



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 08:54 PM UTC

PDB ID : 9KZX / pdb_00009kzx
EMDB ID : EMD-62679
Title : Cryo-EM structure of the HCV IRES-dependently initiated CMV-stalled 80S ribosome (rotated state) in complexed with eIF3
Authors : Iwasaki, W.; Kashiwagi, K.; Sakamoto, A.; Nishimoto, M.; Takahashi, M.; Machida, K.; Imataka, H.; Matsumoto, A.; Shichino, Y.; Iwasaki, S.; Imami, K.; Ito, T.
Deposited on : 2024-12-11
Resolution : 3.30 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

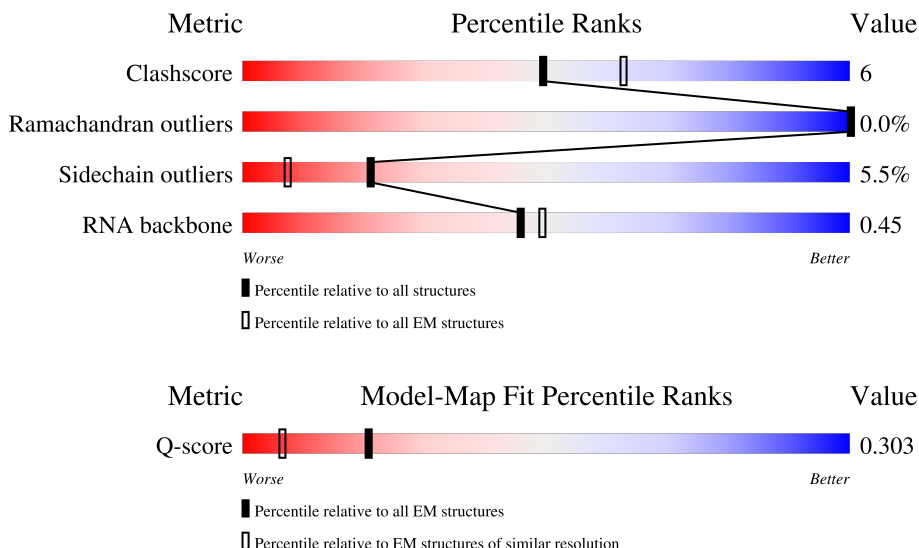
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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.



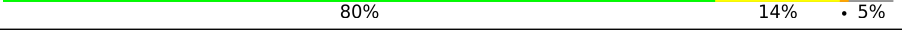
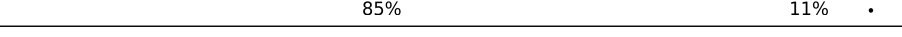
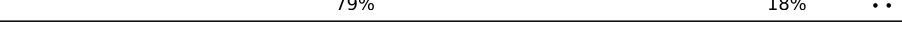
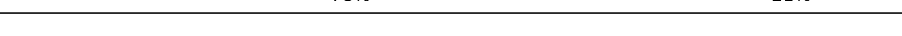
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15087 (2.80 - 3.80)

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	L5	5070	
2	L7	120	
3	L8	156	

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Mol	Chain	Length	Quality of chain
4	LA	257	
5	LB	403	
6	LC	427	
7	LD	297	
8	LE	288	
9	LF	248	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	215	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	
24	LV	140	
25	LW	157	
26	LX	156	
27	LY	145	
28	LZ	136	

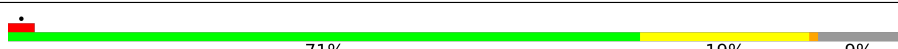
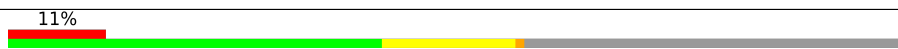
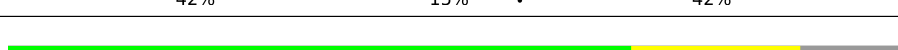
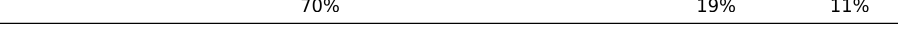
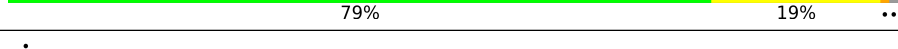
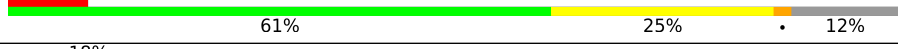
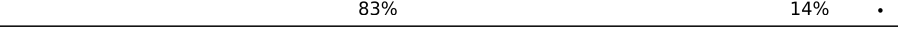
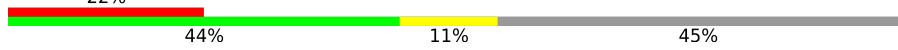
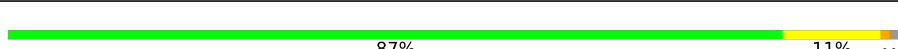
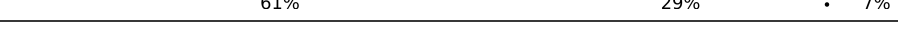
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Mol	Chain	Length	Quality of chain
29	La	148	
30	Lb	159	
31	Lc	115	
32	Ld	125	
33	Le	135	
34	Lf	110	
35	Lg	117	
36	Lh	123	
37	Li	105	
38	Lj	97	
39	Lk	70	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	Lr	137	
46	S2	1869	
47	SA	295	
48	SB	264	
49	SC	293	
50	SD	243	
51	SE	263	
52	SF	204	
53	SG	249	

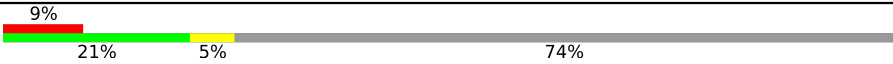
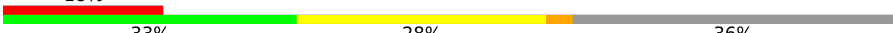
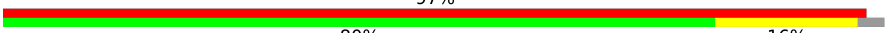
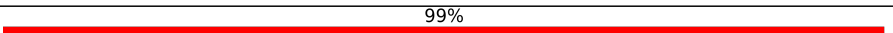
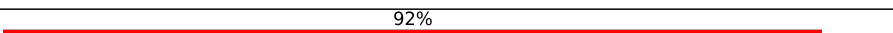
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Mol	Chain	Length	Quality of chain
54	SH	194	
55	SI	208	
56	SJ	194	
57	SK	165	
58	SL	158	
59	SN	151	
60	SO	151	
61	SP	145	
62	SQ	146	
63	SR	135	
64	SS	152	
65	ST	145	
66	SU	119	
67	SV	83	
68	SW	130	
69	SX	143	
70	SY	133	
71	SZ	125	
72	Sa	115	
73	Sb	84	
74	Sc	69	
75	Sd	56	
76	Se	59	
77	Sf	132	
78	Sg	317	

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Mol	Chain	Length	Quality of chain
79	sh	156	
80	zu	75	
80	zy	75	
81	zv	19	
82	zx	31	
83	zz	332	
84	3m	374	
85	3f	357	
86	3a	1382	
87	3e	445	
88	3c	913	
89	3h	352	
90	3d	548	
91	3k	218	
92	3l	564	

2 Entry composition

There are 94 unique types of molecules in this entry. The entry contains 238047 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 RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L5	3589	Total	C	N	O	P	0	0
			76925	34255	14066	25016	3588		

- Molecule 2 is a RNA chain called 5S_ribosomal_RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 3 is a RNA chain called 5.8S_ribosomal_RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 4 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LA	248	Total	C	N	O	S	0	0
			1886	1183	386	311	6		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LB	393	Total	C	N	O	S	0	0
			3101	1979	583	525	14		

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LC	365	Total	C	N	O	S	0	0
			2894	1819	578	482	15		

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LD	293	Total	C	N	O	S	0	0
			2287	1455	426	392	14		

- Molecule 8 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LE	220	Total	C	N	O	S	0	0
			1713	1104	326	279	4		

- Molecule 9 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LF	225	Total	C	N	O	S	0	0
			1844	1189	355	291	9		

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LG	237	Total	C	N	O	S	0	0
			1797	1145	350	298	4		

- Molecule 11 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LH	189	Total	C	N	O	S	0	0
			1439	910	273	250	6		

- Molecule 12 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LI	203	Total	C	N	O	S	0	0
			1581	1007	306	254	14		

- Molecule 13 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LJ	167	Total	C	N	O	S	0	0
			1226	780	228	212	6		

- Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LL	204	Total	C	N	O	S	0	0
			1580	992	335	249	4		

- Molecule 15 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LM	136	Total	C	N	O	S	0	0
			1097	705	211	174	7		

- Molecule 16 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LN	203	Total	C	N	O	S	0	0
			1693	1068	359	262	4		

- Molecule 17 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LO	201	Total	C	N	O	S	0	0
			1613	1042	318	248	5		

- Molecule 18 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LP	153	Total	C	N	O	S	0	0
			1203	754	238	202	9		

- Molecule 19 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LQ	187	Total	C	N	O	S	0	0
			1493	931	311	246	5		

- Molecule 20 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LR	178	Total	C	N	O	S	0	0
			1434	888	316	222	8		

- Molecule 21 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LS	175	Total	C	N	O	S	0	0
			1436	915	281	230	10		

- Molecule 22 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LT	159	Total	C	N	O	S	0	0
			1268	805	249	209	5		

- Molecule 23 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LU	101	Total	C	N	O	S	0	0
			768	497	136	133	2		

- Molecule 24 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LV	131	Total	C	N	O	S	0	0
			954	604	180	165	5		

- Molecule 25 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LW	115	Total	C	N	O	S	0	0
			784	493	154	135	2		

- Molecule 26 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LX	120	Total	C	N	O	S	0	0
			950	611	182	156	1		

- Molecule 27 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LY	134	Total	C	N	O	S	0	0
			1084	681	220	180	3		

- Molecule 28 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LZ	135	Total	C	N	O	S	0	0
			1082	703	207	169	3		

- Molecule 29 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	La	146	Total	C	N	O	S	0	0
			1145	726	233	183	3		

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lb	63	Total	C	N	O	S	0	0
			499	310	107	80	2		

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lc	93	Total	C	N	O	S	0	0
			716	456	125	129	6		

- Molecule 32 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ld	107	Total	C	N	O	S	0	0
			856	546	168	140	2		

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Le	127	Total	C	N	O	S	0	0
			1045	661	215	164	5		

- Molecule 34 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lf	109	Total	C	N	O	S	0	0
			864	547	173	141	3		

- Molecule 35 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lg	110	Total	C	N	O	S	0	0
			851	531	175	139	6		

- Molecule 36 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lh	121	Total	C	N	O	S	0	0
			975	617	200	157	1		

- Molecule 37 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Li	101	Total	C	N	O	S	0	0
			797	500	170	122	5		

- Molecule 38 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lj	86	Total	C	N	O	S	0	0
			701	431	154	111	5		

- Molecule 39 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lk	69	Total	C	N	O	S	0	0
			528	339	99	89	1		

- Molecule 40 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ll	50	Total	C	N	O	S	0	0
			440	278	97	64	1		

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lm	50	Total	C	N	O	S	0	0
			393	244	82	61	6		

- Molecule 42 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 43 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lo	98	Total	C	N	O	S	0	0
			774	488	159	121	6		

- Molecule 44 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lp	91	Total	C	N	O	S	0	0
			689	436	132	114	7		

- Molecule 45 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lr	125	Total	C	N	O	S	0	0
			982	609	205	164	4		

- Molecule 46 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	S2	1691	Total	C	N	O	P	0	0
			35873	16003	6419	11761	1690		

- Molecule 47 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SA	212	Total	C	N	O	S	0	0
			1575	1016	285	266	8		

- Molecule 48 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SB	214	Total	C	N	O	S	0	0
			1627	1041	296	277	13		

- Molecule 49 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SC	217	Total	C	N	O	S	0	0
			1590	1039	276	266	9		

- Molecule 50 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SD	212	Total	C	N	O	S	0	0
			1458	939	264	248	7		

- Molecule 51 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SE	257	Total	C	N	O	S	0	0
			1891	1218	358	307	8		

- Molecule 52 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SF	180	Total	C	N	O	S	0	0
			1365	861	261	237	6		

- Molecule 53 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SG	233	Total	C	N	O	S	0	0
			1740	1084	356	294	6		

- Molecule 54 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SH	178	Total	C	N	O	S	0	0
			1363	883	253	226	1		

- Molecule 55 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SI	202	Total	C	N	O	S	0	0
			1551	972	305	269	5		

- Molecule 56 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SJ	176	Total	C	N	O	S	0	0
			1407	899	280	226	2		

- Molecule 57 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SK	95	Total	C	N	O	S	0	0
			736	482	131	119	4		

- Molecule 58 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SL	140	Total	C	N	O	S	0	0
			1139	725	214	194	6		

- Molecule 59 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SN	150	Total	C	N	O	S	0	0
			1199	766	229	203	1		

- Molecule 60 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SO	135	Total	C	N	O	S	0	0
			1003	615	198	184	6		

- Molecule 61 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SP	127	Total	C	N	O	S	0	0
			1001	636	188	170	7		

- Molecule 62 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SQ	141	Total	C	N	O	S	0	0
			1078	690	207	178	3		

- Molecule 63 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SR	125	Total	C	N	O	S	0	0
			879	551	166	159	3		

- Molecule 64 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SS	138	Total	C	N	O	S	0	0
			1080	684	220	175	1		

- Molecule 65 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	ST	138	Total	C	N	O	S	0	0
			975	612	192	169	2		

- Molecule 66 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SU	98	Total	C	N	O	S	0	0
			737	461	142	132	2		

- Molecule 67 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SV	83	Total	C	N	O	S	0	0
			589	369	111	104	5		

- Molecule 68 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SW	129	Total	C	N	O	S	0	0
			1027	655	192	174	6		

- Molecule 69 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SX	141	Total	C	N	O	S	0	0
			1048	663	206	176	3		

- Molecule 70 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SY	126	Total	C	N	O	S	0	0
			943	599	182	158	4		

- Molecule 71 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SZ	69	Total	C	N	O	S	0	0
			479	305	89	84	1		

- Molecule 72 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Sa	99	Total	C	N	O	S	0	0
			762	478	157	122	5		

- Molecule 73 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Sb	83	Total	C	N	O	S	0	0
			617	390	114	109	4		

- Molecule 74 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Sc	61	Total	C	N	O	S	0	0
			430	267	83	78	2		

- Molecule 75 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Sd	52	Total	C	N	O	S	0	0
			420	264	83	69	4		

- Molecule 76 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Se	51	Total	C	N	O	S	0	0
			386	240	83	62	1		

- Molecule 77 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Sf	78	Total	C	N	O	S	0	0
			483	307	90	82	4		

- Molecule 78 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sg	282	Total	C	N	O	S	0	0
			1948	1241	340	358	9		

- Molecule 79 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	sh	41	Total	C	N	O	S	0	0
			269	168	54	44	3		

- Molecule 80 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	zy	75	Total	C	N	O	P	0	0
			1599	713	284	528	74		
80	zu	72	Total	C	N	O	P	0	0
			1537	685	273	508	71		

- Molecule 81 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	zv	9	Total	C	N	O	P	0	0
			183	82	26	66	9		

- Molecule 82 is a protein called nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
82	zx	20	Total	C	N	O	0	0
			111	71	20	20		

- Molecule 83 is a RNA chain called HCV IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	zz	211	Total	C	N	O	P	0	0
			4503	2005	801	1486	211		

- Molecule 84 is a protein called Eukaryotic translation initiation factor 3 subunit M.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	3m	363	Total	C	N	O	S	0	0
			2639	1666	450	511	12		

- Molecule 85 is a protein called Eukaryotic translation initiation factor 3 subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	3f	269	Total	C	N	O	S	0	0
			2063	1303	354	394	12		

- Molecule 86 is a protein called Eukaryotic translation initiation factor 3 subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	3a	592	Total	C	N	O	S	0	0
			4497	2849	805	822	21		

- Molecule 87 is a protein called Eukaryotic translation initiation factor 3 subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	3e	429	Total	C	N	O	S	0	0
			3218	2050	560	592	16		

- Molecule 88 is a protein called Eukaryotic translation initiation factor 3 subunit C.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	3c	646	Total	C	N	O	S	0	0
			4794	3015	876	876	27		

- Molecule 89 is a protein called Eukaryotic translation initiation factor 3 subunit H.

Mol	Chain	Residues	Atoms					AltConf	Trace
89	3h	318	Total	C	N	O	S	0	0
			2520	1599	431	475	15		

- Molecule 90 is a protein called Eukaryotic translation initiation factor 3 subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
90	3d	55	Total	C	N	O	S	0	0
			347	222	65	59	1		

- Molecule 91 is a protein called Eukaryotic translation initiation factor 3 subunit K.

Mol	Chain	Residues	Atoms					AltConf	Trace
91	3k	215	Total	C	N	O	S	0	0
			1475	932	251	282	10		

- Molecule 92 is a protein called Eukaryotic translation initiation factor 3 subunit L.

Mol	Chain	Residues	Atoms					AltConf	Trace
92	3l	520	Total	C	N	O	S	0	0
			4331	2805	714	793	19		

- Molecule 93 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
93	L5	52	Total	Mg	0
			52	52	
93	L7	1	Total	Mg	0
			1	1	
93	L8	3	Total	Mg	0
			3	3	
93	LV	1	Total	Mg	0
			1	1	
93	Le	1	Total	Mg	0
			1	1	
93	S2	8	Total	Mg	0
			8	8	

- Molecule 94 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
94	Lg	1	Total	Zn	0
			1	1	
94	Lj	1	Total	Zn	0
			1	1	
94	Lm	1	Total	Zn	0
			1	1	
94	Lo	1	Total	Zn	0
			1	1	
94	Lp	1	Total	Zn	0
			1	1	
94	Sa	1	Total	Zn	0
			1	1	

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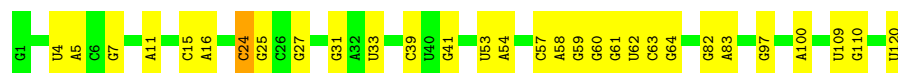
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Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
94	Sd	1	1	1	0





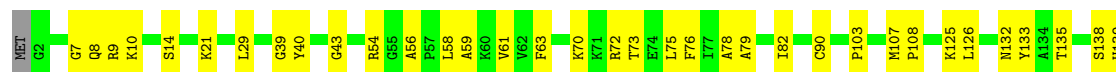
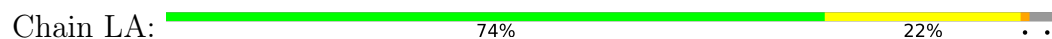




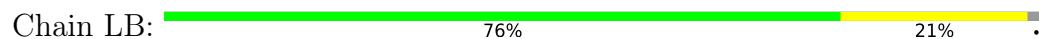
• Molecule 3: 5.8S_ribosomal_RNA



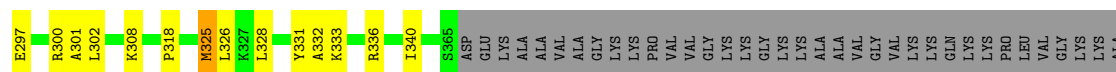
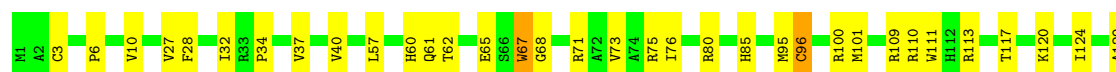
• Molecule 4: 60S ribosomal protein L8



• Molecule 5: 60S ribosomal protein L3

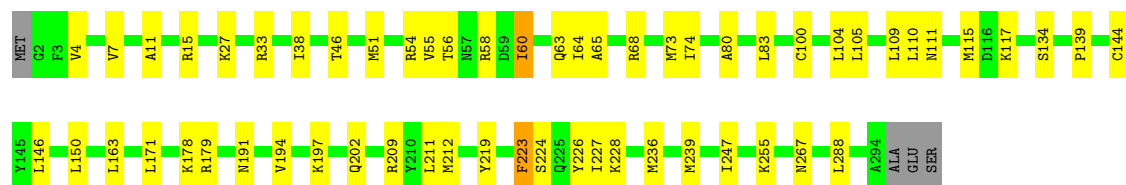


• Molecule 6: 60S ribosomal protein L4

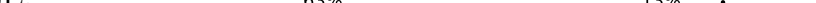


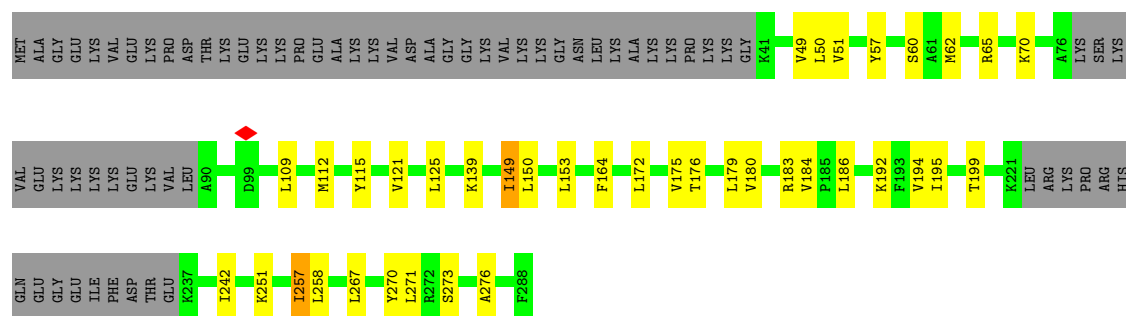
- Molecule 7: 60S ribosomal protein L5

Chain LD: 79% 19% ..

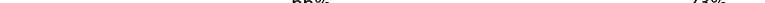


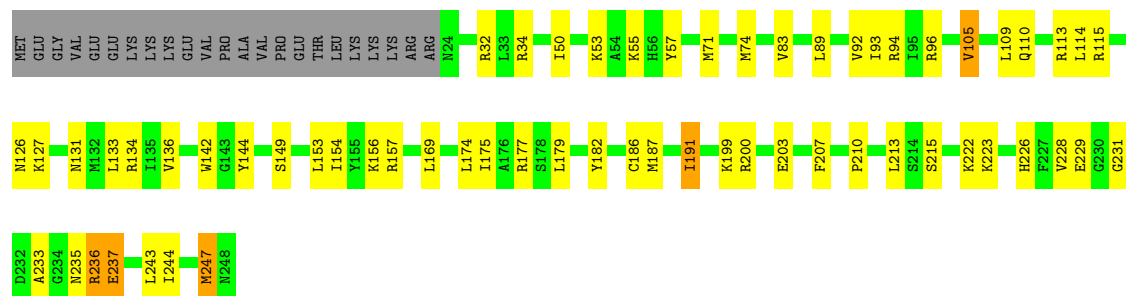
- Molecule 8: 60S ribosomal protein L6

Chain LE: 



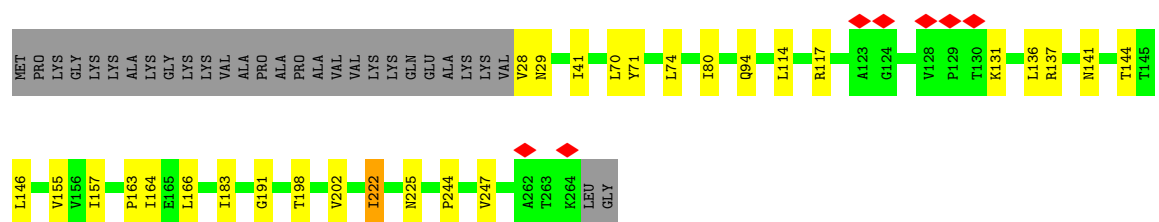
- Molecule 9: 60S ribosomal protein L7

Chain LF: 

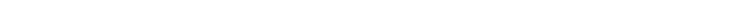


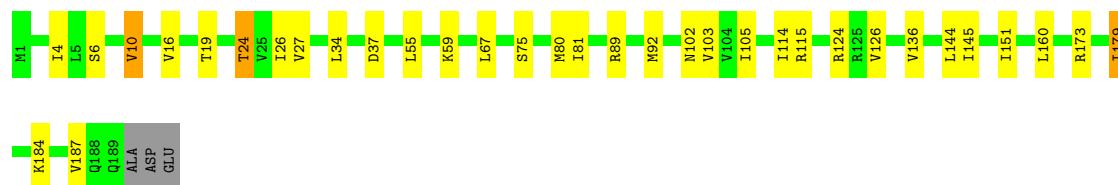
- Molecule 10: 60S ribosomal protein L7a

Chain LG: 



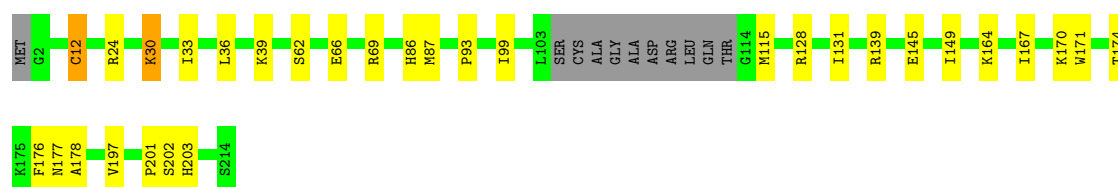
- Molecule 11: 60S ribosomal protein L9

Chain LH:  81% 16% . .

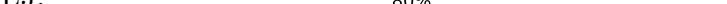


- Molecule 12: 60S ribosomal protein L10-like

Chain LI:  80% 14% • 5%

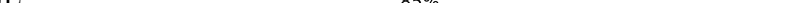


- Molecule 13: 60S ribosomal protein L11

Chain LJ:  80% 12% • 6%

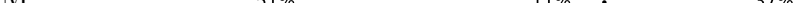


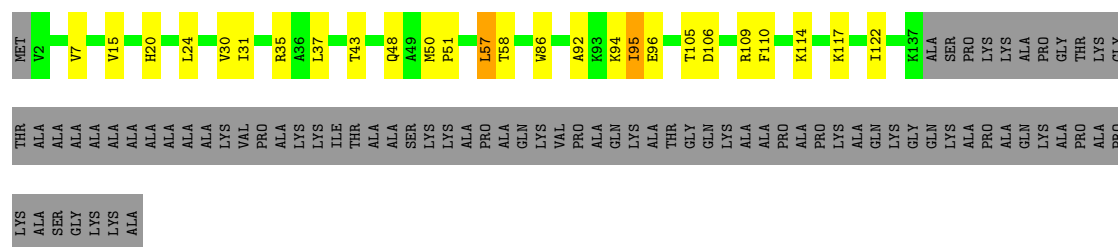
- Molecule 14: 60S ribosomal protein L13

Chain LL:  85% 11% .



- Molecule 15: 60S ribosomal protein L14

Chain LM:  51% 11% 37%



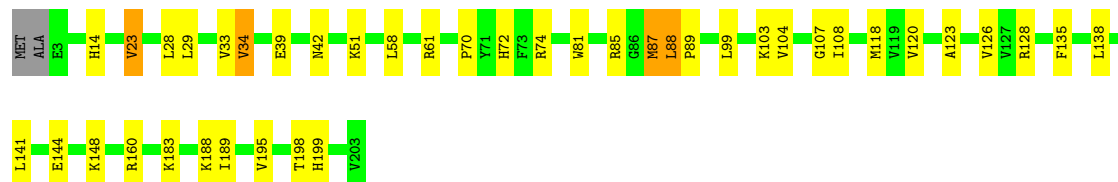
- Molecule 16: 60S ribosomal protein L15

Chain LN: 83% 15%



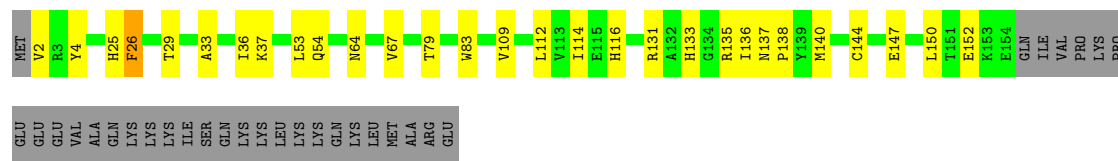
- Molecule 17: 60S ribosomal protein L13a

Chain LO: 79% 18% ..



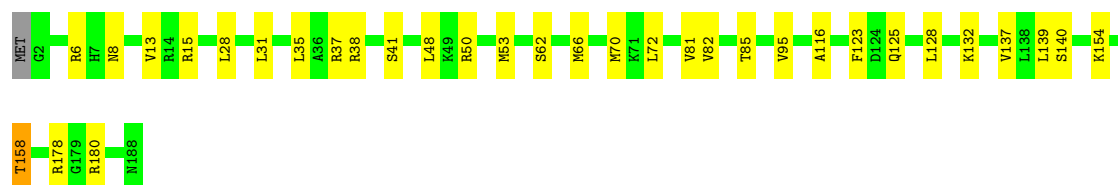
- Molecule 18: 60S ribosomal protein L17

Chain LP: 67% 15% 17%



- Molecule 19: 60S ribosomal protein L18

Chain LQ: 82% 17% ..



- Molecule 20: 60S ribosomal protein L19

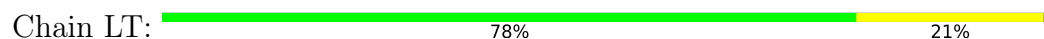
Chain LR: 72% 18% 9%



- Molecule 21: 60S ribosomal protein L18a

Chain LS: 73% 24% ..

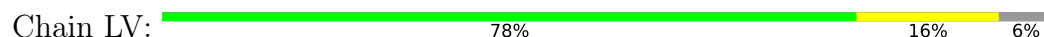
- Molecule 22: 60S ribosomal protein L21



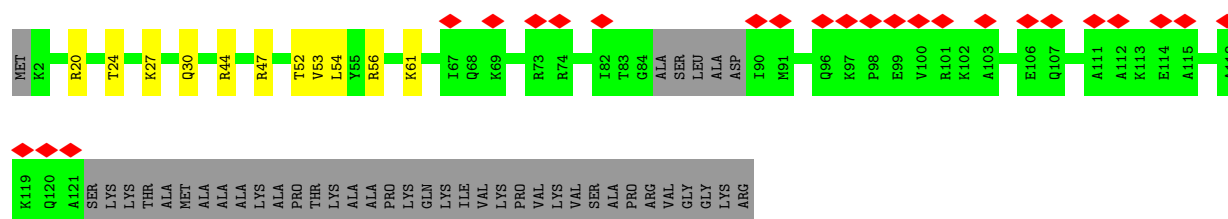
- Molecule 23: 60S ribosomal protein L22



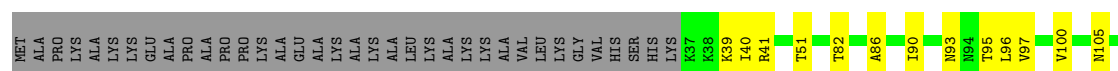
- Molecule 24: 60S ribosomal protein L23



- Molecule 25: 60S ribosomal protein L24

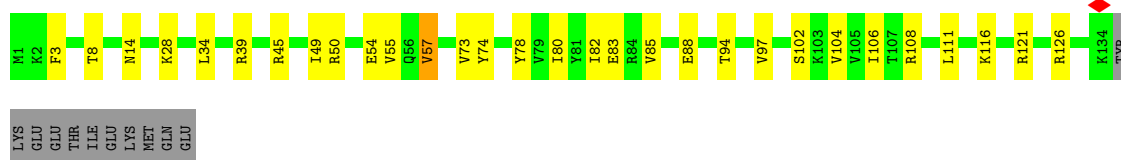


- Molecule 26: 60S ribosomal protein L23a

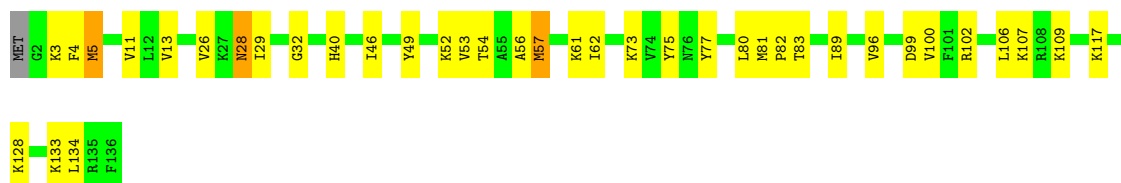




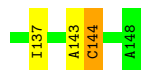
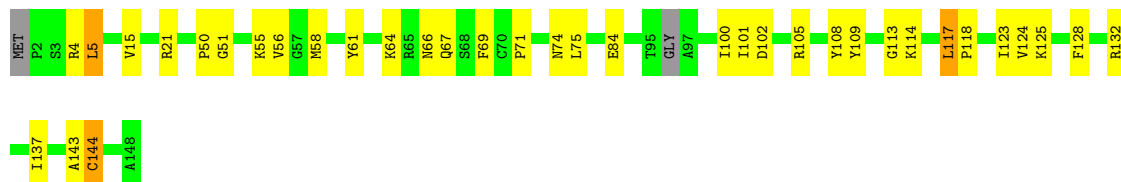
- Molecule 27: 60S ribosomal protein L26



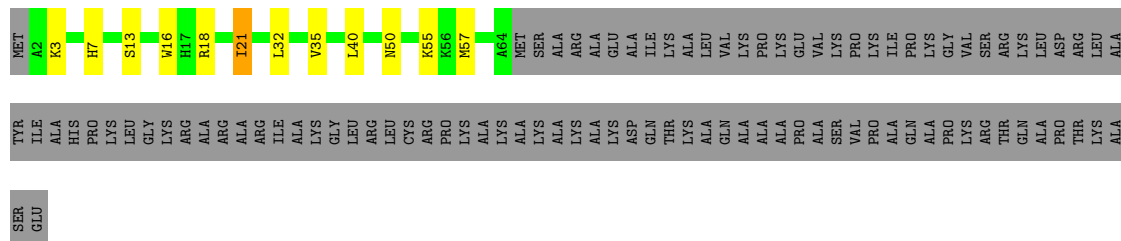
- Molecule 28: 60S ribosomal protein L27



- Molecule 29: 60S ribosomal protein L27a

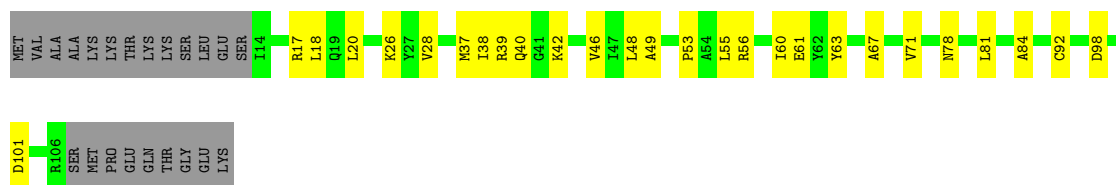


- Molecule 30: 60S ribosomal protein L29



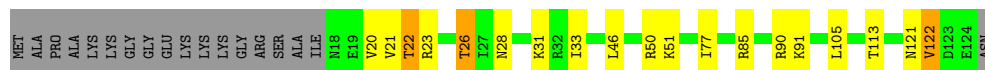
- Molecule 31: 60S ribosomal protein L30





- Molecule 32: 60S ribosomal protein L31

Chain Ld: 70% 13% 14%



- Molecule 33: 60S ribosomal protein L32

Chain Le: 79% 15% 6%



- Molecule 34: 60S ribosomal protein L35a

Chain Lf: 86% 13% 1%



- Molecule 35: 60S ribosomal protein L34

Chain Lg: 72% 21% 6%



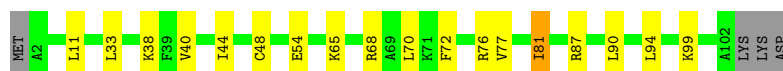
- Molecule 36: 60S ribosomal protein L35

Chain Lh: 82% 16% 2%



- Molecule 37: 60S ribosomal protein L36

Chain Li: 79% 16% 5%



- Molecule 38: 60S ribosomal protein L37

Chain Lj:  79% 9% 11%



- Molecule 39: 60S ribosomal protein L38

Chain Lk:  81% 17%



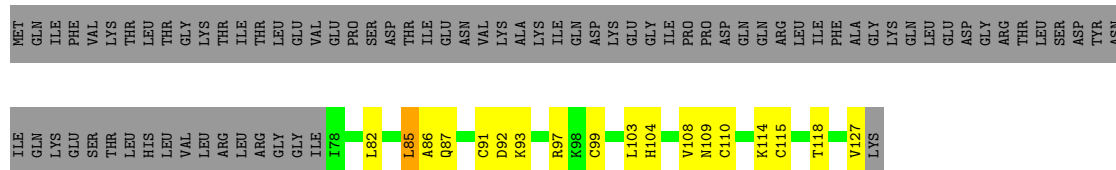
- Molecule 40: 60S ribosomal protein L39

Chain Ll:  69% 27%



- Molecule 41: Ubiquitin-60S ribosomal protein L40

Chain Lm:  25% 13% 61%



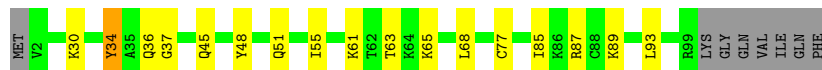
- Molecule 42: 60S ribosomal protein L41

Chain Ln:  84% 12%



- Molecule 43: 60S ribosomal protein L36a

Chain Lo:  76% 15% 8%

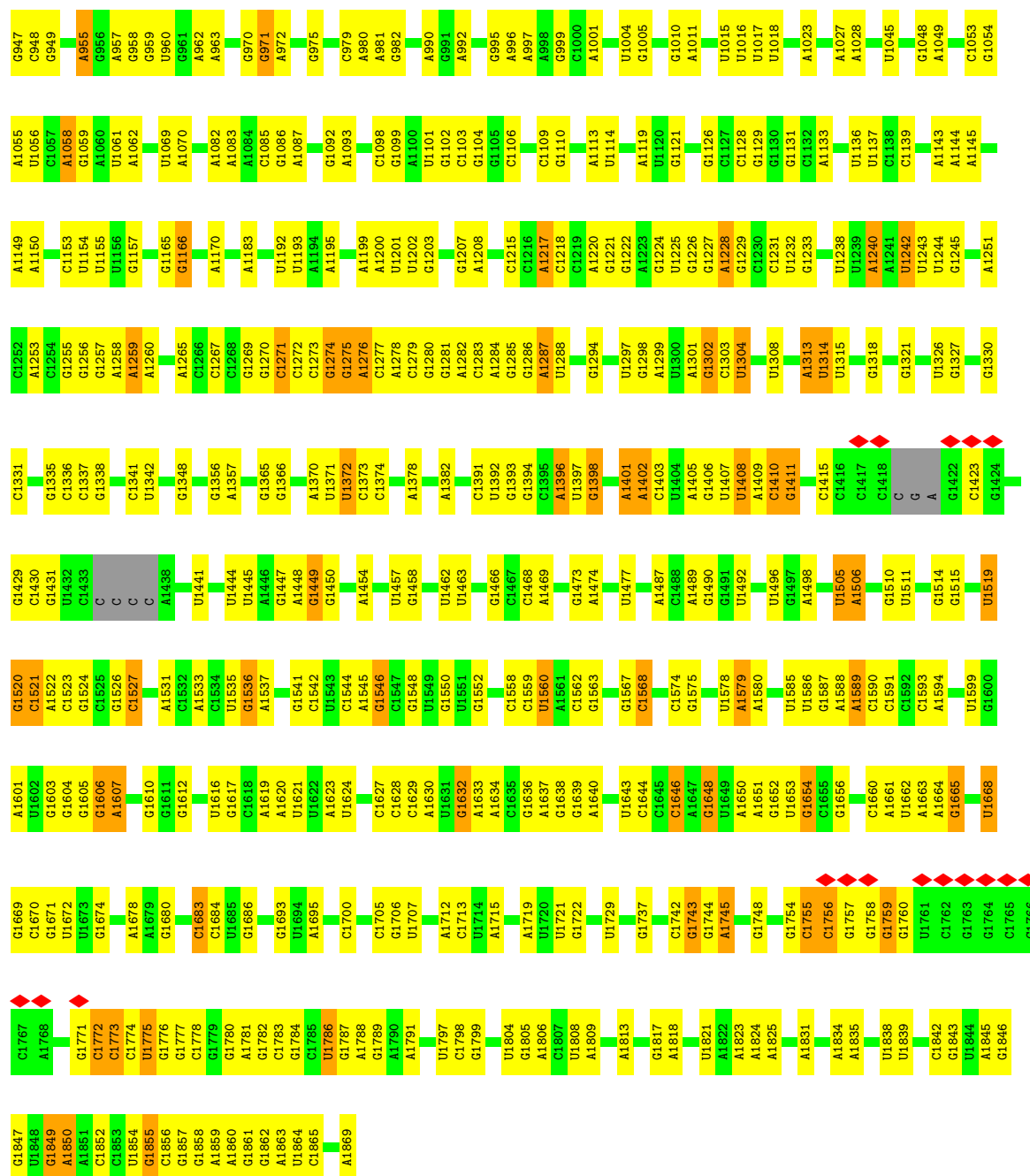


- Molecule 44: 60S ribosomal protein L37a

Chain Lp:  78% 21%

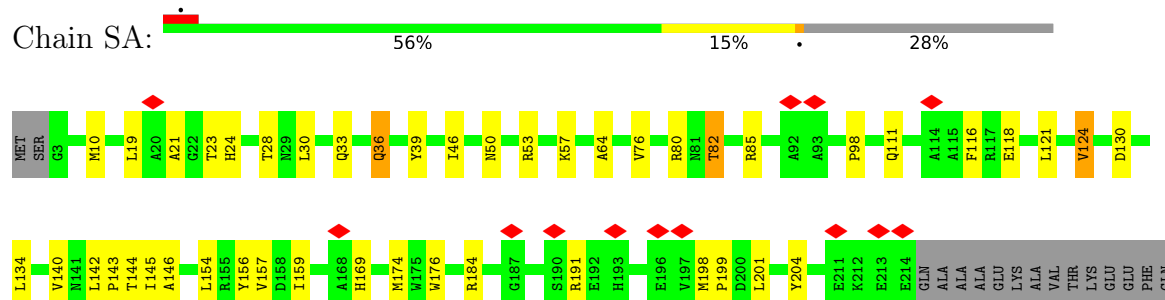


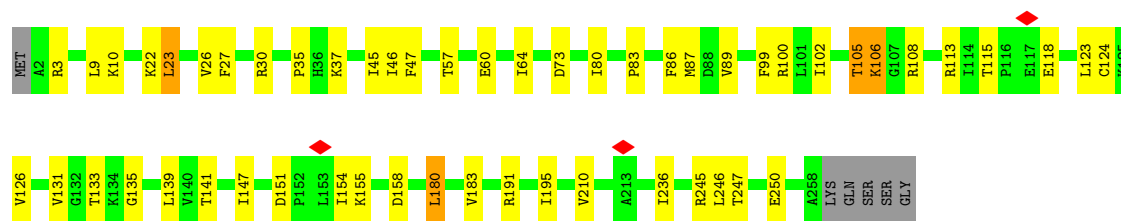
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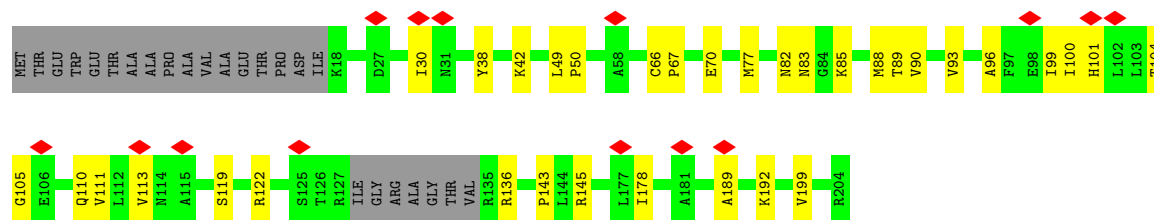
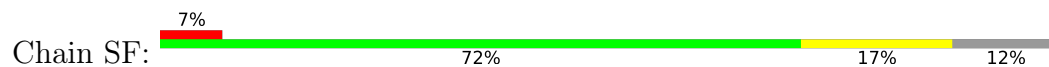
• Molecule 47: Small ribosomal subunit protein uS2

Chain SA:

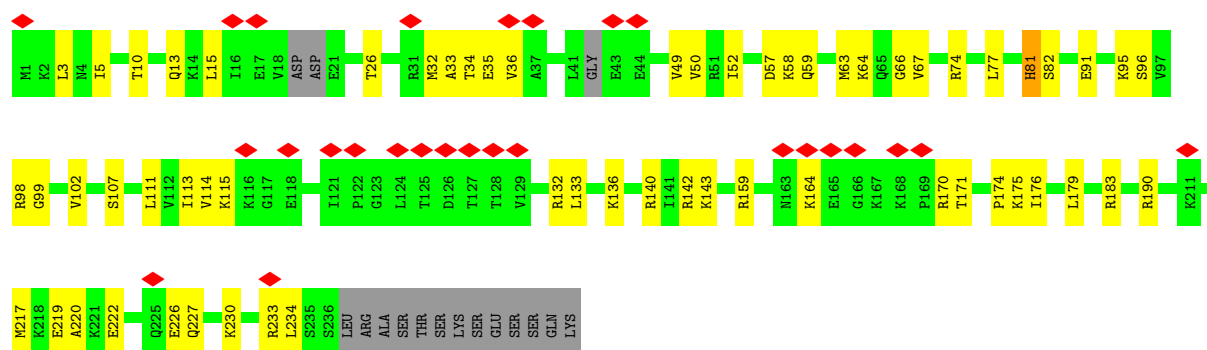




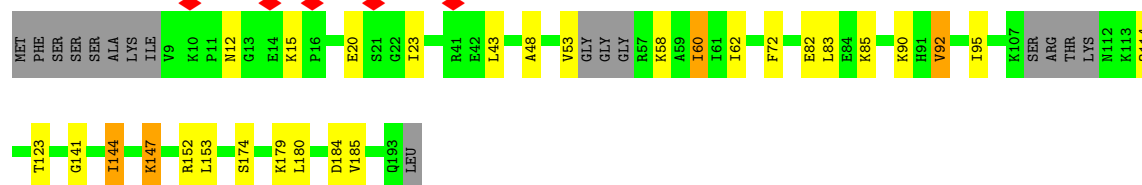
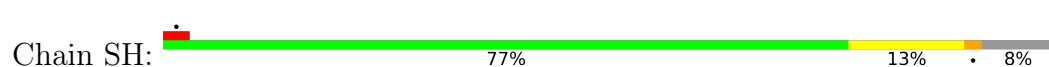
• Molecule 52: 40S ribosomal protein S5



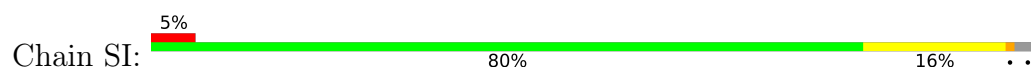
• Molecule 53: 40S ribosomal protein S6

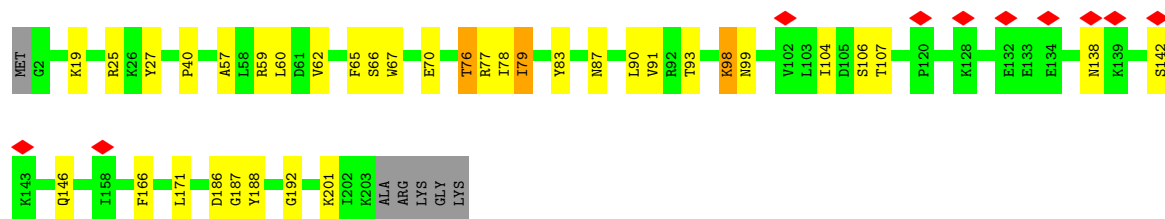


• Molecule 54: 40S ribosomal protein S7

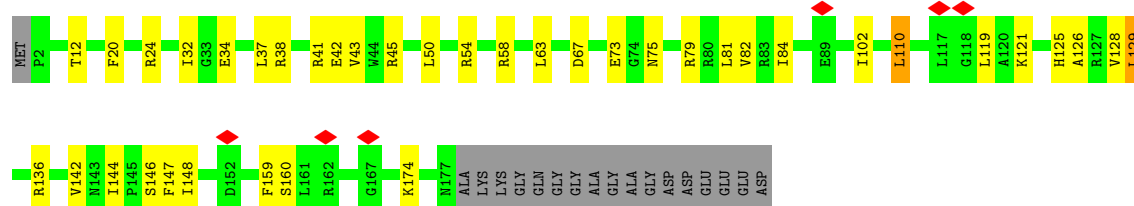


• Molecule 55: 40S ribosomal protein S8

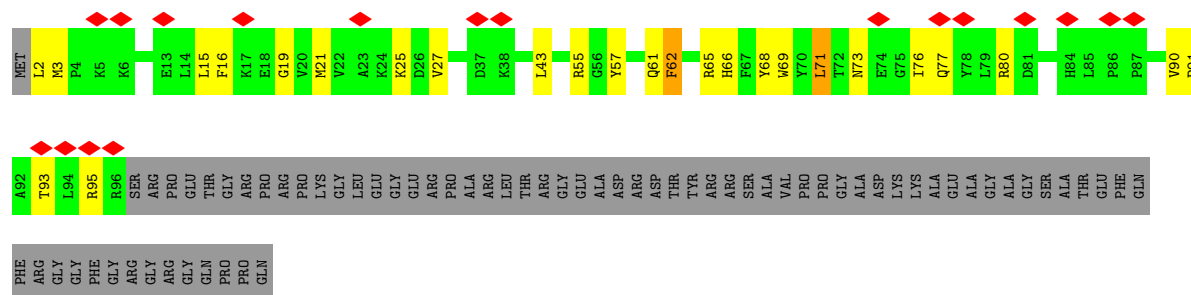
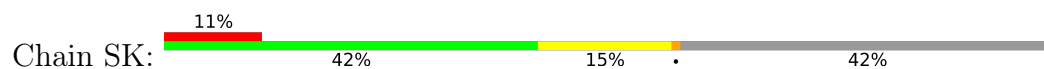




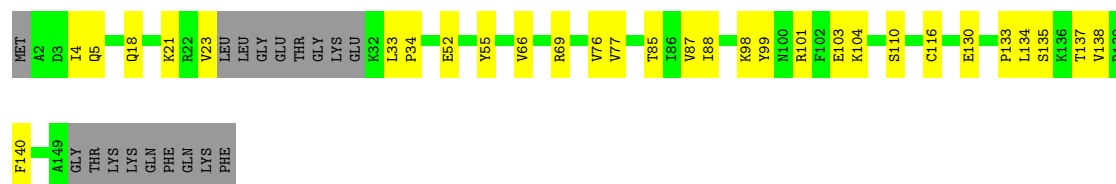
- Molecule 56: 40S ribosomal protein S9



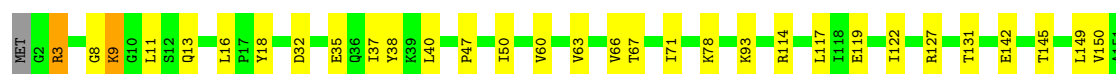
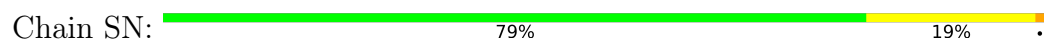
- Molecule 57: 40S ribosomal protein S10



- Molecule 58: 40S ribosomal protein S11



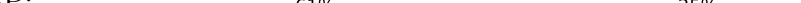
- Molecule 59: 40S ribosomal protein S13



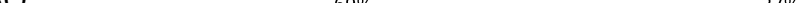
- Molecule 60: 40S ribosomal protein S14

MET	ALA	PRO	ARG	LYS	GLY	GLU	GLU	LYS	GLU	GLN	GLN	ILE	ILE	SER	L17	G18	P19	Q20	V21	A22	E23	G24	V27	F28	G29	V30	C31	H32	T40	F41	V42	H43	V44	I53	V56	M60	K63	R66	V81	K86	G89	I90	T91	A92	L93	A99																																																					
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

Diagram illustrating a protein structure with residues G101, M124, K125, R128, I 129, T133, P134, I 135, and L151. A red arrow points to residue I 129.

- Chain SP: 

[illegible]

- Chain SQ: 

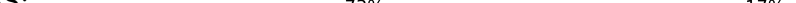
[illegible]

	A103	S104	K105	K106	E107	I108	K109	D110	I111	L112	I113	Q114	Y115		L119	L120	K130	G134	P135		R138	A139	R140	Y141	Q142		R146
--	------	------	------	------	------	------	------	------	------	------	------	------	------	--	------	------	------	------	------	--	------	------	------	------	------	--	------

- Chain SR: 

MET	G2	R3	V4	R5	K10	V15	T22	T30	V34 C35	I38	A39 I40	I41	P42	S43	L46	A51	G52	V53	V54	L57	I61	Q62	R63	G64	I69	S70	I71	P86	E87	V88	Q93	I96	E97	V98	D99	P100	K103	L109	D110	F111
-----	----	----	----	----	-----	-----	-----	-----	------------	-----	------------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------

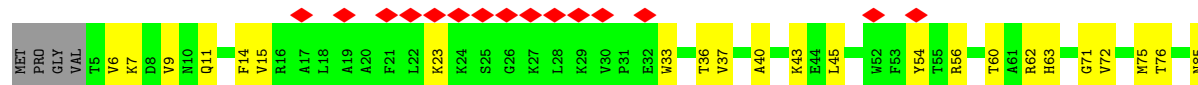
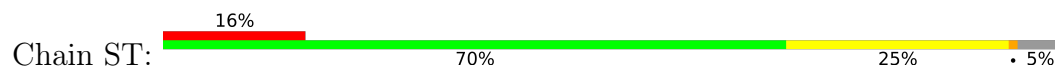
N116	L117	Q118	M126	ASN	PHE	LYS	THR	PRO	ARG	GLY	PRO	VAL
------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Chain SS: 

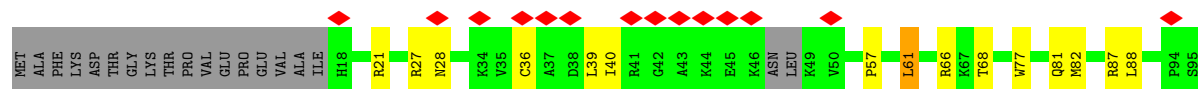
[illegible]



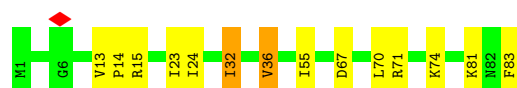
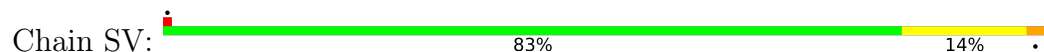
- Molecule 65: 40S ribosomal protein S19



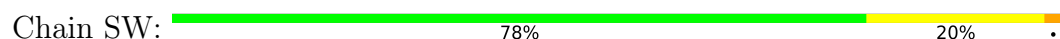
- Molecule 66: 40S ribosomal protein S20



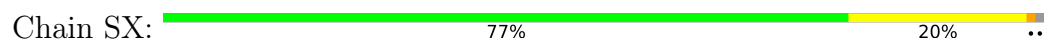
- Molecule 67: 40S ribosomal protein S21



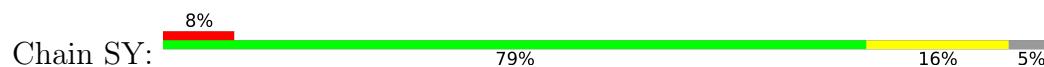
- Molecule 68: 40S ribosomal protein S15a

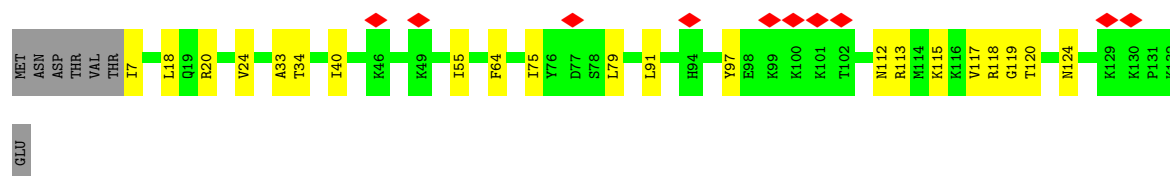


- Molecule 69: 40S ribosomal protein S23

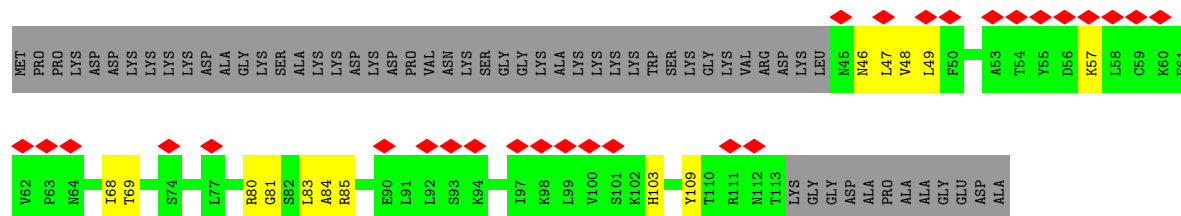


- Molecule 70: 40S ribosomal protein S24





- Molecule 71: 40S ribosomal protein S25



- Molecule 72: 40S ribosomal protein S26



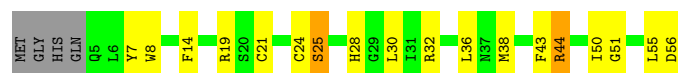
- Molecule 73: 40S ribosomal protein S27



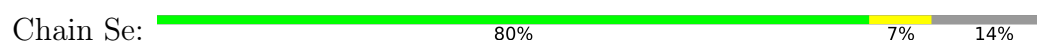
- Molecule 74: 40S ribosomal protein S28

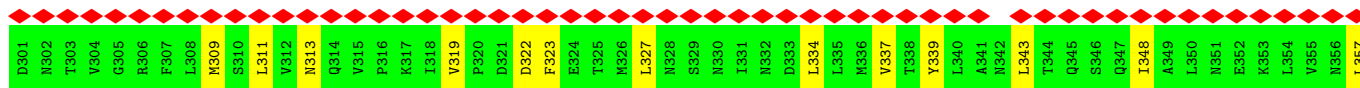
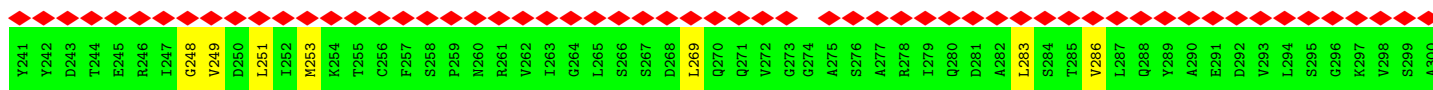


- Molecule 75: 40S ribosomal protein S29

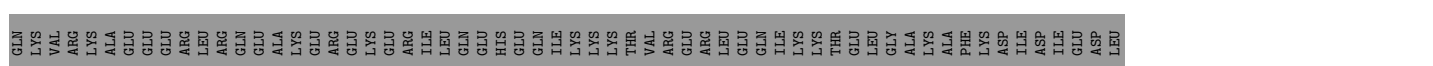
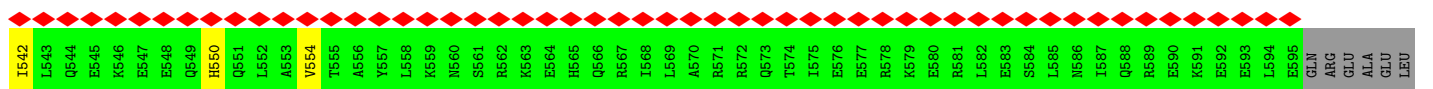
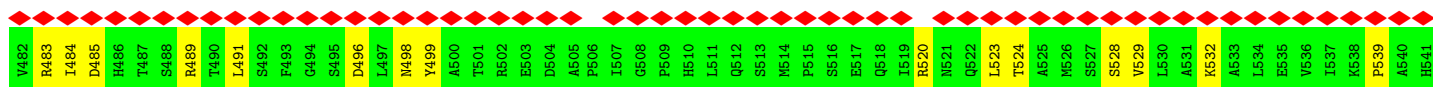
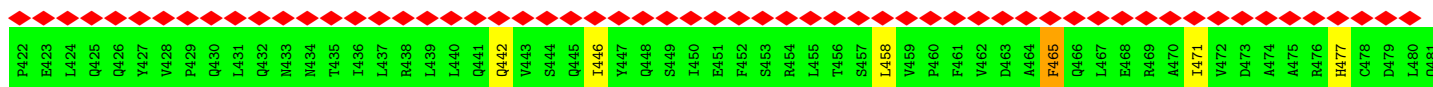
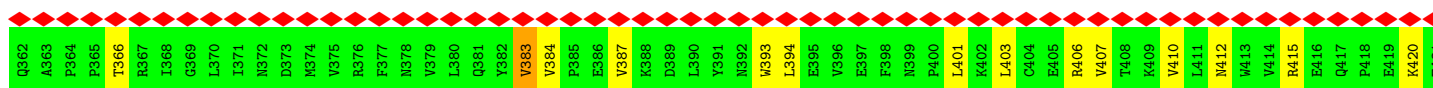
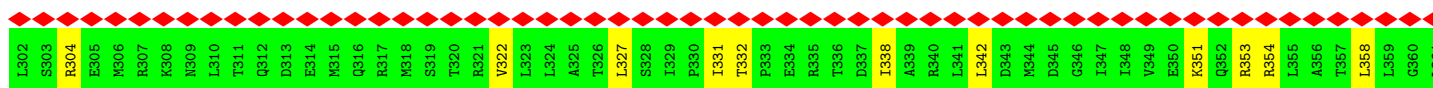
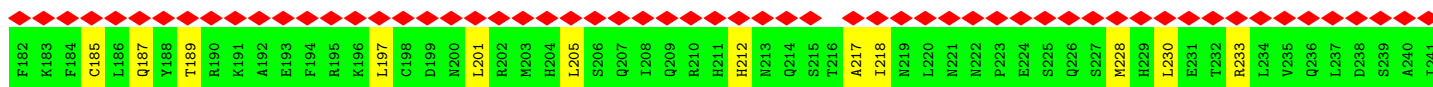
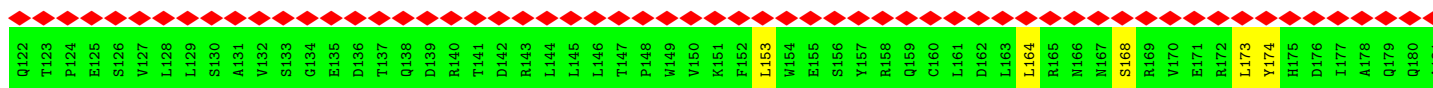
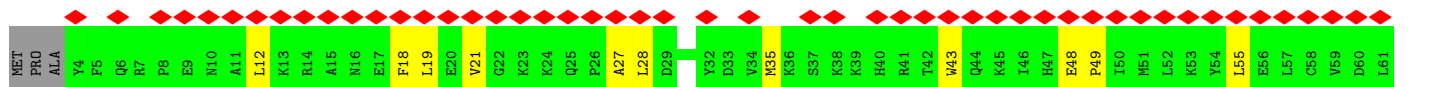
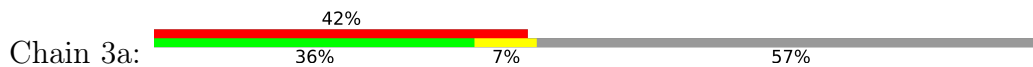


- Molecule 76: 40S ribosomal protein S30

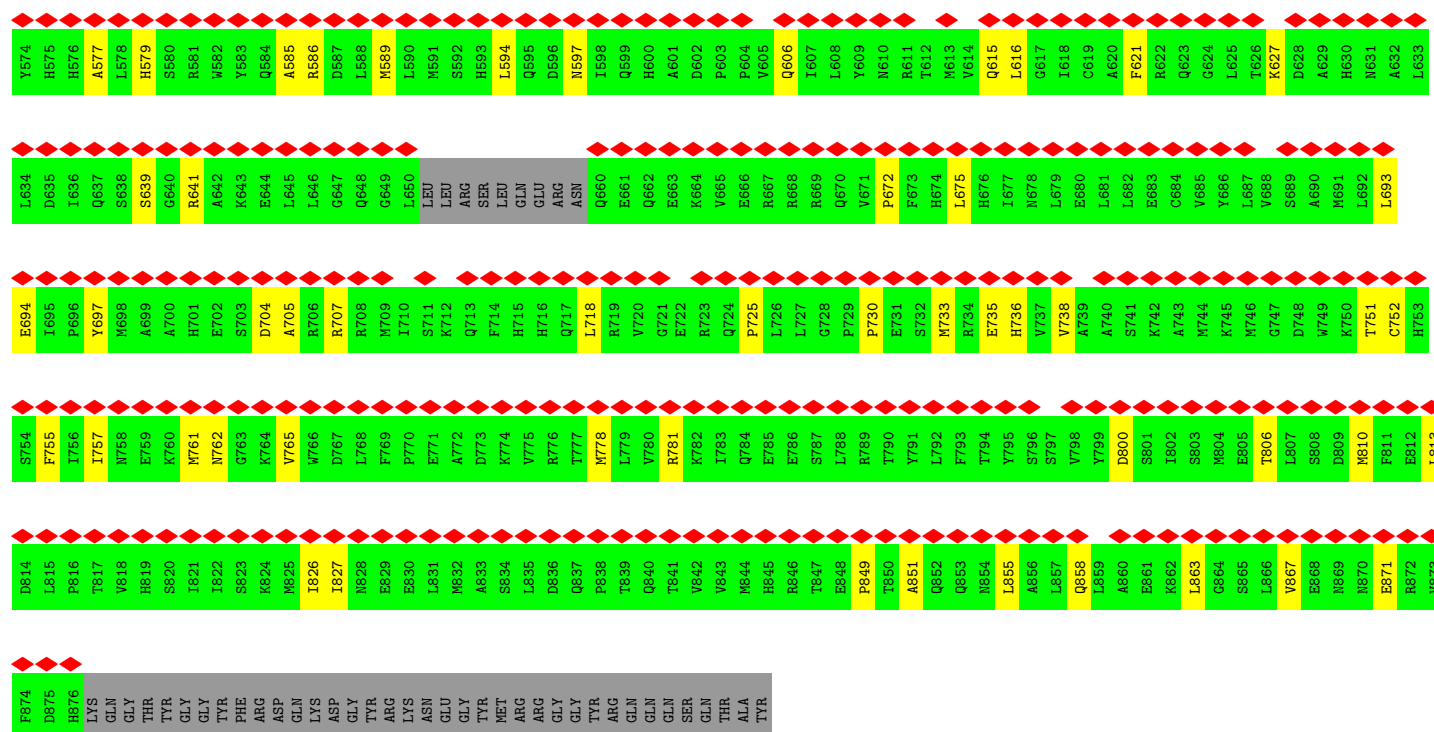




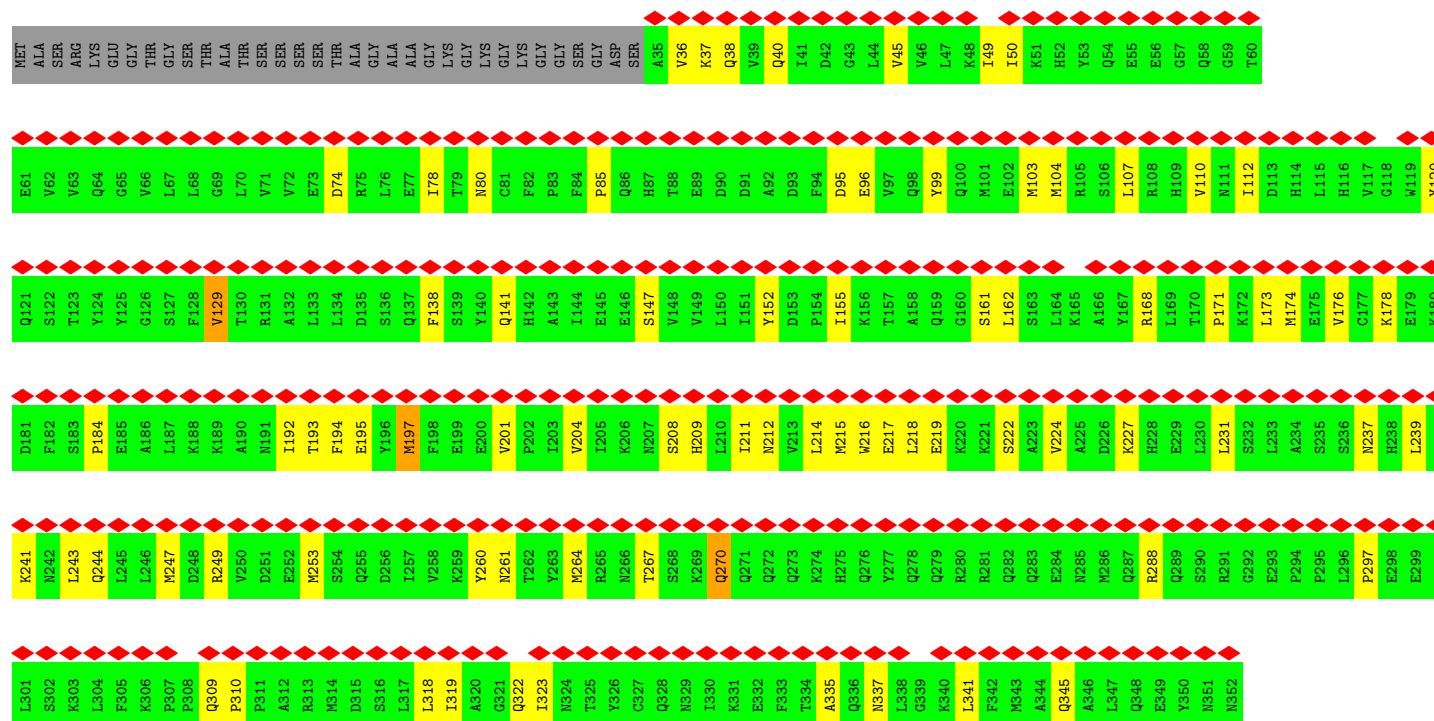
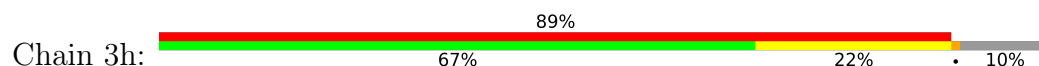
• Molecule 86: Eukaryotic translation initiation factor 3 subunit A







• Molecule 89: Eukaryotic translation initiation factor 3 subunit H

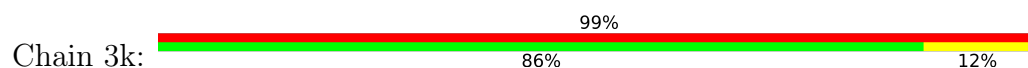


• Molecule 90: Eukaryotic translation initiation factor 3 subunit D



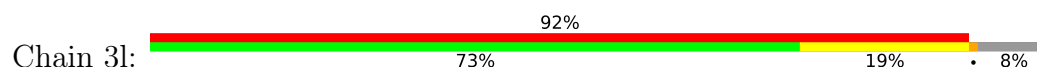
GLU

- Molecule 91: Eukaryotic translation initiation factor 3 subunit K



MET	A2	M3	F4	E5	Q6	M7	R8	A9	N10	V11	G12	K13	L14	L15	K16	G17	I18	D19	R20	Y21	N22	P23	E24	N25	L26	A27	T28	L29	E30	R31	Y32	V33	E34	T35	Q36	A37	K38	E39	N40	A41	Y42	D43	L44	E45	A46	N47	L48	A49	V50	L51	K52	L53	Y54	Q55	F56	N57	P58	A59	F60																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
	F61	Q62	T63	T64	V65	T66	A67	Q68	I69	L70	L71	K72	A73	L74	T75	N76	L77	P78	H79	T80	D81	F82	T83	L84	C85	K86	C87	M88	I89	D90	Q91	A92	H93	Q94	E95	E96	R97	P98	I99	R100	Q101	I102	L103	Y104	L105	G106	D107	L108	L109	E110	T111	C112	H113	F114	Q115	A116	F117	W118	Q119	A120																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
L121	D122	E123	N124	M125	D126	L127	L128	E129	G130	I131	T132	G133	F134	E135	D136	S137	V138	R139	K140	F141	I142	C143	H144	V145	V146	G147	I148	T149	Y150	Q151	H152	I153	D154	R155	V156	L157	L158	A159	E160	M161	L162	G163	D164	L165	S166	D167	S168	Q169	L170	K171	V172	M173	M174	S175	K176	Y177	G178	W179	S180																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
A181	D182	E183	S184	G185	Q186	I187	F188	I189	C190	S191	Q192	E193	E194	S195	I196	K197	P198	K199	N200	I201	V202	E203	K204	I205	D206	F207	D208	S209	V210	S211	S212	I213	M214	A215	S216	SER	GLN																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								

- Molecule 92: Eukaryotic translation initiation factor 3 subunit L



MET	SER	TYR	PRO	ALA	ASP	ASP	TYR	GLU	SER	GLU	ALA	ALA	TYR	ASP	PRO	TYR	ALA	TYR	PRO	SER	ASP	TYR	ASP	GLN	ASP	LEU	ALA	TYR	GLU	ARG	GLN	TYR	GLU	GLN	GLN	THR	Y45	Q46	V47	I48	P49	E50	V51	I52	K53	N54	F55	I56	Q57	Y58	F59	H60
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

D541	K61	Q121	Q181	N361	L421	L481	D501
F542	T62	V122	W182	K362	S422	T482	F502
F543	V63	G123	L183	Q363	P423	E483	F503
T544	S64	N124	W184	M364	V424	Q484	T504
R545	D65	D125	D185	Y365	V425	E485	S504
Q546	L66	A126	I186	Q366	P426	F486	G505
T547	I67	V127	I187	M367	N427	R487	T506
H548	D68	F128	D188	H368	Y428	T488	S507
K549	Q69	F129	E189	A369	D429	Q489	A508
F550	K70	I130	F190	L370	N430	L490	L509
E551	V71	L131	I191	L371	V431	L491	D510
E552	Y72	Y132	Y192	A372	H432	V492	E512
L553	E73	K133	Q193	I373	P433	F493	F513
N554	L74	E134	F194	T314	N434	K494	Q514
R555	Q75	L135	Q195	T315	Y435	H495	S515
T556	A76	L136	Q196	Y316	H436	K496	A516
L557	S77	Y137	S196	T317	K437	F497	S517
K558	R78	R138	S198	Y318	E438	K498	E518
K559	V79	H139	Q199	V319	P439	N499	V519
M560	S80	I140	Y200	G320	F440	L500	D520
G561	S81	Y141	R201	F321	L441	V501	F521
Q562	D82	A142	C202	A322	Q442	F502	I523
R563	V83	K143	K203	Y323	Q443	T503	D524
P564	I84	V144	T204	L324	L444	S504	K465
	D85	S145	A205	M325	K445	G505	L464
	Q86	G146	K206	M326	V446	T506	K466
	K87	G147	K207	R327	F447	S507	Y467
	V88	P148	S208	R328	S448	A508	T468
	Y89	S149	E209	Y329	D449	L509	T469
	E90	L150	E210	Q330	E450	D510	N470
	I91	E151	E211	D331	V451	G511	P471
	Q92	Q152	I212	A332	Q452	E512	V472
	D93	R153	D213	I333	Q453	F513	A473
	I94	F154	F214	R334	Q454	Q514	K474
	Y95	E155	L215	V335	A455	S515	L475
	E96	S156	R216	F336	Q456	A516	A476
	N97	Y157	S217	A337	L457	S517	G477
	S98	Y158	N218	N338	S458	E518	L479
	W99	N159	P219	I339	T459	V519	D480
	T100	Y160	K220	L340	T460	D520	
	K101	C161	I221	L341	R461	F521	
	L102	N162	V222	Y342	S462	Y522	
	T103	L163	N223	I343	F463	I523	
	E104	F164	V224	Q344	L464	D524	
	R105	N165	H225	R345	K465	K525	
	F106	Y166	S226	T346	P466	D526	
	F107	I167	V227	K347	Q467	M527	
	K108	L168	L228	S348	V468	I528	
	N109	N169	N229	M349	Y469	H529	
	T110	A170	V230	F350	E410	I530	
	P111	D171	L231	Q351	E411	A531	
	W112	G172	H232	T352	L412	D532	
	P113	P173	S233	T353	F413	T533	
	E114	A174	L234	T354	S414	K534	
	A115	P175	V235	Y355	Y415	V535	
	E116	L176	D236	K356	S416	A536	
	A117	E177	I297	Y357	C417	R537	
	I118	L178	E298	E358	P418	R538	
	A119	P179	L299	M359	K419	G540	
	P120	N180	N300	I360	F420		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	13805	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	56.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.136	Depositor
Minimum map value	-0.027	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.015	Depositor
Map size ($\text{\AA}$)	742.0, 742.0, 742.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.484, 1.484, 1.484	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	L5	0.19	0/86040	0.33	0/134204
2	L7	0.18	0/2858	0.30	0/4455
3	L8	0.19	0/3701	0.32	0/5766
4	LA	0.21	0/1924	0.51	0/2581
5	LB	0.19	0/3168	0.44	0/4253
6	LC	0.22	0/2948	0.46	0/3960
7	LD	0.17	0/2333	0.44	0/3139
8	LE	0.19	0/1747	0.46	0/2354
9	LF	0.23	0/1879	0.55	1/2507 (0.0%)
10	LG	0.18	0/1830	0.45	0/2484
11	LH	0.20	0/1458	0.50	0/1973
12	LI	0.19	0/1619	0.47	1/2170 (0.0%)
13	LJ	0.20	0/1249	0.49	0/1690
14	LL	0.18	0/1611	0.39	0/2167
15	LM	0.21	0/1119	0.51	0/1501
16	LN	0.23	0/1738	0.45	0/2328
17	LO	0.22	0/1645	0.50	0/2205
18	LP	0.21	0/1229	0.49	0/1655
19	LQ	0.20	0/1517	0.45	0/2030
20	LR	0.21	0/1450	0.52	0/1927
21	LS	0.22	0/1476	0.50	2/1983 (0.1%)
22	LT	0.20	0/1296	0.48	0/1734
23	LU	0.20	0/782	0.56	0/1057
24	LV	0.22	0/968	0.55	0/1303
25	LW	0.19	0/798	0.51	0/1081
26	LX	0.23	0/967	0.58	0/1304
27	LY	0.19	0/1101	0.44	0/1469
28	LZ	0.23	0/1105	0.45	0/1475
29	La	0.22	0/1173	0.47	0/1568
30	Lb	0.22	0/509	0.58	0/675
31	Lc	0.20	0/726	0.48	0/977
32	Ld	0.20	0/871	0.46	0/1176

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.21	0/1063	0.45	0/1418
34	Lf	0.23	0/883	0.59	0/1185
35	Lg	0.21	0/861	0.51	0/1153
36	Lh	0.17	0/983	0.41	0/1304
37	Li	0.20	0/808	0.51	0/1074
38	Lj	0.20	0/716	0.40	0/948
39	Lk	0.20	0/534	0.52	0/712
40	Ll	0.22	0/450	0.44	0/595
41	Lm	0.23	0/399	0.74	2/532 (0.4%)
42	Ln	0.22	0/231	0.58	0/294
43	Lo	0.20	0/787	0.46	0/1042
44	Lp	0.17	0/699	0.45	0/931
45	Lr	0.23	0/997	0.59	0/1341
46	S2	0.16	0/40097	0.33	0/62465
47	SA	0.20	0/1612	0.56	0/2203
48	SB	0.17	0/1654	0.45	0/2227
49	SC	0.20	0/1626	0.53	0/2211
50	SD	0.18	0/1482	0.50	0/2018
51	SE	0.15	0/1933	0.41	0/2623
52	SF	0.18	0/1385	0.49	0/1870
53	SG	0.17	0/1761	0.51	0/2362
54	SH	0.20	0/1384	0.54	0/1862
55	SI	0.19	0/1580	0.46	0/2131
56	SJ	0.19	0/1432	0.53	1/1926 (0.1%)
57	SK	0.20	0/759	0.61	0/1036
58	SL	0.20	0/1159	0.50	0/1555
59	SN	0.19	0/1223	0.53	0/1644
60	SO	0.18	0/1016	0.51	0/1363
61	SP	0.21	0/1020	0.55	0/1369
62	SQ	0.19	0/1096	0.51	0/1473
63	SR	0.23	0/890	0.64	0/1207
64	SS	0.18	0/1098	0.49	0/1480
65	ST	0.20	0/993	0.53	0/1345
66	SU	0.20	0/746	0.53	0/1007
67	SV	0.20	0/596	0.54	0/800
68	SW	0.20	0/1044	0.51	0/1398
69	SX	0.21	0/1066	0.58	0/1434
70	SY	0.18	0/960	0.52	0/1287
71	SZ	0.18	0/485	0.53	0/661
72	Sa	0.18	0/775	0.47	0/1042
73	Sb	0.19	0/631	0.54	0/853
74	Sc	0.20	0/432	0.62	0/582
75	Sd	0.21	0/430	0.52	0/573

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Se	0.16	0/390	0.40	0/515
77	Sf	0.11	0/485	0.36	0/661
78	Sg	0.14	0/1989	0.41	0/2725
79	sh	0.09	0/270	0.27	0/359
80	zu	0.12	0/1717	0.28	0/2677
80	zy	0.12	0/1786	0.26	0/2784
81	zv	0.18	0/201	0.47	0/309
82	zx	0.25	0/113	0.64	0/158
83	zz	0.12	0/5030	0.29	0/7842
84	3m	0.15	0/2676	0.40	0/3635
85	3f	0.15	0/2099	0.38	0/2856
86	3a	0.16	0/4583	0.40	0/6237
87	3e	0.14	0/3282	0.37	0/4467
88	3c	0.15	0/4872	0.40	2/6599 (0.0%)
89	3h	0.16	0/2571	0.41	1/3484 (0.0%)
90	3d	0.14	0/358	0.35	0/493
91	3k	0.17	0/1502	0.48	1/2052 (0.0%)
92	3l	0.17	0/4442	0.42	0/6009
All	All	0.18	0/254977	0.39	11/373549 (0.0%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	Lm	86	ALA	CA-C-N	-6.57	110.49	122.38
41	Lm	86	ALA	C-N-CA	-6.57	110.49	122.38
56	SJ	129	LEU	CA-CB-CG	5.88	136.86	116.30
12	LI	30	LYS	CA-CB-CG	5.64	125.37	114.10
91	3k	148	ILE	N-CA-C	-5.48	107.01	113.42
89	3h	270	GLN	CA-CB-CG	5.41	124.92	114.10
21	LS	163	HIS	CA-C-N	5.33	134.79	121.80
21	LS	163	HIS	C-N-CA	5.33	134.79	121.80
88	3c	694	GLU	CA-C-N	5.32	123.59	120.24
88	3c	694	GLU	C-N-CA	5.32	123.59	120.24
9	LF	229	GLU	CA-CB-CG	5.14	124.39	114.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L5	76925	0	38887	570	0
2	L7	2558	0	1296	10	0
3	L8	3314	0	1683	26	0
4	LA	1886	0	1973	37	0
5	LB	3101	0	3177	44	0
6	LC	2894	0	3061	50	0
7	LD	2287	0	2254	32	0
8	LE	1713	0	1812	18	0
9	LF	1844	0	1961	35	0
10	LG	1797	0	1833	14	0
11	LH	1439	0	1469	15	0
12	LI	1581	0	1574	15	0
13	LJ	1226	0	1168	11	0
14	LL	1580	0	1646	12	0
15	LM	1097	0	1142	13	0
16	LN	1693	0	1741	25	0
17	LO	1613	0	1737	29	0
18	LP	1203	0	1210	12	0
19	LQ	1493	0	1587	17	0
20	LR	1434	0	1539	20	0
21	LS	1436	0	1457	27	0
22	LT	1268	0	1309	18	0
23	LU	768	0	762	3	0
24	LV	954	0	994	9	0
25	LW	784	0	662	8	0
26	LX	950	0	1010	12	0
27	LY	1084	0	1143	15	0
28	LZ	1082	0	1152	25	0
29	La	1145	0	1178	23	0
30	Lb	499	0	506	7	0
31	Lc	716	0	742	14	0
32	Ld	856	0	890	12	0
33	Le	1045	0	1133	8	0
34	Lf	864	0	888	8	0
35	Lg	851	0	908	13	0
36	Lh	975	0	1081	10	0
37	Li	797	0	859	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	Lj	701	0	726	5	0
39	Lk	528	0	554	7	0
40	Ll	440	0	472	10	0
41	Lm	393	0	410	11	0
42	Ln	230	0	276	1	0
43	Lo	774	0	819	9	0
44	Lp	689	0	731	9	0
45	Lr	982	0	1026	16	0
46	S2	35873	0	18084	360	0
47	SA	1575	0	1533	25	0
48	SB	1627	0	1616	26	0
49	SC	1590	0	1606	24	0
50	SD	1458	0	1379	22	0
51	SE	1891	0	1867	30	0
52	SF	1365	0	1367	21	0
53	SG	1740	0	1737	40	0
54	SH	1363	0	1405	12	0
55	SI	1551	0	1515	22	0
56	SJ	1407	0	1450	23	0
57	SK	736	0	691	17	0
58	SL	1139	0	1185	18	0
59	SN	1199	0	1274	18	0
60	SO	1003	0	1028	16	0
61	SP	1001	0	1011	23	0
62	SQ	1078	0	1124	27	0
63	SR	879	0	816	11	0
64	SS	1080	0	1092	15	0
65	ST	975	0	908	25	0
66	SU	737	0	750	12	0
67	SV	589	0	566	12	0
68	SW	1027	0	1067	15	0
69	SX	1048	0	1065	18	0
70	SY	943	0	933	13	0
71	SZ	479	0	442	8	0
72	Sa	762	0	800	10	0
73	Sb	617	0	602	7	0
74	Sc	430	0	425	9	0
75	Sd	420	0	397	10	0
76	Se	386	0	411	4	0
77	Sf	483	0	399	5	0
78	Sg	1948	0	1654	26	0
79	sh	269	0	221	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	zu	1537	0	777	13	0
80	zy	1599	0	810	14	0
81	zv	183	0	97	1	0
82	zx	111	0	74	3	0
83	zz	4503	0	2278	33	0
84	3m	2639	0	2442	37	0
85	3f	2063	0	2054	38	0
86	3a	4497	0	4224	63	0
87	3e	3218	0	2920	34	0
88	3c	4794	0	4416	46	0
89	3h	2520	0	2445	55	0
90	3d	347	0	259	1	0
91	3k	1475	0	1239	16	0
92	3l	4331	0	4261	70	0
93	L5	52	0	0	0	0
93	L7	1	0	0	0	0
93	L8	3	0	0	0	0
93	LV	1	0	0	0	0
93	Le	1	0	0	0	0
93	S2	8	0	0	0	0
94	Lg	1	0	0	0	0
94	Lj	1	0	0	0	0
94	Lm	1	0	0	0	0
94	Lo	1	0	0	0	0
94	Lp	1	0	0	0	0
94	Sa	1	0	0	0	0
94	Sd	1	0	0	0	0
All	All	238047	0	175154	2358	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 6.

All (2358) 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)
80:zu:10:G:H1	80:zu:24:U:H3	1.04	0.99
1:L5:493:G:N1	1:L5:660:A:C2	2.31	0.99
1:L5:493:G:N1	1:L5:660:A:H2	1.61	0.98
46:S2:1656:G:H1	46:S2:1668:U:H3	1.08	0.98
1:L5:2557:G:H1	1:L5:2570:U:H3	1.08	0.98
46:S2:92:A:H62	46:S2:444:G:N2	1.62	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:zz:144:U:H3	83:zz:249:G:H1	1.01	0.97
83:zz:140:A:C2	83:zz:285:G:N1	2.33	0.95
1:L5:1667:G:H21	1:L5:2282:A:H62	1.11	0.94
46:S2:1743:G:N2	46:S2:1791:A:H62	1.66	0.92
46:S2:1748:G:H1	46:S2:1786:U:H3	1.09	0.92
1:L5:1095:A:H2	1:L5:1200:G:H1	0.94	0.91
1:L5:1095:A:C2	1:L5:1200:G:N1	2.37	0.91
46:S2:92:A:N6	46:S2:444:G:H21	1.66	0.91
46:S2:1729:U:H3	46:S2:1805:G:H1	0.92	0.91
46:S2:92:A:H62	46:S2:444:G:H21	0.92	0.90
83:zz:140:A:H2	83:zz:285:G:H1	1.03	0.90
46:S2:1743:G:H21	46:S2:1791:A:H62	0.93	0.90
80:zu:11:U:H3	80:zu:22:G:H1	1.20	0.88
1:L5:1095:A:H2	1:L5:1200:G:N1	1.70	0.87
46:S2:130:G:N2	46:S2:181:A:H61	1.71	0.87
46:S2:1737:G:H1	46:S2:1797:U:H3	1.20	0.86
46:S2:1743:G:H21	46:S2:1791:A:N6	1.74	0.84
1:L5:1667:G:H21	1:L5:2282:A:N6	1.75	0.83
1:L5:1667:G:N2	1:L5:2282:A:H62	1.76	0.83
46:S2:677:G:H21	46:S2:1028:A:H62	1.25	0.82
83:zz:140:A:H2	83:zz:285:G:N1	1.73	0.81
46:S2:130:G:H21	46:S2:181:A:N6	1.78	0.81
41:Lm:87:GLN:HB2	41:Lm:91:CYS:HB2	1.64	0.79
1:L5:493:G:H1	1:L5:660:A:H2	0.87	0.79
46:S2:1849:G:HO2'	46:S2:1850:A:H8	1.29	0.79
1:L5:2263:A:H5''	45:Lr:108:MET:HE3	1.65	0.79
46:S2:692:G:N2	46:S2:738:C:O2	2.15	0.79
46:S2:878:G:H1	46:S2:908:A:H2	1.27	0.78
46:S2:1607:A:H62	46:S2:1632:G:H21	1.30	0.78
46:S2:810:A:H5'	46:S2:811:A:H5''	1.65	0.78
7:LD:115:MET:HE1	7:LD:139:PRO:HB2	1.65	0.78
46:S2:442:C:H42	46:S2:449:A:H62	1.30	0.77
46:S2:692:G:N2	46:S2:738:C:C2	2.53	0.77
1:L5:1759:G:H1	1:L5:1773:U:H3	1.34	0.76
8:LE:57:TYR:HB2	8:LE:62:MET:HE3	1.68	0.75
1:L5:3697:U:H5''	1:L5:3698:G:H5'	1.69	0.74
3:L8:71:A:H62	3:L8:87:G:H21	1.33	0.73
78:Sg:17:TRP:H	78:Sg:36:ARG:H	1.34	0.73
51:SE:87:MET:HE1	51:SE:123:LEU:H	1.53	0.73
88:3c:555:ILE:O	88:3c:559:ASP:HB2	1.88	0.73
46:S2:443:U:H3	46:S2:447:A:H62	1.34	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
91:3k:135:GLU:HB3	91:3k:139:ARG:HH21	1.54	0.73
19:LQ:154:LYS:HE2	19:LQ:158:THR:HG21	1.70	0.73
46:S2:1771:G:H21	46:S2:1772:C:H41	1.37	0.73
46:S2:692:G:C2	46:S2:738:C:O2	2.42	0.73
3:L8:71:A:H62	3:L8:87:G:N2	1.87	0.72
46:S2:1106:C:H5''	73:Sb:70:LYS:HE2	1.71	0.72
22:LT:154:ILE:HD12	22:LT:155:PRO:HD2	1.71	0.72
46:S2:116:U:H3	46:S2:347:G:H1	1.36	0.72
1:L5:1094:G:H1	1:L5:1201:U:H3	1.34	0.71
1:L5:1961:G:H21	1:L5:2025:A:H62	1.37	0.71
29:La:100:ILE:HD11	29:La:125:LYS:HE2	1.72	0.71
91:3k:133:GLY:O	91:3k:137:SER:HB2	1.91	0.71
1:L5:2373:C:H5'	32:Ld:46:LEU:HD21	1.73	0.71
1:L5:3615:G:H1'	25:LW:44:ARG:HE	1.55	0.70
1:L5:1306:C:H2'	1:L5:1307:A:H8	1.55	0.70
46:S2:16:G:H5'	46:S2:669:A:H61	1.56	0.70
4:LA:219:ILE:HG22	4:LA:221:LYS:H	1.57	0.70
61:SP:72:LYS:HE2	61:SP:92:SER:HA	1.72	0.70
1:L5:958:G:H21	8:LE:125:LEU:H	1.40	0.70
21:LS:101:THR:HG23	21:LS:104:GLY:H	1.57	0.70
46:S2:130:G:H21	46:S2:181:A:H61	1.35	0.70
68:SW:14:ILE:HD11	68:SW:65:LEU:HD11	1.74	0.70
46:S2:1643:U:H1'	62:SQ:142:GLN:HE22	1.56	0.69
63:SR:10:LYS:HG3	63:SR:53:TYR:HE1	1.56	0.69
89:3h:173:LEU:HD21	89:3h:192:ILE:HG21	1.74	0.69
46:S2:1271:C:H42	46:S2:1511:U:H3	1.40	0.69
89:3h:129:VAL:HB	89:3h:322:GLN:HG2	1.74	0.69
1:L5:759:G:H22	1:L5:904:C:H2'	1.56	0.69
8:LE:62:MET:HA	8:LE:65:ARG:HB3	1.73	0.69
85:3f:348:ILE:HG22	89:3h:253:MET:HE1	1.73	0.69
1:L5:493:G:O6	1:L5:660:A:N1	2.26	0.69
6:LC:302:LEU:HG	19:LQ:38:ARG:HG2	1.75	0.68
88:3c:855:LEU:HD13	89:3h:244:GLN:HE22	1.56	0.68
5:LB:90:VAL:HG22	5:LB:104:THR:HG22	1.74	0.68
62:SQ:15:ARG:HA	62:SQ:19:ALA:HB3	1.74	0.68
83:zz:140:A:N1	83:zz:285:G:O6	2.27	0.68
1:L5:1100:U:H3	1:L5:1195:G:H1	1.40	0.68
2:L7:59:G:H4'	7:LD:267:ASN:HD21	1.58	0.68
12:LI:30:LYS:HE3	12:LI:66:GLU:HG2	1.76	0.67
1:L5:1913:C:H1'	17:LO:87:MET:HG2	1.77	0.67
29:La:75:LEU:HB2	29:La:113:GLY:HA2	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:SG:34:THR:H	53:SG:52:ILE:HG22	1.60	0.67
56:SJ:38:ARG:HH22	56:SJ:41:ARG:HH21	1.40	0.67
62:SQ:95:TYR:O	62:SQ:99:TYR:HB2	1.95	0.67
13:LJ:141:ILE:HA	13:LJ:144:LYS:HZ1	1.60	0.67
1:L5:515:C:H41	1:L5:647:G:H21	1.43	0.67
1:L5:4910:G:H22	17:LO:107:GLY:HA3	1.60	0.67
1:L5:2845:A:H61	1:L5:3843:C:H42	1.43	0.66
46:S2:149:A:N7	46:S2:169:U:O2	2.28	0.66
46:S2:383:G:H21	58:SL:133:PRO:HG2	1.60	0.66
48:SB:105:LEU:HD22	48:SB:110:MET:HG3	1.77	0.66
46:S2:957:A:H2'	46:S2:958:G:H21	1.60	0.66
92:3l:475:LEU:HD22	92:3l:486:PHE:HD1	1.61	0.66
58:SL:101:ARG:HB2	69:SX:10:ALA:HB2	1.77	0.66
83:zz:141:U:H2'	83:zz:142:A:H8	1.61	0.66
92:3l:328:ARG:HH22	92:3l:509:LEU:HA	1.60	0.66
4:LA:54:ARG:HG2	4:LA:56:ALA:H	1.58	0.66
9:LF:182:TYR:HB3	9:LF:200:ARG:HG3	1.78	0.66
13:LJ:24:ILE:HD11	13:LJ:40:LEU:HD21	1.77	0.66
47:SA:184:ARG:HD2	47:SA:191:ARG:HG3	1.76	0.66
1:L5:4765:G:H21	21:LS:173:ASN:HD21	1.42	0.66
74:Sc:20:ARG:HH21	74:Sc:26:GLN:HA	1.59	0.66
1:L5:502:C:H5'	1:L5:503:C:H3'	1.78	0.66
46:S2:573:U:H2'	46:S2:574:A:H2'	1.78	0.66
46:S2:1398:G:O6	46:S2:1448:A:N1	2.29	0.66
52:SF:100:ILE:HG21	52:SF:111:VAL:HG11	1.78	0.66
58:SL:135:SER:HB3	58:SL:138:VAL:HB	1.76	0.66
61:SP:44:ARG:HH22	61:SP:84:ILE:H	1.44	0.66
33:Le:46:ARG:HA	33:Le:55:MET:HE1	1.78	0.66
6:LC:65:GLU:HG3	6:LC:80:ARG:HE	1.61	0.65
9:LF:222:LYS:HB3	9:LF:231:GLY:HA2	1.76	0.65
46:S2:587:A:H5''	46:S2:592:C:H41	1.59	0.65
1:L5:4875:G:H2'	21:LS:169:THR:HG22	1.77	0.65
9:LF:149:SER:HB2	9:LF:244:ILE:HD11	1.79	0.65
46:S2:955:A:H62	46:S2:971:G:H21	1.43	0.65
80:zy:15:G:N2	80:zy:47:C:O2	2.29	0.65
46:S2:681:U:H4'	69:SX:9:THR:HG22	1.78	0.65
1:L5:4389:C:H2'	1:L5:4390:A:H8	1.61	0.65
1:L5:1952:G:H4'	21:LS:93:MET:HG3	1.79	0.65
1:L5:4563:U:H2'	1:L5:4564:A:H8	1.62	0.65
7:LD:56:THR:HG23	7:LD:58:ARG:H	1.62	0.65
32:Ld:20:VAL:HG12	32:Ld:91:LYS:HA	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3754:G:H1	1:L5:3770:U:H3	1.44	0.65
19:LQ:50:ARG:HH12	19:LQ:140:SER:HB2	1.62	0.65
80:zy:53:U:O2	80:zy:57:A:N7	2.30	0.65
54:SH:144:ILE:HD11	54:SH:152:ARG:HE	1.60	0.65
46:S2:828:G:H4'	51:SE:23:LEU:HD21	1.79	0.64
46:S2:1113:A:H4'	48:SB:202:GLN:HE22	1.63	0.64
1:L5:1332:C:H2'	1:L5:1333:A:H8	1.61	0.64
5:LB:254:ILE:HB	5:LB:266:VAL:HG11	1.78	0.64
53:SG:32:MET:HE3	53:SG:33:ALA:H	1.62	0.64
1:L5:2095:A:H8	9:LF:32:ARG:HH22	1.43	0.64
46:S2:878:G:O6	46:S2:908:A:N1	2.29	0.64
89:3h:171:PRO:HA	89:3h:174:MET:HB3	1.79	0.64
1:L5:1906:U:H2'	1:L5:1907:A:H8	1.62	0.64
29:La:71:PRO:HD2	29:La:109:TYR:HB2	1.80	0.64
1:L5:1095:A:N1	1:L5:1200:G:O6	2.30	0.64
89:3h:141:GLN:HG2	89:3h:147:SER:HB2	1.80	0.64
1:L5:1700:G:H22	9:LF:177:ARG:HH12	1.44	0.64
89:3h:104:MET:HA	89:3h:107:LEU:HB3	1.79	0.64
43:Lo:65:LYS:HB3	43:Lo:87:ARG:HE	1.63	0.64
1:L5:2411:C:H2'	1:L5:2412:A:H8	1.61	0.64
46:S2:316:G:H5''	53:SG:183:ARG:HH12	1.63	0.64
46:S2:1396:A:N7	46:S2:1449:G:O6	2.31	0.64
79:sh:136:CYS:HB2	79:sh:141:LEU:H	1.63	0.64
20:LR:126:LYS:HG2	20:LR:131:VAL:HG11	1.79	0.63
46:S2:1004:U:H2'	46:S2:1005:G:H8	1.63	0.63
1:L5:98:A:H5'	16:LN:195:ARG:HD2	1.80	0.63
46:S2:1550:G:H3'	46:S2:1579:A:H61	1.62	0.63
15:LM:7:VAL:HG12	15:LM:57:LEU:HD11	1.80	0.63
68:SW:104:LEU:HB3	68:SW:125:ILE:HD13	1.80	0.63
86:3a:353:ARG:HH21	86:3a:354:ARG:HH21	1.46	0.63
52:SF:136:ARG:HH22	52:SF:199:VAL:HB	1.62	0.63
5:LB:57:VAL:HG13	5:LB:366:LYS:HB3	1.81	0.63
9:LF:199:LYS:HD2	9:LF:200:ARG:HG2	1.80	0.63
28:LZ:57:MET:HG2	28:LZ:61:LYS:HZ2	1.64	0.63
83:zz:242:C:H2'	83:zz:243:G:H8	1.62	0.63
41:Lm:99:CYS:HB2	41:Lm:115:CYS:HB3	1.80	0.63
41:Lm:103:LEU:HD11	41:Lm:110:CYS:HA	1.79	0.63
46:S2:563:G:H2'	46:S2:564:A:H8	1.62	0.63
46:S2:1335:G:H1	46:S2:1492:U:H3	1.44	0.63
4:LA:103:PRO:HA	4:LA:163:ARG:H	1.64	0.63
78:Sg:123:GLY:HA2	78:Sg:129:ILE:HG23	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:zy:15:G:N2	80:zy:47:C:C2	2.67	0.62
1:L5:2461:G:H4'	16:LN:108:ARG:HH12	1.64	0.62
46:S2:130:G:N2	46:S2:181:A:N6	2.39	0.62
58:SL:104:LYS:HE2	69:SX:8:ARG:HH12	1.62	0.62
1:L5:3932:U:H2'	1:L5:3933:G:H8	1.64	0.62
6:LC:67:TRP:HD1	6:LC:68:GLY:H	1.48	0.62
31:Lc:48:LEU:HD21	31:Lc:60:ILE:HG21	1.81	0.62
46:S2:955:A:H62	46:S2:971:G:N2	1.97	0.62
86:3a:164:LEU:HB3	86:3a:174:TYR:HB2	1.82	0.62
9:LF:154:ILE:HD11	9:LF:191:ILE:HG13	1.82	0.62
27:LY:111:LEU:HD12	27:LY:116:LYS:HE2	1.80	0.62
89:3h:37:LYS:HG2	89:3h:74:ASP:HB3	1.80	0.62
46:S2:527:C:H4'	56:SJ:121:LYS:HD3	1.82	0.62
92:3l:523:ILE:HB	92:3l:528:ILE:HG23	1.81	0.62
1:L5:300:A:H2'	1:L5:301:G:H8	1.64	0.62
1:L5:4174:U:H2'	1:L5:4175:G:H8	1.65	0.62
7:LD:33:ARG:HH11	22:LT:27:LEU:HD23	1.64	0.62
87:3e:298:CYS:HA	87:3e:302:ASN:HB2	1.80	0.62
11:LH:102:ASN:HB3	11:LH:115:ARG:HB2	1.81	0.62
1:L5:194:C:H1'	27:LY:121:ARG:HH12	1.64	0.62
61:SP:79:HIS:HB3	61:SP:97:TYR:HB3	1.80	0.62
66:SU:66:ARG:HG3	66:SU:68:THR:HG22	1.81	0.62
35:Lg:15:THR:HG22	35:Lg:18:ASN:HB2	1.82	0.62
56:SJ:20:PHE:H	56:SJ:24:ARG:HH21	1.47	0.62
28:LZ:29:ILE:HG22	28:LZ:32:GLY:H	1.64	0.62
46:S2:1314:U:H2'	57:SK:3:MET:HE1	1.81	0.62
1:L5:1947:U:H2'	41:Lm:109:ASN:HD22	1.65	0.61
34:Lf:50:VAL:HG12	34:Lf:69:VAL:HG12	1.82	0.61
1:L5:3848:U:H2'	1:L5:3849:A:H8	1.63	0.61
1:L5:3870:C:H2'	1:L5:3871:A:H8	1.65	0.61
4:LA:70:LYS:HD2	4:LA:72:ARG:HH11	1.65	0.61
61:SP:50:ARG:H	61:SP:53:GLN:HE22	1.49	0.61
4:LA:138:SER:HB3	4:LA:147:ARG:HD3	1.81	0.61
46:S2:581:U:H1'	70:SY:34:THR:HG23	1.81	0.61
35:Lg:15:THR:HG23	35:Lg:17:SER:H	1.65	0.61
87:3e:363:THR:HG22	87:3e:365:GLU:H	1.66	0.61
18:LP:26:PHE:HB2	18:LP:144:CYS:HB3	1.83	0.61
1:L5:2865:U:H1'	20:LR:78:ILE:HD11	1.83	0.61
1:L5:4622:A:H4'	5:LB:13:SER:HB2	1.83	0.61
1:L5:5006:U:H4'	1:L5:5007:A:H5'	1.82	0.61
7:LD:104:LEU:HB2	7:LD:247:ILE:HD12	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:132:G:H2'	1:L5:133:C:H4'	1.81	0.60
11:LH:10:VAL:HG13	11:LH:55:LEU:HB3	1.81	0.60
1:L5:4352:U:H1'	29:La:58:MET:HE1	1.82	0.60
7:LD:191:ASN:HD21	7:LD:194:VAL:H	1.49	0.60
87:3e:174:ALA:HA	87:3e:177:ILE:HD12	1.84	0.60
1:L5:1177:U:H3'	1:L5:1180:C:H41	1.66	0.60
91:3k:148:ILE:HG21	92:3l:498:LYS:HD2	1.84	0.60
46:S2:164:A:H5''	53:SG:82:SER:HB3	1.83	0.60
55:SI:57:ALA:HB1	55:SI:60:LEU:HD21	1.83	0.60
80:zu:10:G:O6	80:zu:24:U:O4	2.18	0.60
1:L5:1503:A:H4'	1:L5:1504:G:H5'	1.83	0.60
21:LS:34:ALA:HB1	21:LS:39:VAL:HG13	1.82	0.60
49:SC:166:ARG:HG2	49:SC:181:PRO:HG3	1.83	0.60
53:SG:142:ARG:HH21	53:SG:143:LYS:HG2	1.66	0.60
64:SS:25:LYS:HE3	64:SS:52:LEU:HD12	1.83	0.60
7:LD:110:LEU:HD22	7:LD:115:MET:HB2	1.84	0.60
48:SB:182:LYS:HE2	48:SB:231:LEU:HA	1.83	0.60
1:L5:323:C:H2'	1:L5:324:A:H8	1.67	0.60
6:LC:328:LEU:HD13	9:LF:187:MET:HE1	1.83	0.60
1:L5:1348:U:H2'	1:L5:1349:G:H8	1.67	0.60
1:L5:951:G:H2'	1:L5:952:G:H8	1.67	0.59
6:LC:224:ILE:HB	6:LC:227:ILE:HD11	1.83	0.59
17:LO:58:LEU:HA	17:LO:72:HIS:HD2	1.66	0.59
50:SD:203:PRO:HG2	63:SR:42:PRO:HG3	1.82	0.59
57:SK:15:LEU:HD12	57:SK:19:GLY:HA2	1.82	0.59
9:LF:244:ILE:HA	9:LF:247:MET:HB2	1.84	0.59
12:LI:170:LYS:HA	12:LI:177:ASN:HA	1.84	0.59
15:LM:35:ARG:HA	15:LM:51:PRO:HA	1.84	0.59
46:S2:616:A:H62	46:S2:625:G:H21	1.50	0.59
1:L5:2838:G:H5'	5:LB:247:GLY:HA2	1.85	0.59
3:L8:8:U:H2'	3:L8:9:A:H8	1.67	0.59
11:LH:34:LEU:HB3	11:LH:80:MET:HE3	1.83	0.59
26:LX:117:TYR:HB3	26:LX:119:ILE:HG12	1.83	0.59
92:3l:550:PHE:HA	92:3l:553:LEU:HB2	1.83	0.59
85:3f:337:VAL:HG21	89:3h:239:LEU:HD11	1.83	0.59
7:LD:60:ILE:HG12	7:LD:80:ALA:HB2	1.84	0.59
45:Lr:63:VAL:HG12	45:Lr:79:ARG:HG2	1.84	0.59
86:3a:403:LEU:HA	86:3a:406:ARG:HD2	1.85	0.59
14:LL:91:ALA:HB1	14:LL:96:ILE:HB	1.83	0.59
1:L5:2295:C:H2'	1:L5:2296:G:H8	1.68	0.59
65:ST:72:VAL:HG21	65:ST:101:ARG:HG3	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:3f:159:LEU:HD13	89:3h:103:MET:HE1	1.84	0.59
92:3l:291:ILE:HG13	92:3l:326:MET:HE1	1.84	0.59
16:LN:36:LEU:HD12	16:LN:64:ILE:HD11	1.84	0.59
84:3m:165:LEU:HD23	84:3m:184:VAL:HG13	1.84	0.59
1:L5:4985:U:H4'	5:LB:175:GLN:HG3	1.83	0.59
51:SE:247:THR:HG23	51:SE:250:GLU:H	1.68	0.59
53:SG:219:GLU:HA	53:SG:222:GLU:HB3	1.84	0.59
5:LB:56:ILE:HD13	5:LB:368:ILE:HD13	1.85	0.58
5:LB:242:ARG:HA	5:LB:248:LEU:HD21	1.84	0.58
46:S2:409:C:H5''	46:S2:426:A:H5'	1.85	0.58
49:SC:156:ILE:HD13	49:SC:159:LYS:HZ3	1.67	0.58
1:L5:420:A:H61	3:L8:15:G:H1'	1.68	0.58
11:LH:173:ARG:HH21	41:Lm:127:VAL:H	1.51	0.58
18:LP:112:LEU:HA	18:LP:152:GLU:HA	1.84	0.58
24:LV:94:VAL:HG11	25:LW:20:ARG:HH21	1.68	0.58
51:SE:100:ARG:HH22	51:SE:236:ILE:HD12	1.66	0.58
67:SV:74:LYS:HZ3	67:SV:83:PHE:HD2	1.49	0.58
1:L5:318:A:H2'	1:L5:319:A:H8	1.68	0.58
7:LD:64:ILE:HG13	7:LD:105:LEU:HD21	1.85	0.58
26:LX:86:ALA:HB1	26:LX:97:VAL:HG21	1.85	0.58
47:SA:80:ARG:HD3	47:SA:82:THR:HG23	1.85	0.58
51:SE:57:THR:HG23	51:SE:60:GLU:H	1.69	0.58
1:L5:1914:C:H4'	17:LO:89:PRO:HD3	1.85	0.58
1:L5:4246:G:H2'	1:L5:4247:G:H8	1.68	0.58
55:SI:62:VAL:HA	55:SI:76:THR:O	2.02	0.58
92:3l:179:PRO:HG2	92:3l:182:TRP:HB2	1.85	0.58
9:LF:50:ILE:HD12	9:LF:186:CYS:HB3	1.83	0.58
51:SE:126:VAL:HG12	51:SE:158:ASP:H	1.68	0.58
1:L5:3805:U:H2'	1:L5:3806:G:H8	1.69	0.58
46:S2:1092:G:H2'	46:S2:1093:A:H8	1.69	0.58
47:SA:57:LYS:HE2	67:SV:70:LEU:HD21	1.85	0.58
68:SW:37:PHE:HE1	68:SW:103:VAL:HG11	1.67	0.58
1:L5:197:A:H5''	27:LY:126:ARG:HE	1.68	0.58
19:LQ:41:SER:HB3	19:LQ:132:LYS:HD3	1.85	0.58
20:LR:175:GLU:HA	20:LR:178:GLN:HE21	1.68	0.58
21:LS:80:ILE:HG22	21:LS:129:VAL:HG23	1.86	0.58
48:SB:91:VAL:HG23	48:SB:96:CYS:HA	1.86	0.58
78:Sg:86:THR:HG21	78:Sg:102:VAL:HA	1.85	0.58
80:zu:17:G:H21	80:zu:57:A:H5'	1.67	0.58
92:3l:102:LEU:HB3	92:3l:107:PHE:HE2	1.68	0.58
1:L5:1837:A:H2'	1:L5:1838:A:H8	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:SH:147:LYS:HD3	54:SH:153:LEU:HD21	1.86	0.58
69:SX:115:ILE:HG13	69:SX:118:VAL:HG21	1.85	0.58
83:zz:140:A:N1	83:zz:285:G:C6	2.72	0.58
1:L5:493:G:C6	1:L5:660:A:N1	2.72	0.58
1:L5:3711:A:H2'	1:L5:3712:A:H8	1.69	0.58
21:LS:85:ASP:HB2	21:LS:123:SER:HB2	1.86	0.58
46:S2:649:U:H2'	46:S2:650:A:H8	1.69	0.58
46:S2:1864:U:H3'	72:Sa:5:ARG:HH21	1.69	0.58
61:SP:111:MET:HB3	64:SS:117:ILE:HG21	1.86	0.58
62:SQ:39:LEU:HB3	62:SQ:51:LEU:HD21	1.86	0.58
17:LO:58:LEU:HA	17:LO:72:HIS:CD2	2.38	0.57
47:SA:140:VAL:HG13	47:SA:142:LEU:HD23	1.85	0.57
58:SL:21:LYS:HG2	58:SL:23:VAL:H	1.69	0.57
62:SQ:47:LEU:HD13	62:SQ:81:ILE:HG21	1.86	0.57
66:SU:21:ARG:HD3	66:SU:88:LEU:HD12	1.86	0.57
1:L5:490:C:H2'	1:L5:491:G:H8	1.67	0.57
53:SG:5:ILE:O	53:SG:13:GLN:HA	2.03	0.57
29:La:101:ILE:O	29:La:124:VAL:HA	2.04	0.57
46:S2:920:A:H4'	68:SW:57:ARG:HG2	1.85	0.57
16:LN:51:LEU:HD13	16:LN:117:ASN:HD22	1.69	0.57
46:S2:1143:A:H5'	49:SC:190:SER:HB3	1.86	0.57
46:S2:1521:C:H5'	61:SP:126:VAL:HB	1.87	0.57
46:S2:1808:U:H2'	46:S2:1809:A:H8	1.70	0.57
70:SY:40:ILE:H	70:SY:40:ILE:HD12	1.69	0.57
87:3e:421:ASN:HA	87:3e:424:LYS:HD2	1.86	0.57
29:La:117:LEU:HD13	29:La:118:PRO:HD2	1.87	0.57
17:LO:81:TRP:HB2	17:LO:104:VAL:HG21	1.86	0.57
45:Lr:103:ARG:HG2	45:Lr:106:LEU:HD22	1.85	0.57
46:S2:1101:U:H2'	46:S2:1102:G:H8	1.70	0.57
50:SD:190:LEU:HD12	50:SD:191:PRO:HD2	1.86	0.57
92:3l:471:PRO:HD2	92:3l:474:LYS:HD3	1.86	0.57
1:L5:1802:A:H5''	1:L5:1803:G:H5'	1.85	0.57
9:LF:126:ASN:HD21	22:LT:132:PRO:HG2	1.69	0.57
33:Le:24:GLN:HG2	33:Le:27:ARG:HD3	1.86	0.57
1:L5:3937:C:H1'	16:LN:125:SER:HB3	1.85	0.57
1:L5:4348:A:N1	1:L5:4364:G:O6	2.38	0.57
18:LP:114:ILE:HG22	18:LP:150:LEU:HG	1.85	0.57
21:LS:127:MET:HB3	22:LT:153:PRO:HG2	1.87	0.57
46:S2:1653:U:O2	46:S2:1671:G:N2	2.34	0.57
53:SG:57:ASP:HA	53:SG:107:SER:H	1.70	0.57
74:Sc:10:LYS:HZ1	74:Sc:34:PHE:HD1	1.52	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
91:3k:171:LYS:HA	91:3k:174:MET:HE3	1.87	0.57
1:L5:2908:U:H3	1:L5:3586:G:H22	1.50	0.57
49:SC:183:LYS:HG2	49:SC:196:ILE:HG22	1.87	0.57
9:LF:94:ARG:HD2	9:LF:109:LEU:HD13	1.86	0.57
84:3m:162:HIS:HA	84:3m:188:LEU:HD11	1.87	0.57
88:3c:586:ARG:HA	88:3c:589:MET:HG2	1.87	0.57
21:LS:77:ASN:HD21	21:LS:98:ARG:HH11	1.52	0.56
46:S2:1786:U:H2'	46:S2:1787:G:H8	1.70	0.56
58:SL:87:VAL:HA	58:SL:110:SER:HA	1.86	0.56
89:3h:249:ARG:HB3	89:3h:319:ILE:HD11	1.87	0.56
1:L5:1100:U:O2	1:L5:1195:G:N2	2.30	0.56
1:L5:1207:C:H2'	1:L5:1208:G:H8	1.70	0.56
1:L5:1238:A:H5''	8:LE:60:SER:HB3	1.86	0.56
57:SK:27:VAL:HB	57:SK:43:LEU:HD21	1.86	0.56
86:3a:407:VAL:HA	86:3a:410:VAL:HG12	1.87	0.56
1:L5:2075:G:H2'	1:L5:2076:G:H8	1.70	0.56
7:LD:197:LYS:HB2	7:LD:202:GLN:HB2	1.87	0.56
45:Lr:108:MET:HA	45:Lr:111:ILE:HD12	1.86	0.56
56:SJ:125:HIS:HA	56:SJ:128:VAL:HG12	1.86	0.56
58:SL:33:LEU:HD12	58:SL:34:PRO:HD2	1.87	0.56
80:zy:51:G:H2'	80:zy:52:G:H8	1.71	0.56
83:zz:291:G:O6	83:zz:302:U:O2	2.22	0.56
1:L5:4122:G:H4'	35:Lg:90:ARG:HD2	1.88	0.56
54:SH:60:ILE:HG12	54:SH:92:VAL:HG13	1.87	0.56
86:3a:279:VAL:O	86:3a:283:PHE:HB2	2.05	0.56
46:S2:1536:G:H2'	46:S2:1537:A:H8	1.71	0.56
85:3f:209:GLY:HA2	86:3a:554:VAL:HG11	1.88	0.56
92:3l:470:MET:HE2	92:3l:475:LEU:HB2	1.88	0.56
6:LC:289:LEU:HD12	6:LC:292:ILE:HD11	1.88	0.56
19:LQ:125:GLN:HA	19:LQ:128:LEU:HB2	1.87	0.56
34:Lf:45:LYS:HD3	34:Lf:105:LEU:HA	1.88	0.56
43:Lo:45:GLN:HE22	43:Lo:51:GLN:HA	1.71	0.56
46:S2:1845:A:H2'	46:S2:1846:G:H8	1.71	0.56
92:3l:546:GLN:HA	92:3l:549:LYS:HD3	1.88	0.56
1:L5:2386:U:H2'	1:L5:2387:G:H8	1.71	0.56
16:LN:174:LEU:HA	16:LN:183:THR:HG21	1.86	0.56
17:LO:88:LEU:HD13	17:LO:89:PRO:HD2	1.88	0.56
46:S2:1748:G:N2	46:S2:1786:U:O2	2.34	0.56
92:3l:89:TYR:HA	92:3l:92:GLN:HG2	1.87	0.56
1:L5:1464:C:H5''	30:Lb:32:LEU:HD23	1.86	0.56
5:LB:234:ARG:HB3	5:LB:235:TRP:HD1	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LN:9:GLU:HB3	37:Li:44:ILE:HG21	1.87	0.56
41:Lm:115:CYS:HB2	41:Lm:118:THR:HG22	1.88	0.56
46:S2:958:G:H2'	46:S2:959:G:C8	2.40	0.56
48:SB:72:ALA:HB3	60:SO:128:ARG:HH21	1.69	0.56
48:SB:213:ARG:HH22	48:SB:214:LYS:HD3	1.71	0.56
92:3l:481:LEU:HD13	92:3l:485:GLU:HB3	1.86	0.56
1:L5:2750:G:H5'	35:Lg:72:LYS:HD2	1.87	0.56
10:LG:137:ARG:HD3	10:LG:146:LEU:HD11	1.87	0.56
11:LH:92:MET:HE2	11:LH:144:LEU:HD21	1.88	0.56
28:LZ:28:ASN:C	28:LZ:28:ASN:HD22	2.14	0.56
46:S2:926:A:H61	46:S2:1015:U:H3	1.52	0.56
46:S2:928:G:H2'	46:S2:929:G:C8	2.41	0.56
60:SO:31:CYS:HB2	60:SO:44:VAL:HG12	1.88	0.56
78:Sg:31:ILE:HG21	78:Sg:299:PHE:HE1	1.71	0.56
86:3a:98:GLU:HG2	86:3a:153:LEU:HD21	1.86	0.56
48:SB:161:VAL:HA	48:SB:164:ILE:HG22	1.88	0.56
51:SE:35:PRO:HD2	51:SE:83:PRO:HG2	1.88	0.56
52:SF:122:ARG:HD3	74:Sc:9:ILE:HG23	1.87	0.55
56:SJ:144:ILE:HB	56:SJ:147:PHE:HB2	1.88	0.55
16:LN:59:TYR:HE1	16:LN:142:ILE:HD11	1.70	0.55
26:LX:93:ASN:HB3	26:LX:95:THR:HG22	1.88	0.55
92:3l:475:LEU:HD22	92:3l:486:PHE:CD1	2.41	0.55
46:S2:696:G:H21	46:S2:735:C:H5'	1.71	0.55
62:SQ:40:GLU:HB2	62:SQ:48:GLN:HE22	1.70	0.55
86:3a:483:ARG:HD2	88:3c:800:ASP:HB2	1.87	0.55
88:3c:704:ASP:HB3	88:3c:707:ARG:HH12	1.70	0.55
1:L5:4093:G:H2'	1:L5:4094:G:H8	1.71	0.55
65:ST:14:PHE:HB2	65:ST:138:VAL:HG11	1.87	0.55
75:Sd:21:CYS:HB2	75:Sd:38:MET:HA	1.89	0.55
1:L5:1175:A:H2	1:L5:1185:G:H22	1.53	0.55
27:LY:54:GLU:HB2	27:LY:108:ARG:HB3	1.87	0.55
55:SI:104:ILE:HG23	55:SI:171:LEU:HB2	1.89	0.55
84:3m:354:LEU:HD22	85:3f:286:VAL:HG11	1.88	0.55
1:L5:2749:C:H5'	35:Lg:65:MET:HB2	1.86	0.55
50:SD:137:VAL:HG12	50:SD:151:LYS:HG3	1.88	0.55
61:SP:30:TYR:HA	61:SP:33:LEU:HB2	1.89	0.55
80:zy:14:A:H3'	80:zy:15:G:H8	1.72	0.55
1:L5:1645:C:H2'	1:L5:1646:A:C8	2.41	0.55
1:L5:3873:G:H2'	1:L5:3874:G:C8	2.42	0.55
51:SE:115:THR:HG23	51:SE:118:GLU:H	1.72	0.55
84:3m:111:HIS:HB3	85:3f:234:PRO:HD2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:3a:484:ILE:HG12	86:3a:491:LEU:HG	1.89	0.55
46:S2:391:C:H2'	46:S2:392:A:H8	1.72	0.55
46:S2:857:U:H2'	46:S2:858:A:C8	2.42	0.55
92:3l:326:MET:HE3	92:3l:328:ARG:HE	1.70	0.55
1:L5:4301:U:H4'	22:LT:54:HIS:CD2	2.41	0.55
1:L5:4910:G:H21	5:LB:96:PRO:HG2	1.72	0.55
47:SA:124:VAL:HG11	47:SA:134:LEU:HD21	1.89	0.55
51:SE:131:VAL:HB	51:SE:135:GLY:HA2	1.88	0.55
66:SU:27:ARG:HH22	75:Sd:51:GLY:HA3	1.71	0.55
70:SY:112:ASN:HA	70:SY:115:LYS:HZ2	1.72	0.55
78:Sg:5:MET:HE2	78:Sg:310:TRP:HB3	1.88	0.55
1:L5:268:G:H2'	1:L5:269:G:H8	1.70	0.55
43:Lo:63:THR:HG21	43:Lo:89:LYS:HG2	1.89	0.55
46:S2:28:U:H2'	46:S2:29:G:H8	1.72	0.55
65:ST:6:VAL:HG13	65:ST:7:LYS:HD3	1.89	0.55
86:3a:18:PHE:HA	86:3a:21:VAL:HG22	1.89	0.55
92:3l:130:ILE:HG21	92:3l:163:LEU:HB2	1.87	0.55
1:L5:1332:C:H2'	1:L5:1333:A:C8	2.40	0.54
6:LC:67:TRP:CD1	6:LC:68:GLY:H	2.25	0.54
23:LU:87:THR:O	23:LU:91:LEU:HD12	2.06	0.54
27:LY:73:VAL:HG22	27:LY:80:ILE:HG23	1.87	0.54
61:SP:108:LYS:H	61:SP:111:MET:HE1	1.73	0.54
86:3a:212:HIS:HA	86:3a:217:ALA:HB3	1.89	0.54
92:3l:243:GLN:HE22	92:3l:253:PRO:HB3	1.73	0.54
1:L5:10:A:H2'	1:L5:11:G:H8	1.72	0.54
86:3a:168:SER:HA	86:3a:218:ILE:HD11	1.89	0.54
86:3a:483:ARG:HH12	86:3a:485:ASP:HB2	1.72	0.54
88:3c:606:GLN:HB3	90:3d:43:ALA:HB1	1.88	0.54
1:L5:2520:C:H2'	1:L5:2521:G:H8	1.72	0.54
29:La:71:PRO:HG2	29:La:108:TYR:HA	1.89	0.54
44:Lp:38:THR:HG22	44:Lp:45:THR:HG22	1.89	0.54
50:SD:48:ILE:HB	50:SD:86:LEU:HD13	1.89	0.54
54:SH:20:GLU:HA	54:SH:23:ILE:HB	1.89	0.54
65:ST:76:THR:HG23	65:ST:94:ARG:HD2	1.89	0.54
80:zu:9:G:H1'	80:zu:44:G:H2'	1.89	0.54
89:3h:193:THR:HG23	89:3h:195:GLU:H	1.72	0.54
1:L5:217:C:H3'	1:L5:218:A:H4'	1.90	0.54
1:L5:2091:C:H4'	1:L5:2092:G:H5'	1.90	0.54
17:LO:70:PRO:HB2	17:LO:72:HIS:CE1	2.41	0.54
46:S2:59:U:H2'	46:S2:60:A:H2'	1.89	0.54
46:S2:1644:C:H4'	62:SQ:140:ARG:HB2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
92:3l:66:LEU:HD13	92:3l:177:GLU:HG2	1.89	0.54
1:L5:691:C:H2'	1:L5:692:A:H8	1.71	0.54
21:LS:83:ARG:HG2	21:LS:127:MET:HE1	1.90	0.54
50:SD:47:GLU:HA	50:SD:85:GLU:HG3	1.90	0.54
1:L5:3848:U:H2'	1:L5:3849:A:C8	2.41	0.54
46:S2:1232:U:H2'	46:S2:1233:G:H8	1.72	0.54
46:S2:1629:C:H2'	46:S2:1630:A:H8	1.72	0.54
58:SL:4:ILE:HG23	58:SL:5:GLN:HG2	1.89	0.54
62:SQ:34:VAL:HG12	62:SQ:39:LEU:HD22	1.89	0.54
70:SY:91:LEU:HB3	70:SY:97:TYR:HB2	1.89	0.54
92:3l:286:ASP:HB3	92:3l:289:GLN:HB2	1.89	0.54
1:L5:1907:A:H4'	9:LF:223:LYS:HD3	1.90	0.54
1:L5:4537:C:H2'	1:L5:4538:G:H8	1.72	0.54
92:3l:244:LEU:HD21	92:3l:296:ASN:H	1.73	0.54
1:L5:1538:U:H2'	1:L5:1539:G:H8	1.72	0.54
1:L5:2020:U:H2'	1:L5:2021:G:H8	1.72	0.54
27:LY:57:VAL:HA	27:LY:104:VAL:HG23	1.88	0.54
50:SD:204:LEU:HB2	50:SD:207:HIS:HB3	1.90	0.54
86:3a:496:ASP:HB3	86:3a:499:TYR:HB2	1.90	0.54
1:L5:187:U:H5''	1:L5:188:G:H5'	1.89	0.54
1:L5:1095:A:N1	1:L5:1200:G:C6	2.76	0.54
1:L5:4239:A:H2'	1:L5:4240:G:H8	1.73	0.54
9:LF:127:LYS:HB2	22:LT:133:ALA:HB3	1.90	0.54
32:Ld:22:THR:HB	32:Ld:122:VAL:HG13	1.89	0.54
46:S2:1729:U:O4	46:S2:1805:G:O6	2.26	0.54
86:3a:471:ILE:HD13	86:3a:484:ILE:HD11	1.90	0.54
1:L5:100:C:H2'	1:L5:101:A:H8	1.71	0.54
1:L5:665:C:H2'	1:L5:669:C:H41	1.73	0.54
1:L5:679:C:H2'	1:L5:680:G:H8	1.73	0.54
1:L5:1514:U:H2'	1:L5:1515:A:H8	1.72	0.54
1:L5:3861:A:H2'	1:L5:3862:A:H8	1.73	0.54
6:LC:152:LEU:HD21	6:LC:174:LEU:HD12	1.90	0.54
16:LN:47:LYS:HD2	16:LN:50:ARG:HH22	1.73	0.54
46:S2:1454:A:H5'	63:SR:5:ARG:HH22	1.72	0.54
1:L5:2407:G:C4	40:LI:13:LEU:HD21	2.43	0.53
1:L5:2543:A:H2	1:L5:2773:G:H22	1.56	0.53
1:L5:4274:A:H2'	1:L5:4275:G:H8	1.74	0.53
12:LI:36:LEU:HD21	12:LI:69:ARG:HH11	1.73	0.53
46:S2:1854:U:H2'	46:S2:1855:G:H8	1.74	0.53
87:3e:371:ILE:HD13	87:3e:391:VAL:HG21	1.90	0.53
12:LI:86:HIS:HB3	12:LI:139:ARG:HG3	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1520:G:H21	61:SP:126:VAL:HG11	1.72	0.53
48:SB:181:LEU:HA	48:SB:184:VAL:HG12	1.89	0.53
80:zu:11:U:O2	80:zu:22:G:O6	2.26	0.53
77:Sf:31:LEU:HD22	77:Sf:33:ARG:HD3	1.90	0.53
88:3c:124:LYS:HA	88:3c:127:LYS:HZ3	1.73	0.53
89:3h:40:GLN:HG2	89:3h:204:VAL:HB	1.89	0.53
46:S2:1447:G:H2'	46:S2:1448:A:C8	2.42	0.53
66:SU:66:ARG:HA	66:SU:77:TRP:CD1	2.43	0.53
88:3c:718:LEU:HD12	88:3c:738:VAL:HG22	1.91	0.53
92:3l:464:LEU:HD22	92:3l:530:ILE:HG21	1.91	0.53
1:L5:2641:A:H62	1:L5:2693:G:N2	2.07	0.53
31:Lc:40:GLN:HE22	31:Lc:42:LYS:HG3	1.72	0.53
63:SR:54:VAL:HA	63:SR:57:LEU:HD23	1.90	0.53
69:SX:47:ALA:HB1	69:SX:74:LEU:HD11	1.90	0.53
83:zz:186:C:N4	83:zz:212:U:N3	2.56	0.53
88:3c:424:ILE:HB	88:3c:439:ARG:HD2	1.91	0.53
1:L5:987:C:C4	1:L5:988:C:N4	2.76	0.53
1:L5:3664:G:H2'	1:L5:3665:G:H8	1.74	0.53
46:S2:941:C:H2'	46:S2:942:G:C8	2.44	0.53
46:S2:1712:A:H2'	46:S2:1713:C:C6	2.44	0.53
48:SB:123:ALA:HB2	48:SB:165:ARG:HG3	1.91	0.53
80:zy:53:U:N3	80:zy:57:A:C8	2.75	0.53
80:zy:53:U:C2	80:zy:57:A:N7	2.76	0.53
83:zz:186:C:N4	83:zz:212:U:H3	2.07	0.53
16:LN:88:GLY:HA3	43:Lo:48:TYR:CE1	2.43	0.53
40:Ll:43:HIS:HB3	40:Ll:46:ARG:HD3	1.91	0.53
46:S2:145:G:H2'	46:S2:146:G:C8	2.44	0.53
51:SE:139:LEU:HD13	51:SE:147:ILE:HD11	1.90	0.53
92:3l:401:MET:HG2	92:3l:409:TYR:HE1	1.73	0.53
7:LD:65:ALA:HB2	7:LD:74:ILE:HD13	1.90	0.53
46:S2:54:A:H3'	46:S2:451:G:H22	1.74	0.53
74:Sc:33:GLU:HG3	74:Sc:35:MET:H	1.74	0.53
1:L5:4582:C:H4'	5:LB:99:LEU:HB3	1.90	0.53
6:LC:326:LEU:HD11	6:LC:333:LYS:HB2	1.89	0.53
8:LE:164:PHE:HA	8:LE:175:VAL:HG23	1.90	0.53
46:S2:74:G:H22	53:SG:170:ARG:HA	1.74	0.53
46:S2:306:C:H4'	46:S2:307:G:H5''	1.91	0.53
46:S2:677:G:N2	46:S2:1028:A:H62	2.00	0.53
46:S2:1546:G:H21	46:S2:1670:C:H1'	1.74	0.53
84:3m:62:SER:HB2	85:3f:222:GLY:H	1.74	0.53
86:3a:267:PRO:HB2	86:3a:272:MET:HG2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:3a:351:LYS:HD2	88:3c:725:PRO:HA	1.91	0.53
88:3c:479:VAL:O	88:3c:483:ILE:HG13	2.09	0.53
1:L5:3916:G:H2'	1:L5:3917:A:H8	1.74	0.53
69:SX:107:ARG:HG2	69:SX:110:HIS:HB3	1.91	0.53
84:3m:74:LEU:HD12	84:3m:75:GLU:H	1.73	0.53
92:3l:376:THR:HB	92:3l:401:MET:HE2	1.91	0.53
1:L5:4088:C:H2'	1:L5:4089:G:H8	1.73	0.52
4:LA:39:GLY:HA3	10:LG:41:ILE:HD11	1.90	0.52
9:LF:113:ARG:HH11	9:LF:210:PRO:HD3	1.73	0.52
63:SR:100:PRO:HA	63:SR:103:LYS:HE2	1.90	0.52
72:Sa:50:VAL:HA	72:Sa:53:ILE:HG22	1.90	0.52
89:3h:36:VAL:HA	89:3h:74:ASP:HA	1.91	0.52
1:L5:1461:C:H2'	1:L5:1462:A:H8	1.75	0.52
1:L5:1524:A:H61	1:L5:1651:G:H22	1.57	0.52
1:L5:2106:G:H2'	1:L5:2107:C:H4'	1.90	0.52
5:LB:26:ARG:HD2	5:LB:181:MET:HB2	1.92	0.52
7:LD:224:SER:HA	7:LD:227:ILE:HD12	1.91	0.52
12:LI:36:LEU:H	12:LI:87:MET:HB3	1.73	0.52
27:LY:39:ARG:HD2	27:LY:45:ARG:HD2	1.91	0.52
46:S2:223:C:H2'	46:S2:224:A:C8	2.44	0.52
48:SB:197:ILE:HG21	48:SB:210:VAL:HG21	1.91	0.52
89:3h:37:LYS:HG3	89:3h:38:GLN:HG2	1.92	0.52
1:L5:137:G:H2'	1:L5:138:G:H8	1.73	0.52
1:L5:1613:A:H5''	4:LA:183:GLY:HA3	1.91	0.52
1:L5:3943:A:H2'	1:L5:3944:G:H8	1.73	0.52
1:L5:4704:C:H2'	1:L5:4705:A:C8	2.45	0.52
20:LR:102:LEU:HD13	20:LR:138:LEU:HD22	1.90	0.52
26:LX:90:ILE:HD11	26:LX:96:LEU:HD23	1.90	0.52
56:SJ:32:ILE:HG13	56:SJ:37:LEU:HB2	1.91	0.52
89:3h:218:LEU:O	89:3h:222:SER:HB2	2.08	0.52
1:L5:2745:A:H2'	1:L5:2746:A:H8	1.73	0.52
46:S2:508:A:H3'	46:S2:509:G:H8	1.73	0.52
55:SI:40:PRO:HG2	55:SI:59:ARG:HD3	1.92	0.52
84:3m:120:ARG:HH12	84:3m:124:TYR:HB2	1.74	0.52
87:3e:384:ILE:HG13	87:3e:391:VAL:HG22	1.91	0.52
91:3k:149:THR:HA	92:3l:494:LYS:HE3	1.91	0.52
1:L5:4704:C:H2'	1:L5:4705:A:H8	1.74	0.52
1:L5:5018:C:H2'	1:L5:5019:A:H8	1.73	0.52
5:LB:54:THR:HG22	5:LB:373:LYS:HZ1	1.75	0.52
15:LM:106:ASP:HA	15:LM:109:ARG:HE	1.75	0.52
46:S2:300:U:H2'	46:S2:301:A:C8	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:432:G:H2'	46:S2:433:A:C8	2.45	0.52
46:S2:639:C:H2'	46:S2:640:A:C8	2.44	0.52
59:SN:66:VAL:HG12	59:SN:67:THR:HG23	1.90	0.52
80:zy:9:G:H1'	80:zy:45:G:H5''	1.91	0.52
1:L5:1259:G:H2'	1:L5:1260:G:H8	1.74	0.52
1:L5:1732:C:H2'	1:L5:1733:G:C8	2.45	0.52
14:LL:29:PRO:O	14:LL:33:ILE:HG12	2.09	0.52
46:S2:1468:C:H2'	46:S2:1469:A:H8	1.75	0.52
83:zz:255:C:H1'	83:zz:278:G:H22	1.74	0.52
1:L5:490:C:H2'	1:L5:491:G:C8	2.44	0.52
1:L5:4093:G:H2'	1:L5:4094:G:C8	2.44	0.52
46:S2:212:C:H2'	46:S2:213:G:C8	2.45	0.52
46:S2:962:A:H5''	60:SO:66:ARG:HB2	1.91	0.52
46:S2:1729:U:O2	46:S2:1805:G:N2	2.33	0.52
46:S2:1775:U:H3'	46:S2:1776:G:H21	1.74	0.52
55:SI:142:SER:HA	55:SI:146:GLN:HB3	1.91	0.52
59:SN:37:ILE:HA	59:SN:40:LEU:HD12	1.92	0.52
1:L5:956:A:H1'	1:L5:2076:G:H5''	1.91	0.52
1:L5:1824:G:H2'	1:L5:1825:A:C8	2.45	0.52
1:L5:2641:A:H62	1:L5:2693:G:H21	1.56	0.52
1:L5:3715:U:C2	80:zu:71:C:H5'	2.44	0.52
6:LC:336:ARG:O	6:LC:340:ILE:HG13	2.10	0.52
7:LD:109:LEU:HD23	7:LD:171:LEU:HD21	1.91	0.52
9:LF:228:VAL:HG13	21:LS:39:VAL:HG23	1.91	0.52
16:LN:113:LEU:HB2	16:LN:137:PRO:HD3	1.92	0.52
46:S2:1607:A:H62	46:S2:1632:G:N2	2.05	0.52
56:SJ:81:LEU:HA	56:SJ:84:ILE:HG12	1.90	0.52
85:3f:99:LEU:HB3	89:3h:214:LEU:HD21	1.91	0.52
1:L5:4239:A:H2'	1:L5:4240:G:C8	2.45	0.52
1:L5:4892:A:H5''	17:LO:188:LYS:HE3	1.92	0.52
5:LB:45:ALA:HB3	5:LB:183:ILE:HG23	1.91	0.52
31:Lc:38:ILE:HD11	31:Lc:46:VAL:HG11	1.91	0.52
46:S2:442:C:N4	46:S2:449:A:H62	2.03	0.52
46:S2:659:G:H21	69:SX:17:ARG:HH22	1.57	0.52
46:S2:1693:G:H21	46:S2:1834:A:H8	1.58	0.52
48:SB:157:GLN:HB2	48:SB:160:GLN:HG2	1.91	0.52
54:SH:43:LEU:HB2	54:SH:72:PHE:HE1	1.74	0.52
1:L5:1270:A:H8	1:L5:2106:G:H21	1.58	0.52
1:L5:4642:U:H2'	1:L5:4643:G:H8	1.75	0.52
29:La:64:LYS:HE2	29:La:67:GLN:HE22	1.73	0.52
29:La:137:ILE:HD11	29:La:144:CYS:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:106:C:H2'	46:S2:107:A:H8	1.75	0.52
46:S2:941:C:H2'	46:S2:942:G:H8	1.75	0.52
46:S2:1098:C:H2'	46:S2:1099:G:C8	2.45	0.52
46:S2:1562:C:H2'	46:S2:1563:G:H8	1.74	0.52
65:ST:40:ALA:HB3	65:ST:43:LYS:HG2	1.92	0.52
4:LA:7:GLY:HA2	4:LA:10:LYS:HE3	1.91	0.51
6:LC:32:ILE:HD12	6:LC:130:ALA:HB2	1.92	0.51
12:LI:33:ILE:HB	12:LI:69:ARG:HH12	1.75	0.51
46:S2:1562:C:H2'	46:S2:1563:G:C8	2.45	0.51
84:3m:64:MET:HE1	84:3m:101:LEU:HB2	1.92	0.51
84:3m:102:ARG:HE	84:3m:130:VAL:HG21	1.75	0.51
1:L5:228:C:H2'	1:L5:229:G:H8	1.75	0.51
1:L5:1633:G:C6	4:LA:207:VAL:HG21	2.45	0.51
1:L5:2375:A:H2'	1:L5:2376:A:H8	1.75	0.51
1:L5:4459:U:H2'	1:L5:4460:U:C6	2.46	0.51
3:L8:8:U:H2'	3:L8:9:A:C8	2.44	0.51
8:LE:276:ALA:HA	34:Lf:3:GLY:HA3	1.91	0.51
46:S2:691:G:H3'	46:S2:692:G:H4'	1.91	0.51
83:zz:179:A:H2'	83:zz:180:G:H8	1.75	0.51
1:L5:2884:G:H2'	1:L5:2885:A:H8	1.76	0.51
12:LI:36:LEU:HD21	12:LI:69:ARG:HD3	1.92	0.51
16:LN:6:TYR:HE1	37:Li:40:VAL:HA	1.75	0.51
46:S2:1804:U:H2'	46:S2:1805:G:C8	2.45	0.51
1:L5:1089:G:H2'	1:L5:1090:G:H8	1.75	0.51
1:L5:3589:G:H2'	1:L5:3590:G:C8	2.45	0.51
6:LC:294:LYS:HA	6:LC:294:LYS:HE3	1.91	0.51
17:LO:14:HIS:HD2	17:LO:123:ALA:HB3	1.76	0.51
20:LR:4:LEU:HD12	20:LR:24:LEU:HD13	1.91	0.51
46:S2:110:U:O2	46:S2:351:G:N2	2.39	0.51
46:S2:223:C:H2'	46:S2:224:A:H8	1.75	0.51
46:S2:454:U:H2'	46:S2:455:A:H8	1.75	0.51
78:Sg:121:VAL:HA	78:Sg:131:LEU:HA	1.93	0.51
1:L5:1350:C:H2'	1:L5:1351:G:H8	1.75	0.51
1:L5:1824:G:H2'	1:L5:1825:A:H8	1.75	0.51
1:L5:4389:C:H2'	1:L5:4390:A:C8	2.43	0.51
39:Lk:52:LYS:HB3	39:Lk:55:LYS:HE3	1.93	0.51
46:S2:925:G:H22	46:S2:1017:U:H3	1.57	0.51
86:3a:401:LEU:HA	86:3a:458:LEU:HD11	1.92	0.51
6:LC:117:THR:HA	6:LC:120:LYS:HD3	1.93	0.51
18:LP:4:TYR:HD1	18:LP:147:GLU:HG3	1.75	0.51
46:S2:1858:G:H2'	46:S2:1859:A:H8	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:SE:26:VAL:HG23	51:SE:27:PHE:HD1	1.75	0.51
60:SO:42:VAL:HG23	60:SO:43:HIS:H	1.75	0.51
92:3l:299:LEU:HD11	92:3l:338:ASN:HD21	1.76	0.51
1:L5:4274:A:H2'	1:L5:4275:G:C8	2.46	0.51
85:3f:92:VAL:HG13	85:3f:129:VAL:HG23	1.92	0.51
89:3h:260:TYR:HE1	89:3h:310:PRO:HB3	1.76	0.51
1:L5:1461:C:H2'	1:L5:1462:A:C8	2.45	0.51
1:L5:5055:G:H2'	1:L5:5056:A:H8	1.76	0.51
6:LC:57:LEU:HB3	6:LC:61:GLN:HE21	1.75	0.51
14:LL:70:VAL:HG22	14:LL:159:ASN:HB3	1.93	0.51
46:S2:919:A:H5'	59:SN:16:LEU:HD12	1.92	0.51
83:zz:139:C:H42	83:zz:286:G:H1	1.58	0.51
84:3m:38:LEU:HD21	84:3m:70:LEU:HB3	1.93	0.51
86:3a:532:LYS:HE3	89:3h:224:VAL:HG13	1.93	0.51
88:3c:733:MET:HA	88:3c:736:HIS:HB2	1.92	0.51
3:L8:133:G:H2'	3:L8:134:G:H8	1.75	0.51
4:LA:204:MET:HG3	4:LA:209:HIS:HB2	1.92	0.51
16:LN:138:PHE:HZ	36:Lh:93:ARG:HB3	1.74	0.51
37:Li:54:GLU:HB2	37:Li:90:LEU:HD11	1.92	0.51
46:S2:509:G:H4'	51:SE:26:VAL:HG21	1.93	0.51
68:SW:82:GLN:HB2	68:SW:85:ASP:HB2	1.93	0.51
74:Sc:18:LEU:HB2	74:Sc:29:GLN:HE21	1.75	0.51
79:sh:128:ALA:HB3	79:sh:135:TYR:HB3	1.93	0.51
86:3a:197:LEU:O	86:3a:201:LEU:HD12	2.11	0.51
1:L5:287:U:H2'	1:L5:288:G:C8	2.46	0.51
1:L5:3610:A:H2'	1:L5:3611:A:H8	1.75	0.51
3:L8:28:C:H2'	3:L8:29:G:H8	1.75	0.51
11:LH:4:ILE:HB	21:LS:144:GLN:HE21	1.74	0.51
22:LT:12:ARG:HD3	22:LT:13:TYR:CZ	2.46	0.51
1:L5:1628:C:H3'	4:LA:9:ARG:HH22	1.76	0.50
1:L5:1933:G:H2'	1:L5:1934:A:C8	2.45	0.50
1:L5:3917:A:H2'	1:L5:3918:G:H8	1.77	0.50
6:LC:212:ASN:HD22	6:LC:255:SER:HB2	1.76	0.50
17:LO:70:PRO:HB2	17:LO:72:HIS:HE1	1.76	0.50
28:LZ:134:LEU:HD21	35:Lg:95:PHE:HB2	1.92	0.50
46:S2:878:G:N1	46:S2:908:A:C2	2.63	0.50
46:S2:948:C:H2'	46:S2:949:G:H8	1.76	0.50
52:SF:119:SER:HB2	52:SF:189:ALA:HB1	1.93	0.50
68:SW:32:LYS:HA	68:SW:35:VAL:HG12	1.92	0.50
78:Sg:109:LEU:H	78:Sg:125:ARG:NH2	2.09	0.50
84:3m:193:THR:HG23	84:3m:195:ASP:H	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:2557:G:O6	1:L5:2570:U:O4	2.30	0.50
6:LC:301:ALA:HB1	19:LQ:132:LYS:HZ3	1.76	0.50
24:LV:96:LEU:HB2	25:LW:20:ARG:HB3	1.93	0.50
45:Lr:44:ILE:H	45:Lr:44:ILE:HD12	1.76	0.50
46:S2:878:G:C6	46:S2:908:A:N1	2.80	0.50
50:SD:109:LEU:HD11	50:SD:175:VAL:HG11	1.92	0.50
67:SV:15:ARG:HH21	67:SV:24:ILE:HG21	1.75	0.50
88:3c:67:ILE:O	88:3c:71:MET:HG2	2.11	0.50
89:3h:80:ASN:HD22	89:3h:112:ILE:HG21	1.77	0.50
1:L5:3612:C:H1'	1:L5:5016:A:H8	1.76	0.50
5:LB:279:GLU:HB3	5:LB:282:LYS:HE2	1.93	0.50
19:LQ:70:MET:HE1	19:LQ:137:VAL:HG11	1.93	0.50
78:Sg:152:SER:HB3	78:Sg:168:CYS:HB3	1.94	0.50
80:zu:10:G:N2	80:zu:24:U:O2	2.43	0.50
1:L5:126:C:H2'	1:L5:127:G:H8	1.77	0.50
9:LF:110:GLN:HG3	9:LF:115:ARG:HH12	1.76	0.50
28:LZ:13:VAL:HG13	28:LZ:75:TYR:HE2	1.75	0.50
46:S2:1430:C:H2'	46:S2:1431:G:C8	2.46	0.50
50:SD:198:ILE:H	50:SD:198:ILE:HD12	1.75	0.50
92:3l:345:ARG:HA	92:3l:553:LEU:HD21	1.94	0.50
1:L5:4313:A:H1'	22:LT:90:ASN:HD22	1.77	0.50
47:SA:144:THR:HG23	47:SA:157:VAL:HG23	1.92	0.50
68:SW:53:ILE:H	68:SW:53:ILE:HD12	1.76	0.50
1:L5:1336:G:H21	1:L5:2349:A:N6	2.10	0.50
1:L5:1876:U:H2'	1:L5:1877:G:H8	1.76	0.50
51:SE:9:LEU:HG	51:SE:30:ARG:HD3	1.94	0.50
85:3f:334:LEU:HD21	89:3h:337:ASN:HD22	1.75	0.50
88:3c:672:PRO:HD2	88:3c:675:LEU:HD12	1.93	0.50
89:3h:173:LEU:HA	89:3h:176:VAL:HB	1.94	0.50
1:L5:153:G:H2'	1:L5:154:G:H8	1.77	0.50
1:L5:668:C:H5'	6:LC:6:PRO:HB3	1.93	0.50
1:L5:1617:G:H1'	1:L5:2513:A:H61	1.77	0.50
10:LG:157:ILE:HB	10:LG:183:ILE:HG22	1.93	0.50
17:LO:23:VAL:HG13	17:LO:33:VAL:HG11	1.94	0.50
24:LV:120:PRO:HA	24:LV:138:SER:HB3	1.93	0.50
46:S2:1705:C:H2'	46:S2:1706:G:C8	2.46	0.50
52:SF:110:GLN:HA	52:SF:113:VAL:HG12	1.94	0.50
59:SN:142:GLU:HB2	59:SN:145:THR:HG22	1.92	0.50
62:SQ:134:GLY:HA2	62:SQ:141:TYR:CE1	2.46	0.50
78:Sg:286:CYS:HA	78:Sg:302:TYR:HB3	1.93	0.50
92:3l:60:HIS:HA	92:3l:63:VAL:HG22	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1380:G:H4'	1:L5:1381:U:H5'	1.93	0.50
1:L5:1759:G:O6	1:L5:1773:U:O4	2.29	0.50
1:L5:4635:A:H2	1:L5:4663:G:H21	1.59	0.50
6:LC:331:TYR:HE2	9:LF:55:LYS:HA	1.75	0.50
28:LZ:57:MET:HE2	28:LZ:62:ILE:HG22	1.93	0.50
37:Li:65:LYS:HZ2	37:Li:68:ARG:HB3	1.77	0.50
46:S2:1010:G:H2'	46:S2:1011:A:H8	1.77	0.50
46:S2:1337:C:H2'	46:S2:1338:G:H8	1.76	0.50
49:SC:142:LYS:HZ3	49:SC:144:SER:HB3	1.75	0.50
78:Sg:99:ARG:NH1	78:Sg:99:ARG:HA	2.26	0.50
83:zz:317:C:H2'	83:zz:318:G:C8	2.47	0.50
1:L5:1514:U:H2'	1:L5:1515:A:C8	2.46	0.50
1:L5:4363:A:H5''	43:Lo:36:GLN:HG2	1.94	0.50
2:L7:15:C:H2'	2:L7:16:A:H8	1.75	0.50
18:LP:138:PRO:HB3	18:LP:140:MET:HE3	1.94	0.50
46:S2:885:U:H1'	46:S2:902:G:H22	1.76	0.50
46:S2:1228:A:H2'	46:S2:1229:G:C8	2.47	0.50
91:3k:149:THR:HG23	91:3k:150:TYR:HB2	1.93	0.50
1:L5:1478:C:H2'	1:L5:1479:G:H8	1.77	0.49
1:L5:2343:G:C2	6:LC:101:MET:HE1	2.46	0.49
5:LB:286:LYS:H	5:LB:332:MET:HB3	1.77	0.49
46:S2:943:U:H2'	46:S2:944:A:H8	1.77	0.49
59:SN:93:LYS:HG3	59:SN:150:VAL:HG11	1.94	0.49
1:L5:3736:A:H2'	1:L5:3737:A:C8	2.47	0.49
17:LO:51:LYS:HD2	17:LO:144:GLU:HG2	1.94	0.49
46:S2:903:A:H2'	46:S2:904:A:C4	2.47	0.49
46:S2:923:G:H2'	46:S2:924:G:H8	1.77	0.49
47:SA:21:ALA:HB1	47:SA:169:HIS:HB3	1.93	0.49
51:SE:151:ASP:HB3	51:SE:154:ILE:HG13	1.94	0.49
51:SE:183:VAL:HG12	51:SE:191:ARG:H	1.76	0.49
85:3f:249:VAL:O	85:3f:253:MET:HG2	2.12	0.49
92:3l:336:PHE:HD2	92:3l:371:LEU:HG	1.77	0.49
1:L5:2275:G:H2'	1:L5:2276:A:C8	2.47	0.49
1:L5:4537:C:H2'	1:L5:4538:G:C8	2.46	0.49
1:L5:4680:G:H2'	1:L5:4681:A:C8	2.47	0.49
31:Lc:49:ALA:HB2	31:Lc:81:LEU:HD22	1.95	0.49
46:S2:92:A:H1'	51:SE:3:ARG:HE	1.77	0.49
49:SC:210:PRO:HB3	49:SC:240:THR:HG21	1.93	0.49
1:L5:923:C:H2'	1:L5:925:C:H5	1.76	0.49
1:L5:1534:A:H2'	1:L5:1637:A:C6	2.48	0.49
1:L5:1845:U:H2'	1:L5:1846:G:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4319:C:H2'	1:L5:4320:G:H8	1.77	0.49
1:L5:4742:G:H2'	1:L5:4743:G:H8	1.77	0.49
7:LD:209:ARG:HA	7:LD:212:MET:HG2	1.95	0.49
13:LJ:18:ARG:H	13:LJ:134:LEU:HA	1.76	0.49
46:S2:955:A:N6	46:S2:971:G:H21	2.08	0.49
46:S2:1004:U:H2'	46:S2:1005:G:C8	2.45	0.49
46:S2:1808:U:H2'	46:S2:1809:A:C8	2.46	0.49
78:Sg:122:SER:HB3	78:Sg:132:TRP:HE1	1.76	0.49
92:3l:341:LEU:HD11	92:3l:549:LYS:HD2	1.94	0.49
45:Lr:26:SER:HB2	45:Lr:28:GLU:OE2	2.12	0.49
46:S2:201:C:H3'	46:S2:202:G:H8	1.78	0.49
46:S2:582:U:H2'	46:S2:583:A:C8	2.47	0.49
49:SC:157:LEU:HA	49:SC:160:LEU:HB2	1.93	0.49
49:SC:188:CYS:HB3	49:SC:239:ALA:HB2	1.94	0.49
57:SK:77:GLN:HA	57:SK:80:ARG:HG2	1.94	0.49
86:3a:498:ASN:HA	86:3a:520:ARG:HH22	1.78	0.49
92:3l:65:ASP:HA	92:3l:68:ASP:HB2	1.94	0.49
92:3l:523:ILE:HD12	92:3l:528:ILE:HG12	1.95	0.49
1:L5:691:C:H2'	1:L5:692:A:C8	2.46	0.49
1:L5:1271:G:N1	1:L5:2107:C:C2	2.80	0.49
1:L5:1350:C:H2'	1:L5:1351:G:C8	2.48	0.49
1:L5:2017:A:H5''	1:L5:2018:C:H5	1.77	0.49
7:LD:27:LYS:HE2	13:LJ:147:ARG:HH11	1.77	0.49
15:LM:30:VAL:HG11	21:LS:150:ILE:HD13	1.94	0.49
28:LZ:73:LYS:HE2	28:LZ:75:TYR:HE1	1.78	0.49
46:S2:375:U:H2'	46:S2:376:A:C8	2.47	0.49
46:S2:1228:A:H2'	46:S2:1229:G:H8	1.76	0.49
46:S2:1276:A:H62	46:S2:1321:G:H8	1.59	0.49
53:SG:77:LEU:HD11	53:SG:95:LYS:HB2	1.95	0.49
56:SJ:119:LEU:HD13	56:SJ:159:PHE:HE1	1.78	0.49
57:SK:71:LEU:HD12	57:SK:76:ILE:HG12	1.94	0.49
70:SY:18:LEU:HD23	70:SY:20:ARG:HD2	1.94	0.49
72:Sa:21:ILE:HD11	72:Sa:32:LYS:HE3	1.94	0.49
77:Sf:89:VAL:HG11	77:Sf:106:CYS:HB2	1.95	0.49
85:3f:248:GLY:HA3	89:3h:50:ILE:HD13	1.95	0.49
88:3c:430:ASN:HB3	88:3c:439:ARG:H	1.77	0.49
1:L5:325:U:H2'	1:L5:326:C:C6	2.48	0.49
1:L5:1955:G:H2'	1:L5:1956:A:H8	1.76	0.49
4:LA:192:LYS:HD3	4:LA:193:ARG:HH21	1.78	0.49
29:La:4:ARG:HG2	29:La:5:LEU:HD23	1.94	0.49
29:La:74:ASN:HB3	29:La:114:LYS:HB3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Ld:28:ASN:HD21	32:Ld:31:LYS:HB2	1.78	0.49
46:S2:303:C:H2'	46:S2:304:C:C2	2.48	0.49
46:S2:1231:C:H42	46:S2:1527:C:H41	1.60	0.49
51:SE:99:PHE:HB3	51:SE:113:ARG:HA	1.95	0.49
57:SK:25:LYS:HE3	57:SK:62:PHE:HE1	1.77	0.49
57:SK:66:HIS:HB2	57:SK:68:TYR:HE1	1.77	0.49
85:3f:90:ARG:HH21	85:3f:217:VAL:HG11	1.77	0.49
88:3c:379:ILE:HD11	88:3c:405:ILE:HA	1.95	0.49
88:3c:781:ARG:HH22	88:3c:813:LEU:HD11	1.77	0.49
1:L5:496:G:H2'	1:L5:497:G:H4'	1.95	0.49
1:L5:2540:C:H2'	1:L5:2541:G:H8	1.77	0.49
21:LS:76:LYS:HD3	21:LS:131:GLU:HG3	1.95	0.49
27:LY:55:VAL:HG22	27:LY:104:VAL:HG22	1.95	0.49
46:S2:147:A:HO2'	46:S2:148:U:H6	1.60	0.49
62:SQ:39:LEU:HD12	62:SQ:51:LEU:HD11	1.95	0.49
77:Sf:20:GLU:HA	77:Sf:23:LYS:HE2	1.93	0.49
87:3e:169:LEU:HB3	87:3e:192:LEU:HD13	1.95	0.49
1:L5:4146:G:H2'	1:L5:4147:G:H8	1.76	0.49
28:LZ:99:ASP:HB2	28:LZ:102:ARG:HH21	1.78	0.49
46:S2:1337:C:H2'	46:S2:1338:G:C8	2.47	0.49
61:SP:67:ALA:HB2	61:SP:73:PRO:HB3	1.95	0.49
86:3a:301:HIS:HA	86:3a:304:ARG:HG2	1.95	0.49
89:3h:45:VAL:HG21	89:3h:78:ILE:HG22	1.94	0.49
1:L5:1541:C:H5''	4:LA:21:LYS:HG2	1.93	0.49
1:L5:1942:A:H2'	1:L5:1943:A:C8	2.48	0.49
18:LP:133:HIS:HB2	18:LP:135:ARG:HG3	1.95	0.49
20:LR:15:LEU:HD13	20:LR:52:ARG:HG2	1.95	0.49
28:LZ:29:ILE:HD12	28:LZ:40:HIS:CE1	2.48	0.49
83:zz:138:C:H2'	83:zz:139:C:H6	1.77	0.49
84:3m:208:ILE:HG21	84:3m:237:ILE:HG23	1.95	0.49
1:L5:2610:G:H2'	1:L5:2611:A:H8	1.78	0.48
1:L5:3707:U:H2'	1:L5:3708:C:C6	2.48	0.48
1:L5:4954:G:H2'	1:L5:4955:A:H8	1.78	0.48
5:LB:47:LEU:HD21	5:LB:181:MET:HB3	1.95	0.48
46:S2:429:C:H2'	46:S2:430:C:H6	1.78	0.48
46:S2:529:A:H2'	46:S2:530:U:C6	2.47	0.48
46:S2:1568:C:H5''	65:ST:96:SER:HB2	1.95	0.48
59:SN:47:PRO:HA	59:SN:50:ILE:HB	1.95	0.48
86:3a:18:PHE:HB2	86:3a:27:ALA:HB2	1.95	0.48
1:L5:1195:G:H2'	1:L5:1196:G:H8	1.78	0.48
1:L5:1604:G:H2'	1:L5:1605:G:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:5018:C:H2'	1:L5:5019:A:C8	2.48	0.48
46:S2:1505:U:H5'	46:S2:1506:A:H5'	1.94	0.48
46:S2:1643:U:H2'	46:S2:1644:C:C6	2.47	0.48
46:S2:1653:U:H2'	46:S2:1654:G:C8	2.48	0.48
47:SA:176:TRP:CD2	47:SA:199:PRO:HG3	2.48	0.48
86:3a:550:HIS:CE1	89:3h:217:GLU:HG2	2.48	0.48
1:L5:3736:A:H2'	1:L5:3737:A:H8	1.77	0.48
1:L5:3870:C:H2'	1:L5:3871:A:C8	2.47	0.48
15:LM:122:ILE:HG21	17:LO:189:ILE:HD11	1.95	0.48
17:LO:85:ARG:HG3	17:LO:99:LEU:HD21	1.95	0.48
73:Sb:14:GLU:O	73:Sb:18:LYS:HB2	2.14	0.48
84:3m:181:ALA:O	84:3m:185:MET:HG2	2.14	0.48
1:L5:9:C:H2'	1:L5:10:A:H8	1.78	0.48
1:L5:486:C:H2'	1:L5:487:G:H8	1.78	0.48
1:L5:661:C:H2'	1:L5:662:C:C6	2.49	0.48
1:L5:1702:C:H4'	6:LC:308:LYS:HD2	1.96	0.48
1:L5:4324:A:H2'	1:L5:4325:A:C8	2.48	0.48
1:L5:4716:C:H2'	1:L5:4717:A:H8	1.77	0.48
3:L8:67:U:H2'	3:L8:68:G:H8	1.77	0.48
46:S2:317:C:H2'	46:S2:318:A:C4	2.48	0.48
46:S2:1562:C:H5''	65:ST:71:GLY:HA3	1.94	0.48
46:S2:1665:G:C6	65:ST:88:MET:HE1	2.49	0.48
53:SG:143:LYS:HA	53:SG:143:LYS:HD3	1.60	0.48
85:3f:118:GLY:HA2	85:3f:136:SER:HA	1.94	0.48
88:3c:705:ALA:HB2	88:3c:858:GLN:HB2	1.96	0.48
1:L5:4967:A:H2'	1:L5:4968:A:H8	1.79	0.48
17:LO:118:MET:HE2	17:LO:118:MET:HB2	1.78	0.48
46:S2:1755:C:H42	46:S2:1778:C:H42	1.61	0.48
58:SL:103:GLU:HB3	69:SX:10:ALA:HB3	1.94	0.48
61:SP:43:ARG:HE	61:SP:47:ARG:HH21	1.62	0.48
85:3f:348:ILE:HD13	89:3h:323:ILE:HG22	1.96	0.48
86:3a:338:ILE:O	86:3a:342:LEU:HB2	2.13	0.48
86:3a:489:ARG:HH12	88:3c:806:THR:HG21	1.79	0.48
87:3e:232:ILE:O	87:3e:236:PHE:HB2	2.13	0.48
1:L5:2275:G:H2'	1:L5:2276:A:H8	1.79	0.48
1:L5:3732:A:H2'	1:L5:3733:A:C8	2.49	0.48
14:LL:57:PRO:HB3	14:LL:76:PHE:CZ	2.48	0.48
18:LP:136:ILE:HG21	82:zx:5:VAL:HG11	1.94	0.48
67:SV:67:ASP:O	67:SV:71:ARG:HG3	2.13	0.48
72:Sa:37:LYS:HB3	72:Sa:37:LYS:HE2	1.65	0.48
75:Sd:36:LEU:HD11	75:Sd:43:PHE:HE2	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
88:3c:573:ILE:HG23	88:3c:585:ALA:HB1	1.95	0.48
92:3l:401:MET:HG2	92:3l:409:TYR:CE1	2.49	0.48
1:L5:1961:G:N2	1:L5:2025:A:H62	2.08	0.48
1:L5:2521:G:H2'	1:L5:2522:G:H8	1.79	0.48
46:S2:354:U:H2'	46:S2:355:G:C8	2.49	0.48
46:S2:1845:A:H2'	46:S2:1846:G:C8	2.47	0.48
84:3m:144:LEU:HA	84:3m:147:VAL:HB	1.95	0.48
91:3k:146:VAL:HA	91:3k:149:THR:HG22	1.96	0.48
1:L5:318:A:H2'	1:L5:319:A:C8	2.47	0.48
1:L5:3855:C:H2'	1:L5:3856:A:H8	1.77	0.48
1:L5:4344:U:H2'	1:L5:4345:C:C6	2.49	0.48
28:LZ:54:THR:HG23	28:LZ:56:ALA:H	1.78	0.48
31:Lc:28:VAL:HG21	31:Lc:37:MET:HG3	1.96	0.48
46:S2:145:G:H2'	46:S2:146:G:H8	1.79	0.48
61:SP:35:GLN:HA	61:SP:42:ARG:HD3	1.96	0.48
61:SP:111:MET:HG3	61:SP:119:PHE:HZ	1.79	0.48
66:SU:61:LEU:HG	66:SU:82:MET:HB2	1.96	0.48
92:3l:150:LEU:HA	92:3l:153:ARG:HB2	1.96	0.48
4:LA:79:ALA:HA	4:LA:169:VAL:HA	1.95	0.48
21:LS:106:VAL:HA	21:LS:109:CYS:HB3	1.96	0.48
49:SC:227:ARG:HD3	49:SC:228:GLY:H	1.79	0.48
53:SG:98:ARG:HD2	53:SG:99:GLY:H	1.79	0.48
87:3e:364:PRO:HA	87:3e:367:ALA:HB3	1.96	0.48
89:3h:264:MET:HA	89:3h:267:THR:HG22	1.95	0.48
1:L5:352:G:C2	6:LC:196:MET:HE3	2.49	0.48
1:L5:742:G:H2'	1:L5:743:G:H8	1.79	0.48
1:L5:1346:C:H2'	1:L5:1347:G:H8	1.79	0.48
1:L5:4967:A:H2'	1:L5:4968:A:C8	2.48	0.48
1:L5:5024:C:H41	1:L5:5029:C:H1'	1.78	0.48
17:LO:39:GLU:CD	17:LO:39:GLU:H	2.22	0.48
31:Lc:78:ASN:HD21	31:Lc:92:CYS:HB2	1.79	0.48
57:SK:55:ARG:HB2	57:SK:57:TYR:CE2	2.49	0.48
65:ST:85:ASN:HB2	65:ST:88:MET:HB2	1.95	0.48
86:3a:296:LEU:HB3	86:3a:322:VAL:HG23	1.95	0.48
1:L5:1876:U:H2'	1:L5:1877:G:C8	2.48	0.47
1:L5:2568:C:H2'	1:L5:2569:G:C8	2.49	0.47
1:L5:3731:C:H2'	1:L5:3732:A:H8	1.78	0.47
10:LG:244:PRO:HA	10:LG:247:VAL:HG12	1.96	0.47
30:Lb:35:VAL:HG23	30:Lb:40:LEU:HD12	1.96	0.47
36:Lh:88:THR:HG23	36:Lh:90:ALA:H	1.79	0.47
46:S2:1221:G:H2'	46:S2:1222:G:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69: SX:100: VAL: HG23	69: SX:125: VAL: HA	1.96	0.47
84: 3m:236: LEU: HD13	84: 3m:262: PHE: CD2	2.49	0.47
85: 3f:311: LEU: HD13	86: 3a:529: VAL: HB	1.95	0.47
87: 3e:418: LEU: HD11	88: 3c:871: GLU: HB2	1.96	0.47
1: L5:33: A: H5''	1: L5:47: A: H61	1.79	0.47
1: L5:261: G: H2'	1: L5:262: G: H8	1.79	0.47
1: L5:1443: A: H2'	1: L5:1444: G: H8	1.78	0.47
1: L5:2822: G: H5''	20: LR:18: GLY: HA3	1.96	0.47
52: SF:77: MET: HG3	52: SF:83: ASN: HA	1.96	0.47
54: SH:58: LYS: HB2	54: SH:90: LYS: HD3	1.95	0.47
60: SO:44: VAL: HG23	60: SO:53: ILE: HB	1.95	0.47
92: 3l:184: TRP: O	92: 3l:188: ASP: HB2	2.14	0.47
1: L5:287: U: H2'	1: L5:288: G: H8	1.79	0.47
21: LS:110: TYR: HE1	21: LS:126: ILE: HD11	1.79	0.47
30: Lb:13: SER: HA	30: Lb:16: TRP: NE1	2.29	0.47
46: S2:549: C: H2'	46: S2:550: C: C6	2.49	0.47
46: S2:1048: G: H21	46: S2:1070: A: H62	1.61	0.47
53: SG:174: PRO: HG2	53: SG:176: ILE: HD11	1.97	0.47
53: SG:233: ARG: HE	53: SG:234: LEU: HD23	1.80	0.47
56: SJ:42: GLU: HA	56: SJ:45: ARG: HB3	1.96	0.47
58: SL:77: VAL: HA	58: SL:88: ILE: HG22	1.96	0.47
58: SL:130: GLU: HG2	58: SL:140: PHE: HE2	1.78	0.47
65: ST:11: GLN: HG3	65: ST:62: ARG: HH21	1.79	0.47
78: Sg:191: HIS: HE1	78: Sg:210: GLY: HA2	1.79	0.47
78: Sg:251: ALA: HB2	78: Sg:289: LEU: HD21	1.95	0.47
1: L5:284: G: H2'	1: L5:285: G: H8	1.80	0.47
1: L5:1333: A: H2'	1: L5:1334: A: H8	1.80	0.47
1: L5:1346: C: H2'	1: L5:1347: G: C8	2.49	0.47
1: L5:4699: U: H1'	1: L5:4700: A: H5''	1.95	0.47
5: LB:373: LYS: HA	5: LB:373: LYS: HD3	1.68	0.47
8: LE:179: LEU: HD12	8: LE:183: ARG: HA	1.96	0.47
17: LO:23: VAL: HG22	17: LO:33: VAL: HG21	1.96	0.47
28: LZ:49: TYR: HD1	28: LZ:133: LYS: HG2	1.79	0.47
32: Ld:26: THR: HB	32: Ld:85: ARG: HE	1.79	0.47
41: Lm:82: LEU: HA	41: Lm:85: LEU: HD23	1.96	0.47
46: S2:696: G: H1	46: S2:737: G: H1	1.61	0.47
47: SA:39: TYR: CE2	47: SA:50: ASN: HA	2.50	0.47
47: SA:85: ARG: HD3	47: SA:204: TYR: HA	1.96	0.47
52: SF:30: ILE: HG12	52: SF:42: LYS: HE2	1.95	0.47
54: SH:48: ALA: HB2	54: SH:62: ILE: HD13	1.95	0.47
80: zy:51: G: H2'	80: zy:52: G: C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:3m:46:ILE:HD12	84:3m:86:LEU:HD12	1.97	0.47
91:3k:196:ILE:HG21	92:3l:522:TYR:HD1	1.80	0.47
1:L5:1320:U:H5'	1:L5:1855:G:H1'	1.96	0.47
1:L5:1919:G:H21	21:LS:164:LYS:H	1.62	0.47
1:L5:3916:G:H2'	1:L5:3917:A:C8	2.49	0.47
1:L5:4689:U:H4'	11:LH:151:ILE:HG21	1.96	0.47
17:LO:108:ILE:HD13	17:LO:160:ARG:HH12	1.79	0.47
22:LT:73:GLY:HA2	22:LT:89:ILE:O	2.15	0.47
24:LV:48:ARG:HG3	24:LV:49:LEU:H	1.79	0.47
39:Lk:23:VAL:HG23	39:Lk:66:VAL:HA	1.96	0.47
46:S2:106:C:H2'	46:S2:107:A:C8	2.50	0.47
46:S2:388:U:H2'	46:S2:389:A:H8	1.78	0.47
46:S2:618:C:H3'	46:S2:619:A:H8	1.80	0.47
46:S2:1144:A:H2'	46:S2:1145:A:C8	2.50	0.47
46:S2:1650:A:H5''	62:SQ:139:ALA:HB2	1.95	0.47
46:S2:1706:G:H2'	46:S2:1707:U:H6	1.79	0.47
49:SC:81:ILE:HG23	49:SC:86:LEU:HB2	1.96	0.47
59:SN:13:GLN:HE21	73:Sb:21:LYS:NZ	2.12	0.47
59:SN:63:VAL:HG11	59:SN:71:ILE:HG13	1.95	0.47
68:SW:35:VAL:O	68:SW:39:THR:HG23	2.15	0.47
86:3a:420:LYS:HA	86:3a:420:LYS:HD2	1.78	0.47
87:3e:341:PHE:HD2	87:3e:374:LEU:HD21	1.79	0.47
1:L5:467:U:H3	1:L5:689:U:H3	1.62	0.47
1:L5:1504:G:H2'	1:L5:1505:C:H6	1.79	0.47
1:L5:4736:C:H2'	1:L5:4737:G:H8	1.79	0.47
4:LA:58:LEU:HD13	4:LA:75:LEU:HD12	1.97	0.47
6:LC:34:PRO:HA	6:LC:37:VAL:HG12	1.96	0.47
6:LC:60:HIS:NE2	6:LC:100:ARG:HD3	2.29	0.47
6:LC:109:ARG:HD2	6:LC:111:TRP:CE2	2.50	0.47
36:Lh:69:LEU:HD22	36:Lh:83:LEU:HD11	1.97	0.47
46:S2:28:U:H2'	46:S2:29:G:C8	2.50	0.47
46:S2:130:G:C2	46:S2:181:A:N6	2.79	0.47
83:zz:294:U:H2'	83:zz:295:G:H2'	1.97	0.47
85:3f:120:LEU:HD11	85:3f:173:TYR:HB3	1.95	0.47
86:3a:43:TRP:HH2	86:3a:48:GLU:HG2	1.79	0.47
92:3l:373:ILE:HG13	92:3l:377:MET:HE1	1.97	0.47
1:L5:1368:A:H2'	1:L5:1369:C:O4'	2.15	0.47
1:L5:1645:C:H2'	1:L5:1646:A:H8	1.79	0.47
1:L5:1847:C:H2'	1:L5:1848:C:C6	2.50	0.47
1:L5:4146:G:H2'	1:L5:4147:G:C8	2.49	0.47
1:L5:4273:A:H2'	1:L5:4274:A:C8	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4743:G:H2'	1:L5:4744:A:C8	2.49	0.47
21:LS:2:LYS:HE2	21:LS:35:PRO:HD3	1.97	0.47
46:S2:692:G:H1	46:S2:738:C:H1'	1.80	0.47
46:S2:1225:U:H2'	46:S2:1226:G:C8	2.50	0.47
46:S2:1589:A:H2'	46:S2:1590:C:C6	2.50	0.47
46:S2:1646:C:H5''	62:SQ:138:ARG:HH11	1.79	0.47
48:SB:87:ILE:HG22	48:SB:101:HIS:HB2	1.97	0.47
62:SQ:80:GLN:O	62:SQ:84:ILE:HG12	2.14	0.47
65:ST:33:TRP:HD1	65:ST:37:VAL:HG22	1.79	0.47
83:zz:144:U:O2	83:zz:249:G:N2	2.37	0.47
83:zz:179:A:H2'	83:zz:180:G:C8	2.50	0.47
91:3k:131:ILE:HD13	91:3k:134:PHE:HB2	1.97	0.47
91:3k:153:ILE:HG21	91:3k:158:LEU:HD13	1.97	0.47
91:3k:182:ASP:HB3	91:3k:186:GLN:HB3	1.95	0.47
92:3l:84:ILE:O	92:3l:88:VAL:HG12	2.14	0.47
1:L5:441:G:H2'	1:L5:442:G:H8	1.80	0.47
1:L5:1443:A:H2'	1:L5:1444:G:C8	2.49	0.47
3:L8:28:C:H2'	3:L8:29:G:C8	2.50	0.47
6:LC:85:HIS:CG	82:zx:4:LEU:HD21	2.49	0.47
44:Lp:37:TYR:HB2	44:Lp:47:MET:HB3	1.95	0.47
45:Lr:108:MET:HA	45:Lr:111:ILE:CD1	2.44	0.47
46:S2:1220:A:H4'	52:SF:145:ARG:HH22	1.80	0.47
46:S2:1612:G:H5'	64:SS:88:LYS:HB2	1.96	0.47
46:S2:1619:A:H5''	61:SP:44:ARG:HD3	1.96	0.47
56:SJ:125:HIS:O	56:SJ:129:LEU:HD12	2.15	0.47
64:SS:67:VAL:HG23	64:SS:71:MET:HE3	1.96	0.47
1:L5:1500:A:H5''	1:L5:1501:C:H5''	1.96	0.47
1:L5:1968:G:H2'	1:L5:1969:G:C4	2.50	0.47
1:L5:3911:C:H2'	1:L5:3912:U:H6	1.80	0.47
1:L5:4232:U:H1'	1:L5:4233:A:C2	2.50	0.47
1:L5:4584:A:H2'	1:L5:4585:U:O4'	2.15	0.47
8:LE:192:LYS:HG2	34:Lf:107:PRO:HA	1.96	0.47
9:LF:131:ASN:HA	9:LF:134:ARG:HB3	1.97	0.47
26:LX:155:ILE:H	26:LX:155:ILE:HD12	1.79	0.47
46:S2:149:A:N7	46:S2:169:U:C2	2.83	0.47
46:S2:639:C:H2'	46:S2:640:A:H8	1.79	0.47
46:S2:921:G:H5'	73:Sb:21:LYS:HZ1	1.78	0.47
46:S2:1128:C:H2'	46:S2:1129:G:C8	2.49	0.47
85:3f:163:VAL:HG22	89:3h:85:PRO:HD3	1.97	0.47
1:L5:1333:A:H2'	1:L5:1334:A:C8	2.50	0.47
1:L5:2277:C:H2'	1:L5:2278:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:2568:C:H2'	1:L5:2569:G:H8	1.79	0.47
1:L5:4188:U:H2'	1:L5:4189:U:C6	2.49	0.47
3:L8:47:C:H1'	3:L8:61:A:H2'	1.97	0.47
6:LC:137:VAL:HG21	6:LC:150:LEU:HD11	1.96	0.47
7:LD:73:MET:HA	7:LD:73:MET:HE3	1.97	0.47
11:LH:114:ILE:HB	11:LH:124:ARG:HB2	1.96	0.47
46:S2:95:G:H21	46:S2:474:G:H5'	1.79	0.47
46:S2:388:U:H2'	46:S2:389:A:C8	2.49	0.47
46:S2:1217:A:H2'	46:S2:1218:C:C6	2.49	0.47
46:S2:1396:A:N7	46:S2:1449:G:C6	2.82	0.47
53:SG:159:ARG:HB3	53:SG:171:THR:HB	1.96	0.47
1:L5:926:G:H2'	1:L5:927:G:H8	1.80	0.46
1:L5:1292:C:H2'	1:L5:1293:G:C4	2.50	0.46
1:L5:4088:C:H2'	1:L5:4089:G:C8	2.50	0.46
1:L5:4112:C:H5''	1:L5:4113:U:H5	1.79	0.46
1:L5:4716:C:H2'	1:L5:4717:A:C8	2.50	0.46
6:LC:318:PRO:HB3	6:LC:325:MET:HG2	1.97	0.46
17:LO:34:VAL:HG22	17:LO:103:LYS:HB2	1.96	0.46
46:S2:334:C:H5	53:SG:190:ARG:HH12	1.64	0.46
46:S2:1454:A:H5''	63:SR:3:ARG:HD3	1.96	0.46
46:S2:1560:U:O2	46:S2:1575:G:O6	2.33	0.46
46:S2:1671:G:H2'	46:S2:1672:U:H6	1.80	0.46
62:SQ:96:TYR:HA	62:SQ:100:VAL:HG22	1.96	0.46
63:SR:43:SER:HB3	63:SR:46:LEU:HD23	1.97	0.46
80:zu:62:C:H2'	80:zu:63:G:H8	1.80	0.46
84:3m:254:LYS:HE3	84:3m:254:LYS:HB3	1.64	0.46
1:L5:2475:G:H1	26:LX:51:THR:H	1.64	0.46
1:L5:3642:A:C4	38:Lj:3:LYS:HB3	2.49	0.46
1:L5:3661:G:H4'	1:L5:3662:A:H5'	1.96	0.46
1:L5:4954:G:H2'	1:L5:4955:A:C8	2.50	0.46
18:LP:37:LYS:HA	18:LP:114:ILE:HD11	1.97	0.46
31:Lc:17:ARG:H	31:Lc:17:ARG:HG2	1.57	0.46
46:S2:1391:C:H4'	75:Sd:55:LEU:HD21	1.97	0.46
47:SA:19:LEU:HG	47:SA:24:HIS:HD2	1.80	0.46
60:SO:101:GLY:HA3	60:SO:134:PRO:HD2	1.96	0.46
84:3m:136:ALA:HB1	84:3m:139:TYR:HD2	1.80	0.46
84:3m:228:PRO:HA	84:3m:231:PHE:HB2	1.97	0.46
88:3c:733:MET:HE1	88:3c:765:VAL:HG11	1.97	0.46
1:L5:161:G:H2'	1:L5:162:A:H8	1.80	0.46
1:L5:1094:G:O6	1:L5:1201:U:O4	2.33	0.46
1:L5:2411:C:H2'	1:L5:2412:A:C8	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:2744:A:H2'	1:L5:2745:A:C8	2.50	0.46
1:L5:4238:G:H2'	1:L5:4239:A:H8	1.80	0.46
1:L5:4697:U:H4'	41:Lm:104:HIS:CD2	2.51	0.46
3:L8:71:A:N6	3:L8:87:G:H21	2.07	0.46
6:LC:67:TRP:CD1	6:LC:73:VAL:HG21	2.50	0.46
12:LI:33:ILE:HB	12:LI:69:ARG:HH22	1.79	0.46
17:LO:148:LYS:H	17:LO:148:LYS:HG2	1.59	0.46
53:SG:67:VAL:HG21	53:SG:99:GLY:HA2	1.97	0.46
60:SO:125:LYS:HG3	72:Sa:58:VAL:HG23	1.97	0.46
64:SS:86:ARG:HE	64:SS:89:ASP:HA	1.80	0.46
92:3l:333:ILE:HD12	92:3l:380:MET:HE3	1.97	0.46
1:L5:1636:U:H5''	1:L5:1637:A:H5'	1.97	0.46
1:L5:1751:A:H2'	1:L5:1752:G:H8	1.80	0.46
1:L5:3607:U:H2'	1:L5:3608:A:C8	2.50	0.46
14:LL:55:ILE:HD11	14:LL:120:TYR:CE1	2.51	0.46
19:LQ:180:ARG:HH21	29:La:50:PRO:HB2	1.80	0.46
60:SO:63:LYS:HA	60:SO:63:LYS:HD2	1.72	0.46
65:ST:134:ILE:H	65:ST:134:ILE:HD12	1.79	0.46
70:SY:119:GLY:HA2	70:SY:124:ASN:HD21	1.79	0.46
84:3m:60:VAL:HA	84:3m:63:VAL:HG22	1.98	0.46
84:3m:165:LEU:HD22	84:3m:188:LEU:HD13	1.97	0.46
87:3e:118:ALA:HA	87:3e:123:PHE:HB2	1.97	0.46
92:3l:372:ALA:HA	92:3l:390:LEU:HD11	1.98	0.46
1:L5:1327:C:H2'	1:L5:1328:G:H8	1.79	0.46
1:L5:1918:U:O2	1:L5:2064:G:O6	2.33	0.46
1:L5:2079:G:H2'	1:L5:2080:U:C6	2.51	0.46
1:L5:4291:G:H5'	1:L5:4293:U:C6	2.51	0.46
1:L5:4336:A:H5''	1:L5:4337:C:H5'	1.97	0.46
6:LC:297:GLU:HA	6:LC:300:ARG:HH12	1.80	0.46
8:LE:150:LEU:HB3	8:LE:194:VAL:HG13	1.98	0.46
31:Lc:18:LEU:HD11	31:Lc:84:ALA:HB1	1.96	0.46
36:Lh:88:THR:HG22	36:Lh:91:MET:HE2	1.97	0.46
46:S2:151:C:H2'	46:S2:152:U:C6	2.51	0.46
46:S2:1521:C:N4	64:SS:137:LYS:HE3	2.31	0.46
51:SE:105:THR:HG21	51:SE:245:ARG:HA	1.97	0.46
63:SR:30:THR:O	63:SR:34:VAL:HG12	2.16	0.46
71:SZ:81:GLY:HA2	71:SZ:84:ALA:HB3	1.98	0.46
87:3e:179:MET:HE2	87:3e:179:MET:HB3	1.82	0.46
1:L5:1857:C:H2'	1:L5:1858:A:C8	2.51	0.46
1:L5:4507:A:H2'	1:L5:4508:C:C6	2.51	0.46
1:L5:5023:C:H3'	1:L5:5024:C:H4'	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:LA:61:VAL:O	4:LA:73:THR:HA	2.15	0.46
46:S2:115:U:H2'	46:S2:116:U:C6	2.51	0.46
46:S2:352:U:H2'	46:S2:353:C:C6	2.51	0.46
52:SF:67:PRO:HG2	52:SF:70:GLU:HB3	1.97	0.46
61:SP:38:SER:HB2	61:SP:41:GLN:HB3	1.98	0.46
84:3m:64:MET:HG3	84:3m:105:LEU:HD11	1.96	0.46
87:3e:263:THR:HG23	87:3e:331:ASP:HB2	1.98	0.46
1:L5:257:C:H2'	1:L5:258:G:C8	2.51	0.46
1:L5:4627:U:H4'	5:LB:373:LYS:HD2	1.98	0.46
1:L5:4935:C:H2'	1:L5:4936:G:C8	2.51	0.46
4:LA:246:LEU:HD23	4:LA:246:LEU:H	1.81	0.46
16:LN:6:TYR:CE1	37:Li:40:VAL:HG22	2.50	0.46
21:LS:55:LYS:HB2	21:LS:55:LYS:HE3	1.82	0.46
45:Lr:90:LEU:CD1	45:Lr:111:ILE:HG23	2.46	0.46
46:S2:64:A:H61	46:S2:82:G:H3'	1.80	0.46
46:S2:1259:A:H61	46:S2:1519:U:H5'	1.80	0.46
46:S2:1617:G:H22	46:S2:1620:A:H5''	1.80	0.46
46:S2:1737:G:O6	46:S2:1797:U:O4	2.34	0.46
1:L5:1089:G:H2'	1:L5:1090:G:C8	2.51	0.46
1:L5:1306:C:H2'	1:L5:1307:A:C8	2.41	0.46
1:L5:2274:C:H2'	1:L5:2275:G:C8	2.50	0.46
1:L5:3932:U:H2'	1:L5:3933:G:C8	2.46	0.46
5:LB:389:MET:HE2	5:LB:392:LEU:HD21	1.97	0.46
7:LD:223:PHE:HB2	7:LD:226:TYR:HB2	1.97	0.46
19:LQ:6:ARG:NH1	19:LQ:8:ASN:HD21	2.14	0.46
46:S2:996:A:H2'	46:S2:997:A:C8	2.51	0.46
50:SD:103:GLU:HA	50:SD:106:ARG:HG2	1.98	0.46
51:SE:155:LYS:HA	51:SE:155:LYS:HD3	1.70	0.46
53:SG:227:GLN:HA	53:SG:230:LYS:HE3	1.97	0.46
58:SL:69:ARG:O	58:SL:130:GLU:HB2	2.16	0.46
85:3f:323:PHE:HZ	89:3h:345:GLN:HA	1.81	0.46
91:3k:150:TYR:CE2	92:3l:523:ILE:HG12	2.51	0.46
92:3l:340:LEU:HB2	92:3l:367:MET:HE1	1.97	0.46
1:L5:1197:C:H2'	1:L5:1198:G:C8	2.50	0.46
1:L5:2352:U:H1'	6:LC:96:CYS:HA	1.98	0.46
22:LT:57:TYR:HE1	22:LT:78:LYS:HB2	1.81	0.46
29:La:101:ILE:HB	29:La:124:VAL:HG12	1.97	0.46
31:Lc:20:LEU:HD21	31:Lc:101:ASP:HB3	1.98	0.46
46:S2:901:G:H2'	46:S2:902:G:C8	2.51	0.46
46:S2:1628:C:H4'	64:SS:82:TRP:HZ3	1.81	0.46
88:3c:757:ILE:HG22	88:3c:762:ASN:HD21	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
88:3c:851:ALA:O	88:3c:855:LEU:HG	2.15	0.46
1:L5:10:A:H2'	1:L5:11:G:C8	2.49	0.46
1:L5:243:A:H5''	27:LY:3:PHE:HB2	1.97	0.46
1:L5:2413:U:H2'	1:L5:2414:G:H8	1.81	0.46
1:L5:3898:G:N3	5:LB:261:ARG:HA	2.31	0.46
1:L5:4629:U:H2'	1:L5:4630:G:H8	1.81	0.46
12:LI:174:THR:HG23	12:LI:176:PHE:H	1.81	0.46
47:SA:143:PRO:HB3	67:SV:32:ILE:HG12	1.98	0.46
65:ST:75:MET:O	65:ST:75:MET:HE3	2.15	0.46
69:SX:73:GLN:HE22	69:SX:78:GLY:HA2	1.81	0.46
79:sh:127:MET:HE2	79:sh:127:MET:HB2	1.83	0.46
88:3c:577:ALA:HB3	88:3c:615:GLN:HG3	1.98	0.46
1:L5:294:G:C8	29:La:61:TYR:HE2	2.34	0.45
1:L5:1697:G:H2'	1:L5:1698:C:H4'	1.96	0.45
1:L5:2274:C:H2'	1:L5:2275:G:H8	1.80	0.45
1:L5:2749:C:H2'	1:L5:2750:G:H8	1.81	0.45
4:LA:40:TYR:HA	4:LA:90:CYS:O	2.15	0.45
4:LA:133:TYR:HB3	4:LA:168:VAL:HG22	1.98	0.45
34:Lf:97:ILE:H	34:Lf:97:ILE:HD12	1.82	0.45
46:S2:600:G:H2'	46:S2:601:G:H8	1.79	0.45
46:S2:1103:C:H2'	46:S2:1104:G:C8	2.51	0.45
49:SC:110:MET:HB2	49:SC:125:LYS:HG2	1.98	0.45
66:SU:81:GLN:HE22	75:Sd:56:ASP:H	1.64	0.45
69:SX:124:LYS:HA	69:SX:129:SER:HA	1.97	0.45
83:zz:154:A:H61	83:zz:173:A:H1'	1.81	0.45
85:3f:319:VAL:HG13	85:3f:322:ASP:HB2	1.98	0.45
1:L5:1563:A:H2'	1:L5:1564:A:C8	2.51	0.45
1:L5:1738:A:H2'	1:L5:1739:G:H8	1.81	0.45
1:L5:4872:G:C8	15:LM:94:LYS:HD3	2.51	0.45
32:Ld:51:LYS:HE3	32:Ld:51:LYS:HB2	1.56	0.45
53:SG:3:LEU:O	53:SG:15:LEU:HA	2.17	0.45
62:SQ:32:ILE:HG22	62:SQ:39:LEU:HD23	1.97	0.45
62:SQ:130:LYS:HD2	62:SQ:135:PRO:HA	1.98	0.45
1:L5:676:C:H2'	1:L5:677:G:H8	1.81	0.45
1:L5:1327:C:H2'	1:L5:1328:G:C8	2.51	0.45
1:L5:1340:C:H2'	1:L5:1341:U:H6	1.82	0.45
1:L5:3921:U:H1'	1:L5:4543:G:H21	1.81	0.45
1:L5:4523:A:H5''	1:L5:4524:G:H5'	1.99	0.45
1:L5:5055:G:H2'	1:L5:5056:A:C8	2.50	0.45
8:LE:149:ILE:HD12	8:LE:270:TYR:HE2	1.81	0.45
28:LZ:4:PHE:HD2	31:Lc:67:ALA:HB2	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:Li:81:ILE:H	37:Li:81:ILE:HG13	1.63	0.45
46:S2:1523:C:H2'	46:S2:1524:G:C8	2.51	0.45
46:S2:1748:G:O6	46:S2:1786:U:O4	2.34	0.45
46:S2:1856:C:H2'	46:S2:1857:G:C8	2.52	0.45
51:SE:73:ASP:HA	51:SE:89:VAL:HG23	1.99	0.45
52:SF:66:CYS:HB2	52:SF:70:GLU:HG3	1.97	0.45
74:Sc:10:LYS:NZ	74:Sc:34:PHE:HA	2.31	0.45
87:3e:236:PHE:HE2	87:3e:253:ILE:HG13	1.81	0.45
1:L5:262:G:H2'	1:L5:263:G:C8	2.52	0.45
1:L5:2521:G:H2'	1:L5:2522:G:C8	2.52	0.45
3:L8:70:G:H22	3:L8:87:G:H1'	1.81	0.45
31:Lc:53:PRO:HG2	31:Lc:56:ARG:HD2	1.98	0.45
46:S2:1607:A:N6	46:S2:1632:G:H21	2.07	0.45
48:SB:52:THR:HG22	48:SB:58:ALA:H	1.81	0.45
51:SE:37:LYS:HE2	51:SE:37:LYS:HB2	1.74	0.45
53:SG:3:LEU:HD11	53:SG:111:LEU:HD23	1.98	0.45
65:ST:23:LYS:HE3	65:ST:54:TYR:CE2	2.51	0.45
78:Sg:195:LEU:HA	78:Sg:211:GLY:HA3	1.98	0.45
92:3l:559:LYS:HE3	92:3l:559:LYS:HB3	1.81	0.45
1:L5:2402:G:H21	35:Lg:13:TYR:HE2	1.63	0.45
1:L5:3896:C:H1'	5:LB:268:ARG:HH22	1.81	0.45
2:L7:59:G:H2'	2:L7:60:G:H8	1.81	0.45
28:LZ:77:TYR:CD1	31:Lc:39:ARG:HD3	2.51	0.45
35:Lg:85:LYS:HA	35:Lg:88:ARG:HH11	1.81	0.45
46:S2:520:A:H2'	46:S2:521:A:C8	2.51	0.45
46:S2:649:U:H2'	46:S2:650:A:C8	2.49	0.45
46:S2:1468:C:H2'	46:S2:1469:A:C8	2.51	0.45
52:SF:50:PRO:HG2	52:SF:90:VAL:HG12	1.98	0.45
61:SP:65:LYS:HA	61:SP:65:LYS:HD3	1.65	0.45
67:SV:74:LYS:HE2	67:SV:74:LYS:HB2	1.82	0.45
87:3e:25:PHE:HA	87:3e:28:VAL:HG12	1.98	0.45
89:3h:36:VAL:HG23	89:3h:168:ARG:HH12	1.80	0.45
92:3l:334:ARG:HA	92:3l:334:ARG:HD2	1.70	0.45
1:L5:755:C:H2'	1:L5:756:G:H8	1.82	0.45
1:L5:1669:A:H4'	1:L5:1685:G:N2	2.32	0.45
1:L5:3658:C:H2'	1:L5:3659:G:H8	1.82	0.45
2:L7:4:U:H2'	2:L7:5:A:H8	1.81	0.45
2:L7:15:C:H2'	2:L7:16:A:C8	2.52	0.45
4:LA:180:LEU:HD12	44:Lp:14:TYR:HE1	1.81	0.45
5:LB:222:VAL:HG13	5:LB:343:ARG:HD2	1.98	0.45
6:LC:211:TYR:CZ	6:LC:218:ILE:HD11	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:LR:15:LEU:HD11	20:LR:45:ILE:HD11	1.99	0.45
46:S2:878:G:N1	46:S2:908:A:H2	2.05	0.45
46:S2:1192:U:H2'	46:S2:1193:U:C6	2.51	0.45
46:S2:1683:C:H2'	46:S2:1684:C:H6	1.81	0.45
50:SD:177:LEU:HG	50:SD:179:GLN:H	1.82	0.45
53:SG:58:LYS:H	53:SG:58:LYS:HG2	1.57	0.45
55:SI:192:GLY:HA3	58:SL:18:GLN:HE22	1.82	0.45
81:zv:2:C:H2'	81:zv:3:U:C6	2.52	0.45
84:3m:335:SER:HA	85:3f:313:ASN:HB3	1.99	0.45
85:3f:339:TYR:HB2	92:3l:547:ILE:HG23	1.98	0.45
86:3a:230:LEU:HD22	86:3a:260:PHE:HE1	1.81	0.45
89:3h:129:VAL:HG12	89:3h:318:LEU:HD23	1.98	0.45
1:L5:1095:A:H2	1:L5:1200:G:C2	2.34	0.45
1:L5:2285:A:H2'	1:L5:2286:G:H8	1.82	0.45
1:L5:3607:U:H2'	1:L5:3608:A:H8	1.82	0.45
21:LS:15:ARG:HD2	21:LS:25:PRO:HG2	1.98	0.45
46:S2:222:U:H2'	46:S2:223:C:C6	2.52	0.45
46:S2:1755:C:C4	46:S2:1756:C:N4	2.85	0.45
57:SK:73:ASN:HA	57:SK:76:ILE:HB	1.98	0.45
69:SX:94:ILE:HG22	69:SX:125:VAL:HG21	1.99	0.45
86:3a:66:LEU:HD23	86:3a:66:LEU:HA	1.80	0.45
1:L5:1248:C:H2'	1:L5:1249:C:C6	2.52	0.45
1:L5:1571:G:H4'	20:LR:130:ASN:HD22	1.82	0.45
1:L5:1691:G:H5'	19:LQ:15:ARG:HG2	1.99	0.45
1:L5:1905:U:P	34:Lf:76:ARG:HH12	2.40	0.45
1:L5:4260:U:H2'	1:L5:4261:C:C6	2.52	0.45
1:L5:4526:U:H4'	5:LB:243:LYS:HE3	1.99	0.45
6:LC:152:LEU:HD23	6:LC:251:ILE:HG12	1.97	0.45
6:LC:326:LEU:HD22	6:LC:332:ALA:HB3	1.99	0.45
7:LD:178:LYS:HG2	7:LD:179:ARG:HH11	1.82	0.45
9:LF:142:TRP:CZ2	9:LF:235:ASN:HB3	2.52	0.45
12:LI:12:CYS:HB3	12:LI:128:ARG:HH12	1.81	0.45
18:LP:25:HIS:O	18:LP:29:THR:HG23	2.16	0.45
20:LR:175:GLU:HA	20:LR:178:GLN:NE2	2.31	0.45
38:Lj:12:ARG:H	38:Lj:12:ARG:HG2	1.64	0.45
46:S2:807:G:H2'	46:S2:808:A:C8	2.51	0.45
46:S2:979:C:H2'	46:S2:980:A:C8	2.52	0.45
46:S2:1232:U:H2'	46:S2:1233:G:C8	2.51	0.45
46:S2:1648:G:H22	46:S2:1674:G:H3'	1.82	0.45
49:SC:74:LYS:HB3	49:SC:269:PHE:HE2	1.82	0.45
50:SD:27:ARG:NH2	57:SK:62:PHE:H	2.14	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:SQ:33:LYS:O	62:SQ:69:ARG:HA	2.17	0.45
65:ST:14:PHE:HE2	65:ST:62:ARG:HD2	1.82	0.45
80:zy:66:C:H2'	80:zy:67:G:C8	2.51	0.45
85:3f:115:ARG:HH21	85:3f:174:ALA:HB1	1.82	0.45
87:3e:191:ARG:HA	87:3e:194:GLU:HG2	1.98	0.45
1:L5:1749:A:H2'	1:L5:1750:G:C8	2.52	0.45
2:L7:57:C:H2'	2:L7:58:A:H8	1.82	0.45
10:LG:136:LEU:HD11	10:LG:202:VAL:HB	1.97	0.45
26:LX:105:ASN:O	26:LX:109:ILE:HG13	2.17	0.45
46:S2:155:G:H2'	46:S2:156:G:C8	2.52	0.45
46:S2:615:C:H2'	46:S2:616:A:C8	2.52	0.45
46:S2:981:A:H2'	46:S2:982:G:C8	2.52	0.45
46:S2:1287:A:N1	46:S2:1313:A:H1'	2.32	0.45
56:SJ:144:ILE:HG22	56:SJ:146:SER:H	1.82	0.45
60:SO:99:ALA:H	60:SO:133:THR:HB	1.82	0.45
69:SX:67:ARG:HE	69:SX:115:ILE:HG21	1.82	0.45
70:SY:118:ARG:HG3	70:SY:120:THR:HG23	1.99	0.45
73:Sb:21:LYS:HD2	73:Sb:21:LYS:HA	1.70	0.45
89:3h:288:ARG:HH12	89:3h:297:PRO:HB3	1.82	0.45
1:L5:261:G:H2'	1:L5:262:G:C8	2.52	0.45
27:LY:34:LEU:HG	27:LY:106:ILE:HD11	1.99	0.45
46:S2:1653:U:H3	46:S2:1671:G:H1	1.64	0.45
46:S2:1805:G:H2'	46:S2:1806:A:C8	2.52	0.45
53:SG:58:LYS:HB2	53:SG:59:GLN:NE2	2.32	0.45
53:SG:63:MET:HB3	53:SG:98:ARG:HB3	1.99	0.45
63:SR:51:ALA:HA	63:SR:54:VAL:HG22	1.99	0.45
65:ST:11:GLN:HG3	65:ST:62:ARG:NH2	2.32	0.45
67:SV:32:ILE:HG22	67:SV:55:ILE:HB	1.99	0.45
78:Sg:205:SER:HB3	78:Sg:221:LEU:H	1.81	0.45
87:3e:372:VAL:HG21	92:3l:467:TYR:CZ	2.52	0.45
1:L5:228:C:H2'	1:L5:229:G:C8	2.52	0.44
1:L5:2060:G:H2'	1:L5:2061:U:C6	2.52	0.44
1:L5:2520:C:H2'	1:L5:2521:G:C8	2.52	0.44
1:L5:2634:C:H2'	1:L5:2635:U:H6	1.82	0.44
1:L5:4081:G:H2'	1:L5:4082:G:C8	2.52	0.44
1:L5:4174:U:H2'	1:L5:4175:G:C8	2.50	0.44
1:L5:4493:U:H2'	1:L5:4494:G:H8	1.82	0.44
5:LB:87:VAL:O	5:LB:107:ALA:HB2	2.16	0.44
9:LF:153:LEU:HD12	9:LF:153:LEU:HA	1.83	0.44
21:LS:51:LEU:HD21	22:LT:153:PRO:HA	1.99	0.44
36:Lh:112:ARG:HG2	36:Lh:113:LEU:HD23	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:Lr:89:THR:O	45:Lr:93:ILE:HG13	2.18	0.44
55:SI:83:TYR:CE1	55:SI:201:LYS:HG2	2.52	0.44
55:SI:98:LYS:HE2	55:SI:99:ASN:HB2	1.99	0.44
58:SL:4:ILE:HD12	58:SL:4:ILE:HA	1.87	0.44
59:SN:32:ASP:HA	59:SN:35:GLU:HG2	2.00	0.44
61:SP:20:VAL:HG12	61:SP:25:LEU:HG	1.99	0.44
74:Sc:44:ARG:CZ	74:Sc:45:ASN:H	2.30	0.44
80:zu:51:G:H2'	80:zu:52:G:H8	1.83	0.44
83:zz:213:C:H2'	83:zz:214:A:C8	2.52	0.44
85:3f:228:MET:HE3	85:3f:228:MET:O	2.17	0.44
91:3k:85:CYS:HA	91:3k:88:MET:HG2	2.00	0.44
91:3k:200:ASN:HD21	92:3l:538:ARG:HH22	1.65	0.44
1:L5:1955:G:H2'	1:L5:1956:A:C8	2.52	0.44
1:L5:2282:A:H4'	29:La:21:ARG:HB2	2.00	0.44
1:L5:2333:G:H5''	6:LC:195:LYS:HE2	1.98	0.44
3:L8:147:G:H2'	3:L8:148:A:H8	1.81	0.44
4:LA:248:GLY:HA3	46:S2:1069:U:H5''	1.99	0.44
19:LQ:95:VAL:HG23	19:LQ:116:ALA:HB2	1.99	0.44
46:S2:807:G:H2'	46:S2:808:A:H8	1.82	0.44
46:S2:1401:A:H2'	46:S2:1402:A:C8	2.51	0.44
48:SB:41:ILE:HB	48:SB:74:LEU:HA	1.99	0.44
50:SD:76:ARG:HG3	50:SD:77:PHE:HD1	1.83	0.44
55:SI:25:ARG:HD3	55:SI:25:ARG:HA	1.70	0.44
55:SI:65:PHE:HA	55:SI:187:GLY:O	2.18	0.44
69:SX:81:ILE:HD13	69:SX:120:PHE:CD1	2.51	0.44
86:3a:327:LEU:HD22	86:3a:394:LEU:HD13	1.98	0.44
89:3h:212:ASN:HA	89:3h:215:MET:HE2	1.97	0.44
92:3l:440:PHE:O	92:3l:444:LEU:HD22	2.16	0.44
1:L5:2765:A:H2'	1:L5:2766:A:H8	1.83	0.44
1:L5:3731:C:H2'	1:L5:3732:A:C8	2.52	0.44
1:L5:4761:G:H2'	1:L5:4762:A:C8	2.52	0.44
1:L5:4909:A:H8	5:LB:156:TYR:HE2	1.65	0.44
1:L5:5001:U:H4'	5:LB:317:LEU:HG	2.00	0.44
3:L8:9:A:H2'	3:L8:10:G:H8	1.82	0.44
5:LB:91:GLY:HA3	5:LB:153:MET:HE1	1.99	0.44
11:LH:92:MET:HE3	11:LH:179:ILE:HB	1.99	0.44
12:LI:62:SER:HB2	12:LI:93:PRO:HG3	1.99	0.44
17:LO:42:ASN:OD1	17:LO:135:PHE:HB2	2.17	0.44
32:Ld:23:ARG:HG3	32:Ld:121:ASN:HA	2.00	0.44
42:Ln:8:LYS:HE2	42:Ln:8:LYS:HB2	1.84	0.44
46:S2:77:A:N7	53:SG:179:LEU:HD22	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:442:C:H42	46:S2:449:A:N6	2.08	0.44
46:S2:652:U:H2'	46:S2:653:A:C8	2.52	0.44
46:S2:1521:C:H3'	64:SS:129:LEU:HD21	1.99	0.44
48:SB:125:VAL:O	48:SB:136:ARG:HA	2.17	0.44
72:Sa:44:ILE:HG12	72:Sa:67:LEU:HB3	1.99	0.44
84:3m:131:ALA:HA	84:3m:134:CYS:HB2	1.98	0.44
86:3a:523:LEU:HD12	89:3h:231:LEU:HB2	1.98	0.44
88:3c:419:PHE:HB3	88:3c:439:ARG:HH22	1.82	0.44
1:L5:1631:A:C6	4:LA:204:MET:HE1	2.53	0.44
1:L5:3893:C:H2'	1:L5:3894:A:H8	1.82	0.44
24:LV:26:ILE:HD13	24:LV:26:ILE:HA	1.79	0.44
28:LZ:57:MET:HG2	28:LZ:61:LYS:HG2	1.99	0.44
52:SF:85:LYS:HB3	52:SF:88:MET:HG2	1.98	0.44
56:SJ:54:ARG:O	56:SJ:58:ARG:HG2	2.16	0.44
57:SK:61:GLN:HB3	57:SK:68:TYR:HB2	1.99	0.44
1:L5:503:C:H4'	1:L5:504:G:H5''	1.99	0.44
1:L5:1308:C:H2'	1:L5:1309:C:C6	2.53	0.44
1:L5:1942:A:H2'	1:L5:1943:A:H8	1.83	0.44
1:L5:4743:G:H2'	1:L5:4744:A:H8	1.82	0.44
8:LE:153:LEU:HD11	8:LE:195:ILE:HG12	1.98	0.44
9:LF:50:ILE:HD13	9:LF:50:ILE:HA	1.84	0.44
10:LG:131:LYS:HD2	10:LG:131:LYS:HA	1.88	0.44
16:LN:170:LYS:HE3	16:LN:170:LYS:HB3	1.81	0.44
19:LQ:82:VAL:HG12	19:LQ:139:LEU:HB2	1.98	0.44
27:LY:88:GLU:HG3	27:LY:94:THR:HG22	1.99	0.44
37:Li:33:LEU:HD21	37:Li:38:LYS:HD3	2.00	0.44
45:Lr:18:ILE:HD11	45:Lr:20:ARG:HH11	1.81	0.44
46:S2:1225:U:H2'	46:S2:1226:G:H8	1.82	0.44
46:S2:1798:C:H2'	46:S2:1799:G:O4'	2.17	0.44
53:SG:217:MET:HA	53:SG:220:ALA:HB3	2.00	0.44
56:SJ:75:ASN:HB2	56:SJ:79:ARG:HH12	1.83	0.44
65:ST:7:LYS:HB2	65:ST:7:LYS:HE2	1.80	0.44
72:Sa:43:ASN:HA	72:Sa:66:LYS:HA	2.00	0.44
83:zz:248:U:H2'	83:zz:249:G:C8	2.52	0.44
86:3a:383:VAL:HG12	86:3a:387:VAL:HG23	2.00	0.44
1:L5:139:G:H2'	1:L5:140:G:H8	1.83	0.44
1:L5:493:G:C2	1:L5:660:A:H2	2.29	0.44
1:L5:926:G:H2'	1:L5:927:G:C8	2.53	0.44
1:L5:1302:U:H3'	1:L5:1303:A:C8	2.52	0.44
1:L5:1341:U:H2'	1:L5:1342:A:H8	1.83	0.44
1:L5:3883:U:H2'	1:L5:3884:U:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3893:C:H2'	1:L5:3894:A:C8	2.52	0.44
1:L5:4685:U:H2'	1:L5:4686:G:C8	2.52	0.44
6:LC:124:ILE:HD11	6:LC:235:LEU:HD12	2.00	0.44
9:LF:179:LEU:HD11	9:LF:207:PHE:CG	2.53	0.44
31:Lc:26:LYS:H	31:Lc:98:ASP:HB3	1.82	0.44
39:Lk:45:LEU:HD12	39:Lk:45:LEU:HA	1.86	0.44
44:Lp:28:LYS:HG3	44:Lp:29:ILE:HD13	2.00	0.44
49:SC:73:MET:HE2	49:SC:73:MET:HA	2.00	0.44
50:SD:123:LEU:O	50:SD:127:MET:HG2	2.18	0.44
55:SI:76:THR:HB	55:SI:104:ILE:HD11	1.99	0.44
56:SJ:37:LEU:HD12	56:SJ:43:VAL:HG22	1.99	0.44
65:ST:56:ARG:HD3	65:ST:56:ARG:HA	1.85	0.44
71:SZ:46:ASN:HD21	71:SZ:80:ARG:HA	1.82	0.44
78:Sg:79:LEU:HD11	78:Sg:87:LEU:HD13	1.99	0.44
80:zy:8:U:H5'	80:zy:48:C:H5'	2.00	0.44
84:3m:68:VAL:HG21	84:3m:105:LEU:HD22	2.00	0.44
85:3f:91:VAL:HG21	85:3f:238:LYS:HE2	2.00	0.44
85:3f:124:VAL:HG13	85:3f:129:VAL:HG12	1.98	0.44
88:3c:627:LYS:HG2	88:3c:693:LEU:HD11	2.00	0.44
88:3c:751:THR:O	88:3c:755:PHE:HB2	2.18	0.44
88:3c:858:GLN:HE21	89:3h:247:MET:HE1	1.81	0.44
1:L5:4089:G:H2'	1:L5:4090:G:H8	1.83	0.44
1:L5:4563:U:H2'	1:L5:4564:A:C8	2.49	0.44
2:L7:4:U:H2'	2:L7:5:A:C8	2.53	0.44
9:LF:236:ARG:HH11	9:LF:243:LEU:HD22	1.82	0.44
32:Ld:50:ARG:HE	32:Ld:50:ARG:HB2	1.57	0.44
36:Lh:88:THR:HG22	36:Lh:91:MET:HG2	2.00	0.44
37:Li:72:PHE:HE1	37:Li:76:ARG:HH21	1.65	0.44
46:S2:153:G:H21	53:SG:13:GLN:HE22	1.65	0.44
46:S2:1593:C:H2'	46:S2:1594:A:C8	2.53	0.44
55:SI:65:PHE:HE2	55:SI:78:ILE:HD11	1.82	0.44
59:SN:119:GLU:HA	59:SN:122:ILE:HD12	1.99	0.44
68:SW:43:LYS:HD2	68:SW:43:LYS:HA	1.84	0.44
87:3e:409:LYS:HD2	87:3e:409:LYS:HA	1.73	0.44
88:3c:483:ILE:HA	88:3c:486:VAL:HG22	1.99	0.44
89:3h:120:TYR:HE1	89:3h:152:TYR:HB2	1.83	0.44
92:3l:357:TYR:HA	92:3l:360:ILE:HB	1.98	0.44
1:L5:679:C:H2'	1:L5:680:G:C8	2.53	0.44
1:L5:2029:A:H2'	1:L5:2030:A:C8	2.53	0.44
35:Lg:19:LYS:HD3	35:Lg:19:LYS:HA	1.60	0.44
46:S2:560:A:H5'	56:SJ:174:LYS:HE3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:SD:77:PHE:HB3	50:SD:79:PHE:CE2	2.53	0.44
51:SE:195:ILE:HA	51:SE:210:VAL:HG23	2.00	0.44
66:SU:106:ILE:HD12	66:SU:106:ILE:HA	1.85	0.44
71:SZ:48:VAL:HG22	71:SZ:49:LEU:H	1.83	0.44
85:3f:343:LEU:HD23	85:3f:343:LEU:HA	1.84	0.44
1:L5:181:C:H2'	1:L5:182:G:C8	2.53	0.44
1:L5:432:U:H4'	1:L5:433:A:H5''	2.00	0.44
1:L5:1755:C:H2'	1:L5:1756:U:C6	2.53	0.44
1:L5:3612:C:H1'	1:L5:5016:A:C8	2.52	0.44
1:L5:3660:C:H2'	1:L5:3682:A:H61	1.82	0.44
1:L5:3726:A:H2'	1:L5:3727:A:C8	2.53	0.44
1:L5:4218:U:H4'	30:Lb:7:HIS:NE2	2.32	0.44
1:L5:4881:U:OP2	15:LM:117:LYS:HD2	2.18	0.44
3:L8:90:C:H2'	3:L8:91:A:C8	2.53	0.44
4:LA:246:LEU:HG	4:LA:247:ARG:H	1.82	0.44
5:LB:390:GLY:HA3	5:LB:391:PRO:HD3	1.88	0.44
6:LC:28:PHE:HA	6:LC:129:ALA:HA	2.00	0.44
6:LC:124:ILE:HD11	6:LC:235:LEU:HB2	1.99	0.44
15:LM:37:LEU:HD12	15:LM:37:LEU:HA	1.82	0.44
17:LO:183:LYS:HA	17:LO:183:LYS:HD2	1.86	0.44
33:Le:18:LYS:HE3	33:Le:18:LYS:HB2	1.74	0.44
46:S2:869:A:C4	46:S2:915:G:H1'	2.52	0.44
46:S2:1053:C:H2'	46:S2:1054:G:H8	1.82	0.44
46:S2:1201:U:H2'	46:S2:1202:U:C6	2.52	0.44
46:S2:1229:G:H21	65:ST:87:VAL:HG21	1.82	0.44
46:S2:1274:G:H3'	46:S2:1275:G:H5'	2.00	0.44
46:S2:1336:C:H4'	75:Sd:44:ARG:HH12	1.82	0.44
46:S2:1365:G:H2'	46:S2:1366:G:C8	2.53	0.44
46:S2:1392:U:H2'	46:S2:1393:G:C8	2.53	0.44
68:SW:10:ALA:O	68:SW:14:ILE:HG22	2.18	0.44
69:SX:41:PHE:HB3	69:SX:44:ALA:HB3	2.00	0.44
77:Sf:53:ALA:HB3	77:Sf:85:LEU:HD12	1.99	0.44
83:zz:317:C:H2'	83:zz:318:G:H8	1.82	0.44
84:3m:337:SER:HA	85:3f:309:MET:HE1	2.00	0.44
86:3a:43:TRP:CD1	86:3a:78:CYS:HA	2.53	0.44
1:L5:254:G:H2'	1:L5:255:C:O4'	2.17	0.43
1:L5:372:A:N3	1:L5:1531:U:H1'	2.33	0.43
1:L5:923:C:H2'	1:L5:925:C:C5	2.53	0.43
1:L5:2749:C:H2'	1:L5:2750:G:C8	2.53	0.43
1:L5:4933:C:H2'	1:L5:4934:A:C8	2.53	0.43
1:L5:5057:C:H2'	1:L5:5058:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:LS:9:GLU:OE1	21:LS:67:VAL:HG22	2.17	0.43
46:S2:828:G:H5''	51:SE:22:LYS:HE3	1.99	0.43
53:SG:35:GLU:HA	53:SG:50:VAL:O	2.18	0.43
86:3a:55:LEU:HD13	86:3a:93:TYR:HB2	1.99	0.43
91:3k:170:LEU:HG	91:3k:174:MET:HE2	2.00	0.43
92:3l:330:GLN:HG3	92:3l:501:VAL:HG23	1.99	0.43
1:L5:452:A:H1'	1:L5:453:G:N2	2.34	0.43
1:L5:1197:C:H2'	1:L5:1198:G:H8	1.83	0.43
1:L5:2386:U:H2'	1:L5:2387:G:C8	2.51	0.43
1:L5:4262:C:H2'	1:L5:4263:C:H6	1.83	0.43
4:LA:180:LEU:HD21	44:Lp:22:LEU:HD12	1.99	0.43
5:LB:238:LYS:HD3	5:LB:238:LYS:HA	1.75	0.43
9:LF:96:ARG:HA	9:LF:223:LYS:HZ3	1.82	0.43
9:LF:113:ARG:HG2	9:LF:210:PRO:HG3	2.00	0.43
9:LF:144:TYR:CE2	9:LF:237:GLU:HB2	2.54	0.43
46:S2:212:C:H2'	46:S2:213:G:H8	1.83	0.43
46:S2:654:A:C8	46:S2:655:A:H2'	2.53	0.43
46:S2:675:U:H2'	46:S2:676:C:H6	1.83	0.43
46:S2:1302:G:H21	79:sh:90:ARG:HG2	1.83	0.43
46:S2:1410:C:H2'	46:S2:1411:G:C8	2.53	0.43
46:S2:1670:C:H2'	46:S2:1671:G:C8	2.53	0.43
60:SO:124:MET:HA	60:SO:124:MET:HE2	2.00	0.43
66:SU:66:ARG:HA	66:SU:66:ARG:HD2	1.87	0.43
68:SW:42:MET:HE2	68:SW:42:MET:HA	1.99	0.43
75:Sd:36:LEU:HD23	75:Sd:38:MET:H	1.83	0.43
92:3l:183:LEU:HD12	92:3l:183:LEU:HA	1.85	0.43
1:L5:677:G:H2'	1:L5:678:C:H6	1.83	0.43
1:L5:1522:G:H2'	1:L5:1653:A:H61	1.83	0.43
1:L5:1812:C:H2'	1:L5:1813:U:C6	2.53	0.43
1:L5:1846:G:H2'	1:L5:1847:C:C6	2.53	0.43
1:L5:2264:C:H5'	45:Lr:112:ARG:HH21	1.83	0.43
1:L5:3933:G:H2'	1:L5:3934:G:H8	1.84	0.43
1:L5:4991:U:H2'	1:L5:4992:G:C8	2.53	0.43
6:LC:71:ARG:HB2	6:LC:73:VAL:HG13	1.99	0.43
6:LC:138:MET:HG2	6:LC:144:ILE:HD11	2.00	0.43
8:LE:180:VAL:HG21	8:LE:258:LEU:HD11	2.00	0.43
10:LG:191:GLY:HA3	10:LG:198:THR:HA	2.00	0.43
22:LT:84:ILE:HD11	30:Lb:21:ILE:HD11	2.01	0.43
46:S2:959:G:H2'	46:S2:960:U:C6	2.53	0.43
46:S2:1136:U:H2'	46:S2:1137:U:C6	2.53	0.43
46:S2:1244:U:H2'	46:S2:1245:G:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1244:U:H2'	46:S2:1245:G:C8	2.53	0.43
46:S2:1776:G:H2'	46:S2:1777:G:C8	2.53	0.43
47:SA:10:MET:HE2	47:SA:10:MET:HA	2.00	0.43
47:SA:36:GLN:H	47:SA:36:GLN:HG3	1.70	0.43
53:SG:98:ARG:HH11	53:SG:99:GLY:H	1.66	0.43
57:SK:2:LEU:HD12	57:SK:2:LEU:HA	1.73	0.43
83:zz:130:C:H2'	83:zz:131:G:H8	1.83	0.43
84:3m:354:LEU:HD23	85:3f:283:LEU:HD23	2.00	0.43
87:3e:21:PRO:HB2	87:3e:323:PHE:HZ	1.84	0.43
88:3c:639:SER:HB2	88:3c:641:ARG:HH21	1.84	0.43
92:3l:122:VAL:HG12	92:3l:125:ASP:H	1.83	0.43
1:L5:1739:G:H2'	1:L5:1740:C:C6	2.53	0.43
1:L5:2413:U:H2'	1:L5:2414:G:C8	2.53	0.43
1:L5:2611:A:H2'	1:L5:2612:G:C8	2.54	0.43
1:L5:4246:G:H2'	1:L5:4247:G:C8	2.50	0.43
11:LH:16:VAL:HG11	11:LH:81:ILE:HD11	1.98	0.43
20:LR:99:MET:HE1	20:LR:127:VAL:HG12	2.00	0.43
24:LV:82:ILE:HG23	24:LV:121:VAL:HG13	2.01	0.43
37:Li:70:LEU:HG	37:Li:87:ARG:HH22	1.84	0.43
40:Ll:16:LYS:HE3	40:Ll:16:LYS:HB3	1.84	0.43
46:S2:429:C:H5''	51:SE:10:LYS:HG3	2.01	0.43
46:S2:1846:G:H2'	46:S2:1847:G:H8	1.83	0.43
48:SB:124:HIS:HB3	48:SB:138:PHE:HD1	1.83	0.43
49:SC:193:VAL:HG21	49:SC:240:THR:HG22	2.00	0.43
52:SF:96:ALA:HA	52:SF:99:ILE:HD12	2.00	0.43
76:Se:94:LYS:HA	76:Se:94:LYS:HD3	1.75	0.43
77:Sf:18:LEU:H	77:Sf:18:LEU:HD12	1.84	0.43
86:3a:283:PHE:HE1	86:3a:288:ASN:HB2	1.84	0.43
92:3l:111:PRO:HA	92:3l:139:HIS:HE1	1.84	0.43
92:3l:184:TRP:HA	92:3l:272:PHE:CE2	2.54	0.43
1:L5:2295:C:H2'	1:L5:2296:G:C8	2.51	0.43
1:L5:3599:A:H2'	1:L5:3600:G:C8	2.52	0.43
25:LW:20:ARG:HD3	25:LW:30:GLN:HB3	2.01	0.43
27:LY:49:ILE:HG12	27:LY:80:ILE:HD13	2.00	0.43
46:S2:806:U:H2'	46:S2:807:G:H8	1.84	0.43
46:S2:921:G:C2	73:Sb:22:LYS:HG2	2.54	0.43
46:S2:1393:G:H2'	46:S2:1394:G:C8	2.53	0.43
46:S2:1805:G:H2'	46:S2:1806:A:H8	1.84	0.43
52:SF:77:MET:HA	52:SF:82:ASN:HD21	1.84	0.43
55:SI:66:SER:H	55:SI:188:TYR:HA	1.83	0.43
55:SI:90:LEU:HA	55:SI:93:THR:HG22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:SL:104:LYS:HE2	69:SX:8:ARG:NH1	2.32	0.43
65:ST:60:THR:HG22	65:ST:75:MET:SD	2.58	0.43
66:SU:36:CYS:O	66:SU:40:ILE:HG12	2.19	0.43
84:3m:42:LEU:HD21	84:3m:71:LEU:HD21	1.99	0.43
1:L5:480:C:H2'	1:L5:481:G:H8	1.83	0.43
1:L5:678:C:H2'	1:L5:679:C:H6	1.82	0.43
1:L5:2624:G:H2'	1:L5:2625:U:H6	1.83	0.43
1:L5:3896:C:H2'	1:L5:3897:G:C4	2.54	0.43
1:L5:4992:G:H2'	1:L5:4993:G:C8	2.53	0.43
11:LH:24:THR:HA	11:LH:37:ASP:HA	1.99	0.43
20:LR:25:ASP:HA	20:LR:26:PRO:HD3	1.83	0.43
38:Lj:54:LYS:O	38:Lj:58:THR:HB	2.18	0.43
46:S2:454:U:H2'	46:S2:455:A:C8	2.54	0.43
46:S2:582:U:H3	46:S2:584:A:H62	1.64	0.43
46:S2:806:U:H2'	46:S2:807:G:C8	2.53	0.43
46:S2:1202:U:H2'	46:S2:1203:G:H8	1.83	0.43
46:S2:1670:C:H2'	46:S2:1671:G:H8	1.83	0.43
78:Sg:162:ASN:HA	78:Sg:163:PRO:HD3	1.86	0.43
84:3m:120:ARG:HD2	84:3m:120:ARG:HA	1.79	0.43
86:3a:35:MET:HA	86:3a:35:MET:HE2	2.00	0.43
88:3c:730:PRO:HB3	88:3c:735:GLU:HB3	1.99	0.43
92:3l:168:LEU:HD13	92:3l:233:SER:HB2	2.00	0.43
92:3l:553:LEU:HD23	92:3l:553:LEU:HA	1.89	0.43
1:L5:4186:A:H2'	1:L5:4187:G:C8	2.53	0.43
7:LD:27:LYS:HE2	13:LJ:147:ARG:HD2	2.01	0.43
7:LD:117:LYS:HB2	7:LD:117:LYS:HE2	1.61	0.43
25:LW:56:ARG:HA	25:LW:56:ARG:HD2	1.88	0.43
35:Lg:11:LEU:HD23	35:Lg:13:TYR:H	1.83	0.43
46:S2:89:C:H2'	46:S2:90:G:C8	2.54	0.43
51:SE:46:ILE:HD12	51:SE:46:ILE:HA	1.85	0.43
58:SL:55:TYR:CE1	58:SL:116:CYS:HB3	2.53	0.43
60:SO:135:ILE:HD12	60:SO:135:ILE:HA	1.94	0.43
64:SS:127:TRP:HB3	64:SS:129:LEU:HD12	2.00	0.43
65:ST:134:ILE:O	65:ST:138:VAL:HG12	2.18	0.43
68:SW:37:PHE:CE1	68:SW:103:VAL:HG11	2.51	0.43
87:3e:169:LEU:HD12	87:3e:169:LEU:HA	1.86	0.43
88:3c:439:ARG:HH11	88:3c:440:VAL:H	1.67	0.43
88:3c:863:LEU:O	88:3c:867:VAL:HG22	2.19	0.43
1:L5:162:A:H2'	1:L5:163:A:H8	1.84	0.43
1:L5:651:C:H2'	1:L5:652:G:C8	2.54	0.43
1:L5:1326:A:H2'	1:L5:1327:C:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:2277:C:H2'	1:L5:2278:G:H8	1.84	0.43
1:L5:2370:A:C2	32:Ld:77:ILE:HD12	2.54	0.43
1:L5:2448:G:H2'	1:L5:2449:A:C8	2.53	0.43
1:L5:2610:G:H2'	1:L5:2611:A:C8	2.54	0.43
1:L5:4675:U:H2'	1:L5:4676:G:C8	2.54	0.43
3:L8:27:U:H2'	3:L8:28:C:C6	2.53	0.43
9:LF:213:LEU:HD13	9:LF:247:MET:HB3	2.01	0.43
10:LG:222:ILE:H	10:LG:222:ILE:HG12	1.68	0.43
16:LN:57:GLN:HB3	16:LN:139:HIS:CD2	2.53	0.43
35:Lg:78:TYR:HB3	35:Lg:82:MET:HB2	2.01	0.43
40:Ll:27:ILE:HG13	40:Ll:30:LYS:HE2	2.01	0.43
45:Lr:114:ALA:HA	45:Lr:117:ILE:HG22	1.99	0.43
46:S2:67:C:C4	53:SG:170:ARG:HG2	2.54	0.43
46:S2:1221:G:H2'	46:S2:1222:G:C8	2.53	0.43
46:S2:1304:U:H5'	79:sh:89:LYS:HA	2.00	0.43
52:SF:192:LYS:HA	52:SF:192:LYS:HD2	1.72	0.43
53:SG:64:LYS:NZ	53:SG:81:HIS:HB2	2.33	0.43
59:SN:117:LEU:HD23	59:SN:117:LEU:HA	1.85	0.43
60:SO:27:VAL:HG22	60:SO:91:THR:HG22	2.00	0.43
80:zy:23:A:H3'	80:zy:24:U:H6	1.82	0.43
83:zz:256:G:H2'	83:zz:257:A:C8	2.53	0.43
1:L5:1339:U:H2'	1:L5:1340:C:C6	2.54	0.43
1:L5:1730:U:H2'	1:L5:1731:C:C6	2.54	0.43
1:L5:2101:C:H2'	1:L5:2102:G:H2'	2.00	0.43
1:L5:4458:C:H2'	1:L5:4459:U:C6	2.54	0.43
1:L5:4466:C:H2'	1:L5:4467:A:H8	1.84	0.43
26:LX:39:LYS:HE2	26:LX:39:LYS:HB2	1.77	0.43
33:Le:44:ARG:CZ	33:Le:52:GLN:HE22	2.32	0.43
40:Ll:12:PHE:O	40:Ll:16:LYS:HG2	2.19	0.43
46:S2:801:U:H2'	46:S2:802:A:H8	1.83	0.43
46:S2:946:U:H2'	46:S2:947:G:C8	2.54	0.43
46:S2:1370:A:H2'	46:S2:1372:U:H5'	2.01	0.43
49:SC:209:VAL:HG23	49:SC:210:PRO:HD3	2.01	0.43
50:SD:163:PRO:O	50:SD:167:TYR:HB2	2.19	0.43
50:SD:168:VAL:HA	50:SD:189:MET:HA	2.00	0.43
53:SG:74:ARG:HA	53:SG:96:SER:HA	2.00	0.43
57:SK:16:PHE:O	57:SK:91:PRO:HB3	2.19	0.43
86:3a:338:ILE:O	86:3a:342:LEU:CB	2.67	0.43
87:3e:289:LYS:HD2	87:3e:289:LYS:HA	1.73	0.43
1:L5:133:C:H41	36:Lh:74:LYS:HD2	1.84	0.43
1:L5:133:C:H5	36:Lh:74:LYS:HE2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:742:G:H2'	1:L5:743:G:C8	2.54	0.43
1:L5:1683:U:H2'	1:L5:1684:A:H8	1.84	0.43
1:L5:2385:U:H2'	1:L5:2386:U:C6	2.53	0.43
1:L5:4460:U:H2'	1:L5:4461:C:H6	1.84	0.43
1:L5:4565:C:H2'	1:L5:4566:U:H6	1.84	0.43
6:LC:73:VAL:HG23	6:LC:75:ARG:H	1.84	0.43
6:LC:130:ALA:HB1	6:LC:136:LEU:HD22	2.01	0.43
8:LE:251:LYS:HE2	8:LE:251:LYS:HB3	1.83	0.43
41:Lm:114:LYS:HE3	41:Lm:114:LYS:HB2	1.88	0.43
46:S2:909:G:H2'	46:S2:910:G:C8	2.54	0.43
47:SA:33:GLN:HB2	47:SA:154:LEU:HD23	2.01	0.43
56:SJ:136:ARG:HB2	56:SJ:160:SER:HA	2.01	0.43
73:Sb:70:LYS:H	73:Sb:70:LYS:HG2	1.60	0.43
74:Sc:10:LYS:HZ1	74:Sc:34:PHE:HA	1.83	0.43
78:Sg:248:LEU:O	78:Sg:258:ILE:HA	2.19	0.43
84:3m:249:LEU:HD22	84:3m:277:MET:HE2	2.00	0.43
89:3h:194:PHE:HA	89:3h:197:MET:HE1	2.00	0.43
92:3l:366:GLN:O	92:3l:370:LEU:HG	2.19	0.43
1:L5:25:A:H2'	1:L5:26:C:H6	1.83	0.42
1:L5:1195:G:H2'	1:L5:1196:G:C8	2.54	0.42
1:L5:1947:U:H2'	41:Lm:109:ASN:ND2	2.33	0.42
1:L5:4733:C:H1'	1:L5:4734:A:H2'	2.00	0.42
3:L8:148:A:H2'	3:L8:149:G:C8	2.55	0.42
6:LC:209:ILE:HG23	6:LC:229:LEU:HD13	1.99	0.42
7:LD:68:ARG:HA	7:LD:68:ARG:HD2	1.75	0.42
14:LL:87:HIS:HB3	14:LL:90:VAL:HG12	2.00	0.42
17:LO:61:ARG:HA	17:LO:70:PRO:HD2	2.01	0.42
17:LO:99:LEU:HD12	17:LO:99:LEU:HA	1.82	0.42
19:LQ:178:ARG:H	29:La:51:GLY:HA2	1.84	0.42
22:LT:87:LYS:HB3	22:LT:87:LYS:HE3	1.84	0.42
28:LZ:52:LYS:HA	28:LZ:52:LYS:HD3	1.84	0.42
28:LZ:89:ILE:HD11	28:LZ:117:LYS:HB3	2.01	0.42
44:Lp:50:ARG:HH21	44:Lp:56:HIS:CG	2.36	0.42
46:S2:677:G:H21	46:S2:1028:A:N6	2.03	0.42
46:S2:1606:G:H1'	46:S2:1632:G:H22	1.83	0.42
49:SC:155:ILE:O	49:SC:159:LYS:HG2	2.19	0.42
68:SW:53:ILE:HD11	68:SW:62:VAL:HG23	2.01	0.42
84:3m:183:LYS:HA	84:3m:183:LYS:HD3	1.82	0.42
86:3a:230:LEU:HB2	86:3a:271:LEU:HD21	2.01	0.42
86:3a:539:PRO:HG2	86:3a:542:ILE:HB	2.00	0.42
89:3h:219:GLU:HA	89:3h:222:SER:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
92:3l:467:TYR:HB2	92:3l:530:ILE:HD11	2.01	0.42
1:L5:147:A:H1'	16:LN:57:GLN:HE22	1.84	0.42
1:L5:150:U:H3	10:LG:163:PRO:HD2	1.84	0.42
1:L5:1870:C:H2'	1:L5:1871:A:H8	1.84	0.42
1:L5:2777:G:H5''	1:L5:2778:G:H5'	2.01	0.42
5:LB:5:LYS:HE2	5:LB:5:LYS:HB3	1.85	0.42
8:LE:257:ILE:HD13	8:LE:257:ILE:HA	1.84	0.42
9:LF:105:VAL:HG23	9:LF:136:VAL:HG23	2.01	0.42
10:LG:70:LEU:O	10:LG:74:LEU:HD12	2.19	0.42
14:LL:65:ARG:HG3	29:La:69:PHE:CD1	2.53	0.42
14:LL:182:LEU:HD21	29:La:128:PHE:HD1	1.84	0.42
21:LS:104:GLY:O	21:LS:108:GLN:HG2	2.19	0.42
23:LU:21:PHE:HB2	23:LU:72:VAL:HG13	2.00	0.42
31:Lc:38:ILE:HG21	31:Lc:63:TYR:HB3	2.00	0.42
33:Le:20:PHE:HZ	33:Le:60:TYR:CE2	2.36	0.42
46:S2:432:G:H2'	46:S2:433:A:H8	1.83	0.42
46:S2:1279:C:H2'	46:S2:1280:G:C8	2.54	0.42
46:S2:1405:A:H2'	46:S2:1406:G:C8	2.54	0.42
51:SE:64:ILE:HD13	70:SY:18:LEU:HD13	2.01	0.42
51:SE:126:VAL:HG23	51:SE:139:LEU:HG	2.01	0.42
52:SF:89:THR:O	52:SF:93:VAL:HG22	2.18	0.42
55:SI:106:SER:HB2	55:SI:166:PHE:CE1	2.54	0.42
61:SP:105:VAL:HG11	61:SP:119:PHE:HD2	1.84	0.42
78:Sg:230:LEU:HB3	78:Sg:259:TRP:HH2	1.84	0.42
85:3f:108:ARG:NH1	89:3h:110:VAL:HB	2.34	0.42
88:3c:730:PRO:HG2	88:3c:736:HIS:CE1	2.54	0.42
1:L5:2335:C:H2'	1:L5:2336:G:H8	1.85	0.42
1:L5:2758:G:H2'	1:L5:2759:G:C8	2.54	0.42
1:L5:3667:C:H4'	4:LA:8:GLN:HA	2.00	0.42
5:LB:356:LYS:HE2	5:LB:356:LYS:HB3	1.82	0.42
16:LN:22:LEU:HA	16:LN:22:LEU:HD13	1.80	0.42
19:LQ:178:ARG:N	29:La:51:GLY:HA2	2.33	0.42
28:LZ:100:VAL:HG23	28:LZ:106:LEU:HD23	2.02	0.42
43:Lo:93:LEU:HD12	43:Lo:93:LEU:HA	1.81	0.42
46:S2:457:C:H2'	46:S2:458:A:H8	1.84	0.42
46:S2:533:A:H2'	46:S2:534:G:C8	2.54	0.42
46:S2:1430:C:H2'	46:S2:1431:G:H8	1.83	0.42
47:SA:46:ILE:HD12	47:SA:46:ILE:HA	1.89	0.42
47:SA:53:ARG:HB3	67:SV:83:PHE:CE1	2.54	0.42
47:SA:146:ALA:HB2	47:SA:157:VAL:HG21	2.02	0.42
49:SC:166:ARG:HB2	49:SC:248:TYR:CE1	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:SO:86:LYS:HD2	60:SO:86:LYS:HA	1.78	0.42
61:SP:30:TYR:HD2	61:SP:45:LEU:HD12	1.85	0.42
88:3c:502:ILE:HA	88:3c:505:LEU:HG	2.02	0.42
1:L5:161:G:H2'	1:L5:162:A:C8	2.54	0.42
1:L5:1751:A:H2'	1:L5:1752:G:C8	2.55	0.42
1:L5:2535:G:N2	1:L5:2640:G:H22	2.16	0.42
1:L5:4238:G:H2'	1:L5:4239:A:C8	2.54	0.42
28:LZ:109:LYS:HE3	28:LZ:109:LYS:HB2	1.89	0.42
35:Lg:86:CYS:O	35:Lg:90:ARG:HG2	2.20	0.42
46:S2:1858:G:H2'	46:S2:1859:A:C8	2.54	0.42
56:SJ:148:ILE:HD13	56:SJ:148:ILE:HA	1.89	0.42
57:SK:65:ARG:HH12	75:Sd:25:SER:HB3	1.84	0.42
64:SS:60:THR:O	64:SS:64:VAL:HG22	2.20	0.42
67:SV:81:LYS:HE3	67:SV:81:LYS:HB3	1.82	0.42
68:SW:69:LEU:HD11	68:SW:72:CYS:HB3	2.00	0.42
86:3a:153:LEU:HD12	86:3a:153:LEU:HA	1.88	0.42
86:3a:185:CYS:O	86:3a:189:THR:HA	2.20	0.42
86:3a:266:PRO:HA	86:3a:267:PRO:HD3	1.95	0.42
89:3h:231:LEU:HD23	89:3h:231:LEU:H	1.84	0.42
92:3l:147:GLY:HA3	92:3l:148:PRO:HD3	1.90	0.42
1:L5:272:U:H2'	1:L5:273:U:C6	2.54	0.42
1:L5:2062:C:H4'	21:LS:4:SER:HB3	2.00	0.42
1:L5:2079:G:H2'	1:L5:2080:U:H6	1.84	0.42
1:L5:3927:U:H2'	1:L5:3928:A:H8	1.84	0.42
3:L8:7:U:H2'	3:L8:8:U:C6	2.54	0.42
3:L8:67:U:H2'	3:L8:68:G:C8	2.54	0.42
5:LB:165:HIS:HA	5:LB:179:HIS:O	2.19	0.42
12:LI:12:CYS:HB3	12:LI:128:ARG:NH1	2.35	0.42
12:LI:201:PRO:HB2	12:LI:203:HIS:CD2	2.55	0.42
13:LJ:94:LEU:O	13:LJ:174:ILE:HA	2.19	0.42
15:LM:110:PHE:CZ	15:LM:114:LYS:HE3	2.55	0.42
16:LN:26:ARG:HB3	16:LN:30:TYR:HE2	1.84	0.42
18:LP:33:ALA:HA	18:LP:36:ILE:HG22	2.00	0.42
21:LS:41:LYS:HD2	21:LS:61:ILE:HD13	2.02	0.42
22:LT:111:GLU:HA	22:LT:114:GLN:HE21	1.84	0.42
26:LX:115:LYS:HE3	26:LX:115:LYS:HB2	1.86	0.42
28:LZ:100:VAL:HG22	28:LZ:107:LYS:HA	2.02	0.42
39:Lk:36:VAL:HG12	39:Lk:43:TYR:HB2	2.01	0.42
46:S2:616:A:H62	46:S2:625:G:N2	2.15	0.42
46:S2:1536:G:H2'	46:S2:1537:A:C8	2.52	0.42
59:SN:3:ARG:HD2	59:SN:3:ARG:HA	1.76	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:3m:110:PHE:HD1	84:3m:120:ARG:HE	1.66	0.42
1:L5:92:C:C2	29:La:55:LYS:HD2	2.55	0.42
1:L5:255:C:H2'	1:L5:256:G:H8	1.85	0.42
1:L5:714:G:H2'	1:L5:715:G:H8	1.85	0.42
1:L5:1086:C:H2'	1:L5:1087:A:H8	1.85	0.42
1:L5:2375:A:H2'	1:L5:2376:A:C8	2.53	0.42
1:L5:3608:A:H2'	1:L5:3609:G:H8	1.83	0.42
2:L7:39:C:H4'	13:LJ:47:THR:HG23	2.02	0.42
3:L8:83:C:H42	27:LY:50:ARG:NH1	2.17	0.42
8:LE:70:LYS:HB2	8:LE:70:LYS:HE3	1.74	0.42
13:LJ:20:LEU:HD13	13:LJ:132:VAL:HB	2.00	0.42
22:LT:17:ARG:HD2	22:LT:17:ARG:HA	1.92	0.42
28:LZ:46:ILE:HB	28:LZ:49:TYR:HE2	1.84	0.42
39:Lk:23:VAL:HG12	39:Lk:36:VAL:HG23	2.00	0.42
41:Lm:92:ASP:O	41:Lm:93:LYS:HD3	2.20	0.42
44:Lp:7:LYS:HE2	44:Lp:7:LYS:HB3	1.83	0.42
46:S2:53:C:P	70:SY:112:ASN:HD22	2.42	0.42
46:S2:375:U:H2'	46:S2:376:A:H8	1.84	0.42
46:S2:1396:A:H4'	46:S2:1396:A:OP1	2.18	0.42
52:SF:49:LEU:HD22	62:SQ:50:LYS:HG2	2.01	0.42
53:SG:49:VAL:HG22	53:SG:115:LYS:HB2	2.02	0.42
55:SI:77:ARG:HH12	55:SI:79:ILE:HG23	1.85	0.42
59:SN:114:ARG:HD3	59:SN:114:ARG:HA	1.82	0.42
61:SP:95:GLY:HA2	61:SP:103:ASN:O	2.20	0.42
68:SW:125:ILE:HD13	68:SW:125:ILE:HA	1.88	0.42
83:zz:144:U:O4	83:zz:249:G:O6	2.38	0.42
87:3e:341:PHE:HE2	87:3e:371:ILE:HG13	1.85	0.42
92:3l:215:LEU:HD12	92:3l:215:LEU:HA	1.91	0.42
1:L5:1705:G:H2'	1:L5:1706:A:O4'	2.19	0.42
1:L5:3834:C:H2'	1:L5:3835:C:H6	1.84	0.42
1:L5:4197:G:H2'	1:L5:4198:G:H8	1.84	0.42
1:L5:4255:A:H2'	1:L5:4256:A:O4'	2.20	0.42
1:L5:4890:G:H2'	1:L5:4891:G:C8	2.54	0.42
6:LC:289:LEU:HD11	19:LQ:31:LEU:HB2	2.02	0.42
7:LD:211:LEU:HB3	7:LD:219:TYR:HB2	2.01	0.42
8:LE:176:THR:HB	8:LE:186:LEU:HA	2.02	0.42
10:LG:164:ILE:HG23	16:LN:22:LEU:HD11	2.01	0.42
11:LH:6:SER:OG	11:LH:59:LYS:HB3	2.20	0.42
22:LT:8:ARG:HH21	22:LT:52:MET:HE3	1.85	0.42
36:Lh:73:TYR:CD1	36:Lh:80:PRO:HD3	2.55	0.42
46:S2:655:A:H4'	46:S2:656:G:H5'	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:SB:185:VAL:O	48:SB:189:ILE:HG13	2.19	0.42
50:SD:119:CYS:HA	50:SD:122:VAL:HG12	2.02	0.42
56:SJ:34:GLU:N	76:Se:108:ARG:HH21	2.16	0.42
62:SQ:112:LEU:HD12	62:SQ:112:LEU:HA	1.89	0.42
89:3h:237:ASN:O	89:3h:241:LYS:HG2	2.19	0.42
1:L5:1806:G:H2'	1:L5:1807:C:H6	1.85	0.42
1:L5:2902:G:N2	1:L5:3597:G:H22	2.17	0.42
1:L5:4208:U:H2'	1:L5:4209:G:C8	2.54	0.42
4:LA:126:LEU:HD21	4:LA:150:LEU:HD11	2.02	0.42
7:LD:236:MET:HA	7:LD:239:MET:HG3	2.00	0.42
13:LJ:19:LYS:HD3	13:LJ:75:ARG:NH1	2.35	0.42
15:LM:24:LEU:HD11	15:LM:86:TRP:CE2	2.55	0.42
33:Le:10:PRO:HD2	33:Le:69:MET:HE1	2.02	0.42
34:Lf:92:LEU:HA	34:Lf:93:PRO:HD3	1.90	0.42
38:Lj:83:THR:HA	38:Lj:84:PRO:HD3	1.92	0.42
46:S2:373:G:OP1	58:SL:137:THR:HG22	2.20	0.42
54:SH:82:GLU:O	54:SH:85:LYS:HG3	2.20	0.42
55:SI:77:ARG:NH1	55:SI:79:ILE:HG23	2.35	0.42
60:SO:19:PRO:HG3	60:SO:89:GLY:HA3	2.00	0.42
78:Sg:67:SER:H	78:Sg:82:SER:HA	1.84	0.42
83:zz:151:C:H2'	83:zz:152:G:C8	2.54	0.42
85:3f:269:LEU:HD21	89:3h:335:ALA:HB1	2.01	0.42
86:3a:278:LYS:HD3	86:3a:278:LYS:HA	1.83	0.42
86:3a:528:SER:HB2	89:3h:227:LYS:HG3	2.02	0.42
88:3c:594:LEU:HA	88:3c:597:ASN:HB2	2.01	0.42
1:L5:1186:U:H2'	1:L5:1187:G:N3	2.35	0.42
1:L5:1315:C:H2'	1:L5:1316:G:H8	1.84	0.42
1:L5:1366:G:C2	14:LL:33:ILE:HG21	2.55	0.42
1:L5:2283:G:H2'	1:L5:2284:G:H8	1.85	0.42
1:L5:4552:U:H2'	1:L5:4553:A:C8	2.55	0.42
5:LB:112:ASP:O	5:LB:116:ARG:HG3	2.20	0.42
8:LE:115:TYR:HE1	45:Lr:119:ARG:HB2	1.85	0.42
17:LO:138:LEU:HA	17:LO:141:LEU:HB3	2.02	0.42
45:Lr:7:TRP:CE2	45:Lr:38:PHE:HB2	2.55	0.42
46:S2:1199:A:H2'	46:S2:1200:A:C8	2.54	0.42
46:S2:1514:G:H2'	46:S2:1515:G:H8	1.85	0.42
49:SC:116:THR:HG23	49:SC:118:ALA:H	1.85	0.42
51:SE:180:LEU:HD12	51:SE:180:LEU:HA	1.79	0.42
62:SQ:119:LEU:HD23	62:SQ:120:LEU:HD12	2.02	0.42
64:SS:23:ARG:HH21	71:SZ:80:ARG:HE	1.66	0.42
86:3a:62:ARG:HA	86:3a:62:ARG:HD2	1.72	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
86:3a:284:TRP:HB2	86:3a:292:HIS:CG	2.55	0.42
87:3e:175:SER:O	87:3e:179:MET:HE3	2.20	0.42
87:3e:346:ARG:HD2	87:3e:346:ARG:HA	1.81	0.42
92:3l:278:LEU:HD11	92:3l:294:LEU:HD13	2.02	0.42
1:L5:483:G:N7	1:L5:485:C:H5''	2.34	0.42
1:L5:2624:G:H2'	1:L5:2625:U:C6	2.55	0.42
1:L5:3848:U:H4'	1:L5:4634:U:C4	2.55	0.42
1:L5:4153:C:H2'	1:L5:4154:G:H8	1.84	0.42
1:L5:4208:U:H2'	1:L5:4209:G:H8	1.85	0.42
1:L5:4378:A:O2'	1:L5:4379:A:H2'	2.20	0.42
6:LC:110:ARG:HB2	16:LN:204:ARG:NH2	2.34	0.42
6:LC:113:ARG:HA	6:LC:113:ARG:HD3	1.87	0.42
14:LL:117:LEU:HD23	14:LL:117:LEU:HA	1.81	0.42
17:LO:128:ARG:HA	17:LO:128:ARG:HD2	1.69	0.42
20:LR:84:THR:HG23	20:LR:87:ALA:H	1.85	0.42
20:LR:174:GLU:O	20:LR:178:GLN:HG3	2.20	0.42
24:LV:84:GLN:HA	24:LV:101:ASN:HB3	2.01	0.42
37:Li:65:LYS:NZ	37:Li:68:ARG:HB3	2.35	0.42
46:S2:366:U:H3	46:S2:394:G:H1	1.67	0.42
46:S2:582:U:H4'	70:SY:33:ALA:HB2	2.00	0.42
46:S2:1605:G:H2'	46:S2:1606:G:C4	2.55	0.42
46:S2:1745:A:H1'	53:SG:66:GLY:HA2	2.02	0.42
54:SH:83:LEU:HD13	54:SH:92:VAL:HG23	2.01	0.42
57:SK:21:MET:HB3	57:SK:69:TRP:CD1	2.54	0.42
61:SP:76:VAL:H	61:SP:93:MET:HE1	1.84	0.42
63:SR:35:CYS:HA	63:SR:38:ILE:HG22	2.02	0.42
65:ST:9:VAL:HG21	65:ST:139:ALA:HA	2.02	0.42
69:SX:91:LEU:HD12	69:SX:94:ILE:HD11	2.01	0.42
72:Sa:53:ILE:HD12	72:Sa:53:ILE:HA	1.85	0.42
78:Sg:216:ALA:HB2	78:Sg:236:ILE:HD12	2.02	0.42
80:zy:68:A:H2'	80:zy:69:G:H8	1.84	0.42
83:zz:284:U:H2'	83:zz:285:G:C8	2.54	0.42
84:3m:282:PHE:HB2	84:3m:311:PHE:CZ	2.54	0.42
86:3a:12:LEU:HD11	86:3a:49:PRO:HB2	2.00	0.42
87:3e:182:TRP:HA	87:3e:185:ALA:HB3	2.01	0.42
89:3h:243:LEU:O	89:3h:247:MET:HG3	2.20	0.42
1:L5:1314:C:C2	1:L5:1315:C:C5	3.08	0.41
1:L5:1779:U:H2'	1:L5:1780:A:C8	2.54	0.41
1:L5:2078:C:H2'	1:L5:2079:G:C8	2.55	0.41
1:L5:2535:G:H21	1:L5:2640:G:H22	1.68	0.41
1:L5:3727:A:H2'	1:L5:3728:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3943:A:H2	1:L5:4071:U:H5	1.68	0.41
1:L5:4610:A:H2'	1:L5:4611:A:O4'	2.20	0.41
4:LA:180:LEU:HD11	44:Lp:26:VAL:HG21	2.02	0.41
5:LB:206:PRO:HG2	5:LB:209:GLN:HG3	2.02	0.41
7:LD:51:MET:HE3	7:LD:51:MET:HB2	1.90	0.41
29:La:123:ILE:HD13	29:La:143:ALA:H	1.85	0.41
33:Le:75:ARG:HB2	33:Le:95:TYR:CD1	2.55	0.41
46:S2:332:G:H2'	46:S2:333:G:H8	1.85	0.41
46:S2:1365:G:H2'	46:S2:1366:G:H8	1.85	0.41
47:SA:111:GLN:HA	47:SA:116:PHE:CG	2.54	0.41
52:SF:101:HIS:HA	52:SF:105:GLY:HA2	2.01	0.41
60:SO:56:VAL:HG23	60:SO:60:MET:HG3	2.02	0.41
83:zz:177:C:H2'	83:zz:178:C:C6	2.55	0.41
89:3h:138:PHE:HE1	89:3h:178:LYS:HG3	1.84	0.41
1:L5:58:G:H2'	3:L8:33:G:H3'	2.02	0.41
1:L5:139:G:H2'	1:L5:140:G:C8	2.55	0.41
1:L5:1631:A:C8	4:LA:199:VAL:HG11	2.54	0.41
1:L5:2450:G:H2'	1:L5:2451:A:H8	1.85	0.41
1:L5:3682:A:H3'	4:LA:132:ASN:HD21	1.85	0.41
2:L7:24:C:H2'	2:L7:25:G:O4'	2.20	0.41
5:LB:161:ARG:HD2	5:LB:182:GLU:OE2	2.20	0.41
6:LC:40:VAL:HG12	6:LC:237:ILE:HG21	2.02	0.41
9:LF:226:HIS:HA	9:LF:233:ALA:HB3	2.03	0.41
12:LI:171:TRP:HB2	12:LI:178:ALA:HA	2.02	0.41
16:LN:142:ILE:HD13	16:LN:142:ILE:HA	1.83	0.41
19:LQ:66:MET:HE3	19:LQ:66:MET:HB2	1.79	0.41
27:LY:55:VAL:HG23	27:LY:106:ILE:HA	2.02	0.41
37:Li:99:LYS:HD3	37:Li:99:LYS:HA	1.80	0.41
46:S2:640:A:H2'	46:S2:641:A:C8	2.55	0.41
46:S2:1797:U:H2'	46:S2:1798:C:C6	2.54	0.41
46:S2:1842:C:H2'	46:S2:1843:G:H8	1.85	0.41
48:SB:139:CYS:SG	48:SB:168:MET:HE2	2.59	0.41
50:SD:80:PRO:HG2	50:SD:83:SER:HB2	2.02	0.41
59:SN:38:TYR:CE1	59:SN:78:LYS:HG2	2.55	0.41
71:SZ:57:LYS:HA	71:SZ:57:LYS:HD2	1.77	0.41
74:Sc:17:VAL:HA	74:Sc:30:VAL:HG23	2.02	0.41
87:3e:400:PRO:HG2	88:3c:849:PRO:HB3	2.02	0.41
88:3c:55:LYS:HD3	88:3c:55:LYS:HA	1.79	0.41
92:3l:456:GLN:HG2	92:3l:489:GLN:NE2	2.35	0.41
1:L5:271:C:H2'	1:L5:272:U:C6	2.54	0.41
1:L5:367:C:H5''	40:Ll:47:THR:HG21	2.00	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:424:U:H2'	1:L5:425:U:C6	2.56	0.41
1:L5:442:G:H2'	1:L5:443:G:H8	1.86	0.41
1:L5:1092:G:H2'	1:L5:1093:C:C6	2.56	0.41
1:L5:1334:A:H2'	1:L5:1335:G:H8	1.85	0.41
1:L5:1743:A:H5'	7:LD:11:ALA:HB1	2.02	0.41
1:L5:2539:C:H2'	1:L5:2540:C:C6	2.55	0.41
1:L5:5054:C:H4'	1:L5:5055:G:H5'	2.03	0.41
13:LJ:113:ILE:HD12	13:LJ:113:ILE:HA	1.89	0.41
15:LM:92:ALA:HA	15:LM:95:ILE:HG22	2.03	0.41
16:LN:185:GLY:H	16:LN:191:ALA:HB2	1.85	0.41
26:LX:147:LEU:HD13	26:LX:147:LEU:HA	1.91	0.41
30:Lb:3:LYS:HE3	30:Lb:3:LYS:HB3	1.92	0.41
46:S2:1053:C:H2'	46:S2:1054:G:C8	2.55	0.41
46:S2:1605:G:H2'	46:S2:1606:G:N3	2.35	0.41
46:S2:1628:C:H2'	46:S2:1629:C:C6	2.54	0.41
48:SB:158:HIS:HA	48:SB:161:VAL:HG22	2.01	0.41
49:SC:232:THR:HG23	49:SC:235:ASN:OD1	2.20	0.41
64:SS:68:ILE:O	64:SS:72:GLN:HG2	2.20	0.41
67:SV:32:ILE:HD12	67:SV:32:ILE:HA	1.89	0.41
71:SZ:49:LEU:HB2	71:SZ:83:LEU:HD13	2.03	0.41
79:sh:91:LYS:HA	79:sh:91:LYS:HD2	1.77	0.41
86:3a:412:ASN:HA	86:3a:415:ARG:HD3	2.03	0.41
87:3e:196:ILE:HD12	87:3e:214:LEU:HD13	2.02	0.41
87:3e:227:LYS:HD2	87:3e:227:LYS:HA	1.86	0.41
91:3k:174:MET:HG2	91:3k:179:TRP:HB2	2.03	0.41
1:L5:173:C:H5''	14:LL:129:ARG:HH12	1.84	0.41
1:L5:666:G:H1'	1:L5:667:A:H2'	2.02	0.41
1:L5:911:U:H2'	1:L5:912:G:O4'	2.21	0.41
1:L5:1966:C:H2'	1:L5:1967:A:C8	2.55	0.41
1:L5:2689:C:H2'	1:L5:2690:C:C6	2.56	0.41
1:L5:4147:G:H2'	1:L5:4148:C:C6	2.56	0.41
1:L5:4991:U:H2'	1:L5:4992:G:H8	1.85	0.41
7:LD:255:LYS:HD3	7:LD:255:LYS:HA	1.89	0.41
9:LF:71:MET:HA	9:LF:74:MET:HG2	2.03	0.41
17:LO:58:LEU:HD11	17:LO:74:ARG:HH22	1.84	0.41
25:LW:61:LYS:HD2	25:LW:61:LYS:HA	1.73	0.41
27:LY:28:LYS:HB3	27:LY:28:LYS:HE2	1.82	0.41
28:LZ:11:VAL:HG23	28:LZ:82:PRO:HA	2.01	0.41
35:Lg:99:GLU:HA	35:Lg:102:ILE:HG22	2.03	0.41
46:S2:479:C:H2'	46:S2:480:G:H8	1.85	0.41
46:S2:917:U:H2'	46:S2:918:U:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:1058:A:H2'	46:S2:1059:G:C8	2.56	0.41
46:S2:1277:C:H2'	46:S2:1278:A:C8	2.56	0.41
59:SN:8:GLY:O	59:SN:9:LYS:HG2	2.20	0.41
62:SQ:57:LEU:HD23	62:SQ:57:LEU:HA	1.90	0.41
62:SQ:108:ILE:HA	62:SQ:111:ILE:HG22	2.02	0.41
65:ST:112:MET:HA	65:ST:127:GLY:HA3	2.02	0.41
83:zz:180:G:H2'	83:zz:181:G:C8	2.56	0.41
85:3f:221:MET:HA	85:3f:221:MET:HE3	2.02	0.41
87:3e:236:PHE:CG	87:3e:257:LEU:HD13	2.56	0.41
87:3e:347:ILE:HG23	88:3c:826:ILE:HG21	2.01	0.41
92:3l:69:GLN:HE22	92:3l:83:VAL:HG22	1.85	0.41
1:L5:1264:C:H2'	1:L5:1265:G:C8	2.55	0.41
1:L5:1507:C:H2'	1:L5:1508:A:H8	1.84	0.41
1:L5:1742:A:H2'	1:L5:1743:A:H8	1.85	0.41
1:L5:2634:C:H2'	1:L5:2635:U:C6	2.56	0.41
1:L5:2747:U:H2'	1:L5:2748:C:C6	2.55	0.41
1:L5:2907:G:H2'	1:L5:2908:U:C6	2.55	0.41
1:L5:2908:U:H3	1:L5:3586:G:H1	1.67	0.41
1:L5:3940:U:H2'	1:L5:3941:G:C8	2.55	0.41
1:L5:4153:C:H2'	1:L5:4154:G:C8	2.55	0.41
1:L5:4344:U:H2'	1:L5:4345:C:H6	1.84	0.41
7:LD:212:MET:HE1	7:LD:219:TYR:CZ	2.56	0.41
20:LR:80:LYS:HA	20:LR:80:LYS:HD2	1.89	0.41
26:LX:41:ARG:HA	26:LX:41:ARG:HD3	1.62	0.41
46:S2:5:U:H2'	46:S2:6:G:C8	2.56	0.41
46:S2:349:A:H4'	55:SI:27:TYR:CE2	2.56	0.41
46:S2:941:C:H5''	48:SB:136:ARG:NH1	2.35	0.41
46:S2:1373:C:H2'	46:S2:1374:C:H6	1.86	0.41
46:S2:1406:G:H2'	46:S2:1407:U:H6	1.84	0.41
46:S2:1445:U:H4'	66:SU:57:PRO:HB3	2.02	0.41
46:S2:1665:G:C5	65:ST:88:MET:HE1	2.55	0.41
47:SA:124:VAL:HG13	47:SA:146:ALA:HA	2.02	0.41
49:SC:74:LYS:HE2	49:SC:272:HIS:ND1	2.36	0.41
52:SF:178:ILE:HD13	52:SF:178:ILE:HA	1.89	0.41
54:SH:141:GLY:HA2	59:SN:18:TYR:HE1	1.85	0.41
1:L5:84:A:H61	1:L5:98:A:H3'	1.85	0.41
1:L5:677:G:H2'	1:L5:678:C:C6	2.55	0.41
1:L5:1344:C:H2'	1:L5:1345:A:C8	2.55	0.41
1:L5:2608:G:H2'	1:L5:2609:G:H8	1.85	0.41
1:L5:4299:U:H2'	1:L5:4300:U:H6	1.86	0.41
3:L8:52:A:H62	40:L1:27:ILE:HD13	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:LA:59:ALA:HB2	4:LA:78:ALA:HB2	2.03	0.41
5:LB:19:ARG:HD2	5:LB:234:ARG:NH1	2.36	0.41
5:LB:47:LEU:HD13	5:LB:47:LEU:HA	1.91	0.41
28:LZ:128:LYS:HE3	28:LZ:128:LYS:HB2	1.86	0.41
30:Lb:55:LYS:H	30:Lb:55:LYS:HG2	1.57	0.41
33:Le:111:ILE:HD13	33:Le:111:ILE:HA	1.86	0.41
46:S2:77:A:C4	53:SG:179:LEU:HD13	2.56	0.41
46:S2:158:A:H2'	46:S2:159:A:O4'	2.21	0.41
46:S2:437:G:H3'	46:S2:438:G:H21	1.85	0.41
46:S2:582:U:H2'	46:S2:583:A:H8	1.85	0.41
46:S2:927:C:H2'	46:S2:928:G:C8	2.55	0.41
46:S2:941:C:H5''	48:SB:136:ARG:HH11	1.84	0.41
46:S2:1558:C:H2'	46:S2:1559:C:C6	2.56	0.41
46:S2:1712:A:H2'	46:S2:1713:C:H6	1.83	0.41
47:SA:30:LEU:HD23	47:SA:30:LEU:HA	1.84	0.41
52:SF:49:LEU:HD13	62:SQ:50:LYS:HG2	2.00	0.41
59:SN:35:GLU:HA	59:SN:38:TYR:HB2	2.03	0.41
62:SQ:112:LEU:HD11	62:SQ:119:LEU:HD11	2.02	0.41
67:SV:14:PRO:HG2	67:SV:23:ILE:HD11	2.02	0.41
69:SX:101:LEU:HD23	69:SX:124:LYS:HB2	2.01	0.41
70:SY:113:ARG:O	70:SY:117:VAL:HG12	2.20	0.41
89:3h:216:TRP:O	89:3h:219:GLU:HG3	2.20	0.41
1:L5:253:G:H2'	1:L5:254:G:C8	2.56	0.41
1:L5:1271:G:N1	1:L5:2107:C:N3	2.68	0.41
1:L5:2765:A:H2'	1:L5:2766:A:C8	2.55	0.41
1:L5:2847:G:H3'	1:L5:2848:G:C8	2.56	0.41
1:L5:3911:C:H2'	1:L5:3912:U:C6	2.56	0.41
5:LB:179:HIS:CE1	5:LB:344:VAL:HG21	2.56	0.41
9:LF:53:LYS:HG2	9:LF:57:TYR:CE2	2.56	0.41
15:LM:20:HIS:CD2	15:LM:48:GLN:HE22	2.38	0.41
15:LM:50:MET:HA	15:LM:51:PRO:HD3	1.92	0.41
20:LR:99:MET:O	20:LR:103:ARG:HB2	2.21	0.41
21:LS:70:LYS:HD3	21:LS:70:LYS:HA	1.81	0.41
24:LV:26:ILE:HG23	24:LV:102:ALA:HA	2.03	0.41
32:Ld:91:LYS:HZ2	32:Ld:105:LEU:HD11	1.85	0.41
36:Lh:81:LEU:HD23	36:Lh:81:LEU:HA	1.80	0.41
40:Ll:9:ILE:HD13	40:Ll:9:ILE:HA	1.85	0.41
46:S2:4:C:H4'	49:SC:207:ALA:HB2	2.03	0.41
46:S2:10:G:H1'	49:SC:115:GLN:HG2	2.02	0.41
46:S2:162:C:H2'	46:S2:163:U:O4'	2.20	0.41
46:S2:224:A:H61	46:S2:297:A:H61	1.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:520:A:H5''	56:SJ:12:THR:HG23	2.02	0.41
46:S2:1407:U:H2'	46:S2:1408:U:C6	2.56	0.41
46:S2:1408:U:H2'	46:S2:1409:A:H8	1.84	0.41
46:S2:1759:G:H22	46:S2:1773:C:H5'	1.85	0.41
47:SA:19:LEU:HG	47:SA:24:HIS:CD2	2.55	0.41
47:SA:64:ALA:HA	67:SV:36:VAL:HA	2.03	0.41
48:SB:150:ILE:HD12	48:SB:150:ILE:HA	1.94	0.41
49:SC:142:LYS:HE3	49:SC:142:LYS:HB3	1.92	0.41
66:SU:66:ARG:HA	66:SU:77:TRP:HD1	1.85	0.41
71:SZ:68:ILE:HB	71:SZ:109:TYR:HB2	2.02	0.41
75:Sd:19:ARG:HH22	75:Sd:32:ARG:HE	1.69	0.41
78:Sg:106:LYS:HD3	78:Sg:125:ARG:HB2	2.02	0.41
83:zz:291:G:C6	83:zz:302:U:O2	2.73	0.41
1:L5:101:A:H1'	29:La:66:ASN:ND2	2.36	0.41
1:L5:451:C:H3'	1:L5:1294:A:H2	1.85	0.41
1:L5:1800:U:H2'	1:L5:1801:A:H8	1.85	0.41
1:L5:2540:C:H2'	1:L5:2541:G:C8	2.55	0.41
1:L5:4342:C:O3'	43:Lo:37:GLY:HA3	2.21	0.41
1:L5:4630:G:H2'	1:L5:4631:G:H8	1.86	0.41
1:L5:4775:C:H42	1:L5:4859:C:N4	2.18	0.41
3:L8:133:G:H2'	3:L8:134:G:C8	2.54	0.41
3:L8:141:C:H2'	3:L8:142:U:C6	2.55	0.41
7:LD:38:ILE:HD13	7:LD:38:ILE:HA	1.81	0.41
23:LU:85:TYR:HD2	23:LU:86:LEU:HD22	1.83	0.41
28:LZ:134:LEU:HD12	28:LZ:134:LEU:HA	1.88	0.41
46:S2:65:C:P	53:SG:136:LYS:HZ1	2.43	0.41
46:S2:644:G:H2'	46:S2:645:C:C6	2.56	0.41
48:SB:138:PHE:HB2	48:SB:213:ARG:HB2	2.02	0.41
50:SD:210:ILE:HG13	63:SR:15:VAL:HG11	2.02	0.41
55:SI:19:LYS:HE3	55:SI:19:LYS:HB2	1.86	0.41
84:3m:57:ASP:O	84:3m:61:GLU:HB3	2.20	0.41
85:3f:139:HIS:H	85:3f:139:HIS:CD2	2.38	0.41
86:3a:205:LEU:HD12	86:3a:205:LEU:HA	1.90	0.41
1:L5:286:U:H2'	1:L5:287:U:C6	2.55	0.41
1:L5:428:G:H2'	1:L5:429:A:C8	2.55	0.41
1:L5:429:A:H2'	1:L5:430:G:C8	2.56	0.41
1:L5:441:G:H2'	1:L5:442:G:C8	2.56	0.41
1:L5:486:C:H2'	1:L5:487:G:C8	2.56	0.41
1:L5:722:G:H2'	1:L5:723:A:C8	2.56	0.41
1:L5:1098:G:H2'	1:L5:1099:C:C6	2.56	0.41
1:L5:1338:G:H4'	1:L5:1339:U:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1839:U:H2'	1:L5:1840:G:C8	2.56	0.41
1:L5:1857:C:H2'	1:L5:1858:A:H8	1.86	0.41
1:L5:1932:A:H2'	1:L5:1933:G:C8	2.56	0.41
1:L5:1952:G:H5''	21:LS:139:ARG:HH21	1.86	0.41
1:L5:2281:U:H2'	1:L5:2282:A:H8	1.86	0.41
1:L5:2657:G:H2'	1:L5:2658:G:C4	2.56	0.41
1:L5:4089:G:H2'	1:L5:4090:G:C8	2.56	0.41
1:L5:5027:C:H4'	1:L5:5028:G:O5'	2.19	0.41
4:LA:61:VAL:HG21	4:LA:76:PHE:CE1	2.56	0.41
4:LA:107:MET:HA	4:LA:108:PRO:HD3	1.84	0.41
4:LA:186:TYR:HB2	4:LA:196:TRP:CZ3	2.56	0.41
4:LA:225:ILE:HD12	4:LA:225:ILE:HA	1.91	0.41
6:LC:144:ILE:H	6:LC:144:ILE:HG13	1.80	0.41
6:LC:211:TYR:O	6:LC:232:VAL:HG23	2.20	0.41
7:LD:150:LEU:HD12	7:LD:150:LEU:HA	1.90	0.41
10:LG:141:ASN:HA	10:LG:144:THR:HG22	2.03	0.41
11:LH:19:THR:HG23	11:LH:26:ILE:HB	2.03	0.41
11:LH:89:ARG:HG3	11:LH:145:ILE:HG23	2.02	0.41
12:LI:99:ILE:HD13	12:LI:99:ILE:HA	1.94	0.41
18:LP:131:ARG:HG3	18:LP:137:ASN:HB2	2.02	0.41
20:LR:123:LEU:O	20:LR:127:VAL:HG23	2.21	0.41
24:LV:42:VAL:HA	24:LV:61:VAL:HG13	2.03	0.41
28:LZ:5:MET:HE3	28:LZ:5:MET:HB2	1.73	0.41
39:Lk:12:LEU:HD12	39:Lk:16:ARG:HH12	1.85	0.41
43:Lo:30:LYS:H	43:Lo:30:LYS:HG2	1.63	0.41
43:Lo:34:TYR:HD1	43:Lo:34:TYR:HA	1.71	0.41
46:S2:26:U:H2'	46:S2:27:A:C8	2.56	0.41
46:S2:64:A:H3'	53:SG:175:LYS:HE2	2.03	0.41
46:S2:110:U:H2'	46:S2:111:A:C8	2.56	0.41
46:S2:314:U:H2'	46:S2:315:C:C6	2.56	0.41
46:S2:661:U:H3'	46:S2:662:G:H2'	2.03	0.41
46:S2:1166:G:H1	46:S2:1193:U:H3	1.69	0.41
46:S2:1242:U:H4'	46:S2:1243:U:H5''	2.02	0.41
46:S2:1298:G:H2'	46:S2:1299:A:O4'	2.21	0.41
48:SB:119:THR:H	48:SB:143:THR:HG22	1.86	0.41
51:SE:124:CYS:HB3	51:SE:141:THR:HB	2.03	0.41
55:SI:87:ASN:HD22	55:SI:90:LEU:HD23	1.86	0.41
56:SJ:110:LEU:HD21	56:SJ:142:VAL:HG21	2.03	0.41
56:SJ:126:ALA:HA	56:SJ:129:LEU:HD12	2.03	0.41
57:SK:93:THR:HG22	57:SK:95:ARG:HG2	2.03	0.41
58:SL:98:LYS:HE3	58:SL:99:TYR:HE1	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:SP:18:ARG:NH1	64:SS:88:LYS:HB3	2.36	0.41
61:SP:56:LEU:HD13	61:SP:80:LEU:HD12	2.03	0.41
64:SS:40:TYR:O	64:SS:44:VAL:HG22	2.21	0.41
70:SY:79:LEU:HD23	70:SY:79:LEU:HA	1.90	0.41
83:zz:172:A:H2'	83:zz:173:A:C8	2.54	0.41
85:3f:159:LEU:HD22	89:3h:99:TYR:HE1	1.85	0.41
85:3f:251:LEU:HD22	89:3h:162:LEU:HB2	2.02	0.41
86:3a:80:GLN:HA	86:3a:83:ILE:HD11	2.03	0.41
86:3a:331:ILE:H	86:3a:331:ILE:HG13	1.74	0.41
86:3a:465:PHE:HB2	88:3c:810:MET:SD	2.61	0.41
89:3h:49:ILE:HD13	89:3h:49:ILE:HA	1.88	0.41
92:3l:140:ILE:HD12	92:3l:144:VAL:HG21	2.03	0.41
1:L5:1341:U:H2'	1:L5:1342:A:C8	2.55	0.41
1:L5:2772:C:H2'	1:L5:2773:G:H8	1.86	0.41
1:L5:3748:A:H5''	4:LA:243:THR:OG1	2.21	0.41
1:L5:4597:U:H2'	1:L5:4598:C:O4'	2.21	0.41
5:LB:315:ASN:HD21	5:LB:325:GLU:HA	1.86	0.41
7:LD:146:LEU:HD13	7:LD:163:LEU:HD22	2.03	0.41
20:LR:4:LEU:HD13	20:LR:7:GLN:HE21	1.86	0.41
20:LR:65:LYS:HE3	20:LR:65:LYS:HB2	1.69	0.41
39:Lk:56:LEU:H	39:Lk:56:LEU:HD12	1.86	0.41
45:Lr:90:LEU:HD11	45:Lr:111:ILE:HG23	2.03	0.41
46:S2:482:G:H21	46:S2:484:A:H8	1.69	0.41
46:S2:980:A:H2'	46:S2:981:A:C8	2.56	0.41
46:S2:1165:G:H4'	46:S2:1166:G:H5''	2.03	0.41
46:S2:1240:A:O2'	46:S2:1267:C:H4'	2.21	0.41
47:SA:121:LEU:HD11	47:SA:145:ILE:HG12	2.03	0.41
50:SD:73:VAL:HA	50:SD:76:ARG:HB3	2.03	0.41
53:SG:164:LYS:H	53:SG:164:LYS:HG2	1.69	0.41
54:SH:179:LYS:HE3	54:SH:180:LEU:HD23	2.03	0.41
55:SI:67:TRP:CD1	55:SI:70:GLU:H	2.39	0.41
56:SJ:34:GLU:H	76:Se:108:ARG:HH21	1.69	0.41
56:SJ:79:ARG:HA	56:SJ:82:VAL:HG22	2.02	0.41
62:SQ:84:ILE:O	62:SQ:88:ILE:HG12	2.21	0.41
70:SY:55:ILE:HD12	70:SY:75:ILE:HG12	2.03	0.41
82:zx:5:VAL:HG23	82:zx:6:LEU:H	1.86	0.41
85:3f:251:LEU:HD11	89:3h:161:SER:HB2	2.03	0.41
88:3c:67:ILE:HG12	88:3c:82:GLU:HB3	2.01	0.41
89:3h:208:SER:H	89:3h:211:ILE:HD12	1.85	0.41
1:L5:1382:G:H2'	1:L5:1383:G:H8	1.85	0.40
1:L5:3861:A:H2'	1:L5:3862:A:C8	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L7:82:G:H2'	2:L7:83:A:C8	2.56	0.40
3:L8:45:C:H2'	3:L8:46:G:C8	2.56	0.40
5:LB:379:PHE:HD2	5:LB:385:LYS:HD2	1.85	0.40
6:LC:95:MET:HE2	6:LC:95:MET:HB3	1.96	0.40
7:LD:228:LYS:HE3	7:LD:228:LYS:HB2	1.77	0.40
9:LF:156:LYS:HE3	9:LF:157:ARG:NH1	2.36	0.40
10:LG:117:ARG:HA	10:LG:117:ARG:HD3	1.89	0.40
13:LJ:108:GLY:HA2	13:LJ:129:ASP:HA	2.03	0.40
17:LO:195:VAL:HA	17:LO:198:THR:HG22	2.03	0.40
22:LT:5:LYS:HE2	22:LT:5:LYS:HB2	1.90	0.40
26:LX:100:VAL:HG23	26:LX:134:LYS:HD3	2.04	0.40
32:Ld:21:VAL:HG22	32:Ld:90:ARG:HB3	2.03	0.40
46:S2:12:U:H2'	46:S2:13:C:C6	2.56	0.40
46:S2:1640:A:H1'	80:zu:40:G:H1'	2.03	0.40
47:SA:76:VAL:HG13	47:SA:98:PRO:HA	2.03	0.40
50:SD:222:PRO:HB3	78:Sg:227:LEU:HD11	2.03	0.40
51:SE:106:LYS:HD2	51:SE:108:ARG:HH22	1.85	0.40
53:SG:113:ILE:HD12	53:SG:114:VAL:H	1.85	0.40
54:SH:12:ASN:H	54:SH:15:LYS:HE2	1.85	0.40
55:SI:67:TRP:NE1	55:SI:70:GLU:H	2.19	0.40
86:3a:28:LEU:HD23	86:3a:28:LEU:HA	1.86	0.40
86:3a:91:ARG:HG2	86:3a:173:LEU:HD21	2.03	0.40
86:3a:254:GLU:HG2	86:3a:358:LEU:HD21	2.02	0.40
86:3a:393:TRP:CZ3	86:3a:406:ARG:HD3	2.56	0.40
87:3e:289:LYS:HE3	87:3e:294:GLU:HG2	2.03	0.40
87:3e:303:PHE:HE1	88:3c:827:ILE:HD12	1.86	0.40
88:3c:621:PHE:O	88:3c:778:MET:HE3	2.22	0.40
89:3h:309:GLN:HA	89:3h:310:PRO:HD3	1.96	0.40
92:3l:174:ALA:HA	92:3l:175:PRO:HD3	1.95	0.40
92:3l:244:LEU:HD11	92:3l:296:ASN:C	2.46	0.40
1:L5:25:A:C8	1:L5:341:G:C8	3.08	0.40
1:L5:162:A:H2'	1:L5:163:A:C8	2.56	0.40
1:L5:1220:G:H2'	1:L5:1221:G:C8	2.57	0.40
1:L5:2381:A:H1'	1:L5:2383:C:OP2	2.21	0.40
1:L5:4935:C:H2'	1:L5:4936:G:H8	1.86	0.40
1:L5:5043:A:H2'	1:L5:5044:A:H8	1.86	0.40
5:LB:161:ARG:HG2	5:LB:184:GLN:HA	2.03	0.40
5:LB:177:LYS:HB2	5:LB:177:LYS:HE3	1.81	0.40
7:LD:83:LEU:HD21	7:LD:100:CYS:HB3	2.02	0.40
9:LF:169:LEU:HA	9:LF:174:LEU:HD11	2.03	0.40
25:LW:53:VAL:HA	25:LW:56:ARG:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LZ:3:LYS:HB3	28:LZ:3:LYS:HE2	1.85	0.40
29:La:102:ASP:OD1	29:La:105:ARG:HB2	2.22	0.40
46:S2:338:G:H2'	46:S2:339:A:C8	2.56	0.40
46:S2:374:G:H2'	46:S2:375:U:C6	2.56	0.40
46:S2:1817:G:H2'	46:S2:1818:A:C8	2.56	0.40
48:SB:62:LEU:HD12	48:SB:62:LEU:HA	1.85	0.40
48:SB:111:CYS:SG	72:Sa:68:TYR:HB2	2.61	0.40
50:SD:27:ARG:HH21	57:SK:62:PHE:H	1.68	0.40
52:SF:38:TYR:HE2	52:SF:143:PRO:HB2	1.85	0.40
53:SG:222:GLU:O	53:SG:226:GLU:HB3	2.20	0.40
60:SO:29:GLY:C	60:SO:93:LEU:HB2	2.46	0.40
62:SQ:16:LYS:HA	62:SQ:16:LYS:HD2	1.73	0.40
64:SS:79:ILE:HG13	64:SS:80:PRO:HD2	2.02	0.40
80:zu:51:G:H2'	80:zu:52:G:C8	2.55	0.40
84:3m:91:VAL:HG13	84:3m:129:LYS:HG2	2.03	0.40
84:3m:280:LEU:HD12	84:3m:280:LEU:HA	1.86	0.40
1:L5:74:G:H5'	14:LL:59:VAL:HB	2.04	0.40
1:L5:422:C:H2'	1:L5:423:G:H8	1.87	0.40
1:L5:1794:A:H5''	1:L5:4214:A:N6	2.37	0.40
1:L5:4460:U:H2'	1:L5:4461:C:C6	2.56	0.40
1:L5:4878:C:H2'	1:L5:4879:C:H6	1.85	0.40
4:LA:43:GLY:HA3	4:LA:63:PHE:CD2	2.56	0.40
5:LB:171:LEU:HD23	5:LB:171:LEU:HA	1.89	0.40
6:LC:179:ASP:OD2	6:LC:207:PRO:HD3	2.22	0.40
10:LG:80:ILE:HD11	16:LN:22:LEU:HD21	2.03	0.40
11:LH:6:SER:HB3	11:LH:67:LEU:HD11	2.03	0.40
16:LN:184:ILE:HA	16:LN:184:ILE:HD13	1.89	0.40
18:LP:54:GLN:HG3	18:LP:83:TRP:CD1	2.56	0.40
32:Ld:20:VAL:HA	32:Ld:90:ARG:O	2.21	0.40
34:Lf:55:ASN:HB2	34:Lf:68:ARG:NH2	2.36	0.40
40:Ll:28:ARG:HA	40:Ll:33:ASN:HD21	1.86	0.40
46:S2:168:C:H2'	53:SG:133:LEU:HD23	2.04	0.40
46:S2:612:U:H4'	76:Se:84:LYS:HZ1	1.86	0.40
46:S2:979:C:H2'	46:S2:980:A:H8	1.86	0.40
46:S2:1457:U:H2'	46:S2:1458:G:H8	1.87	0.40
49:SC:130:ILE:HD12	49:SC:130:ILE:HA	1.93	0.40
66:SU:81:GLN:HE21	75:Sd:55:LEU:HB3	1.86	0.40
78:Sg:38:LYS:HA	78:Sg:66:VAL:HG22	2.03	0.40
78:Sg:104:HIS:CE1	78:Sg:124:SER:HB2	2.56	0.40
78:Sg:121:VAL:HG23	78:Sg:156:PHE:HZ	1.86	0.40
86:3a:351:LYS:HB2	86:3a:351:LYS:HE3	1.88	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
87:3e:233:ILE:H	87:3e:233:ILE:HG13	1.73	0.40
92:3l:91:ILE:HD13	92:3l:91:ILE:HA	1.96	0.40
92:3l:538:ARG:HA	92:3l:538:ARG:HD3	1.84	0.40
1:L5:240:G:H2'	1:L5:241:G:O4'	2.22	0.40
1:L5:655:C:H2'	1:L5:656:C:C6	2.56	0.40
1:L5:699:C:H1'	1:L5:968:C:N3	2.37	0.40
1:L5:1244:G:H2'	1:L5:1245:C:C6	2.56	0.40
1:L5:1399:G:H2'	1:L5:1400:G:H8	1.87	0.40
1:L5:1446:C:H2'	1:L5:1447:C:C6	2.56	0.40
1:L5:1693:U:P	19:LQ:53:MET:HE1	2.61	0.40
1:L5:2118:G:O2'	1:L5:2119:C:H2'	2.22	0.40
1:L5:3608:A:H2'	1:L5:3609:G:C8	2.57	0.40
1:L5:3681:G:N7	4:LA:125:LYS:HB2	2.36	0.40
1:L5:5043:A:H2'	1:L5:5044:A:C8	2.56	0.40
3:L8:94:G:C5	38:Lj:84:PRO:HG3	2.57	0.40
20:LR:138:LEU:HD12	20:LR:138:LEU:HA	1.93	0.40
25:LW:27:LYS:HA	25:LW:27:LYS:HD3	1.83	0.40
40:Ll:23:ILE:HD12	40:Ll:24:PRO:HD2	2.04	0.40
45:Lr:35:ARG:HG2	45:Lr:37:SER:HB2	2.04	0.40
46:S2:13:C:H4'	46:S2:1356:G:H21	1.86	0.40
46:S2:89:C:H2'	46:S2:90:G:H8	1.86	0.40
46:S2:1275:G:H5''	46:S2:1506:A:H61	1.86	0.40
46:S2:1846:G:H2'	46:S2:1847:G:C8	2.56	0.40
59:SN:127:ARG:O	59:SN:131:THR:HG22	2.20	0.40
62:SQ:16:LYS:NZ	62:SQ:17:LYS:HB3	2.36	0.40
72:Sa:41:ILE:HD13	72:Sa:41:ILE:HA	1.90	0.40
80:zu:23:A:H2'	80:zu:24:U:C6	2.57	0.40
85:3f:95:HIS:H	85:3f:98:ILE:HG12	1.86	0.40
86:3a:43:TRP:HD1	86:3a:78:CYS:HA	1.87	0.40
86:3a:63:LYS:HA	86:3a:63:LYS:HD3	1.78	0.40
88:3c:514:PHE:CE1	88:3c:579:HIS:HA	2.57	0.40
88:3c:549:GLU:HG3	88:3c:572:HIS:CE1	2.56	0.40
89:3h:184:PRO:HG2	89:3h:310:PRO:HG2	2.02	0.40
92:3l:115:ALA:HB2	92:3l:133:LYS:HE3	2.03	0.40
92:3l:189:GLU:HA	92:3l:192:TYR:HB3	2.02	0.40
92:3l:340:LEU:HD23	92:3l:386:ILE:HD12	2.04	0.40
1:L5:1271:G:H5'	1:L5:1271:G:N3	2.36	0.40
1:L5:1291:G:H2'	1:L5:1292:C:C6	2.57	0.40
1:L5:1315:C:H2'	1:L5:1316:G:C8	2.56	0.40
1:L5:2358:G:H2'	1:L5:2359:U:O4'	2.21	0.40
1:L5:2376:A:H2'	1:L5:2377:C:C6	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3654:G:H1	1:L5:3690:U:H3	1.69	0.40
1:L5:3921:U:H1'	1:L5:4543:G:N2	2.36	0.40
1:L5:4263:C:H2'	1:L5:4264:G:O4'	2.21	0.40
8:LE:50:LEU:HG	8:LE:51:VAL:HG12	2.03	0.40
9:LF:182:TYR:CZ	9:LF:203:GLU:HG2	2.56	0.40
22:LT:133:ALA:HA	22:LT:134:PRO:HD3	1.88	0.40
44:Lp:13:LYS:HE2	44:Lp:14:TYR:HE2	1.86	0.40
46:S2:1665:G:H5'	65:ST:89:PRO:HD2	2.04	0.40
71:SZ:85:ARG:H	71:SZ:85:ARG:HG2	1.71	0.40
80:zy:33:A:H2'	80:zy:34:G:C8	2.57	0.40
83:zz:178:C:H2'	83:zz:179:A:C8	2.56	0.40
84:3m:169:TYR:HB2	84:3m:185:MET:HE1	2.03	0.40
85:3f:327:LEU:HD12	89:3h:341:LEU:HD22	2.04	0.40
86:3a:442:GLN:O	86:3a:446:ILE:HG22	2.21	0.40
89:3h:267:THR:HA	89:3h:270:GLN:NE2	2.37	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	LA	246/257 (96%)	213 (87%)	33 (13%)	0	100	100
5	LB	389/403 (96%)	353 (91%)	36 (9%)	0	100	100
6	LC	363/427 (85%)	336 (93%)	27 (7%)	0	100	100
7	LD	291/297 (98%)	277 (95%)	14 (5%)	0	100	100
8	LE	214/288 (74%)	199 (93%)	15 (7%)	0	100	100
9	LF	223/248 (90%)	212 (95%)	11 (5%)	0	100	100
10	LG	235/266 (88%)	218 (93%)	17 (7%)	0	100	100
11	LH	187/192 (97%)	174 (93%)	13 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	LI	199/214 (93%)	187 (94%)	12 (6%)	0	100	100
13	LJ	165/178 (93%)	155 (94%)	10 (6%)	0	100	100
14	LL	202/211 (96%)	186 (92%)	16 (8%)	0	100	100
15	LM	134/215 (62%)	127 (95%)	7 (5%)	0	100	100
16	LN	201/204 (98%)	190 (94%)	11 (6%)	0	100	100
17	LO	199/203 (98%)	192 (96%)	7 (4%)	0	100	100
18	LP	151/184 (82%)	140 (93%)	11 (7%)	0	100	100
19	LQ	185/188 (98%)	180 (97%)	5 (3%)	0	100	100
20	LR	176/196 (90%)	175 (99%)	1 (1%)	0	100	100
21	LS	173/176 (98%)	160 (92%)	12 (7%)	1 (1%)	21	52
22	LT	157/160 (98%)	142 (90%)	15 (10%)	0	100	100
23	LU	99/128 (77%)	92 (93%)	7 (7%)	0	100	100
24	LV	129/140 (92%)	117 (91%)	12 (9%)	0	100	100
25	LW	111/157 (71%)	104 (94%)	7 (6%)	0	100	100
26	LX	118/156 (76%)	107 (91%)	11 (9%)	0	100	100
27	LY	132/145 (91%)	122 (92%)	10 (8%)	0	100	100
28	LZ	133/136 (98%)	128 (96%)	5 (4%)	0	100	100
29	La	142/148 (96%)	132 (93%)	10 (7%)	0	100	100
30	Lb	61/159 (38%)	58 (95%)	3 (5%)	0	100	100
31	Lc	91/115 (79%)	90 (99%)	1 (1%)	0	100	100
32	Ld	105/125 (84%)	99 (94%)	6 (6%)	0	100	100
33	Le	125/135 (93%)	117 (94%)	8 (6%)	0	100	100
34	Lf	107/110 (97%)	95 (89%)	12 (11%)	0	100	100
35	Lg	108/117 (92%)	102 (94%)	6 (6%)	0	100	100
36	Lh	119/123 (97%)	117 (98%)	2 (2%)	0	100	100
37	Li	99/105 (94%)	97 (98%)	2 (2%)	0	100	100
38	Lj	84/97 (87%)	81 (96%)	3 (4%)	0	100	100
39	Lk	67/70 (96%)	60 (90%)	7 (10%)	0	100	100
40	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
41	Lm	48/128 (38%)	48 (100%)	0	0	100	100
42	Ln	22/25 (88%)	22 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	Lo	96/106 (91%)	91 (95%)	5 (5%)	0	100	100
44	Lp	89/92 (97%)	86 (97%)	3 (3%)	0	100	100
45	Lr	123/137 (90%)	114 (93%)	9 (7%)	0	100	100
47	SA	210/295 (71%)	195 (93%)	15 (7%)	0	100	100
48	SB	212/264 (80%)	203 (96%)	9 (4%)	0	100	100
49	SC	215/293 (73%)	201 (94%)	14 (6%)	0	100	100
50	SD	206/243 (85%)	188 (91%)	17 (8%)	1 (0%)	24	55
51	SE	255/263 (97%)	235 (92%)	20 (8%)	0	100	100
52	SF	176/204 (86%)	166 (94%)	10 (6%)	0	100	100
53	SG	227/249 (91%)	205 (90%)	21 (9%)	1 (0%)	30	60
54	SH	172/194 (89%)	155 (90%)	17 (10%)	0	100	100
55	SI	200/208 (96%)	179 (90%)	21 (10%)	0	100	100
56	SJ	174/194 (90%)	165 (95%)	8 (5%)	1 (1%)	21	52
57	SK	93/165 (56%)	85 (91%)	8 (9%)	0	100	100
58	SL	136/158 (86%)	126 (93%)	10 (7%)	0	100	100
59	SN	148/151 (98%)	136 (92%)	12 (8%)	0	100	100
60	SO	133/151 (88%)	118 (89%)	15 (11%)	0	100	100
61	SP	123/145 (85%)	111 (90%)	11 (9%)	1 (1%)	16	45
62	SQ	139/146 (95%)	129 (93%)	10 (7%)	0	100	100
63	SR	123/135 (91%)	106 (86%)	17 (14%)	0	100	100
64	SS	136/152 (90%)	124 (91%)	12 (9%)	0	100	100
65	ST	136/145 (94%)	126 (93%)	10 (7%)	0	100	100
66	SU	94/119 (79%)	89 (95%)	5 (5%)	0	100	100
67	SV	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
68	SW	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
69	SX	139/143 (97%)	119 (86%)	20 (14%)	0	100	100
70	SY	124/133 (93%)	119 (96%)	5 (4%)	0	100	100
71	SZ	67/125 (54%)	61 (91%)	6 (9%)	0	100	100
72	Sa	97/115 (84%)	91 (94%)	6 (6%)	0	100	100
73	Sb	81/84 (96%)	66 (82%)	15 (18%)	0	100	100
74	Sc	59/69 (86%)	49 (83%)	10 (17%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
75	Sd	50/56 (89%)	50 (100%)	0	0	100	100
76	Se	47/59 (80%)	43 (92%)	4 (8%)	0	100	100
77	Sf	68/132 (52%)	60 (88%)	8 (12%)	0	100	100
78	Sg	258/317 (81%)	228 (88%)	30 (12%)	0	100	100
79	sh	35/156 (22%)	31 (89%)	4 (11%)	0	100	100
82	zx	18/31 (58%)	11 (61%)	7 (39%)	0	100	100
84	3m	361/374 (96%)	346 (96%)	15 (4%)	0	100	100
85	3f	267/357 (75%)	263 (98%)	4 (2%)	0	100	100
86	3a	590/1382 (43%)	573 (97%)	17 (3%)	0	100	100
87	3e	427/445 (96%)	407 (95%)	20 (5%)	0	100	100
88	3c	638/913 (70%)	618 (97%)	20 (3%)	0	100	100
89	3h	316/352 (90%)	311 (98%)	5 (2%)	0	100	100
90	3d	53/548 (10%)	47 (89%)	6 (11%)	0	100	100
91	3k	213/218 (98%)	202 (95%)	11 (5%)	0	100	100
92	3l	518/564 (92%)	504 (97%)	14 (3%)	0	100	100
All	All	14288/17872 (80%)	13376 (94%)	907 (6%)	5 (0%)	100	100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	LS	164	LYS
53	SG	132	ARG
61	SP	73	PRO
56	SJ	110	LEU
50	SD	191	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	LA	187/199 (94%)	178 (95%)	9 (5%)	23	52
5	LB	324/349 (93%)	299 (92%)	25 (8%)	12	37
6	LC	301/348 (86%)	285 (95%)	16 (5%)	20	49
7	LD	218/250 (87%)	205 (94%)	13 (6%)	17	46
8	LE	179/252 (71%)	165 (92%)	14 (8%)	11	36
9	LF	187/215 (87%)	173 (92%)	14 (8%)	12	38
10	LG	173/223 (78%)	164 (95%)	9 (5%)	21	49
11	LH	150/171 (88%)	138 (92%)	12 (8%)	11	36
12	LI	156/181 (86%)	145 (93%)	11 (7%)	13	40
13	LJ	113/149 (76%)	103 (91%)	10 (9%)	9	32
14	LL	152/177 (86%)	145 (95%)	7 (5%)	24	53
15	LM	110/161 (68%)	102 (93%)	8 (7%)	13	39
16	LN	169/172 (98%)	161 (95%)	8 (5%)	23	52
17	LO	163/174 (94%)	154 (94%)	9 (6%)	19	48
18	LP	124/163 (76%)	116 (94%)	8 (6%)	15	43
19	LQ	159/165 (96%)	148 (93%)	11 (7%)	14	41
20	LR	143/175 (82%)	132 (92%)	11 (8%)	12	37
21	LS	151/157 (96%)	139 (92%)	12 (8%)	11	36
22	LT	130/140 (93%)	119 (92%)	11 (8%)	10	33
23	LU	77/115 (67%)	67 (87%)	10 (13%)	4	17
24	LV	94/107 (88%)	86 (92%)	8 (8%)	10	33
25	LW	54/126 (43%)	50 (93%)	4 (7%)	13	38
26	LX	98/133 (74%)	94 (96%)	4 (4%)	27	55
27	LY	116/135 (86%)	106 (91%)	10 (9%)	10	33
28	LZ	109/118 (92%)	100 (92%)	9 (8%)	10	34
29	La	116/121 (96%)	109 (94%)	7 (6%)	17	46
30	Lb	49/126 (39%)	45 (92%)	4 (8%)	10	35
31	Lc	76/97 (78%)	73 (96%)	3 (4%)	28	56
32	Ld	88/110 (80%)	83 (94%)	5 (6%)	18	47
33	Le	113/121 (93%)	107 (95%)	6 (5%)	20	49
34	Lf	85/89 (96%)	83 (98%)	2 (2%)	43	65
35	Lg	88/100 (88%)	78 (89%)	10 (11%)	5	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	Lh	100/110 (91%)	92 (92%)	8 (8%)	11	36
37	Li	79/89 (89%)	74 (94%)	5 (6%)	16	44
38	Lj	72/80 (90%)	69 (96%)	3 (4%)	26	55
39	Lk	52/65 (80%)	50 (96%)	2 (4%)	29	57
40	Ll	46/48 (96%)	43 (94%)	3 (6%)	15	43
41	Lm	42/116 (36%)	39 (93%)	3 (7%)	13	40
42	Ln	23/24 (96%)	21 (91%)	2 (9%)	9	32
43	Lo	79/94 (84%)	73 (92%)	6 (8%)	12	37
44	Lp	70/75 (93%)	64 (91%)	6 (9%)	10	33
45	Lr	103/121 (85%)	96 (93%)	7 (7%)	14	42
47	SA	147/243 (60%)	135 (92%)	12 (8%)	10	35
48	SB	162/231 (70%)	157 (97%)	5 (3%)	35	60
49	SC	155/225 (69%)	148 (96%)	7 (4%)	24	53
50	SD	125/202 (62%)	118 (94%)	7 (6%)	19	47
51	SE	176/225 (78%)	165 (94%)	11 (6%)	16	44
52	SF	133/170 (78%)	132 (99%)	1 (1%)	73	79
53	SG	160/218 (73%)	153 (96%)	7 (4%)	25	54
54	SH	137/174 (79%)	126 (92%)	11 (8%)	11	36
55	SI	149/180 (83%)	142 (95%)	7 (5%)	23	52
56	SJ	140/168 (83%)	135 (96%)	5 (4%)	31	58
57	SK	68/136 (50%)	65 (96%)	3 (4%)	25	54
58	SL	124/142 (87%)	119 (96%)	5 (4%)	28	56
59	SN	127/131 (97%)	122 (96%)	5 (4%)	28	56
60	SO	103/119 (87%)	96 (93%)	7 (7%)	14	42
61	SP	103/130 (79%)	96 (93%)	7 (7%)	14	42
62	SQ	105/121 (87%)	101 (96%)	4 (4%)	29	57
63	SR	77/122 (63%)	74 (96%)	3 (4%)	28	56
64	SS	103/132 (78%)	96 (93%)	7 (7%)	14	42
65	ST	80/115 (70%)	72 (90%)	8 (10%)	7	27
66	SU	77/107 (72%)	72 (94%)	5 (6%)	15	43
67	SV	53/67 (79%)	50 (94%)	3 (6%)	18	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	SW	110/113 (97%)	99 (90%)	11 (10%)	7	27
69	SX	101/115 (88%)	92 (91%)	9 (9%)	9	32
70	SY	87/115 (76%)	84 (97%)	3 (3%)	32	59
71	SZ	39/103 (38%)	36 (92%)	3 (8%)	12	37
72	Sa	79/98 (81%)	74 (94%)	5 (6%)	16	44
73	Sb	64/76 (84%)	58 (91%)	6 (9%)	8	30
74	Sc	41/62 (66%)	35 (85%)	6 (15%)	3	14
75	Sd	42/49 (86%)	33 (79%)	9 (21%)	1	5
76	Se	37/48 (77%)	36 (97%)	1 (3%)	39	63
77	Sf	30/108 (28%)	27 (90%)	3 (10%)	7	27
78	Sg	167/275 (61%)	151 (90%)	16 (10%)	8	29
79	sh	17/140 (12%)	17 (100%)	0	100	100
82	zx	5/29 (17%)	5 (100%)	0	100	100
84	3m	252/335 (75%)	245 (97%)	7 (3%)	38	62
85	3f	229/289 (79%)	226 (99%)	3 (1%)	61	74
86	3a	439/1259 (35%)	426 (97%)	13 (3%)	36	61
87	3e	301/406 (74%)	295 (98%)	6 (2%)	48	68
88	3c	442/811 (54%)	430 (97%)	12 (3%)	39	63
89	3h	272/310 (88%)	264 (97%)	8 (3%)	37	62
90	3d	20/494 (4%)	19 (95%)	1 (5%)	22	50
91	3k	121/193 (63%)	115 (95%)	6 (5%)	22	50
92	3l	474/515 (92%)	467 (98%)	7 (2%)	57	72
All	All	10991/15442 (71%)	10381 (94%)	610 (6%)	21	48

All (610) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	LA	14	SER
4	LA	29	LEU
4	LA	82	ILE
4	LA	135	THR
4	LA	139	HIS
4	LA	165	VAL
4	LA	169	VAL

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Mol	Chain	Res	Type
4	LA	235	VAL
4	LA	246	LEU
5	LB	2	SER
5	LB	31	SER
5	LB	46	PHE
5	LB	67	VAL
5	LB	72	VAL
5	LB	73	VAL
5	LB	76	VAL
5	LB	78	ILE
5	LB	110	ILE
5	LB	134	CYS
5	LB	190	VAL
5	LB	194	LEU
5	LB	210	VAL
5	LB	214	ASP
5	LB	219	VAL
5	LB	222	VAL
5	LB	248	LEU
5	LB	251	VAL
5	LB	258	HIS
5	LB	262	VAL
5	LB	305	THR
5	LB	338	VAL
5	LB	352	LEU
5	LB	371	THR
5	LB	381	THR
6	LC	3	CYS
6	LC	10	VAL
6	LC	27	VAL
6	LC	62	THR
6	LC	67	TRP
6	LC	76	ILE
6	LC	96	CYS
6	LC	144	ILE
6	LC	159	GLU
6	LC	174	LEU
6	LC	209	ILE
6	LC	240	LEU
6	LC	260	LEU
6	LC	279	LEU
6	LC	281	MET

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Mol	Chain	Res	Type
6	LC	325	MET
7	LD	4	VAL
7	LD	7	VAL
7	LD	15	ARG
7	LD	46	THR
7	LD	54	ARG
7	LD	55	VAL
7	LD	60	ILE
7	LD	63	GLN
7	LD	111	ASN
7	LD	134	SER
7	LD	144	CYS
7	LD	223	PHE
7	LD	288	LEU
8	LE	49	VAL
8	LE	109	LEU
8	LE	112	MET
8	LE	121	VAL
8	LE	139	LYS
8	LE	149	ILE
8	LE	172	LEU
8	LE	184	VAL
8	LE	199	THR
8	LE	242	ILE
8	LE	257	ILE
8	LE	267	LEU
8	LE	271	LEU
8	LE	273	SER
9	LF	34	ARG
9	LF	83	VAL
9	LF	89	LEU
9	LF	92	VAL
9	LF	93	ILE
9	LF	105	VAL
9	LF	114	LEU
9	LF	133	LEU
9	LF	175	ILE
9	LF	191	ILE
9	LF	215	SER
9	LF	236	ARG
9	LF	237	GLU
9	LF	247	MET

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Mol	Chain	Res	Type
10	LG	28	VAL
10	LG	29	ASN
10	LG	71	TYR
10	LG	94	GLN
10	LG	114	LEU
10	LG	155	VAL
10	LG	166	LEU
10	LG	222	ILE
10	LG	225	ASN
11	LH	10	VAL
11	LH	24	THR
11	LH	27	VAL
11	LH	75	SER
11	LH	103	VAL
11	LH	105	ILE
11	LH	126	VAL
11	LH	136	VAL
11	LH	160	LEU
11	LH	179	ILE
11	LH	184	LYS
11	LH	187	VAL
12	LI	12	CYS
12	LI	24	ARG
12	LI	39	LYS
12	LI	115	MET
12	LI	131	ILE
12	LI	145	GLU
12	LI	149	ILE
12	LI	164	LYS
12	LI	167	ILE
12	LI	197	VAL
12	LI	202	SER
13	LJ	22	LEU
13	LJ	25	CYS
13	LJ	47	THR
13	LJ	57	VAL
13	LJ	72	CYS
13	LJ	94	LEU
13	LJ	132	VAL
13	LJ	133	VAL
13	LJ	161	GLU
13	LJ	163	MET

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Mol	Chain	Res	Type
14	LL	58	ILE
14	LL	63	THR
14	LL	80	GLU
14	LL	81	LEU
14	LL	94	ILE
14	LL	125	ILE
14	LL	170	THR
15	LM	15	VAL
15	LM	31	ILE
15	LM	43	THR
15	LM	57	LEU
15	LM	58	THR
15	LM	95	ILE
15	LM	96	GLU
15	LM	105	THR
16	LN	22	LEU
16	LN	33	LEU
16	LN	36	LEU
16	LN	61	ILE
16	LN	87	HIS
16	LN	89	VAL
16	LN	142	ILE
16	LN	147	ASP
17	LO	23	VAL
17	LO	28	LEU
17	LO	29	LEU
17	LO	34	VAL
17	LO	87	MET
17	LO	88	LEU
17	LO	120	VAL
17	LO	126	VAL
17	LO	199	HIS
18	LP	2	VAL
18	LP	26	PHE
18	LP	53	LEU
18	LP	64	ASN
18	LP	67	VAL
18	LP	79	THR
18	LP	109	VAL
18	LP	116	HIS
19	LQ	13	VAL
19	LQ	28	LEU

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Mol	Chain	Res	Type
19	LQ	35	LEU
19	LQ	37	ARG
19	LQ	48	LEU
19	LQ	62	SER
19	LQ	72	LEU
19	LQ	81	VAL
19	LQ	85	THR
19	LQ	123	PHE
19	LQ	158	THR
20	LR	12	SER
20	LR	17	CYS
20	LR	22	VAL
20	LR	45	ILE
20	LR	53	LYS
20	LR	59	SER
20	LR	63	CYS
20	LR	66	ASN
20	LR	154	LEU
20	LR	155	LEU
20	LR	168	GLU
21	LS	7	LEU
21	LS	13	VAL
21	LS	23	HIS
21	LS	51	LEU
21	LS	57	SER
21	LS	61	ILE
21	LS	90	THR
21	LS	91	HIS
21	LS	106	VAL
21	LS	150	ILE
21	LS	158	VAL
21	LS	174	THR
22	LT	7	LYS
22	LT	11	THR
22	LT	42	ILE
22	LT	45	MET
22	LT	67	VAL
22	LT	69	GLN
22	LT	75	VAL
22	LT	91	VAL
22	LT	96	ILE
22	LT	121	GLU

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Mol	Chain	Res	Type
22	LT	143	THR
23	LU	18	VAL
23	LU	19	LEU
23	LU	43	LEU
23	LU	49	VAL
23	LU	68	SER
23	LU	72	VAL
23	LU	73	THR
23	LU	76	VAL
23	LU	78	PHE
23	LU	102	VAL
24	LV	16	ILE
24	LV	27	ASN
24	LV	32	THR
24	LV	76	VAL
24	LV	99	GLU
24	LV	104	VAL
24	LV	117	ILE
24	LV	128	LEU
25	LW	24	THR
25	LW	47	ARG
25	LW	52	THR
25	LW	54	LEU
26	LX	40	ILE
26	LX	82	THR
26	LX	115	LYS
26	LX	144	TYR
27	LY	8	THR
27	LY	14	ASN
27	LY	57	VAL
27	LY	74	TYR
27	LY	78	TYR
27	LY	82	ILE
27	LY	83	GLU
27	LY	85	VAL
27	LY	97	VAL
27	LY	102	SER
28	LZ	5	MET
28	LZ	26	VAL
28	LZ	28	ASN
28	LZ	53	VAL
28	LZ	57	MET

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Mol	Chain	Res	Type
28	LZ	80	LEU
28	LZ	81	MET
28	LZ	83	THR
28	LZ	96	VAL
29	La	5	LEU
29	La	15	VAL
29	La	56	VAL
29	La	84	GLU
29	La	117	LEU
29	La	132	ARG
29	La	144	CYS
30	Lb	18	ARG
30	Lb	21	ILE
30	Lb	50	ASN
30	Lb	57	MET
31	Lc	55	LEU
31	Lc	61	GLU
31	Lc	71	VAL
32	Ld	22	THR
32	Ld	26	THR
32	Ld	33	ILE
32	Ld	113	THR
32	Ld	122	VAL
33	Le	4	LEU
33	Le	43	ASN
33	Le	45	VAL
33	Le	79	VAL
33	Le	99	ILE
33	Le	118	LEU
34	Lf	4	ARG
34	Lf	81	SER
35	Lg	25	THR
35	Lg	32	TYR
35	Lg	38	VAL
35	Lg	54	ARG
35	Lg	56	VAL
35	Lg	59	VAL
35	Lg	67	LEU
35	Lg	71	LYS
35	Lg	83	CYS
35	Lg	86	CYS
36	Lh	18	LEU

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Mol	Chain	Res	Type
36	Lh	23	ASP
36	Lh	36	VAL
36	Lh	45	SER
36	Lh	47	ILE
36	Lh	57	VAL
36	Lh	61	ILE
36	Lh	104	THR
37	Li	11	LEU
37	Li	48	CYS
37	Li	77	VAL
37	Li	81	ILE
37	Li	94	LEU
38	Lj	50	SER
38	Lj	68	LYS
38	Lj	69	ILE
39	Lk	39	SER
39	Lk	46	VAL
40	Ll	6	THR
40	Ll	27	ILE
40	Ll	48	LYS
41	Lm	85	LEU
41	Lm	97	ARG
41	Lm	108	VAL
42	Ln	23	ARG
42	Ln	24	SER
43	Lo	34	TYR
43	Lo	55	ILE
43	Lo	61	LYS
43	Lo	68	LEU
43	Lo	77	CYS
43	Lo	85	ILE
44	Lp	8	VAL
44	Lp	33	GLN
44	Lp	54	ILE
44	Lp	70	THR
44	Lp	79	VAL
44	Lp	83	ILE
45	Lr	6	GLN
45	Lr	18	ILE
45	Lr	21	ASN
45	Lr	80	THR
45	Lr	81	THR

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Mol	Chain	Res	Type
45	Lr	106	LEU
45	Lr	118	LEU
47	SA	23	THR
47	SA	28	THR
47	SA	36	GLN
47	SA	82	THR
47	SA	118	GLU
47	SA	124	VAL
47	SA	130	ASP
47	SA	156	TYR
47	SA	159	ILE
47	SA	174	MET
47	SA	198	MET
47	SA	201	LEU
48	SB	39	PHE
48	SB	43	ASN
48	SB	48	LEU
48	SB	139	CYS
48	SB	171	ILE
49	SC	64	THR
49	SC	75	ILE
49	SC	96	PHE
49	SC	98	LEU
49	SC	122	THR
49	SC	191	VAL
49	SC	193	VAL
50	SD	46	THR
50	SD	76	ARG
50	SD	97	CYS
50	SD	134	CYS
50	SD	137	VAL
50	SD	164	VAL
50	SD	186	VAL
51	SE	23	LEU
51	SE	45	ILE
51	SE	47	PHE
51	SE	80	ILE
51	SE	86	PHE
51	SE	102	ILE
51	SE	105	THR
51	SE	106	LYS
51	SE	133	THR

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Mol	Chain	Res	Type
51	SE	180	LEU
51	SE	246	LEU
52	SF	104	THR
53	SG	10	THR
53	SG	26	THR
53	SG	36	VAL
53	SG	81	HIS
53	SG	91	GLU
53	SG	102	VAL
53	SG	140	ARG
54	SH	53	VAL
54	SH	60	ILE
54	SH	92	VAL
54	SH	95	ILE
54	SH	114	GLN
54	SH	123	THR
54	SH	144	ILE
54	SH	147	LYS
54	SH	174	SER
54	SH	184	ASP
54	SH	185	VAL
55	SI	76	THR
55	SI	79	ILE
55	SI	91	VAL
55	SI	98	LYS
55	SI	107	THR
55	SI	138	ASN
55	SI	186	ASP
56	SJ	50	LEU
56	SJ	63	LEU
56	SJ	67	ASP
56	SJ	73	GLU
56	SJ	102	ILE
57	SK	62	PHE
57	SK	71	LEU
57	SK	90	VAL
58	SL	52	GLU
58	SL	66	VAL
58	SL	76	VAL
58	SL	85	THR
58	SL	134	LEU
59	SN	3	ARG

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Mol	Chain	Res	Type
59	SN	9	LYS
59	SN	11	LEU
59	SN	60	VAL
59	SN	149	LEU
60	SO	30	VAL
60	SO	32	HIS
60	SO	40	THR
60	SO	56	VAL
60	SO	81	VAL
60	SO	133	THR
60	SO	135	ILE
61	SP	16	THR
61	SP	56	LEU
61	SP	85	ILE
61	SP	90	VAL
61	SP	107	ILE
61	SP	111	MET
61	SP	115	TYR
62	SQ	18	THR
62	SQ	20	THR
62	SQ	31	LEU
62	SQ	70	VAL
63	SR	40	ILE
63	SR	62	GLN
63	SR	70	SER
64	SS	12	ILE
64	SS	18	THR
64	SS	31	THR
64	SS	52	LEU
64	SS	83	PHE
64	SS	103	LEU
64	SS	131	VAL
65	ST	15	VAL
65	ST	36	THR
65	ST	45	LEU
65	ST	63	HIS
65	ST	87	VAL
65	ST	99	VAL
65	ST	110	LEU
65	ST	123	LEU
66	SU	28	ASN
66	SU	39	LEU

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Mol	Chain	Res	Type
66	SU	61	LEU
66	SU	87	ARG
66	SU	114	VAL
67	SV	13	VAL
67	SV	32	ILE
67	SV	36	VAL
68	SW	11	LEU
68	SW	16	ASN
68	SW	30	CYS
68	SW	34	ILE
68	SW	74	VAL
68	SW	75	ILE
68	SW	83	LEU
68	SW	93	LEU
68	SW	103	VAL
68	SW	104	LEU
68	SW	105	THR
69	SX	7	LEU
69	SX	13	LEU
69	SX	34	THR
69	SX	66	ILE
69	SX	70	VAL
69	SX	74	LEU
69	SX	97	ASN
69	SX	122	VAL
69	SX	125	VAL
70	SY	7	ILE
70	SY	24	VAL
70	SY	64	PHE
71	SZ	47	LEU
71	SZ	69	THR
71	SZ	103	HIS
72	Sa	54	SER
72	Sa	71	LEU
72	Sa	74	CYS
72	Sa	86	ASN
72	Sa	88	SER
73	Sb	11	SER
73	Sb	18	LYS
73	Sb	61	THR
73	Sb	64	CYS
73	Sb	73	LEU

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Mol	Chain	Res	Type
73	Sb	84	HIS
74	Sc	13	ARG
74	Sc	17	VAL
74	Sc	18	LEU
74	Sc	28	THR
74	Sc	30	VAL
74	Sc	32	VAL
75	Sd	7	TYR
75	Sd	8	TRP
75	Sd	14	PHE
75	Sd	24	CYS
75	Sd	25	SER
75	Sd	28	HIS
75	Sd	30	LEU
75	Sd	44	ARG
75	Sd	50	ILE
76	Se	116	VAL
77	Sf	51	VAL
77	Sf	89	VAL
77	Sf	104	VAL
78	Sg	23	THR
78	Sg	57	ARG
78	Sg	74	ASP
78	Sg	83	TRP
78	Sg	91	ASP
78	Sg	94	THR
78	Sg	124	SER
78	Sg	140	TYR
78	Sg	147	HIS
78	Sg	150	TRP
78	Sg	153	CYS
78	Sg	206	LEU
78	Sg	227	LEU
78	Sg	236	ILE
78	Sg	259	TRP
78	Sg	306	LEU
84	3m	122	THR
84	3m	163	THR
84	3m	169	TYR
84	3m	173	VAL
84	3m	192	TYR
84	3m	255	PHE

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Mol	Chain	Res	Type
84	3m	266	LEU
85	3f	91	VAL
85	3f	148	VAL
85	3f	357	LEU
86	3a	19	LEU
86	3a	62	ARG
86	3a	187	GLN
86	3a	228	MET
86	3a	233	ARG
86	3a	297	HIS
86	3a	332	THR
86	3a	366	THR
86	3a	383	VAL
86	3a	384	VAL
86	3a	465	PHE
86	3a	477	HIS
86	3a	524	THR
87	3e	161	THR
87	3e	186	MET
87	3e	315	CYS
87	3e	326	VAL
87	3e	342	GLU
87	3e	351	ILE
88	3c	67	ILE
88	3c	86	LEU
88	3c	120	LEU
88	3c	123	ASP
88	3c	138	LEU
88	3c	152	PHE
88	3c	470	VAL
88	3c	571	CYS
88	3c	616	LEU
88	3c	697	TYR
88	3c	752	CYS
88	3c	761	MET
89	3h	95	ASP
89	3h	96	GLU
89	3h	129	VAL
89	3h	155	ILE
89	3h	197	MET
89	3h	201	VAL
89	3h	209	HIS

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Mol	Chain	Res	Type
89	3h	261	ASN
90	3d	26	ARG
91	3k	84	LEU
91	3k	125	MET
91	3k	161	MET
91	3k	187	ILE
91	3k	189	ILE
91	3k	194	GLU
92	3l	59	PHE
92	3l	95	TYR
92	3l	266	TYR
92	3l	296	ASN
92	3l	336	PHE
92	3l	353	THR
92	3l	444	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (107) such sidechains are listed below:

Mol	Chain	Res	Type
4	LA	187	HIS
5	LB	213	GLN
5	LB	354	GLN
5	LB	376	HIS
6	LC	85	HIS
6	LC	89	GLN
6	LC	187	GLN
6	LC	198	ASN
6	LC	329	ASN
7	LD	157	ASN
7	LD	225	GLN
7	LD	267	ASN
8	LE	245	GLN
8	LE	284	HIS
9	LF	80	ASN
9	LF	205	ASN
9	LF	239	GLN
10	LG	81	ASN
10	LG	159	HIS
11	LH	106	GLN
12	LI	59	GLN
14	LL	87	HIS
15	LM	20	HIS

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Mol	Chain	Res	Type
15	LM	48	GLN
15	LM	70	GLN
16	LN	8	GLN
17	LO	14	HIS
17	LO	26	GLN
18	LP	97	ASN
19	LQ	44	ASN
19	LQ	125	GLN
21	LS	77	ASN
22	LT	69	GLN
26	LX	107	HIS
27	LY	96	HIS
28	LZ	40	HIS
28	LZ	127	ASN
29	La	17	HIS
29	La	28	HIS
29	La	67	GLN
29	La	89	ASN
31	Lc	40	GLN
31	Lc	77	ASN
31	Lc	78	ASN
32	Ld	28	ASN
32	Ld	121	ASN
36	Lh	63	GLN
38	Lj	28	HIS
40	Ll	17	GLN
41	Lm	104	HIS
43	Lo	51	GLN
45	Lr	23	GLN
45	Lr	31	ASN
47	SA	111	GLN
47	SA	164	ASN
48	SB	92	GLN
48	SB	202	GLN
50	SD	159	HIS
52	SF	74	ASN
55	SI	165	GLN
55	SI	181	GLN
58	SL	83	GLN
59	SN	13	GLN
61	SP	32	GLN
61	SP	53	GLN

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Mol	Chain	Res	Type
62	SQ	35	ASN
62	SQ	142	GLN
64	SS	10	GLN
65	ST	12	GLN
66	SU	81	GLN
69	SX	77	ASN
70	SY	124	ASN
71	SZ	89	GLN
72	Sa	8	ASN
72	Sa	86	ASN
74	Sc	24	GLN
76	Se	110	GLN
77	Sf	82	ASN
78	Sg	64	HIS
78	Sg	196	ASN
84	3m	104	GLN
84	3m	111	HIS
84	3m	259	ASN
85	3f	133	ASN
86	3a	175	HIS
86	3a	180	GLN
86	3a	219	ASN
87	3e	181	ASN
87	3e	335	ASN
87	3e	396	ASN
88	3c	143	GLN
88	3c	572	HIS
88	3c	576	HIS
88	3c	584	GLN
88	3c	615	GLN
88	3c	630	HIS
88	3c	762	ASN
88	3c	845	HIS
88	3c	858	GLN
89	3h	261	ASN
89	3h	266	ASN
89	3h	283	GLN
89	3h	351	ASN
92	3l	243	GLN
92	3l	363	GLN
92	3l	402	GLN
92	3l	495	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3572/5070 (70%)	798 (22%)	14 (0%)
2	L7	119/120 (99%)	17 (14%)	1 (0%)
3	L8	155/156 (99%)	36 (23%)	2 (1%)
46	S2	1662/1869 (88%)	480 (28%)	13 (0%)
80	zu	71/75 (94%)	20 (28%)	0
80	zy	74/75 (98%)	16 (21%)	0
81	zv	8/19 (42%)	5 (62%)	0
83	zz	210/332 (63%)	73 (34%)	0
All	All	5871/7716 (76%)	1445 (24%)	30 (0%)

All (1445) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	17	A
1	L5	21	G
1	L5	25	A
1	L5	26	C
1	L5	30	C
1	L5	39	A
1	L5	42	A
1	L5	48	G
1	L5	59	A
1	L5	64	A
1	L5	65	A
1	L5	71	C
1	L5	72	C
1	L5	73	A
1	L5	76	A
1	L5	84	A
1	L5	91	G
1	L5	104	G
1	L5	106	A
1	L5	109	G
1	L5	110	C
1	L5	116	G
1	L5	119	G
1	L5	120	A
1	L5	122	U
1	L5	124	C
1	L5	128	C
1	L5	133	C

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Mol	Chain	Res	Type
1	L5	134	G
1	L5	135	G
1	L5	136	C
1	L5	137	G
1	L5	149	A
1	L5	150	U
1	L5	152	U
1	L5	159	C
1	L5	165	A
1	L5	166	C
1	L5	181	C
1	L5	183	C
1	L5	184	U
1	L5	185	C
1	L5	188	G
1	L5	189	G
1	L5	190	G
1	L5	200	U
1	L5	216	C
1	L5	218	A
1	L5	220	C
1	L5	225	G
1	L5	232	G
1	L5	234	G
1	L5	258	G
1	L5	261	G
1	L5	265	C
1	L5	266	C
1	L5	276	C
1	L5	280	G
1	L5	281	U
1	L5	296	A
1	L5	297	U
1	L5	306	A
1	L5	309	C
1	L5	315	G
1	L5	316	U
1	L5	340	C
1	L5	341	G
1	L5	345	C
1	L5	350	C
1	L5	354	U

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Mol	Chain	Res	Type
1	L5	358	C
1	L5	364	G
1	L5	373	G
1	L5	387	G
1	L5	388	A
1	L5	407	A
1	L5	409	G
1	L5	410	A
1	L5	412	G
1	L5	413	G
1	L5	414	C
1	L5	437	G
1	L5	440	U
1	L5	449	C
1	L5	450	G
1	L5	452	A
1	L5	454	U
1	L5	456	C
1	L5	457	G
1	L5	465	G
1	L5	467	U
1	L5	483	G
1	L5	484	U
1	L5	485	C
1	L5	486	C
1	L5	487	G
1	L5	489	C
1	L5	493	G
1	L5	494	U
1	L5	496	G
1	L5	497	G
1	L5	498	C
1	L5	500	G
1	L5	501	C
1	L5	502	C
1	L5	503	C
1	L5	504	G
1	L5	505	G
1	L5	509	A
1	L5	510	U
1	L5	512	U
1	L5	513	U

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Mol	Chain	Res	Type
1	L5	514	U
1	L5	516	C
1	L5	517	C
1	L5	519	C
1	L5	643	C
1	L5	644	G
1	L5	646	G
1	L5	653	U
1	L5	654	C
1	L5	655	C
1	L5	657	C
1	L5	666	G
1	L5	667	A
1	L5	668	C
1	L5	669	C
1	L5	673	C
1	L5	674	G
1	L5	685	C
1	L5	686	A
1	L5	687	U
1	L5	688	U
1	L5	696	C
1	L5	703	G
1	L5	704	C
1	L5	705	G
1	L5	708	G
1	L5	729	G
1	L5	731	G
1	L5	738	C
1	L5	739	G
1	L5	745	G
1	L5	758	G
1	L5	904	C
1	L5	905	C
1	L5	913	U
1	L5	914	U
1	L5	915	A
1	L5	917	A
1	L5	918	G
1	L5	923	C
1	L5	924	C
1	L5	932	A

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Mol	Chain	Res	Type
1	L5	933	G
1	L5	934	C
1	L5	935	A
1	L5	937	U
1	L5	941	C
1	L5	943	A
1	L5	944	A
1	L5	945	U
1	L5	946	C
1	L5	957	G
1	L5	959	G
1	L5	960	A
1	L5	961	G
1	L5	962	C
1	L5	963	G
1	L5	965	G
1	L5	968	C
1	L5	969	C
1	L5	970	G
1	L5	971	U
1	L5	982	U
1	L5	985	C
1	L5	988	C
1	L5	989	U
1	L5	990	C
1	L5	991	C
1	L5	992	C
1	L5	1070	G
1	L5	1072	C
1	L5	1074	G
1	L5	1082	C
1	L5	1083	U
1	L5	1094	G
1	L5	1095	A
1	L5	1168	G
1	L5	1170	G
1	L5	1171	G
1	L5	1173	G
1	L5	1179	U
1	L5	1180	C
1	L5	1182	C
1	L5	1183	C

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Mol	Chain	Res	Type
1	L5	1184	A
1	L5	1202	C
1	L5	1203	G
1	L5	1211	G
1	L5	1214	C
1	L5	1215	C
1	L5	1216	C
1	L5	1217	G
1	L5	1218	G
1	L5	1220	G
1	L5	1222	A
1	L5	1235	G
1	L5	1241	C
1	L5	1243	C
1	L5	1245	C
1	L5	1246	G
1	L5	1252	C
1	L5	1253	G
1	L5	1259	G
1	L5	1262	G
1	L5	1266	G
1	L5	1268	G
1	L5	1269	G
1	L5	1271	G
1	L5	1272	C
1	L5	1273	G
1	L5	1274	A
1	L5	1275	G
1	L5	1280	C
1	L5	1284	G
1	L5	1293	G
1	L5	1294	A
1	L5	1295	C
1	L5	1296	G
1	L5	1301	C
1	L5	1320	U
1	L5	1326	A
1	L5	1337	A
1	L5	1344	C
1	L5	1354	A
1	L5	1358	G
1	L5	1359	G

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Mol	Chain	Res	Type
1	L5	1365	C
1	L5	1366	G
1	L5	1367	C
1	L5	1370	G
1	L5	1379	C
1	L5	1381	U
1	L5	1387	A
1	L5	1394	G
1	L5	1397	A
1	L5	1399	G
1	L5	1405	C
1	L5	1407	C
1	L5	1408	G
1	L5	1409	C
1	L5	1410	U
1	L5	1420	A
1	L5	1421	G
1	L5	1439	C
1	L5	1441	C
1	L5	1442	C
1	L5	1444	G
1	L5	1447	C
1	L5	1482	G
1	L5	1483	C
1	L5	1497	A
1	L5	1498	G
1	L5	1502	G
1	L5	1518	A
1	L5	1523	A
1	L5	1525	A
1	L5	1534	A
1	L5	1543	G
1	L5	1547	A
1	L5	1564	A
1	L5	1565	A
1	L5	1566	C
1	L5	1578	U
1	L5	1591	U
1	L5	1592	G
1	L5	1596	U
1	L5	1597	G
1	L5	1612	G

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Mol	Chain	Res	Type
1	L5	1614	C
1	L5	1624	G
1	L5	1625	G
1	L5	1626	G
1	L5	1631	A
1	L5	1633	G
1	L5	1634	A
1	L5	1637	A
1	L5	1640	C
1	L5	1641	G
1	L5	1654	G
1	L5	1660	U
1	L5	1661	C
1	L5	1676	C
1	L5	1677	U
1	L5	1679	A
1	L5	1681	G
1	L5	1685	G
1	L5	1697	G
1	L5	1698	C
1	L5	1699	A
1	L5	1703	C
1	L5	1704	C
1	L5	1705	G
1	L5	1707	C
1	L5	1716	G
1	L5	1717	C
1	L5	1719	A
1	L5	1724	G
1	L5	1731	C
1	L5	1742	A
1	L5	1750	G
1	L5	1757	U
1	L5	1758	G
1	L5	1760	G
1	L5	1761	G
1	L5	1762	C
1	L5	1772	C
1	L5	1787	A
1	L5	1804	A
1	L5	1806	G
1	L5	1810	G

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Mol	Chain	Res	Type
1	L5	1819	G
1	L5	1821	G
1	L5	1822	U
1	L5	1836	G
1	L5	1837	A
1	L5	1842	G
1	L5	1855	G
1	L5	1869	G
1	L5	1881	C
1	L5	1897	A
1	L5	1916	G
1	L5	1918	U
1	L5	1919	G
1	L5	1920	C
1	L5	1921	C
1	L5	1922	G
1	L5	1925	G
1	L5	1931	C
1	L5	1932	A
1	L5	1936	C
1	L5	1948	G
1	L5	1951	G
1	L5	1959	U
1	L5	1960	A
1	L5	1961	G
1	L5	1962	A
1	L5	1966	C
1	L5	1968	G
1	L5	1969	G
1	L5	1994	C
1	L5	1996	C
1	L5	1997	U
1	L5	1998	A
1	L5	1999	A
1	L5	2000	G
1	L5	2018	C
1	L5	2019	C
1	L5	2020	U
1	L5	2022	C
1	L5	2023	C
1	L5	2024	G
1	L5	2025	A

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Mol	Chain	Res	Type
1	L5	2026	A
1	L5	2045	G
1	L5	2046	G
1	L5	2048	U
1	L5	2055	G
1	L5	2056	G
1	L5	2064	G
1	L5	2065	G
1	L5	2069	A
1	L5	2084	C
1	L5	2089	G
1	L5	2091	C
1	L5	2092	G
1	L5	2093	A
1	L5	2095	A
1	L5	2096	G
1	L5	2097	U
1	L5	2098	G
1	L5	2099	G
1	L5	2101	C
1	L5	2102	G
1	L5	2103	G
1	L5	2107	C
1	L5	2116	C
1	L5	2117	G
1	L5	2118	G
1	L5	2119	C
1	L5	2120	G
1	L5	2122	G
1	L5	2123	C
1	L5	2255	C
1	L5	2256	C
1	L5	2257	C
1	L5	2258	C
1	L5	2269	C
1	L5	2289	C
1	L5	2300	A
1	L5	2301	G
1	L5	2306	G
1	L5	2313	A
1	L5	2316	G
1	L5	2331	G

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Mol	Chain	Res	Type
1	L5	2332	A
1	L5	2333	G
1	L5	2342	G
1	L5	2346	C
1	L5	2348	G
1	L5	2349	A
1	L5	2351	C
1	L5	2360	A
1	L5	2382	A
1	L5	2397	G
1	L5	2398	U
1	L5	2402	G
1	L5	2410	C
1	L5	2417	A
1	L5	2421	G
1	L5	2422	C
1	L5	2424	G
1	L5	2425	U
1	L5	2437	C
1	L5	2441	C
1	L5	2442	G
1	L5	2453	A
1	L5	2464	C
1	L5	2465	C
1	L5	2470	C
1	L5	2471	G
1	L5	2474	G
1	L5	2475	G
1	L5	2478	C
1	L5	2483	G
1	L5	2484	A
1	L5	2485	U
1	L5	2487	G
1	L5	2488	C
1	L5	2489	C
1	L5	2490	U
1	L5	2493	G
1	L5	2494	U
1	L5	2495	U
1	L5	2496	G
1	L5	2503	G
1	L5	2504	C

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Mol	Chain	Res	Type
1	L5	2505	C
1	L5	2506	G
1	L5	2507	A
1	L5	2511	A
1	L5	2513	A
1	L5	2518	G
1	L5	2519	U
1	L5	2527	A
1	L5	2529	A
1	L5	2537	A
1	L5	2544	G
1	L5	2546	G
1	L5	2547	G
1	L5	2554	U
1	L5	2557	G
1	L5	2558	C
1	L5	2560	C
1	L5	2565	A
1	L5	2583	C
1	L5	2586	G
1	L5	2587	A
1	L5	2589	C
1	L5	2601	A
1	L5	2602	G
1	L5	2618	G
1	L5	2627	C
1	L5	2638	G
1	L5	2653	C
1	L5	2658	G
1	L5	2662	G
1	L5	2664	G
1	L5	2669	C
1	L5	2670	C
1	L5	2673	G
1	L5	2675	G
1	L5	2676	A
1	L5	2687	U
1	L5	2694	G
1	L5	2695	A
1	L5	2696	A
1	L5	2703	G
1	L5	2707	U

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Mol	Chain	Res	Type
1	L5	2711	G
1	L5	2714	G
1	L5	2719	C
1	L5	2721	G
1	L5	2724	G
1	L5	2726	G
1	L5	2739	C
1	L5	2742	G
1	L5	2743	A
1	L5	2754	G
1	L5	2758	G
1	L5	2759	G
1	L5	2761	U
1	L5	2763	U
1	L5	2764	A
1	L5	2770	C
1	L5	2788	U
1	L5	2790	U
1	L5	2791	C
1	L5	2794	C
1	L5	2799	G
1	L5	2814	C
1	L5	2815	A
1	L5	2826	U
1	L5	2827	G
1	L5	2838	G
1	L5	2842	G
1	L5	2848	G
1	L5	2855	G
1	L5	2867	C
1	L5	2877	G
1	L5	2902	G
1	L5	2903	G
1	L5	2904	U
1	L5	2905	C
1	L5	3588	C
1	L5	3591	C
1	L5	3592	G
1	L5	3593	C
1	L5	3596	A
1	L5	3597	G
1	L5	3604	A

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Mol	Chain	Res	Type
1	L5	3605	C
1	L5	3606	U
1	L5	3615	G
1	L5	3618	C
1	L5	3626	G
1	L5	3630	A
1	L5	3635	A
1	L5	3646	A
1	L5	3662	A
1	L5	3664	G
1	L5	3673	C
1	L5	3674	G
1	L5	3682	A
1	L5	3683	C
1	L5	3710	G
1	L5	3711	A
1	L5	3716	C
1	L5	3717	A
1	L5	3726	A
1	L5	3727	A
1	L5	3735	G
1	L5	3736	A
1	L5	3750	G
1	L5	3756	A
1	L5	3757	G
1	L5	3758	U
1	L5	3760	A
1	L5	3763	A
1	L5	3769	C
1	L5	3773	U
1	L5	3774	A
1	L5	3776	G
1	L5	3777	G
1	L5	3778	U
1	L5	3783	A
1	L5	3784	A
1	L5	3786	U
1	L5	3791	C
1	L5	3798	U
1	L5	3802	U
1	L5	3810	C
1	L5	3811	G

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Mol	Chain	Res	Type
1	L5	3814	U
1	L5	3817	A
1	L5	3818	U
1	L5	3819	G
1	L5	3822	U
1	L5	3823	G
1	L5	3838	U
1	L5	3839	G
1	L5	3840	U
1	L5	3843	C
1	L5	3867	A
1	L5	3877	A
1	L5	3878	C
1	L5	3879	G
1	L5	3880	G
1	L5	3890	A
1	L5	3892	U
1	L5	3897	G
1	L5	3898	G
1	L5	3901	A
1	L5	3905	A
1	L5	3906	A
1	L5	3907	G
1	L5	3908	A
1	L5	3915	U
1	L5	3920	U
1	L5	3926	C
1	L5	3939	G
1	L5	3942	A
1	L5	3943	A
1	L5	3945	A
1	L5	3946	G
1	L5	4069	U
1	L5	4071	U
1	L5	4076	G
1	L5	4084	G
1	L5	4086	G
1	L5	4099	G
1	L5	4100	C
1	L5	4110	C
1	L5	4111	U
1	L5	4113	U

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Mol	Chain	Res	Type
1	L5	4114	C
1	L5	4115	G
1	L5	4116	C
1	L5	4117	U
1	L5	4119	C
1	L5	4121	G
1	L5	4122	G
1	L5	4127	A
1	L5	4141	G
1	L5	4142	C
1	L5	4143	G
1	L5	4144	C
1	L5	4150	G
1	L5	4157	A
1	L5	4162	C
1	L5	4163	U
1	L5	4170	A
1	L5	4183	G
1	L5	4184	G
1	L5	4191	G
1	L5	4194	U
1	L5	4203	A
1	L5	4206	C
1	L5	4222	G
1	L5	4225	G
1	L5	4228	G
1	L5	4229	U
1	L5	4233	A
1	L5	4234	A
1	L5	4243	C
1	L5	4251	A
1	L5	4254	G
1	L5	4257	A
1	L5	4258	C
1	L5	4265	U
1	L5	4268	A
1	L5	4273	A
1	L5	4291	G
1	L5	4297	G
1	L5	4305	G
1	L5	4306	U
1	L5	4314	C

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Mol	Chain	Res	Type
1	L5	4319	C
1	L5	4329	G
1	L5	4330	G
1	L5	4332	C
1	L5	4349	C
1	L5	4354	U
1	L5	4364	G
1	L5	4373	G
1	L5	4377	G
1	L5	4378	A
1	L5	4380	A
1	L5	4381	A
1	L5	4387	C
1	L5	4391	G
1	L5	4393	G
1	L5	4394	A
1	L5	4422	A
1	L5	4424	A
1	L5	4437	U
1	L5	4444	C
1	L5	4448	G
1	L5	4449	A
1	L5	4453	C
1	L5	4464	A
1	L5	4465	U
1	L5	4466	C
1	L5	4471	U
1	L5	4488	A
1	L5	4500	U
1	L5	4510	A
1	L5	4512	U
1	L5	4513	A
1	L5	4522	G
1	L5	4525	C
1	L5	4545	G
1	L5	4548	A
1	L5	4554	G
1	L5	4560	C
1	L5	4573	G
1	L5	4575	G
1	L5	4584	A
1	L5	4589	A

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Mol	Chain	Res	Type
1	L5	4590	A
1	L5	4599	A
1	L5	4600	G
1	L5	4601	U
1	L5	4608	G
1	L5	4610	A
1	L5	4612	C
1	L5	4617	G
1	L5	4636	U
1	L5	4652	G
1	L5	4656	A
1	L5	4658	G
1	L5	4670	C
1	L5	4671	C
1	L5	4672	A
1	L5	4687	A
1	L5	4693	C
1	L5	4695	C
1	L5	4700	A
1	L5	4707	A
1	L5	4708	A
1	L5	4709	U
1	L5	4730	C
1	L5	4731	G
1	L5	4733	C
1	L5	4734	A
1	L5	4740	G
1	L5	4741	C
1	L5	4742	G
1	L5	4745	G
1	L5	4754	G
1	L5	4757	C
1	L5	4759	C
1	L5	4761	G
1	L5	4765	G
1	L5	4769	G
1	L5	4775	C
1	L5	4776	G
1	L5	4859	C
1	L5	4860	G
1	L5	4864	U
1	L5	4870	G

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Mol	Chain	Res	Type
1	L5	4871	C
1	L5	4875	G
1	L5	4877	G
1	L5	4880	C
1	L5	4881	U
1	L5	4882	U
1	L5	4883	C
1	L5	4888	U
1	L5	4889	G
1	L5	4895	C
1	L5	4896	G
1	L5	4898	G
1	L5	4900	C
1	L5	4901	G
1	L5	4910	G
1	L5	4912	G
1	L5	4914	C
1	L5	4923	C
1	L5	4927	G
1	L5	4937	C
1	L5	4943	A
1	L5	4944	C
1	L5	4947	U
1	L5	4949	G
1	L5	4951	G
1	L5	4955	A
1	L5	4960	G
1	L5	4961	G
1	L5	4963	G
1	L5	4966	A
1	L5	4976	U
1	L5	4988	U
1	L5	4989	U
1	L5	4990	C
1	L5	4991	U
1	L5	5006	U
1	L5	5013	C
1	L5	5017	G
1	L5	5020	G
1	L5	5022	U
1	L5	5023	C
1	L5	5024	C

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Mol	Chain	Res	Type
1	L5	5025	C
1	L5	5028	G
1	L5	5029	C
1	L5	5030	U
1	L5	5032	C
1	L5	5034	A
1	L5	5040	U
1	L5	5041	G
1	L5	5050	C
1	L5	5054	C
1	L5	5055	G
1	L5	5061	A
1	L5	5062	G
1	L5	5069	U
2	L7	7	G
2	L7	11	A
2	L7	24	C
2	L7	27	G
2	L7	31	G
2	L7	33	U
2	L7	41	G
2	L7	53	U
2	L7	54	A
2	L7	61	G
2	L7	62	U
2	L7	63	C
2	L7	64	G
2	L7	97	G
2	L7	100	A
2	L7	110	G
2	L7	120	U
3	L8	16	G
3	L8	22	U
3	L8	23	C
3	L8	34	U
3	L8	35	C
3	L8	39	G
3	L8	48	A
3	L8	58	G
3	L8	59	A
3	L8	62	A
3	L8	63	U

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Mol	Chain	Res	Type
3	L8	79	G
3	L8	80	A
3	L8	82	A
3	L8	83	C
3	L8	84	A
3	L8	85	U
3	L8	86	U
3	L8	87	G
3	L8	88	A
3	L8	94	G
3	L8	103	A
3	L8	105	C
3	L8	107	C
3	L8	109	C
3	L8	110	U
3	L8	111	U
3	L8	112	G
3	L8	114	G
3	L8	123	U
3	L8	124	U
3	L8	125	C
3	L8	127	U
3	L8	147	G
3	L8	150	C
3	L8	154	G
46	S2	2	A
46	S2	11	A
46	S2	17	C
46	S2	33	G
46	S2	38	A
46	S2	41	G
46	S2	42	A
46	S2	44	U
46	S2	46	A
46	S2	56	G
46	S2	61	A
46	S2	62	G
46	S2	64	A
46	S2	65	C
46	S2	67	C
46	S2	68	A
46	S2	72	C

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Mol	Chain	Res	Type
46	S2	73	C
46	S2	74	G
46	S2	75	G
46	S2	76	U
46	S2	81	U
46	S2	93	U
46	S2	103	A
46	S2	113	G
46	S2	122	G
46	S2	126	G
46	S2	127	C
46	S2	129	C
46	S2	130	G
46	S2	140	U
46	S2	141	A
46	S2	142	C
46	S2	143	U
46	S2	148	U
46	S2	158	A
46	S2	160	U
46	S2	161	U
46	S2	162	C
46	S2	164	A
46	S2	168	C
46	S2	170	A
46	S2	171	A
46	S2	173	A
46	S2	179	C
46	S2	181	A
46	S2	184	G
46	S2	190	G
46	S2	196	C
46	S2	197	U
46	S2	198	U
46	S2	199	C
46	S2	200	G
46	S2	203	G
46	S2	205	G
46	S2	206	G
46	S2	209	A
46	S2	211	G
46	S2	212	C

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Mol	Chain	Res	Type
46	S2	214	U
46	S2	215	G
46	S2	220	U
46	S2	223	C
46	S2	294	U
46	S2	295	C
46	S2	297	A
46	S2	306	C
46	S2	307	G
46	S2	308	G
46	S2	309	G
46	S2	311	C
46	S2	312	G
46	S2	316	G
46	S2	318	A
46	S2	319	C
46	S2	320	G
46	S2	321	C
46	S2	322	C
46	S2	328	U
46	S2	329	G
46	S2	331	C
46	S2	335	G
46	S2	339	A
46	S2	347	G
46	S2	351	G
46	S2	356	C
46	S2	360	A
46	S2	362	C
46	S2	364	A
46	S2	368	U
46	S2	369	C
46	S2	370	G
46	S2	376	A
46	S2	380	G
46	S2	381	C
46	S2	385	G
46	S2	386	C
46	S2	400	C
46	S2	408	A
46	S2	409	C
46	S2	421	G

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Mol	Chain	Res	Type
46	S2	447	A
46	S2	448	A
46	S2	450	C
46	S2	452	G
46	S2	465	A
46	S2	471	G
46	S2	472	C
46	S2	473	A
46	S2	474	G
46	S2	483	C
46	S2	487	U
46	S2	488	U
46	S2	489	A
46	S2	492	C
46	S2	493	A
46	S2	496	C
46	S2	501	C
46	S2	502	C
46	S2	503	C
46	S2	517	C
46	S2	522	A
46	S2	523	A
46	S2	528	A
46	S2	530	U
46	S2	532	C
46	S2	533	A
46	S2	536	A
46	S2	548	C
46	S2	549	C
46	S2	551	U
46	S2	554	A
46	S2	556	U
46	S2	557	U
46	S2	559	G
46	S2	560	A
46	S2	575	A
46	S2	576	A
46	S2	583	A
46	S2	587	A
46	S2	588	G
46	S2	590	A
46	S2	591	U

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Mol	Chain	Res	Type
46	S2	592	C
46	S2	593	C
46	S2	596	U
46	S2	604	A
46	S2	605	A
46	S2	606	G
46	S2	607	U
46	S2	608	C
46	S2	612	U
46	S2	613	G
46	S2	614	C
46	S2	615	C
46	S2	617	G
46	S2	627	U
46	S2	628	A
46	S2	629	A
46	S2	630	U
46	S2	632	C
46	S2	634	A
46	S2	643	A
46	S2	644	G
46	S2	655	A
46	S2	656	G
46	S2	660	C
46	S2	668	A
46	S2	669	A
46	S2	671	A
46	S2	672	A
46	S2	673	G
46	S2	683	G
46	S2	684	G
46	S2	687	C
46	S2	688	U
46	S2	689	U
46	S2	690	G
46	S2	691	G
46	S2	692	G
46	S2	693	A
46	S2	696	G
46	S2	735	C
46	S2	737	G
46	S2	738	C

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Mol	Chain	Res	Type
46	S2	739	C
46	S2	797	C
46	S2	798	G
46	S2	799	U
46	S2	809	A
46	S2	810	A
46	S2	811	A
46	S2	821	G
46	S2	822	U
46	S2	827	A
46	S2	830	A
46	S2	835	C
46	S2	840	C
46	S2	842	C
46	S2	847	A
46	S2	851	C
46	S2	856	C
46	S2	857	U
46	S2	869	A
46	S2	870	A
46	S2	872	A
46	S2	874	G
46	S2	878	G
46	S2	880	G
46	S2	881	G
46	S2	882	U
46	S2	883	U
46	S2	885	U
46	S2	889	U
46	S2	890	U
46	S2	891	G
46	S2	892	U
46	S2	893	U
46	S2	894	G
46	S2	895	G
46	S2	896	U
46	S2	898	U
46	S2	899	U
46	S2	900	C
46	S2	901	G
46	S2	902	G
46	S2	904	A

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Mol	Chain	Res	Type
46	S2	906	U
46	S2	911	C
46	S2	913	A
46	S2	914	U
46	S2	919	A
46	S2	920	A
46	S2	933	G
46	S2	955	A
46	S2	963	A
46	S2	970	G
46	S2	971	G
46	S2	972	A
46	S2	975	G
46	S2	990	A
46	S2	992	A
46	S2	995	G
46	S2	999	G
46	S2	1001	A
46	S2	1016	U
46	S2	1018	U
46	S2	1023	A
46	S2	1027	A
46	S2	1045	U
46	S2	1049	A
46	S2	1055	A
46	S2	1056	U
46	S2	1058	A
46	S2	1061	U
46	S2	1062	A
46	S2	1082	A
46	S2	1083	A
46	S2	1085	C
46	S2	1086	G
46	S2	1087	A
46	S2	1109	C
46	S2	1110	G
46	S2	1114	U
46	S2	1119	A
46	S2	1121	G
46	S2	1126	G
46	S2	1131	G
46	S2	1133	A

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Mol	Chain	Res	Type
46	S2	1139	C
46	S2	1149	A
46	S2	1150	A
46	S2	1153	C
46	S2	1154	U
46	S2	1155	U
46	S2	1157	G
46	S2	1166	G
46	S2	1170	A
46	S2	1183	A
46	S2	1195	A
46	S2	1207	G
46	S2	1208	A
46	S2	1215	C
46	S2	1217	A
46	S2	1224	G
46	S2	1227	G
46	S2	1228	A
46	S2	1238	U
46	S2	1240	A
46	S2	1242	U
46	S2	1251	A
46	S2	1253	A
46	S2	1255	G
46	S2	1256	G
46	S2	1257	G
46	S2	1258	A
46	S2	1259	A
46	S2	1260	A
46	S2	1265	A
46	S2	1269	G
46	S2	1270	G
46	S2	1271	C
46	S2	1272	C
46	S2	1273	C
46	S2	1274	G
46	S2	1275	G
46	S2	1276	A
46	S2	1281	G
46	S2	1282	A
46	S2	1283	C
46	S2	1284	A

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Mol	Chain	Res	Type
46	S2	1285	G
46	S2	1286	G
46	S2	1287	A
46	S2	1288	U
46	S2	1294	G
46	S2	1297	U
46	S2	1301	A
46	S2	1302	G
46	S2	1303	C
46	S2	1304	U
46	S2	1308	U
46	S2	1313	A
46	S2	1314	U
46	S2	1315	U
46	S2	1318	G
46	S2	1326	U
46	S2	1327	G
46	S2	1330	G
46	S2	1331	C
46	S2	1341	C
46	S2	1342	U
46	S2	1348	G
46	S2	1357	A
46	S2	1371	U
46	S2	1372	U
46	S2	1378	A
46	S2	1382	A
46	S2	1396	A
46	S2	1397	U
46	S2	1398	G
46	S2	1401	A
46	S2	1402	A
46	S2	1403	C
46	S2	1408	U
46	S2	1410	C
46	S2	1411	G
46	S2	1415	C
46	S2	1423	C
46	S2	1429	G
46	S2	1441	U
46	S2	1444	U
46	S2	1449	G

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Mol	Chain	Res	Type
46	S2	1450	G
46	S2	1462	U
46	S2	1463	U
46	S2	1466	G
46	S2	1473	G
46	S2	1474	A
46	S2	1477	U
46	S2	1487	A
46	S2	1489	A
46	S2	1490	G
46	S2	1496	U
46	S2	1498	A
46	S2	1505	U
46	S2	1506	A
46	S2	1510	G
46	S2	1519	U
46	S2	1520	G
46	S2	1521	C
46	S2	1522	A
46	S2	1526	G
46	S2	1527	C
46	S2	1531	A
46	S2	1533	A
46	S2	1535	U
46	S2	1536	G
46	S2	1541	G
46	S2	1542	C
46	S2	1544	C
46	S2	1545	A
46	S2	1546	G
46	S2	1548	G
46	S2	1552	G
46	S2	1560	U
46	S2	1567	G
46	S2	1568	C
46	S2	1574	C
46	S2	1578	U
46	S2	1579	A
46	S2	1580	A
46	S2	1585	U
46	S2	1586	U
46	S2	1587	G

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Mol	Chain	Res	Type
46	S2	1588	A
46	S2	1589	A
46	S2	1591	C
46	S2	1599	U
46	S2	1601	A
46	S2	1603	G
46	S2	1604	G
46	S2	1606	G
46	S2	1607	A
46	S2	1610	G
46	S2	1616	U
46	S2	1621	U
46	S2	1623	A
46	S2	1624	U
46	S2	1627	C
46	S2	1632	G
46	S2	1633	A
46	S2	1634	A
46	S2	1636	G
46	S2	1637	A
46	S2	1638	G
46	S2	1639	G
46	S2	1646	C
46	S2	1648	G
46	S2	1651	A
46	S2	1652	G
46	S2	1654	G
46	S2	1660	C
46	S2	1662	U
46	S2	1663	A
46	S2	1664	A
46	S2	1665	G
46	S2	1668	U
46	S2	1669	G
46	S2	1678	A
46	S2	1680	G
46	S2	1683	C
46	S2	1686	G
46	S2	1695	A
46	S2	1700	C
46	S2	1715	A
46	S2	1719	A

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Mol	Chain	Res	Type
46	S2	1721	U
46	S2	1722	G
46	S2	1742	C
46	S2	1743	G
46	S2	1744	G
46	S2	1745	A
46	S2	1754	G
46	S2	1755	C
46	S2	1756	C
46	S2	1757	G
46	S2	1758	G
46	S2	1759	G
46	S2	1760	G
46	S2	1772	C
46	S2	1773	C
46	S2	1774	C
46	S2	1775	U
46	S2	1780	G
46	S2	1781	A
46	S2	1782	G
46	S2	1783	C
46	S2	1784	G
46	S2	1786	U
46	S2	1789	G
46	S2	1813	A
46	S2	1821	U
46	S2	1823	A
46	S2	1824	A
46	S2	1825	A
46	S2	1831	A
46	S2	1835	A
46	S2	1838	U
46	S2	1839	U
46	S2	1849	G
46	S2	1850	A
46	S2	1852	C
46	S2	1855	G
46	S2	1860	A
46	S2	1861	G
46	S2	1862	G
46	S2	1863	A
46	S2	1865	C

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Mol	Chain	Res	Type
46	S2	1869	A
80	zy	8	U
80	zy	9	G
80	zy	14	A
80	zy	16	G
80	zy	17	G
80	zy	18	G
80	zy	19	U
80	zy	21	U
80	zy	22	G
80	zy	23	A
80	zy	35	G
80	zy	53	U
80	zy	57	A
80	zy	59	U
80	zy	73	C
80	zy	74	C
80	zu	2	G
80	zu	8	U
80	zu	9	G
80	zu	16	G
80	zu	17	G
80	zu	18	G
80	zu	19	U
80	zu	21	U
80	zu	22	G
80	zu	23	A
80	zu	40	G
80	zu	42	G
80	zu	45	G
80	zu	48	C
80	zu	57	A
80	zu	58	A
80	zu	68	A
80	zu	70	C
80	zu	71	C
80	zu	72	C
81	zv	-3	C
81	zv	-2	C
81	zv	-1	C
81	zv	3	U
81	zv	4	U

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Mol	Chain	Res	Type
83	zz	120	C
83	zz	124	C
83	zz	126	C
83	zz	135	G
83	zz	136	A
83	zz	137	G
83	zz	143	G
83	zz	144	U
83	zz	145	G
83	zz	150	G
83	zz	154	A
83	zz	157	C
83	zz	161	G
83	zz	163	G
83	zz	164	U
83	zz	165	A
83	zz	166	C
83	zz	168	C
83	zz	169	C
83	zz	171	G
83	zz	172	A
83	zz	175	U
83	zz	177	C
83	zz	184	G
83	zz	185	A
83	zz	187	C
83	zz	189	G
83	zz	190	G
83	zz	191	U
83	zz	195	U
83	zz	196	U
83	zz	197	C
83	zz	198	U
83	zz	202	A
83	zz	208	C
83	zz	209	C
83	zz	210	G
83	zz	213	C
83	zz	216	U
83	zz	217	G
83	zz	224	G
83	zz	228	U

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Mol	Chain	Res	Type
83	zz	229	G
83	zz	232	C
83	zz	234	U
83	zz	237	C
83	zz	244	A
83	zz	252	A
83	zz	253	G
83	zz	256	G
83	zz	258	G
83	zz	263	G
83	zz	265	U
83	zz	266	G
83	zz	268	G
83	zz	270	C
83	zz	271	G
83	zz	280	C
83	zz	282	U
83	zz	285	G
83	zz	288	A
83	zz	291	G
83	zz	295	G
83	zz	296	A
83	zz	297	U
83	zz	303	G
83	zz	305	U
83	zz	306	U
83	zz	307	G
83	zz	315	C
83	zz	325	C
83	zz	328	G
83	zz	329	U

All (30) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	406	C
1	L5	914	U
1	L5	1082	C
1	L5	1271	G
1	L5	2019	C
1	L5	2416	G
1	L5	2675	G

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Mol	Chain	Res	Type
1	L5	2760	G
1	L5	3614	G
1	L5	3673	C
1	L5	3735	G
1	L5	4699	U
1	L5	4913	G
1	L5	5027	C
2	L7	109	U
3	L8	86	U
3	L8	87	G
46	S2	129	C
46	S2	532	C
46	S2	604	A
46	S2	688	U
46	S2	1207	G
46	S2	1273	C
46	S2	1519	U
46	S2	1585	U
46	S2	1661	A
46	S2	1664	A
46	S2	1788	A
46	S2	1824	A
46	S2	1860	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 73 ligands modelled in this entry, 73 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

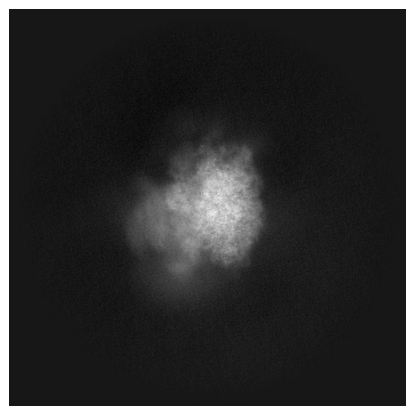
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62679. These allow visual inspection of the internal detail of the map and identification of artifacts.

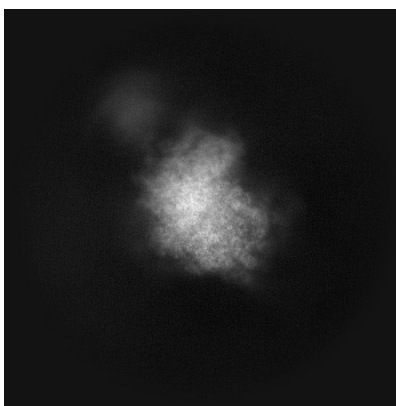
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

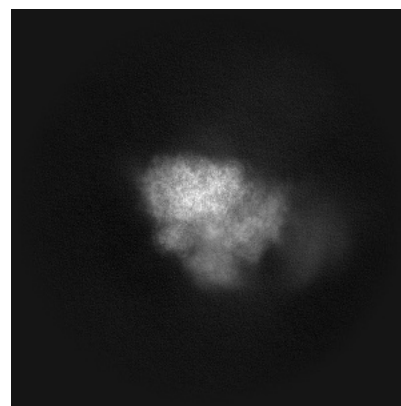
6.1.1 Primary map



X

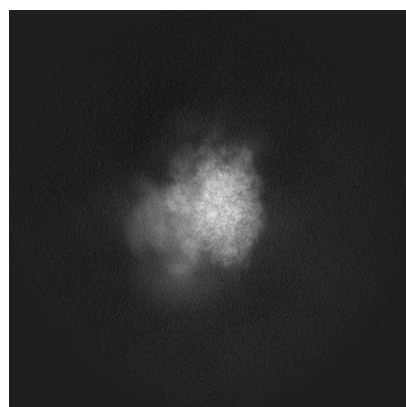


Y

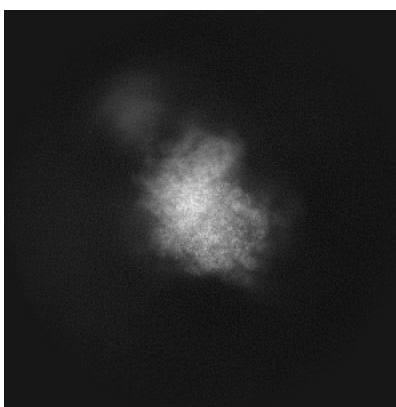


Z

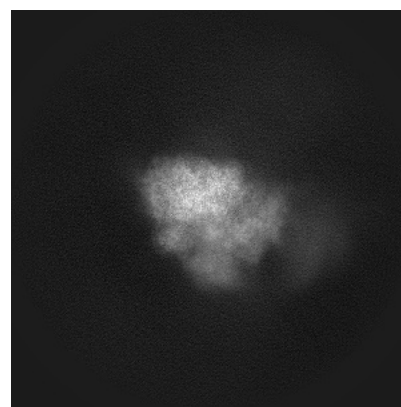
6.1.2 Raw map



X



Y

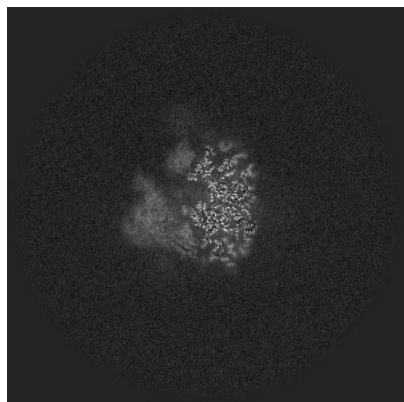


Z

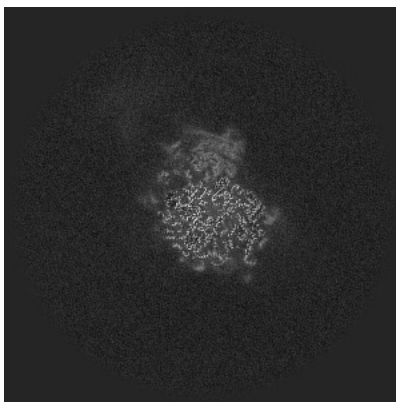
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

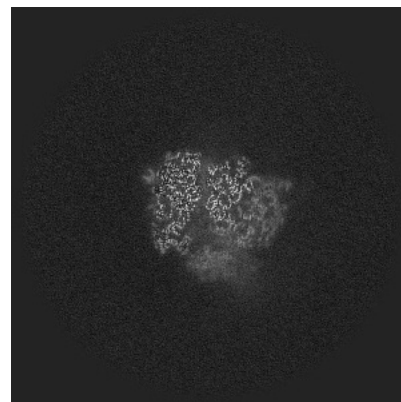
6.2.1 Primary map



X Index: 250

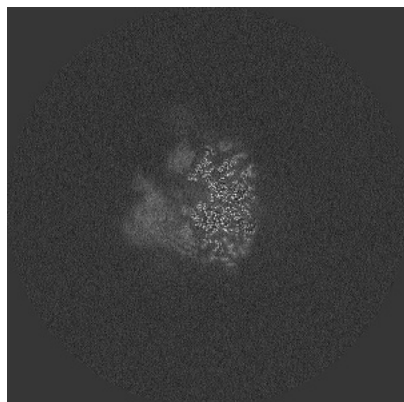


Y Index: 250

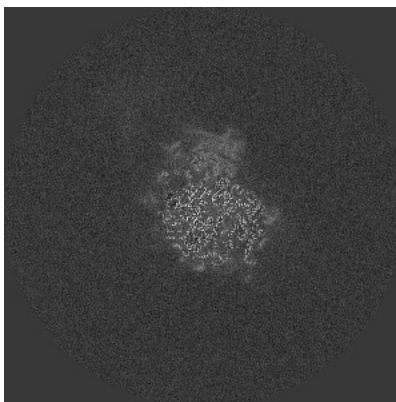


Z Index: 250

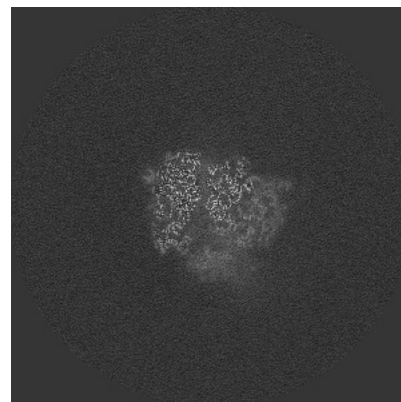
6.2.2 Raw map



X Index: 250



Y Index: 250

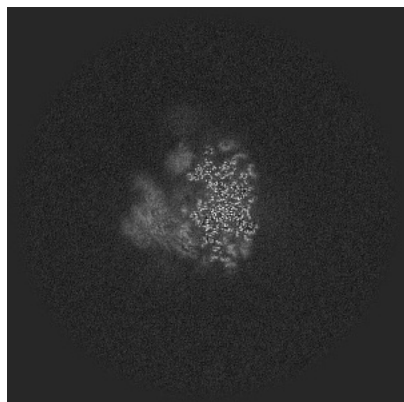


Z Index: 250

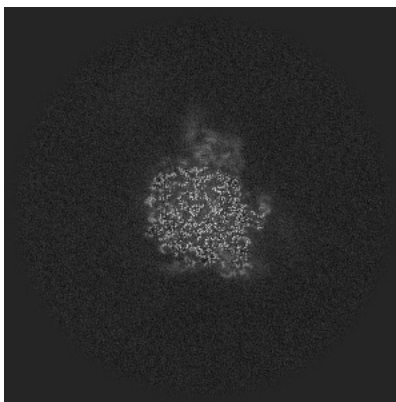
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

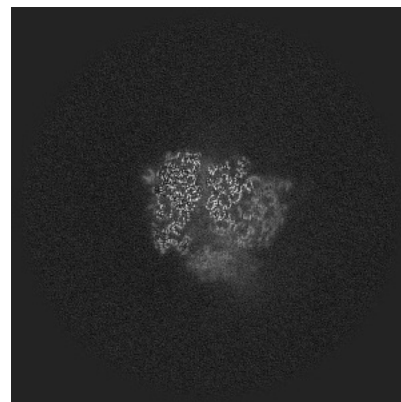
6.3.1 Primary map



X Index: 251

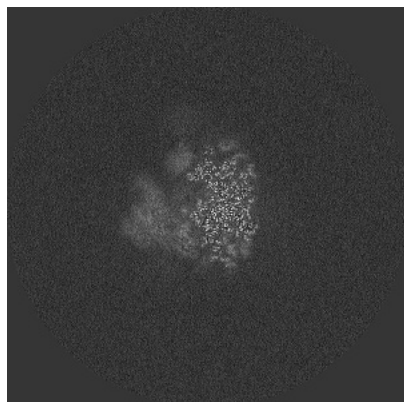


Y Index: 270

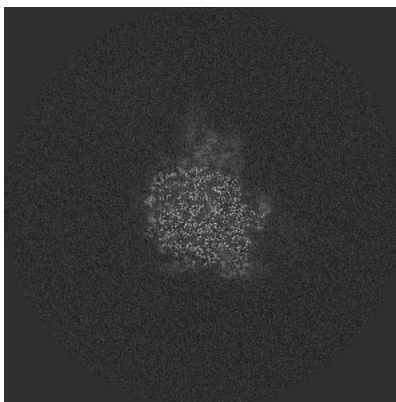


Z Index: 250

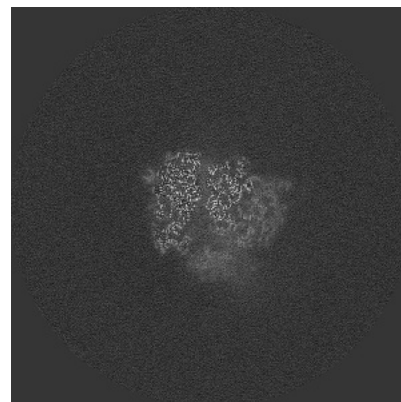
6.3.2 Raw map



X Index: 251



Y Index: 270

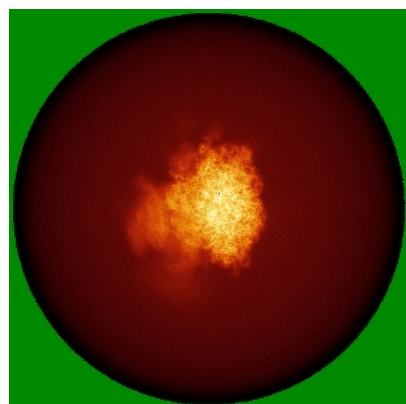


Z Index: 250

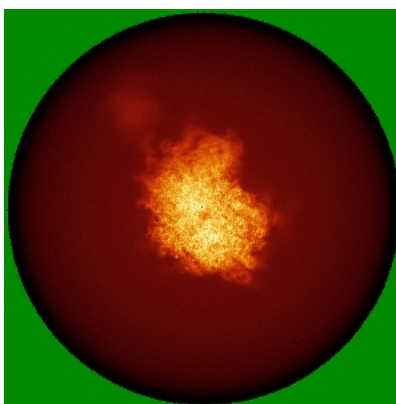
The images above show the largest variance slices of the map in three orthogonal directions.

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

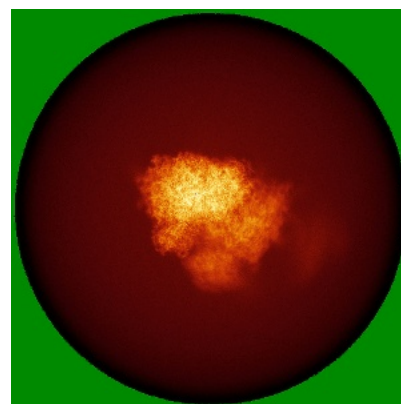
6.4.1 Primary map



X

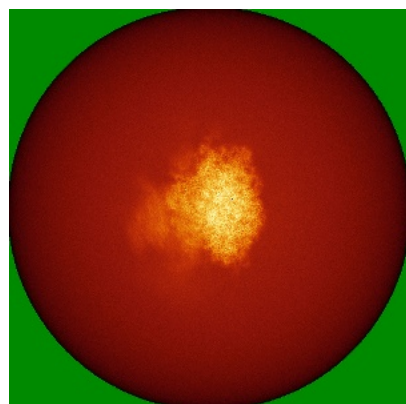


Y

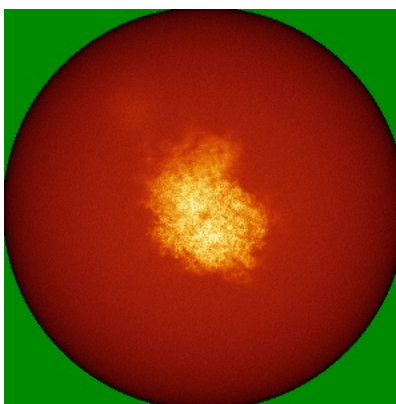


Z

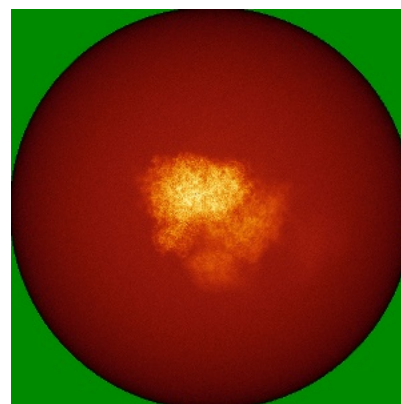
6.4.2 Raw map



X



Y

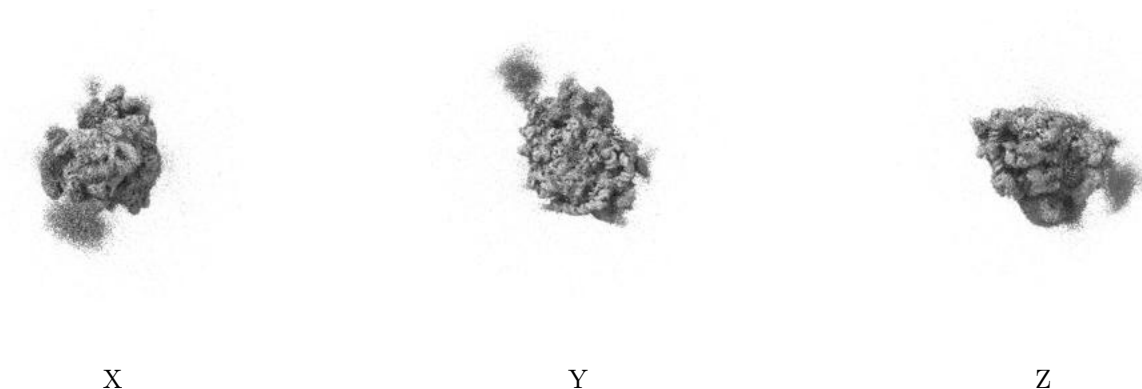


Z

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

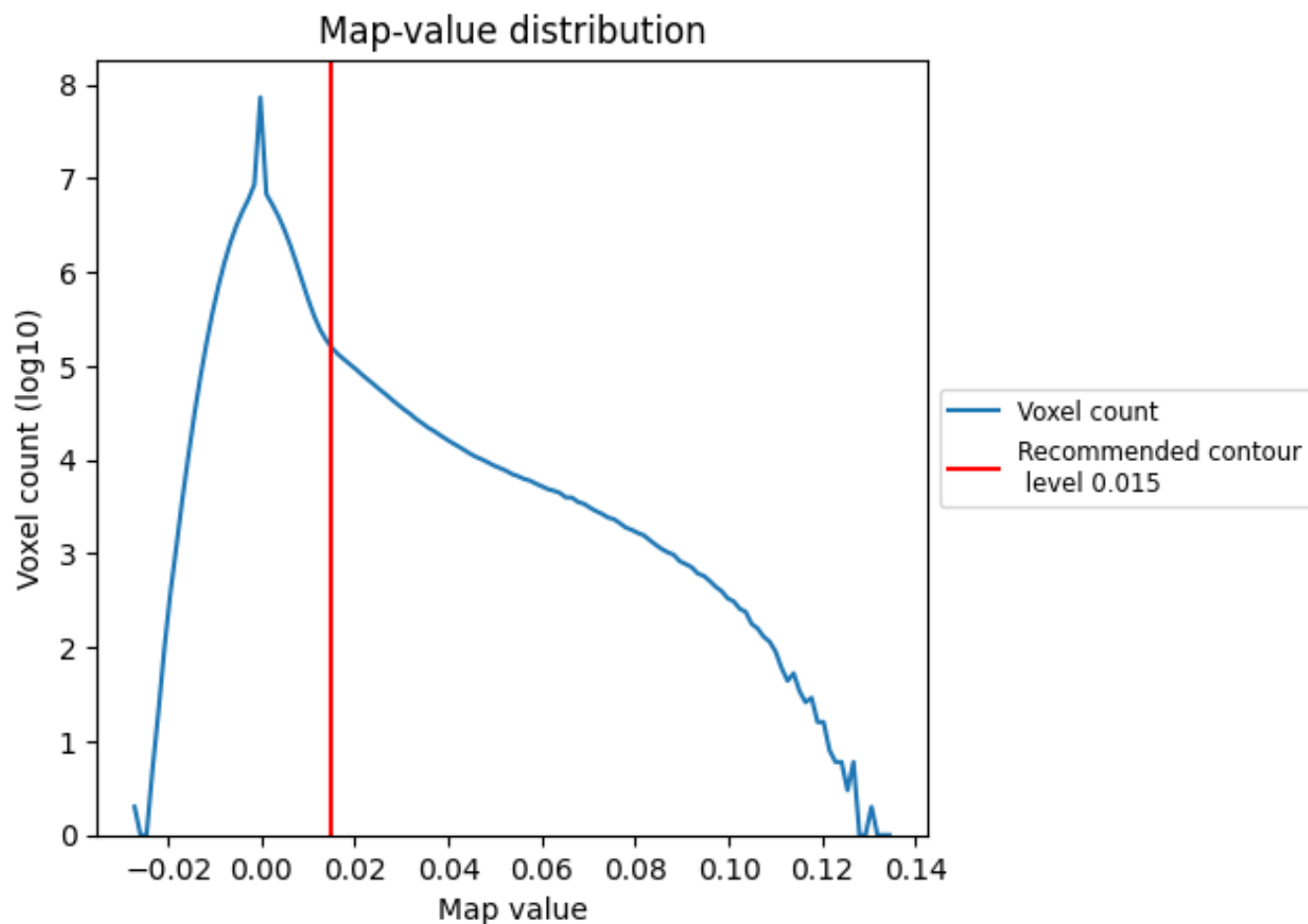
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

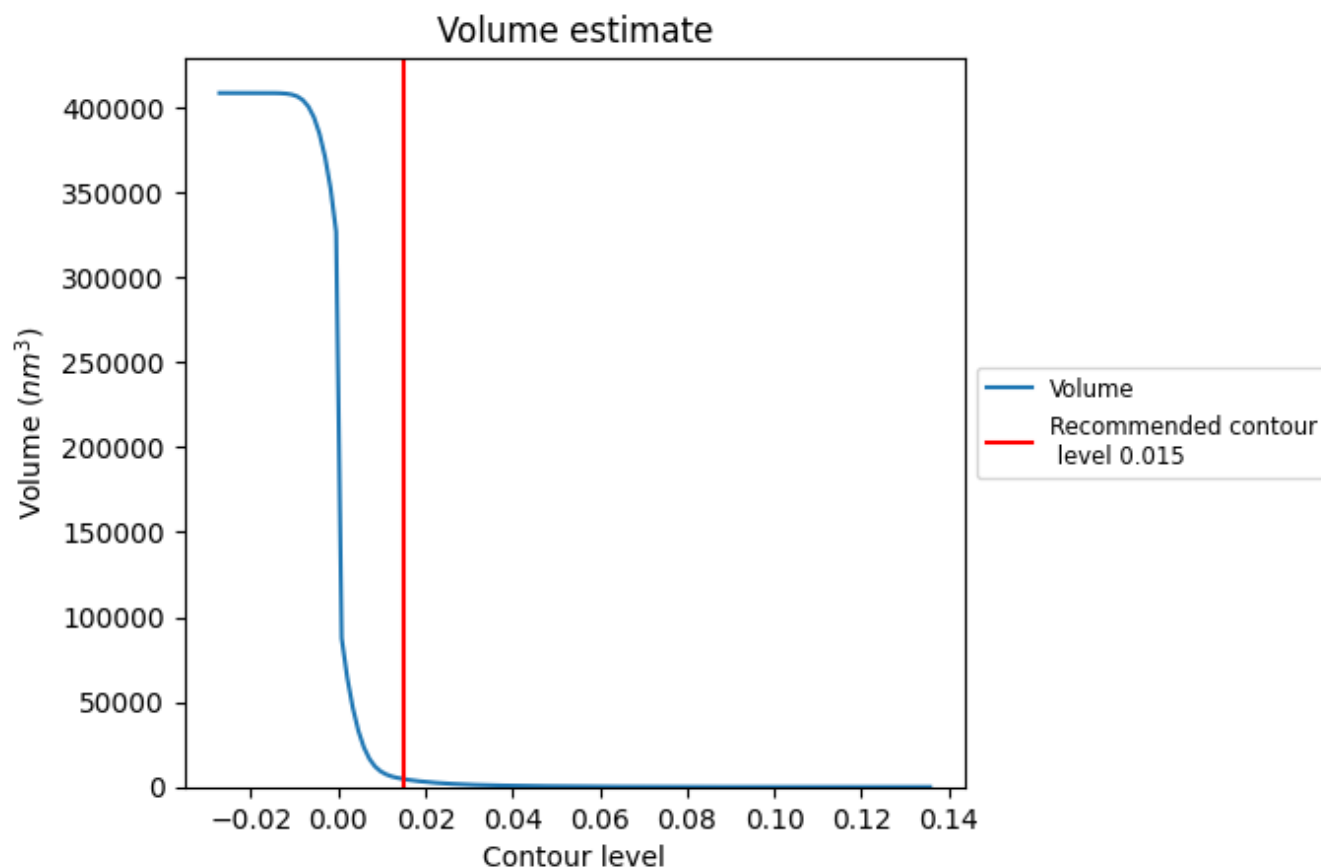
This section contains the results of statistical analysis of the map.

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.

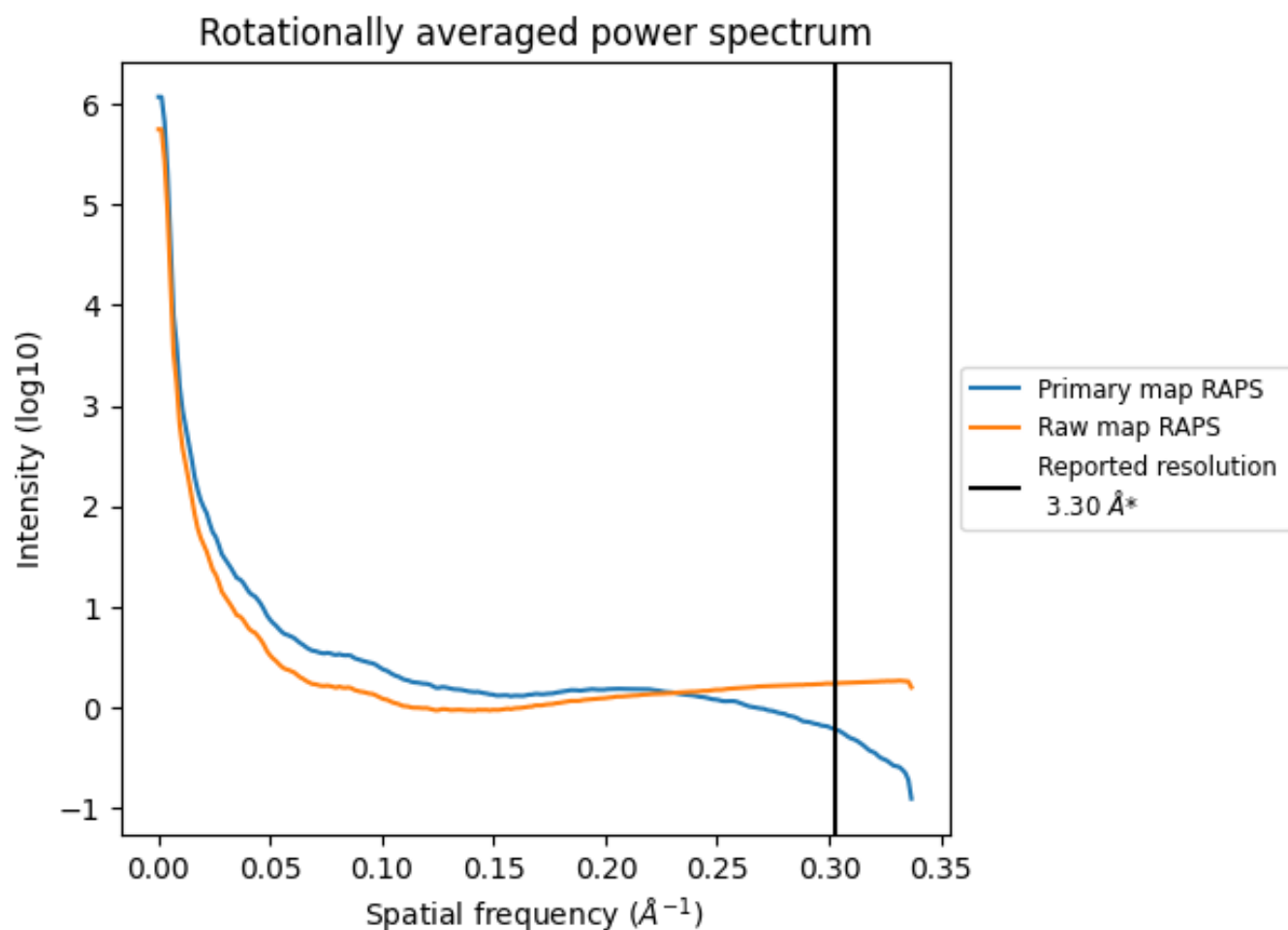
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4651 nm^3 ; this corresponds to an approximate mass of 4201 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 ⓘ

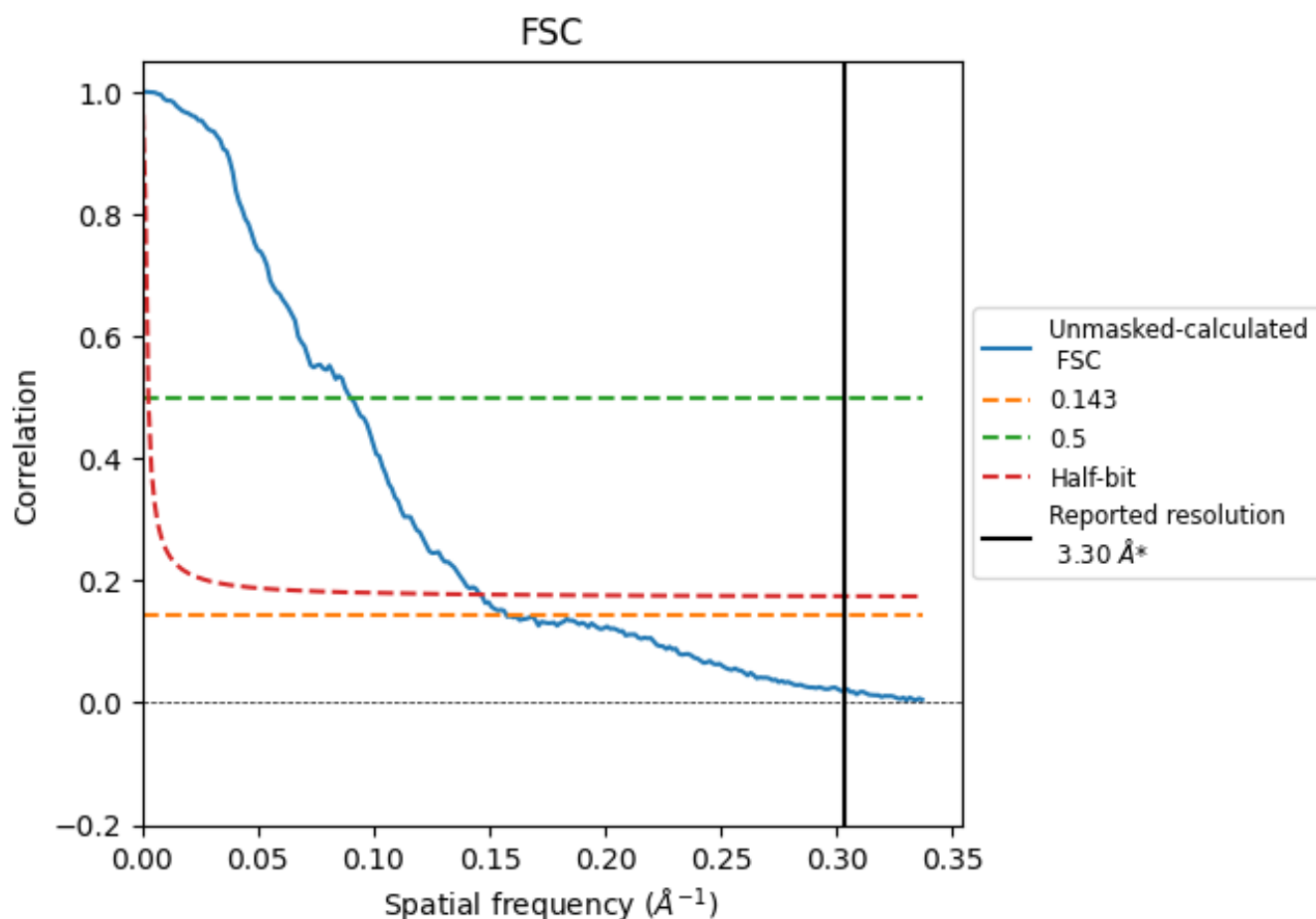


*Reported resolution corresponds to spatial frequency of 0.303 $\text{\AA}^{-1}$

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 0.303 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

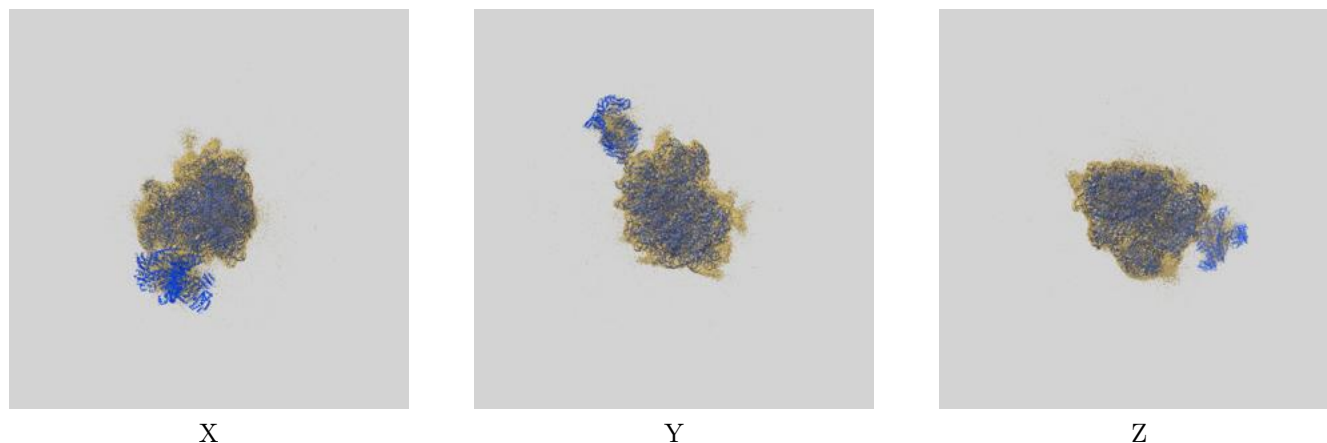
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.35	11.12	6.85

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.35 differs from the reported value 3.3 by more than 10 %

9 Map-model fit [i](#)

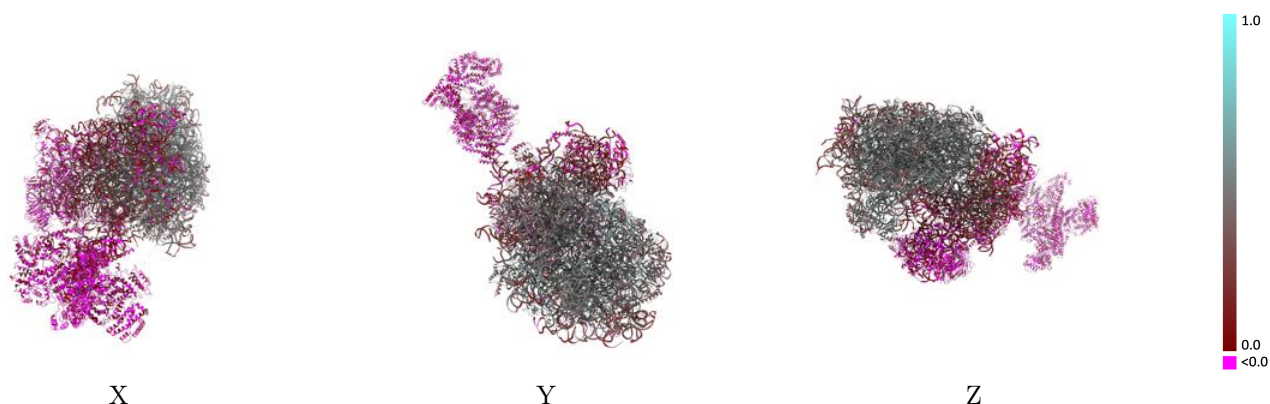
This section contains information regarding the fit between EMDB map EMD-62679 and PDB model 9KZX. Per-residue inclusion information can be found in [section 3](#) on [page 22](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

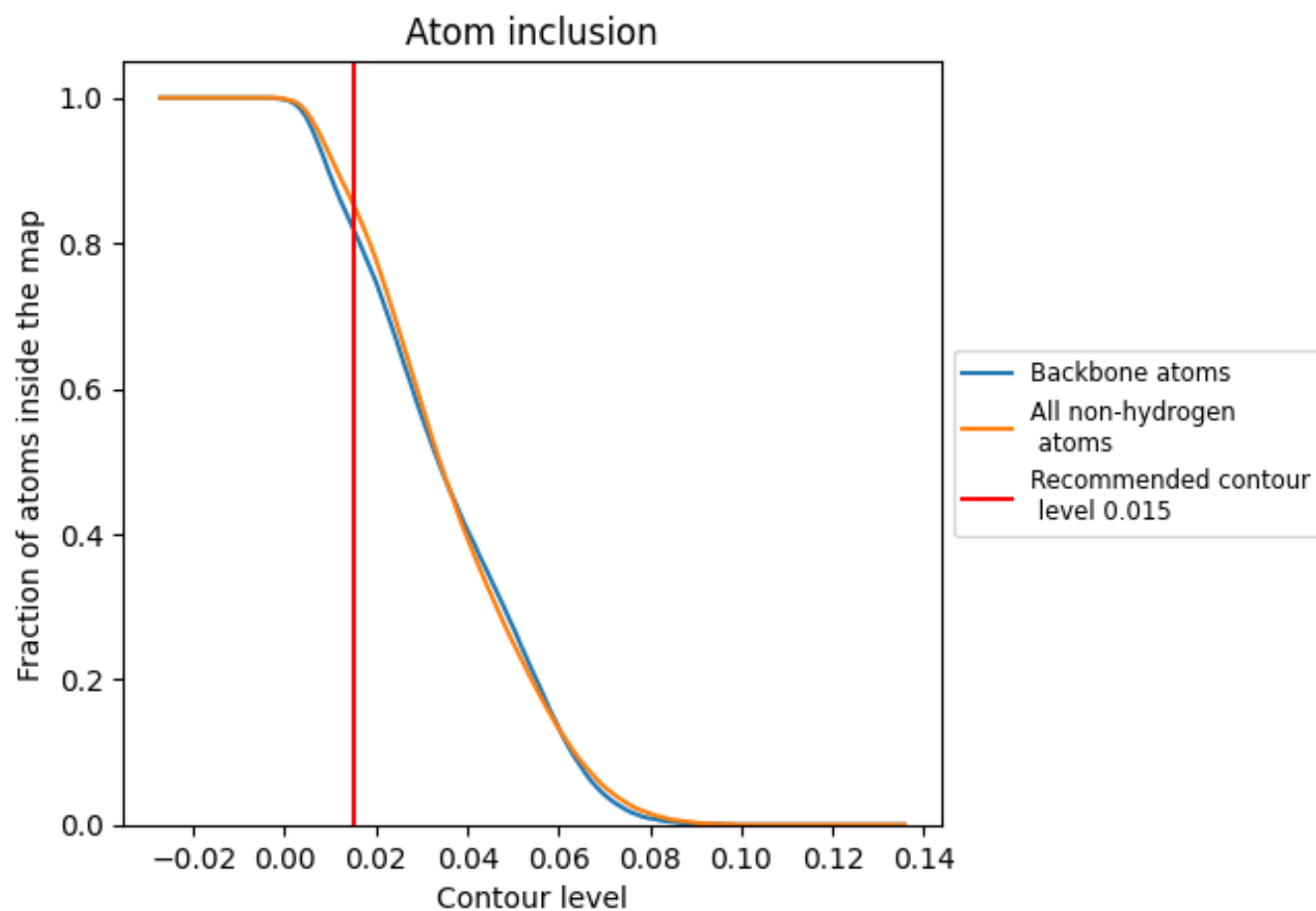


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 85% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8540	 0.3030
3a	 0.0720	 0.0320
3c	 0.1340	 0.0740
3d	 0.0350	 0.0220
3e	 0.0220	 0.0120
3f	 0.0370	 0.0300
3h	 0.0680	 0.0240
3k	 0.0030	 0.0030
3l	 0.0120	 0.0280
3m	 0.0080	 0.0160
L5	 0.9920	 0.4470
L7	 0.9970	 0.4960
L8	 0.9870	 0.4470
LA	 0.9860	 0.4760
LB	 0.9860	 0.4820
LC	 0.9810	 0.4580
LD	 0.9680	 0.4410
LE	 0.9690	 0.4020
LF	 0.9930	 0.4700
LG	 0.9500	 0.4070
LH	 0.9810	 0.4600
LI	 0.9870	 0.4640
LJ	 0.9750	 0.4190
LL	 0.9830	 0.4670
LM	 0.9780	 0.4520
LN	 0.9960	 0.5210
LO	 0.9900	 0.4830
LP	 0.9920	 0.4790
LQ	 0.9880	 0.4810
LR	 0.9800	 0.4360
LS	 0.9880	 0.4900
LT	 0.9920	 0.4760
LU	 0.9520	 0.4230
LV	 0.9860	 0.4660
LW	 0.8200	 0.3240



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Chain	Atom inclusion	Q-score
LX	 0.9770	 0.4390
LY	 0.9740	 0.4430
LZ	 0.9630	 0.4130
La	 0.9770	 0.4530
Lb	 0.9980	 0.4630
Lc	 0.9640	 0.4180
Ld	 0.9770	 0.4570
Le	 0.9920	 0.4750
Lf	 0.9930	 0.4850
Lg	 0.9840	 0.4370
Lh	 0.9810	 0.4530
Li	 0.9780	 0.4470
Lj	 0.9990	 0.4990
Lk	 0.9440	 0.4150
Ll	 0.9950	 0.4710
Lm	 0.9870	 0.4570
Ln	 1.0000	 0.3860
Lo	 0.9960	 0.4870
Lp	 0.9870	 0.4760
Lr	 0.9870	 0.4540
S2	 0.9710	 0.1730
SA	 0.8540	 0.1460
SB	 0.8490	 0.1170
SC	 0.9200	 0.1780
SD	 0.8080	 0.0260
SE	 0.9420	 0.1600
SF	 0.8310	 0.0140
SG	 0.8420	 0.1160
SH	 0.8830	 0.2120
SI	 0.9080	 0.1390
SJ	 0.9280	 0.1310
SK	 0.7290	 0.0010
SL	 0.9830	 0.2650
SN	 0.9620	 0.2890
SO	 0.9120	 0.0760
SP	 0.8370	 0.0840
SQ	 0.7710	 0.0070
SR	 0.7510	 0.0560
SS	 0.7690	 0.0510
ST	 0.7760	 0.0150
SU	 0.7530	 0.0320
SV	 0.8840	 0.2360

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Chain	Atom inclusion	Q-score
SW	 0.9690	 0.3350
SX	 0.9800	 0.2540
SY	 0.8850	 0.1080
SZ	 0.5920	 0.0140
Sa	 0.9610	 0.1460
Sb	 0.9360	 0.2050
Sc	 0.8790	 0.0030
Sd	 0.9800	 0.0110
Se	 0.9250	 0.0920
Sf	 0.3510	 0.0500
Sg	 0.5700	 0.0160
sh	 0.6690	 0.0640
zu	 0.9370	 0.1280
zv	 1.0000	 0.1440
zx	 1.0000	 0.2020
zy	 0.6500	 0.0660
zz	 0.6200	 0.0620