



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 07:45 AM UTC

PDB ID : 6ZMI / pdb_00006zmi
EMDB ID : EMD-11292
Title : SARS-CoV-2 Nsp1 bound to the human LYAR-80S 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 : 2.60 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

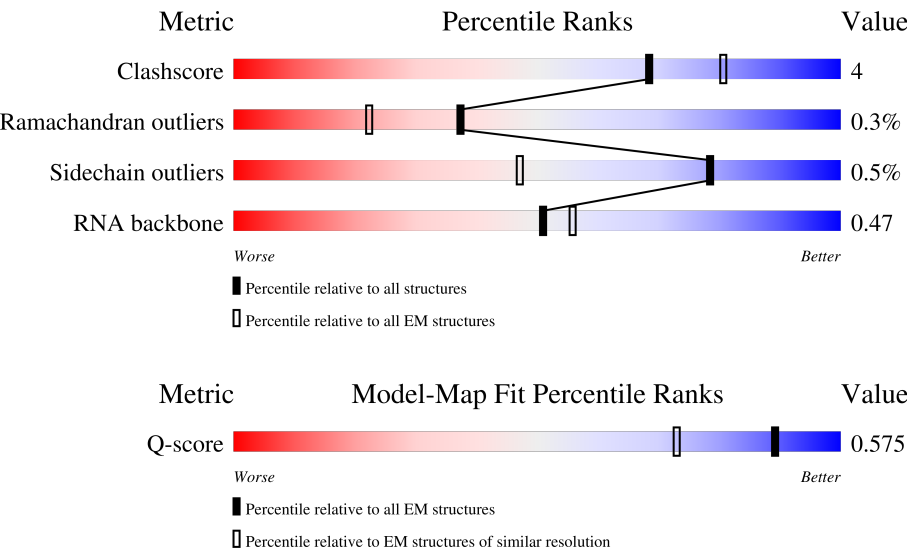
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.60 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.



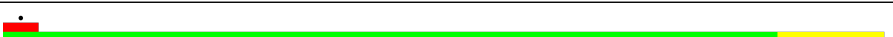
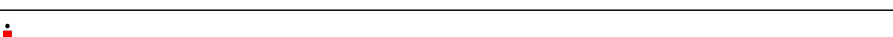
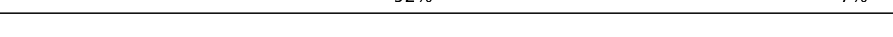
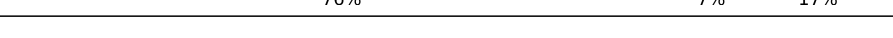
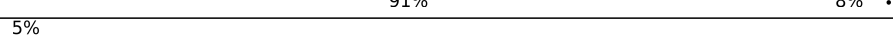
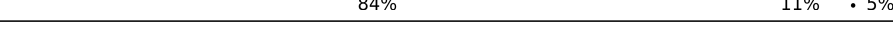
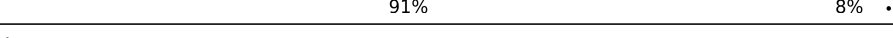
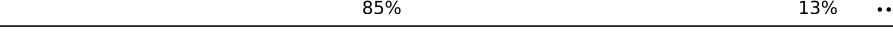
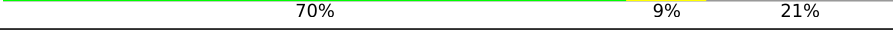
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8728 (2.10 - 3.10)

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	

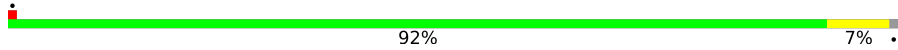
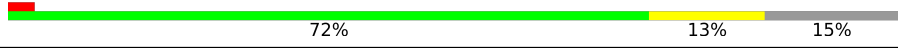
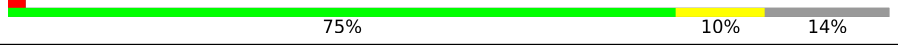
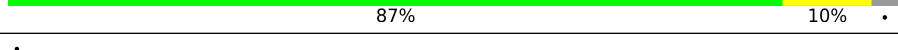
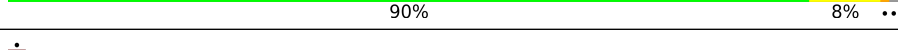
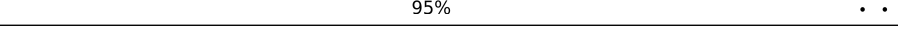
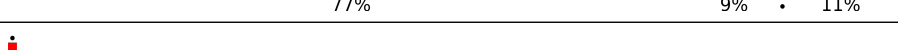
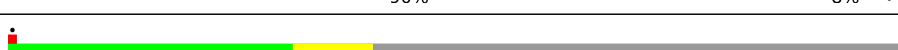
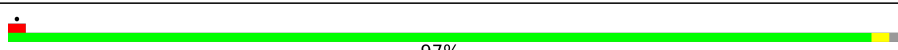
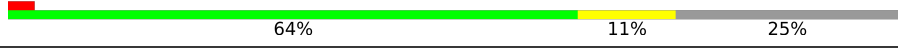
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Mol	Chain	Length	Quality of chain
4	LA	257	
5	LB	403	
6	LC	427	
7	LD	297	
8	LE	288	
9	LF	248	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	215	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	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

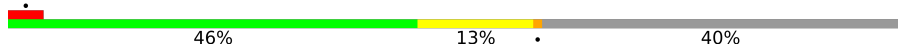
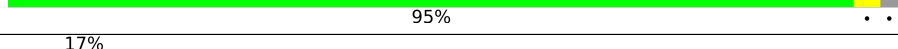
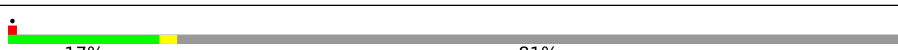
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Mol	Chain	Length	Quality of chain
54	SF	204	
55	SH	194	
56	SI	208	
57	SK	165	
58	SL	158	
59	SP	145	
60	SQ	146	
61	SR	135	
62	SS	152	
63	ST	145	
64	SU	119	
65	SV	83	
66	SX	143	
67	Sa	115	
68	Sc	69	
69	Sd	56	
70	Sg	317	
71	SC	293	
72	SG	249	
73	SJ	194	
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	 46%
80	Sb	84	 85%
81	Se	59	 95%
82	Sf	156	 57%
83	CA	394	 66%
84	CC	75	 49%
85	CE	379	 81%
86	i	180	 82%

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 225122 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
			443	271	98	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 Cell growth-regulating nucleolar protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
85	CE	72	Total	C	N	O	0	0
			603	395	105	103		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
86	i	33	Total	C	N	O	S	0	0
			263	160	47	55	1		

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

Mol	Chain	Residues	Atoms		AltConf
87	L5	212	Total	Mg	0
			212	212	
87	L7	3	Total	Mg	0
			3	3	
87	L8	4	Total	Mg	0
			4	4	
87	LA	1	Total	Mg	0
			1	1	
87	LI	1	Total	Mg	0
			1	1	
87	LP	1	Total	Mg	0
			1	1	
87	LV	1	Total	Mg	0
			1	1	
87	Le	1	Total	Mg	0
			1	1	
87	Lg	1	Total	Mg	0
			1	1	
87	Lj	1	Total	Mg	0
			1	1	
87	S2	30	Total	Mg	0
			30	30	

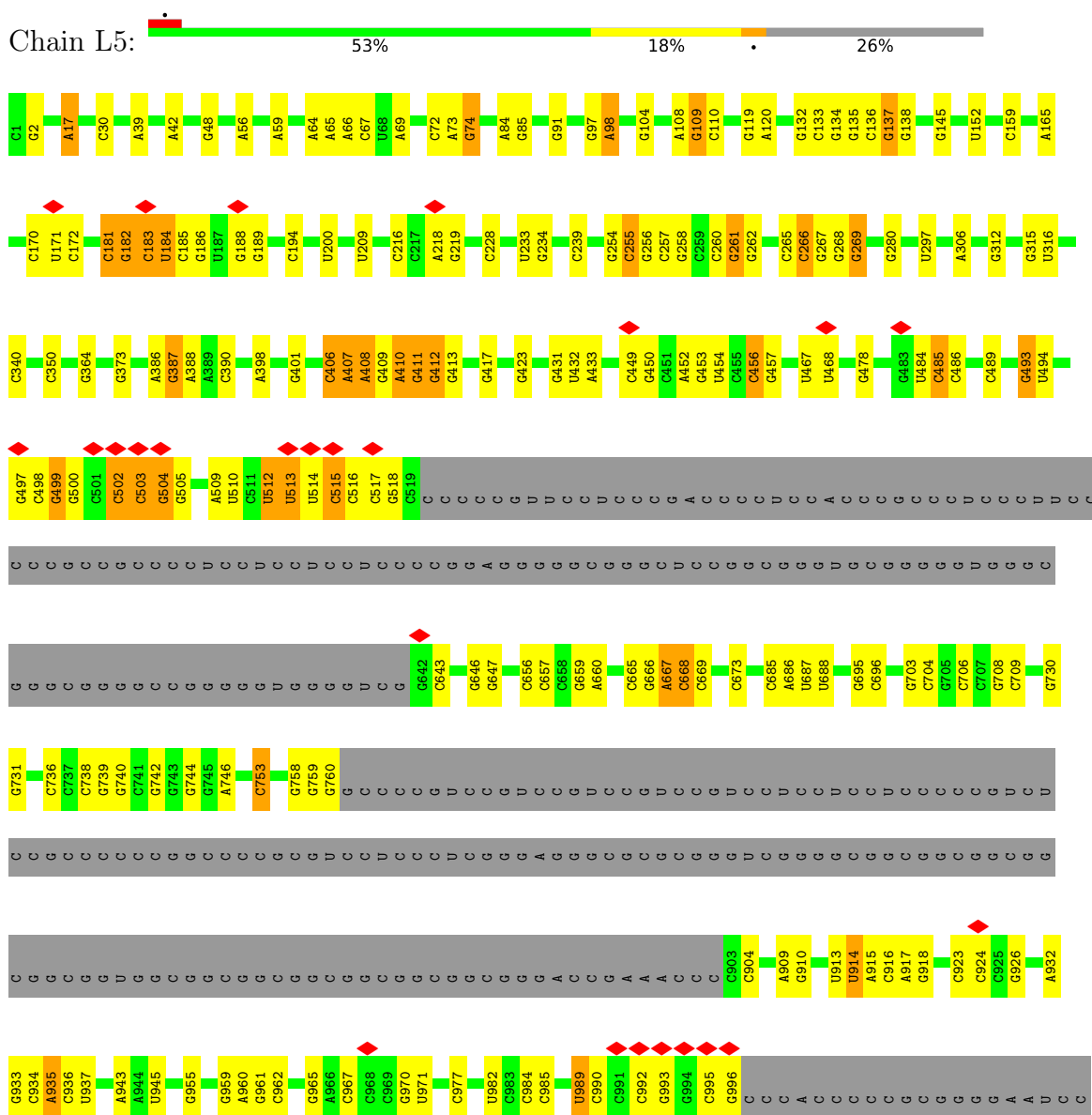
- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn).

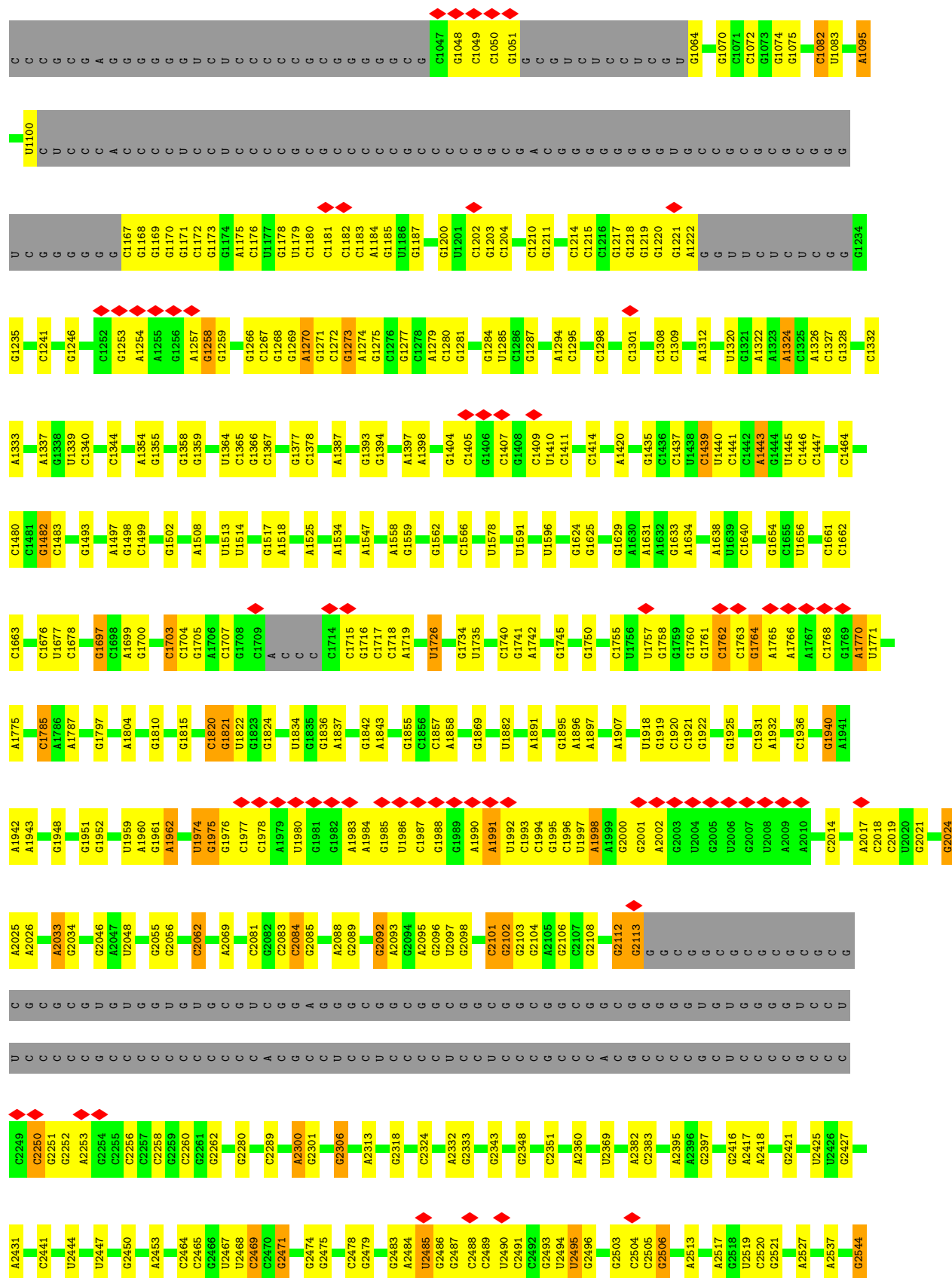
Mol	Chain	Residues	Atoms		AltConf
88	Lg	1	Total 1	Zn 1	0
88	Lj	1	Total 1	Zn 1	0
88	Lm	1	Total 1	Zn 1	0
88	Lo	1	Total 1	Zn 1	0
88	Lp	1	Total 1	Zn 1	0
88	Sa	1	Total 1	Zn 1	0
88	Sd	1	Total 1	Zn 1	0
88	Sf	1	Total 1	Zn 1	0

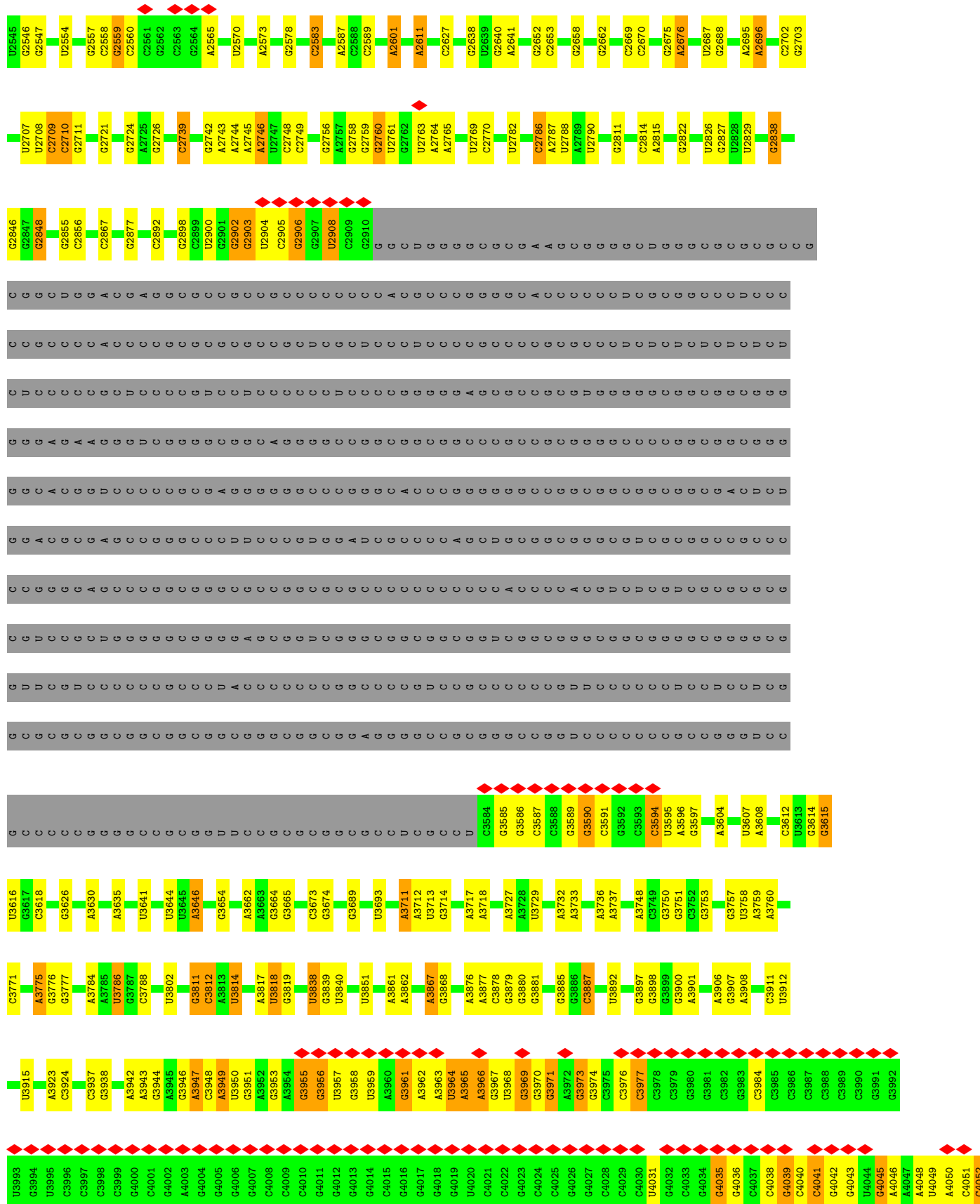
3 Residue-property plots

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



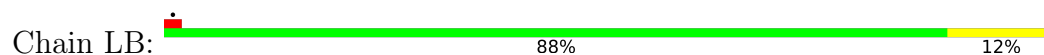




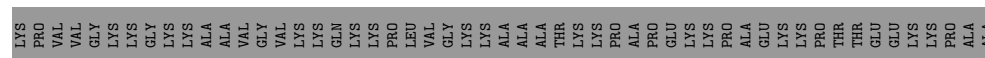
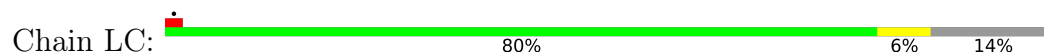




• Molecule 5: 60S ribosomal protein L3



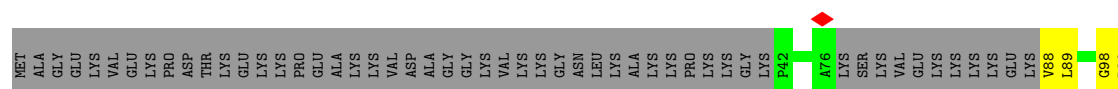
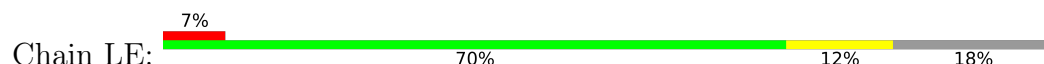
• Molecule 6: 60S ribosomal protein L4



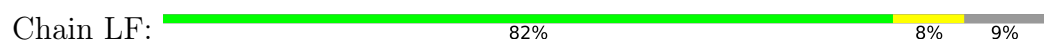
• Molecule 7: 60S ribosomal protein L5

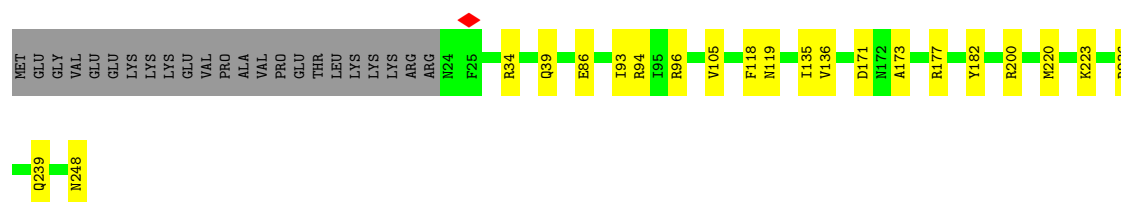


• Molecule 8: 60S ribosomal protein L6

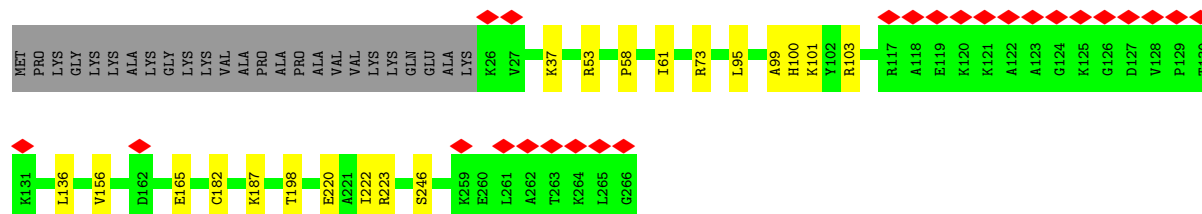
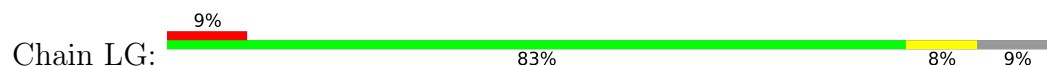


• Molecule 9: 60S ribosomal protein L7

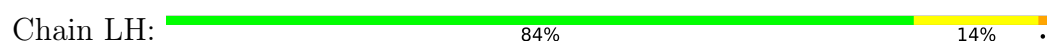




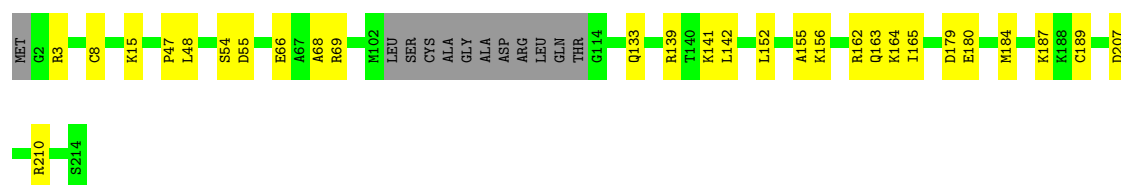
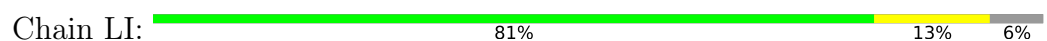
- Molecule 10: 60S ribosomal protein L7a



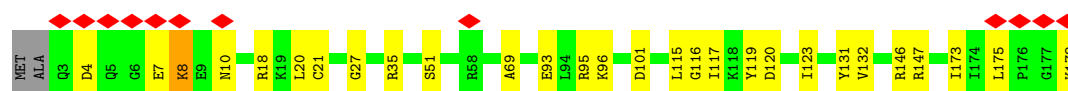
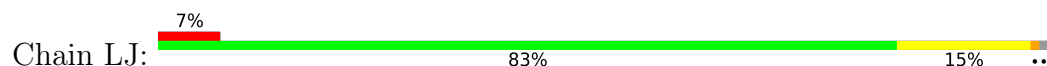
- Molecule 11: 60S ribosomal protein L9



- Molecule 12: 60S ribosomal protein L10-like

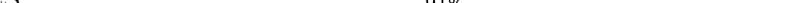


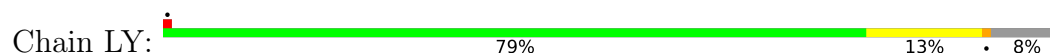
- Molecule 13: 60S ribosomal protein L11



- Molecule 14: 60S ribosomal protein L13



- Chain LS:  91% 8%





- Molecule 28: 60S ribosomal protein L27

Chain LZ: 89% 10% .



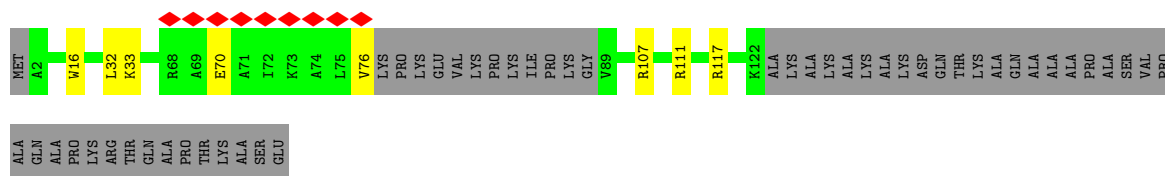
- Molecule 29: 60S ribosomal protein L27a

Chain La: 92% 7% .



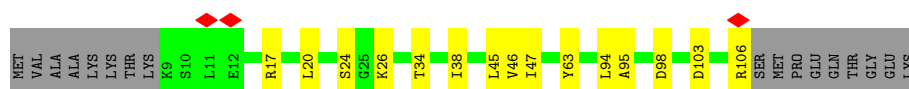
- Molecule 30: 60S ribosomal protein L29

Chain Lb: 6% 64% 5% 31%



- Molecule 31: 60S ribosomal protein L30

Chain Lc: 72% 13% 15%



- Molecule 32: 60S ribosomal protein L31

Chain Ld: 75% 10% 14%



- Molecule 33: 60S ribosomal protein L32

Chain Le: 88% 7% 5%



- Molecule 34: 60S ribosomal protein L35a

Chain Lf:  85% 13% ..



- Molecule 35: 60S ribosomal protein L34

Chain Lg:  5% 87% 10% .

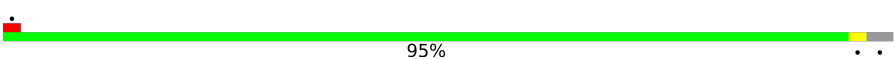


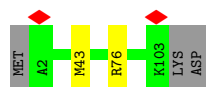
- Molecule 36: 60S ribosomal protein L35

Chain Lh:  90% 8% ..



- Molecule 37: 60S ribosomal protein L36

Chain Li:  95% ..



- Molecule 38: 60S ribosomal protein L37

Chain Lj:  77% 9% . 11%



- Molecule 39: 60S ribosomal protein L38

Chain Lk:  80% 19% .

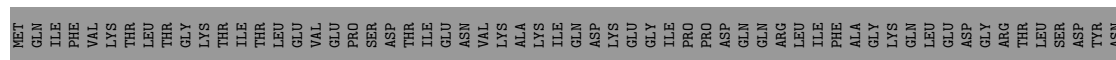
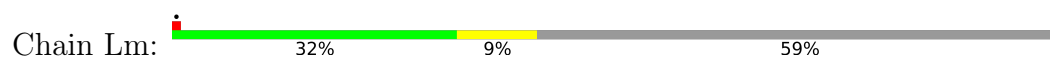


- Molecule 40: 60S ribosomal protein L39

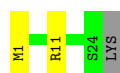
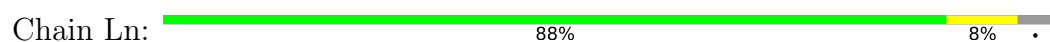
Chain Ll:  90% 8% .



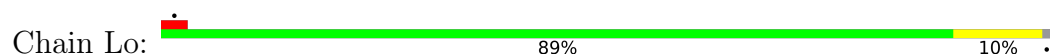
- Molecule 41: Ubiquitin-60S ribosomal protein L40



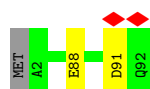
- Molecule 42: 60S ribosomal protein L41



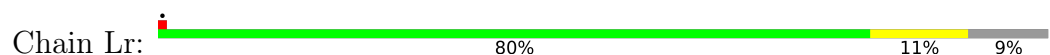
- Molecule 43: 60S ribosomal protein L36a



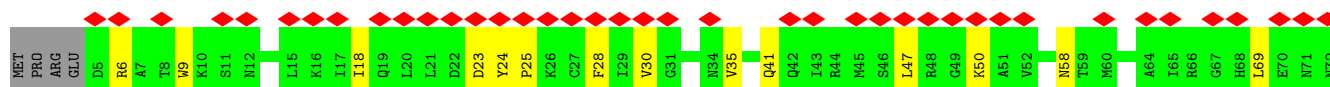
- Molecule 44: 60S ribosomal protein L37a

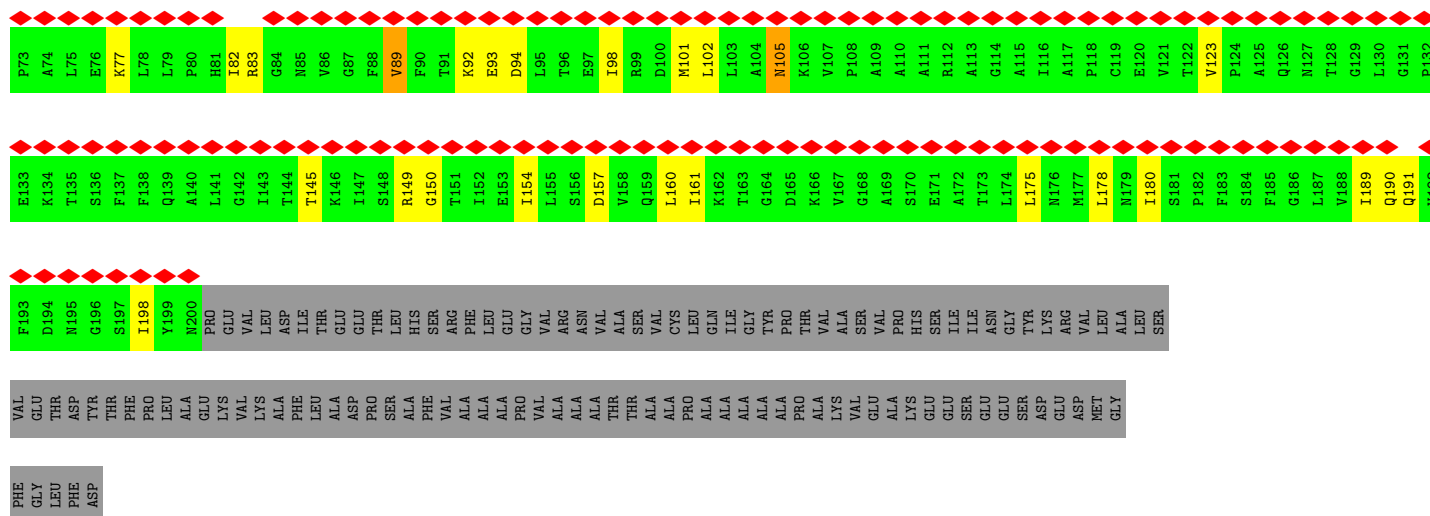


- Molecule 45: 60S ribosomal protein L28

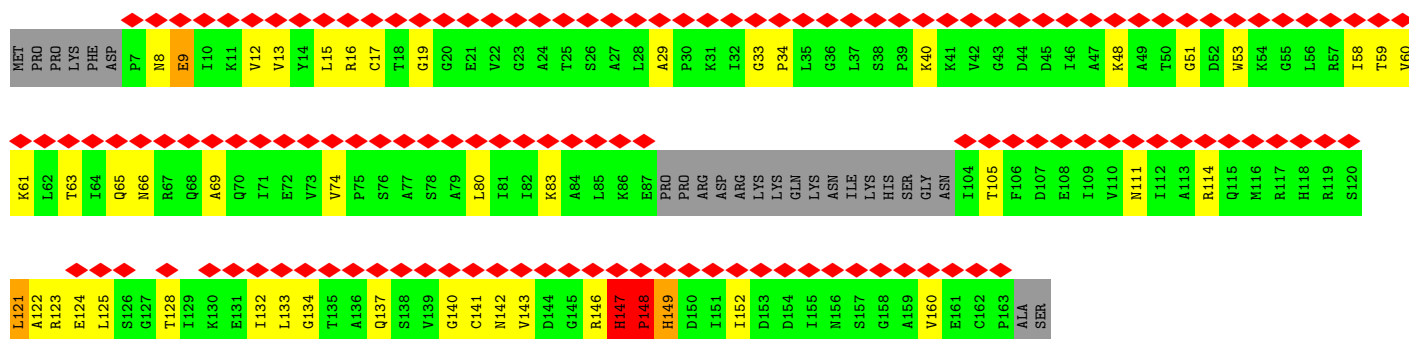
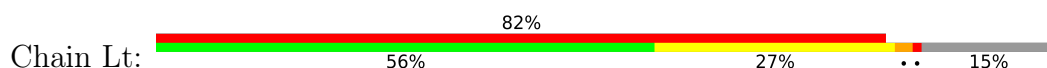


- Molecule 46: 60S acidic ribosomal protein P0

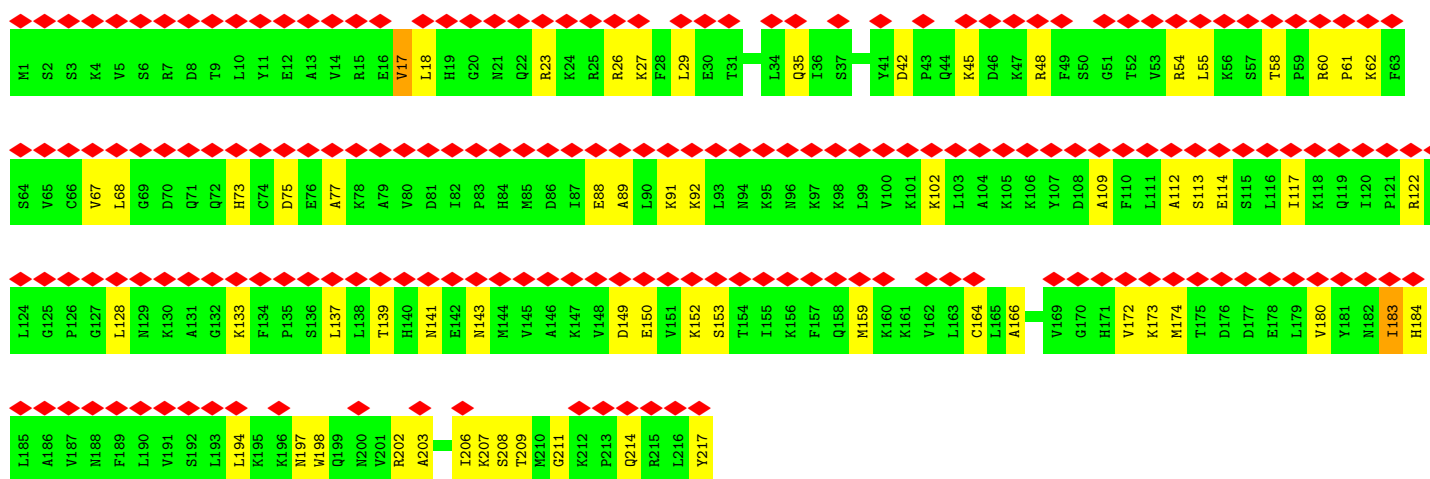
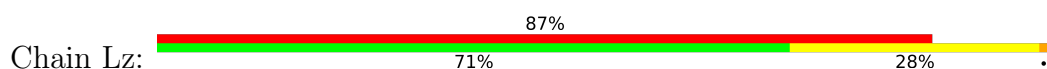




• Molecule 47: 60S ribosomal protein L12

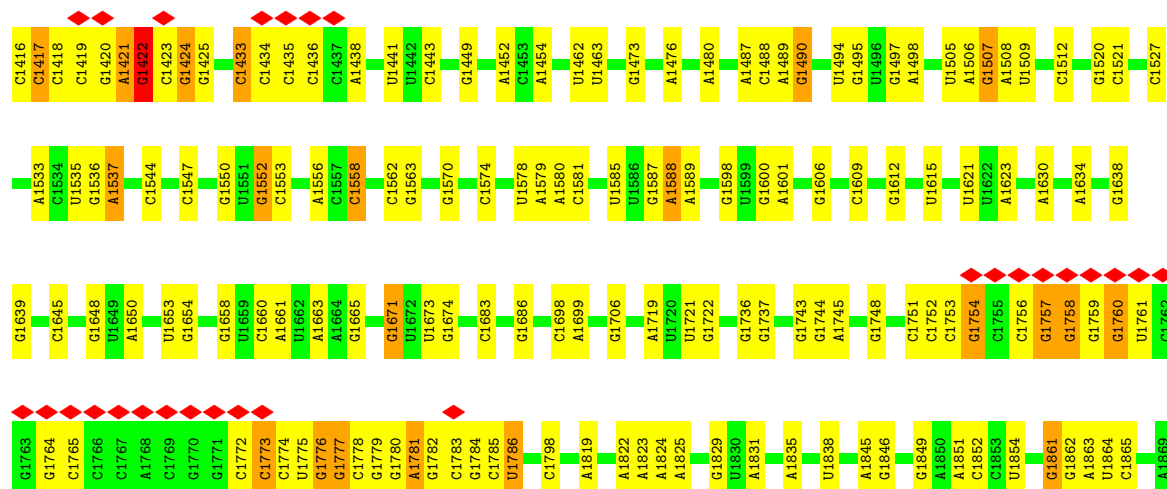


• Molecule 48: 60S ribosomal protein L10a

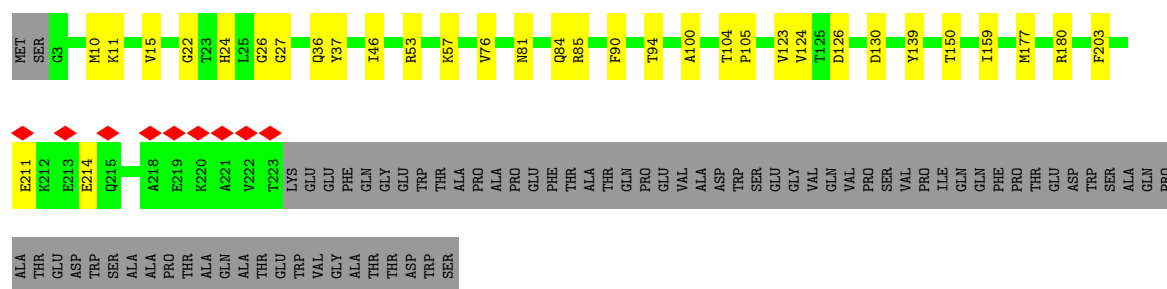


• Molecule 49: 18S ribosomal RNA

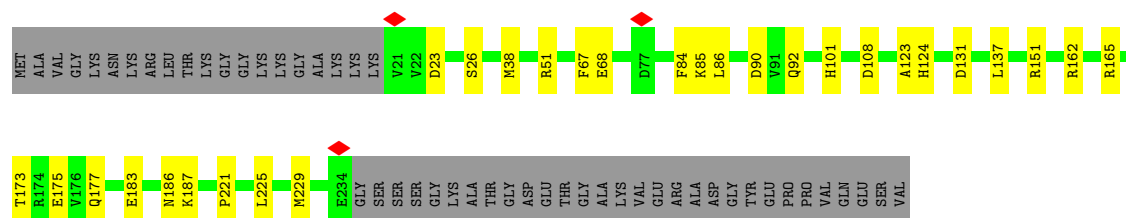




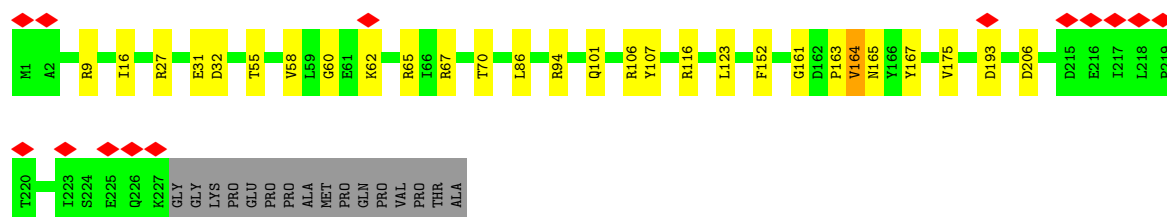
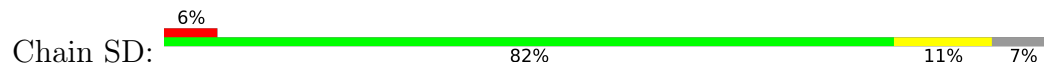
• Molecule 50: 40S ribosomal protein SA



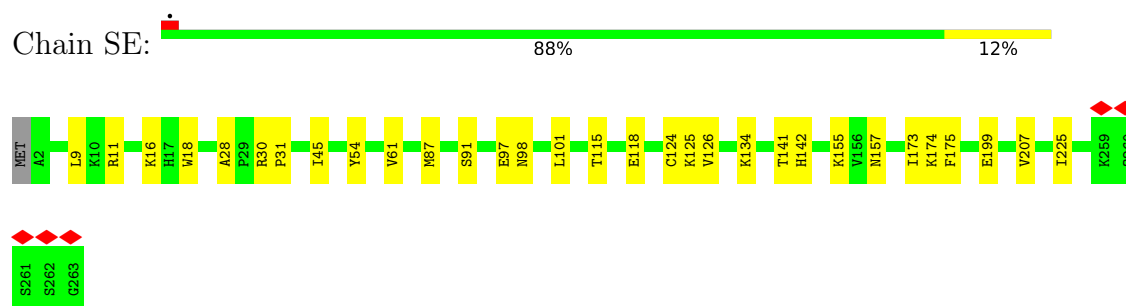
• Molecule 51: 40S ribosomal protein S3a



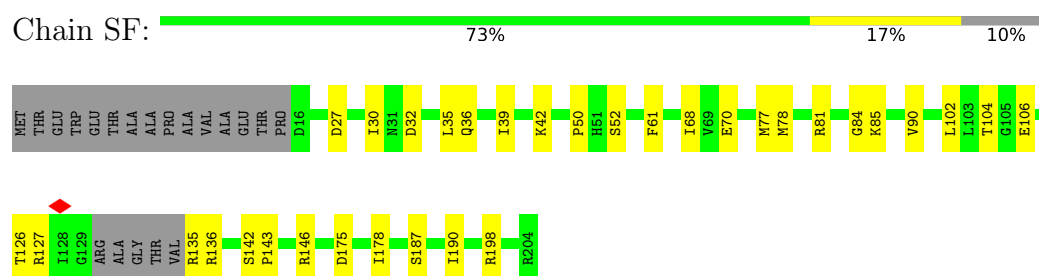
• Molecule 52: 40S ribosomal protein S3



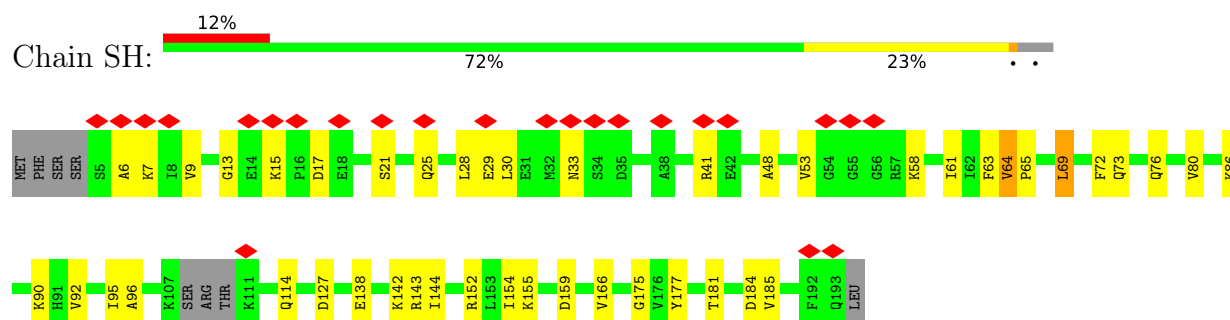
- Molecule 53: 40S ribosomal protein S4, X isoform



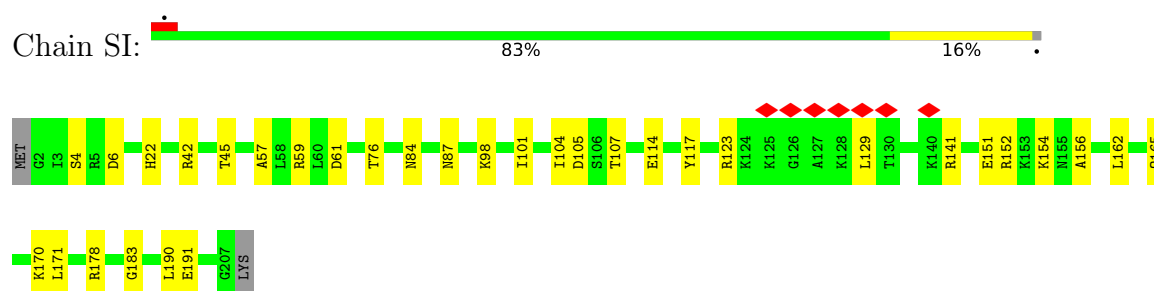
- Molecule 54: 40S ribosomal protein S5



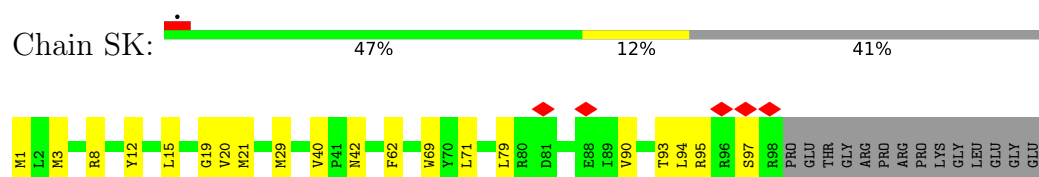
- Molecule 55: 40S ribosomal protein S7



- Molecule 56: 40S ribosomal protein S8



- Molecule 57: 40S ribosomal protein S10



ARG GLY GLU ALA ASP ARG ASP THR TYR ARG ARG SER SER ALA VAL PRO PRO GLY ALA ASP LYS LYS ALA GLU ALA GLY ALA GLY SER SER THR ALA PHE GLN PHE PHE GLY GLY PHE GLY ARG ARG GLN PRO PRO GLN

- Molecule 58: 40S ribosomal protein S11

Chain SL: 7% 92% 5% .

MET A2 K21 R22 V23 L24 L25 G26 E27 T28 G29 K30 E31 E49 K59 M82 R118 D119 V126 V145 Q154 PHE GLN LYS PHE

- Molecule 59: 40S ribosomal protein S15

Chain SP: 6% 74% 14% 11%

MET ALA VAL GLU GLN LYS LYS R10 T11 F12 R13 R18 G19 V20 D21 Q24 L25 L26 D27 M28 L33 L36 R40 K52 K65 H70 E71 V75 L80 G91 S92 M93 I107 Y115 E118 Y123 I133 S138 SER ARG PHE

- Molecule 60: 40S ribosomal protein S16

Chain SQ: 1% 84% 14% ..

MET PRO S3 R4 G5 P6 L7 L31 L32 K33 I42 E43 P44 R45 K50 L51 L52 E53 P54 K73 I81 R85 Q97 K105 D110 I113 G134 A139 R140 Q142 R146

- Molecule 61: 40S ribosomal protein S17

Chain SR: 5% 87% 13%

M1 R5 K10 E36 E37 R47 R67 G68 I69 Q74 E79 R80 R81 D82 R83 Y84 E87 E94 I95 I96 E97 G112 S113 L114 T120 V135

- Molecule 62: 40S ribosomal protein S18

Chain SS: 1% 76% 18% 5%

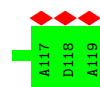
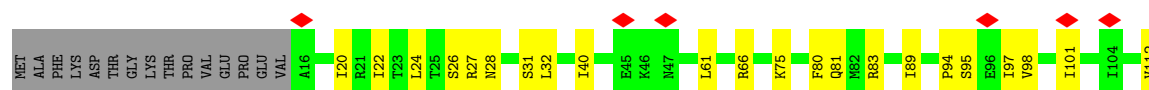
M1 S2 L3 V4 I5 K8 F9 Q10 H11 I12 V15 I20 R24 A29 I30 T31 A32 G35 V36 G37 R38 R39 Y40 T60 E61 D62 I68 R86 Q87 N105 R108 E109 D110 K115 R124 H125 F126 W127 R141 R142 G143 R144 T145 VAL GLY

- Molecule 63: 40S ribosomal protein S19

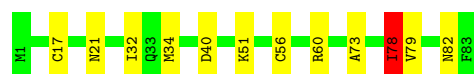
Chain ST: 1% 82% 17% .



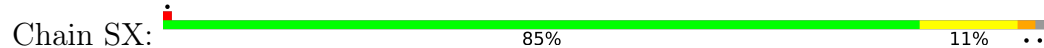
- Molecule 64: 40S ribosomal protein S20



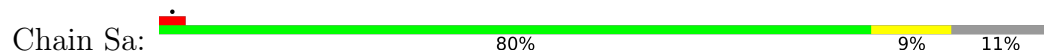
- Molecule 65: 40S ribosomal protein S21



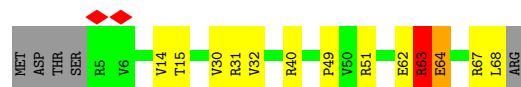
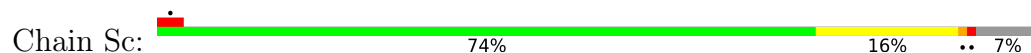
- Molecule 66: 40S ribosomal protein S23



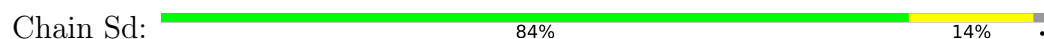
- Molecule 67: 40S ribosomal protein S26



- Molecule 68: 40S ribosomal protein S28

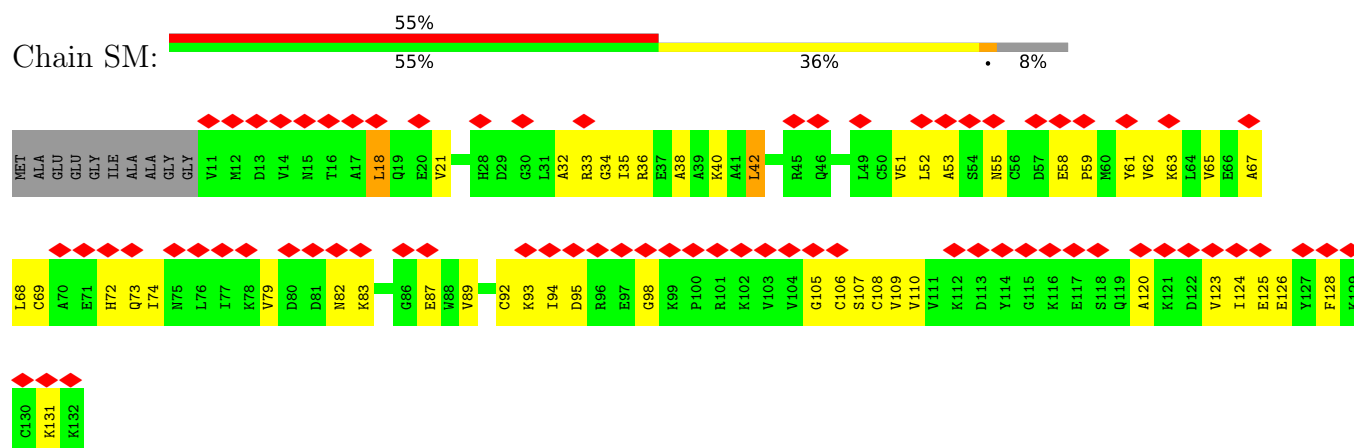


- Molecule 69: 40S ribosomal protein S29

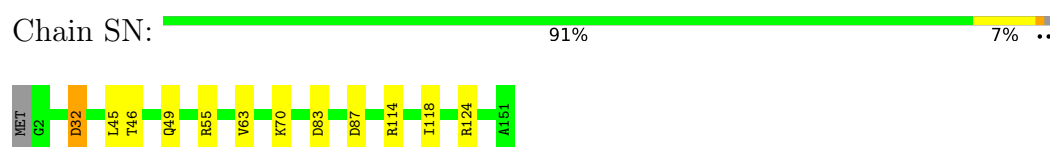




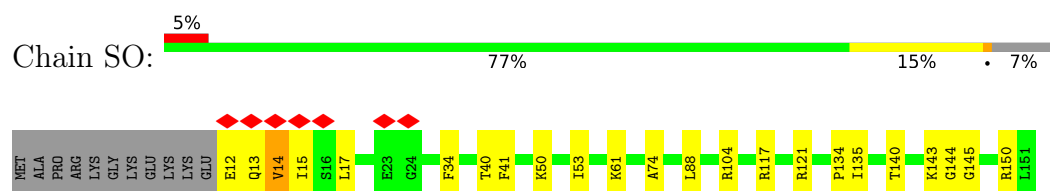
- Molecule 74: 40S ribosomal protein S12



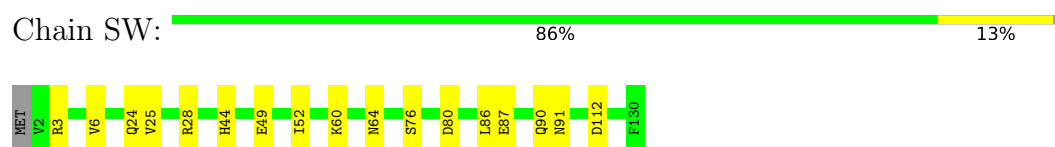
- Molecule 75: 40S ribosomal protein S13



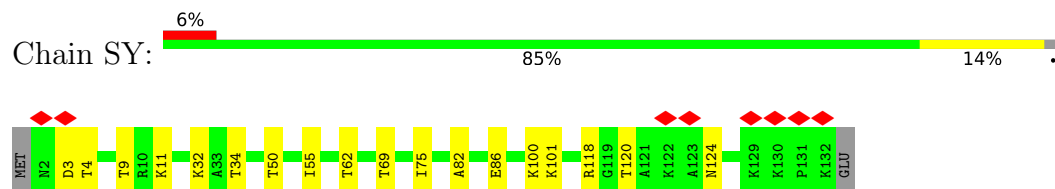
- Molecule 76: 40S ribosomal protein S14



- Molecule 77: 40S ribosomal protein S15a

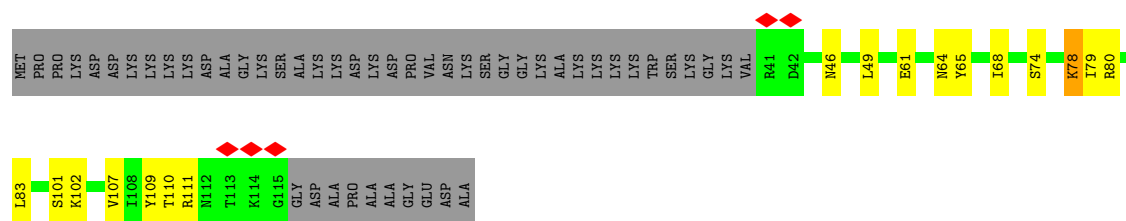


- Molecule 78: 40S ribosomal protein S24

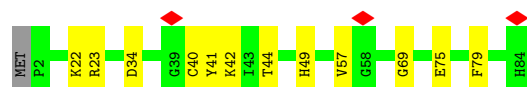
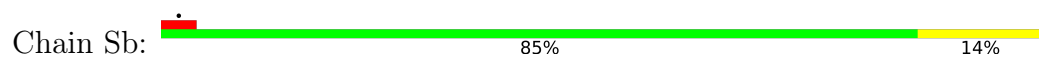


- Molecule 79: 40S ribosomal protein S25

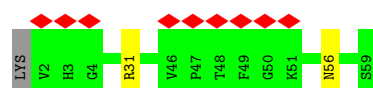




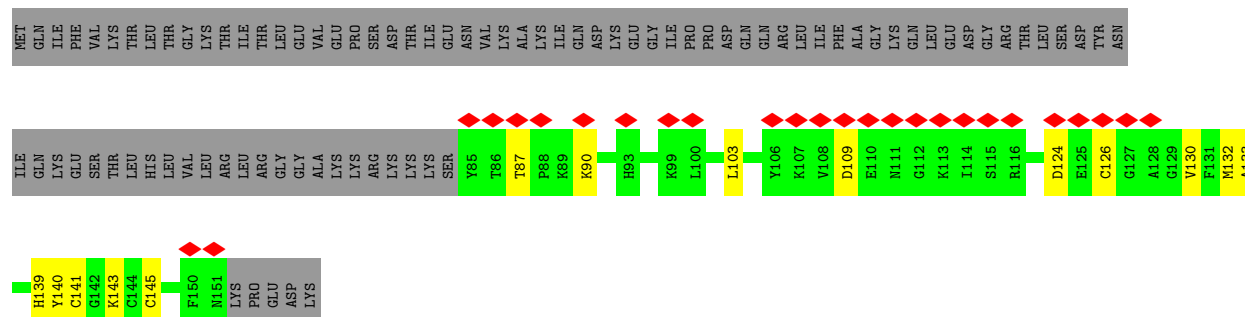
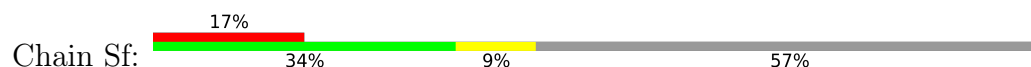
- Molecule 80: 40S ribosomal protein S27



- Molecule 81: 40S ribosomal protein S30

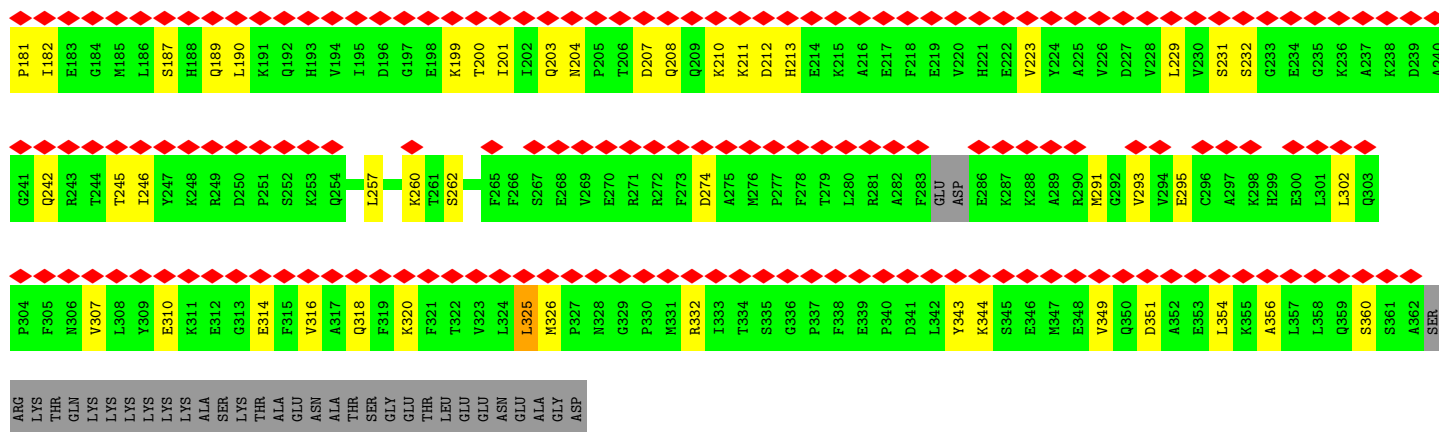


- Molecule 82: Ubiquitin-40S ribosomal protein S27a

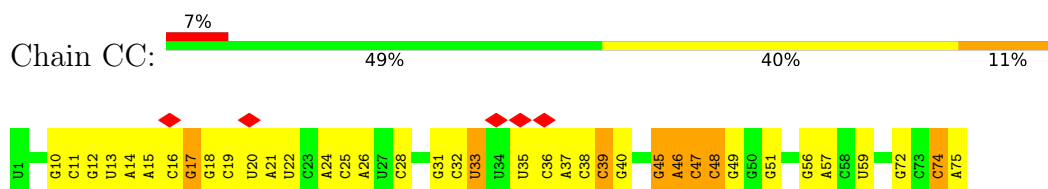


- Molecule 83: Proliferation-associated protein 2G4

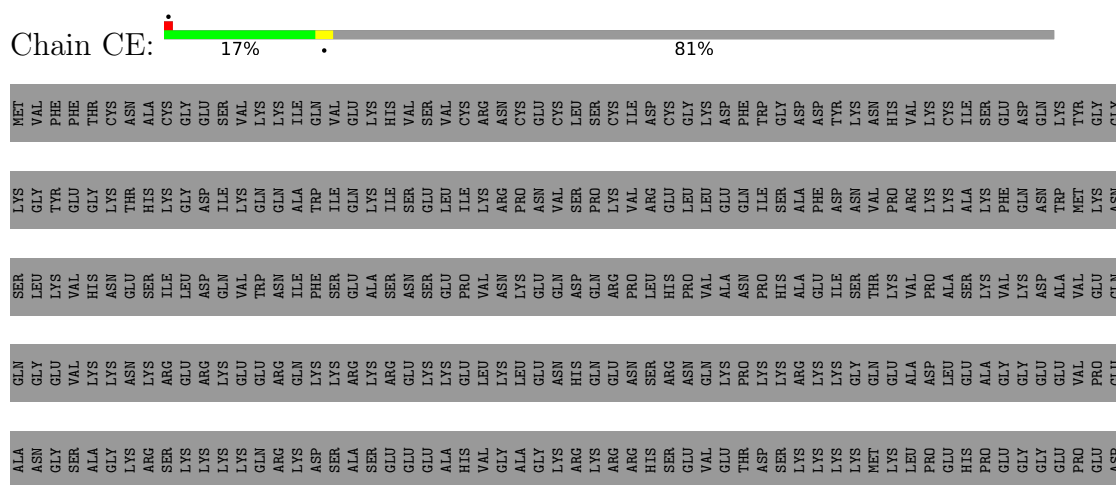




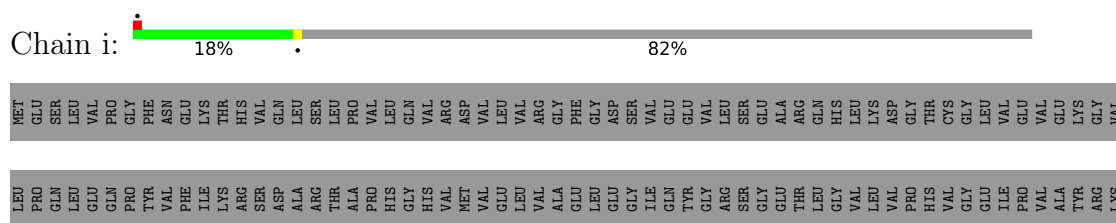
Molecule 84: tRNA



Molecule 85: Cell growth-regulating nucleolar protein



Molecule 86: Non-structural protein 1



VAL	LEU	LEU	ARG	LYS	ASN	GLY	ASN	LYS	GLY	ALA	GLY	GLY	HIS	SER	TYR	GLY	ALA	ASP	LEU	LYS	SER	PHE	ASP	LEU	GLY	ASP	E148	D152	G180
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	107149	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	0.518	Depositor
Minimum map value	-0.107	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.05	Depositor
Map size ($\text{\AA}$)	423.6, 423.6, 423.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.059, 1.059, 1.059	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	L5	0.41	0/89595	0.44	8/139686 (0.0%)
2	L7	0.38	0/2861	0.38	0/4459
3	L8	0.41	0/3701	0.39	0/5766
4	LA	0.43	0/1936	0.73	2/2596 (0.1%)
5	LB	0.38	0/3306	0.62	0/4424
6	LC	0.39	0/2981	0.65	4/4002 (0.1%)
7	LD	0.31	0/2428	0.57	0/3252
8	LE	0.31	0/1942	0.64	0/2606
9	LF	0.39	0/1905	0.65	2/2539 (0.1%)
10	LG	0.35	0/1960	0.65	0/2637
11	LH	0.35	0/1537	0.57	0/2066
12	LI	0.37	0/1673	0.59	0/2233
13	LJ	0.29	0/1433	0.74	3/1915 (0.2%)
14	LL	0.36	0/1732	0.65	0/2315
15	LM	0.36	0/1161	0.68	2/1554 (0.1%)
16	LN	0.42	0/1746	0.68	2/2338 (0.1%)
17	LO	0.37	0/1682	0.53	0/2250
18	LP	0.37	0/1268	0.57	0/1701
19	LQ	0.40	0/1537	0.58	0/2052
20	LR	0.35	0/1582	0.59	2/2091 (0.1%)
21	LS	0.37	0/1493	0.52	0/2003
22	LT	0.37	0/1326	0.60	0/1770
23	LU	0.30	0/839	0.68	0/1126
24	LV	0.35	0/993	0.57	0/1332
25	LW	0.33	0/1030	0.64	0/1364
26	LX	0.34	0/1002	0.55	0/1345
27	LY	0.37	0/1132	0.62	0/1504
28	LZ	0.34	0/1130	0.59	1/1507 (0.1%)
29	La	0.39	0/1191	0.59	0/1591
30	Lb	0.31	0/889	0.63	0/1175
31	Lc	0.37	0/774	0.63	0/1038
32	Ld	0.36	0/903	0.60	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.40	0/1071	0.64	0/1429
34	Lf	0.40	0/895	0.65	0/1198
35	Lg	0.36	0/916	0.56	0/1220
36	Lh	0.32	0/1023	0.49	0/1351
37	Li	0.30	0/843	0.53	0/1115
38	Lj	0.43	0/720	0.69	0/952
39	Lk	0.29	0/575	0.56	0/761
40	Ll	0.39	0/454	0.60	0/599
41	Lm	0.37	0/435	0.60	0/575
42	Ln	0.33	0/231	0.56	0/294
43	Lo	0.35	0/876	0.56	0/1156
44	Lp	0.38	0/718	0.55	0/953
45	Lr	0.37	0/1017	0.60	0/1364
46	Ls	0.30	0/1519	0.77	2/2052 (0.1%)
47	Lt	0.41	1/1058 (0.1%)	0.96	3/1430 (0.2%)
48	Lz	0.28	0/1769	0.76	0/2371
49	S2	0.36	0/41245	0.44	8/64265 (0.0%)
50	SA	0.34	0/1778	0.62	0/2416
51	SB	0.32	0/1765	0.59	0/2362
52	SD	0.30	0/1793	0.65	2/2414 (0.1%)
53	SE	0.33	0/2118	0.64	0/2849
54	SF	0.29	0/1481	0.62	0/1988
55	SH	0.34	0/1519	0.72	0/2033
56	SI	0.34	0/1715	0.62	2/2287 (0.1%)
57	SK	0.26	0/851	0.55	0/1147
58	SL	0.36	0/1268	0.58	0/1696
59	SP	0.26	0/1082	0.69	2/1446 (0.1%)
60	SQ	0.31	0/1160	0.65	0/1553
61	SR	0.28	0/1105	0.72	0/1484
62	SS	0.27	0/1216	0.59	0/1628
63	ST	0.27	0/1131	0.57	0/1515
64	SU	0.30	0/831	0.67	0/1115
65	SV	0.34	0/643	0.68	0/860
66	SX	0.36	0/1116	0.65	1/1490 (0.1%)
67	Sa	0.37	0/836	0.66	0/1121
68	Sc	0.32	0/508	0.76	2/680 (0.3%)
69	Sd	0.31	0/470	0.63	0/623
70	Sg	0.28	0/2493	0.69	0/3394
71	SC	0.37	0/1762	0.67	2/2381 (0.1%)
72	SG	0.29	0/1946	0.62	2/2590 (0.1%)
73	SJ	0.33	0/1550	0.60	0/2069
74	SM	0.30	0/950	0.90	2/1275 (0.2%)
75	SN	0.33	0/1232	0.55	0/1656

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SO	0.34	0/1062	0.66	2/1425 (0.1%)
77	SW	0.36	0/1051	0.55	0/1406
78	SY	0.28	0/1083	0.56	0/1438
79	SZ	0.33	0/604	0.79	0/810
80	Sb	0.31	0/665	0.57	0/891
81	Se	0.27	0/448	0.55	0/592
82	Sf	0.24	0/560	0.78	2/745 (0.3%)
83	CA	0.30	0/2810	0.78	2/3780 (0.1%)
84	CC	0.21	0/1773	0.40	1/2759 (0.0%)
85	CE	0.23	0/613	0.57	0/819
86	i	0.27	0/268	0.51	0/361
All	All	0.37	1/241289 (0.0%)	0.52	61/353636 (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	2
5	LB	0	2
8	LE	0	1
11	LH	0	2
12	LI	0	1
14	LL	0	1
15	LM	0	2
17	LO	0	1
22	LT	0	3
29	La	0	1
32	Ld	0	1
34	Lf	0	2
36	Lh	0	1
38	Lj	0	1
45	Lr	0	1
46	Ls	0	1
47	Lt	0	6
48	Lz	0	1
51	SB	0	1
52	SD	0	1
54	SF	0	2
55	SH	0	2
60	SQ	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
61	SR	0	1
63	ST	0	1
65	SV	0	1
66	SX	0	4
68	Sc	0	1
73	SJ	0	1
79	SZ	0	2
80	Sb	0	1
All	All	0	49

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	Lt	29	ALA	C-N	6.34	1.40	1.34

All (61) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	SP	107	ILE	CA-C-N	9.35	151.06	121.98
59	SP	107	ILE	C-N-CA	9.35	151.06	121.98
74	SM	98	GLY	CA-C-N	8.89	143.50	121.80
74	SM	98	GLY	C-N-CA	8.89	143.50	121.80
47	Lt	149	HIS	N-CA-C	6.82	121.87	112.04
46	Ls	105	ASN	CA-C-N	6.79	134.52	121.54
46	Ls	105	ASN	C-N-CA	6.79	134.52	121.54
15	LM	87	ALA	CA-C-N	6.70	134.33	121.54
15	LM	87	ALA	C-N-CA	6.70	134.33	121.54
6	LC	2	ALA	CA-C-N	6.66	133.69	121.70
6	LC	2	ALA	C-N-CA	6.66	133.69	121.70
49	S2	583	A	C1'-C2'-O2'	-6.36	98.86	108.40
49	S2	1417	C	N3-C4-N4	-6.35	98.96	118.00
47	Lt	8	ASN	CA-C-N	6.30	133.57	121.54
47	Lt	8	ASN	C-N-CA	6.30	133.57	121.54
76	SO	14	VAL	CA-C-N	6.20	132.86	121.70
76	SO	14	VAL	C-N-CA	6.20	132.86	121.70
9	LF	220	MET	CA-C-N	6.01	133.03	121.54
9	LF	220	MET	C-N-CA	6.01	133.03	121.54
84	CC	74	C	C2'-C3'-O3'	5.98	122.67	113.70
13	LJ	8	LYS	N-CA-C	-5.86	107.36	114.75
68	Sc	63	ARG	CA-C-N	5.84	132.69	121.54
68	Sc	63	ARG	C-N-CA	5.84	132.69	121.54
28	LZ	75	TYR	N-CA-C	5.77	117.74	110.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	LJ	117	ILE	CA-C-N	5.75	129.00	120.90
13	LJ	117	ILE	C-N-CA	5.75	129.00	120.90
82	Sf	90	LYS	CA-C-N	5.67	132.37	121.54
82	Sf	90	LYS	C-N-CA	5.67	132.37	121.54
56	SI	129	LEU	CA-C-N	5.65	130.50	121.62
56	SI	129	LEU	C-N-CA	5.65	130.50	121.62
20	LR	38	ARG	CA-C-N	5.60	132.24	121.54
20	LR	38	ARG	C-N-CA	5.60	132.24	121.54
1	L5	456	C	O4'-C1'-N1	5.53	116.49	108.20
49	S2	585	C	C4'-C3'-O3'	5.49	121.24	113.00
16	LN	123	GLU	CA-C-N	5.49	132.02	121.54
16	LN	123	GLU	C-N-CA	5.49	132.02	121.54
71	SC	63	VAL	CA-C-N	5.33	131.72	121.54
71	SC	63	VAL	C-N-CA	5.33	131.72	121.54
49	S2	582	U	C1'-C2'-O2'	-5.32	100.42	108.40
66	SX	127	ASN	N-CA-C	5.31	122.10	110.80
4	LA	55	GLY	CA-C-N	5.26	134.64	121.80
4	LA	55	GLY	C-N-CA	5.26	134.64	121.80
52	SD	193	ASP	N-CA-C	5.25	120.70	113.77
49	S2	1422	G	N1-C6-O6	-5.22	104.24	119.90
49	S2	420	G	C2'-C3'-O3'	5.20	121.50	113.70
1	L5	406	C	C2'-C3'-O3'	5.14	121.41	113.70
1	L5	485	C	C2-N1-C1'	5.14	134.23	118.80
6	LC	47	ASN	CA-C-N	-5.13	113.74	122.56
6	LC	47	ASN	C-N-CA	-5.13	113.74	122.56
49	S2	688	U	P-O3'-C3'	5.10	127.86	120.20
1	L5	2760	G	P-O3'-C3'	5.08	127.82	120.20
83	CA	325	LEU	CA-C-N	5.08	132.20	123.11
83	CA	325	LEU	C-N-CA	5.08	132.20	123.11
1	L5	417	G	O4'-C1'-N9	5.06	115.80	108.20
1	L5	1082	C	P-O3'-C3'	5.06	127.79	120.20
1	L5	914	U	P-O3'-C3'	5.05	127.78	120.20
49	S2	1417	C	C5-C4-N4	5.05	135.35	120.20
72	SG	81	HIS	CA-C-N	5.04	131.16	121.54
72	SG	81	HIS	C-N-CA	5.04	131.16	121.54
52	SD	165	ASN	N-CA-C	-5.03	106.50	113.18
1	L5	2786	C	C2'-C3'-O3'	5.00	121.20	113.70

There are no chirality outliers.

All (49) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	LA	110	GLY	Peptide
4	LA	54	ARG	Peptide
5	LB	17	LEU	Peptide
5	LB	258	HIS	Peptide
8	LE	129	GLY	Peptide
11	LH	106	GLN	Peptide
11	LH	173	ARG	Peptide
12	LI	54	SER	Peptide
14	LL	154	VAL	Peptide
15	LM	87	ALA	Peptide
15	LM	88	ALA	Peptide
17	LO	110	PRO	Peptide
22	LT	135	PRO	Peptide
22	LT	136	ARG	Peptide
22	LT	80	VAL	Peptide
29	La	22	ILE	Peptide
32	Ld	59	THR	Peptide
34	Lf	103	VAL	Peptide
34	Lf	106	TYR	Peptide
36	Lh	86	LYS	Peptide
38	Lj	39	TYR	Peptide
45	Lr	20	ARG	Peptide
46	Ls	149	ARG	Peptide
47	Lt	140	GLY	Peptide
47	Lt	141	CYS	Peptide
47	Lt	147	HIS	Peptide
47	Lt	148	PRO	Peptide
47	Lt	53	TRP	Peptide
47	Lt	9	GLU	Peptide
48	Lz	183	ILE	Peptide
51	SB	221	PRO	Peptide
52	SD	164	VAL	Peptide
54	SF	126	THR	Peptide
54	SF	78	MET	Peptide
55	SH	13	GLY	Peptide
55	SH	15	LYS	Peptide
73	SJ	137	VAL	Peptide
60	SQ	43	GLU	Peptide
61	SR	84	TYR	Peptide
63	ST	46	ALA	Peptide
65	SV	78	ILE	Peptide
66	SX	125	VAL	Peptide
66	SX	126	ALA	Peptide

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Mol	Chain	Res	Type	Group
66	SX	77	ASN	Peptide
66	SX	86	PRO	Peptide
79	SZ	46	ASN	Peptide
79	SZ	78	LYS	Peptide
80	Sb	75	GLU	Peptide
68	Sc	63	ARG	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L5	80138	0	40380	321	0
2	L7	2561	0	1295	6	0
3	L8	3314	0	1683	6	0
4	LA	1898	0	1993	9	0
5	LB	3238	0	3376	29	0
6	LC	2927	0	3104	16	0
7	LD	2382	0	2410	15	0
8	LE	1904	0	2055	22	0
9	LF	1870	0	1996	15	0
10	LG	1927	0	2074	13	0
11	LH	1518	0	1601	17	0
12	LI	1634	0	1671	17	0
13	LJ	1410	0	1441	18	0
14	LL	1701	0	1818	17	0
15	LM	1138	0	1204	12	0
16	LN	1701	0	1749	8	0
17	LO	1650	0	1794	9	0
18	LP	1242	0	1269	9	0
19	LQ	1513	0	1628	10	0
20	LR	1566	0	1729	14	0
21	LS	1453	0	1490	10	0
22	LT	1298	0	1366	16	0
23	LU	825	0	850	7	0
24	LV	979	0	1039	4	0
25	LW	1015	0	1079	15	0
26	LX	985	0	1066	8	0
27	LY	1115	0	1205	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	LZ	1107	0	1182	8	0
29	La	1162	0	1213	7	0
30	Lb	876	0	948	6	0
31	Lc	764	0	804	8	0
32	Ld	888	0	930	7	0
33	Le	1053	0	1147	7	0
34	Lf	876	0	912	9	0
35	Lg	906	0	998	7	0
36	Lh	1015	0	1148	8	0
37	Li	832	0	917	2	0
38	Lj	705	0	736	8	0
39	Lk	569	0	637	9	0
40	Ll	444	0	483	3	0
41	Lm	429	0	465	9	0
42	Ln	230	0	276	2	0
43	Lo	862	0	929	6	0
44	Lp	708	0	756	1	0
45	Lr	1002	0	1068	10	0
46	Ls	1496	0	1540	25	0
47	Lt	1046	0	1076	22	0
48	Lz	1741	0	1854	41	0
49	S2	36899	0	18602	188	0
50	SA	1741	0	1746	23	0
51	SB	1738	0	1809	20	0
52	SD	1765	0	1865	17	0
53	SE	2076	0	2177	16	0
54	SF	1461	0	1511	22	0
55	SH	1497	0	1590	28	0
56	SI	1686	0	1772	21	0
57	SK	827	0	854	13	0
58	SL	1247	0	1323	6	0
59	SP	1061	0	1107	14	0
60	SQ	1142	0	1213	13	0
61	SR	1090	0	1149	10	0
62	SS	1198	0	1261	18	0
63	ST	1112	0	1146	15	0
64	SU	821	0	883	16	0
65	SV	636	0	637	9	0
66	SX	1098	0	1167	9	0
67	Sa	821	0	870	8	0
68	Sc	506	0	536	9	0
69	Sd	459	0	452	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
70	Sg	2436	0	2393	51	0
71	SC	1725	0	1813	12	0
72	SG	1923	0	2089	26	0
73	SJ	1525	0	1640	12	0
74	SM	940	0	965	49	0
75	SN	1208	0	1294	9	0
76	SO	1049	0	1073	16	0
77	SW	1034	0	1080	10	0
78	SY	1065	0	1142	13	0
79	SZ	598	0	656	11	0
80	Sb	651	0	672	7	0
81	Se	443	0	469	2	0
82	Sf	548	0	553	11	0
83	CA	2764	0	2779	59	0
84	CC	1589	0	810	20	0
85	CE	603	0	660	5	0
86	i	263	0	234	1	0
87	L5	212	0	0	0	0
87	L7	3	0	0	0	0
87	L8	4	0	0	0	0
87	LA	1	0	0	0	0
87	LI	1	0	0	0	0
87	LP	1	0	0	0	0
87	LV	1	0	0	0	0
87	Le	1	0	0	0	0
87	Lg	1	0	0	0	0
87	Lj	1	0	0	0	0
87	S2	30	0	0	0	0
88	Lg	1	0	0	0	0
88	Lj	1	0	0	0	0
88	Lm	1	0	0	0	0
88	Lo	1	0	0	0	0
88	Lp	1	0	0	0	0
88	Sa	1	0	0	0	0
88	Sd	1	0	0	0	0
88	Sf	1	0	0	0	0
All	All	225122	0	168376	1408	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (1408) 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)
74:SM:52:LEU:CD2	74:SM:108:CYS:HB3	1.68	1.22
74:SM:52:LEU:HD23	74:SM:108:CYS:HB3	1.23	1.11
49:S2:1756:C:H42	49:S2:1776:G:N2	1.49	1.09
49:S2:1756:C:N4	49:S2:1776:G:H22	1.52	1.06
74:SM:52:LEU:HD23	74:SM:108:CYS:CB	1.86	1.05
49:S2:886:A:N6	49:S2:901:G:C4	2.25	1.04
74:SM:52:LEU:HD11	74:SM:65:VAL:CG2	1.90	1.01
74:SM:52:LEU:CD2	74:SM:108:CYS:CB	2.39	1.00
1:L5:1443:A:C2	1:L5:2103:G:N1	2.30	0.99
1:L5:1175:A:C2	1:L5:1185:G:N1	2.31	0.98
1:L5:1175:A:H2	1:L5:1185:G:N1	1.60	0.98
1:L5:1176:C:H42	1:L5:1184:A:N6	1.61	0.97
1:L5:1176:C:N4	1:L5:1184:A:H61	1.61	0.96
74:SM:52:LEU:HD11	74:SM:65:VAL:HG21	1.46	0.96
1:L5:1762:C:N4	1:L5:1770:A:C2	2.34	0.95
84:CC:11:C:H42	84:CC:24:A:H61	1.07	0.95
1:L5:1095:A:H2	1:L5:1200:G:H1	1.06	0.95
84:CC:11:C:H42	84:CC:24:A:N6	1.64	0.95
1:L5:1443:A:H2	1:L5:2103:G:H1	1.10	0.94
1:L5:1175:A:H2	1:L5:1185:G:H1	0.98	0.92
49:S2:1609:C:H42	49:S2:1630:A:H61	0.97	0.92
66:SX:101:LEU:HB3	66:SX:123:VAL:O	1.71	0.91
1:L5:4906:U:H3	1:L5:4915:G:H1	1.21	0.87
83:CA:80:ILE:HA	83:CA:107:LYS:O	1.75	0.87
1:L5:1445:U:C2	1:L5:2102:G:O6	2.29	0.86
84:CC:11:C:N4	84:CC:24:A:H61	1.73	0.85
1:L5:493:G:H1	1:L5:660:A:H2	1.20	0.85
49:S2:1609:C:N4	49:S2:1630:A:H61	1.74	0.84
1:L5:1095:A:C2	1:L5:1200:G:N1	2.45	0.84
49:S2:1609:C:H42	49:S2:1630:A:N6	1.75	0.83
1:L5:1976:G:N1	1:L5:1991:A:C2	2.48	0.82
1:L5:1996:C:H42	1:L5:2000:G:N2	1.78	0.82
11:LH:12:ILE:HB	11:LH:53:LYS:O	1.79	0.81
1:L5:1443:A:H2	1:L5:2103:G:N1	1.74	0.81
51:SB:173:THR:O	51:SB:177:GLN:HB2	1.80	0.81
52:SD:163:PRO:O	52:SD:167:TYR:HB2	1.81	0.80
49:S2:925:G:H1	49:S2:1017:U:H3	1.28	0.80
1:L5:2557:G:H1	1:L5:2570:U:H3	1.28	0.80
41:Lm:98:LYS:HD2	41:Lm:118:THR:HG21	1.65	0.78
5:LB:223:THR:HG22	5:LB:275:HIS:H	1.48	0.78
83:CA:78:THR:HA	83:CA:109:ASP:O	1.84	0.77
11:LH:59:LYS:HE3	11:LH:66:GLU:HB3	1.66	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:1095:A:H2	1:L5:1200:G:N1	1.82	0.76
49:S2:928:G:H1	49:S2:1013:U:H3	1.32	0.76
1:L5:4242:U:H3	1:L5:4281:A:H2	1.33	0.75
55:SH:72:PHE:O	55:SH:76:GLN:HB2	1.85	0.75
1:L5:2112:G:H2'	1:L5:2113:G:H5''	1.69	0.74
1:L5:387:G:HO2'	1:L5:412:G:H1	1.32	0.74
83:CA:134:GLN:HE22	83:CA:344:LYS:HB2	1.52	0.73
1:L5:1445:U:O2	1:L5:2102:G:C6	2.41	0.73
49:S2:60:G:H22	49:S2:316:G:H21	1.36	0.73
15:LM:77:TRP:O	15:LM:81:ASP:HA	1.89	0.73
70:Sg:46:THR:O	70:Sg:52:TYR:HA	1.89	0.72
74:SM:52:LEU:HD13	74:SM:65:VAL:HG11	1.70	0.72
49:S2:563:G:H1	49:S2:592:C:H5	1.39	0.70
70:Sg:174:VAL:HB	70:Sg:188:HIS:HB2	1.73	0.70
83:CA:81:SER:HB2	83:CA:107:LYS:HD2	1.73	0.70
1:L5:3751:G:H21	1:L5:3775:A:H8	1.35	0.70
16:LN:124:ASP:HB3	16:LN:127:TYR:H	1.56	0.70
1:L5:493:G:N1	1:L5:660:A:C2	2.59	0.70
72:SG:21:GLU:O	72:SG:25:ARG:HB2	1.91	0.70
49:S2:886:A:N6	49:S2:901:G:C5	2.60	0.69
49:S2:582:U:O2'	49:S2:583:A:H5''	1.91	0.69
84:CC:15:A:N1	84:CC:47:C:N3	2.41	0.69
1:L5:1996:C:N4	1:L5:2000:G:H22	1.91	0.69
13:LJ:21:CYS:HB2	13:LJ:131:TYR:O	1.93	0.68
1:L5:3955:G:C2	1:L5:3966:A:N7	2.61	0.68
74:SM:52:LEU:HD11	74:SM:65:VAL:HG22	1.73	0.68
73:SJ:113:GLN:O	73:SJ:117:LEU:HB2	1.92	0.68
5:LB:92:TYR:HB2	5:LB:159:VAL:HB	1.76	0.68
49:S2:837:A:H61	78:SY:9:THR:H	1.40	0.68
1:L5:2517:A:H5'	35:Lg:62:LYS:HD3	1.76	0.68
83:CA:138:ARG:HE	83:CA:232:SER:HB2	1.58	0.68
1:L5:1976:G:C6	1:L5:1991:A:N1	2.62	0.67
1:L5:4093:G:N1	1:L5:4114:C:C2	2.62	0.67
82:Sf:141:CYS:O	82:Sf:145:CYS:HA	1.95	0.67
1:L5:1176:C:N3	1:L5:1184:A:N1	2.44	0.66
1:L5:2469:C:H5	1:L5:2471:G:H1	1.43	0.66
70:Sg:30:MET:HA	70:Sg:43:TRP:O	1.95	0.66
16:LN:135:ILE:HG23	16:LN:142:ILE:HD13	1.78	0.66
49:S2:940:U:H3	49:S2:1002:U:H3	1.43	0.66
83:CA:154:LEU:HD11	83:CA:332:ARG:HB2	1.77	0.66
6:LC:218:ILE:O	6:LC:222:ARG:HB3	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:1609:C:N3	49:S2:1630:A:N1	2.44	0.65
22:LT:43:LYS:O	22:LT:58:HIS:ND1	2.28	0.65
54:SF:104:THR:HG23	54:SF:106:GLU:H	1.61	0.65
10:LG:187:LYS:HG2	10:LG:198:THR:HB	1.78	0.65
52:SD:106:ARG:HG2	52:SD:175:VAL:HG22	1.77	0.65
1:L5:3951:G:N1	1:L5:4060:U:N3	2.45	0.65
70:Sg:247:TRP:HA	70:Sg:259:TRP:O	1.97	0.65
66:SX:123:VAL:HG12	66:SX:124:LYS:HG3	1.78	0.65
84:CC:10:G:N7	84:CC:45:G:N1	2.44	0.65
78:SY:82:ALA:O	78:SY:86:GLU:HB3	1.96	0.64
84:CC:11:C:N3	84:CC:24:A:N1	2.45	0.64
46:Ls:28:PHE:HB2	46:Ls:89:VAL:HG22	1.78	0.64
1:L5:4891:G:H1	1:L5:4928:C:H5	1.45	0.64
1:L5:2902:G:N7	1:L5:2903:G:N2	2.45	0.64
57:SK:29:MET:SD	57:SK:42:ASN:ND2	2.70	0.64
1:L5:4985:U:O2	5:LB:174:ARG:NH1	2.30	0.64
49:S2:885:U:H3	49:S2:901:G:H1	1.46	0.64
13:LJ:7:GLU:HG3	13:LJ:10:ASN:HD21	1.63	0.64
14:LL:16:LYS:O	14:LL:21:ARG:NH1	2.31	0.63
72:SG:33:ALA:N	72:SG:52:ILE:O	2.31	0.63
83:CA:158:LYS:NZ	83:CA:326:MET:O	2.31	0.63
21:LS:77:ASN:HB2	21:LS:132:ILE:O	1.99	0.63
68:Sc:40:ARG:HH11	76:SO:117:ARG:HH22	1.44	0.63
17:LO:27:VAL:HG13	17:LO:98:ALA:HB1	1.81	0.63
49:S2:1754:G:N7	49:S2:1779:G:N2	2.47	0.63
83:CA:181:PRO:HB2	83:CA:204:ASN:HB2	1.78	0.63
1:L5:2021:G:H5"	46:Ls:58:ASN:HB2	1.81	0.63
1:L5:4093:G:N1	1:L5:4114:C:N3	2.48	0.62
14:LL:50:PRO:HB3	14:LL:150:LEU:HB3	1.81	0.62
1:L5:3955:G:N2	1:L5:3966:A:C5	2.68	0.62
1:L5:3967:G:N1	1:L5:4055:U:N3	2.47	0.62
83:CA:86:VAL:HG12	83:CA:316:VAL:HG11	1.81	0.62
1:L5:1095:A:N1	1:L5:1200:G:O6	2.33	0.62
55:SH:30:LEU:O	55:SH:33:ASN:ND2	2.32	0.62
1:L5:512:U:H3	1:L5:647:G:H1	1.48	0.62
1:L5:3949:A:H62	1:L5:4064:C:H42	1.46	0.62
55:SH:154:ILE:HB	55:SH:185:VAL:HG12	1.82	0.62
49:S2:1756:C:N3	49:S2:1776:G:N1	2.46	0.62
55:SH:80:VAL:HG23	55:SH:92:VAL:HB	1.82	0.62
74:SM:68:LEU:HD23	74:SM:69:CYS:SG	2.40	0.62
8:LE:190:HIS:HD2	8:LE:192:LYS:H	1.48	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LH:120:GLU:OE2	11:LH:124:ARG:NH2	2.32	0.61
46:Ls:102:LEU:O	46:Ls:105:ASN:C	2.43	0.61
8:LE:141:ARG:NH2	8:LE:191:GLN:O	2.33	0.61
62:SS:141:ARG:O	62:SS:144:ARG:C	2.42	0.61
74:SM:106:CYS:SG	74:SM:107:SER:N	2.72	0.61
84:CC:15:A:N6	84:CC:47:C:O2	2.30	0.61
49:S2:1158:G:H5''	77:SW:76:SER:HB3	1.83	0.61
49:S2:1488:C:O2'	49:S2:1490:G:OP2	2.16	0.61
62:SS:4:VAL:HG12	62:SS:5:ILE:HG22	1.83	0.61
74:SM:52:LEU:HD22	74:SM:108:CYS:HB3	1.77	0.61
1:L5:493:G:O6	1:L5:660:A:N1	2.33	0.61
47:Lt:13:VAL:HA	47:Lt:63:THR:O	2.01	0.61
47:Lt:15:LEU:HA	47:Lt:61:LYS:O	2.00	0.61
48:Lz:203:ALA:HA	48:Lz:217:TYR:HA	1.82	0.61
49:S2:60:G:H22	49:S2:316:G:N2	1.99	0.61
49:S2:1751:C:H42	49:S2:1782:G:H21	1.47	0.61
74:SM:52:LEU:CD1	74:SM:65:VAL:HG21	2.28	0.61
48:Lz:58:THR:H	48:Lz:152:LYS:HZ3	1.49	0.61
1:L5:1445:U:C2	1:L5:2102:G:C6	2.89	0.61
55:SH:144:ILE:HG23	77:SW:52:ILE:HB	1.81	0.61
70:Sg:120:ILE:HB	70:Sg:132:TRP:HB2	1.83	0.60
71:SC:128:VAL:HG11	71:SC:155:ILE:HG22	1.82	0.60
1:L5:1996:C:H42	1:L5:2000:G:H22	1.43	0.60
22:LT:51:GLY:HA3	22:LT:92:ARG:HG3	1.84	0.60
46:Ls:47:LEU:HD11	46:Ls:101:MET:HE1	1.82	0.60
26:LX:129:ARG:O	26:LX:132:GLY:N	2.32	0.60
48:Lz:206:ILE:HG21	48:Lz:214:GLN:HB2	1.83	0.60
9:LF:105:VAL:HG13	9:LF:136:VAL:HG12	1.83	0.60
46:Ls:102:LEU:O	46:Ls:105:ASN:O	2.20	0.60
26:LX:87:MET:HB3	83:CA:291:MET:HE3	1.83	0.60
49:S2:1192:U:OP2	66:SX:119:ARG:NH2	2.34	0.60
1:L5:3971:G:N2	1:L5:3973:G:N3	2.49	0.60
70:Sg:247:TRP:HB3	70:Sg:258:ILE:HD11	1.83	0.60
1:L5:1513:U:H4'	14:LL:4:SER:HB2	1.83	0.60
18:LP:73:ALA:O	18:LP:76:TRP:O	2.20	0.60
1:L5:2611:A:H5'	1:L5:2688:G:H4'	1.83	0.60
6:LC:152:LEU:HD23	6:LC:251:ILE:HG12	1.84	0.60
1:L5:1364:U:OP2	14:LL:36:ARG:NH1	2.35	0.59
49:S2:959:G:OP1	76:SO:104:ARG:NH2	2.35	0.59
1:L5:1508:A:OP1	6:LC:110:ARG:NH1	2.36	0.59
55:SH:63:PHE:HA	55:SH:95:ILE:O	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:65:C:N4	72:SG:134:GLY:O	2.36	0.59
49:S2:582:U:C2'	49:S2:583:A:H5''	2.32	0.59
61:SR:79:GLU:O	61:SR:83:ASN:HB2	2.03	0.59
64:SU:80:PHE:HB3	69:Sd:52:PHE:HB3	1.84	0.59
74:SM:73:GLN:H	74:SM:74:ILE:HD12	1.68	0.59
1:L5:194:C:O2	27:LY:121:ARG:NH2	2.36	0.59
1:L5:4732:G:N2	1:L5:4734:A:N7	2.48	0.59
5:LB:356:LYS:O	5:LB:359:ALA:C	2.45	0.59
31:Lc:34:THR:HG23	31:Lc:95:ALA:HB2	1.83	0.59
83:CA:159:PRO:HD3	83:CA:325:LEU:HD11	1.83	0.59
1:L5:1762:C:N4	1:L5:1770:A:H2	1.94	0.59
1:L5:3589:G:N2	1:L5:3590:G:N7	2.51	0.59
11:LH:106:GLN:HB2	11:LH:111:LEU:HB3	1.83	0.59
48:Lz:54:ARG:HH22	48:Lz:153:SER:H	1.51	0.59
51:SB:85:LYS:HB3	51:SB:101:HIS:HB3	1.84	0.59
84:CC:10:G:N7	84:CC:45:G:C2	2.71	0.59
1:L5:4092:G:N7	1:L5:4114:C:N4	2.51	0.59
8:LE:223:ARG:HH11	8:LE:234:ASP:HB2	1.67	0.59
23:LU:56:LEU:HD12	23:LU:61:VAL:HB	1.84	0.59
49:S2:582:U:HO2'	49:S2:583:A:H5''	1.67	0.59
70:Sg:107:ASP:N	70:Sg:107:ASP:OD1	2.36	0.58
70:Sg:199:THR:HG21	70:Sg:240:CYS:HA	1.83	0.58
74:SM:42:LEU:HD13	74:SM:69:CYS:SG	2.43	0.58
1:L5:109:G:OP2	14:LL:74:ARG:NH2	2.35	0.58
49:S2:191:A:OP1	56:SI:141:ARG:NH2	2.36	0.58
74:SM:92:CYS:SG	74:SM:93:LYS:N	2.75	0.58
12:LI:156:LYS:HG3	12:LI:163:GLN:HB2	1.86	0.58
45:Lr:26:SER:OG	45:Lr:28:GLU:OE1	2.21	0.58
55:SH:25:GLN:HA	55:SH:28:LEU:HB2	1.85	0.58
1:L5:3951:G:H1	1:L5:4060:U:H3	1.48	0.58
7:LD:120:GLU:O	7:LD:248:ARG:NH1	2.37	0.58
27:LY:31:SER:HA	27:LY:48:PRO:HA	1.85	0.58
74:SM:128:PHE:HA	74:SM:131:LYS:HG2	1.84	0.58
25:LW:73:ARG:NH1	49:S2:1781:A:OP2	2.37	0.58
55:SH:58:LYS:HB2	55:SH:90:LYS:HG2	1.84	0.58
59:SP:33:LEU:HA	59:SP:36:LEU:HB2	1.85	0.58
75:SN:46:THR:H	75:SN:49:GLN:HE21	1.50	0.58
5:LB:356:LYS:O	5:LB:359:ALA:O	2.22	0.58
11:LH:31:ARG:NH1	11:LH:149:ASN:OD1	2.37	0.58
45:Lr:63:VAL:HG22	45:Lr:79:ARG:HB3	1.85	0.58
48:Lz:128:LEU:HD22	48:Lz:133:LYS:HD3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:1417:C:H42	49:S2:1422:G:H1	1.50	0.58
53:SE:45:ILE:HA	53:SE:61:VAL:HG11	1.84	0.58
83:CA:293:VAL:HG23	83:CA:302:LEU:HD12	1.86	0.58
7:LD:41:LYS:NZ	22:LT:32:ARG:O	2.37	0.58
12:LI:187:LYS:NZ	12:LI:189:CYS:SG	2.74	0.58
27:LY:39:ARG:O	27:LY:42:TYR:O	2.22	0.58
76:SO:14:VAL:HG21	76:SO:17:LEU:HB2	1.86	0.58
83:CA:173:VAL:HG23	83:CA:354:LEU:HD13	1.85	0.58
1:L5:2578:G:N7	28:LZ:17:ARG:NH1	2.52	0.58
49:S2:834:C:H42	49:S2:839:C:H42	1.50	0.58
1:L5:4041:C:O2'	48:Lz:102:LYS:O	2.22	0.57
64:SU:61:LEU:O	64:SU:81:GLN:HA	2.03	0.57
74:SM:59:PRO:HA	74:SM:62:VAL:HG22	1.85	0.57
47:Lt:105:THR:HA	47:Lt:143:VAL:HG22	1.86	0.57
76:SO:34:PHE:HB3	76:SO:41:PHE:HB2	1.86	0.57
84:CC:25:C:H2'	84:CC:26:A:H8	1.68	0.57
4:LA:137:ILE:HD11	4:LA:149:LYS:HB2	1.86	0.57
74:SM:52:LEU:HD21	74:SM:108:CYS:CB	2.33	0.57
1:L5:1175:A:N1	1:L5:1185:G:O6	2.38	0.57
1:L5:1952:G:H4'	21:LS:93:MET:HG3	1.85	0.57
1:L5:4882:U:OP1	15:LM:117:LYS:NZ	2.36	0.57
49:S2:581:U:C2'	49:S2:582:U:H5'	2.34	0.57
64:SU:22:ILE:HD11	64:SU:112:VAL:HG13	1.87	0.57
67:Sa:32:LYS:O	67:Sa:37:LYS:NZ	2.37	0.57
85:CE:360:LYS:O	85:CE:364:LYS:HB2	2.03	0.57
11:LH:12:ILE:HD13	11:LH:18:ILE:HG21	1.86	0.57
13:LJ:35:ARG:HD2	13:LJ:123:ILE:HA	1.85	0.57
61:SR:36:GLU:OE1	61:SR:47:ARG:NH1	2.37	0.57
70:Sg:73:SER:OG	70:Sg:117:ASN:ND2	2.38	0.57
1:L5:1100:U:O3'	1:L5:1167:C:N4	2.38	0.57
1:L5:1443:A:H61	1:L5:2104:G:H21	1.50	0.57
13:LJ:51:SER:HB2	13:LJ:69:ALA:HB3	1.86	0.57
49:S2:1284:A:N7	74:SM:33:ARG:NH2	2.53	0.57
13:LJ:95:ARG:HH21	13:LJ:178:LYS:HD3	1.70	0.57
49:S2:672:A:N6	49:S2:1027:A:OP1	2.33	0.57
49:S2:874:G:H21	55:SH:114:GLN:HE22	1.53	0.57
50:SA:37:TYR:OH	50:SA:57:LYS:NZ	2.38	0.57
74:SM:89:VAL:HG21	74:SM:109:VAL:HG11	1.87	0.57
1:L5:2092:G:O2'	1:L5:2262:G:N2	2.38	0.56
1:L5:260:C:H2'	1:L5:261:G:H8	1.70	0.56
1:L5:364:G:O6	38:Lj:55:ARG:NH1	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:SH:69:LEU:HD13	55:SH:96:ALA:HB2	1.87	0.56
74:SM:69:CYS:O	74:SM:72:HIS:C	2.48	0.56
84:CC:13:U:H2'	84:CC:14:A:H8	1.71	0.56
41:Lm:98:LYS:HD2	41:Lm:118:THR:CG2	2.35	0.56
49:S2:1005:G:OP2	51:SB:162:ARG:NH1	2.38	0.56
54:SF:39:ILE:HG23	54:SF:68:ILE:HG13	1.87	0.56
59:SP:123:TYR:OH	62:SS:124:ARG:NH1	2.39	0.56
83:CA:182:ILE:HD11	83:CA:229:LEU:HD13	1.88	0.56
1:L5:1762:C:N3	1:L5:1770:A:N1	2.53	0.56
1:L5:4431:U:OP2	12:LI:3:ARG:NH2	2.38	0.56
6:LC:149:GLU:OE2	45:Lr:71:ARG:NH2	2.39	0.56
85:CE:346:GLU:OE1	85:CE:349:ARG:NH2	2.39	0.56
70:Sg:46:THR:OG1	70:Sg:51:ASN:O	2.22	0.56
49:S2:1017:U:H5'	75:SN:55:ARG:HD3	1.88	0.56
49:S2:1756:C:H42	49:S2:1776:G:H22	0.72	0.56
50:SA:10:MET:HE3	50:SA:15:VAL:HG22	1.87	0.56
51:SB:183:GLU:HA	51:SB:186:ASN:HB2	1.88	0.56
74:SM:42:LEU:CD1	74:SM:69:CYS:SG	2.94	0.56
1:L5:4546:A:N7	4:LA:215:ASN:ND2	2.54	0.56
49:S2:126:G:OP2	72:SG:198:ARG:NH1	2.39	0.56
52:SD:55:THR:HA	52:SD:58:VAL:HG12	1.88	0.56
55:SH:184:ASP:OD1	55:SH:184:ASP:N	2.38	0.56
77:SW:49:GLU:HB2	77:SW:64:ASN:HD22	1.71	0.56
1:L5:2000:G:N2	1:L5:2000:G:OP2	2.39	0.56
1:L5:2431:A:OP1	40:LI:41:ARG:NH1	2.38	0.56
19:LQ:122:THR:H	19:LQ:125:GLN:HE21	1.52	0.56
31:Lc:45:LEU:HD13	31:Lc:106:ARG:HH22	1.71	0.56
55:SH:7:LYS:HZ3	55:SH:17:ASP:HB3	1.70	0.56
83:CA:138:ARG:NH2	83:CA:178:ASN:O	2.38	0.56
1:L5:2427:G:OP1	20:LR:5:ARG:NH2	2.39	0.55
1:L5:3955:G:C2	1:L5:3966:A:C8	2.94	0.55
55:SH:144:ILE:HD11	55:SH:152:ARG:HB2	1.87	0.55
56:SI:162:LEU:HD23	56:SI:165:GLN:HE21	1.70	0.55
1:L5:2710:C:H5''	83:CA:260:LYS:HZ1	1.71	0.55
11:LH:171:ASP:O	11:LH:174:LYS:O	2.24	0.55
1:L5:493:G:N1	1:L5:660:A:H2	1.96	0.55
1:L5:1962:A:H5''	1:L5:2024:G:H22	1.71	0.55
1:L5:2468:U:O2'	1:L5:2506:G:N2	2.39	0.55
1:L5:2486:G:O6	1:L5:2493:G:O6	2.24	0.55
36:Lh:86:LYS:O	36:Lh:92:ARG:NH1	2.40	0.55
47:Lt:17:CYS:HA	47:Lt:59:THR:O	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:Lz:143:ASN:ND2	48:Lz:150:GLU:OE2	2.39	0.55
54:SF:187:SER:HB2	54:SF:190:ILE:HG12	1.88	0.55
1:L5:1996:C:N4	1:L5:2000:G:N2	2.49	0.55
46:Ls:18:ILE:HG23	46:Ls:69:LEU:HD12	1.88	0.55
46:Ls:98:ILE:HA	46:Ls:101:MET:HB3	1.89	0.55
1:L5:1697:G:N2	1:L5:2084:C:OP1	2.39	0.55
5:LB:117:ARG:HG2	5:LB:180:LEU:HD13	1.87	0.55
74:SM:125:GLU:HA	74:SM:128:PHE:HB2	1.87	0.55
1:L5:1273:G:OP2	30:Lb:117:ARG:NH2	2.37	0.55
1:L5:4031:U:OP2	48:Lz:26:ARG:NE	2.39	0.55
54:SF:32:ASP:O	54:SF:36:GLN:HB2	2.07	0.55
46:Ls:145:THR:HG22	46:Ls:154:ILE:HG13	1.89	0.55
49:S2:1414:A:O2'	63:ST:128:GLN:NE2	2.39	0.55
1:L5:1270:A:H8	1:L5:2106:G:H21	1.54	0.55
1:L5:2709:C:H5'	20:LR:43:LYS:HD2	1.88	0.54
43:Lo:33:LEU:HA	43:Lo:38:LYS:HG2	1.89	0.54
1:L5:1499:C:OP1	19:LQ:150:ARG:NH2	2.40	0.54
3:L8:96:C:OP1	36:Lh:70:ARG:NH1	2.40	0.54
45:Lr:7:TRP:O	45:Lr:11:ARG:HB2	2.07	0.54
46:Ls:25:PRO:HD2	46:Ls:92:LYS:HB3	1.88	0.54
54:SF:81:ARG:O	54:SF:85:LYS:NZ	2.39	0.54
74:SM:52:LEU:CD2	74:SM:108:CYS:HB2	2.31	0.54
1:L5:4281:A:H2'	1:L5:4282:A:H2'	1.89	0.54
1:L5:4377:G:O6	29:La:42:ARG:NH2	2.39	0.54
16:LN:120:TRP:HE1	16:LN:123:GLU:HG3	1.72	0.54
50:SA:126:ASP:O	50:SA:130:ASP:HB2	2.07	0.54
51:SB:131:ASP:OD1	51:SB:131:ASP:N	2.40	0.54
1:L5:2601:A:N6	1:L5:2744:A:OP2	2.39	0.54
21:LS:161:ARG:HE	21:LS:164:LYS:HB2	1.72	0.54
1:L5:2838:G:H5'	5:LB:247:GLY:HA2	1.89	0.54
55:SH:143:ARG:HB2	55:SH:155:LYS:HB2	1.89	0.54
74:SM:52:LEU:HD13	74:SM:65:VAL:CG1	2.37	0.54
1:L5:1279:A:O2'	6:LC:323:ARG:NH2	2.41	0.54
1:L5:2658:G:N2	1:L5:2676:A:OP2	2.32	0.54
1:L5:3955:G:C2	1:L5:3966:A:C5	2.96	0.54
46:Ls:190:GLN:HG3	46:Ls:191:GLN:HE21	1.73	0.54
50:SA:36:GLN:O	50:SA:53:ARG:NH1	2.41	0.54
1:L5:387:G:O2'	1:L5:412:G:N1	2.36	0.54
1:L5:2019:C:OP1	46:Ls:6:ARG:NH2	2.39	0.54
25:LW:106:GLU:HA	25:LW:109:ILE:HG22	1.90	0.54
49:S2:643:A:OP1	73:SJ:38:ARG:NH1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:SJ:122:SER:O	73:SJ:125:HIS:N	2.40	0.54
1:L5:1656:U:OP2	29:La:26:ARG:NH2	2.39	0.54
38:Lj:33:THR:HA	38:Lj:40:PRO:HD3	1.90	0.54
67:Sa:22:ARG:NH1	76:SO:145:GLY:O	2.41	0.54
1:L5:3969:G:O2'	1:L5:4054:C:N4	2.41	0.54
5:LB:220:ILE:HG12	5:LB:278:THR:HG23	1.89	0.54
8:LE:120:ASP:OD2	45:Lr:112:ARG:NH1	2.41	0.54
46:Ls:30:VAL:HG22	46:Ls:189:ILE:HG22	1.90	0.54
49:S2:326:C:O2	49:S2:327:G:N2	2.40	0.54
1:L5:4472:G:O2'	41:Lm:100:TYR:O	2.26	0.54
49:S2:127:C:O2	53:SE:134:LYS:NZ	2.41	0.54
62:SS:105:ASN:OD1	62:SS:108:ARG:NH2	2.40	0.54
84:CC:10:G:O6	84:CC:45:G:O6	2.26	0.54
1:L5:1995:G:H4'	47:Lt:128:THR:HB	1.89	0.53
59:SP:52:LYS:HD2	59:SP:80:LEU:HD11	1.90	0.53
83:CA:74:ILE:HA	83:CA:112:VAL:HA	1.90	0.53
20:LR:183:GLU:HA	20:LR:186:LYS:HD2	1.90	0.53
22:LT:88:ARG:NH1	30:Lb:33:LYS:O	2.40	0.53
70:Sg:5:MET:HB2	70:Sg:270:LEU:HD21	1.90	0.53
83:CA:190:LEU:HB3	83:CA:223:VAL:HB	1.89	0.53
1:L5:1976:G:O6	1:L5:1991:A:N1	2.41	0.53
1:L5:2822:G:N7	20:LR:20:LYS:NZ	2.54	0.53
62:SS:8:LYS:NZ	62:SS:10:GLN:OE1	2.41	0.53
1:L5:3955:G:N2	1:L5:3966:A:C4	2.76	0.53
1:L5:5022:U:O4	56:SI:170:LYS:NZ	2.40	0.53
10:LG:58:PRO:HD2	10:LG:61:ILE:HD12	1.90	0.53
49:S2:606:G:H5''	81:Se:56:ASN:HB3	1.90	0.53
71:SC:183:LYS:HA	71:SC:195:LEU:O	2.08	0.53
49:S2:433:A:H5''	56:SI:22:HIS:HB3	1.89	0.53
49:S2:1658:G:OP2	49:S2:1660:C:N4	2.41	0.53
1:L5:2033:A:OP1	12:LI:162:ARG:NH1	2.42	0.53
3:L8:67:U:H5''	38:Lj:86:PRO:HA	1.91	0.53
13:LJ:120:ASP:HB3	13:LJ:123:ILE:HG12	1.91	0.53
14:LL:141:ALA:O	14:LL:145:LYS:HB2	2.09	0.53
48:Lz:23:ARG:NH2	48:Lz:174:MET:O	2.42	0.53
59:SP:11:THR:O	59:SP:13:ARG:NH2	2.41	0.53
75:SN:45:LEU:HB3	75:SN:49:GLN:HG3	1.91	0.53
1:L5:3711:A:H2'	1:L5:3712:A:H8	1.73	0.53
54:SF:35:LEU:HD12	54:SF:117:ILE:HD13	1.91	0.53
1:L5:2898:G:OP2	20:LR:135:LYS:NZ	2.40	0.53
22:LT:93:ILE:HA	22:LT:96:ILE:HG12	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:LU:61:VAL:HG13	23:LU:74:SER:HB2	1.89	0.53
25:LW:107:GLN:OE1	25:LW:110:ARG:NH1	2.42	0.53
26:LX:129:ARG:NH2	26:LX:133:GLU:OE2	2.41	0.53
28:LZ:88:ASP:OD1	28:LZ:88:ASP:N	2.42	0.53
44:Lp:88:GLU:O	44:Lp:91:ASP:O	2.27	0.53
46:Ls:160:LEU:HG	46:Ls:161:ILE:HG23	1.91	0.53
55:SH:65:PRO:O	55:SH:69:LEU:N	2.41	0.53
70:Sg:72:SER:OG	70:Sg:74:ASP:OD1	2.26	0.53
84:CC:22:U:OP2	84:CC:46:A:N6	2.42	0.53
18:LP:7:ASP:N	18:LP:7:ASP:OD1	2.39	0.53
25:LW:81:ALA:HB2	25:LW:87:LEU:HD12	1.91	0.53
49:S2:1674:G:H4'	54:SF:77:MET:HE1	1.89	0.53
49:S2:1473:G:N1	49:S2:1476:A:OP2	2.42	0.53
1:L5:1907:A:H4'	9:LF:223:LYS:HE3	1.91	0.52
1:L5:2083:C:OP2	19:LQ:14:ARG:NH2	2.38	0.52
1:L5:3956:G:O5'	1:L5:3966:A:N6	2.42	0.52
8:LE:222:LEU:HB3	8:LE:237:LYS:HD2	1.91	0.52
9:LF:236:ARG:HD3	9:LF:239:GLN:HB2	1.89	0.52
32:Ld:54:MET:O	32:Ld:57:MET:O	2.26	0.52
49:S2:307:G:N2	56:SI:45:THR:O	2.41	0.52
70:Sg:159:ASN:ND2	70:Sg:161:SER:O	2.41	0.52
79:SZ:68:ILE:HB	79:SZ:109:TYR:HB2	1.92	0.52
14:LL:205:GLN:O	14:LL:208:GLU:C	2.52	0.52
52:SD:67:ARG:NH1	57:SK:93:THR:O	2.42	0.52
66:SX:63:ASN:ND2	66:SX:114:ASP:OD2	2.39	0.52
70:Sg:286:CYS:HA	70:Sg:302:TYR:HA	1.92	0.52
1:L5:1703:C:O2'	9:LF:39:GLN:NE2	2.42	0.52
18:LP:84:PRO:HB2	18:LP:87:SER:HB2	1.90	0.52
49:S2:71:G:O6	72:SG:170:ARG:NH1	2.41	0.52
65:SV:73:ALA:HB1	65:SV:78:ILE:HB	1.91	0.52
1:L5:1095:A:N1	1:L5:1200:G:C6	2.77	0.52
24:LV:10:SER:OG	24:LV:11:GLY:N	2.43	0.52
48:Lz:29:LEU:HD22	48:Lz:60:ARG:HD3	1.91	0.52
48:Lz:88:GLU:HA	48:Lz:91:LYS:HG2	1.90	0.52
49:S2:1024:A:OP2	75:SN:124:ARG:NH2	2.39	0.52
54:SF:102:LEU:HD11	79:SZ:110:THR:HB	1.90	0.52
57:SK:15:LEU:O	57:SK:19:GLY:HA2	2.10	0.52
70:Sg:40:ILE:HB	70:Sg:59:LEU:HB2	1.91	0.52
50:SA:85:ARG:NH1	50:SA:203:PHE:O	2.38	0.52
72:SG:78:SER:OG	72:SG:79:LYS:N	2.42	0.52
79:SZ:65:TYR:HA	79:SZ:111:ARG:HH21	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:706:C:HO2'	1:L5:1298:C:HO2'	1.56	0.52
1:L5:4040:C:H5'	1:L5:4045:G:H22	1.75	0.52
1:L5:4279:A:H5'	1:L5:4281:A:H1'	1.90	0.52
49:S2:1507:G:H22	82:Sf:87:THR:HA	1.74	0.52
52:SD:123:LEU:HD11	52:SD:152:PHE:HB3	1.92	0.52
70:Sg:146:SER:OG	70:Sg:147:HIS:N	2.42	0.52
70:Sg:283:PRO:O	70:Sg:285:GLN:NE2	2.43	0.52
74:SM:52:LEU:HD21	74:SM:65:VAL:HG21	1.91	0.52
2:L7:74:A:N3	21:LS:53:LYS:NZ	2.58	0.52
31:Lc:26:LYS:HB2	31:Lc:98:ASP:HB3	1.90	0.52
49:S2:1047:C:H5'	76:SO:143:LYS:HB2	1.90	0.52
49:S2:1228:A:H2'	49:S2:1229:G:C8	2.44	0.52
70:Sg:11:LEU:HB2	70:Sg:307:VAL:HG13	1.91	0.52
83:CA:203:GLN:NE2	83:CA:229:LEU:O	2.42	0.52
48:Lz:55:LEU:HD22	48:Lz:183:ILE:HG12	1.91	0.52
49:S2:1536:G:H2'	49:S2:1537:A:C8	2.45	0.52
15:LM:81:ASP:OD1	15:LM:81:ASP:N	2.39	0.52
49:S2:1612:G:OP1	59:SP:18:ARG:NH2	2.43	0.52
9:LF:86:GLU:HG3	22:LT:135:PRO:HB3	1.92	0.52
29:La:89:ASN:O	29:La:93:ASN:HB2	2.09	0.52
47:Lt:111:ASN:HA	47:Lt:114:ARG:HD2	1.92	0.52
48:Lz:62:LYS:NZ	48:Lz:152:LYS:O	2.40	0.52
50:SA:76:VAL:HG12	50:SA:123:VAL:HB	1.92	0.52
56:SI:61:ASP:OD1	56:SI:61:ASP:N	2.42	0.52
56:SI:152:ARG:O	56:SI:156:ALA:HB2	2.10	0.52
74:SM:35:ILE:HD12	82:Sf:103:LEU:HD22	1.92	0.52
74:SM:52:LEU:CD1	74:SM:65:VAL:HG11	2.37	0.52
1:L5:3937:C:H1'	16:LN:125:SER:HB2	1.90	0.51
5:LB:85:VAL:HA	5:LB:203:GLN:O	2.10	0.51
20:LR:176:ARG:NH1	49:S2:909:G:OP1	2.43	0.51
49:S2:694:G:H5''	49:S2:730:C:H5	1.75	0.51
1:L5:3868:G:H22	1:L5:3900:G:H1'	1.75	0.51
1:L5:4946:U:HO2'	34:Lf:2:SER:N	2.08	0.51
31:Lc:20:LEU:O	31:Lc:24:SER:OG	2.23	0.51
48:Lz:75:ASP:OD1	48:Lz:75:ASP:N	2.41	0.51
49:S2:21:U:O2	73:SJ:17:ARG:NH2	2.43	0.51
74:SM:32:ALA:HB3	74:SM:110:VAL:HB	1.92	0.51
63:ST:42:HIS:HB2	63:ST:83:GLN:HB2	1.91	0.51
1:L5:1439:C:OP2	9:LF:34:ARG:NH1	2.44	0.51
1:L5:2527:A:OP2	20:LR:38:ARG:NH2	2.37	0.51
48:Lz:42:ASP:HB3	48:Lz:45:LYS:HG2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:SE:11:ARG:HA	53:SE:28:ALA:HB2	1.90	0.51
83:CA:81:SER:H	83:CA:107:LYS:HB3	1.76	0.51
83:CA:231:SER:OG	83:CA:314:GLU:OE2	2.28	0.51
1:L5:2709:C:N4	83:CA:257:LEU:O	2.43	0.51
1:L5:2848:G:O2'	1:L5:3838:U:O4	2.27	0.51
13:LJ:20:LEU:O	13:LJ:131:TYR:O	2.29	0.51
46:Ls:157:ASP:OD1	46:Ls:157:ASP:N	2.41	0.51
72:SG:98:ARG:NH2	72:SG:103:ASP:OD1	2.44	0.51
1:L5:257:C:H2'	1:L5:258:G:C8	2.45	0.51
1:L5:1179:U:OP2	7:LD:289:ARG:NH1	2.43	0.51
1:L5:1824:G:H5''	22:LT:35:LYS:HE3	1.92	0.51
1:L5:4139:G:H21	1:L5:4140:C:H41	1.57	0.51
31:Lc:17:ARG:HD3	31:Lc:103:ASP:HA	1.93	0.51
39:Lk:24:LYS:HA	39:Lk:67:LYS:O	2.11	0.51
49:S2:197:U:OP2	49:S2:203:G:N2	2.41	0.51
49:S2:581:U:C3'	49:S2:582:U:H5'	2.40	0.51
49:S2:1102:G:OP2	51:SB:151:ARG:NH2	2.42	0.51
52:SD:116:ARG:NH2	86:i:152:ASP:OD2	2.42	0.51
62:SS:24:ARG:HB2	62:SS:29:ALA:HB2	1.93	0.51
1:L5:182:G:N2	1:L5:255:C:O2'	2.43	0.51
11:LH:186:THR:O	11:LH:189:GLN:NE2	2.44	0.51
27:LY:80:ILE:HD11	27:LY:104:VAL:HG11	1.92	0.51
34:Lf:37:ASP:OD1	34:Lf:37:ASP:N	2.37	0.51
49:S2:1563:G:OP1	63:ST:121:ARG:NH2	2.44	0.51
55:SH:144:ILE:HD11	55:SH:152:ARG:HD3	1.91	0.51
1:L5:478:G:OP1	45:Lr:66:ARG:NH1	2.44	0.51
1:L5:512:U:O4	1:L5:647:G:O6	2.29	0.51
5:LB:215:GLU:OE2	5:LB:349:LYS:NZ	2.39	0.51
6:LC:66:SER:HA	6:LC:77:PRO:HA	1.93	0.51
23:LU:28:PRO:HB2	23:LU:34:MET:HG2	1.93	0.51
24:LV:35:LYS:HB2	24:LV:67:LYS:HG3	1.93	0.51
35:Lg:5:LEU:HD21	35:Lg:30:ILE:HG22	1.92	0.51
49:S2:377:G:H5'	56:SI:98:LYS:HB3	1.92	0.51
49:S2:1550:G:H3'	49:S2:1579:A:H61	1.76	0.51
56:SI:162:LEU:HD11	56:SI:191:GLU:HG2	1.92	0.51
75:SN:83:ASP:OD1	75:SN:83:ASP:N	2.44	0.51
12:LI:48:LEU:O	12:LI:139:ARG:HA	2.09	0.51
14:LL:211:LYS:HG2	48:Lz:184:HIS:HB2	1.93	0.51
48:Lz:194:LEU:HG	48:Lz:197:ASN:HD22	1.75	0.51
49:S2:1403:C:N4	49:S2:1433:C:OP1	2.43	0.51
50:SA:22:GLY:O	50:SA:24:HIS:ND1	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:SH:177:TYR:O	55:SH:181:THR:HB	2.11	0.51
60:SQ:43:GLU:O	60:SQ:45:ARG:N	2.43	0.51
74:SM:36:ARG:HH21	74:SM:40:LYS:HE3	1.76	0.51
1:L5:186:G:H1'	1:L5:1366:G:H21	1.76	0.51
1:L5:1270:A:OP1	30:Lb:107:ARG:NH2	2.40	0.51
1:L5:1895:G:OP1	9:LF:96:ARG:NH2	2.44	0.51
1:L5:4424:A:OP2	41:Lm:97:ARG:NH2	2.44	0.51
7:LD:80:ALA:HA	7:LD:83:LEU:HD13	1.93	0.51
25:LW:92:ALA:O	25:LW:96:GLN:NE2	2.44	0.51
31:Lc:47:ILE:HD12	31:Lc:94:LEU:HD11	1.93	0.51
49:S2:987:A:OP1	67:Sa:32:LYS:NZ	2.44	0.51
8:LE:157:HIS:HB3	8:LE:160:LYS:HD2	1.93	0.50
8:LE:161:ARG:NH2	8:LE:273:SER:OG	2.44	0.50
8:LE:281:ILE:HD12	8:LE:286:LEU:HD11	1.93	0.50
49:S2:570:C:O2'	78:SY:34:THR:O	2.27	0.50
1:L5:2300:A:H61	6:LC:178:ASN:HD22	1.58	0.50
6:LC:327:LYS:NZ	9:LF:171:ASP:OD1	2.45	0.50
49:S2:1252:C:OP1	64:SU:75:LYS:NZ	2.42	0.50
49:S2:1757:G:H8	49:S2:1758:G:H1'	1.77	0.50
54:SF:143:PRO:HA	54:SF:146:ARG:HG2	1.93	0.50
56:SI:101:ILE:HD12	56:SI:190:LEU:HD11	1.93	0.50
74:SM:52:LEU:CD1	74:SM:65:VAL:CG1	2.89	0.50
83:CA:153:ALA:HA	83:CA:156:LEU:HG	1.92	0.50
83:CA:242:GLN:HB3	83:CA:307:VAL:HG21	1.93	0.50
1:L5:2088:A:OP2	19:LQ:37:ARG:NH1	2.44	0.50
38:Lj:48:ASN:OD1	38:Lj:54:LYS:NZ	2.43	0.50
51:SB:175:GLU:OE1	51:SB:187:LYS:NZ	2.37	0.50
54:SF:135:ARG:N	84:CC:33:U:OP2	2.44	0.50
36:Lh:87:LYS:NZ	38:Lj:78:PHE:O	2.43	0.50
52:SD:27:ARG:NH1	57:SK:62:PHE:O	2.44	0.50
68:Sc:62:GLU:OE1	76:SO:121:ARG:NH2	2.44	0.50
1:L5:1996:C:O2	46:Ls:41:GLN:NE2	2.38	0.50
1:L5:3955:G:H22	1:L5:3966:A:H3'	1.75	0.50
8:LE:274:VAL:HG21	34:Lf:2:SER:HB3	1.93	0.50
28:LZ:36:ARG:NH1	28:LZ:38:TYR:OH	2.44	0.50
49:S2:382:C:H2'	49:S2:383:G:H8	1.77	0.50
63:ST:113:VAL:HG12	63:ST:123:LEU:HD23	1.91	0.50
70:Sg:163:PRO:HB2	70:Sg:179:LEU:HB2	1.93	0.50
83:CA:44:SER:HG	83:CA:47:SER:HG	1.59	0.50
2:L7:1:G:H4'	7:LD:265:ARG:HD2	1.93	0.50
12:LI:47:PRO:HD2	12:LI:141:LYS:HA	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LZ:90:PRO:O	28:LZ:117:LYS:NZ	2.42	0.50
49:S2:145:G:H2'	49:S2:146:G:C8	2.46	0.50
60:SQ:31:LEU:HD11	60:SQ:33:LYS:HE2	1.92	0.50
80:Sb:34:ASP:O	80:Sb:79:PHE:HA	2.11	0.50
80:Sb:49:HIS:ND1	80:Sb:69:GLY:O	2.45	0.50
1:L5:97:G:OP1	14:LL:16:LYS:NZ	2.45	0.50
1:L5:2544:G:N1	3:L8:124:U:OP1	2.41	0.50
1:L5:3967:G:O6	1:L5:4055:U:O4	2.28	0.50
2:L7:23:A:N3	2:L7:118:C:O2'	2.39	0.50
38:Lj:20:ARG:NH2	38:Lj:39:TYR:OH	2.45	0.50
49:S2:1854:U:OP1	76:SO:150:ARG:NH1	2.41	0.50
60:SQ:139:ALA:O	60:SQ:140:ARG:NH2	2.45	0.50
72:SG:23:LYS:HE2	72:SG:42:GLY:H	1.77	0.50
74:SM:120:ALA:HA	74:SM:123:VAL:HG22	1.94	0.50
6:LC:362:GLN:O	6:LC:366:ASP:HB2	2.11	0.50
49:S2:697:G:OP2	49:S2:733:C:N4	2.44	0.50
49:S2:874:G:H2'	49:S2:875:A:H8	1.77	0.50
72:SG:59:GLN:OE1	72:SG:72:ARG:NH2	2.45	0.50
83:CA:231:SER:OG	83:CA:232:SER:N	2.45	0.50
1:L5:2062:C:O2'	21:LS:111:ARG:NH1	2.44	0.50
1:L5:2782:U:OP2	40:LI:10:LYS:NZ	2.43	0.50
1:L5:3689:G:O2'	1:L5:3818:U:OP2	2.25	0.50
19:LQ:159:PRO:HD3	19:LQ:188:ASN:HD21	1.77	0.50
27:LY:54:GLU:HB2	27:LY:108:ARG:HB3	1.94	0.50
63:ST:129:ARG:HH11	63:ST:133:ARG:HH22	1.60	0.50
1:L5:182:G:H1	1:L5:254:G:H1	1.58	0.49
1:L5:4745:G:H1	1:L5:4955:A:H61	1.60	0.49
8:LE:153:LEU:HD11	8:LE:195:ILE:HG13	1.93	0.49
11:LH:187:VAL:HG12	11:LH:188:GLN:HG3	1.93	0.49
48:Lz:48:ARG:NH1	48:Lz:159:MET:O	2.39	0.49
54:SF:198:ARG:NH1	84:CC:40:G:O2'	2.43	0.49
70:Sg:7:LEU:HA	70:Sg:309:VAL:O	2.12	0.49
1:L5:989:U:O2	1:L5:1064:G:O6	2.29	0.49
12:LI:179:ASP:N	12:LI:179:ASP:OD1	2.45	0.49
34:Lf:33:VAL:HG23	34:Lf:38:GLU:HB2	1.94	0.49
64:SU:95:SER:HA	64:SU:98:VAL:HG22	1.93	0.49
70:Sg:51:ASN:HB3	70:Sg:54:ILE:HD11	1.92	0.49
80:Sb:40:CYS:SG	80:Sb:41:TYR:N	2.85	0.49
1:L5:4054:C:N3	48:Lz:35:GLN:NE2	2.60	0.49
15:LM:123:ILE:HD11	17:LO:189:ILE:HD13	1.94	0.49
39:Lk:30:ASP:OD1	39:Lk:30:ASP:N	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:581:U:H2'	49:S2:582:U:H5'	1.94	0.49
51:SB:26:SER:O	51:SB:51:ARG:NH1	2.45	0.49
62:SS:141:ARG:O	62:SS:144:ARG:O	2.30	0.49
68:Sc:15:THR:OG1	68:Sc:31:ARG:O	2.27	0.49
82:Sf:126:CYS:HB2	82:Sf:130:VAL:H	1.77	0.49
1:L5:1175:A:H2	1:L5:1185:G:C2	2.26	0.49
62:SS:115:LYS:HD3	62:SS:126:PHE:HB2	1.94	0.49
65:SV:17:CYS:O	65:SV:21:ASN:N	2.45	0.49
1:L5:493:G:C6	1:L5:660:A:N1	2.80	0.49
1:L5:2702:C:OP1	23:LU:101:ARG:NH2	2.41	0.49
1:L5:2739:C:O2	4:LA:188:LYS:NZ	2.46	0.49
17:LO:7:LEU:HD22	17:LO:31:ARG:HH21	1.77	0.49
23:LU:106:SER:OG	23:LU:107:LYS:N	2.45	0.49
49:S2:1020:A:OP2	75:SN:70:LYS:NZ	2.45	0.49
1:L5:736:C:OP1	15:LM:74:ARG:NH1	2.45	0.49
12:LI:55:ASP:N	12:LI:55:ASP:OD1	2.43	0.49
20:LR:151:ARG:NH1	58:SL:119:ASP:OD2	2.40	0.49
32:Ld:98:SER:OG	32:Ld:100:ASN:OD1	2.31	0.49
1:L5:1976:G:C6	1:L5:1991:A:C2	3.00	0.49
1:L5:5063:G:O6	5:LB:124:LYS:NZ	2.46	0.49
15:LM:52:PHE:HA	15:LM:55:MET:HG2	1.93	0.49
46:Ls:175:LEU:HA	46:Ls:178:LEU:HG	1.95	0.49
49:S2:695:C:N4	49:S2:736:C:O2'	2.46	0.49
62:SS:35:GLY:O	62:SS:97:GLN:NE2	2.46	0.49
1:L5:2280:G:OP1	33:Le:48:ARG:NH2	2.46	0.49
46:Ls:175:LEU:HD22	46:Ls:180:ILE:HD12	1.94	0.49
49:S2:928:G:H2'	49:S2:929:G:C8	2.48	0.49
49:S2:944:A:H5''	76:SO:134:PRO:HB3	1.94	0.49
75:SN:87:ASP:OD1	75:SN:87:ASP:N	2.45	0.49
1:L5:4910:A:H4'	5:LB:95:THR:HG22	1.94	0.49
3:L8:123:U:O2'	3:L8:126:C:N4	2.44	0.49
15:LM:3:PHE:H	21:LS:175:PHE:HZ	1.60	0.49
49:S2:583:A:H2'	49:S2:584:A:C8	2.48	0.49
59:SP:24:GLN:O	59:SP:28:MET:HB2	2.13	0.49
77:SW:86:LEU:HG	77:SW:90:GLN:HE21	1.76	0.49
1:L5:4163:U:OP2	10:LG:53:ARG:NH2	2.46	0.49
16:LN:123:GLU:HG2	16:LN:128:LYS:HG2	1.94	0.49
5:LB:80:GLU:OE1	5:LB:323:TYR:OH	2.29	0.48
5:LB:90:VAL:HG13	5:LB:104:THR:HG22	1.95	0.48
8:LE:177:GLY:HA3	8:LE:184:VAL:HB	1.95	0.48
13:LJ:101:ASP:OD2	13:LJ:101:ASP:N	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Lk:52:LYS:HA	39:Lk:55:LYS:HG2	1.95	0.48
55:SH:48:ALA:HA	55:SH:61:ILE:O	2.12	0.48
78:SY:82:ALA:O	78:SY:86:GLU:CB	2.61	0.48
1:L5:1762:C:H5''	1:L5:1764:G:H1	1.78	0.48
1:L5:3788:C:N4	1:L5:3812:C:OP2	2.46	0.48
43:Lo:26:TYR:HB3	43:Lo:67:VAL:HB	1.95	0.48
74:SM:34:GLY:O	74:SM:38:ALA:HB2	2.12	0.48
1:L5:4992:G:H2'	1:L5:4993:G:C8	2.48	0.48
47:Lt:12:VAL:HB	47:Lt:65:GLN:HG3	1.94	0.48
47:Lt:33:GLY:HA3	47:Lt:40:LYS:HZ3	1.78	0.48
49:S2:886:A:C6	49:S2:901:G:N3	2.82	0.48
54:SF:52:SER:N	54:SF:70:GLU:OE2	2.46	0.48
70:Sg:82:SER:OG	70:Sg:84:ASP:OD1	2.24	0.48
72:SG:70:HIS:HA	72:SG:98:ARG:HH12	1.78	0.48
1:L5:709:C:OP1	34:Lf:89:ARG:NH1	2.45	0.48
1:L5:1726:U:H5'	9:LF:135:ILE:HD11	1.96	0.48
8:LE:223:ARG:NH1	8:LE:236:GLU:O	2.45	0.48
57:SK:90:VAL:HB	57:SK:94:LEU:HD12	1.94	0.48
77:SW:44:HIS:NE2	77:SW:112:ASP:OD2	2.47	0.48
5:LB:322:HIS:O	5:LB:342:LYS:NZ	2.41	0.48
10:LG:182:CYS:HB3	10:LG:222:ILE:HD12	1.94	0.48
15:LM:15:VAL:O	15:LM:22:GLY:N	2.47	0.48
48:Lz:198:TRP:HE1	48:Lz:202:ARG:HB2	1.77	0.48
61:SR:37:GLU:HG3	70:Sg:150:TRP:HE1	1.77	0.48
1:L5:502:C:H3'	1:L5:503:C:H3'	1.95	0.48
1:L5:3654:G:O2'	1:L5:3693:U:OP1	2.29	0.48
1:L5:4052:C:H1'	48:Lz:209:THR:HA	1.95	0.48
9:LF:182:TYR:HB3	9:LF:200:ARG:HG3	1.95	0.48
25:LW:96:GLN:HB3	25:LW:100:VAL:HB	1.96	0.48
49:S2:318:A:H61	72:SG:186:GLN:HE22	1.60	0.48
49:S2:1311:C:OP1	82:Sf:143:LYS:NZ	2.41	0.48
49:S2:1598:G:O2'	79:SZ:80:ARG:O	2.28	0.48
74:SM:69:CYS:O	74:SM:72:HIS:O	2.32	0.48
1:L5:1762:C:C4	1:L5:1770:A:N1	2.81	0.48
1:L5:1994:C:H1'	47:Lt:132:ILE:HA	1.96	0.48
1:L5:2306:G:OP1	33:Le:128:ARG:NH2	2.45	0.48
1:L5:3717:A:H2'	1:L5:3718:A:C8	2.48	0.48
1:L5:3964:U:O2'	1:L5:3966:A:O4'	2.31	0.48
13:LJ:115:LEU:HD12	13:LJ:116:GLY:HA2	1.95	0.48
39:Lk:26:LYS:HB2	39:Lk:69:LEU:HD12	1.95	0.48
46:Ls:123:VAL:HG13	46:Ls:160:LEU:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:Lz:113:SER:OG	48:Lz:114:GLU:N	2.45	0.48
49:S2:1256:G:C8	64:SU:66:ARG:HB2	2.49	0.48
2:L7:12:U:O3'	2:L7:109:U:O2'	2.30	0.48
14:LL:205:GLN:O	14:LL:208:GLU:O	2.32	0.48
46:Ls:23:ASP:OD1	46:Ls:24:TYR:N	2.47	0.48
49:S2:1277:C:H2'	49:S2:1278:A:H8	1.79	0.48
59:SP:21:ASP:H	59:SP:24:GLN:NE2	2.12	0.48
60:SQ:42:ILE:HG21	60:SQ:51:LEU:HD22	1.96	0.48
6:LC:209:ILE:HB	6:LC:229:LEU:HD13	1.93	0.48
29:La:72:THR:HG22	29:La:110:LYS:HB3	1.94	0.48
32:Ld:53:ALA:HA	32:Ld:88:LEU:HD21	1.95	0.48
34:Lf:78:HIS:HB2	34:Lf:85:ARG:HG3	1.95	0.48
49:S2:1562:C:H2'	49:S2:1563:G:H8	1.79	0.48
53:SE:87:MET:N	53:SE:101:LEU:O	2.46	0.48
57:SK:15:LEU:HD13	57:SK:21:MET:HG2	1.96	0.48
72:SG:2:LYS:HB3	72:SG:15:LEU:HD11	1.95	0.48
78:SY:3:ASP:OD1	78:SY:3:ASP:N	2.44	0.48
1:L5:17:A:OP2	26:LX:60:TYR:OH	2.29	0.48
1:L5:1187:G:OP2	1:L5:1187:G:N2	2.38	0.48
22:LT:28:ALA:HA	22:LT:31:MET:HG2	1.95	0.48
22:LT:72:VAL:HG11	22:LT:96:ILE:HD13	1.95	0.48
25:LW:104:GLN:HA	25:LW:107:GLN:HB3	1.95	0.48
50:SA:27:GLY:HA3	50:SA:46:ILE:HA	1.96	0.48
54:SF:50:PRO:HG2	54:SF:90:VAL:HG22	1.96	0.48
1:L5:4099:G:H2'	1:L5:4101:C:H41	1.79	0.47
2:L7:13:A:OP2	2:L7:66:G:N2	2.42	0.47
62:SS:36:VAL:HG13	62:SS:40:TYR:HD2	1.78	0.47
64:SU:94:PRO:HD2	64:SU:97:ILE:HD11	1.96	0.47
1:L5:2112:G:C2'	1:L5:2113:G:H5''	2.41	0.47
1:L5:4208:U:OP2	22:LT:4:THR:OG1	2.30	0.47
8:LE:151:ILE:HA	8:LE:160:LYS:O	2.13	0.47
20:LR:86:ASN:HD22	20:LR:91:GLU:HG3	1.79	0.47
78:SY:4:THR:O	78:SY:32:LYS:NZ	2.47	0.47
1:L5:2696:A:H62	39:Lk:35:LYS:HE2	1.79	0.47
17:LO:37:ARG:HD2	17:LO:108:ILE:HD11	1.97	0.47
19:LQ:70:MET:HE1	19:LQ:137:VAL:HB	1.96	0.47
49:S2:197:U:N3	49:S2:202:G:N7	2.61	0.47
49:S2:750:C:O2	49:S2:752:G:N1	2.47	0.47
49:S2:828:G:OP1	73:SJ:6:SER:OG	2.32	0.47
51:SB:67:PHE:O	51:SB:85:LYS:C	2.57	0.47
65:SV:17:CYS:HB2	65:SV:56:CYS:HB3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LJ:96:LYS:HG2	13:LJ:175:LEU:HA	1.95	0.47
47:Lt:114:ARG:HE	47:Lt:133:LEU:HB2	1.80	0.47
48:Lz:141:ASN:ND2	48:Lz:150:GLU:OE2	2.48	0.47
49:S2:1417:C:N3	49:S2:1422:G:O6	2.47	0.47
52:SD:94:ARG:O	52:SD:101:GLN:NE2	2.44	0.47
55:SH:53:VAL:HG23	55:SH:175:GLY:HA3	1.96	0.47
73:SJ:44:TRP:HA	73:SJ:47:LYS:HG2	1.96	0.47
1:L5:390:C:H5'	83:CA:211:LYS:HG3	1.95	0.47
11:LH:48:LEU:HD21	11:LH:56:ARG:HH21	1.79	0.47
23:LU:35:ASP:OD2	23:LU:35:ASP:N	2.48	0.47
48:Lz:54:ARG:NE	48:Lz:149:ASP:OD2	2.47	0.47
62:SS:62:ASP:OD2	62:SS:62:ASP:N	2.47	0.47
74:SM:18:LEU:HA	74:SM:21:VAL:HG12	1.96	0.47
1:L5:3736:A:H2'	1:L5:3737:A:C8	2.50	0.47
17:LO:3:GLU:N	34:Lf:31:GLU:OE2	2.48	0.47
18:LP:73:ALA:O	18:LP:76:TRP:C	2.58	0.47
56:SI:114:GLU:OE1	56:SI:123:ARG:NH1	2.47	0.47
56:SI:165:GLN:HG3	56:SI:171:LEU:HD23	1.95	0.47
63:ST:22:LEU:HD13	63:ST:28:LEU:HD11	1.96	0.47
70:Sg:193:GLY:N	70:Sg:213:ASP:OD1	2.48	0.47
83:CA:356:ALA:O	83:CA:360:SER:OG	2.30	0.47
1:L5:3977:C:N4	1:L5:3984:C:OP1	2.48	0.47
1:L5:4162:C:H5	10:LG:73:ARG:HH12	1.63	0.47
18:LP:10:ASN:N	18:LP:10:ASN:OD1	2.47	0.47
29:La:76:ASP:N	29:La:76:ASP:OD1	2.48	0.47
31:Lc:38:ILE:HD11	31:Lc:46:VAL:HG21	1.96	0.47
33:Le:108:ARG:HD2	33:Le:128:ARG:HB2	1.97	0.47
49:S2:943:U:O2'	76:SO:135:ILE:O	2.31	0.47
49:S2:1512:C:H5'	69:Sd:8:TRP:HZ3	1.80	0.47
52:SD:16:ILE:HD11	69:Sd:36:LEU:HD13	1.96	0.47
70:Sg:39:THR:HG22	70:Sg:60:ARG:HG2	1.96	0.47
70:Sg:99:ARG:NH1	70:Sg:135:LEU:O	2.47	0.47
72:SG:4:ASN:HB3	72:SG:110:ASN:HD22	1.80	0.47
83:CA:118:ILE:HB	83:CA:190:LEU:HD21	1.96	0.47
83:CA:274:ASP:OD1	83:CA:274:ASP:N	2.47	0.47
1:L5:67:C:OP2	1:L5:312:G:N2	2.47	0.47
49:S2:553:U:H3	49:S2:554:A:H62	1.63	0.47
70:Sg:251:ALA:HA	70:Sg:256:ILE:HG22	1.97	0.47
74:SM:34:GLY:O	74:SM:38:ALA:CB	2.63	0.47
7:LD:103:LEU:HG	7:LD:247:ILE:HG21	1.95	0.47
12:LI:55:ASP:OD2	12:LI:164:LYS:NZ	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LI:152:LEU:HB3	12:LI:165:ILE:HD12	1.96	0.47
49:S2:640:A:H2'	49:S2:641:A:C8	2.50	0.47
50:SA:159:ILE:HD11	65:SV:34:MET:HE1	1.96	0.47
53:SE:115:THR:HG23	53:SE:118:GLU:H	1.80	0.47
71:SC:194:ARG:HD3	71:SC:196:ILE:HD11	1.96	0.47
77:SW:3:ARG:HD3	77:SW:6:VAL:HG12	1.96	0.47
83:CA:156:LEU:HD13	83:CA:166:VAL:HG22	1.96	0.47
1:L5:386:A:OP2	27:LY:89:LYS:NZ	2.39	0.47
1:L5:1974:U:H4'	1:L5:1975:G:H3'	1.96	0.47
1:L5:2856:C:O2	5:LB:242:ARG:NH2	2.45	0.47
47:Lt:80:LEU:HA	47:Lt:83:LYS:HE2	1.97	0.47
49:S2:656:G:O2'	71:SC:227:ARG:NH2	2.48	0.47
51:SB:67:PHE:O	51:SB:86:LEU:HB2	2.15	0.47
74:SM:53:ALA:HA	74:SM:79:VAL:O	2.15	0.47
76:SO:13:GLN:HG3	76:SO:15:ILE:HA	1.96	0.47
83:CA:208:GLN:O	83:CA:212:ASP:HB2	2.15	0.47
1:L5:4093:G:H2'	1:L5:4094:G:C8	2.50	0.46
48:Lz:172:VAL:HG12	48:Lz:174:MET:H	1.80	0.46
54:SF:142:SER:OG	68:Sc:49:PRO:O	2.32	0.46
79:SZ:49:LEU:H	79:SZ:83:LEU:HD22	1.79	0.46
1:L5:3946:G:H21	1:L5:3947:A:H62	1.63	0.46
36:Lh:82:ASP:OD1	36:Lh:82:ASP:N	2.43	0.46
49:S2:1261:C:O2	69:Sd:10:HIS:NE2	2.34	0.46
49:S2:1589:A:N3	49:S2:1653:U:O2'	2.41	0.46
52:SD:32:ASP:OD2	52:SD:65:ARG:NH1	2.38	0.46
54:SF:30:ILE:HG12	54:SF:113:VAL:HG11	1.97	0.46
56:SI:57:ALA:HB2	56:SI:183:GLY:HA2	1.97	0.46
77:SW:60:LYS:NZ	80:Sb:23:ARG:O	2.48	0.46
1:L5:3951:G:N2	1:L5:4060:U:O2	2.47	0.46
1:L5:4260:U:H2'	1:L5:4261:C:C6	2.51	0.46
12:LI:180:GLU:HG3	12:LI:184:MET:HE2	1.97	0.46
22:LT:81:LYS:HB3	30:Lb:16:TRP:CZ3	2.50	0.46
48:Lz:117:ILE:O	48:Lz:122:ARG:NH1	2.48	0.46
49:S2:1199:A:OP1	67:Sa:2:THR:N	2.49	0.46
50:SA:84:GLN:HG2	50:SA:100:ALA:HB1	1.97	0.46
55:SH:9:VAL:HG11	55:SH:41:ARG:HH22	1.80	0.46
58:SL:21:LYS:HD2	58:SL:21:LYS:HA	1.77	0.46
84:CC:17:G:O2'	84:CC:56:G:N2	2.48	0.46
49:S2:747:U:N3	49:S2:796:G:N1	2.63	0.46
51:SB:124:HIS:HA	51:SB:137:LEU:O	2.14	0.46
55:SH:6:ALA:O	55:SH:25:GLN:NE2	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:SU:26:SER:OG	64:SU:27:ARG:N	2.48	0.46
70:Sg:120:ILE:O	70:Sg:131:LEU:HA	2.15	0.46
46:Ls:82:ILE:O	46:Ls:83:ARG:NH1	2.49	0.46
76:SO:40:THR:HG21	76:SO:74:ALA:HB2	1.97	0.46
78:SY:62:THR:HA	78:SY:69:THR:HA	1.98	0.46
59:SP:75:VAL:HG22	59:SP:93:MET:HB3	1.98	0.46
70:Sg:222:ASN:OD1	70:Sg:222:ASN:N	2.43	0.46
82:Sf:109:ASP:N	82:Sf:109:ASP:OD2	2.48	0.46
82:Sf:133:ALA:O	82:Sf:139:HIS:ND1	2.48	0.46
83:CA:138:ARG:HA	83:CA:141:ASP:HB3	1.97	0.46
1:L5:1175:A:N1	1:L5:1185:G:C6	2.84	0.46
1:L5:4741:C:H4'	1:L5:4742:G:H5'	1.98	0.46
12:LI:47:PRO:HG2	12:LI:142:LEU:HG	1.98	0.46
49:S2:527:C:H2'	49:S2:528:A:C8	2.51	0.46
49:S2:1353:A:OP1	50:SA:139:TYR:OH	2.26	0.46
49:S2:1527:C:OP1	60:SQ:142:GLN:NE2	2.42	0.46
56:SI:105:ASP:OD2	56:SI:107:THR:OG1	2.30	0.46
60:SQ:50:LYS:HD2	60:SQ:85:ARG:HE	1.80	0.46
64:SU:40:ILE:HD11	64:SU:89:ILE:HD12	1.96	0.46
70:Sg:11:LEU:HD22	70:Sg:53:GLY:HA3	1.98	0.46
1:L5:85:G:N2	1:L5:98:A:OP2	2.37	0.46
1:L5:1443:A:N1	1:L5:2103:G:O6	2.49	0.46
1:L5:2811:G:N1	1:L5:2814:C:OP2	2.37	0.46
25:LW:99:GLU:HA	25:LW:102:LYS:HE2	1.97	0.46
55:SH:144:ILE:HD13	55:SH:154:ILE:HG12	1.98	0.46
56:SI:117:TYR:HD1	56:SI:152:ARG:HB3	1.80	0.46
1:L5:1339:U:H2'	1:L5:1340:C:C6	2.50	0.46
1:L5:4101:C:N4	1:L5:4107:G:O6	2.49	0.46
1:L5:4742:G:H2'	1:L5:4743:G:H8	1.81	0.46
50:SA:85:ARG:HD2	61:SR:81:ARG:HH11	1.81	0.46
63:ST:3:GLY:HA2	63:ST:4:VAL:HA	1.81	0.46
1:L5:4257:A:H2	13:LJ:27:GLY:HA2	1.80	0.46
14:LL:130:LYS:HD2	14:LL:131:PRO:HD2	1.97	0.46
22:LT:83:LYS:HD2	22:LT:85:LEU:HD21	1.98	0.46
49:S2:824:C:H1'	73:SJ:144:ILE:HG21	1.98	0.46
50:SA:177:MET:SD	50:SA:180:ARG:NH2	2.88	0.46
70:Sg:297:THR:HA	70:Sg:310:TRP:O	2.15	0.46
74:SM:52:LEU:HD21	74:SM:108:CYS:HB2	1.97	0.46
9:LF:93:ILE:HA	9:LF:119:ASN:O	2.16	0.45
14:LL:116:ARG:NH1	14:LL:155:MET:O	2.45	0.45
51:SB:68:GLU:HA	51:SB:84:PHE:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SD:62:LYS:O	52:SD:67:ARG:NH2	2.49	0.45
52:SD:161:GLY:O	52:SD:164:VAL:C	2.59	0.45
55:SH:69:LEU:O	55:SH:73:GLN:HG2	2.16	0.45
70:Sg:152:SER:OG	70:Sg:196:ASN:O	2.34	0.45
74:SM:83:LYS:HD3	74:SM:105:GLY:H	1.81	0.45
1:L5:1443:A:H2	1:L5:2103:G:C2	2.34	0.45
8:LE:152:ILE:O	8:LE:159:GLY:N	2.48	0.45
18:LP:94:MET:HE2	18:LP:148:MET:HE3	1.98	0.45
26:LX:91:GLU:HG2	83:CA:291:MET:HE1	1.98	0.45
69:Sd:2:GLY:HA2	69:Sd:3:HIS:HA	1.77	0.45
83:CA:140:ALA:HB1	83:CA:343:TYR:HB3	1.98	0.45
83:CA:229:LEU:HD23	83:CA:318:GLN:HB3	1.98	0.45
1:L5:2444:U:HO2'	3:L8:112:G:HO2'	1.63	0.45
1:L5:3951:G:O6	1:L5:4060:U:O4	2.33	0.45
1:L5:4474:A:H5''	41:Lm:125:LYS:HD2	1.99	0.45
47:Lt:19:GLY:H	47:Lt:58:ILE:HD12	1.82	0.45
49:S2:1759:G:N2	49:S2:1760:G:O6	2.49	0.45
60:SQ:43:GLU:HB2	60:SQ:81:ILE:HD11	1.96	0.45
63:ST:39:LEU:HD23	63:ST:39:LEU:HA	1.81	0.45
70:Sg:201:SER:OG	70:Sg:203:ASP:O	2.32	0.45
1:L5:407:A:O2'	1:L5:410:A:OP1	2.30	0.45
1:L5:499:G:H2'	1:L5:504:G:H22	1.81	0.45
1:L5:753:C:H41	1:L5:910:G:H1	1.64	0.45
1:L5:1518:A:H61	14:LL:19:GLN:HE22	1.63	0.45
1:L5:3968:U:O2'	48:Lz:164:CYS:O	2.33	0.45
1:L5:4031:U:O5'	48:Lz:27:LYS:NZ	2.46	0.45
1:L5:4126:C:OP1	10:LG:37:LYS:NZ	2.49	0.45
47:Lt:66:ASN:N	47:Lt:69:ALA:O	2.40	0.45
49:S2:1418:C:H1'	49:S2:1421:A:H2	1.82	0.45
74:SM:58:GLU:HG2	74:SM:61:TYR:HB2	1.98	0.45
49:S2:996:A:H2'	49:S2:997:A:C8	2.52	0.45
52:SD:70:THR:HB	52:SD:86:LEU:HG	1.98	0.45
63:ST:9:VAL:HG21	63:ST:138:VAL:HG13	1.97	0.45
72:SG:33:ALA:CA	72:SG:52:ILE:O	2.64	0.45
79:SZ:102:LYS:HA	79:SZ:107:VAL:HG12	1.98	0.45
83:CA:245:THR:HG23	83:CA:246:ILE:HG13	1.97	0.45
1:L5:1896:A:OP1	9:LF:223:LYS:NZ	2.49	0.45
1:L5:4600:G:O2'	1:L5:4609:G:N1	2.48	0.45
1:L5:4940:C:OP2	8:LE:219:LYS:NZ	2.40	0.45
4:LA:45:VAL:O	4:LA:85:GLY:N	2.49	0.45
8:LE:207:LYS:O	8:LE:256:GLN:NE2	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:Lo:104:ILE:HA	43:Lo:105:GLN:HA	1.68	0.45
49:S2:57:U:OP1	49:S2:504:G:O2'	2.35	0.45
53:SE:54:TYR:OH	53:SE:97:GLU:OE2	2.34	0.45
53:SE:199:GLU:HG3	53:SE:207:VAL:HG23	1.99	0.45
60:SQ:134:GLY:HA3	60:SQ:140:ARG:HA	1.97	0.45
1:L5:4113:U:O2'	1:L5:4115:G:OP2	2.33	0.45
5:LB:168:MET:HA	5:LB:171:LEU:HD12	1.97	0.45
11:LH:17:ASP:HB2	11:LH:28:LYS:HB3	1.98	0.45
19:LQ:66:MET:HE3	19:LQ:98:LEU:HD13	1.99	0.45
20:LR:44:LEU:HD22	20:LR:49:LEU:HD12	1.99	0.45
20:LR:77:GLY:O	20:LR:81:ARG:NE	2.50	0.45
49:S2:72:C:N4	49:S2:74:G:O6	2.50	0.45
49:S2:1247:C:H3'	85:CE:330:LYS:HD3	1.99	0.45
57:SK:71:LEU:HD21	57:SK:79:LEU:HD12	1.98	0.45
1:L5:1355:G:OP1	19:LQ:108:ARG:NH1	2.40	0.45
1:L5:4274:A:H2'	1:L5:4275:G:C8	2.51	0.45
4:LA:36:GLU:OE1	4:LA:163:ARG:NH1	2.49	0.45
12:LI:66:GLU:OE1	12:LI:69:ARG:NH1	2.37	0.45
13:LJ:4:ASP:O	13:LJ:8:LYS:HB2	2.17	0.45
20:LR:3:MET:HE3	20:LR:5:ARG:HB2	1.99	0.45
45:Lr:21:ASN:OD1	45:Lr:21:ASN:N	2.47	0.45
48:Lz:109:ALA:HB1	48:Lz:139:THR:HG23	1.97	0.45
49:S2:1215:C:O2'	49:S2:1645:C:OP2	2.34	0.45
66:SX:77:ASN:O	66:SX:79:LYS:N	2.49	0.45
70:Sg:121:VAL:HG11	70:Sg:165:ILE:HD11	1.98	0.45
83:CA:82:VAL:HG12	83:CA:106:VAL:HG12	1.98	0.45
83:CA:174:ALA:O	83:CA:179:CYS:N	2.45	0.45
83:CA:187:SER:O	83:CA:200:THR:OG1	2.29	0.45
84:CC:21:A:H61	84:CC:46:A:H2'	1.81	0.45
1:L5:2324:C:O2'	33:Le:98:GLU:OE1	2.35	0.45
1:L5:2906:G:H1'	1:L5:2908:U:H1'	1.99	0.45
27:LY:53:ASP:HB3	27:LY:110:LYS:H	1.81	0.45
28:LZ:13:VAL:O	28:LZ:20:GLY:N	2.47	0.45
78:SY:100:LYS:NZ	78:SY:101:LYS:O	2.40	0.45
1:L5:4612:C:C2	11:LH:120:GLU:HB2	2.52	0.45
20:LR:105:LEU:HD23	20:LR:138:LEU:HD23	1.99	0.45
49:S2:1421:A:H5''	49:S2:1422:G:H2'	1.99	0.45
49:S2:1748:G:H1	49:S2:1786:U:H3	1.65	0.45
50:SA:26:GLY:O	50:SA:150:THR:OG1	2.29	0.45
59:SP:20:VAL:HG12	59:SP:25:LEU:HG	1.99	0.45
61:SR:5:ARG:O	61:SR:10:LYS:NZ	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:SU:22:ILE:HG23	64:SU:89:ILE:HB	1.99	0.45
73:SJ:164:PRO:HB3	73:SJ:170:PRO:HA	1.99	0.45
78:SY:120:THR:O	78:SY:124:ASN:HB2	2.17	0.45
83:CA:46:LEU:HD11	83:CA:93:LYS:HD3	1.98	0.45
83:CA:122:ALA:HB3	83:CA:320:LYS:HG3	1.98	0.45
1:L5:170:C:H42	1:L5:266:C:H42	1.65	0.44
8:LE:88:VAL:HA	8:LE:89:LEU:HA	1.75	0.44
36:Lh:96:ASN:O	36:Lh:100:GLU:HB2	2.17	0.44
49:S2:1588:A:H2'	49:S2:1589:A:C8	2.51	0.44
55:SH:127:ASP:OD1	55:SH:142:LYS:NZ	2.50	0.44
56:SI:84:ASN:HD22	56:SI:87:ASN:H	1.64	0.44
58:SL:126:VAL:HG12	58:SL:145:VAL:HG22	1.99	0.44
73:SJ:93:LYS:HE2	73:SJ:96:TYR:HE2	1.82	0.44
1:L5:137:G:H2'	1:L5:138:G:H8	1.82	0.44
33:Le:38:PRO:HD2	33:Le:55:MET:HE3	1.98	0.44
39:Lk:24:LYS:HD2	39:Lk:69:LEU:HD21	1.99	0.44
49:S2:1579:A:O2'	49:S2:1581:C:OP2	2.30	0.44
52:SD:206:ASP:OD1	52:SD:206:ASP:N	2.46	0.44
68:Sc:63:ARG:HB3	68:Sc:64:GLU:H	1.70	0.44
79:SZ:102:LYS:HA	79:SZ:102:LYS:HD2	1.77	0.44
1:L5:1857:C:H2'	1:L5:1858:A:H8	1.82	0.44
1:L5:3976:C:N4	1:L5:4035:G:OP2	2.51	0.44
1:L5:4054:C:H1'	48:Lz:207:LYS:HB2	2.00	0.44
16:LN:84:PRO:HA	16:LN:87:HIS:CG	2.52	0.44
26:LX:64:SER:HB2	36:Lh:69:LEU:HD13	1.99	0.44
27:LY:56:GLN:HB3	27:LY:67:ILE:HD13	1.99	0.44
35:Lg:42:PRO:HB2	35:Lg:53:LEU:HD12	1.99	0.44
47:Lt:148:PRO:HD2	47:Lt:149:HIS:CD2	2.52	0.44
49:S2:1845:A:H2'	49:S2:1846:G:C8	2.52	0.44
60:SQ:97:GLN:HB3	60:SQ:105:LYS:HG3	1.99	0.44
70:Sg:236:ILE:HG12	70:Sg:252:THR:HG22	1.99	0.44
79:SZ:74:SER:HA	79:SZ:79:ILE:HB	1.99	0.44
1:L5:2495:U:H2'	1:L5:2496:G:H8	1.83	0.44
1:L5:3955:G:N3	1:L5:3966:A:N7	2.65	0.44
1:L5:4537:C:H2'	1:L5:4538:G:C8	2.52	0.44
1:L5:4712:C:OP1	17:LO:74:ARG:NH2	2.50	0.44
5:LB:380:GLN:N	5:LB:384:GLU:OE2	2.48	0.44
10:LG:99:ALA:HB1	10:LG:136:LEU:HD11	2.00	0.44
42:Ln:1:MET:HB2	49:S2:1706:G:H5'	1.98	0.44
49:S2:693:A:N6	49:S2:738:C:O2'	2.50	0.44
54:SF:175:ASP:HA	54:SF:178:ILE:HG12	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:ST:122:LYS:HB3	63:ST:122:LYS:HE2	1.72	0.44
64:SU:24:LEU:HB3	64:SU:32:LEU:HD11	1.98	0.44
69:Sd:49:ASP:OD1	69:Sd:49:ASP:N	2.37	0.44
74:SM:51:VAL:O	74:SM:108:CYS:HA	2.17	0.44
1:L5:2745:A:H2'	1:L5:2746:A:C8	2.52	0.44
1:L5:2902:G:O6	1:L5:3594:C:N4	2.50	0.44
1:L5:4967:A:H2'	1:L5:4968:A:C8	2.52	0.44
78:SY:55:ILE:HG12	78:SY:75:ILE:HG12	2.00	0.44
82:Sf:141:CYS:O	82:Sf:145:CYS:CA	2.64	0.44
1:L5:74:G:H5'	14:LL:59:VAL:HG13	2.00	0.44
1:L5:1279:A:O2'	1:L5:1281:G:N7	2.51	0.44
1:L5:1320:U:O2'	1:L5:1891:A:N1	2.50	0.44
1:L5:1942:A:H2'	1:L5:1943:A:C8	2.53	0.44
1:L5:4743:G:H2'	1:L5:4744:A:C8	2.52	0.44
23:LU:84:LYS:HE2	23:LU:88:LYS:HE3	1.98	0.44
26:LX:104:ALA:O	26:LX:134:LYS:NZ	2.48	0.44
48:Lz:35:GLN:HG3	48:Lz:166:ALA:HA	1.99	0.44
49:S2:1441:U:O2	49:S2:1443:C:N4	2.49	0.44
49:S2:1759:G:N2	49:S2:1773:C:OP1	2.51	0.44
50:SA:81:ASN:HA	50:SA:84:GLN:HB2	1.99	0.44
53:SE:126:VAL:O	53:SE:157:ASN:HA	2.18	0.44
60:SQ:110:ASP:HA	60:SQ:113:ILE:HG12	1.99	0.44
63:ST:42:HIS:HB3	63:ST:93:SER:HB2	2.00	0.44
1:L5:84:A:OP2	29:La:65:ARG:NH2	2.51	0.44
1:L5:3811:G:O2'	1:L5:3814:U:OP2	2.23	0.44
7:LD:208:MET:HB3	7:LD:233:PRO:HG3	2.00	0.44
10:LG:165:GLU:OE2	16:LN:26:ARG:NH1	2.42	0.44
14:LL:94:ILE:HD13	14:LL:94:ILE:HA	1.88	0.44
35:Lg:103:VAL:HA	35:Lg:106:VAL:HG22	2.00	0.44
49:S2:1653:U:H3	49:S2:1671:G:H1	1.66	0.44
55:SH:64:VAL:O	55:SH:96:ALA:HA	2.18	0.44
59:SP:91:GLY:N	59:SP:107:ILE:O	2.47	0.44
61:SR:69:ILE:HD12	61:SR:74:GLN:HG3	1.99	0.44
63:ST:9:VAL:O	63:ST:11:GLN:NE2	2.51	0.44
67:Sa:36:ILE:HB	67:Sa:73:TYR:HB2	1.98	0.44
72:SG:162:LEU:HB2	72:SG:170:ARG:O	2.17	0.44
73:SJ:127:ARG:HD3	81:Se:31:ARG:HD3	1.99	0.44
24:LV:92:ASP:OD1	24:LV:92:ASP:N	2.49	0.44
34:Lf:10:ILE:HA	34:Lf:99:HIS:O	2.17	0.44
42:Ln:11:ARG:NH2	49:S2:1184:G:OP1	2.51	0.44
50:SA:27:GLY:H	50:SA:46:ILE:HG23	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:SQ:73:LYS:HA	60:SQ:73:LYS:HD3	1.73	0.44
83:CA:189:GLN:HE21	83:CA:199:LYS:HB2	1.83	0.44
83:CA:262:SER:OG	83:CA:295:GLU:OE1	2.33	0.44
1:L5:4478:G:O2'	1:L5:4602:A:N1	2.51	0.44
6:LC:134:PRO:HA	6:LC:150:LEU:HD22	2.00	0.44
49:S2:10:G:O2'	71:SC:113:GLN:NE2	2.51	0.44
51:SB:38:MET:HE2	51:SB:38:MET:HB3	1.80	0.44
77:SW:87:GLU:O	77:SW:91:ASN:ND2	2.51	0.44
82:Sf:124:ASP:OD1	82:Sf:124:ASP:N	2.50	0.44
83:CA:31:VAL:HG12	83:CA:55:MET:HE1	2.00	0.44
83:CA:310:GLU:HG3	83:CA:314:GLU:HB3	2.00	0.44
1:L5:2846:G:O2'	24:LV:19:GLY:O	2.28	0.43
46:Ls:77:LYS:HG2	46:Ls:198:ILE:HD13	2.00	0.43
70:Sg:15:ASN:OD1	70:Sg:15:ASN:N	2.49	0.43
83:CA:164:THR:OG1	83:CA:165:GLN:N	2.50	0.43
1:L5:1322:A:O2'	1:L5:1324:A:OP2	2.36	0.43
15:LM:93:LYS:HB3	15:LM:93:LYS:HE2	1.72	0.43
49:S2:85:A:H5''	78:SY:118:ARG:HH12	1.83	0.43
49:S2:951:C:O2'	76:SO:50:LYS:NZ	2.48	0.43
49:S2:981:A:H2'	49:S2:982:G:C8	2.53	0.43
49:S2:1764:G:H5'	49:S2:1765:C:H5''	2.00	0.43
54:SF:135:ARG:HA	54:SF:135:ARG:HD3	1.81	0.43
67:Sa:45:VAL:HG11	67:Sa:64:LEU:HD13	1.99	0.43
70:Sg:32:LEU:HD12	70:Sg:71:ILE:HG12	1.99	0.43
1:L5:2758:G:O2'	1:L5:2765:A:N3	2.41	0.43
5:LB:107:ALA:HB2	5:LB:201:LEU:HG	2.01	0.43
11:LH:114:ILE:HB	11:LH:124:ARG:HG3	2.01	0.43
12:LI:207:ASP:OD1	12:LI:210:ARG:NH2	2.50	0.43
21:LS:69:GLU:HG2	21:LS:101:THR:HG22	2.00	0.43
49:S2:94:G:O2'	49:S2:508:A:O2'	2.34	0.43
49:S2:1536:G:H2'	49:S2:1537:A:H8	1.80	0.43
55:SH:21:SER:OG	55:SH:25:GLN:OE1	2.24	0.43
63:ST:43:LYS:HB3	63:ST:43:LYS:HE2	1.76	0.43
72:SG:217:MET:HA	72:SG:220:ALA:HB3	1.99	0.43
1:L5:935:A:O2'	15:LM:44:GLN:O	2.36	0.43
1:L5:3612:C:H1'	1:L5:5016:A:C8	2.53	0.43
1:L5:3786:U:OP1	1:L5:4550:G:O2'	2.34	0.43
8:LE:190:HIS:HB3	8:LE:193:PHE:HD2	1.83	0.43
41:Lm:94:MET:HG2	41:Lm:105:PRO:HA	2.00	0.43
45:Lr:94:ARG:HB2	45:Lr:111:ILE:HD11	2.00	0.43
50:SA:85:ARG:HG3	61:SR:81:ARG:HD2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SD:60:GLY:HA3	52:SD:65:ARG:H	1.83	0.43
59:SP:133:ILE:HG21	85:CE:318:ILE:HD11	2.00	0.43
82:Sf:132:MET:HG2	82:Sf:141:CYS:HB2	1.99	0.43
1:L5:1445:U:O2	1:L5:2102:G:O6	2.26	0.43
1:L5:2318:G:O6	33:Le:19:LYS:NZ	2.49	0.43
1:L5:2382:A:N1	1:L5:2829:U:O2'	2.47	0.43
1:L5:5053:U:H5'	1:L5:5054:C:C4	2.52	0.43
5:LB:155:LYS:HE3	5:LB:155:LYS:HB2	1.80	0.43
5:LB:378:ARG:HG2	25:LW:32:LEU:HD21	2.00	0.43
11:LH:59:LYS:HD2	11:LH:59:LYS:HA	1.75	0.43
68:Sc:14:VAL:HG13	68:Sc:30:VAL:HB	2.01	0.43
70:Sg:252:THR:O	70:Sg:252:THR:OG1	2.35	0.43
74:SM:52:LEU:HD23	74:SM:108:CYS:HB2	1.89	0.43
1:L5:257:C:H2'	1:L5:258:G:H8	1.84	0.43
1:L5:2748:C:O2'	35:Lg:61:PRO:O	2.32	0.43
39:Lk:61:PRO:HA	39:Lk:62:PRO:HD3	1.88	0.43
43:Lo:45:GLN:HE22	43:Lo:52:THR:H	1.66	0.43
49:S2:372:U:O2'	58:SL:82:MET:SD	2.75	0.43
49:S2:750:C:N4	49:S2:752:G:OP2	2.51	0.43
53:SE:91:SER:OG	53:SE:98:ASN:ND2	2.52	0.43
84:CC:48:C:H2'	84:CC:49:G:H8	1.82	0.43
1:L5:3615:G:H1'	25:LW:44:ARG:HD3	2.00	0.43
1:L5:3961:G:N2	1:L5:3965:A:N7	2.57	0.43
4:LA:28:ARG:HD2	4:LA:123:ARG:HD2	1.99	0.43
31:Lc:38:ILE:HG21	31:Lc:63:TYR:HB3	2.00	0.43
47:Lt:146:ARG:HH12	47:Lt:152:ILE:HD12	1.83	0.43
51:SB:23:ASP:OD1	51:SB:23:ASP:N	2.51	0.43
53:SE:175:PHE:HE1	53:SE:225:ILE:HG21	1.83	0.43
63:ST:76:THR:HG23	63:ST:94:ARG:HE	1.83	0.43
83:CA:17:VAL:HA	83:CA:20:LYS:HG2	2.01	0.43
1:L5:1327:C:H2'	1:L5:1328:G:C8	2.54	0.43
1:L5:2101:C:H2'	1:L5:2102:G:H2'	2.00	0.43
6:LC:7:LEU:HG	6:LC:21:ASN:HB3	2.00	0.43
10:LG:100:HIS:HA	10:LG:103:ARG:HG3	2.00	0.43
47:Lt:124:GLU:HG3	47:Lt:125:LEU:H	1.82	0.43
49:S2:104:A:H62	49:S2:356:C:H5	1.67	0.43
57:SK:20:VAL:HA	57:SK:69:TRP:O	2.18	0.43
57:SK:21:MET:HB2	57:SK:69:TRP:HB2	2.00	0.43
80:Sb:42:LYS:HE2	80:Sb:57:VAL:HG12	2.00	0.43
83:CA:207:ASP:HA	83:CA:210:LYS:HE2	2.00	0.43
1:L5:3664:G:H2'	1:L5:3665:G:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LI:68:ALA:HB1	12:LI:155:ALA:HB1	2.00	0.43
49:S2:886:A:N6	49:S2:901:G:N9	2.65	0.43
71:SC:196:ILE:HB	71:SC:223:TYR:HB2	2.00	0.43
84:CC:48:C:H2'	84:CC:49:G:C8	2.54	0.43
1:L5:667:A:H5''	1:L5:668:C:H5''	2.01	0.43
1:L5:1308:C:H2'	1:L5:1309:C:C6	2.54	0.43
1:L5:1995:G:H21	47:Lt:122:ALA:HB3	1.83	0.43
1:L5:3923:A:H2'	1:L5:3924:C:C6	2.54	0.43
1:L5:4405:G:H5'	12:LI:8:CYS:SG	2.59	0.43
1:L5:4699:U:H1'	1:L5:4700:A:H5''	2.00	0.43
7:LD:27:LYS:HE2	13:LJ:147:ARG:HD3	2.01	0.43
27:LY:63:LYS:HE2	27:LY:63:LYS:HB3	1.83	0.43
49:S2:483:C:H5''	66:SX:48:LYS:HE2	1.99	0.43
49:S2:837:A:N1	78:SY:9:THR:OG1	2.52	0.43
49:S2:1256:G:H8	64:SU:66:ARG:HB2	1.83	0.43
53:SE:155:LYS:HG2	53:SE:174:LYS:HE3	2.01	0.43
54:SF:27:ASP:OD1	54:SF:27:ASP:N	2.52	0.43
70:Sg:98:THR:OG1	70:Sg:99:ARG:N	2.52	0.43
1:L5:1176:C:O2'	7:LD:282:GLN:NE2	2.52	0.42
7:LD:199:ILE:HG22	7:LD:200:MET:HE2	2.00	0.42
21:LS:43:ARG:HD2	21:LS:43:ARG:HA	1.84	0.42
32:Ld:29:ILE:O	32:Ld:33:ILE:HB	2.19	0.42
32:Ld:123:ASP:OD1	32:Ld:123:ASP:N	2.44	0.42
41:Lm:95:ILE:HA	41:Lm:101:ALA:O	2.19	0.42
49:S2:746:C:O2	49:S2:798:G:O6	2.36	0.42
49:S2:886:A:C6	49:S2:901:G:C4	3.03	0.42
49:S2:1232:U:H2'	49:S2:1233:G:H8	1.84	0.42
49:S2:1247:C:O2	85:CE:334:LYS:NZ	2.41	0.42
55:SH:86:LYS:HE3	55:SH:86:LYS:HB3	1.75	0.42
58:SL:49:GLU:OE1	58:SL:118:ARG:NH2	2.52	0.42
77:SW:24:GLN:NE2	77:SW:64:ASN:OD1	2.51	0.42
80:Sb:34:ASP:HA	80:Sb:44:THR:O	2.18	0.42
49:S2:750:C:H41	49:S2:793:G:H21	1.68	0.42
49:S2:1232:U:H2'	49:S2:1233:G:C8	2.53	0.42
49:S2:1552:G:O4'	52:SD:9:ARG:NH2	2.52	0.42
55:SH:138:GLU:H	55:SH:159:ASP:HB2	1.83	0.42
62:SS:60:THR:OG1	62:SS:62:ASP:OD2	2.25	0.42
74:SM:63:LYS:O	74:SM:67:ALA:HB3	2.18	0.42
83:CA:61:GLY:O	83:CA:65:LYS:NZ	2.36	0.42
1:L5:261:G:H2'	1:L5:262:G:C8	2.55	0.42
1:L5:3607:U:H2'	1:L5:3608:A:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:4717:A:OP2	5:LB:30:LYS:NZ	2.42	0.42
2:L7:27:G:OP1	13:LJ:146:ARG:NH2	2.53	0.42
7:LD:65:ALA:HB2	7:LD:74:ILE:HD13	2.02	0.42
10:LG:95:LEU:HD21	10:LG:156:VAL:HG21	2.01	0.42
48:Lz:60:ARG:HH21	48:Lz:61:PRO:HG3	1.84	0.42
48:Lz:73:HIS:O	48:Lz:77:ALA:HB2	2.19	0.42
48:Lz:208:SER:H	48:Lz:211:GLY:HA3	1.84	0.42
51:SB:123:ALA:HB2	51:SB:165:ARG:HG3	2.01	0.42
54:SF:42:LYS:HA	54:SF:42:LYS:HD2	1.82	0.42
62:SS:124:ARG:O	62:SS:127:TRP:C	2.62	0.42
8:LE:141:ARG:NH1	34:Lf:110:ILE:O	2.51	0.42
19:LQ:159:PRO:HA	19:LQ:160:HIS:HA	1.80	0.42
48:Lz:112:ALA:HB1	48:Lz:137:LEU:HD22	2.01	0.42
49:S2:508:A:H3'	49:S2:509:G:H8	1.84	0.42
57:SK:1:MET:HG3	57:SK:3:MET:HB2	2.01	0.42
73:SJ:30:LYS:O	73:SJ:34:GLU:HB2	2.20	0.42
74:SM:95:ASP:OD1	74:SM:95:ASP:N	2.46	0.42
83:CA:164:THR:OG1	83:CA:165:GLN:OE1	2.37	0.42
1:L5:239:C:OP1	27:LY:46:SER:OG	2.34	0.42
1:L5:909:A:H2'	1:L5:910:G:H8	1.85	0.42
1:L5:1258:G:H2'	1:L5:1259:G:C8	2.54	0.42
1:L5:4425:G:OP1	41:Lm:100:TYR:OH	2.31	0.42
7:LD:191:ASN:HD22	7:LD:194:VAL:HG23	1.84	0.42
47:Lt:48:LYS:O	47:Lt:51:GLY:C	2.63	0.42
50:SA:57:LYS:HD2	50:SA:57:LYS:HA	1.81	0.42
53:SE:9:LEU:HB2	53:SE:30:ARG:HD3	2.00	0.42
70:Sg:256:ILE:HG21	70:Sg:289:LEU:HD21	2.02	0.42
1:L5:2520:C:H2'	1:L5:2521:G:C8	2.54	0.42
1:L5:4135:G:H2'	1:L5:4136:G:C8	2.55	0.42
1:L5:4736:C:H2'	1:L5:4737:G:H8	1.84	0.42
22:LT:116:LYS:HB3	22:LT:116:LYS:HE2	1.93	0.42
25:LW:80:ARG:HD3	72:SG:131:ARG:HH11	1.85	0.42
33:Le:76:LYS:O	45:Lr:23:GLN:NE2	2.50	0.42
38:Lj:67:LEU:HD23	38:Lj:67:LEU:HA	1.90	0.42
49:S2:380:G:O6	56:SI:178:ARG:NH2	2.53	0.42
49:S2:900:C:H5'	49:S2:901:G:N7	2.35	0.42
49:S2:1650:A:H5''	60:SQ:139:ALA:HB2	2.01	0.42
62:SS:15:VAL:HG13	62:SS:68:ILE:HD11	2.02	0.42
64:SU:81:GLN:HE21	64:SU:83:ARG:HE	1.66	0.42
1:L5:1940:G:H22	1:L5:4434:C:H5''	1.84	0.42
1:L5:2558:C:H2'	1:L5:2559:G:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3861:A:H2'	1:L5:3862:A:C8	2.54	0.42
1:L5:4083:U:OP1	4:LA:123:ARG:NH2	2.52	0.42
28:LZ:41:ALA:HB2	28:LZ:77:TYR:HE1	1.84	0.42
49:S2:94:G:HO2'	49:S2:508:A:HO2'	1.65	0.42
56:SI:42:ARG:HH21	56:SI:59:ARG:HH12	1.67	0.42
64:SU:28:ASN:HD22	64:SU:31:SER:H	1.67	0.42
70:Sg:214:GLY:HA2	70:Sg:236:ILE:HG13	2.02	0.42
1:L5:1464:C:H5''	30:Lb:32:LEU:HD12	2.02	0.42
1:L5:1662:C:H2'	1:L5:1663:C:C6	2.55	0.42
1:L5:1820:C:O2'	1:L5:1821:G:N7	2.48	0.42
1:L5:2583:C:OP2	35:Lg:76:ARG:NH1	2.46	0.42
11:LH:56:ARG:NH1	11:LH:58:ASP:OD1	2.53	0.42
13:LJ:93:GLU:HG3	13:LJ:173:ILE:HB	2.01	0.42
13:LJ:119:TYR:HD2	62:SS:12:ILE:HG21	1.84	0.42
15:LM:50:MET:HA	15:LM:51:PRO:HD3	1.93	0.42
16:LN:159:ARG:HB3	16:LN:164:LEU:HB2	2.00	0.42
25:LW:71:ARG:HA	25:LW:71:ARG:HD3	1.75	0.42
43:Lo:11:PHE:O	43:Lo:81:ARG:NH1	2.51	0.42
47:Lt:121:LEU:HB3	47:Lt:123:ARG:HB3	2.01	0.42
49:S2:51:U:H2'	49:S2:52:G:C8	2.55	0.42
49:S2:1275:G:N2	49:S2:1506:A:OP2	2.45	0.42
51:SB:67:PHE:O	51:SB:85:LYS:O	2.37	0.42
53:SE:18:TRP:HH2	53:SE:31:PRO:HD3	1.85	0.42
72:SG:2:LYS:HG2	72:SG:15:LEU:HD21	2.02	0.42
83:CA:79:SER:HB2	83:CA:109:ASP:HB2	2.02	0.42
84:CC:39:C:H2'	84:CC:40:G:C8	2.55	0.42
1:L5:1220:G:H2'	1:L5:1221:G:C8	2.55	0.42
5:LB:193:LYS:HE2	5:LB:193:LYS:HB3	1.82	0.42
17:LO:194:GLU:O	17:LO:198:THR:OG1	2.33	0.42
18:LP:54:GLN:HA	18:LP:83:TRP:CD1	2.55	0.42
36:Lh:80:PRO:HD2	36:Lh:83:LEU:HD12	2.02	0.42
47:Lt:34:PRO:HD3	47:Lt:40:LYS:HZ1	1.84	0.42
49:S2:201:C:H3'	49:S2:202:G:H21	1.85	0.42
49:S2:1101:U:H2'	49:S2:1102:G:C8	2.54	0.42
51:SB:225:LEU:HD11	51:SB:229:MET:HE2	2.02	0.42
56:SI:4:SER:OG	56:SI:6:ASP:OD1	2.35	0.42
57:SK:95:ARG:NE	57:SK:97:SER:O	2.52	0.42
63:ST:2:PRO:HA	63:ST:3:GLY:HA3	1.76	0.42
70:Sg:26:GLN:HE21	70:Sg:75:GLY:HA3	1.85	0.42
70:Sg:220:ASP:HB3	70:Sg:227:LEU:HG	2.01	0.42
83:CA:201:ILE:HA	83:CA:213:HIS:HE1	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:182:G:N1	1:L5:255:C:O2	2.53	0.42
1:L5:408:A:O2'	1:L5:411:G:OP2	2.32	0.42
1:L5:1268:G:N7	30:Lb:111:ARG:NH2	2.65	0.42
1:L5:4363:A:H5''	43:Lo:36:GLN:HG2	2.02	0.42
13:LJ:4:ASP:O	13:LJ:8:LYS:CB	2.68	0.42
37:Li:43:MET:HE3	37:Li:43:MET:HB3	1.81	0.42
38:Lj:3:LYS:H	38:Lj:3:LYS:HG2	1.59	0.42
46:Ls:47:LEU:HA	46:Ls:50:LYS:HB3	2.01	0.42
47:Lt:134:GLY:HA2	47:Lt:137:GLN:HG2	2.01	0.42
49:S2:71:G:N2	49:S2:73:C:OP1	2.52	0.42
49:S2:142:C:N4	49:S2:330:G:OP2	2.50	0.42
51:SB:38:MET:H	51:SB:38:MET:HG2	1.54	0.42
61:SR:97:GLU:HB2	61:SR:120:THR:HG23	2.02	0.42
65:SV:34:MET:HE2	65:SV:34:MET:HB3	1.81	0.42
70:Sg:37:ASP:OD1	70:Sg:37:ASP:N	2.41	0.42
70:Sg:99:ARG:HA	70:Sg:99:ARG:HD2	1.88	0.42
72:SG:50:VAL:HG12	72:SG:113:ILE:HG12	2.02	0.42
83:CA:207:ASP:HA	83:CA:210:LYS:HG2	2.01	0.42
1:L5:513:U:O2'	1:L5:515:C:N4	2.53	0.41
28:LZ:68:ILE:O	28:LZ:115:LYS:NZ	2.52	0.41
49:S2:118:C:H1'	49:S2:445:A:C5	2.55	0.41
61:SR:95:ILE:HD13	61:SR:95:ILE:HA	1.93	0.41
64:SU:98:VAL:HA	64:SU:101:ILE:HG22	2.02	0.41
70:Sg:42:MET:SD	70:Sg:56:GLN:NE2	2.91	0.41
70:Sg:206:LEU:HD12	70:Sg:218:LEU:HD12	2.02	0.41
1:L5:1998:A:H4'	46:Ls:9:TRP:HZ2	1.85	0.41
1:L5:3732:A:H2'	1:L5:3733:A:C8	2.55	0.41
1:L5:4324:A:H2'	1:L5:4325:A:C8	2.55	0.41
1:L5:4976:U:H1'	5:LB:343:ARG:HH21	1.85	0.41
9:LF:86:GLU:HG2	22:LT:136:ARG:H	1.85	0.41
27:LY:55:VAL:HG13	27:LY:104:VAL:HB	2.02	0.41
48:Lz:173:LYS:HE2	48:Lz:173:LYS:HB2	1.84	0.41
49:S2:921:G:C6	80:Sb:22:LYS:HA	2.56	0.41
49:S2:1861:G:H5''	67:Sa:3:LYS:HA	2.02	0.41
50:SA:81:ASN:OD1	50:SA:81:ASN:N	2.52	0.41
51:SB:108:ASP:OD1	51:SB:108:ASP:N	2.51	0.41
56:SI:76:THR:HG21	56:SI:104:ILE:HD12	2.02	0.41
76:SO:53:ILE:HG23	76:SO:88:LEU:HD23	2.00	0.41
79:SZ:101:SER:OG	79:SZ:102:LYS:N	2.53	0.41
83:CA:349:VAL:HG12	83:CA:351:ASP:H	1.84	0.41
1:L5:228:C:O2'	27:LY:14:ASN:ND2	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:2486:G:N7	1:L5:2493:G:N1	2.61	0.41
14:LL:88:LYS:HG3	14:LL:89:LYS:HG3	2.02	0.41
28:LZ:50:PRO:HD3	28:LZ:68:ILE:HG12	2.02	0.41
46:Ls:58:ASN:HD21	46:Ls:83:ARG:HA	1.86	0.41
49:S2:550:C:H2'	49:S2:551:U:C6	2.55	0.41
57:SK:29:MET:HB3	57:SK:42:ASN:HD22	1.85	0.41
59:SP:75:VAL:HA	59:SP:93:MET:O	2.20	0.41
59:SP:115:TYR:HB2	59:SP:118:GLU:HG2	2.01	0.41
72:SG:85:ARG:O	72:SG:87:ARG:NH1	2.52	0.41
82:Sf:133:ALA:N	82:Sf:140:TYR:O	2.52	0.41
1:L5:183:C:H1'	1:L5:184:U:H5	1.85	0.41
15:LM:100:ARG:HA	15:LM:103:LYS:HG2	2.00	0.41
20:LR:39:GLN:HA	20:LR:42:ARG:HB2	2.02	0.41
37:Li:76:ARG:HA	37:Li:76:ARG:HD3	1.73	0.41
47:Lt:16:ARG:O	47:Lt:60:VAL:HA	2.20	0.41
49:S2:746:C:O2'	49:S2:798:G:N1	2.39	0.41
49:S2:1226:G:N1	49:S2:1639:G:OP2	2.38	0.41
49:S2:1615:U:O4	59:SP:40:ARG:NH2	2.53	0.41
49:S2:1736:G:H2'	49:S2:1737:G:C8	2.56	0.41
53:SE:124:CYS:HB3	53:SE:141:THR:HB	2.03	0.41
54:SF:127:ARG:HB2	54:SF:136:ARG:HB2	2.02	0.41
60:SQ:53:GLU:HG3	60:SQ:54:PRO:HD3	2.02	0.41
64:SU:20:ILE:HD13	64:SU:98:VAL:HG21	2.02	0.41
65:SV:32:ILE:HG12	65:SV:60:ARG:HD2	2.01	0.41
65:SV:82:ASN:N	65:SV:82:ASN:OD1	2.54	0.41
66:SX:132:ALA:HB1	66:SX:137:LYS:HB2	2.02	0.41
72:SG:33:ALA:HA	72:SG:52:ILE:O	2.19	0.41
83:CA:41:SER:OG	83:CA:128:ASP:OD2	2.38	0.41
1:L5:4742:G:H2'	1:L5:4743:G:C8	2.55	0.41
9:LF:173:ALA:O	9:LF:177:ARG:HB2	2.20	0.41
49:S2:588:G:H4'	49:S2:589:G:H5'	2.03	0.41
49:S2:641:A:O2'	49:S2:645:C:OP1	2.38	0.41
49:S2:902:G:O2'	49:S2:903:A:O4'	2.39	0.41
49:S2:1203:G:H2'	49:S2:1204:A:C8	2.55	0.41
49:S2:1777:G:H2'	49:S2:1778:C:C6	2.56	0.41
71:SC:68:ARG:HG2	71:SC:277:HIS:HB2	2.03	0.41
1:L5:268:G:H2'	1:L5:269:G:H8	1.85	0.41
1:L5:695:G:OP1	8:LE:226:ARG:NE	2.54	0.41
1:L5:1785:C:OP1	12:LI:133:GLN:NE2	2.54	0.41
1:L5:2343:G:OP2	6:LC:109:ARG:NH1	2.33	0.41
1:L5:3880:G:H2'	1:L5:3881:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L5:3911:C:H2'	1:L5:3912:U:C6	2.56	0.41
5:LB:238:LYS:HB2	5:LB:238:LYS:HE2	1.89	0.41
10:LG:101:LYS:HE2	10:LG:101:LYS:HB3	1.93	0.41
18:LP:94:MET:HE2	18:LP:94:MET:HB3	1.93	0.41
21:LS:13:VAL:HA	21:LS:28:TYR:O	2.20	0.41
49:S2:562:U:H2'	49:S2:563:G:C8	2.56	0.41
49:S2:1424:G:H2'	49:S2:1425:G:C8	2.56	0.41
50:SA:11:LYS:HA	50:SA:11:LYS:HD3	1.75	0.41
61:SR:67:ARG:HA	61:SR:68:GLY:HA3	1.64	0.41
68:Sc:14:VAL:HG22	68:Sc:32:VAL:HG12	2.02	0.41
71:SC:213:LEU:HD23	71:SC:213:LEU:HA	1.95	0.41
1:L5:181:C:H3'	1:L5:182:G:H8	1.84	0.41
1:L5:1629:G:H1	4:LA:208:GLU:HG2	1.85	0.41
1:L5:4054:C:H1'	48:Lz:207:LYS:HD3	2.03	0.41
4:LA:158:ILE:HB	4:LA:162:ASN:HD22	1.85	0.41
27:LY:130:LYS:HA	27:LY:130:LYS:HD3	1.86	0.41
29:La:23:GLY:HA3	29:La:24:LYS:HA	1.70	0.41
48:Lz:89:ALA:HB1	48:Lz:92:LYS:HE3	2.03	0.41
49:S2:13:C:H5'	71:SC:232:THR:HG21	2.03	0.41
49:S2:453:C:O2'	72:SG:92:ARG:O	2.31	0.41
65:SV:51:LYS:HD2	65:SV:78:ILE:HD11	2.03	0.41
66:SX:52:LEU:HD11	66:SX:73:GLN:HB2	2.03	0.41
1:L5:1480:C:O2'	1:L5:1482:G:OP2	2.38	0.41
1:L5:4039:G:N2	1:L5:4050:A:O2'	2.54	0.41
6:LC:293:LEU:O	6:LC:299:GLN:NE2	2.47	0.41
10:LG:220:GLU:HA	10:LG:223:ARG:HG2	2.03	0.41
45:Lr:28:GLU:OE2	45:Lr:31:ASN:ND2	2.44	0.41
48:Lz:17:VAL:HG13	48:Lz:18:LEU:H	1.86	0.41
49:S2:1785:C:O2'	49:S2:1786:U:O4'	2.39	0.41
66:SX:101:LEU:CB	66:SX:123:VAL:O	2.57	0.41
72:SG:219:GLU:HA	72:SG:222:GLU:HG2	2.03	0.41
74:SM:123:VAL:O	74:SM:126:GLU:HG3	2.20	0.41
75:SN:32:ASP:OD1	75:SN:32:ASP:N	2.33	0.41
1:L5:433:A:C2	1:L5:3867:A:H4'	2.56	0.41
1:L5:2250:C:H2'	1:L5:2251:G:C8	2.56	0.41
1:L5:2640:G:H2'	1:L5:2641:A:C8	2.56	0.41
1:L5:4075:U:OP1	10:LG:246:SER:OG	2.34	0.41
1:L5:4457:U:H1'	5:LB:252:ALA:HB3	2.02	0.41
7:LD:41:LYS:HE3	22:LT:93:ILE:HD13	2.03	0.41
11:LH:7:ASN:HA	11:LH:57:VAL:O	2.21	0.41
11:LH:92:MET:HE2	11:LH:179:ILE:HG22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Lk:22:SER:OG	39:Lk:23:VAL:N	2.54	0.41
46:Ls:93:GLU:HG2	46:Ls:94:ASP:H	1.86	0.41
48:Lz:67:VAL:HA	48:Lz:68:LEU:HA	1.54	0.41
49:S2:107:A:H2'	49:S2:108:G:C8	2.55	0.41
49:S2:223:C:H2'	49:S2:224:A:C8	2.55	0.41
49:S2:568:C:C5	49:S2:583:A:N6	2.89	0.41
49:S2:831:G:N7	78:SY:11:LYS:NZ	2.66	0.41
49:S2:1673:U:O2'	54:SF:84:GLY:O	2.30	0.41
49:S2:1757:G:O2'	49:S2:1776:G:O6	2.39	0.41
50:SA:104:THR:HA	50:SA:105:PRO:HD3	1.95	0.41
51:SB:90:ASP:OD2	51:SB:92:GLN:NE2	2.54	0.41
53:SE:16:LYS:HA	53:SE:16:LYS:HD2	1.97	0.41
68:Sc:67:ARG:HH11	68:Sc:68:LEU:H	1.69	0.41
70:Sg:92:LEU:HD13	70:Sg:92:LEU:HA	1.95	0.41
73:SJ:125:HIS:HA	73:SJ:128:VAL:HG12	2.03	0.41
75:SN:114:ARG:O	75:SN:118:ILE:HG12	2.20	0.41
1:L5:1332:C:H2'	1:L5:1333:A:C8	2.56	0.41
1:L5:2485:U:H4'	1:L5:2486:G:N2	2.36	0.41
5:LB:113:GLU:H	5:LB:113:GLU:HG2	1.67	0.41
21:LS:128:LYS:HE3	21:LS:128:LYS:HB2	1.82	0.41
22:LT:42:ILE:O	22:LT:59:GLY:N	2.50	0.41
25:LW:54:LEU:HD23	25:LW:54:LEU:HA	1.93	0.41
32:Ld:47:LYS:HB3	32:Ld:47:LYS:HE2	1.83	0.41
36:Lh:52:LYS:HA	36:Lh:52:LYS:HD3	1.84	0.41
48:Lz:17:VAL:HG11	48:Lz:180:VAL:HG22	2.03	0.41
49:S2:921:G:C6	77:SW:28:ARG:HD2	2.55	0.41
53:SE:125:LYS:HB3	53:SE:142:HIS:HB3	2.03	0.41
62:SS:86:ARG:NH2	62:SS:110:ASP:OD2	2.54	0.41
70:Sg:34:ALA:HB2	70:Sg:69:VAL:HB	2.02	0.41
70:Sg:155:ARG:HA	70:Sg:155:ARG:HD3	1.84	0.41
76:SO:12:GLU:HA	76:SO:13:GLN:HA	1.78	0.41
79:SZ:78:LYS:HA	79:SZ:78:LYS:HD3	1.80	0.41
83:CA:33:ARG:HA	83:CA:36:VAL:HG22	2.03	0.41
1:L5:2749:C:H5'	35:Lg:65:MET:HA	2.03	0.40
1:L5:3967:G:N2	1:L5:4055:U:O2	2.54	0.40
7:LD:86:TYR:CZ	7:LD:247:ILE:HD11	2.56	0.40
7:LD:150:LEU:HD12	13:LJ:146:ARG:HG3	2.02	0.40
8:LE:223:ARG:HB3	8:LE:224:LYS:HG2	2.01	0.40
9:LF:94:ARG:O	9:LF:118:PHE:N	2.52	0.40
26:LX:100:VAL:HG23	26:LX:134:LYS:HB3	2.03	0.40
49:S2:374:G:OP1	58:SL:59:LYS:NZ	2.50	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:S2:629:A:O2'	49:S2:631:U:OP1	2.38	0.40
49:S2:639:C:H2'	49:S2:640:A:C8	2.55	0.40
49:S2:1060:A:O2'	49:S2:1062:A:N7	2.51	0.40
49:S2:1550:G:O2'	49:S2:1558:C:O2	2.40	0.40
62:SS:20:ILE:HG12	62:SS:32:ALA:HB3	2.04	0.40
79:SZ:61:GLU:HA	79:SZ:64:ASN:HD21	1.86	0.40
83:CA:81:SER:HB3	83:CA:85:CYS:HB2	2.03	0.40
1:L5:171:U:OP2	1:L5:172:C:N4	2.55	0.40
1:L5:423:G:OP1	18:LP:62:ARG:NH2	2.54	0.40
1:L5:1558:A:H2'	1:L5:1559:G:C8	2.57	0.40
1:L5:2081:C:H5''	19:LQ:11:ARG:HG3	2.04	0.40
1:L5:2558:C:H2'	1:L5:2559:G:H8	1.86	0.40
5:LB:165:HIS:HA	5:LB:179:HIS:O	2.21	0.40
6:LC:281:MET:HE3	6:LC:281:MET:HB3	1.97	0.40
39:Lk:9:LYS:HE2	39:Lk:9:LYS:HB2	1.92	0.40
41:Lm:110:CYS:SG	41:Lm:111:ARG:N	2.94	0.40
49:S2:735:C:H5''	49:S2:736:C:C2	2.56	0.40
50:SA:211:GLU:HA	50:SA:214:GLU:HG2	2.02	0.40
70:Sg:84:ASP:OD1	70:Sg:84:ASP:N	2.55	0.40
71:SC:176:LYS:HA	71:SC:176:LYS:HD3	1.90	0.40
74:SM:55:ASN:ND2	74:SM:82:ASN:OD1	2.49	0.40
76:SO:61:LYS:HA	76:SO:61:LYS:HD2	1.85	0.40
83:CA:59:GLU:HB2	83:CA:62:LYS:HE3	2.03	0.40
1:L5:3641:U:H5	1:L5:3646:A:N7	2.19	0.40
3:L8:8:U:H2'	3:L8:9:A:C8	2.57	0.40
14:LL:162:LYS:HD2	14:LL:162:LYS:HA	1.93	0.40
25:LW:71:ARG:HD2	25:LW:73:ARG:HH11	1.86	0.40
25:LW:77:LYS:HZ1	72:SG:9:ALA:HA	1.86	0.40
49:S2:115:U:H2'	49:S2:116:U:C6	2.56	0.40
52:SD:31:GLU:HG3	52:SD:107:TYR:CZ	2.57	0.40
54:SF:61:PHE:CZ	68:Sc:51:ARG:HB2	2.57	0.40
56:SI:151:GLU:O	56:SI:154:LYS:HG3	2.22	0.40
62:SS:31:THR:HG21	62:SS:38:ARG:HG3	2.03	0.40
65:SV:40:ASP:N	65:SV:40:ASP:OD1	2.52	0.40
1:L5:1443:A:N1	1:L5:2103:G:C6	2.89	0.40
40:Ll:42:ARG:HG3	40:Ll:47:THR:HG23	2.02	0.40
49:S2:1310:U:P	74:SM:36:ARG:HH22	2.44	0.40
50:SA:90:PHE:O	50:SA:94:THR:OG1	2.36	0.40
57:SK:8:ARG:NH1	57:SK:12:TYR:OH	2.55	0.40
67:Sa:45:VAL:HG21	67:Sa:64:LEU:HD13	2.04	0.40
71:SC:187:ARG:HD3	71:SC:192:LEU:HD12	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:SG:168:LYS:HE2	72:SG:168:LYS:HB2	1.88	0.40
74:SM:106:CYS:HG	74:SM:107:SER:H	1.68	0.40
1:L5:3887:C:OP2	17:LO:85:ARG:NH2	2.41	0.40
1:L5:4967:A:H2'	1:L5:4968:A:H8	1.87	0.40
5:LB:132:LYS:H	5:LB:132:LYS:HG2	1.70	0.40
6:LC:1:MET:HB3	6:LC:2:ALA:H	1.79	0.40
8:LE:98:GLY:HA3	8:LE:99:ASP:HA	1.88	0.40
17:LO:121:PRO:HA	17:LO:124:LEU:HD12	2.03	0.40
32:Ld:117:LEU:HD23	32:Ld:117:LEU:HA	1.93	0.40
71:SC:185:THR:HA	71:SC:193:VAL:O	2.22	0.40
72:SG:26:THR:HG21	72:SG:40:ALA:HB3	2.02	0.40
74:SM:87:GLU:HG2	74:SM:94:ILE:HD11	2.02	0.40
84:CC:11:C:H2'	84:CC:12:G:C8	2.57	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%)	225 (92%)	20 (8%)	1 (0%)	30	51
5	LB	400/403 (99%)	380 (95%)	17 (4%)	3 (1%)	16	34
6	LC	366/427 (86%)	341 (93%)	25 (7%)	0	100	100
7	LD	291/297 (98%)	267 (92%)	24 (8%)	0	100	100
8	LE	232/288 (81%)	211 (91%)	21 (9%)	0	100	100
9	LF	223/248 (90%)	214 (96%)	9 (4%)	0	100	100
10	LG	239/266 (90%)	224 (94%)	15 (6%)	0	100	100
11	LH	188/192 (98%)	172 (92%)	16 (8%)	0	100	100
12	LI	198/214 (92%)	183 (92%)	14 (7%)	1 (0%)	24	46
13	LJ	174/178 (98%)	157 (90%)	16 (9%)	1 (1%)	21	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	LL	208/211 (99%)	191 (92%)	17 (8%)	0	100	100
15	LM	137/215 (64%)	130 (95%)	6 (4%)	1 (1%)	18	38
16	LN	201/204 (98%)	191 (95%)	8 (4%)	2 (1%)	12	28
17	LO	199/203 (98%)	189 (95%)	10 (5%)	0	100	100
18	LP	151/184 (82%)	140 (93%)	10 (7%)	1 (1%)	18	38
19	LQ	185/188 (98%)	177 (96%)	8 (4%)	0	100	100
20	LR	185/196 (94%)	180 (97%)	5 (3%)	0	100	100
21	LS	173/176 (98%)	161 (93%)	12 (7%)	0	100	100
22	LT	157/160 (98%)	148 (94%)	8 (5%)	1 (1%)	21	42
23	LU	99/128 (77%)	86 (87%)	13 (13%)	0	100	100
24	LV	129/140 (92%)	120 (93%)	9 (7%)	0	100	100
25	LW	122/157 (78%)	111 (91%)	11 (9%)	0	100	100
26	LX	118/156 (76%)	116 (98%)	2 (2%)	0	100	100
27	LY	132/145 (91%)	123 (93%)	9 (7%)	0	100	100
28	LZ	133/136 (98%)	123 (92%)	10 (8%)	0	100	100
29	La	145/148 (98%)	136 (94%)	9 (6%)	0	100	100
30	Lb	105/159 (66%)	98 (93%)	7 (7%)	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%)	119 (94%)	6 (5%)	1 (1%)	16	34
34	Lf	107/110 (97%)	99 (92%)	6 (6%)	2 (2%)	6	13
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%)	93 (93%)	7 (7%)	0	100	100
38	Lj	84/97 (87%)	75 (89%)	8 (10%)	1 (1%)	10	23
39	Lk	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
40	Ll	48/51 (94%)	48 (100%)	0	0	100	100
41	Lm	50/128 (39%)	50 (100%)	0	0	100	100
42	Ln	22/25 (88%)	22 (100%)	0	0	100	100
43	Lo	103/106 (97%)	98 (95%)	5 (5%)	0	100	100
44	Lp	89/92 (97%)	84 (94%)	5 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	Lr	123/137 (90%)	114 (93%)	9 (7%)	0	100	100
46	Ls	194/317 (61%)	166 (86%)	27 (14%)	1 (0%)	24	46
47	Lt	137/165 (83%)	100 (73%)	33 (24%)	4 (3%)	3	6
48	Lz	215/217 (99%)	160 (74%)	55 (26%)	0	100	100
50	SA	219/295 (74%)	202 (92%)	17 (8%)	0	100	100
51	SB	212/264 (80%)	201 (95%)	11 (5%)	0	100	100
52	SD	225/243 (93%)	201 (89%)	24 (11%)	0	100	100
53	SE	260/263 (99%)	246 (95%)	14 (5%)	0	100	100
54	SF	180/204 (88%)	164 (91%)	16 (9%)	0	100	100
55	SH	182/194 (94%)	161 (88%)	21 (12%)	0	100	100
56	SI	204/208 (98%)	196 (96%)	8 (4%)	0	100	100
57	SK	96/165 (58%)	85 (88%)	11 (12%)	0	100	100
58	SL	151/158 (96%)	140 (93%)	11 (7%)	0	100	100
59	SP	127/145 (88%)	119 (94%)	8 (6%)	0	100	100
60	SQ	142/146 (97%)	128 (90%)	13 (9%)	1 (1%)	18	38
61	SR	133/135 (98%)	116 (87%)	16 (12%)	1 (1%)	16	34
62	SS	143/152 (94%)	131 (92%)	12 (8%)	0	100	100
63	ST	141/145 (97%)	130 (92%)	10 (7%)	1 (1%)	18	38
64	SU	102/119 (86%)	93 (91%)	9 (9%)	0	100	100
65	SV	81/83 (98%)	74 (91%)	5 (6%)	2 (2%)	4	8
66	SX	139/143 (97%)	131 (94%)	4 (3%)	4 (3%)	3	6
67	Sa	100/115 (87%)	92 (92%)	7 (7%)	1 (1%)	12	28
68	Sc	62/69 (90%)	52 (84%)	9 (14%)	1 (2%)	7	16
69	Sd	53/56 (95%)	50 (94%)	2 (4%)	1 (2%)	6	13
70	Sg	311/317 (98%)	269 (86%)	41 (13%)	1 (0%)	36	58
71	SC	220/293 (75%)	205 (93%)	15 (7%)	0	100	100
72	SG	235/249 (94%)	222 (94%)	13 (6%)	0	100	100
73	SJ	183/194 (94%)	169 (92%)	12 (7%)	2 (1%)	11	25
74	SM	120/132 (91%)	109 (91%)	11 (9%)	0	100	100
75	SN	148/151 (98%)	142 (96%)	6 (4%)	0	100	100
76	SO	138/151 (91%)	127 (92%)	9 (6%)	2 (1%)	9	19

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
77	SW	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
78	SY	129/133 (97%)	123 (95%)	6 (5%)	0	100	100
79	SZ	73/125 (58%)	60 (82%)	13 (18%)	0	100	100
80	Sb	81/84 (96%)	71 (88%)	10 (12%)	0	100	100
81	Se	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
82	Sf	65/156 (42%)	55 (85%)	10 (15%)	0	100	100
83	CA	350/394 (89%)	328 (94%)	22 (6%)	0	100	100
85	CE	70/379 (18%)	67 (96%)	3 (4%)	0	100	100
86	i	31/180 (17%)	29 (94%)	2 (6%)	0	100	100
All	All	12323/14340 (86%)	11364 (92%)	922 (8%)	37 (0%)	37	58

All (37) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	LN	124	ASP
47	Lt	147	HIS
66	SX	127	ASN
47	Lt	142	ASN
47	Lt	148	PRO
63	ST	41	LYS
65	SV	79	VAL
68	Sc	64	GLU
5	LB	302	ASN
5	LB	360	LEU
15	LM	88	ALA
33	Le	73	GLY
66	SX	78	GLY
67	Sa	47	ALA
34	Lf	80	ASN
34	Lf	107	PRO
60	SQ	44	PRO
66	SX	126	ALA
69	Sd	14	PHE
73	SJ	138	ARG
5	LB	18	PRO
13	LJ	18	ARG
16	LN	83	LYS
22	LT	137	GLU
61	SR	94	GLU

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Mol	Chain	Res	Type
76	SO	140	THR
38	Lj	40	PRO
47	Lt	9	GLU
66	SX	87	ASN
70	Sg	246	TYR
12	LI	15	LYS
65	SV	78	ILE
4	LA	55	GLY
76	SO	144	GLY
18	LP	77	GLY
46	Ls	150	GLY
73	SJ	123	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%)	189 (100%)	1 (0%)	81	92
5	LB	348/349 (100%)	345 (99%)	3 (1%)	70	87
6	LC	306/348 (88%)	306 (100%)	0	100	100
7	LD	246/250 (98%)	245 (100%)	1 (0%)	84	93
8	LE	209/252 (83%)	209 (100%)	0	100	100
9	LF	194/215 (90%)	193 (100%)	1 (0%)	81	92
10	LG	203/223 (91%)	203 (100%)	0	100	100
11	LH	169/171 (99%)	169 (100%)	0	100	100
12	LI	172/181 (95%)	172 (100%)	0	100	100
13	LJ	148/149 (99%)	147 (99%)	1 (1%)	76	89
14	LL	176/177 (99%)	172 (98%)	4 (2%)	44	71
15	LM	118/161 (73%)	117 (99%)	1 (1%)	73	88
16	LN	171/172 (99%)	171 (100%)	0	100	100
17	LO	173/174 (99%)	172 (99%)	1 (1%)	78	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	LP	134/163 (82%)	133 (99%)	1 (1%)	76	89
19	LQ	164/165 (99%)	163 (99%)	1 (1%)	78	91
20	LR	166/175 (95%)	164 (99%)	2 (1%)	63	83
21	LS	156/157 (99%)	156 (100%)	0	100	100
22	LT	139/140 (99%)	139 (100%)	0	100	100
23	LU	91/115 (79%)	91 (100%)	0	100	100
24	LV	101/107 (94%)	100 (99%)	1 (1%)	68	86
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%)	122 (98%)	2 (2%)	55	79
28	LZ	117/118 (99%)	117 (100%)	0	100	100
29	La	120/121 (99%)	120 (100%)	0	100	100
30	Lb	88/126 (70%)	86 (98%)	2 (2%)	44	71
31	Lc	83/97 (86%)	83 (100%)	0	100	100
32	Ld	98/110 (89%)	97 (99%)	1 (1%)	68	86
33	Le	114/121 (94%)	114 (100%)	0	100	100
34	Lf	88/89 (99%)	87 (99%)	1 (1%)	65	84
35	Lg	98/100 (98%)	96 (98%)	2 (2%)	48	74
36	Lh	109/110 (99%)	109 (100%)	0	100	100
37	Li	86/89 (97%)	86 (100%)	0	100	100
38	Lj	73/80 (91%)	73 (100%)	0	100	100
39	Lk	64/65 (98%)	64 (100%)	0	100	100
40	Ll	47/48 (98%)	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%)	93 (100%)	0	100	100
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%)	160 (99%)	2 (1%)	63	83
47	Lt	112/137 (82%)	108 (96%)	4 (4%)	31	58
48	Lz	195/196 (100%)	194 (100%)	1 (0%)	81	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
50	SA	183/243 (75%)	182 (100%)	1 (0%)	81	92
51	SB	195/231 (84%)	195 (100%)	0	100	100
52	SD	190/202 (94%)	190 (100%)	0	100	100
53	SE	224/225 (100%)	223 (100%)	1 (0%)	84	93
54	SF	156/170 (92%)	156 (100%)	0	100	100
55	SH	166/174 (95%)	162 (98%)	4 (2%)	43	70
56	SI	178/180 (99%)	178 (100%)	0	100	100
57	SK	89/136 (65%)	88 (99%)	1 (1%)	65	84
58	SL	137/142 (96%)	137 (100%)	0	100	100
59	SP	115/130 (88%)	115 (100%)	0	100	100
60	SQ	119/121 (98%)	119 (100%)	0	100	100
61	SR	122/122 (100%)	122 (100%)	0	100	100
62	SS	126/132 (96%)	125 (99%)	1 (1%)	73	88
63	ST	113/115 (98%)	113 (100%)	0	100	100
64	SU	94/107 (88%)	94 (100%)	0	100	100
65	SV	67/67 (100%)	67 (100%)	0	100	100
66	SX	113/115 (98%)	113 (100%)	0	100	100
67	Sa	89/98 (91%)	89 (100%)	0	100	100
68	Sc	57/62 (92%)	57 (100%)	0	100	100
69	Sd	48/49 (98%)	48 (100%)	0	100	100
70	Sg	272/275 (99%)	267 (98%)	5 (2%)	51	76
71	SC	188/225 (84%)	185 (98%)	3 (2%)	55	79
72	SG	207/218 (95%)	207 (100%)	0	100	100
73	SJ	161/168 (96%)	160 (99%)	1 (1%)	78	91
74	SM	102/108 (94%)	99 (97%)	3 (3%)	37	65
75	SN	130/131 (99%)	128 (98%)	2 (2%)	57	80
76	SO	110/119 (92%)	110 (100%)	0	100	100
77	SW	112/113 (99%)	110 (98%)	2 (2%)	51	76
78	SY	113/115 (98%)	112 (99%)	1 (1%)	70	87
79	SZ	66/103 (64%)	66 (100%)	0	100	100
80	Sb	75/76 (99%)	75 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
81	Se	43/48 (90%)	43 (100%)	0	100	100
82	Sf	60/140 (43%)	60 (100%)	0	100	100
83	CA	303/336 (90%)	302 (100%)	1 (0%)	86	94
85	CE	68/338 (20%)	68 (100%)	0	100	100
86	i	28/151 (18%)	28 (100%)	0	100	100
All	All	10729/12217 (88%)	10670 (100%)	59 (0%)	78	92

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	LA	207	VAL
5	LB	162	VAL
5	LB	223	THR
5	LB	337	VAL
7	LD	37	VAL
9	LF	248	ASN
13	LJ	132	VAL
14	LL	59	VAL
14	LL	63	THR
14	LL	70	VAL
14	LL	90	VAL
15	LM	38	VAL
17	LO	27	VAL
18	LP	24	VAL
19	LQ	83	VAL
20	LR	177	LEU
20	LR	182	GLU
24	LV	22	VAL
27	LY	55	VAL
27	LY	79	VAL
30	Lb	70	GLU
30	Lb	76	VAL
32	Ld	46	LEU
34	Lf	33	VAL
35	Lg	2	VAL
35	Lg	63	VAL
46	Ls	35	VAL
46	Ls	89	VAL
47	Lt	74	VAL
47	Lt	121	LEU

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Mol	Chain	Res	Type
47	Lt	147	HIS
47	Lt	160	VAL
48	Lz	17	VAL
50	SA	124	VAL
53	SE	173	ILE
55	SH	29	GLU
55	SH	64	VAL
55	SH	69	LEU
55	SH	166	VAL
57	SK	40	VAL
62	SS	68	ILE
70	Sg	18	VAL
70	Sg	108	VAL
70	Sg	142	VAL
70	Sg	222	ASN
70	Sg	307	VAL
71	SC	64	THR
71	SC	112	VAL
71	SC	137	VAL
73	SJ	137	VAL
74	SM	18	LEU
74	SM	42	LEU
74	SM	124	ILE
75	SN	32	ASP
75	SN	63	VAL
77	SW	25	VAL
77	SW	80	ASP
78	SY	50	THR
83	CA	143	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (183) such sidechains are listed below:

Mol	Chain	Res	Type
4	LA	95	GLN
4	LA	97	ASN
4	LA	132	ASN
4	LA	205	ASN
4	LA	216	HIS
5	LB	138	GLN
5	LB	145	GLN
5	LB	213	GLN
5	LB	301	ASN

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Mol	Chain	Res	Type
6	LC	48	ASN
6	LC	119	GLN
6	LC	178	ASN
6	LC	223	ASN
6	LC	231	ASN
6	LC	310	HIS
6	LC	329	ASN
7	LD	191	ASN
7	LD	202	GLN
7	LD	282	GLN
8	LE	190	HIS
9	LF	39	GLN
9	LF	63	GLN
9	LF	126	ASN
9	LF	248	ASN
10	LG	38	ASN
10	LG	153	GLN
10	LG	208	ASN
11	LH	98	HIS
11	LH	140	GLN
12	LI	59	GLN
13	LJ	104	ASN
14	LL	115	GLN
14	LL	205	GLN
15	LM	20	HIS
15	LM	34	ASN
15	LM	48	GLN
16	LN	32	GLN
16	LN	109	HIS
16	LN	196	ASN
17	LO	26	GLN
17	LO	42	ASN
17	LO	180	GLN
17	LO	184	ASN
18	LP	21	ASN
18	LP	25	HIS
18	LP	34	GLN
18	LP	97	ASN
18	LP	116	HIS
18	LP	133	HIS
19	LQ	7	HIS
19	LQ	21	GLN

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Mol	Chain	Res	Type
19	LQ	44	ASN
19	LQ	125	GLN
19	LQ	188	ASN
20	LR	34	ASN
20	LR	86	ASN
20	LR	130	ASN
21	LS	77	ASN
21	LS	108	GLN
22	LT	90	ASN
23	LU	94	ASN
24	LV	27	ASN
25	LW	17	HIS
26	LX	73	HIS
27	LY	4	ASN
27	LY	14	ASN
28	LZ	78	ASN
28	LZ	127	ASN
29	La	28	HIS
29	La	39	HIS
29	La	60	HIS
29	La	85	GLN
30	Lb	6	ASN
30	Lb	7	HIS
30	Lb	19	ASN
30	Lb	60	ASN
31	Lc	15	ASN
33	Le	92	ASN
33	Le	107	ASN
33	Le	117	GLN
34	Lf	20	ASN
34	Lf	80	ASN
34	Lf	99	HIS
35	Lg	100	GLN
36	Lh	98	HIS
36	Lh	108	GLN
38	Lj	76	HIS
40	Ll	33	ASN
43	Lo	19	GLN
43	Lo	45	GLN
43	Lo	51	GLN
44	Lp	56	HIS
45	Lr	31	ASN

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Mol	Chain	Res	Type
45	Lr	41	ASN
45	Lr	70	GLN
45	Lr	100	ASN
46	Ls	81	HIS
46	Ls	190	GLN
46	Ls	191	GLN
46	Ls	195	ASN
47	Lt	70	GLN
47	Lt	115	GLN
47	Lt	149	HIS
48	Lz	21	ASN
48	Lz	35	GLN
48	Lz	40	ASN
48	Lz	129	ASN
48	Lz	197	ASN
48	Lz	200	ASN
50	SA	9	GLN
50	SA	141	ASN
51	SB	43	ASN
51	SB	149	GLN
51	SB	179	ASN
51	SB	186	ASN
51	SB	202	GLN
53	SE	67	GLN
53	SE	98	ASN
53	SE	138	HIS
53	SE	188	ASN
54	SF	31	ASN
54	SF	95	HIS
54	SF	148	ASN
55	SH	73	GLN
55	SH	91	HIS
55	SH	114	GLN
55	SH	157	HIS
56	SI	7	ASN
56	SI	35	ASN
56	SI	52	ASN
56	SI	84	ASN
56	SI	116	HIS
56	SI	138	ASN
56	SI	165	GLN
57	SK	39	ASN

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Mol	Chain	Res	Type
58	SL	19	ASN
58	SL	94	HIS
58	SL	100	ASN
59	SP	128	HIS
60	SQ	80	GLN
61	SR	31	ASN
62	SS	11	HIS
62	SS	101	ASN
63	ST	42	HIS
63	ST	128	GLN
64	SU	28	ASN
64	SU	81	GLN
65	SV	35	ASN
66	SX	23	HIS
66	SX	61	GLN
68	Sc	26	GLN
70	Sg	117	ASN
70	Sg	311	GLN
71	SC	113	GLN
71	SC	136	HIS
72	SG	56	ASN
72	SG	110	ASN
72	SG	163	ASN
73	SJ	125	HIS
74	SM	15	ASN
74	SM	19	GLN
75	SN	49	GLN
77	SW	5	ASN
77	SW	82	GLN
77	SW	90	GLN
77	SW	91	ASN
77	SW	98	GLN
78	SY	112	ASN
79	SZ	45	ASN
79	SZ	64	ASN
79	SZ	112	ASN
80	Sb	26	GLN
83	CA	123	HIS
83	CA	134	GLN
83	CA	163	ASN
83	CA	178	ASN
83	CA	204	ASN

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Mol	Chain	Res	Type
83	CA	209	GLN
83	CA	306	ASN
83	CA	328	ASN
85	CE	325	ASN
86	i	158	GLN
86	i	165	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3705/5066 (73%)	830 (22%)	18 (0%)
2	L7	119/121 (98%)	11 (9%)	0
3	L8	155/157 (98%)	27 (17%)	0
49	S2	1715/1869 (91%)	406 (23%)	11 (0%)
84	CC	74/75 (98%)	23 (31%)	2 (2%)
All	All	5768/7288 (79%)	1297 (22%)	31 (0%)

All (1297) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	2	G
1	L5	17	A
1	L5	30	C
1	L5	39	A
1	L5	42	A
1	L5	48	G
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
1	L5	108	A
1	L5	109	G
1	L5	110	C

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Mol	Chain	Res	Type
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	145	G
1	L5	152	U
1	L5	159	C
1	L5	165	A
1	L5	181	C
1	L5	182	G
1	L5	183	C
1	L5	184	U
1	L5	185	C
1	L5	188	G
1	L5	189	G
1	L5	200	U
1	L5	209	U
1	L5	216	C
1	L5	218	A
1	L5	219	G
1	L5	233	U
1	L5	234	G
1	L5	255	C
1	L5	256	G
1	L5	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
1	L5	315	G
1	L5	316	U
1	L5	340	C
1	L5	350	C
1	L5	373	G
1	L5	387	G

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Mol	Chain	Res	Type
1	L5	388	A
1	L5	398	A
1	L5	401	G
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	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	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
1	L5	502	C
1	L5	503	C
1	L5	504	G
1	L5	505	G
1	L5	509	A
1	L5	510	U
1	L5	512	U
1	L5	513	U
1	L5	514	U
1	L5	515	C
1	L5	516	C

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Mol	Chain	Res	Type
1	L5	517	C
1	L5	518	G
1	L5	643	C
1	L5	646	G
1	L5	656	C
1	L5	657	C
1	L5	659	G
1	L5	665	C
1	L5	666	G
1	L5	667	A
1	L5	668	C
1	L5	669	C
1	L5	673	C
1	L5	685	C
1	L5	686	A
1	L5	687	U
1	L5	688	U
1	L5	696	C
1	L5	703	G
1	L5	704	C
1	L5	708	G
1	L5	730	G
1	L5	731	G
1	L5	738	C
1	L5	739	G
1	L5	740	G
1	L5	742	G
1	L5	744	G
1	L5	746	A
1	L5	753	C
1	L5	758	G
1	L5	759	G
1	L5	760	G
1	L5	904	C
1	L5	913	U
1	L5	914	U
1	L5	915	A
1	L5	916	C
1	L5	917	A
1	L5	918	G
1	L5	923	C
1	L5	924	C

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Mol	Chain	Res	Type
1	L5	926	G
1	L5	932	A
1	L5	933	G
1	L5	934	C
1	L5	935	A
1	L5	936	C
1	L5	937	U
1	L5	943	A
1	L5	945	U
1	L5	959	G
1	L5	960	A
1	L5	961	G
1	L5	962	C
1	L5	965	G
1	L5	967	C
1	L5	970	G
1	L5	971	U
1	L5	977	C
1	L5	982	U
1	L5	984	C
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
1	L5	1070	G
1	L5	1072	C
1	L5	1074	G
1	L5	1075	G
1	L5	1082	C
1	L5	1083	U
1	L5	1095	A
1	L5	1168	G
1	L5	1169	G
1	L5	1170	G
1	L5	1171	G

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Mol	Chain	Res	Type
1	L5	1172	C
1	L5	1173	G
1	L5	1178	G
1	L5	1180	C
1	L5	1181	C
1	L5	1182	C
1	L5	1183	C
1	L5	1202	C
1	L5	1203	G
1	L5	1204	C
1	L5	1210	C
1	L5	1211	G
1	L5	1214	C
1	L5	1215	C
1	L5	1217	G
1	L5	1218	G
1	L5	1219	G
1	L5	1222	A
1	L5	1235	G
1	L5	1241	C
1	L5	1246	G
1	L5	1253	G
1	L5	1254	A
1	L5	1257	A
1	L5	1258	G
1	L5	1266	G
1	L5	1267	C
1	L5	1269	G
1	L5	1270	A
1	L5	1271	G
1	L5	1272	C
1	L5	1273	G
1	L5	1274	A
1	L5	1275	G
1	L5	1277	G
1	L5	1280	C
1	L5	1284	G
1	L5	1285	U
1	L5	1287	G
1	L5	1294	A
1	L5	1295	C
1	L5	1301	C

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Mol	Chain	Res	Type
1	L5	1312	A
1	L5	1324	A
1	L5	1326	A
1	L5	1337	A
1	L5	1344	C
1	L5	1354	A
1	L5	1358	G
1	L5	1359	G
1	L5	1365	C
1	L5	1367	C
1	L5	1377	G
1	L5	1378	C
1	L5	1387	A
1	L5	1393	G
1	L5	1394	G
1	L5	1397	A
1	L5	1398	A
1	L5	1404	G
1	L5	1405	C
1	L5	1407	C
1	L5	1409	C
1	L5	1410	U
1	L5	1411	C
1	L5	1414	C
1	L5	1420	A
1	L5	1435	G
1	L5	1437	C
1	L5	1439	C
1	L5	1440	U
1	L5	1441	C
1	L5	1443	A
1	L5	1446	C
1	L5	1447	C
1	L5	1482	G
1	L5	1483	C
1	L5	1493	G
1	L5	1497	A
1	L5	1498	G
1	L5	1502	G
1	L5	1514	U
1	L5	1517	G
1	L5	1525	A

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Mol	Chain	Res	Type
1	L5	1534	A
1	L5	1547	A
1	L5	1562	G
1	L5	1566	C
1	L5	1578	U
1	L5	1591	U
1	L5	1596	U
1	L5	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	1654	G
1	L5	1661	C
1	L5	1676	C
1	L5	1677	U
1	L5	1678	C
1	L5	1697	G
1	L5	1699	A
1	L5	1700	G
1	L5	1703	C
1	L5	1704	C
1	L5	1705	G
1	L5	1707	C
1	L5	1715	C
1	L5	1716	G
1	L5	1717	C
1	L5	1718	C
1	L5	1719	A
1	L5	1726	U
1	L5	1734	G
1	L5	1735	U
1	L5	1740	C
1	L5	1741	G
1	L5	1742	A
1	L5	1745	G
1	L5	1750	G
1	L5	1755	C
1	L5	1757	U
1	L5	1758	G

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Mol	Chain	Res	Type
1	L5	1760	G
1	L5	1761	G
1	L5	1762	C
1	L5	1763	C
1	L5	1764	G
1	L5	1765	A
1	L5	1766	A
1	L5	1768	C
1	L5	1770	A
1	L5	1771	U
1	L5	1775	A
1	L5	1785	C
1	L5	1787	A
1	L5	1797	G
1	L5	1804	A
1	L5	1810	G
1	L5	1815	G
1	L5	1820	C
1	L5	1821	G
1	L5	1822	U
1	L5	1834	U
1	L5	1836	G
1	L5	1837	A
1	L5	1842	G
1	L5	1843	A
1	L5	1855	G
1	L5	1869	G
1	L5	1882	U
1	L5	1897	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	1948	G
1	L5	1951	G
1	L5	1959	U

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Mol	Chain	Res	Type
1	L5	1960	A
1	L5	1961	G
1	L5	1962	A
1	L5	1974	U
1	L5	1975	G
1	L5	1978	C
1	L5	1980	U
1	L5	1983	A
1	L5	1984	A
1	L5	1985	G
1	L5	1986	U
1	L5	1987	C
1	L5	1988	G
1	L5	1990	A
1	L5	1991	A
1	L5	1992	U
1	L5	1993	C
1	L5	1997	U
1	L5	1998	A
1	L5	2001	G
1	L5	2002	A
1	L5	2014	C
1	L5	2017	A
1	L5	2018	C
1	L5	2024	G
1	L5	2025	A
1	L5	2026	A
1	L5	2033	A
1	L5	2034	G
1	L5	2046	G
1	L5	2048	U
1	L5	2055	G
1	L5	2056	G
1	L5	2062	C
1	L5	2069	A
1	L5	2084	C
1	L5	2085	G
1	L5	2089	G
1	L5	2092	G
1	L5	2093	A
1	L5	2095	A
1	L5	2096	G

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Mol	Chain	Res	Type
1	L5	2097	U
1	L5	2098	G
1	L5	2101	C
1	L5	2102	G
1	L5	2108	G
1	L5	2112	G
1	L5	2113	G
1	L5	2250	C
1	L5	2252	G
1	L5	2253	A
1	L5	2256	C
1	L5	2258	C
1	L5	2260	C
1	L5	2289	C
1	L5	2300	A
1	L5	2301	G
1	L5	2306	G
1	L5	2313	A
1	L5	2332	A
1	L5	2333	G
1	L5	2348	G
1	L5	2351	C
1	L5	2360	A
1	L5	2369	U
1	L5	2383	C
1	L5	2395	A
1	L5	2397	G
1	L5	2417	A
1	L5	2418	A
1	L5	2421	G
1	L5	2425	U
1	L5	2441	C
1	L5	2447	U
1	L5	2450	G
1	L5	2453	A
1	L5	2464	C
1	L5	2465	C
1	L5	2467	U
1	L5	2469	C
1	L5	2471	G
1	L5	2474	G
1	L5	2475	G

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Mol	Chain	Res	Type
1	L5	2478	C
1	L5	2479	G
1	L5	2483	G
1	L5	2484	A
1	L5	2485	U
1	L5	2487	G
1	L5	2488	C
1	L5	2489	C
1	L5	2490	U
1	L5	2491	C
1	L5	2494	U
1	L5	2495	U
1	L5	2503	G
1	L5	2504	C
1	L5	2505	C
1	L5	2506	G
1	L5	2513	A
1	L5	2519	U
1	L5	2537	A
1	L5	2544	G
1	L5	2546	G
1	L5	2547	G
1	L5	2554	U
1	L5	2559	G
1	L5	2560	C
1	L5	2565	A
1	L5	2573	A
1	L5	2583	C
1	L5	2587	A
1	L5	2589	C
1	L5	2601	A
1	L5	2611	A
1	L5	2627	C
1	L5	2638	G
1	L5	2652	G
1	L5	2653	C
1	L5	2662	G
1	L5	2669	C
1	L5	2670	C
1	L5	2675	G
1	L5	2676	A
1	L5	2687	U

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Mol	Chain	Res	Type
1	L5	2695	A
1	L5	2696	A
1	L5	2703	G
1	L5	2707	U
1	L5	2708	U
1	L5	2709	C
1	L5	2710	C
1	L5	2711	G
1	L5	2721	G
1	L5	2724	G
1	L5	2726	G
1	L5	2739	C
1	L5	2742	G
1	L5	2743	A
1	L5	2746	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	2815	A
1	L5	2826	U
1	L5	2827	G
1	L5	2838	G
1	L5	2848	G
1	L5	2855	G
1	L5	2867	C
1	L5	2877	G
1	L5	2892	C
1	L5	2900	U
1	L5	2902	G
1	L5	2903	G
1	L5	2904	U
1	L5	2905	C
1	L5	2906	G
1	L5	2908	U
1	L5	3585	G

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Mol	Chain	Res	Type
1	L5	3586	G
1	L5	3587	C
1	L5	3590	G
1	L5	3591	C
1	L5	3594	C
1	L5	3595	U
1	L5	3596	A
1	L5	3597	G
1	L5	3604	A
1	L5	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	3662	A
1	L5	3673	C
1	L5	3674	G
1	L5	3711	A
1	L5	3713	U
1	L5	3714	G
1	L5	3727	A
1	L5	3729	U
1	L5	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	3771	C
1	L5	3775	A
1	L5	3776	G
1	L5	3777	G
1	L5	3784	A
1	L5	3786	U
1	L5	3802	U
1	L5	3811	G
1	L5	3812	C
1	L5	3814	U

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Mol	Chain	Res	Type
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	3851	U
1	L5	3867	A
1	L5	3877	A
1	L5	3878	C
1	L5	3879	G
1	L5	3885	G
1	L5	3887	C
1	L5	3892	U
1	L5	3897	G
1	L5	3898	G
1	L5	3901	A
1	L5	3906	A
1	L5	3907	G
1	L5	3908	A
1	L5	3915	U
1	L5	3938	G
1	L5	3942	A
1	L5	3943	A
1	L5	3944	G
1	L5	3947	A
1	L5	3948	C
1	L5	3949	A
1	L5	3950	U
1	L5	3953	G
1	L5	3955	G
1	L5	3956	G
1	L5	3957	U
1	L5	3958	G
1	L5	3959	U
1	L5	3961	G
1	L5	3962	A
1	L5	3963	A
1	L5	3964	U
1	L5	3965	A
1	L5	3966	A
1	L5	3969	G

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Mol	Chain	Res	Type
1	L5	3970	G
1	L5	3971	G
1	L5	3973	G
1	L5	3974	G
1	L5	3977	C
1	L5	4035	G
1	L5	4036	G
1	L5	4038	C
1	L5	4039	G
1	L5	4041	C
1	L5	4042	G
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
1	L5	4086	G
1	L5	4096	C
1	L5	4097	G
1	L5	4099	G
1	L5	4101	C
1	L5	4102	C
1	L5	4103	C
1	L5	4104	G
1	L5	4107	G
1	L5	4108	G
1	L5	4111	U

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Mol	Chain	Res	Type
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	4162	C
1	L5	4163	U
1	L5	4168	G
1	L5	4170	A
1	L5	4177	C
1	L5	4183	G
1	L5	4184	G
1	L5	4191	G
1	L5	4196	G
1	L5	4203	A
1	L5	4222	G
1	L5	4228	G
1	L5	4229	U
1	L5	4233	A
1	L5	4237	C
1	L5	4249	G
1	L5	4251	A
1	L5	4254	G
1	L5	4257	A
1	L5	4265	U
1	L5	4268	A
1	L5	4273	A
1	L5	4281	A
1	L5	4291	G
1	L5	4295	U
1	L5	4304	A
1	L5	4305	G

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Mol	Chain	Res	Type
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	4349	C
1	L5	4354	U
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	4387	C
1	L5	4391	G
1	L5	4394	A
1	L5	4405	G
1	L5	4422	A
1	L5	4426	C
1	L5	4448	G
1	L5	4449	A
1	L5	4453	C
1	L5	4464	A
1	L5	4475	G
1	L5	4488	A
1	L5	4500	U
1	L5	4512	U
1	L5	4513	A
1	L5	4519	C
1	L5	4524	G
1	L5	4531	U
1	L5	4545	G
1	L5	4548	A
1	L5	4549	G
1	L5	4557	U
1	L5	4560	C
1	L5	4567	G
1	L5	4573	G
1	L5	4575	G
1	L5	4589	A
1	L5	4590	A

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Mol	Chain	Res	Type
1	L5	4600	G
1	L5	4617	G
1	L5	4636	U
1	L5	4637	G
1	L5	4656	A
1	L5	4670	C
1	L5	4672	A
1	L5	4679	G
1	L5	4684	A
1	L5	4687	A
1	L5	4694	G
1	L5	4695	C
1	L5	4700	A
1	L5	4708	A
1	L5	4709	U
1	L5	4719	G
1	L5	4720	C
1	L5	4731	G
1	L5	4733	C
1	L5	4734	A
1	L5	4740	G
1	L5	4741	C
1	L5	4742	G
1	L5	4745	G
1	L5	4754	G
1	L5	4757	C
1	L5	4759	C
1	L5	4761	G
1	L5	4764	A
1	L5	4765	G
1	L5	4771	C
1	L5	4772	C
1	L5	4775	C
1	L5	4859	C
1	L5	4863	G
1	L5	4870	G
1	L5	4871	C
1	L5	4875	G
1	L5	4881	U
1	L5	4882	U
1	L5	4883	C
1	L5	4888	U

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Mol	Chain	Res	Type
1	L5	4889	G
1	L5	4895	C
1	L5	4896	G
1	L5	4900	C
1	L5	4901	G
1	L5	4902	C
1	L5	4910	A
1	L5	4912	G
1	L5	4914	C
1	L5	4922	C
1	L5	4923	C
1	L5	4925	U
1	L5	4927	G
1	L5	4928	C
1	L5	4934	A
1	L5	4940	C
1	L5	4941	G
1	L5	4943	A
1	L5	4944	C
1	L5	4951	G
1	L5	4955	A
1	L5	4960	G
1	L5	4961	G
1	L5	4963	G
1	L5	4966	A
1	L5	4976	U
1	L5	4979	A
1	L5	4988	U
1	L5	4989	U
1	L5	4990	C
1	L5	4991	U
1	L5	5007	A
1	L5	5013	C
1	L5	5014	A
1	L5	5017	G
1	L5	5022	U
1	L5	5023	C
1	L5	5024	C
1	L5	5025	C
1	L5	5026	U
1	L5	5028	G
1	L5	5029	C

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Mol	Chain	Res	Type
1	L5	5031	G
1	L5	5034	A
1	L5	5041	G
1	L5	5047	C
1	L5	5050	C
1	L5	5053	U
1	L5	5054	C
1	L5	5055	G
1	L5	5058	A
1	L5	5061	A
1	L5	5069	U
2	L7	4	U
2	L7	33	U
2	L7	38	U
2	L7	42	A
2	L7	53	U
2	L7	63	C
2	L7	64	G
2	L7	100	A
2	L7	102	U
2	L7	110	G
2	L7	111	C
3	L8	2	G
3	L8	25	G
3	L8	34	U
3	L8	35	C
3	L8	48	A
3	L8	59	A
3	L8	60	G
3	L8	62	A
3	L8	63	U
3	L8	82	A
3	L8	83	C
3	L8	84	A
3	L8	85	U
3	L8	86	U
3	L8	87	G
3	L8	94	G
3	L8	103	A
3	L8	105	C
3	L8	110	U
3	L8	111	U

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Mol	Chain	Res	Type
3	L8	114	G
3	L8	123	U
3	L8	124	U
3	L8	125	C
3	L8	126	C
3	L8	127	U
3	L8	156	U
49	S2	4	C
49	S2	17	C
49	S2	23	G
49	S2	33	G
49	S2	41	G
49	S2	44	U
49	S2	45	A
49	S2	46	A
49	S2	56	G
49	S2	58	C
49	S2	59	U
49	S2	64	A
49	S2	67	C
49	S2	68	A
49	S2	72	C
49	S2	73	C
49	S2	74	G
49	S2	76	U
49	S2	92	A
49	S2	99	A
49	S2	103	A
49	S2	113	G
49	S2	114	G
49	S2	115	U
49	S2	121	U
49	S2	126	G
49	S2	129	C
49	S2	130	G
49	S2	140	U
49	S2	143	U
49	S2	158	A
49	S2	159	A
49	S2	160	U
49	S2	162	C
49	S2	170	A

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Mol	Chain	Res	Type
49	S2	175	A
49	S2	179	C
49	S2	190	G
49	S2	191	A
49	S2	196	C
49	S2	197	U
49	S2	198	U
49	S2	199	C
49	S2	200	G
49	S2	203	G
49	S2	204	G
49	S2	206	G
49	S2	208	G
49	S2	211	G
49	S2	212	C
49	S2	214	U
49	S2	290	U
49	S2	291	G
49	S2	292	A
49	S2	293	C
49	S2	295	C
49	S2	302	A
49	S2	306	C
49	S2	307	G
49	S2	308	G
49	S2	309	G
49	S2	311	C
49	S2	318	A
49	S2	319	C
49	S2	323	C
49	S2	324	C
49	S2	325	C
49	S2	326	C
49	S2	327	G
49	S2	328	U
49	S2	329	G
49	S2	332	G
49	S2	335	G
49	S2	338	G
49	S2	339	A
49	S2	360	A
49	S2	362	C

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Mol	Chain	Res	Type
49	S2	363	A
49	S2	364	A
49	S2	368	U
49	S2	369	C
49	S2	370	G
49	S2	374	G
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	429	C
49	S2	438	G
49	S2	448	A
49	S2	449	A
49	S2	450	C
49	S2	452	G
49	S2	464	A
49	S2	465	A
49	S2	466	G
49	S2	471	G
49	S2	472	C
49	S2	473	A
49	S2	474	G
49	S2	482	G
49	S2	487	U
49	S2	488	U
49	S2	492	C
49	S2	493	A
49	S2	502	C
49	S2	516	A
49	S2	517	C
49	S2	525	A
49	S2	529	A
49	S2	531	A
49	S2	532	C
49	S2	533	A
49	S2	536	A
49	S2	537	C
49	S2	540	U

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Mol	Chain	Res	Type
49	S2	542	U
49	S2	545	A
49	S2	546	G
49	S2	547	G
49	S2	551	U
49	S2	554	A
49	S2	556	U
49	S2	557	U
49	S2	558	G
49	S2	559	G
49	S2	560	A
49	S2	563	G
49	S2	564	A
49	S2	566	U
49	S2	576	A
49	S2	582	U
49	S2	583	A
49	S2	584	A
49	S2	587	A
49	S2	589	G
49	S2	590	A
49	S2	591	U
49	S2	596	U
49	S2	597	G
49	S2	600	G
49	S2	604	A
49	S2	607	U
49	S2	608	C
49	S2	614	C
49	S2	627	U
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	664	A
49	S2	668	A
49	S2	669	A
49	S2	671	A
49	S2	672	A
49	S2	673	G

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Mol	Chain	Res	Type
49	S2	688	U
49	S2	689	U
49	S2	690	G
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
49	S2	788	G
49	S2	791	C
49	S2	792	C
49	S2	797	C
49	S2	798	G
49	S2	810	A
49	S2	821	G
49	S2	822	U
49	S2	823	U
49	S2	824	C
49	S2	830	A
49	S2	835	C
49	S2	836	G
49	S2	837	A
49	S2	838	G
49	S2	839	C
49	S2	840	C
49	S2	841	G
49	S2	842	C
49	S2	847	A
49	S2	869	A
49	S2	873	G
49	S2	874	G
49	S2	878	G
49	S2	880	G
49	S2	882	U

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Mol	Chain	Res	Type
49	S2	883	U
49	S2	887	U
49	S2	888	U
49	S2	889	U
49	S2	891	G
49	S2	894	G
49	S2	896	U
49	S2	897	U
49	S2	898	U
49	S2	899	U
49	S2	900	C
49	S2	901	G
49	S2	903	A
49	S2	913	A
49	S2	914	U
49	S2	917	U
49	S2	920	A
49	S2	922	A
49	S2	930	C
49	S2	933	G
49	S2	934	G
49	S2	943	U
49	S2	963	A
49	S2	971	G
49	S2	972	A
49	S2	990	A
49	S2	992	A
49	S2	999	G
49	S2	1017	U
49	S2	1018	U
49	S2	1023	A
49	S2	1027	A
49	S2	1028	A
49	S2	1033	G
49	S2	1061	U
49	S2	1062	A
49	S2	1078	C
49	S2	1083	A
49	S2	1085	C
49	S2	1088	U
49	S2	1109	C
49	S2	1114	U

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Mol	Chain	Res	Type
49	S2	1115	U
49	S2	1116	C
49	S2	1118	C
49	S2	1119	A
49	S2	1121	G
49	S2	1123	C
49	S2	1133	A
49	S2	1138	C
49	S2	1148	A
49	S2	1153	C
49	S2	1154	U
49	S2	1195	A
49	S2	1203	G
49	S2	1207	G
49	S2	1208	A
49	S2	1215	C
49	S2	1216	C
49	S2	1217	A
49	S2	1224	G
49	S2	1227	G
49	S2	1242	U
49	S2	1243	U
49	S2	1251	A
49	S2	1253	A
49	S2	1256	G
49	S2	1257	G
49	S2	1259	A
49	S2	1265	A
49	S2	1274	G
49	S2	1275	G
49	S2	1283	C
49	S2	1284	A
49	S2	1286	G
49	S2	1294	G
49	S2	1295	A
49	S2	1301	A
49	S2	1302	G
49	S2	1303	C
49	S2	1306	U
49	S2	1308	U
49	S2	1312	G
49	S2	1320	G

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Mol	Chain	Res	Type
49	S2	1342	U
49	S2	1343	U
49	S2	1344	A
49	S2	1348	G
49	S2	1363	C
49	S2	1371	U
49	S2	1372	U
49	S2	1373	C
49	S2	1378	A
49	S2	1396	A
49	S2	1402	A
49	S2	1404	U
49	S2	1409	A
49	S2	1415	C
49	S2	1416	C
49	S2	1419	C
49	S2	1420	G
49	S2	1421	A
49	S2	1422	G
49	S2	1423	C
49	S2	1424	G
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	1495	G
49	S2	1497	G
49	S2	1498	A
49	S2	1505	U
49	S2	1507	G
49	S2	1508	A
49	S2	1509	U

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Mol	Chain	Res	Type
49	S2	1520	G
49	S2	1521	C
49	S2	1533	A
49	S2	1535	U
49	S2	1537	A
49	S2	1544	C
49	S2	1547	C
49	S2	1552	G
49	S2	1553	C
49	S2	1556	A
49	S2	1558	C
49	S2	1570	G
49	S2	1574	C
49	S2	1578	U
49	S2	1580	A
49	S2	1585	U
49	S2	1587	G
49	S2	1588	A
49	S2	1600	G
49	S2	1601	A
49	S2	1606	G
49	S2	1621	U
49	S2	1623	A
49	S2	1634	A
49	S2	1638	G
49	S2	1648	G
49	S2	1654	G
49	S2	1661	A
49	S2	1663	A
49	S2	1665	G
49	S2	1671	G
49	S2	1683	C
49	S2	1686	G
49	S2	1698	C
49	S2	1699	A
49	S2	1719	A
49	S2	1721	U
49	S2	1722	G
49	S2	1743	G
49	S2	1744	G
49	S2	1745	A
49	S2	1752	C

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Mol	Chain	Res	Type
49	S2	1753	C
49	S2	1754	G
49	S2	1757	G
49	S2	1758	G
49	S2	1760	G
49	S2	1761	U
49	S2	1772	C
49	S2	1773	C
49	S2	1774	C
49	S2	1775	U
49	S2	1776	G
49	S2	1777	G
49	S2	1780	G
49	S2	1781	A
49	S2	1783	C
49	S2	1784	G
49	S2	1786	U
49	S2	1798	C
49	S2	1819	A
49	S2	1822	A
49	S2	1823	A
49	S2	1824	A
49	S2	1825	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	16	C
84	CC	17	G
84	CC	18	G
84	CC	19	C
84	CC	20	U
84	CC	28	C
84	CC	31	G

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Mol	Chain	Res	Type
84	CC	32	C
84	CC	33	U
84	CC	35	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	51	G
84	CC	57	A
84	CC	59	U
84	CC	72	G
84	CC	75	A

All (31) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	406	C
1	L5	493	G
1	L5	914	U
1	L5	955	G
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	4699	U
1	L5	4913	G
49	S2	60	G
49	S2	92	A
49	S2	112	U
49	S2	158	A

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Mol	Chain	Res	Type
49	S2	291	G
49	S2	417	C
49	S2	420	G
49	S2	563	G
49	S2	668	A
49	S2	688	U
49	S2	1434	C
84	CC	35	U
84	CC	74	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

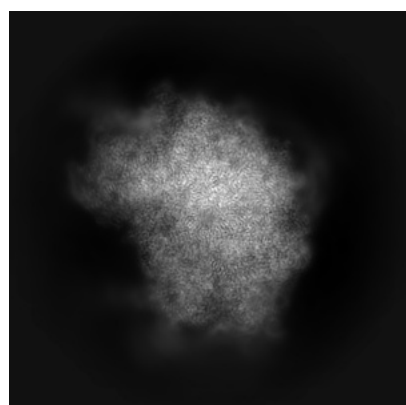
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11292. These allow visual inspection of the internal detail of the map and identification of artifacts.

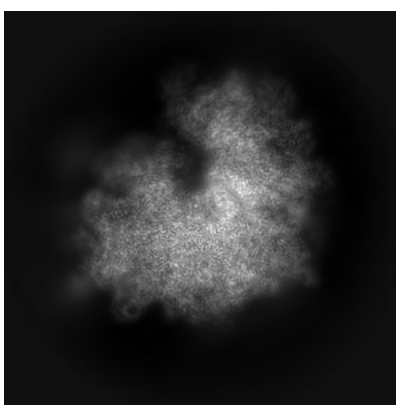
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

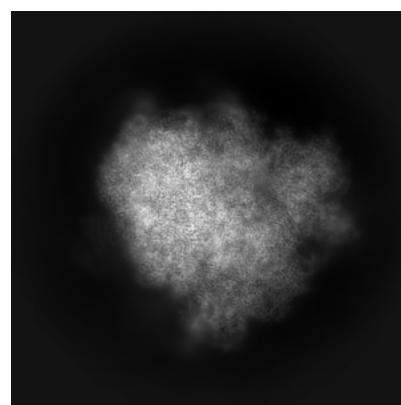
6.1.1 Primary map



X



Y

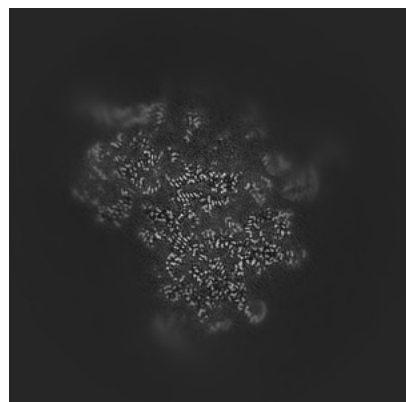


Z

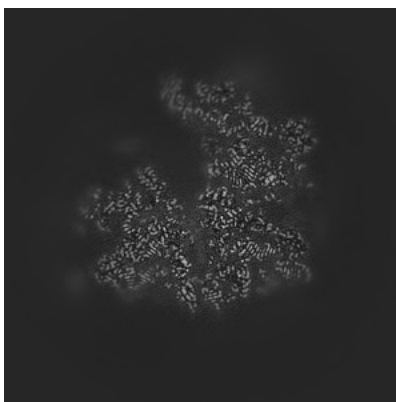
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

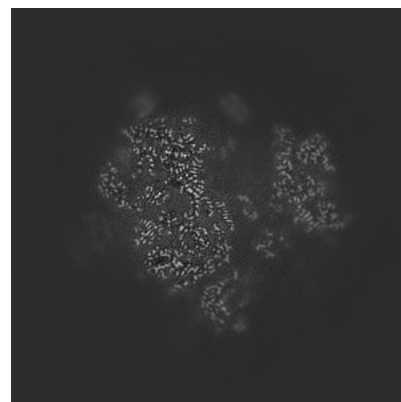
6.2.1 Primary map



X Index: 200



Y Index: 200

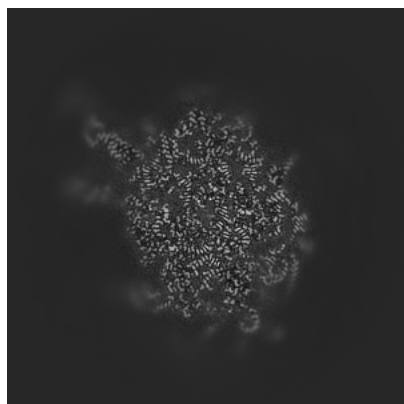


Z Index: 200

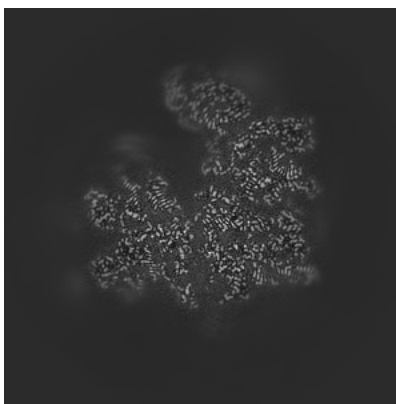
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

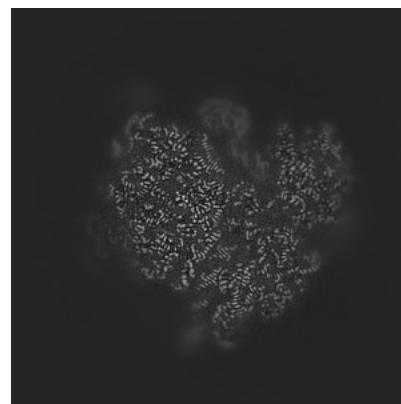
6.3.1 Primary map



X Index: 178



Y Index: 194

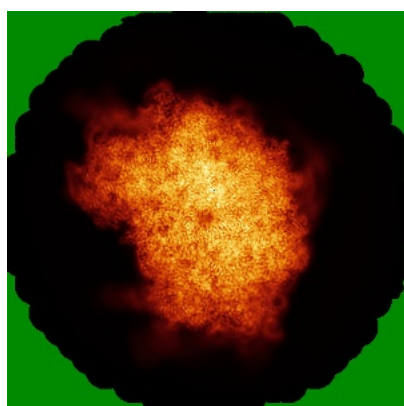


Z Index: 224

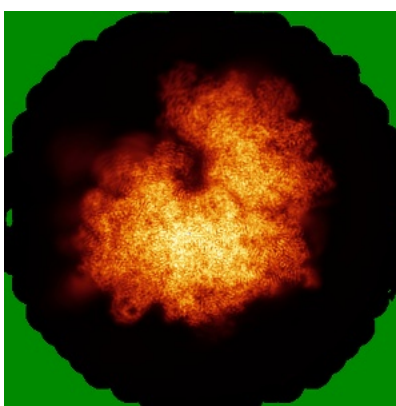
The images above show the largest variance slices of the map in three orthogonal directions.

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

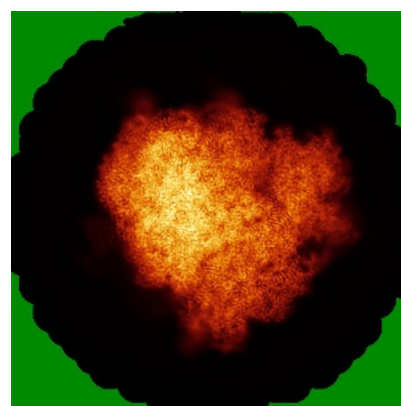
6.4.1 Primary map



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

This section was not generated.

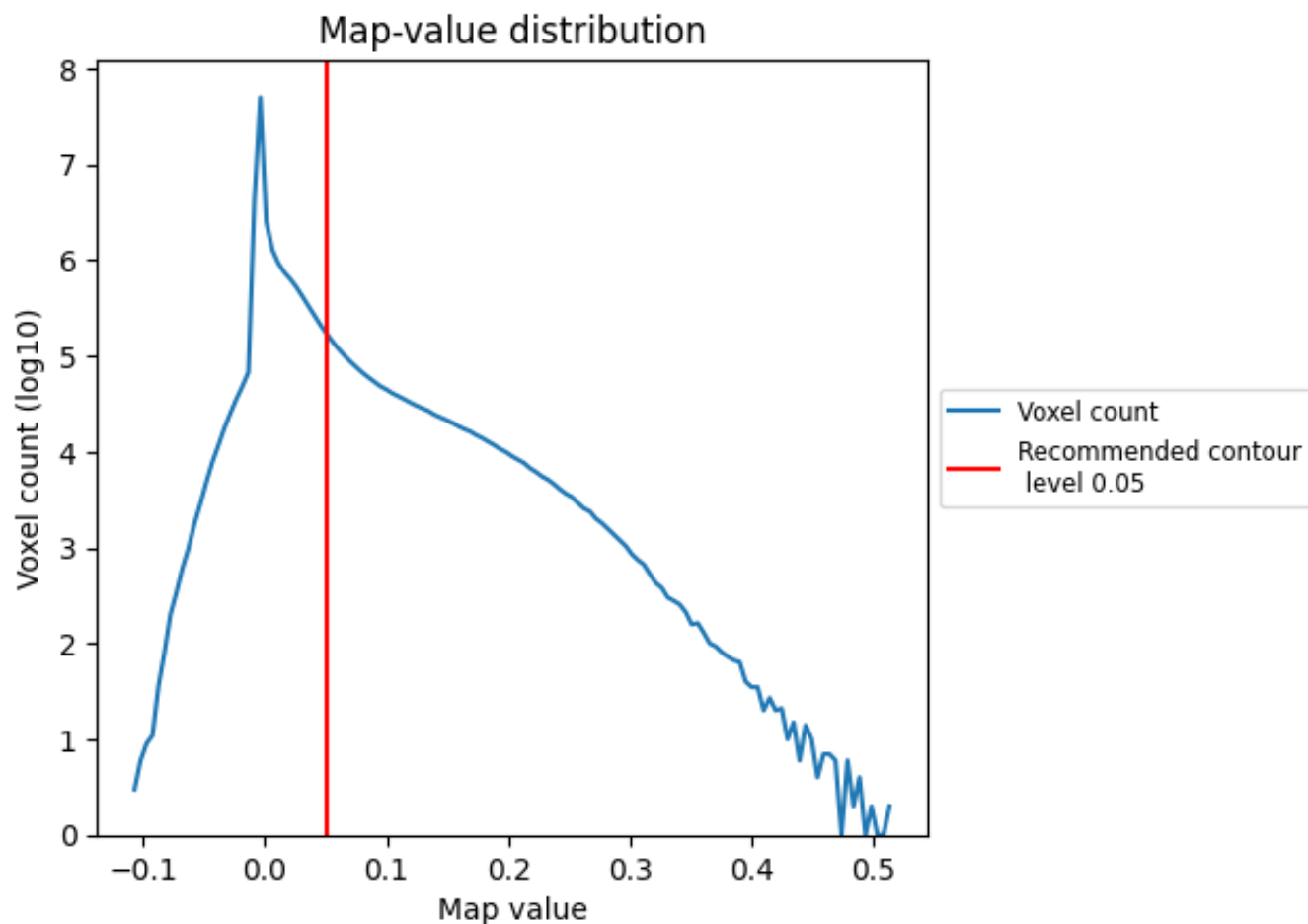
6.6 Mask visualisation

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

7 Map analysis [i](#)

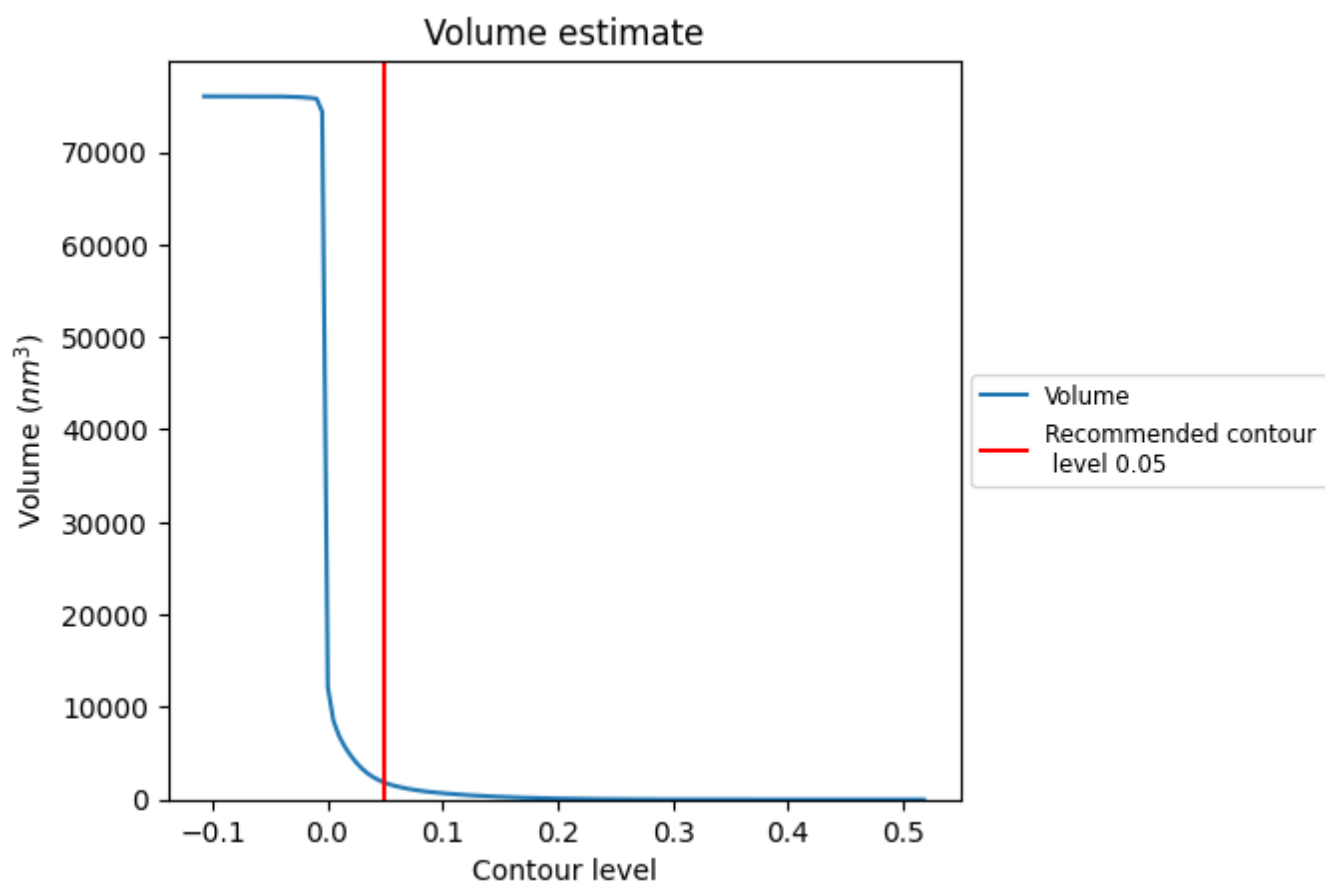
This section contains the results of statistical analysis of the map.

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.

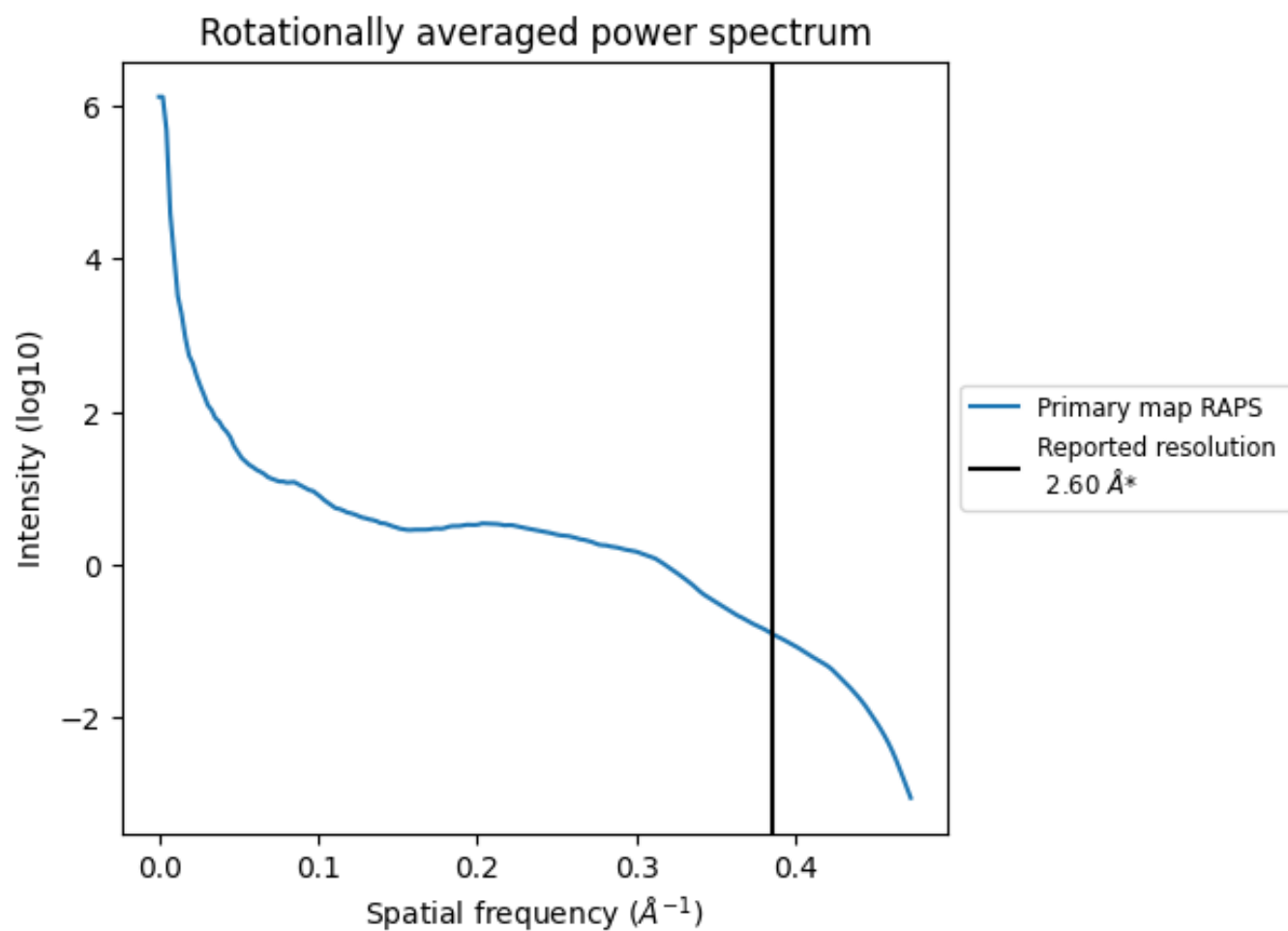
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1822 nm^3 ; this corresponds to an approximate mass of 1646 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 ⓘ

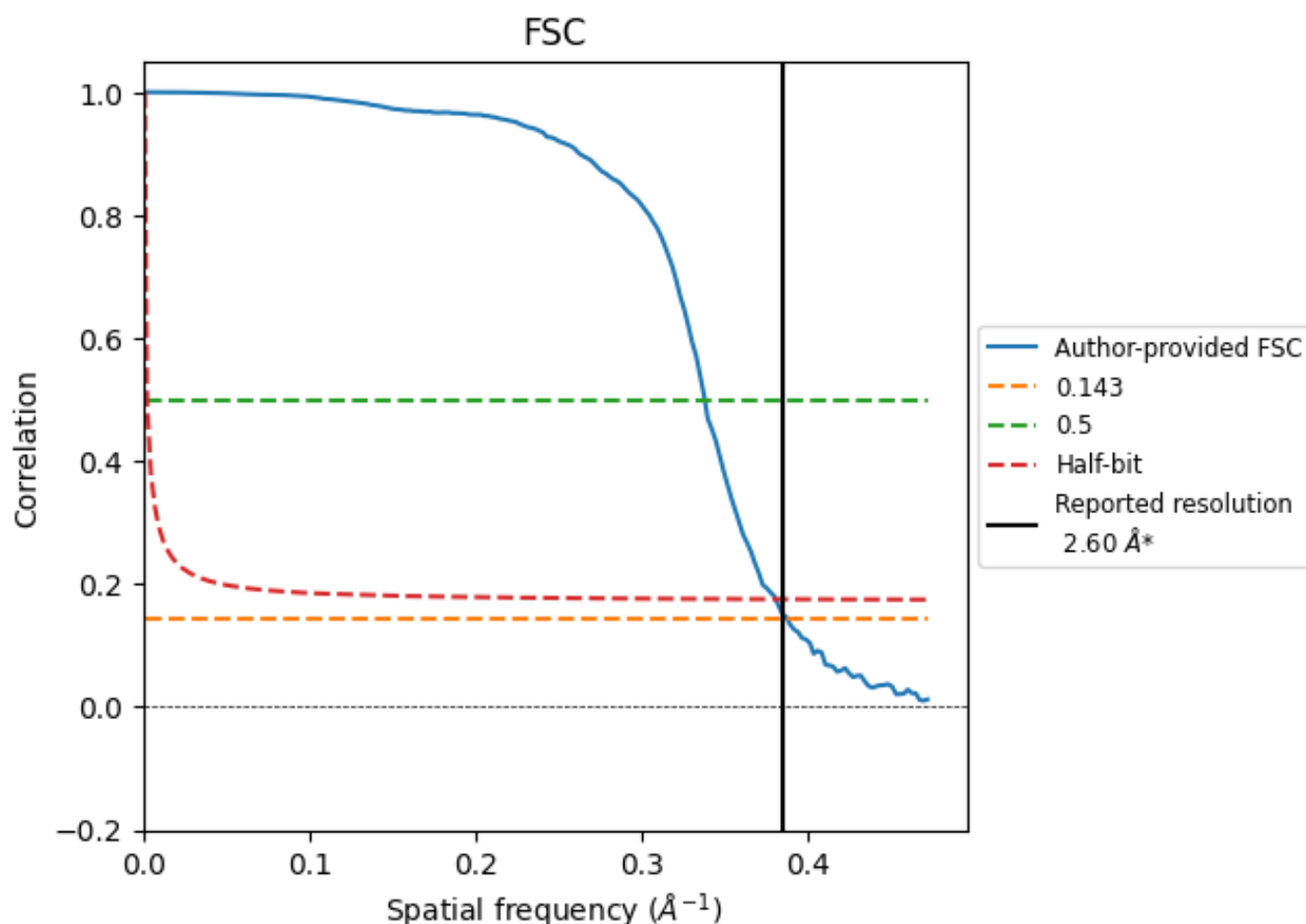


*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

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 0.385 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.58	2.96	2.63
Unmasked-calculated*	-	-	-

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

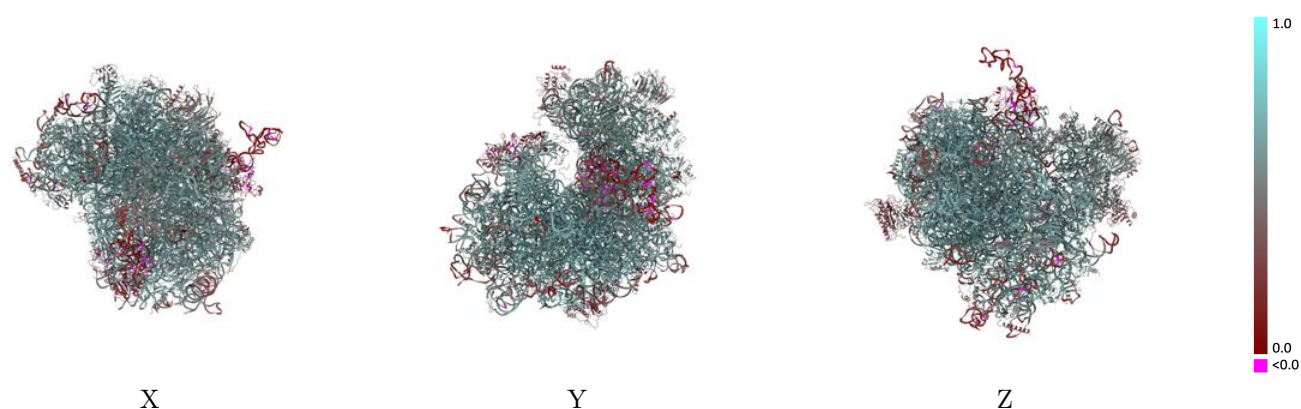
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11292 and PDB model 6ZMI. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)

This section was not generated.

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

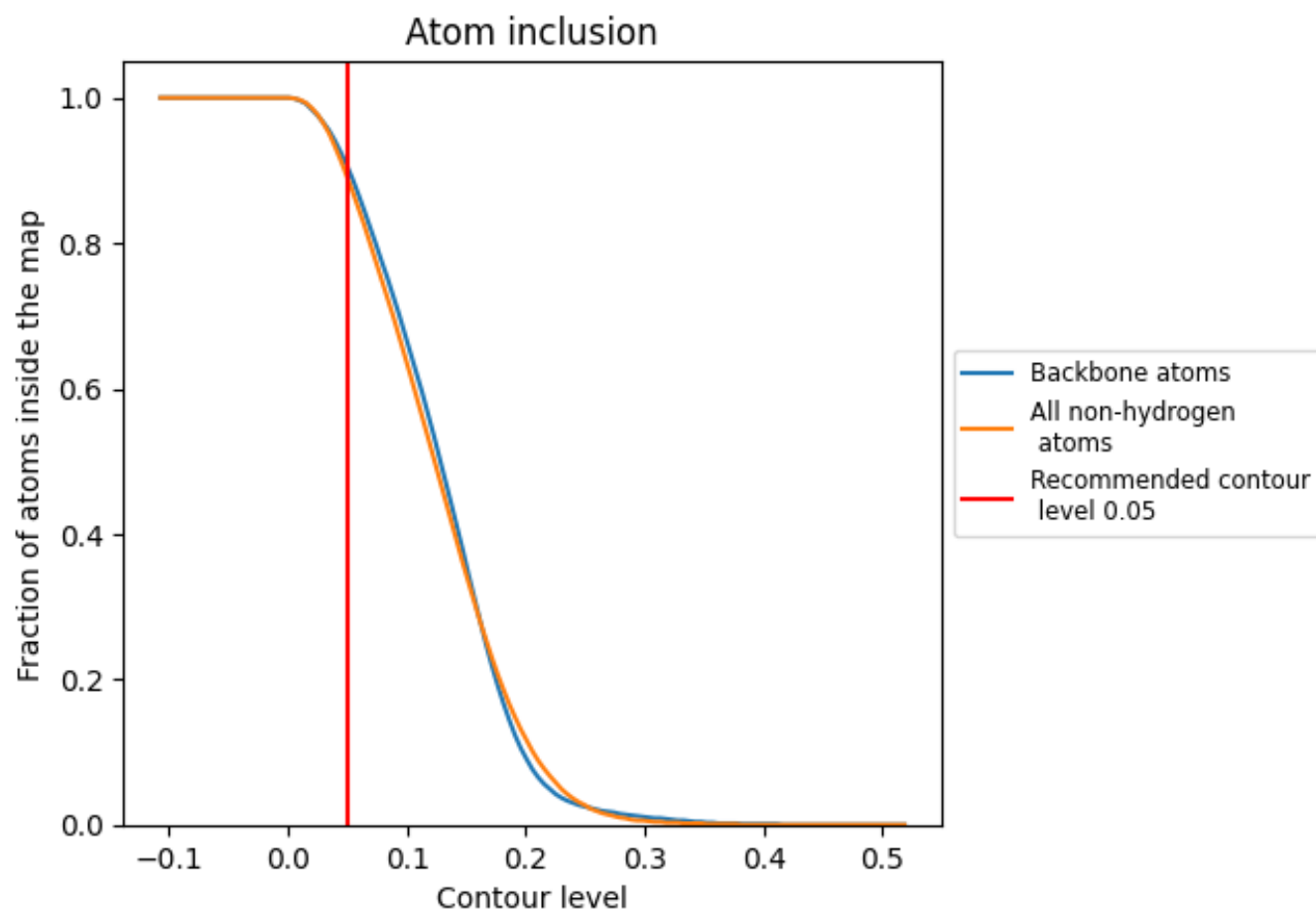


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 89% 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	 0.8900	 0.5750
CA	 0.0380	 0.3190
CC	 0.8400	 0.3510
CE	 0.7730	 0.5450
L5	 0.9300	 0.5890
L7	 0.9930	 0.6360
L8	 0.9670	 0.6210
LA	 0.9870	 0.6800
LB	 0.9410	 0.6450
LC	 0.9450	 0.6340
LD	 0.9100	 0.5870
LE	 0.8540	 0.5600
LF	 0.9640	 0.6440
LG	 0.8450	 0.5730
LH	 0.9320	 0.6090
LI	 0.9470	 0.6230
LJ	 0.8180	 0.5110
LL	 0.8970	 0.6040
LM	 0.9360	 0.6020
LN	 0.9940	 0.6820
LO	 0.9570	 0.6500
LP	 0.9610	 0.6610
LQ	 0.9770	 0.6630
LR	 0.8910	 0.6040
LS	 0.9790	 0.6520
LT	 0.9370	 0.6170
LU	 0.8430	 0.5310
LV	 0.9660	 0.6550
LW	 0.7010	 0.4780
LX	 0.9310	 0.6250
LY	 0.9260	 0.6210
LZ	 0.9390	 0.6170
La	 0.9710	 0.6630
Lb	 0.8620	 0.5650
Lc	 0.9300	 0.6230



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Chain	Atom inclusion	Q-score
Ld	 0.9210	 0.6190
Le	 0.9770	 0.6620
Lf	 0.9810	 0.6610
Lg	 0.9260	 0.6430
Lh	 0.9270	 0.6080
Li	 0.9220	 0.6050
Lj	 0.9820	 0.6680
Lk	 0.8470	 0.5640
Ll	 0.9760	 0.6380
Lm	 0.9280	 0.6240
Ln	 0.9860	 0.6670
Lo	 0.9310	 0.6350
Lp	 0.9590	 0.6680
Lr	 0.9600	 0.6310
Ls	 0.1440	 0.1380
Lt	 0.0350	 0.0940
Lz	 0.1310	 0.1510
S2	 0.9430	 0.5820
SA	 0.8890	 0.5810
SB	 0.9120	 0.5940
SC	 0.9370	 0.6100
SD	 0.8390	 0.5240
SE	 0.9290	 0.5940
SF	 0.8920	 0.5370
SG	 0.7920	 0.5060
SH	 0.7540	 0.4980
SI	 0.8970	 0.5850
SJ	 0.9060	 0.5760
SK	 0.7910	 0.4830
SL	 0.8940	 0.6120
SM	 0.3120	 0.2690
SN	 0.9570	 0.6320
SO	 0.8990	 0.5910
SP	 0.7810	 0.4850
SQ	 0.8640	 0.5450
SR	 0.8070	 0.5240
SS	 0.8140	 0.5060
ST	 0.8610	 0.5300
SU	 0.7790	 0.4950
SV	 0.9150	 0.5870
SW	 0.9640	 0.6400
SX	 0.9510	 0.6340

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Chain	Atom inclusion	Q-score
SY	 0.8170	 0.5290
SZ	 0.7270	 0.4700
Sa	 0.9210	 0.6060
Sb	 0.8860	 0.5710
Sc	 0.8170	 0.5250
Sd	 0.9460	 0.5890
Se	 0.8060	 0.5460
Sf	 0.4720	 0.3380
Sg	 0.6880	 0.4630
i	 0.9260	 0.6210