



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 09:15 PM UTC

PDB ID : 6ZM7 / pdb_00006zm7
EMDB ID : EMD-11288
Title : SARS-CoV-2 Nsp1 bound to the human CCDC124-80S-EBP1 ribosome complex
Authors : Thoms, M.; Buschauer, R.; Ameismeier, M.; Denk, T.; Kratzat, H.; Mackens-Kiani, T.; Cheng, J.; Berninghausen, O.; Becker, T.; Beckmann, R.
Deposited on : 2020-07-01
Resolution : 2.70 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

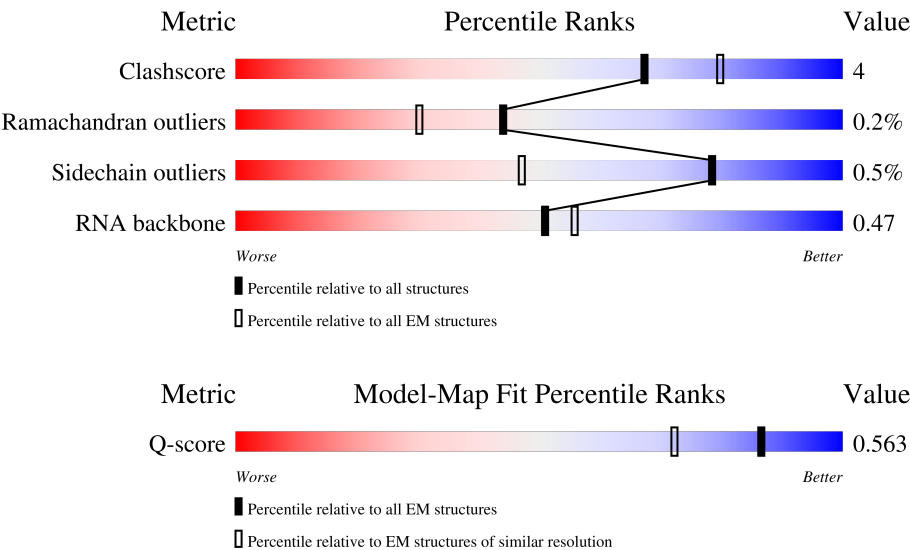
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.70 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.



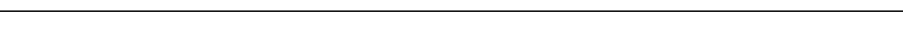
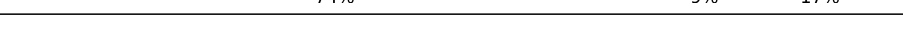
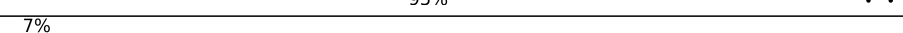
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10327 (2.20 - 3.20)

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	5066	
2	L7	121	
3	L8	157	

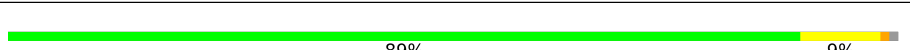
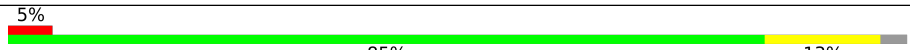
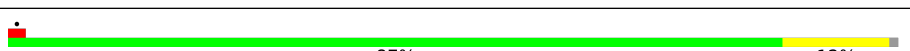
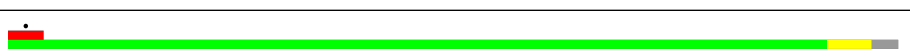
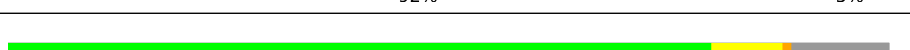
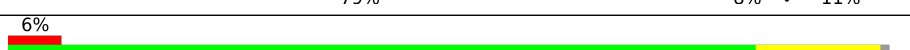
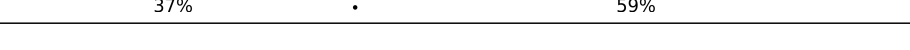
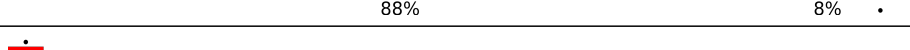
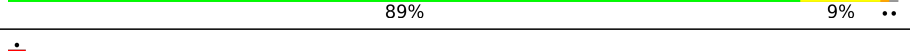
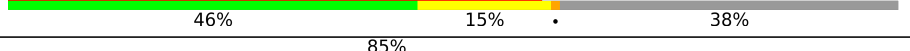
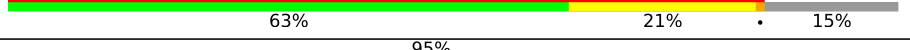
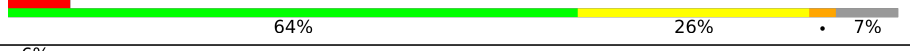
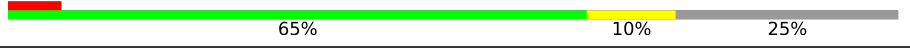
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Mol	Chain	Length	Quality of chain
4	LA	257	
5	LB	403	
6	LC	427	
7	LD	297	
8	LE	288	
9	LF	248	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	215	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	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

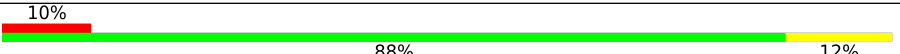
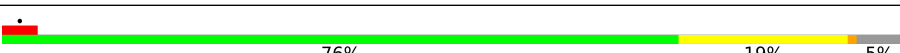
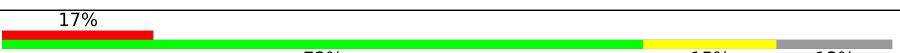
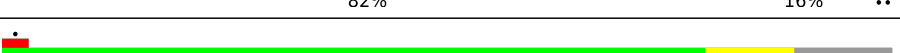
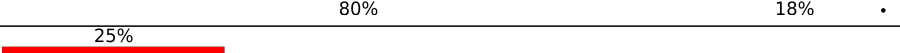
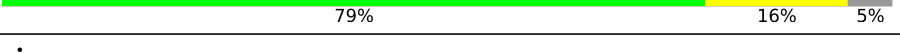
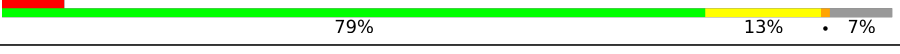
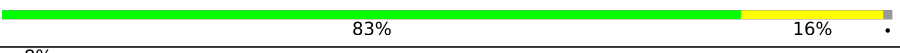
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Mol	Chain	Length	Quality of chain
29	La	148	
30	Lb	159	
31	Lc	115	
32	Ld	125	
33	Le	135	
34	Lf	110	
35	Lg	117	
36	Lh	123	
37	Li	105	
38	Lj	97	
39	Lk	70	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	Lr	137	
46	Ls	317	
47	Lt	165	
48	Lz	217	
49	S2	1869	
50	SA	295	
51	SB	264	
52	SD	243	
53	SE	263	

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Mol	Chain	Length	Quality of chain
54	SF	204	
55	SH	194	
56	SI	208	
57	SK	165	
58	SL	158	
59	SP	145	
60	SQ	146	
61	SR	135	
62	SS	152	
63	ST	145	
64	SU	119	
65	SV	83	
66	SX	143	
67	Sa	115	
68	Sc	69	
69	Sd	56	
70	Sg	317	
71	SC	293	
72	SG	249	
73	SJ	194	
74	SM	132	
75	SN	151	
76	SO	151	
77	SW	130	
78	SY	133	

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Mol	Chain	Length	Quality of chain
79	SZ	125	
80	Sb	84	
81	Se	59	
82	Sf	156	
83	CA	394	
84	CC	75	
85	CE	223	
86	CF	180	

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 225534 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L5	3773	Total	C	N	O	P	0	0
			80138	35655	14589	26122	3772		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LA	248	Total	C	N	O	S	0	0
			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	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LF	225	Total	C	N	O	S	0	0
			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-like.

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	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	101	Total	C	N	O	S	0	0
			825	529	144	150	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	134	Total	C	N	O	S	0	0
			1115	700	226	186	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
			876	546	189	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 60S ribosomal protein L37.

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 Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lm	52	Total	C	N	O	S	0	0
			429	266	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 60S ribosomal protein L12.

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 60S ribosomal protein L10a.

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

- Molecule 49 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S2	1740	Total	C	N	O	P	0	0
			36899	16459	6598	12103	1739		

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

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

- Molecule 51 is a protein called 40S ribosomal protein S3a.

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

- Molecule 52 is a protein called 40S ribosomal protein S3.

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

- Molecule 53 is a protein called 40S ribosomal protein S4, X isoform.

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

- Molecule 54 is a protein called 40S ribosomal protein S5.

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

- Molecule 55 is a protein called 40S ribosomal protein S7.

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

- Molecule 56 is a protein called 40S ribosomal protein S8.

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

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

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

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

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

- Molecule 59 is a protein called 40S ribosomal protein S15.

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

- Molecule 60 is a protein called 40S ribosomal protein S16.

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

- Molecule 61 is a protein called 40S ribosomal protein S17.

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

- Molecule 62 is a protein called 40S ribosomal protein S18.

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

- Molecule 63 is a protein called 40S ribosomal protein S19.

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

- Molecule 64 is a protein called 40S ribosomal protein S20.

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

- Molecule 65 is a protein called 40S ribosomal protein S21.

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

- Molecule 66 is a protein called 40S ribosomal protein S23.

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

- Molecule 67 is a protein called 40S ribosomal protein S26.

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

- Molecule 68 is a protein called 40S ribosomal protein S28.

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

- Molecule 69 is a protein called 40S ribosomal protein S29.

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

- Molecule 70 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 71 is a protein called 40S ribosomal protein S2.

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

- Molecule 72 is a protein called 40S ribosomal protein S6.

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

- Molecule 73 is a protein called 40S ribosomal protein S9.

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

- Molecule 74 is a protein called 40S ribosomal protein S12.

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

- Molecule 75 is a protein called 40S ribosomal protein S13.

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

- Molecule 76 is a protein called 40S ribosomal protein S14.

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

- Molecule 77 is a protein called 40S ribosomal protein S15a.

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

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

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

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

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

- Molecule 80 is a protein called 40S ribosomal protein 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 S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Se	58	Total	C	N	O	S	0	0
			439	268	97	73	1		

- Molecule 82 is a protein called Ubiquitin-40S ribosomal protein S27a.

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

- Molecule 83 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	CA	354	Total	C	N	O	S	4	0
			2764	1744	475	528	17		

- Molecule 84 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	CC	75	Total	C	N	O	P	0	0
			1589	710	279	525	75		

- Molecule 85 is a protein called Coiled-coil domain-containing protein 124.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	CE	124	Total	C	N	O	S	0	0
			1043	637	208	194	4		

- Molecule 86 is a protein called Non-structural protein 1.

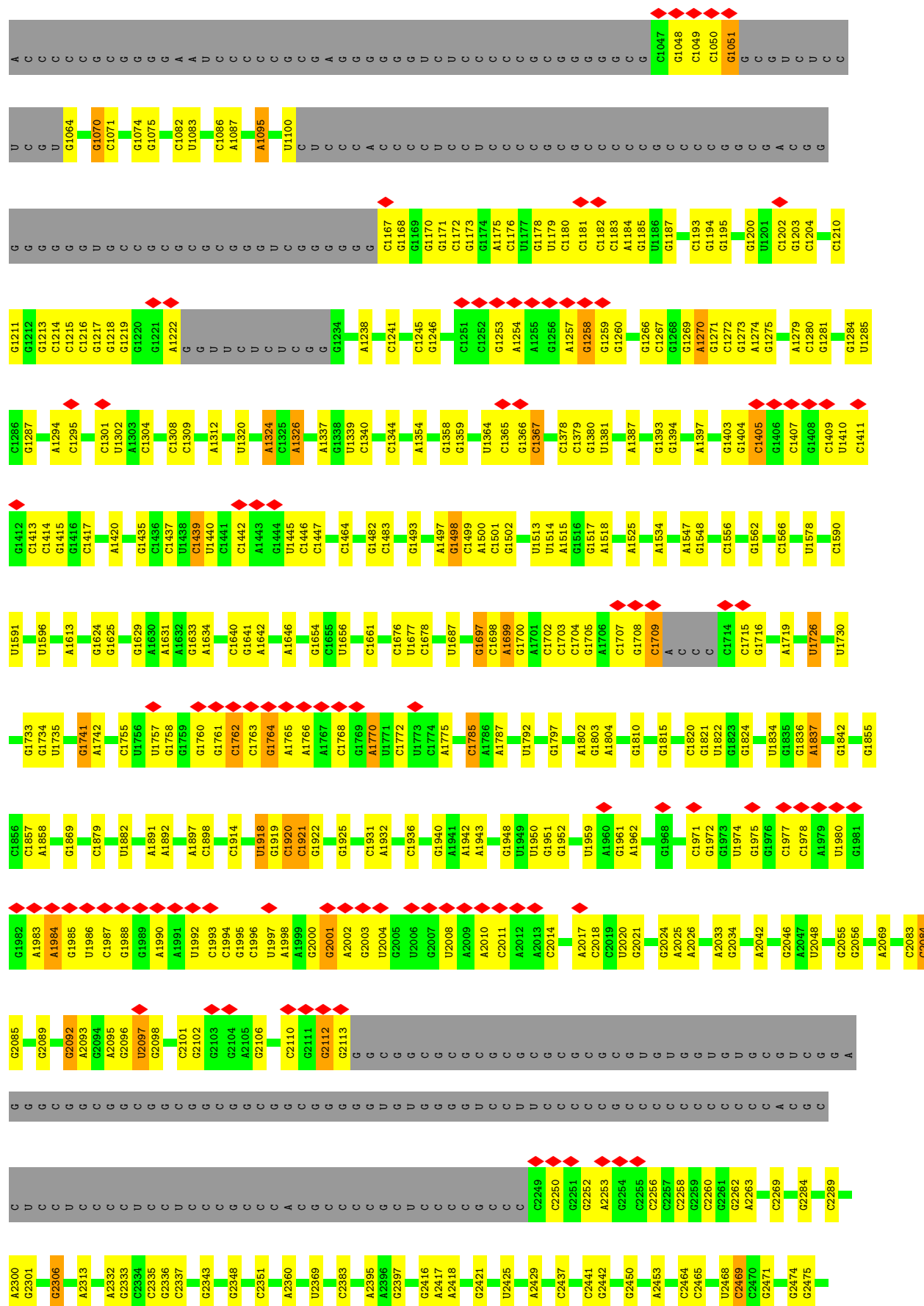
Mol	Chain	Residues	Atoms					AltConf	Trace
86	CF	29	Total	C	N	O	S	0	0
			239	145	43	50	1		

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

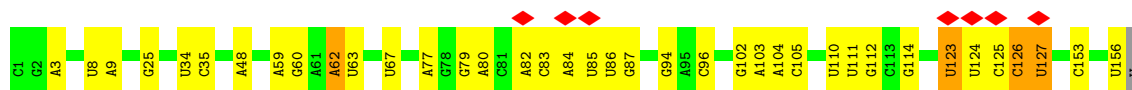
Mol	Chain	Residues	Atoms		AltConf
87	L5	212	Total	Mg	0
			212	212	
87	L7	3	Total	Mg	0
			3	3	
87	L8	4	Total	Mg	0
			4	4	
87	LA	1	Total	Mg	0
			1	1	
87	LI	1	Total	Mg	0
			1	1	
87	LP	1	Total	Mg	0
			1	1	
87	LT	1	Total	Mg	0
			1	1	
87	LV	1	Total	Mg	0
			1	1	
87	Le	1	Total	Mg	0
			1	1	
87	Lg	1	Total	Mg	0
			1	1	
87	S2	29	Total	Mg	0
			29	29	
87	SG	1	Total	Mg	0
			1	1	

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

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

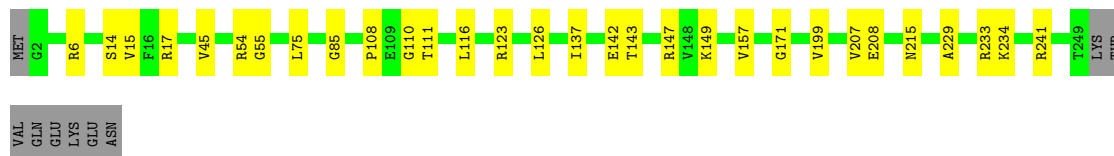






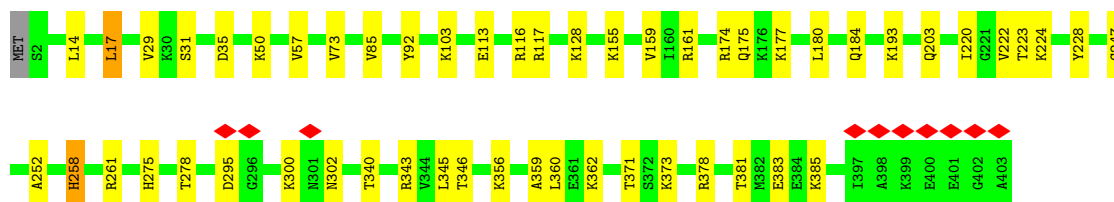
- Molecule 4: 60S ribosomal protein L8

Chain LA: 85% 12%



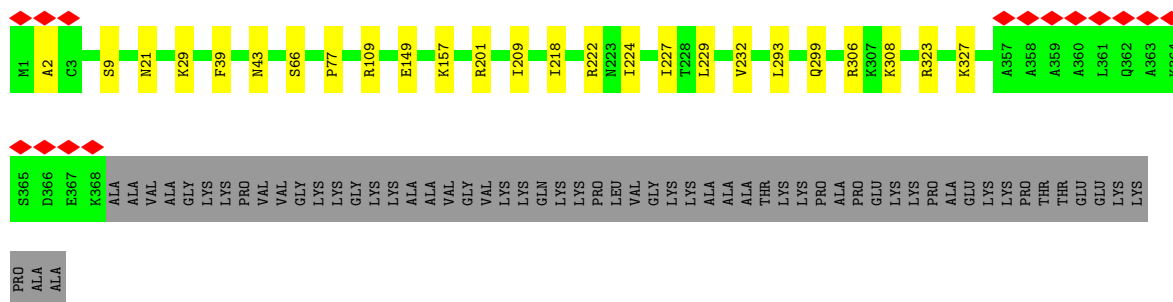
- Molecule 5: 60S ribosomal protein L3

Chain LB: 87% 13%



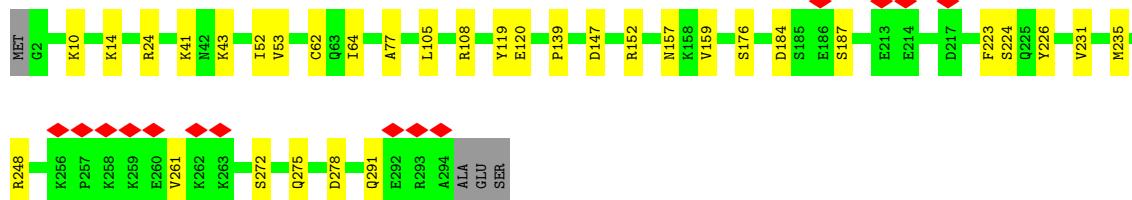
- Molecule 6: 60S ribosomal protein L4

Chain LC: 80% 6% 14%



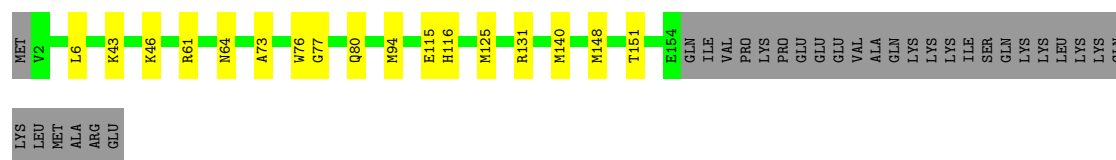
- Molecule 7: 60S ribosomal protein L5

Chain LD: 5% 88% 11%

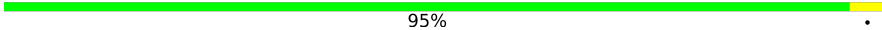


- Molecule 8: 60S ribosomal protein L6

Chain LP:  74% 9% 17%



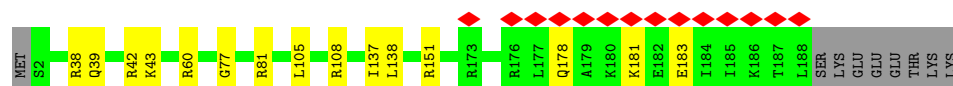
- Molecule 19: 60S ribosomal protein L18

Chain LQ:  95% . .



- Molecule 20: 60S ribosomal protein L19

Chain LR:  7% 88% 8% 5%



- Molecule 21: 60S ribosomal protein L18a

Chain LS:  86% 13% .



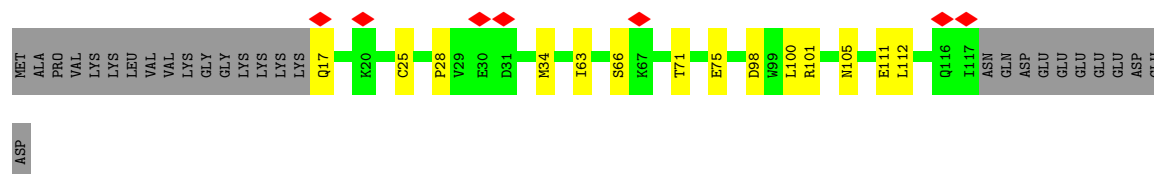
- Molecule 22: 60S ribosomal protein L21

Chain LT:  87% 12% ..



- Molecule 23: 60S ribosomal protein L22

Chain LU:  5% 68% 11% 21%

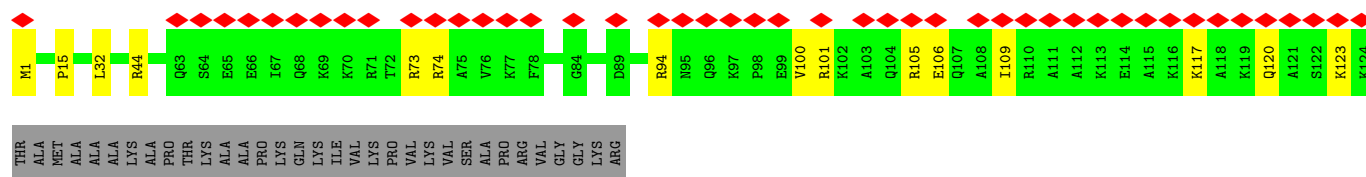
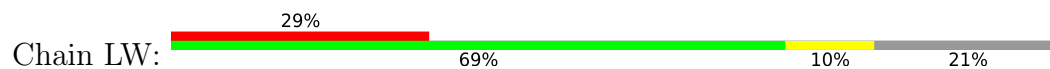


- Molecule 24: 60S ribosomal protein L23

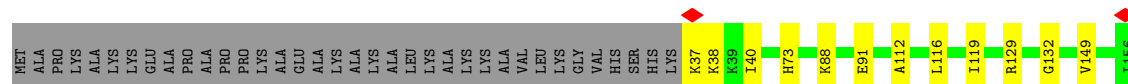
Chain LV:  84% 10% 6%



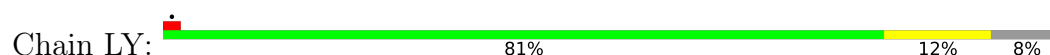
- Molecule 25: 60S ribosomal protein L24



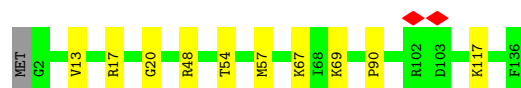
- Molecule 26: 60S ribosomal protein L23a



- Molecule 27: 60S ribosomal protein L26



- Molecule 28: 60S ribosomal protein L27

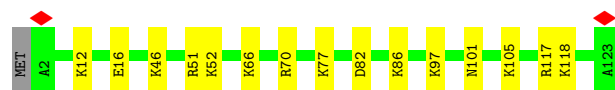


- Molecule 29: 60S ribosomal protein L27a



- Molecule 30: 60S ribosomal protein L29

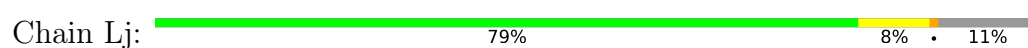




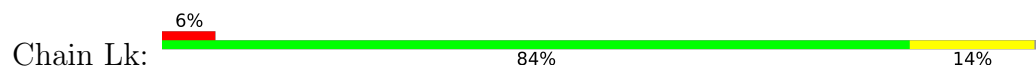
- Molecule 37: 60S ribosomal protein L36



- Molecule 38: 60S ribosomal protein L37



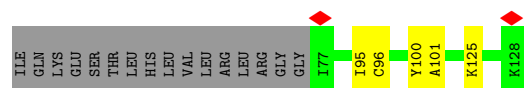
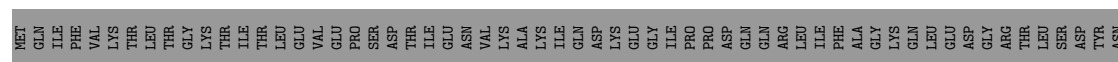
- Molecule 39: 60S ribosomal protein L38



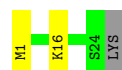
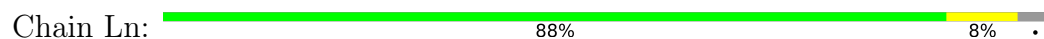
- Molecule 40: 60S ribosomal protein L39



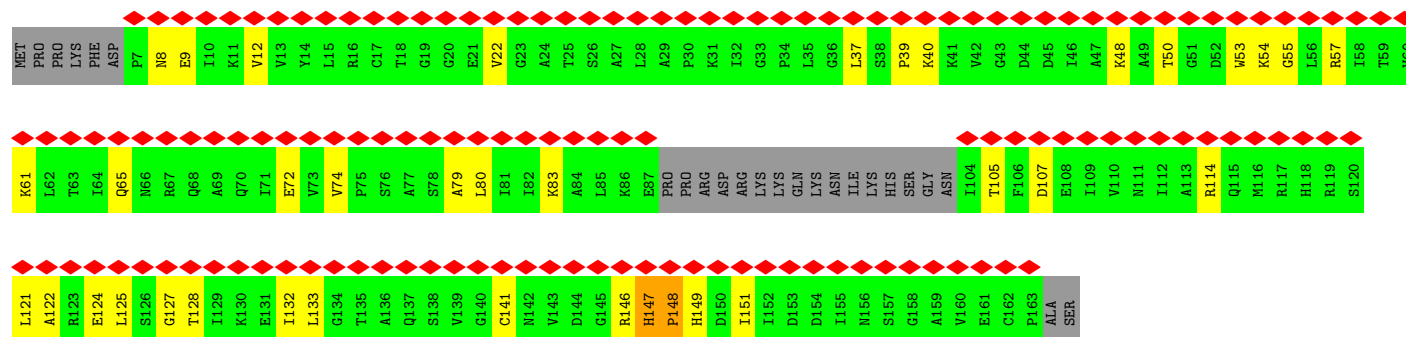
- Molecule 41: Ubiquitin-60S ribosomal protein L40



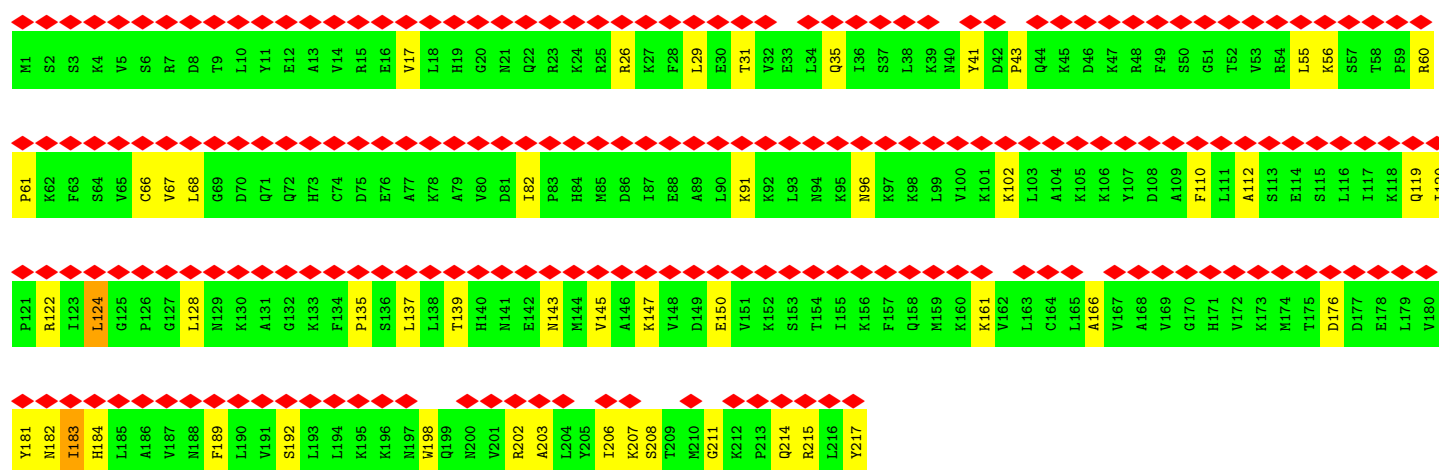
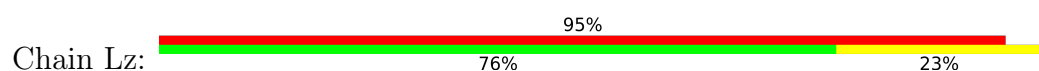
- Molecule 42: 60S ribosomal protein L41



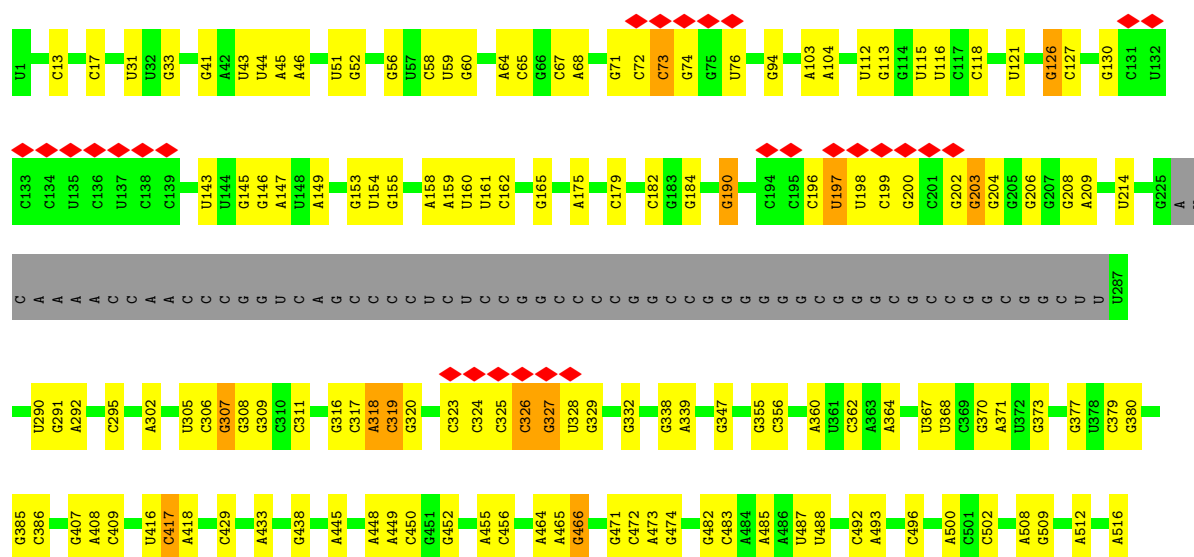
- Chain Lt: 63% 21% 15% 5%

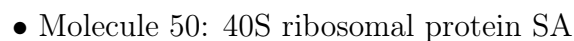


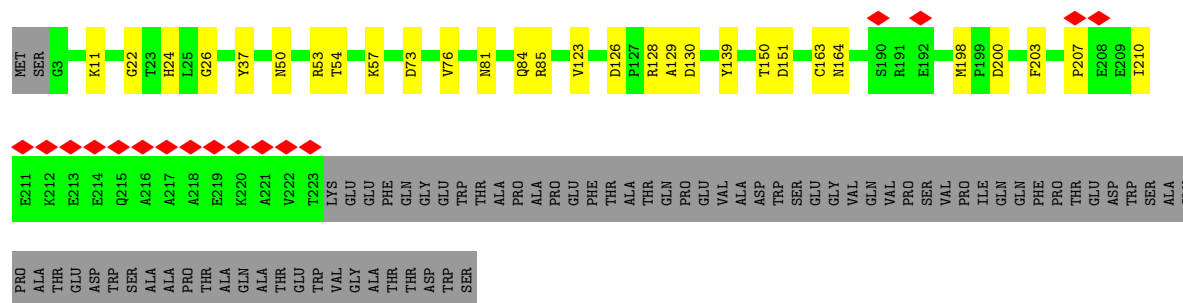
• Molecule 48: 60S ribosomal protein L10a



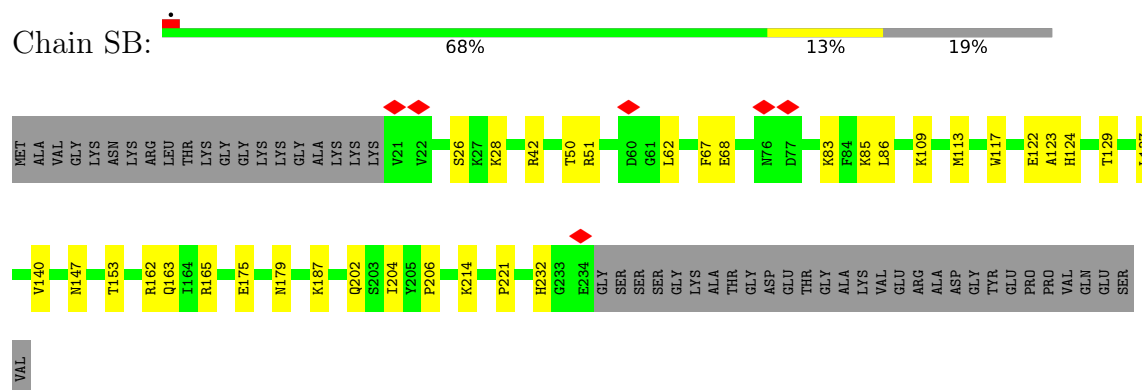
• Molecule 49: 18S ribosomal RNA



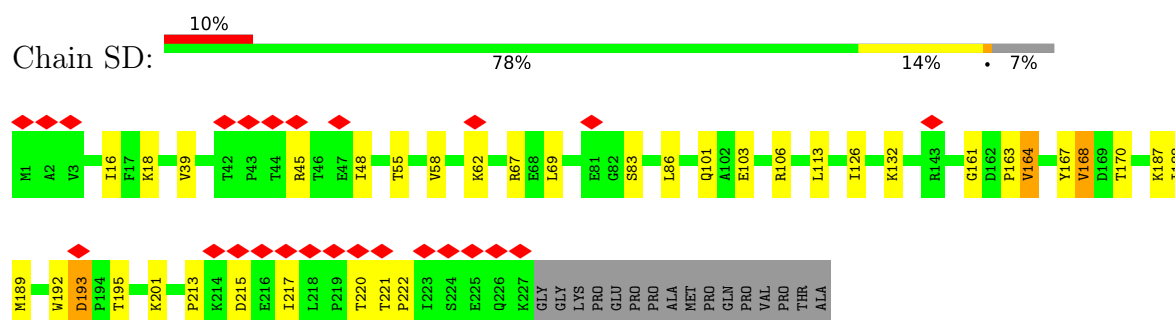




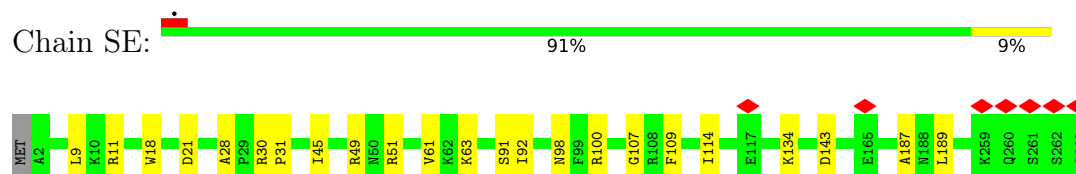
- Molecule 51: 40S ribosomal protein S3a



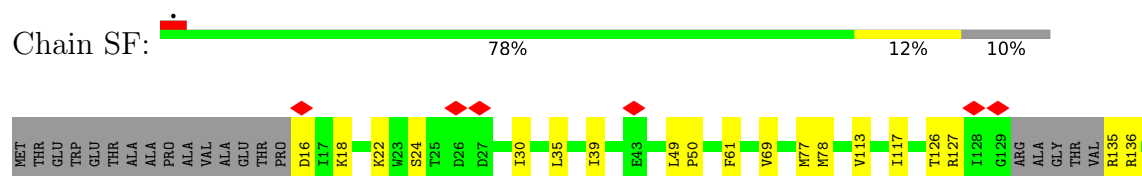
- Molecule 52: 40S ribosomal protein S3



- Molecule 53: 40S ribosomal protein S4, X isoform



- Molecule 54: 40S ribosomal protein S5





ILE
PRO
LEU
LYS

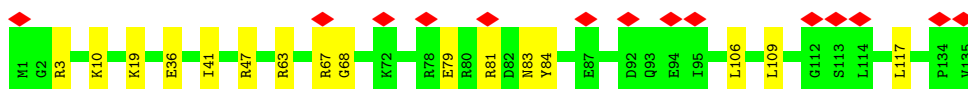
- Molecule 60: 40S ribosomal protein S16

Chain SQ: 5% 78% 18% ..



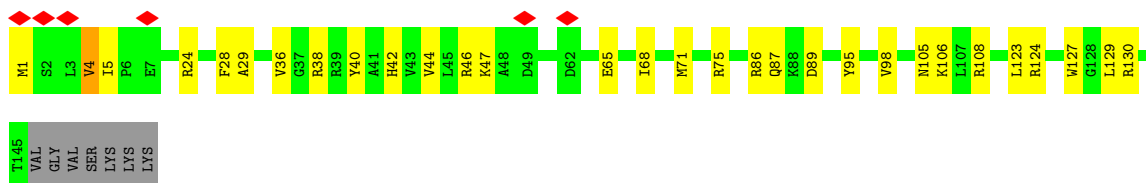
- Molecule 61: 40S ribosomal protein S17

Chain SR: 10% 88% 12%



- Molecule 62: 40S ribosomal protein S18

Chain SS: 76% 19% 5%



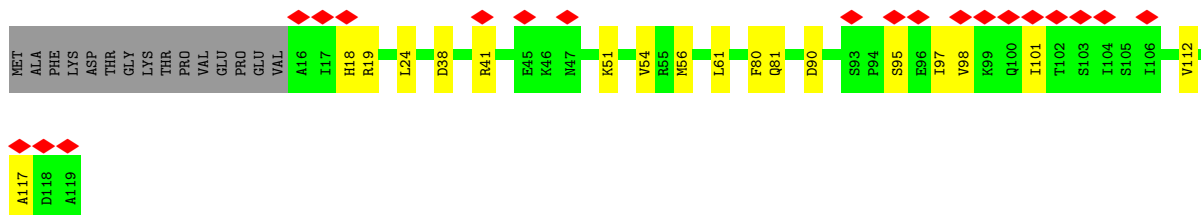
- Molecule 63: 40S ribosomal protein S19

Chain ST: 6% 81% 17%



- Molecule 64: 40S ribosomal protein S20

Chain SU: 17% 72% 15% 13%

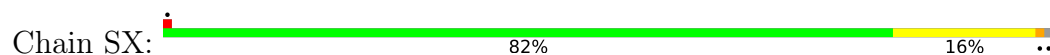


- Molecule 65: 40S ribosomal protein S21

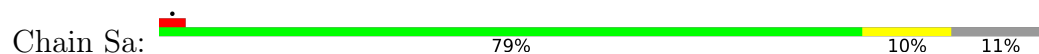
Chain SV: 83% 17%



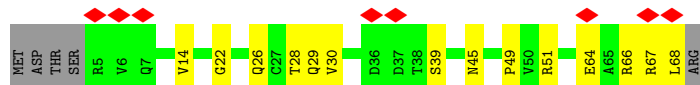
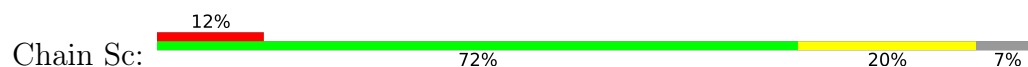
- Molecule 66: 40S ribosomal protein S23



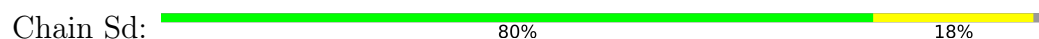
- Molecule 67: 40S ribosomal protein S26



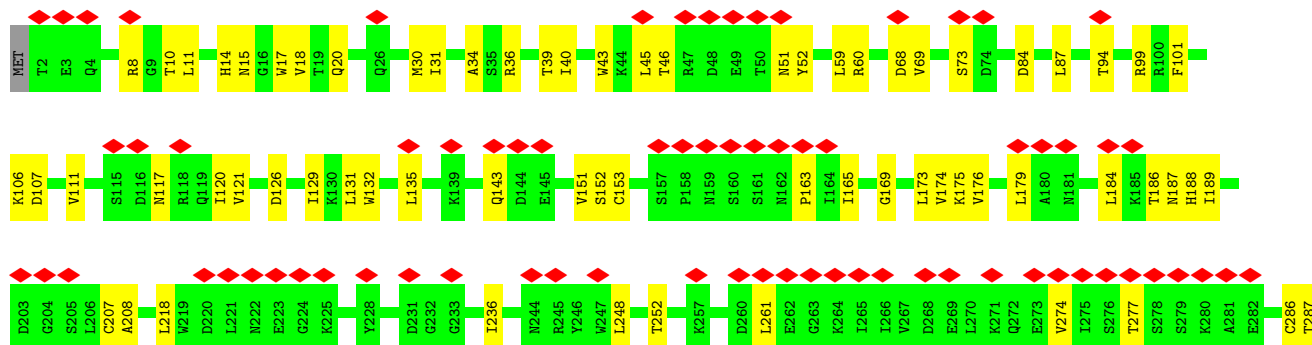
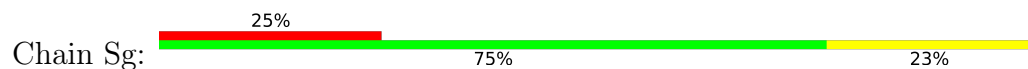
- Molecule 68: 40S ribosomal protein S28



- Molecule 69: 40S ribosomal protein S29

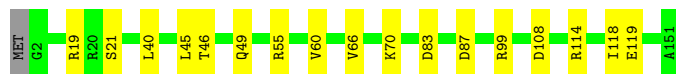


- Molecule 70: Receptor of activated protein C kinase 1



- Molecule 75: 40S ribosomal protein S13

Chain SN:  88% 11%



- Molecule 76: 40S ribosomal protein S14

Chain SO:  7% 79% 13% 7%



- Molecule 77: 40S ribosomal protein S15a

Chain SW:  83% 16%

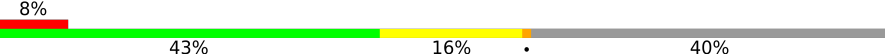


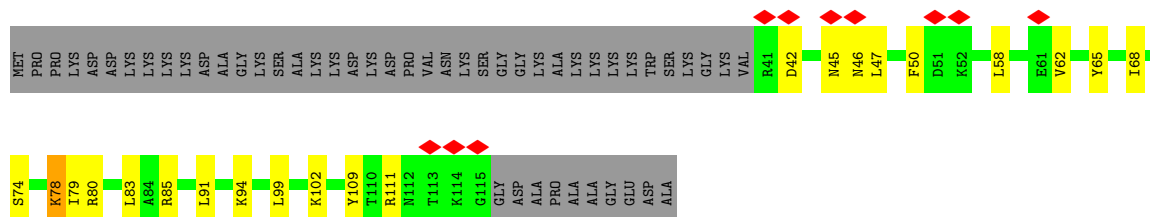
- Molecule 78: 40S ribosomal protein S24

Chain SY:  8% 80% 18% ..



- Molecule 79: 40S ribosomal protein S25

Chain SZ:  8% 43% 16% 40%

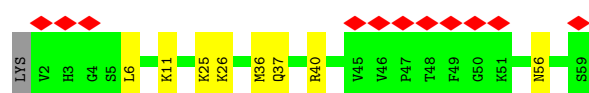


- Molecule 80: 40S ribosomal protein S27

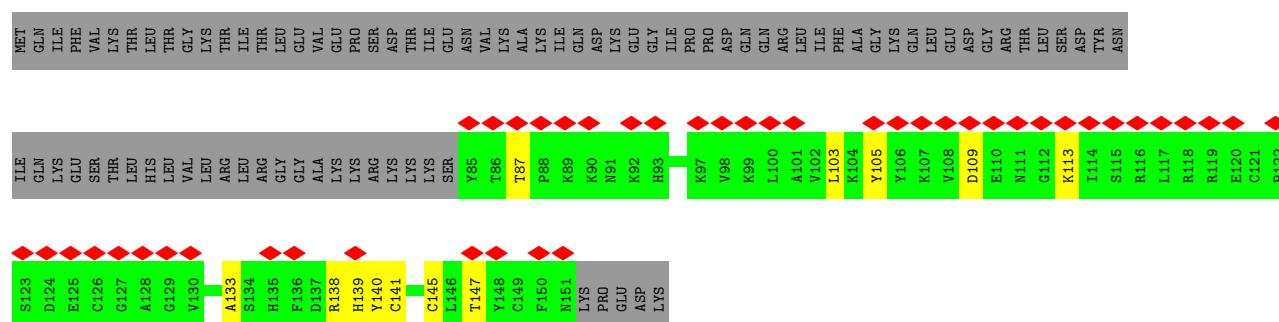
Chain Sb:  10% 88% 11%



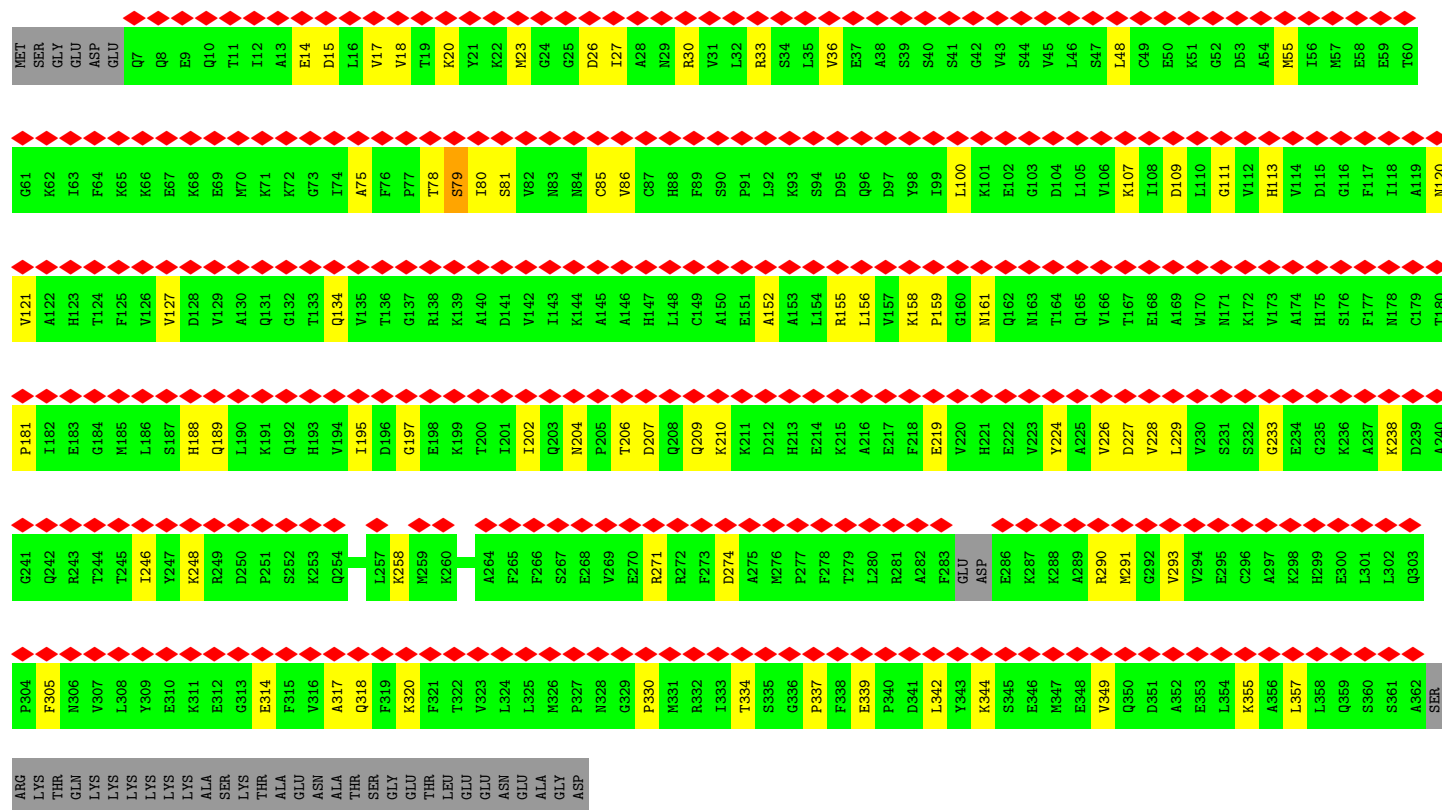
- Molecule 81: 40S ribosomal protein S30



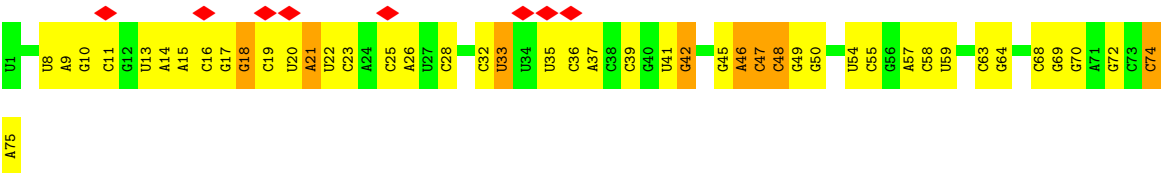
Chain Sf: 29% 35% 8% 57%



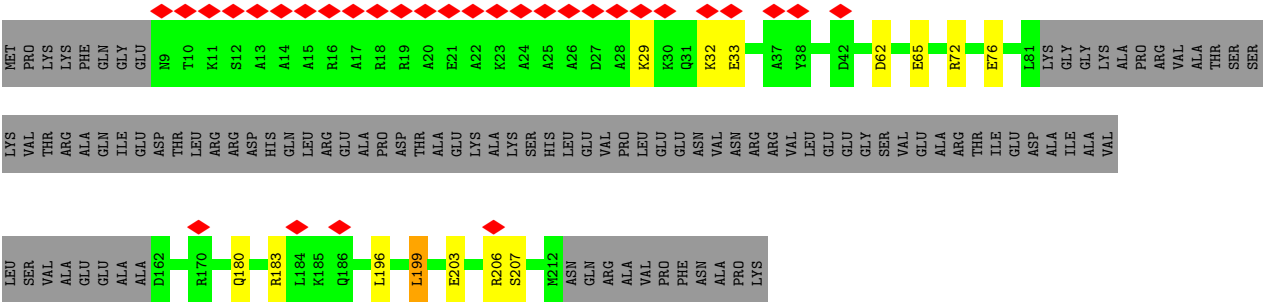
Chain CA:



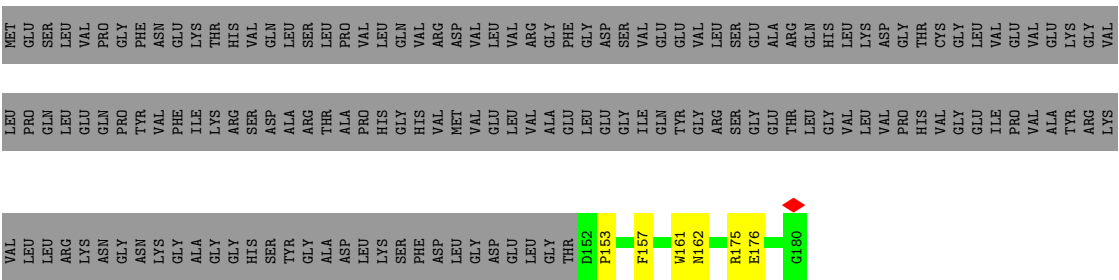
Chain CC:



● Molecule 85: Coiled-coil domain-containing protein 124



● Molecule 86: Non-structural protein 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	52512	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.527	Depositor
Minimum map value	-0.124	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.06	Depositor
Map size ($\text{\AA}$)	423.6, 423.6, 423.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.059, 1.059, 1.059	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	L5	0.37	0/89595	0.43	13/139686 (0.0%)
2	L7	0.34	0/2861	0.37	0/4459
3	L8	0.37	0/3701	0.38	0/5766
4	LA	0.39	0/1936	0.70	4/2596 (0.2%)
5	LB	0.35	0/3306	0.61	0/4424
6	LC	0.37	0/2981	0.63	2/4002 (0.0%)
7	LD	0.29	0/2428	0.57	2/3252 (0.1%)
8	LE	0.29	0/1942	0.62	0/2606
9	LF	0.36	0/1905	0.59	2/2539 (0.1%)
10	LG	0.32	0/1960	0.58	1/2637 (0.0%)
11	LH	0.32	0/1537	0.57	0/2066
12	LI	0.32	0/1673	0.57	0/2233
13	LJ	0.28	0/1433	0.70	1/1915 (0.1%)
14	LL	0.33	0/1732	0.61	1/2315 (0.0%)
15	LM	0.32	0/1161	0.64	2/1554 (0.1%)
16	LN	0.39	0/1746	0.63	0/2338
17	LO	0.34	0/1682	0.49	0/2250
18	LP	0.34	0/1268	0.56	0/1701
19	LQ	0.35	0/1537	0.55	0/2052
20	LR	0.33	0/1582	0.57	2/2091 (0.1%)
21	LS	0.33	0/1493	0.52	0/2003
22	LT	0.34	0/1326	0.62	0/1770
23	LU	0.31	0/839	0.77	2/1126 (0.2%)
24	LV	0.33	0/993	0.58	0/1332
25	LW	0.28	0/1030	0.53	0/1364
26	LX	0.32	0/1002	0.52	0/1345
27	LY	0.32	0/1132	0.55	0/1504
28	LZ	0.32	0/1130	0.54	0/1507
29	La	0.35	0/1191	0.55	0/1591
30	Lb	0.29	0/889	0.62	0/1175
31	Lc	0.34	0/774	0.60	0/1038
32	Ld	0.32	0/903	0.53	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.36	0/1071	0.61	0/1429
34	Lf	0.39	0/895	0.67	0/1198
35	Lg	0.34	0/916	0.57	0/1220
36	Lh	0.29	0/1023	0.47	0/1351
37	Li	0.26	0/843	0.48	0/1115
38	Lj	0.39	0/720	0.68	0/952
39	Lk	0.28	0/575	0.55	0/761
40	Ll	0.36	0/454	0.63	0/599
41	Lm	0.34	0/435	0.62	0/575
42	Ln	0.30	0/231	0.52	0/294
43	Lo	0.32	0/876	0.49	0/1156
44	Lp	0.35	0/718	0.51	0/953
45	Lr	0.34	0/1017	0.59	0/1364
46	Ls	0.25	0/1519	0.64	0/2052
47	Lt	0.36	0/1058	0.94	4/1430 (0.3%)
48	Lz	0.26	0/1769	0.67	0/2371
49	S2	0.33	0/41245	0.41	5/64265 (0.0%)
50	SA	0.32	0/1778	0.61	0/2416
51	SB	0.29	0/1765	0.58	0/2362
52	SD	0.28	0/1793	0.64	0/2414
53	SE	0.29	0/2118	0.61	2/2849 (0.1%)
54	SF	0.30	0/1481	0.59	0/1988
55	SH	0.32	0/1519	0.66	0/2033
56	SI	0.31	0/1715	0.59	0/2287
57	SK	0.24	0/851	0.55	0/1147
58	SL	0.33	0/1268	0.55	0/1696
59	SP	0.26	0/1082	0.69	2/1446 (0.1%)
60	SQ	0.29	0/1160	0.67	0/1553
61	SR	0.26	0/1105	0.64	0/1484
62	SS	0.25	0/1216	0.55	0/1628
63	ST	0.26	0/1131	0.60	0/1515
64	SU	0.28	0/831	0.67	1/1115 (0.1%)
65	SV	0.28	0/643	0.57	0/860
66	SX	0.34	0/1116	0.64	0/1490
67	Sa	0.33	0/836	0.60	0/1121
68	Sc	0.30	0/508	0.75	0/680
69	Sd	0.29	0/470	0.58	0/623
70	Sg	0.26	0/2493	0.67	2/3394 (0.1%)
71	SC	0.34	0/1762	0.61	0/2381
72	SG	0.27	0/1946	0.59	0/2590
73	SJ	0.31	0/1550	0.63	0/2069
74	SM	0.28	0/950	0.69	0/1275
75	SN	0.31	0/1232	0.54	0/1656

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
76	SO	0.34	0/1062	0.70	2/1425 (0.1%)
77	SW	0.32	0/1051	0.52	0/1406
78	SY	0.26	0/1083	0.55	0/1438
79	SZ	0.29	0/604	0.82	0/810
80	Sb	0.27	0/665	0.55	0/891
81	Se	0.24	0/444	0.55	0/588
82	Sf	0.23	0/560	0.72	0/745
83	CA	0.30	0/2810	0.74	2/3780 (0.1%)
84	CC	0.20	0/1773	0.41	1/2759 (0.0%)
85	CE	0.26	0/1055	0.63	0/1400
86	CF	0.26	0/244	0.43	0/328
All	All	0.34	0/241703	0.51	53/354180 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	L5	0	1
4	LA	0	2
5	LB	0	2
11	LH	0	1
13	LJ	0	1
14	LL	0	1
15	LM	0	2
17	LO	0	1
18	LP	0	1
22	LT	0	1
29	La	0	1
34	Lf	0	2
36	Lh	0	1
38	Lj	0	1
46	Ls	0	2
47	Lt	0	3
48	Lz	0	1
51	SB	0	1
52	SD	0	3
54	SF	0	2
55	SH	0	1
56	SI	0	1
60	SQ	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
61	SR	0	1
63	ST	0	1
65	SV	0	1
66	SX	0	3
68	Sc	0	1
73	SJ	0	1
74	SM	0	1
79	SZ	0	2
80	Sb	0	1
All	All	0	45

There are no bond length outliers.

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L5	4910	A	C4'-C3'-O3'	-10.51	93.64	109.40
1	L5	2112	G	C1'-C2'-O2'	-10.43	92.76	108.40
1	L5	4904	G	C4'-C3'-O3'	9.13	126.70	113.00
59	SP	107	ILE	CA-C-N	8.23	138.94	123.55
59	SP	107	ILE	C-N-CA	8.23	138.94	123.55
83	CA	79	SER	CA-C-N	7.45	128.65	121.65
83	CA	79	SER	C-N-CA	7.45	128.65	121.65
6	LC	2	ALA	CA-C-N	7.06	134.41	121.70
6	LC	2	ALA	C-N-CA	7.06	134.41	121.70
1	L5	4906	U	N1-C1'-C2'	-6.92	101.61	112.00
15	LM	87	ALA	CA-C-N	6.77	134.47	121.54
15	LM	87	ALA	C-N-CA	6.77	134.47	121.54
1	L5	4904	G	C2'-C3'-O3'	-6.36	104.16	113.70
1	L5	4906	U	C4'-C3'-O3'	6.29	122.44	113.00
49	S2	1417	C	N3-C4-N4	-6.22	99.33	118.00
47	Lt	9	GLU	CA-C-N	6.12	128.09	121.97
47	Lt	9	GLU	C-N-CA	6.12	128.09	121.97
10	LG	27	VAL	N-CA-C	-6.01	105.51	111.88
4	LA	171	GLY	CA-C-N	5.91	133.00	121.41
4	LA	171	GLY	C-N-CA	5.91	133.00	121.41
84	CC	74	C	C2'-C3'-O3'	5.86	122.49	113.70
76	SO	14	VAL	CA-C-N	5.78	132.10	121.70
76	SO	14	VAL	C-N-CA	5.78	132.10	121.70
20	LR	38	ARG	CA-C-N	5.71	132.45	121.54
20	LR	38	ARG	C-N-CA	5.71	132.45	121.54
23	LU	66	SER	CA-C-N	5.56	132.15	121.54
23	LU	66	SER	C-N-CA	5.56	132.15	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	Lt	8	ASN	CA-C-N	5.49	132.02	121.54
47	Lt	8	ASN	C-N-CA	5.49	132.02	121.54
4	LA	142	GLU	CA-C-N	5.45	131.95	121.54
4	LA	142	GLU	C-N-CA	5.45	131.95	121.54
14	LL	62	PRO	CA-C-O	-5.43	117.20	121.38
1	L5	485	C	C2-N1-C1'	5.34	134.82	118.80
1	L5	4904	G	C3'-C2'-C1'	5.29	106.59	101.30
49	S2	1422	G	N1-C6-O6	-5.26	104.13	119.90
1	L5	4904	G	C3'-C2'-O2'	5.23	118.55	110.70
9	LF	220	MET	CA-C-N	5.20	131.48	121.54
9	LF	220	MET	C-N-CA	5.20	131.48	121.54
64	SU	97	ILE	N-CA-C	-5.20	107.33	111.81
53	SE	92	ILE	CA-C-N	5.20	131.47	121.54
53	SE	92	ILE	C-N-CA	5.20	131.47	121.54
1	L5	2786	C	C2'-C3'-O3'	5.12	121.39	113.70
49	S2	583	A	C4'-C3'-O3'	5.12	120.68	113.00
7	LD	43	LYS	CA-C-N	5.12	131.31	121.54
7	LD	43	LYS	C-N-CA	5.12	131.31	121.54
49	S2	688	U	P-O3'-C3'	5.09	127.83	120.20
1	L5	406	C	C2'-C3'-O3'	5.08	121.32	113.70
13	LJ	95	ARG	CA-CB-CG	5.06	124.23	114.10
49	S2	584	A	C4'-C3'-O3'	5.06	120.59	113.00
70	Sg	143	GLN	CA-C-N	5.06	129.51	122.08
70	Sg	143	GLN	C-N-CA	5.06	129.51	122.08
1	L5	914	U	P-O3'-C3'	5.05	127.78	120.20
1	L5	2760	G	P-O3'-C3'	5.05	127.77	120.20

There are no chirality outliers.

All (45) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	L5	4906	U	Sidechain
4	LA	110	GLY	Peptide
4	LA	54	ARG	Peptide
5	LB	17	LEU	Peptide
5	LB	258	HIS	Peptide
11	LH	106	GLN	Peptide
13	LJ	94	LEU	Peptide
14	LL	154	VAL	Peptide
15	LM	87	ALA	Peptide
15	LM	88	ALA	Peptide
17	LO	110	PRO	Peptide

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Mol	Chain	Res	Type	Group
18	LP	131	ARG	Peptide
22	LT	135	PRO	Peptide
29	La	22	ILE	Peptide
34	Lf	103	VAL	Peptide
34	Lf	106	TYR	Peptide
36	Lh	86	LYS	Peptide
38	Lj	39	TYR	Peptide
46	Ls	148	SER	Peptide
46	Ls	149	ARG	Peptide
47	Lt	141	CYS	Peptide
47	Lt	147	HIS	Peptide
47	Lt	53	TRP	Peptide
48	Lz	183	ILE	Peptide
51	SB	221	PRO	Peptide
52	SD	164	VAL	Peptide
52	SD	192	TRP	Peptide
52	SD	193	ASP	Peptide
54	SF	126	THR	Peptide
54	SF	78	MET	Peptide
55	SH	15	LYS	Peptide
56	SI	130	THR	Peptide
73	SJ	137	VAL	Peptide
74	SM	43	ASP	Peptide
60	SQ	43	GLU	Peptide
61	SR	84	TYR	Peptide
63	ST	46	ALA	Peptide
65	SV	78	ILE	Peptide
66	SX	125	VAL	Peptide
66	SX	126	ALA	Peptide
66	SX	86	PRO	Peptide
79	SZ	46	ASN	Peptide
79	SZ	78	LYS	Peptide
80	Sb	75	GLU	Peptide
68	Sc	64	GLU	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L5	80138	0	40380	331	0
2	L7	2561	0	1295	10	0
3	L8	3314	0	1683	13	0
4	LA	1898	0	1993	15	0
5	LB	3238	0	3376	33	0
6	LC	2927	0	3104	17	0
7	LD	2382	0	2410	20	0
8	LE	1904	0	2055	29	0
9	LF	1870	0	1996	21	0
10	LG	1927	0	2074	13	0
11	LH	1518	0	1601	15	0
12	LI	1634	0	1671	23	0
13	LJ	1410	0	1441	18	0
14	LL	1701	0	1818	14	0
15	LM	1138	0	1204	19	0
16	LN	1701	0	1749	16	0
17	LO	1650	0	1794	13	0
18	LP	1242	0	1269	10	0
19	LQ	1513	0	1628	7	0
20	LR	1566	0	1729	10	0
21	LS	1453	0	1490	17	0
22	LT	1298	0	1366	13	0
23	LU	825	0	850	8	0
24	LV	979	0	1039	8	0
25	LW	1015	0	1079	11	0
26	LX	985	0	1066	8	0
27	LY	1115	0	1205	9	0
28	LZ	1107	0	1182	6	0
29	La	1162	0	1213	8	0
30	Lb	876	0	948	5	0
31	Lc	764	0	804	17	0
32	Ld	888	0	930	6	0
33	Le	1053	0	1147	7	0
34	Lf	876	0	912	6	0
35	Lg	906	0	998	12	0
36	Lh	1015	0	1148	12	0
37	Li	832	0	917	5	0
38	Lj	705	0	736	7	0
39	Lk	569	0	637	7	0
40	Ll	444	0	483	3	0
41	Lm	429	0	465	4	0
42	Ln	230	0	276	2	0
43	Lo	862	0	929	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	Lp	708	0	756	6	0
45	Lr	1002	0	1068	14	0
46	Ls	1496	0	1540	27	0
47	Lt	1046	0	1076	19	0
48	Lz	1741	0	1854	33	0
49	S2	36899	0	18602	181	0
50	SA	1741	0	1746	19	0
51	SB	1738	0	1809	19	0
52	SD	1765	0	1865	24	0
53	SE	2076	0	2177	14	0
54	SF	1461	0	1511	16	0
55	SH	1497	0	1590	30	0
56	SI	1686	0	1772	23	0
57	SK	827	0	854	11	0
58	SL	1247	0	1323	9	0
59	SP	1061	0	1107	10	0
60	SQ	1142	0	1213	21	0
61	SR	1090	0	1149	12	0
62	SS	1198	0	1261	21	0
63	ST	1112	0	1146	15	0
64	SU	821	0	883	10	0
65	SV	636	0	637	10	0
66	SX	1098	0	1167	12	0
67	Sa	821	0	870	7	0
68	Sc	506	0	536	8	0
69	Sd	459	0	449	7	0
70	Sg	2436	0	2393	45	0
71	SC	1725	0	1813	16	0
72	SG	1923	0	2089	28	0
73	SJ	1525	0	1640	11	0
74	SM	940	0	965	24	0
75	SN	1208	0	1294	12	0
76	SO	1049	0	1073	15	0
77	SW	1034	0	1080	14	0
78	SY	1065	0	1142	17	0
79	SZ	598	0	656	12	0
80	Sb	651	0	672	4	0
81	Se	439	0	458	7	0
82	Sf	548	0	553	10	0
83	CA	2764	0	2779	52	0
84	CC	1589	0	810	20	0
85	CE	1043	0	1062	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	CF	239	0	211	4	0
87	L5	212	0	0	0	0
87	L7	3	0	0	0	0
87	L8	4	0	0	0	0
87	LA	1	0	0	0	0
87	LI	1	0	0	0	0
87	LP	1	0	0	0	0
87	LT	1	0	0	0	0
87	LV	1	0	0	0	0
87	Le	1	0	0	0	0
87	Lg	1	0	0	0	0
87	S2	29	0	0	0	0
87	SG	1	0	0	0	0
88	Lg	1	0	0	0	0
88	Lj	1	0	0	0	0
88	Lm	1	0	0	0	0
88	Lo	1	0	0	0	0
88	Lp	1	0	0	0	0
88	Sa	1	0	0	0	0
88	Sd	1	0	0	0	0
88	Sf	1	0	0	0	0
All	All	225534	0	168741	1448	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 4.

All (1448) 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)
83:CA:80:ILE:HA	83:CA:107:LYS:O	1.46	1.15
49:S2:1756:C:H42	49:S2:1776:G:N2	1.50	1.07
83:CA:78:THR:HA	83:CA:109:ASP:O	1.54	1.07
49:S2:1756:C:N4	49:S2:1776:G:H22	1.53	1.05
1:L5:1176:C:H42	1:L5:1184:A:N6	1.57	1.02
49:S2:886:A:N6	49:S2:901:G:C4	2.30	1.00
1:L5:1176:C:N4	1:L5:1184:A:H61	1.59	1.00
1:L5:1762:C:N4	1:L5:1770:A:C2	2.30	1.00
1:L5:1996:C:H42	1:L5:2000:G:N2	1.64	0.96
49:S2:885:U:H3	49:S2:901:G:H1	1.09	0.95
1:L5:2557:G:H1	1:L5:2570:U:H3	1.15	0.95
1:L5:4910:A:O2'	1:L5:4911:A:H8	1.50	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1175:A:H2	1:L5:1185:G:H1	1.15	0.92
70:Sg:46:THR:O	70:Sg:52:TYR:HA	1.70	0.91
1:L5:1175:A:C2	1:L5:1185:G:N1	2.38	0.90
1:L5:4910:A:O2'	1:L5:4911:A:C8	2.24	0.90
1:L5:1095:A:H2	1:L5:1200:G:H1	1.17	0.89
55:SH:163:GLN:O	55:SH:167:GLU:HB3	1.72	0.89
1:L5:4903:G:O2'	1:L5:4904:G:H5'	1.73	0.88
49:S2:928:G:H1	49:S2:1013:U:H3	1.21	0.86
1:L5:1175:A:H2	1:L5:1185:G:N1	1.70	0.85
1:L5:4903:G:C2'	1:L5:4904:G:H5'	2.08	0.84
49:S2:925:G:H1	49:S2:1017:U:H3	1.24	0.83
1:L5:1996:C:H42	1:L5:2000:G:H22	1.21	0.83
1:L5:3951:G:H1	1:L5:4060:U:H3	1.27	0.82
1:L5:4906:U:H3	1:L5:4915:G:H1	1.24	0.82
15:LM:77:TRP:O	15:LM:81:ASP:HA	1.81	0.81
1:L5:1996:C:N4	1:L5:2000:G:H22	1.79	0.80
54:SF:16:ASP:N	54:SF:24:SER:HG	1.79	0.80
1:L5:512:U:H3	1:L5:647:G:H1	1.30	0.78
74:SM:53:ALA:HA	74:SM:79:VAL:O	1.83	0.78
6:LC:218:ILE:O	6:LC:222:ARG:HB2	1.83	0.78
55:SH:72:PHE:O	55:SH:76:GLN:HB2	1.85	0.77
1:L5:1095:A:C2	1:L5:1200:G:N1	2.50	0.77
48:Lz:120:ILE:O	48:Lz:124:LEU:HB2	1.85	0.76
1:L5:4242:U:H3	1:L5:4281:A:H2	1.33	0.76
74:SM:52:LEU:CD2	74:SM:108:CYS:SG	2.73	0.76
5:LB:223:THR:HG22	5:LB:275:HIS:H	1.52	0.75
82:Sf:141:CYS:O	82:Sf:145:CYS:HA	1.87	0.75
56:SI:135:GLU:O	56:SI:139:LYS:HB3	1.88	0.74
21:LS:77:ASN:HB2	21:LS:132:ILE:O	1.89	0.73
1:L5:1176:C:H42	1:L5:1184:A:H61	0.79	0.72
5:LB:261:ARG:HE	17:LO:64:THR:HG21	1.55	0.72
61:SR:79:GLU:O	61:SR:83:ASN:HB2	1.89	0.71
49:S2:886:A:N6	49:S2:901:G:C5	2.58	0.71
13:LJ:21:CYS:HB2	13:LJ:131:TYR:O	1.91	0.70
1:L5:3751:G:H21	1:L5:3775:A:H8	1.37	0.70
84:CC:15:A:N1	84:CC:47:C:N3	2.39	0.69
1:L5:493:G:H1	1:L5:660:A:H2	1.40	0.69
11:LH:12:ILE:HB	11:LH:53:LYS:O	1.93	0.68
1:L5:1095:A:H2	1:L5:1200:G:N1	1.90	0.68
1:L5:1176:C:N3	1:L5:1184:A:N1	2.43	0.67
1:L5:3955:G:C2	1:L5:3966:A:N7	2.62	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:563:G:H1	49:S2:592:C:H5	1.41	0.67
50:SA:126:ASP:O	50:SA:130:ASP:HB2	1.93	0.67
48:Lz:110:PHE:HB2	48:Lz:135:PRO:HB3	1.77	0.66
22:LT:43:LYS:O	22:LT:58:HIS:ND1	2.26	0.66
55:SH:63:PHE:HA	55:SH:95:ILE:O	1.95	0.66
55:SH:140:VAL:HG12	75:SN:19:ARG:HD3	1.77	0.66
52:SD:163:PRO:O	52:SD:167:TYR:HB2	1.95	0.66
54:SF:187:SER:HB2	54:SF:190:ILE:HG12	1.77	0.66
52:SD:101:GLN:HG3	52:SD:126:ILE:HD11	1.76	0.66
64:SU:80:PHE:HB3	69:Sd:52:PHE:HB3	1.78	0.66
84:CC:10:G:N7	84:CC:45:G:N1	2.42	0.66
85:CE:203:GLU:O	85:CE:207:SER:HB2	1.96	0.65
49:S2:1756:C:N3	49:S2:1776:G:N1	2.45	0.65
79:SZ:47:LEU:HD22	79:SZ:79:ILE:HG22	1.78	0.65
1:L5:4093:G:N1	1:L5:4114:C:C2	2.65	0.65
83:CA:229:LEU:HA	83:CA:317:ALA:O	1.97	0.65
47:Lt:146:ARG:HE	47:Lt:151:ILE:HG21	1.61	0.64
1:L5:3971:G:N2	1:L5:3973:G:N3	2.45	0.64
76:SO:34:PHE:HB3	76:SO:41:PHE:HB2	1.80	0.64
49:S2:874:G:H21	55:SH:114:GLN:HE22	1.45	0.64
52:SD:161:GLY:O	52:SD:164:VAL:C	2.40	0.64
1:L5:3967:G:N1	1:L5:4055:U:N3	2.45	0.64
83:CA:228:VAL:O	83:CA:318:GLN:HA	1.98	0.63
46:Ls:110:ALA:HB1	46:Ls:176:ASN:HD21	1.64	0.63
1:L5:4906:U:O2'	1:L5:4907:G:O4'	2.15	0.63
14:LL:50:PRO:HB3	14:LL:150:LEU:HB3	1.79	0.63
45:Lr:7:TRP:O	45:Lr:11:ARG:HB2	1.99	0.63
49:S2:940:U:H3	49:S2:1002:U:H3	1.46	0.63
1:L5:2469:C:H5	1:L5:2471:G:H1	1.44	0.63
78:SY:120:THR:O	78:SY:124:ASN:HB2	1.98	0.63
84:CC:10:G:N7	84:CC:45:G:C2	2.67	0.63
48:Lz:147:LYS:HE2	48:Lz:150:GLU:H	1.64	0.62
49:S2:583:A:O2'	49:S2:584:A:H5'	1.99	0.62
49:S2:1756:C:H42	49:S2:1776:G:H22	0.74	0.62
14:LL:16:LYS:O	14:LL:21:ARG:NH1	2.32	0.62
55:SH:80:VAL:HG23	55:SH:92:VAL:HG13	1.82	0.62
46:Ls:124:PRO:HB2	46:Ls:126:GLN:HG2	1.81	0.62
1:L5:2343:G:OP2	6:LC:109:ARG:NH1	2.32	0.62
72:SG:142:ARG:HB2	72:SG:147:LEU:HB2	1.81	0.62
49:S2:1192:U:OP2	66:SX:119:ARG:NH2	2.32	0.62
31:Lc:34:THR:HG23	31:Lc:95:ALA:HB2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:Lf:78:HIS:HB2	34:Lf:85:ARG:HG3	1.82	0.62
1:L5:186:G:N3	1:L5:1366:G:N2	2.48	0.62
27:LY:54:GLU:HB2	27:LY:108:ARG:HB3	1.82	0.62
1:L5:1952:G:H4'	21:LS:93:MET:HG3	1.82	0.61
1:L5:2707:U:H5'	83:CA:271:ARG:HH22	1.66	0.61
5:LB:92:TYR:HB2	5:LB:159:VAL:HB	1.83	0.61
1:L5:4092:G:N7	1:L5:4114:C:N4	2.48	0.61
43:Lo:45:GLN:HE22	43:Lo:52:THR:H	1.47	0.61
48:Lz:206:ILE:HG21	48:Lz:214:GLN:HB2	1.82	0.61
57:SK:29:MET:SD	57:SK:42:ASN:ND2	2.74	0.61
1:L5:2468:U:O2'	1:L5:2506:G:N2	2.34	0.61
49:S2:606:G:H5''	81:Se:56:ASN:HB3	1.81	0.61
49:S2:1674:G:H4'	54:SF:77:MET:HE1	1.82	0.61
1:L5:4093:G:N1	1:L5:4114:C:N3	2.47	0.61
70:Sg:129:ILE:HD11	70:Sg:151:VAL:HG21	1.82	0.61
1:L5:4946:U:HO2'	34:Lf:2:SER:N	1.99	0.61
49:S2:1158:G:H5''	77:SW:76:SER:HB3	1.83	0.61
1:L5:1730:U:H4'	22:LT:100:LYS:HB2	1.83	0.60
1:L5:1762:C:C4	1:L5:1770:A:N1	2.69	0.60
5:LB:356:LYS:O	5:LB:359:ALA:C	2.44	0.60
48:Lz:56:LYS:H	48:Lz:182:ASN:HD21	1.49	0.60
1:L5:4985:U:O2	5:LB:174:ARG:NH1	2.34	0.60
49:S2:1488:C:O2'	49:S2:1490:G:OP2	2.19	0.60
55:SH:144:ILE:HG23	77:SW:52:ILE:HB	1.83	0.60
1:L5:1095:A:N1	1:L5:1200:G:O6	2.34	0.60
25:LW:74:ARG:NH1	49:S2:1749:G:N7	2.48	0.60
49:S2:202:G:OP1	56:SI:143:LYS:NZ	2.35	0.60
49:S2:1020:A:N7	75:SN:70:LYS:NZ	2.49	0.60
55:SH:53:VAL:O	55:SH:57:ARG:HB2	2.02	0.60
11:LH:31:ARG:NH1	11:LH:149:ASN:OD1	2.34	0.60
83:CA:33:ARG:HH12	83:CA:337:PRO:HD3	1.65	0.60
48:Lz:143:ASN:ND2	48:Lz:150:GLU:OE2	2.35	0.60
1:L5:1656:U:OP2	29:La:26:ARG:NH2	2.36	0.59
35:Lg:82:MET:HE1	35:Lg:90:ARG:HD3	1.84	0.59
70:Sg:120:ILE:HB	70:Sg:132:TRP:HB2	1.83	0.59
83:CA:156:LEU:O	83:CA:161:ASN:ND2	2.35	0.59
49:S2:153:G:N3	72:SG:13:GLN:NE2	2.50	0.59
49:S2:1658:G:OP2	49:S2:1660:C:N4	2.36	0.59
70:Sg:236:ILE:HD13	70:Sg:252:THR:HB	1.83	0.59
12:LI:48:LEU:O	12:LI:139:ARG:HA	2.02	0.59
55:SH:154:ILE:HB	55:SH:185:VAL:HG12	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:SY:26:ASP:N	78:SY:26:ASP:OD1	2.35	0.59
5:LB:14:LEU:HD23	5:LB:17:LEU:HD21	1.85	0.59
26:LX:129:ARG:O	26:LX:132:GLY:N	2.32	0.59
49:S2:65:C:N4	72:SG:134:GLY:O	2.35	0.59
46:Ls:107:VAL:HG21	46:Ls:186:GLY:HA3	1.84	0.59
84:CC:25:C:H2'	84:CC:26:A:H8	1.68	0.59
1:L5:4472:G:O2'	41:Lm:100:TYR:O	2.20	0.59
1:L5:4732:G:N2	1:L5:4734:A:N7	2.49	0.59
5:LB:381:THR:HG22	5:LB:383:GLU:H	1.68	0.59
7:LD:120:GLU:O	7:LD:248:ARG:NH1	2.35	0.59
11:LH:94:SER:HB2	11:LH:142:ASP:HB3	1.85	0.59
1:L5:1499:C:OP1	19:LQ:150:ARG:NH2	2.36	0.59
36:Lh:97:LYS:O	36:Lh:101:ASN:ND2	2.35	0.59
71:SC:128:VAL:HG11	71:SC:155:ILE:HG22	1.85	0.59
49:S2:878:G:H1	49:S2:908:A:H2	1.46	0.58
70:Sg:207:CYS:SG	70:Sg:208:ALA:N	2.76	0.58
83:CA:26:ASP:OD2	83:CA:30:ARG:NH2	2.37	0.58
49:S2:433:A:H5''	56:SI:22:HIS:HB3	1.86	0.58
49:S2:583:A:H2'	49:S2:584:A:C8	2.38	0.58
59:SP:123:TYR:OH	62:SS:124:ARG:NH1	2.36	0.58
84:CC:15:A:N6	84:CC:47:C:O2	2.32	0.58
1:L5:4884:G:N7	8:LE:272:ARG:NH2	2.50	0.58
1:L5:1762:C:C4	1:L5:1770:A:C2	2.90	0.58
46:Ls:65:ILE:HB	46:Ls:75:LEU:HD12	1.85	0.58
47:Lt:57:ARG:HD2	47:Lt:83:LYS:HB2	1.86	0.58
74:SM:128:PHE:HA	74:SM:131:LYS:HG2	1.84	0.58
1:L5:2611:A:H5'	1:L5:2688:G:H4'	1.85	0.58
13:LJ:35:ARG:HD2	13:LJ:123:ILE:HA	1.85	0.58
74:SM:106:CYS:SG	74:SM:107:SER:N	2.77	0.58
23:LU:25:CYS:HB3	23:LU:112:LEU:HD13	1.85	0.58
46:Ls:19:GLN:O	46:Ls:23:ASP:HB2	2.04	0.58
1:L5:493:G:O6	1:L5:660:A:N1	2.36	0.58
1:L5:4377:G:O6	29:La:42:ARG:NH2	2.37	0.58
1:L5:2483:G:H1	1:L5:2495:U:H3	1.52	0.58
49:S2:834:C:H42	49:S2:839:C:H42	1.51	0.58
62:SS:4:VAL:HG22	62:SS:5:ILE:HG22	1.85	0.58
67:Sa:45:VAL:HG21	67:Sa:64:LEU:HD13	1.86	0.58
70:Sg:175:LYS:HD2	70:Sg:184:LEU:HD11	1.86	0.58
1:L5:3711:A:H2'	1:L5:3712:A:H8	1.69	0.57
1:L5:3955:G:N2	1:L5:3966:A:C5	2.72	0.57
25:LW:1:MET:HG2	25:LW:15:PRO:HG3	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LZ:13:VAL:O	28:LZ:20:GLY:N	2.34	0.57
70:Sg:45:LEU:HA	70:Sg:52:TYR:O	2.04	0.57
18:LP:73:ALA:O	18:LP:76:TRP:O	2.21	0.57
29:La:72:THR:HG22	29:La:110:LYS:HB3	1.85	0.57
60:SQ:26:LYS:HB2	60:SQ:67:ASP:HB2	1.85	0.57
70:Sg:46:THR:OG1	70:Sg:51:ASN:O	2.20	0.57
83:CA:75:ALA:HB2	83:CA:113:HIS:HB3	1.86	0.57
9:LF:182:TYR:HB3	9:LF:200:ARG:HG3	1.86	0.57
52:SD:220:THR:OG1	52:SD:221:THR:N	2.37	0.57
3:L8:96:C:OP1	36:Lh:70:ARG:NH1	2.37	0.57
9:LF:105:VAL:HG13	9:LF:136:VAL:HG12	1.85	0.57
57:SK:7:ASN:HD22	57:SK:40:VAL:HB	1.68	0.57
1:L5:194:C:O2	27:LY:121:ARG:NH2	2.37	0.57
10:LG:58:PRO:HD2	10:LG:61:ILE:HD12	1.87	0.57
30:Lb:65:MET:HA	30:Lb:68:ARG:HG2	1.87	0.57
46:Ls:102:LEU:O	46:Ls:105:ASN:C	2.47	0.57
48:Lz:203:ALA:HA	48:Lz:217:TYR:HA	1.86	0.57
83:CA:181:PRO:HB2	83:CA:204:ASN:HB2	1.87	0.57
8:LE:177:GLY:HA3	8:LE:184:VAL:HB	1.87	0.57
1:L5:136:C:N4	36:Lh:77:LYS:O	2.37	0.57
1:L5:1100:U:O3'	1:L5:1167:C:N4	2.38	0.57
1:L5:3589:G:N2	1:L5:3590:G:N7	2.53	0.57
1:L5:3969:G:O2'	1:L5:4054:C:N4	2.37	0.57
1:L5:4905:C:H2'	1:L5:4906:U:C6	2.40	0.57
11:LH:106:GLN:HB2	11:LH:111:LEU:HB3	1.86	0.57
57:SK:15:LEU:O	57:SK:19:GLY:HA2	2.04	0.57
1:L5:1175:A:N1	1:L5:1185:G:O6	2.38	0.57
1:L5:4099:G:H2'	1:L5:4101:C:H41	1.70	0.57
49:S2:190:G:O3'	56:SI:141:ARG:NH2	2.38	0.57
51:SB:122:GLU:HG2	51:SB:140:VAL:HG23	1.86	0.57
1:L5:2092:G:O2'	1:L5:2262:G:N2	2.38	0.56
8:LE:153:LEU:HD11	8:LE:195:ILE:HG13	1.87	0.56
29:La:76:ASP:N	29:La:76:ASP:OD1	2.37	0.56
49:S2:695:C:N4	49:S2:736:C:O2'	2.38	0.56
49:S2:1373:C:O2'	61:SR:10:LYS:NZ	2.37	0.56
62:SS:65:GLU:HA	62:SS:68:ILE:HG12	1.87	0.56
1:L5:2711:G:OP2	20:LR:39:GLN:NE2	2.38	0.56
48:Lz:198:TRP:HE1	48:Lz:202:ARG:HB2	1.70	0.56
54:SF:49:LEU:HD12	60:SQ:50:LYS:HG2	1.87	0.56
55:SH:30:LEU:O	55:SH:33:ASN:ND2	2.38	0.56
65:SV:32:ILE:HG12	65:SV:60:ARG:HD2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:Ls:53:VAL:HG12	46:Ls:89:VAL:HB	1.86	0.56
62:SS:86:ARG:NH1	62:SS:89:ASP:OD1	2.39	0.56
79:SZ:68:ILE:HB	79:SZ:109:TYR:HB2	1.87	0.56
11:LH:120:GLU:OE2	11:LH:124:ARG:NH2	2.37	0.56
13:LJ:115:LEU:HD12	13:LJ:116:GLY:HA2	1.86	0.56
49:S2:1228:A:H2'	49:S2:1229:G:C8	2.41	0.56
55:SH:144:ILE:HD11	55:SH:152:ARG:HB2	1.87	0.56
12:LI:102:MET:SD	12:LI:102:MET:N	2.79	0.56
49:S2:1751:C:H42	49:S2:1782:G:H21	1.54	0.56
1:L5:1697:G:N2	1:L5:2084:C:OP1	2.38	0.56
72:SG:137:ARG:HD2	72:SG:178:ARG:HD3	1.87	0.56
83:CA:27:ILE:HD13	83:CA:30:ARG:HH12	1.70	0.56
1:L5:3946:G:N3	1:L5:3947:A:N6	2.49	0.56
1:L5:2709:C:H5'	20:LR:43:LYS:HD2	1.88	0.56
49:S2:837:A:H61	78:SY:9:THR:H	1.53	0.56
1:L5:182:G:H1	1:L5:254:G:H1	1.54	0.56
1:L5:260:C:H2'	1:L5:261:G:H8	1.71	0.56
1:L5:3937:C:H1'	16:LN:125:SER:HB2	1.87	0.56
4:LA:14:SER:HA	4:LA:17:ARG:HE	1.70	0.56
48:Lz:66:CYS:HB2	48:Lz:82:ILE:HG12	1.87	0.56
49:S2:1230:C:OP1	62:SS:130:ARG:NH2	2.39	0.56
60:SQ:31:LEU:HD11	60:SQ:33:LYS:HE3	1.88	0.56
73:SJ:122:SER:O	73:SJ:125:HIS:N	2.39	0.56
49:S2:71:G:N2	49:S2:73:C:OP1	2.39	0.55
49:S2:126:G:OP1	72:SG:198:ARG:NH1	2.35	0.55
49:S2:1563:G:OP1	63:ST:121:ARG:NH2	2.39	0.55
9:LF:86:GLU:HG3	22:LT:135:PRO:HB3	1.87	0.55
11:LH:171:ASP:O	11:LH:174:LYS:O	2.24	0.55
49:S2:1417:C:H42	49:S2:1422:G:H1	1.54	0.55
74:SM:36:ARG:HH21	74:SM:40:LYS:HE3	1.71	0.55
39:Lk:52:LYS:HA	39:Lk:55:LYS:HG2	1.88	0.55
45:Lr:26:SER:OG	45:Lr:28:GLU:OE1	2.22	0.55
49:S2:878:G:O6	49:S2:908:A:N1	2.39	0.55
1:L5:3961:G:N2	1:L5:3964:U:O3'	2.39	0.55
5:LB:222:VAL:O	5:LB:343:ARG:NH1	2.40	0.55
25:LW:94:ARG:HH21	72:SG:146:ASN:HD21	1.54	0.55
49:S2:922:A:OP1	77:SW:28:ARG:NH2	2.40	0.55
55:SH:49:LYS:O	55:SH:60:ILE:HA	2.07	0.55
1:L5:4250:G:H5''	13:LJ:98:ASN:HD22	1.72	0.55
50:SA:37:TYR:OH	50:SA:57:LYS:NZ	2.40	0.55
70:Sg:17:TRP:H	70:Sg:36:ARG:HB2	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L8:102:G:OP1	38:Lj:20:ARG:NH2	2.36	0.55
22:LT:93:ILE:HA	22:LT:96:ILE:HG12	1.87	0.55
57:SK:31:LYS:NZ	57:SK:39:ASN:OD1	2.40	0.55
72:SG:2:LYS:HD3	72:SG:15:LEU:HD21	1.87	0.55
74:SM:124:ILE:HD12	74:SM:127:TYR:HD2	1.72	0.55
1:L5:4219:A:OP2	22:LT:2:THR:OG1	2.25	0.55
62:SS:47:LYS:NZ	63:ST:35:ASP:OD2	2.40	0.55
1:L5:137:G:H2'	1:L5:138:G:H8	1.72	0.55
8:LE:222:LEU:HB2	8:LE:237:LYS:HD2	1.88	0.55
70:Sg:286:CYS:HA	70:Sg:302:TYR:HA	1.89	0.55
73:SJ:113:GLN:O	73:SJ:117:LEU:HB2	2.07	0.55
13:LJ:44:THR:O	13:LJ:78:LYS:NZ	2.40	0.55
24:LV:43:LYS:HG3	24:LV:60:MET:HG2	1.89	0.55
70:Sg:68:ASP:HB3	70:Sg:111:VAL:HG22	1.89	0.55
74:SM:14:VAL:HG21	74:SM:129:LYS:HE2	1.89	0.55
1:L5:3959:U:O2	1:L5:3960:A:N6	2.40	0.55
12:LI:21:ARG:O	12:LI:24:ARG:NH1	2.40	0.55
49:S2:943:U:OP1	51:SB:214:LYS:NZ	2.40	0.55
49:S2:1464:C:OP2	61:SR:63:ARG:NH2	2.40	0.55
50:SA:128:ARG:NH2	50:SA:151:ASP:O	2.37	0.55
54:SF:30:ILE:HG12	54:SF:113:VAL:HG11	1.89	0.55
63:ST:13:GLU:OE2	63:ST:16:ARG:NH1	2.40	0.55
1:L5:2269:C:H42	19:LQ:21:GLN:HE22	1.55	0.54
1:L5:4233:A:H4'	43:Lo:98:LYS:HE3	1.89	0.54
1:L5:5022:U:O2'	1:L5:5024:C:OP2	2.25	0.54
35:Lg:45:ALA:HB3	35:Lg:82:MET:HG2	1.88	0.54
7:LD:41:LYS:NZ	22:LT:32:ARG:O	2.37	0.54
67:Sa:32:LYS:O	67:Sa:37:LYS:NZ	2.40	0.54
1:L5:3955:G:H22	1:L5:3966:A:H3'	1.72	0.54
24:LV:10:SER:OG	24:LV:11:GLY:N	2.41	0.54
70:Sg:173:LEU:HD22	70:Sg:189:ILE:HG12	1.88	0.54
1:L5:1762:C:N3	1:L5:1770:A:N1	2.55	0.54
3:L8:67:U:H5''	38:Lj:86:PRO:HA	1.87	0.54
4:LA:6:ARG:NH2	4:LA:199:VAL:O	2.41	0.54
50:SA:85:ARG:NH1	50:SA:203:PHE:O	2.40	0.54
54:SF:35:LEU:O	54:SF:39:ILE:HB	2.07	0.54
47:Lt:57:ARG:HE	47:Lt:80:LEU:HB2	1.72	0.54
1:L5:4054:C:N3	48:Lz:35:GLN:NE2	2.56	0.54
46:Ls:102:LEU:O	46:Ls:105:ASN:O	2.26	0.54
48:Lz:55:LEU:HD22	48:Lz:183:ILE:HG12	1.89	0.54
70:Sg:174:VAL:HB	70:Sg:188:HIS:HB2	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4279:A:H5'	1:L5:4281:A:H1'	1.89	0.54
1:L5:4474:A:H5''	41:Lm:125:LYS:HD2	1.89	0.54
1:L5:387:G:O2'	1:L5:412:G:N1	2.34	0.54
1:L5:2495:U:H2'	1:L5:2496:G:H8	1.73	0.54
1:L5:4139:G:H21	1:L5:4140:C:H41	1.55	0.54
5:LB:356:LYS:O	5:LB:359:ALA:O	2.26	0.54
45:Lr:39:ARG:O	45:Lr:103:ARG:NH2	2.40	0.54
51:SB:129:THR:OG1	51:SB:179:ASN:O	2.25	0.54
60:SQ:11:GLN:HA	60:SQ:23:ALA:O	2.07	0.54
70:Sg:84:ASP:OD1	70:Sg:84:ASP:N	2.41	0.54
83:CA:339:GLU:HB3	83:CA:342:LEU:HB3	1.89	0.54
84:CC:22:U:OP2	84:CC:46:A:N6	2.41	0.54
3:L8:123:U:O2'	3:L8:126:C:N4	2.35	0.54
12:LI:209:TRP:O	12:LI:212:LEU:O	2.25	0.54
1:L5:942:G:OP1	9:LF:245:ARG:NH1	2.40	0.54
1:L5:1439:C:OP2	9:LF:34:ARG:NH1	2.41	0.54
2:L7:23:A:N3	2:L7:118:C:O2'	2.38	0.54
14:LL:211:LYS:HG2	48:Lz:184:HIS:HB2	1.88	0.54
25:LW:106:GLU:HA	25:LW:109:ILE:HG22	1.90	0.54
40:LI:21:ARG:NH1	40:LI:22:PRO:O	2.40	0.54
44:Lp:88:GLU:O	44:Lp:91:ASP:O	2.26	0.54
49:S2:656:G:N3	71:SC:227:ARG:NH2	2.54	0.54
77:SW:44:HIS:NE2	77:SW:112:ASP:OD2	2.41	0.54
1:L5:2578:G:N7	28:LZ:17:ARG:NH1	2.55	0.53
7:LD:272:SER:HB3	7:LD:275:GLN:HG3	1.91	0.53
20:LR:178:GLN:HA	20:LR:181:LYS:HE2	1.90	0.53
22:LT:51:GLY:HA3	22:LT:92:ARG:HG3	1.88	0.53
32:Ld:24:GLU:OE2	32:Ld:87:ARG:NH2	2.41	0.53
85:CE:180:GLN:HE21	85:CE:183:ARG:HH21	1.55	0.53
14:LL:48:PRO:HG3	36:Lh:118:LYS:HE3	1.89	0.53
27:LY:39:ARG:O	27:LY:42:TYR:O	2.26	0.53
1:L5:2020:U:H2'	1:L5:2021:G:H8	1.72	0.53
1:L5:3955:G:C2	1:L5:3966:A:C8	2.96	0.53
5:LB:50:LYS:HB2	5:LB:345:LEU:HD11	1.90	0.53
16:LN:124:ASP:HB3	16:LN:127:TYR:H	1.72	0.53
4:LA:137:ILE:HD11	4:LA:149:LYS:HB2	1.89	0.53
14:LL:56:ARG:NH1	14:LL:74:ARG:O	2.39	0.53
27:LY:31:SER:HA	27:LY:48:PRO:HA	1.90	0.53
52:SD:168:VAL:HA	52:SD:188:ILE:O	2.08	0.53
54:SF:127:ARG:O	54:SF:135:ARG:NH1	2.42	0.53
55:SH:65:PRO:O	55:SH:69:LEU:N	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:Sb:49:HIS:ND1	80:Sb:69:GLY:O	2.41	0.53
1:L5:2658:G:N2	1:L5:2676:A:OP2	2.35	0.53
46:Ls:30:VAL:HG22	46:Ls:189:ILE:HG12	1.91	0.53
49:S2:1228:A:H2'	49:S2:1229:G:H8	1.74	0.53
50:SA:50:ASN:HB3	50:SA:53:ARG:HG2	1.90	0.53
59:SP:96:VAL:HG11	59:SP:116:LEU:HB3	1.90	0.53
60:SQ:139:ALA:O	60:SQ:140:ARG:NH2	2.42	0.53
62:SS:105:ASN:OD1	62:SS:108:ARG:NH2	2.41	0.53
63:ST:42:HIS:HB2	63:ST:83:GLN:HB2	1.89	0.53
73:SJ:87:LEU:HD13	73:SJ:100:LEU:HD21	1.91	0.53
76:SO:56:VAL:HG22	76:SO:81:VAL:HG23	1.90	0.53
14:LL:171:GLU:O	14:LL:175:ASN:ND2	2.40	0.53
1:L5:4281:A:H2'	1:L5:4282:A:H2'	1.91	0.53
11:LH:17:ASP:OD1	11:LH:17:ASP:N	2.40	0.53
33:Le:6:PRO:HG3	33:Le:73:GLY:HA3	1.91	0.53
49:S2:886:A:C6	49:S2:901:G:C4	2.97	0.53
66:SX:91:LEU:HD21	81:Se:6:LEU:HD23	1.90	0.53
46:Ls:29:ILE:HG23	46:Ls:86:VAL:HG13	1.90	0.53
49:S2:71:G:O6	72:SG:170:ARG:NH1	2.41	0.53
49:S2:127:C:O2	53:SE:134:LYS:NZ	2.42	0.53
49:S2:1292:C:N3	82:Sf:138:ARG:NH2	2.50	0.53
57:SK:15:LEU:HD13	57:SK:21:MET:HG2	1.90	0.53
1:L5:2702:C:OP1	23:LU:101:ARG:NH2	2.41	0.53
1:L5:5002:U:OP2	5:LB:385:LYS:NZ	2.40	0.53
21:LS:173:ASN:ND2	21:LS:175:PHE:O	2.41	0.53
46:Ls:127:ASN:HD21	46:Ls:151:THR:HG21	1.73	0.53
63:ST:38:LYS:NZ	63:ST:43:LYS:O	2.39	0.53
70:Sg:87:LEU:HB2	70:Sg:101:PHE:HB2	1.91	0.53
21:LS:95:ARG:NH2	21:LS:112:ASP:OD2	2.41	0.52
62:SS:44:VAL:HG11	62:SS:71:MET:HG3	1.91	0.52
8:LE:101:ASN:OD1	8:LE:105:ARG:NH2	2.41	0.52
10:LG:33:GLU:OE2	10:LG:35:ARG:NH1	2.42	0.52
48:Lz:119:GLN:HA	48:Lz:122:ARG:HD2	1.91	0.52
56:SI:165:GLN:HG3	56:SI:171:LEU:HD23	1.92	0.52
66:SX:123:VAL:HG12	66:SX:124:LYS:HG3	1.90	0.52
72:SG:3:LEU:HD12	72:SG:16:ILE:HD11	1.92	0.52
1:L5:109:G:OP2	14:LL:74:ARG:NH2	2.41	0.52
45:Lr:21:ASN:OD1	45:Lr:21:ASN:N	2.41	0.52
55:SH:48:ALA:HA	55:SH:61:ILE:O	2.09	0.52
72:SG:231:ARG:O	72:SG:235:SER:OG	2.26	0.52
1:L5:4431:U:OP2	12:LI:3:ARG:NH2	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:373:G:H4'	58:SL:85:THR:HG21	1.92	0.52
50:SA:163:CYS:SG	50:SA:164:ASN:N	2.79	0.52
65:SV:80:SER:HB3	65:SV:83:PHE:HB3	1.91	0.52
71:SC:194:ARG:HD3	71:SC:196:ILE:HD11	1.90	0.52
75:SN:46:THR:H	75:SN:49:GLN:HE21	1.57	0.52
1:L5:3811:G:O2'	1:L5:3814:U:OP2	2.27	0.52
1:L5:4877:G:OP1	15:LM:101:LYS:NZ	2.40	0.52
5:LB:371:THR:O	5:LB:373:LYS:NZ	2.42	0.52
49:S2:525:A:OP2	81:Se:26:LYS:NZ	2.40	0.52
49:S2:567:C:C2'	49:S2:583:A:H61	2.23	0.52
1:L5:280:G:H5''	16:LN:14:LYS:HE3	1.92	0.52
1:L5:478:G:OP1	45:Lr:66:ARG:NH1	2.43	0.52
1:L5:2284:G:OP1	29:La:7:LYS:NZ	2.41	0.52
77:SW:87:GLU:O	77:SW:91:ASN:ND2	2.42	0.52
83:CA:85:CYS:SG	83:CA:86:VAL:N	2.83	0.52
1:L5:1070:G:OP2	8:LE:65:ARG:NH1	2.43	0.52
1:L5:2601:A:OP1	35:Lg:40:LYS:NZ	2.43	0.52
1:L5:3928:A:OP1	16:LN:90:ASN:ND2	2.42	0.52
3:L8:96:C:H5''	36:Lh:66:LYS:HD2	1.92	0.52
31:Lc:26:LYS:HB2	31:Lc:98:ASP:HB3	1.92	0.52
46:Ls:82:ILE:O	46:Ls:83:ARG:NH1	2.43	0.52
85:CE:72:ARG:NH1	85:CE:76:GLU:OE2	2.43	0.52
49:S2:94:G:O2'	49:S2:508:A:O2'	2.26	0.52
52:SD:215:ASP:HB2	52:SD:217:ILE:HG12	1.92	0.52
1:L5:1950:U:O2'	21:LS:116:ARG:NH1	2.42	0.52
1:L5:3967:G:O6	1:L5:4055:U:O4	2.27	0.52
49:S2:326:C:O2	49:S2:327:G:N2	2.42	0.52
76:SO:14:VAL:H	76:SO:15:ILE:HA	1.75	0.52
7:LD:152:ARG:O	7:LD:157:ASN:ND2	2.43	0.52
70:Sg:11:LEU:HB2	70:Sg:307:VAL:HB	1.92	0.52
70:Sg:120:ILE:O	70:Sg:131:LEU:HA	2.10	0.52
1:L5:407:A:O2'	1:L5:410:A:OP1	2.27	0.51
4:LA:147:ARG:HG2	4:LA:157:VAL:HG22	1.91	0.51
13:LJ:31:ASP:N	13:LJ:31:ASP:OD1	2.41	0.51
21:LS:15:ARG:HB3	21:LS:27:LEU:HD23	1.90	0.51
26:LX:91:GLU:HB2	83:CA:291:MET:HE1	1.91	0.51
1:L5:2601:A:N6	1:L5:2744:A:OP2	2.41	0.51
10:LG:50:ASP:HB2	26:LX:40:ILE:HD12	1.92	0.51
56:SI:101:ILE:HD12	56:SI:190:LEU:HD11	1.91	0.51
64:SU:95:SER:HA	64:SU:98:VAL:HG22	1.91	0.51
80:Sb:34:ASP:OD2	80:Sb:80:ARG:NH2	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:CC:21:A:H61	84:CC:46:A:H2'	1.74	0.51
1:L5:1699:A:O2'	6:LC:306:ARG:NH2	2.44	0.51
1:L5:1708:G:O2'	1:L5:1709:C:O2	2.27	0.51
6:LC:149:GLU:OE2	45:Lr:71:ARG:NH2	2.40	0.51
66:SX:141:PRO:HD2	66:SX:142:ARG:HH21	1.75	0.51
1:L5:3955:G:C2	1:L5:3966:A:C5	2.98	0.51
6:LC:66:SER:HA	6:LC:77:PRO:HA	1.92	0.51
13:LJ:20:LEU:HD22	13:LJ:79:ALA:HA	1.92	0.51
15:LM:100:ARG:HA	15:LM:103:LYS:HG2	1.91	0.51
23:LU:98:ASP:OD1	23:LU:98:ASP:N	2.40	0.51
46:Ls:52:VAL:O	46:Ls:89:VAL:HA	2.11	0.51
49:S2:1650:A:H5''	60:SQ:139:ALA:HB2	1.92	0.51
74:SM:95:ASP:OD1	74:SM:95:ASP:N	2.41	0.51
16:LN:16:SER:O	16:LN:20:ARG:HB2	2.11	0.51
22:LT:28:ALA:HA	22:LT:31:MET:HG2	1.91	0.51
49:S2:590:A:OP1	81:Se:25:LYS:NZ	2.43	0.51
49:S2:643:A:OP1	73:SJ:38:ARG:NH1	2.43	0.51
49:S2:1527:C:OP1	60:SQ:142:GLN:NE2	2.44	0.51
54:SF:143:PRO:HA	54:SF:146:ARG:HG2	1.90	0.51
60:SQ:43:GLU:O	60:SQ:45:ARG:N	2.42	0.51
64:SU:61:LEU:O	64:SU:81:GLN:HA	2.09	0.51
67:Sa:60:ASP:OD1	67:Sa:60:ASP:N	2.44	0.51
70:Sg:152:SER:OG	70:Sg:153:CYS:N	2.39	0.51
5:LB:378:ARG:HG2	25:LW:32:LEU:HD21	1.93	0.51
32:Ld:54:MET:O	32:Ld:57:MET:O	2.29	0.51
49:S2:1598:G:H3'	79:SZ:80:ARG:HD2	1.93	0.51
52:SD:195:THR:HA	52:SD:201:LYS:HG2	1.92	0.51
72:SG:85:ARG:O	72:SG:87:ARG:NH1	2.44	0.51
75:SN:99:ARG:NH2	75:SN:119:GLU:OE2	2.39	0.51
1:L5:453:G:H4'	1:L5:454:U:H5'	1.93	0.51
5:LB:220:ILE:HG12	5:LB:278:THR:HG23	1.93	0.51
13:LJ:20:LEU:O	13:LJ:131:TYR:O	2.29	0.51
47:Lt:50:THR:HG21	47:Lt:72:GLU:HB3	1.91	0.51
49:S2:1536:G:H2'	49:S2:1537:A:C8	2.45	0.51
55:SH:138:GLU:OE2	75:SN:21:SER:OG	2.27	0.51
51:SB:163:GLN:HG3	51:SB:204:ILE:HD13	1.92	0.51
83:CA:158:LYS:HE2	83:CA:330:PRO:HD3	1.93	0.51
1:L5:2562:G:N2	1:L5:2565:A:OP2	2.44	0.51
41:Lm:95:ILE:HA	41:Lm:101:ALA:O	2.11	0.51
49:S2:697:G:OP2	49:S2:733:C:N4	2.44	0.51
49:S2:1868:U:O2'	67:Sa:100:ARG:NH1	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SD:103:GLU:HA	52:SD:106:ARG:HG2	1.92	0.51
57:SK:4:PRO:HD2	57:SK:44:HIS:HE1	1.76	0.51
83:CA:17:VAL:HA	83:CA:20:LYS:HG2	1.92	0.51
1:L5:2083:C:OP2	19:LQ:14:ARG:NH2	2.39	0.50
1:L5:2097:U:OP2	9:LF:35:LYS:NZ	2.43	0.50
10:LG:98:LEU:HD12	10:LG:218:LEU:HD12	1.93	0.50
15:LM:52:PHE:HA	15:LM:55:MET:HG2	1.94	0.50
51:SB:67:PHE:O	51:SB:85:LYS:O	2.29	0.50
74:SM:18:LEU:HA	74:SM:21:VAL:HG12	1.94	0.50
74:SM:69:CYS:O	74:SM:72:HIS:C	2.54	0.50
1:L5:1270:A:H8	1:L5:2106:G:H21	1.59	0.50
1:L5:2838:G:H5'	5:LB:247:GLY:HA2	1.92	0.50
1:L5:3951:G:N2	1:L5:4060:U:O2	2.41	0.50
1:L5:4184:G:H5'	4:LA:233:ARG:HB2	1.94	0.50
15:LM:81:ASP:OD1	15:LM:81:ASP:N	2.44	0.50
62:SS:46:ARG:NH1	63:ST:50:GLU:OE2	2.44	0.50
1:L5:1095:A:N1	1:L5:1200:G:C6	2.79	0.50
31:Lc:17:ARG:HD3	31:Lc:103:ASP:HA	1.92	0.50
71:SC:178:HIS:ND1	71:SC:221:ASP:OD2	2.44	0.50
1:L5:3736:A:H2'	1:L5:3737:A:C8	2.46	0.50
49:S2:886:A:C6	49:S2:901:G:N3	2.80	0.50
63:ST:11:GLN:OE1	63:ST:62:ARG:NH2	2.42	0.50
72:SG:181:THR:HG22	72:SG:183:ARG:H	1.77	0.50
1:L5:183:C:H1'	1:L5:184:U:H5	1.75	0.50
78:SY:27:VAL:HG11	78:SY:35:VAL:HG11	1.94	0.50
83:CA:349:VAL:O	83:CA:355:LYS:NZ	2.45	0.50
1:L5:4725:C:OP1	5:LB:103:LYS:NZ	2.41	0.50
44:Lp:88:GLU:O	44:Lp:91:ASP:C	2.55	0.50
50:SA:85:ARG:NH2	61:SR:81:ARG:O	2.44	0.50
1:L5:512:U:O4	1:L5:647:G:O6	2.29	0.50
8:LE:250:GLN:NE2	8:LE:254:ASP:OD2	2.40	0.50
14:LL:211:LYS:HE3	48:Lz:181:TYR:HA	1.93	0.50
23:LU:28:PRO:HB2	23:LU:34:MET:HG2	1.94	0.50
31:Lc:38:ILE:HD11	31:Lc:46:VAL:HG21	1.94	0.50
39:Lk:13:LEU:HA	39:Lk:16:ARG:HG2	1.93	0.50
49:S2:1420:G:O2'	49:S2:1421:A:N3	2.44	0.50
55:SH:69:LEU:HD13	55:SH:96:ALA:HB2	1.94	0.50
1:L5:2811:G:N1	1:L5:2814:C:OP2	2.36	0.50
1:L5:4929:C:H5''	15:LM:114:LYS:HD2	1.94	0.50
2:L7:49:A:H5''	7:LD:224:SER:HB3	1.94	0.50
31:Lc:104:ILE:O	31:Lc:106:ARG:NH1	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:170:C:H42	1:L5:266:C:H42	1.60	0.50
1:L5:1548:G:O2'	1:L5:2812:A:N3	2.42	0.50
1:L5:2782:U:OP2	40:L1:10:LYS:NZ	2.41	0.50
1:L5:2902:G:O6	1:L5:3594:C:N4	2.45	0.50
44:Lp:30:GLU:HA	44:Lp:33:GLN:HG2	1.93	0.50
46:Ls:160:LEU:HG	46:Ls:161:ILE:HG13	1.93	0.50
52:SD:193:ASP:OD1	52:SD:193:ASP:N	2.44	0.50
80:Sb:40:CYS:SG	80:Sb:41:TYR:N	2.78	0.50
81:Se:37:GLN:HA	81:Se:40:ARG:HG2	1.94	0.50
28:LZ:90:PRO:O	28:LZ:117:LYS:NZ	2.45	0.49
47:Lt:12:VAL:HB	47:Lt:65:GLN:HB2	1.93	0.49
50:SA:81:ASN:OD1	50:SA:81:ASN:N	2.45	0.49
18:LP:115:GLU:OE2	18:LP:151:THR:OG1	2.29	0.49
50:SA:22:GLY:O	50:SA:24:HIS:ND1	2.44	0.49
51:SB:28:LYS:HA	51:SB:50:THR:HA	1.94	0.49
55:SH:177:TYR:O	55:SH:181:THR:HB	2.12	0.49
5:LB:117:ARG:HG2	5:LB:180:LEU:HD13	1.94	0.49
13:LJ:141:ILE:HA	13:LJ:144:LYS:HD3	1.94	0.49
17:LO:166:ILE:HG12	17:LO:169:ARG:HH21	1.77	0.49
49:S2:959:G:OP1	76:SO:104:ARG:NH2	2.37	0.49
52:SD:55:THR:HA	52:SD:58:VAL:HG12	1.93	0.49
52:SD:132:LYS:HD2	52:SD:189:MET:HE2	1.94	0.49
74:SM:119:GLN:HB2	74:SM:122:ASP:HB3	1.93	0.49
77:SW:86:LEU:HG	77:SW:90:GLN:HE21	1.77	0.49
1:L5:3955:G:N2	1:L5:3966:A:C4	2.80	0.49
7:LD:77:ALA:O	7:LD:108:ARG:NH2	2.45	0.49
49:S2:951:C:O2'	76:SO:50:LYS:NZ	2.45	0.49
49:S2:1497:G:O6	57:SK:25:LYS:NZ	2.44	0.49
50:SA:198:MET:HG2	50:SA:200:ASP:H	1.77	0.49
1:L5:1995:G:H4'	47:Lt:128:THR:HB	1.95	0.49
1:L5:2000:G:N2	1:L5:2000:G:OP2	2.46	0.49
10:LG:209:SER:HA	10:LG:212:LYS:HE2	1.95	0.49
43:Lo:19:GLN:NE2	43:Lo:74:GLU:OE1	2.45	0.49
61:SR:36:GLU:HB3	61:SR:47:ARG:HD3	1.94	0.49
65:SV:12:TYR:O	71:SC:248:TYR:OH	2.30	0.49
74:SM:128:PHE:O	74:SM:132:LYS:HB2	2.11	0.49
83:CA:155:ARG:NH2	83:CA:357:LEU:HB3	2.28	0.49
6:LC:66:SER:O	6:LC:66:SER:OG	2.22	0.49
75:SN:87:ASP:OD1	75:SN:87:ASP:N	2.44	0.49
1:L5:3717:A:H2'	1:L5:3718:A:C8	2.47	0.49
1:L5:4194:U:H5'	30:Lb:3:LYS:HD3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LE:281:ILE:HD12	8:LE:286:LEU:HD11	1.95	0.49
15:LM:10:GLY:N	15:LM:27:ILE:O	2.36	0.49
46:Ls:91:THR:OG1	46:Ls:92:LYS:N	2.46	0.49
49:S2:1435:C:H42	64:SU:19:ARG:HH21	1.60	0.49
83:CA:189:GLN:HE21	83:CA:197:GLY:HA3	1.77	0.49
1:L5:651:C:O2	29:La:85:GLN:NE2	2.45	0.49
1:L5:736:C:OP1	15:LM:74:ARG:NH1	2.46	0.49
17:LO:7:LEU:HD22	17:LO:31:ARG:HH21	1.78	0.49
49:S2:355:G:OP2	58:SL:107:LYS:NZ	2.42	0.49
49:S2:1644:C:H4'	60:SQ:140:ARG:HB2	1.94	0.49
70:Sg:163:PRO:HB2	70:Sg:179:LEU:HB2	1.95	0.49
70:Sg:184:LEU:HD21	70:Sg:187:ASN:HB2	1.94	0.49
1:L5:989:U:O2	1:L5:1064:G:O6	2.30	0.49
1:L5:1762:C:H5''	1:L5:1764:G:H1	1.78	0.49
2:L7:13:A:OP2	2:L7:66:G:N2	2.39	0.49
46:Ls:28:PHE:HB2	46:Ls:89:VAL:HG13	1.94	0.49
49:S2:1759:G:N2	49:S2:1760:G:O6	2.45	0.49
53:SE:91:SER:OG	53:SE:98:ASN:ND2	2.46	0.49
62:SS:1:MET:SD	62:SS:1:MET:N	2.84	0.49
74:SM:54:SER:HB3	74:SM:78:LYS:HD2	1.94	0.49
1:L5:3977:C:N4	1:L5:3984:C:OP1	2.46	0.49
21:LS:74:ARG:O	21:LS:76:LYS:NZ	2.44	0.49
84:CC:10:G:O6	84:CC:45:G:O6	2.31	0.49
5:LB:85:VAL:HA	5:LB:203:GLN:O	2.13	0.48
32:Ld:53:ALA:HA	32:Ld:88:LEU:HD21	1.95	0.48
43:Lo:4:VAL:O	43:Lo:94:GLY:N	2.45	0.48
70:Sg:30:MET:HA	70:Sg:43:TRP:O	2.13	0.48
1:L5:182:G:N2	1:L5:255:C:O2'	2.46	0.48
1:L5:1175:A:H2	1:L5:1185:G:C2	2.31	0.48
1:L5:4040:C:H5'	1:L5:4045:G:H22	1.78	0.48
1:L5:4122:G:N1	35:Lg:98:GLU:OE1	2.44	0.48
6:LC:39:PHE:O	6:LC:43:ASN:ND2	2.46	0.48
10:LG:160:ASP:N	10:LG:160:ASP:OD1	2.47	0.48
12:LI:152:LEU:HB3	12:LI:165:ILE:HD12	1.95	0.48
24:LV:35:LYS:HB2	24:LV:67:LYS:HG3	1.94	0.48
44:Lp:46:LYS:HD2	44:Lp:59:SER:HB2	1.94	0.48
56:SI:110:ARG:NH2	56:SI:122:GLY:O	2.47	0.48
69:Sd:25:SER:O	69:Sd:25:SER:OG	2.29	0.48
70:Sg:39:THR:HG22	70:Sg:60:ARG:HG2	1.95	0.48
82:Sf:140:TYR:HB2	82:Sf:147:THR:HG22	1.95	0.48
83:CA:229:LEU:HG	83:CA:318:GLN:HB3	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1187:G:N2	1:L5:1187:G:OP2	2.46	0.48
1:L5:1498:G:OP1	19:LQ:150:ARG:NH1	2.46	0.48
10:LG:101:LYS:NZ	10:LG:211:ASP:OD1	2.44	0.48
50:SA:151:ASP:OD1	50:SA:151:ASP:N	2.43	0.48
51:SB:109:LYS:HG3	51:SB:113:MET:HE2	1.95	0.48
62:SS:24:ARG:HB2	62:SS:29:ALA:HB2	1.94	0.48
83:CA:33:ARG:HA	83:CA:36:VAL:HG22	1.94	0.48
1:L5:1918:U:O2'	1:L5:1920:C:OP2	2.32	0.48
1:L5:2808:G:O3'	20:LR:60:ARG:NH1	2.47	0.48
1:L5:3956:G:O5'	1:L5:3966:A:N6	2.47	0.48
1:L5:4742:G:H2'	1:L5:4743:G:H8	1.79	0.48
8:LE:190:HIS:HD2	8:LE:192:LYS:HB2	1.77	0.48
9:LF:93:ILE:HA	9:LF:119:ASN:O	2.13	0.48
11:LH:128:MET:HE3	11:LH:134:CYS:HB2	1.95	0.48
12:LI:209:TRP:O	12:LI:212:LEU:C	2.57	0.48
46:Ls:74:ALA:HB1	46:Ls:77:LYS:HE3	1.95	0.48
49:S2:1536:G:H2'	49:S2:1537:A:H8	1.79	0.48
71:SC:278:THR:HA	71:SC:279:ARG:HD2	1.93	0.48
1:L5:1320:U:O2'	1:L5:1891:A:N1	2.45	0.48
11:LH:124:ARG:NH1	11:LH:164:ALA:O	2.45	0.48
25:LW:73:ARG:NH1	49:S2:1781:A:OP2	2.46	0.48
49:S2:928:G:H2'	49:S2:929:G:C8	2.48	0.48
54:SF:135:ARG:N	84:CC:33:U:OP2	2.46	0.48
60:SQ:32:ILE:HA	60:SQ:68:ILE:O	2.11	0.48
78:SY:83:LYS:HE2	78:SY:96:LEU:HB3	1.95	0.48
83:CA:207:ASP:HA	83:CA:210:LYS:HE2	1.95	0.48
85:CE:62:ASP:HA	85:CE:65:GLU:HG3	1.95	0.48
1:L5:452:A:H4'	1:L5:453:G:H5'	1.96	0.48
49:S2:1291:A:O2'	82:Sf:145:CYS:SG	2.72	0.48
83:CA:206:THR:O	83:CA:210:LYS:HB2	2.14	0.48
1:L5:4031:U:OP2	48:Lz:26:ARG:NE	2.46	0.48
1:L5:4992:G:H2'	1:L5:4993:G:C8	2.48	0.48
49:S2:380:G:OP2	56:SI:56:ARG:NH2	2.42	0.48
70:Sg:40:ILE:HB	70:Sg:59:LEU:HB2	1.94	0.48
72:SG:159:ARG:HD2	72:SG:173:ALA:HB2	1.95	0.48
1:L5:308:G:O6	16:LN:12:ARG:NH1	2.46	0.48
1:L5:702:U:H5'	8:LE:121:VAL:HG11	1.94	0.48
1:L5:1175:A:N1	1:L5:1185:G:C6	2.82	0.48
7:LD:62:CYS:HB3	7:LD:105:LEU:HD22	1.96	0.48
15:LM:11:ARG:NH1	15:LM:58:THR:O	2.46	0.48
49:S2:60:G:H22	49:S2:316:G:H21	1.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:1005:G:OP2	51:SB:162:ARG:NH1	2.47	0.48
59:SP:28:MET:HE1	59:SP:36:LEU:HG	1.96	0.48
75:SN:40:LEU:HB3	75:SN:45:LEU:HD12	1.94	0.48
83:CA:80:ILE:CA	83:CA:107:LYS:O	2.40	0.48
83:CA:202:ILE:HG21	83:CA:209:GLN:HG3	1.96	0.48
86:CF:153:PRO:HG2	86:CF:176:GLU:HG3	1.95	0.48
4:LA:116:LEU:HB3	4:LA:126:LEU:HB2	1.95	0.48
13:LJ:65:ASN:HB2	43:Lo:103:VAL:HA	1.96	0.48
22:LT:107:LYS:HA	22:LT:110:LYS:HG2	1.96	0.48
33:Le:8:VAL:HG23	33:Le:10:PRO:HD3	1.96	0.48
36:Lh:82:ASP:OD1	36:Lh:82:ASP:N	2.43	0.48
49:S2:1454:A:H5'	61:SR:3:ARG:HD2	1.96	0.48
49:S2:1754:G:N7	49:S2:1779:G:N2	2.62	0.48
56:SI:61:ASP:OD1	56:SI:61:ASP:N	2.46	0.48
60:SQ:33:LYS:HG3	60:SQ:69:ARG:HG3	1.96	0.48
70:Sg:99:ARG:NH1	70:Sg:135:LEU:O	2.47	0.48
70:Sg:274:VAL:HG13	70:Sg:277:THR:HG22	1.95	0.48
1:L5:4906:U:HO2'	1:L5:4907:G:H8	1.61	0.48
8:LE:262:LYS:NZ	8:LE:268:GLN:OE1	2.42	0.48
33:Le:103:VAL:O	33:Le:108:ARG:NH2	2.45	0.48
36:Lh:12:LYS:HD2	36:Lh:16:GLU:HG2	1.96	0.48
46:Ls:97:GLU:O	46:Ls:101:MET:HB2	2.13	0.48
64:SU:98:VAL:HA	64:SU:101:ILE:HB	1.94	0.48
68:Sc:14:VAL:HG13	68:Sc:30:VAL:HB	1.96	0.48
70:Sg:107:ASP:OD1	70:Sg:107:ASP:N	2.35	0.48
78:SY:82:ALA:O	78:SY:86:GLU:HB2	2.13	0.48
4:LA:233:ARG:O	4:LA:233:ARG:NH1	2.42	0.47
12:LI:66:GLU:OE1	12:LI:69:ARG:NH1	2.39	0.47
15:LM:12:VAL:O	15:LM:58:THR:OG1	2.31	0.47
15:LM:90:ARG:HA	15:LM:93:LYS:HG2	1.96	0.47
49:S2:190:G:H5'	56:SI:145:ILE:HD13	1.94	0.47
52:SD:16:ILE:HD11	69:Sd:36:LEU:HD23	1.96	0.47
72:SG:22:ARG:HG3	72:SG:25:ARG:HH12	1.78	0.47
83:CA:188:HIS:ND1	83:CA:195:ILE:O	2.32	0.47
83:CA:233:GLY:N	83:CA:314:GLU:OE2	2.38	0.47
1:L5:3976:C:N4	1:L5:4035:G:OP2	2.46	0.47
15:LM:15:VAL:O	15:LM:22:GLY:N	2.47	0.47
39:Lk:26:LYS:HB2	39:Lk:69:LEU:HD12	1.97	0.47
50:SA:76:VAL:HG12	50:SA:123:VAL:HB	1.96	0.47
64:SU:51:LYS:HB2	64:SU:90:ASP:HB2	1.96	0.47
77:SW:18:GLU:HG2	77:SW:69:LEU:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:935:A:O2'	15:LM:44:GLN:O	2.32	0.47
1:L5:1824:G:H5''	22:LT:35:LYS:HE3	1.96	0.47
1:L5:1914:C:H4'	17:LO:89:PRO:HD3	1.95	0.47
45:Lr:95:HIS:O	45:Lr:99:LYS:HB2	2.14	0.47
45:Lr:103:ARG:HE	45:Lr:106:LEU:HD11	1.79	0.47
49:S2:1521:C:OP2	62:SS:124:ARG:NH2	2.45	0.47
52:SD:161:GLY:O	52:SD:164:VAL:O	2.32	0.47
53:SE:100:ARG:HB2	53:SE:114:ILE:HD13	1.96	0.47
55:SH:50:GLU:HG3	55:SH:60:ILE:HG22	1.97	0.47
1:L5:257:C:H2'	1:L5:258:G:C8	2.50	0.47
1:L5:267:G:H2'	1:L5:268:G:H8	1.80	0.47
45:Lr:47:LYS:HB2	45:Lr:102:TYR:CZ	2.49	0.47
49:S2:640:A:H2'	49:S2:641:A:C8	2.50	0.47
49:S2:1203:G:H2'	49:S2:1204:A:C8	2.49	0.47
77:SW:60:LYS:NZ	80:Sb:23:ARG:O	2.44	0.47
1:L5:1994:C:H2'	1:L5:1995:G:H8	1.79	0.47
1:L5:2745:A:H2'	1:L5:2746:A:C8	2.50	0.47
1:L5:2835:A:O2'	5:LB:228:TYR:O	2.29	0.47
1:L5:4043:G:OP1	1:L5:4045:G:N2	2.47	0.47
1:L5:4601:U:H2'	1:L5:4602:A:H8	1.78	0.47
2:L7:13:A:O2'	7:LD:24:ARG:NH1	2.47	0.47
9:LF:27:GLU:HA	9:LF:30:ILE:HG22	1.95	0.47
27:LY:101:PRO:HA	27:LY:104:VAL:HG22	1.96	0.47
85:CE:203:GLU:O	85:CE:206:ARG:C	2.57	0.47
6:LC:327:LYS:NZ	9:LF:171:ASP:OD1	2.48	0.47
8:LE:152:ILE:HD12	8:LE:189:THR:HG21	1.96	0.47
15:LM:3:PHE:H	21:LS:175:PHE:HZ	1.62	0.47
20:LR:39:GLN:HG3	20:LR:42:ARG:HH21	1.80	0.47
49:S2:661:U:OP1	66:SX:5:ARG:NH2	2.44	0.47
49:S2:1550:G:H3'	49:S2:1579:A:H61	1.79	0.47
68:Sc:67:ARG:HH11	68:Sc:68:LEU:H	1.62	0.47
1:L5:2779:C:O2'	3:L8:112:G:OP1	2.25	0.47
1:L5:3615:G:H1'	25:LW:44:ARG:HD3	1.97	0.47
1:L5:4546:A:N7	4:LA:215:ASN:ND2	2.60	0.47
49:S2:1299:A:OP1	59:SP:59:ARG:NH1	2.48	0.47
51:SB:67:PHE:O	51:SB:85:LYS:C	2.58	0.47
56:SI:139:LYS:HE2	56:SI:141:ARG:HD3	1.96	0.47
66:SX:28:LYS:O	66:SX:32:LEU:HB2	2.13	0.47
66:SX:68:LYS:HB3	66:SX:91:LEU:HD13	1.96	0.47
74:SM:41:ALA:HB1	74:SM:112:LYS:HD2	1.95	0.47
82:Sf:133:ALA:O	82:Sf:139:HIS:ND1	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:CA:111:GLY:HA3	83:CA:120:ASN:HD22	1.80	0.47
83:CA:274:ASP:N	83:CA:274:ASP:OD1	2.47	0.47
86:CF:157:PHE:O	86:CF:161:TRP:HB3	2.15	0.47
1:L5:442:G:OP1	34:Lf:68:ARG:NH1	2.44	0.47
1:L5:1051:G:N2	1:L5:1064:G:OP1	2.47	0.47
1:L5:1086:C:H2'	1:L5:1087:A:H8	1.79	0.47
1:L5:1629:G:H1	4:LA:208:GLU:HG2	1.79	0.47
31:Lc:48:LEU:HD21	31:Lc:60:ILE:HG21	1.97	0.47
49:S2:145:G:H2'	49:S2:146:G:C8	2.50	0.47
49:S2:1757:G:O2'	49:S2:1776:G:O6	2.29	0.47
1:L5:1942:A:H2'	1:L5:1943:A:C8	2.50	0.47
1:L5:4741:C:H2'	1:L5:4950:U:H3	1.80	0.47
13:LJ:97:ASN:N	13:LJ:97:ASN:OD1	2.47	0.47
18:LP:73:ALA:O	18:LP:76:TRP:C	2.58	0.47
19:LQ:159:PRO:HD3	19:LQ:188:ASN:HD21	1.78	0.47
48:Lz:56:LYS:O	48:Lz:182:ASN:ND2	2.48	0.47
49:S2:1597:C:OP2	79:SZ:85:ARG:NH2	2.38	0.47
56:SI:141:ARG:HB3	56:SI:145:ILE:HB	1.96	0.47
66:SX:94:ILE:HD11	66:SX:122:VAL:HG11	1.97	0.47
1:L5:713:C:O2	8:LE:130:LYS:NZ	2.45	0.47
1:L5:4274:A:H2'	1:L5:4275:G:C8	2.50	0.47
1:L5:4966:A:H5'	5:LB:128:LYS:HG3	1.97	0.47
14:LL:204:GLU:HA	14:LL:207:VAL:HG12	1.97	0.47
32:Ld:47:LYS:HB3	32:Ld:47:LYS:HE2	1.76	0.47
47:Lt:22:VAL:HG22	47:Lt:48:LYS:HG2	1.97	0.47
49:S2:377:G:H5'	56:SI:98:LYS:HB3	1.97	0.47
49:S2:874:G:H2'	49:S2:875:A:H8	1.80	0.47
79:SZ:58:LEU:HD12	79:SZ:62:VAL:HG11	1.97	0.47
1:L5:1279:A:O2'	6:LC:323:ARG:NH2	2.48	0.46
1:L5:1590:C:H4'	1:L5:2857:A:H5'	1.96	0.46
5:LB:161:ARG:HG2	5:LB:184:GLN:HA	1.97	0.46
6:LC:293:LEU:O	6:LC:299:GLN:NE2	2.41	0.46
12:LI:193:ASP:N	12:LI:193:ASP:OD1	2.48	0.46
19:LQ:70:MET:HE1	19:LQ:137:VAL:HB	1.96	0.46
20:LR:151:ARG:NH2	58:SL:119:ASP:OD1	2.48	0.46
46:Ls:29:ILE:HB	46:Ls:191:GLN:HB2	1.97	0.46
67:Sa:51:ARG:NH2	68:Sc:39:SER:OG	2.47	0.46
77:SW:3:ARG:NH1	77:SW:9:ASP:OD2	2.47	0.46
1:L5:3964:U:O2'	1:L5:3966:A:O4'	2.32	0.46
1:L5:3969:G:HO2'	1:L5:4054:C:H41	1.61	0.46
12:LI:55:ASP:N	12:LI:55:ASP:OD1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LN:9:GLU:HB2	37:Li:44:ILE:HG13	1.96	0.46
25:LW:120:GLN:HA	25:LW:123:LYS:HD3	1.97	0.46
57:SK:29:MET:HB3	57:SK:42:ASN:HD22	1.80	0.46
12:LI:36:LEU:HB3	12:LI:87:MET:HG3	1.96	0.46
18:LP:64:ASN:HD22	18:LP:80:GLN:HE22	1.62	0.46
26:LX:119:ILE:HD13	26:LX:149:VAL:HG21	1.97	0.46
28:LZ:67:LYS:HE2	28:LZ:67:LYS:HB3	1.77	0.46
35:Lg:42:PRO:HB2	35:Lg:53:LEU:HD12	1.96	0.46
47:Lt:105:THR:HG22	47:Lt:107:ASP:HB2	1.96	0.46
51:SB:42:ARG:NH2	51:SB:232:HIS:O	2.40	0.46
74:SM:40:LYS:HA	74:SM:40:LYS:HD3	1.80	0.46
78:SY:74:MET:HE3	78:SY:74:MET:HB2	1.80	0.46
1:L5:3659:G:OP1	4:LA:241:ARG:NH1	2.46	0.46
8:LE:207:LYS:O	8:LE:256:GLN:NE2	2.48	0.46
16:LN:158:HIS:HB3	16:LN:161:MET:HB2	1.97	0.46
48:Lz:29:LEU:HD22	48:Lz:60:ARG:HD3	1.98	0.46
49:S2:1507:G:H1	82:Sf:87:THR:HG22	1.80	0.46
49:S2:1854:U:OP1	76:SO:150:ARG:NH1	2.43	0.46
70:Sg:46:THR:O	70:Sg:52:TYR:CA	2.54	0.46
78:SY:5:VAL:O	78:SY:43:LYS:NZ	2.48	0.46
1:L5:461:G:H2'	1:L5:462:G:H8	1.80	0.46
1:L5:2517:A:H5'	35:Lg:62:LYS:HD3	1.97	0.46
1:L5:2583:C:OP2	35:Lg:76:ARG:NH1	2.38	0.46
1:L5:3967:G:N2	1:L5:4055:U:O2	2.48	0.46
16:LN:84:PRO:HA	16:LN:87:HIS:CG	2.51	0.46
49:S2:888:U:H2'	49:S2:900:C:H42	1.81	0.46
55:SH:64:VAL:O	55:SH:96:ALA:HA	2.16	0.46
56:SI:150:ASP:HA	56:SI:153:LYS:HG2	1.98	0.46
84:CC:8:U:H5'	84:CC:48:C:H5''	1.97	0.46
14:LL:127:PHE:O	36:Lh:117:ARG:NH2	2.47	0.46
16:LN:123:GLU:HG2	16:LN:128:LYS:HG3	1.98	0.46
47:Lt:148:PRO:HG2	47:Lt:149:HIS:ND1	2.30	0.46
72:SG:136:LYS:NZ	72:SG:175:LYS:O	2.39	0.46
79:SZ:42:ASP:OD1	79:SZ:42:ASP:N	2.47	0.46
49:S2:1417:C:N3	49:S2:1422:G:O6	2.49	0.46
82:Sf:109:ASP:OD1	82:Sf:109:ASP:N	2.47	0.46
1:L5:364:G:O6	38:Lj:55:ARG:NH1	2.46	0.46
1:L5:4041:C:O2'	48:Lz:102:LYS:O	2.27	0.46
1:L5:4054:C:H1'	48:Lz:207:LYS:HB2	1.98	0.46
24:LV:58:GLY:N	24:LV:81:VAL:O	2.44	0.46
38:Lj:33:THR:HA	38:Lj:40:PRO:HD3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:Ln:1:MET:HB2	49:S2:1706:G:H5'	1.98	0.46
46:Ls:47:LEU:HD11	46:Ls:53:VAL:HG22	1.98	0.46
49:S2:1017:U:H5'	75:SN:55:ARG:HD3	1.97	0.46
79:SZ:65:TYR:HA	79:SZ:111:ARG:HH21	1.81	0.46
79:SZ:91:LEU:HA	79:SZ:94:LYS:HG2	1.98	0.46
79:SZ:99:LEU:HD21	79:SZ:102:LYS:HB2	1.97	0.46
1:L5:691:C:H2'	1:L5:692:A:C8	2.51	0.46
49:S2:1611:G:H21	62:SS:87:GLN:HE21	1.63	0.46
67:Sa:3:LYS:HE3	67:Sa:8:ASN:HD21	1.79	0.46
78:SY:80:ASP:N	78:SY:80:ASP:OD1	2.49	0.46
1:L5:235:A:OP1	6:LC:201:ARG:NH2	2.49	0.46
6:LC:9:SER:HA	6:LC:21:ASN:HD22	1.80	0.46
54:SF:18:LYS:HE3	54:SF:22:LYS:HA	1.97	0.46
60:SQ:97:GLN:HB3	60:SQ:105:LYS:HG3	1.98	0.46
61:SR:67:ARG:HA	61:SR:68:GLY:HA3	1.62	0.46
64:SU:56:MET:SD	64:SU:56:MET:N	2.89	0.46
8:LE:152:ILE:O	8:LE:159:GLY:N	2.48	0.45
12:LI:36:LEU:HD22	12:LI:69:ARG:HH21	1.81	0.45
13:LJ:83:LEU:HD13	13:LJ:132:VAL:HG21	1.96	0.45
31:Lc:14:ILE:HA	31:Lc:17:ARG:HG2	1.97	0.45
39:Lk:52:LYS:HA	39:Lk:55:LYS:HZ2	1.82	0.45
55:SH:31:GLU:HG3	55:SH:37:LYS:HD2	1.98	0.45
70:Sg:31:ILE:HG12	70:Sg:43:TRP:HB2	1.97	0.45
74:SM:50:CYS:O	74:SM:76:LEU:HA	2.16	0.45
83:CA:14:GLU:HG2	83:CA:17:VAL:HG12	1.98	0.45
83:CA:121:VAL:HG22	83:CA:334:THR:HG21	1.98	0.45
1:L5:1726:U:H5'	9:LF:135:ILE:HD11	1.97	0.45
1:L5:1984:A:N7	1:L5:2010:A:O2'	2.40	0.45
1:L5:2520:C:H2'	1:L5:2521:G:H8	1.82	0.45
7:LD:223:PHE:HB3	7:LD:226:TYR:HB2	1.98	0.45
8:LE:151:ILE:HA	8:LE:160:LYS:O	2.15	0.45
15:LM:123:ILE:HD11	17:LO:189:ILE:HD13	1.98	0.45
47:Lt:125:LEU:HD12	47:Lt:127:GLY:H	1.81	0.45
49:S2:809:A:OP1	53:SE:187:ALA:N	2.49	0.45
74:SM:17:ALA:O	74:SM:119:GLN:NE2	2.48	0.45
1:L5:3958:G:O5'	84:CC:18:G:O2'	2.35	0.45
1:L5:4743:G:H2'	1:L5:4744:A:C8	2.51	0.45
4:LA:45:VAL:O	4:LA:85:GLY:N	2.49	0.45
84:CC:13:U:H2'	84:CC:14:A:H8	1.81	0.45
1:L5:182:G:N1	1:L5:255:C:O2	2.50	0.45
1:L5:1857:C:H2'	1:L5:1858:A:H8	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LI:156:LYS:HG3	12:LI:163:GLN:HB2	1.97	0.45
17:LO:3:GLU:N	34:Lf:31:GLU:OE2	2.49	0.45
21:LS:2:LYS:HE2	21:LS:35:PRO:HD3	1.97	0.45
76:SO:149:ARG:HH21	76:SO:151:LEU:HD13	1.81	0.45
1:L5:1702:C:O3'	6:LC:308:LYS:NZ	2.49	0.45
3:L8:77:A:O3'	83:CA:238:LYS:NZ	2.49	0.45
9:LF:92:VAL:O	9:LF:120:GLY:HA2	2.17	0.45
60:SQ:29:ASN:OD1	60:SQ:29:ASN:N	2.49	0.45
26:LX:73:HIS:HD2	26:LX:112:ALA:HA	1.81	0.45
46:Ls:26:LYS:HB2	46:Ls:91:THR:HG23	1.98	0.45
55:SH:53:VAL:HG21	55:SH:172:THR:HA	1.99	0.45
59:SP:20:VAL:HG12	59:SP:25:LEU:HG	1.98	0.45
5:LB:175:GLN:HE21	5:LB:177:LYS:HB3	1.82	0.45
49:S2:1562:C:H2'	49:S2:1563:G:H8	1.82	0.45
55:SH:69:LEU:O	55:SH:73:GLN:HG2	2.17	0.45
65:SV:3:ASN:HA	71:SC:173:LYS:HE2	1.99	0.45
65:SV:17:CYS:HB2	65:SV:56:CYS:HB3	1.99	0.45
68:Sc:29:GLN:NE2	68:Sc:66:ARG:O	2.47	0.45
70:Sg:18:VAL:O	70:Sg:287:THR:OG1	2.29	0.45
74:SM:52:LEU:HD23	74:SM:108:CYS:SG	2.55	0.45
83:CA:79:SER:H	83:CA:109:ASP:HB3	1.81	0.45
20:LR:77:GLY:O	20:LR:81:ARG:NE	2.50	0.45
21:LS:76:LYS:HB3	21:LS:131:GLU:HG3	1.98	0.45
49:S2:466:G:O2'	72:SG:72:ARG:NH2	2.50	0.45
49:S2:1221:G:O2'	49:S2:1676:U:O2	2.34	0.45
49:S2:1512:C:H5''	69:Sd:8:TRP:HZ3	1.81	0.45
49:S2:1531:A:H4'	49:S2:1605:G:H4'	1.98	0.45
51:SB:26:SER:O	51:SB:51:ARG:NH1	2.50	0.45
51:SB:123:ALA:HB2	51:SB:165:ARG:HG3	1.99	0.45
71:SC:68:ARG:HG2	71:SC:277:HIS:HB2	1.98	0.45
84:CC:57:A:O2'	84:CC:59:U:OP2	2.31	0.45
1:L5:2429:A:H5''	40:Ll:43:HIS:HE2	1.80	0.45
1:L5:2902:G:N7	1:L5:2903:G:N2	2.65	0.45
4:LA:108:PRO:O	4:LA:111:THR:OG1	2.32	0.45
12:LI:179:ASP:OD1	12:LI:179:ASP:N	2.43	0.45
17:LO:54:TYR:OH	17:LO:73:PHE:O	2.34	0.45
31:Lc:50:ASN:ND2	31:Lc:76:GLY:O	2.50	0.45
50:SA:81:ASN:HA	50:SA:84:GLN:HB2	1.99	0.45
57:SK:20:VAL:HA	57:SK:69:TRP:O	2.17	0.45
1:L5:4939:C:OP1	8:LE:187:ARG:NH1	2.50	0.45
8:LE:191:GLN:HA	8:LE:194:VAL:HG22	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SD:62:LYS:O	52:SD:67:ARG:NH2	2.50	0.45
55:SH:6:ALA:O	55:SH:25:GLN:NE2	2.50	0.45
82:Sf:103:LEU:HD12	82:Sf:105:TYR:H	1.82	0.45
1:L5:29:G:H5''	16:LN:172:ARG:HG2	1.99	0.44
1:L5:98:A:H5'	16:LN:195:ARG:HD3	1.98	0.44
1:L5:1439:C:OP2	9:LF:31:LYS:NZ	2.50	0.44
1:L5:2442:G:O2'	1:L5:2512:A:N3	2.50	0.44
1:L5:3654:G:O2'	1:L5:3693:U:OP1	2.31	0.44
6:LC:209:ILE:HB	6:LC:229:LEU:HD13	1.98	0.44
10:LG:70:LEU:HD23	10:LG:70:LEU:HA	1.88	0.44
16:LN:114:ARG:NH1	16:LN:151:ILE:O	2.50	0.44
23:LU:63:ILE:HA	23:LU:71:THR:O	2.16	0.44
49:S2:527:C:H2'	49:S2:528:A:C8	2.52	0.44
52:SD:213:PRO:HD3	61:SR:19:LYS:HE3	1.99	0.44
57:SK:47:LYS:HA	57:SK:47:LYS:HD3	1.84	0.44
61:SR:36:GLU:OE1	61:SR:47:ARG:NH1	2.50	0.44
68:Sc:28:THR:O	68:Sc:45:ASN:HA	2.17	0.44
69:Sd:49:ASP:OD1	69:Sd:49:ASP:N	2.40	0.44
85:CE:196:LEU:HA	85:CE:199:LEU:HD23	1.99	0.44
1:L5:3689:G:O2'	1:L5:3818:U:OP2	2.25	0.44
1:L5:3712:A:N6	49:S2:970:G:O6	2.50	0.44
31:Lc:20:LEU:O	31:Lc:24:SER:OG	2.22	0.44
31:Lc:47:ILE:HD12	31:Lc:94:LEU:HD11	1.98	0.44
49:S2:902:G:O2'	49:S2:903:A:O4'	2.34	0.44
63:ST:97:LYS:H	63:ST:97:LYS:HG2	1.61	0.44
63:ST:122:LYS:HE2	63:ST:122:LYS:HB3	1.79	0.44
73:SJ:125:HIS:HA	73:SJ:128:VAL:HG22	2.00	0.44
1:L5:1514:U:H2'	1:L5:1515:A:C8	2.52	0.44
1:L5:2846:G:O2'	24:LV:19:GLY:O	2.31	0.44
4:LA:229:ALA:HB3	4:LA:234:LYS:HB3	1.99	0.44
72:SG:148:SER:N	72:SG:151:ASP:OD2	2.50	0.44
78:SY:55:ILE:HG12	78:SY:75:ILE:HG12	1.98	0.44
83:CA:134:GLN:HE21	83:CA:344:LYS:HG2	1.82	0.44
1:L5:2904:U:O4	1:L5:3592:G:N2	2.43	0.44
8:LE:190:HIS:HB3	8:LE:193:PHE:HD2	1.82	0.44
49:S2:104:A:H62	49:S2:356:C:H5	1.63	0.44
50:SA:11:LYS:HA	50:SA:11:LYS:HD3	1.74	0.44
59:SP:24:GLN:O	59:SP:28:MET:HB2	2.18	0.44
59:SP:124:LYS:HB2	59:SP:124:LYS:HE3	1.84	0.44
70:Sg:152:SER:H	70:Sg:169:GLY:HA2	1.83	0.44
85:CE:203:GLU:O	85:CE:206:ARG:O	2.35	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4323:A:H4'	7:LD:176:SER:HB3	1.99	0.44
7:LD:119:TYR:OH	7:LD:139:PRO:O	2.32	0.44
12:LI:68:ALA:HB1	12:LI:155:ALA:HB1	2.00	0.44
42:Ln:16:LYS:HB2	42:Ln:16:LYS:HE2	1.85	0.44
46:Ls:145:THR:HG23	46:Ls:154:ILE:HG13	1.99	0.44
48:Lz:35:GLN:HG3	48:Lz:166:ALA:HA	2.00	0.44
49:S2:379:C:H5'	56:SI:33:ALA:HA	1.98	0.44
49:S2:878:G:C6	49:S2:908:A:N1	2.86	0.44
54:SF:142:SER:OG	68:Sc:49:PRO:O	2.33	0.44
60:SQ:51:LEU:HD12	60:SQ:51:LEU:HA	1.83	0.44
71:SC:187:ARG:HD3	71:SC:192:LEU:HD12	2.00	0.44
1:L5:260:C:H2'	1:L5:261:G:C8	2.52	0.44
1:L5:2306:G:OP1	33:Le:128:ARG:NH2	2.50	0.44
1:L5:2520:C:O2	1:L5:2640:G:N2	2.51	0.44
1:L5:3961:G:O2'	1:L5:3965:A:OP1	2.35	0.44
5:LB:295:ASP:N	5:LB:295:ASP:OD1	2.51	0.44
13:LJ:167:GLN:HA	13:LJ:172:GLY:H	1.83	0.44
21:LS:95:ARG:HH22	21:LS:116:ARG:HD2	1.83	0.44
48:Lz:207:LYS:HE3	48:Lz:215:ARG:HD2	1.98	0.44
51:SB:175:GLU:OE1	51:SB:187:LYS:NZ	2.50	0.44
54:SF:30:ILE:HG23	54:SF:117:ILE:HD11	1.99	0.44
71:SC:179:THR:OG1	71:SC:221:ASP:O	2.34	0.44
13:LJ:120:ASP:HB3	13:LJ:123:ILE:HG12	2.00	0.44
20:LR:105:LEU:HD23	20:LR:138:LEU:HD23	2.00	0.44
23:LU:105:ASN:HB3	23:LU:111:GLU:HG2	1.99	0.44
26:LX:88:LYS:NZ	83:CA:258:LYS:O	2.37	0.44
49:S2:43:U:OP2	49:S2:485:A:N6	2.48	0.44
49:S2:588:G:H4'	49:S2:589:G:H5'	2.00	0.44
61:SR:41:ILE:HD12	61:SR:47:ARG:HG2	1.99	0.44
63:ST:52:TRP:HA	63:ST:55:THR:HG22	1.98	0.44
69:Sd:10:HIS:HB3	69:Sd:12:ARG:HH12	1.82	0.44
83:CA:23:MET:O	83:CA:27:ILE:HG12	2.18	0.44
84:CC:69:G:H2'	84:CC:70:G:C8	2.52	0.44
7:LD:64:ILE:HG13	7:LD:105:LEU:HD21	1.99	0.44
9:LF:57:TYR:OH	9:LF:189:ASP:OD1	2.33	0.44
9:LF:171:ASP:HB2	9:LF:174:LEU:HG	2.00	0.44
26:LX:37:LYS:HA	26:LX:38:LYS:HA	1.62	0.44
31:Lc:47:ILE:HB	31:Lc:94:LEU:HG	1.98	0.44
33:Le:89:LEU:HD12	33:Le:118:LEU:HD21	1.99	0.44
49:S2:996:A:H2'	49:S2:997:A:C8	2.53	0.44
49:S2:1513:C:H2'	49:S2:1514:G:H8	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:SS:75:ARG:HH11	62:SS:95:TYR:HB2	1.83	0.44
1:L5:3917:A:H2'	1:L5:3918:G:H8	1.82	0.44
1:L5:3955:G:N3	1:L5:3966:A:N7	2.65	0.44
17:LO:61:ARG:HA	17:LO:70:PRO:HD2	2.00	0.44
27:LY:56:GLN:HB3	27:LY:67:ILE:HD13	1.99	0.44
45:Lr:105:ASP:OD1	45:Lr:105:ASP:N	2.51	0.44
48:Lz:60:ARG:HH21	48:Lz:61:PRO:HG3	1.83	0.44
49:S2:154:U:O2	72:SG:4:ASN:ND2	2.43	0.44
49:S2:1353:A:OP1	50:SA:139:TYR:OH	2.27	0.44
49:S2:1550:G:O2'	49:S2:1558:C:O2	2.36	0.44
61:SR:106:LEU:HD23	61:SR:109:LEU:HD11	2.00	0.44
62:SS:98:VAL:HG11	62:SS:106:LYS:HG3	1.98	0.44
65:SV:17:CYS:O	65:SV:21:ASN:N	2.51	0.44
1:L5:4293:U:O2'	43:Lo:81:ARG:NH2	2.51	0.43
13:LJ:95:ARG:NH1	13:LJ:97:ASN:OD1	2.38	0.43
36:Lh:52:LYS:HA	36:Lh:52:LYS:HD3	1.82	0.43
48:Lz:41:TYR:CZ	48:Lz:43:PRO:HA	2.53	0.43
49:S2:641:A:O2'	49:S2:645:C:OP1	2.35	0.43
58:SL:21:LYS:HD2	58:SL:21:LYS:HA	1.83	0.43
66:SX:6:GLY:O	66:SX:9:THR:OG1	2.31	0.43
70:Sg:31:ILE:HG23	70:Sg:45:LEU:HD11	2.00	0.43
1:L5:1185:G:O2'	7:LD:278:ASP:OD2	2.33	0.43
7:LD:231:VAL:HA	7:LD:235:MET:HE1	2.00	0.43
8:LE:183:ARG:HD2	8:LE:183:ARG:HA	1.80	0.43
35:Lg:85:LYS:HB2	35:Lg:85:LYS:HE3	1.80	0.43
50:SA:26:GLY:O	50:SA:150:THR:OG1	2.29	0.43
60:SQ:134:GLY:HA3	60:SQ:140:ARG:HA	2.00	0.43
72:SG:4:ASN:HB3	72:SG:110:ASN:HD22	1.83	0.43
1:L5:1339:U:H2'	1:L5:1340:C:C6	2.53	0.43
1:L5:2335:C:H2'	1:L5:2336:G:H8	1.82	0.43
48:Lz:110:PHE:HE2	48:Lz:128:LEU:HD13	1.83	0.43
49:S2:1143:A:OP2	71:SC:187:ARG:NH1	2.42	0.43
53:SE:21:ASP:OD1	53:SE:21:ASP:N	2.44	0.43
1:L5:2485:U:H4'	1:L5:2486:G:N2	2.34	0.43
1:L5:2486:G:O6	1:L5:2493:G:O6	2.36	0.43
25:LW:101:ARG:NH1	72:SG:156:TYR:OH	2.51	0.43
49:S2:496:C:OP1	53:SE:49:ARG:NH1	2.43	0.43
49:S2:606:G:OP2	86:CF:175:ARG:NH2	2.37	0.43
49:S2:981:A:H2'	49:S2:982:G:C8	2.54	0.43
53:SE:107:GLY:HA2	53:SE:189:LEU:HG	2.00	0.43
58:SL:111:VAL:HG12	58:SL:140:PHE:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:SJ:120:ALA:HB2	73:SJ:129:LEU:HD22	1.99	0.43
1:L5:1802:A:H5''	1:L5:1803:G:H5'	2.00	0.43
1:L5:4893:A:OP1	17:LO:188:LYS:NZ	2.44	0.43
3:L8:102:G:OP2	3:L8:104:A:O2'	2.30	0.43
8:LE:223:ARG:NH1	8:LE:236:GLU:O	2.52	0.43
49:S2:305:U:H4'	56:SI:41:ARG:HH11	1.84	0.43
49:S2:921:G:C5	77:SW:28:ARG:HD2	2.54	0.43
49:S2:1221:G:H2'	49:S2:1222:G:C8	2.54	0.43
62:SS:38:ARG:O	62:SS:42:HIS:ND1	2.41	0.43
77:SW:32:LYS:HA	77:SW:35:VAL:HG22	1.99	0.43
1:L5:5027:C:H5	56:SI:79:ILE:HD12	1.84	0.43
18:LP:6:LEU:HD12	18:LP:116:HIS:CD2	2.54	0.43
26:LX:112:ALA:O	26:LX:116:LEU:HB2	2.18	0.43
31:Lc:36:LYS:HB3	31:Lc:36:LYS:HE2	1.79	0.43
37:Li:76:ARG:HA	37:Li:76:ARG:HD3	1.71	0.43
49:S2:60:G:N2	49:S2:317:C:O4'	2.50	0.43
49:S2:549:C:H2'	49:S2:550:C:C6	2.54	0.43
49:S2:1147:C:OP1	67:Sa:6:ARG:NH1	2.51	0.43
49:S2:1845:A:H2'	49:S2:1846:G:C8	2.54	0.43
52:SD:18:LYS:HE2	52:SD:39:VAL:HB	2.01	0.43
54:SF:61:PHE:CZ	68:Sc:51:ARG:HB2	2.53	0.43
55:SH:144:ILE:HD11	55:SH:152:ARG:HD3	1.99	0.43
66:SX:52:LEU:HD11	66:SX:73:GLN:HB2	2.00	0.43
70:Sg:10:THR:HB	70:Sg:306:LEU:HD12	2.00	0.43
70:Sg:176:VAL:HB	70:Sg:186:THR:HG22	2.00	0.43
83:CA:15:ASP:HA	83:CA:18:VAL:HG22	2.00	0.43
1:L5:1837:A:OP2	22:LT:130:ARG:NH2	2.47	0.43
1:L5:2899:C:OP1	20:LR:108:ARG:NH2	2.52	0.43
1:L5:3786:U:OP1	1:L5:4550:G:O2'	2.31	0.43
1:L5:4530:U:H2'	1:L5:4531:U:H2'	2.01	0.43
5:LB:362:LYS:HA	5:LB:362:LYS:HD3	1.92	0.43
6:LC:29:LYS:HD3	6:LC:29:LYS:HA	1.83	0.43
10:LG:57:TRP:O	10:LG:62:ARG:NH1	2.52	0.43
49:S2:318:A:N6	72:SG:186:GLN:OE1	2.51	0.43
49:S2:583:A:H2'	49:S2:584:A:H8	1.82	0.43
49:S2:615:C:O2	81:Se:11:LYS:NZ	2.46	0.43
49:S2:1047:C:H5'	76:SO:143:LYS:HB2	1.99	0.43
52:SD:69:LEU:HD23	52:SD:69:LEU:HA	1.92	0.43
53:SE:51:ARG:NH2	53:SE:109:PHE:O	2.50	0.43
63:ST:105:GLN:HA	63:ST:108:GLU:HG2	2.00	0.43
72:SG:58:LYS:NZ	72:SG:106:LEU:O	2.45	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:SO:67:ASP:OD1	76:SO:67:ASP:N	2.47	0.43
82:Sf:141:CYS:O	82:Sf:145:CYS:CA	2.60	0.43
9:LF:236:ARG:HD3	9:LF:239:GLN:HB2	2.00	0.43
24:LV:82:ILE:HD12	24:LV:121:VAL:HG22	2.01	0.43
49:S2:672:A:N6	49:S2:1027:A:OP1	2.36	0.43
49:S2:857:U:H2'	49:S2:858:A:C8	2.54	0.43
49:S2:1472:C:O3'	70:Sg:15:ASN:ND2	2.52	0.43
49:S2:1705:C:H2'	49:S2:1706:G:C8	2.54	0.43
65:SV:25:GLY:O	71:SC:85:SER:OG	2.37	0.43
78:SY:82:ALA:O	78:SY:86:GLU:CB	2.67	0.43
1:L5:188:G:O2'	1:L5:190:G:OP2	2.33	0.43
1:L5:1971:C:N4	1:L5:2001:G:OP1	2.51	0.43
1:L5:2749:C:H5'	35:Lg:65:MET:HA	2.01	0.43
1:L5:4258:C:H2'	1:L5:4259:C:H6	1.84	0.43
5:LB:35:ASP:OD2	5:LB:193:LYS:NZ	2.52	0.43
7:LD:291:GLN:NE2	12:LI:214:SER:OG	2.52	0.43
8:LE:161:ARG:O	8:LE:182:ASN:ND2	2.51	0.43
9:LF:214:SER:OG	9:LF:215:SER:N	2.51	0.43
49:S2:944:A:H5''	76:SO:134:PRO:HB3	2.01	0.43
66:SX:77:ASN:O	66:SX:79:LYS:N	2.47	0.43
70:Sg:218:LEU:HD22	70:Sg:261:LEU:HD11	2.01	0.43
84:CC:68:C:H2'	84:CC:69:G:C8	2.54	0.43
1:L5:4924:C:O2'	1:L5:4926:C:O2	2.28	0.43
5:LB:155:LYS:HE3	5:LB:155:LYS:HB2	1.94	0.43
7:LD:10:LYS:O	7:LD:14:LYS:HB2	2.18	0.43
10:LG:95:LEU:HD21	10:LG:156:VAL:HG21	1.99	0.43
16:LN:46:ASP:OD1	16:LN:46:ASP:N	2.52	0.43
18:LP:94:MET:HE2	18:LP:148:MET:HE3	2.01	0.43
27:LY:19:PHE:O	27:LY:26:ARG:NH2	2.51	0.43
52:SD:170:THR:HG23	52:SD:187:LYS:HG2	2.01	0.43
53:SE:18:TRP:HH2	53:SE:31:PRO:HD3	1.84	0.43
58:SL:29:GLY:HA3	58:SL:30:LYS:HA	1.64	0.43
72:SG:159:ARG:HH21	72:SG:171:THR:HG23	1.83	0.43
78:SY:14:THR:HB	78:SY:21:LYS:HG2	2.00	0.43
78:SY:62:THR:HA	78:SY:69:THR:HA	2.01	0.43
1:L5:2758:G:O2'	1:L5:2765:A:N3	2.41	0.42
3:L8:8:U:H2'	3:L8:9:A:C8	2.54	0.42
12:LI:47:PRO:HD2	12:LI:141:LYS:HA	2.00	0.42
12:LI:52:MET:HB2	12:LI:152:LEU:HD22	2.00	0.42
19:LQ:159:PRO:HA	19:LQ:160:HIS:HA	1.72	0.42
39:Lk:21:LYS:N	39:Lk:37:ARG:O	2.47	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:Lr:62:VAL:O	45:Lr:79:ARG:HA	2.19	0.42
53:SE:9:LEU:HB2	53:SE:30:ARG:HD3	2.01	0.42
55:SH:20:GLU:O	55:SH:24:SER:OG	2.26	0.42
58:SL:66:VAL:HG11	58:SL:141:ASN:HD22	1.84	0.42
70:Sg:73:SER:OG	70:Sg:117:ASN:ND2	2.47	0.42
70:Sg:99:ARG:HA	70:Sg:99:ARG:HD2	1.87	0.42
78:SY:35:VAL:HG13	78:SY:40:ILE:HD11	2.00	0.42
1:L5:493:G:C6	1:L5:660:A:N1	2.87	0.42
1:L5:4743:G:H2'	1:L5:4744:A:H8	1.84	0.42
49:S2:307:G:O6	56:SI:44:HIS:ND1	2.52	0.42
63:ST:3:GLY:HA2	63:ST:4:VAL:HA	1.86	0.42
70:Sg:106:LYS:HB2	70:Sg:126:ASP:HB3	2.01	0.42
70:Sg:121:VAL:HG11	70:Sg:165:ILE:HD11	2.00	0.42
76:SO:63:LYS:HA	76:SO:63:LYS:HD3	1.89	0.42
1:L5:210:C:O2'	1:L5:233:U:O2	2.37	0.42
1:L5:295:A:H5''	1:L5:296:A:H5'	2.01	0.42
1:L5:1279:A:O2'	1:L5:1281:G:N7	2.52	0.42
1:L5:5066:U:OP1	18:LP:43:LYS:NZ	2.37	0.42
31:Lc:38:ILE:HG21	31:Lc:63:TYR:HB3	2.02	0.42
31:Lc:55:LEU:HD11	35:Lg:92:LYS:HG3	2.02	0.42
48:Lz:67:VAL:HA	48:Lz:68:LEU:HA	1.57	0.42
48:Lz:112:ALA:HB1	48:Lz:137:LEU:HD22	2.00	0.42
49:S2:197:U:OP2	49:S2:203:G:N2	2.40	0.42
49:S2:943:U:O2'	76:SO:135:ILE:O	2.34	0.42
75:SN:83:ASP:OD1	75:SN:83:ASP:N	2.50	0.42
79:SZ:47:LEU:HD21	79:SZ:50:PHE:HA	2.00	0.42
83:CA:48:LEU:HD23	83:CA:80:ILE:HD13	2.01	0.42
1:L5:27:C:OP1	16:LN:193:ARG:NH1	2.52	0.42
2:L7:38:U:N3	2:L7:41:G:OP2	2.40	0.42
12:LI:140:THR:OG1	12:LI:141:LYS:N	2.52	0.42
12:LI:170:LYS:NZ	12:LI:177:ASN:OD1	2.52	0.42
32:Ld:40:LYS:HA	32:Ld:40:LYS:HD3	1.86	0.42
33:Le:70:LEU:HD11	33:Le:76:LYS:HG3	2.01	0.42
43:Lo:59:LYS:HD2	43:Lo:59:LYS:HA	1.77	0.42
48:Lz:176:ASP:OD1	48:Lz:176:ASP:N	2.51	0.42
49:S2:1435:C:O2'	49:S2:1436:C:O4'	2.34	0.42
49:S2:1779:G:H2'	49:S2:1780:G:C8	2.54	0.42
51:SB:124:HIS:HA	51:SB:137:LEU:O	2.18	0.42
53:SE:11:ARG:HA	53:SE:28:ALA:HB2	2.01	0.42
54:SF:50:PRO:HB3	54:SF:69:VAL:HG23	2.01	0.42
56:SI:117:TYR:HD1	56:SI:152:ARG:HB3	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:SJ:67:ASP:HB3	73:SJ:70:ARG:HB3	2.00	0.42
74:SM:59:PRO:HA	74:SM:62:VAL:HG22	2.00	0.42
1:L5:1324:A:O2'	1:L5:1326:A:OP1	2.34	0.42
1:L5:1995:G:H21	47:Lt:122:ALA:HB3	1.83	0.42
1:L5:1998:A:H4'	46:Ls:9:TRP:HZ2	1.84	0.42
1:L5:3861:A:H2'	1:L5:3862:A:C8	2.54	0.42
1:L5:4083:U:OP1	4:LA:123:ARG:NH2	2.52	0.42
1:L5:4146:G:H2'	1:L5:4147:G:C8	2.54	0.42
1:L5:4194:U:O2'	12:LI:116:ARG:NH1	2.52	0.42
14:LL:46:ILE:HB	14:LL:49:ARG:HB2	2.00	0.42
14:LL:116:ARG:NH1	14:LL:155:MET:O	2.49	0.42
46:Ls:133:GLU:HG2	46:Ls:152:ILE:HG13	2.01	0.42
49:S2:118:C:H1'	49:S2:445:A:C5	2.55	0.42
49:S2:1764:G:H5'	49:S2:1765:C:H5''	2.01	0.42
58:SL:75:GLY:HA3	58:SL:88:ILE:HD12	2.02	0.42
64:SU:18:HIS:HB3	64:SU:117:ALA:HB2	2.00	0.42
83:CA:248:LYS:HE2	83:CA:248:LYS:HB2	1.87	0.42
1:L5:1921:C:C6	21:LS:161:ARG:HD3	2.54	0.42
1:L5:1994:C:H1'	47:Lt:132:ILE:HA	2.02	0.42
1:L5:2520:C:H2'	1:L5:2521:G:C8	2.54	0.42
1:L5:4741:C:H4'	1:L5:4742:G:H5'	2.02	0.42
3:L8:62:A:OP1	36:Lh:51:ARG:NH2	2.53	0.42
6:LC:224:ILE:HB	6:LC:227:ILE:HD12	2.01	0.42
11:LH:92:MET:HE2	11:LH:179:ILE:HG22	2.01	0.42
28:LZ:48:ARG:HB2	28:LZ:69:LYS:HB3	2.01	0.42
28:LZ:54:THR:HG23	28:LZ:57:MET:HE3	2.02	0.42
39:Lk:70:LYS:HA	39:Lk:70:LYS:HD3	1.85	0.42
49:S2:319:C:H2'	49:S2:320:G:H8	1.84	0.42
49:S2:550:C:H2'	49:S2:551:U:C6	2.54	0.42
49:S2:1672:U:OP1	60:SQ:18:THR:OG1	2.30	0.42
49:S2:1808:U:H2'	49:S2:1809:A:C8	2.55	0.42
60:SQ:89:SER:HB2	60:SQ:112:LEU:HD13	2.01	0.42
63:ST:22:LEU:O	63:ST:26:GLY:HA2	2.19	0.42
85:CE:29:LYS:HA	85:CE:32:LYS:HG2	2.01	0.42
1:L5:62:A:N3	1:L5:77:U:O2'	2.48	0.42
1:L5:1238:A:O2'	9:LF:52:GLU:OE2	2.32	0.42
1:L5:1500:A:H5''	1:L5:1501:C:H5''	2.00	0.42
1:L5:4896:G:H2'	1:L5:4897:G:C8	2.54	0.42
2:L7:74:A:O2'	21:LS:53:LYS:NZ	2.36	0.42
9:LF:94:ARG:O	9:LF:118:PHE:N	2.52	0.42
45:Lr:63:VAL:HG22	45:Lr:79:ARG:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:1215:C:O2'	49:S2:1645:C:OP2	2.34	0.42
49:S2:1226:G:N1	49:S2:1639:G:OP2	2.38	0.42
59:SP:12:PHE:HD2	59:SP:14:LYS:HE2	1.85	0.42
72:SG:2:LYS:HB3	72:SG:15:LEU:HD11	2.01	0.42
73:SJ:176:LYS:HA	73:SJ:179:LYS:HG2	2.00	0.42
83:CA:55:MET:HE2	83:CA:55:MET:HB2	1.88	0.42
1:L5:1213:G:OP1	9:LF:59:LYS:NZ	2.53	0.42
1:L5:1259:G:H2'	1:L5:1260:G:H8	1.85	0.42
1:L5:2008:U:O2'	1:L5:2010:A:N7	2.50	0.42
1:L5:4478:G:O2'	1:L5:4602:A:N1	2.51	0.42
3:L8:79:G:O2'	36:Lh:46:LYS:NZ	2.41	0.42
12:LI:206:LEU:HD12	12:LI:206:LEU:HA	1.92	0.42
47:Lt:39:PRO:C	47:Lt:40:LYS:HE2	2.45	0.42
54:SF:127:ARG:HB2	54:SF:136:ARG:H	1.83	0.42
56:SI:145:ILE:HA	56:SI:148:LYS:HG2	2.02	0.42
59:SP:92:SER:OG	59:SP:93:MET:N	2.52	0.42
60:SQ:34:VAL:HA	60:SQ:70:VAL:HG22	2.02	0.42
70:Sg:15:ASN:OD1	70:Sg:15:ASN:N	2.52	0.42
71:SC:278:THR:HA	71:SC:279:ARG:HA	1.76	0.42
83:CA:226:VAL:O	83:CA:320:LYS:HA	2.20	0.42
1:L5:230:G:OP1	27:LY:15:ARG:NH1	2.49	0.42
1:L5:460:C:H2'	1:L5:461:G:H8	1.85	0.42
1:L5:1308:C:H2'	1:L5:1309:C:C6	2.54	0.42
1:L5:3868:G:H22	1:L5:3900:G:H1'	1.85	0.42
1:L5:4618:G:H5''	24:LV:15:ARG:HB2	2.00	0.42
15:LM:7:VAL:HG13	15:LM:27:ILE:HD13	2.01	0.42
16:LN:39:ALA:HB3	16:LN:61:ILE:HB	2.01	0.42
31:Lc:60:ILE:HD13	31:Lc:60:ILE:HA	1.93	0.42
36:Lh:105:LYS:HE3	36:Lh:105:LYS:HB2	1.89	0.42
44:Lp:38:THR:HA	44:Lp:45:THR:HA	2.01	0.42
49:S2:367:U:H4'	49:S2:371:A:C8	2.55	0.42
49:S2:455:A:H2'	49:S2:456:C:C6	2.55	0.42
58:SL:119:ASP:O	58:SL:147:LYS:NZ	2.53	0.42
74:SM:21:VAL:HA	74:SM:24:THR:HG22	2.02	0.42
10:LG:99:ALA:HB1	10:LG:193:LEU:HD13	2.02	0.42
30:Lb:8:THR:HB	30:Lb:10:HIS:H	1.85	0.42
47:Lt:61:LYS:HG3	47:Lt:74:VAL:HG22	2.02	0.42
49:S2:955:A:N6	49:S2:971:G:H1'	2.35	0.42
51:SB:83:LYS:NZ	76:SO:130:GLU:OE2	2.47	0.42
53:SE:143:ASP:N	53:SE:143:ASP:OD1	2.44	0.42
57:SK:95:ARG:O	57:SK:96:ARG:NE	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3612:C:H1'	1:L5:5016:A:C8	2.55	0.41
1:L5:3777:G:O2'	1:L5:3815:G:O6	2.35	0.41
1:L5:4169:G:H4'	1:L5:4171:C:C2	2.55	0.41
11:LH:171:ASP:O	11:LH:174:LYS:C	2.63	0.41
24:LV:59:ASP:O	24:LV:80:VAL:HA	2.20	0.41
29:La:100:ILE:HG13	29:La:123:ILE:HB	2.02	0.41
49:S2:1144:A:H2'	49:S2:1145:A:C8	2.54	0.41
62:SS:124:ARG:O	62:SS:127:TRP:C	2.62	0.41
63:ST:2:PRO:HA	63:ST:3:GLY:HA3	1.76	0.41
75:SN:114:ARG:O	75:SN:118:ILE:HG12	2.20	0.41
1:L5:1464:C:H5''	30:Lb:32:LEU:HD12	2.02	0.41
1:L5:4039:G:N2	1:L5:4050:A:O2'	2.53	0.41
18:LP:46:LYS:HE3	18:LP:46:LYS:HB2	1.76	0.41
20:LR:137:ILE:HD13	20:LR:137:ILE:HA	1.94	0.41
22:LT:42:ILE:O	22:LT:59:GLY:N	2.50	0.41
25:LW:105:ARG:NH2	72:SG:151:ASP:OD1	2.49	0.41
34:Lf:37:ASP:OD1	34:Lf:37:ASP:N	2.53	0.41
49:S2:165:G:OP2	49:S2:165:G:N2	2.41	0.41
55:SH:9:VAL:HA	55:SH:44:ASN:HD21	1.85	0.41
64:SU:24:LEU:HD22	64:SU:112:VAL:HG12	2.02	0.41
68:Sc:22:GLY:O	68:Sc:26:GLN:NE2	2.49	0.41
70:Sg:14:HIS:HE1	70:Sg:18:VAL:HG22	1.85	0.41
71:SC:104:ASP:HB3	71:SC:130:ILE:HG13	2.01	0.41
83:CA:152:ALA:O	83:CA:156:LEU:CB	2.68	0.41
84:CC:63:C:H2'	84:CC:64:G:H8	1.85	0.41
1:L5:10:A:H2'	1:L5:11:G:C8	2.54	0.41
1:L5:2491:C:O2'	1:L5:2492:C:O4'	2.34	0.41
5:LB:57:VAL:HG22	5:LB:73:VAL:HG22	2.02	0.41
46:Ls:28:PHE:HZ	46:Ls:95:LEU:HA	1.84	0.41
49:S2:31:U:OP1	66:SX:137:LYS:NZ	2.51	0.41
50:SA:207:PRO:HA	50:SA:210:ILE:HB	2.02	0.41
52:SD:113:LEU:HD23	52:SD:113:LEU:HA	1.94	0.41
55:SH:144:ILE:HD13	55:SH:154:ILE:HG12	2.02	0.41
56:SI:104:ILE:O	56:SI:170:LYS:HA	2.21	0.41
64:SU:38:ASP:HA	64:SU:41:ARG:HG2	2.01	0.41
65:SV:17:CYS:O	65:SV:21:ASN:HA	2.21	0.41
72:SG:33:ALA:N	72:SG:52:ILE:O	2.54	0.41
72:SG:135:PRO:HG2	72:SG:141:ILE:HG12	2.01	0.41
76:SO:84:ARG:NH1	76:SO:87:GLU:OE1	2.53	0.41
83:CA:246:ILE:HB	83:CA:305:PHE:HB2	2.00	0.41
84:CC:41:U:H2'	84:CC:42:G:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:717:U:H2'	1:L5:718:C:C6	2.55	0.41
1:L5:3664:G:H2'	1:L5:3665:G:H8	1.85	0.41
1:L5:3917:A:H2'	1:L5:3918:G:C8	2.56	0.41
1:L5:4736:C:H2'	1:L5:4737:G:H8	1.86	0.41
1:L5:4935:C:H2'	1:L5:4936:G:C8	2.55	0.41
2:L7:94:C:H4'	21:LS:122:HIS:HB2	2.01	0.41
6:LC:157:LYS:HE3	6:LC:157:LYS:HB2	1.92	0.41
7:LD:184:ASP:OD2	7:LD:187:SER:N	2.52	0.41
11:LH:129:ARG:NE	11:LH:156:ASN:OD1	2.51	0.41
34:Lf:36:ARG:HD2	34:Lf:80:ASN:H	1.86	0.41
48:Lz:120:ILE:O	48:Lz:124:LEU:CB	2.63	0.41
48:Lz:161:LYS:NZ	84:CC:54:U:OP1	2.42	0.41
49:S2:1284:A:N7	74:SM:33:ARG:NH2	2.67	0.41
49:S2:1589:A:N3	49:S2:1653:U:O2'	2.50	0.41
52:SD:221:THR:HA	52:SD:222:PRO:HD3	1.91	0.41
79:SZ:79:ILE:HB	79:SZ:83:LEU:HD23	2.03	0.41
1:L5:513:U:O2'	1:L5:515:C:N4	2.52	0.41
1:L5:968:C:O4'	8:LE:110:ARG:NH2	2.54	0.41
1:L5:1258:G:H2'	1:L5:1259:G:C8	2.56	0.41
1:L5:1380:G:N2	1:L5:1381:U:O4	2.46	0.41
1:L5:2493:G:O2'	3:L8:127:U:OP1	2.27	0.41
1:L5:2748:C:O2'	35:Lg:61:PRO:O	2.32	0.41
5:LB:300:LYS:HE3	5:LB:300:LYS:HB2	1.88	0.41
21:LS:13:VAL:HA	21:LS:28:TYR:O	2.21	0.41
47:Lt:61:LYS:HB3	47:Lt:72:GLU:HG2	2.03	0.41
49:S2:51:U:H2'	49:S2:52:G:C8	2.56	0.41
49:S2:416:U:H2'	49:S2:417:C:H5'	2.02	0.41
49:S2:508:A:H3'	49:S2:509:G:H8	1.85	0.41
49:S2:570:C:O2'	78:SY:34:THR:O	2.25	0.41
49:S2:1473:G:N1	49:S2:1476:A:OP2	2.49	0.41
51:SB:86:LEU:HD23	51:SB:86:LEU:HA	1.83	0.41
77:SW:30:CYS:SG	77:SW:31:SER:N	2.93	0.41
79:SZ:74:SER:HA	79:SZ:79:ILE:HG12	2.02	0.41
1:L5:1879:C:O2'	1:L5:1891:A:N3	2.54	0.41
1:L5:4251:A:H5''	13:LJ:108:GLY:HA3	2.01	0.41
2:L7:119:U:C2	7:LD:261:VAL:HG11	2.55	0.41
8:LE:91:THR:HA	8:LE:108:LYS:HA	2.03	0.41
49:S2:838:G:O2'	49:S2:840:C:OP2	2.38	0.41
49:S2:1101:U:H2'	49:S2:1102:G:C8	2.55	0.41
52:SD:161:GLY:O	52:SD:164:VAL:N	2.54	0.41
60:SQ:32:ILE:HD11	60:SQ:88:ILE:HD13	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:SR:106:LEU:HD13	61:SR:117:LEU:HD21	2.03	0.41
70:Sg:8:ARG:HA	70:Sg:8:ARG:HD3	1.92	0.41
73:SJ:169:ARG:HD2	73:SJ:169:ARG:HA	1.85	0.41
1:L5:1513:U:H4'	14:LL:4:SER:HB2	2.02	0.41
1:L5:1994:C:H2'	1:L5:1995:G:C8	2.54	0.41
1:L5:4219:A:H2'	1:L5:4220:A:C8	2.55	0.41
5:LB:224:LYS:HE2	5:LB:340:THR:HG22	2.01	0.41
11:LH:104:VAL:HG22	11:LH:113:GLU:HB2	2.03	0.41
13:LJ:15:LEU:HD12	13:LJ:134:LEU:HD13	2.01	0.41
17:LO:177:LEU:HD23	17:LO:177:LEU:HA	1.92	0.41
21:LS:43:ARG:HD2	21:LS:43:ARG:HA	1.86	0.41
31:Lc:65:MET:HE3	31:Lc:65:MET:HB3	1.99	0.41
32:Ld:70:LYS:HE2	32:Ld:70:LYS:HB3	1.90	0.41
46:Ls:14:PHE:O	46:Ls:18:ILE:HG12	2.20	0.41
47:Lt:79:ALA:O	47:Lt:83:LYS:HG2	2.21	0.41
48:Lz:31:THR:O	48:Lz:208:SER:OG	2.33	0.41
62:SS:36:VAL:HG13	62:SS:40:TYR:HD2	1.86	0.41
82:Sf:113:LYS:HA	82:Sf:113:LYS:HD3	1.73	0.41
83:CA:158:LYS:HA	83:CA:158:LYS:HD2	1.76	0.41
1:L5:1194:G:H2'	1:L5:1195:G:C8	2.55	0.41
1:L5:1741:G:O6	2:L7:103:A:O2'	2.35	0.41
1:L5:2337:C:H4'	45:Lr:19:LYS:HB2	2.03	0.41
1:L5:2515:G:OP1	35:Lg:37:LYS:NZ	2.42	0.41
1:L5:2543:A:H2	1:L5:2773:G:H22	1.69	0.41
8:LE:190:HIS:HD2	8:LE:192:LYS:H	1.69	0.41
23:LU:17:GLN:NE2	23:LU:75:GLU:OE2	2.54	0.41
25:LW:117:LYS:HA	25:LW:120:GLN:HG2	2.03	0.41
37:Li:63:VAL:HG23	37:Li:65:LYS:HG2	2.03	0.41
49:S2:795:A:H2'	49:S2:796:G:C8	2.56	0.41
51:SB:202:GLN:HE22	51:SB:206:PRO:HB3	1.85	0.41
55:SH:60:ILE:O	55:SH:92:VAL:HA	2.21	0.41
63:ST:102:ARG:HA	63:ST:102:ARG:HD3	1.88	0.41
71:SC:132:ASP:OD1	71:SC:132:ASP:N	2.53	0.41
84:CC:49:G:H2'	84:CC:50:G:H8	1.85	0.41
1:L5:1687:U:OP2	30:Lb:19:ASN:ND2	2.53	0.41
1:L5:1785:C:OP1	12:LI:133:GLN:NE2	2.54	0.41
1:L5:2696:A:H62	39:Lk:35:LYS:HE2	1.85	0.41
1:L5:3961:G:H1'	1:L5:3965:A:N1	2.36	0.41
1:L5:4238:G:H2'	1:L5:4239:A:C8	2.55	0.41
1:L5:4239:A:H2'	1:L5:4240:G:C8	2.56	0.41
1:L5:4318:C:O2'	43:Lo:18:HIS:ND1	2.44	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4742:G:H2'	1:L5:4743:G:C8	2.55	0.41
5:LB:113:GLU:HA	5:LB:116:ARG:HD2	2.03	0.41
7:LD:52:ILE:HA	7:LD:147:ASP:HB3	2.02	0.41
8:LE:88:VAL:HA	8:LE:89:LEU:HA	1.79	0.41
10:LG:117:ARG:NH2	10:LG:128:VAL:O	2.45	0.41
23:LU:100:LEU:HD23	23:LU:112:LEU:HD23	2.01	0.41
33:Le:90:MET:HG2	45:Lr:33:LYS:HA	2.02	0.41
44:Lp:73:THR:HG22	44:Lp:75:SER:H	1.85	0.41
47:Lt:54:LYS:HA	47:Lt:55:GLY:HA2	1.84	0.41
49:S2:935:G:O2'	75:SN:108:ASP:OD1	2.34	0.41
49:S2:1588:A:H2'	49:S2:1589:A:C8	2.56	0.41
51:SB:117:TRP:HB3	51:SB:153:THR:HG22	2.03	0.41
52:SD:45:ARG:HA	52:SD:83:SER:O	2.21	0.41
55:SH:10:LYS:HB3	55:SH:10:LYS:HE2	1.78	0.41
56:SI:134:GLU:OE2	56:SI:138:ASN:ND2	2.54	0.41
56:SI:153:LYS:HB3	56:SI:153:LYS:HE2	1.88	0.41
60:SQ:42:ILE:HD12	60:SQ:42:ILE:HA	1.93	0.41
60:SQ:70:VAL:HG21	60:SQ:84:ILE:HD12	2.02	0.41
62:SS:28:PHE:HE1	62:SS:38:ARG:HD2	1.85	0.41
70:Sg:20:GLN:HG2	70:Sg:69:VAL:H	1.86	0.41
72:SG:102:VAL:HG21	72:SG:109:LEU:HD11	2.03	0.41
73:SJ:116:LYS:HB3	73:SJ:116:LYS:HE2	1.84	0.41
78:SY:4:THR:O	78:SY:32:LYS:NZ	2.48	0.41
83:CA:78:THR:CA	83:CA:109:ASP:O	2.46	0.41
83:CA:100:LEU:HD21	83:CA:127:VAL:HG11	2.02	0.41
83:CA:159:PRO:HG3	83:CA:219:GLU:HA	2.02	0.41
83:CA:189:GLN:HA	83:CA:224:TYR:HD1	1.86	0.41
86:CF:162:ASN:OD1	86:CF:162:ASN:N	2.54	0.41
1:L5:186:G:H1'	1:L5:1366:G:H21	1.86	0.41
1:L5:4896:G:H2'	1:L5:4897:G:H8	1.86	0.41
3:L8:3:A:O2'	18:LP:61:ARG:NH2	2.53	0.41
10:LG:132:ARG:HA	10:LG:133:PRO:HD3	1.84	0.41
17:LO:179:LYS:HA	17:LO:179:LYS:HD3	1.94	0.41
48:Lz:189:PHE:O	48:Lz:192:SER:OG	2.38	0.41
49:S2:1354:G:N2	49:S2:1357:A:OP2	2.42	0.41
54:SF:16:ASP:N	54:SF:24:SER:OG	2.47	0.41
55:SH:12:ASN:HD22	55:SH:16:PRO:HG2	1.85	0.41
69:Sd:3:HIS:CE1	69:Sd:5:GLN:HB2	2.55	0.41
81:Se:36:MET:HE2	81:Se:36:MET:HB2	2.01	0.41
1:L5:189:G:H2'	1:L5:190:G:H8	1.86	0.40
1:L5:490:C:H2'	1:L5:491:G:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4699:U:H1'	1:L5:4700:A:H5''	2.02	0.40
2:L7:39:C:H4'	13:LJ:47:THR:HG23	2.04	0.40
8:LE:245:GLN:HA	8:LE:248:ILE:HG12	2.03	0.40
47:Lt:114:ARG:HE	47:Lt:133:LEU:HB2	1.85	0.40
47:Lt:124:GLU:HB3	47:Lt:128:THR:HG21	2.02	0.40
48:Lz:208:SER:H	48:Lz:211:GLY:HA3	1.86	0.40
49:S2:1265:A:H2	49:S2:1517:G:H22	1.69	0.40
65:SV:2:GLN:NE2	65:SV:6:GLY:O	2.54	0.40
77:SW:84:LYS:HE3	77:SW:84:LYS:HB2	1.87	0.40
83:CA:81:SER:HB3	83:CA:107:LYS:HE2	2.03	0.40
1:L5:153:G:H2'	1:L5:154:G:H8	1.86	0.40
1:L5:1556:C:O2'	1:L5:2669:C:OP1	2.33	0.40
1:L5:4195:G:O2'	1:L5:4442:U:OP1	2.29	0.40
9:LF:104:LYS:HB2	9:LF:104:LYS:HE2	1.95	0.40
9:LF:200:ARG:HA	9:LF:200:ARG:HD3	1.88	0.40
15:LM:89:THR:HG23	15:LM:92:ALA:H	1.86	0.40
17:LO:12:ARG:HD3	17:LO:37:ARG:NH1	2.37	0.40
17:LO:27:VAL:HG23	17:LO:98:ALA:HB1	2.03	0.40
29:La:64:LYS:HB2	29:La:67:GLN:HE21	1.85	0.40
31:Lc:57:LYS:HE3	31:Lc:57:LYS:HB2	1.83	0.40
49:S2:570:C:H4'	78:SY:36:PRO:HG3	2.03	0.40
50:SA:126:ASP:HB3	50:SA:129:ALA:HB3	2.03	0.40
53:SE:45:ILE:HA	53:SE:61:VAL:HG11	2.01	0.40
59:SP:91:GLY:N	59:SP:107:ILE:O	2.51	0.40
70:Sg:34:ALA:HB2	70:Sg:69:VAL:HB	2.03	0.40
83:CA:290:ARG:HA	83:CA:293:VAL:HG22	2.03	0.40
1:L5:1405:C:H42	1:L5:1413:C:H42	1.68	0.40
1:L5:1646:A:O2'	38:Lj:49:TRP:O	2.37	0.40
1:L5:3643:A:N7	38:Lj:2:THR:OG1	2.48	0.40
1:L5:4457:U:H1'	5:LB:252:ALA:HB3	2.03	0.40
1:L5:4940:C:OP1	8:LE:156:ARG:NH2	2.50	0.40
1:L5:4967:A:H2'	1:L5:4968:A:C8	2.55	0.40
5:LB:220:ILE:HB	5:LB:346:THR:HB	2.03	0.40
11:LH:113:GLU:HG2	11:LH:125:ARG:HG2	2.04	0.40
37:Li:16:LYS:HA	37:Li:16:LYS:HD3	1.85	0.40
41:Lm:96:CYS:O	41:Lm:100:TYR:N	2.54	0.40
46:Ls:134:LYS:HB3	46:Ls:137:PHE:HB3	2.01	0.40
48:Lz:91:LYS:NZ	48:Lz:96:ASN:OD1	2.53	0.40
49:S2:520:A:O2'	49:S2:825:A:N3	2.46	0.40
49:S2:639:C:H2'	49:S2:640:A:C8	2.56	0.40
49:S2:1217:A:H2'	49:S2:1218:C:H6	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:SA:53:ARG:HD2	65:SV:83:PHE:CD2	2.56	0.40
53:SE:63:LYS:HB3	53:SE:63:LYS:HE2	1.74	0.40
62:SS:123:LEU:HD23	62:SS:123:LEU:HA	1.89	0.40
71:SC:145:LYS:HE2	71:SC:145:LYS:HB3	1.88	0.40
74:SM:93:LYS:HZ1	74:SM:103:VAL:N	2.20	0.40
75:SN:60:VAL:HG13	75:SN:66:VAL:HG21	2.03	0.40
76:SO:33:ILE:HA	76:SO:41:PHE:O	2.21	0.40
83:CA:227:ASP:HB2	83:CA:320:LYS:HD3	2.04	0.40
84:CC:9:A:O2'	84:CC:10:G:N7	2.55	0.40
1:L5:1366:G:O2'	1:L5:1367:C:O2	2.35	0.40
1:L5:2640:G:H2'	1:L5:2641:A:C8	2.57	0.40
1:L5:4093:G:H2'	1:L5:4094:G:C8	2.57	0.40
5:LB:29:VAL:HG12	5:LB:31:SER:H	1.86	0.40
7:LD:53:VAL:HG11	7:LD:159:VAL:HA	2.02	0.40
18:LP:125:MET:O	18:LP:140:MET:HA	2.21	0.40
21:LS:11:LYS:HE3	21:LS:11:LYS:HB2	1.90	0.40
22:LT:64:VAL:HG13	22:LT:72:VAL:HG13	2.03	0.40
27:LY:117:LYS:HE2	27:LY:117:LYS:HB3	1.89	0.40
37:Li:44:ILE:HD13	37:Li:44:ILE:HA	1.92	0.40
49:S2:1285:G:OP1	74:SM:107:SER:N	2.55	0.40
49:S2:1291:A:OP2	49:S2:1302:G:O2'	2.36	0.40
49:S2:1521:C:H5'	62:SS:129:LEU:HD22	2.03	0.40
49:S2:1779:G:H2'	49:S2:1780:G:H8	1.87	0.40
51:SB:147:ASN:OD1	51:SB:147:ASN:N	2.54	0.40
70:Sg:292:SER:OG	70:Sg:297:THR:OG1	2.40	0.40
83:CA:152:ALA:O	83:CA:156:LEU:HB3	2.21	0.40
1:L5:162:A:H2'	1:L5:163:A:C8	2.56	0.40
1:L5:3599:A:H2'	1:L5:3600:G:C8	2.56	0.40
1:L5:4260:U:H2'	1:L5:4261:C:C6	2.57	0.40
4:LA:75:LEU:HD12	4:LA:75:LEU:HA	1.93	0.40
8:LE:223:ARG:HA	8:LE:224:LYS:HA	1.70	0.40
11:LH:11:ASP:OD1	11:LH:11:ASP:N	2.53	0.40
14:LL:94:ILE:HD13	14:LL:94:ILE:HA	1.89	0.40
15:LM:55:MET:HE2	15:LM:55:MET:HB3	1.97	0.40
15:LM:137:LYS:HA	15:LM:137:LYS:HD3	1.89	0.40
38:Lj:25:LYS:HE3	38:Lj:25:LYS:HB3	1.84	0.40
49:S2:1757:G:H8	49:S2:1758:G:H1'	1.85	0.40
52:SD:48:ILE:HB	52:SD:86:LEU:HD23	2.04	0.40
52:SD:126:ILE:HD13	52:SD:126:ILE:HA	1.92	0.40
73:SJ:60:LEU:HD22	73:SJ:70:ARG:HA	2.02	0.40
74:SM:36:ARG:HA	74:SM:36:ARG:HD2	1.90	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:SW:14:ILE:HD11	77:SW:27:ILE:HD11	2.04	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%)	221 (90%)	24 (10%)	1 (0%)	30	54
5	LB	400/403 (99%)	379 (95%)	19 (5%)	2 (0%)	24	48
6	LC	366/427 (86%)	340 (93%)	25 (7%)	1 (0%)	36	60
7	LD	291/297 (98%)	272 (94%)	19 (6%)	0	100	100
8	LE	232/288 (81%)	210 (90%)	22 (10%)	0	100	100
9	LF	223/248 (90%)	212 (95%)	11 (5%)	0	100	100
10	LG	239/266 (90%)	224 (94%)	15 (6%)	0	100	100
11	LH	188/192 (98%)	173 (92%)	15 (8%)	0	100	100
12	LI	198/214 (92%)	180 (91%)	17 (9%)	1 (0%)	24	48
13	LJ	174/178 (98%)	157 (90%)	17 (10%)	0	100	100
14	LL	208/211 (99%)	190 (91%)	18 (9%)	0	100	100
15	LM	137/215 (64%)	129 (94%)	7 (5%)	1 (1%)	18	41
16	LN	201/204 (98%)	189 (94%)	10 (5%)	2 (1%)	12	32
17	LO	199/203 (98%)	192 (96%)	7 (4%)	0	100	100
18	LP	151/184 (82%)	143 (95%)	7 (5%)	1 (1%)	18	41
19	LQ	185/188 (98%)	177 (96%)	8 (4%)	0	100	100
20	LR	185/196 (94%)	180 (97%)	5 (3%)	0	100	100
21	LS	173/176 (98%)	161 (93%)	12 (7%)	0	100	100
22	LT	157/160 (98%)	147 (94%)	10 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	LU	99/128 (77%)	86 (87%)	13 (13%)	0	100	100
24	LV	129/140 (92%)	122 (95%)	7 (5%)	0	100	100
25	LW	122/157 (78%)	114 (93%)	8 (7%)	0	100	100
26	LX	118/156 (76%)	115 (98%)	3 (2%)	0	100	100
27	LY	132/145 (91%)	124 (94%)	8 (6%)	0	100	100
28	LZ	133/136 (98%)	122 (92%)	11 (8%)	0	100	100
29	La	145/148 (98%)	135 (93%)	10 (7%)	0	100	100
30	Lb	105/159 (66%)	97 (92%)	8 (8%)	0	100	100
31	Lc	96/115 (84%)	90 (94%)	6 (6%)	0	100	100
32	Ld	105/125 (84%)	98 (93%)	7 (7%)	0	100	100
33	Le	126/135 (93%)	121 (96%)	4 (3%)	1 (1%)	16	37
34	Lf	107/110 (97%)	98 (92%)	7 (6%)	2 (2%)	6	17
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%)	95 (95%)	5 (5%)	0	100	100
38	Lj	84/97 (87%)	77 (92%)	6 (7%)	1 (1%)	10	27
39	Lk	67/70 (96%)	62 (92%)	5 (8%)	0	100	100
40	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
41	Lm	50/128 (39%)	50 (100%)	0	0	100	100
42	Ln	22/25 (88%)	22 (100%)	0	0	100	100
43	Lo	103/106 (97%)	98 (95%)	5 (5%)	0	100	100
44	Lp	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
45	Lr	123/137 (90%)	116 (94%)	7 (6%)	0	100	100
46	Ls	194/317 (61%)	173 (89%)	19 (10%)	2 (1%)	12	32
47	Lt	137/165 (83%)	107 (78%)	27 (20%)	3 (2%)	5	14
48	Lz	215/217 (99%)	165 (77%)	50 (23%)	0	100	100
50	SA	219/295 (74%)	200 (91%)	19 (9%)	0	100	100
51	SB	212/264 (80%)	200 (94%)	12 (6%)	0	100	100
52	SD	225/243 (93%)	202 (90%)	23 (10%)	0	100	100
53	SE	260/263 (99%)	246 (95%)	14 (5%)	0	100	100
54	SF	180/204 (88%)	161 (89%)	19 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
55	SH	182/194 (94%)	159 (87%)	23 (13%)	0	100	100
56	SI	204/208 (98%)	194 (95%)	10 (5%)	0	100	100
57	SK	96/165 (58%)	81 (84%)	15 (16%)	0	100	100
58	SL	151/158 (96%)	137 (91%)	14 (9%)	0	100	100
59	SP	127/145 (88%)	113 (89%)	14 (11%)	0	100	100
60	SQ	142/146 (97%)	126 (89%)	15 (11%)	1 (1%)	18	41
61	SR	133/135 (98%)	121 (91%)	12 (9%)	0	100	100
62	SS	143/152 (94%)	132 (92%)	11 (8%)	0	100	100
63	ST	141/145 (97%)	127 (90%)	13 (9%)	1 (1%)	18	41
64	SU	102/119 (86%)	93 (91%)	9 (9%)	0	100	100
65	SV	81/83 (98%)	74 (91%)	6 (7%)	1 (1%)	10	27
66	SX	139/143 (97%)	129 (93%)	7 (5%)	3 (2%)	5	14
67	Sa	100/115 (87%)	92 (92%)	7 (7%)	1 (1%)	12	32
68	Sc	62/69 (90%)	51 (82%)	11 (18%)	0	100	100
69	Sd	53/56 (95%)	50 (94%)	2 (4%)	1 (2%)	6	17
70	Sg	311/317 (98%)	267 (86%)	44 (14%)	0	100	100
71	SC	220/293 (75%)	206 (94%)	14 (6%)	0	100	100
72	SG	235/249 (94%)	221 (94%)	14 (6%)	0	100	100
73	SJ	183/194 (94%)	171 (93%)	11 (6%)	1 (0%)	24	48
74	SM	120/132 (91%)	112 (93%)	8 (7%)	0	100	100
75	SN	148/151 (98%)	144 (97%)	4 (3%)	0	100	100
76	SO	138/151 (91%)	124 (90%)	14 (10%)	0	100	100
77	SW	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
78	SY	129/133 (97%)	124 (96%)	5 (4%)	0	100	100
79	SZ	73/125 (58%)	61 (84%)	10 (14%)	2 (3%)	4	10
80	Sb	81/84 (96%)	73 (90%)	8 (10%)	0	100	100
81	Se	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
82	Sf	65/156 (42%)	55 (85%)	10 (15%)	0	100	100
83	CA	350/394 (89%)	326 (93%)	24 (7%)	0	100	100
85	CE	120/223 (54%)	114 (95%)	6 (5%)	0	100	100
86	CF	27/180 (15%)	25 (93%)	2 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	12369/14184 (87%)	11404 (92%)	936 (8%)	29 (0%)	44	68

All (29) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	LN	124	ASP
46	Ls	150	GLY
66	SX	127	ASN
15	LM	88	ALA
47	Lt	148	PRO
63	ST	41	LYS
67	Sa	47	ALA
79	SZ	45	ASN
5	LB	302	ASN
34	Lf	80	ASN
66	SX	126	ALA
47	Lt	147	HIS
60	SQ	44	PRO
5	LB	360	LEU
33	Le	73	GLY
34	Lf	107	PRO
47	Lt	121	LEU
79	SZ	78	LYS
4	LA	55	GLY
16	LN	83	LYS
69	Sd	14	PHE
46	Ls	186	GLY
66	SX	78	GLY
38	Lj	40	PRO
73	SJ	123	ILE
6	LC	232	VAL
18	LP	77	GLY
65	SV	79	VAL
12	LI	15	LYS

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%)	187 (98%)	3 (2%)	55	80
5	LB	348/349 (100%)	347 (100%)	1 (0%)	86	94
6	LC	306/348 (88%)	306 (100%)	0	100	100
7	LD	246/250 (98%)	246 (100%)	0	100	100
8	LE	209/252 (83%)	208 (100%)	1 (0%)	81	92
9	LF	194/215 (90%)	194 (100%)	0	100	100
10	LG	203/223 (91%)	203 (100%)	0	100	100
11	LH	169/171 (99%)	168 (99%)	1 (1%)	78	91
12	LI	172/181 (95%)	172 (100%)	0	100	100
13	LJ	148/149 (99%)	147 (99%)	1 (1%)	76	90
14	LL	176/177 (99%)	173 (98%)	3 (2%)	53	79
15	LM	118/161 (73%)	117 (99%)	1 (1%)	73	88
16	LN	171/172 (99%)	171 (100%)	0	100	100
17	LO	173/174 (99%)	172 (99%)	1 (1%)	78	91
18	LP	134/163 (82%)	134 (100%)	0	100	100
19	LQ	164/165 (99%)	164 (100%)	0	100	100
20	LR	166/175 (95%)	165 (99%)	1 (1%)	78	91
21	LS	156/157 (99%)	155 (99%)	1 (1%)	78	91
22	LT	139/140 (99%)	139 (100%)	0	100	100
23	LU	91/115 (79%)	91 (100%)	0	100	100
24	LV	101/107 (94%)	101 (100%)	0	100	100
25	LW	103/126 (82%)	102 (99%)	1 (1%)	68	86
26	LX	108/133 (81%)	108 (100%)	0	100	100
27	LY	124/135 (92%)	122 (98%)	2 (2%)	55	80
28	LZ	117/118 (99%)	117 (100%)	0	100	100
29	La	120/121 (99%)	119 (99%)	1 (1%)	73	88
30	Lb	88/126 (70%)	88 (100%)	0	100	100
31	Lc	83/97 (86%)	83 (100%)	0	100	100
32	Ld	98/110 (89%)	97 (99%)	1 (1%)	68	86
33	Le	114/121 (94%)	114 (100%)	0	100	100
34	Lf	88/89 (99%)	88 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	Lg	98/100 (98%)	97 (99%)	1 (1%)	68	86
36	Lh	109/110 (99%)	109 (100%)	0	100	100
37	Li	86/89 (97%)	86 (100%)	0	100	100
38	Lj	73/80 (91%)	73 (100%)	0	100	100
39	Lk	64/65 (98%)	64 (100%)	0	100	100
40	Ll	47/48 (98%)	46 (98%)	1 (2%)	47	75
41	Lm	48/116 (41%)	48 (100%)	0	100	100
42	Ln	23/24 (96%)	23 (100%)	0	100	100
43	Lo	93/94 (99%)	92 (99%)	1 (1%)	65	85
44	Lp	74/75 (99%)	74 (100%)	0	100	100
45	Lr	109/121 (90%)	108 (99%)	1 (1%)	70	87
46	Ls	162/258 (63%)	160 (99%)	2 (1%)	63	84
47	Lt	112/137 (82%)	111 (99%)	1 (1%)	70	87
48	Lz	195/196 (100%)	191 (98%)	4 (2%)	47	75
50	SA	183/243 (75%)	181 (99%)	2 (1%)	65	85
51	SB	195/231 (84%)	193 (99%)	2 (1%)	68	86
52	SD	190/202 (94%)	189 (100%)	1 (0%)	81	92
53	SE	224/225 (100%)	224 (100%)	0	100	100
54	SF	156/170 (92%)	156 (100%)	0	100	100
55	SH	166/174 (95%)	164 (99%)	2 (1%)	63	84
56	SI	178/180 (99%)	178 (100%)	0	100	100
57	SK	89/136 (65%)	89 (100%)	0	100	100
58	SL	137/142 (96%)	137 (100%)	0	100	100
59	SP	115/130 (88%)	115 (100%)	0	100	100
60	SQ	119/121 (98%)	116 (98%)	3 (2%)	42	71
61	SR	122/122 (100%)	122 (100%)	0	100	100
62	SS	126/132 (96%)	125 (99%)	1 (1%)	73	88
63	ST	113/115 (98%)	113 (100%)	0	100	100
64	SU	94/107 (88%)	93 (99%)	1 (1%)	65	85
65	SV	67/67 (100%)	67 (100%)	0	100	100
66	SX	113/115 (98%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
67	Sa	89/98 (91%)	89 (100%)	0	100	100
68	Sc	57/62 (92%)	57 (100%)	0	100	100
69	Sd	48/49 (98%)	48 (100%)	0	100	100
70	Sg	272/275 (99%)	269 (99%)	3 (1%)	65	85
71	SC	188/225 (84%)	186 (99%)	2 (1%)	65	85
72	SG	207/218 (95%)	207 (100%)	0	100	100
73	SJ	161/168 (96%)	161 (100%)	0	100	100
74	SM	102/108 (94%)	101 (99%)	1 (1%)	68	86
75	SN	130/131 (99%)	130 (100%)	0	100	100
76	SO	110/119 (92%)	110 (100%)	0	100	100
77	SW	112/113 (99%)	112 (100%)	0	100	100
78	SY	113/115 (98%)	112 (99%)	1 (1%)	70	87
79	SZ	66/103 (64%)	66 (100%)	0	100	100
80	Sb	75/76 (99%)	74 (99%)	1 (1%)	61	83
81	Se	42/48 (88%)	42 (100%)	0	100	100
82	Sf	60/140 (43%)	60 (100%)	0	100	100
83	CA	303/336 (90%)	303 (100%)	0	100	100
85	CE	108/190 (57%)	106 (98%)	2 (2%)	50	77
86	CF	26/151 (17%)	26 (100%)	0	100	100
All	All	10766/12069 (89%)	10714 (100%)	52 (0%)	78	92

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	LA	15	VAL
4	LA	143	THR
4	LA	207	VAL
5	LB	258	HIS
8	LE	189	THR
11	LH	17	ASP
13	LJ	133	VAL
14	LL	59	VAL
14	LL	63	THR
14	LL	144	LEU
15	LM	38	VAL

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Mol	Chain	Res	Type
17	LO	4	VAL
20	LR	183	GLU
21	LS	90	THR
25	LW	100	VAL
27	LY	55	VAL
27	LY	79	VAL
29	La	15	VAL
32	Ld	36	VAL
35	Lg	63	VAL
40	Ll	35	ILE
43	Lo	103	VAL
45	Lr	21	ASN
46	Ls	17	ILE
46	Ls	89	VAL
47	Lt	37	LEU
48	Lz	17	VAL
48	Lz	124	LEU
48	Lz	139	THR
48	Lz	145	VAL
50	SA	54	THR
50	SA	73	ASP
51	SB	62	LEU
51	SB	68	GLU
52	SD	168	VAL
55	SH	69	LEU
55	SH	100	ILE
60	SQ	34	VAL
60	SQ	70	VAL
60	SQ	100	VAL
62	SS	4	VAL
64	SU	54	VAL
70	Sg	94	THR
70	Sg	248	LEU
70	Sg	289	LEU
71	SC	64	THR
71	SC	137	VAL
74	SM	18	LEU
78	SY	26	ASP
80	Sb	53	VAL
85	CE	33	GLU
85	CE	199	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (189)

such sidechains are listed below:

Mol	Chain	Res	Type
4	LA	97	ASN
4	LA	132	ASN
4	LA	205	ASN
5	LB	68	ASN
5	LB	123	HIS
5	LB	138	GLN
5	LB	175	GLN
5	LB	184	GLN
5	LB	213	GLN
5	LB	328	ASN
6	LC	21	ASN
6	LC	89	GLN
6	LC	178	ASN
6	LC	329	ASN
7	LD	122	GLN
7	LD	138	GLN
7	LD	275	GLN
7	LD	291	GLN
8	LE	190	HIS
8	LE	266	GLN
9	LF	63	GLN
10	LG	112	GLN
10	LG	159	HIS
10	LG	208	ASN
11	LH	98	HIS
11	LH	106	GLN
11	LH	138	GLN
11	LH	189	GLN
12	LI	73	ASN
12	LI	144	ASN
13	LJ	3	GLN
13	LJ	98	ASN
13	LJ	167	GLN
14	LL	104	ASN
14	LL	205	GLN
15	LM	48	GLN
15	LM	125	ASN
16	LN	29	GLN
16	LN	32	GLN
16	LN	37	HIS
16	LN	109	HIS
16	LN	145	ASN

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Mol	Chain	Res	Type
16	LN	149	GLN
16	LN	158	HIS
17	LO	26	GLN
18	LP	21	ASN
18	LP	34	GLN
18	LP	80	GLN
18	LP	116	HIS
18	LP	133	HIS
19	LQ	21	GLN
19	LQ	44	ASN
19	LQ	77	ASN
19	LQ	125	GLN
19	LQ	188	ASN
20	LR	40	GLN
20	LR	130	ASN
21	LS	23	HIS
21	LS	108	GLN
22	LT	54	HIS
22	LT	127	GLN
23	LU	17	GLN
23	LU	50	ASN
23	LU	94	ASN
24	LV	27	ASN
25	LW	48	GLN
25	LW	50	ASN
25	LW	96	GLN
27	LY	40	GLN
27	LY	65	GLN
28	LZ	78	ASN
29	La	28	HIS
29	La	67	GLN
29	La	85	GLN
30	Lb	6	ASN
30	Lb	17	HIS
31	Lc	15	ASN
31	Lc	72	HIS
33	Le	23	HIS
33	Le	92	ASN
33	Le	107	ASN
34	Lf	56	ASN
34	Lf	80	ASN
34	Lf	99	HIS

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Mol	Chain	Res	Type
36	Lh	101	ASN
37	Li	12	ASN
37	Li	15	HIS
38	Lj	76	HIS
41	Lm	104	HIS
43	Lo	19	GLN
43	Lo	45	GLN
43	Lo	51	GLN
44	Lp	56	HIS
45	Lr	31	ASN
45	Lr	70	GLN
45	Lr	100	ASN
46	Ls	85	ASN
46	Ls	127	ASN
46	Ls	176	ASN
47	Lt	8	ASN
48	Lz	22	GLN
48	Lz	35	GLN
48	Lz	129	ASN
48	Lz	182	ASN
50	SA	9	GLN
50	SA	131	HIS
50	SA	141	ASN
51	SB	149	GLN
51	SB	179	ASN
51	SB	186	ASN
51	SB	202	GLN
51	SB	208	HIS
52	SD	101	GLN
52	SD	165	ASN
53	SE	98	ASN
53	SE	112	HIS
53	SE	138	HIS
54	SF	29	GLN
54	SF	148	ASN
55	SH	12	ASN
55	SH	33	ASN
55	SH	68	GLN
55	SH	73	GLN
55	SH	114	GLN
56	SI	9	HIS
56	SI	52	ASN

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Mol	Chain	Res	Type
57	SK	7	ASN
57	SK	42	ASN
57	SK	44	HIS
58	SL	11	GLN
58	SL	65	ASN
58	SL	83	GLN
58	SL	94	HIS
58	SL	141	ASN
59	SP	35	GLN
59	SP	54	HIS
59	SP	103	ASN
59	SP	114	HIS
59	SP	137	HIS
60	SQ	77	HIS
61	SR	31	ASN
61	SR	118	GLN
62	SS	11	HIS
63	ST	42	HIS
64	SU	28	ASN
65	SV	49	GLN
65	SV	82	ASN
66	SX	39	ASN
67	Sa	8	ASN
67	Sa	86	ASN
69	Sd	5	GLN
69	Sd	26	ASN
70	Sg	4	GLN
70	Sg	14	HIS
70	Sg	51	ASN
70	Sg	117	ASN
71	SC	115	GLN
72	SG	56	ASN
72	SG	110	ASN
72	SG	146	ASN
72	SG	155	GLN
72	SG	227	GLN
73	SJ	125	HIS
74	SM	82	ASN
75	SN	49	GLN
77	SW	5	ASN
77	SW	90	GLN
77	SW	91	ASN

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Mol	Chain	Res	Type
77	SW	120	HIS
78	SY	89	HIS
78	SY	112	ASN
80	Sb	65	GLN
81	Se	3	HIS
81	Se	58	ASN
83	CA	83	ASN
83	CA	88	HIS
83	CA	120	ASN
83	CA	123	HIS
83	CA	134	GLN
83	CA	203	GLN
83	CA	204	ASN
83	CA	254	GLN
85	CE	51	GLN
85	CE	63	GLN
85	CE	71	GLN
85	CE	180	GLN
85	CE	190	ASN
86	CF	158	GLN
86	CF	165	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3705/5066 (73%)	855 (23%)	20 (0%)
2	L7	119/121 (98%)	13 (10%)	0
3	L8	155/157 (98%)	28 (18%)	0
49	S2	1715/1869 (91%)	380 (22%)	7 (0%)
84	CC	74/75 (98%)	23 (31%)	2 (2%)
All	All	5768/7288 (79%)	1299 (22%)	29 (0%)

All (1299) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	2	G
1	L5	17	A
1	L5	30	C
1	L5	39	A
1	L5	42	A
1	L5	48	G

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Mol	Chain	Res	Type
1	L5	56	A
1	L5	59	A
1	L5	64	A
1	L5	65	A
1	L5	69	A
1	L5	72	C
1	L5	73	A
1	L5	74	G
1	L5	91	G
1	L5	98	A
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	136	C
1	L5	137	G
1	L5	152	U
1	L5	159	C
1	L5	165	A
1	L5	183	C
1	L5	184	U
1	L5	185	C
1	L5	187	U
1	L5	188	G
1	L5	189	G
1	L5	200	U
1	L5	207	G
1	L5	210	C
1	L5	218	A
1	L5	219	G
1	L5	233	U
1	L5	234	G
1	L5	255	C
1	L5	256	G
1	L5	258	G
1	L5	261	G

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Mol	Chain	Res	Type
1	L5	265	C
1	L5	266	C
1	L5	267	G
1	L5	269	G
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	349	A
1	L5	360	A
1	L5	373	G
1	L5	387	G
1	L5	388	A
1	L5	398	A
1	L5	399	G
1	L5	407	A
1	L5	409	G
1	L5	410	A
1	L5	411	G
1	L5	412	G
1	L5	413	G
1	L5	431	G
1	L5	432	U
1	L5	449	C
1	L5	450	G
1	L5	452	A
1	L5	453	G
1	L5	454	U
1	L5	456	C
1	L5	457	G
1	L5	465	G
1	L5	467	U
1	L5	468	U
1	L5	484	U
1	L5	485	C
1	L5	486	C
1	L5	489	C
1	L5	493	G
1	L5	494	U

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Mol	Chain	Res	Type
1	L5	495	C
1	L5	497	G
1	L5	498	C
1	L5	499	G
1	L5	500	G
1	L5	502	C
1	L5	503	C
1	L5	504	G
1	L5	505	G
1	L5	507	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	656	C
1	L5	657	C
1	L5	658	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	673	C
1	L5	685	C
1	L5	686	A
1	L5	687	U
1	L5	688	U
1	L5	696	C
1	L5	703	G
1	L5	704	C
1	L5	708	G
1	L5	731	G
1	L5	738	C
1	L5	739	G
1	L5	742	G

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Mol	Chain	Res	Type
1	L5	746	A
1	L5	753	C
1	L5	758	G
1	L5	759	G
1	L5	760	G
1	L5	904	C
1	L5	913	U
1	L5	914	U
1	L5	915	A
1	L5	916	C
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	936	C
1	L5	941	C
1	L5	945	U
1	L5	958	G
1	L5	959	G
1	L5	960	A
1	L5	961	G
1	L5	962	C
1	L5	965	G
1	L5	966	A
1	L5	967	C
1	L5	969	C
1	L5	970	G
1	L5	977	C
1	L5	982	U
1	L5	985	C
1	L5	989	U
1	L5	990	C
1	L5	992	C
1	L5	993	G
1	L5	995	C
1	L5	996	G
1	L5	1048	G
1	L5	1049	C

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Mol	Chain	Res	Type
1	L5	1050	C
1	L5	1051	G
1	L5	1070	G
1	L5	1071	C
1	L5	1074	G
1	L5	1075	G
1	L5	1082	C
1	L5	1083	U
1	L5	1095	A
1	L5	1168	G
1	L5	1170	G
1	L5	1171	G
1	L5	1172	C
1	L5	1173	G
1	L5	1178	G
1	L5	1179	U
1	L5	1180	C
1	L5	1181	C
1	L5	1182	C
1	L5	1183	C
1	L5	1193	C
1	L5	1202	C
1	L5	1203	G
1	L5	1204	C
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	1218	G
1	L5	1219	G
1	L5	1222	A
1	L5	1241	C
1	L5	1245	C
1	L5	1246	G
1	L5	1253	G
1	L5	1254	A
1	L5	1257	A
1	L5	1258	G
1	L5	1266	G
1	L5	1267	C

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Mol	Chain	Res	Type
1	L5	1269	G
1	L5	1270	A
1	L5	1271	G
1	L5	1272	C
1	L5	1273	G
1	L5	1274	A
1	L5	1275	G
1	L5	1280	C
1	L5	1284	G
1	L5	1285	U
1	L5	1287	G
1	L5	1294	A
1	L5	1295	C
1	L5	1301	C
1	L5	1302	U
1	L5	1304	C
1	L5	1312	A
1	L5	1324	A
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	1367	C
1	L5	1378	C
1	L5	1379	C
1	L5	1387	A
1	L5	1393	G
1	L5	1394	G
1	L5	1397	A
1	L5	1403	G
1	L5	1404	G
1	L5	1405	C
1	L5	1407	C
1	L5	1409	C
1	L5	1410	U
1	L5	1411	C
1	L5	1414	C
1	L5	1415	G

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Mol	Chain	Res	Type
1	L5	1417	C
1	L5	1420	A
1	L5	1435	G
1	L5	1437	C
1	L5	1439	C
1	L5	1440	U
1	L5	1442	C
1	L5	1445	U
1	L5	1446	C
1	L5	1447	C
1	L5	1482	G
1	L5	1483	C
1	L5	1493	G
1	L5	1497	A
1	L5	1498	G
1	L5	1502	G
1	L5	1517	G
1	L5	1518	A
1	L5	1525	A
1	L5	1534	A
1	L5	1547	A
1	L5	1562	G
1	L5	1566	C
1	L5	1578	U
1	L5	1591	U
1	L5	1596	U
1	L5	1613	A
1	L5	1624	G
1	L5	1625	G
1	L5	1631	A
1	L5	1633	G
1	L5	1634	A
1	L5	1640	C
1	L5	1641	G
1	L5	1642	A
1	L5	1654	G
1	L5	1661	C
1	L5	1676	C
1	L5	1677	U
1	L5	1678	C
1	L5	1697	G
1	L5	1698	C

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Mol	Chain	Res	Type
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	1709	C
1	L5	1715	C
1	L5	1716	G
1	L5	1719	A
1	L5	1726	U
1	L5	1734	G
1	L5	1735	U
1	L5	1741	G
1	L5	1742	A
1	L5	1755	C
1	L5	1757	U
1	L5	1758	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	1772	C
1	L5	1775	A
1	L5	1785	C
1	L5	1787	A
1	L5	1792	U
1	L5	1797	G
1	L5	1804	A
1	L5	1810	G
1	L5	1815	G
1	L5	1820	C
1	L5	1821	G
1	L5	1822	U
1	L5	1834	U
1	L5	1836	G
1	L5	1837	A

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Mol	Chain	Res	Type
1	L5	1842	G
1	L5	1855	G
1	L5	1869	G
1	L5	1882	U
1	L5	1892	A
1	L5	1897	A
1	L5	1898	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	1940	G
1	L5	1948	G
1	L5	1951	G
1	L5	1959	U
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
1	L5	1993	C
1	L5	1997	U
1	L5	2001	G
1	L5	2002	A
1	L5	2003	G
1	L5	2004	U
1	L5	2011	C

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Mol	Chain	Res	Type
1	L5	2014	C
1	L5	2017	A
1	L5	2018	C
1	L5	2024	G
1	L5	2025	A
1	L5	2026	A
1	L5	2033	A
1	L5	2034	G
1	L5	2042	A
1	L5	2046	G
1	L5	2048	U
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	2093	A
1	L5	2095	A
1	L5	2096	G
1	L5	2097	U
1	L5	2098	G
1	L5	2101	C
1	L5	2102	G
1	L5	2110	C
1	L5	2112	G
1	L5	2113	G
1	L5	2250	C
1	L5	2252	G
1	L5	2253	A
1	L5	2256	C
1	L5	2258	C
1	L5	2260	C
1	L5	2263	A
1	L5	2289	C
1	L5	2300	A
1	L5	2301	G
1	L5	2306	G
1	L5	2313	A
1	L5	2332	A
1	L5	2333	G

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Mol	Chain	Res	Type
1	L5	2348	G
1	L5	2351	C
1	L5	2360	A
1	L5	2369	U
1	L5	2383	C
1	L5	2395	A
1	L5	2397	G
1	L5	2417	A
1	L5	2418	A
1	L5	2421	G
1	L5	2425	U
1	L5	2437	C
1	L5	2441	C
1	L5	2450	G
1	L5	2453	A
1	L5	2464	C
1	L5	2465	C
1	L5	2469	C
1	L5	2474	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	2491	C
1	L5	2495	U
1	L5	2503	G
1	L5	2504	C
1	L5	2505	C
1	L5	2506	G
1	L5	2513	A
1	L5	2519	U
1	L5	2537	A
1	L5	2544	G
1	L5	2546	G
1	L5	2547	G
1	L5	2554	U

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Mol	Chain	Res	Type
1	L5	2559	G
1	L5	2560	C
1	L5	2573	A
1	L5	2583	C
1	L5	2586	G
1	L5	2587	A
1	L5	2589	C
1	L5	2601	A
1	L5	2611	A
1	L5	2618	G
1	L5	2627	C
1	L5	2652	G
1	L5	2653	C
1	L5	2662	G
1	L5	2669	C
1	L5	2670	C
1	L5	2675	G
1	L5	2676	A
1	L5	2687	U
1	L5	2694	G
1	L5	2695	A
1	L5	2696	A
1	L5	2703	G
1	L5	2707	U
1	L5	2708	U
1	L5	2709	C
1	L5	2710	C
1	L5	2711	G
1	L5	2721	G
1	L5	2724	G
1	L5	2725	A
1	L5	2726	G
1	L5	2739	C
1	L5	2742	G
1	L5	2743	A
1	L5	2746	A
1	L5	2756	G
1	L5	2761	U
1	L5	2763	U
1	L5	2764	A
1	L5	2769	U
1	L5	2770	C

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Mol	Chain	Res	Type
1	L5	2787	A
1	L5	2788	U
1	L5	2790	U
1	L5	2799	G
1	L5	2814	C
1	L5	2815	A
1	L5	2826	U
1	L5	2827	G
1	L5	2835	A
1	L5	2838	G
1	L5	2842	G
1	L5	2848	G
1	L5	2855	G
1	L5	2867	C
1	L5	2877	G
1	L5	2892	C
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

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Mol	Chain	Res	Type
1	L5	3646	A
1	L5	3662	A
1	L5	3664	G
1	L5	3670	C
1	L5	3673	C
1	L5	3674	G
1	L5	3711	A
1	L5	3713	U
1	L5	3714	G
1	L5	3727	A
1	L5	3729	U
1	L5	3735	G
1	L5	3736	A
1	L5	3748	A
1	L5	3750	G
1	L5	3753	G
1	L5	3757	G
1	L5	3758	U
1	L5	3759	A
1	L5	3760	A
1	L5	3761	C
1	L5	3771	C
1	L5	3776	G
1	L5	3777	G
1	L5	3783	A
1	L5	3784	A
1	L5	3786	U
1	L5	3802	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	3839	G
1	L5	3840	U
1	L5	3867	A
1	L5	3877	A
1	L5	3878	C
1	L5	3879	G

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Mol	Chain	Res	Type
1	L5	3885	G
1	L5	3887	C
1	L5	3890	A
1	L5	3892	U
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	3930	U
1	L5	3938	G
1	L5	3939	G
1	L5	3942	A
1	L5	3943	A
1	L5	3944	G
1	L5	3947	A
1	L5	3950	U
1	L5	3953	G
1	L5	3955	G
1	L5	3956	G
1	L5	3957	U
1	L5	3958	G
1	L5	3959	U
1	L5	3961	G
1	L5	3962	A
1	L5	3963	A
1	L5	3964	U
1	L5	3965	A
1	L5	3966	A
1	L5	3969	G
1	L5	3970	G
1	L5	3971	G
1	L5	3973	G
1	L5	3974	G
1	L5	3977	C
1	L5	4035	G
1	L5	4036	G
1	L5	4038	C
1	L5	4039	G
1	L5	4041	C
1	L5	4042	G

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Mol	Chain	Res	Type
1	L5	4043	G
1	L5	4045	G
1	L5	4046	A
1	L5	4048	A
1	L5	4049	U
1	L5	4051	C
1	L5	4052	C
1	L5	4053	A
1	L5	4055	U
1	L5	4056	A
1	L5	4057	C
1	L5	4058	U
1	L5	4059	C
1	L5	4062	A
1	L5	4063	U
1	L5	4064	C
1	L5	4065	G
1	L5	4076	G
1	L5	4084	G
1	L5	4086	G
1	L5	4091	G
1	L5	4096	C
1	L5	4097	G
1	L5	4099	G
1	L5	4101	C
1	L5	4102	C
1	L5	4104	G
1	L5	4106	G
1	L5	4107	G
1	L5	4108	G
1	L5	4111	U
1	L5	4112	C
1	L5	4113	U
1	L5	4114	C
1	L5	4115	G
1	L5	4116	C
1	L5	4117	U
1	L5	4119	C
1	L5	4122	G
1	L5	4127	A
1	L5	4140	C
1	L5	4141	G

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Mol	Chain	Res	Type
1	L5	4142	C
1	L5	4143	G
1	L5	4144	C
1	L5	4146	G
1	L5	4149	C
1	L5	4150	G
1	L5	4160	C
1	L5	4162	C
1	L5	4163	U
1	L5	4168	G
1	L5	4170	A
1	L5	4177	C
1	L5	4183	G
1	L5	4184	G
1	L5	4191	G
1	L5	4196	G
1	L5	4197	G
1	L5	4203	A
1	L5	4222	G
1	L5	4225	G
1	L5	4228	G
1	L5	4229	U
1	L5	4233	A
1	L5	4249	G
1	L5	4251	A
1	L5	4254	G
1	L5	4257	A
1	L5	4265	U
1	L5	4268	A
1	L5	4273	A
1	L5	4291	G
1	L5	4295	U
1	L5	4304	A
1	L5	4305	G
1	L5	4306	U
1	L5	4314	C
1	L5	4319	C
1	L5	4329	G
1	L5	4330	G
1	L5	4332	C
1	L5	4339	A
1	L5	4349	C

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Mol	Chain	Res	Type
1	L5	4371	G
1	L5	4373	G
1	L5	4376	A
1	L5	4377	G
1	L5	4378	A
1	L5	4379	A
1	L5	4380	A
1	L5	4386	C
1	L5	4387	C
1	L5	4391	G
1	L5	4393	G
1	L5	4394	A
1	L5	4398	C
1	L5	4422	A
1	L5	4426	C
1	L5	4448	G
1	L5	4449	A
1	L5	4452	U
1	L5	4453	C
1	L5	4464	A
1	L5	4475	G
1	L5	4488	A
1	L5	4500	U
1	L5	4512	U
1	L5	4513	A
1	L5	4515	G
1	L5	4519	C
1	L5	4524	G
1	L5	4531	U
1	L5	4545	G
1	L5	4548	A
1	L5	4549	G
1	L5	4557	U
1	L5	4560	C
1	L5	4567	G
1	L5	4573	G
1	L5	4575	G
1	L5	4589	A
1	L5	4590	A
1	L5	4600	G
1	L5	4617	G
1	L5	4635	A

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Mol	Chain	Res	Type
1	L5	4636	U
1	L5	4637	G
1	L5	4652	G
1	L5	4656	A
1	L5	4657	U
1	L5	4670	C
1	L5	4672	A
1	L5	4679	G
1	L5	4684	A
1	L5	4687	A
1	L5	4693	C
1	L5	4694	G
1	L5	4695	C
1	L5	4700	A
1	L5	4708	A
1	L5	4709	U
1	L5	4719	G
1	L5	4720	C
1	L5	4730	C
1	L5	4731	G
1	L5	4734	A
1	L5	4740	G
1	L5	4741	C
1	L5	4742	G
1	L5	4745	G
1	L5	4754	G
1	L5	4757	C
1	L5	4759	C
1	L5	4761	G
1	L5	4764	A
1	L5	4765	G
1	L5	4771	C
1	L5	4772	C
1	L5	4775	C
1	L5	4859	C
1	L5	4870	G
1	L5	4871	C
1	L5	4875	G
1	L5	4880	C
1	L5	4881	U
1	L5	4882	U
1	L5	4883	C

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Mol	Chain	Res	Type
1	L5	4888	U
1	L5	4889	G
1	L5	4895	C
1	L5	4896	G
1	L5	4900	C
1	L5	4901	G
1	L5	4902	C
1	L5	4904	G
1	L5	4905	C
1	L5	4906	U
1	L5	4910	A
1	L5	4912	G
1	L5	4914	C
1	L5	4922	C
1	L5	4923	C
1	L5	4924	C
1	L5	4925	U
1	L5	4926	C
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	4960	G
1	L5	4961	G
1	L5	4966	A
1	L5	4976	U
1	L5	4985	U
1	L5	4988	U
1	L5	4989	U
1	L5	4991	U
1	L5	5014	A
1	L5	5017	G
1	L5	5022	U
1	L5	5025	C
1	L5	5026	U
1	L5	5027	C
1	L5	5028	G
1	L5	5029	C

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Mol	Chain	Res	Type
1	L5	5030	U
1	L5	5034	A
1	L5	5041	G
1	L5	5047	C
1	L5	5050	C
1	L5	5054	C
1	L5	5058	A
1	L5	5061	A
1	L5	5069	U
2	L7	4	U
2	L7	5	A
2	L7	33	U
2	L7	38	U
2	L7	49	A
2	L7	53	U
2	L7	54	A
2	L7	63	C
2	L7	64	G
2	L7	97	G
2	L7	100	A
2	L7	110	G
2	L7	111	C
3	L8	25	G
3	L8	34	U
3	L8	35	C
3	L8	48	A
3	L8	59	A
3	L8	60	G
3	L8	62	A
3	L8	63	U
3	L8	80	A
3	L8	82	A
3	L8	83	C
3	L8	84	A
3	L8	85	U
3	L8	86	U
3	L8	87	G
3	L8	94	G
3	L8	103	A
3	L8	105	C
3	L8	110	U
3	L8	111	U

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Mol	Chain	Res	Type
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	153	C
3	L8	156	U
49	S2	13	C
49	S2	17	C
49	S2	33	G
49	S2	41	G
49	S2	44	U
49	S2	45	A
49	S2	46	A
49	S2	56	G
49	S2	58	C
49	S2	59	U
49	S2	64	A
49	S2	67	C
49	S2	68	A
49	S2	72	C
49	S2	73	C
49	S2	74	G
49	S2	76	U
49	S2	103	A
49	S2	113	G
49	S2	115	U
49	S2	116	U
49	S2	121	U
49	S2	126	G
49	S2	130	G
49	S2	143	U
49	S2	147	A
49	S2	149	A
49	S2	155	G
49	S2	158	A
49	S2	159	A
49	S2	160	U
49	S2	161	U
49	S2	162	C
49	S2	175	A

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Mol	Chain	Res	Type
49	S2	179	C
49	S2	182	C
49	S2	184	G
49	S2	190	G
49	S2	196	C
49	S2	197	U
49	S2	198	U
49	S2	199	C
49	S2	200	G
49	S2	203	G
49	S2	204	G
49	S2	206	G
49	S2	208	G
49	S2	209	A
49	S2	214	U
49	S2	290	U
49	S2	291	G
49	S2	292	A
49	S2	295	C
49	S2	302	A
49	S2	306	C
49	S2	307	G
49	S2	308	G
49	S2	309	G
49	S2	311	C
49	S2	318	A
49	S2	319	C
49	S2	323	C
49	S2	324	C
49	S2	325	C
49	S2	326	C
49	S2	327	G
49	S2	328	U
49	S2	329	G
49	S2	332	G
49	S2	338	G
49	S2	339	A
49	S2	347	G
49	S2	360	A
49	S2	362	C
49	S2	364	A
49	S2	368	U

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Mol	Chain	Res	Type
49	S2	370	G
49	S2	385	G
49	S2	386	C
49	S2	407	G
49	S2	408	A
49	S2	409	C
49	S2	417	C
49	S2	418	A
49	S2	429	C
49	S2	438	G
49	S2	448	A
49	S2	449	A
49	S2	450	C
49	S2	452	G
49	S2	464	A
49	S2	465	A
49	S2	466	G
49	S2	471	G
49	S2	472	C
49	S2	473	A
49	S2	474	G
49	S2	482	G
49	S2	483	C
49	S2	487	U
49	S2	488	U
49	S2	492	C
49	S2	493	A
49	S2	500	A
49	S2	502	C
49	S2	512	A
49	S2	516	A
49	S2	525	A
49	S2	529	A
49	S2	531	A
49	S2	532	C
49	S2	533	A
49	S2	536	A
49	S2	537	C
49	S2	540	U
49	S2	542	U
49	S2	546	G
49	S2	547	G

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Mol	Chain	Res	Type
49	S2	556	U
49	S2	557	U
49	S2	558	G
49	S2	559	G
49	S2	563	G
49	S2	564	A
49	S2	576	A
49	S2	583	A
49	S2	584	A
49	S2	587	A
49	S2	589	G
49	S2	590	A
49	S2	591	U
49	S2	597	G
49	S2	604	A
49	S2	607	U
49	S2	608	C
49	S2	614	C
49	S2	623	G
49	S2	628	A
49	S2	629	A
49	S2	631	U
49	S2	643	A
49	S2	644	G
49	S2	655	A
49	S2	660	C
49	S2	668	A
49	S2	669	A
49	S2	671	A
49	S2	672	A
49	S2	673	G
49	S2	683	G
49	S2	687	C
49	S2	688	U
49	S2	689	U
49	S2	692	G
49	S2	693	A
49	S2	695	C
49	S2	696	G
49	S2	697	G
49	S2	698	G
49	S2	732	U

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Mol	Chain	Res	Type
49	S2	733	C
49	S2	734	C
49	S2	736	C
49	S2	738	C
49	S2	749	U
49	S2	751	G
49	S2	752	G
49	S2	753	C
49	S2	788	G
49	S2	791	C
49	S2	792	C
49	S2	798	G
49	S2	810	A
49	S2	811	A
49	S2	821	G
49	S2	822	U
49	S2	823	U
49	S2	824	C
49	S2	830	A
49	S2	835	C
49	S2	836	G
49	S2	837	A
49	S2	838	G
49	S2	839	C
49	S2	840	C
49	S2	842	C
49	S2	847	A
49	S2	869	A
49	S2	870	A
49	S2	873	G
49	S2	874	G
49	S2	878	G
49	S2	880	G
49	S2	882	U
49	S2	883	U
49	S2	887	U
49	S2	888	U
49	S2	889	U
49	S2	891	G
49	S2	893	U
49	S2	894	G
49	S2	896	U

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Mol	Chain	Res	Type
49	S2	897	U
49	S2	898	U
49	S2	899	U
49	S2	900	C
49	S2	901	G
49	S2	903	A
49	S2	913	A
49	S2	914	U
49	S2	920	A
49	S2	930	C
49	S2	933	G
49	S2	934	G
49	S2	943	U
49	S2	963	A
49	S2	971	G
49	S2	972	A
49	S2	990	A
49	S2	992	A
49	S2	999	G
49	S2	1001	A
49	S2	1017	U
49	S2	1018	U
49	S2	1023	A
49	S2	1027	A
49	S2	1028	A
49	S2	1033	G
49	S2	1061	U
49	S2	1062	A
49	S2	1083	A
49	S2	1085	C
49	S2	1089	G
49	S2	1109	C
49	S2	1114	U
49	S2	1115	U
49	S2	1116	C
49	S2	1118	C
49	S2	1121	G
49	S2	1138	C
49	S2	1153	C
49	S2	1154	U
49	S2	1195	A
49	S2	1207	G

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Mol	Chain	Res	Type
49	S2	1208	A
49	S2	1215	C
49	S2	1216	C
49	S2	1217	A
49	S2	1224	G
49	S2	1227	G
49	S2	1242	U
49	S2	1243	U
49	S2	1251	A
49	S2	1253	A
49	S2	1256	G
49	S2	1257	G
49	S2	1259	A
49	S2	1264	C
49	S2	1265	A
49	S2	1274	G
49	S2	1275	G
49	S2	1283	C
49	S2	1284	A
49	S2	1286	G
49	S2	1294	G
49	S2	1295	A
49	S2	1302	G
49	S2	1306	U
49	S2	1308	U
49	S2	1312	G
49	S2	1342	U
49	S2	1343	U
49	S2	1348	G
49	S2	1371	U
49	S2	1372	U
49	S2	1373	C
49	S2	1378	A
49	S2	1402	A
49	S2	1404	U
49	S2	1415	C
49	S2	1419	C
49	S2	1420	G
49	S2	1421	A
49	S2	1422	G
49	S2	1423	C
49	S2	1424	G

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Mol	Chain	Res	Type
49	S2	1433	C
49	S2	1435	C
49	S2	1436	C
49	S2	1438	A
49	S2	1452	A
49	S2	1454	A
49	S2	1455	A
49	S2	1462	U
49	S2	1463	U
49	S2	1480	A
49	S2	1487	A
49	S2	1489	A
49	S2	1490	G
49	S2	1495	G
49	S2	1497	G
49	S2	1498	A
49	S2	1505	U
49	S2	1507	G
49	S2	1509	U
49	S2	1520	G
49	S2	1521	C
49	S2	1533	A
49	S2	1537	A
49	S2	1544	C
49	S2	1552	G
49	S2	1553	C
49	S2	1556	A
49	S2	1558	C
49	S2	1570	G
49	S2	1574	C
49	S2	1578	U
49	S2	1580	A
49	S2	1585	U
49	S2	1587	G
49	S2	1588	A
49	S2	1594	A
49	S2	1601	A
49	S2	1621	U
49	S2	1623	A
49	S2	1634	A
49	S2	1638	G
49	S2	1644	C

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Mol	Chain	Res	Type
49	S2	1647	A
49	S2	1648	G
49	S2	1654	G
49	S2	1661	A
49	S2	1663	A
49	S2	1664	A
49	S2	1665	G
49	S2	1671	G
49	S2	1680	G
49	S2	1683	C
49	S2	1686	G
49	S2	1698	C
49	S2	1699	A
49	S2	1719	A
49	S2	1721	U
49	S2	1722	G
49	S2	1743	G
49	S2	1744	G
49	S2	1745	A
49	S2	1752	C
49	S2	1753	C
49	S2	1754	G
49	S2	1757	G
49	S2	1758	G
49	S2	1761	U
49	S2	1772	C
49	S2	1773	C
49	S2	1774	C
49	S2	1775	U
49	S2	1776	G
49	S2	1777	G
49	S2	1781	A
49	S2	1783	C
49	S2	1784	G
49	S2	1786	U
49	S2	1798	C
49	S2	1822	A
49	S2	1824	A
49	S2	1825	A
49	S2	1826	G
49	S2	1829	G
49	S2	1831	A

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Mol	Chain	Res	Type
49	S2	1835	A
49	S2	1838	U
49	S2	1849	G
49	S2	1851	A
49	S2	1852	C
49	S2	1861	G
49	S2	1862	G
49	S2	1863	A
49	S2	1864	U
49	S2	1865	C
84	CC	11	C
84	CC	16	C
84	CC	17	G
84	CC	18	G
84	CC	19	C
84	CC	20	U
84	CC	21	A
84	CC	23	C
84	CC	28	C
84	CC	32	C
84	CC	33	U
84	CC	35	U
84	CC	36	C
84	CC	37	A
84	CC	39	C
84	CC	42	G
84	CC	46	A
84	CC	47	C
84	CC	48	C
84	CC	55	C
84	CC	58	C
84	CC	72	G
84	CC	75	A

All (29) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	406	C
1	L5	914	U
1	L5	955	G
1	L5	1082	C
1	L5	1633	G

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Mol	Chain	Res	Type
1	L5	1733	G
1	L5	1977	C
1	L5	2033	A
1	L5	2112	G
1	L5	2416	G
1	L5	2675	G
1	L5	2760	G
1	L5	2786	C
1	L5	3614	G
1	L5	3673	C
1	L5	3876	A
1	L5	4378	A
1	L5	4699	U
1	L5	4904	G
1	L5	4913	G
49	S2	112	U
49	S2	291	G
49	S2	417	C
49	S2	563	G
49	S2	688	U
49	S2	1265	A
49	S2	1434	C
84	CC	35	U
84	CC	74	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

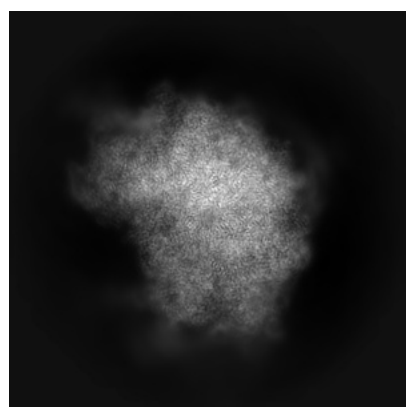
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11288. These allow visual inspection of the internal detail of the map and identification of artifacts.

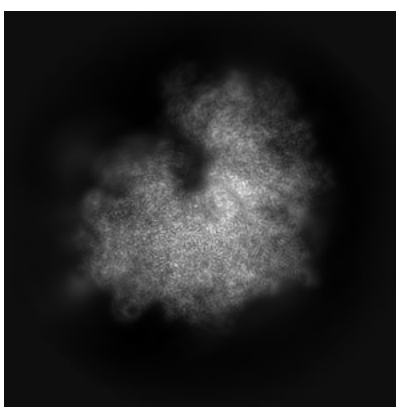
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

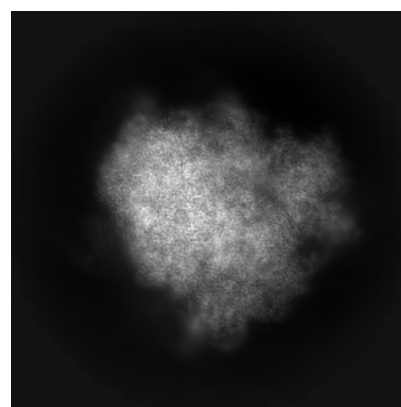
6.1.1 Primary map



X



Y

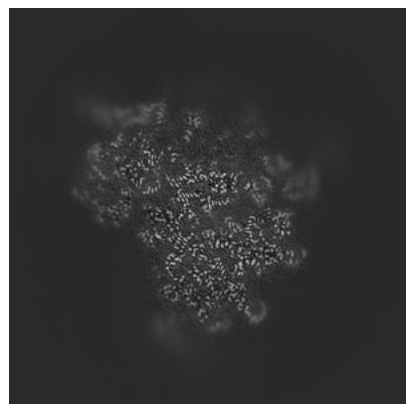


Z

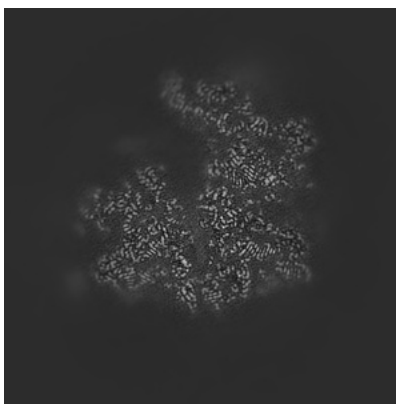
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

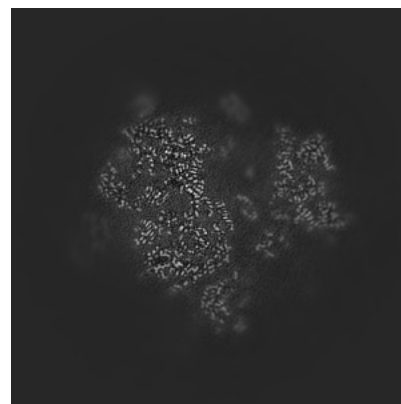
6.2.1 Primary map



X Index: 200



Y Index: 200

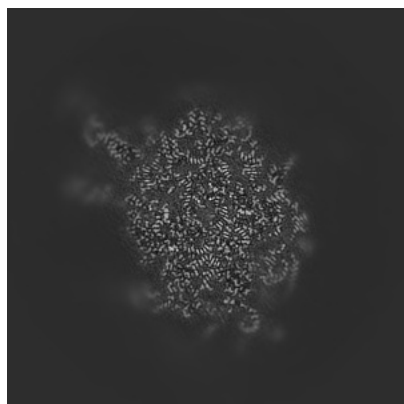


Z Index: 200

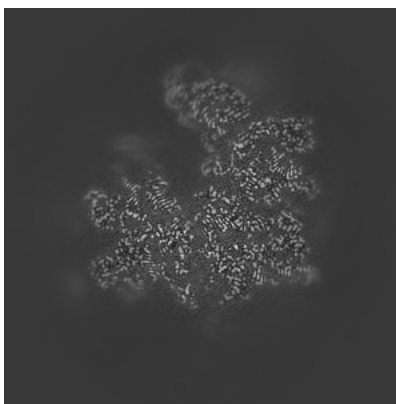
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

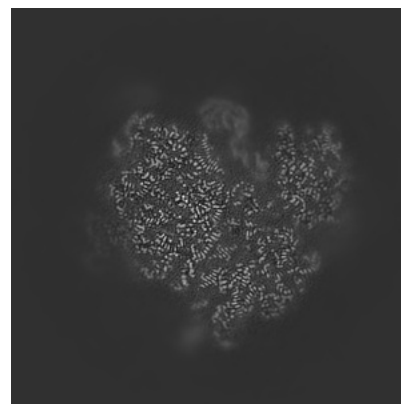
6.3.1 Primary map



X Index: 178



Y Index: 194

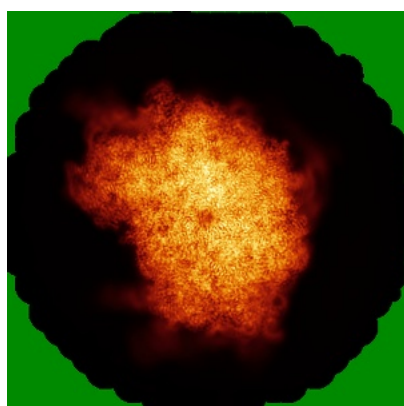


Z Index: 224

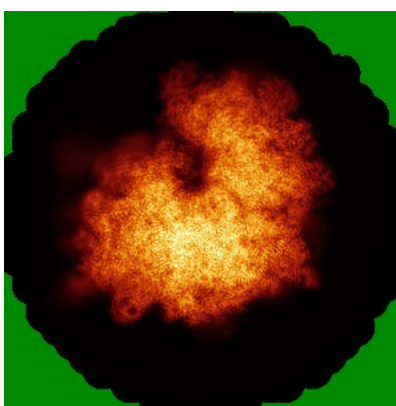
The images above show the largest variance slices of the map in three orthogonal directions.

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

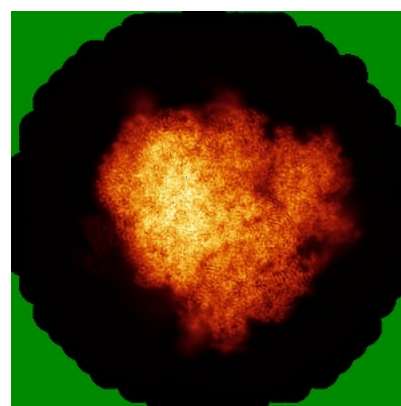
6.4.1 Primary map



X



Y



Z

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

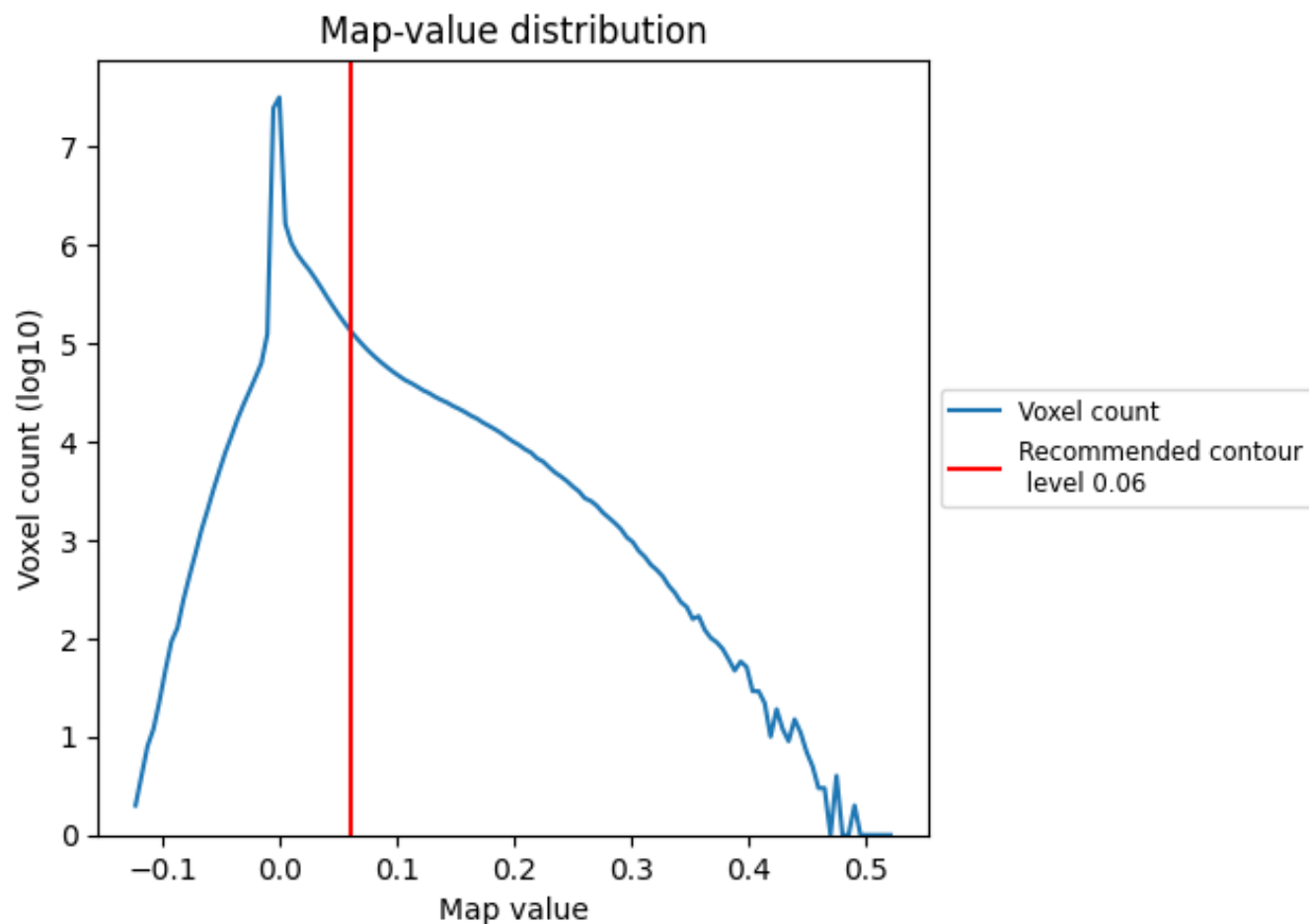
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

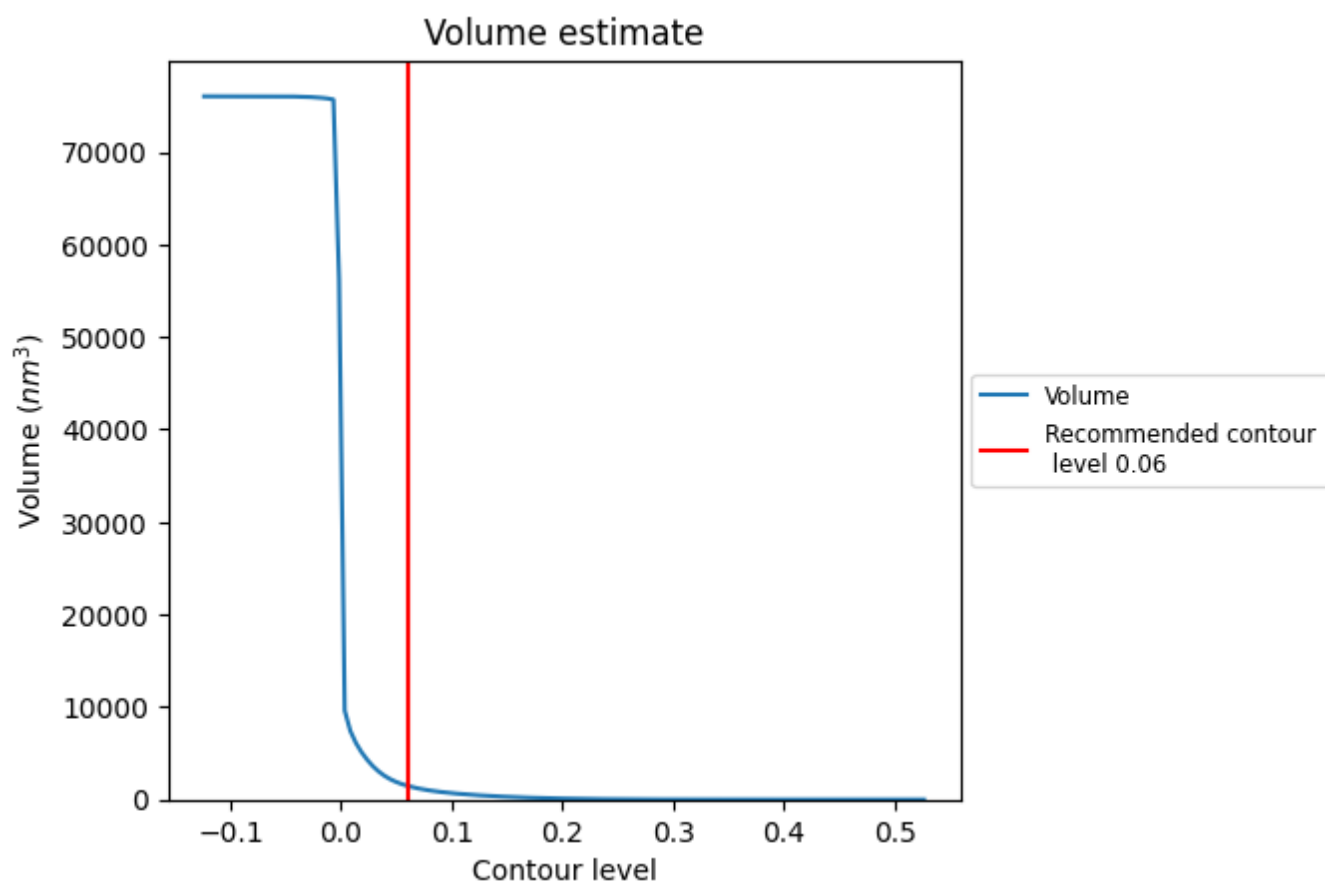
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

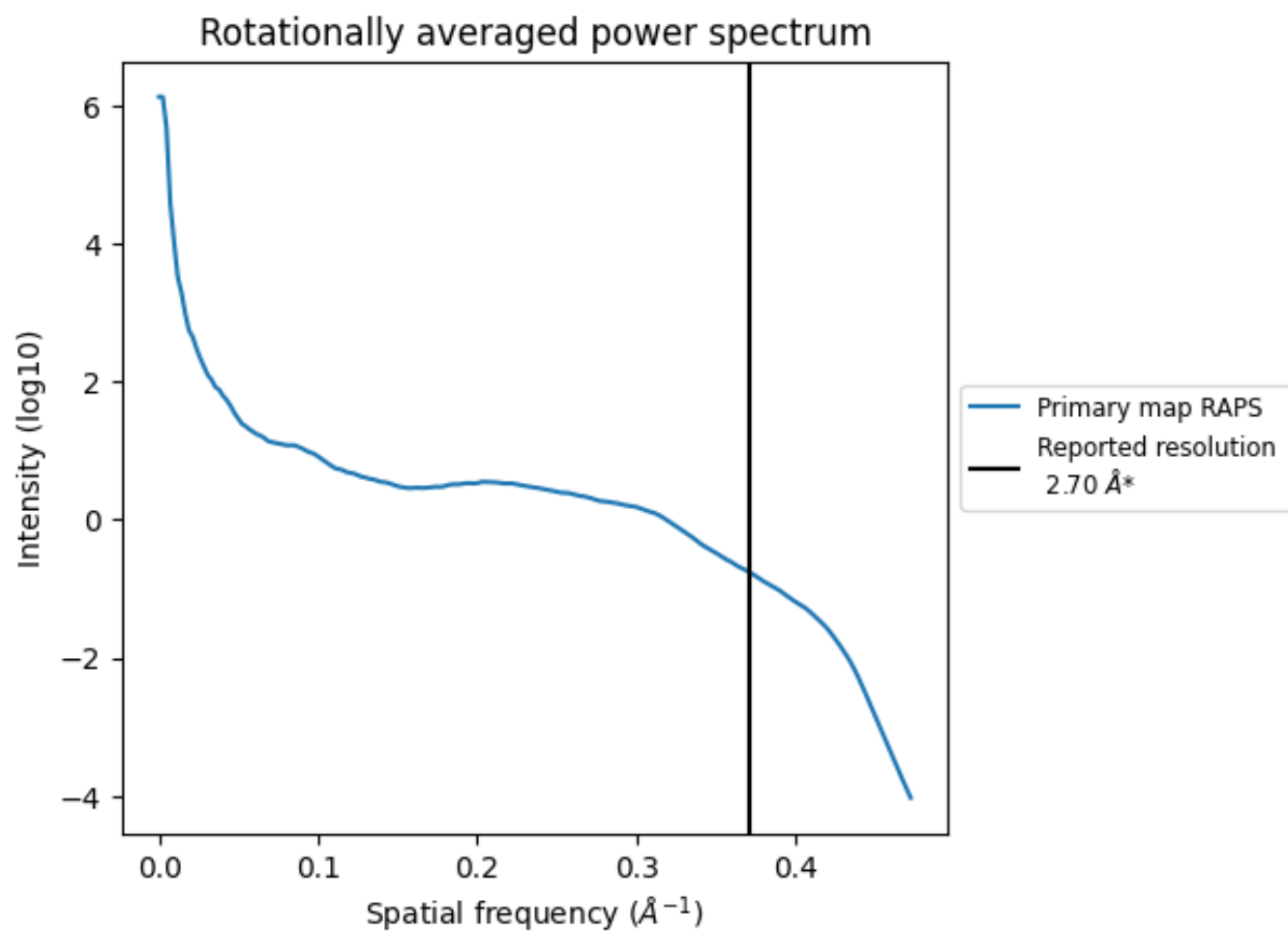
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1485 nm³; this corresponds to an approximate mass of 1342 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

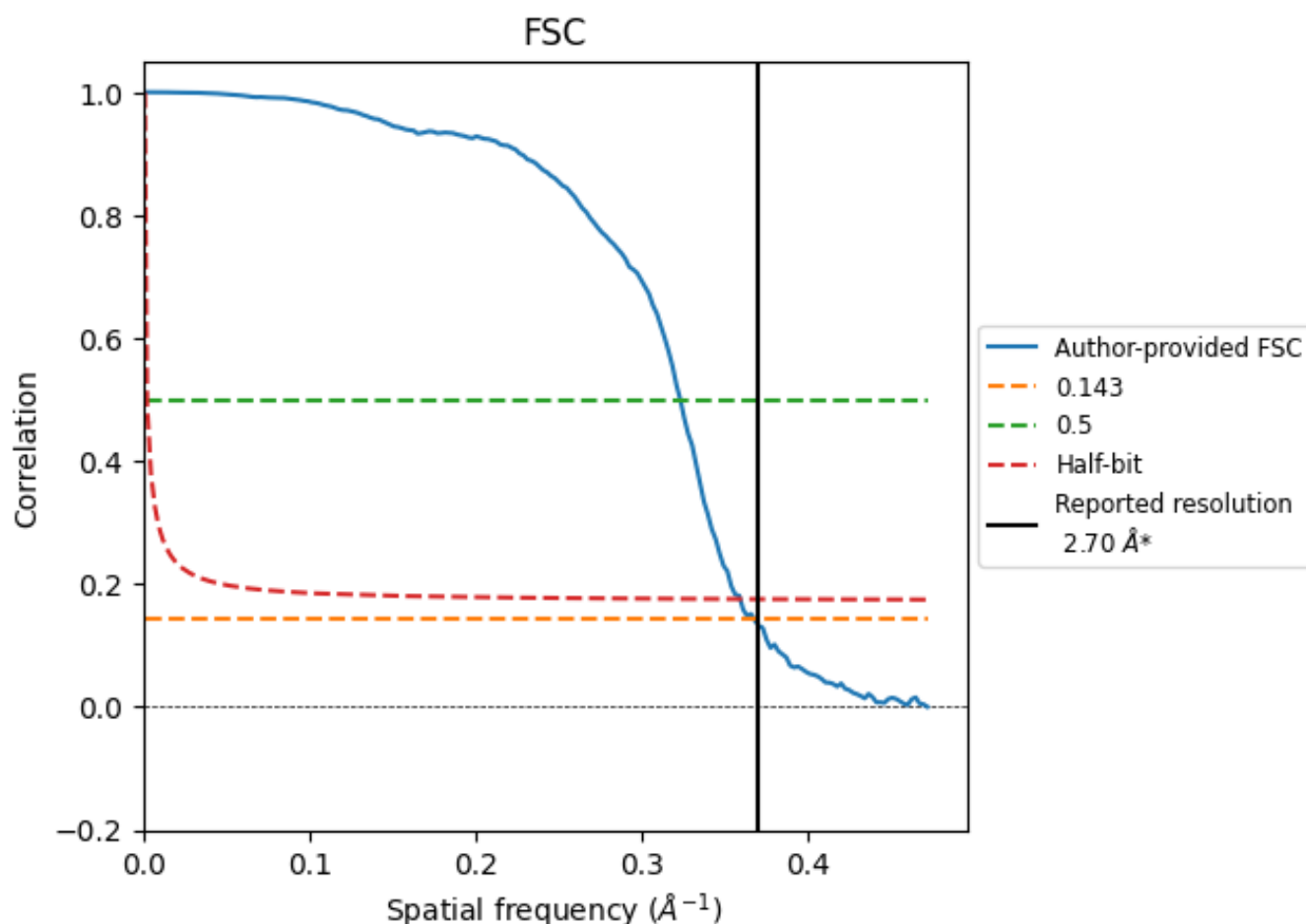


*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.370 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

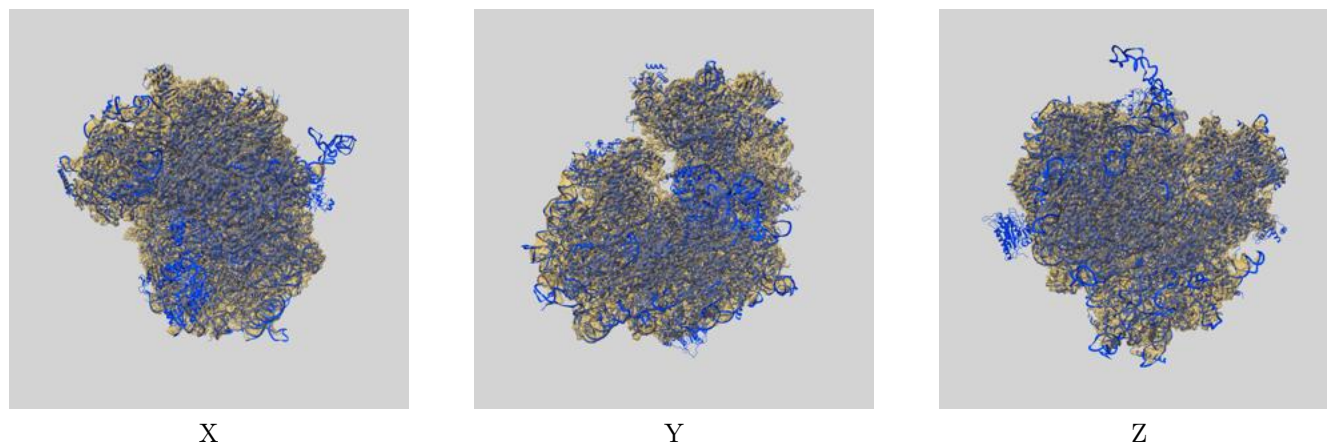
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	2.72	3.09	2.78
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

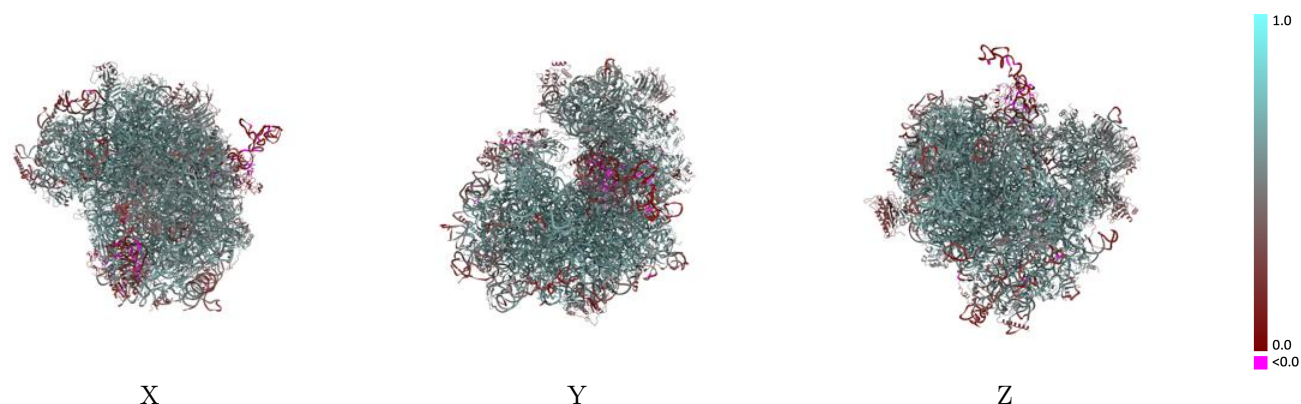
This section contains information regarding the fit between EMDB map EMD-11288 and PDB model 6ZM7. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



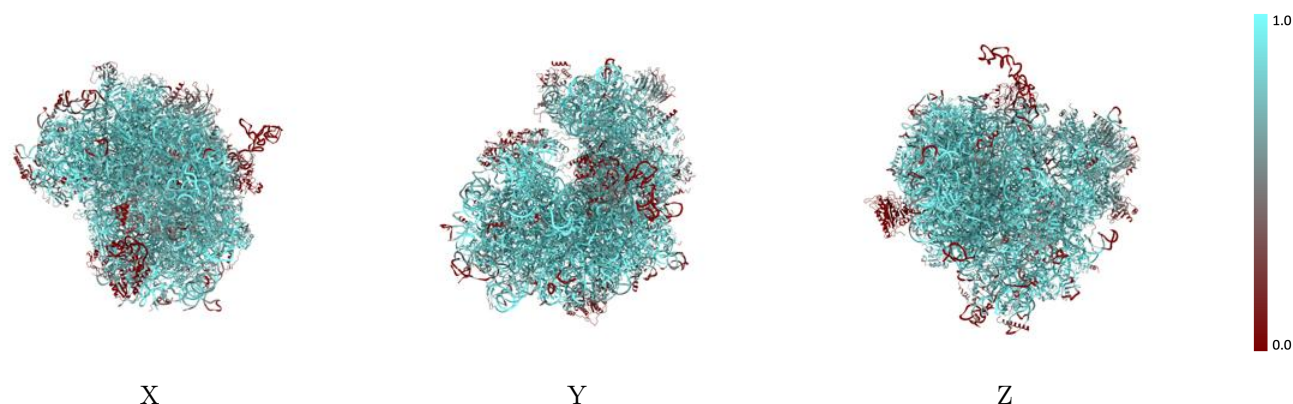
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



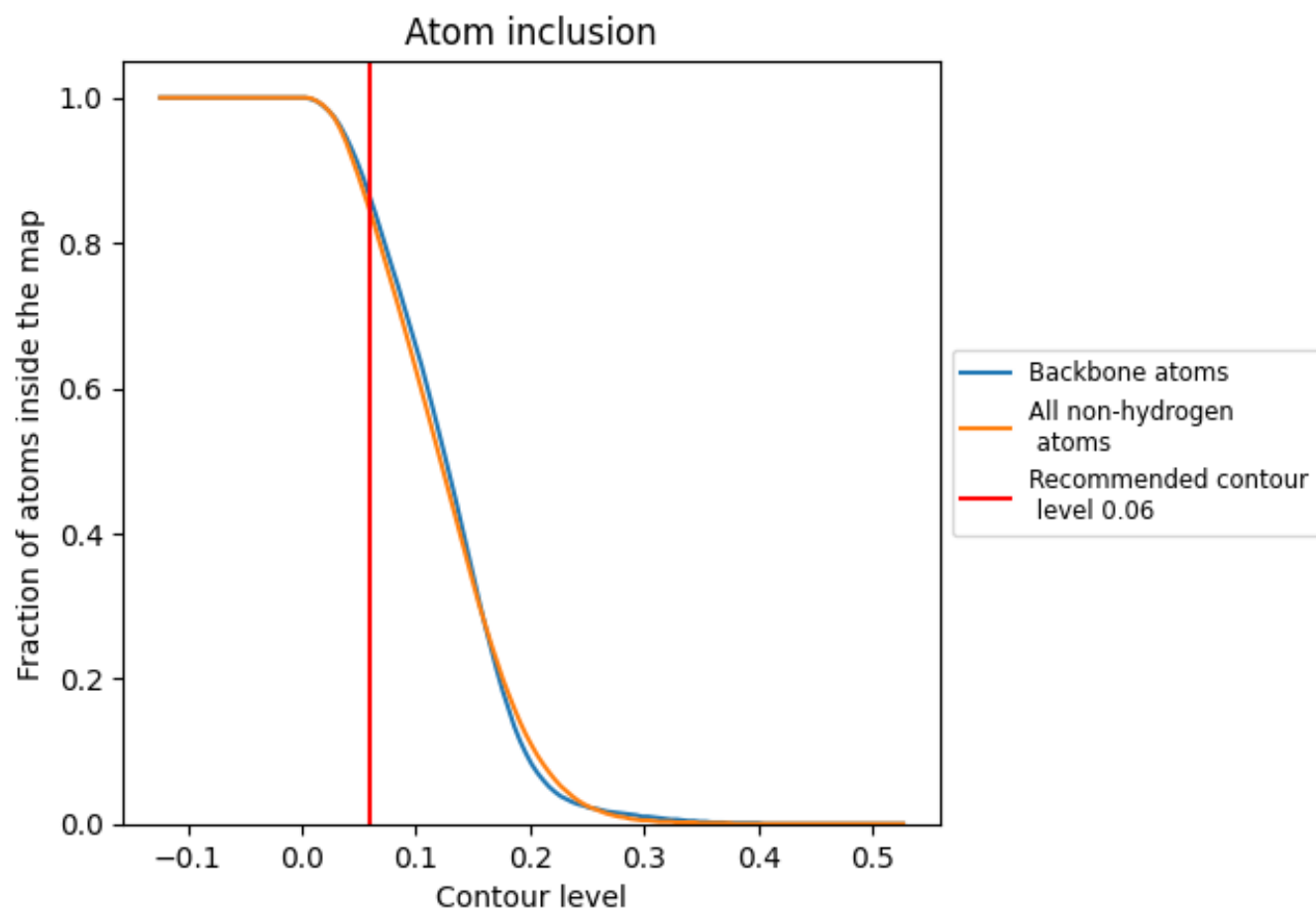
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.06).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 84% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8430	 0.5630
CA	 0.0180	 0.3060
CC	 0.7320	 0.3280
CE	 0.5490	 0.4480
CF	 0.8840	 0.5990
L5	 0.8930	 0.5770
L7	 0.9840	 0.6210
L8	 0.9460	 0.6100
LA	 0.9770	 0.6640
LB	 0.9100	 0.6270
LC	 0.9100	 0.6150
LD	 0.8480	 0.5700
LE	 0.7880	 0.5500
LF	 0.9410	 0.6320
LG	 0.7820	 0.5550
LH	 0.8800	 0.5930
LI	 0.9160	 0.6110
LJ	 0.7380	 0.4940
LL	 0.8610	 0.5910
LM	 0.8850	 0.5830
LN	 0.9810	 0.6660
LO	 0.9340	 0.6370
LP	 0.9410	 0.6450
LQ	 0.9620	 0.6500
LR	 0.8510	 0.5920
LS	 0.9510	 0.6380
LT	 0.8980	 0.6050
LU	 0.7420	 0.5140
LV	 0.9430	 0.6360
LW	 0.5950	 0.4730
LX	 0.9050	 0.6150
LY	 0.8730	 0.6060
LZ	 0.8780	 0.6050
La	 0.9490	 0.6530
Lb	 0.7900	 0.5570



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Chain	Atom inclusion	Q-score
Lc	 0.8890	 0.5970
Ld	 0.8770	 0.6060
Le	 0.9540	 0.6470
Lf	 0.9630	 0.6460
Lg	 0.9090	 0.6250
Lh	 0.8810	 0.5980
Li	 0.8800	 0.5980
Lj	 0.9760	 0.6610
Lk	 0.7590	 0.5520
Ll	 0.9600	 0.6310
Lm	 0.9060	 0.6050
Ln	 0.9470	 0.6440
Lo	 0.8920	 0.6210
Lp	 0.9290	 0.6480
Lr	 0.9350	 0.6120
Ls	 0.0310	 0.1650
Lt	 0.0020	 0.1070
Lz	 0.0590	 0.1400
S2	 0.9060	 0.5720
SA	 0.8270	 0.5640
SB	 0.8530	 0.5840
SC	 0.8900	 0.5970
SD	 0.7200	 0.5010
SE	 0.8660	 0.5850
SF	 0.8040	 0.5390
SG	 0.6860	 0.4930
SH	 0.6410	 0.4830
SI	 0.8440	 0.5740
SJ	 0.8550	 0.5660
SK	 0.6930	 0.4720
SL	 0.8530	 0.6050
SM	 0.1520	 0.2650
SN	 0.9070	 0.6100
SO	 0.8610	 0.5800
SP	 0.6580	 0.4700
SQ	 0.7870	 0.5490
SR	 0.7170	 0.5140
SS	 0.7480	 0.5110
ST	 0.7730	 0.5310
SU	 0.6660	 0.4830
SV	 0.8380	 0.5700
SW	 0.9410	 0.6220

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Chain	Atom inclusion	Q-score
SX	 0.9140	 0.6140
SY	 0.7540	 0.5160
SZ	 0.6310	 0.4800
Sa	 0.8880	 0.5970
Sb	 0.7860	 0.5700
Sc	 0.7100	 0.5110
Sd	 0.9070	 0.5800
Se	 0.7590	 0.5220
Sf	 0.2720	 0.3270
Sg	 0.5520	 0.4590