



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 07:22 AM UTC

PDB ID : 6ZME / pdb_00006zme
EMDB ID : EMD-11289
Title : SARS-CoV-2 Nsp1 bound to the human CCDC124-80S-eERF1 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 : 2020-07-02
Resolution : 3.00 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:

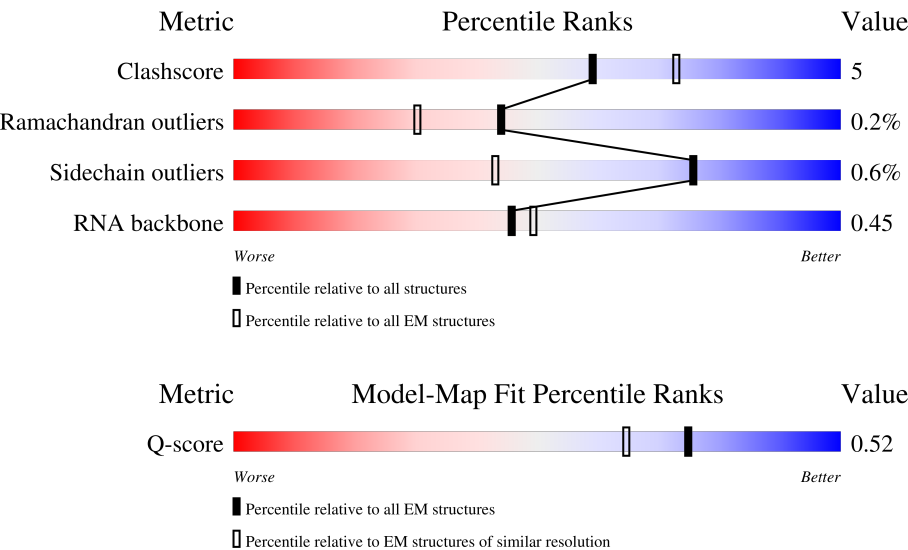
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.00 Å.

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



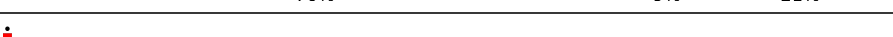
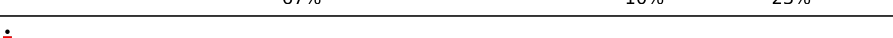
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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

Mol	Chain	Length	Quality of chain
1	L5	5066	
2	L7	121	
3	L8	157	

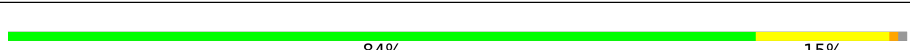
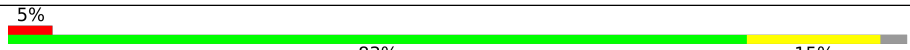
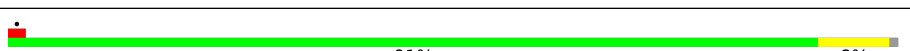
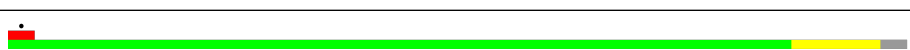
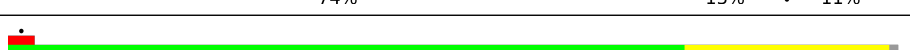
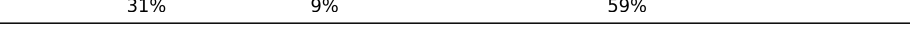
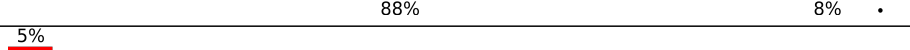
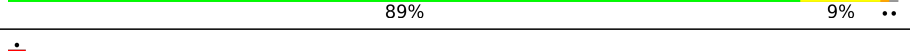
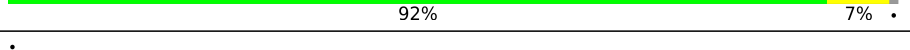
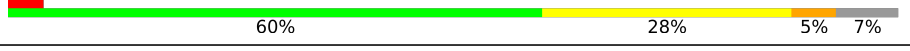
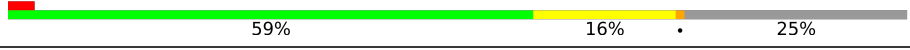
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Mol	Chain	Length	Quality of chain
4	LA	257	
5	LB	403	
6	LC	427	
7	LD	297	
8	LE	288	
9	LF	248	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	215	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	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

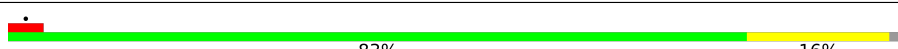
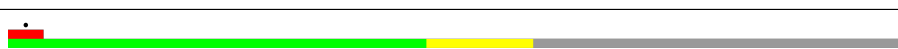
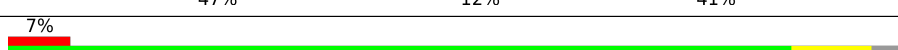
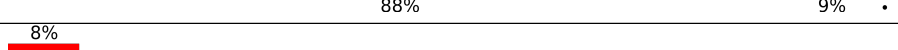
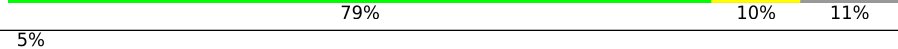
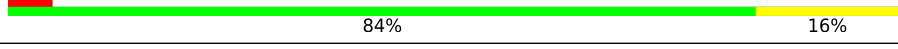
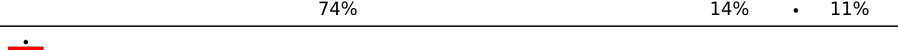
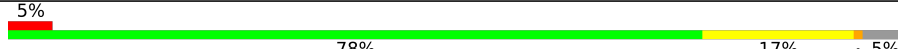
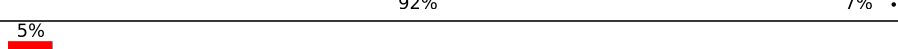
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Mol	Chain	Length	Quality of chain
29	La	148	
30	Lb	159	
31	Lc	115	
32	Ld	125	
33	Le	135	
34	Lf	110	
35	Lg	117	
36	Lh	123	
37	Li	105	
38	Lj	97	
39	Lk	70	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	Lr	137	
46	Ls	317	
47	Lt	165	
48	Lz	217	
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	
87	CI	599	
88	CH	437	

2 Entry composition [i](#)

There are 92 unique types of molecules in this entry. The entry contains 233375 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	117	Total	C	N	O	S	0	0
			998	611	199	184	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 a protein called ATP-binding cassette sub-family E member 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	CI	582	Total	C	N	O	S	0	0
			4586	2931	785	839	31		

- Molecule 88 is a protein called Eukaryotic peptide chain release factor subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	CH	415	Total	C	N	O	S	0	0
			3257	2073	556	617	11		

- Molecule 89 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
89	L5	210	Total	Mg	0
			210	210	
89	L7	3	Total	Mg	0
			3	3	
89	L8	4	Total	Mg	0
			4	4	
89	LA	1	Total	Mg	0
			1	1	
89	LB	1	Total	Mg	0
			1	1	
89	LI	1	Total	Mg	0
			1	1	

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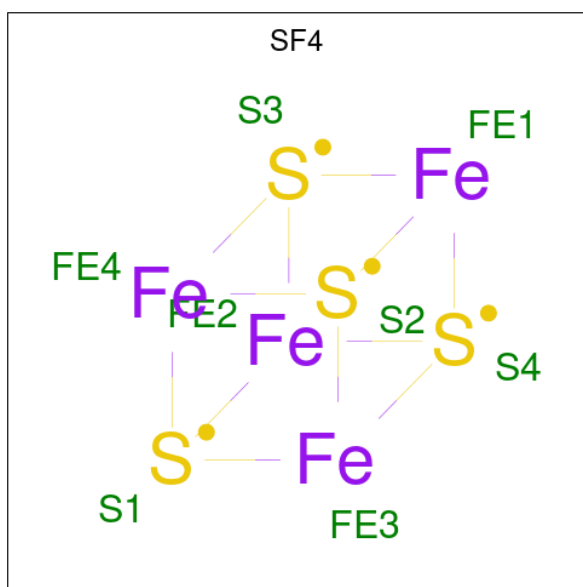
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
89	LP	1	Total 1	Mg 1	0
89	LV	1	Total 1	Mg 1	0
89	LX	1	Total 1	Mg 1	0
89	Le	2	Total 2	Mg 2	0
89	Lg	1	Total 1	Mg 1	0
89	S2	29	Total 29	Mg 29	0
89	SG	1	Total 1	Mg 1	0

- Molecule 90 is ZINC ION (CCD ID: ZN) (formula: Zn).

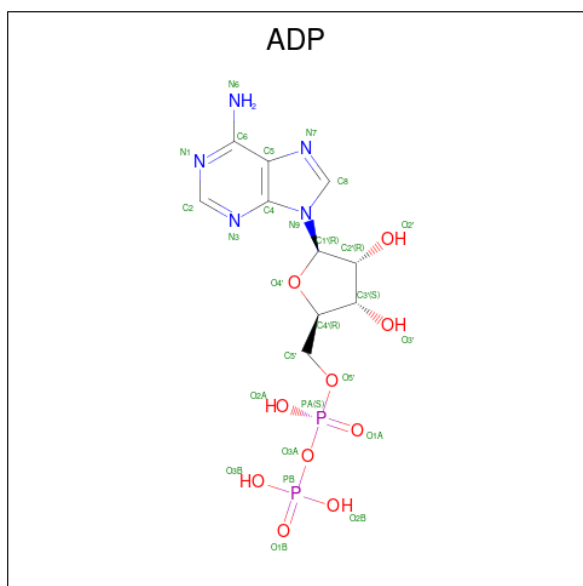
Mol	Chain	Residues	Atoms		AltConf
90	Lg	1	Total 1	Zn 1	0
90	Lj	1	Total 1	Zn 1	0
90	Lm	1	Total 1	Zn 1	0
90	Lo	1	Total 1	Zn 1	0
90	Lp	1	Total 1	Zn 1	0
90	Sa	1	Total 1	Zn 1	0
90	Sd	1	Total 1	Zn 1	0
90	Sf	1	Total 1	Zn 1	0

- Molecule 91 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			AltConf
91	CI	1	Total 8	Fe 4	S 4	0
91	CI	1	Total 8	Fe 4	S 4	0

- Molecule 92 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).

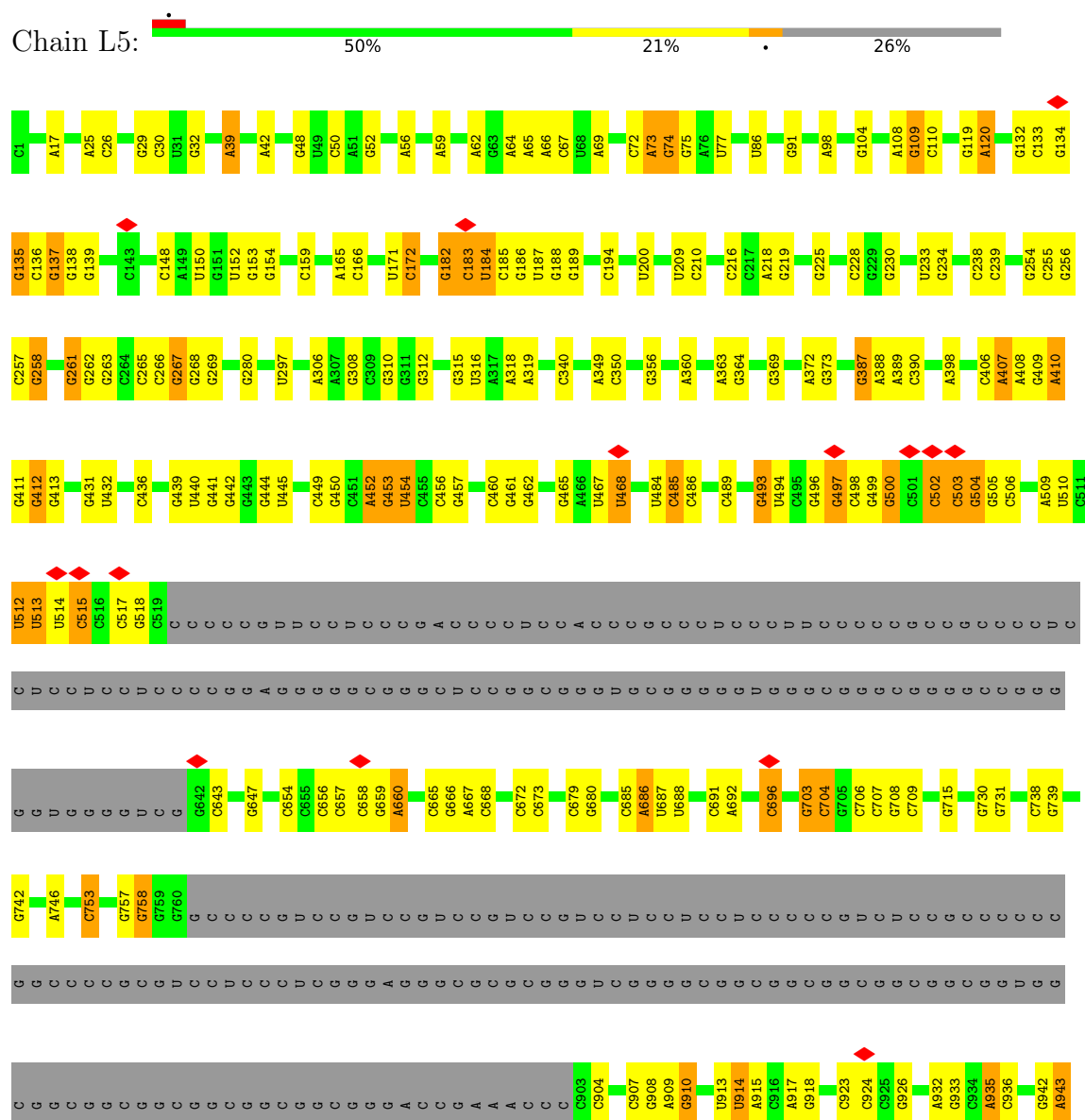


Mol	Chain	Residues	Atoms					AltConf
92	CI	1	Total 27	C 10	N 5	O 10	P 2	0

3 Residue-property plots

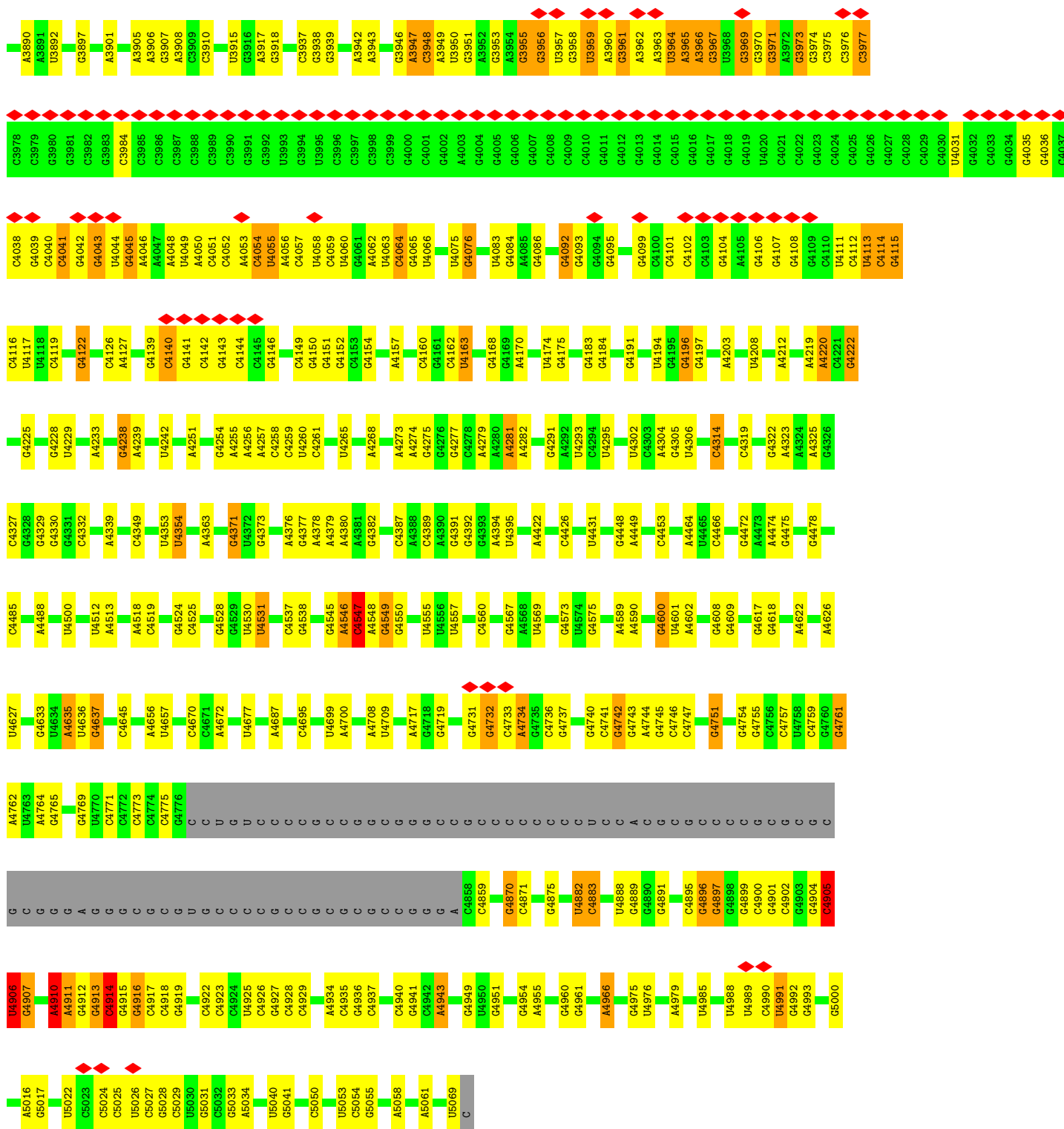
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 28S ribosomal RNA





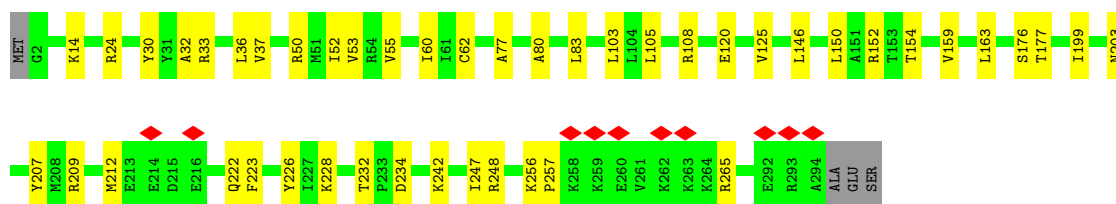




• Molecule 2: 5S ribosomal RNA

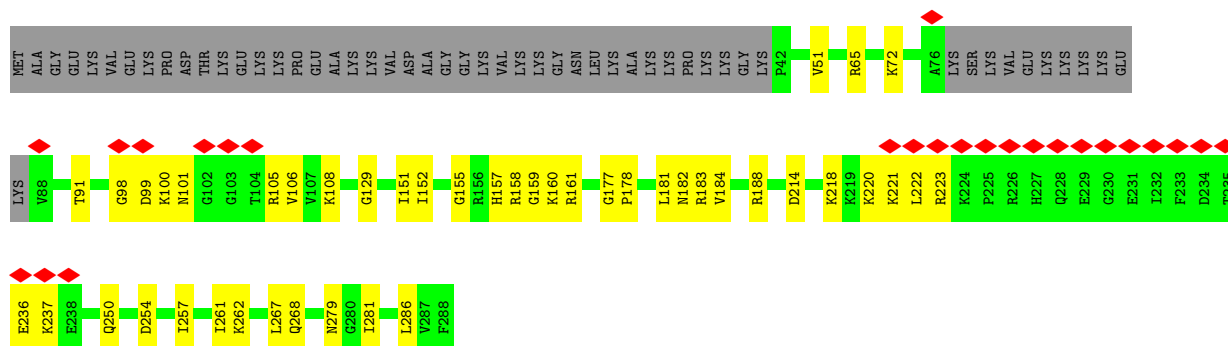
Chain L7: 81% 18%

Chain LD:  83% 15%



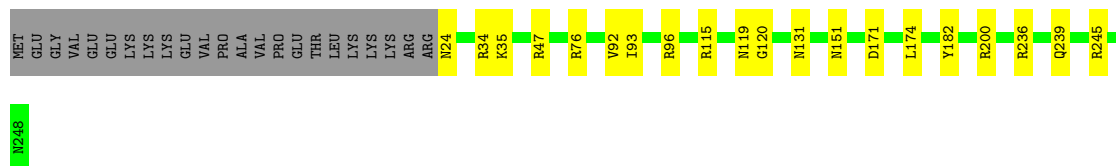
- Molecule 8: 60S ribosomal protein L6

Chain LE:  9% 66% 16% 18%



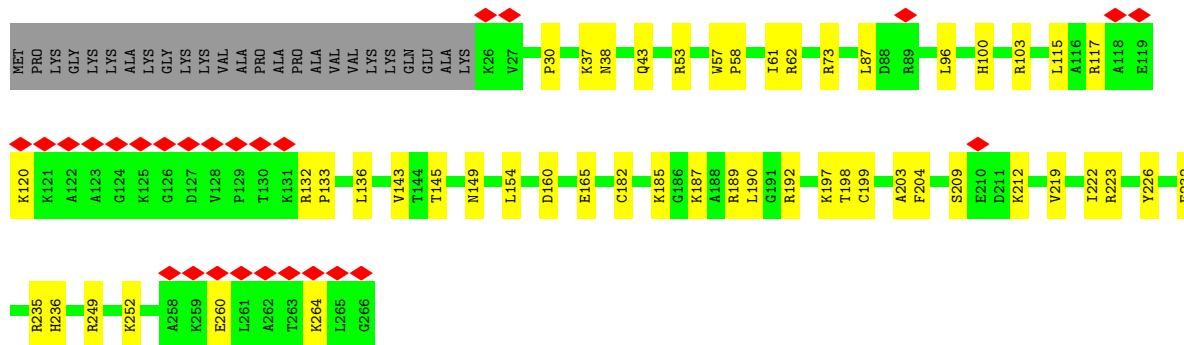
- Molecule 9: 60S ribosomal protein L7

Chain LF:  83% 8% 9%

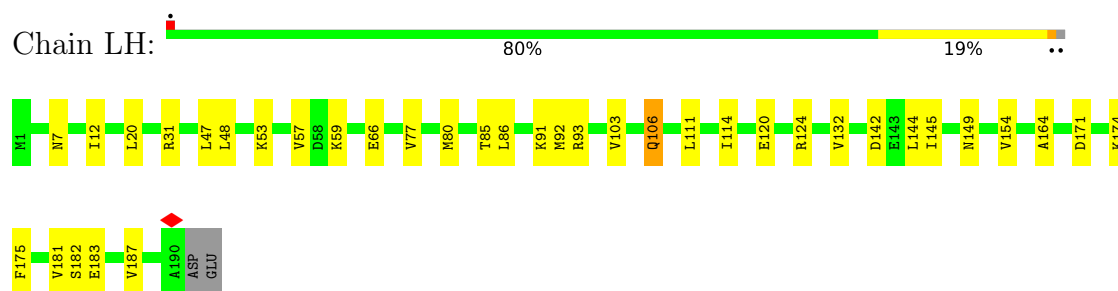


- Molecule 10: 60S ribosomal protein L7a

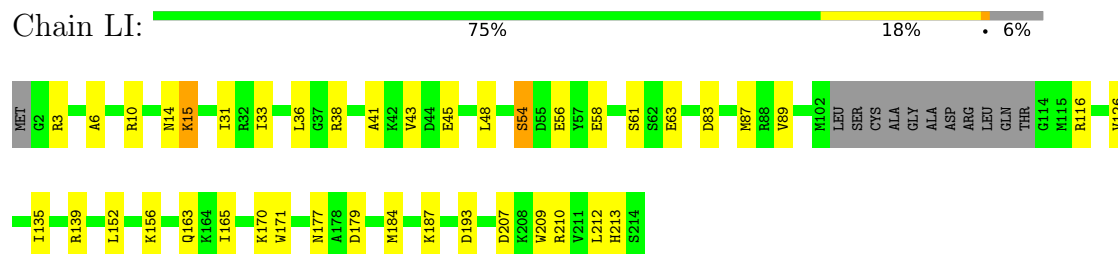
Chain LG:  10% 72% 19% 9%



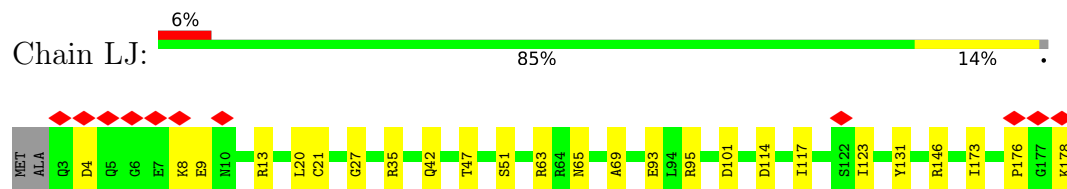
- Molecule 11: 60S ribosomal protein L9



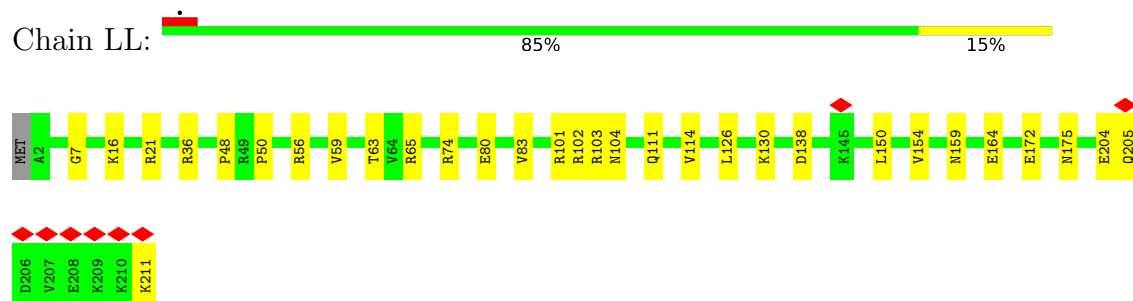
- Molecule 12: 60S ribosomal protein L10-like



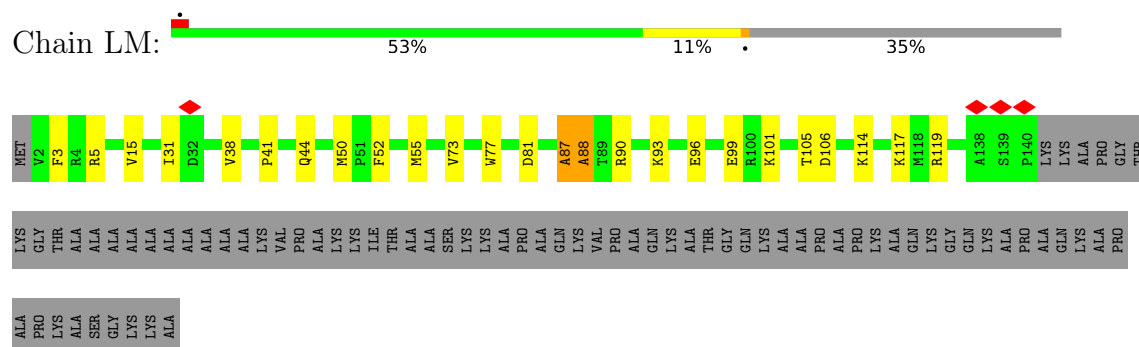
- Molecule 13: 60S ribosomal protein L11



- Molecule 14: 60S ribosomal protein L13

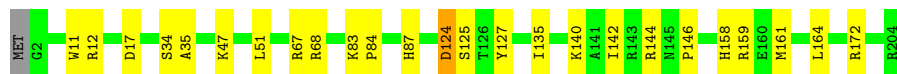


- Molecule 15: 60S ribosomal protein L14



- Molecule 16: 60S ribosomal protein L15

Chain LN:  87% 12%



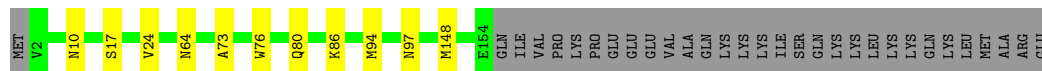
- Molecule 17: 60S ribosomal protein L13a

Chain LO:  88% 10%



- Molecule 18: 60S ribosomal protein L17

Chain LP:  77% 6% 17%



- Molecule 19: 60S ribosomal protein L18

Chain LQ:  89% 10%



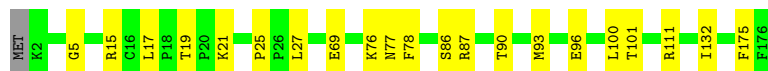
- Molecule 20: 60S ribosomal protein L19

Chain LR:  6% 84% 12% 5%



- Molecule 21: 60S ribosomal protein L18a

Chain LS:  88% 12%



- Molecule 22: 60S ribosomal protein L21

Chain LT:  86% 14%



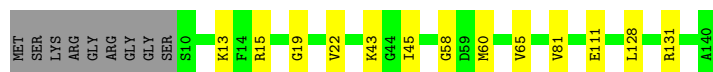
- Molecule 23: 60S ribosomal protein L22

Chain LU:  71% 8% 21%



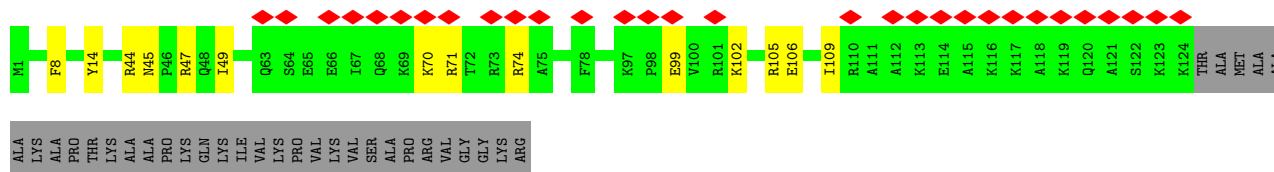
- Molecule 24: 60S ribosomal protein L23

Chain LV:  84% 9% 6%



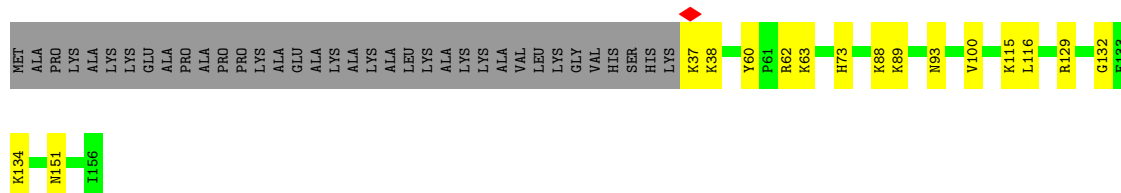
- Molecule 25: 60S ribosomal protein L24

Chain LW:  19% 70% 9% 21%



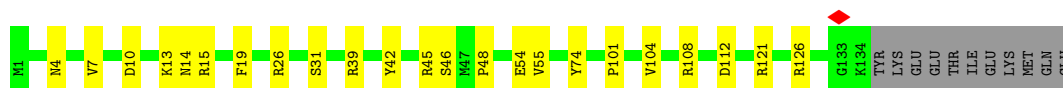
- Molecule 26: 60S ribosomal protein L23a

Chain LX:  67% 10% 23%



- Molecule 27: 60S ribosomal protein L26

Chain LY:  77% 16% 8%

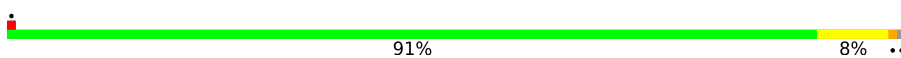


- Molecule 28: 60S ribosomal protein L27

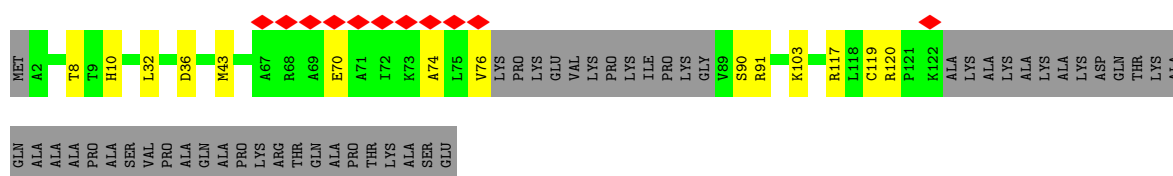
Chain LZ:  87% 12% 1%



• Molecule 29: 60S ribosomal protein L27a

Chain La:  91% 8% ..

• Molecule 30: 60S ribosomal protein L29

Chain Lb:  7% 60% 9% 31%

• Molecule 31: 60S ribosomal protein L30

Chain Lc:  72% 13% 15%

• Molecule 32: 60S ribosomal protein L31

Chain Ld:  74% 11% 14%

• Molecule 33: 60S ribosomal protein L32

Chain Le:  90% 5% 5%

• Molecule 34: 60S ribosomal protein L35a

Chain Lf:  84% 15% ..

• Molecule 35: 60S ribosomal protein L34

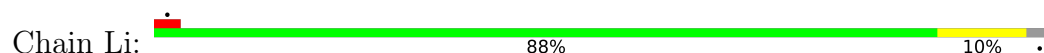
Chain Lg:  5% 83% 15% .



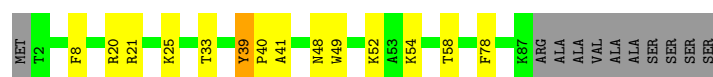
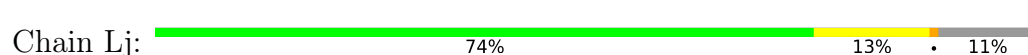
- Molecule 36: 60S ribosomal protein L35



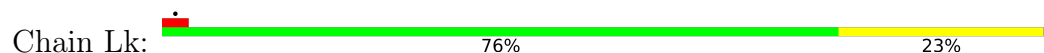
- Molecule 37: 60S ribosomal protein L36



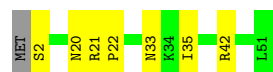
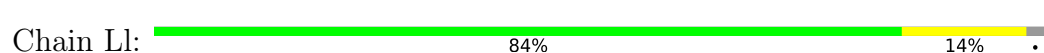
- Molecule 38: 60S ribosomal protein L37



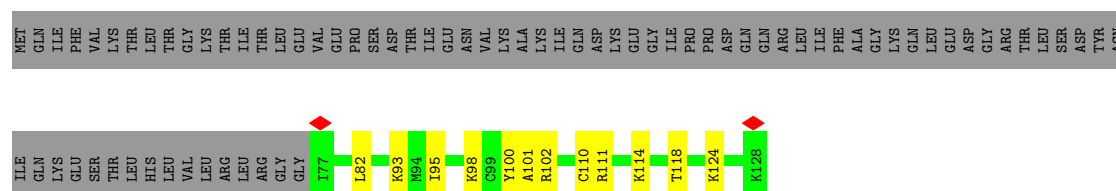
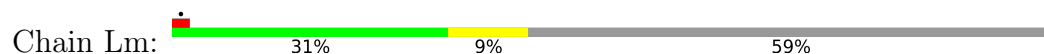
- Molecule 39: 60S ribosomal protein L38

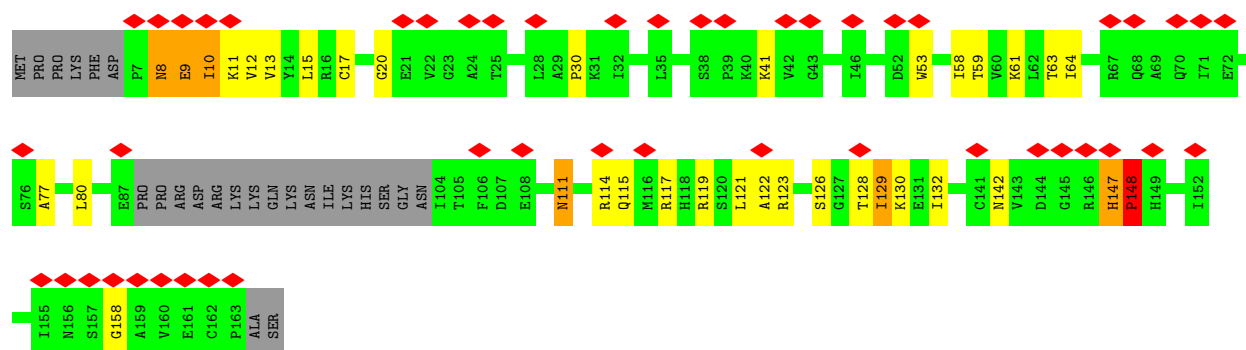


- Molecule 40: 60S ribosomal protein L39

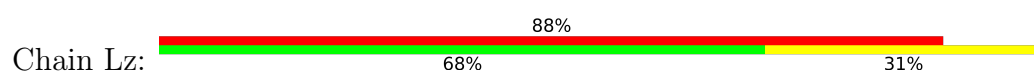


- Molecule 41: Ubiquitin-60S ribosomal protein L40

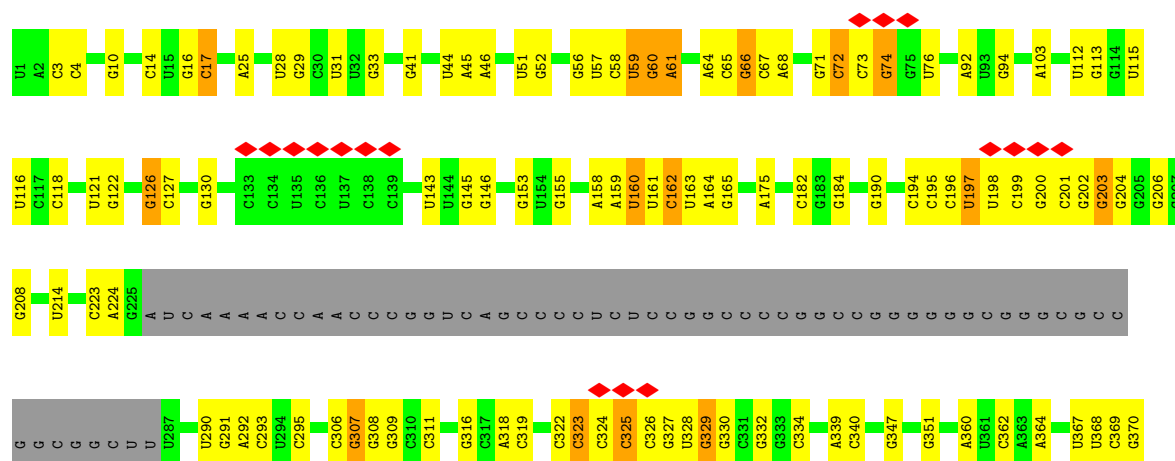


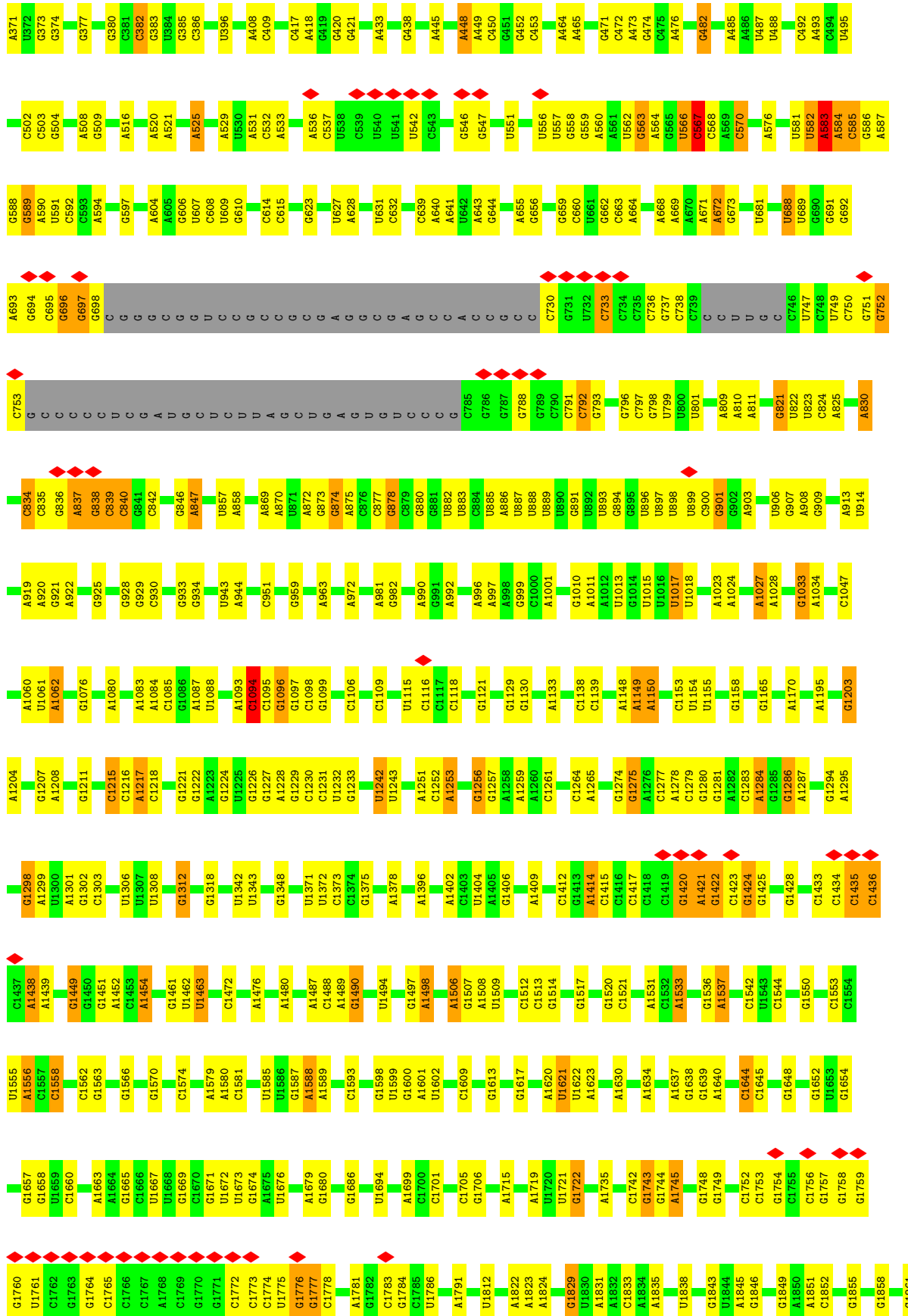


• Molecule 48: 60S ribosomal protein L10a



• Molecule 49: 18S ribosomal RNA

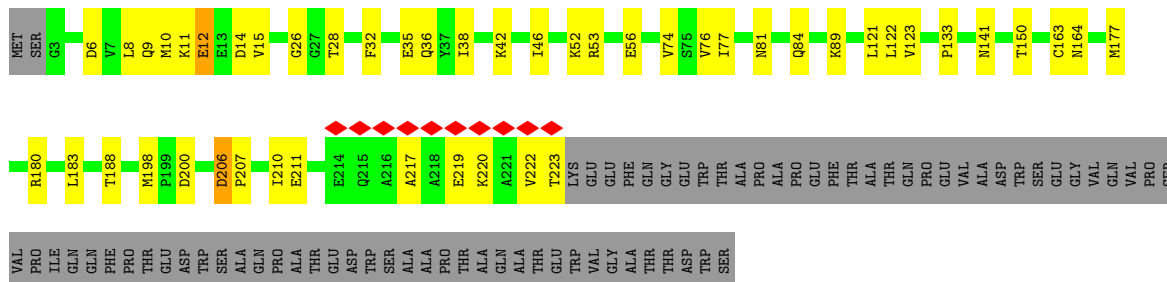




G1862
A1863
U1864
C1865
A1869

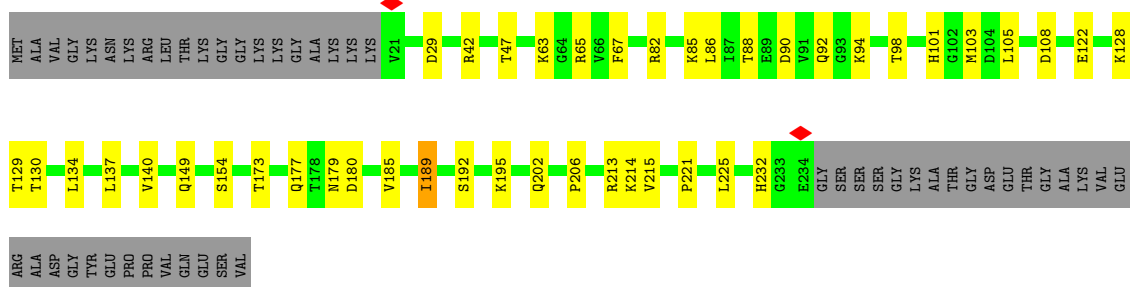
- Molecule 50: 40S ribosomal protein SA

Chain SA:  59% 16% 25%



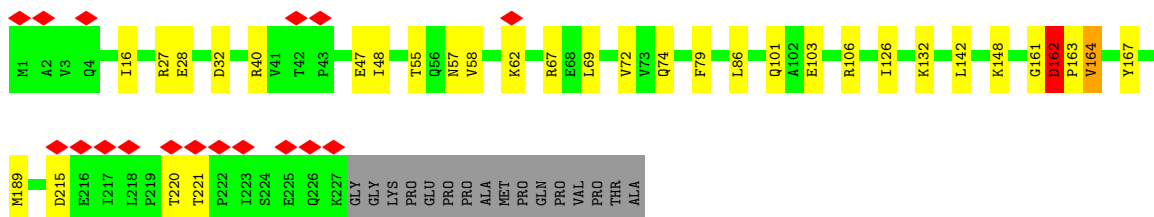
- Molecule 51: 40S ribosomal protein S3a

Chain SB:  65% 16% 19%



- Molecule 52: 40S ribosomal protein S3

Chain SD:  7% 80% 13% 7%



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

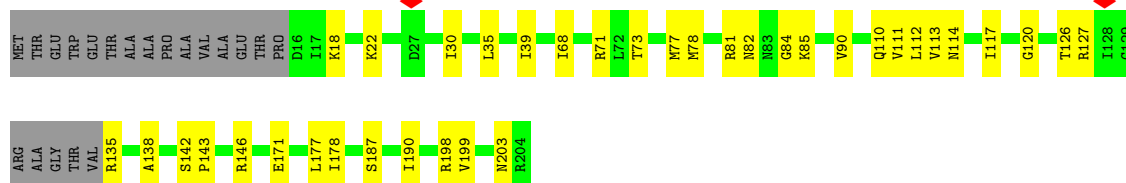
Chain SE:  88% 12%





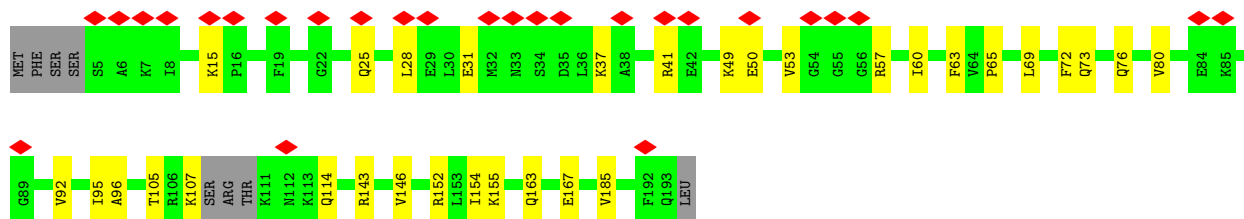
- Molecule 54: 40S ribosomal protein S5

Chain SF: 72% 18% 10%



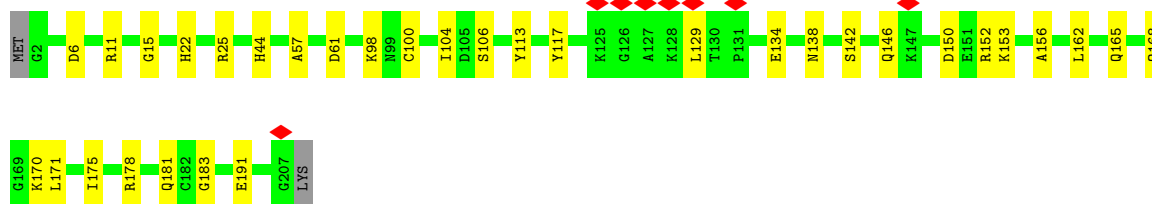
- Molecule 55: 40S ribosomal protein S7

Chain SH: 14% 79% 16%



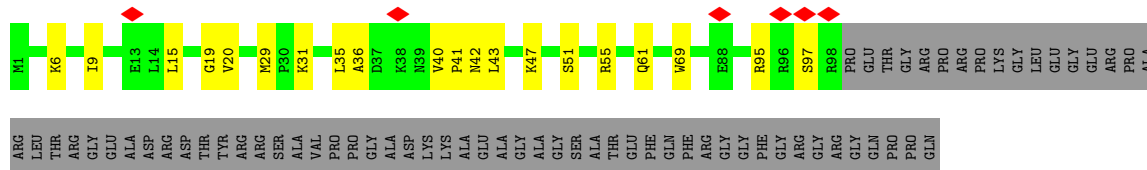
- Molecule 56: 40S ribosomal protein S8

Chain SI: 83% 16%



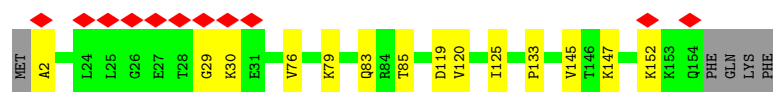
- Molecule 57: 40S ribosomal protein S10

Chain SK: 47% 12% 41%

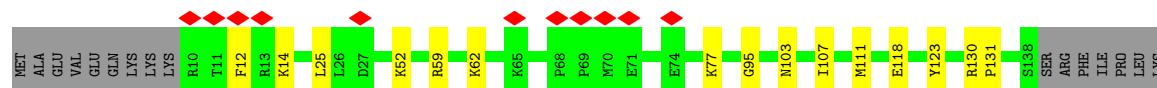
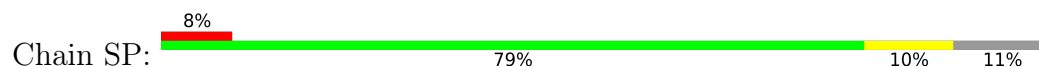


- Molecule 58: 40S ribosomal protein S11

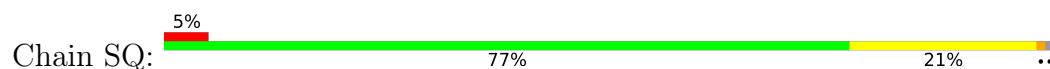
Chain SL: 7% 88% 9%



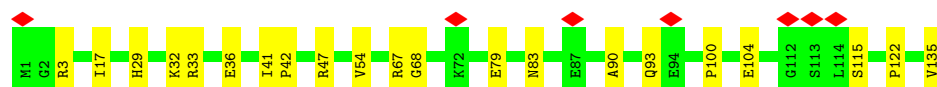
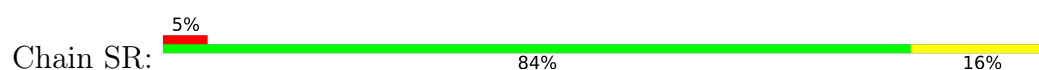
- Molecule 59: 40S ribosomal protein S15



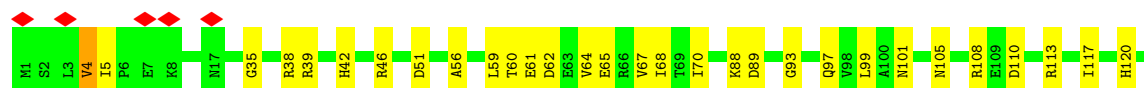
- Molecule 60: 40S ribosomal protein S16



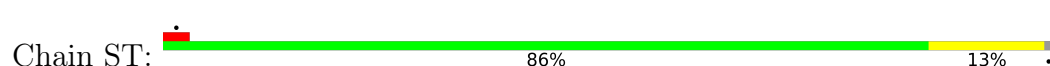
- Molecule 61: 40S ribosomal protein S17



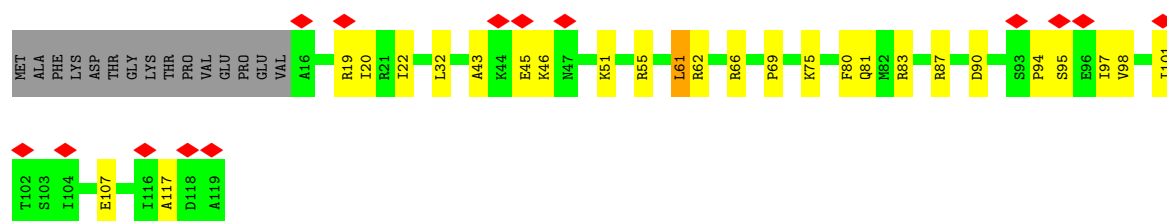
- Molecule 62: 40S ribosomal protein S18



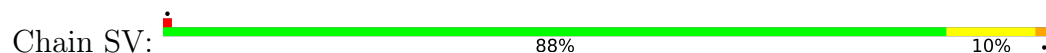
- Molecule 63: 40S ribosomal protein S19



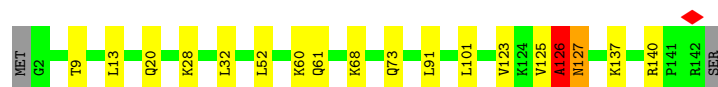
- Molecule 64: 40S ribosomal protein S20



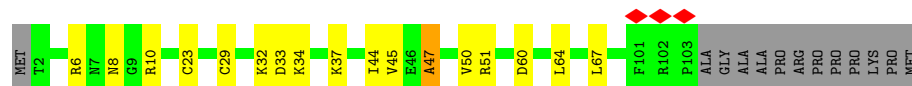
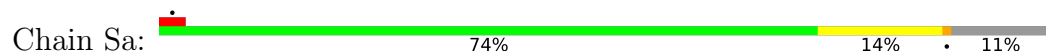
- Molecule 65: 40S ribosomal protein S21



- Molecule 66: 40S ribosomal protein S23



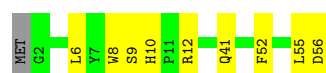
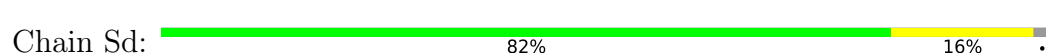
- Molecule 67: 40S ribosomal protein S26



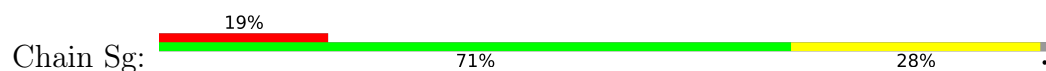
- Molecule 68: 40S ribosomal protein S28



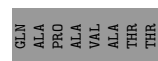
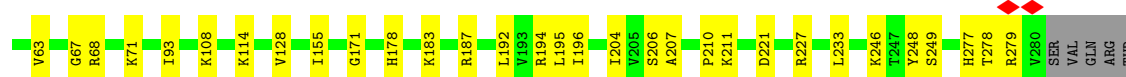
- Molecule 69: 40S ribosomal protein S29



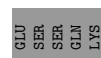
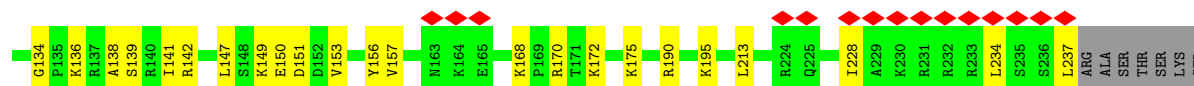
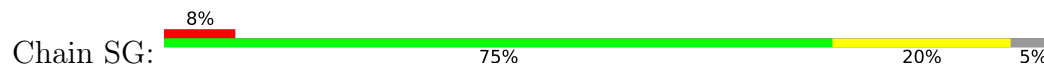
- Molecule 70: Receptor of activated protein C kinase 1



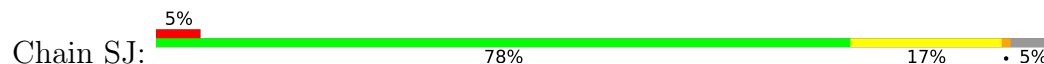
- Molecule 71: 40S ribosomal protein S2

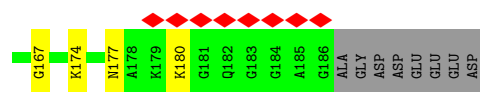


- Molecule 72: 40S ribosomal protein S6

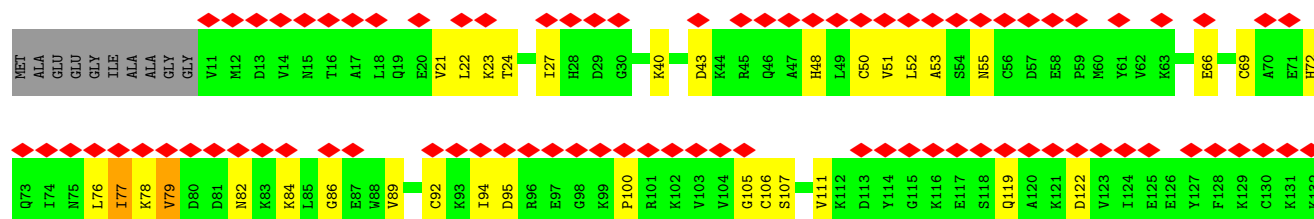


- Molecule 73: 40S ribosomal protein S9





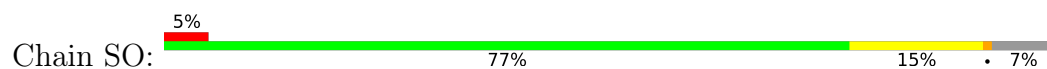
- Molecule 74: 40S ribosomal protein S12



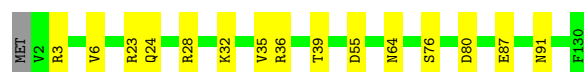
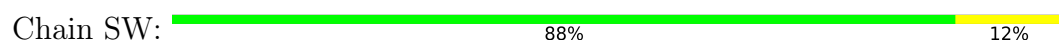
- Molecule 75: 40S ribosomal protein S13



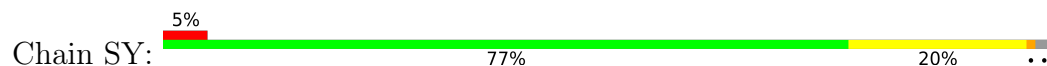
- Molecule 76: 40S ribosomal protein S14



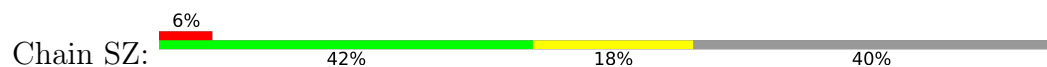
- Molecule 77: 40S ribosomal protein S15a

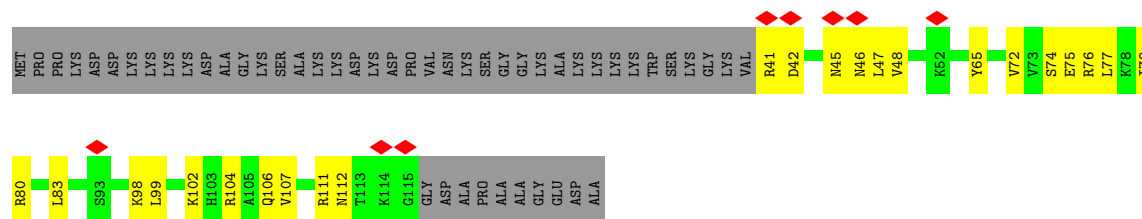


- Molecule 78: 40S ribosomal protein S24

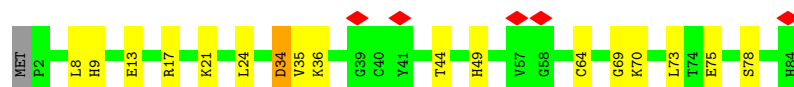
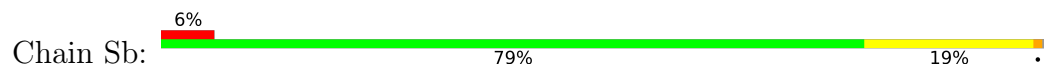


- Molecule 79: 40S ribosomal protein S25

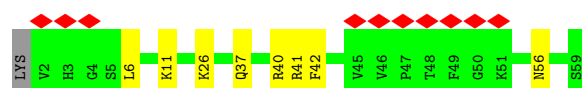
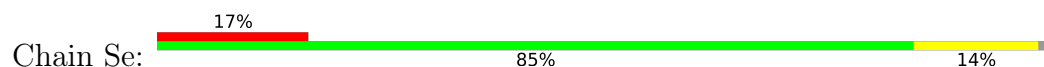




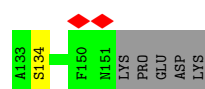
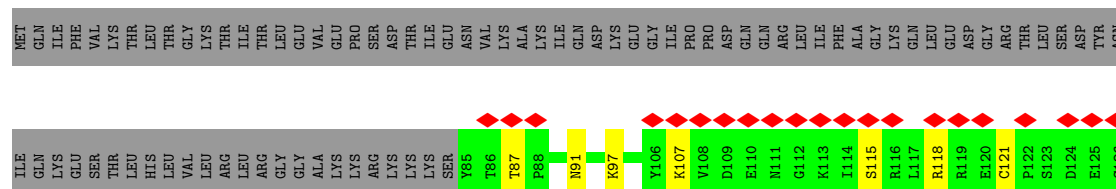
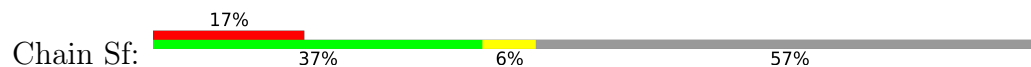
- Molecule 80: 40S ribosomal protein S27



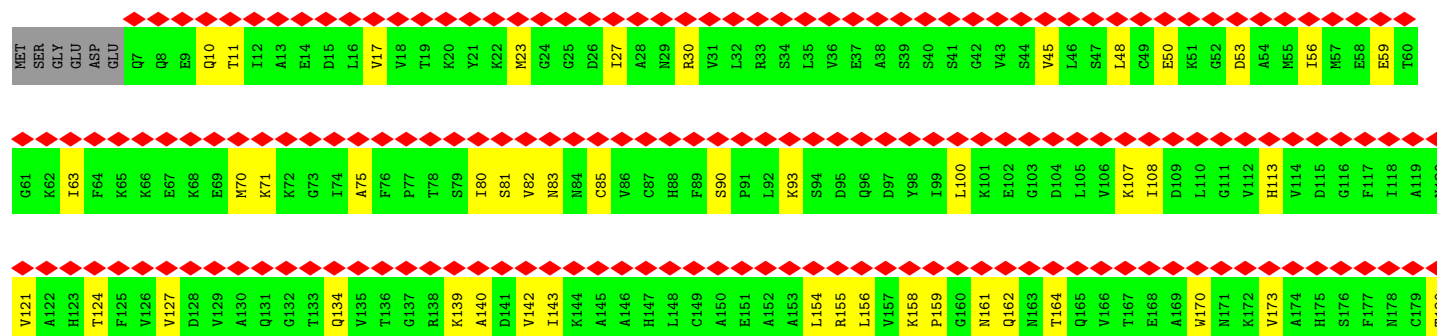
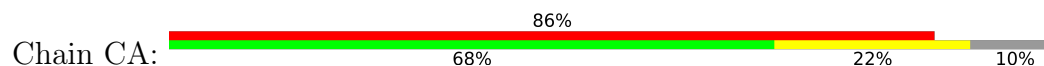
- Molecule 81: 40S ribosomal protein S30

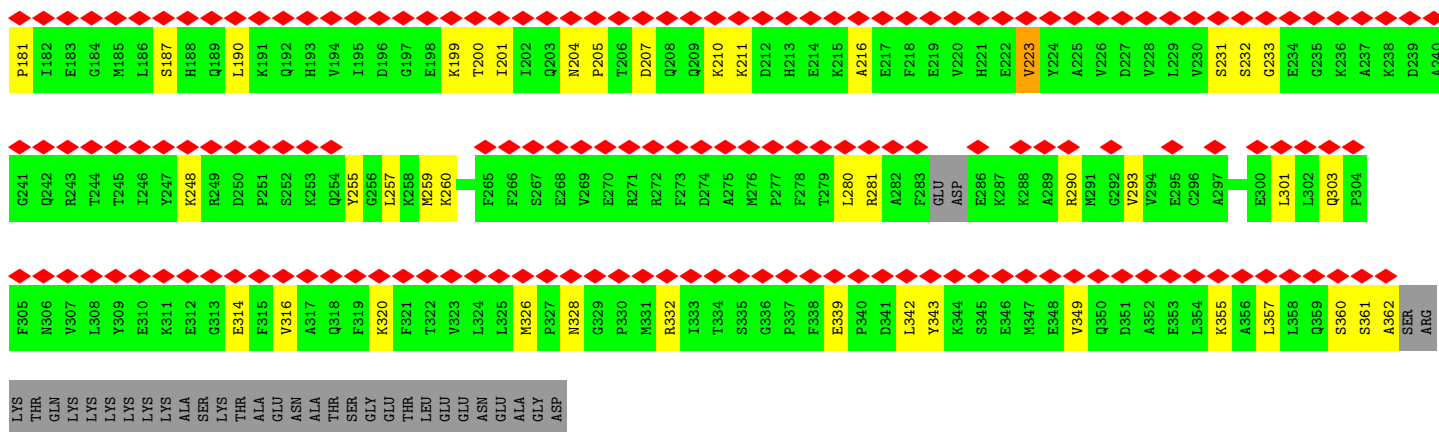


- Molecule 82: Ubiquitin-40S ribosomal protein S27a

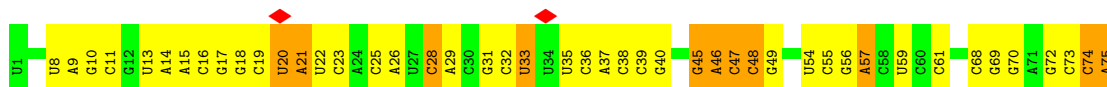


- Molecule 83: Proliferation-associated protein 2G4

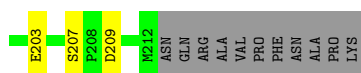
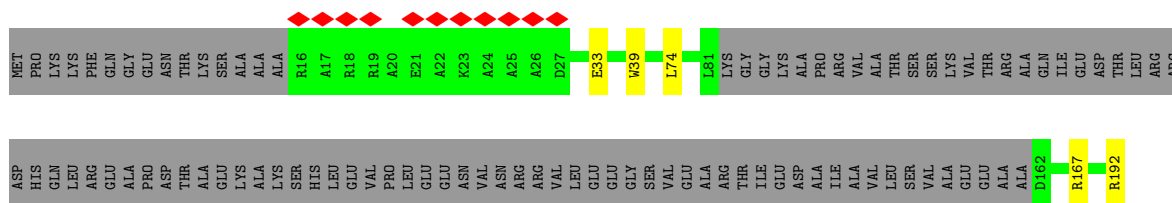




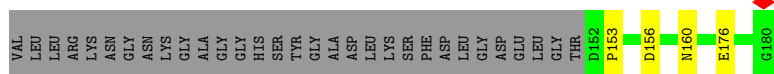
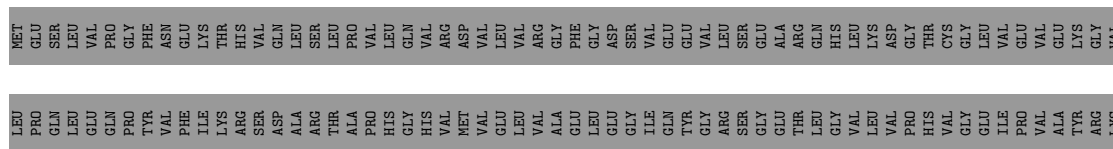
- Molecule 84: tRNA



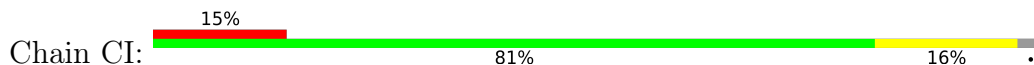
- Molecule 85: Coiled-coil domain-containing protein 124

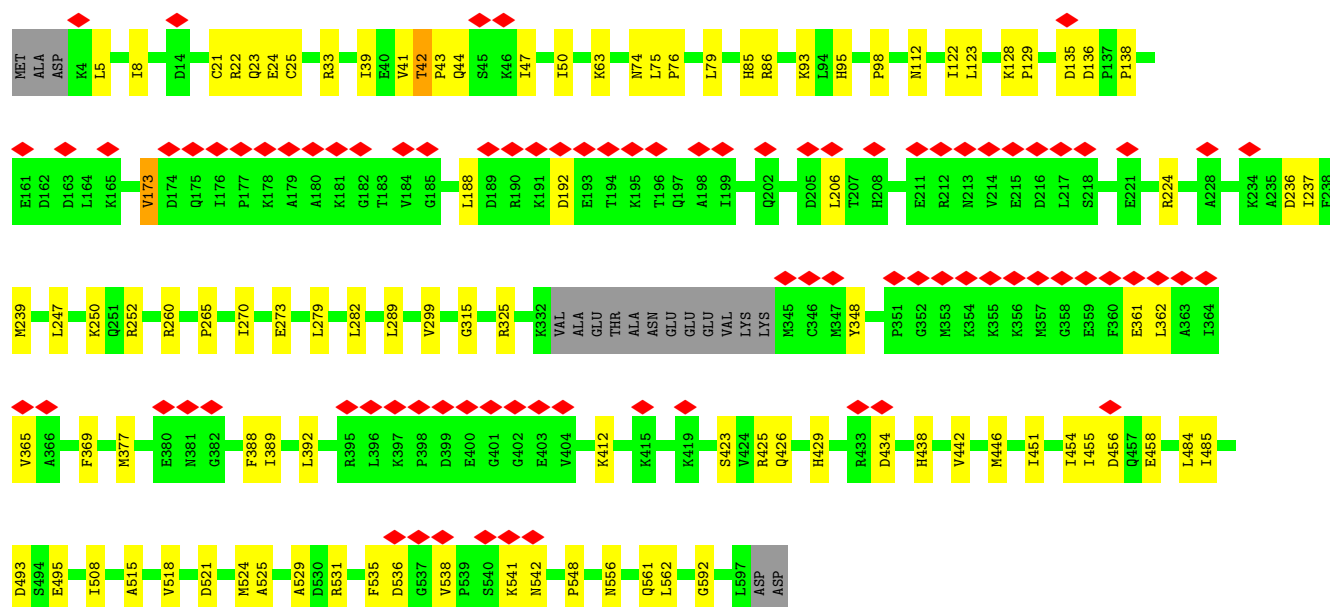


- Molecule 86: Non-structural protein 1

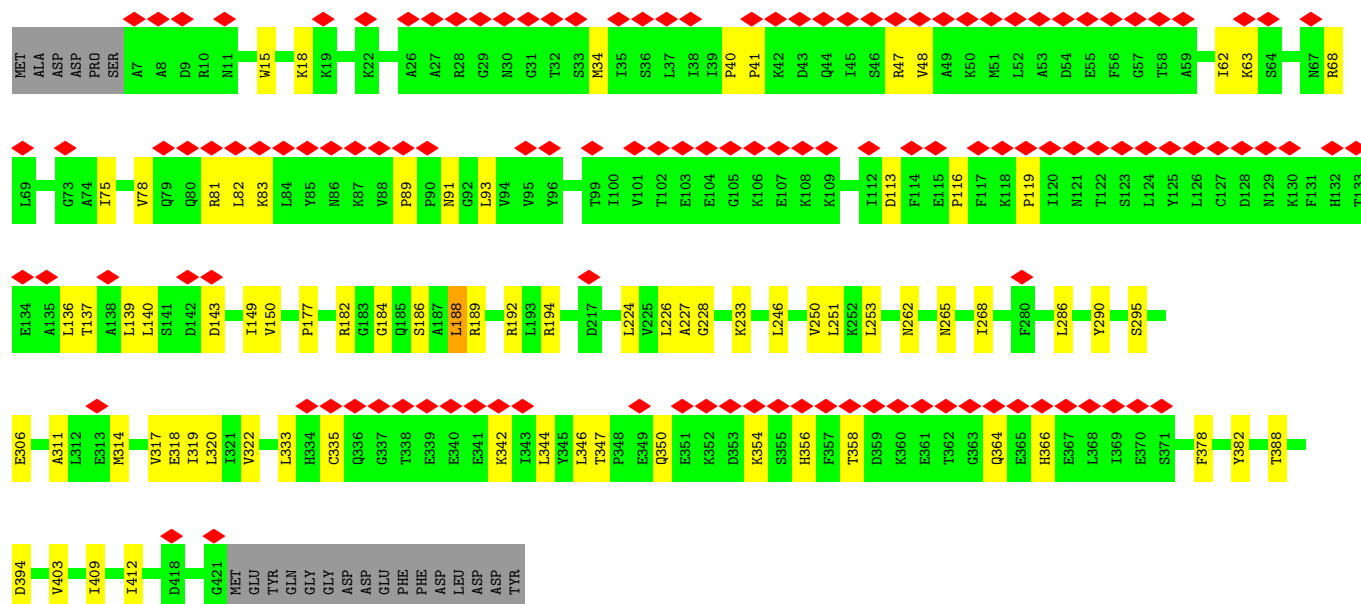
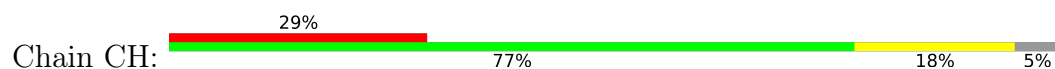


- Molecule 87: ATP-binding cassette sub-family E member 1





- Molecule 88: Eukaryotic peptide chain release factor subunit 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	13337	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	0.457	Depositor
Minimum map value	-0.148	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	423.6, 423.6, 423.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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: MG, ZN, SF4, ADP

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	0.33	2/89595 (0.0%)	0.43	26/139686 (0.0%)
2	L7	0.29	0/2861	0.37	0/4459
3	L8	0.32	0/3701	0.37	0/5766
4	LA	0.37	0/1936	0.66	0/2596
5	LB	0.31	0/3306	0.59	3/4424 (0.1%)
6	LC	0.34	0/2981	0.63	2/4002 (0.0%)
7	LD	0.26	0/2428	0.58	0/3252
8	LE	0.27	0/1942	0.59	0/2606
9	LF	0.33	0/1905	0.60	0/2539
10	LG	0.29	0/1960	0.60	0/2637
11	LH	0.29	0/1537	0.57	0/2066
12	LI	0.29	0/1673	0.55	0/2233
13	LJ	0.27	0/1433	0.67	0/1915
14	LL	0.30	0/1732	0.60	0/2315
15	LM	0.29	0/1161	0.62	2/1554 (0.1%)
16	LN	0.35	0/1746	0.62	0/2338
17	LO	0.32	0/1682	0.51	0/2250
18	LP	0.31	0/1268	0.52	0/1701
19	LQ	0.33	0/1537	0.52	0/2052
20	LR	0.29	0/1582	0.58	2/2091 (0.1%)
21	LS	0.30	0/1493	0.50	0/2003
22	LT	0.34	0/1326	0.61	0/1770
23	LU	0.29	0/839	0.74	2/1126 (0.2%)
24	LV	0.31	0/993	0.56	0/1332
25	LW	0.26	0/1030	0.57	0/1364
26	LX	0.28	0/1002	0.53	0/1345
27	LY	0.29	0/1132	0.53	0/1504
28	LZ	0.28	0/1130	0.49	0/1507
29	La	0.32	0/1191	0.54	0/1591
30	Lb	0.27	0/889	0.58	0/1175
31	Lc	0.30	0/774	0.58	0/1038
32	Ld	0.31	0/903	0.52	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.35	0/1071	0.56	0/1429
34	Lf	0.34	0/895	0.57	0/1198
35	Lg	0.32	0/916	0.56	0/1220
36	Lh	0.26	0/1023	0.48	0/1351
37	Li	0.24	0/843	0.49	0/1115
38	Lj	0.38	0/720	0.63	0/952
39	Lk	0.25	0/575	0.52	0/761
40	Ll	0.33	0/454	0.60	0/599
41	Lm	0.34	0/435	0.55	0/575
42	Ln	0.30	0/231	0.50	0/294
43	Lo	0.28	0/876	0.49	0/1156
44	Lp	0.32	0/718	0.52	0/953
45	Lr	0.30	0/1017	0.54	0/1364
46	Ls	0.28	1/1519 (0.1%)	0.66	0/2052
47	Lt	0.34	0/1058	0.94	4/1430 (0.3%)
48	Lz	0.29	0/1769	0.74	0/2371
49	S2	0.31	3/41245 (0.0%)	0.43	14/64265 (0.0%)
50	SA	0.29	0/1778	0.58	0/2416
51	SB	0.25	0/1765	0.54	0/2362
52	SD	0.26	0/1793	0.63	0/2414
53	SE	0.28	0/2118	0.56	1/2849 (0.0%)
54	SF	0.25	0/1481	0.58	0/1988
55	SH	0.28	0/1519	0.64	0/2033
56	SI	0.30	0/1715	0.59	2/2287 (0.1%)
57	SK	0.24	0/851	0.60	0/1147
58	SL	0.31	0/1268	0.53	0/1696
59	SP	0.23	0/1082	0.71	2/1446 (0.1%)
60	SQ	0.28	0/1160	0.66	0/1553
61	SR	0.25	0/1105	0.67	0/1484
62	SS	0.27	0/1216	0.61	0/1628
63	ST	0.25	0/1131	0.57	0/1515
64	SU	0.28	0/831	0.66	0/1115
65	SV	0.28	0/643	0.63	1/860 (0.1%)
66	SX	0.32	0/1116	0.61	1/1490 (0.1%)
67	Sa	0.33	0/836	0.68	0/1121
68	Sc	0.27	0/508	0.77	2/680 (0.3%)
69	Sd	0.27	0/470	0.60	0/623
70	Sg	0.28	0/2493	0.73	2/3394 (0.1%)
71	SC	0.31	0/1762	0.65	3/2381 (0.1%)
72	SG	0.25	0/1946	0.61	3/2590 (0.1%)
73	SJ	0.29	0/1550	0.59	0/2069
74	SM	0.29	0/950	0.74	0/1275
75	SN	0.28	0/1232	0.52	0/1656

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SO	0.31	0/1062	0.71	4/1425 (0.3%)
77	SW	0.32	0/1051	0.55	0/1406
78	SY	0.26	0/1083	0.55	0/1438
79	SZ	0.32	0/604	0.80	0/810
80	Sb	0.26	0/665	0.54	0/891
81	Se	0.23	0/444	0.60	0/588
82	Sf	0.24	0/560	0.70	0/745
83	CA	0.31	0/2810	0.79	3/3780 (0.1%)
84	CC	0.18	0/1773	0.39	1/2759 (0.0%)
85	CE	0.23	0/1010	0.57	0/1339
86	CF	0.25	0/244	0.46	0/328
87	CI	0.24	0/4672	0.59	1/6308 (0.0%)
88	CH	0.33	0/3309	0.66	2/4450 (0.0%)
All	All	0.31	6/249639 (0.0%)	0.51	83/364877 (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
4	LA	0	1
5	LB	0	3
8	LE	0	1
11	LH	0	1
12	LI	0	3
14	LL	0	1
15	LM	0	3
17	LO	0	2
22	LT	0	1
34	Lf	0	1
36	Lh	0	1
38	Lj	0	1
46	Ls	0	1
47	Lt	0	6
51	SB	0	1
52	SD	0	2
54	SF	0	2
55	SH	0	1
60	SQ	0	1
63	ST	0	1
64	SU	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
65	SV	0	1
66	SX	0	3
73	SJ	0	1
74	SM	0	1
76	SO	0	1
79	SZ	0	1
80	Sb	0	1
87	CI	0	5
88	CH	0	1
All	All	0	51

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	S2	61	A	O3'-P	-6.44	1.51	1.61
1	L5	2113	G	C1'-N9	-6.33	1.37	1.47
1	L5	4546	A	O3'-P	-5.58	1.52	1.61
46	Ls	79	LEU	C-N	5.23	1.37	1.33
49	S2	59	U	O3'-P	-5.22	1.53	1.61
49	S2	1093	A	O3'-P	-5.11	1.53	1.61

All (83) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	S2	1094	C	C1'-C2'-O2'	-13.11	88.74	108.40
1	L5	4905	C	C1'-C2'-O2'	-12.78	89.22	108.40
1	L5	4915	G	C1'-C2'-O2'	-11.00	91.90	108.40
1	L5	4547	C	C1'-C2'-O2'	-10.24	93.05	108.40
49	S2	61	A	C1'-C2'-O2'	-9.59	94.02	108.40
49	S2	1149	A	C4'-C3'-O3'	-9.56	95.05	109.40
49	S2	1094	C	C4'-C3'-O3'	9.36	127.05	113.00
49	S2	1150	A	C4'-C3'-O3'	-9.28	95.49	109.40
1	L5	4905	C	C4'-C3'-O3'	9.11	126.67	113.00
88	CH	182	ARG	N-CA-C	8.54	121.80	110.53
1	L5	4907	G	C4'-C3'-O3'	8.21	125.31	113.00
1	L5	4915	G	C4'-C3'-O3'	8.19	125.29	113.00
1	L5	4914	C	C4'-C3'-O3'	7.93	124.90	113.00
59	SP	107	ILE	CA-C-N	7.86	138.24	123.55
59	SP	107	ILE	C-N-CA	7.86	138.24	123.55
1	L5	4907	G	N9-C1'-C2'	-7.49	100.77	112.00
1	L5	4549	G	N9-C1'-C2'	-7.46	100.81	112.00
6	LC	2	ALA	CA-C-N	7.34	134.92	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	LC	2	ALA	C-N-CA	7.34	134.92	121.70
72	SG	139	SER	N-CA-C	-7.26	106.35	114.62
15	LM	87	ALA	CA-C-N	6.76	134.44	121.54
15	LM	87	ALA	C-N-CA	6.76	134.44	121.54
49	S2	1096	G	N9-C1'-C2'	-6.72	101.93	112.00
47	Lt	8	ASN	CA-C-N	6.61	134.17	121.54
47	Lt	8	ASN	C-N-CA	6.61	134.17	121.54
1	L5	4916	G	N9-C1'-C2'	-6.49	102.26	112.00
1	L5	4549	G	C4'-C3'-O3'	6.45	122.67	113.00
1	L5	4905	C	C2'-C3'-O3'	-6.41	104.08	113.70
1	L5	4914	C	C2'-C3'-O3'	-6.19	104.41	113.70
1	L5	4906	U	C4'-C3'-O3'	6.19	122.28	113.00
1	L5	4914	C	N1-C1'-C2'	-6.17	102.75	112.00
49	S2	1096	G	C4'-C3'-O3'	6.14	122.20	113.00
1	L5	4914	C	C1'-C2'-O2'	-6.12	99.21	108.40
71	SC	171	GLY	N-CA-C	-6.08	102.00	111.00
47	Lt	9	GLU	CA-C-N	6.03	132.81	121.97
47	Lt	9	GLU	C-N-CA	6.03	132.81	121.97
49	S2	1150	A	C2'-C3'-O3'	-5.99	100.51	109.50
68	Sc	63	ARG	CA-C-N	5.99	132.97	121.54
68	Sc	63	ARG	C-N-CA	5.99	132.97	121.54
71	SC	63	VAL	CA-C-N	5.92	132.85	121.54
71	SC	63	VAL	C-N-CA	5.92	132.85	121.54
76	SO	14	VAL	CA-C-N	5.86	132.25	121.70
76	SO	14	VAL	C-N-CA	5.86	132.25	121.70
49	S2	1417	C	N3-C4-N4	-5.85	100.46	118.00
83	CA	223	VAL	CG1-CB-CG2	-5.83	97.97	110.80
49	S2	582	U	C1'-C2'-O2'	-5.78	99.73	108.40
1	L5	4915	G	N9-C1'-C2'	-5.71	103.43	112.00
20	LR	38	ARG	CA-C-N	5.68	132.40	121.54
20	LR	38	ARG	C-N-CA	5.68	132.40	121.54
56	SI	129	LEU	CA-C-N	5.67	130.53	121.62
56	SI	129	LEU	C-N-CA	5.67	130.53	121.62
70	Sg	82	SER	CA-C-N	5.62	132.27	121.54
70	Sg	82	SER	C-N-CA	5.62	132.27	121.54
1	L5	4905	C	N1-C1'-C2'	-5.59	103.61	112.00
49	S2	567	C	C4'-C3'-O3'	5.58	121.37	113.00
83	CA	82	VAL	CA-C-N	5.47	131.99	121.54
83	CA	82	VAL	C-N-CA	5.47	131.99	121.54
84	CC	74	C	C2'-C3'-O3'	5.39	121.78	113.70
72	SG	81	HIS	CA-C-N	5.36	131.78	121.54
72	SG	81	HIS	C-N-CA	5.36	131.78	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
88	CH	137	THR	N-CA-C	-5.36	107.40	114.31
87	CI	173	VAL	N-CA-C	-5.28	107.61	112.83
1	L5	4910	A	C2'-C3'-O3'	-5.27	101.59	109.50
49	S2	1094	C	C2'-C3'-O3'	-5.27	105.80	113.70
23	LU	66	SER	CA-C-N	5.26	131.58	121.54
23	LU	66	SER	C-N-CA	5.26	131.58	121.54
66	SX	127	ASN	N-CA-C	5.25	121.99	110.80
1	L5	485	C	C2-N1-C1'	5.22	134.47	118.80
76	SO	37	PHE	CA-C-N	5.19	131.45	121.54
76	SO	37	PHE	C-N-CA	5.19	131.45	121.54
1	L5	4547	C	N1-C1'-C2'	-5.14	104.28	112.00
53	SE	166	THR	N-CA-C	-5.14	108.76	114.62
5	LB	305	THR	CA-C-N	5.11	131.30	121.54
5	LB	305	THR	C-N-CA	5.11	131.30	121.54
65	SV	79	VAL	N-CA-C	5.11	119.97	109.34
1	L5	2760	G	P-O3'-C3'	5.09	127.84	120.20
49	S2	688	U	P-O3'-C3'	5.09	127.83	120.20
1	L5	1082	C	P-O3'-C3'	5.08	127.82	120.20
1	L5	914	U	P-O3'-C3'	5.07	127.81	120.20
1	L5	4910	A	C3'-C2'-O2'	5.06	122.19	114.60
49	S2	583	A	C1'-C2'-O2'	-5.06	100.81	108.40
5	LB	17	LEU	CA-CB-CG	5.02	133.88	116.30
1	L5	4907	G	C2'-C3'-O3'	-5.02	106.17	113.70

There are no chirality outliers.

All (51) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
88	CH	40	PRO	Peptide
87	CI	236	ASP	Peptide
87	CI	365	VAL	Peptide
87	CI	42	THR	Peptide
87	CI	454	ILE	Peptide
87	CI	95	HIS	Peptide
4	LA	54	ARG	Peptide
5	LB	17	LEU	Peptide
5	LB	258	HIS	Peptide
5	LB	301	ASN	Peptide
8	LE	129	GLY	Peptide
11	LH	106	GLN	Peptide
12	LI	14	ASN	Peptide
12	LI	15	LYS	Peptide

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Mol	Chain	Res	Type	Group
12	LI	54	SER	Peptide
14	LL	154	VAL	Peptide
15	LM	31	ILE	Peptide
15	LM	87	ALA	Peptide
15	LM	88	ALA	Peptide
17	LO	110	PRO	Peptide
17	LO	30	GLY	Peptide
22	LT	135	PRO	Peptide
34	Lf	106	TYR	Peptide
36	Lh	86	LYS	Peptide
38	Lj	39	TYR	Peptide
46	Ls	149	ARG	Peptide
47	Lt	122	ALA	Peptide
47	Lt	147	HIS	Peptide
47	Lt	148	PRO	Peptide
47	Lt	20	GLY	Peptide
47	Lt	53	TRP	Peptide
47	Lt	9	GLU	Peptide
51	SB	221	PRO	Peptide
52	SD	162	ASP	Peptide
52	SD	164	VAL	Peptide
54	SF	126	THR	Peptide
54	SF	78	MET	Peptide
55	SH	15	LYS	Peptide
73	SJ	137	VAL	Peptide
74	SM	43	ASP	Peptide
76	SO	14	VAL	Peptide
60	SQ	43	GLU	Peptide
63	ST	46	ALA	Peptide
64	SU	107	GLU	Peptide
64	SU	61	LEU	Peptide
65	SV	78	ILE	Peptide
66	SX	125	VAL	Peptide
66	SX	126	ALA	Peptide
66	SX	60	LYS	Peptide
79	SZ	46	ASN	Peptide
80	Sb	75	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	40378	400	0
2	L7	2561	0	1295	10	0
3	L8	3314	0	1683	8	0
4	LA	1898	0	1993	22	0
5	LB	3238	0	3376	34	0
6	LC	2927	0	3104	21	0
7	LD	2382	0	2410	30	0
8	LE	1904	0	2055	29	0
9	LF	1870	0	1996	16	0
10	LG	1927	0	2074	35	0
11	LH	1518	0	1601	24	0
12	LI	1634	0	1671	27	0
13	LJ	1410	0	1441	18	0
14	LL	1701	0	1818	24	0
15	LM	1138	0	1204	17	0
16	LN	1701	0	1749	18	0
17	LO	1650	0	1794	13	0
18	LP	1242	0	1269	8	0
19	LQ	1513	0	1628	13	0
20	LR	1566	0	1729	15	0
21	LS	1453	0	1490	12	0
22	LT	1298	0	1366	15	0
23	LU	825	0	850	5	0
24	LV	979	0	1039	7	0
25	LW	1015	0	1079	14	0
26	LX	985	0	1066	11	0
27	LY	1115	0	1205	16	0
28	LZ	1107	0	1182	10	0
29	La	1162	0	1213	11	0
30	Lb	876	0	948	11	0
31	Lc	764	0	804	12	0
32	Ld	888	0	930	9	0
33	Le	1053	0	1147	6	0
34	Lf	876	0	912	10	0
35	Lg	906	0	1000	13	0
36	Lh	1015	0	1148	8	0
37	Li	832	0	917	6	0
38	Lj	705	0	738	10	0
39	Lk	569	0	637	10	0
40	Ll	444	0	483	4	0
41	Lm	429	0	465	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	Ln	230	0	276	2	0
43	Lo	862	0	930	9	0
44	Lp	708	0	756	5	0
45	Lr	1002	0	1068	9	0
46	Ls	1496	0	1540	18	0
47	Lt	1046	0	1076	19	0
48	Lz	1741	0	1854	48	0
49	S2	36899	0	18600	255	0
50	SA	1741	0	1746	29	0
51	SB	1738	0	1809	29	0
52	SD	1765	0	1865	19	0
53	SE	2076	0	2177	20	0
54	SF	1461	0	1511	24	0
55	SH	1497	0	1590	20	0
56	SI	1686	0	1772	23	0
57	SK	827	0	854	12	0
58	SL	1247	0	1323	10	0
59	SP	1061	0	1107	9	0
60	SQ	1142	0	1213	19	0
61	SR	1090	0	1149	14	0
62	SS	1198	0	1261	25	0
63	ST	1112	0	1146	14	0
64	SU	821	0	883	17	0
65	SV	636	0	637	6	0
66	SX	1098	0	1167	11	0
67	Sa	821	0	870	12	0
68	Sc	506	0	536	15	0
69	Sd	459	0	449	9	0
70	Sg	2436	0	2393	48	0
71	SC	1725	0	1813	17	0
72	SG	1923	0	2089	36	0
73	SJ	1525	0	1640	25	0
74	SM	940	0	965	27	0
75	SN	1208	0	1294	10	0
76	SO	1049	0	1073	17	0
77	SW	1034	0	1080	11	0
78	SY	1065	0	1142	21	0
79	SZ	598	0	656	15	0
80	Sb	651	0	672	11	0
81	Se	439	0	458	7	0
82	Sf	548	0	555	6	0
83	CA	2764	0	2779	55	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
84	CC	1589	0	810	23	0
85	CE	998	0	1016	6	0
86	CF	239	0	211	2	0
87	CI	4586	0	4717	54	0
88	CH	3257	0	3297	51	0
89	L5	210	0	0	0	0
89	L7	3	0	0	0	0
89	L8	4	0	0	0	0
89	LA	1	0	0	0	0
89	LB	1	0	0	0	0
89	LI	1	0	0	0	0
89	LP	1	0	0	0	0
89	LV	1	0	0	0	0
89	LX	1	0	0	0	0
89	Le	2	0	0	0	0
89	Lg	1	0	0	0	0
89	S2	29	0	0	0	0
89	SG	1	0	0	0	0
90	Lg	1	0	0	0	0
90	Lj	1	0	0	0	0
90	Lm	1	0	0	0	0
90	Lo	1	0	0	0	0
90	Lp	1	0	0	0	0
90	Sa	1	0	0	0	0
90	Sd	1	0	0	0	0
90	Sf	1	0	0	0	0
91	CI	16	0	0	0	0
92	CI	27	0	12	0	0
All	All	233375	0	176724	1809	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (1809) 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)
1:L5:4904:G:O2'	1:L5:4905:C:H5'	1.37	1.22
41:Lm:98:LYS:HD2	41:Lm:118:THR:HG21	1.27	1.13
49:S2:1756:C:H42	49:S2:1776:G:N2	1.49	1.07
49:S2:1756:C:N4	49:S2:1776:G:H22	1.54	1.05
49:S2:886:A:N6	49:S2:901:G:C4	2.24	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4904:G:C2'	1:L5:4905:C:H5'	1.88	1.02
1:L5:1176:C:H42	1:L5:1184:A:N6	1.59	0.99
1:L5:1176:C:N4	1:L5:1184:A:H61	1.62	0.97
70:Sg:46:THR:O	70:Sg:52:TYR:HA	1.65	0.96
1:L5:2557:G:H1	1:L5:2570:U:H3	0.98	0.95
1:L5:5016:A:C2	1:L5:5033:G:N2	2.33	0.94
49:S2:928:G:H1	49:S2:1013:U:H3	1.17	0.93
1:L5:1095:A:H2	1:L5:1200:G:H1	1.07	0.92
1:L5:4904:G:O2'	1:L5:4905:C:C5'	2.17	0.91
49:S2:1287:A:H62	49:S2:1312:G:H21	0.99	0.91
49:S2:1609:C:H42	49:S2:1630:A:H61	0.93	0.91
49:S2:1609:C:N4	49:S2:1630:A:H61	1.67	0.90
88:CH:189:ARG:HA	88:CH:192:ARG:HG3	1.53	0.90
49:S2:925:G:H1	49:S2:1017:U:H3	1.20	0.90
49:S2:1287:A:H62	49:S2:1312:G:N2	1.70	0.90
49:S2:1609:C:H42	49:S2:1630:A:N6	1.67	0.90
1:L5:1176:C:H42	1:L5:1184:A:H61	0.89	0.89
1:L5:5016:A:H2	1:L5:5033:G:H21	1.21	0.88
1:L5:1762:C:N4	1:L5:1770:A:C2	2.42	0.88
74:SM:53:ALA:HA	74:SM:79:VAL:O	1.74	0.88
1:L5:387:G:HO2'	1:L5:412:G:H1	1.20	0.86
1:L5:1269:G:N2	1:L5:1441:C:C2	2.44	0.85
49:S2:1287:A:N6	49:S2:1312:G:H21	1.73	0.85
1:L5:1095:A:C2	1:L5:1200:G:N1	2.44	0.85
41:Lm:98:LYS:HD2	41:Lm:118:THR:CG2	2.06	0.84
11:LH:59:LYS:HE3	11:LH:66:GLU:HB3	1.64	0.80
14:LL:211:LYS:HE2	48:Lz:184:HIS:HB3	1.65	0.79
31:Lc:20:LEU:O	31:Lc:24:SER:HB3	1.83	0.79
72:SG:34:THR:O	72:SG:51:ARG:HA	1.82	0.78
1:L5:2483:G:H1	1:L5:2495:U:H3	1.27	0.78
1:L5:1095:A:H2	1:L5:1200:G:N1	1.81	0.78
6:LC:218:ILE:O	6:LC:222:ARG:HB2	1.84	0.77
55:SH:72:PHE:O	55:SH:76:GLN:HB2	1.85	0.77
49:S2:1472:C:H42	49:S2:1476:A:H62	1.31	0.77
1:L5:5016:A:H2	1:L5:5033:G:N2	1.79	0.76
1:L5:512:U:H3	1:L5:647:G:H1	1.31	0.75
87:CI:434:ASP:O	87:CI:438:HIS:HB2	1.86	0.75
1:L5:493:G:H1	1:L5:660:A:H2	1.34	0.74
13:LJ:21:CYS:HB2	13:LJ:131:TYR:O	1.88	0.73
47:Lt:111:ASN:HA	47:Lt:114:ARG:HD2	1.70	0.73
57:SK:15:LEU:O	57:SK:19:GLY:HA2	1.88	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:Sg:45:LEU:HA	70:Sg:52:TYR:O	1.90	0.71
48:Lz:186:ALA:O	48:Lz:190:LEU:HB2	1.90	0.70
1:L5:4093:G:N1	1:L5:4114:C:C2	2.60	0.69
83:CA:59:GLU:O	83:CA:63:ILE:HB	1.92	0.69
49:S2:585:C:H2'	49:S2:586:G:C8	2.28	0.69
10:LG:154:LEU:HD11	10:LG:222:ILE:HD11	1.75	0.69
21:LS:77:ASN:HB2	21:LS:132:ILE:O	1.93	0.69
66:SX:101:LEU:HB3	66:SX:123:VAL:O	1.94	0.68
1:L5:216:C:H5''	1:L5:219:G:H21	1.57	0.68
11:LH:93:ARG:HD2	41:Lm:82:LEU:HD21	1.75	0.68
41:Lm:98:LYS:CD	41:Lm:118:THR:HG21	2.16	0.68
1:L5:1176:C:N3	1:L5:1184:A:N1	2.41	0.67
49:S2:566:U:H2'	49:S2:567:C:H5'	1.75	0.67
48:Lz:120:ILE:HG13	48:Lz:135:PRO:HG2	1.77	0.67
87:CI:188:LEU:O	87:CI:192:ASP:HB2	1.95	0.67
1:L5:2578:G:N7	28:LZ:17:ARG:NH1	2.42	0.67
47:Lt:13:VAL:HA	47:Lt:63:THR:O	1.95	0.66
49:S2:567:C:HO2'	49:S2:568:C:H5	1.41	0.66
56:SI:142:SER:O	56:SI:146:GLN:HB2	1.94	0.66
88:CH:333:LEU:HD13	88:CH:342:LYS:HG3	1.77	0.66
84:CC:10:G:N7	84:CC:45:G:N1	2.43	0.66
49:S2:1609:C:N3	49:S2:1630:A:N1	2.43	0.66
1:L5:4546:A:N7	4:LA:215:ASN:ND2	2.43	0.66
49:S2:834:C:H42	49:S2:839:C:H42	1.42	0.66
49:S2:568:C:C5	49:S2:583:A:N6	2.64	0.66
80:Sb:36:LYS:HB3	80:Sb:78:SER:HB3	1.78	0.66
48:Lz:10:LEU:HD23	48:Lz:12:GLU:H	1.61	0.66
49:S2:567:C:O2'	49:S2:568:C:C6	2.49	0.66
49:S2:566:U:C2'	49:S2:567:C:H5'	2.26	0.65
84:CC:15:A:N1	84:CC:47:C:N3	2.45	0.65
14:LL:48:PRO:HG3	36:Lh:118:LYS:HE3	1.78	0.65
88:CH:224:LEU:HB2	88:CH:250:VAL:HA	1.79	0.65
1:L5:1269:G:N2	1:L5:1441:C:O2	2.30	0.65
1:L5:3949:A:H62	1:L5:4064:C:H42	1.45	0.65
49:S2:696:G:H21	49:S2:737:G:H1	1.44	0.65
1:L5:4093:G:N1	1:L5:4114:C:N3	2.45	0.65
49:S2:1756:C:H42	49:S2:1776:G:H22	0.76	0.65
79:SZ:74:SER:HA	79:SZ:79:ILE:HB	1.77	0.65
49:S2:606:G:H5''	81:Se:56:ASN:HB3	1.78	0.65
49:S2:886:A:N6	49:S2:901:G:C5	2.64	0.65
70:Sg:215:GLN:HG3	70:Sg:231:ASP:HB3	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LI:6:ALA:O	12:LI:10:ARG:HB2	1.97	0.64
48:Lz:109:ALA:HB1	48:Lz:139:THR:HG23	1.78	0.64
49:S2:1533:A:H62	49:S2:1602:U:H3	1.46	0.64
87:CI:348:TYR:HB2	87:CI:369:PHE:HB2	1.78	0.64
88:CH:290:TYR:HA	88:CH:412:ILE:HD11	1.79	0.64
1:L5:4910:A:HO2'	1:L5:4911:A:H8	1.46	0.64
16:LN:124:ASP:HB3	16:LN:127:TYR:H	1.62	0.64
1:L5:182:G:H1	1:L5:254:G:H1	1.44	0.64
1:L5:3955:G:C2	1:L5:3966:A:N7	2.65	0.64
79:SZ:48:VAL:HA	79:SZ:83:LEU:HD11	1.79	0.64
83:CA:121:VAL:HA	83:CA:320:LYS:O	1.98	0.64
78:SY:131:PRO:HB3	87:CI:265:PRO:HB2	1.80	0.64
1:L5:3967:G:N1	1:L5:4055:U:N3	2.45	0.64
1:L5:3951:G:N1	1:L5:4060:U:N3	2.45	0.63
5:LB:356:LYS:O	5:LB:359:ALA:C	2.41	0.63
16:LN:135:ILE:HG23	16:LN:142:ILE:HD13	1.79	0.63
49:S2:627:U:H5''	85:CE:192:ARG:HH21	1.64	0.63
18:LP:64:ASN:HD22	18:LP:80:GLN:HE22	1.46	0.63
49:S2:1507:G:H22	82:Sf:87:THR:HA	1.62	0.63
83:CA:349:VAL:O	83:CA:355:LYS:NZ	2.31	0.63
1:L5:4242:U:H3	1:L5:4281:A:H2	1.47	0.63
1:L5:1971:C:O2	46:Ls:41:GLN:NE2	2.32	0.63
1:L5:4546:A:C2'	1:L5:4547:C:H5'	2.29	0.63
22:LT:51:GLY:HA3	22:LT:92:ARG:HG3	1.80	0.63
87:CI:206:LEU:HD11	87:CI:224:ARG:HB3	1.80	0.63
88:CH:378:PHE:O	88:CH:382:TYR:HB3	1.98	0.63
52:SD:162:ASP:OD1	52:SD:162:ASP:N	2.32	0.63
1:L5:1995:G:H4'	47:Lt:128:THR:HB	1.81	0.62
10:LG:209:SER:HA	10:LG:212:LYS:HD2	1.79	0.62
1:L5:1095:A:N1	1:L5:1200:G:O6	2.33	0.62
1:L5:2468:U:O2'	1:L5:2506:G:N2	2.33	0.62
1:L5:1521:C:OP1	6:LC:100:ARG:NH2	2.32	0.62
1:L5:1730:U:H4'	22:LT:100:LYS:HB2	1.81	0.62
49:S2:1658:G:OP2	49:S2:1660:C:N4	2.32	0.62
76:SO:56:VAL:HG12	76:SO:81:VAL:HG23	1.80	0.62
1:L5:3955:G:N2	1:L5:3966:A:C5	2.68	0.62
11:LH:91:LYS:HG2	11:LH:145:ILE:HG22	1.81	0.62
30:Lb:8:THR:HG22	30:Lb:10:HIS:H	1.64	0.62
1:L5:4054:C:N3	48:Lz:35:GLN:NE2	2.46	0.62
49:S2:72:C:H42	72:SG:170:ARG:HB3	1.63	0.62
49:S2:153:G:H21	72:SG:13:GLN:HE22	1.48	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:1461:G:H3'	49:S2:1463:U:H3	1.64	0.62
22:LT:43:LYS:O	22:LT:58:HIS:ND1	2.33	0.62
1:L5:1952:G:H4'	21:LS:93:MET:HG3	1.81	0.61
11:LH:12:ILE:HB	11:LH:53:LYS:O	2.00	0.61
1:L5:3751:G:H21	1:L5:3775:A:H8	1.47	0.61
1:L5:2113:G:H22	1:L5:2249:C:H1'	1.66	0.61
1:L5:2611:A:H5'	1:L5:2688:G:H4'	1.81	0.61
1:L5:4904:G:H2'	1:L5:4905:C:H5'	1.79	0.61
29:La:76:ASP:N	29:La:76:ASP:OD1	2.34	0.61
47:Lt:117:ARG:HG3	47:Lt:121:LEU:HD21	1.82	0.61
55:SH:25:GLN:HA	55:SH:28:LEU:HB2	1.82	0.61
83:CA:181:PRO:HB2	83:CA:204:ASN:HB2	1.82	0.61
10:LG:154:LEU:HB3	10:LG:204:PHE:HB2	1.82	0.61
15:LM:77:TRP:O	15:LM:81:ASP:HA	2.00	0.61
7:LD:62:CYS:HB3	7:LD:105:LEU:HD22	1.83	0.61
83:CA:75:ALA:HB2	83:CA:113:HIS:HB3	1.82	0.61
1:L5:4618:G:H5''	24:LV:15:ARG:HB2	1.81	0.61
46:Ls:55:MET:HG2	46:Ls:87:GLY:HA3	1.82	0.61
49:S2:1396:A:N7	49:S2:1449:G:O6	2.34	0.61
1:L5:493:G:O6	1:L5:660:A:N1	2.33	0.61
48:Lz:93:LEU:O	48:Lz:102:LYS:NZ	2.31	0.61
68:Sc:14:VAL:HG12	68:Sc:32:VAL:HG12	1.83	0.61
74:SM:76:LEU:CD1	74:SM:78:LYS:HE3	2.31	0.61
14:LL:50:PRO:HB3	14:LL:150:LEU:HB3	1.81	0.60
50:SA:206:ASP:OD1	50:SA:206:ASP:N	2.33	0.60
48:Lz:120:ILE:HG23	48:Lz:124:LEU:HD22	1.83	0.60
46:Ls:30:VAL:O	46:Ls:86:VAL:HA	2.02	0.60
1:L5:1404:G:N7	1:L5:1408:G:N2	2.48	0.60
1:L5:3971:G:N2	1:L5:3973:G:N3	2.50	0.60
54:SF:35:LEU:O	54:SF:39:ILE:HB	2.02	0.60
55:SH:143:ARG:HB2	55:SH:155:LYS:HB2	1.83	0.60
68:Sc:44:ARG:NH2	68:Sc:61:SER:O	2.35	0.60
83:CA:81:SER:HG	83:CA:85:CYS:HG	1.46	0.60
49:S2:878:G:H1	49:S2:908:A:H2	1.47	0.60
80:Sb:49:HIS:ND1	80:Sb:69:GLY:O	2.35	0.60
74:SM:51:VAL:HG12	74:SM:77:ILE:HB	1.84	0.60
56:SI:165:GLN:HG3	56:SI:171:LEU:HD23	1.84	0.59
1:L5:513:U:O2'	1:L5:515:C:N4	2.35	0.59
5:LB:222:VAL:O	5:LB:343:ARG:NH1	2.35	0.59
10:LG:187:LYS:HG2	10:LG:198:THR:HB	1.83	0.59
49:S2:847:A:O2'	53:SE:106:LYS:NZ	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:1563:G:OP1	63:ST:121:ARG:NH2	2.35	0.59
64:SU:61:LEU:O	64:SU:81:GLN:HA	2.02	0.59
1:L5:468:U:C4	1:L5:686:A:N1	2.69	0.59
54:SF:135:ARG:N	84:CC:33:U:OP2	2.36	0.59
55:SH:31:GLU:HG3	55:SH:37:LYS:HD2	1.85	0.59
1:L5:75:G:O2'	14:LL:101:ARG:NH1	2.34	0.59
10:LG:260:GLU:OE1	10:LG:264:LYS:NZ	2.36	0.59
1:L5:4929:C:H5''	15:LM:114:LYS:HD2	1.85	0.59
37:Li:2:ALA:N	37:Li:5:TYR:HH	2.01	0.59
70:Sg:173:LEU:HD13	70:Sg:175:LYS:HE3	1.85	0.59
1:L5:3948:C:N3	1:L5:4066:U:O4	2.35	0.59
24:LV:58:GLY:N	24:LV:81:VAL:O	2.36	0.59
62:SS:4:VAL:HG22	62:SS:5:ILE:HG22	1.85	0.59
70:Sg:12:LYS:HG2	70:Sg:306:LEU:HD22	1.84	0.59
11:LH:124:ARG:NH1	11:LH:164:ALA:O	2.36	0.59
41:Lm:110:CYS:SG	41:Lm:111:ARG:N	2.76	0.59
49:S2:374:G:H1'	58:SL:83:GLN:HE21	1.67	0.59
55:SH:53:VAL:O	55:SH:57:ARG:HB2	2.03	0.59
70:Sg:11:LEU:HB2	70:Sg:307:VAL:HB	1.85	0.59
1:L5:1364:U:OP2	14:LL:36:ARG:NH1	2.35	0.59
1:L5:4530:U:H2'	1:L5:4531:U:H2'	1.85	0.59
80:Sb:34:ASP:HA	80:Sb:44:THR:O	2.03	0.59
1:L5:2601:A:N6	1:L5:2744:A:OP2	2.36	0.59
5:LB:230:GLY:O	5:LB:234:ARG:HB2	2.03	0.59
12:LI:38:ARG:HD3	12:LI:83:ASP:HB2	1.84	0.59
1:L5:1443:A:H61	1:L5:2104:G:H21	1.51	0.58
1:L5:3955:G:N2	1:L5:3966:A:C4	2.71	0.58
27:LY:54:GLU:HB2	27:LY:108:ARG:HB3	1.84	0.58
72:SG:2:LYS:HB2	72:SG:108:VAL:HG22	1.84	0.58
1:L5:1656:U:OP2	29:La:26:ARG:NH2	2.36	0.58
88:CH:18:LYS:HZ1	88:CH:140:LEU:HD13	1.68	0.58
1:L5:1378:C:N4	14:LL:159:ASN:O	2.35	0.58
12:LI:156:LYS:HG3	12:LI:163:GLN:HB2	1.84	0.58
48:Lz:160:LYS:HB2	48:Lz:162:VAL:HG12	1.84	0.58
1:L5:4732:G:N2	1:L5:4734:A:N7	2.50	0.58
18:LP:73:ALA:O	18:LP:76:TRP:O	2.21	0.58
66:SX:91:LEU:HD21	81:Se:6:LEU:HD12	1.85	0.58
74:SM:76:LEU:HD13	74:SM:78:LYS:HG3	1.85	0.58
13:LJ:95:ARG:HD3	13:LJ:176:PRO:HG3	1.85	0.58
3:L8:134:G:H5''	26:LX:63:LYS:HD2	1.86	0.58
12:LI:209:TRP:O	12:LI:212:LEU:O	2.22	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:SO:103:ASN:HB3	76:SO:142:ARG:HG3	1.84	0.58
83:CA:170:TRP:HA	83:CA:173:VAL:HG12	1.86	0.58
88:CH:34:MET:SD	88:CH:34:MET:N	2.75	0.58
26:LX:151:ASN:OD1	83:CA:290:ARG:NH1	2.37	0.58
49:S2:567:C:H1'	49:S2:583:A:H61	1.68	0.58
72:SG:64:LYS:HZ1	72:SG:81:HIS:HB3	1.68	0.58
5:LB:92:TYR:HB2	5:LB:159:VAL:HB	1.86	0.58
48:Lz:120:ILE:O	48:Lz:124:LEU:HB3	2.04	0.58
70:Sg:174:VAL:HB	70:Sg:188:HIS:HB2	1.86	0.58
10:LG:96:LEU:HD11	10:LG:189:ARG:HE	1.69	0.57
17:LO:166:ILE:HG12	17:LO:169:ARG:HH21	1.68	0.57
64:SU:95:SER:HA	64:SU:98:VAL:HG22	1.85	0.57
70:Sg:6:THR:O	70:Sg:310:TRP:HA	2.03	0.57
70:Sg:87:LEU:HB2	70:Sg:101:PHE:HB2	1.86	0.57
49:S2:94:G:HO2'	49:S2:508:A:HO2'	1.47	0.57
68:Sc:43:ILE:HG13	68:Sc:65:ALA:HB3	1.85	0.57
84:CC:10:G:N7	84:CC:45:G:C2	2.73	0.57
84:CC:25:C:H2'	84:CC:26:A:H8	1.68	0.57
1:L5:2562:G:N2	1:L5:2565:A:OP2	2.36	0.57
6:LC:152:LEU:HD23	6:LC:251:ILE:HG12	1.86	0.57
74:SM:106:CYS:SG	74:SM:107:SER:N	2.78	0.57
88:CH:317:VAL:HG21	88:CH:320:LEU:HB2	1.85	0.57
1:L5:1762:C:N4	1:L5:1770:A:H2	2.00	0.57
1:L5:2458:C:H5''	16:LN:67:ARG:HD2	1.86	0.57
63:ST:42:HIS:HB2	63:ST:83:GLN:HB2	1.86	0.57
75:SN:99:ARG:NH2	75:SN:119:GLU:OE2	2.34	0.57
87:CI:21:CYS:SG	87:CI:22:ARG:N	2.77	0.57
88:CH:344:LEU:HD13	88:CH:346:LEU:HD23	1.86	0.57
50:SA:177:MET:SD	50:SA:180:ARG:NH2	2.77	0.57
62:SS:110:ASP:HA	62:SS:113:ARG:HG2	1.87	0.57
1:L5:389:A:O2'	83:CA:211:LYS:NZ	2.38	0.57
1:L5:696:C:N4	8:LE:221:LYS:O	2.38	0.57
1:L5:3959:U:O2	1:L5:3960:A:N6	2.38	0.57
1:L5:3969:G:O2'	1:L5:4054:C:N4	2.36	0.57
22:LT:93:ILE:HA	22:LT:96:ILE:HG12	1.85	0.57
55:SH:154:ILE:HB	55:SH:185:VAL:HG12	1.87	0.57
88:CH:47:ARG:HH21	88:CH:48:VAL:HG12	1.70	0.57
1:L5:3955:G:C2	1:L5:3966:A:C5	2.92	0.57
5:LB:113:GLU:HB3	5:LB:178:ALA:HB2	1.86	0.57
49:S2:878:G:O6	49:S2:908:A:N1	2.38	0.57
49:S2:1096:G:H2'	49:S2:1097:G:H8	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:SW:3:ARG:HH12	77:SW:28:ARG:HH21	1.53	0.57
84:CC:21:A:H61	84:CC:46:A:H2'	1.69	0.57
88:CH:347:THR:OG1	88:CH:350:GLN:OE1	2.22	0.57
38:Lj:20:ARG:NH2	38:Lj:39:TYR:OH	2.38	0.57
49:S2:922:A:OP1	77:SW:28:ARG:NH2	2.37	0.57
60:SQ:26:LYS:HB2	60:SQ:67:ASP:HB2	1.86	0.57
72:SG:33:ALA:HA	72:SG:52:ILE:O	2.03	0.57
1:L5:2705:G:O6	20:LR:46:LYS:NZ	2.38	0.56
49:S2:837:A:H61	78:SY:9:THR:H	1.51	0.56
63:ST:38:LYS:NZ	63:ST:43:LYS:O	2.36	0.56
74:SM:22:LEU:HD11	74:SM:89:VAL:HG23	1.87	0.56
1:L5:4985:U:O2	5:LB:174:ARG:NH1	2.38	0.56
22:LT:72:VAL:HG11	22:LT:96:ILE:HD13	1.87	0.56
32:Ld:59:THR:HG1	32:Ld:104:THR:HG1	1.53	0.56
46:Ls:171:GLU:HA	46:Ls:174:LEU:HD23	1.88	0.56
70:Sg:152:SER:HG	70:Sg:168:CYS:HG	1.49	0.56
76:SO:103:ASN:ND2	76:SO:140:THR:O	2.37	0.56
87:CI:98:PRO:HD3	87:CI:299:VAL:HG21	1.86	0.56
9:LF:93:ILE:HA	9:LF:119:ASN:O	2.05	0.56
10:LG:57:TRP:O	10:LG:62:ARG:NH1	2.39	0.56
11:LH:120:GLU:OE2	11:LH:124:ARG:NH2	2.37	0.56
16:LN:140:LYS:O	16:LN:144:ARG:HB2	2.06	0.56
27:LY:31:SER:HA	27:LY:48:PRO:HA	1.87	0.56
61:SR:79:GLU:O	61:SR:83:ASN:HB2	2.05	0.56
70:Sg:199:THR:HG21	70:Sg:240:CYS:HA	1.87	0.56
71:SC:128:VAL:HG11	71:SC:155:ILE:HG22	1.86	0.56
1:L5:4431:U:OP2	12:LI:3:ARG:NH2	2.38	0.56
49:S2:1230:C:OP1	62:SS:130:ARG:NH2	2.38	0.56
78:SY:102:THR:O	78:SY:107:ARG:NH1	2.39	0.56
52:SD:32:ASP:OD1	52:SD:57:ASN:ND2	2.39	0.56
54:SF:199:VAL:O	54:SF:203:ASN:ND2	2.39	0.56
55:SH:146:VAL:HG12	55:SH:152:ARG:HB3	1.88	0.56
49:S2:164:A:H3'	49:S2:165:G:H21	1.70	0.56
54:SF:143:PRO:HA	54:SF:146:ARG:HG2	1.88	0.56
1:L5:2838:G:H5'	5:LB:247:GLY:HA2	1.86	0.56
1:L5:3823:G:OP2	1:L5:3823:G:N2	2.36	0.56
72:SG:33:ALA:N	72:SG:52:ILE:O	2.39	0.56
87:CI:423:SER:HA	87:CI:458:GLU:HA	1.88	0.56
1:L5:1398:A:N1	1:L5:1419:G:O2'	2.39	0.56
1:L5:2739:C:OP2	44:Lp:49:ARG:NH1	2.38	0.56
5:LB:218:ASP:OD2	5:LB:348:ARG:NH1	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:Lb:70:GLU:O	30:Lb:74:ALA:HB3	2.06	0.56
33:Le:90:MET:HG2	45:Lr:33:LYS:HA	1.86	0.56
54:SF:187:SER:HB2	54:SF:190:ILE:HG12	1.88	0.56
1:L5:1175:A:C2	1:L5:1185:G:N1	2.73	0.56
1:L5:3946:G:H21	1:L5:3947:A:H62	1.54	0.56
49:S2:672:A:N6	49:S2:1027:A:OP1	2.36	0.56
52:SD:163:PRO:O	52:SD:167:TYR:HB2	2.06	0.56
28:LZ:17:ARG:NH2	28:LZ:18:TYR:OH	2.37	0.56
48:Lz:14:VAL:HG23	48:Lz:15:ARG:HD2	1.88	0.56
49:S2:1256:G:H8	64:SU:66:ARG:HB2	1.71	0.56
50:SA:122:LEU:HD21	50:SA:133:PRO:HB2	1.88	0.56
70:Sg:99:ARG:NH1	70:Sg:135:LEU:O	2.39	0.56
1:L5:4302:U:H4'	22:LT:5:LYS:HD2	1.87	0.55
50:SA:163:CYS:SG	50:SA:164:ASN:N	2.79	0.55
53:SE:126:VAL:O	53:SE:157:ASN:HA	2.06	0.55
67:Sa:32:LYS:O	67:Sa:37:LYS:NZ	2.38	0.55
88:CH:177:PRO:HG2	88:CH:194:ARG:HG3	1.88	0.55
1:L5:194:C:O2	27:LY:121:ARG:NH2	2.40	0.55
1:L5:709:C:OP1	34:Lf:89:ARG:NH1	2.39	0.55
46:Ls:102:LEU:O	46:Ls:105:ASN:O	2.24	0.55
49:S2:567:C:O2'	49:S2:568:C:C5	2.58	0.55
54:SF:198:ARG:NH1	84:CC:40:G:O2'	2.40	0.55
1:L5:3937:C:H1'	16:LN:125:SER:HB2	1.88	0.55
1:L5:4076:G:OP1	10:LG:73:ARG:NE	2.35	0.55
48:Lz:203:ALA:HA	48:Lz:217:TYR:HA	1.87	0.55
49:S2:380:G:O6	56:SI:178:ARG:NH2	2.39	0.55
50:SA:36:GLN:O	50:SA:53:ARG:NH1	2.39	0.55
56:SI:100:CYS:HB3	56:SI:175:ILE:HD12	1.88	0.55
59:SP:123:TYR:OH	62:SS:124:ARG:NH1	2.39	0.55
70:Sg:132:TRP:HA	70:Sg:138:CYS:HA	1.88	0.55
83:CA:339:GLU:HB2	83:CA:342:LEU:HB3	1.88	0.55
84:CC:13:U:H2'	84:CC:14:A:H8	1.72	0.55
15:LM:3:PHE:H	21:LS:175:PHE:HZ	1.54	0.55
46:Ls:102:LEU:O	46:Ls:105:ASN:C	2.50	0.55
49:S2:1252:C:OP1	64:SU:75:LYS:NZ	2.36	0.55
10:LG:103:ARG:NH2	10:LG:192:ARG:O	2.38	0.55
1:L5:1762:C:H5''	1:L5:1764:G:H1	1.71	0.55
8:LE:281:ILE:HB	8:LE:286:LEU:HD21	1.86	0.55
53:SE:256:LEU:O	53:SE:260:GLN:NE2	2.40	0.55
60:SQ:11:GLN:HA	60:SQ:23:ALA:O	2.06	0.55
1:L5:2469:C:H5	1:L5:2471:G:H1	1.52	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:LQ:124:ASP:N	19:LQ:124:ASP:OD1	2.40	0.55
49:S2:1435:C:H42	64:SU:19:ARG:HH21	1.53	0.55
51:SB:105:LEU:HD13	51:SB:213:ARG:HA	1.88	0.55
1:L5:1439:C:OP2	9:LF:34:ARG:NH1	2.40	0.55
10:LG:154:LEU:HD13	10:LG:219:VAL:HG12	1.88	0.55
49:S2:1488:C:O2'	49:S2:1490:G:OP2	2.21	0.55
71:SC:187:ARG:HH21	71:SC:192:LEU:HD12	1.72	0.55
1:L5:2811:G:N1	1:L5:2814:C:OP2	2.30	0.55
14:LL:16:LYS:O	14:LL:21:ARG:NH1	2.40	0.55
21:LS:19:THR:HG23	21:LS:21:LYS:H	1.70	0.55
88:CH:15:TRP:HA	88:CH:18:LYS:HB2	1.88	0.55
1:L5:1269:G:N2	1:L5:1440:U:O2	2.38	0.55
1:L5:3608:A:OP2	20:LR:81:ARG:NH2	2.38	0.55
13:LJ:9:GLU:HG3	13:LJ:13:ARG:HD3	1.88	0.55
56:SI:61:ASP:OD1	56:SI:61:ASP:N	2.40	0.55
80:Sb:13:GLU:OE1	80:Sb:17:ARG:NH2	2.40	0.55
1:L5:4126:C:OP1	10:LG:37:LYS:NZ	2.40	0.54
54:SF:30:ILE:HG12	54:SF:113:VAL:HG11	1.89	0.54
87:CI:325:ARG:NH2	87:CI:495:GLU:OE2	2.39	0.54
7:LD:176:SER:OG	7:LD:177:THR:N	2.40	0.54
48:Lz:89:ALA:HA	48:Lz:92:LYS:HG2	1.89	0.54
50:SA:81:ASN:HA	50:SA:84:GLN:HB2	1.89	0.54
80:Sb:64:CYS:HB3	80:Sb:73:LEU:HD23	1.89	0.54
87:CI:521:ASP:HB3	87:CI:524:MET:HB2	1.88	0.54
88:CH:82:LEU:HD12	88:CH:83:LYS:HG2	1.89	0.54
1:L5:4043:G:OP1	1:L5:4045:G:N2	2.40	0.54
46:Ls:82:ILE:O	46:Ls:83:ARG:NH1	2.41	0.54
49:S2:1139:C:H5	49:S2:1149:A:H62	1.54	0.54
72:SG:59:GLN:OE1	72:SG:72:ARG:NH2	2.40	0.54
83:CA:232:SER:OG	83:CA:314:GLU:OE1	2.25	0.54
87:CI:76:PRO:HD2	87:CI:79:LEU:HD12	1.89	0.54
1:L5:1762:C:N3	1:L5:1770:A:N1	2.56	0.54
1:L5:4139:G:H21	1:L5:4140:C:H41	1.56	0.54
25:LW:45:ASN:OD1	25:LW:47:ARG:NH1	2.40	0.54
43:Lo:45:GLN:NE2	43:Lo:52:THR:OG1	2.41	0.54
48:Lz:54:ARG:NH1	48:Lz:149:ASP:OD1	2.41	0.54
49:S2:1472:C:N4	49:S2:1476:A:H62	2.01	0.54
60:SQ:31:LEU:HD11	60:SQ:33:LYS:HE3	1.89	0.54
70:Sg:176:VAL:HG13	70:Sg:185:LYS:HB2	1.90	0.54
82:Sf:107:LYS:O	82:Sf:115:SER:OG	2.25	0.54
1:L5:2092:G:O2'	1:L5:2262:G:N2	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Ld:61:ASP:OD2	32:Ld:63:ARG:NH1	2.41	0.54
49:S2:959:G:OP1	76:SO:104:ARG:NH1	2.38	0.54
70:Sg:212:LYS:HG3	70:Sg:235:ILE:HD12	1.90	0.54
73:SJ:140:GLN:NE2	78:SY:64:PHE:O	2.41	0.54
76:SO:67:ASP:OD1	76:SO:67:ASP:N	2.36	0.54
87:CI:425:ARG:NH1	87:CI:456:ASP:OD1	2.41	0.54
1:L5:67:C:OP2	1:L5:312:G:N2	2.40	0.54
2:L7:1:G:H4'	7:LD:265:ARG:HD2	1.90	0.54
55:SH:80:VAL:HG23	55:SH:92:VAL:HB	1.88	0.54
83:CA:50:GLU:OE2	83:CA:93:LYS:NZ	2.40	0.54
83:CA:180:THR:OG1	83:CA:233:GLY:O	2.25	0.54
1:L5:1895:G:OP1	9:LF:96:ARG:NH2	2.41	0.54
8:LE:218:LYS:O	8:LE:220:LYS:NZ	2.40	0.54
39:Lk:26:LYS:HB2	39:Lk:69:LEU:HD12	1.87	0.54
49:S2:943:U:OP1	51:SB:214:LYS:NZ	2.41	0.54
50:SA:76:VAL:HG12	50:SA:123:VAL:HB	1.90	0.54
51:SB:90:ASP:OD2	51:SB:92:GLN:NE2	2.41	0.54
73:SJ:122:SER:O	73:SJ:125:HIS:N	2.40	0.54
1:L5:1070:G:OP2	8:LE:65:ARG:NH1	2.40	0.54
1:L5:2474:G:N2	1:L5:2502:G:O2'	2.40	0.54
1:L5:3961:G:N2	1:L5:3964:U:O3'	2.41	0.54
3:L8:96:C:OP1	36:Lh:70:ARG:NH1	2.37	0.54
26:LX:89:LYS:HD3	26:LX:93:ASN:HD22	1.73	0.54
27:LY:39:ARG:O	27:LY:42:TYR:O	2.25	0.54
27:LY:101:PRO:HA	27:LY:104:VAL:HG22	1.90	0.54
54:SF:127:ARG:O	54:SF:135:ARG:NH1	2.41	0.54
87:CI:39:ILE:HG12	87:CI:50:ILE:HG12	1.90	0.54
1:L5:2899:C:OP1	20:LR:108:ARG:NH2	2.40	0.54
10:LG:145:THR:O	10:LG:149:ASN:ND2	2.41	0.54
31:Lc:30:GLY:O	31:Lc:34:THR:OG1	2.26	0.54
49:S2:747:U:N3	49:S2:796:G:N1	2.56	0.54
83:CA:154:LEU:HD22	83:CA:332:ARG:HD2	1.90	0.54
83:CA:205:PRO:HB2	83:CA:210:LYS:HB3	1.89	0.54
1:L5:453:G:H4'	1:L5:454:U:H5'	1.89	0.54
1:L5:4212:A:OP2	12:LI:15:LYS:NZ	2.40	0.54
20:LR:98:ARG:NH1	20:LR:132:PHE:O	2.40	0.54
48:Lz:58:THR:H	48:Lz:152:LYS:HZ1	1.56	0.54
64:SU:98:VAL:HA	64:SU:101:ILE:HG22	1.90	0.54
1:L5:4163:U:OP2	10:LG:53:ARG:NH2	2.41	0.53
32:Ld:54:MET:O	32:Ld:57:MET:O	2.26	0.53
35:Lg:43:LYS:NZ	35:Lg:50:PRO:O	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:697:G:OP2	49:S2:733:C:N4	2.41	0.53
49:S2:1745:A:H1'	72:SG:66:GLY:HA2	1.89	0.53
88:CH:89:PRO:HG3	88:CH:93:LEU:HD12	1.90	0.53
1:L5:1994:C:H1'	47:Lt:132:ILE:HA	1.90	0.53
1:L5:4281:A:H2'	1:L5:4282:A:H2'	1.90	0.53
16:LN:159:ARG:HB3	16:LN:164:LEU:HB2	1.90	0.53
19:LQ:40:ASN:OD1	19:LQ:132:LYS:NZ	2.41	0.53
49:S2:1550:G:H3'	49:S2:1579:A:H61	1.73	0.53
71:SC:206:SER:HB3	71:SC:210:PRO:HG2	1.89	0.53
74:SM:48:HIS:HB2	74:SM:111:VAL:HG13	1.89	0.53
1:L5:4154:G:OP1	26:LX:37:LYS:NZ	2.39	0.53
9:LF:115:ARG:NH1	19:LQ:4:ASP:O	2.41	0.53
11:LH:106:GLN:HB2	11:LH:111:LEU:HB3	1.90	0.53
20:LR:30:ASN:O	20:LR:34:ASN:ND2	2.42	0.53
74:SM:52:LEU:C	74:SM:52:LEU:HD12	2.34	0.53
74:SM:76:LEU:HD13	74:SM:78:LYS:HE3	1.88	0.53
1:L5:407:A:O2'	1:L5:410:A:OP1	2.26	0.53
1:L5:654:C:H4'	6:LC:269:LYS:HB3	1.90	0.53
1:L5:4371:G:H5'	84:CC:75:A:H62	1.74	0.53
40:LI:21:ARG:NH1	40:LI:22:PRO:O	2.41	0.53
83:CA:155:ARG:NH2	83:CA:360:SER:OG	2.42	0.53
4:LA:116:LEU:HB2	4:LA:126:LEU:HB2	1.91	0.53
12:LI:209:TRP:O	12:LI:212:LEU:C	2.51	0.53
17:LO:27:VAL:HG13	17:LO:98:ALA:HB1	1.89	0.53
32:Ld:29:ILE:O	32:Ld:33:ILE:HB	2.09	0.53
52:SD:161:GLY:O	52:SD:164:VAL:C	2.51	0.53
55:SH:65:PRO:O	55:SH:69:LEU:N	2.41	0.53
56:SI:178:ARG:NH2	56:SI:181:GLN:OE1	2.42	0.53
75:SN:29:THR:OG1	75:SN:30:SER:N	2.41	0.53
77:SW:87:GLU:OE2	77:SW:91:ASN:ND2	2.40	0.53
87:CI:536:ASP:OD1	87:CI:561:GLN:NE2	2.41	0.53
1:L5:2704:C:H2'	1:L5:2705:G:H8	1.73	0.53
1:L5:3711:A:H2'	1:L5:3712:A:H8	1.74	0.53
49:S2:127:C:O2	53:SE:134:LYS:NZ	2.42	0.53
61:SR:90:ALA:O	61:SR:93:GLN:NE2	2.41	0.53
85:CE:203:GLU:O	85:CE:207:SER:HB2	2.09	0.53
1:L5:2260:C:OP1	8:LE:108:LYS:NZ	2.40	0.53
1:L5:5040:U:OP2	5:LB:396:ARG:NH2	2.42	0.53
6:LC:66:SER:HA	6:LC:77:PRO:HA	1.91	0.53
6:LC:339:THR:HG22	6:LC:342:ARG:HH22	1.74	0.53
14:LL:126:LEU:N	14:LL:138:ASP:OD2	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:874:G:H21	55:SH:114:GLN:HE22	1.56	0.53
49:S2:1228:A:H2'	49:S2:1229:G:C8	2.44	0.53
74:SM:50:CYS:O	74:SM:76:LEU:HA	2.07	0.53
1:L5:2486:G:O6	1:L5:2493:G:O6	2.27	0.53
7:LD:77:ALA:O	7:LD:108:ARG:NH2	2.39	0.53
49:S2:74:G:O6	72:SG:168:LYS:NZ	2.41	0.53
49:S2:1228:A:H2'	49:S2:1229:G:H8	1.74	0.53
54:SF:18:LYS:HE3	54:SF:22:LYS:HA	1.91	0.53
65:SV:19:ALA:O	77:SW:23:ARG:NH2	2.42	0.53
1:L5:1885:G:OP1	34:Lf:20:ASN:ND2	2.42	0.53
13:LJ:93:GLU:HG2	13:LJ:173:ILE:HB	1.91	0.53
49:S2:1425:G:OP1	60:SQ:69:ARG:NH2	2.42	0.53
49:S2:1829:G:OP2	85:CE:167:ARG:NH2	2.42	0.53
1:L5:3967:G:O6	1:L5:4055:U:O4	2.26	0.53
20:LR:134:ASN:N	20:LR:134:ASN:OD1	2.42	0.53
49:S2:694:G:H5''	49:S2:730:C:H5	1.74	0.53
68:Sc:22:GLY:O	68:Sc:26:GLN:NE2	2.40	0.53
74:SM:22:LEU:HD21	74:SM:89:VAL:HA	1.91	0.53
6:LC:218:ILE:O	6:LC:222:ARG:CB	2.56	0.52
12:LI:152:LEU:HB3	12:LI:165:ILE:HD12	1.91	0.52
24:LV:13:LYS:HD3	24:LV:128:LEU:HD22	1.90	0.52
34:Lf:37:ASP:N	34:Lf:37:ASP:OD1	2.40	0.52
49:S2:1414:A:O2'	63:ST:128:GLN:NE2	2.42	0.52
60:SQ:139:ALA:O	60:SQ:140:ARG:NH2	2.42	0.52
88:CH:143:ASP:N	88:CH:143:ASP:OD1	2.42	0.52
1:L5:1480:C:O2'	1:L5:1482:G:OP2	2.27	0.52
1:L5:1994:C:H2'	1:L5:1995:G:H8	1.74	0.52
1:L5:3688:U:OP2	4:LA:198:ARG:NH1	2.42	0.52
1:L5:3765:G:O2'	1:L5:3767:C:N4	2.42	0.52
4:LA:137:ILE:HD11	4:LA:149:LYS:HB2	1.90	0.52
5:LB:356:LYS:O	5:LB:359:ALA:O	2.27	0.52
49:S2:1669:G:OP2	60:SQ:130:LYS:NZ	2.40	0.52
57:SK:31:LYS:HD2	57:SK:36:ALA:HA	1.91	0.52
60:SQ:19:ALA:HB2	60:SQ:75:GLY:HA3	1.92	0.52
64:SU:80:PHE:HB3	69:Sd:52:PHE:HB3	1.90	0.52
72:SG:138:ALA:HA	72:SG:141:ILE:HG22	1.91	0.52
50:SA:222:VAL:HG13	50:SA:223:THR:HG23	1.91	0.52
53:SE:126:VAL:O	53:SE:157:ASN:N	2.43	0.52
56:SI:162:LEU:HD11	56:SI:191:GLU:HG2	1.91	0.52
67:Sa:45:VAL:HG21	67:Sa:64:LEU:HD22	1.91	0.52
1:L5:1095:A:N1	1:L5:1200:G:C6	2.77	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1259:G:H2'	1:L5:1260:G:H8	1.74	0.52
1:L5:1760:G:N3	1:L5:1761:G:N1	2.58	0.52
11:LH:31:ARG:NH1	11:LH:149:ASN:OD1	2.41	0.52
12:LI:207:ASP:OD1	12:LI:210:ARG:NH2	2.43	0.52
49:S2:750:C:H41	49:S2:793:G:H21	1.57	0.52
49:S2:1542:C:OP1	63:ST:62:ARG:NH2	2.42	0.52
1:L5:3955:G:C2	1:L5:3966:A:C8	2.98	0.52
7:LD:256:LYS:NZ	7:LD:257:PRO:O	2.42	0.52
10:LG:160:ASP:OD1	10:LG:160:ASP:N	2.42	0.52
25:LW:74:ARG:HH12	49:S2:1748:G:H3'	1.74	0.52
74:SM:94:ILE:HD12	74:SM:100:PRO:HA	1.91	0.52
78:SY:27:VAL:HG22	78:SY:69:THR:HB	1.90	0.52
83:CA:100:LEU:HD21	83:CA:127:VAL:HG11	1.89	0.52
20:LR:184:ILE:HG13	20:LR:185:ILE:HG23	1.90	0.52
40:LI:33:ASN:ND2	40:LI:35:ILE:O	2.43	0.52
48:Lz:17:VAL:O	48:Lz:19:HIS:ND1	2.37	0.52
51:SB:67:PHE:O	51:SB:86:LEU:HB2	2.09	0.52
51:SB:137:LEU:HG	51:SB:215:VAL:HG22	1.92	0.52
75:SN:83:ASP:N	75:SN:83:ASP:OD1	2.41	0.52
1:L5:5000:G:OP1	5:LB:394:LYS:NZ	2.43	0.52
13:LJ:65:ASN:HB2	43:Lo:103:VAL:HA	1.92	0.52
14:LL:56:ARG:NH1	14:LL:74:ARG:O	2.42	0.52
20:LR:176:ARG:NH1	49:S2:909:G:OP1	2.43	0.52
49:S2:585:C:H2'	49:S2:586:G:H8	1.71	0.52
49:S2:1024:A:OP2	75:SN:124:ARG:NH2	2.42	0.52
1:L5:2495:U:H2'	1:L5:2496:G:H8	1.75	0.52
4:LA:14:SER:HA	4:LA:17:ARG:HE	1.75	0.52
26:LX:88:LYS:HE2	83:CA:259:MET:HG2	1.91	0.52
31:Lc:38:ILE:HG21	31:Lc:63:TYR:HB3	1.92	0.52
49:S2:615:C:O2	81:Se:11:LYS:NZ	2.40	0.52
49:S2:1454:A:H5''	61:SR:3:ARG:HD3	1.91	0.52
50:SA:42:LYS:HD2	50:SA:46:ILE:HB	1.91	0.52
70:Sg:251:ALA:HB2	70:Sg:289:LEU:HD23	1.92	0.52
1:L5:512:U:O4	1:L5:647:G:O6	2.28	0.52
1:L5:1499:C:OP1	19:LQ:150:ARG:NH2	2.43	0.52
1:L5:2848:G:O2'	1:L5:3838:U:O4	2.26	0.52
1:L5:4882:U:OP1	15:LM:117:LYS:NZ	2.42	0.52
10:LG:182:CYS:HB3	10:LG:222:ILE:HD12	1.92	0.52
13:LJ:35:ARG:HD2	13:LJ:123:ILE:HA	1.91	0.52
42:Ln:7:LYS:NZ	49:S2:1843:G:OP1	2.40	0.52
62:SS:65:GLU:HA	62:SS:68:ILE:HG12	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1187:G:N2	1:L5:1187:G:OP2	2.42	0.52
7:LD:30:TYR:HA	7:LD:33:ARG:HB3	1.92	0.52
50:SA:217:ALA:HA	50:SA:220:LYS:HD2	1.90	0.52
63:ST:9:VAL:O	63:ST:11:GLN:NE2	2.42	0.52
77:SW:24:GLN:NE2	77:SW:64:ASN:OD1	2.42	0.52
83:CA:27:ILE:HG22	83:CA:30:ARG:HH21	1.75	0.52
88:CH:335:CYS:SG	88:CH:364:GLN:NE2	2.83	0.52
11:LH:114:ILE:HB	11:LH:124:ARG:HG3	1.93	0.51
12:LI:193:ASP:N	12:LI:193:ASP:OD1	2.42	0.51
28:LZ:5:MET:O	28:LZ:28:ASN:ND2	2.43	0.51
51:SB:47:THR:OG1	51:SB:65:ARG:NH2	2.43	0.51
70:Sg:107:ASP:N	70:Sg:107:ASP:OD1	2.43	0.51
87:CI:260:ARG:NH1	87:CI:282:LEU:O	2.43	0.51
1:L5:4041:C:O2'	48:Lz:102:LYS:O	2.28	0.51
42:Ln:1:MET:HG3	49:S2:1706:G:H5'	1.92	0.51
49:S2:1420:G:O2'	49:S2:1421:A:N3	2.42	0.51
72:SG:33:ALA:CA	72:SG:52:ILE:O	2.58	0.51
83:CA:187:SER:O	83:CA:200:THR:OG1	2.28	0.51
38:Lj:21:ARG:NH1	38:Lj:41:ALA:O	2.40	0.51
49:S2:582:U:C2'	49:S2:583:A:H5''	2.40	0.51
49:S2:1536:G:H2'	49:S2:1537:A:H8	1.75	0.51
52:SD:74:GLN:NE2	52:SD:79:PHE:O	2.43	0.51
55:SH:105:THR:HG23	55:SH:107:LYS:H	1.75	0.51
56:SI:134:GLU:O	56:SI:138:ASN:ND2	2.42	0.51
70:Sg:40:ILE:HB	70:Sg:59:LEU:HB2	1.91	0.51
70:Sg:157:SER:OG	70:Sg:159:ASN:OD1	2.28	0.51
1:L5:109:G:OP2	14:LL:74:ARG:NH2	2.41	0.51
1:L5:390:C:H5'	83:CA:211:LYS:HD2	1.91	0.51
1:L5:2483:G:O6	1:L5:2495:U:O4	2.29	0.51
18:LP:73:ALA:O	18:LP:76:TRP:C	2.53	0.51
31:Lc:20:LEU:O	31:Lc:24:SER:CB	2.57	0.51
49:S2:1017:U:H5'	75:SN:55:ARG:HD3	1.92	0.51
49:S2:1644:C:H4'	60:SQ:140:ARG:HB2	1.91	0.51
57:SK:95:ARG:NH2	57:SK:97:SER:O	2.43	0.51
69:Sd:56:ASP:N	69:Sd:56:ASP:OD1	2.44	0.51
83:CA:140:ALA:HA	83:CA:143:ILE:HG22	1.92	0.51
87:CI:42:THR:O	87:CI:44:GLN:N	2.43	0.51
14:LL:65:ARG:HD3	29:La:66:ASN:HD22	1.75	0.51
88:CH:286:LEU:HD11	88:CH:319:ILE:HG21	1.92	0.51
1:L5:2306:G:OP1	33:Le:128:ARG:NH2	2.43	0.51
1:L5:4485:C:O2'	41:Lm:114:LYS:NZ	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:LG:117:ARG:HA	10:LG:120:LYS:HG2	1.92	0.51
12:LI:170:LYS:NZ	12:LI:177:ASN:OD1	2.44	0.51
25:LW:99:GLU:HA	25:LW:102:LYS:HE2	1.92	0.51
53:SE:137:PRO:HG2	53:SE:150:PRO:HD2	1.93	0.51
88:CH:91:ASN:ND2	88:CH:116:PRO:O	2.44	0.51
25:LW:74:ARG:NH1	49:S2:1749:G:OP2	2.43	0.51
49:S2:583:A:H2'	49:S2:584:A:C8	2.45	0.51
49:S2:1673:U:O2'	54:SF:84:GLY:O	2.23	0.51
51:SB:173:THR:O	51:SB:177:GLN:HB2	2.11	0.51
73:SJ:109:ARG:NH1	73:SJ:111:GLN:OE1	2.44	0.51
87:CI:22:ARG:HB3	87:CI:24:GLU:HG3	1.92	0.51
46:Ls:25:PRO:HB2	46:Ls:26:LYS:HD2	1.93	0.51
49:S2:448:A:H5''	56:SI:25:ARG:HA	1.93	0.51
88:CH:188:LEU:O	88:CH:188:LEU:HD13	2.10	0.51
1:L5:4327:C:OP1	22:LT:70:HIS:NE2	2.43	0.51
4:LA:101:VAL:HG22	4:LA:165:VAL:HG22	1.93	0.51
6:LC:209:ILE:HB	6:LC:229:LEU:HD13	1.93	0.51
61:SR:41:ILE:HD12	61:SR:47:ARG:HG2	1.92	0.51
62:SS:56:ALA:HA	62:SS:59:LEU:HD12	1.92	0.51
87:CI:98:PRO:HG2	87:CI:123:LEU:HD11	1.92	0.51
1:L5:2111:G:N1	1:L5:2251:G:O2'	2.42	0.51
1:L5:5022:U:O4	56:SI:170:LYS:NZ	2.44	0.51
22:LT:2:THR:OG1	22:LT:3:ASN:N	2.43	0.51
23:LU:100:LEU:HD23	23:LU:112:LEU:HD23	1.92	0.51
45:Lr:16:PHE:HB3	45:Lr:27:THR:H	1.76	0.51
74:SM:92:CYS:HB2	74:SM:94:ILE:HG12	1.93	0.51
1:L5:1508:A:OP1	6:LC:110:ARG:NH1	2.45	0.50
1:L5:2113:G:N2	1:L5:2249:C:H1'	2.25	0.50
1:L5:2406:G:N7	40:Ll:2:SER:N	2.59	0.50
1:L5:2517:A:H5'	35:Lg:62:LYS:HE3	1.94	0.50
12:LI:212:LEU:HD23	12:LI:213:HIS:H	1.76	0.50
50:SA:77:ILE:HG21	50:SA:133:PRO:HG3	1.93	0.50
1:L5:62:A:OP1	16:LN:172:ARG:NH1	2.41	0.50
1:L5:2658:G:N2	1:L5:2676:A:OP2	2.36	0.50
8:LE:99:ASP:OD1	8:LE:100:LYS:NZ	2.42	0.50
13:LJ:51:SER:HB2	13:LJ:69:ALA:HB3	1.93	0.50
21:LS:86:SER:OG	21:LS:87:ARG:N	2.44	0.50
30:Lb:90:SER:OG	30:Lb:91:ARG:N	2.44	0.50
39:Lk:5:ILE:HD11	39:Lk:43:TYR:HB3	1.93	0.50
49:S2:323:C:H2'	49:S2:327:G:H22	1.77	0.50
54:SF:138:ALA:O	68:Sc:63:ARG:NH1	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:Sc:28:THR:O	68:Sc:45:ASN:HA	2.11	0.50
68:Sc:61:SER:OG	68:Sc:62:GLU:OE1	2.29	0.50
74:SM:24:THR:HA	74:SM:27:ILE:HG12	1.93	0.50
87:CI:289:LEU:HG	87:CI:299:VAL:HG22	1.93	0.50
1:L5:2846:G:O2'	24:LV:19:GLY:O	2.25	0.50
1:L5:4194:U:O2'	12:LI:116:ARG:NH1	2.45	0.50
12:LI:179:ASP:OD1	12:LI:179:ASP:N	2.44	0.50
13:LJ:101:ASP:OD1	13:LJ:101:ASP:N	2.42	0.50
29:La:110:LYS:HG3	29:La:128:PHE:HB2	1.93	0.50
48:Lz:124:LEU:HD21	48:Lz:128:LEU:HD12	1.93	0.50
49:S2:1451:G:OP1	61:SR:32:LYS:NZ	2.42	0.50
49:S2:1652:G:H1	49:S2:1672:U:H3	1.59	0.50
78:SY:47:MET:O	78:SY:49:LYS:NZ	2.44	0.50
84:CC:22:U:OP2	84:CC:46:A:N6	2.44	0.50
1:L5:1100:U:O3'	1:L5:1167:C:N4	2.44	0.50
1:L5:1590:C:H4'	1:L5:2857:A:H5'	1.93	0.50
1:L5:3951:G:O6	1:L5:4060:U:O4	2.29	0.50
14:LL:164:GLU:HG3	29:La:100:ILE:HB	1.92	0.50
49:S2:1679:A:OP1	68:Sc:20:ARG:NH2	2.43	0.50
70:Sg:111:VAL:HA	70:Sg:121:VAL:O	2.11	0.50
72:SG:136:LYS:NZ	72:SG:175:LYS:O	2.37	0.50
83:CA:326:MET:HG3	83:CA:328:ASN:H	1.76	0.50
87:CI:5:LEU:HD13	87:CI:74:ASN:HB3	1.93	0.50
2:L7:13:A:O2'	7:LD:24:ARG:NH1	2.44	0.50
14:LL:172:GLU:O	14:LL:175:ASN:C	2.54	0.50
21:LS:15:ARG:HD2	21:LS:25:PRO:HG2	1.93	0.50
75:SN:87:ASP:OD1	75:SN:87:ASP:N	2.44	0.50
83:CA:10:GLN:HE22	83:CA:17:VAL:HG11	1.76	0.50
1:L5:1727:U:OP1	9:LF:131:ASN:ND2	2.43	0.50
2:L7:34:C:N3	2:L7:46:C:O2'	2.42	0.50
5:LB:384:GLU:OE1	25:LW:14:TYR:OH	2.29	0.50
8:LE:261:ILE:HG23	8:LE:267:LEU:HD23	1.93	0.50
27:LY:45:ARG:HB2	27:LY:126:ARG:HH22	1.75	0.50
49:S2:71:G:O6	72:SG:170:ARG:NH1	2.43	0.50
49:S2:1158:G:H5''	77:SW:76:SER:HB3	1.94	0.50
49:S2:1422:G:N2	49:S2:1424:G:O6	2.44	0.50
69:Sd:6:LEU:HA	69:Sd:9:SER:HB3	1.93	0.50
1:L5:2389:A:H5'	32:Ld:70:LYS:HE3	1.94	0.50
16:LN:17:ASP:N	16:LN:17:ASP:OD1	2.44	0.50
49:S2:145:G:H2'	49:S2:146:G:C8	2.47	0.50
49:S2:570:C:O2	78:SY:34:THR:OG1	2.30	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:1498:A:OP2	52:SD:27:ARG:NH2	2.41	0.50
79:SZ:98:LYS:HE2	79:SZ:112:ASN:HA	1.94	0.50
12:LI:31:ILE:HD11	12:LI:89:VAL:HG21	1.94	0.50
13:LJ:63:ARG:HH21	85:CE:39:TRP:HH2	1.59	0.50
20:LR:182:GLU:O	20:LR:186:LYS:NZ	2.44	0.50
21:LS:76:LYS:NZ	21:LS:100:LEU:O	2.39	0.50
50:SA:81:ASN:OD1	50:SA:81:ASN:N	2.43	0.50
55:SH:163:GLN:O	55:SH:167:GLU:HB2	2.12	0.50
10:LG:185:LYS:O	10:LG:189:ARG:NH2	2.44	0.50
19:LQ:35:LEU:O	19:LQ:39:THR:HB	2.11	0.50
49:S2:830:A:OP2	49:S2:846:G:N2	2.45	0.50
76:SO:83:GLN:NE2	76:SO:87:GLU:OE1	2.45	0.50
80:Sb:34:ASP:OD1	80:Sb:34:ASP:N	2.38	0.50
87:CI:451:ILE:O	87:CI:455:ILE:HB	2.12	0.50
1:L5:74:G:H5'	14:LL:59:VAL:HG13	1.93	0.49
1:L5:2696:A:H62	39:Lk:35:LYS:HE2	1.77	0.49
1:L5:4353:U:H5''	1:L5:4354:U:H5'	1.92	0.49
1:L5:4992:G:H2'	1:L5:4993:G:C8	2.47	0.49
48:Lz:116:LEU:HA	48:Lz:119:GLN:HG3	1.93	0.49
49:S2:525:A:OP2	81:Se:26:LYS:NZ	2.45	0.49
51:SB:108:ASP:N	51:SB:108:ASP:OD1	2.44	0.49
87:CI:412:LYS:HB3	87:CI:485:ILE:HA	1.94	0.49
1:L5:1914:C:H4'	17:LO:89:PRO:HD3	1.95	0.49
1:L5:2083:C:OP2	19:LQ:14:ARG:NH2	2.41	0.49
11:LH:103:VAL:HG11	11:LH:144:LEU:HD11	1.94	0.49
15:LM:90:ARG:HA	15:LM:93:LYS:HG2	1.93	0.49
27:LY:39:ARG:O	27:LY:42:TYR:C	2.56	0.49
47:Lt:123:ARG:HD2	47:Lt:129:ILE:HD11	1.93	0.49
49:S2:1277:C:OP1	57:SK:55:ARG:NH2	2.44	0.49
62:SS:101:ASN:O	62:SS:105:ASN:ND2	2.45	0.49
1:L5:1279:A:O2'	6:LC:323:ARG:NH2	2.45	0.49
1:L5:2113:G:C2	1:L5:2249:C:O2	2.65	0.49
1:L5:4031:U:OP2	48:Lz:26:ARG:NE	2.46	0.49
15:LM:81:ASP:N	15:LM:81:ASP:OD1	2.43	0.49
25:LW:105:ARG:NH1	72:SG:149:LYS:O	2.36	0.49
61:SR:33:ARG:NH1	61:SR:36:GLU:OE1	2.46	0.49
70:Sg:193:GLY:N	70:Sg:213:ASP:OD1	2.45	0.49
72:SG:142:ARG:HB2	72:SG:147:LEU:HB2	1.93	0.49
49:S2:1096:G:H2'	49:S2:1097:G:C8	2.46	0.49
52:SD:62:LYS:O	52:SD:67:ARG:NH2	2.45	0.49
88:CH:265:ASN:HA	88:CH:268:ILE:HD12	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L7:39:C:H4'	13:LJ:47:THR:HG23	1.94	0.49
5:LB:117:ARG:HG2	5:LB:180:LEU:HD13	1.94	0.49
49:S2:944:A:H5''	76:SO:134:PRO:HB3	1.95	0.49
49:S2:1536:G:H2'	49:S2:1537:A:C8	2.47	0.49
71:SC:183:LYS:HA	71:SC:195:LEU:O	2.12	0.49
78:SY:55:ILE:HG12	78:SY:75:ILE:HG12	1.93	0.49
87:CI:85:HIS:HD2	87:CI:129:PRO:HA	1.77	0.49
18:LP:24:VAL:HG12	18:LP:86:LYS:HD3	1.94	0.49
73:SJ:131:ARG:NH2	73:SJ:143:ASN:O	2.46	0.49
87:CI:250:LYS:HB3	87:CI:562:LEU:HD11	1.94	0.49
87:CI:556:ASN:ND2	87:CI:592:GLY:O	2.45	0.49
1:L5:1273:G:OP2	30:Lb:117:ARG:NH2	2.45	0.49
1:L5:3976:C:N4	1:L5:4035:G:OP2	2.46	0.49
1:L5:4220:A:H2'	1:L5:4222:G:H5''	1.93	0.49
1:L5:4966:A:H5'	5:LB:128:LYS:HG3	1.95	0.49
44:Lp:38:THR:HA	44:Lp:45:THR:HA	1.95	0.49
46:Ls:97:GLU:O	46:Ls:101:MET:HB2	2.12	0.49
49:S2:1513:C:H2'	49:S2:1514:G:H8	1.77	0.49
49:S2:1599:U:O2'	79:SZ:41:ARG:NH2	2.46	0.49
51:SB:88:THR:HA	51:SB:98:THR:HA	1.92	0.49
62:SS:35:GLY:HA3	62:SS:99:LEU:HA	1.94	0.49
84:CC:15:A:N6	84:CC:47:C:O2	2.36	0.49
88:CH:75:ILE:HA	88:CH:78:VAL:HG22	1.95	0.49
1:L5:183:C:H1'	1:L5:184:U:H5	1.77	0.49
1:L5:989:U:O2	1:L5:1064:G:O6	2.31	0.49
1:L5:1548:G:O2'	1:L5:2812:A:N3	2.43	0.49
8:LE:155:GLY:O	8:LE:158:ARG:NH1	2.46	0.49
82:Sf:121:CYS:HA	82:Sf:132:MET:HE2	1.94	0.49
48:Lz:206:ILE:HD13	48:Lz:214:GLN:HB2	1.95	0.49
49:S2:566:U:C3'	49:S2:567:C:H5'	2.43	0.49
49:S2:1512:C:H5''	69:Sd:8:TRP:HZ3	1.78	0.49
49:S2:1593:C:OP2	79:SZ:104:ARG:NH2	2.46	0.49
52:SD:215:ASP:N	52:SD:215:ASP:OD1	2.45	0.49
64:SU:62:ARG:NH1	64:SU:81:GLN:OE1	2.46	0.49
87:CI:377:MET:HB3	87:CI:535:PHE:HE1	1.78	0.49
1:L5:1708:G:O2'	1:L5:1709:C:O2	2.31	0.49
18:LP:17:SER:OG	18:LP:97:ASN:ND2	2.40	0.49
18:LP:94:MET:HE2	18:LP:148:MET:HE3	1.95	0.49
20:LR:105:LEU:HD23	20:LR:138:LEU:HD23	1.95	0.49
31:Lc:55:LEU:HD11	35:Lg:93:ARG:HB2	1.95	0.49
49:S2:839:C:H41	78:SY:10:ARG:HA	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:SQ:129:SER:O	60:SQ:131:LYS:NZ	2.43	0.49
72:SG:98:ARG:NH2	72:SG:103:ASP:OD1	2.46	0.49
1:L5:500:G:H1'	1:L5:504:G:H3'	1.94	0.48
1:L5:2793:G:H4'	38:Lj:8:PHE:HD2	1.78	0.48
49:S2:1562:C:H2'	49:S2:1563:G:H8	1.77	0.48
49:S2:1617:G:N1	49:S2:1620:A:OP2	2.45	0.48
72:SG:115:LYS:NZ	72:SG:116:LYS:O	2.45	0.48
82:Sf:118:ARG:HE	82:Sf:134:SER:HB3	1.76	0.48
1:L5:4083:U:OP1	4:LA:123:ARG:NH2	2.46	0.48
40:Ll:20:ASN:ND2	40:Ll:42:ARG:O	2.39	0.48
47:Lt:142:ASN:HD21	47:Lt:148:PRO:HA	1.77	0.48
55:SH:69:LEU:HD22	55:SH:96:ALA:HB2	1.95	0.48
72:SG:2:LYS:O	72:SG:108:VAL:HA	2.13	0.48
73:SJ:177:ASN:OD1	73:SJ:180:LYS:NZ	2.40	0.48
1:L5:715:G:OP1	6:LC:321:ASN:ND2	2.44	0.48
1:L5:4717:A:OP2	5:LB:30:LYS:NZ	2.46	0.48
8:LE:250:GLN:NE2	8:LE:254:ASP:OD2	2.41	0.48
11:LH:171:ASP:O	11:LH:174:LYS:O	2.30	0.48
50:SA:10:MET:HE2	50:SA:15:VAL:HG12	1.95	0.48
56:SI:104:ILE:O	56:SI:170:LYS:HA	2.13	0.48
70:Sg:68:ASP:O	70:Sg:80:SER:HA	2.13	0.48
70:Sg:290:ALA:HB3	70:Sg:299:PHE:HB2	1.94	0.48
87:CI:136:ASP:N	87:CI:136:ASP:OD1	2.46	0.48
1:L5:1279:A:O2'	1:L5:1281:G:N7	2.41	0.48
1:L5:2097:U:OP2	9:LF:35:LYS:NZ	2.46	0.48
1:L5:2739:C:O2	4:LA:188:LYS:NZ	2.46	0.48
5:LB:10:ARG:NH1	5:LB:265:SER:O	2.47	0.48
11:LH:171:ASP:O	11:LH:175:PHE:HB2	2.14	0.48
49:S2:656:G:O2'	71:SC:227:ARG:NH2	2.46	0.48
49:S2:886:A:N6	49:S2:901:G:N3	2.60	0.48
54:SF:68:ILE:HA	54:SF:71:ARG:HG3	1.94	0.48
58:SL:120:VAL:HG22	58:SL:145:VAL:HG11	1.94	0.48
63:ST:9:VAL:HG21	63:ST:138:VAL:HG13	1.94	0.48
88:CH:358:THR:HA	88:CH:366:HIS:H	1.78	0.48
1:L5:52:G:OP2	38:Lj:48:ASN:ND2	2.43	0.48
1:L5:3717:A:H2'	1:L5:3718:A:C8	2.48	0.48
1:L5:4622:A:H4'	5:LB:13:SER:HB2	1.95	0.48
10:LG:143:VAL:HG22	10:LG:203:ALA:HB2	1.94	0.48
20:LR:21:LYS:HE3	20:LR:55:VAL:HA	1.94	0.48
26:LX:100:VAL:HG23	26:LX:134:LYS:HB3	1.94	0.48
34:Lf:11:PHE:O	34:Lf:98:GLY:N	2.41	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:122:G:H21	53:SE:146:THR:HG21	1.78	0.48
68:Sc:31:ARG:HA	68:Sc:43:ILE:HA	1.95	0.48
78:SY:53:ASP:OD1	78:SY:53:ASP:N	2.46	0.48
79:SZ:42:ASP:OD1	79:SZ:42:ASP:N	2.43	0.48
80:Sb:35:VAL:HA	80:Sb:78:SER:O	2.12	0.48
87:CI:525:ALA:O	87:CI:529:ALA:HB2	2.14	0.48
1:L5:308:G:O6	16:LN:12:ARG:NH1	2.46	0.48
5:LB:154:LYS:HG3	5:LB:194:LEU:HD23	1.94	0.48
7:LD:125:VAL:HG11	7:LD:199:ILE:HG21	1.95	0.48
11:LH:77:VAL:HA	11:LH:80:MET:HE3	1.95	0.48
12:LI:83:ASP:OD1	12:LI:83:ASP:N	2.44	0.48
49:S2:567:C:O2'	49:S2:568:C:H6	1.94	0.48
49:S2:1622:U:OP1	62:SS:120:HIS:ND1	2.41	0.48
83:CA:56:ILE:HA	83:CA:59:GLU:HG3	1.96	0.48
86:CF:153:PRO:HG3	86:CF:176:GLU:HG3	1.96	0.48
87:CI:239:MET:HE2	87:CI:270:ILE:HD12	1.94	0.48
1:L5:3736:A:H2'	1:L5:3737:A:C8	2.48	0.48
24:LV:43:LYS:HG3	24:LV:60:MET:HG2	1.96	0.48
43:Lo:26:TYR:HB3	43:Lo:67:VAL:HB	1.96	0.48
44:Lp:88:GLU:O	44:Lp:91:ASP:O	2.31	0.48
51:SB:63:LYS:NZ	51:SB:90:ASP:OD1	2.46	0.48
71:SC:68:ARG:HG2	71:SC:277:HIS:HB2	1.94	0.48
73:SJ:161:LEU:HA	73:SJ:167:GLY:H	1.78	0.48
1:L5:1464:C:H5''	30:Lb:32:LEU:HD12	1.95	0.48
1:L5:1973:G:H5''	47:Lt:117:ARG:HH21	1.77	0.48
1:L5:4742:G:H2'	1:L5:4743:G:H8	1.79	0.48
7:LD:207:TYR:OH	7:LD:222:GLN:NE2	2.46	0.48
10:LG:190:LEU:HB3	10:LG:199:CYS:HB3	1.96	0.48
30:Lb:43:MET:HE2	30:Lb:43:MET:HB3	1.79	0.48
49:S2:334:C:OP2	72:SG:190:ARG:NH2	2.46	0.48
49:S2:1743:G:H21	49:S2:1791:A:H62	1.62	0.48
88:CH:113:ASP:OD1	88:CH:113:ASP:N	2.46	0.48
6:LC:163:LYS:HB2	6:LC:166:GLU:HG2	1.95	0.48
41:Lm:95:ILE:HA	41:Lm:101:ALA:O	2.14	0.48
49:S2:1084:A:OP1	49:S2:1858:G:O2'	2.30	0.48
49:S2:1261:C:O2	69:Sd:10:HIS:NE2	2.42	0.48
50:SA:11:LYS:O	50:SA:14:ASP:N	2.45	0.48
73:SJ:81:LEU:HD12	73:SJ:97:ILE:HD12	1.95	0.48
84:CC:10:G:O6	84:CC:45:G:O6	2.31	0.48
87:CI:531:ARG:HD3	87:CI:548:PRO:HB2	1.96	0.48
88:CH:224:LEU:O	88:CH:251:LEU:N	2.40	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:942:G:OP1	9:LF:245:ARG:NH1	2.47	0.48
1:L5:1077:C:OP1	1:L5:1215:C:O2'	2.30	0.48
1:L5:2335:C:H2'	1:L5:2336:G:H8	1.79	0.48
2:L7:6:C:H4'	7:LD:52:ILE:HD13	1.96	0.48
11:LH:92:MET:HA	11:LH:182:SER:H	1.79	0.48
13:LJ:114:ASP:OD1	13:LJ:114:ASP:N	2.46	0.48
49:S2:928:G:H2'	49:S2:929:G:C8	2.49	0.48
49:S2:1673:U:H5''	60:SQ:78:VAL:HG22	1.95	0.48
71:SC:178:HIS:ND1	71:SC:221:ASP:OD2	2.44	0.48
1:L5:4910:A:O2'	1:L5:4911:A:H8	1.96	0.47
36:Lh:87:LYS:NZ	38:Lj:78:PHE:O	2.45	0.47
46:Ls:69:LEU:HD12	46:Ls:72:ASN:HD21	1.78	0.47
49:S2:307:G:O6	56:SI:44:HIS:ND1	2.47	0.47
49:S2:694:G:OP2	49:S2:696:G:N1	2.42	0.47
49:S2:874:G:H2'	49:S2:875:A:H8	1.79	0.47
52:SD:103:GLU:HG2	52:SD:106:ARG:HH21	1.79	0.47
85:CE:209:ASP:OD1	85:CE:209:ASP:N	2.42	0.47
88:CH:189:ARG:O	88:CH:192:ARG:N	2.47	0.47
1:L5:4363:A:H5''	43:Lo:36:GLN:HG2	1.96	0.47
3:L8:75:G:OP2	27:LY:74:TYR:OH	2.32	0.47
7:LD:150:LEU:HD12	13:LJ:146:ARG:HG3	1.96	0.47
17:LO:3:GLU:N	34:Lf:31:GLU:OE2	2.47	0.47
48:Lz:37:SER:OG	48:Lz:203:ALA:O	2.26	0.47
49:S2:433:A:H5''	56:SI:22:HIS:HB3	1.96	0.47
56:SI:6:ASP:N	56:SI:6:ASP:OD1	2.41	0.47
65:SV:17:CYS:O	65:SV:21:ASN:N	2.47	0.47
66:SX:28:LYS:O	66:SX:32:LEU:HB2	2.14	0.47
78:SY:4:THR:O	78:SY:32:LYS:NZ	2.43	0.47
88:CH:262:ASN:OD1	88:CH:262:ASN:N	2.48	0.47
1:L5:2280:G:OP1	33:Le:48:ARG:NH2	2.47	0.47
1:L5:4645:C:OP2	20:LR:62:ARG:NH1	2.47	0.47
1:L5:4913:G:C4'	1:L5:4914:C:OP2	2.62	0.47
4:LA:28:ARG:HD2	4:LA:123:ARG:HD2	1.96	0.47
11:LH:92:MET:HB3	11:LH:181:VAL:HA	1.96	0.47
46:Ls:53:VAL:HG23	46:Ls:89:VAL:HG22	1.96	0.47
46:Ls:111:ALA:H	46:Ls:182:PRO:HG2	1.79	0.47
49:S2:570:C:O2'	78:SY:34:THR:O	2.31	0.47
49:S2:1087:A:OP2	67:Sa:8:ASN:ND2	2.42	0.47
56:SI:11:ARG:NH1	56:SI:15:GLY:O	2.46	0.47
74:SM:69:CYS:O	74:SM:72:HIS:C	2.57	0.47
1:L5:4274:A:H2'	1:L5:4275:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4883:C:N4	8:LE:181:LEU:O	2.42	0.47
30:Lb:70:GLU:O	30:Lb:74:ALA:CB	2.63	0.47
45:Lr:47:LYS:HA	45:Lr:65:LYS:HB3	1.97	0.47
48:Lz:23:ARG:HA	48:Lz:212:LYS:HE3	1.95	0.47
49:S2:919:A:OP2	75:SN:64:ARG:NH2	2.46	0.47
49:S2:1148:A:OP1	67:Sa:6:ARG:NH2	2.41	0.47
65:SV:74:LYS:HD2	65:SV:83:PHE:HE1	1.79	0.47
87:CI:508:ILE:HG13	87:CI:515:ALA:HB2	1.95	0.47
1:L5:1538:U:H2'	1:L5:1539:G:H8	1.80	0.47
63:ST:2:PRO:HA	63:ST:3:GLY:HA3	1.73	0.47
74:SM:55:ASN:HD21	74:SM:82:ASN:H	1.62	0.47
74:SM:76:LEU:HD11	74:SM:78:LYS:HE3	1.97	0.47
83:CA:70:MET:SD	83:CA:71:LYS:HG2	2.55	0.47
84:CC:57:A:O2'	84:CC:59:U:OP2	2.30	0.47
87:CI:86:ARG:HD2	87:CI:93:LYS:HE3	1.96	0.47
88:CH:91:ASN:HB2	88:CH:119:PRO:HA	1.96	0.47
1:L5:171:U:OP2	1:L5:172:C:N4	2.48	0.47
1:L5:439:G:O3'	34:Lf:91:ASN:ND2	2.48	0.47
1:L5:3964:U:O2'	1:L5:3966:A:O4'	2.32	0.47
1:L5:4113:U:O2'	1:L5:4115:G:OP2	2.32	0.47
1:L5:4472:G:O2'	41:Lm:100:TYR:O	2.30	0.47
12:LI:54:SER:HB3	12:LI:135:ILE:HD11	1.94	0.47
13:LJ:20:LEU:O	13:LJ:131:TYR:O	2.33	0.47
44:Lp:88:GLU:O	44:Lp:91:ASP:C	2.58	0.47
49:S2:28:U:H2'	49:S2:29:G:H8	1.79	0.47
49:S2:639:C:OP1	81:Se:41:ARG:NH2	2.47	0.47
49:S2:1556:A:N6	69:Sd:12:ARG:O	2.48	0.47
1:L5:148:C:OP2	10:LG:197:LYS:NZ	2.47	0.47
1:L5:703:G:H2'	1:L5:704:C:H4'	1.97	0.47
5:LB:195:ASP:HA	5:LB:198:ARG:HG2	1.97	0.47
8:LE:152:ILE:O	8:LE:159:GLY:N	2.47	0.47
10:LG:38:ASN:ND2	10:LG:43:GLN:OE1	2.47	0.47
16:LN:47:LYS:HE3	16:LN:51:LEU:HD11	1.97	0.47
31:Lc:40:GLN:HG3	31:Lc:42:LYS:HG3	1.97	0.47
49:S2:66:G:OP1	72:SG:172:LYS:NZ	2.47	0.47
49:S2:1106:C:H5''	80:Sb:70:LYS:HE3	1.96	0.47
49:S2:1299:A:O2'	59:SP:52:LYS:NZ	2.46	0.47
55:SH:63:PHE:HA	55:SH:95:ILE:O	2.15	0.47
58:SL:119:ASP:O	58:SL:147:LYS:NZ	2.37	0.47
62:SS:60:THR:OG1	62:SS:62:ASP:OD1	2.30	0.47
62:SS:124:ARG:O	62:SS:127:TRP:C	2.57	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:SU:51:LYS:HB2	64:SU:90:ASP:HB2	1.95	0.47
70:Sg:249:CYS:SG	70:Sg:291:TRP:NE1	2.83	0.47
78:SY:90:ARG:HA	78:SY:93:ARG:HB2	1.96	0.47
83:CA:139:LYS:HA	83:CA:142[A]:VAL:HG22	1.96	0.47
87:CI:33:ARG:NH2	88:CH:306:GLU:OE2	2.47	0.47
1:L5:62:A:N3	1:L5:77:U:O2'	2.43	0.47
1:L5:1994:C:H2'	1:L5:1995:G:C8	2.50	0.47
1:L5:3664:G:H2'	1:L5:3665:G:H8	1.79	0.47
1:L5:4474:A:OP2	41:Lm:124:LYS:NZ	2.45	0.47
8:LE:183:ARG:HD2	8:LE:183:ARG:HA	1.78	0.47
47:Lt:15:LEU:HA	47:Lt:61:LYS:O	2.14	0.47
48:Lz:67:VAL:HA	48:Lz:68:LEU:HA	1.50	0.47
53:SE:54:TYR:OH	53:SE:97:GLU:OE2	2.30	0.47
66:SX:126:ALA:HB3	66:SX:140:ARG:HH12	1.80	0.47
2:L7:12:U:O3'	2:L7:109:U:O2'	2.31	0.47
8:LE:177:GLY:HA3	8:LE:184:VAL:HB	1.97	0.47
11:LH:7:ASN:HA	11:LH:57:VAL:O	2.15	0.47
12:LI:48:LEU:O	12:LI:139:ARG:HA	2.14	0.47
19:LQ:88:ASP:OD1	19:LQ:112:ARG:NH1	2.48	0.47
25:LW:106:GLU:HA	25:LW:109:ILE:HG22	1.96	0.47
38:Lj:54:LYS:O	38:Lj:58:THR:HB	2.15	0.47
39:Lk:24:LYS:HD2	39:Lk:69:LEU:HD21	1.96	0.47
49:S2:921:G:OP2	80:Sb:21:LYS:NZ	2.48	0.47
62:SS:38:ARG:O	62:SS:42:HIS:ND1	2.42	0.47
72:SG:234:LEU:HD23	72:SG:237:LEU:HD21	1.96	0.47
1:L5:239:C:OP1	27:LY:46:SER:OG	2.33	0.47
9:LF:171:ASP:HB2	9:LF:174:LEU:HG	1.96	0.47
22:LT:28:ALA:HA	22:LT:31:MET:HG2	1.97	0.47
28:LZ:73:LYS:HD3	28:LZ:75:TYR:CZ	2.50	0.47
49:S2:563:G:H1	49:S2:592:C:H5	1.63	0.47
49:S2:1722:G:O6	49:S2:1812:U:O2	2.32	0.47
50:SA:198:MET:HG2	50:SA:200:ASP:H	1.80	0.47
73:SJ:120:ALA:HB2	73:SJ:129:LEU:HD22	1.97	0.47
1:L5:4916:G:O2'	1:L5:4917:C:O4'	2.31	0.46
2:L7:23:A:N3	2:L7:118:C:O2'	2.40	0.46
9:LF:182:TYR:HB3	9:LF:200:ARG:HG3	1.97	0.46
26:LX:129:ARG:O	26:LX:132:GLY:N	2.44	0.46
45:Lr:65:LYS:O	45:Lr:102:TYR:OH	2.30	0.46
48:Lz:60:ARG:H	48:Lz:171:HIS:HB2	1.78	0.46
49:S2:1579:A:O2'	49:S2:1581:C:OP2	2.29	0.46
49:S2:1657:G:H1	49:S2:1667:U:H3	1.62	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:1759:G:N2	49:S2:1760:G:O6	2.48	0.46
49:S2:1764:G:H5'	49:S2:1765:C:H5''	1.98	0.46
70:Sg:5:MET:HA	70:Sg:311:GLN:O	2.15	0.46
87:CI:273:GLU:HB3	87:CI:279:LEU:HD13	1.97	0.46
1:L5:1708:G:N7	30:Lb:103:LYS:NZ	2.63	0.46
1:L5:2745:A:H2'	1:L5:2746:A:C8	2.50	0.46
1:L5:4076:G:OP2	1:L5:4163:U:N3	2.46	0.46
1:L5:4238:G:H2'	1:L5:4239:A:C8	2.50	0.46
88:CH:333:LEU:HD11	88:CH:344:LEU:HD23	1.97	0.46
7:LD:33:ARG:HE	7:LD:37:VAL:HG11	1.80	0.46
13:LJ:42:GLN:HB2	13:LJ:117:ILE:HD13	1.97	0.46
25:LW:8:PHE:HZ	25:LW:49:ILE:HG13	1.81	0.46
49:S2:1277:C:H2'	49:S2:1278:A:H8	1.80	0.46
49:S2:1824:A:OP2	66:SX:61:GLN:NE2	2.49	0.46
71:SC:204:ILE:O	71:SC:211:LYS:NZ	2.42	0.46
83:CA:200:THR:OG1	83:CA:201:ILE:N	2.49	0.46
1:L5:452:A:H62	1:L5:1293:G:H3'	1.80	0.46
5:LB:139:ASP:O	5:LB:143:LYS:NZ	2.49	0.46
11:LH:171:ASP:O	11:LH:174:LYS:C	2.59	0.46
12:LI:61:SER:HA	12:LI:126:VAL:HG12	1.97	0.46
27:LY:19:PHE:O	27:LY:26:ARG:NH2	2.48	0.46
32:Ld:50:ARG:NH1	32:Ld:62:VAL:O	2.49	0.46
47:Lt:8:ASN:OD1	47:Lt:11:LYS:N	2.48	0.46
49:S2:1284:A:HO2'	74:SM:106:CYS:HG	1.58	0.46
51:SB:82:ARG:NH2	51:SB:189:ILE:O	2.49	0.46
64:SU:43:ALA:HA	64:SU:46:LYS:HB2	1.97	0.46
76:SO:45:THR:HG22	76:SO:52:THR:HA	1.96	0.46
83:CA:134:GLN:HE21	83:CA:343:TYR:HA	1.80	0.46
1:L5:1332:C:H2'	1:L5:1333:A:H8	1.80	0.46
1:L5:1762:C:C4	1:L5:1770:A:N1	2.84	0.46
1:L5:3948:C:O2	1:L5:4066:U:N3	2.48	0.46
21:LS:15:ARG:HB3	21:LS:27:LEU:HD23	1.97	0.46
28:LZ:12:LEU:HB2	28:LZ:81:MET:HB3	1.98	0.46
48:Lz:63:PHE:O	48:Lz:153:SER:OG	2.34	0.46
49:S2:639:C:H2'	49:S2:640:A:C8	2.51	0.46
55:SH:31:GLU:OE2	55:SH:41:ARG:NH1	2.41	0.46
60:SQ:43:GLU:O	60:SQ:45:ARG:N	2.49	0.46
67:Sa:47:ALA:HA	67:Sa:50:VAL:HG13	1.98	0.46
1:L5:1734:G:N2	1:L5:1735:U:O4	2.42	0.46
1:L5:2622:G:OP2	23:LU:84:LYS:NZ	2.47	0.46
4:LA:108:PRO:O	4:LA:111:THR:OG1	2.28	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:LO:7:LEU:HB2	17:LO:31:ARG:HH21	1.80	0.46
64:SU:55:ARG:HG2	64:SU:87:ARG:HG3	1.98	0.46
70:Sg:105:THR:OG1	70:Sg:106:LYS:N	2.49	0.46
1:L5:496:G:O6	1:L5:497:G:N2	2.49	0.46
1:L5:4910:A:H4'	5:LB:95:THR:HG22	1.97	0.46
5:LB:152:SER:O	5:LB:156:TYR:HB2	2.15	0.46
11:LH:142:ASP:OD1	11:LH:142:ASP:N	2.45	0.46
25:LW:105:ARG:NH2	72:SG:151:ASP:OD1	2.49	0.46
27:LY:10:ASP:HB3	27:LY:13:LYS:HB2	1.97	0.46
49:S2:1130:G:OP2	49:S2:1130:G:N2	2.42	0.46
49:S2:1420:G:O2'	49:S2:1421:A:O4'	2.34	0.46
53:SE:141:THR:OG1	53:SE:142:HIS:N	2.48	0.46
55:SH:49:LYS:O	55:SH:60:ILE:HA	2.16	0.46
72:SG:5:ILE:HB	72:SG:124:LEU:HD11	1.96	0.46
74:SM:84:LYS:HE3	74:SM:84:LYS:HB3	1.67	0.46
1:L5:2343:G:OP2	6:LC:109:ARG:NH1	2.35	0.46
12:LI:61:SER:OG	12:LI:63:GLU:OE1	2.34	0.46
35:Lg:56:VAL:HG13	35:Lg:72:LYS:HA	1.97	0.46
60:SQ:48:GLN:HE21	60:SQ:52:LEU:HD21	1.81	0.46
62:SS:46:ARG:NH1	63:ST:50:GLU:OE2	2.48	0.46
71:SC:278:THR:HA	71:SC:279:ARG:HA	1.66	0.46
78:SY:110:ARG:HH11	78:SY:128:GLY:HA3	1.81	0.46
79:SZ:102:LYS:HD2	79:SZ:102:LYS:HA	1.79	0.46
83:CA:231:SER:HA	83:CA:316:VAL:HG12	1.97	0.46
87:CI:361:GLU:O	87:CI:542:ASN:HA	2.16	0.46
1:L5:230:G:OP1	27:LY:15:ARG:NH1	2.46	0.46
14:LL:104:ASN:O	37:Li:20:ASN:ND2	2.43	0.46
17:LO:65:ASN:OD1	17:LO:67:SER:OG	2.29	0.46
25:LW:71:ARG:HD3	25:LW:71:ARG:HA	1.72	0.46
49:S2:521:A:OP1	73:SJ:45:ARG:NH1	2.45	0.46
49:S2:1375:G:OP1	61:SR:67:ARG:NH2	2.48	0.46
70:Sg:120:ILE:O	70:Sg:131:LEU:HA	2.15	0.46
87:CI:247:LEU:O	87:CI:252:ARG:NH2	2.39	0.46
1:L5:2724:G:O2'	1:L5:2726:G:OP2	2.32	0.46
1:L5:3811:G:O2'	1:L5:3814:U:OP2	2.28	0.46
1:L5:4174:U:H2'	1:L5:4175:G:H8	1.81	0.46
1:L5:4736:C:H2'	1:L5:4737:G:H8	1.81	0.46
3:L8:47:C:H1'	3:L8:61:A:H2'	1.98	0.46
10:LG:30:PRO:HB2	28:LZ:125:GLY:HA3	1.97	0.46
25:LW:102:LYS:HA	25:LW:105:ARG:HB2	1.97	0.46
28:LZ:94:THR:O	28:LZ:97:ASN:ND2	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:1613:G:OP1	62:SS:88:LYS:NZ	2.43	0.46
76:SO:63:LYS:HD3	76:SO:63:LYS:HA	1.78	0.46
88:CH:62:ILE:O	88:CH:68:ARG:NH2	2.36	0.46
8:LE:262:LYS:NZ	8:LE:268:GLN:OE1	2.41	0.45
9:LF:236:ARG:HD3	9:LF:239:GLN:HB2	1.99	0.45
18:LP:10:ASN:N	18:LP:10:ASN:OD1	2.49	0.45
49:S2:560:A:O5'	73:SJ:174:LYS:NZ	2.49	0.45
49:S2:886:A:C6	49:S2:901:G:N3	2.84	0.45
52:SD:55:THR:HA	52:SD:58:VAL:HG22	1.97	0.45
73:SJ:44:TRP:HA	73:SJ:47:LYS:HG2	1.98	0.45
78:SY:62:THR:HA	78:SY:69:THR:HA	1.97	0.45
1:L5:39:A:H5''	29:La:35:ALA:HB1	1.98	0.45
1:L5:3589:G:N2	1:L5:3590:G:N7	2.64	0.45
5:LB:317:LEU:HB2	5:LB:372:SER:HB2	1.98	0.45
7:LD:146:LEU:HD13	7:LD:163:LEU:HD12	1.98	0.45
49:S2:1256:G:C8	64:SU:66:ARG:HB2	2.51	0.45
49:S2:1275:G:N2	49:S2:1506:A:OP2	2.44	0.45
67:Sa:60:ASP:OD1	67:Sa:60:ASP:N	2.45	0.45
70:Sg:69:VAL:HA	70:Sg:79:LEU:O	2.17	0.45
74:SM:21:VAL:HA	74:SM:24:THR:HG22	1.97	0.45
83:CA:255:TYR:HB3	83:CA:301:LEU:HD11	1.97	0.45
84:CC:48:C:H2'	84:CC:49:G:H8	1.81	0.45
1:L5:2503:G:O6	4:LA:72:ARG:NH1	2.46	0.45
1:L5:3955:G:H22	1:L5:3966:A:H3'	1.80	0.45
48:Lz:60:ARG:HH21	48:Lz:61:PRO:HG3	1.81	0.45
51:SB:129:THR:OG1	51:SB:130:THR:N	2.50	0.45
53:SE:126:VAL:HG22	53:SE:139:LEU:HD13	1.97	0.45
59:SP:12:PHE:HD2	59:SP:14:LYS:HE2	1.81	0.45
78:SY:78:SER:OG	78:SY:80:ASP:OD1	2.26	0.45
80:Sb:8:LEU:HG	80:Sb:9:HIS:HD2	1.82	0.45
87:CI:377:MET:HB2	87:CI:518:VAL:HG12	1.97	0.45
1:L5:4260:U:H2'	1:L5:4261:C:C6	2.52	0.45
4:LA:56:ALA:HB2	4:LA:130:SER:HB3	1.99	0.45
8:LE:178:PRO:HB2	8:LE:181:LEU:HD12	1.98	0.45
9:LF:24:ASN:N	9:LF:24:ASN:OD1	2.50	0.45
46:Ls:110:ALA:HA	46:Ls:182:PRO:HD2	1.97	0.45
49:S2:1621:U:H1'	59:SP:118:GLU:HB3	1.98	0.45
50:SA:74:VAL:HG22	50:SA:121:LEU:HB3	1.97	0.45
52:SD:220:THR:OG1	52:SD:221:THR:N	2.49	0.45
63:ST:108:GLU:OE2	63:ST:121:ARG:NE	2.50	0.45
87:CI:362:LEU:HD21	87:CI:388:PHE:HB2	1.96	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4258:C:H2'	1:L5:4259:C:H6	1.82	0.45
1:L5:4323:A:H4'	7:LD:176:SER:HB3	1.97	0.45
2:L7:6:C:O2'	7:LD:50:ARG:NH2	2.48	0.45
49:S2:1033:G:N1	49:S2:1080:A:O2'	2.41	0.45
51:SB:180:ASP:OD1	51:SB:180:ASP:N	2.49	0.45
53:SE:89:VAL:HG21	53:SE:164:LEU:HD11	1.98	0.45
54:SF:120:GLY:O	54:SF:146:ARG:NH2	2.50	0.45
64:SU:94:PRO:HD2	64:SU:97:ILE:HD11	1.98	0.45
79:SZ:77:LEU:HB2	79:SZ:79:ILE:HG12	1.99	0.45
84:CC:68:C:H2'	84:CC:69:G:C8	2.52	0.45
1:L5:4392:G:N2	1:L5:4395:U:O2	2.42	0.45
5:LB:14:LEU:HD23	5:LB:17:LEU:HD21	1.98	0.45
5:LB:224:LYS:HG3	5:LB:340:THR:HG22	1.97	0.45
9:LF:92:VAL:O	9:LF:120:GLY:HA2	2.17	0.45
14:LL:111:GLN:HA	14:LL:114:VAL:HG12	1.98	0.45
35:Lg:103:VAL:HA	35:Lg:106:VAL:HG22	1.99	0.45
39:Lk:21:LYS:N	39:Lk:37:ARG:O	2.49	0.45
49:S2:640:A:H2'	49:S2:641:A:C8	2.51	0.45
49:S2:747:U:O4	49:S2:796:G:O6	2.35	0.45
49:S2:1076:G:H5''	75:SN:106:ARG:HH22	1.81	0.45
49:S2:1215:C:O2'	49:S2:1645:C:OP2	2.35	0.45
52:SD:48:ILE:HB	52:SD:86:LEU:HD23	1.99	0.45
60:SQ:43:GLU:HG3	60:SQ:81:ILE:HD11	1.98	0.45
71:SC:246:LYS:HA	71:SC:249:SER:HB3	1.99	0.45
73:SJ:26:ASP:HB2	81:Se:42:PHE:HZ	1.81	0.45
74:SM:86:GLY:HA2	74:SM:89:VAL:HG12	1.99	0.45
1:L5:2709:C:N4	83:CA:257:LEU:O	2.49	0.45
17:LO:54:TYR:OH	17:LO:73:PHE:O	2.33	0.45
31:Lc:37:MET:SD	31:Lc:40:GLN:NE2	2.86	0.45
52:SD:161:GLY:O	52:SD:164:VAL:N	2.50	0.45
65:SV:12:TYR:O	71:SC:248:TYR:OH	2.34	0.45
74:SM:23:LYS:HD2	74:SM:23:LYS:HA	1.67	0.45
1:L5:86:U:OP1	19:LQ:169:SER:OG	2.35	0.45
1:L5:1933:G:H2'	1:L5:1934:A:C8	2.52	0.45
1:L5:3967:G:N2	1:L5:4055:U:O2	2.49	0.45
1:L5:4208:U:OP2	22:LT:4:THR:OG1	2.26	0.45
32:Ld:57:MET:HG2	32:Ld:88:LEU:HD23	1.98	0.45
45:Lr:7:TRP:O	45:Lr:11:ARG:HB2	2.17	0.45
45:Lr:26:SER:OG	45:Lr:28:GLU:OE1	2.30	0.45
49:S2:3:C:O2	73:SJ:18:ARG:NH2	2.46	0.45
49:S2:1756:C:N3	49:S2:1776:G:N1	2.62	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SD:142:LEU:HD12	52:SD:148:LYS:HB2	1.97	0.45
56:SI:117:TYR:HD1	56:SI:152:ARG:HB3	1.81	0.45
1:L5:975:C:O3'	9:LF:47:ARG:NH2	2.49	0.45
1:L5:2748:C:O2'	35:Lg:61:PRO:O	2.34	0.45
1:L5:3956:G:O5'	1:L5:3966:A:N6	2.50	0.45
8:LE:188:ARG:NH2	8:LE:214:ASP:OD1	2.46	0.45
49:S2:57:U:OP1	49:S2:504:G:O2'	2.30	0.45
49:S2:691:G:OP2	49:S2:691:G:N2	2.46	0.45
49:S2:1436:C:O2'	49:S2:1438:A:O5'	2.35	0.45
51:SB:85:LYS:HB3	51:SB:101:HIS:HB3	1.99	0.45
67:Sa:51:ARG:NH1	68:Sc:39:SER:OG	2.41	0.45
74:SM:40:LYS:HD3	74:SM:40:LYS:HA	1.76	0.45
74:SM:95:ASP:OD1	74:SM:95:ASP:N	2.50	0.45
84:CC:69:G:H2'	84:CC:70:G:C8	2.52	0.45
1:L5:460:C:H2'	1:L5:461:G:H8	1.81	0.45
1:L5:461:G:H2'	1:L5:462:G:H8	1.82	0.45
1:L5:947:C:H5''	8:LE:51:VAL:HG11	1.98	0.45
1:L5:1765:A:N7	1:L5:1766:A:O2'	2.49	0.45
1:L5:1942:A:H2'	1:L5:1943:A:C8	2.52	0.45
1:L5:3786:U:OP1	1:L5:4550:G:O2'	2.31	0.45
7:LD:152:ARG:HG3	7:LD:154:THR:HG23	1.98	0.45
8:LE:151:ILE:HA	8:LE:160:LYS:O	2.16	0.45
16:LN:140:LYS:HD3	16:LN:140:LYS:HA	1.76	0.45
39:Lk:57:LYS:HB3	39:Lk:57:LYS:HE2	1.80	0.45
46:Ls:29:ILE:HD11	46:Ls:191:GLN:HG2	1.98	0.45
46:Ls:119:CYS:SG	46:Ls:120:GLU:N	2.90	0.45
51:SB:122:GLU:HG2	51:SB:140:VAL:HG23	1.99	0.45
62:SS:51:ASP:OD1	62:SS:51:ASP:N	2.48	0.45
70:Sg:152:SER:OG	70:Sg:168:CYS:SG	2.62	0.45
1:L5:137:G:H2'	1:L5:138:G:H8	1.81	0.44
1:L5:186:G:N1	1:L5:1366:G:OP1	2.48	0.44
1:L5:228:C:O2'	27:LY:14:ASN:ND2	2.50	0.44
1:L5:308:G:OP2	1:L5:308:G:N2	2.38	0.44
1:L5:3596:A:H1'	58:SL:2:ALA:HA	1.98	0.44
1:L5:4041:C:H1'	48:Lz:103:LEU:HA	1.99	0.44
1:L5:4600:G:O2'	1:L5:4609:G:N1	2.48	0.44
15:LM:101:LYS:HB2	17:LO:200:GLY:HA3	1.98	0.44
49:S2:752:G:OP1	49:S2:792:C:O2'	2.35	0.44
51:SB:42:ARG:NH2	51:SB:232:HIS:O	2.47	0.44
52:SD:40:ARG:HB2	52:SD:47:GLU:HG2	1.99	0.44
52:SD:132:LYS:HE3	52:SD:189:MET:HE2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:SK:47:LYS:HD3	57:SK:47:LYS:HA	1.77	0.44
60:SQ:34:VAL:HG12	60:SQ:70:VAL:HB	1.98	0.44
68:Sc:33:GLU:HG3	68:Sc:41:SER:HB2	1.99	0.44
70:Sg:145:GLU:HG3	70:Sg:177:TRP:HH2	1.82	0.44
77:SW:36:ARG:HA	77:SW:39:THR:HG22	1.99	0.44
84:CC:8:U:H5'	84:CC:48:C:H5''	1.98	0.44
87:CI:135:ASP:OD1	87:CI:135:ASP:N	2.49	0.44
88:CH:150:VAL:HG22	88:CH:227:ALA:HB3	1.99	0.44
1:L5:4743:G:H2'	1:L5:4744:A:C8	2.53	0.44
6:LC:263:LEU:HG	6:LC:273:LEU:HD12	1.99	0.44
10:LG:58:PRO:HD2	10:LG:61:ILE:HD12	1.98	0.44
11:LH:59:LYS:HA	11:LH:59:LYS:HD2	1.79	0.44
12:LI:43:VAL:O	12:LI:171:TRP:NE1	2.46	0.44
48:Lz:53:VAL:HG12	48:Lz:157:PHE:HZ	1.81	0.44
49:S2:1705:C:H2'	49:S2:1706:G:C8	2.52	0.44
51:SB:94:LYS:HA	51:SB:94:LYS:HD3	1.75	0.44
53:SE:11:ARG:HA	53:SE:28:ALA:HB2	1.99	0.44
53:SE:126:VAL:O	53:SE:157:ASN:CA	2.65	0.44
78:SY:68:LYS:HE2	78:SY:68:LYS:HB3	1.86	0.44
1:L5:3961:G:O2'	1:L5:3965:A:OP1	2.34	0.44
4:LA:228:ASP:OD1	4:LA:228:ASP:N	2.38	0.44
7:LD:103:LEU:HG	7:LD:247:ILE:HG21	1.98	0.44
21:LS:17:LEU:HD21	22:LT:136:ARG:HH21	1.82	0.44
26:LX:60:TYR:O	26:LX:62:ARG:NH1	2.50	0.44
49:S2:10:G:H21	71:SC:114:LYS:HA	1.81	0.44
49:S2:197:U:N3	49:S2:202:G:N7	2.65	0.44
49:S2:681:U:H4'	66:SX:9:THR:HG22	1.99	0.44
49:S2:951:C:O2'	76:SO:50:LYS:NZ	2.50	0.44
50:SA:32:PHE:HA	50:SA:35:GLU:HG3	1.99	0.44
68:Sc:12:ALA:HB1	68:Sc:32:VAL:HB	1.99	0.44
83:CA:280:LEU:HD11	83:CA:293:VAL:HG21	1.99	0.44
1:L5:135:G:N2	36:Lh:95:LEU:O	2.50	0.44
1:L5:1857:C:H2'	1:L5:1858:A:H8	1.82	0.44
1:L5:2709:C:H5'	20:LR:43:LYS:HD2	1.99	0.44
1:L5:3788:C:N4	1:L5:3812:C:OP2	2.50	0.44
1:L5:3965:A:O2'	1:L5:4050:A:OP2	2.31	0.44
1:L5:4092:G:H3'	1:L5:4093:G:H21	1.83	0.44
1:L5:4238:G:H2'	1:L5:4239:A:H8	1.83	0.44
1:L5:4322:G:N2	1:L5:4325:A:OP2	2.44	0.44
1:L5:4769:G:OP1	17:LO:176:ARG:NH2	2.44	0.44
6:LC:29:LYS:HA	6:LC:29:LYS:HD3	1.77	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LE:222:LEU:HD13	8:LE:237:LYS:HG3	2.00	0.44
15:LM:93:LYS:HB3	15:LM:93:LYS:HE2	1.77	0.44
45:Lr:105:ASP:OD1	45:Lr:105:ASP:N	2.43	0.44
49:S2:31:U:OP1	66:SX:137:LYS:NZ	2.50	0.44
49:S2:1231:C:O2'	49:S2:1253:A:N6	2.51	0.44
50:SA:219:GLU:O	50:SA:223:THR:OG1	2.32	0.44
61:SR:29:HIS:HA	61:SR:32:LYS:HE2	1.99	0.44
76:SO:124:MET:HE3	76:SO:124:MET:HB3	1.83	0.44
87:CI:8:ILE:HD11	87:CI:75:LEU:HD13	2.00	0.44
87:CI:315:GLY:HA3	87:CI:325:ARG:HB3	2.00	0.44
87:CI:389:ILE:HG21	87:CI:484:LEU:HD22	1.99	0.44
87:CI:426:GLN:HA	87:CI:429:HIS:CD2	2.53	0.44
88:CH:394:ASP:HB3	88:CH:403:VAL:HG11	2.00	0.44
1:L5:962:C:H2'	1:L5:1702:C:H5	1.83	0.44
1:L5:1591:U:N3	1:L5:4555:U:OP1	2.44	0.44
1:L5:2601:A:OP1	35:Lg:40:LYS:NZ	2.51	0.44
1:L5:4761:G:H2'	1:L5:4762:A:C8	2.52	0.44
4:LA:45:VAL:O	4:LA:85:GLY:N	2.51	0.44
27:LY:112:ASP:N	27:LY:112:ASP:OD1	2.49	0.44
36:Lh:4:ILE:HD12	36:Lh:9:LEU:HD11	1.99	0.44
36:Lh:46:LYS:HA	36:Lh:46:LYS:HD3	1.79	0.44
48:Lz:188:ASN:HA	48:Lz:191:VAL:HG22	2.00	0.44
51:SB:67:PHE:O	51:SB:85:LYS:C	2.61	0.44
51:SB:103:MET:HE3	51:SB:103:MET:HB3	1.90	0.44
1:L5:267:G:H2'	1:L5:268:G:H8	1.83	0.44
1:L5:707:C:O2'	1:L5:4943:A:N1	2.40	0.44
1:L5:1364:U:O2	6:LC:234:LYS:NZ	2.48	0.44
1:L5:1405:C:H42	1:L5:1413:C:H42	1.65	0.44
8:LE:98:GLY:HA3	8:LE:99:ASP:HA	1.74	0.44
16:LN:158:HIS:HB3	16:LN:161:MET:HB2	1.98	0.44
48:Lz:12:GLU:HB3	48:Lz:216:LEU:HA	1.99	0.44
53:SE:60:GLU:HA	53:SE:63:LYS:HG2	1.98	0.44
55:SH:53:VAL:HG13	55:SH:57:ARG:HB3	1.98	0.44
56:SI:57:ALA:HB2	56:SI:183:GLY:HA2	1.99	0.44
72:SG:32:MET:HB2	72:SG:100:CYS:HB2	1.99	0.44
83:CA:93:LYS:HZ2	83:CA:281:ARG:HB2	1.83	0.44
83:CA:248:LYS:O	83:CA:303:GLN:N	2.48	0.44
1:L5:2411:C:H2'	1:L5:2412:A:C8	2.52	0.44
1:L5:3689:G:O2'	1:L5:3818:U:OP2	2.29	0.44
1:L5:4279:A:H5'	1:L5:4281:A:H1'	1.98	0.44
1:L5:4991:U:H2'	1:L5:4992:G:H8	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LE:157:HIS:HB3	8:LE:160:LYS:HD2	2.00	0.44
14:LL:63:THR:HG21	29:La:66:ASN:HB3	2.00	0.44
20:LR:77:GLY:O	20:LR:81:ARG:NE	2.51	0.44
31:Lc:65:MET:HE3	31:Lc:65:MET:HB3	1.77	0.44
49:S2:1513:C:OP1	69:Sd:12:ARG:NH1	2.42	0.44
49:S2:1593:C:H1'	63:ST:12:GLN:HE22	1.83	0.44
55:SH:50:GLU:HG3	55:SH:60:ILE:HG22	1.99	0.44
61:SR:17:ILE:HD11	61:SR:54:VAL:HA	1.99	0.44
1:L5:257:C:H2'	1:L5:258:G:C8	2.52	0.44
1:L5:679:C:H2'	1:L5:680:G:H8	1.82	0.44
1:L5:909:A:H2'	1:L5:910:G:H8	1.83	0.44
1:L5:2411:C:H2'	1:L5:2412:A:H8	1.82	0.44
1:L5:2557:G:O6	1:L5:2570:U:O4	2.36	0.44
1:L5:3977:C:N4	1:L5:3984:C:OP1	2.51	0.44
6:LC:66:SER:O	6:LC:66:SER:OG	2.27	0.44
7:LD:223:PHE:HB3	7:LD:226:TYR:HB2	1.99	0.44
10:LG:264:LYS:HD2	51:SB:225:LEU:HD22	2.00	0.44
16:LN:84:PRO:HA	16:LN:87:HIS:CG	2.53	0.44
17:LO:10:ASP:HB2	17:LO:117:ARG:HB3	2.00	0.44
48:Lz:147:LYS:HE2	48:Lz:151:VAL:HG22	2.00	0.44
49:S2:453:C:O2'	72:SG:92:ARG:O	2.30	0.44
53:SE:212:ASP:OD1	53:SE:216:ASN:N	2.51	0.44
62:SS:105:ASN:HA	62:SS:108:ARG:HG2	1.98	0.44
70:Sg:51:ASN:HD21	70:Sg:54:ILE:HD13	1.81	0.44
73:SJ:107:GLU:O	73:SJ:112:THR:OG1	2.34	0.44
81:Se:37:GLN:HA	81:Se:40:ARG:HG2	2.00	0.44
84:CC:54:U:O2'	84:CC:56:G:N7	2.46	0.44
1:L5:4122:G:O2'	28:LZ:136:PHE:OXT	2.36	0.44
1:L5:4991:U:H2'	1:L5:4992:G:C8	2.53	0.44
3:L8:39:G:O2'	3:L8:104:A:N1	2.45	0.44
41:Lm:98:LYS:HD2	41:Lm:118:THR:CB	2.47	0.44
47:Lt:10:ILE:HD13	47:Lt:10:ILE:HA	1.94	0.44
49:S2:1060:A:O2'	49:S2:1062:A:N7	2.43	0.44
49:S2:1165:G:N1	66:SX:20:GLN:OE1	2.41	0.44
50:SA:183:LEU:O	50:SA:188:THR:OG1	2.36	0.44
68:Sc:29:GLN:HA	68:Sc:44:ARG:O	2.17	0.44
87:CI:25:CYS:HB3	87:CI:39:ILE:HD13	1.99	0.44
1:L5:691:C:H2'	1:L5:692:A:C8	2.53	0.43
1:L5:4044:U:N3	48:Lz:95:LYS:O	2.46	0.43
10:LG:100:HIS:HA	10:LG:103:ARG:HG3	2.00	0.43
10:LG:232:GLU:HA	10:LG:235:ARG:HG2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:LM:55:MET:HE2	15:LM:55:MET:HB3	1.83	0.43
21:LS:69:GLU:HB2	21:LS:101:THR:HG23	2.00	0.43
28:LZ:92:ASP:HB3	28:LZ:95:VAL:HG22	2.00	0.43
32:Ld:54:MET:O	32:Ld:57:MET:C	2.60	0.43
49:S2:197:U:OP2	49:S2:203:G:N2	2.46	0.43
50:SA:26:GLY:O	50:SA:150:THR:OG1	2.27	0.43
54:SF:142:SER:OG	68:Sc:49:PRO:O	2.31	0.43
62:SS:61:GLU:HA	62:SS:64:VAL:HG12	1.99	0.43
66:SX:28:LYS:O	66:SX:32:LEU:CB	2.66	0.43
83:CA:10:GLN:NE2	83:CA:11:THR:O	2.51	0.43
5:LB:168:MET:HE1	5:LB:173:LEU:HD12	2.00	0.43
11:LH:132:VAL:HG13	11:LH:154:VAL:HG22	1.99	0.43
12:LI:36:LEU:HB3	12:LI:87:MET:HG3	1.99	0.43
31:Lc:55:LEU:HD21	35:Lg:93:ARG:HA	1.98	0.43
33:Le:85:LEU:HD11	33:Le:111:ILE:HG23	1.99	0.43
57:SK:41:PRO:HB2	57:SK:43:LEU:HD23	2.00	0.43
1:L5:4531:U:H5	88:CH:184:GLY:HA3	1.83	0.43
5:LB:57:VAL:HB	5:LB:367:PHE:HB3	2.01	0.43
39:Lk:24:LYS:HA	39:Lk:67:LYS:O	2.17	0.43
49:S2:857:U:H2'	49:S2:858:A:C8	2.53	0.43
54:SF:111:VAL:HG11	54:SF:178:ILE:HG22	2.00	0.43
56:SI:150:ASP:HA	56:SI:153:LYS:HG2	2.00	0.43
57:SK:29:MET:SD	57:SK:42:ASN:ND2	2.91	0.43
83:CA:207:ASP:HA	83:CA:210:LYS:HE3	1.99	0.43
7:LD:209:ARG:HG2	7:LD:212:MET:HE2	2.00	0.43
12:LI:184:MET:HA	12:LI:187:LYS:HG2	2.01	0.43
48:Lz:17:VAL:HG13	48:Lz:18:LEU:H	1.84	0.43
49:S2:1010:G:H2'	49:S2:1011:A:C8	2.54	0.43
53:SE:162:ILE:HG22	53:SE:169:ILE:HA	1.99	0.43
56:SI:106:SER:HB3	56:SI:171:LEU:HG	2.01	0.43
57:SK:35:LEU:HD22	57:SK:40:VAL:HG21	2.01	0.43
57:SK:51:SER:HB2	57:SK:55:ARG:HH21	1.84	0.43
67:Sa:23:CYS:O	76:SO:142:ARG:NH1	2.51	0.43
70:Sg:84:ASP:OD1	70:Sg:84:ASP:N	2.36	0.43
71:SC:194:ARG:HD3	71:SC:196:ILE:HD11	1.99	0.43
87:CI:369:PHE:HE2	87:CI:392:LEU:HD21	1.83	0.43
1:L5:369:G:N2	1:L5:372:A:OP2	2.42	0.43
1:L5:1332:C:H2'	1:L5:1333:A:C8	2.54	0.43
1:L5:4478:G:O2'	1:L5:4602:A:N1	2.50	0.43
4:LA:107:MET:HE2	4:LA:166:VAL:HG22	2.00	0.43
10:LG:222:ILE:O	10:LG:226:TYR:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LH:91:LYS:HB2	11:LH:183:GLU:HG3	1.99	0.43
15:LM:52:PHE:HA	15:LM:55:MET:HG2	1.99	0.43
49:S2:373:G:H4'	58:SL:85:THR:HG21	2.00	0.43
49:S2:1226:G:N1	49:S2:1639:G:OP2	2.39	0.43
54:SF:110:GLN:NE2	54:SF:114:ASN:OD1	2.47	0.43
70:Sg:239:LEU:HA	70:Sg:250:ALA:HA	2.00	0.43
74:SM:40:LYS:HD2	82:Sf:130:VAL:HG22	2.01	0.43
83:CA:190:LEU:HB3	83:CA:223:VAL:HG23	2.01	0.43
1:L5:2550:G:O2'	1:L5:2587:A:N1	2.45	0.43
1:L5:2903:G:H1'	1:L5:2904:U:H5	1.82	0.43
1:L5:4040:C:H5'	1:L5:4045:G:H22	1.83	0.43
1:L5:4546:A:O2'	1:L5:4547:C:H5'	2.18	0.43
16:LN:146:PRO:HB2	36:Lh:104:THR:HG23	2.01	0.43
19:LQ:70:MET:HE1	19:LQ:137:VAL:HB	2.01	0.43
19:LQ:159:PRO:HD3	19:LQ:188:ASN:HD21	1.83	0.43
37:Li:52:PRO:HA	37:Li:55:ARG:HE	1.83	0.43
49:S2:60:G:H22	49:S2:316:G:H21	1.66	0.43
60:SQ:104:SER:O	60:SQ:108:ILE:HG12	2.18	0.43
62:SS:46:ARG:HA	62:SS:46:ARG:HD3	1.89	0.43
79:SZ:72:VAL:O	79:SZ:76:ARG:HB2	2.18	0.43
88:CH:81:ARG:HA	88:CH:81:ARG:HD3	1.82	0.43
1:L5:1899:G:O2'	33:Le:57:ASN:OD1	2.36	0.43
7:LD:14:LYS:HE3	7:LD:14:LYS:HB2	1.90	0.43
17:LO:177:LEU:HD23	17:LO:177:LEU:HA	1.92	0.43
49:S2:641:A:OP1	73:SJ:40:LYS:NZ	2.40	0.43
49:S2:1550:G:O2'	49:S2:1558:C:O2	2.30	0.43
54:SF:81:ARG:O	54:SF:85:LYS:NZ	2.51	0.43
70:Sg:286:CYS:HA	70:Sg:302:TYR:HA	2.01	0.43
72:SG:153:VAL:HA	72:SG:156:TYR:HB2	2.01	0.43
78:SY:41:ARG:HH12	78:SY:94:HIS:CD2	2.36	0.43
79:SZ:99:LEU:HD21	79:SZ:102:LYS:HB2	2.00	0.43
1:L5:261:G:H2'	1:L5:262:G:C8	2.53	0.43
1:L5:2403:A:OP1	35:Lg:10:ARG:NH1	2.51	0.43
3:L8:62:A:OP1	36:Lh:52:LYS:NZ	2.48	0.43
23:LU:107:LYS:HD3	23:LU:107:LYS:HA	1.91	0.43
24:LV:111:GLU:HG3	24:LV:131:ARG:HE	1.83	0.43
49:S2:1094:C:H2'	49:S2:1095:C:C6	2.53	0.43
62:SS:64:VAL:HA	62:SS:67:VAL:HG22	2.01	0.43
82:Sf:97:LYS:HA	82:Sf:97:LYS:HD3	1.87	0.43
88:CH:149:ILE:HB	88:CH:226:LEU:HD23	2.01	0.43
1:L5:1241:C:O2'	30:Lb:120:ARG:O	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1629:G:H1	4:LA:208:GLU:HG2	1.84	0.43
1:L5:2257:C:H41	1:L5:2261:G:H1	1.67	0.43
1:L5:4935:C:H2'	1:L5:4936:G:C8	2.53	0.43
12:LI:33:ILE:HG21	85:CE:74:LEU:HD13	2.01	0.43
48:Lz:56:LYS:HB3	48:Lz:182:ASN:HD21	1.84	0.43
51:SB:192:SER:HA	51:SB:195:LYS:HG2	2.01	0.43
57:SK:6:LYS:HA	57:SK:9:ILE:HG12	2.00	0.43
66:SX:52:LEU:HD11	66:SX:73:GLN:HB2	2.01	0.43
87:CI:538:VAL:HG13	87:CI:541:LYS:HB2	2.01	0.43
1:L5:935:A:O2'	15:LM:44:GLN:O	2.37	0.43
1:L5:1802:A:H5''	1:L5:1803:G:H5'	2.01	0.43
1:L5:2020:U:H2'	1:L5:2021:G:H8	1.83	0.43
1:L5:2101:C:H2'	1:L5:2102:G:H2'	2.00	0.43
5:LB:302:ASN:O	5:LB:304:SER:N	2.50	0.43
8:LE:223:ARG:NH1	8:LE:236:GLU:O	2.52	0.43
15:LM:105:THR:OG1	15:LM:106:ASP:N	2.49	0.43
32:Ld:23:ARG:HG2	32:Ld:121:ASN:HA	2.00	0.43
38:Lj:33:THR:HA	38:Lj:40:PRO:HD3	2.01	0.43
49:S2:1298:G:H5'	59:SP:77:LYS:HB2	2.01	0.43
52:SD:28:GLU:HG2	57:SK:61:GLN:HG2	2.00	0.43
60:SQ:32:ILE:HA	60:SQ:68:ILE:O	2.19	0.43
67:Sa:29:CYS:SG	76:SO:146:ARG:NH1	2.92	0.43
70:Sg:88:ARG:HH11	70:Sg:97:THR:HG21	1.83	0.43
88:CH:318:GLU:O	88:CH:388:THR:OG1	2.27	0.43
88:CH:322:VAL:HG12	88:CH:409:ILE:HG22	2.00	0.43
1:L5:3687:A:O2'	4:LA:236:GLY:N	2.51	0.42
1:L5:4905:C:H6	1:L5:4905:C:OP2	2.02	0.42
2:L7:8:G:P	7:LD:33:ARG:HH22	2.41	0.42
4:LA:102:LEU:HB2	4:LA:107:MET:HE3	2.00	0.42
24:LV:45:ILE:HD13	24:LV:45:ILE:HA	1.89	0.42
29:La:71:PRO:HG2	29:La:108:TYR:HA	2.00	0.42
39:Lk:52:LYS:HA	39:Lk:55:LYS:HG2	2.00	0.42
46:Ls:24:TYR:HA	46:Ls:25:PRO:HD3	1.87	0.42
49:S2:377:G:H5'	56:SI:98:LYS:HB3	2.01	0.42
49:S2:562:U:H2'	49:S2:563:G:C8	2.54	0.42
61:SR:100:PRO:HG3	61:SR:122:PRO:HD3	2.01	0.42
1:L5:120:A:N1	1:L5:148:C:O2'	2.41	0.42
1:L5:753:C:H41	1:L5:910:G:H1	1.66	0.42
1:L5:4870:G:OP2	15:LM:5:ARG:NH2	2.52	0.42
4:LA:48:ILE:HG22	44:Lp:54:ILE:HG12	2.02	0.42
11:LH:48:LEU:HD23	11:LH:48:LEU:HA	1.90	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LI:41:ALA:HB1	12:LI:45:GLU:HB2	2.00	0.42
16:LN:68:ARG:NH1	16:LN:124:ASP:O	2.53	0.42
37:Li:80:HIS:CD2	37:Li:84:LYS:HD2	2.54	0.42
39:Lk:61:PRO:HA	39:Lk:62:PRO:HD3	1.91	0.42
45:Lr:21:ASN:OD1	45:Lr:21:ASN:N	2.51	0.42
47:Lt:130:LYS:HE2	47:Lt:158:GLY:HA3	2.02	0.42
49:S2:508:A:H3'	49:S2:509:G:H8	1.84	0.42
49:S2:1203:G:H2'	49:S2:1204:A:C8	2.54	0.42
50:SA:6:ASP:HA	50:SA:9:GLN:HG2	2.01	0.42
70:Sg:32:LEU:HA	70:Sg:42:MET:HA	2.01	0.42
78:SY:10:ARG:HG3	78:SY:24:VAL:HG13	2.00	0.42
78:SY:80:ASP:OD1	78:SY:80:ASP:N	2.49	0.42
86:CF:156:ASP:O	86:CF:160:ASN:HB2	2.19	0.42
1:L5:2702:C:OP1	23:LU:101:ARG:NH2	2.51	0.42
1:L5:4896:G:H2'	1:L5:4897:G:C8	2.55	0.42
3:L8:82:A:H62	3:L8:84:A:H3'	1.84	0.42
43:Lo:45:GLN:HE22	43:Lo:52:THR:H	1.66	0.42
49:S2:201:C:H3'	49:S2:202:G:H21	1.83	0.42
49:S2:1855:G:OP2	76:SO:147:ARG:NH2	2.42	0.42
56:SI:142:SER:O	56:SI:146:GLN:CB	2.65	0.42
72:SG:119:LYS:HB3	72:SG:119:LYS:HE2	1.76	0.42
83:CA:155:ARG:NH1	83:CA:357:LEU:O	2.33	0.42
1:L5:356:G:N1	1:L5:360:A:OP2	2.43	0.42
1:L5:757:G:H2'	1:L5:758:G:C8	2.55	0.42
1:L5:3664:G:H2'	1:L5:3665:G:C8	2.54	0.42
1:L5:4151:G:H2'	1:L5:4152:G:H8	1.83	0.42
1:L5:4742:G:H2'	1:L5:4743:G:C8	2.54	0.42
4:LA:126:LEU:HD13	4:LA:150:LEU:HD21	2.01	0.42
5:LB:305:THR:OG1	5:LB:365:LEU:O	2.38	0.42
10:LG:132:ARG:HA	10:LG:133:PRO:HD3	1.85	0.42
47:Lt:17:CYS:HA	47:Lt:59:THR:O	2.20	0.42
49:S2:1232:U:H2'	49:S2:1233:G:C8	2.54	0.42
49:S2:1588:A:H2'	49:S2:1589:A:C8	2.55	0.42
51:SB:202:GLN:HE22	51:SB:206:PRO:HB3	1.84	0.42
55:SH:60:ILE:HD11	55:SH:92:VAL:HG22	2.01	0.42
60:SQ:90:LYS:HA	60:SQ:93:VAL:HG12	2.00	0.42
62:SS:35:GLY:O	62:SS:97:GLN:NE2	2.52	0.42
64:SU:69:PRO:HA	69:Sd:41:GLN:HE21	1.85	0.42
79:SZ:65:TYR:HA	79:SZ:111:ARG:HH21	1.83	0.42
5:LB:213:GLN:HE22	5:LB:286:LYS:HA	1.85	0.42
7:LD:120:GLU:O	7:LD:248:ARG:NH1	2.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:LD:203:ASN:OD1	7:LD:203:ASN:N	2.52	0.42
10:LG:219:VAL:O	10:LG:223:ARG:HB2	2.19	0.42
13:LJ:20:LEU:C	13:LJ:131:TYR:O	2.62	0.42
22:LT:17:ARG:HA	22:LT:17:ARG:HD2	1.87	0.42
39:Lk:49:ASP:N	39:Lk:49:ASP:OD1	2.53	0.42
48:Lz:31:THR:O	48:Lz:208:SER:OG	2.27	0.42
50:SA:12:GLU:OE2	61:SR:115:SER:OG	2.29	0.42
50:SA:28:THR:HG22	50:SA:46:ILE:HD13	2.01	0.42
70:Sg:120:ILE:HB	70:Sg:132:TRP:HB2	2.02	0.42
74:SM:119:GLN:HG3	74:SM:122:ASP:HB3	2.00	0.42
79:SZ:102:LYS:HA	79:SZ:107:VAL:HG12	2.01	0.42
83:CA:90:SER:HB3	83:CA:281:ARG:HH12	1.85	0.42
87:CI:524:MET:HB3	87:CI:524:MET:HE3	1.81	0.42
1:L5:1258:G:H2'	1:L5:1259:G:C8	2.54	0.42
1:L5:3615:G:H1'	25:LW:44:ARG:HD3	2.02	0.42
8:LE:72:LYS:HE3	30:Lb:119:CYS:HB3	2.02	0.42
8:LE:161:ARG:O	8:LE:182:ASN:ND2	2.52	0.42
11:LH:20:LEU:HD12	11:LH:47:LEU:HG	2.01	0.42
27:LY:4:ASN:HB3	27:LY:7:VAL:HG22	2.02	0.42
58:SL:29:GLY:HA3	58:SL:30:LYS:HA	1.69	0.42
61:SR:41:ILE:HA	61:SR:42:PRO:HD3	1.90	0.42
65:SV:73:ALA:HB1	65:SV:78:ILE:HB	2.01	0.42
70:Sg:202:PRO:HG2	70:Sg:243:PRO:HA	2.01	0.42
83:CA:45:VAL:HA	83:CA:48:LEU:HD12	2.01	0.42
84:CC:68:C:H2'	84:CC:69:G:H8	1.83	0.42
88:CH:136:LEU:HB2	88:CH:139:LEU:HD22	2.01	0.42
88:CH:311:ALA:O	88:CH:314:MET:C	2.62	0.42
1:L5:153:G:H2'	1:L5:154:G:H8	1.85	0.42
1:L5:2434:G:O2'	1:L5:2527:A:N1	2.52	0.42
1:L5:3910:C:O2'	1:L5:4196:G:N2	2.53	0.42
1:L5:4075:U:OP1	10:LG:249:ARG:NH2	2.52	0.42
5:LB:216:MET:HG2	5:LB:281:ASN:HA	2.00	0.42
14:LL:80:GLU:OE2	14:LL:102:ARG:NH1	2.53	0.42
26:LX:115:LYS:HA	26:LX:115:LYS:HD3	1.81	0.42
49:S2:16:G:H2'	49:S2:17:C:C6	2.55	0.42
49:S2:996:A:H2'	49:S2:997:A:C8	2.55	0.42
51:SB:128:LYS:HA	51:SB:134:LEU:HA	2.02	0.42
67:Sa:44:ILE:HD11	67:Sa:67:LEU:HD13	2.01	0.42
70:Sg:20:GLN:HB3	70:Sg:34:ALA:HB3	2.00	0.42
77:SW:3:ARG:HD3	77:SW:6:VAL:HG12	2.01	0.42
78:SY:26:ASP:OD1	78:SY:26:ASP:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3654:G:O2'	1:L5:3693:U:OP1	2.34	0.42
1:L5:4277:G:H5''	22:LT:17:ARG:HG2	2.02	0.42
14:LL:7:GLY:O	29:La:49:HIS:NE2	2.42	0.42
49:S2:588:G:H4'	49:S2:589:G:H5'	2.01	0.42
49:S2:1217:A:H2'	49:S2:1218:C:H6	1.84	0.42
70:Sg:255:SER:OG	70:Sg:269:GLU:OE2	2.36	0.42
72:SG:75:LEU:HD23	72:SG:75:LEU:HA	1.93	0.42
1:L5:908:G:H2'	1:L5:909:A:H8	1.85	0.42
5:LB:148:LYS:HD3	5:LB:148:LYS:HA	1.86	0.42
7:LD:53:VAL:HG11	7:LD:159:VAL:HA	2.01	0.42
8:LE:91:THR:HA	8:LE:108:LYS:HA	2.01	0.42
49:S2:838:G:O2'	49:S2:840:C:OP2	2.35	0.42
49:S2:1013:U:OP1	49:S2:1129:G:O2'	2.36	0.42
49:S2:1562:C:H4'	63:ST:119:GLY:HA3	2.00	0.42
49:S2:1845:A:H2'	49:S2:1846:G:C8	2.54	0.42
70:Sg:110:SER:OG	70:Sg:111:VAL:N	2.53	0.42
72:SG:78:SER:OG	72:SG:79:LYS:N	2.52	0.42
72:SG:85:ARG:O	72:SG:87:ARG:NH1	2.53	0.42
83:CA:187:SER:HB3	83:CA:201:ILE:HB	2.01	0.42
88:CH:233:LYS:HD2	88:CH:253:LEU:HB3	2.01	0.42
1:L5:1217:G:H2'	1:L5:1218:G:H8	1.85	0.42
1:L5:3961:G:H1'	1:L5:3965:A:N1	2.35	0.42
7:LD:32:ALA:O	7:LD:36:LEU:HB2	2.20	0.42
10:LG:87:LEU:HD13	10:LG:226:TYR:HE2	1.85	0.42
43:Lo:33:LEU:HA	43:Lo:38:LYS:HG2	2.01	0.42
47:Lt:12:VAL:O	47:Lt:64:ILE:HA	2.20	0.42
49:S2:609:U:H2'	49:S2:610:G:H8	1.85	0.42
49:S2:1566:G:OP2	63:ST:102:ARG:NH1	2.52	0.42
49:S2:1598:G:O2'	79:SZ:80:ARG:O	2.32	0.42
64:SU:20:ILE:HA	64:SU:117:ALA:HA	2.01	0.42
77:SW:32:LYS:HA	77:SW:35:VAL:HG22	2.01	0.42
83:CA:50:GLU:HA	83:CA:53:ASP:HB2	2.01	0.42
83:CA:361:SER:OG	83:CA:362:ALA:N	2.53	0.42
88:CH:354:LYS:NZ	88:CH:356:HIS:HB2	2.35	0.42
1:L5:2480:G:H2'	1:L5:2481:G:H8	1.85	0.41
1:L5:5022:U:N3	56:SI:168:GLN:OE1	2.53	0.41
6:LC:228:THR:OG1	6:LC:248:ARG:NH2	2.52	0.41
7:LD:242:LYS:HB2	7:LD:242:LYS:HE3	1.89	0.41
8:LE:254:ASP:HA	8:LE:257:ILE:HG22	2.01	0.41
15:LM:119:ARG:HE	17:LO:193:THR:HG22	1.85	0.41
18:LP:94:MET:HE2	18:LP:94:MET:HB3	1.78	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:LR:116:ASP:OD1	20:LR:116:ASP:N	2.53	0.41
21:LS:5:GLY:O	21:LS:111:ARG:NH1	2.52	0.41
26:LX:73:HIS:HB3	26:LX:116:LEU:HD23	2.02	0.41
29:La:23:GLY:HA3	29:La:24:LYS:HA	1.67	0.41
43:Lo:100:LYS:HB3	43:Lo:100:LYS:HE2	1.86	0.41
45:Lr:56:ASP:OD1	45:Lr:56:ASP:N	2.39	0.41
49:S2:396:U:OP2	58:SL:79:LYS:NZ	2.46	0.41
49:S2:906:U:H2'	49:S2:907:G:C8	2.55	0.41
52:SD:69:LEU:HA	52:SD:72:VAL:HG22	2.02	0.41
54:SF:127:ARG:HD2	54:SF:127:ARG:HA	1.74	0.41
59:SP:111:MET:HA	62:SS:117:ILE:HD11	2.02	0.41
68:Sc:21:THR:OG1	68:Sc:22:GLY:N	2.52	0.41
83:CA:80:ILE:HG12	83:CA:108:ILE:HG22	2.02	0.41
1:L5:364:G:O6	38:Lj:52:LYS:NZ	2.37	0.41
1:L5:1327:C:H2'	1:L5:1328:G:C8	2.55	0.41
1:L5:1339:U:H2'	1:L5:1340:C:C6	2.54	0.41
1:L5:1373:A:H5''	6:LC:44:LEU:HD13	2.02	0.41
1:L5:4954:G:H2'	1:L5:4955:A:H8	1.85	0.41
10:LG:165:GLU:OE1	16:LN:11:TRP:NE1	2.53	0.41
15:LM:41:PRO:HG3	15:LM:73:VAL:HG23	2.02	0.41
15:LM:96:GLU:HA	15:LM:99:GLU:HG2	2.02	0.41
16:LN:34:SER:OG	16:LN:35:ALA:N	2.53	0.41
37:Li:43:MET:HE3	37:Li:43:MET:HB3	1.86	0.41
46:Ls:83:ARG:HD3	46:Ls:83:ARG:HA	1.91	0.41
48:Lz:199:GLN:H	48:Lz:199:GLN:HG3	1.72	0.41
49:S2:821:G:C6	73:SJ:150:ARG:HG3	2.55	0.41
49:S2:878:G:C6	49:S2:908:A:N1	2.88	0.41
49:S2:1674:G:H4'	54:SF:77:MET:HE1	2.02	0.41
50:SA:141:ASN:HD22	65:SV:29:HIS:HA	1.84	0.41
51:SB:185:VAL:O	51:SB:189:ILE:HD12	2.20	0.41
55:SH:69:LEU:O	55:SH:73:GLN:HG2	2.21	0.41
73:SJ:30:LYS:O	73:SJ:34:GLU:HB2	2.20	0.41
83:CA:200:THR:HG1	83:CA:201:ILE:H	1.67	0.41
87:CI:442:VAL:HA	87:CI:446:MET:HB2	2.01	0.41
1:L5:1481:C:O2'	1:L5:1482:G:N3	2.47	0.41
2:L7:77:A:H62	2:L7:99:G:H21	1.69	0.41
4:LA:210:PRO:O	4:LA:221:LYS:NZ	2.47	0.41
5:LB:231:VAL:HG21	5:LB:251:VAL:HG23	2.03	0.41
8:LE:101:ASN:OD1	8:LE:105:ARG:NH2	2.54	0.41
19:LQ:183:SER:OG	19:LQ:184:ARG:NH1	2.53	0.41
49:S2:582:U:O2'	49:S2:583:A:H5''	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:SP:59:ARG:HA	59:SP:62:LYS:HG2	2.01	0.41
73:SJ:78:LEU:HD23	73:SJ:97:ILE:HD11	2.03	0.41
79:SZ:47:LEU:HD23	79:SZ:79:ILE:HD13	2.01	0.41
83:CA:158:LYS:HD2	83:CA:159:PRO:HD2	2.03	0.41
1:L5:1174:G:H22	1:L5:1187:G:H8	1.69	0.41
1:L5:1523:A:N3	1:L5:4389:C:O2'	2.52	0.41
1:L5:1802:A:N3	22:LT:130:ARG:NH1	2.65	0.41
1:L5:3975:C:H5''	1:L5:4031:U:H5'	2.03	0.41
1:L5:4755:G:OP2	8:LE:279:ASN:ND2	2.43	0.41
1:L5:4913:G:C1'	1:L5:4914:C:OP2	2.68	0.41
7:LD:80:ALA:HA	7:LD:83:LEU:HD13	2.02	0.41
14:LL:172:GLU:O	14:LL:175:ASN:O	2.37	0.41
23:LU:35:ASP:N	23:LU:35:ASP:OD1	2.53	0.41
34:Lf:36:ARG:HD2	34:Lf:80:ASN:H	1.85	0.41
38:Lj:25:LYS:HE3	38:Lj:25:LYS:HB3	1.86	0.41
48:Lz:17:VAL:HG11	48:Lz:180:VAL:HG22	2.02	0.41
49:S2:1777:G:H2'	49:S2:1778:C:C6	2.56	0.41
62:SS:89:ASP:HB3	62:SS:93:GLY:H	1.85	0.41
70:Sg:30:MET:HA	70:Sg:43:TRP:O	2.21	0.41
70:Sg:34:ALA:HB2	70:Sg:69:VAL:HG13	2.02	0.41
1:L5:238:C:OP2	27:LY:45:ARG:NH2	2.53	0.41
1:L5:493:G:C6	1:L5:660:A:N1	2.89	0.41
1:L5:2543:A:H2	1:L5:2773:G:H22	1.69	0.41
1:L5:2675:G:N1	31:Lc:33:GLN:OE1	2.46	0.41
25:LW:70:LYS:HA	25:LW:70:LYS:HD3	1.79	0.41
35:Lg:41:ALA:HB3	35:Lg:52:ARG:HB3	2.03	0.41
48:Lz:206:ILE:HG21	48:Lz:214:GLN:H	1.85	0.41
62:SS:67:VAL:HA	62:SS:70:ILE:HG22	2.02	0.41
71:SC:67:GLY:HA2	71:SC:93:ILE:HD11	2.03	0.41
83:CA:23:MET:HE2	83:CA:23:MET:HB2	1.92	0.41
83:CA:259:MET:HE2	83:CA:259:MET:HB3	1.81	0.41
1:L5:441:G:H2'	1:L5:442:G:H8	1.85	0.41
1:L5:4257:A:H2	13:LJ:27:GLY:HA2	1.85	0.41
5:LB:21:ARG:HG2	5:LB:271:GLN:HG2	2.01	0.41
7:LD:55:VAL:HG22	7:LD:60:ILE:HG12	2.01	0.41
12:LI:3:ARG:NH1	12:LI:63:GLU:OE1	2.53	0.41
13:LJ:176:PRO:HG2	13:LJ:178:LYS:HG2	2.02	0.41
17:LO:8:VAL:HG12	17:LO:117:ARG:HG3	2.02	0.41
47:Lt:115:GLN:NE2	47:Lt:126:SER:OG	2.53	0.41
48:Lz:12:GLU:O	48:Lz:217:TYR:N	2.41	0.41
49:S2:581:U:H5'	49:S2:582:U:OP2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:981:A:H2'	49:S2:982:G:C8	2.55	0.41
50:SA:12:GLU:HA	50:SA:15:VAL:HG22	2.01	0.41
53:SE:139:LEU:O	53:SE:146:THR:HA	2.21	0.41
54:SF:112:LEU:HA	54:SF:177:LEU:HD21	2.02	0.41
54:SF:171:GLU:OE2	79:SZ:106:GLN:NE2	2.43	0.41
57:SK:20:VAL:HA	57:SK:69:TRP:O	2.21	0.41
58:SL:152:LYS:HE3	58:SL:152:LYS:HB3	1.90	0.41
61:SR:67:ARG:HA	61:SR:68:GLY:HA3	1.68	0.41
66:SX:68:LYS:HB3	66:SX:91:LEU:HD22	2.01	0.41
72:SG:141:ILE:HD11	72:SG:157:VAL:HA	2.03	0.41
76:SO:34:PHE:HB3	76:SO:41:PHE:HB2	2.02	0.41
87:CI:63:LYS:NZ	88:CH:295:SER:O	2.53	0.41
1:L5:4314:C:O2'	30:Lb:36:ASP:OD1	2.34	0.41
1:L5:5016:A:N1	1:L5:5033:G:C2	2.89	0.41
6:LC:25:PRO:HD2	6:LC:28:PHE:HD2	1.85	0.41
8:LE:105:ARG:HA	8:LE:105:ARG:HD3	1.85	0.41
19:LQ:176:ARG:HB2	29:La:56:VAL:HG21	2.02	0.41
22:LT:12:ARG:O	22:LT:16:SER:HB3	2.20	0.41
26:LX:37:LYS:HA	26:LX:38:LYS:HA	1.73	0.41
50:SA:89:LYS:HD3	50:SA:89:LYS:HA	1.90	0.41
51:SB:29:ASP:OD1	51:SB:29:ASP:N	2.54	0.41
51:SB:149:GLN:HE22	51:SB:154:SER:HB3	1.86	0.41
54:SF:73:THR:HG21	54:SF:90:VAL:HG12	2.02	0.41
54:SF:114:ASN:HA	54:SF:117:ILE:HG12	2.03	0.41
60:SQ:12:VAL:HG21	60:SQ:90:LYS:HB3	2.03	0.41
64:SU:83:ARG:HH21	69:Sd:55:LEU:HD23	1.85	0.41
73:SJ:129:LEU:HG	73:SJ:134:HIS:HB2	2.03	0.41
87:CI:23:GLN:HB3	87:CI:41:VAL:HG21	2.03	0.41
1:L5:943:A:H62	9:LF:151:ASN:HD21	1.68	0.41
7:LD:228:LYS:HA	7:LD:228:LYS:HD2	1.93	0.41
9:LF:35:LYS:HE2	9:LF:35:LYS:HB3	1.92	0.41
48:Lz:23:ARG:NH2	48:Lz:174:MET:O	2.53	0.41
49:S2:65:C:N4	72:SG:134:GLY:O	2.54	0.41
49:S2:1076:G:OP1	75:SN:106:ARG:NH2	2.54	0.41
51:SB:129:THR:OG1	51:SB:179:ASN:O	2.31	0.41
52:SD:101:GLN:HG3	52:SD:126:ILE:HD11	2.02	0.41
70:Sg:181:ASN:HB2	70:Sg:183:LYS:HE2	2.03	0.41
73:SJ:111:GLN:NE2	73:SJ:127:ARG:HB2	2.36	0.41
87:CI:47:ILE:HD12	87:CI:47:ILE:HA	1.90	0.41
1:L5:32:G:H21	1:L5:50:C:H5	1.68	0.41
1:L5:262:G:H2'	1:L5:263:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:730:G:OP2	9:LF:76:ARG:NE	2.44	0.41
1:L5:1197:C:H2'	1:L5:1198:G:C8	2.56	0.41
1:L5:1503:A:H4'	1:L5:1504:G:H5'	2.02	0.41
1:L5:2491:C:O2'	1:L5:2492:C:O4'	2.33	0.41
1:L5:2520:C:H2'	1:L5:2521:G:C8	2.55	0.41
1:L5:2710:C:H5''	83:CA:260:LYS:HE3	2.03	0.41
1:L5:3722:G:H2'	1:L5:3723:A:H8	1.85	0.41
1:L5:3726:A:H2'	1:L5:3727:A:C8	2.55	0.41
1:L5:3951:G:N2	1:L5:4060:U:O2	2.53	0.41
12:LI:56:GLU:HB3	12:LI:58:GLU:HG2	2.02	0.41
14:LL:130:LYS:HA	14:LL:130:LYS:HD2	1.83	0.41
14:LL:204:GLU:OE1	14:LL:205:GLN:NE2	2.54	0.41
25:LW:105:ARG:HH11	72:SG:150:GLU:HG2	1.85	0.41
31:Lc:42:LYS:HE2	31:Lc:42:LYS:HB3	1.95	0.41
34:Lf:45:LYS:HD2	34:Lf:105:LEU:HA	2.02	0.41
35:Lg:63:VAL:HA	35:Lg:66:ARG:HG2	2.03	0.41
47:Lt:30:PRO:HB2	88:CH:314:MET:HE2	2.03	0.41
48:Lz:161:LYS:HD3	84:CC:54:U:H5'	2.03	0.41
48:Lz:208:SER:OG	48:Lz:209:THR:N	2.51	0.41
49:S2:329:G:H2'	49:S2:330:G:C8	2.56	0.41
49:S2:367:U:H4'	49:S2:371:A:C8	2.56	0.41
49:S2:809:A:OP1	53:SE:187:ALA:N	2.53	0.41
50:SA:38:ILE:HA	50:SA:38:ILE:HD13	1.76	0.41
50:SA:207:PRO:HA	50:SA:210:ILE:HG22	2.03	0.41
53:SE:138:HIS:HD2	53:SE:148:ARG:HG2	1.86	0.41
56:SI:113:TYR:OH	56:SI:156:ALA:O	2.38	0.41
59:SP:95:GLY:HA2	59:SP:103:ASN:O	2.20	0.41
62:SS:39:ARG:HH11	63:ST:38:LYS:HB2	1.86	0.41
67:Sa:10:ARG:HB3	67:Sa:34:LYS:HG3	2.02	0.41
70:Sg:126:ASP:OD1	70:Sg:126:ASP:N	2.44	0.41
70:Sg:308:ARG:HD3	70:Sg:308:ARG:HA	1.86	0.41
71:SC:60:TRP:O	71:SC:71:LYS:NZ	2.44	0.41
73:SJ:151:LEU:HD23	73:SJ:151:LEU:HA	1.95	0.41
74:SM:86:GLY:HA3	74:SM:105:GLY:HA3	2.03	0.41
77:SW:80:ASP:OD1	77:SW:80:ASP:N	2.36	0.41
88:CH:63:LYS:HA	88:CH:63:LYS:HD3	1.88	0.41
88:CH:346:LEU:HG	88:CH:354:LYS:HE3	2.03	0.41
1:L5:1195:G:H2'	1:L5:1196:G:C8	2.56	0.41
1:L5:1514:U:H2'	1:L5:1515:A:C8	2.55	0.41
1:L5:2558:C:H2'	1:L5:2559:G:C8	2.56	0.41
1:L5:4635:A:O2'	1:L5:4637:G:OP1	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:Lf:78:HIS:HB2	34:Lf:85:ARG:HG3	2.03	0.41
49:S2:1221:G:O2'	49:S2:1676:U:O2	2.37	0.41
51:SB:65:ARG:H	51:SB:88:THR:HG22	1.86	0.41
62:SS:123:LEU:HD23	62:SS:123:LEU:HA	1.90	0.41
70:Sg:52:TYR:CZ	70:Sg:309:VAL:HG21	2.56	0.41
73:SJ:112:THR:HG22	73:SJ:123:ILE:HD11	2.02	0.41
76:SO:61:LYS:HA	76:SO:61:LYS:HD2	1.90	0.41
80:Sb:24:LEU:HD23	80:Sb:24:LEU:HA	1.89	0.41
83:CA:156:LEU:HB2	83:CA:161:ASN:ND2	2.36	0.41
83:CA:231:SER:OG	83:CA:232:SER:N	2.53	0.41
84:CC:28:C:H2'	84:CC:29:A:H8	1.85	0.41
87:CI:112:ASN:ND2	87:CI:493:ASP:OD1	2.53	0.41
88:CH:224:LEU:HD11	88:CH:246:LEU:HD22	2.03	0.41
1:L5:29:G:H5''	16:LN:172:ARG:HG2	2.03	0.40
1:L5:453:G:N2	1:L5:1293:G:N7	2.60	0.40
1:L5:1646:A:O2'	38:Lj:49:TRP:O	2.31	0.40
1:L5:3732:A:H2'	1:L5:3733:A:C8	2.56	0.40
1:L5:4906:U:H2'	1:L5:4907:G:H8	1.86	0.40
4:LA:47:ASP:HB2	4:LA:60:LYS:HB3	2.03	0.40
10:LG:136:LEU:HD23	10:LG:136:LEU:HA	1.91	0.40
11:LH:85:THR:HG23	11:LH:86:LEU:HG	2.02	0.40
13:LJ:4:ASP:O	13:LJ:8:LYS:HB3	2.21	0.40
31:Lc:47:ILE:HD12	31:Lc:94:LEU:HD11	2.03	0.40
41:Lm:93:LYS:HD3	41:Lm:102:ARG:HG2	2.03	0.40
48:Lz:185:LEU:O	48:Lz:189:PHE:HB2	2.21	0.40
48:Lz:207:LYS:HE2	48:Lz:207:LYS:HB2	1.90	0.40
49:S2:223:C:H2'	49:S2:224:A:C8	2.56	0.40
49:S2:520:A:O2'	49:S2:825:A:N3	2.49	0.40
49:S2:560:A:OP2	73:SJ:177:ASN:ND2	2.50	0.40
49:S2:608:C:H2'	49:S2:609:U:C6	2.57	0.40
49:S2:885:U:H3	49:S2:901:G:H1	1.69	0.40
49:S2:1015:U:O2'	75:SN:55:ARG:NH1	2.54	0.40
54:SF:82:ASN:OD1	54:SF:82:ASN:N	2.51	0.40
60:SQ:12:VAL:O	60:SQ:22:VAL:HA	2.21	0.40
83:CA:162:GLN:HG3	83:CA:164:THR:H	1.86	0.40
1:L5:2297:G:H4'	6:LC:242:PRO:HB2	2.03	0.40
1:L5:4219:A:H2'	1:L5:4220:A:C8	2.57	0.40
1:L5:4751:G:N7	34:Lf:52:LYS:NZ	2.53	0.40
15:LM:15:VAL:HG22	15:LM:50:MET:HE1	2.03	0.40
28:LZ:13:VAL:O	28:LZ:20:GLY:N	2.52	0.40
33:Le:36:ARG:HA	33:Le:36:ARG:HD3	1.93	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:Ls:122:THR:OG1	46:Ls:157:ASP:OD1	2.39	0.40
47:Lt:77:ALA:H	47:Lt:80:LEU:HD11	1.86	0.40
48:Lz:69:GLY:O	48:Lz:71:GLN:N	2.54	0.40
58:SL:76:VAL:HG12	58:SL:125:ILE:HG13	2.02	0.40
67:Sa:33:ASP:OD1	67:Sa:33:ASP:N	2.53	0.40
72:SG:14:LYS:HE3	72:SG:124:LEU:HD12	2.03	0.40
73:SJ:129:LEU:HD21	73:SJ:159:PHE:HE1	1.85	0.40
73:SJ:143:ASN:OD1	73:SJ:143:ASN:N	2.54	0.40
84:CC:20:U:O2'	84:CC:21:A:N7	2.55	0.40
88:CH:34:MET:HE3	88:CH:34:MET:HB3	1.95	0.40
88:CH:228:GLY:O	88:CH:233:LYS:NZ	2.52	0.40
1:L5:73:A:N7	14:LL:103:ARG:NH2	2.69	0.40
1:L5:1198:G:H2'	1:L5:1199:G:C8	2.57	0.40
1:L5:1677:U:H4'	1:L5:1680:G:C2	2.56	0.40
1:L5:2520:C:H2'	1:L5:2521:G:H8	1.86	0.40
1:L5:2583:C:OP2	35:Lg:76:ARG:NH1	2.43	0.40
1:L5:2758:G:O2'	1:L5:2765:A:N3	2.41	0.40
1:L5:4918:C:H2'	1:L5:4919:G:C8	2.57	0.40
21:LS:78:PHE:O	21:LS:96:GLU:HA	2.21	0.40
37:Li:75:LYS:HA	37:Li:75:LYS:HD2	1.85	0.40
48:Lz:85:MET:HE2	48:Lz:85:MET:HB3	1.99	0.40
49:S2:126:G:OP2	72:SG:195:LYS:NZ	2.40	0.40
49:S2:568:C:C4	49:S2:583:A:C5	3.09	0.40
49:S2:1098:C:H2'	49:S2:1099:G:C8	2.57	0.40
49:S2:1221:G:H2'	49:S2:1222:G:C8	2.55	0.40
49:S2:1242:U:O2	49:S2:1517:G:O2'	2.38	0.40
49:S2:1279:C:H2'	49:S2:1280:G:C8	2.56	0.40
49:S2:1562:C:H2'	49:S2:1563:G:C8	2.56	0.40
64:SU:32:LEU:HD12	64:SU:32:LEU:HA	1.93	0.40
71:SC:108:LYS:HB2	71:SC:233:LEU:HD22	2.04	0.40
77:SW:55:ASP:OD1	77:SW:55:ASP:N	2.43	0.40
83:CA:199:LYS:HZ2	83:CA:216:ALA:HB3	1.86	0.40
84:CC:9:A:O2'	84:CC:10:G:N7	2.54	0.40
87:CI:122:ILE:HG23	87:CI:129:PRO:HG3	2.03	0.40
87:CI:128:LYS:NZ	87:CI:138:PRO:O	2.52	0.40
88:CH:346:LEU:HD12	88:CH:350:GLN:HG2	2.03	0.40
1:L5:138:G:H2'	1:L5:139:G:H8	1.87	0.40
1:L5:318:A:H2'	1:L5:319:A:C8	2.57	0.40
1:L5:502:C:H3'	1:L5:503:C:H3'	2.04	0.40
1:L5:1197:C:H2'	1:L5:1198:G:H8	1.87	0.40
1:L5:2081:C:H5''	19:LQ:11:ARG:HG3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:2908:U:O2'	1:L5:3586:G:O6	2.35	0.40
1:L5:3917:A:H2'	1:L5:3918:G:H8	1.86	0.40
1:L5:4293:U:O2'	43:Lo:81:ARG:NH2	2.54	0.40
1:L5:4537:C:H2'	1:L5:4538:G:C8	2.56	0.40
14:LL:83:VAL:HG23	14:LL:114:VAL:HG21	2.02	0.40
47:Lt:117:ARG:O	47:Lt:119:ARG:NH1	2.54	0.40
48:Lz:13:ALA:HA	48:Lz:217:TYR:HB3	2.02	0.40
49:S2:323:C:O2'	49:S2:325:C:N4	2.54	0.40
49:S2:382:C:H2'	49:S2:383:G:H8	1.86	0.40
49:S2:482:G:N1	49:S2:485:A:OP2	2.45	0.40
49:S2:1284:A:H5''	49:S2:1286:G:H5'	2.03	0.40
49:S2:1694:U:O2'	49:S2:1833:C:O2'	2.39	0.40
49:S2:1869:A:H2'	61:SR:135:VAL:HG21	2.04	0.40
51:SB:86:LEU:HD23	51:SB:86:LEU:HA	1.88	0.40
70:Sg:39:THR:HG22	70:Sg:60:ARG:HG2	2.03	0.40
83:CA:107:LYS:HB3	83:CA:124:THR:HG22	2.02	0.40
1:L5:444:G:H2'	1:L5:445:U:C6	2.56	0.40
1:L5:2395:A:HO2'	1:L5:2806:A:HO2'	1.54	0.40
1:L5:2554:U:O2	1:L5:2764:A:N7	2.55	0.40
3:L8:123:U:O2'	3:L8:126:C:N4	2.55	0.40
7:LD:232:THR:OG1	7:LD:234:ASP:O	2.36	0.40
10:LG:232:GLU:O	10:LG:236:HIS:HB2	2.21	0.40
10:LG:252:LYS:HB3	10:LG:252:LYS:HE2	1.80	0.40
35:Lg:100:GLN:HA	35:Lg:103:VAL:HG12	2.03	0.40
43:Lo:82:MET:HE3	43:Lo:82:MET:HB3	2.01	0.40
47:Lt:41:LYS:HA	47:Lt:41:LYS:HD2	1.92	0.40
49:S2:4:C:H4'	71:SC:207:ALA:HB2	2.04	0.40
49:S2:51:U:H2'	49:S2:52:G:C8	2.57	0.40
49:S2:118:C:H1'	49:S2:445:A:C5	2.56	0.40
49:S2:160:U:O2'	49:S2:162:C:OP2	2.33	0.40
49:S2:194:C:H2'	49:S2:195:C:H6	1.86	0.40
49:S2:329:G:H2'	49:S2:330:G:H8	1.86	0.40
49:S2:383:G:O2'	58:SL:133:PRO:O	2.36	0.40
49:S2:495:U:O2'	53:SE:27:PHE:O	2.34	0.40
49:S2:567:C:H1'	49:S2:583:A:N6	2.36	0.40
49:S2:1232:U:H2'	49:S2:1233:G:H8	1.86	0.40
49:S2:1438:A:H2'	49:S2:1439:A:C8	2.56	0.40
50:SA:52:LYS:O	50:SA:56:GLU:HG2	2.21	0.40
59:SP:130:ARG:HA	59:SP:131:PRO:HD3	1.98	0.40
76:SO:40:THR:HG21	76:SO:74:ALA:HB2	2.04	0.40
88:CH:188:LEU:O	88:CH:188:LEU:CD1	2.70	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%)	223 (91%)	22 (9%)	1 (0%)	30	65
5	LB	400/403 (99%)	374 (94%)	25 (6%)	1 (0%)	36	70
6	LC	366/427 (86%)	337 (92%)	29 (8%)	0	100	100
7	LD	291/297 (98%)	266 (91%)	25 (9%)	0	100	100
8	LE	232/288 (81%)	212 (91%)	20 (9%)	0	100	100
9	LF	223/248 (90%)	216 (97%)	7 (3%)	0	100	100
10	LG	239/266 (90%)	223 (93%)	16 (7%)	0	100	100
11	LH	188/192 (98%)	172 (92%)	16 (8%)	0	100	100
12	LI	198/214 (92%)	182 (92%)	16 (8%)	0	100	100
13	LJ	174/178 (98%)	154 (88%)	20 (12%)	0	100	100
14	LL	208/211 (99%)	190 (91%)	18 (9%)	0	100	100
15	LM	137/215 (64%)	125 (91%)	11 (8%)	1 (1%)	18	53
16	LN	201/204 (98%)	191 (95%)	8 (4%)	2 (1%)	12	45
17	LO	199/203 (98%)	186 (94%)	13 (6%)	0	100	100
18	LP	151/184 (82%)	141 (93%)	10 (7%)	0	100	100
19	LQ	185/188 (98%)	175 (95%)	10 (5%)	0	100	100
20	LR	185/196 (94%)	176 (95%)	9 (5%)	0	100	100
21	LS	173/176 (98%)	163 (94%)	10 (6%)	0	100	100
22	LT	157/160 (98%)	146 (93%)	11 (7%)	0	100	100
23	LU	99/128 (77%)	84 (85%)	13 (13%)	2 (2%)	6	28
24	LV	129/140 (92%)	120 (93%)	9 (7%)	0	100	100
25	LW	122/157 (78%)	113 (93%)	9 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	LX	118/156 (76%)	113 (96%)	5 (4%)	0	100	100
27	LY	132/145 (91%)	123 (93%)	9 (7%)	0	100	100
28	LZ	133/136 (98%)	124 (93%)	9 (7%)	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%)	97 (92%)	8 (8%)	0	100	100
33	Le	126/135 (93%)	117 (93%)	9 (7%)	0	100	100
34	Lf	107/110 (97%)	97 (91%)	8 (8%)	2 (2%)	6	30
35	Lg	112/117 (96%)	110 (98%)	2 (2%)	0	100	100
36	Lh	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
37	Li	100/105 (95%)	96 (96%)	4 (4%)	0	100	100
38	Lj	84/97 (87%)	76 (90%)	8 (10%)	0	100	100
39	Lk	67/70 (96%)	63 (94%)	4 (6%)	0	100	100
40	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
41	Lm	50/128 (39%)	49 (98%)	1 (2%)	0	100	100
42	Ln	22/25 (88%)	22 (100%)	0	0	100	100
43	Lo	103/106 (97%)	97 (94%)	6 (6%)	0	100	100
44	Lp	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
45	Lr	123/137 (90%)	114 (93%)	9 (7%)	0	100	100
46	Ls	194/317 (61%)	173 (89%)	20 (10%)	1 (0%)	24	60
47	Lt	137/165 (83%)	107 (78%)	27 (20%)	3 (2%)	5	26
48	Lz	215/217 (99%)	159 (74%)	56 (26%)	0	100	100
50	SA	219/295 (74%)	194 (89%)	24 (11%)	1 (0%)	24	60
51	SB	212/264 (80%)	199 (94%)	13 (6%)	0	100	100
52	SD	225/243 (93%)	200 (89%)	25 (11%)	0	100	100
53	SE	260/263 (99%)	242 (93%)	18 (7%)	0	100	100
54	SF	180/204 (88%)	163 (91%)	17 (9%)	0	100	100
55	SH	182/194 (94%)	157 (86%)	25 (14%)	0	100	100
56	SI	204/208 (98%)	194 (95%)	10 (5%)	0	100	100
57	SK	96/165 (58%)	86 (90%)	10 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
58	SL	151/158 (96%)	140 (93%)	11 (7%)	0	100	100
59	SP	127/145 (88%)	116 (91%)	11 (9%)	0	100	100
60	SQ	142/146 (97%)	124 (87%)	17 (12%)	1 (1%)	18	53
61	SR	133/135 (98%)	117 (88%)	16 (12%)	0	100	100
62	SS	143/152 (94%)	132 (92%)	11 (8%)	0	100	100
63	ST	141/145 (97%)	129 (92%)	11 (8%)	1 (1%)	18	53
64	SU	102/119 (86%)	89 (87%)	13 (13%)	0	100	100
65	SV	81/83 (98%)	72 (89%)	8 (10%)	1 (1%)	10	40
66	SX	139/143 (97%)	130 (94%)	7 (5%)	2 (1%)	9	36
67	Sa	100/115 (87%)	90 (90%)	9 (9%)	1 (1%)	12	45
68	Sc	62/69 (90%)	49 (79%)	12 (19%)	1 (2%)	7	34
69	Sd	53/56 (95%)	48 (91%)	5 (9%)	0	100	100
70	Sg	311/317 (98%)	269 (86%)	41 (13%)	1 (0%)	36	70
71	SC	220/293 (75%)	206 (94%)	14 (6%)	0	100	100
72	SG	235/249 (94%)	219 (93%)	16 (7%)	0	100	100
73	SJ	183/194 (94%)	171 (93%)	12 (7%)	0	100	100
74	SM	120/132 (91%)	109 (91%)	11 (9%)	0	100	100
75	SN	148/151 (98%)	141 (95%)	7 (5%)	0	100	100
76	SO	138/151 (91%)	126 (91%)	11 (8%)	1 (1%)	18	53
77	SW	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
78	SY	129/133 (97%)	122 (95%)	7 (5%)	0	100	100
79	SZ	73/125 (58%)	59 (81%)	13 (18%)	1 (1%)	9	36
80	Sb	81/84 (96%)	72 (89%)	9 (11%)	0	100	100
81	Se	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
82	Sf	65/156 (42%)	54 (83%)	11 (17%)	0	100	100
83	CA	350/394 (89%)	331 (95%)	18 (5%)	1 (0%)	36	70
85	CE	113/223 (51%)	109 (96%)	4 (4%)	0	100	100
86	CF	27/180 (15%)	26 (96%)	1 (4%)	0	100	100
87	CI	578/599 (96%)	537 (93%)	39 (7%)	2 (0%)	36	70
88	CH	413/437 (94%)	388 (94%)	24 (6%)	1 (0%)	43	76
All	All	13353/15220 (88%)	12258 (92%)	1067 (8%)	28 (0%)	44	76

All (28) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	LN	124	ASP
66	SX	127	ASN
15	LM	88	ALA
23	LU	59	GLY
47	Lt	10	ILE
47	Lt	148	PRO
63	ST	41	LYS
67	Sa	47	ALA
79	SZ	45	ASN
83	CA	83	ASN
34	Lf	80	ASN
46	Ls	150	GLY
47	Lt	147	HIS
66	SX	126	ALA
76	SO	140	THR
4	LA	55	GLY
5	LB	302	ASN
50	SA	12	GLU
68	Sc	64	GLU
87	CI	43	PRO
34	Lf	107	PRO
70	Sg	246	TYR
16	LN	83	LYS
23	LU	67	LYS
60	SQ	44	PRO
88	CH	41	PRO
65	SV	79	VAL
87	CI	237	ILE

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	79
5	LB	348/349 (100%)	348 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	LC	306/348 (88%)	303 (99%)	3 (1%)	68	84
7	LD	246/250 (98%)	246 (100%)	0	100	100
8	LE	209/252 (83%)	208 (100%)	1 (0%)	81	89
9	LF	194/215 (90%)	194 (100%)	0	100	100
10	LG	203/223 (91%)	202 (100%)	1 (0%)	81	89
11	LH	169/171 (99%)	168 (99%)	1 (1%)	78	88
12	LI	172/181 (95%)	172 (100%)	0	100	100
13	LJ	148/149 (99%)	148 (100%)	0	100	100
14	LL	176/177 (99%)	176 (100%)	0	100	100
15	LM	118/161 (73%)	117 (99%)	1 (1%)	73	86
16	LN	171/172 (99%)	171 (100%)	0	100	100
17	LO	173/174 (99%)	171 (99%)	2 (1%)	63	82
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	88
21	LS	156/157 (99%)	155 (99%)	1 (1%)	78	88
22	LT	139/140 (99%)	138 (99%)	1 (1%)	76	86
23	LU	91/115 (79%)	90 (99%)	1 (1%)	65	83
24	LV	101/107 (94%)	99 (98%)	2 (2%)	48	76
25	LW	103/126 (82%)	103 (100%)	0	100	100
26	LX	108/133 (81%)	108 (100%)	0	100	100
27	LY	124/135 (92%)	123 (99%)	1 (1%)	73	86
28	LZ	117/118 (99%)	116 (99%)	1 (1%)	70	85
29	La	120/121 (99%)	119 (99%)	1 (1%)	73	86
30	Lb	88/126 (70%)	87 (99%)	1 (1%)	65	83
31	Lc	83/97 (86%)	82 (99%)	1 (1%)	63	82
32	Ld	98/110 (89%)	98 (100%)	0	100	100
33	Le	114/121 (94%)	114 (100%)	0	100	100
34	Lf	88/89 (99%)	87 (99%)	1 (1%)	65	83
35	Lg	98/100 (98%)	98 (100%)	0	100	100
36	Lh	109/110 (99%)	109 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	Li	86/89 (97%)	85 (99%)	1 (1%)	63	82
38	Lj	73/80 (91%)	73 (100%)	0	100	100
39	Lk	64/65 (98%)	63 (98%)	1 (2%)	55	79
40	Ll	47/48 (98%)	47 (100%)	0	100	100
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	83
44	Lp	74/75 (99%)	74 (100%)	0	100	100
45	Lr	109/121 (90%)	109 (100%)	0	100	100
46	Ls	162/258 (63%)	159 (98%)	3 (2%)	50	76
47	Lt	112/137 (82%)	109 (97%)	3 (3%)	39	71
48	Lz	195/196 (100%)	194 (100%)	1 (0%)	81	89
50	SA	183/243 (75%)	180 (98%)	3 (2%)	55	79
51	SB	195/231 (84%)	194 (100%)	1 (0%)	81	89
52	SD	190/202 (94%)	188 (99%)	2 (1%)	65	83
53	SE	224/225 (100%)	222 (99%)	2 (1%)	70	85
54	SF	156/170 (92%)	156 (100%)	0	100	100
55	SH	166/174 (95%)	166 (100%)	0	100	100
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%)	114 (99%)	1 (1%)	70	85
60	SQ	119/121 (98%)	117 (98%)	2 (2%)	53	78
61	SR	122/122 (100%)	121 (99%)	1 (1%)	73	86
62	SS	126/132 (96%)	125 (99%)	1 (1%)	73	86
63	ST	113/115 (98%)	113 (100%)	0	100	100
64	SU	94/107 (88%)	92 (98%)	2 (2%)	47	75
65	SV	67/67 (100%)	67 (100%)	0	100	100
66	SX	113/115 (98%)	112 (99%)	1 (1%)	70	85
67	Sa	89/98 (91%)	89 (100%)	0	100	100
68	Sc	57/62 (92%)	57 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	Sd	48/49 (98%)	48 (100%)	0	100	100
70	Sg	272/275 (99%)	268 (98%)	4 (2%)	57	80
71	SC	188/225 (84%)	188 (100%)	0	100	100
72	SG	207/218 (95%)	205 (99%)	2 (1%)	68	84
73	SJ	161/168 (96%)	160 (99%)	1 (1%)	78	88
74	SM	102/108 (94%)	99 (97%)	3 (3%)	37	70
75	SN	130/131 (99%)	129 (99%)	1 (1%)	73	86
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	85
79	SZ	66/103 (64%)	65 (98%)	1 (2%)	57	80
80	Sb	75/76 (99%)	74 (99%)	1 (1%)	61	81
81	Se	42/48 (88%)	42 (100%)	0	100	100
82	Sf	60/140 (43%)	59 (98%)	1 (2%)	53	78
83	CA	303/336 (90%)	303 (100%)	0	100	100
85	CE	104/190 (55%)	103 (99%)	1 (1%)	68	84
86	CF	26/151 (17%)	26 (100%)	0	100	100
87	CI	511/526 (97%)	510 (100%)	1 (0%)	87	92
88	CH	353/376 (94%)	351 (99%)	2 (1%)	78	88
All	All	11626/12971 (90%)	11557 (99%)	69 (1%)	76	88

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	LA	45	VAL
4	LA	207	VAL
4	LA	249	THR
6	LC	158	VAL
6	LC	257	PHE
6	LC	266	THR
8	LE	106	VAL
10	LG	115	LEU
11	LH	187	VAL
15	LM	38	VAL
17	LO	6	VAL

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Mol	Chain	Res	Type
17	LO	27	VAL
20	LR	175	GLU
21	LS	90	THR
22	LT	118	GLU
23	LU	45	GLU
24	LV	22	VAL
24	LV	65	VAL
27	LY	55	VAL
28	LZ	74	VAL
29	La	76	ASP
30	Lb	76	VAL
31	Lc	35	LEU
34	Lf	33	VAL
37	Li	34	THR
39	Lk	66	VAL
43	Lo	103	VAL
46	Ls	21	LEU
46	Ls	82	ILE
46	Ls	174	LEU
47	Lt	58	ILE
47	Lt	111	ASN
47	Lt	129	ILE
48	Lz	17	VAL
50	SA	8	LEU
50	SA	206	ASP
50	SA	211	GLU
51	SB	189	ILE
52	SD	16	ILE
52	SD	162	ASP
53	SE	69	PHE
53	SE	208	VAL
59	SP	25	LEU
60	SQ	22	VAL
60	SQ	113	ILE
61	SR	104	GLU
62	SS	4	VAL
64	SU	22	ILE
64	SU	45	GLU
66	SX	13	LEU
70	Sg	18	VAL
70	Sg	102	VAL
70	Sg	151	VAL

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Mol	Chain	Res	Type
70	Sg	186	THR
72	SG	213	LEU
72	SG	228	ILE
73	SJ	137	VAL
74	SM	66	GLU
74	SM	77	ILE
74	SM	79	VAL
75	SN	60	VAL
78	SY	27	VAL
79	SZ	75	GLU
80	Sb	34	ASP
82	Sf	91	ASN
85	CE	33	GLU
87	CI	173	VAL
88	CH	186	SER
88	CH	188	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (198) such sidechains are listed below:

Mol	Chain	Res	Type
4	LA	83	HIS
4	LA	132	ASN
4	LA	205	ASN
5	LB	138	GLN
5	LB	208	ASN
5	LB	245	HIS
5	LB	258	HIS
5	LB	301	ASN
6	LC	43	ASN
6	LC	60	HIS
6	LC	89	GLN
6	LC	223	ASN
6	LC	231	ASN
6	LC	317	ASN
6	LC	329	ASN
7	LD	111	ASN
7	LD	122	GLN
7	LD	202	GLN
7	LD	275	GLN
8	LE	191	GLN
8	LE	245	GLN
8	LE	266	GLN

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Mol	Chain	Res	Type
9	LF	24	ASN
9	LF	80	ASN
9	LF	205	ASN
10	LG	149	ASN
10	LG	153	GLN
10	LG	236	HIS
11	LH	8	GLN
12	LI	73	ASN
12	LI	203	HIS
14	LL	175	ASN
14	LL	205	GLN
15	LM	48	GLN
15	LM	56	GLN
16	LN	109	HIS
16	LN	149	GLN
16	LN	158	HIS
16	LN	196	ASN
17	LO	184	ASN
18	LP	25	HIS
18	LP	34	GLN
18	LP	56	GLN
18	LP	80	GLN
18	LP	97	ASN
18	LP	116	HIS
19	LQ	7	HIS
19	LQ	21	GLN
19	LQ	188	ASN
20	LR	34	ASN
20	LR	86	ASN
20	LR	178	GLN
22	LT	66	ASN
22	LT	95	HIS
22	LT	131	GLN
23	LU	94	ASN
25	LW	17	HIS
25	LW	95	ASN
27	LY	14	ASN
28	LZ	127	ASN
29	La	66	ASN
29	La	67	GLN
29	La	89	ASN
30	Lb	6	ASN

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Mol	Chain	Res	Type
30	Lb	17	HIS
31	Lc	15	ASN
32	Ld	121	ASN
33	Le	34	ASN
33	Le	107	ASN
34	Lf	56	ASN
34	Lf	80	ASN
34	Lf	99	HIS
35	Lg	28	ASN
36	Lh	101	ASN
37	Li	12	ASN
37	Li	80	HIS
38	Lj	13	ASN
38	Lj	30	GLN
38	Lj	76	HIS
41	Lm	104	HIS
41	Lm	117	HIS
43	Lo	45	GLN
43	Lo	51	GLN
45	Lr	4	HIS
45	Lr	31	ASN
45	Lr	83	ASN
45	Lr	100	ASN
46	Ls	139	GLN
46	Ls	159	GLN
46	Ls	176	ASN
46	Ls	195	ASN
47	Lt	70	GLN
47	Lt	115	GLN
47	Lt	142	ASN
47	Lt	156	ASN
48	Lz	21	ASN
48	Lz	40	ASN
48	Lz	44	GLN
48	Lz	129	ASN
48	Lz	158	GLN
48	Lz	182	ASN
48	Lz	200	ASN
50	SA	9	GLN
50	SA	113	GLN
50	SA	141	ASN
51	SB	147	ASN

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Mol	Chain	Res	Type
51	SB	149	GLN
51	SB	179	ASN
51	SB	202	GLN
52	SD	159	HIS
53	SE	98	ASN
53	SE	138	HIS
53	SE	157	ASN
53	SE	188	ASN
53	SE	260	GLN
54	SF	29	GLN
54	SF	148	ASN
55	SH	157	HIS
55	SH	186	ASN
56	SI	87	ASN
56	SI	146	GLN
56	SI	165	GLN
57	SK	50	GLN
57	SK	73	ASN
58	SL	11	GLN
58	SL	19	ASN
58	SL	83	GLN
58	SL	94	HIS
59	SP	104	GLN
60	SQ	86	GLN
61	SR	48	ASN
61	SR	118	GLN
62	SS	76	GLN
62	SS	105	ASN
63	ST	12	GLN
63	ST	128	GLN
64	SU	47	ASN
64	SU	85	HIS
65	SV	82	ASN
66	SX	23	HIS
66	SX	61	GLN
66	SX	77	ASN
67	Sa	72	HIS
69	Sd	16	GLN
69	Sd	37	ASN
70	Sg	4	GLN
70	Sg	14	HIS
70	Sg	51	ASN

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Mol	Chain	Res	Type
70	Sg	143	GLN
70	Sg	178	ASN
70	Sg	215	GLN
71	SC	277	HIS
72	SG	13	GLN
72	SG	81	HIS
72	SG	110	ASN
72	SG	225	GLN
73	SJ	75	ASN
74	SM	119	GLN
75	SN	90	HIS
75	SN	105	ASN
76	SO	32	HIS
78	SY	89	HIS
78	SY	112	ASN
79	SZ	46	ASN
79	SZ	64	ASN
80	Sb	9	HIS
80	Sb	26	GLN
80	Sb	65	GLN
82	Sf	139	HIS
83	CA	10	GLN
83	CA	131[B]	GLN
83	CA	134	GLN
83	CA	193	HIS
83	CA	209	GLN
83	CA	359	GLN
85	CE	45	HIS
85	CE	180	GLN
85	CE	188	ASN
87	CI	85	HIS
87	CI	112	ASN
87	CI	251	GLN
87	CI	414	GLN
87	CI	440	GLN
87	CI	460	GLN
87	CI	520	HIS
87	CI	546	ASN
87	CI	556	ASN
87	CI	561	GLN
88	CH	11	ASN
88	CH	121	ASN

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Mol	Chain	Res	Type
88	CH	129	ASN
88	CH	162	GLN
88	CH	247	GLN
88	CH	265	ASN
88	CH	277	ASN
88	CH	364	GLN
88	CH	380	ASN
88	CH	381	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3705/5066 (73%)	903 (24%)	20 (0%)
2	L7	119/121 (98%)	9 (7%)	0
3	L8	155/157 (98%)	27 (17%)	0
49	S2	1715/1869 (91%)	402 (23%)	12 (0%)
84	CC	74/75 (98%)	26 (35%)	2 (2%)
All	All	5768/7288 (79%)	1367 (23%)	34 (0%)

All (1367) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	17	A
1	L5	25	A
1	L5	26	C
1	L5	30	C
1	L5	39	A
1	L5	42	A
1	L5	48	G
1	L5	56	A
1	L5	59	A
1	L5	64	A
1	L5	65	A
1	L5	66	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

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Mol	Chain	Res	Type
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	150	U
1	L5	152	U
1	L5	159	C
1	L5	165	A
1	L5	166	C
1	L5	172	C
1	L5	182	G
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	209	U
1	L5	210	C
1	L5	218	A
1	L5	225	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
1	L5	265	C
1	L5	266	C
1	L5	267	G
1	L5	269	G
1	L5	280	G
1	L5	297	U
1	L5	306	A

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Mol	Chain	Res	Type
1	L5	310	G
1	L5	315	G
1	L5	316	U
1	L5	340	C
1	L5	349	A
1	L5	350	C
1	L5	363	A
1	L5	373	G
1	L5	387	G
1	L5	388	A
1	L5	398	A
1	L5	407	A
1	L5	408	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	436	C
1	L5	440	U
1	L5	449	C
1	L5	450	G
1	L5	452	A
1	L5	453	G
1	L5	454	U
1	L5	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
1	L5	497	G
1	L5	498	C
1	L5	499	G
1	L5	500	G

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Mol	Chain	Res	Type
1	L5	502	C
1	L5	503	C
1	L5	504	G
1	L5	505	G
1	L5	506	C
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	517	C
1	L5	518	G
1	L5	643	C
1	L5	656	C
1	L5	657	C
1	L5	658	C
1	L5	659	G
1	L5	660	A
1	L5	665	C
1	L5	666	G
1	L5	667	A
1	L5	668	C
1	L5	672	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	706	C
1	L5	708	G
1	L5	731	G
1	L5	738	C
1	L5	739	G
1	L5	742	G
1	L5	746	A
1	L5	753	C
1	L5	758	G
1	L5	904	C

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Mol	Chain	Res	Type
1	L5	907	C
1	L5	910	G
1	L5	913	U
1	L5	914	U
1	L5	915	A
1	L5	917	A
1	L5	918	G
1	L5	923	C
1	L5	924	C
1	L5	926	G
1	L5	932	A
1	L5	933	G
1	L5	935	A
1	L5	936	C
1	L5	943	A
1	L5	945	U
1	L5	946	C
1	L5	956	A
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	968	C
1	L5	969	C
1	L5	970	G
1	L5	971	U
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
1	L5	1050	C
1	L5	1051	G

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Mol	Chain	Res	Type
1	L5	1070	G
1	L5	1072	C
1	L5	1075	G
1	L5	1082	C
1	L5	1083	U
1	L5	1095	A
1	L5	1168	G
1	L5	1169	G
1	L5	1171	G
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	1200	G
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	1217	G
1	L5	1218	G
1	L5	1219	G
1	L5	1222	A
1	L5	1235	G
1	L5	1241	C
1	L5	1242	G
1	L5	1246	G
1	L5	1247	U
1	L5	1253	G
1	L5	1254	A
1	L5	1257	A
1	L5	1258	G
1	L5	1261	G
1	L5	1262	G
1	L5	1266	G
1	L5	1267	C
1	L5	1269	G

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Mol	Chain	Res	Type
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	1293	G
1	L5	1294	A
1	L5	1295	C
1	L5	1296	G
1	L5	1301	C
1	L5	1302	U
1	L5	1303	A
1	L5	1312	A
1	L5	1314	C
1	L5	1324	A
1	L5	1326	A
1	L5	1337	A
1	L5	1354	A
1	L5	1358	G
1	L5	1359	G
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	1405	C
1	L5	1407	C
1	L5	1409	C
1	L5	1410	U
1	L5	1414	C
1	L5	1417	C
1	L5	1420	A
1	L5	1425	G

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Mol	Chain	Res	Type
1	L5	1435	G
1	L5	1437	C
1	L5	1439	C
1	L5	1443	A
1	L5	1444	G
1	L5	1446	C
1	L5	1447	C
1	L5	1457	G
1	L5	1482	G
1	L5	1483	C
1	L5	1486	C
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	1563	A
1	L5	1566	C
1	L5	1578	U
1	L5	1582	U
1	L5	1591	U
1	L5	1596	U
1	L5	1624	G
1	L5	1625	G
1	L5	1631	A
1	L5	1633	G
1	L5	1634	A
1	L5	1638	A
1	L5	1640	C
1	L5	1641	G
1	L5	1654	G
1	L5	1660	U
1	L5	1661	C
1	L5	1676	C
1	L5	1677	U
1	L5	1678	C
1	L5	1679	A
1	L5	1691	G

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Mol	Chain	Res	Type
1	L5	1697	G
1	L5	1698	C
1	L5	1699	A
1	L5	1700	G
1	L5	1701	A
1	L5	1703	C
1	L5	1704	C
1	L5	1705	G
1	L5	1707	C
1	L5	1715	C
1	L5	1716	G
1	L5	1726	U
1	L5	1731	C
1	L5	1734	G
1	L5	1735	U
1	L5	1741	G
1	L5	1742	A
1	L5	1753	G
1	L5	1755	C
1	L5	1756	U
1	L5	1757	U
1	L5	1758	G
1	L5	1759	G
1	L5	1760	G
1	L5	1761	G
1	L5	1762	C
1	L5	1763	C
1	L5	1764	G
1	L5	1765	A
1	L5	1766	A
1	L5	1768	C
1	L5	1769	G
1	L5	1770	A
1	L5	1771	U
1	L5	1775	A
1	L5	1787	A
1	L5	1792	U
1	L5	1797	G
1	L5	1804	A
1	L5	1806	G
1	L5	1810	G
1	L5	1815	G

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Mol	Chain	Res	Type
1	L5	1820	C
1	L5	1821	G
1	L5	1822	U
1	L5	1834	U
1	L5	1836	G
1	L5	1837	A
1	L5	1842	G
1	L5	1843	A
1	L5	1855	G
1	L5	1869	G
1	L5	1882	U
1	L5	1893	C
1	L5	1897	A
1	L5	1917	A
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	1946	G
1	L5	1948	G
1	L5	1949	U
1	L5	1951	G
1	L5	1959	U
1	L5	1961	G
1	L5	1962	A
1	L5	1971	C
1	L5	1972	G
1	L5	1974	U
1	L5	1975	G
1	L5	1978	C
1	L5	1980	U
1	L5	1981	G
1	L5	1983	A
1	L5	1984	A
1	L5	1985	G
1	L5	1987	C

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Mol	Chain	Res	Type
1	L5	1991	A
1	L5	1992	U
1	L5	1993	C
1	L5	1997	U
1	L5	1999	A
1	L5	2002	A
1	L5	2005	G
1	L5	2017	A
1	L5	2018	C
1	L5	2024	G
1	L5	2026	A
1	L5	2034	G
1	L5	2044	U
1	L5	2046	G
1	L5	2048	U
1	L5	2052	G
1	L5	2055	G
1	L5	2056	G
1	L5	2069	A
1	L5	2084	C
1	L5	2085	G
1	L5	2089	G
1	L5	2090	U
1	L5	2091	C
1	L5	2092	G
1	L5	2093	A
1	L5	2094	G
1	L5	2095	A
1	L5	2096	G
1	L5	2097	U
1	L5	2098	G
1	L5	2100	A
1	L5	2101	C
1	L5	2102	G
1	L5	2108	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

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Mol	Chain	Res	Type
1	L5	2258	C
1	L5	2260	C
1	L5	2262	G
1	L5	2289	C
1	L5	2300	A
1	L5	2301	G
1	L5	2306	G
1	L5	2313	A
1	L5	2322	G
1	L5	2331	G
1	L5	2332	A
1	L5	2333	G
1	L5	2348	G
1	L5	2351	C
1	L5	2357	G
1	L5	2360	A
1	L5	2369	U
1	L5	2395	A
1	L5	2397	G
1	L5	2408	U
1	L5	2417	A
1	L5	2418	A
1	L5	2421	G
1	L5	2425	U
1	L5	2436	U
1	L5	2441	C
1	L5	2460	A
1	L5	2464	C
1	L5	2465	C
1	L5	2467	U
1	L5	2471	G
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

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Mol	Chain	Res	Type
1	L5	2491	C
1	L5	2494	U
1	L5	2503	G
1	L5	2504	C
1	L5	2505	C
1	L5	2506	G
1	L5	2511	A
1	L5	2513	A
1	L5	2514	G
1	L5	2519	U
1	L5	2520	C
1	L5	2529	A
1	L5	2537	A
1	L5	2544	G
1	L5	2546	G
1	L5	2547	G
1	L5	2554	U
1	L5	2555	G
1	L5	2559	G
1	L5	2560	C
1	L5	2573	A
1	L5	2583	C
1	L5	2587	A
1	L5	2589	C
1	L5	2601	A
1	L5	2603	C
1	L5	2611	A
1	L5	2627	C
1	L5	2638	G
1	L5	2652	G
1	L5	2653	C
1	L5	2661	U
1	L5	2662	G
1	L5	2669	C
1	L5	2670	C
1	L5	2676	A
1	L5	2687	U
1	L5	2694	G
1	L5	2695	A
1	L5	2696	A
1	L5	2703	G
1	L5	2707	U

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Mol	Chain	Res	Type
1	L5	2708	U
1	L5	2709	C
1	L5	2710	C
1	L5	2711	G
1	L5	2719	C
1	L5	2723	U
1	L5	2724	G
1	L5	2726	G
1	L5	2739	C
1	L5	2742	G
1	L5	2743	A
1	L5	2756	G
1	L5	2759	G
1	L5	2761	U
1	L5	2763	U
1	L5	2764	A
1	L5	2769	U
1	L5	2770	C
1	L5	2787	A
1	L5	2788	U
1	L5	2790	U
1	L5	2826	U
1	L5	2827	G
1	L5	2835	A
1	L5	2838	G
1	L5	2848	G
1	L5	2855	G
1	L5	2877	G
1	L5	2892	C
1	L5	2894	A
1	L5	2900	U
1	L5	2902	G
1	L5	2903	G
1	L5	2904	U
1	L5	2905	C
1	L5	2906	G
1	L5	2907	G
1	L5	2908	U
1	L5	3585	G
1	L5	3586	G
1	L5	3587	C
1	L5	3590	G

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Mol	Chain	Res	Type
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	3606	U
1	L5	3615	G
1	L5	3616	U
1	L5	3618	C
1	L5	3626	G
1	L5	3630	A
1	L5	3635	A
1	L5	3644	U
1	L5	3646	A
1	L5	3648	A
1	L5	3662	A
1	L5	3664	G
1	L5	3673	C
1	L5	3674	G
1	L5	3680	U
1	L5	3691	G
1	L5	3692	A
1	L5	3711	A
1	L5	3713	U
1	L5	3714	G
1	L5	3726	A
1	L5	3727	A
1	L5	3729	U
1	L5	3735	G
1	L5	3736	A
1	L5	3747	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

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Mol	Chain	Res	Type
1	L5	3775	A
1	L5	3776	G
1	L5	3777	G
1	L5	3783	A
1	L5	3784	A
1	L5	3786	U
1	L5	3790	U
1	L5	3802	U
1	L5	3810	C
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	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
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	3905	A
1	L5	3906	A
1	L5	3907	G
1	L5	3908	A
1	L5	3915	U
1	L5	3938	G
1	L5	3939	G
1	L5	3942	A
1	L5	3943	A
1	L5	3947	A
1	L5	3948	C
1	L5	3950	U
1	L5	3953	G
1	L5	3955	G

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Mol	Chain	Res	Type
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	3967	G
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	4036	G
1	L5	4038	C
1	L5	4039	G
1	L5	4041	C
1	L5	4042	G
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	4054	C
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

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Mol	Chain	Res	Type
1	L5	4086	G
1	L5	4092	G
1	L5	4095	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
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	4157	A
1	L5	4160	C
1	L5	4162	C
1	L5	4163	U
1	L5	4168	G
1	L5	4170	A
1	L5	4183	G
1	L5	4184	G
1	L5	4191	G
1	L5	4196	G
1	L5	4197	G
1	L5	4203	A
1	L5	4220	A
1	L5	4222	G

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Mol	Chain	Res	Type
1	L5	4225	G
1	L5	4228	G
1	L5	4229	U
1	L5	4233	A
1	L5	4238	G
1	L5	4251	A
1	L5	4254	G
1	L5	4255	A
1	L5	4256	A
1	L5	4265	U
1	L5	4268	A
1	L5	4273	A
1	L5	4281	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
1	L5	4354	U
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	4382	G
1	L5	4387	C
1	L5	4391	G
1	L5	4394	A
1	L5	4422	A
1	L5	4426	C
1	L5	4448	G
1	L5	4449	A
1	L5	4453	C

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Mol	Chain	Res	Type
1	L5	4464	A
1	L5	4466	C
1	L5	4475	G
1	L5	4488	A
1	L5	4500	U
1	L5	4512	U
1	L5	4513	A
1	L5	4518	A
1	L5	4519	C
1	L5	4524	G
1	L5	4525	C
1	L5	4528	G
1	L5	4531	U
1	L5	4545	G
1	L5	4547	C
1	L5	4548	A
1	L5	4549	G
1	L5	4557	U
1	L5	4560	C
1	L5	4567	G
1	L5	4569	U
1	L5	4573	G
1	L5	4575	G
1	L5	4589	A
1	L5	4590	A
1	L5	4600	G
1	L5	4601	U
1	L5	4608	G
1	L5	4617	G
1	L5	4626	A
1	L5	4627	U
1	L5	4633	G
1	L5	4635	A
1	L5	4636	U
1	L5	4637	G
1	L5	4656	A
1	L5	4657	U
1	L5	4670	C
1	L5	4672	A
1	L5	4677	U
1	L5	4687	A
1	L5	4695	C

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Mol	Chain	Res	Type
1	L5	4700	A
1	L5	4708	A
1	L5	4709	U
1	L5	4719	G
1	L5	4731	G
1	L5	4732	G
1	L5	4733	C
1	L5	4734	A
1	L5	4740	G
1	L5	4741	C
1	L5	4742	G
1	L5	4745	G
1	L5	4746	C
1	L5	4747	C
1	L5	4751	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	4773	C
1	L5	4775	C
1	L5	4859	C
1	L5	4870	G
1	L5	4871	C
1	L5	4875	G
1	L5	4882	U
1	L5	4883	C
1	L5	4888	U
1	L5	4889	G
1	L5	4891	G
1	L5	4895	C
1	L5	4896	G
1	L5	4897	G
1	L5	4899	G
1	L5	4900	C
1	L5	4901	G
1	L5	4902	C
1	L5	4905	C
1	L5	4906	U

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Mol	Chain	Res	Type
1	L5	4910	A
1	L5	4911	A
1	L5	4912	G
1	L5	4914	C
1	L5	4922	C
1	L5	4923	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	4949	G
1	L5	4951	G
1	L5	4960	G
1	L5	4961	G
1	L5	4966	A
1	L5	4975	G
1	L5	4976	U
1	L5	4979	A
1	L5	4988	U
1	L5	4989	U
1	L5	4990	C
1	L5	4991	U
1	L5	5017	G
1	L5	5024	C
1	L5	5025	C
1	L5	5026	U
1	L5	5027	C
1	L5	5028	G
1	L5	5029	C
1	L5	5031	G
1	L5	5034	A
1	L5	5041	G
1	L5	5050	C
1	L5	5053	U
1	L5	5054	C
1	L5	5055	G
1	L5	5058	A

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Mol	Chain	Res	Type
1	L5	5061	A
1	L5	5069	U
2	L7	4	U
2	L7	22	A
2	L7	38	U
2	L7	53	U
2	L7	54	A
2	L7	63	C
2	L7	64	G
2	L7	100	A
2	L7	110	G
3	L8	25	G
3	L8	34	U
3	L8	35	C
3	L8	48	A
3	L8	52	A
3	L8	59	A
3	L8	62	A
3	L8	63	U
3	L8	80	A
3	L8	81	C
3	L8	82	A
3	L8	83	C
3	L8	84	A
3	L8	85	U
3	L8	87	G
3	L8	103	A
3	L8	105	C
3	L8	110	U
3	L8	111	U
3	L8	114	G
3	L8	123	U
3	L8	124	U
3	L8	125	C
3	L8	126	C
3	L8	127	U
3	L8	150	C
3	L8	156	U
49	S2	14	C
49	S2	17	C
49	S2	25	A
49	S2	33	G

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Mol	Chain	Res	Type
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	61	A
49	S2	64	A
49	S2	66	G
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	92	A
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	155	G
49	S2	158	A
49	S2	159	A
49	S2	160	U
49	S2	161	U
49	S2	162	C
49	S2	163	U
49	S2	175	A
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

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Mol	Chain	Res	Type
49	S2	204	G
49	S2	206	G
49	S2	208	G
49	S2	214	U
49	S2	290	U
49	S2	292	A
49	S2	293	C
49	S2	295	C
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	322	C
49	S2	323	C
49	S2	324	C
49	S2	325	C
49	S2	326	C
49	S2	328	U
49	S2	329	G
49	S2	332	G
49	S2	339	A
49	S2	340	C
49	S2	347	G
49	S2	351	G
49	S2	360	A
49	S2	362	C
49	S2	364	A
49	S2	368	U
49	S2	369	C
49	S2	370	G
49	S2	382	C
49	S2	385	G
49	S2	386	C
49	S2	408	A
49	S2	409	C
49	S2	417	C
49	S2	418	A
49	S2	421	G
49	S2	438	G

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Mol	Chain	Res	Type
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	471	G
49	S2	472	C
49	S2	473	A
49	S2	474	G
49	S2	476	A
49	S2	482	G
49	S2	487	U
49	S2	488	U
49	S2	492	C
49	S2	493	A
49	S2	502	C
49	S2	503	C
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	542	U
49	S2	546	G
49	S2	547	G
49	S2	551	U
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	566	U
49	S2	567	C
49	S2	570	C
49	S2	576	A
49	S2	583	A
49	S2	584	A

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Mol	Chain	Res	Type
49	S2	585	C
49	S2	587	A
49	S2	589	G
49	S2	590	A
49	S2	591	U
49	S2	594	A
49	S2	597	G
49	S2	604	A
49	S2	607	U
49	S2	614	C
49	S2	623	G
49	S2	628	A
49	S2	631	U
49	S2	632	C
49	S2	643	A
49	S2	644	G
49	S2	655	A
49	S2	659	G
49	S2	660	C
49	S2	662	G
49	S2	663	C
49	S2	664	A
49	S2	668	A
49	S2	669	A
49	S2	671	A
49	S2	672	A
49	S2	673	G
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	733	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

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Mol	Chain	Res	Type
49	S2	788	G
49	S2	791	C
49	S2	792	C
49	S2	798	G
49	S2	799	U
49	S2	801	U
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	834	C
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	872	A
49	S2	873	G
49	S2	874	G
49	S2	877	C
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
49	S2	897	U
49	S2	898	U
49	S2	899	U

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Mol	Chain	Res	Type
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	963	A
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	1034	A
49	S2	1047	C
49	S2	1061	U
49	S2	1062	A
49	S2	1083	A
49	S2	1085	C
49	S2	1088	U
49	S2	1094	C
49	S2	1109	C
49	S2	1115	U
49	S2	1116	C
49	S2	1118	C
49	S2	1121	G
49	S2	1133	A
49	S2	1138	C
49	S2	1150	A
49	S2	1153	C
49	S2	1154	U
49	S2	1155	U
49	S2	1170	A
49	S2	1195	A

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Mol	Chain	Res	Type
49	S2	1203	G
49	S2	1207	G
49	S2	1208	A
49	S2	1211	G
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	1281	G
49	S2	1283	C
49	S2	1284	A
49	S2	1286	G
49	S2	1294	G
49	S2	1295	A
49	S2	1298	G
49	S2	1301	A
49	S2	1302	G
49	S2	1303	C
49	S2	1306	U
49	S2	1308	U
49	S2	1312	G
49	S2	1318	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

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Mol	Chain	Res	Type
49	S2	1404	U
49	S2	1406	G
49	S2	1409	A
49	S2	1412	C
49	S2	1414	A
49	S2	1415	C
49	S2	1420	G
49	S2	1421	A
49	S2	1422	G
49	S2	1423	C
49	S2	1424	G
49	S2	1428	G
49	S2	1433	C
49	S2	1435	C
49	S2	1436	C
49	S2	1438	A
49	S2	1449	G
49	S2	1452	A
49	S2	1454	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	1494	U
49	S2	1497	G
49	S2	1498	A
49	S2	1506	A
49	S2	1508	A
49	S2	1509	U
49	S2	1520	G
49	S2	1521	C
49	S2	1531	A
49	S2	1533	A
49	S2	1537	A
49	S2	1544	C
49	S2	1553	C
49	S2	1555	U
49	S2	1556	A
49	S2	1558	C
49	S2	1570	G

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Mol	Chain	Res	Type
49	S2	1574	C
49	S2	1580	A
49	S2	1585	U
49	S2	1587	G
49	S2	1588	A
49	S2	1600	G
49	S2	1601	A
49	S2	1621	U
49	S2	1623	A
49	S2	1634	A
49	S2	1637	A
49	S2	1638	G
49	S2	1640	A
49	S2	1644	C
49	S2	1648	G
49	S2	1654	G
49	S2	1663	A
49	S2	1665	G
49	S2	1671	G
49	S2	1680	G
49	S2	1686	G
49	S2	1699	A
49	S2	1701	C
49	S2	1715	A
49	S2	1719	A
49	S2	1721	U
49	S2	1722	G
49	S2	1735	A
49	S2	1742	C
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

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Mol	Chain	Res	Type
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	1822	A
49	S2	1823	A
49	S2	1829	G
49	S2	1831	A
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	31	G
84	CC	32	C
84	CC	33	U
84	CC	36	C
84	CC	37	A
84	CC	38	C
84	CC	39	C
84	CC	45	G
84	CC	46	A
84	CC	47	C
84	CC	48	C
84	CC	55	C
84	CC	57	A

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Mol	Chain	Res	Type
84	CC	61	C
84	CC	72	G
84	CC	73	C
84	CC	75	A

All (34) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	406	C
1	L5	504	G
1	L5	914	U
1	L5	1082	C
1	L5	1633	G
1	L5	1977	C
1	L5	2033	A
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	4548	A
1	L5	4699	U
1	L5	4910	A
1	L5	4913	G
1	L5	4914	C
49	S2	60	G
49	S2	112	U
49	S2	158	A
49	S2	291	G
49	S2	369	C
49	S2	417	C
49	S2	420	G
49	S2	563	G
49	S2	567	C
49	S2	688	U
49	S2	797	C
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 267 ligands modelled in this entry, 264 are monoatomic - leaving 3 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
91	SF4	CI	602	-	0,12,12	-	-	-		
91	SF4	CI	601	-	0,12,12	-	-	-		
92	ADP	CI	603	-	28,29,29	1.42	5 (17%)	43,45,45	1.84	9 (20%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
91	SF4	CI	602	-	-	-	0/6/5/5
91	SF4	CI	601	-	-	-	0/6/5/5
92	ADP	CI	603	-	-	6/16/32/32	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
92	CI	603	ADP	C5-C4	4.60	1.47	1.39
92	CI	603	ADP	C5-C6	2.68	1.48	1.41
92	CI	603	ADP	C8-N7	2.35	1.36	1.31
92	CI	603	ADP	C5-N7	-2.30	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
92	CI	603	ADP	PA-O3A	2.13	1.61	1.59

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
92	CI	603	ADP	C5-C4-N3	-5.81	118.71	126.72
92	CI	603	ADP	N3-C4-N9	4.51	134.84	127.17
92	CI	603	ADP	C2-N3-C4	3.74	120.96	111.83
92	CI	603	ADP	C4-C5-N7	-3.57	106.50	110.58
92	CI	603	ADP	N3-C2-N1	-3.30	123.59	128.58
92	CI	603	ADP	C5-N7-C8	2.62	107.56	103.45
92	CI	603	ADP	C4-N9-C8	2.59	108.46	105.74
92	CI	603	ADP	C6-C5-N7	2.21	136.35	132.09
92	CI	603	ADP	N9-C8-N7	-2.05	111.02	113.94

There are no chirality outliers.

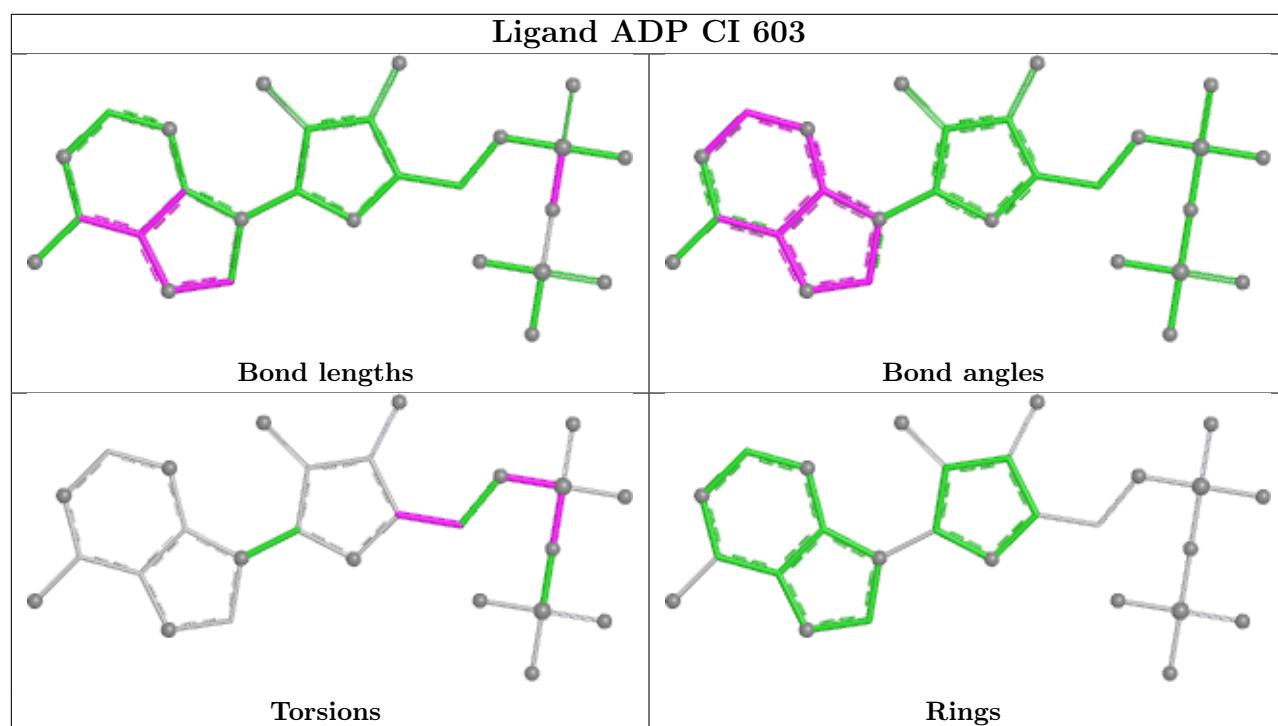
All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
92	CI	603	ADP	PB-O3A-PA-O5'
92	CI	603	ADP	C5'-O5'-PA-O1A
92	CI	603	ADP	C5'-O5'-PA-O2A
92	CI	603	ADP	C5'-O5'-PA-O3A
92	CI	603	ADP	O4'-C4'-C5'-O5'
92	CI	603	ADP	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

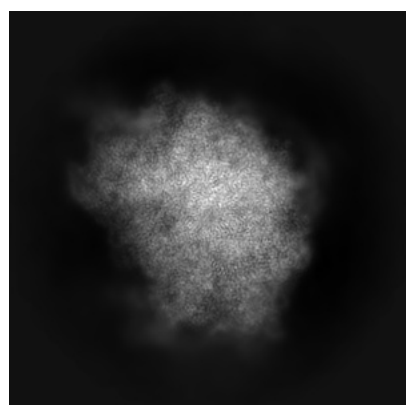
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11289. These allow visual inspection of the internal detail of the map and identification of artifacts.

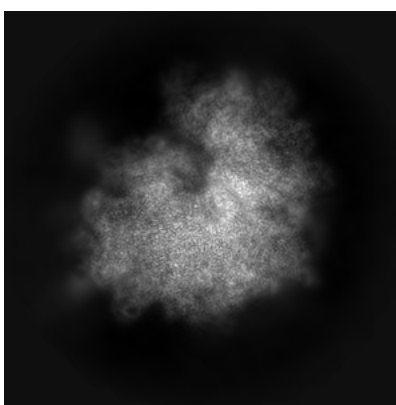
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

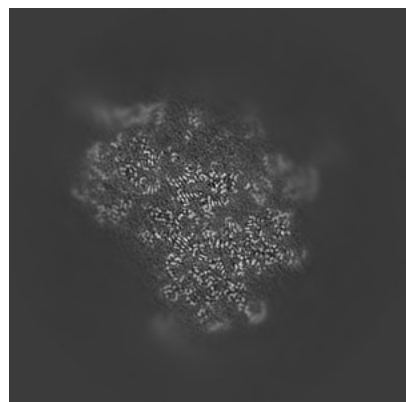


Z

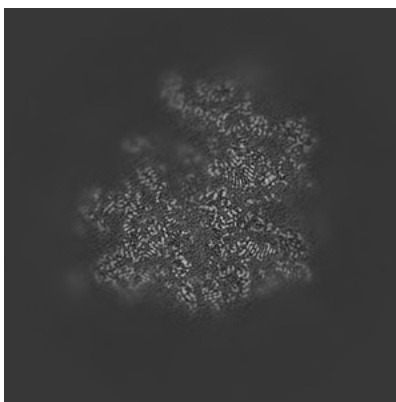
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

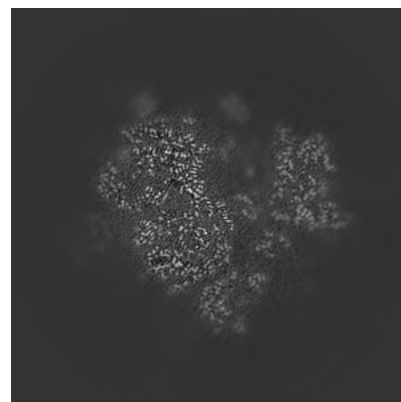
6.2.1 Primary map



X Index: 200



Y Index: 200

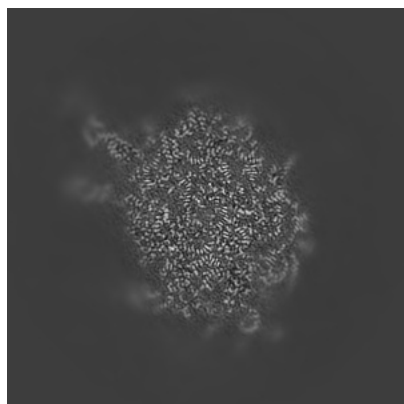


Z Index: 200

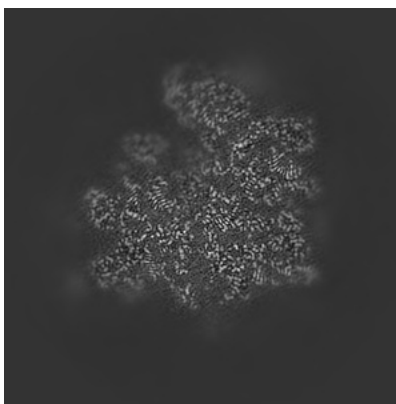
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

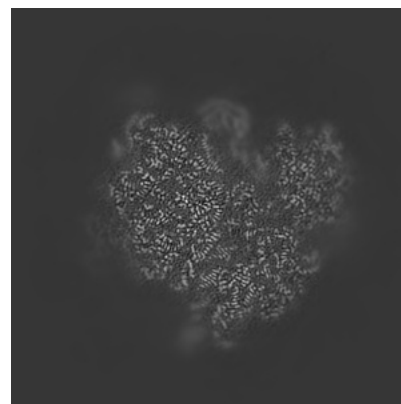
6.3.1 Primary map



X Index: 178



Y Index: 194

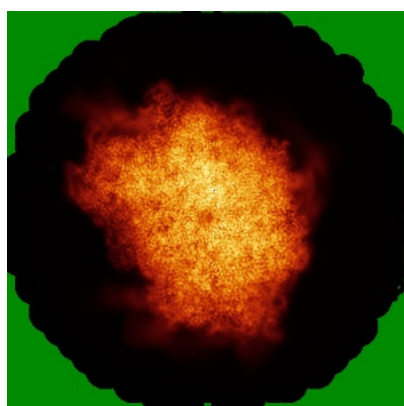


Z Index: 224

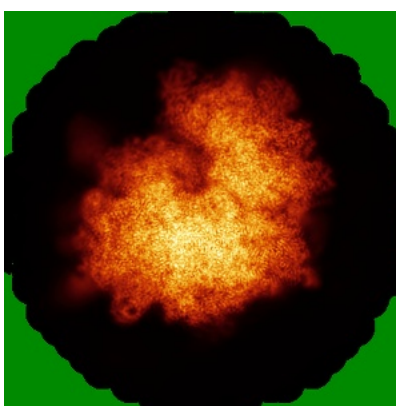
The images above show the largest variance slices of the map in three orthogonal directions.

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

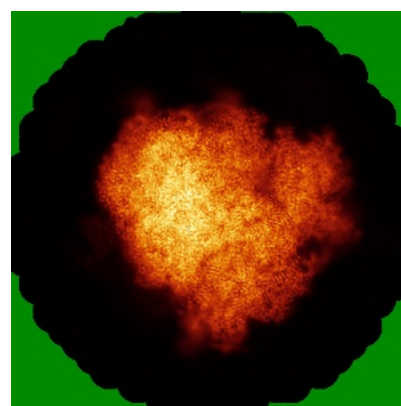
6.4.1 Primary map



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

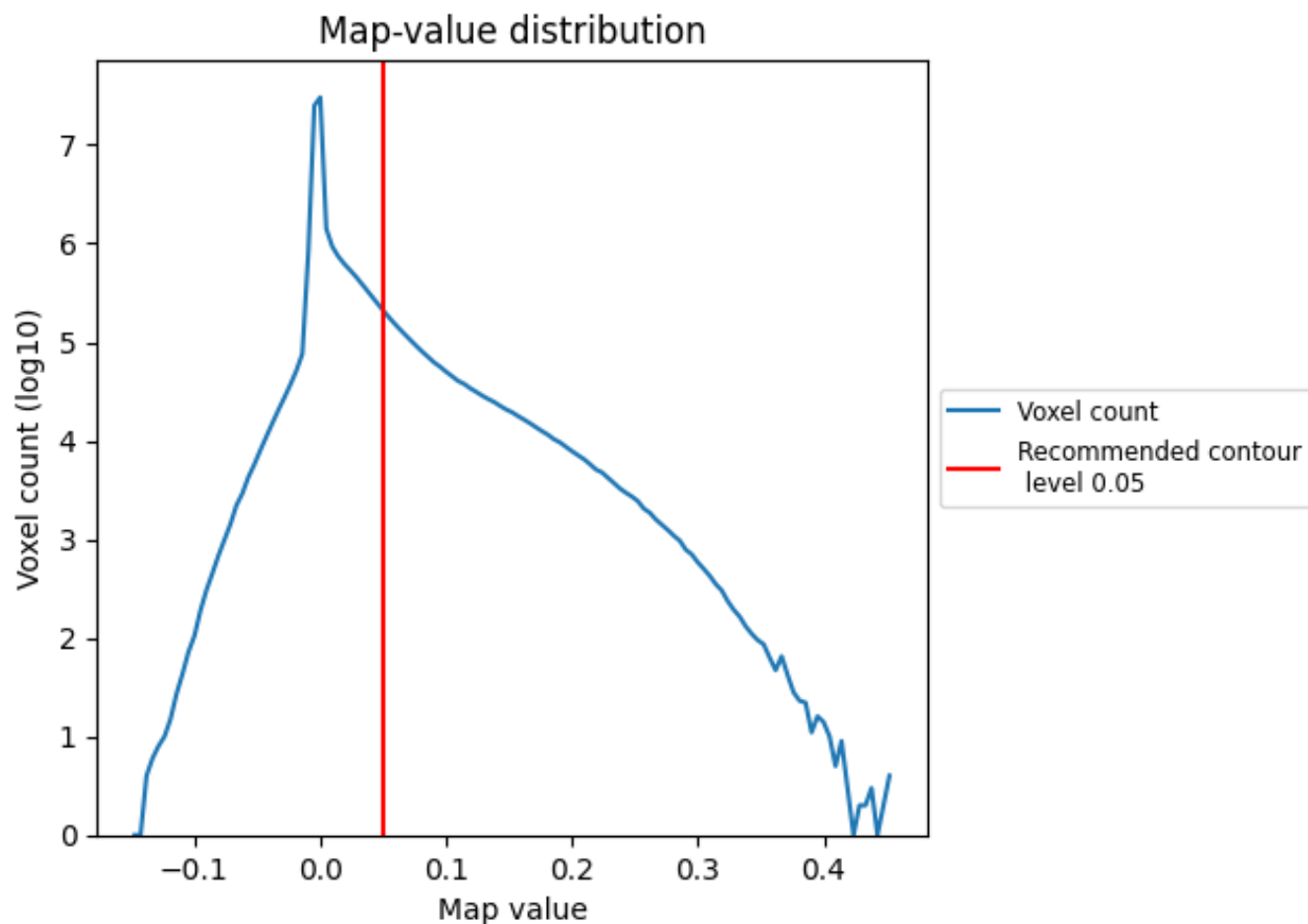
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

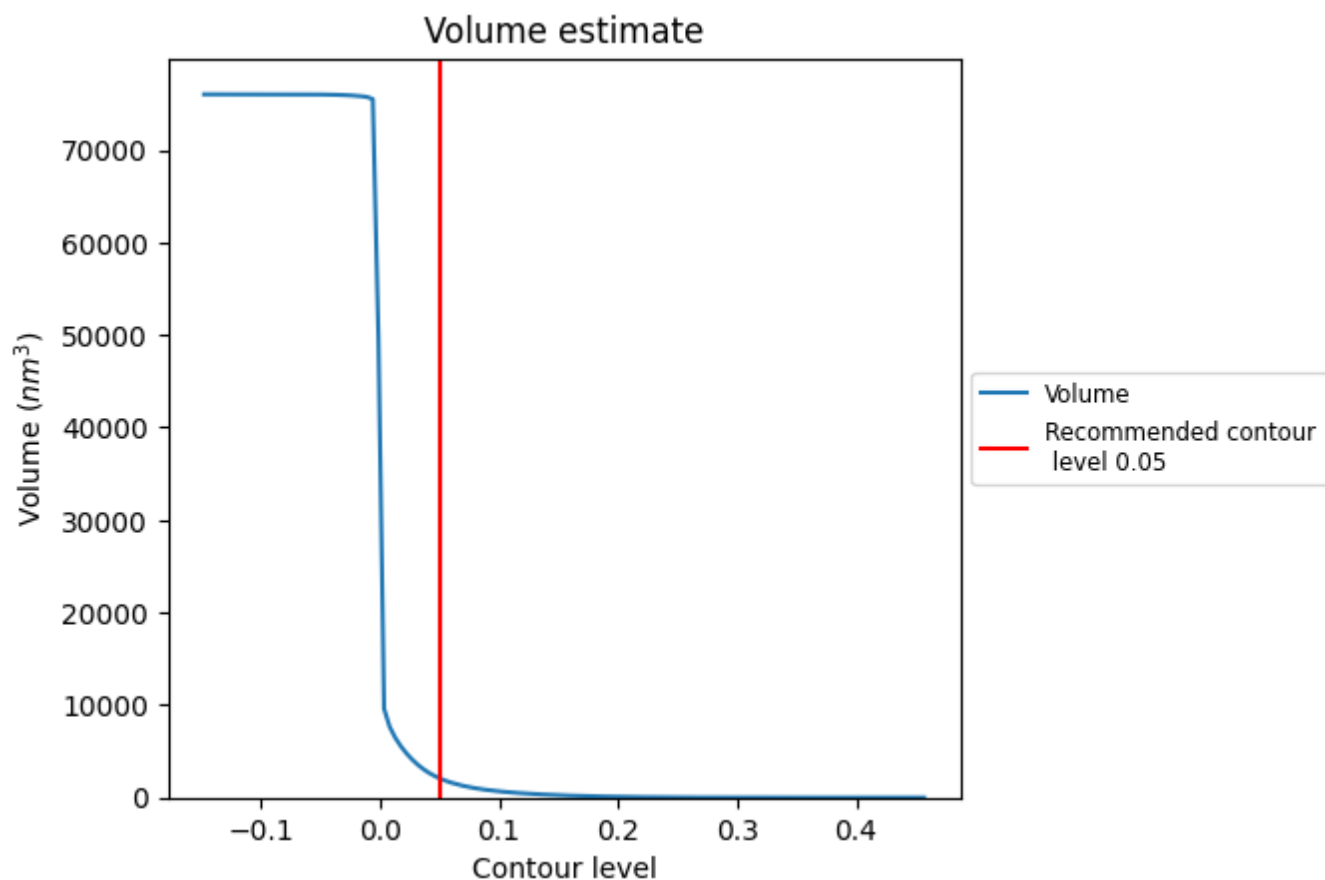
This section contains the results of statistical analysis of the map.

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.

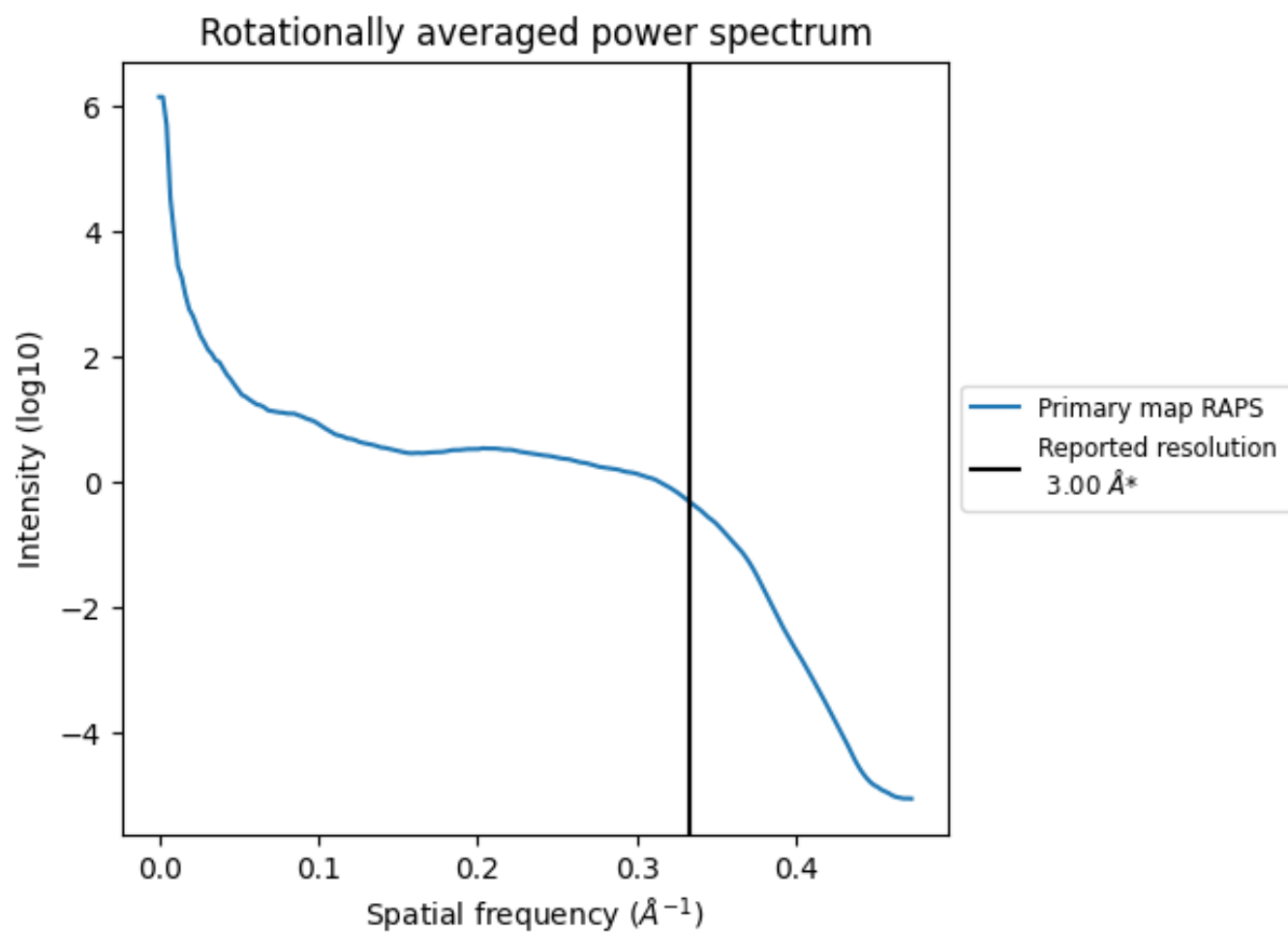
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2092 nm³; this corresponds to an approximate mass of 1890 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 ⓘ

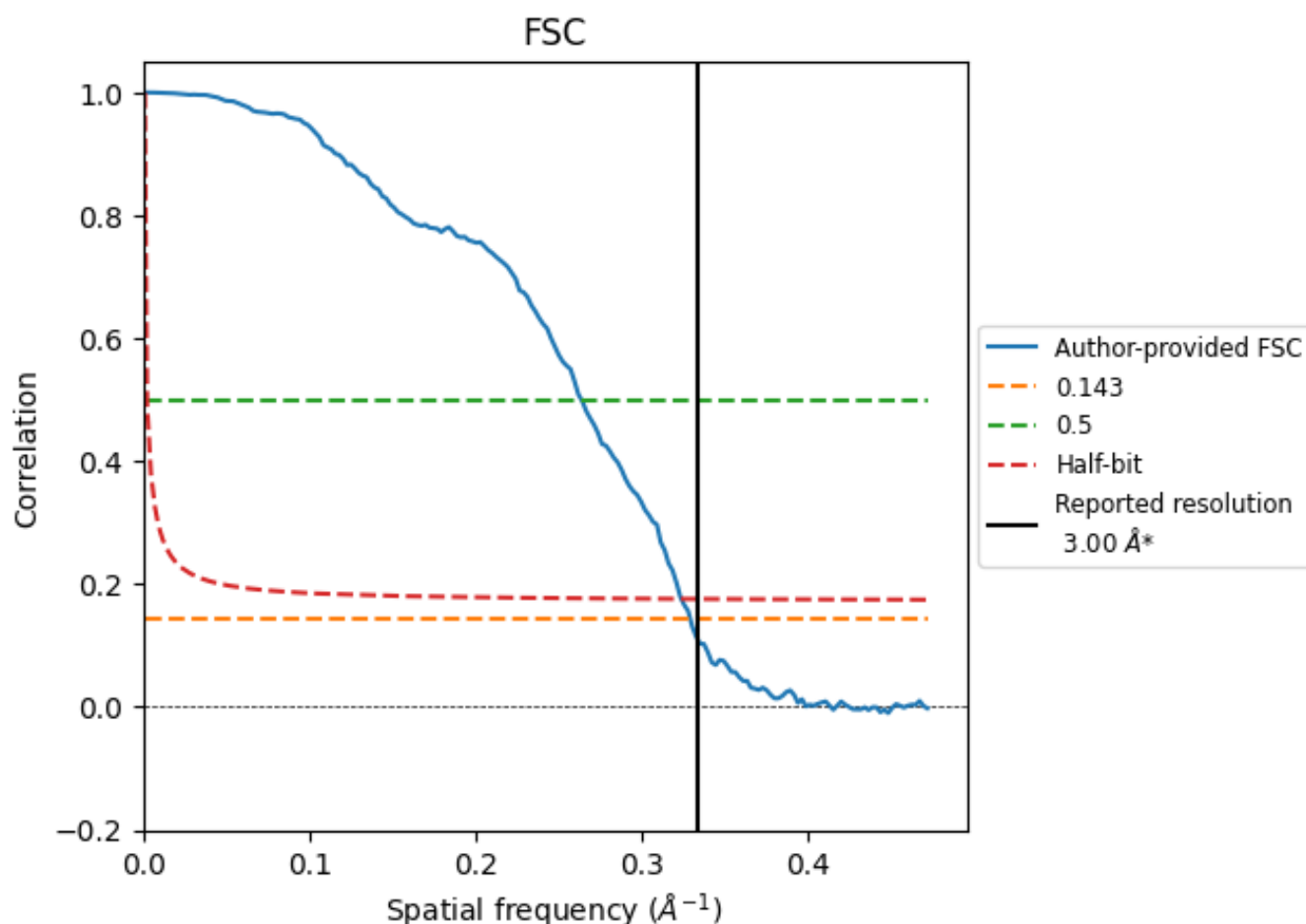


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

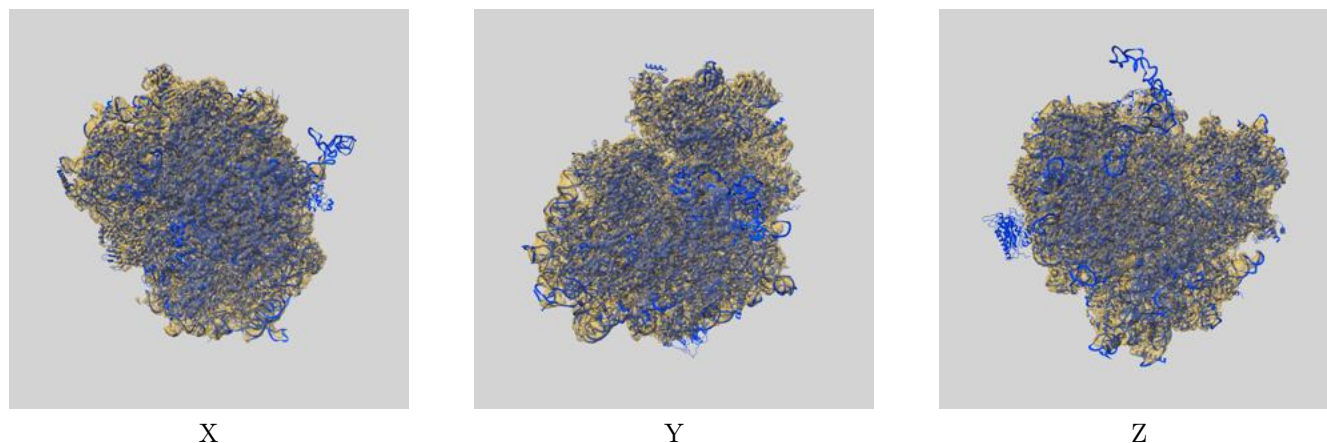
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.04	3.79	3.09
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

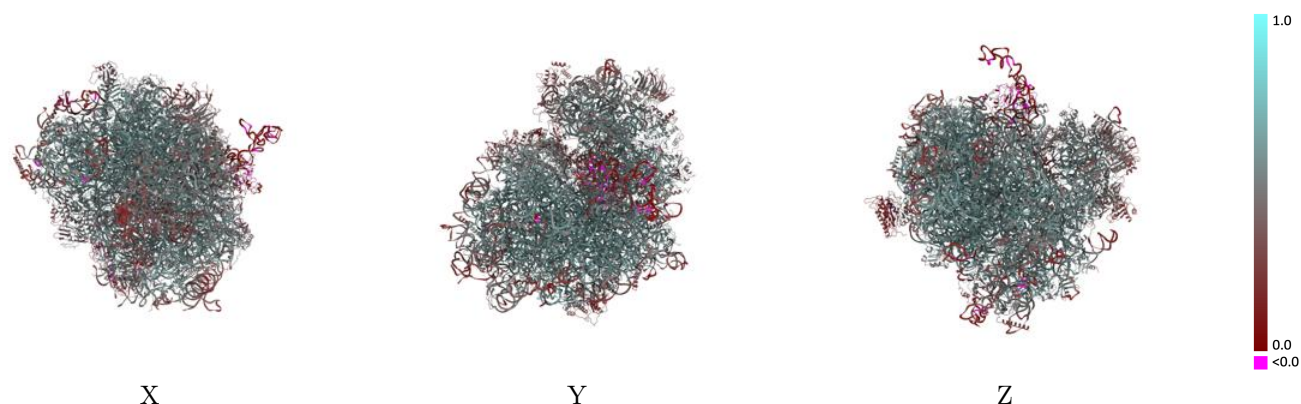
This section contains information regarding the fit between EMDB map EMD-11289 and PDB model 6ZME. Per-residue inclusion information can be found in section [3](#) on page [22](#).

9.1 Map-model overlay [i](#)



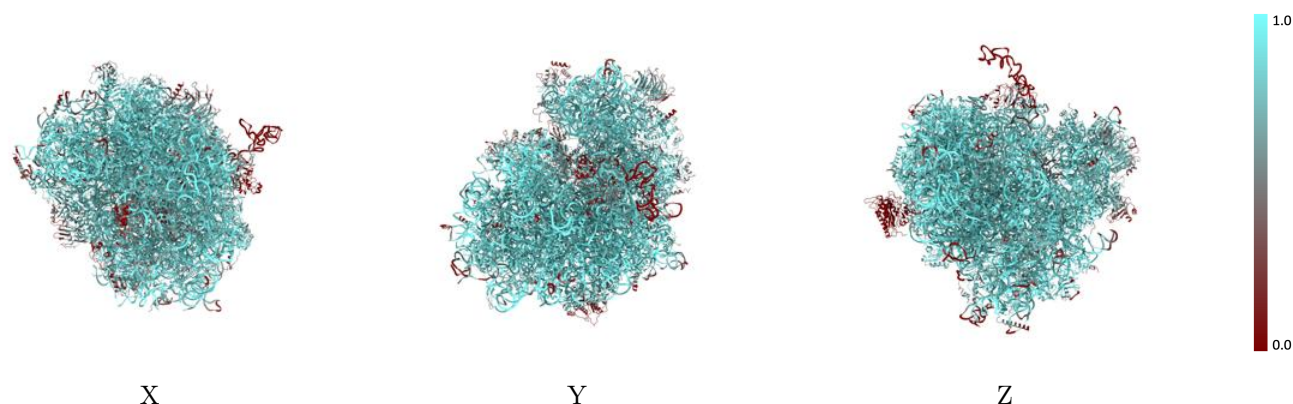
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



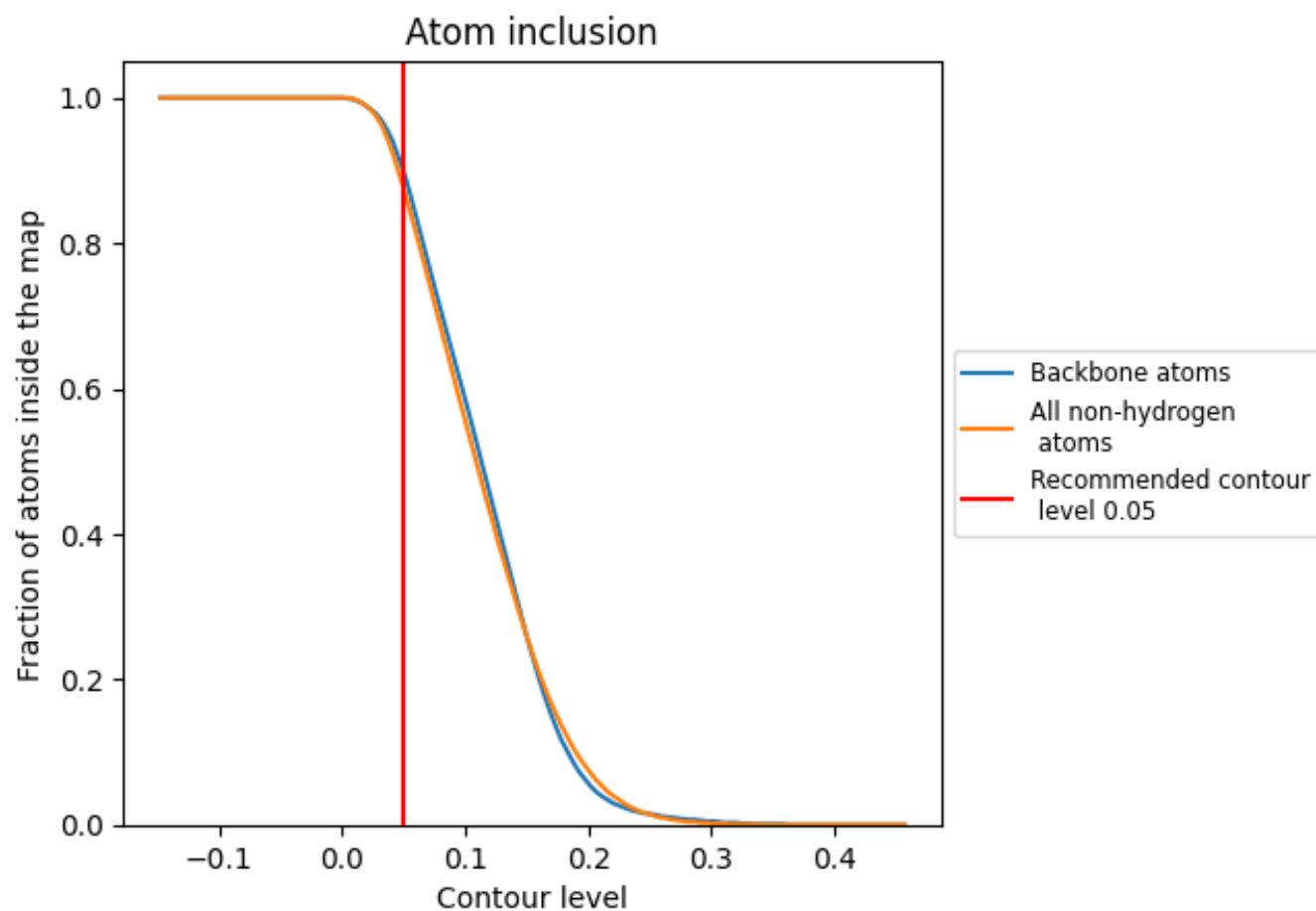
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 88% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8750	 0.5200
CA	 0.0420	 0.2520
CC	 0.8740	 0.2970
CE	 0.7320	 0.4260
CF	 0.9230	 0.5470
CH	 0.5680	 0.3700
CI	 0.6840	 0.4610
L5	 0.9330	 0.5400
L7	 0.9860	 0.5750
L8	 0.9660	 0.5680
LA	 0.9810	 0.6180
LB	 0.9340	 0.5870
LC	 0.9280	 0.5780
LD	 0.8680	 0.5220
LE	 0.8250	 0.4970
LF	 0.9630	 0.5860
LG	 0.8070	 0.5060
LH	 0.9050	 0.5490
LI	 0.9360	 0.5660
LJ	 0.7790	 0.4470
LL	 0.8820	 0.5450
LM	 0.9160	 0.5440
LN	 0.9870	 0.6250
LO	 0.9440	 0.5940
LP	 0.9580	 0.6110
LQ	 0.9680	 0.6020
LR	 0.8750	 0.5450
LS	 0.9640	 0.5930
LT	 0.9310	 0.5590
LU	 0.8150	 0.4710
LV	 0.9680	 0.5970
LW	 0.7010	 0.4520
LX	 0.9190	 0.5670
LY	 0.9030	 0.5640
LZ	 0.8990	 0.5590



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Chain	Atom inclusion	Q-score
La	 0.9540	 0.6050
Lb	 0.8300	 0.5030
Lc	 0.9120	 0.5520
Ld	 0.9120	 0.5680
Le	 0.9680	 0.5970
Lf	 0.9670	 0.6100
Lg	 0.9210	 0.5790
Lh	 0.9000	 0.5490
Li	 0.8970	 0.5450
Lj	 0.9810	 0.6110
Lk	 0.7770	 0.5000
Ll	 0.9810	 0.5910
Lm	 0.9330	 0.5710
Ln	 0.9860	 0.6110
Lo	 0.9100	 0.5780
Lp	 0.9460	 0.6000
Lr	 0.9490	 0.5740
Ls	 0.3310	 0.2650
Lt	 0.4750	 0.2590
Lz	 0.1140	 0.1150
S2	 0.9380	 0.5330
SA	 0.8450	 0.5200
SB	 0.8860	 0.5350
SC	 0.9140	 0.5530
SD	 0.7770	 0.4540
SE	 0.9100	 0.5520
SF	 0.8550	 0.4850
SG	 0.7750	 0.4650
SH	 0.7210	 0.4510
SI	 0.8780	 0.5330
SJ	 0.8800	 0.5310
SK	 0.7440	 0.4100
SL	 0.8980	 0.5670
SM	 0.2510	 0.2210
SN	 0.9300	 0.5670
SO	 0.8780	 0.5390
SP	 0.7340	 0.4250
SQ	 0.8090	 0.4820
SR	 0.7600	 0.4670
SS	 0.7860	 0.4500
ST	 0.8270	 0.4790
SU	 0.7340	 0.4230

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Chain	Atom inclusion	Q-score
SV	 0.8760	 0.5390
SW	 0.9460	 0.5830
SX	 0.9420	 0.5810
SY	 0.8180	 0.5020
SZ	 0.7100	 0.4320
Sa	 0.9200	 0.5630
Sb	 0.8390	 0.5140
Sc	 0.7390	 0.4570
Sd	 0.9530	 0.5380
Se	 0.8180	 0.5030
Sf	 0.4490	 0.2880
Sg	 0.6100	 0.3900