



Full wwPDB EM Validation Report ⓘ

Sep 23, 2026 – 06:45 pm BST

PDB ID : 9T6D / pdb_00009t6d
EMDB ID : EMD-55613
Title : NAA40-NAC bound human 80S (combined translation states)
Authors : Guan, D.; Berninghausen, O.; Beckmann, R.
Deposited on : 2025-11-07
Resolution : 2.67 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:

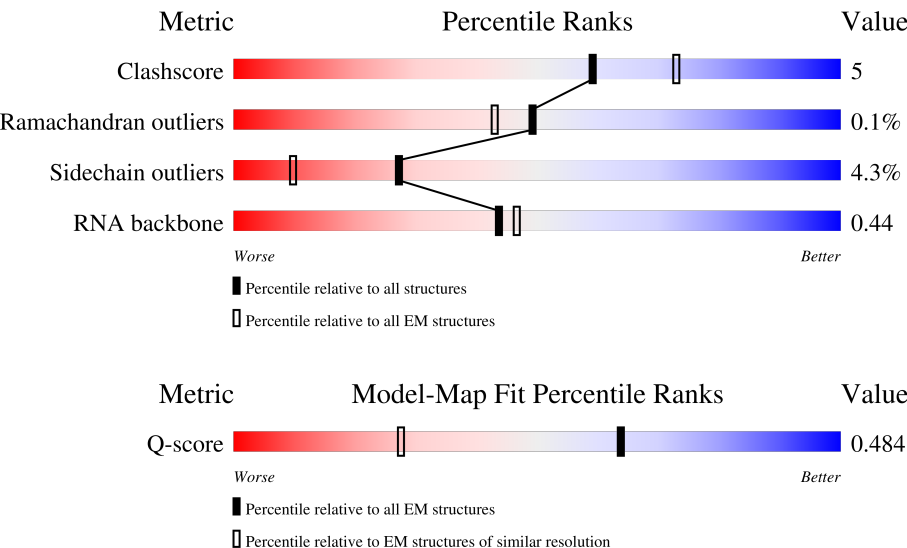
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.67 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.



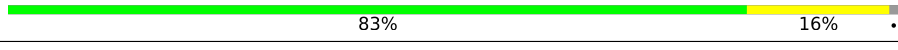
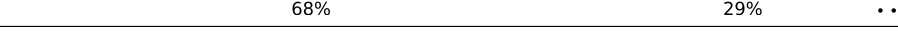
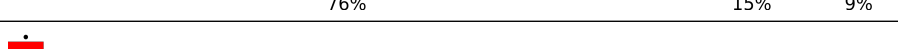
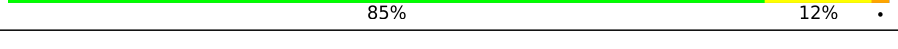
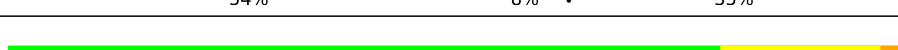
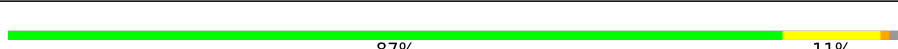
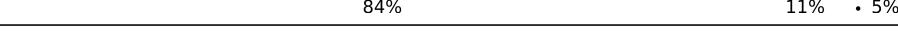
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	9182 (2.17 - 3.17)

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	CB	858	10% 78% 20% ..
2	CC	85	12% 69% 27% .
3	CD	402	12% 86%

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Mol	Chain	Length	Quality of chain
4	L5	5070	
5	L7	121	
6	L8	157	
7	LA	257	
8	LB	403	
9	LC	427	
10	LD	297	
11	LE	288	
12	LF	248	
13	LG	266	
14	LH	192	
15	LI	214	
16	LJ	178	
17	LL	211	
18	LM	215	
19	LN	204	
20	LO	203	
21	LP	184	
22	LQ	188	
23	LR	196	
24	LS	176	
25	LT	160	
26	LU	128	
27	LV	140	
28	LW	157	

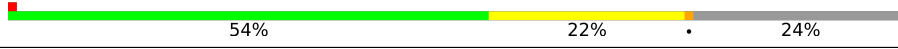
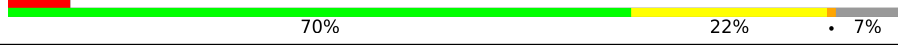
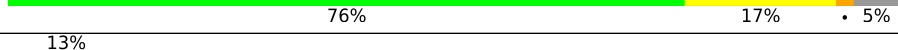
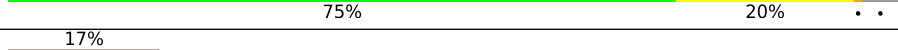
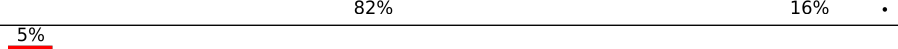
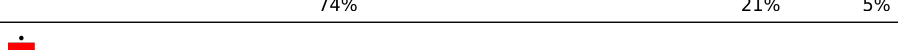
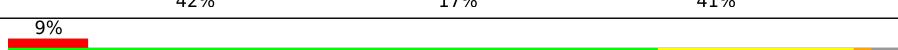
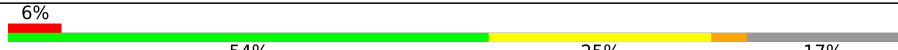
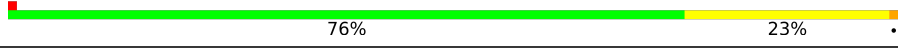
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Mol	Chain	Length	Quality of chain
29	LX	156	
30	LY	145	
31	LZ	136	
32	La	148	
33	Lb	159	
34	Lc	115	
35	Ld	125	
36	Le	135	
37	Lf	110	
38	Lg	117	
39	Lh	123	
40	Li	105	
41	Lj	97	
42	Lk	70	
43	Ll	51	
44	Lm	128	
45	Ln	25	
46	Lo	106	
47	Lp	92	
48	Lr	137	
49	Lz	217	
50	N4	237	
51	NA	215	
52	NB	206	
53	S2	1869	

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Mol	Chain	Length	Quality of chain
54	SA	295	
55	SB	264	
56	SC	293	
57	SD	243	
58	SE	263	
59	SF	204	
60	SG	249	
61	SH	194	
62	SI	208	
63	SJ	194	
64	SK	165	
65	SL	158	
66	SM	132	
67	SN	151	
68	SO	151	
69	SP	145	
70	SQ	146	
71	SR	135	
72	SS	152	
73	ST	145	
74	SU	119	
75	SV	83	
76	SW	130	
77	SX	143	
78	SY	133	

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Mol	Chain	Length	Quality of chain
79	SZ	125	
80	Sa	115	
81	Sb	84	
82	Sc	69	
83	Sd	56	
84	Se	133	
85	Sf	156	
86	Sg	317	

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 229537 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	CB	846	Total	C	N	O	S	0	0
			6605	4193	1136	1232	44		

- Molecule 2 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	CC	85	Total	C	N	O	P	0	0
			1813	808	322	598	85		

- Molecule 3 is a protein called Isoform 2 of SERPINE1 mRNA-binding protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	CD	55	Total	C	N	O	0	0
			440	263	87	90		

- Molecule 4 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L5	3772	Total	C	N	O	P	0	0
			80116	35645	14585	26115	3771		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

- Molecule 6 is a RNA chain called 5.8S rRNA.

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

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

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

- Molecule 8 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LB	402	Total	C	N	O	S	0	0
			3238	2060	608	556	14		

- Molecule 9 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LC	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		

- Molecule 10 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LD	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 11 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LE	236	Total	C	N	O	S	0	0
			1904	1222	361	317	4		

- Molecule 12 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 13 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 14 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 15 is a protein called Ribosomal protein uL16-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LI	202	Total	C	N	O	S	0	0
			1634	1037	314	269	14		

- Molecule 16 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LJ	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		

- Molecule 17 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 18 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 19 is a protein called 60S ribosomal protein L15.

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

- Molecule 20 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 21 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 22 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 23 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LR	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

- Molecule 24 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 25 is a protein called 60S ribosomal protein L21.

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

- Molecule 26 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LU	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 27 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 28 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LW	118	Total	C	N	O	S	0	0
			965	604	199	158	4		

- Molecule 29 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LX	120	Total	C	N	O	S	0	0
			985	630	185	169	1		

- Molecule 30 is a protein called 60S ribosomal protein L26.

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

- Molecule 31 is a protein called 60S ribosomal protein L27.

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

- Molecule 32 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	La	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 33 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lb	109	Total	C	N	O	S	0	0
			876	546	189	137	4		

- Molecule 34 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 35 is a protein called 60S ribosomal protein L31.

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

- Molecule 36 is a protein called 60S ribosomal protein L32.

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

- Molecule 37 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lf	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 38 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lg	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 39 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 40 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 41 is a protein called Large ribosomal subunit protein eL37.

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

- Molecule 42 is a protein called 60S ribosomal protein L38.

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

- Molecule 43 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 44 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lm	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 45 is a protein called 60S ribosomal protein L41.

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

- Molecule 46 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 47 is a protein called 60S ribosomal protein L37a.

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

- Molecule 48 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 49 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Lz	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		

- Molecule 50 is a protein called N-alpha-acetyltransferase 40.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	N4	221	Total	C	N	O	S	0	0
			1795	1128	313	339	15		

- Molecule 51 is a protein called Nascent polypeptide-associated complex subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	NA	105	Total	C	N	O	S	0	0
			817	511	148	154	4		

- Molecule 52 is a protein called Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	NB	104	Total	C	N	O	S	0	0
			805	503	151	149	2		

- Molecule 53 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	S2	1740	Total	C	N	O	P	0	0
			36898	16459	6598	12102	1739		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SA	221	Total	C	N	O	S	0	0
			1741	1106	305	322	8		

- Molecule 55 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SB	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 56 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SC	222	Total	C	N	O	S	0	0
			1725	1115	298	302	10		

- Molecule 57 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 58 is a protein called Small ribosomal subunit protein eS4, X isoform.

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

- Molecule 59 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SF	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 60 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 61 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SH	186	Total	C	N	O	S	0	0
			1497	956	274	266	1		

- Molecule 62 is a protein called 40S ribosomal protein S8.

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

- Molecule 63 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 64 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 65 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SL	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 66 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SM	122	Total	C	N	O	S	0	0
			940	590	164	177	9		

- Molecule 67 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 68 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SO	140	Total	C	N	O	S	0	0
			1049	642	204	197	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SP	121	Total	C	N	O	S	0	0
			985	623	185	170	7		

- Molecule 70 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SQ	144	Total	C	N	O	S	0	0
			1142	726	216	197	3		

- Molecule 71 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SR	135	Total	C	N	O	S	0	0
			1090	685	202	198	5		

- Molecule 72 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SS	145	Total	C	N	O	S	0	0
			1198	751	242	203	2		

- Molecule 73 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	ST	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 74 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SU	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 75 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 76 is a protein called 40S ribosomal protein S15a.

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

- Molecule 77 is a protein called 40S ribosomal protein S23.

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

- Molecule 78 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SY	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		

- Molecule 79 is a protein called 40S ribosomal protein S25.

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

- Molecule 80 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sa	102	Total	C	N	O	S	0	0
			821	512	171	133	5		

- Molecule 81 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 82 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Sc	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 83 is a protein called 40S ribosomal protein S29.

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

- Molecule 84 is a protein called Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Se	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

- Molecule 85 is a protein called Ubiquitin.

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

- Molecule 86 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 87 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
87	CC	1	Total	Mg	0
			1	1	
87	L5	214	Total	Mg	0
			214	214	
87	L7	3	Total	Mg	0
			3	3	
87	L8	3	Total	Mg	0
			3	3	
87	LA	1	Total	Mg	0
			1	1	
87	LI	1	Total	Mg	0
			1	1	
87	LP	1	Total	Mg	0
			1	1	
87	LV	1	Total	Mg	0
			1	1	
87	Le	1	Total	Mg	0
			1	1	
87	Lg	1	Total	Mg	0
			1	1	
87	S2	29	Total	Mg	0
			29	29	

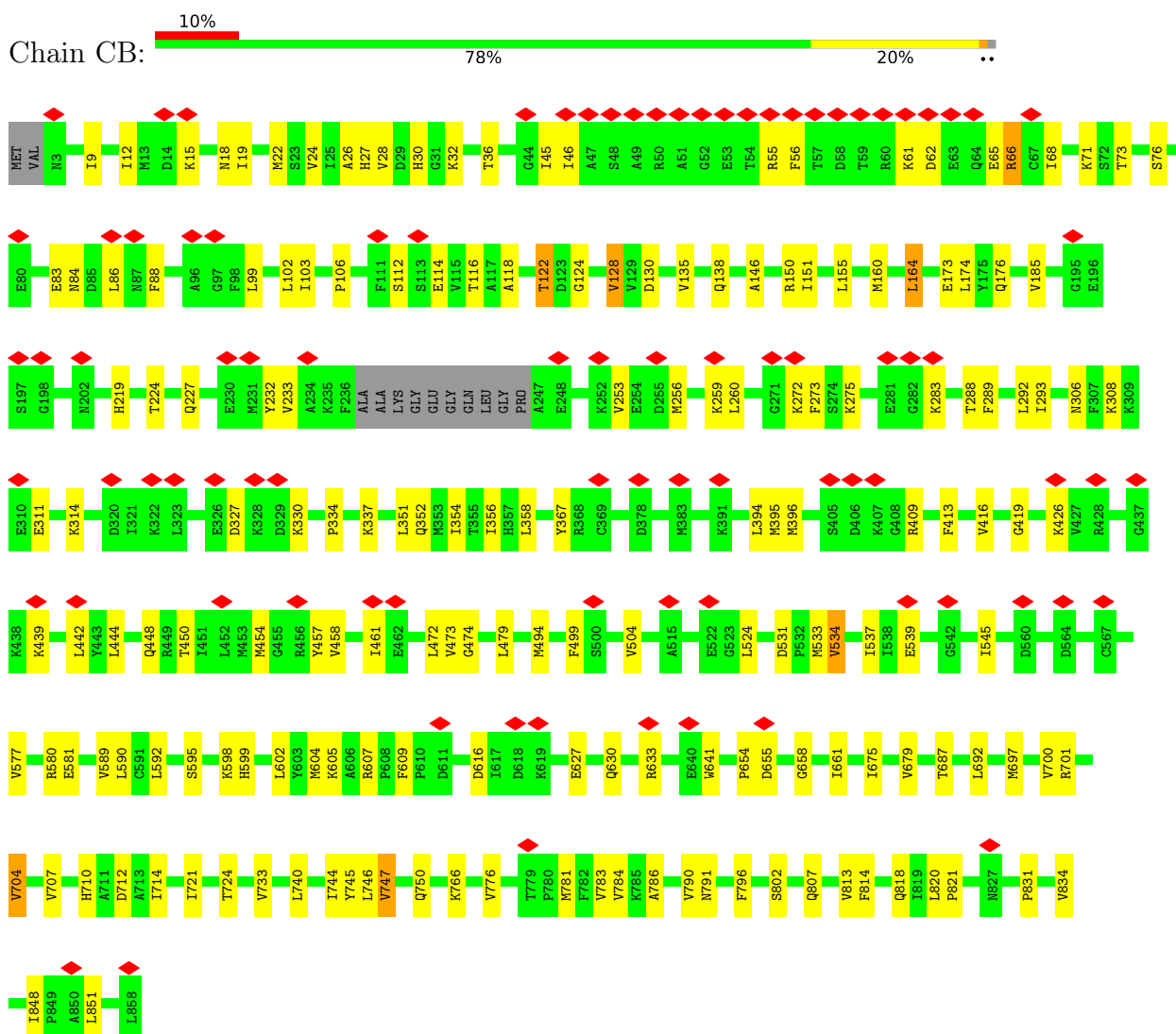
- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
88	Lg	1	Total 1	Zn 1	0
88	Lj	1	Total 1	Zn 1	0
88	Lm	1	Total 1	Zn 1	0
88	Lo	1	Total 1	Zn 1	0
88	Lp	1	Total 1	Zn 1	0
88	SM	1	Total 1	Zn 1	0
88	Sa	1	Total 1	Zn 1	0
88	Sd	1	Total 1	Zn 1	0

3 Residue-property plots

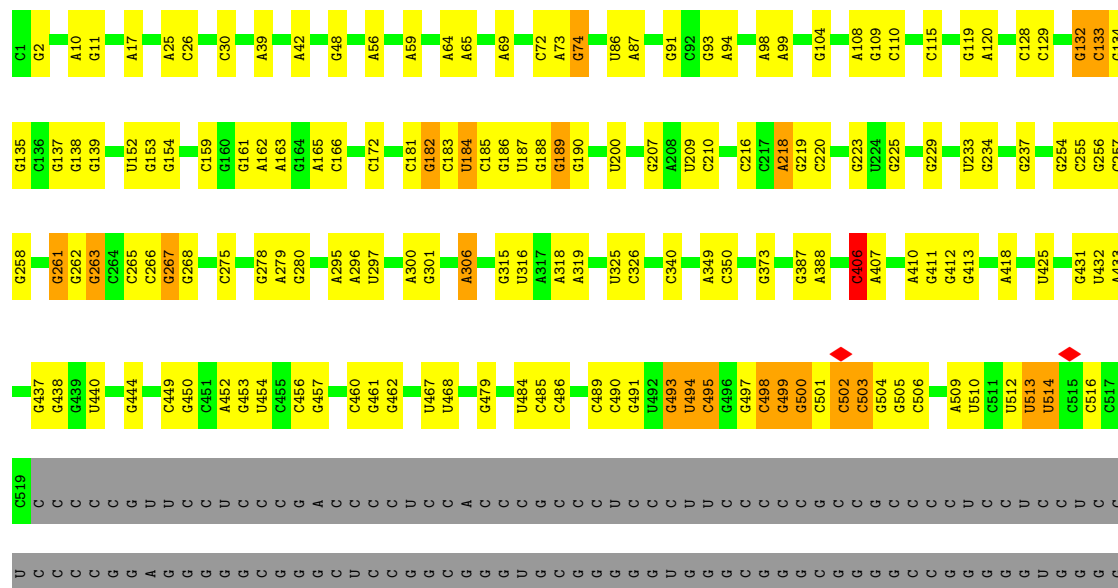
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: Elongation factor 2



• Molecule 2: E-site tRNA









U5030	U4925	G	C4773	A4656	A4513	A4348	A4239	U4118	C4041	G3974	U3992	G3750	A3635
A5034	C4926	C	C4774	U4657	C4519	C4349	G4240	C4119	G4042	C3975	G3897	A3756	U3641
G5041	G4927	G	G4775	G4658	G4524	A4363	C4243	C4122	U4044	C3977	G3900	A3759	U3644
C5060	C4928	G	G4776	G4659	C4525	C4364	G4249	A4127	A4045	C3978	A3901	A3760	U3645
	U4932	U	C	C4670	G4528	G4371	G4250	A4128	A4047	G3979	G3905	C3761	A3646
A4934	C4933	C	U	C4671	G4529	G4372	A4251		A4048	G3980	A3906		A3647
C5054	A4934	C	U	C4672	U4530	G4373	G4254	C4133	U4049	G3981	G3907	U3771	A3648
A5056	G4935	C	U	U4530	U4531	G4374	A4255	C4134	A4050	C3982	A3908	U3772	
C5057	C4937	C	C	G4679	U4533	A4376	G4255	C4139	C4052	G3983	C3909	U3773	A3656
A5058	C4940	C	C	A4687	C4537	G4377	U4260	G4140	A4053	G3984	C3910	A3774	U3657
	G4941	C	G	A4691	G4538	A4378	C4261	C4141	C4054	C3985	C3911		A3662
A5061	C4942	G	C	G4694	G4545	A4380	U4265	C4142	U4055	C3986	G3775		A3663
U5069	A4943	C	C	G4695	A4548	C4387	A4268	C4143	C4057	C3987	A3784		A3664
C	A4944	C	C	U4699	G4549	A4388	G4276	C4144	U4058	C3988	A3785		C3670
	G4949	G	G	A4700	U4557	C4389	A4273	C4145	U4059	C3989	U3786		C3673
	U4950	C	G	A4708	C4560	A4390	A4274	C4146	U4060	C3990	A3917		G3674
	G4951	C	G	U4709	G4567	A4394	G4275	C4147	C4061	C3991	G3918		U3680
	A4955	C	C	G4719	G4573	G4405	G4277	C4160	U4062	C3992	C3923		
		A	C	C4720	U4574	A4422	C4278	C4161	U4063	C3993	A3924		
		G	C	A4727	G4575	C4426	A4281	U4163	U4064	C3994	G3810		U3697
		G	C	C4733	A4584	C4434	G4282	C4170	U4065	C3995	G3811		C3698
		C	C	A4734	C4589	U4438	A4290	U4174	U4066	C3996	U3814		C3699
		C	C	G4740	A4590	U4439	G4291	C4175	G4081	C3997	A3817		C3701
		U	U	G4741	U4591	C4444	A4292	C4176	G4082	C3998	U3818		U3707
		C	C	G4742	C4592	G4448	C4293	C4183	U4083	C3999	G3819		C3708
		C	C	G4743	G4600	G4449	C4294	C4184	G4084	C4000	G3823		U3709
		C	C	A4744	U4601	U4452	U4295	C4188	G4091	C4001	U3824		G3710
		C	A	G4745	A4602	C4453	G4304	U4189	G4092	C4002	A3947		A3711
		G	C	U4748	G4611	U4457	G4305	U4190	G4093	C4003	C3948		A3712
		C	C	G4750	C4612	C4458	U4306	G4191	G4094	C4004	U3950		U3713
		C	C	G4754	G4617	U4459	G4309	C4196	G4095	C4005	G3951		A3717
		C	C	C4757	G4618	U4464	C4314	A4203	G4096	C4006	U3957		A3718
		G	C	U4758	C4625	C4465	C4319	A4214	G4097	C4007	G3958		A3719
		C	C	C4759	A4626	C4466	G4323		G4098	C4008	A3856		G3720
		C	C	G4760	U4627	G4475	G4326	U4219	C4100	C4009	A3857		A3723
		C	C	G4761	G4631	U4476	G4329	A4220	C4101	C4010	G3960		A3724
		C	C	U4762	U4632	C4477	G4330	C4221	C4102	C4011	A3867		A3727
		C	C	U4763	G4633	C4478	G4331	C4222	C4103	C4012	G3868		A3732
		C	C	G4765	U4634	U4500	C4332	G4228	C4104	C4013	A3876		A3733
		C	C		A4635	U4507	C4338	U4229	U4108	C4014	U3877		G3735
		C	C	G4769	U4636	C4508	G4347	A4233	C4109	C4015	C3878		A3736
		A	G	U4770	G4637	U4512		G4238	U4110	C4016	G3967		A3737
		G	G	C4771	G4652				U4111	C4021	U3968		U3745
		C	C	C4772					U4112	C4022	G3970		A3746
									C4114	C4023	G3971		A3747
									C4115	C4024	G3972		A3748
									C4116	C4025	G3973		C3749
									U4117	C4026			
										G4027			
										C4033			
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										C4037			
										G4038			
										G4039			
										G4040			

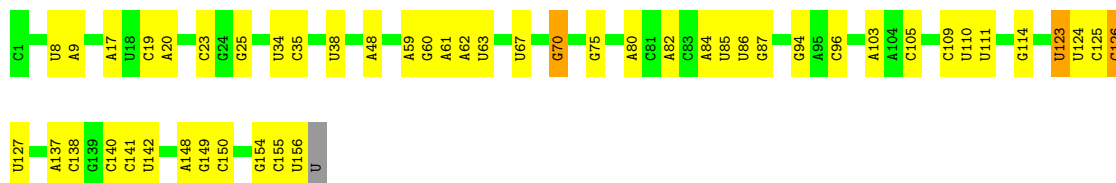
- Molecule 5: 5S rRNA

Chain L7:  83% 16%



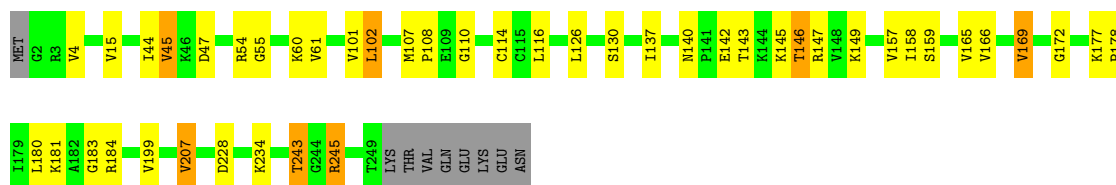
- Molecule 6: 5.8S rRNA

Chain L8:  68% 29%



- Molecule 7: 60S ribosomal protein L8

Chain LA:  79% 15%



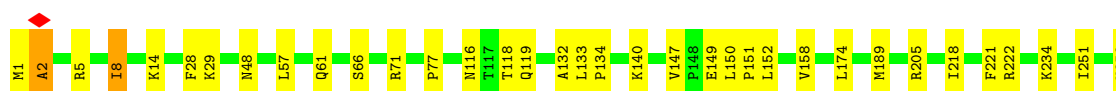
- Molecule 8: 60S ribosomal protein L3

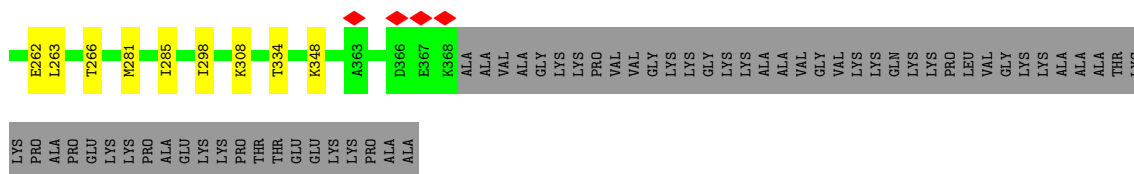
Chain LB:  85% 14%



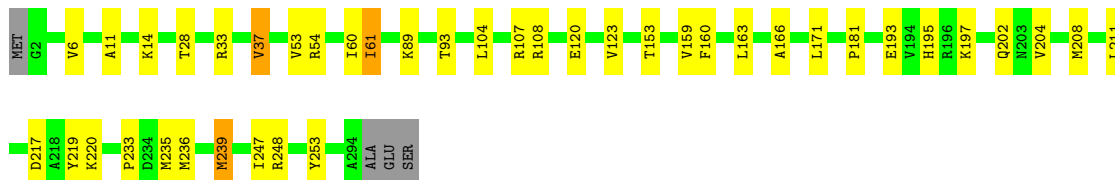
- Molecule 9: 60S ribosomal protein L4

Chain LC:  76% 10% 14%

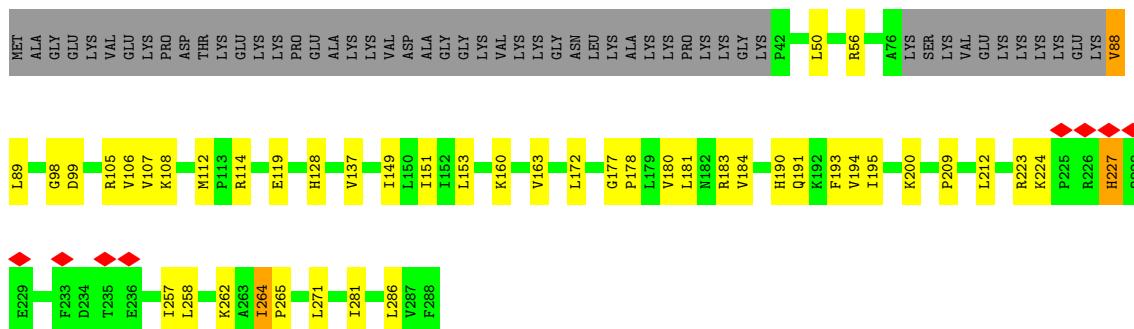




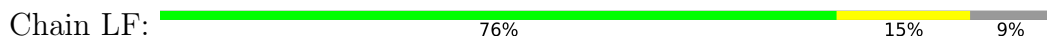
- Molecule 10: 60S ribosomal protein L5



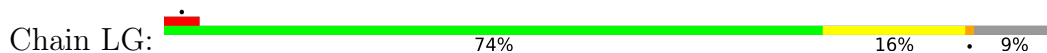
- Molecule 11: Large ribosomal subunit protein eL6

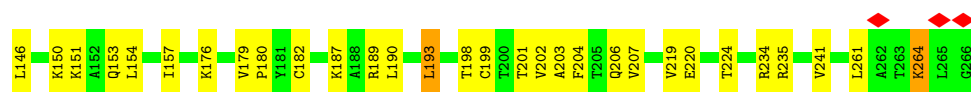


- Molecule 12: Large ribosomal subunit protein uL30



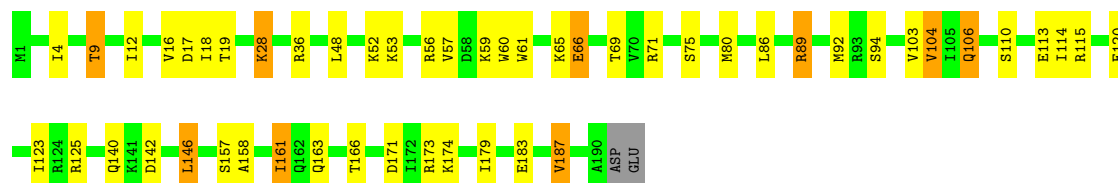
- Molecule 13: 60S ribosomal protein L7a





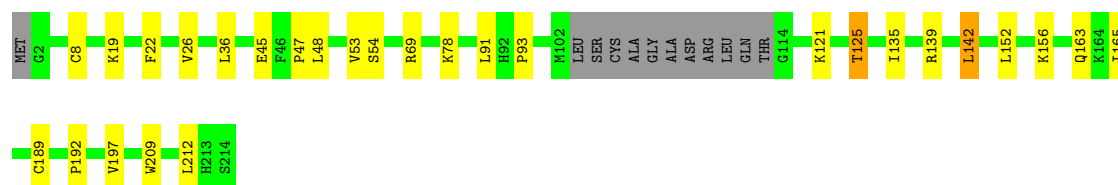
- Molecule 14: 60S ribosomal protein L9

Chain LH: 72% 22% 5%



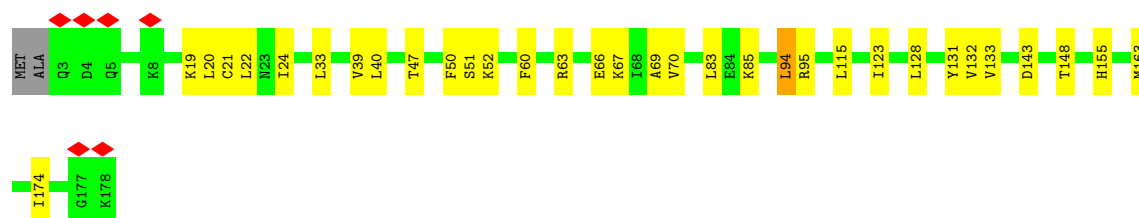
- Molecule 15: Ribosomal protein uL16-like

Chain LI: 81% 12% 6%



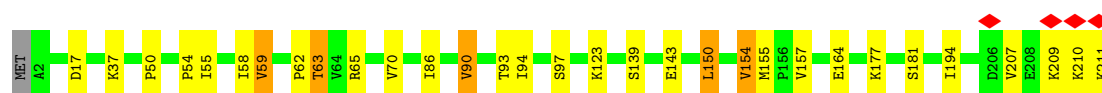
- Molecule 16: 60S ribosomal protein L11

Chain LJ: 80% 18% 2%



- Molecule 17: Large ribosomal subunit protein eL13

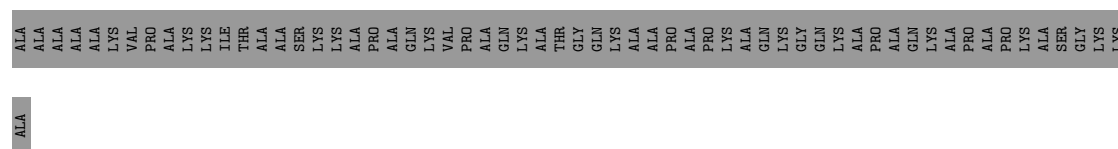
Chain LL: 85% 12% 3%



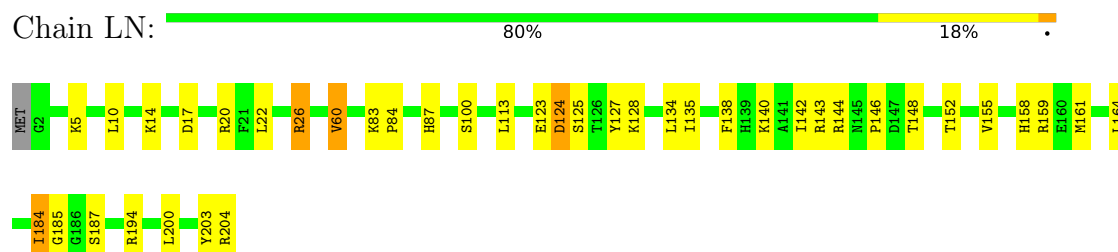
- Molecule 18: 60S ribosomal protein L14

Chain LM: 54% 8% 35%

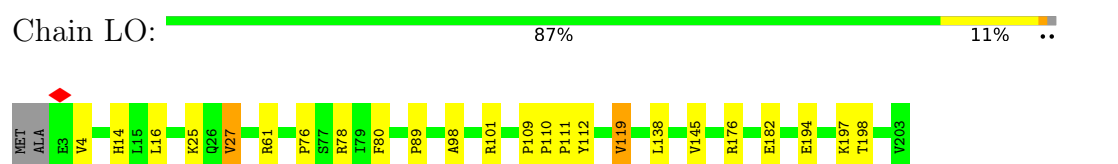




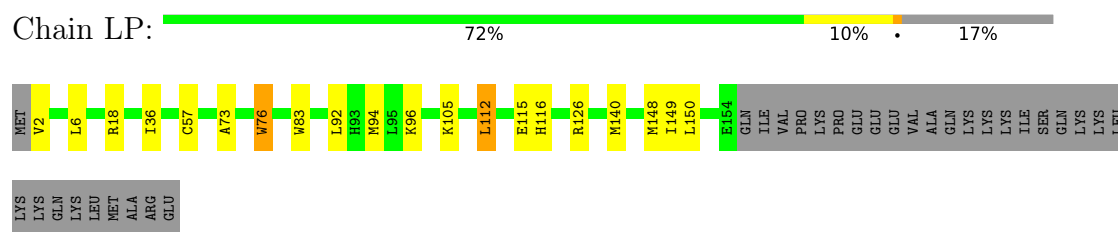
• Molecule 19: 60S ribosomal protein L15



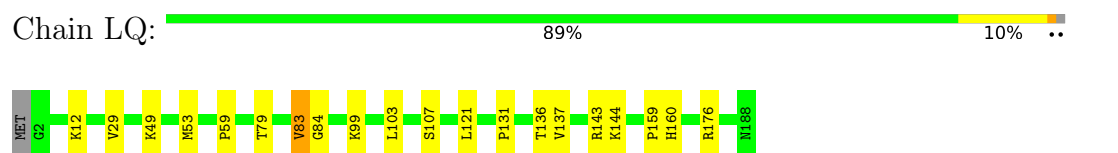
• Molecule 20: 60S ribosomal protein L13a



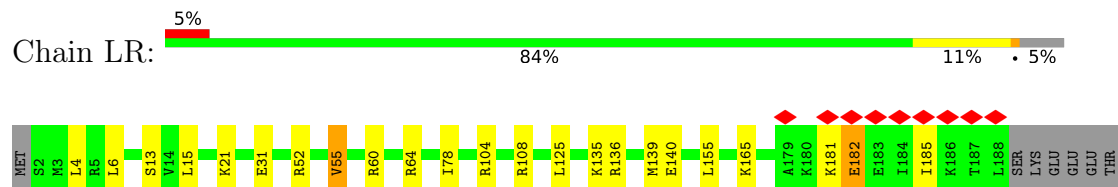
• Molecule 21: 60S ribosomal protein L17



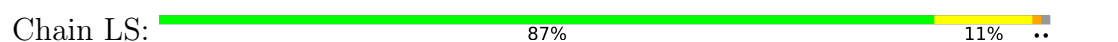
• Molecule 22: 60S ribosomal protein L18



• Molecule 23: 60S ribosomal protein L19



• Molecule 24: 60S ribosomal protein L18a



Chain LY:  75% 17% 8%



- Molecule 31: 60S ribosomal protein L27

Chain LZ:  88% 12% .



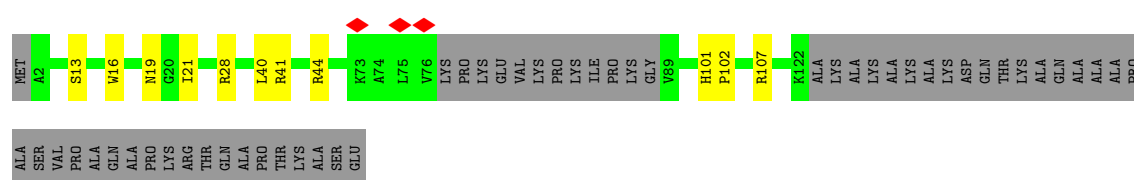
- Molecule 32: 60S ribosomal protein L27a

Chain La:  89% 10% ..



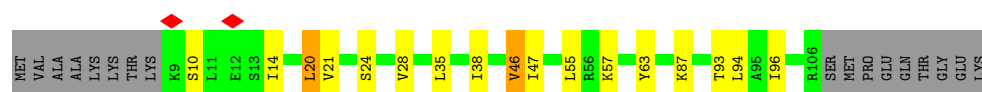
- Molecule 33: 60S ribosomal protein L29

Chain Lb:  62% 7% 31%



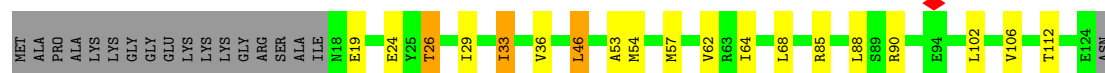
- Molecule 34: 60S ribosomal protein L30

Chain Lc:  70% 13% . 15%



- Molecule 35: 60S ribosomal protein L31

Chain Ld:  70% 13% . 14%



- Molecule 36: 60S ribosomal protein L32

Chain Le:  83% 11% . 5%





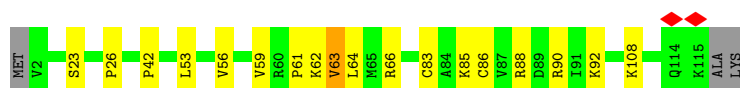
- Molecule 37: 60S ribosomal protein L35a

Chain Lf: 85% 13% ..



- Molecule 38: 60S ribosomal protein L34

Chain Lg: 82% 15% ..



- Molecule 39: 60S ribosomal protein L35

Chain Lh: 86% 11% ..



- Molecule 40: 60S ribosomal protein L36

Chain Li: 90% 8% .



- Molecule 41: Large ribosomal subunit protein eL37

Chain Lj: 76% 10% 11%



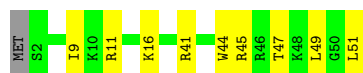
- Molecule 42: 60S ribosomal protein L38

Chain Lk: 81% 17% ..



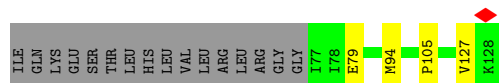
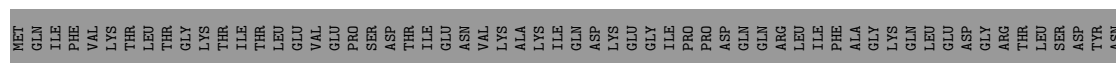
- Molecule 43: 60S ribosomal protein L39

Chain Ll:  80% 18% .



- Molecule 44: Ubiquitin-60S ribosomal protein L40

Chain Lm:  38% 59% .



- Molecule 45: 60S ribosomal protein L41

Chain Ln:  76% 20% .



- Molecule 46: 60S ribosomal protein L36a

Chain Lo:  85% 13% ..



- Molecule 47: 60S ribosomal protein L37a

Chain Lp:  82% 16% ..



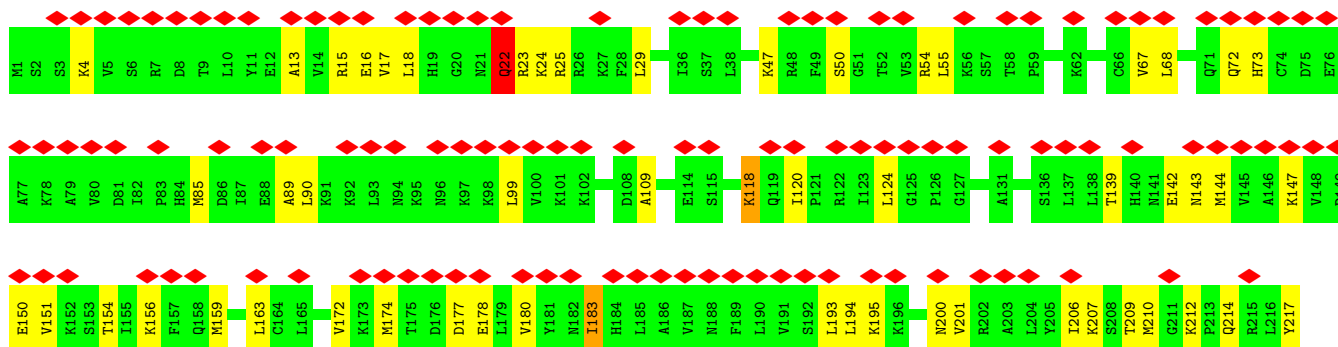
- Molecule 48: 60S ribosomal protein L28

Chain Lr:  84% 7% 9%

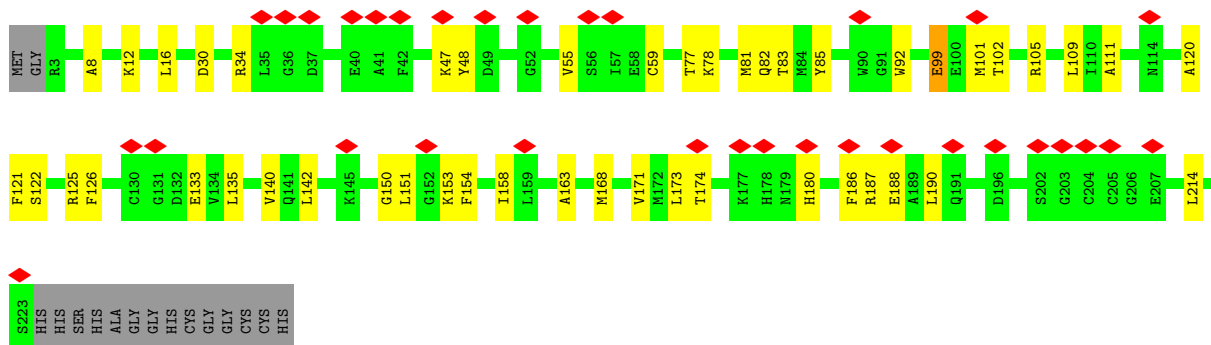


- Molecule 49: 60S ribosomal protein L10a

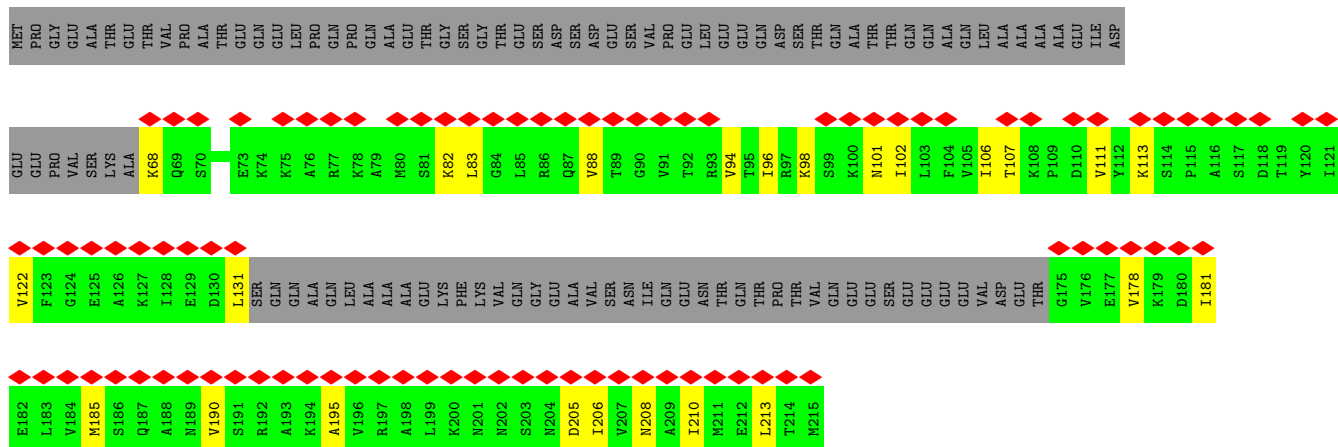
Chain Lz:  54% 74% 24% .



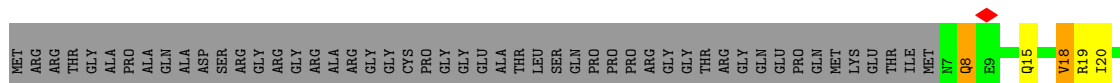
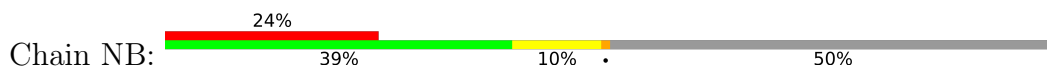
- Molecule 50: N-alpha-acetyltransferase 40



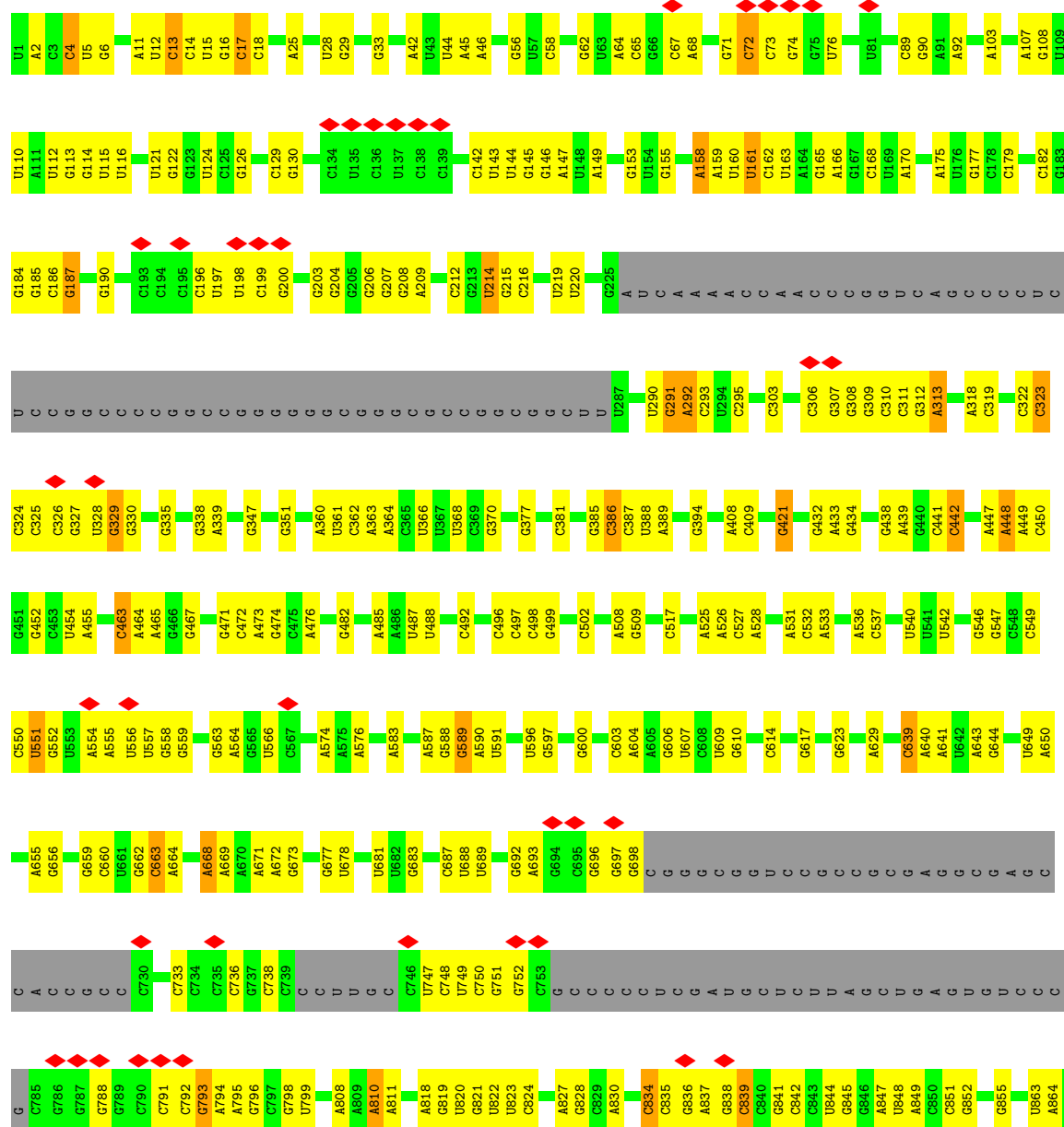
- Molecule 51: Nascent polypeptide-associated complex subunit alpha

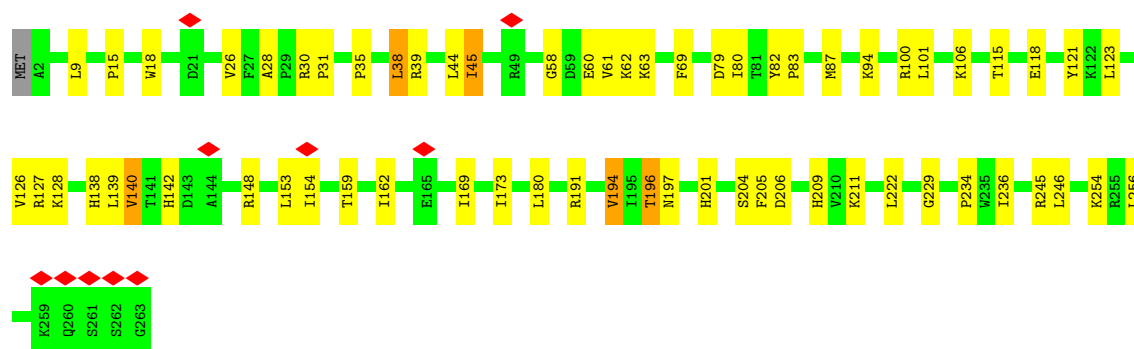


- Molecule 52: Transcription factor BTF3

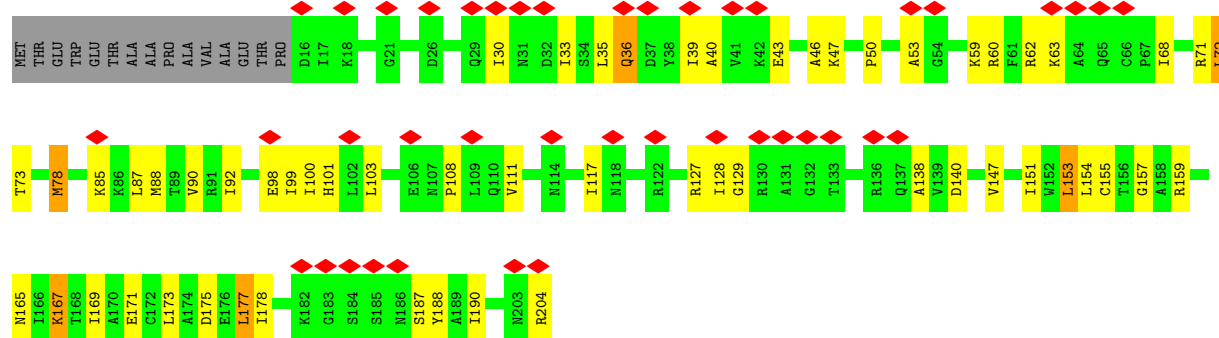


- Molecule 53: 18S rRNA

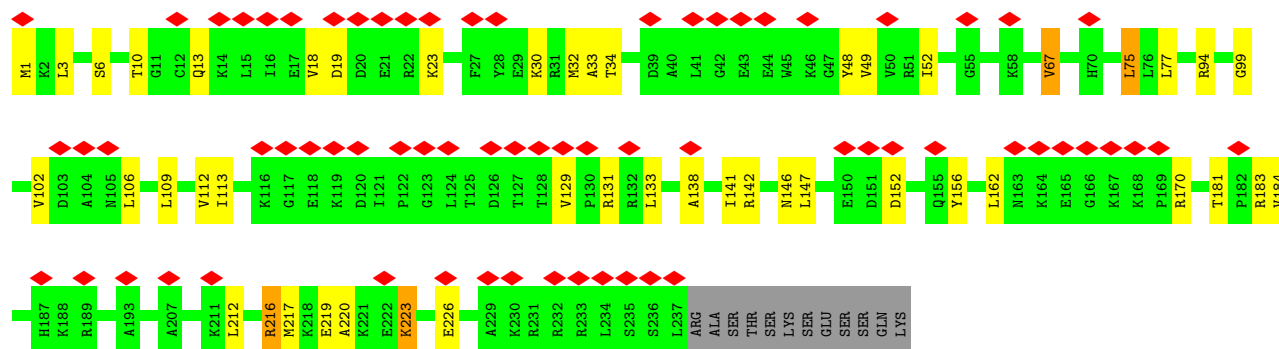
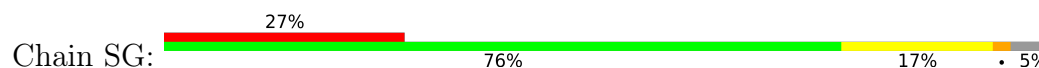




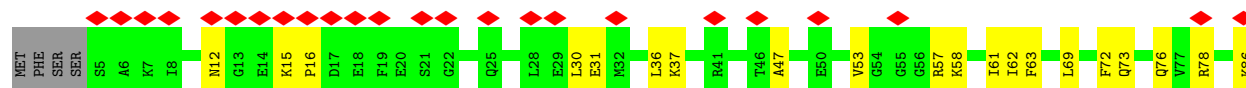
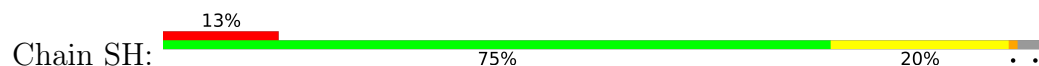
- Molecule 59: 40S ribosomal protein S5

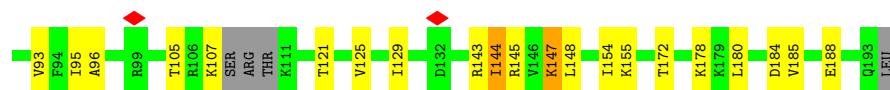


- Molecule 60: 40S ribosomal protein S6

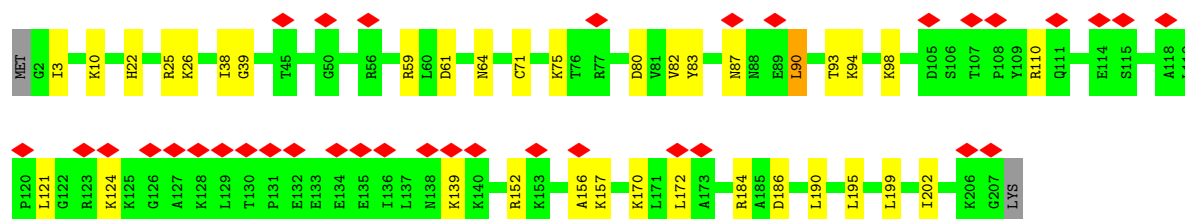
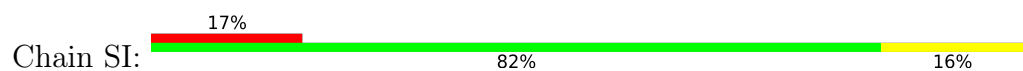


- Molecule 61: 40S ribosomal protein S7

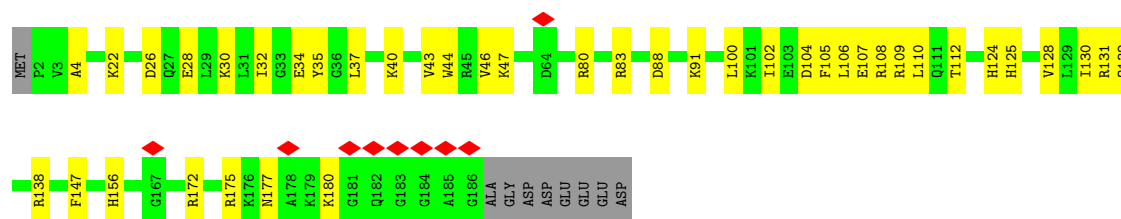
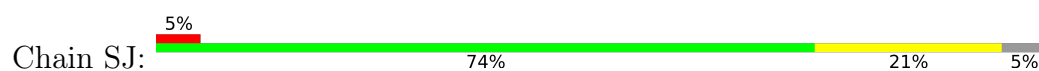




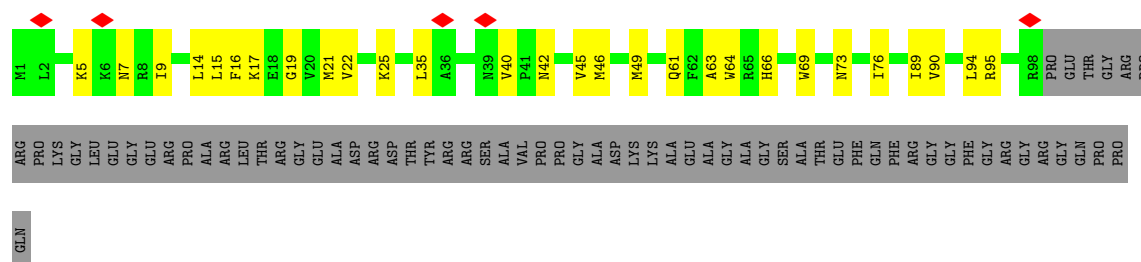
• Molecule 62: 40S ribosomal protein S8



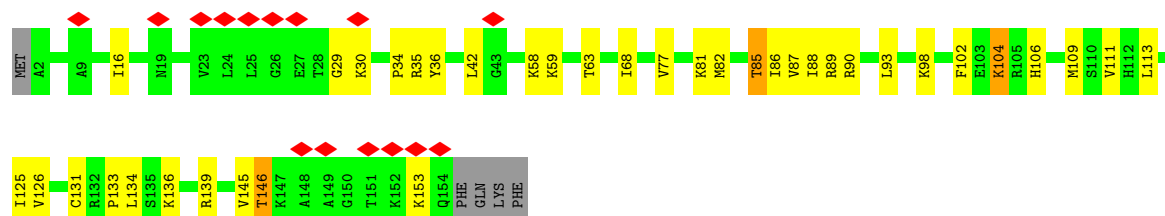
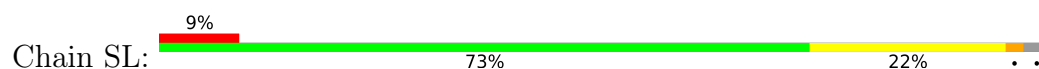
• Molecule 63: 40S ribosomal protein S9



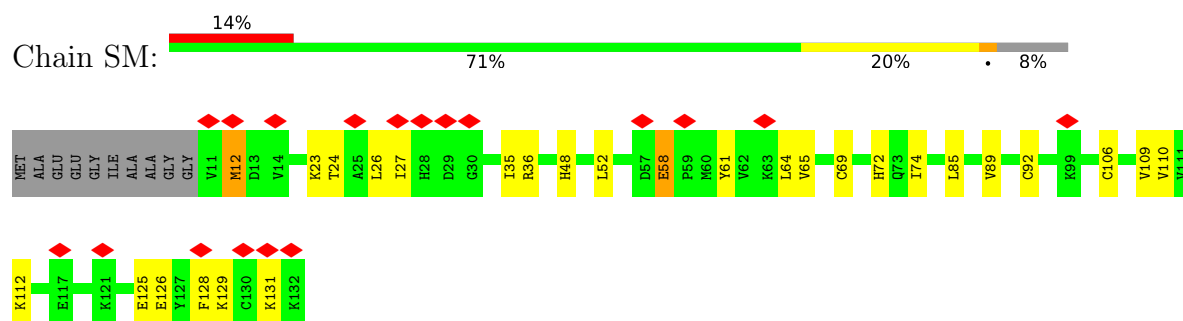
• Molecule 64: 40S ribosomal protein S10



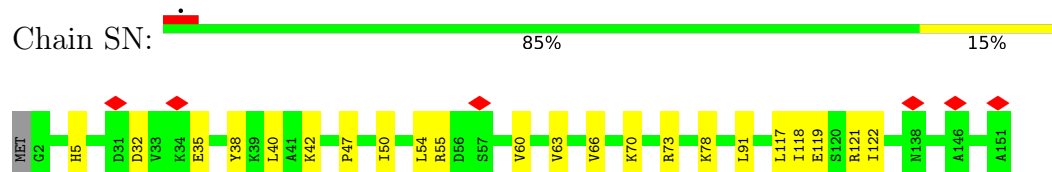
• Molecule 65: 40S ribosomal protein S11



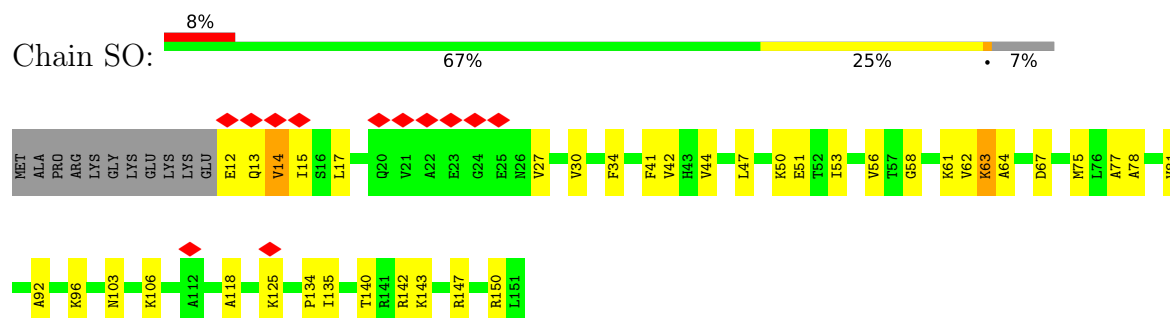
- Molecule 66: 40S ribosomal protein S12



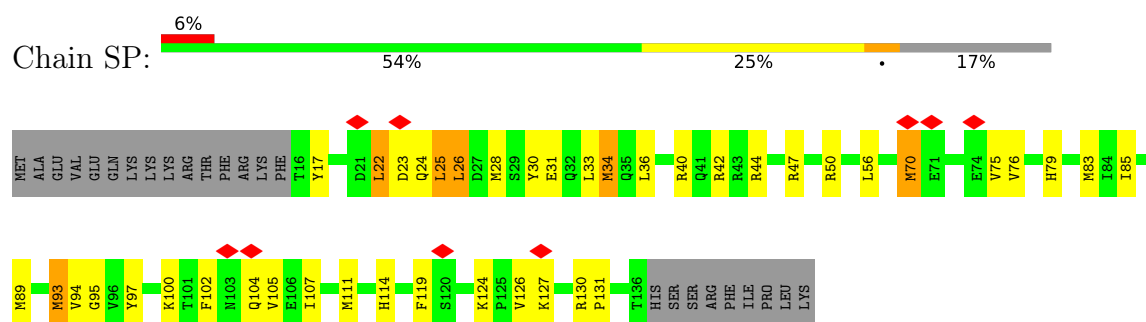
- Molecule 67: 40S ribosomal protein S13



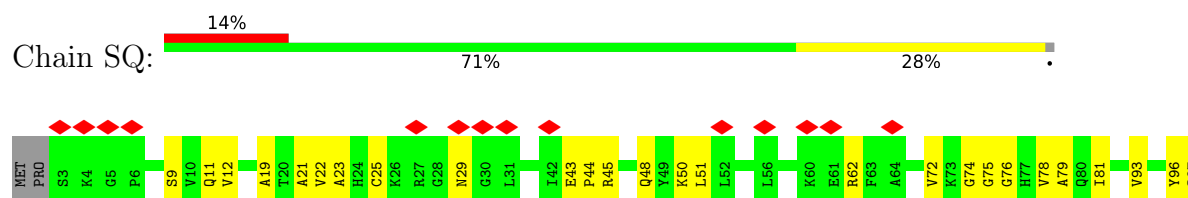
- Molecule 68: 40S ribosomal protein S14

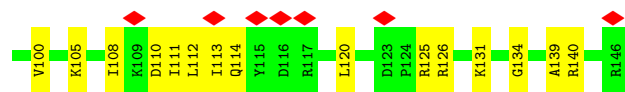


- Molecule 69: 40S ribosomal protein S15

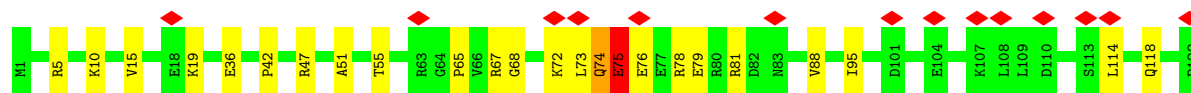
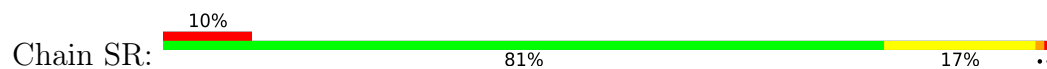


- Molecule 70: 40S ribosomal protein S16





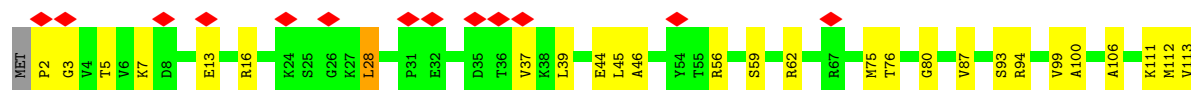
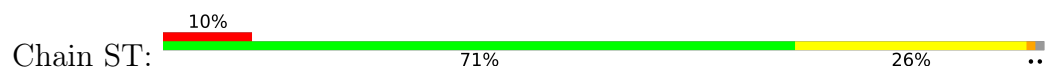
- Molecule 71: 40S ribosomal protein S17



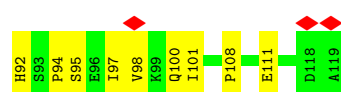
- Molecule 72: 40S ribosomal protein S18



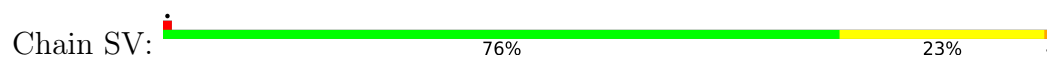
- Molecule 73: 40S ribosomal protein S19



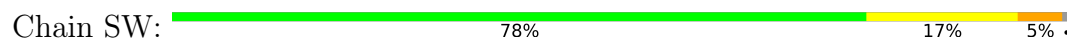
- Molecule 74: 40S ribosomal protein S20



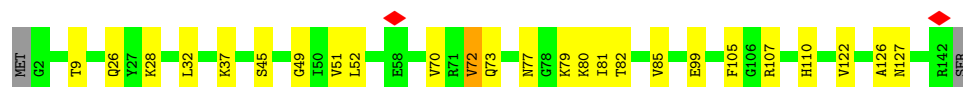
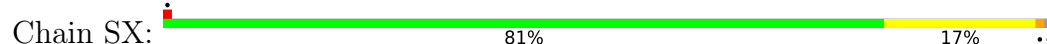
- Molecule 75: 40S ribosomal protein S21



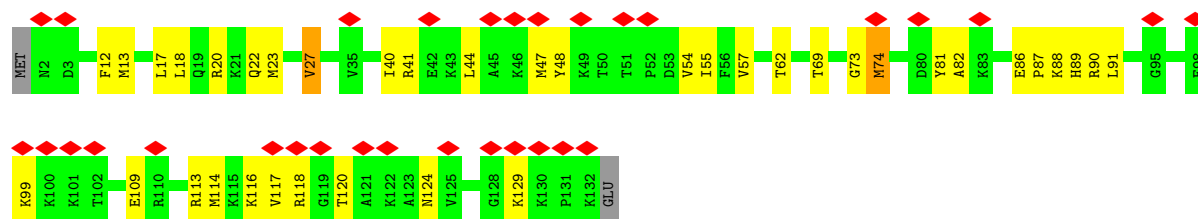
- Molecule 76: 40S ribosomal protein S15a



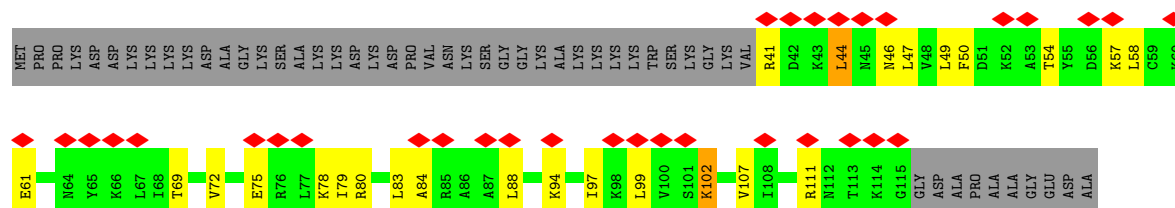
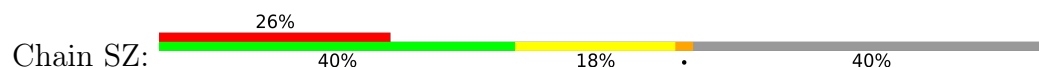
- Molecule 77: 40S ribosomal protein S23



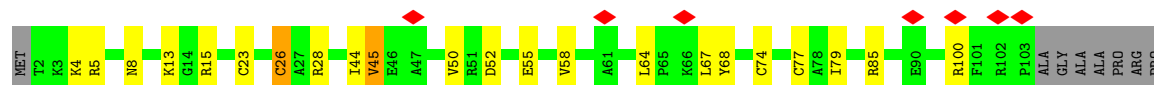
- Molecule 78: 40S ribosomal protein S24



- Molecule 79: 40S ribosomal protein S25



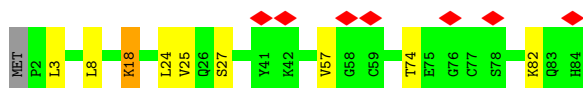
- Molecule 80: 40S ribosomal protein S26



PRO
PRO
LYS
PRO
MET

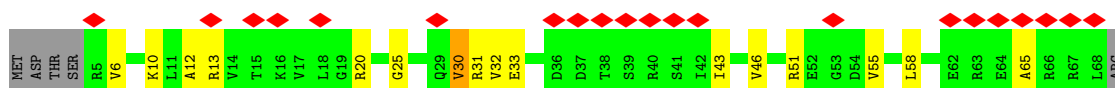
- Molecule 81: 40S ribosomal protein S27

Chain Sb:  8% 88% 10% ..



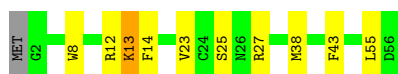
- Molecule 82: 40S ribosomal protein S28

Chain Sc:  30% 70% 22% 7%



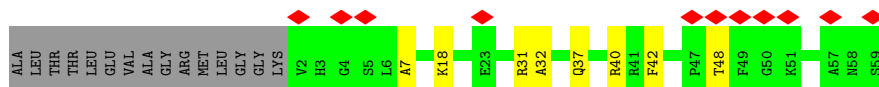
- Molecule 83: 40S ribosomal protein S29

Chain Sd:  80% 16% ..



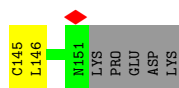
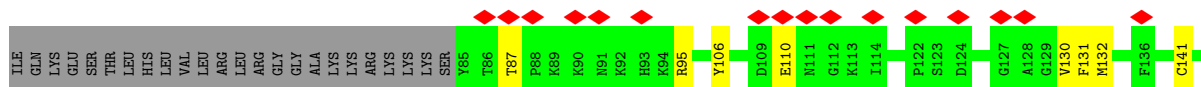
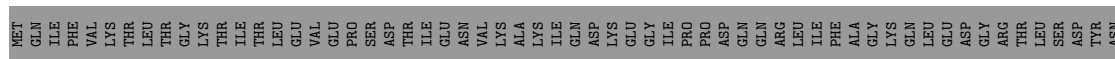
- Molecule 84: Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein

Chain Se:  8% 38% 6% 56%

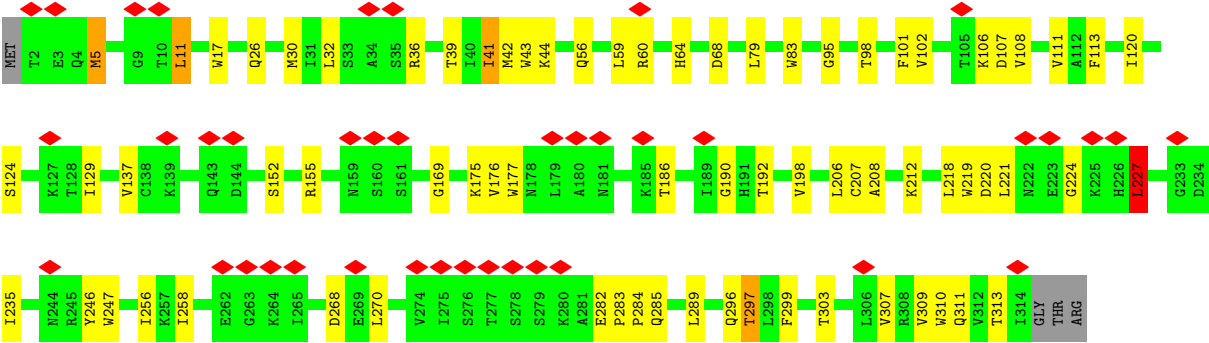
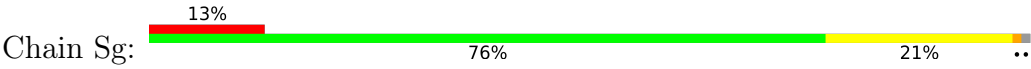


- Molecule 85: Ubiquitin

Chain Sf:  11% 37% 6% 57%



- Molecule 86: Receptor of activated protein C kinase 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	47197	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	4.817	Depositor
Minimum map value	-2.521	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.101	Depositor
Recommended contour level	0.13	Depositor
Map size (Å)	465.28, 465.28, 465.28	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.727, 0.727, 0.727	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	CB	0.22	0/6734	0.59	2/9094 (0.0%)
2	CC	0.15	0/2025	0.32	0/3155
3	CD	0.21	0/447	0.61	0/592
4	L5	0.25	0/89570	0.38	2/139647 (0.0%)
5	L7	0.24	0/2861	0.33	0/4459
6	L8	0.25	0/3701	0.34	0/5766
7	LA	0.27	0/1936	0.59	0/2596
8	LB	0.25	0/3306	0.55	0/4424
9	LC	0.27	0/2981	0.53	2/4002 (0.0%)
10	LD	0.24	0/2428	0.59	0/3252
11	LE	0.23	0/1942	0.56	0/2606
12	LF	0.27	0/1905	0.52	0/2539
13	LG	0.25	0/1960	0.57	0/2637
14	LH	0.28	0/1537	0.61	1/2066 (0.0%)
15	LI	0.23	0/1673	0.52	0/2233
16	LJ	0.26	0/1433	0.66	0/1915
17	LL	0.24	0/1732	0.49	0/2315
18	LM	0.25	0/1161	0.60	2/1554 (0.1%)
19	LN	0.28	0/1746	0.59	1/2338 (0.0%)
20	LO	0.25	0/1682	0.46	0/2250
21	LP	0.24	0/1268	0.49	0/1701
22	LQ	0.25	0/1537	0.51	0/2052
23	LR	0.22	0/1582	0.45	0/2091
24	LS	0.24	0/1493	0.44	0/2003
25	LT	0.24	0/1326	0.48	0/1770
26	LU	0.25	0/839	0.61	1/1126 (0.1%)
27	LV	0.23	0/993	0.50	0/1332
28	LW	0.22	0/979	0.49	0/1295
29	LX	0.23	0/1002	0.56	0/1345
30	LY	0.22	0/1132	0.46	0/1504
31	LZ	0.25	0/1130	0.60	2/1507 (0.1%)
32	La	0.25	0/1191	0.48	0/1591

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Lb	0.24	0/889	0.60	0/1175
34	Lc	0.23	0/774	0.56	0/1038
35	Ld	0.24	0/903	0.49	0/1216
36	Le	0.26	0/1071	0.53	0/1429
37	Lf	0.28	0/895	0.55	0/1198
38	Lg	0.24	0/916	0.50	0/1220
39	Lh	0.21	0/1023	0.45	0/1351
40	Li	0.20	0/843	0.48	0/1115
41	Lj	0.31	0/720	0.60	0/952
42	Lk	0.22	0/575	0.52	0/761
43	Ll	0.27	0/454	0.48	0/599
44	Lm	0.20	0/435	0.41	0/575
45	Ln	0.20	0/231	0.36	0/294
46	Lo	0.23	0/876	0.50	0/1156
47	Lp	0.26	0/718	0.52	0/953
48	Lr	0.25	0/1017	0.49	0/1364
49	Lz	0.24	0/1769	0.70	2/2371 (0.1%)
50	N4	0.22	0/1831	0.66	1/2456 (0.0%)
51	NA	0.20	0/821	0.56	0/1096
52	NB	0.23	0/813	0.61	1/1091 (0.1%)
53	S2	0.16	0/41244	0.34	0/64263
54	SA	0.25	0/1778	0.61	0/2416
55	SB	0.22	0/1765	0.64	1/2362 (0.0%)
56	SC	0.27	0/1762	0.71	1/2381 (0.0%)
57	SD	0.23	0/1793	0.67	0/2414
58	SE	0.21	0/2118	0.58	0/2849
59	SF	0.25	0/1516	0.71	2/2037 (0.1%)
60	SG	0.22	0/1946	0.64	4/2590 (0.2%)
61	SH	0.27	0/1519	0.68	2/2033 (0.1%)
62	SI	0.22	0/1715	0.58	1/2287 (0.0%)
63	SJ	0.24	0/1550	0.60	0/2069
64	SK	0.30	0/851	0.79	0/1147
65	SL	0.22	0/1268	0.53	0/1696
66	SM	0.22	0/950	0.70	2/1275 (0.2%)
67	SN	0.22	0/1232	0.59	0/1656
68	SO	0.24	0/1062	0.62	2/1425 (0.1%)
69	SP	0.33	0/1003	0.90	7/1342 (0.5%)
70	SQ	0.30	0/1160	0.76	2/1553 (0.1%)
71	SR	0.29	0/1105	0.85	4/1484 (0.3%)
72	SS	0.23	0/1216	0.63	1/1628 (0.1%)
73	ST	0.28	0/1131	0.76	2/1515 (0.1%)
74	SU	0.25	0/831	0.77	3/1115 (0.3%)
75	SV	0.23	0/643	0.64	0/860

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
76	SW	0.23	0/1051	0.51	0/1406
77	SX	0.22	0/1116	0.61	1/1490 (0.1%)
78	SY	0.23	0/1083	0.63	1/1438 (0.1%)
79	SZ	0.29	0/604	0.92	1/810 (0.1%)
80	Sa	0.29	0/836	0.57	0/1121
81	Sb	0.23	0/665	0.62	1/891 (0.1%)
82	Sc	0.27	0/508	0.82	0/680
83	Sd	0.22	0/470	0.69	2/623 (0.3%)
84	Se	0.23	0/465	0.63	0/612
85	Sf	0.25	0/560	0.81	1/745 (0.1%)
86	Sg	0.23	0/2493	0.71	4/3394 (0.1%)
All	All	0.24	0/245815	0.47	62/359774 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	CB	0	1
7	LA	0	2
8	LB	0	2
14	LH	0	2
16	LJ	0	1
17	LL	0	1
18	LM	0	2
20	LO	0	1
25	LT	0	1
28	LW	0	1
31	LZ	0	1
37	Lf	0	1
39	Lh	0	1
41	Lj	0	1
49	Lz	0	1
57	SD	0	1
59	SF	0	1
60	SG	0	1
61	SH	0	1
69	SP	0	1
70	SQ	0	1
72	SS	0	1
73	ST	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
75	SV	0	1
77	SX	0	2
79	SZ	0	1
85	Sf	0	1
86	Sg	0	1
All	All	0	33

There are no bond length outliers.

All (62) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	NB	8	GLN	CA-CB-CG	6.62	127.34	114.10
56	SC	80	GLU	CA-CB-CG	6.36	126.83	114.10
19	LN	184	ILE	N-CA-C	-6.28	106.32	111.91
60	SG	223	LYS	CB-CG-CD	6.27	125.73	111.30
73	ST	112	MET	CB-CG-SD	6.26	131.49	112.70
69	SP	34	MET	CA-CB-CG	6.17	126.45	114.10
59	SF	177	LEU	CA-CB-CG	6.17	137.89	116.30
71	SR	74	GLN	CA-C-N	-6.16	110.82	121.66
71	SR	74	GLN	C-N-CA	-6.16	110.82	121.66
86	Sg	227	LEU	CA-CB-CG	6.09	137.60	116.30
60	SG	223	LYS	CA-CB-CG	6.04	126.19	114.10
18	LM	87	ALA	CA-C-N	6.04	133.07	121.54
18	LM	87	ALA	C-N-CA	6.04	133.07	121.54
9	LC	2	ALA	CA-C-N	6.03	132.54	121.70
9	LC	2	ALA	C-N-CA	6.03	132.54	121.70
71	SR	74	GLN	CA-CB-CG	5.82	125.74	114.10
61	SH	58	LYS	CB-CG-CD	5.80	124.65	111.30
61	SH	147	LYS	CB-CG-CD	5.78	124.59	111.30
49	Lz	22	GLN	CA-CB-CG	5.75	125.59	114.10
83	Sd	13	LYS	CA-CB-CG	5.71	125.52	114.10
86	Sg	5	MET	CB-CG-SD	5.69	129.76	112.70
1	CB	71	LYS	CB-CG-CD	5.64	124.26	111.30
60	SG	19	ASP	N-CA-C	-5.63	107.41	114.56
81	Sb	18	LYS	CB-CG-CD	5.62	124.22	111.30
55	SB	110	MET	CB-CG-SD	5.61	129.52	112.70
74	SU	43	ALA	CA-C-N	-5.60	113.71	122.73
74	SU	43	ALA	C-N-CA	-5.60	113.71	122.73
60	SG	223	LYS	N-CA-CB	5.49	119.51	110.39
14	LH	28	LYS	CB-CG-CD	5.49	123.92	111.30
70	SQ	44	PRO	N-CA-C	5.41	123.61	112.47
69	SP	70	MET	CB-CG-SD	5.40	128.91	112.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
77	SX	37	LYS	CA-CB-CG	5.39	124.89	114.10
31	LZ	29	ILE	CA-C-N	5.37	131.80	121.54
31	LZ	29	ILE	C-N-CA	5.37	131.80	121.54
74	SU	44	LYS	CA-CB-CG	5.35	124.80	114.10
69	SP	124	LYS	CB-CG-CD	5.34	123.59	111.30
83	Sd	13	LYS	N-CA-C	-5.34	99.43	110.80
68	SO	14	VAL	CA-C-N	5.33	131.29	121.70
68	SO	14	VAL	C-N-CA	5.33	131.29	121.70
49	Lz	118	LYS	CB-CG-CD	5.31	123.51	111.30
86	Sg	11	LEU	CA-CB-CG	5.27	134.74	116.30
86	Sg	282	GLU	CA-CB-CG	5.25	124.61	114.10
70	SQ	50	LYS	CA-CB-CG	5.25	124.59	114.10
78	SY	74	MET	CB-CG-SD	5.20	128.30	112.70
69	SP	70	MET	CA-CB-CG	5.18	124.47	114.10
62	SI	110	ARG	CG-CD-NE	5.18	123.39	112.00
71	SR	75	GLU	CA-CB-CG	5.17	124.44	114.10
50	N4	101	MET	CB-CG-SD	5.15	128.14	112.70
66	SM	12	MET	CA-CB-CG	5.14	124.37	114.10
85	Sf	110	GLU	CA-CB-CG	5.12	124.33	114.10
26	LU	108	GLU	CA-CB-CG	5.12	124.33	114.10
66	SM	58	GLU	CA-CB-CG	5.10	124.31	114.10
59	SF	153	LEU	CA-CB-CG	5.10	134.15	116.30
69	SP	26	LEU	CA-CB-CG	5.10	134.15	116.30
79	SZ	58	LEU	CA-CB-CG	5.09	134.12	116.30
69	SP	33	LEU	CA-CB-CG	5.09	134.11	116.30
72	SS	76	GLN	CB-CG-CD	5.08	121.24	112.60
73	ST	137	GLN	CB-CG-CD	5.07	121.21	112.60
69	SP	93	MET	CA-CB-CG	5.05	124.21	114.10
4	L5	406	C	C2'-C3'-O3'	5.02	121.23	113.70
4	L5	1082	C	P-O3'-C3'	5.02	127.72	120.20
1	CB	164	LEU	CA-CB-CG	5.00	133.81	116.30

There are no chirality outliers.

All (33) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	CB	807	GLN	Peptide
7	LA	110	GLY	Peptide
7	LA	54	ARG	Peptide
8	LB	17	LEU	Peptide
8	LB	258	HIS	Peptide
14	LH	106	GLN	Peptide

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Mol	Chain	Res	Type	Group
14	LH	173	ARG	Peptide
16	LJ	94	LEU	Peptide
17	LL	154	VAL	Peptide
18	LM	87	ALA	Peptide
18	LM	88	ALA	Peptide
20	LO	110	PRO	Peptide
25	LT	136	ARG	Peptide
28	LW	3	VAL	Peptide
31	LZ	124	THR	Peptide
37	Lf	106	TYR	Peptide
39	Lh	86	LYS	Peptide
41	Lj	39	TYR	Peptide
49	Lz	183	ILE	Peptide
57	SD	164	VAL	Peptide
59	SF	78	MET	Peptide
60	SG	216	ARG	Sidechain
61	SH	15	LYS	Peptide
69	SP	127	LYS	Peptide
70	SQ	43	GLU	Peptide
72	SS	66	ARG	Sidechain
73	ST	46	ALA	Peptide
75	SV	78	ILE	Peptide
77	SX	126	ALA	Peptide
77	SX	77	ASN	Peptide
79	SZ	46	ASN	Peptide
85	Sf	131	PHE	Peptide
86	Sg	227	LEU	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CB	6605	0	6681	94	0
2	CC	1813	0	917	6	0
3	CD	440	0	402	4	0
4	L5	80116	0	40368	331	0
5	L7	2561	0	1295	2	0
6	L8	3314	0	1683	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	LA	1898	0	1993	25	0
8	LB	3238	0	3376	33	0
9	LC	2927	0	3104	21	0
10	LD	2382	0	2410	19	0
11	LE	1904	0	2055	22	0
12	LF	1870	0	1996	18	0
13	LG	1927	0	2074	23	0
14	LH	1518	0	1601	28	0
15	LI	1634	0	1671	17	0
16	LJ	1410	0	1441	18	0
17	LL	1701	0	1818	18	0
18	LM	1138	0	1204	13	0
19	LN	1701	0	1749	24	0
20	LO	1650	0	1794	14	0
21	LP	1242	0	1269	12	0
22	LQ	1513	0	1628	10	0
23	LR	1566	0	1729	11	0
24	LS	1453	0	1490	9	0
25	LT	1298	0	1365	15	0
26	LU	825	0	850	15	0
27	LV	979	0	1039	10	0
28	LW	965	0	1029	11	0
29	LX	985	0	1066	13	0
30	LY	1115	0	1205	11	0
31	LZ	1107	0	1182	7	0
32	La	1162	0	1213	10	0
33	Lb	876	0	948	6	0
34	Lc	764	0	804	11	0
35	Ld	888	0	930	9	0
36	Le	1053	0	1147	7	0
37	Lf	876	0	912	6	0
38	Lg	906	0	998	13	0
39	Lh	1015	0	1148	13	0
40	Li	832	0	917	4	0
41	Lj	705	0	737	9	0
42	Lk	569	0	637	8	0
43	Ll	444	0	483	5	0
44	Lm	429	0	465	1	0
45	Ln	230	0	276	3	0
46	Lo	862	0	929	6	0
47	Lp	708	0	756	11	0
48	Lr	1002	0	1068	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	Lz	1741	0	1854	33	0
50	N4	1795	0	1754	25	0
51	NA	817	0	877	15	0
52	NB	805	0	847	17	0
53	S2	36898	0	18601	237	0
54	SA	1741	0	1746	33	0
55	SB	1738	0	1809	29	0
56	SC	1725	0	1813	37	0
57	SD	1765	0	1865	34	0
58	SE	2076	0	2177	41	0
59	SF	1495	0	1549	39	0
60	SG	1923	0	2089	28	0
61	SH	1497	0	1590	22	0
62	SI	1686	0	1772	23	0
63	SJ	1525	0	1640	24	0
64	SK	827	0	854	21	0
65	SL	1247	0	1323	23	0
66	SM	940	0	965	15	0
67	SN	1208	0	1294	13	0
68	SO	1049	0	1073	30	0
69	SP	985	0	1031	23	0
70	SQ	1142	0	1213	30	0
71	SR	1090	0	1149	16	0
72	SS	1198	0	1261	27	0
73	ST	1112	0	1146	20	0
74	SU	821	0	883	22	0
75	SV	636	0	637	9	0
76	SW	1034	0	1080	15	0
77	SX	1098	0	1167	13	0
78	SY	1065	0	1142	25	0
79	SZ	598	0	656	12	0
80	Sa	821	0	870	16	0
81	Sb	651	0	672	5	0
82	Sc	506	0	536	11	0
83	Sd	459	0	451	9	0
84	Se	459	0	503	6	0
85	Sf	548	0	555	4	0
86	Sg	2436	0	2393	39	0
87	CC	1	0	0	0	0
87	L5	214	0	0	0	0
87	L7	3	0	0	0	0
87	L8	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
87	LA	1	0	0	0	0
87	LI	1	0	0	0	0
87	LP	1	0	0	0	0
87	LV	1	0	0	0	0
87	Le	1	0	0	0	0
87	Lg	1	0	0	0	0
87	S2	29	0	0	0	0
88	Lg	1	0	0	0	0
88	Lj	1	0	0	0	0
88	Lm	1	0	0	0	0
88	Lo	1	0	0	0	0
88	Lp	1	0	0	0	0
88	SM	1	0	0	0	0
88	Sa	1	0	0	0	0
88	Sd	1	0	0	0	0
All	All	229537	0	172689	1830	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 5.

All (1830) 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)
4:L5:1176:C:H42	4:L5:1184:A:N6	1.49	1.10
4:L5:1176:C:N4	4:L5:1184:A:H61	1.51	1.08
53:S2:886:A:N6	53:S2:901:G:C4	2.21	1.07
4:L5:1269:G:N2	4:L5:1441:C:C2	2.25	1.04
59:SF:35:LEU:O	59:SF:39:ILE:HB	1.58	1.03
4:L5:1762:C:N4	4:L5:1770:A:C2	2.29	1.01
18:LM:77:TRP:O	18:LM:81:ASP:HA	1.59	0.99
53:S2:1743:G:N2	53:S2:1791:A:H62	1.59	0.99
53:S2:1652:G:H1	53:S2:1672:U:H3	1.08	0.98
53:S2:925:G:H1	53:S2:1017:U:H3	1.01	0.98
53:S2:366:U:H3	53:S2:394:G:H1	1.04	0.97
53:S2:1748:G:H1	53:S2:1786:U:H3	1.05	0.96
55:SB:67:PHE:O	55:SB:86:LEU:HB2	1.64	0.96
4:L5:3944:G:H1	4:L5:4069:U:H3	1.01	0.96
53:S2:1743:G:H21	53:S2:1791:A:N6	1.63	0.95
58:SE:87:MET:HA	58:SE:101:LEU:O	1.66	0.95
53:S2:820:U:H3	53:S2:828:G:H1	1.10	0.93
28:LW:4:GLU:O	28:LW:12:LYS:HA	1.69	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:SH:53:VAL:O	61:SH:57:ARG:HB2	1.70	0.91
34:Lc:20:LEU:O	34:Lc:24:SER:HB2	1.71	0.91
53:S2:748:C:H42	53:S2:795:A:N6	1.71	0.88
4:L5:3955:G:N2	4:L5:3966:A:C5	2.43	0.87
4:L5:4887:C:H42	4:L5:4932:U:H3	1.22	0.86
56:SC:266:TYR:O	56:SC:270:THR:HB	1.76	0.85
1:CB:604:MET:HB3	1:CB:704:VAL:HA	1.60	0.83
65:SL:82:MET:HB3	65:SL:85:THR:HG23	1.62	0.82
53:S2:1656:G:H1	53:S2:1668:U:H3	1.28	0.81
1:CB:450:THR:HB	1:CB:461:ILE:O	1.80	0.80
4:L5:1095:A:H2	4:L5:1200:G:H1	1.24	0.79
53:S2:1743:G:H21	53:S2:1791:A:H62	0.82	0.79
82:Sc:10:LYS:HB3	82:Sc:58:LEU:O	1.83	0.78
53:S2:748:C:N4	53:S2:795:A:H61	1.81	0.77
4:L5:493:G:H1	4:L5:660:A:H2	1.32	0.77
56:SC:214:LEU:HB3	56:SC:219:ILE:HD11	1.65	0.77
50:N4:105:ARG:HG3	50:N4:125:ARG:HD3	1.67	0.76
58:SE:201:HIS:HB2	58:SE:205:PHE:O	1.86	0.76
66:SM:52:LEU:HD11	66:SM:65:VAL:HG11	1.68	0.75
4:L5:3955:G:C2	4:L5:3966:A:C5	2.75	0.74
20:LO:27:VAL:HG13	20:LO:98:ALA:HB1	1.70	0.73
61:SH:72:PHE:O	61:SH:76:GLN:HB2	1.87	0.73
4:L5:3937:C:H1'	19:LN:125:SER:HB2	1.70	0.73
79:SZ:99:LEU:HD21	79:SZ:102:LYS:HB2	1.69	0.73
19:LN:124:ASP:HB3	19:LN:127:TYR:H	1.53	0.73
56:SC:90:GLU:HB2	56:SC:93:ILE:HG23	1.70	0.72
55:SB:111:CYS:HA	55:SB:114:VAL:HG12	1.70	0.72
4:L5:2483:G:H1	4:L5:2495:U:H3	1.35	0.72
31:LZ:93:LYS:O	31:LZ:97:ASN:HB3	1.89	0.72
58:SE:9:LEU:HB2	58:SE:30:ARG:HD3	1.70	0.71
53:S2:886:A:N6	53:S2:901:G:C5	2.59	0.71
59:SF:85:LYS:HB3	59:SF:88:MET:HG2	1.72	0.71
1:CB:26:ALA:HB2	1:CB:128:VAL:HG13	1.72	0.71
59:SF:59:LYS:HB2	59:SF:62:ARG:HE	1.56	0.70
61:SH:63:PHE:HA	61:SH:95:ILE:O	1.92	0.70
53:S2:748:C:N4	53:S2:795:A:N6	2.37	0.70
49:Lz:142:GLU:HG3	49:Lz:144:MET:HE3	1.72	0.70
53:S2:158:A:C2	53:S2:463:C:O2	2.44	0.70
70:SQ:131:LYS:HB2	70:SQ:140:ARG:HH22	1.55	0.70
16:LJ:21:CYS:HB2	16:LJ:131:TYR:O	1.90	0.70
4:L5:4748:U:H3	4:L5:4952:G:H1	1.36	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:S2:1550:G:H3'	53:S2:1579:A:H61	1.57	0.69
86:Sg:258:ILE:HB	86:Sg:268:ASP:HB2	1.74	0.69
4:L5:2517:A:H5'	38:Lg:62:LYS:HD3	1.75	0.69
15:LI:36:LEU:HD21	15:LI:69:ARG:HH11	1.56	0.69
4:L5:2611:A:H5'	4:L5:2688:G:H4'	1.75	0.68
60:SG:152:ASP:O	60:SG:156:TYR:HB2	1.93	0.68
53:S2:153:G:H21	60:SG:13:GLN:HE22	1.39	0.68
19:LN:158:HIS:HB3	19:LN:161:MET:HB2	1.75	0.68
68:SO:125:LYS:HB3	80:Sa:58:VAL:HG22	1.76	0.68
4:L5:498:C:H42	4:L5:657:C:H42	1.40	0.68
47:Lp:36:LYS:HE3	47:Lp:48:LYS:HD2	1.76	0.68
53:S2:1324:G:H1	53:S2:1504:U:H3	1.41	0.68
72:SS:46:ARG:HH22	72:SS:52:LEU:HB2	1.59	0.68
4:L5:3961:G:N2	4:L5:3965:A:C5	2.63	0.67
86:Sg:246:TYR:HD1	86:Sg:247:TRP:H	1.39	0.67
1:CB:454:MET:HB2	1:CB:457:TYR:HB2	1.76	0.67
53:S2:1287:A:H62	53:S2:1312:G:H21	1.42	0.67
79:SZ:97:ILE:HG22	79:SZ:111:ARG:HA	1.75	0.67
1:CB:118:ALA:O	1:CB:122:THR:HB	1.94	0.67
86:Sg:206:LEU:HD11	86:Sg:218:LEU:HD12	1.77	0.67
64:SK:94:LEU:HD23	64:SK:95:ARG:HG2	1.77	0.67
9:LC:218:ILE:O	9:LC:222:ARG:HB3	1.95	0.67
71:SR:36:GLU:HB3	71:SR:47:ARG:HD3	1.77	0.67
53:S2:851:C:H5''	53:S2:852:G:H5'	1.76	0.67
86:Sg:256:ILE:HB	86:Sg:270:LEU:HB3	1.78	0.66
21:LP:73:ALA:O	21:LP:76:TRP:O	2.13	0.66
53:S2:1347:U:H5''	56:SC:121:ARG:HH12	1.59	0.66
53:S2:1864:U:H5'	80:Sa:79:ILE:HD11	1.77	0.66
38:Lg:83:CYS:SG	38:Lg:86:CYS:HB2	2.34	0.66
56:SC:167:ARG:HB3	56:SC:177:PRO:HB2	1.77	0.66
4:L5:1095:A:C2	4:L5:1200:G:N1	2.57	0.66
16:LJ:52:LYS:HD3	16:LJ:67:LYS:HD3	1.76	0.66
1:CB:354:ILE:HG23	1:CB:358:LEU:HD12	1.78	0.66
4:L5:3951:G:N1	4:L5:4060:U:N3	2.43	0.66
4:L5:3967:G:O6	4:L5:4055:U:O4	2.14	0.65
11:LE:50:LEU:HD23	11:LE:56:ARG:HA	1.76	0.65
53:S2:1398:G:H1	53:S2:1448:A:H2	1.43	0.65
4:L5:1269:G:N2	4:L5:1441:C:O2	2.28	0.65
1:CB:116:THR:HG21	1:CB:499:PHE:HB3	1.79	0.65
73:ST:5:THR:HG23	73:ST:7:LYS:H	1.61	0.65
62:SI:190:LEU:HD12	62:SI:195:LEU:HA	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:1460:C:H5''	22:LQ:144:LYS:HB2	1.78	0.65
4:L5:5024:C:H41	4:L5:5028:G:H21	1.44	0.65
53:S2:165:G:H2'	53:S2:166:A:H8	1.61	0.65
68:SO:58:GLY:HA2	68:SO:61:LYS:HD3	1.79	0.65
28:LW:45:ASN:HB3	28:LW:48:GLN:HG3	1.78	0.64
28:LW:82:ILE:HD13	60:SG:131:ARG:HB3	1.79	0.64
57:SD:49:ILE:HG22	57:SD:87:TYR:HB2	1.79	0.64
63:SJ:104:ASP:HA	63:SJ:107:GLU:HB3	1.79	0.64
72:SS:3:LEU:HD12	72:SS:4:VAL:HG12	1.78	0.64
4:L5:493:G:O6	4:L5:660:A:N1	2.30	0.64
25:LT:93:ILE:HA	25:LT:96:ILE:HG12	1.79	0.64
68:SO:106:LYS:HE2	68:SO:135:ILE:HG23	1.80	0.64
54:SA:59:LEU:HD12	75:SV:79:VAL:HG11	1.78	0.64
14:LH:17:ASP:O	14:LH:28:LYS:HB2	1.97	0.64
76:SW:27:ILE:HB	76:SW:61:ILE:HG23	1.80	0.64
8:LB:286:LYS:HG2	8:LB:332:MET:HB3	1.79	0.64
53:S2:158:A:H2	53:S2:463:C:O2	1.81	0.64
53:S2:1095:C:N3	53:S2:1149:A:N1	2.46	0.64
49:Lz:147:LYS:HE2	49:Lz:151:VAL:H	1.61	0.64
57:SD:131:ALA:HA	57:SD:191:PRO:HD3	1.78	0.64
61:SH:143:ARG:HB2	61:SH:155:LYS:O	1.98	0.64
55:SB:60:ASP:HA	55:SB:63:LYS:HG2	1.80	0.63
35:Ld:29:ILE:O	35:Ld:33:ILE:HB	1.98	0.63
58:SE:201:HIS:O	58:SE:204:SER:C	2.41	0.63
3:CD:285:ASP:HA	3:CD:288:LYS:HE2	1.78	0.63
4:L5:3955:G:C2	4:L5:3966:A:N7	2.66	0.63
70:SQ:111:ILE:HA	70:SQ:114:GLN:HE21	1.64	0.63
2:CC:15:G:N2	2:CC:57:C:O2	2.31	0.63
4:L5:1176:C:N3	4:L5:1184:A:N1	2.46	0.63
4:L5:4093:G:N1	4:L5:4114:C:C2	2.66	0.63
19:LN:123:GLU:HB3	19:LN:128:LYS:HG3	1.79	0.63
56:SC:203:GLY:O	56:SC:221:ASP:HA	1.99	0.63
62:SI:152:ARG:O	62:SI:156:ALA:HB2	1.98	0.63
8:LB:163:ILE:HG22	8:LB:180:LEU:HD22	1.79	0.63
58:SE:35:PRO:HD2	58:SE:83:PRO:HG2	1.81	0.62
66:SM:89:VAL:HG11	66:SM:109:VAL:HG21	1.81	0.62
68:SO:34:PHE:HB3	68:SO:41:PHE:HB2	1.80	0.62
86:Sg:30:MET:HA	86:Sg:43:TRP:O	1.99	0.62
28:LW:80:ARG:HD3	60:SG:131:ARG:HH21	1.63	0.62
53:S2:72:C:H42	60:SG:170:ARG:HB3	1.64	0.62
64:SK:63:ALA:HB3	64:SK:66:HIS:HB2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:4887:C:N4	4:L5:4932:U:H3	1.96	0.62
64:SK:64:TRP:HB3	83:Sd:23:VAL:HA	1.79	0.62
12:LF:105:VAL:HG13	12:LF:136:VAL:HG12	1.79	0.62
57:SD:205:PRO:HA	71:SR:42:PRO:HG2	1.80	0.62
15:LI:54:SER:HB2	15:LI:135:ILE:HD11	1.81	0.62
55:SB:108:ASP:O	55:SB:112:SER:HB3	1.99	0.62
4:L5:3955:G:N2	4:L5:3966:A:C6	2.66	0.62
59:SF:35:LEU:HG	59:SF:117:ILE:HG12	1.81	0.62
72:SS:141:ARG:O	72:SS:144:ARG:C	2.43	0.62
4:L5:184:U:O2	4:L5:254:G:C6	2.52	0.62
4:L5:753:C:H41	4:L5:910:G:H1	1.47	0.62
53:S2:1392:U:H5'	74:SU:83:ARG:HH22	1.64	0.62
4:L5:1095:A:N1	4:L5:1200:G:O6	2.33	0.61
4:L5:444:G:H22	4:L5:1303:A:H2	1.48	0.61
59:SF:127:ARG:HE	59:SF:128:ILE:H	1.48	0.61
1:CB:675:ILE:HD11	1:CB:721:ILE:HG13	1.82	0.61
8:LB:356:LYS:O	8:LB:359:ALA:C	2.43	0.61
10:LD:236:MET:HA	10:LD:239:MET:HG2	1.81	0.61
78:SY:82:ALA:O	78:SY:86:GLU:HB3	2.00	0.61
31:LZ:50:PRO:HD3	31:LZ:68:ILE:HG12	1.82	0.61
68:SO:103:ASN:HB3	68:SO:142:ARG:HG3	1.82	0.61
4:L5:4093:G:H22	4:L5:4114:C:N4	1.99	0.61
14:LH:12:ILE:HB	14:LH:53:LYS:O	2.00	0.61
6:L8:109:C:H2'	41:Lj:20:ARG:HH21	1.66	0.61
53:S2:1218:C:H1'	53:S2:1683:C:H42	1.65	0.61
4:L5:3948:C:N3	4:L5:4066:U:O4	2.34	0.61
11:LE:119:GLU:HG3	36:Le:7:LEU:HD22	1.82	0.61
58:SE:162:ILE:HG22	58:SE:169:ILE:HA	1.81	0.61
14:LH:12:ILE:HD13	14:LH:18:ILE:HG21	1.83	0.60
53:S2:110:U:O2	53:S2:351:G:N2	2.32	0.60
59:SF:140:ASP:HB2	82:Sc:46:VAL:HG12	1.81	0.60
53:S2:1752:C:H42	53:S2:1778:C:H42	1.47	0.60
60:SG:181:THR:HG22	60:SG:183:ARG:H	1.66	0.60
4:L5:1095:A:H2	4:L5:1200:G:N1	1.98	0.60
17:LL:209:LYS:HG3	17:LL:210:LYS:HG2	1.84	0.60
54:SA:81:ASN:HA	54:SA:84:GLN:HB2	1.82	0.60
55:SB:111:CYS:HB3	80:Sa:68:TYR:HE1	1.64	0.60
68:SO:62:VAL:HG21	68:SO:67:ASP:HB2	1.83	0.60
17:LL:50:PRO:HB3	17:LL:150:LEU:HB3	1.84	0.60
54:SA:199:PRO:HA	54:SA:202:TYR:HB2	1.83	0.60
12:LF:182:TYR:HB3	12:LF:200:ARG:HG3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:SH:36:LEU:HD21	61:SH:78:ARG:HE	1.66	0.60
69:SP:75:VAL:HG22	69:SP:93:MET:HG2	1.84	0.60
4:L5:1414:C:H2'	4:L5:1415:G:H8	1.66	0.60
41:Lj:19:CYS:SG	41:Lj:34:CYS:HB2	2.40	0.60
4:L5:1913:C:H5''	20:LO:25:LYS:HD3	1.82	0.60
35:Ld:26:THR:HG22	35:Ld:85:ARG:HH11	1.67	0.60
37:Lf:33:VAL:HG23	37:Lf:38:GLU:HB2	1.84	0.60
54:SA:88:LEU:HB2	71:SR:81:ARG:HH12	1.66	0.60
68:SO:62:VAL:HG22	68:SO:64:ALA:H	1.67	0.60
35:Ld:54:MET:O	35:Ld:57:MET:O	2.19	0.59
36:Le:89:LEU:HD13	36:Le:118:LEU:HD22	1.83	0.59
53:S2:1545:A:H4'	70:SQ:74:GLY:HA2	1.84	0.59
62:SI:172:LEU:HG	62:SI:190:LEU:HD21	1.83	0.59
68:SO:44:VAL:HG13	68:SO:53:ILE:HB	1.84	0.59
60:SG:6:SER:HB3	60:SG:13:GLN:HG3	1.83	0.59
4:L5:1940:G:H22	4:L5:4434:C:H5''	1.67	0.59
34:Lc:47:ILE:HD12	34:Lc:94:LEU:HD11	1.84	0.59
53:S2:574:A:H4'	78:SY:89:HIS:HB2	1.84	0.59
58:SE:9:LEU:HB3	58:SE:28:ALA:HB3	1.85	0.59
53:S2:1650:A:H5''	70:SQ:139:ALA:HB2	1.85	0.59
86:Sg:212:LYS:HA	86:Sg:235:ILE:HG13	1.85	0.59
13:LG:154:LEU:HB3	13:LG:204:PHE:HB2	1.84	0.59
34:Lc:38:ILE:HG21	34:Lc:63:TYR:HB3	1.85	0.59
49:Lz:206:ILE:HD11	49:Lz:214:GLN:HB2	1.85	0.59
66:SM:128:PHE:HA	66:SM:131:LYS:HG2	1.83	0.59
71:SR:5:ARG:HB2	71:SR:10:LYS:HE2	1.85	0.59
4:L5:4093:G:N1	4:L5:4114:C:N3	2.50	0.59
22:LQ:79:THR:HB	22:LQ:136:THR:HG22	1.85	0.59
53:S2:1598:G:H3'	79:SZ:80:ARG:HH11	1.67	0.59
57:SD:106:ARG:HG3	57:SD:175:VAL:HG22	1.85	0.59
57:SD:177:LEU:HD21	57:SD:182:LEU:HD22	1.84	0.59
8:LB:378:ARG:HE	28:LW:32:LEU:HD21	1.68	0.59
19:LN:113:LEU:HB2	19:LN:134:LEU:HD12	1.84	0.58
53:S2:1228:A:H2'	53:S2:1229:G:H8	1.67	0.58
59:SF:33:ILE:HA	59:SF:36:GLN:HG3	1.84	0.58
4:L5:2557:G:H1	4:L5:2570:U:H3	1.51	0.58
42:Lk:26:LYS:HB2	42:Lk:69:LEU:HD12	1.84	0.58
77:SX:49:GLY:O	77:SX:99:GLU:HA	2.03	0.58
15:LI:209:TRP:O	15:LI:212:LEU:C	2.46	0.58
53:S2:186:C:H42	53:S2:214:U:H3	1.51	0.58
57:SD:40:ARG:HB2	57:SD:47:GLU:HB3	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LJ:85:LYS:HD3	16:LJ:115:LEU:HG	1.86	0.58
51:NA:82:LYS:HZ1	52:NB:43:LYS:HE3	1.69	0.58
53:S2:928:G:H2'	53:S2:929:G:C8	2.39	0.58
59:SF:40:ALA:HB3	59:SF:68:ILE:HG12	1.84	0.58
61:SH:148:LEU:HA	76:SW:42:MET:HE3	1.86	0.58
68:SO:147:ARG:HB2	68:SO:150:ARG:HE	1.69	0.58
79:SZ:49:LEU:H	79:SZ:83:LEU:HD13	1.69	0.58
1:CB:19:ILE:HG13	1:CB:99:LEU:HB3	1.86	0.58
15:LI:152:LEU:HB3	15:LI:165:ILE:HD12	1.86	0.58
53:S2:649:U:H2'	53:S2:650:A:H8	1.68	0.58
60:SG:1:MET:HB3	60:SG:18:VAL:HG13	1.86	0.58
4:L5:502:C:H3'	4:L5:503:C:H3'	1.86	0.58
6:L8:67:U:H5''	41:Lj:86:PRO:HA	1.85	0.58
53:S2:421:G:H5'	65:SL:98:LYS:HG3	1.86	0.58
54:SA:118:GLU:HG2	56:SC:65:LYS:HD3	1.86	0.58
69:SP:25:LEU:HD13	69:SP:28:MET:HE1	1.84	0.58
1:CB:308:LYS:HB2	1:CB:311:GLU:HB2	1.86	0.57
11:LE:281:ILE:HD13	11:LE:286:LEU:HD11	1.86	0.57
59:SF:175:ASP:HA	59:SF:178:ILE:HG12	1.85	0.57
7:LA:114:CYS:HB2	7:LA:169:VAL:HG12	1.86	0.57
53:S2:177:G:H22	53:S2:313:A:H5'	1.69	0.57
58:SE:100:ARG:HH22	58:SE:236:ILE:HG21	1.67	0.57
59:SF:127:ARG:HG3	59:SF:129:GLY:H	1.69	0.57
61:SH:47:ALA:HB3	61:SH:63:PHE:HB2	1.84	0.57
86:Sg:296:GLN:HG2	86:Sg:311:GLN:HE22	1.69	0.57
4:L5:2337:C:H4'	48:Lr:19:LYS:HB2	1.85	0.57
4:L5:4601:U:H2'	4:L5:4602:A:H8	1.69	0.57
8:LB:356:LYS:O	8:LB:359:ALA:O	2.23	0.57
11:LE:177:GLY:HA3	11:LE:184:VAL:HB	1.85	0.57
50:N4:126:PHE:HB3	50:N4:168:MET:HE1	1.84	0.57
74:SU:23:THR:HG22	74:SU:88:LEU:HB3	1.87	0.57
86:Sg:176:VAL:HB	86:Sg:186:THR:HB	1.85	0.57
53:S2:878:G:O6	53:S2:908:A:N1	2.37	0.57
4:L5:2495:U:H2'	4:L5:2496:G:H8	1.69	0.57
17:LL:63:THR:HG21	32:La:66:ASN:HD22	1.68	0.57
4:L5:1762:C:C4	4:L5:1770:A:N1	2.72	0.57
28:LW:97:LYS:HG3	28:LW:98:PRO:HD3	1.87	0.57
60:SG:219:GLU:HG2	60:SG:223:LYS:HZ3	1.70	0.57
62:SI:64:ASN:O	62:SI:186:ASP:HA	2.04	0.57
4:L5:184:U:O2	4:L5:254:G:O6	2.22	0.57
4:L5:2469:C:H5	4:L5:2471:G:H1	1.51	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:2838:G:H5'	8:LB:247:GLY:HA2	1.87	0.57
4:L5:3955:G:N2	4:L5:3966:A:C4	2.73	0.57
13:LG:264:LYS:HZ2	55:SB:91:VAL:HG13	1.70	0.57
27:LV:65:VAL:HG22	27:LV:73:ARG:HA	1.87	0.57
50:N4:109:LEU:HB3	50:N4:122:SER:HB2	1.86	0.57
53:S2:329:G:H2'	53:S2:330:G:C8	2.40	0.57
71:SR:75:GLU:HG2	71:SR:78:ARG:HH21	1.68	0.57
4:L5:1914:C:H4'	20:LO:89:PRO:HD3	1.87	0.57
4:L5:4363:A:H5''	46:Lo:36:GLN:HG2	1.86	0.57
15:LI:91:LEU:HD12	15:LI:135:ILE:HG23	1.86	0.57
7:LA:147:ARG:HG3	7:LA:157:VAL:HG22	1.87	0.57
19:LN:17:ASP:HA	19:LN:20:ARG:HG3	1.87	0.56
4:L5:1762:C:N4	4:L5:1770:A:H2	1.97	0.56
9:LC:152:LEU:HD23	9:LC:251:ILE:HG12	1.85	0.56
53:S2:820:U:O2	53:S2:828:G:N2	2.32	0.56
4:L5:99:A:H5''	19:LN:184:ILE:HD13	1.86	0.56
4:L5:1709:C:H42	4:L5:1716:G:H22	1.54	0.56
24:LS:127:MET:HA	25:LT:153:PRO:HG2	1.88	0.56
28:LW:94:ARG:HE	60:SG:146:ASN:HB2	1.70	0.56
53:S2:1432:U:H5''	53:S2:1433:C:H5''	1.87	0.56
54:SA:183:LEU:O	54:SA:186:ARG:C	2.48	0.56
55:SB:224:GLU:HG2	55:SB:227:LYS:HG2	1.86	0.56
58:SE:45:ILE:HD11	58:SE:58:GLY:HA2	1.87	0.56
58:SE:201:HIS:O	58:SE:204:SER:O	2.24	0.56
14:LH:171:ASP:O	14:LH:174:LYS:O	2.23	0.56
49:Lz:193:LEU:HD12	49:Lz:194:LEU:HD23	1.87	0.56
55:SB:103:MET:HB3	55:SB:215:VAL:HB	1.86	0.56
68:SO:30:VAL:HG23	68:SO:47:LEU:HA	1.87	0.56
58:SE:127:ARG:HD2	58:SE:142:HIS:HA	1.86	0.56
53:S2:323:C:H2'	53:S2:327:G:H22	1.71	0.56
56:SC:137:VAL:HG23	56:SC:216:MET:HB2	1.86	0.56
19:LN:135:ILE:HG23	19:LN:142:ILE:HD13	1.88	0.56
57:SD:194:PRO:HG3	57:SD:198:ILE:HG12	1.86	0.56
65:SL:86:ILE:HG13	65:SL:113:LEU:HB2	1.87	0.56
70:SQ:19:ALA:HB2	70:SQ:75:GLY:HA3	1.87	0.56
29:LX:73:HIS:HB2	29:LX:115:LYS:HZ3	1.71	0.56
50:N4:135:LEU:HG	50:N4:163:ALA:HB2	1.88	0.56
53:S2:1228:A:H2'	53:S2:1229:G:C8	2.40	0.56
56:SC:102:LEU:HD12	56:SC:130:ILE:HG12	1.86	0.56
4:L5:1708:G:H2'	4:L5:1709:C:H3'	1.87	0.56
10:LD:60:ILE:HD11	10:LD:93:THR:HA	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:SA:34:MET:HE2	54:SA:150:THR:HA	1.88	0.56
82:Sc:30:VAL:HG21	82:Sc:46:VAL:HG13	1.87	0.56
2:CC:18:G:H2'	4:L5:3958:G:H5'	1.88	0.56
4:L5:1762:C:N3	4:L5:1770:A:N1	2.54	0.56
4:L5:4274:A:H2'	4:L5:4275:G:C8	2.40	0.56
53:S2:110:U:H3	53:S2:351:G:H1	1.54	0.56
63:SJ:177:ASN:HD22	63:SJ:180:LYS:HZ3	1.54	0.56
80:Sa:52:ASP:HA	80:Sa:55:GLU:HG3	1.88	0.56
53:S2:886:A:N6	53:S2:901:G:N3	2.54	0.55
82:Sc:43:ILE:HD13	82:Sc:65:ALA:HB3	1.87	0.55
56:SC:77:SER:HB2	56:SC:80:GLU:H	1.72	0.55
56:SC:264:SER:HB3	56:SC:267:GLN:HG2	1.88	0.55
76:SW:22:LYS:HA	81:Sb:3:LEU:HB3	1.87	0.55
76:SW:33:VAL:HA	76:SW:36:ARG:HD2	1.88	0.55
1:CB:22:MET:HA	1:CB:124:GLY:O	2.07	0.55
9:LC:5:ARG:HH12	9:LC:266:THR:HG23	1.71	0.55
54:SA:14:ASP:HA	54:SA:17:LYS:HD2	1.87	0.55
69:SP:76:VAL:O	69:SP:94:VAL:HA	2.07	0.55
86:Sg:59:LEU:HD21	86:Sg:95:GLY:HA3	1.88	0.55
1:CB:260:LEU:HD11	1:CB:293:ILE:HD11	1.88	0.55
53:S2:1017:U:H5'	67:SN:55:ARG:HE	1.71	0.55
57:SD:55:THR:HA	57:SD:58:VAL:HG12	1.88	0.55
64:SK:14:LEU:HA	64:SK:17:LYS:HG2	1.86	0.55
86:Sg:11:LEU:HD22	86:Sg:307:VAL:HB	1.89	0.55
4:L5:2745:A:H2'	4:L5:2746:A:C8	2.42	0.55
16:LJ:20:LEU:HD11	16:LJ:83:LEU:HB2	1.87	0.55
54:SA:120:ARG:HD2	56:SC:266:TYR:HB3	1.88	0.55
72:SS:124:ARG:O	72:SS:127:TRP:C	2.50	0.55
4:L5:989:U:O2	4:L5:1064:G:O6	2.23	0.55
8:LB:300:LYS:O	8:LB:304:SER:HB3	2.06	0.55
19:LN:138:PHE:HA	19:LN:143:ARG:HD2	1.87	0.55
46:Lo:33:LEU:HA	46:Lo:38:LYS:HG2	1.88	0.55
58:SE:87:MET:CA	58:SE:101:LEU:O	2.50	0.55
72:SS:80:PRO:HG2	72:SS:83:PHE:HB2	1.89	0.55
15:LI:156:LYS:HG3	15:LI:163:GLN:HB2	1.88	0.55
86:Sg:41:ILE:HG13	86:Sg:43:TRP:HE1	1.71	0.55
4:L5:4612:C:C2	14:LH:120:GLU:HB2	2.42	0.55
56:SC:104:ASP:HB3	56:SC:130:ILE:HG13	1.89	0.55
29:LX:82:THR:HG21	39:Lh:37:THR:HG22	1.88	0.55
51:NA:94:VAL:HG21	51:NA:122:VAL:HG11	1.89	0.55
53:S2:1512:C:H5''	83:Sd:8:TRP:HZ3	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:SK:35:LEU:HD12	64:SK:40:VAL:HG11	1.88	0.55
71:SR:95:ILE:HD11	71:SR:118:GLN:HB3	1.89	0.55
13:LG:96:LEU:HD11	13:LG:189:ARG:HD2	1.88	0.55
16:LJ:63:ARG:HG2	16:LJ:66:GLU:HB2	1.89	0.55
39:Lh:88:THR:HG22	39:Lh:91:MET:H	1.71	0.55
53:S2:394:G:H5'	65:SL:81:LYS:HG2	1.89	0.55
57:SD:101:GLN:HG3	57:SD:126:ILE:HD11	1.87	0.55
58:SE:94:LYS:HD3	78:SY:17:LEU:HA	1.89	0.55
30:LY:47:MET:HE1	30:LY:118:ILE:HG23	1.88	0.54
19:LN:159:ARG:HB3	19:LN:164:LEU:HB2	1.89	0.54
72:SS:124:ARG:HG2	72:SS:129:LEU:HD12	1.89	0.54
79:SZ:69:THR:HB	79:SZ:72:VAL:HG12	1.89	0.54
47:Lp:25:MET:HE3	53:S2:1040:G:H5''	1.88	0.54
53:S2:1563:G:H5''	73:ST:121:ARG:HH21	1.72	0.54
1:CB:26:ALA:HB3	1:CB:32:LYS:HD3	1.89	0.54
1:CB:539:GLU:HB2	1:CB:545:ILE:HG12	1.90	0.54
14:LH:9:THR:HG22	14:LH:56:ARG:HG3	1.88	0.54
53:S2:886:A:C6	53:S2:901:G:N3	2.75	0.54
66:SM:126:GLU:HA	66:SM:129:LYS:HG2	1.88	0.54
71:SR:15:VAL:HG22	71:SR:19:LYS:HE2	1.90	0.54
10:LD:197:LYS:HB3	10:LD:202:GLN:HB2	1.89	0.54
53:S2:447:A:H8	62:SI:26:LYS:HZ1	1.55	0.54
53:S2:1705:C:H2'	53:S2:1706:G:C8	2.42	0.54
68:SO:14:VAL:H	68:SO:15:ILE:HA	1.72	0.54
68:SO:92:ALA:HA	68:SO:125:LYS:O	2.07	0.54
77:SX:28:LYS:O	77:SX:32:LEU:HB2	2.07	0.54
15:LI:209:TRP:O	15:LI:212:LEU:O	2.26	0.54
53:S2:377:G:H5'	62:SI:98:LYS:HB3	1.88	0.54
1:CB:409:ARG:HH22	1:CB:474:GLY:HA2	1.71	0.54
4:L5:513:U:H1'	4:L5:516:C:H41	1.73	0.54
10:LD:33:ARG:O	10:LD:37:VAL:HB	2.07	0.54
49:Lz:50:SER:HA	49:Lz:159:MET:HB2	1.89	0.54
4:L5:499:G:H5'	4:L5:500:G:H5''	1.89	0.54
50:N4:99:GLU:HA	50:N4:102:THR:HG22	1.89	0.54
53:S2:433:A:H5''	62:SI:22:HIS:HB3	1.90	0.54
86:Sg:207:CYS:HB3	86:Sg:221:LEU:HD21	1.90	0.54
86:Sg:220:ASP:HB3	86:Sg:224:GLY:HA2	1.90	0.54
8:LB:92:TYR:HB2	8:LB:159:VAL:HG13	1.90	0.54
26:LU:99:TRP:HE1	52:NB:15:GLN:HB2	1.73	0.54
41:Lj:68:LYS:HG3	41:Lj:69:ILE:HD13	1.89	0.54
49:Lz:118:LYS:H	49:Lz:118:LYS:HE2	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:S2:1677:U:H2'	53:S2:1678:A:H8	1.73	0.54
59:SF:92:ILE:HG13	59:SF:169:ILE:HD11	1.90	0.54
4:L5:3717:A:H2'	4:L5:3718:A:C8	2.43	0.54
53:S2:639:C:H2'	53:S2:640:A:H8	1.73	0.54
53:S2:1398:G:O6	53:S2:1448:A:N1	2.40	0.54
77:SX:72:VAL:HG13	77:SX:81:ILE:HG13	1.88	0.53
49:Lz:13:ALA:HA	49:Lz:217:TYR:HB3	1.89	0.53
69:SP:79:HIS:HA	69:SP:97:TYR:HB2	1.90	0.53
72:SS:138:THR:HA	72:SS:141:ARG:HH21	1.73	0.53
12:LF:41:MET:HA	12:LF:44:LYS:HG3	1.90	0.53
12:LF:243:LEU:O	12:LF:247:MET:HB2	2.08	0.53
36:Le:6:PRO:HG3	36:Le:73:GLY:HA3	1.90	0.53
58:SE:106:LYS:HA	58:SE:245:ARG:HH21	1.74	0.53
63:SJ:80:ARG:HA	63:SJ:83:ARG:HG2	1.90	0.53
4:L5:138:G:H2'	4:L5:139:G:C8	2.44	0.53
4:L5:2777:G:H5''	4:L5:2778:G:H5'	1.90	0.53
38:Lg:61:PRO:HA	38:Lg:64:LEU:HD22	1.89	0.53
8:LB:29:VAL:HA	8:LB:220:ILE:HD13	1.90	0.53
15:LI:47:PRO:HG2	15:LI:142:LEU:HD23	1.90	0.53
53:S2:439:A:H4'	53:S2:1799:G:H4'	1.90	0.53
53:S2:810:A:H5''	53:S2:811:A:H5'	1.90	0.53
66:SM:69:CYS:O	66:SM:72:HIS:C	2.51	0.53
1:CB:27:HIS:CD2	1:CB:138:GLN:HB2	2.43	0.53
19:LN:185:GLY:HA3	19:LN:194:ARG:HH12	1.73	0.53
50:N4:150:GLY:HA2	50:N4:153:LYS:HD3	1.89	0.53
53:S2:1764:G:H5'	53:S2:1765:C:H5''	1.90	0.53
64:SK:42:ASN:O	64:SK:46:MET:HG3	2.09	0.53
66:SM:24:THR:HA	66:SM:27:ILE:HG12	1.90	0.53
1:CB:448:GLN:HB3	1:CB:473:VAL:HG23	1.90	0.53
49:Lz:55:LEU:H	49:Lz:154:THR:HG21	1.74	0.53
67:SN:63:VAL:HA	67:SN:66:VAL:HG12	1.89	0.53
4:L5:2705:G:H1	4:L5:2710:C:H5	1.56	0.53
53:S2:943:U:H2'	53:S2:944:A:H8	1.72	0.53
72:SS:124:ARG:O	72:SS:127:TRP:O	2.27	0.53
79:SZ:84:ALA:O	79:SZ:88:LEU:HB2	2.09	0.53
27:LV:57:VAL:HG13	27:LV:84:GLN:HG2	1.90	0.53
49:Lz:68:LEU:HD12	49:Lz:90:LEU:HD22	1.91	0.53
49:Lz:143:ASN:HD21	49:Lz:150:GLU:HB2	1.74	0.53
56:SC:139:LEU:HG	56:SC:241:PHE:HD1	1.74	0.53
70:SQ:96:TYR:HA	70:SQ:100:VAL:HG22	1.91	0.53
4:L5:1176:C:H42	4:L5:1184:A:H61	0.70	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:LD:166:ALA:HB1	10:LD:171:LEU:HD12	1.90	0.53
38:Lg:42:PRO:HB2	38:Lg:53:LEU:HD12	1.91	0.53
51:NA:98:LYS:HB3	51:NA:102:ILE:HB	1.91	0.53
53:S2:588:G:H4'	53:S2:589:G:H5'	1.91	0.53
70:SQ:112:LEU:HB3	70:SQ:120:LEU:HD21	1.91	0.53
86:Sg:155:ARG:HG2	86:Sg:198:VAL:HG23	1.91	0.53
7:LA:116:LEU:HB3	7:LA:126:LEU:HB2	1.89	0.52
53:S2:981:A:H2'	53:S2:982:G:C8	2.44	0.52
54:SA:24:HIS:HA	54:SA:49:ILE:HB	1.91	0.52
1:CB:219:HIS:CG	1:CB:337:LYS:HE2	2.44	0.52
9:LC:66:SER:HA	9:LC:77:PRO:HA	1.91	0.52
58:SE:159:THR:HB	58:SE:173:ILE:HB	1.90	0.52
73:ST:76:THR:HB	73:ST:94:ARG:HB3	1.90	0.52
75:SV:32:ILE:HG12	75:SV:60:ARG:HD2	1.91	0.52
49:Lz:54:ARG:HH22	49:Lz:156:LYS:HE3	1.74	0.52
59:SF:71:ARG:HH12	59:SF:147:VAL:HG23	1.74	0.52
65:SL:85:THR:HA	65:SL:113:LEU:H	1.74	0.52
4:L5:229:G:H5''	30:LY:11:ARG:HG3	1.92	0.52
4:L5:1332:C:H2'	4:L5:1333:A:H8	1.73	0.52
19:LN:60:VAL:HG22	19:LN:134:LEU:HB2	1.92	0.52
53:S2:747:U:N3	53:S2:796:G:N1	2.57	0.52
60:SG:67:VAL:HB	60:SG:99:GLY:HA2	1.92	0.52
4:L5:3944:G:O6	4:L5:4069:U:O4	2.28	0.52
4:L5:3967:G:N1	4:L5:4055:U:N3	2.58	0.52
7:LA:178:PRO:HG2	47:Lp:26:VAL:HG23	1.91	0.52
9:LC:218:ILE:O	9:LC:221:PHE:C	2.52	0.52
36:Le:82:VAL:HG13	36:Le:114:ARG:HG2	1.92	0.52
53:S2:527:C:H2'	53:S2:528:A:C8	2.45	0.52
53:S2:1337:C:H2'	53:S2:1338:G:H8	1.74	0.52
57:SD:109:LEU:HD23	57:SD:182:LEU:HD21	1.90	0.52
61:SH:30:LEU:HD13	61:SH:86:LYS:HZ1	1.72	0.52
63:SJ:46:VAL:HG11	63:SJ:106:LEU:HD21	1.91	0.52
67:SN:70:LYS:HB2	67:SN:73:ARG:HD3	1.92	0.52
14:LH:59:LYS:HE3	14:LH:66:GLU:HB2	1.92	0.52
14:LH:113:GLU:HG2	14:LH:125:ARG:HG2	1.90	0.52
50:N4:142:LEU:HD21	50:N4:151:LEU:HB3	1.92	0.52
56:SC:73:MET:HE1	56:SC:76:LYS:HD3	1.92	0.52
56:SC:184:VAL:HG12	56:SC:195:LEU:HB2	1.90	0.52
4:L5:4052:C:H1'	49:Lz:209:THR:HA	1.92	0.52
29:LX:96:LEU:HG	29:LX:140:LEU:HD11	1.92	0.52
53:S2:186:C:N4	53:S2:214:U:H3	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:S2:1673:U:H5''	70:SQ:78:VAL:HG12	1.90	0.52
72:SS:141:ARG:O	72:SS:144:ARG:O	2.28	0.52
20:LO:14:HIS:HE1	20:LO:119:VAL:HG22	1.75	0.52
53:S2:834:C:H42	53:S2:839:C:H42	1.57	0.52
59:SF:98:GLU:HA	59:SF:101:HIS:CD2	2.45	0.52
4:L5:4093:G:H22	4:L5:4114:C:H42	1.58	0.52
4:L5:4627:U:H4'	8:LB:373:LYS:HE2	1.92	0.52
10:LD:54:ARG:HB2	10:LD:61:ILE:HG23	1.92	0.52
20:LO:109:PRO:HB2	20:LO:111:PRO:HD2	1.92	0.52
53:S2:878:G:H1	53:S2:908:A:H2	1.56	0.52
53:S2:1522:A:H62	69:SP:131:PRO:HD3	1.75	0.52
62:SI:83:TYR:HB2	62:SI:202:ILE:HD11	1.91	0.52
74:SU:85:HIS:HB3	74:SU:87:ARG:HH12	1.75	0.52
29:LX:102:VAL:HA	29:LX:134:LYS:HG3	1.91	0.51
51:NA:88:VAL:HB	51:NA:111:VAL:HG23	1.92	0.51
53:S2:1644:C:H4'	70:SQ:140:ARG:HB2	1.92	0.51
54:SA:15:VAL:HA	54:SA:18:PHE:HB2	1.93	0.51
1:CB:394:LEU:HA	1:CB:419:GLY:HA3	1.92	0.51
53:S2:303:C:H4'	62:SI:75:LYS:HD3	1.91	0.51
1:CB:627:GLU:HB3	1:CB:630:GLN:HE21	1.75	0.51
29:LX:128:ILE:HG12	29:LX:134:LYS:HG2	1.92	0.51
41:Lj:54:LYS:O	41:Lj:58:THR:HB	2.10	0.51
4:L5:3585:G:H2'	4:L5:3586:G:H8	1.75	0.51
15:LI:48:LEU:HB2	15:LI:142:LEU:HD22	1.91	0.51
17:LL:58:ILE:HD13	17:LL:157:VAL:HG22	1.93	0.51
26:LU:48:LYS:HB2	26:LU:53:ALA:HB2	1.92	0.51
53:S2:990:A:H61	53:S2:1001:A:H61	1.58	0.51
54:SA:177:MET:HG2	54:SA:180:ARG:HH21	1.76	0.51
4:L5:4992:G:H2'	4:L5:4993:G:C8	2.46	0.51
34:Lc:38:ILE:HD11	34:Lc:46:VAL:HG11	1.92	0.51
46:Lo:26:TYR:HB3	46:Lo:67:VAL:HB	1.93	0.51
53:S2:944:A:H5''	68:SO:134:PRO:HB3	1.93	0.51
53:S2:1277:C:H2'	53:S2:1278:A:H8	1.75	0.51
62:SI:90:LEU:HA	62:SI:93:THR:HG22	1.92	0.51
1:CB:62:ASP:HA	1:CB:65:GLU:HB3	1.92	0.51
4:L5:1514:U:H2'	4:L5:1515:A:C8	2.46	0.51
4:L5:4139:G:H21	4:L5:4140:C:H41	1.58	0.51
4:L5:4699:U:H1'	4:L5:4700:A:H5''	1.92	0.51
53:S2:1657:G:H1	53:S2:1667:U:H3	1.58	0.51
57:SD:168:VAL:HG12	57:SD:189:MET:HG2	1.92	0.51
58:SE:61:VAL:HG12	58:SE:80:ILE:HD11	1.90	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:4294:C:H4'	46:Lo:13:LYS:HD3	1.92	0.51
13:LG:153:GLN:HE21	13:LG:206:GLN:HA	1.75	0.51
56:SC:246:LYS:HA	56:SC:249:SER:HB3	1.92	0.51
53:S2:145:G:H2'	53:S2:146:G:C8	2.45	0.51
65:SL:93:LEU:HD12	65:SL:102:PHE:HB3	1.93	0.51
86:Sg:175:LYS:HE3	86:Sg:177:TRP:HE1	1.75	0.51
4:L5:2744:A:H2'	4:L5:2745:A:C8	2.46	0.51
4:L5:3697:U:H5''	4:L5:3698:G:H5'	1.92	0.51
7:LA:45:VAL:HB	7:LA:61:VAL:HG22	1.92	0.51
27:LV:68:GLY:H	27:LV:73:ARG:HH21	1.59	0.51
34:Lc:47:ILE:HB	34:Lc:94:LEU:HG	1.92	0.51
61:SH:145:ARG:HH12	81:Sb:8:LEU:HD11	1.76	0.51
67:SN:47:PRO:HA	67:SN:50:ILE:HB	1.92	0.51
75:SV:51:LYS:HE2	75:SV:76:ASP:HB3	1.93	0.51
4:L5:4743:G:H2'	4:L5:4744:A:C8	2.46	0.51
14:LH:104:VAL:HG22	14:LH:113:GLU:HB2	1.93	0.51
14:LH:146:LEU:HD11	14:LH:158:ALA:HB2	1.93	0.51
19:LN:84:PRO:HA	19:LN:87:HIS:CG	2.46	0.51
58:SE:18:TRP:HH2	58:SE:31:PRO:HD3	1.76	0.51
75:SV:1:MET:HG3	75:SV:10:ASP:HB2	1.92	0.50
50:N4:186:PHE:HD2	50:N4:190:LEU:HD12	1.76	0.50
53:S2:28:U:H2'	53:S2:29:G:H8	1.76	0.50
53:S2:609:U:H2'	53:S2:610:G:H8	1.74	0.50
54:SA:77:ILE:HG12	54:SA:99:ILE:HB	1.93	0.50
57:SD:53:THR:HA	57:SD:91:VAL:HG12	1.93	0.50
72:SS:4:VAL:HG22	72:SS:5:ILE:HG22	1.93	0.50
4:L5:1994:C:H2'	4:L5:1995:G:H8	1.77	0.50
4:L5:2520:C:H2'	4:L5:2521:G:C8	2.46	0.50
27:LV:69:LYS:HB2	27:LV:72:LEU:HD12	1.93	0.50
53:S2:1832:A:H5''	53:S2:1840:U:H5''	1.94	0.50
54:SA:84:GLN:HG2	54:SA:100:ALA:HB1	1.92	0.50
61:SH:31:GLU:HA	61:SH:37:LYS:HE3	1.93	0.50
64:SK:15:LEU:O	64:SK:19:GLY:HA2	2.11	0.50
1:CB:232:TYR:HE1	1:CB:292:LEU:HB3	1.76	0.50
4:L5:3932:U:H2'	4:L5:3933:G:H8	1.75	0.50
11:LE:153:LEU:HD11	11:LE:195:ILE:HG13	1.92	0.50
26:LU:65:ARG:HG2	26:LU:67:LYS:H	1.75	0.50
53:S2:677:G:H21	53:S2:1028:A:H62	1.58	0.50
53:S2:1260:A:H61	53:S2:1617:G:H1'	1.77	0.50
53:S2:1652:G:O6	53:S2:1672:U:O4	2.29	0.50
57:SD:75:LYS:HB3	64:SK:22:VAL:HG11	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:SE:100:ARG:HH22	58:SE:236:ILE:HD13	1.75	0.50
77:SX:51:VAL:HG22	77:SX:70:VAL:HG21	1.93	0.50
86:Sg:17:TRP:HB2	86:Sg:36:ARG:HB2	1.93	0.50
1:CB:112:SER:HB3	1:CB:114:GLU:HG2	1.94	0.50
14:LH:94:SER:HB3	14:LH:142:ASP:HB3	1.92	0.50
17:LL:63:THR:HG21	32:La:66:ASN:HB3	1.93	0.50
17:LL:123:LYS:HG2	39:Lh:122:LYS:HG3	1.93	0.50
53:S2:5:U:H2'	53:S2:6:G:H8	1.76	0.50
11:LE:191:GLN:HA	11:LE:194:VAL:HG22	1.93	0.50
28:LW:4:GLU:HB2	28:LW:13:ILE:HB	1.92	0.50
34:Lc:55:LEU:HD11	38:Lg:92:LYS:HG3	1.92	0.50
53:S2:454:U:H5''	60:SG:94:ARG:HB2	1.93	0.50
53:S2:1756:C:N3	53:S2:1776:G:N1	2.59	0.50
58:SE:79:ASP:HB3	58:SE:82:TYR:HB2	1.94	0.50
61:SH:36:LEU:HD11	61:SH:78:ARG:HH21	1.76	0.50
65:SL:68:ILE:HD13	65:SL:131:CYS:HB3	1.93	0.50
4:L5:1095:A:N1	4:L5:1200:G:C6	2.80	0.50
8:LB:85:VAL:HA	8:LB:203:GLN:O	2.12	0.50
13:LG:143:VAL:HG22	13:LG:203:ALA:HB2	1.94	0.50
49:Lz:55:LEU:HD11	49:Lz:183:ILE:HG12	1.92	0.50
50:N4:48:TYR:HB3	50:N4:55:VAL:HB	1.94	0.50
76:SW:111:MET:HE2	76:SW:119:LYS:HD2	1.92	0.50
1:CB:224:THR:HG23	1:CB:227:GLN:H	1.77	0.50
10:LD:208:MET:HB2	10:LD:233:PRO:HG3	1.94	0.50
33:Lb:40:LEU:O	33:Lb:44:ARG:HG3	2.12	0.50
61:SH:144:ILE:HG13	76:SW:52:ILE:HB	1.94	0.50
1:CB:766:LYS:HD2	1:CB:796:PHE:HD1	1.77	0.50
4:L5:4985:U:H4'	8:LB:175:GLN:HG3	1.94	0.50
60:SG:223:LYS:HA	60:SG:226:GLU:HG3	1.94	0.50
64:SK:90:VAL:HG11	64:SK:94:LEU:HD22	1.93	0.50
71:SR:78:ARG:HH12	71:SR:79:GLU:HG3	1.77	0.50
74:SU:20:ILE:HD11	74:SU:91:LEU:HD12	1.93	0.50
77:SX:28:LYS:HG2	77:SX:32:LEU:HD22	1.94	0.50
82:Sc:10:LYS:HE3	82:Sc:12:ALA:HB2	1.94	0.50
4:L5:2411:C:H2'	4:L5:2412:A:H8	1.77	0.49
49:Lz:16:GLU:HG2	49:Lz:18:LEU:HD13	1.92	0.49
51:NA:94:VAL:HB	51:NA:106:ILE:HB	1.94	0.49
60:SG:75:LEU:HD12	60:SG:77:LEU:HD23	1.94	0.49
60:SG:138:ALA:HA	60:SG:141:ILE:HG22	1.94	0.49
78:SY:27:VAL:HG22	78:SY:69:THR:HB	1.94	0.49
4:L5:1444:G:H22	4:L5:2103:G:H1	1.59	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:1762:C:C4	4:L5:1770:A:C2	3.00	0.49
4:L5:3972:A:H1'	4:L5:4050:A:H61	1.76	0.49
4:L5:4279:A:H5'	4:L5:4281:A:H1'	1.92	0.49
6:L8:154:G:H3'	13:LG:89:ARG:HH22	1.77	0.49
16:LJ:22:LEU:HD12	16:LJ:128:LEU:HD12	1.94	0.49
23:LR:182:GLU:HA	23:LR:185:ILE:HG12	1.94	0.49
35:Ld:53:ALA:HA	35:Ld:88:LEU:HD21	1.95	0.49
35:Ld:64:ILE:HG23	35:Ld:68:LEU:HD23	1.94	0.49
54:SA:108:PHE:HD2	54:SA:136:GLU:HB3	1.77	0.49
57:SD:119:CYS:HA	57:SD:122:VAL:HG22	1.93	0.49
69:SP:107:ILE:HA	69:SP:111:MET:SD	2.52	0.49
10:LD:104:LEU:HB2	10:LD:247:ILE:HD12	1.93	0.49
53:S2:146:G:H2'	53:S2:147:A:C8	2.47	0.49
62:SI:38:ILE:HD12	62:SI:94:LYS:HE2	1.94	0.49
68:SO:50:LYS:HE3	68:SO:51:GLU:HG2	1.94	0.49
1:CB:630:GLN:HA	1:CB:633:ARG:HE	1.77	0.49
1:CB:746:LEU:HA	1:CB:786:ALA:O	2.12	0.49
1:CB:820:LEU:HD23	1:CB:831:PRO:HG3	1.95	0.49
4:L5:3951:G:N2	4:L5:4060:U:O2	2.45	0.49
29:LX:124:VAL:HG22	29:LX:138:VAL:HG13	1.95	0.49
49:Lz:17:VAL:HB	49:Lz:180:VAL:HG12	1.93	0.49
50:N4:133:GLU:HB2	50:N4:168:MET:HG3	1.93	0.49
4:L5:1762:C:H5''	4:L5:1764:G:H1	1.77	0.49
4:L5:4260:U:H2'	4:L5:4261:C:C6	2.47	0.49
8:LB:165:HIS:HA	8:LB:179:HIS:O	2.13	0.49
9:LC:298:ILE:HD13	22:LQ:131:PRO:HB3	1.95	0.49
12:LF:107:LYS:HD2	12:LF:110:GLN:HE21	1.77	0.49
34:Lc:20:LEU:O	34:Lc:24:SER:CB	2.53	0.49
73:ST:113:VAL:HA	73:ST:123:LEU:HA	1.94	0.49
4:L5:4611:A:H2	14:LH:120:GLU:HB3	1.76	0.49
17:LL:63:THR:HG22	17:LL:65:ARG:H	1.78	0.49
19:LN:142:ILE:HG23	19:LN:148:THR:HB	1.94	0.49
28:LW:87:LEU:HD12	28:LW:90:ILE:HD11	1.95	0.49
54:SA:62:ALA:HA	54:SA:65:ILE:HG22	1.95	0.49
78:SY:57:VAL:HG12	78:SY:73:GLY:HA2	1.95	0.49
4:L5:994:G:H2'	4:L5:995:C:H4'	1.95	0.49
17:LL:164:GLU:HG2	32:La:100:ILE:HG13	1.95	0.49
22:LQ:84:GLY:H	22:LQ:103:LEU:HB2	1.76	0.49
58:SE:153:LEU:H	60:SG:216:ARG:HH12	1.59	0.49
59:SF:173:LEU:O	59:SF:177:LEU:HD12	2.11	0.49
63:SJ:30:LYS:O	63:SJ:34:GLU:HB2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:4281:A:H2'	4:L5:4282:A:H2'	1.94	0.49
12:LF:92:VAL:O	12:LF:120:GLY:HA2	2.13	0.49
17:LL:139:SER:O	17:LL:143:GLU:HB2	2.12	0.49
17:LL:211:LYS:HZ3	49:Lz:15:ARG:HH12	1.59	0.49
53:S2:508:A:H3'	53:S2:509:G:H8	1.78	0.49
57:SD:61:GLU:H	57:SD:64:ARG:HB2	1.77	0.49
72:SS:60:THR:O	72:SS:64:VAL:HG23	2.13	0.49
4:L5:4277:G:H5''	25:LT:17:ARG:HG2	1.94	0.49
10:LD:211:LEU:HB3	10:LD:219:TYR:HB2	1.94	0.49
11:LE:178:PRO:HB2	11:LE:181:LEU:HD12	1.93	0.49
53:S2:1618:C:H4'	69:SP:50:ARG:HH22	1.76	0.49
56:SC:137:VAL:HB	56:SC:217:ALA:HA	1.94	0.49
57:SD:218:LEU:HD21	86:Sg:190:GLY:HA2	1.95	0.49
86:Sg:297:THR:HA	86:Sg:310:TRP:O	2.13	0.49
1:CB:233:VAL:HG23	1:CB:256:MET:HE3	1.95	0.49
4:L5:1726:U:H5'	12:LF:135:ILE:HD11	1.94	0.49
4:L5:4238:G:H2'	4:L5:4239:A:C8	2.48	0.49
11:LE:209:PRO:HG2	11:LE:212:LEU:HG	1.95	0.49
20:LO:76:PRO:HB3	20:LO:138:LEU:HG	1.95	0.49
52:NB:18:VAL:HG13	52:NB:27:ARG:HB3	1.95	0.49
53:S2:848:U:H2'	53:S2:849:A:H8	1.78	0.49
53:S2:1112:U:O2	53:S2:1121:G:O6	2.29	0.49
63:SJ:28:GLU:HG2	63:SJ:43:VAL:HG11	1.94	0.49
65:SL:88:ILE:HD11	65:SL:109:MET:HE2	1.95	0.49
65:SL:126:VAL:HG12	65:SL:145:VAL:HG12	1.95	0.49
70:SQ:93:VAL:HA	70:SQ:105:LYS:HE2	1.95	0.49
81:Sb:18:LYS:HA	81:Sb:18:LYS:HE3	1.95	0.49
86:Sg:43:TRP:HA	86:Sg:56:GLN:H	1.77	0.49
1:CB:15:LYS:HZ3	1:CB:18:ASN:HB2	1.78	0.48
4:L5:1942:A:H2'	4:L5:1943:A:C8	2.48	0.48
4:L5:4291:G:H5'	4:L5:4293:U:C6	2.48	0.48
7:LA:137:ILE:HD11	7:LA:149:LYS:HB2	1.94	0.48
11:LE:149:ILE:HD12	11:LE:271:LEU:HD21	1.93	0.48
12:LF:85:ALA:HB2	25:LT:138:ALA:H	1.78	0.48
26:LU:100:LEU:HD13	26:LU:112:LEU:HD23	1.94	0.48
56:SC:196:ILE:HB	56:SC:223:TYR:HB2	1.94	0.48
59:SF:50:PRO:HG2	59:SF:90:VAL:HG23	1.93	0.48
83:Sd:13:LYS:HZ2	83:Sd:14:PHE:HB3	1.78	0.48
86:Sg:106:LYS:HD3	86:Sg:107:ASP:H	1.76	0.48
4:L5:318:A:H2'	4:L5:319:A:C8	2.48	0.48
11:LE:190:HIS:HB3	11:LE:193:PHE:HD2	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Lz:174:MET:HE1	49:Lz:178:GLU:HG2	1.95	0.48
70:SQ:11:GLN:HA	70:SQ:23:ALA:O	2.14	0.48
71:SR:15:VAL:O	71:SR:19:LYS:HG3	2.14	0.48
72:SS:36:VAL:HG23	72:SS:99:LEU:HD21	1.94	0.48
4:L5:1258:G:H2'	4:L5:1259:G:C8	2.48	0.48
4:L5:1709:C:O2	4:L5:1716:G:O6	2.31	0.48
4:L5:2692:U:H5'	42:Lk:4:LYS:HE3	1.95	0.48
6:L8:148:A:H2'	6:L8:149:G:C8	2.48	0.48
18:LM:123:ILE:HD13	20:LO:182:GLU:HG2	1.94	0.48
26:LU:115:PHE:HD2	52:NB:29:LYS:HA	1.78	0.48
53:S2:748:C:N3	53:S2:795:A:N1	2.61	0.48
53:S2:943:U:H2'	53:S2:944:A:C8	2.48	0.48
64:SK:73:ASN:HA	64:SK:76:ILE:HG12	1.95	0.48
4:L5:1339:U:H2'	4:L5:1340:C:C6	2.48	0.48
50:N4:30:ASP:HB3	50:N4:34:ARG:HH12	1.76	0.48
50:N4:111:ALA:HB3	50:N4:120:ALA:HB3	1.94	0.48
60:SG:142:ARG:HB2	60:SG:147:LEU:HB2	1.95	0.48
67:SN:5:HIS:HB3	67:SN:117:LEU:HD13	1.95	0.48
4:L5:460:C:H2'	4:L5:461:G:H8	1.78	0.48
12:LF:193:GLU:O	12:LF:196:THR:O	2.31	0.48
13:LG:234:ARG:HD2	13:LG:235:ARG:HH12	1.78	0.48
47:Lp:38:THR:HA	47:Lp:45:THR:HA	1.95	0.48
53:S2:808:A:H2	53:S2:855:G:H22	1.59	0.48
53:S2:1287:A:H62	53:S2:1312:G:N2	2.10	0.48
53:S2:1362:U:H5''	53:S2:1363:C:H5	1.79	0.48
61:SH:178:LYS:HD3	61:SH:184:ASP:HB3	1.95	0.48
86:Sg:17:TRP:CD1	86:Sg:36:ARG:HD2	2.48	0.48
4:L5:74:G:H1'	17:LL:62:PRO:HG3	1.95	0.48
4:L5:2020:U:H2'	4:L5:2021:G:H8	1.78	0.48
4:L5:2405:G:H5''	41:Lj:14:LYS:HE3	1.96	0.48
29:LX:67:ARG:HD2	29:LX:67:ARG:HA	1.63	0.48
49:Lz:23:ARG:HA	49:Lz:212:LYS:HD3	1.96	0.48
58:SE:139:LEU:HD22	58:SE:154:ILE:HG21	1.96	0.48
61:SH:69:LEU:HD13	61:SH:96:ALA:HB2	1.96	0.48
66:SM:48:HIS:H	66:SM:112:LYS:HA	1.79	0.48
70:SQ:105:LYS:HD2	70:SQ:108:ILE:HD11	1.95	0.48
73:ST:140:ALA:HA	73:ST:143:LYS:HE2	1.94	0.48
4:L5:300:A:H2'	4:L5:301:G:H8	1.78	0.48
6:L8:8:U:H2'	6:L8:9:A:C8	2.49	0.48
19:LN:140:LYS:HE3	19:LN:144:ARG:HH21	1.77	0.48
24:LS:15:ARG:HB3	24:LS:27:LEU:HD23	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:S2:1507:G:H22	85:Sf:87:THR:H	1.62	0.48
70:SQ:21:ALA:HB2	70:SQ:72:VAL:HG23	1.94	0.48
74:SU:51:LYS:HG2	74:SU:90:ASP:HB2	1.94	0.48
4:L5:2520:C:H2'	4:L5:2521:G:H8	1.77	0.48
4:L5:3917:A:H2'	4:L5:3918:G:H8	1.78	0.48
40:Li:63:VAL:HG12	40:Li:65:LYS:HG3	1.96	0.48
53:S2:366:U:O4	53:S2:394:G:O6	2.32	0.48
58:SE:31:PRO:HG2	58:SE:38:LEU:HB2	1.95	0.48
58:SE:197:ASN:HB2	58:SE:209:HIS:HB2	1.95	0.48
4:L5:261:G:H2'	4:L5:262:G:C8	2.49	0.48
4:L5:433:A:C2	4:L5:3867:A:H4'	2.49	0.48
4:L5:4389:C:H2'	4:L5:4390:A:C8	2.49	0.48
12:LF:37:PHE:O	12:LF:41:MET:HG2	2.14	0.48
13:LG:264:LYS:HD3	13:LG:264:LYS:HA	1.67	0.48
26:LU:28:PRO:HB2	26:LU:34:MET:HB2	1.95	0.48
47:Lp:51:ALA:HB3	47:Lp:54:ILE:HD12	1.95	0.48
51:NA:178:VAL:HA	51:NA:181:ILE:HD12	1.96	0.48
56:SC:166:ARG:HB2	56:SC:248:TYR:CG	2.49	0.48
4:L5:2373:C:H5'	35:Ld:46:LEU:HD22	1.96	0.48
4:L5:4093:G:C2	4:L5:4114:C:N3	2.81	0.48
4:L5:4093:G:N2	4:L5:4114:C:N3	2.62	0.48
10:LD:107:ARG:HH11	10:LD:248:ARG:HD2	1.79	0.48
15:LI:48:LEU:O	15:LI:139:ARG:HA	2.14	0.48
46:Lo:74:GLU:HG3	46:Lo:76:ASN:H	1.79	0.48
50:N4:12:LYS:O	50:N4:16:LEU:HD22	2.14	0.48
53:S2:186:C:H2'	53:S2:187:G:C8	2.49	0.48
53:S2:750:C:H41	53:S2:793:G:H21	1.62	0.48
53:S2:1096:G:H1	53:S2:1136:U:H3	1.60	0.48
53:S2:1263:U:H4'	83:Sd:27:ARG:HH12	1.79	0.48
57:SD:113:LEU:HD22	57:SD:114:ALA:H	1.77	0.48
59:SF:30:ILE:HG21	59:SF:36:GLN:HB3	1.95	0.48
62:SI:152:ARG:O	62:SI:156:ALA:CB	2.62	0.48
76:SW:93:LEU:HB2	76:SW:102:ILE:HD11	1.96	0.48
78:SY:18:LEU:HD22	78:SY:20:ARG:HH21	1.78	0.48
1:CB:395:MET:HE2	1:CB:494:MET:HE3	1.96	0.47
4:L5:1234:G:H2'	4:L5:1235:G:C8	2.49	0.47
53:S2:1866:A:H61	80:Sa:85:ARG:H	1.60	0.47
68:SO:58:GLY:O	68:SO:62:VAL:HG12	2.14	0.47
4:L5:1468:C:H2'	4:L5:1469:C:C6	2.49	0.47
4:L5:4309:G:H5'	4:L5:4338:G:H5''	1.95	0.47
21:LP:126:ARG:HB2	21:LP:140:MET:HE1	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:Ld:54:MET:O	35:Ld:57:MET:C	2.57	0.47
53:S2:874:G:H2'	53:S2:875:A:H8	1.79	0.47
53:S2:1310:U:P	66:SM:36:ARG:HH22	2.36	0.47
54:SA:84:GLN:HA	54:SA:87:VAL:HG12	1.97	0.47
54:SA:85:ARG:HH21	71:SR:81:ARG:HG2	1.79	0.47
54:SA:207:PRO:HA	54:SA:210:ILE:HG13	1.96	0.47
68:SO:42:VAL:HG11	68:SO:77:ALA:HB1	1.96	0.47
74:SU:24:LEU:HA	74:SU:111:GLU:O	2.13	0.47
1:CB:352:GLN:O	1:CB:356:ILE:HD12	2.14	0.47
4:L5:1332:C:H2'	4:L5:1333:A:C8	2.48	0.47
4:L5:3848:U:H2'	4:L5:3849:A:C8	2.48	0.47
6:L8:70:G:H5''	30:LY:27:ARG:CZ	2.45	0.47
6:L8:137:A:H2'	6:L8:138:C:C6	2.49	0.47
7:LA:108:PRO:HG2	47:Lp:86:LEU:HD13	1.97	0.47
14:LH:163:GLN:HA	14:LH:166:THR:HG23	1.95	0.47
18:LM:63:LYS:HD3	18:LM:63:LYS:HA	1.76	0.47
21:LP:73:ALA:O	21:LP:76:TRP:C	2.56	0.47
24:LS:43:ARG:HA	24:LS:43:ARG:HD2	1.77	0.47
53:S2:550:C:H2'	53:S2:551:U:C6	2.49	0.47
63:SJ:26:ASP:HB2	84:Se:42:PHE:HZ	1.79	0.47
63:SJ:37:LEU:HD11	63:SJ:106:LEU:HD13	1.95	0.47
65:SL:29:GLY:HA3	65:SL:30:LYS:HA	1.54	0.47
1:CB:36:THR:HG22	1:CB:102:LEU:HD11	1.96	0.47
4:L5:295:A:H5''	4:L5:296:A:H5'	1.95	0.47
4:L5:729:G:H5''	12:LF:76:ARG:HD2	1.96	0.47
22:LQ:99:LYS:HE3	22:LQ:121:LEU:HD11	1.95	0.47
45:Ln:12:ARG:HA	45:Ln:15:ARG:HE	1.78	0.47
58:SE:196:THR:HG21	58:SE:211:LYS:HE2	1.97	0.47
60:SG:219:GLU:HG2	60:SG:223:LYS:NZ	2.29	0.47
63:SJ:44:TRP:HA	63:SJ:47:LYS:HE3	1.96	0.47
70:SQ:9:SER:HA	70:SQ:25:CYS:O	2.14	0.47
78:SY:41:ARG:HG2	78:SY:55:ILE:HG23	1.95	0.47
78:SY:114:MET:HA	78:SY:117:VAL:HG12	1.95	0.47
4:L5:490:C:H2'	4:L5:491:G:C8	2.49	0.47
6:L8:19:C:H2'	6:L8:20:A:C8	2.50	0.47
20:LO:27:VAL:HG22	20:LO:101:ARG:HB3	1.94	0.47
61:SH:105:THR:HG23	61:SH:107:LYS:H	1.78	0.47
69:SP:40:ARG:H	69:SP:40:ARG:HD2	1.79	0.47
1:CB:66:ARG:HD2	1:CB:66:ARG:HA	1.65	0.47
4:L5:4238:G:H2'	4:L5:4239:A:H8	1.79	0.47
4:L5:4537:C:H2'	4:L5:4538:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:4976:U:H1'	8:LB:343:ARG:HH21	1.79	0.47
7:LA:181:LYS:HB2	7:LA:184:ARG:HG3	1.96	0.47
26:LU:42:PHE:HZ	26:LU:89:LYS:HG2	1.80	0.47
32:La:75:LEU:HA	32:La:78:LEU:HB3	1.97	0.47
50:N4:47:LYS:HD2	50:N4:47:LYS:HA	1.73	0.47
53:S2:1679:A:H2'	59:SF:60:ARG:HD2	1.96	0.47
58:SE:191:ARG:HH11	58:SE:245:ARG:HD2	1.80	0.47
66:SM:64:LEU:HD11	85:Sf:106:TYR:HB2	1.95	0.47
79:SZ:47:LEU:HD23	79:SZ:78:LYS:HB3	1.97	0.47
80:Sa:23:CYS:HB2	80:Sa:74:CYS:SG	2.55	0.47
86:Sg:152:SER:H	86:Sg:169:GLY:HA2	1.79	0.47
1:CB:173:GLU:HA	1:CB:176:GLN:HB2	1.96	0.47
4:L5:2107:C:H2'	4:L5:2108:G:H8	1.79	0.47
4:L5:4054:C:H1'	49:Lz:207:LYS:HB2	1.97	0.47
8:LB:302:ASN:HD22	8:LB:313:SER:HB2	1.79	0.47
21:LP:92:LEU:O	21:LP:96:LYS:HG2	2.15	0.47
53:S2:4:C:H4'	56:SC:207:ALA:HB2	1.96	0.47
53:S2:863:U:H2'	53:S2:864:A:H8	1.79	0.47
53:S2:1539:U:H2'	53:S2:1540:G:C8	2.50	0.47
55:SB:67:PHE:O	55:SB:85:LYS:C	2.57	0.47
58:SE:15:PRO:HG3	58:SE:39:ARG:HD2	1.97	0.47
58:SE:128:LYS:HB3	58:SE:140:VAL:HG23	1.97	0.47
64:SK:49:MET:HE2	64:SK:49:MET:HA	1.96	0.47
73:ST:44:GLU:HG2	73:ST:45:LEU:HG	1.96	0.47
74:SU:95:SER:HA	74:SU:98:VAL:HG22	1.95	0.47
76:SW:50:PHE:HB3	76:SW:63:VAL:HG23	1.96	0.47
79:SZ:47:LEU:HD11	79:SZ:79:ILE:HA	1.97	0.47
1:CB:654:PRO:HD2	1:CB:658:GLY:HA3	1.96	0.47
14:LH:171:ASP:O	14:LH:174:LYS:C	2.57	0.47
35:Ld:90:ARG:HD3	35:Ld:102:LEU:HD13	1.97	0.47
71:SR:72:LYS:O	71:SR:76:GLU:HB2	2.15	0.47
4:L5:318:A:H2'	4:L5:319:A:H8	1.80	0.47
4:L5:1259:G:H2'	4:L5:1260:G:H8	1.79	0.47
4:L5:1538:U:H2'	4:L5:1539:G:H8	1.79	0.47
4:L5:4219:A:H2'	4:L5:4220:A:C8	2.50	0.47
16:LJ:20:LEU:O	16:LJ:131:TYR:O	2.33	0.47
53:S2:448:A:H5''	62:SI:25:ARG:HA	1.96	0.47
53:S2:1230:C:H5''	72:SS:130:ARG:HH22	1.79	0.47
57:SD:150:MET:HE2	57:SD:150:MET:HB3	1.82	0.47
58:SE:26:VAL:HG22	63:SJ:4:ALA:HB2	1.97	0.47
59:SF:53:ALA:HB1	70:SQ:125:ARG:HH21	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:SL:59:LYS:HB3	65:SL:134:LEU:HD21	1.96	0.47
68:SO:27:VAL:O	68:SO:92:ALA:HB3	2.15	0.47
69:SP:85:ILE:H	69:SP:85:ILE:HD12	1.79	0.47
80:Sa:4:LYS:HB3	80:Sa:5:ARG:HG3	1.97	0.47
4:L5:1730:U:H4'	25:LT:100:LYS:HB2	1.96	0.47
4:L5:4405:G:H5'	15:LI:8:CYS:SG	2.55	0.47
47:Lp:10:ILE:HG22	47:Lp:27:LYS:HG3	1.96	0.47
52:NB:20:ILE:HD13	52:NB:28:ARG:HB3	1.97	0.47
53:S2:1144:A:H2'	53:S2:1145:A:C8	2.50	0.47
53:S2:1588:A:H2'	53:S2:1589:A:H8	1.80	0.47
55:SB:89:GLU:HB3	55:SB:223:PHE:HE1	1.79	0.47
57:SD:171:ALA:HB3	57:SD:186:VAL:HG13	1.96	0.47
59:SF:155:CYS:O	59:SF:159:ARG:HG3	2.15	0.47
4:L5:425:U:H4'	21:LP:6:LEU:HD21	1.97	0.46
4:L5:1730:U:H1'	25:LT:101:SER:HB3	1.97	0.46
7:LA:180:LEU:HD11	47:Lp:26:VAL:HG21	1.98	0.46
23:LR:15:LEU:HD13	23:LR:52:ARG:HB2	1.97	0.46
30:LY:22:PRO:HG2	30:LY:25:ILE:HG12	1.95	0.46
51:NA:206:ILE:O	51:NA:210:ILE:HG12	2.15	0.46
53:S2:1745:A:H62	53:S2:1789:G:N2	2.12	0.46
60:SG:52:ILE:HD11	60:SG:109:LEU:HD22	1.97	0.46
63:SJ:172:ARG:HA	63:SJ:175:ARG:HG2	1.97	0.46
64:SK:17:LYS:HB2	64:SK:17:LYS:HE3	1.73	0.46
78:SY:13:MET:HE3	78:SY:13:MET:HB2	1.84	0.46
83:Sd:13:LYS:HG3	83:Sd:14:PHE:CD2	2.50	0.46
4:L5:717:U:H2'	4:L5:718:C:C6	2.50	0.46
4:L5:2495:U:H2'	4:L5:2496:G:C8	2.49	0.46
4:L5:2745:A:H2'	4:L5:2746:A:H8	1.79	0.46
4:L5:3736:A:H2'	4:L5:3737:A:C8	2.50	0.46
4:L5:4771:C:H2'	4:L5:4772:C:C6	2.50	0.46
7:LA:142:GLU:HG3	7:LA:143:THR:HG23	1.96	0.46
56:SC:193:VAL:HG11	56:SC:240:THR:HG22	1.98	0.46
4:L5:1374:G:H1'	9:LC:234:LYS:HG2	1.97	0.46
4:L5:2554:U:O2	4:L5:2764:A:N7	2.49	0.46
4:L5:3868:G:H22	4:L5:3900:G:H1'	1.80	0.46
4:L5:3951:G:O6	4:L5:4060:U:O4	2.32	0.46
13:LG:99:ALA:HB1	13:LG:136:LEU:HD11	1.96	0.46
22:LQ:59:PRO:HG3	22:LQ:143:ARG:HA	1.97	0.46
49:Lz:109:ALA:HB1	49:Lz:139:THR:HB	1.96	0.46
53:S2:5:U:H2'	53:S2:6:G:C8	2.50	0.46
53:S2:980:A:H2'	53:S2:981:A:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:SH:12:ASN:HB2	61:SH:16:PRO:HD2	1.96	0.46
61:SH:61:ILE:HD11	61:SH:95:ILE:HD12	1.96	0.46
72:SS:66:ARG:HH11	72:SS:70:ILE:HG23	1.81	0.46
74:SU:24:LEU:HD13	74:SU:32:LEU:HD21	1.96	0.46
75:SV:70:LEU:HD21	75:SV:83:PHE:HZ	1.80	0.46
4:L5:1613:A:H5''	7:LA:183:GLY:HA2	1.96	0.46
4:L5:2411:C:H2'	4:L5:2412:A:C8	2.51	0.46
15:LI:93:PRO:HB2	15:LI:125:THR:HB	1.96	0.46
26:LU:111:GLU:HG2	26:LU:113:ARG:HG2	1.97	0.46
50:N4:85:TYR:HB3	50:N4:92:TRP:HB2	1.98	0.46
53:S2:144:U:H2'	53:S2:145:G:H8	1.81	0.46
53:S2:1536:G:H2'	53:S2:1537:A:C8	2.50	0.46
55:SB:109:LYS:O	55:SB:113:MET:HG3	2.16	0.46
55:SB:185:VAL:O	55:SB:189:ILE:HG12	2.16	0.46
78:SY:55:ILE:HA	78:SY:74:MET:O	2.16	0.46
1:CB:396:MET:HE1	1:CB:472:LEU:HD21	1.97	0.46
4:L5:1867:A:H2'	4:L5:1868:A:C8	2.51	0.46
4:L5:3880:G:H2'	4:L5:3881:G:C8	2.50	0.46
4:L5:3932:U:H2'	4:L5:3933:G:C8	2.50	0.46
4:L5:4389:C:H2'	4:L5:4390:A:H8	1.81	0.46
38:Lg:42:PRO:HD2	38:Lg:56:VAL:HG21	1.98	0.46
42:Lk:52:LYS:HG3	42:Lk:55:LYS:HE3	1.97	0.46
49:Lz:67:VAL:HA	49:Lz:68:LEU:HA	1.67	0.46
50:N4:187:ARG:HE	50:N4:188:GLU:HG3	1.80	0.46
54:SA:76:VAL:HG12	54:SA:123:VAL:HB	1.98	0.46
56:SC:212:LYS:O	56:SC:216:MET:HG2	2.15	0.46
57:SD:28:GLU:HG2	64:SK:61:GLN:HE22	1.80	0.46
75:SV:67:ASP:O	75:SV:71:ARG:HG2	2.16	0.46
4:L5:2864:A:H2'	4:L5:2865:U:C6	2.50	0.46
4:L5:3612:C:H1'	4:L5:5016:A:C8	2.51	0.46
53:S2:668:A:H5''	53:S2:1198:G:H4'	1.98	0.46
53:S2:1004:U:H2'	53:S2:1005:G:H8	1.80	0.46
53:S2:1273:C:O2	53:S2:1508:A:N6	2.49	0.46
61:SH:125:VAL:O	61:SH:129:ILE:HG23	2.15	0.46
68:SO:78:ALA:HB3	68:SO:118:ALA:HB3	1.97	0.46
74:SU:94:PRO:HB2	74:SU:97:ILE:HG12	1.97	0.46
1:CB:9:ILE:HA	1:CB:12:ILE:HD12	1.98	0.46
1:CB:84:ASN:O	1:CB:88:PHE:HB2	2.16	0.46
1:CB:311:GLU:HA	1:CB:314:LYS:HG2	1.98	0.46
4:L5:223:G:H4'	4:L5:225:G:N7	2.30	0.46
14:LH:66:GLU:HA	14:LH:69:THR:HG23	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:LI:78:LYS:HB2	15:LI:78:LYS:HE3	1.71	0.46
49:Lz:85:MET:HB2	49:Lz:89:ALA:HB3	1.98	0.46
53:S2:1651:A:H2'	53:S2:1652:G:H8	1.80	0.46
53:S2:1748:G:O6	53:S2:1786:U:O4	2.34	0.46
66:SM:58:GLU:HG2	66:SM:61:TYR:HB2	1.98	0.46
68:SO:147:ARG:HH21	68:SO:150:ARG:HD3	1.80	0.46
70:SQ:110:ASP:O	70:SQ:114:GLN:HG3	2.16	0.46
73:ST:13:GLU:HA	73:ST:16:ARG:HG2	1.98	0.46
78:SY:118:ARG:HD2	78:SY:118:ARG:HA	1.84	0.46
79:SZ:54:THR:HA	79:SZ:57:LYS:HG2	1.98	0.46
86:Sg:256:ILE:HD12	86:Sg:289:LEU:HD21	1.97	0.46
1:CB:330:LYS:HZ2	1:CB:334:PRO:HB2	1.81	0.46
4:L5:3607:U:H2'	4:L5:3608:A:C8	2.50	0.46
4:L5:3917:A:H2'	4:L5:3918:G:C8	2.51	0.46
23:LR:135:LYS:O	23:LR:139:MET:HG3	2.15	0.46
23:LR:165:LYS:HE3	23:LR:165:LYS:HB3	1.71	0.46
30:LY:117:LYS:HB3	30:LY:117:LYS:HE2	1.67	0.46
49:Lz:24:LYS:HD2	49:Lz:29:LEU:HD12	1.96	0.46
53:S2:1779:G:H2'	53:S2:1780:G:C8	2.51	0.46
54:SA:27:GLY:HA2	54:SA:28:THR:HA	1.61	0.46
59:SF:108:PRO:HA	59:SF:111:VAL:HG12	1.98	0.46
65:SL:104:LYS:HB2	65:SL:104:LYS:HE2	1.69	0.46
65:SL:125:ILE:HB	65:SL:146:THR:HG23	1.97	0.46
73:ST:129:ARG:HG2	73:ST:133:ARG:HH12	1.81	0.46
86:Sg:32:LEU:HB3	86:Sg:42:MET:HB3	1.97	0.46
1:CB:581:GLU:HG2	1:CB:692:LEU:HB2	1.98	0.46
3:CD:284:LEU:HD11	64:SK:16:PHE:HB3	1.97	0.46
23:LR:21:LYS:HE3	23:LR:55:VAL:HA	1.98	0.46
25:LT:28:ALA:HA	25:LT:31:MET:HG2	1.96	0.46
42:Lk:8:ILE:HG23	42:Lk:56:LEU:HD12	1.97	0.46
53:S2:1037:G:H4'	53:S2:1845:A:H4'	1.98	0.46
53:S2:1567:G:H4'	73:ST:37:VAL:HG23	1.97	0.46
55:SB:114:VAL:HA	55:SB:142:PHE:HE2	1.81	0.46
56:SC:184:VAL:HG13	56:SC:243:ALA:HB1	1.96	0.46
69:SP:76:VAL:HG13	69:SP:94:VAL:HG12	1.97	0.46
69:SP:83:MET:HE2	69:SP:89:MET:HE1	1.98	0.46
74:SU:94:PRO:HD2	74:SU:97:ILE:HD11	1.97	0.46
4:L5:4591:U:H2'	4:L5:4592:C:C6	2.51	0.46
4:L5:5057:C:H2'	4:L5:5058:A:C8	2.51	0.46
7:LA:245:ARG:HA	7:LA:245:ARG:HD2	1.72	0.46
11:LE:88:VAL:HA	11:LE:89:LEU:HA	1.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Lz:47:LYS:HE3	49:Lz:47:LYS:HB2	1.83	0.46
82:Sc:51:ARG:HA	82:Sc:51:ARG:NH1	2.31	0.46
1:CB:55:ARG:HB3	1:CB:56:PHE:H	1.65	0.45
4:L5:1179:U:H3'	4:L5:1180:C:H5''	1.98	0.45
4:L5:1857:C:H2'	4:L5:1858:A:H8	1.81	0.45
4:L5:4954:G:H2'	4:L5:4955:A:C8	2.52	0.45
6:L8:141:C:H5''	19:LN:60:VAL:HG11	1.97	0.45
11:LE:183:ARG:HA	11:LE:183:ARG:HD2	1.65	0.45
42:Lk:24:LYS:HA	42:Lk:67:LYS:O	2.16	0.45
42:Lk:52:LYS:HB2	42:Lk:52:LYS:HE3	1.72	0.45
43:Ll:41:ARG:HA	43:Ll:41:ARG:HD2	1.69	0.45
53:S2:1394:G:H4'	70:SQ:126:ARG:HH12	1.81	0.45
53:S2:1545:A:H2	53:S2:1671:G:H1'	1.81	0.45
69:SP:34:MET:HB3	69:SP:42:ARG:HG3	1.98	0.45
69:SP:130:ARG:HD3	69:SP:131:PRO:HD2	1.97	0.45
74:SU:42:GLY:HA2	74:SU:45:GLU:HG3	1.97	0.45
1:CB:45:ILE:HD12	1:CB:46:ILE:HD12	1.98	0.45
1:CB:66:ARG:HB3	1:CB:68:ILE:HG12	1.98	0.45
1:CB:609:PHE:HZ	1:CB:661:ILE:HB	1.81	0.45
4:L5:1631:A:C8	7:LA:199:VAL:HG21	2.52	0.45
4:L5:3707:U:H2'	4:L5:3708:C:C6	2.51	0.45
8:LB:293:ILE:HG12	8:LB:297:LYS:HB3	1.98	0.45
11:LE:151:ILE:HA	11:LE:160:LYS:O	2.17	0.45
49:Lz:212:LYS:HB2	49:Lz:214:GLN:HE21	1.81	0.45
54:SA:77:ILE:HD12	54:SA:122:LEU:HD21	1.99	0.45
72:SS:132:ARG:HB2	72:SS:134:GLN:HE22	1.81	0.45
83:Sd:38:MET:HE1	83:Sd:43:PHE:HA	1.99	0.45
1:CB:609:PHE:HE1	1:CB:641:TRP:HZ2	1.64	0.45
4:L5:1461:C:H2'	4:L5:1462:A:C8	2.52	0.45
8:LB:220:ILE:HG12	8:LB:278:THR:HG23	1.99	0.45
19:LN:200:LEU:HD22	19:LN:204:ARG:HD3	1.98	0.45
53:S2:551:U:H2'	53:S2:552:G:C4	2.51	0.45
53:S2:1203:G:H2'	53:S2:1204:A:C8	2.52	0.45
54:SA:126:ASP:HB3	54:SA:129:ALA:HB3	1.99	0.45
78:SY:88:LYS:HA	78:SY:91:LEU:HG	1.98	0.45
78:SY:109:GLU:O	78:SY:113:ARG:HG2	2.16	0.45
1:CB:83:GLU:HA	1:CB:86:LEU:HG	1.99	0.45
4:L5:494:U:H2'	4:L5:495:C:C6	2.52	0.45
4:L5:3848:U:H2'	4:L5:3849:A:H8	1.82	0.45
16:LJ:95:ARG:HD3	16:LJ:95:ARG:H	1.82	0.45
20:LO:78:ARG:HA	20:LO:78:ARG:HD2	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LW:117:LYS:HD3	28:LW:117:LYS:HA	1.82	0.45
41:Lj:51:ALA:HA	41:Lj:54:LYS:HE3	1.98	0.45
46:Lo:23:VAL:HG22	46:Lo:70:LEU:HD22	1.97	0.45
74:SU:49:LYS:HB2	74:SU:92:HIS:HB3	1.98	0.45
77:SX:73:GLN:HB2	77:SX:80:LYS:HZ3	1.82	0.45
80:Sa:45:VAL:HG21	80:Sa:64:LEU:HD23	1.98	0.45
1:CB:595:SER:HA	1:CB:724:THR:HG21	1.98	0.45
4:L5:1359:G:H4'	19:LN:203:TYR:HB2	1.97	0.45
4:L5:3641:U:H5	4:L5:3646:A:N7	2.15	0.45
4:L5:4174:U:H2'	4:L5:4175:G:C8	2.52	0.45
7:LA:101:VAL:HG22	7:LA:165:VAL:HG22	1.97	0.45
22:LQ:83:VAL:HG23	22:LQ:103:LEU:HD22	1.99	0.45
23:LR:104:ARG:O	23:LR:108:ARG:HG2	2.16	0.45
53:S2:1792:G:H2'	53:S2:1793:A:H8	1.81	0.45
55:SB:103:MET:HE2	55:SB:188:LEU:HD21	1.98	0.45
58:SE:115:THR:HG23	58:SE:118:GLU:H	1.82	0.45
60:SG:30:LYS:HD2	60:SG:34:THR:HG21	1.98	0.45
65:SL:89:ARG:HE	65:SL:106:HIS:CG	2.34	0.45
76:SW:87:GLU:HG2	76:SW:117:ARG:HH22	1.82	0.45
1:CB:327:ASP:HA	1:CB:330:LYS:HB3	1.99	0.45
4:L5:679:C:H2'	4:L5:680:G:H8	1.81	0.45
9:LC:1:MET:HB3	9:LC:2:ALA:H	1.54	0.45
16:LJ:163:MET:HB3	16:LJ:174:ILE:HG21	1.99	0.45
53:S2:1144:A:H5'	53:S2:1355:C:H41	1.82	0.45
59:SF:63:LYS:H	59:SF:63:LYS:HG2	1.59	0.45
63:SJ:110:LEU:HD13	63:SJ:147:PHE:HB3	1.98	0.45
72:SS:26:ILE:HA	72:SS:56:ALA:HB2	1.99	0.45
73:ST:122:LYS:HE2	73:ST:122:LYS:HB2	1.76	0.45
4:L5:3897:G:H4'	8:LB:254:ILE:HG12	1.98	0.45
10:LD:11:ALA:HA	10:LD:14:LYS:HB2	1.99	0.45
13:LG:90:GLN:O	13:LG:94:GLN:HG2	2.16	0.45
20:LO:111:PRO:HG2	20:LO:112:TYR:CE1	2.52	0.45
29:LX:37:LYS:HA	29:LX:38:LYS:HA	1.65	0.45
50:N4:135:LEU:HD12	50:N4:171:VAL:HG13	1.99	0.45
53:S2:219:U:H1'	62:SI:184:ARG:HH11	1.81	0.45
53:S2:844:U:H2'	53:S2:845:G:H8	1.81	0.45
56:SC:183:LYS:HA	56:SC:195:LEU:O	2.17	0.45
57:SD:222:PRO:HB3	86:Sg:190:GLY:HA3	1.98	0.45
17:LL:54:PRO:HG2	17:LL:97:SER:HB3	1.99	0.45
23:LR:60:ARG:O	23:LR:64:ARG:HB2	2.15	0.45
51:NA:185:MET:HE1	51:NA:195:ALA:HB3	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:S2:1051:G:H2'	53:S2:1052:A:H8	1.82	0.45
56:SC:70:VAL:HG21	56:SC:93:ILE:HB	1.99	0.45
69:SP:111:MET:HG3	69:SP:119:PHE:CZ	2.51	0.45
72:SS:39:ARG:HH21	73:ST:45:LEU:N	2.14	0.45
73:ST:39:LEU:HD11	73:ST:56:ARG:HH22	1.82	0.45
74:SU:67:LYS:HG3	74:SU:78:ASP:HB2	1.98	0.45
1:CB:396:MET:HG3	1:CB:416:VAL:HG12	1.97	0.45
1:CB:533:MET:O	1:CB:533:MET:HE3	2.17	0.45
4:L5:513:U:H3'	4:L5:514:U:H4'	1.98	0.45
4:L5:1298:C:H2'	4:L5:1299:G:C8	2.52	0.45
4:L5:1662:C:H2'	4:L5:1663:C:C6	2.52	0.45
4:L5:1702:C:H4'	9:LC:308:LYS:HD2	1.99	0.45
4:L5:2539:C:H2'	4:L5:2540:C:C6	2.52	0.45
4:L5:2640:G:H2'	4:L5:2641:A:C8	2.51	0.45
18:LM:51:PRO:HG2	18:LM:54:CYS:HB2	1.99	0.45
24:LS:149:LYS:HB2	24:LS:149:LYS:HE3	1.81	0.45
27:LV:13:LYS:HD2	27:LV:124:GLU:HB3	1.99	0.45
27:LV:91:LYS:HD3	27:LV:91:LYS:HA	1.83	0.45
31:LZ:6:LYS:HA	31:LZ:6:LYS:HD2	1.86	0.45
53:S2:1736:G:H2'	53:S2:1737:G:C8	2.52	0.45
55:SB:192:SER:HA	55:SB:195:LYS:HD3	1.99	0.45
63:SJ:131:ARG:HA	63:SJ:131:ARG:HD2	1.75	0.45
4:L5:128:C:H2'	4:L5:129:C:C6	2.52	0.45
4:L5:406:C:H4'	50:N4:8:ALA:HB1	1.99	0.45
4:L5:1414:C:H2'	4:L5:1415:G:C8	2.51	0.45
9:LC:205:ARG:HA	9:LC:205:ARG:HD3	1.71	0.45
12:LF:184:ILE:HA	12:LF:189:ASP:HB3	1.99	0.45
30:LY:31:SER:HA	30:LY:48:PRO:HA	1.97	0.45
53:S2:165:G:H2'	53:S2:166:A:C8	2.48	0.45
53:S2:656:G:N2	53:S2:663:C:H5''	2.32	0.45
53:S2:945:U:H1'	68:SO:140:THR:HG21	1.99	0.45
59:SF:72:LEU:HA	59:SF:151:ILE:HD11	1.99	0.45
60:SG:48:TYR:HD1	60:SG:113:ILE:HG21	1.81	0.45
63:SJ:138:ARG:HB3	63:SJ:156:HIS:HB3	1.98	0.45
64:SK:15:LEU:HD23	64:SK:21:MET:SD	2.57	0.45
65:SL:153:LYS:HA	65:SL:153:LYS:HD3	1.82	0.45
68:SO:63:LYS:HA	68:SO:63:LYS:HD3	1.74	0.45
1:CB:577:VAL:HG21	1:CB:791:ASN:HB3	1.98	0.44
4:L5:161:G:H2'	4:L5:162:A:H8	1.81	0.44
4:L5:490:C:H2'	4:L5:491:G:H8	1.82	0.44
8:LB:50:LYS:HB2	8:LB:345:LEU:HD11	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LB:220:ILE:HB	8:LB:346:THR:HB	1.99	0.44
14:LH:36:ARG:HB3	14:LH:80:MET:HE1	2.00	0.44
18:LM:17:PHE:HZ	18:LM:53:LYS:HE2	1.82	0.44
20:LO:194:GLU:O	20:LO:198:THR:HG23	2.17	0.44
25:LT:80:VAL:HG12	25:LT:81:LYS:H	1.82	0.44
26:LU:83:LEU:HD23	26:LU:83:LEU:HA	1.85	0.44
30:LY:10:ASP:HB3	30:LY:13:LYS:HB2	1.98	0.44
38:Lg:59:VAL:HG21	38:Lg:63:VAL:HG22	1.99	0.44
50:N4:77:THR:HG23	50:N4:121:PHE:HZ	1.82	0.44
65:SL:133:PRO:HA	65:SL:139:ARG:HG3	1.99	0.44
67:SN:91:LEU:HB3	67:SN:122:ILE:HG12	1.99	0.44
70:SQ:45:ARG:HA	70:SQ:48:GLN:HB2	1.98	0.44
1:CB:426:LYS:HG3	1:CB:444:LEU:HD12	1.99	0.44
1:CB:607:ARG:HE	1:CB:701:ARG:HH21	1.64	0.44
4:L5:1994:C:H2'	4:L5:1995:G:C8	2.52	0.44
4:L5:3967:G:H5'	4:L5:3970:G:H22	1.82	0.44
4:L5:4618:G:H5''	27:LV:15:ARG:HB2	1.99	0.44
4:L5:4761:G:H2'	4:L5:4762:A:C8	2.52	0.44
8:LB:132:LYS:H	8:LB:132:LYS:HG2	1.58	0.44
13:LG:180:PRO:HG3	13:LG:219:VAL:HG13	1.99	0.44
53:S2:184:G:H2'	53:S2:185:G:H8	1.81	0.44
53:S2:640:A:H2'	53:S2:641:A:C8	2.51	0.44
53:S2:681:U:H4'	77:SX:9:THR:HG22	1.99	0.44
69:SP:75:VAL:HG21	69:SP:104:GLN:HE22	1.82	0.44
3:CD:222:LYS:HA	3:CD:222:LYS:HD2	1.81	0.44
4:L5:10:A:H2'	4:L5:11:G:C8	2.53	0.44
4:L5:1503:A:H4'	4:L5:1504:G:H5'	2.00	0.44
4:L5:3732:A:H2'	4:L5:3733:A:C8	2.52	0.44
4:L5:4081:G:H2'	4:L5:4082:G:C8	2.52	0.44
11:LE:224:LYS:HG2	11:LE:227:HIS:HB2	1.98	0.44
39:Lh:73:TYR:HB3	39:Lh:79:LYS:HG2	1.99	0.44
51:NA:190:VAL:HG21	51:NA:213:LEU:HD22	1.97	0.44
53:S2:549:C:H2'	53:S2:550:C:C6	2.52	0.44
55:SB:139:CYS:HB3	55:SB:172:MET:HE1	2.00	0.44
58:SE:211:LYS:HE2	58:SE:211:LYS:HB2	1.80	0.44
69:SP:114:HIS:HB2	69:SP:119:PHE:CZ	2.52	0.44
77:SX:52:LEU:HD23	77:SX:52:LEU:HA	1.77	0.44
4:L5:4239:A:H2'	4:L5:4240:G:C8	2.53	0.44
4:L5:4274:A:H2'	4:L5:4275:G:H8	1.80	0.44
4:L5:4991:U:H2'	4:L5:4992:G:H8	1.83	0.44
12:LF:148:LYS:O	12:LF:152:GLU:HG2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:LQ:49:LYS:HG2	22:LQ:53:MET:HE3	2.00	0.44
53:S2:1860:A:H5''	80:Sa:8:ASN:ND2	2.32	0.44
54:SA:212:LYS:HA	54:SA:212:LYS:HD3	1.84	0.44
55:SB:68:GLU:HB3	55:SB:85:LYS:HD3	1.99	0.44
58:SE:123:LEU:HB2	58:SE:236:ILE:HD11	2.00	0.44
59:SF:100:ILE:HD13	59:SF:103:LEU:HD21	1.99	0.44
73:ST:111:LYS:HD3	73:ST:111:LYS:HA	1.66	0.44
82:Sc:13:ARG:O	82:Sc:32:VAL:HA	2.17	0.44
82:Sc:31:ARG:HD2	82:Sc:43:ILE:HG22	2.00	0.44
1:CB:76:SER:H	1:CB:454:MET:HE1	1.82	0.44
1:CB:744:ILE:HG12	1:CB:818:GLN:HB3	2.00	0.44
4:L5:665:C:H4'	4:L5:666:G:H5'	1.99	0.44
4:L5:1794:A:H5''	4:L5:4214:A:H61	1.83	0.44
9:LC:8:ILE:HD13	9:LC:151:PRO:HB2	1.99	0.44
10:LD:217:ASP:HA	10:LD:220:LYS:HG2	1.99	0.44
16:LJ:51:SER:HB3	16:LJ:69:ALA:HB3	2.00	0.44
17:LL:154:VAL:HG12	17:LL:155:MET:HE3	1.97	0.44
30:LY:120:GLU:O	30:LY:124:LYS:HG2	2.17	0.44
47:Lp:75:SER:O	47:Lp:79:VAL:HG13	2.17	0.44
49:Lz:4:LYS:H	49:Lz:4:LYS:HG2	1.55	0.44
53:S2:1337:C:H2'	53:S2:1338:G:C8	2.53	0.44
53:S2:1468:C:H2'	53:S2:1469:A:C8	2.53	0.44
53:S2:1808:U:H2'	53:S2:1809:A:C8	2.53	0.44
55:SB:46:LYS:NZ	68:SO:27:VAL:HA	2.33	0.44
64:SK:42:ASN:HA	64:SK:45:VAL:HG12	2.00	0.44
67:SN:119:GLU:HA	67:SN:122:ILE:HD12	1.99	0.44
72:SS:10:GLN:HE22	72:SS:57:GLY:HA2	1.82	0.44
77:SX:79:LYS:H	77:SX:79:LYS:HG2	1.61	0.44
6:L8:141:C:H2'	6:L8:142:U:C6	2.52	0.44
19:LN:14:LYS:HB2	19:LN:14:LYS:HE3	1.79	0.44
24:LS:28:TYR:HD1	24:LS:54:MET:HE1	1.82	0.44
38:Lg:63:VAL:HA	38:Lg:66:ARG:HG2	1.99	0.44
42:Lk:10:ASP:HA	42:Lk:13:LEU:HG	2.00	0.44
53:S2:1522:A:H5'	72:SS:144:ARG:HG2	1.99	0.44
56:SC:149:THR:HG22	56:SC:152:ARG:HH22	1.82	0.44
56:SC:210:PRO:HB3	56:SC:240:THR:HG21	1.99	0.44
59:SF:43:GLU:HA	59:SF:46:ALA:HB2	2.00	0.44
61:SH:154:ILE:HB	61:SH:185:VAL:HG22	1.99	0.44
67:SN:38:TYR:CE1	67:SN:78:LYS:HG2	2.52	0.44
69:SP:22:LEU:HA	69:SP:25:LEU:HB2	1.99	0.44
2:CC:79:U:H2'	2:CC:80:A:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:1308:C:H2'	4:L5:1309:C:C6	2.53	0.44
4:L5:1327:C:H2'	4:L5:1328:G:C8	2.53	0.44
4:L5:1560:A:H2'	4:L5:1561:G:C8	2.53	0.44
4:L5:1645:C:H2'	4:L5:1646:A:C8	2.53	0.44
4:L5:1709:C:N4	4:L5:1716:G:H22	2.14	0.44
4:L5:4188:U:H2'	4:L5:4189:U:C6	2.52	0.44
4:L5:4347:G:H2'	4:L5:4348:A:C8	2.53	0.44
4:L5:4691:A:H4'	14:LH:71:ARG:HG2	1.99	0.44
10:LD:181:PRO:HD2	10:LD:195:HIS:CD2	2.53	0.44
17:LL:90:VAL:O	17:LL:94:ILE:HG13	2.18	0.44
25:LT:72:VAL:HG11	25:LT:96:ILE:HD13	1.99	0.44
26:LU:47:ILE:HD12	26:LU:63:ILE:HD11	1.99	0.44
39:Lh:21:LEU:HG	39:Lh:25:LYS:HD2	1.99	0.44
51:NA:205:ASP:HB3	51:NA:208:ASN:HB2	2.00	0.44
52:NB:64:MET:O	52:NB:71:VAL:HA	2.16	0.44
53:S2:121:U:H2'	53:S2:122:G:H8	1.83	0.44
57:SD:50:ILE:HG13	57:SD:88:ALA:HA	2.00	0.44
59:SF:165:ASN:HD21	59:SF:167:LYS:HE3	1.83	0.44
67:SN:42:LYS:HE2	67:SN:42:LYS:N	2.33	0.44
73:ST:28:LEU:HD12	73:ST:106:ALA:HB1	2.00	0.44
78:SY:40:ILE:HD11	78:SY:57:VAL:HG21	1.99	0.44
1:CB:155:LEU:HD22	1:CB:185:VAL:HG11	1.99	0.44
4:L5:162:A:H2'	4:L5:163:A:C8	2.52	0.44
4:L5:325:U:H2'	4:L5:326:C:C6	2.53	0.44
4:L5:3610:A:H2'	4:L5:3611:A:C8	2.52	0.44
29:LX:122:ALA:HB3	29:LX:139:ARG:HG2	1.99	0.44
53:S2:215:G:H2'	53:S2:216:C:H6	1.83	0.44
53:S2:1391:C:H4'	83:Sd:55:LEU:HD21	2.00	0.44
56:SC:185:THR:HA	56:SC:193:VAL:O	2.18	0.44
59:SF:187:SER:HB3	59:SF:190:ILE:HG22	1.99	0.44
62:SI:39:GLY:HA3	62:SI:59:ARG:HD2	2.00	0.44
69:SP:70:MET:HE2	69:SP:70:MET:O	2.18	0.44
85:Sf:132:MET:HE2	85:Sf:132:MET:HA	2.00	0.44
4:L5:4967:A:H2'	4:L5:4968:A:C8	2.53	0.44
7:LA:172:GLY:HA3	47:Lp:68:ALA:H	1.82	0.44
11:LE:98:GLY:HA3	11:LE:99:ASP:HA	1.71	0.44
13:LG:150:LYS:HB2	13:LG:150:LYS:HE3	1.72	0.44
13:LG:187:LYS:HB2	13:LG:198:THR:HG23	1.99	0.44
18:LM:90:ARG:HA	18:LM:93:LYS:HG2	1.98	0.44
25:LT:84:ILE:HD12	33:Lb:21:ILE:HG22	2.00	0.44
31:LZ:71:PHE:HA	31:LZ:111:ARG:HD2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:Ld:19:GLU:HA	35:Ld:90:ARG:HH11	1.83	0.44
52:NB:64:MET:HB3	52:NB:72:ILE:HB	2.00	0.44
53:S2:17:C:H2'	53:S2:18:C:C6	2.53	0.44
53:S2:1669:G:H4'	74:SU:62:ARG:HH22	1.83	0.44
53:S2:1745:A:H62	53:S2:1789:G:H21	1.66	0.44
55:SB:67:PHE:O	55:SB:85:LYS:O	2.35	0.44
73:ST:2:PRO:HA	73:ST:3:GLY:HA3	1.68	0.44
1:CB:30:HIS:CD2	1:CB:130:ASP:H	2.36	0.43
4:L5:279:A:H61	4:L5:306:A:H3'	1.81	0.43
4:L5:1086:C:H2'	4:L5:1087:A:H8	1.82	0.43
51:NA:83:LEU:HD21	52:NB:43:LYS:HD2	1.99	0.43
53:S2:1540:G:H2'	53:S2:1541:G:C8	2.52	0.43
65:SL:59:LYS:HG2	65:SL:134:LEU:HD11	2.00	0.43
69:SP:44:ARG:O	69:SP:47:ARG:C	2.61	0.43
74:SU:49:LYS:HD3	74:SU:92:HIS:HB3	2.00	0.43
86:Sg:30:MET:HB3	86:Sg:44:LYS:HD3	2.00	0.43
1:CB:524:LEU:HD23	1:CB:524:LEU:HA	1.87	0.43
4:L5:1733:G:N3	4:L5:4214:A:H2'	2.33	0.43
29:LX:155:ILE:HA	39:Lh:37:THR:HG21	2.00	0.43
41:Lj:10:LYS:HB3	41:Lj:10:LYS:HE2	1.78	0.43
41:Lj:34:CYS:HB3	41:Lj:39:TYR:H	1.82	0.43
53:S2:549:C:C4	53:S2:550:C:N4	2.86	0.43
54:SA:172:GLY:HA3	54:SA:203:PHE:HD1	1.82	0.43
59:SF:157:GLY:HA2	59:SF:188:TYR:HD2	1.82	0.43
76:SW:31:SER:O	76:SW:35:VAL:HG23	2.18	0.43
78:SY:87:PRO:HG2	78:SY:90:ARG:HH11	1.82	0.43
79:SZ:41:ARG:HH12	79:SZ:44:LEU:HB2	1.82	0.43
4:L5:153:G:H2'	4:L5:154:G:H8	1.83	0.43
4:L5:1333:A:H2'	4:L5:1334:A:C8	2.53	0.43
4:L5:4601:U:H2'	4:L5:4602:A:C8	2.50	0.43
4:L5:4966:A:H5'	8:LB:128:LYS:HG3	1.99	0.43
18:LM:93:LYS:HB3	18:LM:93:LYS:HE2	1.62	0.43
53:S2:1846:G:H2'	53:S2:1847:G:C8	2.52	0.43
86:Sg:5:MET:HA	86:Sg:5:MET:HE3	2.00	0.43
86:Sg:108:VAL:HG12	86:Sg:124:SER:HB2	2.00	0.43
4:L5:1468:C:H2'	4:L5:1469:C:H6	1.82	0.43
4:L5:2386:U:H5'	23:LR:4:LEU:HB2	2.00	0.43
11:LE:262:LYS:HA	11:LE:262:LYS:HD3	1.89	0.43
16:LJ:20:LEU:C	16:LJ:131:TYR:O	2.61	0.43
26:LU:99:TRP:NE1	52:NB:15:GLN:HB2	2.33	0.43
53:S2:1199:A:H2'	53:S2:1200:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:SD:50:ILE:HD12	57:SD:52:ALA:HB2	1.99	0.43
57:SD:60:GLY:HA3	57:SD:65:ARG:H	1.82	0.43
58:SE:254:LYS:HA	58:SE:254:LYS:HD3	1.80	0.43
63:SJ:35:TYR:HD1	63:SJ:112:THR:HG21	1.83	0.43
65:SL:35:ARG:HH21	65:SL:63:THR:HG21	1.83	0.43
86:Sg:283:PRO:HA	86:Sg:284:PRO:HD3	1.85	0.43
1:CB:259:LYS:HE3	1:CB:273:PHE:HD2	1.84	0.43
1:CB:590:LEU:HB2	1:CB:605:LYS:HE2	2.00	0.43
4:L5:267:G:H2'	4:L5:268:G:H8	1.83	0.43
4:L5:4064:C:H2'	4:L5:4065:G:H8	1.84	0.43
12:LF:236:ARG:HB2	12:LF:239:GLN:HB2	2.00	0.43
17:LL:177:LYS:O	17:LL:181:SER:HB3	2.19	0.43
32:La:71:PRO:HG2	32:La:108:TYR:HA	2.01	0.43
49:Lz:25:ARG:HH11	49:Lz:210:MET:HE1	1.83	0.43
49:Lz:47:LYS:NZ	49:Lz:194:LEU:HD13	2.34	0.43
53:S2:1562:C:H2'	53:S2:1563:G:H8	1.83	0.43
64:SK:21:MET:HB2	64:SK:69:TRP:HB2	1.99	0.43
68:SO:56:VAL:HG12	68:SO:61:LYS:NZ	2.33	0.43
70:SQ:76:GLY:H	70:SQ:79:ALA:HB3	1.83	0.43
74:SU:53:PRO:HA	74:SU:89:ILE:HG13	2.00	0.43
78:SY:23:MET:HE1	78:SY:48:TYR:HE2	1.82	0.43
1:CB:602:LEU:HG	1:CB:707:VAL:HG12	2.00	0.43
4:L5:4743:G:H2'	4:L5:4744:A:H8	1.81	0.43
8:LB:29:VAL:HG12	8:LB:31:SER:H	1.84	0.43
13:LG:157:ILE:HA	13:LG:201:THR:HG22	2.01	0.43
14:LH:103:VAL:HG22	14:LH:114:ILE:HG13	2.01	0.43
15:LI:19:LYS:HB3	15:LI:26:VAL:HG21	1.99	0.43
18:LM:38:VAL:O	18:LM:47:ARG:HA	2.18	0.43
50:N4:81:MET:HA	50:N4:81:MET:HE3	2.01	0.43
53:S2:107:A:H2'	53:S2:108:G:C8	2.54	0.43
53:S2:1714:U:H2'	53:S2:1715:A:C8	2.53	0.43
59:SF:78:MET:HG2	59:SF:159:ARG:NH2	2.34	0.43
65:SL:16:ILE:HD11	65:SL:36:TYR:HB2	2.01	0.43
74:SU:27:ARG:HD3	74:SU:82:MET:HE2	2.00	0.43
78:SY:99:LYS:HE2	78:SY:99:LYS:HB3	1.82	0.43
86:Sg:39:THR:HG22	86:Sg:60:ARG:HB3	2.00	0.43
4:L5:1840:G:H1'	12:LF:111:LEU:HD22	2.00	0.43
4:L5:3700:C:H2'	4:L5:3746:A:H61	1.84	0.43
4:L5:3748:A:H5''	7:LA:243:THR:HB	2.00	0.43
4:L5:4108:G:H2'	4:L5:4109:G:H8	1.84	0.43
4:L5:4537:C:H2'	4:L5:4538:G:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LB:36:ASP:HA	8:LB:37:PRO:HD3	1.89	0.43
8:LB:234:ARG:HG3	8:LB:272:LYS:HB2	2.00	0.43
9:LC:134:PRO:HA	9:LC:150:LEU:HD22	2.00	0.43
13:LG:234:ARG:HD2	13:LG:235:ARG:NH1	2.33	0.43
53:S2:1648:G:H5''	70:SQ:125:ARG:HB2	2.01	0.43
68:SO:12:GLU:HA	68:SO:13:GLN:HA	1.72	0.43
70:SQ:62:ARG:HH12	70:SQ:96:TYR:HE1	1.66	0.43
74:SU:30:LYS:HA	74:SU:30:LYS:HE2	2.00	0.43
77:SX:107:ARG:HG3	77:SX:110:HIS:HB3	1.99	0.43
1:CB:283:LYS:HA	1:CB:283:LYS:HD2	1.85	0.43
4:L5:1340:C:H2'	4:L5:1341:U:C6	2.53	0.43
4:L5:4108:G:H2'	4:L5:4109:G:C8	2.54	0.43
29:LX:83:THR:O	29:LX:87:MET:HG2	2.18	0.43
39:Lh:104:THR:O	39:Lh:108:GLN:HG3	2.18	0.43
44:Lm:94:MET:HG2	44:Lm:105:PRO:HA	2.01	0.43
53:S2:941:C:H2'	53:S2:942:G:C8	2.54	0.43
59:SF:33:ILE:HD13	82:Sc:55:VAL:HG11	2.01	0.43
62:SI:170:LYS:HE2	62:SI:170:LYS:HB2	1.80	0.43
73:ST:134:ILE:O	73:ST:138:VAL:HG12	2.19	0.43
4:L5:1788:A:H2'	15:LI:22:PHE:CZ	2.54	0.43
11:LE:223:ARG:HA	11:LE:224:LYS:HA	1.64	0.43
13:LG:87:LEU:HD13	13:LG:182:CYS:HB2	2.00	0.43
19:LN:152:THR:HG21	39:Lh:95:LEU:HD21	2.00	0.43
30:LY:47:MET:HE2	30:LY:119:LEU:HG	2.01	0.43
30:LY:103:LYS:HA	30:LY:103:LYS:HD3	1.86	0.43
33:Lb:13:SER:HA	33:Lb:16:TRP:CE2	2.54	0.43
33:Lb:28:ARG:HE	33:Lb:28:ARG:HB2	1.62	0.43
49:Lz:120:ILE:HG23	49:Lz:124:LEU:HD12	2.01	0.43
53:S2:388:U:H2'	53:S2:389:A:C8	2.54	0.43
53:S2:498:C:H2'	53:S2:499:G:C8	2.54	0.43
53:S2:639:C:H2'	53:S2:640:A:C8	2.52	0.43
54:SA:147:LEU:HD13	54:SA:161:ILE:HB	2.00	0.43
57:SD:69:LEU:HA	57:SD:72:VAL:HG22	2.00	0.43
57:SD:197:LYS:HE2	57:SD:197:LYS:HB2	1.83	0.43
61:SH:53:VAL:HG11	61:SH:172:THR:HA	2.00	0.43
61:SH:72:PHE:O	61:SH:76:GLN:CB	2.61	0.43
63:SJ:128:VAL:O	63:SJ:132:GLN:HG2	2.18	0.43
83:Sd:12:ARG:HD3	83:Sd:12:ARG:HA	1.61	0.43
85:Sf:141:CYS:O	85:Sf:145:CYS:HA	2.18	0.43
86:Sg:219:TRP:HA	86:Sg:227:LEU:HD23	2.01	0.43
1:CB:598:LYS:HE2	1:CB:598:LYS:HB2	1.89	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L5:257:C:H2'	4:L5:258:G:C8	2.54	0.43
4:L5:1465:G:H5'	33:Lb:44:ARG:HH21	1.84	0.43
4:L5:1751:A:H2'	4:L5:1752:G:C8	2.54	0.43
4:L5:2101:C:H2'	4:L5:2102:G:H2'	2.01	0.43
4:L5:3720:G:H22	4:L5:3733:A:H2	1.67	0.43
4:L5:4128:A:H1'	13:LG:35:ARG:HG3	2.00	0.43
4:L5:4708:A:N3	4:L5:4709:U:H5'	2.34	0.43
4:L5:4769:G:H5''	20:LO:176:ARG:HD3	2.01	0.43
4:L5:4896:G:H2'	4:L5:4897:G:C8	2.54	0.43
13:LG:123:ALA:HA	13:LG:124:GLY:HA2	1.76	0.43
19:LN:159:ARG:HA	19:LN:164:LEU:HD12	2.00	0.43
25:LT:102:ARG:HE	25:LT:105:PHE:HD2	1.67	0.43
49:Lz:195:LYS:HD2	49:Lz:195:LYS:HA	1.75	0.43
50:N4:154:PHE:O	50:N4:158:ILE:HG22	2.19	0.43
53:S2:12:U:H2'	53:S2:13:C:C6	2.53	0.43
53:S2:16:G:H2'	53:S2:17:C:C6	2.54	0.43
53:S2:71:G:H2'	53:S2:72:C:H4'	2.00	0.43
53:S2:158:A:N1	53:S2:463:C:O2	2.50	0.43
53:S2:1285:G:H5'	66:SM:35:ILE:HG23	2.01	0.43
53:S2:1562:C:H2'	53:S2:1563:G:C8	2.54	0.43
53:S2:1858:G:H2'	53:S2:1859:A:C8	2.54	0.43
63:SJ:88:ASP:H	63:SJ:91:LYS:NZ	2.16	0.43
72:SS:130:ARG:HG2	72:SS:134:GLN:HB2	2.00	0.43
78:SY:12:PHE:HB2	78:SY:23:MET:HG2	2.01	0.43
81:Sb:82:LYS:HB2	81:Sb:82:LYS:HE3	1.82	0.43
1:CB:697:MET:HE1	1:CB:733:VAL:HG21	2.01	0.42
1:CB:831:PRO:HA	1:CB:834:VAL:HG22	2.01	0.42
4:L5:74:G:H5'	17:LL:59:VAL:HG13	2.01	0.42
4:L5:93:G:H2'	4:L5:94:A:C8	2.54	0.42
4:L5:691:C:H2'	4:L5:692:A:C8	2.53	0.42
4:L5:2696:A:H62	42:Lk:35:LYS:HE2	1.84	0.42
4:L5:4991:U:H2'	4:L5:4992:G:C8	2.54	0.42
7:LA:146:THR:HG23	7:LA:158:ILE:HG13	2.01	0.42
14:LH:115:ARG:HD3	14:LH:123:ILE:HG23	2.00	0.42
24:LS:70:LYS:HD3	24:LS:70:LYS:HA	1.64	0.42
37:Lf:47:CYS:HA	37:Lf:102:ARG:O	2.19	0.42
53:S2:17:C:H2'	53:S2:18:C:H6	1.84	0.42
53:S2:454:U:H2'	53:S2:455:A:H8	1.84	0.42
53:S2:1027:A:H3'	53:S2:1028:A:H8	1.82	0.42
53:S2:1273:C:H4'	53:S2:1274:G:H21	1.84	0.42
57:SD:25:LEU:HA	57:SD:28:GLU:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:SD:161:GLY:O	57:SD:164:VAL:C	2.62	0.42
59:SF:88:MET:HE2	59:SF:88:MET:N	2.34	0.42
64:SK:25:LYS:HA	64:SK:46:MET:HE1	2.01	0.42
68:SO:96:LYS:HA	68:SO:96:LYS:HD3	1.88	0.42
68:SO:147:ARG:HA	80:Sa:28:ARG:HG3	2.00	0.42
69:SP:22:LEU:O	69:SP:26:LEU:HD22	2.19	0.42
71:SR:51:ALA:O	71:SR:55:THR:HG23	2.18	0.42
73:ST:80:GLY:CA	73:ST:93:SER:O	2.67	0.42
80:Sa:44:ILE:HB	80:Sa:67:LEU:HB2	2.00	0.42
86:Sg:64:HIS:HB3	86:Sg:83:TRP:HB3	2.01	0.42
86:Sg:68:ASP:HB3	86:Sg:111:VAL:HG22	2.00	0.42
86:Sg:113:PHE:HA	86:Sg:120:ILE:HD13	2.00	0.42
4:L5:181:C:H3'	4:L5:182:G:H8	1.84	0.42
4:L5:1500:A:H5''	4:L5:1501:C:H5''	2.01	0.42
4:L5:3923:A:H2'	4:L5:3924:C:C6	2.55	0.42
4:L5:3955:G:N3	4:L5:3966:A:N7	2.67	0.42
13:LG:176:LYS:HE2	13:LG:176:LYS:HB2	1.84	0.42
19:LN:5:LYS:HG3	40:Li:40:VAL:HG11	2.02	0.42
21:LP:105:LYS:HB2	21:LP:105:LYS:HE3	1.83	0.42
37:Lf:96:ALA:O	37:Lf:99:HIS:HB2	2.19	0.42
53:S2:525:A:H5''	84:Se:32:ALA:HB2	2.01	0.42
56:SC:255:LEU:HD22	75:SV:14:PRO:HD2	2.01	0.42
57:SD:40:ARG:HG2	74:SU:108:PRO:HG2	2.01	0.42
59:SF:47:LYS:HD2	59:SF:47:LYS:HA	1.72	0.42
66:SM:85:LEU:HD23	66:SM:106:CYS:HB3	2.00	0.42
69:SP:31:GLU:HA	69:SP:34:MET:HE1	2.01	0.42
72:SS:47:LYS:HD3	72:SS:47:LYS:HA	1.78	0.42
86:Sg:79:LEU:HD22	86:Sg:120:ILE:HD12	2.01	0.42
1:CB:439:LYS:HB2	1:CB:439:LYS:HE2	1.81	0.42
4:L5:186:G:H1'	4:L5:1366:G:H21	1.85	0.42
4:L5:1558:A:H2'	4:L5:1559:G:C8	2.55	0.42
20:LO:197:LYS:HE3	20:LO:197:LYS:HB2	1.89	0.42
23:LR:181:LYS:HA	23:LR:181:LYS:HD3	1.88	0.42
37:Lf:35:ALA:HA	37:Lf:81:SER:HA	2.02	0.42
45:Ln:9:ARG:HH22	53:S2:1707:U:H5'	1.84	0.42
53:S2:1047:C:H4'	68:SO:143:LYS:HA	2.00	0.42
58:SE:180:LEU:HA	58:SE:194:VAL:HA	2.01	0.42
59:SF:87:LEU:HA	59:SF:90:VAL:HG12	2.01	0.42
59:SF:167:LYS:H	59:SF:167:LYS:HG3	1.61	0.42
66:SM:69:CYS:HB2	66:SM:74:ILE:HB	2.00	0.42
72:SS:119:ALA:O	72:SS:123:LEU:HD12	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:SU:34:LYS:HE3	74:SU:34:LYS:HB3	1.88	0.42
1:CB:73:THR:O	1:CB:103:ILE:HA	2.18	0.42
1:CB:655:ASP:HA	84:Se:7:ALA:HB1	2.01	0.42
4:L5:1252:C:H2'	4:L5:1254:A:H62	1.84	0.42
4:L5:1604:G:H2'	4:L5:1605:G:C8	2.54	0.42
7:LA:130:SER:HA	7:LA:169:VAL:HG22	2.01	0.42
14:LH:28:LYS:HA	14:LH:28:LYS:HE2	2.01	0.42
53:S2:820:U:O4	53:S2:828:G:O6	2.36	0.42
53:S2:866:U:H2'	53:S2:867:G:C8	2.54	0.42
53:S2:929:G:H2'	53:S2:930:C:O4'	2.19	0.42
53:S2:941:C:H2'	53:S2:942:G:H8	1.83	0.42
53:S2:1468:C:H2'	53:S2:1469:A:H8	1.84	0.42
70:SQ:125:ARG:C	70:SQ:126:ARG:HD2	2.44	0.42
1:CB:150:ARG:HH21	1:CB:367:TYR:HB2	1.84	0.42
1:CB:160:MET:O	1:CB:164:LEU:HD22	2.19	0.42
4:L5:2894:A:H2'	4:L5:2895:A:C8	2.55	0.42
7:LA:102:LEU:HG	7:LA:107:MET:HE3	2.01	0.42
23:LR:136:ARG:O	23:LR:140:GLU:HG3	2.20	0.42
53:S2:526:A:H4'	63:SJ:125:HIS:HB2	2.01	0.42
53:S2:1452:A:H61	53:S2:1473:G:H21	1.67	0.42
54:SA:183:LEU:O	54:SA:186:ARG:O	2.38	0.42
59:SF:138:ALA:HB3	59:SF:204:ARG:HD3	2.02	0.42
70:SQ:134:GLY:N	70:SQ:140:ARG:HH21	2.17	0.42
71:SR:78:ARG:NH1	71:SR:79:GLU:HG3	2.35	0.42
72:SS:36:VAL:HG22	72:SS:40:TYR:HD2	1.85	0.42
78:SY:62:THR:HA	78:SY:69:THR:HA	2.01	0.42
4:L5:2765:A:H2'	4:L5:2766:A:C8	2.55	0.42
4:L5:4530:U:H2'	4:L5:4531:U:H2'	2.02	0.42
4:L5:4764:A:N1	14:LH:60:TRP:HB2	2.35	0.42
6:L8:140:C:H2'	6:L8:141:C:C6	2.55	0.42
11:LE:200:LYS:HE3	11:LE:200:LYS:HB3	1.57	0.42
12:LF:29:LYS:HA	12:LF:32:ARG:HG2	2.01	0.42
13:LG:146:LEU:HD22	13:LG:151:LYS:HB2	2.02	0.42
26:LU:17:GLN:HB2	26:LU:18:VAL:H	1.73	0.42
45:Ln:3:ALA:HA	45:Ln:6:ARG:HB2	2.01	0.42
48:Lr:96:MET:O	48:Lr:100:ASN:HB2	2.18	0.42
53:S2:1410:C:H2'	53:S2:1411:G:C8	2.55	0.42
53:S2:1591:C:O3'	59:SF:88:MET:HE1	2.20	0.42
53:S2:1845:A:H2'	53:S2:1846:G:C8	2.55	0.42
55:SB:28:LYS:HA	55:SB:50:THR:HA	2.00	0.42
55:SB:110:MET:HA	55:SB:113:MET:HE3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:SC:207:ALA:O	56:SC:211:LYS:HB2	2.20	0.42
74:SU:98:VAL:HA	74:SU:101:ILE:HB	2.01	0.42
80:Sa:13:LYS:HD3	80:Sa:13:LYS:HA	1.79	0.42
1:CB:306:ASN:HB2	1:CB:308:LYS:HZ1	1.84	0.42
1:CB:592:LEU:HA	1:CB:602:LEU:O	2.20	0.42
4:L5:1356:U:H2'	4:L5:1357:C:C6	2.55	0.42
4:L5:2621:A:H2'	4:L5:2622:G:C8	2.53	0.42
4:L5:3910:C:H2'	4:L5:3911:C:C6	2.54	0.42
6:L8:123:U:H2'	6:L8:126:C:H41	1.85	0.42
11:LE:108:LYS:NZ	11:LE:112:MET:HE2	2.35	0.42
21:LP:2:VAL:HG21	21:LP:18:ARG:HD2	2.01	0.42
27:LV:16:ILE:HD11	27:LV:56:GLY:HA3	2.02	0.42
39:Lh:17:LEU:HD23	39:Lh:17:LEU:HA	1.89	0.42
53:S2:432:G:H2'	53:S2:433:A:C8	2.54	0.42
53:S2:1334:G:H5'	57:SD:140:GLY:HA2	2.00	0.42
53:S2:1536:G:H2'	53:S2:1537:A:H8	1.85	0.42
53:S2:1593:C:H2'	53:S2:1594:A:C8	2.54	0.42
56:SC:149:THR:HG22	56:SC:152:ARG:NH2	2.34	0.42
70:SQ:97:GLN:HG2	70:SQ:105:LYS:HE3	2.01	0.42
76:SW:32:LYS:O	76:SW:36:ARG:HG3	2.20	0.42
78:SY:120:THR:O	78:SY:124:ASN:HB2	2.18	0.42
1:CB:740:LEU:HD12	1:CB:831:PRO:HB3	2.00	0.42
4:L5:1613:A:H5''	7:LA:183:GLY:CA	2.49	0.42
4:L5:2521:G:H4'	38:Lg:26:PRO:HD2	2.00	0.42
9:LC:29:LYS:HD3	9:LC:29:LYS:HA	1.80	0.42
20:LO:16:LEU:HD12	20:LO:80:PHE:HD1	1.85	0.42
49:Lz:29:LEU:HD12	49:Lz:29:LEU:HA	1.89	0.42
53:S2:11:A:H4'	56:SC:113:GLN:HG3	2.02	0.42
53:S2:124:U:H5'	58:SE:148:ARG:HH12	1.84	0.42
53:S2:291:G:H2'	53:S2:292:A:C8	2.55	0.42
53:S2:1397:U:H3	70:SQ:12:VAL:HA	1.85	0.42
53:S2:1555:U:H5'	53:S2:1556:A:C5	2.55	0.42
53:S2:1568:C:H2'	53:S2:1569:A:C8	2.55	0.42
59:SF:167:LYS:HB2	59:SF:171:GLU:OE2	2.20	0.42
62:SI:124:LYS:HE2	62:SI:124:LYS:HB2	1.91	0.42
62:SI:157:LYS:HD3	62:SI:157:LYS:HA	1.75	0.42
65:SL:16:ILE:HG23	65:SL:34:PRO:HG2	2.02	0.42
72:SS:84:LEU:HG	72:SS:95:TYR:HB3	2.01	0.42
1:CB:289:PHE:CE1	1:CB:293:ILE:HD12	2.55	0.42
4:L5:1695:U:H2'	4:L5:1696:C:C6	2.55	0.42
9:LC:14:LYS:HB3	9:LC:14:LYS:HE3	1.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:LC:259:LYS:O	9:LC:263:LEU:HB2	2.19	0.42
10:LD:193:GLU:O	10:LD:197:LYS:HG2	2.19	0.42
10:LD:235:MET:O	10:LD:239:MET:HB3	2.19	0.42
16:LJ:115:LEU:HD12	16:LJ:115:LEU:HA	1.83	0.42
18:LM:77:TRP:O	18:LM:81:ASP:CA	2.49	0.42
18:LM:130:LEU:HD23	18:LM:130:LEU:HA	1.91	0.42
39:Lh:52:LYS:HA	39:Lh:52:LYS:HD3	1.80	0.42
49:Lz:22:GLN:NE2	49:Lz:22:GLN:O	2.53	0.42
52:NB:43:LYS:HA	52:NB:46:PHE:CD1	2.55	0.42
53:S2:1657:G:H2'	53:S2:1658:G:H8	1.84	0.42
55:SB:46:LYS:HZ3	68:SO:27:VAL:HA	1.84	0.42
55:SB:85:LYS:HD3	55:SB:85:LYS:HA	1.86	0.42
64:SK:5:LYS:O	64:SK:9:ILE:HG12	2.20	0.42
70:SQ:126:ARG:HD2	70:SQ:126:ARG:N	2.35	0.42
1:CB:747:VAL:HG23	1:CB:786:ALA:HB3	2.01	0.42
4:L5:262:G:H2'	4:L5:263:G:C8	2.55	0.42
4:L5:1524:A:H61	4:L5:1651:G:H22	1.68	0.42
4:L5:1907:A:H4'	12:LF:223:LYS:HE3	2.02	0.42
4:L5:3748:A:H2'	4:L5:3749:C:C6	2.55	0.42
4:L5:4457:U:H1'	8:LB:252:ALA:HB3	2.02	0.42
4:L5:4727:A:H5'	8:LB:130:PHE:H	1.85	0.42
4:L5:5055:G:H2'	4:L5:5056:A:C8	2.55	0.42
9:LC:116:ASN:HB2	9:LC:119:GLN:HG3	2.02	0.42
10:LD:108:ARG:CZ	10:LD:253:TYR:HB2	2.50	0.42
12:LF:232:ASP:HB3	12:LF:236:ARG:HH21	1.84	0.42
14:LH:48:LEU:HD21	14:LH:56:ARG:HB2	2.02	0.42
18:LM:100:ARG:HA	18:LM:103:LYS:HG2	2.02	0.42
21:LP:112:LEU:HB3	21:LP:150:LEU:HD23	2.01	0.42
21:LP:116:HIS:HB3	21:LP:149:ILE:HB	2.01	0.42
26:LU:67:LYS:HA	26:LU:67:LYS:HD3	1.92	0.42
27:LV:37:LEU:HD23	27:LV:37:LEU:HA	1.93	0.42
27:LV:62:MET:HE3	27:LV:76:VAL:HG12	2.01	0.42
53:S2:1588:A:H2'	53:S2:1589:A:C8	2.55	0.42
55:SB:181:LEU:HA	55:SB:184:VAL:HB	2.01	0.42
57:SD:37:VAL:HG23	57:SD:50:ILE:HG22	2.02	0.42
57:SD:142:LEU:HD12	57:SD:142:LEU:HA	1.85	0.42
58:SE:60:GLU:HA	58:SE:63:LYS:HE3	2.02	0.42
59:SF:39:ILE:HD12	59:SF:39:ILE:HA	1.86	0.42
80:Sa:28:ARG:HB3	80:Sa:74:CYS:SG	2.59	0.42
86:Sg:285:GLN:O	86:Sg:303:THR:HG23	2.20	0.42
7:LA:47:ASP:HB3	7:LA:60:LYS:HB2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LE:114:ARG:H	11:LE:114:ARG:HG2	1.61	0.41
32:La:22:ILE:H	32:La:22:ILE:HG13	1.70	0.41
34:Lc:57:LYS:HE3	34:Lc:57:LYS:HB2	1.68	0.41
50:N4:78:LYS:O	50:N4:82:GLN:HB3	2.20	0.41
57:SD:185:LYS:HB2	57:SD:185:LYS:HE3	1.75	0.41
65:SL:58:LYS:HG3	65:SL:59:LYS:HG3	2.02	0.41
78:SY:89:HIS:CE1	78:SY:90:ARG:HG3	2.55	0.41
80:Sa:15:ARG:H	80:Sa:15:ARG:HG2	1.72	0.41
80:Sa:26:CYS:HB3	80:Sa:77:CYS:SG	2.59	0.41
1:CB:545:ILE:HD13	1:CB:545:ILE:HA	1.88	0.41
11:LE:264:ILE:HA	11:LE:265:PRO:HD3	1.93	0.41
13:LG:220:GLU:O	13:LG:224:THR:HG22	2.21	0.41
14:LH:157:SER:O	14:LH:161:ILE:HG12	2.20	0.41
25:LT:110:LYS:HA	25:LT:110:LYS:HD2	1.88	0.41
30:LY:72:GLN:HB3	30:LY:81:TYR:HB2	2.02	0.41
32:La:23:GLY:HA3	32:La:24:LYS:HA	1.64	0.41
43:Ll:16:LYS:HG2	43:Ll:49:LEU:HD21	2.01	0.41
51:NA:96:ILE:HG22	52:NB:59:ILE:HD12	2.03	0.41
60:SG:217:MET:HA	60:SG:220:ALA:HB3	2.01	0.41
68:SO:14:VAL:HG11	68:SO:17:LEU:HB2	2.02	0.41
71:SR:65:PRO:HA	71:SR:73:LEU:HD21	2.02	0.41
77:SX:32:LEU:HD12	77:SX:32:LEU:HA	1.86	0.41
4:L5:1346:C:H2'	4:L5:1347:G:H8	1.85	0.41
4:L5:2906:G:H1'	4:L5:2908:U:H1'	2.02	0.41
4:L5:3656:A:H2'	4:L5:3657:U:H6	1.85	0.41
17:LL:90:VAL:HA	17:LL:93:THR:HB	2.01	0.41
23:LR:78:ILE:HD13	23:LR:78:ILE:HA	1.92	0.41
31:LZ:117:LYS:HA	31:LZ:117:LYS:HD3	1.86	0.41
31:LZ:135:ARG:HD2	31:LZ:135:ARG:HA	1.74	0.41
52:NB:80:GLN:HG3	52:NB:89:THR:HB	2.02	0.41
56:SC:253:PRO:HA	56:SC:256:TRP:CG	2.55	0.41
58:SE:153:LEU:N	60:SG:216:ARG:HH22	2.18	0.41
63:SJ:22:LYS:HD3	63:SJ:22:LYS:HA	1.75	0.41
67:SN:118:ILE:HG22	67:SN:121:ARG:HH21	1.86	0.41
70:SQ:12:VAL:O	70:SQ:22:VAL:HA	2.19	0.41
79:SZ:102:LYS:HA	79:SZ:102:LYS:HD2	1.79	0.41
3:CD:284:LEU:HD11	64:SK:16:PHE:HD2	1.85	0.41
4:L5:1278:C:H2'	4:L5:1279:A:O4'	2.20	0.41
4:L5:1298:C:H2'	4:L5:1299:G:H8	1.84	0.41
4:L5:2303:C:H5''	36:Le:104:SER:HB3	2.02	0.41
4:L5:2730:U:H2'	4:L5:2731:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:LD:160:PHE:HA	10:LD:163:LEU:HB3	2.01	0.41
11:LE:180:VAL:HG21	11:LE:258:LEU:HD11	2.02	0.41
14:LH:89:ARG:HB2	14:LH:187:VAL:HG12	2.03	0.41
16:LJ:50:PHE:CD2	16:LJ:67:LYS:HE2	2.55	0.41
19:LN:146:PRO:HB2	39:Lh:104:THR:HG23	2.01	0.41
24:LS:47:PHE:HE1	24:LS:125:GLN:HG3	1.85	0.41
24:LS:85:ASP:HA	24:LS:90:THR:HA	2.01	0.41
43:Ll:9:ILE:HD12	43:Ll:51:LEU:HD11	2.02	0.41
53:S2:161:U:H5'	78:SY:116:LYS:HD2	2.01	0.41
53:S2:1777:G:H2'	53:S2:1778:C:C6	2.56	0.41
70:SQ:51:LEU:HD13	70:SQ:81:ILE:HB	2.03	0.41
84:Se:18:LYS:HD3	84:Se:18:LYS:HA	1.84	0.41
1:CB:272:LYS:HA	1:CB:272:LYS:HD2	1.87	0.41
2:CC:23:G:H2'	2:CC:24:G:H8	1.86	0.41
4:L5:1996:C:N4	4:L5:2000:G:H22	2.17	0.41
4:L5:2082:G:H5''	22:LQ:12:LYS:HG3	2.02	0.41
4:L5:3771:C:H2'	4:L5:3772:U:C6	2.56	0.41
4:L5:4507:A:H2'	4:L5:4508:C:C6	2.55	0.41
9:LC:140:LYS:HD2	9:LC:140:LYS:HA	1.83	0.41
15:LI:36:LEU:HD11	15:LI:69:ARG:HD2	2.02	0.41
15:LI:192:PRO:HA	15:LI:197:VAL:HG12	2.02	0.41
25:LT:71:ALA:HA	25:LT:92:ARG:HA	2.02	0.41
52:NB:59:ILE:HG13	52:NB:79:VAL:HG21	2.03	0.41
53:S2:441:C:H2'	53:S2:442:C:C6	2.55	0.41
54:SA:66:VAL:HG21	54:SA:185:MET:HG2	2.02	0.41
55:SB:68:GLU:HA	55:SB:84:PHE:O	2.20	0.41
62:SI:10:LYS:HE3	65:SL:136:LYS:HZ2	1.86	0.41
62:SI:139:LYS:HE2	62:SI:139:LYS:HB2	1.89	0.41
70:SQ:45:ARG:NH1	70:SQ:48:GLN:HB3	2.36	0.41
72:SS:26:ILE:HD13	72:SS:45:LEU:HD11	2.02	0.41
78:SY:129:LYS:HA	78:SY:129:LYS:HD3	1.89	0.41
80:Sa:100:ARG:HD2	80:Sa:100:ARG:HA	1.93	0.41
82:Sc:20:ARG:HB3	82:Sc:25:GLY:HA2	2.02	0.41
84:Se:37:GLN:HA	84:Se:40:ARG:HG3	2.02	0.41
86:Sg:175:LYS:HE3	86:Sg:175:LYS:HB2	1.78	0.41
1:CB:599:HIS:HB3	1:CB:710:HIS:HB2	2.03	0.41
4:L5:218:A:H1'	4:L5:219:G:C8	2.56	0.41
4:L5:1348:U:H2'	4:L5:1349:G:H8	1.85	0.41
4:L5:1461:C:H2'	4:L5:1462:A:H8	1.85	0.41
4:L5:2693:G:H2'	4:L5:2694:G:N2	2.36	0.41
4:L5:3717:A:H2'	4:L5:3718:A:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:LM:38:VAL:HG21	18:LM:50:MET:HB3	2.02	0.41
40:Li:68:ARG:NH2	40:Li:71:LYS:HE3	2.35	0.41
50:N4:59:CYS:HB2	50:N4:109:LEU:HD23	2.02	0.41
50:N4:173:LEU:HD22	50:N4:174:THR:H	1.85	0.41
53:S2:89:C:H2'	53:S2:90:G:H8	1.85	0.41
53:S2:1010:G:H2'	53:S2:1011:A:C8	2.55	0.41
54:SA:12:GLU:HG3	71:SR:114:LEU:HD11	2.02	0.41
56:SC:278:THR:HA	56:SC:279:ARG:HA	1.68	0.41
69:SP:17:TYR:HE2	69:SP:36:LEU:HG	1.86	0.41
79:SZ:94:LYS:HE2	79:SZ:94:LYS:N	2.35	0.41
1:CB:750:GLN:HG3	1:CB:783:VAL:HG22	2.01	0.41
4:L5:189:G:H2'	4:L5:190:G:H8	1.85	0.41
4:L5:207:G:H5''	50:N4:12:LYS:HD2	2.02	0.41
4:L5:460:C:H2'	4:L5:461:G:C8	2.56	0.41
4:L5:679:C:H2'	4:L5:680:G:C8	2.56	0.41
4:L5:4122:G:H4'	38:Lg:90:ARG:HG2	2.01	0.41
4:L5:4894:A:H3'	4:L5:4895:C:H5'	2.02	0.41
4:L5:4951:G:H2'	4:L5:4952:G:H8	1.86	0.41
38:Lg:108:LYS:HA	38:Lg:108:LYS:HD2	1.91	0.41
48:Lr:37:SER:HB3	48:Lr:40:TYR:HB2	2.02	0.41
51:NA:101:ASN:HB2	51:NA:131:LEU:HB3	2.02	0.41
52:NB:19:ARG:HD2	52:NB:19:ARG:HA	1.89	0.41
53:S2:496:C:H2'	53:S2:497:C:H6	1.85	0.41
53:S2:867:G:H2'	53:S2:868:G:N3	2.35	0.41
53:S2:1858:G:H2'	53:S2:1859:A:H8	1.86	0.41
54:SA:26:GLY:H	54:SA:46:ILE:HG22	1.85	0.41
70:SQ:113:ILE:HD13	70:SQ:113:ILE:HA	1.96	0.41
76:SW:51:GLU:HB3	76:SW:62:VAL:HG23	2.02	0.41
1:CB:146:ALA:HA	1:CB:151:ILE:HD12	2.03	0.41
4:L5:753:C:H5	4:L5:910:G:H22	1.68	0.41
4:L5:908:G:H2'	4:L5:909:A:H8	1.85	0.41
4:L5:1676:C:H41	4:L5:4378:A:H5''	1.85	0.41
4:L5:1852:U:H5''	32:La:22:ILE:HD12	2.03	0.41
4:L5:4934:A:H2'	4:L5:4935:C:C6	2.55	0.41
7:LA:107:MET:HE2	7:LA:166:VAL:HG22	2.01	0.41
7:LA:177:LYS:HD2	47:Lp:69:TRP:CH2	2.56	0.41
8:LB:47:LEU:HD12	8:LB:47:LEU:HA	1.92	0.41
9:LC:28:PHE:CD1	9:LC:132:ALA:HB2	2.55	0.41
14:LH:59:LYS:HD2	14:LH:59:LYS:HA	1.67	0.41
14:LH:65:LYS:HD3	14:LH:65:LYS:HA	1.91	0.41
28:LW:71:ARG:HA	28:LW:71:ARG:HD2	1.74	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:Lc:21:VAL:HG21	34:Lc:96:ILE:HD12	2.03	0.41
52:NB:78:LYS:HB3	52:NB:91:THR:HB	2.03	0.41
53:S2:15:U:H2'	53:S2:16:G:O4'	2.21	0.41
53:S2:1308:U:H2'	53:S2:1309:C:H6	1.85	0.41
53:S2:1649:U:H2'	53:S2:1650:A:H8	1.86	0.41
54:SA:55:TRP:CZ2	54:SA:59:LEU:HD21	2.56	0.41
55:SB:124:HIS:HB3	55:SB:138:PHE:CD2	2.56	0.41
56:SC:182:CYS:SG	76:SW:95:PRO:HB2	2.60	0.41
57:SD:29:LEU:HB2	57:SD:34:TYR:HB2	2.02	0.41
58:SE:80:ILE:HD12	58:SE:80:ILE:HA	1.88	0.41
63:SJ:100:LEU:HD13	63:SJ:105:PHE:HE1	1.85	0.41
63:SJ:124:HIS:HA	84:Se:31:ARG:HH22	1.86	0.41
78:SY:44:LEU:HA	78:SY:47:MET:SD	2.61	0.41
86:Sg:299:PHE:HD1	86:Sg:309:VAL:HG12	1.86	0.41
1:CB:654:PRO:HG3	1:CB:687:THR:HG22	2.01	0.41
1:CB:820:LEU:HA	1:CB:821:PRO:HD3	1.96	0.41
4:L5:162:A:H2'	4:L5:163:A:H8	1.86	0.41
4:L5:300:A:H2'	4:L5:301:G:C8	2.54	0.41
4:L5:1220:G:H2'	4:L5:1221:G:C8	2.56	0.41
4:L5:4169:G:H4'	4:L5:4171:C:C2	2.55	0.41
4:L5:4458:C:H2'	4:L5:4459:U:C6	2.56	0.41
7:LA:145:LYS:HD2	7:LA:159:SER:HA	2.03	0.41
8:LB:50:LYS:HD2	8:LB:337:VAL:HG12	2.01	0.41
8:LB:382:MET:O	8:LB:386:LYS:HG2	2.21	0.41
10:LD:53:VAL:HG11	10:LD:159:VAL:HA	2.03	0.41
16:LJ:24:ILE:HD12	16:LJ:40:LEU:HG	2.02	0.41
17:LL:37:LYS:HE2	17:LL:37:LYS:HB3	1.82	0.41
21:LP:36:ILE:HD13	21:LP:36:ILE:HA	1.84	0.41
21:LP:94:MET:HG2	21:LP:148:MET:SD	2.61	0.41
25:LT:120:LYS:HA	25:LT:120:LYS:HD2	1.79	0.41
26:LU:34:MET:HE3	26:LU:34:MET:HB3	1.90	0.41
29:LX:156:ILE:HD12	29:LX:156:ILE:HA	1.98	0.41
32:La:119:LYS:HB3	32:La:119:LYS:HE3	1.74	0.41
34:Lc:21:VAL:HG21	34:Lc:96:ILE:HG23	2.03	0.41
40:Li:89:GLU:O	40:Li:93:VAL:HG13	2.21	0.41
43:Ll:9:ILE:HG23	43:Ll:51:LEU:HD21	2.03	0.41
51:NA:113:LYS:HA	51:NA:113:LYS:HD2	1.95	0.41
53:S2:907:G:H2'	53:S2:908:A:C8	2.56	0.41
53:S2:1256:G:C8	74:SU:66:ARG:HB2	2.56	0.41
53:S2:1362:U:H5''	53:S2:1363:C:C5	2.56	0.41
53:S2:1508:A:N7	53:S2:1510:G:C6	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:SB:49:VAL:HG21	55:SB:62:LEU:HD22	2.03	0.41
58:SE:62:LYS:HE3	58:SE:62:LYS:HB3	1.94	0.41
58:SE:229:GLY:HA3	58:SE:234:PRO:HA	2.02	0.41
59:SF:99:ILE:HD13	59:SF:171:GLU:HB3	2.02	0.41
60:SG:3:LEU:HG	60:SG:18:VAL:HG11	2.03	0.41
61:SH:147:LYS:HA	61:SH:147:LYS:HE3	2.02	0.41
62:SI:190:LEU:HD23	62:SI:190:LEU:H	1.86	0.41
63:SJ:40:LYS:HA	63:SJ:43:VAL:HB	2.02	0.41
64:SK:89:ILE:HD13	64:SK:89:ILE:HA	1.92	0.41
66:SM:23:LYS:HD3	66:SM:23:LYS:HA	1.82	0.41
67:SN:32:ASP:O	67:SN:35:GLU:HG3	2.21	0.41
71:SR:67:ARG:HA	71:SR:68:GLY:HA3	1.60	0.41
82:Sc:12:ALA:HA	82:Sc:33:GLU:O	2.21	0.41
83:Sd:13:LYS:HG3	83:Sd:14:PHE:H	1.86	0.41
1:CB:358:LEU:HD23	1:CB:358:LEU:HA	1.88	0.41
1:CB:813:VAL:HG23	1:CB:814:PHE:H	1.86	0.41
5:L7:58:A:H2'	5:L7:59:G:C8	2.56	0.41
9:LC:149:GLU:HG2	48:Lr:72:LYS:HG2	2.02	0.41
13:LG:190:LEU:HB3	13:LG:199:CYS:HB3	2.02	0.41
14:LH:4:ILE:HG12	14:LH:61:TRP:CH2	2.56	0.41
16:LJ:33:LEU:HD12	16:LJ:33:LEU:HA	1.89	0.41
34:Lc:10:SER:O	34:Lc:14:ILE:HG22	2.21	0.41
37:Lf:43:LEU:HD12	37:Lf:43:LEU:HA	1.84	0.41
43:Ll:44:TRP:CZ3	43:Ll:45:ARG:HD3	2.56	0.41
52:NB:46:PHE:HA	52:NB:49:LYS:HD2	2.03	0.41
52:NB:65:PHE:HE1	52:NB:106:ILE:HD11	1.84	0.41
53:S2:107:A:H2'	53:S2:108:G:H8	1.86	0.41
53:S2:184:G:H2'	53:S2:185:G:C8	2.56	0.41
53:S2:1653:U:H2'	53:S2:1654:G:C8	2.56	0.41
54:SA:148:CYS:SG	54:SA:160:ALA:HB1	2.61	0.41
60:SG:32:MET:HE3	60:SG:33:ALA:H	1.85	0.41
63:SJ:107:GLU:HG3	63:SJ:108:ARG:HD2	2.03	0.41
65:SL:77:VAL:HA	65:SL:88:ILE:HG22	2.02	0.41
69:SP:95:GLY:HA3	69:SP:102:PHE:HB3	2.03	0.41
75:SV:37:ALA:HA	75:SV:50:PHE:HB3	2.03	0.41
1:CB:354:ILE:O	1:CB:358:LEU:HB2	2.21	0.40
1:CB:580:ARG:HD3	1:CB:580:ARG:HA	1.88	0.40
1:CB:781:MET:HE2	1:CB:781:MET:HA	2.03	0.40
4:L5:86:U:H2'	4:L5:87:A:C8	2.56	0.40
4:L5:418:A:C2	6:L8:17:A:H1'	2.56	0.40
4:L5:1762:C:H6	4:L5:1762:C:H2'	1.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:LU:78:PHE:HE2	26:LU:83:LEU:HG	1.86	0.40
37:Lf:36:ARG:HD2	37:Lf:80:ASN:H	1.86	0.40
53:S2:818:A:H2'	53:S2:819:G:C8	2.56	0.40
53:S2:1181:A:H2'	53:S2:1182:A:C8	2.56	0.40
53:S2:1452:A:H61	53:S2:1473:G:N2	2.20	0.40
55:SB:172:MET:HE2	55:SB:172:MET:HB2	1.92	0.40
67:SN:40:LEU:HD23	67:SN:50:ILE:HG12	2.03	0.40
72:SS:41:ALA:O	72:SS:45:LEU:HD23	2.21	0.40
76:SW:53:ILE:HD11	81:Sb:25:VAL:HG22	2.03	0.40
77:SX:80:LYS:HA	77:SX:80:LYS:HD3	1.84	0.40
86:Sg:208:ALA:HA	86:Sg:218:LEU:HA	2.03	0.40
2:CC:13:G:H21	2:CC:22:A:H62	1.68	0.40
4:L5:1346:C:H2'	4:L5:1347:G:C8	2.55	0.40
4:L5:2461:G:H2'	4:L5:2462:C:C6	2.57	0.40
4:L5:4323:A:C8	10:LD:153:THR:HG21	2.56	0.40
6:L8:96:C:H5''	39:Lh:66:LYS:HG2	2.02	0.40
16:LJ:24:ILE:HB	16:LJ:70:VAL:HG23	2.02	0.40
24:LS:78:PHE:O	24:LS:96:GLU:HA	2.22	0.40
38:Lg:88:ARG:O	38:Lg:92:LYS:HG2	2.21	0.40
39:Lh:16:GLU:H	39:Lh:16:GLU:HG2	1.64	0.40
51:NA:68:LYS:HE3	51:NA:68:LYS:HB3	1.85	0.40
66:SM:125:GLU:HA	66:SM:128:PHE:CZ	2.56	0.40
73:ST:59:SER:HA	73:ST:62:ARG:HG3	2.03	0.40
73:ST:144:LYS:HA	73:ST:144:LYS:HD2	1.77	0.40
76:SW:90:GLN:O	76:SW:94:LEU:HB2	2.21	0.40
1:CB:61:LYS:HA	1:CB:61:LYS:HD3	1.90	0.40
1:CB:256:MET:O	1:CB:260:LEU:HB2	2.21	0.40
1:CB:531:ASP:HB3	1:CB:534:VAL:HG12	2.03	0.40
4:L5:1577:G:H5'	4:L5:1578:U:H5''	2.02	0.40
4:L5:1709:C:H42	4:L5:1716:G:N2	2.17	0.40
4:L5:3599:A:H2'	4:L5:3600:G:C8	2.55	0.40
4:L5:4149:C:H5'	31:LZ:60:LYS:NZ	2.36	0.40
5:L7:55:A:H4'	16:LJ:155:HIS:HB2	2.03	0.40
6:L8:8:U:H2'	6:L8:9:A:H8	1.86	0.40
9:LC:133:LEU:HA	9:LC:133:LEU:HD23	1.86	0.40
9:LC:281:MET:HE3	9:LC:281:MET:HB3	1.92	0.40
13:LG:193:LEU:HD12	13:LG:193:LEU:HA	1.94	0.40
49:Lz:200:ASN:OD1	49:Lz:201:VAL:HG23	2.22	0.40
53:S2:386:C:H2'	53:S2:387:C:C6	2.57	0.40
53:S2:433:A:H2'	53:S2:434:G:C8	2.57	0.40
54:SA:38:ILE:HD13	54:SA:38:ILE:HA	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:SG:23:LYS:HA	60:SG:23:LYS:HD2	1.75	0.40
60:SG:181:THR:HB	60:SG:184:VAL:HG23	2.03	0.40
62:SI:38:ILE:HD13	62:SI:80:ASP:HA	2.04	0.40
62:SI:87:ASN:HB3	62:SI:90:LEU:HB2	2.03	0.40
75:SV:12:TYR:CE1	75:SV:14:PRO:HA	2.57	0.40
1:CB:106:PRO:HG2	1:CB:114:GLU:HG3	2.02	0.40
2:CC:15:G:N2	2:CC:57:C:C2	2.86	0.40
4:L5:1307:A:H2'	4:L5:1308:C:C6	2.57	0.40
4:L5:1779:U:H2'	4:L5:1780:A:C8	2.56	0.40
4:L5:2844:A:O2'	4:L5:4631:G:H4'	2.21	0.40
4:L5:3701:C:N4	4:L5:3745:U:H2'	2.37	0.40
4:L5:3919:C:H5''	7:LA:207:VAL:HG13	2.03	0.40
4:L5:4174:U:H2'	4:L5:4175:G:H8	1.86	0.40
4:L5:4625:C:OP1	8:LB:224:LYS:HG3	2.22	0.40
8:LB:397:ILE:HD12	8:LB:397:ILE:HA	1.91	0.40
29:LX:81:LEU:HG	29:LX:83:THR:HG23	2.02	0.40
33:Lb:101:HIS:HA	33:Lb:102:PRO:HD3	1.99	0.40
36:Le:88:LEU:HA	36:Le:88:LEU:HD23	1.85	0.40
38:Lg:61:PRO:O	38:Lg:64:LEU:HB2	2.20	0.40
53:S2:124:U:H5'	58:SE:148:ARG:NH1	2.37	0.40
53:S2:454:U:H2'	53:S2:455:A:C8	2.56	0.40
53:S2:1004:U:H2'	53:S2:1005:G:C8	2.57	0.40
53:S2:1154:U:H2'	56:SC:192:LEU:HD21	2.04	0.40
55:SB:34:LYS:O	55:SB:98:THR:HG22	2.22	0.40
59:SF:151:ILE:HA	59:SF:154:LEU:HG	2.02	0.40
67:SN:54:LEU:HD23	67:SN:54:LEU:HA	1.96	0.40
73:ST:75:MET:SD	73:ST:100:ALA:HB2	2.61	0.40
78:SY:18:LEU:HB3	78:SY:20:ARG:HE	1.87	0.40
1:CB:275:LYS:HE3	1:CB:275:LYS:HB3	1.92	0.40
4:L5:132:G:H2'	4:L5:133:C:H4'	2.03	0.40
4:L5:461:G:H2'	4:L5:462:G:H8	1.86	0.40
4:L5:1509:C:H5''	32:La:2:PRO:HD2	2.02	0.40
4:L5:2347:A:C4	36:Le:31:ILE:HD11	2.57	0.40
4:L5:3723:A:H2'	4:L5:3724:A:H8	1.85	0.40
4:L5:3856:A:H5''	21:LP:83:TRP:O	2.21	0.40
8:LB:113:GLU:HB2	8:LB:178:ALA:HB2	2.02	0.40
14:LH:92:MET:HE2	14:LH:179:ILE:HG22	2.03	0.40
16:LJ:19:LYS:H	16:LJ:19:LYS:HG3	1.61	0.40
18:LM:10:GLY:HA2	18:LM:64:PHE:CZ	2.56	0.40
19:LN:22:LEU:HB3	19:LN:26:ARG:HH21	1.87	0.40
22:LQ:159:PRO:HA	22:LQ:160:HIS:HA	1.62	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:LT:44:GLY:HA2	25:LT:95:HIS:HD1	1.86	0.40
53:S2:886:A:C5	53:S2:901:G:C2	3.10	0.40
58:SE:206:ASP:HB2	58:SE:222:LEU:HB2	2.03	0.40
60:SG:30:LYS:HD3	60:SG:30:LYS:HA	1.92	0.40
63:SJ:32:ILE:HA	63:SJ:37:LEU:HD12	2.02	0.40
68:SO:42:VAL:HG13	68:SO:81:VAL:HG21	2.04	0.40
72:SS:40:TYR:HA	72:SS:43:VAL:HG12	2.03	0.40
77:SX:85:VAL:HG12	77:SX:122:VAL:HB	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CB	842/858 (98%)	788 (94%)	54 (6%)	0	100	100
3	CD	51/402 (13%)	48 (94%)	3 (6%)	0	100	100
7	LA	246/257 (96%)	226 (92%)	19 (8%)	1 (0%)	30	51
8	LB	400/403 (99%)	376 (94%)	23 (6%)	1 (0%)	36	57
9	LC	366/427 (86%)	339 (93%)	27 (7%)	0	100	100
10	LD	291/297 (98%)	274 (94%)	17 (6%)	0	100	100
11	LE	232/288 (81%)	216 (93%)	16 (7%)	0	100	100
12	LF	223/248 (90%)	216 (97%)	7 (3%)	0	100	100
13	LG	239/266 (90%)	225 (94%)	14 (6%)	0	100	100
14	LH	188/192 (98%)	173 (92%)	15 (8%)	0	100	100
15	LI	198/214 (92%)	185 (93%)	13 (7%)	0	100	100
16	LJ	174/178 (98%)	160 (92%)	14 (8%)	0	100	100
17	LL	208/211 (99%)	192 (92%)	16 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	LM	137/215 (64%)	128 (93%)	8 (6%)	1 (1%)	18	37
19	LN	201/204 (98%)	191 (95%)	8 (4%)	2 (1%)	12	28
20	LO	199/203 (98%)	193 (97%)	6 (3%)	0	100	100
21	LP	151/184 (82%)	143 (95%)	8 (5%)	0	100	100
22	LQ	185/188 (98%)	177 (96%)	8 (4%)	0	100	100
23	LR	185/196 (94%)	182 (98%)	3 (2%)	0	100	100
24	LS	173/176 (98%)	161 (93%)	12 (7%)	0	100	100
25	LT	157/160 (98%)	146 (93%)	11 (7%)	0	100	100
26	LU	99/128 (77%)	94 (95%)	5 (5%)	0	100	100
27	LV	129/140 (92%)	122 (95%)	7 (5%)	0	100	100
28	LW	114/157 (73%)	108 (95%)	6 (5%)	0	100	100
29	LX	118/156 (76%)	115 (98%)	3 (2%)	0	100	100
30	LY	132/145 (91%)	127 (96%)	5 (4%)	0	100	100
31	LZ	133/136 (98%)	121 (91%)	12 (9%)	0	100	100
32	La	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
33	Lb	105/159 (66%)	97 (92%)	8 (8%)	0	100	100
34	Lc	96/115 (84%)	88 (92%)	8 (8%)	0	100	100
35	Ld	105/125 (84%)	99 (94%)	6 (6%)	0	100	100
36	Le	126/135 (93%)	120 (95%)	6 (5%)	0	100	100
37	Lf	107/110 (97%)	99 (92%)	7 (6%)	1 (1%)	14	31
38	Lg	112/117 (96%)	111 (99%)	1 (1%)	0	100	100
39	Lh	120/123 (98%)	117 (98%)	3 (2%)	0	100	100
40	Li	100/105 (95%)	96 (96%)	4 (4%)	0	100	100
41	Lj	84/97 (87%)	74 (88%)	10 (12%)	0	100	100
42	Lk	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
43	Ll	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
44	Lm	50/128 (39%)	50 (100%)	0	0	100	100
45	Ln	22/25 (88%)	22 (100%)	0	0	100	100
46	Lo	103/106 (97%)	97 (94%)	6 (6%)	0	100	100
47	Lp	89/92 (97%)	86 (97%)	3 (3%)	0	100	100
48	Lr	123/137 (90%)	116 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	Lz	215/217 (99%)	164 (76%)	51 (24%)	0	100	100
50	N4	219/237 (92%)	213 (97%)	6 (3%)	0	100	100
51	NA	101/215 (47%)	96 (95%)	5 (5%)	0	100	100
52	NB	102/206 (50%)	99 (97%)	2 (2%)	1 (1%)	12	28
54	SA	219/295 (74%)	197 (90%)	22 (10%)	0	100	100
55	SB	212/264 (80%)	205 (97%)	7 (3%)	0	100	100
56	SC	220/293 (75%)	203 (92%)	17 (8%)	0	100	100
57	SD	225/243 (93%)	202 (90%)	23 (10%)	0	100	100
58	SE	260/263 (99%)	240 (92%)	20 (8%)	0	100	100
59	SF	187/204 (92%)	172 (92%)	15 (8%)	0	100	100
60	SG	235/249 (94%)	219 (93%)	16 (7%)	0	100	100
61	SH	182/194 (94%)	161 (88%)	21 (12%)	0	100	100
62	SI	204/208 (98%)	190 (93%)	14 (7%)	0	100	100
63	SJ	183/194 (94%)	169 (92%)	14 (8%)	0	100	100
64	SK	96/165 (58%)	85 (88%)	11 (12%)	0	100	100
65	SL	151/158 (96%)	139 (92%)	12 (8%)	0	100	100
66	SM	120/132 (91%)	113 (94%)	7 (6%)	0	100	100
67	SN	148/151 (98%)	142 (96%)	6 (4%)	0	100	100
68	SO	138/151 (91%)	124 (90%)	14 (10%)	0	100	100
69	SP	119/145 (82%)	105 (88%)	14 (12%)	0	100	100
70	SQ	142/146 (97%)	131 (92%)	11 (8%)	0	100	100
71	SR	133/135 (98%)	121 (91%)	12 (9%)	0	100	100
72	SS	143/152 (94%)	133 (93%)	10 (7%)	0	100	100
73	ST	141/145 (97%)	130 (92%)	11 (8%)	0	100	100
74	SU	102/119 (86%)	94 (92%)	8 (8%)	0	100	100
75	SV	81/83 (98%)	75 (93%)	6 (7%)	0	100	100
76	SW	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
77	SX	139/143 (97%)	124 (89%)	14 (10%)	1 (1%)	18	37
78	SY	129/133 (97%)	124 (96%)	5 (4%)	0	100	100
79	SZ	73/125 (58%)	58 (80%)	14 (19%)	1 (1%)	9	21
80	Sa	100/115 (87%)	88 (88%)	12 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
81	Sb	81/84 (96%)	74 (91%)	7 (9%)	0	100	100
82	Sc	62/69 (90%)	52 (84%)	10 (16%)	0	100	100
83	Sd	53/56 (95%)	48 (91%)	5 (9%)	0	100	100
84	Se	56/133 (42%)	47 (84%)	9 (16%)	0	100	100
85	Sf	65/156 (42%)	53 (82%)	12 (18%)	0	100	100
86	Sg	311/317 (98%)	269 (86%)	42 (14%)	0	100	100
All	All	12847/14897 (86%)	11924 (93%)	914 (7%)	9 (0%)	49	71

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
52	NB	8	GLN
19	LN	124	ASP
18	LM	88	ALA
79	SZ	50	PHE
8	LB	302	ASN
77	SX	127	ASN
7	LA	55	GLY
19	LN	83	LYS
37	Lf	107	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CB	722/730 (99%)	690 (96%)	32 (4%)	25	50
3	CD	46/322 (14%)	45 (98%)	1 (2%)	45	72
7	LA	190/199 (96%)	177 (93%)	13 (7%)	14	32
8	LB	348/349 (100%)	332 (95%)	16 (5%)	24	48
9	LC	306/348 (88%)	292 (95%)	14 (5%)	24	48
10	LD	246/250 (98%)	237 (96%)	9 (4%)	30	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	LE	209/252 (83%)	198 (95%)	11 (5%)	20	43
12	LF	194/215 (90%)	186 (96%)	8 (4%)	27	52
13	LG	203/223 (91%)	191 (94%)	12 (6%)	18	38
14	LH	169/171 (99%)	152 (90%)	17 (10%)	7	16
15	LI	172/181 (95%)	166 (96%)	6 (4%)	32	58
16	LJ	148/149 (99%)	139 (94%)	9 (6%)	17	37
17	LL	176/177 (99%)	166 (94%)	10 (6%)	18	40
18	LM	118/161 (73%)	114 (97%)	4 (3%)	32	59
19	LN	171/172 (99%)	165 (96%)	6 (4%)	32	58
20	LO	173/174 (99%)	168 (97%)	5 (3%)	37	64
21	LP	134/163 (82%)	130 (97%)	4 (3%)	36	63
22	LQ	164/165 (99%)	159 (97%)	5 (3%)	36	63
23	LR	166/175 (95%)	159 (96%)	7 (4%)	26	52
24	LS	156/157 (99%)	146 (94%)	10 (6%)	16	35
25	LT	139/140 (99%)	135 (97%)	4 (3%)	37	64
26	LU	91/115 (79%)	86 (94%)	5 (6%)	19	41
27	LV	101/107 (94%)	96 (95%)	5 (5%)	22	45
28	LW	97/126 (77%)	95 (98%)	2 (2%)	47	73
29	LX	108/133 (81%)	103 (95%)	5 (5%)	24	48
30	LY	124/135 (92%)	116 (94%)	8 (6%)	15	34
31	LZ	117/118 (99%)	113 (97%)	4 (3%)	32	59
32	La	120/121 (99%)	114 (95%)	6 (5%)	22	45
33	Lb	88/126 (70%)	85 (97%)	3 (3%)	32	59
34	Lc	83/97 (86%)	77 (93%)	6 (7%)	13	29
35	Ld	98/110 (89%)	90 (92%)	8 (8%)	10	24
36	Le	114/121 (94%)	107 (94%)	7 (6%)	17	37
37	Lf	88/89 (99%)	85 (97%)	3 (3%)	32	59
38	Lg	98/100 (98%)	95 (97%)	3 (3%)	35	62
39	Lh	109/110 (99%)	107 (98%)	2 (2%)	51	76
40	Li	86/89 (97%)	85 (99%)	1 (1%)	63	82
41	Lj	73/80 (91%)	72 (99%)	1 (1%)	59	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	Lk	64/65 (98%)	64 (100%)	0	100	100
43	Ll	47/48 (98%)	45 (96%)	2 (4%)	26	51
44	Lm	48/116 (41%)	46 (96%)	2 (4%)	26	52
45	Ln	23/24 (96%)	23 (100%)	0	100	100
46	Lo	93/94 (99%)	87 (94%)	6 (6%)	15	34
47	Lp	74/75 (99%)	72 (97%)	2 (3%)	39	67
48	Lr	109/121 (90%)	105 (96%)	4 (4%)	30	56
49	Lz	195/196 (100%)	188 (96%)	7 (4%)	31	57
50	N4	194/204 (95%)	189 (97%)	5 (3%)	40	68
51	NA	92/183 (50%)	91 (99%)	1 (1%)	65	83
52	NB	88/165 (53%)	84 (96%)	4 (4%)	24	49
54	SA	183/243 (75%)	175 (96%)	8 (4%)	25	50
55	SB	195/231 (84%)	183 (94%)	12 (6%)	16	36
56	SC	188/225 (84%)	176 (94%)	12 (6%)	16	35
57	SD	190/202 (94%)	183 (96%)	7 (4%)	30	56
58	SE	224/225 (100%)	212 (95%)	12 (5%)	20	42
59	SF	159/170 (94%)	154 (97%)	5 (3%)	35	62
60	SG	207/218 (95%)	196 (95%)	11 (5%)	20	43
61	SH	166/174 (95%)	159 (96%)	7 (4%)	26	52
62	SI	178/180 (99%)	171 (96%)	7 (4%)	28	54
63	SJ	161/168 (96%)	158 (98%)	3 (2%)	50	75
64	SK	89/136 (65%)	88 (99%)	1 (1%)	65	83
65	SL	137/142 (96%)	130 (95%)	7 (5%)	21	44
66	SM	102/108 (94%)	98 (96%)	4 (4%)	28	54
67	SN	130/131 (99%)	129 (99%)	1 (1%)	73	87
68	SO	110/119 (92%)	108 (98%)	2 (2%)	51	76
69	SP	107/130 (82%)	98 (92%)	9 (8%)	10	23
70	SQ	119/121 (98%)	118 (99%)	1 (1%)	73	87
71	SR	122/122 (100%)	118 (97%)	4 (3%)	33	60
72	SS	126/132 (96%)	123 (98%)	3 (2%)	43	70
73	ST	113/115 (98%)	107 (95%)	6 (5%)	20	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
74	SU	94/107 (88%)	90 (96%)	4 (4%)	26	51
75	SV	67/67 (100%)	62 (92%)	5 (8%)	12	28
76	SW	112/113 (99%)	102 (91%)	10 (9%)	9	21
77	SX	113/115 (98%)	108 (96%)	5 (4%)	25	50
78	SY	113/115 (98%)	109 (96%)	4 (4%)	32	58
79	SZ	66/103 (64%)	61 (92%)	5 (8%)	12	27
80	Sa	89/98 (91%)	86 (97%)	3 (3%)	32	59
81	Sb	75/76 (99%)	71 (95%)	4 (5%)	20	43
82	Sc	57/62 (92%)	55 (96%)	2 (4%)	32	58
83	Sd	48/49 (98%)	47 (98%)	1 (2%)	47	73
84	Se	47/104 (45%)	46 (98%)	1 (2%)	47	73
85	Sf	60/140 (43%)	57 (95%)	3 (5%)	22	45
86	Sg	272/275 (99%)	262 (96%)	10 (4%)	30	56
All	All	11191/12657 (88%)	10707 (96%)	484 (4%)	27	51

All (484) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	CB	24	VAL
1	CB	28	VAL
1	CB	66	ARG
1	CB	122	THR
1	CB	128	VAL
1	CB	135	VAL
1	CB	174	LEU
1	CB	253	VAL
1	CB	288	THR
1	CB	351	LEU
1	CB	413	PHE
1	CB	442	LEU
1	CB	458	VAL
1	CB	479	LEU
1	CB	504	VAL
1	CB	534	VAL
1	CB	537	ILE
1	CB	589	VAL
1	CB	616	ASP

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Mol	Chain	Res	Type
1	CB	679	VAL
1	CB	700	VAL
1	CB	704	VAL
1	CB	712	ASP
1	CB	714	ILE
1	CB	745	TYR
1	CB	747	VAL
1	CB	776	VAL
1	CB	784	VAL
1	CB	790	VAL
1	CB	802	SER
1	CB	848	ILE
1	CB	851	LEU
3	CD	221	VAL
7	LA	4	VAL
7	LA	15	VAL
7	LA	44	ILE
7	LA	45	VAL
7	LA	102	LEU
7	LA	140	ASN
7	LA	146	THR
7	LA	169	VAL
7	LA	207	VAL
7	LA	228	ASP
7	LA	234	LYS
7	LA	243	THR
7	LA	245	ARG
8	LB	3	HIS
8	LB	34	LYS
8	LB	39	LYS
8	LB	74	GLU
8	LB	136	LYS
8	LB	148	LYS
8	LB	153	MET
8	LB	159	VAL
8	LB	162	VAL
8	LB	209	GLN
8	LB	254	ILE
8	LB	258	HIS
8	LB	317	LEU
8	LB	337	VAL
8	LB	338	VAL

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Mol	Chain	Res	Type
8	LB	362	LYS
9	LC	8	ILE
9	LC	48	ASN
9	LC	57	LEU
9	LC	61	GLN
9	LC	71	ARG
9	LC	118	THR
9	LC	147	VAL
9	LC	158	VAL
9	LC	174	LEU
9	LC	189	MET
9	LC	262	GLU
9	LC	285	ILE
9	LC	334	THR
9	LC	348	LYS
10	LD	6	VAL
10	LD	28	THR
10	LD	37	VAL
10	LD	61	ILE
10	LD	89	LYS
10	LD	120	GLU
10	LD	123	VAL
10	LD	204	VAL
10	LD	239	MET
11	LE	88	VAL
11	LE	105	ARG
11	LE	106	VAL
11	LE	107	VAL
11	LE	128	HIS
11	LE	137	VAL
11	LE	163	VAL
11	LE	172	LEU
11	LE	227	HIS
11	LE	257	ILE
11	LE	264	ILE
12	LF	33	LEU
12	LF	36	LYS
12	LF	86	GLU
12	LF	88	LYS
12	LF	121	THR
12	LF	171	ASP
12	LF	178	SER

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Mol	Chain	Res	Type
12	LF	248	ASN
13	LG	80	ILE
13	LG	84	THR
13	LG	89	ARG
13	LG	91	THR
13	LG	140	VAL
13	LG	179	VAL
13	LG	193	LEU
13	LG	202	VAL
13	LG	207	VAL
13	LG	241	VAL
13	LG	261	LEU
13	LG	264	LYS
14	LH	9	THR
14	LH	16	VAL
14	LH	19	THR
14	LH	52	LYS
14	LH	57	VAL
14	LH	66	GLU
14	LH	75	SER
14	LH	86	LEU
14	LH	89	ARG
14	LH	104	VAL
14	LH	106	GLN
14	LH	110	SER
14	LH	140	GLN
14	LH	146	LEU
14	LH	161	ILE
14	LH	183	GLU
14	LH	187	VAL
15	LI	45	GLU
15	LI	53	VAL
15	LI	121	LYS
15	LI	125	THR
15	LI	142	LEU
15	LI	189	CYS
16	LJ	39	VAL
16	LJ	47	THR
16	LJ	60	PHE
16	LJ	94	LEU
16	LJ	123	ILE
16	LJ	132	VAL

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Mol	Chain	Res	Type
16	LJ	133	VAL
16	LJ	143	ASP
16	LJ	148	THR
17	LL	17	ASP
17	LL	55	ILE
17	LL	59	VAL
17	LL	63	THR
17	LL	70	VAL
17	LL	86	ILE
17	LL	90	VAL
17	LL	150	LEU
17	LL	194	ILE
17	LL	207	VAL
18	LM	25	VAL
18	LM	38	VAL
18	LM	69	HIS
18	LM	90	ARG
19	LN	10	LEU
19	LN	26	ARG
19	LN	60	VAL
19	LN	100	SER
19	LN	155	VAL
19	LN	187	SER
20	LO	4	VAL
20	LO	27	VAL
20	LO	61	ARG
20	LO	119	VAL
20	LO	145	VAL
21	LP	57	CYS
21	LP	76	TRP
21	LP	112	LEU
21	LP	115	GLU
22	LQ	29	VAL
22	LQ	83	VAL
22	LQ	107	SER
22	LQ	137	VAL
22	LQ	176	ARG
23	LR	6	LEU
23	LR	13	SER
23	LR	31	GLU
23	LR	55	VAL
23	LR	125	LEU

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Mol	Chain	Res	Type
23	LR	155	LEU
23	LR	182	GLU
24	LS	16	CYS
24	LS	48	VAL
24	LS	58	SER
24	LS	70	LYS
24	LS	90	THR
24	LS	95	ARG
24	LS	126	ILE
24	LS	135	SER
24	LS	168	THR
24	LS	169	THR
25	LT	29	THR
25	LT	72	VAL
25	LT	104	SER
25	LT	109	VAL
26	LU	17	GLN
26	LU	29	VAL
26	LU	61	VAL
26	LU	71	THR
26	LU	73	THR
27	LV	22	VAL
27	LV	65	VAL
27	LV	71	GLU
27	LV	72	LEU
27	LV	92	ASP
28	LW	12	LYS
28	LW	78	PHE
29	LX	40	ILE
29	LX	102	VAL
29	LX	115	LYS
29	LX	116	LEU
29	LX	121	VAL
30	LY	8	THR
30	LY	44	VAL
30	LY	46	SER
30	LY	55	VAL
30	LY	56	GLN
30	LY	79	VAL
30	LY	91	ASN
30	LY	130	LYS
31	LZ	11	VAL

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Mol	Chain	Res	Type
31	LZ	43	VAL
31	LZ	100	VAL
31	LZ	106	LEU
32	La	12	ARG
32	La	68	SER
32	La	78	LEU
32	La	103	VAL
32	La	106	SER
32	La	140	VAL
33	Lb	19	ASN
33	Lb	41	ARG
33	Lb	107	ARG
34	Lc	20	LEU
34	Lc	28	VAL
34	Lc	35	LEU
34	Lc	46	VAL
34	Lc	87	LYS
34	Lc	93	THR
35	Ld	24	GLU
35	Ld	26	THR
35	Ld	33	ILE
35	Ld	36	VAL
35	Ld	46	LEU
35	Ld	62	VAL
35	Ld	106	VAL
35	Ld	112	THR
36	Le	17	THR
36	Le	45	VAL
36	Le	87	VAL
36	Le	89	LEU
36	Le	94	SER
36	Le	113	GLU
36	Le	129	LEU
37	Lf	33	VAL
37	Lf	57	THR
37	Lf	63	LYS
38	Lg	23	SER
38	Lg	63	VAL
38	Lg	85	LYS
39	Lh	16	GLU
39	Lh	88	THR
40	Li	18	THR

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Mol	Chain	Res	Type
41	Lj	10	LYS
43	Ll	11	ARG
43	Ll	47	THR
44	Lm	79	GLU
44	Lm	127	VAL
46	Lo	2	VAL
46	Lo	7	THR
46	Lo	13	LYS
46	Lo	24	THR
46	Lo	77	CYS
46	Lo	96	ASP
47	Lp	52	VAL
47	Lp	75	SER
48	Lr	49	VAL
48	Lr	63	VAL
48	Lr	80	THR
48	Lr	124	VAL
49	Lz	22	GLN
49	Lz	72	GLN
49	Lz	73	HIS
49	Lz	99	LEU
49	Lz	163	LEU
49	Lz	172	VAL
49	Lz	177	ASP
50	N4	83	THR
50	N4	99	GLU
50	N4	140	VAL
50	N4	180	HIS
50	N4	214	LEU
51	NA	107	THR
52	NB	18	VAL
52	NB	33	VAL
52	NB	48	LEU
52	NB	79	VAL
54	SA	18	PHE
54	SA	30	LEU
54	SA	38	ILE
54	SA	69	GLU
54	SA	134	LEU
54	SA	136	GLU
54	SA	144	THR
54	SA	202	TYR

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Mol	Chain	Res	Type
55	SB	33	VAL
55	SB	90	ASP
55	SB	119	THR
55	SB	120	MET
55	SB	124	HIS
55	SB	125	VAL
55	SB	170	GLU
55	SB	177	GLN
55	SB	181	LEU
55	SB	209	ASP
55	SB	228	LEU
55	SB	231	LEU
56	SC	64	THR
56	SC	68	ARG
56	SC	86	LEU
56	SC	93	ILE
56	SC	101	SER
56	SC	120	GLN
56	SC	128	VAL
56	SC	180	VAL
56	SC	204	ILE
56	SC	247	THR
56	SC	268	GLU
56	SC	280	VAL
57	SD	4	GLN
57	SD	49	ILE
57	SD	110	LEU
57	SD	167	TYR
57	SD	170	THR
57	SD	186	VAL
57	SD	190	LEU
58	SE	38	LEU
58	SE	44	LEU
58	SE	45	ILE
58	SE	69	PHE
58	SE	121	TYR
58	SE	126	VAL
58	SE	138	HIS
58	SE	140	VAL
58	SE	194	VAL
58	SE	196	THR
58	SE	246	LEU

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Mol	Chain	Res	Type
58	SE	256	LEU
59	SF	36	GLN
59	SF	72	LEU
59	SF	73	THR
59	SF	153	LEU
59	SF	167	LYS
60	SG	10	THR
60	SG	49	VAL
60	SG	67	VAL
60	SG	75	LEU
60	SG	102	VAL
60	SG	106	LEU
60	SG	112	VAL
60	SG	129	VAL
60	SG	133	LEU
60	SG	162	LEU
60	SG	212	LEU
61	SH	62	ILE
61	SH	73	GLN
61	SH	93	VAL
61	SH	121	THR
61	SH	144	ILE
61	SH	180	LEU
61	SH	188	GLU
62	SI	3	ILE
62	SI	61	ASP
62	SI	71	CYS
62	SI	82	VAL
62	SI	90	LEU
62	SI	121	LEU
62	SI	199	LEU
63	SJ	102	ILE
63	SJ	109	ARG
63	SJ	130	ILE
64	SK	7	ASN
65	SL	42	LEU
65	SL	85	THR
65	SL	87	VAL
65	SL	90	ARG
65	SL	104	LYS
65	SL	111	VAL
65	SL	146	THR

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Mol	Chain	Res	Type
66	SM	12	MET
66	SM	26	LEU
66	SM	92	CYS
66	SM	110	VAL
67	SN	60	VAL
68	SO	63	LYS
68	SO	75	MET
69	SP	22	LEU
69	SP	23	ASP
69	SP	24	GLN
69	SP	25	LEU
69	SP	30	TYR
69	SP	56	LEU
69	SP	100	LYS
69	SP	105	VAL
69	SP	126	VAL
70	SQ	29	ASN
71	SR	74	GLN
71	SR	75	GLU
71	SR	88	VAL
71	SR	126	MET
72	SS	4	VAL
72	SS	99	LEU
72	SS	129	LEU
73	ST	28	LEU
73	ST	87	VAL
73	ST	99	VAL
73	ST	123	LEU
73	ST	124	THR
73	ST	128	GLN
74	SU	19	ARG
74	SU	31	SER
74	SU	48	LEU
74	SU	100	GLN
75	SV	2	GLN
75	SV	23	ILE
75	SV	33	GLN
75	SV	34	MET
75	SV	78	ILE
76	SW	6	VAL
76	SW	31	SER
76	SW	33	VAL

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Mol	Chain	Res	Type
76	SW	42	MET
76	SW	53	ILE
76	SW	61	ILE
76	SW	62	VAL
76	SW	74	VAL
76	SW	82	GLN
76	SW	104	LEU
77	SX	26	GLN
77	SX	45	SER
77	SX	72	VAL
77	SX	82	THR
77	SX	105	PHE
78	SY	22	GLN
78	SY	27	VAL
78	SY	54	VAL
78	SY	81	TYR
79	SZ	44	LEU
79	SZ	61	GLU
79	SZ	75	GLU
79	SZ	102	LYS
79	SZ	107	VAL
80	Sa	26	CYS
80	Sa	45	VAL
80	Sa	50	VAL
81	Sb	24	LEU
81	Sb	27	SER
81	Sb	57	VAL
81	Sb	74	THR
82	Sc	6	VAL
82	Sc	30	VAL
83	Sd	25	SER
84	Se	48	THR
85	Sf	95	ARG
85	Sf	130	VAL
85	Sf	146	LEU
86	Sg	26	GLN
86	Sg	41	ILE
86	Sg	98	THR
86	Sg	101	PHE
86	Sg	102	VAL
86	Sg	129	ILE
86	Sg	137	VAL

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Mol	Chain	Res	Type
86	Sg	192	THR
86	Sg	297	THR
86	Sg	313	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (130) such sidechains are listed below:

Mol	Chain	Res	Type
1	CB	30	HIS
1	CB	64	GLN
1	CB	168	GLN
1	CB	179	GLN
1	CB	186	ASN
1	CB	448	GLN
1	CB	670	GLN
1	CB	764	ASN
7	LA	38	HIS
7	LA	95	GLN
7	LA	97	ASN
7	LA	215	ASN
8	LB	68	ASN
8	LB	121	ASN
8	LB	175	GLN
8	LB	184	GLN
8	LB	302	ASN
9	LC	48	ASN
9	LC	212	ASN
9	LC	215	ASN
9	LC	286	ASN
9	LC	329	ASN
9	LC	346	ASN
9	LC	347	HIS
10	LD	202	GLN
10	LD	267	ASN
11	LE	191	GLN
11	LE	205	ASN
11	LE	266	GLN
12	LF	80	ASN
13	LG	100	HIS
13	LG	149	ASN
13	LG	153	GLN
13	LG	208	ASN
14	LH	102	ASN

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Mol	Chain	Res	Type
14	LH	108	ASN
14	LH	189	GLN
15	LI	73	ASN
15	LI	123	GLN
15	LI	144	ASN
15	LI	147	HIS
15	LI	213	HIS
16	LJ	23	ASN
16	LJ	98	ASN
18	LM	20	HIS
18	LM	48	GLN
18	LM	56	GLN
19	LN	145	ASN
20	LO	63	ASN
20	LO	96	GLN
20	LO	180	GLN
21	LP	21	ASN
21	LP	75	GLN
21	LP	133	HIS
22	LQ	151	HIS
23	LR	134	ASN
27	LV	84	GLN
28	LW	48	GLN
28	LW	50	ASN
28	LW	96	GLN
28	LW	104	GLN
28	LW	107	GLN
30	LY	18	HIS
30	LY	20	ASN
30	LY	66	GLN
30	LY	72	GLN
30	LY	96	HIS
31	LZ	127	ASN
32	La	19	HIS
32	La	62	HIS
32	La	66	ASN
33	Lb	6	ASN
33	Lb	7	HIS
34	Lc	15	ASN
34	Lc	73	HIS
35	Ld	79	ASN
36	Le	52	GLN

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Mol	Chain	Res	Type
39	Lh	20	GLN
39	Lh	65	GLN
39	Lh	96	ASN
40	Li	80	HIS
41	Lj	30	GLN
41	Lj	57	ASN
48	Lr	30	ASN
49	Lz	94	ASN
49	Lz	143	ASN
50	N4	13	GLN
50	N4	54	ASN
50	N4	167	GLN
50	N4	191	GLN
51	NA	101	ASN
54	SA	132	GLN
55	SB	160	GLN
56	SC	235	ASN
58	SE	17	HIS
58	SE	188	ASN
58	SE	197	ASN
58	SE	214	ASN
59	SF	36	GLN
59	SF	101	HIS
60	SG	155	GLN
61	SH	97	GLN
61	SH	114	GLN
62	SI	52	ASN
62	SI	168	GLN
63	SJ	111	GLN
63	SJ	177	ASN
65	SL	18	GLN
65	SL	39	ASN
65	SL	141	ASN
67	SN	49	GLN
68	SO	113	GLN
71	SR	48	ASN
71	SR	83	ASN
73	ST	42	HIS
74	SU	85	HIS
76	SW	24	GLN
76	SW	82	GLN
78	SY	19	GLN

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Mol	Chain	Res	Type
78	SY	29	HIS
78	SY	89	HIS
79	SZ	112	ASN
81	Sb	29	ASN
81	Sb	65	GLN
83	Sd	26	ASN
83	Sd	28	HIS
83	Sd	37	ASN
84	Se	15	GLN
84	Se	37	GLN
86	Sg	187	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	CC	84/85 (98%)	20 (23%)	1 (1%)
4	L5	3704/5070 (73%)	884 (23%)	17 (0%)
5	L7	119/121 (98%)	16 (13%)	0
53	S2	1715/1869 (91%)	437 (25%)	4 (0%)
6	L8	155/157 (98%)	33 (21%)	0
All	All	5777/7302 (79%)	1390 (24%)	22 (0%)

All (1390) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	CC	7	G
2	CC	8	U
2	CC	9	G
2	CC	14	A
2	CC	16	U
2	CC	17	G
2	CC	18	G
2	CC	19	U
2	CC	20	U
2	CC	21	A
2	CC	22	A
2	CC	26	G
2	CC	45	G
2	CC	48	G
2	CC	49	U
2	CC	50	C

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Mol	Chain	Res	Type
2	CC	56	G
2	CC	57	C
2	CC	70	C
2	CC	85	A
4	L5	2	G
4	L5	17	A
4	L5	25	A
4	L5	26	C
4	L5	30	C
4	L5	39	A
4	L5	42	A
4	L5	48	G
4	L5	56	A
4	L5	59	A
4	L5	64	A
4	L5	65	A
4	L5	69	A
4	L5	72	C
4	L5	73	A
4	L5	74	G
4	L5	91	G
4	L5	98	A
4	L5	104	G
4	L5	108	A
4	L5	109	G
4	L5	110	C
4	L5	115	C
4	L5	119	G
4	L5	120	A
4	L5	132	G
4	L5	133	C
4	L5	134	G
4	L5	135	G
4	L5	137	G
4	L5	152	U
4	L5	159	C
4	L5	165	A
4	L5	166	C
4	L5	172	C
4	L5	182	G
4	L5	183	C
4	L5	184	U

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Mol	Chain	Res	Type
4	L5	185	C
4	L5	187	U
4	L5	188	G
4	L5	189	G
4	L5	200	U
4	L5	209	U
4	L5	210	C
4	L5	216	C
4	L5	218	A
4	L5	220	C
4	L5	233	U
4	L5	234	G
4	L5	237	G
4	L5	255	C
4	L5	256	G
4	L5	261	G
4	L5	263	G
4	L5	265	C
4	L5	266	C
4	L5	267	G
4	L5	275	C
4	L5	280	G
4	L5	297	U
4	L5	306	A
4	L5	315	G
4	L5	316	U
4	L5	340	C
4	L5	349	A
4	L5	350	C
4	L5	373	G
4	L5	387	G
4	L5	388	A
4	L5	407	A
4	L5	410	A
4	L5	411	G
4	L5	412	G
4	L5	413	G
4	L5	431	G
4	L5	432	U
4	L5	437	G
4	L5	438	G
4	L5	440	U

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Mol	Chain	Res	Type
4	L5	449	C
4	L5	450	G
4	L5	452	A
4	L5	453	G
4	L5	454	U
4	L5	456	C
4	L5	457	G
4	L5	467	U
4	L5	468	U
4	L5	479	G
4	L5	484	U
4	L5	485	C
4	L5	486	C
4	L5	489	C
4	L5	493	G
4	L5	494	U
4	L5	495	C
4	L5	497	G
4	L5	498	C
4	L5	499	G
4	L5	500	G
4	L5	501	C
4	L5	502	C
4	L5	503	C
4	L5	504	G
4	L5	505	G
4	L5	506	C
4	L5	509	A
4	L5	510	U
4	L5	512	U
4	L5	513	U
4	L5	514	U
4	L5	518	G
4	L5	643	C
4	L5	646	G
4	L5	654	C
4	L5	655	C
4	L5	656	C
4	L5	657	C
4	L5	658	C
4	L5	659	G
4	L5	665	C

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Mol	Chain	Res	Type
4	L5	666	G
4	L5	667	A
4	L5	668	C
4	L5	673	C
4	L5	674	G
4	L5	685	C
4	L5	686	A
4	L5	687	U
4	L5	696	C
4	L5	703	G
4	L5	704	C
4	L5	708	G
4	L5	731	G
4	L5	738	C
4	L5	739	G
4	L5	742	G
4	L5	753	C
4	L5	758	G
4	L5	759	G
4	L5	904	C
4	L5	907	C
4	L5	913	U
4	L5	914	U
4	L5	915	A
4	L5	917	A
4	L5	918	G
4	L5	923	C
4	L5	924	C
4	L5	926	G
4	L5	932	A
4	L5	933	G
4	L5	935	A
4	L5	936	C
4	L5	937	U
4	L5	941	C
4	L5	945	U
4	L5	946	C
4	L5	956	A
4	L5	958	G
4	L5	959	G
4	L5	960	A
4	L5	961	G

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Mol	Chain	Res	Type
4	L5	962	C
4	L5	965	G
4	L5	966	A
4	L5	967	C
4	L5	968	C
4	L5	969	C
4	L5	970	G
4	L5	971	U
4	L5	982	U
4	L5	985	C
4	L5	989	U
4	L5	990	C
4	L5	992	C
4	L5	993	G
4	L5	995	C
4	L5	1048	G
4	L5	1049	C
4	L5	1050	C
4	L5	1051	G
4	L5	1066	G
4	L5	1070	G
4	L5	1072	C
4	L5	1075	G
4	L5	1082	C
4	L5	1083	U
4	L5	1095	A
4	L5	1168	G
4	L5	1171	G
4	L5	1172	C
4	L5	1173	G
4	L5	1179	U
4	L5	1180	C
4	L5	1181	C
4	L5	1182	C
4	L5	1183	C
4	L5	1202	C
4	L5	1203	G
4	L5	1204	C
4	L5	1210	C
4	L5	1211	G
4	L5	1214	C
4	L5	1215	C

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Mol	Chain	Res	Type
4	L5	1216	C
4	L5	1217	G
4	L5	1218	G
4	L5	1219	G
4	L5	1222	A
4	L5	1241	C
4	L5	1242	G
4	L5	1246	G
4	L5	1253	G
4	L5	1254	A
4	L5	1257	A
4	L5	1258	G
4	L5	1266	G
4	L5	1267	C
4	L5	1269	G
4	L5	1270	A
4	L5	1271	G
4	L5	1272	C
4	L5	1273	G
4	L5	1274	A
4	L5	1275	G
4	L5	1277	G
4	L5	1280	C
4	L5	1284	G
4	L5	1285	U
4	L5	1287	G
4	L5	1293	G
4	L5	1294	A
4	L5	1295	C
4	L5	1296	G
4	L5	1301	C
4	L5	1312	A
4	L5	1313	C
4	L5	1314	C
4	L5	1324	A
4	L5	1326	A
4	L5	1337	A
4	L5	1354	A
4	L5	1358	G
4	L5	1359	G
4	L5	1360	G
4	L5	1365	C

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Mol	Chain	Res	Type
4	L5	1367	C
4	L5	1378	C
4	L5	1379	C
4	L5	1387	A
4	L5	1394	G
4	L5	1397	A
4	L5	1398	A
4	L5	1404	G
4	L5	1405	C
4	L5	1407	C
4	L5	1409	C
4	L5	1410	U
4	L5	1411	C
4	L5	1412	G
4	L5	1414	C
4	L5	1415	G
4	L5	1417	C
4	L5	1420	A
4	L5	1437	C
4	L5	1439	C
4	L5	1441	C
4	L5	1443	A
4	L5	1446	C
4	L5	1447	C
4	L5	1457	G
4	L5	1482	G
4	L5	1483	C
4	L5	1493	G
4	L5	1497	A
4	L5	1498	G
4	L5	1502	G
4	L5	1515	A
4	L5	1517	G
4	L5	1518	A
4	L5	1519	C
4	L5	1525	A
4	L5	1534	A
4	L5	1547	A
4	L5	1562	G
4	L5	1566	C
4	L5	1574	G
4	L5	1576	G

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Mol	Chain	Res	Type
4	L5	1578	U
4	L5	1591	U
4	L5	1596	U
4	L5	1614	C
4	L5	1624	G
4	L5	1625	G
4	L5	1631	A
4	L5	1633	G
4	L5	1634	A
4	L5	1637	A
4	L5	1638	A
4	L5	1640	C
4	L5	1641	G
4	L5	1642	A
4	L5	1643	A
4	L5	1654	G
4	L5	1661	C
4	L5	1663	C
4	L5	1670	G
4	L5	1676	C
4	L5	1677	U
4	L5	1678	C
4	L5	1680	G
4	L5	1681	G
4	L5	1694	C
4	L5	1697	G
4	L5	1698	C
4	L5	1699	A
4	L5	1700	G
4	L5	1703	C
4	L5	1704	C
4	L5	1705	G
4	L5	1707	C
4	L5	1717	C
4	L5	1718	C
4	L5	1719	A
4	L5	1726	U
4	L5	1734	G
4	L5	1740	C
4	L5	1742	A
4	L5	1750	G
4	L5	1753	G

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Mol	Chain	Res	Type
4	L5	1757	U
4	L5	1758	G
4	L5	1760	G
4	L5	1761	G
4	L5	1762	C
4	L5	1763	C
4	L5	1764	G
4	L5	1765	A
4	L5	1766	A
4	L5	1767	A
4	L5	1768	C
4	L5	1769	G
4	L5	1770	A
4	L5	1775	A
4	L5	1787	A
4	L5	1797	G
4	L5	1803	G
4	L5	1804	A
4	L5	1810	G
4	L5	1815	G
4	L5	1820	C
4	L5	1821	G
4	L5	1822	U
4	L5	1834	U
4	L5	1836	G
4	L5	1837	A
4	L5	1842	G
4	L5	1843	A
4	L5	1855	G
4	L5	1869	G
4	L5	1881	C
4	L5	1882	U
4	L5	1892	A
4	L5	1897	A
4	L5	1898	C
4	L5	1916	G
4	L5	1918	U
4	L5	1919	G
4	L5	1920	C
4	L5	1921	C
4	L5	1922	G
4	L5	1925	G

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Mol	Chain	Res	Type
4	L5	1931	C
4	L5	1932	A
4	L5	1936	C
4	L5	1940	G
4	L5	1948	G
4	L5	1949	U
4	L5	1951	G
4	L5	1959	U
4	L5	1961	G
4	L5	1962	A
4	L5	1974	U
4	L5	1975	G
4	L5	1978	C
4	L5	1980	U
4	L5	1981	G
4	L5	1982	G
4	L5	1984	A
4	L5	1985	G
4	L5	1986	U
4	L5	1991	A
4	L5	1992	U
4	L5	1993	C
4	L5	1997	U
4	L5	2002	A
4	L5	2011	C
4	L5	2017	A
4	L5	2018	C
4	L5	2024	G
4	L5	2026	A
4	L5	2033	A
4	L5	2034	G
4	L5	2044	U
4	L5	2046	G
4	L5	2048	U
4	L5	2052	G
4	L5	2055	G
4	L5	2056	G
4	L5	2069	A
4	L5	2084	C
4	L5	2090	U
4	L5	2091	C
4	L5	2092	G

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Mol	Chain	Res	Type
4	L5	2093	A
4	L5	2095	A
4	L5	2096	G
4	L5	2097	U
4	L5	2098	G
4	L5	2101	C
4	L5	2102	G
4	L5	2107	C
4	L5	2111	G
4	L5	2112	G
4	L5	2250	C
4	L5	2252	G
4	L5	2253	A
4	L5	2255	C
4	L5	2256	C
4	L5	2258	C
4	L5	2259	G
4	L5	2260	C
4	L5	2262	G
4	L5	2269	C
4	L5	2289	C
4	L5	2300	A
4	L5	2301	G
4	L5	2306	G
4	L5	2313	A
4	L5	2316	G
4	L5	2331	G
4	L5	2332	A
4	L5	2333	G
4	L5	2348	G
4	L5	2351	C
4	L5	2358	G
4	L5	2360	A
4	L5	2369	U
4	L5	2382	A
4	L5	2395	A
4	L5	2397	G
4	L5	2417	A
4	L5	2418	A
4	L5	2421	G
4	L5	2425	U
4	L5	2437	C

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Mol	Chain	Res	Type
4	L5	2441	C
4	L5	2450	G
4	L5	2463	G
4	L5	2464	C
4	L5	2465	C
4	L5	2467	U
4	L5	2471	G
4	L5	2474	G
4	L5	2475	G
4	L5	2478	C
4	L5	2479	G
4	L5	2483	G
4	L5	2484	A
4	L5	2485	U
4	L5	2487	G
4	L5	2488	C
4	L5	2489	C
4	L5	2490	U
4	L5	2491	C
4	L5	2494	U
4	L5	2503	G
4	L5	2504	C
4	L5	2505	C
4	L5	2506	G
4	L5	2507	A
4	L5	2511	A
4	L5	2513	A
4	L5	2518	G
4	L5	2519	U
4	L5	2520	C
4	L5	2537	A
4	L5	2544	G
4	L5	2546	G
4	L5	2547	G
4	L5	2554	U
4	L5	2555	G
4	L5	2557	G
4	L5	2560	C
4	L5	2565	A
4	L5	2573	A
4	L5	2583	C
4	L5	2587	A

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Mol	Chain	Res	Type
4	L5	2589	C
4	L5	2601	A
4	L5	2611	A
4	L5	2623	A
4	L5	2627	C
4	L5	2638	G
4	L5	2652	G
4	L5	2653	C
4	L5	2662	G
4	L5	2669	C
4	L5	2670	C
4	L5	2673	G
4	L5	2675	G
4	L5	2676	A
4	L5	2687	U
4	L5	2695	A
4	L5	2696	A
4	L5	2707	U
4	L5	2708	U
4	L5	2709	C
4	L5	2710	C
4	L5	2711	G
4	L5	2721	G
4	L5	2724	G
4	L5	2726	G
4	L5	2738	C
4	L5	2739	C
4	L5	2742	G
4	L5	2743	A
4	L5	2746	A
4	L5	2748	C
4	L5	2754	G
4	L5	2756	G
4	L5	2761	U
4	L5	2763	U
4	L5	2764	A
4	L5	2769	U
4	L5	2770	C
4	L5	2787	A
4	L5	2788	U
4	L5	2790	U
4	L5	2826	U

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Mol	Chain	Res	Type
4	L5	2827	G
4	L5	2829	U
4	L5	2838	G
4	L5	2842	G
4	L5	2848	G
4	L5	2855	G
4	L5	2867	C
4	L5	2877	G
4	L5	2892	C
4	L5	2894	A
4	L5	2900	U
4	L5	2902	G
4	L5	2903	G
4	L5	2904	U
4	L5	2905	C
4	L5	2906	G
4	L5	2908	U
4	L5	3587	C
4	L5	3590	G
4	L5	3591	C
4	L5	3594	C
4	L5	3595	U
4	L5	3596	A
4	L5	3597	G
4	L5	3599	A
4	L5	3605	C
4	L5	3615	G
4	L5	3618	C
4	L5	3626	G
4	L5	3630	A
4	L5	3635	A
4	L5	3644	U
4	L5	3646	A
4	L5	3648	A
4	L5	3662	A
4	L5	3664	G
4	L5	3670	C
4	L5	3673	C
4	L5	3674	G
4	L5	3680	U
4	L5	3709	U
4	L5	3710	G

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Mol	Chain	Res	Type
4	L5	3711	A
4	L5	3713	U
4	L5	3727	A
4	L5	3735	G
4	L5	3748	A
4	L5	3750	G
4	L5	3756	A
4	L5	3759	A
4	L5	3761	C
4	L5	3772	U
4	L5	3773	U
4	L5	3774	A
4	L5	3776	G
4	L5	3777	G
4	L5	3784	A
4	L5	3786	U
4	L5	3788	C
4	L5	3802	U
4	L5	3810	C
4	L5	3811	G
4	L5	3814	U
4	L5	3817	A
4	L5	3818	U
4	L5	3819	G
4	L5	3823	G
4	L5	3838	U
4	L5	3839	G
4	L5	3840	U
4	L5	3851	U
4	L5	3867	A
4	L5	3876	A
4	L5	3877	A
4	L5	3878	C
4	L5	3879	G
4	L5	3885	G
4	L5	3887	C
4	L5	3892	U
4	L5	3897	G
4	L5	3901	A
4	L5	3905	A
4	L5	3906	A
4	L5	3907	G

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Mol	Chain	Res	Type
4	L5	3908	A
4	L5	3915	U
4	L5	3916	G
4	L5	3938	G
4	L5	3939	G
4	L5	3942	A
4	L5	3943	A
4	L5	3947	A
4	L5	3948	C
4	L5	3950	U
4	L5	3951	G
4	L5	3955	G
4	L5	3956	G
4	L5	3957	U
4	L5	3958	G
4	L5	3960	A
4	L5	3962	A
4	L5	3963	A
4	L5	3964	U
4	L5	3966	A
4	L5	3968	U
4	L5	3969	G
4	L5	3970	G
4	L5	3972	A
4	L5	3973	G
4	L5	3974	G
4	L5	3975	C
4	L5	3977	C
4	L5	4036	G
4	L5	4038	C
4	L5	4039	G
4	L5	4041	C
4	L5	4042	G
4	L5	4043	G
4	L5	4044	U
4	L5	4045	G
4	L5	4046	A
4	L5	4048	A
4	L5	4049	U
4	L5	4051	C
4	L5	4052	C
4	L5	4053	A

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Mol	Chain	Res	Type
4	L5	4055	U
4	L5	4056	A
4	L5	4057	C
4	L5	4059	C
4	L5	4060	U
4	L5	4062	A
4	L5	4063	U
4	L5	4064	C
4	L5	4065	G
4	L5	4076	G
4	L5	4084	G
4	L5	4091	G
4	L5	4092	G
4	L5	4093	G
4	L5	4095	G
4	L5	4096	C
4	L5	4097	G
4	L5	4099	G
4	L5	4101	C
4	L5	4102	C
4	L5	4103	C
4	L5	4104	G
4	L5	4108	G
4	L5	4111	U
4	L5	4114	C
4	L5	4115	G
4	L5	4116	C
4	L5	4117	U
4	L5	4119	C
4	L5	4127	A
4	L5	4133	C
4	L5	4134	C
4	L5	4140	C
4	L5	4141	G
4	L5	4142	C
4	L5	4143	G
4	L5	4144	C
4	L5	4146	G
4	L5	4150	G
4	L5	4160	C
4	L5	4162	C
4	L5	4163	U

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Mol	Chain	Res	Type
4	L5	4170	A
4	L5	4183	G
4	L5	4184	G
4	L5	4191	G
4	L5	4196	G
4	L5	4203	A
4	L5	4214	A
4	L5	4222	G
4	L5	4228	G
4	L5	4229	U
4	L5	4233	A
4	L5	4243	C
4	L5	4249	G
4	L5	4251	A
4	L5	4254	G
4	L5	4255	A
4	L5	4265	U
4	L5	4268	A
4	L5	4273	A
4	L5	4283	G
4	L5	4290	U
4	L5	4295	U
4	L5	4304	A
4	L5	4305	G
4	L5	4306	U
4	L5	4314	C
4	L5	4319	C
4	L5	4326	G
4	L5	4329	G
4	L5	4330	G
4	L5	4332	C
4	L5	4338	G
4	L5	4349	C
4	L5	4364	G
4	L5	4371	G
4	L5	4373	G
4	L5	4376	A
4	L5	4377	G
4	L5	4378	A
4	L5	4379	A
4	L5	4380	A
4	L5	4387	C

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Mol	Chain	Res	Type
4	L5	4391	G
4	L5	4394	A
4	L5	4422	A
4	L5	4426	C
4	L5	4438	U
4	L5	4444	C
4	L5	4448	G
4	L5	4449	A
4	L5	4452	U
4	L5	4453	C
4	L5	4464	A
4	L5	4466	C
4	L5	4475	G
4	L5	4488	A
4	L5	4500	U
4	L5	4512	U
4	L5	4513	A
4	L5	4519	C
4	L5	4524	G
4	L5	4525	C
4	L5	4528	G
4	L5	4545	G
4	L5	4548	A
4	L5	4549	G
4	L5	4557	U
4	L5	4560	C
4	L5	4567	G
4	L5	4573	G
4	L5	4575	G
4	L5	4584	A
4	L5	4589	A
4	L5	4590	A
4	L5	4600	G
4	L5	4617	G
4	L5	4626	A
4	L5	4627	U
4	L5	4633	G
4	L5	4635	A
4	L5	4636	U
4	L5	4637	G
4	L5	4652	G
4	L5	4656	A

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Mol	Chain	Res	Type
4	L5	4657	U
4	L5	4659	G
4	L5	4670	C
4	L5	4672	A
4	L5	4679	G
4	L5	4687	A
4	L5	4694	G
4	L5	4695	C
4	L5	4700	A
4	L5	4708	A
4	L5	4709	U
4	L5	4719	G
4	L5	4720	C
4	L5	4733	C
4	L5	4734	A
4	L5	4740	G
4	L5	4741	C
4	L5	4742	G
4	L5	4745	G
4	L5	4750	G
4	L5	4754	G
4	L5	4757	C
4	L5	4759	C
4	L5	4761	G
4	L5	4764	A
4	L5	4765	G
4	L5	4771	C
4	L5	4773	C
4	L5	4775	C
4	L5	4776	G
4	L5	4859	C
4	L5	4860	G
4	L5	4870	G
4	L5	4871	C
4	L5	4875	G
4	L5	4880	C
4	L5	4881	U
4	L5	4882	U
4	L5	4883	C
4	L5	4888	U
4	L5	4889	G
4	L5	4895	C

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Mol	Chain	Res	Type
4	L5	4896	G
4	L5	4900	C
4	L5	4901	G
4	L5	4902	C
4	L5	4910	G
4	L5	4912	G
4	L5	4914	C
4	L5	4922	C
4	L5	4925	U
4	L5	4926	C
4	L5	4927	G
4	L5	4928	C
4	L5	4934	A
4	L5	4937	C
4	L5	4940	C
4	L5	4941	G
4	L5	4943	A
4	L5	4949	G
4	L5	4951	G
4	L5	4955	A
4	L5	4960	G
4	L5	4966	A
4	L5	4975	G
4	L5	4976	U
4	L5	4979	A
4	L5	4985	U
4	L5	4988	U
4	L5	4989	U
4	L5	4991	U
4	L5	5009	G
4	L5	5013	C
4	L5	5017	G
4	L5	5022	U
4	L5	5023	C
4	L5	5024	C
4	L5	5025	C
4	L5	5026	U
4	L5	5027	C
4	L5	5028	G
4	L5	5029	C
4	L5	5030	U
4	L5	5034	A

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Mol	Chain	Res	Type
4	L5	5041	G
4	L5	5050	C
4	L5	5054	C
4	L5	5055	G
4	L5	5061	A
4	L5	5069	U
5	L7	3	C
5	L7	4	U
5	L7	13	A
5	L7	22	A
5	L7	33	U
5	L7	38	U
5	L7	49	A
5	L7	53	U
5	L7	54	A
5	L7	63	C
5	L7	64	G
5	L7	97	G
5	L7	100	A
5	L7	109	U
5	L7	110	G
5	L7	120	U
6	L8	23	C
6	L8	25	G
6	L8	34	U
6	L8	35	C
6	L8	38	U
6	L8	48	A
6	L8	59	A
6	L8	60	G
6	L8	61	A
6	L8	62	A
6	L8	63	U
6	L8	70	G
6	L8	75	G
6	L8	80	A
6	L8	82	A
6	L8	84	A
6	L8	85	U
6	L8	86	U
6	L8	87	G
6	L8	94	G

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Mol	Chain	Res	Type
6	L8	103	A
6	L8	105	C
6	L8	110	U
6	L8	111	U
6	L8	114	G
6	L8	123	U
6	L8	124	U
6	L8	125	C
6	L8	126	C
6	L8	127	U
6	L8	150	C
6	L8	155	C
6	L8	156	U
53	S2	2	A
53	S2	4	C
53	S2	13	C
53	S2	14	C
53	S2	17	C
53	S2	25	A
53	S2	33	G
53	S2	42	A
53	S2	44	U
53	S2	45	A
53	S2	46	A
53	S2	56	G
53	S2	58	C
53	S2	62	G
53	S2	64	A
53	S2	65	C
53	S2	67	C
53	S2	68	A
53	S2	72	C
53	S2	73	C
53	S2	74	G
53	S2	76	U
53	S2	92	A
53	S2	103	A
53	S2	113	G
53	S2	114	G
53	S2	115	U
53	S2	116	U
53	S2	126	G

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Mol	Chain	Res	Type
53	S2	129	C
53	S2	130	G
53	S2	142	C
53	S2	143	U
53	S2	149	A
53	S2	155	G
53	S2	158	A
53	S2	159	A
53	S2	160	U
53	S2	161	U
53	S2	162	C
53	S2	163	U
53	S2	168	C
53	S2	170	A
53	S2	175	A
53	S2	179	C
53	S2	182	C
53	S2	187	G
53	S2	190	G
53	S2	196	C
53	S2	197	U
53	S2	198	U
53	S2	199	C
53	S2	200	G
53	S2	203	G
53	S2	204	G
53	S2	206	G
53	S2	207	G
53	S2	208	G
53	S2	209	A
53	S2	212	C
53	S2	214	U
53	S2	220	U
53	S2	290	U
53	S2	291	G
53	S2	292	A
53	S2	293	C
53	S2	295	C
53	S2	306	C
53	S2	307	G
53	S2	308	G
53	S2	309	G

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Mol	Chain	Res	Type
53	S2	310	C
53	S2	311	C
53	S2	312	G
53	S2	313	A
53	S2	318	A
53	S2	319	C
53	S2	322	C
53	S2	323	C
53	S2	324	C
53	S2	325	C
53	S2	326	C
53	S2	328	U
53	S2	329	G
53	S2	335	G
53	S2	338	G
53	S2	339	A
53	S2	347	G
53	S2	360	A
53	S2	361	U
53	S2	362	C
53	S2	363	A
53	S2	364	A
53	S2	368	U
53	S2	370	G
53	S2	381	C
53	S2	385	G
53	S2	386	C
53	S2	408	A
53	S2	409	C
53	S2	421	G
53	S2	438	G
53	S2	442	C
53	S2	448	A
53	S2	449	A
53	S2	450	C
53	S2	452	G
53	S2	463	C
53	S2	464	A
53	S2	465	A
53	S2	467	G
53	S2	471	G
53	S2	472	C

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Mol	Chain	Res	Type
53	S2	473	A
53	S2	474	G
53	S2	476	A
53	S2	482	G
53	S2	485	A
53	S2	487	U
53	S2	488	U
53	S2	492	C
53	S2	502	C
53	S2	517	C
53	S2	531	A
53	S2	532	C
53	S2	533	A
53	S2	536	A
53	S2	537	C
53	S2	540	U
53	S2	542	U
53	S2	546	G
53	S2	547	G
53	S2	551	U
53	S2	554	A
53	S2	555	A
53	S2	556	U
53	S2	557	U
53	S2	558	G
53	S2	559	G
53	S2	563	G
53	S2	564	A
53	S2	566	U
53	S2	576	A
53	S2	583	A
53	S2	587	A
53	S2	589	G
53	S2	590	A
53	S2	591	U
53	S2	596	U
53	S2	597	G
53	S2	600	G
53	S2	603	C
53	S2	604	A
53	S2	606	G
53	S2	607	U

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Mol	Chain	Res	Type
53	S2	614	C
53	S2	617	G
53	S2	623	G
53	S2	629	A
53	S2	639	C
53	S2	643	A
53	S2	644	G
53	S2	655	A
53	S2	659	G
53	S2	660	C
53	S2	662	G
53	S2	663	C
53	S2	664	A
53	S2	668	A
53	S2	669	A
53	S2	671	A
53	S2	672	A
53	S2	673	G
53	S2	678	U
53	S2	683	G
53	S2	687	C
53	S2	689	U
53	S2	692	G
53	S2	693	A
53	S2	696	G
53	S2	697	G
53	S2	698	G
53	S2	733	C
53	S2	736	C
53	S2	738	C
53	S2	749	U
53	S2	751	G
53	S2	752	G
53	S2	788	G
53	S2	791	C
53	S2	792	C
53	S2	793	G
53	S2	794	A
53	S2	798	G
53	S2	799	U
53	S2	810	A
53	S2	821	G

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Mol	Chain	Res	Type
53	S2	822	U
53	S2	823	U
53	S2	824	C
53	S2	827	A
53	S2	830	A
53	S2	834	C
53	S2	835	C
53	S2	836	G
53	S2	837	A
53	S2	838	G
53	S2	839	C
53	S2	841	G
53	S2	842	C
53	S2	847	A
53	S2	869	A
53	S2	870	A
53	S2	871	U
53	S2	872	A
53	S2	873	G
53	S2	878	G
53	S2	882	U
53	S2	888	U
53	S2	889	U
53	S2	891	G
53	S2	896	U
53	S2	897	U
53	S2	898	U
53	S2	899	U
53	S2	900	C
53	S2	901	G
53	S2	903	A
53	S2	913	A
53	S2	914	U
53	S2	919	A
53	S2	920	A
53	S2	922	A
53	S2	933	G
53	S2	954	U
53	S2	955	A
53	S2	971	G
53	S2	990	A
53	S2	992	A

Continued on next page...

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Mol	Chain	Res	Type
53	S2	996	A
53	S2	999	G
53	S2	1001	A
53	S2	1008	A
53	S2	1017	U
53	S2	1023	A
53	S2	1027	A
53	S2	1045	U
53	S2	1061	U
53	S2	1062	A
53	S2	1067	C
53	S2	1083	A
53	S2	1085	C
53	S2	1088	U
53	S2	1109	C
53	S2	1114	U
53	S2	1115	U
53	S2	1116	C
53	S2	1119	A
53	S2	1121	G
53	S2	1126	G
53	S2	1131	G
53	S2	1133	A
53	S2	1138	C
53	S2	1139	C
53	S2	1148	A
53	S2	1153	C
53	S2	1154	U
53	S2	1155	U
53	S2	1195	A
53	S2	1203	G
53	S2	1207	G
53	S2	1208	A
53	S2	1215	C
53	S2	1216	C
53	S2	1217	A
53	S2	1222	G
53	S2	1224	G
53	S2	1227	G
53	S2	1239	U
53	S2	1242	U
53	S2	1243	U

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Mol	Chain	Res	Type
53	S2	1251	A
53	S2	1253	A
53	S2	1256	G
53	S2	1257	G
53	S2	1259	A
53	S2	1264	C
53	S2	1265	A
53	S2	1274	G
53	S2	1275	G
53	S2	1283	C
53	S2	1284	A
53	S2	1286	G
53	S2	1294	G
53	S2	1295	A
53	S2	1302	G
53	S2	1303	C
53	S2	1306	U
53	S2	1308	U
53	S2	1312	G
53	S2	1320	G
53	S2	1333	U
53	S2	1341	C
53	S2	1342	U
53	S2	1364	U
53	S2	1371	U
53	S2	1375	G
53	S2	1376	A
53	S2	1378	A
53	S2	1382	A
53	S2	1396	A
53	S2	1398	G
53	S2	1402	A
53	S2	1404	U
53	S2	1408	U
53	S2	1412	C
53	S2	1414	A
53	S2	1415	C
53	S2	1419	C
53	S2	1420	G
53	S2	1421	A
53	S2	1422	G
53	S2	1423	C

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Mol	Chain	Res	Type
53	S2	1424	G
53	S2	1433	C
53	S2	1434	C
53	S2	1435	C
53	S2	1436	C
53	S2	1438	A
53	S2	1447	G
53	S2	1449	G
53	S2	1450	G
53	S2	1454	A
53	S2	1462	U
53	S2	1463	U
53	S2	1466	G
53	S2	1486	A
53	S2	1489	A
53	S2	1490	G
53	S2	1495	G
53	S2	1497	G
53	S2	1498	A
53	S2	1505	U
53	S2	1507	G
53	S2	1509	U
53	S2	1521	C
53	S2	1522	A
53	S2	1531	A
53	S2	1533	A
53	S2	1534	C
53	S2	1535	U
53	S2	1536	G
53	S2	1537	A
53	S2	1546	G
53	S2	1551	U
53	S2	1552	G
53	S2	1556	A
53	S2	1558	C
53	S2	1570	G
53	S2	1573	G
53	S2	1575	G
53	S2	1580	A
53	S2	1582	C
53	S2	1584	G
53	S2	1585	U

Continued on next page...

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Mol	Chain	Res	Type
53	S2	1586	U
53	S2	1587	G
53	S2	1588	A
53	S2	1598	G
53	S2	1599	U
53	S2	1600	G
53	S2	1601	A
53	S2	1606	G
53	S2	1621	U
53	S2	1623	A
53	S2	1633	A
53	S2	1637	A
53	S2	1638	G
53	S2	1639	G
53	S2	1640	A
53	S2	1646	C
53	S2	1648	G
53	S2	1649	U
53	S2	1654	G
53	S2	1663	A
53	S2	1664	A
53	S2	1665	G
53	S2	1680	G
53	S2	1683	C
53	S2	1698	C
53	S2	1699	A
53	S2	1700	C
53	S2	1705	C
53	S2	1715	A
53	S2	1719	A
53	S2	1721	U
53	S2	1722	G
53	S2	1742	C
53	S2	1743	G
53	S2	1744	G
53	S2	1745	A
53	S2	1752	C
53	S2	1753	C
53	S2	1754	G
53	S2	1756	C
53	S2	1757	G
53	S2	1758	G

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Mol	Chain	Res	Type
53	S2	1761	U
53	S2	1772	C
53	S2	1773	C
53	S2	1774	C
53	S2	1776	G
53	S2	1777	G
53	S2	1782	G
53	S2	1783	C
53	S2	1786	U
53	S2	1787	G
53	S2	1809	A
53	S2	1810	U
53	S2	1812	U
53	S2	1813	A
53	S2	1822	A
53	S2	1823	A
53	S2	1825	A
53	S2	1826	G
53	S2	1829	G
53	S2	1831	A
53	S2	1835	A
53	S2	1836	G
53	S2	1838	U
53	S2	1849	G
53	S2	1852	C
53	S2	1861	G
53	S2	1862	G
53	S2	1863	A
53	S2	1864	U
53	S2	1865	C

All (22) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	CC	18	G
4	L5	278	G
4	L5	406	C
4	L5	914	U
4	L5	955	G
4	L5	1082	C
4	L5	1633	G
4	L5	1977	C

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Mol	Chain	Res	Type
4	L5	2033	A
4	L5	2416	G
4	L5	2675	G
4	L5	2760	G
4	L5	2786	C
4	L5	3614	G
4	L5	3673	C
4	L5	4378	A
4	L5	4699	U
4	L5	4913	G
53	S2	112	U
53	S2	291	G
53	S2	688	U
53	S2	1434	C

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 264 ligands modelled in this entry, 264 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

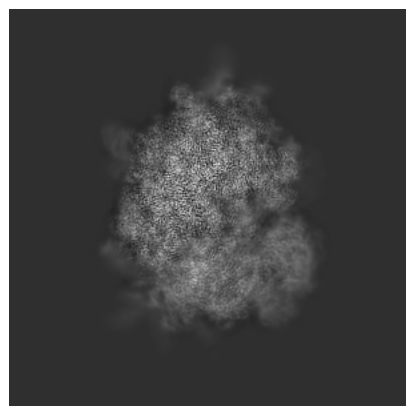
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55613. These allow visual inspection of the internal detail of the map and identification of artifacts.

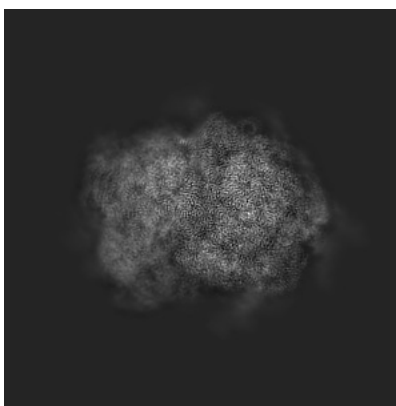
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

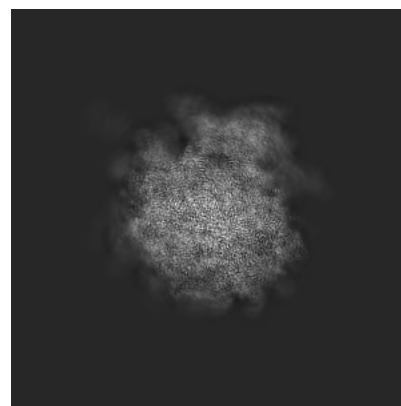
6.1.1 Primary map



X

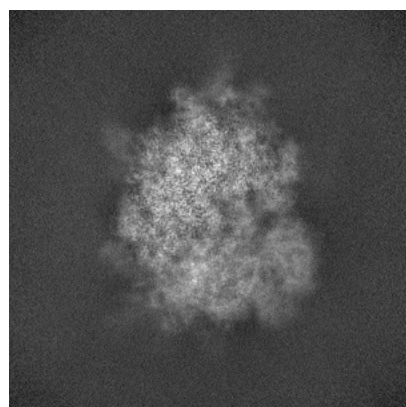


Y

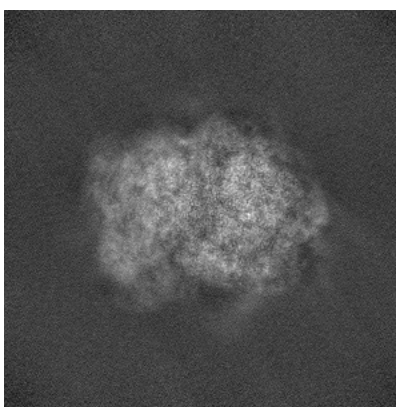


Z

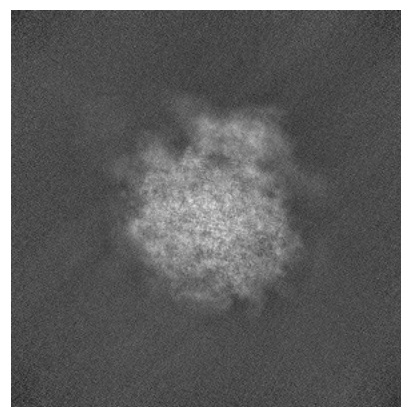
6.1.2 Raw map



X



Y

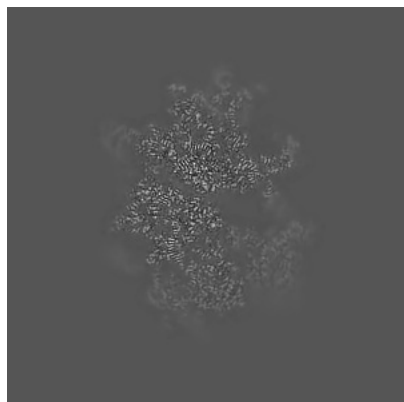


Z

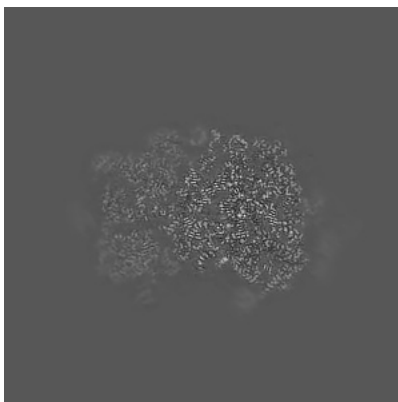
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 320

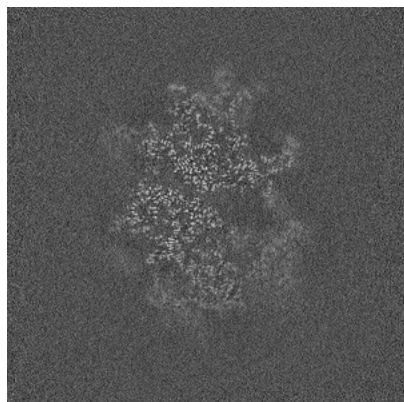


Y Index: 320

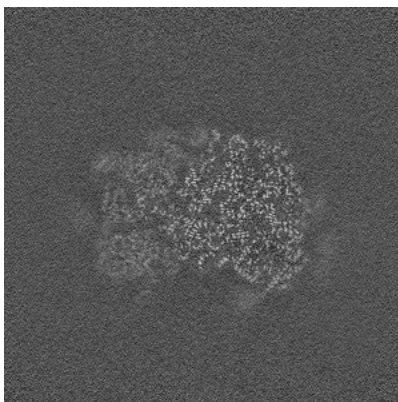


Z Index: 320

6.2.2 Raw map



X Index: 320



Y Index: 320

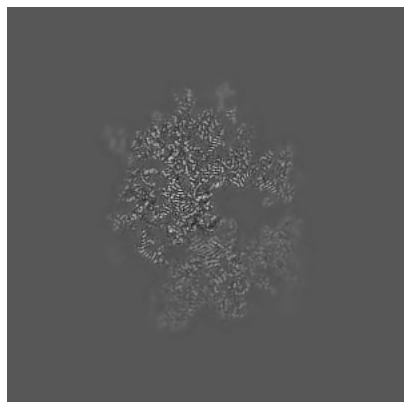


Z Index: 320

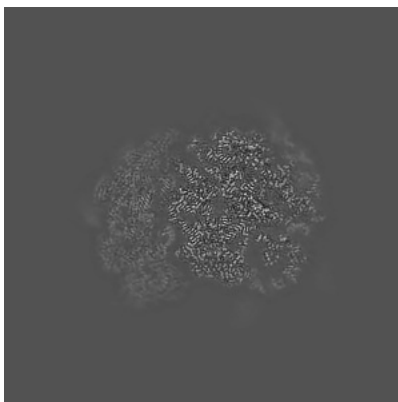
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

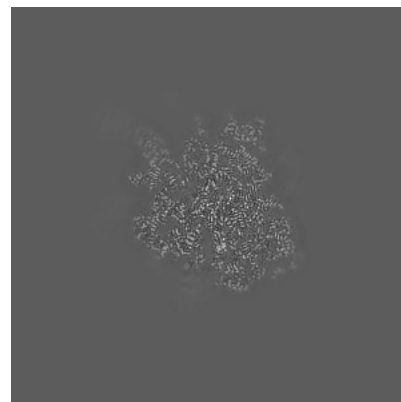
6.3.1 Primary map



X Index: 346

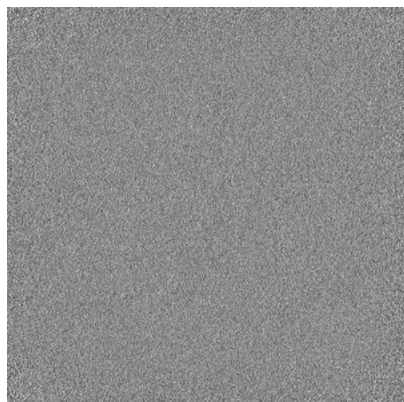


Y Index: 295

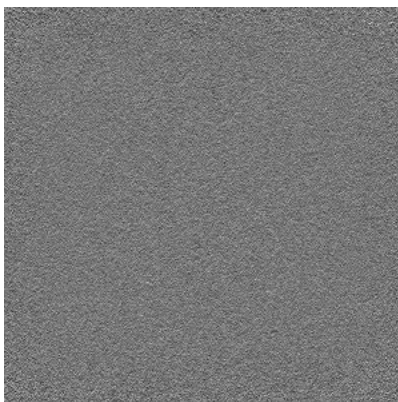


Z Index: 367

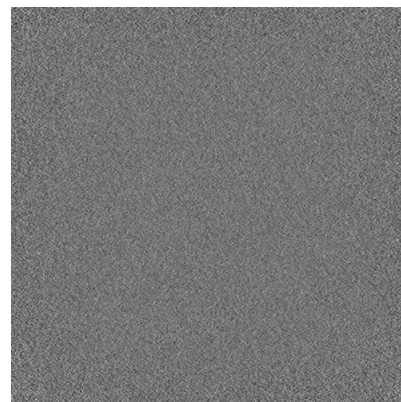
6.3.2 Raw map



X Index: 0



Y Index: 0

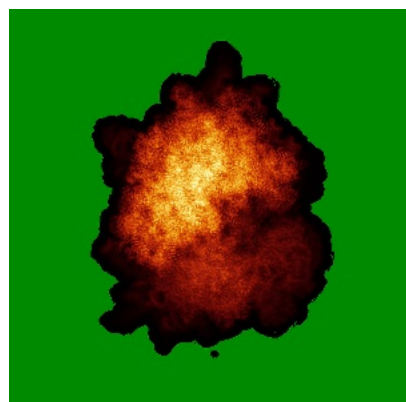


Z Index: 639

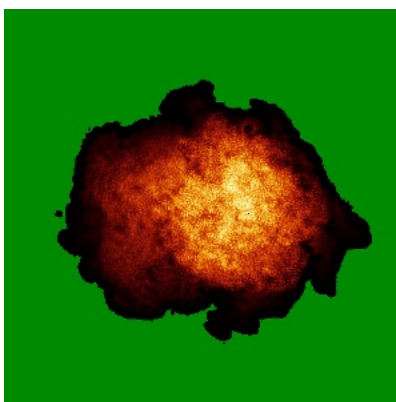
The images above show the largest variance slices of the map in three orthogonal directions.

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

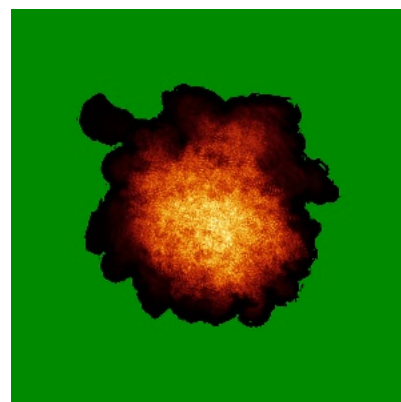
6.4.1 Primary map



X

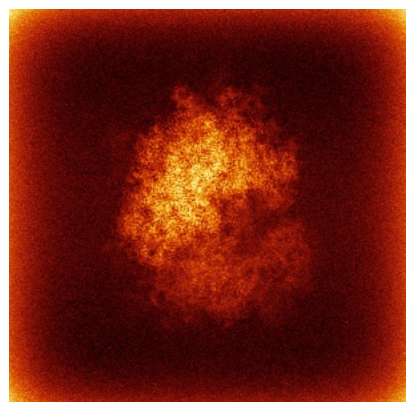


Y

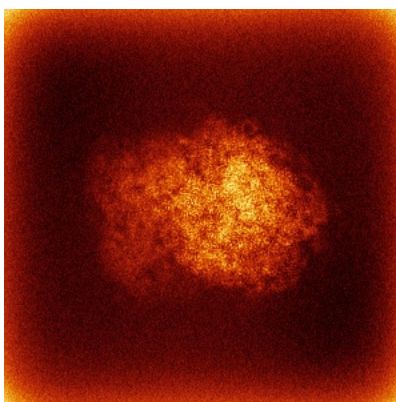


Z

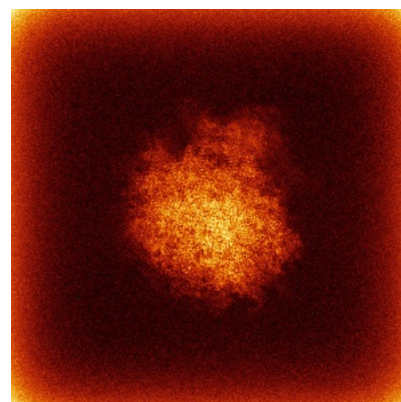
6.4.2 Raw map



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



X



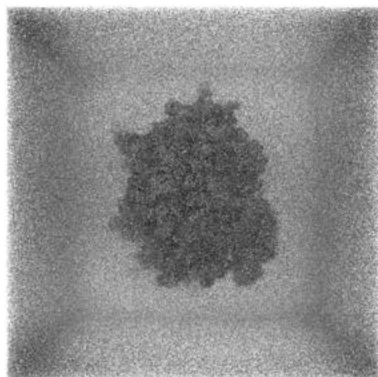
Y



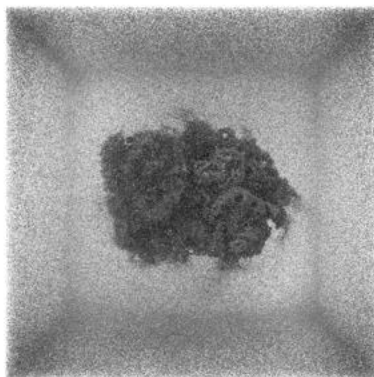
Z

The images above show the 3D surface view of the map at the recommended contour level 0.13. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

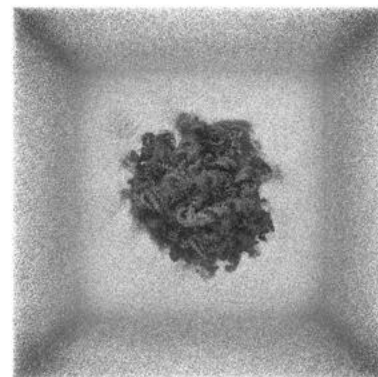
6.5.2 Raw map



X



Y



Z

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

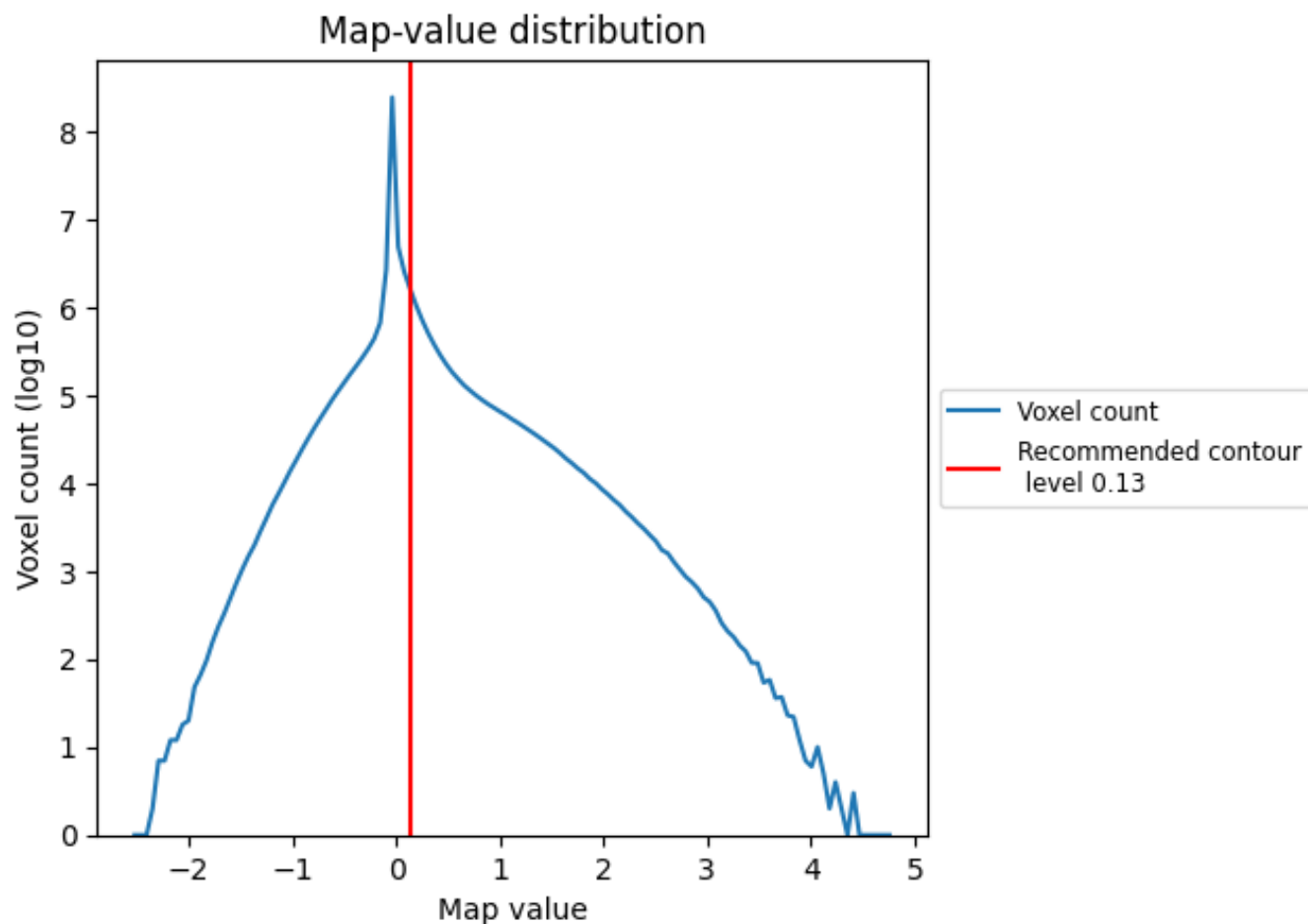
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

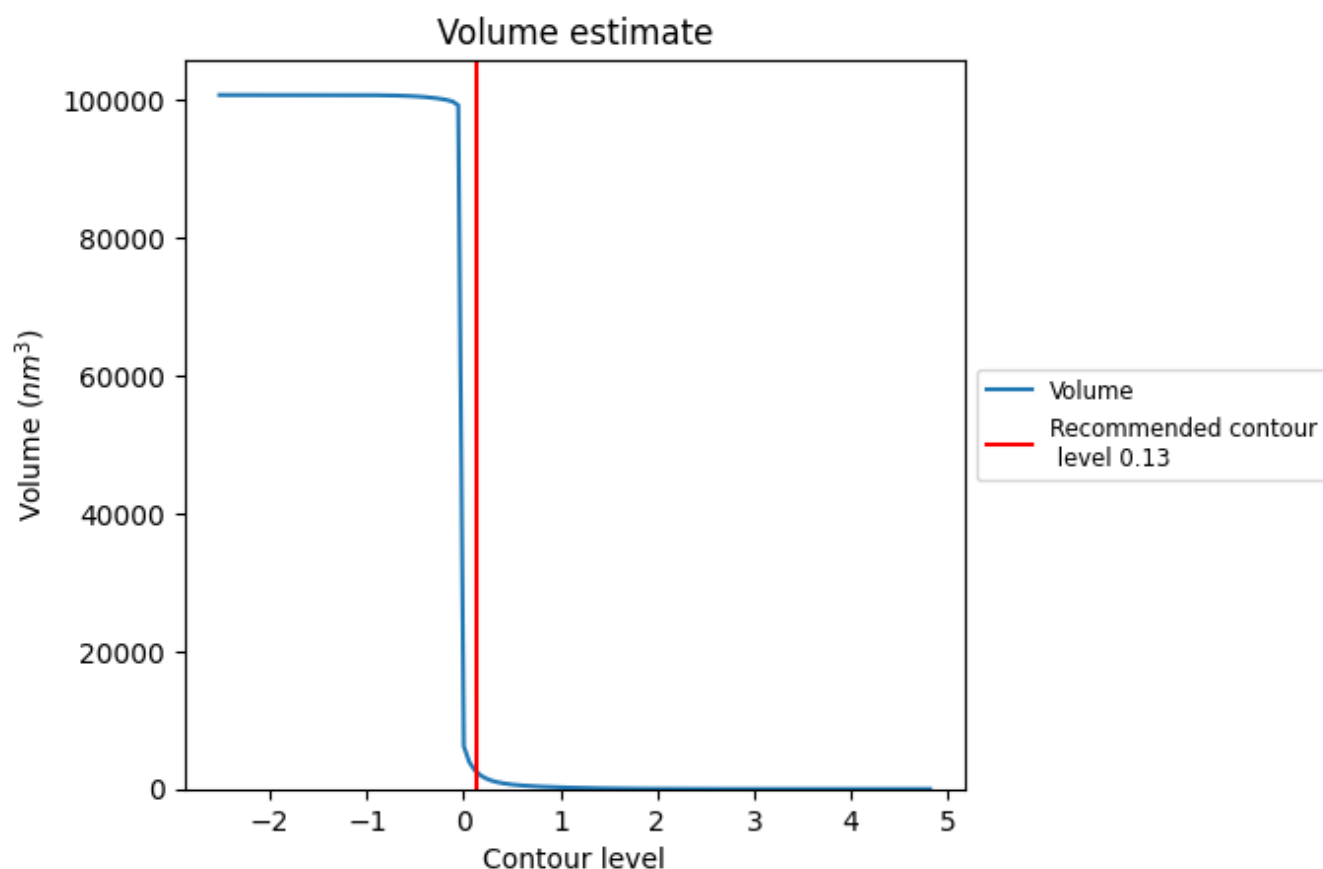
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

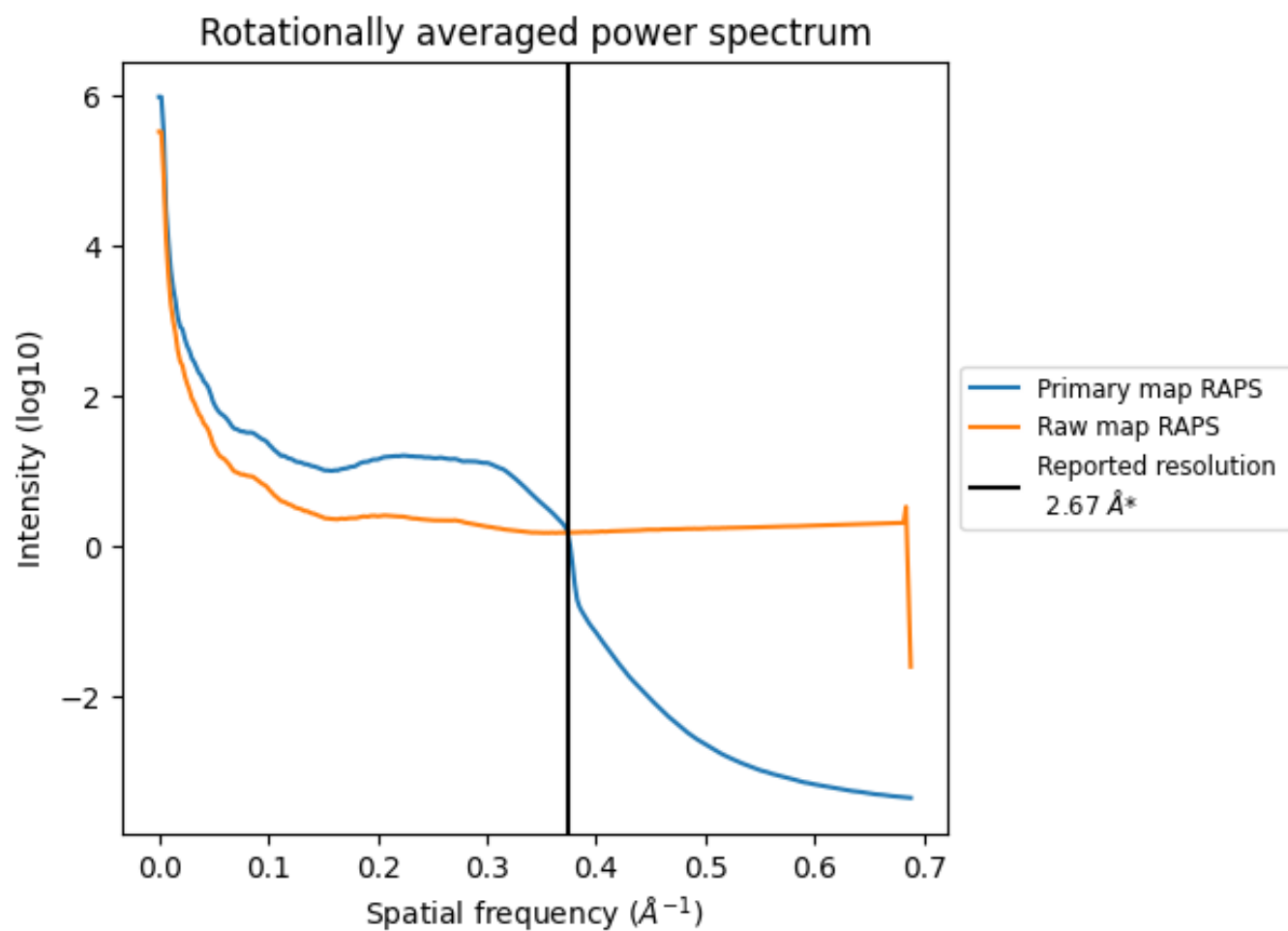
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2535 nm^3 ; this corresponds to an approximate mass of 2290 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 ⓘ

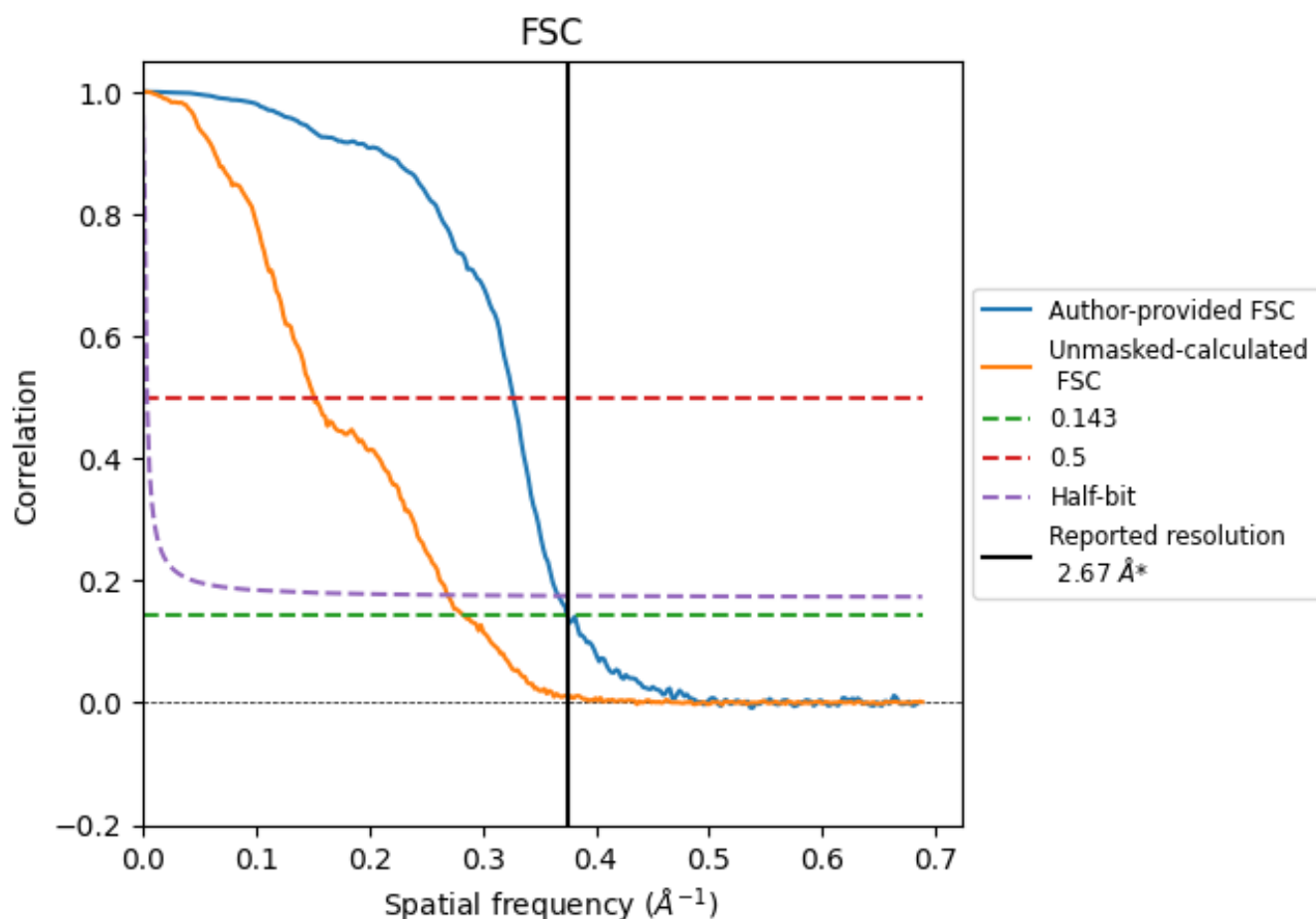


*Reported resolution corresponds to spatial frequency of $0.375 \text{ \AA}^{-1}$

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 0.375 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

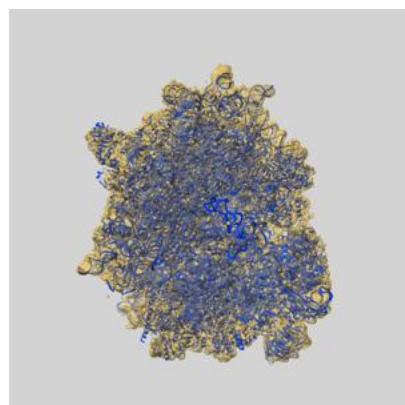
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.67	-	-
Author-provided FSC curve	2.67	3.06	2.73
Unmasked-calculated*	3.52	6.61	3.71

*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 3.52 differs from the reported value 2.67 by more than 10 %

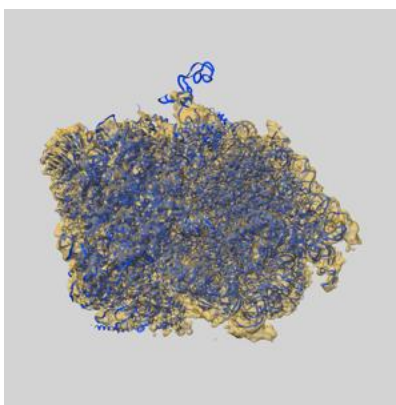
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-55613 and PDB model 9T6D. Per-residue inclusion information can be found in section [3](#) on page [21](#).

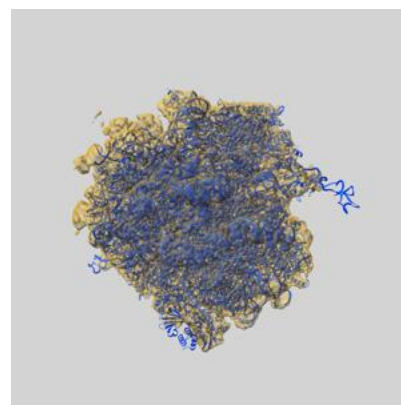
9.1 Map-model overlay [i](#)



X



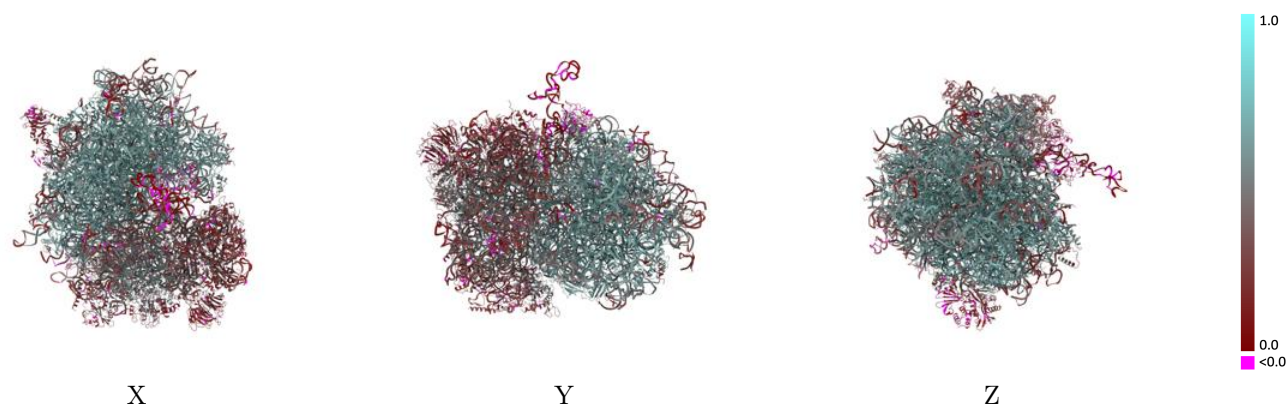
Y



Z

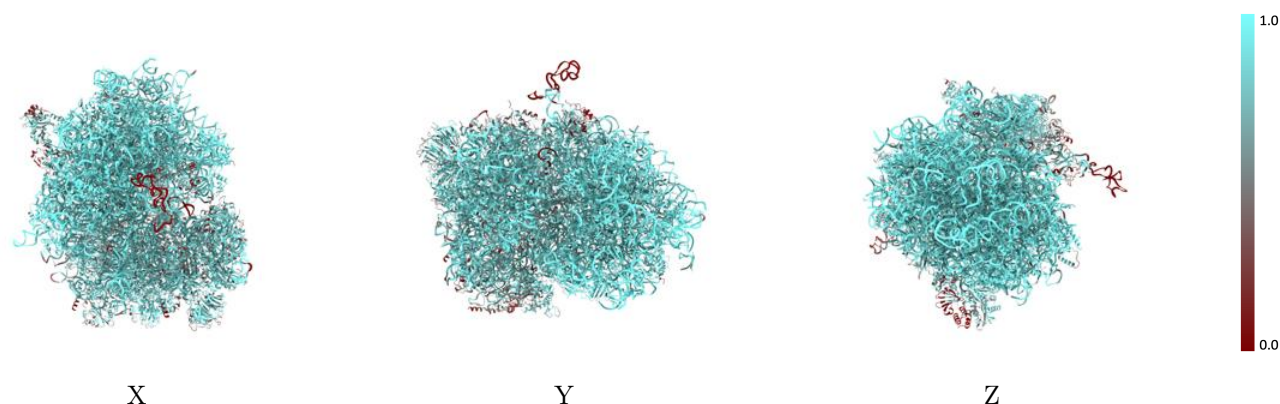
The images above show the 3D surface view of the map at the recommended contour level 0.13 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



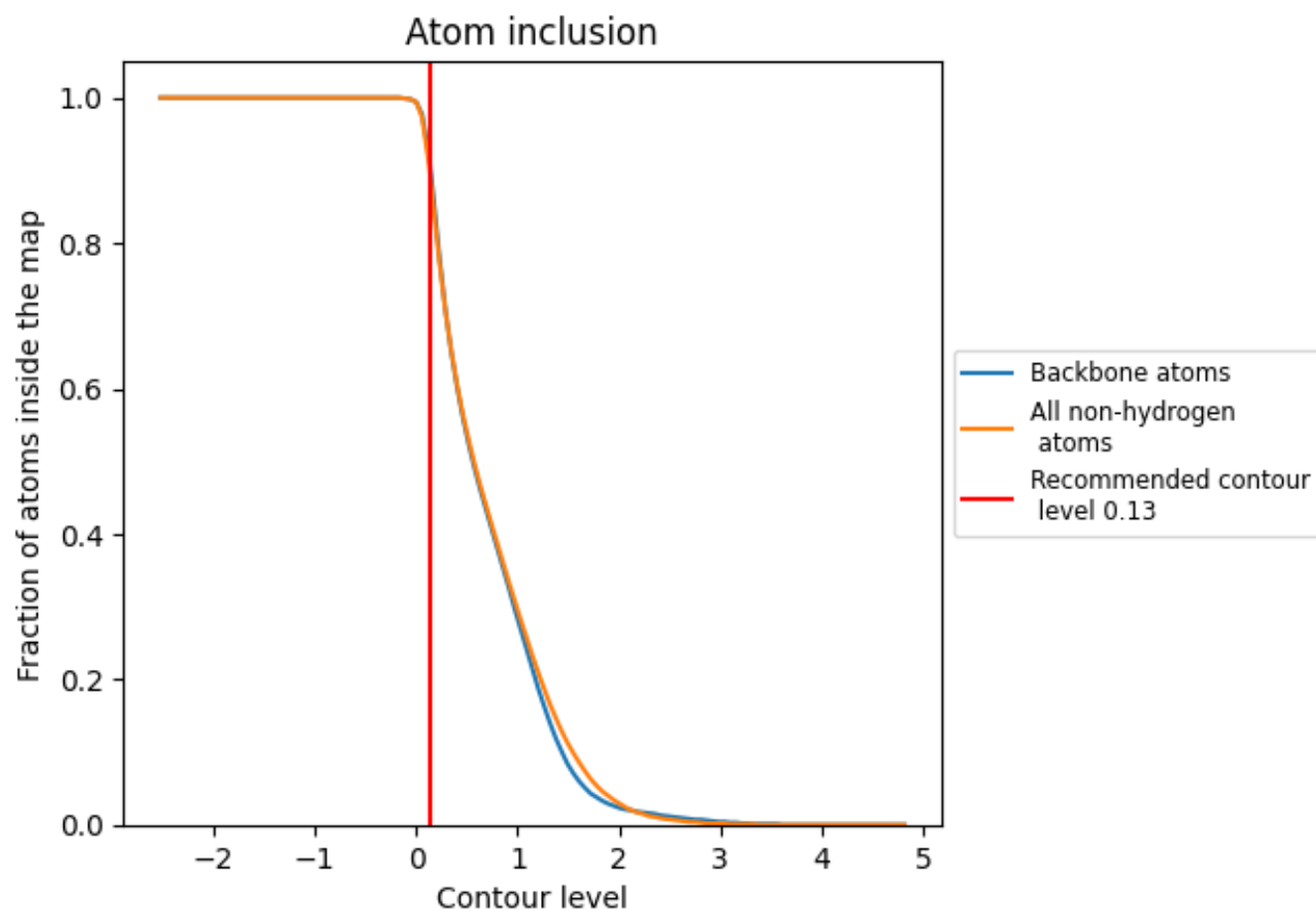
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.13).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 90% 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 (0.13) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9050	 0.4840
CB	 0.7380	 0.3860
CC	 0.7950	 0.2800
CD	 0.7240	 0.3610
L5	 0.9710	 0.5640
L7	 0.9950	 0.6300
L8	 0.9850	 0.6030
LA	 0.9840	 0.6430
LB	 0.9700	 0.6200
LC	 0.9720	 0.6250
LD	 0.9750	 0.5670
LE	 0.9400	 0.5510
LF	 0.9850	 0.6420
LG	 0.9260	 0.5420
LH	 0.9760	 0.6030
LI	 0.9830	 0.6210
LJ	 0.8980	 0.4940
LL	 0.9520	 0.5810
LM	 0.9830	 0.5990
LN	 0.9930	 0.6510
LO	 0.9820	 0.6370
LP	 0.9820	 0.6370
LQ	 0.9950	 0.6490
LR	 0.9210	 0.5640
LS	 0.9900	 0.6430
LT	 0.9620	 0.5930
LU	 0.9280	 0.5200
LV	 0.9820	 0.6390
LW	 0.7120	 0.4250
LX	 0.9660	 0.6060
LY	 0.9860	 0.6270
LZ	 0.9860	 0.5920
La	 0.9850	 0.6430
Lb	 0.9360	 0.5450
Lc	 0.9570	 0.5820



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Chain	Atom inclusion	Q-score
Ld	 0.9590	 0.5990
Le	 0.9910	 0.6470
Lf	 0.9910	 0.6470
Lg	 0.9640	 0.6130
Lh	 0.9610	 0.5930
Li	 0.9740	 0.5840
Lj	 0.9790	 0.6390
Lk	 0.9340	 0.5390
Ll	 0.9840	 0.6210
Lm	 0.9590	 0.6150
Ln	 0.9380	 0.5600
Lo	 0.9550	 0.6040
Lp	 0.9750	 0.6360
Lr	 0.9810	 0.6250
Lz	 0.3960	 0.0660
N4	 0.7160	 0.2150
NA	 0.1340	 0.0850
NB	 0.4280	 0.2060
S2	 0.8930	 0.3800
SA	 0.8590	 0.3850
SB	 0.7900	 0.3400
SC	 0.9130	 0.4610
SD	 0.8220	 0.3380
SE	 0.8430	 0.3370
SF	 0.6440	 0.2290
SG	 0.6150	 0.2170
SH	 0.7480	 0.2870
SI	 0.7190	 0.2760
SJ	 0.8720	 0.3820
SK	 0.8480	 0.2970
SL	 0.8010	 0.3660
SM	 0.7490	 0.1580
SN	 0.8390	 0.3960
SO	 0.7970	 0.3400
SP	 0.7950	 0.2500
SQ	 0.7320	 0.2570
SR	 0.7650	 0.2970
SS	 0.6960	 0.2290
ST	 0.7740	 0.2550
SU	 0.8770	 0.2930
SV	 0.8730	 0.4180
SW	 0.9080	 0.4820

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Chain	Atom inclusion	Q-score
SX	 0.8970	 0.4760
SY	 0.6570	 0.2350
SZ	 0.4750	 0.1730
Sa	 0.8470	 0.3910
Sb	 0.8420	 0.3250
Sc	 0.5330	 0.2460
Sd	 0.9410	 0.4030
Se	 0.7500	 0.3590
Sf	 0.6280	 0.1950
Sg	 0.7520	 0.2080