



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 06:55 PM UTC

PDB ID : 9Y42 / pdb_00009y42
EMDB ID : EMD-72469
Title : Structure of naked mole-rat ribosome with P/E tRNA and eEF2 (rotated)
Authors : Gutierrez-Vargas, C.; De, S.; Maji, S.; Liu, Z.; Nieb, M.; Seluanov, A.; Gorbunova, V.; Frank, J.
Deposited on : 2025-09-02
Resolution : 5.00 Å (reported)
Based on initial models : 4v6x, 707y

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

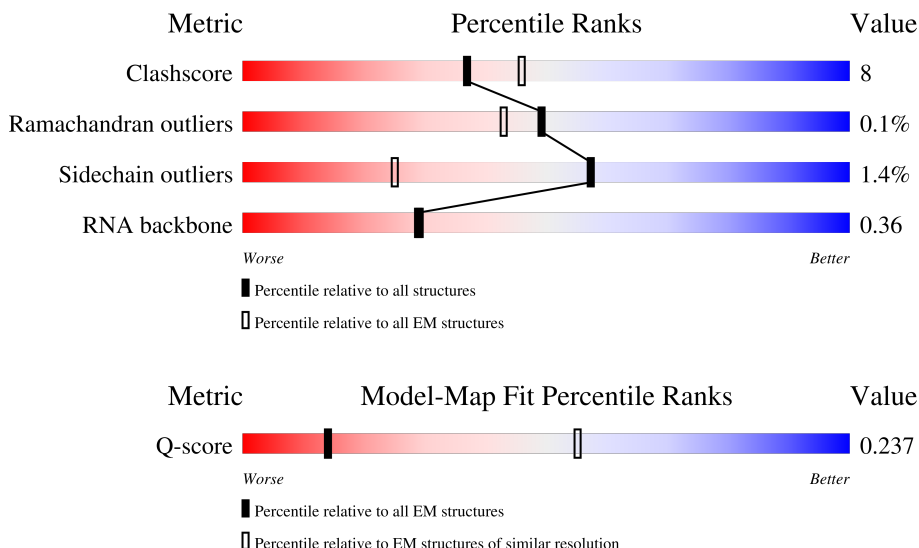
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.00 Å.

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





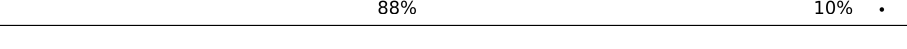
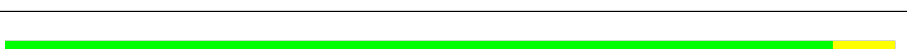



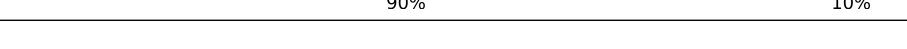


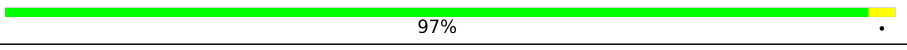
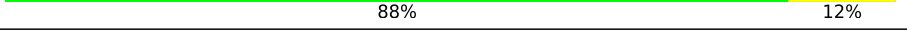
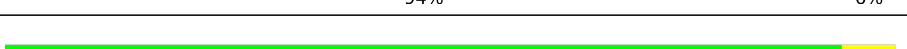
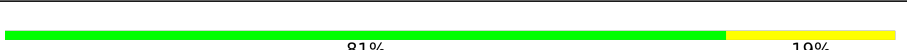

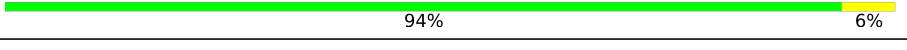
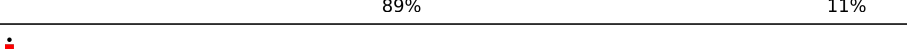



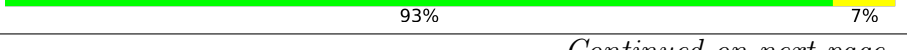



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	1057 (4.50 - 5.50)

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

Mol	Chain	Length	Quality of chain
1	A	248	
2	B	398	
3	C	363	



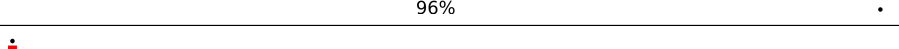
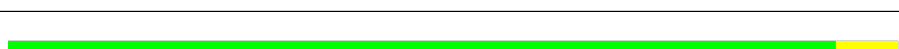
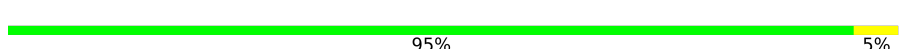
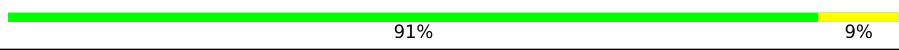
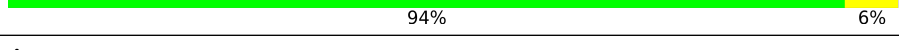
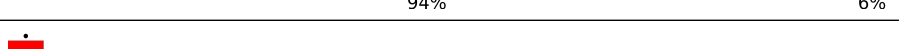
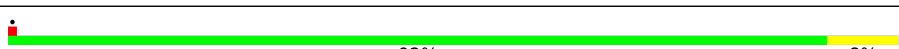

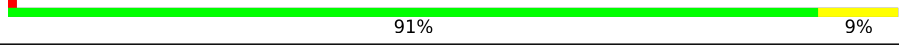
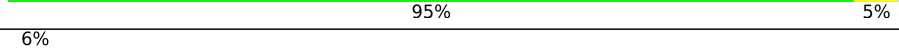

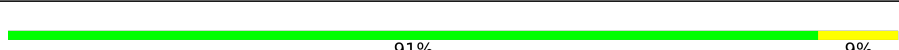
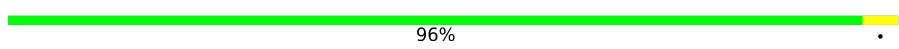

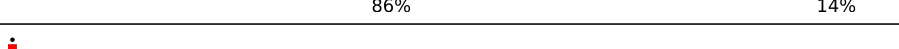



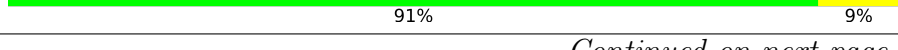



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Mol	Chain	Length	Quality of chain
4	c	121	
5	D	293	
6	E	224	
7	F	225	
8	G	215	
9	H	190	
10	I	213	
11	J	170	
12	L	205	
13	M	136	
14	N	203	
15	O	199	
16	P	153	
17	Q	187	
18	S	176	
19	T	159	
20	U	99	
21	V	131	
22	W	180	
23	X	118	
24	Y	134	
25	Z	135	
26	a	147	
27	b	104	
28	d	107	


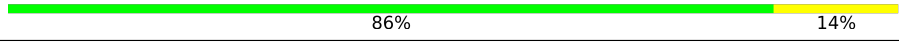
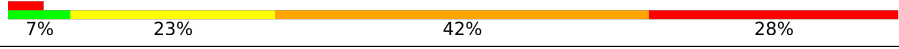
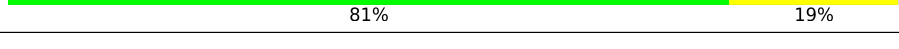

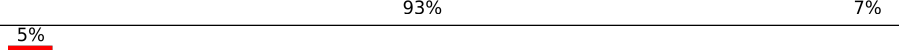
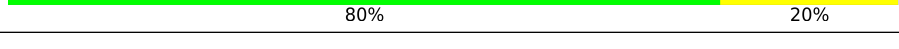
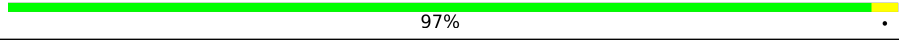

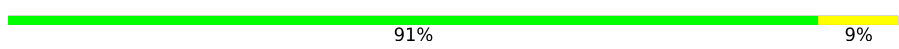
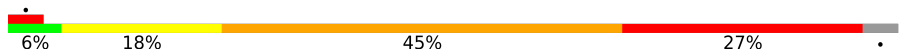
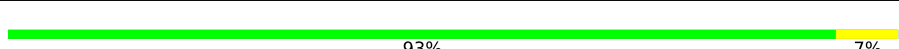

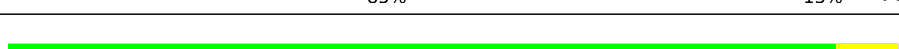
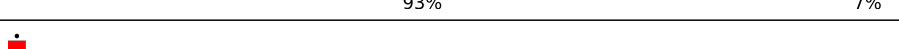
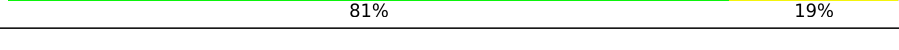
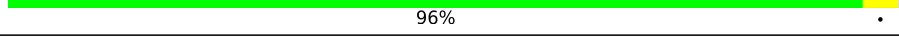
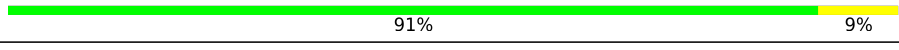
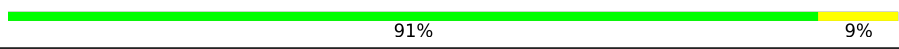
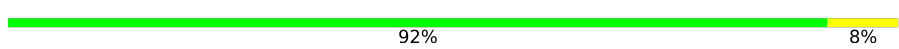




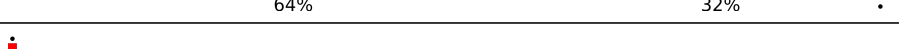
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Mol	Chain	Length	Quality of chain
29	e	128	
30	f	110	
31	g	110	
32	h	121	
33	i	102	
34	j	86	
35	k	69	
36	l	50	
37	m	51	
38	n	25	
39	o	105	
40	p	91	
41	r	127	
42	s	103	
43	t	156	
44	u	100	
45	bb	82	
46	ee	49	
47	aa	98	
48	CC	218	
49	EE	262	
50	GG	228	
51	HH	190	
52	II	206	
53	JJ	180	



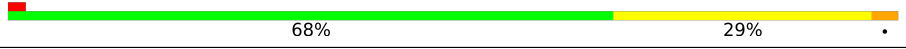



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Mol	Chain	Length	Quality of chain
54	LL	149	
55	NN	149	
56	VV	83	
57	WW	129	
58	XX	141	
59	YY	125	
60	cc	61	
61	ff	67	
62	gg	313	
63	dd	55	
64	AA	214	
65	DD	225	
66	FF	189	
67	KK	96	
68	MM	124	
69	PP	118	
70	QQ	141	
71	SS	145	
72	TT	141	
73	UU	99	
74	ZZ	75	
75	EF	856	
76	Cc	77	
77	A5	1732	
78	A7	121	

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Mol	Chain	Length	Quality of chain
79	A8	157	
80	B2	1837	
81	A6	2122	
82	BB	218	
83	OO	134	
84	RR	132	

2 Entry composition [i](#)

There are 87 unique types of molecules in this entry. The entry contains 225388 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	398	Total	C	N	O	S	0	0
			3206	2042	605	546	13		

- Molecule 3 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	363	Total	C	N	O	S	0	0
			2895	1822	576	483	14		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	1	ACE	-	acetylation	UNP G5AN81
C	262	ASP	GLU	conflict	UNP G5AN81
C	352	GLU	ASP	conflict	UNP G5AN81

- Molecule 4 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	c	115	Total	C	N	O	S	0	0
			938	586	193	155	4		

- Molecule 5 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	293	Total	C	N	O	S	0	0
			2389	1511	437	427	14		

- Molecule 6 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	224	Total	C	N	O	S	0	0
			1789	1149	340	297	3		

- Molecule 7 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 8 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	215	Total	C	N	O	S	0	0
			1741	1111	333	293	4		

- Molecule 9 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 10 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	199	Total	C	N	O	S	0	0
			1620	1029	313	266	12		

- Molecule 11 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	205	Total	C	N	O	S	0	0
			1658	1037	346	271	4		

- Molecule 13 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	136	Total	C	N	O	S	0	0
			1125	720	220	178	7		

- Molecule 14 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 15 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	187	Total	C	N	O	S	0	0
			1512	946	313	249	4		

- Molecule 18 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	176	Total	C	N	O	S	0	0
			1461	930	284	236	11		

- Molecule 19 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 20 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

- Molecule 21 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	131	Total	C	N	O	S	0	0
			973	612	184	172	5		

- Molecule 22 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 23 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 24 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 25 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 26 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	147	Total	C	N	O	S	0	0
			1163	734	239	186	4		

- Molecule 27 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	74	Total	C	N	O	S	0	0
			620	382	141	95	2		

- Molecule 28 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 29 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 30 is a protein called Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	f	110	Total	C	N	O	S	0	0
			884	560	175	144	5		

- Molecule 31 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	g	110	Total	C	N	O	S	0	0
			873	547	180	140	6		

- Molecule 32 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	h	121	Total	C	N	O	S	0	0
			1011	640	204	166	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
h	119	TYR	PHE	conflict	UNP G5B6W3

- Molecule 33 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 34 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	j	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 35 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	k	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 36 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	l	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 37 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	m	51	Total	C	N	O	S	0	0
			422	263	88	65	6		

- Molecule 38 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	n	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 39 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	o	105	Total	C	N	O	S	0	0
			863	543	175	139	6		

- Molecule 40 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 41 is a protein called Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	r	127	Total	C	N	O	S	0	0
			1015	630	209	170	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
r	1	ACE	-	acetylation	UNP G5BVZ2

- Molecule 42 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	s	103	Total	C	N	O	S	0	0
			825	525	150	143	7		

- Molecule 43 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	t	156	Total	C	N	O	S	0	0
			1178	733	221	220	4		

- Molecule 44 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	u	88	Total	C	N	O	S	0	0
			672	425	116	125	6		

- Molecule 45 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	bb	82	Total	C	N	O	S	0	0
			640	402	118	113	7		

- Molecule 46 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	ee	49	Total	C	N	O	S	0	0
			398	243	90	64	1		

- Molecule 47 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	aa	98	Total	C	N	O	S	0	0
			781	486	161	129	5		

- Molecule 48 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	CC	218	Total	C	N	O	S	0	0
			1685	1092	288	296	9		

- Molecule 49 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	EE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 50 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	GG	228	Total	C	N	O	S	0	0
			1848	1155	368	318	7		

- Molecule 51 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	HH	184	Total	C	N	O	S	0	0
			1490	953	271	265	1		

- Molecule 52 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	II	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 53 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	JJ	180	Total	C	N	O	S	0	0
			1499	955	300	242	2		

- Molecule 54 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	LL	141	Total	C	N	O	S	0	0
			1157	737	218	196	6		

- Molecule 55 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	NN	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 56 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	VV	83	Total	C	N	O	S	0	0
			637	392	117	123	5		

- Molecule 57 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	WW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 58 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	XX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 59 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	YY	125	Total	C	N	O	S	0	0
			1015	642	199	169	5		

- Molecule 60 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	cc	61	Total	C	N	O	S	0	0
			479	292	95	90	2		

- Molecule 61 is a protein called Ubiquitin-ribosomal protein eS31 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	ff	67	Total	C	N	O	S	0	0
			548	346	102	93	7		

- Molecule 62 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	gg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 63 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	dd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 64 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AA	205	Total	C	N	O	S	0	0
			1625	1035	283	299	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AA	1	ACE	-	acetylation	UNP A0A0P6K1L6

- Molecule 65 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	DD	225	Total	C	N	O	S	0	0
			1751	1116	315	313	7		

- Molecule 66 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	FF	186	Total	C	N	O	S	0	0
			1475	923	278	267	7		

- Molecule 67 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	KK	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 68 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	MM	124	Total	C	N	O	S	0	0
			958	600	170	179	9		

- Molecule 69 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	PP	118	Total	C	N	O	S	0	0
			979	621	185	166	7		

- Molecule 70 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	QQ	141	Total	C	N	O	S	0	0
			1124	715	212	194	3		

- Molecule 71 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SS	145	Total	C	N	O	S	0	0
			1193	748	241	203	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SS	1	ACE	-	acetylation	UNP G5BAZ4

- Molecule 72 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	TT	141	Total	C	N	O	S	0	0
			1097	687	211	196	3		

- Molecule 73 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	UU	99	Total	C	N	O	S	0	0
			790	495	151	140	4		

- Molecule 74 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	ZZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 75 is a protein called eEF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	EF	856	Total	C	N	O	S	0	0
			6669	4232	1147	1246	44		

- Molecule 76 is a RNA chain called P/E tRNA (77-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Cc	77	Total	C	N	O	P	0	0
			1644	732	298	537	77		

- Molecule 77 is a RNA chain called LSU alpha rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	A5	1732	Total	C	N	O	P	0	0
			36419	16179	6629	11880	1731		

- Molecule 78 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	A7	121	Total	C	N	O	P	0	0
			2578	1150	458	850	120		

- Molecule 79 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	A8	157	Total	C	N	O	P	0	0
			3334	1489	587	1102	156		

- Molecule 80 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	B2	1837	Total	C	N	O	P	0	0
			38185	17001	6745	12603	1836		

- Molecule 81 is a RNA chain called LSU beta rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	A6	2122	Total	C	N	O	P	0	0
			43819	19451	7789	14457	2122		

- Molecule 82 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	BB	218	Total	C	N	O	S	0	0
			1768	1120	320	314	14		

- Molecule 83 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	OO	134	Total	C	N	O	S	0	0
			1002	612	197	187	6		

- Molecule 84 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	RR	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 85 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
85	P	1	Total	Mg	0
			1	1	
85	a	1	Total	Mg	0
			1	1	
85	l	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
85	A5	7	Total 7	Mg 7	0
85	A8	1	Total 1	Mg 1	0
85	B2	6	Total 6	Mg 6	0
85	A6	7	Total 7	Mg 7	0
85	BB	2	Total 2	Mg 2	0

- Molecule 86 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
86	g	1	Total 1	Zn 1	0
86	j	1	Total 1	Zn 1	0
86	m	1	Total 1	Zn 1	0
86	o	1	Total 1	Zn 1	0
86	p	1	Total 1	Zn 1	0
86	aa	1	Total 1	Zn 1	0
86	ff	1	Total 1	Zn 1	0
86	dd	1	Total 1	Zn 1	0


- Molecule 87 is water.

Mol	Chain	Residues	Atoms		AltConf
87	A6	1	Total 1	O 1	0

3 Residue-property plots

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

- Molecule 1: Large ribosomal subunit protein uL2

Chain A:  91% 9%




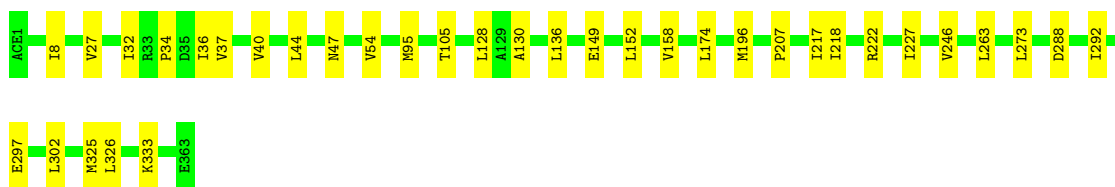
- Molecule 2: 60S ribosomal protein L3

Chain B:  93% 7%




- Molecule 3: Large ribosomal subunit protein uL4

Chain C:  90% 10%




- Molecule 4: Large ribosomal subunit protein eL24

Chain c:  83% 12% 5%

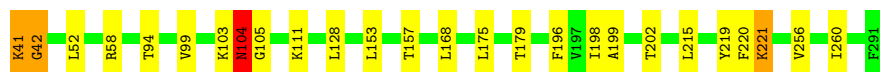


- Molecule 5: Large ribosomal subunit protein uL18

Chain D:  90% 10%



- Molecule 6: 60S ribosomal protein L6



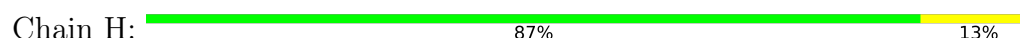
- Molecule 7: 60S ribosomal protein L7



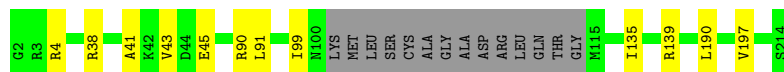
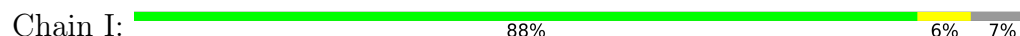
- Molecule 8: 60S ribosomal protein L7a



- Molecule 9: 60S ribosomal protein L9



- Molecule 10: 60S ribosomal protein L10

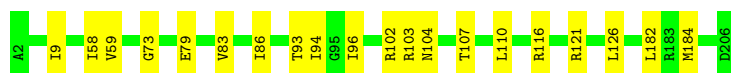


- Molecule 11: Large ribosomal subunit protein uL5



- Molecule 12: 60S ribosomal protein L13





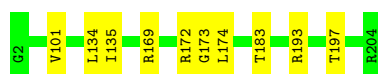
- Molecule 13: Large ribosomal subunit protein eL14

Chain M: 88% 12%



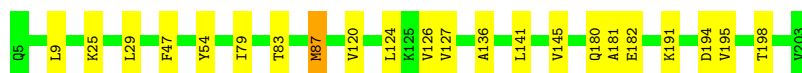
- Molecule 14: Ribosomal protein L15

Chain N: 95% 5%



- Molecule 15: 60S ribosomal protein L13a

Chain O: 89% 11%



- Molecule 16: 60S ribosomal protein L17

Chain P: 97% 3%



- Molecule 17: 60S ribosomal protein L18

Chain Q: 88% 12%



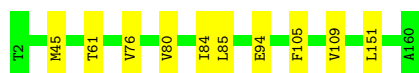
- Molecule 18: Large ribosomal subunit protein eL20

Chain S: 94% 6%



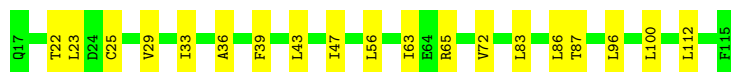
- Molecule 19: Large ribosomal subunit protein eL21

Chain T: 94% 6%



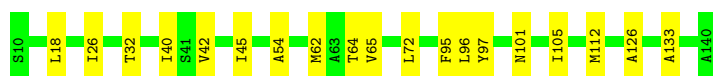
- Molecule 20: 60S ribosomal protein L22

Chain U: 81% 19%



- Molecule 21: Large ribosomal subunit protein uL14

Chain V: 85% 15%



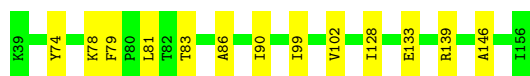
- Molecule 22: Ribosomal protein L19

Chain W: 94% 6%



- Molecule 23: Large ribosomal subunit protein uL23

Chain X: 89% 11%



- Molecule 24: 60S ribosomal protein L26

Chain Y: 89% 11%



- Molecule 25: 60S ribosomal protein L27

Chain Z: 88% 12%



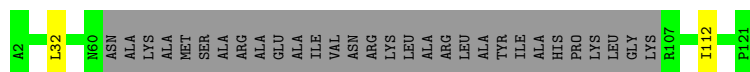
- Molecule 26: 60S ribosomal protein L27a

Chain a: 92% 8%



- Molecule 27: 60S ribosomal protein L29

Chain b: 69% 29%



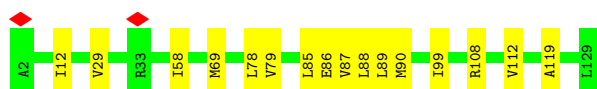
- Molecule 28: Large ribosomal subunit protein eL31

Chain d: 93% 7%



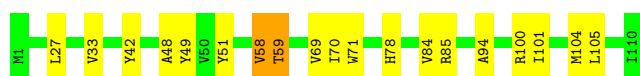
- Molecule 29: 60S ribosomal protein L32

Chain e: 88% 12%



- Molecule 30: Large ribosomal subunit protein eL33

Chain f: 83% 15%



- Molecule 31: Large ribosomal subunit protein eL34

Chain g: 96%



- Molecule 32: Large ribosomal subunit protein uL29

Chain h: 86% 14%



- Molecule 33: 60S ribosomal protein L36

Chain i: 93% 7%



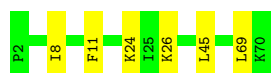
- Molecule 34: Ribosomal protein L37

Chain j: 95% 5%



- Molecule 35: Large ribosomal subunit protein eL38

Chain k: 91% 9%



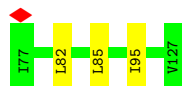
- Molecule 36: 60S ribosomal protein L39

Chain l: 94% 6%



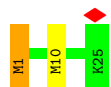
- Molecule 37: Ubiquitin-ribosomal protein eL40 fusion protein

Chain m: 94% 6%



- Molecule 38: 60S ribosomal protein L41

Chain n: 92% 8%



- Molecule 39: 60S ribosomal protein L36a

Chain o: 92% 8%

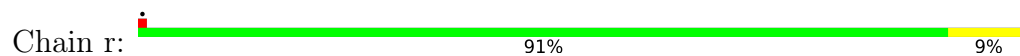


- Molecule 40: Large ribosomal subunit protein eL43

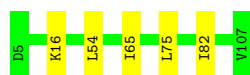
Chain p: 84% 16%



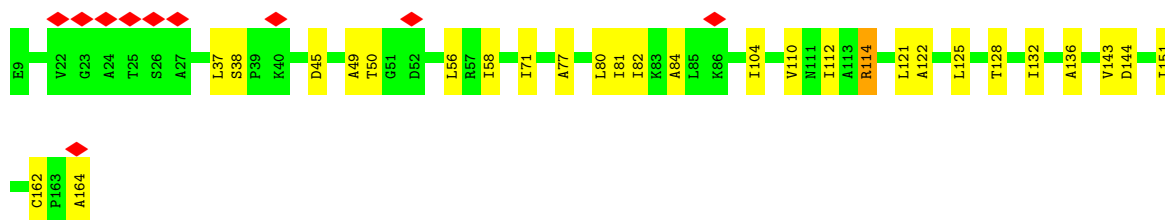
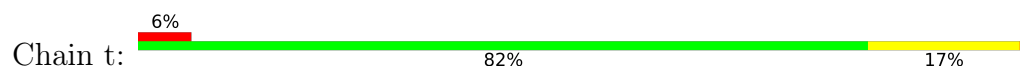
- Molecule 41: Large ribosomal subunit protein eL28



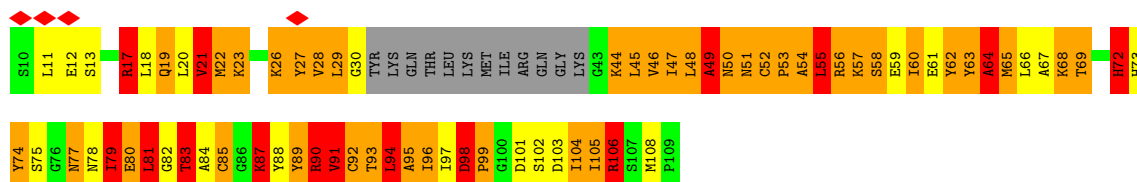
- Molecule 42: 60S acidic ribosomal protein P0



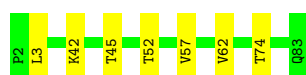
- Molecule 43: 60S ribosomal protein L12



- Molecule 44: Large ribosomal subunit protein eL30



- Molecule 45: 40S ribosomal protein S27



- Molecule 46: 40S ribosomal protein S30

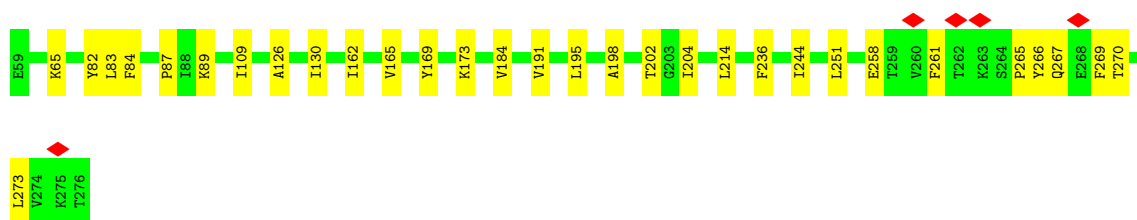
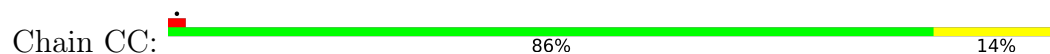




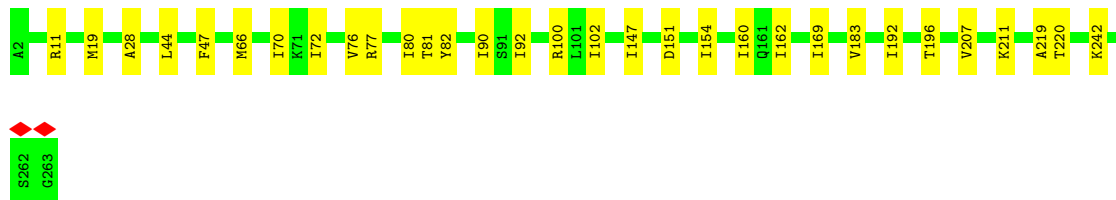
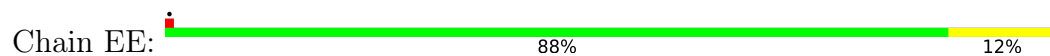
- Molecule 47: 40S ribosomal protein S26



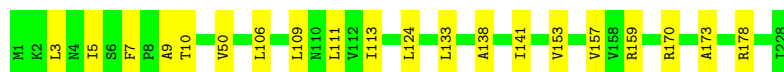
- Molecule 48: 40S ribosomal protein S2



- Molecule 49: 40S ribosomal protein S4, X isoform



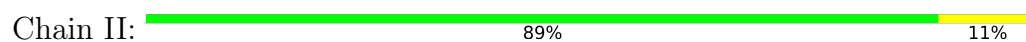
- Molecule 50: 40S ribosomal protein S6



- Molecule 51: 40S ribosomal protein S7



- Molecule 52: 40S ribosomal protein S8





- Molecule 53: Small ribosomal subunit protein uS4

Chain JJ: 91% 9%



- Molecule 54: Small ribosomal subunit protein uS17

Chain LL: 86% 9% 5%



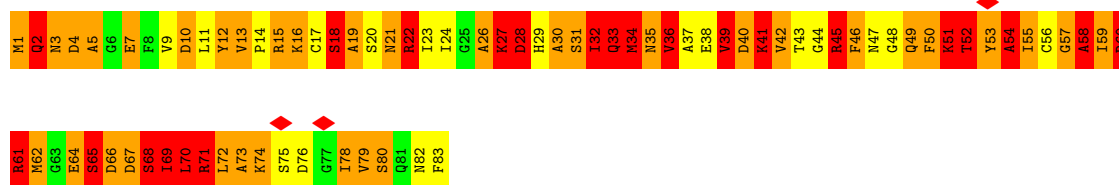
- Molecule 55: Small ribosomal subunit protein uS15

Chain NN: 86% 14%



- Molecule 56: 40S ribosomal protein S21

Chain VV: 7% 23% 42% 28%



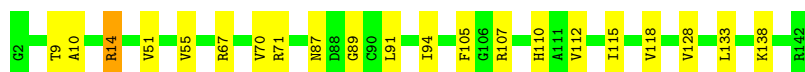
- Molecule 57: Small ribosomal subunit protein uS8

Chain WW: 81% 19%



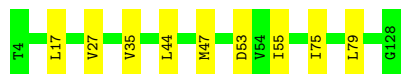
- Molecule 58: Small ribosomal subunit protein uS12

Chain XX: 85% 14%




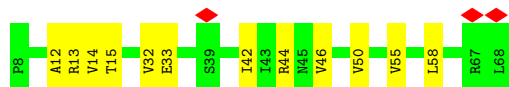
- Molecule 59: 40S ribosomal protein S24

Chain YY:  93% 7%



- Molecule 60: 40S ribosomal protein S28

Chain cc:  5% 80% 20%




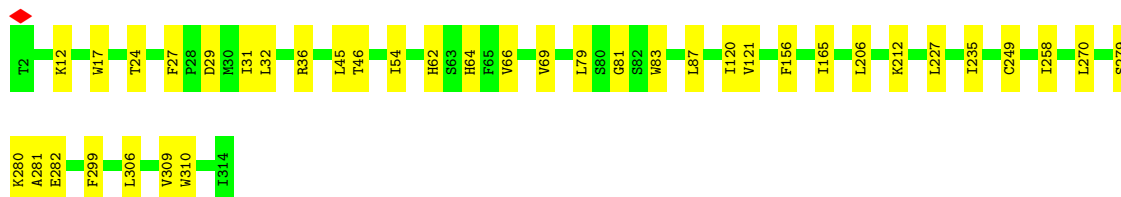
- Molecule 61: Ubiquitin-ribosomal protein eS31 fusion protein

Chain ff:  97% .



- Molecule 62: Small ribosomal subunit protein RACK1

Chain gg:  88% 12%



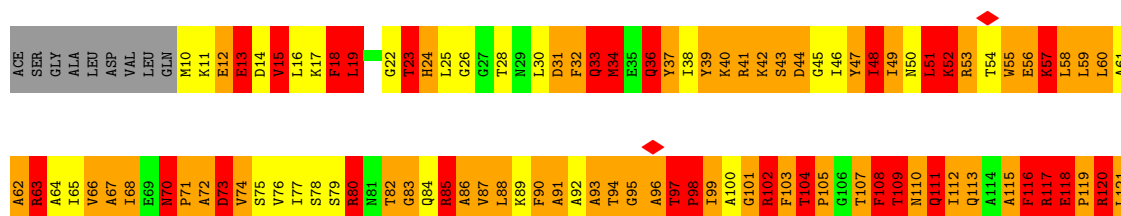
- Molecule 63: Small ribosomal subunit protein uS14

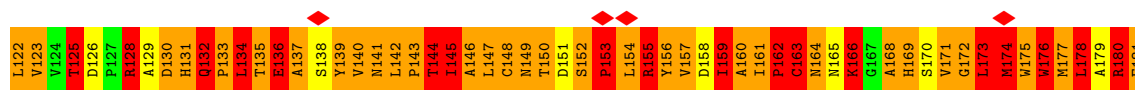
Chain dd:  91% 9%



- Molecule 64: Small ribosomal subunit protein uS2

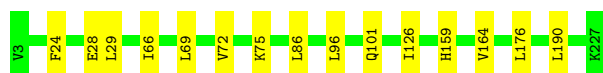
Chain AA:  6% 18% 45% 27% .





- Molecule 65: Small ribosomal subunit protein uS3

Chain DD: 93% 7%



- Molecule 66: Small ribosomal subunit protein uS7

Chain FF: 85% 13% ..



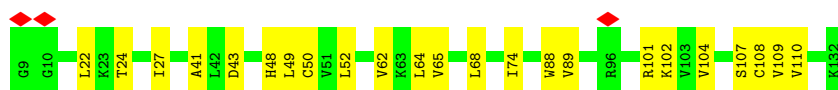
- Molecule 67: Small ribosomal subunit protein eS10

Chain KK: 93% 7%



- Molecule 68: 40S ribosomal protein S12

Chain MM: 81% 19%



- Molecule 69: 40S ribosomal protein S15

Chain PP: 96% .



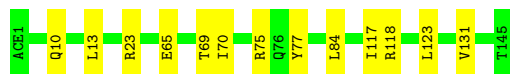
- Molecule 70: Small ribosomal subunit protein uS9

Chain QQ: 91% 9%



- Molecule 71: Small ribosomal subunit protein uS13

Chain SS:  91% 9%



- Molecule 72: Small ribosomal subunit protein eS19

Chain TT:  92% 8%



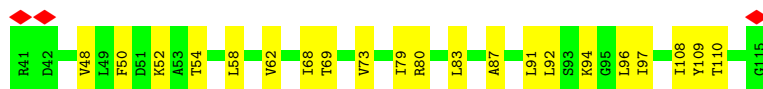
- Molecule 73: 40S ribosomal protein S20

Chain UU:  91% 9%




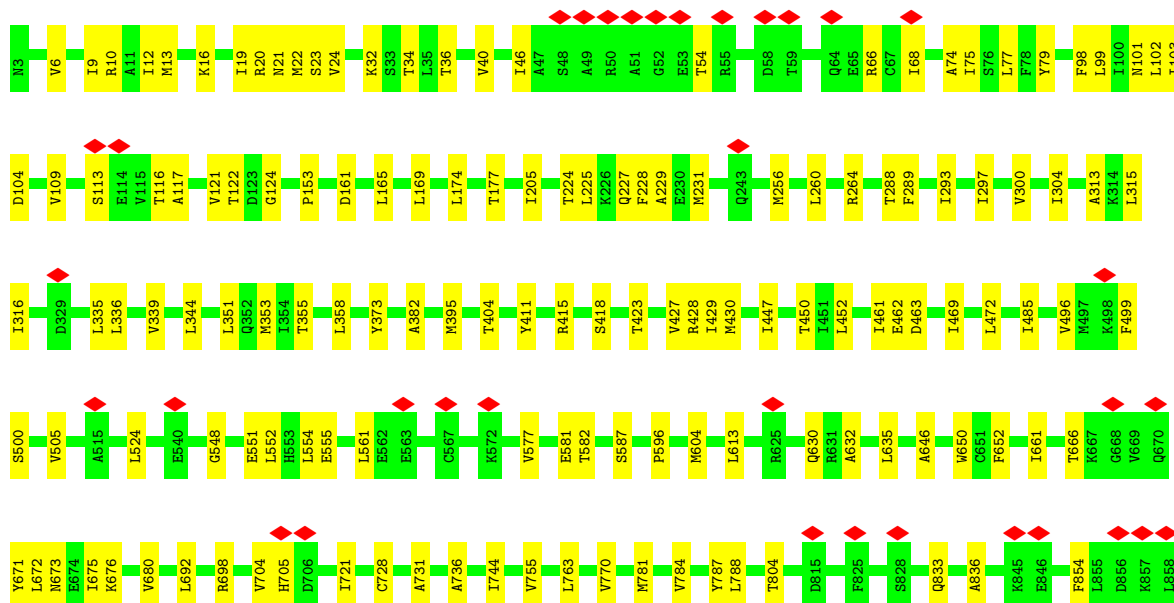
- Molecule 74: 40S ribosomal protein S25

Chain ZZ:  72% 28%



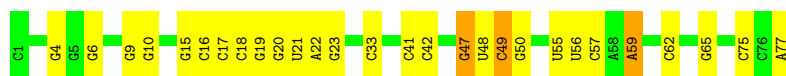
- Molecule 75: eEF2

Chain EF:  83% 17%



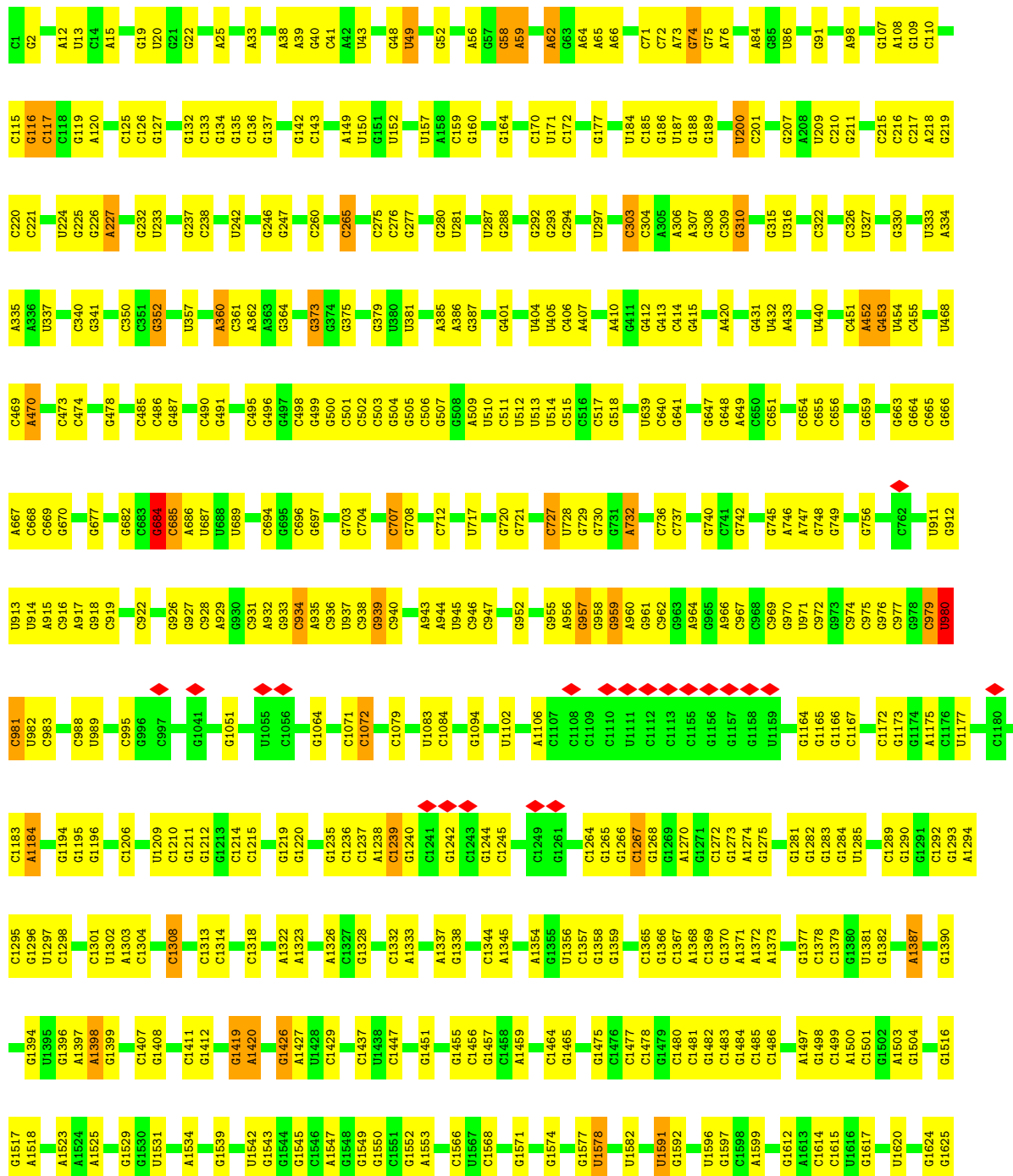
• Molecule 76: P/E tRNA (77-MER)

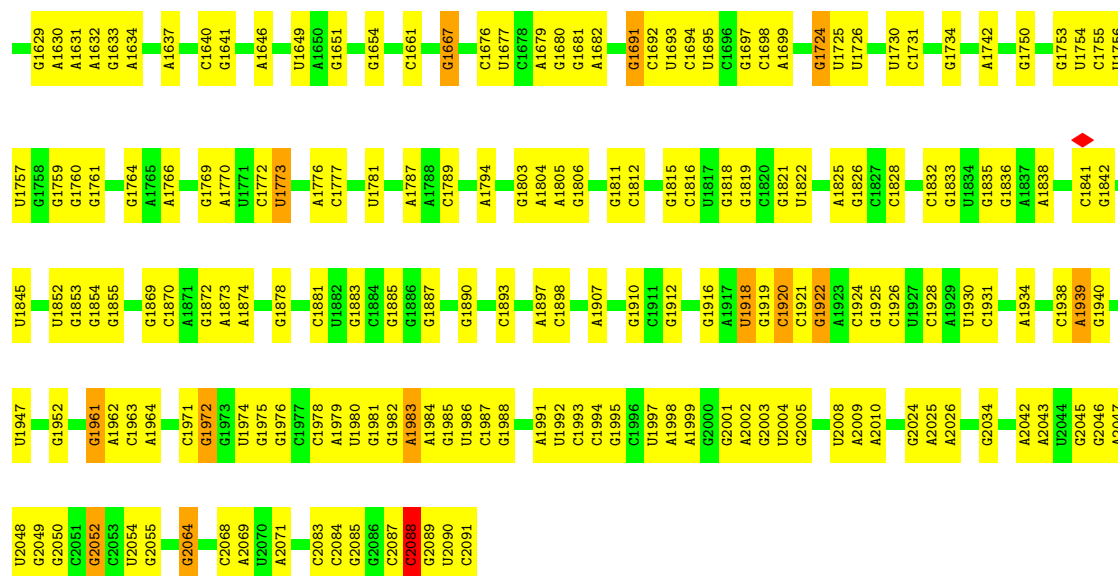
Chain Cc:  64% 32%



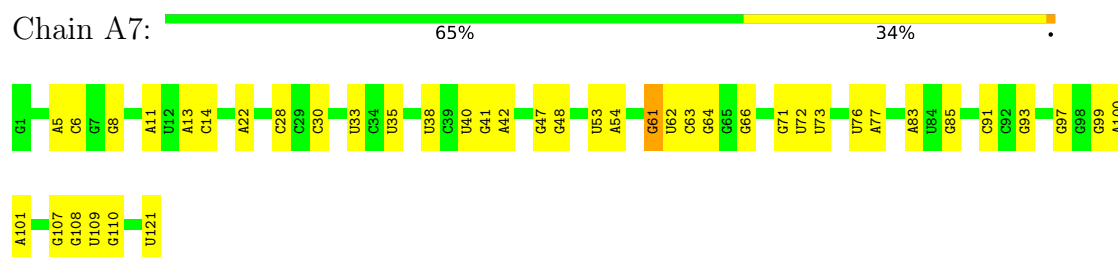
• Molecule 77: LSU alpha rRNA

Chain A5:  62% 35%

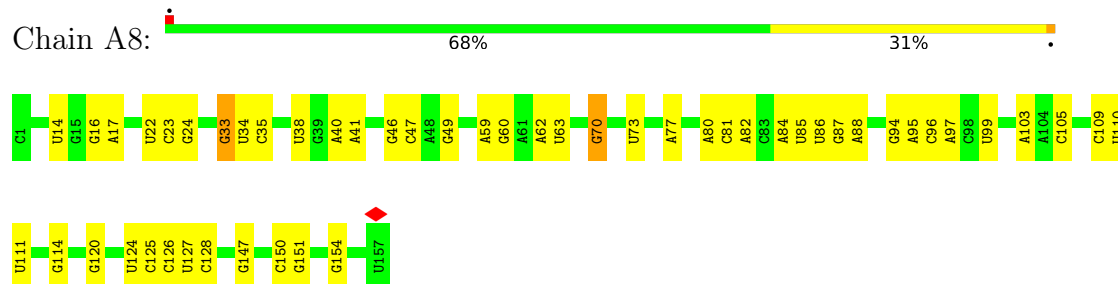




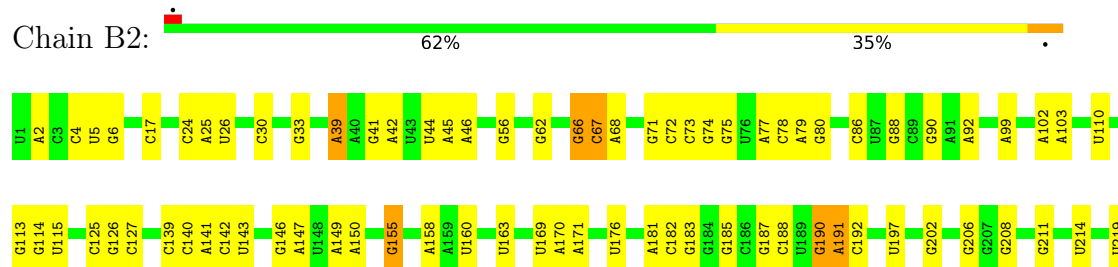
• Molecule 78: 5S ribosomal RNA

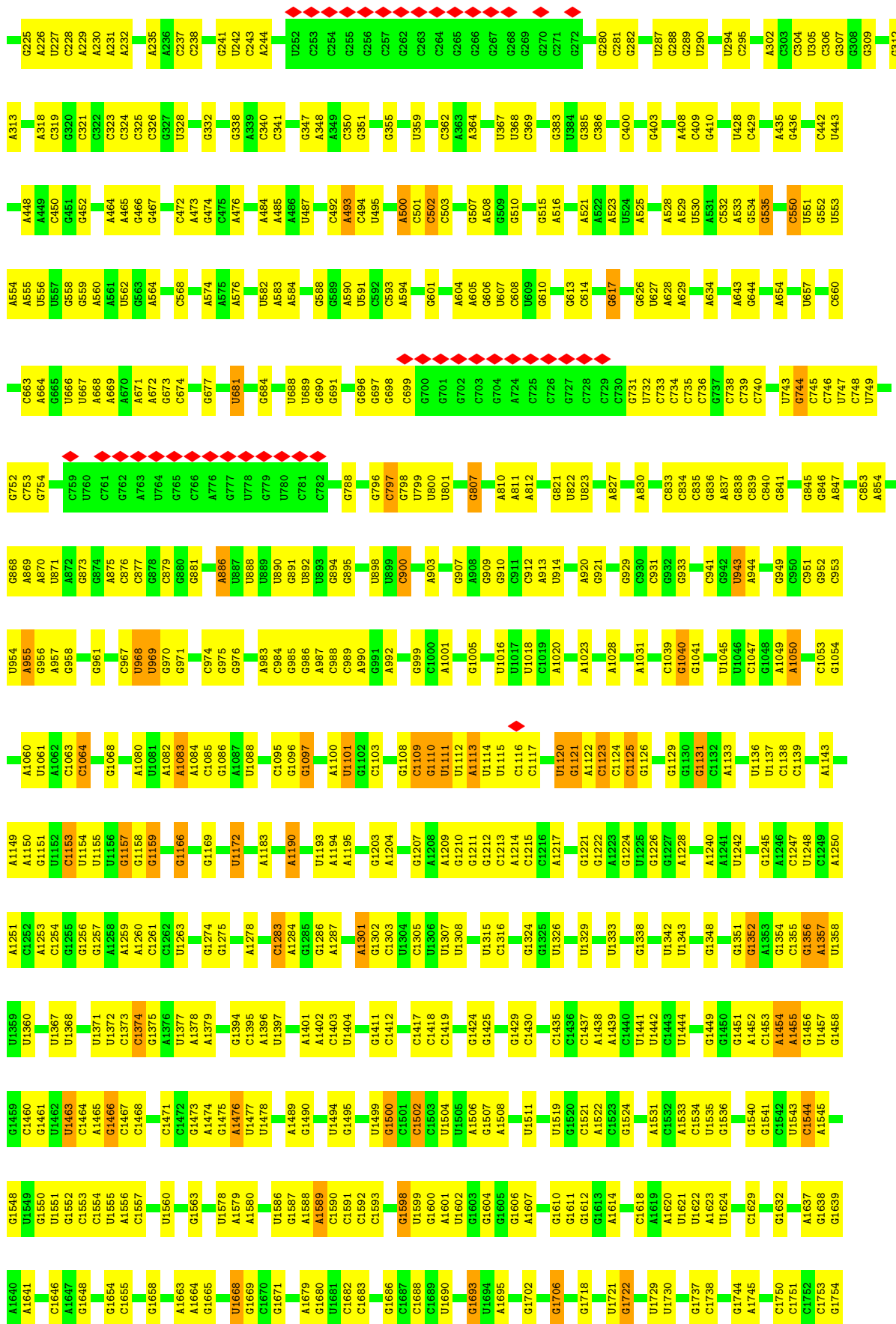


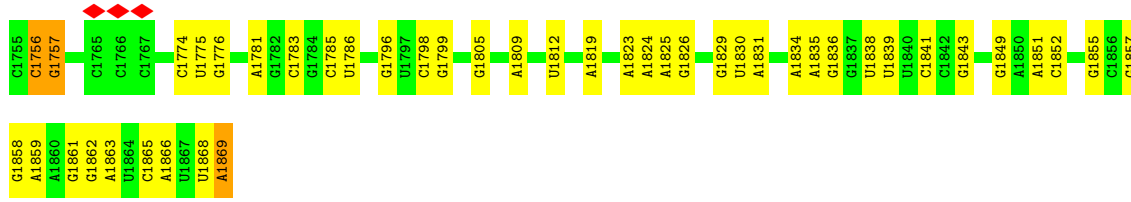
• Molecule 79: 5.8S ribosomal RNA



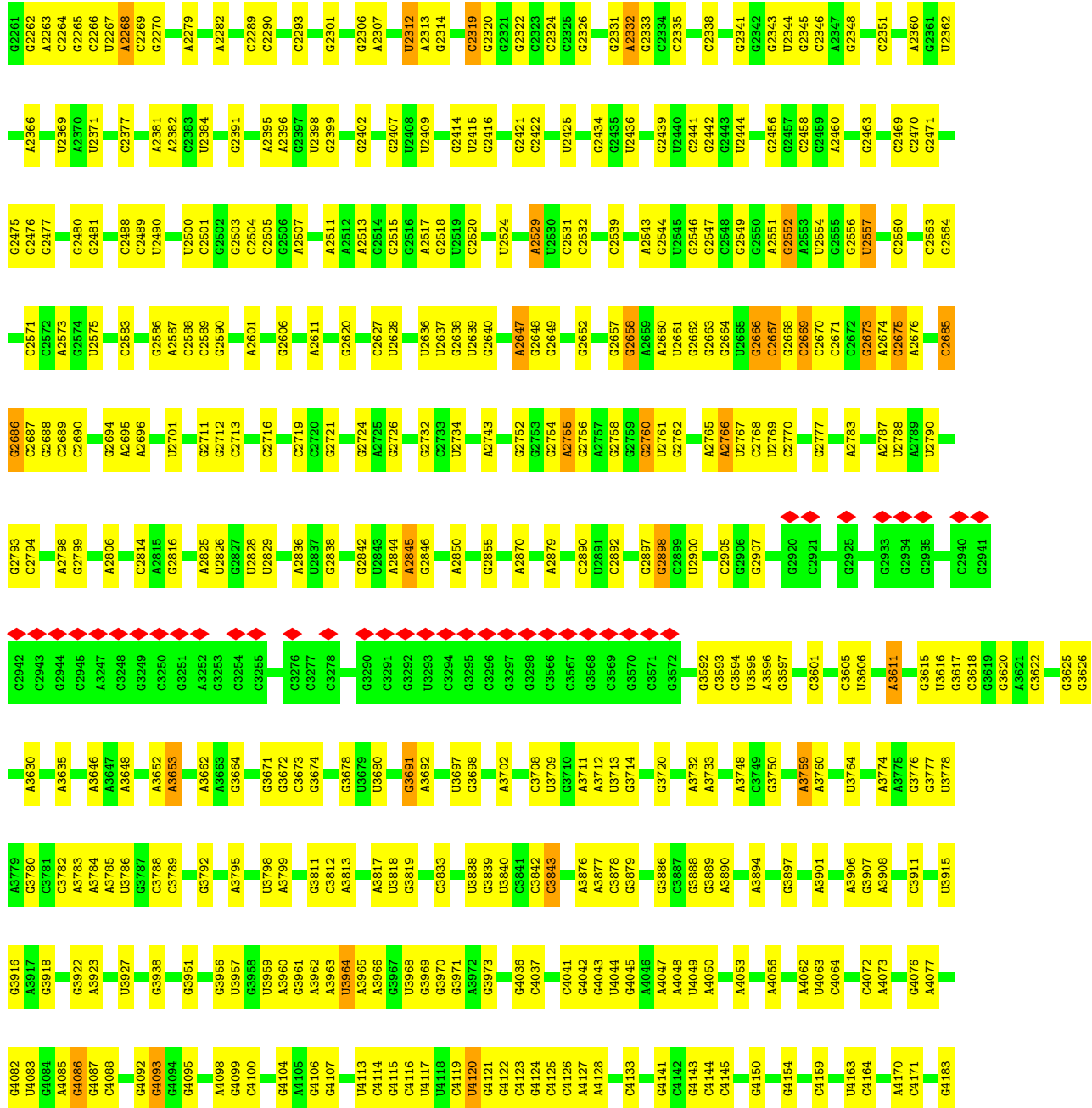
• Molecule 80: 18S ribosomal RNA

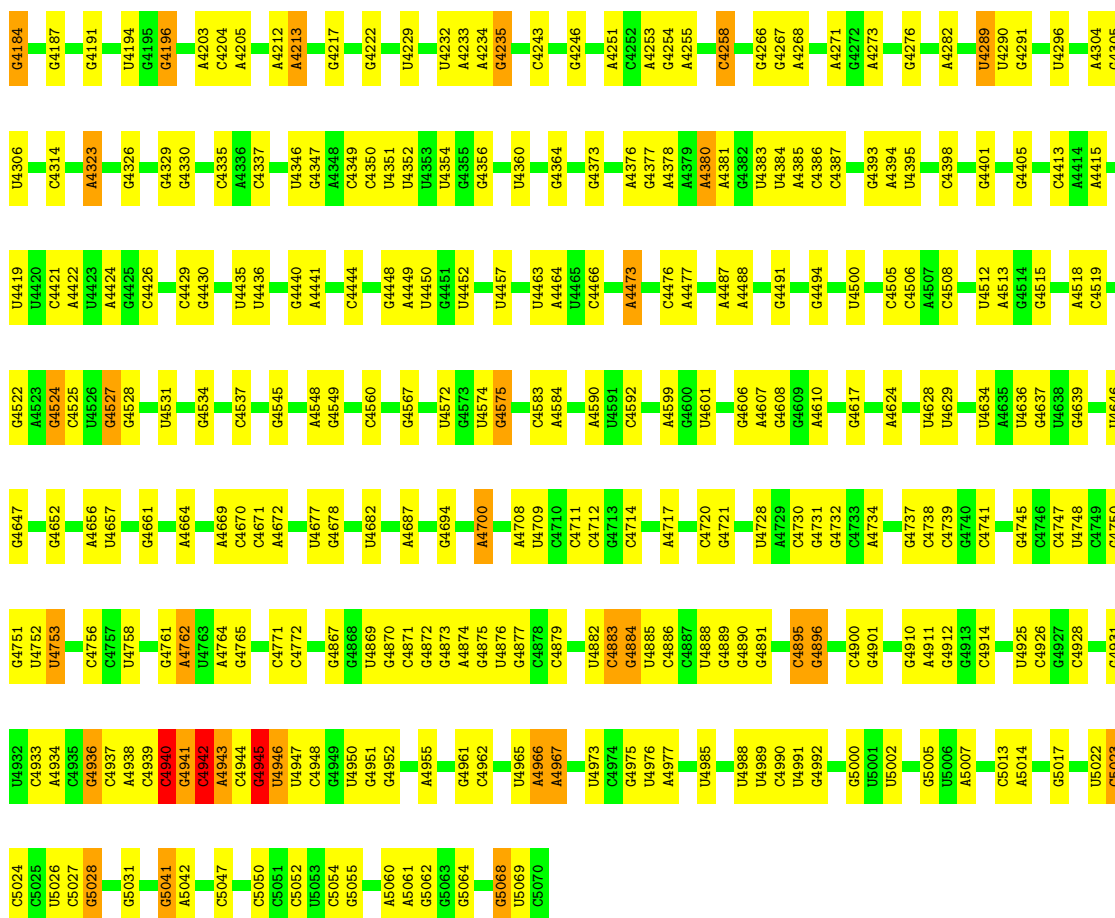




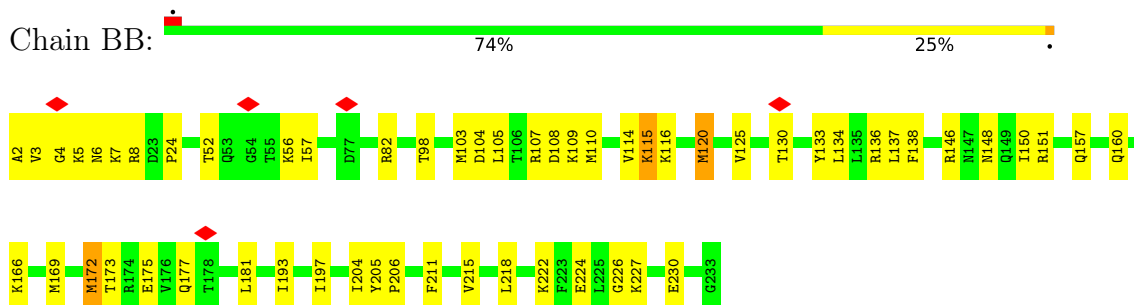


• Molecule 81: LSU beta rRNA

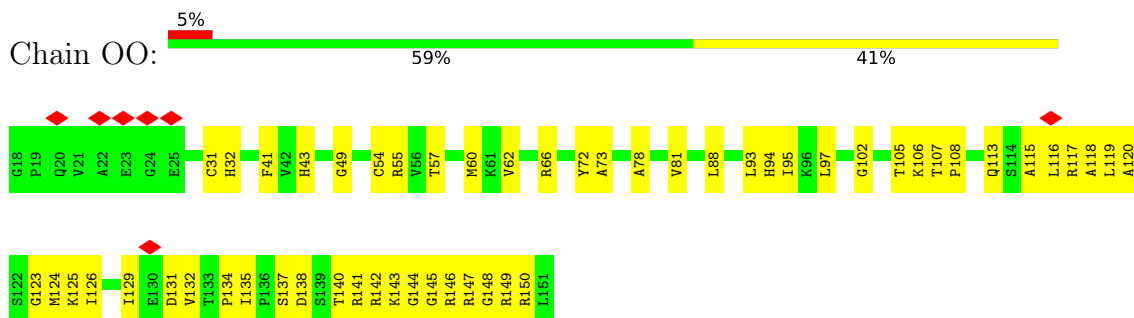




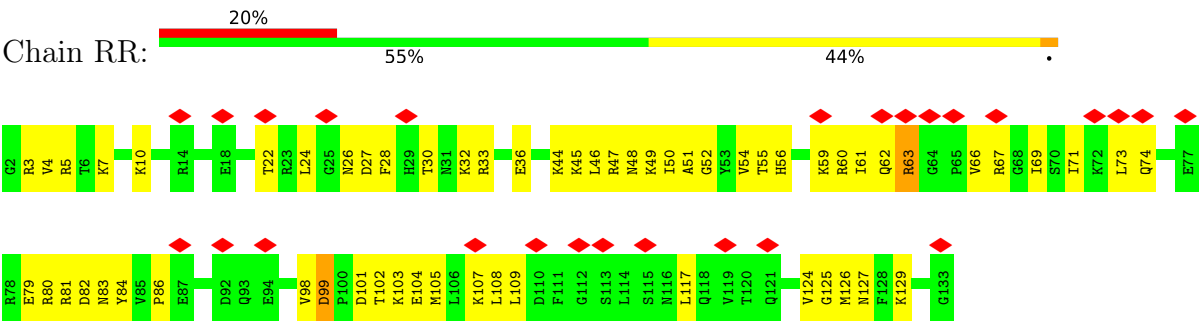
- Molecule 82: 40S ribosomal protein S3a



- Molecule 83: 40S ribosomal protein S14



- Molecule 84: Small ribosomal subunit protein eS17



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	Not provided	
Resolution determination method	Not provided	
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.059	Depositor
Minimum map value	-0.020	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	459.8, 459.8, 459.8	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HIC, MG, ACE, M3L, V5N, NMM, MLZ, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.22	0/1936	0.48	0/2596
2	B	0.20	0/3261	0.47	0/4364
3	C	0.21	0/2948	0.45	0/3959
4	c	0.24	0/952	0.50	0/1262
5	D	0.21	0/2435	0.47	0/3261
6	E	2.87	8/1822 (0.4%)	1.05	11/2442 (0.5%)
7	F	0.22	0/1911	0.51	0/2549
8	G	0.22	0/1772	0.49	0/2387
9	H	0.22	0/1535	0.45	0/2063
10	I	0.20	0/1658	0.45	0/2214
11	J	0.20	0/1385	0.47	0/1852
12	L	0.20	0/1689	0.46	0/2261
13	M	0.20	0/1146	0.43	0/1531
14	N	0.21	0/1746	0.46	0/2338
15	O	0.24	0/1662	0.52	1/2222 (0.0%)
16	P	0.23	0/1268	0.51	0/1700
17	Q	0.19	0/1537	0.46	0/2052
18	S	0.20	0/1501	0.44	0/2013
19	T	0.22	0/1326	0.50	0/1770
20	U	0.21	0/822	0.51	0/1103
21	V	0.24	0/986	0.58	1/1323 (0.1%)
22	W	0.26	0/1524	0.61	0/2013
23	X	0.20	0/984	0.41	0/1323
24	Y	0.25	0/1132	0.50	0/1504
25	Z	0.18	0/1130	0.41	0/1507
26	a	0.17	0/1179	0.41	0/1572
27	b	0.21	0/619	0.50	0/814
28	d	0.22	0/903	0.47	0/1216
29	e	0.21	0/1071	0.47	0/1429
30	f	2.83	4/903 (0.4%)	1.02	6/1208 (0.5%)
31	g	0.19	0/883	0.45	0/1177
32	h	0.22	0/1019	0.51	0/1344

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	i	0.20	0/841	0.51	0/1112
34	j	0.21	0/720	0.50	0/952
35	k	0.20	0/575	0.42	0/761
36	l	0.21	0/459	0.50	0/608
37	m	0.23	0/416	0.55	0/553
38	n	0.28	0/240	0.58	0/305
39	o	0.19	0/866	0.43	0/1141
40	p	0.23	0/718	0.51	0/953
41	r	0.25	0/1028	0.54	0/1377
42	s	0.22	0/837	0.50	0/1121
43	t	0.28	0/1193	0.57	0/1609
44	u	1.58	12/681 (1.8%)	2.72	69/916 (7.5%)
45	bb	0.17	0/653	0.42	0/876
46	ee	0.22	0/399	0.55	0/520
47	aa	0.26	0/794	0.58	0/1065
48	CC	0.23	0/1721	0.46	0/2328
49	EE	0.19	0/2118	0.42	0/2849
50	GG	0.20	0/1871	0.46	0/2492
51	HH	0.19	0/1511	0.40	0/2023
52	II	0.18	0/1715	0.41	0/2287
53	JJ	0.18	0/1524	0.40	0/2035
54	LL	0.28	0/1177	0.52	0/1575
55	NN	0.22	0/1226	0.45	0/1649
56	VV	1.68	16/644 (2.5%)	3.01	88/862 (10.2%)
57	WW	0.21	0/1051	0.50	0/1406
58	XX	0.23	0/1115	0.51	0/1486
59	YY	0.18	0/1032	0.45	0/1371
60	cc	0.23	0/481	0.53	0/643
61	ff	0.22	0/560	0.52	0/745
62	gg	0.20	0/2493	0.48	0/3394
63	dd	0.27	0/470	0.62	0/623
64	AA	1.64	29/1662 (1.7%)	3.25	271/2259 (12.0%)
65	DD	0.20	0/1779	0.43	0/2395
66	FF	0.21	0/1495	0.50	0/2008
67	KK	0.28	0/834	0.57	0/1125
68	MM	0.22	0/968	0.52	1/1296 (0.1%)
69	PP	0.21	0/997	0.46	0/1330
70	QQ	0.21	0/1142	0.50	0/1528
71	SS	0.21	0/1209	0.47	0/1620
72	TT	0.21	0/1102	0.49	0/1476
73	UU	0.20	0/800	0.51	0/1074
74	ZZ	0.31	0/604	0.59	0/810
75	EF	0.24	0/6800	0.55	0/9184

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Cc	0.17	0/1836	0.37	0/2859
77	A5	0.78	11/40680 (0.0%)	0.45	9/63377 (0.0%)
78	A7	0.18	0/2880	0.37	0/4489
79	A8	0.18	0/3723	0.41	0/5800
80	B2	0.18	0/42627	0.42	0/66334
81	A6	0.75	13/48903 (0.0%)	0.42	3/76100 (0.0%)
82	BB	1.60	2/1794 (0.1%)	0.74	4/2396 (0.2%)
83	OO	0.22	0/1015	0.53	0/1361
84	RR	0.28	0/1082	0.63	0/1452
All	All	0.62	95/241706 (0.0%)	0.57	464/354279 (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
3	C	0	1
4	c	0	2
6	E	0	1
12	L	0	2
23	X	0	1
26	a	0	2
30	f	0	1
38	n	0	1
43	t	0	1
44	u	0	4
47	aa	0	2
50	GG	0	1
56	VV	0	14
58	XX	0	1
63	dd	0	1
64	AA	0	19
66	FF	0	1
75	EF	0	1
81	A6	1	0
All	All	1	56

All (95) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	E	104	ASN	CA-C	105.00	2.49	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	f	58	VAL	CA-CB	82.92	2.67	1.54
82	BB	115	LYS	CA-CB	66.18	2.48	1.53
77	A5	684	G	O4'-C1'	61.83	2.65	1.41
77	A5	980	U	C4'-O4'	59.57	2.64	1.45
6	E	221	LYS	CA-CB	58.87	2.32	1.53
81	A6	4945	G	N9-C8	55.31	2.48	1.37
81	A6	4945	G	N9-C4	54.86	2.47	1.38
77	A5	684	G	C4'-O4'	54.71	2.54	1.45
81	A6	4945	G	N7-C5	54.13	2.47	1.39
77	A5	980	U	O4'-C1'	53.48	2.48	1.41
81	A6	4945	G	C8-N7	50.48	2.31	1.30
81	A6	4940	C	C2-N3	49.24	2.34	1.35
81	A6	4940	C	N1-C6	47.12	2.31	1.37
81	A6	4940	C	N1-C2	46.78	2.33	1.40
81	A6	4940	C	N3-C4	46.39	2.26	1.33
81	A6	4940	C	C4-C5	44.40	2.31	1.43
81	A6	4940	C	C5-C6	42.16	2.18	1.34
77	A5	980	U	C2'-C1'	41.61	2.36	1.53
77	A5	684	G	C2'-C1'	41.45	2.36	1.53
77	A5	684	G	C3'-C2'	41.15	2.35	1.53
81	A6	4945	G	C5-C4	40.81	2.19	1.38
77	A5	684	G	C4'-C3'	40.32	2.33	1.52
77	A5	980	U	C4'-C3'	39.16	2.30	1.52
77	A5	980	U	C3'-C2'	39.02	2.31	1.53
64	AA	180	ARG	C-O	-14.39	1.07	1.24
6	E	104	ASN	CA-CB	10.54	1.66	1.53
30	f	58	VAL	CB-CG1	10.21	1.86	1.52
30	f	58	VAL	CB-CG2	10.09	1.85	1.52
44	u	74	TYR	CA-C	9.41	1.64	1.52
44	u	93	THR	N-CA	9.03	1.58	1.46
82	BB	115	LYS	CB-CG	8.58	1.78	1.52
56	VV	51	LYS	C-O	-8.24	1.14	1.23
64	AA	32	PHE	CA-C	-8.01	1.42	1.52
6	E	221	LYS	CB-CG	7.82	1.75	1.52
56	VV	18	SER	CA-CB	-7.76	1.41	1.53
56	VV	66	ASP	C-O	-7.70	1.15	1.24
6	E	42	GLY	N-CA	7.54	1.56	1.45
44	u	64	ALA	C-O	-7.52	1.15	1.24
64	AA	85	ARG	C-O	-7.40	1.15	1.24
64	AA	153	PRO	N-CA	7.17	1.56	1.47
56	VV	73	ALA	CA-CB	-7.17	1.37	1.53
64	AA	116	PHE	CA-C	-7.16	1.42	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
64	AA	71	PRO	N-CA	7.14	1.55	1.47
64	AA	47	TYR	CA-C	-6.92	1.44	1.52
30	f	58	VAL	CA-C	6.83	1.61	1.52
44	u	62	TYR	CA-C	-6.78	1.44	1.52
64	AA	125	THR	CA-C	-6.70	1.44	1.52
64	AA	135	THR	C-N	-6.67	1.25	1.33
81	A6	2666	G	C1'-N9	-6.50	1.38	1.48
64	AA	118	GLU	C-O	-6.47	1.16	1.24
81	A6	2557	U	C1'-N1	6.44	1.58	1.48
64	AA	197	VAL	C-O	-6.29	1.15	1.23
44	u	59	GLU	N-CA	6.27	1.53	1.46
77	A5	2088	C	C1'-N1	6.16	1.56	1.47
64	AA	91	ALA	CA-CB	-6.05	1.43	1.53
56	VV	52	THR	N-CA	6.00	1.53	1.45
64	AA	104	THR	CA-C	-6.00	1.46	1.52
64	AA	99	ILE	N-CA	5.93	1.52	1.46
56	VV	55	ILE	C-O	-5.89	1.17	1.24
56	VV	27	LYS	CA-C	5.85	1.60	1.52
56	VV	59	ILE	N-CA	5.84	1.53	1.46
56	VV	12	TYR	CA-C	-5.80	1.45	1.52
56	VV	65	SER	CA-CB	-5.75	1.44	1.53
64	AA	154	LEU	N-CA	5.70	1.53	1.45
64	AA	201	LEU	N-CA	5.67	1.53	1.46
64	AA	136	GLU	CA-C	-5.67	1.45	1.52
64	AA	135	THR	CA-C	-5.66	1.45	1.52
64	AA	183	LEU	CA-C	5.64	1.60	1.52
64	AA	135	THR	N-CA	5.56	1.53	1.46
64	AA	152	SER	N-CA	5.52	1.51	1.46
44	u	47	ILE	C-O	-5.51	1.18	1.24
64	AA	203	PHE	N-CA	5.50	1.52	1.46
64	AA	144	THR	N-CA	5.49	1.52	1.46
56	VV	27	LYS	N-CA	5.42	1.53	1.46
56	VV	54	ALA	C-N	-5.39	1.27	1.33
64	AA	176	TRP	CA-C	5.38	1.59	1.52
56	VV	13	VAL	C-O	-5.35	1.18	1.25
64	AA	68	ILE	C-O	-5.34	1.18	1.24
44	u	49	ALA	CA-CB	-5.33	1.44	1.53
64	AA	105	PRO	N-CA	-5.31	1.40	1.47
6	E	41	LYS	CA-C	5.31	1.64	1.52
44	u	58	SER	N-CA	5.19	1.52	1.45
44	u	95	ALA	CA-CB	-5.16	1.46	1.53
64	AA	159	ILE	C-O	-5.16	1.18	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
64	AA	180	ARG	CA-C	-5.15	1.46	1.52
64	AA	86	ALA	N-CA	5.14	1.52	1.46
56	VV	28	ASP	N-CA	5.14	1.52	1.46
6	E	104	ASN	C-O	5.11	1.28	1.23
56	VV	60	ARG	N-CA	5.11	1.52	1.45
6	E	104	ASN	C-N	5.10	1.41	1.33
44	u	74	TYR	N-CA	5.09	1.51	1.46
44	u	28	VAL	N-CA	5.08	1.51	1.46
44	u	98	ASP	N-CA	5.05	1.50	1.45
56	VV	32	ILE	CA-C	5.04	1.58	1.52

All (464) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
64	AA	152	SER	N-CA-C	18.92	125.25	108.22
6	E	104	ASN	O-C-N	-18.12	102.81	122.38
6	E	221	LYS	N-CA-C	-17.89	80.51	108.96
64	AA	182	VAL	N-CA-C	-17.12	93.16	110.62
6	E	104	ASN	N-CA-CB	-16.86	84.43	110.39
82	BB	115	LYS	N-CA-C	-16.63	82.14	109.24
6	E	221	LYS	CA-CB-CG	16.06	146.22	114.10
64	AA	134	LEU	N-CA-CB	-16.00	83.45	110.49
64	AA	37	TYR	CB-CA-C	15.95	138.71	110.01
64	AA	200	ASP	N-CA-C	14.79	127.40	111.28
6	E	221	LYS	CB-CA-C	14.67	134.72	110.22
82	BB	115	LYS	CB-CA-C	14.65	133.93	109.75
64	AA	34	MET	N-CA-C	-14.49	93.58	112.41
44	u	59	GLU	N-CA-C	14.22	126.50	111.14
30	f	58	VAL	CB-CA-C	14.19	134.56	111.29
64	AA	181	GLU	CB-CA-C	14.16	139.05	110.17
44	u	91	VAL	N-CA-CB	-14.10	87.97	111.23
64	AA	74	VAL	N-CA-C	13.81	125.82	110.21
64	AA	194	PRO	N-CA-C	-13.72	88.89	111.26
64	AA	143	PRO	CA-C-O	-13.22	105.54	121.67
64	AA	47	TYR	N-CA-CB	-13.15	89.93	110.57
64	AA	92	ALA	N-CA-C	-12.88	96.90	111.71
64	AA	14	ASP	CB-CA-C	12.81	132.64	110.85
82	BB	115	LYS	CA-CB-CG	12.79	139.68	114.10
64	AA	37	TYR	N-CA-CB	-12.70	91.01	110.44
30	f	58	VAL	N-CA-C	-12.70	82.93	109.34
64	AA	204	TYR	N-CA-CB	-12.67	87.97	111.53
30	f	58	VAL	CA-CB-CG2	12.51	131.67	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
64	AA	134	LEU	N-CA-C	12.51	137.44	110.80
30	f	58	VAL	CA-CB-CG1	12.45	131.56	110.40
44	u	99	PRO	N-CA-C	-12.28	96.46	113.53
6	E	41	LYS	CA-C-O	-12.10	100.24	120.80
44	u	60	ILE	N-CA-C	-12.05	101.34	112.90
6	E	104	ASN	CB-CA-C	11.95	133.38	112.00
56	VV	30	ALA	N-CA-C	-11.90	87.05	107.99
64	AA	70	ASN	CB-CA-C	11.84	125.20	110.76
64	AA	58	LEU	N-CA-C	-11.80	98.42	111.28
64	AA	136	GLU	N-CA-CB	-11.70	92.92	110.12
64	AA	63	ARG	N-CA-C	11.67	124.08	111.36
64	AA	211	GLU	CB-CA-C	-11.63	92.62	110.88
64	AA	71	PRO	CB-CA-C	-11.60	95.78	111.21
64	AA	60	LEU	N-CA-C	11.55	127.59	113.38
56	VV	51	LYS	N-CA-CB	-11.51	93.57	110.37
56	VV	46	PHE	N-CA-CB	-11.44	91.78	110.42
6	E	221	LYS	N-CA-CB	11.40	129.32	110.17
56	VV	4	ASP	N-CA-C	-11.26	98.76	111.71
56	VV	58	ALA	CA-C-O	-11.17	104.53	120.51
64	AA	71	PRO	N-CA-C	11.11	128.63	111.19
64	AA	176	TRP	N-CA-C	11.05	123.07	111.14
56	VV	55	ILE	CB-CA-C	11.04	127.05	112.14
56	VV	60	ARG	CB-CA-C	-10.97	94.67	114.52
64	AA	196	GLU	N-CA-C	-10.95	99.35	111.28
6	E	104	ASN	N-CA-C	10.90	131.72	110.56
77	A5	684	G	N9-C1'-C2'	10.71	133.82	112.40
64	AA	195	TRP	CB-CA-C	10.70	127.00	109.89
64	AA	97	THR	N-CA-C	10.68	125.67	110.40
64	AA	52	LYS	CB-CA-C	10.67	130.37	110.63
82	BB	115	LYS	N-CA-CB	10.55	127.63	110.43
64	AA	177	MET	N-CA-C	10.52	122.50	111.14
64	AA	109	THR	CA-CB-OG1	-10.51	93.84	109.60
64	AA	117	ARG	N-CA-C	-10.49	92.18	108.76
44	u	29	LEU	N-CA-CB	-10.48	94.12	110.57
30	f	58	VAL	N-CA-CB	10.44	128.45	111.23
44	u	66	LEU	N-CA-C	-10.33	100.02	111.28
56	VV	40	ASP	CA-CB-CG	10.31	122.91	112.60
56	VV	67	ASP	N-CA-C	-10.17	100.20	111.28
56	VV	35	ASN	N-CA-C	-10.14	96.20	110.50
64	AA	73	ASP	N-CA-C	10.11	132.34	110.80
56	VV	33	GLN	N-CA-CB	10.11	128.29	110.80
64	AA	13	GLU	N-CA-C	-10.10	100.28	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
64	AA	133	PRO	N-CA-C	10.05	127.49	113.53
64	AA	164	ASN	CB-CA-C	-10.03	91.32	109.38
56	VV	33	GLN	CB-CA-C	-9.99	91.62	109.70
64	AA	133	PRO	CB-CA-C	-9.99	96.14	112.62
64	AA	146	ALA	N-CA-C	9.94	121.89	107.88
56	VV	21	ASN	N-CA-C	-9.93	98.33	111.74
44	u	50	ASN	CA-C-O	-9.91	109.92	120.42
64	AA	48	ILE	N-CA-CB	-9.85	93.50	111.92
64	AA	177	MET	CB-CA-C	-9.83	95.37	110.90
44	u	56	ARG	N-CA-C	-9.73	101.42	113.20
64	AA	37	TYR	N-CA-C	-9.73	101.09	113.16
64	AA	203	PHE	CA-CB-CG	9.58	123.38	113.80
64	AA	90	PHE	N-CA-C	9.58	121.32	111.07
64	AA	67	ALA	N-CA-C	9.53	121.67	111.28
64	AA	184	ARG	CB-CA-C	-9.48	95.06	110.79
64	AA	125	THR	N-CA-C	-9.35	101.07	111.07
64	AA	14	ASP	CA-CB-CG	-9.33	103.27	112.60
56	VV	64	GLU	CB-CA-C	9.31	127.60	109.72
64	AA	86	ALA	N-CA-C	9.31	123.58	108.32
64	AA	36	GLN	CB-CA-C	9.29	126.41	110.72
64	AA	63	ARG	CB-CA-C	-9.28	95.07	110.85
64	AA	153	PRO	CA-C-O	-9.20	103.86	120.60
64	AA	194	PRO	CB-CA-C	9.20	123.32	111.64
64	AA	68	ILE	N-CA-C	-9.14	96.78	108.84
44	u	69	THR	N-CA-CB	-9.13	96.05	109.83
64	AA	200	ASP	CA-C-O	-9.08	110.92	120.55
64	AA	172	GLY	N-CA-C	9.08	123.03	112.50
64	AA	32	PHE	N-CA-C	-9.01	101.46	111.28
64	AA	180	ARG	CB-CA-C	-9.01	95.84	110.79
30	f	58	VAL	CG1-CB-CG2	-8.97	91.07	110.80
56	VV	74	LYS	N-CA-C	-8.97	101.60	112.54
64	AA	183	LEU	N-CA-C	8.92	121.08	111.36
64	AA	57	LYS	N-CA-CB	8.84	123.96	110.44
44	u	21	VAL	N-CA-CB	8.79	122.50	110.54
44	u	59	GLU	CB-CA-C	-8.68	97.19	110.90
64	AA	113	GLN	N-CA-CB	8.68	122.94	109.83
64	AA	101	GLY	CA-C-O	-8.66	114.70	122.24
56	VV	55	ILE	CA-C-O	-8.66	111.94	120.95
64	AA	90	PHE	N-CA-CB	-8.66	97.45	110.01
44	u	54	ALA	N-CA-C	8.65	120.70	111.28
64	AA	148	CYS	N-CA-C	8.64	121.22	108.60
44	u	27	TYR	N-CA-CB	-8.54	96.93	109.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
64	AA	70	ASN	CA-C-N	8.49	128.25	119.76
64	AA	70	ASN	C-N-CA	8.49	128.25	119.76
64	AA	117	ARG	CB-CA-C	8.48	125.67	110.16
56	VV	64	GLU	N-CA-CB	-8.39	97.28	110.46
64	AA	153	PRO	CA-N-CD	-8.35	100.32	112.00
64	AA	56	GLU	N-CA-CB	-8.33	97.87	110.12
64	AA	43	SER	N-CA-C	8.29	120.40	111.36
64	AA	212	LYS	CB-CA-C	-8.28	97.88	110.88
56	VV	55	ILE	N-CA-CB	-8.27	99.29	110.54
64	AA	14	ASP	N-CA-CB	-8.26	97.94	110.16
64	AA	178	LEU	N-CA-C	-8.22	102.40	111.36
64	AA	198	MET	N-CA-C	-8.19	91.71	109.81
56	VV	50	PHE	CA-C-O	-8.18	111.26	120.66
81	A6	4942	C	N1-C1'-C2'	8.16	124.24	112.00
56	VV	51	LYS	CB-CA-C	8.15	121.37	110.94
64	AA	183	LEU	CA-C-N	8.14	131.18	120.28
64	AA	183	LEU	C-N-CA	8.14	131.18	120.28
56	VV	30	ALA	CA-C-O	-8.12	112.47	120.92
56	VV	53	TYR	CB-CA-C	8.12	124.17	111.02
64	AA	15	VAL	CA-C-O	-8.12	112.51	120.95
56	VV	60	ARG	N-CA-CB	8.07	126.89	111.15
44	u	90	ARG	CB-CA-C	-8.06	96.35	109.72
64	AA	139	TYR	N-CA-C	-7.99	102.02	112.41
56	VV	74	LYS	N-CA-CB	7.98	123.63	110.39
56	VV	75	SER	N-CA-C	-7.97	102.54	111.71
56	VV	33	GLN	N-CA-C	-7.97	95.29	108.76
64	AA	93	ALA	N-CA-C	-7.96	102.61	111.28
64	AA	60	LEU	CA-C-O	-7.93	110.11	119.15
44	u	83	THR	N-CA-C	-7.87	102.70	111.28
44	u	29	LEU	N-CA-C	7.87	121.73	109.07
56	VV	32	ILE	O-C-N	-7.86	114.71	123.20
64	AA	85	ARG	N-CA-C	7.85	119.47	111.07
56	VV	39	VAL	N-CA-CB	-7.84	98.37	111.38
56	VV	53	TYR	N-CA-C	-7.83	102.23	112.41
64	AA	144	THR	N-CA-CB	-7.82	97.68	110.42
64	AA	176	TRP	CA-C-O	-7.81	112.66	120.70
56	VV	52	THR	CA-CB-OG1	-7.81	97.89	109.60
64	AA	60	LEU	N-CA-CB	-7.80	98.90	110.53
64	AA	116	PHE	CB-CA-C	-7.80	98.93	110.16
44	u	62	TYR	CB-CA-C	-7.77	97.90	110.79
64	AA	51	LEU	N-CA-C	-7.71	103.60	113.16
64	AA	171	VAL	N-CA-CB	-7.68	100.10	110.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
64	AA	52	LYS	N-CA-C	-7.68	102.88	111.71
64	AA	31	ASP	CA-CB-CG	7.67	120.27	112.60
56	VV	26	ALA	CA-C-O	-7.66	112.38	120.58
56	VV	70	LEU	CB-CA-C	-7.64	98.83	110.90
64	AA	39	TYR	CA-C-O	-7.59	112.38	120.42
64	AA	182	VAL	N-CA-CB	7.58	120.86	110.54
44	u	79	ILE	N-CA-C	-7.58	102.89	110.62
64	AA	154	LEU	CA-C-O	-7.57	113.31	121.56
44	u	49	ALA	N-CA-CB	-7.56	97.72	110.49
64	AA	185	MET	N-CA-C	-7.55	103.03	111.71
64	AA	63	ARG	N-CA-CB	7.49	121.24	110.16
56	VV	5	ALA	N-CA-C	-7.48	103.12	111.28
56	VV	7	GLU	CB-CA-C	7.48	125.02	109.68
64	AA	55	TRP	N-CA-C	-7.41	103.20	111.28
64	AA	211	GLU	N-CA-C	7.41	118.99	111.07
64	AA	113	GLN	N-CA-C	-7.37	99.54	110.23
64	AA	115	ALA	N-CA-C	-7.37	103.25	111.28
64	AA	195	TRP	CA-CB-CG	7.36	127.59	113.60
56	VV	51	LYS	CA-C-O	-7.33	111.41	119.98
6	E	220	PHE	CA-C-O	-7.29	109.58	119.05
56	VV	57	GLY	CA-C-O	-7.28	114.55	120.81
64	AA	104	THR	N-CA-C	-7.28	98.64	109.42
64	AA	48	ILE	CB-CA-C	7.28	123.73	110.71
64	AA	133	PRO	CA-N-CD	-7.28	101.81	112.00
44	u	92	CYS	CA-C-O	-7.26	112.72	120.42
64	AA	91	ALA	N-CA-C	-7.25	104.00	112.92
64	AA	171	VAL	CA-C-N	-7.24	111.90	119.94
64	AA	171	VAL	C-N-CA	-7.24	111.90	119.94
64	AA	204	TYR	N-CA-C	7.24	120.45	109.23
64	AA	12	GLU	N-CA-C	-7.23	103.56	112.38
64	AA	182	VAL	CA-C-O	-7.21	113.45	120.95
64	AA	56	GLU	CB-CG-CD	7.19	124.82	112.60
44	u	84	ALA	N-CA-C	-7.17	103.46	111.28
44	u	87	LYS	N-CA-C	-7.14	97.61	109.46
64	AA	181	GLU	N-CA-CB	-7.14	97.90	110.39
64	AA	153	PRO	CA-C-N	7.12	132.12	120.94
64	AA	153	PRO	C-N-CA	7.12	132.12	120.94
64	AA	103	PHE	N-CA-CB	7.11	120.56	109.69
64	AA	39	TYR	N-CA-C	7.08	119.08	111.36
44	u	64	ALA	CA-C-O	-7.06	112.93	120.42
64	AA	195	TRP	CB-CG-CD2	-7.02	116.97	126.80
64	AA	183	LEU	CA-C-O	-6.96	113.04	120.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	u	28	VAL	CA-C-O	-6.93	114.52	121.45
64	AA	59	LEU	N-CA-C	6.92	118.48	111.07
44	u	94	LEU	CA-C-O	-6.90	112.73	120.66
64	AA	119	PRO	CA-C-O	-6.87	113.59	121.56
56	VV	69	ILE	CA-C-O	-6.87	113.81	120.95
64	AA	168	ALA	N-CA-C	6.87	118.76	111.28
44	u	21	VAL	N-CA-C	-6.86	103.62	110.62
64	AA	47	TYR	CB-CA-C	6.86	121.59	109.72
64	AA	155	ARG	N-CA-C	6.86	125.41	110.80
64	AA	177	MET	CA-C-N	-6.84	110.58	120.29
64	AA	177	MET	C-N-CA	-6.84	110.58	120.29
64	AA	152	SER	CA-C-N	6.84	128.39	119.84
64	AA	152	SER	C-N-CA	6.84	128.39	119.84
64	AA	48	ILE	CA-C-O	-6.80	114.07	121.28
64	AA	94	THR	CA-C-O	-6.80	113.34	120.55
44	u	53	PRO	N-CA-C	-6.79	100.55	111.14
44	u	58	SER	N-CA-C	6.79	122.66	113.97
64	AA	134	LEU	CA-C-N	6.78	129.37	120.28
64	AA	134	LEU	C-N-CA	6.78	129.37	120.28
64	AA	83	GLY	CA-C-O	-6.76	114.39	120.75
64	AA	195	TRP	CB-CG-CD1	6.76	137.03	126.90
64	AA	24	HIS	N-CA-C	-6.74	103.93	111.28
44	u	63	TYR	CA-CB-CG	-6.74	101.77	113.90
64	AA	63	ARG	CA-CB-CG	6.74	127.57	114.10
64	AA	151	ASP	CA-C-O	-6.73	112.00	120.28
64	AA	87	VAL	CB-CA-C	-6.72	103.21	112.02
81	A6	4942	C	O4'-C1'-N1	6.72	118.58	108.50
64	AA	205	ARG	N-CA-C	-6.70	101.05	110.50
44	u	87	LYS	CB-CA-C	6.69	120.77	109.80
44	u	63	TYR	N-CA-C	-6.68	104.00	111.28
64	AA	36	GLN	N-CA-C	-6.67	104.28	112.88
64	AA	170	SER	N-CA-C	-6.65	104.26	112.38
56	VV	79	VAL	N-CA-CB	6.65	122.19	111.23
64	AA	196	GLU	CB-CA-C	6.64	121.81	110.79
64	AA	160	ALA	N-CA-C	-6.63	94.85	108.18
64	AA	147	LEU	CA-C-O	-6.61	114.38	121.45
56	VV	59	ILE	N-CA-CB	-6.59	100.35	111.23
64	AA	208	GLU	N-CA-C	-6.58	104.35	112.38
56	VV	46	PHE	N-CA-C	6.58	119.45	108.73
56	VV	27	LYS	N-CA-C	6.56	124.77	110.80
64	AA	63	ARG	CA-C-O	-6.56	113.47	120.42
56	VV	4	ASP	CB-CA-C	6.54	122.73	110.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	u	62	TYR	N-CA-C	-6.54	104.16	111.28
56	VV	52	THR	N-CA-CB	6.54	122.57	111.66
44	u	56	ARG	CB-CA-C	6.49	122.44	110.11
56	VV	41	LYS	CB-CA-C	-6.49	100.02	110.79
44	u	54	ALA	O-C-N	-6.46	115.27	122.12
56	VV	42	VAL	N-CA-C	6.46	117.80	111.67
64	AA	197	VAL	CA-C-O	-6.45	113.86	121.80
56	VV	42	VAL	CA-C-O	-6.44	113.92	120.69
56	VV	61	ARG	N-CA-C	-6.44	97.92	108.67
81	A6	4945	G	C4'-C3'-O3'	6.44	122.66	113.00
44	u	69	THR	N-CA-C	6.42	119.55	110.23
64	AA	155	ARG	CB-CA-C	-6.39	97.70	110.42
64	AA	198	MET	N-CA-CB	6.38	121.73	110.37
64	AA	90	PHE	CA-CB-CG	6.38	120.18	113.80
64	AA	98	PRO	CA-N-CD	-6.38	103.08	112.00
64	AA	140	VAL	N-CA-CB	-6.34	100.77	111.23
44	u	93	THR	N-CA-C	6.33	120.42	107.69
64	AA	80	ARG	N-CA-C	-6.31	101.07	110.23
64	AA	149	ASN	CA-C-O	-6.31	114.06	121.44
64	AA	188	THR	CA-C-O	-6.30	113.87	120.55
64	AA	144	THR	N-CA-C	6.29	118.99	108.73
56	VV	59	ILE	CA-C-O	-6.28	112.94	120.78
77	A5	684	G	C5'-C4'-C3'	6.26	128.53	116.00
56	VV	72	LEU	N-CA-C	-6.25	104.47	111.28
64	AA	135	THR	N-CA-C	6.24	118.08	111.28
64	AA	33	GLN	CB-CA-C	6.23	120.99	111.95
64	AA	56	GLU	CB-CA-C	6.23	121.13	110.79
64	AA	57	LYS	CA-CB-CG	6.23	126.56	114.10
44	u	28	VAL	N-CA-C	-6.22	98.79	108.44
56	VV	59	ILE	N-CA-C	6.20	122.24	109.34
64	AA	62	ALA	CA-C-O	-6.18	111.78	119.38
64	AA	193	HIS	CA-C-O	-6.18	112.95	120.05
64	AA	134	LEU	CA-C-O	-6.17	111.69	120.51
56	VV	10	ASP	CA-CB-CG	6.16	118.76	112.60
56	VV	19	ALA	N-CA-C	6.16	117.79	111.14
56	VV	11	LEU	N-CA-CB	-6.15	101.09	110.01
77	A5	1961	G	O4'-C1'-N9	6.14	117.42	108.20
56	VV	68	SER	N-CA-C	-6.13	104.59	111.28
64	AA	175	TRP	CA-C-O	-6.13	114.05	120.55
64	AA	42	LYS	N-CA-C	-6.09	97.83	110.80
64	AA	109	THR	N-CA-CB	-6.05	102.53	110.88
56	VV	50	PHE	CA-CB-CG	6.03	119.83	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
64	AA	23	THR	N-CA-C	-6.03	98.53	108.49
64	AA	62	ALA	CA-C-N	6.03	128.85	120.29
64	AA	62	ALA	C-N-CA	6.03	128.85	120.29
56	VV	70	LEU	CA-C-O	-6.01	114.51	120.70
64	AA	53	ARG	CB-CA-C	-6.01	100.81	110.79
64	AA	152	SER	CA-C-O	-6.00	114.56	120.26
21	V	95	PHE	N-CA-C	6.00	117.61	108.07
64	AA	213	GLU	CB-CA-C	5.98	121.01	110.85
56	VV	52	THR	CB-CA-C	-5.97	97.61	110.45
64	AA	73	ASP	CA-C-N	5.96	129.76	120.34
64	AA	73	ASP	C-N-CA	5.96	129.76	120.34
64	AA	136	GLU	CB-CA-C	-5.96	100.90	110.79
64	AA	200	ASP	CA-CB-CG	5.96	118.56	112.60
56	VV	2	GLN	N-CA-C	-5.95	101.23	110.10
56	VV	60	ARG	CA-C-N	-5.93	114.39	123.04
56	VV	60	ARG	C-N-CA	-5.93	114.39	123.04
44	u	101	ASP	N-CA-C	-5.92	104.82	111.28
64	AA	180	ARG	CA-C-O	-5.92	114.28	120.55
44	u	58	SER	CA-C-O	-5.90	112.65	118.97
64	AA	136	GLU	CA-C-N	-5.90	112.50	120.82
64	AA	136	GLU	C-N-CA	-5.90	112.50	120.82
64	AA	140	VAL	CA-C-O	-5.90	113.40	120.78
64	AA	99	ILE	N-CA-C	5.90	118.68	108.95
44	u	23	LYS	N-CA-CB	-5.89	101.47	110.01
64	AA	145	ILE	N-CA-C	5.88	116.45	110.05
44	u	12	GLU	N-CA-C	-5.86	104.89	111.28
64	AA	116	PHE	CA-CB-CG	5.86	119.66	113.80
44	u	72	HIS	CA-C-O	-5.85	114.97	121.23
64	AA	23	THR	CB-CA-C	5.84	120.44	111.85
44	u	58	SER	CA-C-N	5.82	128.35	120.44
44	u	58	SER	C-N-CA	5.82	128.35	120.44
64	AA	74	VAL	CA-CB-CG2	5.81	120.28	110.40
64	AA	174	MET	CA-C-N	-5.80	112.51	120.28
64	AA	174	MET	C-N-CA	-5.80	112.51	120.28
44	u	53	PRO	CB-CA-C	5.79	118.93	111.46
56	VV	14	PRO	CA-C-O	-5.78	114.68	122.08
64	AA	58	LEU	CB-CA-C	5.78	120.38	110.79
44	u	21	VAL	CB-CA-C	-5.78	104.34	112.14
56	VV	7	GLU	N-CA-C	-5.77	102.91	110.53
56	VV	60	ARG	CA-C-O	-5.77	115.58	119.68
64	AA	173	LEU	CB-CA-C	-5.77	101.78	110.90
64	AA	85	ARG	CB-CA-C	-5.77	101.82	110.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	u	23	LYS	CB-CA-C	5.75	119.91	110.88
64	AA	137	ALA	N-CA-C	-5.75	101.54	110.10
64	AA	163	CYS	CA-C-O	-5.73	115.03	121.05
64	AA	202	TYR	CB-CA-C	5.73	120.24	110.56
64	AA	161	ILE	N-CA-C	-5.72	102.73	108.96
15	O	87	MET	CA-CB-CG	5.71	125.53	114.10
44	u	108	MET	N-CA-C	-5.71	102.58	109.83
64	AA	164	ASN	N-CA-C	5.70	118.77	109.59
44	u	57	LYS	CA-C-O	-5.70	114.51	120.55
44	u	62	TYR	CA-C-O	-5.69	114.52	120.55
44	u	74	TYR	N-CA-C	5.69	116.91	108.60
56	VV	36	VAL	CA-C-O	-5.68	114.33	120.36
56	VV	64	GLU	CA-C-N	5.68	127.90	120.28
56	VV	64	GLU	C-N-CA	5.68	127.90	120.28
64	AA	117	ARG	N-CA-CB	-5.68	101.45	111.39
64	AA	70	ASN	CA-C-O	-5.67	115.40	120.56
64	AA	111	GLN	N-CA-CB	5.66	118.44	110.12
64	AA	212	LYS	N-CA-CB	5.64	118.19	110.01
64	AA	80	ARG	CA-C-O	-5.64	114.99	121.19
56	VV	60	ARG	N-CA-C	5.62	117.75	108.48
64	AA	95	GLY	N-CA-C	5.62	123.84	115.64
56	VV	17	CYS	CB-CA-C	-5.61	100.40	109.72
64	AA	120	ARG	CD-NE-CZ	5.61	132.26	124.40
64	AA	98	PRO	N-CA-CB	-5.59	97.38	103.25
64	AA	192	GLU	N-CA-C	5.58	119.79	112.92
44	u	81	LEU	N-CA-C	-5.58	105.20	111.28
56	VV	55	ILE	CA-CB-CG2	5.58	119.99	110.50
6	E	42	GLY	N-CA-C	5.58	126.40	113.18
64	AA	154	LEU	N-CA-C	5.58	118.36	110.50
56	VV	69	ILE	N-CA-CB	5.57	118.12	110.54
64	AA	129	ALA	CA-C-O	-5.57	114.52	120.42
64	AA	32	PHE	CA-C-N	-5.57	113.18	122.92
64	AA	32	PHE	C-N-CA	-5.57	113.18	122.92
64	AA	36	GLN	N-CA-CB	-5.56	102.12	110.73
64	AA	118	GLU	CB-CG-CD	5.54	122.02	112.60
44	u	106	ARG	CB-CA-C	-5.54	101.44	110.85
56	VV	28	ASP	CA-C-O	-5.54	113.50	119.98
56	VV	45	ARG	N-CA-CB	-5.54	101.13	110.49
77	A5	980	U	C5'-C4'-O4'	5.54	126.11	109.50
64	AA	107	THR	CA-CB-OG1	-5.53	101.30	109.60
77	A5	684	G	C4'-C3'-C2'	5.52	113.34	102.30
56	VV	50	PHE	N-CA-CB	-5.52	101.01	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
64	AA	110	ASN	N-CA-C	-5.51	98.29	107.99
64	AA	211	GLU	CA-C-O	-5.50	115.04	120.82
64	AA	120	ARG	CB-CA-C	5.49	119.67	110.44
44	u	97	ILE	CA-C-O	-5.48	115.04	120.85
64	AA	73	ASP	CB-CA-C	-5.47	99.52	110.42
64	AA	23	THR	CA-CB-OG1	-5.46	101.42	109.60
64	AA	197	VAL	N-CA-C	-5.45	101.87	109.45
77	A5	684	G	C3'-C2'-C1'	5.43	112.16	101.30
44	u	74	TYR	CA-C-O	-5.42	115.64	121.38
64	AA	130	ASP	CA-CB-CG	5.42	118.02	112.60
64	AA	199	PRO	CB-CA-C	-5.42	103.68	112.62
64	AA	182	VAL	O-C-N	5.41	127.12	121.87
64	AA	55	TRP	CB-CA-C	5.41	119.77	110.79
64	AA	120	ARG	CG-CD-NE	5.41	123.89	112.00
64	AA	108	PHE	CB-CA-C	-5.40	101.67	110.85
64	AA	201	LEU	CA-C-O	-5.40	114.70	120.42
56	VV	17	CYS	CA-C-N	-5.39	113.43	120.44
56	VV	17	CYS	C-N-CA	-5.39	113.43	120.44
56	VV	21	ASN	CA-C-O	-5.39	114.87	121.28
77	A5	684	G	C5'-C4'-O4'	5.38	120.27	109.50
64	AA	180	ARG	N-CA-CB	-5.38	102.21	110.12
56	VV	31	SER	N-CA-C	5.38	117.67	108.90
64	AA	67	ALA	CB-CA-C	-5.38	101.87	110.79
64	AA	137	ALA	CA-C-O	-5.36	114.81	120.92
44	u	47	ILE	CA-C-O	-5.34	114.40	120.65
56	VV	68	SER	CA-C-N	-5.33	113.16	120.46
56	VV	68	SER	C-N-CA	-5.33	113.16	120.46
64	AA	122	LEU	N-CA-CB	-5.33	101.41	109.94
64	AA	123	VAL	CA-C-O	-5.33	116.11	121.59
64	AA	96	ALA	CA-C-O	-5.31	115.22	121.44
64	AA	203	PHE	CB-CA-C	-5.31	100.54	109.72
44	u	55	LEU	CA-C-N	-5.30	111.34	121.94
44	u	55	LEU	C-N-CA	-5.30	111.34	121.94
64	AA	160	ALA	CB-CA-C	5.29	120.70	111.86
56	VV	49	GLN	N-CA-CB	-5.29	101.74	111.37
64	AA	85	ARG	CA-C-O	-5.29	115.26	120.82
64	AA	18	PHE	N-CA-C	-5.28	105.53	111.28
64	AA	182	VAL	CA-C-N	5.28	127.78	120.29
64	AA	182	VAL	C-N-CA	5.28	127.78	120.29
56	VV	41	LYS	CA-C-O	-5.27	114.97	120.55
44	u	94	LEU	N-CA-C	-5.26	100.45	109.24
64	AA	19	LEU	CA-C-O	-5.26	114.97	120.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
64	AA	15	VAL	N-CA-CB	5.25	117.68	110.54
64	AA	39	TYR	CB-CA-C	-5.25	101.93	110.85
64	AA	145	ILE	CA-C-O	-5.25	115.63	121.98
44	u	19	GLN	CB-CA-C	-5.23	102.10	110.79
64	AA	72	ALA	CA-C-O	-5.22	113.06	118.65
64	AA	166	LYS	CA-C-N	5.22	125.78	122.18
64	AA	166	LYS	C-N-CA	5.22	125.78	122.18
64	AA	166	LYS	CB-CA-C	5.21	119.70	110.85
64	AA	156	TYR	CA-C-N	-5.20	115.71	122.94
64	AA	156	TYR	C-N-CA	-5.20	115.71	122.94
44	u	89	TYR	CB-CA-C	5.20	118.54	109.65
56	VV	31	SER	CA-C-O	-5.20	114.75	120.36
64	AA	56	GLU	CA-C-O	-5.19	115.05	120.55
64	AA	144	THR	CA-C-O	-5.19	114.81	120.36
64	AA	190	SER	N-CA-C	5.19	117.51	110.35
64	AA	19	LEU	N-CA-C	5.17	116.92	111.28
64	AA	175	TRP	N-CA-C	-5.17	105.64	111.28
56	VV	66	ASP	CB-CA-C	-5.17	102.22	110.79
64	AA	59	LEU	CA-C-O	-5.17	115.40	120.82
64	AA	39	TYR	CA-CB-CG	5.16	123.18	113.90
64	AA	73	ASP	N-CA-CB	-5.16	101.78	110.49
44	u	22	MET	CA-C-N	-5.15	113.74	120.44
44	u	22	MET	C-N-CA	-5.15	113.74	120.44
64	AA	202	TYR	CA-C-N	5.14	130.10	123.00
64	AA	202	TYR	C-N-CA	5.14	130.10	123.00
64	AA	148	CYS	CB-CA-C	-5.14	101.09	111.17
56	VV	51	LYS	CA-C-N	5.13	130.63	121.75
56	VV	51	LYS	C-N-CA	5.13	130.63	121.75
44	u	90	ARG	CA-C-O	-5.13	115.55	121.19
64	AA	153	PRO	CB-CA-C	-5.13	103.09	111.56
64	AA	172	GLY	CA-C-O	-5.13	115.46	121.00
64	AA	181	GLU	CB-CG-CD	5.13	121.32	112.60
56	VV	26	ALA	N-CA-C	5.13	116.67	108.41
56	VV	34	MET	CB-CA-C	-5.12	100.86	109.72
77	A5	957	G	P-O3'-C3'	5.11	127.86	120.20
44	u	17	ARG	N-CA-C	-5.10	105.72	111.28
64	AA	135	THR	CB-CA-C	-5.10	102.33	110.79
44	u	11	LEU	N-CA-C	-5.09	105.73	111.28
44	u	93	THR	CB-CA-C	-5.09	102.67	111.23
77	A5	980	U	N1-C1'-C2'	5.09	127.68	112.40
64	AA	52	LYS	CB-CG-CD	5.09	123.00	111.30
64	AA	142	LEU	CA-C-O	-5.08	115.28	120.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
64	AA	117	ARG	CA-C-O	-5.08	115.30	120.89
68	MM	101	ARG	CA-CB-CG	5.08	124.26	114.10
56	VV	59	ILE	O-C-N	-5.06	116.25	122.57
64	AA	82	THR	CA-C-O	-5.06	115.19	120.55
64	AA	189	ILE	N-CA-CB	5.05	119.57	111.23
64	AA	131	HIS	N-CA-C	-5.04	106.44	112.59
64	AA	110	ASN	CA-C-N	-5.04	113.53	120.28
64	AA	110	ASN	C-N-CA	-5.04	113.53	120.28
44	u	60	ILE	CA-C-O	-5.03	114.06	119.35
64	AA	191	ARG	N-CA-C	5.03	116.77	111.28
64	AA	192	GLU	CA-C-O	-5.03	113.68	119.56
44	u	50	ASN	O-C-N	5.03	127.88	122.15
64	AA	180	ARG	N-CA-C	5.01	116.75	111.28
64	AA	202	TYR	N-CA-CB	-5.01	103.24	110.56
64	AA	34	MET	N-CA-CB	5.01	119.46	111.20
64	AA	120	ARG	N-CA-CB	-5.00	102.97	111.27

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
81	A6	4942	C	C1'

All (56) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
64	AA	102	ARG	Sidechain
64	AA	117	ARG	Sidechain
64	AA	118	GLU	Mainchain
64	AA	128	ARG	Sidechain
64	AA	132	GLN	Mainchain
64	AA	144	THR	Mainchain
64	AA	153	PRO	Mainchain
64	AA	180	ARG	Sidechain
64	AA	186	ARG	Sidechain
64	AA	191	ARG	Sidechain
64	AA	197	VAL	Mainchain
64	AA	198	MET	Mainchain
64	AA	205	ARG	Sidechain
64	AA	33	GLN	Mainchain
64	AA	41	ARG	Sidechain
64	AA	43	SER	Mainchain
64	AA	63	ARG	Sidechain

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Mol	Chain	Res	Type	Group
64	AA	80	ARG	Sidechain
64	AA	85	ARG	Sidechain
3	C	95	MET	Peptide
6	E	104	ASN	Peptide
75	EF	500	SER	Peptide
66	FF	87	LEU	Peptide
50	GG	170	ARG	Sidechain
12	L	102	ARG	Peptide
12	L	103	ARG	Sidechain
56	VV	15	ARG	Sidechain
56	VV	22	ARG	Sidechain
56	VV	28	ASP	Mainchain
56	VV	36	VAL	Mainchain
56	VV	45	ARG	Sidechain
56	VV	58	ALA	Mainchain
56	VV	60	ARG	Sidechain
56	VV	61	ARG	Sidechain
56	VV	65	SER	Mainchain
56	VV	68	SER	Mainchain
56	VV	69	ILE	Mainchain
56	VV	70	LEU	Mainchain
56	VV	71	ARG	Sidechain
56	VV	80	SER	Mainchain
23	X	139	ARG	Sidechain
58	XX	14	ARG	Sidechain
26	a	39	V5N	Peptide,Mainchain
47	aa	56	ALA	Peptide
47	aa	73	TYR	Peptide
4	c	1	MET	Peptide
4	c	94	ARG	Sidechain
63	dd	12	ARG	Peptide
30	f	59	THR	Peptide
38	n	1	MET	Peptide
43	t	114	ARG	Sidechain
44	u	106	ARG	Sidechain
44	u	17	ARG	Sidechain
44	u	64	ALA	Mainchain
44	u	90	ARG	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1898	0	1993	15	0
2	B	3206	0	3353	23	0
3	C	2895	0	3064	25	0
4	c	938	0	990	12	0
5	D	2389	0	2423	23	0
6	E	1789	0	1941	89	0
7	F	1875	0	1995	17	0
8	G	1741	0	1861	10	0
9	H	1516	0	1597	20	0
10	I	1620	0	1663	10	0
11	J	1362	0	1399	17	0
12	L	1658	0	1766	14	0
13	M	1125	0	1198	15	0
14	N	1701	0	1749	8	0
15	O	1630	0	1778	21	0
16	P	1242	0	1274	4	0
17	Q	1512	0	1629	19	0
18	S	1461	0	1502	9	0
19	T	1298	0	1366	6	0
20	U	808	0	831	16	0
21	V	973	0	1032	16	0
22	W	1508	0	1664	10	0
23	X	967	0	1040	11	0
24	Y	1115	0	1205	11	0
25	Z	1107	0	1182	11	0
26	a	1163	0	1202	12	0
27	b	620	0	665	3	0
28	d	888	0	930	5	0
29	e	1053	0	1147	13	0
30	f	884	0	924	47	0
31	g	873	0	964	6	0
32	h	1011	0	1150	14	0
33	i	830	0	916	8	0
34	j	705	0	737	5	0
35	k	569	0	637	4	0
36	l	447	0	480	3	0
37	m	422	0	458	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	n	239	0	289	2	0
39	o	863	0	929	8	0
40	p	708	0	756	21	0
41	r	1015	0	1085	9	0
42	s	825	0	866	4	0
43	t	1178	0	1235	18	0
44	u	672	0	689	138	0
45	bb	640	0	665	6	0
46	ee	398	0	443	3	0
47	aa	781	0	821	288	0
48	CC	1685	0	1768	53	0
49	EE	2076	0	2177	24	0
50	GG	1848	0	2000	14	0
51	HH	1490	0	1583	10	0
52	II	1686	0	1772	15	0
53	JJ	1499	0	1618	11	0
54	LL	1157	0	1223	13	0
55	NN	1202	0	1289	16	0
56	VV	637	0	630	231	0
57	WW	1034	0	1080	19	0
58	XX	1098	0	1167	19	0
59	YY	1015	0	1086	6	0
60	cc	479	0	507	7	0
61	ff	548	0	552	2	0
62	gg	2436	0	2392	108	0
63	dd	459	0	448	4	0
64	AA	1625	0	1609	572	0
65	DD	1751	0	1846	10	0
66	FF	1475	0	1527	17	0
67	KK	810	0	836	6	0
68	MM	958	0	993	16	0
69	PP	979	0	1029	4	0
70	QQ	1124	0	1193	8	0
71	SS	1193	0	1253	11	0
72	TT	1097	0	1125	7	0
73	UU	790	0	857	6	0
74	ZZ	598	0	656	16	0
75	EF	6669	0	6742	99	0
76	Cc	1644	0	837	5	0
77	A5	36419	0	18340	161	0
78	A7	2578	0	1306	10	0
79	A8	3334	0	1693	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	B2	38185	0	19135	634	0
81	A6	43819	0	21847	237	0
82	BB	1768	0	1837	277	0
83	OO	1002	0	1009	360	0
84	RR	1068	0	1093	467	0
85	A5	7	0	0	0	0
85	A6	7	0	0	0	0
85	A8	1	0	0	0	0
85	B2	6	0	0	0	0
85	BB	2	0	0	0	0
85	P	1	0	0	0	0
85	a	1	0	0	0	0
85	l	1	0	0	0	0
86	aa	1	0	0	0	0
86	dd	1	0	0	0	0
86	ff	1	0	0	0	0
86	g	1	0	0	0	0
86	j	1	0	0	0	0
86	m	1	0	0	0	0
86	o	1	0	0	0	0
86	p	1	0	0	0	0
87	A6	1	0	0	0	0
All	All	225388	0	167538	2943	0

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

All (2943) 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)
64:AA:180:ARG:HD2	64:AA:195:TRP:CH2	1.27	1.69
47:aa:29:CYS:SG	83:OO:146:ARG:HA	1.34	1.61
47:aa:67:LEU:HD13	83:OO:108:PRO:CD	1.18	1.59
47:aa:69:VAL:CG2	83:OO:107:THR:H	1.08	1.59
47:aa:67:LEU:HD13	83:OO:108:PRO:CG	1.28	1.58
47:aa:67:LEU:CD2	83:OO:97:LEU:HD11	1.18	1.58
6:E:221:LYS:CB	6:E:221:LYS:CG	1.75	1.58
80:B2:956:G:C8	82:BB:5:LYS:HG2	1.36	1.58
82:BB:115:LYS:CG	82:BB:115:LYS:CB	1.78	1.57
80:B2:975:G:H1'	83:OO:43:HIS:CE1	1.32	1.57
47:aa:67:LEU:HD23	83:OO:97:LEU:CD1	1.32	1.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:f:58:VAL:CG1	30:f:58:VAL:CB	1.86	1.54
80:B2:1063:C:C4'	83:OO:150:ARG:NH1	1.68	1.54
47:aa:58:VAL:HG21	83:OO:125:LYS:CE	1.38	1.54
30:f:58:VAL:CB	30:f:58:VAL:CG2	1.85	1.53
62:gg:280:LYS:CA	84:RR:59:LYS:HG2	1.32	1.52
47:aa:53:ILE:CA	83:OO:120:ALA:HB2	1.11	1.51
80:B2:955:A:H1'	82:BB:6:ASN:CB	1.33	1.51
80:B2:1111:U:P	84:RR:124:VAL:HG22	1.47	1.51
80:B2:1455:A:N3	84:RR:28:PHE:CD2	1.75	1.51
47:aa:56:ALA:H	83:OO:120:ALA:CA	1.16	1.50
64:AA:214:GLU:CB	84:RR:83:ASN:N	1.75	1.50
81:A6:4099:G:C5'	82:BB:227:LYS:HD3	1.35	1.50
62:gg:280:LYS:CB	84:RR:59:LYS:HG2	1.42	1.49
80:B2:1463:U:H6	84:RR:63:ARG:NH1	1.11	1.49
80:B2:1455:A:N3	84:RR:28:PHE:CE2	1.80	1.49
80:B2:1063:C:H4'	83:OO:150:ARG:CZ	1.39	1.48
47:aa:67:LEU:CD1	83:OO:108:PRO:HG3	1.44	1.48
64:AA:128:ARG:NH2	64:AA:128:ARG:HB3	1.28	1.45
81:A6:4099:G:C5'	82:BB:227:LYS:CD	1.92	1.45
47:aa:67:LEU:CD1	83:OO:108:PRO:CG	1.94	1.45
80:B2:968:U:H3'	82:BB:8:ARG:NH1	1.28	1.44
47:aa:59:PHE:H	83:OO:126:ILE:CB	1.28	1.44
47:aa:59:PHE:N	83:OO:126:ILE:HB	1.16	1.44
80:B2:1463:U:H2'	84:RR:63:ARG:NH2	1.14	1.43
47:aa:58:VAL:CG1	83:OO:125:LYS:HD3	1.26	1.42
47:aa:69:VAL:HG23	83:OO:107:THR:N	1.29	1.42
80:B2:1110:G:N2	82:BB:148:ASN:HD21	1.17	1.42
47:aa:26:CYS:HB2	83:OO:149:ARG:C	1.46	1.41
47:aa:58:VAL:CG1	83:OO:125:LYS:CD	1.81	1.41
47:aa:69:VAL:CG2	83:OO:107:THR:N	1.80	1.41
30:f:58:VAL:HB	81:A6:4945:G:C4	1.56	1.40
47:aa:53:ILE:HA	83:OO:120:ALA:CB	1.51	1.40
30:f:58:VAL:HA	81:A6:4945:G:C8	1.53	1.40
64:AA:17:LYS:CE	64:AA:198:MET:HE1	1.52	1.39
80:B2:1455:A:C4'	84:RR:51:ALA:HB3	0.92	1.39
47:aa:53:ILE:CA	83:OO:120:ALA:CB	1.99	1.39
47:aa:55:GLU:CD	83:OO:121:ARG:NH2	1.80	1.39
80:B2:1463:U:O2'	84:RR:63:ARG:CZ	1.68	1.38
64:AA:180:ARG:CD	64:AA:195:TRP:HH2	1.35	1.38
80:B2:968:U:C3'	82:BB:8:ARG:HH12	1.36	1.37
64:AA:210:ILE:HG22	84:RR:81:ARG:NE	1.38	1.36

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:aa:29:CYS:SG	83:OO:146:ARG:CA	2.11	1.36
47:aa:66:LYS:CD	82:BB:108:ASP:HA	1.51	1.35
47:aa:26:CYS:HA	83:OO:149:ARG:CB	1.26	1.35
62:gg:280:LYS:HB3	84:RR:59:LYS:CE	1.52	1.35
80:B2:1453:C:C4	84:RR:28:PHE:HZ	1.45	1.35
44:u:72:HIS:NE2	44:u:104:ILE:HG22	1.38	1.35
80:B2:1457:U:OP2	84:RR:55:THR:CG2	1.72	1.35
80:B2:986:G:C8	83:OO:137:SER:O	1.80	1.34
47:aa:55:GLU:HG2	83:OO:120:ALA:O	1.21	1.34
47:aa:58:VAL:CG2	83:OO:125:LYS:CE	2.05	1.34
80:B2:1109:C:OP1	84:RR:126:MET:CE	1.76	1.34
80:B2:1466:G:O6	84:RR:56:HIS:CE1	1.80	1.33
81:A6:4099:G:O2'	82:BB:226:GLY:CA	1.74	1.33
47:aa:66:LYS:CE	82:BB:108:ASP:N	1.91	1.33
80:B2:975:G:C1'	83:OO:43:HIS:CE1	2.09	1.33
80:B2:1063:C:H4'	83:OO:150:ARG:NH1	1.18	1.33
80:B2:1463:U:C2'	84:RR:63:ARG:CZ	2.07	1.32
47:aa:28:ARG:CG	83:OO:147:ARG:HA	1.60	1.31
80:B2:1452:A:O4'	84:RR:48:ASN:ND2	1.60	1.31
80:B2:956:G:H5'	82:BB:2:ALA:O	1.17	1.31
62:gg:280:LYS:HB3	84:RR:59:LYS:CD	1.60	1.31
80:B2:1452:A:C4'	84:RR:48:ASN:ND2	1.94	1.31
81:A6:4099:G:O2'	82:BB:226:GLY:HA3	1.30	1.31
47:aa:66:LYS:CD	82:BB:108:ASP:CA	1.97	1.30
62:gg:282:GLU:HG3	84:RR:26:ASN:OD1	1.19	1.30
47:aa:57:SER:OG	83:OO:126:ILE:CB	1.77	1.30
64:AA:42:LYS:CD	84:RR:101:ASP:OD2	1.65	1.30
80:B2:1111:U:P	84:RR:124:VAL:CG2	2.13	1.30
80:B2:1463:U:H2'	84:RR:63:ARG:CZ	1.59	1.30
47:aa:57:SER:CB	83:OO:126:ILE:CG2	2.05	1.30
64:AA:128:ARG:CB	64:AA:128:ARG:HH21	1.45	1.30
80:B2:1373:C:C3'	84:RR:7:LYS:HD3	1.55	1.29
81:A6:4940:C:C5	81:A6:4940:C:C6	2.18	1.29
80:B2:1455:A:H4'	84:RR:51:ALA:CB	0.83	1.29
80:B2:1103:C:OP1	82:BB:157:GLN:NE2	1.65	1.29
47:aa:58:VAL:CG2	83:OO:125:LYS:NZ	1.96	1.29
47:aa:67:LEU:CD1	83:OO:108:PRO:CD	2.04	1.29
64:AA:214:GLU:CD	84:RR:83:ASN:H	1.41	1.29
80:B2:1121:G:H1'	82:BB:204:ILE:O	1.33	1.29
80:B2:957:A:C8	82:BB:5:LYS:HE3	1.65	1.28
81:A6:4945:G:C4	81:A6:4945:G:C5	2.20	1.28

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:aa:55:GLU:OE2	83:OO:121:ARG:NH2	1.65	1.28
47:aa:59:PHE:CD2	83:OO:126:ILE:HG22	1.66	1.28
47:aa:26:CYS:CA	83:OO:149:ARG:HB2	1.63	1.28
64:AA:214:GLU:OE1	84:RR:80:ARG:N	1.64	1.28
80:B2:956:G:N7	82:BB:5:LYS:HG2	1.46	1.27
47:aa:59:PHE:CG	83:OO:126:ILE:HG22	1.66	1.27
80:B2:1373:C:O3'	84:RR:7:LYS:CD	1.81	1.27
62:gg:17:TRP:CH2	84:RR:30:THR:HG23	1.53	1.26
80:B2:955:A:C1'	82:BB:6:ASN:CB	2.11	1.26
80:B2:1374:C:P	84:RR:7:LYS:HD3	1.76	1.26
81:A6:4099:G:H1'	82:BB:224:GLU:CD	1.57	1.26
62:gg:64:HIS:CE1	84:RR:33:ARG:HH12	1.53	1.26
80:B2:956:G:C8	82:BB:5:LYS:CG	1.94	1.26
80:B2:956:G:C3'	82:BB:5:LYS:HE2	1.63	1.26
80:B2:1452:A:C3'	84:RR:44:LYS:HG2	1.53	1.26
80:B2:1456:G:C5'	84:RR:55:THR:OG1	1.84	1.26
81:A6:4100:C:OP1	82:BB:230:GLU:CD	1.76	1.25
80:B2:1111:U:OP1	84:RR:124:VAL:CB	1.85	1.25
80:B2:1121:G:C1'	82:BB:204:ILE:O	1.83	1.25
47:aa:57:SER:CB	83:OO:126:ILE:HG23	1.67	1.25
80:B2:1452:A:H5'	84:RR:48:ASN:CG	1.61	1.25
80:B2:1467:C:O5'	84:RR:3:ARG:HG3	1.07	1.24
80:B2:1463:U:O2'	84:RR:63:ARG:NH1	1.71	1.24
80:B2:1455:A:C4	84:RR:28:PHE:CE2	2.15	1.23
80:B2:1373:C:H3'	84:RR:7:LYS:CE	1.68	1.23
47:aa:55:GLU:CD	83:OO:121:ARG:HH21	1.42	1.23
47:aa:67:LEU:CD2	83:OO:97:LEU:CD1	1.98	1.23
64:AA:210:ILE:HG23	84:RR:81:ARG:CB	1.68	1.23
80:B2:1373:C:C3'	84:RR:7:LYS:CD	2.08	1.22
80:B2:988:C:C5'	82:BB:116:LYS:HD3	1.69	1.22
81:A6:4099:G:H4'	82:BB:227:LYS:CD	1.67	1.22
62:gg:279:SER:HB2	84:RR:63:ARG:N	1.55	1.22
64:AA:128:ARG:NH2	64:AA:128:ARG:CB	2.01	1.22
80:B2:968:U:C3'	82:BB:8:ARG:NH1	1.96	1.21
47:aa:66:LYS:HE3	82:BB:108:ASP:N	1.15	1.21
62:gg:280:LYS:HB3	84:RR:59:LYS:CG	1.70	1.21
62:gg:280:LYS:CB	84:RR:59:LYS:CG	2.17	1.21
80:B2:956:G:OP2	82:BB:4:GLY:CA	1.87	1.21
80:B2:975:G:C1'	83:OO:43:HIS:HE1	1.49	1.20
80:B2:1452:A:H5'	84:RR:48:ASN:ND2	1.54	1.20
80:B2:1452:A:C5'	84:RR:48:ASN:ND2	2.05	1.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:B2:1458:G:OP2	84:RR:59:LYS:CE	1.90	1.20
81:A6:4100:C:P	82:BB:230:GLU:OE1	1.99	1.20
80:B2:1110:G:H21	82:BB:148:ASN:ND2	1.40	1.19
6:E:221:LYS:HA	81:A6:4940:C:C6	1.78	1.19
62:gg:280:LYS:HA	84:RR:59:LYS:CG	1.71	1.19
64:AA:214:GLU:HB3	84:RR:82:ASP:C	1.67	1.19
64:AA:149:ASN:HD21	64:AA:166:LYS:NZ	1.41	1.19
64:AA:214:GLU:HB3	84:RR:83:ASN:N	1.16	1.19
47:aa:52:ASP:OD2	83:OO:116:LEU:HD12	1.40	1.18
47:aa:28:ARG:CB	83:OO:147:ARG:O	1.90	1.18
64:AA:214:GLU:OE2	84:RR:79:GLU:O	1.59	1.18
80:B2:1110:G:N2	82:BB:148:ASN:ND2	1.91	1.18
62:gg:235:ILE:HD11	84:RR:22:THR:OG1	1.02	1.18
47:aa:28:ARG:HB2	83:OO:147:ARG:O	1.02	1.18
80:B2:1455:A:C5'	84:RR:51:ALA:HB3	1.74	1.18
80:B2:1124:C:C5'	82:BB:150:ILE:HB	1.75	1.17
64:AA:214:GLU:OE2	84:RR:82:ASP:HB3	1.38	1.17
80:B2:1456:G:H5''	84:RR:55:THR:OG1	1.40	1.17
81:A6:4940:C:C5	81:A6:4940:C:C4	2.31	1.17
47:aa:28:ARG:CB	83:OO:147:ARG:C	2.16	1.17
81:A6:4099:G:O2'	82:BB:226:GLY:C	1.88	1.17
80:B2:975:G:H5''	83:OO:32:HIS:CE1	1.80	1.16
80:B2:1457:U:OP2	84:RR:55:THR:HG21	1.45	1.16
80:B2:1373:C:H3'	84:RR:7:LYS:NZ	1.60	1.16
81:A6:4099:G:H4'	82:BB:227:LYS:HD2	1.26	1.16
81:A6:4099:G:C4'	82:BB:227:LYS:CD	2.22	1.16
62:gg:280:LYS:CB	84:RR:59:LYS:HE2	1.75	1.16
80:B2:969:U:H5	82:BB:8:ARG:HA	1.04	1.16
62:gg:282:GLU:CG	84:RR:26:ASN:OD1	1.93	1.16
47:aa:28:ARG:HB2	83:OO:147:ARG:C	1.68	1.16
80:B2:1121:G:C2'	82:BB:204:ILE:O	1.95	1.15
80:B2:1467:C:C5'	84:RR:3:ARG:HG3	1.74	1.15
47:aa:67:LEU:HD23	83:OO:97:LEU:HD12	1.28	1.15
80:B2:1857:G:OP2	83:OO:146:ARG:CG	1.94	1.15
81:A6:4099:G:HO2'	82:BB:226:GLY:CA	1.53	1.15
64:AA:213:GLU:HG2	84:RR:86:PRO:CD	1.77	1.15
80:B2:1453:C:C4	84:RR:28:PHE:CZ	2.35	1.15
80:B2:1463:U:C2'	84:RR:63:ARG:NH2	2.08	1.15
64:AA:214:GLU:OE2	84:RR:83:ASN:N	1.76	1.14
80:B2:1453:C:O4'	84:RR:44:LYS:O	1.64	1.14
6:E:104:ASN:HA	77:A5:684:G:O4'	1.44	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:A6:4099:G:C1'	82:BB:224:GLU:CD	2.21	1.14
62:gg:235:ILE:CD1	84:RR:22:THR:OG1	1.95	1.14
64:AA:40:LYS:HE2	84:RR:104:GLU:OE1	1.47	1.14
64:AA:211:GLU:HA	84:RR:81:ARG:HA	1.23	1.14
80:B2:955:A:H1'	82:BB:6:ASN:HB3	1.24	1.14
80:B2:956:G:H5''	82:BB:5:LYS:H	1.12	1.14
80:B2:1112:U:O2	82:BB:146:ARG:CD	1.97	1.13
80:B2:1373:C:H4'	84:RR:7:LYS:N	1.62	1.13
81:A6:4099:G:C4'	82:BB:227:LYS:HD2	1.78	1.13
80:B2:1453:C:N4	84:RR:28:PHE:HZ	1.46	1.13
47:aa:53:ILE:HD13	83:OO:116:LEU:HB2	1.28	1.13
80:B2:1124:C:H5'	82:BB:150:ILE:H	1.07	1.13
47:aa:25:ASN:O	83:OO:149:ARG:HG3	1.49	1.13
47:aa:56:ALA:O	83:OO:124:MET:O	1.66	1.12
47:aa:63:VAL:HG23	83:OO:129:ILE:HD11	1.23	1.12
6:E:104:ASN:HA	77:A5:684:G:C1'	1.78	1.12
80:B2:1368:U:O4'	84:RR:4:VAL:CG1	1.97	1.12
64:AA:210:ILE:CG2	84:RR:81:ARG:HB3	1.78	1.12
80:B2:1124:C:P	82:BB:151:ARG:HB2	1.83	1.12
80:B2:1476:A:C2	84:RR:3:ARG:NH2	2.17	1.12
47:aa:58:VAL:HG13	83:OO:125:LYS:CD	1.47	1.12
62:gg:17:TRP:CH2	84:RR:30:THR:CG2	2.26	1.12
64:AA:214:GLU:CG	84:RR:83:ASN:H	1.62	1.12
80:B2:1452:A:H3'	84:RR:44:LYS:CG	1.78	1.12
80:B2:1476:A:N1	84:RR:3:ARG:NH2	1.97	1.12
80:B2:1453:C:H5	84:RR:32:LYS:HD2	1.08	1.11
47:aa:56:ALA:N	83:OO:120:ALA:HA	0.93	1.11
62:gg:280:LYS:CD	84:RR:59:LYS:HD3	1.79	1.11
80:B2:955:A:C1'	82:BB:6:ASN:HB3	1.74	1.11
47:aa:55:GLU:OE1	83:OO:121:ARG:NH2	1.79	1.11
80:B2:1122:A:H5''	82:BB:205:TYR:CE2	1.85	1.11
80:B2:1368:U:C4'	84:RR:4:VAL:HG13	1.80	1.11
47:aa:58:VAL:HG21	83:OO:125:LYS:NZ	1.60	1.11
80:B2:1466:G:O3'	84:RR:4:VAL:HA	1.29	1.11
80:B2:1124:C:H5''	82:BB:150:ILE:CB	1.81	1.10
47:aa:53:ILE:N	83:OO:117:ARG:NH2	2.00	1.10
80:B2:1109:C:OP1	84:RR:126:MET:HE1	1.44	1.10
64:AA:207:PRO:O	84:RR:81:ARG:NH2	1.83	1.10
80:B2:1455:A:H4'	84:RR:51:ALA:HB1	1.27	1.10
47:aa:58:VAL:HG22	83:OO:125:LYS:NZ	1.64	1.09
64:AA:17:LYS:CE	64:AA:198:MET:CE	2.30	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:B2:1452:A:H5'	84:RR:48:ASN:OD1	1.52	1.09
81:A6:4099:G:H4'	82:BB:227:LYS:CG	1.82	1.09
47:aa:58:VAL:CG2	83:OO:125:LYS:HE2	1.69	1.09
64:AA:210:ILE:CG2	84:RR:81:ARG:NE	2.16	1.09
80:B2:1452:A:H3'	84:RR:44:LYS:HG2	1.22	1.09
80:B2:1112:U:H1'	82:BB:146:ARG:HD3	1.29	1.09
80:B2:1373:C:O3'	84:RR:7:LYS:HD3	0.91	1.09
47:aa:67:LEU:HD13	83:OO:108:PRO:HD3	1.12	1.08
77:A5:980:U:C3'	77:A5:980:U:C4'	2.30	1.08
47:aa:66:LYS:HD2	82:BB:108:ASP:HA	1.32	1.08
47:aa:69:VAL:HG22	83:OO:106:LYS:N	1.67	1.08
62:gg:280:LYS:HB3	84:RR:59:LYS:HE2	1.10	1.08
62:gg:282:GLU:HB3	84:RR:62:GLN:NE2	1.68	1.08
64:AA:17:LYS:HE2	64:AA:198:MET:CE	1.82	1.08
64:AA:214:GLU:CG	84:RR:79:GLU:O	2.01	1.08
80:B2:1111:U:OP1	84:RR:124:VAL:HG23	1.48	1.08
80:B2:1467:C:O5'	84:RR:3:ARG:CG	2.02	1.08
81:A6:4099:G:H5'	82:BB:227:LYS:CD	1.63	1.08
44:u:29:LEU:HD22	81:A6:2673:G:C8	1.88	1.08
47:aa:67:LEU:HD21	83:OO:97:LEU:HD11	1.36	1.08
64:AA:180:ARG:CD	64:AA:195:TRP:CH2	2.17	1.08
80:B2:1452:A:H4'	84:RR:45:LYS:HA	1.33	1.08
80:B2:1466:G:N7	84:RR:5:ARG:NH1	2.02	1.08
64:AA:214:GLU:OE1	84:RR:79:GLU:CA	2.01	1.07
80:B2:1110:G:O3'	84:RR:124:VAL:HG13	1.53	1.07
6:E:221:LYS:CB	6:E:221:LYS:CA	2.32	1.07
77:A5:980:U:C3'	77:A5:980:U:C2'	2.31	1.07
80:B2:1063:C:C4'	83:OO:150:ARG:CZ	2.17	1.07
80:B2:955:A:C1'	82:BB:6:ASN:HB2	1.80	1.07
80:B2:1063:C:O4'	83:OO:150:ARG:NH1	1.86	1.07
47:aa:26:CYS:CA	83:OO:149:ARG:CB	2.16	1.07
47:aa:56:ALA:O	83:OO:124:MET:CB	2.03	1.07
47:aa:66:LYS:HD3	82:BB:108:ASP:CA	1.47	1.07
64:AA:17:LYS:HE2	64:AA:198:MET:HE1	1.13	1.07
64:AA:26:GLY:O	64:AA:44:ASP:HB3	1.54	1.07
77:A5:684:G:C3'	77:A5:684:G:C4'	2.33	1.07
64:AA:210:ILE:HG22	84:RR:81:ARG:CZ	1.85	1.06
80:B2:1456:G:P	84:RR:55:THR:OG1	2.13	1.06
47:aa:26:CYS:HA	83:OO:149:ARG:CG	1.86	1.06
47:aa:28:ARG:HG2	83:OO:147:ARG:HA	1.11	1.06
80:B2:956:G:N7	82:BB:5:LYS:CG	2.10	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:B2:956:G:OP2	82:BB:4:GLY:HA2	1.55	1.06
47:aa:53:ILE:HG12	83:OO:116:LEU:HD13	1.34	1.05
64:AA:213:GLU:HG2	84:RR:86:PRO:HD2	1.33	1.05
80:B2:1456:G:O5'	84:RR:55:THR:OG1	1.72	1.05
64:AA:214:GLU:HG2	84:RR:80:ARG:HA	1.37	1.05
80:B2:1455:A:C4	84:RR:28:PHE:CD2	2.41	1.05
47:aa:58:VAL:HG22	83:OO:125:LYS:HZ3	1.18	1.05
64:AA:211:GLU:O	84:RR:84:TYR:CB	2.05	1.05
80:B2:1465:A:O3'	84:RR:10:LYS:HD2	1.24	1.05
47:aa:53:ILE:C	83:OO:120:ALA:HB2	1.80	1.05
80:B2:1458:G:OP2	84:RR:59:LYS:HE2	1.52	1.04
81:A6:4099:G:C5'	82:BB:227:LYS:HD2	1.75	1.04
6:E:221:LYS:HB3	81:A6:4940:C:N3	1.71	1.04
30:f:58:VAL:HB	81:A6:4945:G:C5	1.92	1.04
47:aa:29:CYS:SG	83:OO:146:ARG:CB	2.45	1.04
77:A5:684:G:C3'	77:A5:684:G:C2'	2.35	1.04
80:B2:956:G:H3'	82:BB:5:LYS:CE	1.86	1.04
47:aa:57:SER:OG	83:OO:126:ILE:HG21	1.22	1.04
47:aa:67:LEU:HD22	83:OO:97:LEU:HD11	1.36	1.04
77:A5:980:U:C2'	77:A5:980:U:C1'	2.36	1.04
80:B2:1063:C:H4'	83:OO:150:ARG:NE	1.70	1.04
47:aa:69:VAL:HG21	83:OO:105:THR:OG1	1.58	1.04
81:A6:4940:C:C4	81:A6:4940:C:N3	2.26	1.04
47:aa:57:SER:OG	83:OO:126:ILE:CG2	0.74	1.03
80:B2:1460:C:N4	84:RR:56:HIS:HE1	1.54	1.03
56:VV:33:GLN:HG2	64:AA:142:LEU:HD12	1.36	1.03
80:B2:1460:C:H42	84:RR:56:HIS:CE1	1.76	1.03
80:B2:1466:G:C3'	84:RR:4:VAL:HA	1.89	1.03
47:aa:53:ILE:HD13	83:OO:116:LEU:CB	1.86	1.03
77:A5:684:G:C1'	77:A5:684:G:C2'	2.36	1.03
80:B2:1121:G:H1'	82:BB:204:ILE:C	1.83	1.03
62:gg:64:HIS:HE1	84:RR:33:ARG:NH1	1.56	1.03
80:B2:1368:U:O4'	84:RR:4:VAL:HG11	1.52	1.03
44:u:72:HIS:NE2	44:u:104:ILE:CG2	2.20	1.02
62:gg:83:TRP:HZ3	84:RR:36:GLU:OE1	1.42	1.02
80:B2:1869:A:H61	82:BB:114:VAL:HG12	1.19	1.02
80:B2:1869:A:C6	82:BB:114:VAL:O	2.12	1.02
81:A6:4099:G:H5''	82:BB:227:LYS:CD	1.85	1.02
64:AA:211:GLU:HA	84:RR:81:ARG:CA	1.89	1.02
80:B2:1452:A:H3'	84:RR:44:LYS:CB	1.88	1.02
64:AA:210:ILE:HD11	84:RR:82:ASP:CG	1.82	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:B2:956:G:C5'	82:BB:2:ALA:O	2.08	1.02
80:B2:974:C:O2'	83:OO:41:PHE:CD2	2.13	1.02
80:B2:1456:G:OP1	84:RR:55:THR:OG1	1.77	1.02
62:gg:280:LYS:HD3	84:RR:59:LYS:CD	1.90	1.02
64:AA:211:GLU:HG3	84:RR:81:ARG:CG	1.89	1.02
80:B2:957:A:H8	82:BB:5:LYS:HE3	0.98	1.02
80:B2:969:U:C5	82:BB:8:ARG:HA	1.92	1.02
80:B2:1124:C:H4'	82:BB:150:ILE:HD12	1.42	1.02
62:gg:282:GLU:HG3	84:RR:26:ASN:CG	1.84	1.01
80:B2:961:G:H5''	83:OO:66:ARG:HH22	1.23	1.01
47:aa:56:ALA:O	83:OO:124:MET:HG3	1.60	1.01
80:B2:1124:C:OP2	82:BB:151:ARG:HB2	1.56	1.01
80:B2:1857:G:OP2	83:OO:146:ARG:CD	2.09	1.01
47:aa:63:VAL:CG2	83:OO:129:ILE:HG13	1.91	1.01
80:B2:1453:C:N4	84:RR:28:PHE:CZ	2.29	1.01
6:E:42:GLY:N	77:A5:980:U:C1'	2.23	1.01
47:aa:52:ASP:OD2	83:OO:117:ARG:N	1.83	1.01
47:aa:57:SER:OG	83:OO:126:ILE:HG22	1.60	1.00
80:B2:1456:G:OP1	84:RR:55:THR:N	1.92	1.00
64:AA:83:GLY:HA2	64:AA:207:PRO:HG2	1.43	1.00
80:B2:988:C:H5''	82:BB:116:LYS:HD3	1.00	1.00
6:E:221:LYS:HA	81:A6:4940:C:N1	1.77	1.00
64:AA:214:GLU:HG2	84:RR:80:ARG:CA	1.91	1.00
80:B2:1466:G:OP2	84:RR:5:ARG:CD	2.02	1.00
30:f:58:VAL:CB	81:A6:4945:G:C8	2.43	1.00
62:gg:280:LYS:HA	84:RR:59:LYS:HG2	1.05	1.00
47:aa:28:ARG:CG	83:OO:147:ARG:CA	2.40	1.00
47:aa:29:CYS:SG	83:OO:146:ARG:CG	2.50	1.00
62:gg:83:TRP:CZ3	84:RR:36:GLU:OE1	2.16	0.99
62:gg:280:LYS:O	84:RR:26:ASN:ND2	1.94	0.99
80:B2:961:G:C5'	83:OO:66:ARG:HH22	1.76	0.99
81:A6:4940:C:C6	81:A6:4940:C:N1	2.31	0.99
6:E:42:GLY:N	77:A5:980:U:O4'	1.95	0.99
47:aa:59:PHE:CD1	83:OO:126:ILE:O	1.87	0.98
47:aa:67:LEU:HD11	83:OO:108:PRO:HG3	1.44	0.98
62:gg:279:SER:O	84:RR:62:GLN:HB2	1.62	0.98
47:aa:56:ALA:O	83:OO:124:MET:C	2.05	0.98
80:B2:1373:C:H3'	84:RR:7:LYS:CD	1.78	0.98
47:aa:26:CYS:CB	83:OO:149:ARG:C	2.34	0.98
47:aa:55:GLU:CG	83:OO:120:ALA:O	2.12	0.98
81:A6:4945:G:C8	81:A6:4945:G:N7	2.31	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:aa:29:CYS:SG	83:OO:146:ARG:HG2	2.03	0.98
47:aa:22:ARG:NH2	83:OO:141:ARG:HG3	1.78	0.98
80:B2:1857:G:OP2	83:OO:146:ARG:HD2	1.63	0.98
62:gg:282:GLU:HB3	84:RR:62:GLN:HE22	1.21	0.97
47:aa:53:ILE:H	83:OO:117:ARG:NH2	1.59	0.97
64:AA:84:GLN:HB2	64:AA:207:PRO:HB3	1.46	0.97
80:B2:1466:G:O3'	84:RR:4:VAL:CA	2.05	0.97
81:A6:2590:G:N3	81:A6:2755:A:N6	2.12	0.97
6:E:104:ASN:CA	77:A5:684:G:O4'	2.12	0.97
47:aa:67:LEU:CD1	83:OO:108:PRO:HD3	1.82	0.97
80:B2:1468:C:OP2	84:RR:3:ARG:NE	1.95	0.97
47:aa:69:VAL:HG22	83:OO:107:THR:N	1.78	0.97
64:AA:128:ARG:HB3	64:AA:128:ARG:CZ	1.91	0.97
64:AA:211:GLU:CG	84:RR:81:ARG:HG2	1.93	0.97
80:B2:956:G:OP2	82:BB:4:GLY:N	1.96	0.97
6:E:42:GLY:N	77:A5:980:U:C4'	2.27	0.97
47:aa:66:LYS:CE	82:BB:108:ASP:H	1.67	0.97
80:B2:941:C:H5'	82:BB:136:ARG:NH2	1.78	0.97
80:B2:1463:U:H2'	84:RR:63:ARG:HH22	1.23	0.97
6:E:104:ASN:CA	77:A5:684:G:C1'	2.43	0.97
47:aa:63:VAL:CG2	83:OO:129:ILE:CG1	2.42	0.97
81:A6:4099:G:H1'	82:BB:224:GLU:CG	1.95	0.97
80:B2:1467:C:P	84:RR:3:ARG:HG3	2.04	0.96
81:A6:4940:C:N1	81:A6:4940:C:C2	2.33	0.96
64:AA:23:THR:OG1	64:AA:164:ASN:ND2	1.98	0.96
80:B2:975:G:C5'	83:OO:32:HIS:CE1	2.48	0.96
49:EE:160:ILE:HD12	49:EE:162:ILE:HD11	1.47	0.96
64:AA:210:ILE:HG23	84:RR:81:ARG:HB3	0.96	0.96
80:B2:1452:A:C3'	84:RR:44:LYS:CG	2.40	0.96
64:AA:42:LYS:HD2	84:RR:101:ASP:OD2	1.62	0.96
47:aa:28:ARG:HG2	83:OO:147:ARG:CA	1.93	0.96
47:aa:69:VAL:HG23	83:OO:107:THR:CA	1.95	0.96
80:B2:1869:A:N6	82:BB:114:VAL:HG12	1.79	0.96
30:f:58:VAL:CA	81:A6:4945:G:C8	2.48	0.96
80:B2:956:G:H5''	82:BB:5:LYS:N	1.81	0.96
80:B2:1453:C:C5	84:RR:32:LYS:HD2	2.00	0.96
80:B2:1869:A:N1	82:BB:114:VAL:O	1.98	0.96
6:E:41:LYS:C	6:E:42:GLY:N	2.24	0.96
56:VV:59:ILE:HG22	56:VV:64:GLU:HB3	1.48	0.96
64:AA:128:ARG:HH21	64:AA:128:ARG:HB2	1.31	0.96
30:f:58:VAL:CB	81:A6:4945:G:N9	2.29	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:aa:56:ALA:N	83:OO:120:ALA:CA	1.86	0.95
47:aa:56:ALA:O	83:OO:124:MET:CG	2.13	0.95
47:aa:59:PHE:HD1	83:OO:126:ILE:O	1.49	0.95
47:aa:28:ARG:CA	83:OO:147:ARG:C	2.38	0.95
80:B2:1111:U:OP1	84:RR:124:VAL:CG2	0.66	0.95
80:B2:1458:G:OP2	84:RR:59:LYS:HE3	1.62	0.95
81:A6:4940:C:N3	81:A6:4940:C:C2	2.34	0.95
64:AA:214:GLU:O	84:RR:80:ARG:HD2	1.67	0.95
80:B2:1122:A:H5'	82:BB:205:TYR:CD2	2.02	0.95
80:B2:1453:C:H4'	84:RR:46:LEU:C	1.62	0.95
80:B2:1456:G:O3'	84:RR:27:ASP:HA	1.65	0.95
64:AA:211:GLU:CG	84:RR:81:ARG:CG	2.44	0.95
80:B2:956:G:H3'	82:BB:5:LYS:HE2	0.97	0.95
80:B2:1124:C:H5''	82:BB:150:ILE:HB	0.95	0.95
80:B2:1452:A:C5'	84:RR:48:ASN:CG	2.36	0.95
64:AA:214:GLU:C	84:RR:81:ARG:CA	2.37	0.95
80:B2:1476:A:N1	84:RR:3:ARG:CZ	2.08	0.95
30:f:58:VAL:CB	81:A6:4945:G:C5	2.49	0.94
64:AA:74:VAL:HG22	64:AA:120:ARG:CB	1.97	0.94
80:B2:1111:U:O2	82:BB:148:ASN:ND2	2.00	0.94
64:AA:214:GLU:HG2	84:RR:80:ARG:C	1.93	0.94
47:aa:69:VAL:HG22	83:OO:107:THR:H	1.32	0.94
64:AA:149:ASN:HD21	64:AA:166:LYS:HZ2	1.13	0.94
81:A6:4099:G:O2'	82:BB:227:LYS:N	2.00	0.94
47:aa:22:ARG:NH2	83:OO:141:ARG:CG	2.28	0.94
6:E:221:LYS:CB	81:A6:4940:C:C2	2.51	0.94
62:gg:235:ILE:HD11	84:RR:22:THR:HG1	1.27	0.94
64:AA:212:LYS:HE2	84:RR:84:TYR:CZ	2.02	0.94
80:B2:969:U:H5	82:BB:8:ARG:CA	1.79	0.94
6:E:104:ASN:C	77:A5:684:G:O4'	2.11	0.94
47:aa:69:VAL:HG21	83:OO:107:THR:H	1.32	0.93
62:gg:280:LYS:CA	84:RR:59:LYS:CG	2.26	0.93
80:B2:988:C:H5''	82:BB:116:LYS:CD	1.96	0.93
47:aa:53:ILE:CD1	83:OO:116:LEU:HB2	1.98	0.93
47:aa:69:VAL:HG22	83:OO:106:LYS:H	1.33	0.93
80:B2:1466:G:C4'	84:RR:4:VAL:HA	1.96	0.93
6:E:104:ASN:C	77:A5:684:G:C4'	2.42	0.93
44:u:64:ALA:HB1	44:u:69:THR:HB	1.51	0.92
80:B2:955:A:H1'	82:BB:6:ASN:HB2	0.94	0.92
64:AA:149:ASN:ND2	64:AA:166:LYS:NZ	2.16	0.92
80:B2:1124:C:OP2	82:BB:151:ARG:CB	2.13	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:f:58:VAL:CA	81:A6:4945:G:N9	2.32	0.92
80:B2:1122:A:C5'	82:BB:205:TYR:CE2	2.52	0.92
80:B2:1456:G:OP1	84:RR:55:THR:CB	2.17	0.92
6:E:221:LYS:HB2	81:A6:4940:C:C2	2.03	0.92
47:aa:22:ARG:HH22	83:OO:141:ARG:CG	1.82	0.92
47:aa:29:CYS:HG	83:OO:146:ARG:HA	1.11	0.92
80:B2:1124:C:H5'	82:BB:150:ILE:N	1.84	0.92
6:E:104:ASN:C	77:A5:684:G:C1'	2.43	0.92
80:B2:1466:G:OP2	84:RR:5:ARG:HD2	1.70	0.92
47:aa:53:ILE:CG1	83:OO:116:LEU:HD13	1.99	0.92
47:aa:58:VAL:CG2	83:OO:125:LYS:HZ1	1.81	0.92
62:gg:280:LYS:HD3	84:RR:59:LYS:HD3	0.95	0.92
80:B2:1467:C:P	84:RR:3:ARG:CG	2.58	0.92
30:f:58:VAL:CB	81:A6:4945:G:N7	2.33	0.92
80:B2:1109:C:OP1	84:RR:126:MET:HE2	1.70	0.92
80:B2:1466:G:P	84:RR:10:LYS:HD2	2.09	0.92
47:aa:63:VAL:HG23	83:OO:129:ILE:CD1	1.98	0.91
64:AA:214:GLU:HG2	84:RR:80:ARG:O	1.69	0.91
80:B2:1374:C:OP2	84:RR:7:LYS:NZ	2.03	0.91
6:E:221:LYS:CB	81:A6:4940:C:C4	2.54	0.91
64:AA:214:GLU:CD	84:RR:79:GLU:O	0.66	0.91
80:B2:1111:U:OP1	84:RR:124:VAL:HG21	1.11	0.91
47:aa:58:VAL:HG21	83:OO:125:LYS:HE2	0.93	0.91
64:AA:210:ILE:HD13	84:RR:82:ASP:OD1	1.70	0.91
64:AA:213:GLU:CG	84:RR:86:PRO:HD2	1.98	0.91
81:A6:2666:G:C2	81:A6:2669:C:O4'	2.15	0.91
81:A6:4099:G:H5''	82:BB:227:LYS:HD2	1.48	0.91
40:p:41:PHE:CZ	44:u:51:ASN:HA	2.05	0.91
80:B2:1455:A:C4'	84:RR:51:ALA:CB	1.75	0.91
62:gg:280:LYS:CB	84:RR:59:LYS:CD	2.44	0.91
80:B2:986:G:H8	83:OO:137:SER:O	1.43	0.91
82:BB:115:LYS:CB	82:BB:115:LYS:CA	2.48	0.91
81:A6:4099:G:H4'	82:BB:227:LYS:HG2	1.50	0.91
47:aa:58:VAL:HG11	83:OO:125:LYS:CE	2.01	0.91
80:B2:1122:A:C5'	82:BB:205:TYR:CD2	2.54	0.91
30:f:58:VAL:CB	81:A6:4945:G:C4	2.51	0.90
80:B2:1466:G:C8	84:RR:5:ARG:NH1	2.38	0.90
30:f:58:VAL:CA	81:A6:4945:G:N7	2.33	0.90
80:B2:1124:C:P	82:BB:151:ARG:CB	2.57	0.90
47:aa:69:VAL:HG22	83:OO:106:LYS:CA	1.99	0.90
64:AA:211:GLU:O	84:RR:84:TYR:HB3	1.69	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:AA:214:GLU:CG	84:RR:83:ASN:N	2.28	0.90
80:B2:1466:G:H5''	84:RR:5:ARG:CG	1.99	0.90
64:AA:210:ILE:CG2	84:RR:81:ARG:CD	2.50	0.90
64:AA:39:TYR:OH	84:RR:108:LEU:HD21	1.72	0.90
6:E:42:GLY:N	77:A5:980:U:C3'	2.34	0.90
77:A5:1183:C:N4	77:A5:1184:A:H62	1.69	0.90
80:B2:969:U:P	82:BB:8:ARG:NH1	2.44	0.90
80:B2:1368:U:H4'	84:RR:4:VAL:HG13	1.54	0.90
80:B2:1465:A:O3'	84:RR:10:LYS:CD	2.18	0.90
47:aa:67:LEU:HD11	83:OO:108:PRO:CG	1.94	0.89
6:E:221:LYS:HB2	81:A6:4940:C:N1	1.87	0.89
80:B2:1456:G:P	84:RR:55:THR:CB	2.59	0.89
47:aa:66:LYS:HE3	82:BB:107:ARG:C	1.95	0.89
80:B2:1452:A:H5''	84:RR:44:LYS:O	1.69	0.89
81:A6:2758:G:N2	81:A6:2766:A:C2	2.40	0.89
64:AA:23:THR:CG2	64:AA:164:ASN:HD22	1.85	0.89
80:B2:955:A:O2'	82:BB:6:ASN:HB3	1.73	0.89
80:B2:1455:A:H4'	84:RR:51:ALA:CA	2.03	0.89
6:E:41:LYS:C	77:A5:980:U:O4'	2.16	0.89
80:B2:943:U:O2'	83:OO:135:ILE:O	1.91	0.89
80:B2:1005:G:OP1	82:BB:166:LYS:NZ	2.05	0.89
30:f:58:VAL:CA	81:A6:4945:G:C4	2.56	0.89
47:aa:59:PHE:CB	83:OO:126:ILE:HG22	2.01	0.89
80:B2:1460:C:N4	84:RR:56:HIS:CE1	2.38	0.89
62:gg:64:HIS:CE1	84:RR:33:ARG:NH1	2.35	0.88
64:AA:210:ILE:CD1	84:RR:82:ASP:OD1	2.21	0.88
64:AA:214:GLU:OE1	84:RR:79:GLU:C	0.64	0.88
47:aa:26:CYS:HB2	83:OO:149:ARG:O	1.73	0.88
64:AA:84:GLN:H	64:AA:207:PRO:HG3	1.39	0.88
80:B2:1367:U:O2'	84:RR:4:VAL:HG12	1.74	0.88
80:B2:1467:C:C5'	84:RR:3:ARG:CG	2.50	0.88
47:aa:58:VAL:CB	83:OO:125:LYS:HD3	2.04	0.88
47:aa:66:LYS:CE	82:BB:107:ARG:HG3	2.04	0.88
47:aa:28:ARG:HA	83:OO:147:ARG:C	1.99	0.88
47:aa:52:ASP:N	83:OO:117:ARG:HD3	1.86	0.88
80:B2:1457:U:OP2	84:RR:55:THR:HG22	1.72	0.88
80:B2:1463:U:C2'	84:RR:63:ARG:NH1	2.32	0.88
47:aa:53:ILE:HG12	83:OO:116:LEU:CD1	2.04	0.88
81:A6:4099:G:HO2'	82:BB:226:GLY:HA3	1.09	0.88
47:aa:65:PRO:HD3	83:OO:129:ILE:HD11	1.56	0.88
44:u:47:ILE:HG21	44:u:81:LEU:HD21	1.55	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:aa:26:CYS:HB2	83:OO:149:ARG:CA	1.93	0.88
64:AA:214:GLU:OE2	84:RR:82:ASP:CB	2.20	0.88
30:f:58:VAL:CA	81:A6:4945:G:C5	2.57	0.87
80:B2:1467:C:H5''	84:RR:3:ARG:HB3	1.55	0.87
47:aa:58:VAL:CG1	83:OO:125:LYS:CE	2.53	0.87
47:aa:59:PHE:HB2	83:OO:126:ILE:CG2	2.05	0.87
56:VV:73:ALA:CB	64:AA:57:LYS:HA	2.04	0.87
47:aa:28:ARG:HG3	83:OO:147:ARG:HA	1.54	0.87
47:aa:54:SER:N	83:OO:120:ALA:HB1	1.90	0.87
47:aa:67:LEU:CD2	83:OO:108:PRO:HG3	2.05	0.87
80:B2:1460:C:H42	84:RR:56:HIS:HE1	0.89	0.87
47:aa:55:GLU:O	83:OO:124:MET:O	1.92	0.87
64:AA:210:ILE:CD1	84:RR:82:ASP:CG	2.47	0.87
80:B2:968:U:C2'	82:BB:8:ARG:NH1	2.38	0.87
80:B2:1109:C:P	84:RR:126:MET:HE1	2.14	0.87
47:aa:63:VAL:HG22	83:OO:129:ILE:CG1	2.04	0.86
47:aa:65:PRO:HB3	83:OO:129:ILE:HD13	1.57	0.86
80:B2:955:A:C2'	82:BB:6:ASN:HB3	2.05	0.86
80:B2:941:C:HO2'	82:BB:138:PHE:HZ	0.90	0.86
64:AA:211:GLU:O	84:RR:84:TYR:CG	2.28	0.86
64:AA:42:LYS:HD3	84:RR:101:ASP:OD2	1.21	0.86
6:E:104:ASN:C	77:A5:684:G:C2'	2.49	0.86
15:O:87:MET:HE1	77:A5:1912:G:H21	1.38	0.86
80:B2:941:C:O2'	82:BB:138:PHE:HZ	1.58	0.86
80:B2:956:G:P	82:BB:4:GLY:H	1.98	0.86
81:A6:4936:G:N2	81:A6:4938:A:H61	1.74	0.86
76:Cc:15:G:N2	76:Cc:49:C:C2	2.44	0.85
80:B2:1101:U:O2	80:B2:1131:G:N1	2.09	0.85
6:E:221:LYS:CB	81:A6:4940:C:C6	2.59	0.85
6:E:104:ASN:CA	77:A5:684:G:C4'	2.54	0.85
47:aa:59:PHE:CD2	83:OO:126:ILE:CG2	2.56	0.85
80:B2:1452:A:H3'	84:RR:44:LYS:HB3	1.58	0.85
64:AA:17:LYS:HE3	64:AA:198:MET:CE	2.07	0.85
80:B2:1063:C:O2'	83:OO:150:ARG:NH2	2.10	0.85
80:B2:1857:G:OP2	83:OO:146:ARG:HG2	1.76	0.85
64:AA:74:VAL:HG22	64:AA:120:ARG:HB2	1.57	0.85
64:AA:83:GLY:CA	64:AA:207:PRO:HG2	2.07	0.85
56:VV:73:ALA:HB3	64:AA:57:LYS:CB	2.07	0.85
6:E:104:ASN:CA	6:E:104:ASN:C	2.49	0.85
47:aa:69:VAL:HG23	83:OO:107:THR:CB	2.07	0.85
6:E:41:LYS:C	77:A5:980:U:C4'	2.50	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:B2:1120:U:O2	82:BB:204:ILE:HG22	1.75	0.85
81:A6:4099:G:H1'	82:BB:224:GLU:OE2	1.77	0.84
47:aa:22:ARG:CZ	83:OO:141:ARG:HG3	2.07	0.84
47:aa:66:LYS:HE3	82:BB:108:ASP:H	1.04	0.84
80:B2:1122:A:N3	82:BB:146:ARG:NH1	2.25	0.84
6:E:42:GLY:N	77:A5:980:U:C2'	2.40	0.84
62:gg:282:GLU:CG	84:RR:26:ASN:CG	2.44	0.84
80:B2:969:U:OP2	82:BB:8:ARG:HD3	1.78	0.84
47:aa:29:CYS:CB	83:OO:146:ARG:HE	1.90	0.84
47:aa:53:ILE:H	83:OO:117:ARG:HH21	1.18	0.84
80:B2:1456:G:C8	84:RR:28:PHE:CB	2.61	0.84
80:B2:1466:G:H5''	84:RR:5:ARG:CD	2.07	0.84
62:gg:279:SER:CB	84:RR:63:ARG:N	2.39	0.84
80:B2:1452:A:H4'	84:RR:45:LYS:CA	2.07	0.84
20:U:23:LEU:HD11	20:U:83:LEU:HD21	1.59	0.84
80:B2:1112:U:O2	82:BB:146:ARG:HD2	1.78	0.84
80:B2:1454:A:N6	84:RR:3:ARG:CZ	2.06	0.84
6:E:221:LYS:CB	81:A6:4940:C:N3	2.39	0.83
64:AA:205:ARG:NH2	84:RR:83:ASN:N	2.03	0.83
80:B2:941:C:H5''	82:BB:136:ARG:CZ	2.08	0.83
80:B2:1453:C:C4'	84:RR:46:LEU:C	2.49	0.83
80:B2:1456:G:H8	84:RR:28:PHE:CB	1.89	0.83
44:u:54:ALA:HA	81:A6:4120:U:C5	2.13	0.83
80:B2:1463:U:C6	84:RR:63:ARG:NH1	2.00	0.83
6:E:104:ASN:CA	77:A5:684:G:C3'	2.56	0.83
47:aa:67:LEU:CG	83:OO:108:PRO:HG3	2.08	0.83
64:AA:17:LYS:HE3	64:AA:198:MET:HE1	1.61	0.83
47:aa:56:ALA:O	83:OO:124:MET:HB3	1.78	0.83
75:EF:666:THR:HG23	75:EF:672:LEU:HD23	1.60	0.83
80:B2:1466:G:C5'	84:RR:5:ARG:CG	2.55	0.83
80:B2:1121:G:H1'	82:BB:204:ILE:CA	2.08	0.82
64:AA:47:TYR:CZ	64:AA:150:THR:HG23	2.14	0.82
80:B2:931:C:C5'	82:BB:157:GLN:OE1	2.27	0.82
80:B2:1373:C:H3'	84:RR:7:LYS:HZ3	1.43	0.82
80:B2:1858:G:OP2	83:OO:146:ARG:NH1	2.13	0.82
6:E:221:LYS:CB	81:A6:4940:C:C5	2.62	0.82
47:aa:28:ARG:HA	83:OO:148:GLY:N	1.95	0.82
81:A6:4099:G:C2'	82:BB:226:GLY:HA3	2.09	0.82
44:u:21:VAL:HG11	44:u:45:LEU:HD23	1.59	0.82
47:aa:59:PHE:CG	83:OO:126:ILE:CG2	2.58	0.82
64:AA:211:GLU:HG3	84:RR:81:ARG:HG3	1.61	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:A6:4945:G:C4	81:A6:4945:G:N9	2.47	0.82
80:B2:941:C:C5'	82:BB:136:ARG:CZ	2.58	0.82
47:aa:53:ILE:C	83:OO:120:ALA:CB	2.45	0.82
81:A6:4945:G:C5	81:A6:4945:G:N7	2.47	0.82
64:AA:213:GLU:HG2	84:RR:86:PRO:HD3	1.61	0.82
81:A6:4945:G:C8	81:A6:4945:G:N9	2.48	0.82
47:aa:26:CYS:HA	83:OO:149:ARG:HB2	0.84	0.82
47:aa:26:CYS:CB	83:OO:149:ARG:O	2.27	0.81
80:B2:1047:C:H5''	83:OO:143:LYS:NZ	1.95	0.81
80:B2:1464:C:O4'	84:RR:60:ARG:NH1	2.14	0.81
64:AA:149:ASN:HD21	64:AA:166:LYS:HZ3	1.27	0.81
80:B2:1466:G:H5''	84:RR:5:ARG:HD2	1.61	0.81
47:aa:65:PRO:CB	83:OO:129:ILE:HD13	2.10	0.81
47:aa:66:LYS:O	83:OO:131:ASP:OD2	1.99	0.81
80:B2:1373:C:H4'	84:RR:7:LYS:H	1.44	0.81
80:B2:1463:U:O2'	84:RR:63:ARG:NE	2.13	0.81
47:aa:53:ILE:CD1	83:OO:116:LEU:HD13	2.10	0.81
80:B2:956:G:C5	82:BB:5:LYS:HG2	2.15	0.81
47:aa:56:ALA:C	83:OO:124:MET:O	2.22	0.81
64:AA:214:GLU:CG	84:RR:80:ARG:O	2.22	0.81
47:aa:65:PRO:HB3	83:OO:129:ILE:CD1	2.11	0.81
6:E:221:LYS:CB	81:A6:4940:C:N1	2.44	0.81
81:A6:2293:C:O2	81:A6:2341:G:N2	2.14	0.81
6:E:221:LYS:CB	6:E:221:LYS:HA	2.11	0.80
80:B2:1374:C:P	84:RR:7:LYS:CD	2.59	0.80
47:aa:65:PRO:CG	83:OO:129:ILE:HD13	2.10	0.80
62:gg:17:TRP:HH2	84:RR:30:THR:HG23	1.39	0.80
64:AA:214:GLU:C	84:RR:81:ARG:HA	2.05	0.80
80:B2:975:G:O4'	83:OO:43:HIS:ND1	2.14	0.80
80:B2:1456:G:H3'	84:RR:55:THR:HG21	1.64	0.80
56:VV:43:THR:HG23	56:VV:45:ARG:HG2	1.63	0.80
47:aa:63:VAL:CG2	83:OO:129:ILE:HD11	2.07	0.80
6:E:41:LYS:C	77:A5:980:U:C1'	2.55	0.80
80:B2:968:U:H3'	82:BB:8:ARG:HH12	0.64	0.80
80:B2:969:U:P	82:BB:8:ARG:HH11	2.05	0.80
80:B2:1456:G:P	84:RR:55:THR:HB	2.22	0.79
6:E:221:LYS:CA	81:A6:4940:C:C2	2.66	0.79
48:CC:84:PHE:CD1	64:AA:67:ALA:CB	2.66	0.79
38:n:10:MET:HE2	80:B2:1172:U:H4'	1.64	0.79
47:aa:63:VAL:CG2	83:OO:129:ILE:CD1	2.60	0.79
80:B2:1468:C:OP2	84:RR:3:ARG:HG2	1.81	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:VV:29:HIS:HB3	64:AA:137:ALA:HB1	1.65	0.79
56:VV:59:ILE:HG23	64:AA:154:LEU:CD2	2.13	0.79
64:AA:149:ASN:ND2	64:AA:166:LYS:HZ3	1.79	0.79
80:B2:1112:U:O2	82:BB:146:ARG:NE	2.14	0.79
64:AA:10:MET:HE1	64:AA:55:TRP:CE3	2.17	0.79
64:AA:74:VAL:HG23	64:AA:94:THR:HG21	1.65	0.79
64:AA:82:THR:O	64:AA:207:PRO:HG2	1.81	0.79
80:B2:1464:C:O5'	84:RR:60:ARG:NH1	2.13	0.79
80:B2:1869:A:H61	82:BB:114:VAL:CG1	1.96	0.79
47:aa:63:VAL:HG22	83:OO:129:ILE:HG13	1.61	0.78
80:B2:1466:G:H4'	84:RR:4:VAL:HA	1.65	0.78
47:aa:27:ALA:HB1	83:OO:143:LYS:O	1.83	0.78
47:aa:29:CYS:CB	83:OO:146:ARG:NE	2.46	0.78
56:VV:73:ALA:HB1	64:AA:57:LYS:HA	1.66	0.78
62:gg:212:LYS:NZ	84:RR:22:THR:CG2	2.47	0.78
47:aa:69:VAL:HG23	83:OO:107:THR:H	0.91	0.78
6:E:221:LYS:CA	81:A6:4940:C:C6	2.65	0.78
47:aa:53:ILE:N	83:OO:117:ARG:HH21	1.71	0.78
80:B2:1458:G:C8	84:RR:59:LYS:NZ	2.52	0.78
77:A5:33:A:N7	77:A5:49:U:C2	2.52	0.78
80:B2:1095:C:N3	80:B2:1149:A:N1	2.33	0.78
80:B2:1467:C:H5''	84:RR:3:ARG:CB	2.14	0.78
64:AA:40:LYS:HB2	84:RR:105:MET:CE	2.14	0.77
81:A6:4099:G:C4'	82:BB:227:LYS:HG2	2.13	0.77
64:AA:173:LEU:HD23	64:AA:174:MET:HA	1.66	0.77
80:B2:1453:C:C5	84:RR:28:PHE:CZ	2.71	0.77
47:aa:28:ARG:HA	83:OO:146:ARG:C	1.84	0.77
56:VV:52:THR:HA	64:AA:61:ALA:HA	1.64	0.77
47:aa:58:VAL:HG21	83:OO:125:LYS:HZ1	1.44	0.77
80:B2:1466:G:O6	84:RR:56:HIS:NE2	2.18	0.77
81:A6:2666:G:H1	81:A6:2669:C:P	1.97	0.77
47:aa:29:CYS:SG	83:OO:146:ARG:NE	2.56	0.77
47:aa:66:LYS:HE2	82:BB:107:ARG:HG3	1.66	0.77
77:A5:1724:G:N1	77:A5:1838:A:C2	2.51	0.77
80:B2:1047:C:H5''	83:OO:143:LYS:HD3	1.67	0.77
80:B2:1166:G:O6	80:B2:1193:U:O2	2.03	0.77
80:B2:1757:G:O6	80:B2:1775:U:O2	2.03	0.77
47:aa:28:ARG:CA	83:OO:148:GLY:N	2.45	0.77
62:gg:279:SER:O	84:RR:62:GLN:OE1	2.02	0.77
80:B2:1455:A:C5'	84:RR:51:ALA:CB	2.38	0.77
6:E:221:LYS:CA	81:A6:4940:C:N1	2.48	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:aa:69:VAL:HG22	83:OO:106:LYS:C	2.10	0.77
80:B2:941:C:O2'	82:BB:138:PHE:CZ	2.36	0.77
64:AA:26:GLY:O	64:AA:44:ASP:CB	2.32	0.76
64:AA:211:GLU:CA	84:RR:81:ARG:HA	2.11	0.76
80:B2:975:G:C1'	83:OO:43:HIS:ND1	2.48	0.76
62:gg:280:LYS:HG2	84:RR:59:LYS:HB3	1.66	0.76
64:AA:174:MET:HE1	64:AA:178:LEU:CD2	2.15	0.76
51:HH:69:LEU:HD22	51:HH:96:ALA:HB2	1.66	0.76
62:gg:17:TRP:CE2	84:RR:30:THR:OG1	2.29	0.76
64:AA:182:VAL:CG1	64:AA:186:ARG:HH22	1.97	0.76
77:A5:727:C:O2	77:A5:939:G:N2	2.19	0.76
56:VV:31:SER:O	56:VV:32:ILE:HD13	1.86	0.76
80:B2:185:G:O6	80:B2:214:U:O2	2.04	0.76
47:aa:59:PHE:CB	83:OO:126:ILE:CG2	2.64	0.76
80:B2:1455:A:C3'	84:RR:51:ALA:CB	2.63	0.76
47:aa:54:SER:N	83:OO:120:ALA:CB	2.49	0.76
47:aa:66:LYS:HE3	82:BB:107:ARG:HG3	1.68	0.75
56:VV:52:THR:HG23	64:AA:61:ALA:HB1	1.68	0.75
56:VV:70:LEU:HD22	64:AA:53:ARG:HD2	1.69	0.75
56:VV:58:ALA:HB3	64:AA:158:ASP:OD1	1.87	0.75
81:A6:4099:G:O4'	82:BB:224:GLU:OE1	2.03	0.75
56:VV:29:HIS:C	64:AA:137:ALA:HB1	2.11	0.75
64:AA:84:GLN:H	64:AA:207:PRO:CG	1.99	0.75
64:AA:149:ASN:ND2	64:AA:166:LYS:HZ2	1.82	0.75
80:B2:1453:C:O2'	84:RR:50:ILE:N	2.18	0.75
80:B2:1855:G:OP2	83:OO:147:ARG:NE	2.18	0.75
81:A6:4098:A:N3	82:BB:224:GLU:OE2	2.19	0.75
56:VV:45:ARG:CB	64:AA:191:ARG:HA	2.17	0.75
30:f:58:VAL:CG1	30:f:58:VAL:CG2	2.65	0.75
56:VV:52:THR:HG23	64:AA:61:ALA:CB	2.15	0.75
64:AA:210:ILE:HG23	84:RR:81:ARG:CD	2.13	0.75
64:AA:214:GLU:OE1	84:RR:80:ARG:CA	2.35	0.74
76:Cc:55:U:O2	76:Cc:59:A:N7	2.20	0.74
47:aa:58:VAL:CB	83:OO:125:LYS:HE2	2.17	0.74
80:B2:1455:A:C3'	84:RR:52:GLY:N	2.50	0.74
47:aa:53:ILE:N	83:OO:117:ARG:CZ	2.50	0.74
64:AA:174:MET:HE1	64:AA:178:LEU:HD23	1.69	0.74
64:AA:214:GLU:CG	84:RR:80:ARG:C	2.60	0.74
80:B2:956:G:P	82:BB:4:GLY:N	2.59	0.74
80:B2:1124:C:O2'	84:RR:127:ASN:ND2	2.20	0.74
80:B2:1124:C:C5	82:BB:151:ARG:NH2	2.55	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:aa:22:ARG:NE	83:OO:141:ARG:NH1	2.35	0.74
80:B2:961:G:C5'	83:OO:66:ARG:NH2	2.50	0.74
80:B2:1368:U:O4'	84:RR:4:VAL:HG13	1.74	0.74
81:A6:4098:A:H1'	82:BB:222:LYS:HE2	1.69	0.74
56:VV:66:ASP:HA	56:VV:69:ILE:HG23	1.69	0.74
81:A6:4936:G:N2	81:A6:4938:A:N6	2.35	0.74
6:E:221:LYS:HB3	81:A6:4940:C:C4	2.23	0.74
80:B2:1857:G:OP2	83:OO:146:ARG:HG3	1.87	0.74
64:AA:210:ILE:HG13	84:RR:81:ARG:O	1.67	0.73
80:B2:1112:U:O2	82:BB:146:ARG:HD3	1.85	0.73
6:E:221:LYS:CA	81:A6:4940:C:C5	2.71	0.73
81:A6:3918:G:O6	81:A6:4383:U:O2	2.06	0.73
6:E:221:LYS:CA	81:A6:4940:C:N3	2.51	0.73
47:aa:29:CYS:HB3	83:OO:146:ARG:HH21	1.52	0.73
47:aa:52:ASP:N	83:OO:117:ARG:CD	2.35	0.73
62:gg:279:SER:CB	84:RR:63:ARG:CA	2.66	0.73
80:B2:1453:C:H4'	84:RR:47:ARG:N	2.04	0.73
6:E:221:LYS:CA	81:A6:4940:C:C4	2.71	0.73
47:aa:65:PRO:HD3	83:OO:129:ILE:CD1	2.18	0.73
64:AA:17:LYS:NZ	64:AA:198:MET:HE1	2.03	0.73
77:A5:1183:C:C4	77:A5:1184:A:N7	2.57	0.73
4:c:81:ALA:HB2	4:c:87:LEU:HD22	1.70	0.73
64:AA:214:GLU:CG	84:RR:80:ARG:HA	2.17	0.73
80:B2:149:A:N7	80:B2:169:U:O2	2.21	0.73
80:B2:1455:A:C3'	84:RR:51:ALA:C	2.56	0.73
80:B2:1453:C:OP1	84:RR:44:LYS:N	2.20	0.73
47:aa:52:ASP:HA	83:OO:121:ARG:HG2	1.70	0.73
81:A6:4099:G:H1'	82:BB:224:GLU:HG2	1.71	0.73
56:VV:51:LYS:C	64:AA:63:ARG:H	1.96	0.73
80:B2:1124:C:H5	82:BB:151:ARG:NH2	1.86	0.73
47:aa:53:ILE:H	83:OO:117:ARG:CZ	2.01	0.73
80:B2:956:G:O5'	82:BB:3:VAL:HA	1.88	0.73
80:B2:989:C:H3'	82:BB:116:LYS:NZ	2.03	0.73
80:B2:1109:C:OP1	84:RR:126:MET:SD	2.47	0.73
80:B2:1111:U:P	84:RR:124:VAL:CG1	2.77	0.73
56:VV:60:ARG:HB3	56:VV:60:ARG:HH11	1.52	0.72
64:AA:74:VAL:HB	64:AA:91:ALA:HB1	1.69	0.72
80:B2:1047:C:C5'	83:OO:143:LYS:NZ	2.51	0.72
80:B2:1121:G:H1'	82:BB:204:ILE:HA	1.69	0.72
80:B2:1869:A:N7	82:BB:116:LYS:CG	2.52	0.72
81:A6:2312:U:O2	81:A6:2326:G:O6	2.06	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:A6:4099:G:C1'	82:BB:224:GLU:OE2	2.33	0.72
30:f:58:VAL:CB	30:f:58:VAL:CA	2.67	0.72
44:u:81:LEU:HD22	44:u:91:VAL:HG12	1.69	0.72
80:B2:1466:G:OP1	84:RR:10:LYS:HG3	1.89	0.72
81:A6:3951:G:H21	81:A6:4062:A:H61	1.36	0.72
64:AA:184:ARG:NH2	64:AA:195:TRP:CZ3	2.57	0.72
80:B2:975:G:O4'	83:OO:43:HIS:CE1	2.43	0.72
56:VV:35:ASN:HD21	64:AA:185:MET:HE3	1.53	0.72
64:AA:214:GLU:C	84:RR:81:ARG:C	2.56	0.72
64:AA:86:ALA:HB1	64:AA:89:LYS:HG3	1.71	0.72
80:B2:956:G:C2'	82:BB:5:LYS:HE2	2.18	0.72
47:aa:63:VAL:HG21	83:OO:129:ILE:HG13	1.72	0.72
64:AA:74:VAL:HG22	64:AA:120:ARG:HB3	1.71	0.72
47:aa:27:ALA:HB3	83:OO:144:GLY:HA3	1.72	0.72
47:aa:28:ARG:CG	83:OO:147:ARG:C	2.62	0.72
62:gg:212:LYS:NZ	84:RR:22:THR:HG22	2.05	0.72
81:A6:4099:G:HO2'	82:BB:226:GLY:N	1.87	0.72
56:VV:76:ASP:HB3	64:AA:59:LEU:HD13	1.72	0.72
60:cc:46:VAL:HG21	60:cc:50:VAL:HG21	1.71	0.72
64:AA:23:THR:HG21	64:AA:164:ASN:O	1.90	0.72
64:AA:210:ILE:HG22	84:RR:81:ARG:HE	1.48	0.72
74:ZZ:58:LEU:HD11	74:ZZ:87:ALA:HB1	1.71	0.72
56:VV:45:ARG:HB2	64:AA:191:ARG:HA	1.72	0.71
80:B2:988:C:C5'	82:BB:116:LYS:CD	2.61	0.71
81:A6:4235:G:O6	81:A6:4289:U:O2	2.07	0.71
2:B:90:VAL:HG22	2:B:104:THR:HG22	1.70	0.71
80:B2:1367:U:O2'	84:RR:4:VAL:CG1	2.37	0.71
64:AA:17:LYS:HE2	64:AA:198:MET:SD	2.30	0.71
64:AA:83:GLY:HA2	64:AA:207:PRO:CG	2.18	0.71
80:B2:974:C:O2'	83:OO:41:PHE:CE2	2.35	0.71
81:A6:2620:G:O6	81:A6:2636:U:O2	2.08	0.71
47:aa:22:ARG:NH1	83:OO:142:ARG:H	1.89	0.71
56:VV:33:GLN:HG2	64:AA:142:LEU:CD1	2.19	0.71
80:B2:1456:G:O5'	84:RR:55:THR:CB	2.37	0.71
6:E:104:ASN:C	77:A5:684:G:C3'	2.63	0.71
47:aa:27:ALA:CB	83:OO:144:GLY:HA3	2.21	0.71
56:VV:59:ILE:HG22	56:VV:64:GLU:CB	2.21	0.71
56:VV:34:MET:SD	64:AA:159:ILE:HD13	2.30	0.71
64:AA:39:TYR:CB	64:AA:48:ILE:HG21	2.21	0.71
80:B2:1467:C:OP2	84:RR:3:ARG:HD2	1.90	0.71
6:E:104:ASN:CA	77:A5:684:G:C2'	2.69	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:B2:1373:C:H4'	84:RR:7:LYS:CA	2.21	0.71
81:A6:4099:G:H5'	82:BB:227:LYS:HD3	0.71	0.71
56:VV:70:LEU:HD22	64:AA:53:ARG:CD	2.21	0.70
80:B2:1456:G:H8	84:RR:28:PHE:HB2	1.55	0.70
80:B2:1466:G:OP2	84:RR:5:ARG:HD3	1.91	0.70
47:aa:50:VAL:C	83:OO:117:ARG:NH1	2.49	0.70
56:VV:79:VAL:HG13	64:AA:10:MET:HB3	1.74	0.70
64:AA:210:ILE:CG2	84:RR:81:ARG:CZ	2.62	0.70
80:B2:956:G:H5'	82:BB:2:ALA:C	2.12	0.70
80:B2:956:G:H3'	82:BB:5:LYS:HB3	1.71	0.70
56:VV:55:ILE:HG22	64:AA:143:PRO:HB3	1.73	0.70
62:gg:279:SER:HB3	84:RR:63:ARG:HA	1.71	0.70
80:B2:957:A:H8	82:BB:5:LYS:CE	1.91	0.70
47:aa:55:GLU:OE2	83:OO:121:ARG:CZ	2.39	0.70
56:VV:3:ASN:CG	56:VV:5:ALA:HB3	2.16	0.70
77:A5:989:U:O2	77:A5:1064:G:O6	2.08	0.70
80:B2:176:U:O2	80:B2:313:A:N7	2.25	0.70
80:B2:1457:U:P	84:RR:55:THR:CG2	2.79	0.70
47:aa:69:VAL:HG23	83:OO:107:THR:HB	1.71	0.70
80:B2:1122:A:H4'	82:BB:205:TYR:CZ	2.26	0.70
80:B2:968:U:C4	82:BB:7:LYS:NZ	2.59	0.70
47:aa:58:VAL:CG2	83:OO:125:LYS:CD	2.70	0.70
75:EF:300:VAL:HG12	75:EF:315:LEU:HD11	1.73	0.70
77:A5:310:G:O6	77:A5:327:U:O2	2.09	0.70
40:p:92:GLN:HB3	82:BB:134:LEU:CD2	2.22	0.70
47:aa:54:SER:N	83:OO:117:ARG:HH22	1.89	0.70
62:gg:279:SER:HB2	84:RR:63:ARG:H	1.54	0.70
6:E:41:LYS:C	77:A5:980:U:C2'	2.65	0.69
80:B2:1857:G:P	83:OO:146:ARG:HD2	2.32	0.69
80:B2:1869:A:O3'	82:BB:115:LYS:HE2	1.92	0.69
80:B2:944:A:H4'	83:OO:102:GLY:HA2	1.72	0.69
80:B2:1452:A:C2'	84:RR:44:LYS:HG2	2.20	0.69
58:XX:55:VAL:HG12	58:XX:71:ARG:NH1	2.07	0.69
56:VV:73:ALA:HB3	64:AA:57:LYS:CA	2.22	0.69
80:B2:1121:G:H21	82:BB:206:PRO:HD3	1.57	0.69
64:AA:12:GLU:HA	64:AA:15:VAL:HB	1.75	0.69
80:B2:1110:G:C8	84:RR:126:MET:SD	2.85	0.69
80:B2:1756:C:O2	80:B2:1776:G:N2	2.26	0.69
47:aa:58:VAL:HG13	83:OO:125:LYS:HD3	0.69	0.69
47:aa:69:VAL:CG2	83:OO:106:LYS:N	2.50	0.69
64:AA:176:TRP:HE1	64:AA:180:ARG:CZ	2.04	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:aa:56:ALA:O	83:OO:124:MET:CA	2.39	0.69
47:aa:58:VAL:CB	83:OO:125:LYS:CE	2.71	0.69
64:AA:42:LYS:HE3	84:RR:99:ASP:HB3	1.74	0.69
80:B2:197:U:O2	80:B2:202:G:O6	2.10	0.69
80:B2:1109:C:P	84:RR:126:MET:CE	2.79	0.69
80:B2:1467:C:H5''	84:RR:3:ARG:CG	2.23	0.69
30:f:58:VAL:HA	81:A6:4945:G:N7	2.06	0.69
80:B2:953:C:O2	83:OO:55:ARG:NH2	2.26	0.69
80:B2:1329:U:O2	80:B2:1500:G:O6	2.10	0.69
80:B2:1452:A:C5'	84:RR:48:ASN:OD1	2.34	0.69
80:B2:944:A:H5''	83:OO:134:PRO:CB	2.23	0.69
80:B2:1111:U:P	84:RR:124:VAL:HG13	2.32	0.69
80:B2:1457:U:OP2	84:RR:55:THR:HG23	1.85	0.69
47:aa:22:ARG:HE	83:OO:141:ARG:NH1	1.92	0.68
80:B2:955:A:HO2'	82:BB:6:ASN:HB3	1.56	0.68
62:gg:212:LYS:NZ	84:RR:22:THR:HG21	2.08	0.68
80:B2:968:U:C2'	82:BB:8:ARG:HH12	1.99	0.68
80:B2:1373:C:C3'	84:RR:7:LYS:CE	2.52	0.68
56:VV:28:ASP:H	64:AA:141:ASN:N	1.91	0.68
80:B2:956:G:OP2	82:BB:4:GLY:C	2.36	0.68
80:B2:1453:C:HO2'	84:RR:50:ILE:H	1.41	0.68
44:u:44:LYS:HB2	44:u:98:ASP:HA	1.74	0.68
62:gg:46:THR:HG21	62:gg:54:ILE:HG23	1.75	0.68
80:B2:1121:G:O2'	82:BB:204:ILE:O	2.11	0.68
18:S:113:MET:HE2	18:S:124:ILE:HG13	1.76	0.68
30:f:58:VAL:HB	30:f:58:VAL:CA	2.23	0.68
62:gg:212:LYS:CD	84:RR:22:THR:HG21	2.24	0.68
81:A6:2758:G:N3	81:A6:2766:A:N1	2.40	0.68
5:D:64:ILE:HG12	5:D:105:LEU:HD21	1.75	0.68
80:B2:961:G:H5''	83:OO:66:ARG:NH2	2.03	0.68
6:E:104:ASN:HA	6:E:104:ASN:C	2.17	0.68
56:VV:19:ALA:HB2	56:VV:72:LEU:HD21	1.75	0.68
43:t:49:ALA:HB2	43:t:71:ILE:HD12	1.76	0.68
64:AA:210:ILE:HG23	84:RR:81:ARG:CG	2.24	0.68
6:E:41:LYS:C	77:A5:980:U:C3'	2.67	0.68
62:gg:279:SER:O	84:RR:62:GLN:CB	2.39	0.68
80:B2:988:C:H5'	82:BB:116:LYS:HD3	1.73	0.68
64:AA:23:THR:CB	64:AA:164:ASN:HD22	2.07	0.68
77:A5:512:U:O2	77:A5:647:G:O6	2.12	0.68
77:A5:1759:G:O6	77:A5:1773:U:O2	2.11	0.68
47:aa:65:PRO:CB	83:OO:129:ILE:CD1	2.70	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:VV:52:THR:HG23	64:AA:61:ALA:CA	2.23	0.67
64:AA:177:MET:SD	64:AA:178:LEU:HD13	2.35	0.67
80:B2:1454:A:N6	84:RR:3:ARG:NE	2.42	0.67
48:CC:270:THR:HG21	64:AA:95:GLY:HA3	1.77	0.67
62:gg:36:ARG:CD	84:RR:33:ARG:HD2	2.14	0.67
80:B2:944:A:H5'	83:OO:134:PRO:HB3	1.76	0.67
80:B2:989:C:H3'	82:BB:116:LYS:HZ2	1.59	0.67
80:B2:1722:G:O6	80:B2:1812:U:O2	2.11	0.67
81:A6:4099:G:O4'	82:BB:224:GLU:CD	2.37	0.67
47:aa:26:CYS:CB	83:OO:149:ARG:HB2	2.25	0.67
49:EE:44:LEU:HD11	49:EE:72:ILE:HD11	1.75	0.67
64:AA:214:GLU:CG	84:RR:80:ARG:CA	2.71	0.67
80:B2:1121:G:H4'	82:BB:160:GLN:NE2	2.09	0.67
30:f:58:VAL:N	81:A6:4945:G:C5	2.62	0.67
40:p:41:PHE:CE2	44:u:51:ASN:HB3	2.30	0.67
44:u:81:LEU:C	44:u:81:LEU:HD23	2.19	0.67
47:aa:58:VAL:C	83:OO:126:ILE:HB	2.12	0.67
64:AA:84:GLN:N	64:AA:207:PRO:CG	2.58	0.67
64:AA:180:ARG:HD2	64:AA:195:TRP:CZ2	2.18	0.67
80:B2:1466:G:C4'	84:RR:4:VAL:CA	2.72	0.67
2:B:217:ILE:HD12	2:B:347:LEU:HD12	1.75	0.67
6:E:99:VAL:HG23	77:A5:685:C:OP1	1.93	0.67
47:aa:68:TYR:O	83:OO:106:LYS:HB2	1.95	0.67
6:E:104:ASN:HB3	77:A5:684:G:H2'	1.76	0.67
17:Q:84:GLY:H	17:Q:103:LEU:HD13	1.59	0.67
37:m:82:LEU:HD12	37:m:85:LEU:HD23	1.77	0.67
47:aa:26:CYS:CB	83:OO:149:ARG:CA	2.54	0.67
56:VV:28:ASP:H	64:AA:141:ASN:H	1.42	0.67
80:B2:1463:U:HO2'	84:RR:63:ARG:NH1	1.88	0.67
40:p:41:PHE:CZ	44:u:51:ASN:CA	2.78	0.67
12:L:182:LEU:HD11	26:a:146:LEU:HD11	1.77	0.67
47:aa:66:LYS:NZ	82:BB:108:ASP:H	1.93	0.67
80:B2:969:U:OP2	82:BB:8:ARG:CD	2.43	0.67
80:B2:1466:G:C5'	84:RR:5:ARG:HG3	2.24	0.67
47:aa:65:PRO:CD	83:OO:129:ILE:HD11	2.25	0.67
56:VV:59:ILE:HD12	64:AA:154:LEU:HD21	1.77	0.67
80:B2:110:U:O2	80:B2:351:G:N2	2.28	0.67
44:u:54:ALA:CA	81:A6:4120:U:C5	2.78	0.66
47:aa:54:SER:N	83:OO:117:ARG:NH2	2.42	0.66
64:AA:176:TRP:CD1	64:AA:180:ARG:HD3	2.30	0.66
64:AA:213:GLU:O	84:RR:83:ASN:O	2.05	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:gg:280:LYS:HB2	84:RR:59:LYS:HE2	1.73	0.66
47:aa:53:ILE:HD13	83:OO:116:LEU:CG	2.24	0.66
56:VV:54:ALA:HB2	64:AA:64:ALA:HB1	1.75	0.66
84:RR:69:ILE:HD13	84:RR:71:ILE:HD11	1.77	0.66
62:gg:279:SER:HB2	84:RR:63:ARG:CA	2.24	0.66
80:B2:968:U:H2'	82:BB:8:ARG:NH1	2.11	0.66
47:aa:54:SER:H	83:OO:117:ARG:HH22	1.41	0.66
47:aa:59:PHE:HB2	83:OO:126:ILE:HG22	1.68	0.66
83:OO:78:ALA:HB3	83:OO:118:ALA:HB3	1.78	0.66
64:AA:39:TYR:HB2	64:AA:48:ILE:HG21	1.78	0.66
77:A5:33:A:N7	77:A5:49:U:O2	2.28	0.66
80:B2:1113:A:C8	82:BB:146:ARG:NH2	2.63	0.66
15:O:126:VAL:HG21	81:A6:4762:A:H2'	1.77	0.66
47:aa:53:ILE:CG1	83:OO:116:LEU:HB2	2.24	0.66
61:ff:114:ILE:HD13	68:MM:68:LEU:HD12	1.78	0.66
62:gg:282:GLU:HG2	84:RR:26:ASN:H	1.61	0.66
80:B2:941:C:H5''	82:BB:136:ARG:NH1	2.10	0.66
80:B2:1466:G:H4'	84:RR:4:VAL:CA	2.25	0.66
56:VV:70:LEU:HB3	64:AA:53:ARG:CB	2.26	0.66
56:VV:73:ALA:HB3	64:AA:57:LYS:CG	2.26	0.66
64:AA:211:GLU:HG3	84:RR:81:ARG:CD	2.25	0.66
80:B2:956:G:C3'	82:BB:5:LYS:HB3	2.25	0.66
80:B2:974:C:H1'	83:OO:41:PHE:HE2	1.61	0.66
80:B2:1454:A:N6	84:RR:3:ARG:HD2	2.11	0.66
80:B2:1456:G:OP1	84:RR:55:THR:CA	2.43	0.66
80:B2:1869:A:C6	82:BB:114:VAL:HG12	2.30	0.66
6:E:104:ASN:N	77:A5:684:G:C4'	2.59	0.66
6:E:221:LYS:N	81:A6:4940:C:C2	2.63	0.66
45:bb:3:LEU:HD13	56:VV:71:ARG:HH21	1.60	0.66
48:CC:265:PRO:HG3	64:AA:68:ILE:HB	1.76	0.66
62:gg:212:LYS:HZ2	84:RR:22:THR:CG2	2.08	0.66
74:ZZ:48:VAL:HG22	74:ZZ:80:ARG:HD2	1.78	0.66
75:EF:427:VAL:HG13	75:EF:485:ILE:HG23	1.78	0.66
80:B2:1452:A:H2'	84:RR:44:LYS:HE2	1.76	0.66
81:A6:3927:U:O2	81:A6:4184:G:O6	2.14	0.66
6:E:221:LYS:CG	6:E:221:LYS:HB3	2.15	0.65
47:aa:56:ALA:C	83:OO:124:MET:HB3	2.21	0.65
47:aa:58:VAL:HG11	83:OO:125:LYS:HE2	1.78	0.65
62:gg:212:LYS:HZ2	84:RR:22:THR:HG22	1.57	0.65
64:AA:73:ASP:C	64:AA:96:ALA:HB3	2.22	0.65
30:f:58:VAL:HB	81:A6:4945:G:N9	2.09	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:VV:76:ASP:HB2	64:AA:56:GLU:O	1.96	0.65
64:AA:210:ILE:N	84:RR:81:ARG:CD	2.59	0.65
80:B2:1457:U:P	84:RR:55:THR:HG21	2.37	0.65
62:gg:17:TRP:HH2	84:RR:30:THR:CG2	1.97	0.65
64:AA:172:GLY:HA2	64:AA:203:PHE:CB	2.26	0.65
47:aa:53:ILE:HA	83:OO:120:ALA:HB2	0.65	0.65
47:aa:66:LYS:HD3	82:BB:108:ASP:HA	1.22	0.65
47:aa:22:ARG:HE	83:OO:141:ARG:HH12	1.43	0.65
47:aa:26:CYS:CA	83:OO:149:ARG:CG	2.68	0.65
56:VV:73:ALA:HB3	64:AA:57:LYS:HA	1.79	0.65
80:B2:957:A:C8	82:BB:5:LYS:CE	2.61	0.65
80:B2:1063:C:H4'	83:OO:150:ARG:HE	1.61	0.65
56:VV:29:HIS:H	64:AA:137:ALA:C	2.05	0.64
64:AA:213:GLU:OE2	84:RR:86:PRO:HD2	1.96	0.64
80:B2:941:C:C5'	82:BB:136:ARG:NH2	2.53	0.64
80:B2:956:G:C5'	82:BB:5:LYS:H	2.01	0.64
44:u:91:VAL:HG13	44:u:94:LEU:HD11	1.79	0.64
64:AA:195:TRP:CD1	64:AA:197:VAL:O	2.51	0.64
80:B2:1368:U:C1'	84:RR:4:VAL:HG11	2.26	0.64
81:A6:4098:A:C2	82:BB:224:GLU:OE2	2.50	0.64
64:AA:173:LEU:HD23	64:AA:174:MET:CA	2.27	0.64
77:A5:33:A:C8	77:A5:49:U:N3	2.65	0.64
62:gg:280:LYS:CD	84:RR:59:LYS:CD	2.63	0.64
62:gg:280:LYS:CG	84:RR:59:LYS:CG	2.76	0.64
64:AA:154:LEU:HD23	64:AA:155:ARG:N	2.13	0.64
76:Cc:15:G:N2	76:Cc:49:C:O2	2.29	0.64
64:AA:12:GLU:O	64:AA:13:GLU:C	2.41	0.64
64:AA:172:GLY:HA2	64:AA:203:PHE:HB2	1.80	0.64
80:B2:956:G:C4'	82:BB:5:LYS:HB3	2.27	0.64
62:gg:279:SER:HB2	84:RR:62:GLN:C	2.22	0.64
83:OO:31:CYS:HB3	83:OO:93:LEU:HD11	1.78	0.64
3:C:44:LEU:HD12	3:C:47:ASN:HD22	1.63	0.64
47:aa:51:ARG:HB3	83:OO:121:ARG:HD2	1.79	0.64
47:aa:69:VAL:CG2	83:OO:106:LYS:H	2.07	0.64
47:aa:54:SER:H	83:OO:117:ARG:NH2	1.96	0.64
56:VV:49:GLN:C	64:AA:185:MET:HE2	2.22	0.64
56:VV:59:ILE:HG23	64:AA:154:LEU:HD23	1.80	0.64
44:u:27:TYR:CA	44:u:96:ILE:HA	2.28	0.64
9:H:41:ILE:HD13	9:H:73:ILE:HD11	1.79	0.63
47:aa:67:LEU:CD1	83:OO:108:PRO:HD2	2.22	0.63
75:EF:770:VAL:HG23	75:EF:784:VAL:HG13	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:B2:1468:C:P	84:RR:3:ARG:HG2	2.38	0.63
44:u:45:LEU:C	44:u:45:LEU:HD12	2.23	0.63
44:u:72:HIS:CD2	44:u:104:ILE:CG2	2.81	0.63
75:EF:16:LYS:HA	75:EF:19:ILE:HD12	1.80	0.63
56:VV:28:ASP:N	64:AA:141:ASN:H	1.95	0.63
64:AA:205:ARG:HH22	84:RR:83:ASN:N	1.92	0.63
64:AA:212:LYS:CE	84:RR:84:TYR:CZ	2.72	0.63
47:aa:58:VAL:CB	83:OO:125:LYS:CD	2.70	0.63
80:B2:1064:C:OP1	83:OO:150:ARG:O	2.16	0.63
57:WW:74:VAL:HG23	57:WW:126:LEU:O	1.99	0.63
81:A6:4100:C:H5'	82:BB:226:GLY:O	1.99	0.63
80:B2:956:G:C5'	82:BB:5:LYS:HB3	2.28	0.63
81:A6:2758:G:C2	81:A6:2766:A:N1	2.66	0.63
80:B2:974:C:C1'	83:OO:41:PHE:CE2	2.82	0.63
81:A6:2477:G:N2	81:A6:2501:C:O2	2.32	0.63
57:WW:4:MET:HE2	80:B2:1158:G:H21	1.62	0.63
57:WW:30:CYS:SG	57:WW:61:ILE:HD11	2.38	0.63
65:DD:66:ILE:HD11	65:DD:86:LEU:HB3	1.81	0.63
81:A6:2524:U:O2	81:A6:2529:A:N7	2.32	0.63
6:E:104:ASN:HB3	77:A5:684:G:C2'	2.29	0.62
6:E:221:LYS:CG	6:E:221:LYS:HB2	2.15	0.62
20:U:100:LEU:HD12	20:U:112:LEU:HB3	1.81	0.62
44:u:27:TYR:HA	44:u:96:ILE:HA	1.81	0.62
47:aa:65:PRO:CD	83:OO:129:ILE:CD1	2.77	0.62
64:AA:182:VAL:HG12	64:AA:186:ARG:HH22	1.62	0.62
81:A6:2552:G:C4	81:A6:2765:A:N6	2.67	0.62
47:aa:56:ALA:N	83:OO:120:ALA:C	2.56	0.62
80:B2:1368:U:C4'	84:RR:4:VAL:CG1	2.60	0.62
30:f:58:VAL:HA	81:A6:4945:G:N9	2.11	0.62
40:p:41:PHE:CD2	44:u:51:ASN:HB3	2.33	0.62
65:DD:66:ILE:HD12	65:DD:69:LEU:HD12	1.81	0.62
80:B2:1124:C:C5'	82:BB:150:ILE:CB	2.57	0.62
80:B2:1373:C:O3'	84:RR:7:LYS:CG	2.45	0.62
9:H:66:GLU:O	9:H:70:VAL:HG23	1.99	0.62
44:u:47:ILE:HB	44:u:94:LEU:HD12	1.81	0.62
56:VV:73:ALA:CB	64:AA:57:LYS:CA	2.78	0.62
64:AA:180:ARG:NE	64:AA:195:TRP:CH2	2.66	0.62
75:EF:264:ARG:O	75:EF:288:THR:HG22	1.99	0.62
80:B2:1452:A:C4'	84:RR:44:LYS:C	2.73	0.62
80:B2:1455:A:OP2	84:RR:54:VAL:N	2.30	0.62
56:VV:55:ILE:HG23	64:AA:158:ASP:HB3	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:gg:280:LYS:HA	84:RR:59:LYS:HA	1.80	0.62
62:gg:282:GLU:HG2	84:RR:26:ASN:CG	2.24	0.62
9:H:65:LYS:O	9:H:69:THR:HG23	1.99	0.62
49:EE:207:VAL:CG2	49:EE:219:ALA:HB1	2.30	0.62
80:B2:931:C:H5'	82:BB:157:GLN:OE1	1.99	0.62
81:A6:4098:A:H1'	82:BB:222:LYS:CE	2.30	0.62
3:C:44:LEU:HD11	77:A5:1373:A:H5''	1.80	0.62
56:VV:59:ILE:HA	64:AA:156:TYR:H	1.65	0.62
64:AA:80:ARG:HB3	64:AA:125:THR:HG21	1.82	0.62
80:B2:1112:U:C1'	82:BB:146:ARG:HD3	2.18	0.62
80:B2:1452:A:H5''	84:RR:44:LYS:C	2.25	0.62
15:O:191:LYS:O	15:O:195:VAL:HG23	2.00	0.62
44:u:22:MET:HG2	44:u:96:ILE:HD11	1.81	0.62
80:B2:1452:A:C4'	84:RR:45:LYS:HA	2.21	0.62
80:B2:1452:A:C5'	84:RR:44:LYS:O	2.44	0.62
11:J:87:LEU:HD21	11:J:166:PHE:CE1	2.35	0.62
56:VV:43:THR:HG23	56:VV:45:ARG:CG	2.29	0.62
62:gg:280:LYS:HA	84:RR:59:LYS:CB	2.29	0.62
80:B2:1454:A:N6	84:RR:3:ARG:CD	2.63	0.62
5:D:52:ILE:HG21	78:A7:6:C:H4'	1.81	0.62
17:Q:18:PRO:HG3	17:Q:29:VAL:HG21	1.81	0.62
56:VV:32:ILE:HG13	64:AA:145:ILE:H	1.65	0.62
56:VV:70:LEU:HA	64:AA:53:ARG:HB2	1.81	0.62
62:gg:281:ALA:HA	84:RR:26:ASN:HD21	1.65	0.62
64:AA:74:VAL:HG13	64:AA:121:LEU:N	2.15	0.62
6:E:105:GLY:N	77:A5:684:G:C3'	2.63	0.61
77:A5:59:A:N7	77:A5:337:U:O2	2.32	0.61
77:A5:980:U:C1'	77:A5:980:U:O4'	2.48	0.61
80:B2:1455:A:C4	84:RR:28:PHE:CG	2.81	0.61
81:A6:4100:C:H5'	82:BB:226:GLY:CA	2.30	0.61
64:AA:74:VAL:C	64:AA:91:ALA:HB3	2.25	0.61
80:B2:975:G:H5'	83:OO:32:HIS:CE1	2.34	0.61
80:B2:1454:A:H61	84:RR:3:ARG:CZ	2.10	0.61
81:A6:2477:G:H1	81:A6:2500:U:H3	1.47	0.61
29:e:99:ILE:HG21	29:e:108:ARG:HG2	1.80	0.61
40:p:41:PHE:CE2	44:u:51:ASN:HA	2.34	0.61
56:VV:58:ALA:O	56:VV:59:ILE:HD13	2.00	0.61
56:VV:66:ASP:O	56:VV:70:LEU:HD23	2.01	0.61
77:A5:1545:G:N2	77:A5:1615:C:C2	2.68	0.61
81:A6:4100:C:H5'	82:BB:226:GLY:C	2.25	0.61
5:D:153:THR:HG21	81:A6:4323:A:N1	2.16	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:EF:524:LEU:HD23	75:EF:561:LEU:HD11	1.81	0.61
80:B2:956:G:H5''	82:BB:5:LYS:CB	2.30	0.61
81:A6:3918:G:C6	81:A6:4383:U:O2	2.53	0.61
82:BB:115:LYS:CB	82:BB:115:LYS:HA	2.30	0.61
3:C:32:ILE:HG22	3:C:34:PRO:HD3	1.81	0.61
47:aa:29:CYS:HB3	83:OO:146:ARG:NH2	2.15	0.61
64:AA:58:LEU:HD21	64:AA:177:MET:HE2	1.82	0.61
75:EF:755:VAL:HG13	75:EF:804:THR:HG22	1.82	0.61
80:B2:956:G:C5'	82:BB:3:VAL:HA	2.30	0.61
7:F:132:LEU:HD21	7:F:141:TRP:NE1	2.15	0.61
44:u:47:ILE:CG2	44:u:81:LEU:HD21	2.29	0.61
47:aa:53:ILE:HA	83:OO:120:ALA:CA	2.29	0.61
56:VV:29:HIS:CB	64:AA:137:ALA:HB1	2.29	0.61
56:VV:54:ALA:HB2	64:AA:64:ALA:CB	2.30	0.61
64:AA:210:ILE:CB	84:RR:81:ARG:CZ	2.79	0.61
77:A5:310:G:O6	77:A5:327:U:C2	2.53	0.61
80:B2:155:G:O6	80:B2:163:U:O2	2.19	0.61
80:B2:956:G:H5''	82:BB:5:LYS:HB3	1.83	0.61
81:A6:4098:A:H2'	82:BB:224:GLU:OE1	2.00	0.61
44:u:89:TYR:CE2	81:A6:2660:A:C6	2.89	0.61
47:aa:65:PRO:HG3	83:OO:129:ILE:HD13	1.81	0.61
19:T:45:MET:HE1	19:T:94:GLU:O	2.00	0.61
56:VV:29:HIS:CA	64:AA:137:ALA:HB1	2.31	0.61
47:aa:22:ARG:HH22	83:OO:141:ARG:HG2	1.63	0.61
47:aa:27:ALA:CB	83:OO:143:LYS:O	2.47	0.61
47:aa:50:VAL:N	83:OO:117:ARG:HD2	2.14	0.61
56:VV:55:ILE:HG23	64:AA:158:ASP:CB	2.30	0.61
56:VV:69:ILE:HA	64:AA:57:LYS:NZ	2.15	0.61
80:B2:957:A:N7	82:BB:5:LYS:HE3	2.14	0.61
47:aa:22:ARG:NH1	83:OO:142:ARG:N	2.48	0.61
56:VV:55:ILE:HB	64:AA:143:PRO:HG3	1.83	0.61
56:VV:65:SER:HB2	64:AA:158:ASP:C	2.26	0.61
62:gg:281:ALA:HA	84:RR:26:ASN:ND2	2.16	0.61
80:B2:956:G:OP2	82:BB:5:LYS:N	2.34	0.61
44:u:21:VAL:HB	44:u:96:ILE:HD13	1.83	0.60
56:VV:59:ILE:HA	64:AA:156:TYR:N	2.16	0.60
75:EF:34:THR:OG1	75:EF:54:THR:HG21	1.99	0.60
17:Q:72:LEU:HD13	77:A5:1457:G:H5'	1.83	0.60
77:A5:86:U:O2	77:A5:98:A:N7	2.34	0.60
80:B2:1869:A:O3'	82:BB:115:LYS:CE	2.49	0.60
83:OO:31:CYS:CB	83:OO:93:LEU:HD11	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:u:26:LYS:C	44:u:96:ILE:HA	2.25	0.60
52:II:145:ILE:HG21	80:B2:190:G:H5''	1.83	0.60
72:TT:5:THR:HG23	72:TT:7:LYS:H	1.66	0.60
6:E:202:THR:HG21	13:M:107:PHE:CB	2.32	0.60
64:AA:18:PHE:CE1	64:AA:174:MET:HE3	2.37	0.60
64:AA:82:THR:O	64:AA:207:PRO:CG	2.49	0.60
64:AA:213:GLU:CD	84:RR:86:PRO:HD2	2.26	0.60
77:A5:1691:G:O6	77:A5:1845:U:O2	2.18	0.60
80:B2:1869:A:O3'	82:BB:115:LYS:NZ	2.34	0.60
14:N:172:ARG:CZ	14:N:174:LEU:HD11	2.31	0.60
20:U:39:PHE:HZ	20:U:87:THR:HG22	1.65	0.60
48:CC:258:GLU:HB3	64:AA:63:ARG:HH21	1.66	0.60
56:VV:50:PHE:HA	64:AA:62:ALA:HB1	1.83	0.60
62:gg:121:VAL:HG22	62:gg:156:PHE:CE2	2.37	0.60
64:AA:58:LEU:HD21	64:AA:177:MET:CE	2.31	0.60
80:B2:323:C:N3	80:B2:328:U:O4	2.35	0.60
80:B2:1063:C:C5'	83:OO:150:ARG:NH1	2.61	0.60
80:B2:1112:U:H1'	82:BB:146:ARG:CD	2.20	0.60
64:AA:177:MET:SD	64:AA:178:LEU:HD22	2.42	0.60
80:B2:1869:A:N7	82:BB:116:LYS:HG2	2.17	0.60
7:F:227:VAL:HA	18:S:39:VAL:HG22	1.82	0.60
10:I:4:ARG:HE	10:I:99:ILE:HD11	1.67	0.60
75:EF:79:TYR:HE1	75:EF:351:LEU:HD13	1.64	0.60
77:A5:352:G:H21	77:A5:360:A:N6	2.00	0.60
80:B2:1869:A:C2	82:BB:114:VAL:O	2.55	0.60
6:E:202:THR:HG21	13:M:107:PHE:HB3	1.83	0.60
47:aa:27:ALA:O	83:OO:145:GLY:O	2.19	0.60
64:AA:182:VAL:HG13	64:AA:186:ARG:HH22	1.65	0.60
80:B2:1123:C:H5''	82:BB:151:ARG:NH2	2.16	0.60
7:F:131:MET:O	7:F:135:VAL:HG22	2.00	0.60
30:f:104:MET:N	30:f:104:MET:HE2	2.17	0.60
43:t:84:ALA:HB1	43:t:104:ILE:HG23	1.84	0.60
56:VV:51:LYS:H	64:AA:62:ALA:HB3	1.67	0.60
77:A5:1072:C:H41	77:A5:1239:C:H41	1.48	0.60
80:B2:975:G:C5'	83:OO:32:HIS:ND1	2.65	0.60
31:g:96:LEU:HD11	44:u:55:LEU:CA	2.32	0.59
56:VV:52:THR:HG23	64:AA:61:ALA:HA	1.84	0.59
74:ZZ:68:ILE:HD13	74:ZZ:97:ILE:HG22	1.84	0.59
80:B2:961:G:O5'	83:OO:66:ARG:NH2	2.35	0.59
80:B2:1476:A:C5	84:RR:3:ARG:NH1	2.70	0.59
81:A6:4099:G:N9	82:BB:224:GLU:OE2	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:104:ASN:CB	77:A5:684:G:C2'	2.81	0.59
22:W:29:THR:HA	22:W:32:ILE:HD12	1.84	0.59
48:CC:169:TYR:OH	56:VV:9:VAL:HG11	2.02	0.59
57:WW:35:VAL:O	57:WW:39:THR:HG23	2.01	0.59
5:D:273:LEU:HD22	78:A7:108:G:P	2.42	0.59
20:U:43:LEU:HD23	20:U:86:LEU:HD21	1.84	0.59
48:CC:84:PHE:CD1	64:AA:67:ALA:HB3	2.37	0.59
62:gg:36:ARG:HD3	84:RR:33:ARG:HD2	1.84	0.59
80:B2:956:G:N7	82:BB:5:LYS:HG3	2.09	0.59
44:u:64:ALA:O	44:u:68:LYS:N	2.35	0.59
56:VV:59:ILE:HG23	64:AA:154:LEU:HG	1.84	0.59
56:VV:83:PHE:CE1	64:AA:50:ASN:HA	2.38	0.59
62:gg:280:LYS:CB	84:RR:59:LYS:CE	2.42	0.59
81:A6:2590:G:H21	81:A6:2755:A:H62	1.50	0.59
80:B2:941:C:H5'	82:BB:136:ARG:CZ	2.28	0.59
3:C:302:LEU:HD22	17:Q:38:ARG:HB2	1.83	0.59
7:F:86:PRO:O	7:F:124:LEU:HD12	2.03	0.59
7:F:153:ILE:HG21	7:F:190:ILE:HD11	1.84	0.59
14:N:193:ARG:O	14:N:197:THR:HG23	2.03	0.59
62:gg:79:LEU:HD22	62:gg:120:ILE:HD12	1.84	0.59
74:ZZ:48:VAL:C	74:ZZ:83:LEU:HD22	2.27	0.59
80:B2:1111:U:OP1	84:RR:124:VAL:CG1	2.49	0.59
6:E:104:ASN:O	77:A5:684:G:O4'	2.20	0.59
13:M:24:LEU:HD11	13:M:86:TRP:CG	2.38	0.59
44:u:89:TYR:HB3	81:A6:2673:G:H22	1.66	0.59
56:VV:33:GLN:O	64:AA:65:ILE:HD13	2.03	0.59
56:VV:48:GLY:C	64:AA:185:MET:SD	2.85	0.59
62:gg:279:SER:HB3	84:RR:63:ARG:CA	2.32	0.59
64:AA:210:ILE:CG2	84:RR:81:ARG:HD2	2.26	0.59
75:EF:395:MET:HE2	75:EF:418:SER:HB3	1.83	0.59
80:B2:969:U:C5	82:BB:8:ARG:CA	2.52	0.59
80:B2:1466:G:H5''	84:RR:5:ARG:HG3	1.81	0.59
9:H:69:THR:HG22	81:A6:4700:A:C2	2.37	0.59
15:O:87:MET:HE1	77:A5:1912:G:N2	2.13	0.59
43:t:144:ASP:OD2	43:t:151:ILE:HG21	2.02	0.59
48:CC:87:PRO:HA	64:AA:139:TYR:CB	2.33	0.59
56:VV:45:ARG:HB3	64:AA:191:ARG:HA	1.83	0.59
64:AA:34:MET:HE2	64:AA:53:ARG:HH12	1.67	0.59
64:AA:97:THR:HG21	64:AA:117:ARG:HH21	1.68	0.59
47:aa:59:PHE:HB2	83:OO:126:ILE:HG21	1.83	0.59
56:VV:40:ASP:CB	64:AA:191:ARG:NE	2.65	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:B2:1467:C:P	84:RR:3:ARG:CD	2.90	0.59
2:B:57:VAL:HG23	4:c:14:TYR:OH	2.03	0.59
80:B2:1454:A:O2'	84:RR:52:GLY:HA3	1.99	0.59
40:p:92:GLN:HB3	82:BB:134:LEU:HD22	1.84	0.58
62:gg:36:ARG:HD3	84:RR:33:ARG:CD	2.33	0.58
23:X:78:LYS:HD2	23:X:99:ILE:HG22	1.86	0.58
56:VV:60:ARG:HB2	64:AA:157:VAL:HB	1.84	0.58
80:B2:955:A:C2	82:BB:8:ARG:O	2.56	0.58
80:B2:975:G:H5''	83:OO:32:HIS:ND1	2.13	0.58
83:OO:115:ALA:O	83:OO:119:LEU:HD22	2.03	0.58
6:E:94:THR:HG22	6:E:111:LYS:HA	1.85	0.58
47:aa:29:CYS:HB2	83:OO:146:ARG:NE	2.18	0.58
56:VV:60:ARG:O	56:VV:61:ARG:C	2.46	0.58
64:AA:195:TRP:CD1	64:AA:197:VAL:C	2.81	0.58
80:B2:1050:A:H62	80:B2:1068:G:H21	1.50	0.58
33:i:33:LEU:HD23	33:i:38:LYS:HD2	1.84	0.58
56:VV:60:ARG:HH12	64:AA:134:LEU:HD13	1.68	0.58
62:gg:17:TRP:CZ3	84:RR:30:THR:HG23	2.30	0.58
64:AA:132:GLN:N	64:AA:133:PRO:HD2	2.18	0.58
75:EF:671:TYR:CE2	75:EF:675:ILE:HG23	2.38	0.58
80:B2:1452:A:C3'	84:RR:44:LYS:C	2.77	0.58
80:B2:1467:C:H3'	84:RR:3:ARG:HG2	1.85	0.58
36:l:13:LEU:HD22	81:A6:2407:G:H2'	1.85	0.58
56:VV:72:LEU:HB2	64:AA:57:LYS:NZ	2.19	0.58
74:ZZ:79:ILE:HB	74:ZZ:83:LEU:HD23	1.84	0.58
80:B2:1063:C:C3'	83:OO:150:ARG:CZ	2.81	0.58
81:A6:2845:A:N1	81:A6:3843:C:C4	2.71	0.58
81:A6:4936:G:H21	81:A6:4938:A:N6	2.01	0.58
2:B:389:MET:HE3	2:B:389:MET:O	2.03	0.58
48:CC:261:PHE:HB3	64:AA:66:VAL:HB	1.84	0.58
56:VV:51:LYS:N	64:AA:63:ARG:N	2.52	0.58
80:B2:931:C:H5''	82:BB:157:GLN:OE1	2.03	0.58
81:A6:2590:G:N2	81:A6:2755:A:H62	2.01	0.58
6:E:215:LEU:HD23	6:E:219:TYR:OH	2.04	0.58
47:aa:52:ASP:CA	83:OO:117:ARG:O	2.51	0.58
62:gg:36:ARG:CD	84:RR:33:ARG:CD	2.81	0.58
75:EF:24:VAL:HG12	75:EF:32:LYS:HD2	1.85	0.58
80:B2:1454:A:H4'	84:RR:48:ASN:O	2.04	0.58
9:H:92:MET:HE1	9:H:181:VAL:HG22	1.86	0.58
64:AA:214:GLU:OE2	84:RR:82:ASP:C	2.45	0.58
80:B2:1110:G:H21	82:BB:148:ASN:HD21	0.62	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:168:MET:HB3	2:B:171:LEU:HD12	1.86	0.58
56:VV:70:LEU:CA	64:AA:53:ARG:HB2	2.33	0.58
64:AA:195:TRP:CG	64:AA:197:VAL:O	2.57	0.58
30:f:48:ALA:HB1	30:f:69:VAL:CG2	2.34	0.58
80:B2:1063:C:O2'	83:OO:150:ARG:CZ	2.52	0.58
6:E:221:LYS:C	81:A6:4940:C:C4	2.82	0.57
47:aa:26:CYS:HB3	83:OO:149:ARG:O	2.02	0.57
56:VV:76:ASP:CB	64:AA:56:GLU:O	2.52	0.57
80:B2:974:C:H1'	83:OO:41:PHE:CE2	2.39	0.57
80:B2:983:A:C2	83:OO:140:THR:HG22	2.39	0.57
47:aa:28:ARG:CG	83:OO:147:ARG:O	2.51	0.57
80:B2:1869:A:N7	82:BB:116:LYS:N	2.51	0.57
43:t:45:ASP:OD1	43:t:71:ILE:HD13	2.04	0.57
56:VV:28:ASP:N	64:AA:141:ASN:N	2.50	0.57
56:VV:50:PHE:HA	64:AA:62:ALA:CB	2.34	0.57
57:WW:6:VAL:HG23	57:WW:34:ILE:HD11	1.86	0.57
62:gg:212:LYS:HZ3	84:RR:22:THR:CG2	2.16	0.57
64:AA:34:MET:CE	64:AA:53:ARG:HH22	2.18	0.57
76:Cc:55:U:C2	76:Cc:59:A:N7	2.73	0.57
80:B2:1113:A:H8	82:BB:146:ARG:HH21	1.48	0.57
80:B2:1544:C:O2	80:B2:1589:A:N6	2.38	0.57
9:H:118:LEU:HD11	9:H:167:VAL:HG22	1.86	0.57
64:AA:15:VAL:HG13	64:AA:19:LEU:HD12	1.86	0.57
3:C:263:LEU:HD23	3:C:273:LEU:HD22	1.87	0.57
47:aa:50:VAL:O	83:OO:117:ARG:NH1	2.38	0.57
76:Cc:23:G:N7	76:Cc:47:G:N2	2.48	0.57
4:c:3:VAL:HG13	4:c:15:PRO:HD3	1.85	0.57
44:u:49:ALA:HB1	44:u:74:TYR:C	2.29	0.57
64:AA:31:ASP:HB3	64:AA:34:MET:HB2	1.87	0.57
75:EF:423:THR:HG22	75:EF:450:THR:H	1.69	0.57
80:B2:1454:A:H62	84:RR:3:ARG:HD2	1.68	0.57
82:BB:115:LYS:CG	82:BB:115:LYS:HB3	2.19	0.57
80:B2:931:C:H4'	82:BB:157:GLN:OE1	2.05	0.57
80:B2:1103:C:H5''	82:BB:157:GLN:OE1	2.05	0.57
80:B2:1456:G:C8	84:RR:28:PHE:CG	2.93	0.57
1:A:80:GLU:O	1:A:98:ILE:HG21	2.05	0.57
25:Z:120:GLU:O	25:Z:124:THR:HG23	2.05	0.57
30:f:58:VAL:CG2	81:A6:4945:G:N7	2.68	0.57
44:u:61:GLU:O	44:u:64:ALA:HB3	2.05	0.57
52:II:31:ARG:NH2	52:II:48:VAL:HG12	2.20	0.57
64:AA:45:GLY:O	64:AA:46:ILE:C	2.46	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:B2:1466:G:P	84:RR:10:LYS:CD	2.89	0.57
30:f:58:VAL:CG1	81:A6:4945:G:N9	2.68	0.57
47:aa:63:VAL:HG22	83:OO:129:ILE:HG12	1.84	0.57
64:AA:145:ILE:HD13	64:AA:146:ALA:N	2.20	0.57
64:AA:180:ARG:O	64:AA:183:LEU:CA	2.53	0.57
64:AA:208:GLU:C	84:RR:81:ARG:NH2	2.63	0.57
81:A6:4095:G:O6	81:A6:4113:U:C2	2.57	0.57
44:u:64:ALA:HB1	44:u:69:THR:CB	2.31	0.56
56:VV:58:ALA:C	64:AA:156:TYR:HA	2.30	0.56
80:B2:1124:C:HO2'	84:RR:127:ASN:ND2	2.01	0.56
31:g:96:LEU:HD11	44:u:55:LEU:HB3	1.87	0.56
43:t:56:LEU:HD21	43:t:82:ILE:HG21	1.86	0.56
62:gg:281:ALA:C	84:RR:26:ASN:ND2	2.63	0.56
6:E:41:LYS:CA	77:A5:980:U:C2'	2.83	0.56
8:G:51:LEU:O	8:G:55:VAL:HG23	2.05	0.56
44:u:29:LEU:HD23	44:u:93:THR:O	2.06	0.56
56:VV:30:ALA:N	64:AA:137:ALA:CB	2.68	0.56
56:VV:43:THR:HG22	64:AA:191:ARG:O	2.05	0.56
56:VV:55:ILE:CG2	64:AA:158:ASP:HB2	2.35	0.56
56:VV:65:SER:HB2	64:AA:158:ASP:CA	2.36	0.56
80:B2:535:G:N2	80:B2:550:C:O2	2.37	0.56
80:B2:1063:C:C4'	83:OO:150:ARG:NE	2.55	0.56
5:D:118:ILE:HG23	5:D:135:ILE:HD11	1.86	0.56
44:u:45:LEU:HD11	44:u:47:ILE:HG13	1.86	0.56
56:VV:78:ILE:HD12	64:AA:59:LEU:CD1	2.34	0.56
62:gg:281:ALA:CA	84:RR:26:ASN:ND2	2.68	0.56
64:AA:212:LYS:HE2	84:RR:84:TYR:CE1	2.39	0.56
1:A:180:LEU:O	1:A:180:LEU:HD23	2.06	0.56
13:M:123:ILE:HD11	15:O:182:GLU:OE2	2.05	0.56
48:CC:198:ALA:HB1	48:CC:202:THR:HG21	1.87	0.56
56:VV:40:ASP:HB2	64:AA:191:ARG:NE	2.19	0.56
64:AA:211:GLU:O	84:RR:84:TYR:CD2	2.55	0.56
80:B2:1452:A:H4'	84:RR:44:LYS:C	2.30	0.56
64:AA:51:LEU:HD13	64:AA:55:TRP:CZ2	2.41	0.56
68:MM:52:LEU:HD21	68:MM:62:VAL:HG13	1.86	0.56
80:B2:1453:C:H3'	84:RR:49:LYS:HG2	1.86	0.56
80:B2:1455:A:H3'	84:RR:52:GLY:N	2.20	0.56
75:EF:428:ARG:HB3	75:EF:430:MET:HE3	1.88	0.56
80:B2:1467:C:C3'	84:RR:3:ARG:HG2	2.35	0.56
64:AA:23:THR:HG23	64:AA:164:ASN:HD22	1.69	0.56
64:AA:206:ASP:HB2	64:AA:209:GLU:HB3	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:B2:1455:A:H61	80:B2:1471:C:H42	1.52	0.56
80:B2:1456:G:H8	84:RR:28:PHE:CG	2.23	0.56
2:B:45:ALA:HB3	2:B:183:ILE:HD12	1.88	0.56
3:C:34:PRO:HA	3:C:37:VAL:HG22	1.87	0.56
77:A5:1106:A:H62	77:A5:1164:G:H21	1.53	0.56
80:B2:1124:C:C5'	82:BB:150:ILE:CA	2.84	0.56
43:t:121:LEU:HD22	77:A5:1972:G:O2'	2.06	0.56
44:u:81:LEU:HD22	44:u:91:VAL:O	2.05	0.56
51:HH:30:LEU:HD21	51:HH:36:LEU:HD12	1.88	0.56
5:D:64:ILE:CG1	5:D:105:LEU:HD21	2.36	0.55
80:B2:1110:G:C8	84:RR:126:MET:CE	2.89	0.55
7:F:156:ARG:HE	7:F:212:LEU:HD13	1.71	0.55
56:VV:39:VAL:HG22	56:VV:44:GLY:HA2	1.88	0.55
64:AA:84:GLN:CB	64:AA:207:PRO:HB3	2.28	0.55
64:AA:112:ILE:O	64:AA:113:GLN:C	2.50	0.55
64:AA:136:GLU:HB2	80:B2:1352:G:H5''	1.87	0.55
75:EF:423:THR:HG23	75:EF:462:GLU:CB	2.36	0.55
80:B2:1103:C:OP1	82:BB:157:GLN:CD	2.46	0.55
11:J:89:VAL:HG11	11:J:109:ILE:HD12	1.87	0.55
42:s:16:LYS:HZ2	42:s:54:LEU:HD11	1.71	0.55
57:WW:94:LEU:HD13	57:WW:100:GLY:O	2.06	0.55
64:AA:18:PHE:CZ	64:AA:177:MET:HE3	2.42	0.55
47:aa:59:PHE:CG	83:OO:126:ILE:C	2.47	0.55
64:AA:173:LEU:HD12	64:AA:176:TRP:CZ3	2.41	0.55
75:EF:731:ALA:HB2	75:EF:854:PHE:HB3	1.87	0.55
80:B2:955:A:C2	82:BB:8:ARG:C	2.85	0.55
80:B2:1121:G:H2'	82:BB:204:ILE:O	1.98	0.55
57:WW:60:LYS:O	57:WW:61:ILE:HD13	2.07	0.55
62:gg:280:LYS:CG	84:RR:59:LYS:CD	2.84	0.55
64:AA:140:VAL:HG12	64:AA:142:LEU:H	1.70	0.55
64:AA:176:TRP:CE2	64:AA:198:MET:HB2	2.42	0.55
21:V:32:THR:HG21	21:V:105:ILE:CG2	2.36	0.55
77:A5:684:G:O4'	77:A5:684:G:C4'	2.54	0.55
20:U:63:ILE:HD12	20:U:72:VAL:HG22	1.89	0.55
44:u:89:TYR:CD2	81:A6:2660:A:C6	2.94	0.55
47:aa:43:ASN:HB3	47:aa:45:VAL:HG22	1.88	0.55
48:CC:87:PRO:HG3	56:VV:29:HIS:CE1	2.42	0.55
57:WW:6:VAL:CG2	57:WW:34:ILE:HD11	2.36	0.55
64:AA:198:MET:SD	64:AA:199:PRO:HD3	2.47	0.55
75:EF:228:PHE:HA	75:EF:231:MET:HE3	1.88	0.55
83:OO:54:CYS:SG	83:OO:81:VAL:HG12	2.47	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:44:LEU:HD11	77:A5:1373:A:C5'	2.36	0.55
6:E:128:LEU:HB2	77:A5:959:G:H21	1.71	0.55
13:M:126:GLU:OE1	15:O:181:ALA:HB1	2.07	0.55
44:u:49:ALA:HB2	44:u:74:TYR:HB3	1.89	0.55
51:HH:30:LEU:HD22	51:HH:40:LEU:HD11	1.88	0.55
64:AA:10:MET:HE3	64:AA:15:VAL:HG23	1.87	0.55
64:AA:136:GLU:O	64:AA:137:ALA:C	2.46	0.55
75:EF:224:THR:HG21	75:EF:353:MET:HE2	1.89	0.55
56:VV:60:ARG:HD2	64:AA:160:ALA:HB2	1.89	0.55
56:VV:64:GLU:CD	64:AA:32:PHE:CD2	2.85	0.55
28:d:90:ARG:HD2	28:d:102:LEU:HD13	1.88	0.55
56:VV:67:ASP:HB2	64:AA:33:GLN:CD	2.32	0.55
56:VV:70:LEU:CB	64:AA:53:ARG:HB2	2.37	0.55
75:EF:429:ILE:C	75:EF:430:MET:HE2	2.32	0.55
80:B2:1453:C:O2'	84:RR:47:ARG:O	2.14	0.55
81:A6:4099:G:C4'	82:BB:227:LYS:CG	2.61	0.55
7:F:178:LEU:HD12	7:F:189:LEU:HD21	1.89	0.54
48:CC:87:PRO:HA	64:AA:139:TYR:HB3	1.88	0.54
51:HH:36:LEU:HD13	51:HH:75:ILE:HD12	1.89	0.54
56:VV:33:GLN:HE21	64:AA:142:LEU:HD13	1.72	0.54
56:VV:82:ASN:C	64:AA:52:LYS:HD2	2.33	0.54
80:B2:1063:C:O3'	83:OO:150:ARG:NE	2.40	0.54
80:B2:1111:U:C2	82:BB:148:ASN:ND2	2.66	0.54
80:B2:1120:U:O2	82:BB:204:ILE:HA	2.07	0.54
80:B2:1453:C:OP1	84:RR:44:LYS:CA	2.55	0.54
80:B2:1544:C:N3	80:B2:1589:A:N7	2.54	0.54
82:BB:82:ARG:HB3	82:BB:103:MET:HE1	1.88	0.54
27:b:32:LEU:HD22	77:A5:1464:C:H5''	1.89	0.54
56:VV:52:THR:CA	64:AA:61:ALA:HA	2.37	0.54
56:VV:52:THR:H	64:AA:63:ARG:HB3	1.72	0.54
56:VV:52:THR:OG1	64:AA:61:ALA:C	2.50	0.54
56:VV:68:SER:O	56:VV:69:ILE:C	2.49	0.54
64:AA:200:ASP:HA	64:AA:203:PHE:HB3	1.89	0.54
77:A5:1539:G:O6	77:A5:1620:U:O2	2.25	0.54
80:B2:975:G:C4'	83:OO:43:HIS:ND1	2.70	0.54
81:A6:2890:C:H42	81:A6:3611:A:H61	1.56	0.54
47:aa:56:ALA:H	83:OO:120:ALA:CB	2.09	0.54
53:JJ:53:ILE:CD1	53:JJ:81:LEU:HD21	2.37	0.54
64:AA:39:TYR:HB3	64:AA:48:ILE:HG21	1.87	0.54
80:B2:944:A:C2	83:OO:140:THR:HG21	2.42	0.54
2:B:389:MET:HE1	81:A6:5041:G:C4	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:VV:40:ASP:HB2	64:AA:191:ARG:HE	1.73	0.54
77:A5:1183:C:N3	77:A5:1184:A:N7	2.55	0.54
80:B2:1124:C:H5''	82:BB:150:ILE:CA	2.36	0.54
81:A6:5023:C:H42	81:A6:5028:G:H21	1.54	0.54
32:h:41:ALA:HA	32:h:44:LEU:HD12	1.90	0.54
42:s:16:LYS:NZ	42:s:54:LEU:HD11	2.23	0.54
44:u:18:LEU:HA	44:u:21:VAL:HG23	1.90	0.54
47:aa:28:ARG:HA	83:OO:147:ARG:CA	2.37	0.54
56:VV:58:ALA:C	64:AA:156:TYR:CA	2.81	0.54
80:B2:1110:G:H8	84:RR:126:MET:HE1	1.73	0.54
8:G:173:LEU:HD12	8:G:177:MET:HE1	1.88	0.54
34:j:64:MET:HE2	34:j:64:MET:H	1.71	0.54
45:bb:62:VAL:HG13	45:bb:74:THR:HG21	1.89	0.54
65:DD:101:GLN:HG3	65:DD:126:ILE:HD11	1.88	0.54
70:QQ:31:LEU:O	70:QQ:32:ILE:HD13	2.07	0.54
77:A5:1542:U:O2	77:A5:1617:G:O6	2.25	0.54
79:A8:70:G:H21	79:A8:88:A:H62	1.53	0.54
80:B2:1453:C:C4'	84:RR:47:ARG:N	2.68	0.54
80:B2:1461:G:H1	84:RR:56:HIS:HE2	1.55	0.54
6:E:42:GLY:CA	77:A5:980:U:O4'	2.56	0.54
47:aa:28:ARG:HG2	83:OO:146:ARG:O	2.08	0.54
47:aa:58:VAL:CG2	83:OO:125:LYS:HD3	2.38	0.54
49:EE:207:VAL:HG21	49:EE:219:ALA:HB1	1.88	0.54
64:AA:173:LEU:HA	64:AA:199:PRO:CB	2.37	0.54
9:H:150:ASP:O	9:H:154:VAL:HG23	2.08	0.54
23:X:99:ILE:HG23	23:X:133:GLU:CD	2.33	0.54
43:t:143:VAL:CG2	43:t:151:ILE:HD11	2.38	0.54
64:AA:74:VAL:HA	64:AA:119:PRO:HA	1.89	0.54
81:A6:4765:G:O6	81:A6:4869:U:O2	2.25	0.54
28:d:20:VAL:HG22	28:d:91:LYS:HA	1.89	0.54
30:f:48:ALA:HB2	30:f:71:TRP:CZ3	2.42	0.54
44:u:54:ALA:HA	81:A6:4120:U:C6	2.42	0.54
49:EE:219:ALA:HB3	80:B2:807:G:O2'	2.07	0.54
75:EF:10:ARG:HA	75:EF:13:MET:HE2	1.90	0.54
80:B2:1110:G:O2'	84:RR:125:GLY:N	2.24	0.54
3:C:196:MET:HE3	79:A8:22:U:H2'	1.89	0.54
71:SS:10:GLN:CD	71:SS:13:LEU:HD21	2.32	0.54
80:B2:1467:C:H3'	84:RR:3:ARG:CG	2.37	0.54
69:PP:111:MET:CE	71:SS:117:ILE:HD11	2.38	0.53
80:B2:185:G:C6	80:B2:214:U:O2	2.60	0.53
80:B2:969:U:P	82:BB:8:ARG:HD3	2.47	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:223:THR:HG23	2:B:275:HIS:O	2.07	0.53
4:c:3:VAL:HG11	4:c:12:LYS:HE3	1.90	0.53
17:Q:25:LEU:O	17:Q:29:VAL:HG23	2.09	0.53
29:e:99:ILE:HD11	29:e:112:VAL:CG1	2.38	0.53
44:u:21:VAL:HG21	44:u:45:LEU:CD2	2.39	0.53
44:u:27:TYR:HA	44:u:96:ILE:CA	2.38	0.53
47:aa:25:ASN:O	83:OO:149:ARG:CG	2.40	0.53
47:aa:53:ILE:HD13	83:OO:116:LEU:HD22	1.90	0.53
56:VV:15:ARG:HH12	56:VV:54:ALA:HB2	1.73	0.53
56:VV:38:GLU:N	64:AA:181:GLU:OE1	2.40	0.53
56:VV:51:LYS:O	64:AA:60:LEU:C	2.51	0.53
56:VV:83:PHE:CE2	64:AA:49:ILE:C	2.87	0.53
71:SS:118:ARG:HD2	71:SS:123:LEU:HD11	1.91	0.53
77:A5:1918:U:O2	77:A5:2064:G:O6	2.26	0.53
80:B2:1126:G:OP1	84:RR:129:LYS:HD3	2.07	0.53
13:M:58:THR:HG22	13:M:91:TRP:CZ3	2.43	0.53
15:O:124:LEU:HB2	15:O:127:VAL:HG12	1.90	0.53
64:AA:136:GLU:CG	80:B2:1352:G:H5''	2.38	0.53
80:B2:956:G:C3'	82:BB:5:LYS:CE	2.58	0.53
11:J:26:VAL:HG21	11:J:32:ARG:HB3	1.91	0.53
58:XX:105:PHE:CG	58:XX:112:VAL:HG21	2.44	0.53
64:AA:36:GLN:C	64:AA:37:TYR:CD2	2.87	0.53
75:EF:613:LEU:HD13	75:EF:635:LEU:HD22	1.90	0.53
80:B2:110:U:O2	80:B2:351:G:C2	2.61	0.53
80:B2:1120:U:C2	82:BB:204:ILE:HA	2.44	0.53
80:B2:1124:C:C5'	82:BB:150:ILE:N	2.67	0.53
80:B2:1452:A:H4'	84:RR:48:ASN:ND2	2.13	0.53
81:A6:2845:A:N6	81:A6:3843:C:C2	2.75	0.53
25:Z:95:VAL:HG13	25:Z:96:VAL:HG23	1.91	0.53
48:CC:273:LEU:HG	64:AA:71:PRO:HB2	1.90	0.53
64:AA:180:ARG:NE	64:AA:195:TRP:CZ3	2.76	0.53
26:a:112:LEU:HD23	77:A5:1387:A:N6	2.24	0.53
29:e:78:LEU:HD21	81:A6:2324:C:H4'	1.90	0.53
56:VV:55:ILE:HG22	64:AA:158:ASP:HB2	1.89	0.53
62:gg:79:LEU:CD2	62:gg:120:ILE:HD12	2.38	0.53
74:ZZ:50:PHE:HD1	74:ZZ:54:THR:HG22	1.73	0.53
80:B2:1122:A:H4'	82:BB:205:TYR:CE1	2.44	0.53
80:B2:1464:C:C4'	84:RR:60:ARG:NH1	2.71	0.53
82:BB:125:VAL:HG22	82:BB:172:MET:HE2	1.91	0.53
17:Q:34:PHE:CD1	77:A5:2088:C:C5	2.97	0.53
44:u:45:LEU:HD12	44:u:46:VAL:N	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:VV:59:ILE:N	64:AA:157:VAL:N	2.57	0.53
75:EF:225:LEU:HD11	75:EF:260:LEU:HD13	1.90	0.53
80:B2:1458:G:P	84:RR:59:LYS:HE2	2.47	0.53
6:E:52:LEU:HD22	6:E:58:ARG:HA	1.91	0.53
21:V:65:VAL:HG11	21:V:72:LEU:HG	1.90	0.53
47:aa:54:SER:HB2	83:OO:121:ARG:HH22	1.72	0.53
64:AA:19:LEU:HD21	84:RR:109:LEU:HD11	1.90	0.53
64:AA:63:ARG:NH1	64:AA:64:ALA:HB2	2.24	0.53
77:A5:1591:U:H5	81:A6:4527:G:H21	1.57	0.53
79:A8:70:G:N2	79:A8:88:A:H62	2.07	0.53
81:A6:4098:A:C2'	82:BB:224:GLU:OE1	2.57	0.53
9:H:111:LEU:HD21	9:H:125:ARG:NH1	2.24	0.53
15:O:194:ASP:O	15:O:198:THR:HG23	2.09	0.53
47:aa:58:VAL:CG1	83:OO:125:LYS:HE2	2.29	0.53
58:XX:105:PHE:HB3	58:XX:112:VAL:HG11	1.90	0.53
81:A6:2312:U:O2	81:A6:2326:G:C6	2.62	0.53
9:H:147:GLU:OE1	9:H:187:VAL:HG22	2.09	0.53
29:e:79:VAL:HG21	29:e:85:LEU:HB3	1.91	0.53
47:aa:46:GLU:CB	83:OO:113:GLN:HE21	1.93	0.53
49:EE:151:ASP:HB3	49:EE:154:ILE:HD12	1.91	0.53
56:VV:30:ALA:N	64:AA:137:ALA:HB1	2.23	0.53
64:AA:97:THR:H	64:AA:117:ARG:HB3	1.74	0.53
64:AA:214:GLU:OE2	84:RR:82:ASP:CA	2.56	0.53
66:FF:39:ILE:HD11	66:FF:116:ILE:HG21	1.91	0.53
66:FF:112:LEU:CD2	66:FF:177:LEU:HD22	2.39	0.53
75:EF:228:PHE:HE2	75:EF:297:ILE:HD11	1.74	0.53
80:B2:1456:G:C8	84:RR:28:PHE:HB2	2.37	0.53
44:u:29:LEU:HG	44:u:94:LEU:HA	1.91	0.52
47:aa:56:ALA:CA	83:OO:124:MET:HB3	2.39	0.52
56:VV:78:ILE:HG21	64:AA:55:TRP:HB3	1.91	0.52
75:EF:524:LEU:HD23	75:EF:561:LEU:CD1	2.39	0.52
80:B2:1463:U:H6	84:RR:63:ARG:CZ	2.06	0.52
15:O:79:ILE:O	15:O:83:THR:HG23	2.08	0.52
20:U:23:LEU:HD21	20:U:87:THR:HG21	1.92	0.52
47:aa:67:LEU:HD12	83:OO:108:PRO:CD	2.28	0.52
56:VV:33:GLN:HE21	64:AA:142:LEU:CD1	2.21	0.52
80:B2:1110:G:C8	84:RR:126:MET:HE1	2.44	0.52
5:D:106:ALA:HB1	5:D:171:LEU:HD13	1.92	0.52
12:L:79:GLU:O	12:L:83:VAL:HG23	2.08	0.52
41:r:89:THR:O	41:r:93:ILE:HD12	2.09	0.52
44:u:60:ILE:HA	44:u:63:TYR:HB2	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:u:61:GLU:O	44:u:65:MET:N	2.42	0.52
64:AA:213:GLU:N	84:RR:86:PRO:HD3	2.24	0.52
66:FF:156:THR:HG22	66:FF:159:ARG:HH12	1.74	0.52
74:ZZ:92:LEU:HD22	74:ZZ:109:TYR:HE2	1.75	0.52
75:EF:13:MET:HA	75:EF:19:ILE:HD11	1.92	0.52
80:B2:944:A:H5''	83:OO:134:PRO:HB2	1.90	0.52
80:B2:1063:C:C1'	83:OO:150:ARG:NH1	2.70	0.52
80:B2:1083:A:H62	80:B2:1841:C:H1'	1.75	0.52
22:W:128:LYS:NZ	81:A6:2666:G:O6	2.39	0.52
80:B2:1453:C:O2'	84:RR:46:LEU:O	2.23	0.52
83:OO:57:THR:HG22	83:OO:60:MET:SD	2.49	0.52
8:G:147:VAL:HG22	8:G:179:VAL:HG11	1.91	0.52
25:Z:5:MET:HE1	44:u:65:MET:HG2	1.91	0.52
40:p:41:PHE:CD1	44:u:51:ASN:OD1	2.62	0.52
64:AA:176:TRP:CD1	64:AA:180:ARG:CD	2.93	0.52
70:QQ:89:SER:O	70:QQ:93:VAL:HG23	2.10	0.52
73:UU:64:THR:HG21	80:B2:1668:U:H4'	1.92	0.52
75:EF:66:ARG:HG3	75:EF:68:ILE:HG23	1.92	0.52
77:A5:420:A:H61	79:A8:14:U:H3	1.57	0.52
2:B:252:ALA:HB1	81:A6:4524:G:C2	2.44	0.52
6:E:221:LYS:CG	81:A6:4940:C:C5	2.92	0.52
36:l:46:ARG:NH1	36:l:47:THR:HG22	2.24	0.52
47:aa:53:ILE:H	83:OO:117:ARG:NE	2.08	0.52
48:CC:261:PHE:CE2	64:AA:64:ALA:HA	2.44	0.52
49:EE:183:VAL:HG13	49:EE:220:THR:HG21	1.92	0.52
50:GG:3:LEU:HD12	50:GG:111:LEU:HD23	1.92	0.52
64:AA:172:GLY:CA	64:AA:203:PHE:HB2	2.39	0.52
64:AA:180:ARG:O	64:AA:183:LEU:N	2.42	0.52
75:EF:260:LEU:HD22	75:EF:293:ILE:HD11	1.91	0.52
80:B2:968:U:C3'	82:BB:8:ARG:HH11	2.11	0.52
80:B2:1467:C:C5'	84:RR:3:ARG:CB	2.85	0.52
30:f:100:ARG:O	30:f:101:ILE:HD13	2.09	0.52
47:aa:66:LYS:HZ1	82:BB:108:ASP:H	1.57	0.52
77:A5:1298:C:H5''	81:A6:4945:G:H22	1.75	0.52
82:BB:52:THR:HG23	82:BB:57:ILE:HA	1.92	0.52
46:ee:83:VAL:HG13	80:B2:617:G:OP1	2.10	0.52
77:A5:379:G:O6	79:A8:22:U:O4	2.27	0.52
80:B2:191:A:H62	80:B2:208:G:H21	1.58	0.52
80:B2:359:U:O2	80:B2:403:G:O6	2.28	0.52
80:B2:1166:G:C6	80:B2:1193:U:O2	2.63	0.52
82:BB:105:LEU:HD22	82:BB:109:LYS:HG2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:i:34:THR:HG21	77:A5:275:C:O5'	2.09	0.52
49:EE:72:ILE:HD13	49:EE:82:TYR:CD2	2.45	0.52
56:VV:29:HIS:HB3	64:AA:137:ALA:CB	2.39	0.52
58:XX:55:VAL:HG12	58:XX:71:ARG:HH12	1.73	0.52
64:AA:176:TRP:NE1	64:AA:180:ARG:NH2	2.57	0.52
64:AA:189:ILE:HG12	64:AA:195:TRP:CD1	2.44	0.52
64:AA:210:ILE:CG1	84:RR:81:ARG:O	2.51	0.52
67:KK:15:LEU:HD23	67:KK:15:LEU:O	2.10	0.52
70:QQ:77:HIS:CE1	80:B2:1590:C:H42	2.28	0.52
78:A7:83:A:N1	78:A7:93:G:O6	2.43	0.52
80:B2:1455:A:H3'	84:RR:52:GLY:CA	2.39	0.52
29:e:29:VAL:HG11	77:A5:420:A:H5''	1.92	0.52
30:f:27:LEU:HD13	30:f:78:HIS:NE2	2.25	0.52
34:j:64:MET:HE2	34:j:64:MET:N	2.25	0.52
47:aa:55:GLU:O	83:OO:123:GLY:C	2.53	0.52
62:gg:83:TRP:CZ3	84:RR:33:ARG:NH1	2.78	0.52
64:AA:135:THR:O	64:AA:136:GLU:C	2.52	0.52
66:FF:152:TRP:O	66:FF:156:THR:HG23	2.09	0.52
80:B2:1456:G:O3'	84:RR:27:ASP:CA	2.51	0.52
84:RR:98:VAL:HG12	84:RR:102:THR:HG21	1.91	0.52
6:E:104:ASN:O	77:A5:684:G:C1'	2.57	0.51
44:u:72:HIS:O	44:u:73:HIS:CG	2.63	0.51
44:u:81:LEU:CD2	44:u:91:VAL:HG12	2.40	0.51
64:AA:40:LYS:CE	84:RR:104:GLU:OE1	2.39	0.51
64:AA:80:ARG:CB	64:AA:125:THR:HG21	2.40	0.51
64:AA:183:LEU:HD11	64:AA:202:TYR:OH	2.10	0.51
64:AA:201:LEU:HB3	64:AA:202:TYR:CZ	2.44	0.51
10:I:90:ARG:O	10:I:91:LEU:HD22	2.10	0.51
62:gg:235:ILE:HG12	84:RR:22:THR:O	2.10	0.51
64:AA:180:ARG:O	64:AA:184:ARG:N	2.43	0.51
64:AA:211:GLU:CG	84:RR:81:ARG:HG3	2.28	0.51
80:B2:956:G:H5'	82:BB:3:VAL:HA	1.92	0.51
80:B2:1123:C:C5'	82:BB:151:ARG:NH2	2.72	0.51
80:B2:1375:G:OP1	84:RR:67:ARG:NH2	2.43	0.51
26:a:43:ILE:HD11	77:A5:1682:A:N3	2.26	0.51
26:a:112:LEU:HD23	77:A5:1387:A:C6	2.45	0.51
44:u:47:ILE:O	44:u:93:THR:HA	2.11	0.51
64:AA:162:PRO:C	64:AA:163:CYS:SG	2.93	0.51
72:TT:28:LEU:HD23	72:TT:54:TYR:CE2	2.46	0.51
77:A5:40:G:H21	81:A6:4380:A:H62	1.57	0.51
80:B2:1111:U:P	84:RR:124:VAL:HG21	2.14	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:BB:133:TYR:CE2	82:BB:181:LEU:HD22	2.45	0.51
9:H:161:ILE:O	9:H:165:THR:HG22	2.09	0.51
30:f:33:VAL:HG11	30:f:42:TYR:CE1	2.45	0.51
44:u:21:VAL:HG22	44:u:102:SER:OG	2.11	0.51
5:D:109:LEU:HD21	5:D:142:PHE:CE2	2.46	0.51
47:aa:59:PHE:N	83:OO:126:ILE:CB	2.11	0.51
50:GG:7:PHE:CE2	50:GG:9:ALA:HB3	2.45	0.51
53:JJ:144:ILE:HD12	80:B2:521:A:O2'	2.09	0.51
62:gg:279:SER:O	84:RR:62:GLN:CD	2.54	0.51
64:AA:107:THR:HG23	64:AA:115:ALA:C	2.36	0.51
64:AA:174:MET:O	64:AA:175:TRP:C	2.53	0.51
77:A5:1934:A:N1	77:A5:2052:G:O6	2.43	0.51
80:B2:984:C:O2	83:OO:138:ASP:OD1	2.29	0.51
6:E:153:LEU:HD23	6:E:199:ALA:HA	1.93	0.51
43:t:114:ARG:NH2	43:t:125:LEU:HD22	2.26	0.51
49:EE:72:ILE:HD12	49:EE:77:ARG:HG2	1.93	0.51
64:AA:44:ASP:O	64:AA:45:GLY:C	2.51	0.51
64:AA:90:PHE:CE1	64:AA:179:ALA:HB1	2.46	0.51
68:MM:41:ALA:HB3	68:MM:110:VAL:HG21	1.92	0.51
81:A6:3918:G:O6	81:A6:4383:U:C2	2.63	0.51
3:C:54:VAL:HG13	3:C:105:THR:OG1	2.10	0.51
53:JJ:130:ILE:HG13	53:JJ:135:ILE:HD13	1.91	0.51
80:B2:1457:U:P	84:RR:55:THR:HG23	2.50	0.51
80:B2:1467:C:P	84:RR:3:ARG:HD2	2.50	0.51
9:H:80:MET:HE2	9:H:80:MET:HA	1.93	0.51
10:I:43:VAL:HG21	10:I:197:VAL:CG1	2.40	0.51
34:j:59:THR:HG23	79:A8:41:A:O3'	2.11	0.51
41:r:32:LEU:HD23	41:r:106:LEU:HD12	1.93	0.51
47:aa:55:GLU:H	83:OO:120:ALA:HB1	1.75	0.51
47:aa:69:VAL:HA	83:OO:106:LYS:HB2	1.91	0.51
53:JJ:46:VAL:HG21	53:JJ:106:LEU:CD2	2.40	0.51
56:VV:45:ARG:HD2	64:AA:195:TRP:HB2	1.93	0.51
58:XX:133:LEU:HD23	58:XX:138:LYS:O	2.11	0.51
62:gg:280:LYS:CG	84:RR:59:LYS:HD3	2.37	0.51
77:A5:1550:G:O6	77:A5:1578:U:C4	2.64	0.51
80:B2:944:A:C5'	83:OO:134:PRO:HB2	2.41	0.51
6:E:221:LYS:CB	6:E:221:LYS:CD	2.80	0.51
17:Q:34:PHE:CD1	77:A5:2088:C:H5	2.29	0.51
42:s:65:ILE:HG13	42:s:75:LEU:HD23	1.93	0.51
56:VV:60:ARG:H	64:AA:155:ARG:C	2.18	0.51
64:AA:31:ASP:O	64:AA:32:PHE:C	2.49	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:AA:160:ALA:O	64:AA:161:ILE:C	2.53	0.51
75:EF:452:LEU:HD13	75:EF:461:ILE:HB	1.92	0.51
80:B2:1373:C:C3'	84:RR:7:LYS:NZ	2.54	0.51
81:A6:4098:A:H1'	82:BB:222:LYS:NZ	2.26	0.51
14:N:134:LEU:O	14:N:135:ILE:HD13	2.11	0.51
44:u:78:ASN:O	44:u:79:ILE:C	2.54	0.51
54:LL:18:GLN:HB3	54:LL:33:LEU:HD11	1.91	0.51
62:gg:206:LEU:HD22	62:gg:227:LEU:HD11	1.93	0.51
77:A5:1183:C:N4	77:A5:1184:A:N6	2.51	0.51
13:M:123:ILE:O	13:M:127:VAL:HG12	2.11	0.50
24:Y:79:VAL:O	24:Y:80:ILE:HD13	2.10	0.50
62:gg:280:LYS:HA	84:RR:59:LYS:CA	2.41	0.50
68:MM:24:THR:HA	68:MM:27:ILE:HD12	1.92	0.50
75:EF:496:VAL:HG12	75:EF:496:VAL:O	2.11	0.50
80:B2:1452:A:H4'	84:RR:44:LYS:O	2.10	0.50
80:B2:1453:C:C3'	84:RR:49:LYS:HG2	2.25	0.50
81:A6:4413:C:H5	81:A6:4429:C:H42	1.59	0.50
14:N:174:LEU:HD13	77:A5:62:A:C5'	2.41	0.50
17:Q:49:LYS:O	17:Q:53:MET:HE3	2.11	0.50
40:p:74:THR:O	40:p:78:THR:HG23	2.11	0.50
44:u:80:GLU:O	44:u:81:LEU:C	2.52	0.50
56:VV:72:LEU:HD12	64:AA:57:LYS:NZ	2.27	0.50
62:gg:212:LYS:CE	84:RR:22:THR:HG21	2.42	0.50
64:AA:172:GLY:HA3	64:AA:203:PHE:CD1	2.46	0.50
64:AA:184:ARG:HH22	64:AA:195:TRP:HZ3	1.57	0.50
64:AA:189:ILE:CG1	64:AA:195:TRP:CD1	2.94	0.50
80:B2:1121:G:H21	82:BB:206:PRO:CD	2.23	0.50
56:VV:12:TYR:O	56:VV:12:TYR:CG	2.64	0.50
58:XX:9:THR:HG22	80:B2:681:U:H4'	1.93	0.50
58:XX:91:LEU:HD13	58:XX:94:ILE:HD11	1.94	0.50
80:B2:1858:G:OP2	83:OO:146:ARG:CZ	2.59	0.50
2:B:57:VAL:HG23	4:c:14:TYR:CZ	2.46	0.50
16:P:115:GLU:OE2	16:P:151:THR:HG23	2.11	0.50
21:V:126:ALA:HB1	21:V:133:ALA:HB2	1.94	0.50
52:II:29:LEU:HD12	52:II:29:LEU:O	2.11	0.50
56:VV:51:LYS:HA	64:AA:63:ARG:HB3	1.93	0.50
56:VV:52:THR:OG1	64:AA:61:ALA:O	2.29	0.50
64:AA:193:HIS:O	64:AA:194:PRO:C	2.46	0.50
39:o:21:HIS:CB	39:o:70:LEU:HD12	2.42	0.50
44:u:27:TYR:O	44:u:27:TYR:CG	2.65	0.50
44:u:91:VAL:HG12	44:u:91:VAL:O	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:aa:67:LEU:HD22	83:OO:108:PRO:HG3	1.91	0.50
56:VV:36:VAL:H	64:AA:62:ALA:CB	2.25	0.50
56:VV:55:ILE:CG2	64:AA:158:ASP:CB	2.89	0.50
64:AA:34:MET:SD	64:AA:37:TYR:C	2.95	0.50
75:EF:763:LEU:CD2	75:EF:788:LEU:HD11	2.41	0.50
80:B2:956:G:N9	82:BB:5:LYS:HG2	2.10	0.50
44:u:27:TYR:N	44:u:96:ILE:HA	2.26	0.50
44:u:72:HIS:CD2	44:u:104:ILE:HG22	2.32	0.50
55:NN:102:LEU:HD13	55:NN:115:LEU:HD12	1.94	0.50
64:AA:211:GLU:O	84:RR:84:TYR:HB2	2.04	0.50
81:A6:4098:A:H1'	82:BB:222:LYS:HZ3	1.76	0.50
7:F:92:ILE:HD13	7:F:118:ASN:O	2.12	0.50
47:aa:53:ILE:CD1	83:OO:116:LEU:HD22	2.42	0.50
47:aa:53:ILE:CD1	83:OO:116:LEU:CD1	2.87	0.50
49:EE:72:ILE:HD12	49:EE:77:ARG:CG	2.41	0.50
54:LL:72:ILE:HD12	54:LL:128:VAL:O	2.11	0.50
54:LL:93:LEU:HD12	54:LL:102:PHE:HB3	1.94	0.50
75:EF:335:LEU:O	75:EF:339:VAL:HG23	2.12	0.50
81:A6:2556:G:C5	81:A6:2557:U:C5	3.00	0.50
7:F:240:ASN:HA	7:F:243:ILE:HD12	1.93	0.50
31:g:96:LEU:HD11	44:u:55:LEU:HA	1.94	0.50
43:t:125:LEU:HD11	43:t:164:ALA:HB3	1.93	0.50
64:AA:86:ALA:CB	64:AA:89:LYS:HG3	2.41	0.50
64:AA:87:VAL:HG13	64:AA:99:ILE:CA	2.42	0.50
64:AA:159:ILE:HD11	64:AA:161:ILE:HD11	1.94	0.50
66:FF:88:MET:HE2	80:B2:1591:C:H5''	1.94	0.50
80:B2:1329:U:C2	80:B2:1500:G:O6	2.65	0.50
43:t:81:ILE:HD13	43:t:136:ALA:CA	2.41	0.50
44:u:48:LEU:O	44:u:73:HIS:HA	2.12	0.50
49:EE:11:ARG:HA	49:EE:28:ALA:HB2	1.94	0.50
68:MM:102:LYS:CE	80:B2:1283:C:H42	2.25	0.50
75:EF:161:ASP:O	75:EF:165:LEU:HD23	2.11	0.50
77:A5:1887:G:H21	77:A5:1938:C:H42	1.60	0.50
80:B2:1869:A:N7	82:BB:116:LYS:CB	2.75	0.50
48:CC:270:THR:O	48:CC:270:THR:HG22	2.12	0.49
56:VV:1:MET:O	56:VV:2:GLN:C	2.52	0.49
56:VV:40:ASP:HB3	64:AA:191:ARG:NE	2.26	0.49
80:B2:1452:A:C4'	84:RR:48:ASN:CG	2.72	0.49
80:B2:1452:A:H4'	84:RR:45:LYS:N	2.27	0.49
5:D:4:VAL:HG11	81:A6:4246:G:O2'	2.13	0.49
5:D:118:ILE:CG2	5:D:135:ILE:HD11	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:41:LYS:HA	77:A5:980:U:C2'	2.42	0.49
6:E:42:GLY:CA	77:A5:980:U:C4'	2.90	0.49
22:W:48:GLY:HA2	22:W:51:ILE:HD11	1.94	0.49
47:aa:53:ILE:HD13	83:OO:116:LEU:CD2	2.43	0.49
56:VV:70:LEU:CB	64:AA:53:ARG:CB	2.90	0.49
62:gg:235:ILE:HD11	84:RR:22:THR:CB	2.25	0.49
64:AA:31:ASP:CB	64:AA:34:MET:HB2	2.41	0.49
64:AA:212:LYS:HE2	84:RR:84:TYR:OH	2.10	0.49
75:EF:505:VAL:HG11	75:EF:551:GLU:HG2	1.93	0.49
75:EF:652:PHE:CD1	75:EF:661:ILE:HD13	2.48	0.49
77:A5:1106:A:H62	77:A5:1164:G:N2	2.10	0.49
80:B2:1869:A:N1	82:BB:114:VAL:HG12	2.27	0.49
10:I:43:VAL:HG21	10:I:197:VAL:HG13	1.94	0.49
30:f:58:VAL:C	81:A6:4945:G:C4	2.90	0.49
44:u:46:VAL:CG1	44:u:48:LEU:HD12	2.42	0.49
62:gg:249:CYS:HB3	62:gg:258:ILE:HD13	1.94	0.49
64:AA:12:GLU:HA	64:AA:15:VAL:CB	2.42	0.49
68:MM:107:SER:O	68:MM:109:VAL:HG13	2.12	0.49
80:B2:952:G:N2	83:OO:55:ARG:NH1	2.59	0.49
80:B2:1064:C:OP1	83:OO:150:ARG:HG3	2.12	0.49
80:B2:1122:A:N3	82:BB:146:ARG:CZ	2.74	0.49
41:r:97:ILE:HD11	41:r:103:ARG:O	2.13	0.49
49:EE:19:MET:HE3	80:B2:846:G:H2'	1.95	0.49
52:II:66:SER:HA	52:II:73:THR:HG22	1.94	0.49
56:VV:62:MET:HB3	64:AA:152:SER:OG	2.13	0.49
64:AA:197:VAL:O	64:AA:198:MET:CG	2.60	0.49
64:AA:210:ILE:HG23	84:RR:81:ARG:C	2.37	0.49
75:EF:24:VAL:HG23	75:EF:102:LEU:HD13	1.93	0.49
75:EF:548:GLY:HA3	75:EF:554:LEU:HD13	1.94	0.49
3:C:136:LEU:HD11	41:r:9:ILE:HD12	1.95	0.49
6:E:221:LYS:C	81:A6:4940:C:C5	2.90	0.49
10:I:4:ARG:NE	10:I:99:ILE:HD11	2.27	0.49
10:I:91:LEU:HD23	10:I:135:ILE:HA	1.94	0.49
58:XX:112:VAL:HG22	58:XX:118:VAL:O	2.12	0.49
58:XX:128:VAL:HG11	58:XX:133:LEU:HD21	1.94	0.49
64:AA:91:ALA:C	64:AA:94:THR:H	2.20	0.49
80:B2:983:A:H2	83:OO:140:THR:HG22	1.76	0.49
80:B2:1456:G:C3'	84:RR:55:THR:HG21	2.37	0.49
2:B:317:LEU:HD21	2:B:380:GLN:O	2.13	0.49
12:L:58:ILE:HD12	12:L:116:ARG:HD2	1.93	0.49
23:X:83:THR:HG23	23:X:86:ALA:H	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Z:2:GLY:HA2	44:u:65:MET:HE2	1.94	0.49
52:II:174:CYS:HB2	52:II:190:LEU:HD21	1.95	0.49
56:VV:35:ASN:CB	64:AA:65:ILE:HG21	2.43	0.49
56:VV:36:VAL:O	56:VV:37:ALA:C	2.54	0.49
56:VV:69:ILE:HD13	64:AA:161:ILE:HG23	1.94	0.49
64:AA:18:PHE:HE1	64:AA:174:MET:HE3	1.78	0.49
64:AA:42:LYS:HE3	84:RR:99:ASP:CB	2.42	0.49
64:AA:85:ARG:HD3	64:AA:202:TYR:C	2.37	0.49
77:A5:1667:G:H21	81:A6:2282:A:H62	1.59	0.49
2:B:338:VAL:HG12	81:A6:4624:A:H4'	1.94	0.49
9:H:34:LEU:HD12	9:H:84:VAL:HG23	1.94	0.49
39:o:21:HIS:HB2	39:o:70:LEU:HD12	1.95	0.49
55:NN:98:VAL:HG23	55:NN:115:LEU:CD2	2.43	0.49
56:VV:16:LYS:HE2	56:VV:21:ASN:HD22	1.78	0.49
56:VV:46:PHE:N	56:VV:46:PHE:CD1	2.80	0.49
61:ff:108:VAL:HG11	68:MM:64:LEU:HA	1.95	0.49
64:AA:40:LYS:HB2	84:RR:105:MET:HE2	1.91	0.49
64:AA:77:ILE:HD13	64:AA:122:LEU:HD13	1.94	0.49
64:AA:176:TRP:CD2	64:AA:198:MET:HB2	2.47	0.49
66:FF:100:ILE:O	66:FF:104:THR:HG22	2.12	0.49
77:A5:58:G:H2'	79:A8:33:G:H2'	1.95	0.49
81:A6:2573:A:H62	81:A6:2760:G:N2	2.11	0.49
22:W:101:ILE:HD11	81:A6:2898:G:OP1	2.13	0.49
30:f:58:VAL:HG11	30:f:58:VAL:HG21	1.95	0.49
44:u:44:LYS:HB2	44:u:98:ASP:CA	2.42	0.49
56:VV:66:ASP:HA	56:VV:69:ILE:CG2	2.40	0.49
64:AA:17:LYS:HE3	64:AA:198:MET:HE3	1.89	0.49
64:AA:73:ASP:CB	64:AA:118:GLU:O	2.61	0.49
71:SS:23:ARG:O	74:ZZ:48:VAL:HG21	2.12	0.49
83:OO:132:VAL:O	83:OO:132:VAL:HG22	2.12	0.49
31:g:32:TYR:C	31:g:33:LEU:HD12	2.38	0.49
36:l:46:ARG:HH11	36:l:47:THR:HG22	1.78	0.49
48:CC:83:LEU:HA	56:VV:12:TYR:CD2	2.48	0.49
80:B2:1458:G:N7	84:RR:59:LYS:NZ	2.61	0.49
17:Q:124:ASP:O	17:Q:128:LEU:HD23	2.13	0.49
40:p:44:LYS:HG3	44:u:90:ARG:NE	2.27	0.49
47:aa:52:ASP:O	83:OO:121:ARG:N	2.44	0.49
48:CC:251:LEU:HD12	56:VV:23:ILE:HD11	1.94	0.49
48:CC:269:PHE:CE1	64:AA:70:ASN:CB	2.95	0.49
56:VV:59:ILE:O	56:VV:65:SER:N	2.46	0.49
64:AA:90:PHE:CD2	64:AA:91:ALA:HB2	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:AA:90:PHE:CZ	64:AA:179:ALA:HB1	2.48	0.49
71:SS:65:GLU:O	71:SS:69:THR:HG23	2.12	0.49
75:EF:117:ALA:O	75:EF:121:VAL:HG12	2.13	0.49
75:EF:731:ALA:HB2	75:EF:854:PHE:CB	2.42	0.49
77:A5:1437:C:H42	77:A5:1447:C:H42	1.61	0.49
14:N:174:LEU:HD13	77:A5:62:A:H5'	1.94	0.48
16:P:112:LEU:HD12	16:P:150:LEU:CB	2.43	0.48
44:u:105:ILE:O	44:u:105:ILE:HD12	2.12	0.48
47:aa:22:ARG:NH1	83:OO:142:ARG:O	2.45	0.48
57:WW:47:ILE:HD11	57:WW:69:LEU:HD13	1.94	0.48
57:WW:75:ILE:HD11	57:WW:93:LEU:HD11	1.95	0.48
64:AA:74:VAL:HB	64:AA:91:ALA:CB	2.42	0.48
64:AA:172:GLY:HA2	64:AA:203:PHE:CA	2.42	0.48
64:AA:176:TRP:CD2	64:AA:198:MET:C	2.91	0.48
6:E:175:LEU:HD21	81:A6:4941:G:C6	2.48	0.48
17:Q:61:LEU:HD21	17:Q:66:MET:HB2	1.95	0.48
20:U:36:ALA:HB3	20:U:65:ARG:CZ	2.44	0.48
30:f:58:VAL:O	81:A6:4945:G:C4	2.67	0.48
54:LL:73:LEU:HD23	54:LL:90:ARG:CD	2.42	0.48
56:VV:36:VAL:HB	64:AA:62:ALA:HB2	1.95	0.48
56:VV:66:ASP:O	56:VV:69:ILE:N	2.46	0.48
62:gg:280:LYS:C	84:RR:26:ASN:HD22	2.05	0.48
64:AA:175:TRP:CB	64:AA:202:TYR:HB2	2.43	0.48
64:AA:189:ILE:HD13	64:AA:193:HIS:ND1	2.28	0.48
80:B2:677:G:H21	80:B2:1028:A:H62	1.61	0.48
3:C:8:ILE:HD12	3:C:149:GLU:OE2	2.13	0.48
11:J:56:THR:HG23	11:J:62:ILE:O	2.13	0.48
16:P:14:SER:HB2	16:P:151:THR:HG22	1.95	0.48
39:o:82:MET:HE1	81:A6:4346:U:O4'	2.14	0.48
44:u:51:ASN:ND2	44:u:51:ASN:N	2.60	0.48
44:u:90:ARG:CB	44:u:90:ARG:CZ	2.87	0.48
47:aa:69:VAL:HG21	83:OO:107:THR:HG22	1.96	0.48
56:VV:15:ARG:HH12	56:VV:54:ALA:CB	2.26	0.48
56:VV:65:SER:CB	64:AA:157:VAL:O	2.61	0.48
62:gg:282:GLU:HG2	84:RR:26:ASN:CB	2.44	0.48
64:AA:110:ASN:O	64:AA:111:GLN:C	2.56	0.48
65:DD:176:LEU:HD11	80:B2:1499:U:C5'	2.43	0.48
80:B2:1005:G:OP1	82:BB:166:LYS:CE	2.60	0.48
1:A:5:ILE:HD12	1:A:209:HIS:HA	1.94	0.48
4:c:13:ILE:HD13	4:c:32:LEU:HA	1.96	0.48
12:L:126:LEU:HD11	32:h:117:ARG:CZ	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:u:54:ALA:CB	81:A6:4120:U:C6	2.96	0.48
52:II:83:TYR:HA	52:II:91:VAL:HG11	1.93	0.48
56:VV:32:ILE:O	64:AA:143:PRO:O	2.30	0.48
62:gg:282:GLU:HG2	84:RR:26:ASN:N	2.26	0.48
64:AA:211:GLU:CA	84:RR:81:ARG:CA	2.78	0.48
81:A6:2647:A:H62	81:A6:2686:G:H8	1.59	0.48
2:B:77:THR:HG21	2:B:337:VAL:HG12	1.94	0.48
3:C:36:ILE:O	3:C:40:VAL:HG22	2.14	0.48
32:h:28:LEU:HA	32:h:31:LEU:HD12	1.95	0.48
56:VV:76:ASP:HB2	64:AA:56:GLU:CA	2.43	0.48
59:YY:44:LEU:HD13	59:YY:47:MET:HE3	1.94	0.48
64:AA:18:PHE:CD1	64:AA:51:LEU:HD11	2.48	0.48
64:AA:168:ALA:O	64:AA:171:VAL:HG23	2.14	0.48
75:EF:79:TYR:CE1	75:EF:351:LEU:HD13	2.46	0.48
75:EF:704:VAL:HG12	75:EF:705:HIS:O	2.13	0.48
20:U:47:ILE:HD11	20:U:56:LEU:HG	1.94	0.48
38:n:1:MET:HE1	80:B2:1706:G:H4'	1.96	0.48
44:u:22:MET:SD	44:u:27:TYR:HB3	2.54	0.48
54:LL:111:VAL:HG11	54:LL:128:VAL:HG12	1.95	0.48
62:gg:12:LYS:HE3	62:gg:306:LEU:HD23	1.96	0.48
64:AA:188:THR:CG2	64:AA:197:VAL:HG11	2.43	0.48
6:E:175:LEU:HD21	81:A6:4941:G:C5	2.48	0.48
48:CC:65:LYS:HB2	64:AA:72:ALA:CB	2.43	0.48
50:GG:5:ILE:HG23	50:GG:124:LEU:HD11	1.96	0.48
51:HH:50:GLU:HG3	51:HH:60:ILE:HD13	1.95	0.48
51:HH:116:ARG:NE	51:HH:121:THR:HG22	2.28	0.48
56:VV:46:PHE:CE2	64:AA:184:ARG:HA	2.48	0.48
64:AA:176:TRP:CE3	64:AA:199:PRO:N	2.81	0.48
75:EF:373:TYR:CD2	75:EF:382:ALA:HB2	2.49	0.48
80:B2:176:U:C2	80:B2:313:A:N7	2.80	0.48
81:A6:3911:C:H5'	81:A6:4196:G:H21	1.79	0.48
81:A6:4753:U:O4	81:A6:4879:C:N3	2.47	0.48
44:u:91:VAL:CG1	44:u:94:LEU:HD11	2.43	0.48
48:CC:109:ILE:HD12	48:CC:126:ALA:HA	1.95	0.48
62:gg:31:ILE:HD13	62:gg:299:PHE:CE1	2.49	0.48
64:AA:34:MET:SD	64:AA:37:TYR:CB	3.02	0.48
77:A5:1550:G:O6	77:A5:1578:U:O4	2.31	0.48
80:B2:956:G:H3'	82:BB:5:LYS:CB	2.40	0.48
6:E:168:LEU:HD11	6:E:179:THR:HG22	1.96	0.48
14:N:101:VAL:HG23	81:A6:2460:A:H4'	1.95	0.48
22:W:128:LYS:CE	81:A6:2666:G:O6	2.62	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:VV:60:ARG:CD	64:AA:157:VAL:HG11	2.44	0.48
8:G:51:LEU:HD11	81:A6:4086:G:C2	2.49	0.48
10:I:41:ALA:HB1	10:I:45:GLU:OE2	2.14	0.48
20:U:25:CYS:O	20:U:29:VAL:HG22	2.14	0.48
34:j:5:THR:HG22	81:A6:2793:G:O2'	2.13	0.48
48:CC:265:PRO:HA	64:AA:70:ASN:CA	2.44	0.48
49:EE:66:MET:HE1	80:B2:502:C:O2	2.14	0.48
56:VV:40:ASP:CB	64:AA:191:ARG:CZ	2.92	0.48
77:A5:1691:G:O6	77:A5:1845:U:C2	2.67	0.48
80:B2:944:A:H2	83:OO:140:THR:HG21	1.79	0.48
80:B2:1103:C:H5''	82:BB:157:GLN:CD	2.39	0.48
81:A6:2620:G:C6	81:A6:2636:U:O2	2.67	0.48
2:B:217:ILE:CD1	2:B:347:LEU:HD12	2.44	0.47
2:B:235:TRP:CD1	2:B:267:ALA:HB1	2.49	0.47
48:CC:265:PRO:HA	64:AA:70:ASN:HA	1.96	0.47
50:GG:5:ILE:HD12	50:GG:111:LEU:HB3	1.96	0.47
56:VV:33:GLN:HE22	56:VV:55:ILE:N	2.12	0.47
56:VV:36:VAL:O	64:AA:181:GLU:OE2	2.32	0.47
62:gg:279:SER:C	84:RR:62:GLN:HB2	2.37	0.47
64:AA:32:PHE:CE1	80:B2:1097:G:H4'	2.49	0.47
64:AA:183:LEU:HD13	64:AA:188:THR:HG21	1.96	0.47
77:A5:352:G:N2	77:A5:360:A:C6	2.78	0.47
80:B2:1374:C:H5	84:RR:7:LYS:NZ	2.12	0.47
81:A6:2666:G:C6	81:A6:2669:C:C6	3.02	0.47
33:i:36:HIS:O	33:i:40:VAL:HG23	2.14	0.47
44:u:48:LEU:HD11	44:u:93:THR:HG23	1.95	0.47
44:u:82:GLY:HA2	44:u:85:CYS:HB3	1.94	0.47
56:VV:55:ILE:HB	64:AA:143:PRO:CG	2.43	0.47
56:VV:73:ALA:CB	64:AA:60:LEU:HD22	2.43	0.47
64:AA:136:GLU:CB	80:B2:1352:G:H5''	2.44	0.47
64:AA:189:ILE:HD12	64:AA:190:SER:N	2.28	0.47
80:B2:968:U:H2'	82:BB:8:ARG:HH11	1.76	0.47
80:B2:1124:C:H5'	82:BB:150:ILE:CA	2.44	0.47
3:C:158:VAL:O	3:C:217:ILE:HD12	2.14	0.47
6:E:256:VAL:HG12	6:E:260:ILE:HD12	1.96	0.47
17:Q:42:THR:O	17:Q:46:VAL:HG23	2.14	0.47
44:u:48:LEU:HD11	44:u:93:THR:OG1	2.14	0.47
45:bb:3:LEU:HD13	56:VV:71:ARG:NH2	2.27	0.47
62:gg:282:GLU:CB	84:RR:62:GLN:HE22	2.10	0.47
71:SS:75:ARG:CG	71:SS:84:LEU:HD11	2.44	0.47
75:EF:650:TRP:N	75:EF:661:ILE:HD11	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:B2:956:G:H5'	82:BB:3:VAL:CA	2.44	0.47
80:B2:974:C:O2'	83:OO:41:PHE:HD2	1.86	0.47
5:D:271:MET:HE1	78:A7:61:G:H5''	1.95	0.47
6:E:41:LYS:O	77:A5:980:U:O4'	2.30	0.47
21:V:62:MET:HE2	81:A6:4508:C:H5'	1.97	0.47
51:HH:61:ILE:HG23	51:HH:95:ILE:HD12	1.95	0.47
55:NN:71:ILE:HD11	80:B2:1018:U:H5'	1.96	0.47
56:VV:40:ASP:C	56:VV:40:ASP:OD1	2.56	0.47
62:gg:121:VAL:HG11	62:gg:165:ILE:HD13	1.95	0.47
62:gg:280:LYS:HG2	84:RR:59:LYS:CB	2.40	0.47
64:AA:99:ILE:HG22	64:AA:100:ALA:N	2.29	0.47
64:AA:172:GLY:C	64:AA:199:PRO:HB3	2.38	0.47
77:A5:1426:G:H3'	77:A5:1457:G:H22	1.79	0.47
80:B2:1063:C:C2'	83:OO:150:ARG:CZ	2.93	0.47
80:B2:1373:C:C4'	84:RR:7:LYS:H	2.20	0.47
47:aa:59:PHE:CA	83:OO:126:ILE:HB	2.27	0.47
48:CC:84:PHE:CG	64:AA:67:ALA:CB	2.96	0.47
56:VV:27:LYS:H	64:AA:141:ASN:HB2	1.79	0.47
56:VV:41:LYS:HE2	56:VV:42:VAL:HG13	1.94	0.47
56:VV:83:PHE:CZ	64:AA:50:ASN:HA	2.49	0.47
77:A5:1691:G:C6	77:A5:1845:U:O2	2.68	0.47
80:B2:957:A:H3'	80:B2:958:G:H21	1.79	0.47
80:B2:1693:G:H21	80:B2:1834:A:C1'	2.27	0.47
82:BB:137:LEU:HD22	82:BB:215:VAL:HG22	1.97	0.47
1:A:41:ILE:HG22	1:A:90:CYS:O	2.15	0.47
2:B:318:GLY:CA	81:A6:5000:G:H21	2.28	0.47
14:N:173:GLY:O	14:N:183:THR:HG21	2.14	0.47
15:O:87:MET:CE	77:A5:1912:G:H21	2.19	0.47
17:Q:88:ASP:HB2	17:Q:109:ALA:HB2	1.96	0.47
17:Q:105:VAL:HG12	17:Q:109:ALA:HB3	1.97	0.47
44:u:89:TYR:HB3	81:A6:2673:G:N2	2.30	0.47
56:VV:60:ARG:CD	64:AA:160:ALA:HB2	2.44	0.47
60:cc:13:ARG:N	60:cc:55:VAL:HG23	2.29	0.47
64:AA:173:LEU:HA	64:AA:199:PRO:HB3	1.95	0.47
64:AA:180:ARG:O	64:AA:183:LEU:CB	2.62	0.47
65:DD:96:LEU:HD12	65:DD:190:LEU:HD23	1.95	0.47
68:MM:52:LEU:HD13	68:MM:108:CYS:HB2	1.95	0.47
22:W:128:LYS:HE2	81:A6:2666:G:O6	2.15	0.47
24:Y:55:VAL:O	24:Y:67:ILE:HD12	2.13	0.47
48:CC:266:TYR:OH	64:AA:120:ARG:HB3	2.15	0.47
49:EE:47:PHE:CE2	49:EE:90:ILE:HG21	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:LL:78:THR:HG21	54:LL:89:ARG:HB2	1.95	0.47
59:YY:27:VAL:HG11	59:YY:35:VAL:HG11	1.97	0.47
59:YY:44:LEU:HD12	59:YY:75:ILE:HD11	1.97	0.47
59:YY:53:ASP:OD2	59:YY:79:LEU:HD11	2.14	0.47
62:gg:83:TRP:CE3	84:RR:33:ARG:NH1	2.82	0.47
64:AA:34:MET:SD	64:AA:37:TYR:HB2	2.54	0.47
64:AA:77:ILE:HD12	64:AA:77:ILE:N	2.29	0.47
71:SS:10:GLN:OE1	71:SS:13:LEU:HD21	2.15	0.47
75:EF:12:ILE:HG13	75:EF:99:LEU:HD22	1.96	0.47
77:A5:708:G:H21	81:A6:4942:C:N4	2.13	0.47
80:B2:796:G:H3'	80:B2:797:C:H5'	1.97	0.47
80:B2:1121:G:H4'	82:BB:160:GLN:HE21	1.78	0.47
80:B2:1455:A:O4'	84:RR:48:ASN:HA	2.15	0.47
6:E:41:LYS:O	77:A5:980:U:C4'	2.63	0.47
44:u:54:ALA:O	81:A6:4120:U:C5	2.68	0.47
47:aa:59:PHE:N	83:OO:126:ILE:CA	2.78	0.47
56:VV:38:GLU:HG3	56:VV:47:ASN:HD21	1.79	0.47
56:VV:51:LYS:H	64:AA:62:ALA:CB	2.28	0.47
64:AA:169:HIS:C	64:AA:171:VAL:N	2.68	0.47
69:PP:22:LEU:HA	69:PP:25:LEU:HD12	1.97	0.47
74:ZZ:68:ILE:HD12	74:ZZ:110:THR:C	2.40	0.47
8:G:66:GLN:HA	8:G:69:ILE:HD12	1.96	0.47
23:X:99:ILE:HG23	23:X:133:GLU:CG	2.44	0.47
24:Y:58:VAL:HG21	77:A5:200:U:C5	2.50	0.47
44:u:89:TYR:CG	81:A6:2660:A:N6	2.82	0.47
47:aa:28:ARG:HA	83:OO:147:ARG:N	2.27	0.47
48:CC:265:PRO:CG	64:AA:68:ILE:HB	2.44	0.47
50:GG:138:ALA:HB3	50:GG:178:ARG:O	2.14	0.47
56:VV:62:MET:CB	64:AA:152:SER:CB	2.93	0.47
62:gg:270:LEU:HD23	62:gg:310:TRP:CD2	2.50	0.47
64:AA:171:VAL:HG12	64:AA:203:PHE:HA	1.97	0.47
64:AA:189:ILE:HG12	64:AA:195:TRP:HA	1.97	0.47
80:B2:1452:A:C5'	84:RR:44:LYS:C	2.88	0.47
80:B2:1467:C:C3'	84:RR:3:ARG:CG	2.93	0.47
82:BB:136:ARG:HB2	82:BB:218:LEU:HD11	1.97	0.47
1:A:107:MET:SD	1:A:111:THR:HG21	2.55	0.47
10:I:190:LEU:HD22	10:I:197:VAL:HB	1.97	0.47
18:S:33:PHE:CD1	18:S:106:VAL:HG21	2.49	0.47
44:u:17:ARG:O	44:u:18:LEU:C	2.58	0.47
44:u:48:LEU:HD21	44:u:56:ARG:CZ	2.45	0.47
56:VV:82:ASN:C	64:AA:52:LYS:HG3	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:AA:74:VAL:HA	64:AA:120:ARG:H	1.79	0.47
3:C:44:LEU:HD12	3:C:47:ASN:ND2	2.28	0.46
4:c:21:TYR:HD2	4:c:28:VAL:HG23	1.79	0.46
9:H:95:VAL:HG22	37:m:82:LEU:HD11	1.97	0.46
33:i:33:LEU:HD21	33:i:41:ARG:CZ	2.46	0.46
44:u:21:VAL:HA	44:u:102:SER:HB3	1.96	0.46
47:aa:52:ASP:HA	83:OO:117:ARG:O	2.14	0.46
49:EE:70:ILE:O	49:EE:76:VAL:HG13	2.15	0.46
52:II:84:ASN:ND2	52:II:90:LEU:HD13	2.30	0.46
64:AA:12:GLU:O	64:AA:15:VAL:N	2.48	0.46
64:AA:189:ILE:HG23	64:AA:195:TRP:HD1	1.80	0.46
74:ZZ:68:ILE:HD13	74:ZZ:97:ILE:CG2	2.44	0.46
81:A6:4401:G:O6	81:A6:4441:A:N1	2.49	0.46
8:G:215:LEU:O	8:G:219:VAL:HG23	2.16	0.46
53:JJ:61:LEU:HD23	53:JJ:70:ARG:NH2	2.30	0.46
64:AA:85:ARG:NH2	64:AA:203:PHE:O	2.48	0.46
75:EF:36:THR:O	75:EF:40:VAL:HG23	2.14	0.46
80:B2:1453:C:C5	84:RR:28:PHE:CE1	3.03	0.46
13:M:25:VAL:HG12	13:M:40:GLY:HA3	1.97	0.46
50:GG:141:ILE:HG21	50:GG:153:VAL:HG13	1.97	0.46
56:VV:9:VAL:O	56:VV:10:ASP:C	2.58	0.46
64:AA:73:ASP:CA	64:AA:96:ALA:HB3	2.45	0.46
64:AA:91:ALA:C	64:AA:93:ALA:N	2.66	0.46
66:FF:166:ILE:HA	80:B2:1598:G:H21	1.81	0.46
80:B2:1120:U:O2	82:BB:204:ILE:CG2	2.55	0.46
80:B2:1455:A:C3'	84:RR:51:ALA:HB1	2.41	0.46
19:T:105:PHE:O	19:T:109:VAL:HG23	2.15	0.46
20:U:43:LEU:HD23	20:U:86:LEU:CD2	2.46	0.46
21:V:96:LEU:HD23	21:V:97:TYR:O	2.14	0.46
23:X:78:LYS:CD	23:X:99:ILE:HG22	2.45	0.46
23:X:79:PHE:CD2	32:h:36:VAL:HG11	2.50	0.46
56:VV:32:ILE:HG13	64:AA:145:ILE:N	2.30	0.46
56:VV:51:LYS:CA	64:AA:63:ARG:H	2.28	0.46
56:VV:52:THR:H	64:AA:63:ARG:CB	2.28	0.46
56:VV:70:LEU:O	56:VV:74:LYS:N	2.47	0.46
62:gg:282:GLU:CG	84:RR:26:ASN:H	2.26	0.46
64:AA:74:VAL:HG12	64:AA:75:SER:N	2.30	0.46
64:AA:115:ALA:O	64:AA:116:PHE:C	2.53	0.46
64:AA:173:LEU:HA	64:AA:199:PRO:HA	1.98	0.46
75:EF:21:ASN:OD1	75:EF:122:THR:HG22	2.15	0.46
75:EF:75:ILE:HG21	75:EF:102:LEU:HD23	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:EF:300:VAL:HG12	75:EF:315:LEU:CD1	2.42	0.46
80:B2:1455:A:C4'	84:RR:51:ALA:HB1	2.07	0.46
81:A6:2556:G:C6	81:A6:2557:U:C4	3.02	0.46
3:C:207:PRO:O	3:C:227:ILE:HD12	2.15	0.46
30:f:84:VAL:HG22	30:f:85:ARG:H	1.80	0.46
39:o:23:VAL:HG22	39:o:70:LEU:HD11	1.98	0.46
44:u:47:ILE:HD11	44:u:96:ILE:HD12	1.98	0.46
56:VV:28:ASP:HB3	64:AA:141:ASN:HA	1.97	0.46
64:AA:49:ILE:HD13	64:AA:49:ILE:N	2.30	0.46
64:AA:119:PRO:CG	64:AA:122:LEU:HD11	2.45	0.46
64:AA:172:GLY:HA2	64:AA:203:PHE:HA	1.96	0.46
66:FF:19:LEU:HD12	66:FF:48:TYR:O	2.15	0.46
77:A5:38:A:H61	77:A5:41:C:H3'	1.79	0.46
78:A7:77:A:H62	78:A7:99:G:H21	1.63	0.46
7:F:64:TYR:CZ	7:F:68:ILE:HD11	2.50	0.46
9:H:88:PHE:H	9:H:187:VAL:HG23	1.80	0.46
17:Q:167:VAL:HG11	17:Q:175:GLU:OE1	2.15	0.46
31:g:96:LEU:HD11	44:u:55:LEU:CB	2.44	0.46
39:o:82:MET:O	39:o:83:LEU:HD22	2.15	0.46
44:u:21:VAL:HG13	44:u:102:SER:HB3	1.98	0.46
44:u:89:TYR:CD2	81:A6:2660:A:N1	2.84	0.46
47:aa:57:SER:HG	83:OO:126:ILE:CG2	1.22	0.46
48:CC:267:GLN:OE1	64:AA:185:MET:HB2	2.16	0.46
56:VV:18:SER:HB3	56:VV:53:TYR:HB2	1.97	0.46
58:XX:110:HIS:O	58:XX:112:VAL:HG13	2.16	0.46
64:AA:211:GLU:HG3	84:RR:81:ARG:HD3	1.96	0.46
80:B2:1456:G:P	84:RR:28:PHE:HB2	2.41	0.46
11:J:22:LEU:HD12	11:J:128:LEU:HD11	1.97	0.46
12:L:107:THR:HG23	33:i:20:ASN:HA	1.98	0.46
41:r:6:GLN:O	41:r:10:VAL:HG22	2.15	0.46
49:EE:100:ARG:HD2	49:EE:102:ILE:HD11	1.98	0.46
56:VV:18:SER:CB	56:VV:53:TYR:HB2	2.46	0.46
58:XX:10:ALA:HB1	58:XX:14:ARG:NH1	2.31	0.46
62:gg:299:PHE:CD1	62:gg:309:VAL:HG12	2.50	0.46
64:AA:39:TYR:HB2	64:AA:48:ILE:CG2	2.44	0.46
82:BB:103:MET:HE3	82:BB:104:ASP:H	1.81	0.46
3:C:130:ALA:HB3	3:C:246:VAL:HG21	1.98	0.46
31:g:92:LYS:NZ	44:u:54:ALA:HB3	2.30	0.46
40:p:31:ILE:O	40:p:35:ALA:HB2	2.15	0.46
44:u:64:ALA:O	44:u:67:ALA:HB3	2.16	0.46
47:aa:56:ALA:HA	83:OO:124:MET:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:JJ:46:VAL:HG21	53:JJ:106:LEU:HD21	1.97	0.46
53:JJ:50:LEU:HD13	53:JJ:105:PHE:HE2	1.81	0.46
56:VV:59:ILE:HG23	64:AA:154:LEU:CG	2.45	0.46
64:AA:118:GLU:O	64:AA:119:PRO:C	2.57	0.46
64:AA:195:TRP:HB3	64:AA:198:MET:HG2	1.98	0.46
72:TT:28:LEU:HD23	72:TT:54:TYR:CD2	2.51	0.46
75:EF:113:SER:O	75:EF:117:ALA:HB2	2.16	0.46
75:EF:604:MET:HE3	75:EF:728:CYS:SG	2.56	0.46
80:B2:968:U:N3	82:BB:7:LYS:NZ	2.64	0.46
81:A6:3720:G:H22	81:A6:3733:A:H2	1.64	0.46
4:c:3:VAL:HG11	4:c:12:LYS:CE	2.46	0.46
8:G:158:ALA:HB3	8:G:161:VAL:HG13	1.96	0.46
30:f:51:TYR:OH	30:f:70:ILE:HD11	2.15	0.46
30:f:58:VAL:CB	30:f:58:VAL:HA	2.43	0.46
41:r:125:MET:HE2	41:r:125:MET:N	2.31	0.46
44:u:74:TYR:CZ	44:u:75:SER:O	2.69	0.46
48:CC:184:VAL:HG23	48:CC:195:LEU:HB2	1.97	0.46
55:NN:98:VAL:HG23	55:NN:115:LEU:HD23	1.98	0.46
55:NN:112:LYS:O	55:NN:116:ILE:HD12	2.16	0.46
56:VV:27:LYS:HB3	64:AA:141:ASN:CG	2.41	0.46
66:FF:166:ILE:HD12	80:B2:1598:G:O2'	2.15	0.46
77:A5:40:G:N2	81:A6:4380:A:H62	2.13	0.46
81:A6:4098:A:O2'	82:BB:224:GLU:OE1	2.34	0.46
82:BB:115:LYS:CG	82:BB:115:LYS:HB2	2.19	0.46
1:A:182:ALA:HB2	81:A6:3652:A:O2'	2.15	0.46
11:J:87:LEU:HD21	11:J:166:PHE:HE1	1.78	0.46
26:a:82:VAL:HG11	26:a:101:ILE:HG21	1.97	0.46
29:e:99:ILE:HD11	29:e:112:VAL:HG13	1.98	0.46
40:p:29:ILE:HD11	40:p:69:TRP:CD1	2.51	0.46
48:CC:204:ILE:HD13	48:CC:214:LEU:HB2	1.98	0.46
49:EE:80:ILE:HG13	49:EE:81:THR:HG23	1.97	0.46
56:VV:24:ILE:HD11	56:VV:56:CYS:HB3	1.98	0.46
64:AA:34:MET:HE2	64:AA:53:ARG:HH22	1.81	0.46
75:EF:13:MET:HE1	75:EF:461:ILE:HG22	1.97	0.46
77:A5:1298:C:H5''	81:A6:4945:G:H1	1.81	0.46
77:A5:1887:G:H21	77:A5:1938:C:N4	2.13	0.46
77:A5:1979:A:H61	77:A5:1983:A:H2'	1.80	0.46
80:B2:1456:G:P	84:RR:55:THR:HG1	2.14	0.46
80:B2:1456:G:C3'	84:RR:27:ASP:HA	2.46	0.46
83:OO:62:VAL:HG21	83:OO:73:ALA:HB2	1.97	0.46
5:D:195:HIS:NE2	5:D:199:ILE:HD11	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:68:ILE:HD11	81:A6:4258:C:H5'	1.97	0.45
12:L:9:ILE:H	12:L:9:ILE:HD12	1.81	0.45
15:O:9:LEU:HD12	15:O:120:VAL:HG23	1.97	0.45
44:u:48:LEU:O	44:u:73:HIS:CA	2.64	0.45
48:CC:266:TYR:CD1	64:AA:94:THR:HG23	2.51	0.45
62:gg:24:THR:HG23	62:gg:27:PHE:H	1.81	0.45
64:AA:73:ASP:C	64:AA:118:GLU:O	2.59	0.45
67:KK:49:MET:HE1	67:KK:69:TRP:CD2	2.51	0.45
75:EF:22:MET:O	75:EF:122:THR:HG21	2.16	0.45
75:EF:613:LEU:CD1	75:EF:635:LEU:HD22	2.45	0.45
1:A:20:VAL:HG23	1:A:20:VAL:O	2.16	0.45
4:c:29:PHE:HB2	21:V:96:LEU:HD12	1.99	0.45
5:D:115:MET:HB2	5:D:118:ILE:HD12	1.98	0.45
32:h:21:LEU:HD11	32:h:58:LEU:HD21	1.99	0.45
44:u:26:LYS:O	44:u:96:ILE:HA	2.17	0.45
44:u:82:GLY:O	44:u:83:THR:C	2.58	0.45
45:bb:42:LYS:HE2	45:bb:57:VAL:HG22	1.99	0.45
45:bb:52:THR:HG21	55:NN:53:ILE:HG22	1.98	0.45
48:CC:87:PRO:HA	64:AA:139:TYR:HB2	1.98	0.45
48:CC:130:ILE:HG21	48:CC:162:ILE:HD11	1.98	0.45
50:GG:106:LEU:HD13	50:GG:109:LEU:HD12	1.97	0.45
56:VV:73:ALA:O	64:AA:56:GLU:HB3	2.15	0.45
64:AA:87:VAL:HG12	64:AA:98:PRO:HD2	1.99	0.45
66:FF:28:VAL:HG11	66:FF:109:LEU:CB	2.47	0.45
74:ZZ:69:THR:O	74:ZZ:73:VAL:HG22	2.17	0.45
80:B2:931:C:C4'	82:BB:157:GLN:OE1	2.64	0.45
11:J:15:LEU:HD12	11:J:165:TRP:CG	2.52	0.45
12:L:94:ILE:HG23	12:L:96:ILE:CD1	2.46	0.45
13:M:130:LEU:HD13	15:O:180:GLN:HE22	1.80	0.45
23:X:102:VAL:HG23	23:X:128:ILE:HD11	1.97	0.45
24:Y:55:VAL:HG12	24:Y:106:ILE:HA	1.98	0.45
52:II:81:VAL:HG12	52:II:91:VAL:HG12	1.98	0.45
64:AA:147:LEU:HD23	64:AA:148:CYS:N	2.30	0.45
64:AA:173:LEU:HA	64:AA:199:PRO:CA	2.46	0.45
77:A5:1437:C:N4	77:A5:1447:C:H42	2.15	0.45
77:A5:1920:C:H2'	77:A5:1922:G:H5''	1.99	0.45
80:B2:1047:C:H5''	83:OO:143:LYS:CD	2.42	0.45
80:B2:1463:U:O2'	84:RR:63:ARG:CD	2.64	0.45
25:Z:46:ILE:HG23	25:Z:68:ILE:HG23	1.98	0.45
30:f:48:ALA:HB1	30:f:69:VAL:HG22	1.97	0.45
56:VV:66:ASP:CG	56:VV:67:ASP:N	2.72	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:VV:73:ALA:HB2	64:AA:60:LEU:HD22	1.99	0.45
64:AA:177:MET:HA	64:AA:180:ARG:HH21	1.81	0.45
65:DD:28:GLU:C	65:DD:29:LEU:HD22	2.41	0.45
70:QQ:45:ARG:HE	80:B2:1593:C:H4'	1.81	0.45
72:TT:15:VAL:HG11	80:B2:1541:G:H4'	1.97	0.45
72:TT:21:PHE:CD2	72:TT:134:ILE:HD11	2.52	0.45
75:EF:304:ILE:HD12	75:EF:336:LEU:HG	1.98	0.45
77:A5:1337:A:N6	81:A6:2346:C:O2	2.49	0.45
80:B2:674:C:H42	80:B2:1031:A:H61	1.64	0.45
2:B:219:VAL:HG21	2:B:337:VAL:CG2	2.46	0.45
6:E:202:THR:HG23	13:M:105:THR:HG21	1.98	0.45
15:O:47:PHE:HA	15:O:136:ALA:HB2	1.98	0.45
25:Z:10:VAL:CG2	25:Z:87:VAL:HG23	2.47	0.45
44:u:46:VAL:HG22	44:u:95:ALA:CB	2.47	0.45
44:u:105:ILE:CG2	44:u:106:ARG:HH21	2.30	0.45
47:aa:22:ARG:NH1	83:OO:141:ARG:HG3	2.28	0.45
47:aa:53:ILE:CG1	83:OO:116:LEU:CD1	2.78	0.45
56:VV:51:LYS:H	64:AA:62:ALA:CA	2.30	0.45
56:VV:67:ASP:HA	56:VV:70:LEU:HG	1.97	0.45
64:AA:177:MET:O	64:AA:178:LEU:C	2.56	0.45
75:EF:313:ALA:HA	75:EF:316:ILE:HD12	1.98	0.45
77:A5:1398:A:H61	77:A5:1419:G:C2'	2.30	0.45
80:B2:1453:C:OP1	84:RR:44:LYS:HB3	2.16	0.45
81:A6:4895:C:H1'	81:A6:4896:G:C8	2.51	0.45
2:B:252:ALA:HB3	81:A6:4457:U:O2	2.16	0.45
5:D:52:ILE:HG23	5:D:147:ASP:OD2	2.16	0.45
22:W:101:ILE:HG23	22:W:135:LYS:NZ	2.32	0.45
23:X:81:LEU:HD12	23:X:83:THR:HG22	1.98	0.45
29:e:87:VAL:HG13	29:e:88:LEU:HD22	1.99	0.45
35:k:11:PHE:HB2	35:k:45:LEU:HD22	1.98	0.45
47:aa:29:CYS:SG	83:OO:146:ARG:CD	3.05	0.45
47:aa:54:SER:H	83:OO:120:ALA:HB1	1.75	0.45
48:CC:173:LYS:HB2	56:VV:4:ASP:H	1.81	0.45
48:CC:265:PRO:HB3	64:AA:68:ILE:HB	1.99	0.45
75:EF:19:ILE:HG12	75:EF:99:LEU:HD23	1.98	0.45
77:A5:980:U:C4'	77:A5:980:U:O4'	2.64	0.45
40:p:41:PHE:CZ	44:u:51:ASN:CB	3.00	0.45
44:u:44:LYS:CB	44:u:98:ASP:HA	2.43	0.45
44:u:46:VAL:HG12	44:u:48:LEU:HD12	1.98	0.45
44:u:89:TYR:H	81:A6:2660:A:H61	1.64	0.45
48:CC:266:TYR:CB	64:AA:94:THR:HG23	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:VV:62:MET:HB2	64:AA:152:SER:CA	2.47	0.45
56:VV:82:ASN:N	64:AA:52:LYS:CD	2.79	0.45
64:AA:87:VAL:HG22	64:AA:100:ALA:N	2.32	0.45
64:AA:88:LEU:HB2	64:AA:98:PRO:HD3	1.98	0.45
64:AA:176:TRP:CG	64:AA:198:MET:C	2.95	0.45
64:AA:180:ARG:CG	64:AA:195:TRP:HH2	2.18	0.45
77:A5:379:G:N1	79:A8:22:U:C4	2.85	0.45
80:B2:944:A:C5'	83:OO:134:PRO:CB	2.91	0.45
80:B2:976:G:C1'	83:OO:49:GLY:O	2.65	0.45
80:B2:1452:A:C4'	84:RR:44:LYS:O	2.65	0.45
7:F:135:VAL:O	7:F:139:ILE:HG22	2.17	0.45
21:V:40:ILE:HD11	21:V:64:THR:HG23	1.99	0.45
43:t:50:THR:HG21	43:t:58:ILE:HG21	1.98	0.45
44:u:91:VAL:O	44:u:91:VAL:CG1	2.65	0.45
48:CC:269:PHE:CE1	64:AA:70:ASN:HB3	2.51	0.45
50:GG:50:VAL:HG12	50:GG:113:ILE:HA	1.99	0.45
56:VV:66:ASP:HA	56:VV:69:ILE:HG12	1.99	0.45
57:WW:103:VAL:HG23	57:WW:126:LEU:HB2	1.98	0.45
64:AA:154:LEU:O	64:AA:155:ARG:CB	2.64	0.45
64:AA:183:LEU:HD13	64:AA:188:THR:CG2	2.47	0.45
26:a:112:LEU:HD21	77:A5:1396:G:C2	2.52	0.45
29:e:12:ILE:HD11	29:e:69:MET:HB3	1.98	0.45
29:e:58:ILE:HD12	81:A6:2319:C:N3	2.32	0.45
44:u:81:LEU:C	44:u:81:LEU:CD2	2.88	0.45
55:NN:61:ALA:HB1	80:B2:1016:U:C6	2.52	0.45
56:VV:76:ASP:CB	64:AA:59:LEU:HD13	2.46	0.45
73:UU:48:LEU:HD22	73:UU:97:ILE:HG21	1.99	0.45
77:A5:684:G:O4'	77:A5:684:G:C1'	2.65	0.45
80:B2:664:A:P	80:B2:1153:C:H41	2.40	0.45
2:B:318:GLY:HA2	81:A6:5000:G:H21	1.81	0.45
3:C:302:LEU:HD23	17:Q:39:THR:CG2	2.47	0.45
11:J:89:VAL:CG1	11:J:109:ILE:HD12	2.46	0.45
21:V:42:VAL:O	21:V:45:ILE:HG22	2.17	0.45
25:Z:41:ALA:HB2	25:Z:77:TYR:CE1	2.52	0.45
26:a:25:HIS:CG	77:A5:1338:G:H22	2.35	0.45
47:aa:57:SER:CB	83:OO:126:ILE:HG21	2.13	0.45
48:CC:84:PHE:CD1	64:AA:67:ALA:HB2	2.49	0.45
56:VV:31:SER:OG	64:AA:140:VAL:HG11	2.16	0.45
56:VV:33:GLN:NE2	56:VV:54:ALA:HB1	2.31	0.45
56:VV:65:SER:OG	56:VV:66:ASP:N	2.49	0.45
64:AA:175:TRP:HB3	64:AA:202:TYR:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:AA:212:LYS:HD3	84:RR:86:PRO:HD3	0.79	0.45
77:A5:59:A:N7	77:A5:337:U:C2	2.84	0.45
77:A5:170:C:H42	77:A5:265:C:H42	1.64	0.45
80:B2:956:G:C4	82:BB:5:LYS:HG2	2.50	0.45
80:B2:1064:C:P	83:OO:150:ARG:HG3	2.57	0.45
30:f:58:VAL:CG2	30:f:58:VAL:HG11	2.47	0.44
33:i:34:THR:HG23	77:A5:276:C:H5'	1.98	0.44
43:t:37:LEU:HD12	43:t:38:SER:H	1.82	0.44
63:dd:14:PHE:HZ	80:B2:1618:C:H41	1.64	0.44
64:AA:77:ILE:HD13	64:AA:122:LEU:CD1	2.47	0.44
64:AA:176:TRP:CB	64:AA:198:MET:O	2.65	0.44
70:QQ:13:PHE:HB3	70:QQ:22:VAL:HG22	1.99	0.44
77:A5:1890:G:N2	77:A5:1939:A:H61	2.16	0.44
83:OO:93:LEU:HD13	83:OO:94:HIS:C	2.42	0.44
22:W:126:LYS:HD3	22:W:131:VAL:HG21	2.00	0.44
29:e:90:MET:HE1	41:r:113:ARG:HB2	2.00	0.44
47:aa:51:ARG:O	83:OO:121:ARG:CD	2.55	0.44
48:CC:267:GLN:HE22	64:AA:185:MET:HB2	1.82	0.44
54:LL:72:ILE:C	54:LL:73:LEU:HD12	2.42	0.44
55:NN:4:MET:HA	55:NN:4:MET:HE3	1.98	0.44
64:AA:139:TYR:C	64:AA:140:VAL:HG23	2.43	0.44
64:AA:143:PRO:HB2	64:AA:159:ILE:HG22	1.98	0.44
75:EF:20:ARG:HD2	75:EF:355:THR:HG23	1.98	0.44
80:B2:369:C:H42	80:B2:1730:U:H5''	1.81	0.44
80:B2:886:A:H61	80:B2:900:C:N4	2.15	0.44
80:B2:1455:A:O3'	84:RR:51:ALA:HB1	2.17	0.44
20:U:63:ILE:HD13	20:U:72:VAL:HG13	1.98	0.44
44:u:48:LEU:HD23	44:u:92:CYS:SG	2.58	0.44
44:u:52:CYS:O	44:u:53:PRO:C	2.61	0.44
58:XX:107:ARG:HG3	58:XX:112:VAL:HG12	1.97	0.44
58:XX:128:VAL:CG1	58:XX:133:LEU:HD21	2.48	0.44
64:AA:57:LYS:O	64:AA:58:LEU:C	2.60	0.44
67:KK:90:VAL:HB	67:KK:94:LEU:HD22	1.99	0.44
75:EF:415:ARG:NH1	75:EF:469:ILE:HG23	2.32	0.44
77:A5:1106:A:N6	77:A5:1164:G:H21	2.14	0.44
7:F:94:ILE:HD12	7:F:231:ASP:CG	2.43	0.44
9:H:41:ILE:CD1	9:H:73:ILE:HD11	2.45	0.44
39:o:7:THR:HA	39:o:23:VAL:HG23	1.99	0.44
47:aa:59:PHE:CE2	83:OO:95:ILE:CD1	3.01	0.44
52:II:190:LEU:HD22	52:II:194:GLU:OE2	2.17	0.44
53:JJ:3:VAL:HG12	80:B2:510:G:OP2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:VV:35:ASN:ND2	64:AA:185:MET:HE3	2.27	0.44
56:VV:70:LEU:HD22	64:AA:53:ARG:CB	2.48	0.44
64:AA:102:ARG:O	64:AA:103:PHE:C	2.58	0.44
64:AA:164:ASN:CG	64:AA:165:ASN:N	2.69	0.44
64:AA:195:TRP:C	64:AA:197:VAL:O	2.60	0.44
80:B2:956:G:H5''	82:BB:5:LYS:CA	2.45	0.44
80:B2:1451:G:C8	84:RR:44:LYS:HD3	2.51	0.44
81:A6:4745:G:N2	81:A6:4955:A:H62	2.15	0.44
2:B:58:ARG:NH2	2:B:72:VAL:HG11	2.33	0.44
23:X:74:TYR:HE1	32:h:26:VAL:HG12	1.82	0.44
25:Z:2:GLY:CA	44:u:65:MET:HE2	2.46	0.44
44:u:54:ALA:O	81:A6:4120:U:C4	2.70	0.44
46:ee:80:LEU:HD11	58:XX:55:VAL:C	2.43	0.44
48:CC:65:LYS:HB2	64:AA:72:ALA:HB1	1.99	0.44
64:AA:54:THR:O	64:AA:55:TRP:C	2.60	0.44
64:AA:136:GLU:HG2	64:AA:137:ALA:N	2.32	0.44
64:AA:173:LEU:HD23	64:AA:174:MET:N	2.32	0.44
75:EF:36:THR:HG21	75:EF:104:ASP:OD2	2.18	0.44
75:EF:174:LEU:HD12	75:EF:177:THR:OG1	2.17	0.44
80:B2:985:G:H4'	83:OO:138:ASP:HB3	2.00	0.44
80:B2:1857:G:O5'	83:OO:146:ARG:HD2	2.17	0.44
23:X:74:TYR:CE1	32:h:26:VAL:HG12	2.52	0.44
30:f:58:VAL:C	81:A6:4945:G:N9	2.75	0.44
47:aa:52:ASP:C	83:OO:117:ARG:CZ	2.77	0.44
54:LL:18:GLN:CB	54:LL:33:LEU:HD11	2.48	0.44
56:VV:62:MET:HB2	64:AA:152:SER:CB	2.47	0.44
64:AA:10:MET:SD	64:AA:55:TRP:CG	3.11	0.44
64:AA:39:TYR:OH	84:RR:108:LEU:HD11	2.17	0.44
64:AA:188:THR:HG22	64:AA:197:VAL:HG11	1.99	0.44
64:AA:189:ILE:HG23	64:AA:195:TRP:CD1	2.53	0.44
80:B2:1455:A:O3'	84:RR:51:ALA:CB	2.64	0.44
22:W:26:PRO:HA	22:W:29:THR:HG23	1.99	0.44
39:o:52:THR:HG22	77:A5:43:U:H4'	2.00	0.44
40:p:41:PHE:CZ	44:u:51:ASN:HB3	2.52	0.44
40:p:41:PHE:CZ	44:u:50:ASN:O	2.71	0.44
40:p:82:ALA:O	40:p:86:LEU:HD23	2.18	0.44
43:t:143:VAL:HG23	43:t:151:ILE:HD11	1.99	0.44
44:u:27:TYR:HA	44:u:96:ILE:N	2.32	0.44
47:aa:26:CYS:C	83:OO:149:ARG:HG2	2.42	0.44
56:VV:82:ASN:N	64:AA:52:LYS:HD2	2.33	0.44
57:WW:26:LEU:HD21	57:WW:60:LYS:HD3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:gg:299:PHE:HD1	62:gg:309:VAL:HG12	1.83	0.44
64:AA:83:GLY:C	64:AA:207:PRO:HG2	2.43	0.44
64:AA:88:LEU:HD12	64:AA:88:LEU:O	2.18	0.44
64:AA:103:PHE:CZ	64:AA:107:THR:HB	2.53	0.44
68:MM:49:LEU:HD23	68:MM:50:CYS:N	2.33	0.44
75:EF:450:THR:HG23	75:EF:472:LEU:HD13	1.99	0.44
81:A6:3961:G:H22	81:A6:3964:U:H3'	1.82	0.44
82:BB:114:VAL:HA	82:BB:120:MET:HE2	1.99	0.44
6:E:104:ASN:HB2	77:A5:684:G:H3'	1.99	0.44
13:M:130:LEU:HD13	15:O:180:GLN:NE2	2.33	0.44
17:Q:72:LEU:HD13	77:A5:1457:G:C5'	2.47	0.44
48:CC:130:ILE:CG2	48:CC:162:ILE:HD11	2.47	0.44
56:VV:52:THR:HB	56:VV:54:ALA:H	1.82	0.44
56:VV:70:LEU:HB3	64:AA:53:ARG:HB3	2.00	0.44
56:VV:83:PHE:CD2	64:AA:49:ILE:O	2.71	0.44
62:gg:32:LEU:HB3	62:gg:69:VAL:HG21	1.99	0.44
66:FF:35:LEU:HD12	66:FF:117:ILE:HG22	1.98	0.44
18:S:113:MET:HE2	18:S:124:ILE:CG1	2.43	0.44
21:V:96:LEU:HD23	21:V:97:TYR:N	2.33	0.44
24:Y:58:VAL:HG22	24:Y:103:LYS:C	2.43	0.44
44:u:21:VAL:HG21	44:u:45:LEU:HD23	2.00	0.44
48:CC:169:TYR:CD1	56:VV:1:MET:HE1	2.53	0.44
48:CC:270:THR:OG1	64:AA:71:PRO:HG3	2.18	0.44
56:VV:46:PHE:CD1	64:AA:189:ILE:O	2.71	0.44
64:AA:79:SER:HA	64:AA:101:GLY:HA2	2.00	0.44
64:AA:175:TRP:CE3	64:AA:202:TYR:O	2.71	0.44
80:B2:1452:A:H3'	84:RR:44:LYS:C	2.42	0.44
80:B2:1466:G:P	84:RR:10:LYS:CG	3.06	0.44
19:T:61:THR:O	19:T:76:VAL:HG23	2.17	0.43
44:u:22:MET:HE3	44:u:85:CYS:HA	1.99	0.43
44:u:61:GLU:HA	44:u:64:ALA:HB3	1.99	0.43
47:aa:28:ARG:HG3	83:OO:147:ARG:CA	2.29	0.43
53:JJ:50:LEU:HD13	53:JJ:105:PHE:CE2	2.53	0.43
56:VV:52:THR:HG1	64:AA:61:ALA:C	2.26	0.43
64:AA:104:THR:O	64:AA:105:PRO:C	2.60	0.43
64:AA:176:TRP:NE1	64:AA:180:ARG:CZ	2.79	0.43
66:FF:87:LEU:HD23	80:B2:1592:C:H5'	1.99	0.43
68:MM:48:HIS:C	68:MM:74:ILE:HD11	2.42	0.43
77:A5:1759:G:C6	77:A5:1773:U:O2	2.70	0.43
80:B2:493:A:H61	80:B2:510:G:H1'	1.82	0.43
81:A6:2377:C:O2	81:A6:2381:A:N6	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:MET:CE	1:A:136:VAL:HG21	2.48	0.43
11:J:12:MET:HE1	78:A7:28:C:O2	2.18	0.43
20:U:33:ILE:HD12	20:U:96:LEU:HD22	2.00	0.43
30:f:59:THR:HG1	81:A6:4946:U:H5	1.65	0.43
47:aa:27:ALA:HB1	83:OO:144:GLY:HA3	1.97	0.43
47:aa:29:CYS:CB	83:OO:146:ARG:CZ	2.96	0.43
50:GG:157:VAL:HG13	50:GG:159:ARG:HG3	1.99	0.43
56:VV:76:ASP:HB2	64:AA:56:GLU:C	2.43	0.43
57:WW:4:MET:HE1	80:B2:1159:G:C1'	2.48	0.43
60:cc:14:VAL:HG22	60:cc:32:VAL:HG12	1.99	0.43
64:AA:47:TYR:CD1	64:AA:164:ASN:HB2	2.54	0.43
75:EF:40:VAL:HG22	75:EF:77:LEU:HD11	1.99	0.43
75:EF:577:VAL:O	75:EF:577:VAL:HG13	2.18	0.43
80:B2:1112:U:C2	82:BB:146:ARG:NE	2.83	0.43
80:B2:1124:C:C4'	82:BB:150:ILE:HB	2.43	0.43
80:B2:1463:U:C6	84:RR:63:ARG:CZ	2.91	0.43
1:A:91:GLY:O	1:A:102:LEU:HD13	2.18	0.43
44:u:30:GLY:C	81:A6:2675:G:O6	2.61	0.43
44:u:98:ASP:O	44:u:99:PRO:C	2.60	0.43
47:aa:57:SER:HA	83:OO:126:ILE:HA	1.67	0.43
48:CC:266:TYR:CG	64:AA:94:THR:HG23	2.53	0.43
52:II:43:ILE:HD11	52:II:60:LEU:HD21	2.00	0.43
52:II:174:CYS:CB	52:II:190:LEU:HD21	2.48	0.43
56:VV:76:ASP:OD2	64:AA:60:LEU:HD13	2.19	0.43
62:gg:79:LEU:HD11	62:gg:87:LEU:HB3	2.01	0.43
62:gg:279:SER:HA	84:RR:62:GLN:HB3	1.99	0.43
64:AA:144:THR:H	64:AA:157:VAL:HG13	1.82	0.43
68:MM:52:LEU:HD22	68:MM:65:VAL:CG2	2.48	0.43
75:EF:169:LEU:CD2	75:EF:174:LEU:HD13	2.49	0.43
75:EF:404:THR:HG21	75:EF:411:TYR:CD2	2.53	0.43
80:B2:88:G:H21	80:B2:500:A:H5'	1.83	0.43
80:B2:1455:A:C8	84:RR:48:ASN:HB3	2.54	0.43
81:A6:2306:G:H21	81:A6:2332:A:H62	1.66	0.43
4:c:40:PHE:CE2	21:V:96:LEU:HD11	2.54	0.43
6:E:221:LYS:HA	81:A6:4940:C:C5	2.52	0.43
15:O:25:LYS:O	15:O:29:LEU:HD23	2.18	0.43
15:O:141:LEU:O	15:O:145:VAL:HG22	2.19	0.43
48:CC:265:PRO:CB	64:AA:68:ILE:HB	2.48	0.43
53:JJ:32:ILE:HD11	53:JJ:40:LYS:HD3	2.00	0.43
56:VV:46:PHE:CE1	64:AA:189:ILE:O	2.71	0.43
57:WW:52:ILE:HG23	57:WW:61:ILE:HD13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:MM:43:ASP:OD1	68:MM:68:LEU:HD11	2.18	0.43
75:EF:581:GLU:HG2	75:EF:692:LEU:HD12	2.01	0.43
75:EF:673:ASN:ND2	80:B2:1502:C:H4'	2.33	0.43
3:C:297:GLU:OE2	17:Q:128:LEU:HD13	2.19	0.43
13:M:36:ALA:HB2	13:M:52:PHE:CE1	2.54	0.43
15:O:141:LEU:O	15:O:145:VAL:HG13	2.18	0.43
19:T:84:ILE:C	19:T:85:LEU:HD12	2.43	0.43
26:a:137:ILE:HD11	26:a:144:CYS:SG	2.59	0.43
40:p:35:ALA:HB3	40:p:37:TYR:CZ	2.54	0.43
48:CC:191:VAL:HG11	48:CC:236:PHE:HA	1.99	0.43
75:EF:673:ASN:HD22	80:B2:1502:C:H4'	1.83	0.43
81:A6:2685:C:O2'	81:A6:2686:G:H5''	2.18	0.43
1:A:75:LEU:HD23	1:A:75:LEU:H	1.84	0.43
3:C:325:MET:HE3	3:C:325:MET:O	2.19	0.43
9:H:34:LEU:HD11	9:H:149:ASN:O	2.18	0.43
12:L:93:THR:HA	32:h:116:LEU:HD13	2.01	0.43
26:a:116:LYS:CG	77:A5:1420:A:H62	2.31	0.43
54:LL:73:LEU:HD23	54:LL:90:ARG:HD2	2.01	0.43
60:cc:12:ALA:HB3	60:cc:58:LEU:HD13	2.01	0.43
64:AA:39:TYR:CZ	84:RR:108:LEU:HD11	2.54	0.43
64:AA:85:ARG:HD3	64:AA:202:TYR:CA	2.48	0.43
64:AA:176:TRP:HB3	64:AA:198:MET:O	2.18	0.43
64:AA:182:VAL:O	64:AA:186:ARG:NH1	2.51	0.43
75:EF:169:LEU:HD23	75:EF:174:LEU:HD13	2.01	0.43
80:B2:369:C:H42	80:B2:1730:U:C5'	2.31	0.43
81:A6:2477:G:N2	81:A6:2501:C:C2	2.86	0.43
81:A6:3759:A:N7	81:A6:3764:U:O2	2.52	0.43
6:E:105:GLY:H	77:A5:684:G:C3'	2.31	0.43
8:G:167:VAL:HG22	8:G:167:VAL:O	2.18	0.43
12:L:86:ILE:HD11	12:L:121:ARG:HD3	2.01	0.43
21:V:26:ILE:HG22	21:V:101:ASN:HB2	2.01	0.43
32:h:9:LEU:HD22	32:h:57:VAL:HG23	2.00	0.43
33:i:33:LEU:HD21	33:i:41:ARG:NH1	2.34	0.43
44:u:89:TYR:H	81:A6:2660:A:N6	2.16	0.43
47:aa:56:ALA:HA	83:OO:124:MET:N	2.33	0.43
56:VV:31:SER:C	56:VV:32:ILE:HD13	2.42	0.43
56:VV:32:ILE:HG23	64:AA:120:ARG:O	2.18	0.43
58:XX:51:VAL:HG13	58:XX:70:VAL:HG11	1.99	0.43
64:AA:94:THR:O	64:AA:94:THR:HG22	2.17	0.43
64:AA:181:GLU:O	64:AA:182:VAL:C	2.57	0.43
64:AA:210:ILE:HG23	84:RR:81:ARG:HD2	1.90	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:DD:75:LYS:HB2	67:KK:22:VAL:HG21	2.01	0.43
68:MM:52:LEU:HD11	68:MM:62:VAL:HG22	2.00	0.43
75:EF:101:ASN:O	75:EF:122:THR:HG21	2.19	0.43
75:EF:582:THR:HG23	75:EF:698:ARG:O	2.18	0.43
77:A5:979:C:H2'	77:A5:981:C:H41	1.83	0.43
80:B2:1466:G:O6	84:RR:56:HIS:HE1	1.76	0.43
81:A6:4099:G:C1'	82:BB:224:GLU:HG2	2.46	0.43
83:OO:78:ALA:CB	83:OO:118:ALA:HB3	2.48	0.43
1:A:179:ILE:HG21	1:A:185:ALA:HB2	2.01	0.43
4:c:74:ARG:NH2	80:B2:1781:A:H62	2.17	0.43
5:D:132:VAL:HG13	5:D:172:SER:HB2	2.01	0.43
9:H:69:THR:HG22	81:A6:4700:A:N3	2.34	0.43
11:J:27:GLY:O	11:J:62:ILE:HG22	2.18	0.43
11:J:28:GLU:HA	11:J:68:ILE:HG22	2.01	0.43
20:U:23:LEU:CD2	20:U:87:THR:HG21	2.48	0.43
26:a:79:TRP:HE1	26:a:122:VAL:HG21	1.84	0.43
28:d:86:VAL:HG12	28:d:107:THR:O	2.19	0.43
44:u:29:LEU:O	81:A6:2658:G:C8	2.72	0.43
44:u:60:ILE:O	44:u:64:ALA:N	2.48	0.43
47:aa:69:VAL:CG2	83:OO:106:LYS:C	2.65	0.43
48:CC:82:TYR:HE1	56:VV:26:ALA:HB2	1.84	0.43
56:VV:3:ASN:C	56:VV:5:ALA:N	2.70	0.43
60:cc:15:THR:HG23	60:cc:33:GLU:OE1	2.19	0.43
64:AA:46:ILE:N	64:AA:46:ILE:HD13	2.34	0.43
64:AA:181:GLU:HA	64:AA:184:ARG:HB3	2.01	0.43
64:AA:210:ILE:CA	84:RR:81:ARG:CZ	2.62	0.43
71:SS:131:VAL:HG11	80:B2:1610:G:OP1	2.19	0.43
75:EF:461:ILE:HG22	75:EF:461:ILE:O	2.19	0.43
77:A5:1724:G:C6	77:A5:1838:A:N1	2.86	0.43
80:B2:1110:G:H21	82:BB:148:ASN:CG	2.16	0.43
81:A6:4099:G:H2'	82:BB:226:GLY:HA3	1.96	0.43
5:D:195:HIS:CE1	5:D:199:ILE:HD11	2.54	0.43
6:E:202:THR:HG21	13:M:107:PHE:HB2	1.98	0.43
21:V:18:LEU:HD12	21:V:54:ALA:HB3	2.00	0.43
29:e:86:GLU:O	29:e:89:LEU:HD22	2.18	0.43
49:EE:19:MET:HE1	80:B2:846:G:C5	2.53	0.43
54:LL:111:VAL:HG13	54:LL:140:PHE:C	2.44	0.43
56:VV:66:ASP:C	56:VV:69:ILE:H	2.27	0.43
64:AA:176:TRP:HE1	64:AA:180:ARG:NH2	2.16	0.43
68:MM:104:VAL:HG21	80:B2:1283:C:O2	2.18	0.43
77:A5:303:C:H2'	77:A5:304:C:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:B2:1455:A:P	84:RR:50:ILE:O	2.71	0.43
80:B2:1467:C:O3'	84:RR:3:ARG:HG2	2.19	0.43
81:A6:2606:G:H21	81:A6:2667:C:H41	1.65	0.43
24:Y:109:LEU:HD23	24:Y:110:LYS:C	2.44	0.43
30:f:48:ALA:HB1	30:f:69:VAL:HG21	2.01	0.43
49:EE:19:MET:HE1	80:B2:846:G:C4	2.54	0.43
64:AA:132:GLN:N	64:AA:132:GLN:CD	2.75	0.43
75:EF:833:GLN:O	75:EF:836:ALA:HB3	2.18	0.43
80:B2:1356:G:H4'	80:B2:1357:A:OP1	2.18	0.43
80:B2:1545:A:H61	80:B2:1655:C:H1'	1.83	0.43
80:B2:1757:G:C6	80:B2:1775:U:O2	2.72	0.43
81:A6:3927:U:O2	81:A6:4184:G:C6	2.71	0.43
84:RR:61:ILE:HD11	84:RR:69:ILE:HD11	2.01	0.43
21:V:112:MET:HE2	21:V:112:MET:HA	2.01	0.42
44:u:60:ILE:O	44:u:60:ILE:HG22	2.19	0.42
56:VV:60:ARG:HB3	56:VV:60:ARG:NH1	2.28	0.42
56:VV:76:ASP:HB2	64:AA:56:GLU:HA	2.01	0.42
64:AA:91:ALA:HB1	64:AA:94:THR:OG1	2.19	0.42
64:AA:189:ILE:HG21	64:AA:196:GLU:CD	2.43	0.42
64:AA:201:LEU:HB3	64:AA:202:TYR:CE1	2.54	0.42
75:EF:98:PHE:CE1	75:EF:355:THR:HG21	2.53	0.42
75:EF:124:GLY:CA	75:EF:358:LEU:HD22	2.49	0.42
77:A5:452:A:H4'	77:A5:453:G:OP2	2.19	0.42
80:B2:39:A:H61	80:B2:515:G:H1'	1.84	0.42
80:B2:953:C:OP1	82:BB:24:PRO:CB	2.67	0.42
84:RR:61:ILE:HD12	84:RR:66:VAL:HG21	2.01	0.42
35:k:26:LYS:HB2	35:k:69:LEU:HD12	2.00	0.42
44:u:89:TYR:CD2	81:A6:2660:A:N6	2.87	0.42
45:bb:45:THR:HG21	55:NN:59:GLY:HA3	2.01	0.42
47:aa:56:ALA:HA	83:OO:124:MET:H	1.85	0.42
56:VV:32:ILE:HG13	64:AA:145:ILE:HG22	2.01	0.42
64:AA:40:LYS:CB	84:RR:105:MET:CE	2.92	0.42
66:FF:17:ILE:HG21	66:FF:46:ALA:C	2.44	0.42
71:SS:131:VAL:HG11	80:B2:1610:G:P	2.59	0.42
74:ZZ:52:LYS:HA	74:ZZ:52:LYS:HE3	2.01	0.42
80:B2:969:U:OP1	82:BB:8:ARG:CZ	2.67	0.42
80:B2:1169:G:H1'	80:B2:1190:A:H61	1.84	0.42
5:D:204:VAL:HG22	78:A7:47:G:H5''	2.02	0.42
6:E:103:LYS:HD2	6:E:104:ASN:OD1	2.19	0.42
44:u:44:LYS:HG3	44:u:99:PRO:HD3	2.01	0.42
47:aa:65:PRO:CD	83:OO:129:ILE:HD13	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:VV:56:CYS:SG	56:VV:57:GLY:N	2.90	0.42
56:VV:59:ILE:HG22	56:VV:59:ILE:O	2.19	0.42
56:VV:60:ARG:N	64:AA:157:VAL:H	2.17	0.42
60:cc:42:ILE:HD13	60:cc:44:ARG:HH21	1.85	0.42
64:AA:188:THR:HB	64:AA:195:TRP:HE1	1.84	0.42
75:EF:505:VAL:HG11	75:EF:551:GLU:CG	2.49	0.42
78:A7:66:G:O6	78:A7:109:U:O2	2.37	0.42
80:B2:974:C:H4'	83:OO:41:PHE:CZ	2.54	0.42
80:B2:1110:G:H8	84:RR:126:MET:CE	2.31	0.42
80:B2:1120:U:N3	82:BB:204:ILE:HA	2.34	0.42
80:B2:1122:A:H4'	82:BB:205:TYR:CE2	2.53	0.42
80:B2:1124:C:C6	82:BB:151:ARG:NH2	2.82	0.42
80:B2:1468:C:OP2	84:RR:3:ARG:CG	2.59	0.42
7:F:164:LYS:HB3	7:F:166:ILE:HD11	2.01	0.42
12:L:59:VAL:HG21	12:L:73:GLY:CA	2.50	0.42
20:U:22:THR:C	20:U:23:LEU:HD12	2.43	0.42
35:k:24:LYS:HB3	35:k:69:LEU:HD11	2.01	0.42
44:u:72:HIS:C	44:u:73:HIS:CG	2.97	0.42
48:CC:89:LYS:HG2	64:AA:139:TYR:CZ	2.54	0.42
56:VV:73:ALA:HB2	64:AA:60:LEU:HB2	2.01	0.42
56:VV:83:PHE:CD1	64:AA:50:ASN:HA	2.54	0.42
64:AA:74:VAL:HG13	64:AA:121:LEU:H	1.84	0.42
64:AA:203:PHE:CD1	64:AA:203:PHE:C	2.97	0.42
66:FF:99:ILE:HD11	74:ZZ:108:ILE:HD11	2.01	0.42
74:ZZ:62:VAL:HG11	74:ZZ:91:LEU:HD13	2.00	0.42
77:A5:307:A:H3'	77:A5:308:G:H21	1.84	0.42
6:E:202:THR:HG23	13:M:105:THR:CG2	2.49	0.42
9:H:88:PHE:N	9:H:187:VAL:HG23	2.34	0.42
22:W:97:ARG:O	22:W:101:ILE:HG22	2.19	0.42
47:aa:51:ARG:O	83:OO:121:ARG:HD2	2.20	0.42
56:VV:66:ASP:O	56:VV:67:ASP:C	2.58	0.42
58:XX:10:ALA:O	58:XX:14:ARG:HG2	2.19	0.42
58:XX:67:ARG:HG3	58:XX:115:ILE:HG22	2.01	0.42
63:dd:6:LEU:HD11	80:B2:1301:A:O4'	2.19	0.42
73:UU:20:ILE:HG21	73:UU:98:VAL:HG21	2.01	0.42
77:A5:379:G:C6	79:A8:22:U:N3	2.87	0.42
77:A5:732:A:H61	77:A5:934:C:H42	1.68	0.42
77:A5:1874:A:H1'	81:A6:4213:A:H62	1.85	0.42
82:BB:103:MET:HE3	82:BB:104:ASP:N	2.35	0.42
3:C:152:LEU:HD21	3:C:174:LEU:HD22	2.00	0.42
28:d:29:ILE:H	28:d:29:ILE:HD12	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:e:119:ALA:HB3	41:r:119:ARG:HH12	1.85	0.42
43:t:122:ALA:HB3	43:t:128:THR:HG23	2.01	0.42
44:u:88:TYR:N	81:A6:2660:A:H62	2.18	0.42
44:u:89:TYR:CD1	44:u:89:TYR:N	2.85	0.42
64:AA:87:VAL:HG13	64:AA:99:ILE:HA	2.02	0.42
66:FF:147:VAL:HG12	66:FF:151:ILE:HD12	2.01	0.42
74:ZZ:94:LYS:HD2	74:ZZ:96:LEU:HD12	2.02	0.42
77:A5:1332:C:H2'	77:A5:1333:A:C8	2.54	0.42
80:B2:975:G:H1'	83:OO:43:HIS:HE1	0.54	0.42
80:B2:1351:G:O6	80:B2:1360:U:O4	2.38	0.42
81:A6:4883:C:H3'	81:A6:4884:G:H5''	2.00	0.42
7:F:236:GLU:OE1	18:S:38:VAL:HG22	2.19	0.42
11:J:109:ILE:HG22	11:J:111:GLU:H	1.85	0.42
15:O:54:TYR:HE2	15:O:145:VAL:HG21	1.84	0.42
25:Z:14:LEU:HD21	25:Z:81:MET:HB2	2.02	0.42
35:k:8:ILE:HD13	35:k:45:LEU:HD21	2.01	0.42
63:dd:48:LYS:HE3	63:dd:48:LYS:HA	2.01	0.42
64:AA:34:MET:HE3	64:AA:47:TYR:HE2	1.85	0.42
66:FF:27:ASP:OD1	66:FF:28:VAL:HG13	2.19	0.42
75:EF:632:ALA:HA	75:EF:646:ALA:HB1	2.02	0.42
75:EF:744:ILE:HD11	75:EF:787:TYR:HB3	2.01	0.42
77:A5:1979:A:H61	77:A5:1983:A:C2'	2.32	0.42
80:B2:975:G:HO2'	83:OO:43:HIS:CE1	2.37	0.42
81:A6:2377:C:N3	81:A6:2381:A:N7	2.68	0.42
81:A6:3653:A:N6	81:A6:3691:G:C4	2.87	0.42
82:BB:137:LEU:CD2	82:BB:215:VAL:HG22	2.49	0.42
2:B:90:VAL:CG2	2:B:104:THR:HG22	2.45	0.42
7:F:225:HIS:HB2	7:F:227:VAL:HG22	2.02	0.42
18:S:113:MET:SD	18:S:119:ALA:HB3	2.59	0.42
30:f:49:TYR:C	30:f:69:VAL:HG23	2.45	0.42
46:ee:83:VAL:HG12	58:XX:89:GLY:HA2	2.02	0.42
51:HH:166:VAL:O	51:HH:170:VAL:HG13	2.20	0.42
55:NN:114:ARG:HD3	55:NN:117:LEU:HD12	2.00	0.42
56:VV:76:ASP:CG	64:AA:60:LEU:HD13	2.45	0.42
59:YY:55:ILE:HD12	59:YY:75:ILE:CD1	2.49	0.42
70:QQ:78:VAL:HA	70:QQ:81:ILE:HD12	2.01	0.42
75:EF:13:MET:HE1	75:EF:461:ILE:CG2	2.49	0.42
80:B2:1122:A:O4'	82:BB:206:PRO:HD2	2.20	0.42
80:B2:1466:G:OP1	84:RR:10:LYS:CG	2.63	0.42
81:A6:2666:G:C6	81:A6:2669:C:C5	3.07	0.42
82:BB:105:LEU:HB2	82:BB:110:MET:HE3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:29:LEU:HD11	1:A:101:VAL:HG11	2.02	0.42
1:A:133:TYR:HB3	1:A:168:VAL:HG12	2.01	0.42
3:C:27:VAL:HG22	3:C:128:LEU:HD11	2.02	0.42
8:G:223:ARG:HE	8:G:227:ASN:HB2	1.84	0.42
9:H:92:MET:SD	9:H:181:VAL:HG22	2.60	0.42
20:U:39:PHE:CZ	20:U:87:THR:HG22	2.49	0.42
24:Y:58:VAL:HG23	24:Y:59:ARG:HG2	2.01	0.42
26:a:112:LEU:HD21	77:A5:1396:G:C4	2.55	0.42
30:f:58:VAL:O	81:A6:4945:G:H2'	2.19	0.42
42:s:82:ILE:HG23	42:s:82:ILE:O	2.20	0.42
52:II:100:CYS:SG	52:II:175:ILE:HD13	2.59	0.42
54:LL:111:VAL:HG11	54:LL:128:VAL:CG1	2.50	0.42
55:NN:60:VAL:HG11	55:NN:63:VAL:HG12	2.02	0.42
56:VV:55:ILE:CB	64:AA:143:PRO:HG3	2.50	0.42
64:AA:40:LYS:CB	84:RR:105:MET:HE2	2.50	0.42
64:AA:84:GLN:N	64:AA:207:PRO:HG2	2.35	0.42
64:AA:198:MET:CG	64:AA:199:PRO:HD3	2.50	0.42
80:B2:149:A:N7	80:B2:169:U:C2	2.88	0.42
80:B2:1373:C:H5''	84:RR:7:LYS:HE2	1.47	0.42
80:B2:1374:C:OP2	84:RR:7:LYS:CD	2.68	0.42
81:A6:4092:G:H3'	81:A6:4093:G:H21	1.85	0.42
4:c:12:LYS:HZ1	4:c:14:TYR:HD1	1.67	0.42
11:J:113:ILE:HD13	11:J:119:TYR:HB2	2.02	0.42
18:S:102:THR:O	18:S:106:VAL:HG23	2.20	0.42
21:V:18:LEU:HD23	21:V:18:LEU:H	1.85	0.42
25:Z:10:VAL:HG21	25:Z:87:VAL:HG23	2.02	0.42
29:e:119:ALA:HB3	41:r:119:ARG:NH1	2.35	0.42
30:f:58:VAL:CG1	81:A6:4945:G:C8	3.03	0.42
32:h:59:THR:HG22	32:h:63:GLN:CD	2.45	0.42
44:u:54:ALA:O	44:u:56:ARG:N	2.53	0.42
47:aa:53:ILE:CA	83:OO:117:ARG:HH21	2.32	0.42
47:aa:55:GLU:O	83:OO:124:MET:C	2.60	0.42
56:VV:32:ILE:HG13	64:AA:145:ILE:HB	2.02	0.42
56:VV:40:ASP:OD1	56:VV:42:VAL:N	2.53	0.42
56:VV:71:ARG:O	56:VV:72:LEU:C	2.63	0.42
57:WW:46:TYR:C	57:WW:47:ILE:HD12	2.45	0.42
62:gg:81:GLY:HA2	62:gg:87:LEU:HD23	2.02	0.42
64:AA:85:ARG:NH1	64:AA:204:TYR:CD2	2.88	0.42
64:AA:103:PHE:CZ	64:AA:108:PHE:CE1	3.08	0.42
64:AA:198:MET:O	64:AA:199:PRO:C	2.58	0.42
75:EF:9:ILE:HD11	75:EF:46:ILE:HG13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:EF:229:ALA:HB1	75:EF:256:MET:HE3	2.01	0.42
77:A5:1874:A:H4'	81:A6:4217:G:H22	1.84	0.42
14:N:169:ARG:HG3	14:N:174:LEU:HD12	2.02	0.41
30:f:58:VAL:CG1	30:f:58:VAL:HG21	2.47	0.41
32:h:44:LEU:HA	32:h:47:ILE:HD12	2.02	0.41
44:u:29:LEU:CD2	44:u:94:LEU:HA	2.50	0.41
44:u:54:ALA:CA	81:A6:4120:U:C6	3.02	0.41
48:CC:267:GLN:NE2	64:AA:185:MET:HB2	2.34	0.41
51:HH:107:LYS:CE	80:B2:744:G:H21	2.33	0.41
52:II:144:LYS:HE2	52:II:145:ILE:HD11	2.02	0.41
56:VV:3:ASN:HB2	56:VV:5:ALA:H	1.84	0.41
62:gg:29:ASP:O	62:gg:45:LEU:HD23	2.20	0.41
62:gg:279:SER:CB	84:RR:63:ARG:CB	2.98	0.41
64:AA:176:TRP:CE3	64:AA:198:MET:C	2.98	0.41
65:DD:24:PHE:CZ	65:DD:72:VAL:HG11	2.55	0.41
69:PP:108:LYS:HB2	71:SS:117:ILE:HD11	2.01	0.41
80:B2:185:G:O6	80:B2:214:U:C2	2.73	0.41
80:B2:1123:C:O2'	82:BB:148:ASN:O	2.38	0.41
81:A6:4765:G:C6	81:A6:4869:U:O2	2.73	0.41
81:A6:4966:A:H2'	81:A6:4967:A:O4'	2.20	0.41
82:BB:130:THR:HG23	82:BB:177:GLN:O	2.20	0.41
82:BB:175:GLU:OE2	82:BB:193:ILE:HG23	2.20	0.41
5:D:6:VAL:HG13	5:D:9:ASN:HB3	2.03	0.41
5:D:157:ASN:OD1	5:D:159:VAL:HG22	2.20	0.41
5:D:211:LEU:HD12	5:D:223:PHE:CE2	2.54	0.41
16:P:112:LEU:HD12	16:P:150:LEU:HB2	2.01	0.41
34:j:53:ALA:HB2	77:A5:373:G:C5'	2.51	0.41
40:p:75:SER:O	40:p:79:VAL:HG13	2.20	0.41
49:EE:147:ILE:HG21	49:EE:169:ILE:HD11	2.00	0.41
56:VV:18:SER:N	56:VV:53:TYR:O	2.52	0.41
60:cc:12:ALA:CB	60:cc:58:LEU:HD13	2.50	0.41
64:AA:47:TYR:CG	64:AA:164:ASN:HB2	2.55	0.41
67:KK:49:MET:HE1	67:KK:69:TRP:CE2	2.55	0.41
3:C:288:ASP:O	3:C:292:ILE:HD12	2.19	0.41
5:D:273:LEU:HD22	78:A7:107:G:O3'	2.20	0.41
32:h:24:LEU:HD22	32:h:50:VAL:HG23	2.01	0.41
44:u:27:TYR:HB3	44:u:96:ILE:HG13	2.01	0.41
44:u:27:TYR:CD2	44:u:27:TYR:C	2.93	0.41
44:u:87:LYS:HD2	44:u:87:LYS:N	2.35	0.41
44:u:88:TYR:H	81:A6:2660:A:H62	1.67	0.41
52:II:113:TYR:CE1	52:II:158:ILE:HD11	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:VV:20:SER:HB3	56:VV:22:ARG:HD3	2.01	0.41
56:VV:59:ILE:CA	64:AA:156:TYR:N	2.83	0.41
56:VV:62:MET:HB2	64:AA:152:SER:HB3	2.02	0.41
56:VV:65:SER:HB2	64:AA:157:VAL:O	2.20	0.41
56:VV:69:ILE:O	64:AA:57:LYS:CD	2.68	0.41
56:VV:83:PHE:N	64:AA:52:LYS:HG3	2.35	0.41
64:AA:47:TYR:CE1	64:AA:150:THR:HG23	2.55	0.41
64:AA:204:TYR:CD2	64:AA:205:ARG:O	2.73	0.41
68:MM:22:LEU:HD23	68:MM:88:TRP:HB3	2.02	0.41
75:EF:227:GLN:NE2	75:EF:344:LEU:HD22	2.35	0.41
75:EF:676:LYS:O	75:EF:680:VAL:HG22	2.20	0.41
75:EF:755:VAL:O	75:EF:755:VAL:HG12	2.20	0.41
80:B2:956:G:O5'	82:BB:4:GLY:N	2.54	0.41
23:X:90:ILE:HG13	23:X:146:ALA:HB1	2.02	0.41
33:i:33:LEU:HD13	77:A5:308:G:O2'	2.20	0.41
43:t:112:ILE:HG22	43:t:132:ILE:HD13	2.03	0.41
44:u:20:LEU:HD23	44:u:102:SER:HA	2.01	0.41
44:u:27:TYR:HA	44:u:95:ALA:C	2.45	0.41
44:u:29:LEU:HD23	44:u:94:LEU:HA	2.03	0.41
44:u:74:TYR:CG	44:u:75:SER:N	2.89	0.41
48:CC:266:TYR:HB3	64:AA:186:ARG:HH21	1.85	0.41
64:AA:99:ILE:HD11	64:AA:115:ALA:HB1	2.03	0.41
64:AA:198:MET:CB	64:AA:199:PRO:HD3	2.50	0.41
75:EF:153:PRO:HG2	75:EF:205:ILE:HD11	2.02	0.41
80:B2:1757:G:O6	80:B2:1775:U:C2	2.72	0.41
80:B2:1858:G:OP2	83:OO:146:ARG:NH2	2.54	0.41
2:B:71:GLU:HG3	2:B:73:VAL:HG13	2.01	0.41
5:D:261:VAL:HG23	5:D:261:VAL:O	2.21	0.41
6:E:157:THR:HG21	6:E:196:PHE:HD2	1.86	0.41
21:V:26:ILE:HG22	21:V:101:ASN:CB	2.49	0.41
27:b:32:LEU:HD22	77:A5:1464:C:C5'	2.50	0.41
37:m:95:ILE:HD12	81:A6:4473:A:H5''	2.03	0.41
43:t:110:VAL:HG22	43:t:162:CYS:SG	2.60	0.41
44:u:105:ILE:HD12	44:u:105:ILE:C	2.46	0.41
48:CC:165:VAL:HG22	48:CC:244:ILE:CG2	2.50	0.41
56:VV:40:ASP:OD1	56:VV:43:THR:N	2.54	0.41
56:VV:65:SER:HB2	64:AA:158:ASP:HA	2.03	0.41
58:XX:14:ARG:HG2	58:XX:14:ARG:HH11	1.85	0.41
64:AA:197:VAL:HG12	64:AA:198:MET:N	2.35	0.41
64:AA:208:GLU:C	84:RR:81:ARG:HH22	2.28	0.41
65:DD:159:HIS:C	65:DD:164:VAL:HG21	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:FF:195:GLU:O	66:FF:199:VAL:HG23	2.21	0.41
75:EF:427:VAL:HG13	75:EF:485:ILE:CG2	2.49	0.41
75:EF:781:MET:HA	75:EF:781:MET:HE3	2.01	0.41
80:B2:941:C:H5'	82:BB:136:ARG:HH22	1.77	0.41
81:A6:2590:G:H1'	81:A6:2755:A:H61	1.85	0.41
81:A6:2666:G:N3	81:A6:2669:C:O4'	2.50	0.41
6:E:105:GLY:N	77:A5:684:G:C4'	2.82	0.41
6:E:221:LYS:N	81:A6:4940:C:N3	2.69	0.41
44:u:27:TYR:O	44:u:27:TYR:CD1	2.73	0.41
44:u:29:LEU:HD13	81:A6:2673:G:N7	2.34	0.41
47:aa:58:VAL:HG22	47:aa:58:VAL:O	2.20	0.41
48:CC:266:TYR:HB3	64:AA:94:THR:HG23	2.01	0.41
56:VV:37:ALA:HA	64:AA:181:GLU:HB2	2.02	0.41
75:EF:24:VAL:HG23	75:EF:102:LEU:CD1	2.50	0.41
75:EF:587:SER:OG	75:EF:736:ALA:HB2	2.21	0.41
77:A5:470:A:C8	77:A5:684:G:N2	2.84	0.41
77:A5:707:C:H4'	81:A6:4943:A:H61	1.86	0.41
80:B2:956:G:C5'	82:BB:3:VAL:CA	2.96	0.41
80:B2:968:U:C2'	82:BB:8:ARG:HH11	2.24	0.41
80:B2:1125:C:O5'	84:RR:129:LYS:NZ	2.54	0.41
9:H:69:THR:HG22	81:A6:4700:A:H2	1.84	0.41
15:O:54:TYR:CD2	15:O:145:VAL:HG11	2.56	0.41
18:S:28:TYR:HD1	19:T:151:LEU:HD22	1.85	0.41
47:aa:52:ASP:C	83:OO:117:ARG:O	2.63	0.41
48:CC:84:PHE:CG	64:AA:67:ALA:HB1	2.56	0.41
55:NN:129:TYR:HB2	55:NN:135:LEU:HD12	2.02	0.41
63:dd:52:PHE:HA	73:UU:82:MET:HE1	2.02	0.41
77:A5:116:G:HO2'	77:A5:117:C:H6	1.69	0.41
80:B2:976:G:H1'	83:OO:49:GLY:O	2.21	0.41
84:RR:103:LYS:O	84:RR:107:LYS:HD2	2.20	0.41
1:A:111:THR:HG22	40:p:86:LEU:HG	2.02	0.41
48:CC:266:TYR:CE2	64:AA:74:VAL:HG21	2.56	0.41
49:EE:92:ILE:HG21	59:YY:17:LEU:HD21	2.03	0.41
51:HH:107:LYS:HE3	80:B2:744:G:H21	1.86	0.41
55:NN:94:LYS:O	55:NN:98:VAL:HG22	2.20	0.41
56:VV:12:TYR:O	56:VV:13:VAL:C	2.61	0.41
64:AA:84:GLN:HB2	64:AA:204:TYR:HE1	1.86	0.41
69:PP:112:ILE:HD12	69:PP:112:ILE:H	1.86	0.41
75:EF:22:MET:HE3	75:EF:23:SER:H	1.85	0.41
75:EF:74:ALA:HA	75:EF:103:ILE:HD13	2.03	0.41
80:B2:1476:A:C8	84:RR:49:LYS:NZ	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:326:LEU:HD22	3:C:333:LYS:HB2	2.03	0.41
6:E:198:ILE:HD11	30:f:105:LEU:CD1	2.51	0.41
7:F:36:PHE:CE2	7:F:40:MET:HE3	2.55	0.41
7:F:90:PHE:CZ	7:F:92:ILE:HD11	2.55	0.41
8:G:161:VAL:HG21	8:G:167:VAL:HG11	2.02	0.41
11:J:56:THR:HG21	39:o:106:PHE:C	2.46	0.41
11:J:130:PHE:CE2	11:J:132:VAL:HG23	2.55	0.41
12:L:104:ASN:HB2	12:L:110:LEU:HD21	2.03	0.41
24:Y:7:VAL:HG21	77:A5:242:U:OP1	2.21	0.41
24:Y:101:PRO:HA	24:Y:104:VAL:HG12	2.02	0.41
28:d:19:GLU:OE1	28:d:20:VAL:HG23	2.21	0.41
40:p:25:MET:HE1	80:B2:1040:G:C5'	2.51	0.41
44:u:72:HIS:CD2	44:u:104:ILE:HG21	2.55	0.41
44:u:77:ASN:O	44:u:78:ASN:C	2.64	0.41
44:u:103:ASP:HA	44:u:106:ARG:CZ	2.51	0.41
47:aa:28:ARG:CG	83:OO:146:ARG:O	2.69	0.41
47:aa:65:PRO:HB3	83:OO:129:ILE:HD12	1.97	0.41
48:CC:258:GLU:HB3	64:AA:63:ARG:NH2	2.35	0.41
55:NN:40:LEU:HD23	55:NN:43:LYS:CE	2.50	0.41
55:NN:88:LEU:CD2	55:NN:125:LEU:HD23	2.50	0.41
56:VV:18:SER:HA	56:VV:53:TYR:HB2	2.02	0.41
57:WW:4:MET:HE1	80:B2:1159:G:O4'	2.21	0.41
62:gg:212:LYS:HD2	84:RR:22:THR:HG21	1.98	0.41
64:AA:55:TRP:HA	64:AA:58:LEU:HG	2.02	0.41
64:AA:102:ARG:NH1	80:B2:1377:U:C5	2.89	0.41
64:AA:172:GLY:CA	64:AA:203:PHE:CB	2.98	0.41
72:TT:112:MET:HE2	72:TT:112:MET:HA	2.03	0.41
73:UU:76:THR:HG21	80:B2:1338:G:H5''	2.03	0.41
75:EF:6:VAL:HG22	75:EF:461:ILE:HG12	2.03	0.41
75:EF:552:LEU:HD12	75:EF:555:GLU:OE2	2.21	0.41
80:B2:1373:C:C3'	84:RR:7:LYS:HZ3	2.24	0.41
80:B2:1465:A:H5''	84:RR:10:LYS:HG2	1.86	0.41
80:B2:1611:G:H2'	80:B2:1612:G:O4'	2.20	0.41
81:A6:2666:G:C2	81:A6:2668:G:H3'	2.56	0.41
81:A6:4745:G:H21	81:A6:4955:A:H62	1.68	0.41
84:RR:73:LEU:HD12	84:RR:74:GLN:H	1.86	0.41
1:A:113:VAL:HG23	1:A:116:LEU:HD21	2.03	0.41
5:D:99:TYR:CG	5:D:199:ILE:HG23	2.56	0.41
15:O:54:TYR:CE2	15:O:145:VAL:HG11	2.56	0.41
19:T:80:VAL:HG21	19:T:85:LEU:HD13	2.03	0.41
26:a:112:LEU:HD21	77:A5:1396:G:N3	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:112:ILE:HD11	77:A5:1267:C:H5	1.86	0.41
50:GG:50:VAL:CG2	50:GG:111:LEU:HD12	2.51	0.41
54:LL:93:LEU:HD12	54:LL:102:PHE:CB	2.50	0.41
56:VV:16:LYS:CG	56:VV:21:ASN:HA	2.51	0.41
56:VV:78:ILE:HG23	64:AA:10:MET:HB2	2.02	0.41
57:WW:75:ILE:HG23	80:B2:1157:G:C5	2.56	0.41
64:AA:85:ARG:HB2	64:AA:204:TYR:HB2	2.02	0.41
64:AA:188:THR:HB	64:AA:195:TRP:NE1	2.36	0.41
68:MM:22:LEU:HD11	68:MM:89:VAL:HG12	2.02	0.41
74:ZZ:48:VAL:O	74:ZZ:83:LEU:HD22	2.20	0.41
82:BB:193:ILE:HG22	82:BB:197:ILE:HD12	2.02	0.41
3:C:302:LEU:HD22	17:Q:38:ARG:CB	2.48	0.40
10:I:38:ARG:HG3	10:I:41:ALA:HB2	2.02	0.40
11:J:83:LEU:HD12	11:J:132:VAL:HG21	2.02	0.40
12:L:184:MET:HA	12:L:184:MET:HE2	2.03	0.40
17:Q:61:LEU:HD21	17:Q:66:MET:CB	2.50	0.40
30:f:94:ALA:HB3	77:A5:1308:C:O2'	2.21	0.40
43:t:56:LEU:CD2	43:t:82:ILE:HG21	2.50	0.40
43:t:77:ALA:HA	43:t:80:LEU:HD12	2.03	0.40
47:aa:24:THR:HA	83:OO:142:ARG:NH1	2.36	0.40
48:CC:261:PHE:CD1	64:AA:63:ARG:CD	3.05	0.40
49:EE:192:ILE:HD12	49:EE:242:LYS:C	2.47	0.40
50:GG:133:LEU:HD12	80:B2:169:U:H1'	2.03	0.40
53:JJ:78:LEU:HD23	53:JJ:97:ILE:HD11	2.03	0.40
55:NN:102:LEU:HD13	55:NN:115:LEU:CD1	2.51	0.40
56:VV:83:PHE:CD1	56:VV:83:PHE:N	2.88	0.40
62:gg:62:HIS:CD2	62:gg:66:VAL:HG22	2.56	0.40
64:AA:131:HIS:C	64:AA:133:PRO:HD2	2.45	0.40
64:AA:149:ASN:HD21	64:AA:166:LYS:CE	2.26	0.40
64:AA:176:TRP:HE1	64:AA:180:ARG:CD	2.34	0.40
75:EF:13:MET:HE3	75:EF:463:ASP:O	2.21	0.40
77:A5:2087:C:H2'	81:A6:2268:A:H61	1.86	0.40
78:A7:5:A:H2'	78:A7:6:C:O4'	2.20	0.40
80:B2:1124:C:H4'	82:BB:150:ILE:CD1	2.32	0.40
80:B2:1455:A:H3'	84:RR:52:GLY:HA2	2.02	0.40
3:C:218:ILE:HG22	3:C:222:ARG:HD3	2.03	0.40
10:I:41:ALA:HB3	10:I:139:ARG:HH22	1.86	0.40
18:S:45:TRP:NE1	18:S:61:ILE:HD11	2.37	0.40
20:U:33:ILE:HD11	20:U:100:LEU:HD21	2.04	0.40
40:p:41:PHE:CE2	44:u:51:ASN:CB	3.04	0.40
44:u:45:LEU:C	44:u:45:LEU:CD1	2.90	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:EE:196:THR:HG21	49:EE:211:LYS:HE2	2.02	0.40
52:II:121:LEU:HD11	52:II:166:PHE:CD2	2.57	0.40
57:WW:83:LEU:HA	57:WW:86:LEU:HD22	2.02	0.40
64:AA:86:ALA:HB2	64:AA:89:LYS:NZ	2.37	0.40
64:AA:164:ASN:HD21	64:AA:166:LYS:H	1.69	0.40
75:EF:225:LEU:HD13	75:EF:289:PHE:CE1	2.56	0.40
77:A5:287:U:H2'	77:A5:288:G:C8	2.56	0.40
77:A5:379:G:N1	79:A8:22:U:N3	2.69	0.40
77:A5:379:G:C6	79:A8:22:U:C4	3.08	0.40
80:B2:969:U:OP1	82:BB:8:ARG:NH1	2.54	0.40
12:L:59:VAL:HG13	77:A5:74:G:H4'	2.04	0.40
25:Z:53:VAL:HB	25:Z:62:ILE:HD12	2.02	0.40
32:h:21:LEU:HD11	32:h:58:LEU:CD2	2.51	0.40
50:GG:7:PHE:CD2	50:GG:10:THR:HG23	2.57	0.40
56:VV:51:LYS:N	64:AA:62:ALA:HB3	2.34	0.40
64:AA:214:GLU:CD	84:RR:82:ASP:HB3	2.33	0.40
67:KK:22:VAL:HG13	67:KK:68:TYR:HE1	1.86	0.40
70:QQ:16:LYS:HG3	70:QQ:17:LYS:H	1.87	0.40
72:TT:11:GLN:O	72:TT:15:VAL:HG23	2.22	0.40
73:UU:46:LYS:HE2	73:UU:101:ILE:HD11	2.04	0.40
77:A5:52:G:H4'	77:A5:1529:G:H4'	2.03	0.40
77:A5:352:G:N2	77:A5:360:A:N1	2.69	0.40
2:B:77:THR:HG21	2:B:337:VAL:CG1	2.51	0.40
21:V:126:ALA:CB	21:V:133:ALA:HB2	2.51	0.40
24:Y:1:MET:HE2	77:A5:227:A:OP2	2.21	0.40
24:Y:77:LYS:O	24:Y:79:VAL:HG13	2.22	0.40
49:EE:151:ASP:CB	49:EE:154:ILE:HD12	2.51	0.40
56:VV:79:VAL:HG22	64:AA:10:MET:HE2	2.04	0.40
57:WW:7:LEU:HD21	57:WW:33:VAL:HG23	2.03	0.40
64:AA:89:LYS:HD2	64:AA:201:LEU:HG	2.02	0.40
64:AA:176:TRP:NE1	64:AA:180:ARG:CD	2.85	0.40
64:AA:189:ILE:HG21	64:AA:196:GLU:HG2	2.03	0.40
64:AA:198:MET:HB2	64:AA:199:PRO:HD3	2.02	0.40
65:DD:66:ILE:HD11	65:DD:86:LEU:CB	2.50	0.40
70:QQ:13:PHE:CB	70:QQ:22:VAL:HG22	2.51	0.40
75:EF:116:THR:HG21	75:EF:499:PHE:HB3	2.04	0.40
75:EF:427:VAL:CG2	75:EF:447:ILE:HD11	2.52	0.40
75:EF:596:PRO:HD2	75:EF:721:ILE:HG23	2.03	0.40
80:B2:176:U:O2	80:B2:313:A:C5	2.74	0.40
80:B2:988:C:H5'	82:BB:116:LYS:CD	2.44	0.40
80:B2:1125:C:O5'	84:RR:129:LYS:HE2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:BB:169:MET:O	82:BB:173:THR:HG23	2.22	0.40
83:OO:78:ALA:HB3	83:OO:118:ALA:CB	2.49	0.40
12:L:126:LEU:HD11	32:h:117:ARG:NH2	2.36	0.40
13:M:117:LYS:HE3	13:M:118:MET:HE1	2.03	0.40
15:O:47:PHE:CE1	15:O:141:LEU:HD22	2.56	0.40
47:aa:26:CYS:CB	83:OO:149:ARG:CB	2.82	0.40
50:GG:133:LEU:HD11	80:B2:150:A:N1	2.35	0.40
50:GG:157:VAL:CG2	50:GG:173:ALA:HB1	2.51	0.40
54:LL:93:LEU:HD13	54:LL:103:GLU:C	2.47	0.40
56:VV:28:ASP:CA	64:AA:138:SER:HA	2.51	0.40
56:VV:33:GLN:NE2	64:AA:143:PRO:CD	2.85	0.40
64:AA:76:VAL:HB	64:AA:123:VAL:HB	2.03	0.40
64:AA:109:THR:HB	64:AA:136:GLU:CD	2.46	0.40
71:SS:70:ILE:HG22	71:SS:77:TYR:CE1	2.56	0.40
75:EF:552:LEU:HD11	81:A6:4607:A:H4'	2.02	0.40
80:B2:66:G:N2	80:B2:67:C:H42	2.19	0.40
80:B2:1374:C:C5	84:RR:7:LYS:NZ	2.90	0.40
80:B2:1452:A:OP1	84:RR:47:ARG:NH1	2.53	0.40
80:B2:1453:C:H6	84:RR:47:ARG:HG2	1.87	0.40
81:A6:2845:A:N1	81:A6:3843:C:N3	2.69	0.40
81:A6:4575:G:H21	81:A6:5068:G:H5'	1.86	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	A	246/248 (99%)	228 (93%)	18 (7%)	0	100	100
2	B	395/398 (99%)	361 (91%)	34 (9%)	0	100	100
3	C	361/363 (99%)	348 (96%)	13 (4%)	0	100	100
4	c	111/121 (92%)	104 (94%)	6 (5%)	1 (1%)	14	50

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	D	291/293 (99%)	271 (93%)	20 (7%)	0	100	100
6	E	217/224 (97%)	197 (91%)	20 (9%)	0	100	100
7	F	223/225 (99%)	208 (93%)	15 (7%)	0	100	100
8	G	211/215 (98%)	201 (95%)	10 (5%)	0	100	100
9	H	188/190 (99%)	177 (94%)	11 (6%)	0	100	100
10	I	195/213 (92%)	186 (95%)	9 (5%)	0	100	100
11	J	168/170 (99%)	154 (92%)	14 (8%)	0	100	100
12	L	203/205 (99%)	192 (95%)	11 (5%)	0	100	100
13	M	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
14	N	201/203 (99%)	185 (92%)	16 (8%)	0	100	100
15	O	197/199 (99%)	189 (96%)	8 (4%)	0	100	100
16	P	151/153 (99%)	145 (96%)	6 (4%)	0	100	100
17	Q	185/187 (99%)	171 (92%)	14 (8%)	0	100	100
18	S	174/176 (99%)	165 (95%)	9 (5%)	0	100	100
19	T	157/159 (99%)	148 (94%)	9 (6%)	0	100	100
20	U	97/99 (98%)	95 (98%)	2 (2%)	0	100	100
21	V	129/131 (98%)	115 (89%)	14 (11%)	0	100	100
22	W	178/180 (99%)	173 (97%)	5 (3%)	0	100	100
23	X	116/118 (98%)	107 (92%)	9 (8%)	0	100	100
24	Y	132/134 (98%)	127 (96%)	5 (4%)	0	100	100
25	Z	133/135 (98%)	124 (93%)	9 (7%)	0	100	100
26	a	144/147 (98%)	138 (96%)	6 (4%)	0	100	100
27	b	69/104 (66%)	67 (97%)	2 (3%)	0	100	100
28	d	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
29	e	126/128 (98%)	119 (94%)	7 (6%)	0	100	100
30	f	108/110 (98%)	99 (92%)	9 (8%)	0	100	100
31	g	108/110 (98%)	101 (94%)	7 (6%)	0	100	100
32	h	119/121 (98%)	115 (97%)	4 (3%)	0	100	100
33	i	100/102 (98%)	95 (95%)	5 (5%)	0	100	100
34	j	84/86 (98%)	79 (94%)	5 (6%)	0	100	100
35	k	67/69 (97%)	67 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	l	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
37	m	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
38	n	23/25 (92%)	23 (100%)	0	0	100	100
39	o	102/105 (97%)	93 (91%)	9 (9%)	0	100	100
40	p	89/91 (98%)	82 (92%)	7 (8%)	0	100	100
41	r	125/127 (98%)	116 (93%)	9 (7%)	0	100	100
42	s	101/103 (98%)	94 (93%)	7 (7%)	0	100	100
43	t	154/156 (99%)	140 (91%)	14 (9%)	0	100	100
44	u	84/100 (84%)	81 (96%)	2 (2%)	1 (1%)	10	42
45	bb	80/82 (98%)	75 (94%)	5 (6%)	0	100	100
46	ee	45/49 (92%)	43 (96%)	2 (4%)	0	100	100
47	aa	96/98 (98%)	79 (82%)	17 (18%)	0	100	100
48	CC	216/218 (99%)	199 (92%)	17 (8%)	0	100	100
49	EE	260/262 (99%)	249 (96%)	11 (4%)	0	100	100
50	GG	226/228 (99%)	212 (94%)	14 (6%)	0	100	100
51	HH	178/190 (94%)	167 (94%)	11 (6%)	0	100	100
52	II	204/206 (99%)	199 (98%)	5 (2%)	0	100	100
53	JJ	178/180 (99%)	173 (97%)	5 (3%)	0	100	100
54	LL	137/149 (92%)	131 (96%)	6 (4%)	0	100	100
55	NN	147/149 (99%)	140 (95%)	7 (5%)	0	100	100
56	VV	81/83 (98%)	68 (84%)	11 (14%)	2 (2%)	4	25
57	WW	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
58	XX	137/141 (97%)	125 (91%)	11 (8%)	1 (1%)	18	55
59	YY	123/125 (98%)	117 (95%)	6 (5%)	0	100	100
60	cc	59/61 (97%)	53 (90%)	6 (10%)	0	100	100
61	ff	65/67 (97%)	60 (92%)	5 (8%)	0	100	100
62	gg	311/313 (99%)	276 (89%)	35 (11%)	0	100	100
63	dd	53/55 (96%)	51 (96%)	2 (4%)	0	100	100
64	AA	203/214 (95%)	179 (88%)	17 (8%)	7 (3%)	3	20
65	DD	223/225 (99%)	211 (95%)	12 (5%)	0	100	100
66	FF	182/189 (96%)	175 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
67	KK	94/96 (98%)	87 (93%)	7 (7%)	0	100	100
68	MM	122/124 (98%)	111 (91%)	11 (9%)	0	100	100
69	PP	116/118 (98%)	107 (92%)	9 (8%)	0	100	100
70	QQ	139/141 (99%)	124 (89%)	15 (11%)	0	100	100
71	SS	143/145 (99%)	131 (92%)	12 (8%)	0	100	100
72	TT	138/141 (98%)	131 (95%)	6 (4%)	1 (1%)	18	55
73	UU	97/99 (98%)	95 (98%)	2 (2%)	0	100	100
74	ZZ	73/75 (97%)	69 (94%)	4 (6%)	0	100	100
75	EF	854/856 (100%)	743 (87%)	109 (13%)	2 (0%)	43	77
82	BB	214/218 (98%)	204 (95%)	10 (5%)	0	100	100
83	OO	132/134 (98%)	122 (92%)	10 (8%)	0	100	100
84	RR	130/132 (98%)	124 (95%)	6 (5%)	0	100	100
All	All	12180/12459 (98%)	11346 (93%)	819 (7%)	15 (0%)	49	83

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
64	AA	98	PRO
64	AA	155	ARG
64	AA	162	PRO
64	AA	198	MET
56	VV	80	SER
64	AA	22	GLY
75	EF	109	VAL
44	u	49	ALA
56	VV	54	ALA
64	AA	153	PRO
72	TT	66	LEU
64	AA	132	GLN
75	EF	630	GLN
58	XX	87	ASN
4	c	15	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	190/190 (100%)	190 (100%)	0	100	100
2	B	344/344 (100%)	344 (100%)	0	100	100
3	C	303/303 (100%)	303 (100%)	0	100	100
4	c	94/100 (94%)	94 (100%)	0	100	100
5	D	247/247 (100%)	247 (100%)	0	100	100
6	E	197/197 (100%)	197 (100%)	0	100	100
7	F	196/196 (100%)	196 (100%)	0	100	100
8	G	187/187 (100%)	187 (100%)	0	100	100
9	H	169/169 (100%)	169 (100%)	0	100	100
10	I	170/180 (94%)	170 (100%)	0	100	100
11	J	143/143 (100%)	143 (100%)	0	100	100
12	L	170/170 (100%)	170 (100%)	0	100	100
13	M	116/116 (100%)	116 (100%)	0	100	100
14	N	171/171 (100%)	171 (100%)	0	100	100
15	O	171/171 (100%)	171 (100%)	0	100	100
16	P	134/134 (100%)	134 (100%)	0	100	100
17	Q	164/164 (100%)	164 (100%)	0	100	100
18	S	157/157 (100%)	157 (100%)	0	100	100
19	T	139/139 (100%)	139 (100%)	0	100	100
20	U	89/89 (100%)	89 (100%)	0	100	100
21	V	100/101 (99%)	100 (100%)	0	100	100
22	W	159/159 (100%)	159 (100%)	0	100	100
23	X	106/106 (100%)	106 (100%)	0	100	100
24	Y	124/124 (100%)	124 (100%)	0	100	100
25	Z	117/117 (100%)	117 (100%)	0	100	100
26	a	118/118 (100%)	118 (100%)	0	100	100
27	b	63/84 (75%)	63 (100%)	0	100	100
28	d	98/98 (100%)	98 (100%)	0	100	100
29	e	114/114 (100%)	114 (100%)	0	100	100
30	f	89/89 (100%)	89 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	g	94/94 (100%)	94 (100%)	0	100	100
32	h	109/109 (100%)	109 (100%)	0	100	100
33	i	86/86 (100%)	86 (100%)	0	100	100
34	j	73/73 (100%)	73 (100%)	0	100	100
35	k	64/64 (100%)	64 (100%)	0	100	100
36	l	47/47 (100%)	47 (100%)	0	100	100
37	m	46/46 (100%)	46 (100%)	0	100	100
38	n	24/24 (100%)	24 (100%)	0	100	100
39	o	92/92 (100%)	92 (100%)	0	100	100
40	p	74/74 (100%)	74 (100%)	0	100	100
41	r	110/110 (100%)	110 (100%)	0	100	100
42	s	90/90 (100%)	90 (100%)	0	100	100
43	t	128/128 (100%)	128 (100%)	0	100	100
44	u	74/85 (87%)	39 (53%)	35 (47%)	0	0
45	bb	74/74 (100%)	74 (100%)	0	100	100
46	ee	41/41 (100%)	41 (100%)	0	100	100
47	aa	85/85 (100%)	85 (100%)	0	100	100
48	CC	182/183 (100%)	182 (100%)	0	100	100
49	EE	224/224 (100%)	224 (100%)	0	100	100
50	GG	199/199 (100%)	199 (100%)	0	100	100
51	HH	167/170 (98%)	167 (100%)	0	100	100
52	II	178/178 (100%)	178 (100%)	0	100	100
53	JJ	160/160 (100%)	160 (100%)	0	100	100
54	LL	128/134 (96%)	128 (100%)	0	100	100
55	NN	130/130 (100%)	130 (100%)	0	100	100
56	VV	68/68 (100%)	45 (66%)	23 (34%)	0	2
57	WW	112/112 (100%)	112 (100%)	0	100	100
58	XX	113/113 (100%)	113 (100%)	0	100	100
59	YY	107/107 (100%)	107 (100%)	0	100	100
60	cc	54/54 (100%)	54 (100%)	0	100	100
61	ff	60/60 (100%)	60 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
62	gg	272/272 (100%)	272 (100%)	0	100	100
63	dd	48/48 (100%)	48 (100%)	0	100	100
64	AA	172/179 (96%)	96 (56%)	76 (44%)	0	0
65	DD	189/189 (100%)	189 (100%)	0	100	100
66	FF	158/159 (99%)	158 (100%)	0	100	100
67	KK	87/87 (100%)	87 (100%)	0	100	100
68	MM	104/104 (100%)	104 (100%)	0	100	100
69	PP	107/107 (100%)	107 (100%)	0	100	100
70	QQ	117/117 (100%)	117 (100%)	0	100	100
71	SS	125/125 (100%)	125 (100%)	0	100	100
72	TT	110/110 (100%)	110 (100%)	0	100	100
73	UU	92/92 (100%)	92 (100%)	0	100	100
74	ZZ	66/66 (100%)	66 (100%)	0	100	100
75	EF	727/728 (100%)	727 (100%)	0	100	100
82	BB	197/197 (100%)	192 (98%)	5 (2%)	42	62
83	OO	104/104 (100%)	102 (98%)	2 (2%)	50	66
84	RR	119/119 (100%)	115 (97%)	4 (3%)	32	54
All	All	10626/10694 (99%)	10481 (99%)	145 (1%)	57	72

All (145) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	u	13	SER
44	u	17	ARG
44	u	19	GLN
44	u	21	VAL
44	u	23	LYS
44	u	26	LYS
44	u	28	VAL
44	u	44	LYS
44	u	45	LEU
44	u	46	VAL
44	u	48	LEU
44	u	51	ASN
44	u	52	CYS
44	u	55	LEU

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Mol	Chain	Res	Type
44	u	57	LYS
44	u	58	SER
44	u	62	TYR
44	u	65	MET
44	u	68	LYS
44	u	72	HIS
44	u	77	ASN
44	u	79	ILE
44	u	80	GLU
44	u	81	LEU
44	u	83	THR
44	u	85	CYS
44	u	87	LYS
44	u	90	ARG
44	u	91	VAL
44	u	94	LEU
44	u	96	ILE
44	u	98	ASP
44	u	104	ILE
44	u	105	ILE
44	u	106	ARG
56	VV	1	MET
56	VV	2	GLN
56	VV	3	ASN
56	VV	7	GLU
56	VV	16	LYS
56	VV	18	SER
56	VV	22	ARG
56	VV	27	LYS
56	VV	32	ILE
56	VV	33	GLN
56	VV	34	MET
56	VV	39	VAL
56	VV	41	LYS
56	VV	45	ARG
56	VV	51	LYS
56	VV	52	THR
56	VV	61	ARG
56	VV	62	MET
56	VV	68	SER
56	VV	69	ILE
56	VV	70	LEU

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Mol	Chain	Res	Type
56	VV	71	ARG
56	VV	78	ILE
64	AA	11	LYS
64	AA	13	GLU
64	AA	15	VAL
64	AA	16	LEU
64	AA	18	PHE
64	AA	19	LEU
64	AA	23	THR
64	AA	24	HIS
64	AA	25	LEU
64	AA	28	THR
64	AA	30	LEU
64	AA	33	GLN
64	AA	34	MET
64	AA	36	GLN
64	AA	38	ILE
64	AA	40	LYS
64	AA	41	ARG
64	AA	44	ASP
64	AA	48	ILE
64	AA	49	ILE
64	AA	51	LEU
64	AA	52	LYS
64	AA	57	LYS
64	AA	63	ARG
64	AA	66	VAL
64	AA	70	ASN
64	AA	73	ASP
64	AA	78	SER
64	AA	85	ARG
64	AA	88	LEU
64	AA	97	THR
64	AA	98	PRO
64	AA	102	ARG
64	AA	104	THR
64	AA	108	PHE
64	AA	109	THR
64	AA	111	GLN
64	AA	112	ILE
64	AA	116	PHE
64	AA	117	ARG

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Mol	Chain	Res	Type
64	AA	120	ARG
64	AA	121	LEU
64	AA	125	THR
64	AA	126	ASP
64	AA	128	ARG
64	AA	130	ASP
64	AA	132	GLN
64	AA	134	LEU
64	AA	136	GLU
64	AA	141	ASN
64	AA	145	ILE
64	AA	150	THR
64	AA	157	VAL
64	AA	159	ILE
64	AA	162	PRO
64	AA	163	CYS
64	AA	166	LYS
64	AA	169	HIS
64	AA	173	LEU
64	AA	174	MET
64	AA	176	TRP
64	AA	178	LEU
64	AA	180	ARG
64	AA	186	ARG
64	AA	188	THR
64	AA	189	ILE
64	AA	193	HIS
64	AA	198	MET
64	AA	202	TYR
64	AA	203	PHE
64	AA	205	ARG
64	AA	206	ASP
64	AA	209	GLU
64	AA	212	LYS
64	AA	213	GLU
64	AA	214	GLU
82	BB	56	LYS
82	BB	98	THR
82	BB	120	MET
82	BB	172	MET
82	BB	211	PHE
83	OO	72	TYR

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Mol	Chain	Res	Type
83	OO	88	LEU
84	RR	24	LEU
84	RR	63	ARG
84	RR	99	ASP
84	RR	117	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (54) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	25	HIS
2	B	236	HIS
3	C	142	HIS
4	c	120	GLN
7	F	57	HIS
7	F	125	ASN
8	G	149	ASN
9	H	102	ASN
12	L	113	ASN
13	M	33	GLN
15	O	150	GLN
16	P	75	GLN
16	P	97	ASN
16	P	133	HIS
17	Q	7	HIS
19	T	3	ASN
24	Y	18	HIS
25	Z	127	ASN
26	a	49	HIS
26	a	62	HIS
26	a	85	GLN
33	i	26	HIS
36	l	25	GLN
37	m	90	ASN
45	bb	9	HIS
45	bb	83	GLN
51	HH	97	GLN
52	II	44	HIS
52	II	88	ASN
52	II	165	GLN
53	JJ	140	GLN
54	LL	65	ASN
56	VV	21	ASN

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Mol	Chain	Res	Type
56	VV	33	GLN
56	VV	35	ASN
56	VV	81	GLN
57	WW	64	ASN
59	YY	89	HIS
62	gg	64	HIS
62	gg	188	HIS
64	AA	84	GLN
64	AA	113	GLN
64	AA	149	ASN
64	AA	164	ASN
66	FF	101	HIS
72	TT	142	ASN
73	UU	47	ASN
75	EF	202	ASN
75	EF	630	GLN
82	BB	158	HIS
82	BB	160	GLN
83	OO	113	GLN
84	RR	56	HIS
84	RR	127	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
76	Cc	76/77 (98%)	25 (32%)	0
77	A5	1668/1732 (96%)	582 (34%)	82 (4%)
78	A7	120/121 (99%)	29 (24%)	1 (0%)
79	A8	156/157 (99%)	46 (29%)	5 (3%)
80	B2	1756/1837 (95%)	581 (33%)	53 (3%)
81	A6	1995/2122 (94%)	607 (30%)	56 (2%)
All	All	5771/6046 (95%)	1870 (32%)	197 (3%)

All (1870) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
76	Cc	4	G
76	Cc	6	G
76	Cc	9	G
76	Cc	10	G
76	Cc	16	C

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Mol	Chain	Res	Type
76	Cc	17	C
76	Cc	18	C
76	Cc	19	G
76	Cc	20	G
76	Cc	21	U
76	Cc	22	A
76	Cc	33	C
76	Cc	41	C
76	Cc	42	C
76	Cc	47	G
76	Cc	48	U
76	Cc	49	C
76	Cc	50	G
76	Cc	56	U
76	Cc	57	C
76	Cc	59	A
76	Cc	62	C
76	Cc	65	G
76	Cc	75	C
76	Cc	77	A
77	A5	2	G
77	A5	12	A
77	A5	13	U
77	A5	15	A
77	A5	19	G
77	A5	20	U
77	A5	22	G
77	A5	25	A
77	A5	39	A
77	A5	48	G
77	A5	49	U
77	A5	56	A
77	A5	58	G
77	A5	59	A
77	A5	62	A
77	A5	64	A
77	A5	65	A
77	A5	66	A
77	A5	71	C
77	A5	72	C
77	A5	73	A
77	A5	74	G

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Mol	Chain	Res	Type
77	A5	75	G
77	A5	76	A
77	A5	84	A
77	A5	91	G
77	A5	107	G
77	A5	108	A
77	A5	109	G
77	A5	110	C
77	A5	115	C
77	A5	116	G
77	A5	117	C
77	A5	119	G
77	A5	120	A
77	A5	126	C
77	A5	127	G
77	A5	132	G
77	A5	133	C
77	A5	134	G
77	A5	135	G
77	A5	136	C
77	A5	137	G
77	A5	142	G
77	A5	143	C
77	A5	149	A
77	A5	150	U
77	A5	152	U
77	A5	157	U
77	A5	159	C
77	A5	160	G
77	A5	164	G
77	A5	171	U
77	A5	172	C
77	A5	177	G
77	A5	184	U
77	A5	185	C
77	A5	187	U
77	A5	188	G
77	A5	189	G
77	A5	200	U
77	A5	201	C
77	A5	207	G
77	A5	209	U

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Mol	Chain	Res	Type
77	A5	210	C
77	A5	211	G
77	A5	216	C
77	A5	217	C
77	A5	218	A
77	A5	219	G
77	A5	220	C
77	A5	221	C
77	A5	224	U
77	A5	225	G
77	A5	226	G
77	A5	227	A
77	A5	232	G
77	A5	233	U
77	A5	237	G
77	A5	238	C
77	A5	246	G
77	A5	247	G
77	A5	260	C
77	A5	265	C
77	A5	277	G
77	A5	280	G
77	A5	281	U
77	A5	292	G
77	A5	294	G
77	A5	297	U
77	A5	303	C
77	A5	306	A
77	A5	309	C
77	A5	310	G
77	A5	315	G
77	A5	316	U
77	A5	322	C
77	A5	326	C
77	A5	330	G
77	A5	334	A
77	A5	335	A
77	A5	340	C
77	A5	341	G
77	A5	350	C
77	A5	352	G
77	A5	357	U

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Mol	Chain	Res	Type
77	A5	360	A
77	A5	361	C
77	A5	362	A
77	A5	364	G
77	A5	373	G
77	A5	375	G
77	A5	381	U
77	A5	385	A
77	A5	386	A
77	A5	387	G
77	A5	401	G
77	A5	404	U
77	A5	405	U
77	A5	406	C
77	A5	407	A
77	A5	410	A
77	A5	412	G
77	A5	413	G
77	A5	414	C
77	A5	415	G
77	A5	432	U
77	A5	433	A
77	A5	440	U
77	A5	451	C
77	A5	452	A
77	A5	453	G
77	A5	454	U
77	A5	455	C
77	A5	468	U
77	A5	469	C
77	A5	470	A
77	A5	473	C
77	A5	474	C
77	A5	478	G
77	A5	485	C
77	A5	486	C
77	A5	487	G
77	A5	491	G
77	A5	495	C
77	A5	496	G
77	A5	498	C
77	A5	499	G

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Mol	Chain	Res	Type
77	A5	500	G
77	A5	501	C
77	A5	502	C
77	A5	503	C
77	A5	504	G
77	A5	505	G
77	A5	506	C
77	A5	507	G
77	A5	509	A
77	A5	510	U
77	A5	511	C
77	A5	513	U
77	A5	514	U
77	A5	515	C
77	A5	517	C
77	A5	518	G
77	A5	639	U
77	A5	640	C
77	A5	641	G
77	A5	648	G
77	A5	649	A
77	A5	651	C
77	A5	654	C
77	A5	656	C
77	A5	659	G
77	A5	663	G
77	A5	664	G
77	A5	665	C
77	A5	666	G
77	A5	667	A
77	A5	668	C
77	A5	669	C
77	A5	670	G
77	A5	677	G
77	A5	682	G
77	A5	684	G
77	A5	685	C
77	A5	686	A
77	A5	687	U
77	A5	689	U
77	A5	694	C
77	A5	696	C

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Mol	Chain	Res	Type
77	A5	697	G
77	A5	704	C
77	A5	707	C
77	A5	712	C
77	A5	717	U
77	A5	720	G
77	A5	721	G
77	A5	727	C
77	A5	728	U
77	A5	729	G
77	A5	730	G
77	A5	732	A
77	A5	736	C
77	A5	737	C
77	A5	740	G
77	A5	742	G
77	A5	745	G
77	A5	746	A
77	A5	747	A
77	A5	748	G
77	A5	749	G
77	A5	756	G
77	A5	911	U
77	A5	912	G
77	A5	913	U
77	A5	914	U
77	A5	916	C
77	A5	918	G
77	A5	919	C
77	A5	922	C
77	A5	926	G
77	A5	927	G
77	A5	928	C
77	A5	929	A
77	A5	931	C
77	A5	932	A
77	A5	933	G
77	A5	935	A
77	A5	936	C
77	A5	937	U
77	A5	938	C
77	A5	939	G

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Mol	Chain	Res	Type
77	A5	940	C
77	A5	943	A
77	A5	944	A
77	A5	945	U
77	A5	946	C
77	A5	947	C
77	A5	952	G
77	A5	955	G
77	A5	956	A
77	A5	957	G
77	A5	958	G
77	A5	959	G
77	A5	960	A
77	A5	961	G
77	A5	962	C
77	A5	964	A
77	A5	966	A
77	A5	967	C
77	A5	969	C
77	A5	970	G
77	A5	971	U
77	A5	972	C
77	A5	974	C
77	A5	975	C
77	A5	976	G
77	A5	977	C
77	A5	979	C
77	A5	980	U
77	A5	981	C
77	A5	982	U
77	A5	983	C
77	A5	988	C
77	A5	995	C
77	A5	1051	G
77	A5	1071	C
77	A5	1072	C
77	A5	1079	C
77	A5	1083	U
77	A5	1084	C
77	A5	1094	G
77	A5	1102	U
77	A5	1165	G

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Mol	Chain	Res	Type
77	A5	1166	G
77	A5	1167	C
77	A5	1172	C
77	A5	1173	G
77	A5	1175	A
77	A5	1177	U
77	A5	1184	A
77	A5	1194	G
77	A5	1195	G
77	A5	1196	G
77	A5	1206	C
77	A5	1209	U
77	A5	1210	C
77	A5	1211	G
77	A5	1212	G
77	A5	1214	C
77	A5	1215	C
77	A5	1219	G
77	A5	1220	G
77	A5	1235	G
77	A5	1237	C
77	A5	1239	C
77	A5	1240	G
77	A5	1242	G
77	A5	1244	G
77	A5	1245	C
77	A5	1264	C
77	A5	1265	G
77	A5	1266	G
77	A5	1267	C
77	A5	1268	G
77	A5	1270	A
77	A5	1272	C
77	A5	1273	G
77	A5	1274	A
77	A5	1275	G
77	A5	1281	G
77	A5	1282	G
77	A5	1283	G
77	A5	1284	G
77	A5	1285	U
77	A5	1289	C

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Mol	Chain	Res	Type
77	A5	1290	G
77	A5	1292	C
77	A5	1293	G
77	A5	1294	A
77	A5	1295	C
77	A5	1296	G
77	A5	1297	U
77	A5	1301	C
77	A5	1302	U
77	A5	1303	A
77	A5	1304	C
77	A5	1308	C
77	A5	1313	C
77	A5	1314	C
77	A5	1318	C
77	A5	1322	A
77	A5	1323	A
77	A5	1326	A
77	A5	1328	G
77	A5	1344	C
77	A5	1345	A
77	A5	1354	A
77	A5	1357	C
77	A5	1358	G
77	A5	1359	G
77	A5	1365	C
77	A5	1366	G
77	A5	1367	C
77	A5	1368	A
77	A5	1369	C
77	A5	1370	G
77	A5	1371	A
77	A5	1372	A
77	A5	1377	G
77	A5	1378	C
77	A5	1379	C
77	A5	1381	U
77	A5	1382	G
77	A5	1387	A
77	A5	1390	G
77	A5	1394	G
77	A5	1397	A

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Mol	Chain	Res	Type
77	A5	1399	G
77	A5	1407	C
77	A5	1408	G
77	A5	1411	C
77	A5	1412	G
77	A5	1419	G
77	A5	1420	A
77	A5	1427	A
77	A5	1429	C
77	A5	1451	G
77	A5	1455	G
77	A5	1456	C
77	A5	1459	A
77	A5	1465	G
77	A5	1475	G
77	A5	1477	C
77	A5	1478	C
77	A5	1480	C
77	A5	1481	C
77	A5	1482	G
77	A5	1483	C
77	A5	1484	G
77	A5	1485	C
77	A5	1486	C
77	A5	1497	A
77	A5	1498	G
77	A5	1499	C
77	A5	1501	C
77	A5	1503	A
77	A5	1504	G
77	A5	1516	G
77	A5	1517	G
77	A5	1518	A
77	A5	1523	A
77	A5	1525	A
77	A5	1531	U
77	A5	1534	A
77	A5	1543	G
77	A5	1547	A
77	A5	1549	G
77	A5	1552	G
77	A5	1553	A

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Mol	Chain	Res	Type
77	A5	1566	C
77	A5	1568	C
77	A5	1571	G
77	A5	1574	G
77	A5	1577	G
77	A5	1578	U
77	A5	1582	U
77	A5	1591	U
77	A5	1592	G
77	A5	1596	U
77	A5	1597	G
77	A5	1599	A
77	A5	1612	G
77	A5	1614	C
77	A5	1624	G
77	A5	1625	G
77	A5	1629	G
77	A5	1630	A
77	A5	1631	A
77	A5	1632	A
77	A5	1633	G
77	A5	1634	A
77	A5	1637	A
77	A5	1640	C
77	A5	1641	G
77	A5	1646	A
77	A5	1649	U
77	A5	1651	G
77	A5	1654	G
77	A5	1661	C
77	A5	1667	G
77	A5	1676	C
77	A5	1677	U
77	A5	1679	A
77	A5	1680	G
77	A5	1681	G
77	A5	1691	G
77	A5	1692	C
77	A5	1693	U
77	A5	1694	C
77	A5	1695	U
77	A5	1697	G

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Mol	Chain	Res	Type
77	A5	1698	C
77	A5	1699	A
77	A5	1724	G
77	A5	1725	U
77	A5	1726	U
77	A5	1730	U
77	A5	1731	C
77	A5	1734	G
77	A5	1742	A
77	A5	1750	G
77	A5	1753	G
77	A5	1754	U
77	A5	1755	C
77	A5	1756	U
77	A5	1757	U
77	A5	1760	G
77	A5	1761	G
77	A5	1764	G
77	A5	1766	A
77	A5	1769	G
77	A5	1770	A
77	A5	1772	C
77	A5	1773	U
77	A5	1776	A
77	A5	1777	C
77	A5	1781	U
77	A5	1787	A
77	A5	1789	C
77	A5	1794	A
77	A5	1803	G
77	A5	1804	A
77	A5	1805	A
77	A5	1806	G
77	A5	1811	G
77	A5	1812	C
77	A5	1815	G
77	A5	1816	C
77	A5	1818	G
77	A5	1819	G
77	A5	1821	G
77	A5	1822	U
77	A5	1825	A

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Mol	Chain	Res	Type
77	A5	1826	G
77	A5	1828	C
77	A5	1832	C
77	A5	1833	G
77	A5	1835	G
77	A5	1836	G
77	A5	1841	C
77	A5	1842	G
77	A5	1852	U
77	A5	1853	G
77	A5	1854	G
77	A5	1855	G
77	A5	1869	G
77	A5	1870	C
77	A5	1872	G
77	A5	1873	A
77	A5	1878	G
77	A5	1881	C
77	A5	1883	G
77	A5	1885	G
77	A5	1893	C
77	A5	1897	A
77	A5	1898	C
77	A5	1907	A
77	A5	1910	G
77	A5	1916	G
77	A5	1918	U
77	A5	1919	G
77	A5	1920	C
77	A5	1921	C
77	A5	1922	G
77	A5	1924	C
77	A5	1925	G
77	A5	1926	C
77	A5	1928	C
77	A5	1930	U
77	A5	1931	C
77	A5	1939	A
77	A5	1940	G
77	A5	1947	U
77	A5	1952	G
77	A5	1961	G

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Mol	Chain	Res	Type
77	A5	1962	A
77	A5	1963	C
77	A5	1964	A
77	A5	1971	C
77	A5	1972	G
77	A5	1974	U
77	A5	1975	G
77	A5	1976	G
77	A5	1978	C
77	A5	1980	U
77	A5	1981	G
77	A5	1982	G
77	A5	1983	A
77	A5	1984	A
77	A5	1985	G
77	A5	1987	C
77	A5	1988	G
77	A5	1991	A
77	A5	1992	U
77	A5	1993	C
77	A5	1994	C
77	A5	1995	G
77	A5	1997	U
77	A5	1998	A
77	A5	1999	A
77	A5	2001	G
77	A5	2002	A
77	A5	2003	G
77	A5	2004	U
77	A5	2005	G
77	A5	2008	U
77	A5	2009	A
77	A5	2010	A
77	A5	2024	G
77	A5	2025	A
77	A5	2026	A
77	A5	2034	G
77	A5	2042	A
77	A5	2043	A
77	A5	2045	G
77	A5	2047	A
77	A5	2048	U

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Mol	Chain	Res	Type
77	A5	2049	G
77	A5	2050	G
77	A5	2052	G
77	A5	2054	U
77	A5	2055	G
77	A5	2064	G
77	A5	2069	A
77	A5	2071	A
77	A5	2084	C
77	A5	2085	G
77	A5	2088	C
77	A5	2089	G
77	A5	2090	U
77	A5	2091	C
78	A7	8	G
78	A7	11	A
78	A7	13	A
78	A7	14	C
78	A7	22	A
78	A7	30	C
78	A7	33	U
78	A7	35	U
78	A7	38	U
78	A7	40	U
78	A7	41	G
78	A7	42	A
78	A7	48	G
78	A7	53	U
78	A7	54	A
78	A7	61	G
78	A7	62	U
78	A7	63	C
78	A7	64	G
78	A7	71	G
78	A7	73	U
78	A7	76	U
78	A7	85	G
78	A7	91	C
78	A7	97	G
78	A7	100	A
78	A7	101	A
78	A7	110	G

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Mol	Chain	Res	Type
78	A7	121	U
79	A8	16	G
79	A8	17	A
79	A8	23	C
79	A8	24	G
79	A8	33	G
79	A8	34	U
79	A8	35	C
79	A8	38	U
79	A8	40	A
79	A8	46	G
79	A8	47	C
79	A8	49	G
79	A8	59	A
79	A8	60	G
79	A8	62	A
79	A8	63	U
79	A8	70	G
79	A8	73	U
79	A8	77	A
79	A8	80	A
79	A8	81	C
79	A8	82	A
79	A8	84	A
79	A8	85	U
79	A8	86	U
79	A8	87	G
79	A8	95	A
79	A8	96	C
79	A8	97	A
79	A8	99	U
79	A8	103	A
79	A8	105	C
79	A8	109	C
79	A8	110	U
79	A8	111	U
79	A8	114	G
79	A8	120	G
79	A8	124	U
79	A8	125	C
79	A8	126	C
79	A8	127	U

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Mol	Chain	Res	Type
79	A8	128	C
79	A8	147	G
79	A8	150	C
79	A8	151	G
79	A8	154	G
80	B2	2	A
80	B2	4	C
80	B2	5	U
80	B2	6	G
80	B2	17	C
80	B2	25	A
80	B2	26	U
80	B2	30	C
80	B2	33	G
80	B2	39	A
80	B2	41	G
80	B2	42	A
80	B2	44	U
80	B2	45	A
80	B2	46	A
80	B2	56	G
80	B2	62	G
80	B2	66	G
80	B2	67	C
80	B2	68	A
80	B2	71	G
80	B2	72	C
80	B2	73	C
80	B2	74	G
80	B2	75	G
80	B2	77	A
80	B2	78	C
80	B2	79	A
80	B2	80	G
80	B2	86	C
80	B2	90	G
80	B2	92	A
80	B2	99	A
80	B2	103	A
80	B2	113	G
80	B2	114	G
80	B2	115	U

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Mol	Chain	Res	Type
80	B2	125	C
80	B2	126	G
80	B2	127	C
80	B2	140	C
80	B2	141	A
80	B2	142	C
80	B2	143	U
80	B2	146	G
80	B2	147	A
80	B2	155	G
80	B2	158	A
80	B2	160	U
80	B2	170	A
80	B2	171	A
80	B2	181	A
80	B2	182	C
80	B2	183	G
80	B2	187	G
80	B2	188	C
80	B2	190	G
80	B2	191	A
80	B2	192	C
80	B2	206	G
80	B2	211	G
80	B2	219	U
80	B2	226	A
80	B2	227	U
80	B2	228	C
80	B2	229	A
80	B2	230	A
80	B2	231	A
80	B2	232	A
80	B2	235	A
80	B2	237	C
80	B2	238	C
80	B2	241	G
80	B2	242	U
80	B2	243	C
80	B2	244	A
80	B2	280	G
80	B2	281	C
80	B2	282	G

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Mol	Chain	Res	Type
80	B2	287	U
80	B2	288	G
80	B2	289	G
80	B2	290	U
80	B2	294	U
80	B2	295	C
80	B2	302	A
80	B2	304	C
80	B2	305	U
80	B2	306	C
80	B2	307	G
80	B2	309	G
80	B2	312	G
80	B2	318	A
80	B2	319	C
80	B2	321	C
80	B2	324	C
80	B2	325	C
80	B2	326	C
80	B2	332	G
80	B2	338	G
80	B2	340	C
80	B2	341	C
80	B2	347	G
80	B2	348	A
80	B2	350	C
80	B2	355	G
80	B2	362	C
80	B2	364	A
80	B2	367	U
80	B2	368	U
80	B2	383	G
80	B2	385	G
80	B2	386	C
80	B2	400	C
80	B2	408	A
80	B2	409	C
80	B2	410	G
80	B2	428	U
80	B2	429	C
80	B2	435	A
80	B2	436	G

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Mol	Chain	Res	Type
80	B2	442	C
80	B2	443	U
80	B2	448	A
80	B2	450	C
80	B2	452	G
80	B2	464	A
80	B2	465	A
80	B2	466	G
80	B2	467	G
80	B2	472	C
80	B2	473	A
80	B2	474	G
80	B2	476	A
80	B2	484	A
80	B2	485	A
80	B2	487	U
80	B2	492	C
80	B2	493	A
80	B2	494	C
80	B2	495	U
80	B2	500	A
80	B2	501	C
80	B2	502	C
80	B2	503	C
80	B2	507	G
80	B2	508	A
80	B2	516	A
80	B2	523	A
80	B2	525	A
80	B2	528	A
80	B2	530	U
80	B2	532	C
80	B2	533	A
80	B2	535	G
80	B2	550	C
80	B2	551	U
80	B2	552	G
80	B2	553	U
80	B2	555	A
80	B2	556	U
80	B2	558	G
80	B2	559	G

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Mol	Chain	Res	Type
80	B2	560	A
80	B2	562	U
80	B2	564	A
80	B2	568	C
80	B2	574	A
80	B2	576	A
80	B2	582	U
80	B2	583	A
80	B2	584	A
80	B2	588	G
80	B2	590	A
80	B2	591	U
80	B2	593	C
80	B2	594	A
80	B2	601	G
80	B2	604	A
80	B2	605	A
80	B2	606	G
80	B2	607	U
80	B2	608	C
80	B2	610	G
80	B2	613	G
80	B2	614	C
80	B2	617	G
80	B2	626	G
80	B2	627	U
80	B2	628	A
80	B2	629	A
80	B2	634	A
80	B2	643	A
80	B2	644	G
80	B2	654	A
80	B2	657	U
80	B2	660	C
80	B2	663	C
80	B2	666	U
80	B2	667	U
80	B2	668	A
80	B2	669	A
80	B2	671	A
80	B2	672	A
80	B2	673	G

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Mol	Chain	Res	Type
80	B2	681	U
80	B2	684	G
80	B2	688	U
80	B2	689	U
80	B2	690	G
80	B2	691	G
80	B2	696	G
80	B2	697	G
80	B2	698	G
80	B2	699	C
80	B2	731	G
80	B2	732	U
80	B2	733	C
80	B2	734	C
80	B2	735	C
80	B2	736	C
80	B2	738	C
80	B2	739	C
80	B2	740	C
80	B2	743	U
80	B2	744	G
80	B2	745	C
80	B2	747	U
80	B2	748	C
80	B2	749	U
80	B2	752	G
80	B2	753	C
80	B2	754	G
80	B2	788	G
80	B2	797	C
80	B2	798	G
80	B2	799	U
80	B2	800	U
80	B2	801	U
80	B2	807	G
80	B2	810	A
80	B2	811	A
80	B2	812	A
80	B2	822	U
80	B2	823	U
80	B2	827	A
80	B2	830	A

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Mol	Chain	Res	Type
80	B2	834	C
80	B2	835	C
80	B2	836	G
80	B2	837	A
80	B2	838	G
80	B2	839	C
80	B2	840	C
80	B2	841	G
80	B2	845	G
80	B2	847	A
80	B2	853	C
80	B2	854	A
80	B2	868	G
80	B2	870	A
80	B2	871	U
80	B2	873	G
80	B2	875	A
80	B2	876	C
80	B2	877	C
80	B2	879	C
80	B2	881	G
80	B2	886	A
80	B2	888	U
80	B2	890	U
80	B2	891	G
80	B2	892	U
80	B2	894	G
80	B2	895	G
80	B2	898	U
80	B2	900	C
80	B2	903	A
80	B2	907	G
80	B2	909	G
80	B2	910	G
80	B2	912	C
80	B2	913	A
80	B2	914	U
80	B2	920	A
80	B2	921	G
80	B2	929	G
80	B2	933	G
80	B2	943	U

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Mol	Chain	Res	Type
80	B2	949	G
80	B2	951	C
80	B2	954	U
80	B2	955	A
80	B2	967	C
80	B2	968	U
80	B2	969	U
80	B2	970	G
80	B2	971	G
80	B2	987	A
80	B2	990	A
80	B2	992	A
80	B2	999	G
80	B2	1001	A
80	B2	1020	A
80	B2	1023	A
80	B2	1039	C
80	B2	1040	G
80	B2	1041	G
80	B2	1045	U
80	B2	1049	A
80	B2	1050	A
80	B2	1053	C
80	B2	1054	G
80	B2	1060	A
80	B2	1061	U
80	B2	1064	C
80	B2	1080	A
80	B2	1082	A
80	B2	1083	A
80	B2	1084	A
80	B2	1085	C
80	B2	1086	G
80	B2	1088	U
80	B2	1096	G
80	B2	1097	G
80	B2	1100	A
80	B2	1101	U
80	B2	1108	G
80	B2	1109	C
80	B2	1110	G
80	B2	1111	U

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Mol	Chain	Res	Type
80	B2	1113	A
80	B2	1114	U
80	B2	1115	U
80	B2	1116	C
80	B2	1117	C
80	B2	1120	U
80	B2	1121	G
80	B2	1123	C
80	B2	1125	C
80	B2	1129	G
80	B2	1131	G
80	B2	1133	A
80	B2	1136	U
80	B2	1137	U
80	B2	1138	C
80	B2	1139	C
80	B2	1143	A
80	B2	1150	A
80	B2	1151	G
80	B2	1153	C
80	B2	1154	U
80	B2	1155	U
80	B2	1157	G
80	B2	1159	G
80	B2	1166	G
80	B2	1172	U
80	B2	1183	A
80	B2	1190	A
80	B2	1194	A
80	B2	1195	A
80	B2	1203	G
80	B2	1204	A
80	B2	1207	G
80	B2	1209	A
80	B2	1210	G
80	B2	1211	G
80	B2	1212	G
80	B2	1213	C
80	B2	1214	A
80	B2	1215	C
80	B2	1217	A
80	B2	1221	G

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Mol	Chain	Res	Type
80	B2	1222	G
80	B2	1224	G
80	B2	1226	G
80	B2	1228	A
80	B2	1240	A
80	B2	1242	U
80	B2	1245	G
80	B2	1247	C
80	B2	1248	U
80	B2	1250	A
80	B2	1251	A
80	B2	1253	A
80	B2	1254	C
80	B2	1256	G
80	B2	1257	G
80	B2	1259	A
80	B2	1260	A
80	B2	1261	C
80	B2	1263	U
80	B2	1274	G
80	B2	1275	G
80	B2	1278	A
80	B2	1284	A
80	B2	1286	G
80	B2	1287	A
80	B2	1301	A
80	B2	1302	G
80	B2	1303	C
80	B2	1305	C
80	B2	1308	U
80	B2	1315	U
80	B2	1316	C
80	B2	1324	G
80	B2	1326	U
80	B2	1333	U
80	B2	1342	U
80	B2	1343	U
80	B2	1348	G
80	B2	1352	G
80	B2	1354	G
80	B2	1355	C
80	B2	1357	A

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Mol	Chain	Res	Type
80	B2	1358	U
80	B2	1371	U
80	B2	1372	U
80	B2	1374	C
80	B2	1378	A
80	B2	1379	A
80	B2	1394	G
80	B2	1395	C
80	B2	1396	A
80	B2	1397	U
80	B2	1401	A
80	B2	1402	A
80	B2	1403	C
80	B2	1404	U
80	B2	1411	G
80	B2	1412	C
80	B2	1417	C
80	B2	1418	C
80	B2	1419	C
80	B2	1424	G
80	B2	1425	G
80	B2	1430	C
80	B2	1435	C
80	B2	1437	C
80	B2	1438	A
80	B2	1439	A
80	B2	1441	U
80	B2	1442	U
80	B2	1444	U
80	B2	1449	G
80	B2	1454	A
80	B2	1455	A
80	B2	1463	U
80	B2	1466	G
80	B2	1473	G
80	B2	1475	G
80	B2	1476	A
80	B2	1477	U
80	B2	1478	U
80	B2	1489	A
80	B2	1490	G
80	B2	1494	U

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Mol	Chain	Res	Type
80	B2	1495	G
80	B2	1500	G
80	B2	1502	C
80	B2	1504	U
80	B2	1506	A
80	B2	1507	G
80	B2	1508	A
80	B2	1511	U
80	B2	1519	U
80	B2	1521	C
80	B2	1522	A
80	B2	1524	G
80	B2	1531	A
80	B2	1533	A
80	B2	1534	C
80	B2	1535	U
80	B2	1536	G
80	B2	1540	G
80	B2	1543	U
80	B2	1544	C
80	B2	1548	G
80	B2	1550	G
80	B2	1551	U
80	B2	1552	G
80	B2	1553	C
80	B2	1554	C
80	B2	1555	U
80	B2	1556	A
80	B2	1557	C
80	B2	1560	U
80	B2	1563	G
80	B2	1578	U
80	B2	1579	A
80	B2	1580	A
80	B2	1586	U
80	B2	1587	G
80	B2	1588	A
80	B2	1589	A
80	B2	1598	G
80	B2	1599	U
80	B2	1600	G
80	B2	1601	A

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Mol	Chain	Res	Type
80	B2	1602	U
80	B2	1604	G
80	B2	1606	G
80	B2	1607	A
80	B2	1614	A
80	B2	1620	A
80	B2	1621	U
80	B2	1622	U
80	B2	1623	A
80	B2	1624	U
80	B2	1629	C
80	B2	1632	G
80	B2	1637	A
80	B2	1638	G
80	B2	1639	G
80	B2	1641	A
80	B2	1646	C
80	B2	1648	G
80	B2	1654	G
80	B2	1658	G
80	B2	1663	A
80	B2	1665	G
80	B2	1668	U
80	B2	1669	G
80	B2	1671	G
80	B2	1679	A
80	B2	1680	G
80	B2	1682	C
80	B2	1683	C
80	B2	1686	G
80	B2	1688	C
80	B2	1690	U
80	B2	1693	G
80	B2	1695	A
80	B2	1702	G
80	B2	1706	G
80	B2	1718	G
80	B2	1721	U
80	B2	1722	G
80	B2	1729	U
80	B2	1737	G
80	B2	1738	C

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Mol	Chain	Res	Type
80	B2	1744	G
80	B2	1745	A
80	B2	1750	C
80	B2	1751	C
80	B2	1753	C
80	B2	1754	G
80	B2	1756	C
80	B2	1757	G
80	B2	1774	C
80	B2	1783	C
80	B2	1785	C
80	B2	1786	U
80	B2	1796	G
80	B2	1798	C
80	B2	1799	G
80	B2	1805	G
80	B2	1809	A
80	B2	1819	A
80	B2	1823	A
80	B2	1824	A
80	B2	1825	A
80	B2	1826	G
80	B2	1829	G
80	B2	1831	A
80	B2	1835	A
80	B2	1836	G
80	B2	1838	U
80	B2	1839	U
80	B2	1843	G
80	B2	1849	G
80	B2	1851	A
80	B2	1852	C
80	B2	1859	A
80	B2	1861	G
80	B2	1862	G
80	B2	1863	A
80	B2	1865	C
80	B2	1866	A
80	B2	1868	U
80	B2	1869	A
81	A6	2262	G
81	A6	2263	A

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Mol	Chain	Res	Type
81	A6	2264	C
81	A6	2265	G
81	A6	2267	U
81	A6	2269	C
81	A6	2270	G
81	A6	2279	A
81	A6	2289	C
81	A6	2290	C
81	A6	2301	G
81	A6	2307	A
81	A6	2313	A
81	A6	2314	G
81	A6	2320	G
81	A6	2322	G
81	A6	2331	G
81	A6	2332	A
81	A6	2333	G
81	A6	2335	C
81	A6	2338	C
81	A6	2343	G
81	A6	2344	U
81	A6	2345	G
81	A6	2348	G
81	A6	2351	C
81	A6	2360	A
81	A6	2362	U
81	A6	2366	A
81	A6	2369	U
81	A6	2371	U
81	A6	2382	A
81	A6	2384	U
81	A6	2391	G
81	A6	2395	A
81	A6	2396	A
81	A6	2399	G
81	A6	2402	G
81	A6	2409	U
81	A6	2414	G
81	A6	2415	U
81	A6	2416	G
81	A6	2421	G
81	A6	2422	C

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Mol	Chain	Res	Type
81	A6	2425	U
81	A6	2434	G
81	A6	2436	U
81	A6	2439	G
81	A6	2441	C
81	A6	2442	G
81	A6	2444	U
81	A6	2456	G
81	A6	2458	C
81	A6	2463	G
81	A6	2469	C
81	A6	2470	C
81	A6	2471	G
81	A6	2475	G
81	A6	2476	G
81	A6	2480	G
81	A6	2481	G
81	A6	2488	C
81	A6	2489	C
81	A6	2490	U
81	A6	2503	G
81	A6	2504	C
81	A6	2505	C
81	A6	2507	A
81	A6	2511	A
81	A6	2513	A
81	A6	2515	G
81	A6	2517	A
81	A6	2518	G
81	A6	2520	C
81	A6	2529	A
81	A6	2531	C
81	A6	2532	C
81	A6	2539	C
81	A6	2543	A
81	A6	2544	G
81	A6	2546	G
81	A6	2547	G
81	A6	2549	G
81	A6	2551	A
81	A6	2552	G
81	A6	2554	U

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Mol	Chain	Res	Type
81	A6	2560	C
81	A6	2563	C
81	A6	2564	G
81	A6	2571	C
81	A6	2575	U
81	A6	2583	C
81	A6	2586	G
81	A6	2587	A
81	A6	2588	C
81	A6	2589	C
81	A6	2601	A
81	A6	2611	A
81	A6	2627	C
81	A6	2628	U
81	A6	2637	U
81	A6	2638	G
81	A6	2639	U
81	A6	2640	G
81	A6	2647	A
81	A6	2648	G
81	A6	2649	G
81	A6	2652	G
81	A6	2657	G
81	A6	2658	G
81	A6	2661	U
81	A6	2662	G
81	A6	2663	G
81	A6	2664	G
81	A6	2667	C
81	A6	2669	C
81	A6	2670	C
81	A6	2671	C
81	A6	2673	G
81	A6	2674	A
81	A6	2675	G
81	A6	2676	A
81	A6	2685	C
81	A6	2686	G
81	A6	2687	C
81	A6	2688	G
81	A6	2689	C
81	A6	2690	C

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Mol	Chain	Res	Type
81	A6	2694	G
81	A6	2695	A
81	A6	2696	A
81	A6	2701	U
81	A6	2711	G
81	A6	2712	G
81	A6	2713	C
81	A6	2716	C
81	A6	2719	C
81	A6	2721	G
81	A6	2724	G
81	A6	2726	G
81	A6	2732	G
81	A6	2734	U
81	A6	2743	A
81	A6	2752	G
81	A6	2754	G
81	A6	2755	A
81	A6	2756	G
81	A6	2760	G
81	A6	2761	U
81	A6	2762	G
81	A6	2766	A
81	A6	2767	U
81	A6	2768	C
81	A6	2769	U
81	A6	2770	C
81	A6	2777	G
81	A6	2783	A
81	A6	2787	A
81	A6	2788	U
81	A6	2790	U
81	A6	2794	C
81	A6	2798	A
81	A6	2799	G
81	A6	2806	A
81	A6	2814	C
81	A6	2816	G
81	A6	2825	A
81	A6	2826	U
81	A6	2828	U
81	A6	2829	U

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Mol	Chain	Res	Type
81	A6	2836	A
81	A6	2838	G
81	A6	2842	G
81	A6	2844	A
81	A6	2845	A
81	A6	2846	G
81	A6	2850	A
81	A6	2855	G
81	A6	2870	A
81	A6	2879	A
81	A6	2892	C
81	A6	2897	G
81	A6	2898	G
81	A6	2900	U
81	A6	2905	C
81	A6	2907	G
81	A6	3592	G
81	A6	3593	C
81	A6	3594	C
81	A6	3595	U
81	A6	3596	A
81	A6	3597	G
81	A6	3601	C
81	A6	3605	C
81	A6	3606	U
81	A6	3611	A
81	A6	3615	G
81	A6	3617	G
81	A6	3618	C
81	A6	3620	G
81	A6	3622	C
81	A6	3625	G
81	A6	3626	G
81	A6	3630	A
81	A6	3635	A
81	A6	3646	A
81	A6	3648	A
81	A6	3653	A
81	A6	3662	A
81	A6	3664	G
81	A6	3672	G
81	A6	3673	C

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Mol	Chain	Res	Type
81	A6	3674	G
81	A6	3678	G
81	A6	3680	U
81	A6	3691	G
81	A6	3692	A
81	A6	3698	G
81	A6	3702	A
81	A6	3708	C
81	A6	3709	U
81	A6	3711	A
81	A6	3712	A
81	A6	3713	U
81	A6	3714	G
81	A6	3732	A
81	A6	3748	A
81	A6	3750	G
81	A6	3759	A
81	A6	3760	A
81	A6	3774	A
81	A6	3776	G
81	A6	3777	G
81	A6	3778	U
81	A6	3780	G
81	A6	3782	C
81	A6	3783	A
81	A6	3784	A
81	A6	3785	A
81	A6	3786	U
81	A6	3789	C
81	A6	3792	G
81	A6	3795	A
81	A6	3798	U
81	A6	3799	A
81	A6	3811	G
81	A6	3812	C
81	A6	3813	A
81	A6	3817	A
81	A6	3818	U
81	A6	3819	G
81	A6	3833	C
81	A6	3838	U
81	A6	3839	G

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Mol	Chain	Res	Type
81	A6	3840	U
81	A6	3842	C
81	A6	3843	C
81	A6	3877	A
81	A6	3878	C
81	A6	3879	G
81	A6	3886	G
81	A6	3888	G
81	A6	3889	G
81	A6	3890	A
81	A6	3894	A
81	A6	3897	G
81	A6	3901	A
81	A6	3906	A
81	A6	3907	G
81	A6	3908	A
81	A6	3915	U
81	A6	3916	G
81	A6	3922	G
81	A6	3923	A
81	A6	3938	G
81	A6	3956	G
81	A6	3957	U
81	A6	3960	A
81	A6	3962	A
81	A6	3963	A
81	A6	3964	U
81	A6	3965	A
81	A6	3966	A
81	A6	3969	G
81	A6	3970	G
81	A6	3971	G
81	A6	3973	G
81	A6	4036	G
81	A6	4037	C
81	A6	4041	C
81	A6	4042	G
81	A6	4043	G
81	A6	4044	U
81	A6	4045	G
81	A6	4048	A
81	A6	4049	U

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Mol	Chain	Res	Type
81	A6	4050	A
81	A6	4053	A
81	A6	4056	A
81	A6	4063	U
81	A6	4064	C
81	A6	4072	C
81	A6	4073	A
81	A6	4076	G
81	A6	4077	A
81	A6	4083	U
81	A6	4085	A
81	A6	4086	G
81	A6	4087	G
81	A6	4088	C
81	A6	4093	G
81	A6	4104	G
81	A6	4106	G
81	A6	4107	G
81	A6	4114	C
81	A6	4115	G
81	A6	4116	C
81	A6	4117	U
81	A6	4119	C
81	A6	4120	U
81	A6	4121	G
81	A6	4122	G
81	A6	4123	C
81	A6	4124	G
81	A6	4125	C
81	A6	4126	C
81	A6	4127	A
81	A6	4128	A
81	A6	4133	C
81	A6	4141	G
81	A6	4143	G
81	A6	4144	C
81	A6	4145	C
81	A6	4150	G
81	A6	4154	G
81	A6	4159	C
81	A6	4163	U
81	A6	4164	C

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Mol	Chain	Res	Type
81	A6	4170	A
81	A6	4171	C
81	A6	4183	G
81	A6	4184	G
81	A6	4187	G
81	A6	4191	G
81	A6	4194	U
81	A6	4196	G
81	A6	4203	A
81	A6	4204	C
81	A6	4205	A
81	A6	4212	A
81	A6	4213	A
81	A6	4222	G
81	A6	4229	U
81	A6	4232	U
81	A6	4233	A
81	A6	4234	A
81	A6	4235	G
81	A6	4243	C
81	A6	4251	A
81	A6	4253	A
81	A6	4254	G
81	A6	4255	A
81	A6	4258	C
81	A6	4266	G
81	A6	4267	G
81	A6	4268	A
81	A6	4271	A
81	A6	4273	A
81	A6	4276	G
81	A6	4282	A
81	A6	4289	U
81	A6	4290	U
81	A6	4291	G
81	A6	4296	U
81	A6	4304	A
81	A6	4305	G
81	A6	4306	U
81	A6	4314	C
81	A6	4323	A
81	A6	4326	G

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Mol	Chain	Res	Type
81	A6	4329	G
81	A6	4330	G
81	A6	4335	C
81	A6	4337	C
81	A6	4347	G
81	A6	4349	C
81	A6	4350	C
81	A6	4351	U
81	A6	4352	U
81	A6	4354	U
81	A6	4356	G
81	A6	4360	U
81	A6	4364	G
81	A6	4373	G
81	A6	4376	A
81	A6	4377	G
81	A6	4378	A
81	A6	4380	A
81	A6	4381	A
81	A6	4384	U
81	A6	4385	A
81	A6	4386	C
81	A6	4387	C
81	A6	4393	G
81	A6	4394	A
81	A6	4395	U
81	A6	4398	C
81	A6	4405	G
81	A6	4415	A
81	A6	4419	U
81	A6	4421	C
81	A6	4422	A
81	A6	4424	A
81	A6	4426	C
81	A6	4430	G
81	A6	4435	U
81	A6	4436	U
81	A6	4440	G
81	A6	4444	C
81	A6	4448	G
81	A6	4449	A
81	A6	4450	U

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Mol	Chain	Res	Type
81	A6	4452	U
81	A6	4463	U
81	A6	4464	A
81	A6	4466	C
81	A6	4473	A
81	A6	4476	C
81	A6	4477	A
81	A6	4487	A
81	A6	4488	A
81	A6	4491	G
81	A6	4494	G
81	A6	4500	U
81	A6	4505	C
81	A6	4506	C
81	A6	4512	U
81	A6	4513	A
81	A6	4515	G
81	A6	4518	A
81	A6	4519	C
81	A6	4522	G
81	A6	4524	G
81	A6	4525	C
81	A6	4527	G
81	A6	4528	G
81	A6	4531	U
81	A6	4534	G
81	A6	4537	C
81	A6	4545	G
81	A6	4548	A
81	A6	4549	G
81	A6	4560	C
81	A6	4567	G
81	A6	4572	U
81	A6	4574	U
81	A6	4575	G
81	A6	4583	C
81	A6	4584	A
81	A6	4590	A
81	A6	4592	C
81	A6	4599	A
81	A6	4601	U
81	A6	4606	G

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Mol	Chain	Res	Type
81	A6	4608	G
81	A6	4610	A
81	A6	4617	G
81	A6	4628	U
81	A6	4629	U
81	A6	4634	U
81	A6	4636	U
81	A6	4637	G
81	A6	4639	G
81	A6	4646	U
81	A6	4647	G
81	A6	4652	G
81	A6	4656	A
81	A6	4657	U
81	A6	4661	G
81	A6	4664	A
81	A6	4669	A
81	A6	4670	C
81	A6	4671	C
81	A6	4672	A
81	A6	4677	U
81	A6	4678	G
81	A6	4682	U
81	A6	4687	A
81	A6	4694	G
81	A6	4700	A
81	A6	4708	A
81	A6	4709	U
81	A6	4711	C
81	A6	4712	C
81	A6	4714	C
81	A6	4717	A
81	A6	4720	C
81	A6	4721	G
81	A6	4728	U
81	A6	4730	C
81	A6	4731	G
81	A6	4732	G
81	A6	4734	A
81	A6	4737	G
81	A6	4739	C
81	A6	4741	C

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Mol	Chain	Res	Type
81	A6	4747	C
81	A6	4748	U
81	A6	4750	G
81	A6	4751	G
81	A6	4752	U
81	A6	4753	U
81	A6	4756	C
81	A6	4758	U
81	A6	4761	G
81	A6	4762	A
81	A6	4764	A
81	A6	4771	C
81	A6	4772	C
81	A6	4867	G
81	A6	4870	G
81	A6	4871	C
81	A6	4872	G
81	A6	4873	G
81	A6	4874	A
81	A6	4875	G
81	A6	4876	U
81	A6	4877	G
81	A6	4882	U
81	A6	4883	C
81	A6	4884	G
81	A6	4885	U
81	A6	4886	C
81	A6	4888	U
81	A6	4889	G
81	A6	4890	G
81	A6	4891	G
81	A6	4895	C
81	A6	4896	G
81	A6	4900	C
81	A6	4901	G
81	A6	4910	G
81	A6	4911	A
81	A6	4912	G
81	A6	4914	C
81	A6	4925	U
81	A6	4926	C
81	A6	4928	C

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Mol	Chain	Res	Type
81	A6	4931	G
81	A6	4933	C
81	A6	4934	A
81	A6	4936	G
81	A6	4937	C
81	A6	4939	C
81	A6	4940	C
81	A6	4941	G
81	A6	4942	C
81	A6	4943	A
81	A6	4944	C
81	A6	4945	G
81	A6	4946	U
81	A6	4947	U
81	A6	4948	C
81	A6	4950	U
81	A6	4951	G
81	A6	4952	G
81	A6	4961	G
81	A6	4962	C
81	A6	4965	U
81	A6	4966	A
81	A6	4967	A
81	A6	4973	U
81	A6	4975	G
81	A6	4976	U
81	A6	4977	A
81	A6	4985	U
81	A6	4988	U
81	A6	4989	U
81	A6	4990	C
81	A6	4991	U
81	A6	4992	G
81	A6	5002	U
81	A6	5005	G
81	A6	5007	A
81	A6	5013	C
81	A6	5014	A
81	A6	5017	G
81	A6	5022	U
81	A6	5023	C
81	A6	5024	C

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Mol	Chain	Res	Type
81	A6	5026	U
81	A6	5027	C
81	A6	5028	G
81	A6	5031	G
81	A6	5041	G
81	A6	5042	A
81	A6	5047	C
81	A6	5050	C
81	A6	5052	C
81	A6	5054	C
81	A6	5055	G
81	A6	5060	A
81	A6	5061	A
81	A6	5062	G
81	A6	5064	G
81	A6	5068	G
81	A6	5069	U

All (197) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
77	A5	12	A
77	A5	64	A
77	A5	125	C
77	A5	142	G
77	A5	184	U
77	A5	186	G
77	A5	200	U
77	A5	215	C
77	A5	219	G
77	A5	220	C
77	A5	226	G
77	A5	293	G
77	A5	333	U
77	A5	406	C
77	A5	431	G
77	A5	451	C
77	A5	452	A
77	A5	490	C
77	A5	505	G
77	A5	509	A
77	A5	648	G

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Mol	Chain	Res	Type
77	A5	655	C
77	A5	668	C
77	A5	684	G
77	A5	703	G
77	A5	727	C
77	A5	746	A
77	A5	915	A
77	A5	917	A
77	A5	926	G
77	A5	928	C
77	A5	931	C
77	A5	934	C
77	A5	936	C
77	A5	939	G
77	A5	955	G
77	A5	957	G
77	A5	958	G
77	A5	959	G
77	A5	971	U
77	A5	974	C
77	A5	979	C
77	A5	980	U
77	A5	1210	C
77	A5	1211	G
77	A5	1236	C
77	A5	1238	A
77	A5	1239	C
77	A5	1267	C
77	A5	1274	A
77	A5	1281	G
77	A5	1284	G
77	A5	1294	A
77	A5	1296	G
77	A5	1356	U
77	A5	1358	G
77	A5	1365	C
77	A5	1370	G
77	A5	1371	A
77	A5	1398	A
77	A5	1419	G
77	A5	1426	G
77	A5	1455	G

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Mol	Chain	Res	Type
77	A5	1480	C
77	A5	1481	C
77	A5	1482	G
77	A5	1500	A
77	A5	1629	G
77	A5	1633	G
77	A5	1804	A
77	A5	1835	G
77	A5	1841	C
77	A5	1853	G
77	A5	1919	G
77	A5	1921	C
77	A5	1986	U
77	A5	1998	A
77	A5	2009	A
77	A5	2046	G
77	A5	2068	C
77	A5	2083	C
77	A5	2089	G
78	A7	72	U
79	A8	85	U
79	A8	94	G
79	A8	96	C
79	A8	124	U
79	A8	126	C
80	B2	24	C
80	B2	66	G
80	B2	72	C
80	B2	102	A
80	B2	127	C
80	B2	139	C
80	B2	140	C
80	B2	141	A
80	B2	181	A
80	B2	225	G
80	B2	228	C
80	B2	465	A
80	B2	529	A
80	B2	534	G
80	B2	552	G
80	B2	554	A
80	B2	604	A

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Mol	Chain	Res	Type
80	B2	668	A
80	B2	688	U
80	B2	732	U
80	B2	734	C
80	B2	746	C
80	B2	797	C
80	B2	810	A
80	B2	821	G
80	B2	833	C
80	B2	839	C
80	B2	869	A
80	B2	970	G
80	B2	1214	A
80	B2	1253	A
80	B2	1283	C
80	B2	1307	U
80	B2	1356	G
80	B2	1378	A
80	B2	1394	G
80	B2	1395	C
80	B2	1396	A
80	B2	1401	A
80	B2	1429	G
80	B2	1474	A
80	B2	1543	U
80	B2	1556	A
80	B2	1599	U
80	B2	1601	A
80	B2	1637	A
80	B2	1664	A
80	B2	1756	C
80	B2	1823	A
80	B2	1824	A
80	B2	1825	A
80	B2	1830	U
80	B2	1868	U
81	A6	2263	A
81	A6	2264	C
81	A6	2266	C
81	A6	2268	A
81	A6	2312	U
81	A6	2313	A

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Mol	Chain	Res	Type
81	A6	2319	C
81	A6	2398	U
81	A6	2488	C
81	A6	2517	A
81	A6	2531	C
81	A6	2546	G
81	A6	2661	U
81	A6	2670	C
81	A6	2695	A
81	A6	2766	A
81	A6	2769	U
81	A6	2825	A
81	A6	2828	U
81	A6	3605	C
81	A6	3616	U
81	A6	3671	G
81	A6	3697	U
81	A6	3788	C
81	A6	3876	A
81	A6	3888	G
81	A6	3959	U
81	A6	3965	A
81	A6	3968	U
81	A6	4036	G
81	A6	4047	A
81	A6	4072	C
81	A6	4082	G
81	A6	4085	A
81	A6	4119	C
81	A6	4121	G
81	A6	4127	A
81	A6	4163	U
81	A6	4170	A
81	A6	4232	U
81	A6	4448	G
81	A6	4656	A
81	A6	4738	C
81	A6	4871	C
81	A6	4874	A
81	A6	4882	U
81	A6	4885	U
81	A6	4889	G

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Mol	Chain	Res	Type
81	A6	4925	U
81	A6	4942	C
81	A6	4943	A
81	A6	4945	G
81	A6	4966	A
81	A6	4991	U
81	A6	5022	U
81	A6	5027	C

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

6 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
39	MLZ	o	53	39	8,9,10	0.77	0	4,9,11	0.52	0
27	MLZ	b	5	27	8,9,10	0.79	0	4,9,11	0.62	0
72	NMM	TT	67	72	8,11,12	0.76	0	7,12,14	1.21	1 (14%)
37	M3L	m	98	37	10,11,12	0.40	0	9,14,16	0.32	0
26	V5N	a	39	26	8,11,12	0.57	0	8,14,16	1.00	0
2	HIC	B	245	2	10,11,12	0.52	0	9,14,16	0.61	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	MLZ	o	53	39	-	2/7/8/10	-
27	MLZ	b	5	27	-	2/7/8/10	-
72	NMM	TT	67	72	-	0/9/11/13	-
37	M3L	m	98	37	-	0/9/10/12	-
26	V5N	a	39	26	-	4/9/10/12	0/1/1/1
2	HIC	B	245	2	-	0/5/6/8	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
72	TT	67	NMM	NE-CZ-NH1	2.09	124.10	120.26

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
39	o	53	MLZ	CD-CE-NZ-CM
26	a	39	V5N	O-C-CA-CB
26	a	39	V5N	C-CA-CB-CG
26	a	39	V5N	C-CA-CB-O2
27	b	5	MLZ	N-CA-CB-CG
27	b	5	MLZ	C-CA-CB-CG
26	a	39	V5N	N-CA-CB-O2
39	o	53	MLZ	CE-CD-CG-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 34 ligands modelled in this entry, 34 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
77	A5	9
81	A6	4
6	E	3
80	B2	3
82	BB	1
8	G	1
46	ee	1
58	XX	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A5	1703:C	O3'	1720:C	P	20.34
1	E	78:ALA	C	90:LYS	N	20.05
1	BB	8:ARG	C	23:ASP	N	19.98
1	B2	704:G	O3'	724:A	P	19.89
1	B2	766:C	O3'	776:A	P	18.72
1	A5	1249:C	O3'	1261:G	P	17.48
1	A5	1221:G	O3'	1234:G	P	15.93
1	A5	1438:U	O3'	1447:C	P	15.70
1	A5	889:C	O3'	895:C	P	15.14
1	A5	1113:C	O3'	1155:C	P	15.03
1	B2	257:C	O3'	262:G	P	14.52
1	A6	3983:G	O3'	4029:C	P	14.40
1	G	113:ARG	C	133:PRO	N	12.67
1	A5	524:C	O3'	633:G	P	12.51
1	A5	1000:A	O3'	1041:G	P	12.33
1	ee	119:VAL	C	126:LYS	N	12.00
1	A6	3298:G	O3'	3566:C	P	11.60
1	A5	765:C	O3'	884:G	P	10.55
1	A6	2945:C	O3'	3247:A	P	9.59
1	E	224:LYS	C	241:GLU	N	8.62
1	A6	4779:U	O3'	4855:G	P	5.46
1	XX	61:GLN	C	62:PRO	N	4.06
1	E	41:LYS	C	42:GLY	N	2.24

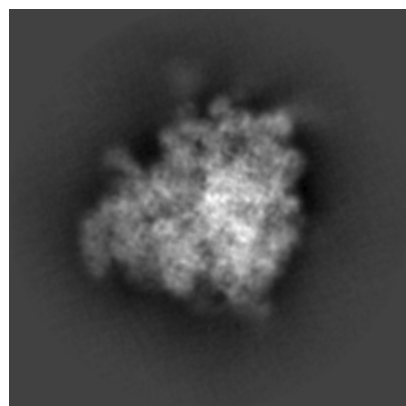
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72469. These allow visual inspection of the internal detail of the map and identification of artifacts.

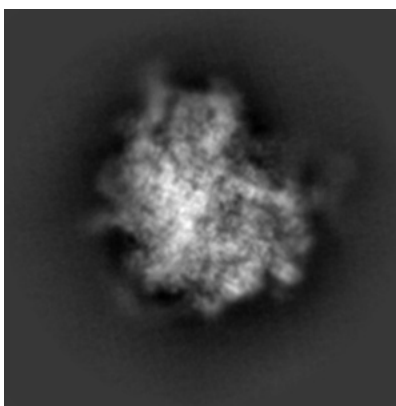
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

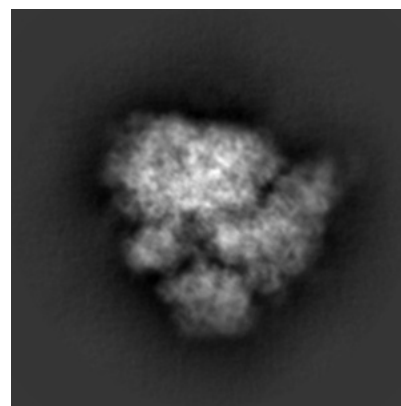
6.1.1 Primary map



X

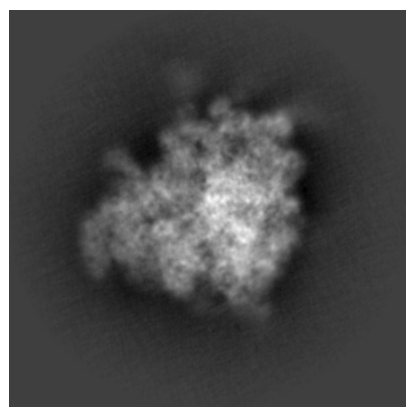


Y

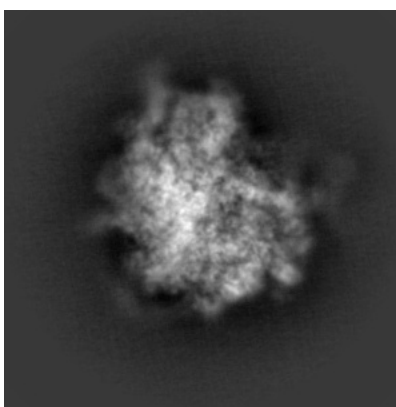


Z

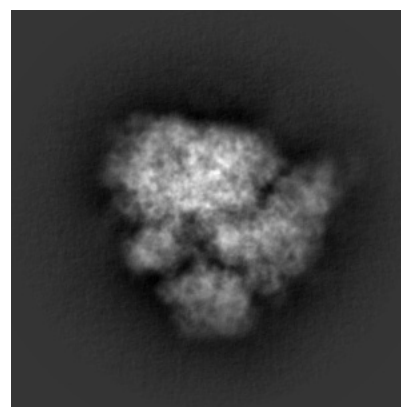
6.1.2 Raw map



X



Y

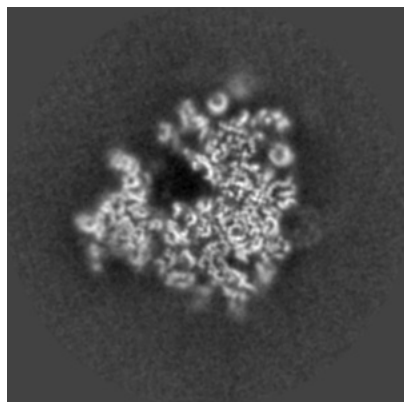


Z

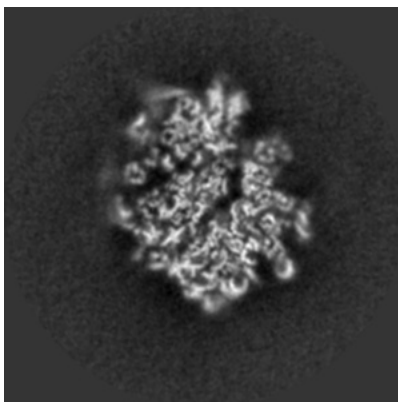
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

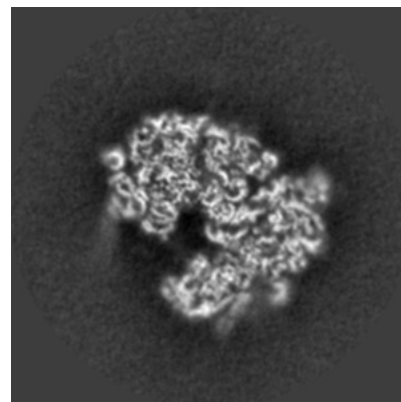
6.2.1 Primary map



X Index: 220

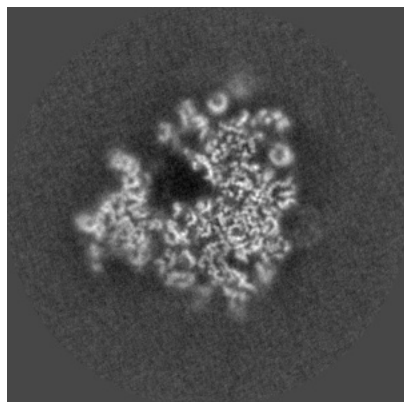


Y Index: 220

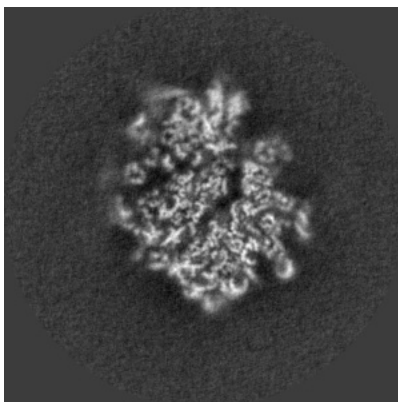


Z Index: 220

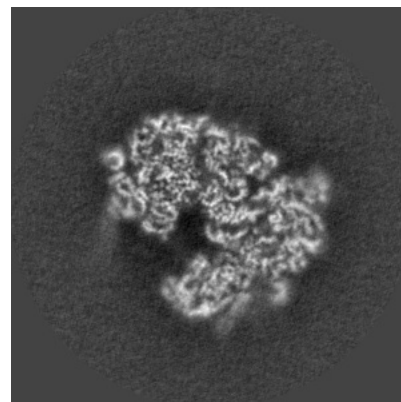
6.2.2 Raw map



X Index: 220



Y Index: 220

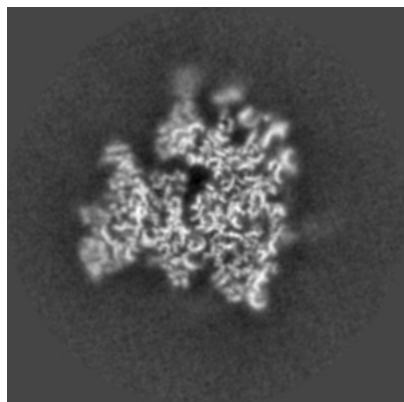


Z Index: 220

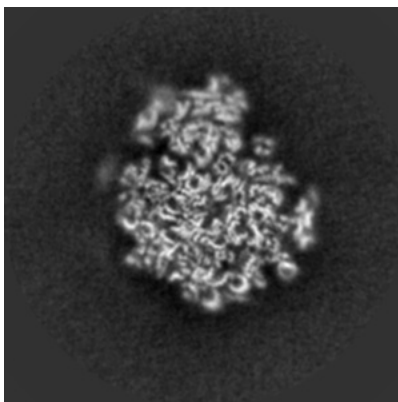
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

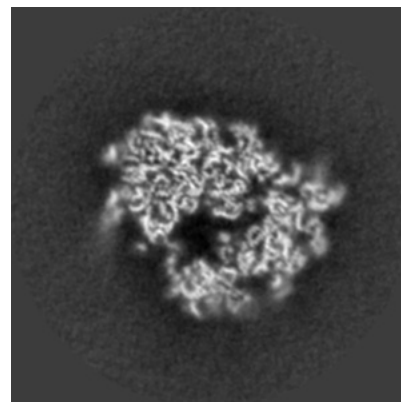
6.3.1 Primary map



X Index: 236

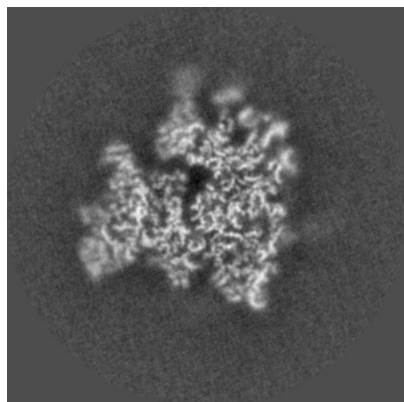


Y Index: 228

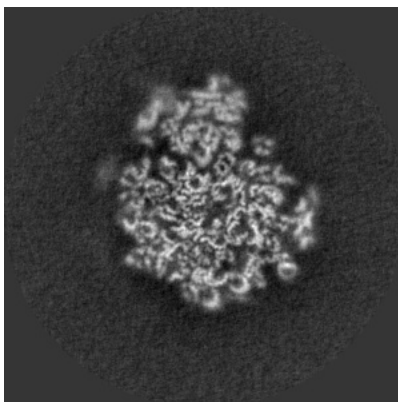


Z Index: 229

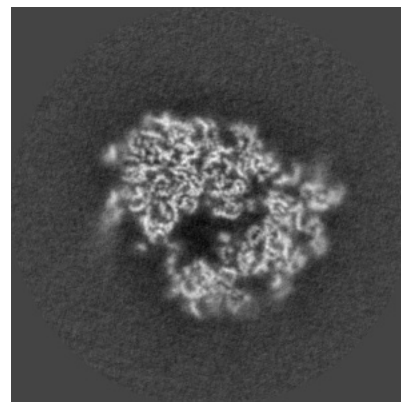
6.3.2 Raw map



X Index: 236



Y Index: 229

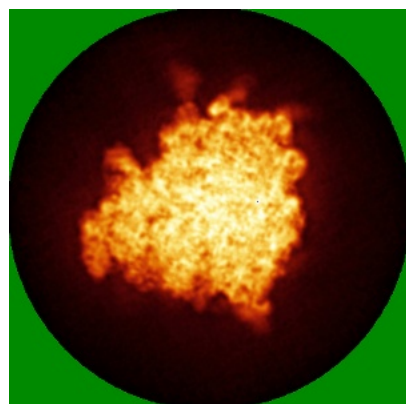


Z Index: 229

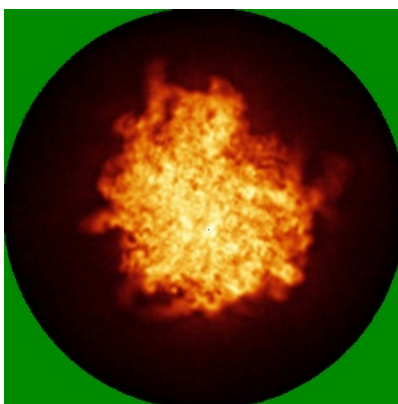
The images above show the largest variance slices of the map in three orthogonal directions.

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

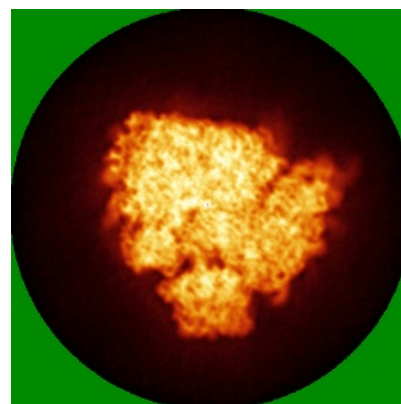
6.4.1 Primary map



X

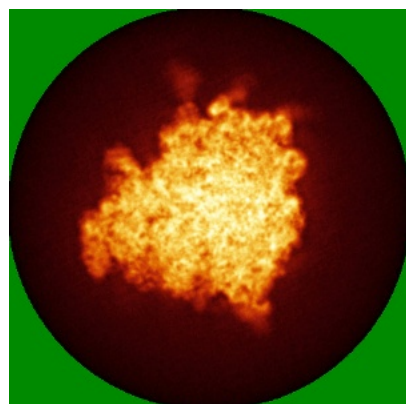


Y

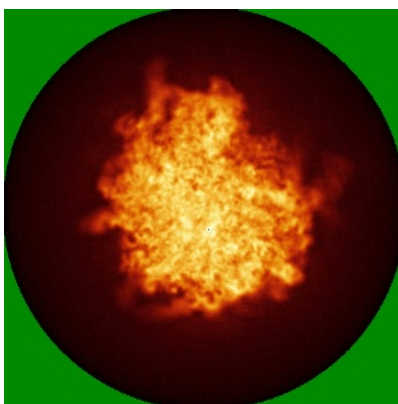


Z

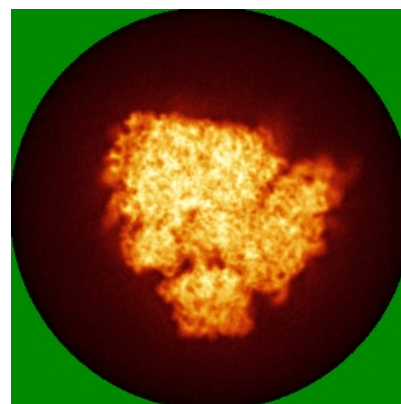
6.4.2 Raw map



X



Y

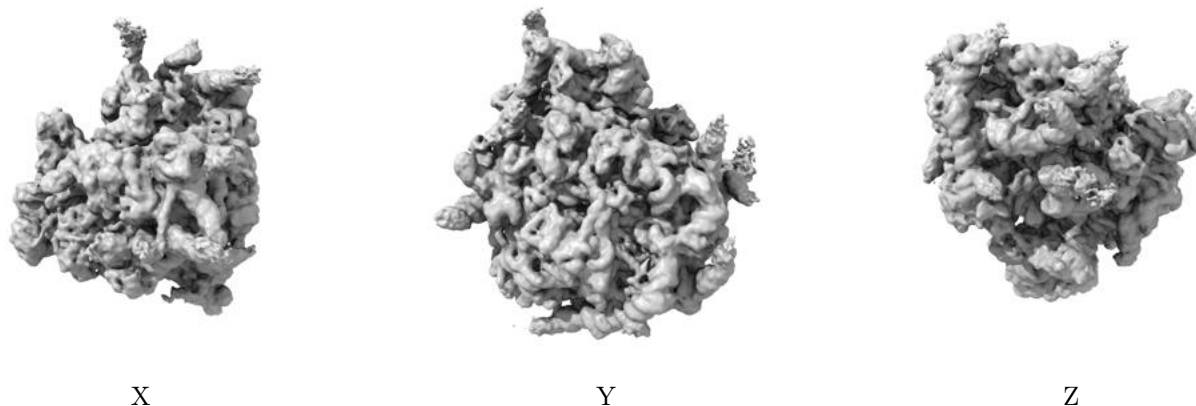


Z

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 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

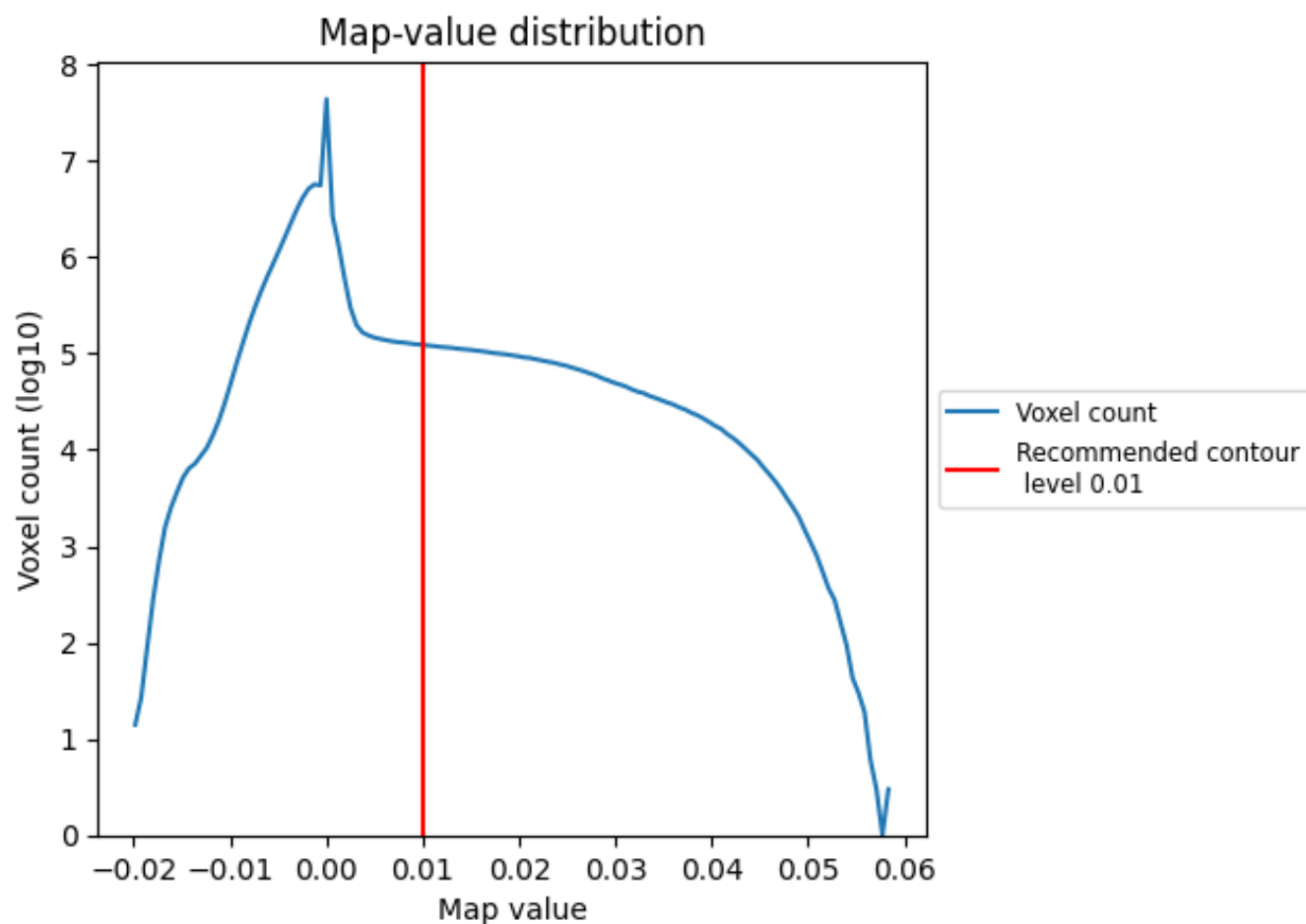
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

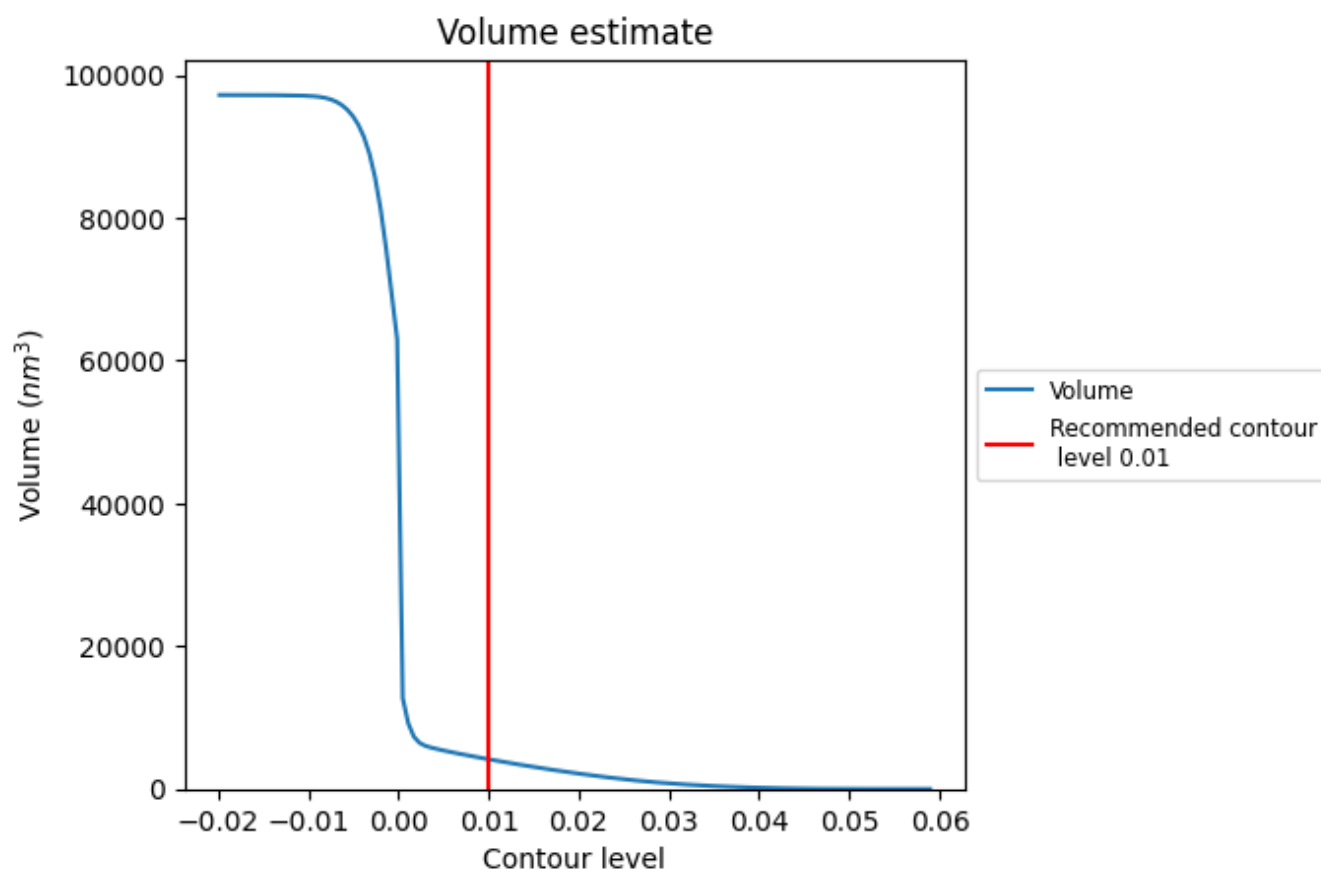
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

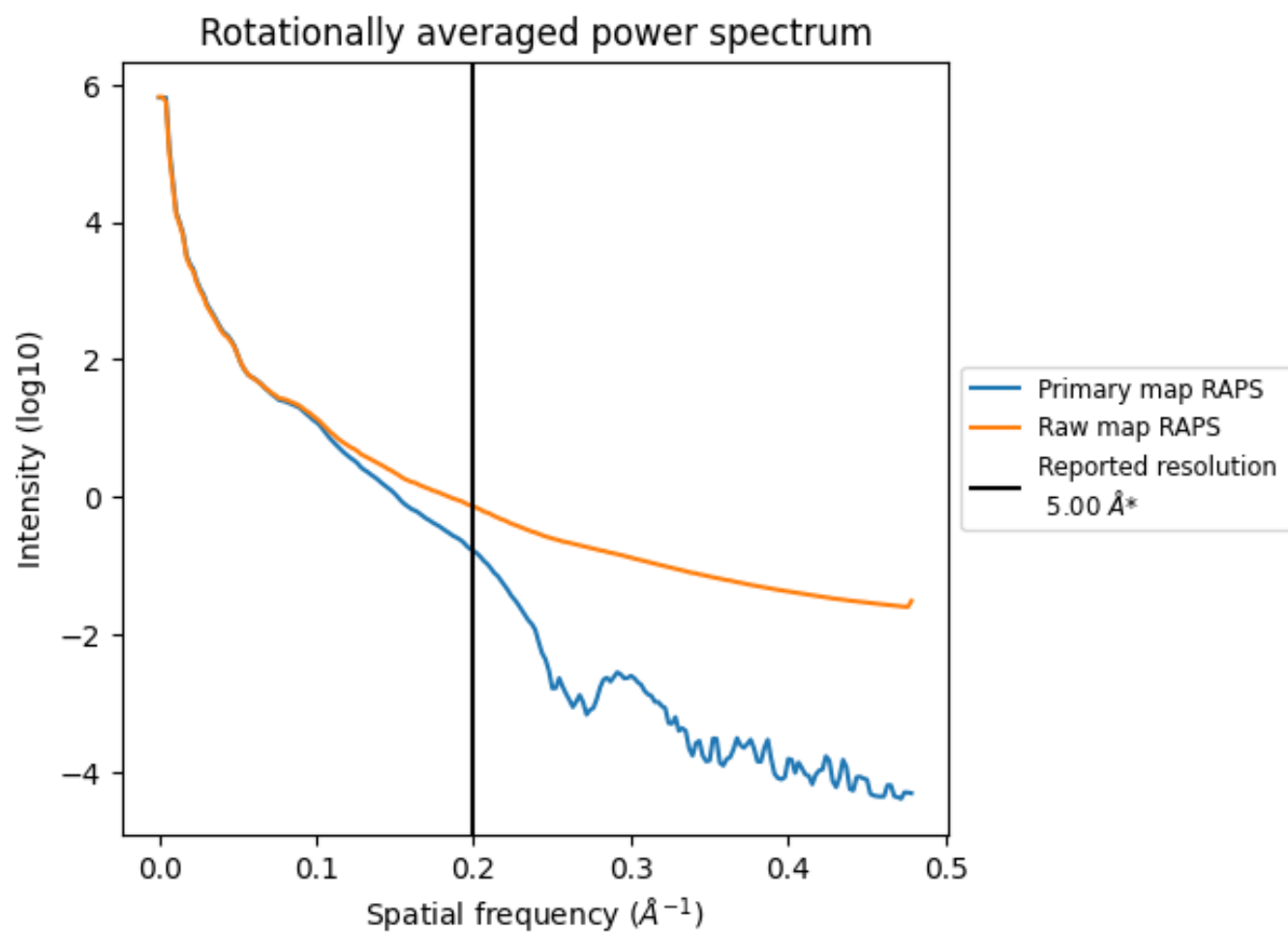
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4156 nm^3 ; this corresponds to an approximate mass of 3755 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 ⓘ

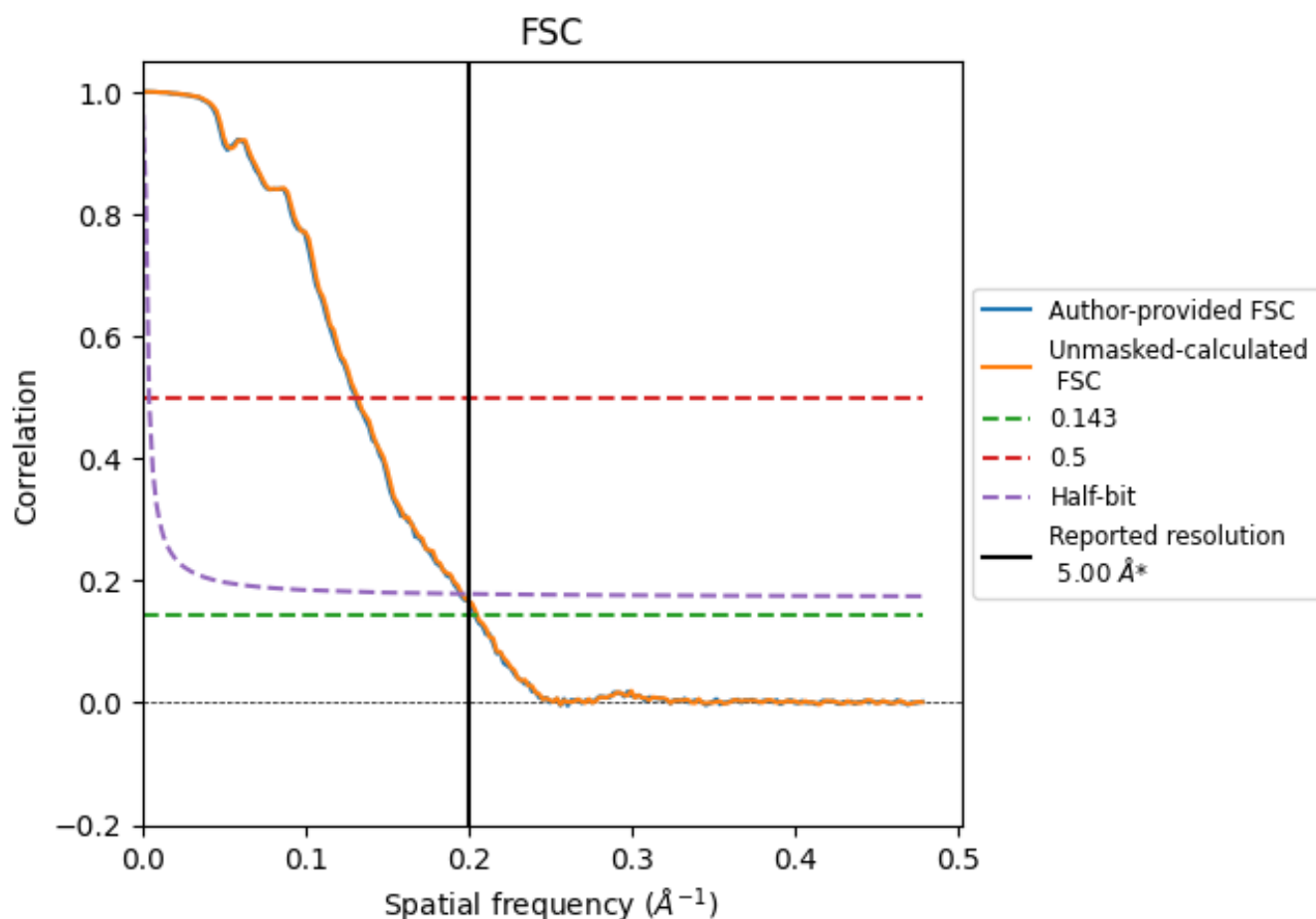


*Reported resolution corresponds to spatial frequency of 0.200 \AA^{-1}

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 0.200 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	-	-
Author-provided FSC curve	4.90	7.64	5.13
Unmasked-calculated*	4.87	7.58	5.10

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

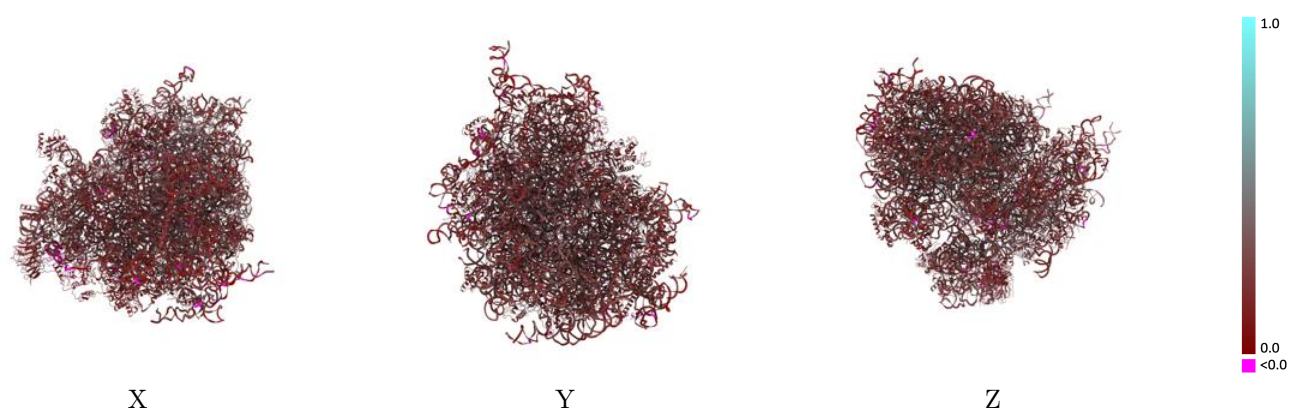
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-72469 and PDB model 9Y42. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)

This section was not generated.

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

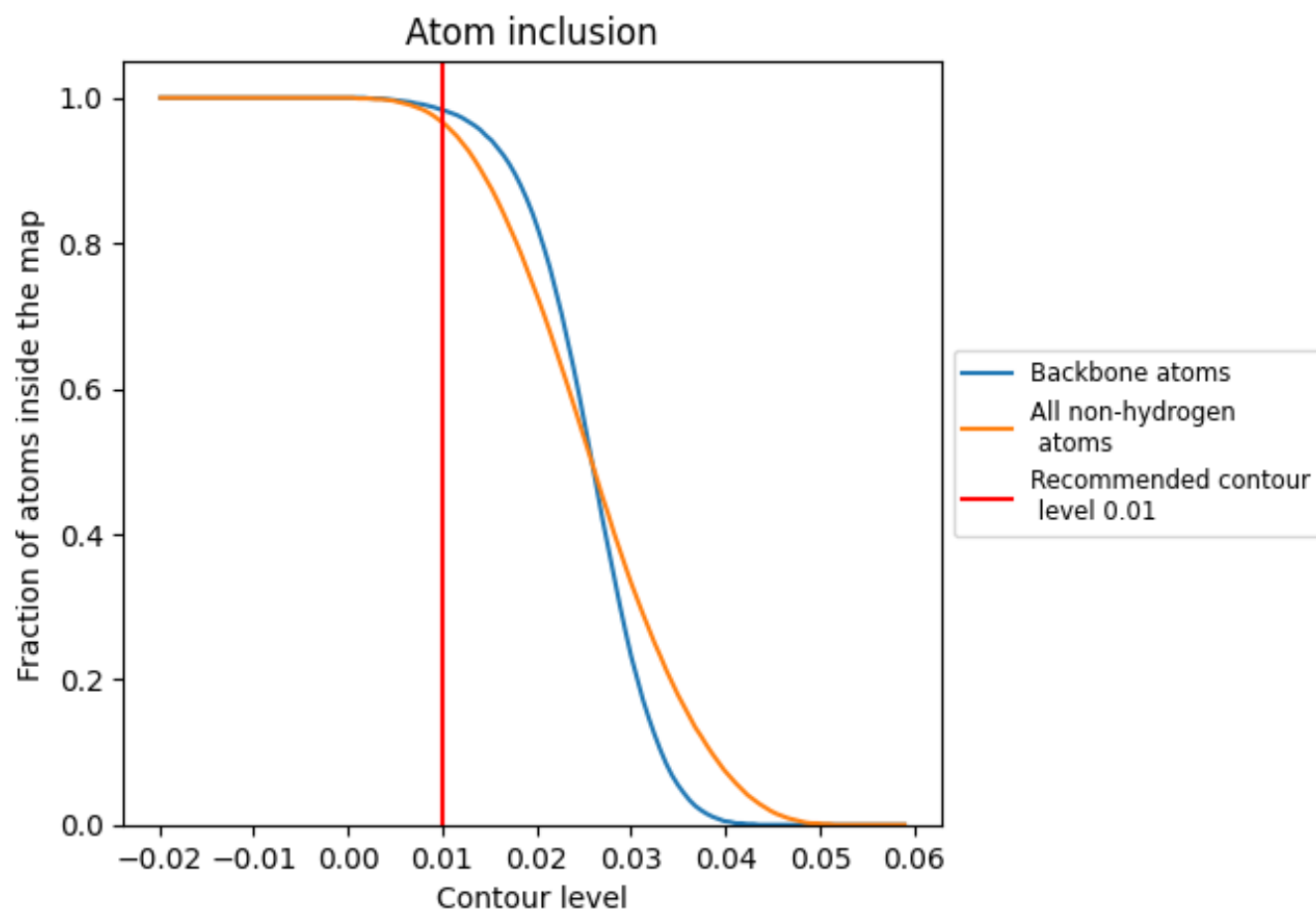


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 97% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9660	 0.2370
A	 0.9140	 0.2370
A5	 0.9870	 0.2570
A6	 0.9900	 0.2680
A7	 0.9980	 0.2760
A8	 0.9930	 0.2580
AA	 0.8950	 0.1840
B	 0.9490	 0.2330
B2	 0.9850	 0.2500
BB	 0.9060	 0.1380
C	 0.9520	 0.2360
CC	 0.9100	 0.2210
Cc	 0.9880	 0.2470
D	 0.9840	 0.2080
DD	 0.9430	 0.2260
E	 0.9720	 0.2280
EE	 0.9680	 0.2120
EF	 0.8390	 0.1890
F	 0.9370	 0.2220
FF	 0.9610	 0.1810
G	 0.9590	 0.2130
GG	 0.9660	 0.1780
H	 0.9400	 0.2250
HH	 0.9170	 0.2060
I	 0.9440	 0.2460
II	 0.9560	 0.1950
J	 0.9800	 0.2030
JJ	 0.9720	 0.2010
KK	 0.9920	 0.1980
L	 0.9590	 0.2350
LL	 0.9180	 0.2350
M	 0.9750	 0.2270
MM	 0.9490	 0.1840
N	 0.9620	 0.2160
NN	 0.9260	 0.2010



















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Chain	Atom inclusion	Q-score
O	 0.9240	 0.2250
OO	 0.8970	 0.1160
P	 0.9500	 0.2260
PP	 0.9760	 0.1940
Q	 0.9280	 0.2400
QQ	 0.9810	 0.1790
RR	 0.7460	 0.0790
S	 0.9680	 0.2360
SS	 0.9700	 0.1830
T	 0.9490	 0.2450
TT	 0.9900	 0.1770
U	 0.9810	 0.2110
UU	 0.9790	 0.2010
V	 0.8730	 0.2370
VV	 0.8590	 0.2030
W	 0.9420	 0.2020
WW	 0.9250	 0.2210
X	 0.9700	 0.2310
XX	 0.9380	 0.2500
Y	 0.9680	 0.2200
YY	 0.9830	 0.1850
Z	 0.9800	 0.2130
ZZ	 0.9500	 0.1580
a	 0.9690	 0.2450
aa	 0.9270	 0.1880
b	 0.9580	 0.1830
bb	 0.9670	 0.2210
c	 0.9380	 0.1830
cc	 0.9330	 0.2010
d	 0.9640	 0.2340
dd	 0.9750	 0.1860
e	 0.9280	 0.2540
ee	 0.9820	 0.2050
f	 0.9460	 0.2380
ff	 0.9790	 0.1870
g	 0.9510	 0.2210
gg	 0.9790	 0.1900
h	 0.9640	 0.2100
i	 0.9490	 0.2170
j	 0.9760	 0.2110
k	 0.9570	 0.2020
l	 0.9700	 0.2290

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Chain	Atom inclusion	Q-score
m	 0.9440	 0.2290
n	 0.8670	 0.1580
o	 0.9390	 0.2250
p	 0.8850	 0.2290
r	 0.9360	 0.2500
s	 0.9800	 0.1910
t	 0.8940	 0.1390
u	 0.8560	 0.2190