



Full wwPDB EM Validation Report ⓘ

Sep 23, 2026 – 06:45 pm BST

PDB ID : 9T6I / pdb_00009t6i
EMDB ID : EMD-55616
Title : In vitro reconstituted METAP1-NAA40-NAC bound 80S - State 2
Authors : Guan, D.; Berninghausen, O.; Beckmann, R.
Deposited on : 2025-11-07
Resolution : 3.44 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:

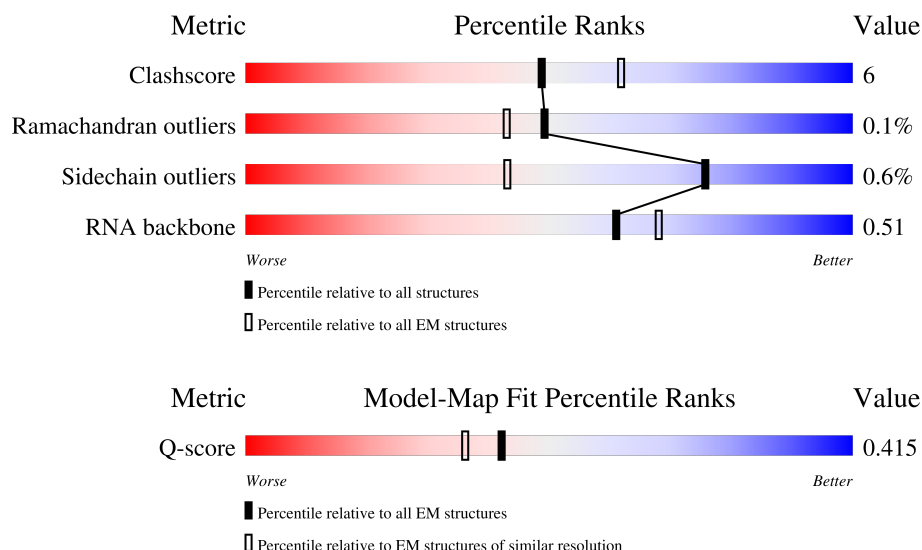
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal 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

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

The reported resolution of this entry is 3.44 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.



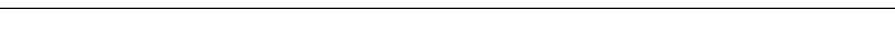
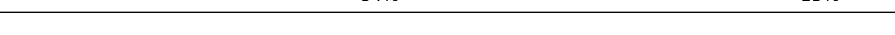
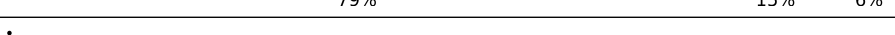
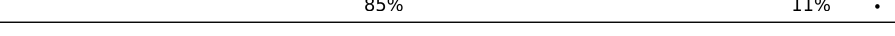
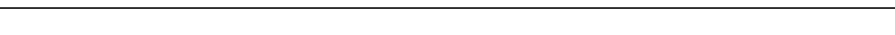
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13877 (2.94 - 3.94)

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

Mol	Chain	Length	Quality of chain
1	L5	5070	
2	L7	121	
3	L8	157	

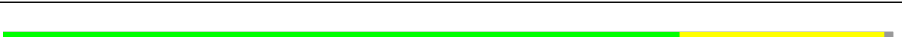
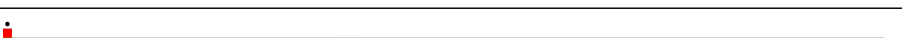
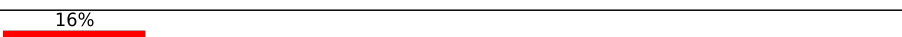
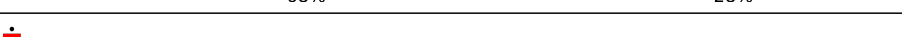
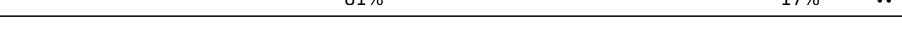
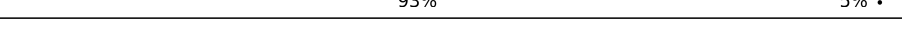
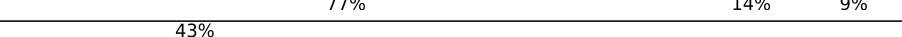
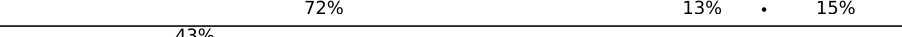
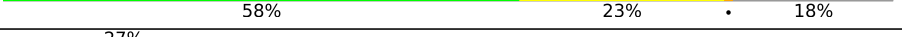
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Mol	Chain	Length	Quality of chain
4	LA	257	
5	LB	403	
6	LC	427	
7	LD	297	
8	LE	288	
9	LF	248	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	215	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	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

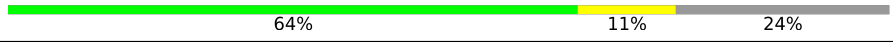
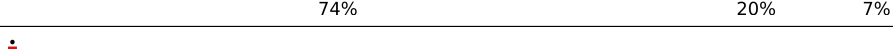
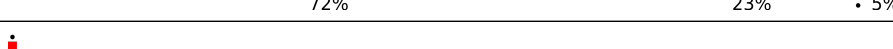
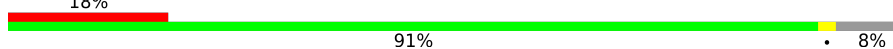
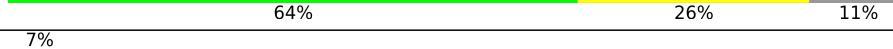
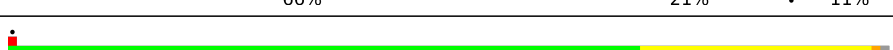
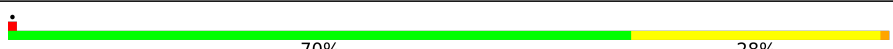
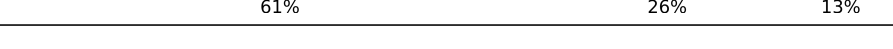
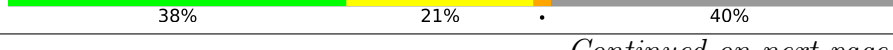
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Mol	Chain	Length	Quality of chain
29	La	148	
30	Lb	159	
31	Lc	115	
32	Ld	125	
33	Le	135	
34	Lf	110	
35	Lg	117	
36	Lh	123	
37	Li	105	
38	Lj	97	
39	Lk	70	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	Lr	137	
46	Ls	317	
47	Lt	165	
48	MA	386	
49	N4	237	
50	NA	215	
51	NB	162	
52	S2	1869	
53	SA	295	

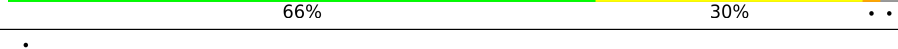
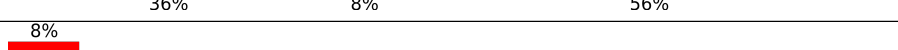
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Mol	Chain	Length	Quality of chain
54	SB	264	
55	SC	293	
56	SD	243	
57	SE	263	
58	SF	204	
59	SG	249	
60	SH	194	
61	SI	208	
62	SJ	194	
63	SK	165	
64	SL	158	
65	SM	132	
66	SN	151	
67	SO	151	
68	SP	145	
69	SQ	146	
70	SR	135	
71	SS	152	
72	ST	145	
73	SU	119	
74	SV	83	
75	SW	130	
76	SX	143	
77	SY	133	
78	SZ	125	

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

2 Entry composition [i](#)

There are 87 unique types of molecules in this entry. The entry contains 221549 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L5	3670	Total	C	N	O	P	0	0
			78678	35036	14400	25573	3669		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L5	2113	C	G	conflict	GB 86475748

- Molecule 2 is a RNA chain called 5S rRNA.

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

- Molecule 3 is a RNA chain called 5.8S rRNA.

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LC	365	Total	C	N	O	S	0	0
			2908	1829	580	486	13		

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

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

- Molecule 8 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LE	221	Total	C	N	O	S	0	0
			1774	1142	336	292	4		

- Molecule 9 is a protein called Large ribosomal subunit protein uL30.

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LI	202	Total	C	N	O	S	0	0
			1639	1041	316	269	13		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LJ	171	Total	C	N	O	S	0	0
			1371	867	256	242	6		

- Molecule 14 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LL	207	Total	C	N	O	S	0	0
			1673	1046	346	277	4		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LU	100	Total	C	N	O	S	0	0
			816	524	142	148	2		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LW	124	Total	C	N	O	S	0	0
			1015	634	207	170	4		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LY	133	Total	C	N	O	S	0	0
			1106	694	224	185	3		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lb	109	Total	C	N	O	S	0	0
			882	549	192	137	4		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 38 is a protein called Large ribosomal subunit protein eL37.

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

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

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

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

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

- Molecule 41 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lm	52	Total	C	N	O	S	0	0
			430	267	90	67	6		

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

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

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

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

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

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

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

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

- Molecule 46 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Ls	196	Total	C	N	O	S	0	0
			1496	952	259	276	9		

- Molecule 47 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lt	141	Total	C	N	O	S	0	0
			1046	652	191	199	4		

- Molecule 48 is a protein called Methionine aminopeptidase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	MA	315	Total	C	N	O	S	0	0
			2485	1562	443	462	18		

- Molecule 49 is a protein called N-alpha-acetyltransferase 40.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	N4	223	Total	C	N	O	S	0	0
			1809	1136	317	341	15		

- Molecule 50 is a protein called Nascent polypeptide-associated complex subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	NA	108	Total	C	N	O	S	0	0
			841	524	153	160	4		

- Molecule 51 is a protein called Isoform 2 of Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	NB	106	Total	C	N	O	S	0	0
			821	514	153	151	3		

- Molecule 52 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	S2	1719	Total	C	N	O	P	0	0
			36456	16264	6516	11958	1718		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S2	582	C	U	conflict	GB 36162
S2	583	C	A	conflict	GB 36162
S2	584	G	A	conflict	GB 36162
S2	798	A	G	conflict	GB 36162
S2	1095	U	C	conflict	GB 36162

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

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

- Molecule 54 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SB	221	Total	C	N	O	S	0	0
			1791	1135	323	319	14		

- Molecule 55 is a protein called 40S ribosomal protein S2.

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

- Molecule 56 is a protein called 40S ribosomal protein S3.

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

- Molecule 57 is a protein called Small ribosomal subunit protein eS4, X isoform.

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

- Molecule 58 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SF	184	Total	C	N	O	S	0	0
			1461	914	276	264	7		

- Molecule 59 is a protein called 40S ribosomal protein S6.

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

- Molecule 60 is a protein called 40S ribosomal protein S7.

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

- Molecule 61 is a protein called 40S ribosomal protein S8.

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

- Molecule 62 is a protein called 40S ribosomal protein S9.

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

- Molecule 63 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SK	95	Total	C	N	O	S	0	0
			799	524	139	130	6		

- Molecule 64 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SL	144	Total	C	N	O	S	0	0
			1182	752	224	200	6		

- Molecule 65 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms				AltConf	Trace
65	SM	122	Total	C	N	O	0	0
			604	359	122	123		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SM	52	GLN	LEU	conflict	UNP P25398
SM	69	LEU	CYS	conflict	UNP P25398
SM	99	ASN	LYS	conflict	UNP P25398

- Molecule 66 is a protein called 40S ribosomal protein S13.

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

- Molecule 67 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SO	135	Total	C	N	O	S	0	0
			1010	618	198	188	6		

- Molecule 68 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SP	129	Total	C	N	O	S	0	0
			1061	672	202	180	7		

- Molecule 69 is a protein called 40S ribosomal protein S16.

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

- Molecule 70 is a protein called 40S ribosomal protein S17.

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

- Molecule 71 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SS	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 72 is a protein called 40S ribosomal protein S19.

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

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

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

- Molecule 74 is a protein called 40S ribosomal protein S21.

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

- Molecule 75 is a protein called 40S ribosomal protein S15a.

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

- Molecule 76 is a protein called 40S ribosomal protein S23.

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

- Molecule 77 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SY	126	Total	C	N	O	S	0	0
			1027	648	201	173	5		

- Molecule 78 is a protein called 40S ribosomal protein S25.

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

- Molecule 79 is a protein called 40S ribosomal protein S26.

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

- Molecule 80 is a protein called 40S ribosomal protein S27.

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

- Molecule 81 is a protein called 40S ribosomal protein S28.

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

- Molecule 82 is a protein called 40S ribosomal protein S29.

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

- Molecule 83 is a protein called Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein.

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

- Molecule 84 is a protein called Ubiquitin.

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

- Molecule 85 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	L5	213	Total	Mg	0
			213	213	
86	L7	3	Total	Mg	0
			3	3	
86	L8	4	Total	Mg	0
			4	4	
86	LA	1	Total	Mg	0
			1	1	
86	LI	1	Total	Mg	0
			1	1	
86	LP	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
86	LV	1	Total 1	Mg 1	0
86	Le	1	Total 1	Mg 1	0
86	Lj	1	Total 1	Mg 1	0
86	S2	31	Total 31	Mg 31	0

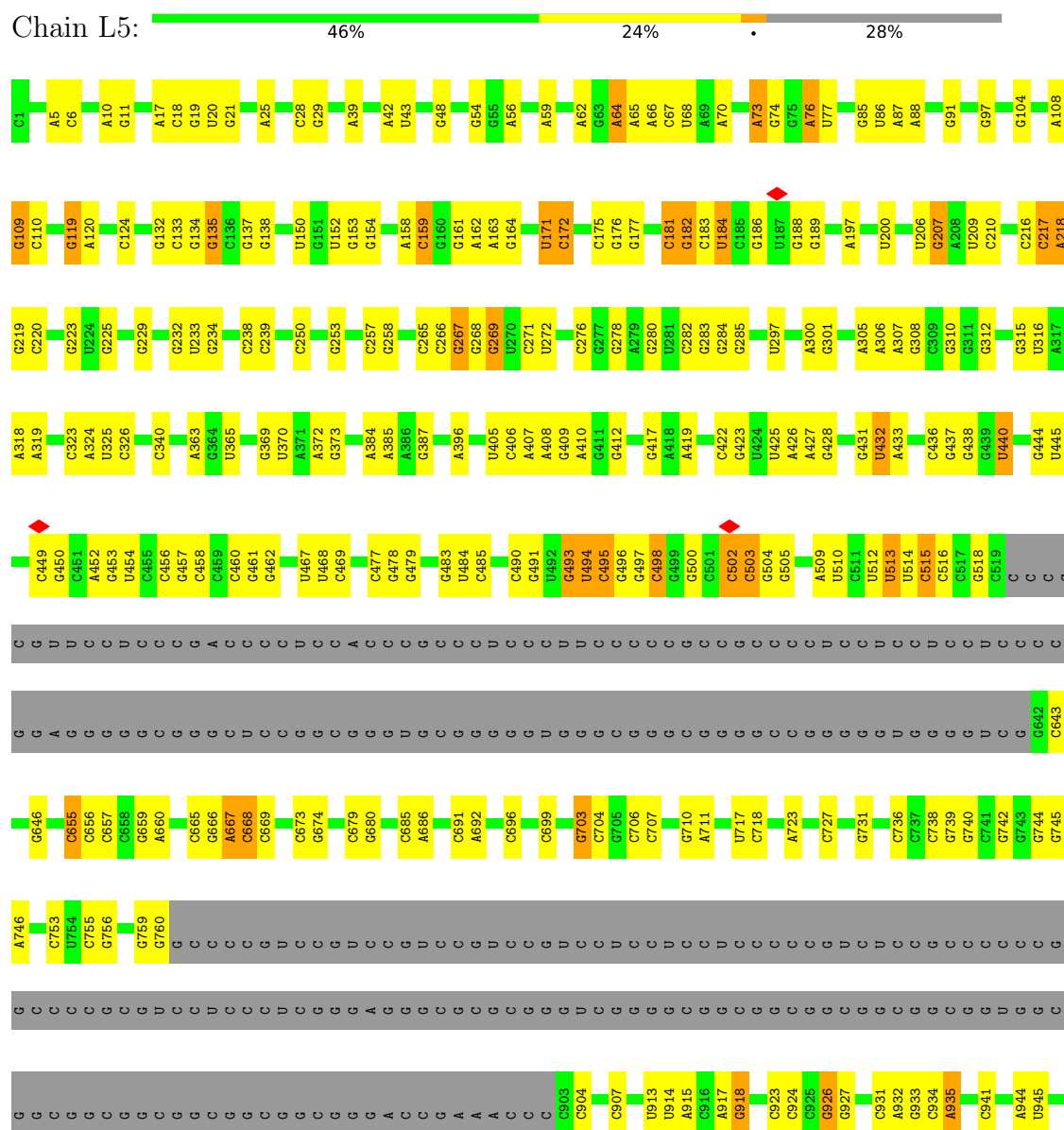
- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
87	Lg	1	Total 1	Zn 1	0
87	Lj	1	Total 1	Zn 1	0
87	Lm	1	Total 1	Zn 1	0
87	Lo	1	Total 1	Zn 1	0
87	Lp	1	Total 1	Zn 1	0
87	Sa	1	Total 1	Zn 1	0
87	Sd	1	Total 1	Zn 1	0
87	Sf	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: 28S rRNA



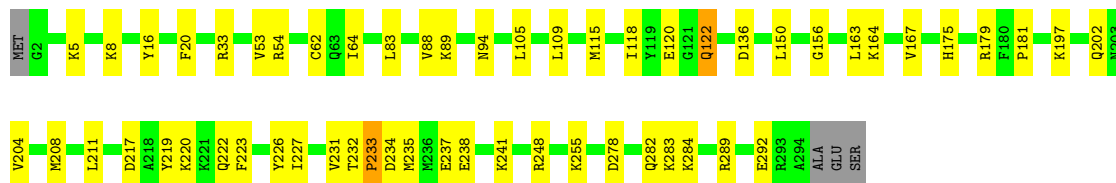


G3654	G	U2788	A2696	U2545	G2450	G2321	G
G3661	C	A2789	C2699	G2546	G2456	G2326	C
A3662	G	U2790	G2700	G2547	G2457	G2326	C
G3663	C	G2793	U2701	U2554	C2458	A	C
G3664	G	C2794	C2702	G2555	G2459	U2329	C
G3665	C	A2806	G2703	G2556	C2462	G2330	G
C3666	C	G2809	U2707	C2557	G2462	G2331	C
C3667	C	G2809	U2708	C2558	G2471	A2332	C
C3673	C	A2812	G2709	U2559	C2471	G2333	C
G3674	C	G2813	G2710	C2560	G2475	C2335	G
U3680	U	C2814	G2711	A2565	C2478	G2336	C
U3684	U	G2712	G2713	C2568	C2479	G2342	U
G3685	G	C2714	G2714	G2569	G2479	G2343	C
G3686	G	A2825	G2715	U2570	G2483	C	C
G3687	G	U2826	G2719	A2573	A2484	A2349	C
G3688	C	G2827	C2720	G2578	U2485	U2350	G
G3689	C	A2835	G2721	G2579	G2486	C2351	C
G3690	C	U2836	G2724	C2582	C2488	U2352	C
G3691	C	G2837	A2725	C2583	C2489	A2360	C
G3692	C	G2842	G2726	G2587	U2490	G2361	C
G3693	C	A2845	U2730	C2588	U2495	A2382	C
G3694	C	G2846	C2731	C2589	G2496	A2382	C
G3695	C	G2847	G2739	A2598	G2503	U2385	C
G3696	C	G2848	C2742	A2601	C2504	U2386	C
G3697	C	G2855	A2743	A2611	G2505	U2387	C
G3698	C	C2856	A2744	A2611	C2506	C2258	C
U3707	U	G2863	A2745	A2623	A2507	G2259	C
C3708	C	G2877	G2749	C2627	A2508	G2262	C
C3709	C	G2884	G2750	A2627	C2509	A2268	C
C3710	C	A2885	G2751	G2640	G2510	G2405	C
A3711	A	G2890	G2752	A2641	A2511	G2406	C
A3712	A	U2891	G2756	C2653	A2512	G2407	C
A3713	A	A2894	G2760	G2652	A2513	C2410	C
U3714	U	A2895	U2761	C2669	G2514	A2412	C
A3717	A	G2896	G2762	C2670	G2515	G2283	C
A3718	A	G2897	U2763	C2671	A2517	C2289	C
A3719	A	G2898	U2769	C2672	U2519	G2296	C
U3720	U	U2900	C2770	A2675	C2520	G2297	C
U3721	U	G2901	G2771	A2676	G2521	A2417	C
U3722	U	G2902	C2772	U2538	A2529	G2421	C
A3723	A	G2903	G2773	C2539	C2532	C2422	C
A3726	A	U2904	C2780	G2541	A2537	A2423	C
A3727	A	G2905	G2781	G2542	U2538	G2424	C
A3733	A	G2906	U2907	A2543	C2537	G2443	C
U3734	U	U2907	C2909	A2595	A2537	G2448	C
G3735	G	G2908	C2909	A2695	U2537	A2449	C
A3736	A	G2909	C2909	A2695	A2537	A2449	C
A3737	A	G2910	C2909	A2695	A2537	A2449	C
A3748	A	G2911	C2909	A2695	A2537	A2449	C
C3749	C	G2912	C2909	A2695	A2537	A2449	C
G3750	G	G2913	C2909	A2695	A2537	A2449	C
G3753	G	G2914	C2909	A2695	A2537	A2449	C
A3759	A	G2915	C2909	A2695	A2537	A2449	C
A3760	A	G2916	C2909	A2695	A2537	A2449	C
C3761	C	G2917	C2909	A2695	A2537	A2449	C



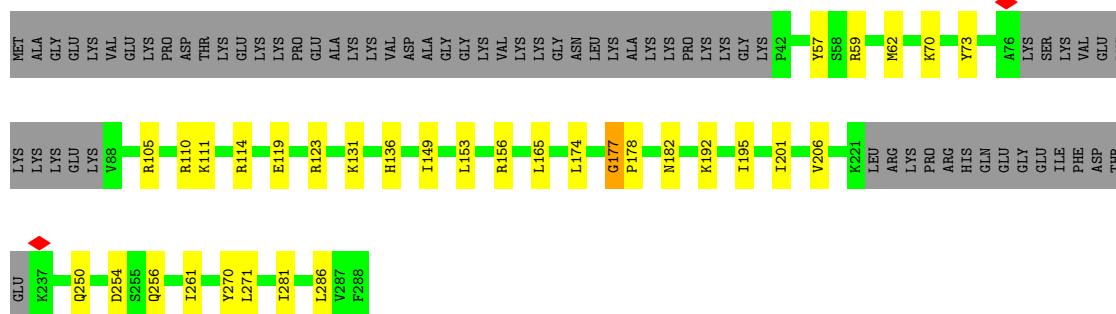
- Molecule 7: 60S ribosomal protein L5

Chain LD:  80% 18% ..



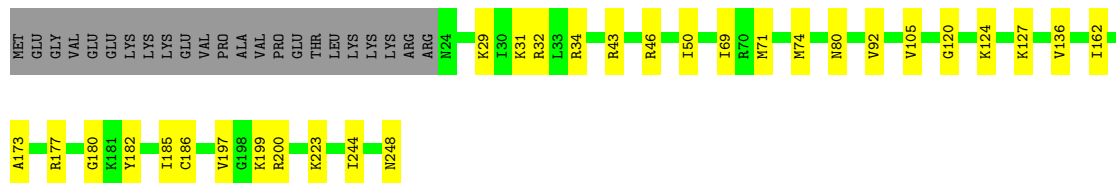
- Molecule 8: Large ribosomal subunit protein eL6

Chain LE:  65% 11% 23%



- Molecule 9: Large ribosomal subunit protein uL30

Chain LF:  79% 12% 9%



- Molecule 10: 60S ribosomal protein L7a

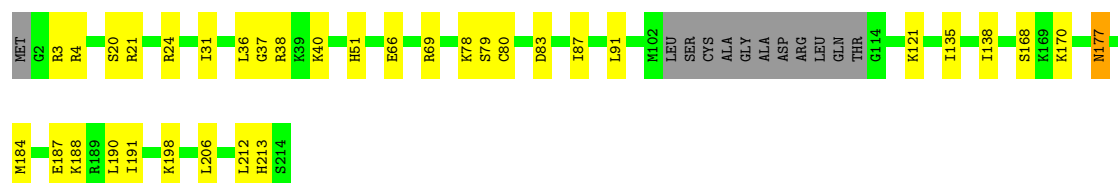
Chain LG:  71% 20% 9%

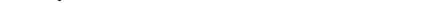


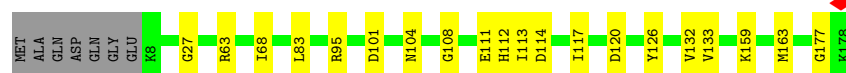
- Molecule 11: 60S ribosomal protein L9

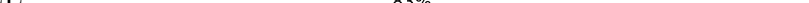
#1
Q8
T9
V10
D11
E44
K51
R66
V57
D58
R64
R71
K91
S94
V103
E107
L111
V112
E113
I114
R115
R125
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N156
I161
Q162
Q163
R173
L176
E183
A190
ASP

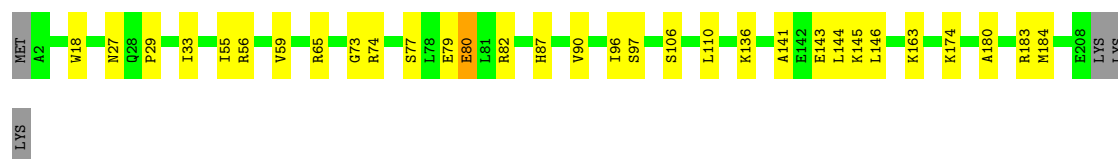
- Chain LI:  79% 15% 6%

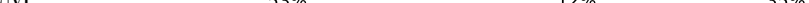


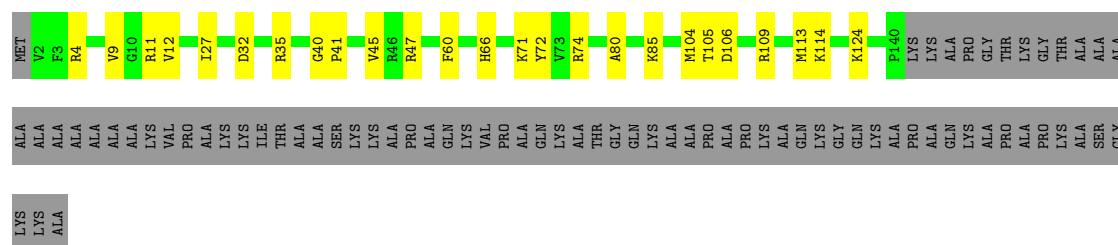
- Chain LJ:  85% 11% .



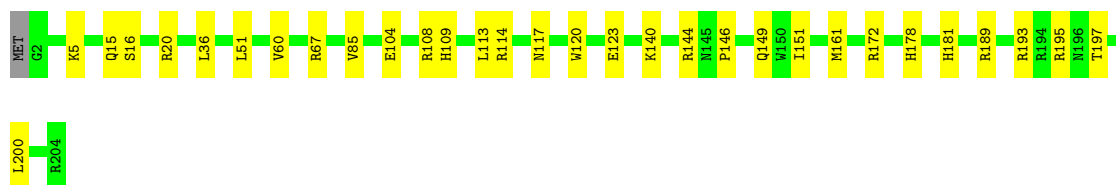
- Chain LL:  83% 14%



- Chain LM:  53% 12% 35%



- Chain LN: 



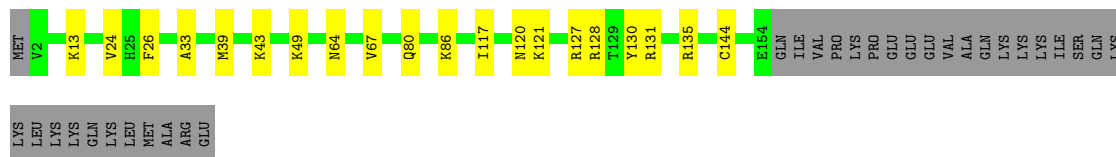
- Molecule 17: 60S ribosomal protein L13a

Chain LO: 89% 10% .



- Molecule 18: 60S ribosomal protein L17

Chain LP: 72% 11% 17%



- Molecule 19: 60S ribosomal protein L18

Chain LQ: 89% 10% ..



- Molecule 20: 60S ribosomal protein L19

Chain LR: 82% 13% 5%



- Molecule 21: 60S ribosomal protein L18a

Chain LS: 84% 15% .



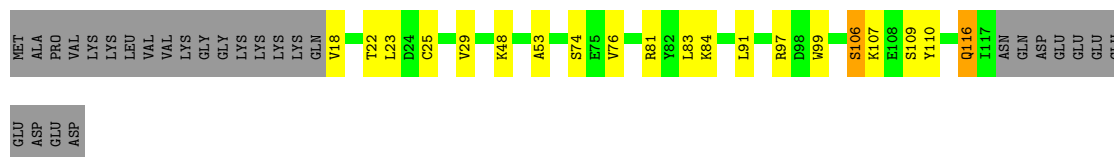
- Molecule 22: 60S ribosomal protein L21

Chain LT: 84% 16% .



- Molecule 23: 60S ribosomal protein L22

Chain LU: 62% 14% 22%



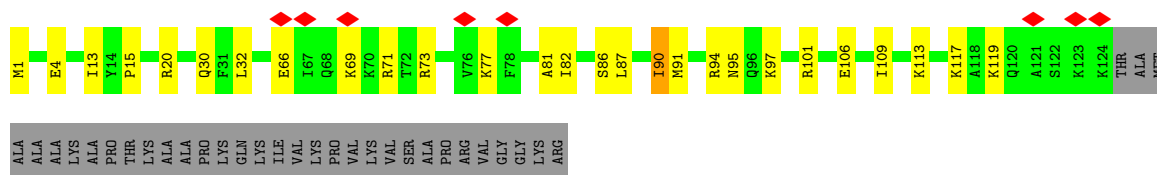
- Molecule 24: 60S ribosomal protein L23

Chain LV: 84% 9% 6%



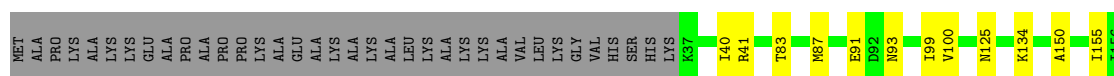
- Molecule 25: 60S ribosomal protein L24

Chain LW: 5% 62% 17% 21%



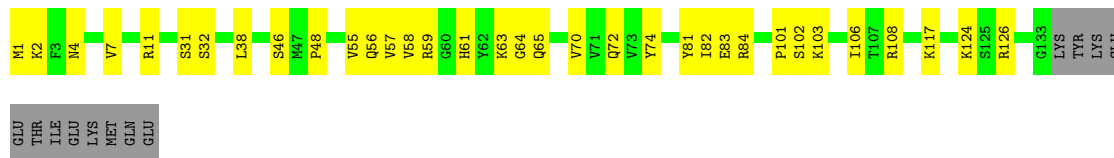
- Molecule 26: 60S ribosomal protein L23a

Chain LX: 69% 8% 23%



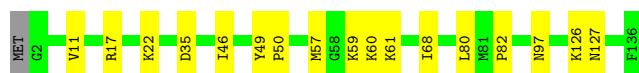
- Molecule 27: 60S ribosomal protein L26

Chain LY: 68% 23% 8%



- Molecule 28: 60S ribosomal protein L27

Chain LZ: 87% 12% 1%



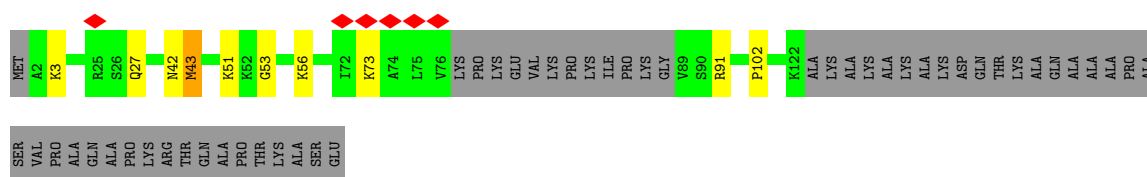
- Molecule 29: 60S ribosomal protein L27a

Chain La: 86% 14%



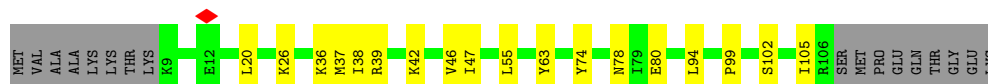
- Molecule 30: 60S ribosomal protein L29

Chain Lb: 62% 6% 31%



- Molecule 31: 60S ribosomal protein L30

Chain Lc: 70% 16% 15%



- Molecule 32: 60S ribosomal protein L31

Chain Ld: 70% 16% 14%



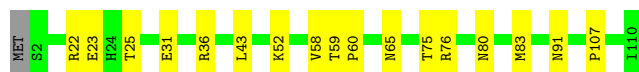
- Molecule 33: 60S ribosomal protein L32

Chain Le: 79% 16% 5%



- Molecule 34: 60S ribosomal protein L35a

Chain Lf: 84% 15%



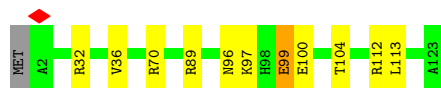
- Molecule 35: 60S ribosomal protein L34

Chain Lg:  83% 15% .



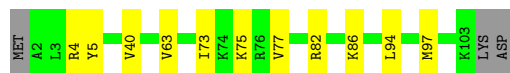
- Molecule 36: 60S ribosomal protein L35

Chain Lh:  90% 8% ..



- Molecule 37: 60S ribosomal protein L36

Chain Li:  87% 10% .



- Molecule 38: Large ribosomal subunit protein eL37

Chain Lj:  73% 15% 11%



- Molecule 39: 60S ribosomal protein L38

Chain Lk:  76% 23% .



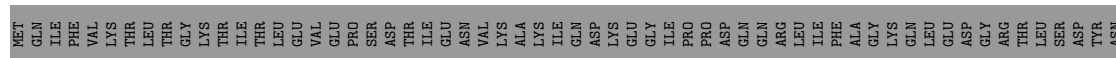
- Molecule 40: 60S ribosomal protein L39

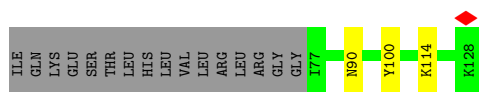
Chain Ll:  78% 20% .



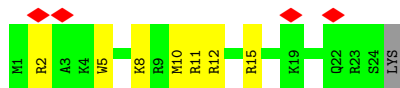
- Molecule 41: Large ribosomal subunit protein eL40

Chain Lm:  38% 59%

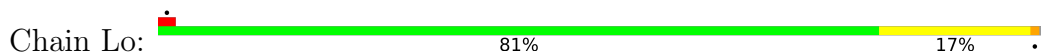




- Molecule 42: 60S ribosomal protein L41



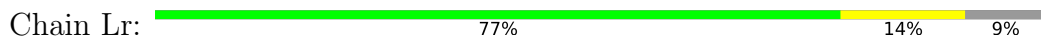
- Molecule 43: 60S ribosomal protein L36a



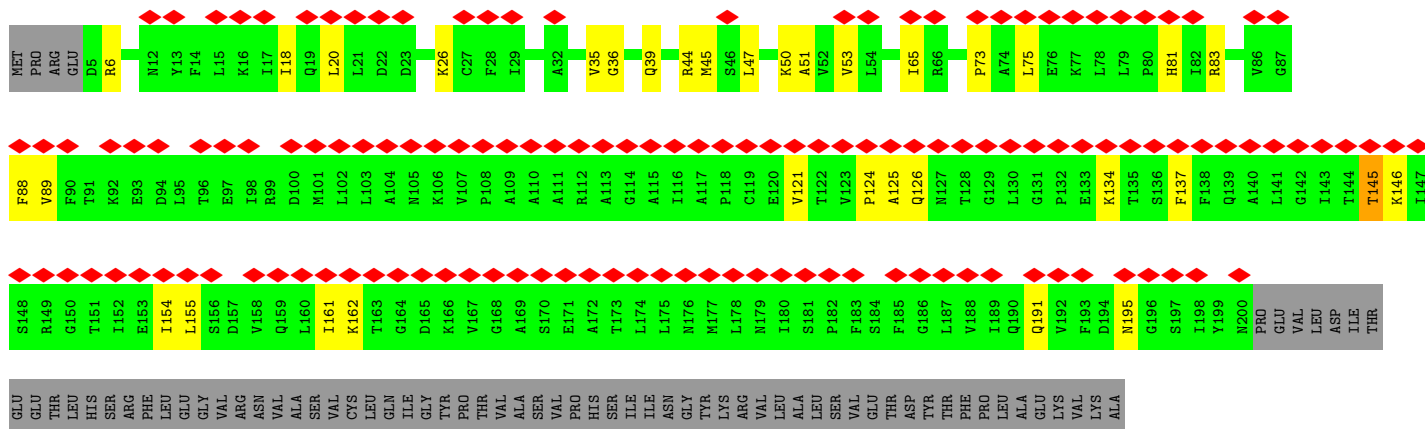
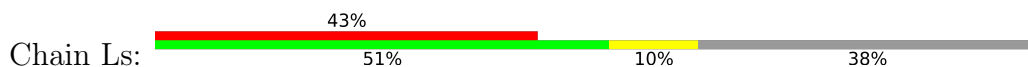
- Molecule 44: 60S ribosomal protein L37a



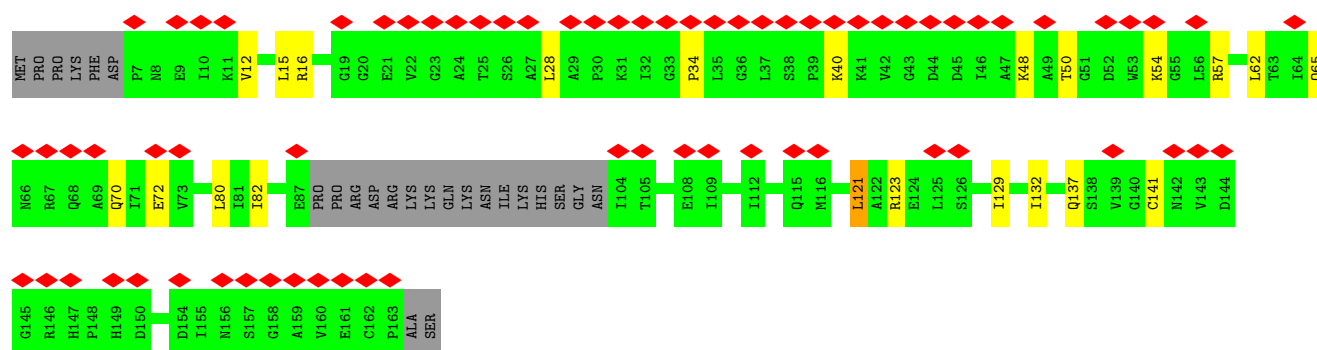
- Molecule 45: 60S ribosomal protein L28



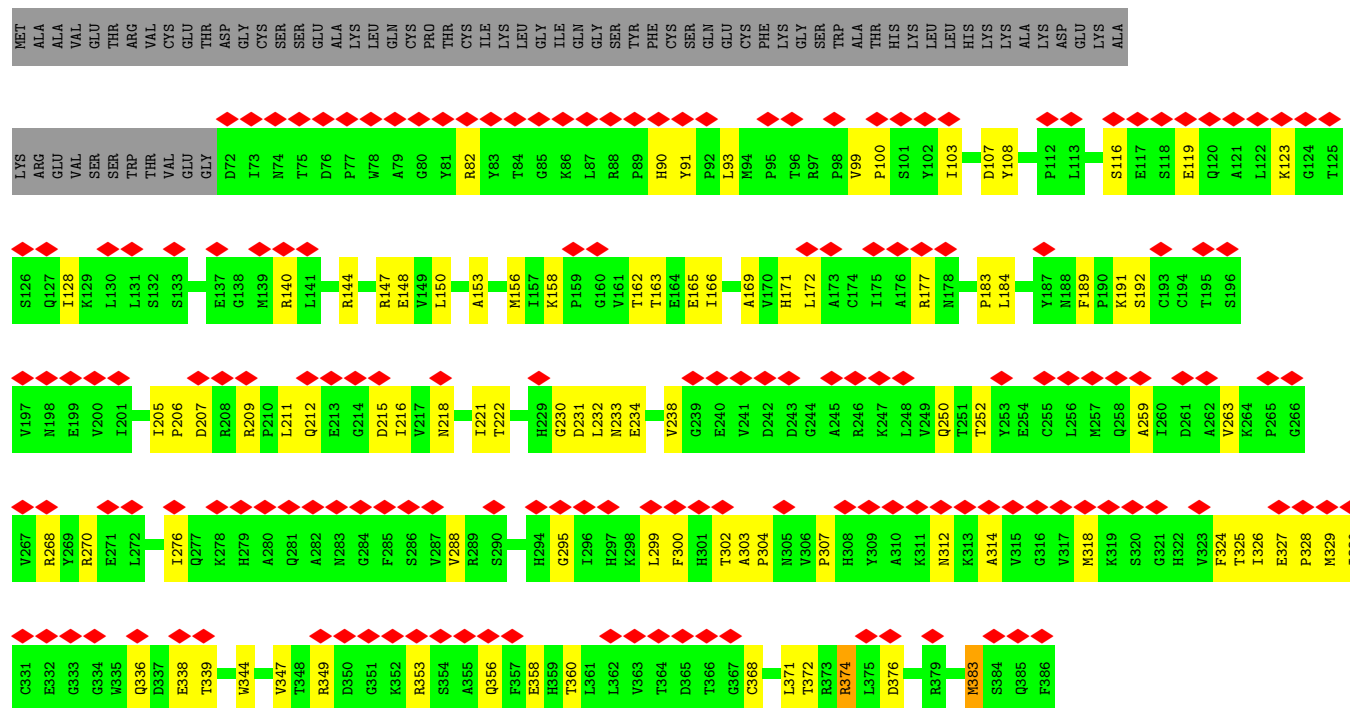
- Molecule 46: 60S acidic ribosomal protein P0



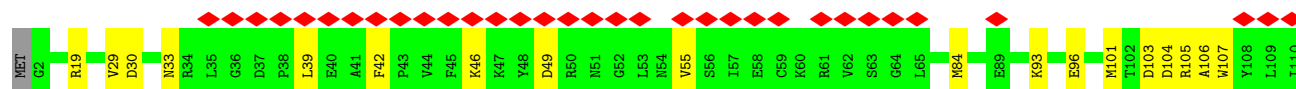
Chain Lt: 43% 72% 13% 15%

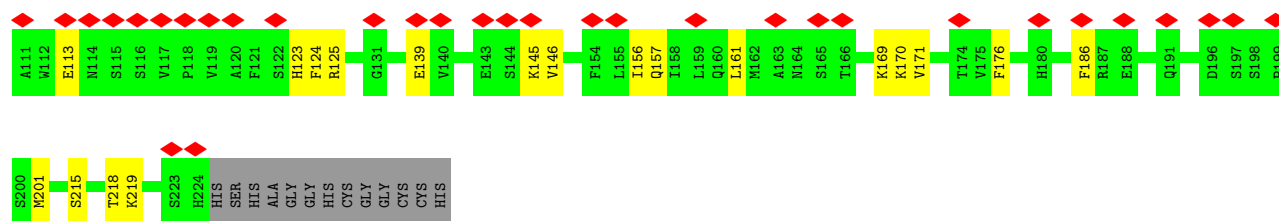


Chain MA:



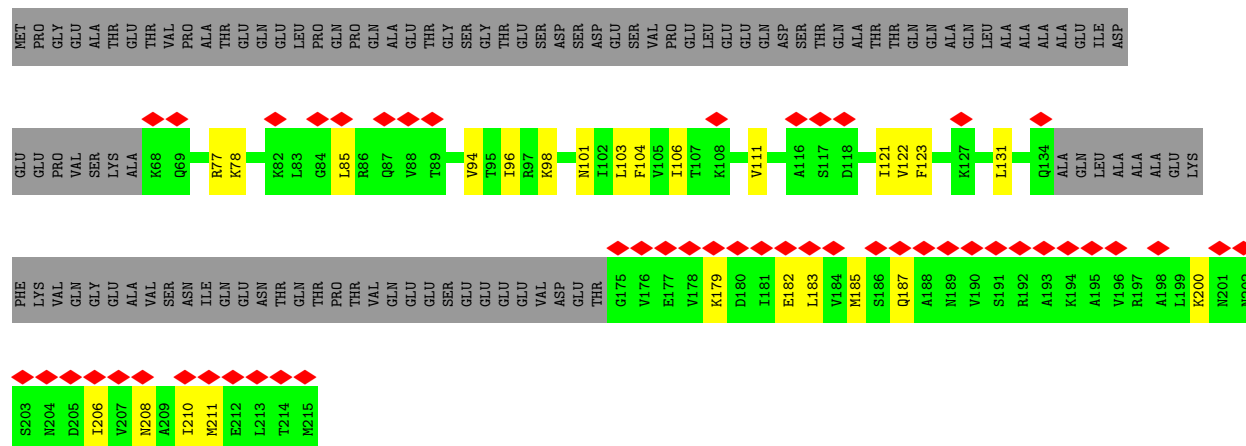
Chain N4:





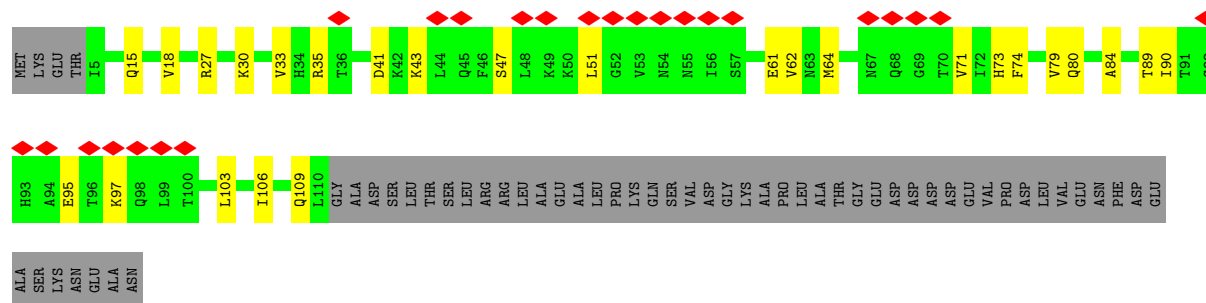
- Molecule 50: Nascent polypeptide-associated complex subunit alpha

Chain NA: 23% 39% 12% 50%



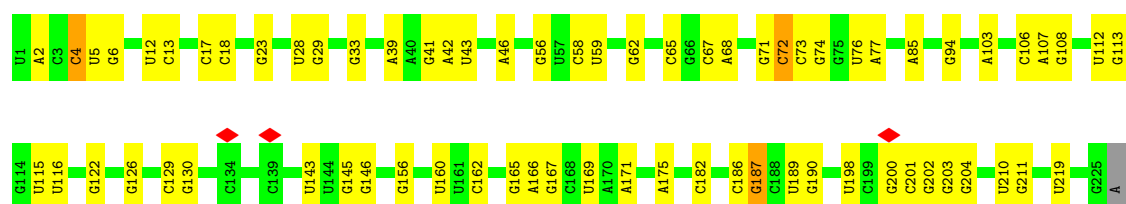
- Molecule 51: Isoform 2 of Transcription factor BTF3

Chain NB: 15% 49% 16% 35%

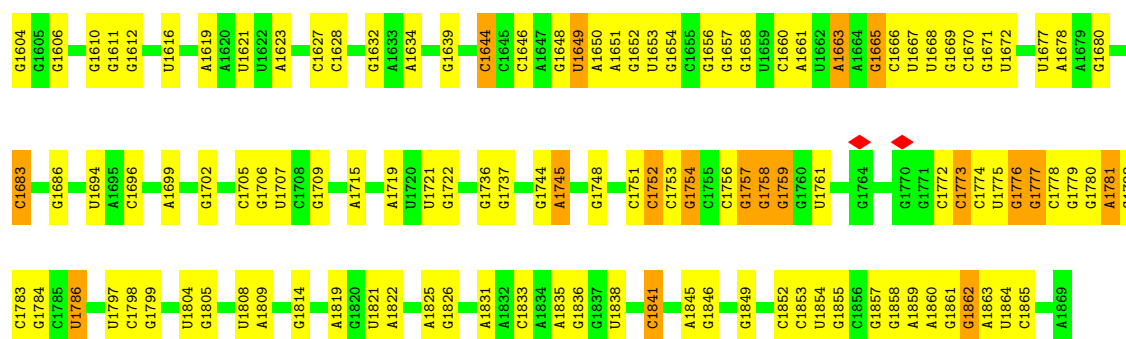


- Molecule 52: 18S rRNA

Chain S2: 55% 33% 8%

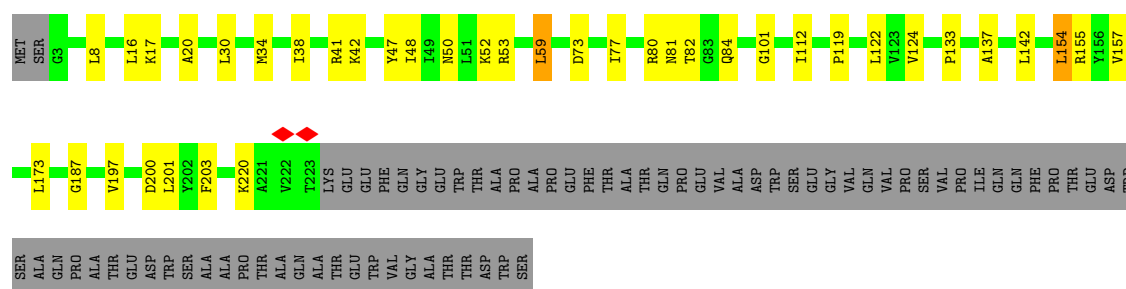






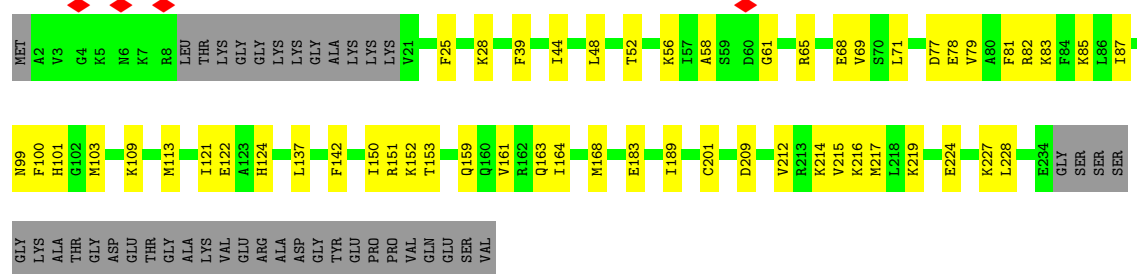
• Molecule 53: 40S ribosomal protein SA

Chain SA: 62% 13% 25%



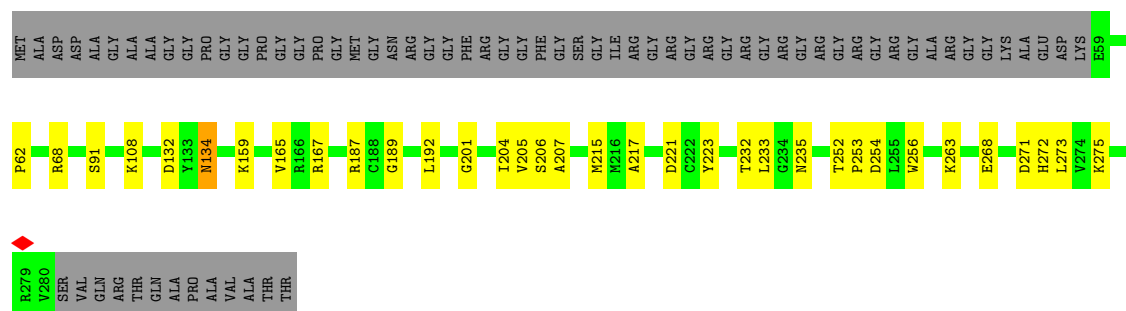
• Molecule 54: 40S ribosomal protein S3a

Chain SB: 63% 20% 16%

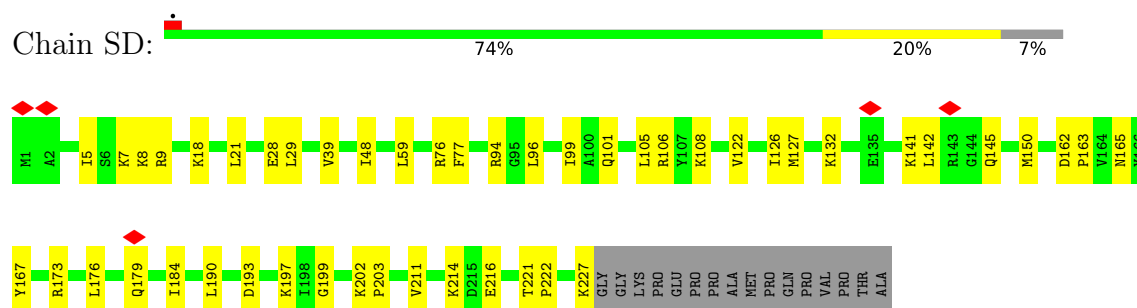


• Molecule 55: 40S ribosomal protein S2

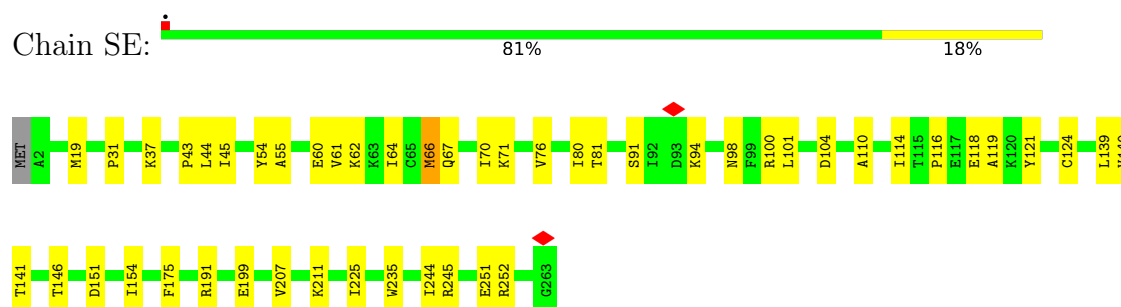
Chain SC: 64% 11% 24%



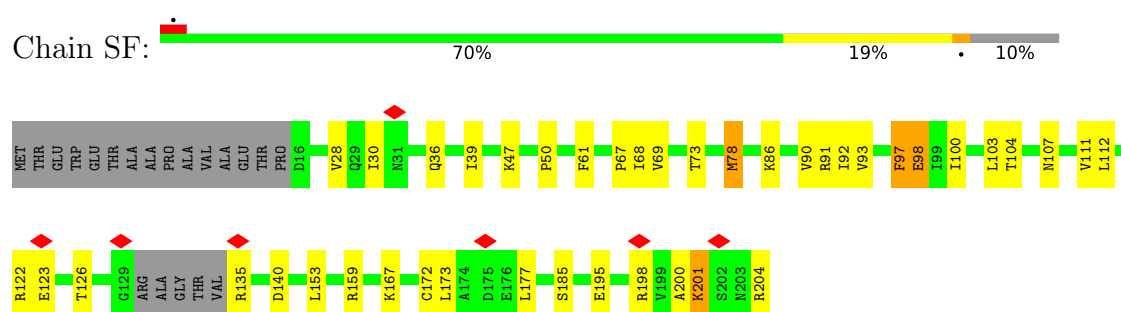
- Molecule 56: 40S ribosomal protein S3



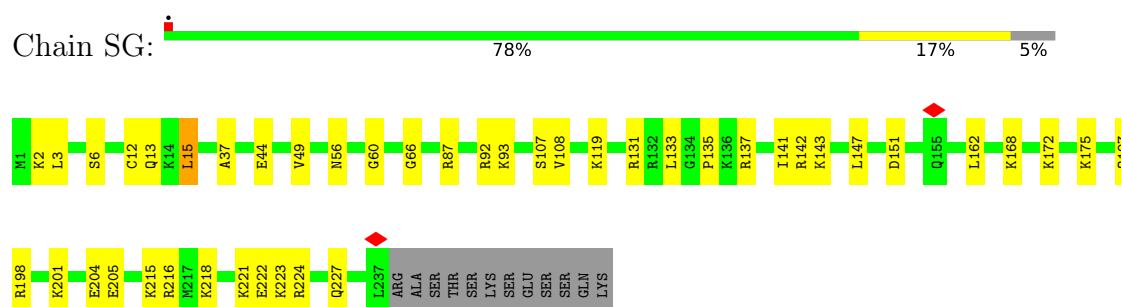
- Molecule 57: Small ribosomal subunit protein eS4, X isoform



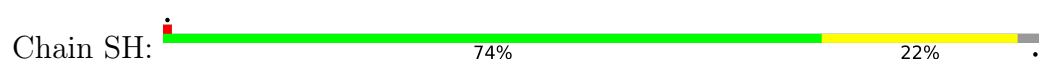
- Molecule 58: 40S ribosomal protein S5

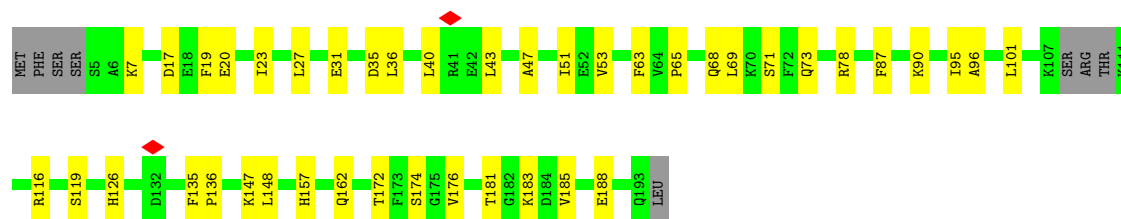


- Molecule 59: 40S ribosomal protein S6



- Molecule 60: 40S ribosomal protein S7





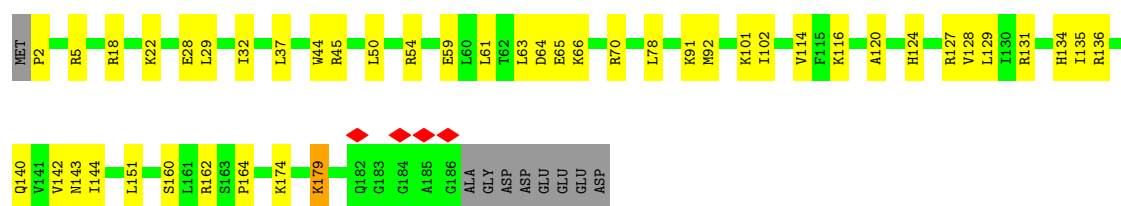
- Molecule 61: 40S ribosomal protein S8

Chain SI: 78% 20% .



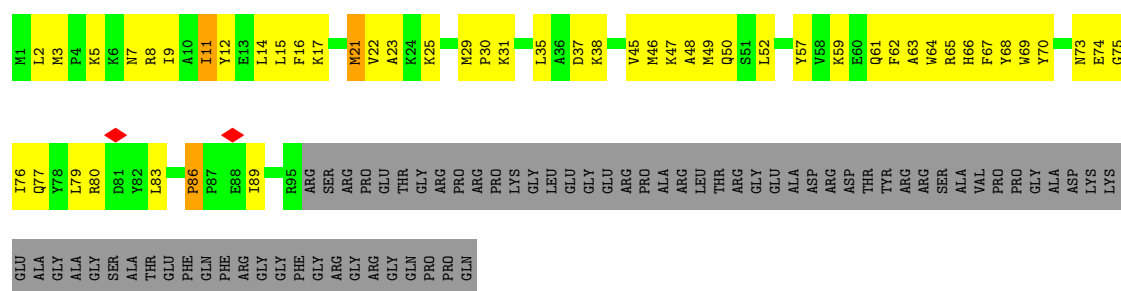
- Molecule 62: 40S ribosomal protein S9

Chain SJ: 72% 23% . 5%



- Molecule 63: 40S ribosomal protein S10

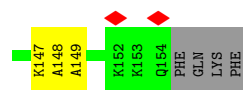
Chain SK: 27% 29% . 42%



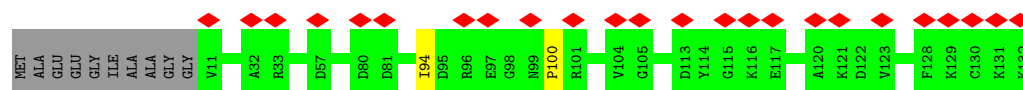
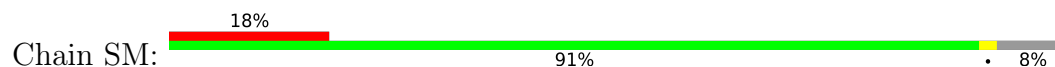
- Molecule 64: 40S ribosomal protein S11

Chain SL: 73% 18% 9%

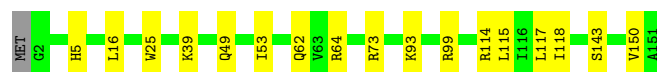




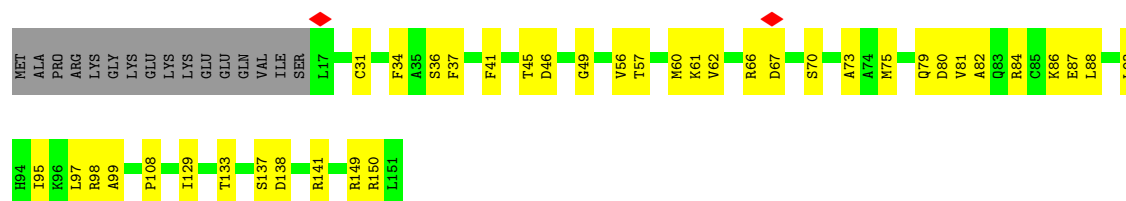
- Molecule 65: 40S ribosomal protein S12



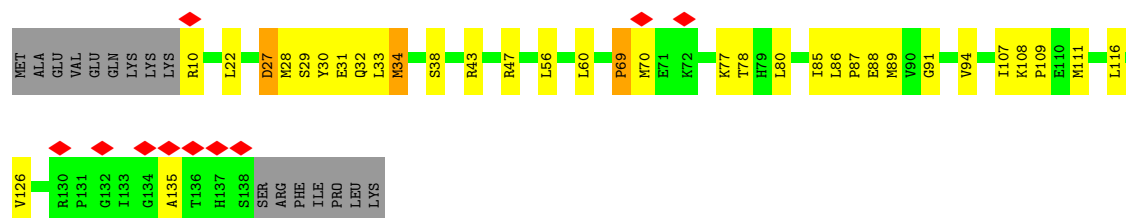
- Molecule 66: 40S ribosomal protein S13



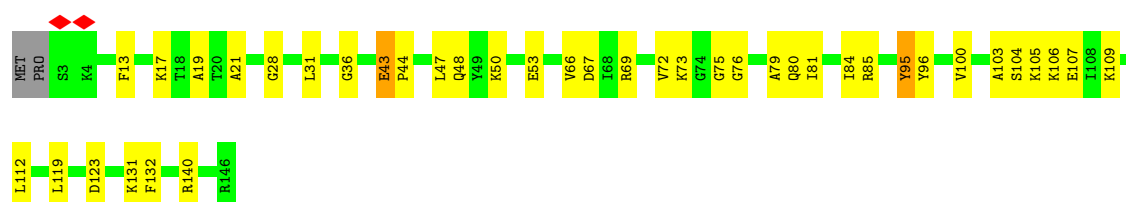
- Molecule 67: 40S ribosomal protein S14



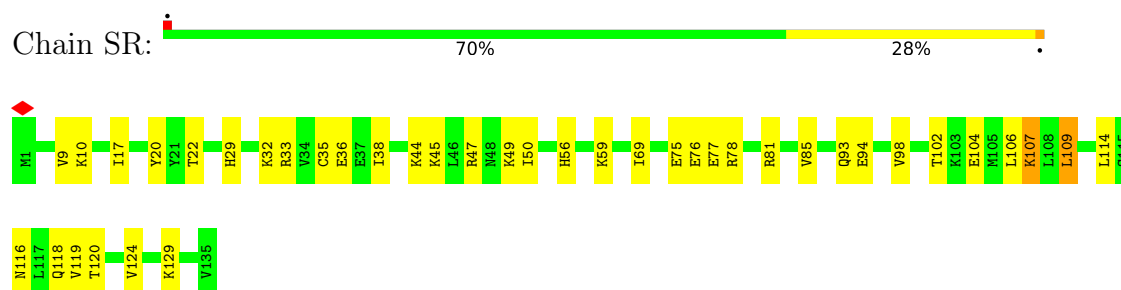
- Molecule 68: 40S ribosomal protein S15



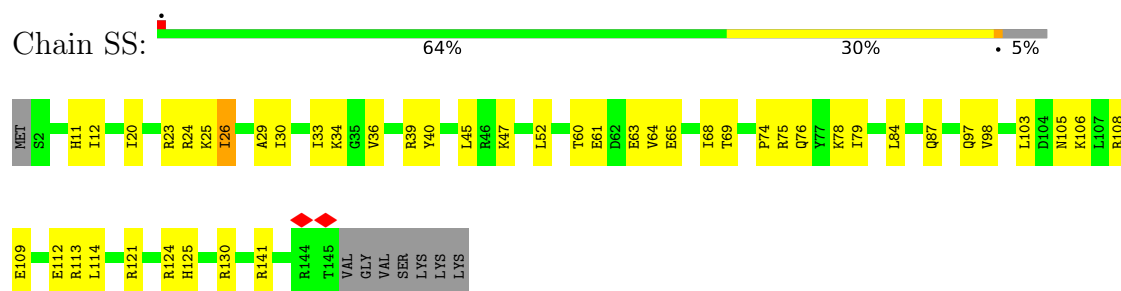
- Molecule 69: 40S ribosomal protein S16



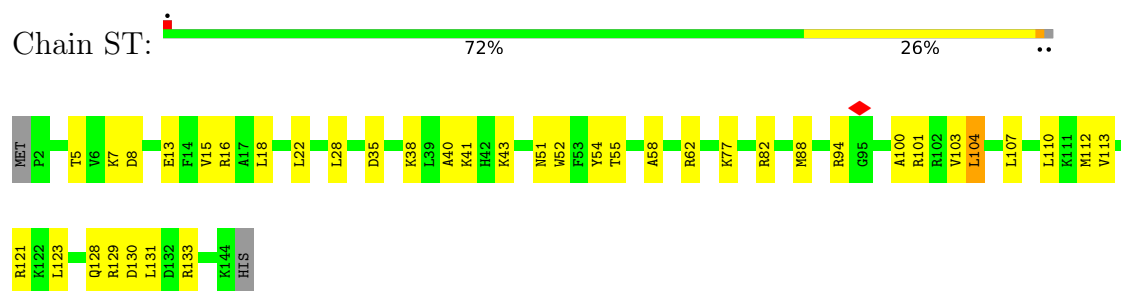
- Molecule 70: 40S ribosomal protein S17



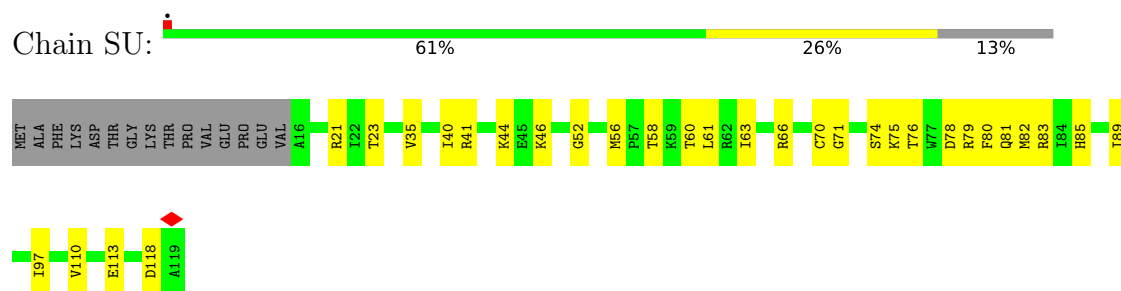
- Molecule 71: 40S ribosomal protein S18



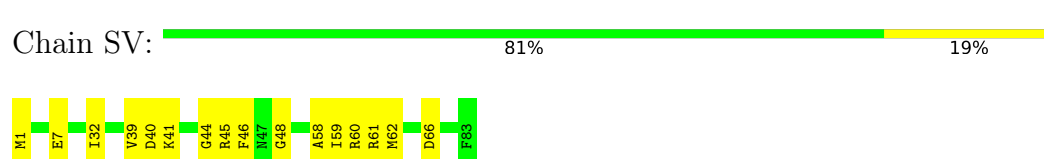
- Molecule 72: 40S ribosomal protein S19



- Molecule 73: 40S ribosomal protein S20

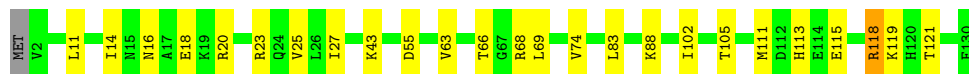


- Molecule 74: 40S ribosomal protein S21



- Molecule 75: 40S ribosomal protein S15a

Chain SW:  80% 18% ..



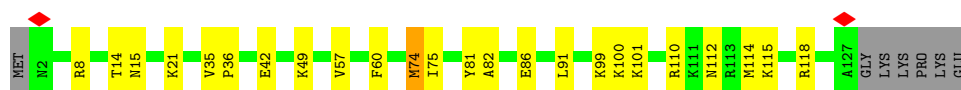
- Molecule 76: 40S ribosomal protein S23

Chain SX:  87% 12% .

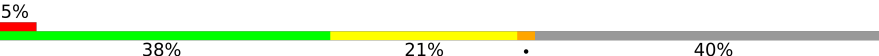


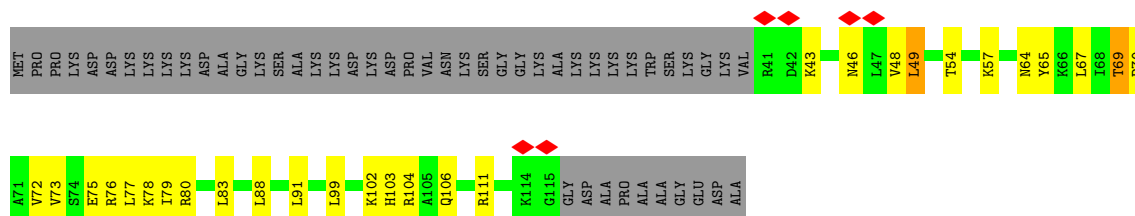
- Molecule 77: 40S ribosomal protein S24

Chain SY:  77% 17% . 5%



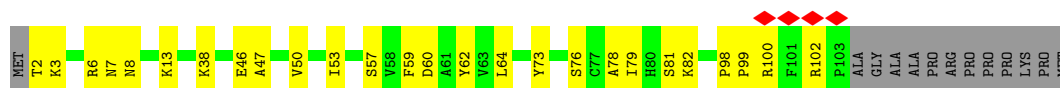
- Molecule 78: 40S ribosomal protein S25

Chain SZ:  5% 38% 21% . 40%



- Molecule 79: 40S ribosomal protein S26

Chain Sa:  66% 23% 11%

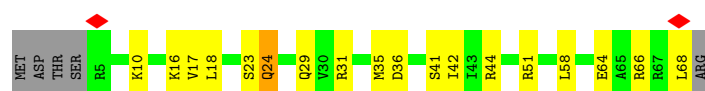


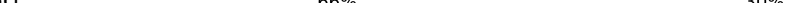
- Molecule 80: 40S ribosomal protein S27

Chain Sb:  83% 14% ..



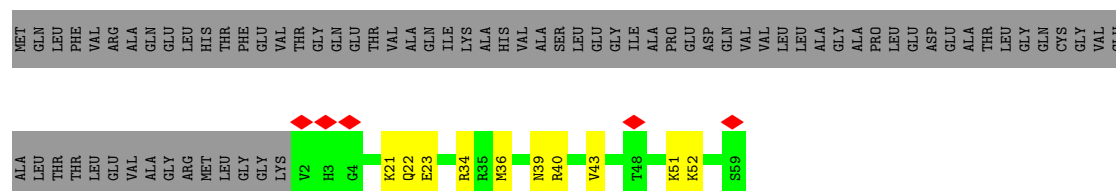
- Molecule 81: 40S ribosomal protein S28

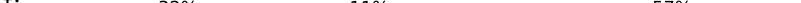


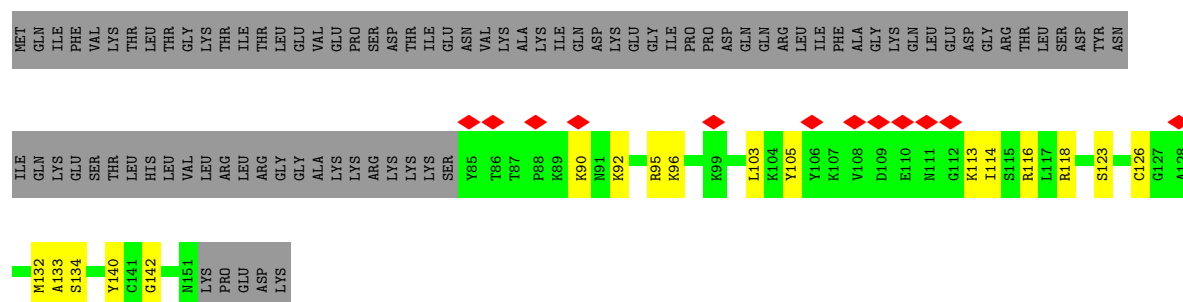
- Chain Sd:  66% 30% 4%

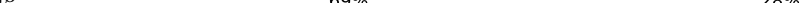


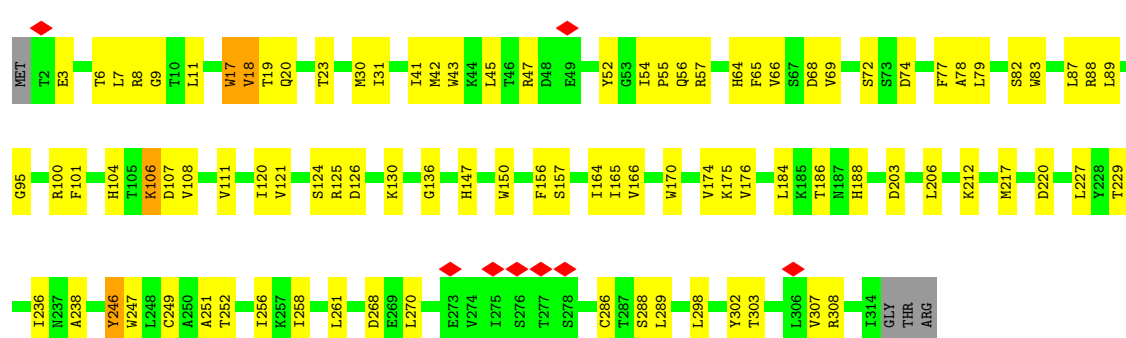
- Chain Se: 



- Chain Sf: 



- Chain Sg:  69% 28% ..



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	15772	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	2.471	Depositor
Minimum map value	-1.464	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.076	Depositor
Recommended contour level	0.11	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: MG, ZN, MLZ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	L5	0.15	0/88012	0.32	0/137296
2	L7	0.14	0/2861	0.29	0/4459
3	L8	0.14	0/3701	0.30	0/5766
4	LA	0.20	0/1936	0.46	0/2596
5	LB	0.19	0/3306	0.47	1/4424 (0.0%)
6	LC	0.19	0/2962	0.41	0/3977
7	LD	0.22	0/2428	0.59	4/3252 (0.1%)
8	LE	0.21	0/1808	0.70	2/2425 (0.1%)
9	LF	0.19	0/1905	0.45	0/2539
10	LG	0.24	0/1960	0.56	0/2637
11	LH	0.22	0/1537	0.48	1/2066 (0.0%)
12	LI	0.20	0/1677	0.51	1/2237 (0.0%)
13	LJ	0.22	0/1394	0.53	0/1863
14	LL	0.20	0/1704	0.49	0/2282
15	LM	0.21	0/1161	0.55	0/1554
16	LN	0.17	0/1746	0.40	0/2338
17	LO	0.20	0/1682	0.47	0/2250
18	LP	0.15	0/1268	0.36	0/1701
19	LQ	0.18	0/1537	0.44	0/2052
20	LR	0.20	0/1582	0.46	0/2091
21	LS	0.18	0/1493	0.39	0/2003
22	LT	0.20	0/1326	0.50	0/1770
23	LU	0.23	0/830	0.63	1/1114 (0.1%)
24	LV	0.16	0/993	0.38	0/1332
25	LW	0.21	0/1030	0.57	2/1364 (0.1%)
26	LX	0.17	0/1002	0.45	0/1345
27	LY	0.20	0/1123	0.49	1/1493 (0.1%)
28	LZ	0.20	0/1130	0.46	0/1507
29	La	0.16	0/1191	0.38	0/1591
30	Lb	0.21	0/895	0.63	0/1182
31	Lc	0.18	0/774	0.43	0/1038
32	Ld	0.21	0/903	0.54	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.19	0/1071	0.45	0/1429
34	Lf	0.20	0/895	0.49	3/1198 (0.3%)
35	Lg	0.17	0/916	0.38	0/1220
36	Lh	0.17	0/1023	0.43	0/1351
37	Li	0.19	0/843	0.55	0/1115
38	Lj	0.17	0/720	0.41	0/952
39	Lk	0.23	0/575	0.60	0/761
40	Ll	0.16	0/454	0.38	0/599
41	Lm	0.13	0/425	0.36	0/561
42	Ln	0.34	0/231	0.80	1/294 (0.3%)
43	Lo	0.16	0/876	0.46	0/1156
44	Lp	0.15	0/718	0.38	0/953
45	Lr	0.18	0/1017	0.43	0/1364
46	Ls	0.24	0/1519	0.64	2/2052 (0.1%)
47	Lt	0.22	0/1058	0.65	0/1430
48	MA	0.18	0/2549	0.49	0/3462
49	N4	0.18	0/1846	0.52	0/2476
50	NA	0.24	0/845	0.63	0/1128
51	NB	0.25	0/829	0.63	0/1112
52	S2	0.13	0/40751	0.31	0/63496
53	SA	0.24	0/1778	0.64	3/2416 (0.1%)
54	SB	0.22	0/1817	0.61	1/2428 (0.0%)
55	SC	0.25	0/1762	0.61	1/2381 (0.0%)
56	SD	0.22	0/1793	0.57	2/2414 (0.1%)
57	SE	0.21	0/2118	0.60	4/2849 (0.1%)
58	SF	0.28	0/1481	0.78	6/1988 (0.3%)
59	SG	0.22	0/1946	0.63	3/2590 (0.1%)
60	SH	0.25	0/1519	0.65	2/2033 (0.1%)
61	SI	0.21	0/1715	0.55	1/2287 (0.0%)
62	SJ	0.24	0/1550	0.65	3/2069 (0.1%)
63	SK	0.36	0/823	1.03	7/1111 (0.6%)
64	SL	0.20	0/1202	0.53	1/1606 (0.1%)
65	SM	0.09	0/603	0.25	0/837
66	SN	0.16	0/1232	0.39	0/1656
67	SO	0.23	0/1023	0.70	2/1372 (0.1%)
68	SP	0.29	0/1082	0.82	4/1446 (0.3%)
69	SQ	0.28	0/1160	0.75	0/1553
70	SR	0.27	0/1105	0.73	2/1484 (0.1%)
71	SS	0.26	0/1208	0.70	1/1618 (0.1%)
72	ST	0.28	0/1131	0.73	1/1515 (0.1%)
73	SU	0.31	0/831	0.77	2/1115 (0.2%)
74	SV	0.22	0/643	0.57	1/860 (0.1%)
75	SW	0.27	0/1051	0.56	0/1406

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SX	0.19	0/1116	0.45	0/1490
77	SY	0.24	0/1044	0.65	2/1388 (0.1%)
78	SZ	0.40	0/604	1.06	3/810 (0.4%)
79	Sa	0.21	0/836	0.52	0/1121
80	Sb	0.20	0/665	0.51	0/891
81	Sc	0.21	0/508	0.61	0/680
82	Sd	0.30	0/470	0.68	0/623
83	Se	0.22	0/465	0.56	0/612
84	Sf	0.22	0/560	0.66	1/745 (0.1%)
85	Sg	0.22	0/2493	0.62	2/3394 (0.1%)
All	All	0.18	0/237352	0.43	74/347657 (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
8	LE	0	1
48	MA	0	2
68	SP	0	1
75	SW	0	1
85	Sg	0	2
All	All	0	7

There are no bond length outliers.

All (74) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	LE	111	LYS	CA-C-N	18.39	145.95	120.39
8	LE	111	LYS	C-N-CA	18.39	145.95	120.39
53	SA	197	VAL	CA-C-N	9.94	133.99	120.67
53	SA	197	VAL	C-N-CA	9.94	133.99	120.67
46	Ls	73	PRO	CA-N-CD	-8.69	99.83	112.00
63	SK	86	PRO	CA-N-CD	-8.53	100.06	112.00
68	SP	69	PRO	CA-N-CD	-8.32	100.35	112.00
58	SF	78	MET	CA-C-N	7.85	135.82	121.70
58	SF	78	MET	C-N-CA	7.85	135.82	121.70
7	LD	233	PRO	CA-N-CD	-7.79	101.09	112.00
58	SF	97	PHE	CA-C-N	-7.65	107.75	121.14
58	SF	97	PHE	C-N-CA	-7.65	107.75	121.14
63	SK	8	ARG	CA-CB-CG	7.10	128.30	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
73	SU	75	LYS	CB-CG-CD	6.68	126.67	111.30
77	SY	42	GLU	CA-CB-CG	6.65	127.40	114.10
57	SE	19	MET	CA-CB-CG	6.50	127.09	114.10
70	SR	107	LYS	CA-CB-CG	6.19	126.47	114.10
63	SK	11	ILE	CA-C-N	-6.18	111.19	122.38
63	SK	11	ILE	C-N-CA	-6.18	111.19	122.38
67	SO	137	SER	CA-C-N	6.18	133.35	121.54
67	SO	137	SER	C-N-CA	6.18	133.35	121.54
46	Ls	45	MET	CB-CG-SD	6.16	131.18	112.70
78	SZ	49	LEU	CA-CB-CG	6.16	137.85	116.30
34	Lf	60	PRO	CA-N-CD	-6.14	103.40	112.00
78	SZ	69	THR	N-CA-C	-6.07	102.66	108.13
70	SR	76	GLU	CA-CB-CG	5.99	126.07	114.10
57	SE	66	MET	CA-C-N	-5.91	112.84	122.65
57	SE	66	MET	C-N-CA	-5.91	112.84	122.65
62	SJ	59	GLU	N-CA-CB	5.87	119.34	110.30
58	SF	98	GLU	N-CA-CB	5.86	119.94	110.40
27	LY	124	LYS	CA-CB-CG	5.75	125.60	114.10
23	LU	116	GLN	CA-CB-CG	5.72	125.54	114.10
77	SY	74	MET	CB-CG-SD	5.62	129.57	112.70
72	ST	104	LEU	CA-CB-CG	5.59	135.86	116.30
73	SU	82	MET	CA-CB-CG	5.58	125.25	114.10
56	SD	59	LEU	CA-CB-CG	5.55	135.72	116.30
59	SG	223	LYS	CA-CB-CG	5.51	125.11	114.10
7	LD	284	LYS	CA-CB-CG	5.50	125.09	114.10
7	LD	89	LYS	CA-CB-CG	5.48	125.07	114.10
71	SS	112	GLU	CA-CB-CG	5.48	125.06	114.10
74	SV	41	LYS	CB-CG-CD	5.46	123.86	111.30
63	SK	21	MET	CB-CG-SD	5.42	128.95	112.70
7	LD	122	GLN	CA-CB-CG	5.41	124.92	114.10
42	Ln	10	MET	CB-CG-SD	-5.39	96.53	112.70
54	SB	56	LYS	CB-CG-CD	5.37	123.66	111.30
59	SG	143	LYS	CA-CB-CG	5.31	124.71	114.10
78	SZ	57	LYS	CA-CB-CG	5.27	124.64	114.10
61	SI	154	LYS	CA-CB-CG	5.26	124.63	114.10
84	Sf	90	LYS	CA-CB-CG	5.25	124.60	114.10
11	LH	107	GLU	CA-CB-CG	5.22	124.54	114.10
60	SH	31	GLU	CA-C-N	-5.21	113.94	122.54
60	SH	31	GLU	C-N-CA	-5.21	113.94	122.54
68	SP	69	PRO	N-CA-C	5.21	123.19	112.47
58	SF	201	LYS	CA-CB-CG	5.20	124.49	114.10
62	SJ	59	GLU	CA-CB-CG	5.20	124.49	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	SG	143	LYS	CB-CG-CD	5.19	123.25	111.30
5	LB	138	GLN	CA-CB-CG	5.19	124.47	114.10
25	LW	90	ILE	CA-C-N	-5.19	112.06	121.14
25	LW	90	ILE	C-N-CA	-5.19	112.06	121.14
56	SD	197	LYS	CA-CB-CG	5.18	124.45	114.10
62	SJ	179	LYS	CB-CG-CD	5.16	123.16	111.30
12	LI	187	GLU	CA-CB-CG	5.14	124.38	114.10
85	Sg	64	HIS	CA-C-N	5.11	129.61	121.99
85	Sg	64	HIS	C-N-CA	5.11	129.61	121.99
53	SA	154	LEU	CA-CB-CG	5.11	134.18	116.30
68	SP	34	MET	CA-CB-CG	5.09	124.28	114.10
34	Lf	58	VAL	CA-C-N	5.05	129.71	121.83
34	Lf	58	VAL	C-N-CA	5.05	129.71	121.83
57	SE	211	LYS	CA-CB-CG	5.05	124.20	114.10
64	SL	45	LYS	CB-CG-CD	5.04	122.90	111.30
63	SK	48	ALA	CA-C-N	-5.03	113.90	122.56
63	SK	48	ALA	C-N-CA	-5.03	113.90	122.56
55	SC	215	MET	CB-CG-SD	5.02	127.77	112.70
68	SP	28	MET	CA-CB-CG	5.02	124.14	114.10

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	LE	177	GLY	Peptide
48	MA	303	ALA	Peptide
48	MA	91	TYR	Peptide
68	SP	27	ASP	Peptide
75	SW	118	ARG	Sidechain
85	Sg	106	LYS	Peptide
85	Sg	246	TYR	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	L5	78678	0	39756	588	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	L7	2561	0	1295	16	0
3	L8	3314	0	1683	26	0
4	LA	1898	0	1993	29	0
5	LB	3238	0	3376	47	0
6	LC	2908	0	3082	32	0
7	LD	2382	0	2410	38	0
8	LE	1774	0	1929	23	0
9	LF	1870	0	1996	21	0
10	LG	1927	0	2074	36	0
11	LH	1518	0	1601	17	0
12	LI	1639	0	1687	21	0
13	LJ	1371	0	1412	13	0
14	LL	1673	0	1779	24	0
15	LM	1138	0	1204	19	0
16	LN	1701	0	1749	23	0
17	LO	1650	0	1794	18	0
18	LP	1242	0	1269	14	0
19	LQ	1513	0	1628	16	0
20	LR	1566	0	1729	18	0
21	LS	1453	0	1490	19	0
22	LT	1298	0	1366	19	0
23	LU	816	0	842	11	0
24	LV	979	0	1039	9	0
25	LW	1015	0	1079	20	0
26	LX	985	0	1066	8	0
27	LY	1106	0	1192	25	0
28	LZ	1107	0	1182	13	0
29	La	1162	0	1213	16	0
30	Lb	882	0	959	9	0
31	Lc	764	0	804	13	0
32	Ld	888	0	930	13	0
33	Le	1053	0	1147	15	0
34	Lf	876	0	912	11	0
35	Lg	906	0	998	11	0
36	Lh	1015	0	1148	10	0
37	Li	832	0	917	8	0
38	Lj	705	0	737	12	0
39	Lk	569	0	637	10	0
40	Ll	444	0	483	8	0
41	Lm	430	0	465	3	0
42	Ln	230	0	276	7	0
43	Lo	862	0	929	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	Lp	708	0	756	4	0
45	Lr	1002	0	1068	13	0
46	Ls	1496	0	1540	22	0
47	Lt	1046	0	1076	15	0
48	MA	2485	0	2414	65	0
49	N4	1809	0	1764	24	0
50	NA	841	0	898	19	0
51	NB	821	0	867	17	0
52	S2	36456	0	18381	333	0
53	SA	1741	0	1746	27	0
54	SB	1791	0	1870	33	0
55	SC	1725	0	1813	22	0
56	SD	1765	0	1865	36	0
57	SE	2076	0	2177	30	0
58	SF	1461	0	1511	29	0
59	SG	1923	0	2089	34	0
60	SH	1497	0	1590	23	0
61	SI	1686	0	1772	27	0
62	SJ	1525	0	1640	29	0
63	SK	799	0	823	40	0
64	SL	1182	0	1253	18	0
65	SM	604	0	281	1	0
66	SN	1208	0	1294	13	0
67	SO	1010	0	1034	28	0
68	SP	1061	0	1107	24	0
69	SQ	1142	0	1212	30	0
70	SR	1090	0	1149	26	0
71	SS	1190	0	1249	36	0
72	ST	1112	0	1146	31	0
73	SU	821	0	883	26	0
74	SV	636	0	637	12	0
75	SW	1034	0	1080	24	0
76	SX	1098	0	1167	12	0
77	SY	1027	0	1093	17	0
78	SZ	598	0	656	21	0
79	Sa	821	0	870	19	0
80	Sb	651	0	672	10	0
81	Sc	506	0	536	13	0
82	Sd	459	0	448	23	0
83	Se	459	0	503	7	0
84	Sf	548	0	551	10	0
85	Sg	2436	0	2393	59	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	L5	213	0	0	0	0
86	L7	3	0	0	0	0
86	L8	4	0	0	0	0
86	LA	1	0	0	0	0
86	LI	1	0	0	0	0
86	LP	1	0	0	0	0
86	LV	1	0	0	0	0
86	Le	1	0	0	0	0
86	Lj	1	0	0	0	0
86	S2	31	0	0	0	0
87	Lg	1	0	0	0	0
87	Lj	1	0	0	0	0
87	Lm	1	0	0	0	0
87	Lo	1	0	0	0	0
87	Lp	1	0	0	0	0
87	Sa	1	0	0	0	0
87	Sd	1	0	0	0	0
87	Sf	1	0	0	0	0
All	All	221549	0	166131	2199	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (2199) 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)
52:S2:1756:C:H42	52:S2:1776:G:N2	1.51	1.07
52:S2:1756:C:N4	52:S2:1776:G:H22	1.51	1.07
49:N4:107:TRP:HB2	49:N4:124:PHE:O	1.54	1.06
1:L5:1762:C:N4	1:L5:1770:A:C2	2.33	0.95
52:S2:677:G:H21	52:S2:1028:A:H62	1.01	0.94
48:MA:119:GLU:O	48:MA:123:LYS:HB2	1.68	0.93
1:L5:2557:G:H1	1:L5:2570:U:H3	1.05	0.89
42:Ln:5:TRP:HE1	52:S2:1853:C:H41	1.20	0.89
1:L5:2483:G:H1	1:L5:2495:U:H3	1.25	0.85
1:L5:1762:C:N4	1:L5:1770:A:H2	1.75	0.84
52:S2:1657:G:H1	52:S2:1667:U:H3	1.23	0.84
52:S2:677:G:N2	52:S2:1028:A:H62	1.78	0.81
52:S2:1656:G:H1	52:S2:1668:U:H3	1.26	0.78
52:S2:940:U:H3	52:S2:1002:U:H3	1.31	0.78
1:L5:184:U:H3	1:L5:253:G:H21	1.32	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:SC:62:PRO:HG2	55:SC:68:ARG:HH21	1.49	0.77
52:S2:677:G:H21	52:S2:1028:A:N6	1.81	0.77
69:SQ:76:GLY:O	69:SQ:80:GLN:HB2	1.85	0.77
85:Sg:65:PHE:HB3	85:Sg:83:TRP:HB2	1.66	0.76
1:L5:4745:G:H1	1:L5:4955:A:H61	1.33	0.75
43:Lo:99:ARG:HB2	43:Lo:102:GLN:HE22	1.50	0.75
7:LD:197:LYS:HG3	7:LD:202:GLN:HB2	1.70	0.74
52:S2:1401:A:H4'	73:SU:52:GLY:HA3	1.70	0.73
27:LY:72:GLN:HB3	27:LY:81:TYR:HB2	1.69	0.73
1:L5:2845:A:H61	1:L5:3843:C:H42	1.37	0.72
48:MA:299:LEU:HD21	48:MA:302:THR:HB	1.71	0.72
7:LD:208:MET:HE3	7:LD:233:PRO:HD3	1.71	0.72
48:MA:232:LEU:HD13	48:MA:372:THR:HB	1.73	0.71
80:Sb:42:LYS:NZ	80:Sb:43:ILE:O	2.21	0.70
10:LG:114:LEU:HA	10:LG:117:ARG:HE	1.57	0.70
48:MA:302:THR:HG23	48:MA:304:PRO:HD2	1.74	0.69
71:SS:26:ILE:HD11	71:SS:52:LEU:HA	1.73	0.69
25:LW:97:LYS:HA	25:LW:101:ARG:HD3	1.75	0.69
53:SA:30:LEU:HD11	53:SA:38:ILE:HG21	1.75	0.69
67:SO:34:PHE:HB3	67:SO:41:PHE:HB2	1.75	0.69
78:SZ:69:THR:HG22	78:SZ:72:VAL:HG12	1.74	0.69
73:SU:61:LEU:O	73:SU:81:GLN:HA	1.93	0.69
52:S2:1751:C:H42	52:S2:1782:G:H21	1.39	0.69
1:L5:2262:G:OP1	45:Lr:94:ARG:NH1	2.25	0.69
52:S2:1756:C:H42	52:S2:1776:G:H22	0.76	0.69
52:S2:1349:G:H21	53:SA:112:ILE:HD11	1.58	0.68
56:SD:142:LEU:HG	56:SD:150:MET:HE1	1.75	0.68
67:SO:75:MET:SD	67:SO:79:GLN:NE2	2.67	0.68
13:LJ:95:ARG:HE	13:LJ:177:GLY:HA2	1.58	0.68
53:SA:17:LYS:HB3	53:SA:173:LEU:HD11	1.74	0.67
48:MA:326:ILE:O	48:MA:358:GLU:HA	1.95	0.67
52:S2:165:G:H2'	52:S2:166:A:H8	1.58	0.67
62:SJ:101:LYS:HE3	62:SJ:102:ILE:H	1.58	0.67
1:L5:54:G:O2'	16:LN:108:ARG:NH2	2.28	0.67
9:LF:182:TYR:HB3	9:LF:200:ARG:HG3	1.77	0.67
1:L5:703:G:O2'	33:Le:5:ARG:NH2	2.28	0.67
56:SD:105:LEU:HD11	56:SD:122:VAL:HG21	1.76	0.67
70:SR:32:LYS:HG3	70:SR:47:ARG:HE	1.59	0.67
1:L5:1959:U:H4'	1:L5:1960:A:H5''	1.77	0.66
75:SW:118:ARG:HH12	75:SW:119:LYS:HB3	1.60	0.66
52:S2:1652:G:H1	52:S2:1672:U:H3	1.43	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:SA:77:ILE:HB	53:SA:124:VAL:HG12	1.77	0.66
1:L5:4139:G:H21	1:L5:4140:C:H41	1.41	0.66
52:S2:867:G:H5''	64:SL:149:ALA:HB2	1.77	0.66
59:SG:131:ARG:HE	59:SG:133:LEU:H	1.43	0.66
1:L5:493:G:H1	1:L5:660:A:H2	1.42	0.66
71:SS:36:VAL:HG23	71:SS:40:TYR:HB3	1.76	0.66
78:SZ:46:ASN:HB2	78:SZ:78:LYS:HE3	1.77	0.66
1:L5:2342:G:H5''	6:LC:109:ARG:HH22	1.61	0.66
53:SA:155:ARG:HH12	74:SV:61:ARG:HG3	1.60	0.66
48:MA:222:THR:HA	48:MA:230:GLY:O	1.95	0.65
85:Sg:87:LEU:HD21	85:Sg:111:VAL:HG11	1.78	0.65
25:LW:82:ILE:HA	59:SG:131:ARG:HB3	1.79	0.65
1:L5:1976:G:H1	1:L5:1990:A:H61	1.45	0.65
1:L5:3877:A:O2'	1:L5:4400:G:N2	2.30	0.65
10:LG:114:LEU:HB3	10:LG:117:ARG:HH21	1.62	0.65
52:S2:563:G:H1	52:S2:592:C:H5	1.45	0.65
52:S2:1079:C:H4'	52:S2:1182:A:H61	1.60	0.65
60:SH:87:PHE:HB3	60:SH:90:LYS:HD2	1.79	0.65
52:S2:1658:G:OP2	52:S2:1660:C:N4	2.30	0.64
69:SQ:43:GLU:HG2	69:SQ:44:PRO:HD3	1.79	0.64
5:LB:84:MET:O	5:LB:204:GLN:HA	1.97	0.64
11:LH:44:GLU:HB2	11:LH:58:ASP:HB2	1.79	0.64
19:LQ:50:ARG:HB3	19:LQ:83:VAL:HG21	1.80	0.64
1:L5:1762:C:N3	1:L5:1770:A:N1	2.45	0.64
52:S2:851:C:H5''	52:S2:852:G:H5'	1.79	0.64
1:L5:4093:G:N1	1:L5:4114:C:C2	2.66	0.64
63:SK:25:LYS:HA	63:SK:46:MET:HE1	1.80	0.64
23:LU:99:TRP:HE1	51:NB:15:GLN:HB3	1.62	0.64
39:Lk:12:LEU:HD22	39:Lk:16:ARG:HH21	1.62	0.64
66:SN:99:ARG:HH12	66:SN:143:SER:HB2	1.62	0.64
36:Lh:96:ASN:O	36:Lh:100:GLU:HB2	1.98	0.64
1:L5:493:G:O6	1:L5:660:A:N1	2.31	0.64
75:SW:23:ARG:HH12	80:Sb:4:ALA:HA	1.62	0.64
85:Sg:289:LEU:HD11	85:Sg:298:LEU:HD22	1.80	0.64
69:SQ:31:LEU:O	69:SQ:67:ASP:HA	1.97	0.63
1:L5:4581:G:OP1	5:LB:26:ARG:NH1	2.32	0.63
48:MA:191:LYS:HG3	48:MA:206:PRO:HD2	1.79	0.63
52:S2:1461:G:H3'	52:S2:1463:U:H3	1.64	0.63
71:SS:26:ILE:HD12	71:SS:45:LEU:HD13	1.81	0.63
52:S2:167:G:H21	59:SG:131:ARG:HH22	1.46	0.63
62:SJ:65:GLU:HG3	62:SJ:66:LYS:HD2	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1365:C:O2'	1:L5:1367:C:N4	2.31	0.63
52:S2:1754:G:N7	52:S2:1779:G:N2	2.47	0.63
1:L5:977:C:OP2	8:LE:59:ARG:NH1	2.31	0.63
70:SR:75:GLU:HB3	70:SR:78:ARG:HH21	1.64	0.63
27:LY:108:ARG:NH2	49:N4:104:ASP:OD1	2.32	0.62
48:MA:183:PRO:HD3	48:MA:222:THR:HB	1.80	0.62
48:MA:295:GLY:HA3	48:MA:304:PRO:HG2	1.81	0.62
1:L5:956:A:H1'	1:L5:2076:G:H5''	1.82	0.62
76:SX:123:VAL:HG12	76:SX:124:LYS:HG3	1.80	0.62
10:LG:58:PRO:HD2	10:LG:61:ILE:HD12	1.80	0.62
50:NA:96:ILE:HB	50:NA:104:PHE:HB2	1.80	0.62
12:LI:20:SER:OG	12:LI:21:ARG:N	2.32	0.62
25:LW:1:MET:HE3	25:LW:15:PRO:HB3	1.81	0.62
43:Lo:103:VAL:HG12	43:Lo:104:ILE:HD12	1.81	0.62
1:L5:4353:U:H5''	1:L5:4354:U:H5'	1.82	0.62
8:LE:57:TYR:HB2	8:LE:62:MET:HE2	1.80	0.62
52:S2:960:U:O2	67:SO:66:ARG:NH2	2.33	0.62
63:SK:47:LYS:HA	63:SK:50:GLN:HG2	1.80	0.62
1:L5:2845:A:H61	1:L5:3843:C:N4	1.97	0.62
1:L5:4431:U:OP2	12:LI:3:ARG:NH2	2.33	0.62
48:MA:268:ARG:HG3	48:MA:270:ARG:H	1.64	0.62
69:SQ:47:LEU:HD23	69:SQ:81:ILE:HD13	1.81	0.62
82:Sd:16:GLN:HE22	82:Sd:27:ARG:HB3	1.65	0.62
12:LI:170:LYS:HA	12:LI:177:ASN:HA	1.82	0.61
18:LP:128:ARG:NH1	18:LP:130:TYR:OH	2.33	0.61
70:SR:33:ARG:HG3	85:Sg:83:TRP:HZ3	1.65	0.61
84:Sf:118:ARG:HD2	84:Sf:134:SER:HB3	1.82	0.61
42:Ln:11:ARG:NH1	52:S2:1845:A:OP2	2.30	0.61
11:LH:91:LYS:HB2	11:LH:183:GLU:HB3	1.81	0.61
52:S2:1748:G:H1	52:S2:1786:U:H3	1.46	0.61
52:S2:566:U:H3	52:S2:584:G:H1	1.49	0.61
58:SF:198:ARG:HA	58:SF:201:LYS:HE3	1.82	0.61
1:L5:2434:G:H5''	26:LX:83:THR:HG22	1.83	0.61
34:Lf:75:THR:HG23	34:Lf:76:ARG:HG2	1.81	0.61
46:Ls:124:PRO:HG2	46:Ls:126:GLN:HE22	1.66	0.61
52:S2:1261:C:O2	82:Sd:10:HIS:NE2	2.31	0.61
55:SC:91:SER:HB2	55:SC:159:LYS:HD3	1.82	0.61
85:Sg:7:LEU:HD13	85:Sg:9:GLY:H	1.64	0.61
32:Ld:87:ARG:HH21	32:Ld:122:VAL:HG11	1.66	0.61
52:S2:1324:G:H1	52:S2:1504:U:H3	1.48	0.61
75:SW:118:ARG:HH22	75:SW:119:LYS:HZ2	1.49	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:ST:40:ALA:HB3	72:ST:43:LYS:HG3	1.83	0.61
1:L5:1977:C:OP1	47:Lt:57:ARG:NH2	2.33	0.61
3:L8:94:G:OP2	38:Lj:72:ARG:NH1	2.33	0.61
1:L5:1391:A:OP1	19:LQ:181:ARG:NH2	2.32	0.60
27:LY:83:GLU:HG3	27:LY:84:ARG:HD2	1.83	0.60
1:L5:2262:G:OP2	45:Lr:98:ARG:NH2	2.34	0.60
1:L5:4212:A:N1	22:LT:3:ASN:ND2	2.42	0.60
1:L5:4987:C:H2'	5:LB:123:HIS:CE1	2.37	0.60
49:N4:169:LYS:HG2	49:N4:170:LYS:HG2	1.82	0.60
52:S2:391:C:H2'	52:S2:392:A:H8	1.65	0.60
29:La:71:PRO:HG2	29:La:108:TYR:HA	1.83	0.60
48:MA:233:ASN:H	48:MA:358:GLU:HB3	1.65	0.60
52:S2:928:G:H2'	52:S2:929:G:C8	2.36	0.60
1:L5:2611:A:H5'	1:L5:2688:G:H4'	1.83	0.60
52:S2:323:C:H2'	52:S2:327:G:H22	1.66	0.60
58:SF:97:PHE:HA	58:SF:100:ILE:HG12	1.81	0.60
74:SV:46:PHE:HD1	74:SV:48:GLY:H	1.47	0.60
1:L5:4225:G:OP1	12:LI:24:ARG:NH2	2.35	0.60
16:LN:5:LYS:HG3	37:Li:40:VAL:HG11	1.84	0.60
1:L5:308:G:N2	1:L5:308:G:OP2	2.34	0.60
1:L5:4077:A:N1	1:L5:4171:C:N4	2.50	0.60
9:LF:29:LYS:HE2	9:LF:32:ARG:HH21	1.66	0.60
81:Sc:66:ARG:HH12	81:Sc:68:LEU:HD23	1.67	0.60
85:Sg:217:MET:SD	85:Sg:229:THR:OG1	2.57	0.60
1:L5:2742:G:OP1	4:LA:24:LYS:NZ	2.32	0.60
3:L8:96:C:OP1	36:Lh:70:ARG:NH1	2.34	0.60
52:S2:419:G:O3'	75:SW:88:LYS:NZ	2.35	0.60
1:L5:3641:U:OP2	1:L5:3646:A:N6	2.35	0.60
1:L5:4163:U:H5'	1:L5:4164:C:H5''	1.83	0.60
3:L8:19:C:H2'	3:L8:20:A:H8	1.66	0.60
1:L5:1732:C:H5''	22:LT:43:LYS:HD2	1.83	0.59
1:L5:3689:G:O2'	1:L5:3818:U:OP2	2.19	0.59
1:L5:1271:G:H1'	9:LF:34:ARG:HH22	1.66	0.59
1:L5:1950:U:O2'	21:LS:116:ARG:NH1	2.35	0.59
9:LF:46:ARG:HH22	30:Lb:102:PRO:HG3	1.67	0.59
61:SI:164:GLU:OE2	61:SI:168:GLN:NE2	2.34	0.59
78:SZ:65:TYR:OH	78:SZ:76:ARG:NH1	2.35	0.59
14:LL:141:ALA:HA	14:LL:144:LEU:HB2	1.83	0.59
52:S2:1231:C:O2'	52:S2:1253:A:N6	2.35	0.59
57:SE:251:GLU:OE1	57:SE:252:ARG:NH1	2.35	0.59
85:Sg:79:LEU:HD21	85:Sg:120:ILE:HG12	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:2020:U:H2'	1:L5:2021:G:H8	1.67	0.59
1:L5:2458:C:H5''	16:LN:67:ARG:HD2	1.84	0.59
1:L5:4472:G:O2'	41:Lm:100:TYR:O	2.19	0.59
51:NB:33:VAL:HG13	51:NB:35:ARG:HH12	1.67	0.59
61:SI:84:ASN:HB2	61:SI:91:VAL:HG23	1.83	0.59
76:SX:49:GLY:O	76:SX:99:GLU:HA	2.02	0.59
1:L5:76:A:N7	14:LL:74:ARG:NH2	2.50	0.59
1:L5:4873:G:N7	17:LO:179:LYS:NZ	2.45	0.59
29:La:71:PRO:HD2	29:La:109:TYR:HB2	1.84	0.59
1:L5:62:A:N3	1:L5:77:U:O2'	2.34	0.59
1:L5:1703:C:N4	1:L5:2097:U:O2'	2.36	0.59
5:LB:73:VAL:O	24:LV:89:ARG:NH2	2.36	0.59
32:Ld:32:ARG:HB3	32:Ld:48:GLU:HG3	1.84	0.59
1:L5:959:G:O4'	8:LE:123:ARG:NH1	2.35	0.59
1:L5:2407:G:N2	1:L5:2407:G:OP2	2.34	0.59
6:LC:208:CYS:HB2	6:LC:248:ARG:HE	1.68	0.59
13:LJ:101:ASP:OD2	13:LJ:101:ASP:N	2.36	0.59
52:S2:1209:A:O3'	79:Sa:82:LYS:NZ	2.36	0.59
68:SP:27:ASP:OD2	68:SP:27:ASP:N	2.36	0.59
62:SJ:114:VAL:HG21	62:SJ:135:ILE:HD13	1.84	0.59
16:LN:120:TRP:HE1	16:LN:123:GLU:HB3	1.68	0.59
22:LT:17:ARG:HD2	22:LT:47:THR:HB	1.84	0.59
51:NB:61:GLU:HB2	51:NB:73:HIS:HE1	1.68	0.59
52:S2:1597:C:H5''	71:SS:25:LYS:HZ3	1.67	0.59
1:L5:4220:A:OP2	22:LT:2:THR:OG1	2.19	0.58
75:SW:14:ILE:HG13	75:SW:27:ILE:HD11	1.85	0.58
1:L5:723:A:OP1	1:L5:934:C:N4	2.37	0.58
7:LD:83:LEU:HB3	7:LD:88:VAL:HB	1.85	0.58
23:LU:22:THR:OG1	23:LU:109:SER:OG	2.21	0.58
51:NB:18:VAL:HG22	51:NB:27:ARG:HB3	1.85	0.58
68:SP:78:THR:HG22	68:SP:80:LEU:H	1.69	0.58
1:L5:1996:C:H42	1:L5:2000:G:N2	2.01	0.58
2:L7:99:G:N7	21:LS:55:LYS:NZ	2.48	0.58
57:SE:104:ASP:HB3	57:SE:110:ALA:HB2	1.85	0.58
1:L5:5055:G:N2	32:Ld:118:GLN:OE1	2.35	0.58
5:LB:154:LYS:HD3	5:LB:194:LEU:HD23	1.84	0.58
15:LM:40:GLY:HA3	15:LM:45:VAL:HB	1.85	0.58
52:S2:547:G:H1'	52:S2:549:C:H41	1.67	0.58
56:SD:94:ARG:O	56:SD:101:GLN:NE2	2.36	0.58
57:SE:31:PRO:HG3	57:SE:43:PRO:HG3	1.85	0.58
60:SH:69:LEU:HD22	60:SH:96:ALA:HB2	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:SK:46:MET:HE2	63:SK:67:PHE:HD2	1.69	0.58
1:L5:3697:U:H5''	1:L5:3698:G:H5'	1.84	0.58
4:LA:117:GLU:HG2	4:LA:124:GLY:H	1.66	0.58
6:LC:152:LEU:HD23	6:LC:251:ILE:HD12	1.86	0.58
52:S2:830:A:OP2	52:S2:846:G:N2	2.35	0.58
47:Lt:123:ARG:HD3	47:Lt:129:ILE:HD11	1.86	0.58
56:SD:162:ASP:OD1	56:SD:165:ASN:ND2	2.37	0.58
56:SD:163:PRO:O	56:SD:167:TYR:HB2	2.02	0.58
77:SY:82:ALA:O	77:SY:86:GLU:HB2	2.02	0.58
85:Sg:256:ILE:HB	85:Sg:270:LEU:HB2	1.85	0.58
23:LU:106:SER:OG	23:LU:107:LYS:N	2.36	0.58
58:SF:126:THR:HA	58:SF:135:ARG:HH21	1.68	0.58
69:SQ:19:ALA:HB2	69:SQ:75:GLY:HA3	1.86	0.58
77:SY:14:THR:HG22	77:SY:21:LYS:HE2	1.85	0.58
78:SZ:54:THR:HB	78:SZ:77:LEU:HD21	1.84	0.58
1:L5:4363:A:H5''	43:Lo:36:GLN:HG2	1.86	0.58
1:L5:5022:U:O4	61:SI:170:LYS:NZ	2.36	0.58
9:LF:173:ALA:HB1	9:LF:177:ARG:HH12	1.69	0.58
54:SB:101:HIS:HA	54:SB:217:MET:HE2	1.85	0.58
56:SD:96:LEU:HD12	56:SD:190:LEU:HD12	1.85	0.58
52:S2:377:G:H5'	61:SI:98:LYS:HB3	1.85	0.58
69:SQ:36:GLY:HA3	72:ST:7:LYS:HE2	1.84	0.58
1:L5:1819:G:H1'	7:LD:115:MET:HE1	1.86	0.58
1:L5:2352:U:OP1	6:LC:78:ARG:NH2	2.37	0.58
1:L5:3944:G:H1	1:L5:4069:U:H3	1.51	0.58
15:LM:105:THR:OG1	15:LM:106:ASP:N	2.37	0.58
52:S2:1547:C:N4	52:S2:1586:U:O4	2.37	0.58
77:SY:110:ARG:O	77:SY:114:MET:HB2	2.03	0.58
77:SY:112:ASN:HA	77:SY:115:LYS:HE2	1.86	0.58
1:L5:257:C:H2'	1:L5:258:G:H8	1.70	0.57
1:L5:1214:C:OP2	30:Lb:91:ARG:NH2	2.35	0.57
25:LW:101:ARG:NH2	59:SG:151:ASP:OD2	2.37	0.57
1:L5:28:C:OP2	16:LN:189:ARG:NH2	2.37	0.57
6:LC:218:ILE:HG23	6:LC:229:LEU:HD13	1.86	0.57
52:S2:962:A:N1	52:S2:1055:A:O2'	2.37	0.57
54:SB:124:HIS:HA	54:SB:137:LEU:O	2.03	0.57
1:L5:1516:G:O2'	14:LL:18:TRP:NE1	2.33	0.57
1:L5:4093:G:N1	1:L5:4114:C:N3	2.51	0.57
1:L5:4274:A:H2'	1:L5:4275:G:H8	1.69	0.57
69:SQ:112:LEU:HD21	69:SQ:119:LEU:HB2	1.85	0.57
85:Sg:6:THR:OG1	85:Sg:8:ARG:NH1	2.36	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:Sg:31:ILE:HG12	85:Sg:45:LEU:HD21	1.86	0.57
1:L5:2837:U:OP1	5:LB:249:ARG:NH1	2.38	0.57
48:MA:263:VAL:HG12	48:MA:368:CYS:HB2	1.87	0.57
1:L5:305:A:OP2	16:LN:15:GLN:NE2	2.37	0.57
1:L5:1942:A:OP2	1:L5:2040:A:N6	2.37	0.57
25:LW:81:ALA:HB2	25:LW:87:LEU:HB2	1.87	0.57
85:Sg:238:ALA:HB3	85:Sg:251:ALA:HB3	1.87	0.57
1:L5:727:C:H4'	9:LF:69:ILE:HD12	1.86	0.57
1:L5:2343:G:OP2	6:LC:109:ARG:NH2	2.35	0.57
6:LC:205:ARG:HD2	6:LC:248:ARG:HH12	1.69	0.57
45:Lr:41:ASN:HD22	45:Lr:44:ILE:HD13	1.69	0.57
52:S2:1513:C:OP1	82:Sd:12:ARG:NH2	2.38	0.57
1:L5:2406:G:N7	40:Ll:2:SER:N	2.53	0.57
1:L5:3940:U:H5''	10:LG:75:LYS:HD2	1.87	0.57
23:LU:116:GLN:HE21	51:NB:30:LYS:HD2	1.69	0.57
56:SD:18:LYS:HG2	56:SD:39:VAL:HG21	1.86	0.57
77:SY:57:VAL:HB	77:SY:60:PHE:HE2	1.70	0.57
1:L5:265:C:H1'	36:Lh:112:ARG:HH12	1.70	0.57
1:L5:3887:C:OP2	17:LO:85:ARG:NH2	2.37	0.57
1:L5:4745:G:H1	1:L5:4955:A:N6	2.01	0.57
1:L5:4769:G:OP1	17:LO:176:ARG:NH1	2.37	0.57
45:Lr:26:SER:OG	45:Lr:28:GLU:OE1	2.23	0.57
52:S2:1860:A:H3'	79:Sa:8:ASN:HB3	1.86	0.57
84:Sf:113:LYS:NZ	84:Sf:114:ILE:O	2.37	0.57
56:SD:126:ILE:HG23	56:SD:127:MET:HE2	1.87	0.57
72:ST:35:ASP:OD2	72:ST:35:ASP:N	2.35	0.57
78:SZ:103:HIS:HB2	78:SZ:106:GLN:HE21	1.69	0.57
1:L5:2000:G:N2	1:L5:2000:G:OP2	2.38	0.56
21:LS:71:SER:O	21:LS:76:LYS:NZ	2.38	0.56
57:SE:54:TYR:O	77:SY:15:ASN:ND2	2.38	0.56
70:SR:22:THR:O	85:Sg:212:LYS:NZ	2.37	0.56
71:SS:60:THR:OG1	71:SS:61:GLU:N	2.34	0.56
1:L5:4229:U:OP1	43:Lo:63:THR:OG1	2.23	0.56
9:LF:71:MET:HA	9:LF:74:MET:HG2	1.87	0.56
68:SP:69:PRO:HD2	68:SP:70:MET:H	1.70	0.56
69:SQ:104:SER:HA	69:SQ:107:GLU:HG2	1.87	0.56
1:L5:1487:G:H4'	14:LL:183:ARG:HB3	1.87	0.56
14:LL:174:LYS:NZ	29:La:142:GLY:O	2.38	0.56
29:La:68:SER:O	29:La:68:SER:OG	2.21	0.56
52:S2:649:U:H2'	52:S2:650:A:H8	1.70	0.56
52:S2:1256:G:O4'	82:Sd:40:ARG:NH2	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:S2:1536:G:H2'	52:S2:1537:A:H8	1.69	0.56
52:S2:1854:U:OP1	67:SO:150:ARG:NH2	2.37	0.56
63:SK:52:LEU:HB3	63:SK:57:TYR:HD1	1.70	0.56
1:L5:438:G:N2	34:Lf:23:GLU:OE2	2.37	0.56
1:L5:2404:A:H1'	38:Lj:12:ARG:HH11	1.71	0.56
1:L5:4951:G:H2'	1:L5:4952:G:H8	1.70	0.56
48:MA:209:ARG:NH2	48:MA:212:GLN:OE1	2.38	0.56
48:MA:218:ASN:ND2	48:MA:356:GLN:O	2.38	0.56
52:S2:844:U:H2'	52:S2:845:G:H8	1.70	0.56
61:SI:81:VAL:HG22	61:SI:102:VAL:HG12	1.87	0.56
71:SS:23:ARG:HH21	78:SZ:48:VAL:HG23	1.71	0.56
1:L5:1332:C:H2'	1:L5:1333:A:H8	1.70	0.56
1:L5:4626:A:OP2	5:LB:224:LYS:NZ	2.32	0.56
52:S2:874:G:H2'	52:S2:875:A:H8	1.71	0.56
52:S2:1123:C:OP1	54:SB:151:ARG:NH2	2.38	0.56
57:SE:199:GLU:HB2	57:SE:207:VAL:HG23	1.88	0.56
61:SI:87:ASN:HB3	61:SI:90:LEU:HD23	1.87	0.56
1:L5:691:C:OP1	8:LE:114:ARG:NH1	2.38	0.56
1:L5:1914:C:H4'	17:LO:89:PRO:HD3	1.87	0.56
1:L5:5027:C:H5	61:SI:79:ILE:HG12	1.71	0.56
51:NB:43:LYS:NZ	51:NB:47:SER:OG	2.37	0.56
52:S2:560:A:H5'	62:SJ:174:LYS:HD3	1.88	0.56
1:L5:4589:A:N1	1:L5:4621:C:O2'	2.36	0.56
55:SC:263:LYS:HG2	55:SC:268:GLU:HB2	1.87	0.56
42:Ln:2:ARG:NH1	52:S2:1841:C:OP2	2.38	0.56
50:NA:111:VAL:HG22	50:NA:122:VAL:HG22	1.87	0.56
1:L5:3680:U:OP1	4:LA:54:ARG:NH2	2.35	0.56
54:SB:77:ASP:N	54:SB:77:ASP:OD2	2.37	0.56
71:SS:39:ARG:HH22	72:ST:38:LYS:HB3	1.70	0.56
71:SS:114:LEU:HD21	71:SS:121:ARG:HG2	1.87	0.56
85:Sg:106:LYS:HG2	85:Sg:126:ASP:HB3	1.88	0.56
1:L5:4594:U:H2'	1:L5:4595:G:H8	1.71	0.56
29:La:89:ASN:OD1	29:La:92:LYS:NZ	2.39	0.56
48:MA:205:ILE:HD11	48:MA:344:TRP:HD1	1.71	0.56
49:N4:30:ASP:HA	49:N4:33:ASN:HD22	1.70	0.56
63:SK:76:ILE:O	63:SK:80:ARG:HG2	2.06	0.56
52:S2:1550:G:H3'	52:S2:1579:A:H61	1.70	0.55
67:SO:56:VAL:HG12	67:SO:81:VAL:HG23	1.88	0.55
1:L5:4769:G:H5''	17:LO:176:ARG:HD3	1.88	0.55
54:SB:68:GLU:OE1	54:SB:83:LYS:NZ	2.36	0.55
71:SS:98:VAL:HG21	71:SS:106:LYS:HG3	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:LB:230:GLY:O	5:LB:234:ARG:HB2	2.06	0.55
22:LT:114:GLN:NE2	22:LT:118:GLU:OE2	2.39	0.55
27:LY:32:SER:OG	27:LY:101:PRO:O	2.23	0.55
52:S2:1548:G:OP1	73:SU:60:THR:OG1	2.23	0.55
1:L5:2083:C:OP2	19:LQ:14:ARG:NH2	2.39	0.55
1:L5:4194:U:H5'	30:Lb:3:LYS:HG2	1.87	0.55
52:S2:604:A:OP1	62:SJ:22:LYS:NZ	2.39	0.55
7:LD:232:THR:HG22	7:LD:234:ASP:H	1.71	0.55
52:S2:1862:G:N2	79:Sa:76:SER:OG	2.39	0.55
56:SD:150:MET:N	56:SD:150:MET:SD	2.79	0.55
1:L5:207:G:O2'	1:L5:232:G:N2	2.39	0.55
52:S2:355:G:OP1	64:SL:105:ARG:NH1	2.40	0.55
52:S2:1628:C:OP1	72:ST:38:LYS:NZ	2.40	0.55
54:SB:61:GLY:O	54:SB:65:ARG:NH1	2.39	0.55
70:SR:36:GLU:HB3	70:SR:47:ARG:HD2	1.88	0.55
70:SR:118:GLN:NE2	70:SR:119:VAL:O	2.40	0.55
1:L5:974:C:O3'	9:LF:43:ARG:NH2	2.34	0.55
20:LR:103:ARG:HG2	20:LR:124:TYR:HE1	1.71	0.55
52:S2:1854:U:H2'	52:S2:1855:G:H8	1.72	0.55
53:SA:187:GLY:HA2	74:SV:45:ARG:HH11	1.71	0.55
58:SF:47:LYS:HG3	58:SF:67:PRO:HG3	1.89	0.55
64:SL:68:ILE:HG21	64:SL:143:LEU:HD11	1.88	0.55
1:L5:365:U:O2'	40:Ll:40:LYS:NZ	2.38	0.55
7:LD:231:VAL:HA	7:LD:235:MET:HE2	1.89	0.55
31:Lc:38:ILE:HG21	31:Lc:63:TYR:HB3	1.87	0.55
47:Lt:12:VAL:HB	47:Lt:65:GLN:HB3	1.89	0.55
54:SB:224:GLU:HB2	54:SB:227:LYS:HB2	1.88	0.55
1:L5:1517:G:H22	6:LC:103:ALA:HA	1.72	0.55
48:MA:231:ASP:HB3	48:MA:325:THR:HG21	1.88	0.55
52:S2:156:G:O2'	59:SG:56:ASN:ND2	2.40	0.55
52:S2:1752:C:H42	52:S2:1778:C:H42	1.55	0.55
85:Sg:203:ASP:OD2	85:Sg:203:ASP:N	2.40	0.55
58:SF:172:CYS:SG	58:SF:173:LEU:N	2.78	0.55
1:L5:109:G:OP2	14:LL:74:ARG:NH1	2.35	0.54
1:L5:1517:G:H1	6:LC:104:PRO:HD2	1.71	0.54
1:L5:2695:A:OP1	39:Lk:35:LYS:NZ	2.38	0.54
1:L5:3809:G:OP2	1:L5:3809:G:N2	2.33	0.54
16:LN:104:GLU:HG3	16:LN:161:MET:HG3	1.89	0.54
52:S2:4:C:H1'	62:SJ:18:ARG:HH12	1.72	0.54
57:SE:44:LEU:HD21	57:SE:70:ILE:HG21	1.89	0.54
57:SE:100:ARG:HB2	57:SE:114:ILE:HD13	1.87	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:926:G:H2'	1:L5:927:G:H8	1.71	0.54
53:SA:200:ASP:HA	53:SA:203:PHE:HB2	1.88	0.54
64:SL:16:ILE:HD11	64:SL:34:PRO:HG2	1.89	0.54
67:SO:41:PHE:HA	67:SO:57:THR:HG22	1.87	0.54
83:Se:36:MET:SD	83:Se:40:ARG:NH2	2.79	0.54
1:L5:4185:G:OP1	4:LA:2:GLY:N	2.40	0.54
1:L5:4537:C:H2'	1:L5:4538:G:H8	1.71	0.54
64:SL:86:ILE:HG13	64:SL:111:VAL:HG23	1.88	0.54
75:SW:119:LYS:HG3	75:SW:121:THR:HG23	1.90	0.54
1:L5:496:G:H2'	1:L5:498:C:H5''	1.89	0.54
1:L5:1198:G:O2'	1:L5:1200:G:OP1	2.25	0.54
52:S2:309:G:OP2	61:SI:55:TYR:OH	2.23	0.54
53:SA:42:LYS:HD3	53:SA:48:ILE:HD11	1.89	0.54
53:SA:77:ILE:HG21	53:SA:133:PRO:HG3	1.89	0.54
54:SB:52:THR:HG22	54:SB:58:ALA:H	1.72	0.54
54:SB:183:GLU:OE1	54:SB:183:GLU:N	2.40	0.54
55:SC:108:LYS:HB2	55:SC:233:LEU:HD13	1.88	0.54
67:SO:36:SER:OG	67:SO:37:PHE:N	2.39	0.54
45:Lr:16:PHE:HB3	45:Lr:27:THR:H	1.71	0.54
58:SF:104:THR:HG21	58:SF:111:VAL:HG21	1.89	0.54
60:SH:147:LYS:HD2	60:SH:148:LEU:H	1.72	0.54
1:L5:4274:A:H2'	1:L5:4275:G:C8	2.43	0.54
1:L5:4301:U:OP2	1:L5:4303:C:N4	2.40	0.54
56:SD:8:LYS:HB3	73:SU:61:LEU:HD21	1.89	0.54
73:SU:118:ASP:OD2	73:SU:118:ASP:N	2.35	0.54
1:L5:2772:C:O2'	39:Lk:17:ARG:NH1	2.40	0.54
3:L8:94:G:N3	38:Lj:82:THR:OG1	2.40	0.54
15:LM:104:MET:HE3	15:LM:109:ARG:HG2	1.90	0.54
32:Ld:92:ARG:HG2	32:Ld:94:GLU:HG2	1.89	0.54
48:MA:209:ARG:NH2	48:MA:215:ASP:OD2	2.40	0.54
52:S2:1373:C:H4'	70:SR:10:LYS:HE3	1.90	0.54
52:S2:1521:C:H5'	68:SP:126:VAL:HG11	1.89	0.54
56:SD:227:LYS:HD2	85:Sg:184:LEU:HD23	1.89	0.54
72:ST:104:LEU:HD22	72:ST:121:ARG:HH11	1.71	0.54
78:SZ:77:LEU:HD23	78:SZ:79:ILE:HD11	1.89	0.54
1:L5:1479:G:H21	14:LL:184:MET:HE1	1.73	0.54
1:L5:2793:G:H5''	1:L5:2794:C:H5''	1.90	0.54
1:L5:4128:A:H1'	10:LG:35:ARG:HB2	1.90	0.54
7:LD:278:ASP:O	7:LD:282:GLN:HG3	2.08	0.54
48:MA:268:ARG:NH2	48:MA:314:ALA:O	2.41	0.54
72:ST:77:LYS:HB2	72:ST:94:ARG:HH21	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1994:C:H1'	47:Lt:132:ILE:HA	1.90	0.54
1:L5:3932:U:H2'	1:L5:3933:G:H8	1.72	0.54
27:LY:55:VAL:HG12	27:LY:106:ILE:HA	1.90	0.54
52:S2:1192:U:OP2	76:SX:119:ARG:NH2	2.40	0.54
14:LL:79:GLU:OE2	14:LL:82:ARG:NH2	2.41	0.53
25:LW:77:LYS:HE2	52:S2:1778:C:H5''	1.90	0.53
48:MA:263:VAL:HG13	48:MA:318:MET:HE1	1.89	0.53
51:NB:33:VAL:O	51:NB:35:ARG:NH1	2.41	0.53
71:SS:25:LYS:O	71:SS:29:ALA:CB	2.56	0.53
1:L5:153:G:H2'	1:L5:154:G:H8	1.74	0.53
9:LF:127:LYS:HB2	22:LT:133:ALA:HB3	1.90	0.53
9:LF:180:GLY:HA2	9:LF:185:ILE:HG22	1.90	0.53
17:LO:34:VAL:HG22	17:LO:103:LYS:HB2	1.90	0.53
35:Lg:41:ALA:HB3	35:Lg:52:ARG:HD3	1.89	0.53
46:Ls:145:THR:HG23	46:Ls:154:ILE:HG13	1.90	0.53
48:MA:184:LEU:HB2	48:MA:192:SER:HA	1.89	0.53
85:Sg:41:ILE:HG21	85:Sg:55:PRO:HB3	1.90	0.53
1:L5:2520:C:H2'	1:L5:2521:G:H8	1.73	0.53
12:LI:87:ILE:HG12	12:LI:138:ILE:HG12	1.90	0.53
18:LP:24:VAL:HG23	18:LP:86:LYS:HD3	1.89	0.53
19:LQ:27:LEU:HA	19:LQ:30:LYS:HD3	1.90	0.53
52:S2:43:U:OP2	52:S2:485:A:N6	2.42	0.53
69:SQ:123:ASP:OD2	69:SQ:123:ASP:N	2.42	0.53
73:SU:41:ARG:HA	73:SU:44:LYS:HZ3	1.74	0.53
1:L5:5:A:O2'	10:LG:192:ARG:NH1	2.39	0.53
1:L5:67:C:OP2	1:L5:312:G:N2	2.41	0.53
52:S2:1033:G:N1	52:S2:1080:A:O2'	2.36	0.53
67:SO:45:THR:OG1	67:SO:46:ASP:N	2.42	0.53
1:L5:2045:G:O6	1:L5:3870:C:O2'	2.27	0.53
14:LL:65:ARG:HG2	29:La:69:PHE:HD2	1.73	0.53
25:LW:71:ARG:HD2	25:LW:73:ARG:HH21	1.74	0.53
51:NB:73:HIS:HB3	51:NB:97:LYS:HZ1	1.73	0.53
57:SE:175:PHE:HE2	57:SE:225:ILE:HG21	1.73	0.53
1:L5:1850:A:N3	1:L5:2283:G:O2'	2.40	0.53
1:L5:4992:G:H2'	1:L5:4993:G:C8	2.43	0.53
14:LL:29:PRO:O	14:LL:33:ILE:HD12	2.09	0.53
46:Ls:125:ALA:HA	46:Ls:154:ILE:HB	1.90	0.53
52:S2:4:C:H4'	55:SC:207:ALA:HB2	1.91	0.53
52:S2:1446:A:H5''	73:SU:58:THR:HG23	1.91	0.53
52:S2:1566:G:O6	72:ST:101:ARG:NH1	2.41	0.53
1:L5:1961:G:OP1	46:Ls:6:ARG:NH2	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:LM:47:ARG:HG2	21:LS:73:LEU:HD22	1.91	0.53
52:S2:509:G:H2'	52:S2:510:G:H8	1.74	0.53
52:S2:1488:C:O2'	52:S2:1490:G:OP2	2.21	0.53
54:SB:99:ASN:OD1	54:SB:100:PHE:N	2.41	0.53
62:SJ:78:LEU:HB3	62:SJ:92:MET:HG2	1.91	0.53
73:SU:23:THR:HB	73:SU:113:GLU:HB3	1.89	0.53
1:L5:2407:G:H2'	40:Ll:13:LEU:HD22	1.90	0.53
47:Lt:82:ILE:HG21	47:Lt:137:GLN:HG3	1.91	0.53
48:MA:189:PHE:HD1	48:MA:191:LYS:H	1.55	0.53
52:S2:1644:C:H4'	69:SQ:140:ARG:HB2	1.90	0.53
85:Sg:236:ILE:HA	85:Sg:252:THR:HG22	1.91	0.53
1:L5:976:G:H4'	6:LC:326:LEU:HD23	1.89	0.53
1:L5:1996:C:H42	1:L5:2000:G:H22	1.55	0.53
65:SM:94:ILE:HA	65:SM:100:PRO:HA	1.91	0.53
81:Sc:44:ARG:HE	81:Sc:58:LEU:HD13	1.74	0.53
1:L5:4272:G:OP2	1:L5:4272:G:N2	2.34	0.53
1:L5:4587:G:N2	5:LB:15:GLY:O	2.39	0.53
12:LI:79:SER:OG	12:LI:80:CYS:SG	2.61	0.53
27:LY:57:VAL:HB	27:LY:63:LYS:HA	1.89	0.53
49:N4:106:ALA:O	49:N4:124:PHE:O	2.26	0.53
52:S2:837:A:N7	77:SY:8:ARG:NH1	2.57	0.53
52:S2:991:G:N7	79:Sa:7:ASN:ND2	2.54	0.53
75:SW:66:THR:OG1	75:SW:68:ARG:NH1	2.41	0.53
1:L5:307:A:N3	1:L5:310:G:O2'	2.39	0.52
1:L5:1996:C:N4	1:L5:2000:G:H22	2.06	0.52
4:LA:30:ARG:NH1	4:LA:36:GLU:OE1	2.41	0.52
8:LE:165:LEU:HD12	8:LE:174:LEU:HG	1.91	0.52
52:S2:822:U:H5'	52:S2:823:U:H5''	1.90	0.52
52:S2:1171:G:O2'	52:S2:1187:G:O6	2.25	0.52
61:SI:133:GLU:HA	61:SI:136:ILE:HG22	1.91	0.52
63:SK:3:MET:HE1	63:SK:7:ASN:HD22	1.74	0.52
68:SP:30:TYR:HA	68:SP:33:LEU:HG	1.90	0.52
74:SV:7:GLU:N	74:SV:7:GLU:OE2	2.42	0.52
85:Sg:121:VAL:HG21	85:Sg:165:ILE:HD11	1.90	0.52
1:L5:300:A:H2'	1:L5:301:G:H8	1.74	0.52
1:L5:4686:G:N3	11:LH:163:GLN:NE2	2.43	0.52
19:LQ:27:LEU:HD11	45:Lr:4:HIS:HB3	1.90	0.52
40:Ll:27:ILE:O	40:Ll:33:ASN:ND2	2.41	0.52
46:Ls:146:LYS:HE2	46:Ls:155:LEU:HD13	1.91	0.52
52:S2:1657:G:O2'	82:Sd:33:LYS:NZ	2.42	0.52
66:SN:114:ARG:O	66:SN:118:ILE:HD12	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1503:A:H4'	1:L5:1504:G:H5'	1.91	0.52
1:L5:4581:G:HO2'	5:LB:92:TYR:HH	1.55	0.52
48:MA:140:ARG:HG2	48:MA:371:LEU:HD22	1.92	0.52
49:N4:201:MET:N	49:N4:201:MET:SD	2.82	0.52
57:SE:71:LYS:HD3	57:SE:76:VAL:HG12	1.92	0.52
1:L5:4926:C:H5''	1:L5:4927:G:H21	1.75	0.52
1:L5:4966:A:H5''	5:LB:128:LYS:HG3	1.91	0.52
48:MA:307:PRO:HB2	48:MA:312:ASN:HB2	1.91	0.52
52:S2:201:C:H3'	52:S2:202:G:H21	1.75	0.52
73:SU:63:ILE:HG12	82:Sd:33:LYS:HG2	1.92	0.52
73:SU:66:ARG:HH22	73:SU:71:GLY:HA2	1.74	0.52
1:L5:158:A:H5''	1:L5:159:C:H2'	1.91	0.52
1:L5:1896:A:OP1	9:LF:223:LYS:NZ	2.42	0.52
1:L5:3811:G:O2'	1:L5:3814:U:OP2	2.28	0.52
1:L5:4174:U:H2'	1:L5:4175:G:H8	1.75	0.52
3:L8:141:C:H5''	16:LN:60:VAL:HG11	1.90	0.52
4:LA:177:LYS:HB2	44:Lp:29:ILE:HG21	1.90	0.52
14:LL:80:GLU:HG3	14:LL:110:LEU:HD12	1.90	0.52
16:LN:16:SER:O	16:LN:20:ARG:HB2	2.08	0.52
60:SH:27:LEU:HD21	60:SH:40:LEU:HD11	1.91	0.52
70:SR:114:LEU:HD23	70:SR:116:ASN:H	1.74	0.52
85:Sg:23:THR:HG22	85:Sg:31:ILE:HG23	1.91	0.52
1:L5:2326:G:OP1	33:Le:108:ARG:NH2	2.43	0.52
1:L5:5046:U:OP2	32:Ld:83:ARG:NH2	2.42	0.52
31:Lc:20:LEU:HB3	31:Lc:102:SER:HB2	1.91	0.52
35:Lg:5:LEU:HD21	35:Lg:30:ILE:HG22	1.91	0.52
39:Lk:37:ARG:HH21	39:Lk:42:LEU:HB2	1.75	0.52
48:MA:327:GLU:HB2	48:MA:356:GLN:HE21	1.75	0.52
52:S2:603:C:N4	52:S2:620:G:O6	2.41	0.52
61:SI:6:ASP:N	61:SI:6:ASP:OD1	2.34	0.52
72:ST:129:ARG:O	72:ST:133:ARG:HG3	2.09	0.52
1:L5:229:G:OP1	27:LY:11:ARG:NH1	2.37	0.52
5:LB:79:VAL:HB	5:LB:331:VAL:HG12	1.92	0.52
31:Lc:74:TYR:HE2	31:Lc:80:GLU:HG3	1.75	0.52
45:Lr:97:ILE:HD13	45:Lr:107:ARG:HA	1.91	0.52
48:MA:336:GLN:HE21	48:MA:349:ARG:HB3	1.74	0.52
52:S2:793:G:H2'	52:S2:794:A:H8	1.74	0.52
52:S2:1669:G:OP1	73:SU:79:ARG:NH2	2.32	0.52
67:SO:62:VAL:HG21	67:SO:67:ASP:HB2	1.92	0.52
72:ST:18:LEU:HD22	72:ST:58:ALA:HA	1.91	0.52
1:L5:1306:C:H2'	1:L5:1307:A:H8	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:N4:156:ILE:HD12	49:N4:186:PHE:HE1	1.74	0.52
59:SG:3:LEU:O	59:SG:15:LEU:HA	2.09	0.52
59:SG:224:ARG:HA	59:SG:227:GLN:HE21	1.73	0.52
1:L5:1942:A:H2'	1:L5:1943:A:C8	2.45	0.52
1:L5:4765:G:O6	15:LM:4:ARG:NH2	2.43	0.52
1:L5:4873:G:H22	17:LO:172:LYS:HG2	1.74	0.52
7:LD:62:CYS:HB3	7:LD:105:LEU:HD22	1.92	0.52
23:LU:74:SER:OG	23:LU:76:VAL:O	2.28	0.52
1:L5:458:C:OP1	45:Lr:87:ARG:NH2	2.43	0.52
1:L5:4541:G:N2	1:L5:4544:A:OP2	2.38	0.52
8:LE:149:ILE:HG21	8:LE:270:TYR:HE1	1.75	0.52
54:SB:164:ILE:O	54:SB:168:MET:HG3	2.10	0.52
60:SH:19:PHE:CE1	60:SH:23:ILE:HD11	2.44	0.52
66:SN:25:TRP:HE1	80:Sb:84:HIS:HB3	1.75	0.52
75:SW:115:GLU:HG2	75:SW:118:ARG:HH21	1.75	0.52
1:L5:422:C:H2'	1:L5:423:G:H8	1.75	0.51
1:L5:1933:G:H2'	1:L5:1934:A:C8	2.45	0.51
1:L5:3930:U:H3	1:L5:4180:G:H1	1.57	0.51
5:LB:162:VAL:O	5:LB:182:GLU:HA	2.10	0.51
5:LB:378:ARG:HG2	25:LW:32:LEU:HD21	1.91	0.51
49:N4:55:VAL:HG12	49:N4:113:GLU:HG2	1.92	0.51
52:S2:380:G:N1	52:S2:383:G:OP2	2.41	0.51
56:SD:105:LEU:HB3	56:SD:184:ILE:HD13	1.90	0.51
1:L5:1457:G:O2'	19:LQ:75:ARG:NH2	2.41	0.51
4:LA:147:ARG:HG3	4:LA:157:VAL:HG22	1.93	0.51
54:SB:137:LEU:HG	54:SB:215:VAL:HG22	1.90	0.51
67:SO:97:LEU:HD21	67:SO:108:PRO:HB3	1.92	0.51
85:Sg:18:VAL:HG11	85:Sg:307:VAL:HG22	1.92	0.51
85:Sg:286:CYS:HA	85:Sg:302:TYR:HA	1.92	0.51
1:L5:283:G:O2'	37:Li:82:ARG:NH2	2.43	0.51
1:L5:4134:C:H2'	1:L5:4135:G:H8	1.76	0.51
25:LW:66:GLU:HG2	25:LW:69:LYS:HD2	1.91	0.51
37:Li:94:LEU:HA	37:Li:97:MET:HG3	1.92	0.51
48:MA:119:GLU:HA	48:MA:299:LEU:HD12	1.92	0.51
1:L5:29:G:H5''	16:LN:172:ARG:HG2	1.92	0.51
52:S2:1857:G:OP1	67:SO:141:ARG:NH1	2.44	0.51
82:Sd:49:ASP:OD1	82:Sd:49:ASP:N	2.39	0.51
1:L5:238:C:O2	27:LY:102:SER:OG	2.29	0.51
1:L5:3664:G:H2'	1:L5:3665:G:H8	1.75	0.51
1:L5:4892:A:H5''	17:LO:188:LYS:HD3	1.92	0.51
52:S2:523:A:OP1	62:SJ:127:ARG:NH1	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:SZ:65:TYR:HA	78:SZ:111:ARG:HH21	1.76	0.51
1:L5:265:C:H4'	36:Lh:112:ARG:HH22	1.76	0.51
1:L5:2725:A:N6	20:LR:88:ARG:O	2.44	0.51
25:LW:91:MET:HA	25:LW:94:ARG:HG2	1.93	0.51
52:S2:641:A:OP2	83:Se:34:ARG:NH2	2.36	0.51
55:SC:271:ASP:OD2	55:SC:272:HIS:N	2.44	0.51
72:ST:28:LEU:HA	72:ST:110:LEU:HD21	1.92	0.51
72:ST:100:ALA:O	72:ST:104:LEU:HD12	2.10	0.51
75:SW:18:GLU:HG2	75:SW:69:LEU:HB3	1.91	0.51
85:Sg:166:VAL:HG12	85:Sg:176:VAL:HG22	1.93	0.51
1:L5:679:C:H2'	1:L5:680:G:H8	1.76	0.51
1:L5:2578:G:N7	28:LZ:17:ARG:NH2	2.59	0.51
1:L5:4163:U:OP2	10:LG:53:ARG:NH2	2.44	0.51
1:L5:4457:U:OP1	24:LV:50:ASN:ND2	2.42	0.51
16:LN:193:ARG:O	16:LN:197:THR:OG1	2.25	0.51
32:Ld:64:ILE:HG23	32:Ld:68:LEU:HD23	1.92	0.51
52:S2:1579:A:O2'	52:S2:1582:C:N4	2.43	0.51
56:SD:76:ARG:HG3	56:SD:77:PHE:HD2	1.75	0.51
85:Sg:157:SER:HB3	85:Sg:164:ILE:HB	1.91	0.51
1:L5:3668:C:OP1	4:LA:8:GLN:NE2	2.41	0.51
12:LI:177:ASN:N	12:LI:177:ASN:OD1	2.43	0.51
64:SL:65:ASN:O	64:SL:132:ARG:NH1	2.44	0.51
71:SS:75:ARG:HA	71:SS:79:ILE:HG22	1.92	0.51
84:Sf:103:LEU:HD23	84:Sf:105:TYR:H	1.75	0.51
1:L5:85:G:O2'	1:L5:97:G:O6	2.28	0.51
5:LB:224:LYS:HG3	5:LB:340:THR:HB	1.93	0.51
80:Sb:33:MET:HE2	80:Sb:48:SER:HA	1.91	0.51
84:Sf:123:SER:OG	84:Sf:126:CYS:SG	2.68	0.51
52:S2:453:C:O2'	59:SG:92:ARG:O	2.23	0.51
52:S2:661:U:OP2	76:SX:3:LYS:NZ	2.44	0.51
52:S2:1203:G:H2'	52:S2:1204:A:C8	2.46	0.51
77:SY:21:LYS:HG3	77:SY:75:ILE:HB	1.92	0.51
51:NB:80:GLN:HB2	51:NB:89:THR:HG23	1.91	0.50
52:S2:1218:C:H1'	52:S2:1683:C:H42	1.76	0.50
61:SI:38:ILE:HG13	61:SI:96:LEU:HD21	1.92	0.50
62:SJ:28:GLU:OE1	62:SJ:44:TRP:NE1	2.39	0.50
73:SU:35:VAL:HG21	73:SU:110:VAL:HG21	1.92	0.50
1:L5:1188:C:H2'	1:L5:1189:G:H8	1.76	0.50
1:L5:2385:U:OP1	20:LR:5:ARG:NH1	2.44	0.50
1:L5:4420:U:O4	1:L5:4475:G:N2	2.44	0.50
2:L7:7:G:OP1	7:LD:33:ARG:NH1	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L8:13:G:O2'	18:LP:121:LYS:O	2.28	0.50
3:L8:19:C:H2'	3:L8:20:A:C8	2.44	0.50
4:LA:247:ARG:HB3	52:S2:1069:U:H4'	1.93	0.50
8:LE:153:LEU:HD11	8:LE:195:ILE:HG13	1.94	0.50
52:S2:913:A:N6	60:SH:119:SER:O	2.44	0.50
52:S2:1420:G:H21	52:S2:1421:A:H1'	1.75	0.50
52:S2:1556:A:H1'	82:Sd:13:LYS:HG3	1.92	0.50
85:Sg:108:VAL:HA	85:Sg:124:SER:HA	1.93	0.50
1:L5:1332:C:H2'	1:L5:1333:A:C8	2.45	0.50
1:L5:2503:G:O4'	1:L5:4084:G:N2	2.44	0.50
21:LS:86:SER:OG	21:LS:89:GLY:O	2.27	0.50
43:Lo:26:TYR:HB3	43:Lo:67:VAL:HB	1.92	0.50
52:S2:919:A:OP2	66:SN:64:ARG:NH2	2.44	0.50
52:S2:1004:U:H2'	52:S2:1005:G:H8	1.76	0.50
52:S2:1228:A:H2'	52:S2:1229:G:H8	1.77	0.50
70:SR:35:CYS:HA	70:SR:38:ILE:HG22	1.94	0.50
72:ST:13:GLU:HA	72:ST:16:ARG:HG3	1.93	0.50
75:SW:55:ASP:HB3	80:Sb:25:VAL:HG12	1.92	0.50
1:L5:1548:G:O2'	1:L5:2812:A:N3	2.37	0.50
1:L5:2845:A:N6	1:L5:3843:C:H42	2.06	0.50
1:L5:3688:U:OP2	4:LA:198:ARG:NH1	2.44	0.50
45:Lr:39:ARG:O	45:Lr:103:ARG:NH2	2.44	0.50
48:MA:349:ARG:NE	48:MA:349:ARG:O	2.44	0.50
52:S2:1095:U:O3'	75:SW:20:ARG:NH1	2.44	0.50
52:S2:1243:U:OP2	52:S2:1518:C:O2'	2.25	0.50
54:SB:122:GLU:N	54:SB:122:GLU:OE2	2.44	0.50
73:SU:46:LYS:HD3	73:SU:97:ILE:HD11	1.93	0.50
1:L5:2835:A:O2'	5:LB:228:TYR:O	2.25	0.50
1:L5:2884:G:H2'	1:L5:2885:A:H8	1.76	0.50
1:L5:3839:G:N2	1:L5:3843:C:O2'	2.45	0.50
2:L7:12:U:OP2	2:L7:67:C:O2'	2.30	0.50
5:LB:29:VAL:HA	5:LB:220:ILE:HD13	1.94	0.50
11:LH:111:LEU:HD13	11:LH:127:ARG:HE	1.77	0.50
31:Lc:78:ASN:OD1	31:Lc:78:ASN:N	2.45	0.50
52:S2:582:C:H5''	62:SJ:162:ARG:HH12	1.76	0.50
52:S2:1239:U:H3	52:S2:1242:U:H5''	1.76	0.50
52:S2:1244:U:H2'	52:S2:1245:G:H8	1.77	0.50
57:SE:191:ARG:HD2	57:SE:245:ARG:HE	1.76	0.50
1:L5:436:C:H2'	1:L5:437:G:H8	1.76	0.50
1:L5:2333:G:H5''	6:LC:195:LYS:HE3	1.93	0.50
6:LC:209:ILE:O	6:LC:229:LEU:HA	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:LD:202:GLN:NE2	7:LD:237:GLU:OE1	2.45	0.50
12:LI:66:GLU:OE1	12:LI:69:ARG:NH2	2.37	0.50
42:Ln:5:TRP:HE1	52:S2:1853:C:N4	2.01	0.50
52:S2:520:A:O2'	52:S2:825:A:N3	2.41	0.50
52:S2:1277:C:H2'	52:S2:1278:A:C8	2.46	0.50
52:S2:1360:U:O2'	52:S2:1379:A:OP2	2.28	0.50
63:SK:37:ASP:OD2	63:SK:38:LYS:NZ	2.45	0.50
69:SQ:132:PHE:HE1	73:SU:76:THR:HA	1.77	0.50
1:L5:1460:C:H5''	19:LQ:144:LYS:HB2	1.94	0.50
1:L5:4277:G:H5''	22:LT:17:ARG:HG3	1.93	0.50
6:LC:163:LYS:HB2	6:LC:166:GLU:HG3	1.93	0.50
10:LG:96:LEU:O	10:LG:100:HIS:HB2	2.12	0.50
16:LN:181:HIS:O	16:LN:195:ARG:NH2	2.43	0.50
28:LZ:11:VAL:HB	28:LZ:80:LEU:HD22	1.93	0.50
35:Lg:84:ALA:O	35:Lg:88:ARG:HG3	2.12	0.50
48:MA:150:LEU:HD13	48:MA:221:ILE:HG12	1.94	0.50
48:MA:259:ALA:HB2	48:MA:276:ILE:HD11	1.94	0.50
60:SH:47:ALA:HB3	60:SH:63:PHE:HB2	1.93	0.50
63:SK:57:TYR:HB3	63:SK:75:GLY:HA2	1.94	0.50
1:L5:1443:A:H2	1:L5:2102:G:H22	1.60	0.50
1:L5:2411:C:H2'	1:L5:2412:A:H8	1.76	0.50
1:L5:2899:C:OP1	20:LR:108:ARG:NH2	2.40	0.50
1:L5:4485:C:O2'	41:Lm:114:LYS:NZ	2.39	0.50
50:NA:101:ASN:HB3	50:NA:131:LEU:HB3	1.94	0.50
52:S2:165:G:OP2	52:S2:165:G:N2	2.36	0.50
69:SQ:13:PHE:HA	69:SQ:21:ALA:O	2.11	0.50
71:SS:84:LEU:O	71:SS:87:GLN:NE2	2.38	0.50
85:Sg:19:THR:O	85:Sg:288:SER:OG	2.26	0.50
1:L5:2745:A:H2'	1:L5:2746:A:H8	1.77	0.50
5:LB:291:TYR:HB3	5:LB:298:LEU:HD11	1.93	0.50
7:LD:202:GLN:HE22	7:LD:237:GLU:HB2	1.76	0.50
10:LG:105:GLU:N	10:LG:105:GLU:OE1	2.42	0.50
32:Ld:36:VAL:HG21	32:Ld:44:ARG:HG2	1.93	0.50
48:MA:288:VAL:HB	48:MA:329:MET:HE3	1.94	0.50
52:S2:1627:C:H5''	72:ST:41:LYS:HD2	1.94	0.50
53:SA:154:LEU:HD21	74:SV:66:ASP:HB3	1.92	0.50
55:SC:254:ASP:OD2	74:SV:1:MET:N	2.45	0.50
58:SF:91:ARG:HH21	58:SF:92:ILE:HG13	1.77	0.50
80:Sb:33:MET:HG3	80:Sb:46:VAL:HG13	1.94	0.50
85:Sg:47:ARG:HG3	85:Sg:52:TYR:HE1	1.76	0.50
1:L5:3661:G:N7	4:LA:152:SER:OG	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:LD:289:ARG:HA	7:LD:292:GLU:HG3	1.93	0.49
10:LG:102:TYR:HE1	10:LG:207:VAL:HG22	1.77	0.49
16:LN:114:ARG:NH1	16:LN:151:ILE:O	2.45	0.49
70:SR:29:HIS:HA	70:SR:32:LYS:HE2	1.94	0.49
1:L5:268:G:H2'	1:L5:269:G:H8	1.78	0.49
1:L5:691:C:P	8:LE:114:ARG:HH12	2.34	0.49
1:L5:1604:G:H2'	1:L5:1605:G:C8	2.48	0.49
1:L5:2361:G:O2'	1:L5:3859:G:O6	2.28	0.49
1:L5:3654:G:O2'	1:L5:3693:U:OP1	2.28	0.49
6:LC:101:MET:HE3	6:LC:104:PRO:HA	1.94	0.49
46:Ls:81:HIS:HB3	46:Ls:191:GLN:HG3	1.93	0.49
50:NA:94:VAL:HB	50:NA:106:ILE:HB	1.93	0.49
52:S2:1665:G:C5	72:ST:88:MET:HE1	2.47	0.49
67:SO:99:ALA:H	67:SO:133:THR:HG23	1.76	0.49
69:SQ:48:GLN:OE1	69:SQ:48:GLN:N	2.36	0.49
84:Sf:116:ARG:NE	84:Sf:118:ARG:O	2.45	0.49
2:L7:117:G:OP2	7:LD:255:LYS:NZ	2.43	0.49
51:NB:41:ASP:OD1	51:NB:41:ASP:N	2.44	0.49
52:S2:1550:G:O2'	52:S2:1558:C:O2	2.25	0.49
53:SA:52:LYS:HG3	70:SR:109:LEU:HD11	1.94	0.49
55:SC:134:ASN:O	55:SC:167:ARG:NH1	2.41	0.49
1:L5:2395:A:HO2'	1:L5:2806:A:HO2'	1.56	0.49
1:L5:3917:A:H2'	1:L5:3918:G:H8	1.77	0.49
26:LX:87:MET:O	26:LX:91:GLU:HG3	2.13	0.49
52:S2:639:C:H2'	52:S2:640:A:H8	1.78	0.49
60:SH:73:GLN:HB2	60:SH:135:PHE:CZ	2.47	0.49
61:SI:162:LEU:HD21	61:SI:191:GLU:HG2	1.94	0.49
71:SS:20:ILE:HD11	71:SS:33:ILE:HG23	1.95	0.49
85:Sg:107:ASP:O	85:Sg:125:ARG:N	2.41	0.49
18:LP:64:ASN:ND2	18:LP:80:GLN:OE1	2.43	0.49
27:LY:58:VAL:HG13	27:LY:59:ARG:HG2	1.95	0.49
43:Lo:34:TYR:O	43:Lo:39:ARG:NH1	2.45	0.49
48:MA:148:GLU:HB3	48:MA:177:ARG:HH21	1.77	0.49
52:S2:169:U:H5''	59:SG:135:PRO:HA	1.95	0.49
59:SG:2:LYS:HB2	59:SG:108:VAL:HG22	1.93	0.49
1:L5:267:G:H2'	1:L5:268:G:H8	1.76	0.49
1:L5:1563:A:H2'	1:L5:1564:A:C8	2.48	0.49
24:LV:30:ASP:HB3	24:LV:104:VAL:HG12	1.94	0.49
42:Ln:5:TRP:NE1	52:S2:1853:C:H41	1.98	0.49
48:MA:153:ALA:HA	48:MA:156:MET:HE3	1.95	0.49
48:MA:216:ILE:HG12	48:MA:353:ARG:HH21	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:ST:22:LEU:HD13	72:ST:28:LEU:HD21	1.95	0.49
82:Sd:10:HIS:O	82:Sd:12:ARG:NH1	2.45	0.49
1:L5:4135:G:H2'	1:L5:4136:G:H8	1.78	0.49
1:L5:5047:C:O2'	1:L5:5050:C:OP2	2.31	0.49
5:LB:107:ALA:HB2	5:LB:201:LEU:HD22	1.93	0.49
8:LE:286:LEU:HD13	15:LM:109:ARG:HH12	1.77	0.49
11:LH:113:GLU:OE1	11:LH:115:ARG:NH2	2.45	0.49
22:LT:154:ILE:HD12	22:LT:155:PRO:HD2	1.95	0.49
49:N4:145:LYS:HG3	49:N4:146:VAL:HG13	1.94	0.49
52:S2:862:A:N3	75:SW:105:THR:OG1	2.40	0.49
63:SK:12:TYR:HA	63:SK:15:LEU:HB3	1.93	0.49
68:SP:86:LEU:HG	68:SP:88:GLU:H	1.78	0.49
76:SX:39:ASN:OD1	76:SX:42:GLY:N	2.45	0.49
85:Sg:258:ILE:HG12	85:Sg:268:ASP:HB2	1.95	0.49
1:L5:232:G:H1	27:LY:61:HIS:HB2	1.78	0.49
1:L5:1558:A:H2'	1:L5:1559:G:C8	2.48	0.49
6:LC:59:GLY:HA3	6:LC:100:ARG:HB2	1.95	0.49
28:LZ:35:ASP:OD1	28:LZ:35:ASP:N	2.44	0.49
52:S2:1694:U:O2'	52:S2:1833:C:O2'	2.30	0.49
52:S2:1705:C:H2'	52:S2:1706:G:C8	2.48	0.49
1:L5:2297:G:H4'	6:LC:242:PRO:HB2	1.95	0.49
24:LV:32:THR:HG23	24:LV:34:ALA:H	1.77	0.49
52:S2:145:G:H2'	52:S2:146:G:C8	2.48	0.49
58:SF:195:GLU:HA	58:SF:198:ARG:HG2	1.94	0.49
85:Sg:7:LEU:HD21	85:Sg:308:ARG:HB3	1.95	0.49
1:L5:934:C:H4'	1:L5:935:A:H5''	1.95	0.49
1:L5:1762:C:H5''	1:L5:1764:G:H1	1.78	0.49
1:L5:3932:U:H2'	1:L5:3933:G:C8	2.48	0.49
1:L5:4092:G:H3'	1:L5:4093:G:H21	1.78	0.49
1:L5:4761:G:H2'	1:L5:4762:A:H8	1.78	0.49
27:LY:59:ARG:HB2	27:LY:103:LYS:HD2	1.94	0.49
27:LY:108:ARG:NH1	49:N4:103:ASP:OD2	2.46	0.49
28:LZ:46:ILE:HG23	28:LZ:68:ILE:HG23	1.94	0.49
52:S2:527:C:H2'	52:S2:528:A:H8	1.78	0.49
53:SA:122:LEU:HD21	53:SA:133:PRO:HB2	1.93	0.49
60:SH:101:LEU:O	60:SH:116:ARG:NH1	2.46	0.49
73:SU:78:ASP:HB3	82:Sd:54:LYS:HZ3	1.77	0.49
75:SW:25:VAL:HG22	75:SW:63:VAL:HB	1.95	0.49
1:L5:1086:C:H2'	1:L5:1087:A:H8	1.78	0.48
1:L5:1645:C:H2'	1:L5:1646:A:C8	2.47	0.48
1:L5:1743:A:N1	1:L5:1789:C:O2'	2.39	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:2309:G:O2'	3:L8:18:U:O2	2.29	0.48
1:L5:2699:C:H2'	1:L5:2700:G:H8	1.78	0.48
22:LT:75:VAL:HG12	22:LT:88:ARG:HG2	1.94	0.48
23:LU:91:LEU:HB3	23:LU:97:ARG:HG2	1.95	0.48
52:S2:1130:G:N2	52:S2:1130:G:OP2	2.46	0.48
58:SF:50:PRO:HB3	58:SF:69:VAL:HG23	1.95	0.48
73:SU:80:PHE:HB3	82:Sd:52:PHE:HB3	1.95	0.48
81:Sc:35:MET:N	81:Sc:35:MET:SD	2.86	0.48
25:LW:20:ARG:NH1	25:LW:30:GLN:OE1	2.43	0.48
48:MA:100:PRO:HD2	48:MA:103:ILE:HD12	1.95	0.48
48:MA:147:ARG:NE	48:MA:372:THR:O	2.41	0.48
51:NB:79:VAL:HG22	51:NB:90:ILE:HG12	1.94	0.48
52:S2:1277:C:H2'	52:S2:1278:A:H8	1.77	0.48
52:S2:1396:A:O2'	52:S2:1398:G:N7	2.43	0.48
78:SZ:70:PRO:HD3	78:SZ:88:LEU:HD21	1.94	0.48
85:Sg:176:VAL:HB	85:Sg:186:THR:HB	1.95	0.48
1:L5:1071:C:O2	8:LE:70:LYS:NZ	2.38	0.48
1:L5:1996:C:O2'	46:Ls:44:ARG:NH1	2.44	0.48
1:L5:2809:G:O2'	1:L5:4644:G:OP1	2.30	0.48
1:L5:5066:U:OP1	18:LP:43:LYS:NZ	2.44	0.48
5:LB:165:HIS:HA	5:LB:179:HIS:O	2.12	0.48
6:LC:209:ILE:HD13	6:LC:251:ILE:HB	1.95	0.48
8:LE:192:LYS:HD3	34:Lf:107:PRO:HB3	1.94	0.48
19:LQ:61:LEU:HD21	19:LQ:66:MET:HB2	1.94	0.48
52:S2:1010:G:H2'	52:S2:1011:A:H8	1.77	0.48
52:S2:1864:U:H5'	79:Sa:79:ILE:HD11	1.94	0.48
59:SG:56:ASN:HD22	59:SG:60:GLY:HA2	1.78	0.48
67:SO:60:MET:SD	67:SO:60:MET:N	2.80	0.48
1:L5:2318:G:N2	1:L5:2321:G:OP2	2.38	0.48
4:LA:33:ASP:N	4:LA:33:ASP:OD1	2.45	0.48
10:LG:103:ARG:HE	10:LG:195:HIS:CE1	2.31	0.48
10:LG:232:GLU:O	10:LG:236:HIS:HB2	2.14	0.48
18:LP:26:PHE:HB2	18:LP:144:CYS:HB3	1.94	0.48
51:NB:62:VAL:HB	51:NB:74:PHE:HD2	1.78	0.48
52:S2:1228:A:H2'	52:S2:1229:G:C8	2.48	0.48
53:SA:119:PRO:HG2	53:SA:142:LEU:HD21	1.94	0.48
58:SF:93:VAL:HG23	58:SF:97:PHE:CE1	2.49	0.48
60:SH:43:LEU:HD11	60:SH:71:SER:HB2	1.95	0.48
70:SR:56:HIS:HA	70:SR:59:LYS:HD2	1.96	0.48
85:Sg:111:VAL:HA	85:Sg:121:VAL:O	2.13	0.48
1:L5:307:A:OP1	37:Li:86:LYS:NZ	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1802:A:H5''	1:L5:1803:G:H5'	1.96	0.48
1:L5:2335:C:H2'	1:L5:2336:G:H8	1.78	0.48
1:L5:4466:C:H2'	1:L5:4467:A:H8	1.78	0.48
35:Lg:42:PRO:HB2	35:Lg:53:LEU:HD12	1.95	0.48
48:MA:222:THR:HG21	48:MA:300:PHE:HE1	1.78	0.48
49:N4:171:VAL:O	49:N4:215:SER:HA	2.13	0.48
52:S2:383:G:O2'	64:SL:133:PRO:O	2.26	0.48
52:S2:1256:G:N2	82:Sd:30:LEU:O	2.38	0.48
52:S2:1528:G:O2'	52:S2:1666:C:OP1	2.31	0.48
52:S2:1536:G:H2'	52:S2:1537:A:C8	2.48	0.48
53:SA:154:LEU:HG	53:SA:157:VAL:HB	1.95	0.48
54:SB:25:PHE:HA	54:SB:28:LYS:HG2	1.95	0.48
55:SC:205:VAL:HG23	55:SC:223:TYR:HA	1.95	0.48
83:Se:22:GLN:NE2	83:Se:23:GLU:O	2.46	0.48
85:Sg:11:LEU:HB2	85:Sg:307:VAL:HB	1.96	0.48
1:L5:161:G:H2'	1:L5:162:A:H8	1.78	0.48
1:L5:419:A:N3	1:L5:1332:C:O2'	2.44	0.48
1:L5:1906:U:H2'	1:L5:1907:A:H8	1.78	0.48
48:MA:211:LEU:HB3	48:MA:238:VAL:HG11	1.95	0.48
52:S2:122:G:H21	57:SE:146:THR:HG21	1.78	0.48
68:SP:22:LEU:HD21	68:SP:109:PRO:HG3	1.95	0.48
82:Sd:16:GLN:NE2	82:Sd:27:ARG:HB3	2.28	0.48
1:L5:323:C:H2'	1:L5:324:A:H8	1.78	0.48
1:L5:513:U:O2'	1:L5:515:C:N4	2.47	0.48
1:L5:673:C:H2'	1:L5:674:G:H8	1.78	0.48
1:L5:1947:U:O2	1:L5:4693:C:N4	2.45	0.48
1:L5:2517:A:N3	1:L5:2539:C:O2'	2.45	0.48
45:Lr:113:ARG:O	45:Lr:117:ILE:HG13	2.14	0.48
81:Sc:42:ILE:HD11	81:Sc:64:GLU:HG3	1.96	0.48
85:Sg:20:GLN:HG3	85:Sg:68:ASP:HA	1.95	0.48
1:L5:370:U:O2'	38:Lj:16:HIS:ND1	2.44	0.48
1:L5:1494:U:H2'	1:L5:1495:G:H8	1.79	0.48
1:L5:3848:U:H2'	1:L5:3849:A:H8	1.79	0.48
1:L5:4975:G:O2'	1:L5:4977:A:N6	2.46	0.48
2:L7:95:C:OP1	21:LS:43:ARG:NH2	2.46	0.48
6:LC:242:PRO:HG3	6:LC:248:ARG:HH11	1.79	0.48
7:LD:53:VAL:O	7:LD:54:ARG:NE	2.46	0.48
11:LH:112:VAL:HG11	11:LH:161:ILE:HD11	1.95	0.48
27:LY:70:VAL:HA	27:LY:82:ILE:HG22	1.95	0.48
39:Lk:40:ARG:HG2	39:Lk:41:TYR:CD1	2.49	0.48
46:Ls:53:VAL:HG12	46:Ls:89:VAL:HG22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:MA:338:GLU:HG2	48:MA:347:VAL:HG23	1.95	0.48
52:S2:681:U:H4'	76:SX:9:THR:HG22	1.96	0.48
55:SC:272:HIS:HA	55:SC:275:LYS:HG2	1.96	0.48
57:SE:98:ASN:HD22	57:SE:116:PRO:HG3	1.78	0.48
61:SI:101:ILE:HD12	61:SI:190:LEU:HD11	1.95	0.48
63:SK:63:ALA:HB3	63:SK:68:TYR:HE2	1.79	0.48
31:Lc:47:ILE:HB	31:Lc:94:LEU:HG	1.96	0.48
52:S2:656:G:H21	52:S2:663:C:H5''	1.79	0.48
52:S2:1255:G:H5'	73:SU:66:ARG:HH12	1.77	0.48
63:SK:21:MET:HB3	63:SK:69:TRP:HB2	1.95	0.48
63:SK:23:ALA:O	63:SK:66:HIS:HA	2.12	0.48
67:SO:67:ASP:HA	67:SO:70:SER:HB3	1.95	0.48
1:L5:727:C:H5''	9:LF:69:ILE:HG21	1.96	0.48
1:L5:1482:G:N2	1:L5:1482:G:OP2	2.46	0.48
1:L5:1514:U:H2'	1:L5:1515:A:H8	1.79	0.48
1:L5:1558:A:H2'	1:L5:1559:G:H8	1.78	0.48
1:L5:1646:A:O2'	38:Lj:49:TRP:O	2.31	0.48
3:L8:45:C:OP2	40:Ll:15:LYS:NZ	2.37	0.48
5:LB:150:PHE:O	5:LB:154:LYS:HG2	2.14	0.48
8:LE:131:LYS:O	8:LE:136:HIS:NE2	2.44	0.48
11:LH:94:SER:HB3	11:LH:142:ASP:HB3	1.96	0.48
21:LS:159:LEU:HD11	21:LS:161:ARG:HB2	1.96	0.48
48:MA:374:ARG:NH1	48:MA:374:ARG:HB2	2.29	0.48
52:S2:1597:C:H5''	71:SS:25:LYS:NZ	2.29	0.48
56:SD:5:ILE:HG23	56:SD:9:ARG:HG3	1.96	0.48
57:SE:31:PRO:HA	57:SE:81:THR:HB	1.96	0.48
1:L5:1415:G:H2'	1:L5:1416:G:H8	1.79	0.47
1:L5:3717:A:H2'	1:L5:3718:A:H8	1.77	0.47
1:L5:3855:C:H2'	1:L5:3856:A:H8	1.79	0.47
1:L5:4622:A:H4'	5:LB:13:SER:HB2	1.94	0.47
7:LD:94:ASN:HD22	7:LD:204:VAL:HG21	1.78	0.47
10:LG:209:SER:HA	10:LG:212:LYS:HE2	1.95	0.47
52:S2:1232:U:H2'	52:S2:1233:G:H8	1.79	0.47
62:SJ:124:HIS:O	62:SJ:128:VAL:HG23	2.13	0.47
63:SK:59:LYS:HZ3	63:SK:70:TYR:HB3	1.79	0.47
64:SL:147:LYS:HD2	64:SL:148:ALA:N	2.29	0.47
68:SP:56:LEU:HD22	68:SP:78:THR:HG21	1.95	0.47
71:SS:47:LYS:HD3	71:SS:78:LYS:HE3	1.96	0.47
1:L5:239:C:H5''	27:LY:46:SER:HB2	1.96	0.47
1:L5:461:G:H2'	1:L5:462:G:H8	1.78	0.47
1:L5:1434:G:H21	1:L5:1708:G:H5'	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1481:C:H41	37:Li:4:ARG:HD2	1.79	0.47
1:L5:1749:A:H2'	1:L5:1750:G:C8	2.48	0.47
3:L8:110:U:H5'	40:Li:8:ARG:HH12	1.77	0.47
15:LM:104:MET:HE2	15:LM:104:MET:HB3	1.81	0.47
52:S2:1653:U:H2'	52:S2:1654:G:C8	2.49	0.47
60:SH:17:ASP:HB3	60:SH:20:GLU:HG3	1.96	0.47
62:SJ:28:GLU:O	62:SJ:32:ILE:HG22	2.14	0.47
63:SK:21:MET:HE2	63:SK:21:MET:HA	1.95	0.47
1:L5:5:A:H2'	1:L5:6:C:C6	2.49	0.47
19:LQ:35:LEU:O	19:LQ:39:THR:OG1	2.29	0.47
52:S2:1013:U:H2'	52:S2:1014:G:H8	1.78	0.47
72:ST:107:LEU:HD12	72:ST:113:VAL:HB	1.95	0.47
1:L5:1478:C:H2'	1:L5:1479:G:H8	1.79	0.47
1:L5:1514:U:H2'	1:L5:1515:A:C8	2.48	0.47
1:L5:1762:C:C4	1:L5:1770:A:N1	2.82	0.47
1:L5:1976:G:H1	1:L5:1990:A:N6	2.11	0.47
10:LG:131:LYS:HD2	10:LG:131:LYS:HA	1.73	0.47
12:LI:190:LEU:HA	12:LI:198:LYS:O	2.15	0.47
19:LQ:95:VAL:HG11	19:LQ:112:ARG:HD3	1.96	0.47
43:Lo:33:LEU:HA	43:Lo:38:LYS:HG2	1.96	0.47
54:SB:121:ILE:HD12	54:SB:161:VAL:HG13	1.97	0.47
57:SE:80:ILE:HG13	57:SE:81:THR:HG23	1.95	0.47
69:SQ:53:GLU:OE1	69:SQ:85:ARG:NH1	2.47	0.47
74:SV:58:ALA:O	74:SV:62:MET:HG3	2.15	0.47
1:L5:1683:U:H2'	1:L5:1684:A:H8	1.79	0.47
6:LC:218:ILE:O	6:LC:222:ARG:HB2	2.13	0.47
13:LJ:114:ASP:OD1	13:LJ:114:ASP:N	2.37	0.47
32:Ld:22:THR:HA	32:Ld:88:LEU:O	2.15	0.47
49:N4:157:GLN:O	49:N4:161:LEU:HD12	2.14	0.47
52:S2:39:A:OP1	62:SJ:5:ARG:NH1	2.42	0.47
63:SK:49:MET:HA	63:SK:52:LEU:HG	1.96	0.47
81:Sc:36:ASP:OD2	81:Sc:36:ASP:N	2.44	0.47
85:Sg:88:ARG:HD3	85:Sg:100:ARG:HG2	1.97	0.47
1:L5:4563:U:H2'	1:L5:4564:A:H8	1.79	0.47
7:LD:238:GLU:HA	7:LD:241:LYS:HB2	1.96	0.47
12:LI:91:LEU:HD12	12:LI:135:ILE:HG23	1.96	0.47
20:LR:162:ARG:NH2	52:S2:873:G:N3	2.57	0.47
33:Le:24:GLN:HG2	33:Le:27:ARG:HD3	1.96	0.47
43:Lo:24:THR:HA	43:Lo:93:LEU:HD11	1.96	0.47
54:SB:87:ILE:H	54:SB:101:HIS:HB2	1.79	0.47
55:SC:256:TRP:CG	75:SW:68:ARG:HD2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:SI:65:PHE:HA	61:SI:187:GLY:O	2.14	0.47
62:SJ:179:LYS:HE2	62:SJ:179:LYS:HA	1.96	0.47
63:SK:11:ILE:HD12	63:SK:45:VAL:HG22	1.97	0.47
63:SK:16:PHE:HD1	63:SK:83:LEU:HD13	1.79	0.47
1:L5:43:U:H5''	16:LN:85:VAL:HB	1.96	0.47
1:L5:250:C:O3'	38:Lj:85:LYS:NZ	2.47	0.47
1:L5:1787:A:N3	1:L5:4210:U:O2'	2.48	0.47
1:L5:2483:G:O6	1:L5:2495:U:O4	2.32	0.47
1:L5:2543:A:H2	1:L5:2773:G:H22	1.62	0.47
1:L5:4537:C:H2'	1:L5:4538:G:C8	2.49	0.47
1:L5:4635:A:OP1	1:L5:4636:U:O2'	2.25	0.47
2:L7:112:U:H2'	2:L7:113:G:H8	1.79	0.47
14:LL:143:GLU:HA	14:LL:146:LEU:HG	1.97	0.47
16:LN:51:LEU:HD13	16:LN:117:ASN:HB3	1.97	0.47
23:LU:48:LYS:HG2	23:LU:53:ALA:HB2	1.95	0.47
28:LZ:11:VAL:HG12	28:LZ:82:PRO:HA	1.96	0.47
33:Le:57:ASN:OD1	33:Le:57:ASN:N	2.44	0.47
48:MA:163:THR:HA	48:MA:166:ILE:HD12	1.96	0.47
49:N4:107:TRP:HD1	49:N4:125:ARG:HA	1.79	0.47
50:NA:94:VAL:HG21	50:NA:122:VAL:HG11	1.97	0.47
50:NA:182:GLU:HA	50:NA:185:MET:HG2	1.96	0.47
52:S2:639:C:H2'	52:S2:640:A:C8	2.49	0.47
52:S2:963:A:H8	67:SO:66:ARG:HH22	1.63	0.47
52:S2:1010:G:H2'	52:S2:1011:A:C8	2.49	0.47
52:S2:1098:C:H2'	52:S2:1099:G:C8	2.50	0.47
52:S2:1651:A:H2'	52:S2:1652:G:H8	1.80	0.47
52:S2:1797:U:H2'	52:S2:1798:C:C6	2.50	0.47
58:SF:86:LYS:O	58:SF:90:VAL:HG23	2.14	0.47
63:SK:35:LEU:HD22	63:SK:38:LYS:HZ1	1.80	0.47
66:SN:93:LYS:HA	66:SN:150:VAL:HG21	1.96	0.47
68:SP:31:GLU:HA	68:SP:34:MET:HE2	1.95	0.47
78:SZ:102:LYS:HD2	78:SZ:102:LYS:HA	1.69	0.47
85:Sg:66:VAL:HA	85:Sg:82:SER:HA	1.96	0.47
1:L5:10:A:H2'	1:L5:11:G:C8	2.50	0.47
1:L5:679:C:H2'	1:L5:680:G:C8	2.50	0.47
1:L5:2809:G:N2	1:L5:4643:G:O2'	2.46	0.47
52:S2:681:U:O2'	52:S2:1160:U:OP1	2.30	0.47
56:SD:163:PRO:O	56:SD:167:TYR:CB	2.62	0.47
57:SE:116:PRO:HA	57:SE:119:ALA:HB3	1.96	0.47
59:SG:87:ARG:NH2	59:SG:93:LYS:HD3	2.29	0.47
62:SJ:32:ILE:HA	62:SJ:37:LEU:HD12	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:SO:95:ILE:HB	67:SO:129:ILE:HG12	1.97	0.47
77:SY:86:GLU:HB3	77:SY:91:LEU:HD21	1.97	0.47
1:L5:1074:G:H2'	1:L5:1075:G:H8	1.80	0.47
1:L5:4246:G:H2'	1:L5:4247:G:H8	1.79	0.47
5:LB:199:GLU:HG3	5:LB:200:ARG:HG3	1.96	0.47
10:LG:44:ASP:OD1	10:LG:44:ASP:N	2.48	0.47
46:Ls:65:ILE:HG23	46:Ls:75:LEU:HD22	1.96	0.47
53:SA:8:LEU:HB3	53:SA:59:LEU:HD21	1.97	0.47
85:Sg:65:PHE:O	85:Sg:83:TRP:N	2.45	0.47
1:L5:4083:U:OP1	4:LA:123:ARG:NH1	2.47	0.47
6:LC:170:LEU:HD23	6:LC:221:PHE:HZ	1.80	0.47
20:LR:183:GLU:HA	20:LR:186:LYS:HG2	1.97	0.47
30:Lb:27:GLN:OE1	30:Lb:27:GLN:N	2.47	0.47
38:Lj:69:ILE:HD12	38:Lj:72:ARG:HH21	1.79	0.47
52:S2:1101:U:H2'	52:S2:1102:G:C8	2.50	0.47
59:SG:162:LEU:HD13	59:SG:172:LYS:HD3	1.96	0.47
74:SV:32:ILE:HD13	74:SV:60:ARG:HH11	1.79	0.47
1:L5:1866:U:OP1	12:LI:4:ARG:NH1	2.32	0.46
1:L5:1882:U:OP2	33:Le:46:ARG:NH2	2.48	0.46
4:LA:101:VAL:HG22	4:LA:165:VAL:HG22	1.97	0.46
5:LB:238:LYS:HE2	5:LB:238:LYS:HB2	1.68	0.46
52:S2:525:A:H2'	52:S2:526:A:H8	1.80	0.46
58:SF:97:PHE:HE2	58:SF:112:LEU:HD13	1.80	0.46
77:SY:74:MET:HA	77:SY:74:MET:HE3	1.98	0.46
1:L5:4101:C:N4	1:L5:4107:G:O6	2.47	0.46
1:L5:4281:A:H2'	1:L5:4282:A:H2'	1.97	0.46
1:L5:4991:U:H2'	1:L5:4992:G:H8	1.80	0.46
11:LH:103:VAL:HG21	11:LH:144:LEU:HD21	1.96	0.46
32:Ld:64:ILE:HA	32:Ld:106:VAL:HG23	1.97	0.46
52:S2:454:U:H2'	52:S2:455:A:C8	2.51	0.46
52:S2:1610:G:H2'	52:S2:1611:G:C8	2.51	0.46
53:SA:84:GLN:OE1	53:SA:101:GLY:N	2.48	0.46
54:SB:113:MET:HE3	54:SB:142:PHE:HE2	1.80	0.46
59:SG:6:SER:HA	59:SG:13:GLN:HB3	1.98	0.46
67:SO:84:ARG:HH22	67:SO:88:LEU:HG	1.80	0.46
69:SQ:28:GLY:H	69:SQ:66:VAL:HA	1.79	0.46
1:L5:162:A:H2'	1:L5:163:A:H8	1.80	0.46
1:L5:444:G:H2'	1:L5:445:U:H6	1.80	0.46
1:L5:667:A:N3	45:Lr:46:ARG:NH2	2.50	0.46
1:L5:4743:G:H2'	1:L5:4744:A:H8	1.79	0.46
4:LA:242:ARG:NH2	4:LA:243:THR:O	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:LB:165:HIS:ND1	5:LB:166:THR:O	2.47	0.46
6:LC:108:TRP:HB2	16:LN:200:LEU:HD23	1.96	0.46
35:Lg:87:VAL:O	35:Lg:91:ILE:HG12	2.15	0.46
46:Ls:35:VAL:HB	46:Ls:39:GLN:NE2	2.30	0.46
46:Ls:121:VAL:HG22	46:Ls:161:ILE:HB	1.97	0.46
52:S2:5:U:H2'	52:S2:6:G:H8	1.80	0.46
52:S2:72:C:H41	59:SG:168:LYS:HG3	1.80	0.46
52:S2:948:C:H2'	52:S2:949:G:H8	1.79	0.46
52:S2:1777:G:H2'	52:S2:1778:C:C6	2.51	0.46
53:SA:16:LEU:HD21	70:SR:114:LEU:HD21	1.97	0.46
54:SB:152:LYS:HG3	54:SB:153:THR:HG23	1.95	0.46
56:SD:132:LYS:HB2	56:SD:132:LYS:HE2	1.69	0.46
58:SF:78:MET:HG3	58:SF:159:ARG:HE	1.79	0.46
58:SF:103:LEU:HG	78:SZ:67:LEU:HD11	1.96	0.46
59:SG:201:LYS:HA	59:SG:204:GLU:HG2	1.98	0.46
1:L5:4148:C:H5''	28:LZ:59:LYS:HE3	1.97	0.46
4:LA:136:VAL:HA	4:LA:148:VAL:HG12	1.97	0.46
11:LH:8:GLN:HE22	11:LH:71:ARG:HA	1.80	0.46
11:LH:11:ASP:OD2	11:LH:11:ASP:N	2.44	0.46
40:Ll:9:ILE:HD12	40:Ll:51:LEU:HD11	1.97	0.46
44:Lp:30:GLU:HA	44:Lp:33:GLN:HG2	1.97	0.46
49:N4:218:THR:HB	50:NA:211:MET:HE1	1.96	0.46
52:S2:1199:A:OP1	79:Sa:2:THR:N	2.49	0.46
52:S2:1220:A:N3	52:S2:1677:U:O2'	2.35	0.46
52:S2:1657:G:H2'	52:S2:1658:G:C8	2.51	0.46
52:S2:1719:A:N6	52:S2:1814:G:O2'	2.48	0.46
52:S2:1779:G:H2'	52:S2:1780:G:C8	2.49	0.46
1:L5:10:A:H2'	1:L5:11:G:H8	1.80	0.46
1:L5:88:A:N7	19:LQ:173:LYS:NZ	2.63	0.46
1:L5:460:C:H2'	1:L5:461:G:H8	1.80	0.46
1:L5:1207:C:H2'	1:L5:1208:G:H8	1.81	0.46
1:L5:1818:G:OP2	1:L5:1818:G:N2	2.43	0.46
1:L5:4135:G:H2'	1:L5:4136:G:C8	2.50	0.46
5:LB:168:MET:HG3	5:LB:178:ALA:HA	1.96	0.46
23:LU:84:LYS:HB2	23:LU:110:TYR:CZ	2.50	0.46
52:S2:189:U:OP1	61:SI:152:ARG:NH2	2.41	0.46
52:S2:445:A:OP2	61:SI:47:ARG:NH2	2.45	0.46
52:S2:1094:C:O2	75:SW:16:ASN:ND2	2.48	0.46
52:S2:1649:U:H2'	52:S2:1650:A:H8	1.80	0.46
52:S2:1657:G:O3'	82:Sd:33:LYS:NZ	2.47	0.46
54:SB:68:GLU:HG2	54:SB:85:LYS:HD3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:SH:35:ASP:OD1	60:SH:78:ARG:NH2	2.49	0.46
1:L5:691:C:H2'	1:L5:692:A:C8	2.50	0.46
1:L5:1193:C:H2'	1:L5:1194:G:H8	1.80	0.46
1:L5:1245:C:H2'	1:L5:1246:G:H8	1.80	0.46
1:L5:1333:A:H2'	1:L5:1334:A:H8	1.81	0.46
1:L5:1994:C:H2'	1:L5:1995:G:H8	1.79	0.46
1:L5:2520:C:H2'	1:L5:2521:G:C8	2.51	0.46
1:L5:4761:G:OP2	17:LO:37:ARG:NH1	2.47	0.46
7:LD:122:GLN:O	7:LD:248:ARG:NH1	2.49	0.46
9:LF:105:VAL:HG13	9:LF:136:VAL:HG12	1.98	0.46
10:LG:146:LEU:HD22	10:LG:151:LYS:HB2	1.98	0.46
31:Lc:47:ILE:HD12	31:Lc:94:LEU:HD11	1.98	0.46
52:S2:1598:G:OP1	71:SS:25:LYS:NZ	2.49	0.46
57:SE:94:LYS:HE3	57:SE:94:LYS:HB3	1.75	0.46
58:SF:39:ILE:HG23	58:SF:68:ILE:HD13	1.98	0.46
62:SJ:142:VAL:HG12	62:SJ:144:ILE:H	1.81	0.46
76:SX:60:LYS:H	76:SX:114:ASP:HB2	1.80	0.46
81:Sc:18:LEU:HB2	81:Sc:29:GLN:HG2	1.96	0.46
85:Sg:206:LEU:HA	85:Sg:220:ASP:HA	1.97	0.46
1:L5:2275:G:H2'	1:L5:2276:A:C8	2.50	0.46
1:L5:2601:A:N6	1:L5:2744:A:OP2	2.40	0.46
1:L5:3610:A:H2'	1:L5:3611:A:H8	1.81	0.46
1:L5:4108:G:H2'	1:L5:4109:G:C8	2.50	0.46
1:L5:4711:C:O2'	17:LO:145:VAL:O	2.32	0.46
1:L5:4967:A:H2'	1:L5:4968:A:H8	1.81	0.46
7:LD:217:ASP:N	7:LD:217:ASP:OD2	2.47	0.46
15:LM:80:ALA:O	15:LM:85:LYS:NZ	2.39	0.46
31:Lc:38:ILE:HD11	31:Lc:46:VAL:HG21	1.98	0.46
52:S2:1050:A:OP1	52:S2:1846:G:N2	2.46	0.46
64:SL:113:LEU:HD11	64:SL:120:VAL:HG11	1.98	0.46
79:Sa:3:LYS:NZ	79:Sa:8:ASN:OD1	2.49	0.46
1:L5:66:A:O2'	1:L5:326:C:O2	2.29	0.46
1:L5:171:U:H3'	1:L5:172:C:H4'	1.97	0.46
1:L5:1541:C:H5''	4:LA:21:LYS:HG2	1.96	0.46
7:LD:208:MET:HG3	7:LD:219:TYR:CE2	2.51	0.46
47:Lt:50:THR:HG21	47:Lt:72:GLU:HB2	1.98	0.46
76:SX:58:GLU:OE2	76:SX:58:GLU:N	2.40	0.46
1:L5:5:A:H2'	1:L5:6:C:H6	1.81	0.46
1:L5:4280:A:H62	7:LD:150:LEU:HD21	1.81	0.46
1:L5:4620:U:OP2	1:L5:4670:C:N4	2.49	0.46
48:MA:250:GLN:HE22	48:MA:383:MET:HE1	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:S2:94:G:O2'	52:S2:508:A:O2'	2.25	0.46
52:S2:309:G:OP2	61:SI:53:LYS:NZ	2.49	0.46
52:S2:1064:C:O3'	67:SO:149:ARG:NH1	2.49	0.46
53:SA:220:LYS:HA	53:SA:220:LYS:HD3	1.74	0.46
66:SN:49:GLN:O	66:SN:53:ILE:HG13	2.16	0.46
70:SR:94:GLU:OE1	70:SR:94:GLU:N	2.41	0.46
1:L5:318:A:H2'	1:L5:319:A:C8	2.51	0.46
1:L5:1078:A:H61	1:L5:1221:G:H1	1.63	0.46
1:L5:1669:A:H4'	1:L5:1685:G:N2	2.31	0.46
1:L5:1814:C:O2'	30:Lb:42:ASN:ND2	2.49	0.46
1:L5:2514:G:O2'	1:L5:2743:A:N6	2.49	0.46
1:L5:3848:U:H2'	1:L5:3849:A:C8	2.51	0.46
10:LG:215:LEU:O	10:LG:219:VAL:HG12	2.15	0.46
47:Lt:65:GLN:HA	47:Lt:70:GLN:HA	1.98	0.46
52:S2:878:G:H22	52:S2:908:A:H2	1.63	0.46
52:S2:1084:A:OP1	52:S2:1858:G:O2'	2.33	0.46
52:S2:1524:G:OP2	71:SS:141:ARG:NE	2.49	0.46
52:S2:1759:G:H21	52:S2:1773:C:H4'	1.79	0.46
64:SL:61:PRO:HD3	64:SL:141:ASN:HD22	1.81	0.46
85:Sg:227:LEU:HD23	85:Sg:227:LEU:HA	1.82	0.46
1:L5:673:C:H2'	1:L5:674:G:C8	2.52	0.45
1:L5:1187:G:OP2	1:L5:1187:G:N2	2.36	0.45
1:L5:1825:A:O2'	30:Lb:43:MET:SD	2.74	0.45
1:L5:4661:G:N2	1:L5:5004:C:O3'	2.48	0.45
46:Ls:44:ARG:HA	46:Ls:47:LEU:HD12	1.97	0.45
49:N4:105:ARG:HB2	49:N4:125:ARG:HD3	1.98	0.45
52:S2:345:U:H5''	57:SE:37:LYS:HG3	1.98	0.45
52:S2:373:G:OP1	64:SL:137:THR:OG1	2.31	0.45
52:S2:521:A:OP1	62:SJ:45:ARG:NH1	2.40	0.45
54:SB:103:MET:HE1	54:SB:212:VAL:HG12	1.98	0.45
55:SC:206:SER:OG	55:SC:207:ALA:O	2.33	0.45
58:SF:123:GLU:HA	58:SF:140:ASP:HA	1.98	0.45
1:L5:197:A:H5''	27:LY:126:ARG:HE	1.81	0.45
1:L5:1577:G:O2'	1:L5:1612:G:H4'	2.17	0.45
1:L5:1596:U:O2'	18:LP:135:ARG:NH2	2.48	0.45
1:L5:2495:U:H2'	1:L5:2496:G:C8	2.51	0.45
2:L7:47:G:N2	7:LD:222:GLN:OE1	2.40	0.45
3:L8:67:U:H2'	3:L8:68:G:H8	1.80	0.45
5:LB:240:LEU:HB2	5:LB:248:LEU:HA	1.98	0.45
28:LZ:59:LYS:HE2	28:LZ:59:LYS:HB2	1.74	0.45
52:S2:5:U:H2'	52:S2:6:G:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:S2:388:U:H2'	52:S2:389:A:C8	2.52	0.45
52:S2:642:U:H4'	52:S2:644:G:H4'	1.98	0.45
52:S2:1513:C:H2'	52:S2:1514:G:H8	1.82	0.45
60:SH:63:PHE:HA	60:SH:95:ILE:O	2.16	0.45
61:SI:76:THR:HG21	61:SI:104:ILE:HD12	1.98	0.45
71:SS:60:THR:N	71:SS:63:GLU:OE1	2.48	0.45
78:SZ:64:ASN:OD1	78:SZ:64:ASN:N	2.42	0.45
79:Sa:47:ALA:HA	79:Sa:50:VAL:HG13	1.98	0.45
82:Sd:47:ALA:HB1	82:Sd:52:PHE:HB2	1.96	0.45
1:L5:1824:G:H2'	1:L5:1825:A:C8	2.51	0.45
1:L5:2532:C:OP1	26:LX:125:ASN:ND2	2.43	0.45
1:L5:4238:G:H2'	1:L5:4239:A:H8	1.81	0.45
31:Lc:99:PRO:HG3	31:Lc:105:ILE:HD11	1.98	0.45
54:SB:28:LYS:HE2	54:SB:48:LEU:HD12	1.99	0.45
56:SD:106:ARG:HH21	56:SD:173:ARG:HD2	1.81	0.45
63:SK:29:MET:N	63:SK:29:MET:SD	2.89	0.45
71:SS:65:GLU:O	71:SS:69:THR:HG23	2.17	0.45
85:Sg:174:VAL:HB	85:Sg:188:HIS:HB2	1.98	0.45
1:L5:124:C:OP1	16:LN:144:ARG:NH1	2.48	0.45
1:L5:325:U:H2'	1:L5:326:C:C6	2.51	0.45
1:L5:456:C:H2'	1:L5:457:G:H8	1.82	0.45
1:L5:469:C:N3	8:LE:105:ARG:NH2	2.63	0.45
1:L5:710:G:H2'	1:L5:711:A:H8	1.80	0.45
1:L5:1969:G:H4'	46:Ls:36:GLY:HA2	1.97	0.45
1:L5:4743:G:H2'	1:L5:4744:A:C8	2.51	0.45
5:LB:132:LYS:HA	5:LB:135:LYS:HG2	1.97	0.45
50:NA:85:LEU:HG	50:NA:121:ILE:HD13	1.97	0.45
52:S2:1593:C:OP2	78:SZ:104:ARG:NH2	2.48	0.45
52:S2:1808:U:H2'	52:S2:1809:A:C8	2.51	0.45
56:SD:202:LYS:HD3	56:SD:203:PRO:HD2	1.99	0.45
57:SE:151:ASP:HB3	57:SE:154:ILE:HD12	1.97	0.45
59:SG:137:ARG:O	59:SG:141:ILE:HD12	2.16	0.45
63:SK:5:LYS:O	63:SK:9:ILE:HG22	2.17	0.45
69:SQ:105:LYS:HD2	69:SQ:109:LYS:HD2	1.98	0.45
70:SR:44:LYS:HG3	70:SR:47:ARG:HH12	1.79	0.45
78:SZ:99:LEU:HD11	78:SZ:102:LYS:HB2	1.98	0.45
1:L5:229:G:H5''	27:LY:11:ARG:HG3	1.98	0.45
1:L5:369:G:N2	1:L5:372:A:OP2	2.37	0.45
1:L5:494:U:H2'	1:L5:495:C:C6	2.51	0.45
1:L5:1338:G:H4'	1:L5:1339:U:H6	1.80	0.45
1:L5:1702:C:H5''	6:LC:308:LYS:HD2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3610:A:H2'	1:L5:3611:A:C8	2.51	0.45
1:L5:4672:A:OP1	24:LV:15:ARG:NH2	2.47	0.45
11:LH:152:GLU:O	11:LH:156:ASN:HB2	2.17	0.45
47:Lt:34:PRO:HG3	47:Lt:40:LYS:HE3	1.98	0.45
47:Lt:48:LYS:HD2	47:Lt:48:LYS:HA	1.76	0.45
47:Lt:54:LYS:HA	47:Lt:54:LYS:HD3	1.84	0.45
52:S2:1103:C:H2'	52:S2:1104:G:C8	2.52	0.45
52:S2:1677:U:H2'	52:S2:1678:A:H8	1.82	0.45
53:SA:155:ARG:NH1	74:SV:61:ARG:O	2.49	0.45
58:SF:185:SER:O	58:SF:185:SER:OG	2.34	0.45
60:SH:7:LYS:HA	60:SH:7:LYS:HD3	1.76	0.45
66:SN:16:LEU:HD11	66:SN:62:GLN:HG3	1.99	0.45
67:SO:31:CYS:HB2	67:SO:93:LEU:HD13	1.98	0.45
70:SR:45:LYS:HE3	70:SR:49:LYS:HE2	1.97	0.45
80:Sb:36:LYS:NZ	80:Sb:40:CYS:O	2.44	0.45
84:Sf:132:MET:SD	84:Sf:133:ALA:N	2.89	0.45
1:L5:2884:G:H2'	1:L5:2885:A:C8	2.51	0.45
6:LC:254:GLU:OE2	6:LC:258:ARG:NH2	2.50	0.45
10:LG:46:GLN:OE1	10:LG:49:ARG:NH1	2.41	0.45
14:LL:180:ALA:O	14:LL:184:MET:HG2	2.17	0.45
20:LR:15:LEU:HD22	20:LR:52:ARG:HD3	1.98	0.45
21:LS:12:VAL:HG11	21:LS:44:PHE:HB2	1.98	0.45
48:MA:99:VAL:HG22	48:MA:171:HIS:HE1	1.81	0.45
51:NB:95:GLU:O	51:NB:97:LYS:NZ	2.50	0.45
52:S2:106:C:H2'	52:S2:107:A:C8	2.51	0.45
52:S2:1401:A:H2'	52:S2:1402:A:C8	2.51	0.45
58:SF:153:LEU:HD23	58:SF:153:LEU:HA	1.87	0.45
60:SH:136:PRO:O	60:SH:162:GLN:NE2	2.48	0.45
85:Sg:30:MET:HA	85:Sg:43:TRP:O	2.16	0.45
85:Sg:156:PHE:HA	85:Sg:165:ILE:HD12	1.99	0.45
1:L5:135:G:C6	36:Lh:97:LYS:HE2	2.52	0.45
1:L5:1629:G:N2	4:LA:208:GLU:OE1	2.46	0.45
1:L5:4752:U:O4	34:Lf:52:LYS:NZ	2.50	0.45
10:LG:187:LYS:HB2	10:LG:198:THR:HG23	1.99	0.45
12:LI:191:ILE:HD11	12:LI:212:LEU:HD11	1.99	0.45
16:LN:146:PRO:HB2	36:Lh:104:THR:HG23	1.97	0.45
21:LS:9:GLU:OE2	21:LS:31:ARG:NH2	2.50	0.45
24:LV:107:ASN:HD21	24:LV:111:GLU:HB2	1.81	0.45
46:Ls:50:LYS:HE3	46:Ls:51:ALA:HB3	1.99	0.45
52:S2:1392:U:OP1	73:SU:83:ARG:NH2	2.48	0.45
59:SG:2:LYS:O	59:SG:108:VAL:HA	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:SI:128:LYS:NZ	61:SI:129:LEU:O	2.42	0.45
62:SJ:131:ARG:HA	62:SJ:131:ARG:HD2	1.69	0.45
67:SO:56:VAL:HG11	67:SO:80:ASP:HB3	1.99	0.45
85:Sg:77:PHE:HB3	85:Sg:89:LEU:HD11	1.98	0.45
1:L5:2296:G:O2'	6:LC:242:PRO:O	2.27	0.45
1:L5:2443:G:OP2	1:L5:2516:G:N2	2.44	0.45
9:LF:92:VAL:O	9:LF:120:GLY:HA2	2.16	0.45
14:LL:77:SER:N	14:LL:80:GLU:OE1	2.45	0.45
14:LL:163:LYS:HA	14:LL:163:LYS:HD2	1.81	0.45
20:LR:178:GLN:HA	20:LR:181:LYS:HG2	1.99	0.45
24:LV:29:ALA:HB3	24:LV:82:ILE:HD11	1.98	0.45
52:S2:527:C:H2'	52:S2:528:A:C8	2.52	0.45
52:S2:1134:G:OP1	79:Sa:6:ARG:NE	2.46	0.45
67:SO:129:ILE:HD12	79:Sa:64:LEU:HD11	1.99	0.45
1:L5:318:A:H2'	1:L5:319:A:H8	1.82	0.45
1:L5:1687:U:H2'	1:L5:1688:G:C8	2.52	0.45
1:L5:1769:G:H1'	68:SP:10:ARG:HH22	1.81	0.45
1:L5:3717:A:H2'	1:L5:3718:A:C8	2.52	0.45
1:L5:4238:G:H2'	1:L5:4239:A:C8	2.52	0.45
1:L5:4991:U:H2'	1:L5:4992:G:C8	2.52	0.45
3:L8:37:A:OP2	36:Lh:89:ARG:NH1	2.50	0.45
16:LN:140:LYS:HD3	16:LN:140:LYS:HA	1.73	0.45
17:LO:3:GLU:N	34:Lf:31:GLU:OE2	2.49	0.45
46:Ls:162:LYS:HA	46:Ls:162:LYS:HD3	1.64	0.45
52:S2:656:G:H5'	52:S2:662:G:N2	2.31	0.45
59:SG:142:ARG:HA	59:SG:147:LEU:HB2	1.98	0.45
61:SI:147:LYS:HA	61:SI:147:LYS:HD3	1.80	0.45
62:SJ:91:LYS:HA	62:SJ:91:LYS:HD3	1.73	0.45
63:SK:65:ARG:HH22	82:Sd:20:SER:HB2	1.82	0.45
67:SO:61:LYS:NZ	67:SO:80:ASP:OD2	2.48	0.45
70:SR:9:VAL:HG23	70:SR:50:ILE:HG13	1.98	0.45
1:L5:3786:U:OP1	1:L5:4550:G:O2'	2.33	0.45
1:L5:4699:U:H1'	1:L5:4700:A:H5''	1.99	0.45
5:LB:317:LEU:HD11	5:LB:382:MET:HG3	1.98	0.45
14:LL:56:ARG:NH1	14:LL:74:ARG:O	2.49	0.45
33:Le:19:LYS:HE3	33:Le:19:LYS:HB3	1.78	0.45
48:MA:374:ARG:HB2	48:MA:374:ARG:HH11	1.81	0.45
49:N4:123:HIS:HB3	49:N4:139:GLU:HB2	1.98	0.45
52:S2:375:U:H2'	52:S2:376:A:C8	2.52	0.45
52:S2:540:U:H2'	52:S2:541:U:H6	1.83	0.45
52:S2:907:G:H2'	52:S2:908:A:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:S2:1232:U:H2'	52:S2:1233:G:C8	2.52	0.45
52:S2:1259:A:H62	52:S2:1518:C:H3'	1.82	0.45
52:S2:1468:C:H2'	52:S2:1469:A:H8	1.82	0.45
52:S2:1657:G:H2'	52:S2:1658:G:H8	1.82	0.45
54:SB:159:GLN:O	54:SB:163:GLN:HG3	2.16	0.45
58:SF:200:ALA:O	58:SF:204:ARG:HB3	2.17	0.45
62:SJ:63:LEU:O	62:SJ:70:ARG:NH1	2.48	0.45
1:L5:1207:C:H2'	1:L5:1208:G:C8	2.51	0.44
1:L5:1328:G:O2'	1:L5:2349:A:OP1	2.34	0.44
1:L5:1461:C:H2'	1:L5:1462:A:C8	2.52	0.44
1:L5:2000:G:O2'	1:L5:2001:G:N7	2.47	0.44
1:L5:2308:A:N3	3:L8:19:C:O2'	2.46	0.44
16:LN:36:LEU:HD21	16:LN:109:HIS:CG	2.52	0.44
27:LY:2:LYS:HE3	27:LY:2:LYS:HB3	1.82	0.44
51:NB:64:MET:O	51:NB:71:VAL:HA	2.17	0.44
52:S2:595:U:H2'	52:S2:596:U:C6	2.52	0.44
52:S2:1355:C:O2	55:SC:235:ASN:ND2	2.50	0.44
52:S2:1468:C:H2'	52:S2:1469:A:C8	2.53	0.44
56:SD:76:ARG:HB2	63:SK:22:VAL:HG11	1.99	0.44
57:SE:45:ILE:HA	57:SE:61:VAL:HG11	1.99	0.44
68:SP:85:ILE:HD11	68:SP:116:LEU:HG	1.98	0.44
1:L5:73:A:OP1	14:LL:106:SER:OG	2.33	0.44
1:L5:74:G:H5'	14:LL:59:VAL:HG13	1.97	0.44
1:L5:2751:G:H2'	1:L5:2752:G:H8	1.81	0.44
3:L8:153:C:H2'	3:L8:154:G:H8	1.83	0.44
4:LA:27:ALA:HB3	4:LA:128:ARG:HH21	1.81	0.44
11:LH:51:LYS:HD3	11:LH:51:LYS:HA	1.81	0.44
19:LQ:95:VAL:HG23	19:LQ:116:ALA:HB2	1.99	0.44
31:Lc:55:LEU:HD11	35:Lg:92:LYS:HB3	1.98	0.44
48:MA:90:HIS:H	48:MA:207:ASP:HB2	1.82	0.44
51:NB:103:LEU:HA	51:NB:106:ILE:HG22	1.99	0.44
52:S2:502:C:H4'	57:SE:62:LYS:HZ1	1.83	0.44
52:S2:502:C:H5'	57:SE:66:MET:HE3	1.99	0.44
52:S2:1298:G:P	68:SP:77:LYS:HZ2	2.41	0.44
52:S2:1808:U:H2'	52:S2:1809:A:H8	1.82	0.44
58:SF:122:ARG:HE	58:SF:122:ARG:HB2	1.68	0.44
59:SG:198:ARG:HG2	59:SG:201:LYS:HE3	2.00	0.44
60:SH:53:VAL:HG21	60:SH:172:THR:HA	1.97	0.44
64:SL:77:VAL:HA	64:SL:88:ILE:HG22	2.00	0.44
71:SS:34:LYS:HG2	71:SS:103:LEU:HD22	1.99	0.44
72:ST:52:TRP:HA	72:ST:55:THR:HG22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:SW:118:ARG:HH22	75:SW:119:LYS:NZ	2.16	0.44
1:L5:425:U:H2'	1:L5:426:A:H8	1.82	0.44
1:L5:699:C:O2'	1:L5:968:C:O2	2.34	0.44
1:L5:707:C:O2'	1:L5:4943:A:N1	2.43	0.44
1:L5:2485:U:H4'	1:L5:2486:G:N2	2.32	0.44
1:L5:4685:U:H2'	1:L5:4686:G:C8	2.52	0.44
1:L5:5037:U:H2'	1:L5:5038:A:H8	1.83	0.44
4:LA:137:ILE:HD11	4:LA:149:LYS:HB2	1.99	0.44
7:LD:136:ASP:OD2	7:LD:136:ASP:N	2.49	0.44
38:Lj:52:LYS:HA	38:Lj:55:ARG:HG2	2.00	0.44
50:NA:77:ARG:HB2	50:NA:123:PHE:CZ	2.53	0.44
52:S2:329:G:H2'	52:S2:330:G:C8	2.51	0.44
52:S2:981:A:H2'	52:S2:982:G:C8	2.53	0.44
53:SA:80:ARG:HG2	53:SA:82:THR:H	1.83	0.44
59:SG:37:ALA:HA	59:SG:49:VAL:HG12	1.99	0.44
1:L5:745:G:H2'	1:L5:746:A:C8	2.52	0.44
1:L5:1435:G:H1'	1:L5:1708:G:H5''	1.99	0.44
1:L5:1918:U:O4'	1:L5:2065:G:N2	2.50	0.44
1:L5:3720:G:H22	1:L5:3733:A:H2	1.66	0.44
1:L5:3860:A:H2	18:LP:131:ARG:HH22	1.65	0.44
3:L8:102:G:OP2	3:L8:104:A:O2'	2.31	0.44
7:LD:156:GLY:HA2	7:LD:181:PRO:HG3	1.97	0.44
8:LE:281:ILE:HG23	8:LE:286:LEU:HD21	1.99	0.44
23:LU:25:CYS:O	23:LU:29:VAL:HG22	2.17	0.44
42:Ln:15:ARG:NH1	52:S2:1182:A:O3'	2.51	0.44
48:MA:162:THR:HG23	48:MA:165:GLU:H	1.81	0.44
48:MA:327:GLU:HB3	48:MA:358:GLU:HB2	1.99	0.44
52:S2:17:C:H2'	52:S2:18:C:C6	2.52	0.44
52:S2:1670:C:H2'	52:S2:1671:G:C8	2.53	0.44
56:SD:214:LYS:HE2	56:SD:216:GLU:H	1.82	0.44
58:SF:173:LEU:HG	58:SF:177:LEU:HD13	2.00	0.44
59:SG:44:GLU:HA	59:SG:119:LYS:HD2	1.99	0.44
69:SQ:132:PHE:H	69:SQ:132:PHE:HD2	1.66	0.44
72:ST:51:ASN:HB2	72:ST:54:TYR:HB2	2.00	0.44
73:SU:78:ASP:HB3	82:Sd:54:LYS:NZ	2.32	0.44
82:Sd:16:GLN:HA	82:Sd:19:ARG:HB2	2.00	0.44
1:L5:161:G:H2'	1:L5:162:A:C8	2.53	0.44
1:L5:2863:G:O2'	20:LR:82:LYS:O	2.33	0.44
1:L5:4208:U:OP1	1:L5:4334:U:O2'	2.34	0.44
1:L5:4594:U:H2'	1:L5:4595:G:C8	2.52	0.44
2:L7:46:C:H2'	2:L7:47:G:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:LB:92:TYR:HB2	5:LB:159:VAL:HB	1.99	0.44
14:LL:136:LYS:HA	14:LL:136:LYS:HD2	1.81	0.44
35:Lg:11:LEU:O	35:Lg:18:ASN:ND2	2.46	0.44
48:MA:116:SER:HB3	48:MA:119:GLU:HB2	2.00	0.44
52:S2:656:G:N2	52:S2:663:C:H5'	2.32	0.44
53:SA:50:ASN:HD22	53:SA:53:ARG:HE	1.65	0.44
54:SB:71:LEU:HD22	54:SB:82:ARG:HG3	2.00	0.44
55:SC:201:GLY:N	55:SC:221:ASP:OD1	2.50	0.44
61:SI:115:SER:HB3	61:SI:136:ILE:HD11	1.99	0.44
61:SI:131:PRO:HA	61:SI:134:GLU:OE1	2.18	0.44
71:SS:68:ILE:HD12	71:SS:68:ILE:HA	1.90	0.44
81:Sc:10:LYS:HD2	81:Sc:10:LYS:HA	1.76	0.44
83:Se:39:ASN:HA	83:Se:43:VAL:HG12	1.98	0.44
85:Sg:57:ARG:HD3	85:Sg:95:GLY:HA3	1.99	0.44
85:Sg:104:HIS:NE2	85:Sg:130:LYS:HG3	2.32	0.44
1:L5:982:U:OP1	8:LE:73:TYR:OH	2.29	0.44
1:L5:2640:G:H2'	1:L5:2641:A:C8	2.53	0.44
4:LA:58:LEU:HD23	4:LA:75:LEU:HD22	1.98	0.44
21:LS:77:ASN:OD1	21:LS:98:ARG:NH1	2.50	0.44
21:LS:95:ARG:HD2	21:LS:113:MET:HE2	2.00	0.44
27:LY:31:SER:HA	27:LY:48:PRO:HA	1.99	0.44
47:Lt:121:LEU:HB3	47:Lt:123:ARG:HB3	1.98	0.44
48:MA:326:ILE:HG22	48:MA:328:PRO:HD3	2.00	0.44
49:N4:39:LEU:HB3	49:N4:46:LYS:HE2	1.99	0.44
52:S2:12:U:H2'	52:S2:13:C:C6	2.52	0.44
52:S2:558:G:H2'	52:S2:559:G:C8	2.52	0.44
56:SD:28:GLU:HB3	56:SD:29:LEU:HD23	1.98	0.44
60:SH:174:SER:OG	60:SH:185:VAL:O	2.31	0.44
67:SO:62:VAL:HG13	67:SO:73:ALA:HB2	1.99	0.44
77:SY:99:LYS:O	77:SY:101:LYS:NZ	2.40	0.44
85:Sg:30:MET:HG3	85:Sg:42:MET:HE2	1.99	0.44
1:L5:197:A:N1	1:L5:225:G:O2'	2.42	0.44
1:L5:1354:A:N1	1:L5:1385:G:O2'	2.44	0.44
1:L5:1494:U:H2'	1:L5:1495:G:C8	2.51	0.44
1:L5:2079:G:H4'	33:Le:58:ILE:HD11	2.00	0.44
1:L5:2386:U:H2'	1:L5:2387:G:H8	1.83	0.44
1:L5:2422:C:H2'	1:L5:2423:A:C8	2.53	0.44
1:L5:4319:C:H2'	1:L5:4320:G:H8	1.83	0.44
1:L5:4742:G:H2'	1:L5:4743:G:H8	1.82	0.44
5:LB:56:ILE:HG22	5:LB:368:ILE:HA	1.99	0.44
21:LS:83:ARG:HG3	21:LS:125:GLN:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:LW:106:GLU:HA	25:LW:109:ILE:HG22	1.99	0.44
31:Lc:55:LEU:HD22	35:Lg:93:ARG:HE	1.82	0.44
38:Lj:64:MET:HB3	38:Lj:68:LYS:HG3	1.99	0.44
46:Ls:53:VAL:HA	46:Ls:88:PHE:O	2.17	0.44
51:NB:51:LEU:HB3	51:NB:84:ALA:HB2	1.99	0.44
52:S2:454:U:H2'	52:S2:455:A:H8	1.83	0.44
52:S2:1030:A:H2'	52:S2:1031:A:H8	1.82	0.44
71:SS:26:ILE:O	71:SS:30:ILE:HG12	2.18	0.44
77:SY:110:ARG:O	77:SY:114:MET:CB	2.66	0.44
79:Sa:73:TYR:HB3	79:Sa:78:ALA:HB2	1.99	0.44
1:L5:1365:C:H41	1:L5:1366:G:H21	1.66	0.44
1:L5:2495:U:H2'	1:L5:2496:G:H8	1.83	0.44
1:L5:3711:A:H2	1:L5:3735:G:H5''	1.83	0.44
1:L5:4577:U:H2'	1:L5:4578:G:C8	2.53	0.44
5:LB:331:VAL:HG11	5:LB:347:LEU:HD21	1.99	0.44
11:LH:9:THR:HG22	11:LH:56:ARG:HG3	2.00	0.44
21:LS:127:MET:HG2	22:LT:153:PRO:HB2	1.99	0.44
33:Le:78:LEU:HD23	33:Le:98:GLU:HG3	1.99	0.44
39:Lk:13:LEU:HD23	39:Lk:16:ARG:HH22	1.83	0.44
39:Lk:49:ASP:HB2	39:Lk:52:LYS:HG3	2.00	0.44
50:NA:96:ILE:O	50:NA:103:LEU:HA	2.17	0.44
50:NA:103:LEU:HD21	51:NB:109:GLN:HG2	2.00	0.44
52:S2:388:U:H2'	52:S2:389:A:H8	1.82	0.44
52:S2:823:U:N3	62:SJ:143:ASN:OD1	2.46	0.44
56:SD:48:ILE:HD13	56:SD:48:ILE:HA	1.87	0.44
57:SE:244:ILE:HD12	57:SE:244:ILE:HA	1.85	0.44
63:SK:25:LYS:HE3	63:SK:62:PHE:CZ	2.53	0.44
1:L5:438:G:OP1	33:Le:16:ARG:NH2	2.51	0.44
1:L5:1339:U:H2'	1:L5:1340:C:C6	2.53	0.44
1:L5:1512:G:OP1	29:La:7:LYS:NZ	2.45	0.44
1:L5:1617:G:H2'	1:L5:1618:G:H8	1.83	0.44
1:L5:3717:A:OP2	1:L5:3735:G:N2	2.48	0.44
1:L5:4279:A:H5'	1:L5:4281:A:H1'	2.00	0.44
8:LE:206:VAL:HG23	8:LE:256:GLN:HB2	2.00	0.44
10:LG:157:ILE:HG23	10:LG:201:THR:HG22	2.00	0.44
13:LJ:83:LEU:HD22	13:LJ:132:VAL:HG11	1.99	0.44
22:LT:102:ARG:HD2	22:LT:102:ARG:HA	1.79	0.44
22:LT:104:SER:HA	22:LT:107:LYS:NZ	2.33	0.44
54:SB:142:PHE:HD2	54:SB:209:ASP:HB2	1.83	0.44
63:SK:2:LEU:HD12	63:SK:2:LEU:HA	1.86	0.44
72:ST:103:VAL:O	72:ST:107:LEU:HD23	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:Sc:44:ARG:HH21	81:Sc:58:LEU:HB3	1.83	0.44
85:Sg:147:HIS:NE2	85:Sg:175:LYS:HG3	2.33	0.44
1:L5:2508:U:H2'	1:L5:2509:C:H6	1.83	0.43
1:L5:4459:U:H2'	1:L5:4460:U:C6	2.52	0.43
7:LD:64:ILE:HG13	7:LD:109:LEU:HD21	1.99	0.43
11:LH:173:ARG:HE	11:LH:173:ARG:HB2	1.56	0.43
12:LI:121:LYS:HA	12:LI:121:LYS:HD2	1.87	0.43
17:LO:173:GLN:HG2	17:LO:176:ARG:HH21	1.82	0.43
22:LT:79:GLN:HG3	22:LT:84:ILE:HG12	2.00	0.43
46:Ls:26:LYS:NZ	46:Ls:195:ASN:OD1	2.51	0.43
62:SJ:136:ARG:HD3	62:SJ:160:SER:HA	1.99	0.43
68:SP:60:LEU:HD21	68:SP:89:MET:HB3	1.99	0.43
72:ST:123:LEU:HG	72:ST:128:GLN:HB2	2.00	0.43
83:Se:51:LYS:HD2	83:Se:51:LYS:HA	1.87	0.43
1:L5:1088:C:H2'	1:L5:1089:G:C8	2.53	0.43
1:L5:4061:G:H2'	1:L5:4062:A:C8	2.53	0.43
2:L7:63:C:H5'	2:L7:64:G:H5''	2.00	0.43
8:LE:119:GLU:OE1	33:Le:94:SER:OG	2.34	0.43
13:LJ:159:LYS:O	13:LJ:163:MET:HG3	2.18	0.43
17:LO:43:ILE:HD11	17:LO:138:LEU:HD13	2.00	0.43
47:Lt:15:LEU:HB2	47:Lt:62:LEU:HD23	2.00	0.43
47:Lt:57:ARG:HH11	47:Lt:80:LEU:HB3	1.84	0.43
50:NA:179:LYS:HE3	50:NA:183:LEU:HD11	2.00	0.43
52:S2:1144:A:H2'	52:S2:1145:A:C8	2.52	0.43
52:S2:1391:C:H2'	52:S2:1392:U:H6	1.82	0.43
55:SC:187:ARG:NH2	55:SC:189:GLY:O	2.51	0.43
60:SH:126:HIS:CE1	60:SH:181:THR:HG23	2.52	0.43
60:SH:157:HIS:HA	60:SH:188:GLU:O	2.18	0.43
78:SZ:78:LYS:HA	78:SZ:78:LYS:HD2	1.75	0.43
84:Sf:96:LYS:HE2	84:Sf:96:LYS:HB2	1.65	0.43
1:L5:86:U:H2'	1:L5:87:A:C8	2.53	0.43
7:LD:220:LYS:HD3	7:LD:227:ILE:HD13	1.99	0.43
27:LY:64:GLY:HA2	49:N4:19:ARG:HH21	1.83	0.43
31:Lc:37:MET:HE3	31:Lc:42:LYS:HB2	1.99	0.43
33:Le:82:VAL:HG13	33:Le:114:ARG:HG2	2.00	0.43
48:MA:156:MET:O	48:MA:158:LYS:NZ	2.49	0.43
49:N4:49:ASP:H	50:NA:179:LYS:NZ	2.16	0.43
49:N4:101:MET:N	49:N4:101:MET:SD	2.91	0.43
52:S2:1757:G:H8	52:S2:1758:G:H1'	1.82	0.43
55:SC:132:ASP:OD2	55:SC:132:ASP:N	2.39	0.43
57:SE:139:LEU:O	57:SE:146:THR:HA	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:SL:88:ILE:HD11	64:SL:109:MET:HE3	2.00	0.43
73:SU:21:ARG:HA	73:SU:89:ILE:O	2.17	0.43
74:SV:39:VAL:HB	74:SV:44:GLY:HA2	2.00	0.43
1:L5:162:A:H2'	1:L5:163:A:C8	2.52	0.43
1:L5:217:C:H3'	1:L5:218:A:H2'	2.00	0.43
1:L5:267:G:H4'	36:Lh:113:LEU:HD21	2.00	0.43
1:L5:4578:G:H2'	1:L5:4579:U:C6	2.53	0.43
3:L8:75:G:OP2	27:LY:74:TYR:OH	2.34	0.43
15:LM:41:PRO:HB2	15:LM:74:ARG:HB2	2.01	0.43
18:LP:67:VAL:HG12	18:LP:80:GLN:HB3	2.01	0.43
43:Lo:93:LEU:HD23	43:Lo:93:LEU:HA	1.90	0.43
48:MA:128:ILE:HG23	48:MA:304:PRO:HG3	2.00	0.43
50:NA:98:LYS:HE2	50:NA:104:PHE:HE1	1.83	0.43
52:S2:77:A:H2	59:SG:175:LYS:HG3	1.83	0.43
52:S2:835:C:O2'	52:S2:836:G:N7	2.49	0.43
52:S2:1203:G:H2'	52:S2:1204:A:H8	1.83	0.43
56:SD:211:VAL:O	70:SR:20:TYR:OH	2.34	0.43
58:SF:30:ILE:HG21	58:SF:36:GLN:HA	2.01	0.43
60:SH:181:THR:HG22	60:SH:183:LYS:HG3	2.00	0.43
62:SJ:63:LEU:HD12	62:SJ:64:ASP:H	1.82	0.43
63:SK:80:ARG:NH2	63:SK:89:ILE:O	2.40	0.43
75:SW:111:MET:HB2	75:SW:115:GLU:OE2	2.18	0.43
85:Sg:147:HIS:CE1	85:Sg:175:LYS:HG3	2.53	0.43
1:L5:1368:A:C4	27:LY:1:MET:HE1	2.53	0.43
1:L5:1443:A:N6	1:L5:2103:G:O6	2.51	0.43
1:L5:1509:C:H5''	29:La:2:PRO:HD3	1.99	0.43
1:L5:2258:C:N4	1:L5:2259:G:O6	2.51	0.43
1:L5:2598:A:OP1	35:Lg:52:ARG:NH2	2.51	0.43
1:L5:2730:U:H2'	1:L5:2731:C:C6	2.54	0.43
2:L7:11:A:N6	7:LD:16:TYR:O	2.50	0.43
13:LJ:112:HIS:ND1	13:LJ:117:ILE:HD12	2.33	0.43
30:Lb:73:LYS:HD3	30:Lb:73:LYS:HA	1.73	0.43
34:Lf:59:THR:OG1	34:Lf:65:ASN:OD1	2.37	0.43
39:Lk:67:LYS:HE2	39:Lk:67:LYS:HB2	1.76	0.43
56:SD:173:ARG:HD3	56:SD:173:ARG:HA	1.70	0.43
57:SE:55:ALA:HB1	57:SE:60:GLU:HB3	2.00	0.43
61:SI:37:LYS:HB2	61:SI:59:ARG:HD3	2.01	0.43
68:SP:108:LYS:HD2	68:SP:109:PRO:HD2	1.99	0.43
73:SU:66:ARG:NH2	73:SU:70:CYS:O	2.51	0.43
75:SW:14:ILE:HG12	75:SW:25:VAL:HG21	2.00	0.43
1:L5:440:U:O2'	34:Lf:91:ASN:O	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1631:A:N7	4:LA:199:VAL:HG21	2.34	0.43
1:L5:1637:A:OP1	1:L5:1640:C:N4	2.43	0.43
1:L5:1645:C:H2'	1:L5:1646:A:H8	1.83	0.43
1:L5:2848:G:O2'	1:L5:3838:U:O4	2.34	0.43
1:L5:3868:G:H22	1:L5:3900:G:H1'	1.84	0.43
1:L5:4251:A:H5''	13:LJ:108:GLY:HA3	1.99	0.43
7:LD:163:LEU:HD21	7:LD:175:HIS:CG	2.54	0.43
46:Ls:50:LYS:HG2	46:Ls:51:ALA:H	1.83	0.43
59:SG:151:ASP:OD1	59:SG:151:ASP:N	2.30	0.43
66:SN:99:ARG:HH21	66:SN:115:LEU:HD21	1.84	0.43
74:SV:40:ASP:OD1	74:SV:44:GLY:N	2.52	0.43
81:Sc:23:SER:C	81:Sc:24:GLN:HE21	2.26	0.43
1:L5:20:U:H3'	1:L5:21:G:H8	1.83	0.43
1:L5:755:C:H2'	1:L5:756:G:H8	1.83	0.43
1:L5:1503:A:H1'	1:L5:1504:G:C8	2.53	0.43
1:L5:1952:G:H4'	21:LS:93:MET:HG2	2.01	0.43
1:L5:2540:C:H2'	1:L5:2541:G:H8	1.83	0.43
1:L5:4996:C:OP1	32:Ld:32:ARG:NH1	2.52	0.43
5:LB:218:ASP:OD2	5:LB:348:ARG:NH2	2.51	0.43
12:LI:36:LEU:HD12	12:LI:37:GLY:H	1.83	0.43
12:LI:188:LYS:HB2	12:LI:213:HIS:HE2	1.84	0.43
33:Le:90:MET:N	33:Le:90:MET:HE2	2.33	0.43
34:Lf:83:MET:HE3	34:Lf:83:MET:HB3	1.92	0.43
46:Ls:134:LYS:HB2	46:Ls:137:PHE:HB3	2.01	0.43
52:S2:300:U:H2'	52:S2:301:A:H8	1.84	0.43
52:S2:1627:C:H2'	52:S2:1628:C:H6	1.84	0.43
52:S2:1821:U:H2'	52:S2:1822:A:H8	1.83	0.43
52:S2:1858:G:H2'	52:S2:1859:A:H8	1.83	0.43
71:SS:76:GLN:CD	71:SS:76:GLN:H	2.27	0.43
74:SV:59:ILE:H	74:SV:59:ILE:HD12	1.83	0.43
85:Sg:150:TRP:HB2	85:Sg:170:TRP:CD1	2.54	0.43
85:Sg:246:TYR:HB3	85:Sg:261:LEU:HD13	2.00	0.43
1:L5:64:A:H1'	1:L5:76:A:H1'	2.01	0.43
1:L5:1950:U:OP2	11:LH:64:ARG:NH1	2.42	0.43
1:L5:4750:G:H2'	1:L5:4751:G:H8	1.83	0.43
1:L5:4954:G:H2'	1:L5:4955:A:C8	2.54	0.43
4:LA:178:PRO:HD2	44:Lp:26:VAL:HG12	2.00	0.43
5:LB:61:ASP:OD1	5:LB:61:ASP:N	2.52	0.43
5:LB:223:THR:HG22	5:LB:338:VAL:HB	2.01	0.43
9:LF:50:ILE:HD12	9:LF:186:CYS:SG	2.59	0.43
16:LN:149:GLN:NE2	36:Lh:99:GLU:HB2	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LZ:60:LYS:HE2	28:LZ:60:LYS:HB3	1.84	0.43
48:MA:252:THR:HG23	48:MA:330:ILE:HD12	2.01	0.43
52:S2:329:G:H2'	52:S2:330:G:H8	1.82	0.43
52:S2:635:G:H5''	83:Se:21:LYS:HG2	2.01	0.43
52:S2:929:G:H2'	52:S2:930:C:O4'	2.19	0.43
52:S2:1405:A:H2'	52:S2:1406:G:O4'	2.18	0.43
52:S2:1457:U:H2'	52:S2:1458:G:H8	1.83	0.43
70:SR:94:GLU:H	70:SR:94:GLU:CD	2.27	0.43
72:ST:130:ASP:N	72:ST:130:ASP:OD1	2.52	0.43
1:L5:1088:C:H2'	1:L5:1089:G:H8	1.83	0.43
1:L5:1340:C:H2'	1:L5:1341:U:H6	1.84	0.43
1:L5:2579:G:N2	1:L5:2582:A:OP2	2.38	0.43
1:L5:2856:C:O2	5:LB:242:ARG:NH2	2.44	0.43
2:L7:82:G:H2'	2:L7:83:A:C8	2.54	0.43
21:LS:82:LEU:HD11	21:LS:113:MET:HE3	2.01	0.43
27:LY:4:ASN:HB3	27:LY:7:VAL:HG22	2.01	0.43
28:LZ:126:LYS:HD3	28:LZ:127:ASN:H	1.84	0.43
52:S2:964:A:H2'	52:S2:965:U:H6	1.84	0.43
52:S2:1302:G:H21	84:Sf:95:ARG:HE	1.67	0.43
52:S2:1317:C:H2'	52:S2:1318:G:H8	1.83	0.43
53:SA:137:ALA:HB1	53:SA:142:LEU:HB3	2.00	0.43
61:SI:62:VAL:HA	61:SI:77:ARG:HA	2.01	0.43
75:SW:115:GLU:O	75:SW:118:ARG:NH2	2.52	0.43
85:Sg:3:GLU:HG2	85:Sg:247:TRP:HH2	1.84	0.43
1:L5:1074:G:H2'	1:L5:1075:G:C8	2.54	0.43
1:L5:1333:A:H2'	1:L5:1334:A:C8	2.54	0.43
1:L5:1578:U:OP1	1:L5:3637:U:O2'	2.26	0.43
1:L5:1618:G:OP1	38:Lj:13:ASN:ND2	2.48	0.43
1:L5:1629:G:N7	4:LA:9:ARG:NH2	2.66	0.43
3:L8:26:C:O2'	6:LC:53:ALA:O	2.34	0.43
3:L8:141:C:H5'	16:LN:113:LEU:HD11	2.01	0.43
15:LM:12:VAL:HB	15:LM:60:PHE:HB2	2.01	0.43
17:LO:185:VAL:HG22	17:LO:188:LYS:HB2	2.00	0.43
39:Lk:23:VAL:HG22	39:Lk:36:VAL:HG22	2.00	0.43
43:Lo:45:GLN:HE22	43:Lo:51:GLN:HA	1.83	0.43
52:S2:382:C:H2'	52:S2:383:G:H8	1.83	0.43
58:SF:28:VAL:HG23	58:SF:107:ASN:HD22	1.84	0.43
59:SG:197:GLN:O	59:SG:201:LYS:HG3	2.18	0.43
70:SR:17:ILE:HG22	70:SR:69:ILE:HG21	2.01	0.43
85:Sg:101:PHE:CD2	85:Sg:136:GLY:HA2	2.53	0.43
1:L5:710:G:H2'	1:L5:711:A:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:931:C:OP1	6:LC:350:ARG:NH1	2.52	0.42
1:L5:1177:U:H2'	1:L5:1178:G:C8	2.54	0.42
1:L5:1438:U:O3'	9:LF:31:LYS:NZ	2.48	0.42
1:L5:1500:A:H5''	1:L5:1501:C:H5''	2.00	0.42
1:L5:2079:G:H2'	1:L5:2080:U:C6	2.54	0.42
1:L5:4584:A:H2'	1:L5:4585:U:O4'	2.19	0.42
1:L5:4712:C:OP1	17:LO:74:ARG:NH2	2.52	0.42
1:L5:5006:U:H4'	1:L5:5007:A:H5'	2.00	0.42
3:L8:148:A:H2'	3:L8:149:G:C8	2.54	0.42
5:LB:366:LYS:HB3	5:LB:366:LYS:HE2	1.78	0.42
10:LG:34:LYS:HB3	10:LG:34:LYS:HE3	1.87	0.42
14:LL:87:HIS:HB3	14:LL:90:VAL:HG23	2.01	0.42
25:LW:73:ARG:NH2	52:S2:1781:A:OP2	2.52	0.42
28:LZ:22:LYS:N	28:LZ:49:TYR:OH	2.51	0.42
34:Lf:43:LEU:HD23	34:Lf:43:LEU:HA	1.90	0.42
35:Lg:103:VAL:HA	35:Lg:106:VAL:HG22	2.00	0.42
47:Lt:121:LEU:HD23	47:Lt:123:ARG:HB3	2.01	0.42
49:N4:219:LYS:H	50:NA:211:MET:HE1	1.83	0.42
52:S2:647:U:H2'	52:S2:648:A:H8	1.84	0.42
52:S2:1263:U:H5''	52:S2:1264:C:H5''	1.99	0.42
52:S2:1337:C:H2'	52:S2:1338:G:H8	1.83	0.42
52:S2:1406:G:H2'	52:S2:1407:U:C6	2.54	0.42
54:SB:78:GLU:HB2	54:SB:79:VAL:H	1.69	0.42
56:SD:108:LYS:HA	56:SD:108:LYS:HD3	1.72	0.42
67:SO:98:ARG:HB2	67:SO:133:THR:HA	2.00	0.42
69:SQ:105:LYS:HB3	69:SQ:105:LYS:HE3	1.77	0.42
1:L5:175:C:H2'	1:L5:176:G:H8	1.84	0.42
1:L5:1390:G:N2	1:L5:1393:G:OP2	2.44	0.42
1:L5:2422:C:H5'	1:L5:3857:G:H21	1.84	0.42
1:L5:2516:G:OP1	35:Lg:60:ARG:NH2	2.38	0.42
1:L5:3736:A:H2'	1:L5:3737:A:H8	1.83	0.42
1:L5:4151:G:H2'	1:L5:4152:G:H8	1.84	0.42
10:LG:250:ILE:HD13	10:LG:250:ILE:HA	1.91	0.42
20:LR:158:GLN:OE1	20:LR:162:ARG:NE	2.39	0.42
25:LW:113:LYS:O	25:LW:117:LYS:HG2	2.18	0.42
48:MA:250:GLN:NE2	48:MA:383:MET:HE1	2.34	0.42
49:N4:29:VAL:O	49:N4:33:ASN:ND2	2.52	0.42
52:S2:1562:C:H2'	52:S2:1563:G:H8	1.84	0.42
52:S2:1798:C:H2'	52:S2:1799:G:O4'	2.18	0.42
56:SD:28:GLU:HG2	63:SK:61:GLN:NE2	2.34	0.42
57:SE:121:TYR:OH	57:SE:235:TRP:O	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:SJ:29:LEU:HD23	62:SJ:29:LEU:HA	1.83	0.42
63:SK:86:PRO:HD2	63:SK:86:PRO:O	2.18	0.42
68:SP:91:GLY:H	68:SP:107:ILE:HB	1.84	0.42
75:SW:11:LEU:HD12	75:SW:74:VAL:HG13	2.01	0.42
80:Sb:20:LYS:O	80:Sb:26:GLN:HB2	2.20	0.42
1:L5:2448:G:H1'	1:L5:2743:A:H2	1.85	0.42
1:L5:4909:A:OP2	5:LB:156:TYR:OH	2.30	0.42
5:LB:307:TYR:CD2	5:LB:366:LYS:HG2	2.54	0.42
6:LC:60:HIS:HA	6:LC:92:PHE:HE1	1.83	0.42
14:LL:59:VAL:HG21	14:LL:73:GLY:HA3	2.01	0.42
19:LQ:8:ASN:HD22	19:LQ:8:ASN:C	2.27	0.42
20:LR:182:GLU:HA	20:LR:185:ILE:HG12	2.02	0.42
29:La:119:LYS:HA	29:La:140:VAL:HG13	2.00	0.42
52:S2:367:U:H4'	52:S2:371:A:C8	2.54	0.42
52:S2:428:U:H1'	62:SJ:2:PRO:HA	2.00	0.42
52:S2:609:U:H2'	52:S2:610:G:H8	1.84	0.42
52:S2:1610:G:OP1	71:SS:125:HIS:NE2	2.52	0.42
52:S2:1660:C:H4'	52:S2:1663:A:H62	1.85	0.42
59:SG:221:LYS:HE3	59:SG:221:LYS:HB3	1.85	0.42
63:SK:49:MET:HE2	63:SK:49:MET:HB3	1.68	0.42
63:SK:64:TRP:CD1	82:Sd:23:VAL:HG13	2.54	0.42
71:SS:61:GLU:HA	71:SS:64:VAL:HG22	2.01	0.42
1:L5:86:U:O2'	29:La:65:ARG:NH2	2.53	0.42
1:L5:1308:C:H2'	1:L5:1309:C:C6	2.54	0.42
1:L5:3871:A:H2'	1:L5:3872:A:C8	2.55	0.42
1:L5:4086:G:C4	10:LG:51:LEU:HD11	2.54	0.42
1:L5:4234:A:OP1	43:Lo:100:LYS:NZ	2.46	0.42
1:L5:4929:C:H5''	15:LM:114:LYS:HD3	2.00	0.42
6:LC:192:GLY:O	6:LC:195:LYS:NZ	2.51	0.42
7:LD:20:PHE:HE2	22:LT:24:VAL:HG13	1.85	0.42
7:LD:211:LEU:HD23	7:LD:219:TYR:HA	2.00	0.42
9:LF:199:LYS:HE2	9:LF:199:LYS:HB2	1.81	0.42
10:LG:55:VAL:HG21	26:LX:41:ARG:HD2	2.00	0.42
11:LH:176:LEU:HD23	41:Lm:90:ASN:HD22	1.84	0.42
25:LW:91:MET:O	25:LW:95:ASN:HB2	2.18	0.42
48:MA:324:PHE:HE2	48:MA:326:ILE:HD11	1.84	0.42
50:NA:206:ILE:O	50:NA:210:ILE:HG12	2.19	0.42
52:S2:186:C:H2'	52:S2:187:G:C8	2.54	0.42
52:S2:356:C:OP1	64:SL:105:ARG:NH2	2.52	0.42
52:S2:963:A:H2'	52:S2:964:A:C8	2.55	0.42
52:S2:1016:U:H4'	66:SN:16:LEU:HD22	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:S2:1199:A:H5''	79:Sa:2:THR:HB	2.01	0.42
54:SB:44:ILE:HD12	54:SB:69:VAL:HG21	2.00	0.42
56:SD:141:LYS:HE3	56:SD:179:GLN:HB3	2.00	0.42
59:SG:216:ARG:HD3	59:SG:216:ARG:HA	1.88	0.42
70:SR:77:GLU:OE1	70:SR:81:ARG:HG3	2.19	0.42
1:L5:417:G:OP1	1:L5:2329:U:O2'	2.35	0.42
1:L5:968:C:H5'	8:LE:110:ARG:HH11	1.84	0.42
1:L5:1180:C:O4'	7:LD:289:ARG:NH1	2.49	0.42
1:L5:1994:C:H2'	1:L5:1995:G:C8	2.54	0.42
1:L5:2895:A:H2'	1:L5:2896:G:C8	2.54	0.42
1:L5:3736:A:H2'	1:L5:3737:A:C8	2.54	0.42
1:L5:4208:U:H2'	1:L5:4209:G:H8	1.84	0.42
3:L8:67:U:H2'	3:L8:68:G:C8	2.55	0.42
13:LJ:27:GLY:HA2	13:LJ:68:ILE:HB	2.00	0.42
14:LL:55:ILE:HG22	14:LL:96:ILE:HA	2.02	0.42
15:LM:9:VAL:HG21	15:LM:66:HIS:HB3	2.01	0.42
20:LR:2:SER:HB2	20:LR:3:MET:H	1.63	0.42
29:La:103:VAL:HB	29:La:108:TYR:HB2	2.02	0.42
30:Lb:51:LYS:HB3	30:Lb:51:LYS:HE3	1.74	0.42
49:N4:93:LYS:HG3	49:N4:96:GLU:H	1.85	0.42
52:S2:980:A:H2'	52:S2:981:A:C8	2.54	0.42
52:S2:1004:U:H2'	52:S2:1005:G:C8	2.53	0.42
52:S2:1593:C:H2'	52:S2:1594:A:C8	2.54	0.42
56:SD:7:LYS:HD3	56:SD:7:LYS:HA	1.79	0.42
56:SD:193:ASP:HB3	56:SD:199:GLY:HA3	2.02	0.42
57:SE:124:CYS:HB3	57:SE:141:THR:HB	2.01	0.42
58:SF:91:ARG:HH12	78:SZ:106:GLN:HG2	1.84	0.42
64:SL:110:SER:HB3	64:SL:138:VAL:HG22	2.02	0.42
67:SO:82:ALA:O	67:SO:86:LYS:NZ	2.52	0.42
68:SP:29:SER:H	68:SP:32:GLN:NE2	2.16	0.42
68:SP:111:MET:HE2	68:SP:111:MET:N	2.34	0.42
72:ST:128:GLN:HA	72:ST:131:LEU:HD12	2.01	0.42
1:L5:502:C:H3'	1:L5:503:C:H3'	2.01	0.42
1:L5:1662:C:H2'	1:L5:1663:C:C6	2.55	0.42
1:L5:1803:G:C6	22:LT:109:VAL:HG23	2.55	0.42
1:L5:2568:C:H2'	1:L5:2569:G:C8	2.54	0.42
1:L5:4906:C:H2'	1:L5:4907:G:H8	1.84	0.42
8:LE:177:GLY:HA2	8:LE:178:PRO:HD3	1.87	0.42
12:LI:40:LYS:HD3	12:LI:40:LYS:HA	1.90	0.42
34:Lf:36:ARG:HB2	34:Lf:80:ASN:HA	2.01	0.42
52:S2:107:A:H2'	52:S2:108:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:S2:1179:G:N2	52:S2:1182:A:OP2	2.43	0.42
52:S2:1199:A:H2'	52:S2:1200:A:C8	2.54	0.42
52:S2:1702:G:O6	52:S2:1836:G:N2	2.52	0.42
59:SG:215:LYS:HA	59:SG:218:LYS:HE3	2.01	0.42
69:SQ:50:LYS:HE2	69:SQ:50:LYS:HB2	1.77	0.42
71:SS:124:ARG:NH2	71:SS:130:ARG:O	2.46	0.42
72:ST:107:LEU:HA	72:ST:110:LEU:HB2	2.01	0.42
75:SW:83:LEU:HD23	75:SW:83:LEU:HA	1.89	0.42
79:Sa:38:LYS:HE3	79:Sa:38:LYS:HB3	1.79	0.42
1:L5:119:G:C6	10:LG:132:ARG:HG3	2.55	0.42
1:L5:181:C:H2'	1:L5:182:G:C8	2.55	0.42
1:L5:918:G:H5'	15:LM:72:TYR:HE2	1.85	0.42
3:L8:6:C:H2'	3:L8:7:U:C6	2.55	0.42
7:LD:283:LYS:HD2	12:LI:206:LEU:HD23	2.02	0.42
17:LO:125:LYS:HB3	17:LO:125:LYS:HE3	1.77	0.42
20:LR:32:ILE:HD13	20:LR:44:LEU:HD13	2.02	0.42
48:MA:169:ALA:HA	48:MA:172:LEU:HD12	2.02	0.42
48:MA:207:ASP:OD1	48:MA:207:ASP:N	2.53	0.42
52:S2:1426:U:P	69:SQ:69:ARG:HH22	2.43	0.42
56:SD:5:ILE:HD13	56:SD:5:ILE:HA	1.95	0.42
58:SF:123:GLU:HG2	58:SF:200:ALA:HB1	2.02	0.42
59:SG:201:LYS:O	59:SG:205:GLU:HG3	2.20	0.42
60:SH:36:LEU:HD13	60:SH:40:LEU:HD23	2.00	0.42
60:SH:51:ILE:HD11	60:SH:176:VAL:HG22	2.02	0.42
64:SL:104:LYS:NZ	76:SX:8:ARG:HH21	2.17	0.42
66:SN:39:LYS:HD3	66:SN:39:LYS:HA	1.86	0.42
71:SS:25:LYS:O	71:SS:29:ALA:HB3	2.20	0.42
84:Sf:92:LYS:HD2	84:Sf:92:LYS:HA	1.82	0.42
1:L5:736:C:O5'	15:LM:71:LYS:NZ	2.46	0.42
1:L5:1655:C:O2	1:L5:4390:A:O2'	2.37	0.42
1:L5:1847:C:H2'	1:L5:1848:C:C6	2.55	0.42
1:L5:2824:C:H2'	1:L5:2825:A:C8	2.54	0.42
1:L5:3707:U:H2'	1:L5:3708:C:C6	2.55	0.42
1:L5:3726:A:H2'	1:L5:3727:A:C8	2.55	0.42
1:L5:4153:C:H2'	1:L5:4154:G:C8	2.53	0.42
1:L5:4174:U:H2'	1:L5:4175:G:C8	2.54	0.42
1:L5:4188:U:H2'	1:L5:4189:U:C6	2.55	0.42
1:L5:4611:A:H2'	1:L5:4612:C:H6	1.84	0.42
2:L7:46:C:H2'	2:L7:47:G:C8	2.54	0.42
5:LB:307:TYR:HD2	5:LB:366:LYS:HG2	1.85	0.42
7:LD:120:GLU:O	7:LD:248:ARG:NH2	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:LF:80:ASN:HB3	22:LT:142:ARG:HA	2.02	0.42
10:LG:170:LEU:HD12	10:LG:170:LEU:HA	1.87	0.42
15:LM:32:ASP:OD1	15:LM:35:ARG:NH1	2.53	0.42
17:LO:9:LEU:HD13	17:LO:33:VAL:HG13	2.02	0.42
18:LP:49:LYS:HE3	18:LP:49:LYS:HB2	1.84	0.42
48:MA:252:THR:HA	48:MA:330:ILE:HD13	2.02	0.42
50:NA:200:LYS:O	50:NA:200:LYS:NZ	2.44	0.42
52:S2:640:A:H2'	52:S2:641:A:C8	2.55	0.42
52:S2:1438:A:H2'	52:S2:1439:A:C8	2.55	0.42
59:SG:218:LYS:O	59:SG:222:GLU:HG2	2.19	0.42
63:SK:14:LEU:HA	63:SK:17:LYS:HZ2	1.83	0.42
68:SP:30:TYR:O	68:SP:34:MET:HG3	2.20	0.42
75:SW:115:GLU:OE1	75:SW:119:LYS:NZ	2.51	0.42
1:L5:926:G:H2'	1:L5:927:G:C8	2.53	0.42
1:L5:1097:C:H2'	1:L5:1098:G:H8	1.85	0.42
1:L5:1629:G:N1	4:LA:208:GLU:OE1	2.53	0.42
1:L5:2456:G:H2'	1:L5:2457:G:C8	2.55	0.42
1:L5:3933:G:H2'	1:L5:3934:G:H8	1.85	0.42
1:L5:4307:A:H4'	19:LQ:186:TYR:CG	2.55	0.42
1:L5:4492:U:O2'	1:L5:4512:U:O2	2.26	0.42
5:LB:57:VAL:HG22	5:LB:73:VAL:HG22	2.02	0.42
12:LI:38:ARG:HD3	12:LI:83:ASP:HB2	2.01	0.42
21:LS:17:LEU:HD23	21:LS:17:LEU:HA	1.90	0.42
52:S2:210:U:H2'	52:S2:211:G:H8	1.85	0.42
52:S2:432:G:H2'	52:S2:433:A:C8	2.54	0.42
52:S2:525:A:H2'	52:S2:526:A:C8	2.55	0.42
52:S2:561:A:H5''	62:SJ:164:PRO:HG2	2.00	0.42
52:S2:1256:G:H1	82:Sd:31:ILE:HG22	1.84	0.42
53:SA:38:ILE:HD11	53:SA:47:TYR:HB3	2.01	0.42
70:SR:98:VAL:O	70:SR:120:THR:N	2.49	0.42
79:Sa:60:ASP:OD1	79:Sa:60:ASP:N	2.52	0.42
85:Sg:54:ILE:HD12	85:Sg:54:ILE:HA	1.99	0.42
1:L5:918:G:H5'	15:LM:72:TYR:CE2	2.55	0.42
1:L5:1662:C:H2'	1:L5:1663:C:H6	1.85	0.42
1:L5:2274:C:H2'	1:L5:2275:G:C8	2.55	0.42
1:L5:4258:C:H5'	13:LJ:68:ILE:HD11	2.02	0.42
1:L5:4263:C:O3'	7:LD:8:LYS:NZ	2.40	0.42
3:L8:29:G:H5''	14:LL:27:ASN:HB3	2.01	0.42
52:S2:291:G:H2'	52:S2:292:A:C8	2.54	0.42
52:S2:996:A:H2'	52:S2:997:A:C8	2.55	0.42
52:S2:1499:U:H4'	56:SD:176:LEU:HD11	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:SD:76:ARG:HG3	56:SD:77:PHE:CD2	2.55	0.42
58:SF:69:VAL:O	58:SF:73:THR:HG23	2.20	0.42
66:SN:99:ARG:HE	66:SN:115:LEU:HD21	1.84	0.42
1:L5:268:G:H2'	1:L5:269:G:C8	2.55	0.41
1:L5:4195:G:C8	1:L5:4442:U:H5''	2.55	0.41
1:L5:4967:A:H2'	1:L5:4968:A:C8	2.55	0.41
9:LF:244:ILE:O	9:LF:248:ASN:HB3	2.20	0.41
11:LH:111:LEU:HD21	11:LH:125:ARG:HD3	2.02	0.41
15:LM:124:LYS:HE3	15:LM:124:LYS:HB2	1.79	0.41
17:LO:54:TYR:OH	17:LO:73:PHE:O	2.38	0.41
27:LY:117:LYS:HE2	27:LY:117:LYS:HB3	1.83	0.41
30:Lb:53:GLY:HA2	30:Lb:56:LYS:HE3	2.02	0.41
36:Lh:32:ARG:O	36:Lh:36:VAL:HG13	2.20	0.41
52:S2:106:C:H2'	52:S2:107:A:H8	1.85	0.41
52:S2:300:U:H2'	52:S2:301:A:C8	2.55	0.41
52:S2:1113:A:H2'	52:S2:1114:U:C6	2.55	0.41
52:S2:1133:A:H4'	79:Sa:13:LYS:HD2	2.01	0.41
52:S2:1580:A:H5''	73:SU:56:MET:HE1	2.02	0.41
52:S2:1619:A:OP2	68:SP:47:ARG:NH2	2.53	0.41
56:SD:21:LEU:HA	56:SD:21:LEU:HD12	1.85	0.41
56:SD:99:ILE:HD11	56:SD:173:ARG:HH22	1.85	0.41
71:SS:105:ASN:HB3	71:SS:108:ARG:HH21	1.85	0.41
72:ST:5:THR:N	72:ST:8:ASP:OD2	2.50	0.41
85:Sg:249:CYS:HB3	85:Sg:258:ILE:HG22	2.02	0.41
1:L5:223:G:H4'	1:L5:225:G:C8	2.55	0.41
1:L5:1876:U:H2'	1:L5:1877:G:C8	2.55	0.41
1:L5:4260:U:H2'	1:L5:4261:C:C6	2.55	0.41
6:LC:348:LYS:HB3	6:LC:348:LYS:HE3	1.88	0.41
21:LS:82:LEU:HD13	21:LS:124:ILE:HG23	2.02	0.41
22:LT:125:TRP:NE1	22:LT:127:GLN:HE22	2.18	0.41
26:LX:150:ALA:HB1	26:LX:155:ILE:HB	2.03	0.41
28:LZ:57:MET:HB3	28:LZ:61:LYS:HD3	2.02	0.41
38:Lj:27:TYR:HA	38:Lj:34:CYS:HA	2.02	0.41
48:MA:107:ASP:N	48:MA:107:ASP:OD1	2.53	0.41
52:S2:928:G:H21	80:Sb:68:GLY:HA2	1.85	0.41
52:S2:1124:C:H5''	54:SB:150:ILE:HG13	2.03	0.41
52:S2:1610:G:H2'	52:S2:1611:G:H8	1.85	0.41
52:S2:1845:A:H2'	52:S2:1846:G:C8	2.54	0.41
53:SA:20:ALA:HB1	70:SR:93:GLN:HE22	1.85	0.41
54:SB:214:LYS:HD3	54:SB:216:LYS:HD3	2.02	0.41
79:Sa:100:ARG:HE	79:Sa:102:ARG:HH22	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:Sg:108:VAL:HG12	85:Sg:124:SER:HB3	2.02	0.41
1:L5:86:U:H2'	1:L5:87:A:H8	1.86	0.41
1:L5:150:U:OP2	10:LG:200:THR:OG1	2.33	0.41
1:L5:444:G:H2'	1:L5:445:U:C6	2.55	0.41
1:L5:1097:C:H2'	1:L5:1098:G:C8	2.54	0.41
1:L5:1252:C:O2	1:L5:1254:A:N6	2.53	0.41
1:L5:2456:G:H2'	1:L5:2457:G:H8	1.85	0.41
1:L5:4093:G:H22	1:L5:4114:C:N4	2.17	0.41
10:LG:83:PHE:HD2	10:LG:159:HIS:HA	1.85	0.41
10:LG:89:ARG:O	10:LG:93:THR:HG23	2.20	0.41
10:LG:253:LEU:HD23	10:LG:253:LEU:HA	1.85	0.41
15:LM:11:ARG:HB3	15:LM:27:ILE:HD12	2.02	0.41
20:LR:65:LYS:HE3	20:LR:65:LYS:HB2	1.84	0.41
26:LX:40:ILE:HD12	26:LX:40:ILE:HA	1.95	0.41
52:S2:917:U:H2'	52:S2:918:U:C6	2.55	0.41
52:S2:1218:C:H2'	52:S2:1219:C:H6	1.85	0.41
52:S2:1413:G:H2'	52:S2:1414:A:C8	2.56	0.41
52:S2:1736:G:H2'	52:S2:1737:G:C8	2.55	0.41
56:SD:221:THR:HA	56:SD:222:PRO:HD3	1.93	0.41
57:SE:60:GLU:O	57:SE:64:ILE:HG12	2.20	0.41
58:SF:61:PHE:CE2	81:Sc:51:ARG:HG3	2.56	0.41
58:SF:93:VAL:O	58:SF:97:PHE:HD1	2.02	0.41
59:SG:135:PRO:HG2	59:SG:141:ILE:HG13	2.02	0.41
71:SS:11:HIS:HB2	71:SS:12:ILE:HD12	2.01	0.41
1:L5:1194:G:H2'	1:L5:1195:G:H8	1.85	0.41
1:L5:1290:G:H2'	1:L5:1291:G:C8	2.56	0.41
1:L5:2421:G:H4'	18:LP:127:ARG:HH21	1.85	0.41
1:L5:3760:A:H62	52:S2:1709:G:H22	1.68	0.41
1:L5:4635:A:H3'	1:L5:4636:U:H4'	2.03	0.41
1:L5:4718:G:OP1	5:LB:23:SER:OG	2.38	0.41
8:LE:201:ILE:HD13	8:LE:261:ILE:HG12	2.02	0.41
21:LS:36:ASN:OD1	21:LS:36:ASN:N	2.51	0.41
28:LZ:50:PRO:HD3	28:LZ:68:ILE:HG12	2.02	0.41
29:La:145:VAL:HG13	37:Li:5:TYR:CZ	2.55	0.41
34:Lf:22:ARG:HA	34:Lf:22:ARG:HD3	1.78	0.41
37:Li:73:ILE:O	37:Li:77:VAL:HG22	2.20	0.41
39:Lk:60:LEU:HD23	39:Lk:61:PRO:HD2	2.02	0.41
42:Ln:8:LYS:O	42:Ln:12:ARG:HG3	2.20	0.41
50:NA:77:ARG:HH22	50:NA:78:LYS:HE2	1.86	0.41
52:S2:352:U:H2'	52:S2:353:C:C6	2.56	0.41
52:S2:509:G:H2'	52:S2:510:G:C8	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:S2:1338:G:H4'	73:SU:74:SER:H	1.86	0.41
52:S2:1600:G:H5''	78:SZ:43:LYS:HD2	2.02	0.41
52:S2:1745:A:H1'	59:SG:66:GLY:HA2	2.02	0.41
67:SO:61:LYS:HD2	67:SO:61:LYS:HA	1.81	0.41
76:SX:130:LEU:HD23	76:SX:130:LEU:HA	1.83	0.41
77:SY:35:VAL:HA	77:SY:36:PRO:HD3	1.92	0.41
84:Sf:140:TYR:CZ	84:Sf:142:GLY:HA2	2.55	0.41
1:L5:300:A:H2'	1:L5:301:G:C8	2.55	0.41
1:L5:477:C:H2'	1:L5:478:G:H8	1.86	0.41
1:L5:478:G:H2'	1:L5:479:G:H8	1.85	0.41
1:L5:493:G:C6	1:L5:660:A:N1	2.88	0.41
1:L5:1093:C:H2'	1:L5:1094:G:H8	1.86	0.41
1:L5:1383:G:N2	1:L5:1505:C:O3'	2.53	0.41
1:L5:4286:C:H2'	1:L5:4287:G:C8	2.55	0.41
3:L8:144:U:H2'	3:L8:145:C:C6	2.55	0.41
4:LA:27:ALA:HB1	4:LA:77:ILE:HG12	2.02	0.41
6:LC:13:GLU:OE1	6:LC:161:TYR:OH	2.35	0.41
10:LG:165:GLU:HA	10:LG:168:VAL:HG12	2.01	0.41
19:LQ:91:ARG:HE	19:LQ:91:ARG:HB2	1.59	0.41
24:LV:96:LEU:HD13	25:LW:20:ARG:HG2	2.01	0.41
25:LW:119:LYS:HD3	25:LW:119:LYS:HA	1.83	0.41
27:LY:56:GLN:NE2	27:LY:65:GLN:OE1	2.53	0.41
48:MA:150:LEU:HD21	48:MA:234:GLU:HB2	2.03	0.41
48:MA:376:ASP:OD1	48:MA:376:ASP:N	2.53	0.41
52:S2:28:U:H2'	52:S2:29:G:H8	1.85	0.41
52:S2:842:C:H2'	52:S2:843:C:C6	2.55	0.41
52:S2:1101:U:H2'	52:S2:1102:G:H8	1.86	0.41
52:S2:1256:G:OP2	82:Sd:40:ARG:NH2	2.44	0.41
55:SC:253:PRO:HA	55:SC:256:TRP:NE1	2.36	0.41
58:SF:167:LYS:NZ	78:SZ:75:GLU:HB3	2.36	0.41
72:ST:22:LEU:HD22	72:ST:28:LEU:HD11	2.01	0.41
73:SU:40:ILE:HG22	73:SU:44:LYS:HZ2	1.86	0.41
77:SY:49:LYS:HD3	77:SY:49:LYS:O	2.21	0.41
1:L5:137:G:H2'	1:L5:138:G:H8	1.86	0.41
1:L5:1195:G:H2'	1:L5:1196:G:H8	1.85	0.41
1:L5:1442:C:H2'	1:L5:1443:A:C8	2.56	0.41
1:L5:3598:C:H2'	1:L5:3599:A:H8	1.84	0.41
1:L5:4153:C:H2'	1:L5:4154:G:H8	1.86	0.41
1:L5:4694:G:H5'	1:L5:4695:C:H5	1.86	0.41
2:L7:4:U:H2'	2:L7:5:A:H8	1.84	0.41
23:LU:23:LEU:HD21	23:LU:83:LEU:HD22	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:LW:86:SER:O	25:LW:90:ILE:HG23	2.21	0.41
25:LW:113:LYS:HD3	25:LW:113:LYS:HA	1.89	0.41
33:Le:85:LEU:HD21	33:Le:115:ALA:HB2	2.02	0.41
45:Lr:7:TRP:HB2	45:Lr:44:ILE:HD12	2.03	0.41
48:MA:82:ARG:HH12	48:MA:349:ARG:HH12	1.69	0.41
52:S2:1457:U:H2'	52:S2:1458:G:C8	2.55	0.41
52:S2:1677:U:H2'	52:S2:1678:A:C8	2.55	0.41
55:SC:232:THR:HG22	55:SC:235:ASN:H	1.84	0.41
63:SK:65:ARG:NH2	82:Sd:21:CYS:O	2.54	0.41
63:SK:65:ARG:NH2	82:Sd:25:SER:HA	2.36	0.41
68:SP:86:LEU:HD12	68:SP:87:PRO:HD2	2.02	0.41
69:SQ:17:LYS:HE3	69:SQ:17:LYS:HB3	1.86	0.41
69:SQ:28:GLY:HA3	69:SQ:67:ASP:CG	2.45	0.41
71:SS:23:ARG:NH2	78:SZ:80:ARG:HH22	2.19	0.41
78:SZ:91:LEU:HD12	78:SZ:91:LEU:HA	1.91	0.41
81:Sc:31:ARG:NH2	81:Sc:41:SER:OG	2.54	0.41
1:L5:490:C:H2'	1:L5:491:G:C8	2.55	0.41
1:L5:1346:C:H2'	1:L5:1347:G:H8	1.85	0.41
1:L5:2568:C:H2'	1:L5:2569:G:H8	1.85	0.41
1:L5:2899:C:P	20:LR:108:ARG:HH22	2.44	0.41
1:L5:4940:C:H5'	1:L5:4941:G:H5''	2.03	0.41
3:L8:93:C:HO2'	3:L8:94:G:H8	1.67	0.41
4:LA:186:TYR:HB2	4:LA:196:TRP:CZ3	2.55	0.41
5:LB:217:ILE:HD11	5:LB:333:LEU:HD21	2.02	0.41
7:LD:179:ARG:HD3	7:LD:179:ARG:HA	1.86	0.41
12:LI:51:HIS:CD2	12:LI:168:SER:HB3	2.56	0.41
29:La:117:LEU:HB2	29:La:140:VAL:HG21	2.03	0.41
33:Le:91:CYS:HB3	33:Le:95:TYR:HD2	1.86	0.41
44:Lp:6:LYS:HE2	44:Lp:6:LYS:HB3	1.81	0.41
46:Ls:18:ILE:HD13	46:Ls:18:ILE:HA	1.95	0.41
46:Ls:83:ARG:HD3	46:Ls:83:ARG:HA	1.85	0.41
48:MA:144:ARG:HD3	48:MA:144:ARG:HA	1.89	0.41
52:S2:71:G:H2'	52:S2:72:C:H4'	2.02	0.41
52:S2:1337:C:H2'	52:S2:1338:G:C8	2.56	0.41
64:SL:73:LEU:HD13	64:SL:90:ARG:HH12	1.85	0.41
64:SL:128:VAL:HG12	64:SL:142:VAL:HA	2.02	0.41
67:SO:45:THR:HG21	67:SO:49:GLY:HA2	2.01	0.41
70:SR:102:THR:O	70:SR:106:LEU:HD23	2.21	0.41
71:SS:78:LYS:NZ	72:ST:35:ASP:OD1	2.54	0.41
78:SZ:70:PRO:HA	78:SZ:73:VAL:HG22	2.01	0.41
1:L5:1431:C:H2'	1:L5:1432:G:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:2749:C:H2'	1:L5:2750:G:H8	1.85	0.41
1:L5:4761:G:H2'	1:L5:4762:A:C8	2.55	0.41
12:LI:184:MET:HE2	12:LI:190:LEU:HD11	2.03	0.41
13:LJ:63:ARG:HH12	43:Lo:103:VAL:HA	1.85	0.41
14:LL:141:ALA:C	14:LL:145:LYS:HZ2	2.29	0.41
29:La:119:LYS:HE3	29:La:119:LYS:HB3	1.94	0.41
31:Lc:36:LYS:HA	31:Lc:39:ARG:HG2	2.03	0.41
40:Ll:34:LYS:HB3	40:Ll:34:LYS:HE3	1.91	0.41
43:Lo:6:LYS:O	43:Lo:23:VAL:N	2.45	0.41
48:MA:108:TYR:HB3	48:MA:116:SER:HB2	2.03	0.41
52:S2:1189:A:H2'	52:S2:1190:A:H8	1.86	0.41
52:S2:1332:A:O2'	56:SD:145:GLN:O	2.36	0.41
52:S2:1362:U:H5''	52:S2:1363:C:H5	1.85	0.41
52:S2:1779:G:H2'	52:S2:1780:G:H8	1.84	0.41
55:SC:252:THR:HG22	55:SC:254:ASP:H	1.85	0.41
69:SQ:73:LYS:HD3	69:SQ:73:LYS:HA	1.78	0.41
69:SQ:96:TYR:HA	69:SQ:100:VAL:HB	2.02	0.41
70:SR:104:GLU:HG2	70:SR:107:LYS:HE3	2.03	0.41
85:Sg:17:TRP:CE2	85:Sg:303:THR:HG23	2.56	0.41
1:L5:18:C:H2'	1:L5:19:G:H8	1.86	0.41
1:L5:66:A:H61	1:L5:282:C:HO2'	1.68	0.41
1:L5:271:C:H2'	1:L5:272:U:C6	2.56	0.41
1:L5:427:A:H2'	1:L5:428:G:C8	2.56	0.41
1:L5:432:U:H4'	1:L5:433:A:H5''	2.03	0.41
1:L5:717:U:H2'	1:L5:718:C:C6	2.56	0.41
1:L5:1523:A:N3	1:L5:4389:C:O2'	2.49	0.41
1:L5:1778:C:H5''	7:LD:5:LYS:HG2	2.02	0.41
1:L5:2044:U:C2	5:LB:259:PRO:HB3	2.56	0.41
1:L5:2459:G:N2	1:L5:2462:C:OP2	2.53	0.41
1:L5:2623:A:H62	23:LU:81:ARG:HH22	1.68	0.41
1:L5:4742:G:H2'	1:L5:4743:G:C8	2.56	0.41
1:L5:4935:C:H2'	1:L5:4936:G:C8	2.55	0.41
1:L5:5005:G:N2	1:L5:5041:G:O2'	2.54	0.41
1:L5:5055:G:H2'	1:L5:5056:A:H8	1.85	0.41
7:LD:118:ILE:HD12	7:LD:118:ILE:H	1.86	0.41
8:LE:182:ASN:ND2	8:LE:271:LEU:O	2.46	0.41
26:LX:100:VAL:HG23	26:LX:134:LYS:HB3	2.03	0.41
27:LY:38:LEU:HD23	27:LY:38:LEU:HA	1.93	0.41
29:La:75:LEU:HD11	29:La:133:ALA:HA	2.03	0.41
33:Le:81:ASN:HA	33:Le:111:ILE:HD11	2.03	0.41
38:Lj:67:LEU:HD23	38:Lj:67:LEU:HA	1.93	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:Lr:117:ILE:HG22	45:Lr:121:GLN:OE1	2.21	0.41
47:Lt:16:ARG:HD2	47:Lt:28:LEU:HD12	2.02	0.41
48:MA:93:LEU:HD23	48:MA:93:LEU:HA	1.91	0.41
48:MA:231:ASP:O	48:MA:360:THR:OG1	2.39	0.41
48:MA:299:LEU:H	48:MA:299:LEU:HD23	1.86	0.41
52:S2:219:U:H1'	61:SI:184:ARG:HH12	1.86	0.41
52:S2:746:C:H2'	52:S2:747:U:C6	2.56	0.41
52:S2:1174:U:H2'	52:S2:1175:G:H8	1.85	0.41
52:S2:1189:A:H2'	52:S2:1190:A:C8	2.56	0.41
52:S2:1235:G:H21	68:SP:135:ALA:HA	1.85	0.41
52:S2:1279:C:H2'	52:S2:1280:G:C8	2.56	0.41
52:S2:1415:C:H2'	52:S2:1416:C:H6	1.86	0.41
52:S2:1541:G:H4'	72:ST:15:VAL:HG11	2.03	0.41
52:S2:1543:U:OP1	72:ST:62:ARG:NH1	2.53	0.41
53:SA:201:LEU:HD21	70:SR:85:VAL:HG22	2.03	0.41
54:SB:228:LEU:HD12	54:SB:228:LEU:HA	1.83	0.41
55:SC:187:ARG:HD3	55:SC:192:LEU:HD12	2.03	0.41
62:SJ:120:ALA:HB2	62:SJ:129:LEU:HD12	2.01	0.41
62:SJ:134:HIS:CE1	62:SJ:164:PRO:HD2	2.56	0.41
63:SK:49:MET:HG3	63:SK:69:TRP:CE2	2.56	0.41
66:SN:5:HIS:HB3	66:SN:117:LEU:HD13	2.03	0.41
67:SO:84:ARG:NH1	67:SO:87:GLU:HB2	2.36	0.41
69:SQ:106:LYS:O	69:SQ:109:LYS:HG2	2.20	0.41
71:SS:24:ARG:HB2	71:SS:29:ALA:HB2	2.02	0.41
71:SS:105:ASN:O	71:SS:109:GLU:HG3	2.20	0.41
81:Sc:31:ARG:HH12	81:Sc:42:ILE:N	2.19	0.41
85:Sg:42:MET:SD	85:Sg:56:GLN:HB3	2.61	0.41
1:L5:68:U:OP1	16:LN:178:HIS:ND1	2.42	0.41
1:L5:70:A:OP2	29:La:64:LYS:NZ	2.37	0.41
1:L5:1539:G:H4'	4:LA:194:ASN:HB2	2.03	0.41
1:L5:1733:G:N3	1:L5:4214:A:H2'	2.36	0.41
1:L5:2540:C:H2'	1:L5:2541:G:C8	2.56	0.41
1:L5:2671:C:H2'	1:L5:2672:C:C6	2.56	0.41
1:L5:4080:C:H2'	1:L5:4081:G:H8	1.85	0.41
1:L5:4577:U:H2'	1:L5:4578:G:H8	1.86	0.41
2:L7:15:C:H2'	2:L7:16:A:H8	1.86	0.41
2:L7:110:G:H2'	2:L7:111:C:C6	2.56	0.41
3:L8:141:C:H2'	3:L8:142:U:C6	2.55	0.41
6:LC:143:ARG:HG2	6:LC:182:LYS:HD2	2.02	0.41
10:LG:257:LYS:HD3	10:LG:257:LYS:HA	1.94	0.41
52:S2:647:U:H2'	52:S2:648:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:S2:929:G:N2	52:S2:1104:G:H4'	2.36	0.41
52:S2:931:C:H2'	52:S2:932:G:C8	2.56	0.41
52:S2:1037:G:H4'	52:S2:1845:A:H4'	2.04	0.41
52:S2:1580:A:P	73:SU:56:MET:HE1	2.60	0.41
52:S2:1804:U:H2'	52:S2:1805:G:C8	2.56	0.41
57:SE:140:VAL:HG22	57:SE:146:THR:HB	2.02	0.41
62:SJ:50:LEU:HG	62:SJ:54:ARG:HH12	1.85	0.41
63:SK:74:GLU:HA	63:SK:77:GLN:HG3	2.03	0.41
68:SP:69:PRO:HD2	68:SP:70:MET:N	2.32	0.41
71:SS:109:GLU:O	71:SS:113:ARG:HB2	2.21	0.41
75:SW:102:ILE:H	75:SW:113:HIS:CD2	2.38	0.41
80:Sb:42:LYS:HA	80:Sb:42:LYS:HD2	1.86	0.41
1:L5:667:A:H5''	1:L5:668:C:H5''	2.02	0.40
1:L5:1290:G:H2'	1:L5:1291:G:H8	1.86	0.40
1:L5:1676:C:O2	1:L5:4191:G:O2'	2.30	0.40
3:L8:12:G:N2	18:LP:120:ASN:OD1	2.47	0.40
7:LD:164:LYS:HA	7:LD:167:VAL:HG12	2.04	0.40
7:LD:223:PHE:HB3	7:LD:226:TYR:HB2	2.02	0.40
9:LF:124:LYS:HB3	9:LF:124:LYS:HE2	1.81	0.40
13:LJ:104:ASN:HD21	13:LJ:133:VAL:HG13	1.86	0.40
20:LR:21:LYS:HA	20:LR:21:LYS:HD3	1.89	0.40
25:LW:4:GLU:HG2	25:LW:13:ILE:HB	2.02	0.40
28:LZ:57:MET:HE2	28:LZ:61:LYS:HD3	2.03	0.40
32:Ld:20:VAL:HG12	32:Ld:91:LYS:HA	2.04	0.40
32:Ld:91:LYS:HZ2	32:Ld:91:LYS:HG3	1.58	0.40
46:Ls:20:LEU:HD12	46:Ls:20:LEU:HA	1.96	0.40
52:S2:85:A:O3'	77:SY:118:ARG:NH2	2.54	0.40
52:S2:396:U:H4'	61:SI:14:THR:HG22	2.02	0.40
52:S2:1226:G:N1	52:S2:1639:G:OP2	2.47	0.40
52:S2:1562:C:H2'	52:S2:1563:G:C8	2.56	0.40
53:SA:41:ARG:HD3	53:SA:47:TYR:CZ	2.56	0.40
54:SB:39:PHE:CE2	54:SB:189:ILE:HD11	2.56	0.40
55:SC:165:VAL:HG21	55:SC:217:ALA:HB1	2.04	0.40
57:SE:101:LEU:HD23	57:SE:101:LEU:HA	1.90	0.40
59:SG:93:LYS:HE3	59:SG:93:LYS:HB3	1.80	0.40
63:SK:30:PRO:C	63:SK:31:LYS:HZ2	2.29	0.40
63:SK:74:GLU:HA	63:SK:77:GLN:HE21	1.86	0.40
68:SP:22:LEU:HD12	68:SP:22:LEU:H	1.86	0.40
73:SU:83:ARG:HB3	73:SU:85:HIS:CE1	2.57	0.40
76:SX:131:LEU:HD23	76:SX:131:LEU:HA	1.92	0.40
79:Sa:53:ILE:O	79:Sa:57:SER:OG	2.35	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:Sc:16:LYS:NZ	81:Sc:17:VAL:O	2.37	0.40
83:Se:52:LYS:HE2	83:Se:52:LYS:HB3	1.92	0.40
1:L5:655:C:H2'	1:L5:656:C:C6	2.56	0.40
1:L5:975:C:P	9:LF:43:ARG:HH21	2.42	0.40
1:L5:1461:C:H2'	1:L5:1462:A:H8	1.86	0.40
1:L5:2770:C:H2'	1:L5:2771:G:H8	1.85	0.40
1:L5:2780:C:H2'	1:L5:2781:G:H8	1.86	0.40
1:L5:3722:G:H2'	1:L5:3723:A:H8	1.87	0.40
1:L5:4546:A:N7	4:LA:215:ASN:ND2	2.69	0.40
1:L5:4881:U:C2	15:LM:113:MET:HE1	2.56	0.40
1:L5:5055:G:H2'	1:L5:5056:A:C8	2.56	0.40
5:LB:161:ARG:HB3	5:LB:182:GLU:HB3	2.03	0.40
8:LE:250:GLN:O	8:LE:254:ASP:HB2	2.21	0.40
10:LG:107:LYS:HB3	10:LG:107:LYS:HE3	1.92	0.40
13:LJ:111:GLU:HB3	13:LJ:113:ILE:HG22	2.04	0.40
13:LJ:112:HIS:CD2	13:LJ:126:TYR:H	2.39	0.40
19:LQ:179:GLY:HA2	19:LQ:186:TYR:CE1	2.57	0.40
22:LT:33:ILE:HD13	22:LT:33:ILE:HA	1.97	0.40
31:Lc:26:LYS:HE2	31:Lc:26:LYS:HB3	1.94	0.40
52:S2:652:U:H2'	52:S2:653:A:C8	2.57	0.40
52:S2:1036:A:H4'	52:S2:1855:G:N2	2.36	0.40
52:S2:1244:U:H2'	52:S2:1245:G:C8	2.55	0.40
52:S2:1616:U:OP2	68:SP:43:ARG:NH2	2.45	0.40
52:S2:1706:G:H2'	52:S2:1707:U:H6	1.87	0.40
57:SE:71:LYS:HB2	57:SE:91:SER:HB2	2.04	0.40
61:SI:86:SER:OG	61:SI:87:ASN:N	2.54	0.40
63:SK:73:ASN:HA	63:SK:76:ILE:HG22	2.03	0.40
72:ST:112:MET:SD	72:ST:112:MET:N	2.94	0.40
79:Sa:59:PHE:HB2	79:Sa:62:TYR:HB2	2.04	0.40
85:Sg:69:VAL:HA	85:Sg:79:LEU:O	2.20	0.40
1:L5:163:A:H2'	1:L5:164:G:H8	1.85	0.40
1:L5:1511:U:H2'	1:L5:1512:G:H8	1.86	0.40
1:L5:2714:G:H2'	1:L5:2715:G:H8	1.86	0.40
1:L5:2890:C:H2'	1:L5:2891:U:C6	2.56	0.40
1:L5:4088:C:H2'	1:L5:4089:G:C8	2.56	0.40
1:L5:4507:A:O2'	24:LV:41:SER:OG	2.31	0.40
2:L7:23:A:N3	2:L7:118:C:O2'	2.40	0.40
5:LB:43:LEU:HD12	5:LB:205:VAL:HG11	2.03	0.40
22:LT:111:GLU:HA	22:LT:114:GLN:HB3	2.03	0.40
32:Ld:57:MET:HE3	32:Ld:90:ARG:HB2	2.04	0.40
52:S2:570:C:H4'	77:SY:36:PRO:HG3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:S2:652:U:H2'	52:S2:653:A:H8	1.86	0.40
54:SB:164:ILE:HD12	54:SB:201:CYS:HB2	2.04	0.40
54:SB:219:LYS:HD3	54:SB:219:LYS:HA	1.72	0.40
69:SQ:72:VAL:HG11	69:SQ:84:ILE:HD11	2.04	0.40
69:SQ:76:GLY:H	69:SQ:79:ALA:HB3	1.86	0.40
76:SX:76:LYS:HG3	76:SX:77:ASN:ND2	2.36	0.40
85:Sg:78:ALA:O	85:Sg:89:LEU:HA	2.21	0.40
1:L5:284:G:H2'	1:L5:285:G:H8	1.87	0.40
1:L5:1573:G:OP1	20:LR:92:LYS:NZ	2.49	0.40
1:L5:2587:A:H2'	1:L5:2588:C:C2	2.56	0.40
1:L5:2897:G:H5'	20:LR:101:ILE:HG21	2.03	0.40
1:L5:3910:C:H2'	1:L5:3911:C:H6	1.86	0.40
1:L5:4460:U:H2'	1:L5:4461:C:C6	2.57	0.40
10:LG:48:LYS:HA	10:LG:48:LYS:HD2	1.86	0.40
10:LG:178:GLY:O	10:LG:223:ARG:NH2	2.55	0.40
10:LG:207:VAL:HG21	10:LG:215:LEU:HD22	2.04	0.40
18:LP:33:ALA:HB1	18:LP:117:ILE:HG12	2.04	0.40
26:LX:99:ILE:HD13	26:LX:99:ILE:HA	1.85	0.40
37:Li:75:LYS:HA	37:Li:75:LYS:HD2	1.86	0.40
50:NA:208:ASN:OD1	50:NA:208:ASN:N	2.54	0.40
52:S2:916:A:C6	66:SN:73:ARG:HD2	2.57	0.40
52:S2:1589:A:O2'	72:ST:82:ARG:NH1	2.54	0.40
53:SA:73:ASP:OD1	53:SA:73:ASP:N	2.55	0.40
54:SB:81:PHE:CD2	54:SB:109:LYS:HG2	2.56	0.40
55:SC:273:LEU:HD23	55:SC:273:LEU:HA	1.87	0.40
59:SG:107:SER:OG	59:SG:108:VAL:N	2.54	0.40
60:SH:65:PRO:HB2	60:SH:68:GLN:HG3	2.04	0.40
63:SK:14:LEU:HA	63:SK:17:LYS:NZ	2.36	0.40
63:SK:16:PHE:HA	63:SK:79:LEU:HD21	2.04	0.40
69:SQ:95:TYR:HD1	69:SQ:95:TYR:HA	1.79	0.40
69:SQ:103:ALA:HA	69:SQ:106:LYS:HD2	2.01	0.40
71:SS:65:GLU:O	71:SS:68:ILE:HG22	2.22	0.40
71:SS:84:LEU:HD22	71:SS:97:GLN:HB2	2.02	0.40
75:SW:118:ARG:NH1	75:SW:119:LYS:HB3	2.34	0.40
77:SY:100:LYS:HA	77:SY:100:LYS:HD2	1.93	0.40
1:L5:181:C:H2'	1:L5:182:G:H8	1.86	0.40
1:L5:384:A:H61	1:L5:405:U:H4'	1.87	0.40
1:L5:1919:G:N2	21:LS:163:HIS:O	2.51	0.40
1:L5:2087:C:OP1	6:LC:303:ARG:NH1	2.48	0.40
1:L5:3633:C:H2'	1:L5:3634:G:C8	2.56	0.40
1:L5:4593:C:H2'	1:L5:4594:U:H6	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4940:C:OP1	8:LE:156:ARG:NH2	2.41	0.40
1:L5:4970:C:C2	1:L5:4971:A:C8	3.09	0.40
5:LB:341:LYS:H	5:LB:341:LYS:HG2	1.68	0.40
12:LI:78:LYS:HA	12:LI:78:LYS:HE2	2.02	0.40
18:LP:13:LYS:HE3	18:LP:13:LYS:HB3	1.84	0.40
49:N4:84:MET:HE1	49:N4:176:PHE:CD2	2.57	0.40
52:S2:1513:C:H2'	52:S2:1514:G:C8	2.56	0.40
63:SK:16:PHE:CD1	63:SK:83:LEU:HD13	2.56	0.40
69:SQ:131:LYS:HD2	69:SQ:131:LYS:HA	1.89	0.40
79:Sa:98:PRO:HA	79:Sa:99:PRO:HD3	1.97	0.40
85:Sg:72:SER:OG	85:Sg:74:ASP:OD1	2.37	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	
4	LA	246/257 (96%)	228 (93%)	18 (7%)	0	100	100
5	LB	400/403 (99%)	384 (96%)	16 (4%)	0	100	100
6	LC	363/427 (85%)	353 (97%)	9 (2%)	1 (0%)	36	66
7	LD	291/297 (98%)	284 (98%)	7 (2%)	0	100	100
8	LE	215/288 (75%)	205 (95%)	10 (5%)	0	100	100
9	LF	223/248 (90%)	218 (98%)	4 (2%)	1 (0%)	30	61
10	LG	239/266 (90%)	229 (96%)	10 (4%)	0	100	100
11	LH	188/192 (98%)	178 (95%)	10 (5%)	0	100	100
12	LI	198/214 (92%)	190 (96%)	8 (4%)	0	100	100
13	LJ	169/178 (95%)	166 (98%)	3 (2%)	0	100	100
14	LL	205/211 (97%)	196 (96%)	8 (4%)	1 (0%)	24	56

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	LM	137/215 (64%)	131 (96%)	6 (4%)	0	100	100
16	LN	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
17	LO	199/203 (98%)	197 (99%)	2 (1%)	0	100	100
18	LP	151/184 (82%)	145 (96%)	6 (4%)	0	100	100
19	LQ	185/188 (98%)	179 (97%)	6 (3%)	0	100	100
20	LR	185/196 (94%)	183 (99%)	2 (1%)	0	100	100
21	LS	173/176 (98%)	168 (97%)	5 (3%)	0	100	100
22	LT	157/160 (98%)	152 (97%)	5 (3%)	0	100	100
23	LU	98/128 (77%)	97 (99%)	1 (1%)	0	100	100
24	LV	129/140 (92%)	122 (95%)	7 (5%)	0	100	100
25	LW	122/157 (78%)	115 (94%)	7 (6%)	0	100	100
26	LX	118/156 (76%)	116 (98%)	2 (2%)	0	100	100
27	LY	131/145 (90%)	125 (95%)	6 (5%)	0	100	100
28	LZ	133/136 (98%)	132 (99%)	1 (1%)	0	100	100
29	La	145/148 (98%)	139 (96%)	6 (4%)	0	100	100
30	Lb	105/159 (66%)	100 (95%)	5 (5%)	0	100	100
31	Lc	96/115 (84%)	96 (100%)	0	0	100	100
32	Ld	105/125 (84%)	103 (98%)	2 (2%)	0	100	100
33	Le	126/135 (93%)	121 (96%)	5 (4%)	0	100	100
34	Lf	107/110 (97%)	106 (99%)	1 (1%)	0	100	100
35	Lg	112/117 (96%)	111 (99%)	1 (1%)	0	100	100
36	Lh	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
37	Li	100/105 (95%)	98 (98%)	2 (2%)	0	100	100
38	Lj	84/97 (87%)	81 (96%)	3 (4%)	0	100	100
39	Lk	67/70 (96%)	67 (100%)	0	0	100	100
40	Ll	48/51 (94%)	48 (100%)	0	0	100	100
41	Lm	49/128 (38%)	49 (100%)	0	0	100	100
42	Ln	22/25 (88%)	21 (96%)	1 (4%)	0	100	100
43	Lo	103/106 (97%)	97 (94%)	6 (6%)	0	100	100
44	Lp	89/92 (97%)	86 (97%)	3 (3%)	0	100	100
45	Lr	123/137 (90%)	121 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	Ls	194/317 (61%)	182 (94%)	12 (6%)	0	100	100
47	Lt	137/165 (83%)	109 (80%)	26 (19%)	2 (2%)	8	34
48	MA	313/386 (81%)	302 (96%)	11 (4%)	0	100	100
49	N4	221/237 (93%)	214 (97%)	7 (3%)	0	100	100
50	NA	104/215 (48%)	96 (92%)	8 (8%)	0	100	100
51	NB	104/162 (64%)	96 (92%)	8 (8%)	0	100	100
53	SA	219/295 (74%)	210 (96%)	9 (4%)	0	100	100
54	SB	217/264 (82%)	210 (97%)	7 (3%)	0	100	100
55	SC	220/293 (75%)	213 (97%)	7 (3%)	0	100	100
56	SD	225/243 (93%)	215 (96%)	10 (4%)	0	100	100
57	SE	260/263 (99%)	248 (95%)	12 (5%)	0	100	100
58	SF	180/204 (88%)	168 (93%)	12 (7%)	0	100	100
59	SG	235/249 (94%)	229 (97%)	5 (2%)	1 (0%)	30	61
60	SH	182/194 (94%)	179 (98%)	3 (2%)	0	100	100
61	SI	204/208 (98%)	196 (96%)	8 (4%)	0	100	100
62	SJ	183/194 (94%)	181 (99%)	2 (1%)	0	100	100
63	SK	93/165 (56%)	88 (95%)	5 (5%)	0	100	100
64	SL	140/158 (89%)	131 (94%)	9 (6%)	0	100	100
65	SM	120/132 (91%)	113 (94%)	7 (6%)	0	100	100
66	SN	148/151 (98%)	146 (99%)	2 (1%)	0	100	100
67	SO	133/151 (88%)	119 (90%)	13 (10%)	1 (1%)	16	47
68	SP	127/145 (88%)	117 (92%)	10 (8%)	0	100	100
69	SQ	142/146 (97%)	130 (92%)	12 (8%)	0	100	100
70	SR	133/135 (98%)	127 (96%)	5 (4%)	1 (1%)	16	47
71	SS	142/152 (93%)	131 (92%)	10 (7%)	1 (1%)	18	50
72	ST	141/145 (97%)	134 (95%)	7 (5%)	0	100	100
73	SU	102/119 (86%)	96 (94%)	6 (6%)	0	100	100
74	SV	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
75	SW	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
76	SX	139/143 (97%)	135 (97%)	4 (3%)	0	100	100
77	SY	124/133 (93%)	119 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
78	SZ	73/125 (58%)	56 (77%)	17 (23%)	0	100	100
79	Sa	100/115 (87%)	95 (95%)	4 (4%)	1 (1%)	12	42
80	Sb	81/84 (96%)	77 (95%)	4 (5%)	0	100	100
81	Sc	62/69 (90%)	61 (98%)	1 (2%)	0	100	100
82	Sd	53/56 (95%)	51 (96%)	2 (4%)	0	100	100
83	Se	56/133 (42%)	56 (100%)	0	0	100	100
84	Sf	65/156 (42%)	57 (88%)	8 (12%)	0	100	100
85	Sg	311/317 (98%)	274 (88%)	37 (12%)	0	100	100
All	All	12348/14244 (87%)	11816 (96%)	522 (4%)	10 (0%)	49	78

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
67	SO	138	ASP
79	Sa	46	GLU
6	LC	149	GLU
14	LL	97	SER
47	Lt	141	CYS
59	SG	12	CYS
70	SR	129	LYS
47	Lt	121	LEU
71	SS	74	PRO
9	LF	197	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	LA	190/199 (96%)	188 (99%)	2 (1%)	65	74
5	LB	348/349 (100%)	348 (100%)	0	100	100
6	LC	304/348 (87%)	302 (99%)	2 (1%)	76	78
7	LD	246/250 (98%)	246 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	LE	195/252 (77%)	195 (100%)	0	100	100
9	LF	194/215 (90%)	193 (100%)	1 (0%)	81	81
10	LG	203/223 (91%)	201 (99%)	2 (1%)	68	75
11	LH	169/171 (99%)	169 (100%)	0	100	100
12	LI	172/181 (95%)	170 (99%)	2 (1%)	63	73
13	LJ	144/149 (97%)	143 (99%)	1 (1%)	76	78
14	LL	173/177 (98%)	172 (99%)	1 (1%)	78	80
15	LM	118/161 (73%)	118 (100%)	0	100	100
16	LN	171/172 (99%)	171 (100%)	0	100	100
17	LO	173/174 (99%)	173 (100%)	0	100	100
18	LP	134/163 (82%)	133 (99%)	1 (1%)	76	78
19	LQ	164/165 (99%)	163 (99%)	1 (1%)	78	80
20	LR	166/175 (95%)	164 (99%)	2 (1%)	63	73
21	LS	156/157 (99%)	156 (100%)	0	100	100
22	LT	139/140 (99%)	139 (100%)	0	100	100
23	LU	90/115 (78%)	88 (98%)	2 (2%)	45	65
24	LV	101/107 (94%)	101 (100%)	0	100	100
25	LW	103/126 (82%)	103 (100%)	0	100	100
26	LX	108/133 (81%)	107 (99%)	1 (1%)	70	76
27	LY	123/135 (91%)	123 (100%)	0	100	100
28	LZ	117/118 (99%)	116 (99%)	1 (1%)	70	76
29	La	120/121 (99%)	119 (99%)	1 (1%)	73	77
30	Lb	89/126 (71%)	88 (99%)	1 (1%)	65	74
31	Lc	83/97 (86%)	83 (100%)	0	100	100
32	Ld	98/110 (89%)	97 (99%)	1 (1%)	68	75
33	Le	114/121 (94%)	114 (100%)	0	100	100
34	Lf	88/89 (99%)	87 (99%)	1 (1%)	65	74
35	Lg	98/100 (98%)	98 (100%)	0	100	100
36	Lh	109/110 (99%)	108 (99%)	1 (1%)	70	76
37	Li	86/89 (97%)	85 (99%)	1 (1%)	63	73
38	Lj	73/80 (91%)	73 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	Lk	64/65 (98%)	64 (100%)	0	100	100
40	Ll	47/48 (98%)	47 (100%)	0	100	100
41	Lm	47/115 (41%)	47 (100%)	0	100	100
42	Ln	23/24 (96%)	23 (100%)	0	100	100
43	Lo	93/94 (99%)	92 (99%)	1 (1%)	65	74
44	Lp	74/75 (99%)	74 (100%)	0	100	100
45	Lr	109/121 (90%)	109 (100%)	0	100	100
46	Ls	162/258 (63%)	161 (99%)	1 (1%)	78	80
47	Lt	112/137 (82%)	112 (100%)	0	100	100
48	MA	270/330 (82%)	267 (99%)	3 (1%)	65	74
49	N4	195/204 (96%)	194 (100%)	1 (0%)	81	81
50	NA	95/183 (52%)	94 (99%)	1 (1%)	65	74
51	NB	90/136 (66%)	90 (100%)	0	100	100
53	SA	183/243 (75%)	180 (98%)	3 (2%)	55	70
54	SB	200/231 (87%)	200 (100%)	0	100	100
55	SC	188/225 (84%)	186 (99%)	2 (1%)	65	74
56	SD	190/202 (94%)	190 (100%)	0	100	100
57	SE	224/225 (100%)	222 (99%)	2 (1%)	70	76
58	SF	156/170 (92%)	155 (99%)	1 (1%)	78	80
59	SG	207/218 (95%)	206 (100%)	1 (0%)	81	81
60	SH	166/174 (95%)	166 (100%)	0	100	100
61	SI	178/180 (99%)	176 (99%)	2 (1%)	65	74
62	SJ	161/168 (96%)	157 (98%)	4 (2%)	42	63
63	SK	86/136 (63%)	86 (100%)	0	100	100
64	SL	130/142 (92%)	130 (100%)	0	100	100
66	SN	130/131 (99%)	130 (100%)	0	100	100
67	SO	105/119 (88%)	105 (100%)	0	100	100
68	SP	115/130 (88%)	113 (98%)	2 (2%)	53	69
69	SQ	119/121 (98%)	117 (98%)	2 (2%)	53	69
70	SR	122/122 (100%)	120 (98%)	2 (2%)	55	70
71	SS	125/132 (95%)	124 (99%)	1 (1%)	73	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
72	ST	113/115 (98%)	113 (100%)	0	100	100
73	SU	94/107 (88%)	94 (100%)	0	100	100
74	SV	67/67 (100%)	67 (100%)	0	100	100
75	SW	112/113 (99%)	111 (99%)	1 (1%)	70	76
76	SX	113/115 (98%)	113 (100%)	0	100	100
77	SY	109/115 (95%)	108 (99%)	1 (1%)	70	76
78	SZ	66/103 (64%)	64 (97%)	2 (3%)	36	60
79	Sa	89/98 (91%)	88 (99%)	1 (1%)	65	74
80	Sb	75/76 (99%)	74 (99%)	1 (1%)	61	72
81	Sc	57/62 (92%)	56 (98%)	1 (2%)	51	68
82	Sd	48/49 (98%)	47 (98%)	1 (2%)	47	66
83	Se	47/104 (45%)	47 (100%)	0	100	100
84	Sf	60/140 (43%)	60 (100%)	0	100	100
85	Sg	272/275 (99%)	270 (99%)	2 (1%)	76	78
All	All	10647/11996 (89%)	10583 (99%)	64 (1%)	76	80

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	LA	4	VAL
4	LA	243	THR
6	LC	50	GLN
6	LC	146	GLU
9	LF	162	ILE
10	LG	33	GLU
10	LG	240	ASN
12	LI	31	ILE
12	LI	177	ASN
13	LJ	120	ASP
14	LL	80	GLU
18	LP	39	MET
19	LQ	8	ASN
20	LR	8	LYS
20	LR	116	ASP
23	LU	18	VAL
23	LU	106	SER
26	LX	93	ASN

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Mol	Chain	Res	Type
28	LZ	97	ASN
29	La	58	MET
30	Lb	43	MET
32	Ld	86	VAL
34	Lf	25	THR
36	Lh	99	GLU
37	Li	63	VAL
43	Lo	33	LEU
46	Ls	145	THR
48	MA	339	THR
48	MA	374	ARG
48	MA	383	MET
49	N4	42	PHE
50	NA	187	GLN
53	SA	34	MET
53	SA	59	LEU
53	SA	81	ASN
55	SC	134	ASN
55	SC	204	ILE
57	SE	67	GLN
57	SE	118	GLU
58	SF	98	GLU
59	SG	15	LEU
61	SI	91	VAL
61	SI	138	ASN
62	SJ	61	LEU
62	SJ	116	LYS
62	SJ	140	GLN
62	SJ	151	LEU
68	SP	38	SER
68	SP	94	VAL
69	SQ	43	GLU
69	SQ	95	TYR
70	SR	109	LEU
70	SR	124	VAL
71	SS	26	ILE
75	SW	43	LYS
77	SY	81	TYR
78	SZ	49	LEU
78	SZ	83	LEU
79	Sa	81	SER
80	Sb	25	VAL

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Mol	Chain	Res	Type
81	Sc	24	GLN
82	Sd	16	GLN
85	Sg	17	TRP
85	Sg	18	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (108) such sidechains are listed below:

Mol	Chain	Res	Type
4	LA	97	ASN
4	LA	162	ASN
5	LB	213	GLN
5	LB	376	HIS
6	LC	212	ASN
6	LC	215	ASN
6	LC	231	ASN
6	LC	278	ASN
6	LC	329	ASN
7	LD	39	GLN
7	LD	94	ASN
7	LD	202	GLN
7	LD	225	GLN
8	LE	101	ASN
9	LF	39	GLN
10	LG	82	GLN
10	LG	112	GLN
10	LG	240	ASN
11	LH	162	GLN
11	LH	189	GLN
12	LI	73	ASN
14	LL	19	GLN
16	LN	149	GLN
17	LO	167	HIS
18	LP	72	GLN
18	LP	133	HIS
19	LQ	21	GLN
19	LQ	77	ASN
20	LR	7	GLN
20	LR	34	ASN
20	LR	178	GLN
21	LS	125	GLN
22	LT	127	GLN
23	LU	116	GLN

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Mol	Chain	Res	Type
24	LV	135	ASN
25	LW	68	GLN
27	LY	14	ASN
27	LY	56	GLN
28	LZ	78	ASN
28	LZ	127	ASN
31	Lc	72	HIS
32	Ld	28	ASN
32	Ld	69	ASN
33	Le	24	GLN
37	Li	15	HIS
41	Lm	84	GLN
41	Lm	90	ASN
43	Lo	51	GLN
44	Lp	33	GLN
45	Lr	6	GLN
45	Lr	23	GLN
45	Lr	41	ASN
46	Ls	85	ASN
46	Ls	159	GLN
46	Ls	191	GLN
48	MA	74	ASN
48	MA	168	HIS
48	MA	178	ASN
48	MA	198	ASN
48	MA	250	GLN
48	MA	356	GLN
49	N4	33	ASN
49	N4	157	GLN
49	N4	180	HIS
51	NB	7	ASN
51	NB	17	GLN
51	NB	55	ASN
53	SA	33	GLN
53	SA	50	ASN
54	SB	75	GLN
55	SC	113	GLN
55	SC	115	GLN
57	SE	197	ASN
58	SF	118	ASN
58	SF	137	GLN
58	SF	148	ASN

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Mol	Chain	Res	Type
58	SF	186	ASN
59	SG	56	ASN
59	SG	227	GLN
60	SH	25	GLN
60	SH	76	GLN
61	SI	9	HIS
61	SI	35	ASN
63	SK	50	GLN
64	SL	19	ASN
66	SN	36	GLN
68	SP	79	HIS
69	SQ	8	GLN
69	SQ	80	GLN
70	SR	93	GLN
70	SR	118	GLN
71	SS	10	GLN
72	ST	83	GLN
72	ST	137	GLN
75	SW	70	ASN
76	SX	16	HIS
77	SY	15	ASN
77	SY	19	GLN
77	SY	106	GLN
77	SY	124	ASN
78	SZ	106	GLN
82	Sd	16	GLN
82	Sd	28	HIS
82	Sd	37	ASN
85	Sg	4	GLN
85	Sg	119	GLN
85	Sg	296	GLN
85	Sg	305	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3658/5070 (72%)	729 (19%)	16 (0%)
2	L7	119/121 (98%)	13 (10%)	0
3	L8	155/157 (98%)	29 (18%)	0
52	S2	1696/1869 (90%)	350 (20%)	5 (0%)
All	All	5628/7217 (77%)	1121 (19%)	21 (0%)

All (1121) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	17	A
1	L5	25	A
1	L5	39	A
1	L5	42	A
1	L5	48	G
1	L5	56	A
1	L5	59	A
1	L5	64	A
1	L5	65	A
1	L5	73	A
1	L5	76	A
1	L5	91	G
1	L5	104	G
1	L5	108	A
1	L5	109	G
1	L5	110	C
1	L5	119	G
1	L5	120	A
1	L5	132	G
1	L5	133	C
1	L5	134	G
1	L5	135	G
1	L5	152	U
1	L5	159	C
1	L5	171	U
1	L5	172	C
1	L5	177	G
1	L5	181	C
1	L5	182	G
1	L5	183	C
1	L5	184	U
1	L5	186	G
1	L5	188	G
1	L5	189	G
1	L5	200	U
1	L5	207	G
1	L5	209	U
1	L5	210	C
1	L5	216	C
1	L5	217	C
1	L5	218	A
1	L5	219	G

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Mol	Chain	Res	Type
1	L5	220	C
1	L5	233	U
1	L5	234	G
1	L5	266	C
1	L5	267	G
1	L5	269	G
1	L5	276	C
1	L5	278	G
1	L5	280	G
1	L5	297	U
1	L5	306	A
1	L5	315	G
1	L5	316	U
1	L5	340	C
1	L5	363	A
1	L5	373	G
1	L5	385	A
1	L5	387	G
1	L5	396	A
1	L5	407	A
1	L5	408	A
1	L5	409	G
1	L5	410	A
1	L5	412	G
1	L5	431	G
1	L5	432	U
1	L5	440	U
1	L5	449	C
1	L5	450	G
1	L5	452	A
1	L5	453	G
1	L5	454	U
1	L5	467	U
1	L5	468	U
1	L5	483	G
1	L5	484	U
1	L5	485	C
1	L5	493	G
1	L5	494	U
1	L5	495	C
1	L5	497	G
1	L5	498	C

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Mol	Chain	Res	Type
1	L5	500	G
1	L5	502	C
1	L5	503	C
1	L5	504	G
1	L5	505	G
1	L5	509	A
1	L5	510	U
1	L5	512	U
1	L5	513	U
1	L5	514	U
1	L5	515	C
1	L5	516	C
1	L5	518	G
1	L5	643	C
1	L5	646	G
1	L5	655	C
1	L5	657	C
1	L5	659	G
1	L5	665	C
1	L5	666	G
1	L5	667	A
1	L5	668	C
1	L5	669	C
1	L5	685	C
1	L5	686	A
1	L5	696	C
1	L5	703	G
1	L5	704	C
1	L5	706	C
1	L5	731	G
1	L5	738	C
1	L5	739	G
1	L5	740	G
1	L5	742	G
1	L5	744	G
1	L5	753	C
1	L5	759	G
1	L5	760	G
1	L5	904	C
1	L5	907	C
1	L5	913	U
1	L5	914	U

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Mol	Chain	Res	Type
1	L5	915	A
1	L5	917	A
1	L5	918	G
1	L5	923	C
1	L5	924	C
1	L5	926	G
1	L5	932	A
1	L5	933	G
1	L5	935	A
1	L5	941	C
1	L5	944	A
1	L5	945	U
1	L5	956	A
1	L5	959	G
1	L5	960	A
1	L5	961	G
1	L5	962	C
1	L5	964	A
1	L5	965	G
1	L5	966	A
1	L5	967	C
1	L5	969	C
1	L5	970	G
1	L5	972	C
1	L5	982	U
1	L5	988	C
1	L5	989	U
1	L5	990	C
1	L5	992	C
1	L5	993	G
1	L5	995	C
1	L5	1048	G
1	L5	1049	C
1	L5	1050	C
1	L5	1051	G
1	L5	1070	G
1	L5	1072	C
1	L5	1073	G
1	L5	1078	A
1	L5	1170	G
1	L5	1171	G
1	L5	1172	C

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Mol	Chain	Res	Type
1	L5	1173	G
1	L5	1183	C
1	L5	1198	G
1	L5	1199	G
1	L5	1200	G
1	L5	1205	G
1	L5	1210	C
1	L5	1211	G
1	L5	1214	C
1	L5	1215	C
1	L5	1216	C
1	L5	1217	G
1	L5	1219	G
1	L5	1222	A
1	L5	1239	C
1	L5	1253	G
1	L5	1254	A
1	L5	1255	A
1	L5	1262	G
1	L5	1266	G
1	L5	1267	C
1	L5	1271	G
1	L5	1273	G
1	L5	1280	C
1	L5	1284	G
1	L5	1287	G
1	L5	1293	G
1	L5	1294	A
1	L5	1295	C
1	L5	1296	G
1	L5	1301	C
1	L5	1302	U
1	L5	1326	A
1	L5	1337	A
1	L5	1344	C
1	L5	1354	A
1	L5	1358	G
1	L5	1359	G
1	L5	1364	U
1	L5	1365	C
1	L5	1366	G
1	L5	1367	C

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Mol	Chain	Res	Type
1	L5	1379	C
1	L5	1387	A
1	L5	1394	G
1	L5	1397	A
1	L5	1398	A
1	L5	1405	C
1	L5	1407	C
1	L5	1409	C
1	L5	1410	U
1	L5	1414	C
1	L5	1415	G
1	L5	1417	C
1	L5	1420	A
1	L5	1438	U
1	L5	1447	C
1	L5	1448	G
1	L5	1457	G
1	L5	1465	G
1	L5	1472	C
1	L5	1480	C
1	L5	1483	C
1	L5	1497	A
1	L5	1498	G
1	L5	1502	G
1	L5	1518	A
1	L5	1534	A
1	L5	1543	G
1	L5	1547	A
1	L5	1564	A
1	L5	1566	C
1	L5	1574	G
1	L5	1578	U
1	L5	1591	U
1	L5	1596	U
1	L5	1597	G
1	L5	1612	G
1	L5	1613	A
1	L5	1624	G
1	L5	1625	G
1	L5	1631	A
1	L5	1633	G
1	L5	1634	A

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Mol	Chain	Res	Type
1	L5	1640	C
1	L5	1641	G
1	L5	1650	A
1	L5	1654	G
1	L5	1661	C
1	L5	1676	C
1	L5	1677	U
1	L5	1678	C
1	L5	1694	C
1	L5	1699	A
1	L5	1700	G
1	L5	1703	C
1	L5	1704	C
1	L5	1705	G
1	L5	1707	C
1	L5	1708	G
1	L5	1716	G
1	L5	1719	A
1	L5	1724	G
1	L5	1726	U
1	L5	1731	C
1	L5	1734	G
1	L5	1742	A
1	L5	1754	U
1	L5	1755	C
1	L5	1756	U
1	L5	1758	G
1	L5	1759	G
1	L5	1760	G
1	L5	1761	G
1	L5	1762	C
1	L5	1763	C
1	L5	1764	G
1	L5	1765	A
1	L5	1766	A
1	L5	1768	C
1	L5	1770	A
1	L5	1771	U
1	L5	1787	A
1	L5	1804	A
1	L5	1815	G
1	L5	1820	C

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Mol	Chain	Res	Type
1	L5	1821	G
1	L5	1822	U
1	L5	1834	U
1	L5	1836	G
1	L5	1837	A
1	L5	1842	G
1	L5	1855	G
1	L5	1869	G
1	L5	1888	A
1	L5	1891	A
1	L5	1897	A
1	L5	1910	G
1	L5	1915	C
1	L5	1918	U
1	L5	1919	G
1	L5	1920	C
1	L5	1921	C
1	L5	1922	G
1	L5	1925	G
1	L5	1931	C
1	L5	1932	A
1	L5	1936	C
1	L5	1948	G
1	L5	1949	U
1	L5	1951	G
1	L5	1959	U
1	L5	1960	A
1	L5	1961	G
1	L5	1962	A
1	L5	1972	G
1	L5	1974	U
1	L5	1975	G
1	L5	1978	C
1	L5	1980	U
1	L5	1983	A
1	L5	1984	A
1	L5	1985	G
1	L5	1986	U
1	L5	1987	C
1	L5	1988	G
1	L5	1990	A
1	L5	1992	U

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Mol	Chain	Res	Type
1	L5	1993	C
1	L5	1997	U
1	L5	1998	A
1	L5	2001	G
1	L5	2002	A
1	L5	2004	U
1	L5	2017	A
1	L5	2018	C
1	L5	2024	G
1	L5	2026	A
1	L5	2034	G
1	L5	2046	G
1	L5	2048	U
1	L5	2052	G
1	L5	2055	G
1	L5	2056	G
1	L5	2069	A
1	L5	2084	C
1	L5	2085	G
1	L5	2089	G
1	L5	2092	G
1	L5	2095	A
1	L5	2096	G
1	L5	2098	G
1	L5	2099	G
1	L5	2112	G
1	L5	2250	C
1	L5	2252	G
1	L5	2253	A
1	L5	2256	C
1	L5	2268	A
1	L5	2289	C
1	L5	2300	A
1	L5	2301	G
1	L5	2313	A
1	L5	2314	G
1	L5	2316	G
1	L5	2331	G
1	L5	2332	A
1	L5	2333	G
1	L5	2351	C
1	L5	2360	A

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Mol	Chain	Res	Type
1	L5	2382	A
1	L5	2397	G
1	L5	2410	C
1	L5	2417	A
1	L5	2421	G
1	L5	2425	U
1	L5	2441	C
1	L5	2442	G
1	L5	2450	G
1	L5	2471	G
1	L5	2475	G
1	L5	2478	C
1	L5	2479	G
1	L5	2483	G
1	L5	2484	A
1	L5	2485	U
1	L5	2487	G
1	L5	2488	C
1	L5	2489	C
1	L5	2490	U
1	L5	2495	U
1	L5	2503	G
1	L5	2504	C
1	L5	2505	C
1	L5	2506	G
1	L5	2511	A
1	L5	2513	A
1	L5	2519	U
1	L5	2529	A
1	L5	2537	A
1	L5	2544	G
1	L5	2546	G
1	L5	2547	G
1	L5	2554	U
1	L5	2555	G
1	L5	2559	G
1	L5	2560	C
1	L5	2565	A
1	L5	2573	A
1	L5	2583	C
1	L5	2587	A
1	L5	2589	C

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Mol	Chain	Res	Type
1	L5	2601	A
1	L5	2627	C
1	L5	2653	C
1	L5	2662	G
1	L5	2669	C
1	L5	2670	C
1	L5	2676	A
1	L5	2687	U
1	L5	2694	G
1	L5	2695	A
1	L5	2696	A
1	L5	2701	U
1	L5	2703	G
1	L5	2707	U
1	L5	2708	U
1	L5	2709	C
1	L5	2710	C
1	L5	2711	G
1	L5	2712	G
1	L5	2719	C
1	L5	2721	G
1	L5	2724	G
1	L5	2726	G
1	L5	2739	C
1	L5	2742	G
1	L5	2743	A
1	L5	2756	G
1	L5	2761	U
1	L5	2763	U
1	L5	2769	U
1	L5	2770	C
1	L5	2787	A
1	L5	2788	U
1	L5	2790	U
1	L5	2793	G
1	L5	2794	C
1	L5	2814	C
1	L5	2826	U
1	L5	2827	G
1	L5	2835	A
1	L5	2842	G
1	L5	2846	G

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Mol	Chain	Res	Type
1	L5	2855	G
1	L5	2877	G
1	L5	2894	A
1	L5	2900	U
1	L5	2902	G
1	L5	2903	G
1	L5	2904	U
1	L5	2905	C
1	L5	2906	G
1	L5	2907	G
1	L5	2908	U
1	L5	3585	G
1	L5	3587	C
1	L5	3588	C
1	L5	3590	G
1	L5	3591	C
1	L5	3594	C
1	L5	3595	U
1	L5	3596	A
1	L5	3597	G
1	L5	3604	A
1	L5	3605	C
1	L5	3615	G
1	L5	3616	U
1	L5	3618	C
1	L5	3626	G
1	L5	3630	A
1	L5	3635	A
1	L5	3644	U
1	L5	3646	A
1	L5	3648	A
1	L5	3662	A
1	L5	3673	C
1	L5	3674	G
1	L5	3680	U
1	L5	3691	G
1	L5	3710	G
1	L5	3714	G
1	L5	3727	A
1	L5	3748	A
1	L5	3750	G
1	L5	3753	G

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Mol	Chain	Res	Type
1	L5	3759	A
1	L5	3760	A
1	L5	3761	C
1	L5	3776	G
1	L5	3777	G
1	L5	3778	U
1	L5	3783	A
1	L5	3784	A
1	L5	3786	U
1	L5	3811	G
1	L5	3812	C
1	L5	3814	U
1	L5	3817	A
1	L5	3818	U
1	L5	3819	G
1	L5	3823	G
1	L5	3838	U
1	L5	3840	U
1	L5	3851	U
1	L5	3867	A
1	L5	3877	A
1	L5	3878	C
1	L5	3879	G
1	L5	3885	G
1	L5	3887	C
1	L5	3897	G
1	L5	3901	A
1	L5	3906	A
1	L5	3907	G
1	L5	3908	A
1	L5	3915	U
1	L5	3938	G
1	L5	3939	G
1	L5	3947	A
1	L5	3948	C
1	L5	3951	G
1	L5	3955	G
1	L5	4064	C
1	L5	4065	G
1	L5	4076	G
1	L5	4084	G
1	L5	4086	G

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Mol	Chain	Res	Type
1	L5	4092	G
1	L5	4093	G
1	L5	4097	G
1	L5	4099	G
1	L5	4101	C
1	L5	4102	C
1	L5	4103	C
1	L5	4104	G
1	L5	4107	G
1	L5	4108	G
1	L5	4111	U
1	L5	4114	C
1	L5	4115	G
1	L5	4116	C
1	L5	4117	U
1	L5	4122	G
1	L5	4127	A
1	L5	4140	C
1	L5	4141	G
1	L5	4142	C
1	L5	4143	G
1	L5	4144	C
1	L5	4146	G
1	L5	4150	G
1	L5	4162	C
1	L5	4163	U
1	L5	4168	G
1	L5	4170	A
1	L5	4183	G
1	L5	4184	G
1	L5	4191	G
1	L5	4194	U
1	L5	4196	G
1	L5	4203	A
1	L5	4212	A
1	L5	4222	G
1	L5	4228	G
1	L5	4229	U
1	L5	4233	A
1	L5	4234	A
1	L5	4243	C
1	L5	4251	A

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Mol	Chain	Res	Type
1	L5	4254	G
1	L5	4255	A
1	L5	4265	U
1	L5	4268	A
1	L5	4273	A
1	L5	4280	A
1	L5	4281	A
1	L5	4290	U
1	L5	4291	G
1	L5	4295	U
1	L5	4304	A
1	L5	4305	G
1	L5	4314	C
1	L5	4319	C
1	L5	4329	G
1	L5	4330	G
1	L5	4332	C
1	L5	4349	C
1	L5	4350	C
1	L5	4354	U
1	L5	4373	G
1	L5	4377	G
1	L5	4378	A
1	L5	4380	A
1	L5	4387	C
1	L5	4394	A
1	L5	4422	A
1	L5	4437	U
1	L5	4444	C
1	L5	4448	G
1	L5	4449	A
1	L5	4452	U
1	L5	4453	C
1	L5	4464	A
1	L5	4466	C
1	L5	4488	A
1	L5	4500	U
1	L5	4512	U
1	L5	4513	A
1	L5	4515	G
1	L5	4518	A
1	L5	4519	C

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Mol	Chain	Res	Type
1	L5	4524	G
1	L5	4545	G
1	L5	4548	A
1	L5	4549	G
1	L5	4560	C
1	L5	4567	G
1	L5	4573	G
1	L5	4575	G
1	L5	4584	A
1	L5	4590	A
1	L5	4600	G
1	L5	4627	U
1	L5	4635	A
1	L5	4636	U
1	L5	4637	G
1	L5	4652	G
1	L5	4656	A
1	L5	4670	C
1	L5	4672	A
1	L5	4684	A
1	L5	4695	C
1	L5	4700	A
1	L5	4707	A
1	L5	4708	A
1	L5	4709	U
1	L5	4719	G
1	L5	4734	A
1	L5	4741	C
1	L5	4742	G
1	L5	4745	G
1	L5	4754	G
1	L5	4757	C
1	L5	4759	C
1	L5	4761	G
1	L5	4765	G
1	L5	4771	C
1	L5	4772	C
1	L5	4773	C
1	L5	4775	C
1	L5	4859	C
1	L5	4867	G
1	L5	4870	G

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Mol	Chain	Res	Type
1	L5	4871	C
1	L5	4874	A
1	L5	4875	G
1	L5	4882	U
1	L5	4883	C
1	L5	4889	G
1	L5	4895	C
1	L5	4896	G
1	L5	4897	G
1	L5	4899	G
1	L5	4900	C
1	L5	4901	G
1	L5	4910	G
1	L5	4911	A
1	L5	4912	G
1	L5	4914	C
1	L5	4918	C
1	L5	4924	C
1	L5	4925	U
1	L5	4927	G
1	L5	4928	C
1	L5	4934	A
1	L5	4937	C
1	L5	4940	C
1	L5	4941	G
1	L5	4943	A
1	L5	4951	G
1	L5	4955	A
1	L5	4960	G
1	L5	4973	U
1	L5	4975	G
1	L5	4976	U
1	L5	4985	U
1	L5	4988	U
1	L5	4989	U
1	L5	4991	U
1	L5	5006	U
1	L5	5009	G
1	L5	5013	C
1	L5	5014	A
1	L5	5017	G
1	L5	5022	U

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Mol	Chain	Res	Type
1	L5	5023	C
1	L5	5025	C
1	L5	5026	U
1	L5	5027	C
1	L5	5028	G
1	L5	5029	C
1	L5	5030	U
1	L5	5034	A
1	L5	5041	G
1	L5	5048	A
1	L5	5050	C
1	L5	5054	C
1	L5	5055	G
1	L5	5061	A
1	L5	5069	U
2	L7	7	G
2	L7	24	C
2	L7	33	U
2	L7	37	G
2	L7	38	U
2	L7	53	U
2	L7	54	A
2	L7	63	C
2	L7	64	G
2	L7	74	A
2	L7	100	A
2	L7	110	G
2	L7	111	C
3	L8	23	C
3	L8	25	G
3	L8	34	U
3	L8	35	C
3	L8	39	G
3	L8	48	A
3	L8	59	A
3	L8	61	A
3	L8	62	A
3	L8	63	U
3	L8	68	G
3	L8	80	A
3	L8	81	C
3	L8	85	U

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Mol	Chain	Res	Type
3	L8	87	G
3	L8	94	G
3	L8	103	A
3	L8	105	C
3	L8	110	U
3	L8	112	G
3	L8	114	G
3	L8	123	U
3	L8	124	U
3	L8	125	C
3	L8	126	C
3	L8	127	U
3	L8	150	C
3	L8	153	C
3	L8	155	C
52	S2	2	A
52	S2	4	C
52	S2	23	G
52	S2	33	G
52	S2	41	G
52	S2	42	A
52	S2	46	A
52	S2	56	G
52	S2	58	C
52	S2	59	U
52	S2	62	G
52	S2	65	C
52	S2	67	C
52	S2	68	A
52	S2	72	C
52	S2	73	C
52	S2	74	G
52	S2	76	U
52	S2	103	A
52	S2	113	G
52	S2	115	U
52	S2	116	U
52	S2	126	G
52	S2	129	C
52	S2	130	G
52	S2	143	U
52	S2	160	U

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Mol	Chain	Res	Type
52	S2	162	C
52	S2	171	A
52	S2	175	A
52	S2	182	C
52	S2	187	G
52	S2	190	G
52	S2	198	U
52	S2	200	G
52	S2	203	G
52	S2	204	G
52	S2	291	G
52	S2	292	A
52	S2	295	C
52	S2	302	A
52	S2	308	G
52	S2	310	C
52	S2	311	C
52	S2	312	G
52	S2	319	C
52	S2	322	C
52	S2	323	C
52	S2	324	C
52	S2	325	C
52	S2	326	C
52	S2	328	U
52	S2	329	G
52	S2	332	G
52	S2	339	A
52	S2	347	G
52	S2	351	G
52	S2	360	A
52	S2	362	C
52	S2	364	A
52	S2	368	U
52	S2	369	C
52	S2	370	G
52	S2	373	G
52	S2	385	G
52	S2	386	C
52	S2	400	C
52	S2	407	G
52	S2	408	A

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Mol	Chain	Res	Type
52	S2	409	C
52	S2	428	U
52	S2	448	A
52	S2	449	A
52	S2	450	C
52	S2	452	G
52	S2	464	A
52	S2	466	G
52	S2	471	G
52	S2	472	C
52	S2	473	A
52	S2	474	G
52	S2	482	G
52	S2	485	A
52	S2	487	U
52	S2	488	U
52	S2	492	C
52	S2	493	A
52	S2	496	C
52	S2	501	C
52	S2	517	C
52	S2	523	A
52	S2	540	U
52	S2	541	U
52	S2	542	U
52	S2	545	A
52	S2	547	G
52	S2	548	C
52	S2	554	A
52	S2	560	A
52	S2	563	G
52	S2	564	A
52	S2	568	C
52	S2	576	A
52	S2	583	C
52	S2	589	G
52	S2	591	U
52	S2	593	C
52	S2	598	G
52	S2	604	A
52	S2	614	C
52	S2	617	G

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Mol	Chain	Res	Type
52	S2	623	G
52	S2	627	U
52	S2	628	A
52	S2	631	U
52	S2	643	A
52	S2	644	G
52	S2	660	C
52	S2	664	A
52	S2	668	A
52	S2	669	A
52	S2	670	A
52	S2	671	A
52	S2	672	A
52	S2	673	G
52	S2	684	G
52	S2	687	C
52	S2	688	U
52	S2	689	U
52	S2	690	G
52	S2	749	U
52	S2	751	G
52	S2	752	G
52	S2	753	C
52	S2	791	C
52	S2	792	C
52	S2	797	C
52	S2	798	A
52	S2	801	U
52	S2	811	A
52	S2	821	G
52	S2	822	U
52	S2	827	A
52	S2	830	A
52	S2	834	C
52	S2	836	G
52	S2	837	A
52	S2	838	G
52	S2	839	C
52	S2	840	C
52	S2	842	C
52	S2	847	A
52	S2	869	A

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Mol	Chain	Res	Type
52	S2	870	A
52	S2	873	G
52	S2	878	G
52	S2	880	G
52	S2	886	A
52	S2	888	U
52	S2	889	U
52	S2	891	G
52	S2	896	U
52	S2	897	U
52	S2	898	U
52	S2	900	C
52	S2	904	A
52	S2	913	A
52	S2	914	U
52	S2	917	U
52	S2	920	A
52	S2	930	C
52	S2	933	G
52	S2	934	G
52	S2	950	C
52	S2	963	A
52	S2	978	G
52	S2	990	A
52	S2	992	A
52	S2	999	G
52	S2	1001	A
52	S2	1016	U
52	S2	1017	U
52	S2	1023	A
52	S2	1027	A
52	S2	1045	U
52	S2	1067	C
52	S2	1083	A
52	S2	1085	C
52	S2	1089	G
52	S2	1109	C
52	S2	1115	U
52	S2	1116	C
52	S2	1118	C
52	S2	1121	G
52	S2	1133	A

Continued on next page...

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Mol	Chain	Res	Type
52	S2	1138	C
52	S2	1139	C
52	S2	1149	A
52	S2	1150	A
52	S2	1153	C
52	S2	1154	U
52	S2	1155	U
52	S2	1166	G
52	S2	1170	A
52	S2	1195	A
52	S2	1207	G
52	S2	1212	G
52	S2	1215	C
52	S2	1216	C
52	S2	1217	A
52	S2	1221	G
52	S2	1224	G
52	S2	1227	G
52	S2	1240	A
52	S2	1242	U
52	S2	1243	U
52	S2	1251	A
52	S2	1253	A
52	S2	1255	G
52	S2	1256	G
52	S2	1257	G
52	S2	1259	A
52	S2	1264	C
52	S2	1269	G
52	S2	1274	G
52	S2	1275	G
52	S2	1283	C
52	S2	1285	G
52	S2	1286	G
52	S2	1290	G
52	S2	1294	G
52	S2	1295	A
52	S2	1302	G
52	S2	1303	C
52	S2	1306	U
52	S2	1308	U
52	S2	1312	G

Continued on next page...

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Mol	Chain	Res	Type
52	S2	1333	U
52	S2	1341	C
52	S2	1342	U
52	S2	1343	U
52	S2	1348	G
52	S2	1371	U
52	S2	1372	U
52	S2	1378	A
52	S2	1382	A
52	S2	1384	C
52	S2	1394	G
52	S2	1395	C
52	S2	1397	U
52	S2	1398	G
52	S2	1404	U
52	S2	1421	A
52	S2	1423	C
52	S2	1428	G
52	S2	1431	G
52	S2	1433	C
52	S2	1434	C
52	S2	1435	C
52	S2	1436	C
52	S2	1438	A
52	S2	1439	A
52	S2	1454	A
52	S2	1462	U
52	S2	1463	U
52	S2	1464	C
52	S2	1478	U
52	S2	1487	A
52	S2	1489	A
52	S2	1490	G
52	S2	1494	U
52	S2	1495	G
52	S2	1497	G
52	S2	1498	A
52	S2	1505	U
52	S2	1507	G
52	S2	1508	A
52	S2	1520	G
52	S2	1521	C

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Mol	Chain	Res	Type
52	S2	1523	C
52	S2	1533	A
52	S2	1537	A
52	S2	1546	G
52	S2	1552	G
52	S2	1553	C
52	S2	1557	C
52	S2	1570	G
52	S2	1579	A
52	S2	1580	A
52	S2	1585	U
52	S2	1586	U
52	S2	1587	G
52	S2	1588	A
52	S2	1598	G
52	S2	1600	G
52	S2	1601	A
52	S2	1604	G
52	S2	1606	G
52	S2	1612	G
52	S2	1621	U
52	S2	1623	A
52	S2	1632	G
52	S2	1634	A
52	S2	1644	C
52	S2	1646	C
52	S2	1648	G
52	S2	1649	U
52	S2	1661	A
52	S2	1663	A
52	S2	1665	G
52	S2	1680	G
52	S2	1683	C
52	S2	1686	G
52	S2	1696	C
52	S2	1699	A
52	S2	1715	A
52	S2	1721	U
52	S2	1722	G
52	S2	1744	G
52	S2	1745	A
52	S2	1752	C

Continued on next page...

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Mol	Chain	Res	Type
52	S2	1753	C
52	S2	1754	G
52	S2	1757	G
52	S2	1758	G
52	S2	1759	G
52	S2	1761	U
52	S2	1772	C
52	S2	1773	C
52	S2	1774	C
52	S2	1775	U
52	S2	1776	G
52	S2	1777	G
52	S2	1781	A
52	S2	1783	C
52	S2	1784	G
52	S2	1786	U
52	S2	1819	A
52	S2	1825	A
52	S2	1826	G
52	S2	1831	A
52	S2	1835	A
52	S2	1838	U
52	S2	1841	C
52	S2	1849	G
52	S2	1852	C
52	S2	1861	G
52	S2	1862	G
52	S2	1863	A
52	S2	1865	C

All (21) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	206	U
1	L5	218	A
1	L5	406	C
1	L5	914	U
1	L5	1171	G
1	L5	1198	G
1	L5	1633	G
1	L5	1977	C
1	L5	2033	A

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Mol	Chain	Res	Type
1	L5	2675	G
1	L5	2760	G
1	L5	2786	C
1	L5	3614	G
1	L5	3673	C
1	L5	4699	U
1	L5	4913	G
52	S2	112	U
52	S2	291	G
52	S2	563	G
52	S2	688	U
52	S2	1434	C

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
41	MLZ	Lm	98	41	8,9,10	0.77	0	4,9,11	0.62	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
41	MLZ	Lm	98	41	-	0/7/8/10	-

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.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 265 ligands modelled in this entry, 265 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

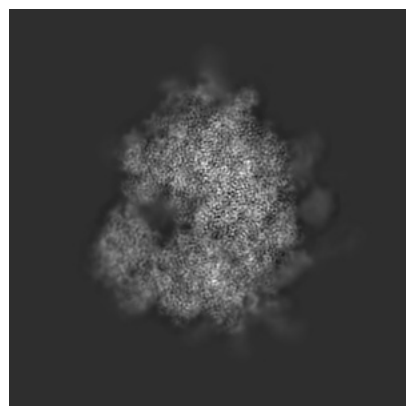
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55616. These allow visual inspection of the internal detail of the map and identification of artifacts.

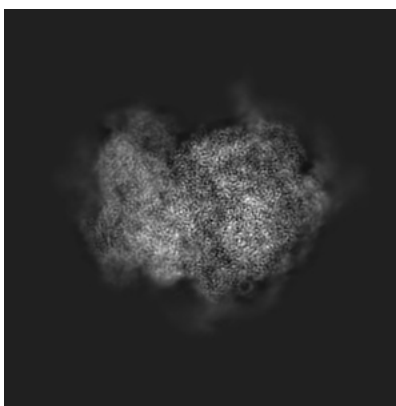
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

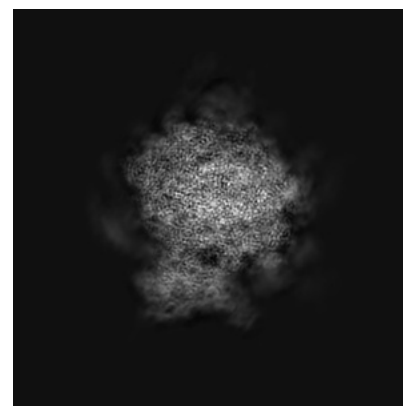
6.1.1 Primary map



X

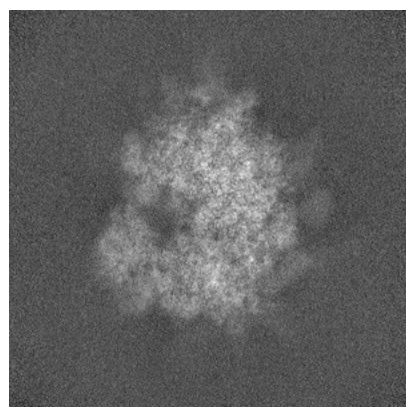


Y

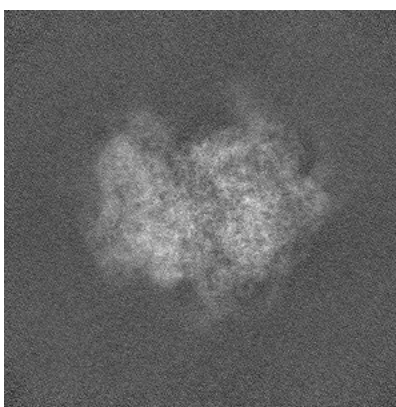


Z

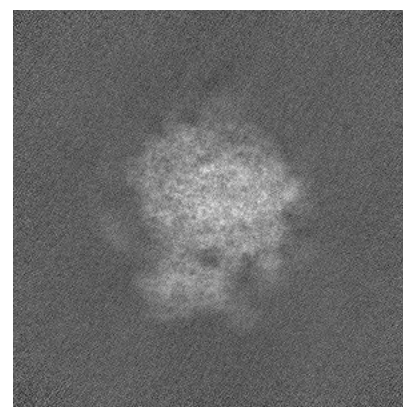
6.1.2 Raw map



X



Y

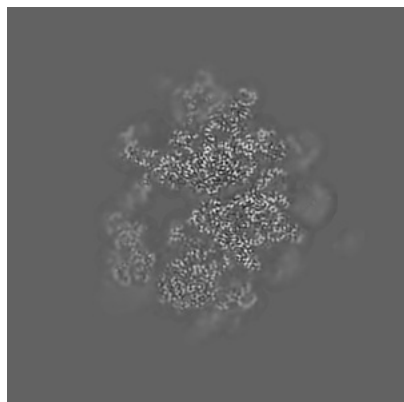


Z

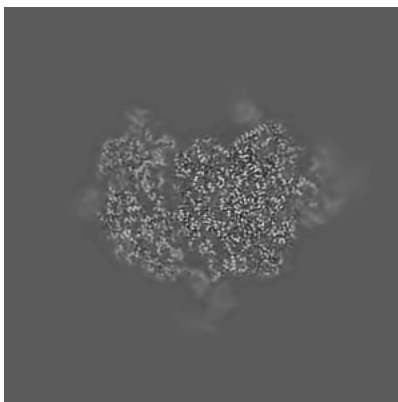
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

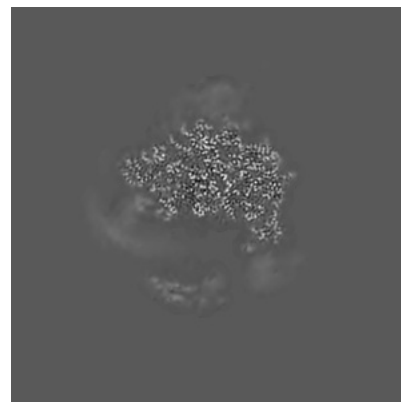
6.2.1 Primary map



X Index: 320

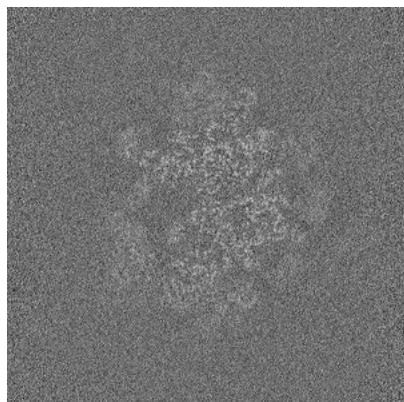


Y Index: 320

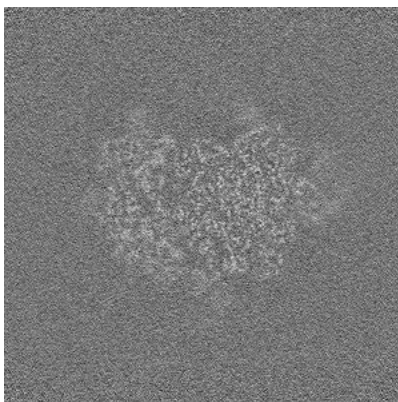


Z Index: 320

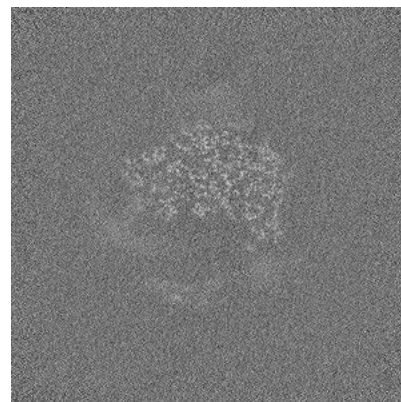
6.2.2 Raw map



X Index: 320



Y Index: 320

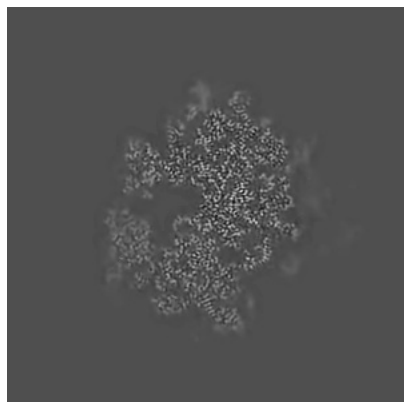


Z Index: 320

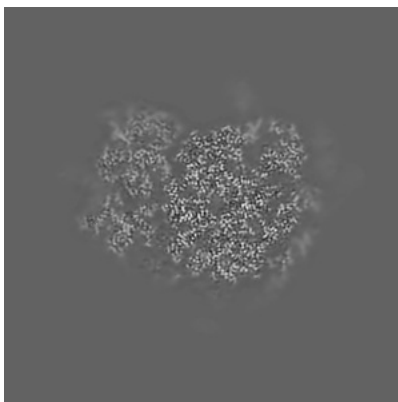
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

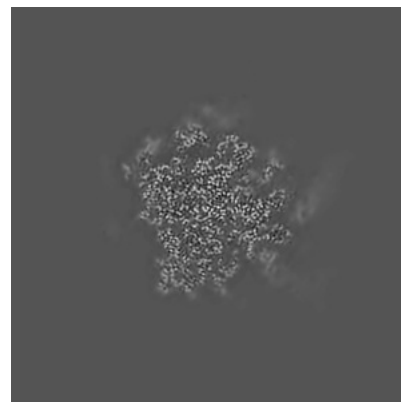
6.3.1 Primary map



X Index: 298

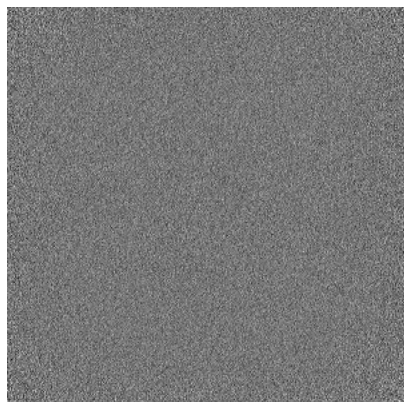


Y Index: 346

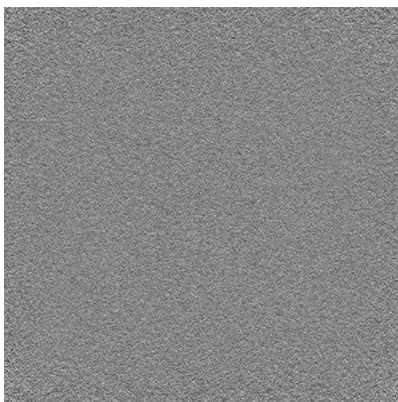


Z Index: 385

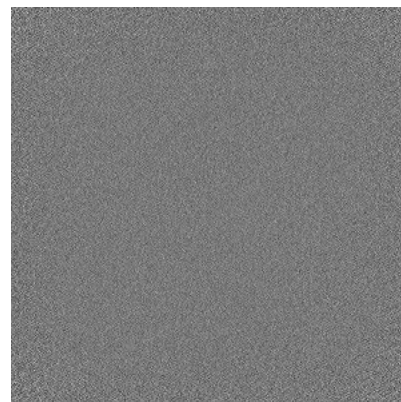
6.3.2 Raw map



X Index: 0



Y Index: 0

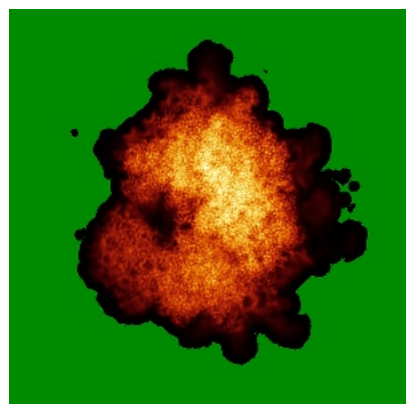


Z Index: 0

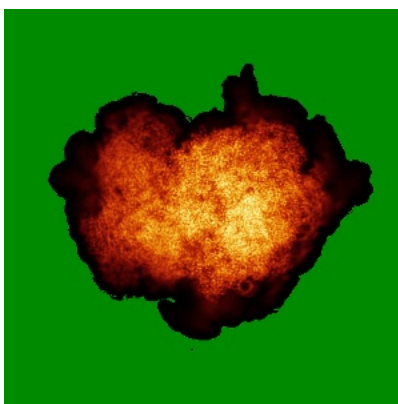
The images above show the largest variance slices of the map in three orthogonal directions.

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

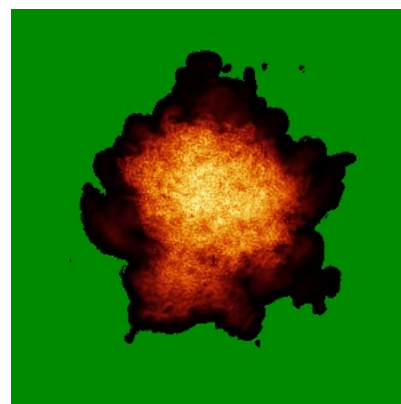
6.4.1 Primary map



X

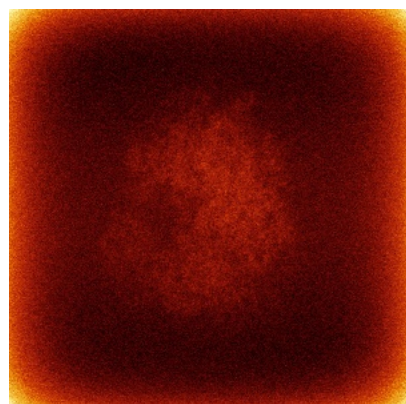


Y

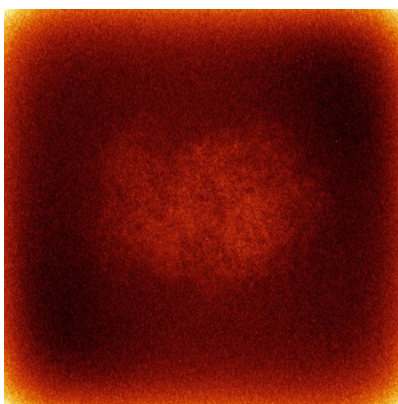


Z

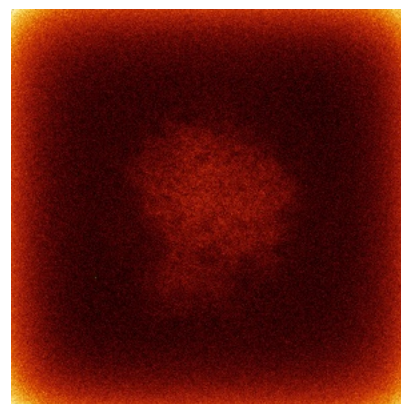
6.4.2 Raw map



X



Y



Z

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

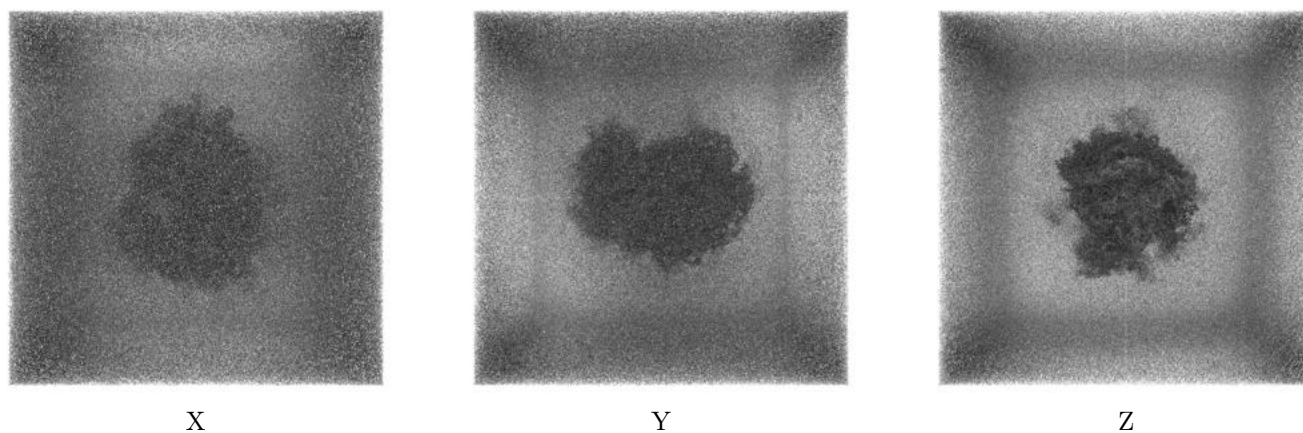
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.11. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

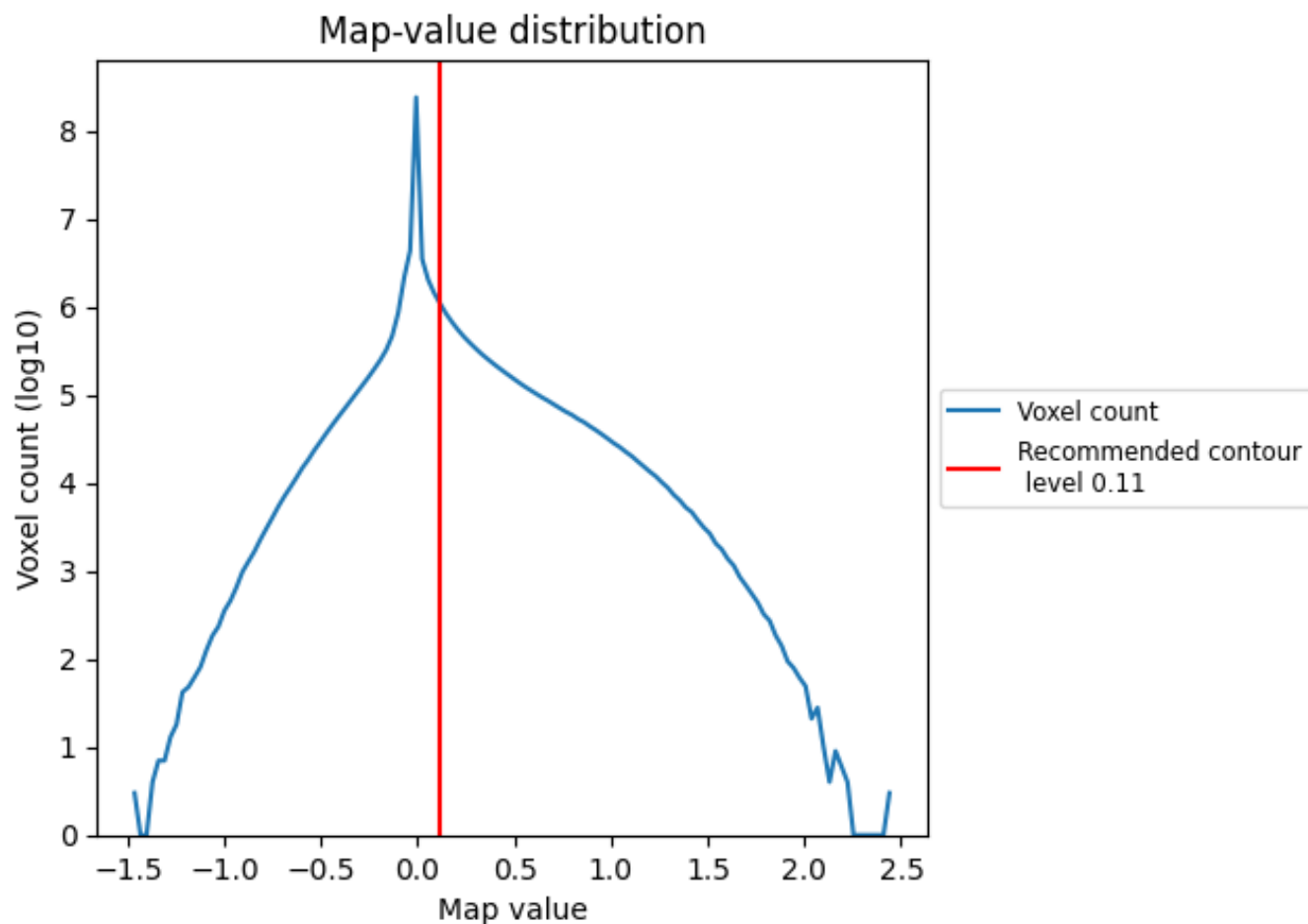
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

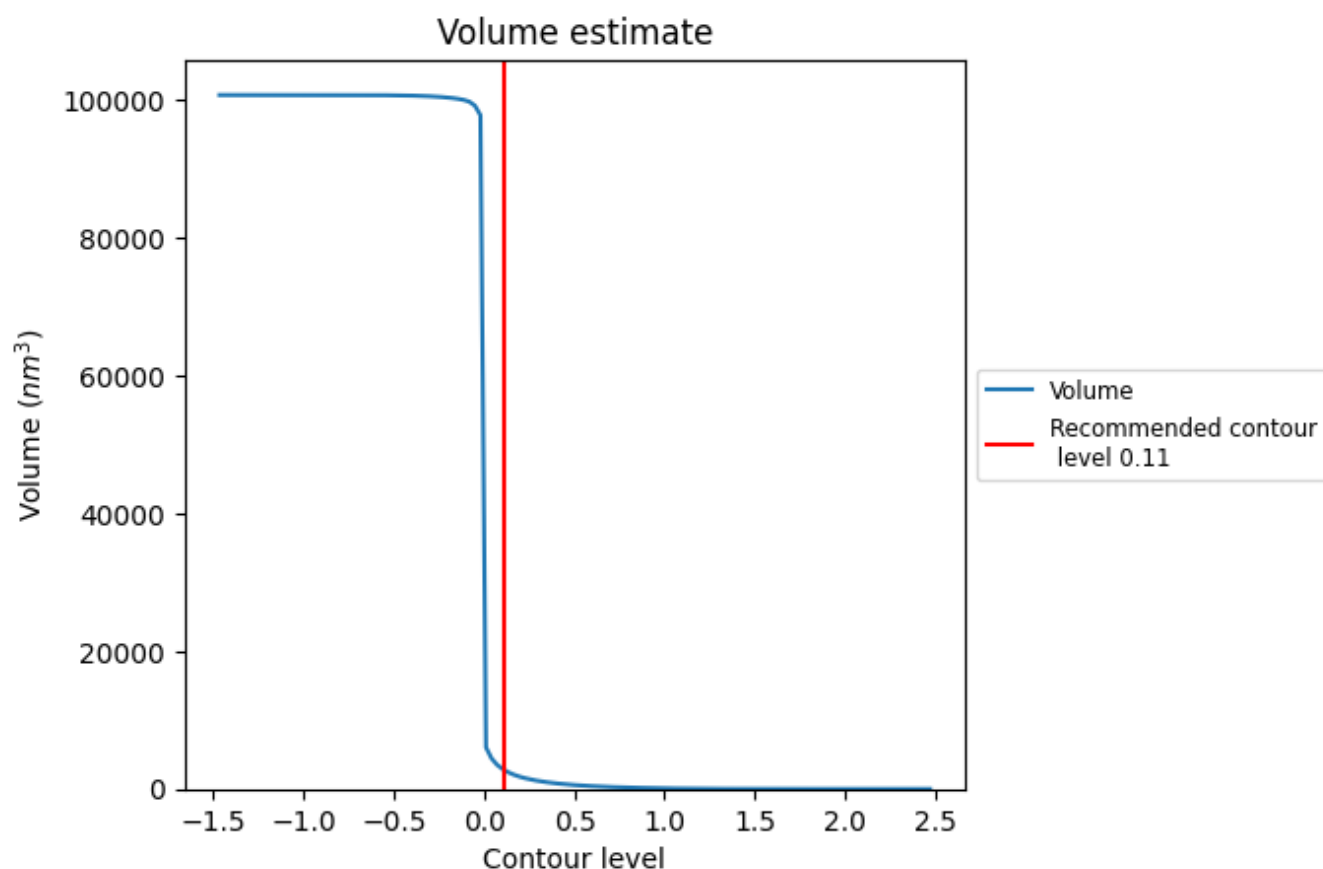
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

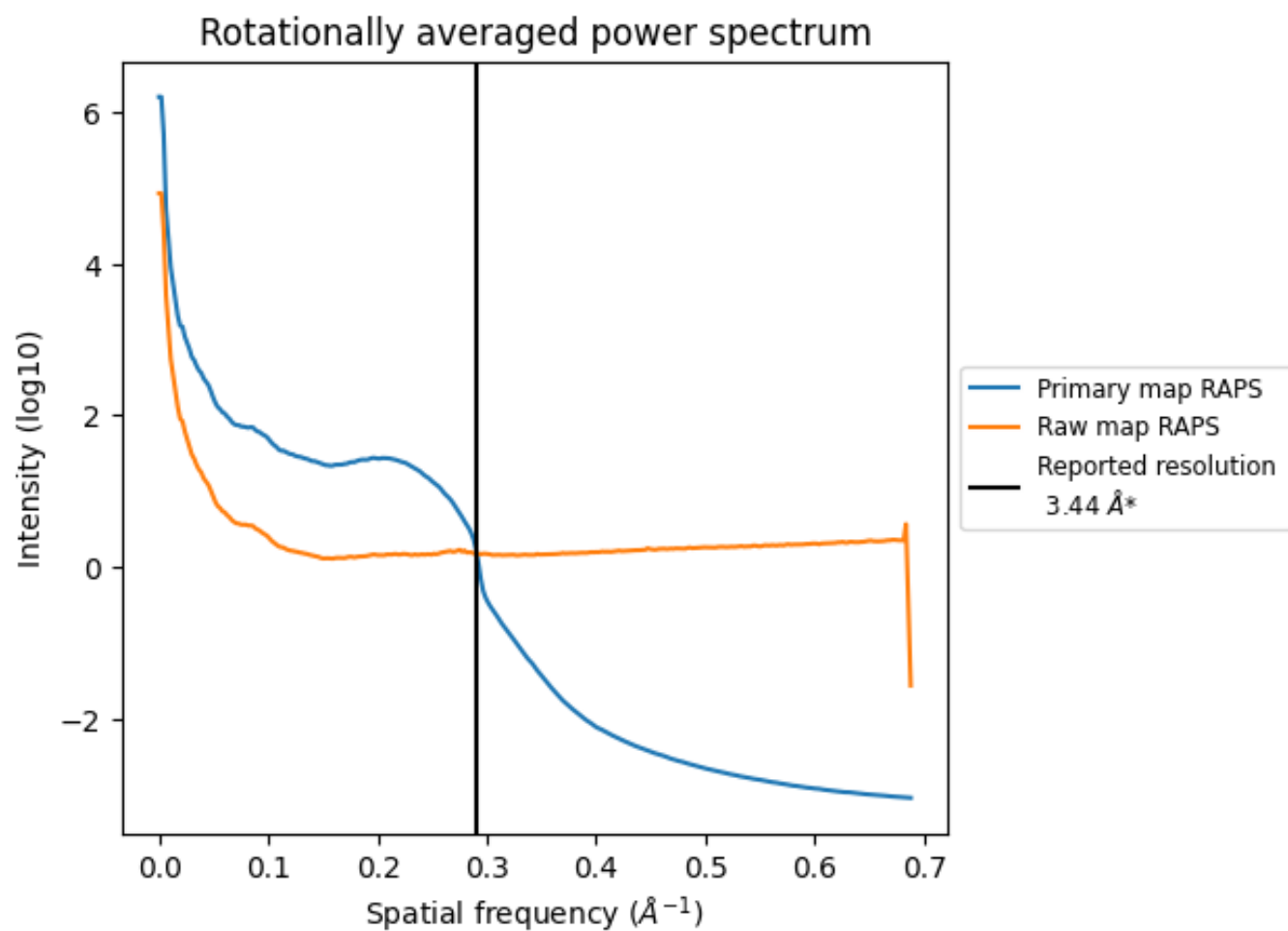
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2790 nm^3 ; this corresponds to an approximate mass of 2521 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 [i](#)

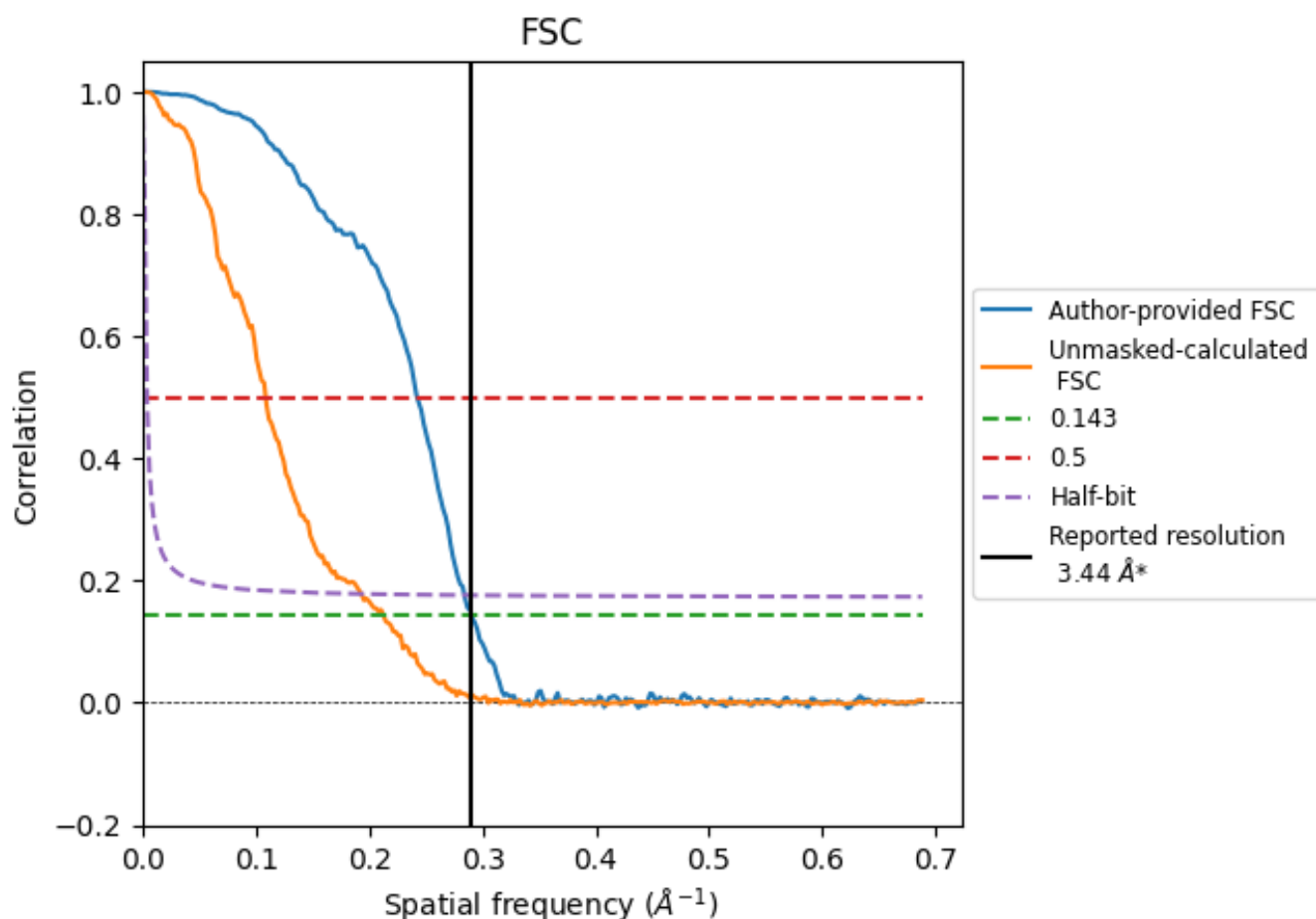


*Reported resolution corresponds to spatial frequency of $0.291 \text{ \AA}^{-1}$

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 $0.291 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

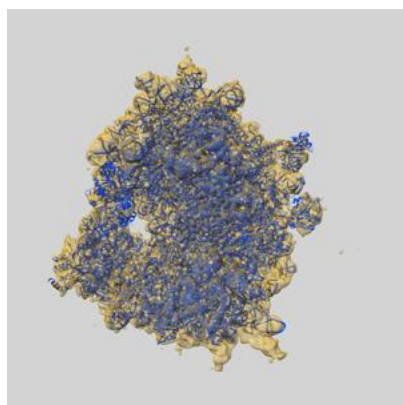
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.44	-	-
Author-provided FSC curve	3.44	4.13	3.52
Unmasked-calculated*	4.70	9.18	5.18

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.70 differs from the reported value 3.44 by more than 10 %

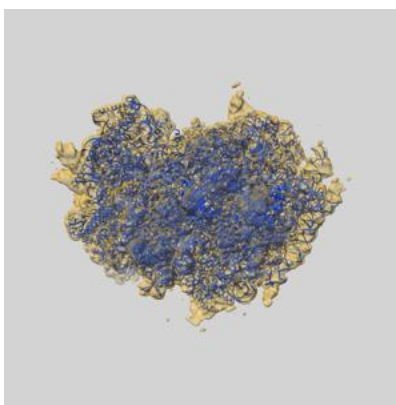
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-55616 and PDB model 9T6I. Per-residue inclusion information can be found in section 3 on page 21.

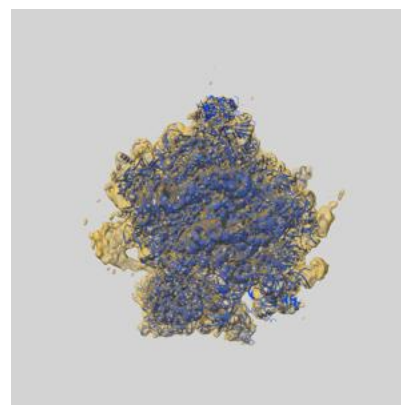
9.1 Map-model overlay [i](#)



X



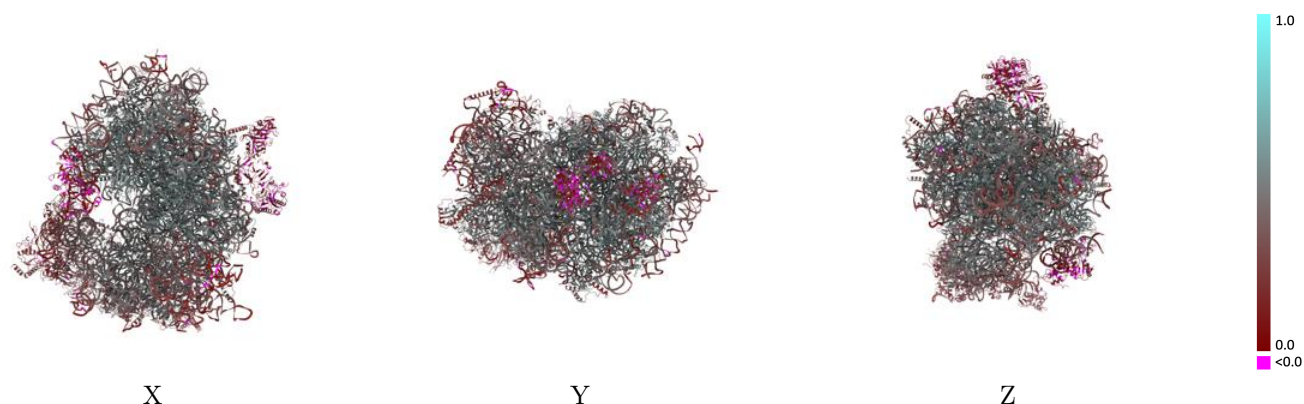
Y



Z

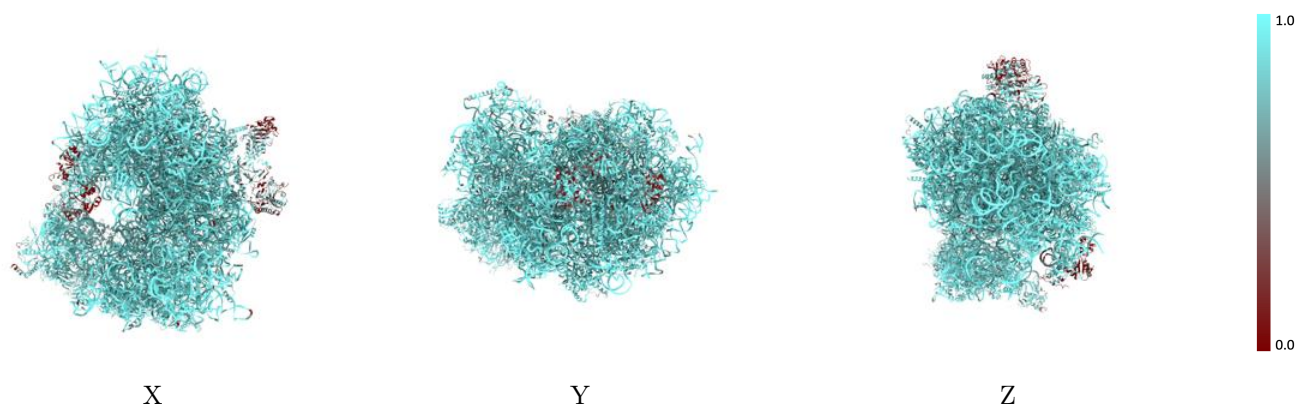
The images above show the 3D surface view of the map at the recommended contour level 0.11 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



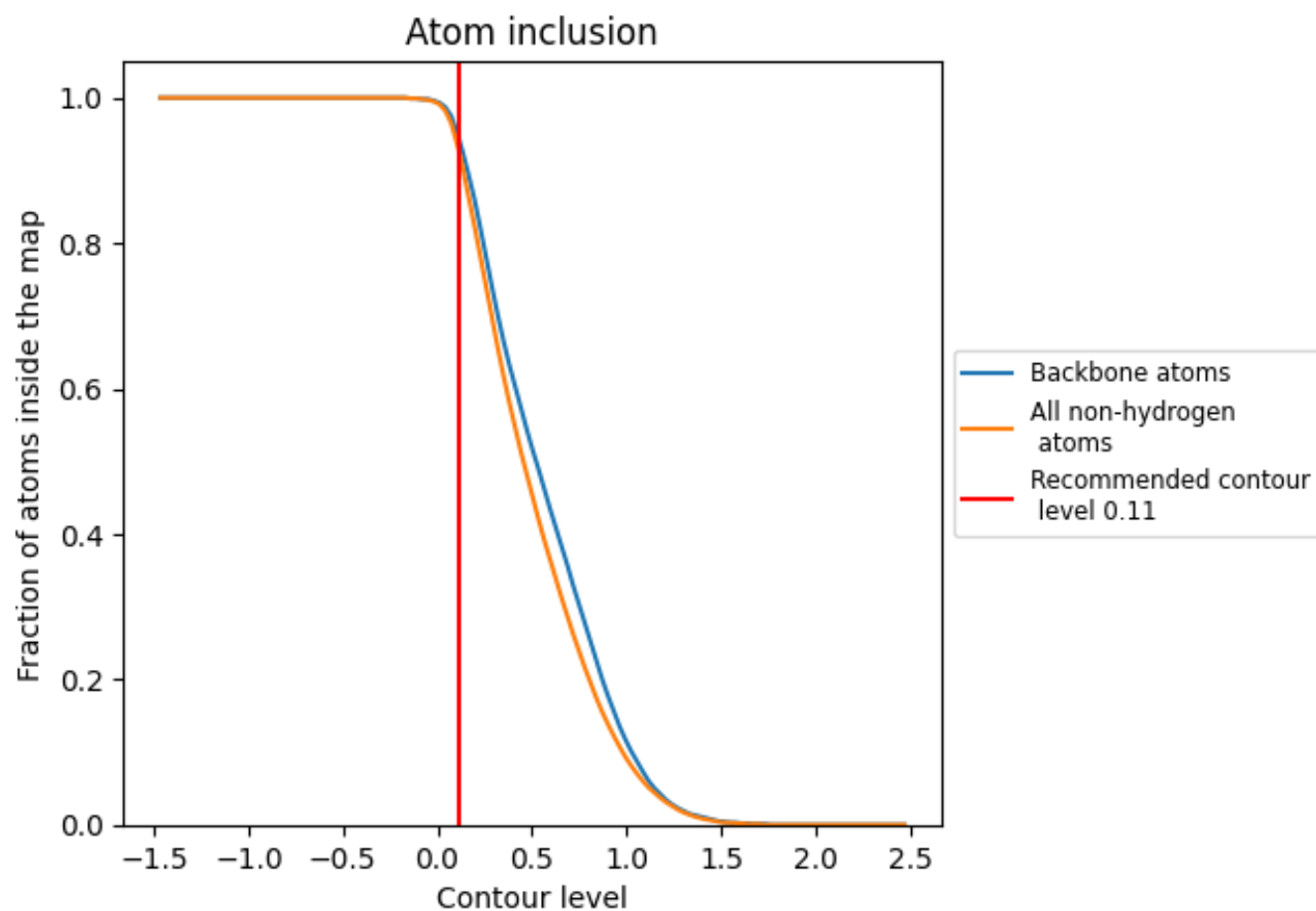
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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 (0.11).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 93% 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 (0.11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9310	 0.4150
L5	 0.9660	 0.4380
L7	 0.9840	 0.4790
L8	 0.9620	 0.4470
LA	 0.9580	 0.5390
LB	 0.9560	 0.5150
LC	 0.9530	 0.5170
LD	 0.9560	 0.4540
LE	 0.9640	 0.4760
LF	 0.9560	 0.5170
LG	 0.9140	 0.4410
LH	 0.9590	 0.4950
LI	 0.9620	 0.5130
LJ	 0.9380	 0.4220
LL	 0.9390	 0.4890
LM	 0.9630	 0.4940
LN	 0.9560	 0.5390
LO	 0.9470	 0.5150
LP	 0.9510	 0.5290
LQ	 0.9610	 0.5310
LR	 0.9210	 0.4620
LS	 0.9690	 0.5350
LT	 0.9450	 0.4970
LU	 0.9540	 0.4450
LV	 0.9570	 0.5210
LW	 0.8490	 0.3480
LX	 0.9160	 0.4860
LY	 0.9470	 0.5010
LZ	 0.9690	 0.4920
La	 0.9630	 0.5250
Lb	 0.8990	 0.4290
Lc	 0.9370	 0.4880
Ld	 0.9310	 0.4900
Le	 0.9630	 0.5370
Lf	 0.9620	 0.5490



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Chain	Atom inclusion	Q-score
Lg	 0.9450	 0.5070
Lh	 0.9380	 0.4770
Li	 0.9400	 0.4740
Lj	 0.9560	 0.5390
Lk	 0.9160	 0.4310
Ll	 0.9670	 0.5340
Lm	 0.9380	 0.5020
Ln	 0.6080	 0.3140
Lo	 0.9340	 0.5000
Lp	 0.9420	 0.5140
Lr	 0.9610	 0.5200
Ls	 0.2890	 0.0790
Lt	 0.4610	 0.0700
MA	 0.4400	 0.0790
N4	 0.6070	 0.1370
NA	 0.4820	 0.1120
NB	 0.7060	 0.1800
S2	 0.9660	 0.3790
SA	 0.9210	 0.4150
SB	 0.9080	 0.4160
SC	 0.9420	 0.4420
SD	 0.8490	 0.3060
SE	 0.9290	 0.4310
SF	 0.8680	 0.2700
SG	 0.9010	 0.3100
SH	 0.9020	 0.3600
SI	 0.9210	 0.4330
SJ	 0.9050	 0.3940
SK	 0.8690	 0.2220
SL	 0.9020	 0.4640
SM	 0.7190	 0.2150
SN	 0.9370	 0.4710
SO	 0.9080	 0.4220
SP	 0.8200	 0.2280
SQ	 0.9040	 0.3010
SR	 0.8910	 0.3350
SS	 0.8590	 0.2340
ST	 0.8890	 0.2610
SU	 0.8950	 0.3000
SV	 0.9520	 0.4310
SW	 0.9300	 0.4750
SX	 0.9390	 0.4800

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Chain	Atom inclusion	Q-score
SY	 0.9300	 0.3540
SZ	 0.8410	 0.2120
Sa	 0.9160	 0.4620
Sb	 0.9470	 0.4330
Sc	 0.9280	 0.3340
Sd	 0.8980	 0.3140
Se	 0.8940	 0.3770
Sf	 0.7290	 0.1530
Sg	 0.8930	 0.2180