



Full wwPDB EM Validation Report ⓘ

Apr 15, 2026 – 03:04 AM UTC

PDB ID : 6XDQ / pdb_00006xdq
EMDB ID : EMD-22141
Title : Cryo-EM structure of an Escherichia coli coupled transcription-translational complex B3 (TTC-B3) containing an mRNA with a 30 nt long spacer, transcription factors NusA and NusG, and fMet-tRNAs at P-site and E-site
Authors : Molodtsov, V.; Ebright, R.H.; Wang, C.; Su, M.
Deposited on : 2020-06-11
Resolution : 3.70 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

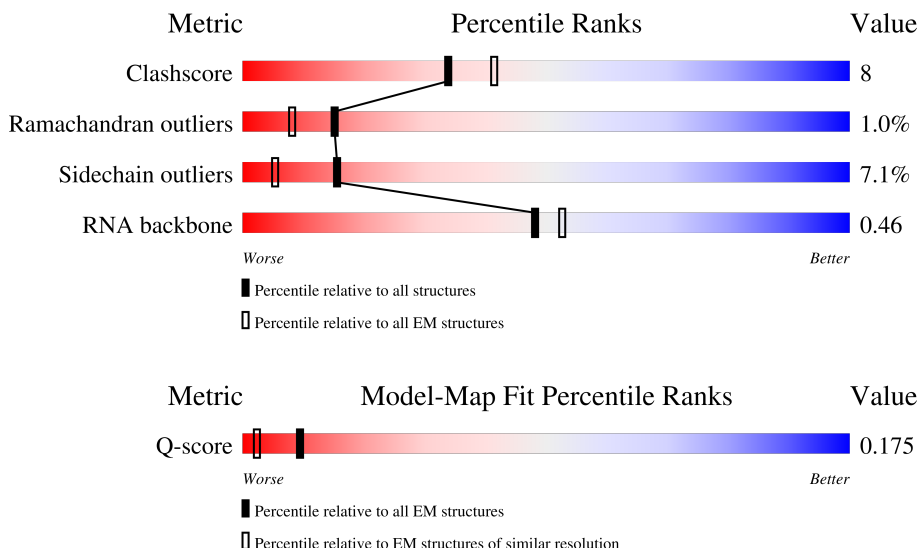
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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.



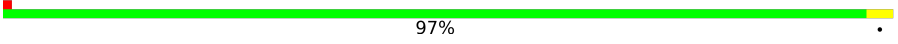
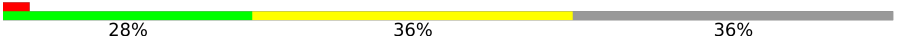
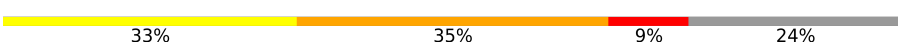
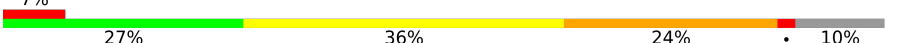
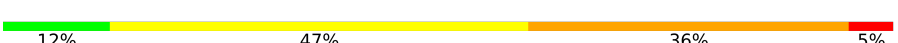
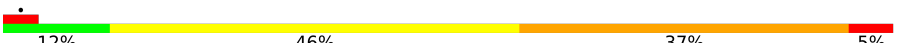
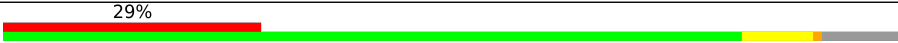
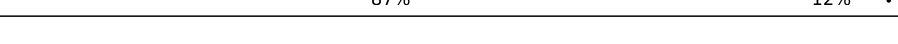
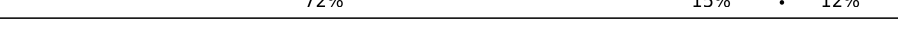
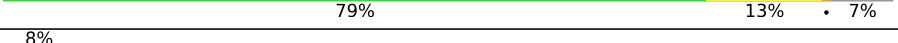
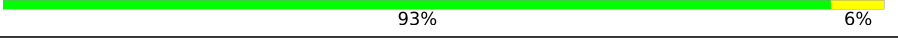
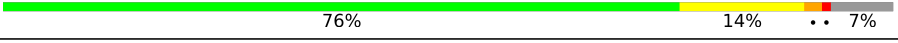
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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

Mol	Chain	Length	Quality of chain
1	0	103	84% 15% .
2	1	110	75% 25%
3	2	100	86% 6% . 6%

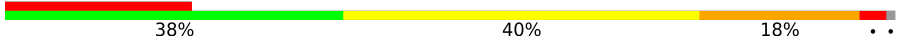
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Mol	Chain	Length	Quality of chain
4	3	104	
5	4	94	
6	5	36	
7	6	36	
8	7	46	
9	9	165	
10	A	76	
10	B	76	
11	AA	1342	
12	AB	181	
13	AC	329	
13	AD	329	
14	AE	1407	
15	AF	91	
16	AG	495	
17	C	75	
18	D	1542	
19	E	87	
20	F	71	
21	G	241	
22	H	557	
23	I	233	
24	J	206	
25	K	167	
26	L	135	

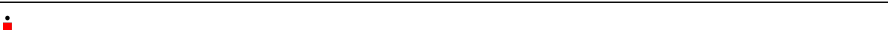
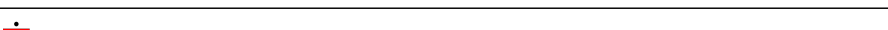
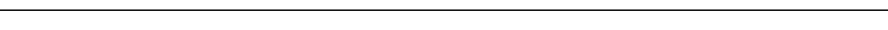
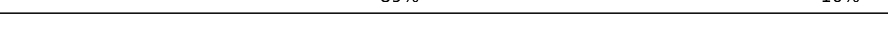
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Mol	Chain	Length	Quality of chain
27	M	179	
28	N	130	
29	O	130	
30	P	103	
31	Q	129	
32	R	124	
33	S	101	
34	T	89	
35	U	82	
36	V	84	
37	W	92	
38	X	118	
39	Y	142	
40	Z	121	
41	a	2904	
42	b	85	
43	c	78	
44	d	120	
45	e	63	
46	f	59	
47	g	70	
48	h	273	
49	i	57	
50	j	209	
51	k	55	

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Mol	Chain	Length	Quality of chain
52	l	201	 85% 13% .
53	m	46	 78% 17% .
54	n	179	 75% 20% ..
55	o	65	 88% 8% ..
56	p	177	 90% 8% .
57	q	38	 89% 8% .
58	r	149	 5% 88% 9% .
59	s	142	 83% 15% .
60	t	123	 80% 18% .
61	u	144	 90% 10%
62	v	136	 91% 8% .
63	w	127	 76% 18% 6%
64	x	117	 84% 15% ..
65	y	115	 89% 10% .
66	z	118	 84% 14% ..

2 Entry composition

There are 68 unique types of molecules in this entry. The entry contains 290243 atoms, of which 109912 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 50S ribosomal protein L21.

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

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

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

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

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

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

Mol	Chain	Residues	Atoms						AltConf	Trace
4	3	103	Total	C	H	N	O		0	0
			1632	498	844	148	142			

- Molecule 5 is a protein called 50S ribosomal protein L25.

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

- Molecule 6 is a DNA chain called NT DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	5	23	Total	C	H	N	O	P	0	0
			732	225	260	87	137	23		

- Molecule 7 is a DNA chain called T DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	6	27	Total	C	H	N	O	P	0	0
			847	259	305	89	167	27		

- Molecule 8 is a RNA chain called mRNA with 30 nt long spacer.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	7	35	Total	C	H	N	O	P	0	0
			824	325	97	100	267	35		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	9	148	Total	C	N	O	S	0	0
			1117	705	196	209	7		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
10	A	76	Total	C	H	N	O	P	0	0
			2446	723	826	295	527	75		
10	B	76	Total	C	H	N	O	P	0	0
			2433	723	813	295	527	75		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AA	1340	Total	C	N	O	S	0	0
			10567	6631	1841	2052	43		

- Molecule 12 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AB	161	Total	C	N	O	S	0	0
			1276	813	221	235	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AC	301	Total	C	N	O	S	0	0
			2091	1295	379	411	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	AD	298	Total	C	N	O	S	0	0
			2073	1284	377	406	6		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
14	AE	1335	Total	C	H	N	O	S	0	0
			21000	6526	10612	1854	1958	50		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AE	1384	VAL	MET	variant	UNP A0A4S1NBU2

- Molecule 15 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AF	82	Total	C	N	O	S	0	0
			650	396	122	131	1		

- Molecule 16 is a protein called Transcription termination/antitermination protein NusA.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	AG	494	Total	C	N	O	0	0
			2442	1454	494	494		

- Molecule 17 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	C	66	Total	C	H	N	O	S	0	0
			1103	344	559	102	97	1		

- Molecule 18 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	D	1524	Total	C	H	N	O	P	0	0
			49126	14585	16423	6003	10591	1524		

- Molecule 19 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	E	86	Total	C	H	N	O	S	0	0
			1388	414	719	138	114	3		

- Molecule 20 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	F	70	Total	C	H	N	O	S	0	0
			1218	366	629	125	97	1		

- Molecule 21 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	G	225	Total	C	H	N	O	S	0	0
			3545	1113	1785	316	323	8		

- Molecule 22 is a protein called 30S ribosomal protein S1.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	H	259	Total	C	H	N	O	S	0	0
			3184	1073	1454	305	349	3		

- Molecule 23 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	I	208	Total	C	H	N	O	S	0	0
			3346	1036	1710	307	290	3		

- Molecule 24 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	J	205	Total	C	H	N	O	S	0	0
			3350	1026	1707	315	298	4		

- Molecule 25 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	K	156	Total	C	H	N	O	S	0	0
			2348	717	1196	217	212	6		

- Molecule 26 is a protein called 30S ribosomal protein S6.

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

- Molecule 27 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	M	151	Total	C	H	N	O	S	0	0
			2416	735	1235	227	215	4		

- Molecule 28 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	N	129	Total	C	H	N	O	S	0	0
			2010	616	1031	173	184	6		

- Molecule 29 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	O	127	Total	C	H	N	O	S	0	0
			2092	634	1070	206	179	3		

- Molecule 30 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	P	99	Total	C	H	N	O	S	0	0
			1621	495	831	151	143	1		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
31	Q	117	Total	C	H	N	O	S	0	0
			1764	540	887	174	160	3		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
32	R	121	Total	C	H	N	O	S	0	0
			1940	580	1001	194	161	4		

- Molecule 33 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	S	100	Total	C	H	N	O	S	0	0
			1649	499	844	164	139	3		

- Molecule 34 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	T	88	Total	C	H	N	O	S	0	0
			1448	439	734	144	130	1		

- Molecule 35 is a protein called 30S ribosomal protein S16.

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

- Molecule 36 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	V	80	Total	C	H	N	O	S	0	0
			1339	411	691	121	113	3		

- Molecule 37 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	W	83	Total	C	H	N	O	S	0	0
			1351	424	688	126	111	2		

- Molecule 38 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	X	116	Total	C	H	N	O	S	0	0
			1864	558	964	181	158	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Y	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 40 is a protein called 50S ribosomal protein L7/L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Z	30	Total	C	N	O	S	0	0
			227	144	33	47	3		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
41	a	2880	Total	C	H	N	O	P	0	0
			92918	27587	31077	11398	19976	2880		

There is a discrepancy between the modelled and reference sequences:

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

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

Mol	Chain	Residues	Atoms						AltConf	Trace
42	b	76	Total	C	H	N	O	S	0	0
			1181	360	599	117	104	1		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
43	c	77	Total	C	H	N	O	S	0	0
			1277	388	652	129	106	2		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
44	d	120	Total	C	H	N	O	P	0	0
			3870	1144	1301	468	837	120		

- Molecule 45 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	e	62	Total	C	H	N	O	S	0	0
			1032	308	531	98	94	1		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
46	f	58	Total	C	H	N	O	S	0	0
			936	281	488	87	78	2		

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

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

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

Mol	Chain	Residues	Atoms						AltConf	Trace
48	h	271	Total	C	H	N	O	S	0	0
			4236	1288	2154	423	364	7		

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

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

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

Mol	Chain	Residues	Atoms						AltConf	Trace
50	j	209	Total	C	H	N	O	S	0	0
			3182	979	1617	288	294	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
51	k	52	Total	C	H	N	O		0	0
			890	275	464	78	73			

- Molecule 52 is a protein called 50S ribosomal protein L4.

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

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

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

- Molecule 54 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	n	177	Total	C	H	N	O	S	0	0
			2853	899	1443	249	256	6		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
55	o	64	Total	C	H	N	O	S	0	0
			1076	323	572	105	74	2		

- Molecule 56 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	p	175	Total	C	H	N	O	S	0	0
			2671	826	1358	241	244	2		

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

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

- Molecule 58 is a protein called 50S ribosomal protein L9.

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

- Molecule 59 is a protein called 50S ribosomal protein L13.

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

- Molecule 60 is a protein called 50S ribosomal protein L14.

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

- Molecule 61 is a protein called 50S ribosomal protein L15.

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

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

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

- Molecule 63 is a protein called 50S ribosomal protein L17.

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

- Molecule 64 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms						AltConf	Trace
64	x	116	Total	C	H	N	O		0	0
			1815	552	923	178	162			

- Molecule 65 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms						AltConf	Trace
65	y	114	Total	C	H	N	O	S	0	0
			1879	574	962	179	163	1		

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

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

- Molecule 67 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 68 is ZINC ION (CCD ID: ZN) (formula: Zn).

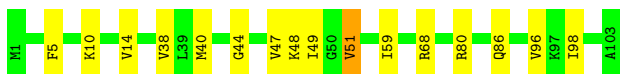
Mol	Chain	Residues	Atoms		AltConf
68	AE	2	Total 2	Zn 2	0

3 Residue-property plots [i](#)

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

- Molecule 1: 50S ribosomal protein L21

Chain 0:  84% 15% .



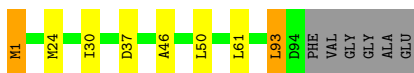
- Molecule 2: 50S ribosomal protein L22

Chain 1:  75% 25%



- Molecule 3: 50S ribosomal protein L23

Chain 2:  86% 6% • 6%

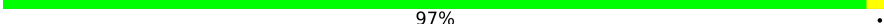


- Molecule 4: 50S ribosomal protein L24

Chain 3:  84% 14% ..

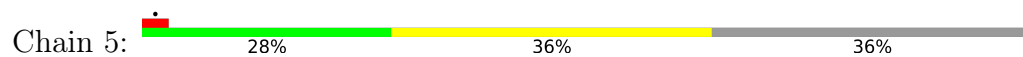


- Molecule 5: 50S ribosomal protein L25

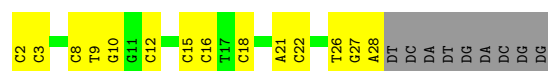
Chain 4:  97% .



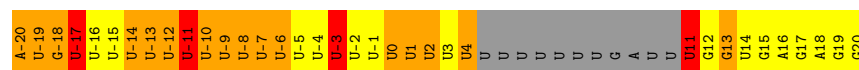
- Molecule 6: NT DNA



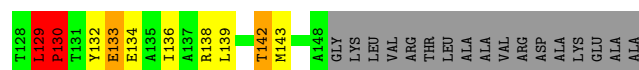
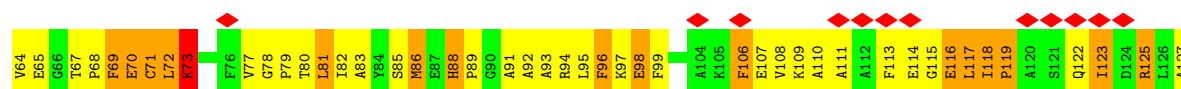
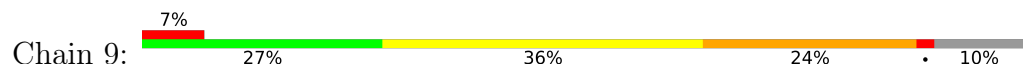
• Molecule 7: T DNA



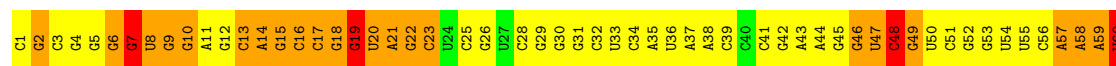
• Molecule 8: mRNA with 30 nt long spacer



• Molecule 9: 50S ribosomal protein L10



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

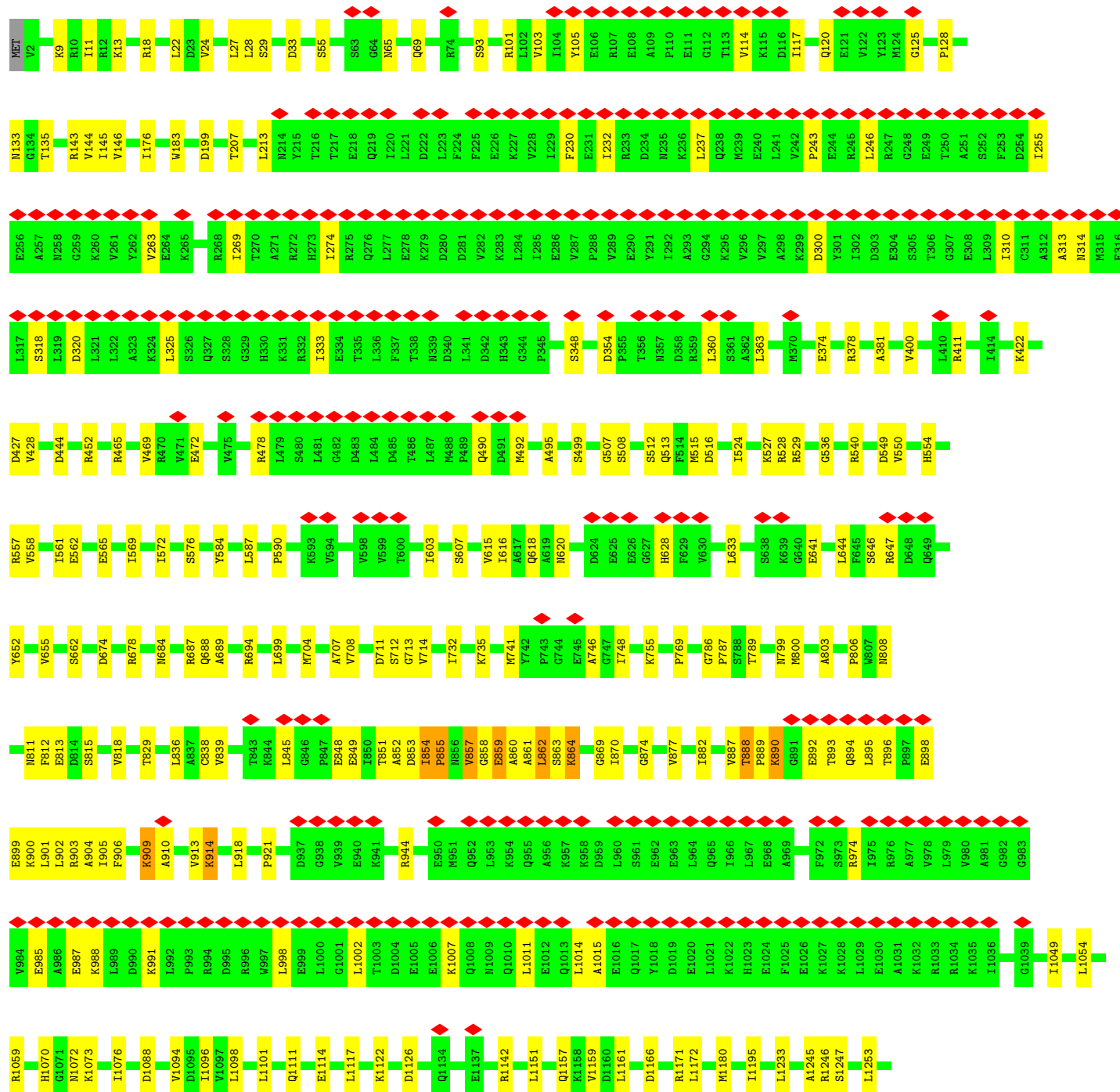
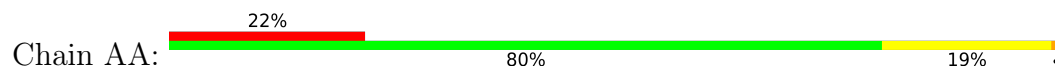


• Molecule 10: E-site and P-site tRNA (fMet)



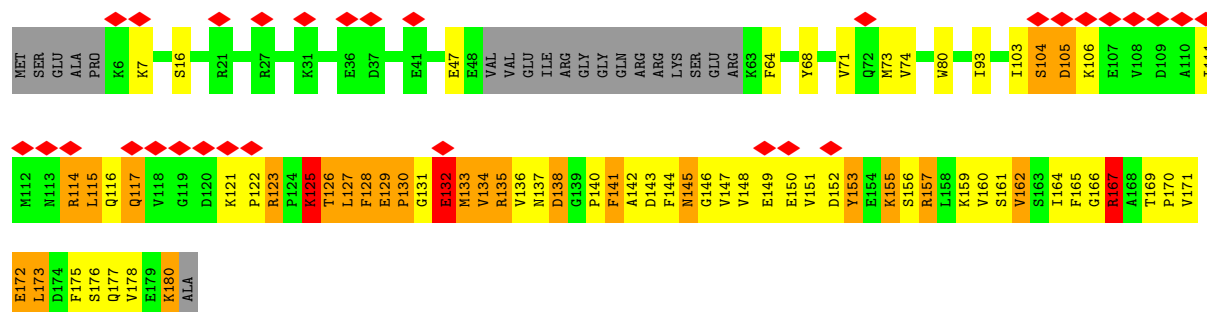


• Molecule 11: DNA-directed RNA polymerase subunit beta

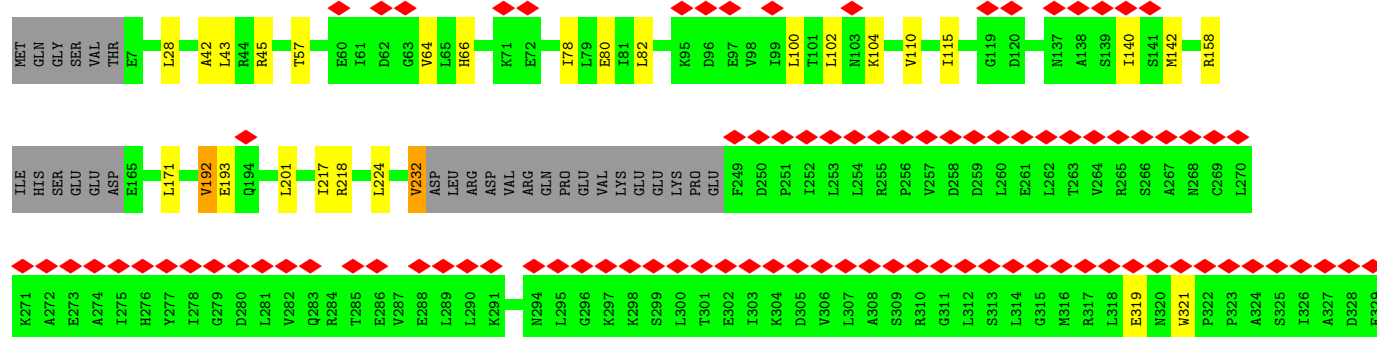
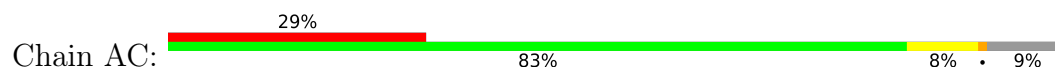




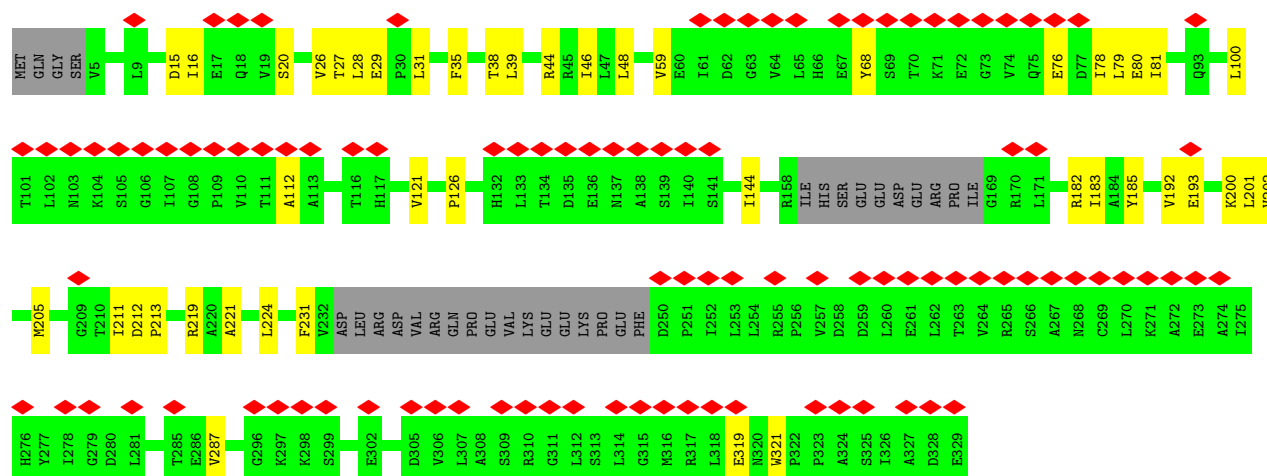
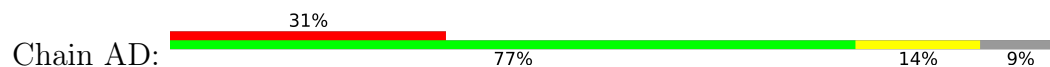
• Molecule 12: Transcription termination/antitermination protein NusG



• Molecule 13: DNA-directed RNA polymerase subunit alpha

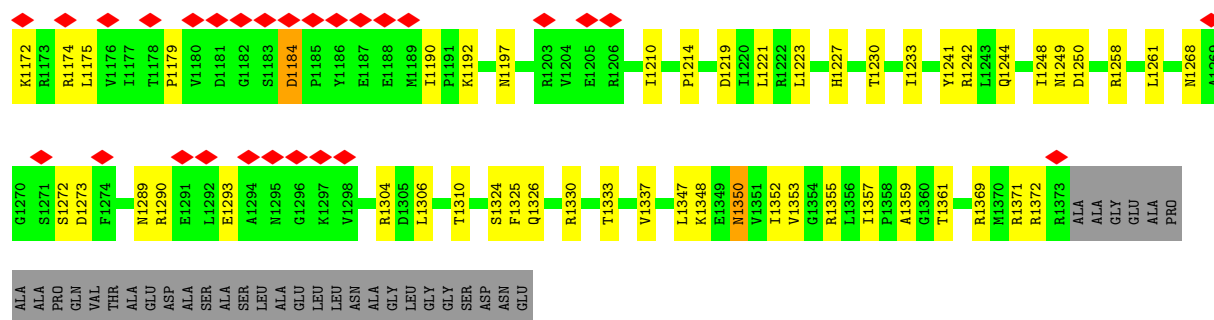


• Molecule 13: DNA-directed RNA polymerase subunit alpha



Chain AE:





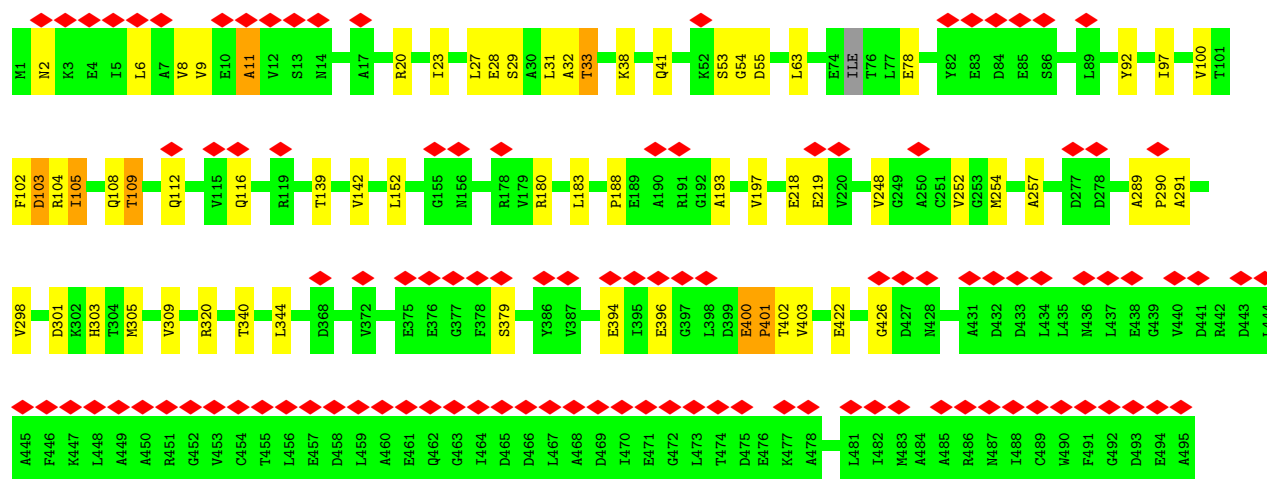
- Molecule 15: DNA-directed RNA polymerase subunit omega

Chain AF: 19% 77% 13% 10%



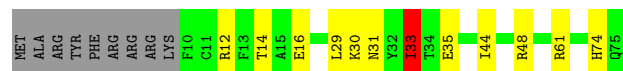
- Molecule 16: Transcription termination/antitermination protein NusA

Chain AG: 22% 87% 12%



- Molecule 17: 30S ribosomal protein S18

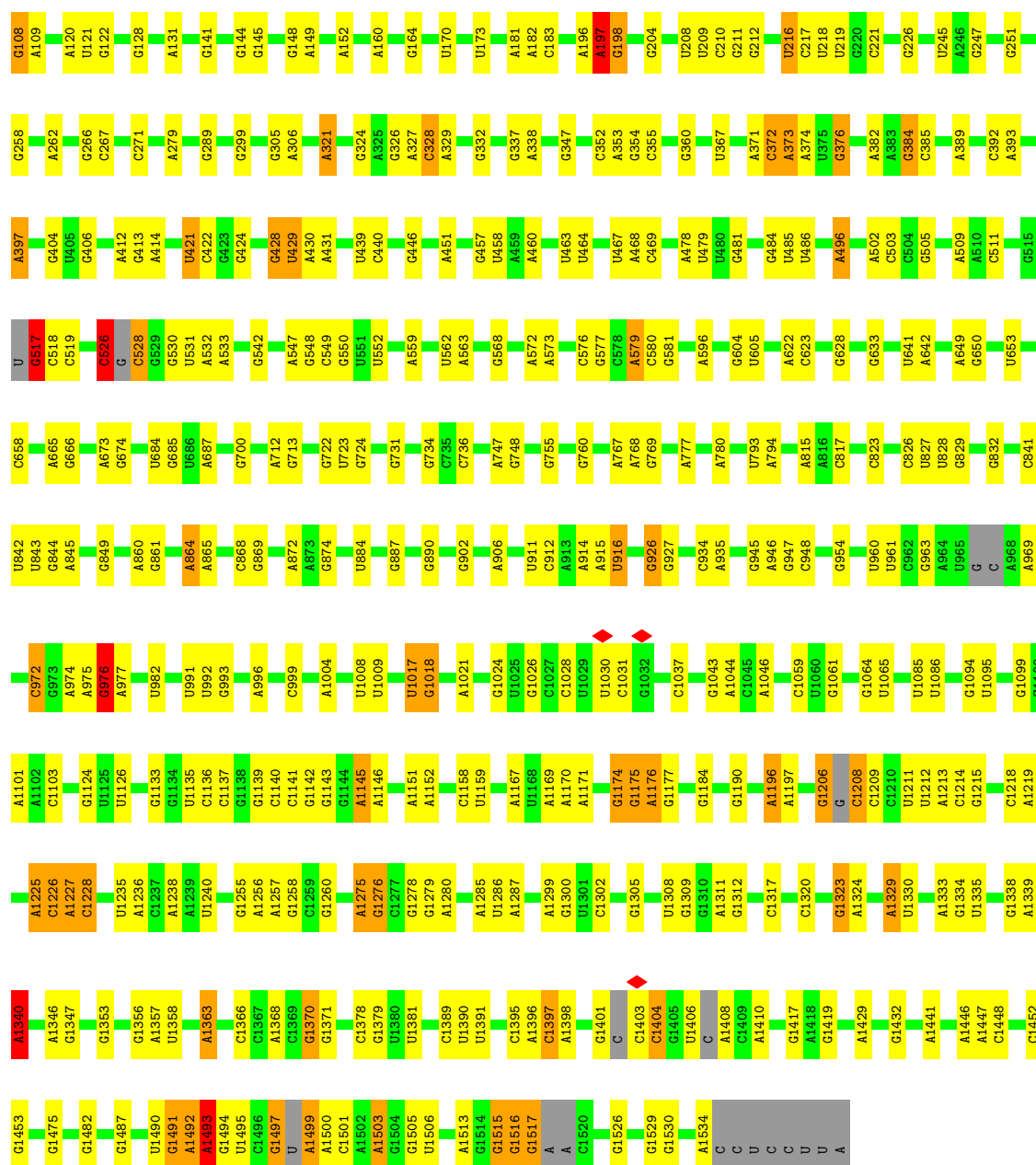
Chain C: 72% 15% 12%



- Molecule 18: 16S rRNA

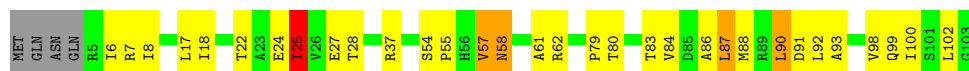
Chain D: 70% 25% 5%





- Molecule 30: 30S ribosomal protein S10

Chain P:  65% 26% . . .



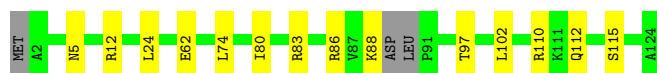
- Molecule 31: 30S ribosomal protein S11

Chain Q:  82% 9% 9%



- Molecule 32: 30S ribosomal protein S12

Chain R:  86% 11% .



- Molecule 33: 30S ribosomal protein S14

Chain S:  89% 8% ...



- Molecule 34: 30S ribosomal protein S15

Chain T:  79% 18% ..



- Molecule 35: 30S ribosomal protein S16

Chain U:  88% 11% .



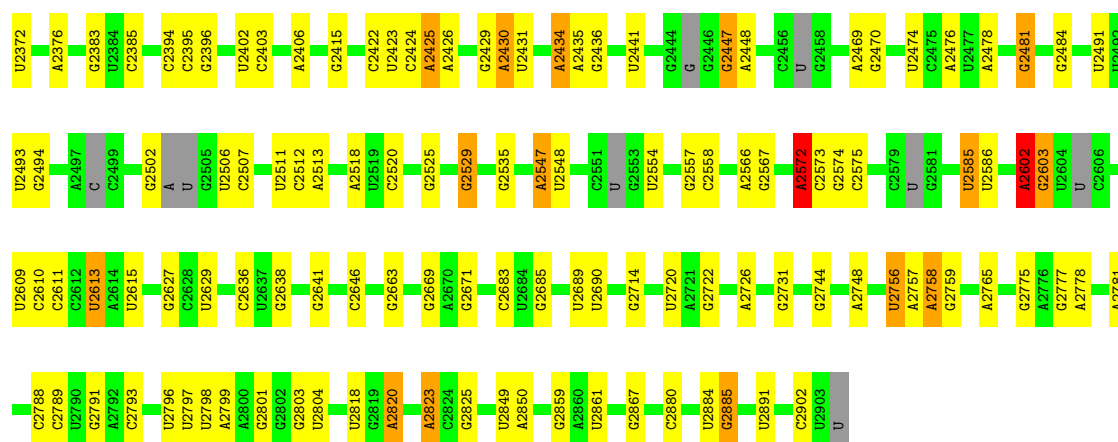
- Molecule 36: 30S ribosomal protein S17

Chain V:  87% 7% . 5%



- Molecule 37: 30S ribosomal protein S19

U2249	G2146	A2051	A1936	G1817	G1649	A1503	C1345	A1133	G1042	A910	G776	G494	A320
G2250	A2147	A2052	A1937	U1818	A1650	A1508	U1352	A1134	C1045	G914	A782	A501	A324
G2252	A2154	G2055	U1938	G1824	G1651	A1509	U1352	C1136	A1046	C915	A783	A502	A324
G2253	G2157	G2056	U1940	A1829	A1568	G1510	A1365	U1141	G1047	A927	G785	A503	U328
A2268	A2158	G2056	U1955	G1833	G1674	A1515	G1368	A1142	A1054	A928	G785	A504	G329
A2273	G2159	A2060	U1955	U1833	A1677	A1529	A1378	A1143	G1055	U929	A800	A505	A330
A2274	G2162	G2061	C1961	G1834	A1677	G1529	U1379	A1169	G1056	G930	G801	C509	A340
A2278	A2163	C2063	U1963	G1836	C1694	A1534	C1380	C1170	U1060	U931	A802	C517	C353
C2283	C2164	G2068	G1965	G1839	G1695	U1535	A1383	A1173	A1062	A941	G805	A522	G359
A2287	C2165	U2068	A1966	G1847	G1703	C1536	A1384	U1174	G1063	C944	U811	C523	U360
A2291	U2167	A2070	C1967	A1848	G1703	G1537	A1385	A1175	C1064	A945	C812	A526	G361
U2292	A2169	C2072	G1964	A1848	U1714	A1538	A1386	A1176	U1065	C946	U813	A527	A362
G2293	A2170	C2073	U1971	A1858	G1715	A1549	C1387	G1177	A1066	A947	U639	A528	A371
C2295	U2172	U2075	C1972	U1859	G1715	U1554	A1392	C1178	G1068	C948	A819	A529	G372
C2296	C2178	A2077	G1980	G1862	G1719	U1569	A1393	G1179	A1069	G953	U827	A532	U373
A2297	U2181	G2083	U1981	U1863	U1720	A1570	U1394	U1180	C1071	G954	U828	A374	A374
A2298	A2182	A2097	U1982	G1864	G1721	A1571	A1395	U1181	G1072	G956	U828	G375	G375
U2299	A2183	U2098	U1991	G1873	G1732	A1578	U1396	U1182	A1073	C961	A845	C540	C353
G2303	A2184	C2100	U1993	G1873	G1732	A1578	U1406	U1183	G1075	A973	U846	G543	G386
U2305	U2188	A2108	C1997	G1889	U1729	U1578	G1407	G1186	C1076	A974	C851	U546	G386
G2308	U2189	U2109	A1998	C1870	C1730	A1579	G1408	U1187	U1079	A983	U852	U547	G396
A2309	A2190	C1999	G1906	A1871	G1730	A1580	U1411	U1188	U1080	A984	G858	G548	A404
U2310	U2191	C2000	G1907	A1872	G1732	G1581	U1412	U1189	U1081	C985	G859	C550	U405
A2311	G2192	C2001	C1908	A1872	A1756	G1582	A1413	A1237	U1082	C995	G869	C551	G411
U2194	G2193	G2002	C1909	U1757	G1756	A1583	C1414	G1238	A1083	U870	U871	U554	A412
A2314	U2194	U2113	G1910	U1757	A1757	G1584	G1415	U1249	A1084	G997	U872	C560	C420
G2315	A2198	C2114	U1912	U1758	U1758	A1584	G1416	G1250	A1086	C998	U872	A563	A423
U2321	G2204	A2116	A1913	C1764	C1764	U1588	A1419	G1253	A1088	U999	A878	C564	G424
A2322	U2210	U2117	U1914	A1773	A1773	U1589	A1420	A1253	A1090	C1005	G879	C565	A424
U2210	G2212	U2118	U1916	A1773	A1773	A1590	G1422	G1256	A1095	C1007	G880	U566	C435
A2211	G2213	G2121	U1918	U1779	U1779	A1591	C1428	G1266	A1096	U1012	G882	U567	G450
U2212	G2123	U2122	A1918	A1784	A1784	A1596	A1433	C1270	A1103	C1013	U884	U568	U451
U2213	G2124	G2125	A1919	A1789	A1789	A1597	A1434	A1271	G1107	U1019	C888	A572	C456
A2225	A2126	G2126	C1920	C1790	C1790	A1603	A1452	A1272	U1108	A1020	U891	U573	A457
C2226	G2127	G2127	U1923	A1791	A1791	A1608	A1453	U1273	G1109	A1021	A892	A574	U464
U2229	G2128	G2128	C1924	C1800	C1800	A1609	U1460	A1274	G1110	G1022	A893	U575	U464
G2230	U2131	U2131	C1925	A1901	A1901	A1610	U1478	A1275	A1111	U1023	U894	U580	G476
U2231	U2132	U2132	U1926	A1908	A1908	A1614	G1482	C1296	G1112	G1025	U895	G585	A477
G2345	G2238	G2238	A1927	A1908	A1908	A1614	G1478	U1296	U1119	G1026	A896	A586	A478
A2346	G2239	A2134	A1928	A1908	A1908	C1617	G1482	U1301	U1119	A1027	A897	A587	A479
C2347	U2243	U2139	U1931	G1930	G1930	A	G1619	A1321	G1122	A1028	C898	U588	A480
C2350	U2244	U2140	A1932	G1931	G1931	G1619	A1490	A1321	G1125	U1033	A899	U603	G481
G2361	U2245	G2141	A1933	G1933	G1933	U1647	G1491	A1327	U1132	G1041	G907	A492	A491
			C2043	C1816	C1816	U1648	U1497	A1328				A609	G493



• Molecule 42: 50S ribosomal protein L27

Chain b: 84% 6% 11%



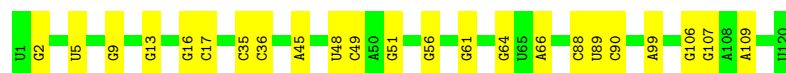
• Molecule 43: 50S ribosomal protein L28

Chain c: 88% 8% 4%



• Molecule 44: 5S rRNA

Chain d: 81% 19%



• Molecule 45: 50S ribosomal protein L29

Chain e: 5% 87% 10% 2%



• Molecule 46: 50S ribosomal protein L30

Chain f: 85% 12% 3%



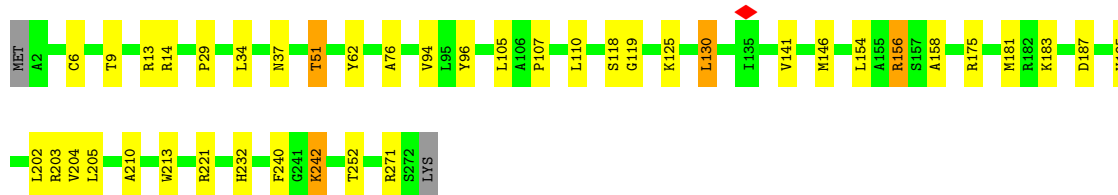
• Molecule 47: 50S ribosomal protein L31

Chain g:  80% 13% • 6%



- Molecule 48: 50S ribosomal protein L2

Chain h:  84% 14% ••



- Molecule 49: 50S ribosomal protein L32

Chain i:  77% 19% ••



- Molecule 50: 50S ribosomal protein L3

Chain j:  88% 11%



- Molecule 51: 50S ribosomal protein L33

Chain k:  89% 5% 5%



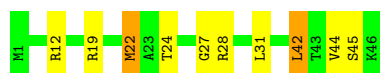
- Molecule 52: 50S ribosomal protein L4

Chain l:  85% 13% •



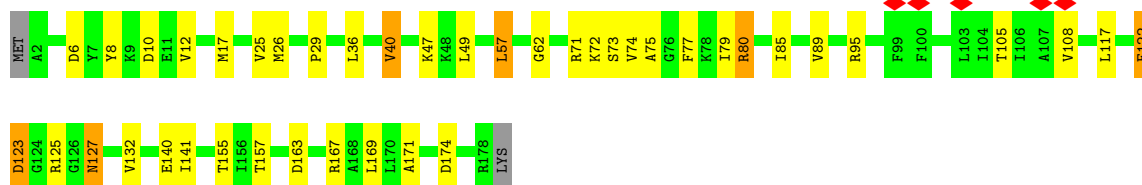
- Molecule 53: 50S ribosomal protein L34

Chain m:  78% 17% •



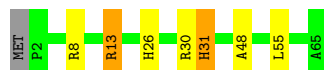
- Molecule 54: 50S ribosomal protein L5

Chain n: 75% 20% . .



- Molecule 55: 50S ribosomal protein L35

Chain o: 88% 8% . .



- Molecule 56: 50S ribosomal protein L6

Chain p: 90% 8% .



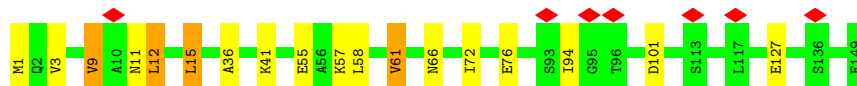
- Molecule 57: 50S ribosomal protein L36

Chain q: 89% 8% .



- Molecule 58: 50S ribosomal protein L9

Chain r: 5% 88% 9% .



- Molecule 59: 50S ribosomal protein L13

Chain s: 83% 15% .

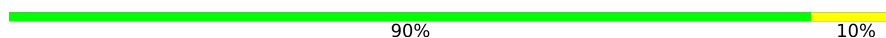


- Molecule 60: 50S ribosomal protein L14

Chain t:  80% 18%



- Molecule 61: 50S ribosomal protein L15

Chain u:  90% 10%



- Molecule 62: 50S ribosomal protein L16

Chain v:  91% 8%



- Molecule 63: 50S ribosomal protein L17

Chain w:  76% 18% 6%



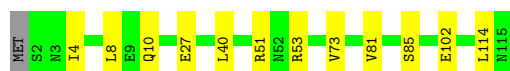
- Molecule 64: 50S ribosomal protein L18

Chain x:  84% 15%



- Molecule 65: 50S ribosomal protein L19

Chain y:  89% 10%



- Molecule 66: 50S ribosomal protein L20

Chain z:  84% 14%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	19967	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.039	Depositor
Minimum map value	-0.009	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.00359	Depositor
Map size ($\text{\AA}$)	532.48, 532.48, 532.48	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.04, 1.04, 1.04	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, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	0.49	0/829	0.74	0/1107
2	1	0.67	0/864	1.08	0/1156
3	2	0.54	0/752	0.89	0/1005
4	3	0.47	0/796	0.77	0/1062
5	4	0.52	0/766	0.88	0/1025
6	5	0.63	1/528 (0.2%)	0.55	0/810
7	6	0.55	1/603 (0.2%)	0.56	0/926
8	7	0.60	3/805 (0.4%)	0.88	4/1246 (0.3%)
9	9	1.15	3/1131 (0.3%)	1.30	4/1524 (0.3%)
10	A	0.36	0/1810	0.72	2/2821 (0.1%)
10	B	0.43	0/1810	0.87	9/2821 (0.3%)
11	AA	0.40	0/10736	0.64	0/14487
12	AB	0.72	0/1304	0.93	1/1759 (0.1%)
13	AC	0.35	0/2110	0.61	0/2873
13	AD	0.29	0/2091	0.59	0/2847
14	AE	0.54	9/10545 (0.1%)	0.74	25/14236 (0.2%)
15	AF	0.29	0/652	0.61	0/879
16	AG	0.64	0/2440	0.90	6/3396 (0.2%)
17	C	0.66	0/553	1.14	2/743 (0.3%)
18	D	0.40	9/36610 (0.0%)	0.75	38/57091 (0.1%)
19	E	0.76	0/675	1.32	0/895
20	F	0.71	0/597	1.20	0/792
21	G	0.65	0/1791	1.08	1/2413 (0.0%)
22	H	0.76	4/1746 (0.2%)	1.58	34/2382 (1.4%)
23	I	0.58	0/1663	0.98	0/2241
24	J	0.63	0/1665	1.08	0/2227
25	K	0.63	0/1165	1.06	2/1568 (0.1%)
26	L	0.58	0/867	0.94	0/1171
27	M	0.68	0/1195	1.19	3/1602 (0.2%)
28	N	0.55	0/989	0.92	0/1326
29	O	0.58	0/1034	1.02	1/1375 (0.1%)
30	P	0.63	0/800	1.14	4/1082 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	Q	0.55	0/893	0.91	0/1205
32	R	0.49	0/952	0.81	0/1274
33	S	0.64	0/817	1.11	1/1088 (0.1%)
34	T	0.69	0/722	1.21	0/964
35	U	0.58	0/659	0.99	0/884
36	V	0.46	0/657	0.73	0/881
37	W	0.51	0/680	0.83	0/915
38	X	0.67	0/909	1.21	3/1215 (0.2%)
39	Y	1.03	0/1046	1.08	0/1410
40	Z	1.02	0/227	1.13	0/304
41	a	0.40	3/69247 (0.0%)	0.75	56/107985 (0.1%)
42	b	0.51	0/589	0.76	0/779
43	c	0.63	0/635	0.97	0/848
44	d	0.37	0/2872	0.69	0/4478
45	e	0.69	0/502	1.19	0/667
46	f	0.62	0/452	1.02	0/605
47	g	0.55	0/531	0.99	1/709 (0.1%)
48	h	0.54	0/2121	0.85	0/2852
49	i	0.52	0/450	0.94	0/599
50	j	0.60	0/1586	0.87	0/2134
51	k	0.47	0/433	0.80	0/576
52	l	0.61	0/1571	1.03	1/2113 (0.0%)
53	m	0.68	0/380	1.22	0/498
54	n	0.62	0/1434	1.18	10/1926 (0.5%)
55	o	0.64	0/513	1.10	1/676 (0.1%)
56	p	0.58	0/1333	0.89	0/1805
57	q	0.50	0/303	0.88	0/397
58	r	0.63	0/1122	0.97	1/1515 (0.1%)
59	s	0.68	0/1152	1.02	2/1551 (0.1%)
60	t	0.57	0/955	0.88	0/1279
61	u	0.55	0/1062	0.96	1/1413 (0.1%)
62	v	0.60	0/1093	0.97	0/1460
63	w	0.67	0/964	1.13	0/1289
64	x	0.61	0/902	1.09	0/1209
65	y	0.53	0/929	0.79	0/1242
66	z	0.80	0/960	1.25	0/1278
All	All	0.49	33/193575 (0.0%)	0.82	213/284911 (0.1%)

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
10	A	0	2
10	B	0	2
11	AA	0	1
13	AC	0	3
13	AD	0	3
14	AE	0	5
16	AG	0	1
22	H	0	3
38	X	0	1
All	All	0	21

All (33) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	9	130	PRO	N-CA	18.15	1.70	1.47
14	AE	93	THR	CA-C	12.17	1.69	1.52
22	H	169	SER	N-CA	11.76	1.61	1.46
18	D	1516	G	O3'-P	-10.73	1.45	1.61
14	AE	70	CYS	CA-CB	-8.81	1.41	1.53
18	D	1339	A	O3'-P	8.39	1.73	1.61
8	7	19	G	C1'-N9	-7.37	1.36	1.48
8	7	-19	U	C1'-N1	7.06	1.59	1.48
22	H	88	LYS	N-CA	7.05	1.55	1.46
6	5	109	DT	O3'-P	6.95	1.71	1.61
18	D	145	G	O3'-P	6.78	1.71	1.61
18	D	196	A	O3'-P	6.60	1.71	1.61
22	H	168	VAL	C-N	6.48	1.42	1.33
18	D	1275	A	O3'-P	6.16	1.70	1.61
41	a	2434	A	O3'-P	6.06	1.70	1.61
18	D	1515	G	O3'-P	-5.85	1.52	1.61
18	D	1395	C	O3'-P	5.77	1.69	1.61
22	H	88	LYS	CA-C	5.75	1.60	1.52
14	AE	90	VAL	CA-C	5.70	1.60	1.52
18	D	1490	U	O3'-P	5.46	1.69	1.61
7	6	10	DG	C1'-N9	-5.37	1.35	1.46
41	a	1905	C	O3'-P	5.28	1.69	1.61
8	7	-3	U	C1'-N1	5.27	1.56	1.48
18	D	1492	A	O3'-P	5.25	1.69	1.61
14	AE	1350	ASN	CG-ND2	-5.24	1.22	1.33
14	AE	777	HIS	ND1-CE1	5.19	1.37	1.32
41	a	2167	U	O3'-P	5.18	1.69	1.61
14	AE	424	ASN	CG-ND2	-5.17	1.22	1.33
14	AE	777	HIS	CD2-NE2	-5.16	1.32	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	9	129	LEU	C-N	5.13	1.45	1.33
9	9	116	GLU	N-CA	5.08	1.49	1.46
14	AE	1108	GLN	CD-OE1	5.08	1.33	1.23
14	AE	1268	ASN	CG-ND2	-5.00	1.22	1.33

All (213) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	D	1516	G	O3'-P-O5'	17.45	130.18	104.00
22	H	88	LYS	CA-C-N	16.90	143.54	120.38
22	H	88	LYS	C-N-CA	16.90	143.54	120.38
10	B	29	G	C3'-C2'-O2'	15.94	134.61	110.70
9	9	129	LEU	CA-C-N	15.85	139.66	119.84
9	9	129	LEU	C-N-CA	15.85	139.66	119.84
18	D	1516	G	P-O3'-C3'	-15.51	96.93	120.20
22	H	332	VAL	N-CA-C	13.67	124.56	110.62
22	H	169	SER	N-CA-C	12.73	137.92	110.80
22	H	330	VAL	N-CA-C	12.18	126.93	109.51
22	H	305	HIS	N-CA-C	11.97	131.12	111.37
14	AE	90	VAL	N-CA-C	9.88	122.17	107.75
41	a	2244	U	C1'-C2'-O2'	-9.78	93.73	108.40
54	n	73	SER	N-CA-CB	-9.56	94.60	110.47
18	D	1206	G	C4'-C3'-O3'	9.51	127.26	113.00
30	P	54	SER	CA-C-N	9.37	129.06	118.85
30	P	54	SER	C-N-CA	9.37	129.06	118.85
41	a	2250	G	C4'-C3'-O3'	-9.22	95.57	109.40
16	AG	104	ARG	N-CA-C	-9.10	96.59	110.70
18	D	1401	G	C4'-C3'-O3'	8.84	126.26	113.00
18	D	428	G	C4'-C3'-O3'	8.75	122.52	109.40
8	7	-20	A	O3'-P-O5'	-8.60	91.09	104.00
9	9	130	PRO	CA-N-CD	-8.59	99.97	112.00
22	H	339	ARG	CA-C-N	8.57	137.91	121.54
22	H	339	ARG	C-N-CA	8.57	137.91	121.54
18	D	1515	G	O3'-P-O5'	-8.48	91.28	104.00
33	S	45	VAL	N-CA-CB	8.46	120.44	110.55
41	a	2296	U	C4'-C3'-O3'	8.36	121.94	109.40
41	a	404	A	C2'-C3'-O3'	8.32	121.98	109.50
8	7	-17	U	C2'-C3'-O3'	8.29	121.94	109.50
30	P	57	VAL	N-CA-C	8.26	119.99	107.77
18	D	197	A	C2'-C3'-O3'	8.19	121.79	109.50
41	a	2252	G	N9-C1'-C2'	-8.16	99.76	112.00
18	D	1401	G	N9-C1'-C2'	-7.93	100.10	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	a	2425	A	C2'-C3'-O3'	7.83	121.25	109.50
22	H	155	LYS	CA-C-N	-7.81	110.88	121.66
22	H	155	LYS	C-N-CA	-7.81	110.88	121.66
41	a	2071	A	C4'-C3'-O3'	-7.73	101.41	113.00
22	H	168	VAL	CA-C-N	7.67	136.19	121.54
22	H	168	VAL	C-N-CA	7.67	136.19	121.54
14	AE	903	LEU	CA-C-N	7.64	136.14	121.54
14	AE	903	LEU	C-N-CA	7.64	136.14	121.54
22	H	84	LEU	N-CA-C	7.62	120.98	110.24
54	n	75	ALA	CA-C-N	7.62	129.66	120.14
54	n	75	ALA	C-N-CA	7.62	129.66	120.14
18	D	1493	A	C2'-C3'-O3'	7.60	125.10	113.70
22	H	52	GLN	N-CA-C	-7.60	104.16	113.50
18	D	1339	A	P-O3'-C3'	7.59	131.59	120.20
38	X	102	THR	CB-CA-C	7.58	123.42	110.84
18	D	1499	A	N9-C1'-C2'	-7.57	100.64	112.00
25	K	60	ILE	N-CA-CB	7.51	119.34	110.55
18	D	528	C	N1-C1'-C2'	-7.48	100.78	112.00
22	H	336	ASP	CB-CA-C	-7.45	98.65	110.79
54	n	73	SER	CB-CA-C	7.40	122.86	110.79
10	B	28	C	P-O3'-C3'	7.36	131.25	120.20
54	n	108	VAL	O-C-N	7.35	125.29	120.07
25	K	56	VAL	O-C-N	7.32	125.11	120.42
41	a	2602	A	C4'-C3'-O3'	7.27	120.31	109.40
41	a	783	A	C4'-C3'-O3'	7.25	123.88	113.00
21	G	47	VAL	O-C-N	7.25	125.06	120.42
10	B	29	G	N9-C1'-C2'	-7.18	101.24	112.00
18	D	196	A	P-O3'-C3'	7.13	130.90	120.20
18	D	1497	G	C1'-C2'-O2'	-7.11	97.73	108.40
41	a	2162	G	C4'-C3'-O3'	7.09	120.04	109.40
41	a	896	A	C4'-C3'-O3'	7.05	119.97	109.40
27	M	27	VAL	N-CA-CB	7.00	118.74	110.55
41	a	1379	U	C2'-C3'-O3'	7.00	124.19	113.70
41	a	2225	A	C4'-C3'-O3'	6.99	119.88	109.40
41	a	2244	U	C4'-C3'-O3'	6.90	123.34	113.00
22	H	140	PRO	N-CA-CB	6.85	110.44	103.25
22	H	340	ARG	CA-C-N	-6.81	112.54	123.23
22	H	340	ARG	C-N-CA	-6.81	112.54	123.23
41	a	2252	G	C4'-C3'-O3'	6.76	123.15	113.00
54	n	71	ARG	CA-C-N	6.75	133.99	122.37
54	n	71	ARG	C-N-CA	6.75	133.99	122.37
16	AG	103	ASP	O-C-N	6.72	131.53	123.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	a	2243	U	C4'-C3'-O3'	6.66	122.99	113.00
22	H	170	ARG	N-CA-C	6.66	119.63	110.24
18	D	517	G	C5'-C4'-C3'	6.65	125.17	115.20
22	H	132	PRO	N-CA-CB	6.58	110.29	103.38
22	H	303	LEU	N-CA-C	6.58	121.15	112.13
41	a	2189	U	C1'-C2'-O2'	-6.57	101.94	111.80
41	a	2167	U	P-O3'-C3'	6.57	130.05	120.20
22	H	87	GLU	N-CA-C	-6.54	104.15	111.28
54	n	127	ASN	CB-CA-C	6.54	121.69	110.77
18	D	526	C	C4'-C3'-O3'	6.54	122.81	113.00
22	H	155	LYS	N-CA-C	-6.54	98.25	108.90
41	a	894	U	C2'-C3'-O3'	6.52	119.28	109.50
22	H	112	ILE	N-CA-C	6.51	117.07	106.72
58	r	61	VAL	N-CA-CB	6.49	118.14	110.55
29	O	72	ILE	N-CA-C	-6.47	105.40	111.48
55	o	13	ARG	N-CA-C	6.46	121.00	113.18
18	D	526	C	N1-C1'-C2'	-6.45	102.32	112.00
18	D	1340	A	C1'-C2'-O2'	6.45	118.07	108.40
14	AE	450	HIS	CB-CG-CD2	-6.43	122.84	131.20
54	n	127	ASN	CA-CB-CG	-6.41	106.19	112.60
41	a	754	U	N1-C1'-C2'	6.39	121.59	112.00
14	AE	93	THR	CA-C-N	6.38	133.06	121.06
14	AE	93	THR	C-N-CA	6.38	133.06	121.06
18	D	69	G	C4'-C3'-O3'	-6.33	103.51	113.00
17	C	33	ILE	CA-C-O	-6.32	114.85	121.93
14	AE	61	ILE	CA-C-N	-6.32	114.06	121.64
14	AE	61	ILE	C-N-CA	-6.32	114.06	121.64
18	D	1208	C	N1-C1'-C2'	-6.29	102.56	112.00
14	AE	777	HIS	CB-CG-CD2	-6.26	123.06	131.20
22	H	153	GLU	N-CA-C	-6.25	97.48	110.80
41	a	2434	A	P-O3'-C3'	6.24	129.56	120.20
8	7	11	U	C4'-C3'-O3'	6.23	118.75	109.40
10	B	28	C	O3'-P-O5'	-6.22	94.67	104.00
22	H	113	ASN	N-CA-C	6.19	118.10	111.36
41	a	2425	A	C4'-C3'-O3'	6.16	118.64	109.40
18	D	1206	G	N9-C1'-C2'	-6.14	102.78	112.00
14	AE	70	CYS	CB-CA-C	6.12	120.33	110.29
41	a	271	G	C4'-C3'-O3'	6.08	118.52	109.40
18	D	1516	G	OP1-P-O3'	-6.05	89.84	108.00
18	D	1408	A	C4'-C3'-O3'	6.01	122.02	113.00
41	a	2210	U	C4'-C3'-O3'	6.01	118.42	109.40
18	D	550	G	C3'-C2'-O2'	6.00	119.71	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	AE	90	VAL	CA-C-O	-5.98	114.17	120.39
41	a	2820	A	C4'-C3'-O3'	-5.97	104.04	113.00
12	AB	122	PRO	N-CA-CB	5.97	109.90	103.33
41	a	1913	A	C2'-C3'-O3'	5.95	118.42	109.50
27	M	92	ARG	CA-C-N	5.91	125.39	119.24
27	M	92	ARG	C-N-CA	5.91	125.39	119.24
41	a	2308	G	C2'-C3'-O3'	-5.88	104.88	113.70
41	a	2756	U	C4'-C3'-O3'	5.87	118.20	109.40
22	H	109	THR	N-CA-C	-5.84	99.14	109.06
52	l	108	ILE	N-CA-CB	5.83	118.48	110.54
54	n	72	LYS	N-CA-C	-5.83	99.16	109.06
22	H	75	VAL	N-CA-C	5.82	116.50	108.12
22	H	150	LYS	N-CA-C	5.82	118.21	110.53
38	X	26	GLY	N-CA-C	-5.81	104.34	112.13
41	a	1905	C	P-O3'-C3'	5.79	128.88	120.20
10	B	29	G	O5'-C5'-C4'	-5.79	102.82	111.50
18	D	1275	A	P-O3'-C3'	5.78	128.87	120.20
41	a	70	G	C4'-C3'-O3'	5.78	118.06	109.40
14	AE	91	GLU	N-CA-C	5.76	123.07	110.80
16	AG	11	ALA	CA-C-N	5.76	132.06	121.70
16	AG	11	ALA	C-N-CA	5.76	132.06	121.70
10	B	48	C	N1-C1'-C2'	5.75	120.63	112.00
10	A	48	C	N1-C1'-C2'	5.73	120.60	112.00
18	D	1490	U	P-O3'-C3'	5.73	128.79	120.20
18	D	1492	A	P-O3'-C3'	5.72	128.78	120.20
18	D	976	G	C4'-C3'-O3'	-5.70	104.45	113.00
18	D	1406	U	N1-C1'-C2'	-5.69	103.46	112.00
18	D	1340	A	C5'-C4'-C3'	5.68	124.53	116.00
41	a	2168	G	C4'-C3'-O3'	-5.68	104.48	113.00
41	a	1757	A	C4'-C3'-O3'	-5.66	104.50	113.00
22	H	114	GLY	N-CA-C	5.61	121.24	111.14
14	AE	450	HIS	CB-CG-ND1	5.59	131.09	122.70
41	a	2017	U	C2'-C3'-O3'	-5.59	105.32	113.70
18	D	780	A	C4'-C3'-O3'	-5.55	104.67	113.00
41	a	1568	G	C4'-C3'-O3'	-5.53	104.71	113.00
41	a	2731	G	C4'-C3'-O3'	-5.53	104.71	113.00
41	a	2447	G	C2'-C3'-O3'	-5.51	101.24	109.50
14	AE	93	THR	CB-CA-C	5.43	121.22	110.42
41	a	2572	A	C4'-C3'-O3'	-5.42	101.27	109.40
18	D	864	A	N9-C1'-C2'	5.42	120.13	112.00
14	AE	69	GLU	CA-C-N	-5.40	113.89	121.72
14	AE	69	GLU	C-N-CA	-5.40	113.89	121.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	D	1145	A	C4'-C3'-O3'	-5.40	104.90	113.00
41	a	2481	G	C4'-C3'-O3'	-5.39	104.92	113.00
41	a	2068	U	C4'-C3'-O3'	-5.38	104.92	113.00
41	a	944	C	C4'-C3'-O3'	-5.38	104.93	113.00
18	D	1499	A	C4'-C3'-O3'	5.37	121.06	113.00
14	AE	70	CYS	N-CA-C	-5.37	101.04	109.25
14	AE	777	HIS	CB-CG-ND1	5.35	130.72	122.70
10	B	35	A	P-O3'-C3'	5.33	128.20	120.20
41	a	1270	C	C2'-C3'-O3'	-5.33	105.71	113.70
18	D	517	G	C4'-C3'-O3'	-5.32	101.42	109.40
41	a	375	G	C2'-C3'-O3'	5.31	121.67	113.70
47	g	5	ILE	N-CA-C	5.31	117.69	111.05
41	a	2020	A	C4'-C3'-O3'	-5.30	105.04	113.00
14	AE	90	VAL	O-C-N	-5.30	117.58	123.20
41	a	2231	U	C1'-C2'-O2'	5.30	116.35	108.40
8	7	-11	U	C2'-C3'-O3'	5.29	117.44	109.50
14	AE	73	GLY	N-CA-C	5.29	125.72	113.18
38	X	102	THR	CA-C-O	-5.29	114.83	121.02
41	a	2529	G	C4'-C3'-O3'	-5.27	105.09	113.00
18	D	145	G	P-O3'-C3'	5.25	128.08	120.20
14	AE	88	CYS	N-CA-C	5.24	120.33	113.88
18	D	1395	C	P-O3'-C3'	5.24	128.06	120.20
41	a	423	A	C2'-C3'-O3'	-5.20	105.90	113.70
61	u	101	ILE	N-CA-C	5.19	116.48	112.12
10	A	60	U	C2'-C3'-O3'	5.18	117.26	109.50
10	B	60	U	C2'-C3'-O3'	5.17	117.26	109.50
22	H	128	ARG	CA-C-N	-5.17	114.13	122.81
22	H	128	ARG	C-N-CA	-5.17	114.13	122.81
18	D	1335	U	C4'-C3'-O3'	-5.16	105.26	113.00
41	a	2245	U	N1-C1'-C2'	-5.14	104.29	112.00
22	H	154	PHE	N-CA-C	-5.13	100.34	109.06
41	a	528	A	C4'-C3'-O3'	-5.13	105.31	113.00
41	a	1834	U	C4'-C3'-O3'	-5.13	105.31	113.00
41	a	328	U	C4'-C3'-O3'	-5.12	105.32	113.00
14	AE	61	ILE	CA-C-O	-5.12	115.62	120.95
41	a	126	A	C4'-C3'-O3'	-5.10	105.34	113.00
30	P	25	ILE	N-CA-CB	5.09	117.46	110.54
41	a	614	A	C2'-C3'-O3'	5.08	117.12	109.50
41	a	479	A	C4'-C3'-O3'	5.07	117.00	109.40
59	s	28	LEU	CA-C-N	5.05	127.01	120.44
59	s	28	LEU	C-N-CA	5.05	127.01	120.44
41	a	1864	U	C4'-C3'-O3'	-5.04	105.44	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	C	35	GLU	N-CA-C	-5.04	105.98	111.82
14	AE	89	GLY	CA-C-N	5.03	129.79	123.10
14	AE	89	GLY	C-N-CA	5.03	129.79	123.10
10	B	19	G	N9-C1'-C2'	5.02	119.53	112.00
41	a	2193	G	C2'-C3'-O3'	5.02	121.23	113.70
22	H	108	VAL	N-CA-C	-5.02	98.90	109.34
14	AE	1184	ASP	N-CA-C	5.02	120.90	109.81
16	AG	104	ARG	CA-C-N	5.02	131.00	121.97
16	AG	104	ARG	C-N-CA	5.02	131.00	121.97
41	a	1025	G	C4'-C3'-O3'	5.01	116.92	109.40
9	9	115	GLY	CA-C-O	-5.00	118.24	122.29

There are no chirality outliers.

All (21) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	A	19	G	Sidechain
10	A	7	G	Sidechain
11	AA	910	ALA	Peptide
13	AC	192	VAL	Peptide
13	AC	319	GLU	Peptide
13	AC	321	TRP	Peptide
13	AD	20	SER	Peptide
13	AD	319	GLU	Peptide
13	AD	321	TRP	Peptide
14	AE	1184	ASP	Peptide
14	AE	1326	GLN	Peptide
14	AE	313	GLY	Peptide
14	AE	416	ILE	Peptide
14	AE	804	ALA	Peptide
16	AG	379	SER	Peptide
10	B	19	G	Sidechain
10	B	7	G	Sidechain
22	H	274	TYR	Peptide
22	H	81	GLU	Peptide
22	H	82	THR	Peptide
38	X	100	GLN	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	0	816	839	839	8	0
2	1	857	922	922	14	0
3	2	746	811	811	6	0
4	3	788	844	844	11	0
5	4	753	780	780	0	0
6	5	472	260	260	20	0
7	6	542	305	306	24	0
8	7	727	97	361	106	0
9	9	1117	0	1153	163	0
10	A	1620	826	826	169	0
10	B	1620	813	827	138	0
11	AA	10567	0	10582	280	0
12	AB	1276	0	1244	234	0
13	AC	2091	0	1892	17	0
13	AD	2073	0	1889	30	0
14	AE	10388	10612	10611	364	0
15	AF	650	0	658	13	0
16	AG	2442	0	1177	83	0
17	C	544	559	560	23	0
18	D	32703	16423	16459	220	0
19	E	669	719	719	3	0
20	F	589	629	629	8	0
21	G	1760	1785	1785	51	0
22	H	1730	1454	1454	211	0
23	I	1636	1710	1710	18	0
24	J	1643	1707	1707	15	0
25	K	1152	1196	1196	22	0
26	L	848	846	846	3	0
27	M	1181	1235	1235	33	0
28	N	979	1031	1031	7	0
29	O	1022	1070	1070	12	0
30	P	790	831	831	103	0
31	Q	877	887	887	4	0
32	R	939	1001	1001	7	0
33	S	805	844	844	5	0
34	T	714	734	734	8	0
35	U	649	666	666	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	V	648	691	691	4	0
37	W	663	688	688	2	0
38	X	900	964	964	57	0
39	Y	1032	0	1088	84	0
40	Z	227	0	237	19	0
41	a	61841	31077	31123	299	0
42	b	582	599	599	3	0
43	c	625	652	652	4	0
44	d	2569	1301	1301	3	0
45	e	501	531	531	4	0
46	f	448	488	488	5	0
47	g	522	520	520	11	0
48	h	2082	2154	2154	20	0
49	i	444	459	458	6	0
50	j	1565	1617	1616	15	0
51	k	426	464	464	0	0
52	l	1552	1619	1619	13	0
53	m	377	418	418	10	0
54	n	1410	1443	1444	28	0
55	o	504	572	572	3	0
56	p	1313	1358	1358	7	0
57	q	302	343	343	1	0
58	r	1111	1148	1148	6	0
59	s	1129	1162	1162	12	0
60	t	946	1023	1023	12	0
61	u	1053	1129	1129	7	0
62	v	1074	1157	1157	5	0
63	w	951	994	994	9	0
64	x	892	923	923	8	0
65	y	917	962	962	4	0
66	z	947	1020	1019	13	0
67	AE	1	0	0	0	0
68	AE	2	0	0	0	0
All	All	180331	109912	130191	2521	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (2521) 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)
22:H:131:LEU:CB	22:H:167:VAL:CA	1.78	1.62
11:AA:902:LEU:CD1	16:AG:27:LEU:CB	1.78	1.58
11:AA:902:LEU:HD13	16:AG:27:LEU:CB	1.23	1.56
17:C:12:ARG:HG3	22:H:264:GLU:CB	1.30	1.54
12:AB:141:PHE:CE2	12:AB:173:LEU:HD11	1.40	1.51
22:H:131:LEU:CB	22:H:167:VAL:HA	1.03	1.48
12:AB:141:PHE:CE1	30:P:102:LEU:CD2	1.97	1.47
9:9:31:ARG:NE	41:a:1054:A:H5'	1.31	1.45
12:AB:141:PHE:CE2	12:AB:173:LEU:CD1	1.96	1.45
9:9:130:PRO:N	9:9:130:PRO:CA	1.70	1.43
12:AB:140:PRO:CD	30:P:102:LEU:HD21	1.46	1.43
12:AB:141:PHE:CE1	30:P:102:LEU:HD23	1.51	1.43
12:AB:140:PRO:HD2	30:P:102:LEU:CD2	1.51	1.39
12:AB:141:PHE:HE1	30:P:102:LEU:CB	1.38	1.37
12:AB:128:PHE:CZ	12:AB:175:PHE:O	1.77	1.36
22:H:71:ALA:C	22:H:72:LEU:HD12	1.49	1.36
18:D:1358:U:O4	18:D:1363:A:N1	1.60	1.35
8:7:-7:U:H5'	23:I:132:ARG:NH1	1.40	1.34
9:9:57:ASN:OD1	9:9:62:ARG:CG	1.75	1.34
41:a:1839:G:H1'	41:a:1927:A:C8	1.62	1.33
8:7:4:U:O2'	11:AA:914:LYS:HD2	1.26	1.32
22:H:118:GLY:O	22:H:133:GLY:CA	1.74	1.32
12:AB:128:PHE:HZ	12:AB:175:PHE:O	1.03	1.29
41:a:1021:A:N1	41:a:1141:U:O4	1.63	1.28
12:AB:167:ARG:NH2	30:P:93:ALA:O	1.66	1.28
11:AA:905:ILE:HG12	16:AG:54:GLY:O	1.30	1.27
9:9:31:ARG:CZ	41:a:1054:A:H5'	1.63	1.27
18:D:1308:U:H2'	38:X:98:ARG:NH2	1.47	1.26
22:H:118:GLY:O	22:H:133:GLY:HA3	1.27	1.25
17:C:12:ARG:CG	22:H:264:GLU:CB	2.15	1.24
18:D:1308:U:H3'	38:X:98:ARG:CZ	1.43	1.24
11:AA:858:GLY:H	11:AA:861:ALA:CB	1.49	1.24
18:D:948:C:OP2	38:X:105:ASN:OD1	1.53	1.23
12:AB:145:ASN:HD22	14:AE:53:ARG:NH2	1.35	1.23
10:A:18:G:N7	10:A:57:A:N6	1.87	1.22
10:B:18:G:N7	10:B:57:A:N6	1.87	1.22
18:D:1227:A:OP2	38:X:110:LYS:HE3	1.35	1.22
18:D:1308:U:C2'	38:X:98:ARG:NH2	2.03	1.22
10:A:32:C:O4'	27:M:144:MET:HE1	1.09	1.21
12:AB:167:ARG:CG	30:P:92:LEU:H	1.52	1.21
16:AG:32:ALA:HB1	16:AG:102:PHE:O	1.36	1.21
22:H:267:TRP:CZ2	22:H:340:ARG:HG2	1.75	1.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:D:563:A:N1	18:D:884:U:O4	1.73	1.20
12:AB:140:PRO:HB3	30:P:79:PRO:CB	1.71	1.19
10:A:70:G:H2'	10:A:71:C:H5''	1.22	1.19
9:9:88:HIS:HB3	9:9:89:PRO:CD	1.70	1.18
12:AB:141:PHE:CE1	30:P:102:LEU:CB	2.26	1.17
9:9:31:ARG:NE	41:a:1054:A:C5'	2.07	1.17
12:AB:47:GLU:HG3	12:AB:64:PHE:CE1	1.80	1.17
9:9:142:THR:HG21	40:Z:7:ILE:HG12	1.21	1.16
11:AA:855:PRO:CB	16:AG:109:THR:H	1.59	1.15
11:AA:854:ILE:HG12	11:AA:855:PRO:CD	1.77	1.15
12:AB:144:PHE:CB	12:AB:164:ILE:HD13	1.55	1.15
18:D:1329:A:OP1	38:X:28:THR:HB	1.47	1.15
21:G:19:GLN:CD	22:H:76:GLU:HB3	1.67	1.15
12:AB:144:PHE:HB2	12:AB:164:ILE:HG21	1.27	1.14
10:B:70:G:H2'	10:B:71:C:H5''	1.22	1.14
8:7:11:U:O2	11:AA:1253:LEU:HD12	1.48	1.13
11:AA:855:PRO:HG3	16:AG:108:GLN:CB	1.79	1.13
11:AA:854:ILE:HG12	11:AA:855:PRO:HD2	1.17	1.13
17:C:44:ILE:HD13	22:H:339:ARG:CG	1.78	1.12
11:AA:859:GLU:O	11:AA:863:SER:HB3	1.46	1.12
12:AB:144:PHE:CB	12:AB:164:ILE:CD1	2.27	1.12
11:AA:848:GLU:HG2	11:AA:888:THR:HG22	1.15	1.12
11:AA:906:PHE:CE2	16:AG:31:LEU:CB	2.32	1.12
9:9:57:ASN:OD1	9:9:62:ARG:HG3	1.44	1.12
10:A:32:C:O4'	27:M:144:MET:CE	1.97	1.12
11:AA:904:ALA:N	16:AG:8:VAL:CB	2.12	1.12
22:H:119:GLY:HA2	22:H:133:GLY:HA2	1.14	1.12
22:H:135:LEU:CB	22:H:167:VAL:CB	2.27	1.12
12:AB:141:PHE:CZ	30:P:102:LEU:HD23	1.85	1.11
21:G:19:GLN:CD	22:H:76:GLU:CB	2.19	1.11
12:AB:47:GLU:HG3	12:AB:64:PHE:HE1	1.01	1.11
22:H:267:TRP:CE2	22:H:340:ARG:HG2	1.84	1.11
41:a:1839:G:C8	41:a:1927:A:H1'	1.87	1.09
22:H:267:TRP:CH2	22:H:340:ARG:HG2	1.87	1.09
9:9:129:LEU:N	9:9:130:PRO:HD3	1.66	1.09
17:C:44:ILE:HD13	22:H:339:ARG:HG2	1.18	1.09
18:D:1308:U:C2'	38:X:98:ARG:HH21	1.63	1.09
18:D:1308:U:C3'	38:X:98:ARG:NH2	2.16	1.09
8:7:4:U:H5''	11:AA:890:LYS:HD2	1.32	1.08
9:9:50:VAL:HG22	39:Y:119:ALA:CB	1.82	1.08
11:AA:858:GLY:H	11:AA:861:ALA:HB3	1.12	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:G:19:GLN:CG	22:H:75:VAL:HG22	1.84	1.08
9:9:88:HIS:CB	9:9:89:PRO:HD3	1.82	1.08
12:AB:141:PHE:CZ	12:AB:173:LEU:CD1	2.37	1.08
12:AB:144:PHE:HB2	12:AB:164:ILE:CG2	1.83	1.08
18:D:1308:U:C3'	38:X:98:ARG:CZ	2.31	1.07
24:J:162:ALA:HA	24:J:165:ARG:CZ	1.83	1.07
13:AC:232:VAL:C	13:AD:221:ALA:HB3	1.80	1.07
8:7:-18:G:H5''	18:D:1500:A:N6	1.70	1.06
12:AB:128:PHE:HZ	12:AB:175:PHE:C	1.62	1.06
9:9:129:LEU:H	9:9:130:PRO:HD3	0.90	1.06
12:AB:141:PHE:CE2	12:AB:173:LEU:HD12	1.84	1.06
12:AB:144:PHE:HB2	12:AB:164:ILE:HD13	1.35	1.06
11:AA:857:VAL:HG12	11:AA:861:ALA:CB	1.84	1.05
10:B:18:G:N2	10:B:55:U:O2	1.90	1.05
22:H:71:ALA:O	22:H:72:LEU:HD12	1.54	1.05
14:AE:24:LEU:HG	14:AE:232:ASN:HD21	1.17	1.05
12:AB:145:ASN:ND2	14:AE:53:ARG:NH2	2.05	1.05
12:AB:140:PRO:HB3	30:P:79:PRO:HB2	1.05	1.04
8:7:-7:U:C5'	23:I:132:ARG:HH12	1.68	1.04
11:AA:1313:HIS:CD2	15:AF:31:GLN:HE22	1.75	1.04
22:H:162:LYS:CB	22:H:298:GLU:CD	2.30	1.04
18:D:1308:U:H2'	38:X:98:ARG:HH21	1.06	1.04
8:7:-10:U:O2'	25:K:33:PHE:CE1	2.11	1.03
10:A:56:C:H2'	10:A:57:A:H5''	1.39	1.03
18:D:1227:A:OP2	38:X:110:LYS:CE	2.06	1.03
10:A:18:G:N2	10:A:55:U:O2	1.90	1.03
16:AG:32:ALA:CB	16:AG:102:PHE:O	2.05	1.03
10:A:70:G:C2'	10:A:71:C:H5''	1.89	1.03
10:B:70:G:C2'	10:B:71:C:H5''	1.89	1.03
10:B:56:C:O4'	54:n:80:ARG:NH2	1.91	1.02
22:H:19:ARG:O	22:H:72:LEU:HB2	1.58	1.02
10:B:56:C:H5'	54:n:80:ARG:CZ	1.90	1.02
11:AA:857:VAL:HG12	11:AA:861:ALA:HB1	1.03	1.02
21:G:38:VAL:CG2	22:H:75:VAL:HG21	1.90	1.02
9:9:93:ALA:O	9:9:129:LEU:HD12	1.60	1.01
11:AA:549:ASP:OD2	14:AE:750:PRO:HB3	1.60	1.01
12:AB:141:PHE:CZ	12:AB:173:LEU:HD11	1.95	1.01
12:AB:136:VAL:HG11	12:AB:141:PHE:HD2	1.23	1.01
18:D:1329:A:OP1	38:X:28:THR:CB	2.07	1.01
41:a:2297:A:N1	41:a:2321:U:C4	2.29	1.01
11:AA:855:PRO:HB3	16:AG:109:THR:H	1.22	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:167:ARG:HG3	30:P:92:LEU:HD12	1.41	1.00
22:H:290:TYR:O	22:H:305:HIS:O	1.77	1.00
12:AB:141:PHE:CE1	30:P:102:LEU:HD22	1.93	1.00
11:AA:901:LEU:HA	16:AG:9:VAL:HA	1.43	1.00
12:AB:137:ASN:OD1	12:AB:143:ASP:HA	1.61	1.00
21:G:19:GLN:HG3	22:H:75:VAL:HG22	1.38	1.00
21:G:38:VAL:HG22	22:H:75:VAL:HG21	1.44	1.00
11:AA:902:LEU:HD12	16:AG:27:LEU:CB	1.85	1.00
18:D:13:U:N3	18:D:915:A:C6	2.29	0.99
22:H:131:LEU:CB	22:H:167:VAL:CB	2.40	0.99
10:B:56:C:H2'	10:B:57:A:H5''	1.39	0.99
18:D:13:U:O4	18:D:20:U:O4	1.79	0.99
12:AB:141:PHE:CE1	30:P:102:LEU:HB3	1.97	0.99
14:AE:111:THR:HG23	14:AE:300:GLN:CD	1.86	0.99
12:AB:47:GLU:CG	12:AB:64:PHE:HE1	1.76	0.98
13:AC:232:VAL:C	13:AD:221:ALA:CB	2.37	0.98
11:AA:1268:GLN:NE2	14:AE:352:ARG:HD2	1.78	0.98
9:9:129:LEU:H	9:9:130:PRO:CD	1.77	0.97
18:D:1308:U:H3'	38:X:98:ARG:NH2	1.76	0.97
41:a:1839:G:C1'	41:a:1927:A:C8	2.47	0.97
12:AB:171:VAL:HG13	12:AB:173:LEU:HD22	1.45	0.97
12:AB:141:PHE:HE1	30:P:102:LEU:HB2	1.28	0.97
10:A:32:C:O2'	27:M:86:GLN:CG	2.12	0.97
22:H:118:GLY:O	22:H:133:GLY:HA2	1.63	0.97
30:P:87:LEU:HD23	30:P:90:LEU:O	1.63	0.97
10:A:32:C:C4'	27:M:144:MET:HE1	1.93	0.97
12:AB:140:PRO:CB	30:P:79:PRO:HB2	1.95	0.96
8:7:-7:U:C5'	23:I:132:ARG:NH1	2.26	0.96
11:AA:906:PHE:CZ	16:AG:31:LEU:CB	2.48	0.96
41:a:1839:G:O4'	41:a:1927:A:O4'	1.82	0.96
11:AA:887:VAL:HG22	11:AA:913:VAL:HG22	1.45	0.96
8:7:-19:U:P	18:D:1505:G:H8	1.87	0.96
11:AA:906:PHE:HE2	16:AG:31:LEU:CB	1.79	0.96
11:AA:849:GLU:HB2	11:AA:887:VAL:CG1	1.96	0.95
11:AA:903:ARG:HB3	16:AG:8:VAL:CB	1.95	0.95
9:9:31:ARG:CD	41:a:1054:A:H5'	1.94	0.95
22:H:119:GLY:CA	22:H:133:GLY:HA2	1.95	0.95
12:AB:141:PHE:HE1	30:P:102:LEU:CG	1.78	0.95
12:AB:140:PRO:HG2	30:P:102:LEU:CD1	1.96	0.95
12:AB:167:ARG:CD	30:P:92:LEU:H	1.78	0.95
9:9:88:HIS:CB	9:9:89:PRO:CD	2.41	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:1839:G:O4'	41:a:1927:A:C1'	2.15	0.94
11:AA:904:ALA:H	16:AG:8:VAL:CB	1.76	0.94
10:A:72:A:H2'	10:A:73:A:H5''	1.49	0.94
9:9:142:THR:HG21	40:Z:7:ILE:CG1	1.95	0.94
41:a:67:U:N3	41:a:74:A:C6	2.36	0.94
7:6:15:DC:N4	7:6:16:DC:N4	2.15	0.94
9:9:57:ASN:OD1	9:9:62:ARG:HG2	1.64	0.94
11:AA:887:VAL:CG2	11:AA:913:VAL:CG2	2.46	0.94
12:AB:167:ARG:HG3	30:P:92:LEU:CD1	1.97	0.94
14:AE:68:TYR:O	14:AE:75:TYR:CE2	2.20	0.94
11:AA:1313:HIS:HD2	15:AF:31:GLN:HE22	0.99	0.94
10:B:68:C:H2'	10:B:69:C:H5''	1.50	0.93
11:AA:858:GLY:H	11:AA:861:ALA:HB2	1.33	0.93
22:H:135:LEU:HA	22:H:157:ILE:CB	1.98	0.93
10:A:68:C:H2'	10:A:69:C:H5''	1.51	0.93
11:AA:857:VAL:CG1	11:AA:861:ALA:HB1	1.97	0.93
18:D:13:U:C4	18:D:915:A:N6	2.36	0.93
16:AG:400:GLU:O	16:AG:401:PRO:O	1.85	0.93
10:A:32:C:O2'	27:M:86:GLN:HG3	1.68	0.93
10:B:72:A:H2'	10:B:73:A:H5''	1.49	0.93
18:D:13:U:N3	18:D:915:A:N6	2.16	0.93
8:7:4:U:O2'	11:AA:914:LYS:CD	2.16	0.92
12:AB:166:GLY:HA2	30:P:87:LEU:HB3	1.50	0.92
22:H:119:GLY:HA3	22:H:131:LEU:O	1.68	0.92
9:9:50:VAL:HG22	39:Y:119:ALA:HB1	1.50	0.92
10:B:75:C:OP1	41:a:2602:A:C8	2.23	0.92
11:AA:855:PRO:HB2	16:AG:109:THR:H	1.34	0.91
10:A:56:C:H1'	41:a:2112:G:C6	2.06	0.91
8:7:-17:U:O2'	18:D:1403:C:O2	1.87	0.91
11:AA:858:GLY:N	11:AA:861:ALA:CB	2.33	0.91
12:AB:125:LYS:HG2	12:AB:153:TYR:HB2	1.53	0.91
12:AB:167:ARG:HG2	30:P:91:ASP:HA	1.53	0.91
18:D:13:U:C4	18:D:20:U:O4	2.24	0.91
41:a:1406:U:O2'	41:a:1407:G:C5'	2.19	0.91
12:AB:169:THR:OG1	30:P:99:GLN:HA	1.69	0.91
12:AB:141:PHE:HE2	12:AB:173:LEU:CD1	1.63	0.90
12:AB:144:PHE:HB2	12:AB:164:ILE:CD1	1.95	0.90
12:AB:167:ARG:CG	30:P:92:LEU:N	2.34	0.90
14:AE:136:GLU:OE1	14:AE:312:ARG:NH1	2.04	0.90
12:AB:117:GLN:HE21	12:AB:117:GLN:HA	1.36	0.90
12:AB:129:GLU:OE1	12:AB:130:PRO:HD2	1.72	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:146:GLY:N	12:AB:162:VAL:HG22	1.83	0.90
41:a:2013:A:N6	41:a:2613:U:H3	1.68	0.90
10:A:18:G:N2	10:A:58:A:N7	2.19	0.90
11:AA:857:VAL:HG11	11:AA:862:LEU:HD12	1.53	0.90
39:Y:104:GLN:HG2	39:Y:108:ILE:HD11	1.53	0.90
14:AE:24:LEU:HB2	14:AE:232:ASN:OD1	1.72	0.90
8:7:-19:U:P	18:D:1505:G:C8	2.64	0.90
9:9:93:ALA:O	9:9:129:LEU:CD1	2.19	0.90
11:AA:641:GLU:OE2	14:AE:749:LYS:NZ	2.03	0.90
22:H:279:LYS:HA	22:H:331:MET:HB3	1.54	0.90
39:Y:21:PRO:HB2	39:Y:22:PRO:HD3	1.54	0.89
11:AA:848:GLU:HG2	11:AA:888:THR:CG2	2.02	0.89
12:AB:93:ILE:HG22	14:AE:290:ILE:CG2	2.02	0.89
9:9:88:HIS:HB3	9:9:89:PRO:HD3	0.93	0.89
9:9:129:LEU:N	9:9:130:PRO:CD	2.34	0.89
41:a:2314:A:H1'	54:n:155:THR:HG21	1.54	0.89
11:AA:887:VAL:HG22	11:AA:913:VAL:CG2	2.00	0.89
8:7:-18:G:C5'	18:D:1500:A:H62	1.85	0.89
10:B:18:G:N2	10:B:58:A:N7	2.19	0.89
9:9:31:ARG:CZ	41:a:1054:A:C5'	2.49	0.89
14:AE:202:ARG:HG2	14:AE:202:ARG:HH11	1.35	0.89
6:5:114:DC:H5''	14:AE:1148:ARG:NH2	1.87	0.88
11:AA:1313:HIS:HD2	15:AF:31:GLN:NE2	1.71	0.88
12:AB:144:PHE:HB2	12:AB:164:ILE:CG1	2.02	0.88
14:AE:68:TYR:C	14:AE:75:TYR:HE2	1.80	0.88
11:AA:857:VAL:HG11	11:AA:862:LEU:CD1	2.04	0.88
9:9:50:VAL:CG2	39:Y:119:ALA:HB3	2.04	0.88
10:A:33:U:H5''	27:M:84:THR:HG21	1.55	0.88
22:H:71:ALA:C	22:H:72:LEU:CD1	2.42	0.88
17:C:31:ASN:OD1	22:H:268:VAL:HG22	1.74	0.88
12:AB:145:ASN:C	12:AB:162:VAL:HG22	1.99	0.88
12:AB:141:PHE:CD1	30:P:102:LEU:HD22	2.07	0.87
22:H:162:LYS:N	22:H:298:GLU:OE2	2.06	0.87
11:AA:858:GLY:O	11:AA:861:ALA:N	2.07	0.87
12:AB:136:VAL:HG11	12:AB:141:PHE:CD2	2.10	0.87
12:AB:141:PHE:CE1	30:P:102:LEU:CG	2.55	0.87
12:AB:138:ASP:HB2	12:AB:177:GLN:HA	1.55	0.87
12:AB:167:ARG:HG3	30:P:92:LEU:H	1.37	0.87
47:g:16:CYS:CB	47:g:37:CYS:HB3	2.05	0.87
9:9:142:THR:CG2	40:Z:7:ILE:HG12	2.02	0.87
22:H:119:GLY:HA2	22:H:133:GLY:CA	2.01	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:J:61:VAL:HG21	24:J:200:ILE:HD11	1.57	0.87
9:9:52:MET:C	9:9:52:MET:HE3	2.00	0.87
16:AG:219:GLU:O	21:G:157:LEU:HD12	1.74	0.87
22:H:131:LEU:CB	22:H:167:VAL:N	2.37	0.87
11:AA:901:LEU:CD2	16:AG:23:ILE:CB	2.53	0.86
14:AE:24:LEU:HG	14:AE:232:ASN:ND2	1.90	0.86
12:AB:137:ASN:OD1	12:AB:143:ASP:CA	2.23	0.86
14:AE:425:ARG:NH1	14:AE:458:ASN:O	2.08	0.86
39:Y:81:LYS:O	39:Y:81:LYS:HE3	1.75	0.86
11:AA:887:VAL:CG2	11:AA:913:VAL:HG22	2.05	0.86
11:AA:888:THR:HB	11:AA:889:PRO:HD2	1.55	0.86
21:G:18:HIS:HA	22:H:43:LYS:HD2	1.55	0.86
22:H:348:GLN:N	22:H:348:GLN:OE1	2.08	0.86
11:AA:855:PRO:HB3	16:AG:108:GLN:N	1.90	0.86
22:H:267:TRP:CD2	22:H:340:ARG:HG2	2.11	0.86
10:B:18:G:N7	10:B:57:A:C6	2.44	0.85
10:A:16:C:O2	41:a:2181:U:H5'	1.76	0.85
4:3:34:VAL:HG13	4:3:67:VAL:HG22	1.58	0.85
12:AB:136:VAL:HG22	12:AB:178:VAL:HG12	1.57	0.85
24:J:162:ALA:HB2	24:J:165:ARG:NH2	1.90	0.85
12:AB:171:VAL:HG13	12:AB:173:LEU:CD2	2.06	0.85
14:AE:68:TYR:HB3	14:AE:75:TYR:OH	1.76	0.85
9:9:31:ARG:CD	41:a:1054:A:H4'	2.06	0.85
22:H:267:TRP:CZ3	22:H:340:ARG:HG2	2.11	0.85
41:a:783:A:N3	41:a:783:A:H2'	1.89	0.85
18:D:197:A:C6	18:D:221:C:H4'	2.11	0.85
22:H:332:VAL:HG11	22:H:335:ILE:HG13	1.58	0.85
9:9:31:ARG:HH11	9:9:31:ARG:HG3	1.41	0.85
8:7:4:U:HO2'	11:AA:914:LYS:HD2	1.37	0.85
9:9:125:ARG:NH1	9:9:125:ARG:HA	1.92	0.85
10:A:18:G:N7	10:A:57:A:C6	2.44	0.85
22:H:135:LEU:CB	22:H:167:VAL:C	2.50	0.85
41:a:2303:G:C2	41:a:2314:A:C2	2.66	0.84
12:AB:144:PHE:CB	12:AB:164:ILE:HG21	2.07	0.84
21:G:16:PHE:HB3	22:H:43:LYS:HA	1.60	0.84
41:a:67:U:N3	41:a:74:A:N6	2.25	0.84
39:Y:20:SER:HB3	39:Y:21:PRO:HD3	1.59	0.84
12:AB:111:ILE:O	12:AB:115:LEU:HD22	1.77	0.84
22:H:131:LEU:CB	22:H:166:VAL:O	2.26	0.84
17:C:12:ARG:HH22	22:H:268:VAL:CG2	1.90	0.83
22:H:267:TRP:CH2	22:H:340:ARG:CG	2.61	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:26:SER:HB2	14:AE:236:TRP:CZ2	2.12	0.83
10:B:68:C:C2'	10:B:69:C:H5''	2.08	0.83
30:P:80:THR:HG1	30:P:83:THR:HG1	1.16	0.83
39:Y:60:VAL:HG13	39:Y:66:PHE:HB3	1.58	0.83
9:9:62:ARG:HG2	9:9:62:ARG:HH21	1.44	0.83
25:K:111:MET:HE2	25:K:125:ALA:HB1	1.59	0.83
14:AE:68:TYR:O	14:AE:75:TYR:HE2	1.58	0.83
7:6:21:DA:N1	8:7:15:G:N2	2.26	0.83
9:9:31:ARG:CD	41:a:1054:A:C4'	2.56	0.83
12:AB:140:PRO:HG2	30:P:102:LEU:HD11	1.57	0.83
16:AG:401:PRO:O	16:AG:403:VAL:N	2.11	0.83
9:9:57:ASN:OD1	9:9:62:ARG:CD	2.27	0.83
10:A:72:A:C2'	10:A:73:A:H5''	2.08	0.83
11:AA:913:VAL:HG12	16:AG:108:GLN:CB	2.09	0.83
10:A:68:C:C2'	10:A:69:C:H5''	2.08	0.83
39:Y:102:ARG:HB3	39:Y:141:ASP:HA	1.61	0.83
12:AB:141:PHE:CD1	30:P:102:LEU:CD2	2.62	0.82
41:a:1019:U:H3	41:a:1142:A:N6	1.77	0.82
10:B:72:A:C2'	10:B:73:A:H5''	2.09	0.82
18:D:1227:A:H5'	38:X:110:LYS:NZ	1.94	0.82
8:7:-19:U:OP2	18:D:1505:G:C8	2.32	0.82
8:7:-18:G:C5'	18:D:1500:A:N6	2.42	0.82
12:AB:141:PHE:CE1	30:P:102:LEU:HB2	2.06	0.82
7:6:18:DC:H42	8:7:17:G:H1	1.27	0.82
9:9:28:ALA:H	9:9:110:ALA:HA	1.44	0.82
10:B:56:C:H5'	54:n:80:ARG:NE	1.93	0.82
11:AA:808:ASN:H	14:AE:633:ALA:HB2	1.45	0.82
9:9:3:LEU:HD13	9:9:5:LEU:HG	1.61	0.82
10:A:54:U:H3	10:A:58:A:N6	1.77	0.82
11:AA:855:PRO:CB	16:AG:109:THR:N	2.42	0.82
18:D:37:U:N3	18:D:397:A:N6	2.28	0.82
12:AB:137:ASN:OD1	12:AB:143:ASP:N	2.13	0.82
8:7:-19:U:OP1	18:D:1505:G:C8	2.32	0.82
10:B:76:A:H1'	41:a:2494:G:P	2.20	0.82
11:AA:858:GLY:N	11:AA:861:ALA:HB3	1.94	0.81
17:C:12:ARG:CB	22:H:264:GLU:CB	2.59	0.81
22:H:305:HIS:CD2	22:H:306:VAL:H	1.98	0.81
41:a:1021:A:N6	41:a:1141:U:H3	1.77	0.81
41:a:1406:U:O2'	41:a:1407:G:H5''	1.79	0.81
14:AE:141:PHE:HE2	14:AE:296:LYS:HB2	1.44	0.81
41:a:1839:G:C1'	41:a:1927:A:N9	2.43	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:22:G:H2'	10:B:23:C:C6	2.16	0.81
10:B:56:C:C2'	10:B:57:A:H5''	2.11	0.81
11:AA:905:ILE:CG1	16:AG:54:GLY:O	2.24	0.81
14:AE:141:PHE:CE2	14:AE:296:LYS:HB2	2.15	0.81
39:Y:72:THR:OG1	39:Y:73:PRO:HD2	1.81	0.81
10:A:22:G:H2'	10:A:23:C:C6	2.16	0.81
11:AA:887:VAL:CG2	11:AA:913:VAL:HG21	2.11	0.81
11:AA:901:LEU:HD23	16:AG:23:ILE:CB	2.11	0.81
7:6:21:DA:N1	8:7:15:G:C2	2.49	0.81
10:A:7:G:H4'	10:A:8:U:OP1	1.81	0.81
10:A:56:C:C2'	10:A:57:A:H5''	2.11	0.81
14:AE:1169:THR:OG1	14:AE:1192:LYS:NZ	2.13	0.80
10:B:7:G:H4'	10:B:8:U:OP1	1.81	0.80
22:H:267:TRP:CZ3	22:H:340:ARG:CG	2.63	0.80
22:H:155:LYS:CB	22:H:169:SER:CB	2.58	0.80
10:B:54:U:H3	10:B:58:A:N6	1.77	0.80
9:9:31:ARG:HD2	41:a:1054:A:H4'	1.62	0.80
41:a:585:G:N7	66:z:6:ARG:NH1	2.29	0.80
41:a:1019:U:H3	41:a:1142:A:H61	1.28	0.80
41:a:2297:A:N1	41:a:2321:U:O4	2.14	0.80
14:AE:37:GLU:O	14:AE:61:ILE:HD11	1.81	0.80
14:AE:144:TYR:HE1	14:AE:162:GLU:OE2	1.64	0.80
10:B:58:A:O2'	10:B:59:A:H3'	1.82	0.80
18:D:972:C:O2'	30:P:57:VAL:CG2	2.29	0.80
9:9:43:LYS:HD2	9:9:43:LYS:C	2.05	0.80
39:Y:27:LEU:HD12	39:Y:27:LEU:O	1.81	0.80
22:H:270:ILE:CG2	22:H:337:GLU:HB3	2.12	0.80
24:J:162:ALA:CA	24:J:165:ARG:NH2	2.44	0.80
8:7:-7:U:H5'	23:I:132:ARG:HH12	1.01	0.80
11:AA:887:VAL:HG21	11:AA:913:VAL:HG21	1.63	0.80
24:J:162:ALA:HA	24:J:165:ARG:NH2	1.95	0.80
18:D:1397:C:OP1	18:D:1397:C:H2'	1.81	0.79
10:A:58:A:O2'	10:A:59:A:H3'	1.82	0.79
11:AA:854:ILE:HG13	11:AA:887:VAL:HB	1.62	0.79
14:AE:111:THR:HG23	14:AE:300:GLN:OE1	1.81	0.79
18:D:1329:A:P	38:X:28:THR:HB	2.22	0.79
11:AA:848:GLU:CG	11:AA:888:THR:HG22	2.06	0.79
11:AA:855:PRO:HB3	16:AG:109:THR:N	1.96	0.79
12:AB:169:THR:HG21	30:P:100:ILE:H	1.46	0.79
10:B:18:G:N2	10:B:58:A:C5	2.50	0.79
10:A:76:A:H2'	41:a:2394:C:H42	1.48	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:H:122:VAL:O	22:H:129:ALA:N	2.13	0.79
54:n:125:ARG:O	54:n:127:ASN:ND2	2.14	0.79
24:J:162:ALA:CB	24:J:165:ARG:NH2	2.44	0.79
47:g:18:CYS:HB3	47:g:40:CYS:CB	2.12	0.79
41:a:1021:A:H61	41:a:1141:U:H3	1.29	0.79
41:a:2298:A:C4	41:a:2321:U:C5	2.70	0.79
9:9:50:VAL:CG2	39:Y:119:ALA:CB	2.59	0.79
12:AB:141:PHE:CD2	12:AB:173:LEU:HD11	2.17	0.79
12:AB:160:VAL:HG12	12:AB:162:VAL:HG23	1.65	0.79
24:J:162:ALA:HB2	24:J:165:ARG:HH22	1.47	0.79
10:A:18:G:N2	10:A:58:A:C5	2.50	0.79
12:AB:148:VAL:HB	12:AB:160:VAL:HG22	1.63	0.79
21:G:16:PHE:CZ	22:H:41:GLY:O	2.36	0.79
11:AA:618:GLN:HG3	14:AE:770:LEU:HD13	1.64	0.78
12:AB:167:ARG:CD	30:P:92:LEU:N	2.46	0.78
9:9:11:ILE:HD11	9:9:62:ARG:HA	1.66	0.78
22:H:19:ARG:HD3	22:H:73:ASP:CG	2.09	0.78
22:H:162:LYS:CA	22:H:298:GLU:OE2	2.17	0.78
9:9:3:LEU:H	9:9:3:LEU:HD12	1.47	0.78
41:a:1406:U:O2'	41:a:1407:G:P	2.41	0.78
41:a:2189:U:OP1	41:a:2189:U:O4'	2.00	0.78
50:j:4:LEU:HD23	50:j:29:VAL:HG11	1.65	0.78
12:AB:146:GLY:HA3	12:AB:162:VAL:HA	1.63	0.78
9:9:39:THR:HA	9:9:42:ARG:HD2	1.64	0.78
9:9:78:GLY:N	9:9:79:PRO:HD2	1.97	0.78
16:AG:298:VAL:HA	16:AG:305:MET:HA	1.65	0.78
9:9:50:VAL:HG22	39:Y:119:ALA:HB3	1.60	0.78
12:AB:117:GLN:HA	12:AB:117:GLN:NE2	1.94	0.78
14:AE:90:VAL:HG13	14:AE:90:VAL:O	1.81	0.78
10:B:5:G:H2'	10:B:6:G:H5'	1.66	0.78
10:B:70:G:H2'	10:B:71:C:C5'	2.11	0.78
41:a:1406:U:O2'	41:a:1407:G:O5'	2.01	0.78
47:g:16:CYS:HB2	47:g:37:CYS:HB3	1.63	0.78
8:7:4:U:OP1	11:AA:890:LYS:HE3	1.83	0.78
9:9:31:ARG:CD	41:a:1054:A:C5'	2.58	0.78
14:AE:186:GLN:HG3	14:AE:238:ILE:HG13	1.65	0.78
10:A:5:G:H2'	10:A:6:G:H5'	1.66	0.77
14:AE:1075:ARG:NH2	14:AE:1168:GLU:OE2	2.17	0.77
22:H:123:GLU:HA	22:H:128:ARG:HA	1.63	0.77
10:A:15:G:N1	10:A:20:U:O2	2.17	0.77
7:6:18:DC:N3	8:7:17:G:N2	2.31	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:7:-19:U:OP1	18:D:1505:G:H8	1.63	0.77
10:A:33:U:O3'	27:M:84:THR:OG1	2.02	0.77
16:AG:32:ALA:CA	16:AG:102:PHE:O	2.32	0.77
22:H:305:HIS:CD2	22:H:306:VAL:N	2.53	0.77
10:B:15:G:N1	10:B:20:U:O2	2.17	0.77
39:Y:32:VAL:HG13	39:Y:60:VAL:HG21	1.66	0.77
10:A:68:C:C3'	10:A:69:C:H5''	2.15	0.77
10:B:18:G:C5	10:B:57:A:C6	2.72	0.77
41:a:2756:U:N3	41:a:2758:A:C6	2.53	0.77
41:a:2756:U:N3	41:a:2758:A:N6	2.32	0.77
10:A:18:G:C5	10:A:57:A:C6	2.72	0.77
7:6:15:DC:C4	7:6:16:DC:N4	2.53	0.76
14:AE:123:ARG:HG3	14:AE:1337:VAL:HG11	1.67	0.76
9:9:31:ARG:NE	41:a:1054:A:C4'	2.48	0.76
10:A:70:G:H2'	10:A:71:C:C5'	2.11	0.76
11:AA:854:ILE:CG1	11:AA:855:PRO:HD2	2.08	0.76
18:D:1358:U:C4	18:D:1363:A:N1	2.53	0.76
21:G:35:ARG:HD2	22:H:14:LYS:HD3	1.65	0.76
10:B:68:C:C3'	10:B:69:C:H5''	2.15	0.76
11:AA:902:LEU:HD11	16:AG:27:LEU:CB	2.12	0.76
12:AB:140:PRO:CB	30:P:79:PRO:CB	2.60	0.76
11:AA:906:PHE:CZ	16:AG:28:GLU:HA	2.20	0.76
39:Y:74:PRO:HG2	39:Y:77:VAL:HB	1.67	0.76
9:9:52:MET:HG3	9:9:95:LEU:HD11	1.68	0.76
12:AB:141:PHE:HE2	12:AB:173:LEU:HD12	1.31	0.76
12:AB:160:VAL:CG1	12:AB:162:VAL:HG23	2.16	0.76
9:9:27:VAL:HG23	9:9:83:ALA:HB3	1.67	0.75
12:AB:128:PHE:CB	12:AB:180:LYS:HB2	2.16	0.75
22:H:109:THR:HA	22:H:153:GLU:HA	1.68	0.75
47:g:18:CYS:CB	47:g:40:CYS:HB3	2.16	0.75
12:AB:144:PHE:CB	12:AB:164:ILE:CG1	2.61	0.75
12:AB:138:ASP:CB	12:AB:177:GLN:HA	2.16	0.75
9:9:60:LEU:HD23	9:9:64:VAL:HG21	1.67	0.75
9:9:97:LYS:HD3	9:9:127:ALA:HA	1.68	0.75
12:AB:140:PRO:HG3	30:P:79:PRO:HG2	1.66	0.75
25:K:137:VAL:O	25:K:140:THR:OG1	2.04	0.75
41:a:2298:A:C4	41:a:2321:U:H5	2.05	0.75
10:A:6:G:O2'	10:A:7:G:O5'	2.05	0.75
10:A:41:C:O4'	27:M:143:ARG:NH1	2.20	0.75
11:AA:858:GLY:N	11:AA:861:ALA:HB2	1.96	0.75
12:AB:136:VAL:CG1	12:AB:141:PHE:HD2	1.98	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Y:85:ILE:H	39:Y:85:ILE:HD12	1.52	0.75
64:x:31:THR:O	64:x:102:ARG:NH1	2.19	0.75
8:7:-18:G:H5''	18:D:1500:A:H62	1.40	0.74
10:B:6:G:O2'	10:B:7:G:O5'	2.05	0.74
21:G:35:ARG:HG3	22:H:10:GLU:OE2	1.86	0.74
10:A:32:C:C1'	27:M:144:MET:HE1	2.16	0.74
11:AA:857:VAL:CG1	11:AA:862:LEU:CD1	2.65	0.74
12:AB:135:ARG:HG2	12:AB:135:ARG:HH11	1.50	0.74
14:AE:110:PRO:HG2	14:AE:183:GLU:HG3	1.68	0.74
18:D:1227:A:H5'	38:X:110:LYS:HZ3	1.51	0.74
22:H:131:LEU:CB	22:H:166:VAL:C	2.60	0.74
22:H:109:THR:CA	22:H:153:GLU:HA	2.17	0.74
10:A:41:C:H1'	27:M:143:ARG:HH12	1.52	0.74
14:AE:120:LEU:O	14:AE:1330:ARG:NH1	2.21	0.74
22:H:19:ARG:HB2	22:H:73:ASP:OD2	1.88	0.74
10:A:18:G:H1'	10:A:58:A:C2	2.23	0.74
12:AB:167:ARG:HG2	30:P:91:ASP:CA	2.18	0.74
21:G:19:GLN:CG	22:H:76:GLU:HB2	2.18	0.74
22:H:304:VAL:HG12	22:H:309:MET:SD	2.28	0.74
6:5:115:DA:OP1	14:AE:1148:ARG:NE	2.21	0.74
9:9:78:GLY:N	9:9:79:PRO:CD	2.51	0.74
11:AA:845:LEU:HD23	11:AA:889:PRO:HB2	1.70	0.74
10:B:18:G:H1'	10:B:58:A:C2	2.23	0.74
10:B:76:A:H2'	10:B:76:A:N3	2.03	0.74
18:D:197:A:N6	18:D:221:C:H4'	2.01	0.74
14:AE:202:ARG:HG2	14:AE:202:ARG:NH1	1.99	0.73
14:AE:1143:ASP:OD1	14:AE:1148:ARG:NH1	2.21	0.73
8:7:14:U:H4'	14:AE:322:ARG:CD	2.18	0.73
11:AA:901:LEU:HA	16:AG:9:VAL:CA	2.17	0.73
14:AE:44:ILE:HD12	14:AE:252:LEU:CD2	2.18	0.73
14:AE:211:GLU:HG2	14:AE:215:LYS:HE3	1.70	0.73
10:B:18:G:O2'	10:B:60:U:C2	2.41	0.73
4:3:36:VAL:HG11	4:3:39:ILE:HD12	1.68	0.73
10:A:33:U:H5''	27:M:84:THR:CG2	2.19	0.73
12:AB:132:GLU:HB2	12:AB:147:VAL:HG22	1.71	0.73
18:D:1228:C:OP1	38:X:107:ARG:NH1	2.21	0.73
14:AE:105:ILE:HD12	14:AE:242:LEU:HD22	1.71	0.73
10:B:70:G:C3'	10:B:71:C:H5''	2.17	0.73
10:B:76:A:H1'	41:a:2494:G:OP1	1.88	0.73
14:AE:395:LYS:HZ2	14:AE:399:LYS:CD	2.00	0.73
8:7:-12:U:N3	18:D:1196:A:C8	2.57	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:864:LYS:HE3	11:AA:877:VAL:HG12	1.70	0.73
12:AB:145:ASN:HD22	14:AE:53:ARG:HH22	1.28	0.73
12:AB:146:GLY:CA	12:AB:162:VAL:HG22	2.19	0.73
14:AE:210:SER:HB3	14:AE:213:LYS:HB2	1.71	0.73
18:D:517:G:O2'	18:D:530:G:H4'	1.88	0.73
10:A:70:G:C3'	10:A:71:C:H5''	2.18	0.73
17:C:44:ILE:CD1	22:H:339:ARG:CG	2.62	0.73
39:Y:36:GLU:OE1	39:Y:36:GLU:HA	1.88	0.73
41:a:1021:A:N1	41:a:1141:U:C4	2.55	0.73
41:a:1913:A:OP2	41:a:1913:A:H3'	1.89	0.73
9:9:77:VAL:HG12	9:9:82:ILE:HG21	1.71	0.73
41:a:2013:A:N6	41:a:2613:U:N3	2.33	0.73
16:AG:401:PRO:C	16:AG:403:VAL:H	1.97	0.73
22:H:110:GLY:CA	22:H:153:GLU:O	2.36	0.73
14:AE:68:TYR:C	14:AE:75:TYR:CE2	2.65	0.72
29:O:84:THR:HG21	29:O:103:PHE:HB3	1.71	0.72
41:a:1839:G:C1'	41:a:1927:A:C1'	2.67	0.72
9:9:18:VAL:HA	9:9:86:MET:HE2	1.71	0.72
12:AB:145:ASN:ND2	14:AE:53:ARG:CZ	2.52	0.72
12:AB:141:PHE:CZ	12:AB:173:LEU:HD12	2.15	0.72
17:C:44:ILE:HD13	22:H:339:ARG:HG3	1.70	0.72
10:A:18:G:O2'	10:A:60:U:C2	2.41	0.72
11:AA:905:ILE:HG12	16:AG:54:GLY:C	2.14	0.72
22:H:267:TRP:CE3	22:H:340:ARG:HG2	2.25	0.72
32:R:86:ARG:HG3	32:R:86:ARG:O	1.89	0.72
41:a:67:U:C4	41:a:74:A:N6	2.57	0.72
7:6:21:DA:C6	8:7:15:G:N2	2.57	0.72
14:AE:107:LEU:HD11	14:AE:242:LEU:HB2	1.70	0.72
12:AB:146:GLY:HA3	12:AB:162:VAL:CG2	2.20	0.72
18:D:827:U:H3	18:D:872:A:N6	1.87	0.72
22:H:267:TRP:CE3	22:H:340:ARG:CG	2.72	0.72
10:A:72:A:C3'	10:A:73:A:H5''	2.20	0.71
10:B:72:A:C3'	10:B:73:A:H5''	2.20	0.71
21:G:19:GLN:OE1	22:H:75:VAL:O	1.85	0.71
22:H:70:VAL:HA	22:H:85:SER:CB	2.20	0.71
10:B:46:G:H1'	10:B:47:U:C5	2.25	0.71
10:B:18:G:C5	10:B:57:A:N6	2.59	0.71
17:C:12:ARG:HB2	22:H:264:GLU:CB	2.20	0.71
41:a:742:A:H2'	41:a:743:A:C8	2.26	0.71
8:7:-12:U:O4	18:D:1196:A:N9	2.24	0.71
14:AE:220:ARG:HG2	14:AE:220:ARG:HH11	1.55	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:140:PRO:CG	30:P:102:LEU:HD21	2.19	0.71
16:AG:219:GLU:CB	21:G:157:LEU:HG	2.19	0.71
12:AB:128:PHE:HB2	12:AB:180:LYS:HB2	1.71	0.71
12:AB:155:LYS:HE3	18:D:1276:G:OP2	1.90	0.71
14:AE:54:ASP:OD1	14:AE:54:ASP:N	2.24	0.71
18:D:1308:U:C3'	38:X:98:ARG:HH21	1.92	0.71
30:P:87:LEU:CD2	30:P:90:LEU:O	2.37	0.71
9:9:3:LEU:HD12	9:9:3:LEU:N	2.05	0.71
41:a:2314:A:C1'	54:n:155:THR:HG21	2.21	0.71
47:g:18:CYS:CB	47:g:40:CYS:CB	2.68	0.71
10:A:15:G:H2'	10:A:15:G:N3	2.06	0.71
10:A:46:G:H1'	10:A:47:U:C5	2.25	0.71
12:AB:138:ASP:CG	12:AB:177:GLN:HA	2.15	0.71
14:AE:142:GLU:HG3	14:AE:142:GLU:O	1.89	0.71
10:B:76:A:H2'	41:a:2493:U:H5''	1.72	0.71
12:AB:144:PHE:HB3	12:AB:164:ILE:CD1	2.21	0.70
38:X:96:PRO:HG2	38:X:102:THR:CG2	2.20	0.70
11:AA:903:ARG:C	16:AG:8:VAL:CB	2.63	0.70
18:D:1308:U:O5'	38:X:98:ARG:HG3	1.90	0.70
12:AB:169:THR:CG2	30:P:100:ILE:H	2.03	0.70
14:AE:44:ILE:HD12	14:AE:252:LEU:HD21	1.71	0.70
21:G:19:GLN:CD	22:H:76:GLU:HB2	2.08	0.70
22:H:70:VAL:HA	22:H:85:SER:CA	2.22	0.70
8:7:14:U:H4'	14:AE:322:ARG:HD2	1.74	0.70
14:AE:157:GLN:OE1	14:AE:157:GLN:HA	1.88	0.70
21:G:16:PHE:CB	22:H:43:LYS:HA	2.20	0.70
10:A:18:G:C5	10:A:57:A:N6	2.59	0.70
10:A:32:C:C1'	27:M:144:MET:CE	2.69	0.70
10:A:41:C:C1'	27:M:143:ARG:NH1	2.55	0.70
16:AG:32:ALA:HA	16:AG:103:ASP:O	1.92	0.70
18:D:1309:G:H8	38:X:98:ARG:NH2	1.89	0.70
9:9:31:ARG:HD2	41:a:1054:A:C5'	2.22	0.70
11:AA:888:THR:HB	11:AA:889:PRO:CD	2.22	0.70
22:H:86:ARG:O	22:H:89:ALA:HB3	1.91	0.70
41:a:1021:A:H3'	41:a:1021:A:N3	2.07	0.70
41:a:2310:C:O2'	54:n:74:VAL:CG1	2.40	0.70
11:AA:65:ASN:HB3	11:AA:105:TYR:HB2	1.73	0.70
11:AA:905:ILE:HA	16:AG:54:GLY:C	2.17	0.70
39:Y:21:PRO:CB	39:Y:22:PRO:HD3	2.22	0.69
11:AA:849:GLU:HB2	11:AA:887:VAL:HG12	1.72	0.69
12:AB:140:PRO:CD	30:P:102:LEU:CD2	2.35	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:80:ARG:NH2	41:a:572:A:OP2	2.25	0.69
9:9:58:THR:HG21	9:9:81:LEU:HG	1.74	0.69
12:AB:159:LYS:HG3	12:AB:170:PRO:HB2	1.74	0.69
18:D:972:C:O2'	30:P:57:VAL:HG23	1.92	0.69
14:AE:39:LYS:O	14:AE:273:ILE:CG2	2.41	0.69
18:D:37:U:H3	18:D:397:A:N6	1.90	0.69
11:AA:855:PRO:HB2	16:AG:109:THR:N	2.05	0.69
10:B:15:G:H2'	10:B:15:G:N3	2.06	0.69
18:D:915:A:N6	18:D:916:U:C4	2.60	0.69
41:a:1596:A:H2'	41:a:1597:A:C8	2.28	0.69
9:9:50:VAL:HG13	39:Y:119:ALA:CB	2.22	0.69
12:AB:144:PHE:CB	12:AB:164:ILE:CG2	2.69	0.69
13:AC:232:VAL:C	13:AD:221:ALA:HB1	2.15	0.69
10:B:11:A:H2'	10:B:12:G:O4'	1.92	0.69
48:h:146:MET:HE3	48:h:154:LEU:HD21	1.74	0.69
12:AB:164:ILE:O	30:P:88:MET:HB2	1.93	0.69
14:AE:832:LYS:C	14:AE:1242:ARG:HH12	2.01	0.69
18:D:13:U:O4	18:D:21:G:C2	2.46	0.69
11:AA:887:VAL:HG21	11:AA:913:VAL:CG2	2.20	0.69
11:AA:1268:GLN:HE22	14:AE:352:ARG:HD2	1.57	0.69
14:AE:128:LEU:HD11	14:AE:189:LEU:HG	1.73	0.69
22:H:19:ARG:HD3	22:H:73:ASP:OD1	1.92	0.69
22:H:267:TRP:CE2	22:H:340:ARG:CG	2.73	0.69
7:6:21:DA:C2	8:7:15:G:N2	2.61	0.68
10:A:11:A:H2'	10:A:12:G:O4'	1.92	0.68
10:A:16:C:O2	41:a:2181:U:C5'	2.40	0.68
38:X:96:PRO:CG	38:X:102:THR:CG2	2.71	0.68
10:A:19:G:N2	41:a:2112:G:C8	2.62	0.68
41:a:2756:U:C4	41:a:2758:A:N6	2.61	0.68
13:AD:48:LEU:HB2	13:AD:183:ILE:HD11	1.76	0.68
22:H:110:GLY:HA3	22:H:153:GLU:O	1.93	0.68
11:AA:1332:SER:O	14:AE:243:PRO:HG2	1.93	0.68
14:AE:94:GLN:HB2	14:AE:97:VAL:HG23	1.76	0.68
14:AE:141:PHE:CD2	14:AE:293:ARG:O	2.47	0.68
12:AB:128:PHE:CE1	12:AB:175:PHE:O	2.45	0.68
14:AE:395:LYS:HZ2	14:AE:399:LYS:HD3	1.59	0.68
22:H:19:ARG:HD3	22:H:73:ASP:OD2	1.92	0.68
39:Y:14:ALA:HB2	39:Y:54:ILE:HD12	1.76	0.68
41:a:927:A:H2'	41:a:928:A:C8	2.28	0.68
7:6:8:DC:C6	7:6:9:DT:H72	2.29	0.68
41:a:1153:C:OP1	66:z:92:ARG:NH1	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:2310:C:O2'	54:n:74:VAL:HG12	1.94	0.68
41:a:1839:G:C4	41:a:1927:A:C4	2.81	0.68
39:Y:58:ILE:HD13	39:Y:58:ILE:N	2.09	0.68
41:a:1839:G:H8	41:a:1927:A:H1'	1.55	0.68
9:9:73:LYS:HB2	9:9:117:LEU:HD21	1.75	0.68
12:AB:140:PRO:CG	30:P:79:PRO:HG2	2.24	0.68
22:H:267:TRP:CD2	22:H:340:ARG:CG	2.76	0.68
41:a:1920:C:O5'	41:a:1920:C:H6	1.77	0.68
14:AE:117:LEU:HD12	14:AE:117:LEU:O	1.94	0.67
10:B:5:G:H2'	10:B:6:G:C5'	2.24	0.67
14:AE:984:LEU:HB3	14:AE:993:GLU:HB2	1.76	0.67
9:9:43:LYS:HD2	9:9:43:LYS:O	1.94	0.67
14:AE:1355:ARG:NH1	14:AE:1369:ARG:HH12	1.93	0.67
18:D:1358:U:O4	18:D:1363:A:C2	2.47	0.67
11:AA:905:ILE:HG23	16:AG:55:ASP:HA	1.75	0.67
14:AE:108:ALA:CB	14:AE:279:LEU:HD22	2.25	0.67
16:AG:219:GLU:CB	21:G:157:LEU:H	2.08	0.67
22:H:117:LYS:CB	22:H:279:LYS:O	2.41	0.67
38:X:96:PRO:CG	38:X:102:THR:HG22	2.25	0.67
12:AB:149:GLU:N	12:AB:149:GLU:OE1	2.27	0.67
7:6:16:DC:H1'	14:AE:426:ALA:HB1	1.77	0.67
14:AE:108:ALA:HB3	14:AE:279:LEU:HD22	1.77	0.67
10:B:66:C:H5'	10:B:66:C:H6	1.60	0.67
36:V:25:ILE:HD11	36:V:61:ILE:HD11	1.77	0.67
12:AB:144:PHE:HB2	12:AB:164:ILE:CB	2.25	0.67
41:a:1839:G:C8	41:a:1927:A:C1'	2.74	0.67
8:7:-6:U:OP1	23:I:136:ARG:NH2	2.28	0.67
12:AB:167:ARG:CG	30:P:92:LEU:HD12	2.23	0.67
41:a:1779:U:H5	41:a:1784:A:N7	1.93	0.66
56:p:24:ILE:HD13	56:p:72:LEU:HD21	1.77	0.66
9:9:11:ILE:CD1	9:9:62:ARG:HD3	2.24	0.66
9:9:118:ILE:HB	9:9:119:PRO:HD3	1.76	0.66
14:AE:161:THR:HG22	14:AE:164:GLN:HB2	1.75	0.66
23:I:75:ILE:O	23:I:75:ILE:HD13	1.95	0.66
10:A:56:C:C5	41:a:2168:G:C6	2.83	0.66
14:AE:978:ARG:HG2	14:AE:1197:ASN:HD21	1.60	0.66
18:D:563:A:N1	18:D:884:U:C4	2.60	0.66
38:X:96:PRO:HG3	38:X:102:THR:HG22	1.78	0.66
9:9:67:THR:N	9:9:68:PRO:CD	2.58	0.66
10:A:5:G:H2'	10:A:6:G:C5'	2.24	0.66
11:AA:849:GLU:HB2	11:AA:887:VAL:HG13	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:H:270:ILE:HG23	22:H:337:GLU:HB3	1.78	0.66
11:AA:904:ALA:HB2	16:AG:9:VAL:H	1.61	0.66
10:A:66:C:H6	10:A:66:C:H5'	1.60	0.66
12:AB:129:GLU:OE1	12:AB:130:PRO:CD	2.43	0.66
14:AE:193:ASP:HB3	14:AE:196:GLN:HB2	1.78	0.66
21:G:16:PHE:HZ	22:H:41:GLY:O	1.77	0.66
22:H:162:LYS:CB	22:H:298:GLU:OE1	2.44	0.66
9:9:142:THR:HG21	40:Z:7:ILE:CD1	2.26	0.66
59:s:114:LEU:HG	59:s:118:MET:HE3	1.78	0.66
10:A:32:C:C4'	27:M:144:MET:CE	2.66	0.66
22:H:110:GLY:N	22:H:153:GLU:C	2.53	0.66
41:a:1923:U:H2'	41:a:1923:U:OP2	1.96	0.66
10:B:56:C:H5'	54:n:80:ARG:NH2	2.11	0.66
8:7:-12:U:O4	18:D:1196:A:O4'	2.13	0.65
9:9:61:ARG:NH1	41:a:1047:G:N7	2.44	0.65
12:AB:93:ILE:HG22	14:AE:290:ILE:HG22	1.79	0.65
10:B:37:A:H3'	10:B:37:A:OP2	1.96	0.65
39:Y:116:MET:HB3	39:Y:124:MET:HG2	1.76	0.65
21:G:19:GLN:CG	22:H:75:VAL:CG2	2.70	0.65
22:H:70:VAL:HA	22:H:85:SER:HA	1.77	0.65
22:H:110:GLY:H	22:H:153:GLU:CA	2.08	0.65
11:AA:901:LEU:HD21	16:AG:23:ILE:CB	2.27	0.65
12:AB:125:LYS:CG	12:AB:153:TYR:HB2	2.24	0.65
12:AB:152:ASP:HB2	12:AB:157:ARG:HB3	1.78	0.65
22:H:135:LEU:CA	22:H:157:ILE:CB	2.74	0.65
9:9:60:LEU:HA	9:9:64:VAL:HB	1.77	0.65
14:AE:68:TYR:HB3	14:AE:75:TYR:CE2	2.32	0.65
10:B:3:C:H2'	10:B:4:G:H8	1.62	0.65
8:7:-10:U:O2'	25:K:33:PHE:HE1	1.77	0.65
10:A:3:C:H2'	10:A:4:G:H8	1.62	0.65
10:A:18:G:C8	10:A:57:A:C6	2.85	0.65
10:B:22:G:H2'	10:B:23:C:H6	1.62	0.65
9:9:11:ILE:HG13	9:9:65:GLU:HB3	1.79	0.65
9:9:78:GLY:H	9:9:79:PRO:CD	2.10	0.65
18:D:1227:A:OP2	38:X:110:LYS:NZ	2.29	0.65
22:H:19:ARG:O	22:H:72:LEU:CB	2.41	0.65
22:H:118:GLY:C	22:H:133:GLY:CA	2.68	0.65
22:H:267:TRP:CE3	22:H:340:ARG:HG3	2.32	0.65
9:9:50:VAL:CG1	39:Y:119:ALA:HB3	2.26	0.65
12:AB:140:PRO:CG	30:P:102:LEU:CD2	2.74	0.65
12:AB:167:ARG:HG2	30:P:92:LEU:H	1.58	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:84:ILE:O	14:AE:84:ILE:HG13	1.96	0.65
10:B:21:A:H4'	10:B:21:A:OP1	1.95	0.65
22:H:52:GLN:O	22:H:53:PHE:CD1	2.50	0.65
22:H:332:VAL:HG12	22:H:334:ASP:H	1.62	0.65
8:7:-12:U:N3	18:D:1196:A:N7	2.44	0.65
10:A:41:C:C4'	27:M:143:ARG:NH1	2.60	0.65
14:AE:162:GLU:OE1	14:AE:162:GLU:HA	1.97	0.65
18:D:197:A:C6	18:D:221:C:C4'	2.80	0.65
9:9:29:ASP:HB2	9:9:56:ARG:HD3	1.79	0.64
10:A:21:A:H4'	10:A:21:A:OP1	1.95	0.64
10:B:18:G:C8	10:B:57:A:C6	2.85	0.64
22:H:85:SER:O	22:H:88:LYS:CB	2.45	0.64
8:7:-13:U:OP2	18:D:1397:C:N3	2.30	0.64
11:AA:901:LEU:HD21	16:AG:20:ARG:O	1.97	0.64
14:AE:111:THR:CG2	14:AE:300:GLN:CD	2.66	0.64
41:a:1082:U:N3	41:a:1086:A:N6	2.45	0.64
12:AB:146:GLY:HA3	12:AB:162:VAL:HG22	1.80	0.64
10:B:75:C:OP1	41:a:2602:A:N9	2.30	0.64
18:D:1358:U:N3	18:D:1363:A:N6	2.46	0.64
12:AB:171:VAL:CG1	12:AB:173:LEU:HD22	2.25	0.64
18:D:1308:U:O5'	38:X:98:ARG:CG	2.45	0.64
18:D:1308:U:H5''	38:X:98:ARG:HG2	1.78	0.64
55:o:26:HIS:CE1	55:o:48:ALA:HB2	2.32	0.64
10:A:50:U:H2'	10:A:51:C:C6	2.33	0.64
12:AB:128:PHE:HB2	12:AB:180:LYS:HG3	1.79	0.64
18:D:1358:U:H3	18:D:1363:A:N6	1.96	0.64
11:AA:314:ASN:HD21	11:AA:348:SER:HA	1.62	0.64
14:AE:975:ILE:HG22	14:AE:977:SER:H	1.62	0.64
12:AB:138:ASP:HB2	12:AB:177:GLN:HG2	1.80	0.64
12:AB:171:VAL:CG1	12:AB:173:LEU:CD2	2.75	0.64
10:B:76:A:H1'	41:a:2493:U:O3'	1.97	0.64
33:S:47:LYS:O	33:S:50:THR:OG1	2.12	0.64
12:AB:128:PHE:HB2	12:AB:180:LYS:CB	2.28	0.64
8:7:-7:U:H5'	23:I:132:ARG:CZ	2.26	0.64
14:AE:1037:PHE:HB3	14:AE:1040:MET:HB2	1.78	0.64
10:B:50:U:H2'	10:B:51:C:C6	2.33	0.64
21:G:35:ARG:HH21	22:H:10:GLU:HG2	1.62	0.64
11:AA:528:ARG:NH2	11:AA:576:SER:O	2.30	0.63
11:AA:858:GLY:C	11:AA:861:ALA:H	2.03	0.63
12:AB:141:PHE:HA	30:P:84:VAL:CG2	2.28	0.63
21:G:19:GLN:CG	22:H:76:GLU:CB	2.76	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:H:270:ILE:HG21	22:H:337:GLU:HB3	1.80	0.63
41:a:1909:C:O5'	41:a:1909:C:H6	1.81	0.63
2:1:36:LEU:HD13	2:1:48:LYS:HA	1.80	0.63
10:A:56:C:O2	41:a:2112:G:C4	2.52	0.63
14:AE:44:ILE:CD1	14:AE:252:LEU:HD21	2.29	0.63
9:9:11:ILE:HD12	9:9:62:ARG:HD3	1.80	0.63
9:9:57:ASN:CG	9:9:62:ARG:CG	2.68	0.63
11:AA:1280:ALA:HB1	14:AE:918:ILE:HG22	1.80	0.63
41:a:2297:A:C2	41:a:2321:U:C4	2.86	0.63
41:a:2303:G:N3	41:a:2314:A:C2	2.66	0.63
9:9:23:LEU:HB3	9:9:92:ALA:HA	1.81	0.63
10:A:31:G:O2'	27:M:144:MET:SD	2.56	0.63
11:AA:120:GLN:NE2	11:AA:490:GLN:OE1	2.32	0.63
11:AA:1287:LEU:HD13	14:AE:1357:ILE:HD11	1.81	0.63
18:D:13:U:O4	18:D:20:U:C4	2.52	0.63
22:H:49:PRO:CD	22:H:84:LEU:HD11	2.29	0.63
22:H:119:GLY:CA	22:H:131:LEU:O	2.46	0.63
41:a:1839:G:O4'	41:a:1927:A:H1'	1.97	0.63
9:9:57:ASN:OD1	9:9:62:ARG:HD2	1.98	0.63
14:AE:67:ASP:OD1	14:AE:95:THR:OG1	2.15	0.63
22:H:162:LYS:CB	22:H:298:GLU:OE2	2.45	0.63
39:Y:116:MET:HE2	39:Y:116:MET:HA	1.79	0.63
1:0:40:MET:HE1	66:z:105:ALA:HB1	1.80	0.63
12:AB:167:ARG:NE	30:P:92:LEU:HB2	2.14	0.63
56:p:121:ILE:HD12	56:p:141:ILE:HG22	1.79	0.63
18:D:1329:A:P	38:X:28:THR:CB	2.83	0.63
14:AE:141:PHE:HD2	14:AE:293:ARG:O	1.80	0.63
18:D:1309:G:C8	38:X:98:ARG:NH2	2.66	0.63
24:J:162:ALA:CB	24:J:165:ARG:HH22	2.08	0.63
41:a:1998:A:OP2	50:j:141:ARG:NH2	2.32	0.63
14:AE:245:LEU:HG	14:AE:246:PRO:HD2	1.79	0.62
18:D:1059:C:O2	30:P:55:PRO:HG3	1.99	0.62
41:a:1789:A:OP2	48:h:221:ARG:NH1	2.32	0.62
14:AE:128:LEU:HA	14:AE:192:MET:HE1	1.81	0.62
16:AG:142:VAL:HA	16:AG:152:LEU:HA	1.81	0.62
10:B:6:G:HO2'	10:B:7:G:H8	1.46	0.62
9:9:92:ALA:HB3	9:9:129:LEU:HB2	1.82	0.62
14:AE:136:GLU:CD	14:AE:312:ARG:HH22	2.06	0.62
6:5:101:DT:OP2	14:AE:275:ARG:NH2	2.31	0.62
8:7:-14:U:H5''	8:7:-14:U:H6	1.64	0.62
9:9:57:ASN:CG	9:9:62:ARG:HG2	2.25	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:813:GLU:HB2	14:AE:461:PHE:HD2	1.63	0.62
11:AA:862:LEU:HD22	11:AA:862:LEU:N	2.14	0.62
41:a:1839:G:N9	41:a:1927:A:N9	2.48	0.62
9:9:18:VAL:HG13	9:9:71:CYS:HB2	1.81	0.62
13:AD:211:ILE:HG12	13:AD:219:ARG:HH12	1.65	0.62
10:B:69:C:H2'	10:B:70:G:O4'	1.99	0.62
18:D:37:U:O2	18:D:548:G:C2	2.52	0.62
18:D:827:U:N3	18:D:872:A:N6	2.45	0.62
41:a:2885:G:N7	49:i:40:ARG:NH2	2.46	0.62
6:5:98:DA:C2'	6:5:99:DT:H72	2.28	0.62
11:AA:1101:LEU:HD23	14:AE:725:MET:SD	2.40	0.62
14:AE:1355:ARG:NH1	14:AE:1369:ARG:NH1	2.47	0.62
22:H:110:GLY:N	22:H:153:GLU:O	2.32	0.62
12:AB:141:PHE:CZ	30:P:102:LEU:HB3	2.35	0.62
10:A:69:C:H2'	10:A:70:G:O4'	1.99	0.62
12:AB:171:VAL:O	12:AB:173:LEU:HD22	1.98	0.62
21:G:18:HIS:HA	22:H:43:LYS:CD	2.27	0.62
27:M:23:LEU:O	27:M:27:VAL:HG13	1.99	0.62
38:X:101:ARG:O	38:X:101:ARG:HD3	2.00	0.62
41:a:2189:U:O4'	41:a:2189:U:P	2.57	0.62
3:2:50:LEU:HD23	45:e:26:PHE:CE1	2.35	0.62
10:A:37:A:O2'	10:A:38:A:H5'	1.99	0.62
13:AC:45:ARG:HD3	13:AD:38:THR:HB	1.82	0.62
10:B:54:U:N3	10:B:58:A:N6	2.47	0.62
21:G:38:VAL:HG22	22:H:75:VAL:CG2	2.24	0.62
30:P:28:THR:HG22	30:P:86:ALA:HB1	1.82	0.62
30:P:57:VAL:O	30:P:58:ASN:CG	2.43	0.62
14:AE:92:VAL:O	14:AE:92:VAL:HG12	1.99	0.62
14:AE:111:THR:CG2	14:AE:300:GLN:NE2	2.63	0.62
8:7:-7:U:OP1	23:I:132:ARG:NH1	2.33	0.61
10:A:42:G:H2'	10:A:43:A:H8	1.65	0.61
17:C:29:LEU:O	17:C:33:ILE:HG23	2.00	0.61
22:H:270:ILE:CG2	22:H:337:GLU:CB	2.77	0.61
10:A:54:U:N3	10:A:58:A:N6	2.48	0.61
39:Y:32:VAL:HA	39:Y:60:VAL:HG11	1.81	0.61
10:A:33:U:H4'	27:M:84:THR:HB	1.82	0.61
12:AB:167:ARG:HD3	30:P:92:LEU:N	2.14	0.61
14:AE:24:LEU:CG	14:AE:232:ASN:ND2	2.63	0.61
14:AE:90:VAL:O	14:AE:90:VAL:CG1	2.48	0.61
14:AE:201:LEU:HB2	14:AE:221:ILE:HD13	1.80	0.61
14:AE:223:LEU:HG	14:AE:223:LEU:O	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:65:C:H2'	10:A:66:C:H5'	1.82	0.61
10:A:22:G:H2'	10:A:23:C:H6	1.62	0.61
12:AB:125:LYS:HG2	12:AB:153:TYR:CB	2.30	0.61
12:AB:165:PHE:CE2	12:AB:171:VAL:HG11	2.35	0.61
10:B:3:C:H2'	10:B:4:G:C8	2.36	0.61
41:a:84:A:N1	41:a:98:G:O2'	2.33	0.61
7:6:15:DC:C4	7:6:16:DC:C4	2.89	0.61
10:A:3:C:H2'	10:A:4:G:C8	2.36	0.61
12:AB:159:LYS:HG2	12:AB:170:PRO:HB3	1.82	0.61
14:AE:342:LEU:HD23	14:AE:1352:ILE:HG23	1.83	0.61
22:H:304:VAL:HG12	22:H:304:VAL:O	1.99	0.61
8:7:17:G:OP2	11:AA:540:ARG:NH1	2.33	0.61
16:AG:219:GLU:CB	21:G:157:LEU:N	2.64	0.61
22:H:71:ALA:O	22:H:72:LEU:CD1	2.42	0.61
9:9:136:ILE:HD12	9:9:139:LEU:HD12	1.83	0.61
10:B:42:G:H2'	10:B:43:A:H8	1.65	0.61
18:D:1308:U:H2'	38:X:98:ARG:HH22	1.61	0.61
21:G:19:GLN:HG3	22:H:76:GLU:HB2	1.82	0.61
25:K:107:ALA:HB2	25:K:125:ALA:HB3	1.82	0.61
41:a:754:U:H2'	41:a:755:U:C6	2.35	0.61
11:AA:549:ASP:OD2	14:AE:750:PRO:CB	2.44	0.60
11:AA:1268:GLN:HE21	14:AE:352:ARG:HD2	1.66	0.60
12:AB:145:ASN:N	12:AB:145:ASN:OD1	2.34	0.60
14:AE:144:TYR:CE1	14:AE:162:GLU:OE2	2.51	0.60
27:M:69:VAL:HG23	27:M:100:ALA:HB1	1.83	0.60
11:AA:862:LEU:HD22	11:AA:862:LEU:H	1.66	0.60
11:AA:1072:ASN:ND2	11:AA:1111:GLN:OE1	2.34	0.60
12:AB:135:ARG:HH11	12:AB:135:ARG:CG	2.14	0.60
10:B:56:C:C4'	54:n:80:ARG:NH2	2.63	0.60
21:G:19:GLN:CD	22:H:75:VAL:HG22	2.25	0.60
9:9:6:GLN:OE1	9:9:6:GLN:HA	2.00	0.60
10:A:41:C:H4'	27:M:143:ARG:CZ	2.31	0.60
12:AB:167:ARG:HG2	30:P:92:LEU:N	2.15	0.60
14:AE:951:GLN:NE2	14:AE:1014:GLY:O	2.35	0.60
17:C:44:ILE:CD1	22:H:339:ARG:HG3	2.28	0.60
18:D:1218:C:H2'	18:D:1219:A:C8	2.36	0.60
12:AB:140:PRO:HG2	30:P:102:LEU:HD13	1.78	0.60
12:AB:166:GLY:CA	30:P:87:LEU:HB3	2.27	0.60
14:AE:395:LYS:NZ	14:AE:399:LYS:HD3	2.15	0.60
18:D:13:U:C5	18:D:20:U:O4	2.53	0.60
22:H:84:LEU:HD22	22:H:84:LEU:N	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:H:305:HIS:HD2	22:H:306:VAL:H	1.49	0.60
35:U:21:VAL:HG21	35:U:60:TRP:CD1	2.36	0.60
40:Z:7:ILE:HG23	40:Z:7:ILE:O	2.01	0.60
41:a:2720:U:OP1	65:y:53:ARG:NH2	2.34	0.60
9:9:77:VAL:HG12	9:9:77:VAL:O	2.01	0.60
10:A:76:A:H2'	41:a:2394:C:N4	2.11	0.60
12:AB:165:PHE:HB3	30:P:84:VAL:HG13	1.82	0.60
14:AE:68:TYR:HB3	14:AE:75:TYR:CZ	2.35	0.60
14:AE:154:LEU:HD21	14:AE:160:LEU:HD21	1.83	0.60
14:AE:412:LEU:HD22	14:AE:441:LEU:HD21	1.84	0.60
10:B:65:C:H2'	10:B:66:C:H5'	1.82	0.60
40:Z:20:VAL:O	40:Z:20:VAL:HG12	2.02	0.60
41:a:2297:A:C2	41:a:2321:U:C5	2.89	0.60
53:m:31:LEU:HD22	53:m:42:LEU:HD13	1.84	0.60
12:AB:128:PHE:HB3	12:AB:180:LYS:HB2	1.82	0.60
12:AB:156:SER:O	12:AB:156:SER:OG	2.16	0.60
12:AB:159:LYS:HG2	12:AB:159:LYS:O	2.00	0.60
22:H:331:MET:N	22:H:331:MET:SD	2.75	0.60
11:AA:55:SER:OG	11:AA:465:ARG:NH1	2.33	0.60
22:H:270:ILE:HG21	22:H:337:GLU:CB	2.32	0.60
11:AA:69:GLN:HE21	11:AA:101:ARG:HD2	1.67	0.60
14:AE:201:LEU:HD11	14:AE:220:ARG:HH11	1.67	0.60
14:AE:370:LYS:HG2	14:AE:441:LEU:HD23	1.84	0.60
22:H:305:HIS:O	22:H:306:VAL:HB	2.00	0.60
41:a:1921:G:O5'	41:a:1921:G:H8	1.84	0.60
10:A:34:C:P	27:M:84:THR:OG1	2.60	0.60
11:AA:855:PRO:CG	16:AG:108:GLN:CB	2.69	0.60
11:AA:1282:GLY:HA3	15:AF:17:PHE:HE1	1.67	0.60
41:a:70:G:H4'	41:a:71:A:OP1	2.02	0.60
22:H:305:HIS:CD2	22:H:307:SER:H	2.20	0.60
39:Y:54:ILE:O	39:Y:54:ILE:HG22	2.00	0.60
41:a:1406:U:HO2'	41:a:1407:G:C5'	2.07	0.60
18:D:13:U:C2	18:D:915:A:N6	2.70	0.59
8:7:20:G:OP1	11:AA:1073:LYS:NZ	2.26	0.59
10:A:47:U:O2'	10:A:50:U:P	2.61	0.59
11:AA:901:LEU:CA	16:AG:9:VAL:HA	2.25	0.59
18:D:404:G:N7	24:J:2:ALA:HB3	2.17	0.59
18:D:658:C:H1'	34:T:22:THR:HG21	1.83	0.59
21:G:35:ARG:HD2	22:H:14:LYS:CD	2.32	0.59
13:AD:112:ALA:HB3	13:AD:126:PRO:HA	1.83	0.59
22:H:267:TRP:CZ2	22:H:340:ARG:CG	2.68	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:H:280:LEU:N	22:H:330:VAL:O	2.32	0.59
14:AE:416:ILE:HG13	14:AE:441:LEU:HD11	1.83	0.59
18:D:1225:A:H4'	37:W:78:ARG:NH1	2.18	0.59
22:H:117:LYS:CB	22:H:278:THR:HG23	2.32	0.59
35:U:4:ILE:HG12	35:U:21:VAL:HG22	1.84	0.59
41:a:2683:C:OP1	65:y:51:ARG:NH2	2.32	0.59
7:6:15:DC:N4	7:6:16:DC:H41	1.96	0.59
9:9:31:ARG:HD2	41:a:1054:A:H5'	1.80	0.59
11:AA:618:GLN:CG	14:AE:770:LEU:HD13	2.32	0.59
9:9:31:ARG:HD2	41:a:1054:A:C4'	2.29	0.59
18:D:1308:U:C5'	38:X:98:ARG:HG2	2.32	0.59
46:f:24:LEU:HD11	46:f:54:MET:HE2	1.84	0.59
9:9:19:ALA:HA	9:9:70:GLU:HG2	1.84	0.59
11:AA:857:VAL:CG1	11:AA:862:LEU:HD13	2.31	0.59
14:AE:1161:GLY:HA3	14:AE:1179:PRO:HA	1.83	0.59
20:F:4:ILE:CD1	20:F:19:PHE:HA	2.33	0.59
21:G:217:VAL:O	21:G:220:THR:HG22	2.02	0.59
14:AE:99:ARG:HG3	14:AE:99:ARG:NH1	2.17	0.59
14:AE:161:THR:HG23	14:AE:164:GLN:H	1.68	0.59
10:B:58:A:H1'	10:B:60:U:C5	2.38	0.59
50:j:33:ARG:NH1	50:j:53:GLY:O	2.36	0.59
10:A:34:C:P	27:M:84:THR:HG1	2.25	0.59
10:A:58:A:H1'	10:A:60:U:C5	2.38	0.59
11:AA:838:CYS:HB2	11:AA:918:LEU:HD22	1.85	0.59
12:AB:138:ASP:OD1	12:AB:138:ASP:N	2.35	0.59
14:AE:67:ASP:OD1	14:AE:67:ASP:N	2.34	0.59
14:AE:97:VAL:HG11	14:AE:101:ARG:NH2	2.18	0.59
18:D:563:A:N6	18:D:884:U:N3	2.51	0.59
9:9:47:GLU:HG3	9:9:95:LEU:HD21	1.83	0.59
11:AA:1142:ARG:NH1	11:AA:1161:LEU:O	2.36	0.59
9:9:54:VAL:O	9:9:54:VAL:HG22	2.03	0.58
12:AB:128:PHE:CZ	12:AB:175:PHE:C	2.55	0.58
14:AE:118:LYS:HD2	14:AE:312:ARG:NH2	2.17	0.58
39:Y:78:LEU:HD13	39:Y:108:ILE:HG22	1.85	0.58
41:a:2572:A:C8	50:j:149:ASN:OD1	2.56	0.58
14:AE:926:PRO:HG2	14:AE:1248:ILE:HD11	1.84	0.58
10:B:47:U:O2'	10:B:50:U:P	2.60	0.58
18:D:439:U:O2	18:D:440:C:C6	2.56	0.58
21:G:19:GLN:HG3	22:H:75:VAL:CG2	2.23	0.58
22:H:72:LEU:HD12	22:H:72:LEU:N	2.11	0.58
41:a:1590:A:H2'	41:a:1591:A:C8	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:9:52:MET:HE3	9:9:52:MET:O	2.03	0.58
10:A:35:A:H2'	10:A:36:U:C6	2.38	0.58
12:AB:144:PHE:CB	12:AB:164:ILE:HG12	2.32	0.58
12:AB:157:ARG:HD2	12:AB:172:GLU:HB3	1.86	0.58
10:B:56:C:C5'	54:n:80:ARG:CZ	2.76	0.58
22:H:284:VAL:HG12	22:H:294:VAL:HB	1.84	0.58
14:AE:275:ARG:NH1	14:AE:278:ARG:NH1	2.51	0.58
22:H:36:VAL:HB	22:H:48:ILE:HB	1.84	0.58
2:1:20:VAL:HG11	2:1:44:ALA:HA	1.86	0.58
9:9:61:ARG:CZ	41:a:1047:G:N7	2.67	0.58
10:A:18:G:C8	10:A:57:A:N6	2.69	0.58
11:AA:903:ARG:CB	16:AG:8:VAL:CB	2.76	0.58
14:AE:514:THR:HG21	14:AE:596:LEU:HD12	1.84	0.58
22:H:118:GLY:C	22:H:133:GLY:HA2	2.27	0.58
12:AB:164:ILE:O	30:P:88:MET:CB	2.51	0.58
38:X:104:THR:O	38:X:104:THR:HG22	2.03	0.58
39:Y:112:LYS:HZ2	39:Y:112:LYS:HB3	1.69	0.58
14:AE:615:LYS:HG2	15:AF:5:THR:HG21	1.85	0.58
22:H:110:GLY:H	22:H:153:GLU:C	2.12	0.58
41:a:2314:A:O2'	54:n:155:THR:CG2	2.52	0.58
8:7:-12:U:O4	18:D:1196:A:C1'	2.52	0.58
8:7:-12:U:O4	18:D:1196:A:C8	2.57	0.58
18:D:1227:A:H5'	38:X:110:LYS:HZ1	1.69	0.58
18:D:1329:A:P	38:X:28:THR:OG1	2.62	0.58
19:E:25:ARG:HA	19:E:66:LEU:HD21	1.85	0.58
22:H:267:TRP:CH2	22:H:340:ARG:CB	2.86	0.58
8:7:-11:U:H5''	8:7:-11:U:O2	2.03	0.58
9:9:34:THR:HG22	9:9:38:MET:HE3	1.85	0.58
11:AA:707:ALA:O	11:AA:711:ASP:HB2	2.03	0.58
11:AA:854:ILE:HG12	11:AA:855:PRO:HD3	1.80	0.58
14:AE:491:LEU:HB2	14:AE:904:ALA:HA	1.86	0.58
14:AE:1046:ILE:HD12	14:AE:1059:LEU:HB3	1.86	0.58
22:H:119:GLY:HA3	22:H:132:PRO:C	2.28	0.58
8:7:-14:U:H5''	8:7:-14:U:C6	2.39	0.57
11:AA:1328:LYS:HE2	14:AE:100:GLU:HA	1.85	0.57
14:AE:1167:LYS:HZ2	14:AE:1170:LYS:HB2	1.69	0.57
18:D:496:A:N3	18:D:496:A:H2'	2.18	0.57
39:Y:7:TYR:HB2	39:Y:57:VAL:HG22	1.86	0.57
39:Y:59:THR:HG22	39:Y:61:TYR:HE1	1.69	0.57
7:6:18:DC:N4	8:7:17:G:H1	1.99	0.57
8:7:-9:U:H3'	8:7:-9:U:H6	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:60:U:P	10:A:61:C:H41	2.27	0.57
12:AB:140:PRO:HB3	30:P:79:PRO:HB3	1.76	0.57
10:B:50:U:H2'	10:B:51:C:H6	1.69	0.57
6:5:115:DA:OP2	14:AE:1148:ARG:HG3	2.04	0.57
11:AA:516:ASP:OD1	11:AA:516:ASP:O	2.22	0.57
14:AE:198:CYS:HA	14:AE:221:ILE:HD11	1.86	0.57
39:Y:137:LEU:N	39:Y:137:LEU:HD23	2.19	0.57
41:a:2245:U:O2'	41:a:2436:G:OP2	2.22	0.57
6:5:100:DA:H4'	12:AB:16:SER:OG	2.03	0.57
11:AA:1122:LYS:NZ	11:AA:1126:ASP:OD1	2.38	0.57
14:AE:241:VAL:HG12	14:AE:241:VAL:O	2.04	0.57
14:AE:438:GLU:HG3	14:AE:485:MET:HE1	1.84	0.57
14:AE:741:ALA:O	14:AE:762:ASN:ND2	2.38	0.57
18:D:1526:G:OP2	20:F:42:THR:HG23	2.04	0.57
39:Y:77:VAL:O	39:Y:77:VAL:HG12	2.05	0.57
12:AB:138:ASP:OD2	12:AB:176:SER:O	2.23	0.57
14:AE:343:LEU:HD11	14:AE:1324:SER:HB3	1.87	0.57
14:AE:510:LEU:HD22	14:AE:601:ILE:HD12	1.86	0.57
17:C:44:ILE:CD1	22:H:339:ARG:HG2	2.12	0.57
4:3:36:VAL:CG1	4:3:39:ILE:HD12	2.32	0.57
13:AD:287:VAL:CB	16:AG:78:GLU:CB	2.82	0.57
14:AE:99:ARG:HH11	14:AE:99:ARG:CG	2.18	0.57
10:B:56:C:C5'	54:n:80:ARG:NH2	2.67	0.57
10:A:6:G:HO2'	10:A:7:G:H8	1.51	0.57
21:G:19:GLN:NE2	22:H:75:VAL:HG22	2.19	0.57
22:H:49:PRO:HD3	22:H:84:LEU:HD11	1.87	0.57
22:H:110:GLY:N	22:H:153:GLU:CA	2.67	0.57
30:P:6:ILE:HG23	30:P:100:ILE:HG23	1.87	0.57
10:A:41:C:C1'	27:M:143:ARG:HH12	2.12	0.57
13:AC:82:LEU:HD11	13:AC:171:LEU:HD23	1.86	0.57
14:AE:124:ILE:HG22	14:AE:124:ILE:O	2.04	0.57
10:B:11:A:H2'	10:B:12:G:C8	2.40	0.57
10:B:32:C:OP2	29:O:130:ARG:NH2	2.38	0.57
11:AA:818:VAL:HG22	11:AA:1096:ILE:HG12	1.87	0.57
11:AA:839:VAL:HG12	11:AA:1049:ILE:HG12	1.87	0.57
11:AA:858:GLY:O	11:AA:861:ALA:HB3	2.04	0.57
12:AB:169:THR:OG1	30:P:98:VAL:O	2.22	0.57
41:a:1021:A:C2	41:a:1141:U:O4	2.51	0.57
41:a:1839:G:N9	41:a:1927:A:C4	2.72	0.57
14:AE:638:SER:OG	14:AE:639:VAL:N	2.36	0.56
6:5:99:DT:H2''	6:5:100:DA:H5''	1.85	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:7:-12:U:C4	18:D:1196:A:C8	2.93	0.56
10:A:11:A:H2'	10:A:12:G:C8	2.40	0.56
10:A:60:U:O2'	10:A:61:C:OP1	2.23	0.56
14:AE:160:LEU:HD22	14:AE:164:GLN:HB3	1.86	0.56
14:AE:247:PRO:HA	14:AE:250:ARG:HG3	1.87	0.56
25:K:56:VAL:O	25:K:60:ILE:HG23	2.04	0.56
1:0:51:VAL:HG23	66:z:86:ALA:O	2.05	0.56
2:1:93:ALA:HB2	41:a:1614:A:C2	2.40	0.56
8:7:-20:A:H2'	8:7:-19:U:H6	1.70	0.56
12:AB:144:PHE:HB3	12:AB:164:ILE:HG12	1.86	0.56
14:AE:802:ASP:OD1	14:AE:1348:LYS:NZ	2.31	0.56
10:B:60:U:P	10:B:61:C:H41	2.27	0.56
41:a:580:U:O3'	66:z:31:VAL:HG13	2.05	0.56
52:l:104:ALA:O	52:l:108:ILE:HG23	2.05	0.56
12:AB:134:VAL:HG12	12:AB:180:LYS:HA	1.87	0.56
13:AC:28:LEU:HD22	13:AC:201:LEU:HD23	1.88	0.56
14:AE:130:MET:HE2	14:AE:135:ILE:HG12	1.87	0.56
22:H:330:VAL:HB	22:H:344:LEU:HD23	1.86	0.56
31:Q:67:ALA:HB2	31:Q:96:THR:HG23	1.86	0.56
41:a:404:A:O2'	41:a:405:U:OP2	2.22	0.56
41:a:1818:U:OP2	48:h:156:ARG:NH1	2.38	0.56
8:7:-9:U:H5''	25:K:56:VAL:HG21	1.87	0.56
10:A:76:A:C2'	41:a:2394:C:H42	2.16	0.56
21:G:148:LEU:HD22	21:G:151:ILE:HD11	1.86	0.56
47:g:16:CYS:CB	47:g:37:CYS:CB	2.82	0.56
10:A:56:C:C6	41:a:2168:G:C6	2.94	0.56
12:AB:93:ILE:HG22	14:AE:290:ILE:HG23	1.85	0.56
12:AB:117:GLN:HE21	12:AB:117:GLN:CA	2.16	0.56
12:AB:169:THR:OG1	12:AB:170:PRO:HD2	2.06	0.56
18:D:769:G:H4'	18:D:1513:A:H4'	1.88	0.56
8:7:-10:U:O2	8:7:-10:U:H2'	2.06	0.56
12:AB:148:VAL:HG13	12:AB:148:VAL:O	2.06	0.56
61:u:77:ILE:HD11	61:u:108:ALA:HB1	1.87	0.56
14:AE:102:MET:HG2	14:AE:246:PRO:HG3	1.87	0.56
16:AG:63:LEU:HA	16:AG:92:TYR:HA	1.87	0.56
22:H:291:GLY:HA2	22:H:305:HIS:HA	1.86	0.56
43:c:31:PRO:HG2	43:c:33:LEU:HD13	1.87	0.56
8:7:-18:G:H5''	18:D:1501:C:N4	2.21	0.56
9:9:17:GLU:HB3	9:9:86:MET:HB2	1.87	0.56
11:AA:806:PRO:O	14:AE:633:ALA:HA	2.06	0.56
12:AB:169:THR:HB	30:P:98:VAL:HG23	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:144:TYR:HE1	14:AE:162:GLU:CD	2.14	0.56
10:A:11:A:O5'	10:A:11:A:H8	1.89	0.55
10:B:11:A:H8	10:B:11:A:O5'	1.89	0.55
62:v:66:ARG:NH1	62:v:104:GLU:OE1	2.39	0.55
9:9:35:VAL:HA	9:9:38:MET:HB2	1.88	0.55
11:AA:905:ILE:HA	16:AG:55:ASP:N	2.22	0.55
14:AE:74:LYS:HD2	14:AE:85:CYS:SG	2.45	0.55
16:AG:32:ALA:HA	16:AG:102:PHE:O	2.06	0.55
28:N:10:MET:HE3	28:N:61:LEU:HD11	1.87	0.55
41:a:2314:A:O2'	54:n:155:THR:HG21	2.06	0.55
47:g:16:CYS:HB3	47:g:37:CYS:HB3	1.86	0.55
7:6:26:DT:H2''	7:6:27:DG:H5'	1.88	0.55
10:A:50:U:H2'	10:A:51:C:H6	1.69	0.55
14:AE:1175:LEU:HD22	14:AE:1190:ILE:HD11	1.88	0.55
34:T:5:THR:O	34:T:8:THR:OG1	2.18	0.55
14:AE:833:GLU:HB2	14:AE:1242:ARG:NH1	2.22	0.55
16:AG:112:GLN:O	16:AG:116:GLN:CB	2.54	0.55
22:H:267:TRP:CH2	22:H:340:ARG:HB3	2.41	0.55
41:a:2303:G:C4	41:a:2314:A:C2	2.95	0.55
11:AA:13:LYS:HB2	11:AA:1180:MET:HE2	1.86	0.55
18:D:528:C:H6	18:D:528:C:H5''	1.71	0.55
7:6:22:DC:H4'	11:AA:508:SER:OG	2.07	0.55
11:AA:985:GLU:HB3	11:AA:988:LYS:HB2	1.89	0.55
12:AB:169:THR:CB	30:P:98:VAL:O	2.55	0.55
39:Y:96:LYS:HE3	39:Y:136:GLY:HA3	1.87	0.55
6:5:110:DA:N7	11:AA:183:TRP:CH2	2.75	0.55
7:6:21:DA:N6	8:7:15:G:H1	2.04	0.55
10:A:38:A:H2'	10:A:39:C:H5'	1.88	0.55
11:AA:633:LEU:HD13	11:AA:644:LEU:HD23	1.89	0.55
12:AB:166:GLY:HA2	30:P:87:LEU:HD22	1.87	0.55
16:AG:218:GLU:HA	21:G:104:TRP:HD1	1.71	0.55
22:H:119:GLY:CA	22:H:133:GLY:CA	2.74	0.55
40:Z:2:ILE:HB	40:Z:5:ASP:HB3	1.89	0.55
9:9:50:VAL:HG13	39:Y:119:ALA:HB3	1.88	0.55
14:AE:759:ILE:HG23	14:AE:771:GLN:HB3	1.89	0.55
14:AE:1166:GLY:HA3	14:AE:1174:ARG:HB2	1.88	0.55
18:D:563:A:N6	18:D:884:U:H3	2.05	0.55
11:AA:906:PHE:HZ	16:AG:31:LEU:CB	2.12	0.55
14:AE:37:GLU:O	14:AE:61:ILE:CD1	2.52	0.55
14:AE:124:ILE:HG23	14:AE:128:LEU:HD12	1.89	0.55
14:AE:903:LEU:HD21	14:AE:1249:ASN:HD22	1.70	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AF:3:ARG:NH1	15:AF:55:GLU:OE2	2.40	0.55
22:H:45:GLU:OE1	22:H:45:GLU:N	2.40	0.55
22:H:154:PHE:CB	22:H:168:VAL:CB	2.85	0.55
8:7:-20:A:C4	8:7:-19:U:C5	2.95	0.55
8:7:-13:U:H5'	18:D:1397:C:N3	2.22	0.55
10:A:56:C:H2'	10:A:57:A:C5'	2.27	0.55
14:AE:136:GLU:OE1	14:AE:312:ARG:CZ	2.55	0.55
18:D:961:U:O4	18:D:974:A:N1	2.40	0.55
22:H:22:SER:N	22:H:69:ASP:OD2	2.40	0.55
14:AE:26:SER:HB2	14:AE:236:TRP:CE2	2.42	0.54
14:AE:804:ALA:O	14:AE:806:ASP:N	2.41	0.54
39:Y:57:VAL:O	39:Y:57:VAL:HG12	2.07	0.54
9:9:51:TYR:CD1	9:9:51:TYR:C	2.85	0.54
14:AE:171:GLU:HA	14:AE:171:GLU:OE1	2.06	0.54
37:W:15:LEU:HD13	37:W:33:THR:HG21	1.88	0.54
41:a:2249:U:H3'	41:a:2250:G:C5'	2.36	0.54
52:l:108:ILE:HD11	52:l:180:LEU:HD13	1.89	0.54
12:AB:165:PHE:HB3	30:P:84:VAL:CG1	2.37	0.54
14:AE:58:CYS:SG	14:AE:59:ALA:N	2.80	0.54
18:D:439:U:O2	18:D:440:C:C5	2.61	0.54
18:D:1515:G:H2'	18:D:1516:G:H8	1.72	0.54
30:P:8:ILE:HD12	30:P:25:ILE:HD11	1.89	0.54
11:AA:360:LEU:HD13	11:AA:378:ARG:HH11	1.72	0.54
18:D:13:U:C2	18:D:915:A:C6	2.95	0.54
22:H:52:GLN:OE1	22:H:86:ARG:CB	2.55	0.54
30:P:28:THR:HG22	30:P:86:ALA:CB	2.38	0.54
11:AA:103:VAL:HB	11:AA:114:VAL:HG11	1.89	0.54
13:AC:100:LEU:HD23	13:AC:115:ILE:HG21	1.89	0.54
14:AE:39:LYS:O	14:AE:273:ILE:HG21	2.06	0.54
14:AE:46:TYR:CD1	14:AE:46:TYR:C	2.85	0.54
18:D:321:A:N7	18:D:328:C:O2'	2.34	0.54
18:D:945:G:C2	18:D:946:A:C8	2.96	0.54
22:H:84:LEU:HD22	22:H:84:LEU:H	1.72	0.54
22:H:290:TYR:C	22:H:305:HIS:O	2.47	0.54
39:Y:12:VAL:HG12	39:Y:23:VAL:HG21	1.90	0.54
39:Y:19:PRO:HG2	39:Y:24:GLY:H	1.73	0.54
41:a:1056:G:O2'	41:a:1103:A:N6	2.41	0.54
8:7:-18:G:C4'	18:D:1500:A:H62	2.21	0.54
11:AA:684:ASN:OD1	11:AA:687:ARG:NH2	2.41	0.54
22:H:116:VAL:C	22:H:279:LYS:HB2	2.33	0.54
22:H:332:VAL:CG1	22:H:335:ILE:HG13	2.33	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:2192:U:H2'	41:a:2193:G:C8	2.43	0.54
8:7:-18:G:C3'	18:D:1500:A:N6	2.71	0.54
11:AA:143:ARG:NH2	11:AA:512:SER:O	2.40	0.54
11:AA:1117:LEU:HD12	11:AA:1195:ILE:HG12	1.90	0.54
12:AB:165:PHE:HB3	30:P:84:VAL:O	2.08	0.54
14:AE:814:CYS:SG	14:AE:883:ARG:NH2	2.81	0.54
14:AE:1155:ILE:HG13	14:AE:1210:ILE:HB	1.88	0.54
16:AG:401:PRO:C	16:AG:403:VAL:N	2.62	0.54
21:G:38:VAL:CG2	22:H:75:VAL:CG2	2.77	0.54
32:R:80:ILE:HD12	32:R:97:THR:HG22	1.89	0.54
8:7:-18:G:H3'	18:D:1500:A:N6	2.23	0.54
8:7:-4:U:H2'	8:7:-3:U:H5''	1.90	0.54
10:A:56:C:C2	41:a:2112:G:C8	2.96	0.54
16:AG:289:ALA:HA	16:AG:291:ALA:H	1.72	0.54
39:Y:116:MET:HG3	39:Y:124:MET:HB3	1.89	0.54
11:AA:243:PRO:HB2	11:AA:274:ILE:HG23	1.90	0.54
11:AA:1142:ARG:NH2	11:AA:1166:ASP:OD1	2.38	0.54
12:AB:47:GLU:CG	12:AB:64:PHE:CE1	2.64	0.54
12:AB:148:VAL:HA	12:AB:160:VAL:HA	1.90	0.54
12:AB:164:ILE:O	30:P:88:MET:HA	2.07	0.54
14:AE:746:LEU:HG	14:AE:758:PRO:HG3	1.90	0.54
18:D:13:U:C4	18:D:915:A:C6	2.92	0.54
3:2:50:LEU:HD23	45:e:26:PHE:CZ	2.42	0.54
14:AE:78:LEU:O	14:AE:78:LEU:HD13	2.08	0.54
10:B:17:C:O2	10:B:17:C:H2'	2.08	0.54
18:D:823:C:HO2'	28:N:2:SER:N	2.06	0.54
41:a:1906:G:H5''	41:a:1906:G:H8	1.73	0.54
10:A:72:A:H2'	10:A:73:A:C5'	2.32	0.53
11:AA:857:VAL:CG1	11:AA:861:ALA:CB	2.71	0.53
12:AB:142:ALA:H	30:P:84:VAL:HG11	1.73	0.53
12:AB:165:PHE:HE2	12:AB:171:VAL:HG11	1.74	0.53
13:AD:100:LEU:HD21	13:AD:121:VAL:HG11	1.91	0.53
10:B:12:G:H2'	10:B:13:C:OP1	2.08	0.53
10:B:56:C:H2'	10:B:57:A:C5'	2.27	0.53
18:D:1228:C:OP2	38:X:110:LYS:NZ	2.41	0.53
22:H:84:LEU:H	22:H:84:LEU:CD2	2.21	0.53
41:a:811:U:H2'	61:u:21:ARG:HA	1.89	0.53
7:6:2:DC:H2''	7:6:3:DC:C5	2.43	0.53
11:AA:1284:ALA:HB3	14:AE:1361:THR:HB	1.90	0.53
14:AE:205:LEU:HG	14:AE:217:LEU:HB3	1.90	0.53
39:Y:109:ALA:HB2	39:Y:128:ILE:HG13	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:523:C:O2	41:a:554:U:O2'	2.25	0.53
52:l:130:LYS:HB2	52:l:133:LEU:HD12	1.89	0.53
64:x:27:VAL:HG21	64:x:40:ILE:HD12	1.89	0.53
64:x:35:ILE:HG21	64:x:71:ALA:HA	1.90	0.53
8:7:-10:U:O2'	25:K:33:PHE:CZ	2.52	0.53
9:9:123:ILE:O	9:9:123:ILE:HG12	2.08	0.53
11:AA:628:HIS:HB3	11:AA:647:ARG:HH21	1.74	0.53
12:AB:128:PHE:C	12:AB:180:LYS:HG3	2.34	0.53
14:AE:39:LYS:O	14:AE:273:ILE:HG23	2.08	0.53
14:AE:72:CYS:SG	14:AE:73:GLY:N	2.81	0.53
22:H:332:VAL:O	22:H:334:ASP:N	2.40	0.53
47:g:18:CYS:HB3	47:g:40:CYS:HB2	1.88	0.53
11:AA:29:SER:O	11:AA:33:ASP:HB2	2.07	0.53
12:AB:129:GLU:N	12:AB:180:LYS:HG3	2.23	0.53
14:AE:111:THR:HG22	14:AE:300:GLN:NE2	2.23	0.53
18:D:1329:A:OP1	38:X:28:THR:N	2.41	0.53
22:H:135:LEU:CB	22:H:167:VAL:CA	2.86	0.53
25:K:94:VAL:HG13	25:K:111:MET:HE1	1.91	0.53
41:a:995:C:O2	59:s:3:THR:OG1	2.24	0.53
9:9:125:ARG:HA	9:9:125:ARG:CZ	2.38	0.53
9:9:139:LEU:HD11	40:Z:11:VAL:HG13	1.90	0.53
14:AE:209:ASN:HA	14:AE:214:ARG:HH21	1.74	0.53
14:AE:785:ASP:O	14:AE:789:LYS:HB2	2.08	0.53
39:Y:116:MET:HE2	39:Y:117:THR:H	1.73	0.53
8:7:15:G:H2'	8:7:16:A:C8	2.43	0.53
11:AA:618:GLN:HG3	14:AE:770:LEU:CD1	2.38	0.53
11:AA:1070:HIS:NE2	11:AA:1114:GLU:OE1	2.36	0.53
12:AB:144:PHE:CD2	12:AB:164:ILE:HG21	2.43	0.53
14:AE:99:ARG:HG3	14:AE:99:ARG:HH11	1.74	0.53
18:D:767:A:H2'	18:D:768:A:O4'	2.08	0.53
41:a:2315:G:O2'	54:n:125:ARG:HD3	2.09	0.53
58:r:58:LEU:O	58:r:61:VAL:HG22	2.08	0.53
9:9:43:LYS:HG2	9:9:98:GLU:HG2	1.90	0.53
14:AE:832:LYS:HB3	14:AE:1242:ARG:NH1	2.24	0.53
10:B:6:G:O2'	10:B:7:G:H8	1.92	0.53
39:Y:33:ASN:H	39:Y:66:PHE:HE1	1.56	0.53
41:a:2000:C:OP1	63:w:5:LYS:NZ	2.36	0.53
14:AE:30:ILE:HG21	14:AE:241:VAL:O	2.08	0.53
14:AE:215:LYS:HA	14:AE:218:THR:HG22	1.91	0.53
25:K:99:ALA:HB1	25:K:103:THR:HG21	1.89	0.53
10:A:16:C:O2	10:A:16:C:H2'	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:159:LYS:CG	12:AB:170:PRO:CB	2.86	0.53
14:AE:145:VAL:HG23	14:AE:159:ILE:HG22	1.89	0.53
2:1:59:GLU:CG	2:1:66:ILE:HD11	2.38	0.53
9:9:31:ARG:HH11	9:9:31:ARG:CG	2.14	0.53
9:9:58:THR:HG21	9:9:81:LEU:HA	1.90	0.53
10:A:38:A:C2'	10:A:39:C:H5'	2.39	0.53
14:AE:201:LEU:HD12	14:AE:224:LEU:HD12	1.91	0.53
10:B:60:U:O2'	10:B:61:C:OP1	2.23	0.53
22:H:49:PRO:HD2	22:H:84:LEU:CD1	2.39	0.53
22:H:321:VAL:HG13	22:H:322:VAL:HG23	1.90	0.53
29:O:81:HIS:O	29:O:84:THR:OG1	2.23	0.53
39:Y:138:VAL:HG12	39:Y:138:VAL:O	2.08	0.53
22:H:24:VAL:HG12	22:H:69:ASP:H	1.74	0.52
23:I:77:ILE:HA	23:I:84:VAL:HG23	1.91	0.52
29:O:98:LEU:HB3	29:O:104:VAL:HG13	1.92	0.52
41:a:523:C:H4'	41:a:540:C:O2	2.10	0.52
41:a:2298:A:C5	41:a:2321:U:O4	2.62	0.52
52:l:131:THR:HG22	52:l:160:ALA:O	2.08	0.52
60:t:7:MET:HE1	60:t:44:LYS:HD2	1.91	0.52
10:A:6:G:O2'	10:A:7:G:H8	1.92	0.52
11:AA:811:ASN:HA	11:AA:815:SER:HB2	1.90	0.52
13:AD:16:ILE:HG23	13:AD:26:VAL:HG22	1.91	0.52
14:AE:56:LEU:CD1	14:AE:273:ILE:HD12	2.39	0.52
14:AE:975:ILE:HD11	14:AE:1003:LEU:HD11	1.90	0.52
54:n:8:TYR:HA	54:n:12:VAL:HB	1.91	0.52
8:7:17:G:H2'	8:7:18:A:C8	2.44	0.52
10:A:12:G:H2'	10:A:13:C:OP1	2.08	0.52
12:AB:93:ILE:CG2	14:AE:290:ILE:HG22	2.39	0.52
13:AD:28:LEU:HD12	13:AD:201:LEU:HD23	1.91	0.52
10:B:12:G:C2'	10:B:13:C:OP1	2.57	0.52
10:B:18:G:C2	10:B:58:A:C5	2.96	0.52
10:A:18:G:C2	10:A:58:A:C5	2.96	0.52
10:A:56:C:C3'	10:A:57:A:H5''	2.40	0.52
11:AA:714:VAL:HB	11:AA:787:PRO:HD2	1.92	0.52
12:AB:128:PHE:HB2	12:AB:180:LYS:CG	2.39	0.52
13:AC:43:LEU:HD13	13:AC:217:ILE:HD11	1.90	0.52
13:AD:205:MET:HE3	13:AD:213:PRO:HB3	1.91	0.52
18:D:13:U:C4	18:D:21:G:C2	2.96	0.52
22:H:279:LYS:HA	22:H:331:MET:CB	2.33	0.52
42:b:37:ILE:HD11	42:b:82:ILE:HD11	1.90	0.52
2:1:93:ALA:HB2	41:a:1614:A:N1	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:13:VAL:CG2	4:3:39:ILE:HD13	2.38	0.52
11:AA:143:ARG:NH1	11:AA:507:GLY:O	2.32	0.52
13:AC:140:ILE:HD12	13:AC:142:MET:HE3	1.92	0.52
18:D:673:A:H2'	18:D:674:G:C8	2.44	0.52
39:Y:37:PHE:CZ	39:Y:56:VAL:HG11	2.44	0.52
12:AB:133:MET:HE2	12:AB:133:MET:O	2.10	0.52
12:AB:166:GLY:HA2	30:P:87:LEU:CB	2.30	0.52
14:AE:68:TYR:CA	14:AE:75:TYR:HE2	2.22	0.52
10:B:22:G:O2'	10:B:23:C:P	2.67	0.52
10:B:76:A:N3	41:a:2493:U:H4'	2.24	0.52
18:D:1308:U:OP1	38:X:100:GLN:OE1	2.22	0.52
39:Y:59:THR:HG22	39:Y:61:TYR:CE1	2.45	0.52
39:Y:100:ILE:HB	39:Y:105:LEU:HD11	1.92	0.52
9:9:71:CYS:HA	9:9:117:LEU:HD13	1.90	0.52
12:AB:159:LYS:CG	12:AB:170:PRO:HB2	2.40	0.52
12:AB:169:THR:HB	30:P:98:VAL:O	2.10	0.52
12:AB:171:VAL:HG13	12:AB:171:VAL:O	2.10	0.52
10:B:18:G:C8	10:B:57:A:N6	2.70	0.52
17:C:61:ARG:NH2	18:D:736:C:OP1	2.43	0.52
41:a:2328:A:H2'	41:a:2329:U:C6	2.45	0.52
66:z:58:ARG:HA	66:z:61:TRP:CE3	2.45	0.52
8:7:20:G:O2'	14:AE:425:ARG:NH2	2.40	0.52
9:9:78:GLY:H	9:9:79:PRO:HD2	1.68	0.52
10:A:41:C:H4'	27:M:143:ARG:NH1	2.25	0.52
11:AA:374:GLU:HB2	12:AB:80:TRP:HH2	1.75	0.52
11:AA:524:ILE:HG21	11:AA:708:VAL:HG13	1.92	0.52
10:B:15:G:N3	10:B:15:G:C2'	2.73	0.52
18:D:1308:U:P	38:X:98:ARG:HG3	2.50	0.52
24:J:61:VAL:HG21	24:J:200:ILE:CD1	2.35	0.52
41:a:2093:G:O2'	41:a:2198:A:N1	2.41	0.52
8:7:-18:G:C4'	18:D:1500:A:N6	2.73	0.52
8:7:-7:U:H6	8:7:-7:U:H3'	1.75	0.52
8:7:16:A:H2'	8:7:17:G:C8	2.45	0.52
10:A:17:C:O2	10:A:17:C:H2'	2.08	0.52
22:H:135:LEU:CB	22:H:157:ILE:CB	2.87	0.52
39:Y:27:LEU:HD12	39:Y:27:LEU:C	2.35	0.52
10:A:12:G:C2'	10:A:13:C:OP1	2.58	0.52
11:AA:255:ILE:HB	11:AA:263:VAL:HB	1.92	0.52
12:AB:159:LYS:HG3	12:AB:170:PRO:CB	2.39	0.52
10:B:16:C:O2	10:B:16:C:H2'	2.09	0.52
10:B:56:C:C3'	10:B:57:A:H5''	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:D:1228:C:OP1	38:X:107:ARG:CZ	2.58	0.52
41:a:639:U:H2'	41:a:640:C:C6	2.45	0.52
53:m:31:LEU:HD22	53:m:42:LEU:CD1	2.40	0.52
63:w:38:LEU:N	63:w:39:PRO:CD	2.73	0.52
9:9:93:ALA:O	9:9:129:LEU:HD13	2.06	0.51
11:AA:1313:HIS:CD2	15:AF:31:GLN:NE2	2.57	0.51
14:AE:99:ARG:HA	14:AE:248:ASP:HB2	1.92	0.51
14:AE:112:ALA:HA	14:AE:238:ILE:HA	1.91	0.51
22:H:19:ARG:O	22:H:72:LEU:HD22	2.09	0.51
22:H:308:GLU:O	22:H:310:ASP:N	2.43	0.51
41:a:587:C:OP2	61:u:21:ARG:NH1	2.43	0.51
41:a:2636:C:HO2'	50:j:45:TYR:HH	1.57	0.51
11:AA:974:ARG:HD2	11:AA:1014:LEU:HD21	1.92	0.51
14:AE:850:LYS:HB2	14:AE:857:LEU:HB2	1.91	0.51
41:a:560:C:O2	66:z:48:ARG:NH1	2.41	0.51
41:a:1839:G:N9	41:a:1927:A:H1'	2.23	0.51
4:3:94:ARG:HB3	4:3:103:ILE:HD12	1.91	0.51
9:9:3:LEU:HD13	9:9:5:LEU:H	1.75	0.51
14:AE:390:LEU:N	14:AE:390:LEU:CD1	2.73	0.51
39:Y:112:LYS:NZ	39:Y:112:LYS:CB	2.73	0.51
8:7:15:G:H2'	8:7:16:A:H8	1.75	0.51
9:9:125:ARG:HG3	9:9:125:ARG:O	2.10	0.51
11:AA:125:GLY:HA2	11:AA:499:SER:HB2	1.92	0.51
12:AB:146:GLY:HA3	12:AB:162:VAL:CA	2.35	0.51
14:AE:144:TYR:CE1	14:AE:162:GLU:CD	2.88	0.51
16:AG:139:THR:HA	16:AG:180:ARG:HA	1.91	0.51
10:B:18:G:C2	10:B:58:A:C6	2.99	0.51
10:B:24:U:O2'	41:a:1922:G:O3'	2.29	0.51
18:D:864:A:C2	18:D:865:A:C2	2.98	0.51
18:D:1499:A:O2'	18:D:1500:A:H5'	2.10	0.51
34:T:40:GLN:CA	34:T:40:GLN:HE21	2.23	0.51
41:a:1839:G:H1'	41:a:1927:A:N9	2.03	0.51
44:d:106:G:H2'	44:d:107:G:O4'	2.10	0.51
56:p:121:ILE:HD12	56:p:141:ILE:CG2	2.41	0.51
9:9:7:ASP:OD1	9:9:7:ASP:N	2.36	0.51
9:9:62:ARG:CG	9:9:62:ARG:HH21	2.14	0.51
12:AB:167:ARG:HG3	30:P:92:LEU:HD13	1.88	0.51
18:D:5:U:O2	18:D:5:U:O4'	2.29	0.51
20:F:4:ILE:HD12	20:F:19:PHE:HA	1.93	0.51
60:t:43:ILE:HD12	60:t:56:ASP:HB2	1.93	0.51
60:t:71:ARG:NH2	60:t:123:LEU:O	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:22:G:O2'	10:A:23:C:P	2.68	0.51
11:AA:845:LEU:HB3	11:AA:889:PRO:HB2	1.93	0.51
12:AB:123:ARG:H	12:AB:123:ARG:HD2	1.75	0.51
10:B:72:A:H2'	10:B:73:A:C5'	2.33	0.51
8:7:-19:U:H2'	8:7:-18:G:C8	2.45	0.51
9:9:11:ILE:CD1	9:9:11:ILE:N	2.73	0.51
10:A:76:A:O2'	41:a:2395:C:C2	2.64	0.51
12:AB:160:VAL:HG11	12:AB:162:VAL:HG23	1.92	0.51
41:a:929:U:H1'	46:f:26:GLY:O	2.10	0.51
10:A:15:G:H22	10:A:20:U:H3	1.59	0.51
11:AA:93:SER:HA	11:AA:128:PRO:HA	1.93	0.51
11:AA:786:GLY:N	11:AA:789:THR:OG1	2.41	0.51
11:AA:857:VAL:HB	11:AA:862:LEU:HD11	1.93	0.51
12:AB:172:GLU:N	12:AB:172:GLU:OE1	2.44	0.51
10:B:5:G:C2'	10:B:6:G:H5'	2.40	0.51
22:H:332:VAL:C	22:H:334:ASP:H	2.18	0.51
41:a:1266:G:OP2	49:i:17:ARG:NE	2.43	0.51
60:t:113:MET:O	60:t:116:ILE:HG13	2.11	0.51
9:9:41:LEU:HD12	39:Y:117:THR:HG22	1.92	0.51
14:AE:395:LYS:HZ2	14:AE:399:LYS:CE	2.23	0.51
30:P:57:VAL:O	30:P:57:VAL:HG13	2.11	0.51
41:a:1814:G:H4'	48:h:51:THR:HG21	1.92	0.51
41:a:2243:U:H2'	41:a:2244:U:C6	2.46	0.51
6:5:101:DT:H72	14:AE:271:ARG:CZ	2.41	0.51
10:A:56:C:C5	41:a:2168:G:O6	2.64	0.51
11:AA:246:LEU:HB3	11:AA:269:ILE:HD13	1.92	0.51
12:AB:146:GLY:CA	12:AB:162:VAL:HA	2.36	0.51
14:AE:683:ILE:HD12	14:AE:754:ILE:HG21	1.93	0.51
41:a:1141:U:O2	41:a:1142:A:N6	2.44	0.51
10:A:15:G:N3	10:A:15:G:C2'	2.73	0.50
10:A:18:G:C2	10:A:58:A:C6	2.98	0.50
10:A:28:C:H2'	10:A:29:G:H8	1.76	0.50
11:AA:904:ALA:HB2	16:AG:9:VAL:N	2.25	0.50
11:AA:1101:LEU:HD21	14:AE:508:LEU:HD22	1.92	0.50
14:AE:972:LYS:HD2	14:AE:1004:ALA:HA	1.93	0.50
17:C:30:LYS:HA	17:C:33:ILE:HD13	1.91	0.50
41:a:2557:G:H2'	41:a:2558:C:C6	2.47	0.50
41:a:2627:G:O2'	41:a:2781:A:N1	2.37	0.50
2:1:59:GLU:HG3	2:1:66:ILE:HD11	1.92	0.50
9:9:44:ALA:HB1	9:9:52:MET:HB3	1.93	0.50
11:AA:862:LEU:O	11:AA:862:LEU:HD23	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:D:1276:G:O5'	18:D:1276:G:H8	1.93	0.50
44:d:5:U:OP1	44:d:61:G:O2'	2.26	0.50
59:s:30:THR:HG22	59:s:31:GLU:N	2.27	0.50
1:0:14:VAL:HG21	1:0:98:ILE:HG13	1.94	0.50
11:AA:904:ALA:CB	16:AG:9:VAL:H	2.24	0.50
12:AB:171:VAL:CG1	12:AB:173:LEU:HD21	2.42	0.50
16:AG:29:SER:O	16:AG:33:THR:N	2.44	0.50
18:D:108:G:H5''	18:D:108:G:N3	2.27	0.50
21:G:18:HIS:CA	22:H:43:LYS:HD2	2.29	0.50
21:G:35:ARG:NH2	22:H:10:GLU:HG2	2.25	0.50
34:T:21:ASP:O	34:T:22:THR:HG22	2.12	0.50
41:a:118:A:C8	41:a:119:A:C8	2.99	0.50
41:a:1693:U:O2'	48:h:14:ARG:NH2	2.43	0.50
41:a:1910:G:O5'	41:a:1910:G:H8	1.93	0.50
59:s:17:VAL:HG23	59:s:137:PRO:HB2	1.93	0.50
66:z:47:TYR:CD1	66:z:47:TYR:C	2.90	0.50
11:AA:146:VAL:HG21	11:AA:513:GLN:HE21	1.77	0.50
14:AE:88:CYS:HB3	14:AE:90:VAL:HG12	1.92	0.50
18:D:1404:C:H2'	18:D:1404:C:O2	2.10	0.50
28:N:3:MET:HA	28:N:3:MET:HE3	1.94	0.50
41:a:2297:A:C6	41:a:2321:U:O4	2.65	0.50
9:9:57:ASN:CG	9:9:62:ARG:HG3	2.30	0.50
12:AB:133:MET:HE1	12:AB:180:LYS:HE3	1.92	0.50
12:AB:141:PHE:HA	30:P:84:VAL:HG21	1.92	0.50
18:D:927:G:O2'	18:D:1503:A:N7	2.36	0.50
54:n:127:ASN:ND2	54:n:127:ASN:N	2.60	0.50
6:5:96:DT:H2''	6:5:97:DC:C5	2.46	0.50
9:9:52:MET:HE3	9:9:52:MET:CA	2.42	0.50
10:A:37:A:H2'	10:A:38:A:H8	1.77	0.50
16:AG:103:ASP:C	16:AG:105:ILE:H	2.19	0.50
41:a:1964:G:H4'	41:a:1965:C:OP2	2.11	0.50
14:AE:275:ARG:HH12	14:AE:278:ARG:NH1	2.09	0.50
10:B:34:C:O2	10:B:34:C:H2'	2.11	0.50
21:G:35:ARG:CD	22:H:14:LYS:HD3	2.40	0.50
22:H:117:LYS:CB	22:H:278:THR:CG2	2.90	0.50
41:a:1824:G:O2'	48:h:252:THR:HG21	2.11	0.50
48:h:107:PRO:HD2	48:h:110:LEU:HD22	1.94	0.50
10:A:5:G:C2'	10:A:6:G:H5'	2.40	0.50
41:a:783:A:N3	41:a:783:A:C2'	2.70	0.50
56:p:35:ARG:HD3	56:p:71:LEU:HD13	1.93	0.50
59:s:32:LEU:CD2	59:s:54:ILE:HG21	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:x:51:ALA:HB3	64:x:78:VAL:HB	1.94	0.50
10:A:48:C:H2'	10:A:48:C:O2	2.11	0.50
10:B:48:C:O2	10:B:48:C:H2'	2.11	0.50
18:D:1208:C:H2'	18:D:1209:C:C6	2.47	0.50
25:K:81:LEU:HD13	25:K:123:VAL:HG12	1.92	0.50
36:V:48:ASP:HB3	36:V:75:LEU:HD23	1.94	0.50
41:a:1869:G:N2	41:a:1871:A:O2'	2.44	0.50
4:3:12:ILE:HG21	4:3:80:ALA:HB2	1.92	0.49
6:5:98:DA:N9	6:5:99:DT:H72	2.27	0.49
8:7:-15:U:C2	18:D:1493:A:C2	3.00	0.49
10:A:59:A:H2'	10:A:60:U:H5'	1.94	0.49
10:A:76:A:C2'	41:a:2394:C:N4	2.75	0.49
22:H:132:PRO:N	22:H:167:VAL:CB	2.75	0.49
25:K:114:VAL:HG21	25:K:141:ILE:HD12	1.94	0.49
43:c:3:ARG:HD2	43:c:30:LEU:HD22	1.95	0.49
2:1:24:ILE:HD13	2:1:36:LEU:HD11	1.93	0.49
9:9:23:LEU:HA	9:9:118:ILE:HG13	1.92	0.49
11:AA:554:HIS:HD2	11:AA:558:VAL:HB	1.77	0.49
12:AB:71:VAL:HG12	12:AB:73:MET:HB2	1.93	0.49
10:B:39:C:O5'	10:B:39:C:H6	1.95	0.49
18:D:1356:G:H2'	18:D:1357:A:C8	2.47	0.49
34:T:4:SER:O	34:T:8:THR:HG23	2.12	0.49
41:a:2646:C:O5'	41:a:2646:C:H6	1.95	0.49
46:f:24:LEU:HD11	46:f:54:MET:CE	2.42	0.49
8:7:-19:U:OP2	18:D:926:G:N2	2.45	0.49
11:AA:400:VAL:HG21	11:AA:452:ARG:HE	1.76	0.49
11:AA:529:ARG:HH11	11:AA:572:ILE:HG22	1.77	0.49
11:AA:857:VAL:HB	11:AA:862:LEU:CD1	2.43	0.49
16:AG:183:LEU:HA	16:AG:197:VAL:HA	1.95	0.49
18:D:1499:A:H3'	18:D:1499:A:OP2	2.12	0.49
22:H:267:TRP:CZ3	22:H:340:ARG:HG3	2.43	0.49
41:a:2303:G:C6	41:a:2314:A:N1	2.81	0.49
45:e:18:LEU:HB2	45:e:53:VAL:HG11	1.94	0.49
63:w:67:PHE:O	63:w:71:ARG:N	2.45	0.49
2:1:55:ILE:HG23	2:1:66:ILE:HD12	1.93	0.49
8:7:-15:U:C2	18:D:1493:A:H2	2.31	0.49
11:AA:18:ARG:HE	11:AA:620:ASN:HA	1.77	0.49
12:AB:135:ARG:CG	12:AB:135:ARG:NH1	2.73	0.49
16:AG:340:THR:O	16:AG:344:LEU:N	2.43	0.49
18:D:50:A:O2'	18:D:360:G:N2	2.45	0.49
18:D:1410:A:C2	18:D:1491:G:C2	2.99	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:H:318:PRO:HA	22:H:321:VAL:HG12	1.95	0.49
41:a:1980:G:O2'	41:a:1982:U:OP2	2.28	0.49
63:w:55:ALA:HA	63:w:80:PHE:CE1	2.47	0.49
8:7:-13:U:OP2	18:D:1397:C:C2	2.65	0.49
11:AA:411:ARG:NH2	11:AA:427:ASP:OD2	2.44	0.49
12:AB:165:PHE:HA	30:P:84:VAL:O	2.11	0.49
14:AE:220:ARG:HG2	14:AE:220:ARG:NH1	2.26	0.49
14:AE:800:LEU:HB3	14:AE:920:ALA:HB1	1.95	0.49
22:H:49:PRO:HD2	22:H:84:LEU:HD11	1.92	0.49
41:a:1406:U:HO2'	41:a:1407:G:P	2.29	0.49
4:3:7:ARG:HB2	41:a:85:G:OP2	2.13	0.49
10:A:56:C:H1'	41:a:2112:G:C5	2.46	0.49
14:AE:749:LYS:HB3	14:AE:755:ILE:HD11	1.93	0.49
14:AE:1371:ARG:HE	14:AE:1372:ARG:NH1	2.10	0.49
16:AG:103:ASP:C	16:AG:105:ILE:N	2.69	0.49
18:D:13:U:O4	18:D:21:G:N3	2.46	0.49
22:H:120:PHE:CB	22:H:136:VAL:CB	2.91	0.49
41:a:1412:U:C4	41:a:1413:A:N7	2.81	0.49
41:a:1433:A:H2'	41:a:1434:A:O4'	2.13	0.49
41:a:2298:A:N3	41:a:2321:U:C5	2.80	0.49
53:m:22:MET:O	53:m:28:ARG:NH1	2.45	0.49
8:7:-13:U:H5'	18:D:1397:C:C2	2.48	0.49
11:AA:836:LEU:HD13	11:AA:1054:LEU:HD13	1.95	0.49
11:AA:1336:ASN:ND2	14:AE:29:MET:HG2	2.27	0.49
10:B:25:C:H2'	10:B:26:G:H5'	1.94	0.49
50:j:4:LEU:HD23	50:j:29:VAL:CG1	2.39	0.49
6:5:108:DT:H73	11:AA:199:ASP:HB3	1.94	0.49
6:5:110:DA:N7	11:AA:183:TRP:HH2	2.11	0.49
10:A:47:U:H2'	10:A:48:C:H4'	1.94	0.49
11:AA:857:VAL:CB	11:AA:862:LEU:CD1	2.91	0.49
11:AA:862:LEU:C	11:AA:862:LEU:CD2	2.85	0.49
14:AE:437:PHE:HZ	14:AE:453:VAL:HG11	1.76	0.49
14:AE:550:VAL:O	14:AE:569:LEU:HA	2.13	0.49
14:AE:799:ARG:HG2	14:AE:1325:PHE:HZ	1.77	0.49
18:D:872:A:H2'	18:D:872:A:N3	2.27	0.49
48:h:210:ALA:HA	48:h:213:TRP:CE3	2.48	0.49
58:r:3:VAL:HG22	58:r:36:ALA:HB1	1.95	0.49
9:9:50:VAL:CG1	39:Y:119:ALA:CB	2.88	0.49
9:9:51:TYR:CG	9:9:89:PRO:HD2	2.47	0.49
11:AA:812:PHE:HA	14:AE:505:ASP:OD2	2.13	0.49
41:a:464:U:O3'	53:m:12:ARG:NH2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:b:37:ILE:HG21	42:b:80:ILE:HG21	1.95	0.49
10:A:11:A:H2'	10:A:12:G:C1'	2.42	0.49
10:A:25:C:H2'	10:A:26:G:H5'	1.94	0.49
11:AA:232:ILE:HG12	11:AA:237:LEU:HG	1.94	0.49
11:AA:400:VAL:HG11	11:AA:452:ARG:HD2	1.94	0.49
12:AB:140:PRO:HG2	30:P:102:LEU:CD2	2.42	0.49
12:AB:167:ARG:HG3	30:P:92:LEU:N	2.14	0.49
13:AD:15:ASP:OD1	13:AD:27:THR:OG1	2.30	0.49
14:AE:115:TRP:O	14:AE:1333:THR:HG21	2.13	0.49
14:AE:123:ARG:HD3	14:AE:123:ARG:HA	1.48	0.49
8:7:2:U:H2'	8:7:3:U:C6	2.48	0.48
9:9:23:LEU:HD22	9:9:92:ALA:HB1	1.95	0.48
11:AA:904:ALA:O	16:AG:53:SER:O	2.31	0.48
12:AB:140:PRO:HD2	30:P:102:LEU:HD21	0.63	0.48
12:AB:144:PHE:CG	12:AB:164:ILE:HG21	2.48	0.48
14:AE:117:LEU:HG	14:AE:118:LYS:HG3	1.95	0.48
10:B:59:A:H2'	10:B:60:U:H5'	1.94	0.48
10:A:18:G:C5	10:A:57:A:C5	3.01	0.48
10:A:76:A:N6	41:a:2422:C:O4'	2.46	0.48
14:AE:102:MET:HG2	14:AE:246:PRO:HD3	1.95	0.48
14:AE:421:VAL:O	14:AE:436:ALA:HA	2.12	0.48
14:AE:809:VAL:HG21	14:AE:909:ILE:HG12	1.95	0.48
18:D:1366:C:O2'	30:P:62:ARG:NH2	2.44	0.48
26:L:18:VAL:N	26:L:19:PRO:CD	2.76	0.48
30:P:6:ILE:HG23	30:P:100:ILE:CG2	2.43	0.48
53:m:24:THR:HG23	53:m:27:GLY:H	1.78	0.48
11:AA:9:LYS:HG2	11:AA:1171:ARG:HH12	1.77	0.48
11:AA:363:LEU:HB3	11:AA:381:ALA:HB1	1.96	0.48
10:B:11:A:H2'	10:B:12:G:C1'	2.43	0.48
18:D:1017:U:O2'	18:D:1018:G:O4'	2.31	0.48
18:D:1169:A:H2'	18:D:1170:A:C8	2.48	0.48
18:D:1329:A:OP1	38:X:28:THR:OG1	2.31	0.48
22:H:23:ILE:N	22:H:69:ASP:OD2	2.47	0.48
39:Y:77:VAL:HG13	39:Y:80:LYS:HE3	1.95	0.48
41:a:742:A:C2	41:a:743:A:C6	3.00	0.48
50:j:156:PHE:CE1	59:s:81:ILE:HD13	2.48	0.48
7:6:21:DA:N6	8:7:15:G:N1	2.61	0.48
10:A:19:G:C5	41:a:2112:G:H4'	2.44	0.48
10:B:47:U:H2'	10:B:48:C:H4'	1.94	0.48
18:D:1311:A:OP1	47:g:59:ARG:NH1	2.46	0.48
39:Y:80:LYS:HG3	39:Y:86:LYS:HA	1.93	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:2038:G:H2'	41:a:2039:U:O4'	2.13	0.48
50:j:25:THR:HG21	50:j:193:VAL:HG22	1.94	0.48
12:AB:93:ILE:O	14:AE:290:ILE:HG21	2.13	0.48
14:AE:103:GLY:H	14:AE:244:VAL:HG22	1.79	0.48
30:P:6:ILE:CG2	30:P:100:ILE:HG23	2.43	0.48
9:9:31:ARG:NE	41:a:1054:A:O4'	2.46	0.48
10:A:49:G:H8	10:A:49:G:O5'	1.96	0.48
13:AD:100:LEU:HB2	13:AD:144:ILE:HG23	1.94	0.48
10:B:18:G:N3	10:B:58:A:C6	2.82	0.48
41:a:565:C:H2'	41:a:566:U:O4'	2.13	0.48
1:0:14:VAL:CG2	1:0:98:ILE:HG13	2.43	0.48
10:A:37:A:H2'	10:A:38:A:C8	2.48	0.48
10:A:42:G:H2'	10:A:43:A:C8	2.47	0.48
14:AE:145:VAL:HG12	14:AE:184:ALA:HB1	1.94	0.48
36:V:75:LEU:C	36:V:75:LEU:HD12	2.38	0.48
10:A:15:G:C2	10:A:20:U:O2	2.66	0.48
11:AA:565:GLU:HA	11:AA:569:ILE:HG12	1.95	0.48
14:AE:201:LEU:HD11	14:AE:220:ARG:HG2	1.95	0.48
10:B:49:G:O5'	10:B:49:G:H8	1.95	0.48
18:D:974:A:OP1	33:S:69:ARG:NH1	2.46	0.48
41:a:2685:G:OP1	60:t:78:ARG:NH2	2.47	0.48
1:0:40:MET:HE3	1:0:49:ILE:CD1	2.43	0.48
10:B:60:U:H4'	10:B:61:C:OP2	2.14	0.48
18:D:371:A:H2'	18:D:372:C:O4'	2.14	0.48
39:Y:77:VAL:HG13	39:Y:80:LYS:CE	2.44	0.48
41:a:742:A:C2	41:a:755:U:N3	2.80	0.48
2:1:25:ARG:NH1	2:1:74:ILE:O	2.46	0.48
8:7:-2:U:O2	8:7:-2:U:H2'	2.12	0.48
10:A:14:A:H2'	10:A:14:A:N3	2.29	0.48
10:A:58:A:OP2	10:A:58:A:C8	2.67	0.48
12:AB:169:THR:HG21	30:P:100:ILE:N	2.21	0.48
14:AE:1146:GLU:OE2	14:AE:1310:THR:HG22	2.14	0.48
16:AG:248:VAL:O	16:AG:252:VAL:CB	2.62	0.48
10:B:18:G:C5	10:B:57:A:C5	3.01	0.48
10:B:42:G:H2'	10:B:43:A:C8	2.48	0.48
10:B:68:C:H3'	10:B:69:C:H5''	1.96	0.48
41:a:686:U:O4	53:m:12:ARG:HB2	2.14	0.48
41:a:1814:G:C4'	48:h:51:THR:HG21	2.44	0.48
9:9:51:TYR:CD1	9:9:88:HIS:HB2	2.49	0.47
11:AA:732:ILE:HD11	11:AA:769:PRO:HB3	1.95	0.47
12:AB:140:PRO:CG	30:P:102:LEU:HD11	2.37	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:47:ARG:CZ	14:AE:47:ARG:HB2	2.44	0.47
14:AE:152:THR:HB	14:AE:172:PHE:CZ	2.48	0.47
14:AE:526:VAL:HG12	14:AE:549:LYS:HB2	1.96	0.47
10:B:15:G:C2	10:B:20:U:O2	2.66	0.47
39:Y:133:ARG:O	39:Y:133:ARG:HG2	2.14	0.47
3:2:61:LEU:C	3:2:61:LEU:HD12	2.39	0.47
9:9:17:GLU:HG2	9:9:88:HIS:NE2	2.29	0.47
11:AA:808:ASN:N	14:AE:633:ALA:HB2	2.21	0.47
18:D:911:U:H2'	18:D:912:C:C6	2.49	0.47
22:H:52:GLN:O	22:H:53:PHE:HD1	1.95	0.47
22:H:330:VAL:HG12	22:H:345:GLY:O	2.14	0.47
24:J:162:ALA:O	24:J:165:ARG:O	2.33	0.47
55:o:13:ARG:HD3	61:u:58:TYR:O	2.14	0.47
1:0:5:PHE:HB3	1:0:59:ILE:HD12	1.96	0.47
9:9:31:ARG:HE	41:a:1054:A:C5'	2.18	0.47
11:AA:207:THR:OG1	11:AA:354:ASP:OD2	2.32	0.47
14:AE:114:ILE:HG12	14:AE:311:ARG:HD2	1.95	0.47
14:AE:1027:VAL:HB	14:AE:1121:LEU:HB2	1.95	0.47
14:AE:1347:LEU:HG	14:AE:1357:ILE:HG23	1.96	0.47
18:D:13:U:O2	18:D:915:A:N7	2.47	0.47
18:D:604:G:H2'	18:D:605:U:O4'	2.14	0.47
18:D:1227:A:P	38:X:110:LYS:HZ1	2.36	0.47
2:1:4:ILE:HG12	2:1:106:VAL:HG22	1.96	0.47
9:9:8:LYS:NZ	41:a:1046:A:H61	2.11	0.47
9:9:48:ALA:HB3	9:9:51:TYR:CD2	2.50	0.47
9:9:62:ARG:CG	9:9:62:ARG:NH2	2.73	0.47
10:A:18:G:N3	10:A:58:A:C6	2.82	0.47
10:A:68:C:C4	10:A:69:C:C5	3.02	0.47
14:AE:128:LEU:HD21	14:AE:188:LEU:HB3	1.97	0.47
18:D:1174:G:H2'	18:D:1175:G:H5'	1.95	0.47
19:E:54:MET:O	19:E:57:ILE:HG22	2.15	0.47
41:a:2303:G:C2	41:a:2314:A:N3	2.82	0.47
10:A:33:U:H2'	10:A:35:A:OP2	2.14	0.47
10:A:41:C:H5'	27:M:143:ARG:HD2	1.95	0.47
11:AA:400:VAL:HG22	11:AA:584:TYR:HB3	1.96	0.47
14:AE:395:LYS:NZ	14:AE:399:LYS:CE	2.77	0.47
10:B:14:A:N3	10:B:14:A:H2'	2.29	0.47
10:B:68:C:C4	10:B:69:C:C5	3.02	0.47
18:D:552:U:O2'	32:R:83:ARG:O	2.27	0.47
25:K:99:ALA:CB	25:K:103:THR:HG21	2.43	0.47
39:Y:79:LEU:HD13	39:Y:132:ALA:HA	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:1021:A:N6	41:a:1141:U:N3	2.47	0.47
41:a:1266:G:OP1	49:i:16:ARG:NE	2.45	0.47
41:a:1588:G:C6	41:a:1589:U:O4	2.67	0.47
11:AA:858:GLY:C	11:AA:860:ALA:N	2.72	0.47
11:AA:861:ALA:O	11:AA:882:ILE:HD13	2.14	0.47
11:AA:1286:THR:O	11:AA:1290:MET:HB2	2.14	0.47
12:AB:145:ASN:HD21	14:AE:53:ARG:CZ	2.25	0.47
14:AE:108:ALA:HB1	14:AE:279:LEU:HD22	1.96	0.47
18:D:526:C:P	32:R:88:LYS:HE3	2.54	0.47
22:H:316:ILE:HD11	22:H:321:VAL:HG11	1.97	0.47
38:X:16:VAL:HG23	38:X:17:ILE:HD12	1.97	0.47
9:9:31:ARG:HG3	9:9:31:ARG:NH1	2.17	0.47
9:9:118:ILE:HB	9:9:119:PRO:CD	2.45	0.47
11:AA:689:ALA:HB2	11:AA:1233:LEU:HD23	1.97	0.47
12:AB:123:ARG:H	12:AB:123:ARG:CD	2.27	0.47
12:AB:159:LYS:HG2	12:AB:170:PRO:CB	2.45	0.47
13:AD:59:VAL:HG22	13:AD:144:ILE:HA	1.97	0.47
13:AD:182:ARG:O	13:AD:205:MET:HA	2.13	0.47
14:AE:891:ASP:OD2	14:AE:1290:ARG:NH2	2.47	0.47
14:AE:902:ASP:OD2	14:AE:905:ARG:HB2	2.15	0.47
10:B:9:G:H5''	10:B:10:G:OP2	2.14	0.47
10:B:58:A:C8	10:B:58:A:OP2	2.67	0.47
18:D:1308:U:P	38:X:98:ARG:CG	3.03	0.47
28:N:102:ALA:HB3	28:N:113:ASP:HB3	1.96	0.47
30:P:28:THR:CG2	30:P:86:ALA:C	2.88	0.47
40:Z:4:LYS:O	40:Z:4:LYS:HD2	2.15	0.47
41:a:1839:G:N9	41:a:1927:A:C1'	2.77	0.47
41:a:2168:G:H8	41:a:2168:G:OP1	1.97	0.47
41:a:2756:U:C4	41:a:2759:G:C6	3.03	0.47
47:g:18:CYS:HB2	47:g:40:CYS:HB3	1.96	0.47
50:j:121:THR:HB	50:j:127:PHE:CD2	2.49	0.47
64:x:27:VAL:CG2	64:x:40:ILE:HD12	2.44	0.47
9:9:43:LYS:NZ	9:9:95:LEU:HD13	2.30	0.47
9:9:132:TYR:CE1	40:Z:19:VAL:HG22	2.50	0.47
18:D:526:C:OP2	32:R:88:LYS:HE3	2.15	0.47
18:D:1064:G:O2'	18:D:1190:G:N2	2.47	0.47
23:I:75:ILE:HD13	23:I:75:ILE:C	2.40	0.47
36:V:8:LEU:HD23	36:V:25:ILE:HG21	1.97	0.47
40:Z:18:ASP:HB3	40:Z:22:LEU:CD1	2.45	0.47
59:s:84:ILE:HG23	59:s:84:ILE:O	2.14	0.47
7:6:21:DA:C6	8:7:15:G:C2	3.03	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:7:-14:U:C6	8:7:-14:U:C3'	2.97	0.47
10:A:5:G:C2'	10:A:6:G:C5'	2.93	0.47
10:A:9:G:H5''	10:A:10:G:OP2	2.14	0.47
14:AE:395:LYS:NZ	14:AE:399:LYS:CD	2.74	0.47
14:AE:968:ASN:HA	14:AE:1117:SER:HB2	1.96	0.47
14:AE:1150:PRO:HG3	14:AE:1214:PRO:HB2	1.96	0.47
14:AE:1261:LEU:HD12	14:AE:1304:ARG:HH21	1.78	0.47
10:B:18:G:C8	10:B:57:A:N1	2.83	0.47
39:Y:21:PRO:CB	39:Y:22:PRO:CD	2.90	0.47
41:a:517:C:OP2	49:i:10:ARG:NH2	2.48	0.47
41:a:1394:U:H4'	41:a:1603:A:H4'	1.97	0.47
41:a:1993:U:H4'	50:j:133:THR:HG22	1.96	0.47
4:3:94:ARG:CB	4:3:103:ILE:HD12	2.45	0.47
8:7:16:A:H2'	8:7:17:G:H8	1.80	0.47
10:A:18:G:C6	10:A:57:A:N7	2.83	0.47
10:A:60:U:H4'	10:A:61:C:OP2	2.14	0.47
11:AA:318:SER:OG	11:AA:320:ASP:OD1	2.31	0.47
11:AA:858:GLY:O	11:AA:861:ALA:CB	2.62	0.47
12:AB:166:GLY:C	30:P:87:LEU:HD22	2.40	0.47
14:AE:842:ARG:HH22	14:AE:1250:ASP:HB2	1.80	0.47
17:C:12:ARG:NH2	22:H:268:VAL:CG2	2.71	0.47
18:D:373:A:C2	18:D:374:A:C8	3.03	0.47
41:a:1021:A:N3	41:a:1021:A:C3'	2.78	0.47
41:a:2315:G:H5'	54:n:157:THR:HG23	1.97	0.47
2:1:29:VAL:HB	2:1:55:ILE:HD11	1.95	0.46
10:A:18:G:C8	10:A:57:A:N1	2.83	0.46
18:D:915:A:C8	18:D:915:A:H3'	2.50	0.46
41:a:784:G:H5'	41:a:785:G:OP1	2.15	0.46
9:9:1:MET:SD	9:9:2:ALA:N	2.88	0.46
9:9:31:ARG:CG	9:9:31:ARG:NH1	2.73	0.46
9:9:58:THR:HB	9:9:82:ILE:H	1.80	0.46
10:A:6:G:O2'	10:A:7:G:C5'	2.64	0.46
11:AA:230:PHE:HB2	11:AA:333:ILE:HB	1.97	0.46
11:AA:735:LYS:HA	11:AA:748:ILE:HG22	1.97	0.46
13:AC:102:LEU:HD12	13:AC:115:ILE:HG12	1.96	0.46
14:AE:319:SER:HA	14:AE:320:ASN:HA	1.64	0.46
14:AE:1036:ARG:HE	14:AE:1081:VAL:HG11	1.79	0.46
18:D:1225:A:OP1	38:X:101:ARG:HB2	2.15	0.46
50:j:152:PRO:HG3	50:j:156:PHE:CZ	2.50	0.46
3:2:30:ILE:HD13	3:2:93:LEU:HD12	1.97	0.46
11:AA:27:LEU:O	11:AA:528:ARG:NH1	2.43	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:103:VAL:HG12	11:AA:117:ILE:HG22	1.97	0.46
11:AA:862:LEU:HD11	16:AG:105:ILE:CB	2.46	0.46
11:AA:903:ARG:CA	16:AG:8:VAL:CB	2.94	0.46
13:AD:212:ASP:OD1	13:AD:212:ASP:N	2.48	0.46
14:AE:1060:VAL:HG13	14:AE:1106:ILE:HG12	1.96	0.46
14:AE:1167:LYS:NZ	14:AE:1170:LYS:HB2	2.30	0.46
10:B:15:G:H22	10:B:20:U:H3	1.59	0.46
18:D:868:C:H2'	18:D:869:G:O4'	2.16	0.46
18:D:1255:G:O2'	18:D:1258:G:N3	2.47	0.46
22:H:135:LEU:CB	22:H:167:VAL:O	2.63	0.46
8:7:-7:U:C3'	8:7:-7:U:C6	2.98	0.46
9:9:24:SER:HB2	9:9:116:GLU:HG2	1.98	0.46
11:AA:1245:ALA:O	14:AE:375:GLU:HG2	2.15	0.46
11:AA:1336:ASN:OD1	14:AE:33:TRP:HZ2	1.97	0.46
12:AB:149:GLU:N	12:AB:149:GLU:CD	2.73	0.46
14:AE:105:ILE:HD12	14:AE:242:LEU:CD2	2.44	0.46
10:B:18:G:C6	10:B:57:A:N7	2.83	0.46
18:D:1228:C:P	38:X:107:ARG:HH12	2.38	0.46
30:P:8:ILE:HD12	30:P:25:ILE:CD1	2.46	0.46
60:t:18:ARG:HB2	60:t:45:GLU:HB3	1.97	0.46
8:7:-20:A:H2'	8:7:-19:U:C6	2.50	0.46
9:9:139:LEU:HD21	40:Z:11:VAL:HG22	1.97	0.46
11:AA:909:LYS:NZ	16:AG:2:ASN:O	2.48	0.46
12:AB:138:ASP:HB2	12:AB:177:GLN:CA	2.36	0.46
12:AB:141:PHE:HA	30:P:84:VAL:HG22	1.98	0.46
14:AE:109:SER:HB2	14:AE:296:LYS:HG2	1.98	0.46
14:AE:420:PRO:HA	14:AE:437:PHE:O	2.15	0.46
14:AE:1219:ASP:O	14:AE:1223:LEU:HB2	2.15	0.46
10:B:6:G:O2'	10:B:7:G:C5'	2.64	0.46
18:D:946:A:H2'	18:D:947:G:C8	2.50	0.46
18:D:1103:C:O2	21:G:106:THR:HG21	2.15	0.46
18:D:1517:G:H1'	41:a:1919:A:O2'	2.16	0.46
22:H:33:LYS:HA	22:H:34:ASP:HA	1.61	0.46
22:H:69:ASP:O	22:H:85:SER:CB	2.63	0.46
41:a:1020:A:C6	41:a:1141:U:O2	2.68	0.46
62:v:96:ILE:HG21	62:v:126:ILE:HD12	1.97	0.46
9:9:60:LEU:HB2	9:9:61:ARG:NH2	2.31	0.46
11:AA:618:GLN:CD	14:AE:770:LEU:HD13	2.40	0.46
11:AA:845:LEU:HD13	11:AA:892:GLU:HB2	1.97	0.46
12:AB:167:ARG:HH12	30:P:93:ALA:C	2.24	0.46
12:AB:172:GLU:N	12:AB:172:GLU:CD	2.73	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:C:33:ILE:O	17:C:33:ILE:HG12	2.15	0.46
18:D:429:U:N3	18:D:431:A:N6	2.64	0.46
41:a:1406:U:H3	41:a:1596:A:H2	1.59	0.46
6:5:114:DC:H5''	14:AE:1148:ARG:CZ	2.46	0.46
9:9:39:THR:HA	9:9:42:ARG:HH11	1.81	0.46
10:A:11:A:C2'	10:A:12:G:O4'	2.60	0.46
10:A:14:A:H1'	10:A:22:G:N2	2.31	0.46
10:A:29:G:H2'	10:A:30:G:O4'	2.15	0.46
11:AA:712:SER:OG	11:AA:713:GLY:N	2.49	0.46
12:AB:137:ASN:HA	12:AB:142:ALA:HA	1.96	0.46
14:AE:1221:LEU:HD22	14:AE:1306:LEU:HB2	1.96	0.46
10:B:14:A:H1'	10:B:22:G:N2	2.31	0.46
30:P:99:GLN:O	30:P:99:GLN:HG2	2.16	0.46
3:2:1:MET:N	41:a:142:A:O2'	2.48	0.46
10:A:58:A:C1'	10:A:60:U:C5	2.99	0.46
11:AA:28:LEU:HD21	11:AA:524:ILE:HG13	1.98	0.46
13:AD:185:TYR:HA	13:AD:202:VAL:O	2.16	0.46
21:G:16:PHE:CD2	22:H:42:LEU:O	2.69	0.46
41:a:1275:A:N1	41:a:1295:C:O2'	2.46	0.46
41:a:2168:G:OP1	41:a:2168:G:C8	2.68	0.46
9:9:111:ALA:HB3	9:9:114:GLU:HG3	1.98	0.46
13:AC:64:VAL:HG11	13:AC:78:ILE:HG21	1.97	0.46
14:AE:198:CYS:HA	14:AE:221:ILE:CD1	2.45	0.46
14:AE:833:GLU:N	14:AE:1242:ARG:HH12	2.12	0.46
18:D:1175:G:N3	18:D:1176:A:C8	2.83	0.46
25:K:96:MET:CE	25:K:115:LEU:HD11	2.45	0.46
29:O:63:LEU:HD13	29:O:65:ILE:HD11	1.98	0.46
39:Y:23:VAL:HB	39:Y:24:GLY:H	1.65	0.46
39:Y:37:PHE:CE1	39:Y:56:VAL:HG11	2.51	0.46
54:n:36:LEU:HB3	54:n:57:LEU:HD21	1.97	0.46
8:7:1:U:O2	8:7:1:U:H2'	2.14	0.46
9:9:67:THR:H	9:9:68:PRO:HD3	1.80	0.46
9:9:127:ALA:O	9:9:130:PRO:HG2	2.16	0.46
10:A:48:C:N4	10:A:59:A:C5	2.84	0.46
11:AA:1314:GLN:HB2	15:AF:28:ARG:HH12	1.81	0.46
14:AE:43:THR:HG22	14:AE:57:PHE:HE1	1.80	0.46
14:AE:209:ASN:HA	14:AE:214:ARG:NH2	2.31	0.46
10:B:11:A:C2'	10:B:12:G:O4'	2.60	0.46
10:B:48:C:N4	10:B:59:A:C5	2.84	0.46
17:C:12:ARG:CZ	22:H:264:GLU:HA	2.46	0.46
18:D:35:G:N3	32:R:115:SER:OG	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:1906:G:H4'	41:a:1906:G:OP1	2.16	0.46
41:a:2291:U:H2'	41:a:2292:U:C6	2.51	0.46
63:w:28:LEU:HD23	63:w:48:VAL:HG21	1.98	0.46
10:A:60:U:OP2	10:A:61:C:N4	2.45	0.45
11:AA:176:ILE:HD11	11:AA:428:VAL:HG21	1.98	0.45
21:G:114:LEU:HA	21:G:144:LEU:HD13	1.98	0.45
39:Y:42:ASN:HA	39:Y:45:THR:HB	1.98	0.45
11:AA:562:GLU:OE1	11:AA:662:SER:OG	2.28	0.45
11:AA:852:ALA:HB2	11:AA:869:GLY:HA2	1.97	0.45
11:AA:1311:GLY:O	15:AF:31:GLN:NE2	2.49	0.45
14:AE:115:TRP:HB3	14:AE:1333:THR:CG2	2.46	0.45
14:AE:385:LEU:HD23	14:AE:390:LEU:HB2	1.98	0.45
18:D:1240:U:OP1	27:M:116:MET:HB2	2.16	0.45
31:Q:34:ILE:HG12	31:Q:70:CYS:SG	2.56	0.45
41:a:1385:A:O2'	41:a:1396:U:O2	2.35	0.45
41:a:1695:G:N7	48:h:14:ARG:NH2	2.64	0.45
41:a:2298:A:C6	41:a:2299:U:C2	3.04	0.45
8:7:-13:U:OP2	18:D:1397:C:O2	2.34	0.45
8:7:11:U:C2	11:AA:1253:LEU:HD12	2.37	0.45
8:7:17:G:H2'	8:7:18:A:H8	1.80	0.45
9:9:27:VAL:HG22	9:9:99:PHE:HE2	1.80	0.45
10:A:41:C:C5'	27:M:143:ARG:HD2	2.46	0.45
11:AA:887:VAL:HG21	11:AA:913:VAL:HG11	1.97	0.45
13:AD:35:PHE:HA	13:AD:38:THR:HG22	1.97	0.45
14:AE:201:LEU:CD1	14:AE:224:LEU:HD12	2.46	0.45
23:I:117:ALA:HB2	23:I:200:VAL:CG1	2.46	0.45
26:L:67:PRO:O	26:L:70:VAL:HG22	2.15	0.45
38:X:106:ALA:HB3	38:X:110:LYS:HD2	1.98	0.45
39:Y:124:MET:HE2	39:Y:124:MET:HB2	1.77	0.45
41:a:1327:A:H2'	41:a:1328:A:O4'	2.17	0.45
41:a:2547:A:H2'	41:a:2548:U:C6	2.52	0.45
9:9:106:PHE:CG	9:9:106:PHE:O	2.69	0.45
18:D:1176:A:H2'	18:D:1177:G:O4'	2.16	0.45
23:I:155:GLY:HA2	23:I:163:ALA:HB1	1.99	0.45
46:f:25:LEU:C	46:f:25:LEU:HD13	2.41	0.45
48:h:76:ALA:HB2	48:h:96:TYR:CD1	2.51	0.45
7:6:15:DC:C4	7:6:16:DC:C5	3.05	0.45
10:A:48:C:C5	10:A:59:A:C8	3.05	0.45
16:AG:254:MET:O	16:AG:257:ALA:HB2	2.17	0.45
10:B:37:A:N3	10:B:37:A:H5''	2.32	0.45
21:G:208:ARG:HH12	22:H:29:VAL:HG11	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:H:309:MET:HE2	22:H:318:PRO:HB3	1.97	0.45
22:H:332:VAL:HG13	22:H:342:ILE:HG23	1.98	0.45
41:a:2585:U:O2	41:a:2585:U:O4'	2.32	0.45
56:p:24:ILE:CD1	56:p:72:LEU:HD21	2.44	0.45
12:AB:47:GLU:HG3	12:AB:64:PHE:CD1	2.44	0.45
12:AB:111:ILE:O	12:AB:114:ARG:O	2.33	0.45
12:AB:144:PHE:CD2	12:AB:164:ILE:CG2	3.00	0.45
14:AE:53:ARG:HA	14:AE:54:ASP:HA	1.56	0.45
14:AE:395:LYS:HE3	14:AE:395:LYS:HB3	1.45	0.45
14:AE:926:PRO:HB2	14:AE:1241:TYR:HE1	1.81	0.45
15:AF:25:ARG:NH1	15:AF:61:ASN:OD1	2.49	0.45
10:B:58:A:HO2'	10:B:60:U:H5	1.61	0.45
10:B:58:A:C1'	10:B:60:U:C5	2.99	0.45
17:C:61:ARG:HG2	26:L:88:MET:HE1	1.98	0.45
18:D:1340:A:H8	18:D:1340:A:O5'	1.99	0.45
27:M:27:VAL:HG12	27:M:43:VAL:HG11	1.98	0.45
39:Y:116:MET:CB	39:Y:124:MET:HG2	2.46	0.45
39:Y:125:THR:HA	39:Y:128:ILE:HG12	1.98	0.45
1:O:51:VAL:HG22	1:O:51:VAL:O	2.15	0.45
6:5:110:DA:N1	11:AA:536:GLY:O	2.49	0.45
9:9:50:VAL:HG22	39:Y:119:ALA:C	2.41	0.45
10:A:18:G:O2'	10:A:60:U:N3	2.48	0.45
11:AA:694:ARG:HH22	13:AC:80:GLU:HG3	1.82	0.45
14:AE:141:PHE:CE2	14:AE:296:LYS:CB	2.94	0.45
20:F:67:ARG:HD3	20:F:67:ARG:N	2.31	0.45
27:M:24:ALA:O	27:M:27:VAL:HG22	2.16	0.45
41:a:954:G:OP2	62:v:16:ARG:NH2	2.50	0.45
54:n:57:LEU:HD22	54:n:89:VAL:CG2	2.47	0.45
6:5:108:DT:O4	11:AA:199:ASP:OD2	2.35	0.45
9:9:139:LEU:CD2	40:Z:11:VAL:HG22	2.47	0.45
11:AA:24:VAL:HG11	11:AA:704:MET:HE1	1.99	0.45
11:AA:1002:LEU:HD21	11:AA:1007:LYS:HB2	1.98	0.45
10:B:76:A:N3	10:B:76:A:C2'	2.74	0.45
18:D:17:U:H2'	18:D:18:C:C6	2.52	0.45
22:H:291:GLY:HA2	22:H:305:HIS:O	2.15	0.45
24:J:165:ARG:NH1	24:J:165:ARG:HB2	2.32	0.45
41:a:1720:U:H2'	41:a:1721:G:O4'	2.16	0.45
41:a:2070:A:H2'	41:a:2071:A:O4'	2.16	0.45
54:n:77:PHE:N	54:n:77:PHE:CD1	2.82	0.45
58:r:15:LEU:HD13	58:r:15:LEU:C	2.42	0.45
59:s:30:THR:CG2	59:s:31:GLU:N	2.79	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:9:34:THR:HG22	9:9:38:MET:CE	2.47	0.45
11:AA:557:ARG:NH2	11:AA:607:SER:O	2.49	0.45
11:AA:1332:SER:C	14:AE:243:PRO:HG2	2.42	0.45
14:AE:388:ARG:HG2	14:AE:388:ARG:NH1	2.32	0.45
14:AE:1227:HIS:HA	14:AE:1230:THR:HG22	1.99	0.45
16:AG:298:VAL:CA	16:AG:305:MET:HA	2.43	0.45
10:B:5:G:C2'	10:B:6:G:C5'	2.93	0.45
21:G:19:GLN:OE1	22:H:76:GLU:HB3	2.12	0.45
22:H:72:LEU:CD1	22:H:72:LEU:N	2.73	0.45
34:T:21:ASP:OD1	34:T:22:THR:N	2.49	0.45
39:Y:71:LYS:HB3	39:Y:72:THR:H	1.58	0.45
41:a:1007:C:OP1	59:s:37:ARG:NH2	2.50	0.45
44:d:48:U:H2'	44:d:49:C:C6	2.52	0.45
50:j:186:LEU:HD21	65:y:4:ILE:HG21	1.98	0.45
8:7:-8:U:H5''	8:7:-8:U:H6	1.82	0.45
9:9:125:ARG:NH1	9:9:125:ARG:CA	2.73	0.45
10:A:25:C:C2'	10:A:26:G:H5'	2.47	0.45
11:AA:1334:GLY:O	14:AE:25:ALA:HB3	2.17	0.45
12:AB:152:ASP:HB2	12:AB:157:ARG:CB	2.46	0.45
12:AB:155:LYS:HD3	12:AB:155:LYS:HA	1.53	0.45
12:AB:165:PHE:CZ	12:AB:171:VAL:HG11	2.52	0.45
14:AE:75:TYR:CD2	14:AE:75:TYR:O	2.70	0.45
14:AE:190:LYS:HB2	14:AE:190:LYS:HE3	1.41	0.45
22:H:84:LEU:N	22:H:84:LEU:CD2	2.78	0.45
41:a:39:G:H1'	52:l:43:THR:HG21	1.99	0.45
41:a:340:A:O2'	52:l:162:ARG:NH1	2.50	0.45
52:l:149:ILE:CD1	52:l:188:MET:HE3	2.46	0.45
7:6:15:DC:N3	7:6:16:DC:C4	2.84	0.44
9:9:62:ARG:HG2	9:9:62:ARG:NH2	2.20	0.44
9:9:106:PHE:O	9:9:106:PHE:CD2	2.70	0.44
11:AA:1314:GLN:HA	15:AF:28:ARG:HH22	1.82	0.44
10:B:34:C:C5	10:B:34:C:OP1	2.70	0.44
18:D:337:G:H2'	18:D:338:A:C8	2.52	0.44
21:G:114:LEU:HD13	21:G:144:LEU:CB	2.46	0.44
22:H:19:ARG:O	22:H:72:LEU:HD13	2.16	0.44
54:n:17:MET:HE2	54:n:25:VAL:HA	1.98	0.44
58:r:55:GLU:HA	58:r:58:LEU:HD12	1.99	0.44
9:9:16:SER:HB2	9:9:20:LYS:NZ	2.33	0.44
9:9:50:VAL:CG2	39:Y:120:ASP:N	2.79	0.44
11:AA:829:THR:HG23	11:AA:1059:ARG:HG2	2.00	0.44
13:AD:68:TYR:HE1	13:AD:79:LEU:HD13	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:161:THR:H	14:AE:164:GLN:HB2	1.82	0.44
10:B:18:G:O2'	10:B:60:U:N3	2.48	0.44
10:B:25:C:C2'	10:B:26:G:H5'	2.47	0.44
10:B:48:C:C5	10:B:59:A:C8	3.05	0.44
10:B:49:G:C2'	10:B:50:U:H5'	2.47	0.44
21:G:114:LEU:HD13	21:G:144:LEU:HB3	1.99	0.44
38:X:75:MET:HA	38:X:75:MET:HE3	1.99	0.44
53:m:12:ARG:HG3	53:m:44:VAL:HG11	2.00	0.44
2:1:17:VAL:HG12	2:1:76:VAL:HG21	1.98	0.44
10:A:76:A:C2	55:o:31:HIS:NE2	2.85	0.44
11:AA:674:ASP:OD2	11:AA:1070:HIS:ND1	2.50	0.44
14:AE:201:LEU:CB	14:AE:221:ILE:HD13	2.47	0.44
10:B:9:G:O2'	10:B:45:G:H2'	2.17	0.44
18:D:1397:C:O5'	18:D:1397:C:C6	2.70	0.44
18:D:1493:A:C8	18:D:1493:A:OP1	2.70	0.44
24:J:197:GLU:HA	24:J:200:ILE:HD12	1.99	0.44
25:K:111:MET:CE	25:K:125:ALA:HB1	2.39	0.44
29:O:80:ARG:O	29:O:84:THR:HG23	2.17	0.44
39:Y:37:PHE:CD2	39:Y:37:PHE:O	2.70	0.44
40:Z:29:LYS:HE2	40:Z:29:LYS:HB2	1.46	0.44
41:a:57:C:H2'	41:a:58:G:O4'	2.18	0.44
41:a:68:G:N2	41:a:74:A:OP2	2.49	0.44
41:a:645:C:H2'	41:a:647:G:C8	2.52	0.44
8:7:-12:U:C6	8:7:-12:U:OP2	2.71	0.44
10:A:49:G:C2'	10:A:50:U:H5'	2.47	0.44
11:AA:855:PRO:HG3	11:AA:913:VAL:HG12	1.99	0.44
11:AA:887:VAL:HG21	11:AA:913:VAL:CG1	2.47	0.44
18:D:13:U:C2	18:D:915:A:C5	3.06	0.44
18:D:915:A:H8	18:D:915:A:O5'	2.00	0.44
21:G:206:ALA:O	21:G:210:VAL:HG23	2.18	0.44
41:a:74:A:N7	41:a:88:G:C5	2.86	0.44
41:a:930:G:H1'	46:f:25:LEU:HD11	1.98	0.44
41:a:1589:U:C2	41:a:1590:A:C8	3.06	0.44
8:7:14:U:H2'	8:7:15:G:C8	2.51	0.44
10:A:9:G:O2'	10:A:45:G:H2'	2.18	0.44
11:AA:557:ARG:HB3	11:AA:587:LEU:HD13	2.00	0.44
12:AB:116:GLN:HG2	12:AB:116:GLN:O	2.17	0.44
14:AE:68:TYR:HB3	14:AE:75:TYR:HE2	1.81	0.44
14:AE:213:LYS:HA	14:AE:213:LYS:HE3	1.99	0.44
14:AE:1106:ILE:O	14:AE:1123:ARG:N	2.46	0.44
10:B:1:C:C5	10:B:2:G:N7	2.86	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:22:G:H2'	10:B:23:C:C5	2.52	0.44
18:D:376:G:C2	18:D:389:A:C2	3.05	0.44
18:D:1515:G:H2'	18:D:1516:G:C8	2.52	0.44
20:F:21:ARG:HH22	22:H:341:ARG:HD2	1.81	0.44
22:H:38:VAL:HG22	22:H:48:ILE:HD11	1.99	0.44
39:Y:35:MET:HE3	39:Y:35:MET:HB3	1.90	0.44
39:Y:95:ASP:OD2	39:Y:95:ASP:N	2.50	0.44
11:AA:11:ILE:HG22	11:AA:1172:LEU:HD11	1.99	0.44
11:AA:855:PRO:HB3	16:AG:108:GLN:CA	2.48	0.44
12:AB:144:PHE:CG	12:AB:164:ILE:CG2	3.00	0.44
14:AE:894:VAL:HG22	14:AE:1258:ARG:HH11	1.83	0.44
14:AE:1357:ILE:HG22	14:AE:1359:ALA:H	1.82	0.44
10:B:34:C:O5'	10:B:34:C:C6	2.70	0.44
18:D:109:A:C6	18:D:326:G:C6	3.05	0.44
22:H:294:VAL:HG21	22:H:330:VAL:HG21	1.99	0.44
39:Y:121:ILE:HA	39:Y:124:MET:SD	2.58	0.44
39:Y:140:GLU:OE1	39:Y:140:GLU:N	2.50	0.44
40:Z:1:SER:HB3	40:Z:2:ILE:H	1.61	0.44
41:a:1668:A:O2'	41:a:1674:G:N7	2.44	0.44
48:h:6:CYS:SG	48:h:13:ARG:NH1	2.89	0.44
8:7:-9:U:C3'	8:7:-9:U:C6	3.00	0.44
9:9:71:CYS:CA	9:9:117:LEU:HD13	2.48	0.44
11:AA:998:LEU:HG	11:AA:1011:LEU:HB3	1.99	0.44
11:AA:1088:ASP:OD1	11:AA:1088:ASP:N	2.51	0.44
11:AA:1157:GLN:HG3	11:AA:1159:VAL:HG13	2.00	0.44
13:AC:218:ARG:NH1	13:AD:231:PHE:O	2.50	0.44
14:AE:26:SER:HB2	14:AE:236:TRP:CH2	2.51	0.44
14:AE:978:ARG:HD3	14:AE:999:TYR:H	1.82	0.44
14:AE:1158:GLU:HA	14:AE:1223:LEU:HD21	1.99	0.44
10:B:26:G:N2	10:B:45:G:N2	2.66	0.44
10:B:57:A:O5'	10:B:58:A:P	2.76	0.44
10:B:60:U:OP2	10:B:61:C:N4	2.45	0.44
17:C:12:ARG:HD3	17:C:16:GLU:OE1	2.18	0.44
38:X:23:TYR:CD2	38:X:69:LEU:HD23	2.53	0.44
41:a:813:U:H2'	41:a:814:C:C6	2.53	0.44
41:a:1927:A:C8	41:a:1927:A:O5'	2.70	0.44
9:9:9:GLN:CD	9:9:9:GLN:C	2.85	0.44
10:A:22:G:H2'	10:A:23:C:C5	2.52	0.44
12:AB:68:TYR:OH	14:AE:294:ASN:ND2	2.51	0.44
12:AB:128:PHE:CD2	12:AB:128:PHE:N	2.85	0.44
13:AD:192:VAL:HG12	13:AD:193:GLU:H	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:211:GLU:CG	14:AE:215:LYS:HE3	2.44	0.44
14:AE:1108:GLN:HG3	14:AE:1109:LEU:HD12	1.99	0.44
18:D:198:G:OP2	18:D:198:G:C8	2.70	0.44
38:X:106:ALA:HB3	38:X:110:LYS:CD	2.47	0.44
39:Y:19:PRO:HG2	39:Y:24:GLY:N	2.32	0.44
41:a:214:G:N2	41:a:216:A:N3	2.66	0.44
45:e:59:GLU:O	45:e:63:ALA:HB3	2.18	0.44
66:z:76:TYR:OH	66:z:92:ARG:NH1	2.51	0.44
8:7:-7:U:H3'	8:7:-7:U:C6	2.52	0.44
11:AA:561:ILE:HG21	14:AE:772:TYR:HE2	1.82	0.44
11:AA:901:LEU:HA	16:AG:8:VAL:C	2.42	0.44
11:AA:906:PHE:CE1	16:AG:28:GLU:HA	2.52	0.44
11:AA:1298:VAL:HG11	14:AE:96:LYS:NZ	2.33	0.44
12:AB:132:GLU:CB	12:AB:147:VAL:HG13	2.47	0.44
12:AB:132:GLU:HB3	12:AB:147:VAL:HG13	1.99	0.44
12:AB:165:PHE:CB	30:P:84:VAL:O	2.66	0.44
14:AE:76:LYS:HB3	14:AE:76:LYS:NZ	2.32	0.44
14:AE:111:THR:CG2	14:AE:300:GLN:HA	2.48	0.44
14:AE:395:LYS:NZ	14:AE:399:LYS:HE2	2.32	0.44
14:AE:824:PRO:HD3	14:AE:835:LEU:HD12	2.00	0.44
14:AE:850:LYS:HB3	14:AE:855:ASP:HB2	2.00	0.44
14:AE:1079:LYS:HD3	14:AE:1098:GLN:HB3	1.99	0.44
10:B:22:G:O2'	10:B:23:C:O5'	2.36	0.44
18:D:397:A:H3'	18:D:397:A:N3	2.32	0.44
41:a:998:C:OP2	66:z:58:ARG:NH2	2.49	0.44
41:a:1209:U:O2'	41:a:1237:A:N1	2.40	0.44
8:7:11:U:C5	8:7:11:U:OP2	2.71	0.43
9:9:43:LYS:HZ1	9:9:95:LEU:HD13	1.83	0.43
9:9:106:PHE:CD2	9:9:106:PHE:C	2.95	0.43
10:A:46:G:O2'	10:A:47:U:H5''	2.19	0.43
10:A:56:C:OP1	41:a:2168:G:C4	2.71	0.43
10:A:57:A:O5'	10:A:58:A:P	2.76	0.43
11:AA:1282:GLY:O	14:AE:1361:THR:OG1	2.33	0.43
14:AE:515:ARG:HH12	14:AE:724:MET:HG2	1.83	0.43
14:AE:1046:ILE:HG22	14:AE:1061:VAL:HA	2.00	0.43
15:AF:58:LEU:HD12	15:AF:59:ILE:HG12	2.00	0.43
60:t:24:VAL:HG13	60:t:33:ALA:HB2	2.00	0.43
8:7:0:U:OP1	23:I:80:LYS:HB3	2.18	0.43
10:A:22:G:O2'	10:A:23:C:O5'	2.36	0.43
11:AA:811:ASN:ND2	11:AA:1098:LEU:O	2.51	0.43
11:AA:1247:SER:HB3	14:AE:375:GLU:O	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:167:ARG:CZ	30:P:93:ALA:O	2.55	0.43
13:AD:29:GLU:HB3	13:AD:200:LYS:HG3	1.99	0.43
14:AE:111:THR:HG21	14:AE:303:VAL:HB	2.00	0.43
14:AE:506:VAL:HG23	14:AE:628:GLY:HA3	1.99	0.43
19:E:55:GLN:N	19:E:56:PRO:HD2	2.32	0.43
22:H:61:GLU:HG2	22:H:62:ILE:HG23	2.00	0.43
25:K:153:VAL:HG23	25:K:164:ILE:HD13	2.00	0.43
41:a:2133:G:O2'	41:a:2157:G:N2	2.51	0.43
41:a:2395:C:H2'	41:a:2396:G:O4'	2.18	0.43
59:s:73:VAL:HG11	59:s:75:TYR:CZ	2.53	0.43
62:v:35:ALA:HB2	62:v:102:LEU:HD11	2.00	0.43
8:7:11:U:OP2	8:7:11:U:C4	2.70	0.43
10:A:49:G:O5'	10:A:49:G:C8	2.71	0.43
14:AE:120:LEU:HA	14:AE:121:PRO:HA	1.84	0.43
14:AE:126:LEU:HD12	14:AE:223:LEU:HD22	1.99	0.43
14:AE:222:LYS:HD2	14:AE:222:LYS:HA	1.32	0.43
14:AE:478:LEU:HD21	15:AF:47:THR:HG23	1.99	0.43
18:D:976:G:C8	18:D:1358:U:O2	2.71	0.43
18:D:1126:U:OP1	30:P:7:ARG:NH2	2.51	0.43
21:G:16:PHE:CG	22:H:43:LYS:HA	2.53	0.43
22:H:335:ILE:HG12	22:H:342:ILE:HG23	2.00	0.43
23:I:50:ALA:HB2	23:I:75:ILE:HD12	2.00	0.43
39:Y:7:TYR:CD2	39:Y:7:TYR:O	2.70	0.43
41:a:1925:C:C5	41:a:1925:C:OP2	2.70	0.43
64:x:18:LEU:HD23	64:x:25:ARG:HD2	1.99	0.43
6:5:116:DG:C6	6:5:117:DA:C6	3.06	0.43
11:AA:859:GLU:H	11:AA:859:GLU:HG3	1.38	0.43
13:AD:78:ILE:HA	13:AD:81:ILE:HG22	2.00	0.43
14:AE:128:LEU:CD2	14:AE:188:LEU:HB3	2.47	0.43
14:AE:1033:GLY:HA3	14:AE:1081:VAL:O	2.18	0.43
18:D:1417:G:C6	18:D:1482:G:C6	3.06	0.43
21:G:76:ALA:CB	21:G:210:VAL:HG11	2.48	0.43
22:H:109:THR:C	22:H:153:GLU:HA	2.43	0.43
41:a:2252:G:O2'	41:a:2253:G:H5'	2.18	0.43
7:6:18:DC:C2	8:7:17:G:N2	2.78	0.43
8:7:-7:U:P	23:I:132:ARG:HH12	2.41	0.43
10:A:1:C:C5	10:A:2:G:N7	2.86	0.43
11:AA:646:SER:OG	11:AA:647:ARG:N	2.51	0.43
25:K:150:PRO:O	25:K:153:VAL:HG22	2.19	0.43
39:Y:123:ALA:HA	39:Y:126:ARG:HG3	2.00	0.43
41:a:631:A:N3	41:a:2415:G:O2'	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:1020:A:C2	41:a:1141:U:C2	3.07	0.43
41:a:1082:U:H3	41:a:1086:A:N6	2.15	0.43
54:n:29:PRO:HB2	54:n:169:LEU:HD22	1.99	0.43
4:3:12:ILE:CG2	4:3:80:ALA:HB2	2.49	0.43
9:9:52:MET:HE1	9:9:85:SER:HB2	2.00	0.43
9:9:72:LEU:HD22	9:9:72:LEU:C	2.42	0.43
11:AA:1246:ARG:HH11	11:AA:1266:GLY:HA2	1.82	0.43
12:AB:7:LYS:HG2	12:AB:74:VAL:HG13	2.01	0.43
13:AD:31:LEU:HD21	13:AD:39:LEU:HD12	2.00	0.43
14:AE:62:PHE:N	14:AE:62:PHE:CD1	2.86	0.43
14:AE:141:PHE:HE2	14:AE:296:LYS:CB	2.22	0.43
14:AE:1026:PRO:HB2	14:AE:1028:ILE:HG23	2.00	0.43
25:K:156:LYS:HG2	28:N:71:VAL:HG13	2.00	0.43
35:U:6:LEU:HG	35:U:17:TYR:HB3	2.00	0.43
41:a:705:A:O4'	48:h:9:THR:HG21	2.18	0.43
41:a:1067:A:O2'	41:a:1068:G:O4'	2.31	0.43
14:AE:50:LYS:HD3	14:AE:50:LYS:HA	1.71	0.43
18:D:324:G:N2	18:D:327:A:C8	2.86	0.43
18:D:842:U:H3'	18:D:843:U:C5'	2.48	0.43
18:D:1333:A:H2'	18:D:1334:G:O4'	2.19	0.43
18:D:1499:A:O2'	18:D:1500:A:C5'	2.67	0.43
22:H:76:GLU:HA	22:H:76:GLU:OE2	2.18	0.43
22:H:136:VAL:HA	22:H:168:VAL:O	2.18	0.43
7:6:12:DC:O5'	7:6:12:DC:H6	2.01	0.43
11:AA:300:ASP:OD1	11:AA:313:ALA:N	2.51	0.43
11:AA:904:ALA:CB	16:AG:9:VAL:N	2.82	0.43
14:AE:586:GLY:HA3	14:AE:612:LEU:HD11	2.01	0.43
18:D:684:U:H2'	18:D:685:G:O4'	2.18	0.43
29:O:84:THR:HG21	29:O:103:PHE:CB	2.45	0.43
11:AA:1275:VAL:HG13	11:AA:1287:LEU:HD11	2.01	0.43
12:AB:128:PHE:HZ	12:AB:175:PHE:CA	2.28	0.43
12:AB:144:PHE:HB3	12:AB:164:ILE:CG1	2.38	0.43
12:AB:153:TYR:CD2	12:AB:153:TYR:N	2.81	0.43
14:AE:107:LEU:HA	14:AE:276:ASN:ND2	2.33	0.43
14:AE:394:ILE:O	14:AE:394:ILE:HG13	2.18	0.43
14:AE:609:TYR:HD2	14:AE:610:ARG:NH1	2.17	0.43
14:AE:950:ILE:HB	14:AE:1018:ALA:HB3	2.01	0.43
10:B:49:G:O5'	10:B:49:G:C8	2.71	0.43
18:D:563:A:C2	18:D:884:U:O4	2.62	0.43
41:a:1095:A:H2'	41:a:1096:A:C8	2.53	0.43
41:a:2310:C:HO2'	54:n:74:VAL:HG12	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:t:76:VAL:HG12	65:y:73:VAL:HB	2.01	0.43
60:t:107:LEU:HD21	60:t:115:ILE:HG21	2.01	0.43
4:3:36:VAL:HG11	4:3:39:ILE:CD1	2.44	0.43
6:5:98:DA:C2'	6:5:99:DT:C7	2.96	0.43
6:5:115:DA:P	14:AE:1148:ARG:HG3	2.58	0.43
11:AA:900:LYS:HB2	16:AG:11:ALA:HB2	1.05	0.43
11:AA:905:ILE:CG1	16:AG:54:GLY:C	2.88	0.43
12:AB:136:VAL:HG21	12:AB:173:LEU:CD2	2.49	0.43
14:AE:24:LEU:CD1	14:AE:232:ASN:ND2	2.82	0.43
14:AE:102:MET:HG2	14:AE:246:PRO:CG	2.49	0.43
14:AE:242:LEU:C	14:AE:242:LEU:HD23	2.44	0.43
14:AE:797:THR:HG22	14:AE:924:GLY:HA3	2.01	0.43
22:H:119:GLY:CA	22:H:132:PRO:C	2.92	0.43
22:H:152:LEU:CB	22:H:171:ARG:H	2.32	0.43
31:Q:88:GLY:H	31:Q:114:THR:HG22	1.84	0.43
39:Y:100:ILE:HB	39:Y:101:SER:H	1.71	0.43
41:a:973:A:O4'	41:a:1188:U:C6	2.72	0.43
41:a:1142:A:H2'	41:a:1142:A:N3	2.34	0.43
41:a:1394:U:C4	41:a:1395:A:C6	3.07	0.43
41:a:1932:A:H2'	41:a:1933:G:O4'	2.19	0.43
41:a:2511:U:O4	41:a:2575:C:N3	2.52	0.43
8:7:2:U:H3'	8:7:2:U:H6	1.84	0.42
10:A:18:G:N3	10:A:58:A:C5	2.87	0.42
11:AA:1268:GLN:NE2	14:AE:352:ARG:HB2	2.34	0.42
14:AE:126:LEU:CD1	14:AE:223:LEU:HD22	2.49	0.42
14:AE:647:PRO:HG3	14:AE:697:MET:HB3	2.01	0.42
18:D:429:U:O2	18:D:430:A:C8	2.72	0.42
22:H:119:GLY:O	22:H:120:PHE:C	2.62	0.42
22:H:280:LEU:HB2	22:H:330:VAL:O	2.19	0.42
39:Y:104:GLN:HB3	39:Y:105:LEU:H	1.74	0.42
41:a:1095:A:O2'	41:a:1096:A:O4'	2.33	0.42
41:a:2252:G:H2'	41:a:2253:G:H8	1.84	0.42
8:7:-14:U:H6	8:7:-14:U:H3'	1.84	0.42
11:AA:22:LEU:HB3	11:AA:655:VAL:HG11	2.01	0.42
11:AA:616:ILE:HG13	11:AA:652:TYR:HB2	2.01	0.42
12:AB:157:ARG:HD3	12:AB:157:ARG:HA	1.33	0.42
12:AB:166:GLY:O	30:P:87:LEU:O	2.37	0.42
14:AE:201:LEU:HD11	14:AE:220:ARG:NH1	2.32	0.42
18:D:421:U:O2	18:D:421:U:O4'	2.36	0.42
40:Z:28:GLU:H	40:Z:28:GLU:HG3	1.58	0.42
41:a:567:U:OP2	61:u:29:LYS:NZ	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:1386:C:H2'	41:a:1387:A:C8	2.53	0.42
41:a:1921:G:C2'	41:a:1922:G:H5'	2.49	0.42
41:a:2469:A:N6	41:a:2481:G:O2'	2.52	0.42
41:a:2756:U:C4	41:a:2759:G:O6	2.72	0.42
43:c:37:ARG:HG2	43:c:48:THR:HG23	2.00	0.42
48:h:37:ASN:HB2	48:h:62:TYR:HB2	2.01	0.42
10:A:26:G:N2	10:A:45:G:N2	2.66	0.42
11:AA:469:VAL:HA	11:AA:472:GLU:HG2	2.02	0.42
11:AA:590:PRO:HB2	11:AA:655:VAL:HG21	2.01	0.42
11:AA:741:MET:HE3	11:AA:974:ARG:HH12	1.85	0.42
13:AD:76:GLU:HB3	13:AD:80:GLU:HB3	2.01	0.42
14:AE:58:CYS:SG	14:AE:60:ARG:HG2	2.59	0.42
14:AE:568:SER:HB3	14:AE:570:LYS:NZ	2.34	0.42
14:AE:616:PRO:HA	14:AE:619:ILE:HG22	2.02	0.42
10:B:18:G:N3	10:B:58:A:C5	2.87	0.42
18:D:37:U:O2	18:D:548:G:N2	2.53	0.42
18:D:622:A:C8	18:D:623:C:C6	3.07	0.42
21:G:35:ARG:CG	22:H:10:GLU:OE2	2.63	0.42
29:O:55:VAL:O	29:O:57:MET:N	2.52	0.42
41:a:2638:G:O2'	41:a:2775:G:N2	2.41	0.42
48:h:240:PHE:CD2	48:h:240:PHE:O	2.73	0.42
52:l:145:ASP:HA	52:l:166:LYS:HB3	2.02	0.42
60:t:38:ILE:HD11	60:t:112:PHE:CZ	2.54	0.42
63:w:9:GLN:O	63:w:17:ARG:NH2	2.51	0.42
8:7:11:U:H6	8:7:11:U:H2'	1.68	0.42
10:A:34:C:OP1	27:M:84:THR:OG1	2.35	0.42
11:AA:901:LEU:HD11	16:AG:20:ARG:O	2.19	0.42
12:AB:115:LEU:HD13	12:AB:115:LEU:HA	1.73	0.42
12:AB:166:GLY:CA	30:P:87:LEU:HD22	2.49	0.42
14:AE:141:PHE:CD2	14:AE:297:ARG:HB2	2.54	0.42
14:AE:144:TYR:CE1	14:AE:162:GLU:OE1	2.73	0.42
14:AE:559:ALA:HB3	14:AE:562:GLU:HB3	2.01	0.42
10:B:46:G:O2'	10:B:47:U:H5''	2.19	0.42
18:D:1371:G:O3'	29:O:71:GLY:HA3	2.19	0.42
22:H:274:TYR:HD1	22:H:335:ILE:HD12	1.84	0.42
24:J:48:LEU:N	24:J:48:LEU:HD13	2.33	0.42
30:P:57:VAL:O	30:P:58:ASN:ND2	2.52	0.42
39:Y:34:ILE:HG22	39:Y:34:ILE:O	2.18	0.42
41:a:1250:G:OP2	61:u:21:ARG:NH2	2.53	0.42
57:q:3:VAL:HA	57:q:36:ARG:O	2.19	0.42
59:s:32:LEU:HD23	59:s:54:ILE:HD13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:t:113:MET:HE3	60:t:116:ILE:HD11	2.01	0.42
10:A:68:C:H3'	10:A:69:C:H5''	1.96	0.42
11:AA:144:VAL:HG23	11:AA:515:MET:HB2	2.02	0.42
11:AA:478:ARG:HD2	11:AA:492:MET:HA	2.02	0.42
14:AE:47:ARG:HA	14:AE:47:ARG:NE	2.34	0.42
14:AE:244:VAL:HA	14:AE:269:TYR:OH	2.19	0.42
18:D:826:C:O2	28:N:16:ASN:ND2	2.52	0.42
22:H:110:GLY:H	22:H:153:GLU:N	2.17	0.42
41:a:1047:G:N2	41:a:1110:G:O2'	2.50	0.42
41:a:2803:G:H2'	41:a:2804:U:C5	2.55	0.42
9:9:72:LEU:HD22	9:9:72:LEU:O	2.19	0.42
10:A:15:G:H1	10:A:20:U:H3	1.67	0.42
10:A:53:G:C2	10:A:54:U:C5	3.07	0.42
11:AA:133:ASN:O	11:AA:527:LYS:NZ	2.42	0.42
11:AA:444:ASP:OD1	11:AA:444:ASP:N	2.51	0.42
10:B:53:G:C2	10:B:54:U:C5	3.07	0.42
18:D:1329:A:OP1	38:X:28:THR:CA	2.67	0.42
40:Z:18:ASP:HB3	40:Z:22:LEU:HD12	2.00	0.42
41:a:36:G:N3	41:a:450:G:O2'	2.53	0.42
47:g:37:CYS:N	47:g:40:CYS:SG	2.77	0.42
9:9:18:VAL:HA	9:9:86:MET:CE	2.44	0.42
11:AA:678:ARG:HD3	11:AA:678:ARG:HA	1.84	0.42
14:AE:109:SER:HA	14:AE:110:PRO:HD3	1.96	0.42
14:AE:385:LEU:CD2	14:AE:390:LEU:HB2	2.50	0.42
17:C:44:ILE:HG21	22:H:339:ARG:HA	2.01	0.42
18:D:384:G:H2'	18:D:385:C:C6	2.54	0.42
18:D:1308:U:O5'	38:X:98:ARG:HG2	2.16	0.42
18:D:1323:G:H2'	18:D:1324:A:C8	2.55	0.42
40:Z:7:ILE:HD12	40:Z:7:ILE:HA	1.77	0.42
40:Z:23:ILE:HA	40:Z:23:ILE:HD12	1.77	0.42
41:a:126:A:OP1	53:m:45:SER:OG	2.38	0.42
41:a:320:A:H2'	52:l:131:THR:HG21	2.01	0.42
52:l:48:THR:HG23	52:l:86:ALA:HB3	2.02	0.42
61:u:109:LYS:HG2	61:u:126:ARG:HB2	2.01	0.42
11:AA:125:GLY:H	11:AA:495:ALA:HB1	1.84	0.42
14:AE:513:MET:HG3	14:AE:544:LEU:HD11	2.01	0.42
18:D:548:G:C6	18:D:549:C:C4	3.08	0.42
29:O:28:ILE:HD12	29:O:28:ILE:N	2.35	0.42
39:Y:64:ARG:HE	39:Y:64:ARG:HB2	1.52	0.42
41:a:819:A:C4	41:a:1189:A:C2	3.07	0.42
41:a:948:C:H1'	41:a:984:A:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:1028:A:N6	41:a:1125:G:H2'	2.34	0.42
48:h:119:GLY:O	48:h:130:LEU:HB3	2.20	0.42
9:9:80:THR:O	41:a:1108:U:OP1	2.38	0.42
14:AE:1272:SER:OG	14:AE:1273:ASP:N	2.53	0.42
21:G:47:VAL:N	21:G:48:PRO:HD2	2.34	0.42
22:H:302:GLY:HA3	22:H:344:LEU:HD13	2.00	0.42
27:M:22:LEU:HD13	27:M:97:ASN:ND2	2.35	0.42
38:X:96:PRO:HG2	38:X:102:THR:HG23	1.97	0.42
41:a:1082:U:N3	41:a:1086:A:C6	2.87	0.42
41:a:2683:C:O2	60:t:70:ARG:NH2	2.52	0.42
48:h:76:ALA:HB2	48:h:96:TYR:CE1	2.55	0.42
50:j:172:VAL:HG11	50:j:175:LEU:HD21	2.01	0.42
7:6:27:DG:H1'	7:6:28:DA:C5	2.55	0.42
9:9:71:CYS:SG	9:9:117:LEU:HB2	2.60	0.42
11:AA:135:THR:HG22	11:AA:144:VAL:HG22	2.02	0.42
14:AE:848:VAL:HB	14:AE:858:VAL:HG22	2.02	0.42
14:AE:1024:THR:HG23	14:AE:1123:ARG:HA	2.00	0.42
16:AG:422:GLU:O	16:AG:426:GLY:N	2.52	0.42
10:B:58:A:OP2	10:B:58:A:H8	2.02	0.42
10:B:65:C:C2'	10:B:66:C:H5'	2.49	0.42
21:G:208:ARG:NH1	22:H:29:VAL:HG11	2.34	0.42
22:H:292:CYS:SG	22:H:304:VAL:HB	2.60	0.42
23:I:9:GLY:HA3	33:S:89:MET:HE3	2.01	0.42
25:K:133:PRO:HA	25:K:136:VAL:HG12	2.02	0.42
39:Y:20:SER:CB	39:Y:21:PRO:HD3	2.39	0.42
39:Y:41:PHE:HA	39:Y:68:PHE:CE2	2.54	0.42
41:a:126:A:O5'	53:m:19:ARG:HG3	2.19	0.42
41:a:851:C:H2'	41:a:852:U:C6	2.55	0.42
41:a:2602:A:H5''	41:a:2603:G:C5'	2.49	0.42
53:m:12:ARG:CG	53:m:44:VAL:HG11	2.50	0.42
64:x:99:TYR:OH	64:x:111:ARG:NH1	2.53	0.42
66:z:65:ILE:CD1	66:z:92:ARG:HB2	2.49	0.42
9:9:61:ARG:C	9:9:65:GLU:HB2	2.45	0.41
11:AA:1245:ALA:HB3	14:AE:375:GLU:HB3	2.01	0.41
11:AA:1278:LEU:HD21	14:AE:484:MET:CE	2.50	0.41
14:AE:144:TYR:N	14:AE:144:TYR:CD1	2.88	0.41
14:AE:242:LEU:HA	14:AE:243:PRO:HD3	1.95	0.41
14:AE:390:LEU:N	14:AE:390:LEU:HD13	2.35	0.41
14:AE:395:LYS:HZ2	14:AE:399:LYS:HE2	1.84	0.41
14:AE:515:ARG:NH2	14:AE:718:SER:O	2.48	0.41
10:B:26:G:C2	10:B:45:G:N2	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:C:12:ARG:O	17:C:16:GLU:HG3	2.19	0.41
18:D:502:A:H2'	18:D:503:C:O4'	2.20	0.41
20:F:67:ARG:HD3	20:F:67:ARG:H	1.85	0.41
21:G:187:VAL:HG21	21:G:199:VAL:HG23	2.02	0.41
41:a:879:G:H2'	41:a:880:G:O4'	2.19	0.41
41:a:2788:C:H2'	41:a:2789:C:C6	2.55	0.41
56:p:25:THR:HG22	56:p:34:THR:HG23	2.02	0.41
2:1:92:ARG:NE	2:1:94:ASP:OD1	2.53	0.41
8:7:18:A:O3'	11:AA:688:GLN:NE2	2.53	0.41
10:A:36:U:H2'	10:A:37:A:O4'	2.19	0.41
10:A:56:C:C2	41:a:2112:G:C5	3.07	0.41
10:A:58:A:OP2	10:A:58:A:H8	2.02	0.41
11:AA:755:LYS:HD2	11:AA:755:LYS:HA	1.86	0.41
11:AA:836:LEU:HD21	11:AA:921:PRO:HD3	2.02	0.41
14:AE:139:LEU:HD23	14:AE:139:LEU:HA	1.90	0.41
14:AE:515:ARG:HG2	14:AE:516:ASP:H	1.85	0.41
18:D:37:U:C4	18:D:397:A:N6	2.87	0.41
18:D:1061:G:H5'	30:P:61:ALA:HB2	2.02	0.41
22:H:155:LYS:O	22:H:169:SER:CB	2.69	0.41
34:T:43:PHE:CE2	34:T:56:LEU:HD22	2.56	0.41
41:a:742:A:N1	41:a:755:U:O4	2.53	0.41
41:a:1082:U:C4	41:a:1086:A:N6	2.88	0.41
41:a:1182:G:H2'	41:a:1183:U:O4'	2.20	0.41
41:a:1570:A:H2'	41:a:1571:A:C8	2.55	0.41
41:a:2615:U:C2	49:i:4:GLN:HA	2.55	0.41
54:n:123:ASP:C	54:n:123:ASP:OD1	2.62	0.41
6:5:98:DA:H2'	6:5:99:DT:H72	2.01	0.41
8:7:20:G:H21	14:AE:427:PRO:HD3	1.86	0.41
12:AB:103:ILE:HG13	12:AB:104:SER:H	1.85	0.41
14:AE:68:TYR:O	14:AE:75:TYR:CD2	2.70	0.41
14:AE:1289:ASN:O	14:AE:1293:GLU:HB2	2.20	0.41
18:D:429:U:O2	18:D:430:A:N7	2.53	0.41
20:F:32:VAL:HG11	31:Q:89:PRO:HG3	2.01	0.41
38:X:4:ILE:CG1	38:X:9:ILE:HD12	2.50	0.41
39:Y:102:ARG:HD2	39:Y:103:ALA:N	2.36	0.41
41:a:1925:C:OP2	41:a:1925:C:C6	2.73	0.41
41:a:2294:G:OP1	64:x:10:ARG:HD3	2.21	0.41
3:2:46:ALA:O	3:2:50:LEU:HB2	2.20	0.41
10:A:26:G:H1	10:A:44:A:N6	2.18	0.41
12:AB:125:LYS:HB3	12:AB:126:THR:H	1.60	0.41
14:AE:136:GLU:OE1	14:AE:312:ARG:NH2	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:388:ARG:HG2	14:AE:388:ARG:HH11	1.84	0.41
18:D:1235:U:H2'	18:D:1236:A:O4'	2.20	0.41
22:H:342:ILE:HG22	22:H:344:LEU:HD12	2.01	0.41
25:K:136:VAL:O	25:K:140:THR:HG23	2.20	0.41
41:a:548:G:H3'	41:a:549:G:O4'	2.20	0.41
41:a:1406:U:O2'	41:a:1407:G:OP2	2.39	0.41
48:h:175:ARG:NH1	48:h:181:MET:HE2	2.36	0.41
49:i:43:ILE:HG22	49:i:49:TYR:HB2	2.01	0.41
63:w:49:GLU:HB2	63:w:50:PRO:HD3	2.01	0.41
8:7:13:G:H8	8:7:13:G:H5''	1.84	0.41
10:A:26:G:C2	10:A:45:G:N2	2.89	0.41
11:AA:1278:LEU:HD23	11:AA:1278:LEU:HA	1.86	0.41
12:AB:141:PHE:HB2	12:AB:165:PHE:CE1	2.55	0.41
14:AE:51:PRO:HB2	14:AE:52:GLU:H	1.65	0.41
17:C:14:THR:CG2	17:C:48:ARG:HE	2.33	0.41
18:D:216:U:H2'	18:D:217:C:C6	2.55	0.41
18:D:860:A:H2'	18:D:861:G:O4'	2.21	0.41
18:D:1175:G:HO2'	18:D:1176:A:P	2.43	0.41
41:a:207:A:H2'	41:a:208:C:O4'	2.21	0.41
41:a:984:A:N3	41:a:984:A:H2'	2.35	0.41
41:a:2006:C:O2'	41:a:2823:A:N3	2.47	0.41
54:n:171:ALA:O	54:n:174:ASP:N	2.54	0.41
11:AA:22:LEU:HD22	11:AA:603:ILE:HG21	2.02	0.41
11:AA:699:LEU:HG	11:AA:799:ASN:HD22	1.85	0.41
11:AA:998:LEU:HD21	11:AA:1015:ALA:HB2	2.02	0.41
12:AB:127:LEU:HD12	12:AB:127:LEU:HA	1.87	0.41
14:AE:279:LEU:HD13	14:AE:299:LEU:HD13	2.02	0.41
18:D:977:A:H1'	18:D:982:U:O4	2.20	0.41
18:D:1526:G:P	20:F:42:THR:HG23	2.61	0.41
24:J:61:VAL:CG2	24:J:200:ILE:HD11	2.39	0.41
33:S:41:ARG:O	33:S:45:VAL:HG12	2.20	0.41
41:a:197:A:N6	41:a:2430:A:H2'	2.36	0.41
41:a:1548:A:H2'	41:a:1549:A:C8	2.55	0.41
41:a:1839:G:C4	41:a:1927:A:C5	3.08	0.41
50:j:175:LEU:CD1	50:j:193:VAL:HG12	2.51	0.41
52:l:170:ARG:NH2	52:l:176:ASP:OD1	2.49	0.41
54:n:122:PHE:CZ	54:n:167:ARG:HA	2.56	0.41
56:p:52:PHE:CZ	56:p:72:LEU:HD22	2.56	0.41
9:9:25:ALA:HA	9:9:96:PHE:HE1	1.85	0.41
10:A:56:C:OP1	41:a:2168:G:N3	2.53	0.41
11:AA:310:ILE:HG21	11:AA:325:LEU:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:1279:GLU:HG2	14:AE:1357:ILE:HD13	2.02	0.41
14:AE:390:LEU:HD13	14:AE:390:LEU:H	1.86	0.41
14:AE:847:ASP:OD1	14:AE:847:ASP:N	2.49	0.41
14:AE:1050:THR:HG23	14:AE:1057:SER:HB3	2.03	0.41
18:D:218:U:H2'	18:D:219:U:O4'	2.21	0.41
39:Y:102:ARG:H	39:Y:102:ARG:HG3	1.59	0.41
41:a:17:G:H2'	41:a:18:U:C6	2.56	0.41
63:w:67:PHE:O	63:w:71:ARG:HG2	2.21	0.41
66:z:66:ASN:OD1	66:z:70:ARG:NE	2.54	0.41
8:7:13:G:H8	8:7:13:G:C5'	2.33	0.41
9:9:8:LYS:NZ	41:a:1046:A:N6	2.69	0.41
9:9:48:ALA:HB3	9:9:51:TYR:HD2	1.86	0.41
9:9:67:THR:N	9:9:68:PRO:HD2	2.36	0.41
11:AA:741:MET:SD	11:AA:974:ARG:NH2	2.93	0.41
11:AA:746:ALA:O	11:AA:974:ARG:NH2	2.45	0.41
13:AC:57:THR:HG23	13:AC:158:ARG:HH21	1.86	0.41
14:AE:47:ARG:NE	14:AE:47:ARG:CA	2.83	0.41
18:D:1368:A:OP1	29:O:113:ARG:NH2	2.54	0.41
25:K:154:ALA:HA	25:K:164:ILE:HD11	2.03	0.41
28:N:11:LEU:HD22	28:N:75:ILE:HD11	2.03	0.41
39:Y:21:PRO:HD2	39:Y:22:PRO:HD2	2.03	0.41
41:a:476:G:H4'	41:a:502:A:N1	2.35	0.41
41:a:526:A:O2'	41:a:2043:C:O2	2.39	0.41
41:a:2273:A:H2'	41:a:2274:A:C8	2.55	0.41
62:v:73:ILE:HG21	62:v:91:TYR:CZ	2.55	0.41
63:w:29:VAL:HG11	63:w:75:ILE:HG23	2.03	0.41
2:1:75:PHE:CZ	2:1:104:THR:HG21	2.56	0.41
8:7:-7:U:P	23:I:132:ARG:NH1	2.94	0.41
8:7:4:U:O2'	11:AA:914:LYS:CG	2.68	0.41
9:9:23:LEU:HA	9:9:118:ILE:CG1	2.51	0.41
9:9:47:GLU:HG3	9:9:95:LEU:CD2	2.49	0.41
11:AA:862:LEU:HD23	11:AA:862:LEU:C	2.46	0.41
11:AA:874:GLY:HA2	13:AC:66:HIS:HB3	2.03	0.41
12:AB:133:MET:O	12:AB:133:MET:SD	2.79	0.41
12:AB:146:GLY:CA	12:AB:162:VAL:CG2	2.86	0.41
13:AC:42:ALA:HB1	13:AC:224:LEU:HD11	2.03	0.41
13:AD:79:LEU:HD11	14:AE:526:VAL:HG21	2.02	0.41
14:AE:24:LEU:CB	14:AE:232:ASN:OD1	2.54	0.41
14:AE:68:TYR:CB	14:AE:75:TYR:HE2	2.34	0.41
14:AE:1350:ASN:HA	14:AE:1353:VAL:HG12	2.01	0.41
16:AG:400:GLU:C	16:AG:401:PRO:O	2.62	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:15:G:N2	10:B:20:U:C2	2.88	0.41
10:B:26:G:H1	10:B:44:A:N6	2.18	0.41
18:D:152:A:N6	18:D:170:U:C2	2.89	0.41
18:D:712:A:H2'	18:D:713:G:O4'	2.21	0.41
18:D:915:A:C6	18:D:916:U:C4	3.08	0.41
18:D:1330:U:OP2	38:X:26:GLY:HA3	2.21	0.41
23:I:6:HIS:HA	23:I:7:PRO:HD3	1.96	0.41
39:Y:35:MET:O	39:Y:35:MET:SD	2.79	0.41
41:a:5:A:H2'	41:a:6:A:C8	2.56	0.41
41:a:221:A:N1	41:a:265:A:O2'	2.54	0.41
41:a:493:G:H2'	41:a:494:G:O4'	2.20	0.41
41:a:1169:A:H5''	41:a:1169:A:N3	2.36	0.41
41:a:1406:U:C2'	41:a:1407:G:OP2	2.69	0.41
41:a:1421:G:C2	41:a:1422:G:C8	3.09	0.41
4:3:39:ILE:HG22	4:3:40:ASN:N	2.34	0.41
8:7:-4:U:OP1	8:7:-4:U:H4'	2.21	0.41
9:9:73:LYS:CB	9:9:117:LEU:HD11	2.51	0.41
10:A:32:C:H4'	27:M:144:MET:CE	2.51	0.41
10:A:46:G:H2'	10:A:47:U:OP2	2.21	0.41
11:AA:800:MET:HE3	11:AA:800:MET:HB2	1.69	0.41
11:AA:870:ILE:HB	11:AA:944:ARG:HD3	2.03	0.41
13:AD:44:ARG:HA	13:AD:183:ILE:HD12	2.03	0.41
13:AD:46:ILE:HD11	13:AD:224:LEU:HD13	2.02	0.41
14:AE:820:ILE:HG12	14:AE:884:SER:HB2	2.02	0.41
18:D:580:C:H2'	18:D:581:G:O4'	2.21	0.41
22:H:123:GLU:CA	22:H:128:ARG:HA	2.43	0.41
33:S:16:LEU:HD13	33:S:54:ASP:HB2	2.03	0.41
41:a:1019:U:N3	41:a:1142:A:N6	2.49	0.41
41:a:2298:A:C5	41:a:2321:U:C4	3.09	0.41
48:h:232:HIS:HA	48:h:242:LYS:HE3	2.03	0.41
58:r:9:VAL:HG11	58:r:12:LEU:HD21	2.03	0.41
9:9:31:ARG:HD3	41:a:1054:A:H4'	1.96	0.40
11:AA:803:ALA:HB2	11:AA:1094:VAL:HG21	2.03	0.40
14:AE:213:LYS:HE3	14:AE:213:LYS:CA	2.47	0.40
14:AE:506:VAL:H	14:AE:506:VAL:HG12	1.59	0.40
10:B:15:G:N2	10:B:20:U:H3	2.20	0.40
22:H:332:VAL:HG11	22:H:335:ILE:CG1	2.38	0.40
39:Y:14:ALA:HB3	39:Y:50:LYS:HA	2.03	0.40
41:a:2572:A:N7	50:j:150:GLN:NE2	2.69	0.40
9:9:8:LYS:HZ1	41:a:1046:A:H61	1.68	0.40
9:9:60:LEU:HD23	9:9:60:LEU:HA	1.94	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:136:VAL:CG1	12:AB:141:PHE:CD2	2.87	0.40
13:AC:104:LYS:HG2	13:AC:110:VAL:HG22	2.03	0.40
14:AE:113:HIS:ND1	14:AE:115:TRP:HB2	2.37	0.40
14:AE:734:ALA:O	14:AE:738:ARG:HB2	2.22	0.40
14:AE:839:VAL:HG12	14:AE:864:LEU:HD12	2.02	0.40
18:D:197:A:C5	18:D:221:C:H4'	2.53	0.40
18:D:972:C:O2'	30:P:57:VAL:HG21	2.18	0.40
18:D:1208:C:H2'	18:D:1209:C:H6	1.85	0.40
18:D:1370:G:C2	18:D:1371:G:C8	3.09	0.40
32:R:110:ARG:NH1	32:R:112:GLN:O	2.53	0.40
38:X:16:VAL:O	38:X:20:THR:HG23	2.21	0.40
41:a:2311:A:C2	54:n:85:ILE:HD11	2.55	0.40
52:l:149:ILE:HD11	52:l:188:MET:HE3	2.02	0.40
58:r:57:LYS:O	58:r:61:VAL:HG13	2.21	0.40
11:AA:524:ILE:HD12	11:AA:712:SER:HB2	2.02	0.40
11:AA:550:VAL:HG13	14:AE:777:HIS:CD2	2.56	0.40
11:AA:1245:ALA:CB	14:AE:375:GLU:HB3	2.52	0.40
12:AB:167:ARG:HE	30:P:92:LEU:HB2	1.83	0.40
14:AE:109:SER:CB	14:AE:296:LYS:HG2	2.51	0.40
14:AE:182:ALA:HB1	14:AE:238:ILE:CG2	2.52	0.40
14:AE:368:LEU:HA	14:AE:369:PRO:HD3	1.96	0.40
10:B:8:U:OP2	10:B:8:U:H6	2.04	0.40
18:D:579:A:O2'	34:T:54:ARG:NH1	2.54	0.40
22:H:29:VAL:HG23	22:H:37:LEU:HD12	2.04	0.40
25:K:150:PRO:HA	25:K:153:VAL:HG22	2.03	0.40
27:M:27:VAL:HG12	27:M:43:VAL:HG21	2.04	0.40
39:Y:72:THR:HG1	39:Y:73:PRO:HD2	1.82	0.40
8:7:-11:U:O2	8:7:-11:U:C3'	2.69	0.40
10:A:71:C:H2'	10:A:72:A:C1'	2.52	0.40
11:AA:213:LEU:HD13	11:AA:422:LYS:HG2	2.03	0.40
11:AA:888:THR:CB	11:AA:889:PRO:CD	2.93	0.40
11:AA:987:GLU:HG2	11:AA:991:LYS:HE3	2.03	0.40
13:AD:211:ILE:HD12	13:AD:211:ILE:HA	1.92	0.40
14:AE:67:ASP:CG	14:AE:95:THR:HG1	2.24	0.40
16:AG:188:PRO:HA	16:AG:193:ALA:HB2	2.04	0.40
10:B:25:C:H2'	10:B:26:G:C5'	2.51	0.40
18:D:1225:A:H2'	18:D:1226:C:C5	2.56	0.40
18:D:1389:C:H2'	18:D:1390:U:O4'	2.22	0.40
22:H:110:GLY:N	22:H:153:GLU:HA	2.37	0.40
30:P:22:THR:HA	30:P:25:ILE:HG22	2.04	0.40
41:a:871:U:H2'	41:a:872:U:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:h:29:PRO:HG2	48:h:34:LEU:HD11	2.03	0.40
66:z:18:LEU:HD13	66:z:18:LEU:HA	1.95	0.40
10:A:7:G:O6	10:A:49:G:O6	2.39	0.40
12:AB:138:ASP:OD2	12:AB:177:GLN:HA	2.21	0.40
14:AE:111:THR:HG23	14:AE:300:GLN:HA	2.03	0.40
14:AE:117:LEU:HD22	14:AE:139:LEU:CD1	2.52	0.40
14:AE:245:LEU:CG	14:AE:246:PRO:HD2	2.47	0.40
14:AE:820:ILE:HD11	14:AE:822:MET:HE2	2.02	0.40
14:AE:930:LEU:HA	14:AE:1244:GLN:HG3	2.02	0.40
18:D:890:G:O2'	18:D:906:A:N6	2.55	0.40
22:H:305:HIS:CG	22:H:306:VAL:N	2.90	0.40
29:O:9:THR:O	29:O:85:ARG:HD2	2.21	0.40
30:P:99:GLN:O	30:P:99:GLN:CG	2.70	0.40
38:X:16:VAL:HG13	38:X:34:LEU:CD1	2.51	0.40
41:a:67:U:C4	41:a:74:A:C6	3.04	0.40
41:a:1365:A:O5'	43:c:28:ARG:NH2	2.52	0.40
41:a:2641:G:OP1	59:s:78:THR:HG22	2.21	0.40
42:b:59:LEU:HD12	42:b:80:ILE:HD12	2.03	0.40
52:l:188:MET:HE2	52:l:193:VAL:HA	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	101/103 (98%)	97 (96%)	3 (3%)	1 (1%)	12	43
2	1	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	2	92/100 (92%)	90 (98%)	2 (2%)	0	100	100
4	3	101/104 (97%)	96 (95%)	4 (4%)	1 (1%)	12	43
5	4	92/94 (98%)	90 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	9	146/165 (88%)	95 (65%)	37 (25%)	14 (10%)	0	7
11	AA	1338/1342 (100%)	1209 (90%)	126 (9%)	3 (0%)	43	72
12	AB	157/181 (87%)	128 (82%)	22 (14%)	7 (4%)	2	18
13	AC	295/329 (90%)	274 (93%)	19 (6%)	2 (1%)	18	50
13	AD	292/329 (89%)	270 (92%)	22 (8%)	0	100	100
14	AE	1329/1407 (94%)	1198 (90%)	122 (9%)	9 (1%)	18	50
15	AF	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
16	AG	490/495 (99%)	421 (86%)	51 (10%)	18 (4%)	2	22
17	C	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
19	E	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
20	F	68/71 (96%)	68 (100%)	0	0	100	100
21	G	223/241 (92%)	210 (94%)	13 (6%)	0	100	100
22	H	255/557 (46%)	188 (74%)	55 (22%)	12 (5%)	2	18
23	I	206/233 (88%)	197 (96%)	8 (4%)	1 (0%)	24	56
24	J	203/206 (98%)	198 (98%)	5 (2%)	0	100	100
25	K	154/167 (92%)	146 (95%)	7 (4%)	1 (1%)	21	52
26	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	12	43
27	M	149/179 (83%)	144 (97%)	4 (3%)	1 (1%)	18	50
28	N	127/130 (98%)	121 (95%)	5 (4%)	1 (1%)	16	48
29	O	125/130 (96%)	115 (92%)	9 (7%)	1 (1%)	16	48
30	P	97/103 (94%)	87 (90%)	9 (9%)	1 (1%)	12	43
31	Q	115/129 (89%)	104 (90%)	9 (8%)	2 (2%)	7	34
32	R	117/124 (94%)	116 (99%)	1 (1%)	0	100	100
33	S	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
34	T	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
35	U	80/82 (98%)	75 (94%)	4 (5%)	1 (1%)	9	38
36	V	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
37	W	81/92 (88%)	78 (96%)	3 (4%)	0	100	100
38	X	114/118 (97%)	107 (94%)	5 (4%)	2 (2%)	6	34
39	Y	139/142 (98%)	102 (73%)	25 (18%)	12 (9%)	0	8
40	Z	28/121 (23%)	19 (68%)	7 (25%)	2 (7%)	1	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	b	74/85 (87%)	69 (93%)	5 (7%)	0	100	100
43	c	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
45	e	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
46	f	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
47	g	64/70 (91%)	63 (98%)	1 (2%)	0	100	100
48	h	269/273 (98%)	259 (96%)	9 (3%)	1 (0%)	30	60
49	i	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
50	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
51	k	50/55 (91%)	50 (100%)	0	0	100	100
52	l	199/201 (99%)	190 (96%)	8 (4%)	1 (0%)	24	56
53	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
54	n	175/179 (98%)	162 (93%)	11 (6%)	2 (1%)	11	42
55	o	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
56	p	173/177 (98%)	161 (93%)	12 (7%)	0	100	100
57	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
58	r	147/149 (99%)	136 (92%)	11 (8%)	0	100	100
59	s	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
60	t	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
61	u	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
62	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
63	w	117/127 (92%)	107 (92%)	10 (8%)	0	100	100
64	x	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
65	y	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
66	z	115/118 (98%)	110 (96%)	4 (4%)	1 (1%)	14	45
All	All	10154/11072 (92%)	9318 (92%)	738 (7%)	98 (1%)	15	43

All (98) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	9	88	HIS
16	AG	6	LEU
16	AG	100	VAL
16	AG	400	GLU
16	AG	401	PRO

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Mol	Chain	Res	Type
16	AG	402	THR
22	H	139	ARG
22	H	153	GLU
22	H	169	SER
22	H	306	VAL
22	H	340	ARG
29	O	56	ASP
38	X	103	LYS
39	Y	48	ILE
9	9	33	VAL
9	9	119	PRO
11	AA	853	ASP
12	AB	125	LYS
12	AB	131	GLY
14	AE	175	GLU
16	AG	33	THR
16	AG	41	GLN
16	AG	109	THR
16	AG	303	HIS
22	H	108	VAL
22	H	309	MET
22	H	333	LEU
23	I	80	LYS
39	Y	93	ASN
48	h	158	ALA
52	l	142	ALA
66	z	3	ARG
9	9	48	ALA
9	9	91	ALA
9	9	118	ILE
9	9	130	PRO
14	AE	51	PRO
14	AE	805	GLN
16	AG	38	LYS
16	AG	309	VAL
16	AG	396	GLU
22	H	76	GLU
22	H	142	ARG
27	M	130	ASN
30	P	58	ASN
31	Q	119	ASN
38	X	105	ASN

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Mol	Chain	Res	Type
39	Y	20	SER
39	Y	64	ARG
39	Y	106	GLN
9	9	69	PHE
9	9	73	LYS
9	9	108	VAL
9	9	129	LEU
9	9	133	GLU
12	AB	105	ASP
13	AC	193	GLU
14	AE	174	ASP
14	AE	193	ASP
16	AG	301	ASP
16	AG	394	GLU
39	Y	83	ALA
40	Z	21	GLU
54	n	40	VAL
12	AB	130	PRO
12	AB	132	GLU
12	AB	167	ARG
14	AE	91	GLU
16	AG	97	ILE
16	AG	320	ARG
22	H	70	VAL
22	H	82	THR
39	Y	22	PRO
39	Y	62	ALA
39	Y	71	LYS
39	Y	89	SER
40	Z	7	ILE
4	3	39	ILE
9	9	28	ALA
12	AB	121	LYS
13	AC	192	VAL
14	AE	49	PHE
14	AE	73	GLY
14	AE	904	ALA
16	AG	105	ILE
26	L	96	VAL
39	Y	23	VAL
39	Y	100	ILE
1	0	44	GLY

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Mol	Chain	Res	Type
25	K	44	GLY
31	Q	74	VAL
35	U	64	GLY
9	9	54	VAL
11	AA	855	PRO
11	AA	1317	PRO
54	n	62	GLY
28	N	75	ILE
16	AG	290	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	84/84 (100%)	76 (90%)	8 (10%)	8	31
2	1	93/93 (100%)	86 (92%)	7 (8%)	12	39
3	2	81/84 (96%)	77 (95%)	4 (5%)	22	48
4	3	84/85 (99%)	79 (94%)	5 (6%)	17	44
5	4	78/78 (100%)	75 (96%)	3 (4%)	29	53
9	9	112/123 (91%)	63 (56%)	49 (44%)	0	0
11	AA	1155/1157 (100%)	1135 (98%)	20 (2%)	53	67
12	AB	138/158 (87%)	108 (78%)	30 (22%)	1	7
13	AC	185/286 (65%)	184 (100%)	1 (0%)	81	80
13	AD	185/286 (65%)	185 (100%)	0	100	100
14	AE	1120/1168 (96%)	1047 (94%)	73 (6%)	15	43
15	AF	70/75 (93%)	69 (99%)	1 (1%)	59	70
17	C	57/65 (88%)	55 (96%)	2 (4%)	32	54
19	E	65/66 (98%)	61 (94%)	4 (6%)	16	44
20	F	60/61 (98%)	57 (95%)	3 (5%)	22	48
21	G	187/199 (94%)	174 (93%)	13 (7%)	14	41
22	H	137/461 (30%)	124 (90%)	13 (10%)	8	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	I	171/190 (90%)	162 (95%)	9 (5%)	20	46
24	J	172/173 (99%)	164 (95%)	8 (5%)	23	48
25	K	119/126 (94%)	111 (93%)	8 (7%)	15	42
26	L	91/116 (78%)	84 (92%)	7 (8%)	12	38
27	M	124/147 (84%)	113 (91%)	11 (9%)	9	33
28	N	104/105 (99%)	101 (97%)	3 (3%)	37	57
29	O	105/107 (98%)	99 (94%)	6 (6%)	18	45
30	P	86/90 (96%)	78 (91%)	8 (9%)	8	32
31	Q	90/99 (91%)	88 (98%)	2 (2%)	45	63
32	R	101/104 (97%)	95 (94%)	6 (6%)	18	44
33	S	83/84 (99%)	79 (95%)	4 (5%)	23	48
34	T	76/77 (99%)	65 (86%)	11 (14%)	3	17
35	U	65/65 (100%)	60 (92%)	5 (8%)	12	38
36	V	74/78 (95%)	71 (96%)	3 (4%)	27	52
37	W	72/79 (91%)	66 (92%)	6 (8%)	10	35
38	X	94/96 (98%)	87 (93%)	7 (7%)	13	39
39	Y	109/110 (99%)	69 (63%)	40 (37%)	0	1
40	Z	26/85 (31%)	10 (38%)	16 (62%)	0	0
42	b	58/63 (92%)	57 (98%)	1 (2%)	53	67
43	c	67/68 (98%)	64 (96%)	3 (4%)	24	49
45	e	54/55 (98%)	51 (94%)	3 (6%)	19	46
46	f	48/49 (98%)	43 (90%)	5 (10%)	7	28
47	g	59/62 (95%)	54 (92%)	5 (8%)	10	35
48	h	216/218 (99%)	199 (92%)	17 (8%)	11	37
49	i	47/48 (98%)	41 (87%)	6 (13%)	4	21
50	j	164/164 (100%)	156 (95%)	8 (5%)	22	48
51	k	47/49 (96%)	44 (94%)	3 (6%)	16	43
52	l	165/165 (100%)	151 (92%)	14 (8%)	10	35
53	m	38/38 (100%)	36 (95%)	2 (5%)	20	46
54	n	148/150 (99%)	130 (88%)	18 (12%)	5	22
55	o	51/52 (98%)	47 (92%)	4 (8%)	11	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	p	136/138 (99%)	130 (96%)	6 (4%)	25	50
57	q	34/34 (100%)	31 (91%)	3 (9%)	9	33
58	r	114/114 (100%)	102 (90%)	12 (10%)	6	28
59	s	116/116 (100%)	106 (91%)	10 (9%)	10	34
60	t	104/104 (100%)	97 (93%)	7 (7%)	15	42
61	u	103/103 (100%)	96 (93%)	7 (7%)	14	42
62	v	109/109 (100%)	105 (96%)	4 (4%)	30	54
63	w	99/103 (96%)	91 (92%)	8 (8%)	11	36
64	x	86/87 (99%)	80 (93%)	6 (7%)	14	41
65	y	99/100 (99%)	91 (92%)	8 (8%)	11	36
66	z	89/90 (99%)	85 (96%)	4 (4%)	24	49
All	All	7904/8739 (90%)	7344 (93%)	560 (7%)	15	40

All (560) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	10	LYS
1	0	38	VAL
1	0	47	VAL
1	0	48	LYS
1	0	51	VAL
1	0	68	ARG
1	0	86	GLN
1	0	96	VAL
2	1	19	LEU
2	1	30	SER
2	1	41	LYS
2	1	69	LEU
2	1	97	LEU
2	1	107	VAL
2	1	110	ARG
3	2	1	MET
3	2	24	MET
3	2	37	ASP
3	2	93	LEU
4	3	52	LEU
4	3	70	VAL
4	3	72	ILE

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Mol	Chain	Res	Type
4	3	99	ASN
4	3	101	GLU
5	4	40	ILE
5	4	69	GLU
5	4	71	LYS
9	9	1	MET
9	9	3	LEU
9	9	4	ASN
9	9	5	LEU
9	9	6	GLN
9	9	7	ASP
9	9	11	ILE
9	9	14	GLU
9	9	23	LEU
9	9	24	SER
9	9	27	VAL
9	9	31	ARG
9	9	33	VAL
9	9	34	THR
9	9	35	VAL
9	9	36	ASP
9	9	37	LYS
9	9	39	THR
9	9	42	ARG
9	9	43	LYS
9	9	52	MET
9	9	54	VAL
9	9	55	VAL
9	9	56	ARG
9	9	57	ASN
9	9	61	ARG
9	9	69	PHE
9	9	70	GLU
9	9	71	CYS
9	9	72	LEU
9	9	73	LYS
9	9	81	LEU
9	9	86	MET
9	9	94	ARG
9	9	96	PHE
9	9	98	GLU
9	9	106	PHE

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Mol	Chain	Res	Type
9	9	107	GLU
9	9	109	LYS
9	9	113	PHE
9	9	117	LEU
9	9	122	GLN
9	9	123	ILE
9	9	125	ARG
9	9	133	GLU
9	9	134	GLU
9	9	138	ARG
9	9	142	THR
9	9	143	MET
11	AA	145	ILE
11	AA	615	VAL
11	AA	851	THR
11	AA	854	ILE
11	AA	857	VAL
11	AA	859	GLU
11	AA	862	LEU
11	AA	864	LYS
11	AA	888	THR
11	AA	890	LYS
11	AA	893	THR
11	AA	894	GLN
11	AA	895	LEU
11	AA	896	THR
11	AA	898	GLU
11	AA	899	GLU
11	AA	909	LYS
11	AA	914	LYS
11	AA	1076	ILE
11	AA	1151	LEU
12	AB	104	SER
12	AB	105	ASP
12	AB	106	LYS
12	AB	114	ARG
12	AB	115	LEU
12	AB	117	GLN
12	AB	123	ARG
12	AB	125	LYS
12	AB	126	THR
12	AB	127	LEU

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Mol	Chain	Res	Type
12	AB	128	PHE
12	AB	129	GLU
12	AB	132	GLU
12	AB	133	MET
12	AB	134	VAL
12	AB	135	ARG
12	AB	138	ASP
12	AB	141	PHE
12	AB	145	ASN
12	AB	150	GLU
12	AB	151	VAL
12	AB	153	TYR
12	AB	155	LYS
12	AB	157	ARG
12	AB	161	SER
12	AB	162	VAL
12	AB	167	ARG
12	AB	172	GLU
12	AB	173	LEU
12	AB	180	LYS
13	AC	232	VAL
14	AE	40	LYS
14	AE	42	GLU
14	AE	44	ILE
14	AE	46	TYR
14	AE	47	ARG
14	AE	49	PHE
14	AE	50	LYS
14	AE	52	GLU
14	AE	53	ARG
14	AE	54	ASP
14	AE	56	LEU
14	AE	60	ARG
14	AE	66	LYS
14	AE	67	ASP
14	AE	70	CYS
14	AE	74	LYS
14	AE	76	LYS
14	AE	78	LEU
14	AE	80	HIS
14	AE	81	ARG
14	AE	88	CYS

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Mol	Chain	Res	Type
14	AE	91	GLU
14	AE	94	GLN
14	AE	95	THR
14	AE	96	LYS
14	AE	99	ARG
14	AE	100	GLU
14	AE	114	ILE
14	AE	117	LEU
14	AE	119	SER
14	AE	123	ARG
14	AE	132	LEU
14	AE	135	ILE
14	AE	142	GLU
14	AE	144	TYR
14	AE	145	VAL
14	AE	146	VAL
14	AE	147	ILE
14	AE	152	THR
14	AE	154	LEU
14	AE	157	GLN
14	AE	159	ILE
14	AE	175	GLU
14	AE	180	MET
14	AE	190	LYS
14	AE	193	ASP
14	AE	196	GLN
14	AE	210	SER
14	AE	212	THR
14	AE	216	LYS
14	AE	222	LYS
14	AE	223	LEU
14	AE	227	PHE
14	AE	233	LYS
14	AE	237	MET
14	AE	238	ILE
14	AE	239	LEU
14	AE	240	THR
14	AE	244	VAL
14	AE	271	ARG
14	AE	324	LEU
14	AE	385	LEU
14	AE	386	GLU

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Mol	Chain	Res	Type
14	AE	387	LEU
14	AE	390	LEU
14	AE	393	THR
14	AE	394	ILE
14	AE	395	LYS
14	AE	506	VAL
14	AE	514	THR
14	AE	839	VAL
14	AE	1172	LYS
14	AE	1233	ILE
15	AF	63	ILE
17	C	33	ILE
17	C	74	HIS
19	E	6	SER
19	E	10	ARG
19	E	48	GLN
19	E	64	LYS
20	F	34	ARG
20	F	62	ARG
20	F	67	ARG
21	G	8	ASP
21	G	45	LYS
21	G	59	LYS
21	G	105	LYS
21	G	108	ARG
21	G	117	LEU
21	G	128	LYS
21	G	129	LEU
21	G	132	LYS
21	G	135	LEU
21	G	161	LEU
21	G	174	LYS
21	G	208	ARG
22	H	9	PHE
22	H	31	ILE
22	H	43	LYS
22	H	54	LYS
22	H	62	ILE
22	H	70	VAL
22	H	294	VAL
22	H	305	HIS
22	H	336	ASP

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Mol	Chain	Res	Type
22	H	337	GLU
22	H	338	GLU
22	H	339	ARG
22	H	340	ARG
23	I	14	ILE
23	I	21	THR
23	I	33	LEU
23	I	75	ILE
23	I	80	LYS
23	I	89	LYS
23	I	175	LEU
23	I	178	LEU
23	I	200	VAL
24	J	47	ARG
24	J	48	LEU
24	J	95	GLU
24	J	104	ARG
24	J	105	MET
24	J	116	GLN
24	J	138	SER
24	J	143	VAL
25	K	10	GLU
25	K	15	LEU
25	K	60	ILE
25	K	114	VAL
25	K	115	LEU
25	K	138	ARG
25	K	141	ILE
25	K	162	GLU
26	L	7	VAL
26	L	16	GLU
26	L	24	ARG
26	L	36	ILE
26	L	38	ARG
26	L	54	LEU
26	L	86	ARG
27	M	7	ILE
27	M	17	LYS
27	M	21	GLU
27	M	23	LEU
27	M	27	VAL
27	M	50	LEU

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Mol	Chain	Res	Type
27	M	79	ARG
27	M	91	VAL
27	M	109	ARG
27	M	130	ASN
27	M	146	GLU
28	N	96	MET
28	N	104	VAL
28	N	117	ARG
29	O	27	LYS
29	O	60	LYS
29	O	61	LEU
29	O	63	LEU
29	O	116	VAL
29	O	118	LEU
30	P	17	LEU
30	P	18	ILE
30	P	24	GLU
30	P	25	ILE
30	P	27	GLU
30	P	37	ARG
30	P	87	LEU
30	P	90	LEU
31	Q	15	GLN
31	Q	107	ILE
32	R	5	ASN
32	R	12	ARG
32	R	24	LEU
32	R	62	GLU
32	R	74	LEU
32	R	102	LEU
33	S	45	VAL
33	S	46	LEU
33	S	89	MET
33	S	92	GLU
34	T	10	LYS
34	T	22	THR
34	T	39	LEU
34	T	40	GLN
34	T	64	ARG
34	T	66	LEU
34	T	67	LEU
34	T	70	LEU

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Mol	Chain	Res	Type
34	T	73	LYS
34	T	84	ARG
34	T	85	LEU
35	U	1	MET
35	U	2	VAL
35	U	6	LEU
35	U	19	VAL
35	U	50	THR
36	V	46	VAL
36	V	75	LEU
36	V	81	LYS
37	W	21	LYS
37	W	33	THR
37	W	49	ILE
37	W	58	VAL
37	W	79	THR
37	W	81	ARG
38	X	16	VAL
38	X	25	VAL
38	X	29	ARG
38	X	59	GLU
38	X	93	ARG
38	X	101	ARG
38	X	117	LYS
39	Y	4	VAL
39	Y	10	LEU
39	Y	16	MET
39	Y	23	VAL
39	Y	27	LEU
39	Y	30	GLN
39	Y	36	GLU
39	Y	44	LYS
39	Y	45	THR
39	Y	48	ILE
39	Y	50	LYS
39	Y	52	LEU
39	Y	57	VAL
39	Y	58	ILE
39	Y	60	VAL
39	Y	61	TYR
39	Y	64	ARG
39	Y	65	SER

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Mol	Chain	Res	Type
39	Y	67	THR
39	Y	71	LYS
39	Y	78	LEU
39	Y	80	LYS
39	Y	81	LYS
39	Y	91	LYS
39	Y	94	LYS
39	Y	95	ASP
39	Y	99	LYS
39	Y	100	ILE
39	Y	102	ARG
39	Y	104	GLN
39	Y	108	ILE
39	Y	112	LYS
39	Y	116	MET
39	Y	124	MET
39	Y	125	THR
39	Y	126	ARG
39	Y	133	ARG
39	Y	135	MET
39	Y	137	LEU
39	Y	138	VAL
40	Z	1	SER
40	Z	2	ILE
40	Z	3	THR
40	Z	4	LYS
40	Z	6	GLN
40	Z	7	ILE
40	Z	8	ILE
40	Z	14	MET
40	Z	16	VAL
40	Z	17	MET
40	Z	19	VAL
40	Z	23	ILE
40	Z	26	MET
40	Z	28	GLU
40	Z	29	LYS
40	Z	30	PHE
42	b	70	GLU
43	c	33	LEU
43	c	48	THR
43	c	71	LEU

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Mol	Chain	Res	Type
45	e	18	LEU
45	e	58	ASN
45	e	60	LYS
46	f	3	LYS
46	f	11	ARG
46	f	25	LEU
46	f	45	ARG
46	f	55	VAL
47	g	3	LYS
47	g	16	CYS
47	g	24	ILE
47	g	36	VAL
47	g	47	LYS
48	h	51	THR
48	h	94	VAL
48	h	105	LEU
48	h	118	SER
48	h	125	LYS
48	h	130	LEU
48	h	141	VAL
48	h	156	ARG
48	h	183	LYS
48	h	187	ASP
48	h	195	VAL
48	h	202	LEU
48	h	203	ARG
48	h	204	VAL
48	h	205	LEU
48	h	242	LYS
48	h	271	ARG
49	i	9	THR
49	i	12	LYS
49	i	26	THR
49	i	27	SER
49	i	29	SER
49	i	40	ARG
50	j	13	ARG
50	j	18	ASP
50	j	91	THR
50	j	99	GLU
50	j	104	VAL
50	j	177	VAL

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Mol	Chain	Res	Type
50	j	189	VAL
50	j	193	VAL
51	k	5	ILE
51	k	17	THR
51	k	24	THR
52	l	17	THR
52	l	22	ASP
52	l	40	ARG
52	l	48	THR
52	l	57	LYS
52	l	69	ARG
52	l	77	ILE
52	l	80	SER
52	l	108	ILE
52	l	109	LEU
52	l	111	GLU
52	l	122	GLU
52	l	149	ILE
52	l	179	SER
53	m	22	MET
53	m	42	LEU
54	n	6	ASP
54	n	10	ASP
54	n	26	MET
54	n	40	VAL
54	n	47	LYS
54	n	49	LEU
54	n	57	LEU
54	n	79	ILE
54	n	80	ARG
54	n	95	ARG
54	n	105	THR
54	n	117	LEU
54	n	122	PHE
54	n	123	ASP
54	n	132	VAL
54	n	140	GLU
54	n	141	ILE
54	n	163	ASP
55	o	8	ARG
55	o	30	ARG
55	o	31	HIS

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Mol	Chain	Res	Type
55	o	55	LEU
56	p	11	VAL
56	p	85	LYS
56	p	95	ARG
56	p	125	CYS
56	p	168	VAL
56	p	171	THR
57	q	3	VAL
57	q	26	ILE
57	q	34	LYS
58	r	1	MET
58	r	9	VAL
58	r	11	ASN
58	r	12	LEU
58	r	15	LEU
58	r	41	LYS
58	r	66	ASN
58	r	72	ILE
58	r	76	GLU
58	r	94	ILE
58	r	101	ASP
58	r	127	GLU
59	s	1	MET
59	s	30	THR
59	s	31	GLU
59	s	43	GLU
59	s	57	LEU
59	s	123	LYS
59	s	124	VAL
59	s	139	VAL
59	s	140	LEU
59	s	142	ILE
60	t	7	MET
60	t	35	VAL
60	t	49	ARG
60	t	67	LYS
60	t	70	ARG
60	t	80	ASP
60	t	104	THR
61	u	5	THR
61	u	27	LEU
61	u	59	ARG

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Mol	Chain	Res	Type
61	u	73	ILE
61	u	76	GLU
61	u	78	ARG
61	u	84	LYS
62	v	110	GLU
62	v	126	ILE
62	v	127	LYS
62	v	128	THR
63	w	2	ARG
63	w	20	MET
63	w	24	MET
63	w	51	LEU
63	w	65	LEU
63	w	69	ARG
63	w	95	THR
63	w	116	VAL
64	x	13	ARG
64	x	31	THR
64	x	47	VAL
64	x	48	LEU
64	x	91	SER
64	x	116	GLN
65	y	8	LEU
65	y	10	GLN
65	y	27	GLU
65	y	40	LEU
65	y	81	VAL
65	y	85	SER
65	y	102	GLU
65	y	114	LEU
66	z	18	LEU
66	z	51	ARG
66	z	109	LEU
66	z	117	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (85) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	86	GLN
2	1	31	GLN
2	1	61	ASN
3	2	28	ASN

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Mol	Chain	Res	Type
3	2	59	ASN
4	3	54	GLN
5	4	12	GLN
9	9	103	ASN
9	9	122	GLN
11	AA	69	GLN
11	AA	314	ASN
11	AA	330	HIS
11	AA	343	HIS
11	AA	513	GLN
11	AA	554	HIS
11	AA	688	GLN
11	AA	762	ASN
11	AA	808	ASN
11	AA	1237	HIS
11	AA	1268	GLN
11	AA	1313	HIS
12	AB	117	GLN
12	AB	145	ASN
12	AB	177	GLN
13	AC	23	HIS
13	AD	37	HIS
13	AD	66	HIS
13	AD	84	ASN
13	AD	117	HIS
13	AD	128	HIS
13	AD	227	GLN
14	AE	196	GLN
14	AE	294	ASN
14	AE	424	ASN
14	AE	469	HIS
14	AE	865	HIS
14	AE	1195	GLN
14	AE	1238	GLN
14	AE	1249	ASN
14	AE	1259	GLN
15	AF	7	GLN
15	AF	31	GLN
15	AF	62	GLN
17	C	31	ASN
19	E	3	ASN
19	E	55	GLN

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Mol	Chain	Res	Type
19	E	61	GLN
21	G	18	HIS
21	G	58	ASN
21	G	94	HIS
23	I	6	HIS
23	I	25	ASN
23	I	123	GLN
24	J	36	GLN
24	J	40	GLN
24	J	41	HIS
25	K	97	GLN
26	L	11	HIS
26	L	46	GLN
26	L	63	ASN
26	L	94	HIS
27	M	97	ASN
27	M	148	ASN
29	O	81	HIS
30	P	58	ASN
32	R	72	HIS
33	S	60	GLN
34	T	40	GLN
35	U	59	HIS
38	X	12	HIS
38	X	105	ASN
47	g	33	ASN
47	g	41	HIS
48	h	70	ASN
51	k	26	ASN
55	o	28	ASN
56	p	48	ASN
56	p	88	GLN
57	q	35	GLN
58	r	11	ASN
58	r	18	GLN
58	r	20	ASN
58	r	133	GLN
60	t	88	ASN
65	y	15	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	75/76 (98%)	29 (38%)	6 (8%)
10	B	75/76 (98%)	35 (46%)	6 (8%)
18	D	1514/1542 (98%)	289 (19%)	34 (2%)
41	a	2859/2904 (98%)	542 (18%)	0
44	d	119/120 (99%)	17 (14%)	0
8	7	34/46 (73%)	21 (61%)	4 (11%)
All	All	4676/4764 (98%)	933 (19%)	50 (1%)

All (933) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	-18	G
8	7	-17	U
8	7	-16	U
8	7	-14	U
8	7	-13	U
8	7	-12	U
8	7	-11	U
8	7	-10	U
8	7	-9	U
8	7	-8	U
8	7	-7	U
8	7	-6	U
8	7	-5	U
8	7	-3	U
8	7	-1	U
8	7	0	U
8	7	1	U
8	7	2	U
8	7	4	U
8	7	12	G
8	7	13	G
10	A	2	G
10	A	6	G
10	A	7	G
10	A	8	U
10	A	10	G
10	A	13	C
10	A	14	A
10	A	15	G
10	A	16	C
10	A	17	C
10	A	18	G

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Mol	Chain	Res	Type
10	A	19	G
10	A	20	U
10	A	21	A
10	A	22	G
10	A	23	C
10	A	46	G
10	A	47	U
10	A	48	C
10	A	49	G
10	A	52	G
10	A	57	A
10	A	58	A
10	A	59	A
10	A	61	C
10	A	66	C
10	A	69	C
10	A	71	C
10	A	73	A
10	B	2	G
10	B	6	G
10	B	7	G
10	B	8	U
10	B	10	G
10	B	13	C
10	B	14	A
10	B	15	G
10	B	16	C
10	B	17	C
10	B	18	G
10	B	19	G
10	B	20	U
10	B	21	A
10	B	22	G
10	B	23	C
10	B	30	G
10	B	31	G
10	B	32	C
10	B	36	U
10	B	37	A
10	B	38	A
10	B	46	G
10	B	47	U

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Mol	Chain	Res	Type
10	B	48	C
10	B	49	G
10	B	52	G
10	B	57	A
10	B	58	A
10	B	59	A
10	B	61	C
10	B	66	C
10	B	69	C
10	B	71	C
10	B	73	A
18	D	4	U
18	D	5	U
18	D	9	G
18	D	22	G
18	D	29	U
18	D	32	A
18	D	39	G
18	D	41	G
18	D	47	C
18	D	48	C
18	D	50	A
18	D	51	A
18	D	52	C
18	D	54	C
18	D	69	G
18	D	70	U
18	D	71	A
18	D	72	A
18	D	74	A
18	D	76	G
18	D	82	G
18	D	83	C
18	D	84	U
18	D	87	C
18	D	90	C
18	D	94	G
18	D	95	C
18	D	96	U
18	D	108	G
18	D	120	A
18	D	122	G

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Mol	Chain	Res	Type
18	D	128	G
18	D	131	A
18	D	141	G
18	D	144	G
18	D	148	G
18	D	149	A
18	D	160	A
18	D	164	G
18	D	173	U
18	D	181	A
18	D	182	A
18	D	197	A
18	D	198	G
18	D	204	G
18	D	208	U
18	D	209	U
18	D	210	C
18	D	211	G
18	D	212	G
18	D	216	U
18	D	226	G
18	D	245	U
18	D	247	G
18	D	251	G
18	D	258	G
18	D	262	A
18	D	266	G
18	D	267	C
18	D	271	C
18	D	279	A
18	D	289	G
18	D	299	G
18	D	306	A
18	D	321	A
18	D	328	C
18	D	329	A
18	D	332	G
18	D	347	G
18	D	352	C
18	D	353	A
18	D	354	G
18	D	355	C

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Mol	Chain	Res	Type
18	D	367	U
18	D	372	C
18	D	373	A
18	D	376	G
18	D	382	A
18	D	384	G
18	D	392	C
18	D	393	A
18	D	397	A
18	D	406	G
18	D	412	A
18	D	413	G
18	D	414	A
18	D	421	U
18	D	422	C
18	D	424	G
18	D	429	U
18	D	446	G
18	D	451	A
18	D	457	G
18	D	458	U
18	D	460	A
18	D	463	U
18	D	464	U
18	D	467	U
18	D	468	A
18	D	469	C
18	D	478	A
18	D	479	U
18	D	481	G
18	D	484	G
18	D	485	U
18	D	486	U
18	D	505	G
18	D	509	A
18	D	511	C
18	D	518	C
18	D	519	C
18	D	526	C
18	D	531	U
18	D	532	A
18	D	533	A

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Mol	Chain	Res	Type
18	D	542	G
18	D	547	A
18	D	559	A
18	D	562	U
18	D	568	G
18	D	572	A
18	D	573	A
18	D	576	C
18	D	577	G
18	D	579	A
18	D	596	A
18	D	628	G
18	D	633	G
18	D	641	U
18	D	642	A
18	D	649	A
18	D	650	G
18	D	653	U
18	D	665	A
18	D	666	G
18	D	687	A
18	D	700	G
18	D	723	U
18	D	724	G
18	D	731	G
18	D	734	G
18	D	747	A
18	D	748	G
18	D	755	G
18	D	760	G
18	D	777	A
18	D	793	U
18	D	794	A
18	D	815	A
18	D	817	C
18	D	828	U
18	D	829	G
18	D	832	G
18	D	841	C
18	D	844	G
18	D	845	A
18	D	849	G

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Mol	Chain	Res	Type
18	D	874	G
18	D	887	G
18	D	902	G
18	D	914	A
18	D	916	U
18	D	926	G
18	D	934	C
18	D	935	A
18	D	954	G
18	D	960	U
18	D	963	G
18	D	969	A
18	D	972	C
18	D	975	A
18	D	976	G
18	D	991	U
18	D	992	U
18	D	993	G
18	D	996	A
18	D	999	C
18	D	1004	A
18	D	1008	U
18	D	1009	U
18	D	1017	U
18	D	1018	G
18	D	1021	A
18	D	1024	G
18	D	1026	G
18	D	1028	C
18	D	1030	U
18	D	1031	C
18	D	1037	C
18	D	1043	G
18	D	1044	A
18	D	1046	A
18	D	1065	U
18	D	1085	U
18	D	1086	U
18	D	1094	G
18	D	1095	U
18	D	1099	G
18	D	1101	A

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Mol	Chain	Res	Type
18	D	1124	G
18	D	1133	G
18	D	1135	U
18	D	1136	C
18	D	1137	C
18	D	1139	G
18	D	1140	C
18	D	1141	C
18	D	1142	G
18	D	1143	G
18	D	1145	A
18	D	1146	A
18	D	1151	A
18	D	1152	A
18	D	1158	C
18	D	1159	U
18	D	1167	A
18	D	1171	A
18	D	1174	G
18	D	1175	G
18	D	1176	A
18	D	1184	G
18	D	1196	A
18	D	1197	A
18	D	1206	G
18	D	1211	U
18	D	1212	U
18	D	1213	A
18	D	1214	C
18	D	1215	G
18	D	1226	C
18	D	1227	A
18	D	1228	C
18	D	1238	A
18	D	1256	A
18	D	1257	A
18	D	1260	G
18	D	1275	A
18	D	1276	G
18	D	1278	G
18	D	1279	G
18	D	1280	A

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Mol	Chain	Res	Type
18	D	1285	A
18	D	1286	U
18	D	1287	A
18	D	1299	A
18	D	1300	G
18	D	1302	C
18	D	1305	G
18	D	1312	G
18	D	1317	C
18	D	1320	C
18	D	1323	G
18	D	1329	A
18	D	1338	G
18	D	1340	A
18	D	1346	A
18	D	1347	G
18	D	1353	G
18	D	1363	A
18	D	1370	G
18	D	1378	C
18	D	1379	G
18	D	1381	U
18	D	1391	U
18	D	1396	A
18	D	1397	C
18	D	1398	A
18	D	1404	C
18	D	1419	G
18	D	1429	A
18	D	1441	A
18	D	1446	A
18	D	1447	A
18	D	1448	C
18	D	1452	C
18	D	1453	G
18	D	1475	G
18	D	1487	G
18	D	1492	A
18	D	1493	A
18	D	1494	G
18	D	1495	U
18	D	1497	G

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Mol	Chain	Res	Type
18	D	1503	A
18	D	1506	U
18	D	1517	G
18	D	1529	G
18	D	1530	G
18	D	1534	A
41	a	10	A
41	a	15	G
41	a	34	U
41	a	35	G
41	a	46	G
41	a	58	G
41	a	60	G
41	a	63	A
41	a	71	A
41	a	74	A
41	a	75	G
41	a	83	A
41	a	84	A
41	a	85	G
41	a	93	G
41	a	96	C
41	a	102	U
41	a	103	A
41	a	110	G
41	a	114	U
41	a	118	A
41	a	119	A
41	a	120	U
41	a	122	G
41	a	131	A
41	a	136	G
41	a	139	U
41	a	140	C
41	a	141	G
41	a	145	C
41	a	163	C
41	a	165	A
41	a	181	A
41	a	196	A
41	a	199	A
41	a	200	U

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Mol	Chain	Res	Type
41	a	215	G
41	a	216	A
41	a	222	A
41	a	225	C
41	a	248	G
41	a	249	C
41	a	261	G
41	a	264	C
41	a	265	A
41	a	266	G
41	a	267	C
41	a	271	G
41	a	272	A
41	a	275	C
41	a	276	U
41	a	278	A
41	a	285	G
41	a	311	A
41	a	324	A
41	a	329	G
41	a	330	A
41	a	353	C
41	a	359	G
41	a	361	G
41	a	362	A
41	a	371	A
41	a	372	G
41	a	373	U
41	a	375	G
41	a	383	C
41	a	386	G
41	a	396	G
41	a	405	U
41	a	411	G
41	a	412	A
41	a	420	C
41	a	424	G
41	a	435	C
41	a	451	U
41	a	456	C
41	a	457	A
41	a	477	A

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Mol	Chain	Res	Type
41	a	481	G
41	a	491	G
41	a	501	A
41	a	503	A
41	a	504	A
41	a	505	A
41	a	509	C
41	a	522	A
41	a	529	A
41	a	532	A
41	a	543	G
41	a	546	U
41	a	547	A
41	a	548	G
41	a	549	G
41	a	551	G
41	a	563	A
41	a	569	U
41	a	573	U
41	a	575	A
41	a	588	U
41	a	603	A
41	a	609	A
41	a	613	A
41	a	614	A
41	a	615	U
41	a	616	A
41	a	618	G
41	a	620	G
41	a	621	A
41	a	627	A
41	a	637	A
41	a	645	C
41	a	647	G
41	a	654	A
41	a	664	G
41	a	668	A
41	a	685	A
41	a	686	U
41	a	710	U
41	a	717	C
41	a	730	A

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Mol	Chain	Res	Type
41	a	738	G
41	a	757	G
41	a	764	A
41	a	765	C
41	a	775	G
41	a	776	G
41	a	782	A
41	a	784	G
41	a	785	G
41	a	800	A
41	a	802	A
41	a	805	G
41	a	812	C
41	a	819	A
41	a	827	U
41	a	828	U
41	a	845	A
41	a	846	U
41	a	858	G
41	a	859	G
41	a	869	G
41	a	878	A
41	a	881	G
41	a	883	G
41	a	884	U
41	a	885	C
41	a	888	C
41	a	891	G
41	a	892	A
41	a	893	C
41	a	895	U
41	a	896	A
41	a	897	C
41	a	899	A
41	a	907	G
41	a	910	A
41	a	914	G
41	a	915	C
41	a	931	U
41	a	941	A
41	a	945	A
41	a	946	C

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Mol	Chain	Res	Type
41	a	953	G
41	a	961	C
41	a	974	G
41	a	983	A
41	a	984	A
41	a	985	C
41	a	995	C
41	a	996	A
41	a	999	U
41	a	1005	C
41	a	1012	U
41	a	1013	C
41	a	1022	G
41	a	1023	U
41	a	1026	G
41	a	1033	U
41	a	1041	G
41	a	1042	G
41	a	1045	C
41	a	1046	A
41	a	1047	G
41	a	1060	U
41	a	1061	U
41	a	1062	G
41	a	1063	G
41	a	1064	C
41	a	1065	U
41	a	1066	U
41	a	1067	A
41	a	1068	G
41	a	1069	A
41	a	1070	A
41	a	1071	G
41	a	1073	A
41	a	1074	G
41	a	1076	C
41	a	1079	C
41	a	1080	A
41	a	1081	U
41	a	1082	U
41	a	1083	U
41	a	1084	A

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Mol	Chain	Res	Type
41	a	1087	G
41	a	1088	A
41	a	1090	A
41	a	1095	A
41	a	1096	A
41	a	1107	G
41	a	1110	G
41	a	1111	A
41	a	1112	G
41	a	1119	U
41	a	1122	G
41	a	1132	U
41	a	1134	A
41	a	1135	C
41	a	1142	A
41	a	1143	A
41	a	1169	A
41	a	1170	C
41	a	1173	U
41	a	1174	U
41	a	1175	A
41	a	1176	U
41	a	1177	G
41	a	1178	C
41	a	1179	G
41	a	1180	U
41	a	1186	G
41	a	1238	G
41	a	1248	G
41	a	1253	A
41	a	1256	G
41	a	1266	G
41	a	1271	G
41	a	1272	A
41	a	1273	U
41	a	1301	A
41	a	1321	A
41	a	1345	C
41	a	1352	U
41	a	1365	A
41	a	1368	G
41	a	1378	A

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Mol	Chain	Res	Type
41	a	1379	U
41	a	1380	G
41	a	1383	A
41	a	1387	A
41	a	1392	A
41	a	1395	A
41	a	1406	U
41	a	1407	G
41	a	1408	G
41	a	1411	U
41	a	1414	C
41	a	1415	U
41	a	1416	G
41	a	1417	C
41	a	1419	A
41	a	1420	A
41	a	1428	C
41	a	1452	G
41	a	1453	A
41	a	1460	U
41	a	1478	G
41	a	1482	G
41	a	1490	A
41	a	1491	G
41	a	1497	U
41	a	1503	A
41	a	1508	A
41	a	1509	A
41	a	1510	G
41	a	1515	A
41	a	1529	G
41	a	1534	U
41	a	1535	A
41	a	1536	C
41	a	1537	G
41	a	1554	U
41	a	1559	U
41	a	1566	A
41	a	1569	A
41	a	1578	U
41	a	1580	A
41	a	1581	G

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Mol	Chain	Res	Type
41	a	1582	C
41	a	1583	A
41	a	1584	U
41	a	1589	U
41	a	1590	A
41	a	1608	A
41	a	1609	A
41	a	1610	A
41	a	1647	U
41	a	1648	U
41	a	1649	G
41	a	1651	G
41	a	1674	G
41	a	1677	A
41	a	1703	G
41	a	1714	U
41	a	1715	G
41	a	1718	G
41	a	1729	U
41	a	1730	C
41	a	1732	C
41	a	1738	G
41	a	1750	G
41	a	1755	A
41	a	1758	U
41	a	1764	C
41	a	1773	A
41	a	1791	A
41	a	1800	C
41	a	1801	A
41	a	1808	A
41	a	1811	G
41	a	1816	C
41	a	1829	A
41	a	1833	C
41	a	1847	A
41	a	1848	A
41	a	1858	A
41	a	1859	U
41	a	1862	G
41	a	1864	U
41	a	1869	G

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Mol	Chain	Res	Type
41	a	1870	C
41	a	1872	A
41	a	1873	G
41	a	1905	C
41	a	1906	G
41	a	1907	G
41	a	1913	A
41	a	1914	C
41	a	1919	A
41	a	1920	C
41	a	1922	G
41	a	1923	U
41	a	1924	C
41	a	1925	C
41	a	1926	U
41	a	1928	A
41	a	1929	G
41	a	1930	G
41	a	1936	A
41	a	1938	A
41	a	1955	U
41	a	1965	C
41	a	1967	C
41	a	1970	A
41	a	1971	U
41	a	1972	G
41	a	1987	A
41	a	1991	U
41	a	1992	G
41	a	1993	U
41	a	1997	C
41	a	2002	G
41	a	2022	U
41	a	2023	C
41	a	2027	G
41	a	2033	A
41	a	2043	C
41	a	2051	A
41	a	2052	A
41	a	2055	C
41	a	2056	G
41	a	2060	A

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Mol	Chain	Res	Type
41	a	2061	G
41	a	2062	A
41	a	2063	C
41	a	2077	A
41	a	2093	G
41	a	2097	A
41	a	2099	U
41	a	2100	G
41	a	2108	A
41	a	2110	G
41	a	2111	U
41	a	2113	U
41	a	2115	G
41	a	2116	G
41	a	2117	A
41	a	2118	U
41	a	2121	G
41	a	2122	U
41	a	2124	G
41	a	2125	G
41	a	2126	A
41	a	2127	G
41	a	2128	G
41	a	2131	U
41	a	2132	U
41	a	2133	G
41	a	2134	A
41	a	2139	U
41	a	2141	G
41	a	2146	C
41	a	2147	A
41	a	2154	A
41	a	2157	G
41	a	2158	A
41	a	2159	G
41	a	2162	G
41	a	2163	A
41	a	2164	C
41	a	2165	C
41	a	2169	A
41	a	2171	A
41	a	2172	U

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Mol	Chain	Res	Type
41	a	2178	C
41	a	2182	U
41	a	2183	A
41	a	2185	U
41	a	2188	U
41	a	2189	U
41	a	2190	G
41	a	2191	A
41	a	2193	G
41	a	2194	U
41	a	2198	A
41	a	2204	G
41	a	2210	U
41	a	2211	A
41	a	2212	A
41	a	2213	U
41	a	2225	A
41	a	2226	C
41	a	2229	U
41	a	2238	G
41	a	2239	G
41	a	2244	U
41	a	2250	G
41	a	2268	A
41	a	2278	A
41	a	2283	C
41	a	2287	A
41	a	2297	A
41	a	2305	U
41	a	2308	G
41	a	2309	A
41	a	2315	G
41	a	2322	A
41	a	2325	G
41	a	2327	A
41	a	2333	A
41	a	2339	C
41	a	2345	G
41	a	2347	C
41	a	2350	C
41	a	2361	G
41	a	2372	U

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Mol	Chain	Res	Type
41	a	2376	A
41	a	2383	G
41	a	2385	C
41	a	2402	U
41	a	2403	C
41	a	2406	A
41	a	2423	U
41	a	2424	C
41	a	2425	A
41	a	2426	A
41	a	2429	G
41	a	2430	A
41	a	2431	U
41	a	2434	A
41	a	2435	A
41	a	2441	U
41	a	2447	G
41	a	2448	A
41	a	2470	G
41	a	2474	U
41	a	2476	A
41	a	2478	A
41	a	2484	G
41	a	2491	U
41	a	2502	G
41	a	2506	U
41	a	2507	C
41	a	2512	C
41	a	2513	A
41	a	2518	A
41	a	2520	C
41	a	2525	G
41	a	2529	G
41	a	2535	G
41	a	2547	A
41	a	2554	U
41	a	2566	A
41	a	2567	G
41	a	2572	A
41	a	2573	C
41	a	2574	G
41	a	2585	U

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Mol	Chain	Res	Type
41	a	2586	U
41	a	2602	A
41	a	2603	G
41	a	2609	U
41	a	2610	C
41	a	2611	C
41	a	2613	U
41	a	2629	U
41	a	2663	G
41	a	2669	G
41	a	2671	G
41	a	2689	U
41	a	2690	U
41	a	2714	G
41	a	2722	G
41	a	2726	A
41	a	2744	G
41	a	2748	A
41	a	2757	A
41	a	2758	A
41	a	2765	A
41	a	2777	G
41	a	2778	A
41	a	2791	G
41	a	2793	C
41	a	2796	U
41	a	2797	U
41	a	2798	U
41	a	2799	A
41	a	2801	G
41	a	2818	U
41	a	2820	A
41	a	2823	A
41	a	2825	G
41	a	2849	U
41	a	2850	A
41	a	2859	G
41	a	2861	U
41	a	2867	G
41	a	2880	C
41	a	2884	U
41	a	2885	G

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Mol	Chain	Res	Type
41	a	2891	U
41	a	2902	C
44	d	2	G
44	d	9	G
44	d	13	G
44	d	16	G
44	d	17	C
44	d	35	C
44	d	36	C
44	d	45	A
44	d	51	G
44	d	56	G
44	d	64	G
44	d	66	A
44	d	88	C
44	d	89	U
44	d	90	C
44	d	99	A
44	d	109	A

All (50) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	7	-17	U
8	7	-14	U
8	7	-11	U
8	7	11	U
10	A	6	G
10	A	7	G
10	A	9	G
10	A	22	G
10	A	60	U
10	A	70	G
10	B	6	G
10	B	7	G
10	B	9	G
10	B	22	G
10	B	37	A
10	B	60	U
18	D	7	A
18	D	70	U
18	D	121	U

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Mol	Chain	Res	Type
18	D	181	A
18	D	183	C
18	D	197	A
18	D	209	U
18	D	305	G
18	D	328	C
18	D	428	G
18	D	496	A
18	D	517	G
18	D	531	U
18	D	532	A
18	D	562	U
18	D	641	U
18	D	722	G
18	D	793	U
18	D	991	U
18	D	992	U
18	D	1145	A
18	D	1196	A
18	D	1211	U
18	D	1212	U
18	D	1213	A
18	D	1214	C
18	D	1225	A
18	D	1299	A
18	D	1396	A
18	D	1432	G
18	D	1447	A
18	D	1491	G
18	D	1492	A
18	D	1493	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

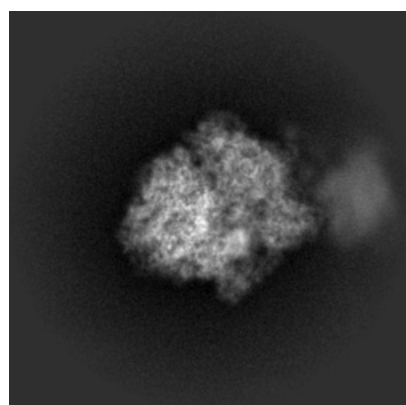
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22141. These allow visual inspection of the internal detail of the map and identification of artifacts.

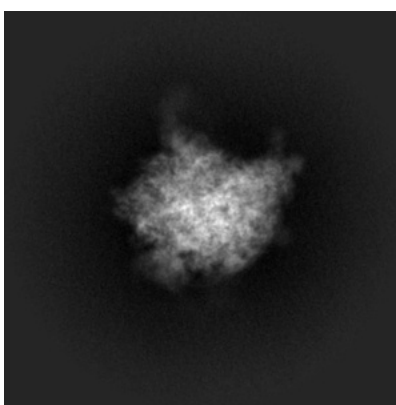
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

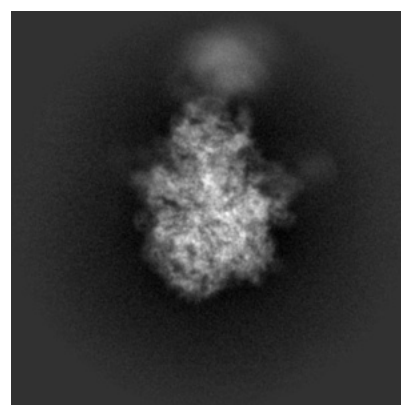
6.1.1 Primary map



X



Y

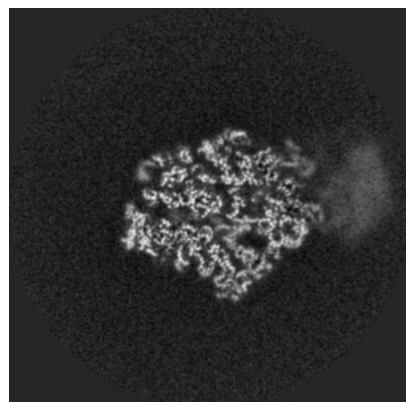


Z

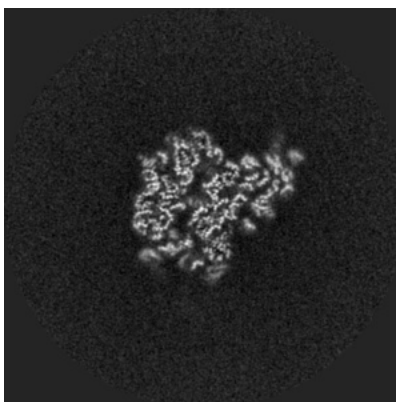
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

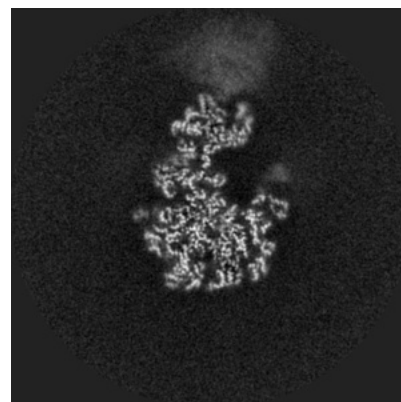
6.2.1 Primary map



X Index: 256



Y Index: 256

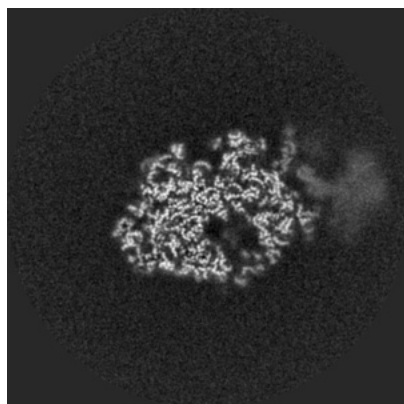


Z Index: 256

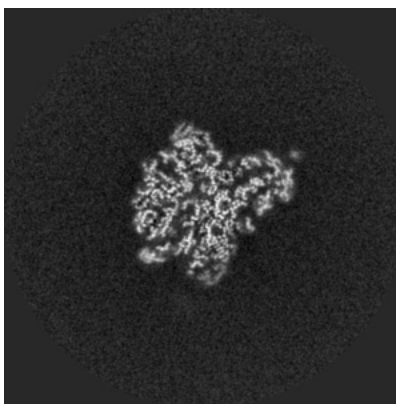
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

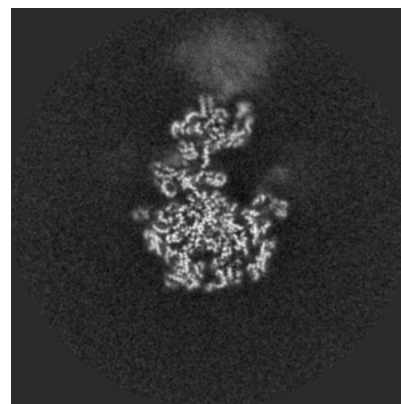
6.3.1 Primary map



X Index: 239



Y Index: 251

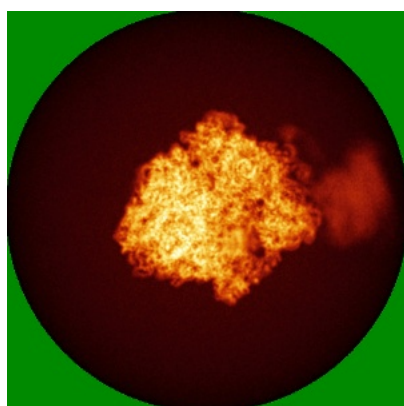


Z Index: 258

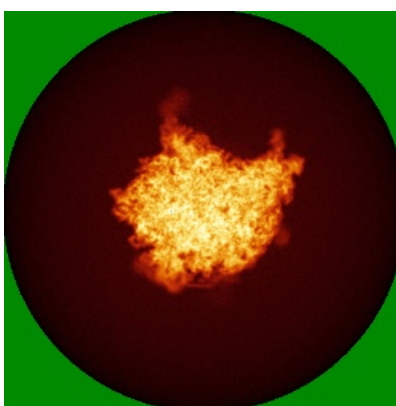
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



Y

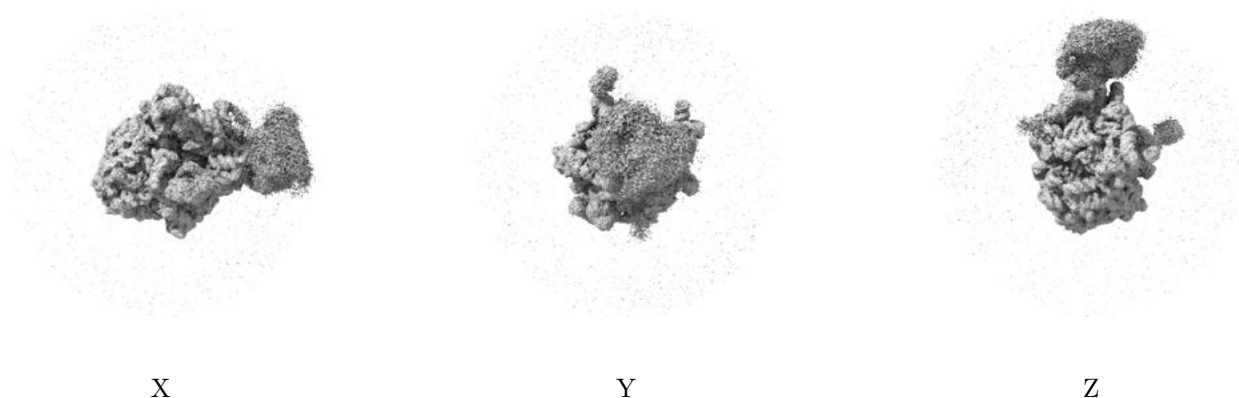


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00359. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

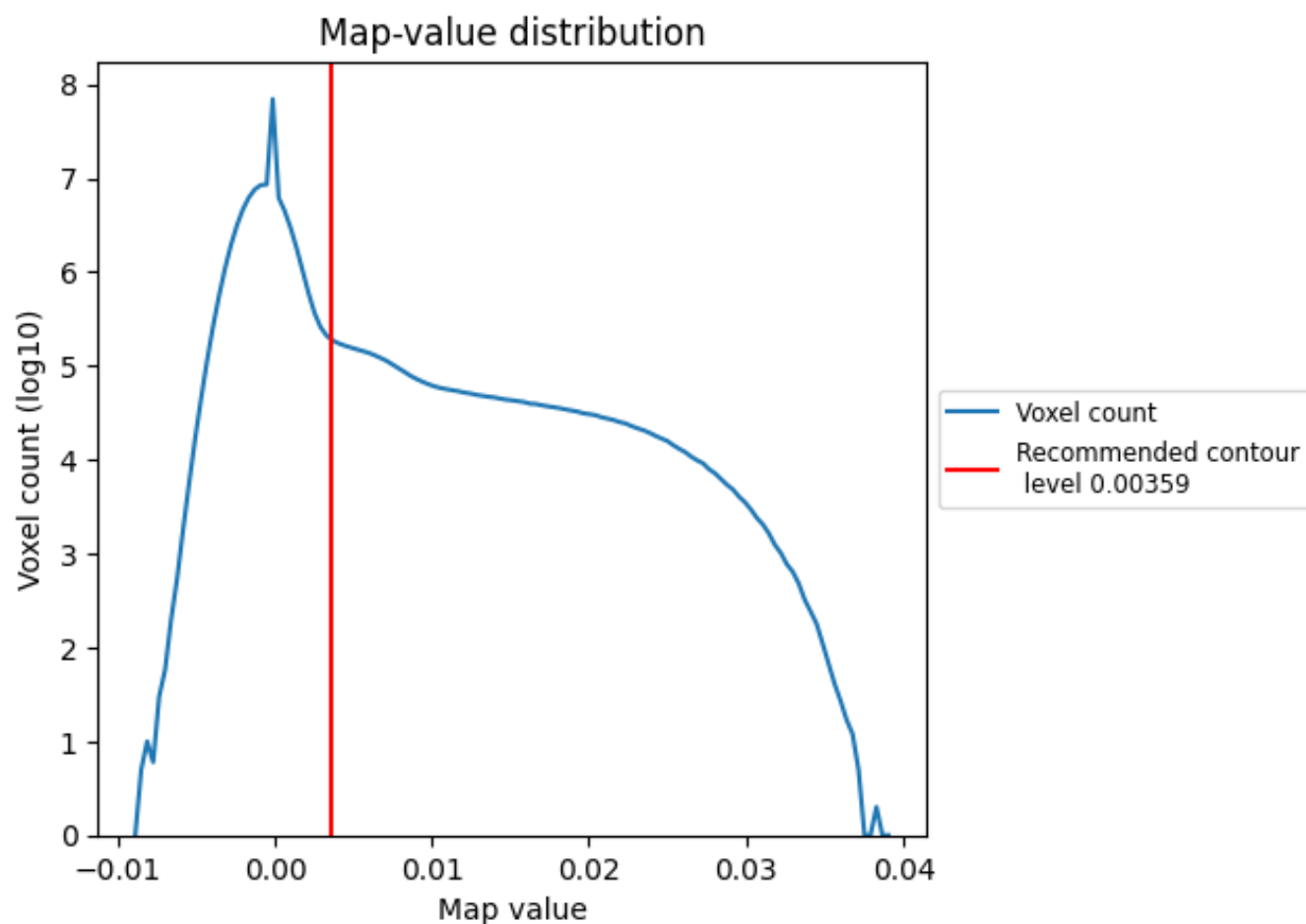
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

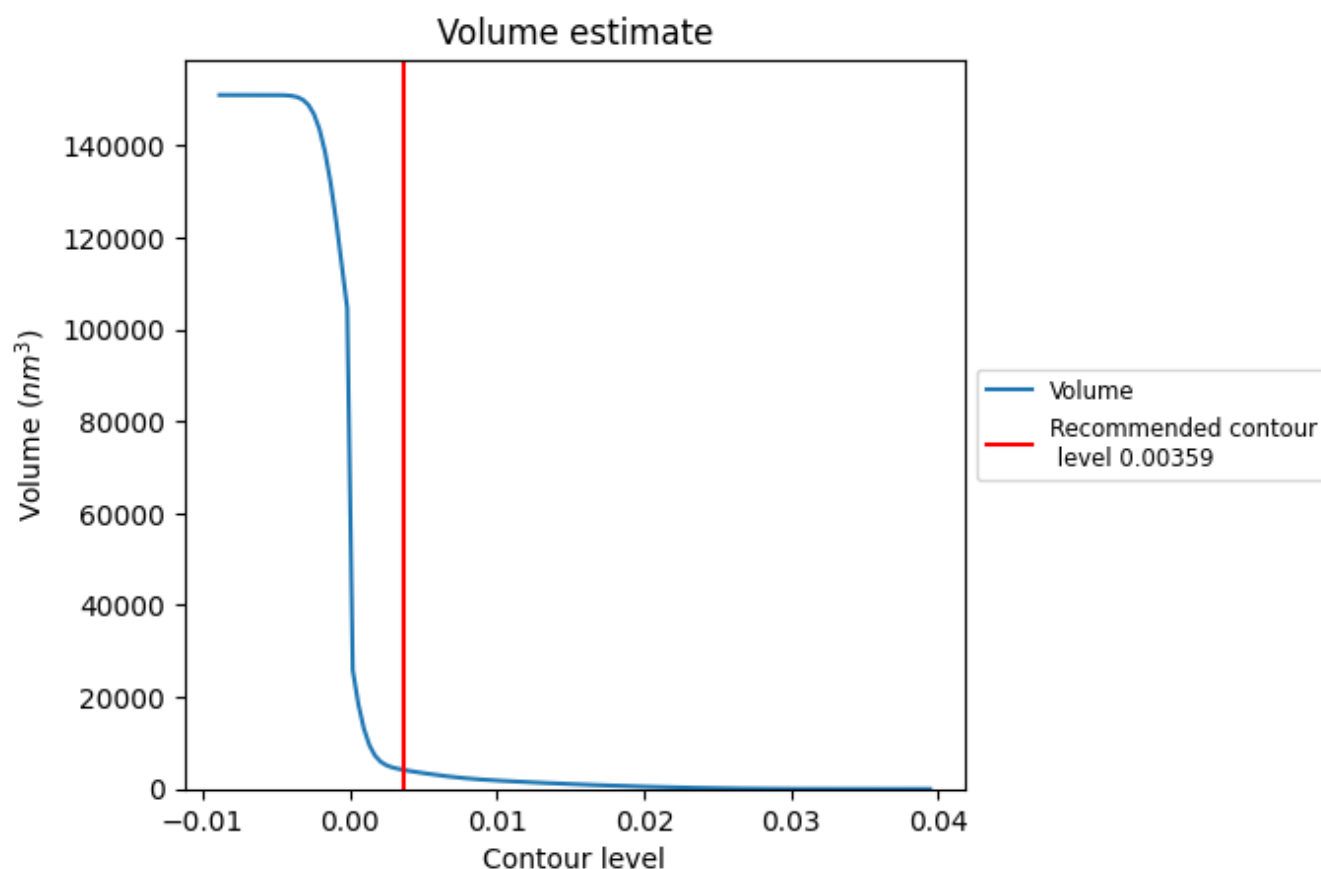
This section contains the results of statistical analysis of the map.

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.

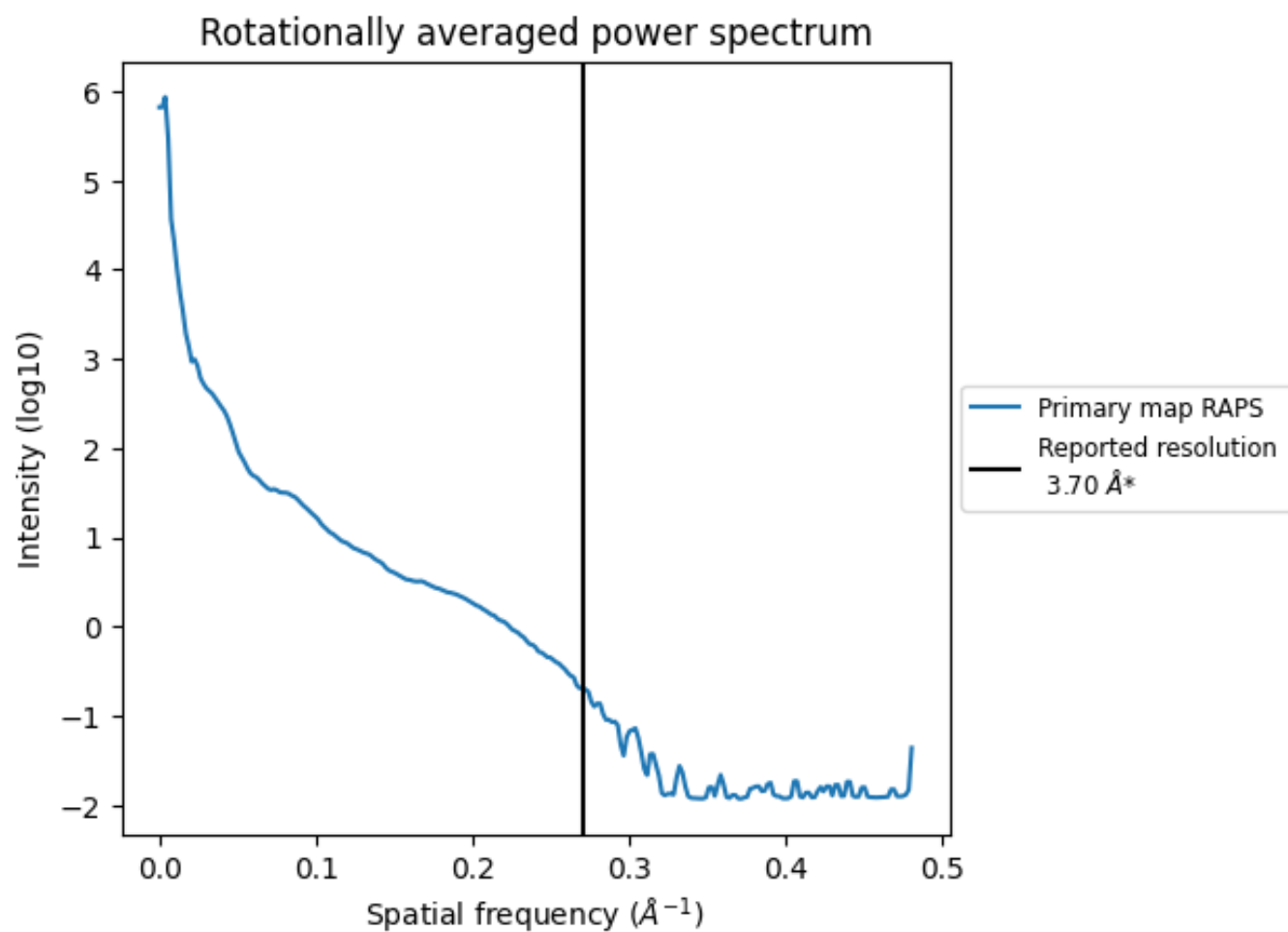
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4172 nm^3 ; this corresponds to an approximate mass of 3769 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 0.270 $\text{\AA}^{-1}$

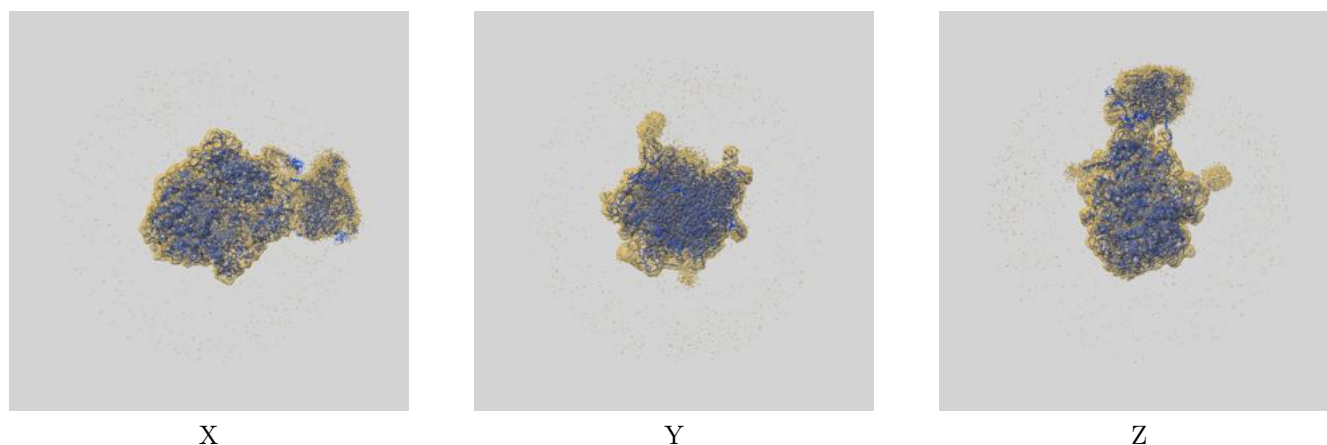
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

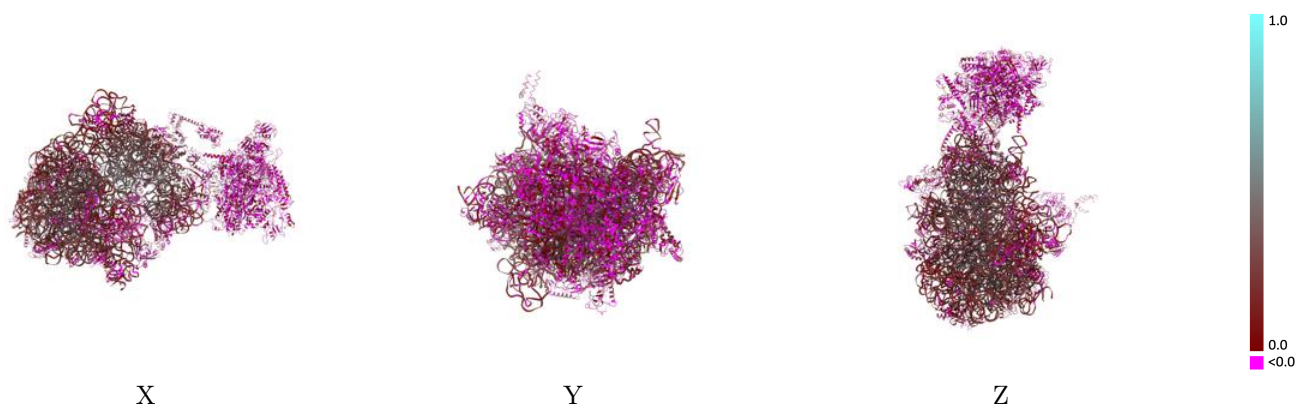
This section contains information regarding the fit between EMDB map EMD-22141 and PDB model 6XDQ. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



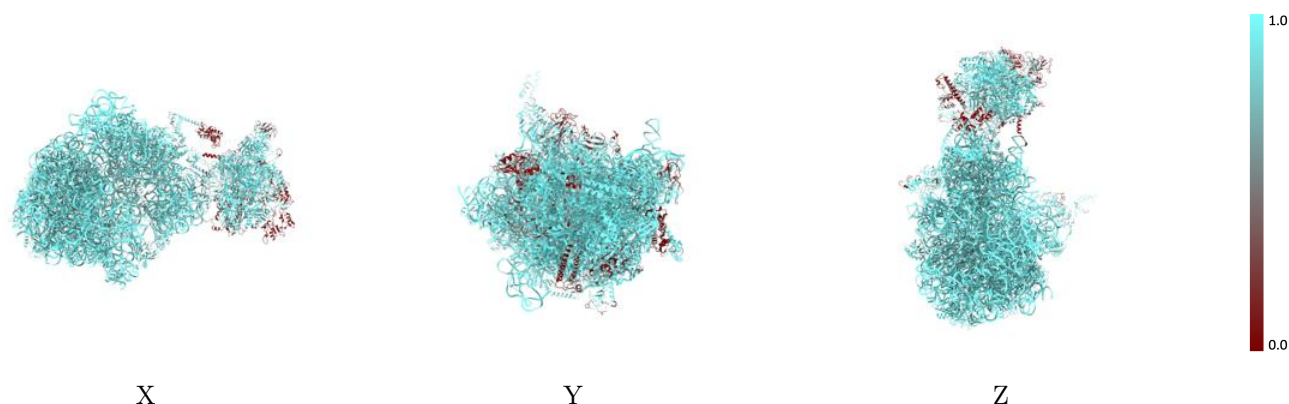
The images above show the 3D surface view of the map at the recommended contour level 0.00359 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



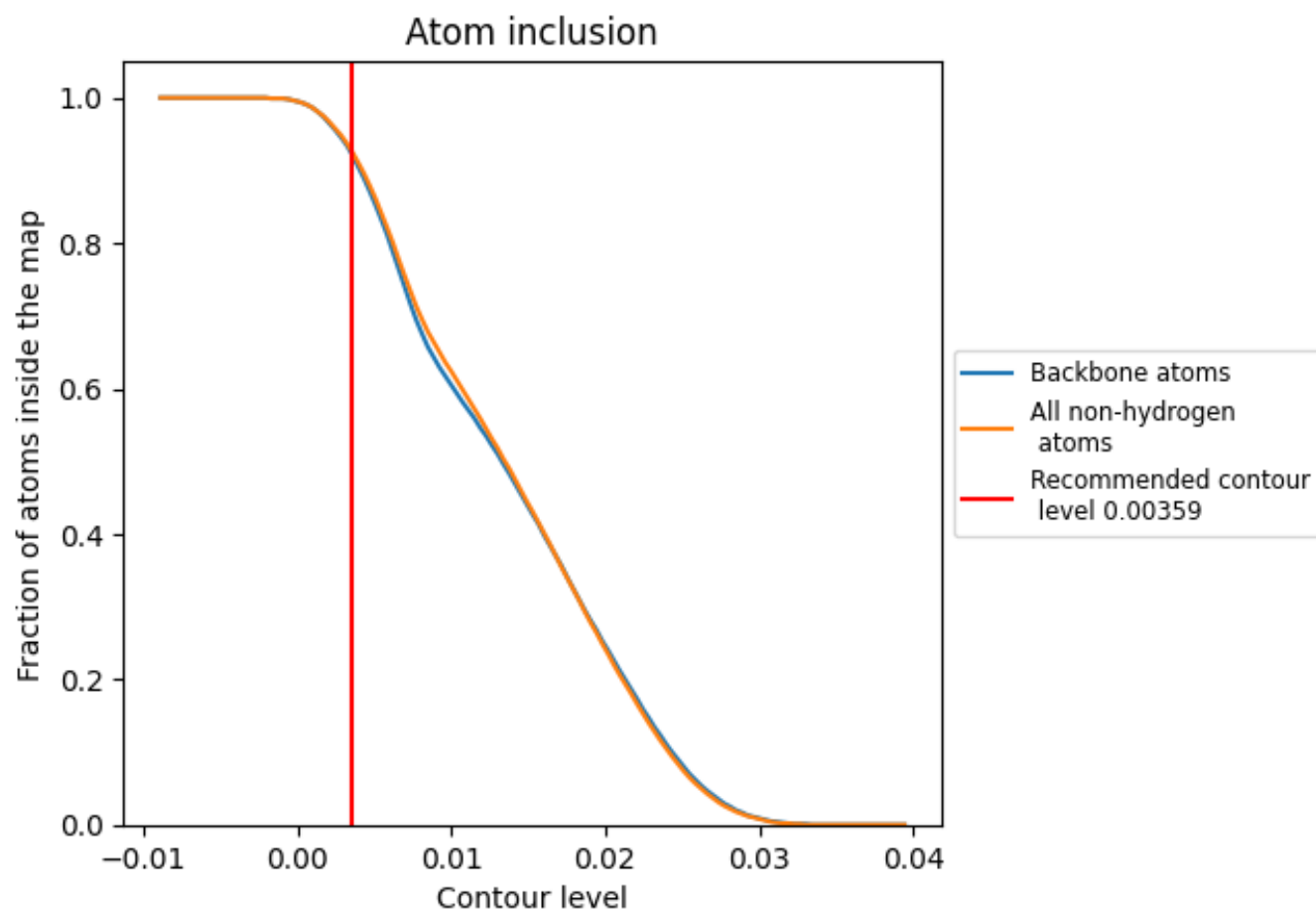
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.00359).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.00359) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9250	 0.1750
0	 0.9360	 0.1880
1	 0.9380	 0.2750
2	 0.9140	 0.1340
3	 0.9450	 0.1200
4	 0.9400	 0.1220
5	 0.8900	 0.0180
6	 0.9610	 0.0240
7	 0.9440	 0.0680
9	 0.8770	 0.0300
A	 0.9980	 0.1920
AA	 0.7490	 0.0110
AB	 0.7330	 0.0390
AC	 0.7050	 0.0230
AD	 0.6300	 0.0140
AE	 0.8150	 0.0130
AF	 0.7080	 -0.0110
AG	 0.7700	 0.0870
B	 0.8930	 0.0740
C	 0.9560	 0.1710
D	 0.9930	 0.2500
E	 0.9620	 0.1080
F	 0.9450	 0.2240
G	 0.9230	 0.1830
H	 0.7990	 0.0360
I	 0.9400	 0.2120
J	 0.9500	 0.1860
K	 0.9660	 0.3140
L	 0.9180	 0.1040
M	 0.9340	 0.1710
N	 0.9540	 0.2430
O	 0.9480	 0.1460
P	 0.9230	 0.1430
Q	 0.9630	 0.1940
R	 0.9750	 0.3010



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Chain	Atom inclusion	Q-score
S	 0.9560	 0.1410
T	 0.9640	 0.2030
U	 0.9590	 0.1030
V	 0.9480	 0.2250
W	 0.8690	 0.0450
X	 0.9020	 0.0720
Y	 0.7380	 0.0150
Z	 0.8330	 0.0180
a	 0.9930	 0.2350
b	 0.9470	 0.1360
c	 0.9470	 0.1970
d	 0.9880	 0.1350
e	 0.9120	 0.0940
f	 0.9500	 0.1830
g	 0.9290	 0.0380
h	 0.9490	 0.1910
i	 0.9580	 0.2310
j	 0.9490	 0.1660
k	 0.9280	 0.0880
l	 0.9340	 0.1680
m	 0.9750	 0.3110
n	 0.9130	 0.0610
o	 0.9470	 0.1880
p	 0.9320	 0.0620
q	 0.9520	 0.1030
r	 0.8490	 0.0530
s	 0.9510	 0.1750
t	 0.9140	 0.1690
u	 0.9470	 0.1790
v	 0.9550	 0.1880
w	 0.9440	 0.1840
x	 0.9320	 0.0210
y	 0.9230	 0.1170
z	 0.9630	 0.2310