



Full wwPDB EM Validation Report ⓘ

Jul 15, 2025 – 11:58 AM EDT

PDB ID : 8VOR / pdb_00008vor
EMDB ID : EMD-43390
Title : Escherichia coli transcription-translation loosely coupled complex (TTC-LC) containing mRNA with a 51 nt long spacer, NusG, NusA, and fMet-tRNAs in E-site and P-site
Authors : Molodtsov, V.; Wang, C.; Ebright, R.H.
Deposited on : 2024-01-15
Resolution : 3.60 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.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

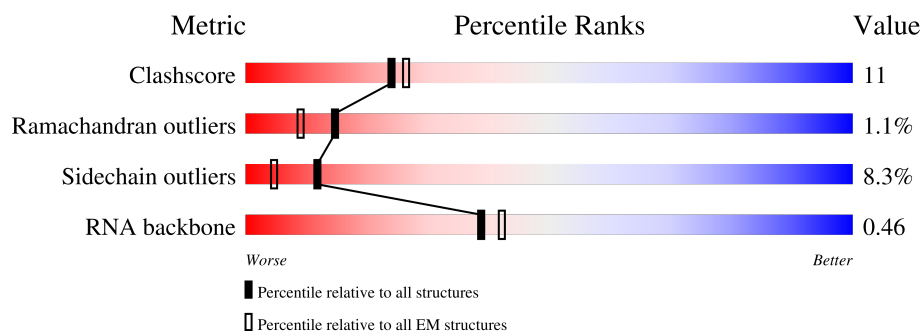
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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% 7% . 6%
4	3	104	84% 14% ..
5	4	94	97% .
6	5	36	6% 28% 36% 36%
7	6	36	36% 39% 25%









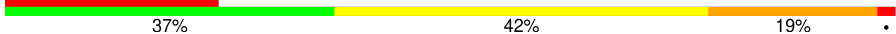
















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Mol	Chain	Length	Quality of chain
8	7	68	
9	9	165	
10	A	76	
10	B	76	
11	AA	1342	
12	AB	181	
13	AC	329	
13	AD	329	
14	AE	1407	
15	AF	91	
16	AG	495	
17	C	75	
18	D	1542	
19	E	87	
20	F	71	
21	G	241	
22	H	557	
23	I	233	
24	J	206	
25	K	167	
26	L	135	
27	M	179	
28	N	130	
29	O	130	
30	P	103	

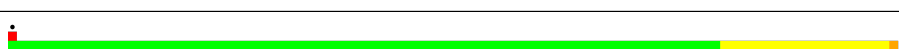

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Mol	Chain	Length	Quality of chain
31	Q	129	
32	R	124	
33	S	101	
34	T	89	
35	U	82	
36	V	84	
37	W	92	
38	X	118	
39	Y	142	
40	Z	121	
41	a	2904	
42	b	85	
43	c	78	
44	d	120	
45	e	63	
46	f	59	
47	g	70	
48	h	273	
49	i	57	
50	j	209	
51	k	55	
52	l	201	
53	m	46	
54	n	179	
55	o	65	

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Mol	Chain	Length	Quality of chain
56	p	177	 90% 8% •
57	q	38	 89% 8% •
58	r	149	 88% 9% •
59	s	142	 82% 16% •
60	t	123	 80% 19% •
61	u	144	 89% 10% •
62	v	136	 91% 8% •
63	w	127	 77% 17% 6%
64	x	117	 82% 16% ••
65	y	115	 89% 10% •
66	z	118	 84% 15% •

2 Entry composition [i](#)

There are 68 unique types of molecules in this entry. The entry contains 291173 atoms, of which 109913 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Ribosomal protein L21.

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

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

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

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

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

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

Mol	Chain	Residues	Atoms						AltConf	Trace
4	3	103	Total	C	H	N	O		0	0
			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 51 nt long spacer.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	7	31	Total	C	H	N	O	P	0	0
			744	289	97	92	235	31		

- 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
			2434	723	814	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	220	Total	C	N	O	S	0	0
			1690	1056	298	330	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		

- 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	495	Total	C	N	O	S	0	0
			3852	2396	669	774	13		

- 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 Small ribosomal subunit protein uS15.

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	conflict	GB 937521852

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

Mol	Chain	Residues	Atoms						AltConf	Trace
42	b	76	Total	C	H	N	O	S	0	0
			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	Mg	0
			1	1	


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

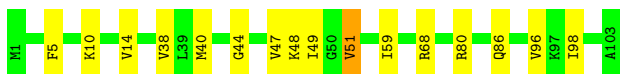
Mol	Chain	Residues	Atoms		AltConf
68	AE	2	Total	Zn	0
			2	2	

3 Residue-property plots [i](#)

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

- Molecule 1: Ribosomal protein L21

Chain 0:  84% 15% .




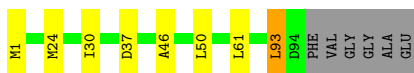
- Molecule 2: 50S ribosomal protein L22

Chain 1:  75% 25%




- Molecule 3: 50S ribosomal protein L23

Chain 2:  86% 7% . 6%



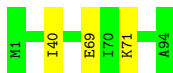
- Molecule 4: 50S ribosomal protein L24

Chain 3:  84% 14% ..

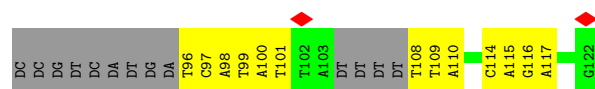
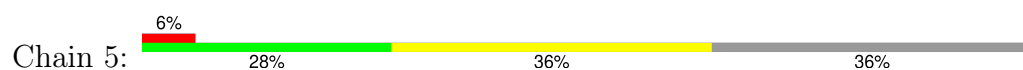


- Molecule 5: 50S ribosomal protein L25

Chain 4:  97% .



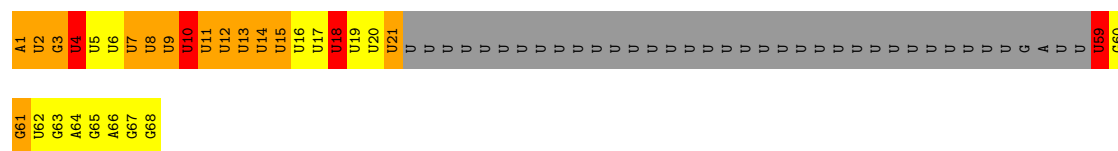
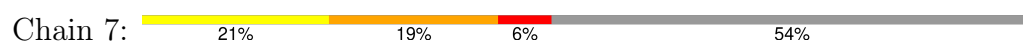
- Molecule 6: NT DNA



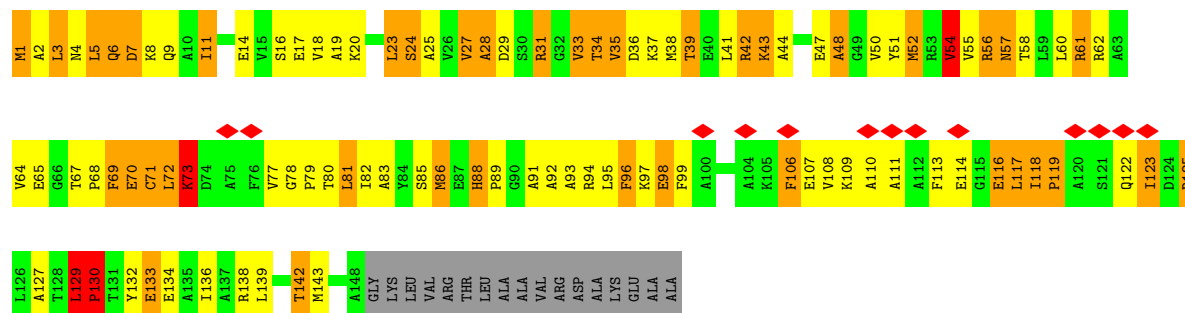
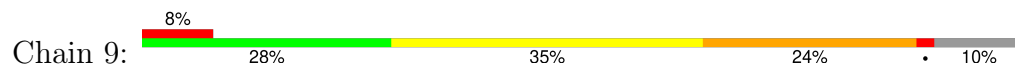
• Molecule 7: T DNA



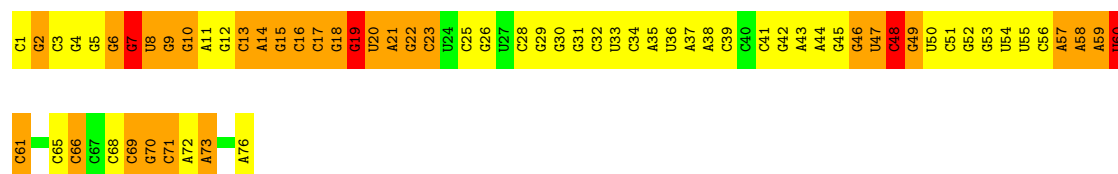
• Molecule 8: mRNA with 51 nt long spacer



• Molecule 9: 50S ribosomal protein L10

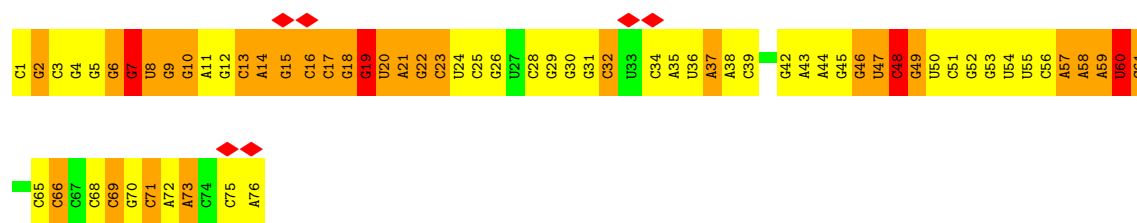


• Molecule 10: E-site and P-site tRNA (fMet)

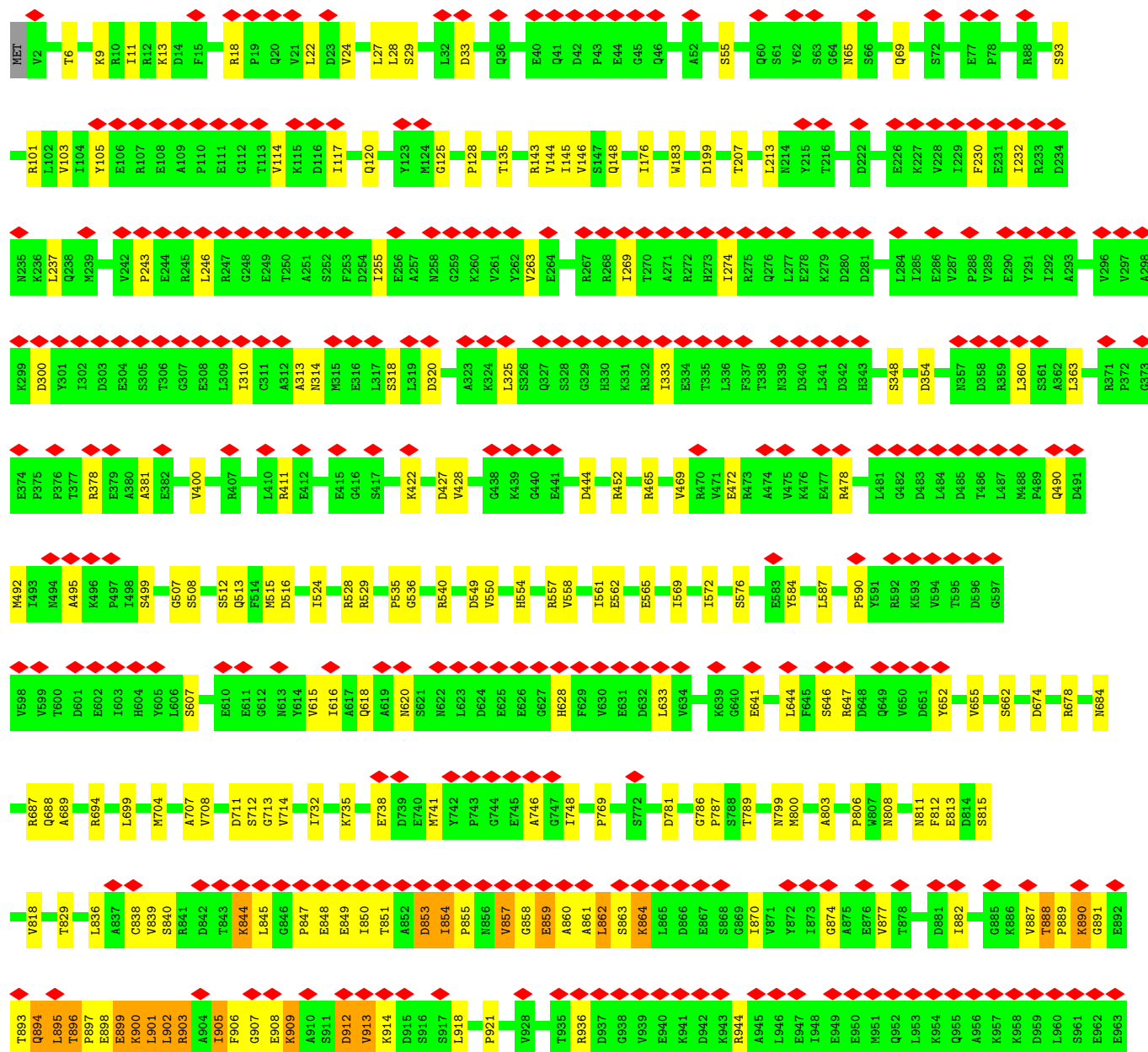
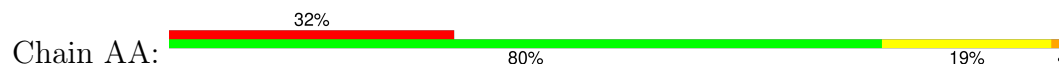


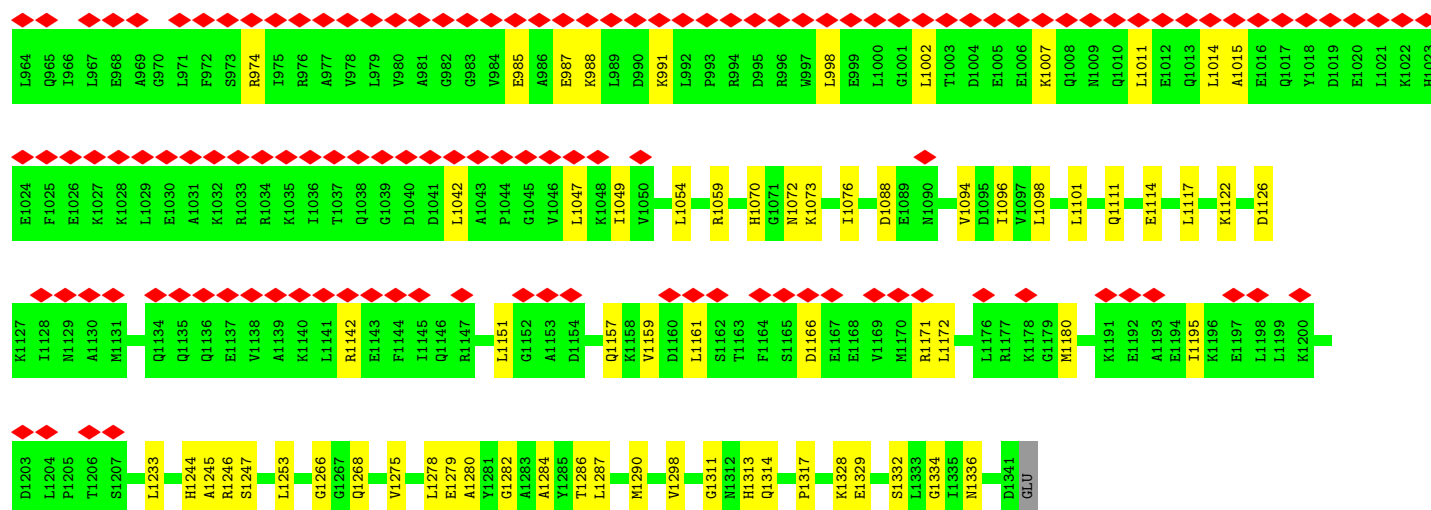
• Molecule 10: E-site and P-site tRNA (fMet)



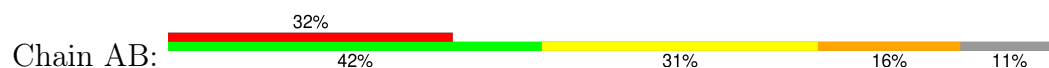


• Molecule 11: DNA-directed RNA polymerase subunit beta

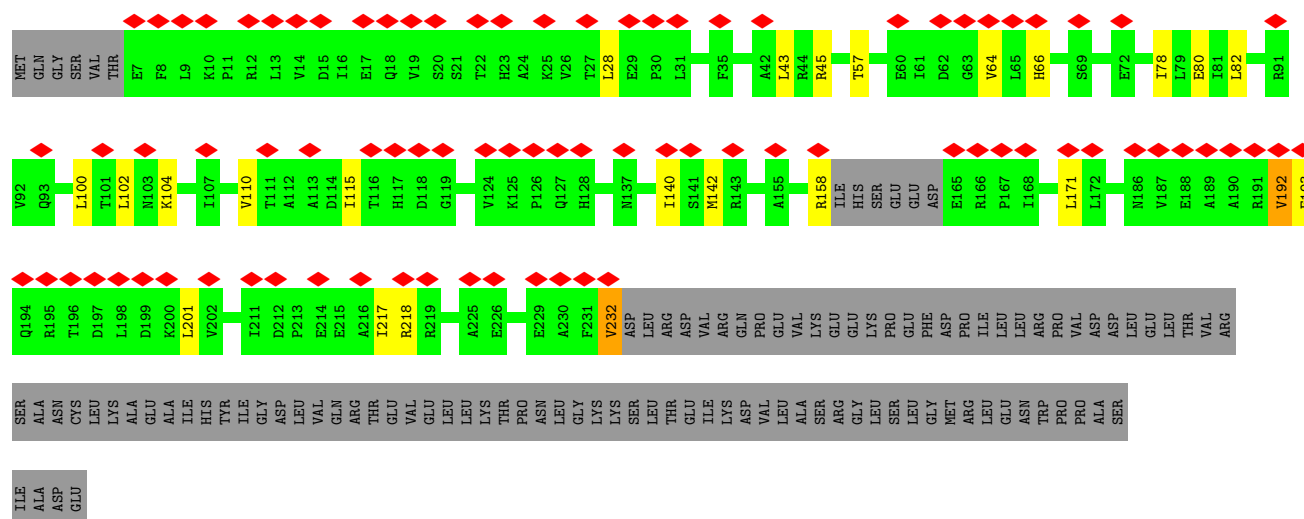




• Molecule 12: Transcription termination/antitermination protein NusG

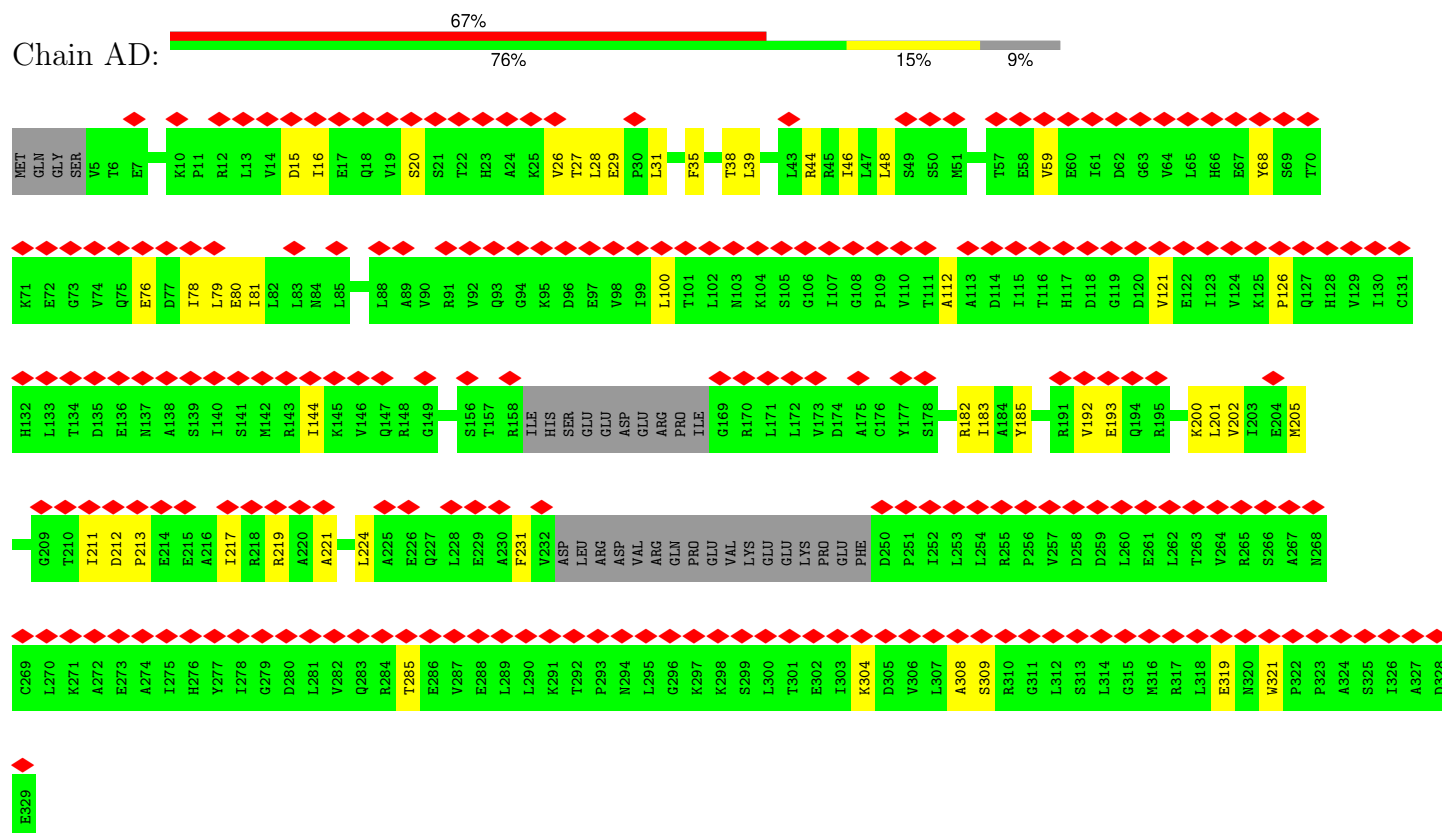


• Molecule 13: DNA-directed RNA polymerase subunit alpha



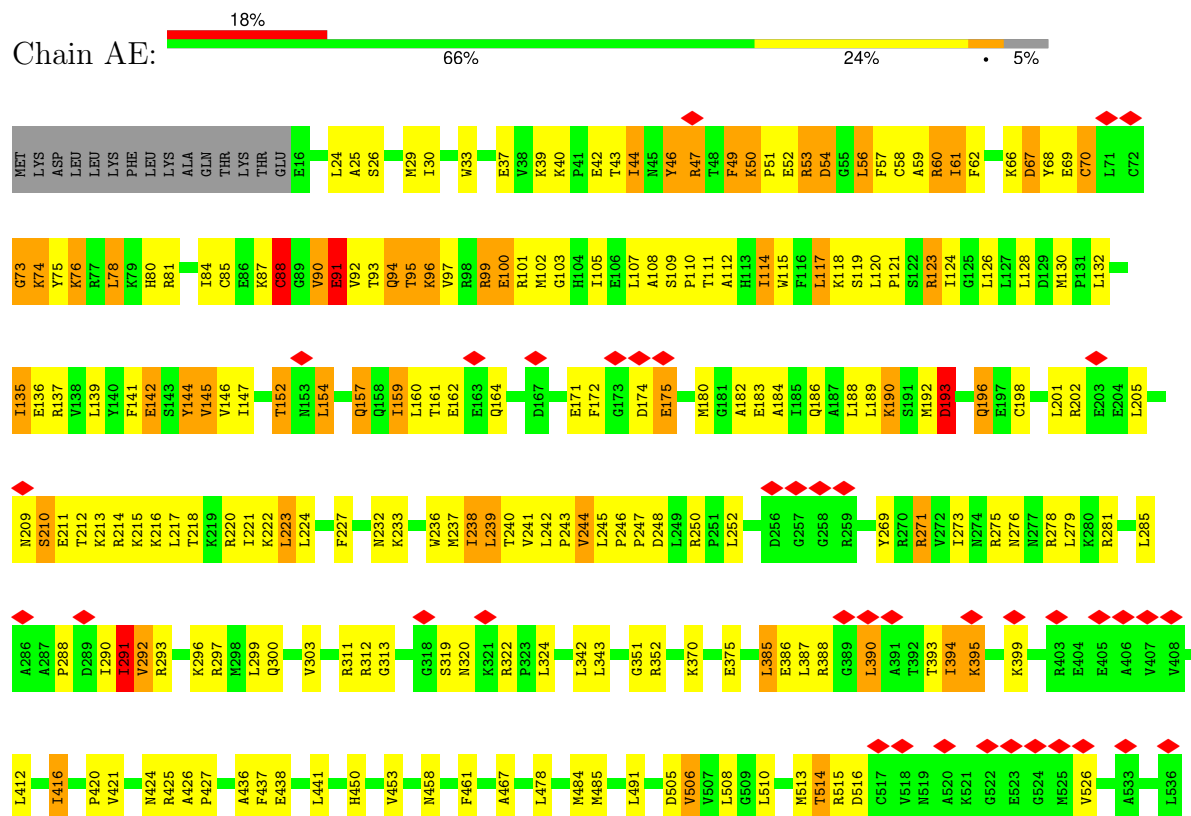
• Molecule 13: DNA-directed RNA polymerase subunit alpha

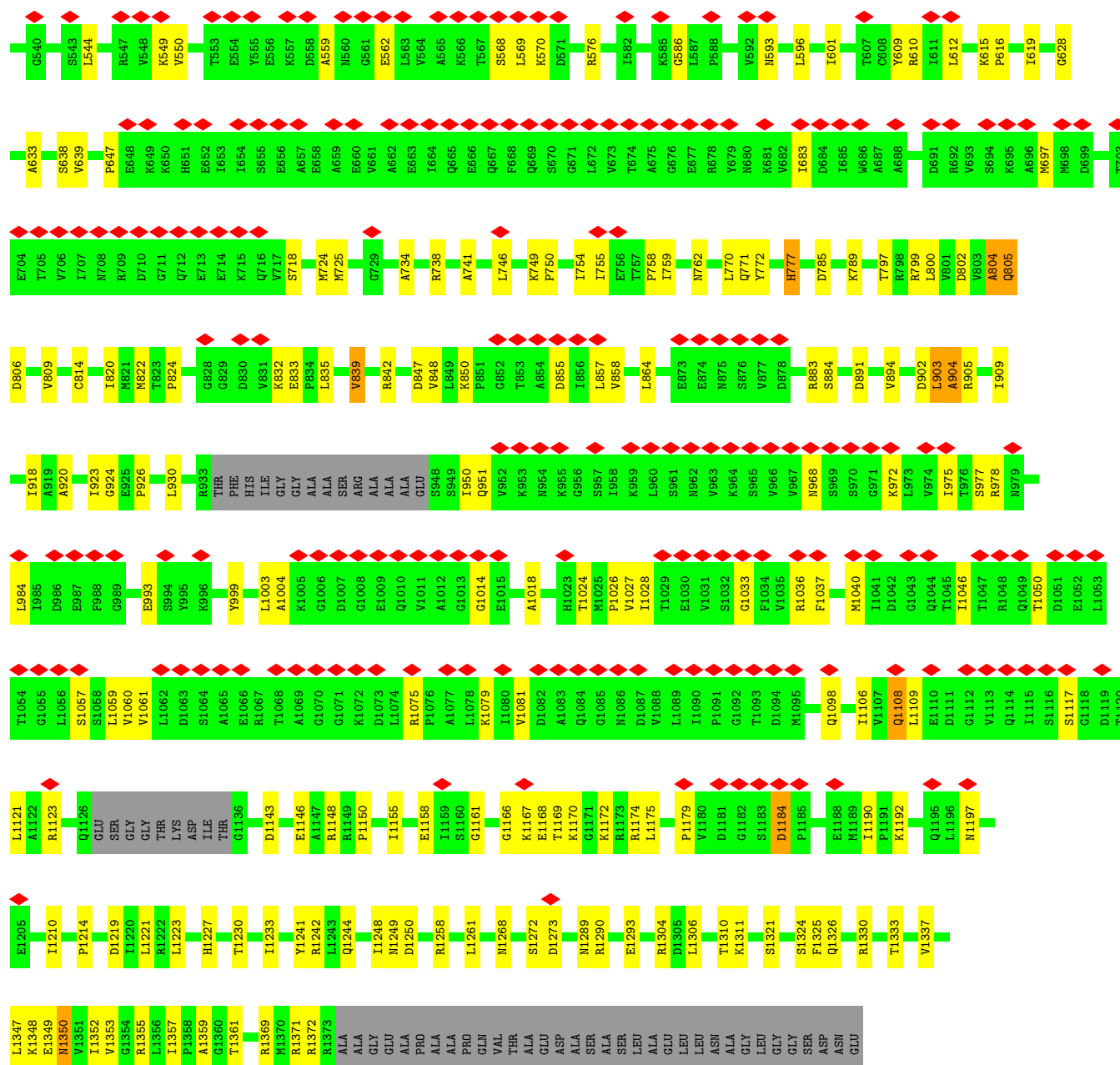
Chain AD:



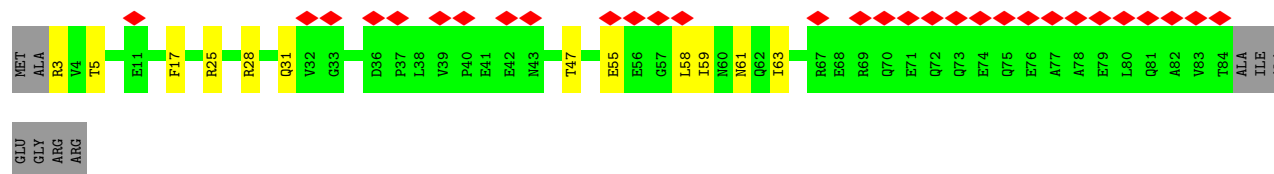
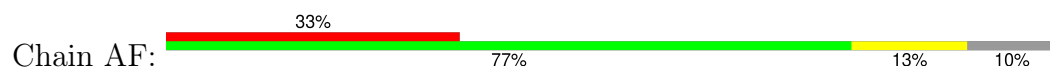
• Molecule 14: DNA-directed RNA polymerase subunit beta'

Chain AE:



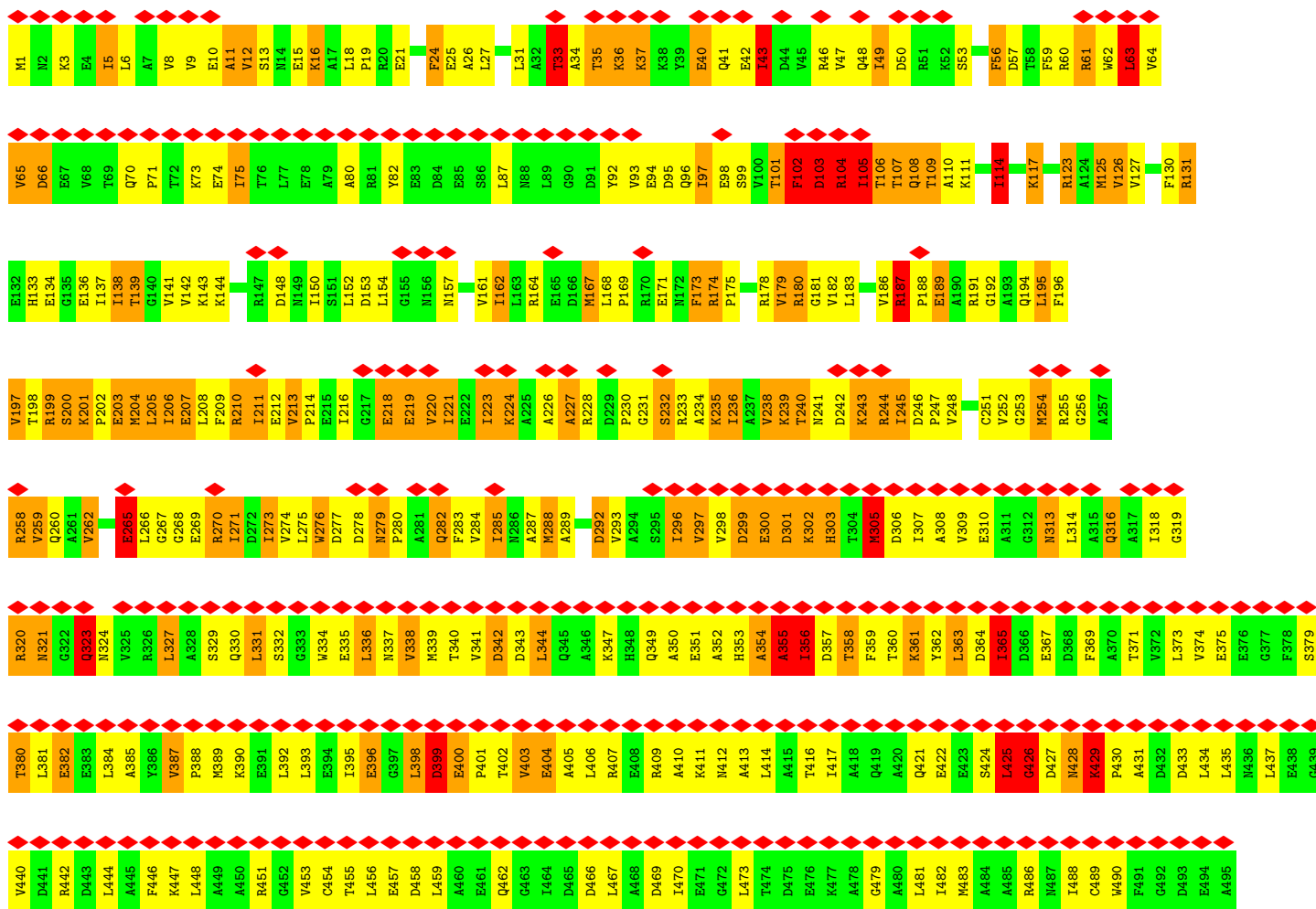


• Molecule 15: DNA-directed RNA polymerase subunit omega



• Molecule 16: Transcription termination/antitermination protein NusA





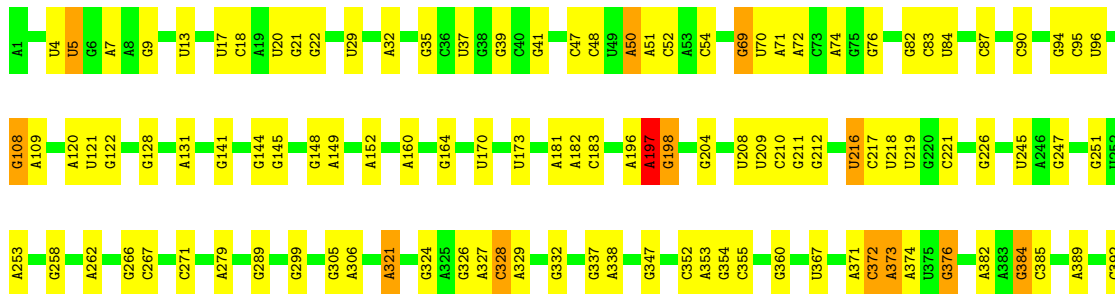
• Molecule 17: 30S ribosomal protein S18

Chain C: 73% 13% 12%

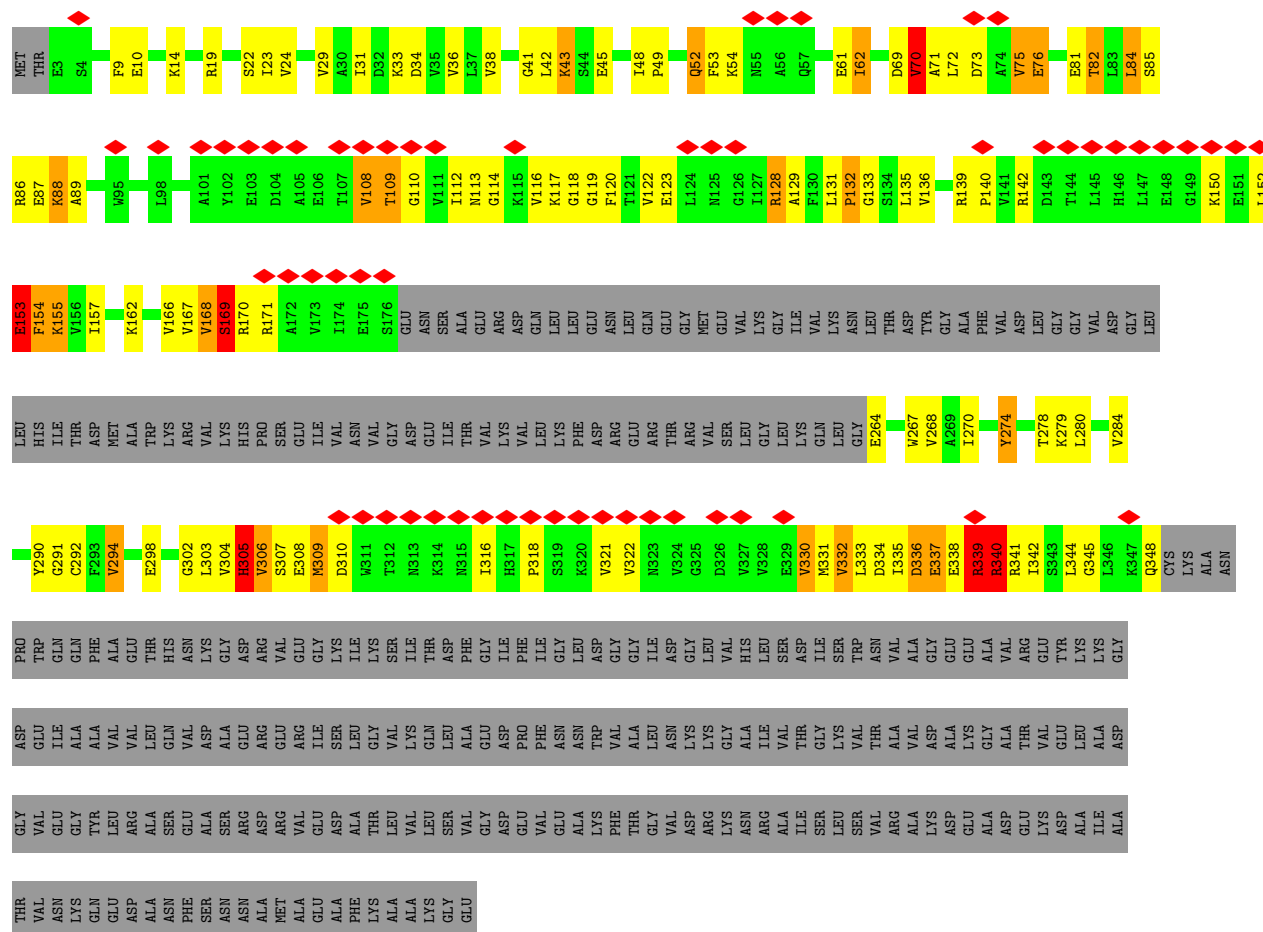


• Molecule 18: 16S rRNA

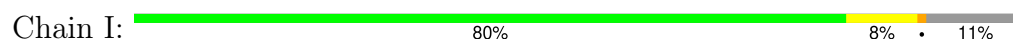
Chain D: 70% 25%



- Molecule 22: 30S ribosomal protein S1



- Molecule 23: 30S ribosomal protein S3



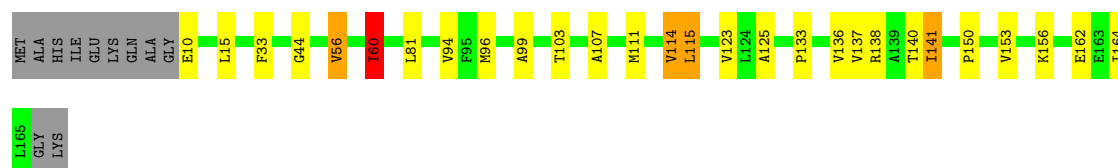
- Molecule 24: 30S ribosomal protein S4

Chain J:  92% 7%



- Molecule 25: 30S ribosomal protein S5

Chain K:  77% 14% 7%



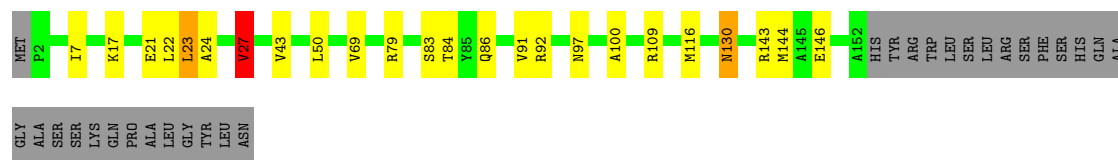
- Molecule 26: 30S ribosomal protein S6

Chain L:  67% 10% 23%



- Molecule 27: 30S ribosomal protein S7

Chain M:  71% 12% 16%




- Molecule 28: 30S ribosomal protein S8

Chain N:  90% 8%



- Molecule 29: 30S ribosomal protein S9

Chain O:  80% 17%

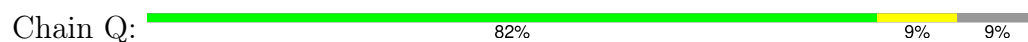


- Molecule 30: 30S ribosomal protein S10

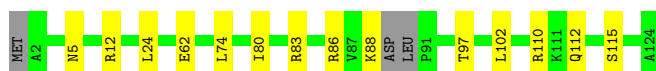
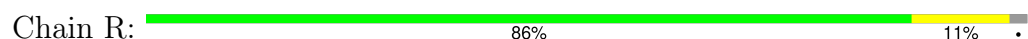
Chain P:  66% 21% 8%



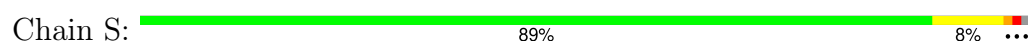
- Molecule 31: 30S ribosomal protein S11



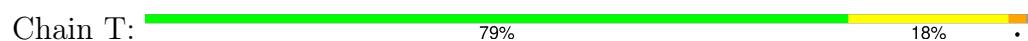
- Molecule 32: 30S ribosomal protein S12



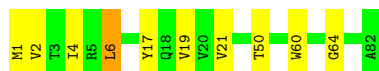
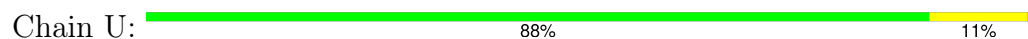
- Molecule 33: 30S ribosomal protein S14



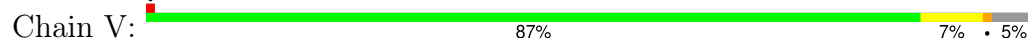
- Molecule 34: Small ribosomal subunit protein uS15



- Molecule 35: 30S ribosomal protein S16



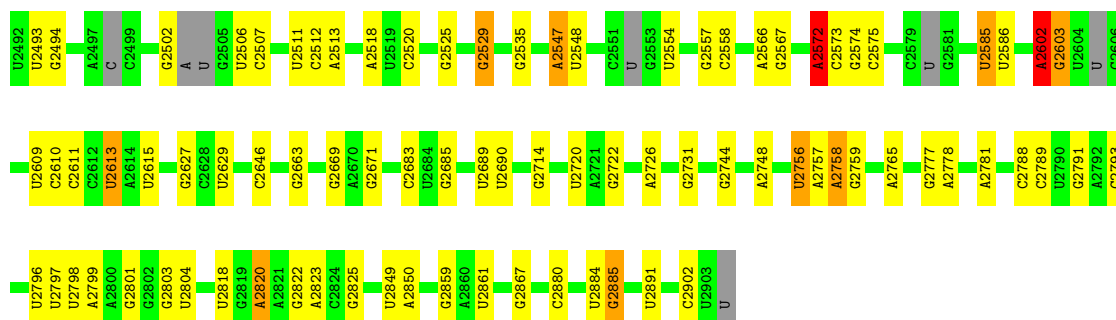
- Molecule 36: 30S ribosomal protein S17



- Molecule 37: 30S ribosomal protein S19



G2372	A2376	G2383	U2384	C2385	C2394	C2395	G2396	U2402	C2403	A2406	G2415	C2422	U2423	C2424	A2425	A2426	G2429	A2430	U2431	A2434	A2435	A2436	U2441	G2444	G2446	G2447	A2448	C2456	U2458	A2469	G2470	U2474	C2475	A2476	U2477	A2478	G2481	G2484	U2491							
G2253	A2268	A2273	A2274	A2278	C2283	A2287	U2291	U2292	G2293	G2294	G2295	C2296	A2297	U2298	U2299	G2303	G2304	U2305	G2308	A2309	C2310	A2311	A2314	G2315	U2321	A2322	G2325	C2326	A2327	A2328	U2329	G2330	C2331	G2332	A2333	U2334	A2335	A2336	C2339	G2345	A2346	C2347	C2350	G2361		
G2157	A2158	G2159	G2162	A2163	C2164	C2165	U2166	U2167	G2168	A2169	U2170	A2171	U2172	C2178	U2181	A2182	U2183	A2184	U2185	U2188	G2189	A2190	A2191	U2192	G2193	U2194	A2198	G2204	U2210	A2211	A2212	U2213	A2225	C2226	U2229	G2230	U2231	A2238	G2239	U2243	U2244	U2245	U2249	G2250	G2252	
C2055	G2056	A2060	G2061	A2062	C2063	U2068	G2070	A2071	C2072	C2073	U2075	U2076	A2077	G2093	A2097	U2098	G2100	A2108	U2109	G2110	U2111	G2112	U2113	A2114	G2115	G2116	A2117	U2118	G2121	U2122	G2123	G2124	G2125	A2126	G2127	U2131	A2132	G2133	A2134	U2139	G2140	G2141	C2146	A2147	A2154	
A1938	U1940	U1955	C1961	U1963	C1964	C1965	A1966	C1967	A1970	U1971	G1972	G1980	A1981	U1982	A1987	U1991	G1992	U1993	C1997	G1998	C1999	C2000	C2001	G2002	A2013	U2017	A2020	C2021	U2022	C2023	G2027	U2028	G2029	A2031	C2032	A2033	U2038	U2039	C2043	A2051	A2052					
G1824	A1829	C1833	U1834	G1836	G1839	A1847	A1848	A1858	U1859	G1862	G1863	U1864	G1869	C1870	A1871	A1872	G1873	C1905	G1906	G1907	C1908	C1909	U1910	A1912	A1913	C1914	U1916	U1918	A1919	C1920	G1921	G1922	U1923	C1924	C1925	U1926	A1927	A1928	G1929	G1930	U1931	A1932	G1933	A1936	A1937	
A1509	G1510	A1515	G1529	U1534	A1535	G1537	A1548	A1549	U1554	U1559	C1565	A1566	G1567	G1568	A1569	A1570	A1571	U1578	A1579	A1580	G1581	C1582	A1583	U1584	G1588	U1589	A1590	A1591	A1596	A1597	A1603	A1608	A1609	A1610	A1614	C1617	A1619	U1647	U1648	G1649	A1650	G1651				
G1674	A1677	U1693	C1694	G1695	G1703	U1714	G1715	A1718	G1719	U1720	G1721	U1729	C1730	G1731	C1732	G1738	G1750	A1755	G1756	A1757	U1758	C1764	A1773	U1779	A1784	A1789	C1790	A1791	U1796	G1797	C1800	A1808	A1809	G1810	C1811	G1814	A1815	G1816	U1817							
U1352	C1363	G1364	A1365	G1368	A1378	U1379	G1380	A1383	A1384	C1386	A1387	U1394	A1395	U1396	U1406	G1407	G1408	U1411	A1412	A1413	C1414	U1415	G1416	C1417	A1418	A1419	A1420	C1428	A1433	A1434	G1452	A1453	U1460	G1478	G1482	A1490	G1491	U1497	A1503	A1508						
G1122	G1125	U1132	A1133	A1134	C1135	U1141	A1142	A1143	C1153	A1169	C1170	U1173	U1174	U1175	U1176	G1177	C1178	G1179	U1180	U1181	G1182	U1183	G1186	G1187	U1188	A1189	G1238	U1249	G1250	A1253	G1256	G1266	C1270	G1271	A1272	U1273	A1301	A1321	A1327	A1328	C1345					
A1028	U1033	G1041	A1042	C1045	A1046	G1047	U1054	G1055	U1060	U1061	G1062	G1063	C1064	A1065	U1066	A1067	G1068	A1069	A1070	C1071	G1072	A1073	G1074	C1075	C1076	C1079	A1080	U1081	U1082	A1084	U1085	A1086	G1087	A1088	U1089	A1090	A1095	A1096	A1103	G1107	U1108	C1109	G1110	A1111	G1112	U1119
C997	C998	A999	G907	A910	G914	C915	A927	A928	U929	U931	A941	C944	A945	C946	A947	C948	G953	G954	U954	G956	A957	U958	C961	A973	G974	A983	A984	C985	C995	A996	G997	C998	U999	C1005	C1006	C1007	U1012	C1013	U1019	A1020	A1021	G1022	U1023	G1026	A1027	
G757	A764	C765	G775	G776	A782	A783	G784	G785	A800	A802	G805	U811	C812	U813	C814	A819	U827	U828	A845	U846	C851	U852	G858	U859	G869	U870	U871	U872	A878	G879	G880	G881	G882	U883	U884	C885	C888	G891	A892	C893	U894	U895	A896			
A609	A613	A614	U615	A616	G617	G618	G619	G620	A621	A627	A631	A637	G638	U639	C640	U641	U642	A643	A644	C645	G647	A654	G664	A668	A685	U686	A705	U710	U717	A730	G738	A742	A743	U744	G748	A753	U754	U755	A756							



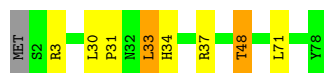
- Molecule 42: 50S ribosomal protein L27

Chain b: 84% 6% 11%



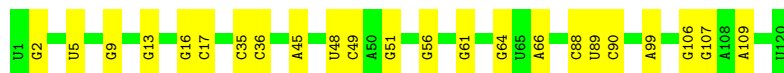
- Molecule 43: 50S ribosomal protein L28

Chain c: 88% 8% ..



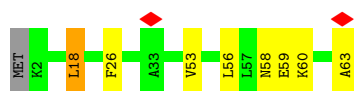
- Molecule 44: 5S rRNA

Chain d: 81% 19%



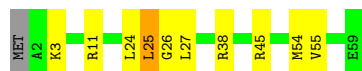
- Molecule 45: 50S ribosomal protein L29

Chain e: 86% 11% ..



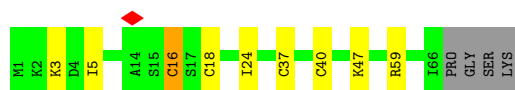
- Molecule 46: 50S ribosomal protein L30

Chain f: 81% 15% ..



- Molecule 47: 50S ribosomal protein L31

Chain g: 81% 11% 6%



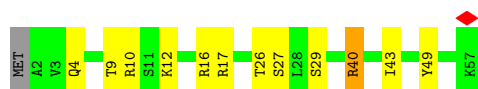
- Molecule 48: 50S ribosomal protein L2

Chain h: 84% 14% ..



- Molecule 49: 50S ribosomal protein L32

Chain i: 77% 19% ..



- Molecule 50: 50S ribosomal protein L3

Chain j: 88% 11%



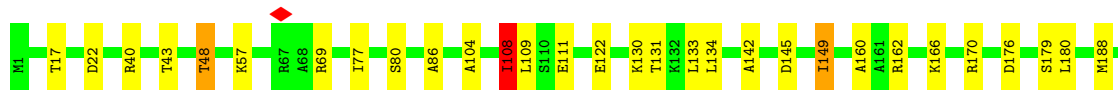
- Molecule 51: 50S ribosomal protein L33

Chain k: 89% 5% 5%



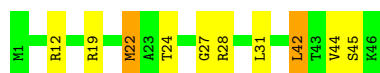
- Molecule 52: 50S ribosomal protein L4

Chain l: 85% 14% .



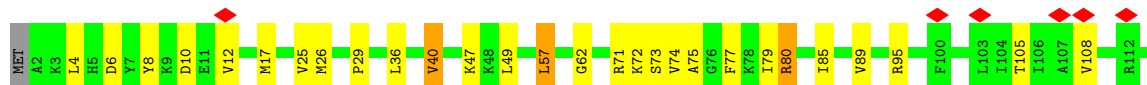
- Molecule 53: 50S ribosomal protein L34

Chain m: 78% 17% .



- Molecule 54: 50S ribosomal protein L5

Chain n: 75% 21% . .



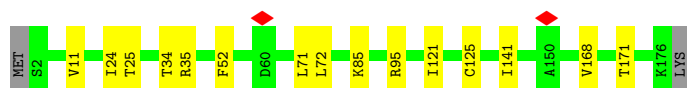
- Molecule 55: 50S ribosomal protein L35

Chain o: 88% 6% 5% .



- 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: 88% 9% .

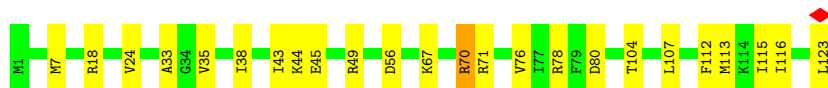
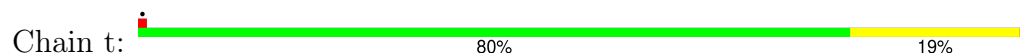


- Molecule 59: 50S ribosomal protein L13

Chain s: 82% 16% .



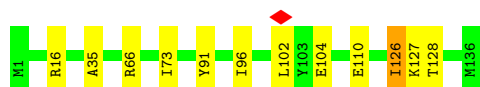
- Molecule 60: 50S ribosomal protein L14



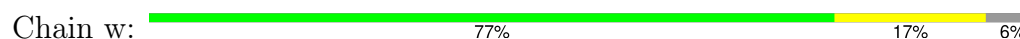
- Molecule 61: 50S ribosomal protein L15



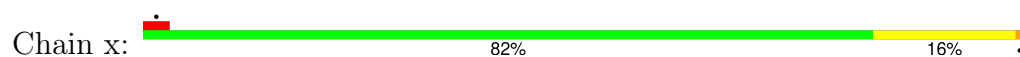
- Molecule 62: 50S ribosomal protein L16



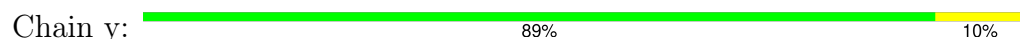
- Molecule 63: 50S ribosomal protein L17



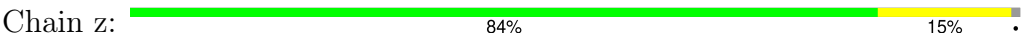
- Molecule 64: 50S ribosomal protein L18



- Molecule 65: 50S ribosomal protein L19



- Molecule 66: 50S ribosomal protein L20



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	24109	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1250	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.043	Depositor
Minimum map value	-0.011	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0039	Depositor
Map size (\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 (\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: MG, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.50	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	0.64	1/528 (0.2%)	0.55	0/810
7	6	0.56	1/603 (0.2%)	0.56	0/926
8	7	0.62	3/717 (0.4%)	0.90	4/1110 (0.4%)
9	9	1.15	3/1131 (0.3%)	1.30	3/1524 (0.2%)
10	A	0.36	0/1810	0.72	2/2821 (0.1%)
10	B	0.44	0/1810	0.87	9/2821 (0.3%)
11	AA	0.38	0/10736	0.63	0/14487
12	AB	0.56	0/1304	0.82	2/1759 (0.1%)
13	AC	0.38	0/1710	0.61	0/2317
13	AD	0.30	0/2091	0.59	0/2847
14	AE	0.56	11/10545 (0.1%)	0.79	27/14236 (0.2%)
15	AF	0.30	0/652	0.61	0/879
16	AG	0.97	5/3897 (0.1%)	1.40	49/5273 (0.9%)
17	C	0.66	0/553	1.14	1/743 (0.1%)
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	0.72	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	0.59	0/1663	0.99	0/2241
24	J	0.63	0/1665	1.08	0/2227
25	K	0.64	1/1165 (0.1%)	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	0.56	0/989	0.92	0/1326
29	O	0.59	0/1034	1.02	1/1375 (0.1%)
30	P	0.64	0/800	1.13	4/1082 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	Q	0.55	0/893	0.92	0/1205
32	R	0.50	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	1.04	0/1046	1.09	1/1410 (0.1%)
40	Z	1.02	0/227	1.12	0/304
41	a	0.41	3/69247 (0.0%)	0.75	54/107985 (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	0.56	0/531	0.99	1/709 (0.1%)
48	h	0.54	0/2121	0.85	0/2852
49	i	0.53	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	0.69	0/380	1.22	0/498
54	n	0.63	0/1434	1.18	10/1926 (0.5%)
55	o	0.64	0/513	1.11	1/676 (0.1%)
56	p	0.58	0/1333	0.89	0/1805
57	q	0.51	0/303	0.88	0/397
58	r	0.63	0/1122	0.98	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	0.95	1/1413 (0.1%)
62	v	0.60	0/1093	0.97	0/1460
63	w	0.68	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	0.50	41/194544 (0.0%)	0.84	256/286096 (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
12	AB	0	1
13	AC	0	1
13	AD	0	3
14	AE	0	5
16	AG	0	6
22	H	0	3
38	X	0	1
All	All	0	24

All (41) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	9	130	PRO	N-CA	18.20	1.70	1.47
16	AG	429	LYS	C-N	13.87	1.51	1.33
14	AE	93	THR	CA-C	12.12	1.69	1.52
22	H	169	SER	N-CA	11.79	1.61	1.46
14	AE	291	ILE	CA-C	11.49	1.67	1.52
18	D	1516	G	O3'-P	-10.70	1.45	1.61
14	AE	70	CYS	CA-CB	-8.85	1.41	1.53
18	D	1339	A	O3'-P	8.44	1.73	1.61
8	7	67	G	C1'-N9	-7.45	1.36	1.48
8	7	2	U	C1'-N1	7.11	1.59	1.48
16	AG	246	ASP	C-N	7.02	1.50	1.33
22	H	88	LYS	N-CA	6.95	1.55	1.46
6	5	109	DT	O3'-P	6.88	1.71	1.61
18	D	145	G	O3'-P	6.72	1.71	1.61
18	D	196	A	O3'-P	6.57	1.71	1.61
22	H	168	VAL	C-N	6.38	1.42	1.33
18	D	1275	A	O3'-P	6.34	1.70	1.61
16	AG	355	ALA	N-CA	6.26	1.54	1.46
41	a	2434	A	O3'-P	6.04	1.70	1.61
16	AG	355	ALA	CA-C	5.95	1.60	1.52
18	D	1515	G	O3'-P	-5.90	1.52	1.61
18	D	1395	C	O3'-P	5.71	1.69	1.61
22	H	88	LYS	CA-C	5.69	1.60	1.52
14	AE	90	VAL	CA-C	5.60	1.60	1.52
18	D	1490	U	O3'-P	5.53	1.69	1.61
7	6	10	DG	C1'-N9	-5.35	1.35	1.46
25	K	56	VAL	CA-CB	5.34	1.57	1.54
41	a	1905	C	O3'-P	5.26	1.69	1.61
14	AE	424	ASN	CG-ND2	-5.25	1.22	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	7	18	U	C1'-N1	5.25	1.56	1.48
18	D	1492	A	O3'-P	5.24	1.69	1.61
41	a	2167	U	O3'-P	5.21	1.69	1.61
14	AE	777	HIS	CD2-NE2	-5.21	1.32	1.37
14	AE	1350	ASN	CG-ND2	-5.20	1.22	1.33
14	AE	777	HIS	ND1-CE1	5.16	1.37	1.32
16	AG	99	SER	N-CA	5.15	1.49	1.46
9	9	116	GLU	N-CA	5.12	1.49	1.46
9	9	129	LEU	C-N	5.10	1.45	1.33
14	AE	291	ILE	N-CA	5.09	1.52	1.46
14	AE	1268	ASN	CG-ND2	-5.05	1.22	1.33
14	AE	1108	GLN	CD-OE1	5.03	1.33	1.23

All (256) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	AE	291	ILE	CA-C-N	20.30	158.51	121.97
14	AE	291	ILE	C-N-CA	20.30	158.51	121.97
16	AG	104	ARG	CA-C-N	17.90	154.18	121.97
16	AG	104	ARG	C-N-CA	17.90	154.18	121.97
18	D	1516	G	O3'-P-O5'	17.52	130.27	104.00
22	H	88	LYS	CA-C-N	17.06	143.75	120.38
22	H	88	LYS	C-N-CA	17.06	143.75	120.38
10	B	29	G	C3'-C2'-O2'	16.00	134.70	110.70
9	9	129	LEU	CA-C-N	15.90	139.72	119.84
9	9	129	LEU	C-N-CA	15.90	139.72	119.84
18	D	1516	G	P-O3'-C3'	-15.59	96.82	120.20
16	AG	246	ASP	CA-C-N	14.47	137.93	119.84
16	AG	246	ASP	C-N-CA	14.47	137.93	119.84
16	AG	354	ALA	O-C-N	-13.70	107.30	122.09
22	H	332	VAL	N-CA-C	13.69	124.58	110.62
22	H	169	SER	N-CA-C	12.77	138.01	110.80
22	H	330	VAL	N-CA-C	12.16	126.89	109.51
22	H	305	HIS	N-CA-C	11.93	131.05	111.37
16	AG	429	LYS	CA-C-N	11.49	132.22	119.92
16	AG	429	LYS	C-N-CA	11.49	132.22	119.92
12	AB	122	PRO	N-CA-CB	11.37	110.38	102.65
14	AE	291	ILE	CB-CA-C	10.69	128.83	111.29
16	AG	24	PHE	CA-CB-CG	-10.58	103.22	113.80
16	AG	105	ILE	CA-C-N	10.23	136.97	120.60
16	AG	105	ILE	C-N-CA	10.23	136.97	120.60
14	AE	90	VAL	N-CA-C	9.90	122.21	107.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	a	2244	U	C1'-C2'-O2'	-9.81	93.68	108.40
54	n	73	SER	N-CA-CB	-9.62	94.50	110.47
18	D	1206	G	C4'-C3'-O3'	9.54	127.31	113.00
30	P	54	SER	CA-C-N	9.36	129.06	118.85
30	P	54	SER	C-N-CA	9.36	129.06	118.85
41	a	2250	G	C4'-C3'-O3'	-9.19	95.61	109.40
16	AG	103	ASP	CA-CB-CG	9.01	121.61	112.60
18	D	1401	G	C4'-C3'-O3'	8.74	126.11	113.00
18	D	428	G	C4'-C3'-O3'	8.70	122.45	109.40
9	9	130	PRO	CA-N-CD	-8.64	99.90	112.00
8	7	1	A	O3'-P-O5'	-8.62	91.07	104.00
22	H	339	ARG	CA-C-N	8.55	137.87	121.54
22	H	339	ARG	C-N-CA	8.55	137.87	121.54
33	S	45	VAL	N-CA-CB	8.43	120.42	110.55
41	a	2296	U	C4'-C3'-O3'	8.41	122.01	109.40
18	D	1515	G	O3'-P-O5'	-8.40	91.39	104.00
41	a	404	A	C2'-C3'-O3'	8.39	122.09	109.50
8	7	4	U	C2'-C3'-O3'	8.33	121.99	109.50
30	P	57	VAL	N-CA-C	8.28	120.03	107.77
16	AG	35	THR	CA-CB-OG1	-8.24	97.23	109.60
16	AG	292	ASP	O-C-N	-8.24	107.44	122.44
16	AG	109	THR	CB-CA-C	8.17	124.74	110.85
41	a	2252	G	N9-C1'-C2'	-8.16	99.75	112.00
18	D	197	A	C2'-C3'-O3'	8.12	121.68	109.50
16	AG	108	GLN	N-CA-CB	8.04	123.50	110.40
18	D	1401	G	N9-C1'-C2'	-7.93	100.10	112.00
41	a	2425	A	C2'-C3'-O3'	7.84	121.26	109.50
22	H	155	LYS	CA-C-N	-7.82	110.87	121.66
22	H	155	LYS	C-N-CA	-7.82	110.87	121.66
18	D	1493	A	C2'-C3'-O3'	7.74	125.31	113.70
41	a	2071	A	C4'-C3'-O3'	-7.71	101.43	113.00
14	AE	903	LEU	CA-C-N	7.65	136.15	121.54
14	AE	903	LEU	C-N-CA	7.65	136.15	121.54
22	H	84	LEU	N-CA-C	7.64	121.02	110.24
22	H	52	GLN	N-CA-C	-7.64	104.10	113.50
22	H	168	VAL	CA-C-N	7.64	136.13	121.54
22	H	168	VAL	C-N-CA	7.64	136.13	121.54
54	n	75	ALA	CA-C-N	7.62	129.67	120.14
54	n	75	ALA	C-N-CA	7.62	129.67	120.14
18	D	1339	A	P-O3'-C3'	7.61	131.62	120.20
38	X	102	THR	CB-CA-C	7.61	123.47	110.84
25	K	60	ILE	N-CA-CB	7.56	119.39	110.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	D	1499	A	N9-C1'-C2'	-7.54	100.69	112.00
16	AG	33	THR	CA-C-N	7.51	135.89	121.54
16	AG	33	THR	C-N-CA	7.51	135.89	121.54
18	D	528	C	N1-C1'-C2'	-7.50	100.75	112.00
16	AG	102	PHE	CA-C-N	7.48	135.83	121.54
16	AG	102	PHE	C-N-CA	7.48	135.83	121.54
25	K	56	VAL	O-C-N	7.44	125.18	120.42
54	n	73	SER	CB-CA-C	7.43	122.90	110.79
10	B	28	C	P-O3'-C3'	7.42	131.33	120.20
22	H	336	ASP	CB-CA-C	-7.42	98.69	110.79
21	G	47	VAL	O-C-N	7.33	125.11	120.42
16	AG	108	GLN	N-CA-C	-7.32	103.81	112.89
41	a	783	A	C4'-C3'-O3'	7.32	123.98	113.00
18	D	1497	G	C1'-C2'-O2'	-7.27	97.50	108.40
41	a	2602	A	C4'-C3'-O3'	7.24	120.26	109.40
16	AG	426	GLY	O-C-N	-7.21	113.33	122.70
54	n	108	VAL	O-C-N	7.18	125.17	120.07
10	B	29	G	N9-C1'-C2'	-7.17	101.24	112.00
41	a	896	A	C4'-C3'-O3'	7.14	120.11	109.40
18	D	196	A	P-O3'-C3'	7.10	130.85	120.20
41	a	2162	G	C4'-C3'-O3'	7.08	120.02	109.40
41	a	1379	U	C2'-C3'-O3'	7.02	124.23	113.70
41	a	2225	A	C4'-C3'-O3'	7.01	119.92	109.40
27	M	27	VAL	N-CA-CB	6.96	118.69	110.55
41	a	2244	U	C4'-C3'-O3'	6.96	123.44	113.00
22	H	140	PRO	N-CA-CB	6.93	110.53	103.25
41	a	2252	G	C4'-C3'-O3'	6.85	123.27	113.00
22	H	340	ARG	CA-C-N	-6.82	112.52	123.23
22	H	340	ARG	C-N-CA	-6.82	112.52	123.23
54	n	71	ARG	CA-C-N	6.80	134.07	122.37
54	n	71	ARG	C-N-CA	6.80	134.07	122.37
16	AG	102	PHE	N-CA-C	6.79	125.27	110.80
16	AG	104	ARG	O-C-N	6.70	131.50	122.59
18	D	517	G	C5'-C4'-C3'	6.65	125.18	115.20
22	H	170	ARG	N-CA-C	6.64	119.61	110.24
41	a	2243	U	C4'-C3'-O3'	6.64	122.97	113.00
18	D	526	C	C4'-C3'-O3'	6.61	122.92	113.00
22	H	87	GLU	N-CA-C	-6.60	104.09	111.28
22	H	303	LEU	N-CA-C	6.57	121.13	112.13
29	O	72	ILE	N-CA-C	-6.57	105.30	111.48
54	n	127	ASN	CB-CA-C	6.55	121.72	110.77
58	r	61	VAL	N-CA-CB	6.54	118.20	110.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	a	2189	U	C1'-C2'-O2'	-6.53	102.00	111.80
41	a	894	U	C2'-C3'-O3'	6.52	119.28	109.50
22	H	132	PRO	N-CA-CB	6.51	110.22	103.38
41	a	2167	U	P-O3'-C3'	6.51	129.97	120.20
22	H	112	ILE	N-CA-C	6.50	117.06	106.72
14	AE	450	HIS	CB-CG-CD2	-6.49	122.76	131.20
16	AG	106	THR	OG1-CB-CG2	-6.49	96.31	109.30
22	H	155	LYS	N-CA-C	-6.49	98.32	108.90
18	D	1340	A	C1'-C2'-O2'	6.48	118.12	108.40
18	D	526	C	N1-C1'-C2'	-6.47	102.29	112.00
55	o	13	ARG	N-CA-C	6.46	120.99	113.18
54	n	127	ASN	CA-CB-CG	-6.41	106.19	112.60
16	AG	355	ALA	CB-CA-C	6.38	123.11	110.42
41	a	754	U	N1-C1'-C2'	6.37	121.56	112.00
18	D	69	G	C4'-C3'-O3'	-6.35	103.47	113.00
16	AG	103	ASP	CA-C-N	6.34	133.65	121.54
16	AG	103	ASP	C-N-CA	6.34	133.65	121.54
14	AE	61	ILE	CA-C-N	-6.34	114.04	121.64
14	AE	61	ILE	C-N-CA	-6.34	114.04	121.64
18	D	1208	C	N1-C1'-C2'	-6.33	102.50	112.00
41	a	2434	A	P-O3'-C3'	6.31	129.67	120.20
8	7	59	U	C4'-C3'-O3'	6.29	118.84	109.40
16	AG	109	THR	N-CA-C	-6.26	104.54	111.36
14	AE	777	HIS	CB-CG-CD2	-6.25	123.08	131.20
17	C	33	ILE	CA-C-O	-6.24	114.94	121.93
22	H	153	GLU	N-CA-C	-6.24	97.52	110.80
41	a	2425	A	C4'-C3'-O3'	6.24	118.75	109.40
10	B	28	C	O3'-P-O5'	-6.20	94.70	104.00
16	AG	403	VAL	N-CA-C	-6.18	104.27	111.00
22	H	113	ASN	N-CA-C	6.14	118.05	111.36
14	AE	70	CYS	CB-CA-C	6.13	120.35	110.29
18	D	1206	G	N9-C1'-C2'	-6.13	102.80	112.00
16	AG	404	GLU	N-CA-C	-6.11	104.93	112.38
16	AG	108	GLN	CB-CA-C	-6.10	97.24	109.99
18	D	1516	G	OP1-P-O3'	-6.05	89.85	108.00
41	a	271	G	C4'-C3'-O3'	6.04	118.46	109.40
16	AG	71	PRO	N-CA-C	6.04	122.56	113.81
18	D	1408	A	C4'-C3'-O3'	6.04	122.06	113.00
41	a	2210	U	C4'-C3'-O3'	5.99	118.39	109.40
16	AG	33	THR	CA-CB-CG2	5.99	120.67	110.50
18	D	550	G	C3'-C2'-O2'	5.98	119.67	110.70
14	AE	90	VAL	CA-C-O	-5.96	114.20	120.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	a	2820	A	C4'-C3'-O3'	-5.96	104.07	113.00
41	a	1913	A	C2'-C3'-O3'	5.95	118.43	109.50
27	M	92	ARG	CA-C-N	5.94	125.42	119.24
27	M	92	ARG	C-N-CA	5.94	125.42	119.24
52	l	108	ILE	N-CA-CB	5.89	118.56	110.54
22	H	109	THR	N-CA-C	-5.88	99.07	109.06
41	a	2308	G	C2'-C3'-O3'	-5.87	104.90	113.70
38	X	26	GLY	N-CA-C	-5.84	104.30	112.13
22	H	150	LYS	N-CA-C	5.83	118.22	110.53
14	AE	291	ILE	N-CA-CB	-5.83	101.61	111.23
41	a	2756	U	C4'-C3'-O3'	5.82	118.14	109.40
22	H	75	VAL	N-CA-C	5.82	116.50	108.12
18	D	1275	A	P-O3'-C3'	5.81	128.92	120.20
54	n	72	LYS	N-CA-C	-5.80	99.20	109.06
41	a	1905	C	P-O3'-C3'	5.79	128.88	120.20
14	AE	91	GLU	N-CA-C	5.78	123.10	110.80
16	AG	66	ASP	N-CA-C	-5.78	103.97	111.71
18	D	1406	U	N1-C1'-C2'	-5.77	103.35	112.00
10	A	48	C	N1-C1'-C2'	5.76	120.64	112.00
18	D	1490	U	P-O3'-C3'	5.76	128.84	120.20
41	a	70	G	C4'-C3'-O3'	5.76	118.03	109.40
10	B	29	G	O5'-C5'-C4'	-5.75	102.87	111.50
18	D	1492	A	P-O3'-C3'	5.74	128.81	120.20
18	D	976	G	C4'-C3'-O3'	-5.74	104.39	113.00
41	a	2168	G	C4'-C3'-O3'	-5.70	104.45	113.00
10	B	48	C	N1-C1'-C2'	5.69	120.53	112.00
16	AG	220	VAL	N-CA-C	-5.68	108.32	113.71
41	a	1757	A	C4'-C3'-O3'	-5.66	104.51	113.00
14	AE	450	HIS	CB-CG-ND1	5.64	131.16	122.70
41	a	2017	U	C2'-C3'-O3'	-5.63	105.25	113.70
18	D	1340	A	C5'-C4'-C3'	5.62	124.44	116.00
16	AG	101	THR	CA-CB-OG1	5.60	118.00	109.60
22	H	114	GLY	N-CA-C	5.60	121.22	111.14
41	a	2731	G	C4'-C3'-O3'	-5.60	104.61	113.00
18	D	780	A	C4'-C3'-O3'	-5.56	104.66	113.00
41	a	1568	G	C4'-C3'-O3'	-5.51	104.73	113.00
16	AG	74	GLU	CB-CA-C	-5.51	101.65	110.14
41	a	2447	G	C2'-C3'-O3'	-5.50	101.25	109.50
14	AE	93	THR	CA-C-N	5.47	133.15	121.45
14	AE	93	THR	C-N-CA	5.47	133.15	121.45
14	AE	93	THR	CB-CA-C	5.46	121.28	110.42
16	AG	354	ALA	CA-C-N	-5.44	111.16	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	AG	354	ALA	C-N-CA	-5.44	111.16	121.54
18	D	1499	A	C4'-C3'-O3'	5.43	121.14	113.00
41	a	2572	A	C4'-C3'-O3'	-5.42	101.28	109.40
16	AG	355	ALA	N-CA-CB	5.40	119.61	110.49
14	AE	777	HIS	CB-CG-ND1	5.38	130.78	122.70
14	AE	69	GLU	CA-C-N	-5.38	113.92	121.72
14	AE	69	GLU	C-N-CA	-5.38	113.92	121.72
18	D	517	G	C4'-C3'-O3'	-5.36	101.36	109.40
41	a	944	C	C4'-C3'-O3'	-5.36	104.96	113.00
18	D	1145	A	C4'-C3'-O3'	-5.36	104.96	113.00
41	a	2068	U	C4'-C3'-O3'	-5.36	104.97	113.00
41	a	2481	G	C4'-C3'-O3'	-5.35	104.97	113.00
41	a	375	G	C2'-C3'-O3'	5.35	121.73	113.70
14	AE	70	CYS	N-CA-C	-5.35	101.06	109.25
18	D	864	A	N9-C1'-C2'	5.34	120.02	112.00
18	D	145	G	P-O3'-C3'	5.34	128.21	120.20
10	B	35	A	P-O3'-C3'	5.34	128.21	120.20
41	a	2020	A	C4'-C3'-O3'	-5.33	105.00	113.00
14	AE	90	VAL	O-C-N	-5.33	117.55	123.20
41	a	1270	C	C2'-C3'-O3'	-5.33	105.70	113.70
14	AE	73	GLY	N-CA-C	5.32	125.79	113.18
16	AG	105	ILE	N-CA-CB	-5.30	102.48	111.23
8	7	10	U	C2'-C3'-O3'	5.30	117.44	109.50
47	g	5	ILE	N-CA-C	5.29	117.66	111.05
18	D	1395	C	P-O3'-C3'	5.28	128.13	120.20
41	a	2231	U	C1'-C2'-O2'	5.26	116.30	108.40
41	a	2529	G	C4'-C3'-O3'	-5.26	105.11	113.00
61	u	101	ILE	N-CA-C	5.25	116.53	112.12
14	AE	88	CYS	N-CA-C	5.23	120.32	113.88
38	X	102	THR	CA-C-O	-5.22	114.91	121.02
10	B	60	U	C2'-C3'-O3'	5.22	117.32	109.50
10	A	60	U	C2'-C3'-O3'	5.21	117.32	109.50
41	a	479	A	C4'-C3'-O3'	5.20	117.20	109.40
39	Y	5	GLN	O-C-N	5.20	124.68	120.83
16	AG	107	THR	CA-C-N	-5.19	112.06	121.14
16	AG	107	THR	C-N-CA	-5.19	112.06	121.14
14	AE	61	ILE	CA-C-O	-5.18	115.56	120.95
41	a	1834	U	C4'-C3'-O3'	-5.17	105.24	113.00
18	D	1335	U	C4'-C3'-O3'	-5.17	105.25	113.00
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
41	a	2245	U	N1-C1'-C2'	-5.15	104.27	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	a	423	A	C2'-C3'-O3'	-5.14	105.99	113.70
16	AG	114	ILE	N-CA-C	-5.14	105.49	110.42
41	a	126	A	C4'-C3'-O3'	-5.12	105.31	113.00
41	a	528	A	C4'-C3'-O3'	-5.10	105.34	113.00
16	AG	105	ILE	O-C-N	5.10	128.95	122.57
30	P	25	ILE	N-CA-CB	5.10	117.48	110.54
16	AG	65	VAL	CA-C-N	5.08	131.66	121.81
16	AG	65	VAL	C-N-CA	5.08	131.66	121.81
14	AE	1184	ASP	N-CA-C	5.06	121.00	109.81
22	H	154	PHE	N-CA-C	-5.06	100.46	109.06
12	AB	120	ASP	CB-CA-C	-5.05	110.73	116.54
41	a	328	U	C4'-C3'-O3'	-5.03	105.45	113.00
16	AG	356	ILE	N-CA-C	-5.03	107.83	111.90
10	B	19	G	N9-C1'-C2'	5.03	119.54	112.00
41	a	2335	A	C4'-C3'-O3'	-5.02	105.47	113.00
22	H	108	VAL	N-CA-C	-5.02	98.90	109.34
16	AG	107	THR	CA-C-O	-5.02	113.21	119.18
41	a	614	A	C2'-C3'-O3'	5.02	117.02	109.50
59	s	28	LEU	CA-C-N	5.00	126.94	120.44
59	s	28	LEU	C-N-CA	5.00	126.94	120.44

There are no chirality outliers.

All (24) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	A	19	G	Sidechain
10	A	7	G	Sidechain
12	AB	44	VAL	Mainchain
13	AC	192	VAL	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	102	PHE	Peptide
16	AG	104	ARG	Mainchain,Peptide
16	AG	11	ALA	Peptide
16	AG	292	ASP	Mainchain
16	AG	426	GLY	Mainchain

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Mol	Chain	Res	Type	Group
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 [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	816	839	839	8	0
2	1	857	922	922	14	0
3	2	746	811	811	5	0
4	3	788	844	844	10	0
5	4	753	780	780	0	0
6	5	472	260	260	26	0
7	6	542	305	306	23	0
8	7	647	97	321	97	0
9	9	1117	0	1153	167	0
10	A	1620	826	826	173	0
10	B	1620	814	827	139	0
11	AA	10567	0	10584	320	0
12	AB	1276	0	1244	273	0
13	AC	1690	0	1714	16	0
13	AD	2073	0	1889	46	0
14	AE	10388	10612	10610	394	0
15	AF	650	0	658	13	0
16	AG	3852	0	3826	802	0
17	C	544	559	560	23	0
18	D	32703	16423	16459	233	0
19	E	669	719	719	3	0
20	F	589	629	629	7	0
21	G	1760	1785	1785	44	0
22	H	1730	1454	1454	208	0
23	I	1636	1710	1710	32	0
24	J	1643	1707	1707	16	0
25	K	1152	1196	1196	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	L	848	846	846	3	0
27	M	1181	1235	1235	34	0
28	N	979	1031	1031	6	0
29	O	1022	1070	1070	12	0
30	P	790	831	831	112	0
31	Q	877	887	887	4	0
32	R	939	1001	1001	8	0
33	S	805	844	844	5	0
34	T	714	734	734	8	0
35	U	649	666	666	3	0
36	V	648	691	691	4	0
37	W	663	688	688	2	0
38	X	900	964	964	55	0
39	Y	1032	0	1088	83	0
40	Z	227	0	237	20	0
41	a	61841	31077	31123	296	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	5	0
46	f	448	488	488	6	0
47	g	522	520	520	10	0
48	h	2082	2154	2154	20	0
49	i	444	459	458	6	0
50	j	1565	1617	1616	14	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	4	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	8	0
62	v	1074	1157	1157	5	0
63	w	951	994	994	8	0
64	x	892	923	923	9	0
65	y	917	962	962	4	0
66	z	947	1020	1019	12	0
67	AE	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
68	AE	2	0	0	0	0
All	All	181260	109913	132623	3318	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (3318) 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)
16:AG:425:LEU:CD2	16:AG:429:LYS:HE2	1.21	1.62
16:AG:287:ALA:CA	16:AG:331:LEU:HD12	1.19	1.62
11:AA:901:LEU:CD1	16:AG:8:VAL:HG13	1.31	1.60
22:H:131:LEU:CB	22:H:167:VAL:CA	1.78	1.57
17:C:12:ARG:HG3	22:H:264:GLU:CB	1.30	1.55
16:AG:393:LEU:CB	16:AG:398:LEU:CD2	1.83	1.54
16:AG:168:LEU:CD2	16:AG:231:GLY:HA3	1.34	1.54
16:AG:363:LEU:CD2	16:AG:410:ALA:H	1.24	1.50
16:AG:425:LEU:CA	16:AG:429:LYS:HE3	1.40	1.50
16:AG:287:ALA:CB	16:AG:331:LEU:HD12	1.41	1.50
22:H:131:LEU:CB	22:H:167:VAL:HA	1.03	1.50
16:AG:287:ALA:HA	16:AG:331:LEU:CD1	1.38	1.49
16:AG:425:LEU:HD23	16:AG:429:LYS:CE	1.45	1.46
12:AB:139:GLY:HA3	30:P:102:LEU:CD1	1.46	1.45
9:9:31:ARG:NE	41:a:1054:A:H5'	1.31	1.44
16:AG:187:ARG:HB3	16:AG:188:PRO:CD	1.45	1.43
16:AG:363:LEU:CD2	16:AG:410:ALA:N	1.82	1.41
16:AG:393:LEU:CD2	16:AG:398:LEU:CD2	1.99	1.39
9:9:130:PRO:N	9:9:130:PRO:CA	1.70	1.39
16:AG:168:LEU:HD22	16:AG:231:GLY:CA	1.49	1.38
16:AG:168:LEU:CD2	16:AG:231:GLY:CA	1.98	1.38
22:H:71:ALA:C	22:H:72:LEU:HD12	1.49	1.37
16:AG:437:LEU:HD21	16:AG:456:LEU:CD1	1.54	1.37
12:AB:173:LEU:HD11	30:P:102:LEU:CD2	1.49	1.37
16:AG:385:ALA:CB	16:AG:411:LYS:HE3	1.56	1.35
9:9:57:ASN:OD1	9:9:62:ARG:CG	1.75	1.35
11:AA:901:LEU:HD11	16:AG:8:VAL:CG1	1.55	1.35
41:a:1839:G:H1'	41:a:1927:A:C8	1.62	1.35
16:AG:393:LEU:CD2	16:AG:398:LEU:HD21	1.57	1.34
22:H:118:GLY:O	22:H:133:GLY:CA	1.74	1.34
16:AG:393:LEU:CA	16:AG:398:LEU:CD2	2.05	1.34
16:AG:387:VAL:HG12	16:AG:388:PRO:CD	1.57	1.33

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AG:393:LEU:CA	16:AG:398:LEU:HD22	1.59	1.32
8:7:14:U:H5'	23:I:132:ARG:NH1	1.40	1.31
18:D:1358:U:O4	18:D:1363:A:N1	1.60	1.31
16:AG:434:LEU:CD2	16:AG:456:LEU:HA	1.58	1.31
16:AG:434:LEU:HD22	16:AG:459:LEU:CD1	1.58	1.31
41:a:1021:A:N1	41:a:1141:U:O4	1.63	1.31
11:AA:854:ILE:N	16:AG:105:ILE:HG23	1.44	1.29
13:AD:285:THR:CB	16:AG:82:TYR:CE1	2.14	1.29
16:AG:448:LEU:HD21	16:AG:473:LEU:CD1	1.61	1.29
9:9:31:ARG:CZ	41:a:1054:A:H5'	1.63	1.28
16:AG:363:LEU:HD23	16:AG:410:ALA:N	1.38	1.28
16:AG:393:LEU:CG	16:AG:398:LEU:HD21	1.63	1.27
18:D:1308:U:H3'	38:X:98:ARG:CZ	1.43	1.27
12:AB:65:PHE:CE2	12:AB:111:ILE:HD11	1.70	1.27
16:AG:434:LEU:HA	16:AG:456:LEU:CD2	1.64	1.26
18:D:1308:U:H2'	38:X:98:ARG:NH2	1.48	1.26
11:AA:849:GLU:HG2	16:AG:104:ARG:NH1	1.45	1.26
16:AG:425:LEU:HA	16:AG:429:LYS:CE	1.64	1.26
16:AG:287:ALA:CA	16:AG:331:LEU:CD1	2.02	1.26
11:AA:858:GLY:H	11:AA:861:ALA:CB	1.49	1.25
10:A:32:C:O4'	27:M:144:MET:HE1	1.09	1.25
16:AG:353:HIS:O	16:AG:356:ILE:HG23	1.13	1.25
16:AG:387:VAL:CG1	16:AG:388:PRO:HD2	1.67	1.25
16:AG:393:LEU:HB3	16:AG:398:LEU:CD2	1.51	1.25
16:AG:355:ALA:CB	16:AG:382:GLU:CD	2.10	1.24
17:C:12:ARG:CG	22:H:264:GLU:CB	2.15	1.24
6:5:100:DA:OP1	12:AB:16:SER:O	1.56	1.23
11:AA:853:ASP:C	16:AG:105:ILE:HG23	1.64	1.23
12:AB:165:PHE:N	30:P:88:MET:HG3	1.52	1.23
16:AG:355:ALA:HA	16:AG:382:GLU:OE2	1.37	1.23
10:A:18:G:N7	10:A:57:A:N6	1.87	1.23
16:AG:353:HIS:C	16:AG:356:ILE:HG23	1.62	1.22
18:D:1227:A:OP2	38:X:110:LYS:HE3	1.35	1.22
16:AG:355:ALA:HB2	16:AG:382:GLU:OE1	1.40	1.22
9:9:88:HIS:HB3	9:9:89:PRO:CD	1.70	1.22
22:H:267:TRP:CZ2	22:H:340:ARG:HG2	1.75	1.22
16:AG:433:ASP:O	16:AG:456:LEU:HD11	1.35	1.21
12:AB:140:PRO:CD	30:P:102:LEU:HB2	1.70	1.21
12:AB:167:ARG:NE	23:I:61:ALA:O	1.73	1.21
16:AG:123:ARG:NH1	16:AG:191:ARG:C	1.98	1.21
16:AG:287:ALA:CB	16:AG:331:LEU:CD1	2.16	1.21

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:18:G:N7	10:B:57:A:N6	1.87	1.21
6:5:100:DA:OP1	12:AB:16:SER:OG	1.58	1.21
16:AG:363:LEU:HD23	16:AG:409:ARG:C	1.63	1.21
16:AG:362:TYR:O	16:AG:413:ALA:HB2	1.35	1.21
18:D:563:A:N1	18:D:884:U:O4	1.73	1.21
12:AB:23:ALA:HB2	12:AB:44:VAL:CG2	1.70	1.20
12:AB:139:GLY:CA	30:P:102:LEU:HD13	1.70	1.20
18:D:948:C:OP2	38:X:105:ASN:OD1	1.53	1.20
12:AB:19:GLU:O	12:AB:44:VAL:HG11	1.37	1.20
16:AG:425:LEU:CG	16:AG:429:LYS:HE2	1.69	1.20
18:D:1308:U:C2'	38:X:98:ARG:NH2	2.03	1.20
11:AA:849:GLU:CG	16:AG:104:ARG:HH11	1.55	1.19
16:AG:442:ARG:O	16:AG:446:PHE:CD2	1.95	1.19
16:AG:393:LEU:HD22	16:AG:398:LEU:CD1	1.73	1.19
12:AB:65:PHE:CD2	12:AB:111:ILE:HD11	1.78	1.19
21:G:19:GLN:CD	22:H:76:GLU:HB3	1.67	1.18
22:H:118:GLY:O	22:H:133:GLY:HA3	1.27	1.18
16:AG:353:HIS:O	16:AG:357:ASP:N	1.77	1.17
9:9:31:ARG:NE	41:a:1054:A:C5'	2.07	1.17
16:AG:437:LEU:CD2	16:AG:456:LEU:HD13	1.74	1.16
16:AG:393:LEU:HA	16:AG:398:LEU:CD2	1.69	1.16
16:AG:381:LEU:HA	16:AG:384:LEU:HD12	1.21	1.15
16:AG:434:LEU:HA	16:AG:456:LEU:HD21	1.25	1.15
9:9:57:ASN:OD1	9:9:62:ARG:HG3	1.44	1.15
11:AA:859:GLU:O	11:AA:863:SER:HB3	1.46	1.15
16:AG:355:ALA:HB1	16:AG:382:GLU:CG	1.77	1.14
11:AA:853:ASP:OD1	16:AG:105:ILE:HG21	1.47	1.14
16:AG:123:ARG:HH12	16:AG:191:ARG:CA	1.36	1.14
17:C:44:ILE:HD13	22:H:339:ARG:CG	1.78	1.14
16:AG:393:LEU:HD22	16:AG:398:LEU:CD2	1.71	1.14
16:AG:355:ALA:HA	16:AG:382:GLU:CD	1.71	1.14
16:AG:393:LEU:CB	16:AG:398:LEU:HD21	1.58	1.13
22:H:135:LEU:CB	22:H:167:VAL:CB	2.27	1.13
22:H:119:GLY:HA2	22:H:133:GLY:HA2	1.15	1.13
16:AG:285:ILE:HG23	16:AG:293:VAL:HG12	1.25	1.13
12:AB:173:LEU:CD1	30:P:102:LEU:HD23	1.79	1.13
12:AB:173:LEU:CD1	30:P:102:LEU:CD2	2.26	1.12
22:H:267:TRP:CE2	22:H:340:ARG:HG2	1.84	1.12
16:AG:393:LEU:CD2	16:AG:398:LEU:CD1	2.27	1.12
18:D:1329:A:OP1	38:X:28:THR:HB	1.47	1.12
10:A:32:C:O4'	27:M:144:MET:CE	1.97	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AG:285:ILE:CG1	16:AG:293:VAL:HG11	1.79	1.12
10:A:70:G:H2'	10:A:71:C:H5''	1.22	1.12
12:AB:155:LYS:HB2	18:D:1277:C:OP2	1.48	1.12
16:AG:123:ARG:NH1	16:AG:191:ARG:O	1.80	1.12
10:B:70:G:H2'	10:B:71:C:H5''	1.23	1.12
16:AG:424:SER:O	16:AG:429:LYS:HG2	1.47	1.11
13:AD:285:THR:CB	16:AG:82:TYR:CD1	2.32	1.11
30:P:87:LEU:HD23	30:P:100:ILE:HD13	1.32	1.11
12:AB:140:PRO:HD3	30:P:102:LEU:HB2	1.32	1.11
16:AG:422:GLU:HA	16:AG:426:GLY:CA	1.79	1.11
16:AG:425:LEU:HA	16:AG:429:LYS:CG	1.80	1.11
9:9:142:THR:HG21	40:Z:7:ILE:HG12	1.21	1.11
16:AG:430:PRO:HG2	16:AG:435:LEU:HD21	1.29	1.11
16:AG:393:LEU:HD22	16:AG:398:LEU:HD21	1.26	1.10
12:AB:23:ALA:HB2	12:AB:44:VAL:HG21	1.25	1.10
16:AG:279:ASN:OD1	16:AG:280:PRO:HD3	1.50	1.10
16:AG:353:HIS:O	16:AG:356:ILE:CG2	1.99	1.10
11:AA:909:LYS:HD3	11:AA:909:LYS:H	1.16	1.10
12:AB:19:GLU:HG2	12:AB:44:VAL:HG13	1.20	1.10
8:7:59:U:O2	11:AA:1253:LEU:HD12	1.48	1.10
11:AA:858:GLY:H	11:AA:861:ALA:HB3	1.12	1.10
12:AB:23:ALA:HB2	12:AB:44:VAL:CB	1.81	1.10
16:AG:363:LEU:HD21	16:AG:410:ALA:H	0.94	1.10
16:AG:425:LEU:CD2	16:AG:429:LYS:CE	2.13	1.10
16:AG:434:LEU:CD2	16:AG:459:LEU:HD12	1.81	1.10
22:H:267:TRP:CH2	22:H:340:ARG:HG2	1.87	1.10
12:AB:66:PRO:HG2	14:AE:281:ARG:NH2	1.66	1.09
16:AG:451:ARG:NH1	16:AG:467:LEU:HA	1.68	1.09
12:AB:165:PHE:CZ	30:P:91:ASP:HA	1.88	1.09
16:AG:393:LEU:HB3	16:AG:398:LEU:HD23	1.26	1.09
16:AG:425:LEU:HA	16:AG:429:LYS:HG3	1.33	1.09
18:D:1308:U:C2'	38:X:98:ARG:HH21	1.63	1.09
41:a:1839:G:C8	41:a:1927:A:H1'	1.87	1.09
18:D:1308:U:C3'	38:X:98:ARG:CZ	2.30	1.08
16:AG:187:ARG:HB3	16:AG:188:PRO:HD2	1.21	1.08
17:C:44:ILE:HD13	22:H:339:ARG:HG2	1.18	1.08
9:9:50:VAL:HG22	39:Y:119:ALA:CB	1.82	1.08
16:AG:181:GLY:HA2	16:AG:204:MET:SD	1.92	1.08
16:AG:385:ALA:HB1	16:AG:411:LYS:HE3	1.35	1.08
24:J:162:ALA:HA	24:J:165:ARG:CZ	1.83	1.08
16:AG:123:ARG:HH12	16:AG:191:ARG:C	1.57	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AG:451:ARG:HH12	16:AG:467:LEU:C	1.62	1.08
9:9:88:HIS:CB	9:9:89:PRO:HD3	1.82	1.07
16:AG:442:ARG:O	16:AG:446:PHE:HD2	1.34	1.07
18:D:1308:U:C3'	38:X:98:ARG:NH2	2.16	1.07
11:AA:913:VAL:HG21	16:AG:108:GLN:NE2	1.56	1.07
12:AB:165:PHE:HA	30:P:88:MET:O	1.53	1.07
16:AG:393:LEU:HD22	16:AG:398:LEU:HD11	1.28	1.07
12:AB:155:LYS:NZ	18:D:1278:G:OP2	1.88	1.07
11:AA:857:VAL:HG12	11:AA:861:ALA:CB	1.84	1.06
13:AC:232:VAL:C	13:AD:221:ALA:HB3	1.80	1.06
21:G:19:GLN:CG	22:H:75:VAL:HG22	1.84	1.06
12:AB:138:ASP:HB3	12:AB:177:GLN:HA	1.37	1.06
16:AG:434:LEU:HD21	16:AG:456:LEU:HA	1.26	1.06
22:H:71:ALA:O	22:H:72:LEU:HD12	1.54	1.06
8:7:3:G:H5''	18:D:1500:A:N6	1.70	1.06
12:AB:125:LYS:HG2	12:AB:153:TYR:HB2	1.30	1.06
14:AE:24:LEU:HG	14:AE:232:ASN:HD21	1.17	1.06
16:AG:385:ALA:CB	16:AG:411:LYS:CE	2.33	1.06
16:AG:434:LEU:CD2	16:AG:456:LEU:CA	2.33	1.06
16:AG:187:ARG:HB3	16:AG:188:PRO:HD3	1.32	1.05
8:7:14:U:C5'	23:I:132:ARG:HH12	1.68	1.05
16:AG:365:ILE:HD13	16:AG:406:LEU:HD22	1.37	1.05
21:G:19:GLN:CD	22:H:76:GLU:CB	2.19	1.05
11:AA:848:GLU:HG2	11:AA:888:THR:HG22	1.14	1.05
16:AG:285:ILE:HG23	16:AG:293:VAL:CG1	1.87	1.05
16:AG:365:ILE:HD13	16:AG:406:LEU:CD2	1.85	1.05
16:AG:434:LEU:HD23	16:AG:456:LEU:HD23	1.10	1.05
9:9:129:LEU:N	9:9:130:PRO:HD3	1.66	1.05
10:B:18:G:N2	10:B:55:U:O2	1.90	1.05
12:AB:140:PRO:HD2	30:P:102:LEU:HD13	1.32	1.05
16:AG:363:LEU:HG	16:AG:410:ALA:HB2	1.37	1.05
12:AB:165:PHE:CE1	30:P:91:ASP:HA	1.92	1.04
16:AG:285:ILE:HG13	16:AG:293:VAL:CG1	1.86	1.04
22:H:19:ARG:O	22:H:72:LEU:HB2	1.57	1.04
10:A:18:G:N2	10:A:55:U:O2	1.90	1.04
11:AA:887:VAL:HG21	11:AA:913:VAL:HG22	1.33	1.04
16:AG:302:LYS:H	16:AG:302:LYS:HE3	1.16	1.04
21:G:19:GLN:HG3	22:H:75:VAL:HG22	1.38	1.04
10:B:56:C:O4'	54:n:80:ARG:NH2	1.91	1.04
8:7:11:U:O2'	25:K:33:PHE:CE1	2.11	1.04
11:AA:854:ILE:HG12	11:AA:855:PRO:CD	1.89	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:128:PHE:HB2	12:AB:180:LYS:HB2	1.36	1.03
18:D:1227:A:OP2	38:X:110:LYS:CE	2.06	1.03
12:AB:11:VAL:HG23	12:AB:103:ILE:HD11	1.39	1.03
16:AG:434:LEU:HD23	16:AG:456:LEU:HA	1.34	1.03
11:AA:1313:HIS:CD2	15:AF:31:GLN:HE22	1.75	1.03
16:AG:422:GLU:HA	16:AG:426:GLY:HA3	1.33	1.03
9:9:129:LEU:H	9:9:130:PRO:HD3	0.90	1.03
10:A:56:C:H2'	10:A:57:A:H5''	1.39	1.03
16:AG:168:LEU:HD22	16:AG:231:GLY:HA2	1.40	1.03
16:AG:168:LEU:HD21	16:AG:231:GLY:CA	1.83	1.03
16:AG:387:VAL:HG12	16:AG:388:PRO:HD2	1.06	1.03
16:AG:434:LEU:HD21	16:AG:456:LEU:CA	1.89	1.03
16:AG:437:LEU:CD2	16:AG:456:LEU:CD1	2.34	1.03
12:AB:155:LYS:NZ	18:D:1277:C:H3'	1.71	1.03
16:AG:187:ARG:CB	16:AG:188:PRO:CD	2.37	1.03
16:AG:361:LYS:HE2	16:AG:417:ILE:HG12	1.39	1.02
22:H:162:LYS:CB	22:H:298:GLU:CD	2.30	1.02
12:AB:155:LYS:HZ1	18:D:1277:C:C3'	1.72	1.02
16:AG:422:GLU:HA	16:AG:426:GLY:N	1.74	1.02
16:AG:448:LEU:CD2	16:AG:473:LEU:CD1	2.36	1.02
10:B:56:C:H2'	10:B:57:A:H5''	1.39	1.02
12:AB:154:GLU:O	18:D:1276:G:OP2	1.75	1.02
16:AG:355:ALA:HB1	16:AG:382:GLU:HG3	1.41	1.02
11:AA:549:ASP:OD2	14:AE:750:PRO:HB3	1.60	1.02
22:H:290:TYR:O	22:H:305:HIS:O	1.77	1.02
11:AA:857:VAL:HG12	11:AA:861:ALA:HB1	1.03	1.02
16:AG:287:ALA:HA	16:AG:331:LEU:HD11	1.41	1.02
16:AG:363:LEU:HD23	16:AG:409:ARG:CA	1.89	1.02
16:AG:425:LEU:CG	16:AG:429:LYS:CE	2.34	1.01
16:AG:425:LEU:C	16:AG:429:LYS:HE3	1.84	1.01
10:A:70:G:C2'	10:A:71:C:H5''	1.89	1.01
16:AG:393:LEU:CG	16:AG:398:LEU:CD2	2.30	1.01
12:AB:140:PRO:HD2	30:P:102:LEU:CD1	1.91	1.01
12:AB:155:LYS:HZ1	18:D:1277:C:H3'	1.25	1.01
14:AE:111:THR:HG23	14:AE:300:GLN:CD	1.86	1.01
16:AG:365:ILE:CG2	16:AG:409:ARG:NH1	2.23	1.01
16:AG:131:ARG:O	16:AG:134:GLU:HG3	1.61	1.01
16:AG:393:LEU:HD23	16:AG:398:LEU:HD22	1.43	1.00
30:P:17:LEU:HD21	30:P:93:ALA:CB	1.90	1.00
16:AG:123:ARG:NH1	16:AG:191:ARG:CA	2.11	1.00
10:B:56:C:H5'	54:n:80:ARG:CZ	1.90	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:70:G:C2'	10:B:71:C:H5''	1.89	1.00
21:G:38:VAL:CG2	22:H:75:VAL:HG21	1.90	1.00
16:AG:361:LYS:CE	16:AG:417:ILE:HG12	1.90	1.00
18:D:1329:A:OP1	38:X:28:THR:CB	2.07	1.00
41:a:2297:A:N1	41:a:2321:U:C4	2.29	1.00
18:D:13:U:O4	18:D:20:U:O4	1.79	1.00
11:AA:854:ILE:HG12	11:AA:855:PRO:HD2	1.39	1.00
16:AG:168:LEU:HD21	16:AG:231:GLY:N	1.76	1.00
16:AG:287:ALA:HB2	16:AG:331:LEU:CD1	1.92	1.00
21:G:38:VAL:HG22	22:H:75:VAL:HG21	1.44	1.00
9:9:93:ALA:O	9:9:129:LEU:HD12	1.60	1.00
18:D:13:U:N3	18:D:915:A:C6	2.29	1.00
13:AD:308:ALA:CB	16:AG:96:GLN:HB3	1.92	0.99
16:AG:362:TYR:O	16:AG:413:ALA:CB	2.10	0.99
16:AG:434:LEU:HD23	16:AG:456:LEU:CD2	1.91	0.99
16:AG:363:LEU:CD2	16:AG:409:ARG:HB2	1.91	0.99
16:AG:434:LEU:CD2	16:AG:456:LEU:HD23	1.92	0.99
22:H:131:LEU:CB	22:H:167:VAL:CB	2.40	0.99
11:AA:901:LEU:CD1	16:AG:8:VAL:CG1	2.28	0.99
12:AB:140:PRO:CD	30:P:102:LEU:CB	2.41	0.99
11:AA:849:GLU:HB2	11:AA:887:VAL:CG1	1.93	0.99
16:AG:393:LEU:HD22	16:AG:398:LEU:CG	1.93	0.99
8:7:14:U:C5'	23:I:132:ARG:NH1	2.26	0.98
41:a:1839:G:C1'	41:a:1927:A:C8	2.47	0.98
10:A:32:C:C4'	27:M:144:MET:HE1	1.93	0.98
11:AA:1268:GLN:NE2	14:AE:352:ARG:HD2	1.78	0.98
12:AB:165:PHE:H	30:P:88:MET:HA	1.27	0.98
16:AG:168:LEU:HD21	16:AG:230:PRO:C	1.89	0.98
13:AC:232:VAL:C	13:AD:221:ALA:CB	2.37	0.97
11:AA:1313:HIS:HD2	15:AF:31:GLN:HE22	0.99	0.97
16:AG:393:LEU:CD2	16:AG:398:LEU:HD11	1.90	0.97
10:A:32:C:O2'	27:M:86:GLN:CG	2.12	0.97
16:AG:387:VAL:HG12	16:AG:388:PRO:HD3	1.47	0.97
9:9:31:ARG:CD	41:a:1054:A:H5'	1.94	0.97
16:AG:424:SER:O	16:AG:429:LYS:CG	2.13	0.97
11:AA:853:ASP:C	16:AG:105:ILE:CG2	2.38	0.97
16:AG:393:LEU:CA	16:AG:398:LEU:HD23	1.88	0.97
22:H:119:GLY:CA	22:H:133:GLY:HA2	1.95	0.96
16:AG:279:ASN:CG	16:AG:280:PRO:CD	2.38	0.96
12:AB:64:PHE:HB2	14:AE:285:LEU:HD21	1.46	0.96
16:AG:285:ILE:HG13	16:AG:293:VAL:HG11	1.45	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:9:142:THR:HG21	40:Z:7:ILE:CG1	1.95	0.96
11:AA:895:LEU:HD23	11:AA:895:LEU:H	1.29	0.96
16:AG:380:THR:O	16:AG:384:LEU:CD1	2.13	0.96
16:AG:433:ASP:O	16:AG:456:LEU:CD1	2.13	0.96
41:a:1839:G:O4'	41:a:1927:A:O4'	1.82	0.96
12:AB:140:PRO:CD	30:P:102:LEU:HD13	1.96	0.96
8:7:2:U:P	18:D:1505:G:H8	1.87	0.96
16:AG:214:PRO:O	16:AG:218:GLU:OE2	1.83	0.96
8:7:14:U:H5'	23:I:132:ARG:HH12	1.01	0.96
9:9:129:LEU:H	9:9:130:PRO:CD	1.77	0.96
10:A:72:A:H2'	10:A:73:A:H5''	1.48	0.95
16:AG:228:ARG:HA	16:AG:327:LEU:HD11	1.46	0.95
11:AA:900:LYS:HZ2	16:AG:11:ALA:CB	1.78	0.95
6:5:100:DA:P	12:AB:16:SER:HG	1.90	0.95
12:AB:19:GLU:O	12:AB:44:VAL:CG1	2.13	0.95
16:AG:123:ARG:HH12	16:AG:191:ARG:HA	1.32	0.95
16:AG:336:LEU:HD12	16:AG:336:LEU:H	1.26	0.95
18:D:1308:U:H3'	38:X:98:ARG:NH2	1.76	0.95
16:AG:258:ARG:HH11	16:AG:258:ARG:HG2	1.31	0.95
16:AG:451:ARG:NH1	16:AG:467:LEU:CA	2.30	0.95
16:AG:440:VAL:CG2	16:AG:481:LEU:HD22	1.97	0.94
12:AB:141:PHE:CE2	12:AB:171:VAL:HG11	2.02	0.94
16:AG:355:ALA:HB2	16:AG:382:GLU:CD	1.83	0.94
7:6:15:DC:N4	7:6:16:DC:N4	2.15	0.94
11:AA:887:VAL:CG2	11:AA:913:VAL:HG22	1.97	0.94
12:AB:128:PHE:CZ	12:AB:178:VAL:HG21	2.00	0.94
18:D:1308:U:H2'	38:X:98:ARG:HH21	1.06	0.94
30:P:17:LEU:HD21	30:P:93:ALA:HB1	1.49	0.94
22:H:135:LEU:HA	22:H:157:ILE:CB	1.98	0.94
16:AG:365:ILE:CD1	16:AG:406:LEU:HD22	1.97	0.94
22:H:118:GLY:O	22:H:133:GLY:HA2	1.63	0.94
9:9:50:VAL:HG22	39:Y:119:ALA:HB1	1.50	0.94
16:AG:240:THR:OG1	16:AG:247:PRO:HG3	1.68	0.94
18:D:13:U:C4	18:D:915:A:N6	2.36	0.94
41:a:67:U:N3	41:a:74:A:C6	2.35	0.94
11:AA:900:LYS:NZ	16:AG:11:ALA:CB	2.31	0.94
16:AG:425:LEU:CA	16:AG:429:LYS:CE	2.30	0.94
11:AA:900:LYS:NZ	16:AG:11:ALA:HB1	1.82	0.93
41:a:1839:G:O4'	41:a:1927:A:C1'	2.16	0.93
10:A:32:C:O2'	27:M:86:GLN:HG3	1.68	0.93
16:AG:123:ARG:CZ	16:AG:191:ARG:O	2.17	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:H:119:GLY:HA3	22:H:131:LEU:O	1.68	0.93
11:AA:901:LEU:CG	16:AG:8:VAL:HG13	1.98	0.93
14:AE:68:TYR:O	14:AE:75:TYR:CE2	2.20	0.93
16:AG:168:LEU:HD22	16:AG:231:GLY:HA3	1.00	0.93
16:AG:393:LEU:HA	16:AG:398:LEU:HD22	0.95	0.93
11:AA:853:ASP:OD2	16:AG:103:ASP:HB2	1.69	0.93
16:AG:363:LEU:HG	16:AG:410:ALA:CB	1.97	0.93
11:AA:858:GLY:H	11:AA:861:ALA:HB2	1.34	0.93
13:AD:308:ALA:CB	16:AG:96:GLN:CB	2.34	0.93
16:AG:363:LEU:CG	16:AG:410:ALA:HB2	1.99	0.93
18:D:13:U:N3	18:D:915:A:N6	2.16	0.93
9:9:57:ASN:OD1	9:9:62:ARG:HG2	1.64	0.93
30:P:87:LEU:CD2	30:P:100:ILE:HD13	1.99	0.93
10:B:72:A:H2'	10:B:73:A:H5''	1.49	0.93
16:AG:174:ARG:HB3	16:AG:175:PRO:HD2	1.51	0.92
16:AG:448:LEU:HD21	16:AG:473:LEU:HD11	1.48	0.92
10:B:75:C:OP1	41:a:2602:A:C8	2.22	0.92
16:AG:451:ARG:NH1	16:AG:466:ASP:O	2.02	0.92
12:AB:65:PHE:CE2	12:AB:111:ILE:CD1	2.51	0.92
16:AG:171:GLU:OE2	16:AG:267:GLY:HA3	1.68	0.92
41:a:2013:A:N6	41:a:2613:U:H3	1.68	0.92
16:AG:279:ASN:CG	16:AG:280:PRO:HD3	1.93	0.92
16:AG:448:LEU:HD21	16:AG:473:LEU:HD13	1.48	0.92
11:AA:641:GLU:OE2	14:AE:749:LYS:NZ	2.03	0.92
16:AG:385:ALA:HB3	16:AG:411:LYS:CE	2.00	0.92
16:AG:393:LEU:HD23	16:AG:398:LEU:CD2	1.93	0.92
9:9:88:HIS:HB3	9:9:89:PRO:HD3	0.93	0.92
12:AB:139:GLY:CA	30:P:102:LEU:CD1	2.36	0.91
12:AB:165:PHE:N	30:P:88:MET:HA	1.82	0.91
16:AG:363:LEU:HD22	16:AG:409:ARG:HB2	1.53	0.91
16:AG:425:LEU:HA	16:AG:429:LYS:CD	2.01	0.91
16:AG:422:GLU:HA	16:AG:426:GLY:H	1.34	0.91
16:AG:434:LEU:HD21	16:AG:455:THR:O	1.69	0.91
12:AB:140:PRO:HD2	30:P:102:LEU:CG	2.00	0.91
10:A:56:C:H1'	41:a:2112:G:C6	2.06	0.91
11:AA:858:GLY:N	11:AA:861:ALA:CB	2.33	0.91
16:AG:183:LEU:HG	16:AG:197:VAL:HG13	1.51	0.91
41:a:1406:U:O2'	41:a:1407:G:C5'	2.19	0.91
14:AE:136:GLU:OE1	14:AE:312:ARG:NH1	2.04	0.91
16:AG:453:VAL:HG13	16:AG:458:ASP:CB	2.00	0.91
8:7:2:U:P	18:D:1505:G:C8	2.64	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:857:VAL:CG1	11:AA:861:ALA:HB1	1.97	0.90
16:AG:363:LEU:HD23	16:AG:409:ARG:CB	2.00	0.90
8:7:4:U:O2'	18:D:1403:C:O2	1.87	0.90
11:AA:900:LYS:HZ2	16:AG:11:ALA:HB3	1.36	0.90
16:AG:200:SER:O	16:AG:230:PRO:HG2	1.71	0.90
10:A:68:C:H2'	10:A:69:C:H5''	1.51	0.90
14:AE:24:LEU:HB2	14:AE:232:ASN:OD1	1.71	0.90
22:H:71:ALA:C	22:H:72:LEU:CD1	2.42	0.90
41:a:2314:A:H1'	54:n:155:THR:HG21	1.54	0.90
16:AG:434:LEU:HD22	16:AG:459:LEU:HD12	0.93	0.90
13:AD:285:THR:CB	16:AG:82:TYR:HE1	1.72	0.90
10:B:18:G:N2	10:B:58:A:N7	2.19	0.90
10:A:18:G:N2	10:A:58:A:N7	2.19	0.90
12:AB:128:PHE:CE1	12:AB:178:VAL:CG2	2.55	0.90
10:B:68:C:H2'	10:B:69:C:H5''	1.51	0.90
16:AG:434:LEU:HA	16:AG:456:LEU:HD23	1.53	0.90
18:D:13:U:C4	18:D:20:U:O4	2.24	0.90
12:AB:167:ARG:HG2	12:AB:167:ARG:HH21	1.35	0.90
16:AG:240:THR:OG1	16:AG:247:PRO:CG	2.20	0.89
22:H:279:LYS:HA	22:H:331:MET:HB3	1.54	0.89
8:7:3:G:C5'	18:D:1500:A:H62	1.85	0.89
16:AG:365:ILE:HG21	16:AG:409:ARG:NH1	1.87	0.89
16:AG:453:VAL:HG23	16:AG:462:GLN:NE2	1.87	0.89
30:P:87:LEU:HD23	30:P:100:ILE:CD1	2.02	0.89
9:9:93:ALA:O	9:9:129:LEU:CD1	2.19	0.89
14:AE:68:TYR:C	14:AE:75:TYR:HE2	1.80	0.89
16:AG:425:LEU:CA	16:AG:429:LYS:HG3	2.02	0.89
6:5:114:DC:H5''	14:AE:1148:ARG:NH2	1.87	0.89
39:Y:104:GLN:HG2	39:Y:108:ILE:HD11	1.53	0.89
11:AA:848:GLU:HG2	11:AA:888:THR:CG2	2.03	0.89
11:AA:913:VAL:CG2	16:AG:108:GLN:NE2	2.10	0.89
9:9:129:LEU:N	9:9:130:PRO:CD	2.34	0.89
12:AB:65:PHE:HD1	14:AE:285:LEU:HD23	1.38	0.89
14:AE:202:ARG:HG2	14:AE:202:ARG:HH11	1.35	0.89
16:AG:422:GLU:CA	16:AG:426:GLY:HA3	2.02	0.89
11:AA:855:PRO:CB	16:AG:109:THR:HG21	2.02	0.89
11:AA:857:VAL:HG11	11:AA:862:LEU:HD12	1.53	0.89
12:AB:128:PHE:HB2	12:AB:180:LYS:CB	2.02	0.89
11:AA:1313:HIS:HD2	15:AF:31:GLN:NE2	1.71	0.88
16:AG:302:LYS:HE3	16:AG:302:LYS:N	1.87	0.88
16:AG:363:LEU:HG	16:AG:410:ALA:CA	2.04	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:9:142:THR:CG2	40:Z:7:ILE:HG12	2.03	0.88
12:AB:167:ARG:CZ	23:I:61:ALA:O	2.20	0.88
12:AB:95:GLY:O	14:AE:162:GLU:CD	2.16	0.88
12:AB:165:PHE:H	30:P:88:MET:HG3	1.32	0.88
11:AA:857:VAL:HG11	11:AA:862:LEU:CD1	2.04	0.88
16:AG:355:ALA:HB1	16:AG:382:GLU:CD	1.94	0.88
16:AG:434:LEU:HD21	16:AG:455:THR:C	1.97	0.88
39:Y:21:PRO:HB2	39:Y:22:PRO:HD3	1.54	0.88
12:AB:11:VAL:HG23	12:AB:103:ILE:CD1	2.03	0.88
12:AB:23:ALA:CB	12:AB:44:VAL:HG21	2.04	0.88
16:AG:434:LEU:HD23	16:AG:456:LEU:CA	2.00	0.88
21:G:18:HIS:HA	22:H:43:LYS:HD2	1.55	0.88
9:9:50:VAL:CG2	39:Y:119:ALA:HB3	2.04	0.88
12:AB:140:PRO:CB	30:P:6:ILE:HD11	2.04	0.88
16:AG:362:TYR:C	16:AG:413:ALA:HB2	1.99	0.88
22:H:162:LYS:N	22:H:298:GLU:OE2	2.06	0.88
17:C:31:ASN:OD1	22:H:268:VAL:HG22	1.74	0.87
12:AB:140:PRO:HD2	30:P:102:LEU:CB	2.03	0.87
16:AG:302:LYS:O	16:AG:302:LYS:NZ	2.08	0.87
12:AB:173:LEU:HD11	30:P:102:LEU:HD23	0.88	0.87
22:H:119:GLY:HA2	22:H:133:GLY:CA	2.01	0.87
41:a:783:A:N3	41:a:783:A:H2'	1.89	0.87
12:AB:44:VAL:HG22	12:AB:69:VAL:HG13	1.56	0.87
16:AG:141:VAL:HG22	16:AG:178:ARG:HG2	1.57	0.87
16:AG:61:ARG:HD3	16:AG:63:LEU:HD21	1.57	0.87
22:H:131:LEU:CB	22:H:167:VAL:N	2.37	0.87
11:AA:913:VAL:HG21	16:AG:108:GLN:HE21	1.36	0.87
30:P:17:LEU:CD2	30:P:93:ALA:HB3	2.03	0.87
16:AG:171:GLU:CD	16:AG:267:GLY:HA3	1.99	0.86
12:AB:167:ARG:NH1	23:I:62:LYS:O	2.07	0.86
22:H:348:GLN:N	22:H:348:GLN:OE1	2.08	0.86
10:A:33:U:H5''	27:M:84:THR:HG21	1.55	0.86
12:AB:19:GLU:HG2	12:AB:44:VAL:CG1	2.04	0.86
12:AB:103:ILE:HD12	12:AB:107:GLU:CD	2.00	0.86
12:AB:128:PHE:CZ	12:AB:178:VAL:CG2	2.58	0.86
16:AG:385:ALA:HB3	16:AG:411:LYS:HE3	1.57	0.86
16:AG:453:VAL:HG13	16:AG:458:ASP:HB2	1.55	0.86
12:AB:11:VAL:CG2	12:AB:103:ILE:HD11	2.03	0.86
16:AG:248:VAL:HG13	16:AG:273:ILE:HB	1.56	0.86
12:AB:136:VAL:HG22	12:AB:178:VAL:HG12	1.57	0.86
14:AE:425:ARG:NH1	14:AE:458:ASN:O	2.08	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:34:VAL:HG13	4:3:67:VAL:HG22	1.58	0.86
24:J:162:ALA:HB2	24:J:165:ARG:NH2	1.90	0.86
11:AA:858:GLY:O	11:AA:861:ALA:N	2.07	0.86
12:AB:128:PHE:CE2	12:AB:134:VAL:HG11	2.11	0.86
12:AB:155:LYS:NZ	18:D:1278:G:P	2.48	0.86
16:AG:362:TYR:C	16:AG:413:ALA:CB	2.48	0.86
47:g:16:CYS:CB	47:g:37:CYS:HB3	2.05	0.85
10:A:16:C:O2	41:a:2181:U:H5'	1.76	0.85
16:AG:168:LEU:HD23	16:AG:231:GLY:HA3	1.56	0.85
16:AG:254:MET:HA	16:AG:254:MET:HE3	1.55	0.85
16:AG:434:LEU:HD12	16:AG:454:CYS:O	1.75	0.85
12:AB:173:LEU:HD11	30:P:102:LEU:HD21	1.57	0.85
9:9:125:ARG:NH1	9:9:125:ARG:HA	1.92	0.85
14:AE:24:LEU:HG	14:AE:232:ASN:ND2	1.90	0.85
16:AG:355:ALA:CA	16:AG:382:GLU:CD	2.49	0.85
10:A:18:G:N7	10:A:57:A:C6	2.44	0.85
16:AG:387:VAL:CB	16:AG:388:PRO:HD2	2.06	0.85
16:AG:448:LEU:CD2	16:AG:473:LEU:HD11	2.05	0.85
24:J:61:VAL:HG21	24:J:200:ILE:HD11	1.57	0.85
13:AD:308:ALA:HB2	16:AG:96:GLN:CB	1.77	0.85
16:AG:210:ARG:HG3	16:AG:216:ILE:HB	1.59	0.85
18:D:197:A:C6	18:D:221:C:H4'	2.11	0.85
9:9:52:MET:C	9:9:52:MET:HE3	2.00	0.85
11:AA:854:ILE:HG13	11:AA:887:VAL:HB	1.58	0.85
16:AG:430:PRO:HG2	16:AG:435:LEU:CD2	2.05	0.85
39:Y:81:LYS:O	39:Y:81:LYS:HE3	1.75	0.85
41:a:67:U:N3	41:a:74:A:N6	2.25	0.85
12:AB:141:PHE:CZ	12:AB:171:VAL:HG11	2.12	0.84
12:AB:167:ARG:HH11	23:I:62:LYS:C	1.84	0.84
16:AG:425:LEU:HA	16:AG:429:LYS:HE3	0.95	0.84
22:H:267:TRP:CD2	22:H:340:ARG:HG2	2.12	0.84
9:9:31:ARG:CD	41:a:1054:A:H4'	2.06	0.84
22:H:267:TRP:CZ3	22:H:340:ARG:HG2	2.12	0.84
12:AB:167:ARG:HE	23:I:61:ALA:C	1.85	0.84
14:AE:68:TYR:HB3	14:AE:75:TYR:OH	1.77	0.84
39:Y:60:VAL:HG13	39:Y:66:PHE:HB3	1.58	0.84
22:H:135:LEU:CB	22:H:167:VAL:C	2.50	0.84
22:H:267:TRP:CH2	22:H:340:ARG:CG	2.61	0.84
12:AB:155:LYS:HZ2	18:D:1278:G:P	1.99	0.84
11:AA:855:PRO:HB3	16:AG:109:THR:CG2	2.06	0.84
22:H:332:VAL:HG11	22:H:335:ILE:HG13	1.58	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AG:287:ALA:HA	16:AG:331:LEU:HD12	0.87	0.84
16:AG:365:ILE:CG2	16:AG:409:ARG:HH12	1.91	0.84
10:B:18:G:N7	10:B:57:A:C6	2.44	0.84
41:a:2303:G:C2	41:a:2314:A:C2	2.66	0.84
14:AE:26:SER:HB2	14:AE:236:TRP:CZ2	2.12	0.84
22:H:131:LEU:CB	22:H:166:VAL:O	2.26	0.84
12:AB:96:THR:HB	14:AE:162:GLU:HG3	1.60	0.84
11:AA:848:GLU:CG	11:AA:888:THR:HG22	2.06	0.84
16:AG:187:ARG:CB	16:AG:188:PRO:HD2	2.03	0.84
12:AB:133:MET:H	12:AB:133:MET:HE2	1.42	0.83
16:AG:425:LEU:HG	16:AG:429:LYS:CE	2.08	0.83
16:AG:213:VAL:HG11	16:AG:251:CYS:HA	1.59	0.83
16:AG:365:ILE:HG21	16:AG:409:ARG:HH12	1.42	0.83
16:AG:486:ARG:O	16:AG:490:TRP:HD1	1.58	0.83
10:B:56:C:H5'	54:n:80:ARG:NE	1.93	0.83
13:AD:308:ALA:HB2	16:AG:96:GLN:HB3	1.54	0.83
16:AG:285:ILE:CG2	16:AG:293:VAL:HG12	2.06	0.83
9:9:31:ARG:CZ	41:a:1054:A:C5'	2.49	0.83
16:AG:243:LYS:HB3	16:AG:245:ILE:HD11	1.60	0.83
18:D:1227:A:H5'	38:X:110:LYS:NZ	1.93	0.83
11:AA:849:GLU:HB2	11:AA:887:VAL:HG12	1.59	0.83
12:AB:165:PHE:H	30:P:88:MET:CA	1.91	0.83
16:AG:287:ALA:HB2	16:AG:331:LEU:HD13	1.58	0.83
21:G:16:PHE:HB3	22:H:43:LYS:HA	1.60	0.83
8:7:2:U:OP1	18:D:1505:G:C8	2.32	0.83
9:9:31:ARG:CD	41:a:1054:A:C4'	2.57	0.83
9:9:57:ASN:OD1	9:9:62:ARG:CD	2.27	0.83
16:AG:12:VAL:HB	16:AG:16:LYS:HG3	1.61	0.83
16:AG:127:VAL:CG2	16:AG:192:GLY:HA2	2.09	0.83
16:AG:433:ASP:C	16:AG:456:LEU:HG	2.03	0.83
39:Y:102:ARG:HB3	39:Y:141:ASP:HA	1.61	0.83
9:9:31:ARG:HH11	9:9:31:ARG:HG3	1.41	0.83
12:AB:23:ALA:HB2	12:AB:44:VAL:HB	1.58	0.83
7:6:18:DC:H42	8:7:65:G:H1	1.27	0.83
16:AG:279:ASN:CG	16:AG:280:PRO:HD2	2.03	0.83
41:a:1406:U:O2'	41:a:1407:G:H5''	1.79	0.83
8:7:2:U:OP1	18:D:1505:G:H8	1.62	0.82
14:AE:68:TYR:O	14:AE:75:TYR:HE2	1.58	0.82
16:AG:362:TYR:HA	16:AG:413:ALA:CB	2.09	0.82
9:9:88:HIS:CB	9:9:89:PRO:CD	2.41	0.82
10:A:68:C:C2'	10:A:69:C:H5''	2.08	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:P:17:LEU:CD2	30:P:93:ALA:CB	2.58	0.82
41:a:1019:U:H3	41:a:1142:A:N6	1.77	0.82
8:7:2:U:OP2	18:D:1505:G:C8	2.32	0.82
9:9:28:ALA:H	9:9:110:ALA:HA	1.44	0.82
16:AG:354:ALA:HA	16:AG:357:ASP:HB3	1.60	0.82
16:AG:381:LEU:CA	16:AG:384:LEU:HD12	2.08	0.82
10:A:72:A:C2'	10:A:73:A:H5''	2.08	0.82
14:AE:141:PHE:HE2	14:AE:296:LYS:HB2	1.44	0.82
16:AG:203:GLU:HA	16:AG:206:ILE:HG12	1.60	0.82
17:C:12:ARG:HH22	22:H:268:VAL:CG2	1.91	0.82
16:AG:451:ARG:HH11	16:AG:467:LEU:HA	1.42	0.82
7:6:21:DA:N1	8:7:63:G:N2	2.26	0.82
25:K:111:MET:HE2	25:K:125:ALA:HB1	1.59	0.82
10:B:68:C:C2'	10:B:69:C:H5''	2.08	0.82
22:H:305:HIS:CD2	22:H:306:VAL:H	1.98	0.82
16:AG:285:ILE:CG2	16:AG:293:VAL:CG1	2.57	0.82
10:B:54:U:H3	10:B:58:A:N6	1.78	0.82
10:B:72:A:C2'	10:B:73:A:H5''	2.09	0.82
39:Y:20:SER:HB3	39:Y:21:PRO:HD3	1.59	0.82
16:AG:353:HIS:CA	16:AG:356:ILE:HG23	2.10	0.82
16:AG:361:LYS:CD	16:AG:417:ILE:HG12	2.10	0.82
9:9:43:LYS:HD2	9:9:43:LYS:C	2.05	0.82
12:AB:11:VAL:CG2	12:AB:103:ILE:CD1	2.58	0.82
10:A:56:C:C2'	10:A:57:A:H5''	2.10	0.81
16:AG:380:THR:O	16:AG:384:LEU:HD11	1.80	0.81
41:a:1021:A:N6	41:a:1141:U:H3	1.77	0.81
9:9:3:LEU:HD13	9:9:5:LEU:HG	1.61	0.81
16:AG:133:HIS:ND1	16:AG:136:GLU:OE1	2.13	0.81
14:AE:1169:THR:OG1	14:AE:1192:LYS:NZ	2.13	0.81
16:AG:285:ILE:CB	16:AG:293:VAL:HG11	2.09	0.81
9:9:62:ARG:HG2	9:9:62:ARG:HH21	1.44	0.81
16:AG:434:LEU:CG	16:AG:455:THR:C	2.54	0.81
41:a:1839:G:C1'	41:a:1927:A:N9	2.43	0.81
16:AG:393:LEU:HB3	16:AG:398:LEU:HD21	1.25	0.81
18:D:972:C:O2'	30:P:57:VAL:CG2	2.29	0.81
11:AA:855:PRO:HB2	16:AG:109:THR:HG21	1.62	0.81
22:H:155:LYS:CB	22:H:169:SER:CB	2.58	0.81
12:AB:23:ALA:CB	12:AB:44:VAL:HB	2.10	0.81
12:AB:165:PHE:N	30:P:88:MET:CG	2.41	0.81
10:B:76:A:H1'	41:a:2494:G:P	2.20	0.81
18:D:37:U:N3	18:D:397:A:N6	2.28	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:H:267:TRP:CZ3	22:H:340:ARG:CG	2.63	0.81
16:AG:430:PRO:CG	16:AG:435:LEU:HD21	2.11	0.81
39:Y:27:LEU:HD12	39:Y:27:LEU:O	1.81	0.81
41:a:585:G:N7	66:z:6:ARG:NH1	2.29	0.81
8:7:3:G:C5'	18:D:1500:A:N6	2.42	0.81
16:AG:425:LEU:HD23	16:AG:429:LYS:HE2	0.81	0.81
24:J:162:ALA:CA	24:J:165:ARG:NH2	2.44	0.81
39:Y:72:THR:OG1	39:Y:73:PRO:HD2	1.81	0.81
13:AD:308:ALA:HB1	16:AG:96:GLN:HB3	1.61	0.81
54:n:125:ARG:O	54:n:127:ASN:ND2	2.14	0.81
9:9:50:VAL:CG2	39:Y:119:ALA:CB	2.59	0.80
10:A:54:U:H3	10:A:58:A:N6	1.78	0.80
14:AE:144:TYR:HE1	14:AE:162:GLU:OE2	1.64	0.80
16:AG:287:ALA:HB1	16:AG:331:LEU:HD12	1.62	0.80
10:B:22:G:H2'	10:B:23:C:C6	2.16	0.80
10:B:56:C:C2'	10:B:57:A:H5''	2.11	0.80
8:7:3:G:H5''	18:D:1500:A:H62	1.40	0.80
10:A:58:A:O2'	10:A:59:A:H3'	1.81	0.80
12:AB:140:PRO:CB	30:P:84:VAL:HG21	2.10	0.80
14:AE:141:PHE:CE2	14:AE:296:LYS:HB2	2.15	0.80
16:AG:226:ALA:HA	16:AG:236:ILE:HG13	1.61	0.80
16:AG:451:ARG:NE	16:AG:470:ILE:HG13	1.95	0.80
22:H:122:VAL:O	22:H:129:ALA:N	2.13	0.80
10:A:7:G:H4'	10:A:8:U:OP1	1.81	0.80
14:AE:37:GLU:O	14:AE:61:ILE:HD11	1.82	0.80
16:AG:252:VAL:HA	16:AG:259:VAL:HG23	1.61	0.80
16:AG:362:TYR:HA	16:AG:413:ALA:HB1	1.62	0.80
17:C:12:ARG:CB	22:H:264:GLU:CB	2.59	0.80
7:6:21:DA:N1	8:7:63:G:C2	2.49	0.80
12:AB:125:LYS:CG	12:AB:153:TYR:HB2	2.10	0.80
12:AB:173:LEU:CD1	30:P:102:LEU:HD21	2.08	0.80
11:AA:853:ASP:CA	16:AG:105:ILE:CG2	2.59	0.80
41:a:2298:A:C4	41:a:2321:U:C5	2.70	0.80
10:A:18:G:N2	10:A:58:A:C5	2.50	0.80
11:AA:855:PRO:CB	16:AG:109:THR:CG2	2.59	0.80
16:AG:425:LEU:HG	16:AG:429:LYS:CD	2.10	0.80
11:AA:808:ASN:H	14:AE:633:ALA:HB2	1.44	0.80
16:AG:133:HIS:HD1	16:AG:136:GLU:CD	1.90	0.80
24:J:162:ALA:HA	24:J:165:ARG:NH2	1.95	0.80
41:a:2297:A:N1	41:a:2321:U:O4	2.14	0.80
12:AB:139:GLY:HA3	30:P:102:LEU:HD13	0.83	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:148:VAL:HB	12:AB:160:VAL:HG22	1.63	0.80
14:AE:90:VAL:HG13	14:AE:90:VAL:O	1.81	0.80
16:AG:425:LEU:CA	16:AG:429:LYS:CG	2.60	0.80
18:D:1397:C:OP1	18:D:1397:C:H2'	1.81	0.80
22:H:270:ILE:CG2	22:H:337:GLU:HB3	2.12	0.80
24:J:162:ALA:CB	24:J:165:ARG:NH2	2.44	0.80
9:9:78:GLY:N	9:9:79:PRO:HD2	1.97	0.80
16:AG:189:GLU:HB3	16:AG:194:GLN:HG3	1.64	0.80
47:g:18:CYS:HB3	47:g:40:CYS:CB	2.12	0.80
16:AG:365:ILE:CD1	16:AG:406:LEU:CD2	2.57	0.79
16:AG:440:VAL:CG2	16:AG:481:LEU:CD2	2.60	0.79
9:9:31:ARG:CD	41:a:1054:A:C5'	2.58	0.79
9:9:39:THR:HA	9:9:42:ARG:HD2	1.64	0.79
22:H:123:GLU:HA	22:H:128:ARG:HA	1.63	0.79
9:9:3:LEU:H	9:9:3:LEU:HD12	1.47	0.79
11:AA:858:GLY:N	11:AA:861:ALA:HB2	1.96	0.79
10:B:58:A:O2'	10:B:59:A:H3'	1.82	0.79
47:g:16:CYS:HB2	47:g:37:CYS:HB3	1.63	0.79
12:AB:23:ALA:CB	12:AB:44:VAL:CG2	2.59	0.79
12:AB:64:PHE:HA	12:AB:66:PRO:HD3	1.64	0.79
16:AG:437:LEU:HD21	16:AG:456:LEU:HD13	0.81	0.79
16:AG:451:ARG:NH2	16:AG:470:ILE:HG13	1.97	0.79
10:B:7:G:H4'	10:B:8:U:OP1	1.81	0.79
41:a:2189:U:OP1	41:a:2189:U:O4'	2.00	0.79
16:AG:235:LYS:HD3	16:AG:327:LEU:HG	1.65	0.79
10:B:18:G:N2	10:B:58:A:C5	2.51	0.79
21:G:19:GLN:OE1	22:H:75:VAL:O	1.85	0.79
11:AA:858:GLY:N	11:AA:861:ALA:HB3	1.94	0.79
13:AD:309:SER:CB	16:AG:40:GLU:OE1	2.31	0.79
18:D:1329:A:P	38:X:28:THR:HB	2.22	0.79
16:AG:381:LEU:HA	16:AG:384:LEU:CD1	2.09	0.79
50:j:4:LEU:HD23	50:j:29:VAL:HG11	1.65	0.79
11:AA:900:LYS:HD2	16:AG:11:ALA:HB1	1.65	0.79
10:A:22:G:H2'	10:A:23:C:C6	2.16	0.79
14:AE:111:THR:HG23	14:AE:300:GLN:OE1	1.81	0.79
8:7:21:U:OP1	23:I:80:LYS:HA	1.81	0.79
41:a:1406:U:O2'	41:a:1407:G:O5'	2.01	0.79
10:A:76:A:H2'	41:a:2394:C:H42	1.47	0.78
16:AG:363:LEU:CG	16:AG:410:ALA:N	2.45	0.78
9:9:31:ARG:HD2	41:a:1054:A:H4'	1.62	0.78
12:AB:43:MET:HG2	12:AB:115:LEU:HD22	1.66	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:66:PRO:HG2	14:AE:281:ARG:HH22	1.48	0.78
16:AG:393:LEU:CD2	16:AG:398:LEU:CG	2.58	0.78
16:AG:451:ARG:NH1	16:AG:467:LEU:C	2.40	0.78
39:Y:32:VAL:HG13	39:Y:60:VAL:HG21	1.65	0.78
16:AG:379:SER:OG	16:AG:384:LEU:HD21	1.81	0.78
16:AG:412:ASN:O	16:AG:416:THR:HG23	1.84	0.78
14:AE:186:GLN:HG3	14:AE:238:ILE:HG13	1.65	0.78
14:AE:1075:ARG:NH2	14:AE:1168:GLU:OE2	2.17	0.78
16:AG:434:LEU:CD2	16:AG:456:LEU:N	2.46	0.78
11:AA:888:THR:HB	11:AA:889:PRO:HD2	1.65	0.78
16:AG:402:THR:O	16:AG:405:ALA:HB3	1.84	0.78
12:AB:114:ARG:HE	12:AB:114:ARG:C	1.91	0.78
12:AB:140:PRO:CG	30:P:6:ILE:HD11	2.13	0.78
16:AG:233:ARG:HB2	16:AG:327:LEU:HD23	1.66	0.78
10:A:18:G:C5	10:A:57:A:C6	2.72	0.78
16:AG:447:LYS:O	16:AG:470:ILE:CD1	2.31	0.78
21:G:19:GLN:CD	22:H:76:GLU:HB2	2.08	0.78
24:J:162:ALA:HB2	24:J:165:ARG:HH22	1.47	0.78
30:P:17:LEU:HD21	30:P:93:ALA:HB3	1.62	0.78
41:a:1019:U:H3	41:a:1142:A:H61	1.28	0.78
10:A:15:G:N1	10:A:20:U:O2	2.17	0.77
10:B:5:G:H2'	10:B:6:G:H5'	1.66	0.77
22:H:19:ARG:HD3	22:H:73:ASP:CG	2.09	0.77
16:AG:354:ALA:HA	16:AG:357:ASP:CB	2.14	0.77
22:H:162:LYS:CA	22:H:298:GLU:OE2	2.17	0.77
16:AG:385:ALA:HB1	16:AG:411:LYS:CE	2.04	0.77
18:D:1358:U:C4	18:D:1363:A:N1	2.52	0.77
21:G:16:PHE:CZ	22:H:41:GLY:O	2.37	0.77
41:a:2756:U:N3	41:a:2758:A:N6	2.32	0.77
11:AA:618:GLN:HG3	14:AE:770:LEU:HD13	1.64	0.77
10:B:70:G:H2'	10:B:71:C:C5'	2.11	0.77
12:AB:135:ARG:HG2	12:AB:135:ARG:HH11	1.50	0.77
10:B:18:G:C5	10:B:57:A:C6	2.72	0.77
11:AA:853:ASP:OD1	16:AG:105:ILE:CG2	2.20	0.77
16:AG:425:LEU:HD23	16:AG:429:LYS:NZ	1.99	0.77
12:AB:165:PHE:H	30:P:88:MET:CG	1.95	0.77
16:AG:353:HIS:C	16:AG:356:ILE:CG2	2.50	0.77
39:Y:74:PRO:HG2	39:Y:77:VAL:HB	1.67	0.77
7:6:15:DC:C4	7:6:16:DC:N4	2.53	0.77
11:AA:894:GLN:NE2	11:AA:894:GLN:O	2.17	0.77
12:AB:64:PHE:HB2	14:AE:285:LEU:CD2	2.15	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:64:PHE:CB	14:AE:285:LEU:HD21	2.15	0.77
12:AB:165:PHE:CA	30:P:88:MET:HA	2.14	0.77
16:AG:434:LEU:HD11	16:AG:455:THR:O	1.85	0.77
10:B:15:G:N1	10:B:20:U:O2	2.17	0.77
12:AB:165:PHE:CE1	30:P:91:ASP:CA	2.67	0.77
10:A:68:C:C3'	10:A:69:C:H5''	2.15	0.76
11:AA:909:LYS:HD3	11:AA:909:LYS:N	1.87	0.76
12:AB:23:ALA:CB	12:AB:44:VAL:CB	2.63	0.76
10:B:68:C:C3'	10:B:69:C:H5''	2.15	0.76
41:a:1021:A:H61	41:a:1141:U:H3	1.29	0.76
41:a:1406:U:O2'	41:a:1407:G:P	2.41	0.76
41:a:2756:U:N3	41:a:2758:A:C6	2.53	0.76
14:AE:123:ARG:HG3	14:AE:1337:VAL:HG11	1.67	0.76
10:A:33:U:O3'	27:M:84:THR:OG1	2.02	0.76
16:AG:354:ALA:O	16:AG:356:ILE:N	2.18	0.76
16:AG:451:ARG:CZ	16:AG:470:ILE:HG13	2.16	0.76
16:AG:354:ALA:O	16:AG:355:ALA:C	2.26	0.76
9:9:11:ILE:HD11	9:9:62:ARG:HA	1.65	0.76
10:A:5:G:H2'	10:A:6:G:H5'	1.66	0.76
12:AB:125:LYS:HG2	12:AB:153:TYR:CB	2.11	0.76
16:AG:240:THR:CG2	16:AG:247:PRO:HG3	2.16	0.76
16:AG:283:PHE:CZ	16:AG:331:LEU:O	2.39	0.76
16:AG:284:VAL:HG12	16:AG:296:ILE:HD13	1.66	0.76
16:AG:434:LEU:CD2	16:AG:455:THR:C	2.58	0.76
16:AG:434:LEU:CA	16:AG:456:LEU:HD21	2.12	0.76
9:9:60:LEU:HD23	9:9:64:VAL:HG21	1.67	0.76
11:AA:894:GLN:HE21	11:AA:894:GLN:H	1.32	0.76
11:AA:903:ARG:CB	11:AA:903:ARG:HH11	1.99	0.76
12:AB:140:PRO:HB2	30:P:84:VAL:CG2	2.16	0.76
16:AG:201:LYS:HD2	16:AG:201:LYS:N	2.01	0.76
16:AG:307:ILE:HB	16:AG:338:VAL:HA	1.66	0.76
16:AG:313:ASN:N	16:AG:313:ASN:OD1	2.19	0.76
9:9:31:ARG:NE	41:a:1054:A:C4'	2.48	0.76
16:AG:371:THR:O	16:AG:375:GLU:HG3	1.86	0.76
9:9:97:LYS:HD3	9:9:127:ALA:HA	1.68	0.75
12:AB:155:LYS:HE2	18:D:1277:C:P	2.26	0.75
16:AG:425:LEU:O	16:AG:429:LYS:HE3	1.87	0.75
22:H:305:HIS:CD2	22:H:306:VAL:N	2.53	0.75
11:AA:853:ASP:OD2	16:AG:103:ASP:C	2.29	0.75
13:AD:308:ALA:O	16:AG:96:GLN:OE1	1.96	0.75
16:AG:131:ARG:HA	16:AG:186:VAL:HG11	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:G:35:ARG:HD2	22:H:14:LYS:HD3	1.66	0.75
12:AB:65:PHE:CD1	14:AE:285:LEU:HD23	2.21	0.75
14:AE:202:ARG:HG2	14:AE:202:ARG:NH1	1.99	0.75
16:AG:365:ILE:HG23	16:AG:409:ARG:HH11	1.52	0.75
12:AB:19:GLU:CG	12:AB:44:VAL:HG13	2.09	0.75
18:D:197:A:N6	18:D:221:C:H4'	2.01	0.75
16:AG:354:ALA:C	16:AG:356:ILE:H	1.93	0.75
16:AG:385:ALA:HB3	16:AG:411:LYS:HE2	1.69	0.75
64:x:31:THR:O	64:x:102:ARG:NH1	2.19	0.75
7:6:18:DC:N3	8:7:65:G:N2	2.31	0.75
11:AA:903:ARG:NH1	11:AA:903:ARG:O	2.20	0.75
16:AG:228:ARG:HD2	16:AG:236:ILE:HB	1.68	0.75
41:a:1021:A:N1	41:a:1141:U:C4	2.55	0.75
9:9:52:MET:HG3	9:9:95:LEU:HD11	1.68	0.75
22:H:109:THR:HA	22:H:153:GLU:HA	1.69	0.75
47:g:18:CYS:CB	47:g:40:CYS:HB3	2.16	0.75
11:AA:857:VAL:CG1	11:AA:862:LEU:CD1	2.65	0.75
14:AE:110:PRO:HG2	14:AE:183:GLU:HG3	1.68	0.75
22:H:131:LEU:CB	22:H:166:VAL:C	2.60	0.75
12:AB:44:VAL:CG2	12:AB:69:VAL:HG13	2.15	0.74
16:AG:451:ARG:HH12	16:AG:467:LEU:CA	1.92	0.74
17:C:44:ILE:HD13	22:H:339:ARG:HG3	1.69	0.74
16:AG:336:LEU:HD12	16:AG:336:LEU:N	2.01	0.74
16:AG:393:LEU:CD2	16:AG:398:LEU:HD22	1.90	0.74
12:AB:155:LYS:CE	18:D:1277:C:O5'	2.34	0.74
16:AG:62:TRP:HB3	16:AG:75:ILE:HD11	1.69	0.74
16:AG:248:VAL:HG22	16:AG:273:ILE:HG22	1.68	0.74
21:G:35:ARG:HG3	22:H:10:GLU:OE2	1.87	0.74
25:K:137:VAL:O	25:K:140:THR:OG1	2.04	0.74
14:AE:44:ILE:HD12	14:AE:252:LEU:CD2	2.18	0.74
16:AG:219:GLU:HA	16:AG:219:GLU:OE2	1.87	0.74
39:Y:85:ILE:H	39:Y:85:ILE:HD12	1.52	0.74
41:a:2298:A:C4	41:a:2321:U:H5	2.04	0.74
10:B:70:G:C3'	10:B:71:C:H5''	2.17	0.74
22:H:304:VAL:HG12	22:H:309:MET:SD	2.28	0.74
16:AG:365:ILE:HG23	16:AG:409:ARG:NH1	2.02	0.74
10:B:6:G:O2'	10:B:7:G:O5'	2.05	0.74
18:D:1228:C:OP1	38:X:107:ARG:NH1	2.21	0.74
14:AE:395:LYS:HZ2	14:AE:399:LYS:CD	2.00	0.74
14:AE:1143:ASP:OD1	14:AE:1148:ARG:NH1	2.21	0.74
21:G:19:GLN:CG	22:H:76:GLU:HB2	2.18	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:H:110:GLY:CA	22:H:153:GLU:O	2.36	0.74
6:5:115:DA:OP1	14:AE:1148:ARG:NE	2.21	0.74
10:A:41:C:O4'	27:M:143:ARG:NH1	2.20	0.74
12:AB:165:PHE:CZ	30:P:91:ASP:HB2	2.23	0.74
16:AG:258:ARG:HG2	16:AG:258:ARG:NH1	1.99	0.74
10:A:41:C:H1'	27:M:143:ARG:HH12	1.52	0.74
16:AG:354:ALA:C	16:AG:356:ILE:N	2.43	0.74
10:B:18:G:H1'	10:B:58:A:C2	2.23	0.74
8:7:62:U:H4'	14:AE:322:ARG:CD	2.18	0.74
16:AG:363:LEU:CD1	16:AG:410:ALA:HB2	2.17	0.74
16:AG:393:LEU:C	16:AG:398:LEU:HD23	2.12	0.74
16:AG:451:ARG:HE	16:AG:470:ILE:HG13	1.51	0.74
39:Y:36:GLU:OE1	39:Y:36:GLU:HA	1.87	0.74
9:9:27:VAL:HG23	9:9:83:ALA:HB3	1.67	0.73
10:A:18:G:H1'	10:A:58:A:C2	2.23	0.73
10:A:70:G:C3'	10:A:71:C:H5''	2.17	0.73
11:AA:855:PRO:HB3	16:AG:109:THR:HG21	1.67	0.73
14:AE:120:LEU:O	14:AE:1330:ARG:NH1	2.21	0.73
14:AE:211:GLU:HG2	14:AE:215:LYS:HE3	1.70	0.73
16:AG:425:LEU:CB	16:AG:429:LYS:HE3	2.16	0.73
16:AG:486:ARG:O	16:AG:490:TRP:CD1	2.41	0.73
4:3:36:VAL:HG11	4:3:39:ILE:HD12	1.68	0.73
9:9:78:GLY:N	9:9:79:PRO:CD	2.50	0.73
10:B:76:A:H1'	41:a:2494:G:OP1	1.88	0.73
12:AB:140:PRO:HG3	30:P:6:ILE:HD11	1.69	0.73
16:AG:285:ILE:HG13	16:AG:293:VAL:HG13	1.71	0.73
12:AB:103:ILE:HD12	12:AB:107:GLU:OE2	1.87	0.73
14:AE:157:GLN:OE1	14:AE:157:GLN:HA	1.89	0.73
16:AG:429:LYS:H	16:AG:429:LYS:HD2	1.53	0.73
10:B:76:A:H2'	10:B:76:A:N3	2.02	0.73
16:AG:297:VAL:HG23	16:AG:306:ASP:HB2	1.70	0.73
18:D:517:G:O2'	18:D:530:G:H4'	1.88	0.73
12:AB:165:PHE:CZ	30:P:91:ASP:CA	2.69	0.73
14:AE:68:TYR:C	14:AE:75:TYR:CE2	2.65	0.73
16:AG:425:LEU:HG	16:AG:429:LYS:HE2	1.66	0.73
22:H:19:ARG:HB2	22:H:73:ASP:OD2	1.88	0.73
22:H:109:THR:CA	22:H:153:GLU:HA	2.18	0.73
10:A:6:G:O2'	10:A:7:G:O5'	2.05	0.73
10:A:18:G:O2'	10:A:60:U:C2	2.41	0.73
16:AG:434:LEU:HD21	16:AG:456:LEU:N	2.03	0.73
41:a:1913:A:OP2	41:a:1913:A:H3'	1.89	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AG:434:LEU:HG	16:AG:455:THR:C	2.14	0.73
22:H:267:TRP:CE3	22:H:340:ARG:CG	2.72	0.72
10:A:33:U:H5''	27:M:84:THR:CG2	2.19	0.72
11:AA:849:GLU:HG2	16:AG:104:ARG:HH11	0.66	0.72
12:AB:133:MET:HE2	12:AB:133:MET:N	2.05	0.72
12:AB:155:LYS:CB	18:D:1277:C:OP2	2.33	0.72
16:AG:223:ILE:O	16:AG:223:ILE:HD13	1.89	0.72
16:AG:403:VAL:HG22	16:AG:406:LEU:HD12	1.71	0.72
16:AG:413:ALA:O	16:AG:416:THR:OG1	2.05	0.72
10:B:18:G:O2'	10:B:60:U:C2	2.41	0.72
30:P:102:LEU:HG	30:P:102:LEU:O	1.89	0.72
7:6:21:DA:C6	8:7:63:G:N2	2.58	0.72
9:9:18:VAL:HA	9:9:86:MET:HE2	1.71	0.72
14:AE:210:SER:HB3	14:AE:213:LYS:HB2	1.70	0.72
17:C:44:ILE:CD1	22:H:339:ARG:CG	2.62	0.72
8:7:9:U:N3	18:D:1196:A:C8	2.57	0.72
18:D:827:U:H3	18:D:872:A:N6	1.87	0.72
41:a:67:U:C4	41:a:74:A:N6	2.57	0.72
41:a:1839:G:C1'	41:a:1927:A:C1'	2.67	0.72
11:AA:853:ASP:OD2	16:AG:103:ASP:CB	2.36	0.72
12:AB:167:ARG:HG2	12:AB:167:ARG:NH2	2.04	0.72
14:AE:44:ILE:HD12	14:AE:252:LEU:HD21	1.71	0.72
16:AG:365:ILE:CG2	16:AG:409:ARG:HH11	2.01	0.72
10:A:32:C:C1'	27:M:144:MET:HE1	2.17	0.72
12:AB:140:PRO:HB2	30:P:84:VAL:HG21	1.71	0.72
16:AG:262:VAL:HA	16:AG:265:GLU:HB2	1.72	0.72
10:B:46:G:H1'	10:B:47:U:C5	2.25	0.72
22:H:70:VAL:HA	22:H:85:SER:CB	2.19	0.72
6:5:100:DA:OP1	12:AB:16:SER:C	2.33	0.72
11:AA:901:LEU:HD11	16:AG:8:VAL:HG13	0.73	0.72
16:AG:167:MET:HE1	16:AG:199:ARG:HG3	1.72	0.72
16:AG:254:MET:HA	16:AG:254:MET:CE	2.17	0.72
9:9:77:VAL:HG12	9:9:82:ILE:HG21	1.71	0.72
10:A:46:G:H1'	10:A:47:U:C5	2.25	0.72
16:AG:279:ASN:CB	16:AG:280:PRO:CD	2.66	0.72
16:AG:365:ILE:HD13	16:AG:406:LEU:HD21	1.70	0.72
16:AG:442:ARG:HB3	16:AG:446:PHE:HE2	1.53	0.72
10:B:72:A:C3'	10:B:73:A:H5''	2.20	0.72
12:AB:164:ILE:HA	30:P:88:MET:SD	2.30	0.71
14:AE:107:LEU:HD11	14:AE:242:LEU:HB2	1.70	0.71
16:AG:220:VAL:O	16:AG:240:THR:HG22	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:O:84:THR:HG21	29:O:103:PHE:HB3	1.71	0.71
10:A:70:G:H2'	10:A:71:C:C5'	2.11	0.71
11:AA:864:LYS:HE3	11:AA:877:VAL:HG12	1.70	0.71
14:AE:105:ILE:HD12	14:AE:242:LEU:HD22	1.71	0.71
14:AE:142:GLU:HG3	14:AE:142:GLU:O	1.89	0.71
16:AG:352:ALA:O	16:AG:356:ILE:HG22	1.90	0.71
16:AG:393:LEU:CD2	16:AG:398:LEU:HD13	2.19	0.71
17:C:12:ARG:HB2	22:H:264:GLU:CB	2.19	0.71
18:D:1308:U:C3'	38:X:98:ARG:HH21	1.92	0.71
16:AG:422:GLU:CB	16:AG:426:GLY:HA3	2.21	0.71
8:7:9:U:O4	18:D:1196:A:N9	2.24	0.71
12:AB:139:GLY:HA3	30:P:102:LEU:HD11	1.67	0.71
16:AG:198:THR:HB	16:AG:201:LYS:HD3	1.70	0.71
16:AG:433:ASP:C	16:AG:456:LEU:CG	2.64	0.71
10:A:72:A:C3'	10:A:73:A:H5''	2.20	0.71
11:AA:65:ASN:HB3	11:AA:105:TYR:HB2	1.73	0.71
12:AB:164:ILE:HD11	12:AB:169:THR:HB	1.72	0.71
14:AE:220:ARG:HG2	14:AE:220:ARG:HH11	1.55	0.71
47:g:18:CYS:CB	47:g:40:CYS:CB	2.68	0.71
16:AG:389:MET:O	16:AG:404:GLU:OE2	2.09	0.71
16:AG:355:ALA:CB	16:AG:382:GLU:CG	2.54	0.71
22:H:267:TRP:CE3	22:H:340:ARG:HG2	2.25	0.71
38:X:96:PRO:HG2	38:X:102:THR:CG2	2.21	0.71
16:AG:393:LEU:CB	16:AG:398:LEU:HD23	1.80	0.70
16:AG:393:LEU:HD23	16:AG:398:LEU:CD1	2.19	0.70
41:a:742:A:H2'	41:a:743:A:C8	2.26	0.70
12:AB:138:ASP:HB3	12:AB:177:GLN:CA	2.18	0.70
16:AG:127:VAL:HG22	16:AG:192:GLY:C	2.15	0.70
16:AG:362:TYR:CA	16:AG:413:ALA:CB	2.69	0.70
10:B:18:G:C5	10:B:57:A:N6	2.59	0.70
18:D:1308:U:O5'	38:X:98:ARG:HG3	1.90	0.70
10:A:18:G:C5	10:A:57:A:N6	2.59	0.70
12:AB:95:GLY:O	14:AE:162:GLU:HG3	1.92	0.70
16:AG:282:GLN:NE2	16:AG:282:GLN:HA	2.04	0.70
16:AG:353:HIS:HA	16:AG:356:ILE:CG2	2.21	0.70
32:R:86:ARG:HG3	32:R:86:ARG:O	1.89	0.70
41:a:2314:A:C1'	54:n:155:THR:HG21	2.21	0.70
14:AE:128:LEU:HD11	14:AE:189:LEU:HG	1.73	0.70
10:A:15:G:H2'	10:A:15:G:N3	2.06	0.70
22:H:86:ARG:O	22:H:89:ALA:HB3	1.91	0.70
12:AB:138:ASP:CB	12:AB:177:GLN:HA	2.19	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:900:LYS:HZ1	16:AG:13:SER:N	1.90	0.70
10:B:76:A:H2'	41:a:2493:U:H5''	1.72	0.70
21:G:16:PHE:CB	22:H:43:LYS:HA	2.20	0.70
11:AA:853:ASP:CA	16:AG:105:ILE:HG23	2.21	0.69
10:B:11:A:H2'	10:B:12:G:O4'	1.92	0.69
18:D:915:A:N6	18:D:916:U:C4	2.60	0.69
1:0:80:ARG:NH2	41:a:572:A:OP2	2.25	0.69
9:9:50:VAL:HG13	39:Y:119:ALA:CB	2.22	0.69
10:A:32:C:C1'	27:M:144:MET:CE	2.69	0.69
16:AG:60:ARG:HG3	16:AG:98:GLU:HG3	1.74	0.69
16:AG:433:ASP:O	16:AG:437:LEU:HG	1.92	0.69
48:h:146:MET:HE3	48:h:154:LEU:HD21	1.74	0.69
10:A:11:A:H2'	10:A:12:G:O4'	1.92	0.69
10:A:16:C:O2	41:a:2181:U:C5'	2.40	0.69
10:A:41:C:C1'	27:M:143:ARG:NH1	2.55	0.69
18:D:972:C:O2'	30:P:57:VAL:HG23	1.92	0.69
41:a:2310:C:O2'	54:n:74:VAL:CG1	2.40	0.69
9:9:3:LEU:HD12	9:9:3:LEU:N	2.05	0.69
16:AG:171:GLU:OE2	16:AG:267:GLY:CA	2.41	0.69
16:AG:107:THR:HA	16:AG:110:ALA:HB3	1.75	0.69
16:AG:434:LEU:HD11	16:AG:455:THR:C	2.17	0.69
18:D:1309:G:H8	38:X:98:ARG:NH2	1.89	0.69
22:H:19:ARG:HD3	22:H:73:ASP:OD2	1.92	0.69
41:a:1596:A:H2'	41:a:1597:A:C8	2.28	0.69
12:AB:128:PHE:HB2	12:AB:180:LYS:CG	2.23	0.69
16:AG:355:ALA:C	16:AG:380:THR:HG21	2.18	0.69
16:AG:434:LEU:CA	16:AG:456:LEU:CD2	2.58	0.69
18:D:37:U:H3	18:D:397:A:N6	1.90	0.69
22:H:70:VAL:HA	22:H:85:SER:CA	2.22	0.69
10:A:32:C:C4'	27:M:144:MET:CE	2.66	0.69
11:AA:1332:SER:O	14:AE:243:PRO:HG2	1.93	0.69
12:AB:44:VAL:HG22	12:AB:69:VAL:CG1	2.21	0.69
13:AC:232:VAL:C	13:AD:221:ALA:HB1	2.15	0.69
16:AG:239:LYS:HG3	16:AG:276:TRP:HB3	1.75	0.69
16:AG:266:LEU:H	16:AG:266:LEU:CD2	2.06	0.69
16:AG:279:ASN:CB	16:AG:280:PRO:HD2	2.22	0.69
18:D:563:A:N1	18:D:884:U:C4	2.61	0.69
16:AG:171:GLU:OE1	16:AG:267:GLY:HA3	1.92	0.69
16:AG:235:LYS:HZ2	16:AG:331:LEU:HG	1.58	0.69
16:AG:298:VAL:HA	16:AG:303:HIS:HD1	1.58	0.69
16:AG:353:HIS:C	16:AG:357:ASP:H	2.01	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:9:58:THR:HG21	9:9:81:LEU:HG	1.74	0.69
12:AB:128:PHE:HB2	12:AB:180:LYS:HG3	1.75	0.69
12:AB:165:PHE:HZ	30:P:91:ASP:HB2	1.58	0.69
16:AG:462:GLN:OE1	16:AG:467:LEU:HD21	1.93	0.69
22:H:117:LYS:CB	22:H:279:LYS:O	2.41	0.69
39:Y:21:PRO:CB	39:Y:22:PRO:HD3	2.22	0.69
41:a:1839:G:C4	41:a:1927:A:C4	2.81	0.69
41:a:2756:U:C4	41:a:2758:A:N6	2.61	0.69
7:6:21:DA:C2	8:7:63:G:N2	2.61	0.68
11:AA:855:PRO:HB3	16:AG:109:THR:HG23	1.73	0.68
14:AE:87:LYS:HE3	30:P:81:GLU:CD	2.18	0.68
16:AG:228:ARG:HA	16:AG:327:LEU:CD1	2.22	0.68
16:AG:285:ILE:CD1	16:AG:293:VAL:HG11	2.22	0.68
16:AG:302:LYS:H	16:AG:302:LYS:CE	2.00	0.68
14:AE:39:LYS:O	14:AE:273:ILE:CG2	2.41	0.68
18:D:1227:A:H5'	38:X:110:LYS:HZ1	1.55	0.68
41:a:1021:A:H3'	41:a:1021:A:N3	2.07	0.68
12:AB:19:GLU:C	12:AB:44:VAL:CG1	2.66	0.68
12:AB:96:THR:HB	14:AE:162:GLU:CG	2.23	0.68
16:AG:440:VAL:HG23	16:AG:481:LEU:HD22	1.76	0.68
11:AA:902:LEU:O	11:AA:902:LEU:HD22	1.94	0.68
11:AA:905:ILE:HD12	16:AG:8:VAL:HG11	1.74	0.68
14:AE:54:ASP:OD1	14:AE:54:ASP:N	2.24	0.68
16:AG:453:VAL:CG2	16:AG:462:GLN:NE2	2.56	0.68
10:B:15:G:H2'	10:B:15:G:N3	2.06	0.68
9:9:31:ARG:HD2	41:a:1054:A:C5'	2.22	0.68
12:AB:167:ARG:HH11	23:I:62:LYS:CB	2.06	0.68
16:AG:321:ASN:OD1	16:AG:321:ASN:N	2.25	0.68
16:AG:425:LEU:CB	16:AG:429:LYS:CE	2.71	0.68
38:X:96:PRO:CG	38:X:102:THR:CG2	2.71	0.68
22:H:19:ARG:O	22:H:72:LEU:CB	2.40	0.68
22:H:267:TRP:CD2	22:H:340:ARG:CG	2.76	0.68
9:9:11:ILE:CD1	9:9:62:ARG:HD3	2.24	0.68
9:9:43:LYS:HD2	9:9:43:LYS:O	1.94	0.68
12:AB:95:GLY:O	14:AE:162:GLU:CG	2.42	0.68
16:AG:448:LEU:CD2	16:AG:473:LEU:HD12	2.24	0.68
18:D:13:U:O4	18:D:21:G:C2	2.46	0.68
22:H:19:ARG:HD3	22:H:73:ASP:OD1	1.92	0.68
41:a:927:A:H2'	41:a:928:A:C8	2.28	0.68
11:AA:913:VAL:CG2	16:AG:108:GLN:HE21	1.94	0.68
13:AD:48:LEU:HB2	13:AD:183:ILE:HD11	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AG:207:GLU:HA	16:AG:210:ARG:HB2	1.76	0.68
16:AG:363:LEU:HD21	16:AG:410:ALA:N	1.79	0.68
14:AE:141:PHE:CD2	14:AE:293:ARG:O	2.47	0.68
14:AE:832:LYS:C	14:AE:1242:ARG:HH12	2.01	0.68
14:AE:94:GLN:HB2	14:AE:97:VAL:HG23	1.75	0.67
39:Y:58:ILE:HD13	39:Y:58:ILE:N	2.10	0.67
8:7:62:U:H4'	14:AE:322:ARG:HD2	1.74	0.67
39:Y:14:ALA:HB2	39:Y:54:ILE:HD12	1.76	0.67
41:a:1779:U:H5	41:a:1784:A:N7	1.92	0.67
12:AB:155:LYS:CE	18:D:1277:C:H3'	2.23	0.67
22:H:110:GLY:HA3	22:H:153:GLU:O	1.93	0.67
9:9:67:THR:N	9:9:68:PRO:CD	2.57	0.67
9:9:73:LYS:HB2	9:9:117:LEU:HD21	1.75	0.67
16:AG:453:VAL:HG13	16:AG:458:ASP:HB3	1.77	0.67
22:H:267:TRP:CE2	22:H:340:ARG:CG	2.72	0.67
41:a:1153:C:OP1	66:z:92:ARG:NH1	2.27	0.67
41:a:1920:C:O5'	41:a:1920:C:H6	1.77	0.67
12:AB:165:PHE:HD1	30:P:88:MET:O	1.78	0.67
14:AE:161:THR:HG22	14:AE:164:GLN:HB2	1.75	0.67
14:AE:984:LEU:HB3	14:AE:993:GLU:HB2	1.77	0.67
16:AG:429:LYS:CD	16:AG:429:LYS:H	2.05	0.67
16:AG:434:LEU:CD2	16:AG:459:LEU:CD1	2.54	0.67
7:6:16:DC:H1'	14:AE:426:ALA:HB1	1.77	0.67
14:AE:108:ALA:CB	14:AE:279:LEU:HD22	2.25	0.67
16:AG:102:PHE:HB2	16:AG:106:THR:HG21	1.75	0.67
11:AA:1268:GLN:HE22	14:AE:352:ARG:HD2	1.57	0.67
12:AB:140:PRO:CB	30:P:84:VAL:CG2	2.73	0.67
12:AB:165:PHE:HA	30:P:88:MET:C	2.20	0.67
14:AE:1355:ARG:NH1	14:AE:1369:ARG:HH12	1.93	0.67
16:AG:168:LEU:HB2	16:AG:171:GLU:HB2	1.76	0.67
22:H:267:TRP:CZ2	22:H:340:ARG:CG	2.68	0.67
7:6:8:DC:C6	7:6:9:DT:H72	2.29	0.67
9:9:118:ILE:HB	9:9:119:PRO:HD3	1.75	0.67
14:AE:395:LYS:HZ2	14:AE:399:LYS:HD3	1.59	0.67
22:H:110:GLY:N	22:H:153:GLU:C	2.53	0.67
41:a:2013:A:N6	41:a:2613:U:N3	2.33	0.67
11:AA:902:LEU:O	11:AA:902:LEU:HD13	1.94	0.67
14:AE:117:LEU:HD12	14:AE:117:LEU:O	1.94	0.67
36:V:25:ILE:HD11	36:V:61:ILE:HD11	1.77	0.67
38:X:96:PRO:CG	38:X:102:THR:HG22	2.25	0.67
56:p:24:ILE:HD13	56:p:72:LEU:HD21	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:5:G:H2'	10:A:6:G:C5'	2.24	0.66
11:AA:853:ASP:HA	16:AG:105:ILE:CG2	2.25	0.66
16:AG:323:GLN:HA	16:AG:323:GLN:HE21	1.59	0.66
23:I:75:ILE:O	23:I:75:ILE:HD13	1.95	0.66
41:a:2310:C:O2'	54:n:74:VAL:HG12	1.94	0.66
16:AG:387:VAL:CG1	16:AG:388:PRO:CD	2.41	0.66
9:9:50:VAL:CG1	39:Y:119:ALA:HB3	2.26	0.66
10:B:5:G:H2'	10:B:6:G:C5'	2.24	0.66
11:AA:854:ILE:CG1	11:AA:855:PRO:HD2	2.18	0.66
12:AB:65:PHE:CD2	12:AB:111:ILE:CD1	2.71	0.66
14:AE:108:ALA:HB3	14:AE:279:LEU:HD22	1.77	0.66
16:AG:227:ALA:HB3	16:AG:331:LEU:HA	1.78	0.66
10:A:21:A:H4'	10:A:21:A:OP1	1.95	0.66
38:X:96:PRO:HG3	38:X:102:THR:HG22	1.78	0.66
8:7:15:U:OP1	23:I:136:ARG:NH2	2.28	0.66
10:A:19:G:N2	41:a:2112:G:C8	2.62	0.66
11:AA:900:LYS:CD	16:AG:11:ALA:HB1	2.24	0.66
16:AG:123:ARG:HG2	16:AG:191:ARG:O	1.96	0.66
41:a:1923:U:H2'	41:a:1923:U:OP2	1.96	0.66
9:9:60:LEU:HA	9:9:64:VAL:HB	1.77	0.66
16:AG:308:ALA:HB2	16:AG:344:LEU:HD11	1.77	0.66
16:AG:393:LEU:HD23	16:AG:398:LEU:HD13	1.78	0.66
16:AG:447:LYS:O	16:AG:470:ILE:HD13	1.95	0.66
8:7:9:U:O4	18:D:1196:A:O4'	2.13	0.66
11:AA:894:GLN:HE21	11:AA:894:GLN:N	1.94	0.66
12:AB:149:GLU:N	12:AB:149:GLU:OE1	2.27	0.66
16:AG:64:VAL:HG22	16:AG:75:ILE:HD12	1.78	0.66
39:Y:116:MET:HB3	39:Y:124:MET:HG2	1.76	0.66
9:9:11:ILE:HG13	9:9:65:GLU:HB3	1.79	0.65
10:A:56:C:C5	41:a:2168:G:C6	2.83	0.65
16:AG:174:ARG:HB3	16:AG:175:PRO:CD	2.25	0.65
16:AG:284:VAL:CG1	16:AG:296:ILE:HD13	2.25	0.65
10:B:37:A:H3'	10:B:37:A:OP2	1.96	0.65
10:B:56:C:H5'	54:n:80:ARG:NH2	2.11	0.65
10:B:66:C:H5'	10:B:66:C:H6	1.60	0.65
18:D:1329:A:P	38:X:28:THR:CB	2.83	0.65
9:9:78:GLY:H	9:9:79:PRO:CD	2.09	0.65
10:A:66:C:H6	10:A:66:C:H5'	1.60	0.65
12:AB:66:PRO:CG	14:AE:281:ARG:NH2	2.54	0.65
16:AG:183:LEU:HA	16:AG:197:VAL:HA	1.78	0.65
16:AG:361:LYS:CD	16:AG:417:ILE:CG1	2.75	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:H:110:GLY:H	22:H:153:GLU:CA	2.08	0.65
9:9:61:ARG:NH1	41:a:1047:G:N7	2.44	0.65
10:A:18:G:C8	10:A:57:A:C6	2.85	0.65
16:AG:393:LEU:O	16:AG:398:LEU:HD23	1.95	0.65
18:D:1358:U:O4	18:D:1363:A:C2	2.47	0.65
59:s:114:LEU:HG	59:s:118:MET:HE3	1.78	0.65
12:AB:128:PHE:HZ	12:AB:178:VAL:HG21	1.60	0.65
16:AG:235:LYS:NZ	16:AG:331:LEU:HG	2.11	0.65
16:AG:422:GLU:CA	16:AG:426:GLY:CA	2.65	0.65
10:B:21:A:H4'	10:B:21:A:OP1	1.95	0.65
22:H:70:VAL:HA	22:H:85:SER:HA	1.77	0.65
11:AA:898:GLU:HA	11:AA:898:GLU:OE2	1.96	0.65
12:AB:133:MET:H	12:AB:133:MET:CE	2.08	0.65
12:AB:152:ASP:HB2	12:AB:157:ARG:HB3	1.78	0.65
10:B:75:C:OP1	41:a:2602:A:N9	2.30	0.65
22:H:162:LYS:CB	22:H:298:GLU:OE1	2.44	0.65
12:AB:165:PHE:H	30:P:88:MET:CB	2.09	0.65
14:AE:67:ASP:OD1	14:AE:95:THR:OG1	2.15	0.65
14:AE:975:ILE:HG22	14:AE:977:SER:H	1.62	0.65
16:AG:226:ALA:O	16:AG:228:ARG:HD3	1.97	0.65
18:D:1308:U:H5''	38:X:98:ARG:HG2	1.78	0.65
22:H:135:LEU:CA	22:H:157:ILE:CB	2.74	0.65
9:9:142:THR:HG21	40:Z:7:ILE:CD1	2.26	0.65
14:AE:111:THR:CG2	14:AE:300:GLN:CD	2.66	0.65
16:AG:213:VAL:HG22	16:AG:216:ILE:HG13	1.78	0.65
16:AG:232:SER:HB2	16:AG:323:GLN:OE1	1.96	0.65
8:7:8:U:OP2	18:D:1397:C:N3	2.30	0.65
16:AG:425:LEU:O	16:AG:429:LYS:CE	2.45	0.65
14:AE:141:PHE:HD2	14:AE:293:ARG:O	1.80	0.65
10:B:18:G:C8	10:B:57:A:C6	2.85	0.65
12:AB:163:SER:O	30:P:88:MET:SD	2.54	0.65
16:AG:354:ALA:CA	16:AG:357:ASP:H	2.10	0.65
22:H:52:GLN:O	22:H:53:PHE:CD1	2.50	0.65
10:A:22:G:H2'	10:A:23:C:H6	1.62	0.64
12:AB:161:SER:HA	12:AB:170:PRO:HA	1.79	0.64
14:AE:978:ARG:HG2	14:AE:1197:ASN:HD21	1.60	0.64
10:B:76:A:H1'	41:a:2493:U:O3'	1.97	0.64
18:D:197:A:C6	18:D:221:C:C4'	2.80	0.64
21:G:16:PHE:HZ	22:H:41:GLY:O	1.77	0.64
22:H:85:SER:O	22:H:88:LYS:CB	2.45	0.64
11:AA:314:ASN:HD21	11:AA:348:SER:HA	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:141:PHE:HE2	12:AB:171:VAL:HG11	1.57	0.64
14:AE:193:ASP:HB3	14:AE:196:GLN:HB2	1.78	0.64
14:AE:1037:PHE:HB3	14:AE:1040:MET:HB2	1.77	0.64
16:AG:349:GLN:C	16:AG:351:GLU:H	2.05	0.64
16:AG:363:LEU:CD2	16:AG:409:ARG:CA	2.71	0.64
21:G:19:GLN:CG	22:H:75:VAL:CG2	2.70	0.64
41:a:2303:G:N3	41:a:2314:A:C2	2.66	0.64
10:A:41:C:C4'	27:M:143:ARG:NH1	2.61	0.64
11:AA:900:LYS:HZ3	16:AG:11:ALA:HB1	1.62	0.64
14:AE:68:TYR:HB3	14:AE:75:TYR:CE2	2.32	0.64
18:D:1308:U:O5'	38:X:98:ARG:CG	2.45	0.64
8:7:9:U:N3	18:D:1196:A:N7	2.44	0.64
11:AA:858:GLY:C	11:AA:861:ALA:H	2.03	0.64
12:AB:93:ILE:HG21	14:AE:291:ILE:HA	1.80	0.64
16:AG:422:GLU:HG2	16:AG:426:GLY:HA3	1.80	0.64
16:AG:425:LEU:HG	16:AG:429:LYS:HD3	1.79	0.64
16:AG:434:LEU:HD12	16:AG:454:CYS:C	2.22	0.64
55:o:26:HIS:CE1	55:o:48:ALA:HB2	2.32	0.64
6:5:98:DA:C2'	6:5:99:DT:H72	2.28	0.64
16:AG:385:ALA:HB2	16:AG:411:LYS:HE3	1.69	0.64
16:AG:422:GLU:CA	16:AG:426:GLY:H	2.08	0.64
9:9:11:ILE:HD12	9:9:62:ARG:HD3	1.80	0.64
14:AE:84:ILE:O	14:AE:84:ILE:HG13	1.96	0.64
18:D:827:U:N3	18:D:872:A:N6	2.45	0.64
11:AA:853:ASP:HA	16:AG:105:ILE:HG21	1.80	0.64
14:AE:162:GLU:OE1	14:AE:162:GLU:HA	1.97	0.64
16:AG:380:THR:O	16:AG:384:LEU:HD12	1.95	0.64
18:D:1227:A:OP2	38:X:110:LYS:NZ	2.29	0.64
21:G:19:GLN:CG	22:H:76:GLU:CB	2.76	0.64
21:G:38:VAL:HG22	22:H:75:VAL:CG2	2.25	0.64
22:H:332:VAL:HG12	22:H:334:ASP:H	1.62	0.64
30:P:17:LEU:HD11	30:P:94:ALA:O	1.98	0.64
10:B:50:U:H2'	10:B:51:C:C6	2.33	0.64
18:D:1309:G:C8	38:X:98:ARG:NH2	2.66	0.64
22:H:72:LEU:HD12	22:H:72:LEU:N	2.10	0.64
22:H:267:TRP:CE3	22:H:340:ARG:HG3	2.32	0.64
22:H:270:ILE:HG23	22:H:337:GLU:HB3	1.77	0.64
41:a:1082:U:N3	41:a:1086:A:N6	2.45	0.64
11:AA:895:LEU:H	11:AA:895:LEU:CD2	2.07	0.64
16:AG:353:HIS:CA	16:AG:356:ILE:CG2	2.76	0.64
16:AG:363:LEU:CD2	16:AG:409:ARG:CB	2.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:D:1059:C:O2	30:P:55:PRO:HG3	1.99	0.64
9:9:29:ASP:HB2	9:9:56:ARG:HD3	1.79	0.63
14:AE:136:GLU:CD	14:AE:312:ARG:HH22	2.06	0.63
16:AG:133:HIS:ND1	16:AG:136:GLU:CD	2.55	0.63
22:H:49:PRO:CD	22:H:84:LEU:HD11	2.29	0.63
41:a:1839:G:O4'	41:a:1927:A:H1'	1.97	0.63
8:7:14:U:H5'	23:I:132:ARG:CZ	2.26	0.63
10:A:50:U:H2'	10:A:51:C:C6	2.33	0.63
16:AG:205:LEU:HA	16:AG:208:LEU:HB2	1.80	0.63
16:AG:433:ASP:O	16:AG:456:LEU:CG	2.45	0.63
18:D:1358:U:H3	18:D:1363:A:N6	1.96	0.63
21:G:18:HIS:HA	22:H:43:LYS:CD	2.28	0.63
1:0:40:MET:HE1	66:z:105:ALA:HB1	1.80	0.63
9:9:18:VAL:HG13	9:9:71:CYS:HB2	1.80	0.63
10:A:3:C:H2'	10:A:4:G:H8	1.62	0.63
10:A:31:G:O2'	27:M:144:MET:SD	2.56	0.63
11:AA:1280:ALA:HB1	14:AE:918:ILE:HG22	1.79	0.63
16:AG:63:LEU:HD22	16:AG:92:TYR:HD1	1.63	0.63
16:AG:223:ILE:HA	16:AG:238:VAL:HG12	1.80	0.63
16:AG:323:GLN:HE21	16:AG:323:GLN:CA	2.12	0.63
17:C:44:ILE:CD1	22:H:339:ARG:HG2	2.12	0.63
33:S:47:LYS:O	33:S:50:THR:OG1	2.12	0.63
41:a:1909:C:O5'	41:a:1909:C:H6	1.81	0.63
16:AG:354:ALA:HA	16:AG:357:ASP:CA	2.28	0.63
16:AG:355:ALA:CB	16:AG:382:GLU:OE1	2.18	0.63
21:G:35:ARG:HH21	22:H:10:GLU:HG2	1.62	0.63
39:Y:32:VAL:HA	39:Y:60:VAL:HG11	1.81	0.63
9:9:57:ASN:OD1	9:9:62:ARG:HD2	1.98	0.63
16:AG:162:ILE:HD11	16:AG:199:ARG:HD2	1.80	0.63
41:a:1789:A:OP2	48:h:221:ARG:NH1	2.32	0.63
16:AG:266:LEU:H	16:AG:266:LEU:HD23	1.64	0.63
16:AG:437:LEU:CD2	16:AG:456:LEU:HD11	2.27	0.63
18:D:1358:U:N3	18:D:1363:A:N6	2.46	0.63
2:1:36:LEU:HD13	2:1:48:LYS:HA	1.80	0.63
11:AA:120:GLN:NE2	11:AA:490:GLN:OE1	2.32	0.63
41:a:1839:G:C8	41:a:1927:A:C1'	2.74	0.63
41:a:1839:G:H8	41:a:1927:A:H1'	1.54	0.63
41:a:2189:U:O4'	41:a:2189:U:P	2.57	0.63
56:p:121:ILE:HD12	56:p:141:ILE:HG22	1.79	0.63
16:AG:233:ARG:CB	16:AG:327:LEU:HD23	2.28	0.63
10:B:69:C:H2'	10:B:70:G:O4'	1.99	0.63

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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	0.63
41:a:1998:A:OP2	50:j:141:ARG:NH2	2.32	0.63
6:5:101:DT:OP2	14:AE:275:ARG:NH2	2.31	0.62
10:A:69:C:H2'	10:A:70:G:O4'	1.99	0.62
10:B:3:C:H2'	10:B:4:G:H8	1.62	0.62
14:AE:245:LEU:HG	14:AE:246:PRO:HD2	1.79	0.62
16:AG:434:LEU:CD1	16:AG:454:CYS:C	2.72	0.62
22:H:162:LYS:CB	22:H:298:GLU:OE2	2.45	0.62
39:Y:116:MET:HE2	39:Y:116:MET:HA	1.79	0.62
41:a:2297:A:C2	41:a:2321:U:C4	2.86	0.62
41:a:2683:C:OP1	65:y:51:ARG:NH2	2.32	0.62
10:A:56:C:O2	41:a:2112:G:C4	2.52	0.62
11:AA:901:LEU:CG	16:AG:8:VAL:CG1	2.70	0.62
16:AG:361:LYS:CE	16:AG:417:ILE:CG1	2.74	0.62
22:H:270:ILE:CG2	22:H:337:GLU:CB	2.77	0.62
7:6:15:DC:N4	7:6:16:DC:H41	1.96	0.62
13:AD:211:ILE:HG12	13:AD:219:ARG:HH12	1.65	0.62
14:AE:44:ILE:CD1	14:AE:252:LEU:HD21	2.29	0.62
16:AG:288:MET:SD	16:AG:293:VAL:N	2.73	0.62
18:D:1227:A:H5'	38:X:110:LYS:HZ3	1.64	0.62
41:a:1839:G:N9	41:a:1927:A:N9	2.48	0.62
9:9:57:ASN:CG	9:9:62:ARG:CG	2.68	0.62
10:A:54:U:N3	10:A:58:A:N6	2.48	0.62
11:AA:854:ILE:HG12	11:AA:855:PRO:HD3	1.77	0.62
14:AE:1355:ARG:NH1	14:AE:1369:ARG:NH1	2.47	0.62
16:AG:301:ASP:OD1	16:AG:301:ASP:N	2.32	0.62
16:AG:353:HIS:HA	16:AG:356:ILE:HG23	1.78	0.62
18:D:37:U:O2	18:D:548:G:C2	2.52	0.62
39:Y:112:LYS:HZ2	39:Y:112:LYS:HB3	1.64	0.62
10:A:37:A:O2'	10:A:38:A:H5'	1.99	0.62
12:AB:177:GLN:HE22	30:P:103:GLY:HA3	1.65	0.62
14:AE:201:LEU:HB2	14:AE:221:ILE:HD13	1.80	0.62
41:a:754:U:H2'	41:a:755:U:C6	2.35	0.62
9:9:23:LEU:HB3	9:9:92:ALA:HA	1.81	0.62
9:9:92:ALA:HB3	9:9:129:LEU:HB2	1.81	0.62
16:AG:387:VAL:CB	16:AG:388:PRO:CD	2.76	0.62
16:AG:389:MET:HE3	16:AG:407:ARG:HD2	1.81	0.62
22:H:110:GLY:N	22:H:153:GLU:O	2.32	0.62
24:J:162:ALA:CB	24:J:165:ARG:HH22	2.08	0.62
11:AA:853:ASP:OD2	16:AG:104:ARG:N	2.31	0.62
11:AA:908:GLU:OE1	16:AG:104:ARG:HG2	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AG:428:ASN:O	16:AG:428:ASN:ND2	2.32	0.62
3:2:50:LEU:HD23	45:e:26:PHE:CE1	2.35	0.62
9:9:31:ARG:HD2	41:a:1054:A:H5'	1.80	0.62
10:A:65:C:H2'	10:A:66:C:H5'	1.82	0.62
14:AE:90:VAL:O	14:AE:90:VAL:CG1	2.48	0.62
14:AE:111:THR:CG2	14:AE:300:GLN:NE2	2.63	0.62
14:AE:144:TYR:CE1	14:AE:162:GLU:OE2	2.51	0.62
21:G:19:GLN:CD	22:H:75:VAL:HG22	2.24	0.62
22:H:270:ILE:HG21	22:H:337:GLU:HB3	1.80	0.62
22:H:304:VAL:HG12	22:H:304:VAL:O	1.99	0.62
10:A:41:C:C1'	27:M:143:ARG:HH12	2.12	0.62
11:AA:813:GLU:HB2	14:AE:461:PHE:HD2	1.63	0.62
12:AB:128:PHE:CE1	12:AB:178:VAL:HG23	2.34	0.62
14:AE:24:LEU:CG	14:AE:232:ASN:HD21	2.05	0.62
16:AG:127:VAL:CG2	16:AG:192:GLY:CA	2.78	0.62
16:AG:131:ARG:HG2	16:AG:186:VAL:HG12	1.80	0.62
16:AG:380:THR:C	16:AG:384:LEU:HD11	2.24	0.62
11:AA:901:LEU:HD12	16:AG:8:VAL:HG13	1.68	0.61
14:AE:128:LEU:HA	14:AE:192:MET:HE1	1.81	0.61
16:AG:424:SER:C	16:AG:429:LYS:CG	2.72	0.61
16:AG:440:VAL:HG23	16:AG:481:LEU:CD2	2.29	0.61
10:B:54:U:N3	10:B:58:A:N6	2.47	0.61
10:B:56:C:C4'	54:n:80:ARG:NH2	2.63	0.61
38:X:101:ARG:O	38:X:101:ARG:HD3	2.00	0.61
8:7:65:G:OP2	11:AA:540:ARG:NH1	2.33	0.61
11:AA:1101:LEU:HD23	14:AE:725:MET:SD	2.40	0.61
16:AG:253:GLY:HA3	16:AG:258:ARG:HD2	1.82	0.61
16:AG:425:LEU:O	16:AG:429:LYS:NZ	2.33	0.61
18:D:13:U:C5	18:D:20:U:O4	2.53	0.61
27:M:23:LEU:O	27:M:27:VAL:HG13	1.99	0.61
7:6:15:DC:C4	7:6:16:DC:C4	2.89	0.61
9:9:57:ASN:CG	9:9:62:ARG:HG2	2.25	0.61
11:AA:55:SER:OG	11:AA:465:ARG:NH1	2.33	0.61
12:AB:103:ILE:HD12	12:AB:107:GLU:OE1	2.00	0.61
16:AG:287:ALA:HB1	16:AG:331:LEU:HB3	1.81	0.61
16:AG:433:ASP:C	16:AG:456:LEU:CD1	2.72	0.61
11:AA:862:LEU:HD22	11:AA:862:LEU:N	2.14	0.61
10:B:42:G:H2'	10:B:43:A:H8	1.65	0.61
11:AA:1287:LEU:HD13	14:AE:1357:ILE:HD11	1.81	0.61
16:AG:27:LEU:HD22	16:AG:114:ILE:HG23	1.82	0.61
16:AG:402:THR:O	16:AG:406:LEU:N	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:C:29:LEU:O	17:C:33:ILE:HG23	2.00	0.61
41:a:1839:G:H1'	41:a:1927:A:N9	2.03	0.61
11:AA:857:VAL:CG1	11:AA:862:LEU:HD13	2.30	0.61
12:AB:96:THR:CB	14:AE:162:GLU:HG3	2.29	0.61
12:AB:135:ARG:HH11	12:AB:135:ARG:CG	2.14	0.61
13:AD:285:THR:CB	16:AG:82:TYR:HD1	2.08	0.61
14:AE:342:LEU:HD23	14:AE:1352:ILE:HG23	1.83	0.61
16:AG:63:LEU:HG	16:AG:73:LYS:HB3	1.83	0.61
16:AG:451:ARG:CZ	16:AG:469:ASP:HB2	2.31	0.61
22:H:118:GLY:C	22:H:133:GLY:CA	2.68	0.61
10:A:42:G:H2'	10:A:43:A:H8	1.65	0.61
12:AB:159:LYS:O	12:AB:159:LYS:HG2	2.00	0.61
16:AG:424:SER:C	16:AG:429:LYS:HG3	2.26	0.61
18:D:13:U:O4	18:D:20:U:C4	2.52	0.61
8:7:7:U:H6	8:7:7:U:H5''	1.65	0.61
9:9:6:GLN:OE1	9:9:6:GLN:HA	2.00	0.61
14:AE:223:LEU:HG	14:AE:223:LEU:O	2.00	0.61
14:AE:1161:GLY:HA3	14:AE:1179:PRO:HA	1.83	0.61
16:AG:285:ILE:HD13	16:AG:285:ILE:N	2.15	0.61
16:AG:453:VAL:HG21	16:AG:462:GLN:CD	2.25	0.61
10:B:3:C:H2'	10:B:4:G:C8	2.36	0.61
17:C:44:ILE:CD1	22:H:339:ARG:HG3	2.28	0.61
9:9:136:ILE:HD12	9:9:139:LEU:HD12	1.83	0.61
21:G:19:GLN:HG3	22:H:76:GLU:HB2	1.82	0.61
41:a:2297:A:C2	41:a:2321:U:C5	2.89	0.61
14:AE:395:LYS:NZ	14:AE:399:LYS:HD3	2.15	0.61
16:AG:10:GLU:HA	16:AG:12:VAL:HG22	1.83	0.61
8:7:14:U:OP1	23:I:132:ARG:NH1	2.33	0.60
10:A:33:U:H4'	27:M:84:THR:HB	1.82	0.60
12:AB:42:VAL:HG13	12:AB:42:VAL:O	2.00	0.60
12:AB:133:MET:HE2	12:AB:133:MET:O	2.01	0.60
12:AB:155:LYS:HG3	12:AB:155:LYS:O	2.00	0.60
16:AG:421:GLN:O	16:AG:425:LEU:N	2.34	0.60
16:AG:434:LEU:CD1	16:AG:455:THR:C	2.74	0.60
25:K:107:ALA:HB2	25:K:125:ALA:HB3	1.83	0.60
11:AA:896:THR:HB	11:AA:897:PRO:HD2	1.82	0.60
11:AA:1072:ASN:ND2	11:AA:1111:GLN:OE1	2.34	0.60
14:AE:92:VAL:O	14:AE:92:VAL:HG12	1.99	0.60
22:H:305:HIS:O	22:H:306:VAL:HB	2.00	0.60
22:H:305:HIS:CD2	22:H:307:SER:H	2.19	0.60
27:M:69:VAL:HG23	27:M:100:ALA:HB1	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:P:57:VAL:O	30:P:58:ASN:CG	2.43	0.60
9:9:77:VAL:HG12	9:9:77:VAL:O	2.01	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
16:AG:233:ARG:HG2	16:AG:270:ARG:HB2	1.83	0.60
18:D:658:C:H1'	34:T:22:THR:HG21	1.83	0.60
22:H:119:GLY:CA	22:H:131:LEU:O	2.46	0.60
39:Y:21:PRO:HB2	39:Y:22:PRO:CD	2.30	0.60
41:a:2885:G:N7	49:i:40:ARG:NH2	2.46	0.60
18:D:1218:C:H2'	18:D:1219:A:C8	2.36	0.60
18:D:1308:U:C5'	38:X:98:ARG:HG2	2.31	0.60
41:a:1406:U:HO2'	41:a:1407:G:C5'	2.09	0.60
41:a:2720:U:OP1	65:y:53:ARG:NH2	2.34	0.60
10:A:41:C:H4'	27:M:143:ARG:CZ	2.32	0.60
14:AE:67:ASP:OD1	14:AE:67:ASP:N	2.34	0.60
10:A:34:C:P	27:M:84:THR:OG1	2.59	0.60
12:AB:46:THR:HG22	12:AB:46:THR:O	2.00	0.60
14:AE:412:LEU:HD22	14:AE:441:LEU:HD21	1.84	0.60
16:AG:139:THR:HG22	16:AG:180:ARG:HB3	1.83	0.60
16:AG:197:VAL:HG11	16:AG:199:ARG:HH21	1.66	0.60
16:AG:279:ASN:HB3	16:AG:280:PRO:HD2	1.83	0.60
21:G:19:GLN:HG3	22:H:75:VAL:CG2	2.24	0.60
22:H:84:LEU:HD22	22:H:84:LEU:N	2.16	0.60
22:H:331:MET:N	22:H:331:MET:SD	2.75	0.60
35:U:21:VAL:HG21	35:U:60:TRP:CD1	2.36	0.60
6:5:100:DA:OP1	12:AB:16:SER:CB	2.48	0.60
9:9:47:GLU:HG3	9:9:95:LEU:HD21	1.83	0.60
10:A:3:C:H2'	10:A:4:G:C8	2.36	0.60
11:AA:905:ILE:HD12	16:AG:8:VAL:HG21	1.82	0.60
12:AB:44:VAL:HG12	12:AB:44:VAL:O	2.02	0.60
12:AB:155:LYS:HE2	18:D:1277:C:O5'	2.01	0.60
13:AC:45:ARG:HD3	13:AD:38:THR:HB	1.82	0.60
13:AD:112:ALA:HB3	13:AD:126:PRO:HA	1.83	0.60
14:AE:118:LYS:HD2	14:AE:312:ARG:NH2	2.17	0.60
14:AE:951:GLN:NE2	14:AE:1014:GLY:O	2.35	0.60
16:AG:353:HIS:O	16:AG:356:ILE:C	2.43	0.60
39:Y:54:ILE:O	39:Y:54:ILE:HG22	2.00	0.60
41:a:1921:G:O5'	41:a:1921:G:H8	1.84	0.60
12:AB:96:THR:HB	14:AE:162:GLU:CB	2.31	0.60
16:AG:202:PRO:O	16:AG:205:LEU:HD12	2.02	0.60
16:AG:363:LEU:HD23	16:AG:409:ARG:HB2	1.62	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AG:168:LEU:HD21	16:AG:230:PRO:O	2.00	0.60
8:7:68:G:OP1	11:AA:1073:LYS:NZ	2.26	0.60
16:AG:433:ASP:HB3	16:AG:456:LEU:HD12	1.83	0.60
16:AG:434:LEU:HG	16:AG:456:LEU:N	2.16	0.60
10:B:65:C:H2'	10:B:66:C:H5'	1.82	0.60
30:P:87:LEU:CD2	30:P:100:ILE:CD1	2.71	0.60
41:a:70:G:H4'	41:a:71:A:OP1	2.02	0.60
46:f:24:LEU:HD11	46:f:54:MET:HE2	1.84	0.60
4:3:36:VAL:CG1	4:3:39:ILE:HD12	2.32	0.59
11:AA:903:ARG:HH11	11:AA:903:ARG:CA	2.15	0.59
12:AB:167:ARG:NH1	23:I:62:LYS:C	2.58	0.59
14:AE:370:LYS:HG2	14:AE:441:LEU:HD23	1.84	0.59
14:AE:926:PRO:HG2	14:AE:1248:ILE:HD11	1.84	0.59
10:A:35:A:H2'	10:A:36:U:C6	2.37	0.59
11:AA:905:ILE:HG23	11:AA:905:ILE:O	2.00	0.59
12:AB:145:ASN:N	12:AB:145:ASN:OD1	2.34	0.59
14:AE:416:ILE:HG13	14:AE:441:LEU:HD11	1.83	0.59
16:AG:303:HIS:HB3	16:AG:334:TRP:HZ3	1.66	0.59
16:AG:363:LEU:CG	16:AG:410:ALA:CB	2.71	0.59
22:H:36:VAL:HB	22:H:48:ILE:HB	1.84	0.59
22:H:117:LYS:CB	22:H:278:THR:HG23	2.32	0.59
11:AA:1328:LYS:HE2	14:AE:100:GLU:HA	1.85	0.59
14:AE:24:LEU:CG	14:AE:232:ASN:ND2	2.63	0.59
22:H:118:GLY:C	22:H:133:GLY:HA2	2.28	0.59
22:H:270:ILE:HG21	22:H:337:GLU:CB	2.32	0.59
11:AA:1142:ARG:NH1	11:AA:1161:LEU:O	2.36	0.59
12:AB:165:PHE:HA	30:P:88:MET:HA	1.83	0.59
14:AE:802:ASP:OD1	14:AE:1348:LYS:NZ	2.31	0.59
10:B:47:U:O2'	10:B:50:U:P	2.61	0.59
21:G:217:VAL:O	21:G:220:THR:HG22	2.02	0.59
53:m:31:LEU:HD22	53:m:42:LEU:HD13	1.84	0.59
8:7:11:U:O2'	25:K:33:PHE:HE1	1.76	0.59
11:AA:69:GLN:HE21	11:AA:101:ARG:HD2	1.67	0.59
16:AG:320:ARG:CG	16:AG:320:ARG:HH11	2.14	0.59
16:AG:453:VAL:HG11	16:AG:459:LEU:HG	1.84	0.59
10:A:6:G:HO2'	10:A:7:G:H8	1.48	0.59
11:AA:528:ARG:NH2	11:AA:576:SER:O	2.30	0.59
11:AA:862:LEU:HD22	11:AA:862:LEU:H	1.66	0.59
11:AA:1268:GLN:HE21	14:AE:352:ARG:HD2	1.66	0.59
18:D:404:G:N7	24:J:2:ALA:HB3	2.17	0.59
20:F:4:ILE:CD1	20:F:19:PHE:HA	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:Z:7:ILE:HG23	40:Z:7:ILE:O	2.01	0.59
14:AE:161:THR:HG23	14:AE:164:GLN:H	1.68	0.59
14:AE:438:GLU:HG3	14:AE:485:MET:HE1	1.84	0.59
14:AE:514:THR:HG21	14:AE:596:LEU:HD12	1.84	0.59
14:AE:99:ARG:HG3	14:AE:99:ARG:NH1	2.18	0.59
16:AG:285:ILE:CG2	16:AG:293:VAL:HG11	2.28	0.59
40:Z:20:VAL:O	40:Z:20:VAL:HG12	2.02	0.59
11:AA:845:LEU:O	11:AA:845:LEU:HG	2.03	0.59
11:AA:1282:GLY:HA3	15:AF:17:PHE:HE1	1.67	0.59
16:AG:212:GLU:HB3	16:AG:258:ARG:HB3	1.84	0.59
16:AG:453:VAL:CG2	16:AG:462:GLN:CD	2.76	0.59
8:7:10:U:H5''	8:7:10:U:O2	2.03	0.59
14:AE:87:LYS:CE	30:P:81:GLU:CD	2.76	0.59
14:AE:275:ARG:NH1	14:AE:278:ARG:NH1	2.51	0.59
18:D:439:U:O2	18:D:440:C:C6	2.56	0.59
22:H:119:GLY:HA3	22:H:132:PRO:C	2.28	0.59
9:9:61:ARG:CZ	41:a:1047:G:N7	2.67	0.58
10:A:47:U:O2'	10:A:50:U:P	2.61	0.58
14:AE:201:LEU:HD11	14:AE:220:ARG:HH11	1.67	0.58
16:AG:137:ILE:O	16:AG:137:ILE:HG22	2.03	0.58
16:AG:352:ALA:O	16:AG:356:ILE:CG2	2.51	0.58
16:AG:437:LEU:HD22	16:AG:488:ILE:CD1	2.33	0.58
18:D:563:A:N6	18:D:884:U:N3	2.51	0.58
18:D:1225:A:H4'	37:W:78:ARG:NH1	2.17	0.58
35:U:4:ILE:HG12	35:U:21:VAL:HG22	1.84	0.58
41:a:84:A:N1	41:a:98:G:O2'	2.33	0.58
10:A:18:G:C8	10:A:57:A:N6	2.69	0.58
16:AG:413:ALA:HA	16:AG:416:THR:OG1	2.03	0.58
41:a:2314:A:O2'	54:n:155:THR:CG2	2.51	0.58
9:9:19:ALA:HA	9:9:70:GLU:HG2	1.84	0.58
10:A:58:A:H1'	10:A:60:U:C5	2.38	0.58
11:AA:855:PRO:HB2	16:AG:109:THR:CG2	2.30	0.58
12:AB:133:MET:HE2	12:AB:133:MET:CA	2.32	0.58
12:AB:140:PRO:HG3	30:P:6:ILE:CD1	2.33	0.58
16:AG:63:LEU:HD23	16:AG:63:LEU:H	1.69	0.58
16:AG:434:LEU:N	16:AG:456:LEU:HG	2.17	0.58
10:B:22:G:H2'	10:B:23:C:H6	1.62	0.58
22:H:267:TRP:CH2	22:H:340:ARG:CB	2.87	0.58
22:H:284:VAL:HG12	22:H:294:VAL:HB	1.84	0.58
7:6:18:DC:N4	8:7:65:G:H1	1.99	0.58
10:A:76:A:H2'	41:a:2394:C:N4	2.11	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:615:LYS:HG2	15:AF:5:THR:HG21	1.85	0.58
16:AG:362:TYR:CA	16:AG:413:ALA:HB1	2.31	0.58
22:H:71:ALA:O	22:H:72:LEU:CD1	2.42	0.58
8:7:7:U:H5''	8:7:7:U:C6	2.39	0.58
9:9:52:MET:HE3	9:9:52:MET:O	2.03	0.58
11:AA:707:ALA:O	11:AA:711:ASP:HB2	2.03	0.58
11:AA:858:GLY:O	11:AA:861:ALA:HB3	2.04	0.58
12:AB:165:PHE:CD1	30:P:88:MET:O	2.56	0.58
16:AG:130:PHE:C	16:AG:186:VAL:HG11	2.28	0.58
16:AG:240:THR:CB	16:AG:247:PRO:HG3	2.32	0.58
39:Y:78:LEU:HD13	39:Y:108:ILE:HG22	1.85	0.58
6:5:100:DA:P	12:AB:16:SER:OG	2.48	0.58
14:AE:97:VAL:HG11	14:AE:101:ARG:NH2	2.18	0.58
14:AE:491:LEU:HB2	14:AE:904:ALA:HA	1.86	0.58
16:AG:287:ALA:CB	16:AG:331:LEU:HB3	2.33	0.58
16:AG:354:ALA:HA	16:AG:357:ASP:N	2.17	0.58
41:a:2572:A:C8	50:j:149:ASN:OD1	2.56	0.58
16:AG:31:LEU:HD23	16:AG:110:ALA:HB1	1.85	0.58
16:AG:379:SER:HG	16:AG:384:LEU:HD21	1.66	0.58
39:Y:7:TYR:HB2	39:Y:57:VAL:HG22	1.86	0.58
41:a:1590:A:H2'	41:a:1591:A:C8	2.38	0.58
12:AB:155:LYS:HE3	18:D:1277:C:O5'	2.03	0.58
10:B:58:A:H1'	10:B:60:U:C5	2.38	0.58
38:X:104:THR:O	38:X:104:THR:HG22	2.03	0.58
10:A:60:U:P	10:A:61:C:H41	2.27	0.58
12:AB:157:ARG:HD2	12:AB:172:GLU:HB3	1.86	0.58
13:AC:82:LEU:HD11	13:AC:171:LEU:HD23	1.86	0.58
16:AG:127:VAL:HG21	16:AG:192:GLY:HA2	1.84	0.58
18:D:13:U:C2	18:D:915:A:N6	2.70	0.58
19:E:25:ARG:HA	19:E:66:LEU:HD21	1.85	0.58
25:K:56:VAL:O	25:K:60:ILE:HG23	2.04	0.58
8:7:9:U:O4	18:D:1196:A:C8	2.57	0.58
16:AG:233:ARG:HH12	16:AG:324:ASN:N	2.02	0.58
16:AG:266:LEU:HD23	16:AG:266:LEU:N	2.19	0.58
16:AG:318:ILE:HG12	16:AG:338:VAL:HG11	1.85	0.58
50:j:33:ARG:NH1	50:j:53:GLY:O	2.36	0.58
2:1:20:VAL:HG11	2:1:44:ALA:HA	1.86	0.57
12:AB:103:ILE:CD1	12:AB:107:GLU:OE2	2.52	0.57
12:AB:165:PHE:HA	30:P:88:MET:CA	2.34	0.57
14:AE:510:LEU:HD22	14:AE:601:ILE:HD12	1.86	0.57
16:AG:33:THR:HG23	16:AG:43:ILE:HD11	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AG:162:ILE:HD13	16:AG:167:MET:HE2	1.86	0.57
16:AG:387:VAL:HB	16:AG:388:PRO:HD2	1.85	0.57
18:D:496:A:N3	18:D:496:A:H2'	2.19	0.57
39:Y:137:LEU:N	39:Y:137:LEU:HD23	2.19	0.57
6:5:115:DA:OP2	14:AE:1148:ARG:HG3	2.04	0.57
14:AE:198:CYS:HA	14:AE:221:ILE:HD11	1.87	0.57
16:AG:434:LEU:HD22	16:AG:459:LEU:CG	2.31	0.57
10:B:60:U:P	10:B:61:C:H41	2.27	0.57
41:a:1839:G:N9	41:a:1927:A:C4	2.72	0.57
9:9:34:THR:HG22	9:9:38:MET:HE3	1.85	0.57
11:AA:900:LYS:HZ3	16:AG:11:ALA:CB	2.13	0.57
11:AA:1122:LYS:NZ	11:AA:1126:ASP:OD1	2.38	0.57
12:AB:128:PHE:CB	12:AB:180:LYS:HB2	2.23	0.57
12:AB:167:ARG:HH11	23:I:62:LYS:CA	2.17	0.57
14:AE:241:VAL:HG12	14:AE:241:VAL:O	2.04	0.57
16:AG:354:ALA:CA	16:AG:357:ASP:HB3	2.32	0.57
16:AG:367:GLU:O	16:AG:371:THR:HG23	2.04	0.57
39:Y:77:VAL:O	39:Y:77:VAL:HG12	2.05	0.57
8:7:12:U:H5''	25:K:56:VAL:HG21	1.86	0.57
12:AB:133:MET:N	12:AB:133:MET:SD	2.77	0.57
16:AG:9:VAL:HA	16:AG:24:PHE:CZ	2.40	0.57
16:AG:221:ILE:HD13	16:AG:247:PRO:HA	1.85	0.57
16:AG:240:THR:OG1	16:AG:247:PRO:HG2	2.01	0.57
6:5:99:DT:H2''	6:5:100:DA:H5''	1.85	0.57
12:AB:140:PRO:CA	30:P:84:VAL:HG21	2.34	0.57
14:AE:124:ILE:HG22	14:AE:124:ILE:O	2.04	0.57
16:AG:434:LEU:HD11	16:AG:455:THR:N	2.19	0.57
16:AG:440:VAL:HG22	16:AG:481:LEU:CD2	2.34	0.57
22:H:290:TYR:C	22:H:305:HIS:O	2.47	0.57
22:H:332:VAL:CG1	22:H:335:ILE:HG13	2.33	0.57
28:N:10:MET:HE3	28:N:61:LEU:HD11	1.87	0.57
11:AA:838:CYS:HB2	11:AA:918:LEU:HD22	1.85	0.57
12:AB:140:PRO:HG3	30:P:6:ILE:CG1	2.35	0.57
12:AB:173:LEU:HD12	30:P:102:LEU:CD2	2.30	0.57
14:AE:343:LEU:HD11	14:AE:1324:SER:HB3	1.87	0.57
16:AG:61:ARG:HD2	16:AG:73:LYS:HD3	1.86	0.57
16:AG:392:LEU:CD2	16:AG:395:ILE:HD11	2.34	0.57
16:AG:422:GLU:CG	16:AG:426:GLY:HA3	2.35	0.57
18:D:1526:G:OP2	20:F:42:THR:HG23	2.04	0.57
8:7:9:U:O4	18:D:1196:A:C1'	2.52	0.57
16:AG:362:TYR:CZ	16:AG:382:GLU:HG2	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:G:35:ARG:HD2	22:H:14:LYS:CD	2.33	0.57
21:G:148:LEU:HD22	21:G:151:ILE:HD11	1.86	0.57
22:H:110:GLY:N	22:H:153:GLU:CA	2.67	0.57
39:Y:59:THR:HG22	39:Y:61:TYR:HE1	1.69	0.57
41:a:2245:U:O2'	41:a:2436:G:OP2	2.22	0.57
9:9:54:VAL:O	9:9:54:VAL:HG22	2.03	0.57
12:AB:155:LYS:NZ	18:D:1277:C:C3'	2.44	0.57
12:AB:165:PHE:CZ	30:P:91:ASP:CB	2.87	0.57
16:AG:131:ARG:CA	16:AG:186:VAL:HG11	2.35	0.57
16:AG:354:ALA:HA	16:AG:357:ASP:H	1.70	0.57
18:D:1329:A:P	38:X:28:THR:OG1	2.62	0.57
21:G:19:GLN:NE2	22:H:75:VAL:HG22	2.19	0.57
10:A:76:A:C2'	41:a:2394:C:H42	2.16	0.57
11:AA:516:ASP:OD1	11:AA:516:ASP:O	2.23	0.57
13:AD:308:ALA:HB1	16:AG:96:GLN:CB	2.23	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	2.68	0.57
9:9:17:GLU:HB3	9:9:86:MET:HB2	1.87	0.57
11:AA:1142:ARG:NH2	11:AA:1166:ASP:OD1	2.38	0.57
12:AB:129:GLU:H	12:AB:180:LYS:HD2	1.70	0.57
16:AG:210:ARG:HE	16:AG:216:ILE:HG22	1.69	0.57
61:u:77:ILE:HD11	61:u:108:ALA:HB1	1.87	0.57
14:AE:102:MET:HG2	14:AE:246:PRO:HG3	1.87	0.56
14:AE:130:MET:HE2	14:AE:135:ILE:HG12	1.87	0.56
16:AG:187:ARG:CB	16:AG:188:PRO:HD3	2.20	0.56
16:AG:287:ALA:HB1	16:AG:331:LEU:CB	2.36	0.56
16:AG:392:LEU:HD22	16:AG:395:ILE:HD11	1.87	0.56
22:H:110:GLY:H	22:H:153:GLU:C	2.12	0.56
22:H:291:GLY:HA2	22:H:305:HIS:HA	1.86	0.56
11:AA:850:ILE:O	11:AA:850:ILE:HG22	2.05	0.56
12:AB:47:GLU:HB2	12:AB:63:LYS:HB2	1.87	0.56
12:AB:140:PRO:CG	30:P:102:LEU:CB	2.82	0.56
14:AE:1046:ILE:HD12	14:AE:1059:LEU:HB3	1.86	0.56
22:H:305:HIS:HD2	22:H:306:VAL:H	1.49	0.56
11:AA:888:THR:CB	11:AA:889:PRO:HD2	2.34	0.56
14:AE:247:PRO:HA	14:AE:250:ARG:HG3	1.87	0.56
14:AE:741:ALA:O	14:AE:762:ASN:ND2	2.38	0.56
14:AE:903:LEU:HD21	14:AE:1249:ASN:HD22	1.70	0.56
16:AG:25:GLU:HG3	16:AG:49:ILE:HD11	1.86	0.56
16:AG:63:LEU:HD23	16:AG:63:LEU:N	2.21	0.56
16:AG:130:PHE:HB3	16:AG:186:VAL:HG22	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AG:320:ARG:HB2	16:AG:323:GLN:HB2	1.88	0.56
16:AG:447:LYS:O	16:AG:470:ILE:HD11	2.05	0.56
10:B:32:C:OP2	29:O:130:ARG:NH2	2.38	0.56
7:6:21:DA:N6	8:7:63:G:H1	2.04	0.56
11:AA:618:GLN:CG	14:AE:770:LEU:HD13	2.32	0.56
12:AB:165:PHE:HZ	30:P:91:ASP:CB	2.18	0.56
16:AG:457:GLU:HG2	16:AG:489:CYS:SG	2.45	0.56
10:B:11:A:H2'	10:B:12:G:C8	2.39	0.56
18:D:321:A:N7	18:D:328:C:O2'	2.34	0.56
18:D:528:C:H6	18:D:528:C:H5''	1.71	0.56
47:g:16:CYS:HB3	47:g:37:CYS:HB3	1.86	0.56
2:1:93:ALA:HB2	41:a:1614:A:C2	2.40	0.56
10:A:50:U:H2'	10:A:51:C:H6	1.69	0.56
11:AA:913:VAL:N	16:AG:108:GLN:HG2	2.21	0.56
12:AB:165:PHE:CA	30:P:88:MET:HG3	2.33	0.56
12:AB:172:GLU:HB2	30:P:101:SER:OG	2.06	0.56
16:AG:173:PHE:N	16:AG:173:PHE:CD2	2.73	0.56
16:AG:437:LEU:HD22	16:AG:488:ILE:HD12	1.88	0.56
22:H:330:VAL:HB	22:H:344:LEU:HD23	1.86	0.56
30:P:6:ILE:HG23	30:P:100:ILE:HG23	1.87	0.56
41:a:1818:U:OP2	48:h:156:ARG:NH1	2.38	0.56
8:7:11:U:O2	8:7:11:U:H2'	2.06	0.56
11:AA:901:LEU:HD11	16:AG:8:VAL:CB	2.32	0.56
12:AB:93:ILE:HG22	14:AE:290:ILE:HG22	1.88	0.56
12:AB:156:SER:O	12:AB:156:SER:OG	2.16	0.56
14:AE:37:GLU:O	14:AE:61:ILE:CD1	2.52	0.56
16:AG:233:ARG:O	16:AG:327:LEU:HD21	2.04	0.56
16:AG:307:ILE:HD11	16:AG:336:LEU:HB2	1.87	0.56
22:H:267:TRP:CH2	22:H:340:ARG:HB3	2.41	0.56
31:Q:67:ALA:HB2	31:Q:96:THR:HG23	1.86	0.56
9:9:31:ARG:HD2	41:a:1054:A:C4'	2.29	0.56
9:9:35:VAL:HA	9:9:38:MET:HB2	1.88	0.56
11:AA:818:VAL:HG22	11:AA:1096:ILE:HG12	1.87	0.56
14:AE:171:GLU:HA	14:AE:171:GLU:OE1	2.05	0.56
16:AG:283:PHE:CE2	16:AG:331:LEU:O	2.58	0.56
21:G:18:HIS:CA	22:H:43:LYS:HD2	2.29	0.56
22:H:49:PRO:HD3	22:H:84:LEU:HD11	1.87	0.56
39:Y:96:LYS:HE3	39:Y:136:GLY:HA3	1.87	0.56
8:7:12:U:H3'	8:7:12:U:H6	1.70	0.56
12:AB:164:ILE:C	30:P:88:MET:HG3	2.27	0.56
12:AB:165:PHE:HE1	30:P:91:ASP:CA	2.17	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AG:162:ILE:HG22	16:AG:162:ILE:O	2.06	0.56
16:AG:434:LEU:HD23	16:AG:456:LEU:CG	2.35	0.56
18:D:13:U:C4	18:D:915:A:C6	2.92	0.56
43:c:31:PRO:HG2	43:c:33:LEU:HD13	1.87	0.56
10:A:11:A:O5'	10:A:11:A:H8	1.89	0.56
11:AA:549:ASP:OD2	14:AE:750:PRO:CB	2.44	0.56
16:AG:49:ILE:HG22	16:AG:49:ILE:O	2.04	0.56
16:AG:133:HIS:CE1	16:AG:136:GLU:OE1	2.59	0.56
16:AG:302:LYS:NZ	16:AG:302:LYS:HB2	2.20	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
7:6:26:DT:H2''	7:6:27:DG:H5'	1.89	0.56
8:7:9:U:C4	18:D:1196:A:C8	2.93	0.56
11:AA:839:VAL:HG12	11:AA:1049:ILE:HG12	1.87	0.56
11:AA:854:ILE:H	16:AG:105:ILE:HG23	1.60	0.56
14:AE:39:LYS:O	14:AE:273:ILE:HG21	2.06	0.56
14:AE:74:LYS:HD2	14:AE:85:CYS:SG	2.45	0.56
14:AE:160:LEU:HD22	14:AE:164:GLN:HB3	1.86	0.56
14:AE:1175:LEU:HD22	14:AE:1190:ILE:HD11	1.88	0.56
16:AG:425:LEU:N	16:AG:429:LYS:HG3	2.20	0.56
18:D:769:G:H4'	18:D:1513:A:H4'	1.88	0.56
1:0:51:VAL:HG23	66:z:86:ALA:O	2.05	0.55
8:7:1:A:H2'	8:7:2:U:H6	1.70	0.55
10:A:56:C:C6	41:a:2168:G:C6	2.94	0.55
11:AA:13:LYS:HB2	11:AA:1180:MET:HE2	1.86	0.55
16:AG:285:ILE:O	16:AG:288:MET:CE	2.54	0.55
16:AG:334:TRP:N	16:AG:334:TRP:CD1	2.73	0.55
16:AG:355:ALA:HB1	16:AG:382:GLU:CB	2.36	0.55
10:A:38:A:H2'	10:A:39:C:H5'	1.89	0.55
14:AE:638:SER:OG	14:AE:639:VAL:N	2.36	0.55
8:7:3:G:H5''	18:D:1501:C:N4	2.21	0.55
10:A:11:A:H2'	10:A:12:G:C8	2.40	0.55
12:AB:128:PHE:CE1	12:AB:178:VAL:HG22	2.41	0.55
12:AB:134:VAL:HG12	12:AB:180:LYS:HA	1.87	0.55
10:B:18:G:C8	10:B:57:A:N6	2.69	0.55
11:AA:806:PRO:O	14:AE:633:ALA:HA	2.06	0.55
14:AE:144:TYR:HE1	14:AE:162:GLU:CD	2.14	0.55
14:AE:833:GLU:HB2	14:AE:1242:ARG:NH1	2.22	0.55
16:AG:448:LEU:HD22	16:AG:467:LEU:HD22	1.89	0.55
22:H:84:LEU:HD22	22:H:84:LEU:H	1.72	0.55
16:AG:46:ARG:HH11	16:AG:61:ARG:HB3	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:1155:ILE:HG13	14:AE:1210:ILE:HB	1.88	0.55
16:AG:288:MET:HE2	16:AG:293:VAL:HB	1.89	0.55
16:AG:305:MET:HG3	16:AG:336:LEU:HB3	1.89	0.55
10:B:11:A:H8	10:B:11:A:O5'	1.89	0.55
8:7:1:A:C4	8:7:2:U:C5	2.95	0.55
8:7:8:U:H5'	18:D:1397:C:N3	2.22	0.55
11:AA:1070:HIS:NE2	11:AA:1114:GLU:OE1	2.36	0.55
14:AE:58:CYS:SG	14:AE:59:ALA:N	2.80	0.55
14:AE:1166:GLY:HA3	14:AE:1174:ARG:HB2	1.88	0.55
16:AG:168:LEU:CD2	16:AG:230:PRO:C	2.74	0.55
30:P:8:ILE:HD12	30:P:25:ILE:HD11	1.89	0.55
40:Z:2:ILE:HB	40:Z:5:ASP:HB3	1.89	0.55
52:l:108:ILE:HD11	52:l:180:LEU:HD13	1.89	0.55
22:H:332:VAL:O	22:H:334:ASP:N	2.40	0.55
24:J:61:VAL:HG21	24:J:200:ILE:CD1	2.35	0.55
32:R:80:ILE:HD12	32:R:97:THR:HG22	1.89	0.55
6:5:110:DA:N7	11:AA:183:TRP:CH2	2.75	0.55
11:AA:143:ARG:NH2	11:AA:512:SER:O	2.40	0.55
11:AA:840:SER:HB2	11:AA:850:ILE:HD11	1.89	0.55
11:AA:900:LYS:HD2	16:AG:11:ALA:CB	2.37	0.55
13:AD:308:ALA:HB1	16:AG:60:ARG:HD3	1.89	0.55
14:AE:87:LYS:HB2	30:P:81:GLU:OE1	2.07	0.55
16:AG:320:ARG:NH1	16:AG:320:ARG:HG2	2.22	0.55
10:B:6:G:HO2'	10:B:7:G:H8	1.54	0.55
18:D:1227:A:P	38:X:110:LYS:HZ1	2.30	0.55
11:AA:29:SER:O	11:AA:33:ASP:HB2	2.07	0.55
12:AB:148:VAL:HG13	12:AB:148:VAL:O	2.06	0.55
16:AG:168:LEU:CD2	16:AG:230:PRO:O	2.55	0.55
16:AG:433:ASP:C	16:AG:456:LEU:HD11	2.23	0.55
22:H:45:GLU:OE1	22:H:45:GLU:N	2.40	0.55
39:Y:116:MET:HG3	39:Y:124:MET:HB3	1.89	0.55
41:a:2303:G:C4	41:a:2314:A:C2	2.95	0.55
47:g:18:CYS:HB3	47:g:40:CYS:HB2	1.88	0.55
16:AG:299:ASP:HB2	16:AG:303:HIS:HA	1.89	0.54
22:H:52:GLN:OE1	22:H:86:ARG:CB	2.55	0.54
41:a:2192:U:H2'	41:a:2193:G:C8	2.42	0.54
11:AA:360:LEU:HD13	11:AA:378:ARG:HH11	1.72	0.54
14:AE:124:ILE:HG23	14:AE:128:LEU:HD12	1.89	0.54
37:W:15:LEU:HD13	37:W:33:THR:HG21	1.88	0.54
64:x:35:ILE:HG21	64:x:71:ALA:HA	1.89	0.54
7:6:22:DC:H4'	11:AA:508:SER:OG	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:72:A:H2'	10:A:73:A:C5'	2.32	0.54
11:AA:985:GLU:HB3	11:AA:988:LYS:HB2	1.89	0.54
41:a:1056:G:O2'	41:a:1103:A:N6	2.41	0.54
41:a:2000:C:OP1	63:w:5:LYS:NZ	2.36	0.54
7:6:2:DC:H2''	7:6:3:DC:C5	2.43	0.54
10:A:17:C:O2	10:A:17:C:H2'	2.08	0.54
11:AA:633:LEU:HD13	11:AA:644:LEU:HD23	1.89	0.54
14:AE:46:TYR:CD1	14:AE:46:TYR:C	2.85	0.54
16:AG:327:LEU:HD12	16:AG:327:LEU:O	2.07	0.54
41:a:1021:A:C2	41:a:1141:U:O4	2.51	0.54
41:a:2249:U:H3'	41:a:2250:G:C5'	2.36	0.54
41:a:2314:A:O2'	54:n:155:THR:HG21	2.06	0.54
62:v:66:ARG:NH1	62:v:104:GLU:OE1	2.39	0.54
8:7:63:G:H2'	8:7:64:A:C8	2.43	0.54
11:AA:1117:LEU:HD12	11:AA:1195:ILE:HG12	1.90	0.54
13:AC:28:LEU:HD22	13:AC:201:LEU:HD23	1.88	0.54
14:AE:145:VAL:HG23	14:AE:159:ILE:HG22	1.89	0.54
16:AG:220:VAL:HG12	16:AG:245:ILE:HG21	1.89	0.54
10:B:12:G:H2'	10:B:13:C:OP1	2.08	0.54
10:B:50:U:H2'	10:B:51:C:H6	1.70	0.54
18:D:563:A:N6	18:D:884:U:H3	2.05	0.54
18:D:1228:C:OP2	38:X:110:LYS:NZ	2.41	0.54
22:H:22:SER:N	22:H:69:ASP:OD2	2.40	0.54
22:H:154:PHE:CB	22:H:168:VAL:CB	2.85	0.54
3:2:50:LEU:HD23	45:e:26:PHE:CZ	2.42	0.54
8:7:3:G:C3'	18:D:1500:A:N6	2.71	0.54
13:AC:100:LEU:HD23	13:AC:115:ILE:HG21	1.90	0.54
11:AA:684:ASN:OD1	11:AA:687:ARG:NH2	2.41	0.54
12:AB:148:VAL:HA	12:AB:160:VAL:HA	1.90	0.54
16:AG:374:VAL:O	16:AG:374:VAL:HG12	2.08	0.54
18:D:1515:G:H2'	18:D:1516:G:H8	1.72	0.54
39:Y:19:PRO:HG2	39:Y:24:GLY:H	1.73	0.54
42:b:37:ILE:HD11	42:b:82:ILE:HD11	1.90	0.54
52:l:130:LYS:HB2	52:l:133:LEU:HD12	1.89	0.54
8:7:3:G:C4'	18:D:1500:A:H62	2.21	0.54
8:7:68:G:O2'	14:AE:425:ARG:NH2	2.40	0.54
12:AB:167:ARG:NH1	23:I:61:ALA:O	2.41	0.54
16:AG:362:TYR:CE1	16:AG:414:LEU:HD21	2.43	0.54
18:D:13:U:C4	18:D:21:G:C2	2.96	0.54
18:D:13:U:C2	18:D:915:A:C6	2.95	0.54
18:D:961:U:O4	18:D:974:A:N1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:H:84:LEU:H	22:H:84:LEU:CD2	2.21	0.54
22:H:116:VAL:C	22:H:279:LYS:HB2	2.33	0.54
58:r:58:LEU:O	58:r:61:VAL:HG22	2.08	0.54
11:AA:853:ASP:CG	16:AG:103:ASP:HB2	2.33	0.54
12:AB:63:LYS:O	12:AB:63:LYS:HG2	2.07	0.54
14:AE:26:SER:HB2	14:AE:236:TRP:CE2	2.42	0.54
14:AE:39:LYS:O	14:AE:273:ILE:HG23	2.08	0.54
16:AG:130:PHE:O	16:AG:186:VAL:HG11	2.07	0.54
16:AG:223:ILE:HD13	16:AG:223:ILE:C	2.32	0.54
16:AG:285:ILE:HD12	16:AG:293:VAL:HG11	1.88	0.54
8:7:3:G:H3'	18:D:1500:A:N6	2.23	0.54
14:AE:814:CYS:SG	14:AE:883:ARG:NH2	2.81	0.54
18:D:945:G:C2	18:D:946:A:C8	2.96	0.54
8:7:17:U:H2'	8:7:18:U:H5''	1.90	0.53
9:9:51:TYR:CD1	9:9:51:TYR:C	2.85	0.53
9:9:123:ILE:O	9:9:123:ILE:HG12	2.08	0.53
12:AB:140:PRO:HD2	30:P:102:LEU:CD2	2.38	0.53
14:AE:785:ASP:O	14:AE:789:LYS:HB2	2.08	0.53
16:AG:363:LEU:HG	16:AG:410:ALA:N	2.16	0.53
39:Y:12:VAL:HG12	39:Y:23:VAL:HG21	1.90	0.53
2:1:59:GLU:CG	2:1:66:ILE:HD11	2.38	0.53
10:A:12:G:H2'	10:A:13:C:OP1	2.08	0.53
10:A:18:G:C2	10:A:58:A:C5	2.96	0.53
10:A:60:U:O2'	10:A:61:C:OP1	2.23	0.53
11:AA:811:ASN:HA	11:AA:815:SER:HB2	1.90	0.53
14:AE:30:ILE:HG21	14:AE:241:VAL:O	2.08	0.53
14:AE:759:ILE:HG23	14:AE:771:GLN:HB3	1.89	0.53
14:AE:1167:LYS:HZ2	14:AE:1170:LYS:HB2	1.72	0.53
16:AG:213:VAL:HG22	16:AG:213:VAL:O	2.08	0.53
16:AG:448:LEU:HD11	16:AG:481:LEU:HD13	1.89	0.53
18:D:439:U:O2	18:D:440:C:C5	2.61	0.53
18:D:767:A:H2'	18:D:768:A:O4'	2.08	0.53
18:D:927:G:O2'	18:D:1503:A:N7	2.36	0.53
52:l:131:THR:HG22	52:l:160:ALA:O	2.08	0.53
9:9:139:LEU:HD11	40:Z:11:VAL:HG13	1.90	0.53
12:AB:167:ARG:NH1	23:I:62:LYS:CB	2.71	0.53
13:AD:100:LEU:HD21	13:AD:121:VAL:HG11	1.90	0.53
14:AE:975:ILE:HD11	14:AE:1003:LEU:HD11	1.90	0.53
18:D:1329:A:OP1	38:X:28:THR:N	2.41	0.53
22:H:267:TRP:CZ3	22:H:340:ARG:HG3	2.43	0.53
41:a:811:U:H2'	61:u:21:ARG:HA	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:9:93:ALA:O	9:9:129:LEU:HD13	2.06	0.53
11:AA:903:ARG:HH11	11:AA:903:ARG:C	2.16	0.53
12:AB:167:ARG:NE	23:I:61:ALA:C	2.53	0.53
10:B:60:U:O2'	10:B:61:C:OP1	2.23	0.53
34:T:5:THR:O	34:T:8:THR:OG1	2.18	0.53
39:Y:33:ASN:H	39:Y:66:PHE:HE1	1.56	0.53
39:Y:57:VAL:O	39:Y:57:VAL:HG12	2.07	0.53
39:Y:109:ALA:HB2	39:Y:128:ILE:HG13	1.89	0.53
9:9:78:GLY:H	9:9:79:PRO:HD2	1.68	0.53
9:9:125:ARG:HA	9:9:125:ARG:CZ	2.38	0.53
11:AA:103:VAL:HB	11:AA:114:VAL:HG11	1.89	0.53
13:AD:28:LEU:HD12	13:AD:201:LEU:HD23	1.91	0.53
14:AE:111:THR:HG22	14:AE:300:GLN:NE2	2.23	0.53
14:AE:205:LEU:HG	14:AE:217:LEU:HB3	1.90	0.53
16:AG:358:THR:O	16:AG:358:THR:OG1	2.25	0.53
25:K:94:VAL:HG13	25:K:111:MET:HE1	1.91	0.53
9:9:71:CYS:HA	9:9:117:LEU:HD13	1.91	0.53
12:AB:44:VAL:CG2	12:AB:69:VAL:CG1	2.83	0.53
16:AG:398:LEU:HG	16:AG:398:LEU:O	2.09	0.53
22:H:19:ARG:O	22:H:72:LEU:HD22	2.09	0.53
22:H:24:VAL:HG12	22:H:69:ASP:H	1.74	0.53
64:x:27:VAL:HG21	64:x:40:ILE:HD12	1.89	0.53
14:AE:832:LYS:HB3	14:AE:1242:ARG:NH1	2.24	0.53
16:AG:233:ARG:C	16:AG:327:LEU:HD21	2.34	0.53
16:AG:235:LYS:HG2	16:AG:235:LYS:O	2.07	0.53
16:AG:434:LEU:CG	16:AG:456:LEU:N	2.71	0.53
10:B:16:C:O2	10:B:16:C:H2'	2.09	0.53
22:H:321:VAL:HG13	22:H:322:VAL:HG23	1.90	0.53
41:a:1906:G:H5''	41:a:1906:G:H8	1.73	0.53
11:AA:900:LYS:HZ1	16:AG:13:SER:H	1.54	0.53
16:AG:380:THR:C	16:AG:384:LEU:CD1	2.79	0.53
41:a:523:C:O2	41:a:554:U:O2'	2.25	0.53
8:7:65:G:H2'	8:7:66:A:C8	2.44	0.53
10:A:56:C:C2	41:a:2112:G:C8	2.96	0.53
12:AB:141:PHE:HB3	12:AB:144:PHE:HB2	1.91	0.53
22:H:49:PRO:HD2	22:H:84:LEU:CD1	2.39	0.53
8:7:59:U:C2	11:AA:1253:LEU:HD12	2.37	0.53
13:AC:43:LEU:HD13	13:AC:217:ILE:HD11	1.91	0.53
14:AE:78:LEU:O	14:AE:78:LEU:HD13	2.08	0.53
14:AE:112:ALA:HA	14:AE:238:ILE:HA	1.91	0.53
16:AG:9:VAL:HG22	16:AG:24:PHE:CE2	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:17:C:O2	10:B:17:C:H2'	2.08	0.53
22:H:135:LEU:CB	22:H:167:VAL:CA	2.86	0.53
25:K:99:ALA:HB1	25:K:103:THR:HG21	1.89	0.53
39:Y:37:PHE:CZ	39:Y:56:VAL:HG11	2.44	0.53
10:A:22:G:O2'	10:A:23:C:P	2.68	0.52
10:A:38:A:C2'	10:A:39:C:H5'	2.39	0.52
12:AB:106:LYS:HA	12:AB:109:ASP:HB2	1.91	0.52
14:AE:99:ARG:HG3	14:AE:99:ARG:HH11	1.74	0.52
14:AE:850:LYS:HB2	14:AE:857:LEU:HB2	1.91	0.52
22:H:135:LEU:CB	22:H:157:ILE:CB	2.87	0.52
39:Y:138:VAL:HG12	39:Y:138:VAL:O	2.08	0.52
54:n:8:TYR:HA	54:n:12:VAL:HB	1.91	0.52
4:3:13:VAL:CG2	4:3:39:ILE:HD13	2.38	0.52
9:9:31:ARG:HH11	9:9:31:ARG:CG	2.14	0.52
11:AA:888:THR:HB	11:AA:889:PRO:CD	2.38	0.52
12:AB:165:PHE:HZ	30:P:91:ASP:CA	2.21	0.52
22:H:279:LYS:HA	22:H:331:MET:CB	2.34	0.52
63:w:38:LEU:N	63:w:39:PRO:CD	2.73	0.52
9:9:11:ILE:CD1	9:9:11:ILE:N	2.73	0.52
9:9:43:LYS:HG2	9:9:98:GLU:HG2	1.90	0.52
10:A:16:C:O2	10:A:16:C:H2'	2.09	0.52
11:AA:628:HIS:HB3	11:AA:647:ARG:HH21	1.74	0.52
11:AA:900:LYS:NZ	16:AG:11:ALA:HB3	2.09	0.52
14:AE:56:LEU:CD1	14:AE:273:ILE:HD12	2.39	0.52
14:AE:111:THR:HG23	14:AE:300:GLN:NE2	2.24	0.52
14:AE:136:GLU:OE1	14:AE:312:ARG:CZ	2.55	0.52
16:AG:434:LEU:CD2	16:AG:455:THR:O	2.50	0.52
10:B:6:G:O2'	10:B:7:G:H8	1.92	0.52
10:B:76:A:N3	41:a:2493:U:H4'	2.23	0.52
18:D:864:A:C2	18:D:865:A:C2	2.98	0.52
41:a:2298:A:C5	41:a:2321:U:O4	2.62	0.52
41:a:2315:G:O2'	54:n:125:ARG:HD3	2.09	0.52
9:9:58:THR:HG21	9:9:81:LEU:HA	1.90	0.52
11:AA:786:GLY:N	11:AA:789:THR:OG1	2.41	0.52
11:AA:849:GLU:HB2	11:AA:887:VAL:HG13	1.86	0.52
12:AB:165:PHE:HZ	30:P:91:ASP:HA	1.62	0.52
14:AE:68:TYR:CA	14:AE:75:TYR:HE2	2.22	0.52
10:B:18:G:C2	10:B:58:A:C5	2.97	0.52
41:a:1266:G:OP2	49:i:17:ARG:NE	2.43	0.52
11:AA:243:PRO:HB2	11:AA:274:ILE:HG23	1.90	0.52
16:AG:63:LEU:HA	16:AG:92:TYR:HA	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AG:179:VAL:HB	16:AG:199:ARG:HH11	1.73	0.52
16:AG:266:LEU:CD2	16:AG:266:LEU:N	2.73	0.52
16:AG:285:ILE:HD12	16:AG:293:VAL:HG21	1.92	0.52
9:9:3:LEU:HD13	9:9:5:LEU:H	1.75	0.52
10:A:56:C:C3'	10:A:57:A:H5''	2.40	0.52
11:AA:125:GLY:HA2	11:AA:499:SER:HB2	1.92	0.52
11:AA:894:GLN:NE2	11:AA:894:GLN:H	2.04	0.52
11:AA:901:LEU:HG	16:AG:8:VAL:CG1	2.39	0.52
41:a:1980:G:O2'	41:a:1982:U:OP2	2.28	0.52
11:AA:618:GLN:HG3	14:AE:770:LEU:CD1	2.38	0.52
11:AA:714:VAL:HB	11:AA:787:PRO:HD2	1.92	0.52
11:AA:895:LEU:HD23	11:AA:895:LEU:N	2.12	0.52
14:AE:87:LYS:HZ2	30:P:81:GLU:HG2	1.75	0.52
14:AE:201:LEU:HD12	14:AE:224:LEU:HD12	1.92	0.52
39:Y:116:MET:HE2	39:Y:117:THR:H	1.74	0.52
11:AA:974:ARG:HD2	11:AA:1014:LEU:HD21	1.92	0.52
13:AD:205:MET:HE3	13:AD:213:PRO:HB3	1.91	0.52
16:AG:131:ARG:O	16:AG:134:GLU:CG	2.47	0.52
16:AG:399:ASP:OD2	16:AG:399:ASP:N	2.40	0.52
16:AG:444:LEU:HD22	16:AG:473:LEU:HD21	1.92	0.52
41:a:1910:G:O5'	41:a:1910:G:H8	1.93	0.52
9:9:41:LEU:HD12	39:Y:117:THR:HG22	1.92	0.52
10:A:6:G:O2'	10:A:7:G:H8	1.92	0.52
10:A:12:G:C2'	10:A:13:C:OP1	2.58	0.52
11:AA:855:PRO:HG3	16:AG:108:GLN:OE1	2.10	0.52
11:AA:1284:ALA:HB3	14:AE:1361:THR:HB	1.90	0.52
12:AB:140:PRO:HB2	30:P:84:VAL:CG1	2.39	0.52
13:AD:16:ILE:HG23	13:AD:26:VAL:HG22	1.91	0.52
14:AE:804:ALA:O	14:AE:806:ASP:N	2.41	0.52
18:D:673:A:H2'	18:D:674:G:C8	2.44	0.52
60:t:7:MET:HE1	60:t:44:LYS:HD2	1.91	0.52
11:AA:93:SER:HA	11:AA:128:PRO:HA	1.92	0.52
13:AC:140:ILE:HD12	13:AC:142:MET:HE3	1.92	0.52
14:AE:291:ILE:HG22	14:AE:292:VAL:HG13	1.91	0.52
41:a:523:C:H4'	41:a:540:C:O2	2.09	0.52
14:AE:88:CYS:HB3	14:AE:90:VAL:HG12	1.92	0.51
14:AE:144:TYR:CE1	14:AE:162:GLU:CD	2.88	0.51
14:AE:209:ASN:HA	14:AE:214:ARG:HH21	1.74	0.51
16:AG:360:THR:HG22	16:AG:360:THR:O	2.10	0.51
16:AG:451:ARG:NH2	16:AG:470:ILE:CG1	2.67	0.51
10:B:12:G:C2'	10:B:13:C:OP1	2.57	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:22:G:O2'	10:B:23:C:P	2.67	0.51
22:H:332:VAL:C	22:H:334:ASP:H	2.18	0.51
34:T:40:GLN:CA	34:T:40:GLN:HE21	2.23	0.51
41:a:1814:G:H4'	48:h:51:THR:HG21	1.93	0.51
10:A:18:G:C2	10:A:58:A:C6	2.99	0.51
10:A:34:C:P	27:M:84:THR:HG1	2.30	0.51
14:AE:395:LYS:HZ2	14:AE:399:LYS:CE	2.23	0.51
16:AG:402:THR:HA	16:AG:405:ALA:HB3	1.91	0.51
18:D:1308:U:P	38:X:98:ARG:HG3	2.50	0.51
29:O:81:HIS:O	29:O:84:THR:OG1	2.23	0.51
41:a:2328:A:H2'	41:a:2329:U:C6	2.44	0.51
44:d:5:U:OP1	44:d:61:G:O2'	2.26	0.51
66:z:58:ARG:HA	66:z:61:TRP:CE3	2.45	0.51
8:7:14:U:H3'	8:7:14:U:H6	1.75	0.51
16:AG:362:TYR:CE2	16:AG:382:GLU:HG2	2.45	0.51
23:I:77:ILE:HA	23:I:84:VAL:HG23	1.91	0.51
4:3:94:ARG:HB3	4:3:103:ILE:HD12	1.92	0.51
8:7:64:A:H2'	8:7:65:G:C8	2.46	0.51
9:9:125:ARG:HG3	9:9:125:ARG:O	2.10	0.51
10:A:15:G:N3	10:A:15:G:C2'	2.73	0.51
12:AB:23:ALA:HB2	12:AB:44:VAL:CG1	2.39	0.51
12:AB:135:ARG:CG	12:AB:135:ARG:NH1	2.73	0.51
14:AE:390:LEU:N	14:AE:390:LEU:CD1	2.73	0.51
16:AG:131:ARG:HA	16:AG:186:VAL:CG1	2.38	0.51
18:D:1499:A:O2'	18:D:1500:A:H5'	2.10	0.51
29:O:98:LEU:HB3	29:O:104:VAL:HG13	1.92	0.51
39:Y:27:LEU:HD12	39:Y:27:LEU:C	2.35	0.51
41:a:118:A:C8	41:a:119:A:C8	2.99	0.51
41:a:587:C:OP2	61:u:21:ARG:NH1	2.43	0.51
41:a:639:U:H2'	41:a:640:C:C6	2.45	0.51
2:1:93:ALA:HB2	41:a:1614:A:N1	2.25	0.51
8:7:3:G:C4'	18:D:1500:A:N6	2.73	0.51
10:A:19:G:C5	41:a:2112:G:H4'	2.44	0.51
11:AA:1101:LEU:HD21	14:AE:508:LEU:HD22	1.92	0.51
14:AE:746:LEU:HG	14:AE:758:PRO:HG3	1.90	0.51
16:AG:285:ILE:CD1	16:AG:285:ILE:N	2.73	0.51
16:AG:429:LYS:HD2	16:AG:429:LYS:N	2.24	0.51
10:B:24:U:O2'	41:a:1922:G:O3'	2.29	0.51
10:B:56:C:C3'	10:B:57:A:H5''	2.40	0.51
17:C:30:LYS:HA	17:C:33:ILE:HD13	1.91	0.51
22:H:49:PRO:HD2	22:H:84:LEU:HD11	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Y:112:LYS:NZ	39:Y:112:LYS:CB	2.73	0.51
53:m:31:LEU:HD22	53:m:42:LEU:CD1	2.40	0.51
2:1:59:GLU:HG3	2:1:66:ILE:HD11	1.92	0.51
11:AA:246:LEU:HB3	11:AA:269:ILE:HD13	1.92	0.51
12:AB:140:PRO:CD	30:P:102:LEU:CD1	2.67	0.51
12:AB:141:PHE:HE2	12:AB:171:VAL:CG1	2.23	0.51
14:AE:99:ARG:HA	14:AE:248:ASP:HB2	1.92	0.51
16:AG:12:VAL:HG23	16:AG:16:LYS:HE2	1.92	0.51
17:C:61:ARG:NH2	18:D:736:C:OP1	2.43	0.51
41:a:1693:U:O2'	48:h:14:ARG:NH2	2.43	0.51
41:a:2093:G:O2'	41:a:2198:A:N1	2.41	0.51
50:j:4:LEU:HD23	50:j:29:VAL:CG1	2.39	0.51
60:t:71:ARG:NH2	60:t:123:LEU:O	2.42	0.51
12:AB:155:LYS:HE3	18:D:1277:C:H3'	1.93	0.51
14:AE:215:LYS:HA	14:AE:218:THR:HG22	1.91	0.51
16:AG:21:GLU:HB3	16:AG:49:ILE:HD12	1.91	0.51
16:AG:233:ARG:NH1	16:AG:324:ASN:HB2	2.25	0.51
16:AG:361:LYS:HD2	16:AG:417:ILE:HG12	1.92	0.51
16:AG:365:ILE:HD11	16:AG:406:LEU:HD22	1.87	0.51
18:D:1276:G:O5'	18:D:1276:G:H8	1.93	0.51
41:a:783:A:N3	41:a:783:A:C2'	2.70	0.51
41:a:1964:G:H4'	41:a:1965:C:OP2	2.11	0.51
9:9:23:LEU:HA	9:9:118:ILE:HG13	1.92	0.51
9:9:62:ARG:HG2	9:9:62:ARG:NH2	2.20	0.51
12:AB:172:GLU:N	12:AB:172:GLU:OE1	2.44	0.51
14:AE:275:ARG:HH12	14:AE:278:ARG:NH1	2.09	0.51
16:AG:296:ILE:HD11	16:AG:307:ILE:HD13	1.93	0.51
16:AG:353:HIS:O	16:AG:356:ILE:CB	2.58	0.51
10:B:18:G:C2	10:B:58:A:C6	2.99	0.51
20:F:4:ILE:HD12	20:F:19:PHE:HA	1.93	0.51
25:K:81:LEU:HD13	25:K:123:VAL:HG12	1.92	0.51
39:Y:59:THR:HG22	39:Y:61:TYR:CE1	2.45	0.51
41:a:404:A:O2'	41:a:405:U:OP2	2.22	0.51
8:7:2:U:H2'	8:7:3:G:C8	2.45	0.51
10:A:76:A:O2'	41:a:2395:C:C2	2.64	0.51
11:AA:857:VAL:CG1	11:AA:861:ALA:CB	2.71	0.51
10:B:56:C:C5'	54:n:80:ARG:CZ	2.76	0.51
18:D:1410:A:C2	18:D:1491:G:C2	2.99	0.51
22:H:308:GLU:O	22:H:310:ASP:N	2.43	0.51
30:P:57:VAL:O	30:P:57:VAL:HG13	2.10	0.51
11:AA:524:ILE:HG21	11:AA:708:VAL:HG13	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:68:TYR:CE2	14:AE:291:ILE:HG23	2.46	0.51
12:AB:93:ILE:HG21	14:AE:291:ILE:CA	2.40	0.51
39:Y:80:LYS:HG3	39:Y:86:LYS:HA	1.93	0.51
41:a:2243:U:H2'	41:a:2244:U:C6	2.46	0.51
44:d:106:G:H2'	44:d:107:G:O4'	2.10	0.51
9:9:62:ARG:CG	9:9:62:ARG:NH2	2.73	0.50
11:AA:862:LEU:O	11:AA:862:LEU:HD23	2.11	0.50
60:t:43:ILE:HD12	60:t:56:ASP:HB2	1.93	0.50
8:7:11:U:HO2'	25:K:33:PHE:HE1	1.42	0.50
9:9:31:ARG:HG3	9:9:31:ARG:NH1	2.17	0.50
11:AA:255:ILE:HB	11:AA:263:VAL:HB	1.93	0.50
11:AA:400:VAL:HG21	11:AA:452:ARG:HE	1.76	0.50
16:AG:329:SER:HA	16:AG:336:LEU:HG	1.92	0.50
16:AG:453:VAL:HG11	16:AG:459:LEU:CD2	2.41	0.50
18:D:1228:C:OP1	38:X:107:ARG:CZ	2.58	0.50
21:G:35:ARG:NH2	22:H:10:GLU:HG2	2.25	0.50
10:A:37:A:H2'	10:A:38:A:H8	1.77	0.50
16:AG:11:ALA:HB3	16:AG:12:VAL:HA	1.92	0.50
16:AG:384:LEU:O	16:AG:387:VAL:HG23	2.12	0.50
10:B:34:C:O2	10:B:34:C:H2'	2.11	0.50
22:H:119:GLY:CA	22:H:133:GLY:CA	2.75	0.50
1:0:14:VAL:HG21	1:0:98:ILE:HG13	1.94	0.50
6:5:98:DA:N9	6:5:99:DT:H72	2.27	0.50
8:7:63:G:H2'	8:7:64:A:H8	1.74	0.50
12:AB:63:LYS:HG2	12:AB:66:PRO:HB3	1.92	0.50
16:AG:422:GLU:O	16:AG:427:ASP:N	2.45	0.50
16:AG:448:LEU:CG	16:AG:473:LEU:HD11	2.42	0.50
18:D:1366:C:O2'	30:P:62:ARG:NH2	2.45	0.50
41:a:2298:A:N3	41:a:2321:U:C5	2.80	0.50
10:A:56:C:H1'	41:a:2112:G:C5	2.46	0.50
14:AE:87:LYS:CB	30:P:81:GLU:OE1	2.60	0.50
16:AG:5:ILE:HA	16:AG:8:VAL:HB	1.93	0.50
16:AG:65:VAL:HG12	16:AG:66:ASP:H	1.76	0.50
18:D:1404:C:H2'	18:D:1404:C:O2	2.10	0.50
39:Y:100:ILE:HB	39:Y:105:LEU:HD11	1.92	0.50
41:a:1141:U:O2	41:a:1142:A:N6	2.44	0.50
9:9:44:ALA:HB1	9:9:52:MET:HB3	1.94	0.50
11:AA:400:VAL:HG11	11:AA:452:ARG:HD2	1.94	0.50
13:AD:309:SER:CB	16:AG:40:GLU:CD	2.85	0.50
14:AE:421:VAL:O	14:AE:436:ALA:HA	2.12	0.50
18:D:5:U:O2	18:D:5:U:O4'	2.29	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:D:1308:U:H2'	38:X:98:ARG:HH22	1.62	0.50
18:D:1356:G:H2'	18:D:1357:A:C8	2.47	0.50
28:N:3:MET:HA	28:N:3:MET:HE3	1.94	0.50
41:a:929:U:H1'	46:f:26:GLY:O	2.10	0.50
41:a:1824:G:O2'	48:h:252:THR:HG21	2.11	0.50
4:3:12:ILE:HG21	4:3:80:ALA:HB2	1.92	0.50
8:7:6:U:C2	18:D:1493:A:C2	3.00	0.50
8:7:19:U:O2	8:7:19:U:H2'	2.12	0.50
11:AA:845:LEU:HD23	11:AA:889:PRO:HB2	1.93	0.50
16:AG:433:ASP:O	16:AG:456:LEU:HD21	2.12	0.50
10:B:5:G:C2'	10:B:6:G:H5'	2.39	0.50
18:D:872:A:H2'	18:D:872:A:N3	2.27	0.50
10:A:59:A:H2'	10:A:60:U:H5'	1.94	0.50
11:AA:232:ILE:HG12	11:AA:237:LEU:HG	1.94	0.50
11:AA:900:LYS:HZ3	16:AG:11:ALA:C	2.19	0.50
14:AE:1371:ARG:HE	14:AE:1372:ARG:NH1	2.10	0.50
16:AG:139:THR:HA	16:AG:180:ARG:HA	1.92	0.50
41:a:1869:G:N2	41:a:1871:A:O2'	2.44	0.50
2:1:24:ILE:HD13	2:1:36:LEU:HD11	1.93	0.50
6:5:96:DT:H2''	6:5:97:DC:C5	2.46	0.50
6:5:101:DT:H72	14:AE:271:ARG:CZ	2.41	0.50
8:7:2:U:OP2	18:D:926:G:N2	2.45	0.50
9:9:62:ARG:CG	9:9:62:ARG:HH21	2.14	0.50
11:AA:554:HIS:HD2	11:AA:558:VAL:HB	1.77	0.50
12:AB:64:PHE:O	12:AB:114:ARG:NH1	2.31	0.50
12:AB:103:ILE:CG1	12:AB:107:GLU:OE2	2.60	0.50
14:AE:437:PHE:HZ	14:AE:453:VAL:HG11	1.76	0.50
14:AE:972:LYS:HD2	14:AE:1004:ALA:HA	1.93	0.50
10:B:39:C:O5'	10:B:39:C:H6	1.95	0.50
18:D:1208:C:H2'	18:D:1209:C:C6	2.47	0.50
34:T:4:SER:O	34:T:8:THR:HG23	2.12	0.50
41:a:742:A:C2	41:a:743:A:C6	3.00	0.50
48:h:107:PRO:HD2	48:h:110:LEU:HD22	1.94	0.50
59:s:17:VAL:HG23	59:s:137:PRO:HB2	1.92	0.50
59:s:32:LEU:CD2	59:s:54:ILE:HG21	2.42	0.50
10:A:11:A:H2'	10:A:12:G:C1'	2.42	0.49
11:AA:18:ARG:HE	11:AA:620:ASN:HA	1.77	0.49
14:AE:683:ILE:HD12	14:AE:754:ILE:HG21	1.93	0.49
14:AE:749:LYS:HB3	14:AE:755:ILE:HD11	1.94	0.49
16:AG:171:GLU:OE2	16:AG:267:GLY:C	2.54	0.49
16:AG:305:MET:HG2	16:AG:336:LEU:HA	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:2646:C:O5'	41:a:2646:C:H6	1.95	0.49
43:c:3:ARG:HD2	43:c:30:LEU:HD22	1.94	0.49
60:t:113:MET:O	60:t:116:ILE:HG13	2.11	0.49
10:A:11:A:C2'	10:A:12:G:O4'	2.60	0.49
10:A:28:C:H2'	10:A:29:G:H8	1.76	0.49
11:AA:903:ARG:HH11	11:AA:903:ARG:CG	2.25	0.49
15:AF:3:ARG:NH1	15:AF:55:GLU:OE2	2.40	0.49
16:AG:123:ARG:NH1	16:AG:123:ARG:HG2	2.26	0.49
16:AG:285:ILE:HD13	16:AG:285:ILE:H	1.76	0.49
16:AG:369:PHE:O	16:AG:373:LEU:HG	2.12	0.49
63:w:55:ALA:HA	63:w:80:PHE:CE1	2.47	0.49
6:5:110:DA:N7	11:AA:183:TRP:HH2	2.11	0.49
9:9:7:ASP:OD1	9:9:7:ASP:N	2.36	0.49
9:9:51:TYR:CG	9:9:89:PRO:HD2	2.47	0.49
11:AA:146:VAL:HG21	11:AA:513:GLN:HE21	1.77	0.49
12:AB:71:VAL:HG12	12:AB:73:MET:HB2	1.93	0.49
12:AB:167:ARG:HE	23:I:62:LYS:HB2	1.77	0.49
16:AG:130:PHE:C	16:AG:186:VAL:CG1	2.86	0.49
10:B:48:C:O2	10:B:48:C:H2'	2.11	0.49
18:D:108:G:H5''	18:D:108:G:N3	2.27	0.49
18:D:1499:A:H3'	18:D:1499:A:OP2	2.12	0.49
9:9:8:LYS:HZ2	41:a:1046:A:N6	2.10	0.49
9:9:43:LYS:HZ1	9:9:95:LEU:HD13	1.77	0.49
11:AA:857:VAL:HB	11:AA:862:LEU:HD11	1.93	0.49
16:AG:64:VAL:HA	16:AG:75:ILE:HB	1.94	0.49
16:AG:440:VAL:HG22	16:AG:481:LEU:HD21	1.95	0.49
16:AG:453:VAL:HG11	16:AG:459:LEU:HD23	1.95	0.49
10:B:18:G:C5	10:B:57:A:C5	3.01	0.49
18:D:50:A:O2'	18:D:360:G:N2	2.45	0.49
21:G:38:VAL:CG2	22:H:75:VAL:CG2	2.77	0.49
34:T:21:ASP:O	34:T:22:THR:HG22	2.12	0.49
41:a:2303:G:C6	41:a:2314:A:N1	2.81	0.49
8:7:8:U:H5'	18:D:1397:C:C2	2.48	0.49
9:9:31:ARG:HE	41:a:1054:A:C4'	2.26	0.49
9:9:52:MET:HE3	9:9:52:MET:CA	2.42	0.49
10:A:76:A:C2'	41:a:2394:C:N4	2.75	0.49
11:AA:9:LYS:HG2	11:AA:1171:ARG:HH12	1.77	0.49
11:AA:411:ARG:NH2	11:AA:427:ASP:OD2	2.44	0.49
10:B:15:G:H22	10:B:20:U:H3	1.58	0.49
10:B:49:G:O5'	10:B:49:G:H8	1.96	0.49
41:a:1412:U:C4	41:a:1413:A:N7	2.81	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:2038:G:H2'	41:a:2039:U:O4'	2.12	0.49
41:a:2297:A:C6	41:a:2321:U:O4	2.65	0.49
63:w:67:PHE:O	63:w:71:ARG:N	2.45	0.49
1:0:14:VAL:CG2	1:0:98:ILE:HG13	2.43	0.49
9:9:23:LEU:HD22	9:9:92:ALA:HB1	1.95	0.49
12:AB:11:VAL:CG2	12:AB:103:ILE:HD13	2.38	0.49
14:AE:145:VAL:HG12	14:AE:184:ALA:HB1	1.94	0.49
14:AE:550:VAL:O	14:AE:569:LEU:HA	2.13	0.49
16:AG:216:ILE:HG12	16:AG:221:ILE:HB	1.93	0.49
18:D:13:U:O4	18:D:21:G:N3	2.46	0.49
18:D:1329:A:OP1	38:X:28:THR:OG1	2.31	0.49
41:a:1433:A:H2'	41:a:1434:A:O4'	2.13	0.49
41:a:2557:G:H2'	41:a:2558:C:C6	2.47	0.49
8:7:8:U:OP2	18:D:1397:C:C2	2.66	0.49
10:A:5:G:C2'	10:A:6:G:H5'	2.39	0.49
10:A:48:C:H2'	10:A:48:C:O2	2.11	0.49
10:A:49:G:H8	10:A:49:G:O5'	1.96	0.49
14:AE:799:ARG:HG2	14:AE:1325:PHE:HZ	1.77	0.49
16:AG:18:LEU:HB3	16:AG:19:PRO:HD2	1.95	0.49
10:B:47:U:H2'	10:B:48:C:H4'	1.93	0.49
26:L:18:VAL:N	26:L:19:PRO:CD	2.76	0.49
54:n:127:ASN:ND2	54:n:127:ASN:N	2.59	0.49
56:p:121:ILE:HD12	56:p:141:ILE:CG2	2.41	0.49
59:s:30:THR:HG22	59:s:31:GLU:N	2.27	0.49
2:1:55:ILE:HG23	2:1:66:ILE:HD12	1.93	0.49
4:3:7:ARG:HB2	41:a:85:G:OP2	2.13	0.49
10:A:41:C:H4'	27:M:143:ARG:NH1	2.26	0.49
16:AG:285:ILE:CG1	16:AG:293:VAL:CG1	2.53	0.49
10:B:11:A:C2'	10:B:12:G:O4'	2.60	0.49
18:D:1169:A:H2'	18:D:1170:A:C8	2.48	0.49
22:H:72:LEU:CD1	22:H:72:LEU:N	2.72	0.49
22:H:120:PHE:CB	22:H:136:VAL:CB	2.90	0.49
22:H:132:PRO:N	22:H:167:VAL:CB	2.75	0.49
41:a:1839:G:N9	41:a:1927:A:H1'	2.23	0.49
42:b:37:ILE:HG21	42:b:80:ILE:HG21	1.95	0.49
46:f:24:LEU:HD11	46:f:54:MET:CE	2.42	0.49
48:h:210:ALA:HA	48:h:213:TRP:CE3	2.48	0.49
50:j:25:THR:HG21	50:j:193:VAL:HG22	1.94	0.49
64:x:51:ALA:HB3	64:x:78:VAL:HB	1.95	0.49
10:A:56:C:C5	41:a:2168:G:O6	2.65	0.49
11:AA:812:PHE:HA	14:AE:505:ASP:OD2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AG:283:PHE:CE2	16:AG:332:SER:HA	2.47	0.49
10:B:15:G:N3	10:B:15:G:C2'	2.73	0.49
18:D:974:A:OP1	33:S:69:ARG:NH1	2.46	0.49
22:H:117:LYS:CB	22:H:278:THR:CG2	2.90	0.49
9:9:50:VAL:HG13	39:Y:119:ALA:HB3	1.88	0.49
11:AA:732:ILE:HD11	11:AA:769:PRO:HB3	1.95	0.49
11:AA:900:LYS:CE	16:AG:11:ALA:HB1	2.43	0.49
16:AG:363:LEU:HD11	16:AG:410:ALA:HB2	1.92	0.49
16:AG:448:LEU:HD23	16:AG:473:LEU:HD12	1.95	0.49
10:B:25:C:H2'	10:B:26:G:H5'	1.95	0.49
66:z:47:TYR:CD1	66:z:47:TYR:C	2.90	0.49
1:0:40:MET:HE3	1:0:49:ILE:CD1	2.43	0.48
10:A:15:G:C2	10:A:20:U:O2	2.66	0.48
10:A:18:G:C5	10:A:57:A:C5	3.01	0.48
11:AA:857:VAL:CB	11:AA:862:LEU:CD1	2.91	0.48
11:AA:896:THR:HG23	11:AA:899:GLU:HG2	1.94	0.48
11:AA:1336:ASN:ND2	14:AE:29:MET:HG2	2.27	0.48
13:AD:182:ARG:O	13:AD:205:MET:HA	2.13	0.48
16:AG:244:ARG:CD	16:AG:244:ARG:N	2.73	0.48
16:AG:277:ASP:HB2	16:AG:282:GLN:HG3	1.95	0.48
25:K:114:VAL:HG21	25:K:141:ILE:HD12	1.94	0.48
36:V:48:ASP:HB3	36:V:75:LEU:HD23	1.94	0.48
53:m:24:THR:HG23	53:m:27:GLY:H	1.78	0.48
10:A:76:A:N6	41:a:2422:C:O4'	2.46	0.48
16:AG:440:VAL:HG21	16:AG:481:LEU:HD22	1.88	0.48
10:B:76:A:N3	10:B:76:A:C2'	2.74	0.48
18:D:1174:G:H2'	18:D:1175:G:H5'	1.95	0.48
18:D:1311:A:OP1	47:g:59:ARG:NH1	2.45	0.48
36:V:75:LEU:C	36:V:75:LEU:HD12	2.39	0.48
41:a:742:A:C2	41:a:755:U:N3	2.81	0.48
50:j:156:PHE:CE1	59:s:81:ILE:HD13	2.48	0.48
53:m:22:MET:O	53:m:28:ARG:NH1	2.45	0.48
6:5:108:DT:H73	11:AA:199:ASP:HB3	1.94	0.48
9:9:31:ARG:HE	41:a:1054:A:C5'	2.18	0.48
10:A:47:U:H2'	10:A:48:C:H4'	1.94	0.48
11:AA:903:ARG:HH11	11:AA:903:ARG:HB3	1.76	0.48
12:AB:11:VAL:HG11	14:AE:291:ILE:CG1	2.43	0.48
12:AB:140:PRO:CG	30:P:102:LEU:HB3	2.42	0.48
16:AG:59:PHE:CD1	16:AG:97:ILE:HG23	2.48	0.48
16:AG:248:VAL:HG21	16:AG:275:LEU:HG	1.94	0.48
16:AG:320:ARG:CG	16:AG:320:ARG:NH1	2.73	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:K:99:ALA:CB	25:K:103:THR:HG21	2.43	0.48
30:P:6:ILE:HG23	30:P:100:ILE:CG2	2.43	0.48
41:a:464:U:O3'	53:m:12:ARG:NH2	2.45	0.48
2:1:25:ARG:NH1	2:1:74:ILE:O	2.46	0.48
10:A:41:C:H5'	27:M:143:ARG:HD2	1.96	0.48
11:AA:808:ASN:N	14:AE:633:ALA:HB2	2.21	0.48
11:AA:857:VAL:HB	11:AA:862:LEU:CD1	2.43	0.48
12:AB:155:LYS:HA	18:D:1276:G:OP2	2.13	0.48
14:AE:115:TRP:O	14:AE:1333:THR:HG21	2.13	0.48
14:AE:152:THR:HB	14:AE:172:PHE:CZ	2.48	0.48
14:AE:1027:VAL:HB	14:AE:1121:LEU:HB2	1.95	0.48
14:AE:1261:LEU:HD12	14:AE:1304:ARG:HH21	1.78	0.48
14:AE:1321:SER:OG	14:AE:1349:GLU:OE2	2.22	0.48
16:AG:87:LEU:HD22	16:AG:93:VAL:HG21	1.96	0.48
16:AG:148:ASP:HA	16:AG:164:ARG:CD	2.44	0.48
16:AG:349:GLN:C	16:AG:351:GLU:N	2.71	0.48
16:AG:365:ILE:CD1	16:AG:406:LEU:HD21	2.38	0.48
10:B:59:A:H2'	10:B:60:U:H5'	1.94	0.48
56:p:35:ARG:HD3	56:p:71:LEU:HD13	1.94	0.48
8:7:6:U:C2	18:D:1493:A:H2	2.31	0.48
9:9:51:TYR:CD1	9:9:88:HIS:HB2	2.49	0.48
10:A:14:A:H2'	10:A:14:A:N3	2.29	0.48
10:A:15:G:H22	10:A:20:U:H3	1.59	0.48
11:AA:363:LEU:HB3	11:AA:381:ALA:HB1	1.96	0.48
11:AA:565:GLU:HA	11:AA:569:ILE:HG12	1.95	0.48
12:AB:140:PRO:HD2	30:P:102:LEU:HD22	1.95	0.48
14:AE:201:LEU:HD11	14:AE:220:ARG:HG2	1.95	0.48
10:B:72:A:H2'	10:B:73:A:C5'	2.33	0.48
18:D:1064:G:O2'	18:D:1190:G:N2	2.47	0.48
22:H:330:VAL:HG12	22:H:345:GLY:O	2.14	0.48
30:P:6:ILE:CG2	30:P:100:ILE:HG23	2.43	0.48
39:Y:77:VAL:HG13	39:Y:80:LYS:HE3	1.95	0.48
39:Y:112:LYS:HZ2	39:Y:112:LYS:CB	2.27	0.48
41:a:565:C:H2'	41:a:566:U:O4'	2.13	0.48
41:a:1839:G:N9	41:a:1927:A:C1'	2.77	0.48
58:r:3:VAL:HG22	58:r:36:ALA:HB1	1.95	0.48
10:A:25:C:H2'	10:A:26:G:H5'	1.95	0.48
10:A:37:A:H2'	10:A:38:A:C8	2.48	0.48
11:AA:862:LEU:C	11:AA:862:LEU:CD2	2.86	0.48
12:AB:129:GLU:N	12:AB:180:LYS:HG3	2.29	0.48
12:AB:140:PRO:CG	30:P:102:LEU:HB2	2.36	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AB:153:TYR:CD2	12:AB:153:TYR:N	2.81	0.48
13:AD:100:LEU:HB2	13:AD:144:ILE:HG23	1.94	0.48
14:AE:968:ASN:HA	14:AE:1117:SER:HB2	1.96	0.48
16:AG:183:LEU:HD23	16:AG:197:VAL:HG22	1.94	0.48
16:AG:389:MET:HA	16:AG:407:ARG:NH1	2.29	0.48
16:AG:453:VAL:HG11	16:AG:459:LEU:CG	2.42	0.48
10:B:11:A:H2'	10:B:12:G:C1'	2.43	0.48
22:H:23:ILE:N	22:H:69:ASP:OD2	2.47	0.48
41:a:2685:G:OP1	60:t:78:ARG:NH2	2.47	0.48
10:A:18:G:N3	10:A:58:A:C6	2.82	0.48
11:AA:836:LEU:HD13	11:AA:1054:LEU:HD13	1.95	0.48
16:AG:35:THR:HG21	16:AG:106:THR:HG22	1.96	0.48
41:a:1588:G:C6	41:a:1589:U:O4	2.67	0.48
1:O:5:PHE:HB3	1:O:59:ILE:HD12	1.96	0.48
10:A:58:A:OP2	10:A:58:A:C8	2.67	0.48
11:AA:529:ARG:HH11	11:AA:572:ILE:HG22	1.77	0.48
11:AA:562:GLU:OE1	11:AA:662:SER:OG	2.28	0.48
12:AB:140:PRO:CB	30:P:6:ILE:CD1	2.87	0.48
12:AB:167:ARG:NE	23:I:62:LYS:HB2	2.29	0.48
14:AE:288:PRO:HB2	14:AE:291:ILE:HD12	1.96	0.48
10:B:68:C:C4	10:B:69:C:C5	3.02	0.48
41:a:995:C:O2	59:s:3:THR:OG1	2.24	0.48
2:1:4:ILE:HG12	2:1:106:VAL:HG22	1.95	0.48
10:A:60:U:H4'	10:A:61:C:OP2	2.14	0.48
11:AA:1286:THR:O	11:AA:1290:MET:HB2	2.14	0.48
12:AB:47:GLU:H	12:AB:63:LYS:HG3	1.78	0.48
14:AE:141:PHE:CE2	14:AE:296:LYS:CB	2.94	0.48
16:AG:26:ALA:HB1	16:AG:117:LYS:HG2	1.96	0.48
16:AG:467:LEU:HD12	16:AG:482:ILE:HD11	1.95	0.48
41:a:1067:A:O2'	41:a:1068:G:O4'	2.31	0.48
13:AD:304:LYS:O	16:AG:96:GLN:HG2	2.14	0.48
14:AE:102:MET:HG2	14:AE:246:PRO:HD3	1.95	0.48
14:AE:800:LEU:HB3	14:AE:920:ALA:HB1	1.95	0.48
16:AG:209:PHE:CE1	16:AG:262:VAL:HG21	2.49	0.48
16:AG:288:MET:O	16:AG:288:MET:HG2	2.13	0.48
16:AG:353:HIS:HA	16:AG:356:ILE:HG21	1.94	0.48
10:B:15:G:C2	10:B:20:U:O2	2.66	0.48
18:D:1017:U:O2'	18:D:1018:G:O4'	2.31	0.48
39:Y:133:ARG:O	39:Y:133:ARG:HG2	2.14	0.48
7:6:21:DA:N6	8:7:63:G:N1	2.61	0.47
14:AE:24:LEU:CB	14:AE:232:ASN:OD1	2.54	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:114:ILE:HG12	14:AE:311:ARG:HD2	1.95	0.47
14:AE:1146:GLU:OE2	14:AE:1310:THR:HG22	2.14	0.47
16:AG:27:LEU:HD22	16:AG:114:ILE:HG12	1.96	0.47
16:AG:61:ARG:HD2	16:AG:73:LYS:CD	2.44	0.47
16:AG:62:TRP:CD1	16:AG:95:ASP:HB2	2.49	0.47
16:AG:362:TYR:HA	16:AG:413:ALA:HB3	1.94	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
22:H:318:PRO:HA	22:H:321:VAL:HG12	1.95	0.47
39:Y:21:PRO:CB	39:Y:22:PRO:CD	2.90	0.47
55:o:13:ARG:HD3	61:u:58:TYR:O	2.14	0.47
59:s:84:ILE:HG23	59:s:84:ILE:O	2.14	0.47
3:2:61:LEU:C	3:2:61:LEU:HD12	2.39	0.47
8:7:11:U:O2'	25:K:33:PHE:CZ	2.52	0.47
11:AA:207:THR:OG1	11:AA:354:ASP:OD2	2.32	0.47
14:AE:809:VAL:HG21	14:AE:909:ILE:HG12	1.95	0.47
16:AG:342:ASP:N	16:AG:342:ASP:OD1	2.45	0.47
16:AG:442:ARG:O	16:AG:446:PHE:CE2	2.63	0.47
10:B:14:A:N3	10:B:14:A:H2'	2.29	0.47
22:H:52:GLN:O	22:H:53:PHE:HD1	1.95	0.47
41:a:1814:G:C4'	48:h:51:THR:HG21	2.44	0.47
45:e:18:LEU:HB2	45:e:53:VAL:HG11	1.95	0.47
11:AA:858:GLY:O	11:AA:861:ALA:CB	2.62	0.47
13:AD:59:VAL:HG22	13:AD:144:ILE:HA	1.96	0.47
14:AE:117:LEU:HG	14:AE:118:LYS:HG3	1.95	0.47
16:AG:240:THR:HG21	16:AG:247:PRO:HG3	1.92	0.47
16:AG:299:ASP:CB	16:AG:303:HIS:HA	2.44	0.47
16:AG:444:LEU:HD22	16:AG:473:LEU:CD2	2.43	0.47
10:B:18:G:N3	10:B:58:A:C6	2.82	0.47
18:D:35:G:N3	32:R:115:SER:OG	2.47	0.47
39:Y:77:VAL:HG13	39:Y:80:LYS:CE	2.44	0.47
41:a:1019:U:N3	41:a:1142:A:N6	2.49	0.47
8:7:7:U:C6	8:7:7:U:C3'	2.97	0.47
9:9:48:ALA:HB3	9:9:51:TYR:CD2	2.50	0.47
10:A:33:U:H2'	10:A:35:A:OP2	2.14	0.47
11:AA:905:ILE:CD1	16:AG:8:VAL:HG11	2.43	0.47
12:AB:70:LEU:HB3	12:AB:108:VAL:HG11	1.64	0.47
12:AB:96:THR:CA	14:AE:162:GLU:HG3	2.44	0.47
13:AC:102:LEU:HD12	13:AC:115:ILE:HG12	1.96	0.47
14:AE:891:ASP:OD2	14:AE:1290:ARG:NH2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AG:220:VAL:CG1	16:AG:245:ILE:HG21	2.44	0.47
10:B:56:C:H2'	10:B:57:A:C5'	2.27	0.47
10:B:60:U:H4'	10:B:61:C:OP2	2.14	0.47
18:D:371:A:H2'	18:D:372:C:O4'	2.14	0.47
18:D:1103:C:O2	21:G:106:THR:HG21	2.15	0.47
25:K:111:MET:CE	25:K:125:ALA:HB1	2.39	0.47
41:a:2585:U:O2	41:a:2585:U:O4'	2.32	0.47
64:x:27:VAL:CG2	64:x:40:ILE:HD12	2.44	0.47
16:AG:33:THR:CG2	16:AG:43:ILE:HD11	2.44	0.47
16:AG:233:ARG:HB2	16:AG:327:LEU:CD2	2.42	0.47
16:AG:320:ARG:HH11	16:AG:320:ARG:HG2	1.80	0.47
10:B:58:A:C8	10:B:58:A:OP2	2.67	0.47
17:C:33:ILE:O	17:C:33:ILE:HG12	2.14	0.47
18:D:946:A:H2'	18:D:947:G:C8	2.50	0.47
18:D:1255:G:O2'	18:D:1258:G:N3	2.47	0.47
50:j:121:THR:HB	50:j:127:PHE:CD2	2.49	0.47
10:A:9:G:H5''	10:A:10:G:OP2	2.15	0.47
11:AA:902:LEU:HG	16:AG:111:LYS:HG2	1.97	0.47
14:AE:1150:PRO:HG3	14:AE:1214:PRO:HB2	1.96	0.47
16:AG:36:LYS:HE3	16:AG:43:ILE:HG12	1.95	0.47
16:AG:285:ILE:O	16:AG:288:MET:HE3	2.14	0.47
16:AG:323:GLN:CA	16:AG:323:GLN:NE2	2.75	0.47
41:a:1993:U:H4'	50:j:133:THR:HG22	1.96	0.47
41:a:2303:G:C2	41:a:2314:A:N3	2.82	0.47
9:9:1:MET:SD	9:9:2:ALA:N	2.88	0.47
9:9:8:LYS:NZ	41:a:1046:A:H61	2.11	0.47
11:AA:143:ARG:NH1	11:AA:507:GLY:O	2.32	0.47
12:AB:68:TYR:CZ	14:AE:291:ILE:HG23	2.49	0.47
12:AB:126:THR:CG2	12:AB:130:PRO:HD3	2.44	0.47
13:AD:35:PHE:HA	13:AD:38:THR:HG22	1.97	0.47
14:AE:395:LYS:NZ	14:AE:399:LYS:CE	2.77	0.47
14:AE:526:VAL:HG12	14:AE:549:LYS:HB2	1.96	0.47
14:AE:902:ASP:OD2	14:AE:905:ARG:HB2	2.15	0.47
16:AG:197:VAL:HG11	16:AG:199:ARG:NH2	2.30	0.47
16:AG:207:GLU:HG3	16:AG:210:ARG:HB3	1.96	0.47
16:AG:233:ARG:O	16:AG:327:LEU:CD2	2.62	0.47
16:AG:434:LEU:HD11	16:AG:454:CYS:C	2.39	0.47
16:AG:442:ARG:C	16:AG:446:PHE:CD2	2.85	0.47
16:AG:479:GLY:O	16:AG:483:MET:HG2	2.15	0.47
10:B:60:U:OP2	10:B:61:C:N4	2.45	0.47
18:D:526:C:P	32:R:88:LYS:HE3	2.54	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:N:102:ALA:HB3	28:N:113:ASP:HB3	1.96	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:2168:G:H8	41:a:2168:G:OP1	1.97	0.47
56:p:24:ILE:CD1	56:p:72:LEU:HD21	2.44	0.47
60:t:18:ARG:HB2	60:t:45:GLU:HB3	1.97	0.47
8:7:14:U:C6	8:7:14:U:C3'	2.98	0.47
10:A:68:C:C4	10:A:69:C:C5	3.02	0.47
11:AA:689:ALA:HB2	11:AA:1233:LEU:HD23	1.97	0.47
12:AB:149:GLU:N	12:AB:149:GLU:CD	2.73	0.47
14:AE:103:GLY:H	14:AE:244:VAL:HG22	1.78	0.47
14:AE:833:GLU:N	14:AE:1242:ARG:HH12	2.12	0.47
16:AG:233:ARG:HG2	16:AG:270:ARG:CB	2.45	0.47
10:B:18:G:C6	10:B:57:A:N7	2.83	0.47
18:D:373:A:C2	18:D:374:A:C8	3.03	0.47
18:D:526:C:OP2	32:R:88:LYS:HE3	2.15	0.47
19:E:54:MET:O	19:E:57:ILE:HG22	2.15	0.47
39:Y:64:ARG:HE	39:Y:64:ARG:HB2	1.51	0.47
41:a:1020:A:C6	41:a:1141:U:O2	2.68	0.47
2:1:29:VAL:HB	2:1:55:ILE:HD11	1.96	0.47
8:7:1:A:H2'	8:7:2:U:C6	2.50	0.47
12:AB:172:GLU:N	12:AB:172:GLU:CD	2.73	0.47
13:AD:15:ASP:OD1	13:AD:27:THR:OG1	2.30	0.47
14:AE:1036:ARG:HE	14:AE:1081:VAL:HG11	1.79	0.47
16:AG:243:LYS:O	16:AG:243:LYS:HD3	2.14	0.47
16:AG:288:MET:HE2	16:AG:288:MET:HB3	1.75	0.47
18:D:911:U:H2'	18:D:912:C:C6	2.49	0.47
22:H:84:LEU:N	22:H:84:LEU:CD2	2.78	0.47
22:H:135:LEU:CB	22:H:167:VAL:O	2.63	0.47
41:a:2756:U:C4	41:a:2759:G:C6	3.03	0.47
54:n:36:LEU:HB3	54:n:57:LEU:HD21	1.97	0.47
10:A:18:G:C6	10:A:57:A:N7	2.83	0.47
10:A:29:G:H2'	10:A:30:G:O4'	2.15	0.47
11:AA:230:PHE:HB2	11:AA:333:ILE:HB	1.97	0.47
14:AE:198:CYS:HA	14:AE:221:ILE:CD1	2.45	0.47
14:AE:202:ARG:HH11	14:AE:202:ARG:CG	2.14	0.47
16:AG:36:LYS:HB2	16:AG:101:THR:HG21	1.97	0.47
16:AG:183:LEU:CD2	16:AG:197:VAL:HG22	2.45	0.47
16:AG:353:HIS:O	16:AG:356:ILE:CA	2.63	0.47
22:H:309:MET:HE2	22:H:318:PRO:HB3	1.97	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)
3:2:30:ILE:HD13	3:2:93:LEU:HD12	1.98	0.46
11:AA:618:GLN:CD	14:AE:770:LEU:HD13	2.40	0.46
14:AE:43:THR:HG22	14:AE:57:PHE:HE1	1.80	0.46
16:AG:61:ARG:HA	16:AG:94:GLU:HA	1.97	0.46
16:AG:63:LEU:HD22	16:AG:92:TYR:CD1	2.47	0.46
16:AG:302:LYS:HZ1	16:AG:302:LYS:C	2.12	0.46
10:B:5:G:C2'	10:B:6:G:C5'	2.93	0.46
22:H:316:ILE:HD11	22:H:321:VAL:HG11	1.97	0.46
41:a:1695:G:N7	48:h:14:ARG:NH2	2.63	0.46
9:9:3:LEU:N	9:9:3:LEU:CD1	2.73	0.46
12:AB:133:MET:HE2	12:AB:133:MET:C	2.40	0.46
12:AB:155:LYS:HE3	18:D:1277:C:C6	2.50	0.46
12:AB:173:LEU:HD12	30:P:102:LEU:HG	1.97	0.46
14:AE:50:LYS:HD3	14:AE:50:LYS:HA	1.71	0.46
14:AE:105:ILE:HD12	14:AE:242:LEU:CD2	2.44	0.46
14:AE:1347:LEU:HG	14:AE:1357:ILE:HG23	1.96	0.46
16:AG:1:MET:SD	16:AG:53:SER:HA	2.55	0.46
16:AG:138:ILE:HD12	16:AG:183:LEU:CD1	2.45	0.46
10:B:9:G:H5''	10:B:10:G:OP2	2.15	0.46
10:B:22:G:HO2'	10:B:23:C:P	2.38	0.46
18:D:429:U:N3	18:D:431:A:N6	2.63	0.46
22:H:69:ASP:O	22:H:85:SER:CB	2.63	0.46
40:Z:18:ASP:HB3	40:Z:22:LEU:CD1	2.45	0.46
41:a:1406:U:HO2'	41:a:1407:G:P	2.31	0.46
41:a:2168:G:OP1	41:a:2168:G:C8	2.68	0.46
8:7:64:A:H2'	8:7:65:G:H8	1.80	0.46
9:9:67:THR:H	9:9:68:PRO:HD3	1.80	0.46
10:A:18:G:C8	10:A:57:A:N1	2.83	0.46
11:AA:28:LEU:HD21	11:AA:524:ILE:HG13	1.98	0.46
11:AA:735:LYS:HA	11:AA:748:ILE:HG22	1.98	0.46
11:AA:800:MET:HE3	11:AA:800:MET:HB2	1.69	0.46
11:AA:1336:ASN:OD1	14:AE:33:TRP:HZ2	1.97	0.46
14:AE:1219:ASP:O	14:AE:1223:LEU:HB2	2.15	0.46
16:AG:314:LEU:HB3	16:AG:318:ILE:HD12	1.97	0.46
23:I:75:ILE:HD13	23:I:75:ILE:C	2.40	0.46
25:K:96:MET:CE	25:K:115:LEU:HD11	2.45	0.46
40:Z:4:LYS:O	40:Z:4:LYS:HD2	2.15	0.46
9:9:132:TYR:CE1	40:Z:19:VAL:HG22	2.50	0.46
11:AA:400:VAL:HG22	11:AA:584:TYR:HB3	1.96	0.46
14:AE:108:ALA:HB1	14:AE:279:LEU:HD22	1.96	0.46
14:AE:211:GLU:CG	14:AE:215:LYS:HE3	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:420:PRO:HA	14:AE:437:PHE:O	2.15	0.46
14:AE:515:ARG:NH2	14:AE:718:SER:O	2.48	0.46
14:AE:1167:LYS:NZ	14:AE:1170:LYS:HB2	2.30	0.46
16:AG:208:LEU:HD23	16:AG:208:LEU:HA	1.78	0.46
16:AG:362:TYR:HE1	16:AG:414:LEU:HD21	1.80	0.46
10:B:6:G:O2'	10:B:7:G:C5'	2.63	0.46
18:D:868:C:H2'	18:D:869:G:O4'	2.15	0.46
41:a:2298:A:C6	41:a:2299:U:C2	3.04	0.46
9:9:17:GLU:HG2	9:9:88:HIS:NE2	2.29	0.46
11:AA:1314:GLN:HB2	15:AF:28:ARG:HH12	1.81	0.46
14:AE:1221:LEU:HD22	14:AE:1306:LEU:HB2	1.97	0.46
16:AG:201:LYS:HB3	16:AG:201:LYS:HZ3	1.79	0.46
22:H:332:VAL:HG13	22:H:342:ILE:HG23	1.98	0.46
36:V:8:LEU:HD23	36:V:25:ILE:HG21	1.97	0.46
38:X:16:VAL:HG23	38:X:17:ILE:HD12	1.97	0.46
38:X:106:ALA:HB3	38:X:110:LYS:HD2	1.98	0.46
41:a:2291:U:H2'	41:a:2292:U:C6	2.51	0.46
7:6:21:DA:C6	8:7:63:G:C2	3.03	0.46
12:AB:11:VAL:HG11	14:AE:291:ILE:HD11	1.96	0.46
12:AB:64:PHE:CZ	12:AB:114:ARG:HD2	2.50	0.46
12:AB:126:THR:HG21	12:AB:130:PRO:HD3	1.98	0.46
12:AB:128:PHE:C	12:AB:180:LYS:HG3	2.40	0.46
12:AB:140:PRO:HB3	30:P:79:PRO:HB3	1.98	0.46
13:AC:64:VAL:HG11	13:AC:78:ILE:HG21	1.97	0.46
16:AG:226:ALA:HB1	16:AG:228:ARG:HH11	1.81	0.46
16:AG:393:LEU:CB	16:AG:398:LEU:HD22	1.90	0.46
18:D:1308:U:P	38:X:98:ARG:CG	3.03	0.46
26:L:67:PRO:O	26:L:70:VAL:HG22	2.15	0.46
30:P:8:ILE:HD12	30:P:25:ILE:CD1	2.46	0.46
41:a:686:U:O4	53:m:12:ARG:HB2	2.15	0.46
9:9:18:VAL:HA	9:9:86:MET:CE	2.44	0.46
11:AA:861:ALA:O	11:AA:882:ILE:HD13	2.14	0.46
11:AA:903:ARG:NH1	11:AA:903:ARG:C	2.73	0.46
14:AE:1060:VAL:HG13	14:AE:1106:ILE:HG12	1.96	0.46
16:AG:442:ARG:C	16:AG:446:PHE:HD2	2.15	0.46
10:B:68:C:H3'	10:B:69:C:H5''	1.96	0.46
18:D:1175:G:N3	18:D:1176:A:C8	2.83	0.46
39:Y:37:PHE:CE1	39:Y:56:VAL:HG11	2.51	0.46
41:a:299:A:N1	41:a:322:A:O2'	2.46	0.46
9:9:39:THR:HA	9:9:42:ARG:HH11	1.81	0.46
15:AF:25:ARG:NH1	15:AF:61:ASN:OD1	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:18:G:O2'	10:B:60:U:N3	2.48	0.46
31:Q:34:ILE:HG12	31:Q:70:CYS:SG	2.56	0.46
50:j:152:PRO:HG3	50:j:156:PHE:CZ	2.50	0.46
4:3:94:ARG:CB	4:3:103:ILE:HD12	2.45	0.46
9:9:43:LYS:NZ	9:9:95:LEU:HD13	2.30	0.46
11:AA:858:GLY:C	11:AA:860:ALA:N	2.73	0.46
11:AA:1245:ALA:O	14:AE:375:GLU:HG2	2.15	0.46
12:AB:63:LYS:CG	12:AB:66:PRO:HB3	2.46	0.46
14:AE:385:LEU:HD23	14:AE:390:LEU:HB2	1.98	0.46
16:AG:228:ARG:HB3	16:AG:234:ALA:HA	1.98	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
17:C:12:ARG:NH2	22:H:268:VAL:CG2	2.71	0.46
18:D:1228:C:P	38:X:107:ARG:HH12	2.38	0.46
24:J:162:ALA:O	24:J:165:ARG:O	2.33	0.46
41:a:784:G:H5'	41:a:785:G:OP1	2.15	0.46
41:a:1720:U:H2'	41:a:1721:G:O4'	2.16	0.46
63:w:28:LEU:HD23	63:w:48:VAL:HG21	1.98	0.46
8:7:8:U:OP2	18:D:1397:C:O2	2.34	0.46
9:9:27:VAL:HG22	9:9:99:PHE:HE2	1.80	0.46
9:9:34:THR:HG22	9:9:38:MET:CE	2.46	0.46
9:9:50:VAL:CG2	39:Y:120:ASP:N	2.79	0.46
9:9:111:ALA:HB3	9:9:114:GLU:HG3	1.98	0.46
11:AA:853:ASP:C	16:AG:105:ILE:CB	2.71	0.46
39:Y:72:THR:HG1	39:Y:73:PRO:HD2	1.76	0.46
41:a:1906:G:H4'	41:a:1906:G:OP1	2.16	0.46
41:a:2070:A:H2'	41:a:2071:A:O4'	2.16	0.46
48:h:76:ALA:HB2	48:h:96:TYR:CD1	2.51	0.46
54:n:17:MET:HE2	54:n:25:VAL:HA	1.98	0.46
9:9:50:VAL:HG22	39:Y:119:ALA:C	2.41	0.45
9:9:139:LEU:HD21	40:Z:11:VAL:HG22	1.97	0.45
10:A:14:A:H1'	10:A:22:G:N2	2.31	0.45
10:A:41:C:C5'	27:M:143:ARG:HD2	2.46	0.45
16:AG:200:SER:C	16:AG:230:PRO:HG2	2.38	0.45
16:AG:314:LEU:HD22	16:AG:318:ILE:HD11	1.98	0.45
16:AG:339:MET:HE2	16:AG:343:ASP:HB3	1.98	0.45
16:AG:400:GLU:H	16:AG:400:GLU:HG2	1.40	0.45
18:D:915:A:C8	18:D:915:A:H3'	2.50	0.45
22:H:19:ARG:O	22:H:72:LEU:HD13	2.16	0.45
39:Y:42:ASN:HA	39:Y:45:THR:HB	1.98	0.45
8:7:13:U:H6	8:7:13:U:H5''	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:7:65:G:H2'	8:7:66:A:H8	1.80	0.45
9:9:57:ASN:CG	9:9:62:ARG:HG3	2.30	0.45
9:9:58:THR:HB	9:9:82:ILE:H	1.80	0.45
9:9:60:LEU:HB2	9:9:61:ARG:NH2	2.31	0.45
10:A:6:G:O2'	10:A:7:G:C5'	2.64	0.45
11:AA:900:LYS:NZ	16:AG:13:SER:H	2.14	0.45
14:AE:201:LEU:CD1	14:AE:224:LEU:HD12	2.47	0.45
14:AE:847:ASP:N	14:AE:847:ASP:OD1	2.49	0.45
16:AG:127:VAL:HG22	16:AG:192:GLY:CA	2.46	0.45
16:AG:434:LEU:HD11	16:AG:455:THR:CA	2.46	0.45
10:B:14:A:H1'	10:B:22:G:N2	2.31	0.45
18:D:1225:A:OP1	38:X:101:ARG:HB2	2.15	0.45
18:D:1240:U:OP1	27:M:116:MET:HB2	2.16	0.45
20:F:67:ARG:HD3	20:F:67:ARG:N	2.31	0.45
47:g:16:CYS:CB	47:g:37:CYS:CB	2.82	0.45
1:0:51:VAL:HG22	1:0:51:VAL:O	2.15	0.45
7:6:15:DC:N3	7:6:16:DC:C4	2.85	0.45
8:7:62:U:H2'	8:7:63:G:C8	2.52	0.45
9:9:118:ILE:HB	9:9:119:PRO:CD	2.44	0.45
10:A:42:G:H2'	10:A:43:A:C8	2.47	0.45
11:AA:853:ASP:CG	16:AG:103:ASP:CB	2.89	0.45
11:AA:1311:GLY:O	15:AF:31:GLN:NE2	2.49	0.45
14:AE:26:SER:HB2	14:AE:236:TRP:CH2	2.51	0.45
14:AE:209:ASN:HA	14:AE:214:ARG:NH2	2.31	0.45
16:AG:102:PHE:HB3	16:AG:103:ASP:CG	2.41	0.45
16:AG:227:ALA:CB	16:AG:331:LEU:HA	2.46	0.45
10:B:42:G:H2'	10:B:43:A:C8	2.48	0.45
10:B:58:A:C1'	10:B:60:U:C5	2.99	0.45
50:j:186:LEU:HD21	65:y:4:ILE:HG21	1.98	0.45
9:9:24:SER:HB2	9:9:116:GLU:HG2	1.98	0.45
14:AE:67:ASP:CG	14:AE:95:THR:HG1	2.24	0.45
14:AE:842:ARG:HH22	14:AE:1250:ASP:HB2	1.80	0.45
16:AG:142:VAL:HB	16:AG:175:PRO:HA	1.99	0.45
17:C:61:ARG:HG2	26:L:88:MET:HE1	1.98	0.45
18:D:1308:U:OP1	38:X:100:GLN:OE1	2.22	0.45
21:G:16:PHE:CD2	22:H:42:LEU:O	2.69	0.45
22:H:291:GLY:HA2	22:H:305:HIS:O	2.15	0.45
27:M:27:VAL:HG12	27:M:43:VAL:HG11	1.98	0.45
29:O:63:LEU:HD13	29:O:65:ILE:HD11	1.97	0.45
52:l:149:ILE:CD1	52:l:188:MET:HE3	2.46	0.45
6:5:114:DC:H5''	14:AE:1148:ARG:CZ	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:9:106:PHE:CG	9:9:106:PHE:O	2.69	0.45
10:A:48:C:N4	10:A:59:A:C5	2.84	0.45
11:AA:1002:LEU:HD21	11:AA:1007:LYS:HB2	1.98	0.45
14:AE:395:LYS:NZ	14:AE:399:LYS:CD	2.74	0.45
14:AE:478:LEU:HD21	15:AF:47:THR:HG23	1.99	0.45
16:AG:19:PRO:HG2	16:AG:19:PRO:O	2.17	0.45
10:B:18:G:C8	10:B:57:A:N1	2.83	0.45
20:F:21:ARG:HH22	22:H:341:ARG:HD2	1.82	0.45
21:G:35:ARG:CD	22:H:14:LYS:HD3	2.40	0.45
21:G:208:ARG:HH12	22:H:29:VAL:HG11	1.82	0.45
23:I:117:ALA:HB2	23:I:200:VAL:CG1	2.46	0.45
10:A:58:A:HO2'	10:A:60:U:H5	1.62	0.45
13:AD:308:ALA:HB2	16:AG:96:GLN:HG2	1.06	0.45
14:AE:128:LEU:HD21	14:AE:188:LEU:HB3	1.97	0.45
14:AE:319:SER:HA	14:AE:320:ASN:HA	1.64	0.45
14:AE:395:LYS:NZ	14:AE:399:LYS:HE2	2.32	0.45
16:AG:433:ASP:HB3	16:AG:456:LEU:CD1	2.47	0.45
10:B:48:C:C5	10:B:59:A:C8	3.05	0.45
18:D:17:U:H2'	18:D:18:C:C6	2.52	0.45
18:D:1517:G:H1'	41:a:1919:A:O2'	2.16	0.45
19:E:55:GLN:N	19:E:56:PRO:HD2	2.32	0.45
21:G:114:LEU:HD13	21:G:144:LEU:CB	2.46	0.45
21:G:114:LEU:HA	21:G:144:LEU:HD13	1.98	0.45
10:A:49:G:C2'	10:A:50:U:H5'	2.47	0.45
11:AA:998:LEU:HG	11:AA:1011:LEU:HB3	1.99	0.45
14:AE:76:LYS:HB3	14:AE:76:LYS:NZ	2.32	0.45
14:AE:388:ARG:HG2	14:AE:388:ARG:NH1	2.32	0.45
14:AE:926:PRO:HB2	14:AE:1241:TYR:HE1	1.82	0.45
16:AG:143:LYS:HG3	16:AG:153:ASP:HB2	1.99	0.45
18:D:1308:U:O5'	38:X:98:ARG:HG2	2.16	0.45
22:H:332:VAL:HG11	22:H:335:ILE:CG1	2.38	0.45
27:M:24:ALA:O	27:M:27:VAL:HG22	2.16	0.45
41:a:39:G:H1'	52:l:43:THR:HG21	1.99	0.45
41:a:645:C:H2'	41:a:647:G:C8	2.52	0.45
41:a:2315:G:H5'	54:n:157:THR:HG23	1.97	0.45
41:a:2547:A:H2'	41:a:2548:U:C6	2.52	0.45
44:d:48:U:H2'	44:d:49:C:C6	2.52	0.45
52:l:170:ARG:NH2	52:l:176:ASP:OD1	2.49	0.45
54:n:57:LEU:HD22	54:n:89:VAL:CG2	2.47	0.45
6:5:110:DA:N1	11:AA:536:GLY:O	2.49	0.45
9:9:127:ALA:O	9:9:130:PRO:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:128:LEU:CD2	14:AE:188:LEU:HB3	2.47	0.45
16:AG:3:LYS:HB3	16:AG:6:LEU:HD12	1.99	0.45
16:AG:104:ARG:N	16:AG:105:ILE:HG12	2.32	0.45
21:G:114:LEU:HD13	21:G:144:LEU:HB3	1.99	0.45
29:O:80:ARG:O	29:O:84:THR:HG23	2.17	0.45
30:P:99:GLN:O	30:P:99:GLN:HG2	2.16	0.45
41:a:68:G:N2	41:a:74:A:OP2	2.49	0.45
41:a:2627:G:O2'	41:a:2781:A:N1	2.37	0.45
58:r:15:LEU:HD13	58:r:15:LEU:C	2.42	0.45
6:5:108:DT:O4	11:AA:199:ASP:OD2	2.35	0.45
8:7:59:U:OP2	8:7:59:U:C4	2.70	0.45
9:9:9:GLN:CD	9:9:9:GLN:C	2.85	0.45
9:9:72:LEU:HD22	9:9:72:LEU:C	2.42	0.45
10:A:5:G:C2'	10:A:6:G:C5'	2.93	0.45
10:A:58:A:C1'	10:A:60:U:C5	2.99	0.45
11:AA:103:VAL:HG12	11:AA:117:ILE:HG22	1.97	0.45
11:AA:1247:SER:HB3	14:AE:375:GLU:O	2.17	0.45
11:AA:1334:GLY:O	14:AE:25:ALA:HB3	2.17	0.45
14:AE:109:SER:HB2	14:AE:296:LYS:HG2	1.98	0.45
16:AG:429:LYS:CB	16:AG:430:PRO:HD2	2.47	0.45
18:D:1493:A:C8	18:D:1493:A:OP1	2.70	0.45
48:h:6:CYS:SG	48:h:13:ARG:NH1	2.89	0.45
54:n:29:PRO:HB2	54:n:169:LEU:HD22	1.99	0.45
9:9:31:ARG:CG	9:9:31:ARG:NH1	2.73	0.45
10:A:48:C:C5	10:A:59:A:C8	3.05	0.45
10:A:76:A:C2	55:o:31:HIS:NE2	2.85	0.45
11:AA:24:VAL:HG11	11:AA:704:MET:HE1	1.99	0.45
11:AA:557:ARG:NH2	11:AA:607:SER:O	2.50	0.45
11:AA:678:ARG:HA	11:AA:678:ARG:HD3	1.84	0.45
11:AA:1246:ARG:HH11	11:AA:1266:GLY:HA2	1.82	0.45
12:AB:19:GLU:C	12:AB:44:VAL:HG11	2.23	0.45
13:AD:68:TYR:HE1	13:AD:79:LEU:HD13	1.82	0.45
14:AE:201:LEU:CB	14:AE:221:ILE:HD13	2.47	0.45
16:AG:288:MET:HE3	16:AG:289:ALA:N	2.31	0.45
10:B:34:C:O5'	10:B:34:C:C6	2.70	0.45
18:D:337:G:H2'	18:D:338:A:C8	2.52	0.45
39:Y:95:ASP:OD2	39:Y:95:ASP:N	2.50	0.45
41:a:340:A:O2'	52:l:162:ARG:NH1	2.50	0.45
41:a:954:G:OP2	62:v:16:ARG:NH2	2.50	0.45
46:f:25:LEU:C	46:f:25:LEU:HD13	2.41	0.45
54:n:77:PHE:N	54:n:77:PHE:CD1	2.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:7:9:U:OP2	8:7:9:U:C6	2.70	0.44
9:9:16:SER:HB2	9:9:20:LYS:NZ	2.32	0.44
9:9:139:LEU:CD2	40:Z:11:VAL:HG22	2.47	0.44
11:AA:674:ASP:OD2	11:AA:1070:HIS:ND1	2.50	0.44
11:AA:893:THR:HG22	11:AA:894:GLN:HG3	1.99	0.44
11:AA:1332:SER:C	14:AE:243:PRO:HG2	2.42	0.44
12:AB:128:PHE:CB	12:AB:180:LYS:HG3	2.43	0.44
13:AD:185:TYR:HA	13:AD:202:VAL:O	2.16	0.44
14:AE:75:TYR:CD2	14:AE:75:TYR:O	2.70	0.44
14:AE:126:LEU:HD12	14:AE:223:LEU:HD22	1.99	0.44
14:AE:506:VAL:HG23	14:AE:628:GLY:HA3	1.98	0.44
16:AG:440:VAL:CG2	16:AG:481:LEU:HD21	2.42	0.44
18:D:1176:A:H2'	18:D:1177:G:O4'	2.16	0.44
39:Y:19:PRO:HG2	39:Y:24:GLY:N	2.32	0.44
39:Y:37:PHE:CD2	39:Y:37:PHE:O	2.70	0.44
41:a:930:G:H1'	46:f:25:LEU:HD11	1.98	0.44
62:v:96:ILE:HG21	62:v:126:ILE:HD12	1.98	0.44
8:7:12:U:C3'	8:7:12:U:C6	3.00	0.44
8:7:14:U:H3'	8:7:14:U:C6	2.52	0.44
10:A:60:U:OP2	10:A:61:C:N4	2.45	0.44
11:AA:176:ILE:HD11	11:AA:428:VAL:HG21	1.98	0.44
12:AB:27:ARG:HG3	12:AB:42:VAL:HG11	2.00	0.44
14:AE:115:TRP:HB3	14:AE:1333:THR:CG2	2.46	0.44
14:AE:1227:HIS:HA	14:AE:1230:THR:HG22	1.99	0.44
16:AG:80:ALA:HB1	16:AG:87:LEU:HB2	1.98	0.44
10:B:25:C:C2'	10:B:26:G:H5'	2.47	0.44
18:D:1340:A:H8	18:D:1340:A:O5'	2.00	0.44
18:D:1397:C:O5'	18:D:1397:C:C6	2.70	0.44
21:G:16:PHE:CG	22:H:43:LYS:HA	2.52	0.44
24:J:165:ARG:NH1	24:J:165:ARG:HB2	2.32	0.44
39:Y:34:ILE:HG22	39:Y:34:ILE:O	2.18	0.44
39:Y:125:THR:HA	39:Y:128:ILE:HG12	1.98	0.44
39:Y:140:GLU:OE1	39:Y:140:GLU:N	2.50	0.44
41:a:1266:G:OP1	49:i:16:ARG:NE	2.45	0.44
8:7:59:U:OP2	8:7:59:U:C5	2.71	0.44
10:A:25:C:C2'	10:A:26:G:H5'	2.47	0.44
13:AC:218:ARG:NH1	13:AD:231:PHE:O	2.50	0.44
14:AE:271:ARG:HE	14:AE:271:ARG:HB2	1.58	0.44
16:AG:440:VAL:HG13	16:AG:444:LEU:HB2	2.00	0.44
10:B:9:G:O2'	10:B:45:G:H2'	2.18	0.44
18:D:13:U:C2	18:D:915:A:C5	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:D:915:A:H8	18:D:915:A:O5'	2.00	0.44
22:H:294:VAL:HG21	22:H:330:VAL:HG21	1.99	0.44
24:J:197:GLU:HA	24:J:200:ILE:HD12	1.99	0.44
41:a:1927:A:C8	41:a:1927:A:O5'	2.70	0.44
7:6:15:DC:C4	7:6:16:DC:C5	3.05	0.44
10:A:56:C:H2'	10:A:57:A:C5'	2.27	0.44
11:AA:1088:ASP:OD1	11:AA:1088:ASP:N	2.51	0.44
14:AE:144:TYR:OH	14:AE:162:GLU:OE1	2.34	0.44
14:AE:161:THR:H	14:AE:164:GLN:HB2	1.82	0.44
14:AE:1108:GLN:HG3	14:AE:1109:LEU:HD12	1.99	0.44
14:AE:1158:GLU:HA	14:AE:1223:LEU:HD21	1.99	0.44
16:AG:227:ALA:CB	16:AG:330:GLN:C	2.91	0.44
17:C:12:ARG:HD3	17:C:16:GLU:OE1	2.18	0.44
18:D:109:A:C6	18:D:326:G:C6	3.05	0.44
18:D:376:G:C2	18:D:389:A:C2	3.05	0.44
18:D:397:A:H3'	18:D:397:A:N3	2.32	0.44
22:H:38:VAL:HG22	22:H:48:ILE:HD11	1.99	0.44
38:X:96:PRO:HG2	38:X:102:THR:HG23	1.97	0.44
39:Y:7:TYR:CD2	39:Y:7:TYR:O	2.70	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
60:t:24:VAL:HG13	60:t:33:ALA:HB2	2.00	0.44
10:A:9:G:O2'	10:A:45:G:H2'	2.18	0.44
11:AA:148:GLN:NE2	11:AA:535:PRO:O	2.40	0.44
11:AA:300:ASP:OD1	11:AA:313:ALA:N	2.51	0.44
11:AA:845:LEU:HD23	11:AA:889:PRO:CB	2.48	0.44
11:AA:896:THR:CB	11:AA:897:PRO:HD2	2.48	0.44
14:AE:87:LYS:HE3	30:P:81:GLU:OE1	2.18	0.44
16:AG:15:GLU:HA	16:AG:18:LEU:HB2	2.00	0.44
10:B:49:G:O5'	10:B:49:G:C8	2.71	0.44
23:I:155:GLY:HA2	23:I:163:ALA:HB1	1.99	0.44
41:a:1007:C:OP1	59:s:37:ARG:NH2	2.50	0.44
41:a:1327:A:H2'	41:a:1328:A:O4'	2.17	0.44
41:a:1386:C:H2'	41:a:1387:A:C8	2.53	0.44
11:AA:1298:VAL:HG11	14:AE:96:LYS:NZ	2.33	0.44
12:AB:11:VAL:HG21	12:AB:103:ILE:CD1	2.46	0.44
14:AE:213:LYS:CA	14:AE:213:LYS:HE3	2.47	0.44
14:AE:894:VAL:HG22	14:AE:1258:ARG:HH11	1.83	0.44
16:AG:429:LYS:HB2	16:AG:430:PRO:HD2	1.99	0.44
10:B:37:A:N3	10:B:37:A:H5''	2.32	0.44
18:D:976:G:C8	18:D:1358:U:O2	2.71	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:H:136:VAL:HA	22:H:168:VAL:O	2.18	0.44
41:a:1047:G:N2	41:a:1110:G:O2'	2.50	0.44
41:a:1589:U:C2	41:a:1590:A:C8	3.06	0.44
59:s:30:THR:CG2	59:s:31:GLU:N	2.79	0.44
6:5:116:DG:C6	6:5:117:DA:C6	3.06	0.44
10:A:34:C:OP1	27:M:84:THR:OG1	2.35	0.44
10:A:57:A:O5'	10:A:58:A:P	2.76	0.44
11:AA:561:ILE:HG21	14:AE:772:TYR:HE2	1.82	0.44
11:AA:913:VAL:O	11:AA:913:VAL:HG12	2.17	0.44
11:AA:1314:GLN:HA	15:AF:28:ARG:HH22	1.82	0.44
12:AB:129:GLU:H	12:AB:180:LYS:CD	2.30	0.44
14:AE:62:PHE:N	14:AE:62:PHE:CD1	2.86	0.44
16:AG:126:VAL:HG13	16:AG:130:PHE:CE2	2.53	0.44
10:B:1:C:C5	10:B:2:G:N7	2.86	0.44
18:D:198:G:OP2	18:D:198:G:C8	2.70	0.44
21:G:76:ALA:CB	21:G:210:VAL:HG11	2.48	0.44
21:G:206:ALA:O	21:G:210:VAL:HG23	2.18	0.44
22:H:290:TYR:O	22:H:305:HIS:C	2.56	0.44
41:a:74:A:N7	41:a:88:G:C5	2.86	0.44
41:a:1363:C:O2'	41:a:1809:A:N3	2.46	0.44
41:a:1925:C:C5	41:a:1925:C:OP2	2.70	0.44
9:9:106:PHE:O	9:9:106:PHE:CD2	2.70	0.44
11:AA:6:THR:OG1	11:AA:781:ASP:OD1	2.33	0.44
14:AE:978:ARG:HD3	14:AE:999:TYR:H	1.82	0.44
10:B:49:G:C2'	10:B:50:U:H5'	2.47	0.44
10:B:57:A:O5'	10:B:58:A:P	2.76	0.44
18:D:324:G:N2	18:D:327:A:C8	2.86	0.44
22:H:335:ILE:HG12	22:H:342:ILE:HG23	2.00	0.44
25:K:153:VAL:HG23	25:K:164:ILE:HD13	2.00	0.44
38:X:106:ALA:HB3	38:X:110:LYS:CD	2.47	0.44
39:Y:121:ILE:HA	39:Y:124:MET:SD	2.58	0.44
41:a:57:C:H2'	41:a:58:G:O4'	2.18	0.44
61:u:2:ARG:H	61:u:5:THR:HG1	1.66	0.44
9:9:106:PHE:CD2	9:9:106:PHE:C	2.95	0.44
10:A:1:C:C5	10:A:2:G:N7	2.86	0.44
10:A:32:C:HO2'	27:M:86:GLN:HG3	1.80	0.44
11:AA:1157:GLN:HG3	11:AA:1159:VAL:HG13	2.00	0.44
12:AB:95:GLY:C	14:AE:162:GLU:HG3	2.43	0.44
14:AE:107:LEU:HA	14:AE:276:ASN:ND2	2.33	0.44
14:AE:111:THR:CG2	14:AE:300:GLN:HA	2.48	0.44
14:AE:515:ARG:HH12	14:AE:724:MET:HG2	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AG:123:ARG:HG2	16:AG:123:ARG:HH11	1.81	0.44
16:AG:353:HIS:C	16:AG:357:ASP:HB2	2.43	0.44
41:a:998:C:OP2	66:z:58:ARG:NH2	2.49	0.44
41:a:1095:A:O2'	41:a:1096:A:O4'	2.33	0.44
47:g:18:CYS:HB2	47:g:40:CYS:HB3	1.96	0.44
60:t:76:VAL:HG12	65:y:73:VAL:HB	2.00	0.44
6:5:115:DA:P	14:AE:1148:ARG:HG3	2.58	0.43
9:9:31:ARG:NE	41:a:1054:A:O4'	2.46	0.43
9:9:71:CYS:CA	9:9:117:LEU:HD13	2.48	0.43
11:AA:906:PHE:CD1	11:AA:906:PHE:O	2.71	0.43
12:AB:140:PRO:HB2	30:P:6:ILE:HD11	1.95	0.43
12:AB:141:PHE:CE2	12:AB:173:LEU:HD21	2.52	0.43
13:AD:78:ILE:HA	13:AD:81:ILE:HG22	2.00	0.43
13:AD:212:ASP:OD1	13:AD:212:ASP:N	2.48	0.43
14:AE:111:THR:HG21	14:AE:303:VAL:HB	2.00	0.43
14:AE:213:LYS:HE3	14:AE:213:LYS:HA	1.98	0.43
10:B:26:G:N2	10:B:45:G:N2	2.66	0.43
18:D:684:U:H2'	18:D:685:G:O4'	2.18	0.43
18:D:842:U:H3'	18:D:843:U:C5'	2.48	0.43
38:X:23:TYR:CD2	38:X:69:LEU:HD23	2.53	0.43
41:a:813:U:H2'	41:a:814:C:C6	2.53	0.43
64:x:18:LEU:HD23	64:x:25:ARG:HD2	1.99	0.43
11:AA:318:SER:OG	11:AA:320:ASP:OD1	2.31	0.43
12:AB:128:PHE:CD2	12:AB:128:PHE:O	2.72	0.43
12:AB:140:PRO:HA	30:P:79:PRO:HB2	2.00	0.43
12:AB:152:ASP:HB2	12:AB:157:ARG:CB	2.46	0.43
14:AE:1046:ILE:HG22	14:AE:1061:VAL:HA	2.00	0.43
16:AG:252:VAL:HG13	16:AG:256:GLY:HA2	1.99	0.43
16:AG:287:ALA:HB1	16:AG:331:LEU:CD1	2.32	0.43
16:AG:363:LEU:CD2	16:AG:409:ARG:N	2.81	0.43
18:D:384:G:H2'	18:D:385:C:C6	2.54	0.43
41:a:631:A:N3	41:a:2415:G:O2'	2.48	0.43
4:3:12:ILE:CG2	4:3:80:ALA:HB2	2.49	0.43
6:5:98:DA:C2'	6:5:99:DT:C7	2.96	0.43
8:7:14:U:P	23:I:132:ARG:HH12	2.41	0.43
10:A:56:C:OP1	41:a:2168:G:C4	2.71	0.43
11:AA:11:ILE:HG22	11:AA:1172:LEU:HD11	1.99	0.43
14:AE:58:CYS:SG	14:AE:60:ARG:HG2	2.58	0.43
14:AE:1033:GLY:HA3	14:AE:1081:VAL:O	2.18	0.43
14:AE:1079:LYS:HD3	14:AE:1098:GLN:HB3	2.00	0.43
15:AF:58:LEU:HD12	15:AF:59:ILE:HG12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AG:167:MET:HE3	16:AG:173:PHE:CZ	2.53	0.43
22:H:76:GLU:HA	22:H:76:GLU:OE2	2.18	0.43
25:K:150:PRO:O	25:K:153:VAL:HG22	2.18	0.43
41:a:2189:U:O2'	41:a:2190:G:O4'	2.36	0.43
10:A:18:G:N3	10:A:58:A:C5	2.87	0.43
10:A:22:G:O2'	10:A:23:C:O5'	2.36	0.43
11:AA:902:LEU:HD11	16:AG:111:LYS:NZ	2.33	0.43
16:AG:227:ALA:HB2	16:AG:330:GLN:O	2.18	0.43
10:B:34:C:C5	10:B:34:C:OP1	2.70	0.43
18:D:1417:G:C6	18:D:1482:G:C6	3.06	0.43
22:H:61:GLU:HG2	22:H:62:ILE:HG23	2.00	0.43
41:a:1095:A:H2'	41:a:1096:A:C8	2.53	0.43
41:a:1565:C:O2'	41:a:1567:G:N7	2.48	0.43
50:j:172:VAL:HG11	50:j:175:LEU:HD21	2.01	0.43
11:AA:844:LYS:HD3	11:AA:844:LYS:HA	1.37	0.43
14:AE:141:PHE:HE2	14:AE:296:LYS:CB	2.22	0.43
14:AE:220:ARG:HG2	14:AE:220:ARG:NH1	2.26	0.43
14:AE:568:SER:HB3	14:AE:570:LYS:NZ	2.34	0.43
16:AG:393:LEU:CG	16:AG:398:LEU:HD22	2.22	0.43
16:AG:402:THR:C	16:AG:405:ALA:H	2.26	0.43
16:AG:402:THR:C	16:AG:405:ALA:HB3	2.41	0.43
16:AG:431:ALA:O	16:AG:435:LEU:HG	2.18	0.43
22:H:119:GLY:O	22:H:120:PHE:C	2.62	0.43
24:J:48:LEU:HD13	24:J:48:LEU:N	2.33	0.43
25:K:156:LYS:HG2	28:N:71:VAL:HG13	2.00	0.43
38:X:75:MET:HA	38:X:75:MET:HE3	1.99	0.43
40:Z:29:LYS:HB2	40:Z:29:LYS:HE2	1.45	0.43
41:a:1082:U:H3	41:a:1086:A:N6	2.15	0.43
53:m:12:ARG:HG3	53:m:44:VAL:HG11	1.99	0.43
58:r:55:GLU:HA	58:r:58:LEU:HD12	1.99	0.43
2:1:17:VAL:HG12	2:1:76:VAL:HG21	1.98	0.43
7:6:12:DC:O5'	7:6:12:DC:H6	2.01	0.43
9:9:43:LYS:C	9:9:43:LYS:CD	2.86	0.43
11:AA:694:ARG:HH22	13:AC:80:GLU:HG3	1.82	0.43
12:AB:132:GLU:CB	12:AB:147:VAL:HG13	2.49	0.43
16:AG:10:GLU:C	16:AG:12:VAL:HG22	2.44	0.43
16:AG:162:ILE:HD13	16:AG:167:MET:CE	2.49	0.43
16:AG:320:ARG:HB2	16:AG:323:GLN:CB	2.48	0.43
16:AG:403:VAL:C	16:AG:405:ALA:N	2.73	0.43
23:I:50:ALA:HB2	23:I:75:ILE:HD12	2.00	0.43
41:a:2133:G:O2'	41:a:2157:G:N2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:27:LEU:O	11:AA:528:ARG:NH1	2.43	0.43
11:AA:590:PRO:HB2	11:AA:655:VAL:HG21	2.01	0.43
11:AA:894:GLN:NE2	11:AA:894:GLN:N	2.61	0.43
11:AA:894:GLN:C	11:AA:894:GLN:CD	2.87	0.43
14:AE:1026:PRO:HB2	14:AE:1028:ILE:HG23	2.00	0.43
14:AE:1357:ILE:HG22	14:AE:1359:ALA:H	1.83	0.43
16:AG:305:MET:HE3	16:AG:305:MET:HB3	1.77	0.43
10:B:53:G:C2	10:B:54:U:C5	3.07	0.43
22:H:302:GLY:HA3	22:H:344:LEU:HD13	2.00	0.43
40:Z:26:MET:HE2	40:Z:26:MET:HB2	1.71	0.43
41:a:1020:A:C2	41:a:1141:U:C2	3.07	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
9:9:96:PHE:HD1	9:9:96:PHE:HA	1.70	0.43
10:A:49:G:O5'	10:A:49:G:C8	2.71	0.43
11:AA:646:SER:OG	11:AA:647:ARG:N	2.52	0.43
11:AA:829:THR:HG23	11:AA:1059:ARG:HG2	2.00	0.43
13:AD:29:GLU:HB3	13:AD:200:LYS:HG3	1.99	0.43
14:AE:242:LEU:C	14:AE:242:LEU:HD23	2.44	0.43
14:AE:388:ARG:HG2	14:AE:388:ARG:HH11	1.84	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:824:PRO:HD3	14:AE:835:LEU:HD12	2.00	0.43
16:AG:224:LYS:HB2	16:AG:276:TRP:CH2	2.54	0.43
16:AG:277:ASP:HB2	16:AG:282:GLN:CB	2.49	0.43
16:AG:316:GLN:H	16:AG:316:GLN:HG3	1.54	0.43
10:B:22:G:H2'	10:B:23:C:C5	2.52	0.43
18:D:1371:G:O3'	29:O:71:GLY:HA3	2.19	0.43
41:a:705:A:O4'	48:h:9:THR:HG21	2.19	0.43
41:a:819:A:C4	41:a:1189:A:C2	3.07	0.43
41:a:2331:G:O2'	41:a:2336:A:N1	2.47	0.43
54:n:4:LEU:HD23	54:n:4:LEU:HA	1.96	0.43
63:w:9:GLN:O	63:w:17:ARG:NH2	2.51	0.43
10:A:26:G:N2	10:A:45:G:N2	2.66	0.43
10:A:32:C:O2'	27:M:86:GLN:CD	2.31	0.43
10:A:53:G:C2	10:A:54:U:C5	3.07	0.43
11:AA:712:SER:OG	11:AA:713:GLY:N	2.49	0.43
11:AA:746:ALA:O	11:AA:974:ARG:NH2	2.45	0.43
12:AB:7:LYS:HG2	12:AB:74:VAL:HG13	2.00	0.43
12:AB:140:PRO:HB2	30:P:84:VAL:HG11	2.00	0.43
12:AB:173:LEU:CD1	30:P:102:LEU:CG	2.94	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:1350:ASN:HA	14:AE:1353:VAL:HG12	2.01	0.43
16:AG:168:LEU:CD2	16:AG:231:GLY:HA2	2.09	0.43
16:AG:318:ILE:CG1	16:AG:338:VAL:HG11	2.48	0.43
22:H:72:LEU:HB3	22:H:73:ASP:H	1.68	0.43
41:a:2469:A:N6	41:a:2481:G:O2'	2.51	0.43
11:AA:22:LEU:HB3	11:AA:655:VAL:HG11	2.01	0.43
12:AB:64:PHE:N	12:AB:64:PHE:CD1	2.86	0.43
12:AB:165:PHE:N	30:P:88:MET:CA	2.62	0.43
13:AD:31:LEU:HD21	13:AD:39:LEU:HD12	2.00	0.43
14:AE:102:MET:HG2	14:AE:246:PRO:CG	2.49	0.43
14:AE:513:MET:HG3	14:AE:544:LEU:HD11	2.01	0.43
16:AG:437:LEU:CG	16:AG:456:LEU:CD1	2.92	0.43
18:D:826:C:O2	28:N:16:ASN:ND2	2.52	0.43
18:D:1515:G:H2'	18:D:1516:G:C8	2.52	0.43
22:H:280:LEU:HB2	22:H:330:VAL:O	2.18	0.43
23:I:9:GLY:HA3	33:S:89:MET:HE3	2.01	0.43
23:I:58:GLU:OE1	30:P:94:ALA:HB3	2.18	0.43
41:a:126:A:O5'	53:m:19:ARG:HG3	2.19	0.43
41:a:1028:A:N6	41:a:1125:G:H2'	2.34	0.43
41:a:1385:A:O2'	41:a:1396:U:O2	2.35	0.43
41:a:1406:U:H3	41:a:1596:A:H2	1.59	0.43
41:a:2252:G:O2'	41:a:2253:G:H5'	2.18	0.43
63:w:49:GLU:HB2	63:w:50:PRO:HD3	2.01	0.43
10:A:26:G:H1	10:A:44:A:N6	2.17	0.42
12:AB:105:ASP:OD2	12:AB:105:ASP:N	2.52	0.42
12:AB:136:VAL:HG21	12:AB:173:LEU:CD2	2.49	0.42
12:AB:140:PRO:HB3	30:P:6:ILE:CD1	2.49	0.42
13:AD:192:VAL:HG12	13:AD:193:GLU:H	1.83	0.42
13:AD:308:ALA:HB1	16:AG:60:ARG:CD	2.47	0.42
16:AG:21:GLU:HB3	16:AG:49:ILE:CD1	2.49	0.42
16:AG:131:ARG:HG2	16:AG:186:VAL:CG1	2.48	0.42
16:AG:316:GLN:HE21	16:AG:316:GLN:HB2	1.49	0.42
10:B:22:G:O2'	10:B:23:C:O5'	2.36	0.42
18:D:429:U:O2	18:D:430:A:C8	2.72	0.42
18:D:1126:U:OP1	30:P:7:ARG:NH2	2.51	0.42
34:T:21:ASP:OD1	34:T:22:THR:N	2.49	0.42
41:a:1142:A:H2'	41:a:1142:A:N3	2.34	0.42
41:a:1921:G:C2'	41:a:1922:G:H5'	2.49	0.42
41:a:2395:C:H2'	41:a:2396:G:O4'	2.18	0.42
9:9:31:ARG:HD3	41:a:1054:A:H4'	1.96	0.42
9:9:72:LEU:HD22	9:9:72:LEU:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:444:ASP:OD1	11:AA:444:ASP:N	2.51	0.42
11:AA:557:ARG:HB3	11:AA:587:LEU:HD13	2.00	0.42
11:AA:890:LYS:HB3	11:AA:891:GLY:H	1.61	0.42
11:AA:1268:GLN:NE2	14:AE:352:ARG:HB2	2.34	0.42
14:AE:24:LEU:CD1	14:AE:232:ASN:ND2	2.82	0.42
14:AE:244:VAL:HA	14:AE:269:TYR:OH	2.19	0.42
14:AE:559:ALA:HB3	14:AE:562:GLU:HB3	2.01	0.42
14:AE:1024:THR:HG23	14:AE:1123:ARG:HA	2.00	0.42
22:H:109:THR:C	22:H:153:GLU:HA	2.43	0.42
29:O:28:ILE:HD12	29:O:28:ILE:N	2.34	0.42
40:Z:18:ASP:HB3	40:Z:22:LEU:HD12	2.01	0.42
41:a:320:A:H2'	52:l:131:THR:HG21	2.01	0.42
52:l:145:ASP:HA	52:l:166:LYS:HB3	2.01	0.42
57:q:3:VAL:HA	57:q:36:ARG:O	2.19	0.42
61:u:109:LYS:HG2	61:u:126:ARG:HB2	2.01	0.42
64:x:99:TYR:OH	64:x:111:ARG:NH1	2.52	0.42
8:7:61:G:H5''	8:7:61:G:H8	1.85	0.42
8:7:66:A:O3'	11:AA:688:GLN:NE2	2.53	0.42
10:A:36:U:H2'	10:A:37:A:O4'	2.19	0.42
11:AA:616:ILE:HG13	11:AA:652:TYR:HB2	2.01	0.42
12:AB:43:MET:SD	12:AB:108:VAL:HG12	2.60	0.42
14:AE:47:ARG:HA	14:AE:47:ARG:NE	2.35	0.42
14:AE:141:PHE:CD2	14:AE:297:ARG:HB2	2.54	0.42
14:AE:616:PRO:HA	14:AE:619:ILE:HG22	2.02	0.42
16:AG:87:LEU:CD2	16:AG:93:VAL:HG21	2.49	0.42
16:AG:402:THR:O	16:AG:405:ALA:CB	2.64	0.42
17:C:44:ILE:HG21	22:H:339:ARG:HA	2.01	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	3.08	0.42
21:G:208:ARG:NH1	22:H:29:VAL:HG11	2.34	0.42
22:H:33:LYS:HA	22:H:34:ASP:HA	1.60	0.42
22:H:119:GLY:CA	22:H:132:PRO:C	2.92	0.42
39:Y:23:VAL:HB	39:Y:24:GLY:H	1.65	0.42
40:Z:1:SER:HB3	40:Z:2:ILE:H	1.61	0.42
4:3:39:ILE:HG22	4:3:40:ASN:N	2.34	0.42
9:9:86:MET:H	9:9:86:MET:HG2	1.59	0.42
10:A:46:G:O2'	10:A:47:U:H5''	2.19	0.42
11:AA:478:ARG:HD2	11:AA:492:MET:HA	2.02	0.42
11:AA:811:ASN:ND2	11:AA:1098:LEU:O	2.51	0.42
11:AA:859:GLU:H	11:AA:859:GLU:HG3	1.38	0.42
14:AE:126:LEU:CD1	14:AE:223:LEU:HD22	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:850:LYS:HB3	14:AE:855:ASP:HB2	2.00	0.42
16:AG:218:GLU:H	16:AG:218:GLU:HG2	1.64	0.42
16:AG:226:ALA:O	16:AG:228:ARG:N	2.52	0.42
16:AG:288:MET:HE3	16:AG:288:MET:C	2.45	0.42
10:B:18:G:N3	10:B:58:A:C5	2.87	0.42
18:D:552:U:O2'	32:R:83:ARG:O	2.27	0.42
18:D:1323:G:H2'	18:D:1324:A:C8	2.54	0.42
21:G:187:VAL:HG21	21:G:199:VAL:HG23	2.02	0.42
33:S:41:ARG:O	33:S:45:VAL:HG12	2.20	0.42
41:a:879:G:H2'	41:a:880:G:O4'	2.19	0.42
49:i:43:ILE:HG22	49:i:49:TYR:HB2	2.01	0.42
9:9:47:GLU:HG3	9:9:95:LEU:CD2	2.49	0.42
10:A:56:C:C2	41:a:2112:G:C5	3.07	0.42
11:AA:125:GLY:H	11:AA:495:ALA:HB1	1.84	0.42
11:AA:469:VAL:HA	11:AA:472:GLU:HG2	2.02	0.42
11:AA:699:LEU:HG	11:AA:799:ASN:HD22	1.85	0.42
11:AA:894:GLN:NE2	11:AA:894:GLN:C	2.77	0.42
12:AB:95:GLY:HA2	14:AE:293:ARG:HH12	1.84	0.42
14:AE:220:ARG:NH1	14:AE:220:ARG:CG	2.82	0.42
14:AE:950:ILE:HB	14:AE:1018:ALA:HB3	2.01	0.42
14:AE:1289:ASN:O	14:AE:1293:GLU:HB2	2.20	0.42
16:AG:183:LEU:HD22	16:AG:195:LEU:HD13	2.00	0.42
16:AG:226:ALA:HB1	16:AG:228:ARG:NH1	2.34	0.42
16:AG:282:GLN:HA	16:AG:282:GLN:HE21	1.82	0.42
16:AG:343:ASP:HB3	16:AG:347:LYS:HE3	2.01	0.42
17:C:12:ARG:O	17:C:16:GLU:HG3	2.19	0.42
30:P:57:VAL:O	30:P:58:ASN:ND2	2.52	0.42
41:a:2602:A:H5''	41:a:2603:G:C5'	2.49	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
9:9:52:MET:HE1	9:9:85:SER:HB2	2.00	0.42
9:9:80:THR:O	41:a:1108:U:OP1	2.38	0.42
11:AA:913:VAL:HG21	16:AG:108:GLN:HE22	1.65	0.42
11:AA:1244:HIS:NE2	11:AA:1266:GLY:O	2.44	0.42
14:AE:586:GLY:HA3	14:AE:612:LEU:HD11	2.01	0.42
14:AE:797:THR:HG22	14:AE:924:GLY:HA3	2.01	0.42
16:AG:398:LEU:C	16:AG:398:LEU:HD12	2.44	0.42
22:H:110:GLY:H	22:H:153:GLU:N	2.17	0.42
39:Y:123:ALA:HA	39:Y:126:ARG:HG3	2.00	0.42
41:a:742:A:N1	41:a:755:U:O4	2.53	0.42
41:a:973:A:O4'	41:a:1188:U:C6	2.72	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:h:37:ASN:HB2	48:h:62:TYR:HB2	2.01	0.42
8:7:7:U:H6	8:7:7:U:H3'	1.83	0.42
9:9:50:VAL:CG1	39:Y:119:ALA:CB	2.88	0.42
9:9:67:THR:N	9:9:68:PRO:HD3	2.33	0.42
11:AA:741:MET:SD	11:AA:974:ARG:NH2	2.93	0.42
11:AA:888:THR:CB	11:AA:889:PRO:CD	2.97	0.42
13:AD:76:GLU:HB3	13:AD:80:GLU:HB3	2.01	0.42
14:AE:137:ARG:HA	14:AE:142:GLU:HG2	2.02	0.42
14:AE:144:TYR:CE1	14:AE:162:GLU:OE1	2.73	0.42
14:AE:385:LEU:CD2	14:AE:390:LEU:HB2	2.50	0.42
14:AE:820:ILE:HD11	14:AE:822:MET:HE2	2.02	0.42
14:AE:820:ILE:HG12	14:AE:884:SER:HB2	2.01	0.42
16:AG:56:PHE:CD1	16:AG:56:PHE:N	2.88	0.42
16:AG:296:ILE:CD1	16:AG:307:ILE:HA	2.49	0.42
22:H:274:TYR:HD1	22:H:335:ILE:HD12	1.84	0.42
39:Y:41:PHE:HA	39:Y:68:PHE:CE2	2.54	0.42
41:a:1021:A:N3	41:a:1021:A:C3'	2.78	0.42
41:a:1250:G:OP2	61:u:21:ARG:NH2	2.52	0.42
48:h:240:PHE:CD2	48:h:240:PHE:O	2.72	0.42
60:t:113:MET:HE3	60:t:116:ILE:HD11	2.01	0.42
7:6:27:DG:H1'	7:6:28:DA:C5	2.55	0.42
9:9:67:THR:H	9:9:68:PRO:CD	2.29	0.42
10:A:47:U:O2'	10:A:50:U:OP1	2.38	0.42
11:AA:1282:GLY:O	14:AE:1361:THR:OG1	2.33	0.42
16:AG:37:LYS:HA	16:AG:37:LYS:HD3	1.67	0.42
16:AG:234:ALA:HB3	16:AG:271:ILE:HD13	2.01	0.42
16:AG:285:ILE:O	16:AG:288:MET:HE2	2.19	0.42
16:AG:314:LEU:HD23	16:AG:314:LEU:HA	1.85	0.42
10:B:47:U:O2'	10:B:50:U:OP1	2.37	0.42
18:D:421:U:O2	18:D:421:U:O4'	2.37	0.42
22:H:332:VAL:HG12	22:H:334:ASP:N	2.33	0.42
25:K:133:PRO:HA	25:K:136:VAL:HG12	2.02	0.42
35:U:6:LEU:HG	35:U:17:TYR:HB3	2.00	0.42
41:a:1394:U:C4	41:a:1395:A:C6	3.07	0.42
41:a:2788:C:H2'	41:a:2789:C:C6	2.55	0.42
52:l:134:LEU:HB2	52:l:160:ALA:HB1	2.02	0.42
8:7:61:G:H8	8:7:61:G:C5'	2.33	0.42
11:AA:845:LEU:HD21	11:AA:912:ASP:H	1.84	0.42
11:AA:903:ARG:HD2	11:AA:903:ARG:HA	1.30	0.42
11:AA:998:LEU:HD21	11:AA:1015:ALA:HB2	2.02	0.42
11:AA:1279:GLU:HG2	14:AE:1357:ILE:HD13	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:136:GLU:OE1	14:AE:312:ARG:NH2	2.53	0.42
14:AE:201:LEU:HD11	14:AE:220:ARG:NH1	2.31	0.42
14:AE:390:LEU:N	14:AE:390:LEU:HD13	2.35	0.42
14:AE:1272:SER:OG	14:AE:1273:ASP:N	2.53	0.42
16:AG:422:GLU:CA	16:AG:426:GLY:N	2.62	0.42
41:a:560:C:O2	66:z:48:ARG:NH1	2.41	0.42
41:a:948:C:H1'	41:a:984:A:C8	2.55	0.42
41:a:1932:A:H2'	41:a:1933:G:O4'	2.19	0.42
41:a:2803:G:H2'	41:a:2804:U:C5	2.55	0.42
54:n:123:ASP:OD1	54:n:123:ASP:C	2.62	0.42
59:s:32:LEU:HD23	59:s:54:ILE:HD13	2.01	0.42
11:AA:524:ILE:HD12	11:AA:712:SER:HB2	2.02	0.42
11:AA:1268:GLN:NE2	14:AE:352:ARG:CD	2.66	0.42
14:AE:109:SER:HA	14:AE:110:PRO:HD3	1.96	0.42
14:AE:120:LEU:HA	14:AE:121:PRO:HA	1.84	0.42
14:AE:245:LEU:CG	14:AE:246:PRO:HD2	2.47	0.42
14:AE:839:VAL:HG12	14:AE:864:LEU:HD12	2.02	0.42
14:AE:930:LEU:HA	14:AE:1244:GLN:HG3	2.02	0.42
16:AG:296:ILE:HD11	16:AG:307:ILE:CD1	2.50	0.42
16:AG:307:ILE:CB	16:AG:338:VAL:HA	2.45	0.42
16:AG:354:ALA:O	16:AG:358:THR:HG22	2.19	0.42
16:AG:434:LEU:CD1	16:AG:455:THR:CA	2.98	0.42
10:B:58:A:OP2	10:B:58:A:H8	2.02	0.42
18:D:977:A:H1'	18:D:982:U:O4	2.20	0.42
25:K:136:VAL:O	25:K:140:THR:HG23	2.20	0.42
41:a:493:G:H2'	41:a:494:G:O4'	2.20	0.42
41:a:1925:C:OP2	41:a:1925:C:C6	2.73	0.42
41:a:2511:U:O4	41:a:2575:C:N3	2.52	0.42
48:h:119:GLY:O	48:h:130:LEU:HB3	2.20	0.42
56:p:25:THR:HG22	56:p:34:THR:HG23	2.02	0.42
66:z:76:TYR:OH	66:z:92:ARG:NH1	2.51	0.42
9:9:25:ALA:HA	9:9:96:PHE:HE1	1.85	0.41
10:A:15:G:H1	10:A:20:U:H3	1.67	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
13:AD:79:LEU:HD11	14:AE:526:VAL:HG21	2.02	0.41
14:AE:576:ARG:HD3	14:AE:593:ASN:HA	2.02	0.41
16:AG:244:ARG:N	16:AG:244:ARG:HE	2.18	0.41
16:AG:277:ASP:HB2	16:AG:282:GLN:CG	2.50	0.41
16:AG:307:ILE:HG13	16:AG:338:VAL:HG23	2.02	0.41
10:B:15:G:H1	10:B:20:U:H3	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:46:G:O2'	10:B:47:U:H5''	2.19	0.41
18:D:1499:A:O2'	18:D:1500:A:C5'	2.67	0.41
20:F:32:VAL:HG11	31:Q:89:PRO:HG3	2.02	0.41
22:H:292:CYS:SG	22:H:304:VAL:HB	2.60	0.41
39:Y:100:ILE:HB	39:Y:101:SER:H	1.71	0.41
41:a:244:A:OP2	55:o:8:ARG:NH2	2.50	0.41
41:a:567:U:OP2	61:u:29:LYS:NZ	2.53	0.41
41:a:2252:G:H2'	41:a:2253:G:H8	1.84	0.41
41:a:2822:G:OP1	50:j:164:GLN:NE2	2.47	0.41
45:e:56:LEU:HD23	45:e:56:LEU:HA	1.87	0.41
48:h:76:ALA:HB2	48:h:96:TYR:CE1	2.55	0.41
60:t:38:ILE:HD11	60:t:112:PHE:CZ	2.55	0.41
66:z:65:ILE:CD1	66:z:92:ARG:HB2	2.49	0.41
10:A:18:G:O2'	10:A:60:U:N3	2.48	0.41
10:A:58:A:OP2	10:A:58:A:H8	2.02	0.41
11:AA:836:LEU:HD21	11:AA:921:PRO:HD3	2.02	0.41
12:AB:11:VAL:HG23	12:AB:103:ILE:HD13	1.97	0.41
14:AE:395:LYS:HZ2	14:AE:399:LYS:HE2	1.84	0.41
16:AG:41:GLN:HB2	16:AG:42:GLU:H	1.73	0.41
10:B:26:G:H1	10:B:44:A:N6	2.18	0.41
18:D:548:G:C6	18:D:549:C:C4	3.08	0.41
18:D:1235:U:H2'	18:D:1236:A:O4'	2.20	0.41
21:G:47:VAL:N	21:G:48:PRO:HD2	2.34	0.41
22:H:152:LEU:CB	22:H:171:ARG:H	2.32	0.41
29:O:55:VAL:O	29:O:57:MET:N	2.52	0.41
41:a:2311:A:C2	54:n:85:ILE:HD11	2.55	0.41
54:n:122:PHE:CZ	54:n:167:ARG:HA	2.55	0.41
9:9:118:ILE:H	9:9:119:PRO:HD2	1.86	0.41
11:AA:1275:VAL:HG13	11:AA:1287:LEU:HD11	2.01	0.41
16:AG:26:ALA:CA	16:AG:117:LYS:HG2	2.51	0.41
16:AG:323:GLN:HE21	16:AG:323:GLN:C	2.28	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:1061:G:H5'	30:P:61:ALA:HB2	2.02	0.41
18:D:1333:A:H2'	18:D:1334:G:O4'	2.19	0.41
30:P:87:LEU:HA	30:P:87:LEU:HD12	1.85	0.41
41:a:126:A:OP1	53:m:45:SER:OG	2.38	0.41
41:a:1082:U:N3	41:a:1086:A:C6	2.87	0.41
41:a:1570:A:H2'	41:a:1571:A:C8	2.56	0.41
41:a:2273:A:H2'	41:a:2274:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:2683:C:O2	60:t:70:ARG:NH2	2.52	0.41
66:z:66:ASN:OD1	66:z:70:ARG:NE	2.54	0.41
11:AA:903:ARG:NH1	11:AA:903:ARG:CG	2.82	0.41
14:AE:239:LEU:N	14:AE:239:LEU:HD23	2.36	0.41
14:AE:848:VAL:HB	14:AE:858:VAL:HG22	2.02	0.41
16:AG:105:ILE:HD13	16:AG:105:ILE:H	1.85	0.41
16:AG:434:LEU:CD1	16:AG:455:THR:O	2.62	0.41
18:D:502:A:H2'	18:D:503:C:O4'	2.20	0.41
18:D:791:G:N2	18:D:1497:G:O3'	2.53	0.41
22:H:342:ILE:HG22	22:H:344:LEU:HD12	2.02	0.41
27:M:22:LEU:HD13	27:M:97:ASN:ND2	2.35	0.41
40:Z:23:ILE:HD12	40:Z:23:ILE:HA	1.78	0.41
41:a:1082:U:C4	41:a:1086:A:N6	2.88	0.41
8:7:68:G:H21	14:AE:427:PRO:HD3	1.85	0.41
9:9:61:ARG:C	9:9:65:GLU:HB2	2.45	0.41
9:9:71:CYS:SG	9:9:117:LEU:HB2	2.60	0.41
10:A:22:G:H2'	10:A:23:C:C5	2.52	0.41
10:A:34:C:H41	27:M:83:SER:HA	1.85	0.41
10:A:46:G:H2'	10:A:47:U:OP2	2.21	0.41
11:AA:847:PRO:HB2	11:AA:1047:LEU:HD11	2.03	0.41
11:AA:1329:GLU:HA	14:AE:245:LEU:HD13	2.03	0.41
12:AB:141:PHE:HE2	12:AB:173:LEU:HD21	1.83	0.41
14:AE:144:TYR:N	14:AE:144:TYR:CD1	2.88	0.41
16:AG:434:LEU:HG	16:AG:455:THR:CA	2.50	0.41
18:D:1225:A:H2'	18:D:1226:C:C5	2.56	0.41
41:a:197:A:N6	41:a:2430:A:H2'	2.36	0.41
41:a:548:G:H3'	41:a:549:G:O4'	2.20	0.41
41:a:642:U:O2'	41:a:644:A:N7	2.51	0.41
41:a:2294:G:OP1	64:x:10:ARG:HD3	2.21	0.41
53:m:12:ARG:CG	53:m:44:VAL:HG11	2.50	0.41
60:t:107:LEU:HD21	60:t:115:ILE:HG21	2.01	0.41
3:2:46:ALA:O	3:2:50:LEU:HB2	2.21	0.41
11:AA:135:THR:HG22	11:AA:144:VAL:HG22	2.03	0.41
11:AA:550:VAL:HG13	14:AE:777:HIS:CD2	2.56	0.41
12:AB:43:MET:CE	12:AB:112:MET:HB2	2.51	0.41
12:AB:65:PHE:HE2	12:AB:111:ILE:CD1	2.22	0.41
12:AB:95:GLY:O	14:AE:162:GLU:OE2	2.35	0.41
12:AB:128:PHE:HE2	12:AB:134:VAL:HG11	1.78	0.41
12:AB:133:MET:N	12:AB:133:MET:CE	2.73	0.41
14:AE:123:ARG:HD3	14:AE:123:ARG:HA	1.48	0.41
14:AE:190:LYS:HB2	14:AE:190:LYS:HE3	1.41	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:1106:ILE:O	14:AE:1123:ARG:N	2.46	0.41
16:AG:161:VAL:HB	16:AG:196:PHE:CE1	2.54	0.41
16:AG:202:PRO:C	16:AG:204:MET:N	2.79	0.41
16:AG:206:ILE:HD11	16:AG:226:ALA:HB2	2.02	0.41
16:AG:233:ARG:CB	16:AG:327:LEU:CD2	2.98	0.41
18:D:197:A:C5	18:D:221:C:H4'	2.53	0.41
18:D:429:U:O2	18:D:430:A:N7	2.53	0.41
20:F:67:ARG:HD3	20:F:67:ARG:H	1.85	0.41
39:Y:21:PRO:HD2	39:Y:22:PRO:HD2	2.03	0.41
39:Y:116:MET:HA	39:Y:116:MET:CE	2.50	0.41
40:Z:30:PHE:HD1	40:Z:30:PHE:HA	1.75	0.41
41:a:5:A:H2'	41:a:6:A:C8	2.56	0.41
62:v:73:ILE:HG21	62:v:91:TYR:CZ	2.56	0.41
2:1:92:ARG:NE	2:1:94:ASP:OD1	2.54	0.41
10:A:65:C:C2'	10:A:66:C:H5'	2.49	0.41
11:AA:741:MET:HE3	11:AA:974:ARG:HH12	1.85	0.41
11:AA:895:LEU:HB3	11:AA:903:ARG:HD3	2.02	0.41
12:AB:23:ALA:CA	12:AB:44:VAL:HG21	2.50	0.41
13:AD:46:ILE:HD11	13:AD:224:LEU:HD13	2.02	0.41
14:AE:53:ARG:HA	14:AE:54:ASP:HA	1.56	0.41
16:AG:108:GLN:HA	16:AG:111:LYS:HD2	2.03	0.41
16:AG:300:GLU:HB3	16:AG:301:ASP:H	1.70	0.41
18:D:915:A:C6	18:D:916:U:C4	3.08	0.41
29:O:84:THR:HG21	29:O:103:PHE:CB	2.45	0.41
31:Q:88:GLY:H	31:Q:114:THR:HG22	1.84	0.41
39:Y:102:ARG:HD2	39:Y:103:ALA:N	2.36	0.41
52:l:48:THR:HG23	52:l:86:ALA:HB3	2.02	0.41
2:1:75:PHE:CZ	2:1:104:THR:HG21	2.56	0.41
8:7:17:U:H4'	8:7:17:U:OP1	2.21	0.41
11:AA:144:VAL:HG23	11:AA:515:MET:HB2	2.02	0.41
14:AE:68:TYR:CB	14:AE:75:TYR:HE2	2.34	0.41
14:AE:279:LEU:HD13	14:AE:299:LEU:HD13	2.02	0.41
14:AE:647:PRO:HG3	14:AE:697:MET:HB3	2.01	0.41
16:AG:148:ASP:HA	16:AG:164:ARG:HD2	2.03	0.41
16:AG:168:LEU:CB	16:AG:171:GLU:HB2	2.46	0.41
16:AG:207:GLU:HG3	16:AG:210:ARG:CB	2.50	0.41
16:AG:437:LEU:CD2	16:AG:488:ILE:CD1	2.98	0.41
22:H:155:LYS:O	22:H:169:SER:CB	2.68	0.41
34:T:43:PHE:CE2	34:T:56:LEU:HD22	2.55	0.41
38:X:4:ILE:CG1	38:X:9:ILE:HD12	2.50	0.41
41:a:207:A:H2'	41:a:208:C:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:a:2298:A:C5	41:a:2321:U:C4	3.09	0.41
41:a:2615:U:C2	49:i:4:GLN:HA	2.55	0.41
6:5:98:DA:H2'	6:5:99:DT:H72	2.01	0.41
6:5:116:DG:OP1	14:AE:1311:LYS:NZ	2.46	0.41
8:7:10:U:O2	8:7:10:U:C3'	2.69	0.41
8:7:14:U:P	23:I:132:ARG:NH1	2.94	0.41
9:9:48:ALA:HB3	9:9:51:TYR:HD2	1.86	0.41
10:A:26:G:C2	10:A:45:G:N2	2.89	0.41
11:AA:803:ALA:HB2	11:AA:1094:VAL:HG21	2.03	0.41
11:AA:936:ARG:HB2	11:AA:1042:LEU:HD12	2.03	0.41
11:AA:987:GLU:HG2	11:AA:991:LYS:HE3	2.03	0.41
11:AA:1278:LEU:HD23	11:AA:1278:LEU:HA	1.86	0.41
12:AB:167:ARG:HD2	23:I:61:ALA:HB1	2.03	0.41
13:AD:44:ARG:HA	13:AD:183:ILE:HD12	2.03	0.41
13:AD:205:MET:HE1	13:AD:217:ILE:HG13	2.02	0.41
14:AE:109:SER:CB	14:AE:296:LYS:HG2	2.51	0.41
16:AG:152:LEU:HD11	16:AG:162:ILE:HD12	2.02	0.41
16:AG:284:VAL:HG22	16:AG:305:MET:CE	2.51	0.41
16:AG:285:ILE:CA	16:AG:293:VAL:HG11	2.51	0.41
16:AG:374:VAL:O	16:AG:374:VAL:CG1	2.68	0.41
16:AG:434:LEU:HD22	16:AG:459:LEU:HD11	1.81	0.41
10:B:8:U:OP2	10:B:8:U:H6	2.04	0.41
18:D:537:G:OP1	32:R:110:ARG:NH2	2.48	0.41
32:R:110:ARG:NH1	32:R:112:GLN:O	2.53	0.41
38:X:16:VAL:O	38:X:20:THR:HG23	2.21	0.41
39:Y:104:GLN:HB3	39:Y:105:LEU:H	1.74	0.41
41:a:871:U:H2'	41:a:872:U:C6	2.56	0.41
41:a:984:A:N3	41:a:984:A:H2'	2.35	0.41
41:a:1839:G:C4	41:a:1927:A:C5	3.08	0.41
42:b:59:LEU:HD12	42:b:80:ILE:HD12	2.03	0.41
52:l:188:MET:HE2	52:l:193:VAL:HA	2.03	0.41
8:7:1:A:C6	8:7:2:U:C4	3.09	0.41
9:9:8:LYS:NZ	41:a:1046:A:N6	2.69	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
11:AA:870:ILE:HB	11:AA:944:ARG:HD3	2.03	0.41
14:AE:47:ARG:NE	14:AE:47:ARG:CA	2.83	0.41
14:AE:351:GLY:O	14:AE:467:ALA:HA	2.21	0.41
14:AE:390:LEU:HD13	14:AE:390:LEU:H	1.85	0.41
14:AE:734:ALA:O	14:AE:738:ARG:HB2	2.21	0.41
16:AG:10:GLU:CA	16:AG:12:VAL:HG22	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AG:125:MET:O	16:AG:125:MET:SD	2.79	0.41
16:AG:201:LYS:N	16:AG:201:LYS:CD	2.73	0.41
16:AG:244:ARG:N	16:AG:244:ARG:NE	2.69	0.41
16:AG:302:LYS:HE3	16:AG:302:LYS:CA	2.51	0.41
18:D:152:A:N6	18:D:170:U:C2	2.89	0.41
18:D:218:U:H2'	18:D:219:U:O4'	2.21	0.41
18:D:1368:A:OP1	29:O:113:ARG:NH2	2.54	0.41
41:a:36:G:N3	41:a:450:G:O2'	2.53	0.41
41:a:476:G:H4'	41:a:502:A:N1	2.35	0.41
41:a:753:A:C5	41:a:754:U:C5	3.09	0.41
41:a:2572:A:N7	50:j:150:GLN:NE2	2.69	0.41
54:n:171:ALA:O	54:n:174:ASP:N	2.54	0.41
9:9:23:LEU:HA	9:9:118:ILE:CG1	2.51	0.40
9:9:73:LYS:CB	9:9:117:LEU:HD11	2.51	0.40
10:A:25:C:H2'	10:A:26:G:C5'	2.52	0.40
11:AA:1313:HIS:CD2	15:AF:31:GLN:NE2	2.57	0.40
13:AC:57:THR:HG23	13:AC:158:ARG:HH21	1.86	0.40
13:AC:104:LYS:HG2	13:AC:110:VAL:HG22	2.03	0.40
16:AG:204:MET:SD	16:AG:204:MET:O	2.79	0.40
16:AG:437:LEU:CD2	16:AG:488:ILE:HD13	2.51	0.40
18:D:1330:U:OP2	38:X:26:GLY:HA3	2.21	0.40
25:K:150:PRO:HA	25:K:153:VAL:HG22	2.03	0.40
41:a:17:G:H2'	41:a:18:U:C6	2.56	0.40
41:a:67:U:C4	41:a:74:A:C6	3.04	0.40
48:h:175:ARG:NH1	48:h:181:MET:HE2	2.36	0.40
64:x:53:THR:HG23	64:x:74:VAL:HG21	2.03	0.40
12:AB:173:LEU:HD12	12:AB:173:LEU:HA	1.92	0.40
14:AE:108:ALA:HB2	14:AE:276:ASN:OD1	2.22	0.40
14:AE:395:LYS:HE3	14:AE:395:LYS:HB3	1.45	0.40
14:AE:515:ARG:HG2	14:AE:516:ASP:H	1.85	0.40
14:AE:923:ILE:O	14:AE:1241:TYR:OH	2.31	0.40
16:AG:211:ILE:HA	16:AG:211:ILE:HD12	1.85	0.40
10:B:26:G:C2	10:B:45:G:N2	2.89	0.40
24:J:100:ASN:OD1	24:J:111:ARG:NH1	2.54	0.40
39:Y:35:MET:O	39:Y:35:MET:SD	2.79	0.40
39:Y:122:GLU:O	39:Y:122:GLU:HG2	2.21	0.40
41:a:851:C:H2'	41:a:852:U:C6	2.56	0.40
41:a:1406:U:C2'	41:a:1407:G:OP2	2.69	0.40
48:h:29:PRO:HG2	48:h:34:LEU:HD11	2.03	0.40
59:s:104:ALA:O	59:s:108:MET:HG3	2.21	0.40
12:AB:64:PHE:HA	12:AB:65:PHE:HA	1.74	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AE:26:SER:CB	14:AE:236:TRP:CZ2	2.95	0.40
14:AE:1050:THR:HG23	14:AE:1057:SER:HB3	2.03	0.40
10:B:76:A:N3	41:a:2493:U:H5''	2.37	0.40
18:D:915:A:C8	18:D:915:A:C3'	3.04	0.40
29:O:10:GLY:HA3	29:O:78:ALA:O	2.21	0.40
33:S:16:LEU:HD13	33:S:54:ASP:HB2	2.03	0.40
39:Y:14:ALA:HB3	39:Y:50:LYS:HA	2.03	0.40
41:a:1548:A:H2'	41:a:1549:A:C8	2.55	0.40
43:c:33:LEU:O	43:c:34:HIS:CG	2.75	0.40
48:h:232:HIS:HA	48:h:242:LYS:HE3	2.04	0.40
11:AA:213:LEU:HD13	11:AA:422:LYS:HG2	2.03	0.40
11:AA:738:GLU:HA	11:AA:741:MET:HE2	2.03	0.40
14:AE:117:LEU:HD22	14:AE:139:LEU:CD1	2.52	0.40
16:AG:230:PRO:HA	16:AG:269:GLU:CD	2.47	0.40
16:AG:323:GLN:NE2	16:AG:323:GLN:C	2.79	0.40
18:D:579:A:O2'	34:T:54:ARG:NH1	2.54	0.40
18:D:890:G:O2'	18:D:906:A:N6	2.55	0.40
18:D:1208:C:H2'	18:D:1209:C:H6	1.85	0.40
28:N:11:LEU:HD22	28:N:75:ILE:HD11	2.03	0.40
39:Y:78:LEU:CD1	39:Y:108:ILE:HG22	2.50	0.40
39:Y:124:MET:HE2	39:Y:124:MET:HB2	1.77	0.40
40:Z:28:GLU:H	40:Z:28:GLU:HG3	1.58	0.40
41:a:1182:G:H2'	41:a:1183:U:O4'	2.21	0.40
46:f:27:LEU:O	46:f:38:ARG:NE	2.46	0.40
56:p:52:PHE:CZ	56:p:72:LEU:HD22	2.56	0.40
58:r:9:VAL:HG11	58:r:12:LEU:HD21	2.02	0.40
63:w:67:PHE:O	63:w:71:ARG:HG2	2.21	0.40
10:A:8:U:OP2	10:A:8:U:H6	2.04	0.40
11:AA:687:ARG:HH11	11:AA:687:ARG:HD3	1.74	0.40
11:AA:874:GLY:HA2	13:AC:66:HIS:HB3	2.04	0.40
11:AA:1328:LYS:HD2	14:AE:102:MET:SD	2.62	0.40
12:AB:11:VAL:HG21	12:AB:103:ILE:HD13	2.02	0.40
14:AE:182:ALA:HB1	14:AE:238:ILE:CG2	2.52	0.40
14:AE:805:GLN:HG3	14:AE:1348:LYS:HD3	2.03	0.40
16:AG:18:LEU:HD21	16:AG:125:MET:HE2	2.04	0.40
16:AG:216:ILE:HG12	16:AG:221:ILE:CB	2.52	0.40
16:AG:363:LEU:HD21	16:AG:407:ARG:C	2.46	0.40
10:B:7:G:O6	10:B:49:G:O6	2.39	0.40
10:B:15:G:N2	10:B:20:U:H3	2.19	0.40
18:D:500:G:H2'	18:D:501:C:C6	2.57	0.40
18:D:580:C:H2'	18:D:581:G:O4'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:D:712:A:H2'	18:D:713:G:O4'	2.21	0.40
18:D:1389:C:H2'	18:D:1390:U:O4'	2.22	0.40
24:J:47:ARG:HD3	24:J:47:ARG:HA	1.90	0.40
41:a:1796:U:H2'	41:a:1797:G:C8	2.57	0.40
41:a:2602:A:H5''	41:a:2603:G:H5''	2.03	0.40
58:r:57:LYS:O	58:r:61:VAL:HG13	2.21	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%)	13	46
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%)	13	46
5	4	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
9	9	146/165 (88%)	94 (64%)	38 (26%)	14 (10%)	0	6
11	AA	1338/1342 (100%)	1207 (90%)	127 (10%)	4 (0%)	37	67
12	AB	157/181 (87%)	130 (83%)	20 (13%)	7 (4%)	2	18
13	AC	216/329 (66%)	202 (94%)	12 (6%)	2 (1%)	14	48
13	AD	292/329 (89%)	269 (92%)	23 (8%)	0	100	100
14	AE	1329/1407 (94%)	1198 (90%)	120 (9%)	11 (1%)	16	51
15	AF	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
16	AG	493/495 (100%)	376 (76%)	86 (17%)	31 (6%)	1	13
17	C	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
19	E	84/87 (97%)	83 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	189 (74%)	54 (21%)	12 (5%)	2	18
23	I	206/233 (88%)	196 (95%)	9 (4%)	1 (0%)	25	59
24	J	203/206 (98%)	198 (98%)	5 (2%)	0	100	100
25	K	154/167 (92%)	146 (95%)	7 (4%)	1 (1%)	22	55
26	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	13	46
27	M	149/179 (83%)	144 (97%)	4 (3%)	1 (1%)	19	53
28	N	127/130 (98%)	121 (95%)	5 (4%)	1 (1%)	16	51
29	O	125/130 (96%)	115 (92%)	9 (7%)	1 (1%)	16	51
30	P	97/103 (94%)	87 (90%)	8 (8%)	2 (2%)	5	33
31	Q	115/129 (89%)	104 (90%)	9 (8%)	2 (2%)	7	37
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%)	10	41
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%)	7	35
39	Y	139/142 (98%)	102 (73%)	25 (18%)	12 (9%)	0	7
40	Z	28/121 (23%)	19 (68%)	7 (25%)	2 (7%)	1	11
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	63
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%)	25	59

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
54	n	175/179 (98%)	162 (93%)	11 (6%)	2 (1%)	12	45
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%)	108 (92%)	9 (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	48
All	All	10078/11072 (91%)	9200 (91%)	763 (8%)	115 (1%)	15	45

All (115) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	9	88	HIS
12	AB	118	VAL
12	AB	121	LYS
14	AE	291	ILE
16	AG	34	ALA
16	AG	105	ILE
16	AG	187	ARG
16	AG	227	ALA
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

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Mol	Chain	Res	Type
11	AA	853	ASP
11	AA	905	ILE
11	AA	907	GLY
12	AB	130	PRO
12	AB	163	SER
14	AE	175	GLU
14	AE	292	VAL
16	AG	63	LEU
16	AG	104	ARG
16	AG	242	ASP
16	AG	268	GLY
16	AG	279	ASN
16	AG	365	ILE
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	33	THR
16	AG	102	PHE
16	AG	200	SER
16	AG	305	MET
16	AG	319	GLY
16	AG	350	ALA
16	AG	355	ALA
16	AG	396	GLU
16	AG	425	LEU
22	H	76	GLU
22	H	142	ARG
27	M	130	ASN
30	P	58	ASN
31	Q	119	ASN
39	Y	20	SER

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Mol	Chain	Res	Type
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	67	GLY
12	AB	141	PHE
13	AC	193	GLU
14	AE	174	ASP
14	AE	193	ASP
16	AG	48	GLN
16	AG	265	GLU
16	AG	363	LEU
16	AG	401	PRO
22	H	82	THR
30	P	90	LEU
38	X	105	ASN
39	Y	83	ALA
40	Z	21	GLU
54	n	40	VAL
14	AE	91	GLU
16	AG	224	LYS
16	AG	399	ASP
22	H	70	VAL
39	Y	22	PRO
39	Y	71	LYS
39	Y	89	SER
40	Z	7	ILE
4	3	39	ILE
9	9	28	ALA
13	AC	192	VAL
14	AE	49	PHE
14	AE	73	GLY
14	AE	904	ALA
16	AG	43	ILE
16	AG	70	GLN
16	AG	169	PRO
16	AG	323	GLN
16	AG	364	ASP
16	AG	382	GLU

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Mol	Chain	Res	Type
39	Y	62	ALA
12	AB	42	VAL
26	L	96	VAL
39	Y	23	VAL
39	Y	100	ILE
1	0	44	GLY
25	K	44	GLY
31	Q	74	VAL
35	U	64	GLY
9	9	54	VAL
11	AA	1317	PRO
54	n	62	GLY
28	N	75	ILE

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%)	7	30
2	1	93/93 (100%)	86 (92%)	7 (8%)	11	37
3	2	81/84 (96%)	77 (95%)	4 (5%)	21	50
4	3	84/85 (99%)	79 (94%)	5 (6%)	16	45
5	4	78/78 (100%)	75 (96%)	3 (4%)	28	57
9	9	112/123 (91%)	63 (56%)	49 (44%)	0	0
11	AA	1155/1157 (100%)	1130 (98%)	25 (2%)	47	69
12	AB	138/158 (87%)	108 (78%)	30 (22%)	1	5
13	AC	185/286 (65%)	184 (100%)	1 (0%)	86	93
13	AD	185/286 (65%)	185 (100%)	0	100	100
14	AE	1120/1168 (96%)	1046 (93%)	74 (7%)	14	42
15	AF	70/75 (93%)	69 (99%)	1 (1%)	62	79
16	AG	409/409 (100%)	288 (70%)	121 (30%)	0	2
17	C	57/65 (88%)	55 (96%)	2 (4%)	31	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	E	65/66 (98%)	61 (94%)	4 (6%)	15	44
20	F	60/61 (98%)	57 (95%)	3 (5%)	20	49
21	G	187/199 (94%)	174 (93%)	13 (7%)	12	40
22	H	137/461 (30%)	124 (90%)	13 (10%)	7	30
23	I	171/190 (90%)	163 (95%)	8 (5%)	22	51
24	J	172/173 (99%)	164 (95%)	8 (5%)	22	51
25	K	119/126 (94%)	111 (93%)	8 (7%)	13	41
26	L	91/116 (78%)	84 (92%)	7 (8%)	10	36
27	M	124/147 (84%)	113 (91%)	11 (9%)	8	32
28	N	104/105 (99%)	101 (97%)	3 (3%)	37	63
29	O	105/107 (98%)	99 (94%)	6 (6%)	17	46
30	P	86/90 (96%)	73 (85%)	13 (15%)	2	15
31	Q	90/99 (91%)	88 (98%)	2 (2%)	47	69
32	R	101/104 (97%)	95 (94%)	6 (6%)	16	45
33	S	83/84 (99%)	79 (95%)	4 (5%)	21	51
34	T	76/77 (99%)	65 (86%)	11 (14%)	2	16
35	U	65/65 (100%)	60 (92%)	5 (8%)	10	36
36	V	74/78 (95%)	71 (96%)	3 (4%)	26	55
37	W	72/79 (91%)	66 (92%)	6 (8%)	9	34
38	X	94/96 (98%)	87 (93%)	7 (7%)	11	37
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%)	56	75
43	c	67/68 (98%)	64 (96%)	3 (4%)	23	53
45	e	54/55 (98%)	51 (94%)	3 (6%)	17	47
46	f	48/49 (98%)	43 (90%)	5 (10%)	5	26
47	g	59/62 (95%)	55 (93%)	4 (7%)	13	41
48	h	216/218 (99%)	199 (92%)	17 (8%)	10	35
49	i	47/48 (98%)	41 (87%)	6 (13%)	3	19
50	j	164/164 (100%)	156 (95%)	8 (5%)	21	50
51	k	47/49 (96%)	44 (94%)	3 (6%)	14	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	l	165/165 (100%)	151 (92%)	14 (8%)	8	33
53	m	38/38 (100%)	36 (95%)	2 (5%)	19	48
54	n	148/150 (99%)	130 (88%)	18 (12%)	4	21
55	o	51/52 (98%)	47 (92%)	4 (8%)	10	36
56	p	136/138 (99%)	130 (96%)	6 (4%)	24	53
57	q	34/34 (100%)	31 (91%)	3 (9%)	8	32
58	r	114/114 (100%)	102 (90%)	12 (10%)	5	26
59	s	116/116 (100%)	106 (91%)	10 (9%)	8	33
60	t	104/104 (100%)	98 (94%)	6 (6%)	17	46
61	u	103/103 (100%)	96 (93%)	7 (7%)	13	41
62	v	109/109 (100%)	105 (96%)	4 (4%)	29	58
63	w	99/103 (96%)	91 (92%)	8 (8%)	9	35
64	x	86/87 (99%)	80 (93%)	6 (7%)	12	40
65	y	99/100 (99%)	91 (92%)	8 (8%)	9	35
66	z	89/90 (99%)	85 (96%)	4 (4%)	23	53
All	All	8313/9148 (91%)	7624 (92%)	689 (8%)	12	34

All (689) 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

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Mol	Chain	Res	Type
3	2	37	ASP
3	2	93	LEU
4	3	52	LEU
4	3	70	VAL
4	3	72	ILE
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

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Mol	Chain	Res	Type
9	9	86	MET
9	9	94	ARG
9	9	96	PHE
9	9	98	GLU
9	9	106	PHE
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	844	LYS
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	894	GLN
11	AA	895	LEU
11	AA	896	THR
11	AA	899	GLU
11	AA	900	LYS
11	AA	901	LEU
11	AA	902	LEU
11	AA	903	ARG
11	AA	909	LYS
11	AA	912	ASP
11	AA	913	VAL
11	AA	914	LYS
11	AA	1076	ILE
11	AA	1151	LEU

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Mol	Chain	Res	Type
12	AB	46	THR
12	AB	64	PHE
12	AB	103	ILE
12	AB	105	ASP
12	AB	106	LYS
12	AB	107	GLU
12	AB	108	VAL
12	AB	114	ARG
12	AB	116	GLN
12	AB	117	GLN
12	AB	125	LYS
12	AB	126	THR
12	AB	127	LEU
12	AB	132	GLU
12	AB	133	MET
12	AB	134	VAL
12	AB	135	ARG
12	AB	145	ASN
12	AB	150	GLU
12	AB	151	VAL
12	AB	153	TYR
12	AB	157	ARG
12	AB	161	SER
12	AB	162	VAL
12	AB	167	ARG
12	AB	169	THR
12	AB	171	VAL
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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	291	ILE
14	AE	324	LEU
14	AE	385	LEU
14	AE	386	GLU
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
16	AG	5	ILE
16	AG	12	VAL
16	AG	16	LYS
16	AG	36	LYS
16	AG	37	LYS
16	AG	40	GLU
16	AG	43	ILE
16	AG	47	VAL
16	AG	49	ILE
16	AG	50	ASP
16	AG	56	PHE
16	AG	57	ASP
16	AG	61	ARG
16	AG	63	LEU
16	AG	75	ILE
16	AG	97	ILE
16	AG	103	ASP
16	AG	104	ARG
16	AG	114	ILE
16	AG	117	LYS

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Mol	Chain	Res	Type
16	AG	123	ARG
16	AG	125	MET
16	AG	126	VAL
16	AG	131	ARG
16	AG	138	ILE
16	AG	139	THR
16	AG	144	LYS
16	AG	150	ILE
16	AG	154	LEU
16	AG	157	ASN
16	AG	162	ILE
16	AG	167	MET
16	AG	173	PHE
16	AG	174	ARG
16	AG	179	VAL
16	AG	180	ARG
16	AG	182	VAL
16	AG	187	ARG
16	AG	189	GLU
16	AG	195	LEU
16	AG	197	VAL
16	AG	199	ARG
16	AG	201	LYS
16	AG	203	GLU
16	AG	204	MET
16	AG	205	LEU
16	AG	206	ILE
16	AG	207	GLU
16	AG	210	ARG
16	AG	211	ILE
16	AG	213	VAL
16	AG	218	GLU
16	AG	219	GLU
16	AG	221	ILE
16	AG	223	ILE
16	AG	232	SER
16	AG	235	LYS
16	AG	236	ILE
16	AG	238	VAL
16	AG	239	LYS
16	AG	240	THR
16	AG	241	ASN

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Mol	Chain	Res	Type
16	AG	243	LYS
16	AG	244	ARG
16	AG	245	ILE
16	AG	254	MET
16	AG	255	ARG
16	AG	258	ARG
16	AG	259	VAL
16	AG	260	GLN
16	AG	262	VAL
16	AG	265	GLU
16	AG	270	ARG
16	AG	271	ILE
16	AG	273	ILE
16	AG	274	VAL
16	AG	276	TRP
16	AG	278	ASP
16	AG	282	GLN
16	AG	285	ILE
16	AG	288	MET
16	AG	296	ILE
16	AG	297	VAL
16	AG	299	ASP
16	AG	300	GLU
16	AG	301	ASP
16	AG	302	LYS
16	AG	303	HIS
16	AG	305	MET
16	AG	309	VAL
16	AG	310	GLU
16	AG	313	ASN
16	AG	316	GLN
16	AG	320	ARG
16	AG	321	ASN
16	AG	323	GLN
16	AG	327	LEU
16	AG	331	LEU
16	AG	335	GLU
16	AG	336	LEU
16	AG	337	ASN
16	AG	338	VAL
16	AG	340	THR
16	AG	341	VAL

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Mol	Chain	Res	Type
16	AG	342	ASP
16	AG	344	LEU
16	AG	356	ILE
16	AG	358	THR
16	AG	359	PHE
16	AG	361	LYS
16	AG	365	ILE
16	AG	380	THR
16	AG	387	VAL
16	AG	390	LYS
16	AG	396	GLU
16	AG	398	LEU
16	AG	399	ASP
16	AG	400	GLU
16	AG	425	LEU
16	AG	428	ASN
16	AG	429	LYS
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

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Mol	Chain	Res	Type
22	H	54	LYS
22	H	62	ILE
22	H	70	VAL
22	H	294	VAL
22	H	305	HIS
22	H	336	ASP
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	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

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Mol	Chain	Res	Type
27	M	17	LYS
27	M	21	GLU
27	M	23	LEU
27	M	27	VAL
27	M	50	LEU
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	88	MET
30	P	89	ARG
30	P	90	LEU
30	P	91	ASP
30	P	92	LEU
30	P	102	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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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	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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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	35	VAL

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Mol	Chain	Res	Type
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
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	61	ASN
3	2	28	ASN
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	580	GLN
11	AA	688	GLN
11	AA	808	ASN
11	AA	894	GLN
11	AA	1237	HIS
11	AA	1268	GLN
11	AA	1313	HIS
13	AC	23	HIS
13	AD	66	HIS
13	AD	84	ASN
13	AD	117	HIS
13	AD	128	HIS
13	AD	227	GLN
14	AE	294	ASN
14	AE	424	ASN
14	AE	450	HIS
14	AE	469	HIS
14	AE	865	HIS
14	AE	1195	GLN
14	AE	1238	GLN
14	AE	1249	ASN
15	AF	7	GLN
15	AF	31	GLN
15	AF	62	GLN
16	AG	194	GLN
16	AG	260	GLN
16	AG	282	GLN

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Mol	Chain	Res	Type
16	AG	316	GLN
16	AG	323	GLN
16	AG	324	ASN
16	AG	337	ASN
16	AG	428	ASN
19	E	55	GLN
19	E	61	GLN
21	G	18	HIS
21	G	58	ASN
21	G	94	HIS
23	I	6	HIS
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	63	ASN
26	L	94	HIS
27	M	97	ASN
27	M	148	ASN
29	O	81	HIS
29	O	126	GLN
30	P	58	ASN
31	Q	15	GLN
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
54	n	63	GLN
55	o	28	ASN
56	p	88	GLN
57	q	35	GLN
58	r	20	ASN
58	r	133	GLN
60	t	88	ASN

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Mol	Chain	Res	Type
65	y	15	GLN
65	y	66	ASN

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%)	291 (19%)	34 (2%)
41	a	2859/2904 (98%)	539 (18%)	0
44	d	119/120 (99%)	17 (14%)	0
8	7	30/68 (44%)	18 (60%)	4 (13%)
All	All	4672/4786 (97%)	929 (19%)	50 (1%)

All (929) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	3	G
8	7	4	U
8	7	5	U
8	7	7	U
8	7	8	U
8	7	9	U
8	7	10	U
8	7	11	U
8	7	12	U
8	7	13	U
8	7	14	U
8	7	15	U
8	7	16	U
8	7	18	U
8	7	20	U
8	7	21	U
8	7	60	G
8	7	61	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

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Mol	Chain	Res	Type
10	A	14	A
10	A	15	G
10	A	16	C
10	A	17	C
10	A	18	G
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

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Mol	Chain	Res	Type
10	B	36	U
10	B	37	A
10	B	38	A
10	B	46	G
10	B	47	U
10	B	48	C
10	B	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

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Mol	Chain	Res	Type
18	D	95	C
18	D	96	U
18	D	108	G
18	D	120	A
18	D	122	G
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	253	A
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

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Mol	Chain	Res	Type
18	D	332	G
18	D	347	G
18	D	352	C
18	D	353	A
18	D	354	G
18	D	355	C
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	398	U
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
41	a	1379	U
41	a	1380	G
41	a	1383	A
41	a	1387	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

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Mol	Chain	Res	Type
41	a	1559	U
41	a	1566	A
41	a	1569	A
41	a	1578	U
41	a	1580	A
41	a	1581	G
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	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

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Mol	Chain	Res	Type
41	a	1858	A
41	a	1859	U
41	a	1862	G
41	a	1864	U
41	a	1869	G
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

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Mol	Chain	Res	Type
41	a	2051	A
41	a	2052	A
41	a	2055	C
41	a	2056	G
41	a	2060	A
41	a	2061	G
41	a	2062	A
41	a	2063	C
41	a	2077	A
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

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Mol	Chain	Res	Type
41	a	2165	C
41	a	2169	A
41	a	2171	A
41	a	2172	U
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

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Mol	Chain	Res	Type
41	a	2347	C
41	a	2350	C
41	a	2361	G
41	a	2372	U
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

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Mol	Chain	Res	Type
41	a	2572	A
41	a	2573	C
41	a	2574	G
41	a	2585	U
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

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Mol	Chain	Res	Type
41	a	2867	G
41	a	2880	C
41	a	2884	U
41	a	2885	G
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	4	U
8	7	7	U
8	7	10	U
8	7	59	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

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Mol	Chain	Res	Type
10	B	60	U
18	D	7	A
18	D	70	U
18	D	121	U
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 ⓘ

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

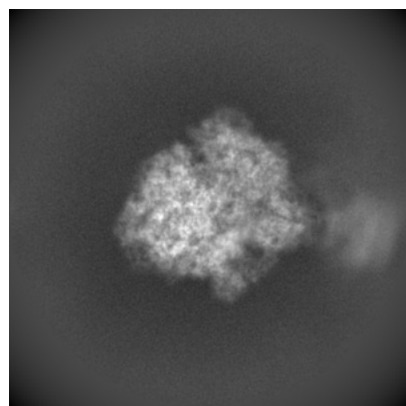
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43390. These allow visual inspection of the internal detail of the map and identification of artifacts.

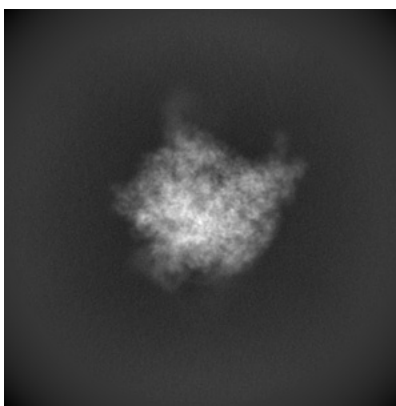
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

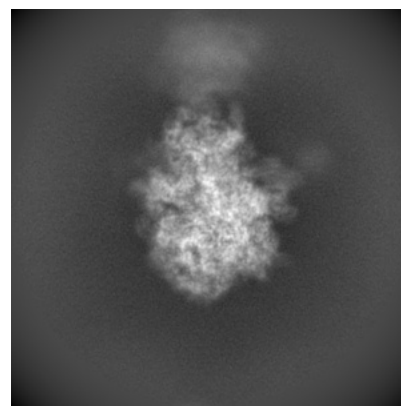
6.1.1 Primary map



X

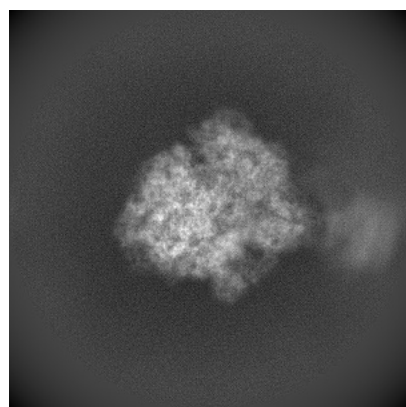


Y

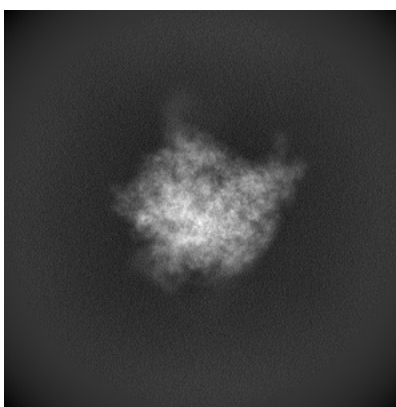


Z

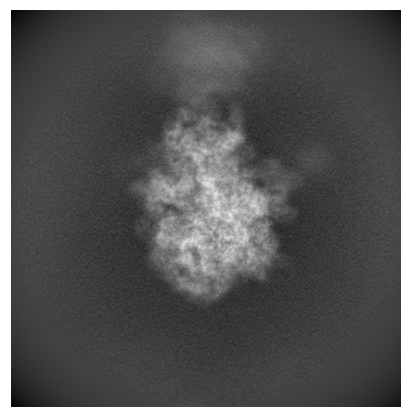
6.1.2 Raw map



X



Y

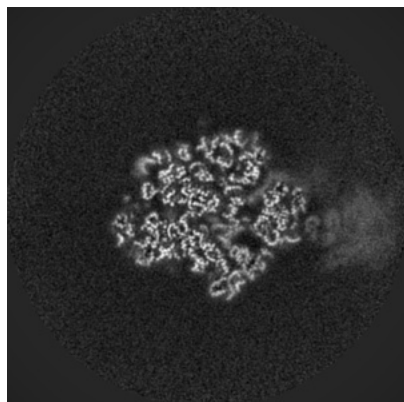


Z

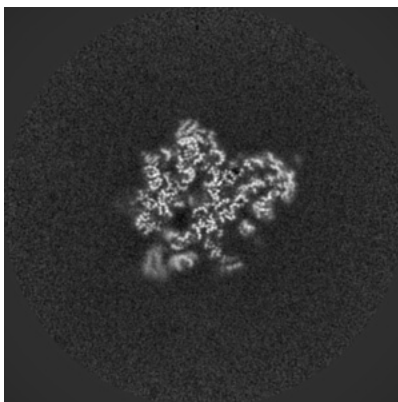
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

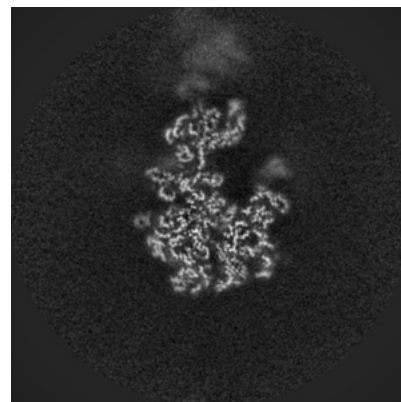
6.2.1 Primary map



X Index: 256

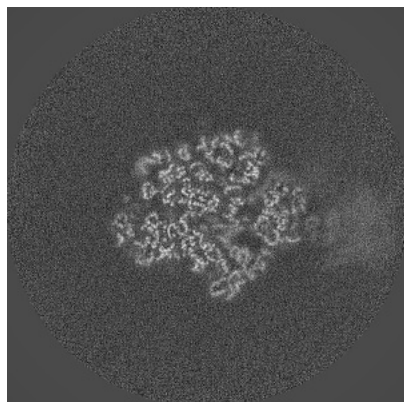


Y Index: 256

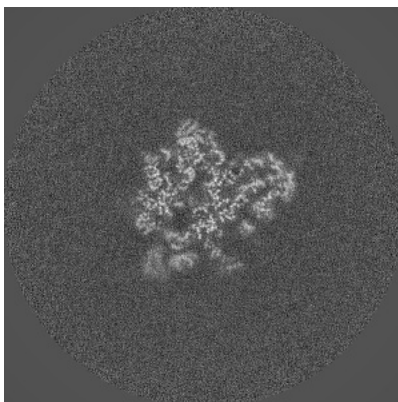


Z Index: 256

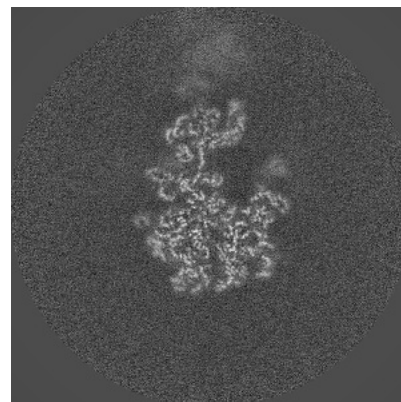
6.2.2 Raw map



X Index: 256



Y Index: 256

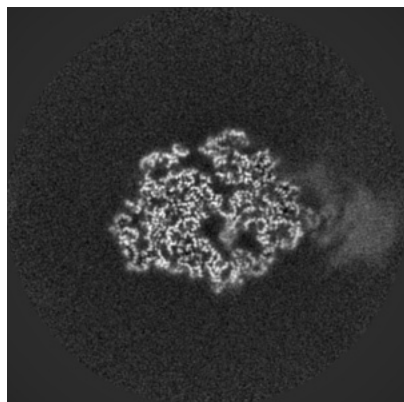


Z Index: 256

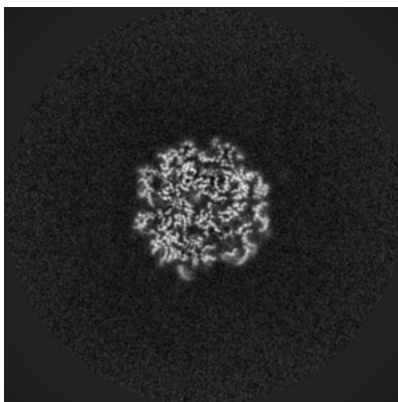
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

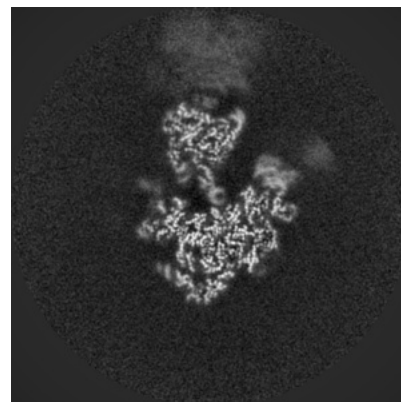
6.3.1 Primary map



X Index: 247

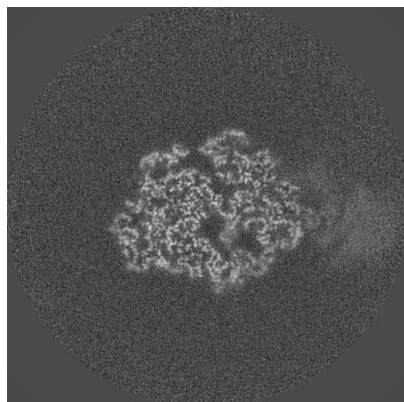


Y Index: 221

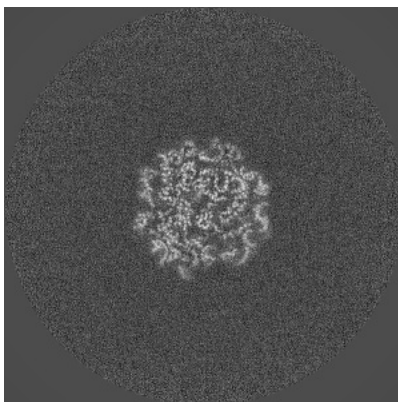


Z Index: 231

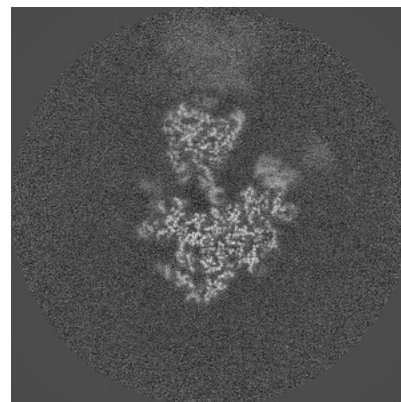
6.3.2 Raw map



X Index: 247



Y Index: 220



Z Index: 231

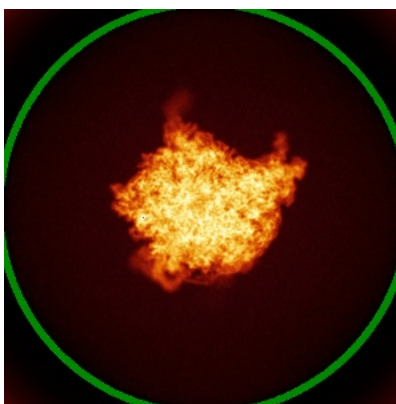
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

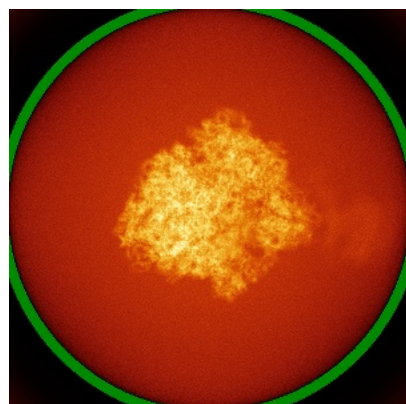


Y

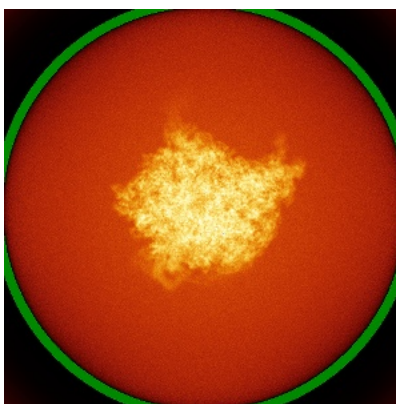


Z

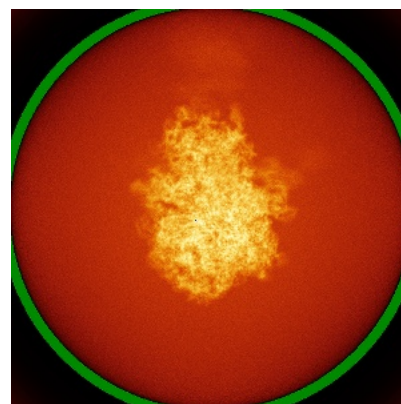
6.4.2 Raw map



X



Y

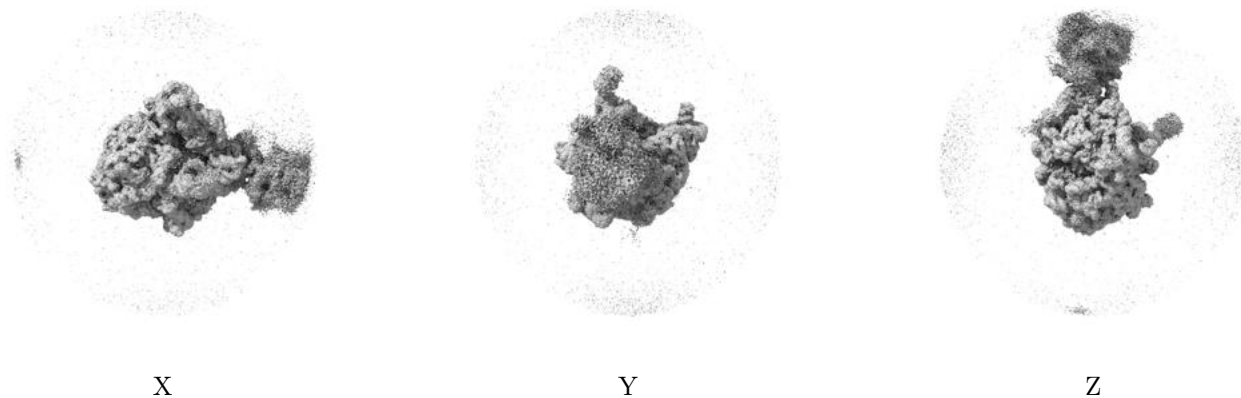


Z

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

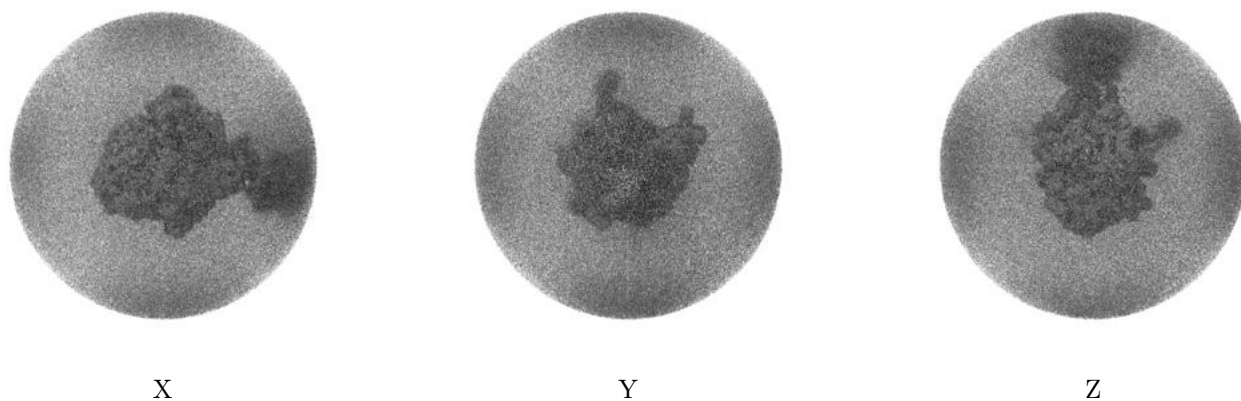
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0039. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

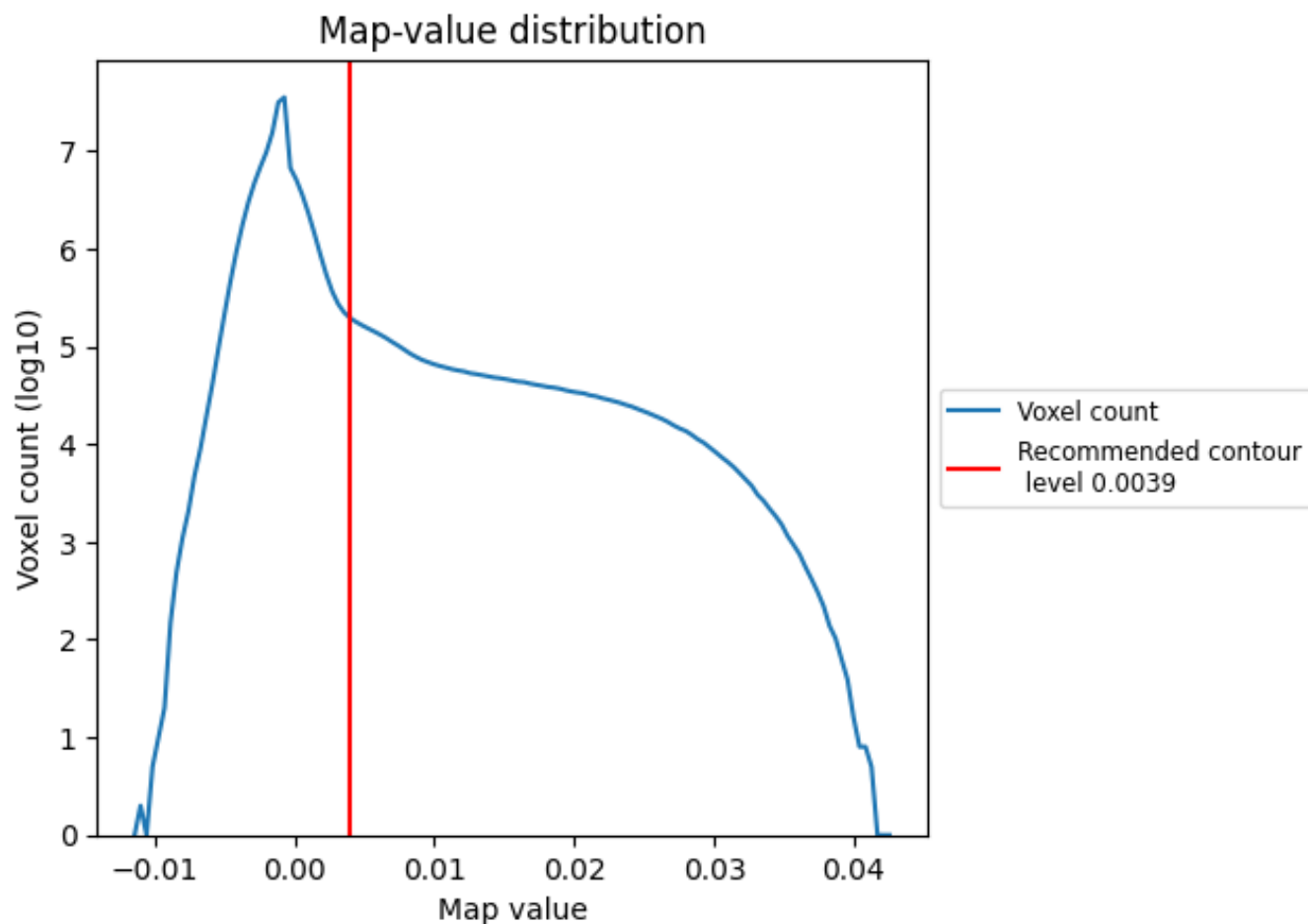
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

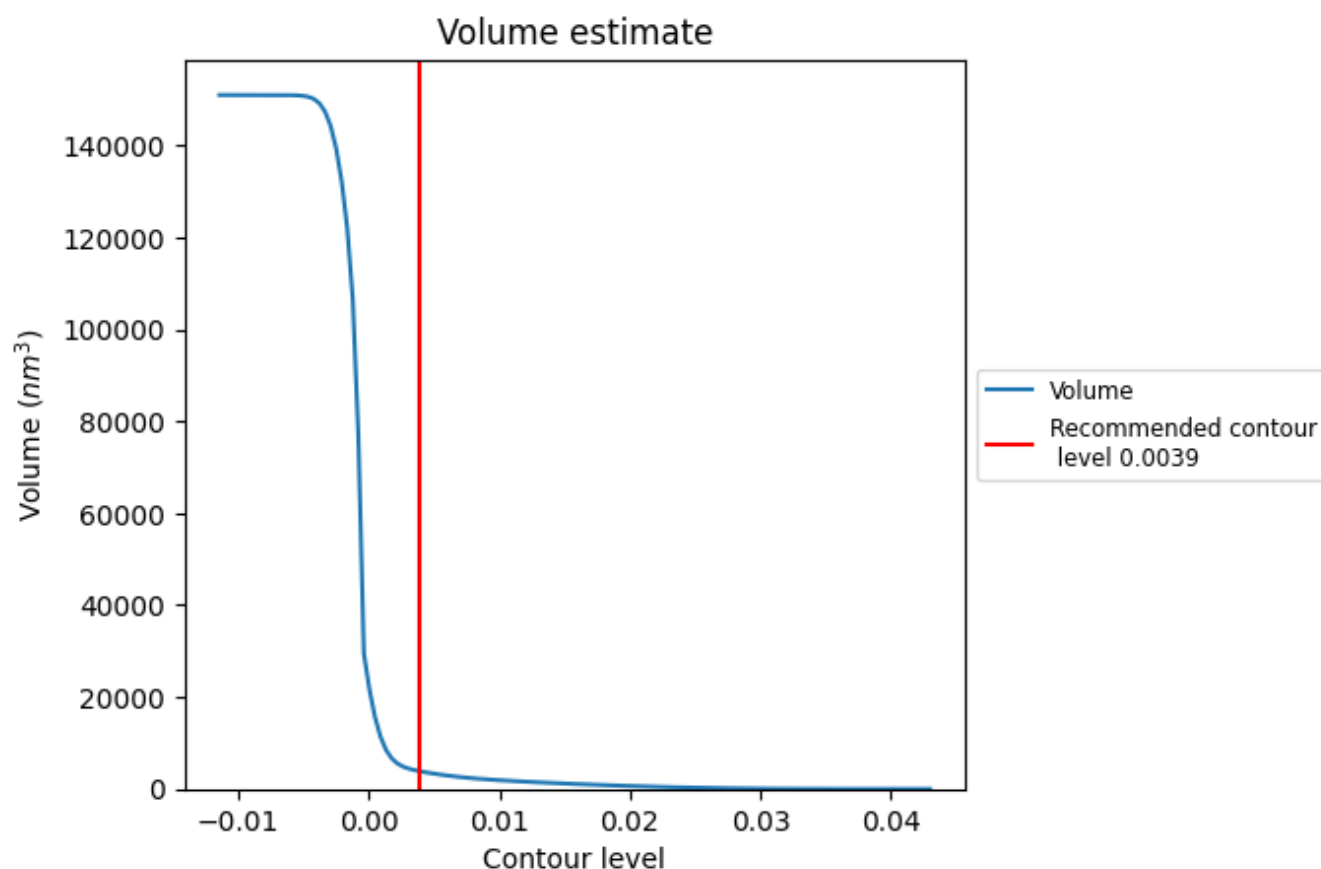
This section contains the results of statistical analysis of the map.

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.

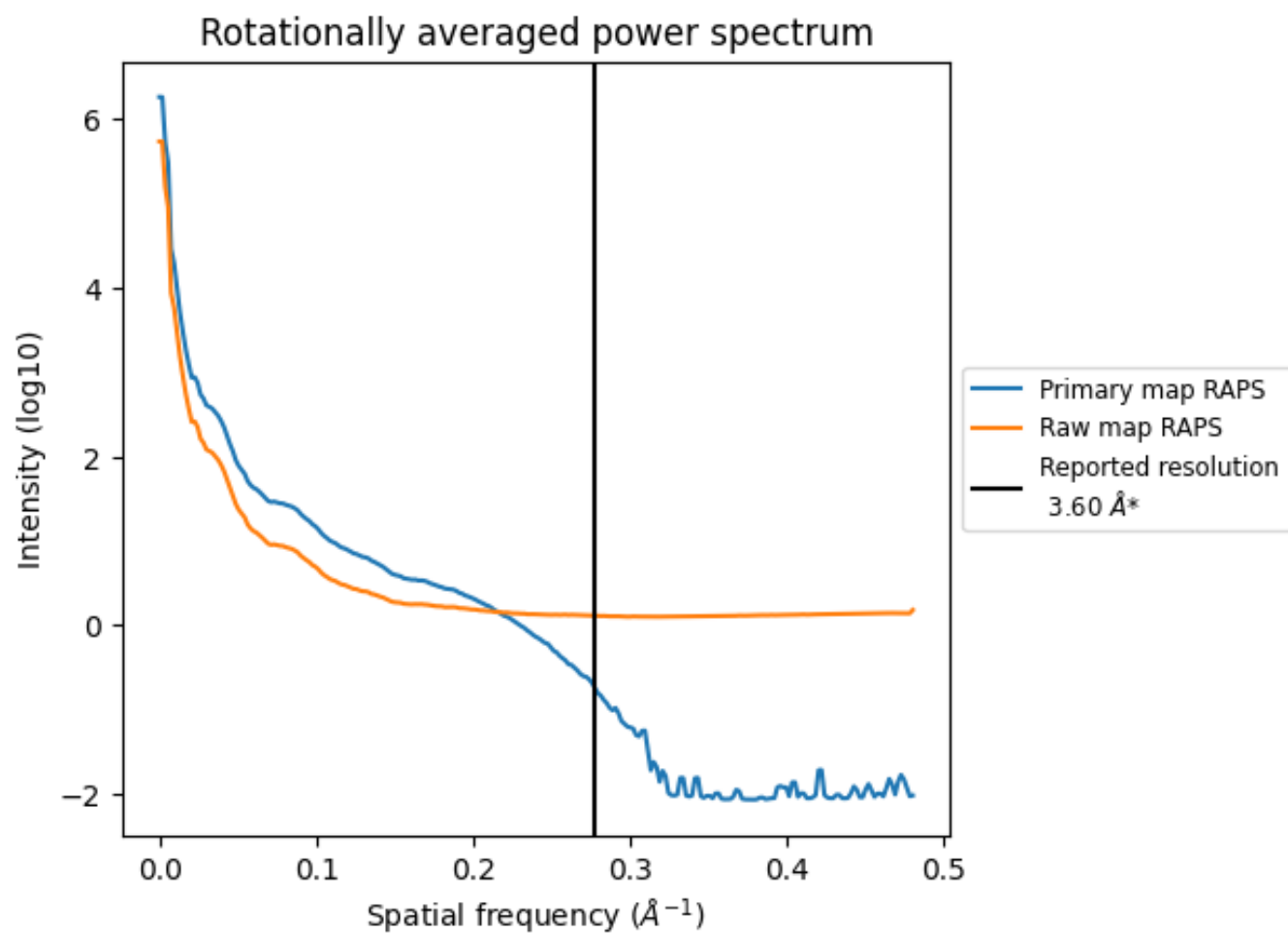
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3859 nm^3 ; this corresponds to an approximate mass of 3486 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 ⓘ

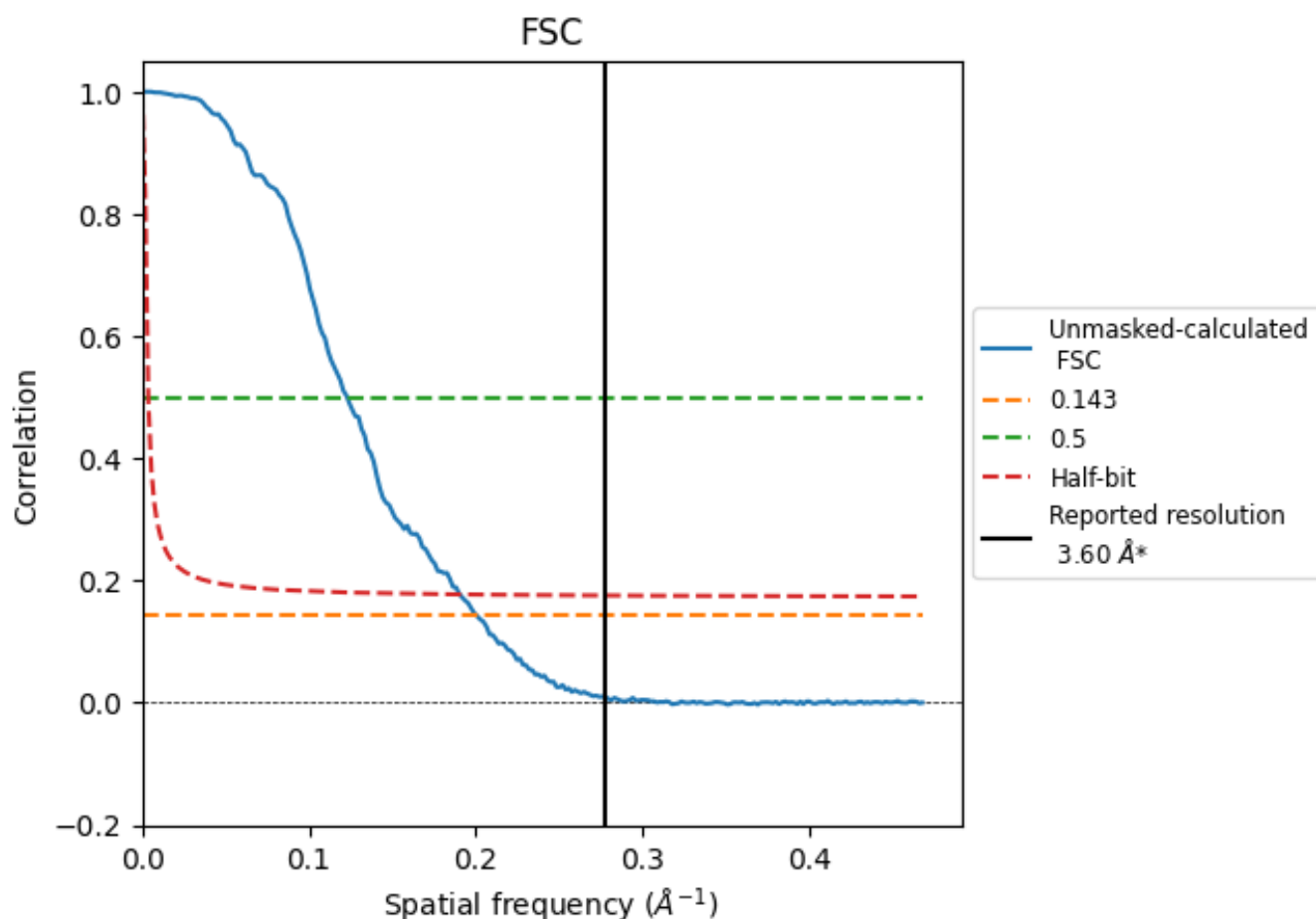


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.278 \AA^{-1}

8.2 Resolution estimates [i](#)

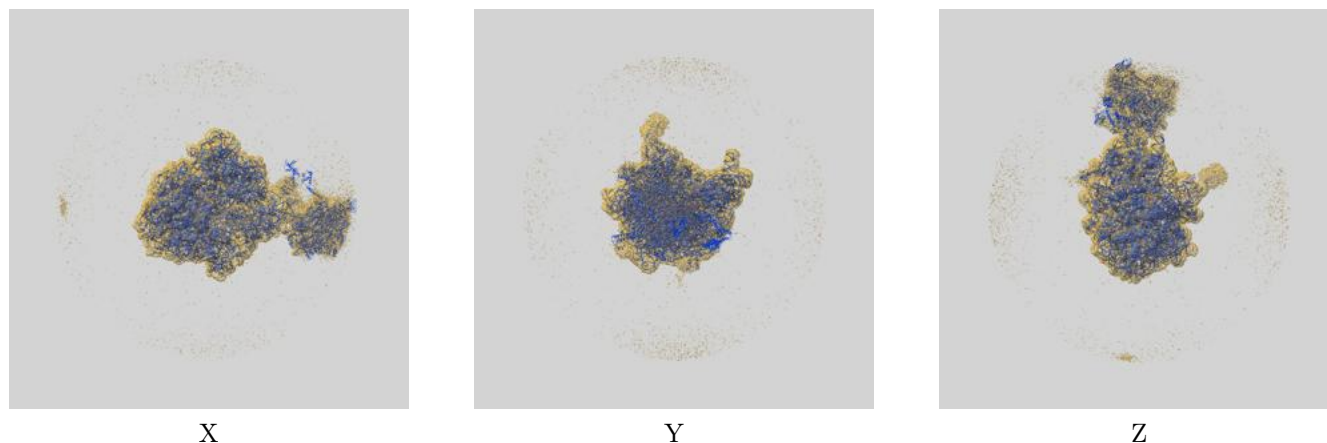
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.99	8.14	5.25

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.99 differs from the reported value 3.6 by more than 10 %

9 Map-model fit [i](#)

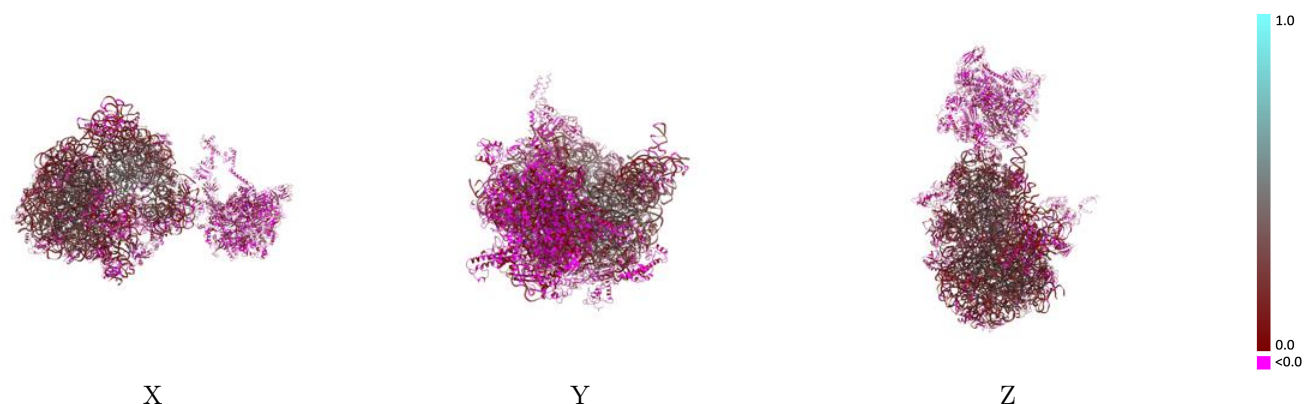
This section contains information regarding the fit between EMDB map EMD-43390 and PDB model 8VOR. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



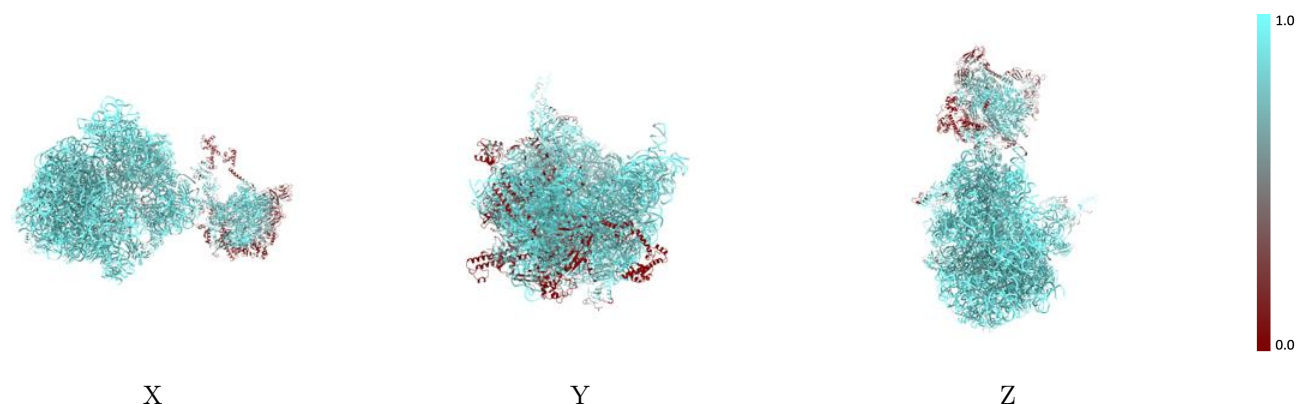
The images above show the 3D surface view of the map at the recommended contour level 0.0039 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



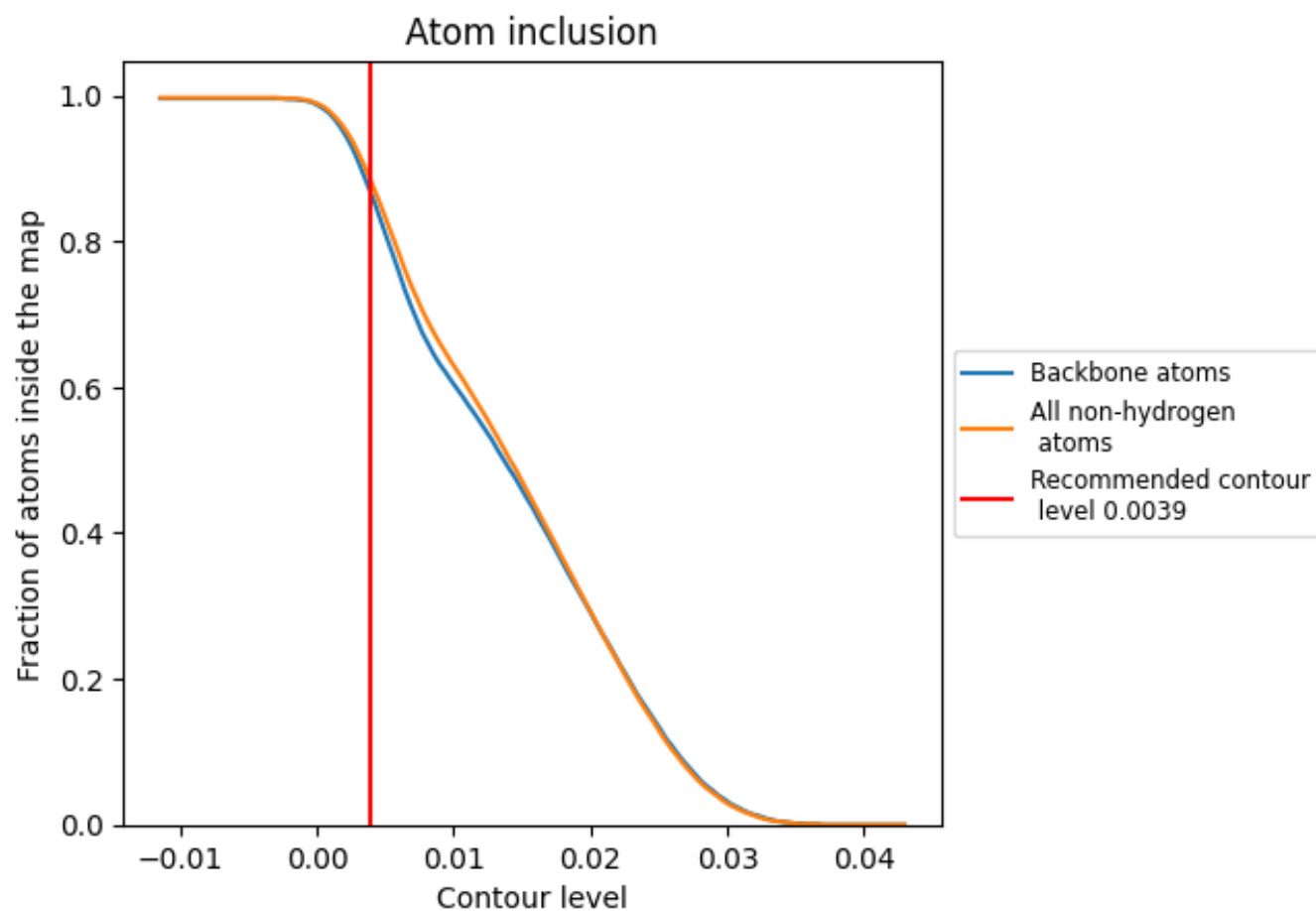
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0039).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 89% 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 (0.0039) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8860	 0.1710
0	 0.9440	 0.1900
1	 0.9400	 0.2830
2	 0.9100	 0.1350
3	 0.9370	 0.0970
4	 0.9500	 0.1260
5	 0.8620	 0.0410
6	 0.8670	 0.0330
7	 0.8900	 0.0820
9	 0.8700	 0.0380
A	 0.9910	 0.1860
AA	 0.6220	 0.0330
AB	 0.5790	 0.0520
AC	 0.5460	 0.0450
AD	 0.2720	 0.0170
AE	 0.7380	 0.0330
AF	 0.6070	 0.0160
AG	 0.3780	 0.0120
B	 0.8590	 0.0720
C	 0.9540	 0.1570
D	 0.9920	 0.2420
E	 0.9530	 0.0920
F	 0.9390	 0.2290
G	 0.9170	 0.1730
H	 0.7390	 0.0180
I	 0.9290	 0.1960
J	 0.9500	 0.1710
K	 0.9570	 0.2970
L	 0.9240	 0.0950
M	 0.9380	 0.1610
N	 0.9550	 0.2360
O	 0.9530	 0.1370
P	 0.8970	 0.1340
Q	 0.9450	 0.1870
R	 0.9640	 0.3070



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Chain	Atom inclusion	Q-score
S	 0.9440	 0.1420
T	 0.9510	 0.1990
U	 0.9570	 0.0840
V	 0.9540	 0.2130
W	 0.8580	 0.0380
X	 0.8780	 0.0700
Y	 0.7150	 0.0400
Z	 0.8240	 0.0420
a	 0.9900	 0.2290
b	 0.9200	 0.1270
c	 0.9130	 0.1820
d	 0.9810	 0.1250
e	 0.9220	 0.0860
f	 0.9520	 0.1860
g	 0.9430	 0.0580
h	 0.9330	 0.1930
i	 0.9420	 0.2460
j	 0.9350	 0.1650
k	 0.9020	 0.0770
l	 0.9290	 0.1590
m	 0.9660	 0.3090
n	 0.9040	 0.0540
o	 0.9210	 0.1680
p	 0.9250	 0.0450
q	 0.9280	 0.0890
r	 0.8600	 0.0470
s	 0.9370	 0.1750
t	 0.8950	 0.1730
u	 0.9450	 0.1540
v	 0.9230	 0.1860
w	 0.9390	 0.1770
x	 0.9330	 0.0070
y	 0.9120	 0.1120
z	 0.9580	 0.2350