.46
5:E:162:SER:HB2	48:5:3219:G:H1	1.79	0.46
7:G:134:TYR:CG	7:G:190:VAL:HG11	2.50	0.46
7:G:239:GLY:O	7:G:240:ASN:C	2.58	0.46
8:H:90:MET:HE2	8:H:179:ILE:HG22	1.97	0.46
8:H:103:ILE:HD11	8:H:134:ILE:HG21	1.97	0.46
12:L:89:TYR:CE2	12:L:93:ILE:HD11	2.50	0.46
12:L:168:ARG:O	12:L:172:LEU:HG	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:14:LYS:HA	14:N:19:LEU:HD23	1.97	0.46
16:P:84:PRO:HB2	16:P:87:SER:HB2	1.96	0.46
29:c:68:TYR:CD1	29:c:68:TYR:C	2.93	0.46
48:5:441:U:O2'	48:5:442:G:O4'	2.22	0.46
48:5:818:C:H2'	48:5:819:U:O4'	2.14	0.46
48:5:1085:A:C8	48:5:1085:A:H5''	2.49	0.46
48:5:1313:G:H2'	48:5:1314:C:H6	1.80	0.46
48:5:1352:A:H1'	48:5:1353:U:H5'	1.97	0.46
48:5:1819:U:C2'	48:5:1820:U:H5'	2.45	0.46
1:A:3:ARG:HD3	48:5:911:C:N4	2.31	0.46
1:A:66:PRO:HB2	1:A:67:TYR:CE2	2.50	0.46
3:C:11:LEU:HD13	3:C:159:ILE:HD11	1.97	0.46
5:E:51:ARG:NH1	13:M:114:ASP:OD2	2.48	0.46
5:E:58:LEU:HD12	5:E:78:ARG:HD3	1.97	0.46
7:G:74:THR:O	7:G:77:GLN:HG3	2.15	0.46
7:G:124:ASP:HA	48:5:120:G:H22	1.79	0.46
18:R:88:ARG:HD2	48:5:1864:A:H5'	1.97	0.46
19:S:155:ARG:NH2	48:5:3206:C:O2	2.48	0.46
24:X:142:ILE:HD11	46:t:417:LYS:O	2.00	0.46
31:e:4:LEU:HD13	31:e:90:LYS:HB3	1.97	0.46
46:t:31:ALA:N	46:t:147:ILE:HD12	2.31	0.46
48:5:123:A:C6	48:5:150:A:C5	3.04	0.46
48:5:620:U:OP2	48:5:620:U:H6	1.98	0.46
48:5:1464:G:N2	48:5:1466:G:H3'	2.31	0.46
48:5:2514:U:C6	48:5:2514:U:OP1	2.68	0.46
1:A:72:ARG:HG3	1:A:72:ARG:NH1	2.31	0.46
1:A:130:SER:HA	1:A:169:ILE:HG22	1.97	0.46
2:B:95:THR:HG22	48:5:3243:A:H4'	1.98	0.46
7:G:149:LYS:HD3	7:G:201:THR:O	2.16	0.46
9:I:169:LYS:O	9:I:170:LYS:HD3	2.15	0.46
10:J:65:ILE:HD13	10:J:65:ILE:HG21	1.60	0.46
10:J:142:LYS:HD3	10:J:142:LYS:HA	1.67	0.46
15:O:10[B]:ASP:HB2	15:O:117[B]:ARG:HG3	1.97	0.46
18:R:43:LYS:HE2	48:5:1765:U:H5'	1.97	0.46
21:U:12:ALA:HB2	21:U:68:THR:HG23	1.97	0.46
31:e:71:HIS:CE1	31:e:118:LYS:HD3	2.49	0.46
32:f:16:TYR:OH	32:f:91:ALA:HB2	2.15	0.46
43:q:53:MET:HB3	43:q:53:MET:HE3	1.69	0.46
46:t:28:TYR:CE2	46:t:150:TYR:HD1	2.33	0.46
46:t:191:MET:N	46:t:321:LEU:HD12	2.25	0.46
46:t:246:ARG:CD	46:t:254:GLN:HG2	2.42	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:5:1239:C:N4	48:5:1249:G:H1	2.10	0.46
48:5:1912:U:N3	48:5:2122:G:OP2	2.46	0.46
48:5:3225:C:H2'	48:5:3226:A:O4'	2.15	0.46
48:5:3340:G:H4'	48:5:3341:U:OP1	2.15	0.46
2:B:68:HIS:CD2	2:B:69:LYS:HG3	2.50	0.46
19:S:48:LEU:O	19:S:49:HIS:ND1	2.49	0.46
20:T:48:ILE:HG13	20:T:94:GLU:HG2	1.97	0.46
26:Z:67:LYS:NZ	48:5:1630:U:OP1	2.49	0.46
26:Z:128:GLN:O	26:Z:130:PHE:N	2.48	0.46
27:a:126:LYS:HA	27:a:146:GLU:O	2.15	0.46
30:d:46:THR:HG21	30:d:91:SER:HB2	1.98	0.46
46:t:188:HIS:NE2	46:t:191:MET:HE3	2.22	0.46
46:t:215:SER:HA	46:t:522:LEU:CD1	2.44	0.46
46:t:250:PHE:C	46:t:388:TYR:CE2	2.90	0.46
48:5:208:C:H2'	48:5:209:A:H5'	1.97	0.46
3:C:209:TYR:O	3:C:230:VAL:HG22	2.16	0.46
3:C:301:PRO:C	17:Q:39:ARG:HH12	2.23	0.46
13:M:121:MET:HG3	48:5:3214:U:C4	2.50	0.46
14:N:160:GLU:OE1	14:N:160:GLU:N	2.41	0.46
15:O:10[B]:ASP:OD2	15:O:37[B]:ARG:NH2	2.35	0.46
15:O:108[B]:ILE:HA	15:O:109[B]:PRO:HD2	1.84	0.46
17:Q:170:ARG:O	17:Q:170:ARG:HG3	2.11	0.46
26:Z:54:THR:HG22	26:Z:57:HIS:NE2	2.31	0.46
27:a:96:LYS:HE2	27:a:142:GLY:O	2.15	0.46
28:b:3:LYS:HD3	48:5:2617:U:H5''	1.98	0.46
29:c:68:TYR:C	29:c:68:TYR:HD1	2.22	0.46
37:k:11:PHE:O	37:k:14:LEU:HB2	2.15	0.46
38:l:3:ALA:H	38:l:5:LYS:HE2	1.81	0.46
48:5:801:A:H4'	48:5:802:C:O5'	2.15	0.46
48:5:1876:U:C5'	48:5:1876:U:C6	2.99	0.46
48:5:2304:C:C5	48:5:2305:G:C6	3.04	0.46
48:5:2681:U:O2'	48:5:2682:C:H5'	2.16	0.46
48:5:2696:A:H2'	48:5:2697:A:C8	2.50	0.46
48:5:2957:G:H5'	48:5:2957:G:C8	2.45	0.46
49:7:22:A:C6	49:7:23:A:C6	3.04	0.46
50:8:83:C:H4'	50:8:85:G:N3	2.31	0.46
6:F:158:LYS:HD2	6:F:159:GLN:N	2.30	0.46
7:G:136:LEU:HD23	7:G:136:LEU:HA	1.72	0.46
10:J:20:ASN:HB3	10:J:126:ASP:HB2	1.98	0.46
15:O:10[A]:ASP:CG	15:O:37[A]:ARG:HH21	2.21	0.46
15:O:25[A]:LYS:HE3	48:5:1176:C:OP1	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:100:THR:O	21:U:101:ASN:HB2	2.14	0.46
25:Y:4:GLN:HB2	48:5:229:G:H5''	1.98	0.46
37:k:18:ALA:C	37:k:20:VAL:N	2.74	0.46
39:m:78:ILE:HG21	39:m:78:ILE:HD13	1.72	0.46
46:t:533:GLN:HB3	46:t:536:TRP:CD2	2.50	0.46
48:5:173:G:H1'	48:5:174:C:H5'	1.98	0.46
48:5:736:A:C4	48:5:737:G:H1'	2.50	0.46
48:5:879:U:O2	48:5:2357:A:H1'	2.14	0.46
48:5:1025:A:H5'	48:5:1026:A:OP2	2.16	0.46
48:5:1232:C:C5	48:5:1261:G:H2'	2.50	0.46
48:5:1710:C:H2'	48:5:1711:C:H6	1.81	0.46
48:5:1815:U:O2'	48:5:1816:A:P	2.72	0.46
48:5:2772:C:H1'	48:5:2773:C:OP2	2.16	0.46
48:5:2947:G:N2	48:5:2948:C:C2	2.83	0.46
50:8:125:U:O2'	50:8:126:A:H5'	2.15	0.46
2:B:148:LEU:HD21	2:B:196:ARG:HD3	1.98	0.46
2:B:229:VAL:HG13	2:B:235:THR:HG21	1.98	0.46
3:C:140:HIS:CG	3:C:247:PHE:HB2	2.50	0.46
9:I:156:ARG:C	9:I:158:LYS:H	2.24	0.46
12:L:46:ILE:HA	12:L:46:ILE:HD13	1.45	0.46
19:S:40:ARG:HD2	19:S:40:ARG:HA	1.55	0.46
19:S:104:GLU:O	19:S:104:GLU:HG3	2.14	0.46
30:d:57:GLN:HG2	48:5:1475:A:H4'	1.96	0.46
36:j:13:ASN:O	48:5:817:A:C4	2.69	0.46
46:t:197:LEU:O	46:t:218:ILE:HD12	2.16	0.46
46:t:244:VAL:CG1	46:t:319:ILE:CA	2.79	0.46
48:5:174:C:H2'	48:5:175:C:C6	2.51	0.46
48:5:546:C:H4'	48:5:547:G:O5'	2.15	0.46
48:5:578:A:H5''	48:5:579:G:O5'	2.15	0.46
48:5:2282:U:O2	48:5:2310:U:H4'	2.16	0.46
48:5:3159:C:H4'	48:5:3395:G:C5	2.51	0.46
48:5:3167:A:O2'	48:5:3168:A:OP1	2.27	0.46
48:5:3174:A:H2'	48:5:3175:U:C5'	2.46	0.46
49:7:43:U:C4	49:7:44:C:C4	3.03	0.46
50:8:9:A:H2'	50:8:10:A:C8	2.50	0.46
2:B:81:THR:O	2:B:81:THR:CG2	2.64	0.46
2:B:244:ARG:HG2	2:B:244:ARG:HH11	1.81	0.46
3:C:196:ASN:ND2	48:5:337:G:OP2	2.37	0.46
4:D:126:GLU:HA	4:D:196:ARG:HD2	1.97	0.46
7:G:160:ILE:HD12	7:G:164:VAL:HG13	1.98	0.46
8:H:139:ASN:OD1	8:H:139:ASN:N	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:86:HIS:ND1	9:I:139:ARG:NH1	2.57	0.46
19:S:139:TYR:CD1	19:S:140:VAL:HG23	2.51	0.46
46:t:39:LEU:CD2	46:t:529:SER:CB	2.37	0.46
1:A:53:GLY:O	1:A:192:LYS:HE3	2.15	0.46
3:C:302:ALA:HB2	17:Q:39:ARG:CZ	2.45	0.46
4:D:187:THR:CG2	4:D:189:GLU:HB2	2.45	0.46
7:G:219:ASP:O	7:G:223:ALA:HB3	2.16	0.46
12:L:126:PHE:HB2	34:h:115:LYS:HB3	1.98	0.46
13:M:50:LYS:HD3	13:M:91:CYS:SG	2.56	0.46
17:Q:94:PHE:CZ	27:a:119:PRO:HD3	2.51	0.46
22:V:46:LEU:HG	22:V:47:ASN:OD1	2.15	0.46
31:e:24:ARG:HG2	31:e:25:TYR:CE2	2.51	0.46
41:o:66:LYS:HG2	48:5:2793:G:H5''	1.98	0.46
46:t:190:ALA:HB3	46:t:321:LEU:HD13	1.98	0.46
46:t:191:MET:N	46:t:321:LEU:HD11	2.12	0.46
46:t:545:PRO:HA	46:t:550:VAL:HG23	1.57	0.46
48:5:253:A:HO2'	48:5:254:A:H8	1.64	0.46
48:5:709:A:H2'	48:5:710:A:O4'	2.16	0.46
48:5:1096:U:H4'	48:5:1097:G:O5'	2.16	0.46
48:5:2514:U:OP1	48:5:2514:U:H6	1.99	0.46
49:7:3:U:H2'	49:7:4:U:C6	2.50	0.46
1:A:96:LEU:O	42:p:87:ARG:HD3	2.16	0.46
6:F:221:LYS:O	6:F:228:SER:O	2.34	0.46
13:M:55:ARG:NH2	13:M:77:ARG:HA	2.31	0.46
15:O:34[B]:VAL:HB	15:O:103[B]:LYS:HB2	1.96	0.46
15:O:124[B]:LEU:O	15:O:128[B]:ARG:HB2	2.15	0.46
21:U:27:VAL:HG21	21:U:107:PHE:HE2	1.80	0.46
43:q:45:LEU:HD22	43:q:49:ALA:HB3	1.97	0.46
46:t:105:CYS:HB2	46:t:391:LYS:CD	2.44	0.46
46:t:247:ILE:O	46:t:248:ARG:NH1	2.48	0.46
46:t:298:PHE:HD1	46:t:302:SER:HB3	1.81	0.46
46:t:505:ASN:HA	46:t:526:THR:HG23	1.97	0.46
48:5:92:G:H5'	48:5:93:C:H5''	1.98	0.46
48:5:642:U:O5'	48:5:642:U:H6	1.99	0.46
48:5:1118:C:O5'	48:5:1118:C:H6	1.99	0.46
48:5:1257:C:H2'	48:5:1258:U:O4'	2.16	0.46
48:5:2746:A:H2'	48:5:2747:A:O4'	2.16	0.46
1:A:137:ILE:HG12	1:A:147:ARG:HG3	1.98	0.45
2:B:188:ILE:HA	2:B:191:LYS:HD2	1.98	0.45
9:I:168:SER:HB2	20:T:160:ILE:C	2.41	0.45
14:N:184:LYS:C	14:N:186:GLY:N	2.73	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:26:PHE:HE1	16:P:120:ASN:HA	1.82	0.45
18:R:18:GLY:HA3	48:5:1874:A:H5''	1.98	0.45
25:Y:103:LYS:HD3	25:Y:103:LYS:HA	1.45	0.45
26:Z:36:HIS:H	26:Z:37:PRO:HD3	1.82	0.45
33:g:99:LYS:O	33:g:102:LYS:N	2.49	0.45
39:m:78:ILE:HD11	39:m:83:LYS:CA	2.44	0.45
42:p:58:SER:O	42:p:61:LYS:NZ	2.40	0.45
43:q:25:LEU:HD21	43:q:76:LEU:HD11	1.96	0.45
46:t:39:LEU:HD23	46:t:529:SER:HB2	0.58	0.45
46:t:190:ALA:C	46:t:321:LEU:HD11	2.40	0.45
48:5:491:C:H5''	48:5:492:U:OP2	2.15	0.45
48:5:1012:G:O2'	48:5:1013:G:H5'	2.16	0.45
48:5:1204:A:H2'	48:5:1205:A:H5'	1.98	0.45
48:5:1354:G:C6	48:5:1358:C:H5'	2.51	0.45
48:5:3238:G:C5'	48:5:3238:G:H8	2.29	0.45
4:D:115:LEU:HD12	4:D:119:TYR:HD2	1.80	0.45
4:D:273:ARG:O	4:D:273:ARG:HG2	2.15	0.45
6:F:151:ARG:NH2	48:5:1334:U:O2'	2.49	0.45
7:G:123:GLN:C	7:G:125:ALA:H	2.24	0.45
7:G:156:ASP:OD2	7:G:183:LYS:HG2	2.15	0.45
8:H:93:VAL:O	8:H:177:ASP:HA	2.16	0.45
15:O:128[B]:ARG:HD3	15:O:128[B]:ARG:HA	1.75	0.45
31:e:75:LEU:HD22	31:e:76:VAL:H	1.81	0.45
41:o:73:GLU:OE2	41:o:80:ARG:NH1	2.49	0.45
46:t:41:TYR:O	46:t:45:LEU:HG	2.16	0.45
46:t:247:ILE:HD11	46:t:318:LEU:HB2	1.98	0.45
48:5:138:U:H2'	48:5:139:G:C8	2.52	0.45
48:5:244:G:C6	48:5:245:U:C4	3.04	0.45
48:5:731:U:H2'	48:5:732:C:C6	2.52	0.45
48:5:2180:G:H2'	48:5:2181:C:C6	2.51	0.45
1:A:224:THR:HG21	48:5:2201:G:N2	2.30	0.45
3:C:145:ILE:HA	3:C:146:PRO:HD3	1.87	0.45
6:F:241:LYS:NZ	48:5:576:C:OP1	2.49	0.45
7:G:138:HIS:CE1	48:5:119:U:C2	3.04	0.45
7:G:202:GLU:O	7:G:203:VAL:HB	2.15	0.45
10:J:13:LYS:HE2	10:J:132:ASN:ND2	2.32	0.45
29:c:22:LYS:HB2	29:c:94:GLU:HB2	1.99	0.45
29:c:103:THR:O	29:c:105:ALA:N	2.49	0.45
31:e:123:LYS:O	31:e:124:GLY:O	2.34	0.45
42:p:13:LYS:HD2	42:p:14:TYR:CZ	2.51	0.45
46:t:161:TYR:CD2	46:t:161:TYR:O	2.69	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:t:197:LEU:O	46:t:218:ILE:CD1	2.65	0.45
46:t:353:LEU:HD12	46:t:439:ILE:CG2	2.45	0.45
46:t:383:ASP:OD1	46:t:383:ASP:C	2.58	0.45
48:5:1831:U:O2'	50:8:114:G:OP1	2.19	0.45
48:5:3287:U:N3	48:5:3288:G:N7	2.64	0.45
50:8:10:A:H2'	50:8:11:C:C6	2.51	0.45
3:C:152:VAL:HG22	3:C:172:VAL:HG21	1.97	0.45
5:E:98:VAL:HA	5:E:101:PHE:HD2	1.80	0.45
6:F:158:LYS:O	6:F:203:TRP:HZ3	1.99	0.45
7:G:73:PRO:HD3	7:G:233:TRP:CG	2.50	0.45
8:H:75:VAL:HG22	8:H:78:MET:CE	2.46	0.45
8:H:90:MET:O	8:H:143:GLU:O	2.34	0.45
14:N:69:GLY:O	48:5:290:G:H4'	2.16	0.45
20:T:68:THR:HG22	20:T:71:SER:N	2.27	0.45
28:b:14:ARG:CZ	28:b:18:ARG:HH11	2.30	0.45
29:c:96:GLY:C	29:c:98:SER:H	2.25	0.45
43:q:12:PHE:HD1	43:q:12:PHE:H	1.64	0.45
46:t:25:LEU:CD2	46:t:508:VAL:HG11	2.46	0.45
46:t:378:LEU:CD1	46:t:422:GLY:N	2.78	0.45
46:t:517:THR:CG2	46:t:518:ASP:C	2.88	0.45
48:5:278:U:O5'	48:5:278:U:H6	2.00	0.45
48:5:958:C:C4	48:5:960:U:H1'	2.51	0.45
48:5:1494:U:H4'	48:5:1495:U:O5'	2.17	0.45
48:5:1686:U:O2	48:5:1688:U:H1'	2.17	0.45
50:8:62:C:H4'	50:8:63:G:O5'	2.16	0.45
50:8:155:A:H2'	50:8:156:U:O4'	2.16	0.45
2:B:5:LYS:HE3	48:5:2878:G:OP1	2.16	0.45
9:I:55:ASN:O	9:I:131:ILE:HG12	2.16	0.45
10:J:171:VAL:HG13	10:J:172:LEU:N	2.31	0.45
12:L:119:TYR:HD1	12:L:145:PHE:CE2	2.35	0.45
17:Q:67:ILE:HG23	17:Q:81:VAL:HG11	1.97	0.45
20:T:160:ILE:HD12	20:T:160:ILE:HA	1.67	0.45
22:V:57:MET:HE3	22:V:57:MET:HB2	1.86	0.45
23:W:102:LYS:HG2	23:W:105:ARG:NH2	2.32	0.45
34:h:119:LYS:HD2	34:h:119:LYS:HA	1.38	0.45
36:j:64:MET:O	36:j:65:ARG:C	2.59	0.45
46:t:215:SER:HA	46:t:509:LEU:HD22	1.96	0.45
48:5:627:U:H4'	48:5:1399:A:O2'	2.16	0.45
48:5:655:C:H2'	48:5:656:A:C8	2.51	0.45
48:5:1284:C:O2'	48:5:1285:G:H5'	2.16	0.45
4:D:261:THR:H	4:D:264:GLN:CD	2.24	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:170:LYS:HG3	9:I:175:ASN:HA	1.98	0.45
22:V:120:LYS:H	22:V:137:VAL:HG23	1.81	0.45
26:Z:28:PRO:O	26:Z:29:HIS:C	2.60	0.45
46:t:181:ALA:HB1	46:t:537:ILE:HG23	1.99	0.45
48:5:499:G:H2'	48:5:500:C:C6	2.52	0.45
48:5:1565:G:C2	48:5:1566:A:H1'	2.51	0.45
48:5:3163:A:C6	48:5:3164:C:N4	2.85	0.45
48:5:3330:A:H8	48:5:3330:A:C5'	2.29	0.45
50:8:154:C:H2'	50:8:155:A:O4'	2.16	0.45
17:Q:184:PHE:CD2	48:5:2730:G:H4'	2.51	0.45
18:R:143:ILE:HG22	18:R:144:GLN:N	2.31	0.45
20:T:14:MET:HE1	20:T:55:LYS:CB	2.46	0.45
22:V:27:ASP:HA	22:V:113:ALA:O	2.17	0.45
26:Z:46:ILE:HD11	26:Z:49:TYR:CE2	2.51	0.45
48:5:90:C:C2'	48:5:91:G:H5'	2.47	0.45
48:5:208:C:O2'	48:5:209:A:H5'	2.16	0.45
48:5:312:C:O2'	48:5:313:A:H5'	2.16	0.45
48:5:1103:A:H3'	48:5:1104:G:H5'	1.99	0.45
48:5:1564:U:H2'	48:5:1565:G:H8	1.80	0.45
48:5:2174:G:H4'	48:5:2175:U:O5'	2.17	0.45
5:E:26:ARG:NH2	48:5:607:A:OP1	2.50	0.45
6:F:173:LEU:HD12	6:F:173:LEU:HA	1.81	0.45
8:H:4:ILE:HD13	8:H:4:ILE:HG21	1.66	0.45
9:I:174:THR:OG1	9:I:175:ASN:N	2.49	0.45
10:J:107:ASP:O	10:J:108:GLU:HG2	2.17	0.45
15:O:8[B]:VAL:HG12	15:O:117[B]:ARG:HB3	1.99	0.45
15:O:122[B]:GLN:NE2	48:5:1181:U:H2'	2.32	0.45
18:R:90:PRO:HG2	18:R:93:VAL:CG2	2.47	0.45
18:R:96:ILE:HG12	48:5:1722:U:O4'	2.17	0.45
27:a:128:ARG:HB2	35:i:8:ALA:CB	2.47	0.45
42:p:80:ARG:HE	42:p:80:ARG:HB2	1.46	0.45
46:t:514:VAL:HG12	46:t:515:SER:H	1.72	0.45
48:5:65:A:C4	48:5:110:G:N7	2.84	0.45
48:5:238:A:H2'	48:5:239:G:O4'	2.17	0.45
48:5:1567:U:H2'	48:5:1568:U:C4'	2.47	0.45
48:5:1614:C:H2'	48:5:1615:C:H6	1.81	0.45
48:5:1801:U:H2'	48:5:1802:C:C6	2.52	0.45
48:5:3245:A:H2	48:5:3246:G:C2	2.35	0.45
48:5:3330:A:C8	48:5:3330:A:C5'	3.00	0.45
7:G:33:ASN:HA	48:5:2549:G:N2	2.32	0.45
9:I:24:ARG:H	9:I:24:ARG:HG3	1.43	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:210:ILE:HA	9:I:217:PHE:HE1	1.79	0.45
15:O:128[A]:ARG:HD3	15:O:128[A]:ARG:HA	1.50	0.45
16:P:69:ARG:NH2	48:5:2992:U:H1'	2.31	0.45
26:Z:46:ILE:HD12	26:Z:47:GLU:N	2.32	0.45
30:d:46:THR:CG2	30:d:47:ASP:N	2.80	0.45
32:f:85:PHE:CZ	32:f:89:LEU:HD11	2.52	0.45
34:h:95:PHE:CD2	48:5:136:G:H5'	2.52	0.45
48:5:1816:A:C2'	48:5:1817:G:H5''	2.46	0.45
48:5:3163:A:O2'	48:5:3164:C:H5'	2.16	0.45
48:5:3275:U:C6	48:5:3275:U:OP1	2.69	0.45
3:C:271:LYS:O	3:C:272:VAL:C	2.60	0.45
4:D:8:LYS:HD2	49:7:15:C:O2'	2.17	0.45
10:J:132:ASN:HD22	10:J:132:ASN:H	1.65	0.45
12:L:116:LEU:HD23	12:L:116:LEU:HA	1.73	0.45
14:N:192:LYS:O	14:N:196:THR:OG1	2.35	0.45
15:O:60[A]:LYS:NZ	48:5:1307:G:H5''	2.32	0.45
17:Q:157:PRO:CB	48:5:2729:U:H4'	2.47	0.45
18:R:8:LYS:NZ	48:5:1473:G:OP2	2.50	0.45
25:Y:83:ASP:O	25:Y:84:LYS:HB2	2.17	0.45
28:b:24:PRO:CD	28:b:25:LYS:H	2.29	0.45
29:c:68:TYR:HD1	29:c:69:TYR:N	2.15	0.45
36:j:18:LEU:HG	38:l:51:ILE:HG21	1.98	0.45
43:q:42:ARG:O	43:q:46:ARG:HG2	2.17	0.45
46:t:60:THR:HB	46:t:131:GLY:C	2.20	0.45
46:t:63:GLU:O	46:t:67:LEU:HG	2.16	0.45
46:t:181:ALA:HB1	46:t:537:ILE:CG2	2.46	0.45
46:t:353:LEU:O	46:t:354:ILE:HG13	2.04	0.45
48:5:422:A:C2	48:5:2363:A:H4'	2.52	0.45
48:5:1580:A:O2'	48:5:1581:C:OP2	2.30	0.45
48:5:2567:C:H42	48:5:2568:C:H41	1.64	0.45
48:5:3085:G:H5''	48:5:3086:A:OP1	2.17	0.45
7:G:99:PRO:HG2	7:G:190:VAL:HG13	1.99	0.44
12:L:2:ALA:N	27:a:33:GLY:O	2.50	0.44
13:M:60:LEU:HD23	13:M:60:LEU:HA	1.83	0.44
15:O:18[A]:ARG:NH2	48:5:1318:A:OP1	2.42	0.44
19:S:26:ARG:HB3	20:T:150:THR:HG22	1.97	0.44
30:d:77:ARG:HG3	30:d:90:PHE:O	2.17	0.44
31:e:119:VAL:O	31:e:122:PRO:HD3	2.17	0.44
44:r:34:UNK:C	44:r:36:UNK:N	2.80	0.44
46:t:89:ILE:O	46:t:387:VAL:HB	2.16	0.44
46:t:218:ILE:HG22	46:t:219:THR:N	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:t:230:ILE:CD1	46:t:543:LEU:HD13	2.47	0.44
46:t:324:ALA:O	46:t:328:HIS:HE1	1.97	0.44
48:5:92:G:H5''	48:5:94:G:N7	2.32	0.44
48:5:181:U:O5'	48:5:181:U:H6	2.00	0.44
1:A:105:GLY:CA	1:A:160:SER:HB3	2.47	0.44
2:B:95:THR:C	2:B:97:ARG:H	2.26	0.44
2:B:102:LEU:O	48:5:3147:G:H4'	2.16	0.44
7:G:236:GLY:O	7:G:237:ILE:HB	2.17	0.44
10:J:132:ASN:HD22	10:J:132:ASN:N	2.16	0.44
15:O:68[A]:ARG:NH1	48:5:2988:C:OP1	2.50	0.44
16:P:31:GLU:CG	16:P:60:PHE:HA	2.46	0.44
16:P:52:LEU:HD13	16:P:88:VAL:HG11	1.99	0.44
17:Q:90:ASP:C	17:Q:92:ARG:H	2.26	0.44
37:k:27:ILE:HD12	37:k:39:ARG:NH2	2.32	0.44
39:m:102:ARG:NE	48:5:2896:A:OP1	2.41	0.44
41:o:12:CYS:SG	41:o:74:CYS:SG	3.15	0.44
48:5:620:U:H5''	48:5:621:A:O5'	2.17	0.44
48:5:625:G:H2'	48:5:626:U:O4'	2.18	0.44
48:5:736:A:C5	48:5:737:G:H1'	2.52	0.44
48:5:1838:G:H4'	48:5:1839:A:N3	2.32	0.44
48:5:2209:U:H1'	48:5:2210:G:H5''	1.99	0.44
48:5:2358:A:H2'	48:5:2359:C:O4'	2.18	0.44
4:D:257:GLU:O	4:D:258:LYS:HD3	2.18	0.44
6:F:25:GLN:O	6:F:28:ALA:N	2.49	0.44
6:F:150:LYS:HE2	6:F:151:ARG:NH1	2.33	0.44
10:J:17:LEU:HD21	10:J:19:LEU:HD21	1.98	0.44
13:M:40:ASP:HA	19:S:143:PHE:CE2	2.52	0.44
17:Q:8:LYS:HB2	17:Q:8:LYS:HE3	1.53	0.44
29:c:24:THR:O	29:c:25:LEU:HD23	2.18	0.44
35:i:55:ARG:O	35:i:58:ILE:HD13	2.18	0.44
36:j:65:ARG:HG3	36:j:65:ARG:NH1	2.31	0.44
46:t:190:ALA:CB	46:t:321:LEU:HD13	2.47	0.44
48:5:622:A:H2'	48:5:623:U:O4'	2.17	0.44
48:5:1560:G:HO2'	48:5:1561:G:P	2.36	0.44
48:5:1807:G:C6	48:5:1808:G:N1	2.86	0.44
48:5:2298:U:O4	48:5:2923:U:H5	2.00	0.44
48:5:2897:A:H2'	48:5:2899:C:H5'	1.97	0.44
1:A:15:ILE:HA	1:A:15:ILE:HD12	1.66	0.44
1:A:96:LEU:HD22	42:p:83:ILE:HG23	1.98	0.44
2:B:331:ASN:OD1	2:B:331:ASN:N	2.49	0.44
3:C:144:LYS:H	3:C:144:LYS:HZ2	1.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:50:ARG:NH1	48:5:267:G:H4'	2.33	0.44
14:N:56:LYS:NZ	14:N:145:ASP:OD2	2.50	0.44
23:W:119:GLU:O	23:W:122:ALA:HB3	2.17	0.44
26:Z:46:ILE:HD13	26:Z:49:TYR:N	2.32	0.44
41:o:71:ARG:NH1	41:o:71:ARG:HG3	2.33	0.44
46:t:505:ASN:CB	46:t:530:LYS:HD2	2.15	0.44
48:5:32:U:H6	48:5:32:U:O5'	2.00	0.44
48:5:182:U:H4'	48:5:182:U:OP1	2.16	0.44
48:5:247:C:N3	48:5:248:U:H1'	2.32	0.44
48:5:839:C:O2'	48:5:1724:U:OP1	2.27	0.44
48:5:1246:G:C8	48:5:1264:G:C6	3.05	0.44
48:5:1758:G:H5''	48:5:1759:C:OP2	2.18	0.44
2:B:106:TRP:CH2	2:B:161:LEU:HD13	2.52	0.44
4:D:95:TRP:HZ3	4:D:156:GLY:O	1.99	0.44
7:G:162:LEU:HD23	14:N:7:LEU:HD21	1.99	0.44
8:H:161:LEU:O	8:H:164:ILE:HG22	2.18	0.44
22:V:84:SER:HA	22:V:94:TYR:HB3	2.00	0.44
24:X:58:ASP:O	24:X:62:VAL:HG23	2.18	0.44
24:X:111:ASN:ND2	48:5:1608:C:H5''	2.33	0.44
25:Y:120:GLN:OE1	25:Y:126:LEU:HD23	2.18	0.44
29:c:99:ASP:O	29:c:100:ILE:C	2.61	0.44
30:d:19:ARG:HD3	30:d:35:GLU:HG3	1.99	0.44
42:p:44:LYS:NZ	48:5:1727:G:OP1	2.45	0.44
46:t:74:THR:O	46:t:78:GLN:HG3	2.17	0.44
46:t:307:ASP:OD1	46:t:308:ASP:N	2.50	0.44
48:5:1024:G:H5''	48:5:1025:A:OP2	2.17	0.44
48:5:1024:G:C2'	48:5:1026:A:H8	2.26	0.44
48:5:1128:U:H2'	48:5:1129:A:O4'	2.18	0.44
48:5:1151:U:H3'	48:5:1152:G:C8	2.53	0.44
48:5:1764:U:H3'	48:5:1765:U:C5'	2.47	0.44
48:5:1817:G:O2'	48:5:1818:U:P	2.76	0.44
48:5:1942:U:H2'	48:5:1943:C:O4'	2.18	0.44
48:5:3195:U:C1'	48:5:3196:U:OP1	2.65	0.44
1:A:226:SER:N	48:5:2202:C:H5''	2.33	0.44
3:C:22:LEU:HA	3:C:23:PRO:HD3	1.68	0.44
4:D:222:LEU:HA	4:D:222:LEU:HD23	1.77	0.44
8:H:92:TYR:CD1	8:H:92:TYR:N	2.84	0.44
12:L:64:LYS:HD2	27:a:66:ALA:HB1	1.99	0.44
12:L:120:GLN:C	12:L:122:LYS:H	2.26	0.44
13:M:77:ARG:NH1	48:5:562:C:OP2	2.49	0.44
26:Z:81:LEU:HD22	26:Z:81:LEU:HA	1.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:h:83:LYS:O	34:h:84:LYS:C	2.61	0.44
48:5:439:C:H4'	48:5:440:A:C5'	2.46	0.44
48:5:611:A:OP2	48:5:611:A:H4'	2.16	0.44
48:5:1481:A:O2'	48:5:1858:A:N3	2.40	0.44
48:5:1565:G:H1'	48:5:1575:A:C2	2.52	0.44
48:5:1753:G:H2'	48:5:1754:G:O5'	2.17	0.44
48:5:3060:C:H1'	48:5:3332:U:H1'	1.99	0.44
1:A:40:TYR:O	48:5:2550:U:H5	2.01	0.44
1:A:144:ASN:O	1:A:160:SER:N	2.45	0.44
2:B:218:ILE:CG1	2:B:276:THR:HG23	2.48	0.44
2:B:221:THR:CG2	2:B:273:HIS:H	2.28	0.44
3:C:131:VAL:O	3:C:135:VAL:HG23	2.18	0.44
7:G:51:LYS:HE3	48:5:1557:A:OP1	2.17	0.44
14:N:73:ARG:HB2	14:N:92:LEU:HD23	2.00	0.44
15:O:61[A]:ALA:CB	15:O:66[A]:LYS:HG3	2.48	0.44
15:O:108[A]:ILE:HA	15:O:109[A]:PRO:HD2	1.90	0.44
22:V:93:LEU:HD23	22:V:93:LEU:H	1.83	0.44
30:d:85:ALA:O	30:d:87:ASN:N	2.51	0.44
34:h:6:ALA:O	34:h:10:ARG:HG3	2.18	0.44
34:h:86:ARG:HG3	34:h:90:ARG:NH2	2.32	0.44
46:t:387:VAL:HG13	46:t:387:VAL:O	2.07	0.44
48:5:48:A:O4'	48:5:50:U:C6	2.71	0.44
48:5:237:G:C2	48:5:238:A:C8	3.06	0.44
48:5:1222:G:HO2'	48:5:1223:A:P	2.40	0.44
48:5:2224:A:H5''	48:5:2225:U:OP2	2.17	0.44
48:5:2667:A:H8	48:5:2667:A:C5'	2.28	0.44
48:5:3362:A:C2	48:5:3363:U:C2	3.06	0.44
2:B:296:THR:HG22	2:B:297:SER:N	2.33	0.44
3:C:182:LEU:HD13	3:C:182:LEU:HA	1.71	0.44
6:F:140:SER:O	6:F:144:ILE:HG13	2.18	0.44
8:H:94:TYR:CD2	8:H:98:PRO:HA	2.52	0.44
9:I:171:TRP:HE3	9:I:178:ARG:HB3	1.82	0.44
15:O:127[B]:LEU:HD11	19:S:168:PRO:HG3	2.00	0.44
20:T:80:VAL:HG11	20:T:85:LEU:HD12	1.99	0.44
25:Y:5:SER:C	25:Y:7:ASP:H	2.24	0.44
26:Z:92:PHE:O	26:Z:93:LYS:C	2.61	0.44
26:Z:129:TRP:O	26:Z:132:SER:OG	2.36	0.44
27:a:132:LYS:O	27:a:136:GLU:HG3	2.18	0.44
30:d:82:GLU:O	30:d:83:GLU:C	2.61	0.44
34:h:89:ARG:HD2	50:8:38:U:C4	2.53	0.44
42:p:50:GLY:O	42:p:51:ALA:HB3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:t:514:VAL:HG12	46:t:515:SER:CA	2.45	0.44
48:5:342:A:C2	48:5:368:G:C8	3.06	0.44
48:5:412:G:H2'	48:5:413:U:C6	2.53	0.44
48:5:1109:U:H2'	48:5:1110:U:O4'	2.17	0.44
48:5:1152:G:OP2	48:5:1152:G:H8	2.01	0.44
48:5:1456:A:H4'	48:5:1457:U:O5'	2.17	0.44
48:5:1655:G:H5''	48:5:1655:G:C8	2.51	0.44
7:G:68:ARG:H	7:G:68:ARG:HG2	1.66	0.44
12:L:16:LYS:HE3	48:5:49:A:OP1	2.18	0.44
15:O:85[B]:ARG:HD3	15:O:90[B]:HIS:ND1	2.33	0.44
18:R:28:GLU:O	18:R:32:ILE:HG13	2.18	0.44
19:S:155:ARG:HD3	19:S:172:TYR:CD2	2.52	0.44
20:T:17:ARG:HH11	20:T:17:ARG:CG	2.31	0.44
23:W:55:PHE:CD1	23:W:55:PHE:C	2.95	0.44
26:Z:36:HIS:N	26:Z:37:PRO:HD3	2.33	0.44
33:g:16:ARG:HH11	33:g:16:ARG:CG	2.29	0.44
37:k:14:LEU:HD23	37:k:17:ARG:HD3	1.99	0.44
44:r:36:UNK:O	44:r:40:UNK:N	2.51	0.44
48:5:1093:A:H2	48:5:1096:U:O2	2.01	0.44
48:5:1565:G:N1	48:5:1574:C:C2	2.83	0.44
48:5:1638:A:H2	48:5:1736:G:N3	2.16	0.44
48:5:1770:G:H5'	48:5:1771:C:OP2	2.18	0.44
48:5:2427:U:H2'	48:5:2428:U:C6	2.53	0.44
48:5:2437:G:H5'	48:5:2437:G:C8	2.44	0.44
48:5:2437:G:H2'	48:5:2438:A:O4'	2.18	0.44
2:B:325:LYS:HG2	2:B:326:GLY:N	2.32	0.43
3:C:8:VAL:O	3:C:16:THR:HB	2.18	0.43
14:N:153:ASP:OD1	14:N:155:VAL:HG22	2.17	0.43
15:O:62[B]:THR:HA	48:5:1306:G:C6	2.53	0.43
15:O:138[B]:LEU:HD12	15:O:138[B]:LEU:HA	1.75	0.43
41:o:63:LYS:NZ	48:5:2761:G:N7	2.63	0.43
46:t:154:VAL:CB	46:t:526:THR:CG2	2.96	0.43
48:5:183:G:C8	48:5:183:G:H3'	2.53	0.43
48:5:1523:U:H3'	48:5:1607:U:O2	2.18	0.43
48:5:1802:C:H2'	48:5:1803:C:C6	2.53	0.43
1:A:174:ARG:HA	42:p:69:TYR:CE2	2.53	0.43
3:C:141:ARG:NH1	3:C:180:LYS:HD3	2.33	0.43
4:D:211:LEU:HD23	4:D:211:LEU:HA	1.71	0.43
15:O:59[B]:ARG:NH1	48:5:1307:G:OP2	2.52	0.43
17:Q:176:ARG:NH2	27:a:46:ASP:OD1	2.51	0.43
21:U:29:ASP:O	21:U:32:SER:N	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:40:LEU:HB3	24:X:41:ALA:H	1.58	0.43
25:Y:59:VAL:O	25:Y:64:LYS:HD2	2.18	0.43
33:g:81:CYS:O	33:g:83:ASN:N	2.51	0.43
34:h:78:LYS:HA	34:h:81:ARG:CD	2.44	0.43
46:t:302:SER:HA	46:t:305:PRO:HD2	1.99	0.43
48:5:163:C:H42	48:5:258:G:H1	1.65	0.43
48:5:178:U:H2'	48:5:179:C:O4'	2.19	0.43
48:5:1313:G:H2'	48:5:1314:C:C6	2.53	0.43
48:5:2101:C:HO2'	48:5:2102:U:P	2.41	0.43
48:5:2192:C:H2'	48:5:2193:U:O4'	2.17	0.43
48:5:2207:A:H2'	48:5:2208:A:O4'	2.19	0.43
1:A:30:ARG:NH2	1:A:33:ASP:OD1	2.51	0.43
1:A:116:VAL:CG1	1:A:134:VAL:HG11	2.48	0.43
3:C:177:ASP:O	3:C:180:LYS:HB3	2.18	0.43
4:D:158:ARG:HD3	49:7:46:A:OP1	2.19	0.43
15:O:177[B]:LYS:HE2	15:O:177[B]:LYS:HB3	1.80	0.43
17:Q:141:ARG:HD3	48:5:743:C:O2	2.17	0.43
18:R:9:ARG:NH2	48:5:1602:A:O3'	2.51	0.43
20:T:129:LYS:HG2	48:5:1095:U:O2	2.17	0.43
21:U:36:TYR:O	21:U:40:HIS:HD2	2.01	0.43
23:W:125:ALA:C	23:W:127:LYS:H	2.26	0.43
32:f:16:TYR:CG	32:f:25:PRO:HA	2.54	0.43
33:g:58:ARG:NH1	48:5:1592:G:OP1	2.50	0.43
48:5:123:A:H5'	48:5:124:U:OP2	2.18	0.43
48:5:174:C:H2'	48:5:175:C:H6	1.84	0.43
48:5:406:G:H1'	50:8:16:G:N2	2.32	0.43
48:5:438:A:H2'	48:5:494:G:N2	2.33	0.43
48:5:702:C:O2	48:5:788:C:H4'	2.18	0.43
48:5:2140:U:O2'	48:5:2978:U:H5'	2.18	0.43
48:5:2768:U:H2'	48:5:2769:A:C8	2.52	0.43
48:5:2949:U:C5	48:5:2950:G:C6	3.05	0.43
48:5:3329:U:H2'	48:5:3330:A:H5''	2.01	0.43
1:A:243:THR:HG23	48:5:2241:U:O2'	2.18	0.43
2:B:328:ILE:HD13	2:B:328:ILE:HG21	1.65	0.43
3:C:338:LYS:O	3:C:340:GLY:N	2.50	0.43
6:F:179:LEU:HD22	6:F:183:ASP:OD2	2.18	0.43
9:I:171:TRP:O	9:I:174:THR:CG2	2.66	0.43
10:J:8:PRO:HD2	10:J:10:ARG:HG2	1.99	0.43
12:L:105:ASN:OD1	12:L:105:ASN:C	2.61	0.43
15:O:15[B]:LEU:HD21	15:O:125[B]:ARG:HG3	2.00	0.43
16:P:4:TYR:CZ	16:P:18:ARG:HG3	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:m:77:ILE:HG13	39:m:78:ILE:N	2.33	0.43
43:q:46:ARG:NH2	48:5:1257:C:O3'	2.51	0.43
46:t:34:ILE:CD1	46:t:76:LEU:HD23	2.48	0.43
46:t:39:LEU:HD23	46:t:529:SER:O	2.16	0.43
46:t:61:VAL:HG13	46:t:106:PRO:HG2	1.88	0.43
46:t:353:LEU:CG	46:t:439:ILE:HD12	2.48	0.43
46:t:507:ILE:CD1	46:t:522:LEU:CD2	2.66	0.43
48:5:15:C:H6	48:5:15:C:C5'	2.27	0.43
48:5:83:U:H2'	48:5:84:U:O4'	2.18	0.43
48:5:863:C:H2'	48:5:864:G:O4'	2.18	0.43
48:5:1498:A:H2'	48:5:1499:C:C6	2.54	0.43
48:5:1510:G:H8	48:5:1510:G:O5'	2.00	0.43
48:5:1614:C:H2'	48:5:1615:C:C6	2.53	0.43
48:5:1620:U:H2'	48:5:1621:A:C8	2.54	0.43
48:5:1655:G:H8	48:5:1655:G:H5'	1.80	0.43
48:5:1715:A:H4'	48:5:1716:U:OP1	2.18	0.43
48:5:1783:U:H2'	48:5:1784:G:C8	2.53	0.43
48:5:1815:U:H1'	48:5:1816:A:O5'	2.19	0.43
48:5:1880:U:H2'	48:5:1881:A:O4'	2.18	0.43
48:5:2511:A:C3'	48:5:2512:C:H5''	2.49	0.43
48:5:2590:A:C2'	48:5:2591:A:O5'	2.67	0.43
1:A:204:MET:HG2	48:5:914:A:N3	2.33	0.43
1:A:242:ARG:HH11	1:A:242:ARG:HG3	1.84	0.43
3:C:89:ALA:O	3:C:90:PHE:O	2.36	0.43
3:C:112:LYS:HB2	3:C:112:LYS:HE2	1.81	0.43
4:D:68:THR:CG2	4:D:70:THR:H	2.31	0.43
4:D:125:VAL:O	4:D:125:VAL:HG12	2.18	0.43
5:E:152:THR:HA	5:E:153:PRO:HD3	1.76	0.43
8:H:7:GLU:HA	8:H:68:LEU:HD11	2.00	0.43
8:H:13:PRO:HG2	8:H:16:VAL:CG1	2.49	0.43
8:H:87:LYS:NZ	8:H:191:LEU:HD21	2.34	0.43
14:N:143:ARG:NH2	34:h:92:LEU:HD23	2.33	0.43
17:Q:176:ARG:HA	17:Q:182:LYS:HB3	2.00	0.43
22:V:120:LYS:H	22:V:137:VAL:CG2	2.30	0.43
27:a:49:HIS:N	27:a:50:PRO:HD3	2.33	0.43
29:c:40:LYS:HB3	29:c:101:LEU:HD11	1.99	0.43
34:h:68:GLN:C	34:h:70:TYR:H	2.25	0.43
46:t:309:PHE:CG	46:t:310:VAL:N	2.85	0.43
48:5:911:C:O2	48:5:917:A:N1	2.51	0.43
48:5:1014:U:H2'	48:5:1015:U:H5''	2.00	0.43
48:5:1483:G:C8	48:5:1485:G:C8	3.07	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:5:1553:U:H1'	48:5:1554:U:H5	1.83	0.43
48:5:1864:A:H2'	48:5:1865:A:C8	2.53	0.43
48:5:1952:G:H1	48:5:2094:C:N4	2.09	0.43
48:5:2406:C:H2'	48:5:2407:C:C6	2.53	0.43
48:5:2585:G:H2'	48:5:2585:G:N3	2.33	0.43
2:B:81:THR:HB	2:B:321:PHE:HA	2.01	0.43
3:C:156:LEU:C	3:C:158:SER:H	2.26	0.43
4:D:59:ASP:OD2	4:D:81:HIS:CD2	2.71	0.43
4:D:99:TYR:CD1	4:D:199:ILE:HG12	2.54	0.43
7:G:190:VAL:O	7:G:190:VAL:HG12	2.18	0.43
12:L:12:ASN:ND2	48:5:797:U:O2	2.47	0.43
12:L:80:VAL:HG12	12:L:85:LEU:O	2.17	0.43
27:a:44:ASN:O	27:a:47:LYS:O	2.36	0.43
41:o:41:ARG:HD2	48:5:284:A:OP2	2.18	0.43
43:q:48:ARG:NH2	43:q:91:GLU:HG3	2.33	0.43
43:q:75:LYS:O	43:q:78:PRO:HD2	2.19	0.43
48:5:183:G:H2'	48:5:184:U:O4'	2.17	0.43
48:5:248:U:C3'	48:5:249:U:H5'	2.48	0.43
48:5:1165:A:H2'	48:5:1166:G:O4'	2.19	0.43
48:5:2518:C:C2	48:5:2590:A:C2	3.07	0.43
48:5:3027:A:H2'	48:5:3028:G:O4'	2.19	0.43
49:7:106:U:H2'	49:7:107:C:O4'	2.19	0.43
3:C:193:LYS:HB2	3:C:193:LYS:HE3	1.66	0.43
4:D:279:LYS:HD3	4:D:282:ARG:CZ	2.48	0.43
7:G:241:LYS:HB2	48:5:2586:G:C5	2.54	0.43
13:M:14:LEU:H	13:M:19:ARG:NH2	2.16	0.43
18:R:110:ARG:O	18:R:110:ARG:HG2	2.19	0.43
18:R:138:LEU:O	18:R:142:ILE:HG13	2.19	0.43
18:R:167:ARG:HG2	18:R:167:ARG:H	1.68	0.43
22:V:87:ARG:HH22	22:V:137:VAL:CG2	2.31	0.43
27:a:22:ILE:HD12	48:5:1114:U:H5''	2.01	0.43
29:c:77:LEU:O	29:c:77:LEU:HD12	2.19	0.43
31:e:67:SER:O	31:e:68:PRO:C	2.60	0.43
46:t:42:VAL:CG2	46:t:68:THR:OG1	2.67	0.43
46:t:193:THR:HG23	46:t:226:ILE:HG21	1.78	0.43
48:5:261:U:H2'	48:5:262:U:C6	2.53	0.43
48:5:378:A:N7	48:5:391:A:H2	2.16	0.43
48:5:437:G:H5''	48:5:438:A:OP2	2.19	0.43
48:5:726:G:H1'	48:5:744:A:N6	2.33	0.43
48:5:1236:G:N2	48:5:1244:A:OP1	2.46	0.43
48:5:1390:A:H5'	48:5:1390:A:N3	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:5:1867:A:H2'	48:5:1868:G:C8	2.54	0.43
48:5:2836:C:O2	48:5:2836:C:O4'	2.33	0.43
48:5:3287:U:N3	48:5:3288:G:C8	2.87	0.43
1:A:181:LYS:HB2	48:5:860:G:C5	2.53	0.43
1:A:217:GLN:O	1:A:218:HIS:HB3	2.18	0.43
2:B:67:PHE:O	2:B:70:ARG:HB2	2.18	0.43
3:C:52:VAL:HG13	3:C:53:SER:O	2.19	0.43
3:C:112:LYS:HD2	48:5:790:U:H5'	2.01	0.43
6:F:32:ALA:O	6:F:35:ALA:HB3	2.19	0.43
11:K:105:UNK:HA	11:K:142:UNK:O	2.19	0.43
12:L:133:PRO:O	12:L:135:ALA:N	2.52	0.43
15:O:138[A]:LEU:HA	15:O:138[A]:LEU:HD12	1.66	0.43
26:Z:61:LYS:O	26:Z:65:ARG:HG2	2.18	0.43
26:Z:135:ARG:HH11	26:Z:135:ARG:CB	2.31	0.43
27:a:14:HIS:C	27:a:15:VAL:O	2.55	0.43
34:h:82:ALA:O	50:8:38:U:H5	2.01	0.43
46:t:76:LEU:HD11	46:t:145:VAL:CG1	2.37	0.43
46:t:96:ASP:OD2	46:t:103:GLY:N	2.52	0.43
46:t:246:ARG:HD2	46:t:256:GLU:OE1	2.19	0.43
48:5:29:C:H4'	48:5:62:A:H4'	2.00	0.43
48:5:79:U:H2'	48:5:80:G:C8	2.54	0.43
48:5:892:U:H2'	48:5:893:C:H5'	2.00	0.43
48:5:1560:G:O2'	48:5:1561:G:P	2.77	0.43
48:5:1763:U:H3'	48:5:1764:U:C5	2.54	0.43
48:5:2656:A:C8	48:5:2658:G:C8	3.07	0.43
48:5:2882:U:H2'	48:5:2883:U:C6	2.54	0.43
1:A:65:ASP:HA	1:A:66:PRO:HD3	1.87	0.43
1:A:68:LYS:HD3	1:A:70:ARG:HH21	1.84	0.43
1:A:129:ALA:O	1:A:130:SER:C	2.62	0.43
2:B:39:LYS:HE2	2:B:39:LYS:HB3	1.69	0.43
3:C:258:LEU:HD12	3:C:258:LEU:HA	1.91	0.43
4:D:40:HIS:HD2	4:D:42:ALA:N	2.06	0.43
5:E:175:LYS:HD2	13:M:111:ALA:HA	2.00	0.43
7:G:81:THR:OG1	7:G:82:LEU:N	2.51	0.43
9:I:36:LEU:N	9:I:36:LEU:HD12	2.33	0.43
15:O:10[B]:ASP:CG	15:O:37[B]:ARG:HH21	2.23	0.43
15:O:25[B]:LYS:HG3	48:5:1175:C:H5''	2.00	0.43
21:U:17:VAL:HB	21:U:63:VAL:HG23	2.01	0.43
22:V:33:ASN:ND2	22:V:64:LYS:HB2	2.33	0.43
22:V:45:ARG:HD3	22:V:45:ARG:HA	1.81	0.43
23:W:63:ILE:HB	23:W:64:THR:H	1.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:a:21:ARG:NH1	48:5:1369:A:OP1	2.52	0.43
34:h:94:LYS:O	34:h:98:SER:HB2	2.19	0.43
35:i:98:ARG:HB3	35:i:99:ARG:H	1.49	0.43
46:t:194:VAL:HG21	46:t:321:LEU:HD21	2.00	0.43
48:5:507:U:H2'	48:5:508:U:C6	2.53	0.43
48:5:1240:A:C2'	48:5:1241:U:H5'	2.48	0.43
48:5:1753:G:C2'	48:5:1754:G:O5'	2.66	0.43
48:5:1760:A:H5'	48:5:1761:C:OP2	2.19	0.43
48:5:2373:A:N7	48:5:2867:C:H1'	2.34	0.43
48:5:2596:U:H2'	48:5:2597:U:C6	2.53	0.43
48:5:2726:C:O2	48:5:2726:C:O5'	2.36	0.43
48:5:2796:G:H5''	48:5:2798:C:O4'	2.19	0.43
48:5:2818:U:C6	48:5:2818:U:C5'	2.95	0.43
48:5:3276:G:H4'	48:5:3277:U:OP1	2.17	0.43
50:8:59:A:H3'	50:8:59:A:OP2	2.19	0.43
1:A:224:THR:HG23	48:5:2202:C:C1'	2.48	0.43
2:B:258:ALA:C	2:B:259:HIS:CG	2.97	0.43
4:D:211:LEU:HD13	4:D:219:PHE:CA	2.46	0.43
6:F:169:ILE:HD13	6:F:181:ILE:HA	2.01	0.43
9:I:81:GLY:C	9:I:83:ASP:N	2.77	0.43
10:J:96:PHE:CD2	10:J:160:VAL:HG23	2.54	0.43
12:L:67:ARG:H	12:L:67:ARG:HG3	1.40	0.43
16:P:127:ARG:HD2	48:5:1505:C:OP1	2.19	0.43
24:X:43:ALA:N	48:5:16:A:OP1	2.47	0.43
24:X:105:VAL:HG13	24:X:130:TYR:CD2	2.53	0.43
26:Z:65:ARG:HG3	26:Z:65:ARG:NH1	2.34	0.43
27:a:42:ARG:NH2	48:5:2799:A:H1'	2.34	0.43
29:c:9:SER:OG	29:c:12:GLN:HB3	2.18	0.43
33:g:10:ARG:O	48:5:1488:G:O2'	2.37	0.43
36:j:14:LYS:HE2	38:l:51:ILE:HG13	2.01	0.43
46:t:24:VAL:HG13	46:t:150:TYR:CE1	2.54	0.43
46:t:76:LEU:HD12	46:t:88:GLY:C	2.44	0.43
48:5:171:G:H1	48:5:247:C:H42	1.67	0.43
48:5:1563:C:N3	48:5:1576:G:O6	2.52	0.43
48:5:1580:A:HO2'	48:5:1581:C:P	2.40	0.43
48:5:1895:A:O2'	48:5:3053:G:H4'	2.18	0.43
48:5:2561:A:O2'	48:5:2562:A:H8	2.02	0.43
48:5:3155:U:C3'	48:5:3156:U:H5''	2.49	0.43
48:5:3227:A:N3	48:5:3227:A:O4'	2.51	0.43
50:8:47:C:H1'	50:8:61:A:H2'	2.00	0.43
2:B:139:GLN:C	2:B:141:GLY:N	2.77	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:186:GLY:O	2:B:190:GLU:HB2	2.19	0.42
4:D:223:PHE:O	4:D:224:LYS:C	2.62	0.42
6:F:148:VAL:HG12	6:F:181:ILE:HD11	2.01	0.42
12:L:121:SER:O	12:L:121:SER:OG	2.29	0.42
13:M:115:PHE:O	13:M:119:GLN:HG3	2.19	0.42
15:O:157[B]:GLU:OE2	15:O:160[B]:ARG:NH1	2.46	0.42
17:Q:125:ASP:OD1	17:Q:125:ASP:N	2.49	0.42
21:U:36:TYR:O	21:U:40:HIS:CD2	2.72	0.42
23:W:97:LYS:O	23:W:100:VAL:HG23	2.18	0.42
33:g:67:LYS:HA	33:g:70:LYS:HE3	2.01	0.42
36:j:11:ARG:HG2	48:5:817:A:O2'	2.19	0.42
37:k:17:ARG:O	37:k:18:ALA:CB	2.67	0.42
42:p:83:ILE:HG22	42:p:87:ARG:NH1	2.34	0.42
48:5:2294:U:C2	48:5:2297:U:C5	3.07	0.42
48:5:3006:A:H2'	48:5:3007:U:O4'	2.19	0.42
48:5:3164:C:O2'	48:5:3165:A:P	2.77	0.42
50:8:121:U:O2'	50:8:122:U:H5'	2.18	0.42
1:A:200:ARG:NH2	48:5:2146:C:OP1	2.49	0.42
2:B:383:LEU:HD23	2:B:383:LEU:HA	1.89	0.42
3:C:80:GLY:O	48:5:357:A:H1'	2.19	0.42
4:D:63:GLN:HB3	4:D:65:ILE:HD11	2.01	0.42
7:G:134:TYR:CD1	7:G:190:VAL:HG11	2.54	0.42
8:H:117:PHE:CE1	8:H:165:CYS:HB3	2.53	0.42
10:J:166:LYS:C	10:J:168:ASP:N	2.77	0.42
12:L:6:ASN:HB2	27:a:48:TYR:CE1	2.54	0.42
29:c:57:GLU:OE2	29:c:69:TYR:OH	2.23	0.42
31:e:32:TRP:HB3	48:5:1407:A:H5'	2.01	0.42
33:g:42:PRO:HG2	33:g:54:ILE:CG2	2.48	0.42
36:j:64:MET:O	36:j:68:LYS:HB3	2.19	0.42
41:o:73:GLU:HG3	41:o:80:ARG:HG2	2.01	0.42
48:5:275:U:H2'	48:5:276:U:C6	2.54	0.42
48:5:622:A:H8	48:5:622:A:O5'	2.03	0.42
48:5:926:A:H2'	48:5:927:C:C6	2.55	0.42
48:5:1480:G:N2	48:5:1872:C:C5	2.87	0.42
48:5:1525:G:C6	48:5:1526:U:O4	2.72	0.42
48:5:2213:A:H61	48:5:2429:G:H1'	1.84	0.42
2:B:169:THR:CG2	2:B:171:LEU:HG	2.49	0.42
3:C:205:PRO:HB3	3:C:247:PHE:CD2	2.53	0.42
4:D:113:LEU:HD12	4:D:113:LEU:HA	1.68	0.42
4:D:214:ASP:O	4:D:215:ASP:HB2	2.18	0.42
6:F:185:ILE:O	6:F:189:ILE:HG22	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:41:ALA:O	9:I:139:ARG:NH2	2.38	0.42
18:R:5:ARG:CZ	18:R:5:ARG:HB2	2.49	0.42
18:R:99:LEU:O	18:R:103:ARG:HG3	2.18	0.42
26:Z:53:VAL:HA	26:Z:57:HIS:CD2	2.53	0.42
30:d:55:LEU:O	30:d:55:LEU:HD22	2.18	0.42
36:j:63:ARG:O	36:j:68:LYS:HE2	2.19	0.42
42:p:83:ILE:O	42:p:84:ARG:C	2.62	0.42
48:5:1014:U:H3'	48:5:1015:U:H5'	2.01	0.42
48:5:1084:A:H2'	48:5:1085:A:H5''	2.00	0.42
48:5:1307:G:H1'	48:5:1308:A:C8	2.54	0.42
48:5:1668:G:H2'	48:5:1669:C:O4'	2.19	0.42
48:5:1940:G:N2	48:5:3362:A:H8	2.17	0.42
48:5:2540:A:O2'	48:5:2541:U:H2'	2.18	0.42
48:5:2770:G:H2'	48:5:2771:U:H5'	1.99	0.42
48:5:3174:A:H2'	48:5:3175:U:H5'	2.02	0.42
50:8:6:U:H2'	50:8:7:U:C6	2.54	0.42
2:B:49:TYR:O	2:B:79:VAL:HG23	2.19	0.42
3:C:23:PRO:HD2	3:C:26:PHE:CD2	2.54	0.42
4:D:269:SER:CB	49:7:1:G:H21	2.32	0.42
5:E:173:MET:HE3	5:E:173:MET:HB3	1.46	0.42
6:F:102:VAL:HG12	6:F:130:ILE:HD12	2.02	0.42
6:F:137:GLY:HA3	6:F:236:ILE:HB	2.01	0.42
8:H:129:ARG:O	8:H:132:VAL:HG13	2.20	0.42
8:H:161:LEU:HD13	8:H:179:ILE:HG21	2.02	0.42
22:V:71:LYS:HE3	22:V:71:LYS:HB3	1.58	0.42
25:Y:103:LYS:HZ3	48:5:221:A:H61	1.67	0.42
26:Z:92:PHE:HA	26:Z:95:VAL:HG23	2.01	0.42
27:a:110:GLY:O	27:a:128:ARG:O	2.37	0.42
40:n:2:ARG:HG3	40:n:3:ALA:N	2.33	0.42
46:t:240:PRO:HD2	46:t:349:LYS:CA	2.47	0.42
48:5:283:G:O6	48:5:304:G:H1'	2.20	0.42
48:5:353:G:O2'	48:5:364:G:O6	2.37	0.42
48:5:492:U:C2'	48:5:493:G:H5'	2.49	0.42
48:5:1622:U:H2'	48:5:1623:G:O4'	2.20	0.42
48:5:2289:U:H2'	48:5:2290:C:C6	2.55	0.42
48:5:3094:A:H2'	48:5:3095:U:C6	2.54	0.42
2:B:199:PHE:C	2:B:201:LYS:H	2.28	0.42
3:C:352:ALA:O	3:C:354:VAL:N	2.52	0.42
4:D:110:LEU:HD23	4:D:110:LEU:C	2.45	0.42
4:D:181:PRO:HD2	4:D:195:LEU:HD13	2.00	0.42
5:E:93:VAL:HG13	5:E:93:VAL:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:93:VAL:HG13	39:m:78:ILE:HD12	2.01	0.42
9:I:47:PRO:HB3	9:I:171:TRP:CZ2	2.55	0.42
10:J:92:ARG:HH12	10:J:94:ARG:HH11	1.67	0.42
13:M:38:ILE:HA	13:M:44:VAL:HG12	2.02	0.42
14:N:38:ARG:NH2	50:8:143:U:OP1	2.41	0.42
17:Q:161:LYS:N	17:Q:161:LYS:HD2	2.35	0.42
20:T:85:LEU:HD23	20:T:85:LEU:HA	1.67	0.42
26:Z:46:ILE:HD12	26:Z:47:GLU:C	2.45	0.42
26:Z:135:ARG:HH11	26:Z:135:ARG:CG	2.32	0.42
32:f:91:ALA:C	32:f:93:THR:N	2.76	0.42
37:k:18:ALA:O	37:k:20:VAL:N	2.53	0.42
46:t:162:PRO:HG3	46:t:167:LYS:HG3	2.01	0.42
46:t:391:LYS:HE3	46:t:393:SER:OG	2.19	0.42
48:5:806:A:H5''	48:5:936:A:H61	1.85	0.42
48:5:999:G:C6	48:5:1000:C:N4	2.87	0.42
48:5:1661:G:H2'	48:5:1662:G:C8	2.53	0.42
48:5:2313:A:H4'	48:5:2314:U:C5'	2.50	0.42
48:5:3279:A:H2'	48:5:3280:U:H5'	2.00	0.42
48:5:3349:C:H2'	48:5:3350:C:O4'	2.20	0.42
48:5:3350:C:H2'	48:5:3351:U:C2	2.53	0.42
2:B:37:ARG:O	2:B:186:GLY:HA3	2.20	0.42
3:C:74:ILE:HD12	3:C:74:ILE:HA	1.89	0.42
6:F:130:ILE:HG21	6:F:130:ILE:HD13	1.60	0.42
7:G:153:ILE:HD13	7:G:166:LEU:HB3	2.00	0.42
7:G:214:LEU:HD12	7:G:214:LEU:HA	1.78	0.42
19:S:117:ARG:HD2	48:5:1322:U:OP1	2.19	0.42
26:Z:17:ARG:HG2	33:g:73:SER:O	2.19	0.42
42:p:74:ALA:O	42:p:78:THR:HG23	2.19	0.42
46:t:162:PRO:HD2	46:t:167:LYS:HB2	2.01	0.42
48:5:242:C:H2'	48:5:243:G:H8	1.83	0.42
48:5:242:C:H2'	48:5:243:G:C8	2.55	0.42
48:5:2441:A:N1	48:5:2507:C:C2	2.87	0.42
50:8:92:A:H2'	50:8:93:U:O4'	2.19	0.42
1:A:200:ARG:HG3	48:5:2147:A:OP1	2.19	0.42
2:B:361:THR:HG23	2:B:371:GLN:O	2.20	0.42
7:G:50:VAL:HG22	7:G:52:TRP:CE2	2.55	0.42
7:G:82:LEU:HD13	7:G:178:ALA:HB1	2.02	0.42
12:L:122:LYS:HG3	34:h:119:LYS:O	2.20	0.42
14:N:6:TYR:CE2	35:i:40:VAL:HG22	2.55	0.42
15:O:68[A]:ARG:NH1	48:5:2988:C:P	2.93	0.42
17:Q:60:PRO:HG2	17:Q:142:GLY:C	2.43	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:127:LYS:HA	23:W:130:SER:OG	2.20	0.42
31:e:103:LYS:HD3	48:5:1391:C:C2	2.55	0.42
43:q:41:VAL:HG21	43:q:185:LEU:HD21	2.01	0.42
46:t:194:VAL:HG13	46:t:198:LEU:HG	2.01	0.42
46:t:360:TYR:OH	46:t:423:MET:SD	2.78	0.42
46:t:505:ASN:CG	46:t:530:LYS:HZ2	2.28	0.42
48:5:735:A:H5''	48:5:735:A:H8	1.84	0.42
48:5:1366:A:C2	48:5:1367:G:C4	3.08	0.42
48:5:1648:A:H2'	48:5:1649:U:O4'	2.19	0.42
48:5:3228:C:HO2'	48:5:3229:G:P	2.41	0.42
49:7:55:A:H2'	49:7:56:A:O4'	2.20	0.42
8:H:91:ARG:HG2	8:H:182:SER:HB3	2.02	0.42
10:J:21:ILE:HG13	10:J:37:LEU:HD11	2.01	0.42
12:L:59:ARG:O	12:L:59:ARG:HG3	2.18	0.42
12:L:157:ARG:NH2	27:a:146:GLU:OE2	2.52	0.42
16:P:30:ARG:HD3	16:P:30:ARG:C	2.44	0.42
17:Q:170:ARG:HD2	27:a:56:VAL:O	2.20	0.42
20:T:54:HIS:CG	20:T:55:LYS:N	2.87	0.42
29:c:61:MET:HE3	29:c:62:LEU:HG	2.02	0.42
33:g:94:LEU:HA	33:g:94:LEU:HD23	1.66	0.42
39:m:110:CYS:SG	39:m:112:LYS:HB2	2.59	0.42
43:q:25:LEU:HD23	43:q:76:LEU:HD21	2.02	0.42
48:5:958:C:OP1	48:5:2799:A:H3'	2.19	0.42
48:5:2436:U:C2'	48:5:2437:G:H5''	2.48	0.42
48:5:3238:G:H8	48:5:3238:G:H5''	1.83	0.42
48:5:3287:U:H2'	48:5:3288:G:H5'	2.00	0.42
1:A:33:ASP:OD1	1:A:33:ASP:N	2.48	0.42
3:C:44:LYS:HB3	3:C:47:ARG:HH11	1.84	0.42
7:G:54:GLU:O	7:G:58:VAL:HG23	2.19	0.42
30:d:44:MET:HB2	30:d:44:MET:HE3	1.40	0.42
31:e:9:ILE:HG12	31:e:63:THR:HB	2.00	0.42
40:n:16:LYS:HE2	40:n:16:LYS:HB3	1.75	0.42
41:o:71:ARG:HG3	41:o:71:ARG:HH11	1.85	0.42
43:q:11:TYR:HE1	43:q:15:LEU:HD12	1.84	0.42
46:t:68:THR:CG2	46:t:93:THR:HG1	2.20	0.42
48:5:173:G:N1	48:5:246:U:C2	2.88	0.42
48:5:396:A:O2'	48:5:399:A:OP1	2.35	0.42
48:5:567:G:H2'	48:5:568:G:C8	2.55	0.42
48:5:630:A:H2'	48:5:631:U:C6	2.54	0.42
48:5:2147:A:H2'	48:5:2148:U:O4'	2.19	0.42
48:5:2682:C:O2'	48:5:2683:U:OP1	2.15	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:5:2827:U:O2	48:5:2827:U:H2'	2.19	0.42
48:5:2896:A:H8	48:5:2896:A:C5'	2.32	0.42
48:5:2995:A:O5'	48:5:2995:A:H8	2.03	0.42
48:5:3294:A:H2'	48:5:3295:A:O4'	2.20	0.42
50:8:126:A:H8	50:8:126:A:OP2	2.02	0.42
2:B:4:ARG:HH11	2:B:4:ARG:HG3	1.84	0.42
4:D:270:LYS:O	4:D:271:LYS:HD3	2.20	0.42
6:F:73:GLY:O	20:T:143:THR:HB	2.20	0.42
6:F:141:TYR:O	6:F:142:SER:C	2.61	0.42
11:K:126:UNK:O	11:K:127:UNK:C	2.68	0.42
12:L:59:ARG:O	12:L:60:ALA:HB3	2.20	0.42
14:N:78:GLY:HA2	14:N:89:VAL:HG21	2.02	0.42
17:Q:90:ASP:O	17:Q:92:ARG:N	2.53	0.42
19:S:137:ARG:HD3	48:5:1213:G:OP1	2.20	0.42
25:Y:11:ASP:HB3	25:Y:14:LYS:HG3	2.02	0.42
34:h:17:LEU:HA	34:h:20:GLN:HB2	2.02	0.42
39:m:98:LYS:HD3	39:m:115:CYS:HB2	2.02	0.42
46:t:43:THR:HA	46:t:46:ILE:HD12	2.02	0.42
46:t:387:VAL:HG12	46:t:389:PRO:O	2.12	0.42
46:t:513:SER:CA	46:t:518:ASP:OD1	2.68	0.42
48:5:248:U:O2	48:5:248:U:H2'	2.20	0.42
48:5:600:G:H5'	48:5:601:U:OP2	2.20	0.42
48:5:748:U:H2'	48:5:749:C:C6	2.55	0.42
48:5:1190:A:C8	48:5:1193:A:H1'	2.55	0.42
48:5:1932:A:H5'	48:5:1933:A:OP2	2.19	0.42
48:5:2314:U:H4'	48:5:2314:U:OP2	2.20	0.42
48:5:2568:C:O2'	48:5:2569:A:O5'	2.28	0.42
48:5:2840:C:H2'	48:5:2841:G:O4'	2.20	0.42
48:5:2935:U:O2	48:5:2935:U:H2'	2.20	0.42
2:B:329:PRO:HA	48:5:3047:U:H5'	2.02	0.41
2:B:346:THR:O	2:B:348:ARG:N	2.53	0.41
2:B:360:ASP:OD1	2:B:361:THR:N	2.52	0.41
5:E:155:LEU:HD23	5:E:155:LEU:HA	1.76	0.41
10:J:116:TYR:O	10:J:117:ASP:C	2.62	0.41
12:L:16:LYS:O	48:5:48:A:OP2	2.38	0.41
14:N:172:ARG:NH2	48:5:63:A:OP1	2.53	0.41
15:O:108[A]:ILE:HD13	15:O:160[A]:ARG:HD2	2.02	0.41
15:O:155[B]:LYS:HE2	15:O:155[B]:LYS:HB3	1.87	0.41
19:S:45:LEU:HA	19:S:45:LEU:HD22	1.67	0.41
27:a:32:ARG:NH1	48:5:799:G:OP2	2.50	0.41
27:a:79:TRP:CZ3	27:a:91:LEU:HD13	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:b:9:ALA:O	28:b:10:HIS:C	2.63	0.41
30:d:46:THR:HG21	30:d:91:SER:CB	2.50	0.41
37:k:5:ILE:HG22	37:k:54:LEU:HB2	2.02	0.41
38:l:5:LYS:O	48:5:1833:G:H4'	2.20	0.41
38:l:7:PHE:CZ	50:8:113:U:C4	3.07	0.41
42:p:20:SER:O	42:p:24:ARG:HB2	2.20	0.41
44:r:29:UNK:C	44:r:31:UNK:N	2.83	0.41
46:t:31:ALA:N	46:t:147:ILE:CD1	2.82	0.41
46:t:227:VAL:HG11	46:t:238:VAL:HG21	1.92	0.41
48:5:314:U:H2'	48:5:315:C:C6	2.55	0.41
48:5:536:U:H1'	48:5:559:A:C8	2.55	0.41
48:5:971:G:H2'	48:5:972:A:O4'	2.20	0.41
48:5:2534:G:H8	48:5:2534:G:OP2	2.03	0.41
48:5:3158:G:C5	48:5:3159:C:C5	3.08	0.41
50:8:157:U:O2'	50:8:158:U:H5'	2.19	0.41
1:A:61:VAL:HG22	1:A:63:PHE:CE1	2.54	0.41
3:C:80:GLY:HA2	3:C:85:SER:OG	2.20	0.41
3:C:93:MET:HE2	3:C:93:MET:H	1.85	0.41
3:C:118:LYS:O	3:C:122:THR:HG22	2.20	0.41
7:G:53:PRO:HD2	7:G:56:VAL:HG21	2.02	0.41
8:H:29:GLY:HA3	8:H:82:VAL:HG13	2.01	0.41
8:H:166:ARG:O	8:H:167:VAL:HB	2.20	0.41
10:J:13:LYS:CE	10:J:132:ASN:HD21	2.32	0.41
12:L:166:ALA:HB1	27:a:147:LEU:HD21	2.01	0.41
27:a:12:ARG:HB3	48:5:943:U:O2'	2.20	0.41
29:c:69:TYR:N	29:c:69:TYR:CD1	2.89	0.41
32:f:77:ASN:ND2	48:5:1326:A:O2'	2.50	0.41
39:m:99:CYS:HB3	39:m:115:CYS:HB3	2.01	0.41
48:5:240:U:O2'	48:5:241:G:H8	2.02	0.41
48:5:806:A:O2'	48:5:807:A:H5'	2.19	0.41
48:5:815:G:C6	48:5:906:A:C4	3.08	0.41
48:5:2573:G:H3'	48:5:2574:G:H5''	2.02	0.41
48:5:2660:G:H4'	48:5:2750:U:O2	2.21	0.41
49:7:11:A:O2'	49:7:13:A:H2'	2.19	0.41
1:A:250:GLN:HG2	1:A:251:LYS:H	1.84	0.41
4:D:49:TYR:CE1	4:D:75:LEU:HD12	2.56	0.41
5:E:154:LEU:HD23	5:E:154:LEU:HA	1.87	0.41
19:S:82:ASP:OD1	19:S:87:THR:HB	2.20	0.41
19:S:106:LEU:HD13	19:S:106:LEU:C	2.45	0.41
25:Y:33:ALA:HB2	25:Y:101:PRO:HB2	2.02	0.41
26:Z:108:GLU:O	26:Z:112:LYS:HG3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:d:26:LYS:HE2	48:5:1456:A:N7	2.35	0.41
30:d:61:LYS:HE2	30:d:61:LYS:HB3	1.39	0.41
31:e:123:LYS:HA	31:e:126:LEU:CG	2.51	0.41
34:h:95:PHE:CG	48:5:136:G:H5'	2.55	0.41
37:k:41:THR:HG21	37:k:62:ALA:HB1	2.03	0.41
37:k:64:LYS:HE2	37:k:65:LEU:HA	2.03	0.41
42:p:30:GLU:HG2	42:p:34:HIS:NE2	2.36	0.41
43:q:19:LEU:HD23	43:q:19:LEU:HA	1.70	0.41
46:t:87:ARG:HH11	46:t:87:ARG:HD3	1.54	0.41
46:t:194:VAL:HA	46:t:223:ILE:HD12	2.02	0.41
48:5:529:A:H2'	48:5:530:G:O4'	2.20	0.41
48:5:726:G:C8	48:5:726:G:C5'	3.01	0.41
48:5:1116:G:H4'	48:5:1117:G:OP2	2.20	0.41
48:5:1690:C:H2'	48:5:1691:U:O4'	2.20	0.41
48:5:2442:G:C2	48:5:2443:A:N7	2.89	0.41
48:5:3393:U:H2'	48:5:3394:U:O4'	2.20	0.41
1:A:23:ARG:C	1:A:24:GLN:O	2.63	0.41
1:A:68:LYS:HG3	1:A:69:TYR:N	2.36	0.41
1:A:241:ARG:NH2	48:5:2156:C:OP2	2.53	0.41
2:B:221:THR:HG22	2:B:272:TYR:N	2.36	0.41
3:C:203:ARG:NH1	3:C:226:GLU:OE2	2.54	0.41
4:D:122:VAL:O	4:D:124:GLU:N	2.44	0.41
6:F:22:THR:HA	6:F:25:GLN:OE1	2.20	0.41
7:G:122:LYS:C	7:G:124:ASP:H	2.28	0.41
9:I:156:ARG:C	9:I:158:LYS:N	2.78	0.41
11:K:134:UNK:O	11:K:136:UNK:N	2.53	0.41
14:N:22:LEU:HD12	14:N:22:LEU:HA	1.86	0.41
20:T:25:VAL:HG22	20:T:30:TYR:HE2	1.85	0.41
20:T:105:PHE:CE1	48:5:1062:A:H4'	2.55	0.41
22:V:87:ARG:HH12	22:V:137:VAL:HG11	1.85	0.41
24:X:70:GLU:HB3	46:t:372:LEU:HD21	2.03	0.41
26:Z:81:LEU:HD12	33:g:93:PHE:CD2	2.55	0.41
29:c:88:GLY:N	48:5:1729:A:OP1	2.53	0.41
32:f:89:LEU:HA	32:f:90:PRO:HD3	1.87	0.41
43:q:63:ILE:HG21	43:q:77:LEU:HD21	2.01	0.41
46:t:28:TYR:CE2	46:t:150:TYR:CD1	3.08	0.41
48:5:339:C:OP1	48:5:1380:G:O2'	2.30	0.41
48:5:916:G:C5'	48:5:917:A:OP1	2.69	0.41
48:5:1471:U:H2'	48:5:1472:U:C6	2.54	0.41
48:5:1939:G:C6	48:5:2110:G:O6	2.74	0.41
48:5:2298:U:C5	48:5:2921:U:H1'	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:5:2403:G:N2	48:5:2404:A:N6	2.66	0.41
48:5:2509:U:H2'	48:5:2510:U:C5'	2.45	0.41
48:5:2663:G:H2'	48:5:2664:C:O4'	2.21	0.41
48:5:3288:G:O2'	48:5:3289:G:P	2.78	0.41
1:A:34:TYR:O	1:A:35:ALA:C	2.62	0.41
4:D:33:ARG:O	4:D:34:LYS:C	2.63	0.41
4:D:155:THR:HG22	4:D:179:ARG:NH1	2.36	0.41
5:E:80:ASN:HB2	48:5:3272:C:O2	2.21	0.41
6:F:96:PRO:HA	6:F:97:PRO:HD3	1.98	0.41
8:H:20:ILE:HG13	13:M:7:VAL:HG22	2.01	0.41
15:O:49[B]:ARG:O	15:O:52[B]:LEU:HB2	2.20	0.41
15:O:54[B]:TYR:O	15:O:57[B]:PHE:HB3	2.20	0.41
15:O:149[A]:TYR:OH	48:5:3006:A:OP1	2.20	0.41
16:P:94:LEU:HD12	16:P:94:LEU:HA	1.71	0.41
17:Q:93:ILE:HG23	48:5:784:A:C6	2.56	0.41
18:R:146:LYS:O	18:R:149:ALA:N	2.53	0.41
19:S:34:GLU:O	19:S:38:LYS:HG3	2.20	0.41
24:X:27:ARG:H	24:X:27:ARG:HG2	1.68	0.41
24:X:105:VAL:HG13	24:X:130:TYR:CG	2.56	0.41
25:Y:102:SER:O	25:Y:103:LYS:HD3	2.20	0.41
26:Z:46:ILE:HD12	26:Z:46:ILE:C	2.46	0.41
27:a:13:GLY:O	31:e:36:LYS:HE2	2.20	0.41
32:f:45:LEU:HA	32:f:71:VAL:HG12	2.02	0.41
46:t:62:PRO:HG3	46:t:130:THR:HG21	2.02	0.41
48:5:438:A:O2'	48:5:439:C:P	2.79	0.41
48:5:973:A:H5''	48:5:974:G:OP2	2.21	0.41
48:5:1014:U:H3'	48:5:1015:U:C5'	2.51	0.41
48:5:1547:G:H2'	48:5:1548:C:C6	2.56	0.41
48:5:1766:G:C2'	48:5:1767:C:H5'	2.51	0.41
48:5:3242:G:C5'	48:5:3245:A:C8	3.03	0.41
2:B:73:VAL:HG13	22:V:89:ASP:C	2.45	0.41
4:D:108:ARG:HA	4:D:251:PRO:HB2	2.03	0.41
4:D:270:LYS:HG3	4:D:273:ARG:HB3	2.01	0.41
6:F:121:LYS:HB2	20:T:133:ALA:HB3	2.03	0.41
7:G:71:VAL:CG2	7:G:76:ALA:HB2	2.50	0.41
8:H:117:PHE:CZ	8:H:165:CYS:HB3	2.55	0.41
8:H:156:GLN:NE2	8:H:160:ASP:OD1	2.46	0.41
9:I:42:THR:CG2	9:I:45:GLU:HG3	2.51	0.41
12:L:46:ILE:HD12	12:L:46:ILE:HG23	1.80	0.41
12:L:144:THR:C	12:L:146:PRO:HD3	2.45	0.41
14:N:183:THR:O	14:N:183:THR:CG2	2.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:36:ILE:O	16:P:39:TRP:HB2	2.21	0.41
17:Q:158:HIS:H	17:Q:186:VAL:CG1	2.28	0.41
19:S:7:TYR:CE2	19:S:34:GLU:HG2	2.56	0.41
22:V:125:LEU:HB3	22:V:126:TRP:CD1	2.55	0.41
25:Y:37:LYS:HE2	25:Y:37:LYS:H	1.85	0.41
25:Y:50:ILE:HD12	25:Y:70:ILE:HG12	2.02	0.41
25:Y:63:LYS:HA	25:Y:63:LYS:HD3	1.82	0.41
26:Z:34:LYS:HA	26:Z:34:LYS:HD2	1.67	0.41
30:d:19:ARG:HD3	30:d:35:GLU:HG2	2.02	0.41
31:e:126:LEU:HD23	31:e:126:LEU:HA	1.78	0.41
32:f:102:LEU:HA	32:f:102:LEU:HD23	1.84	0.41
33:g:96:GLU:O	33:g:99:LYS:HB2	2.21	0.41
35:i:31:GLY:HA3	48:5:299:G:C4	2.55	0.41
35:i:76:ARG:HA	35:i:76:ARG:HE	1.85	0.41
36:j:2:GLY:O	36:j:7:SER:HB3	2.20	0.41
39:m:127:LEU:HD23	39:m:127:LEU:HA	1.66	0.41
43:q:76:LEU:HD22	43:q:76:LEU:HA	1.87	0.41
48:5:174:C:H2'	48:5:175:C:O4'	2.21	0.41
48:5:956:U:H2'	48:5:957:C:C6	2.55	0.41
48:5:1056:U:H2'	48:5:1057:A:O5'	2.21	0.41
48:5:1249:G:H2'	48:5:1250:G:H8	1.83	0.41
48:5:2191:U:H2'	48:5:2192:C:O4'	2.20	0.41
48:5:2405:C:O2	48:5:2819:A:N1	2.53	0.41
48:5:2558:U:O2'	48:5:2559:U:H5'	2.21	0.41
48:5:2911:A:H4'	48:5:2912:G:C8	2.56	0.41
48:5:3278:C:HO2'	48:5:3279:A:P	2.31	0.41
1:A:71:LEU:HA	1:A:71:LEU:HD12	1.83	0.41
6:F:207:LEU:O	48:5:1334:U:H5'	2.20	0.41
7:G:73:PRO:HA	7:G:232:HIS:O	2.21	0.41
8:H:40:HIS:ND1	8:H:41:ILE:HG13	2.36	0.41
8:H:89:LYS:HG2	8:H:145:VAL:HG22	2.03	0.41
12:L:61:PRO:C	12:L:62:THR:HG23	2.45	0.41
15:O:155[A]:LYS:HE2	15:O:155[A]:LYS:HB3	1.87	0.41
18:R:38:ARG:O	18:R:42:ARG:HG3	2.21	0.41
24:X:91:ASN:O	24:X:92:LYS:C	2.64	0.41
26:Z:95:VAL:CG1	26:Z:110:ALA:HA	2.50	0.41
29:c:87:VAL:HB	48:5:1728:G:O2'	2.21	0.41
32:f:18:ARG:HD3	48:5:1178:G:C5'	2.42	0.41
35:i:43:LEU:HD23	35:i:43:LEU:HA	1.82	0.41
37:k:17:ARG:NH2	48:5:1824:U:O3'	2.53	0.41
42:p:35:ALA:HB3	42:p:37:TYR:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:5:1077:U:H2'	48:5:1078:U:C6	2.56	0.41
48:5:1358:C:H2'	48:5:1359:C:O4'	2.21	0.41
48:5:2397:A:C2	48:5:2873:U:H5'	2.55	0.41
4:D:48:LYS:NZ	48:5:2749:G:P	2.94	0.41
4:D:257:GLU:CD	4:D:257:GLU:H	2.29	0.41
6:F:62:ILE:O	6:F:66:LYS:HG3	2.21	0.41
7:G:187:GLY:C	7:G:189:LEU:H	2.28	0.41
8:H:17:THR:O	8:H:17:THR:OG1	2.30	0.41
9:I:212:GLU:C	9:I:214:PRO:HD3	2.46	0.41
14:N:166:ALA:HB2	48:5:320:G:OP1	2.21	0.41
16:P:139:TYR:CE1	48:5:2355:G:H4'	2.55	0.41
23:W:13:ILE:HG12	23:W:32:GLN:HA	2.03	0.41
24:X:23:ALA:O	24:X:24:LEU:HB2	2.21	0.41
31:e:24:ARG:HD3	31:e:25:TYR:CE2	2.56	0.41
46:t:163:VAL:CG2	46:t:165:GLU:H	2.31	0.41
48:5:118:U:C5	48:5:119:U:C4	3.09	0.41
48:5:797:U:O2'	48:5:798:G:H5'	2.21	0.41
48:5:1403:C:C2	48:5:1409:G:C2	3.08	0.41
48:5:1597:C:H5'	48:5:1696:A:H1'	2.01	0.41
48:5:1763:U:H3'	48:5:1764:U:C6	2.56	0.41
48:5:2953:U:H5''	48:5:2954:U:OP2	2.20	0.41
48:5:3028:G:H2'	48:5:3029:A:C8	2.55	0.41
48:5:3089:C:H2'	48:5:3090:U:O4'	2.21	0.41
48:5:3289:G:O2'	48:5:3290:G:OP1	2.36	0.41
1:A:8:GLN:HA	48:5:2163:C:H4'	2.01	0.41
1:A:83:HIS:O	1:A:86:GLN:HB3	2.21	0.41
1:A:180:LEU:HA	1:A:180:LEU:HD23	1.79	0.41
2:B:57:VAL:HG23	2:B:358:TRP:HE3	1.85	0.41
2:B:130:PHE:CE2	48:5:3149:G:H4'	2.56	0.41
3:C:52:VAL:HB	3:C:99:MET:CE	2.51	0.41
4:D:48:LYS:HZ3	48:5:2749:G:P	2.43	0.41
4:D:122:VAL:C	4:D:124:GLU:H	2.29	0.41
4:D:272:TYR:CE2	49:7:22:A:H1'	2.55	0.41
6:F:102:VAL:HG12	6:F:130:ILE:CD1	2.50	0.41
7:G:108:ARG:NH1	48:5:121:A:C4	2.89	0.41
7:G:205:ALA:HA	7:G:208:GLU:OE1	2.21	0.41
8:H:13:PRO:HG2	8:H:16:VAL:HG13	2.02	0.41
8:H:66:ALA:O	8:H:70:THR:HG22	2.21	0.41
8:H:86:TYR:CE1	8:H:151:VAL:HG13	2.56	0.41
9:I:160:PRO:HD3	48:5:2854:U:H5''	2.03	0.41
10:J:151:SER:O	10:J:152:HIS:CB	2.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:109:PHE:O	12:L:113:VAL:HG23	2.20	0.41
14:N:68:ARG:HD2	48:5:291:C:OP1	2.21	0.41
14:N:102:ALA:O	14:N:106:VAL:HG13	2.21	0.41
14:N:193:ARG:HH11	14:N:193:ARG:HD2	1.75	0.41
15:O:88[B]:VAL:HG12	15:O:89[B]:SER:N	2.36	0.41
15:O:116[A]:LYS:HB2	48:5:3180:A:H5''	2.03	0.41
15:O:156[A]:LEU:HD13	48:5:3243:A:C8	2.56	0.41
15:O:156[B]:LEU:HB3	48:5:3243:A:N7	2.36	0.41
19:S:74:ASN:OD1	19:S:95:ARG:NH1	2.54	0.41
20:T:139:ARG:NH1	20:T:139:ARG:CG	2.83	0.41
21:U:90:ARG:HB3	21:U:90:ARG:NH1	2.36	0.41
21:U:100:THR:HA	48:5:1677:G:OP1	2.21	0.41
23:W:120:LYS:O	23:W:123:ARG:HB2	2.21	0.41
25:Y:24:SER:OG	50:8:73:U:OP1	2.34	0.41
26:Z:68:ILE:O	26:Z:115:LYS:HG3	2.21	0.41
27:a:115:LYS:HG3	48:5:715:A:C8	2.55	0.41
31:e:19:ARG:HD2	31:e:28:VAL:CG1	2.51	0.41
32:f:88:ASN:HB2	48:5:429:U:C4'	2.51	0.41
43:q:40:GLU:O	43:q:44:GLU:HB2	2.20	0.41
43:q:44:GLU:OE1	43:q:103:ASN:HB3	2.21	0.41
46:t:39:LEU:CD2	46:t:529:SER:C	2.92	0.41
46:t:39:LEU:CG	46:t:529:SER:HB2	2.35	0.41
46:t:172:PRO:C	46:t:174:GLY:N	2.77	0.41
46:t:176:LEU:HB3	46:t:537:ILE:CD1	2.45	0.41
46:t:387:VAL:HG13	46:t:388:TYR:C	2.46	0.41
48:5:345:G:O2'	50:8:25:G:N3	2.54	0.41
48:5:594:U:C5'	48:5:609:G:H1	2.33	0.41
48:5:1256:G:O6	48:5:1261:G:N2	2.54	0.41
48:5:1480:G:H4'	48:5:1481:A:OP1	2.21	0.41
48:5:1596:C:H2'	48:5:1597:C:C6	2.55	0.41
48:5:1813:A:O2'	48:5:1816:A:N3	2.47	0.41
48:5:1821:U:H4'	48:5:1822:C:OP2	2.21	0.41
48:5:2101:C:O2'	48:5:2102:U:P	2.78	0.41
48:5:2179:C:H4'	48:5:2180:G:OP2	2.20	0.41
48:5:2199:G:H2'	48:5:2200:U:H6	1.86	0.41
48:5:2530:G:C2'	48:5:2531:C:H5'	2.51	0.41
48:5:2985:C:H2'	48:5:2986:U:C6	2.55	0.41
48:5:3205:G:H2'	48:5:3206:C:C5	2.56	0.41
48:5:3257:C:H2'	48:5:3258:U:O4'	2.20	0.41
49:7:4:U:H2'	49:7:5:G:H8	1.86	0.41
1:A:206:PRO:HG3	1:A:213:GLY:CA	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:221:LYS:NZ	48:5:2965:U:O2	2.53	0.41
3:C:99:MET:HE3	3:C:103:THR:H	1.86	0.41
3:C:306:THR:O	3:C:306:THR:HG22	2.21	0.41
6:F:158:LYS:HD2	6:F:158:LYS:C	2.46	0.41
10:J:75:LYS:HB3	10:J:75:LYS:HE2	1.84	0.41
10:J:82:ARG:HB3	10:J:112:LEU:HB2	2.03	0.41
13:M:14:LEU:HA	13:M:14:LEU:HD23	1.82	0.41
14:N:171:SER:O	48:5:288:C:H4'	2.21	0.41
19:S:50:LYS:HZ3	19:S:50:LYS:HG2	1.53	0.41
20:T:68:THR:HG23	20:T:69:LYS:N	2.35	0.41
22:V:128:ARG:HB3	22:V:128:ARG:CZ	2.51	0.41
41:o:34:SER:C	41:o:36:PHE:H	2.29	0.41
43:q:198:PRO:HG2	43:q:200:SER:H	1.86	0.41
46:t:50:TYR:O	46:t:50:TYR:CG	2.69	0.41
48:5:594:U:O2'	48:5:595:G:H5'	2.20	0.41
48:5:1449:A:C2	48:5:2356:A:C4	3.08	0.41
48:5:1685:C:H2'	48:5:1686:U:C6	2.56	0.41
48:5:2222:A:O5'	48:5:2222:A:H8	2.04	0.41
48:5:2910:A:H5''	48:5:2910:A:H8	1.85	0.41
48:5:3255:U:H6	48:5:3255:U:O5'	2.04	0.41
48:5:3351:U:H3'	48:5:3351:U:O2	2.21	0.41
49:7:24:A:H2'	49:7:25:G:O4'	2.21	0.41
49:7:110:G:C6	49:7:111:U:C4	3.08	0.41
1:A:116:VAL:CG1	1:A:126:LEU:HB2	2.47	0.40
2:B:233:TRP:CD1	2:B:265:ALA:HB1	2.56	0.40
14:N:44:ARG:HB3	14:N:47:LYS:HB3	2.02	0.40
15:O:121[A]:PRO:HA	15:O:124[A]:LEU:HD22	2.02	0.40
26:Z:109:GLU:O	26:Z:113:VAL:HG23	2.21	0.40
27:a:79:TRP:CH2	27:a:91:LEU:HD13	2.56	0.40
32:f:37:THR:HB	32:f:39:GLN:OE1	2.21	0.40
37:k:24:THR:HG23	37:k:44:LYS:HB2	2.03	0.40
46:t:321:LEU:O	46:t:502:ARG:HA	2.21	0.40
48:5:371:G:H4'	48:5:396:A:N1	2.36	0.40
48:5:926:A:H2'	48:5:927:C:H6	1.86	0.40
48:5:1072:G:H2'	48:5:1073:U:C6	2.56	0.40
48:5:3245:A:C2	48:5:3246:G:C2	3.08	0.40
48:5:3353:G:H4'	48:5:3354:U:OP2	2.21	0.40
3:C:195:ARG:O	3:C:196:ASN:HB2	2.21	0.40
4:D:257:GLU:CD	4:D:257:GLU:N	2.79	0.40
8:H:37:ASN:OD1	8:H:39:LYS:HB2	2.21	0.40
9:I:24:ARG:O	9:I:25:ALA:HB3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:47:ASP:CG	13:M:55:ARG:HB2	2.46	0.40
13:M:59:ASN:O	13:M:62:GLN:HG2	2.21	0.40
15:O:171[B]:LYS:NZ	48:5:3180:A:OP1	2.54	0.40
17:Q:138:LEU:HD23	17:Q:138:LEU:HA	1.74	0.40
18:R:100:ARG:HH11	18:R:100:ARG:HD2	1.71	0.40
22:V:39:VAL:HG21	22:V:51:ALA:C	2.46	0.40
34:h:82:ALA:O	50:8:38:U:C5	2.74	0.40
37:k:54:LEU:HG	37:k:56:ILE:CD1	2.51	0.40
41:o:43:TYR:OH	41:o:47:GLN:NE2	2.54	0.40
43:q:53:MET:SD	43:q:85:GLY:HA3	2.61	0.40
43:q:67:LEU:HD22	43:q:67:LEU:HA	1.96	0.40
46:t:50:TYR:CD2	46:t:50:TYR:C	2.95	0.40
46:t:181:ALA:CA	46:t:537:ILE:HG23	2.50	0.40
46:t:395:LEU:CB	46:t:419:PHE:HB2	2.51	0.40
48:5:237:G:N2	48:5:238:A:O4'	2.54	0.40
48:5:291:C:H2'	48:5:292:U:C6	2.56	0.40
48:5:384:A:H1'	48:5:1465:A:C8	2.56	0.40
48:5:1018:G:C5	48:5:1035:G:C2	3.10	0.40
48:5:1352:A:H3'	48:5:1352:A:P	2.61	0.40
48:5:2442:G:N2	48:5:2506:U:H3	2.17	0.40
48:5:2697:A:H2'	48:5:2698:G:C8	2.56	0.40
48:5:2775:U:H2'	48:5:2776:C:C6	2.56	0.40
49:7:27:A:H2'	49:7:28:C:C6	2.56	0.40
1:A:179:LEU:O	1:A:184:ARG:HD2	2.21	0.40
4:D:92:LEU:HD23	4:D:92:LEU:HA	1.68	0.40
4:D:124:GLU:O	4:D:125:VAL:HB	2.20	0.40
6:F:236:ILE:O	6:F:240:VAL:HG23	2.20	0.40
10:J:82:ARG:NH1	10:J:112:LEU:O	2.46	0.40
14:N:28:TRP:O	14:N:32:GLN:HG2	2.21	0.40
14:N:93:LYS:HG3	48:5:289:A:N3	2.35	0.40
15:O:64[A]:PHE:CE2	15:O:68[A]:ARG:HD3	2.56	0.40
15:O:95[B]:GLY:O	15:O:98[B]:ALA:HB3	2.22	0.40
15:O:106[B]:GLU:H	15:O:106[B]:GLU:HG2	1.56	0.40
17:Q:63:SER:O	17:Q:66:ARG:HB3	2.22	0.40
18:R:169:ALA:O	18:R:173:ARG:HB3	2.21	0.40
21:U:37:LEU:HD13	21:U:37:LEU:HA	1.91	0.40
24:X:49:LYS:HE3	50:8:135:G:OP1	2.20	0.40
25:Y:39:LEU:HD12	25:Y:43:TYR:HE1	1.87	0.40
26:Z:136:PHE:HB2	33:g:88:ARG:HG3	2.03	0.40
27:a:4:ARG:HH11	27:a:4:ARG:HD2	1.66	0.40
29:c:10:ILE:HD11	29:c:68:TYR:HE2	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:d:23:VAL:O	30:d:28:ARG:NH1	2.54	0.40
31:e:34:LYS:O	31:e:36:LYS:HD3	2.21	0.40
31:e:82:LEU:HD22	31:e:117:ILE:HD13	2.04	0.40
34:h:55:LEU:HD23	34:h:55:LEU:HA	1.86	0.40
39:m:82:LEU:HA	39:m:82:LEU:HD23	1.84	0.40
43:q:46:ARG:NH2	48:5:1258:U:OP1	2.55	0.40
46:t:50:TYR:O	46:t:50:TYR:CD2	2.74	0.40
46:t:60:THR:C	46:t:62:PRO:N	2.80	0.40
48:5:993:G:N3	48:5:2637:A:H2'	2.36	0.40
48:5:1046:A:H2'	48:5:1049:C:C5	2.56	0.40
48:5:1049:C:H2'	48:5:1050:U:C6	2.55	0.40
48:5:1081:U:HO2'	48:5:1082:U:H5''	1.87	0.40
48:5:1262:G:H5''	48:5:1263:A:OP2	2.21	0.40
48:5:2872:A:HO2'	48:5:2873:U:P	2.42	0.40
48:5:2916:U:H5	48:5:2935:U:HO2'	1.60	0.40
48:5:3167:A:H8	48:5:3167:A:O5'	2.05	0.40
48:5:3218:A:H3'	48:5:3218:A:OP1	2.21	0.40
49:7:113:C:H2'	49:7:114:U:O4'	2.22	0.40
2:B:250:ALA:HB1	48:5:2947:G:C2	2.57	0.40
2:B:258:ALA:O	2:B:259:HIS:CD2	2.75	0.40
5:E:47:PHE:CD1	5:E:74:VAL:HG22	2.56	0.40
8:H:57:VAL:HG23	8:H:68:LEU:HG	2.03	0.40
9:I:62:SER:HA	9:I:65:LEU:HD12	2.04	0.40
10:J:142:LYS:HE3	48:5:2664:C:OP2	2.21	0.40
14:N:179:LYS:O	48:5:287:G:H5'	2.21	0.40
15:O:27[A]:LEU:HB3	15:O:98[A]:ALA:O	2.22	0.40
15:O:194[B]:LEU:O	15:O:199[B]:TYR:N	2.48	0.40
21:U:14:THR:HG23	21:U:66:VAL:HG13	2.03	0.40
24:X:55:ASN:OD1	24:X:56:ARG:O	2.39	0.40
29:c:14:LEU:HA	29:c:17:VAL:HG23	2.03	0.40
33:g:57:LEU:HB3	33:g:61:GLN:HB2	2.03	0.40
34:h:100:VAL:HG22	34:h:104:GLN:HB3	2.04	0.40
38:l:7:PHE:CD2	38:l:7:PHE:C	3.00	0.40
41:o:9:LYS:O	48:5:2713:U:H3'	2.21	0.40
41:o:63:LYS:HD2	48:5:2795:U:OP2	2.21	0.40
46:t:163:VAL:CG2	46:t:164:ASP:H	2.24	0.40
48:5:36:C:C2'	48:5:37:U:H5'	2.51	0.40
48:5:139:G:H2'	48:5:140:C:C6	2.56	0.40
48:5:372:A:C6	48:5:373:A:C6	3.09	0.40
48:5:411:U:H2'	48:5:412:G:H8	1.86	0.40
48:5:436:A:H5''	48:5:436:A:H8	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:5:600:G:H5''	48:5:600:G:C8	2.54	0.40
48:5:703:G:O2'	48:5:787:G:H4'	2.22	0.40
48:5:721:G:C2	48:5:722:G:C8	3.10	0.40
48:5:2567:C:N4	48:5:2568:C:H41	2.19	0.40
48:5:3066:U:H2'	48:5:3067:C:C6	2.57	0.40
48:5:3131:U:H2'	48:5:3132:C:C6	2.56	0.40
48:5:3132:C:H2'	48:5:3133:C:C6	2.56	0.40
48:5:3275:U:H4'	48:5:3276:G:OP2	2.19	0.40
1:A:133:TYR:CD2	1:A:168:VAL:HG12	2.57	0.40
2:B:19:ARG:HB3	2:B:232:ARG:NH1	2.37	0.40
3:C:170:LYS:CG	3:C:175:HIS:HB2	2.52	0.40
3:C:341:SER:O	3:C:342:LYS:HB3	2.22	0.40
4:D:18:THR:HA	4:D:19:PRO:HD3	1.95	0.40
4:D:140:ARG:HH11	48:5:1080:A:P	2.44	0.40
7:G:229:VAL:C	7:G:231:LYS:H	2.29	0.40
8:H:31:ARG:HB2	8:H:82:VAL:HA	2.02	0.40
10:J:92:ARG:HG2	10:J:92:ARG:NH1	2.26	0.40
11:K:16:UNK:O	11:K:61:UNK:N	2.54	0.40
27:a:14:HIS:ND1	27:a:14:HIS:N	2.68	0.40
30:d:9:THR:OG1	30:d:76:SER:HB3	2.20	0.40
34:h:24:LEU:O	34:h:27:GLU:HB2	2.22	0.40
46:t:154:VAL:HB	46:t:526:THR:HG22	2.03	0.40
46:t:197:LEU:HB3	46:t:223:ILE:HD13	2.04	0.40
48:5:138:U:H2'	48:5:139:G:H8	1.86	0.40
48:5:167:U:H2'	48:5:168:U:H6	1.86	0.40
48:5:253:A:O2'	48:5:254:A:P	2.80	0.40
48:5:256:G:H2'	48:5:257:U:H6	1.87	0.40
48:5:1064:A:N6	48:5:1096:U:H3	2.19	0.40
48:5:3237:U:H2'	48:5:3238:G:H5''	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	250/254 (98%)	213 (85%)	30 (12%)	7 (3%)	4	24
2	B	384/387 (99%)	341 (89%)	34 (9%)	9 (2%)	5	28
3	C	359/362 (99%)	306 (85%)	32 (9%)	21 (6%)	1	14
4	D	292/297 (98%)	267 (91%)	19 (6%)	6 (2%)	5	30
5	E	153/176 (87%)	134 (88%)	15 (10%)	4 (3%)	4	25
6	F	221/244 (91%)	201 (91%)	15 (7%)	5 (2%)	5	28
7	G	229/256 (90%)	181 (79%)	27 (12%)	21 (9%)	0	8
8	H	189/191 (99%)	172 (91%)	13 (7%)	4 (2%)	5	30
9	I	209/221 (95%)	175 (84%)	22 (10%)	12 (6%)	1	14
10	J	167/174 (96%)	135 (81%)	19 (11%)	13 (8%)	1	10
12	L	192/199 (96%)	161 (84%)	20 (10%)	11 (6%)	1	14
13	M	135/138 (98%)	124 (92%)	10 (7%)	1 (1%)	18	56
14	N	201/204 (98%)	182 (90%)	13 (6%)	6 (3%)	3	23
15	O	352/219 (161%)	324 (92%)	18 (5%)	10 (3%)	4	24
16	P	153/184 (83%)	142 (93%)	9 (6%)	2 (1%)	9	42
17	Q	183/186 (98%)	168 (92%)	9 (5%)	6 (3%)	3	21
18	R	186/189 (98%)	167 (90%)	16 (9%)	3 (2%)	7	38
19	S	170/172 (99%)	163 (96%)	6 (4%)	1 (1%)	21	59
20	T	157/160 (98%)	146 (93%)	9 (6%)	2 (1%)	9	42
21	U	96/121 (79%)	80 (83%)	13 (14%)	3 (3%)	3	22
22	V	134/137 (98%)	124 (92%)	8 (6%)	2 (2%)	8	40
23	W	133/155 (86%)	106 (80%)	19 (14%)	8 (6%)	1	13
24	X	118/142 (83%)	103 (87%)	7 (6%)	8 (7%)	1	11
25	Y	124/127 (98%)	107 (86%)	12 (10%)	5 (4%)	2	18
26	Z	133/136 (98%)	107 (80%)	13 (10%)	13 (10%)	0	7
27	a	146/149 (98%)	123 (84%)	18 (12%)	5 (3%)	3	21
28	b	56/59 (95%)	44 (79%)	7 (12%)	5 (9%)	0	8
29	c	98/105 (93%)	87 (89%)	8 (8%)	3 (3%)	3	22
30	d	107/113 (95%)	88 (82%)	13 (12%)	6 (6%)	1	14
31	e	125/130 (96%)	109 (87%)	10 (8%)	6 (5%)	2	16
32	f	104/107 (97%)	96 (92%)	5 (5%)	3 (3%)	3	23
33	g	110/121 (91%)	93 (84%)	13 (12%)	4 (4%)	2	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	h	117/120 (98%)	99 (85%)	14 (12%)	4 (3%)	3	21
35	i	97/100 (97%)	77 (79%)	13 (13%)	7 (7%)	1	11
36	j	85/88 (97%)	75 (88%)	8 (9%)	2 (2%)	4	27
37	k	75/78 (96%)	61 (81%)	10 (13%)	4 (5%)	1	15
38	l	48/51 (94%)	41 (85%)	6 (12%)	1 (2%)	5	30
39	m	50/128 (39%)	48 (96%)	1 (2%)	1 (2%)	6	31
40	n	23/25 (92%)	22 (96%)	0	1 (4%)	2	17
41	o	103/106 (97%)	90 (87%)	11 (11%)	2 (2%)	6	32
42	p	89/92 (97%)	81 (91%)	8 (9%)	0	100	100
43	q	139/312 (45%)	111 (80%)	21 (15%)	7 (5%)	1	16
46	t	376/614 (61%)	354 (94%)	14 (4%)	8 (2%)	5	30
All	All	6868/7529 (91%)	6028 (88%)	588 (9%)	252 (4%)	4	20

All (252) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	96	LEU
2	B	129	ALA
2	B	140	ASP
2	B	347	SER
3	C	14	GLU
3	C	15	ALA
3	C	90	PHE
3	C	145	ILE
3	C	302	ALA
3	C	311	HIS
3	C	329	PRO
3	C	330	TYR
3	C	361	HIS
4	D	215	ASP
4	D	260	PHE
5	E	97	ASN
5	E	98	VAL
6	F	158	LYS
7	G	25	PRO
7	G	26	LEU
7	G	34	PHE
7	G	122	LYS

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Mol	Chain	Res	Type
9	I	25	ALA
9	I	82	ARG
9	I	170	LYS
9	I	175	ASN
9	I	187	ALA
10	J	8	PRO
10	J	10	ARG
10	J	12	LEU
10	J	94	ARG
10	J	95	ASN
10	J	108	GLU
10	J	115	LYS
10	J	167	TYR
12	L	47	ALA
12	L	129	ASN
12	L	134	GLU
12	L	150	PRO
13	M	136	ALA
14	N	49	ARG
14	N	146	ALA
14	N	147	ARG
15	O	110[A]	PRO
15	O	110[B]	PRO
15	O	111[A]	PRO
15	O	111[B]	PRO
15	O	180[A]	SER
15	O	180[B]	SER
15	O	181[A]	ALA
15	O	181[B]	ALA
17	Q	41	ASP
17	Q	99	THR
18	R	35	ALA
19	S	2	ALA
20	T	136	ARG
22	V	42	SER
23	W	26	SER
23	W	71	ARG
23	W	76	VAL
24	X	24	LEU
24	X	25	LYS
24	X	40	LEU
24	X	44	PRO

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Mol	Chain	Res	Type
24	X	45	LYS
25	Y	77	LYS
25	Y	83	ASP
25	Y	84	LYS
25	Y	125	LYS
25	Y	126	LEU
26	Z	5	LEU
26	Z	125	GLY
26	Z	129	TRP
27	a	76	ASP
28	b	21	ILE
28	b	23	LYS
28	b	25	LYS
28	b	39	PHE
29	c	100	ILE
29	c	104	LEU
30	d	7	VAL
30	d	45	GLY
30	d	84	ASP
31	e	4	LEU
31	e	5	PRO
31	e	27	ARG
32	f	88	ASN
33	g	10	ARG
33	g	100	ILE
34	h	40	SER
34	h	82	ALA
35	i	33	ALA
35	i	63	ASN
35	i	64	SER
35	i	98	ARG
36	j	87	SER
37	k	17	ARG
37	k	18	ALA
38	l	3	ALA
41	o	78	LYS
46	t	62	PRO
46	t	169	ILE
1	A	24	GLN
1	A	194	ASN
2	B	235	THR
2	B	293	ASN

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Mol	Chain	Res	Type
3	C	71	VAL
3	C	190	GLY
3	C	272	VAL
3	C	345	GLU
3	C	353	ALA
4	D	125	VAL
4	D	178	ASN
7	G	81	THR
7	G	121	SER
7	G	188	THR
7	G	203	VAL
7	G	223	ALA
7	G	240	ASN
8	H	144	ILE
8	H	189	GLU
9	I	220	GLN
10	J	55	ARG
12	L	135	ALA
12	L	141	ALA
14	N	184	LYS
16	P	66	SER
16	P	67	ILE
17	Q	91	ALA
17	Q	167	SER
21	U	49	ASN
21	U	91	ASP
22	V	41	GLY
23	W	63	ILE
23	W	77	LYS
26	Z	17	ARG
26	Z	93	LYS
26	Z	130	PHE
26	Z	134	LEU
27	a	24	LYS
29	c	10	ILE
30	d	83	GLU
31	e	6	HIS
31	e	12	LYS
31	e	124	GLY
32	f	91	ALA
34	h	119	LYS
40	n	23	ARG

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Mol	Chain	Res	Type
43	q	47	GLY
43	q	198	PRO
46	t	61	VAL
46	t	354	ILE
1	A	56	ALA
1	A	144	ASN
1	A	249	SER
2	B	138	ALA
2	B	155	ALA
3	C	146	PRO
4	D	270	LYS
5	E	10	TYR
5	E	32	ALA
7	G	39	ALA
7	G	123	GLN
7	G	133	LYS
7	G	237	ILE
9	I	83	ASP
9	I	101	LYS
9	I	174	THR
9	I	176	LEU
12	L	101	ARG
12	L	140	SER
14	N	181	ASN
15	O	12[A]	LYS
15	O	12[B]	LYS
21	U	48	GLY
23	W	74	LYS
23	W	134	GLN
24	X	38	LEU
24	X	47	ALA
24	X	55	ASN
26	Z	16	GLY
27	a	47	LYS
30	d	5	LYS
30	d	86	LYS
33	g	79	SER
35	i	34	SER
43	q	33	VAL
43	q	203	ASP
46	t	173	THR
46	t	175	PRO

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Mol	Chain	Res	Type
1	A	143	GLU
2	B	333	LYS
3	C	233	LEU
3	C	306	THR
3	C	331	ALA
3	C	342	LYS
4	D	124	GLU
6	F	191	VAL
7	G	206	GLU
8	H	167	VAL
9	I	207	GLU
12	L	60	ALA
12	L	76	THR
14	N	48	ALA
18	R	147	ALA
23	W	25	ASP
26	Z	34	LYS
26	Z	36	HIS
27	a	121	VAL
33	g	99	LYS
36	j	85	LYS
37	k	8	ILE
37	k	19	ASP
43	q	102	SER
3	C	5	GLN
6	F	229	PHE
7	G	69	LEU
7	G	120	LYS
7	G	124	ASP
8	H	110	LYS
10	J	111	ASP
10	J	153	LYS
12	L	121	SER
17	Q	98	LYS
18	R	183	ALA
20	T	20	ARG
26	Z	7	ALA
27	a	129	PHE
28	b	24	PRO
35	i	9	ILE
39	m	78	ILE
43	q	197	PHE

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Mol	Chain	Res	Type
2	B	187	SER
3	C	328	ASN
6	F	157	ASN
7	G	202	GLU
9	I	204	GLY
10	J	114	ILE
26	Z	29	HIS
34	h	83	LYS
6	F	178	ILE
7	G	190	VAL
43	q	196	VAL
46	t	389	PRO
26	Z	103	GLN
35	i	3	VAL
41	o	31	GLY
46	t	550	VAL
7	G	73	PRO
10	J	118	PRO
17	Q	42	ALA
32	f	59	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	192/196 (98%)	149 (78%)	43 (22%)	1	6
2	B	321/323 (99%)	242 (75%)	79 (25%)	1	4
3	C	288/289 (100%)	213 (74%)	75 (26%)	0	3
4	D	243/245 (99%)	185 (76%)	58 (24%)	1	4
5	E	135/153 (88%)	113 (84%)	22 (16%)	2	10
6	F	187/205 (91%)	158 (84%)	29 (16%)	2	12
7	G	177/208 (85%)	136 (77%)	41 (23%)	1	5
8	H	171/171 (100%)	128 (75%)	43 (25%)	0	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	I	179/187 (96%)	134 (75%)	45 (25%)	0	4
10	J	147/150 (98%)	113 (77%)	34 (23%)	1	5
12	L	154/159 (97%)	126 (82%)	28 (18%)	2	9
13	M	108/109 (99%)	80 (74%)	28 (26%)	0	3
14	N	175/176 (99%)	139 (79%)	36 (21%)	1	6
15	O	323/179 (180%)	254 (79%)	69 (21%)	1	6
16	P	125/146 (86%)	98 (78%)	27 (22%)	1	6
17	Q	150/151 (99%)	121 (81%)	29 (19%)	1	7
18	R	153/154 (99%)	113 (74%)	40 (26%)	0	3
19	S	156/156 (100%)	119 (76%)	37 (24%)	1	4
20	T	136/137 (99%)	107 (79%)	29 (21%)	1	6
21	U	85/107 (79%)	60 (71%)	25 (29%)	0	2
22	V	104/105 (99%)	93 (89%)	11 (11%)	6	21
23	W	100/129 (78%)	83 (83%)	17 (17%)	2	10
24	X	104/118 (88%)	77 (74%)	27 (26%)	0	3
25	Y	109/110 (99%)	81 (74%)	28 (26%)	0	3
26	Z	115/116 (99%)	87 (76%)	28 (24%)	1	4
27	a	118/119 (99%)	90 (76%)	28 (24%)	1	4
28	b	46/47 (98%)	32 (70%)	14 (30%)	0	2
29	c	84/88 (96%)	65 (77%)	19 (23%)	1	6
30	d	94/97 (97%)	72 (77%)	22 (23%)	1	5
31	e	109/111 (98%)	85 (78%)	24 (22%)	1	6
32	f	90/91 (99%)	80 (89%)	10 (11%)	6	20
33	g	95/103 (92%)	70 (74%)	25 (26%)	0	3
34	h	103/105 (98%)	75 (73%)	28 (27%)	0	3
35	i	80/82 (98%)	51 (64%)	29 (36%)	0	1
36	j	70/71 (99%)	55 (79%)	15 (21%)	1	6
37	k	67/69 (97%)	50 (75%)	17 (25%)	0	3
38	l	45/46 (98%)	30 (67%)	15 (33%)	0	2
39	m	47/116 (40%)	35 (74%)	12 (26%)	0	3
40	n	23/23 (100%)	13 (56%)	10 (44%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	o	90/91 (99%)	72 (80%)	18 (20%)	1	7
42	p	71/72 (99%)	59 (83%)	12 (17%)	2	10
43	q	105/254 (41%)	74 (70%)	31 (30%)	0	2
46	t	332/539 (62%)	331 (100%)	1 (0%)	86	86
All	All	5806/6303 (92%)	4548 (78%)	1258 (22%)	3	6

All (1258) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	ILE
1	A	23	ARG
1	A	32	LEU
1	A	41	ILE
1	A	44	ILE
1	A	45	VAL
1	A	46	LYS
1	A	48	ILE
1	A	61	VAL
1	A	62	VAL
1	A	71	LEU
1	A	82	VAL
1	A	96	LEU
1	A	101	VAL
1	A	104	LEU
1	A	109	GLU
1	A	112	ILE
1	A	113	VAL
1	A	119	LYS
1	A	134	VAL
1	A	137	ILE
1	A	142	ASP
1	A	155	LYS
1	A	157	VAL
1	A	158	ILE
1	A	165	VAL
1	A	169	ILE
1	A	179	LEU
1	A	180	LEU
1	A	181	LYS
1	A	188	LYS
1	A	193	ARG

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Mol	Chain	Res	Type
1	A	202	VAL
1	A	207	VAL
1	A	224	THR
1	A	225	ILE
1	A	226	SER
1	A	227	ARG
1	A	230	VAL
1	A	238	ILE
1	A	241	ARG
1	A	243	THR
1	A	246	LEU
2	B	3	HIS
2	B	4	ARG
2	B	10	ARG
2	B	17	LEU
2	B	19	ARG
2	B	21	ARG
2	B	24	SER
2	B	30	LYS
2	B	37	ARG
2	B	43	LEU
2	B	47	LEU
2	B	50	LYS
2	B	56	ILE
2	B	70	ARG
2	B	73	VAL
2	B	77	THR
2	B	79	VAL
2	B	81	THR
2	B	84	VAL
2	B	85	VAL
2	B	89	VAL
2	B	100	ARG
2	B	103	THR
2	B	114	VAL
2	B	116	ARG
2	B	139	GLN
2	B	145	GLU
2	B	146	ARG
2	B	148	LEU
2	B	150	ARG
2	B	153	LYS

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Mol	Chain	Res	Type
2	B	157	VAL
2	B	169	THR
2	B	175	LYS
2	B	183	LEU
2	B	187	SER
2	B	188	ILE
2	B	192	VAL
2	B	196	ARG
2	B	202	THR
2	B	205	VAL
2	B	213	GLU
2	B	218	ILE
2	B	221	THR
2	B	229	VAL
2	B	232	ARG
2	B	235	THR
2	B	238	LEU
2	B	242	THR
2	B	248	LYS
2	B	249	VAL
2	B	252	ILE
2	B	264	VAL
2	B	275	ARG
2	B	282	ILE
2	B	284	ARG
2	B	287	LYS
2	B	291	GLU
2	B	297	SER
2	B	301	THR
2	B	304	THR
2	B	308	MET
2	B	317	ILE
2	B	322	ILE
2	B	324	VAL
2	B	328	ILE
2	B	338	LEU
2	B	340	LYS
2	B	346	THR
2	B	347	SER
2	B	349	LYS
2	B	354	VAL
2	B	355	SER

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Mol	Chain	Res	Type
2	B	361	THR
2	B	367	LYS
2	B	369	ARG
2	B	380	MET
2	B	382	THR
2	B	386	ASP
3	C	2	SER
3	C	3	ARG
3	C	7	THR
3	C	16	THR
3	C	18	ASN
3	C	25	VAL
3	C	27	SER
3	C	40	THR
3	C	47	ARG
3	C	52	VAL
3	C	53	SER
3	C	55	LYS
3	C	69	ARG
3	C	71	VAL
3	C	85	SER
3	C	93	MET
3	C	98	ARG
3	C	112	LYS
3	C	122	THR
3	C	136	LEU
3	C	138	ARG
3	C	144	LYS
3	C	145	ILE
3	C	150	LEU
3	C	152	VAL
3	C	153	SER
3	C	156	LEU
3	C	158	SER
3	C	161	LYS
3	C	170	LYS
3	C	172	VAL
3	C	176	SER
3	C	177	ASP
3	C	179	LEU
3	C	182	LEU
3	C	186	LYS

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Mol	Chain	Res	Type
3	C	187	LEU
3	C	191	LYS
3	C	198	ARG
3	C	200	THR
3	C	203	ARG
3	C	206	LEU
3	C	215	ILE
3	C	217	LYS
3	C	220	ARG
3	C	222	VAL
3	C	230	VAL
3	C	246	ARG
3	C	258	LEU
3	C	259	ASP
3	C	265	GLU
3	C	267	VAL
3	C	283	THR
3	C	286	VAL
3	C	287	THR
3	C	289	ILE
3	C	290	ILE
3	C	300	ARG
3	C	307	GLN
3	C	313	LEU
3	C	319	LYS
3	C	323	VAL
3	C	327	LEU
3	C	333	VAL
3	C	339	LEU
3	C	342	LYS
3	C	345	GLU
3	C	349	THR
3	C	354	VAL
3	C	356	THR
3	C	357	GLU
3	C	358	THR
3	C	359	LEU
3	C	360	LYS
3	C	362	ASP
4	D	4	GLN
4	D	5	LYS
4	D	13	SER

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Mol	Chain	Res	Type
4	D	34	LYS
4	D	35	ARG
4	D	41	LYS
4	D	51	LEU
4	D	64	ILE
4	D	65	ILE
4	D	68	THR
4	D	69	ILE
4	D	70	THR
4	D	73	VAL
4	D	74	VAL
4	D	88	ILE
4	D	89	THR
4	D	93	THR
4	D	110	LEU
4	D	112	LYS
4	D	113	LEU
4	D	115	LEU
4	D	118	THR
4	D	124	GLU
4	D	128	GLU
4	D	131	LEU
4	D	132	THR
4	D	133	GLU
4	D	136	GLU
4	D	144	VAL
4	D	146	LEU
4	D	148	ILE
4	D	152	ARG
4	D	155	THR
4	D	158	ARG
4	D	163	LEU
4	D	164	LYS
4	D	177	GLU
4	D	185	PHE
4	D	186	GLU
4	D	189	GLU
4	D	190	ILE
4	D	194	LEU
4	D	205	SER
4	D	211	LEU
4	D	218	ARG

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Mol	Chain	Res	Type
4	D	227	LEU
4	D	232	ASP
4	D	236	LEU
4	D	241	THR
4	D	254	LYS
4	D	258	LYS
4	D	259	LYS
4	D	262	LYS
4	D	268	GLU
4	D	273	ARG
4	D	275	THR
4	D	279	LYS
4	D	282	ARG
5	E	8	LYS
5	E	20	LYS
5	E	21	THR
5	E	46	ARG
5	E	50	LYS
5	E	52	VAL
5	E	64	LEU
5	E	65	ILE
5	E	76	LEU
5	E	78	ARG
5	E	79	VAL
5	E	89	THR
5	E	91	VAL
5	E	93	VAL
5	E	98	VAL
5	E	99	GLU
5	E	109	GLU
5	E	143	LYS
5	E	151	LYS
5	E	152	THR
5	E	155	LEU
5	E	162	SER
6	F	22	THR
6	F	26	VAL
6	F	39	GLU
6	F	41	ARG
6	F	45	LEU
6	F	53	LYS
6	F	54	GLU

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Mol	Chain	Res	Type
6	F	56	GLU
6	F	60	ARG
6	F	77	VAL
6	F	83	LEU
6	F	88	ARG
6	F	98	LYS
6	F	101	LYS
6	F	121	LYS
6	F	124	LEU
6	F	130	ILE
6	F	156	ILE
6	F	158	LYS
6	F	159	GLN
6	F	173	LEU
6	F	175	LYS
6	F	179	LEU
6	F	184	LEU
6	F	196	LYS
6	F	206	LYS
6	F	219	LYS
6	F	229	PHE
6	F	239	LEU
7	G	26	LEU
7	G	41	GLN
7	G	50	VAL
7	G	67	ILE
7	G	68	ARG
7	G	70	LYS
7	G	71	VAL
7	G	74	THR
7	G	79	GLN
7	G	81	THR
7	G	89	GLU
7	G	92	LYS
7	G	95	ASN
7	G	110	THR
7	G	126	SER
7	G	128	LYS
7	G	136	LEU
7	G	145	ASN
7	G	146	LYS
7	G	149	LYS

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Mol	Chain	Res	Type
7	G	150	LEU
7	G	153	ILE
7	G	160	ILE
7	G	163	VAL
7	G	169	LEU
7	G	172	LYS
7	G	173	MET
7	G	183	LYS
7	G	185	ARG
7	G	189	LEU
7	G	208	GLU
7	G	213	LYS
7	G	214	LEU
7	G	216	SER
7	G	217	THR
7	G	219	ASP
7	G	222	PHE
7	G	230	LYS
7	G	241	LYS
7	G	245	LYS
7	G	248	LYS
8	H	4	ILE
8	H	5	GLN
8	H	6	THR
8	H	16	VAL
8	H	18	VAL
8	H	19	SER
8	H	20	ILE
8	H	31	ARG
8	H	33	THR
8	H	39	LYS
8	H	43	VAL
8	H	44	THR
8	H	52	LEU
8	H	55	VAL
8	H	62	ARG
8	H	63	LYS
8	H	68	LEU
8	H	69	ARG
8	H	70	THR
8	H	71	VAL
8	H	80	THR

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Mol	Chain	Res	Type
8	H	82	VAL
8	H	92	TYR
8	H	106	LYS
8	H	121	LYS
8	H	123	ILE
8	H	124	ARG
8	H	130	ASP
8	H	132	VAL
8	H	133	THR
8	H	134	ILE
8	H	138	THR
8	H	144	ILE
8	H	151	VAL
8	H	161	LEU
8	H	162	GLN
8	H	164	ILE
8	H	169	ASN
8	H	170	LYS
8	H	173	ARG
8	H	179	ILE
8	H	188	THR
8	H	191	LEU
9	I	19	LYS
9	I	24	ARG
9	I	26	VAL
9	I	31	ILE
9	I	32	ARG
9	I	33	ILE
9	I	36	LEU
9	I	42	THR
9	I	48	LEU
9	I	52	LEU
9	I	53	VAL
9	I	57	LEU
9	I	58	GLU
9	I	63	GLU
9	I	69	ARG
9	I	76	MET
9	I	78	THR
9	I	83	ASP
9	I	87	LEU
9	I	91	VAL

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Mol	Chain	Res	Type
9	I	99	ILE
9	I	129	VAL
9	I	135	ILE
9	I	140	THR
9	I	143	SER
9	I	144	ASN
9	I	145	LYS
9	I	153	ARG
9	I	154	ARG
9	I	167	LEU
9	I	169	LYS
9	I	174	THR
9	I	177	ASP
9	I	178	ARG
9	I	182	LEU
9	I	183	LYS
9	I	197	VAL
9	I	200	LEU
9	I	203	LYS
9	I	206	LEU
9	I	210	ILE
9	I	211	ARG
9	I	212	GLU
9	I	215	GLU
9	I	217	PHE
10	J	10	ARG
10	J	12	LEU
10	J	13	LYS
10	J	16	LYS
10	J	22	SER
10	J	30	LEU
10	J	31	THR
10	J	34	SER
10	J	35	LYS
10	J	44	THR
10	J	46	VAL
10	J	80	LEU
10	J	85	LYS
10	J	87	LYS
10	J	92	ARG
10	J	106	ILE
10	J	107	ASP

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Mol	Chain	Res	Type
10	J	108	GLU
10	J	112	LEU
10	J	114	ILE
10	J	129	VAL
10	J	130	VAL
10	J	132	ASN
10	J	137	ARG
10	J	138	VAL
10	J	140	ARG
10	J	142	LYS
10	J	147	THR
10	J	152	HIS
10	J	158	ASP
10	J	159	THR
10	J	160	VAL
10	J	161	SER
10	J	165	GLN
12	L	45	LYS
12	L	46	ILE
12	L	54	LEU
12	L	58	VAL
12	L	59	ARG
12	L	63	VAL
12	L	67	ARG
12	L	68	LYS
12	L	69	VAL
12	L	73	ARG
12	L	85	LEU
12	L	100	ARG
12	L	107	GLU
12	L	114	GLN
12	L	118	GLU
12	L	121	SER
12	L	123	ILE
12	L	124	ILE
12	L	131	LYS
12	L	152	THR
12	L	154	VAL
12	L	164	GLU
12	L	168	ARG
12	L	171	ARG
12	L	176	GLU

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Mol	Chain	Res	Type
12	L	184	GLU
12	L	189	GLU
12	L	194	GLU
13	M	3	THR
13	M	10	SER
13	M	13	ARG
13	M	15	VAL
13	M	20	VAL
13	M	24	LYS
13	M	27	GLN
13	M	42	LYS
13	M	53	VAL
13	M	58	ILE
13	M	62	GLN
13	M	63	VAL
13	M	64	VAL
13	M	72	LEU
13	M	74	ARG
13	M	80	THR
13	M	82	SER
13	M	92	GLU
13	M	106	ARG
13	M	107	GLU
13	M	108	ARG
13	M	124	ARG
13	M	126	GLN
13	M	128	ARG
13	M	130	THR
13	M	132	LYS
13	M	133	LYS
13	M	135	LEU
14	N	5	LYS
14	N	7	LEU
14	N	8	GLU
14	N	10	LEU
14	N	12	ARG
14	N	15	GLN
14	N	18	VAL
14	N	22	LEU
14	N	24	ARG
14	N	41	ARG
14	N	49	ARG

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Mol	Chain	Res	Type
14	N	54	LYS
14	N	60	VAL
14	N	68	ARG
14	N	80	THR
14	N	83	LYS
14	N	85	THR
14	N	91	GLU
14	N	92	LEU
14	N	96	ARG
14	N	97	SER
14	N	98	LEU
14	N	104	GLU
14	N	105	ARG
14	N	106	VAL
14	N	109	ARG
14	N	134	LEU
14	N	138	GLN
14	N	155	VAL
14	N	170	LYS
14	N	176	LYS
14	N	184	LYS
14	N	190	THR
14	N	194	GLN
14	N	196	THR
14	N	204	LYS
15	O	3[A]	VAL
15	O	3[B]	SER
15	O	12[A]	LYS
15	O	12[B]	LYS
15	O	22[A]	VAL
15	O	22[B]	THR
15	O	25[A]	LYS
15	O	25[B]	LYS
15	O	34[A]	VAL
15	O	34[B]	VAL
15	O	41[A]	LEU
15	O	41[B]	LEU
15	O	58[A]	LEU
15	O	58[B]	LEU
15	O	59[A]	ARG
15	O	59[B]	ARG
15	O	60[A]	LYS

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Mol	Chain	Res	Type
15	O	60[B]	LYS
15	O	67[A]	THR
15	O	67[B]	THR
15	O	74[A]	ARG
15	O	74[B]	ARG
15	O	78[A]	ARG
15	O	78[B]	ARG
15	O	85[A]	ARG
15	O	85[B]	ARG
15	O	100[A]	GLU
15	O	100[B]	GLU
15	O	102[A]	LEU
15	O	102[B]	LEU
15	O	106[A]	GLU
15	O	106[B]	GLU
15	O	108[A]	ILE
15	O	108[B]	ILE
15	O	115[A]	LYS
15	O	115[B]	LYS
15	O	117[A]	ARG
15	O	117[B]	ARG
15	O	124[A]	LEU
15	O	124[B]	LEU
15	O	126[A]	VAL
15	O	126[B]	VAL
15	O	128[A]	ARG
15	O	128[B]	ARG
15	O	129[A]	LEU
15	O	129[B]	LEU
15	O	130[A]	LYS
15	O	130[B]	LYS
15	O	134[A]	LYS
15	O	134[B]	LYS
15	O	140[A]	LYS
15	O	140[B]	LYS
15	O	144[A]	SER
15	O	144[B]	SER
15	O	160[A]	ARG
15	O	160[B]	ARG
15	O	166[A]	GLU
15	O	166[B]	GLU
15	O	171[A]	LYS

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Mol	Chain	Res	Type
15	O	171[B]	LYS
15	O	175[A]	THR
15	O	175[B]	THR
15	O	182[A]	ASN
15	O	182[B]	SER
15	O	184[A]	THR
15	O	187[A]	GLU
15	O	187[B]	GLU
15	O	197[A]	LEU
15	O	197[B]	PHE
16	P	9	THR
16	P	23	ARG
16	P	24	VAL
16	P	29	THR
16	P	31	GLU
16	P	32	THR
16	P	41	LEU
16	P	51	VAL
16	P	52	LEU
16	P	56	ARG
16	P	58	ILE
16	P	69	ARG
16	P	74	LYS
16	P	78	VAL
16	P	79	THR
16	P	80	LYS
16	P	89	LYS
16	P	94	LEU
16	P	103	GLU
16	P	112	LEU
16	P	114	VAL
16	P	119	VAL
16	P	124	LYS
16	P	126	ARG
16	P	127	ARG
16	P	128	ARG
16	P	138	LYS
17	Q	3	ILE
17	Q	7	SER
17	Q	17	THR
17	Q	24	VAL
17	Q	26	LEU

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Mol	Chain	Res	Type
17	Q	31	LYS
17	Q	32	LEU
17	Q	34	THR
17	Q	49	LEU
17	Q	57	ILE
17	Q	64	VAL
17	Q	72	LYS
17	Q	80	THR
17	Q	81	VAL
17	Q	86	THR
17	Q	93	ILE
17	Q	100	THR
17	Q	105	ARG
17	Q	113	LYS
17	Q	129	VAL
17	Q	135	GLN
17	Q	138	LEU
17	Q	141	ARG
17	Q	150	VAL
17	Q	161	LYS
17	Q	165	ILE
17	Q	166	LEU
17	Q	168	THR
17	Q	170	ARG
18	R	5	ARG
18	R	7	GLN
18	R	10	LEU
18	R	14	VAL
18	R	17	VAL
18	R	20	ARG
18	R	27	ASN
18	R	29	THR
18	R	36	ASN
18	R	43	LYS
18	R	49	THR
18	R	55	VAL
18	R	56	THR
18	R	57	VAL
18	R	63	THR
18	R	70	LYS
18	R	71	ARG
18	R	74	ARG

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Mol	Chain	Res	Type
18	R	98	ARG
18	R	99	LEU
18	R	101	VAL
18	R	105	LEU
18	R	106	LEU
18	R	108	LYS
18	R	114	LYS
18	R	117	LYS
18	R	126	GLU
18	R	128	LYS
18	R	133	LYS
18	R	138	LEU
18	R	146	LYS
18	R	152	GLU
18	R	153	LYS
18	R	158	GLU
18	R	162	ARG
18	R	164	LEU
18	R	167	ARG
18	R	173	ARG
18	R	177	VAL
18	R	180	LYS
19	S	1	MET
19	S	13	ARG
19	S	15	PRO
19	S	17	GLU
19	S	21	GLU
19	S	23	LYS
19	S	40	ARG
19	S	45	LEU
19	S	50	LYS
19	S	51	VAL
19	S	52	LYS
19	S	58	ILE
19	S	61	ILE
19	S	71	LYS
19	S	73	LYS
19	S	74	ASN
19	S	80	ARG
19	S	87	THR
19	S	97	VAL
19	S	100	VAL

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Mol	Chain	Res	Type
19	S	104	GLU
19	S	105	THR
19	S	115	ARG
19	S	117	ARG
19	S	130	GLU
19	S	132	THR
19	S	136	LYS
19	S	137	ARG
19	S	146	LYS
19	S	148	LEU
19	S	149	LYS
19	S	155	ARG
19	S	161	LYS
19	S	162	THR
19	S	166	LYS
19	S	169	SER
19	S	172	TYR
20	T	12	ARG
20	T	17	ARG
20	T	25	VAL
20	T	27	LEU
20	T	35	LYS
20	T	36	VAL
20	T	55	LYS
20	T	68	THR
20	T	71	SER
20	T	78	LYS
20	T	80	VAL
20	T	83	ARG
20	T	88	ARG
20	T	89	LEU
20	T	96	ILE
20	T	102	ARG
20	T	104	GLU
20	T	118	GLU
20	T	126	VAL
20	T	130	ARG
20	T	131	GLN
20	T	135	PRO
20	T	139	ARG
20	T	140	ILE
20	T	141	VAL

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Mol	Chain	Res	Type
20	T	143	THR
20	T	149	GLN
20	T	150	THR
20	T	160	ILE
21	U	13	LYS
21	U	14	THR
21	U	16	THR
21	U	17	VAL
21	U	21	SER
21	U	23	THR
21	U	27	VAL
21	U	37	LEU
21	U	38	ILE
21	U	39	ASP
21	U	43	VAL
21	U	50	LEU
21	U	54	VAL
21	U	55	THR
21	U	58	GLU
21	U	61	THR
21	U	62	VAL
21	U	63	VAL
21	U	64	THR
21	U	68	THR
21	U	81	LYS
21	U	90	ARG
21	U	98	THR
21	U	100	THR
21	U	105	LEU
22	V	13	ILE
22	V	32	ARG
22	V	48	ARG
22	V	64	LYS
22	V	66	LYS
22	V	70	ARG
22	V	73	VAL
22	V	88	ARG
22	V	91	VAL
22	V	115	THR
22	V	125	LEU
23	W	1	MET
23	W	5	ILE

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Mol	Chain	Res	Type
23	W	25	ASP
23	W	34	SER
23	W	39	LEU
23	W	57	LYS
23	W	63	ILE
23	W	92	GLU
23	W	95	SER
23	W	97	LYS
23	W	98	PRO
23	W	100	VAL
23	W	105	ARG
23	W	107	GLU
23	W	126	GLU
23	W	127	LYS
23	W	135	SER
24	X	24	LEU
24	X	27	ARG
24	X	34	LEU
24	X	37	THR
24	X	38	LEU
24	X	39	LYS
24	X	40	LEU
24	X	45	LYS
24	X	56	ARG
24	X	57	LEU
24	X	63	ILE
24	X	65	GLN
24	X	70	GLU
24	X	71	THR
24	X	73	MET
24	X	74	LYS
24	X	81	ILE
24	X	86	VAL
24	X	101	GLU
24	X	108	LEU
24	X	109	LYS
24	X	115	ARG
24	X	121	LYS
24	X	125	ARG
24	X	133	LEU
24	X	135	ILE
24	X	142	ILE

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Mol	Chain	Res	Type
25	Y	4	GLN
25	Y	12	ARG
25	Y	13	ARG
25	Y	14	LYS
25	Y	17	LYS
25	Y	37	LYS
25	Y	40	ARG
25	Y	43	TYR
25	Y	45	ILE
25	Y	50	ILE
25	Y	52	ARG
25	Y	56	VAL
25	Y	57	LEU
25	Y	59	VAL
25	Y	66	GLN
25	Y	70	ILE
25	Y	71	SER
25	Y	76	LEU
25	Y	80	VAL
25	Y	83	ASP
25	Y	87	LYS
25	Y	90	VAL
25	Y	94	SER
25	Y	95	VAL
25	Y	97	ILE
25	Y	103	LYS
25	Y	115	ARG
25	Y	120	GLN
26	Z	3	LYS
26	Z	14	VAL
26	Z	17	ARG
26	Z	24	VAL
26	Z	30	ASP
26	Z	31	GLU
26	Z	34	LYS
26	Z	36	HIS
26	Z	55	LYS
26	Z	65	ARG
26	Z	72	ILE
26	Z	81	LEU
26	Z	83	THR
26	Z	86	THR

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Mol	Chain	Res	Type
26	Z	89	VAL
26	Z	93	LYS
26	Z	95	VAL
26	Z	99	GLU
26	Z	100	THR
26	Z	102	GLU
26	Z	103	GLN
26	Z	105	SER
26	Z	119	GLU
26	Z	121	ARG
26	Z	126	LYS
26	Z	127	ASN
26	Z	134	LEU
26	Z	135	ARG
27	a	4	ARG
27	a	6	THR
27	a	8	THR
27	a	12	ARG
27	a	16	SER
27	a	24	LYS
27	a	34	MET
27	a	42	ARG
27	a	44	ASN
27	a	46	ASP
27	a	47	LYS
27	a	56	VAL
27	a	60	TYR
27	a	65	GLN
27	a	78	LEU
27	a	80	THR
27	a	82	ILE
27	a	85	ASP
27	a	91	LEU
27	a	97	GLU
27	a	98	THR
27	a	115	LYS
27	a	124	ILE
27	a	128	ARG
27	a	130	VAL
27	a	132	LYS
27	a	133	LEU
27	a	139	ARG

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Mol	Chain	Res	Type
28	b	3	LYS
28	b	14	ARG
28	b	15	LYS
28	b	21	ILE
28	b	22	LYS
28	b	23	LYS
28	b	26	THR
28	b	33	LYS
28	b	35	VAL
28	b	38	LYS
28	b	50	THR
28	b	52	LYS
28	b	58	LYS
28	b	59	LYS
29	c	8	GLU
29	c	10	ILE
29	c	17	VAL
29	c	18	ILE
29	c	19	LYS
29	c	30	THR
29	c	32	LYS
29	c	33	SER
29	c	34	LEU
29	c	41	LEU
29	c	48	THR
29	c	68	TYR
29	c	69	TYR
29	c	76	GLU
29	c	83	LYS
29	c	86	ARG
29	c	87	VAL
29	c	99	ASP
29	c	100	ILE
30	d	6	ASP
30	d	8	VAL
30	d	13	THR
30	d	16	LEU
30	d	26	LYS
30	d	31	ARG
30	d	34	LYS
30	d	36	ILE
30	d	44	MET

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Mol	Chain	Res	Type
30	d	55	LEU
30	d	61	LYS
30	d	76	SER
30	d	82	GLU
30	d	89	LEU
30	d	90	PHE
30	d	96	VAL
30	d	100	SER
30	d	102	LYS
30	d	104	LEU
30	d	105	GLN
30	d	106	THR
30	d	110	GLU
31	e	4	LEU
31	e	8	LYS
31	e	14	THR
31	e	16	LYS
31	e	18	LYS
31	e	19	ARG
31	e	27	ARG
31	e	31	ASN
31	e	33	ARG
31	e	35	GLN
31	e	38	ILE
31	e	41	VAL
31	e	51	SER
31	e	61	LYS
31	e	73	THR
31	e	75	LEU
31	e	76	VAL
31	e	82	LEU
31	e	87	MET
31	e	91	THR
31	e	106	VAL
31	e	109	LEU
31	e	125	ARG
31	e	126	LEU
32	f	4	SER
32	f	10	LYS
32	f	28	SER
32	f	31	LYS
32	f	49	ILE

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Mol	Chain	Res	Type
32	f	70	LYS
32	f	81	VAL
32	f	84	THR
32	f	98	VAL
32	f	107	ILE
33	g	5	VAL
33	g	9	ARG
33	g	16	ARG
33	g	19	LYS
33	g	20	ILE
33	g	23	VAL
33	g	24	LYS
33	g	29	ILE
33	g	30	LEU
33	g	31	ARG
33	g	35	VAL
33	g	54	ILE
33	g	58	ARG
33	g	65	VAL
33	g	70	LYS
33	g	79	SER
33	g	85	VAL
33	g	86	LYS
33	g	87	GLU
33	g	88	ARG
33	g	90	ILE
33	g	98	GLN
33	g	102	LYS
33	g	104	VAL
33	g	105	VAL
34	h	15	GLU
34	h	20	GLN
34	h	21	LEU
34	h	27	GLU
34	h	28	LEU
34	h	38	ARG
34	h	40	SER
34	h	45	LYS
34	h	47	VAL
34	h	48	ARG
34	h	57	VAL
34	h	62	GLN

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Mol	Chain	Res	Type
34	h	66	VAL
34	h	68	GLN
34	h	69	LEU
34	h	79	ASP
34	h	81	ARG
34	h	84	LYS
34	h	85	THR
34	h	89	ARG
34	h	90	ARG
34	h	94	LYS
34	h	98	SER
34	h	100	VAL
34	h	101	THR
34	h	107	LYS
34	h	115	LYS
34	h	119	LYS
35	i	3	VAL
35	i	7	ILE
35	i	9	ILE
35	i	11	LEU
35	i	17	VAL
35	i	18	THR
35	i	21	THR
35	i	26	ILE
35	i	29	LYS
35	i	34	SER
35	i	36	ARG
35	i	37	THR
35	i	38	LYS
35	i	40	VAL
35	i	43	LEU
35	i	45	ARG
35	i	57	LEU
35	i	58	ILE
35	i	60	LEU
35	i	61	ILE
35	i	66	GLU
35	i	68	ARG
35	i	74	LYS
35	i	75	LYS
35	i	76	ARG
35	i	81	THR

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Mol	Chain	Res	Type
35	i	88	GLU
35	i	94	ILE
35	i	98	ARG
36	j	3	LYS
36	j	17	THR
36	j	25	ARG
36	j	33	THR
36	j	36	SER
36	j	44	THR
36	j	55	ARG
36	j	58	THR
36	j	59	THR
36	j	65	ARG
36	j	67	LEU
36	j	68	LYS
36	j	75	LYS
36	j	80	THR
36	j	84	SER
37	k	5	ILE
37	k	12	LEU
37	k	24	THR
37	k	27	ILE
37	k	31	LEU
37	k	39	ARG
37	k	41	THR
37	k	46	ARG
37	k	50	SER
37	k	53	THR
37	k	61	LYS
37	k	63	LYS
37	k	64	LYS
37	k	65	LEU
37	k	66	ILE
37	k	67	GLN
37	k	68	SER
38	l	11	GLN
38	l	12	LYS
38	l	15	LYS
38	l	17	LYS
38	l	21	ARG
38	l	23	LEU
38	l	27	ILE

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Mol	Chain	Res	Type
38	l	28	ARG
38	l	29	LEU
38	l	30	ARG
38	l	41	ARG
38	l	45	ARG
38	l	47	THR
38	l	48	LYS
38	l	51	ILE
39	m	78	ILE
39	m	83	LYS
39	m	85	LEU
39	m	88	LYS
39	m	91	CYS
39	m	93	LYS
39	m	106	ARG
39	m	112	LYS
39	m	113	ARG
39	m	114	LYS
39	m	126	LYS
39	m	127	LEU
40	n	2	ARG
40	n	6	ARG
40	n	9	ARG
40	n	10	THR
40	n	13	LEU
40	n	16	LYS
40	n	19	LYS
40	n	21	ARG
40	n	23	ARG
40	n	24	SER
41	o	7	THR
41	o	8	ARG
41	o	15	LYS
41	o	16	THR
41	o	18	ARG
41	o	46	LYS
41	o	47	GLN
41	o	61	LYS
41	o	63	LYS
41	o	71	ARG
41	o	78	LYS
41	o	79	THR

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Mol	Chain	Res	Type
41	o	83	LEU
41	o	84	THR
41	o	89	LYS
41	o	93	LEU
41	o	104	LEU
41	o	105	GLN
42	p	3	LYS
42	p	16	VAL
42	p	22	LEU
42	p	24	ARG
42	p	42	CYS
42	p	48	LYS
42	p	49	ARG
42	p	54	ILE
42	p	56	THR
42	p	73	THR
42	p	79	VAL
42	p	90	VAL
43	q	4	ILE
43	q	5	ARG
43	q	10	GLU
43	q	17	GLU
43	q	30	VAL
43	q	32	ASN
43	q	41	VAL
43	q	42	ARG
43	q	43	LYS
43	q	44	GLU
43	q	50	VAL
43	q	51	VAL
43	q	52	LEU
43	q	55	LYS
43	q	57	THR
43	q	67	LEU
43	q	68	SER
43	q	70	LEU
43	q	74	GLU
43	q	76	LEU
43	q	79	PHE
43	q	80	VAL
43	q	81	LYS
43	q	84	VAL

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Mol	Chain	Res	Type
43	q	91	GLU
43	q	93	LEU
43	q	96	ILE
43	q	97	LYS
43	q	185	LEU
43	q	188	VAL
43	q	196	VAL
46	t	417	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (63) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	209	HIS
1	A	215	ASN
2	B	211	GLN
2	B	371	GLN
3	C	5	GLN
3	C	48	GLN
3	C	114	ASN
3	C	116	ASN
3	C	175	HIS
3	C	213	ASN
3	C	221	ASN
3	C	291	ASN
4	D	4	GLN
4	D	40	HIS
4	D	57	ASN
4	D	63	GLN
4	D	81	HIS
5	E	167	ASN
6	F	64	GLN
6	F	225	GLN
7	G	33	ASN
7	G	191	ASN
8	H	59	ASN
8	H	96	HIS
8	H	125	ASN
8	H	162	GLN
9	I	59	GLN
10	J	68	HIS
10	J	95	ASN
10	J	109	HIS

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Mol	Chain	Res	Type
10	J	132	ASN
13	M	126	GLN
16	P	55	GLN
17	Q	9	GLN
17	Q	73	GLN
18	R	34	GLN
18	R	175	GLN
20	T	49	GLN
22	V	7	GLN
22	V	33	ASN
23	W	42	GLN
23	W	59	HIS
24	X	94	GLN
26	Z	36	HIS
26	Z	57	HIS
27	a	44	ASN
27	a	62	HIS
27	a	65	GLN
29	c	71	GLN
31	e	49	ASN
32	f	77	ASN
33	g	52	GLN
37	k	10	GLN
38	l	11	GLN
38	l	33	ASN
43	q	36	GLN
43	q	37	GLN
43	q	83	ASN
46	t	33	GLN
46	t	82	ASN
46	t	156	HIS
46	t	394	HIS
46	t	533	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
47	1	0/114	-	-
48	5	3145/3396 (92%)	747 (23%)	129 (4%)
49	7	120/121 (99%)	18 (15%)	0
50	8	157/158 (99%)	33 (21%)	3 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	3422/3789 (90%)	798 (23%)	132 (3%)

All (798) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
48	5	14	U
48	5	15	C
48	5	16	A
48	5	26	A
48	5	38	U
48	5	40	A
48	5	43	A
48	5	44	U
48	5	49	A
48	5	60	A
48	5	65	A
48	5	66	A
48	5	74	G
48	5	76	G
48	5	77	A
48	5	92	G
48	5	93	C
48	5	94	G
48	5	96	G
48	5	99	A
48	5	109	A
48	5	110	G
48	5	111	C
48	5	116	A
48	5	121	A
48	5	122	A
48	5	133	U
48	5	134	U
48	5	135	C
48	5	136	G
48	5	146	U
48	5	150	A
48	5	152	U
48	5	156	G
48	5	157	A
48	5	160	G
48	5	166	C

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Mol	Chain	Res	Type
48	5	170	G
48	5	171	G
48	5	174	C
48	5	178	U
48	5	180	C
48	5	182	U
48	5	183	G
48	5	184	U
48	5	187	A
48	5	190	U
48	5	191	U
48	5	200	C
48	5	201	A
48	5	210	U
48	5	218	G
48	5	219	A
48	5	221	A
48	5	235	A
48	5	236	G
48	5	238	A
48	5	239	G
48	5	240	U
48	5	242	C
48	5	244	G
48	5	248	U
48	5	249	U
48	5	250	U
48	5	251	G
48	5	252	U
48	5	253	A
48	5	254	A
48	5	258	G
48	5	259	C
48	5	269	G
48	5	283	G
48	5	284	A
48	5	286	U
48	5	294	U
48	5	295	A
48	5	305	U
48	5	322	U
48	5	323	A

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Mol	Chain	Res	Type
48	5	329	U
48	5	334	A
48	5	339	C
48	5	349	A
48	5	350	C
48	5	351	A
48	5	352	A
48	5	370	U
48	5	376	G
48	5	390	G
48	5	395	A
48	5	397	A
48	5	398	A
48	5	399	A
48	5	401	U
48	5	402	A
48	5	403	C
48	5	421	G
48	5	422	A
48	5	436	A
48	5	437	G
48	5	438	A
48	5	439	C
48	5	440	A
48	5	441	U
48	5	442	G
48	5	443	G
48	5	492	U
48	5	493	G
48	5	495	G
48	5	520	U
48	5	521	A
48	5	531	G
48	5	535	G
48	5	538	G
48	5	546	C
48	5	547	G
48	5	548	G
48	5	551	A
48	5	553	U
48	5	555	U
48	5	557	A

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Mol	Chain	Res	Type
48	5	559	A
48	5	578	A
48	5	579	G
48	5	588	G
48	5	589	A
48	5	592	A
48	5	594	U
48	5	595	G
48	5	600	G
48	5	604	G
48	5	609	G
48	5	610	G
48	5	611	A
48	5	612	U
48	5	619	A
48	5	620	U
48	5	621	A
48	5	630	A
48	5	636	C
48	5	649	A
48	5	653	A
48	5	656	A
48	5	660	A
48	5	675	C
48	5	677	A
48	5	681	U
48	5	705	A
48	5	708	G
48	5	712	G
48	5	715	A
48	5	716	A
48	5	719	U
48	5	720	A
48	5	725	G
48	5	726	G
48	5	727	G
48	5	735	A
48	5	736	A
48	5	750	G
48	5	758	C
48	5	766	U
48	5	767	U

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Mol	Chain	Res	Type
48	5	768	C
48	5	776	U
48	5	777	U
48	5	780	A
48	5	781	G
48	5	785	G
48	5	786	A
48	5	787	G
48	5	806	A
48	5	809	G
48	5	817	A
48	5	830	A
48	5	846	A
48	5	851	C
48	5	861	C
48	5	862	U
48	5	871	U
48	5	874	U
48	5	879	U
48	5	891	G
48	5	893	C
48	5	896	A
48	5	897	U
48	5	907	G
48	5	908	G
48	5	914	A
48	5	916	G
48	5	917	A
48	5	921	A
48	5	923	C
48	5	924	G
48	5	937	G
48	5	944	C
48	5	946	U
48	5	947	G
48	5	958	C
48	5	959	C
48	5	960	U
48	5	974	G
48	5	979	U
48	5	980	A
48	5	981	U

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Mol	Chain	Res	Type
48	5	983	A
48	5	993	G
48	5	994	G
48	5	1000	C
48	5	1001	G
48	5	1002	A
48	5	1003	A
48	5	1010	G
48	5	1014	U
48	5	1015	U
48	5	1016	C
48	5	1017	C
48	5	1018	G
48	5	1020	G
48	5	1021	G
48	5	1023	C
48	5	1024	G
48	5	1025	A
48	5	1026	A
48	5	1027	A
48	5	1028	U
48	5	1029	G
48	5	1032	C
48	5	1034	U
48	5	1035	G
48	5	1047	A
48	5	1049	C
48	5	1057	A
48	5	1064	A
48	5	1065	A
48	5	1071	U
48	5	1072	G
48	5	1081	U
48	5	1082	U
48	5	1085	A
48	5	1086	C
48	5	1093	A
48	5	1094	U
48	5	1095	U
48	5	1096	U
48	5	1097	G
48	5	1098	A

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Mol	Chain	Res	Type
48	5	1103	A
48	5	1104	G
48	5	1117	G
48	5	1131	G
48	5	1153	A
48	5	1159	A
48	5	1160	C
48	5	1174	G
48	5	1178	G
48	5	1179	A
48	5	1180	A
48	5	1181	U
48	5	1182	A
48	5	1191	U
48	5	1192	C
48	5	1193	A
48	5	1201	C
48	5	1209	G
48	5	1213	G
48	5	1222	G
48	5	1223	A
48	5	1232	C
48	5	1233	G
48	5	1236	G
48	5	1237	G
48	5	1239	C
48	5	1240	A
48	5	1241	U
48	5	1242	G
48	5	1243	G
48	5	1245	A
48	5	1246	G
48	5	1248	C
48	5	1258	U
48	5	1259	A
48	5	1262	G
48	5	1263	A
48	5	1264	G
48	5	1265	U
48	5	1266	G
48	5	1270	A
48	5	1281	G

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Mol	Chain	Res	Type
48	5	1285	G
48	5	1294	A
48	5	1307	G
48	5	1308	A
48	5	1309	U
48	5	1312	C
48	5	1317	A
48	5	1318	A
48	5	1330	A
48	5	1331	U
48	5	1332	A
48	5	1348	U
48	5	1349	G
48	5	1350	A
48	5	1351	U
48	5	1352	A
48	5	1353	U
48	5	1354	G
48	5	1355	A
48	5	1356	U
48	5	1357	G
48	5	1366	A
48	5	1385	C
48	5	1386	A
48	5	1387	G
48	5	1399	A
48	5	1400	G
48	5	1403	C
48	5	1419	A
48	5	1422	G
48	5	1428	A
48	5	1434	G
48	5	1435	A
48	5	1437	C
48	5	1440	G
48	5	1446	A
48	5	1450	G
48	5	1460	A
48	5	1481	A
48	5	1482	A
48	5	1490	A
48	5	1495	U

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Mol	Chain	Res	Type
48	5	1502	C
48	5	1503	A
48	5	1508	C
48	5	1527	C
48	5	1541	G
48	5	1542	G
48	5	1549	U
48	5	1554	U
48	5	1555	U
48	5	1556	C
48	5	1557	A
48	5	1560	G
48	5	1561	G
48	5	1562	C
48	5	1563	C
48	5	1565	G
48	5	1566	A
48	5	1567	U
48	5	1568	U
48	5	1569	U
48	5	1570	U
48	5	1571	A
48	5	1572	U
48	5	1574	C
48	5	1575	A
48	5	1576	G
48	5	1577	G
48	5	1578	C
48	5	1580	A
48	5	1581	C
48	5	1582	C
48	5	1583	A
48	5	1587	A
48	5	1589	A
48	5	1593	A
48	5	1605	A
48	5	1607	U
48	5	1608	C
48	5	1620	U
48	5	1629	U
48	5	1633	C
48	5	1635	G

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Mol	Chain	Res	Type
48	5	1639	C
48	5	1641	U
48	5	1643	A
48	5	1644	C
48	5	1645	U
48	5	1655	G
48	5	1657	C
48	5	1680	G
48	5	1683	A
48	5	1716	U
48	5	1717	U
48	5	1718	G
48	5	1724	U
48	5	1725	C
48	5	1736	G
48	5	1750	A
48	5	1751	G
48	5	1754	G
48	5	1758	G
48	5	1760	A
48	5	1762	C
48	5	1764	U
48	5	1765	U
48	5	1766	G
48	5	1767	C
48	5	1770	G
48	5	1778	G
48	5	1780	G
48	5	1783	U
48	5	1797	A
48	5	1810	A
48	5	1812	G
48	5	1814	A
48	5	1815	U
48	5	1816	A
48	5	1817	G
48	5	1818	U
48	5	1820	U
48	5	1821	U
48	5	1835	A
48	5	1841	A
48	5	1842	A

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Mol	Chain	Res	Type
48	5	1846	C
48	5	1849	C
48	5	1850	A
48	5	1855	U
48	5	1871	U
48	5	1876	U
48	5	1878	G
48	5	1879	A
48	5	1880	U
48	5	1905	G
48	5	1906	G
48	5	1909	A
48	5	1918	C
48	5	1927	G
48	5	1940	G
48	5	1953	G
48	5	2100	A
48	5	2101	C
48	5	2102	U
48	5	2112	U
48	5	2113	A
48	5	2114	C
48	5	2121	G
48	5	2122	G
48	5	2128	C
48	5	2131	A
48	5	2134	G
48	5	2139	A
48	5	2144	A
48	5	2158	A
48	5	2169	G
48	5	2170	U
48	5	2171	G
48	5	2192	C
48	5	2201	G
48	5	2205	U
48	5	2210	G
48	5	2213	A
48	5	2222	A
48	5	2223	A
48	5	2228	A
48	5	2229	A

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Mol	Chain	Res	Type
48	5	2244	A
48	5	2250	G
48	5	2253	G
48	5	2255	A
48	5	2256	A
48	5	2257	C
48	5	2258	U
48	5	2264	U
48	5	2270	A
48	5	2273	G
48	5	2276	G
48	5	2278	C
48	5	2279	A
48	5	2288	G
48	5	2290	C
48	5	2294	U
48	5	2298	U
48	5	2307	G
48	5	2310	U
48	5	2313	A
48	5	2315	G
48	5	2324	A
48	5	2329	C
48	5	2334	U
48	5	2335	G
48	5	2336	U
48	5	2373	A
48	5	2374	C
48	5	2375	G
48	5	2377	G
48	5	2385	G
48	5	2388	U
48	5	2393	G
48	5	2394	G
48	5	2396	G
48	5	2397	A
48	5	2398	A
48	5	2400	G
48	5	2401	A
48	5	2402	A
48	5	2403	G
48	5	2404	A

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Mol	Chain	Res	Type
48	5	2405	C
48	5	2406	C
48	5	2411	U
48	5	2418	G
48	5	2435	G
48	5	2436	U
48	5	2437	G
48	5	2438	A
48	5	2439	A
48	5	2440	G
48	5	2441	A
48	5	2443	A
48	5	2504	U
48	5	2505	U
48	5	2506	U
48	5	2507	C
48	5	2508	U
48	5	2510	U
48	5	2511	A
48	5	2512	C
48	5	2513	U
48	5	2514	U
48	5	2515	A
48	5	2518	C
48	5	2523	A
48	5	2524	A
48	5	2526	C
48	5	2530	G
48	5	2531	C
48	5	2532	U
48	5	2534	G
48	5	2538	U
48	5	2539	C
48	5	2540	A
48	5	2543	U
48	5	2544	U
48	5	2549	G
48	5	2552	C
48	5	2555	G
48	5	2562	A
48	5	2567	C
48	5	2568	C

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Mol	Chain	Res	Type
48	5	2569	A
48	5	2570	U
48	5	2571	U
48	5	2572	C
48	5	2573	G
48	5	2574	G
48	5	2584	G
48	5	2585	G
48	5	2589	G
48	5	2590	A
48	5	2591	A
48	5	2593	A
48	5	2594	C
48	5	2598	G
48	5	2599	U
48	5	2606	G
48	5	2607	G
48	5	2610	G
48	5	2614	G
48	5	2615	G
48	5	2622	C
48	5	2637	A
48	5	2639	G
48	5	2652	U
48	5	2656	A
48	5	2662	G
48	5	2663	G
48	5	2667	A
48	5	2674	A
48	5	2677	G
48	5	2678	A
48	5	2681	U
48	5	2683	U
48	5	2689	A
48	5	2691	A
48	5	2694	A
48	5	2696	A
48	5	2714	G
48	5	2723	U
48	5	2728	G
48	5	2729	U
48	5	2752	U

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Mol	Chain	Res	Type
48	5	2753	G
48	5	2762	A
48	5	2771	U
48	5	2772	C
48	5	2773	C
48	5	2776	C
48	5	2777	G
48	5	2778	G
48	5	2779	A
48	5	2796	G
48	5	2799	A
48	5	2800	G
48	5	2801	A
48	5	2810	C
48	5	2817	A
48	5	2818	U
48	5	2819	A
48	5	2822	U
48	5	2829	U
48	5	2839	G
48	5	2844	C
48	5	2845	A
48	5	2853	A
48	5	2871	G
48	5	2872	A
48	5	2873	U
48	5	2875	U
48	5	2887	A
48	5	2888	U
48	5	2889	C
48	5	2896	A
48	5	2897	A
48	5	2898	G
48	5	2899	C
48	5	2904	U
48	5	2910	A
48	5	2923	U
48	5	2928	C
48	5	2935	U
48	5	2936	A
48	5	2941	A
48	5	2942	C

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Mol	Chain	Res	Type
48	5	2945	G
48	5	2947	G
48	5	2954	U
48	5	2957	G
48	5	2970	C
48	5	2971	A
48	5	2972	G
48	5	2979	U
48	5	2983	C
48	5	2987	A
48	5	2990	G
48	5	2996	U
48	5	2997	G
48	5	3012	A
48	5	3028	G
48	5	3050	U
48	5	3056	U
48	5	3057	U
48	5	3059	G
48	5	3078	U
48	5	3079	U
48	5	3080	G
48	5	3086	A
48	5	3087	A
48	5	3092	C
48	5	3130	A
48	5	3131	U
48	5	3139	A
48	5	3142	A
48	5	3143	C
48	5	3148	U
48	5	3153	U
48	5	3154	C
48	5	3155	U
48	5	3156	U
48	5	3157	U
48	5	3158	G
48	5	3159	C
48	5	3164	C
48	5	3165	A
48	5	3166	C
48	5	3168	A

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Mol	Chain	Res	Type
48	5	3171	U
48	5	3172	A
48	5	3173	G
48	5	3174	A
48	5	3175	U
48	5	3176	G
48	5	3177	G
48	5	3179	U
48	5	3180	A
48	5	3181	C
48	5	3187	A
48	5	3195	U
48	5	3196	U
48	5	3207	U
48	5	3217	C
48	5	3218	A
48	5	3219	G
48	5	3222	U
48	5	3223	A
48	5	3224	G
48	5	3227	A
48	5	3229	G
48	5	3238	G
48	5	3245	A
48	5	3246	G
48	5	3247	G
48	5	3251	U
48	5	3253	G
48	5	3259	U
48	5	3260	G
48	5	3269	U
48	5	3270	U
48	5	3273	A
48	5	3275	U
48	5	3276	G
48	5	3277	U
48	5	3279	A
48	5	3280	U
48	5	3282	U
48	5	3284	G
48	5	3285	C
48	5	3286	G

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Mol	Chain	Res	Type
48	5	3288	G
48	5	3289	G
48	5	3290	G
48	5	3292	A
48	5	3294	A
48	5	3304	U
48	5	3307	A
48	5	3313	U
48	5	3316	A
48	5	3317	U
48	5	3318	G
48	5	3319	U
48	5	3320	A
48	5	3330	A
48	5	3331	U
48	5	3333	G
48	5	3335	A
48	5	3336	A
48	5	3341	U
48	5	3342	A
48	5	3343	G
48	5	3345	G
48	5	3349	C
48	5	3351	U
48	5	3352	U
48	5	3354	U
48	5	3355	U
48	5	3356	G
48	5	3357	U
48	5	3358	U
48	5	3369	G
48	5	3378	C
48	5	3382	U
48	5	3383	G
48	5	3389	U
48	5	3390	G
48	5	3393	U
48	5	3396	U
49	7	7	G
49	7	22	A
49	7	27	A
49	7	33	U

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Mol	Chain	Res	Type
49	7	38	U
49	7	42	A
49	7	54	U
49	7	61	G
49	7	65	G
49	7	66	A
49	7	73	C
49	7	74	C
49	7	93	C
49	7	101	G
49	7	102	A
49	7	103	A
49	7	104	A
49	7	112	G
50	8	21	C
50	8	34	U
50	8	35	C
50	8	48	A
50	8	52	A
50	8	53	A
50	8	59	A
50	8	62	C
50	8	63	G
50	8	79	A
50	8	80	A
50	8	81	U
50	8	83	C
50	8	84	C
50	8	86	U
50	8	87	G
50	8	90	U
50	8	95	G
50	8	104	A
50	8	105	A
50	8	106	C
50	8	111	A
50	8	112	U
50	8	113	U
50	8	122	U
50	8	125	U
50	8	126	A
50	8	127	U

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Mol	Chain	Res	Type
50	8	138	A
50	8	152	G
50	8	156	U
50	8	157	U
50	8	158	U

All (132) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
48	5	43	A
48	5	65	A
48	5	93	C
48	5	151	A
48	5	169	U
48	5	183	G
48	5	217	U
48	5	238	A
48	5	282	G
48	5	397	A
48	5	436	A
48	5	438	A
48	5	439	C
48	5	545	U
48	5	546	C
48	5	588	G
48	5	611	A
48	5	619	A
48	5	647	A
48	5	705	A
48	5	715	A
48	5	719	U
48	5	726	G
48	5	735	A
48	5	765	C
48	5	786	A
48	5	816	A
48	5	873	C
48	5	896	A
48	5	908	G
48	5	916	G
48	5	937	G
48	5	979	U

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Mol	Chain	Res	Type
48	5	993	G
48	5	1027	A
48	5	1033	U
48	5	1064	A
48	5	1081	U
48	5	1085	A
48	5	1094	U
48	5	1152	G
48	5	1181	U
48	5	1192	C
48	5	1222	G
48	5	1236	G
48	5	1238	C
48	5	1239	C
48	5	1241	U
48	5	1284	C
48	5	1307	G
48	5	1317	A
48	5	1329	U
48	5	1331	U
48	5	1352	A
48	5	1355	A
48	5	1434	G
48	5	1481	A
48	5	1507	G
48	5	1514	G
48	5	1554	U
48	5	1560	G
48	5	1568	U
48	5	1574	C
48	5	1580	A
48	5	1589	A
48	5	1607	U
48	5	1716	U
48	5	1724	U
48	5	1815	U
48	5	1816	A
48	5	1817	G
48	5	1819	U
48	5	1841	A
48	5	1842	A
48	5	1849	C

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Mol	Chain	Res	Type
48	5	1878	G
48	5	1879	A
48	5	2101	C
48	5	2112	U
48	5	2116	G
48	5	2204	C
48	5	2209	U
48	5	2249	G
48	5	2255	A
48	5	2257	C
48	5	2372	A
48	5	2374	C
48	5	2440	G
48	5	2507	C
48	5	2513	U
48	5	2531	C
48	5	2537	U
48	5	2539	C
48	5	2583	C
48	5	2585	G
48	5	2593	A
48	5	2662	G
48	5	2682	C
48	5	2689	A
48	5	2714	G
48	5	2728	G
48	5	2752	U
48	5	2772	C
48	5	2777	G
48	5	2801	A
48	5	2817	A
48	5	2818	U
48	5	2887	A
48	5	2896	A
48	5	2970	C
48	5	2971	A
48	5	2996	U
48	5	3056	U
48	5	3078	U
48	5	3154	C
48	5	3155	U
48	5	3167	A

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Mol	Chain	Res	Type
48	5	3195	U
48	5	3218	A
48	5	3228	C
48	5	3259	U
48	5	3269	U
48	5	3275	U
48	5	3289	G
48	5	3317	U
48	5	3330	A
48	5	3340	G
48	5	3341	U
48	5	3357	U
50	8	111	A
50	8	126	A
50	8	156	U

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
11	K	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	K	52:UNK	C	54:UNK	N	3.86
1	K	23:UNK	C	28:UNK	N	3.48

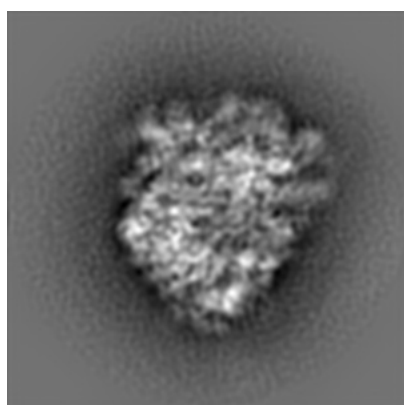
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2169. These allow visual inspection of the internal detail of the map and identification of artifacts.

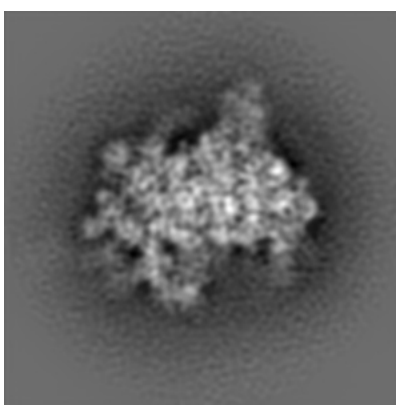
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

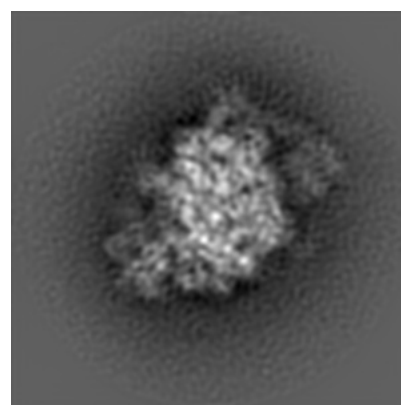
6.1.1 Primary map



X



Y

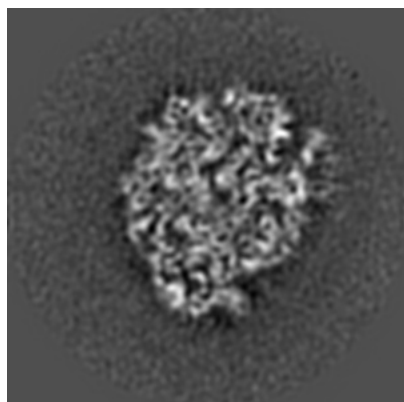


Z

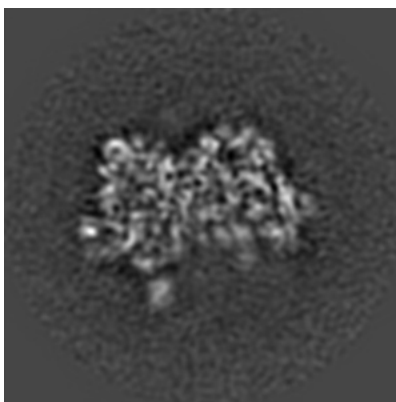
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

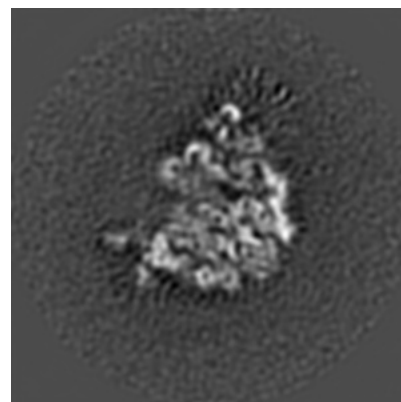
6.2.1 Primary map



X Index: 112



Y Index: 112

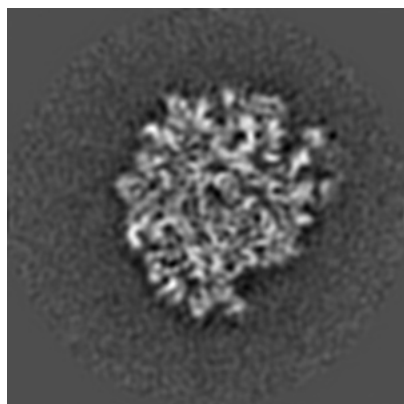


Z Index: 112

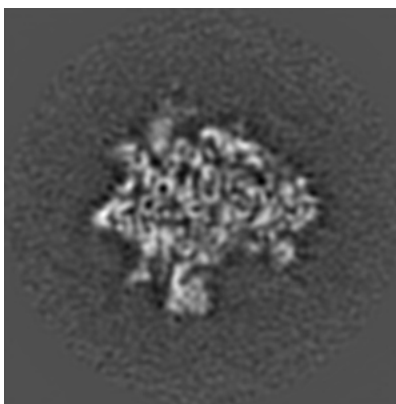
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

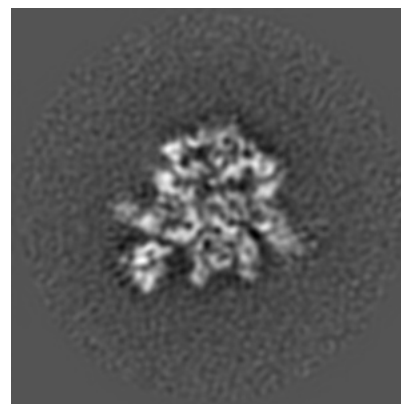
6.3.1 Primary map



X Index: 115



Y Index: 95

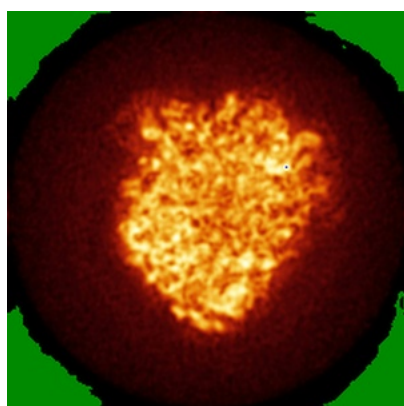


Z Index: 84

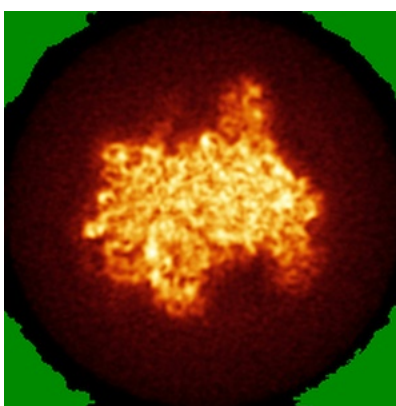
The images above show the largest variance slices of the map in three orthogonal directions.

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

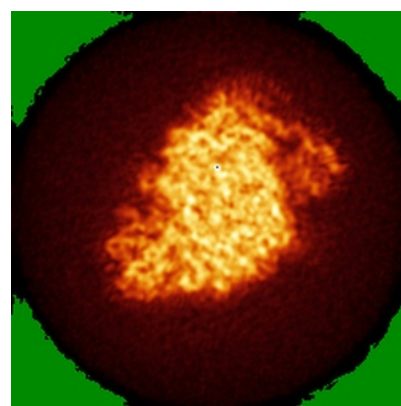
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 35.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

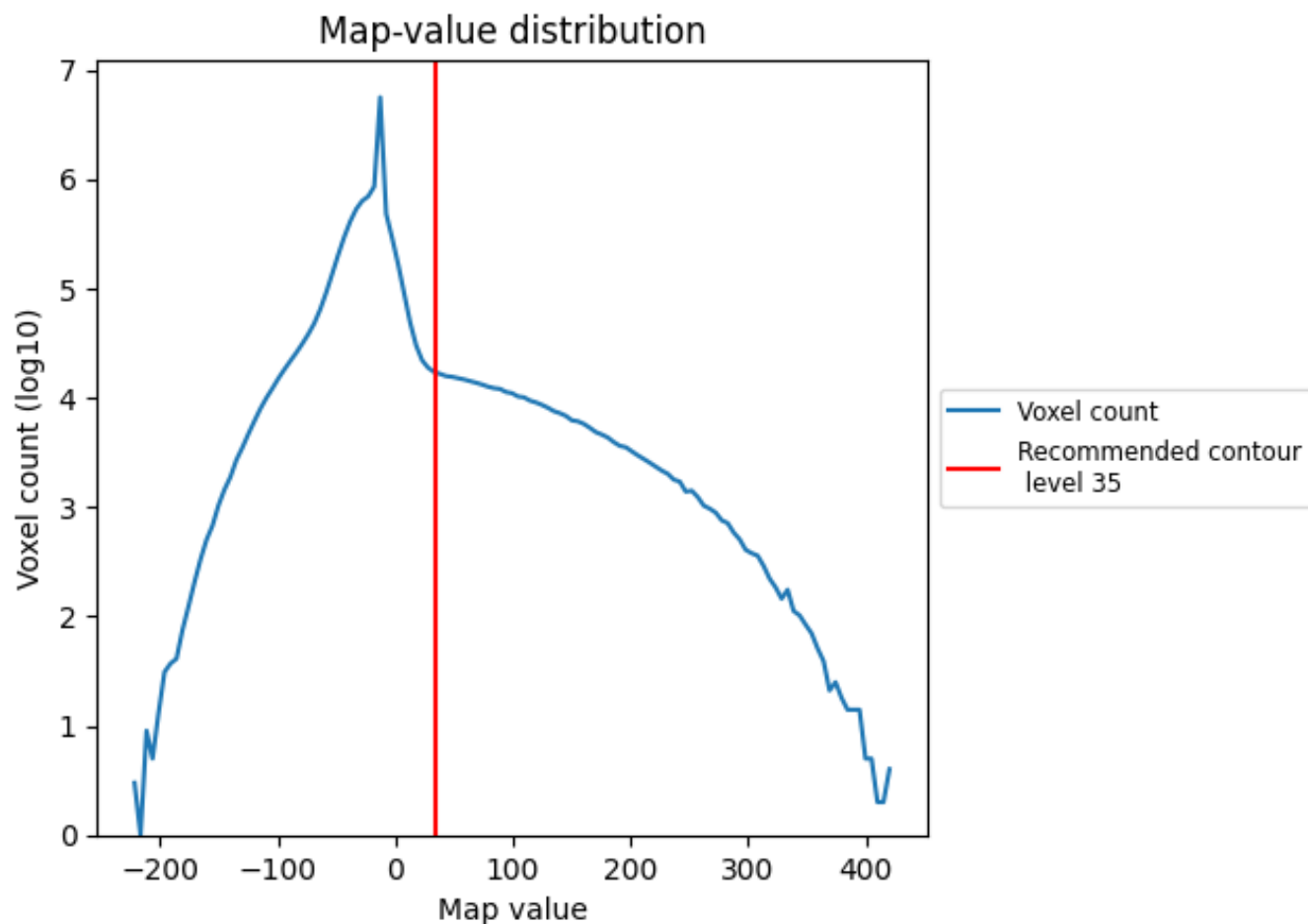
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

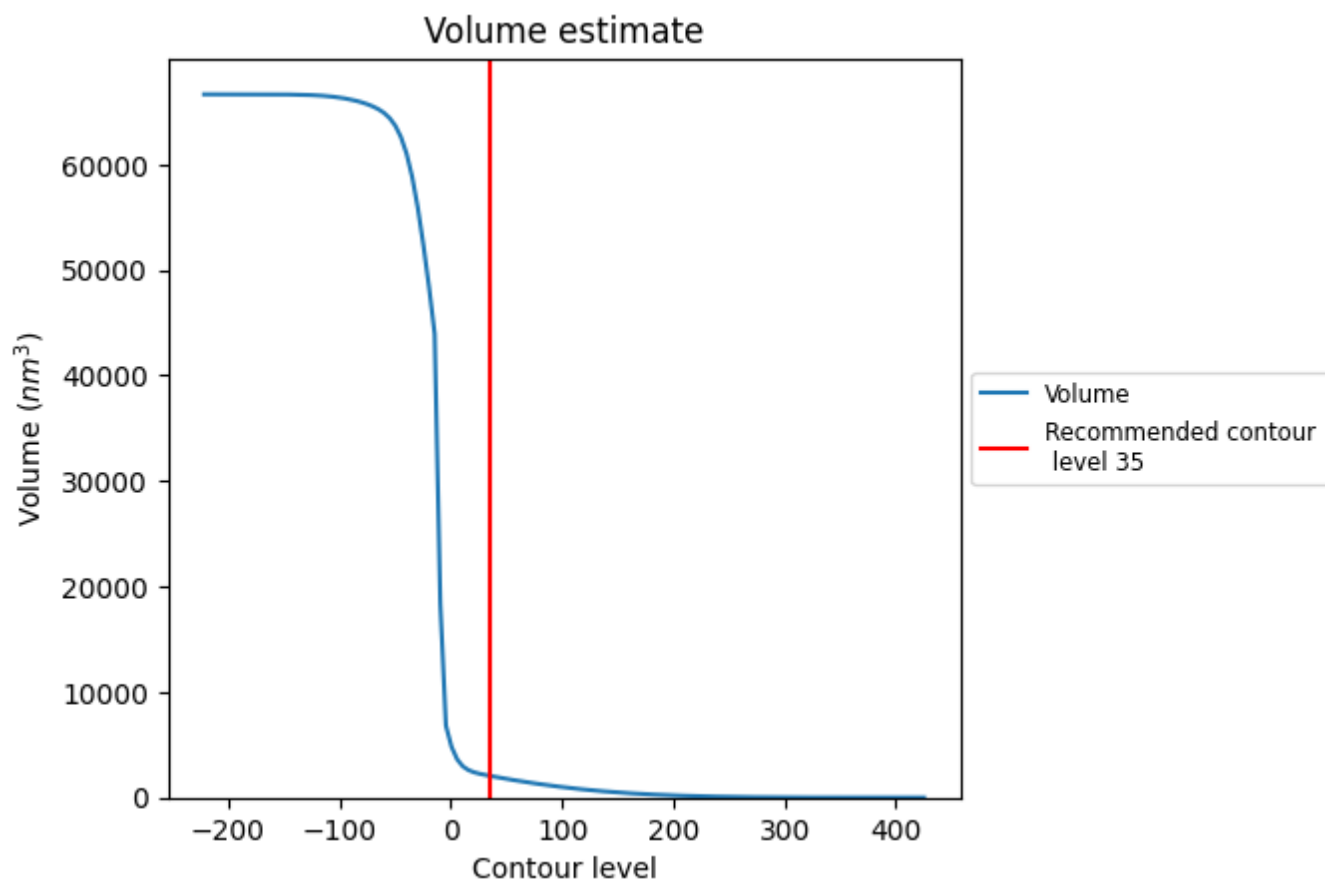
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

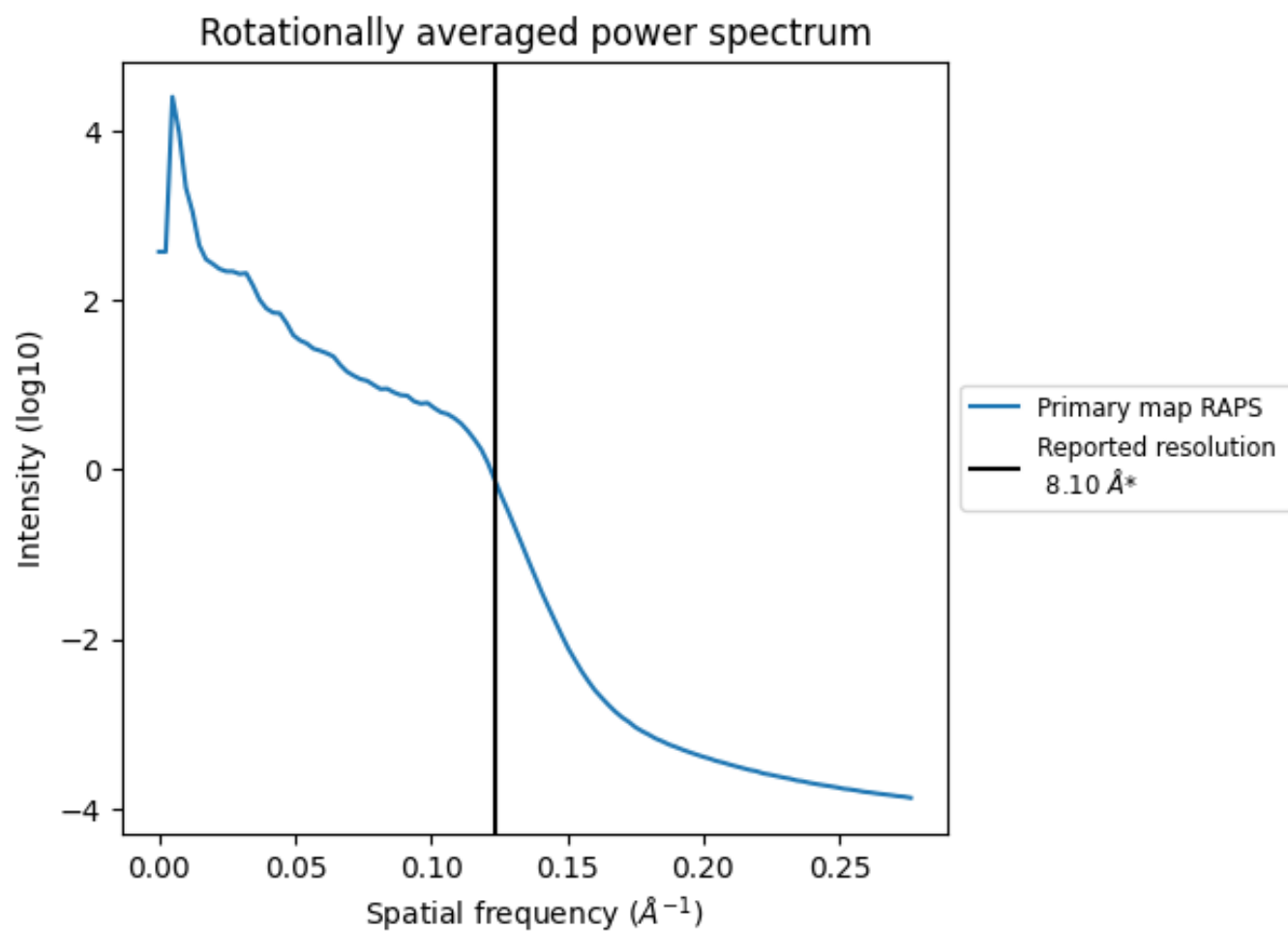
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2057 nm³; this corresponds to an approximate mass of 1858 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 0.123 Å⁻¹

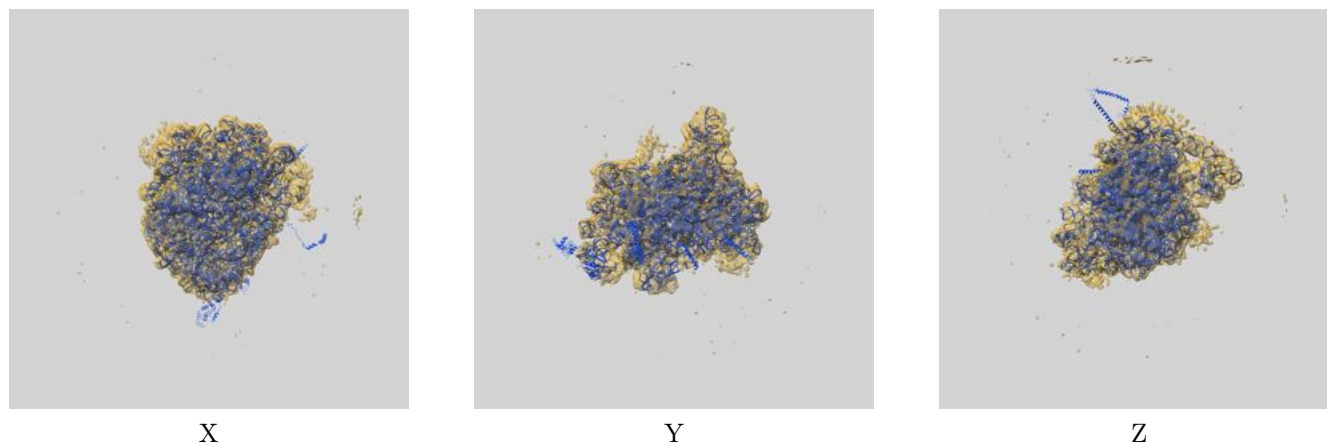
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

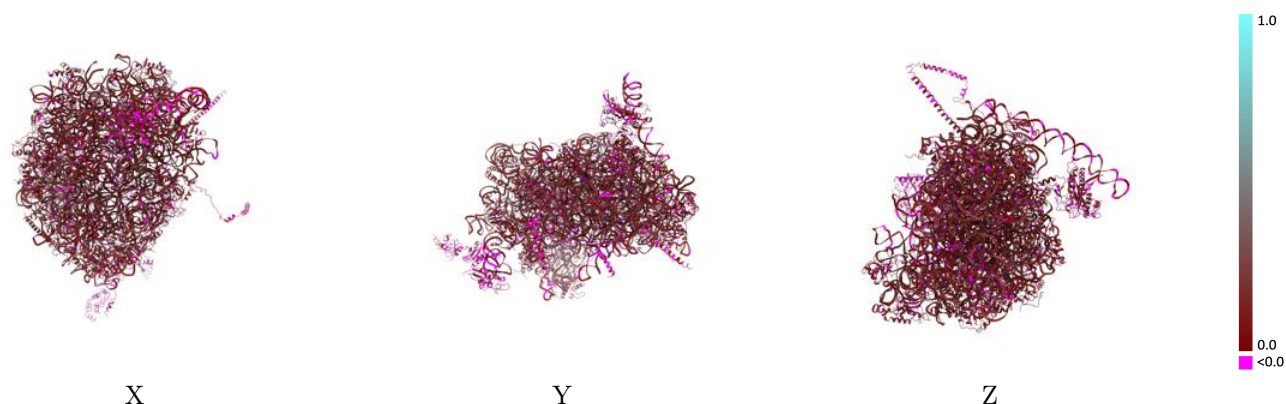
This section contains information regarding the fit between EMDB map EMD-2169 and PDB model 4V8T. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



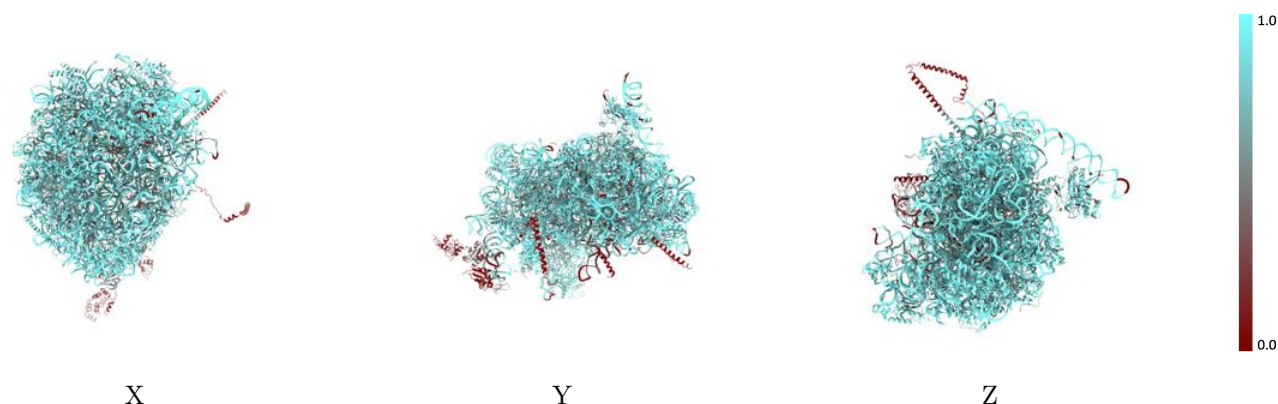
The images above show the 3D surface view of the map at the recommended contour level 35.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



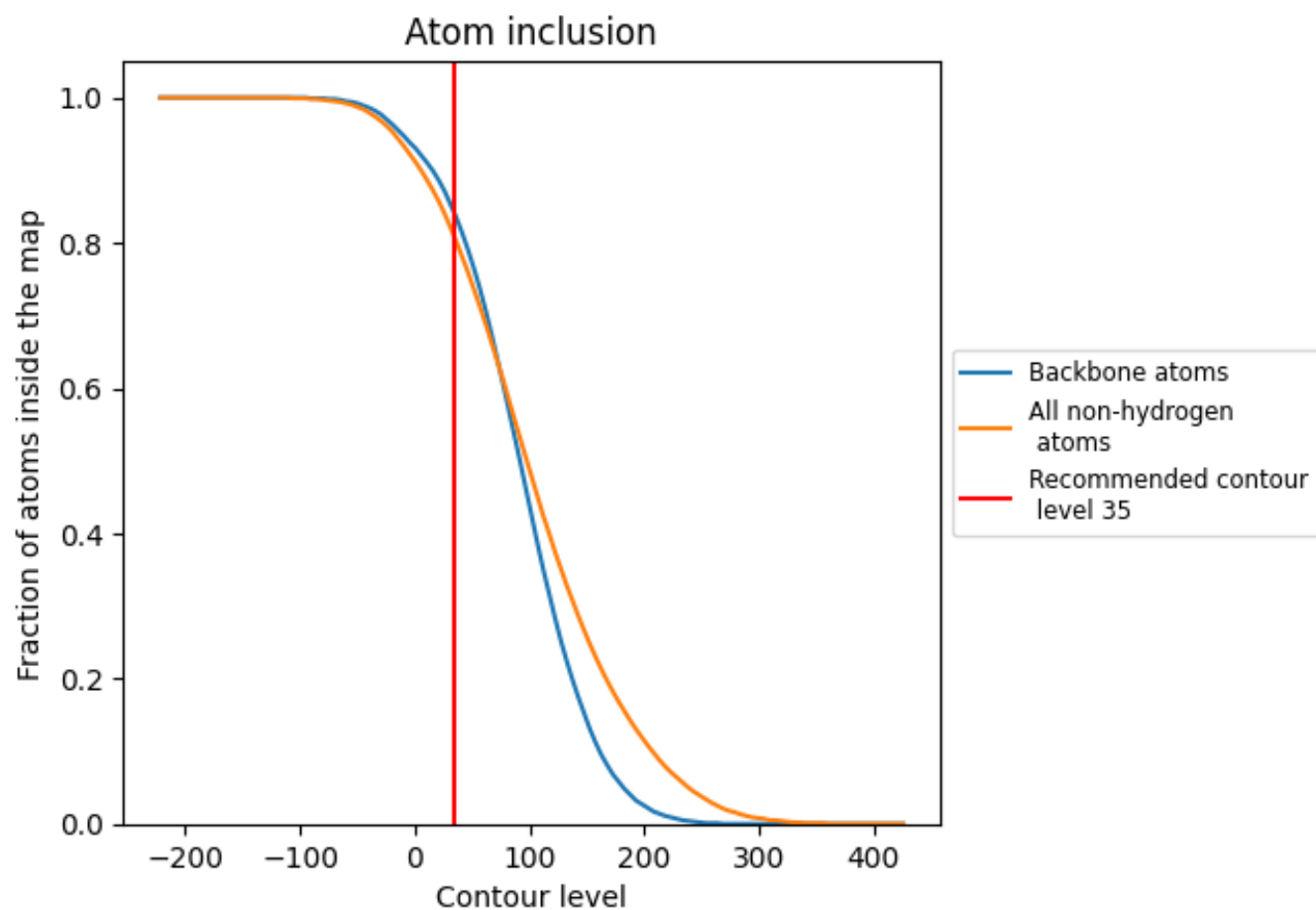
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (35).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 81% 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 (35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8060	 0.1350
1	 0.9210	 0.0730
5	 0.8850	 0.1540
7	 0.9700	 0.1670
8	 0.9200	 0.1690
A	 0.5420	 0.0710
B	 0.7000	 0.1060
C	 0.7170	 0.1120
D	 0.8100	 0.1160
E	 0.8080	 0.1310
F	 0.7420	 0.1380
G	 0.8230	 0.1300
H	 0.8120	 0.1290
I	 0.6820	 0.0940
J	 0.8520	 0.1170
K	 0.1310	 0.0320
L	 0.7830	 0.1380
M	 0.8550	 0.1500
N	 0.5560	 0.0810
O	 0.7690	 0.1420
P	 0.6700	 0.1020
Q	 0.6930	 0.1130
R	 0.5720	 0.1050
S	 0.7620	 0.1180
T	 0.7100	 0.1150
U	 0.7660	 0.1080
V	 0.6610	 0.1040
W	 0.3990	 0.0710
X	 0.7100	 0.1280
Y	 0.7650	 0.1130
Z	 0.7740	 0.1330
a	 0.6720	 0.1030
b	 0.6130	 0.1190
c	 0.7960	 0.1400
d	 0.7210	 0.1200



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Chain	Atom inclusion	Q-score
e	 0.6100	 0.1120
f	 0.7350	 0.1050
g	 0.5900	 0.0950
h	 0.7940	 0.1410
i	 0.7570	 0.1360
j	 0.6720	 0.0960
k	 0.8340	 0.1360
l	 0.5300	 0.1020
m	 0.7150	 0.1130
n	 0.0000	 -0.0490
o	 0.6250	 0.0810
p	 0.7700	 0.1110
q	 0.2200	 0.0110
r	 0.0000	 0.0090
s	 0.0000	 0.0190
t	 0.8060	 0.0840