



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 04:46 PM UTC

PDB ID : 8XT2 / pdb_00008xt2
EMDB ID : EMD-38634
Title : Cryo-EM structure of the human 55S mitoribosome with 10uM Tigecycline
Authors : Li, X.; Wang, M.; Cheng, J.
Deposited on : 2024-01-10
Resolution : 3.30 Å (reported)
Based on initial model : 7A5I

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

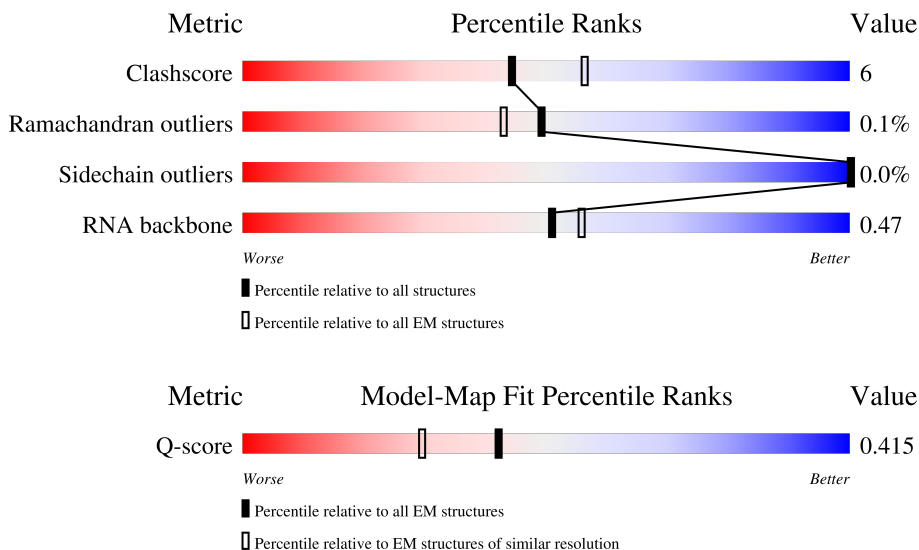
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.30 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	15087 (2.80 - 3.80)

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	L1	1559	60% 32% . .
2	L2	69	45% 33% . 19%
3	LB	305	69% 9% 22%

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Mol	Chain	Length	Quality of chain
4	LC	348	75% 12% 13%
5	LD	311	63% 17% 20%
6	LI	267	27% 9% 64%
7	LJ	261	40% 20% 39%
8	LK	192	78% 14% 9%
9	LM	178	84% 15%
10	LN	145	63% 17% 21%
11	LO	296	82% 15%
12	LP	251	74% 14% 12%
13	LQ	175	75% 11% 13%
14	LR	179	68% 13% 18%
15	LS	292	66% 9% 25%
16	LT	149	86% 8% 6%
17	LU	205	66% 12% 22%
18	LV	212	68% 10% 22%
19	LW	153	72% 22% 7%
20	LX	216	77% 16% 6%
21	La	148	62% 13% 25%
22	Lb	256	88% 7% 5%
23	Lu	250	58% 13% 30%
24	Ld	161	63% 11% 25%
25	Lf	188	52% 6% 43%
26	Lg	65	60% 20% 20%
27	Lh	92	46% 50%
28	Li	188	43% 8% 49%

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Mol	Chain	Length	Quality of chain
29	Lj	103	
30	Lk	423	
31	Ll	380	
32	Lm	338	
33	Ln	206	
34	Lo	137	
35	Lp	142	
36	Lq	215	
37	Lr	332	
38	Ls	306	
39	Lt	279	
40	Lv	212	
41	Lw	166	
42	Lx	158	
43	Ly	128	
44	Lz	123	
45	L3	112	
46	L4	138	
47	L5	128	
48	L6	102	
49	L7	206	
50	L8	222	
51	SR	196	
52	Sf	439	
53	SB	296	

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Mol	Chain	Length	Quality of chain
54	SZ	167	50% 29% 21%
55	SE	430	61% 13% 26%
56	SF	125	80% 18%
57	SG	242	68% 15% 17%
58	SI	396	61% 15% 23%
59	SJ	201	35% 25% 39%
60	SK	194	59% 11% 30%
61	SL	138	67% 12% 22%
62	SN	128	50% 29% 21%
63	SO	257	52% 12% 36%
64	SP	137	55% 29% 15%
65	SQ	130	66% 16% 18%
66	SS	258	53% 19% 28%
67	ST	142	51% 16% 32%
68	SW	87	83% 15%
69	SX	360	7% 66% 16% 18%
70	SY	190	56% 11% 34%
71	Sa	173	78% 15% 6%
72	Sb	205	71% 14% 16%
73	Sc	414	8% 76% 17% 7%
74	Sd	187	41% 11% 48%
75	Se	398	72% 16% 12%
76	Sg	395	19% 8% 73%
77	Si	106	60% 21% 19%
78	Sj	218	68% 24% 8%

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Mol	Chain	Length	Quality of chain
79	Sk	323	
80	Sm	118	
81	Sn	199	
82	So	689	
83	S1	954	

2 Entry composition [i](#)

There are 87 unique types of molecules in this entry. The entry contains 165243 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 16s rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	L1	1500	31847	14290	5750	10307	1500	0	0

- Molecule 2 is a RNA chain called Val tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	L2	56	1191	534	214	387	56	0	0

- Molecule 3 is a protein called Large ribosomal subunit protein uL2m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	LB	237	1851	1151	375	316	9	0	0

- Molecule 4 is a protein called Large ribosomal subunit protein uL3m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	LC	304	2393	1538	415	429	11	0	0

- Molecule 5 is a protein called Large ribosomal subunit protein uL4m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	LD	250	2013	1294	365	348	6	0	0

- Molecule 6 is a protein called Large ribosomal subunit protein bL9m.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	LI	95	784	498	152	134	0	0

- Molecule 7 is a protein called Large ribosomal subunit protein uL10m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	LJ	158	1283	828	235	210	10	0	0

- Molecule 8 is a protein called Large ribosomal subunit protein uL11m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	LK	175	1323	841	237	243	2	0	0

- Molecule 9 is a protein called Large ribosomal subunit protein uL13m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	LM	177	1451	934	259	251	7	0	0

- Molecule 10 is a protein called Large ribosomal subunit protein uL14m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	LN	115	889	559	171	154	5	0	0

- Molecule 11 is a protein called Large ribosomal subunit protein uL15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	LO	287	2305	1472	425	402	6	0	0

- Molecule 12 is a protein called Large ribosomal subunit protein uL16m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	LP	221	1779	1138	325	306	10	0	0

- Molecule 13 is a protein called Large ribosomal subunit protein bL17m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	LQ	152	1245	784	239	215	7	0	0

- Molecule 14 is a protein called Mitochondrial ribosomal protein L18, isoform CRA_b.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	LR	146	1189	743	226	215	5	0	0

- Molecule 15 is a protein called Large ribosomal subunit protein bL19m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	LS	219	1822	1168	322	323	9	0	0

- Molecule 16 is a protein called Large ribosomal subunit protein bL20m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	LT	140	1153	732	231	186	4	0	0

- Molecule 17 is a protein called Large ribosomal subunit protein bL21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	LU	160	1284	829	226	225	4	0	0

- Molecule 18 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	LV	166	1368	875	254	232	7	0	0

- Molecule 19 is a protein called Large ribosomal subunit protein uL23m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	LW	143	1188	752	224	208	4	0	0

- Molecule 20 is a protein called Large ribosomal subunit protein uL24m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	LX	202	1652	1053	294	297	8	0	0

- Molecule 21 is a protein called Large ribosomal subunit protein bL27m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	La	111	871	558	164	146	3	0	0

- Molecule 22 is a protein called Large ribosomal subunit protein bL28m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	Lb	243	2035	1317	351	362	5	0	0

- Molecule 23 is a protein called Large ribosomal subunit protein uL29m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	Lu	176	1517	970	291	252	4	0	0

- Molecule 24 is a protein called Large ribosomal subunit protein uL30m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	Ld	120	978	626	183	166	3	0	0

- Molecule 25 is a protein called Large ribosomal subunit protein bL32m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	Lf	108	880	545	172	157	6	0	0

- Molecule 26 is a protein called Large ribosomal subunit protein bL33m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	Lg	52	433	278	83	70	2	0	0

- Molecule 27 is a protein called Large ribosomal subunit protein bL34m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	Lh	46	376	233	83	59	1	0	0

- Molecule 28 is a protein called Large ribosomal subunit protein bL35m.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Li	95	Total	C	N	O	S	0	0
			831	539	162	127	3		

- Molecule 29 is a protein called Large ribosomal subunit protein bL36m.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Lj	38	Total	C	N	O	S	0	0
			341	217	72	48	4		

- Molecule 30 is a protein called Large ribosomal subunit protein mL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lk	394	Total	C	N	O	S	0	0
			3210	2073	560	566	11		

- Molecule 31 is a protein called Large ribosomal subunit protein mL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Ll	354	Total	C	N	O	S	0	0
			2947	1881	525	532	9		

- Molecule 32 is a protein called Large ribosomal subunit protein mL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lm	293	Total	C	N	O	S	0	0
			2382	1525	404	435	18		

- Molecule 33 is a protein called Large ribosomal subunit protein mL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ln	99	Total	C	N	O	S	0	0
			836	535	144	155	2		

- Molecule 34 is a protein called Large ribosomal subunit protein mL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lo	124	Total	C	N	O	S	0	0
			997	644	170	181	2		

- Molecule 35 is a protein called Large ribosomal subunit protein mL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	Lp	97	815	514	147	149	5	0	0

- Molecule 36 is a protein called Large ribosomal subunit protein mL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	Lq	148	1178	733	229	213	3	0	0

- Molecule 37 is a protein called Large ribosomal subunit protein mL44.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	Lr	275	2217	1415	383	410	9	0	0

- Molecule 38 is a protein called Large ribosomal subunit protein mL45.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	Ls	214	1754	1117	304	320	13	0	0

- Molecule 39 is a protein called Large ribosomal subunit protein mL46.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	Lt	217	1762	1124	310	323	5	0	0

- Molecule 40 is a protein called Large ribosomal subunit protein mL48.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	Lv	131	1035	661	169	201	4	0	0

- Molecule 41 is a protein called Large ribosomal subunit protein mL49.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	Lw	132	1097	710	191	194	2	0	0

- Molecule 42 is a protein called Large ribosomal subunit protein mL50.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	Lx	110	895	568	156	168	3	0	0

- Molecule 43 is a protein called Large ribosomal subunit protein mL51.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	Ly	97	827	532	165	126	4	0	0

- Molecule 44 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	Lz	92	732	454	142	134	2	0	0

- Molecule 45 is a protein called Large ribosomal subunit protein mL53.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	L3	96	743	462	143	133	5	0	0

- Molecule 46 is a protein called Large ribosomal subunit protein mL54.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	L4	83	703	446	124	130	3	0	0

- Molecule 47 is a protein called Large ribosomal subunit protein mL55.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	L5	45	372	232	76	62	2	0	0

- Molecule 48 is a protein called Large ribosomal subunit protein mL63.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	L6	94	797	501	165	128	3	0	0

- Molecule 49 is a protein called Large ribosomal subunit protein mL62.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	L7	127	1058	661	201	192	4	0	0

- Molecule 50 is a protein called Large ribosomal subunit protein mL64.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	L8	128	1076	671	208	192	5	0	0

- Molecule 51 is a protein called Large ribosomal subunit protein mL66.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	SR	146	1203	764	232	199	8	0	0

- Molecule 52 is a protein called Large ribosomal subunit protein mL65.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	Sf	370	3036	1946	542	534	14	0	0

- Molecule 53 is a protein called Small ribosomal subunit protein uS2m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	SB	217	1768	1131	321	306	10	0	0

- Molecule 54 is a protein called Small ribosomal subunit protein uS3m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	SZ	132	1082	699	195	184	4	0	0

- Molecule 55 is a protein called Small ribosomal subunit protein uS5m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	SE	320	2540	1600	473	455	12	0	0

- Molecule 56 is a protein called Small ribosomal subunit protein bS6m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	SF	122	972	614	177	177	4	0	0

- Molecule 57 is a protein called Small ribosomal subunit protein uS7m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	SG	201	1668	1069	305	283	11	0	0

- Molecule 58 is a protein called Small ribosomal subunit protein uS9m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	SI	304	2501	1591	444	452	14	0	0

- Molecule 59 is a protein called Small ribosomal subunit protein uS10m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	SJ	122	999	643	168	185	3	0	0

- Molecule 60 is a protein called Small ribosomal subunit protein uS11m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	SK	136	1011	637	192	178	4	0	0

- Molecule 61 is a protein called Small ribosomal subunit protein uS12m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	SL	108	838	521	169	142	6	0	0

- Molecule 62 is a protein called Small ribosomal subunit protein uS14m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	SN	101	861	537	179	140	5	0	0

- Molecule 63 is a protein called Small ribosomal subunit protein uS15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	SO	164	1382	883	257	235	7	0	0

- Molecule 64 is a protein called Small ribosomal subunit protein bS16m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	SP	116	920	582	182	150	6	0	0

- Molecule 65 is a protein called Small ribosomal subunit protein uS17m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	SQ	107	846	549	153	141	3	0	0

- Molecule 66 is a protein called Small ribosomal subunit protein mS40.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	SS	185	1528	970	285	267	6	0	0

- Molecule 67 is a protein called Small ribosomal subunit protein bS18m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	ST	96	774	498	133	135	8	0	0

- Molecule 68 is a protein called Small ribosomal subunit protein bS21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	SW	86	740	458	150	124	8	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SW	50	ARG	CYS	variant	UNP P82921

- Molecule 69 is a protein called Small ribosomal subunit protein mS22.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SX	295	Total	C	N	O	S	0	0
			2405	1530	413	454	8		

- Molecule 70 is a protein called Small ribosomal subunit protein mS23.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SY	126	Total	C	N	O	S	0	0
			1042	673	183	185	1		

- Molecule 71 is a protein called Small ribosomal subunit protein mS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Sa	162	Total	C	N	O	S	0	0
			1330	850	231	238	11		

- Molecule 72 is a protein called Small ribosomal subunit protein mS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Sb	173	Total	C	N	O	S	0	0
			1454	894	294	262	4		

- Molecule 73 is a protein called Small ribosomal subunit protein mS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Sc	385	Total	C	N	O	S	0	0
			3116	1980	522	603	11		

- Molecule 74 is a protein called Small ribosomal subunit protein bS1m.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Sd	97	Total	C	N	O	S	0	0
			766	486	137	139	4		

- Molecule 75 is a protein called Small ribosomal subunit protein mS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Se	350	Total	C	N	O	S	0	0
			2836	1813	497	515	11		

- Molecule 76 is a protein called Small ribosomal subunit protein mS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Sg	108	Total	C	N	O	S	0	0
			903	587	145	169	2		

- Molecule 77 is a protein called Small ribosomal subunit protein mS33.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Si	86	Total	C	N	O	S	0	0
			731	467	131	129	4		

- Molecule 78 is a protein called Small ribosomal subunit protein mS34.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sj	201	Total	C	N	O	S	0	0
			1680	1062	321	292	5		

- Molecule 79 is a protein called Small ribosomal subunit protein mS35.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sk	256	Total	C	N	O	S	0	0
			2068	1317	349	392	10		

- Molecule 80 is a protein called Small ribosomal subunit protein mS37.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sm	116	Total	C	N	O	S	0	0
			925	574	181	162	8		

- Molecule 81 is a protein called Small ribosomal subunit protein mS38.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Sn	69	Total	C	N	O	S	0	0
			610	393	130	86	1		

- Molecule 82 is a protein called Small ribosomal subunit protein mS39.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	So	616	Total	C	N	O	S	0	0
			4981	3177	849	928	27		

- Molecule 83 is a RNA chain called 12s rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
83	S1	928	19716	8840	3560	6388	928	0	0

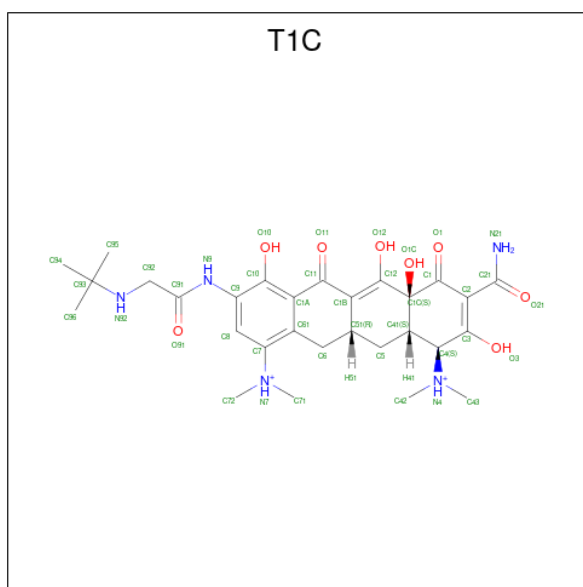
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S1	873	A	U	conflict	GB 587653826

- Molecule 84 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
84	L1	104	Total	Mg	0
			104	104	
84	LB	3	Total	Mg	0
			3	3	
84	LC	1	Total	Mg	0
			1	1	
84	LP	1	Total	Mg	0
			1	1	
84	La	1	Total	Mg	0
			1	1	
84	Lw	1	Total	Mg	0
			1	1	
84	L6	1	Total	Mg	0
			1	1	
84	S1	33	Total	Mg	0
			33	33	

- Molecule 85 is TIGECYCLINE (CCD ID: T1C) (formula: C₂₉H₄₁N₅O₈) (labeled as "Ligand of Interest" by depositor).

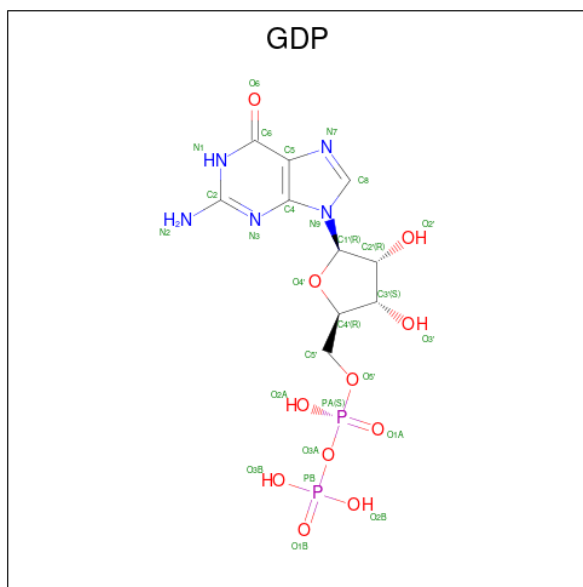


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
85	L1	1	42	29	5	8	0
85	L1	1	42	29	5	8	0
85	S1	1	42	29	5	8	0

- Molecule 86 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
86	Lf	1	1	1	0
86	Lj	1	1	1	0
86	SR	1	1	1	0
86	SB	1	1	1	0
86	SS	1	1	1	0
86	ST	1	1	1	0
86	Sa	1	1	1	0

- Molecule 87 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).




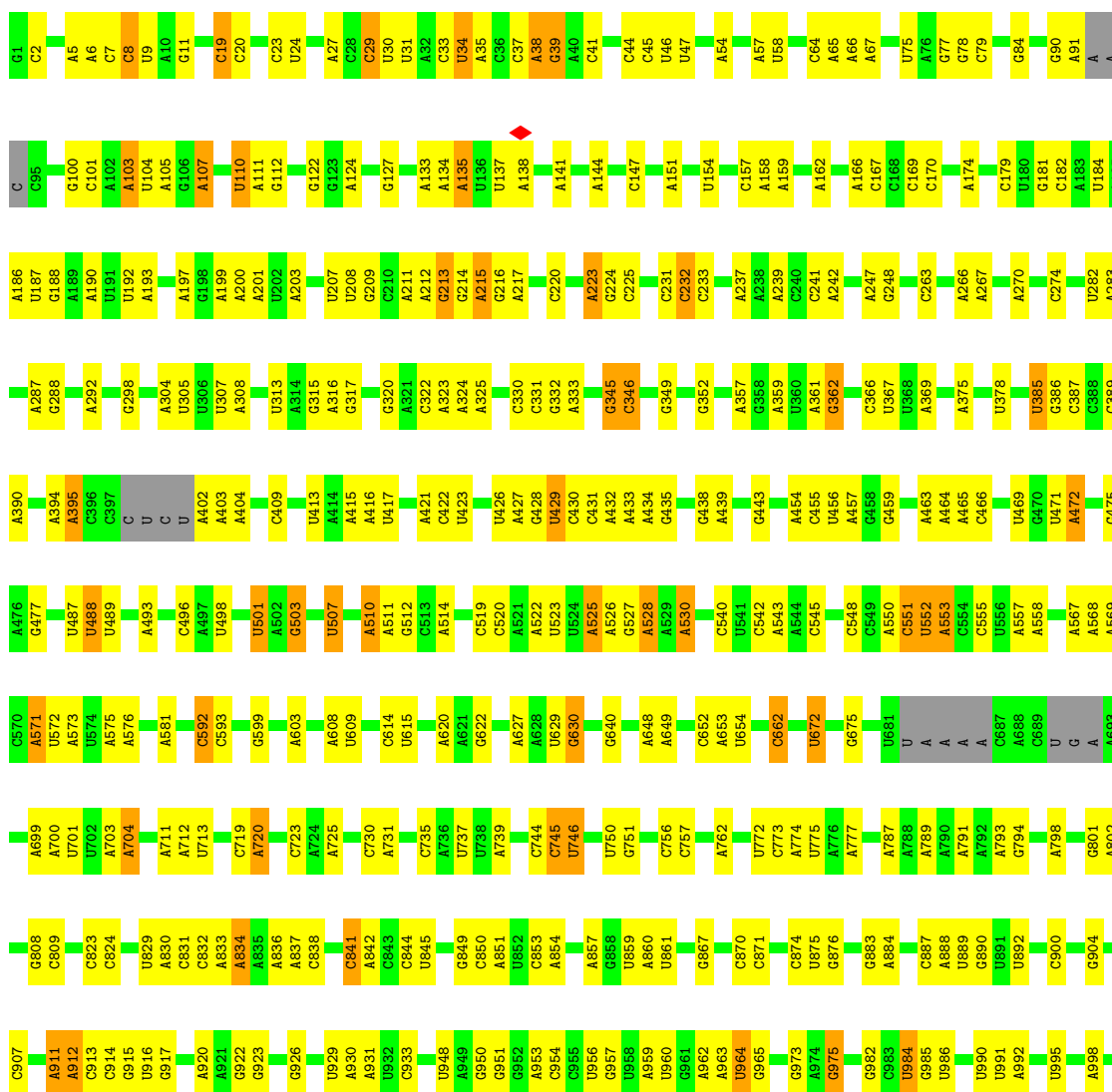
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
87	Se	1	28	10	5	11	2	0

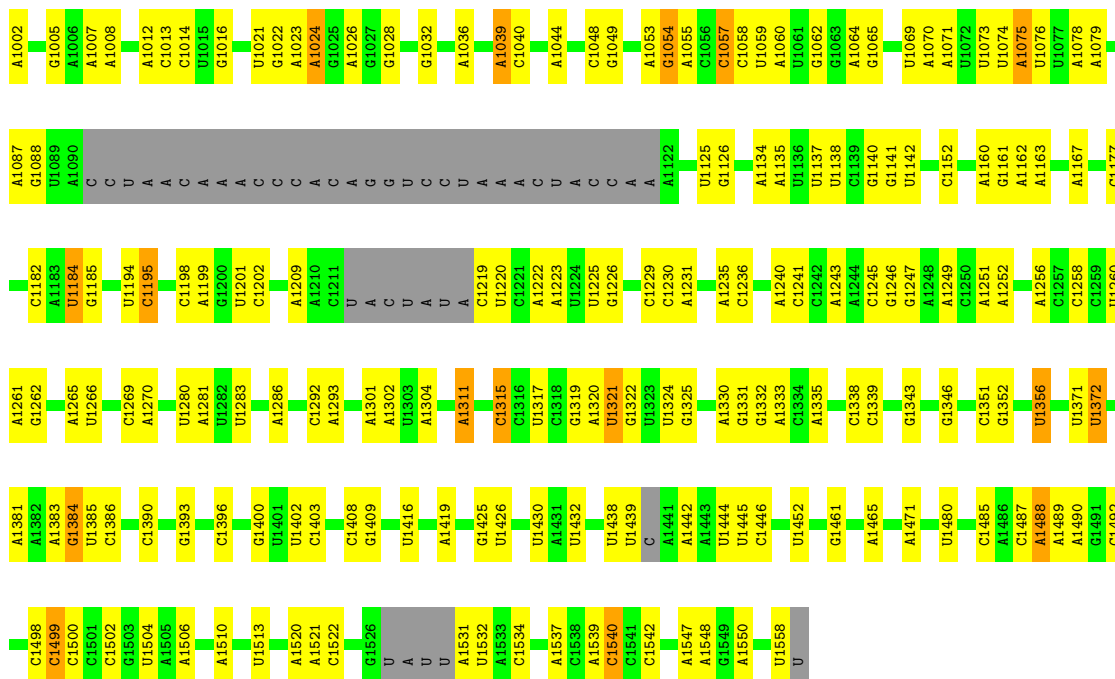
3 Residue-property plots i

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.

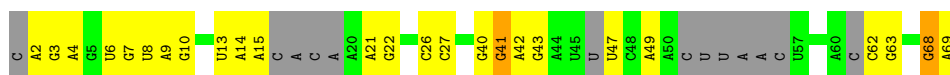
• Molecule 1: 16s rRNA

Chain L1: 

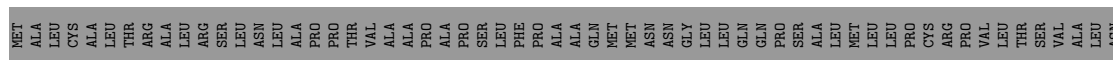




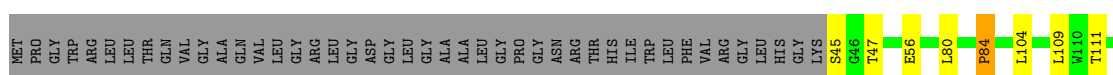
• Molecule 2: Val tRNA

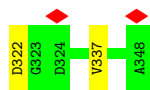


• Molecule 3: Large ribosomal subunit protein uL2m

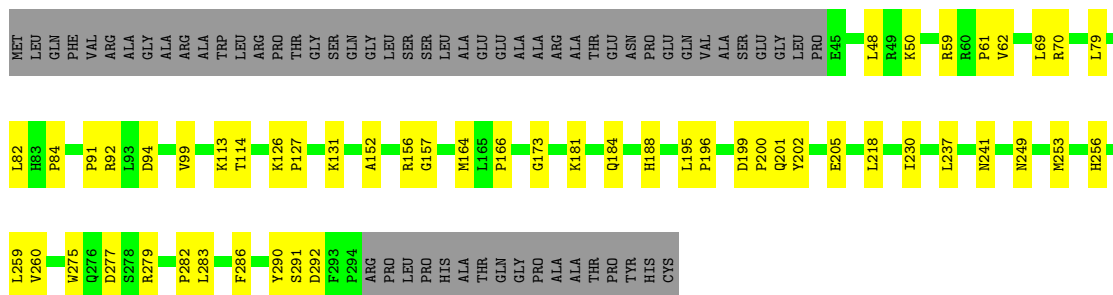


• Molecule 4: Large ribosomal subunit protein uL3m

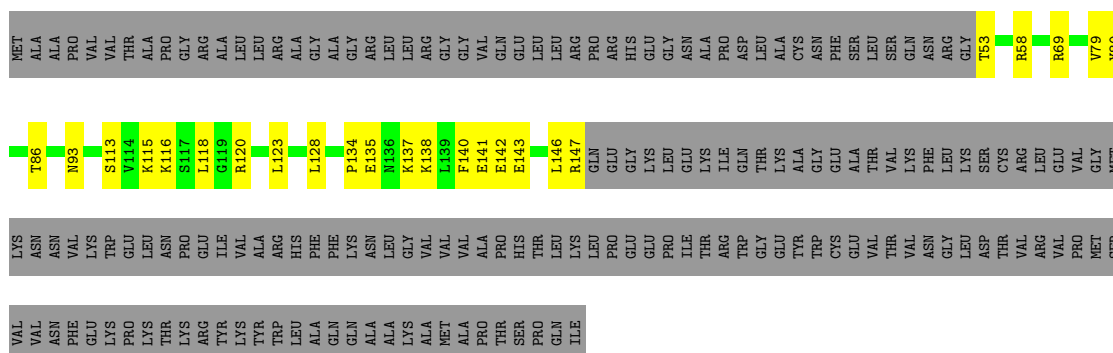




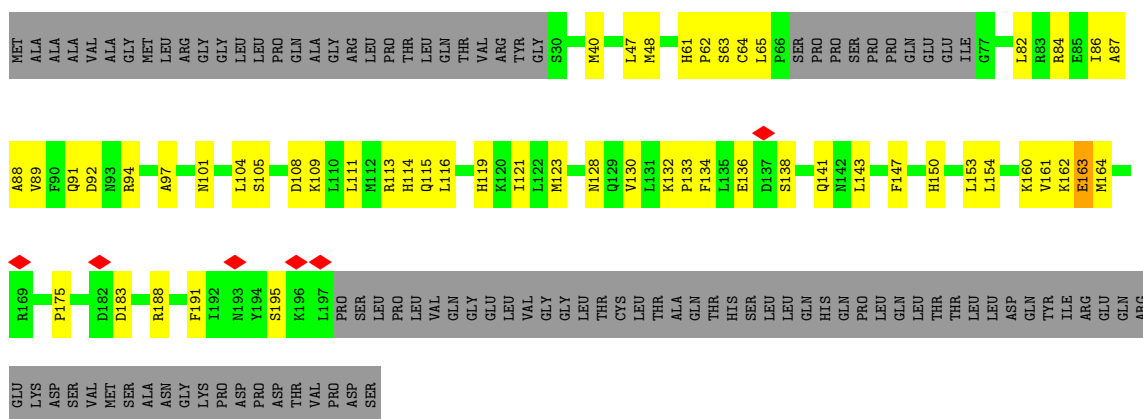
• Molecule 5: Large ribosomal subunit protein uL4m



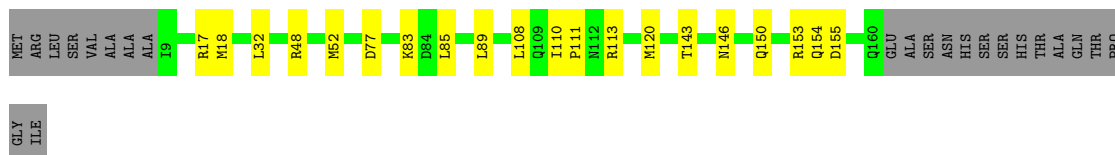
• Molecule 6: Large ribosomal subunit protein bL9m



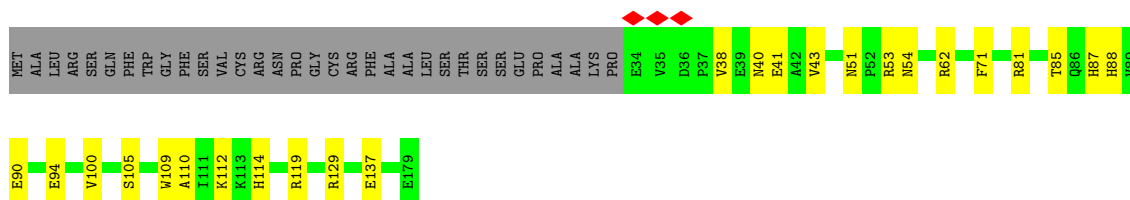
• Molecule 7: Large ribosomal subunit protein uL10m



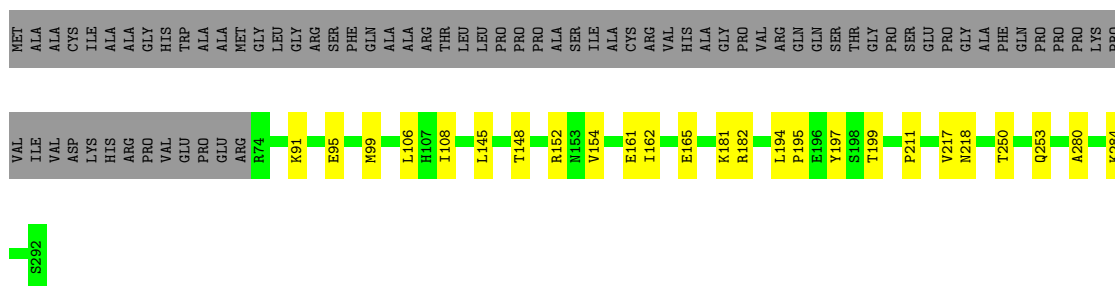
• Molecule 8: Large ribosomal subunit protein uL11m



- Molecule 14: Mitochondrial ribosomal protein L18, isoform CRA_b



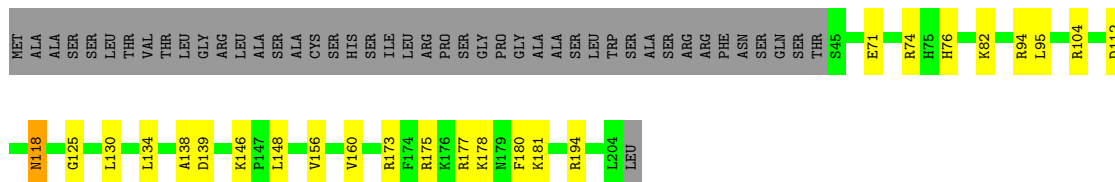
- Molecule 15: Large ribosomal subunit protein bL19m



- Molecule 16: Large ribosomal subunit protein bL20m

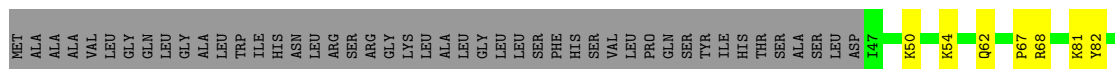


- Molecule 17: Large ribosomal subunit protein bL21m

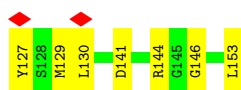
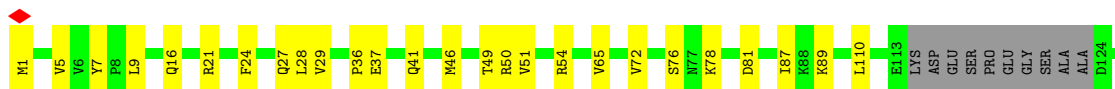


- Molecule 18: 39S ribosomal protein L22, mitochondrial

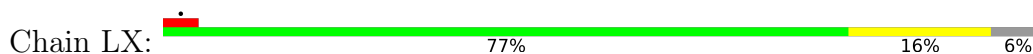




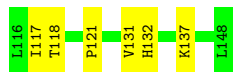
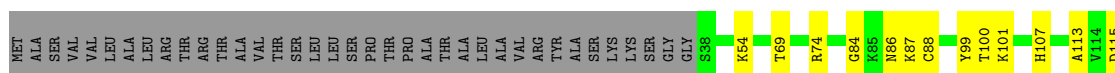
• Molecule 19: Large ribosomal subunit protein uL23m



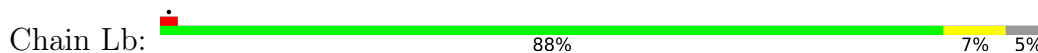
• Molecule 20: Large ribosomal subunit protein uL24m



• Molecule 21: Large ribosomal subunit protein bL27m

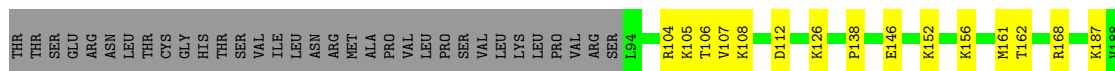


• Molecule 22: Large ribosomal subunit protein bL28m

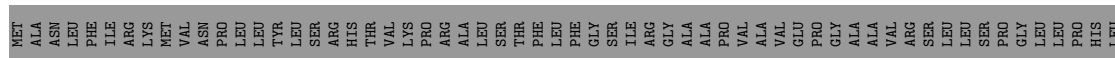


• Molecule 23: Large ribosomal subunit protein uL29m

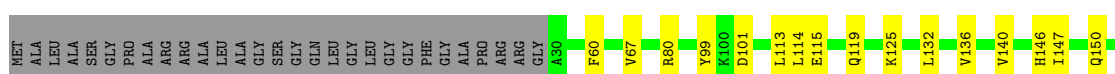
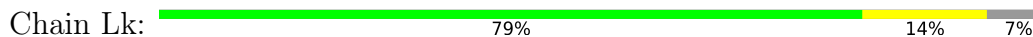




• Molecule 29: Large ribosomal subunit protein bL36m



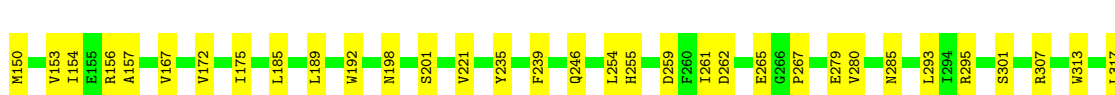
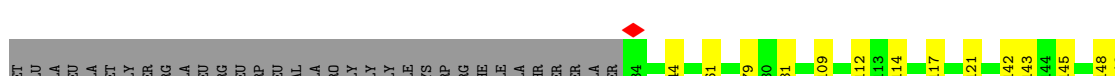
• Molecule 30: Large ribosomal subunit protein mL37

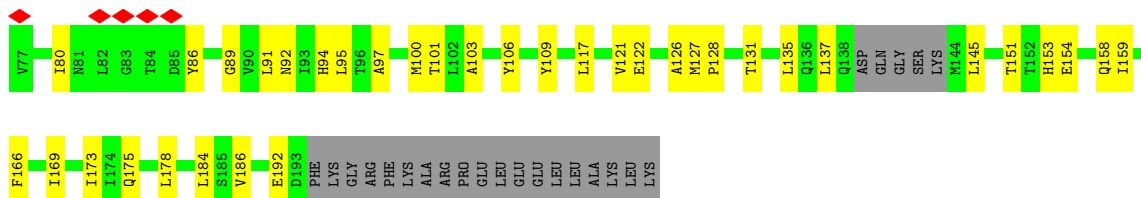


• Molecule 31: Large ribosomal subunit protein mL38

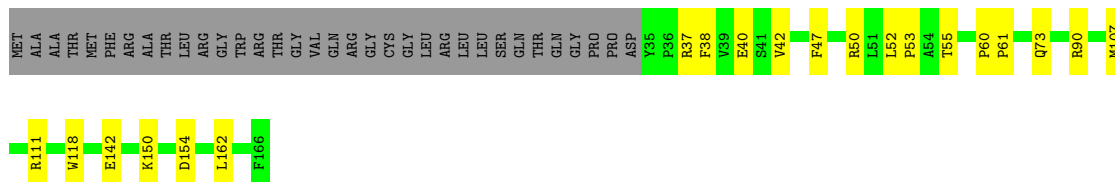


• Molecule 32: Large ribosomal subunit protein mL39

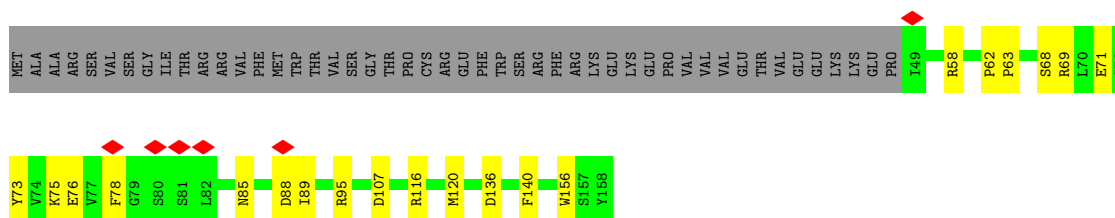




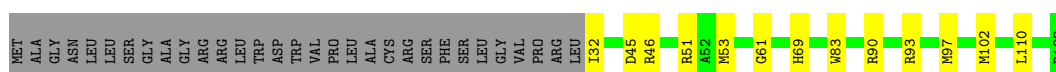
- Molecule 41: Large ribosomal subunit protein mL49



- Molecule 42: Large ribosomal subunit protein mL50



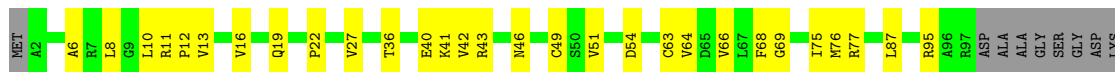
- Molecule 43: Large ribosomal subunit protein mL51



- Molecule 44: 39S ribosomal protein L52, mitochondrial

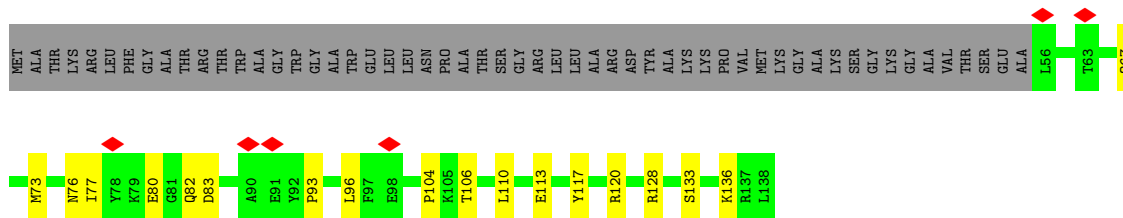


- Molecule 45: Large ribosomal subunit protein mL53

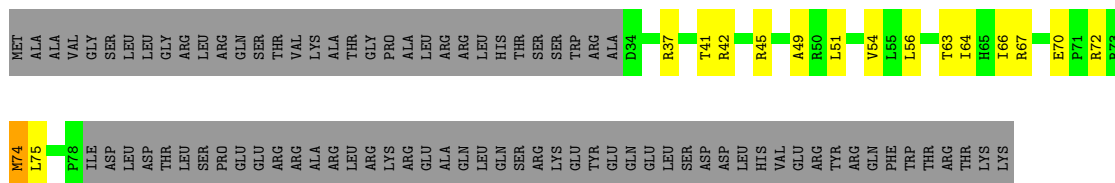


PRO
GLY
ALA
ASP
THR
GLY
ARG

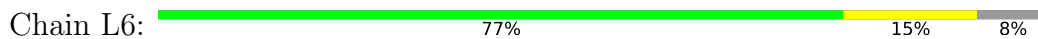
- Molecule 46: Large ribosomal subunit protein mL54



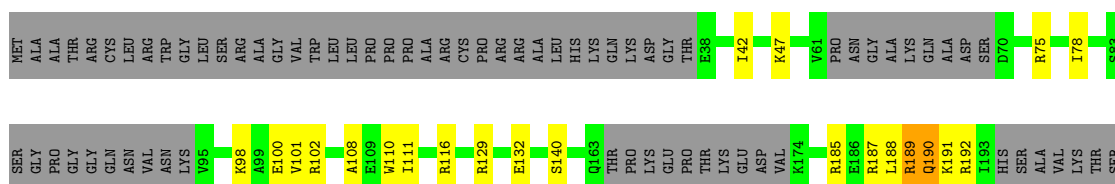
- Molecule 47: Large ribosomal subunit protein mL55



- Molecule 48: Large ribosomal subunit protein mL63



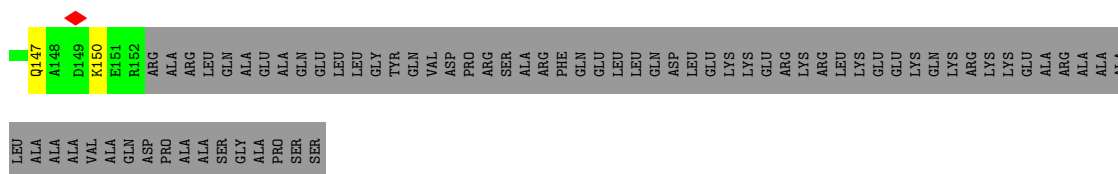
- Molecule 49: Large ribosomal subunit protein mL62



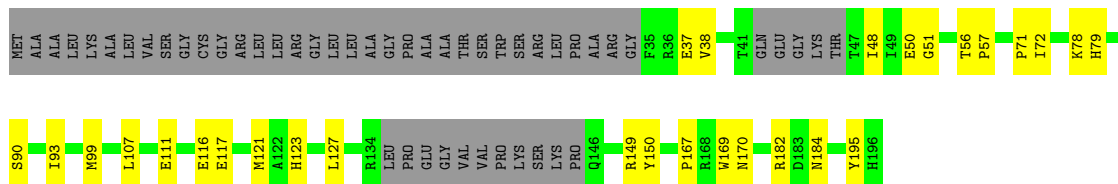
ARG
ARG
VAL
ASP
MET
ASP

- Molecule 50: Large ribosomal subunit protein mL64

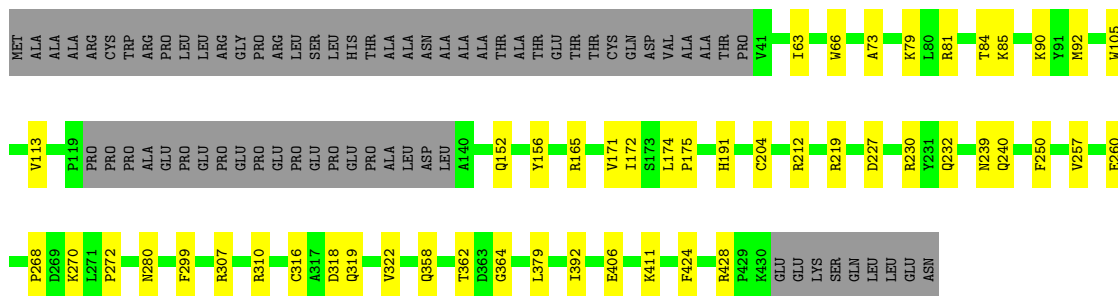




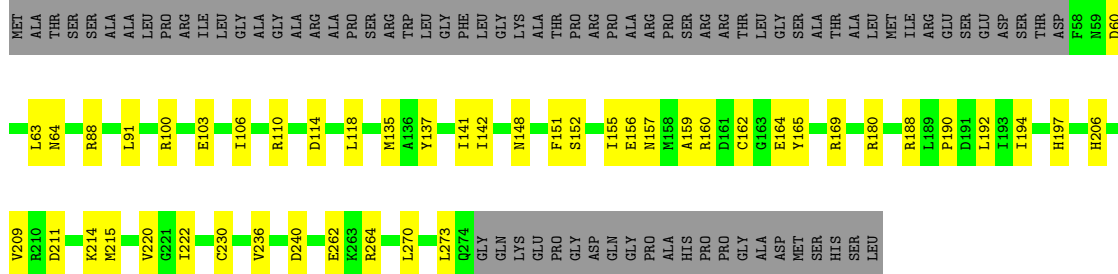
- Molecule 51: Large ribosomal subunit protein mL66



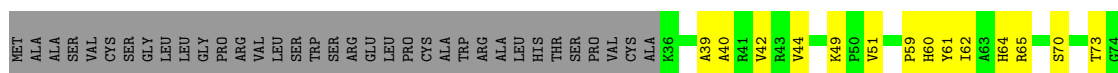
- Molecule 52: Large ribosomal subunit protein mL65

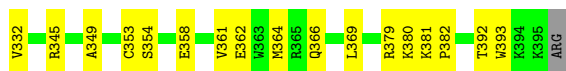


- Molecule 53: Small ribosomal subunit protein uS2m

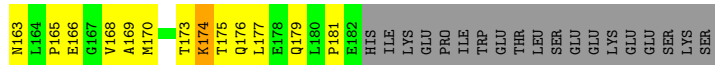
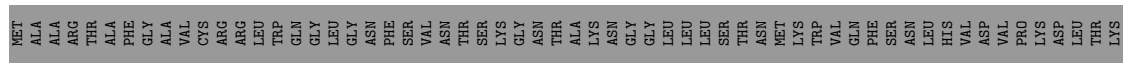
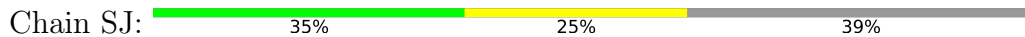


- Molecule 54: Small ribosomal subunit protein uS3m

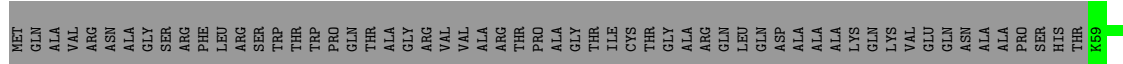




• Molecule 59: Small ribosomal subunit protein uS10m



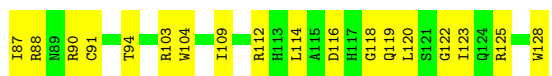
• Molecule 60: Small ribosomal subunit protein uS11m



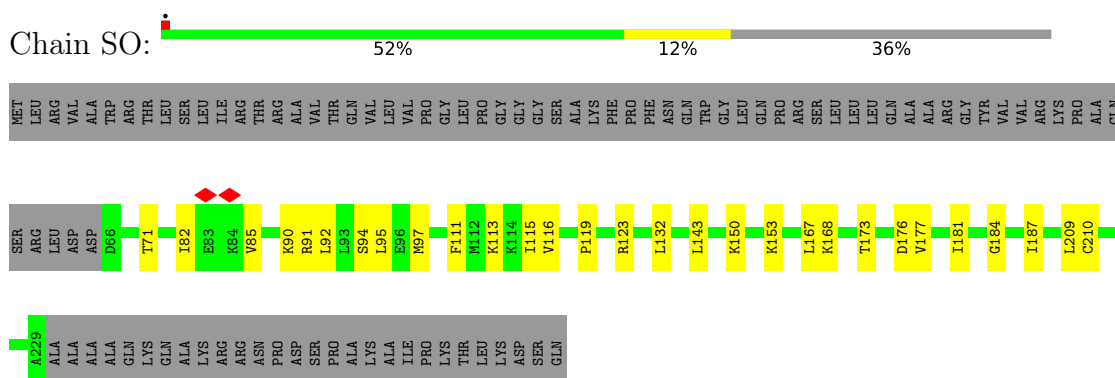
• Molecule 61: Small ribosomal subunit protein uS12m



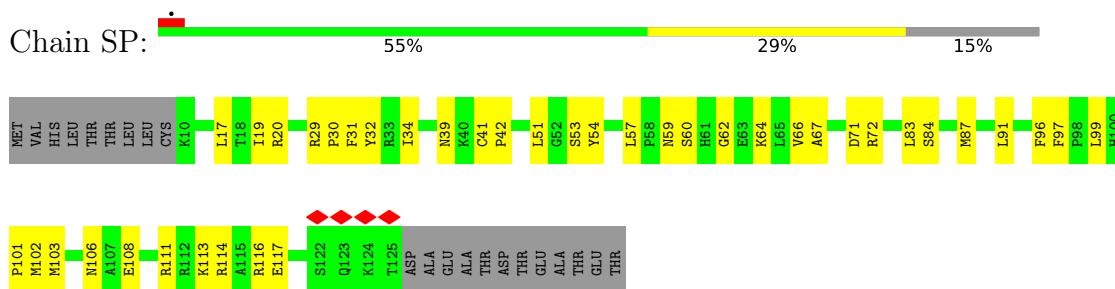
• Molecule 62: Small ribosomal subunit protein uS14m



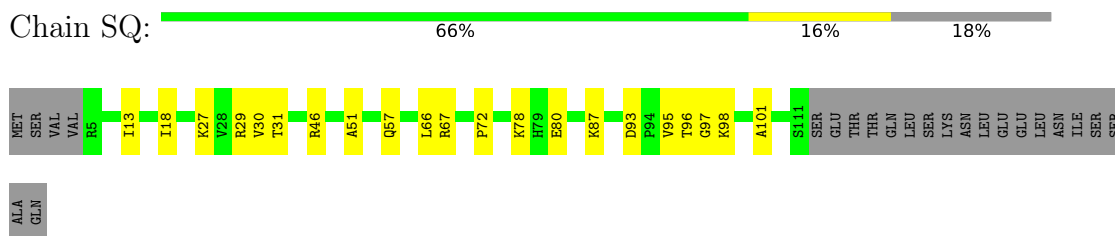
• Molecule 63: Small ribosomal subunit protein uS15m



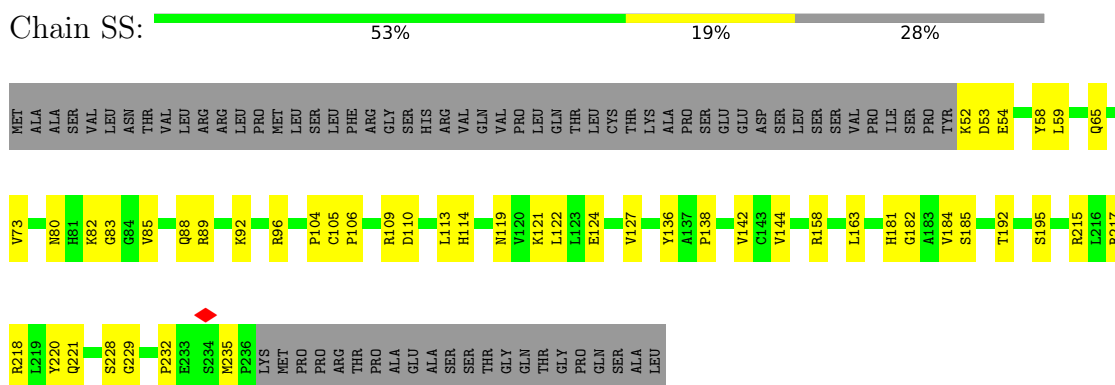
• Molecule 64: Small ribosomal subunit protein bS16m



• Molecule 65: Small ribosomal subunit protein uS17m

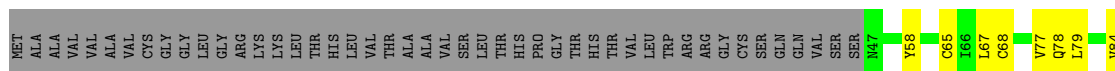


• Molecule 66: Small ribosomal subunit protein mS40

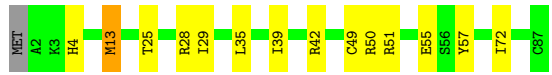
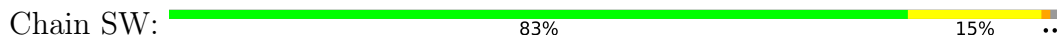


• Molecule 67: Small ribosomal subunit protein bS18m

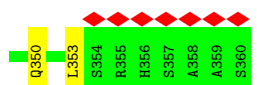
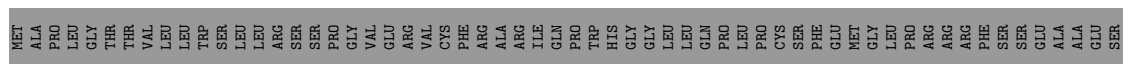




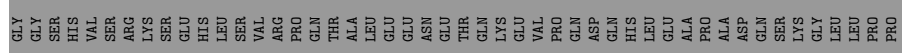
• Molecule 68: Small ribosomal subunit protein bS21m



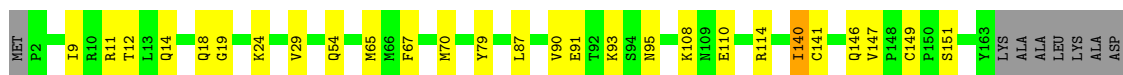
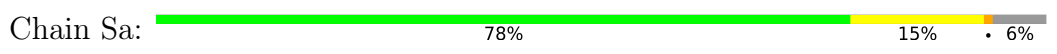
• Molecule 69: Small ribosomal subunit protein mS22



• Molecule 70: Small ribosomal subunit protein mS23

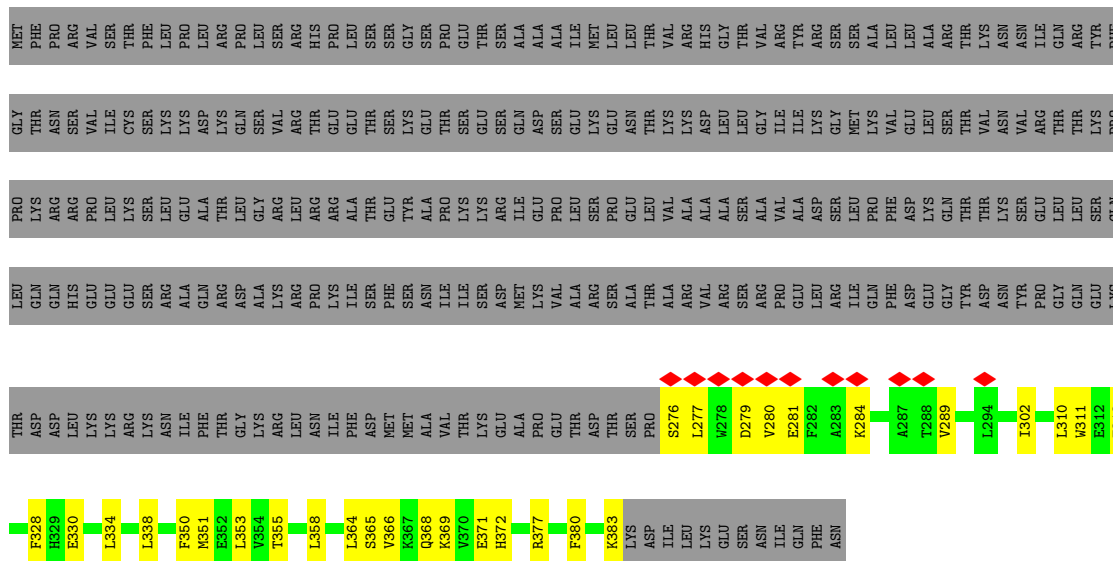


• Molecule 71: Small ribosomal subunit protein mS25

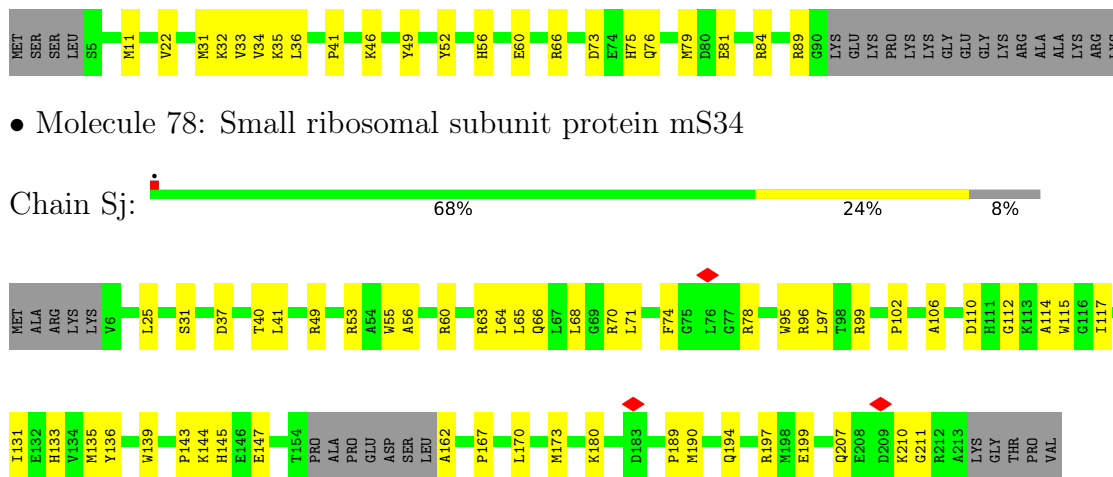




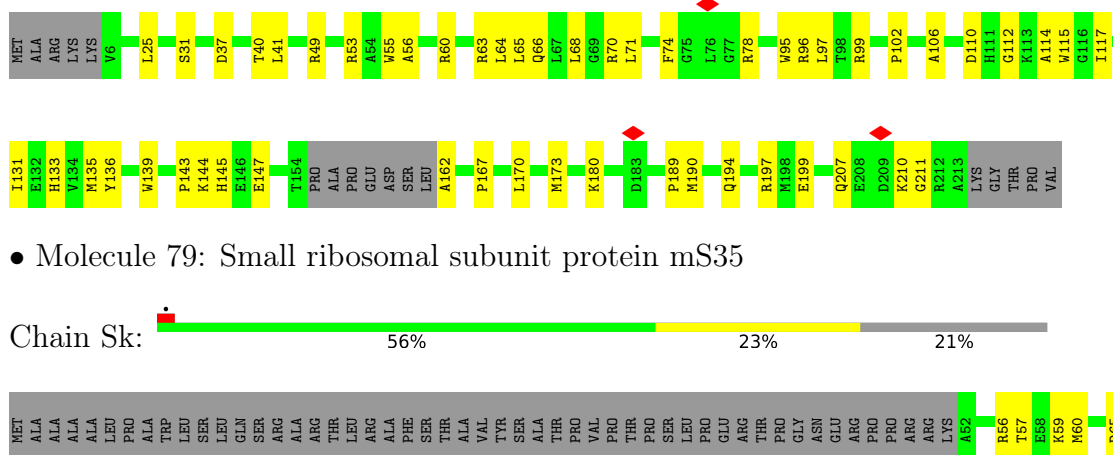
• Molecule 76: Small ribosomal subunit protein mS31



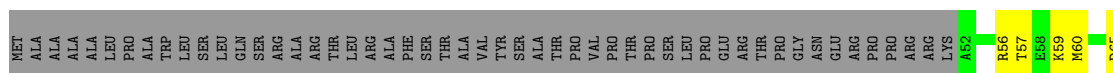
• Molecule 77: Small ribosomal subunit protein mS33

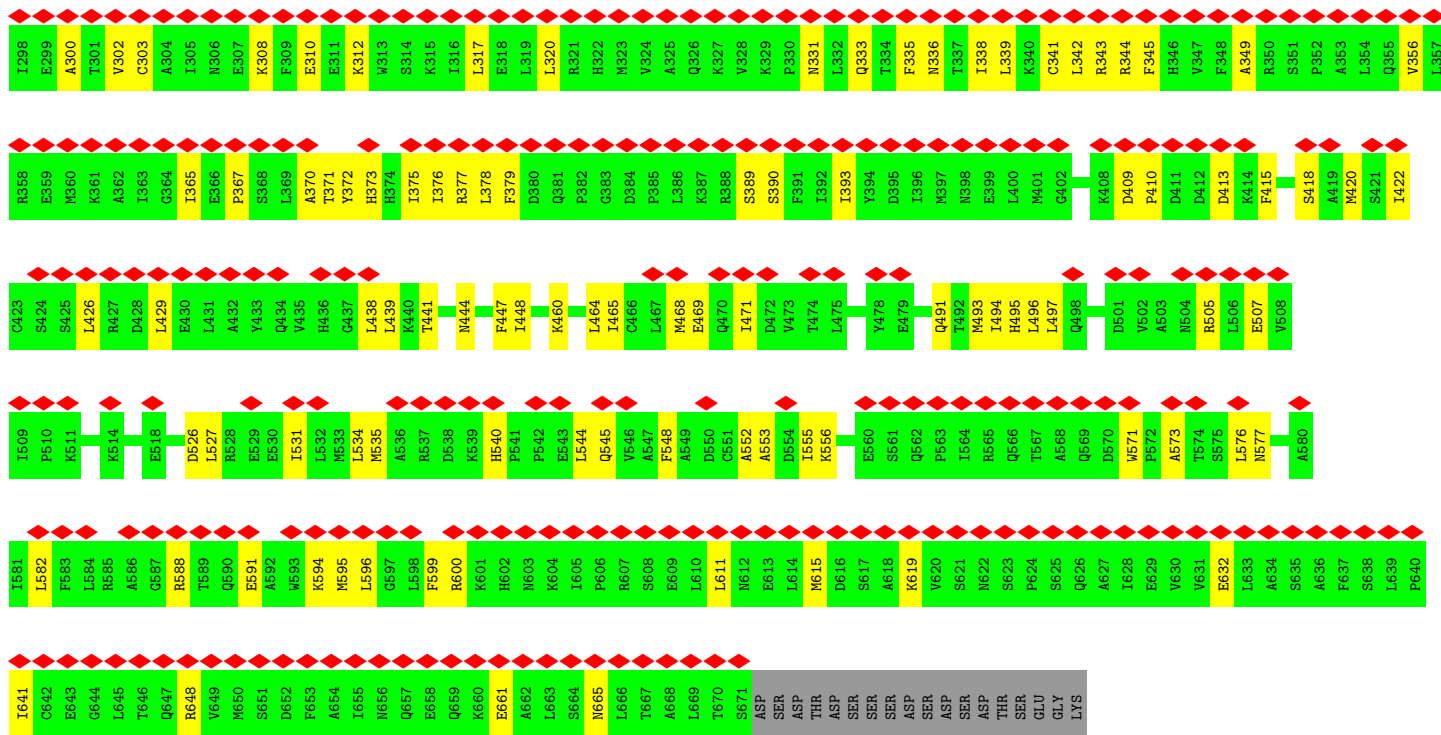


• Molecule 78: Small ribosomal subunit protein mS34

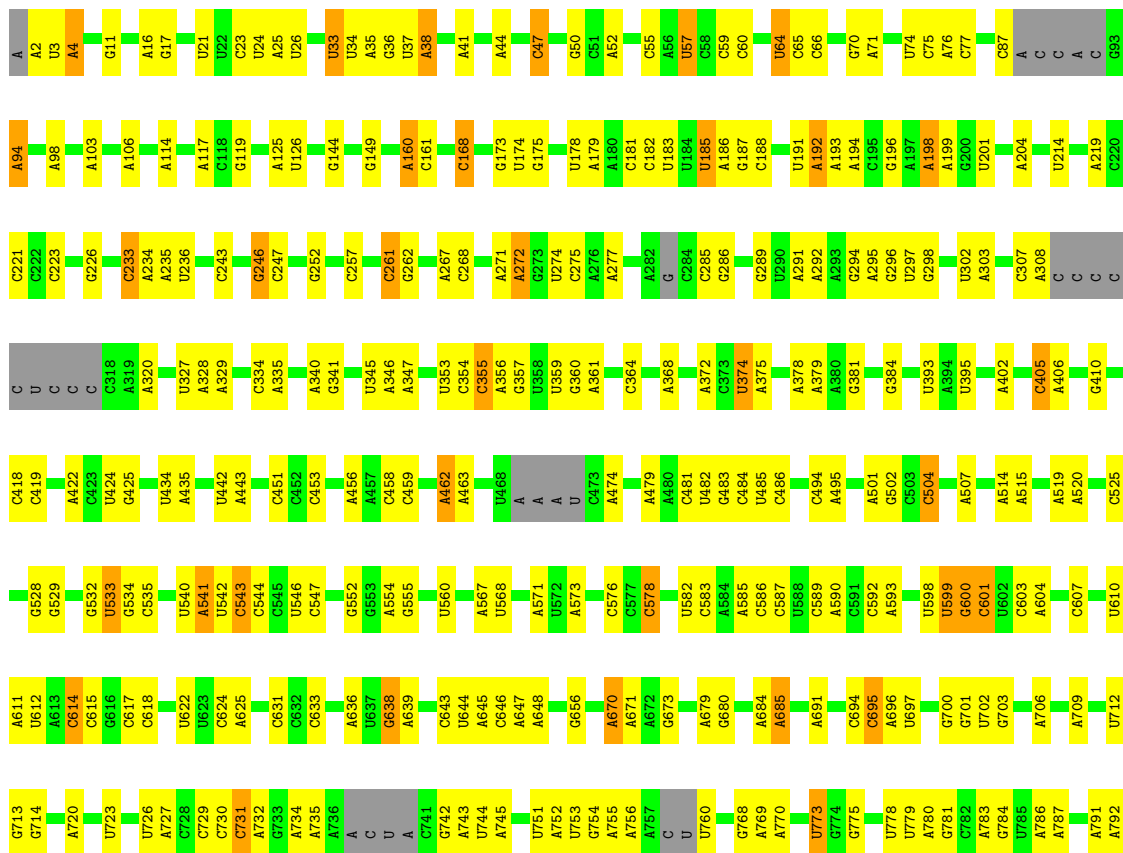


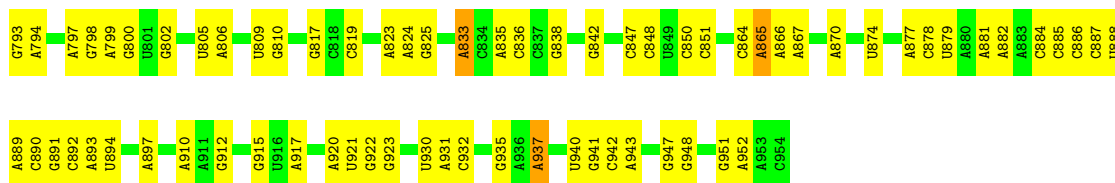
• Molecule 79: Small ribosomal subunit protein mS35





• Molecule 83: 12s rRNA





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	83274	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; Relion	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.065	Depositor
Minimum map value	-0.012	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	446.88, 446.88, 446.88	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.064, 1.064, 1.064	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: T1C, MG, GDP, 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	L1	0.29	0/35628	0.39	0/55448
2	L2	0.15	0/1328	0.30	0/2056
3	LB	0.27	0/1888	0.47	0/2538
4	LC	0.28	0/2462	0.54	1/3340 (0.0%)
5	LD	0.29	0/2071	0.59	0/2817
6	LI	0.28	0/798	0.66	1/1073 (0.1%)
7	LJ	0.33	0/1308	0.85	0/1761
8	LK	0.26	0/1340	0.50	0/1802
9	LM	0.29	0/1495	0.54	0/2029
10	LN	0.24	0/904	0.45	0/1218
11	LO	0.29	0/2359	0.50	0/3185
12	LP	0.27	0/1826	0.55	1/2458 (0.0%)
13	LQ	0.27	0/1269	0.50	0/1708
14	LR	0.27	0/1215	0.49	0/1645
15	LS	0.26	0/1863	0.54	1/2509 (0.0%)
16	LT	0.32	0/1174	0.50	0/1572
17	LU	0.32	0/1311	0.57	0/1778
18	LV	0.28	0/1402	0.48	1/1886 (0.1%)
19	LW	0.28	0/1217	0.49	0/1644
20	LX	0.24	0/1697	0.56	0/2302
21	La	0.29	0/893	0.47	0/1204
22	Lb	0.22	0/2090	0.45	1/2825 (0.0%)
23	Lu	0.28	0/1552	0.53	0/2079
24	Ld	0.28	0/1003	0.51	0/1354
25	Lf	0.24	0/895	0.42	0/1201
26	Lg	0.25	0/438	0.60	0/583
27	Lh	0.32	0/382	0.45	0/507
28	Li	0.29	0/852	0.45	0/1136
29	Lj	0.26	0/349	0.47	0/461
30	Lk	0.23	0/3305	0.48	0/4502
31	Ll	0.25	0/3042	0.54	0/4140
32	Lm	0.23	0/2439	0.53	2/3299 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Ln	0.26	0/855	0.59	0/1152
34	Lo	0.24	0/1025	0.48	0/1379
35	Lp	0.26	0/839	0.47	0/1136
36	Lq	0.29	0/1202	0.54	0/1626
37	Lr	0.25	0/2264	0.55	0/3059
38	Ls	0.24	0/1800	0.57	3/2436 (0.1%)
39	Lt	0.24	0/1797	0.57	0/2422
40	Lv	0.25	0/1051	0.66	2/1422 (0.1%)
41	Lw	0.29	0/1134	0.61	1/1547 (0.1%)
42	Lx	0.25	0/918	0.54	0/1249
43	Ly	0.31	0/849	0.47	0/1135
44	Lz	0.26	0/747	0.64	0/1005
45	L3	0.24	0/754	0.63	0/1017
46	L4	0.27	0/722	0.76	0/978
47	L5	0.25	0/379	0.67	0/510
48	L6	0.29	0/818	0.47	0/1097
49	L7	0.31	0/1071	0.65	1/1433 (0.1%)
50	L8	0.25	0/1107	0.52	0/1498
51	SR	0.26	0/1238	0.52	0/1676
52	Sf	0.25	0/3114	0.50	0/4225
53	SB	0.30	0/1811	0.67	1/2451 (0.0%)
54	SZ	0.29	0/1112	0.65	0/1505
55	SE	0.25	0/2590	0.56	1/3477 (0.0%)
56	SF	0.24	0/989	0.54	0/1335
57	SG	0.22	0/1708	0.53	1/2291 (0.0%)
58	SI	0.22	0/2555	0.54	2/3424 (0.1%)
59	SJ	0.33	0/1019	0.77	1/1379 (0.1%)
60	SK	0.24	0/1031	0.52	0/1390
61	SL	0.27	0/854	0.66	1/1148 (0.1%)
62	SN	0.29	0/879	0.63	0/1182
63	SO	0.26	0/1406	0.56	0/1878
64	SP	0.27	0/941	0.64	0/1265
65	SQ	0.20	0/864	0.44	0/1169
66	SS	0.21	0/1580	0.53	0/2150
67	ST	0.29	0/791	0.66	2/1062 (0.2%)
68	SW	0.31	0/752	0.58	1/1001 (0.1%)
69	SX	0.26	0/2452	0.55	0/3310
70	SY	0.26	0/1069	0.60	0/1441
71	Sa	0.21	0/1361	0.53	1/1829 (0.1%)
72	Sb	0.20	0/1474	0.47	0/1976
73	Sc	0.20	0/3177	0.46	1/4292 (0.0%)
74	Sd	0.27	0/778	0.69	0/1048
75	Se	0.18	0/2908	0.48	0/3936

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Sg	0.23	0/931	0.62	0/1259
77	Si	0.23	0/748	0.62	0/1000
78	Sj	0.22	0/1723	0.60	0/2334
79	Sk	0.32	0/2113	0.74	0/2863
80	Sm	0.31	0/939	0.68	5/1256 (0.4%)
81	Sn	0.26	0/621	0.53	0/820
82	So	0.22	0/5093	0.51	0/6891
83	S1	0.19	0/22053	0.35	0/34324
All	All	0.26	0/173801	0.49	32/246748 (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
7	LJ	0	1
8	LK	0	1
11	LO	0	1
13	LQ	0	1
18	LV	0	1
31	Ll	0	1
39	Lt	0	1
46	L4	0	1
47	L5	0	1
49	L7	0	1
55	SE	0	1
59	SJ	0	1
79	Sk	0	1
All	All	0	13

There are no bond length outliers.

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	L7	75	ARG	CG-CD-NE	-7.84	94.75	112.00
71	Sa	140	ILE	N-CA-C	-6.89	105.81	112.29
6	LI	142	GLU	N-CA-CB	6.73	120.67	110.30
57	SG	66	ARG	CB-CG-CD	6.56	126.39	111.30
32	Lm	246	GLN	CA-C-N	-6.53	112.53	121.61
32	Lm	246	GLN	C-N-CA	-6.53	112.53	121.61
80	Sm	55	CYS	CA-CB-SG	6.29	128.85	114.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	Lw	42	VAL	N-CA-C	-6.19	107.46	113.53
40	Lv	126	ALA	CA-C-N	6.12	131.37	121.83
40	Lv	126	ALA	C-N-CA	6.12	131.37	121.83
38	Ls	172	MET	N-CA-C	-5.96	107.24	114.75
38	Ls	119	GLN	N-CA-CB	5.92	119.46	110.28
53	SB	262	GLU	N-CA-CB	5.80	119.23	110.30
4	LC	84	PRO	CA-N-CD	-5.76	103.93	112.00
15	LS	211	PRO	CA-N-CD	-5.56	104.21	112.00
55	SE	147	PRO	CA-N-CD	-5.51	104.29	112.00
80	Sm	65	ALA	CA-C-N	-5.51	114.94	122.87
80	Sm	65	ALA	C-N-CA	-5.51	114.94	122.87
61	SL	130	TYR	CB-CA-C	-5.43	110.33	116.63
12	LP	172	VAL	N-CA-CB	-5.29	104.36	110.55
59	SJ	174	LYS	CB-CG-CD	5.29	123.47	111.30
80	Sm	53	MET	CB-CG-SD	-5.29	96.83	112.70
68	SW	13	MET	CB-CG-SD	-5.24	96.99	112.70
73	Sc	405	GLN	N-CA-CB	5.24	118.36	110.30
67	ST	84	VAL	CA-C-N	5.20	127.61	120.39
67	ST	84	VAL	C-N-CA	5.20	127.61	120.39
18	LV	161	ARG	CB-CA-C	-5.15	110.61	116.54
22	Lb	55	LYS	N-CA-C	-5.13	106.97	113.43
80	Sm	55	CYS	CB-CA-C	-5.10	102.88	110.88
38	Ls	119	GLN	CA-CB-CG	5.04	124.18	114.10
58	SI	314	MET	CA-C-N	5.00	129.47	121.62
58	SI	314	MET	C-N-CA	5.00	129.47	121.62

There are no chirality outliers.

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
46	L4	106	THR	Peptide
47	L5	74	MET	Peptide
49	L7	189	ARG	Sidechain
7	LJ	163	GLU	Peptide
8	LK	60	ILE	Peptide
11	LO	39	ARG	Sidechain
13	LQ	110	ILE	Peptide
18	LV	129	VAL	Peptide
31	Ll	310	THR	Peptide
39	Lt	269	LEU	Peptide
55	SE	184	LYS	Peptide
59	SJ	169	ALA	Peptide

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Mol	Chain	Res	Type	Group
79	Sk	260	ARG	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L1	31847	0	16178	215	0
2	L2	1191	0	607	11	0
3	LB	1851	0	1909	18	0
4	LC	2393	0	2398	28	0
5	LD	2013	0	2044	43	0
6	LI	784	0	832	18	0
7	LJ	1283	0	1370	42	0
8	LK	1323	0	1400	16	0
9	LM	1451	0	1448	18	0
10	LN	889	0	941	16	0
11	LO	2305	0	2378	34	0
12	LP	1779	0	1808	24	0
13	LQ	1245	0	1283	12	0
14	LR	1189	0	1180	18	0
15	LS	1822	0	1859	15	0
16	LT	1153	0	1214	10	0
17	LU	1284	0	1354	18	0
18	LV	1368	0	1410	16	0
19	LW	1188	0	1180	28	0
20	LX	1652	0	1658	27	0
21	La	871	0	898	15	0
22	Lb	2035	0	2054	15	0
23	Lu	1517	0	1561	28	0
24	Ld	978	0	1030	13	0
25	Lf	880	0	902	8	0
26	Lg	433	0	475	11	0
27	Lh	376	0	406	3	0
28	Li	831	0	883	13	0
29	Lj	341	0	361	7	0
30	Lk	3210	0	3206	40	0
31	Ll	2947	0	2841	58	0
32	Lm	2382	0	2393	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	Ln	836	0	844	17	0
34	Lo	997	0	987	19	0
35	Lp	815	0	792	10	0
36	Lq	1178	0	1180	24	0
37	Lr	2217	0	2220	24	0
38	Ls	1754	0	1732	35	0
39	Lt	1762	0	1767	49	0
40	Lv	1035	0	1040	26	0
41	Lw	1097	0	1085	16	0
42	Lx	895	0	881	12	0
43	Ly	827	0	857	12	0
44	Lz	732	0	730	7	0
45	L3	743	0	758	18	0
46	L4	703	0	693	15	0
47	L5	372	0	387	14	0
48	L6	797	0	804	13	0
49	L7	1058	0	1083	17	0
50	L8	1076	0	1049	14	0
51	SR	1203	0	1219	22	0
52	Sf	3036	0	3022	29	0
53	SB	1768	0	1765	35	0
54	SZ	1082	0	1088	36	0
55	SE	2540	0	2574	39	0
56	SF	972	0	1001	17	0
57	SG	1668	0	1716	25	0
58	SI	2501	0	2486	48	0
59	SJ	999	0	1024	51	0
60	SK	1011	0	1052	14	0
61	SL	838	0	887	11	0
62	SN	861	0	885	40	0
63	SO	1382	0	1472	25	0
64	SP	920	0	951	32	0
65	SQ	846	0	908	16	0
66	SS	1528	0	1488	37	0
67	ST	774	0	801	15	0
68	SW	740	0	754	13	0
69	SX	2405	0	2425	42	0
70	SY	1042	0	1037	17	0
71	Sa	1330	0	1342	20	0
72	Sb	1454	0	1464	26	0
73	Sc	3116	0	3069	45	0
74	Sd	766	0	785	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
75	Se	2836	0	2828	44	0
76	Sg	903	0	843	26	0
77	Si	731	0	734	20	0
78	Sj	1680	0	1674	46	0
79	Sk	2068	0	2087	76	0
80	Sm	925	0	962	9	0
81	Sn	610	0	682	11	0
82	So	4981	0	4959	89	0
83	S1	19716	0	10015	173	0
84	L1	104	0	0	0	0
84	L6	1	0	0	0	0
84	LB	3	0	0	0	0
84	LC	1	0	0	0	0
84	LP	1	0	0	0	0
84	La	1	0	0	0	0
84	Lw	1	0	0	0	0
84	S1	33	0	0	0	0
85	L1	84	0	76	2	0
85	S1	42	0	38	0	0
86	Lf	1	0	0	0	0
86	Lj	1	0	0	0	0
86	SB	1	0	0	0	0
86	SR	1	0	0	0	0
86	SS	1	0	0	0	0
86	ST	1	0	0	0	0
86	Sa	1	0	0	0	0
87	Se	28	0	12	0	0
All	All	165243	0	140475	1948	0

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

All (1948) 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)
36:Lq:75:VAL:O	36:Lq:86:GLU:HA	1.34	1.24
9:LM:81:THR:O	9:LM:86:GLY:HA3	1.52	1.10
83:S1:77:C:N4	83:S1:103:A:H61	1.50	1.09
83:S1:77:C:H42	83:S1:103:A:N6	1.50	1.07
31:L1:179:VAL:O	31:L1:183:ASP:HB2	1.62	0.99
71:Sa:14:GLN:O	71:Sa:18:GLN:HB2	1.67	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:Lj:76:CYS:SG	29:Lj:98:HIS:CE1	2.65	0.90
82:So:531:ILE:O	82:So:535:MET:HB2	1.71	0.89
67:ST:65:CYS:SG	67:ST:68:CYS:HB2	2.14	0.88
30:Lk:313:MET:HE1	30:Lk:353:HIS:HB2	1.62	0.81
52:Sf:362:THR:HG22	52:Sf:364:GLY:H	1.43	0.81
73:Sc:360:VAL:O	73:Sc:364:LEU:HB2	1.80	0.80
79:Sk:56:ARG:O	79:Sk:60:MET:HB2	1.82	0.80
31:Ll:237:LEU:HB3	31:Ll:240:ILE:HD11	1.65	0.78
47:L5:51:LEU:HB3	47:L5:67:ARG:HB3	1.64	0.77
54:SZ:73:THR:OG1	59:SJ:170:MET:SD	2.43	0.76
82:So:393:ILE:HG13	82:So:422:ILE:HG21	1.64	0.76
1:L1:523:U:C2	1:L1:525:A:N7	2.54	0.74
38:Ls:288:LYS:HD2	38:Ls:289:PRO:HD2	1.68	0.74
40:Lv:127:MET:HB3	40:Lv:154:GLU:HB3	1.68	0.74
28:Li:107:VAL:HG21	28:Li:161:MET:HE2	1.69	0.74
72:Sb:52:GLU:O	72:Sb:56:LEU:HB2	1.87	0.74
36:Lq:28:ARG:HH12	37:Lr:177:GLN:HE22	1.35	0.73
53:SB:142:ILE:HA	53:SB:192:LEU:O	1.89	0.73
20:LX:122:LEU:HD23	20:LX:133:ILE:HG13	1.71	0.72
32:Lm:279:GLU:HG2	32:Lm:317:LEU:HD11	1.72	0.72
82:So:619:LYS:HG3	82:So:648:ARG:HH21	1.54	0.72
57:SG:99:MET:HE1	83:S1:810:G:H4'	1.71	0.72
19:LW:129:MET:HG3	38:Ls:82:ALA:HB2	1.70	0.72
7:LJ:119:HIS:HB3	7:LJ:160:LYS:HE3	1.71	0.71
26:Lg:19:ARG:HH12	26:Lg:60:LYS:HE3	1.55	0.71
1:L1:141:A:H4'	18:LV:50:LYS:HD3	1.73	0.71
75:Se:153:LEU:HB3	75:Se:260:VAL:HG12	1.72	0.71
76:Sg:334:LEU:O	76:Sg:338:LEU:HB2	1.90	0.71
1:L1:1343:G:HO2'	29:Lj:66:PHE:N	1.87	0.71
72:Sb:68:ARG:HD2	72:Sb:71:ARG:HH21	1.54	0.71
79:Sk:298:SER:O	79:Sk:302:GLU:HB3	1.91	0.71
54:SZ:76:LEU:HD22	59:SJ:170:MET:HE1	1.72	0.71
39:Lt:128:PHE:HA	47:L5:74:MET:HE1	1.72	0.71
49:L7:102:ARG:NH2	49:L7:132:GLU:OE2	2.24	0.70
39:Lt:177:GLU:O	39:Lt:190:ARG:NH2	2.23	0.70
78:Sj:96:ARG:HB2	78:Sj:117:ILE:HB	1.74	0.70
36:Lq:75:VAL:O	36:Lq:86:GLU:CA	2.28	0.70
7:LJ:113:ARG:HD3	7:LJ:123:MET:HE2	1.71	0.70
5:LD:201:GLN:NE2	5:LD:205:GLU:OE2	2.25	0.70
40:Lv:117:LEU:HD23	40:Lv:166:PHE:HZ	1.55	0.70
42:Lx:73:TYR:OH	42:Lx:107:ASP:OD2	2.09	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:Lv:95:LEU:HD21	40:Lv:106:TYR:HB3	1.73	0.69
83:S1:836:C:N3	83:S1:920:A:N1	2.39	0.69
27:Lh:58:ILE:HD11	34:Lo:27:PRO:HG3	1.74	0.69
59:SJ:83:HIS:H	59:SJ:168:VAL:HG23	1.56	0.69
76:Sg:338:LEU:HD11	76:Sg:351:MET:HB3	1.72	0.69
1:L1:523:U:O2	1:L1:525:A:N7	2.26	0.69
7:LJ:160:LYS:HE2	7:LJ:163:GLU:HG2	1.74	0.69
28:Li:146:GLU:OE2	31:Ll:364:ARG:NH1	2.26	0.69
38:Ls:198:ARG:NH1	38:Ls:199:CYS:O	2.26	0.69
52:Sf:204:CYS:SG	52:Sf:240:GLN:NE2	2.66	0.69
75:Se:67:HIS:HB3	75:Se:98:CYS:HB3	1.73	0.69
1:L1:475:G:N3	17:LU:104:ARG:NH2	2.36	0.69
64:SP:102:MET:HE3	64:SP:106:ASN:HD21	1.58	0.68
60:SK:129:GLN:HE22	80:Sm:47:THR:HG22	1.58	0.68
79:Sk:56:ARG:HA	79:Sk:59:LYS:HB3	1.76	0.68
76:Sg:289:VAL:HG11	82:So:410:PRO:HB3	1.74	0.68
20:LX:77:VAL:HG21	38:Ls:77:HIS:HE1	1.59	0.68
58:SI:314:MET:HE1	75:Se:382:PHE:HB3	1.74	0.68
50:L8:49:ARG:HA	50:L8:52:LEU:HG	1.75	0.68
82:So:420:MET:HE1	82:So:460:LYS:HB2	1.74	0.68
1:L1:1356:U:H5'	29:Lj:68:ASN:HD21	1.58	0.67
37:Lr:94:ASN:OD1	37:Lr:122:ASN:ND2	2.26	0.67
60:SK:182:PRO:O	68:SW:42:ARG:NH1	2.27	0.67
79:Sk:68:SER:HA	82:So:78:VAL:HG23	1.76	0.67
83:S1:77:C:N3	83:S1:103:A:N1	2.41	0.67
1:L1:438:G:N7	12:LP:67:LYS:NZ	2.43	0.67
54:SZ:84:GLU:HA	54:SZ:87:VAL:HG22	1.75	0.67
53:SB:142:ILE:N	53:SB:164:GLU:OE2	2.20	0.67
68:SW:57:TYR:OH	83:S1:951:G:OP1	2.13	0.67
1:L1:488:U:OP1	51:SR:182:ARG:NH2	2.29	0.66
1:L1:973:G:O2'	1:L1:975:G:OP2	2.13	0.66
58:SI:103:ASP:OD1	58:SI:106:ARG:NH1	2.28	0.66
73:Sc:210:LEU:HB2	78:Sj:145:HIS:HE2	1.59	0.66
82:So:336:ASN:ND2	82:So:409:ASP:OD2	2.27	0.66
45:L3:11:ARG:HH21	45:L3:46:ASN:HB2	1.61	0.66
79:Sk:174:ARG:HA	79:Sk:205:LEU:O	1.96	0.66
76:Sg:276:SER:N	76:Sg:279:ASP:OD2	2.29	0.66
58:SI:136:ARG:HH21	58:SI:156:GLN:HE21	1.44	0.66
31:Ll:183:ASP:OD1	49:L7:192:ARG:NH2	2.28	0.66
81:Sn:162:LEU:HD12	81:Sn:195:TYR:HB3	1.78	0.66
80:Sm:109:GLN:NE2	83:S1:644:U:O2	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:SQ:95:VAL:HG22	71:Sa:87:LEU:HD21	1.78	0.65
20:LX:126:MET:SD	20:LX:152:ARG:NH1	2.70	0.65
21:La:100:THR:HG1	21:La:132:HIS:HE2	1.44	0.65
57:SG:114:THR:HG21	57:SG:205:LEU:HD22	1.76	0.65
59:SJ:75:ARG:HA	59:SJ:145:LEU:O	1.97	0.65
70:SY:70:ILE:HD11	70:SY:100:VAL:HG23	1.78	0.65
59:SJ:76:LEU:HD13	59:SJ:175:THR:HG22	1.79	0.65
73:Sc:225:LEU:HB3	73:Sc:283:LEU:HD11	1.78	0.65
10:LN:45:ALA:O	10:LN:49:SER:HB2	1.98	0.64
12:LP:117:ASN:HB2	12:LP:166:ARG:HB2	1.79	0.64
17:LU:175:ARG:HB2	17:LU:180:PHE:HB3	1.80	0.64
31:Ll:173:LEU:HD13	31:Ll:272:LEU:HD22	1.78	0.64
19:LW:27:GLN:HG2	23:Lu:113:LEU:HB3	1.80	0.64
37:Lr:160:LEU:HD21	37:Lr:223:MET:HB3	1.79	0.64
59:SJ:109:HIS:HB3	59:SJ:142:CYS:HB3	1.80	0.64
79:Sk:57:THR:HG23	79:Sk:82:PRO:HA	1.78	0.64
83:S1:817:G:H21	83:S1:819:C:H42	1.46	0.64
1:L1:875:U:H5''	1:L1:876:G:H5'	1.78	0.64
83:S1:57:U:OP1	83:S1:198:A:N6	2.31	0.64
4:LC:129:VAL:HB	4:LC:191:THR:HG22	1.80	0.64
18:LV:126:ASP:OD1	18:LV:130:ARG:NH1	2.30	0.64
69:SX:223:ARG:HG2	69:SX:226:ASP:HB3	1.80	0.64
79:Sk:183:ASP:HB3	79:Sk:187:LYS:HB3	1.80	0.64
7:LJ:48:MET:SD	12:LP:250:ARG:NH1	2.71	0.63
39:Lt:266:PRO:O	39:Lt:270:ALA:N	2.31	0.63
59:SJ:157:LEU:HD11	59:SJ:173:THR:HG21	1.80	0.63
60:SK:158:ARG:NH2	60:SK:177:ASP:OD2	2.31	0.63
1:L1:725:A:H4'	30:Lk:350:ARG:HH12	1.63	0.63
76:Sg:338:LEU:O	76:Sg:377:ARG:NH2	2.31	0.63
5:LD:94:ASP:OD1	48:L6:91:GLN:NE2	2.32	0.63
14:LR:62:ARG:NH2	21:La:137:LYS:O	2.31	0.63
36:Lq:35:ARG:HG3	48:L6:101:TRP:HB2	1.81	0.63
52:Sf:319:GLN:HA	52:Sf:322:VAL:HB	1.80	0.63
64:SP:31:PHE:HZ	64:SP:53:SER:HB2	1.63	0.63
78:Sj:99:ARG:HB2	78:Sj:115:TRP:HB2	1.80	0.63
36:Lq:89:ILE:HA	36:Lq:92:LYS:HD3	1.81	0.63
45:L3:36:THR:HG21	45:L3:87:LEU:HD21	1.80	0.63
49:L7:188:LEU:O	49:L7:191:LYS:NZ	2.26	0.63
5:LD:164:MET:HE3	43:Ly:69:HIS:HE1	1.63	0.63
69:SX:253:ILE:O	69:SX:257:GLY:HA2	1.99	0.63
83:S1:583:C:N4	83:S1:799:A:O2'	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L1:263:C:OP1	30:Lk:395:ARG:NH1	2.32	0.62
1:L1:608:A:OP1	43:Ly:51:ARG:NH1	2.32	0.62
20:LX:102:MET:HG3	20:LX:104:TYR:H	1.62	0.62
31:Ll:187:VAL:HG13	31:Ll:319:PHE:HB3	1.81	0.62
59:SJ:165:PRO:HG3	79:Sk:111:PHE:HZ	1.64	0.62
56:SF:11:LYS:HB3	56:SF:13:MET:HE3	1.81	0.62
19:LW:28:LEU:H	23:Lu:114:THR:HG22	1.64	0.62
31:Ll:221:LEU:HA	31:Ll:231:GLU:HG2	1.79	0.62
66:SS:59:LEU:HD21	66:SS:121:LYS:HB3	1.80	0.62
17:LU:95:LEU:HD23	17:LU:138:ALA:HB2	1.81	0.62
36:Lq:27:GLN:HE21	36:Lq:80:LEU:HD23	1.62	0.62
75:Se:261:ALA:HA	75:Se:307:VAL:O	2.00	0.62
64:SP:113:LYS:HG2	64:SP:116:ARG:HH21	1.64	0.62
66:SS:215:ARG:HG3	66:SS:218:ARG:HH21	1.63	0.62
1:L1:1283:U:H5''	29:Lj:71:VAL:HG22	1.82	0.62
66:SS:92:LYS:NZ	83:S1:272:A:OP1	2.30	0.62
82:So:312:LYS:HD2	82:So:345:PHE:HZ	1.64	0.62
62:SN:28:HIS:N	83:S1:601:C:O2	2.33	0.62
69:SX:165:ILE:O	69:SX:170:ARG:NH1	2.33	0.62
29:Lj:76:CYS:SG	29:Lj:98:HIS:HE1	2.15	0.62
33:Ln:97:LYS:NZ	33:Ln:100:GLU:OE2	2.33	0.61
77:Si:66:ARG:NH1	77:Si:73:ASP:OD1	2.30	0.61
1:L1:394:A:OP1	21:La:101:LYS:NZ	2.33	0.61
23:Lu:93:LYS:HE2	34:Lo:70:LEU:HD11	1.82	0.61
37:Lr:259:ARG:HB2	37:Lr:271:PHE:HB2	1.82	0.61
58:SI:291:GLY:HA2	58:SI:326:HIS:O	1.98	0.61
64:SP:108:GLU:OE2	72:Sb:59:ARG:NH2	2.32	0.61
67:ST:67:LEU:HD21	67:ST:79:LEU:HD21	1.82	0.61
69:SX:258:LYS:HB3	69:SX:261:LEU:HB2	1.82	0.61
79:Sk:298:SER:O	79:Sk:301:ASN:O	2.18	0.61
82:So:556:LYS:HG3	82:So:571:TRP:HH2	1.64	0.61
6:LI:120:ARG:NH1	22:Lb:136:ASP:OD2	2.30	0.61
19:LW:46:MET:HE1	19:LW:72:VAL:HG13	1.82	0.61
59:SJ:173:THR:OG1	79:Sk:155:ASP:OD1	2.17	0.61
4:LC:217:GLY:HA2	4:LC:258:PRO:HB3	1.82	0.61
52:Sf:239:ASN:HB2	52:Sf:299:PHE:HB2	1.82	0.61
64:SP:59:ASN:HB3	64:SP:62:GLY:H	1.66	0.61
66:SS:124:GLU:HA	66:SS:127:VAL:HG12	1.81	0.61
73:Sc:120:ASP:OD1	73:Sc:154:LYS:NZ	2.34	0.61
75:Se:166:ARG:NH2	83:S1:734:A:O3'	2.34	0.61
40:Lv:94:HIS:ND1	40:Lv:154:GLU:OE2	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:L3:13:VAL:HA	45:L3:68:PHE:HA	1.82	0.61
59:SJ:92:GLU:HB2	59:SJ:141:ARG:HD3	1.82	0.61
49:L7:98:LYS:NZ	49:L7:100:GLU:OE2	2.33	0.61
55:SE:173:ILE:HD12	55:SE:176:ARG:HG3	1.83	0.61
46:L4:76:ASN:HD22	46:L4:82:GLN:H	1.49	0.61
75:Se:163:LYS:HG3	75:Se:164:ASN:HD22	1.66	0.61
20:LX:137:PHE:H	20:LX:143:ARG:HH11	1.49	0.61
55:SE:406:LEU:HD11	71:Sa:9:ILE:HG13	1.82	0.61
65:SQ:29:ARG:HD3	65:SQ:46:ARG:HD2	1.82	0.61
40:Lv:80:ILE:HG22	40:Lv:89:GLY:HA2	1.82	0.60
52:Sf:113:VAL:HG21	52:Sf:257:VAL:HG11	1.82	0.60
63:SO:167:LEU:HD11	63:SO:187:ILE:HD12	1.82	0.60
66:SS:113:LEU:HD12	66:SS:122:LEU:HD11	1.81	0.60
72:Sb:41:ARG:O	78:Sj:49:ARG:NH2	2.34	0.60
72:Sb:135:GLN:O	72:Sb:139:GLN:NE2	2.34	0.60
1:L1:37:C:O2	30:Lk:80:ARG:NH2	2.34	0.60
1:L1:216:G:H1	43:Ly:61:GLY:HA3	1.64	0.60
11:LO:180:ASP:OD1	11:LO:180:ASP:N	2.33	0.60
1:L1:426:U:O4	11:LO:57:ARG:NH1	2.34	0.60
39:Lt:203:LYS:HE3	39:Lt:239:LEU:HD11	1.83	0.60
75:Se:324:LEU:HD13	79:Sk:304:GLU:HB2	1.83	0.60
15:LS:182:ARG:HE	15:LS:218:ASN:HB3	1.67	0.60
32:Lm:112:PRO:HB2	32:Lm:267:PRO:HG3	1.84	0.60
79:Sk:123:CYS:HA	79:Sk:126:LEU:HB2	1.83	0.60
1:L1:67:A:H4'	43:Ly:97:MET:HE2	1.83	0.60
1:L1:745:C:H3'	52:Sf:165:ARG:HH22	1.66	0.60
4:LC:129:VAL:O	4:LC:190:GLY:N	2.35	0.60
7:LJ:62:PRO:HA	7:LJ:65:LEU:HB2	1.83	0.60
32:Lm:148:MET:HE2	32:Lm:262:ASP:HB3	1.83	0.60
74:Sd:162:VAL:HG12	74:Sd:164:GLU:HB3	1.82	0.60
82:So:259:TYR:HB3	82:So:282:LEU:HD12	1.83	0.60
1:L1:75:U:O4	28:Li:108:LYS:NZ	2.35	0.60
73:Sc:70:LEU:HD11	73:Sc:389:LEU:HB3	1.83	0.60
1:L1:433:A:HO2'	24:Ld:35:LYS:N	1.99	0.60
1:L1:704:A:N6	52:Sf:272:PRO:O	2.31	0.60
65:SQ:18:ILE:HD11	65:SQ:29:ARG:HB2	1.84	0.60
14:LR:38:VAL:HB	14:LR:41:GLU:HG3	1.83	0.60
30:Lk:201:ARG:HG2	30:Lk:232:THR:HG22	1.84	0.60
31:Ll:92:LEU:HD21	31:Ll:170:ARG:HB2	1.84	0.60
59:SJ:177:LEU:HG	59:SJ:179:GLN:HE22	1.67	0.60
1:L1:395:A:OP1	40:Lv:48:TYR:N	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:SR:79:HIS:HB3	51:SR:184:ASN:HA	1.84	0.60
62:SN:120:LEU:HB3	62:SN:123:ILE:HD13	1.83	0.60
1:L1:662:C:H42	1:L1:772:U:H3	1.50	0.59
38:Ls:157:HIS:O	38:Ls:161:HIS:ND1	2.34	0.59
39:Lt:138:THR:OG1	39:Lt:150:ASN:O	2.16	0.59
60:SK:147:ILE:HG13	60:SK:170:LEU:HD13	1.84	0.59
65:SQ:31:THR:OG1	71:Sa:65:MET:SD	2.60	0.59
83:S1:881:A:H2'	83:S1:882:A:H8	1.67	0.59
60:SK:152:LYS:HG3	60:SK:180:PRO:HD3	1.84	0.59
75:Se:74:ASP:O	75:Se:78:VAL:HB	2.02	0.59
4:LC:45:SER:O	32:Lm:307:ARG:NH2	2.35	0.59
78:Sj:99:ARG:O	78:Sj:114:ALA:HA	2.02	0.59
6:LI:115:LYS:O	6:LI:118:LEU:O	2.19	0.59
65:SQ:31:THR:HG22	65:SQ:46:ARG:HG2	1.84	0.59
83:S1:533:U:OP1	83:S1:923:G:N2	2.32	0.59
1:L1:629:U:H5''	1:L1:630:G:H5''	1.85	0.59
1:L1:991:U:OP2	4:LC:238:ARG:NH2	2.25	0.59
38:Ls:160:LEU:O	38:Ls:164:VAL:HB	2.02	0.59
40:Lv:122:GLU:N	40:Lv:158:GLN:O	2.36	0.59
54:SZ:113:ARG:HB2	59:SJ:166:GLU:HG2	1.85	0.59
8:LK:56:ARG:NH1	8:LK:80:ILE:O	2.35	0.59
76:Sg:277:LEU:HA	76:Sg:280:VAL:HG22	1.84	0.59
36:Lq:77:ALA:O	36:Lq:84:VAL:HA	2.02	0.59
64:SP:29:ARG:NH1	71:Sa:147:VAL:O	2.36	0.59
75:Se:312:GLN:NE2	75:Se:319:PRO:O	2.36	0.59
1:L1:507:U:N3	1:L1:510:A:OP2	2.33	0.59
9:LM:73:GLU:OE2	51:SR:149:ARG:NH2	2.32	0.59
66:SS:158:ARG:HG3	66:SS:163:LEU:HD23	1.84	0.59
69:SX:218:MET:HE1	69:SX:227:VAL:HG22	1.84	0.59
83:S1:805:U:H2'	83:S1:806:A:H8	1.67	0.59
1:L1:603:A:O2'	16:LT:16:ASP:OD2	2.21	0.59
3:LB:130:ARG:NH2	3:LB:131:TYR:O	2.36	0.59
54:SZ:123:VAL:HG11	54:SZ:155:LEU:HD13	1.85	0.59
59:SJ:75:ARG:NH2	79:Sk:150:GLU:OE1	2.35	0.59
62:SN:112:ARG:NH2	83:S1:618:C:OP1	2.30	0.59
66:SS:228:SER:OG	66:SS:229:GLY:N	2.35	0.59
31:L1:194:THR:HG23	49:L7:185:ARG:HH12	1.68	0.58
49:L7:110:TRP:CD1	49:L7:110:TRP:H	2.19	0.58
55:SE:260:LYS:NZ	83:S1:639:A:OP1	2.35	0.58
63:SO:91:ARG:NH1	63:SO:97:MET:SD	2.76	0.58
78:Sj:63:ARG:NH2	78:Sj:110:ASP:OD2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:S1:50:G:N2	83:S1:204:A:C6	2.69	0.58
1:L1:211:A:OP2	41:Lw:111:ARG:NH2	2.36	0.58
51:SR:37:GLU:O	51:SR:51:GLY:HA2	2.02	0.58
55:SE:179:TRP:HA	55:SE:182:LYS:HG2	1.84	0.58
50:L8:143:TRP:O	50:L8:147:GLN:NE2	2.36	0.58
22:Lb:111:GLU:HG2	22:Lb:126:THR:HG22	1.85	0.58
55:SE:366:LYS:HE2	55:SE:368:LEU:HB2	1.85	0.58
58:SI:353:CYS:SG	58:SI:354:SER:N	2.75	0.58
82:So:169:SER:HA	82:So:172:MET:HE2	1.85	0.58
45:L3:19:GLN:HA	45:L3:54:ASP:HB3	1.85	0.58
79:Sk:74:ALA:O	79:Sk:110:ASN:ND2	2.35	0.58
82:So:491:GLN:O	82:So:495:HIS:ND1	2.30	0.58
82:So:611:LEU:HD12	82:So:641:ILE:HD11	1.86	0.58
83:S1:592:C:H2'	83:S1:593:A:H8	1.68	0.58
7:LJ:188:ARG:HA	7:LJ:191:PHE:HD2	1.69	0.58
57:SG:190:GLU:HG3	57:SG:208:LYS:HZ3	1.69	0.58
1:L1:1054:G:OP1	5:LD:131:LYS:NZ	2.34	0.58
7:LJ:136:GLU:HA	7:LJ:141:GLN:HG2	1.86	0.58
30:Lk:146:HIS:O	30:Lk:194:LYS:NZ	2.35	0.58
65:SQ:67:ARG:NH1	65:SQ:80:GLU:OE2	2.36	0.58
70:SY:105:GLU:HA	70:SY:108:LYS:HG2	1.85	0.58
78:Sj:78:ARG:HH21	78:Sj:143:PRO:HA	1.68	0.58
79:Sk:59:LYS:NZ	82:So:83:THR:O	2.36	0.58
1:L1:750:U:H5''	34:Lo:36:ARG:HG2	1.84	0.58
15:LS:152:ARG:NH1	15:LS:161:GLU:OE2	2.36	0.58
40:Lv:131:THR:HG22	40:Lv:151:THR:HG22	1.86	0.58
54:SZ:111:LYS:HB2	54:SZ:118:GLU:HB2	1.86	0.58
54:SZ:162:VAL:HG11	79:Sk:97:MET:HE1	1.85	0.58
75:Se:50:ARG:HG2	75:Se:67:HIS:HB2	1.85	0.58
20:LX:64:ILE:O	20:LX:71:GLY:N	2.36	0.58
22:Lb:7:PRO:HD2	22:Lb:10:LEU:HD12	1.84	0.58
38:Ls:91:PRO:HG2	38:Ls:94:ASP:HB2	1.86	0.58
20:LX:76:VAL:HA	20:LX:88:VAL:HA	1.85	0.58
59:SJ:81:LYS:HB2	59:SJ:170:MET:HE2	1.85	0.58
59:SJ:149:THR:O	59:SJ:153:ALA:HB2	2.04	0.58
75:Se:123:ARG:HH21	75:Se:339:PRO:HD2	1.69	0.58
82:So:390:SER:HB3	82:So:426:LEU:HD11	1.86	0.58
7:LJ:101:ASN:HB3	7:LJ:150:HIS:HB3	1.84	0.57
20:LX:80:ILE:HB	20:LX:85:TRP:HB2	1.85	0.57
32:Lm:201:SER:HA	35:Lp:95:ARG:HH12	1.69	0.57
39:Lt:49:GLY:HA2	39:Lt:232:PHE:HB2	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:Sa:11:ARG:HH21	83:S1:285:C:H5	1.52	0.57
79:Sk:298:SER:O	79:Sk:301:ASN:C	2.47	0.57
1:L1:237:A:N3	1:L1:1260:U:O2'	2.36	0.57
1:L1:1074:U:O2'	1:L1:1076:U:O4	2.21	0.57
5:LD:195:LEU:HD22	5:LD:202:TYR:HE2	1.69	0.57
13:LQ:85:LEU:O	13:LQ:89:LEU:N	2.35	0.57
20:LX:170:TRP:HD1	34:Lo:77:LEU:HG	1.69	0.57
1:L1:551:C:O2'	1:L1:553:A:N6	2.37	0.57
16:LT:148:TYR:OH	17:LU:146:LYS:O	2.23	0.57
19:LW:81:ASP:HB3	19:LW:87:ILE:HD11	1.86	0.57
54:SZ:40:ALA:HB3	54:SZ:59:PRO:HD3	1.86	0.57
82:So:75:ALA:O	82:So:78:VAL:O	2.20	0.57
7:LJ:161:VAL:HA	7:LJ:164:MET:HE2	1.86	0.57
14:LR:53:ARG:NH1	31:Ll:155:TYR:OH	2.37	0.57
56:SF:35:ILE:HD11	63:SO:92:LEU:HD13	1.86	0.57
65:SQ:46:ARG:NH1	83:S1:302:U:O2'	2.38	0.57
83:S1:174:U:H2'	83:S1:175:G:H8	1.68	0.57
4:LC:56:GLU:O	13:LQ:153:ARG:NH2	2.37	0.57
57:SG:126:TYR:HB2	57:SG:139:ARG:HD3	1.87	0.57
58:SI:296:ASN:HD21	58:SI:332:VAL:H	1.53	0.57
82:So:471:ILE:HG21	82:So:505:ARG:HG3	1.85	0.57
1:L1:29:C:N4	23:Lu:171:ASP:OD1	2.37	0.57
17:LU:118:ASN:HD22	17:LU:118:ASN:C	2.11	0.57
72:Sb:135:GLN:HG3	72:Sb:139:GLN:HE22	1.70	0.57
78:Sj:65:LEU:HG	78:Sj:112:GLY:H	1.68	0.57
83:S1:442:U:H2'	83:S1:443:A:H8	1.69	0.57
7:LJ:97:ALA:HB3	7:LJ:154:LEU:HB2	1.87	0.57
56:SF:26:ILE:HD11	56:SF:39:LEU:HD12	1.85	0.57
61:SL:66:PHE:HE1	61:SL:82:ARG:HG3	1.70	0.57
66:SS:114:HIS:O	66:SS:119:ASN:ND2	2.37	0.57
67:ST:142:GLU:H	68:SW:28:ARG:HH21	1.53	0.57
1:L1:911:A:O2'	1:L1:912:A:N7	2.35	0.57
2:L2:8:U:O2	2:L2:15:A:N6	2.37	0.57
20:LX:76:VAL:HG12	20:LX:88:VAL:HG22	1.87	0.57
33:Ln:142:ALA:HB2	39:Lt:274:ARG:HG2	1.85	0.57
57:SG:174:LEU:O	57:SG:179:ARG:NH2	2.36	0.57
62:SN:112:ARG:O	62:SN:116:ASP:HB2	2.05	0.57
1:L1:39:G:H4'	23:Lu:192:LYS:HG2	1.86	0.57
18:LV:91:ALA:O	18:LV:94:ILE:O	2.23	0.57
31:Ll:233:LEU:HD11	31:Ll:236:LEU:HD22	1.86	0.57
47:L5:56:LEU:O	47:L5:63:THR:HA	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:Sf:212:ARG:HD3	52:Sf:379:LEU:HB3	1.86	0.57
75:Se:123:ARG:NH1	75:Se:297:MET:O	2.37	0.57
1:L1:77:G:OP2	1:L1:79:C:N4	2.37	0.56
1:L1:1202:C:O2'	21:La:88:CYS:SG	2.61	0.56
9:LM:25:MET:O	9:LM:149:ARG:NH1	2.37	0.56
42:Lx:85:ASN:ND2	42:Lx:88:ASP:OD2	2.38	0.56
58:SI:87:HIS:O	58:SI:91:MET:HB2	2.04	0.56
82:So:331:ASN:HD21	82:So:333:GLN:HE21	1.53	0.56
83:S1:578:C:HO2'	83:S1:802:G:HO2'	1.53	0.56
1:L1:1356:U:H5'	29:Lj:68:ASN:ND2	2.19	0.56
29:Lj:90:VAL:HB	29:Lj:100:GLN:HB2	1.86	0.56
32:Lm:285:ASN:HB3	32:Lm:293:LEU:HD11	1.87	0.56
48:L6:15:ARG:HB3	48:L6:18:ILE:HG12	1.87	0.56
66:SS:52:LYS:HE3	66:SS:58:TYR:HB2	1.87	0.56
77:Si:76:GLN:HA	77:Si:79:MET:HG2	1.86	0.56
78:Sj:71:LEU:HD13	78:Sj:78:ARG:HG2	1.87	0.56
79:Sk:65:ASP:O	79:Sk:68:SER:OG	2.19	0.56
82:So:438:LEU:O	82:So:444:ASN:ND2	2.35	0.56
12:LP:90:LEU:HD13	12:LP:159:LEU:HD23	1.86	0.56
31:Ll:161:LEU:HD22	31:Ll:300:THR:HG21	1.87	0.56
36:Lq:28:ARG:HH12	37:Lr:177:GLN:NE2	2.03	0.56
64:SP:59:ASN:OD1	64:SP:60:SER:N	2.38	0.56
69:SX:209:ILE:HD12	69:SX:214:ASN:HB3	1.87	0.56
70:SY:67:GLU:OE1	74:Sd:85:ARG:NH1	2.39	0.56
73:Sc:274:LYS:HB3	73:Sc:348:GLU:HB2	1.88	0.56
75:Se:166:ARG:HH22	83:S1:735:A:H5'	1.70	0.56
79:Sk:173:LEU:HD21	79:Sk:226:LEU:HD22	1.87	0.56
79:Sk:244:THR:HB	79:Sk:247:ASP:HB2	1.88	0.56
1:L1:385:U:H2'	1:L1:386:G:H8	1.70	0.56
12:LP:117:ASN:O	12:LP:166:ARG:N	2.38	0.56
37:Lr:60:ARG:HD2	37:Lr:63:LYS:HB2	1.87	0.56
53:SB:106:ILE:HD11	53:SB:114:ASP:HB3	1.87	0.56
53:SB:194:ILE:HG12	53:SB:220:VAL:HB	1.88	0.56
69:SX:276:VAL:HG12	69:SX:307:LEU:HD23	1.87	0.56
82:So:303:CYS:SG	82:So:344:ARG:NH1	2.79	0.56
1:L1:320:G:OP1	3:LB:269:ARG:NH1	2.29	0.56
11:LO:44:ARG:HG3	11:LO:45:ARG:HG3	1.87	0.56
17:LU:125:GLY:N	17:LU:160:VAL:O	2.39	0.56
26:Lg:55:LEU:HD13	50:L8:132:ILE:HD13	1.86	0.56
31:Ll:64:GLU:O	31:Ll:69:HIS:NE2	2.39	0.56
70:SY:70:ILE:HA	70:SY:73:LYS:HG2	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L1:787:A:N3	13:LQ:17:ARG:NH2	2.53	0.56
33:Ln:178:TYR:O	39:Lt:136:ARG:NH2	2.39	0.56
73:Sc:277:ARG:HE	73:Sc:349:SER:HB2	1.70	0.56
1:L1:802:A:OP1	10:LN:56:ARG:NH2	2.34	0.56
1:L1:1070:A:N3	1:L1:1251:A:O2'	2.35	0.56
1:L1:1134:A:H2'	1:L1:1135:A:H8	1.70	0.56
8:LK:149:ARG:HH22	46:L4:104:PRO:HD3	1.70	0.56
31:Ll:157:LEU:O	31:Ll:161:LEU:N	2.38	0.56
32:Lm:201:SER:HB3	35:Lp:95:ARG:HH22	1.69	0.56
53:SB:192:LEU:HD11	53:SB:220:VAL:HG23	1.87	0.56
79:Sk:122:HIS:HD2	82:So:77:THR:HG21	1.70	0.56
82:So:615:MET:O	82:So:648:ARG:NH2	2.39	0.56
83:S1:614:C:H2'	83:S1:615:C:H6	1.70	0.56
1:L1:867:G:O2'	1:L1:964:U:OP2	2.23	0.56
20:LX:64:ILE:HD11	20:LX:88:VAL:HG11	1.87	0.56
39:Lt:214:THR:HB	39:Lt:230:LYS:HD2	1.87	0.56
82:So:342:LEU:HA	82:So:345:PHE:HB2	1.88	0.56
1:L1:520:C:OP2	46:L4:120:ARG:NH1	2.39	0.56
9:LM:27:PRO:HG2	9:LM:30:LYS:HB2	1.88	0.56
21:La:100:THR:OG1	21:La:132:HIS:NE2	2.36	0.56
53:SB:135:MET:HE1	70:SY:31:TRP:HA	1.88	0.56
58:SI:382:PRO:HB2	59:SJ:131:ARG:HB2	1.88	0.56
63:SO:213:VAL:HG23	81:Sn:182:LEU:HD21	1.88	0.56
64:SP:20:ARG:HB2	83:S1:192:A:H5'	1.88	0.56
73:Sc:311:GLU:OE2	78:Sj:60:ARG:NH1	2.39	0.56
82:So:573:ALA:O	82:So:577:ASN:ND2	2.38	0.56
32:Lm:61:ARG:HH22	38:Ls:275:PRO:HD2	1.71	0.56
83:S1:753:U:O2'	83:S1:797:A:N3	2.39	0.56
1:L1:214:G:N3	1:L1:225:C:O2'	2.39	0.55
45:L3:46:ASN:ND2	45:L3:49:CYS:SG	2.80	0.55
83:S1:694:C:H5''	83:S1:695:C:H4'	1.87	0.55
83:S1:784:G:O2'	83:S1:810:G:O6	2.24	0.55
1:L1:38:A:OP2	23:Lu:192:LYS:NZ	2.39	0.55
1:L1:746:U:H4'	34:Lo:52:GLN:HB3	1.86	0.55
7:LJ:64:CYS:SG	51:SR:78:LYS:NZ	2.76	0.55
18:LV:54:LYS:O	38:Ls:227:ARG:NH2	2.39	0.55
18:LV:62:GLN:NE2	18:LV:67:PRO:O	2.39	0.55
57:SG:96:ASN:OD1	57:SG:104:LYS:NZ	2.38	0.55
74:Sd:172:ILE:HG22	74:Sd:173:GLN:HG2	1.88	0.55
3:LB:64:VAL:O	3:LB:80:ARG:NH2	2.39	0.55
5:LD:241:ASN:OD1	5:LD:256:HIS:NE2	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:Lw:37:ARG:HE	41:Lw:38:PHE:H	1.52	0.55
1:L1:122:G:N7	27:Lh:87:ARG:NH2	2.54	0.55
1:L1:1160:A:N6	1:L1:1167:A:OP2	2.37	0.55
6:LI:115:LYS:O	6:LI:118:LEU:C	2.49	0.55
39:Lt:69:GLU:O	39:Lt:72:SER:OG	2.24	0.55
46:L4:133:SER:HA	46:L4:136:LYS:HB2	1.89	0.55
55:SE:362:LEU:O	55:SE:366:LYS:HG2	2.07	0.55
75:Se:338:ASP:O	79:Sk:312:TYR:OH	2.24	0.55
4:LC:196:ALA:O	4:LC:199:ARG:NH1	2.39	0.55
11:LO:175:THR:HG21	11:LO:259:ARG:HH12	1.71	0.55
25:Lf:159:LEU:HB2	25:Lf:174:ILE:HD11	1.88	0.55
30:Lk:113:LEU:HD12	30:Lk:311:ALA:HB1	1.88	0.55
36:Lq:77:ALA:HB3	36:Lq:85:ARG:HB3	1.87	0.55
78:Sj:68:LEU:HD11	78:Sj:97:LEU:HD11	1.89	0.55
1:L1:829:U:OP2	1:L1:834:A:N6	2.30	0.55
34:Lo:91:LEU:O	34:Lo:95:ALA:HB3	2.07	0.55
19:LW:16:GLN:HG2	34:Lo:55:GLU:HA	1.87	0.55
20:LX:36:PRO:HD2	20:LX:39:ILE:HB	1.89	0.55
46:L4:93:PRO:HD2	46:L4:96:LEU:HD13	1.89	0.55
65:SQ:13:ILE:HD12	65:SQ:30:VAL:HG21	1.89	0.55
66:SS:192:THR:O	66:SS:195:SER:C	2.49	0.55
71:Sa:29:VAL:HB	71:Sa:79:TYR:HB2	1.89	0.55
73:Sc:322:THR:HG23	73:Sc:325:SER:H	1.72	0.55
75:Se:348:TYR:HB2	75:Se:386:ALA:HB1	1.89	0.55
76:Sg:302:ILE:HD12	82:So:68:VAL:HG13	1.88	0.55
13:LQ:113:ARG:HD3	13:LQ:120:MET:HE2	1.89	0.55
32:Lm:109:ASP:OD2	32:Lm:121:LYS:NZ	2.40	0.55
37:Lr:220:ILE:HA	37:Lr:223:MET:HG2	1.87	0.55
66:SS:185:SER:O	69:SX:183:LYS:NZ	2.39	0.55
82:So:75:ALA:O	82:So:78:VAL:C	2.50	0.55
83:S1:760:U:H1'	83:S1:798:G:H21	1.72	0.55
24:Ld:101:LYS:HE3	44:Lz:80:LEU:HD22	1.88	0.55
54:SZ:75:ASN:OD1	62:SN:104:TRP:NE1	2.38	0.55
74:Sd:155:GLY:HA3	80:Sm:28:ILE:HG23	1.88	0.55
11:LO:14:ASP:OD1	11:LO:17:ARG:NH1	2.40	0.55
39:Lt:273:ARG:HA	39:Lt:276:VAL:HG12	1.87	0.55
58:SI:123:PRO:HB3	79:Sk:87:MET:HE1	1.89	0.55
78:Sj:144:LYS:HA	78:Sj:147:GLU:HG2	1.89	0.55
1:L1:1184:U:H4'	28:Li:138:PRO:HG2	1.88	0.54
12:LP:89:ILE:HB	12:LP:161:VAL:HG22	1.89	0.54
23:Lu:83:ALA:HB3	34:Lo:74:VAL:HB	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:Ly:102:MET:HE1	43:Ly:110:LEU:HD22	1.88	0.54
55:SE:191:ARG:NH1	66:SS:80:ASN:OD1	2.40	0.54
62:SN:116:ASP:OD1	62:SN:125:ARG:NH1	2.40	0.54
64:SP:30:PRO:HD2	64:SP:57:LEU:HD21	1.88	0.54
79:Sk:243:LYS:HE3	79:Sk:247:ASP:HB3	1.88	0.54
22:Lb:72:PRO:O	22:Lb:75:SER:OG	2.20	0.54
55:SE:335:LYS:HE2	83:S1:2:A:H5''	1.88	0.54
35:Lp:67:ILE:HG13	36:Lq:138:THR:HG21	1.90	0.54
66:SS:217:ARG:HH12	73:Sc:318:ASP:HB2	1.71	0.54
74:Sd:110:ASN:C	74:Sd:110:ASN:HD22	2.14	0.54
82:So:429:LEU:HA	82:So:464:LEU:HD21	1.90	0.54
83:S1:356:A:H2'	83:S1:357:G:H8	1.72	0.54
4:LC:244:ALA:HB1	4:LC:248:ILE:HD11	1.88	0.54
14:LR:114:HIS:HD2	31:Ll:131:PRO:HD2	1.72	0.54
48:L6:56:ARG:HA	48:L6:59:GLU:HG2	1.90	0.54
59:SJ:111:PRO:HB2	59:SJ:140:TYR:HB2	1.89	0.54
1:L1:65:A:H5''	6:LI:69:ARG:HH22	1.72	0.54
59:SJ:161:GLN:HE22	76:Sg:314:PRO:HA	1.72	0.54
63:SO:115:ILE:HD11	63:SO:181:ILE:HA	1.90	0.54
63:SO:209:LEU:HD13	81:Sn:173:LEU:HD22	1.90	0.54
73:Sc:337:LEU:HA	73:Sc:340:LYS:HG2	1.89	0.54
83:S1:712:U:H2'	83:S1:713:G:H8	1.73	0.54
37:Lr:228:LEU:HB2	37:Lr:307:PHE:CD2	2.42	0.54
58:SI:136:ARG:NH1	58:SI:209:LEU:O	2.39	0.54
64:SP:111:ARG:NE	66:SS:235:MET:SD	2.80	0.54
75:Se:276:ARG:NH2	75:Se:286:GLU:OE1	2.39	0.54
79:Sk:253:TRP:HH2	79:Sk:261:ASN:HD22	1.55	0.54
1:L1:421:A:OP2	28:Li:152:LYS:NZ	2.41	0.54
4:LC:210:THR:HG22	4:LC:290:PRO:HB3	1.88	0.54
23:Lu:128:SER:OG	23:Lu:131:ARG:NE	2.28	0.54
64:SP:111:ARG:NH1	66:SS:232:PRO:O	2.41	0.54
69:SX:212:GLU:OE2	69:SX:248:LYS:NZ	2.41	0.54
1:L1:292:A:OP2	1:L1:831:C:N4	2.41	0.54
13:LQ:108:LEU:HD13	25:Lf:122:LEU:HD11	1.90	0.54
39:Lt:264:LEU:HD22	39:Lt:269:LEU:HB3	1.89	0.54
40:Lv:135:LEU:HG	40:Lv:145:LEU:HD22	1.90	0.54
55:SE:182:LYS:HA	55:SE:185:MET:SD	2.48	0.54
82:So:540:HIS:O	82:So:545:GLN:NE2	2.41	0.54
31:Ll:323:TRP:NE1	31:Ll:339:GLU:OE2	2.41	0.54
53:SB:157:ASN:OD1	53:SB:160:ARG:NH2	2.41	0.54
59:SJ:126:ILE:HG22	59:SJ:127:TYR:H	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:LJ:47:LEU:HD22	12:LP:226:ILE:HG12	1.89	0.53
7:LJ:104:LEU:HD23	7:LJ:109:LYS:HD3	1.90	0.53
12:LP:109:ILE:O	12:LP:113:MET:HB3	2.08	0.53
65:SQ:93:ASP:O	65:SQ:97:GLY:HA2	2.08	0.53
41:Lw:73:GLN:HB3	41:Lw:162:LEU:HD11	1.90	0.53
72:Sb:120:ARG:HG2	72:Sb:123:ARG:HH12	1.73	0.53
73:Sc:240:LEU:HA	73:Sc:243:VAL:HG22	1.91	0.53
1:L1:402:A:OP2	31:Ll:27:ARG:N	2.40	0.53
11:LO:30:ASN:O	11:LO:33:SER:OG	2.22	0.53
26:Lg:34:ARG:NH1	26:Lg:35:ASN:O	2.41	0.53
53:SB:148:ASN:HD21	53:SB:197:HIS:CD2	2.25	0.53
53:SB:180:ARG:HH21	55:SE:210:PRO:HG2	1.72	0.53
5:LD:184:GLN:HE22	11:LO:22:VAL:HG23	1.73	0.53
33:Ln:161:ALA:HB1	39:Lt:209:PRO:HD3	1.89	0.53
45:L3:16:VAL:HG12	45:L3:66:VAL:HG22	1.89	0.53
52:Sf:90:LYS:NZ	52:Sf:232:GLN:OE1	2.42	0.53
54:SZ:113:ARG:HE	54:SZ:116:GLN:HE21	1.56	0.53
1:L1:1209:A:O2'	26:Lg:53:ARG:NH1	2.38	0.53
11:LO:31:PRO:HG2	48:L6:86:ARG:HH12	1.72	0.53
26:Lg:40:LYS:HD2	26:Lg:58:GLU:CD	2.34	0.53
30:Lk:307:ASP:HA	30:Lk:310:ARG:HH21	1.73	0.53
38:Ls:200:SER:OG	38:Ls:204:ASN:OD1	2.26	0.53
73:Sc:166:GLU:OE2	73:Sc:170:GLN:NE2	2.40	0.53
79:Sk:71:PRO:HG3	82:So:78:VAL:HG21	1.89	0.53
1:L1:751:G:H5'	34:Lo:24:LYS:HG2	1.89	0.53
5:LD:277:ASP:O	41:Lw:90:ARG:NH1	2.41	0.53
20:LX:77:VAL:HG21	38:Ls:77:HIS:CE1	2.41	0.53
31:Ll:255:LEU:HD12	31:Ll:256:PRO:HD2	1.90	0.53
69:SX:224:HIS:HB2	69:SX:262:LEU:HD21	1.91	0.53
72:Sb:168:ILE:HG12	72:Sb:176:ARG:HG2	1.91	0.53
78:Sj:133:HIS:O	78:Sj:139:TRP:NE1	2.40	0.53
1:L1:1070:A:H2'	1:L1:1071:A:C8	2.44	0.53
3:LB:217:LEU:HD11	3:LB:227:GLN:HB2	1.91	0.53
6:LI:134:PRO:HA	6:LI:137:LYS:HG2	1.90	0.53
16:LT:85:ALA:O	16:LT:89:ASN:ND2	2.40	0.53
52:Sf:171:VAL:HG23	52:Sf:172:ILE:HG13	1.91	0.53
59:SJ:176:GLN:NE2	79:Sk:152:ASP:OD1	2.42	0.53
64:SP:42:PRO:HG3	83:S1:66:C:H5'	1.90	0.53
82:So:379:PHE:HB3	82:So:389:SER:HB2	1.90	0.53
1:L1:346:C:OP2	11:LO:59:ARG:NH1	2.42	0.53
21:La:54:LYS:NZ	21:La:69:THR:OG1	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Lq:78:GLU:HG2	36:Lq:84:VAL:HG22	1.91	0.53
54:SZ:61:TYR:HB3	54:SZ:65:ARG:HB2	1.91	0.53
56:SF:33:GLY:O	63:SO:91:ARG:NH2	2.42	0.53
59:SJ:78:VAL:HG22	59:SJ:173:THR:HG22	1.91	0.53
61:SL:82:ARG:HG2	61:SL:92:VAL:HG22	1.90	0.53
62:SN:62:ILE:HG13	62:SN:63:LEU:HD12	1.91	0.53
1:L1:703:A:OP1	19:LW:50:ARG:NH2	2.39	0.53
5:LD:114:THR:O	5:LD:156:ARG:NH1	2.42	0.53
19:LW:127:TYR:HA	19:LW:130:LEU:HD12	1.90	0.53
19:LW:153:LEU:HD11	38:Ls:240:LYS:HG3	1.91	0.53
31:Ll:311:MET:O	44:Lz:112:LYS:NZ	2.42	0.53
73:Sc:132:LYS:NZ	78:Sj:70:ARG:O	2.41	0.53
76:Sg:330:GLU:HB3	76:Sg:366:VAL:HG21	1.90	0.53
82:So:335:PHE:HD2	82:So:356:VAL:HG13	1.73	0.53
14:LR:129:ARG:HD2	31:Ll:132:LEU:HD11	1.91	0.53
30:Lk:275:ASN:HD21	30:Lk:326:ARG:HH11	1.56	0.53
50:L8:127:LYS:HG2	50:L8:131:MET:HE2	1.90	0.53
82:So:256:GLU:HG2	82:So:287:LEU:HB3	1.91	0.53
83:S1:700:G:H2'	83:S1:701:G:H8	1.74	0.53
1:L1:599:G:N7	11:LO:45:ARG:NH2	2.58	0.52
37:Lr:161:THR:O	37:Lr:192:GLN:NE2	2.42	0.52
39:Lt:50:ALA:HB3	39:Lt:233:PHE:HA	1.91	0.52
46:L4:76:ASN:ND2	46:L4:80:GLU:O	2.42	0.52
66:SS:104:PRO:HB2	66:SS:109:ARG:HB3	1.91	0.52
76:Sg:380:PHE:HD1	76:Sg:383:LYS:HZ1	1.55	0.52
7:LJ:111:LEU:HA	7:LJ:114:HIS:CE1	2.44	0.52
62:SN:43:MET:HE1	62:SN:81:ASP:HB3	1.90	0.52
63:SO:173:THR:HG22	65:SQ:101:ALA:HB1	1.91	0.52
68:SW:72:ILE:HD12	80:Sm:104:LEU:HD22	1.91	0.52
1:L1:79:C:O2'	11:LO:80:LYS:NZ	2.42	0.52
7:LJ:88:ALA:O	7:LJ:92:ASP:HB3	2.09	0.52
30:Lk:409:GLU:HG3	30:Lk:412:ARG:HH21	1.74	0.52
34:Lo:20:LYS:HE2	34:Lo:22:THR:HG22	1.91	0.52
83:S1:178:U:O4	83:S1:181:C:N3	2.43	0.52
1:L1:640:G:OP2	25:Lf:93:ARG:NH2	2.38	0.52
2:L2:41:G:H4'	33:Ln:119:LYS:HD2	1.91	0.52
69:SX:350:GLN:HA	69:SX:353:LEU:HD12	1.92	0.52
73:Sc:74:ARG:NH2	73:Sc:393:GLU:OE2	2.43	0.52
1:L1:791:A:H4'	4:LC:235:LYS:HB3	1.90	0.52
33:Ln:169:PHE:CE2	40:Lv:91:LEU:HD12	2.44	0.52
39:Lt:188:ALA:O	39:Lt:191:THR:OG1	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:Lx:58:ARG:N	42:Lx:136:ASP:OD2	2.41	0.52
48:L6:10:GLY:HA3	51:SR:167:PRO:HG3	1.90	0.52
62:SN:59:LYS:HZ1	77:Si:36:LEU:HB2	1.72	0.52
73:Sc:140:ASP:O	73:Sc:143:THR:OG1	2.24	0.52
83:S1:541:A:N6	83:S1:547:C:C2	2.77	0.52
4:LC:234:THR:O	4:LC:236:THR:N	2.42	0.52
31:Ll:235:TRP:NE1	31:Ll:237:LEU:HG	2.24	0.52
32:Lm:114:ASP:HB2	32:Lm:117:LYS:HB2	1.92	0.52
54:SZ:44:VAL:HG22	54:SZ:167:LEU:HD22	1.92	0.52
58:SI:102:GLU:OE1	58:SI:106:ARG:NH2	2.43	0.52
62:SN:40:ARG:NH2	83:S1:587:C:O3'	2.42	0.52
63:SO:115:ILE:HD12	63:SO:184:GLY:HA3	1.92	0.52
66:SS:192:THR:O	66:SS:195:SER:O	2.27	0.52
82:So:556:LYS:HZ2	82:So:595:MET:HB3	1.73	0.52
83:S1:751:U:H2'	83:S1:752:A:H8	1.74	0.52
1:L1:1317:U:O2'	1:L1:1321:U:OP1	2.27	0.52
4:LC:212:GLY:HA2	4:LC:262:GLY:HA3	1.90	0.52
8:LK:188:GLU:HG3	8:LK:191:LYS:HD2	1.92	0.52
11:LO:142:GLU:HB2	11:LO:162:LEU:HD23	1.92	0.52
12:LP:36:VAL:HG23	46:L4:128:ARG:HD2	1.91	0.52
33:Ln:136:ILE:HD11	40:Lv:173:ILE:HG13	1.92	0.52
36:Lq:44:ARG:NH2	48:L6:99:LYS:O	2.42	0.52
53:SB:141:ILE:HB	53:SB:190:PRO:HA	1.91	0.52
59:SJ:76:LEU:HA	59:SJ:174:LYS:O	2.09	0.52
73:Sc:348:GLU:HG2	73:Sc:350:GLU:H	1.74	0.52
79:Sk:102:ASN:HB2	79:Sk:105:LEU:HD12	1.91	0.52
82:So:531:ILE:O	82:So:535:MET:CB	2.52	0.52
7:LJ:86:ILE:HA	7:LJ:89:VAL:HG22	1.91	0.52
53:SB:214:LYS:HE2	83:S1:633:C:H5''	1.91	0.52
58:SI:358:GLU:HA	58:SI:361:VAL:HG12	1.92	0.52
58:SI:392:THR:OG1	58:SI:393:TRP:N	2.42	0.52
64:SP:101:PRO:HB3	72:Sb:59:ARG:HB3	1.90	0.52
82:So:526:ASP:OD1	82:So:526:ASP:N	2.41	0.52
6:LI:146:LEU:HD23	6:LI:147:ARG:HG2	1.92	0.52
56:SF:36:VAL:HG23	72:Sb:168:ILE:HB	1.92	0.52
58:SI:291:GLY:CA	58:SI:326:HIS:O	2.57	0.52
69:SX:106:MET:HB2	69:SX:110:GLN:HB2	1.92	0.52
75:Se:108:LEU:HD23	75:Se:141:VAL:HG21	1.91	0.52
1:L1:182:C:OP1	17:LU:177:ARG:NH2	2.43	0.52
1:L1:622:G:O2'	16:LT:11:ARG:O	2.27	0.52
17:LU:130:LEU:HB2	17:LU:156:VAL:HB	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Ld:111:LYS:HG3	48:L6:49:LEU:HD23	1.92	0.52
31:Ll:187:VAL:O	31:Ll:317:SER:OG	2.28	0.52
59:SJ:77:SER:HA	59:SJ:144:GLU:HA	1.92	0.52
72:Sb:71:ARG:NH1	83:S1:87:C:O3'	2.43	0.52
76:Sg:334:LEU:HB2	76:Sg:355:THR:HG23	1.91	0.52
82:So:596:LEU:HA	82:So:599:PHE:HD2	1.75	0.52
83:S1:50:G:H21	83:S1:204:A:N6	2.08	0.52
36:Lq:44:ARG:O	36:Lq:48:GLU:HG3	2.10	0.51
39:Lt:82:SER:OG	39:Lt:83:LEU:N	2.43	0.51
49:L7:187:ARG:HA	49:L7:190:GLN:NE2	2.25	0.51
64:SP:91:LEU:HD12	64:SP:96:PHE:HB3	1.91	0.51
75:Se:268:LEU:HD11	75:Se:293:LEU:HB3	1.92	0.51
4:LC:221:ARG:HG3	4:LC:261:MET:HG2	1.92	0.51
25:Lf:118:GLN:HB2	25:Lf:121:VAL:HG22	1.92	0.51
37:Lr:86:ASP:OD1	37:Lr:87:LEU:N	2.42	0.51
1:L1:179:C:OP2	11:LO:53:HIS:NE2	2.44	0.51
1:L1:213:G:OP2	11:LO:109:ARG:NH2	2.42	0.51
50:L8:28:ARG:HH22	50:L8:31:PRO:HG3	1.76	0.51
55:SE:220:THR:HG22	55:SE:247:VAL:HG22	1.92	0.51
55:SE:317:HIS:HD2	83:S1:4:A:H5'	1.74	0.51
66:SS:73:VAL:HG12	66:SS:106:PRO:HB3	1.92	0.51
82:So:267:VAL:HG22	82:So:300:ALA:HB2	1.91	0.51
11:LO:263:ARG:NH1	11:LO:296:SER:O	2.43	0.51
36:Lq:28:ARG:NE	36:Lq:78:GLU:OE1	2.35	0.51
52:Sf:227:ASP:OD1	52:Sf:230:ARG:NH2	2.37	0.51
53:SB:188:ARG:HH11	58:SI:144:GLY:HA3	1.74	0.51
1:L1:1488:A:H2'	1:L1:1489:A:C8	2.46	0.51
6:LI:93:ASN:ND2	6:LI:113:SER:OG	2.43	0.51
15:LS:154:VAL:HB	15:LS:199:THR:HG22	1.92	0.51
53:SB:156:GLU:HG2	58:SI:149:TYR:HE2	1.75	0.51
59:SJ:149:THR:HG1	79:Sk:133:TRP:CD1	2.28	0.51
83:S1:174:U:H2'	83:S1:175:G:C8	2.45	0.51
1:L1:510:A:H2'	1:L1:514:A:H62	1.75	0.51
9:LM:159:THR:OG1	9:LM:162:GLU:OE1	2.28	0.51
49:L7:189:ARG:O	49:L7:191:LYS:N	2.43	0.51
51:SR:71:PRO:HD2	51:SR:107:LEU:HD23	1.93	0.51
51:SR:72:ILE:HD12	51:SR:111:GLU:HB3	1.93	0.51
1:L1:523:U:N3	1:L1:525:A:C8	2.79	0.51
1:L1:1039:A:O2'	25:Lf:98:GLN:OE1	2.25	0.51
14:LR:38:VAL:HG12	14:LR:40:ASN:H	1.75	0.51
24:Ld:78:ARG:HD2	24:Ld:116:LEU:HD21	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:Lk:229:ARG:NH1	30:Lk:231:SER:OG	2.43	0.51
32:Lm:150:MET:O	32:Lm:154:ILE:HG13	2.11	0.51
32:Lm:156:ARG:HH12	32:Lm:259:ASP:HB2	1.76	0.51
46:L4:110:LEU:HD13	46:L4:117:TYR:HA	1.92	0.51
77:Si:32:LYS:HA	77:Si:35:LYS:HE2	1.93	0.51
82:So:339:LEU:HA	82:So:342:LEU:HG	1.93	0.51
1:L1:914:C:H2'	1:L1:915:G:H8	1.75	0.51
3:LB:213:CYS:HB3	3:LB:246:ARG:HG3	1.92	0.51
4:LC:163:GLU:HG2	4:LC:166:ARG:HH21	1.76	0.51
7:LJ:88:ALA:O	7:LJ:92:ASP:CB	2.58	0.51
13:LQ:143:THR:HG1	13:LQ:146:ASN:HD22	1.58	0.51
39:Lt:74:LEU:HD23	39:Lt:77:ILE:HD11	1.93	0.51
49:L7:111:ILE:O	49:L7:116:ARG:NH2	2.44	0.51
53:SB:110:ARG:NH1	70:SY:68:ASP:OD2	2.33	0.51
79:Sk:174:ARG:HG2	79:Sk:206:THR:HG22	1.92	0.51
1:L1:211:A:H62	41:Lw:111:ARG:HD3	1.76	0.51
1:L1:469:U:O4	24:Ld:77:ARG:NH1	2.38	0.51
5:LD:218:LEU:HD22	5:LD:230:ILE:HD11	1.92	0.51
18:LV:62:GLN:HE22	18:LV:68:ARG:HA	1.76	0.51
23:Lu:111:MET:O	23:Lu:114:THR:OG1	2.27	0.51
31:Ll:241:PRO:HB2	31:Ll:244:ARG:HE	1.75	0.51
39:Lt:124:TRP:CD2	47:L5:72:ARG:HG2	2.46	0.51
54:SZ:60:HIS:HA	62:SN:125:ARG:HG3	1.92	0.51
54:SZ:62:ILE:HD11	62:SN:118:GLY:HA2	1.92	0.51
58:SI:361:VAL:HA	58:SI:364:MET:HG3	1.92	0.51
64:SP:19:ILE:HB	64:SP:83:LEU:HD13	1.93	0.51
71:Sa:110:GLU:O	71:Sa:114:ARG:HG2	2.10	0.51
80:Sm:9:ARG:NH2	83:S1:374:U:OP2	2.42	0.51
1:L1:672:U:H5'	19:LW:78:LYS:HB2	1.92	0.51
37:Lr:83:PHE:CD1	37:Lr:88:LEU:HD21	2.45	0.51
39:Lt:146:ARG:HA	39:Lt:151:ARG:HD3	1.93	0.51
52:Sf:318:ASP:N	52:Sf:318:ASP:OD1	2.43	0.51
57:SG:62:GLU:HB3	57:SG:65:VAL:HB	1.93	0.51
71:Sa:110:GLU:OE1	71:Sa:114:ARG:NH1	2.44	0.51
30:Lk:313:MET:HE2	30:Lk:346:GLY:HA3	1.93	0.50
56:SF:112:PRO:HD2	80:Sm:7:ARG:HH22	1.74	0.50
57:SG:129:ALA:HB1	57:SG:133:GLU:HB3	1.92	0.50
71:Sa:140:ILE:HG22	71:Sa:146:GLN:HG3	1.92	0.50
82:So:465:ILE:O	82:So:469:GLU:HB2	2.11	0.50
21:La:84:GLY:O	21:La:87:LYS:N	2.44	0.50
32:Lm:201:SER:HB3	35:Lp:95:ARG:NH2	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Lt:187:THR:HA	39:Lt:190:ARG:HE	1.76	0.50
54:SZ:70:SER:OG	62:SN:119:GLN:O	2.25	0.50
62:SN:53:ARG:HH21	76:Sg:372:HIS:HD2	1.59	0.50
79:Sk:125:ALA:HB1	82:So:73:ALA:HB1	1.93	0.50
6:LI:135:GLU:HA	6:LI:138:LYS:HG2	1.93	0.50
12:LP:191:SER:H	12:LP:194:THR:HG1	1.57	0.50
62:SN:41:ARG:NH2	62:SN:88:ARG:O	2.44	0.50
1:L1:23:C:H2'	23:Lu:162:ARG:HH22	1.76	0.50
1:L1:849:G:N7	3:LB:230:SER:OG	2.44	0.50
5:LD:62:VAL:HG23	5:LD:82:LEU:HB2	1.94	0.50
5:LD:200:PRO:HB3	5:LD:237:LEU:HG	1.92	0.50
5:LD:282:PRO:O	5:LD:290:TYR:OH	2.22	0.50
8:LK:149:ARG:HH12	46:L4:104:PRO:HD3	1.76	0.50
18:LV:91:ALA:O	18:LV:94:ILE:C	2.55	0.50
59:SJ:76:LEU:HD23	59:SJ:148:LEU:HD11	1.92	0.50
70:SY:102:LYS:HA	70:SY:105:GLU:HG3	1.94	0.50
83:S1:261:C:H2'	83:S1:262:G:H8	1.75	0.50
1:L1:1280:U:H2'	1:L1:1281:A:H8	1.76	0.50
10:LN:45:ALA:O	10:LN:49:SER:CB	2.60	0.50
82:So:661:GLU:OE2	82:So:665:ASN:ND2	2.44	0.50
5:LD:253:MET:HE3	5:LD:259:LEU:HD22	1.92	0.50
12:LP:89:ILE:HG13	12:LP:176:LEU:HD22	1.94	0.50
12:LP:123:ARG:NH1	12:LP:162:GLU:OE1	2.43	0.50
16:LT:141:ILE:HG22	35:Lp:51:LEU:HD12	1.93	0.50
37:Lr:170:ALA:HB1	37:Lr:175:VAL:HB	1.93	0.50
55:SE:88:SER:HB3	55:SE:91:THR:HG22	1.94	0.50
59:SJ:124:VAL:HG12	62:SN:109:ILE:HG21	1.93	0.50
59:SJ:181:PRO:HD3	79:Sk:148:PRO:HD2	1.94	0.50
62:SN:59:LYS:NZ	77:Si:32:LYS:HG2	2.26	0.50
78:Sj:135:MET:N	78:Sj:135:MET:SD	2.85	0.50
1:L1:144:A:N3	1:L1:192:U:O2'	2.41	0.50
7:LJ:136:GLU:O	7:LJ:141:GLN:NE2	2.45	0.50
11:LO:168:GLU:OE2	11:LO:220:ARG:NE	2.38	0.50
39:Lt:202:ALA:HA	39:Lt:239:LEU:H	1.77	0.50
49:L7:78:ILE:HG12	49:L7:101:VAL:HG12	1.93	0.50
49:L7:187:ARG:HA	49:L7:190:GLN:HE22	1.77	0.50
55:SE:282:ILE:HG21	55:SE:329:ILE:HD11	1.93	0.50
59:SJ:149:THR:HA	79:Sk:133:TRP:HE1	1.76	0.50
71:Sa:91:GLU:OE2	72:Sb:123:ARG:NH2	2.44	0.50
8:LK:39:LEU:HB3	8:LK:44:VAL:HB	1.94	0.50
35:Lp:141:ASP:OD2	36:Lq:117:LYS:NZ	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Lt:201:GLU:H	39:Lt:241:GLY:HA3	1.77	0.50
44:Lz:83:GLU:OE1	48:L6:66:ARG:NH1	2.45	0.50
53:SB:88:ARG:HB3	53:SB:91:LEU:HD13	1.93	0.50
57:SG:74:ILE:HG13	58:SI:366:GLN:HA	1.93	0.50
63:SO:168:LYS:NZ	83:S1:302:U:OP2	2.44	0.50
69:SX:161:ILE:O	69:SX:170:ARG:NE	2.32	0.50
70:SY:67:GLU:HB2	70:SY:100:VAL:HG21	1.92	0.50
72:Sb:30:ARG:NH2	83:S1:64:U:O2	2.45	0.50
1:L1:892:U:O2'	3:LB:284:ARG:O	2.28	0.50
5:LD:69:LEU:HB3	5:LD:195:LEU:HD23	1.93	0.50
18:LV:109:ASN:OD1	18:LV:110:ASP:N	2.45	0.50
31:Ll:233:LEU:HD21	31:Ll:236:LEU:HB2	1.94	0.50
39:Lt:203:LYS:O	39:Lt:237:LEU:N	2.42	0.50
40:Lv:121:VAL:HG22	40:Lv:159:ILE:HG22	1.94	0.50
52:Sf:63:ILE:HA	52:Sf:66:TRP:CD1	2.47	0.50
63:SO:210:CYS:HA	63:SO:213:VAL:HG12	1.94	0.50
66:SS:105:CYS:HB2	66:SS:142:VAL:HA	1.93	0.50
79:Sk:152:ASP:O	79:Sk:171:VAL:HA	2.12	0.50
7:LJ:143:LEU:HB3	7:LJ:147:PHE:HE2	1.76	0.49
19:LW:76:SER:HB3	19:LW:89:LYS:HE2	1.92	0.49
30:Lk:132:LEU:HG	30:Lk:377:ASP:HB2	1.94	0.49
83:S1:355:C:H2'	83:S1:356:A:H8	1.77	0.49
10:LN:131:GLU:O	10:LN:135:SER:OG	2.22	0.49
17:LU:173:ARG:O	17:LU:181:LYS:HA	2.12	0.49
18:LV:125:GLN:NE2	18:LV:137:ARG:O	2.44	0.49
33:Ln:97:LYS:NZ	39:Lt:84:TYR:HA	2.27	0.49
38:Ls:288:LYS:HG3	38:Ls:290:GLU:HG3	1.93	0.49
58:SI:100:THR:HG23	58:SI:103:ASP:H	1.77	0.49
65:SQ:72:PRO:HB3	65:SQ:78:LYS:HG2	1.93	0.49
78:Sj:41:LEU:HD21	78:Sj:55:TRP:HA	1.94	0.49
1:L1:1012:A:OP1	16:LT:34:ARG:NH2	2.44	0.49
4:LC:80:LEU:HD13	4:LC:84:PRO:HG3	1.94	0.49
12:LP:132:THR:HG22	12:LP:147:ILE:HA	1.94	0.49
36:Lq:16:HIS:HB3	36:Lq:19:LEU:HD12	1.94	0.49
48:L6:65:VAL:O	48:L6:69:GLU:HG2	2.12	0.49
53:SB:230:CYS:SG	70:SY:47:GLN:N	2.79	0.49
57:SG:170:VAL:HG22	57:SG:236:LEU:HB3	1.94	0.49
61:SL:66:PHE:CE1	61:SL:82:ARG:HG3	2.47	0.49
68:SW:25:THR:O	68:SW:29:ILE:HG12	2.12	0.49
1:L1:207:U:O3'	11:LO:30:ASN:ND2	2.46	0.49
1:L1:1302:A:H5''	12:LP:184:PRO:HA	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:LB:228:LEU:O	3:LB:231:LYS:N	2.45	0.49
22:Lb:10:LEU:HD22	50:L8:45:LEU:HD13	1.94	0.49
45:L3:77:ARG:HH12	51:SR:48:ILE:HD13	1.76	0.49
50:L8:40:PRO:HG3	50:L8:51:GLN:HB3	1.94	0.49
56:SF:3:ARG:HB3	56:SF:99:THR:HG21	1.92	0.49
70:SY:102:LYS:HD3	70:SY:125:LEU:HD22	1.93	0.49
83:S1:451:C:OP1	83:S1:504:C:N4	2.45	0.49
1:L1:231:C:O2'	1:L1:232:C:O2	2.29	0.49
11:LO:281:LYS:HD3	41:Lw:40:GLU:OE2	2.12	0.49
19:LW:110:LEU:HD12	23:Lu:118:GLU:HG2	1.95	0.49
20:LX:48:PRO:HD3	23:Lu:234:LEU:HD21	1.95	0.49
63:SO:113:LYS:HD2	63:SO:119:PRO:HG2	1.95	0.49
71:Sa:19:GLY:HA3	71:Sa:54:GLN:HB3	1.95	0.49
79:Sk:56:ARG:NH2	79:Sk:79:SER:OG	2.45	0.49
82:So:370:ALA:HA	82:So:373:HIS:HB3	1.94	0.49
82:So:600:ARG:NH2	82:So:632:GLU:OE1	2.45	0.49
83:S1:786:A:H3'	83:S1:787:A:H8	1.78	0.49
1:L1:719:C:H5''	30:Lk:301:PRO:HB3	1.94	0.49
1:L1:801:G:O2'	1:L1:984:U:O4	2.30	0.49
4:LC:134:SER:OG	4:LC:137:ASN:OD1	2.29	0.49
61:SL:78:ARG:HH21	83:S1:247:C:H41	1.60	0.49
1:L1:105:A:O2'	16:LT:10:LEU:N	2.46	0.49
6:LI:53:THR:N	6:LI:86:THR:HG1	2.10	0.49
8:LK:48:GLN:NE2	8:LK:52:GLU:OE2	2.45	0.49
40:Lv:178:LEU:HD22	40:Lv:184:LEU:HD22	1.94	0.49
53:SB:194:ILE:HA	53:SB:220:VAL:O	2.13	0.49
54:SZ:119:ILE:HB	54:SZ:153:LEU:HG	1.94	0.49
64:SP:64:LYS:HE3	69:SX:154:THR:HB	1.93	0.49
83:S1:780:A:H2'	83:S1:781:G:C8	2.48	0.49
1:L1:1339:C:O2'	1:L1:1445:U:OP1	2.24	0.49
7:LJ:82:LEU:HD13	7:LJ:130:VAL:HG21	1.95	0.49
7:LJ:160:LYS:O	7:LJ:160:LYS:HD3	2.13	0.49
19:LW:49:THR:HG22	19:LW:51:VAL:H	1.77	0.49
19:LW:146:GLY:O	38:Ls:179:LYS:NZ	2.45	0.49
26:Lg:34:ARG:HH21	26:Lg:40:LYS:NZ	2.11	0.49
57:SG:92:SER:O	57:SG:96:ASN:ND2	2.46	0.49
57:SG:116:GLU:O	57:SG:120:ARG:HG2	2.13	0.49
62:SN:60:ASN:HB3	77:Si:33:VAL:HG21	1.94	0.49
80:Sm:62:ARG:HE	80:Sm:65:ALA:HB2	1.78	0.49
30:Lk:140:VAL:HB	30:Lk:416:ALA:HB2	1.95	0.49
69:SX:189:ARG:HE	69:SX:193:ILE:HD11	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:Sn:174:ARG:HA	81:Sn:177:TRP:HE3	1.77	0.49
82:So:376:ILE:HG12	82:So:393:ILE:HD12	1.95	0.49
7:LJ:123:MET:HA	7:LJ:153:LEU:O	2.11	0.49
9:LM:143:GLU:OE1	36:Lq:136:LYS:NZ	2.39	0.49
15:LS:194:LEU:HB2	15:LS:197:TYR:HD2	1.78	0.49
22:Lb:230:TYR:HB3	34:Lo:92:PHE:CD2	2.48	0.49
39:Lt:248:ASN:ND2	39:Lt:250:GLY:O	2.45	0.49
41:Lw:47:PHE:HD1	41:Lw:50:ARG:HH21	1.58	0.49
65:SQ:96:THR:O	65:SQ:98:LYS:N	2.46	0.49
75:Se:138:LEU:HD11	75:Se:261:ALA:HB1	1.95	0.49
79:Sk:173:LEU:O	79:Sk:206:THR:HA	2.12	0.49
39:Lt:260:LEU:HD11	39:Lt:272:VAL:HG23	1.95	0.48
69:SX:276:VAL:HG22	69:SX:281:ILE:HG21	1.95	0.48
75:Se:319:PRO:HG2	75:Se:322:ALA:HB2	1.94	0.48
1:L1:389:C:O2'	1:L1:409:C:N4	2.37	0.48
6:LI:58:ARG:HH21	22:Lb:67:ILE:HD13	1.78	0.48
7:LJ:101:ASN:OD1	7:LJ:109:LYS:NZ	2.45	0.48
7:LJ:175:PRO:O	7:LJ:188:ARG:NH1	2.45	0.48
10:LN:82:LYS:HG2	10:LN:107:LEU:HD23	1.94	0.48
31:Ll:280:ASP:OD1	31:Ll:280:ASP:N	2.46	0.48
33:Ln:139:MET:HB3	40:Lv:169:ILE:HD12	1.94	0.48
46:L4:67:GLN:HE22	46:L4:73:MET:HE1	1.77	0.48
54:SZ:109:VAL:HG12	54:SZ:111:LYS:HG3	1.94	0.48
62:SN:54:ILE:HB	62:SN:75:ILE:HD11	1.95	0.48
73:Sc:315:GLU:OE2	78:Sj:60:ARG:NH2	2.46	0.48
79:Sk:298:SER:O	79:Sk:302:GLU:CB	2.61	0.48
79:Sk:306:GLU:HA	79:Sk:309:ILE:HG22	1.95	0.48
3:LB:127:ILE:HD13	30:Lk:114:LEU:HD11	1.94	0.48
9:LM:40:GLN:HA	9:LM:121:MET:HE2	1.95	0.48
14:LR:87:HIS:HA	14:LR:119:ARG:HH21	1.79	0.48
40:Lv:100:MET:HB3	40:Lv:153:HIS:CD2	2.48	0.48
42:Lx:69:ARG:HG2	42:Lx:73:TYR:CE2	2.49	0.48
62:SN:109:ILE:HD11	83:S1:685:A:C4	2.48	0.48
66:SS:82:LYS:HE2	83:S1:21:U:H5''	1.95	0.48
73:Sc:231:LEU:HA	73:Sc:234:VAL:HG12	1.95	0.48
82:So:373:HIS:HB2	82:So:415:PHE:HA	1.96	0.48
83:S1:560:U:H5''	83:S1:571:A:H61	1.79	0.48
83:S1:592:C:H2'	83:S1:593:A:C8	2.46	0.48
83:S1:793:G:H2'	83:S1:794:A:C8	2.48	0.48
1:L1:457:A:H4'	1:L1:581:A:C5	2.48	0.48
14:LR:137:GLU:HA	49:L7:188:LEU:HD11	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:LU:71:GLU:HA	17:LU:74:ARG:HG3	1.95	0.48
40:Lv:109:TYR:HE1	47:L5:37:ARG:HH21	1.61	0.48
46:L4:76:ASN:HB2	46:L4:83:ASP:HA	1.95	0.48
64:SP:71:ASP:OD1	64:SP:72:ARG:N	2.45	0.48
73:Sc:308:GLN:O	73:Sc:312:LYS:HB2	2.14	0.48
83:S1:930:U:H2'	83:S1:931:A:C8	2.48	0.48
1:L1:1152:C:O2'	1:L1:1245:C:OP2	2.31	0.48
30:Lk:147:ILE:HB	30:Lk:150:GLN:HG3	1.93	0.48
38:Ls:123:ARG:HH21	38:Ls:126:LYS:HD2	1.78	0.48
62:SN:53:ARG:O	62:SN:56:SER:OG	2.27	0.48
73:Sc:175:VAL:HG22	73:Sc:177:SER:H	1.78	0.48
75:Se:110:HIS:HA	75:Se:113:LYS:HD2	1.96	0.48
76:Sg:328:PHE:HB2	79:Sk:217:GLN:HB2	1.95	0.48
82:So:302:VAL:HG21	82:So:341:CYS:HB3	1.95	0.48
83:S1:805:U:H2'	83:S1:806:A:C8	2.48	0.48
20:LX:216:TYR:HE1	23:Lu:191:ASN:HD22	1.62	0.48
31:Ll:98:SER:OG	31:Ll:101:GLN:OE1	2.29	0.48
31:Ll:227:GLU:HG3	31:Ll:229:ASP:H	1.79	0.48
32:Lm:185:LEU:HD12	32:Lm:295:ARG:HH11	1.79	0.48
36:Lq:28:ARG:NH1	37:Lr:177:GLN:HE22	2.07	0.48
39:Lt:151:ARG:NH1	39:Lt:254:TRP:O	2.39	0.48
55:SE:141:TRP:CE3	82:So:116:VAL:HG22	2.48	0.48
60:SK:183:HIS:HB2	83:S1:328:A:H2	1.79	0.48
75:Se:273:THR:HG23	75:Se:316:LEU:HD13	1.95	0.48
83:S1:37:U:H2'	83:S1:38:A:H8	1.77	0.48
83:S1:327:U:O2'	83:S1:328:A:N7	2.41	0.48
5:LD:59:ARG:HH21	5:LD:84:PRO:HB2	1.79	0.48
14:LR:109:TRP:HA	14:LR:112:LYS:HB2	1.95	0.48
52:Sf:73:ALA:O	52:Sf:79:LYS:NZ	2.46	0.48
54:SZ:49:LYS:NZ	54:SZ:167:LEU:HB2	2.29	0.48
59:SJ:163:ASN:HB3	79:Sk:114:LEU:HD11	1.95	0.48
74:Sd:148:GLU:HG3	74:Sd:150:THR:HG23	1.96	0.48
75:Se:149:ASP:HA	75:Se:197:ARG:HH22	1.79	0.48
76:Sg:358:LEU:HB3	76:Sg:369:LYS:HG2	1.96	0.48
82:So:548:PHE:HB3	82:So:582:LEU:HD22	1.95	0.48
83:S1:356:A:H2'	83:S1:357:G:C8	2.49	0.48
83:S1:824:A:H2'	83:S1:825:G:C8	2.49	0.48
1:L1:1007:A:H2'	1:L1:1008:A:C8	2.49	0.48
1:L1:1384:G:H2'	1:L1:1385:U:C6	2.49	0.48
30:Lk:125:LYS:HA	30:Lk:253:LEU:HD11	1.95	0.48
41:Lw:52:LEU:HD12	41:Lw:53:PRO:HD2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:Se:204:VAL:HB	75:Se:208:TYR:HE2	1.78	0.48
78:Sj:133:HIS:HB2	78:Sj:139:TRP:HZ2	1.78	0.48
1:L1:8:C:O2	20:LX:42:ARG:NH1	2.46	0.48
24:Ld:84:ASP:O	24:Ld:88:MET:HG3	2.14	0.48
32:Lm:150:MET:HE2	32:Lm:280:VAL:HG22	1.96	0.48
38:Ls:175:ASP:OD1	38:Ls:175:ASP:N	2.47	0.48
39:Lt:124:TRP:CE2	47:L5:72:ARG:HG2	2.49	0.48
78:Sj:207:GLN:HA	78:Sj:210:LYS:HB2	1.95	0.48
30:Lk:136:VAL:HG12	30:Lk:416:ALA:HB1	1.94	0.48
53:SB:222:ILE:HD13	53:SB:236:VAL:HB	1.96	0.48
57:SG:44:PRO:HD3	57:SG:75:LYS:HG2	1.96	0.48
64:SP:111:ARG:HB3	66:SS:232:PRO:HD2	1.96	0.48
67:ST:124:TYR:HE2	68:SW:4:HIS:HB3	1.79	0.48
69:SX:275:PHE:O	69:SX:279:LYS:HA	2.14	0.48
79:Sk:87:MET:HB2	79:Sk:102:ASN:HD22	1.79	0.48
52:Sf:105:TRP:HZ3	52:Sf:268:PRO:HA	1.79	0.47
58:SI:317:PHE:HB3	58:SI:323:LEU:HA	1.96	0.47
59:SJ:165:PRO:HG3	79:Sk:111:PHE:CZ	2.48	0.47
69:SX:171:PHE:CG	78:Sj:173:MET:HE1	2.49	0.47
69:SX:219:TYR:HE1	69:SX:227:VAL:HG21	1.78	0.47
1:L1:333:A:OP2	1:L1:1064:A:O2'	2.30	0.47
8:LK:187:GLU:HG3	8:LK:191:LYS:HE3	1.96	0.47
19:LW:21:ARG:NH1	23:Lu:143:ASP:OD1	2.39	0.47
36:Lq:85:ARG:NE	36:Lq:87:GLU:OE2	2.47	0.47
58:SI:379:ARG:O	58:SI:381:LYS:NZ	2.40	0.47
59:SJ:69:PRO:HA	82:So:61:LYS:HA	1.95	0.47
61:SL:57:GLN:HB3	61:SL:109:LEU:HD11	1.95	0.47
82:So:507:GLU:HA	82:So:544:LEU:HD11	1.95	0.47
3:LB:126:VAL:HA	3:LB:142:VAL:HG12	1.96	0.47
5:LD:188:HIS:HB2	5:LD:260:VAL:HG22	1.95	0.47
7:LJ:84:ARG:HH12	46:L4:113:GLU:HG3	1.79	0.47
12:LP:203:GLU:O	12:LP:207:ARG:HG3	2.14	0.47
52:Sf:92:MET:HE3	52:Sf:92:MET:HB2	1.79	0.47
57:SG:176:ASP:OD1	57:SG:176:ASP:N	2.48	0.47
64:SP:32:TYR:HD2	64:SP:54:TYR:HD2	1.62	0.47
75:Se:159:HIS:HA	75:Se:162:VAL:HG12	1.95	0.47
83:S1:838:G:O6	83:S1:922:G:N2	2.47	0.47
12:LP:96:TYR:OH	12:LP:129:LYS:NZ	2.44	0.47
26:Lg:34:ARG:HH21	26:Lg:40:LYS:HZ3	1.63	0.47
45:L3:8:LEU:HD21	45:L3:95:ARG:HG3	1.95	0.47
74:Sd:142:LEU:HB3	74:Sd:167:ALA:HB1	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:S1:378:A:H2'	83:S1:379:A:C8	2.49	0.47
1:L1:1521:A:H4'	51:SR:123:HIS:HB3	1.95	0.47
6:LI:146:LEU:O	6:LI:147:ARG:NE	2.44	0.47
30:Lk:173:ARG:NH2	30:Lk:348:ASP:O	2.47	0.47
64:SP:91:LEU:HB3	64:SP:97:PHE:HB2	1.96	0.47
69:SX:67:LYS:HD2	69:SX:307:LEU:HD12	1.96	0.47
69:SX:208:ILE:O	69:SX:214:ASN:ND2	2.47	0.47
1:L1:133:A:N6	1:L1:135:A:N6	2.63	0.47
7:LJ:134:PHE:O	7:LJ:138:SER:CB	2.62	0.47
16:LT:111:LYS:NZ	17:LU:139:ASP:OD1	2.48	0.47
37:Lr:60:ARG:HG2	37:Lr:177:GLN:HE21	1.79	0.47
55:SE:320:ILE:HD11	55:SE:345:LEU:HD11	1.97	0.47
57:SG:63:LYS:HD3	57:SG:66:ARG:HH21	1.79	0.47
69:SX:195:VAL:HG23	69:SX:204:ILE:HG21	1.97	0.47
79:Sk:214:LEU:HB2	79:Sk:217:GLN:HE21	1.80	0.47
83:S1:16:A:H2'	83:S1:17:G:C8	2.50	0.47
83:S1:515:A:N3	83:S1:850:C:O2'	2.45	0.47
1:L1:181:G:H2'	1:L1:1023:A:N7	2.29	0.47
1:L1:472:A:O2'	1:L1:592:C:OP1	2.31	0.47
1:L1:648:A:H2'	1:L1:649:A:C8	2.49	0.47
1:L1:916:U:H2'	1:L1:917:G:H8	1.80	0.47
4:LC:111:THR:O	4:LC:114:GLY:N	2.38	0.47
9:LM:59:ILE:HB	9:LM:127:LEU:HD23	1.97	0.47
12:LP:223:MET:HE3	48:L6:42:GLU:HB3	1.96	0.47
20:LX:144:VAL:HG11	20:LX:153:ILE:HD12	1.96	0.47
38:Ls:144:ILE:HG22	38:Ls:261:MET:HE3	1.97	0.47
40:Lv:137:LEU:HB2	40:Lv:145:LEU:HG	1.96	0.47
44:Lz:63:GLN:OE1	44:Lz:66:ARG:NH1	2.48	0.47
45:L3:64:VAL:HB	45:L3:76:MET:HB2	1.96	0.47
49:L7:42:ILE:HA	49:L7:47:LYS:HD2	1.95	0.47
66:SS:217:ARG:O	66:SS:221:GLN:HB3	2.15	0.47
73:Sc:137:ILE:HG22	73:Sc:139:PRO:HD3	1.96	0.47
75:Se:81:HIS:CD2	75:Se:190:ASN:HB3	2.50	0.47
83:S1:554:A:H2'	83:S1:555:G:C8	2.50	0.47
1:L1:429:U:H2'	1:L1:430:C:C6	2.50	0.47
5:LD:91:PRO:HB3	11:LO:16:LEU:HD11	1.95	0.47
9:LM:85:GLY:O	9:LM:88:ARG:NH2	2.47	0.47
19:LW:9:LEU:N	23:Lu:183:GLN:OE1	2.46	0.47
38:Ls:94:ASP:OD2	38:Ls:215:ARG:NE	2.43	0.47
53:SB:60:ASP:O	53:SB:64:ASN:HB2	2.14	0.47
54:SZ:134:PHE:HD2	54:SZ:135:LEU:HD22	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:SE:258:ILE:HD11	55:SE:343:LEU:HD11	1.97	0.47
55:SE:285:TYR:OH	55:SE:372:GLU:OE1	2.33	0.47
62:SN:52:LEU:HD13	77:Si:41:PRO:HB3	1.96	0.47
73:Sc:139:PRO:HD2	73:Sc:170:GLN:HE22	1.80	0.47
78:Sj:64:LEU:HB2	78:Sj:139:TRP:CD1	2.50	0.47
79:Sk:87:MET:HG2	79:Sk:105:LEU:HG	1.96	0.47
1:L1:209:G:OP1	5:LD:92:ARG:NH1	2.41	0.47
26:Lg:17:LEU:HB2	26:Lg:65:LEU:HD23	1.97	0.47
38:Ls:213:THR:HG22	38:Ls:247:VAL:HG22	1.97	0.47
45:L3:22:PRO:HA	45:L3:27:VAL:HG11	1.96	0.47
68:SW:49:CYS:SG	68:SW:50:ARG:NH1	2.87	0.47
72:Sb:41:ARG:NH2	83:S1:55:C:OP1	2.48	0.47
82:So:157:LEU:HA	82:So:172:MET:HE3	1.97	0.47
83:S1:930:U:H2'	83:S1:931:A:H8	1.80	0.47
11:LO:255:MET:HE3	11:LO:256:LEU:HD12	1.97	0.47
55:SE:343:LEU:HD21	83:S1:638:G:H5'	1.97	0.47
69:SX:209:ILE:HA	69:SX:214:ASN:HD22	1.80	0.47
76:Sg:365:SER:H	76:Sg:368:GLN:NE2	2.13	0.47
1:L1:416:A:H2'	1:L1:417:U:C6	2.51	0.46
1:L1:841:C:H3'	1:L1:842:A:H8	1.80	0.46
1:L1:1134:A:H2'	1:L1:1135:A:C8	2.49	0.46
1:L1:1531:A:H2'	1:L1:1532:U:O4'	2.15	0.46
7:LJ:133:PRO:HA	7:LJ:136:GLU:HG3	1.97	0.46
9:LM:174:GLU:HG2	51:SR:56:THR:HG21	1.97	0.46
36:Lq:30:SER:O	36:Lq:75:VAL:HA	2.14	0.46
39:Lt:70:MET:HB2	39:Lt:70:MET:HE3	1.59	0.46
53:SB:164:GLU:HG3	53:SB:165:TYR:H	1.80	0.46
56:SF:82:LEU:HD12	56:SF:88:VAL:HG11	1.97	0.46
69:SX:259:TYR:O	69:SX:263:ARG:HG3	2.15	0.46
70:SY:97:GLN:HA	70:SY:100:VAL:HG12	1.97	0.46
79:Sk:56:ARG:HH21	79:Sk:80:ALA:HB2	1.81	0.46
81:Sn:139:ASN:ND2	83:S1:494:C:OP1	2.35	0.46
82:So:148:GLN:N	82:So:159:GLU:OE2	2.47	0.46
82:So:302:VAL:HA	82:So:312:LYS:HD3	1.96	0.46
1:L1:789:A:N6	1:L1:998:A:O2'	2.44	0.46
7:LJ:162:LYS:HG3	7:LJ:195:SER:HB2	1.97	0.46
9:LM:172:PRO:HG2	51:SR:57:PRO:HD2	1.97	0.46
15:LS:181:LYS:HB3	15:LS:217:VAL:HG22	1.96	0.46
19:LW:46:MET:HE3	34:Lo:36:ARG:HH21	1.81	0.46
20:LX:165:ILE:HG21	34:Lo:76:TYR:CD2	2.51	0.46
31:Ll:151:LEU:HD23	31:Ll:151:LEU:HA	1.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:SN:91:CYS:HB3	62:SN:94:THR:O	2.15	0.46
66:SS:110:ASP:HB3	66:SS:113:LEU:HD23	1.97	0.46
74:Sd:161:THR:HG22	74:Sd:163:LEU:H	1.79	0.46
75:Se:310:LEU:HD12	75:Se:328:LEU:HB2	1.96	0.46
78:Sj:25:LEU:HD21	83:S1:884:C:H2'	1.97	0.46
1:L1:1141:G:H2'	1:L1:1142:U:H6	1.81	0.46
34:Lo:91:LEU:O	34:Lo:95:ALA:CB	2.63	0.46
39:Lt:97:ARG:HA	39:Lt:100:LYS:HE2	1.96	0.46
39:Lt:164:LYS:HG2	39:Lt:169:ASP:HB3	1.96	0.46
42:Lx:73:TYR:HA	42:Lx:76:GLU:HG3	1.97	0.46
52:Sf:406:GLU:CD	52:Sf:411:LYS:HD3	2.40	0.46
53:SB:159:ALA:O	53:SB:162:CYS:O	2.34	0.46
75:Se:157:ASP:OD2	75:Se:160:LEU:N	2.48	0.46
9:LM:119:ARG:O	9:LM:123:GLU:HG2	2.16	0.46
14:LR:43:VAL:HG12	31:L1:225:LEU:HB3	1.98	0.46
14:LR:51:ASN:HB3	14:LR:54:ASN:HB2	1.96	0.46
31:L1:133:ASP:N	31:L1:133:ASP:OD1	2.48	0.46
41:Lw:150:LYS:NZ	48:L6:79:THR:O	2.45	0.46
55:SE:275:ALA:O	55:SE:278:HIS:C	2.58	0.46
75:Se:259:LEU:HD12	75:Se:305:ALA:HB3	1.96	0.46
82:So:367:PRO:HB3	82:So:371:THR:HG21	1.97	0.46
1:L1:2:C:O2'	18:LV:149:ARG:O	2.28	0.46
1:L1:421:A:OP1	28:Li:156:LYS:NZ	2.37	0.46
1:L1:1325:G:O2'	1:L1:1372:U:OP1	2.33	0.46
8:LK:119:GLU:OE1	8:LK:122:ARG:NH2	2.48	0.46
51:SR:90:SER:HA	51:SR:93:ILE:HG12	1.97	0.46
58:SI:86:ARG:HH12	58:SI:97:GLU:HA	1.81	0.46
82:So:464:LEU:HG	82:So:468:MET:HE1	1.98	0.46
83:S1:24:U:H2'	83:S1:25:A:H8	1.80	0.46
83:S1:35:A:H2'	83:S1:36:G:H8	1.81	0.46
1:L1:501:U:C2	1:L1:503:G:H4'	2.50	0.46
23:Lu:102:TRP:CZ3	23:Lu:139:MET:HB3	2.51	0.46
38:Ls:187:GLU:O	38:Ls:218:THR:OG1	2.32	0.46
44:Lz:99:GLN:HE22	44:Lz:103:ARG:HD2	1.80	0.46
56:SF:22:LEU:HD12	56:SF:39:LEU:HD11	1.97	0.46
59:SJ:83:HIS:N	59:SJ:168:VAL:HG23	2.27	0.46
63:SO:132:LEU:HD21	83:S1:393:U:H5'	1.97	0.46
72:Sb:77:GLU:OE2	72:Sb:80:ARG:NH2	2.46	0.46
73:Sc:226:TYR:HE1	73:Sc:282:VAL:HG21	1.81	0.46
83:S1:160:A:H8	83:S1:161:C:H41	1.64	0.46
1:L1:439:A:H61	1:L1:1311:A:H2	1.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:LW:28:LEU:HD12	23:Lu:67:PHE:HD2	1.81	0.46
26:Lg:19:ARG:HB2	26:Lg:62:ILE:HD11	1.97	0.46
31:Ll:304:TYR:O	31:Ll:308:GLN:HB2	2.15	0.46
32:Lm:221:VAL:HG21	32:Lm:254:LEU:HD12	1.97	0.46
47:L5:56:LEU:HD22	47:L5:66:ILE:HD13	1.96	0.46
54:SZ:64:HIS:HA	58:SI:117:PHE:HB2	1.96	0.46
55:SE:426:LYS:N	66:SS:88:GLN:OE1	2.46	0.46
78:Sj:37:ASP:OD2	78:Sj:40:THR:OG1	2.33	0.46
83:S1:554:A:H2'	83:S1:555:G:H8	1.81	0.46
1:L1:487:U:OP1	51:SR:182:ARG:NH1	2.48	0.46
5:LD:113:LYS:HG3	5:LD:157:GLY:H	1.81	0.46
13:LQ:77:ASP:O	13:LQ:83:LYS:NZ	2.49	0.46
45:L3:6:ALA:HB2	45:L3:41:LYS:HB3	1.96	0.46
50:L8:44:ASP:HB3	50:L8:47:THR:HG23	1.97	0.46
53:SB:215:MET:SD	70:SY:5:ARG:NH2	2.89	0.46
58:SI:298:ILE:HD11	58:SI:303:TYR:HD1	1.80	0.46
77:Si:56:HIS:O	77:Si:60:GLU:HB2	2.16	0.46
83:S1:847:C:H2'	83:S1:848:C:C6	2.51	0.46
1:L1:1230:C:H2'	1:L1:1231:A:H8	1.80	0.46
6:LI:140:PHE:HA	6:LI:143:GLU:HG3	1.98	0.46
12:LP:113:MET:HE3	12:LP:118:MET:HG3	1.98	0.46
15:LS:250:THR:HG22	15:LS:253:GLN:HE21	1.81	0.46
55:SE:394:ASP:OD1	55:SE:394:ASP:N	2.49	0.46
58:SI:136:ARG:HE	58:SI:139:GLN:HE21	1.64	0.46
71:Sa:90:VAL:HA	71:Sa:93:LYS:HD2	1.98	0.46
83:S1:47:C:H2'	83:S1:168:C:H41	1.80	0.46
1:L1:362:G:O2'	1:L1:1195:C:O2	2.26	0.46
5:LD:59:ARG:HE	5:LD:84:PRO:HB2	1.81	0.46
7:LJ:94:ARG:NH2	7:LJ:183:ASP:OD1	2.47	0.46
30:Lk:377:ASP:OD1	30:Lk:380:GLN:NE2	2.49	0.46
54:SZ:42:VAL:HG21	54:SZ:51:VAL:HG21	1.98	0.46
58:SI:164:ASP:O	58:SI:168:MET:HG3	2.16	0.46
59:SJ:128:LYS:HE3	59:SJ:131:ARG:HH21	1.81	0.46
64:SP:34:ILE:O	64:SP:51:LEU:N	2.49	0.46
64:SP:34:ILE:HG22	64:SP:51:LEU:HB2	1.97	0.46
79:Sk:156:TYR:CE2	79:Sk:167:ARG:HG3	2.51	0.46
81:Sn:177:TRP:NE1	81:Sn:186:PRO:HD3	2.31	0.46
82:So:591:GLU:HA	82:So:594:LYS:HG3	1.98	0.46
1:L1:1201:U:O2'	21:La:86:ASN:ND2	2.49	0.45
4:LC:104:LEU:HG	15:LS:91:LYS:HB2	1.98	0.45
15:LS:95:GLU:O	15:LS:99:MET:HG3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:LS:95:GLU:OE2	15:LS:145:LEU:N	2.49	0.45
39:Lt:178:TRP:NE1	39:Lt:182:GLU:O	2.44	0.45
75:Se:260:VAL:HG23	75:Se:306:ILE:HA	1.98	0.45
78:Sj:207:GLN:O	78:Sj:210:LYS:C	2.59	0.45
82:So:302:VAL:O	82:So:312:LYS:NZ	2.40	0.45
83:S1:34:U:H2'	83:S1:35:A:H8	1.80	0.45
1:L1:214:G:H1'	1:L1:225:C:H1'	1.98	0.45
1:L1:307:U:H2'	1:L1:308:A:H8	1.81	0.45
30:Lk:212:THR:HG21	30:Lk:273:VAL:HG13	1.98	0.45
31:Ll:139:TRP:CD1	31:Ll:143:CYS:HG	2.34	0.45
58:SI:349:ALA:HB1	58:SI:364:MET:HE1	1.98	0.45
72:Sb:58:GLU:O	72:Sb:62:HIS:ND1	2.34	0.45
72:Sb:82:VAL:HG11	83:S1:94:A:H5'	1.96	0.45
73:Sc:229:ALA:HB2	73:Sc:283:LEU:HG	1.98	0.45
75:Se:130:LYS:NZ	83:S1:731:C:O2'	2.42	0.45
1:L1:79:C:OP2	1:L1:1229:C:O2'	2.29	0.45
1:L1:548:C:OP2	7:LJ:128:ASN:ND2	2.49	0.45
85:L1:1706:T1C:H941	85:L1:1706:T1C:H921	1.81	0.45
7:LJ:87:ALA:O	7:LJ:91:GLN:HG3	2.16	0.45
19:LW:54:ARG:NH1	19:LW:65:VAL:O	2.49	0.45
32:Lm:143:TRP:HE1	32:Lm:172:VAL:HG23	1.81	0.45
32:Lm:313:TRP:O	32:Lm:317:LEU:HD23	2.16	0.45
52:Sf:191:HIS:O	52:Sf:428:ARG:NH2	2.43	0.45
55:SE:193:TRP:CE3	55:SE:199:GLY:HA3	2.51	0.45
60:SK:179:THR:HG21	68:SW:39:ILE:HD13	1.98	0.45
80:Sm:52:MET:O	80:Sm:55:CYS:HB2	2.16	0.45
83:S1:940:U:H2'	83:S1:941:G:H8	1.81	0.45
1:L1:1338:C:O2'	1:L1:1381:A:N3	2.41	0.45
7:LJ:40:MET:HE1	7:LJ:48:MET:HE2	1.98	0.45
10:LN:118:ARG:HH12	10:LN:120:LYS:HG2	1.81	0.45
14:LR:110:ALA:HA	31:Ll:138:GLU:OE2	2.17	0.45
25:Lf:132:LYS:HD3	38:Ls:290:GLU:HB3	1.99	0.45
31:Ll:275:GLN:HE21	31:Ll:311:MET:HE3	1.82	0.45
31:Ll:374:GLU:OE2	49:L7:140:SER:OG	2.28	0.45
38:Ls:267:PRO:HG2	38:Ls:270:ALA:HB2	1.98	0.45
42:Lx:78:PHE:CD2	42:Lx:89:ILE:HD12	2.52	0.45
54:SZ:96:MET:HE2	54:SZ:153:LEU:HD21	1.99	0.45
54:SZ:131:LYS:NZ	55:SE:144:LEU:HA	2.31	0.45
58:SI:327:ASP:N	58:SI:327:ASP:OD1	2.49	0.45
58:SI:345:ARG:HH11	58:SI:369:LEU:HD23	1.82	0.45
63:SO:115:ILE:HG23	63:SO:116:VAL:HG13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:SO:132:LEU:HD23	63:SO:132:LEU:HA	1.82	0.45
67:ST:77:VAL:HG23	67:ST:120:MET:HE2	1.97	0.45
78:Sj:68:LEU:HG	78:Sj:71:LEU:HD12	1.98	0.45
78:Sj:210:LYS:NZ	83:S1:59:C:O2	2.39	0.45
82:So:494:ILE:HA	82:So:497:LEU:HD12	1.97	0.45
83:S1:25:A:H2'	83:S1:26:U:C6	2.52	0.45
83:S1:552:G:N1	83:S1:775:G:OP2	2.47	0.45
1:L1:187:U:H2'	1:L1:188:G:C8	2.52	0.45
1:L1:197:A:N1	1:L1:349:G:O2'	2.45	0.45
1:L1:662:C:N4	1:L1:772:U:H3	2.15	0.45
27:Lh:72:THR:HG22	27:Lh:74:ALA:H	1.81	0.45
32:Lm:153:VAL:O	32:Lm:157:ALA:HB2	2.16	0.45
55:SE:244:LEU:HD11	55:SE:256:PHE:HD2	1.82	0.45
55:SE:305:MET:HA	55:SE:333:TYR:O	2.15	0.45
58:SI:269:PHE:HB3	58:SI:286:TYR:CD2	2.52	0.45
62:SN:59:LYS:HZ2	77:Si:32:LYS:HG2	1.81	0.45
73:Sc:30:LEU:HD12	73:Sc:149:ASP:HB2	1.99	0.45
81:Sn:138:MET:HE1	83:S1:937:A:H5'	1.99	0.45
83:S1:514:A:H2'	83:S1:515:A:H8	1.82	0.45
1:L1:190:A:O2'	1:L1:1012:A:OP1	2.29	0.45
1:L1:283:A:O2'	1:L1:793:A:OP1	2.34	0.45
10:LN:123:ILE:HD12	10:LN:127:LEU:HD12	1.99	0.45
30:Lk:358:GLN:NE2	30:Lk:360:ASN:OD1	2.41	0.45
33:Ln:173:LYS:HG2	40:Lv:175:GLN:NE2	2.32	0.45
40:Lv:100:MET:HE1	47:L5:45:ARG:HE	1.81	0.45
75:Se:69:ASN:HA	75:Se:97:ALA:O	2.16	0.45
76:Sg:353:LEU:HD23	77:Si:22:VAL:HG11	1.97	0.45
4:LC:109:LEU:HD21	4:LC:337:VAL:HG22	1.98	0.45
5:LD:164:MET:HE3	43:Ly:69:HIS:CE1	2.48	0.45
8:LK:48:GLN:HA	8:LK:51:LYS:HD2	1.98	0.45
32:Lm:142:TYR:OH	32:Lm:301:SER:OG	2.33	0.45
66:SS:220:TYR:HD2	72:Sb:48:VAL:HG11	1.82	0.45
83:S1:791:A:H2'	83:S1:792:A:H8	1.81	0.45
1:L1:64:C:H4'	1:L1:65:A:H5'	1.99	0.45
1:L1:739:A:O2'	30:Lk:270:ILE:O	2.34	0.45
1:L1:1488:A:H2'	1:L1:1489:A:H8	1.82	0.45
3:LB:164:LEU:N	3:LB:180:ASP:OD1	2.40	0.45
5:LD:61:PRO:HA	5:LD:84:PRO:HD3	1.99	0.45
6:LI:53:THR:N	6:LI:86:THR:OG1	2.50	0.45
11:LO:177:ALA:HA	11:LO:222:TYR:CD1	2.51	0.45
20:LX:75:LYS:HE3	20:LX:75:LYS:HB2	1.83	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:La:113:ALA:O	21:La:117:ILE:HG12	2.17	0.45
30:Lk:101:ASP:OD1	30:Lk:101:ASP:N	2.50	0.45
33:Ln:173:LYS:HG2	40:Lv:175:GLN:HE22	1.80	0.45
43:Ly:93:ARG:CZ	43:Ly:97:MET:HE1	2.47	0.45
46:L4:76:ASN:ND2	46:L4:82:GLN:H	2.13	0.45
54:SZ:117:LEU:HD12	54:SZ:151:VAL:HG22	1.97	0.45
58:SI:353:CYS:HB2	58:SI:361:VAL:HG21	1.98	0.45
72:Sb:49:ASP:OD1	72:Sb:49:ASP:N	2.50	0.45
83:S1:35:A:H2'	83:S1:36:G:C8	2.52	0.45
83:S1:700:G:H2'	83:S1:701:G:C8	2.52	0.45
1:L1:220:C:OP2	28:Li:168:ARG:NH1	2.50	0.45
5:LD:292:ASP:OD1	41:Lw:55:THR:OG1	2.31	0.45
10:LN:120:LYS:HB3	10:LN:120:LYS:HE3	1.85	0.45
19:LW:141:ASP:HB3	19:LW:144:ARG:HG2	1.98	0.45
23:Lu:187:PRO:HD2	23:Lu:190:LEU:HD12	1.98	0.45
30:Lk:333:ALA:HB1	30:Lk:363:ASP:HA	1.98	0.45
39:Lt:64:THR:H	39:Lt:67:GLN:HE21	1.65	0.45
55:SE:312:TYR:CZ	55:SE:315:ARG:HD3	2.52	0.45
58:SI:255:GLN:NE2	58:SI:362:GLU:OE1	2.50	0.45
59:SJ:147:HIS:HA	79:Sk:133:TRP:CH2	2.52	0.45
62:SN:62:ILE:HD11	76:Sg:350:PHE:HB2	1.99	0.45
73:Sc:96:ARG:HH12	78:Sj:74:PHE:HE1	1.64	0.45
82:So:553:ALA:HB2	82:So:588:ARG:HH22	1.81	0.45
83:S1:942:C:H2'	83:S1:943:A:C8	2.52	0.45
1:L1:844:C:H2'	1:L1:845:U:H6	1.81	0.45
5:LD:249:ASN:O	5:LD:253:MET:HG3	2.17	0.45
5:LD:275:TRP:O	5:LD:279:ARG:HB2	2.17	0.45
7:LJ:163:GLU:OE1	7:LJ:163:GLU:N	2.49	0.45
21:La:121:PRO:HA	31:Ll:50:LYS:HA	1.99	0.45
23:Lu:232:LYS:O	23:Lu:236:LYS:HD3	2.17	0.45
24:Ld:71:ARG:HD3	24:Ld:86:ILE:HD12	1.99	0.45
37:Lr:150:THR:HA	37:Lr:153:ILE:HG22	1.98	0.45
38:Ls:186:VAL:HG21	38:Ls:239:PRO:HB3	1.99	0.45
57:SG:68:LEU:O	57:SG:72:GLN:HG3	2.16	0.45
65:SQ:18:ILE:HD12	65:SQ:27:LYS:HG2	1.98	0.45
83:S1:160:A:H1'	83:S1:161:C:H5	1.81	0.45
1:L1:27:A:O2'	1:L1:34:U:OP2	2.32	0.44
1:L1:1070:A:H2'	1:L1:1071:A:H8	1.79	0.44
10:LN:133:GLU:OE1	10:LN:133:GLU:N	2.50	0.44
11:LO:259:ARG:HH11	11:LO:259:ARG:HG3	1.83	0.44
30:Lk:60:PHE:HB3	30:Lk:67:VAL:HG12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Ll:307:HIS:O	31:Ll:311:MET:HG2	2.16	0.44
33:Ln:146:ALA:HB1	39:Lt:209:PRO:HB2	1.99	0.44
39:Lt:74:LEU:HD22	47:L5:42:ARG:HB3	1.99	0.44
52:Sf:81:ARG:O	52:Sf:85:LYS:HB3	2.18	0.44
58:Sl:204:GLU:OE2	58:Sl:246:ARG:NH1	2.50	0.44
63:SO:143:LEU:HD11	63:SO:153:LYS:HA	1.98	0.44
74:Sd:104:ILE:HD12	74:Sd:138:THR:HB	1.98	0.44
83:S1:261:C:H2'	83:S1:262:G:C8	2.51	0.44
83:S1:534:G:H2'	83:S1:535:C:C6	2.53	0.44
11:LO:197:GLY:HA3	50:L8:62:ALA:HB2	1.99	0.44
18:LV:81:LYS:HA	18:LV:81:LYS:HD2	1.87	0.44
19:LW:36:PRO:HD3	52:Sf:270:LYS:HB3	1.98	0.44
20:LX:190:CYS:SG	20:LX:191:LEU:N	2.90	0.44
23:Lu:146:VAL:O	23:Lu:150:GLU:HG2	2.17	0.44
31:Ll:217:LEU:O	31:Ll:270:PHE:HA	2.17	0.44
37:Lr:245:LEU:HD12	37:Lr:253:PRO:HD3	1.99	0.44
52:Sf:84:THR:HB	52:Sf:280:ASN:HB2	1.99	0.44
53:SB:270:LEU:HA	53:SB:273:LEU:HG	1.99	0.44
62:SN:37:ASP:O	62:SN:41:ARG:HG2	2.18	0.44
68:SW:35:LEU:O	68:SW:39:ILE:HG13	2.17	0.44
79:Sk:169:ARG:NH2	79:Sk:210:ASP:OD2	2.50	0.44
79:Sk:214:LEU:HB2	79:Sk:217:GLN:HG2	1.99	0.44
79:Sk:257:SER:HA	79:Sk:260:ARG:CZ	2.47	0.44
82:So:317:LEU:HD23	82:So:320:LEU:HD21	1.99	0.44
83:S1:753:U:H2'	83:S1:754:G:C8	2.52	0.44
1:L1:84:G:N7	28:Li:105:LYS:NZ	2.54	0.44
17:LU:82:LYS:HB3	17:LU:82:LYS:HE2	1.74	0.44
20:LX:172:ASP:OD1	20:LX:172:ASP:N	2.48	0.44
54:SZ:105:ALA:HB3	54:SZ:122:VAL:HG13	1.98	0.44
55:SE:229:PHE:H	83:S1:11:G:H4'	1.82	0.44
59:SJ:124:VAL:HG13	83:S1:617:C:H1'	1.99	0.44
61:SL:56:PRO:HD2	83:S1:179:A:C6	2.52	0.44
83:S1:191:U:H2'	83:S1:192:A:H8	1.80	0.44
5:LD:241:ASN:HD22	50:L8:25:TYR:HB2	1.83	0.44
7:LJ:134:PHE:O	7:LJ:138:SER:OG	2.35	0.44
14:LR:114:HIS:CD2	31:Ll:131:PRO:HD2	2.51	0.44
31:Ll:190:GLY:N	31:Ll:318:PHE:O	2.51	0.44
33:Ln:169:PHE:O	33:Ln:171:PHE:N	2.50	0.44
37:Lr:122:ASN:HB3	37:Lr:197:ALA:HB2	1.99	0.44
40:Lv:127:MET:SD	40:Lv:128:PRO:HD2	2.57	0.44
57:SG:176:ASP:HA	57:SG:179:ARG:HG2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:SS:96:ARG:NH1	83:S1:272:A:OP2	2.43	0.44
67:ST:120:MET:HE3	67:ST:120:MET:HB2	1.80	0.44
75:Se:296:MET:HE2	75:Se:296:MET:HB2	1.78	0.44
79:Sk:169:ARG:HH12	79:Sk:210:ASP:C	2.26	0.44
82:So:335:PHE:HA	82:So:338:ILE:HD12	1.99	0.44
82:So:615:MET:SD	82:So:648:ARG:NH1	2.91	0.44
83:S1:614:C:H2'	83:S1:615:C:C6	2.51	0.44
1:L1:35:A:C8	34:Lo:39:LYS:HD3	2.53	0.44
1:L1:192:U:H2'	1:L1:193:A:C8	2.52	0.44
1:L1:640:G:O2'	1:L1:1005:G:O6	2.33	0.44
1:L1:720:A:H4'	30:Lk:301:PRO:HD3	1.99	0.44
5:LD:241:ASN:HB3	43:Ly:53:MET:HE1	2.00	0.44
5:LD:291:SER:N	41:Lw:53:PRO:O	2.51	0.44
12:LP:204:GLU:O	12:LP:208:ASN:ND2	2.51	0.44
31:Ll:136:ARG:NH1	31:Ll:140:GLU:OE2	2.51	0.44
39:Lt:260:LEU:HG	39:Lt:264:LEU:HD12	1.99	0.44
57:SG:129:ALA:HB3	57:SG:134:GLN:HG3	2.00	0.44
75:Se:159:HIS:CD2	75:Se:267:ALA:HB2	2.53	0.44
81:Sn:130:VAL:HG12	81:Sn:133:ILE:HD12	2.00	0.44
82:So:413:ASP:OD1	82:So:413:ASP:N	2.48	0.44
82:So:497:LEU:HB3	82:So:534:LEU:HD12	1.99	0.44
83:S1:77:C:H42	83:S1:103:A:H61	0.68	0.44
83:S1:424:U:H2'	83:S1:425:G:H8	1.82	0.44
1:L1:1125:U:H2'	1:L1:1126:G:H8	1.81	0.44
1:L1:1393:G:O2'	1:L1:1396:C:OP2	2.26	0.44
6:LI:58:ARG:HA	6:LI:80:TYR:HA	2.00	0.44
17:LU:112:ASP:O	17:LU:194:ARG:HA	2.18	0.44
52:Sf:90:LYS:HD2	52:Sf:232:GLN:HB2	1.99	0.44
52:Sf:316:CYS:HB3	52:Sf:319:GLN:HB2	2.00	0.44
54:SZ:39:ALA:HB3	54:SZ:59:PRO:HG3	1.99	0.44
56:SF:78:MET:HG3	56:SF:93:ILE:HD11	1.99	0.44
57:SG:194:LYS:NZ	83:S1:773:U:OP2	2.38	0.44
58:SI:257:ILE:HG23	58:SI:354:SER:HA	1.99	0.44
64:SP:114:ARG:HA	64:SP:117:GLU:HG3	2.00	0.44
73:Sc:360:VAL:O	73:Sc:364:LEU:CB	2.60	0.44
75:Se:123:ARG:HG2	75:Se:306:ILE:HB	2.00	0.44
83:S1:625:A:N1	83:S1:656:G:O2'	2.40	0.44
1:L1:247:A:O2'	1:L1:313:U:O4	2.29	0.44
1:L1:833:A:H5'	1:L1:1425:G:H4'	2.00	0.44
1:L1:1219:C:H2'	1:L1:1220:U:H6	1.83	0.44
13:LQ:18:MET:HE3	13:LQ:48:ARG:HG2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:Lv:101:THR:HG22	47:L5:41:THR:HG23	1.99	0.44
43:Ly:83:TRP:HZ3	43:Ly:90:ARG:HG2	1.83	0.44
58:SI:392:THR:HG21	83:S1:714:G:H4'	2.00	0.44
62:SN:114:LEU:HB3	62:SN:120:LEU:HD23	1.99	0.44
73:Sc:180:LEU:HD13	73:Sc:360:VAL:HG22	2.00	0.44
73:Sc:202:ARG:HD2	73:Sc:247:MET:HE2	1.99	0.44
78:Sj:96:ARG:HH11	78:Sj:96:ARG:HA	1.83	0.44
1:L1:8:C:N4	1:L1:103:A:OP2	2.33	0.44
5:LD:113:LYS:HD2	5:LD:157:GLY:HA2	1.99	0.44
22:Lb:230:TYR:HB3	34:Lo:92:PHE:CE2	2.53	0.44
66:SS:83:GLY:HA3	83:S1:233:C:H5'	1.99	0.44
67:ST:58:TYR:CE1	70:SY:72:ALA:HA	2.53	0.44
78:Sj:31:SER:HB3	78:Sj:106:ALA:HB2	2.00	0.44
81:Sn:177:TRP:HD1	81:Sn:182:LEU:HD11	1.82	0.44
83:S1:359:U:H2'	83:S1:360:G:H8	1.82	0.44
83:S1:779:U:H2'	83:S1:780:A:C8	2.52	0.44
1:L1:169:C:H2'	1:L1:170:C:C6	2.53	0.44
1:L1:223:A:H4'	1:L1:224:G:H5'	2.00	0.44
1:L1:1499:C:H2'	1:L1:1500:C:C6	2.53	0.44
10:LN:98:PRO:HA	15:LS:162:ILE:HG12	2.00	0.44
19:LW:29:VAL:O	19:LW:41:GLN:HB3	2.18	0.44
41:Lw:118:TRP:NE1	41:Lw:142:GLU:OE2	2.41	0.44
61:SL:78:ARG:HB2	61:SL:118:LEU:HD11	2.00	0.44
63:SO:123:ARG:HD2	63:SO:123:ARG:HA	1.83	0.44
78:Sj:162:ALA:O	78:Sj:194:GLN:NE2	2.50	0.44
79:Sk:184:ASP:O	79:Sk:187:LYS:HG2	2.18	0.44
83:S1:836:C:C4	83:S1:920:A:N1	2.86	0.44
1:L1:345:G:H5'	1:L1:346:C:H5	1.83	0.43
1:L1:395:A:C5	21:La:74:ARG:HD2	2.52	0.43
9:LM:138:LEU:HD23	9:LM:141:LEU:HD12	2.00	0.43
30:Lk:309:LEU:HG	30:Lk:313:MET:HE3	1.99	0.43
39:Lt:213:TYR:HB2	39:Lt:233:PHE:HE2	1.83	0.43
41:Lw:107:MET:HE3	41:Lw:107:MET:HB2	1.82	0.43
58:SI:91:MET:HB2	58:SI:91:MET:HE2	1.91	0.43
58:SI:201:ILE:HG13	58:SI:204:GLU:H	1.83	0.43
59:SJ:159:TYR:OH	79:Sk:122:HIS:ND1	2.49	0.43
66:SS:92:LYS:HA	66:SS:144:VAL:HB	2.00	0.43
71:Sa:67:PHE:HB3	71:Sa:70:MET:HE3	1.99	0.43
76:Sg:281:GLU:HA	76:Sg:284:LYS:HG2	1.99	0.43
79:Sk:252:ILE:HG22	79:Sk:253:TRP:H	1.82	0.43
82:So:331:ASN:HA	82:So:365:ILE:HD13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:So:444:ASN:HA	82:So:447:PHE:HB2	1.99	0.43
2:L2:62:C:H2'	2:L2:63:G:H8	1.83	0.43
8:LK:20:ILE:HD11	8:LK:42:ARG:HG2	1.99	0.43
11:LO:175:THR:HG21	11:LO:259:ARG:NH1	2.30	0.43
36:Lq:15:LEU:HD11	37:Lr:169:VAL:HA	2.00	0.43
39:Lt:266:PRO:HB2	39:Lt:267:LYS:H	1.57	0.43
43:Ly:45:ASP:O	43:Ly:51:ARG:NE	2.47	0.43
50:L8:134:ASN:HA	50:L8:137:GLN:HG3	2.00	0.43
52:Sf:219:ARG:HE	52:Sf:219:ARG:HB3	1.62	0.43
56:SF:3:ARG:NH2	56:SF:67:ASP:OD2	2.38	0.43
59:SJ:115:ILE:HA	59:SJ:136:MET:O	2.17	0.43
69:SX:140:ASP:HB2	69:SX:183:LYS:HD3	2.00	0.43
76:Sg:277:LEU:O	76:Sg:281:GLU:HB2	2.17	0.43
79:Sk:137:LEU:HD12	79:Sk:142:LYS:HG3	1.99	0.43
83:S1:168:C:N3	83:S1:173:G:N1	2.66	0.43
83:S1:226:G:N3	83:S1:274:U:O2'	2.50	0.43
83:S1:864:C:H3'	83:S1:865:A:H5''	2.01	0.43
1:L1:1141:G:H2'	1:L1:1142:U:C6	2.53	0.43
1:L1:1280:U:H2'	1:L1:1281:A:C8	2.54	0.43
11:LO:277:MET:HE2	11:LO:277:MET:HB3	1.96	0.43
17:LU:76:HIS:ND1	35:Lp:50:ALA:HA	2.33	0.43
31:Ll:364:ARG:HA	31:Ll:367:ASP:HB2	2.00	0.43
34:Lo:114:LEU:HA	34:Lo:117:TYR:HD2	1.84	0.43
39:Lt:65:PRO:HA	39:Lt:68:GLU:HG2	2.00	0.43
69:SX:75:VAL:HA	69:SX:78:ILE:HG12	2.00	0.43
73:Sc:272:ASP:HA	73:Sc:346:LYS:HE2	2.00	0.43
73:Sc:294:ASP:OD1	73:Sc:294:ASP:N	2.49	0.43
82:So:493:MET:HA	82:So:496:LEU:HG	1.99	0.43
83:S1:515:A:H1'	83:S1:851:C:H5'	2.00	0.43
1:L1:992:A:OP1	1:L1:1489:A:O2'	2.33	0.43
1:L1:1182:C:H5	26:Lg:32:THR:HG21	1.83	0.43
3:LB:176:ALA:HB1	3:LB:244:VAL:HG11	2.00	0.43
7:LJ:105:SER:O	7:LJ:108:ASP:N	2.51	0.43
8:LK:59:ASP:OD1	46:L4:77:ILE:HG13	2.18	0.43
25:Lf:137:ILE:O	25:Lf:141:ILE:HG12	2.18	0.43
32:Lm:61:ARG:NH2	38:Ls:275:PRO:HD2	2.31	0.43
39:Lt:86:ASP:OD1	39:Lt:86:ASP:N	2.51	0.43
54:SZ:115:ASN:HD21	76:Sg:310:LEU:HA	1.84	0.43
56:SF:21:THR:HG23	56:SF:24:ARG:HH21	1.84	0.43
75:Se:117:PHE:HB3	75:Se:303:GLY:HA2	1.99	0.43
76:Sg:364:LEU:HD13	76:Sg:372:HIS:HE1	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:Sj:63:ARG:HB3	78:Sj:66:GLN:HB3	1.99	0.43
79:Sk:211:ARG:NH1	79:Sk:221:TYR:OH	2.52	0.43
83:S1:355:C:H2'	83:S1:356:A:C8	2.53	0.43
1:L1:1058:C:H2'	1:L1:1059:U:C6	2.53	0.43
4:LC:128:HIS:HA	4:LC:191:THR:O	2.19	0.43
23:Lu:102:TRP:HE3	23:Lu:142:LEU:HD22	1.82	0.43
30:Lk:215:ARG:NH2	30:Lk:367:ASN:OD1	2.51	0.43
38:Ls:158:ASP:OD1	38:Ls:158:ASP:N	2.51	0.43
42:Lx:71:GLU:O	42:Lx:75:LYS:HG2	2.18	0.43
44:Lz:99:GLN:HA	44:Lz:102:GLN:HG2	1.99	0.43
45:L3:8:LEU:HD12	45:L3:8:LEU:HA	1.89	0.43
45:L3:63:CYS:SG	45:L3:64:VAL:N	2.91	0.43
55:SE:285:TYR:CD2	55:SE:286:GLU:HG2	2.54	0.43
58:SI:132:PHE:CD1	79:Sk:95:VAL:HG11	2.53	0.43
59:SJ:76:LEU:HD11	59:SJ:173:THR:HB	2.00	0.43
62:SN:38:VAL:HB	77:Si:52:TYR:HD2	1.84	0.43
62:SN:53:ARG:HH21	76:Sg:372:HIS:CD2	2.35	0.43
62:SN:85:VAL:HG22	83:S1:586:C:N4	2.34	0.43
78:Sj:65:LEU:HG	78:Sj:112:GLY:N	2.31	0.43
83:S1:267:A:H2'	83:S1:268:C:C6	2.53	0.43
1:L1:571:A:OP1	51:SR:150:TYR:OH	2.30	0.43
1:L1:1540:C:O2'	4:LC:47:THR:O	2.33	0.43
7:LJ:82:LEU:O	7:LJ:86:ILE:HG12	2.19	0.43
8:LK:122:ARG:HG2	8:LK:137:LEU:HD21	2.01	0.43
25:Lf:179:ARG:NH2	38:Ls:292:GLU:OE1	2.52	0.43
31:Ll:233:LEU:HD12	31:Ll:298:PHE:CD1	2.53	0.43
39:Lt:164:LYS:HA	39:Lt:169:ASP:HA	2.00	0.43
57:SG:168:TYR:HB3	57:SG:236:LEU:HD13	2.01	0.43
69:SX:223:ARG:O	69:SX:227:VAL:HG23	2.18	0.43
70:SY:86:ASP:HA	74:Sd:101:ILE:HG22	2.01	0.43
71:Sa:24:LYS:HA	71:Sa:108:LYS:HE3	2.01	0.43
83:S1:297:U:H2'	83:S1:298:G:C8	2.53	0.43
1:L1:1078:A:H2'	1:L1:1079:A:H8	1.83	0.43
39:Lt:184:LEU:HB3	39:Lt:234:PHE:CZ	2.53	0.43
41:Lw:154:ASP:N	41:Lw:154:ASP:OD1	2.51	0.43
45:L3:12:PRO:O	45:L3:69:GLY:N	2.32	0.43
53:SB:159:ALA:O	53:SB:162:CYS:C	2.62	0.43
58:SI:255:GLN:HE22	58:SI:362:GLU:HA	1.83	0.43
59:SJ:74:LYS:O	59:SJ:176:GLN:HB2	2.19	0.43
59:SJ:149:THR:O	59:SJ:153:ALA:CB	2.67	0.43
67:ST:78:GLN:HE21	72:Sb:190:ALA:HB2	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:SX:271:MET:HE1	69:SX:284:LEU:HD11	2.00	0.43
75:Se:153:LEU:HD11	75:Se:244:LEU:HG	2.00	0.43
79:Sk:108:ILE:HG22	79:Sk:110:ASN:H	1.82	0.43
79:Sk:139:SER:HB3	79:Sk:142:LYS:HB2	2.01	0.43
82:So:115:ASN:HA	82:So:118:LYS:HB2	2.00	0.43
83:S1:485:U:H2'	83:S1:486:C:C6	2.53	0.43
1:L1:609:U:OP2	43:Ly:46:ARG:NH1	2.43	0.43
5:LD:181:LYS:HD3	5:LD:181:LYS:HA	1.75	0.43
19:LW:37:GLU:OE1	19:LW:37:GLU:N	2.52	0.43
24:Ld:46:PHE:CZ	24:Ld:111:LYS:HG2	2.54	0.43
38:Ls:90:PRO:HB2	38:Ls:269:TRP:HE1	1.84	0.43
45:L3:75:ILE:HB	51:SR:48:ILE:HG12	2.01	0.43
53:SB:137:TYR:O	53:SB:264:ARG:NH1	2.49	0.43
60:SK:71:SER:O	60:SK:74:ARG:NH1	2.40	0.43
62:SN:128:TRP:NE1	83:S1:806:A:OP1	2.37	0.43
67:ST:103:LYS:HA	67:ST:103:LYS:HD3	1.73	0.43
73:Sc:304:ASP:OD1	73:Sc:308:GLN:NE2	2.43	0.43
83:S1:406:A:N1	83:S1:453:C:O2'	2.43	0.43
83:S1:599:U:O2	83:S1:600:G:N1	2.51	0.43
1:L1:488:U:OP2	51:SR:195:TYR:OH	2.33	0.43
1:L1:503:G:N7	1:L1:528:A:O2'	2.51	0.43
2:L2:2:A:H2'	2:L2:3:G:C8	2.54	0.43
5:LD:283:LEU:HD12	11:LO:189:LYS:HE2	2.00	0.43
11:LO:104:LEU:HD11	11:LO:126:GLY:HA3	2.00	0.43
13:LQ:32:LEU:HB3	13:LQ:52:MET:HG3	2.00	0.43
20:LX:199:MET:HE3	20:LX:199:MET:HB3	1.95	0.43
31:Ll:215:THR:HB	31:Ll:275:GLN:HE22	1.83	0.43
52:Sf:307:ARG:HE	52:Sf:310:ARG:HB2	1.84	0.43
54:SZ:106:ASP:OD1	54:SZ:122:VAL:HG11	2.19	0.43
55:SE:93:LEU:H	77:Si:75:HIS:CD2	2.37	0.43
56:SF:24:ARG:NH2	56:SF:87:ASP:OD2	2.34	0.43
58:SI:227:LYS:HB3	58:SI:227:LYS:HE2	1.84	0.43
60:SK:80:PHE:CE1	68:SW:13:MET:HE1	2.54	0.43
62:SN:56:SER:HB3	77:Si:36:LEU:HD23	2.00	0.43
63:SO:82:ILE:O	63:SO:85:VAL:HG22	2.19	0.43
79:Sk:142:LYS:HD2	79:Sk:142:LYS:HA	1.82	0.43
1:L1:1269:C:H2'	1:L1:1270:A:C8	2.54	0.43
2:L2:26:C:H2'	2:L2:27:C:H6	1.83	0.43
6:LI:116:LYS:HE3	6:LI:120:ARG:HH12	1.84	0.43
15:LS:148:THR:HG22	15:LS:165:GLU:HG2	2.00	0.43
38:Ls:218:THR:OG1	38:Ls:219:ARG:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Lt:160:LEU:HG	39:Lt:171:TRP:HB3	2.00	0.43
58:SI:315:PHE:HD2	58:SI:369:LEU:HD21	1.83	0.43
64:SP:67:ALA:HB2	69:SX:196:TYR:CZ	2.54	0.43
81:Sn:177:TRP:CD1	81:Sn:182:LEU:HD11	2.53	0.43
83:S1:702:U:H2'	83:S1:703:G:C8	2.54	0.43
1:L1:1024:A:C6	1:L1:1315:C:H1'	2.53	0.42
5:LD:48:LEU:HD21	42:Lx:95:ARG:HB2	2.00	0.42
11:LO:123:ASN:O	11:LO:125:ARG:NH1	2.52	0.42
14:LR:81:ARG:NH2	14:LR:94:GLU:OE2	2.44	0.42
19:LW:130:LEU:HA	20:LX:107:THR:HG21	2.00	0.42
58:SI:380:LYS:HZ3	58:SI:380:LYS:HG2	1.71	0.42
60:SK:192:ARG:HB3	60:SK:194:LEU:HD23	2.00	0.42
76:Sg:311:TRP:HB2	76:Sg:313:PHE:CE2	2.54	0.42
83:S1:246:G:HO2'	83:S1:261:C:HO2'	1.67	0.42
83:S1:865:A:H4'	83:S1:866:A:H3'	2.00	0.42
1:L1:1002:A:OP1	18:LV:111:LYS:NZ	2.37	0.42
6:LI:138:LYS:O	6:LI:141:GLU:HG3	2.19	0.42
14:LR:90:GLU:HG2	14:LR:105:SER:HB2	2.01	0.42
17:LU:118:ASN:C	17:LU:118:ASN:ND2	2.76	0.42
28:Li:106:THR:HG23	28:Li:162:THR:HA	2.01	0.42
31:Ll:161:LEU:HG	31:Ll:221:LEU:HD21	2.01	0.42
32:Lm:44:ARG:HB3	32:Lm:261:ILE:HD12	2.00	0.42
32:Lm:148:MET:HE1	32:Lm:255:HIS:HB2	2.00	0.42
38:Ls:90:PRO:HG2	38:Ls:267:PRO:HA	2.00	0.42
54:SZ:77:ASP:OD2	59:SJ:140:TYR:OH	2.36	0.42
54:SZ:99:THR:HG23	54:SZ:100:PHE:HD1	1.84	0.42
59:SJ:80:VAL:HA	59:SJ:170:MET:O	2.20	0.42
59:SJ:158:GLU:HA	59:SJ:161:GLN:NE2	2.33	0.42
62:SN:58:ARG:NH2	62:SN:71:ALA:O	2.52	0.42
67:ST:94:ARG:NH1	67:ST:101:GLY:HA2	2.35	0.42
83:S1:191:U:H2'	83:S1:192:A:C8	2.53	0.42
83:S1:328:A:H2'	83:S1:329:A:C8	2.54	0.42
83:S1:625:A:N6	83:S1:673:G:O2'	2.51	0.42
83:S1:778:U:H2'	83:S1:779:U:H6	1.84	0.42
1:L1:215:A:H5'	5:LD:166:PRO:HB3	2.02	0.42
1:L1:530:A:O2'	46:L4:133:SER:O	2.37	0.42
1:L1:995:U:OP2	13:LQ:17:ARG:HD2	2.19	0.42
3:LB:292:MET:HE2	3:LB:292:MET:HB3	1.91	0.42
5:LD:199:ASP:OD2	5:LD:202:TYR:N	2.51	0.42
12:LP:89:ILE:O	12:LP:160:VAL:N	2.44	0.42
26:Lg:43:LEU:O	26:Lg:55:LEU:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:L8:37:PRO:HG3	50:L8:68:SER:HA	2.01	0.42
51:SR:38:VAL:HA	51:SR:50:GLU:O	2.19	0.42
54:SZ:97:TRP:HZ3	55:SE:94:THR:HG22	1.84	0.42
59:SJ:115:ILE:HD12	59:SJ:137:ARG:HG2	2.00	0.42
59:SJ:155:VAL:HG21	79:Sk:129:PHE:HB2	2.00	0.42
60:SK:184:ASN:OD1	68:SW:42:ARG:NH2	2.53	0.42
63:SO:92:LEU:HD23	72:Sb:160:LEU:HD21	2.01	0.42
66:SS:89:ARG:NH1	83:S1:23:C:OP1	2.52	0.42
71:Sa:12:THR:HG23	71:Sa:14:GLN:HG2	2.00	0.42
75:Se:165:CYS:HB2	75:Se:168:LEU:HD21	2.00	0.42
78:Sj:56:ALA:O	78:Sj:60:ARG:HG2	2.18	0.42
82:So:439:LEU:HD11	82:So:448:ILE:HG12	2.01	0.42
82:So:576:LEU:HB3	82:So:599:PHE:CZ	2.54	0.42
83:S1:24:U:H2'	83:S1:25:A:C8	2.54	0.42
1:L1:29:C:N4	23:Lu:198:ARG:O	2.50	0.42
1:L1:1075:A:O2'	22:Lb:102:LYS:O	2.28	0.42
13:LQ:155:ASP:OD2	32:Lm:319:ARG:NE	2.35	0.42
21:La:100:THR:HG1	21:La:132:HIS:CD2	2.36	0.42
36:Lq:15:LEU:HD23	36:Lq:15:LEU:HA	1.92	0.42
37:Lr:258:THR:OG1	37:Lr:271:PHE:O	2.35	0.42
61:SL:69:LYS:HD2	61:SL:77:ASN:HB3	2.01	0.42
63:SO:176:ASP:OD1	63:SO:177:VAL:N	2.51	0.42
67:ST:95:HIS:CD2	67:ST:96:ILE:HG13	2.55	0.42
82:So:493:MET:HB3	82:So:527:LEU:HD13	2.00	0.42
83:S1:514:A:H2'	83:S1:515:A:C8	2.55	0.42
1:L1:1040:C:O2'	1:L1:1550:A:N1	2.46	0.42
5:LD:79:LEU:HD12	5:LD:79:LEU:HA	1.89	0.42
8:LK:114:LEU:HA	8:LK:117:VAL:HG12	2.00	0.42
10:LN:73:ILE:HD11	10:LN:105:VAL:HG11	2.02	0.42
13:LQ:150:GLN:O	13:LQ:154:GLN:HG3	2.20	0.42
20:LX:137:PHE:CE1	20:LX:143:ARG:HD3	2.55	0.42
31:Ll:58:ARG:O	31:Ll:62:GLU:HG2	2.20	0.42
32:Lm:167:VAL:HG22	32:Lm:235:TYR:CD2	2.54	0.42
50:L8:108:LEU:HD23	50:L8:108:LEU:HA	1.88	0.42
50:L8:150:LYS:HD3	50:L8:150:LYS:HA	1.74	0.42
52:Sf:257:VAL:HG21	52:Sf:392:ILE:HD12	2.01	0.42
53:SB:118:LEU:HD23	53:SB:118:LEU:HA	1.87	0.42
54:SZ:76:LEU:O	62:SN:103:ARG:NH2	2.52	0.42
54:SZ:94:LYS:NZ	55:SE:89:PHE:O	2.40	0.42
55:SE:225:VAL:HG22	55:SE:243:VAL:HG12	2.02	0.42
61:SL:51:PRO:HG3	61:SL:122:LYS:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:SS:181:HIS:HB3	66:SS:184:VAL:HG22	2.01	0.42
72:Sb:135:GLN:HG3	72:Sb:139:GLN:NE2	2.34	0.42
73:Sc:219:VAL:HG11	73:Sc:356:THR:HG22	2.02	0.42
73:Sc:312:LYS:HB2	73:Sc:312:LYS:HE2	1.91	0.42
82:So:112:SER:O	82:So:116:VAL:HG23	2.20	0.42
82:So:418:SER:O	82:So:422:ILE:HG12	2.20	0.42
1:L1:19:C:H5'	22:Lb:5:LYS:HG2	2.02	0.42
1:L1:357:A:O2'	1:L1:378:U:OP1	2.34	0.42
2:L2:21:A:H2'	2:L2:22:G:C8	2.54	0.42
7:LJ:104:LEU:O	7:LJ:109:LYS:HG2	2.20	0.42
8:LK:130:PHE:O	8:LK:133:GLN:O	2.37	0.42
9:LM:20:LEU:HD22	9:LM:141:LEU:HD13	2.00	0.42
31:Ll:206:TYR:OH	31:Ll:242:GLY:O	2.35	0.42
42:Lx:116:ARG:O	42:Lx:120:MET:HG2	2.18	0.42
56:SF:30:MET:HE2	56:SF:30:MET:HB3	1.84	0.42
56:SF:39:LEU:HD22	72:Sb:180:ALA:HB1	2.02	0.42
58:SI:158:TYR:CE1	58:SI:162:MET:HE2	2.54	0.42
62:SN:41:ARG:HD3	62:SN:87:ILE:HD12	2.02	0.42
64:SP:108:GLU:HA	64:SP:111:ARG:HG2	2.02	0.42
69:SX:275:PHE:O	69:SX:278:ASN:O	2.38	0.42
69:SX:282:ASP:N	69:SX:282:ASP:OD1	2.48	0.42
72:Sb:60:TYR:HB3	72:Sb:64:ARG:NH1	2.34	0.42
75:Se:121:ALA:HA	75:Se:304:GLY:O	2.18	0.42
76:Sg:368:GLN:HA	76:Sg:371:GLU:HG3	2.01	0.42
82:So:342:LEU:HB2	82:So:349:ALA:HB1	2.01	0.42
82:So:343:ARG:HD2	82:So:377:ARG:HB3	2.01	0.42
83:S1:33:U:H2'	83:S1:34:U:H6	1.83	0.42
83:S1:791:A:H2'	83:S1:792:A:C8	2.54	0.42
1:L1:1044:A:P	4:LC:239:ARG:HH21	2.43	0.42
14:LR:94:GLU:HG2	14:LR:100:VAL:HG22	2.02	0.42
15:LS:194:LEU:HB2	15:LS:197:TYR:CD2	2.55	0.42
23:Lu:191:ASN:HB3	23:Lu:194:TYR:HB3	2.02	0.42
30:Lk:211:ALA:HB1	30:Lk:322:LEU:HD23	2.02	0.42
30:Lk:229:ARG:HH21	30:Lk:288:PRO:HG3	1.84	0.42
31:Ll:103:LEU:HG	31:Ll:107:LYS:HE2	2.02	0.42
31:Ll:139:TRP:O	31:Ll:144:GLY:N	2.45	0.42
40:Lv:97:ALA:HB3	40:Lv:103:ALA:HB2	2.01	0.42
73:Sc:288:LYS:O	73:Sc:292:SER:OG	2.31	0.42
79:Sk:126:LEU:HD21	82:So:70:VAL:HG13	2.00	0.42
83:S1:410:G:H4'	83:S1:931:A:H4'	2.02	0.42
1:L1:19:C:N4	22:Lb:14:LEU:HB3	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L1:179:C:O2'	1:L1:181:G:N7	2.45	0.42
1:L1:287:A:C4	18:LV:163:ARG:HD2	2.55	0.42
1:L1:916:U:H2'	1:L1:917:G:C8	2.55	0.42
7:LJ:121:ILE:HG12	7:LJ:164:MET:SD	2.60	0.42
7:LJ:143:LEU:HB3	7:LJ:147:PHE:CE2	2.53	0.42
10:LN:94:PRO:O	10:LN:97:THR:OG1	2.37	0.42
12:LP:38:SER:OG	12:LP:40:GLU:OE2	2.36	0.42
12:LP:118:MET:HE2	12:LP:118:MET:HB3	1.95	0.42
31:L1:113:LEU:HD12	31:L1:119:GLU:HG3	2.02	0.42
31:L1:308:GLN:HE22	44:Lz:109:LEU:HA	1.84	0.42
52:Sf:358:GLN:NE2	52:Sf:424:PHE:O	2.52	0.42
53:SB:197:HIS:NE2	53:SB:240:ASP:HB2	2.35	0.42
63:SO:150:LYS:HD2	83:S1:405:C:H5'	2.02	0.42
73:Sc:341:LEU:HB3	73:Sc:347:ILE:HD11	2.01	0.42
74:Sd:102:GLY:O	74:Sd:139:ARG:HA	2.20	0.42
79:Sk:123:CYS:O	79:Sk:127:LYS:HB2	2.20	0.42
82:So:248:PHE:CZ	82:So:254:LYS:HD3	2.55	0.42
82:So:339:LEU:HD23	82:So:342:LEU:HD21	2.02	0.42
82:So:342:LEU:HD13	82:So:378:LEU:HD22	2.02	0.42
1:L1:1064:A:H2'	1:L1:1065:G:H8	1.83	0.42
85:L1:1705:T1C:H953	85:L1:1705:T1C:H921	1.79	0.42
3:LB:127:ILE:HD11	30:Lk:114:LEU:HD21	2.02	0.42
39:Lt:55:ARG:HA	39:Lt:56:PRO:HD3	1.90	0.42
54:SZ:105:ALA:O	54:SZ:161:LYS:NZ	2.37	0.42
57:SG:157:GLY:O	57:SG:171:PRO:HA	2.19	0.42
58:SI:111:LEU:HD12	79:Sk:112:LEU:HD23	2.02	0.42
64:SP:99:LEU:HD11	69:SX:148:LEU:HD11	2.02	0.42
67:ST:102:LYS:O	67:ST:106:GLU:HG2	2.20	0.42
83:S1:793:G:H2'	83:S1:794:A:H8	1.84	0.42
1:L1:197:A:H5'	5:LD:152:ALA:HB3	2.02	0.42
1:L1:282:U:H2'	1:L1:283:A:C8	2.55	0.42
1:L1:1408:C:H2'	1:L1:1409:G:C8	2.55	0.42
3:LB:73:THR:H	3:LB:106:MET:HE3	1.84	0.42
16:LT:18:TYR:CD1	43:Ly:32:ILE:HD11	2.55	0.42
24:Ld:67:HIS:O	24:Ld:99:VAL:HA	2.20	0.42
28:Li:126:LYS:HE3	28:Li:126:LYS:HB3	1.86	0.42
57:SG:115:LEU:HD13	57:SG:142:TYR:HE1	1.84	0.42
57:SG:187:MET:HE1	57:SG:208:LYS:HB3	2.01	0.42
58:SI:110:TYR:HD2	58:SI:111:LEU:HD22	1.85	0.42
60:SK:150:VAL:HG22	60:SK:176:THR:HB	2.01	0.42
63:SO:71:THR:HB	63:SO:95:LEU:HD12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:SP:84:SER:O	64:SP:87:MET:N	2.52	0.42
71:Sa:95:ASN:OD1	71:Sa:95:ASN:N	2.53	0.42
82:So:438:LEU:O	82:So:441:THR:OG1	2.37	0.42
83:S1:55:C:OP1	83:S1:201:U:O2'	2.38	0.42
83:S1:196:G:N2	83:S1:198:A:H3'	2.35	0.42
83:S1:462:A:H2'	83:S1:463:A:H8	1.85	0.42
1:L1:1332:G:H2'	1:L1:1333:A:H8	1.85	0.41
4:LC:235:LYS:HB2	4:LC:235:LYS:HE3	1.84	0.41
8:LK:103:GLN:HB3	8:LK:106:LYS:HD2	2.02	0.41
30:Lk:99:TYR:HD1	30:Lk:270:ILE:HG12	1.85	0.41
30:Lk:115:GLU:HB2	30:Lk:119:GLN:HB2	2.02	0.41
30:Lk:219:LEU:HA	30:Lk:219:LEU:HD12	1.77	0.41
34:Lo:68:PHE:CE2	34:Lo:70:LEU:HB2	2.54	0.41
38:Ls:152:LEU:HD21	38:Ls:172:MET:HG3	2.02	0.41
53:SB:142:ILE:HG13	53:SB:192:LEU:HB3	2.01	0.41
53:SB:152:SER:OG	53:SB:169:ARG:NH1	2.43	0.41
58:SI:127:HIS:ND1	58:SI:129:GLU:HB3	2.35	0.41
62:SN:37:ASP:HB3	77:Si:52:TYR:HE2	1.85	0.41
66:SS:136:TYR:HD2	66:SS:138:PRO:HD2	1.85	0.41
69:SX:202:ARG:HG3	69:SX:234:GLN:HA	2.02	0.41
75:Se:67:HIS:CD2	75:Se:100:MET:HB3	2.55	0.41
78:Sj:95:TRP:CE2	78:Sj:131:ILE:HG13	2.54	0.41
80:Sm:69:GLU:OE1	80:Sm:69:GLU:N	2.53	0.41
81:Sn:138:MET:HE2	83:S1:842:G:H4'	2.01	0.41
1:L1:241:C:H2'	1:L1:242:A:H8	1.85	0.41
1:L1:1078:A:H2'	1:L1:1079:A:C8	2.54	0.41
7:LJ:115:GLN:NE2	7:LJ:116:LEU:HG	2.34	0.41
20:LX:160:PRO:O	20:LX:161:ARG:HG3	2.21	0.41
31:Ll:257:PRO:HB3	31:Ll:268:LEU:HD21	2.02	0.41
33:Ln:169:PHE:CZ	40:Lv:186:VAL:HB	2.55	0.41
39:Lt:198:ASN:HB2	39:Lt:200:MET:HG2	2.01	0.41
54:SZ:114:GLY:O	79:Sk:160:GLY:N	2.53	0.41
60:SK:187:ARG:O	83:S1:419:C:O2'	2.36	0.41
62:SN:59:LYS:NZ	77:Si:36:LEU:HB2	2.35	0.41
64:SP:17:LEU:HD23	64:SP:17:LEU:HA	1.92	0.41
69:SX:225:VAL:HG11	69:SX:265:THR:HG21	2.01	0.41
69:SX:293:LEU:HB3	69:SX:296:ASP:HB3	2.02	0.41
73:Sc:86:ASP:OD1	73:Sc:124:LYS:NZ	2.54	0.41
83:S1:328:A:H2'	83:S1:329:A:H8	1.85	0.41
83:S1:485:U:H2'	83:S1:486:C:H6	1.85	0.41
83:S1:543:C:H2'	83:S1:544:C:H6	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L2:42:A:N3	33:Ln:126:GLN:NE2	2.66	0.41
24:Ld:53:HIS:O	24:Ld:57:GLY:HA2	2.21	0.41
42:Lx:62:PRO:HA	42:Lx:63:PRO:HD3	1.94	0.41
51:SR:169:TRP:CE3	51:SR:170:ASN:HB2	2.55	0.41
59:SJ:94:PHE:CE1	79:Sk:114:LEU:HD13	2.55	0.41
69:SX:167:HIS:O	69:SX:189:ARG:NH2	2.46	0.41
71:Sa:141:CYS:HB3	71:Sa:149:CYS:HB2	2.02	0.41
1:L1:431:C:H2'	1:L1:432:A:H8	1.86	0.41
6:LI:79:VAL:HA	22:Lb:89:GLN:HB2	2.01	0.41
11:LO:118:LEU:HD23	11:LO:187:VAL:HG13	2.03	0.41
11:LO:123:ASN:CG	41:Lw:53:PRO:HB3	2.46	0.41
11:LO:179:TYR:HH	11:LO:260:LYS:HZ1	1.63	0.41
15:LS:195:PRO:O	15:LS:199:THR:HG23	2.19	0.41
18:LV:169:LYS:HA	18:LV:169:LYS:HD2	1.79	0.41
20:LX:69:ASP:HB3	20:LX:91:LEU:HD12	2.02	0.41
24:Ld:53:HIS:CE1	24:Ld:60:PRO:HG3	2.56	0.41
24:Ld:140:LYS:HB3	24:Ld:140:LYS:HE2	1.69	0.41
30:Lk:125:LYS:HG2	30:Lk:371:LYS:HG3	2.02	0.41
51:SR:99:MET:SD	51:SR:116:GLU:HG3	2.59	0.41
53:SB:214:LYS:HG2	70:SY:7:GLU:OE2	2.20	0.41
55:SE:425:LEU:HD13	66:SS:85:VAL:HG11	2.02	0.41
57:SG:62:GLU:HB2	57:SG:66:ARG:NH1	2.35	0.41
59:SJ:161:GLN:HE21	59:SJ:162:ARG:HH12	1.67	0.41
62:SN:85:VAL:HG21	83:S1:756:A:H62	1.86	0.41
63:SO:90:LYS:O	63:SO:94:SER:HB3	2.21	0.41
65:SQ:51:ALA:HB2	65:SQ:66:LEU:HD13	2.01	0.41
68:SW:51:ARG:O	68:SW:55:GLU:HG2	2.21	0.41
73:Sc:236:LEU:HD11	73:Sc:323:GLU:HB2	2.02	0.41
76:Sg:364:LEU:HD22	76:Sg:368:GLN:HG3	2.02	0.41
79:Sk:66:TRP:HZ2	79:Sk:112:LEU:O	2.03	0.41
79:Sk:192:LYS:HE3	79:Sk:243:LYS:NZ	2.35	0.41
82:So:556:LYS:NZ	82:So:595:MET:HB3	2.34	0.41
83:S1:792:A:H2'	83:S1:793:G:H8	1.85	0.41
83:S1:809:U:H2'	83:S1:810:G:O4'	2.20	0.41
1:L1:725:A:O2'	30:Lk:384:GLN:OE1	2.39	0.41
3:LB:187:LEU:HA	3:LB:187:LEU:HD23	1.85	0.41
4:LC:208:ALA:HB2	4:LC:297:VAL:HG12	2.01	0.41
8:LK:140:VAL:O	8:LK:144:ILE:HG12	2.21	0.41
15:LS:106:LEU:O	15:LS:108:ILE:HG13	2.21	0.41
16:LT:26:LYS:HA	16:LT:29:ARG:HG2	2.03	0.41
23:Lu:223:LYS:O	23:Lu:227:GLU:HG2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Ld:71:ARG:HB2	24:Ld:91:LEU:HB3	2.02	0.41
31:Ll:224:HIS:HA	31:Ll:232:TYR:CZ	2.56	0.41
38:Ls:245:TYR:HB2	38:Ls:265:ILE:HB	2.01	0.41
39:Lt:94:GLU:HB3	39:Lt:116:LEU:HD12	2.02	0.41
45:L3:10:LEU:HD22	45:L3:42:VAL:HB	2.03	0.41
45:L3:40:GLU:OE2	45:L3:43:ARG:NH2	2.53	0.41
51:SR:117:GLU:O	51:SR:121:MET:HG3	2.20	0.41
55:SE:231:MET:HG3	83:S1:833:A:C2	2.56	0.41
62:SN:90:ARG:NH2	83:S1:589:C:OP2	2.52	0.41
64:SP:103:MET:HE1	69:SX:148:LEU:HD22	2.02	0.41
67:ST:139:ARG:NH2	67:ST:141:ARG:O	2.53	0.41
71:Sa:14:GLN:O	71:Sa:18:GLN:CB	2.54	0.41
71:Sa:151:SER:OG	83:S1:37:U:O2'	2.33	0.41
73:Sc:116:CYS:HA	73:Sc:121:ALA:HB3	2.01	0.41
78:Sj:167:PRO:HG2	78:Sj:170:LEU:HD12	2.02	0.41
83:S1:501:A:H2'	83:S1:502:G:C8	2.56	0.41
2:L2:2:A:N6	2:L2:68:G:O6	2.54	0.41
5:LD:237:LEU:HD23	5:LD:237:LEU:HA	1.95	0.41
5:LD:286:PHE:HA	5:LD:290:TYR:HE2	1.86	0.41
37:Lr:96:CYS:HB3	37:Lr:182:GLU:HG2	2.03	0.41
38:Ls:281:MET:HE2	38:Ls:281:MET:HB3	1.91	0.41
47:L5:54:VAL:HG11	47:L5:75:LEU:HD23	2.03	0.41
49:L7:108:ALA:O	49:L7:116:ARG:NH2	2.28	0.41
55:SE:209:GLY:N	55:SE:213:GLU:O	2.53	0.41
61:SL:96:PRO:HG3	61:SL:124:THR:HG23	2.03	0.41
63:SO:111:PHE:O	63:SO:115:ILE:HG22	2.21	0.41
69:SX:129:PRO:HD3	69:SX:266:ARG:HD2	2.01	0.41
1:L1:1330:A:H2'	1:L1:1331:G:C8	2.56	0.41
36:Lq:44:ARG:HD2	48:L6:101:TRP:CD1	2.56	0.41
57:SG:137:ILE:HD13	57:SG:137:ILE:HA	1.96	0.41
58:SI:317:PHE:HB3	58:SI:323:LEU:HD23	2.03	0.41
60:SK:65:PRO:HD3	68:SW:13:MET:HE3	2.03	0.41
64:SP:39:ASN:OD1	64:SP:39:ASN:N	2.54	0.41
66:SS:181:HIS:ND1	78:Sj:180:LYS:HE2	2.36	0.41
72:Sb:45:PRO:HB2	78:Sj:53:ARG:HH21	1.86	0.41
73:Sc:186:LEU:HD13	73:Sc:208:LEU:HG	2.02	0.41
75:Se:244:LEU:HD23	75:Se:296:MET:HE1	2.03	0.41
78:Sj:210:LYS:HB3	78:Sj:211:GLY:H	1.76	0.41
79:Sk:115:THR:O	79:Sk:119:ILE:HG12	2.20	0.41
82:So:308:LYS:HG3	82:So:310:GLU:H	1.85	0.41
83:S1:726:U:H2'	83:S1:727:A:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L1:552:U:H2'	1:L1:553:A:N3	2.36	0.41
1:L1:712:A:H2'	1:L1:713:U:C6	2.56	0.41
1:L1:883:G:H2'	1:L1:884:A:C8	2.56	0.41
4:LC:275:ARG:HB3	4:LC:284:TYR:HB2	2.03	0.41
6:LI:123:LEU:HA	6:LI:128:LEU:HB2	2.03	0.41
9:LM:80:HIS:HA	9:LM:86:GLY:O	2.20	0.41
19:LW:5:VAL:HG23	19:LW:7:TYR:HE1	1.85	0.41
31:Ll:161:LEU:HD13	31:Ll:271:LEU:HD11	2.02	0.41
31:Ll:188:TYR:HE2	49:L7:188:LEU:HD22	1.85	0.41
31:Ll:338:ARG:HG2	49:L7:129:ARG:HD2	2.02	0.41
33:Ln:177:HIS:CD2	47:L5:64:ILE:HD11	2.55	0.41
34:Lo:136:LEU:HD23	34:Lo:136:LEU:HA	1.86	0.41
39:Lt:83:LEU:O	47:L5:49:ALA:HA	2.21	0.41
42:Lx:68:SER:O	42:Lx:71:GLU:HB2	2.21	0.41
47:L5:70:GLU:HG3	47:L5:72:ARG:HG3	2.02	0.41
59:SJ:91:TYR:OH	59:SJ:160:ILE:O	2.36	0.41
70:SY:20:VAL:HG11	70:SY:28:LYS:HG2	2.03	0.41
73:Sc:210:LEU:HD13	78:Sj:145:HIS:CD2	2.55	0.41
75:Se:293:LEU:O	75:Se:297:MET:HG2	2.20	0.41
77:Si:11:MET:HE3	79:Sk:239:TRP:HE1	1.86	0.41
77:Si:89:ARG:NH2	83:S1:691:A:OP2	2.43	0.41
82:So:372:TYR:HA	82:So:375:ILE:HG12	2.03	0.41
83:S1:193:A:H2'	83:S1:194:A:C8	2.56	0.41
83:S1:360:G:H2'	83:S1:361:A:H8	1.86	0.41
83:S1:484:C:H2'	83:S1:485:U:C6	2.56	0.41
83:S1:670:A:H3'	83:S1:671:A:H8	1.86	0.41
1:L1:434:A:OP1	12:LP:73:ARG:NH1	2.51	0.41
1:L1:568:A:N3	9:LM:111:MET:HG2	2.36	0.41
1:L1:842:A:O2'	1:L1:871:C:OP1	2.31	0.41
1:L1:859:U:H2'	3:LB:208:ARG:HB2	2.03	0.41
1:L1:1137:U:H2'	1:L1:1138:U:C6	2.56	0.41
1:L1:1198:C:H2'	1:L1:1199:A:O4'	2.20	0.41
2:L2:6:U:H3	2:L2:63:G:H1	1.68	0.41
4:LC:252:TRP:O	4:LC:255:THR:OG1	2.30	0.41
5:LD:126:LYS:HA	5:LD:127:PRO:HD3	1.96	0.41
7:LJ:128:ASN:HB2	7:LJ:132:LYS:HE2	2.03	0.41
10:LN:111:ASN:HB2	10:LN:113:ASN:HD22	1.86	0.41
11:LO:80:LYS:HE3	28:Li:112:ASP:HB3	2.03	0.41
11:LO:182:ARG:O	11:LO:186:ILE:HG12	2.21	0.41
11:LO:202:LYS:HD2	11:LO:263:ARG:HD2	2.01	0.41
17:LU:134:LEU:HD23	17:LU:148:LEU:HD23	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:LW:1:MET:HB3	19:LW:24:PHE:HE2	1.86	0.41
19:LW:28:LEU:N	23:Lu:114:THR:HG22	2.33	0.41
20:LX:109:ILE:HD12	38:Ls:76:ILE:HG21	2.03	0.41
21:La:115:ASP:HA	21:La:118:THR:HG22	2.02	0.41
22:Lb:238:LEU:HD23	22:Lb:238:LEU:HA	1.89	0.41
31:Ll:99:ARG:HA	31:Ll:99:ARG:HD2	1.87	0.41
32:Lm:79:PHE:HB3	32:Lm:81:MET:SD	2.61	0.41
32:Lm:175:ILE:O	32:Lm:319:ARG:NH2	2.38	0.41
32:Lm:192:TRP:CD1	35:Lp:91:VAL:HG11	2.56	0.41
33:Ln:162:ILE:O	40:Lv:86:TYR:HE2	2.04	0.41
37:Lr:54:PRO:HA	37:Lr:55:PRO:HD3	1.95	0.41
53:SB:63:LEU:HD23	53:SB:63:LEU:HA	1.91	0.41
56:SF:96:HIS:HB3	56:SF:99:THR:HG23	2.02	0.41
59:SJ:83:HIS:CE1	62:SN:122:GLY:HA3	2.56	0.41
59:SJ:91:TYR:CE1	59:SJ:165:PRO:HD3	2.56	0.41
63:SO:115:ILE:HD13	63:SO:181:ILE:HD12	2.03	0.41
65:SQ:78:LYS:HB2	65:SQ:78:LYS:HE3	1.76	0.41
66:SS:182:GLY:O	69:SX:183:LYS:NZ	2.39	0.41
73:Sc:372:ILE:O	73:Sc:376:GLU:HG2	2.21	0.41
74:Sd:115:ASP:OD1	74:Sd:116:PHE:N	2.54	0.41
76:Sg:368:GLN:O	76:Sg:372:HIS:ND1	2.54	0.41
78:Sj:133:HIS:HB3	78:Sj:136:TYR:HB2	2.03	0.41
79:Sk:56:ARG:NH2	82:So:91:ASP:O	2.46	0.41
79:Sk:243:LYS:O	79:Sk:244:THR:OG1	2.30	0.41
82:So:198:TYR:CZ	82:So:203:PRO:HG3	2.56	0.41
83:S1:196:G:C2	83:S1:198:A:H5'	2.55	0.41
83:S1:528:G:H2'	83:S1:529:G:C8	2.55	0.41
83:S1:931:A:H2'	83:S1:932:C:C6	2.55	0.41
4:LC:322:ASP:OD1	4:LC:322:ASP:N	2.44	0.41
9:LM:24:LYS:HD2	9:LM:24:LYS:HA	1.89	0.41
10:LN:69:VAL:HG23	10:LN:89:HIS:CE1	2.56	0.41
18:LV:82:TYR:HD2	18:LV:87:MET:HE2	1.86	0.41
28:Li:187:LYS:HE2	28:Li:187:LYS:HB2	1.92	0.41
30:Lk:238:THR:HG21	30:Lk:339:PRO:HD2	2.02	0.41
32:Lm:145:SER:O	32:Lm:149:MET:HG3	2.21	0.41
32:Lm:239:PHE:HZ	32:Lm:265:GLU:HG2	1.86	0.41
37:Lr:244:GLU:O	37:Lr:248:ARG:HG2	2.21	0.41
40:Lv:92:ASN:ND2	40:Lv:192:GLU:OE2	2.54	0.41
53:SB:151:PHE:O	53:SB:155:ILE:HG12	2.21	0.41
55:SE:192:GLY:C	55:SE:194:SER:H	2.29	0.41
67:ST:125:LYS:HE2	67:ST:130:LEU:HD23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:SX:69:THR:OG1	69:SX:70:PHE:N	2.53	0.41
69:SX:106:MET:HE3	69:SX:106:MET:HB3	1.91	0.41
73:Sc:240:LEU:HD21	73:Sc:253:PRO:HB3	2.03	0.41
78:Sj:64:LEU:HD22	78:Sj:65:LEU:HD22	2.02	0.41
79:Sk:106:LEU:HD12	79:Sk:106:LEU:HA	1.84	0.41
82:So:552:ALA:HA	82:So:555:ILE:HD12	2.03	0.41
83:S1:185:U:H2'	83:S1:186:A:H8	1.85	0.41
83:S1:186:A:H2'	83:S1:187:G:C8	2.55	0.41
83:S1:334:C:H2'	83:S1:335:A:H8	1.86	0.41
1:L1:107:A:N6	1:L1:110:U:OP2	2.46	0.40
1:L1:402:A:H2'	1:L1:403:A:C8	2.56	0.40
1:L1:1021:U:H2'	1:L1:1022:G:C8	2.56	0.40
1:L1:1445:U:H2'	1:L1:1446:C:C6	2.56	0.40
7:LJ:61:HIS:CE1	7:LJ:63:SER:HB2	2.56	0.40
9:LM:154:ARG:HG2	51:SR:127:LEU:HA	2.02	0.40
10:LN:40:VAL:HG11	10:LN:47:GLY:HA3	2.04	0.40
18:LV:129:VAL:HG11	18:LV:137:ARG:HB3	2.02	0.40
22:Lb:29:LEU:O	22:Lb:33:GLU:HG2	2.22	0.40
22:Lb:96:LYS:HB2	22:Lb:96:LYS:HE2	1.90	0.40
23:Lu:156:LEU:HD23	23:Lu:156:LEU:HA	1.90	0.40
31:Ll:252:CYS:HB2	31:Ll:286:ARG:HB2	2.03	0.40
36:Lq:33:VAL:O	36:Lq:67:SER:HA	2.20	0.40
39:Lt:162:ARG:HB3	39:Lt:251:HIS:HB2	2.03	0.40
39:Lt:200:MET:HA	39:Lt:241:GLY:HA3	2.02	0.40
53:SB:206:HIS:HB3	53:SB:209:VAL:HG23	2.03	0.40
55:SE:89:PHE:HA	55:SE:92:LYS:HG2	2.03	0.40
55:SE:166:GLU:HA	55:SE:169:GLU:HG3	2.03	0.40
65:SQ:57:GLN:O	65:SQ:87:LYS:NZ	2.55	0.40
69:SX:218:MET:HE3	69:SX:218:MET:HB3	1.84	0.40
77:Si:81:GLU:HG2	77:Si:84:ARG:HH2	1.86	0.40
78:Sj:102:PRO:HA	78:Sj:112:GLY:HA3	2.03	0.40
78:Sj:189:PRO:O	78:Sj:190:MET:HE2	2.22	0.40
1:L1:801:G:P	10:LN:37:ARG:HH21	2.45	0.40
4:LC:145:LEU:HD23	4:LC:145:LEU:HA	1.94	0.40
14:LR:71:PHE:HB2	21:La:107:HIS:HA	2.03	0.40
17:LU:178:LYS:HA	17:LU:178:LYS:HD3	1.96	0.40
19:LW:144:ARG:HD2	19:LW:144:ARG:HA	1.71	0.40
35:Lp:69:TYR:CD2	37:Lr:278:LYS:HG2	2.56	0.40
38:Ls:232:MET:HE2	38:Ls:232:MET:HB3	1.91	0.40
56:SF:32:ARG:HH11	56:SF:78:MET:HE2	1.86	0.40
59:SJ:145:LEU:HB3	59:SJ:148:LEU:HD22	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:SP:20:ARG:NH2	64:SP:41:CYS:SG	2.94	0.40
70:SY:103:TYR:HD1	70:SY:121:THR:HG21	1.85	0.40
75:Se:206:GLU:HB2	75:Se:208:TYR:CZ	2.56	0.40
77:Si:46:LYS:HA	77:Si:49:TYR:CE2	2.56	0.40
78:Sj:96:ARG:HA	78:Sj:96:ARG:NH1	2.37	0.40
79:Sk:71:PRO:HB3	82:So:78:VAL:HG11	2.03	0.40
1:L1:1057:C:H2'	1:L1:1058:C:C6	2.56	0.40
1:L1:1260:U:H2'	1:L1:1261:A:C8	2.56	0.40
2:L2:41:G:H2'	2:L2:42:A:C8	2.57	0.40
3:LB:260:ALA:O	3:LB:264:ARG:HG2	2.22	0.40
15:LS:280:ALA:O	15:LS:284:LYS:HG2	2.21	0.40
21:La:99:TYR:CE2	21:La:131:VAL:HG22	2.56	0.40
23:Lu:89:GLN:O	23:Lu:93:LYS:HG2	2.21	0.40
32:Lm:198:ASN:HD22	35:Lp:92:LEU:HD12	1.87	0.40
37:Lr:137:LEU:HD11	37:Lr:219:LEU:HD13	2.03	0.40
38:Ls:122:ILE:HD13	38:Ls:134:ILE:HG13	2.04	0.40
41:Lw:60:PRO:HA	41:Lw:61:PRO:HD3	1.99	0.40
42:Lx:140:PHE:HB2	42:Lx:156:TRP:CD2	2.57	0.40
45:L3:16:VAL:HG23	45:L3:51:VAL:HA	2.03	0.40
52:Sf:152:GLN:HA	52:Sf:156:TYR:HB2	2.02	0.40
52:Sf:174:LEU:HB3	52:Sf:175:PRO:HD3	2.02	0.40
64:SP:54:TYR:HD1	64:SP:66:VAL:HB	1.86	0.40
67:ST:103:LYS:O	67:ST:107:ILE:HG12	2.22	0.40
72:Sb:28:LYS:HE2	83:S1:52:A:C8	2.57	0.40
78:Sj:197:ARG:NH1	78:Sj:199:GLU:OE2	2.52	0.40
82:So:160:ARG:HD2	82:So:172:MET:CE	2.51	0.40
83:S1:482:U:H2'	83:S1:483:G:H8	1.86	0.40
1:L1:192:U:H2'	1:L1:193:A:H8	1.85	0.40
1:L1:542:C:H2'	1:L1:543:A:H8	1.87	0.40
2:L2:62:C:H2'	2:L2:63:G:C8	2.56	0.40
5:LD:70:ARG:HA	5:LD:196:PRO:HD3	2.03	0.40
5:LD:99:VAL:HG21	5:LD:173:GLY:HA3	2.04	0.40
12:LP:119:PHE:O	12:LP:163:MET:HG3	2.22	0.40
17:LU:94:ARG:HA	17:LU:94:ARG:HD3	1.96	0.40
23:Lu:110:ASN:O	23:Lu:114:THR:HG23	2.21	0.40
32:Lm:189:LEU:O	32:Lm:295:ARG:NH2	2.54	0.40
58:SI:143:ASP:OD1	58:SI:143:ASP:N	2.53	0.40
73:Sc:176:PRO:HA	73:Sc:179:GLN:HB2	2.02	0.40
79:Sk:248:MET:N	79:Sk:248:MET:SD	2.94	0.40
1:L1:201:A:N3	28:Li:104:ARG:NH2	2.69	0.40
1:L1:950:G:H2'	1:L1:951:G:H8	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:LD:50:LYS:HE3	5:LD:50:LYS:HB3	1.90	0.40
14:LR:85:THR:HG23	14:LR:88:HIS:H	1.87	0.40
30:Lk:384:GLN:N	30:Lk:404:VAL:O	2.53	0.40
53:SB:100:ARG:HA	53:SB:103:GLU:HG3	2.03	0.40
53:SB:211:ASP:HA	53:SB:214:LYS:HG3	2.03	0.40
54:SZ:104:LEU:HD21	54:SZ:108:LEU:HG	2.03	0.40
61:SL:56:PRO:HB3	83:S1:277:A:C2	2.57	0.40
66:SS:53:ASP:OD1	66:SS:54:GLU:N	2.55	0.40
66:SS:119:ASN:ND2	66:SS:122:LEU:HD12	2.36	0.40
66:SS:182:GLY:H	78:Sj:180:LYS:NZ	2.20	0.40
74:Sd:110:ASN:C	74:Sd:110:ASN:ND2	2.78	0.40
75:Se:136:LEU:HD23	75:Se:136:LEU:HA	1.78	0.40
77:Si:31:MET:HE3	77:Si:34:VAL:HB	2.02	0.40
79:Sk:76:PHE:CE2	79:Sk:105:LEU:HD13	2.57	0.40
82:So:243:ASN:O	82:So:247:ILE:HG12	2.21	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	
3	LB	235/305 (77%)	228 (97%)	6 (3%)	1 (0%)	30	60
4	LC	302/348 (87%)	283 (94%)	19 (6%)	0	100	100
5	LD	248/311 (80%)	235 (95%)	13 (5%)	0	100	100
6	LI	93/267 (35%)	87 (94%)	6 (6%)	0	100	100
7	LJ	154/261 (59%)	142 (92%)	12 (8%)	0	100	100
8	LK	173/192 (90%)	166 (96%)	7 (4%)	0	100	100
9	LM	175/178 (98%)	163 (93%)	12 (7%)	0	100	100
10	LN	113/145 (78%)	109 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	LO	285/296 (96%)	274 (96%)	11 (4%)	0	100	100
12	LP	219/251 (87%)	213 (97%)	6 (3%)	0	100	100
13	LQ	150/175 (86%)	139 (93%)	10 (7%)	1 (1%)	18	49
14	LR	144/179 (80%)	142 (99%)	2 (1%)	0	100	100
15	LS	217/292 (74%)	207 (95%)	10 (5%)	0	100	100
16	LT	138/149 (93%)	135 (98%)	3 (2%)	0	100	100
17	LU	158/205 (77%)	154 (98%)	4 (2%)	0	100	100
18	LV	164/212 (77%)	157 (96%)	7 (4%)	0	100	100
19	LW	139/153 (91%)	136 (98%)	3 (2%)	0	100	100
20	LX	200/216 (93%)	191 (96%)	9 (4%)	0	100	100
21	La	109/148 (74%)	105 (96%)	4 (4%)	0	100	100
22	Lb	241/256 (94%)	233 (97%)	8 (3%)	0	100	100
23	Lu	174/250 (70%)	171 (98%)	3 (2%)	0	100	100
24	Ld	118/161 (73%)	112 (95%)	6 (5%)	0	100	100
25	Lf	106/188 (56%)	102 (96%)	4 (4%)	0	100	100
26	Lg	50/65 (77%)	49 (98%)	1 (2%)	0	100	100
27	Lh	44/92 (48%)	43 (98%)	1 (2%)	0	100	100
28	Li	93/188 (50%)	89 (96%)	4 (4%)	0	100	100
29	Lj	36/103 (35%)	35 (97%)	1 (3%)	0	100	100
30	Lk	392/423 (93%)	378 (96%)	14 (4%)	0	100	100
31	Ll	352/380 (93%)	328 (93%)	24 (7%)	0	100	100
32	Lm	291/338 (86%)	277 (95%)	14 (5%)	0	100	100
33	Ln	97/206 (47%)	85 (88%)	12 (12%)	0	100	100
34	Lo	122/137 (89%)	118 (97%)	4 (3%)	0	100	100
35	Lp	93/142 (66%)	88 (95%)	5 (5%)	0	100	100
36	Lq	146/215 (68%)	135 (92%)	11 (8%)	0	100	100
37	Lr	271/332 (82%)	266 (98%)	5 (2%)	0	100	100
38	Ls	210/306 (69%)	203 (97%)	7 (3%)	0	100	100
39	Lt	211/279 (76%)	189 (90%)	21 (10%)	1 (0%)	24	55
40	Lv	125/212 (59%)	121 (97%)	4 (3%)	0	100	100
41	Lw	130/166 (78%)	124 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	Lx	108/158 (68%)	105 (97%)	3 (3%)	0	100	100
43	Ly	95/128 (74%)	90 (95%)	5 (5%)	0	100	100
44	Lz	90/123 (73%)	85 (94%)	5 (6%)	0	100	100
45	L3	94/112 (84%)	81 (86%)	13 (14%)	0	100	100
46	L4	81/138 (59%)	75 (93%)	6 (7%)	0	100	100
47	L5	43/128 (34%)	38 (88%)	5 (12%)	0	100	100
48	L6	92/102 (90%)	91 (99%)	1 (1%)	0	100	100
49	L7	119/206 (58%)	114 (96%)	4 (3%)	1 (1%)	16	45
50	L8	126/222 (57%)	125 (99%)	1 (1%)	0	100	100
51	SR	140/196 (71%)	135 (96%)	5 (4%)	0	100	100
52	Sf	366/439 (83%)	348 (95%)	16 (4%)	2 (0%)	24	55
53	SB	215/296 (73%)	207 (96%)	8 (4%)	0	100	100
54	SZ	130/167 (78%)	115 (88%)	15 (12%)	0	100	100
55	SE	314/430 (73%)	293 (93%)	21 (7%)	0	100	100
56	SF	120/125 (96%)	116 (97%)	4 (3%)	0	100	100
57	SG	197/242 (81%)	193 (98%)	4 (2%)	0	100	100
58	SI	300/396 (76%)	274 (91%)	26 (9%)	0	100	100
59	SJ	120/201 (60%)	105 (88%)	15 (12%)	0	100	100
60	SK	134/194 (69%)	128 (96%)	6 (4%)	0	100	100
61	SL	106/138 (77%)	92 (87%)	13 (12%)	1 (1%)	14	43
62	SN	99/128 (77%)	92 (93%)	7 (7%)	0	100	100
63	SO	162/257 (63%)	155 (96%)	7 (4%)	0	100	100
64	SP	114/137 (83%)	109 (96%)	5 (4%)	0	100	100
65	SQ	105/130 (81%)	96 (91%)	9 (9%)	0	100	100
66	SS	183/258 (71%)	165 (90%)	18 (10%)	0	100	100
67	ST	94/142 (66%)	89 (95%)	5 (5%)	0	100	100
68	SW	84/87 (97%)	82 (98%)	2 (2%)	0	100	100
69	SX	293/360 (81%)	281 (96%)	12 (4%)	0	100	100
70	SY	124/190 (65%)	119 (96%)	5 (4%)	0	100	100
71	Sa	160/173 (92%)	149 (93%)	11 (7%)	0	100	100
72	Sb	171/205 (83%)	167 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
73	Sc	383/414 (92%)	374 (98%)	9 (2%)	0	100	100
74	Sd	95/187 (51%)	87 (92%)	7 (7%)	1 (1%)	11	39
75	Se	348/398 (87%)	332 (95%)	16 (5%)	0	100	100
76	Sg	106/395 (27%)	98 (92%)	8 (8%)	0	100	100
77	Si	84/106 (79%)	82 (98%)	2 (2%)	0	100	100
78	Sj	197/218 (90%)	176 (89%)	21 (11%)	0	100	100
79	Sk	252/323 (78%)	223 (88%)	29 (12%)	0	100	100
80	Sm	114/118 (97%)	107 (94%)	7 (6%)	0	100	100
81	Sn	67/199 (34%)	63 (94%)	4 (6%)	0	100	100
82	So	614/689 (89%)	594 (97%)	20 (3%)	0	100	100
All	All	13557/17977 (75%)	12862 (95%)	687 (5%)	8 (0%)	49	75

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
39	Lt	266	PRO
49	L7	190	GLN
52	Sf	250	PHE
61	SL	72	LYS
74	Sd	109	GLU
52	Sf	260	GLU
3	LB	207	ILE
13	LQ	111	PRO

5.3.2 Protein sidechains [i](#)

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	
3	LB	191/245 (78%)	191 (100%)	0	100	100
4	LC	258/290 (89%)	258 (100%)	0	100	100
5	LD	217/262 (83%)	217 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	LI	86/228 (38%)	86 (100%)	0	100	100
7	LJ	145/232 (62%)	145 (100%)	0	100	100
8	LK	137/150 (91%)	137 (100%)	0	100	100
9	LM	155/156 (99%)	155 (100%)	0	100	100
10	LN	98/124 (79%)	98 (100%)	0	100	100
11	LO	245/249 (98%)	245 (100%)	0	100	100
12	LP	188/211 (89%)	188 (100%)	0	100	100
13	LQ	133/150 (89%)	133 (100%)	0	100	100
14	LR	128/154 (83%)	128 (100%)	0	100	100
15	LS	201/256 (78%)	201 (100%)	0	100	100
16	LT	118/126 (94%)	118 (100%)	0	100	100
17	LU	145/180 (81%)	144 (99%)	1 (1%)	76	80
18	LV	146/182 (80%)	146 (100%)	0	100	100
19	LW	128/135 (95%)	128 (100%)	0	100	100
20	LX	180/191 (94%)	180 (100%)	0	100	100
21	La	91/119 (76%)	91 (100%)	0	100	100
22	Lb	219/229 (96%)	219 (100%)	0	100	100
23	Lu	159/223 (71%)	159 (100%)	0	100	100
24	Ld	111/147 (76%)	111 (100%)	0	100	100
25	Lf	97/164 (59%)	97 (100%)	0	100	100
26	Lg	49/60 (82%)	49 (100%)	0	100	100
27	Lh	40/72 (56%)	40 (100%)	0	100	100
28	Li	88/166 (53%)	88 (100%)	0	100	100
29	Lj	37/89 (42%)	37 (100%)	0	100	100
30	Lk	353/368 (96%)	353 (100%)	0	100	100
31	Ll	313/332 (94%)	313 (100%)	0	100	100
32	Lm	269/303 (89%)	269 (100%)	0	100	100
33	Ln	91/190 (48%)	91 (100%)	0	100	100
34	Lo	104/112 (93%)	104 (100%)	0	100	100
35	Lp	93/133 (70%)	93 (100%)	0	100	100
36	Lq	130/186 (70%)	130 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	Lr	241/288 (84%)	241 (100%)	0	100	100
38	Ls	196/274 (72%)	196 (100%)	0	100	100
39	Lt	188/236 (80%)	188 (100%)	0	100	100
40	Lv	116/188 (62%)	116 (100%)	0	100	100
41	Lw	122/148 (82%)	122 (100%)	0	100	100
42	Lx	104/148 (70%)	104 (100%)	0	100	100
43	Ly	86/110 (78%)	86 (100%)	0	100	100
44	Lz	73/97 (75%)	73 (100%)	0	100	100
45	L3	81/90 (90%)	81 (100%)	0	100	100
46	L4	78/116 (67%)	78 (100%)	0	100	100
47	L5	40/113 (35%)	40 (100%)	0	100	100
48	L6	80/87 (92%)	80 (100%)	0	100	100
49	L7	117/181 (65%)	117 (100%)	0	100	100
50	L8	110/178 (62%)	110 (100%)	0	100	100
51	SR	133/169 (79%)	133 (100%)	0	100	100
52	Sf	326/381 (86%)	326 (100%)	0	100	100
53	SB	191/249 (77%)	191 (100%)	0	100	100
54	SZ	115/143 (80%)	115 (100%)	0	100	100
55	SE	267/357 (75%)	267 (100%)	0	100	100
56	SF	104/107 (97%)	104 (100%)	0	100	100
57	SG	178/209 (85%)	178 (100%)	0	100	100
58	SI	263/342 (77%)	263 (100%)	0	100	100
59	SJ	112/180 (62%)	112 (100%)	0	100	100
60	SK	104/147 (71%)	103 (99%)	1 (1%)	68	76
61	SL	93/118 (79%)	93 (100%)	0	100	100
62	SN	91/113 (80%)	91 (100%)	0	100	100
63	SO	152/226 (67%)	152 (100%)	0	100	100
64	SP	95/113 (84%)	95 (100%)	0	100	100
65	SQ	93/115 (81%)	93 (100%)	0	100	100
66	SS	166/230 (72%)	165 (99%)	1 (1%)	78	81
67	ST	87/123 (71%)	87 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	SW	78/79 (99%)	78 (100%)	0	100	100
69	SX	263/318 (83%)	262 (100%)	1 (0%)	84	84
70	SY	109/164 (66%)	109 (100%)	0	100	100
71	Sa	150/157 (96%)	150 (100%)	0	100	100
72	Sb	148/174 (85%)	147 (99%)	1 (1%)	76	80
73	Sc	338/364 (93%)	338 (100%)	0	100	100
74	Sd	84/158 (53%)	83 (99%)	1 (1%)	63	75
75	Se	310/351 (88%)	310 (100%)	0	100	100
76	Sg	97/357 (27%)	97 (100%)	0	100	100
77	Si	79/95 (83%)	79 (100%)	0	100	100
78	Sj	175/190 (92%)	175 (100%)	0	100	100
79	Sk	235/291 (81%)	235 (100%)	0	100	100
80	Sm	99/101 (98%)	99 (100%)	0	100	100
81	Sn	63/166 (38%)	63 (100%)	0	100	100
82	So	548/609 (90%)	548 (100%)	0	100	100
All	All	12121/15564 (78%)	12115 (100%)	6 (0%)	100	100

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	LU	118	ASN
60	SK	141	GLN
66	SS	65	GLN
69	SX	347	GLN
72	Sb	109	ASN
74	Sd	110	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (122) such sidechains are listed below:

Mol	Chain	Res	Type
4	LC	52	HIS
4	LC	174	GLN
4	LC	286	ASN
5	LD	201	GLN
5	LD	251	HIS
6	LI	93	ASN

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Mol	Chain	Res	Type
6	LI	121	ASN
8	LK	48	GLN
8	LK	84	GLN
8	LK	168	GLN
9	LM	9	GLN
9	LM	61	ASN
9	LM	64	HIS
9	LM	147	GLN
10	LN	48	ASN
10	LN	59	HIS
10	LN	80	GLN
11	LO	99	ASN
11	LO	114	GLN
12	LP	173	GLN
13	LQ	91	GLN
13	LQ	154	GLN
15	LS	172	GLN
15	LS	262	GLN
16	LT	149	HIS
17	LU	84	ASN
18	LV	62	GLN
18	LV	195	HIS
18	LV	210	HIS
19	LW	41	GLN
19	LW	84	ASN
19	LW	98	GLN
21	La	86	ASN
22	Lb	239	GLN
23	Lu	89	GLN
23	Lu	92	ASN
23	Lu	117	GLN
23	Lu	157	GLN
24	Ld	98	GLN
24	Ld	107	ASN
25	Lf	115	HIS
30	Lk	119	GLN
30	Lk	150	GLN
30	Lk	160	HIS
30	Lk	191	GLN
30	Lk	221	GLN
30	Lk	251	HIS
30	Lk	302	HIS

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Mol	Chain	Res	Type
31	Ll	191	ASN
31	Ll	275	GLN
32	Lm	84	ASN
32	Lm	284	HIS
36	Lq	27	GLN
36	Lq	120	HIS
37	Lr	42	GLN
37	Lr	73	GLN
37	Lr	134	GLN
37	Lr	139	GLN
37	Lr	168	HIS
37	Lr	177	GLN
38	Ls	77	HIS
39	Lt	248	ASN
40	Lv	138	GLN
40	Lv	175	GLN
42	Lx	87	GLN
43	Ly	65	ASN
44	Lz	102	GLN
45	L3	46	ASN
46	L4	76	ASN
49	L7	104	HIS
49	L7	152	GLN
52	Sf	164	HIS
52	Sf	240	GLN
52	Sf	339	GLN
52	Sf	373	GLN
52	Sf	375	ASN
52	Sf	386	ASN
52	Sf	420	GLN
53	SB	148	ASN
53	SB	201	ASN
54	SZ	57	HIS
55	SE	196	ASN
55	SE	288	HIS
55	SE	317	HIS
56	SF	59	ASN
57	SG	238	HIS
58	SI	156	GLN
58	SI	261	GLN
58	SI	288	HIS
59	SJ	130	HIS

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Mol	Chain	Res	Type
59	SJ	161	GLN
59	SJ	163	ASN
60	SK	119	ASN
60	SK	129	GLN
62	SN	89	ASN
64	SP	106	ASN
66	SS	147	HIS
67	ST	137	ASN
68	SW	85	GLN
69	SX	299	ASN
69	SX	320	GLN
69	SX	350	GLN
70	SY	66	HIS
71	Sa	51	ASN
72	Sb	131	GLN
72	Sb	139	GLN
72	Sb	147	GLN
72	Sb	188	ASN
73	Sc	358	GLN
73	Sc	381	GLN
73	Sc	388	GLN
75	Se	358	GLN
76	Sg	378	ASN
77	Si	75	HIS
78	Sj	88	GLN
78	Sj	179	GLN
79	Sk	165	ASN
81	Sn	140	HIS
81	Sn	158	GLN
82	So	331	ASN
82	So	436	HIS
82	So	452	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L1	1491/1559 (95%)	354 (23%)	10 (0%)
2	L2	52/69 (75%)	13 (25%)	0
83	S1	921/954 (96%)	186 (20%)	10 (1%)
All	All	2464/2582 (95%)	553 (22%)	20 (0%)

All (553) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L1	5	A
1	L1	6	A
1	L1	7	C
1	L1	8	C
1	L1	9	U
1	L1	11	G
1	L1	19	C
1	L1	20	C
1	L1	24	U
1	L1	29	C
1	L1	30	U
1	L1	31	U
1	L1	34	U
1	L1	38	A
1	L1	39	G
1	L1	41	C
1	L1	44	C
1	L1	45	C
1	L1	46	U
1	L1	47	U
1	L1	54	A
1	L1	57	A
1	L1	58	U
1	L1	66	A
1	L1	78	G
1	L1	90	G
1	L1	91	A
1	L1	100	G
1	L1	101	C
1	L1	103	A
1	L1	104	U
1	L1	107	A
1	L1	110	U
1	L1	111	A
1	L1	112	G
1	L1	124	A
1	L1	127	G
1	L1	134	A
1	L1	135	A
1	L1	137	U
1	L1	138	A
1	L1	147	C
1	L1	151	A

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Mol	Chain	Res	Type
1	L1	154	U
1	L1	157	C
1	L1	158	A
1	L1	159	A
1	L1	162	A
1	L1	166	A
1	L1	167	C
1	L1	174	A
1	L1	184	U
1	L1	186	A
1	L1	199	A
1	L1	200	A
1	L1	203	A
1	L1	208	U
1	L1	212	A
1	L1	213	G
1	L1	215	A
1	L1	217	A
1	L1	223	A
1	L1	232	C
1	L1	233	C
1	L1	239	A
1	L1	248	G
1	L1	266	A
1	L1	267	A
1	L1	270	A
1	L1	274	C
1	L1	288	G
1	L1	298	G
1	L1	304	A
1	L1	305	U
1	L1	315	G
1	L1	316	A
1	L1	317	G
1	L1	322	C
1	L1	323	A
1	L1	324	A
1	L1	325	A
1	L1	330	C
1	L1	331	C
1	L1	332	G
1	L1	345	G

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Mol	Chain	Res	Type
1	L1	346	C
1	L1	352	G
1	L1	359	A
1	L1	361	A
1	L1	362	G
1	L1	366	C
1	L1	367	U
1	L1	369	A
1	L1	375	A
1	L1	385	U
1	L1	387	C
1	L1	390	A
1	L1	395	A
1	L1	404	A
1	L1	413	U
1	L1	415	A
1	L1	422	C
1	L1	423	U
1	L1	427	A
1	L1	428	G
1	L1	429	U
1	L1	435	G
1	L1	443	G
1	L1	454	A
1	L1	455	C
1	L1	456	U
1	L1	459	G
1	L1	463	A
1	L1	464	A
1	L1	465	A
1	L1	466	C
1	L1	471	U
1	L1	472	A
1	L1	477	G
1	L1	488	U
1	L1	489	U
1	L1	493	A
1	L1	496	C
1	L1	498	U
1	L1	501	U
1	L1	503	G
1	L1	507	U

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Mol	Chain	Res	Type
1	L1	510	A
1	L1	511	A
1	L1	512	G
1	L1	519	C
1	L1	522	A
1	L1	525	A
1	L1	526	A
1	L1	527	G
1	L1	528	A
1	L1	530	A
1	L1	540	C
1	L1	545	C
1	L1	550	A
1	L1	551	C
1	L1	552	U
1	L1	553	A
1	L1	555	C
1	L1	557	A
1	L1	558	A
1	L1	567	A
1	L1	569	A
1	L1	571	A
1	L1	572	U
1	L1	573	A
1	L1	575	A
1	L1	576	A
1	L1	592	C
1	L1	593	C
1	L1	614	C
1	L1	615	U
1	L1	620	A
1	L1	627	A
1	L1	630	G
1	L1	652	C
1	L1	653	A
1	L1	654	U
1	L1	662	C
1	L1	672	U
1	L1	675	G
1	L1	699	A
1	L1	700	A
1	L1	701	U

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Mol	Chain	Res	Type
1	L1	704	A
1	L1	711	A
1	L1	720	A
1	L1	723	C
1	L1	730	C
1	L1	731	A
1	L1	735	C
1	L1	737	U
1	L1	744	C
1	L1	745	C
1	L1	746	U
1	L1	756	C
1	L1	757	C
1	L1	762	A
1	L1	773	C
1	L1	774	A
1	L1	775	U
1	L1	777	A
1	L1	794	G
1	L1	798	A
1	L1	808	G
1	L1	809	C
1	L1	823	C
1	L1	824	C
1	L1	830	A
1	L1	832	C
1	L1	834	A
1	L1	836	A
1	L1	837	A
1	L1	838	C
1	L1	841	C
1	L1	850	C
1	L1	851	A
1	L1	853	C
1	L1	854	A
1	L1	857	A
1	L1	860	A
1	L1	861	U
1	L1	870	C
1	L1	874	C
1	L1	887	C
1	L1	888	A

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Mol	Chain	Res	Type
1	L1	889	U
1	L1	890	G
1	L1	900	C
1	L1	904	G
1	L1	907	C
1	L1	911	A
1	L1	912	A
1	L1	913	C
1	L1	920	A
1	L1	922	G
1	L1	923	G
1	L1	926	G
1	L1	929	U
1	L1	930	A
1	L1	931	A
1	L1	933	C
1	L1	948	U
1	L1	953	A
1	L1	954	C
1	L1	956	U
1	L1	957	G
1	L1	959	A
1	L1	960	U
1	L1	962	A
1	L1	963	A
1	L1	964	U
1	L1	965	G
1	L1	975	G
1	L1	982	G
1	L1	984	U
1	L1	985	G
1	L1	986	U
1	L1	990	U
1	L1	1013	C
1	L1	1014	C
1	L1	1016	G
1	L1	1024	A
1	L1	1026	A
1	L1	1028	G
1	L1	1032	G
1	L1	1036	A
1	L1	1039	A

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Mol	Chain	Res	Type
1	L1	1048	C
1	L1	1049	G
1	L1	1053	A
1	L1	1054	G
1	L1	1055	A
1	L1	1057	C
1	L1	1060	A
1	L1	1062	G
1	L1	1069	U
1	L1	1073	U
1	L1	1075	A
1	L1	1087	A
1	L1	1088	G
1	L1	1140	G
1	L1	1161	G
1	L1	1162	A
1	L1	1163	A
1	L1	1177	C
1	L1	1184	U
1	L1	1185	G
1	L1	1194	U
1	L1	1195	C
1	L1	1222	A
1	L1	1223	A
1	L1	1225	U
1	L1	1226	G
1	L1	1236	C
1	L1	1240	A
1	L1	1241	C
1	L1	1243	A
1	L1	1246	G
1	L1	1247	G
1	L1	1249	A
1	L1	1252	A
1	L1	1256	A
1	L1	1258	C
1	L1	1262	G
1	L1	1265	A
1	L1	1266	U
1	L1	1286	A
1	L1	1292	C
1	L1	1293	A

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Mol	Chain	Res	Type
1	L1	1301	A
1	L1	1304	A
1	L1	1311	A
1	L1	1315	C
1	L1	1319	G
1	L1	1320	A
1	L1	1321	U
1	L1	1322	G
1	L1	1324	U
1	L1	1335	A
1	L1	1346	G
1	L1	1351	C
1	L1	1352	G
1	L1	1356	U
1	L1	1371	U
1	L1	1372	U
1	L1	1383	A
1	L1	1384	G
1	L1	1386	C
1	L1	1390	C
1	L1	1400	G
1	L1	1402	U
1	L1	1403	C
1	L1	1416	U
1	L1	1419	A
1	L1	1426	U
1	L1	1430	U
1	L1	1432	U
1	L1	1438	U
1	L1	1439	U
1	L1	1442	A
1	L1	1444	U
1	L1	1452	U
1	L1	1461	G
1	L1	1465	A
1	L1	1471	A
1	L1	1480	U
1	L1	1485	C
1	L1	1487	C
1	L1	1488	A
1	L1	1490	A
1	L1	1492	C

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Mol	Chain	Res	Type
1	L1	1498	C
1	L1	1499	C
1	L1	1502	C
1	L1	1504	U
1	L1	1506	A
1	L1	1510	A
1	L1	1513	U
1	L1	1520	A
1	L1	1522	C
1	L1	1534	C
1	L1	1537	A
1	L1	1539	A
1	L1	1540	C
1	L1	1542	C
1	L1	1547	A
1	L1	1548	A
1	L1	1558	U
2	L2	4	A
2	L2	7	G
2	L2	9	A
2	L2	10	G
2	L2	13	U
2	L2	14	A
2	L2	40	G
2	L2	41	G
2	L2	43	G
2	L2	47	U
2	L2	49	A
2	L2	68	G
2	L2	69	A
83	S1	3	U
83	S1	4	A
83	S1	33	U
83	S1	38	A
83	S1	41	A
83	S1	44	A
83	S1	47	C
83	S1	57	U
83	S1	60	C
83	S1	64	U
83	S1	65	C
83	S1	71	A

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Mol	Chain	Res	Type
83	S1	74	U
83	S1	75	C
83	S1	76	A
83	S1	94	A
83	S1	98	A
83	S1	106	A
83	S1	114	A
83	S1	117	A
83	S1	119	G
83	S1	125	A
83	S1	126	U
83	S1	144	G
83	S1	149	G
83	S1	160	A
83	S1	168	C
83	S1	182	C
83	S1	183	U
83	S1	185	U
83	S1	188	C
83	S1	192	A
83	S1	198	A
83	S1	199	A
83	S1	214	U
83	S1	219	A
83	S1	221	C
83	S1	223	C
83	S1	233	C
83	S1	234	A
83	S1	235	A
83	S1	236	U
83	S1	243	C
83	S1	246	G
83	S1	252	G
83	S1	257	C
83	S1	261	C
83	S1	271	A
83	S1	272	A
83	S1	275	C
83	S1	286	G
83	S1	289	G
83	S1	291	A
83	S1	292	A

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Mol	Chain	Res	Type
83	S1	294	G
83	S1	295	A
83	S1	296	G
83	S1	303	A
83	S1	307	C
83	S1	308	A
83	S1	320	A
83	S1	340	A
83	S1	341	G
83	S1	345	U
83	S1	346	A
83	S1	347	A
83	S1	353	U
83	S1	354	C
83	S1	355	C
83	S1	364	C
83	S1	368	A
83	S1	372	A
83	S1	375	A
83	S1	381	G
83	S1	384	G
83	S1	395	U
83	S1	402	A
83	S1	405	C
83	S1	418	C
83	S1	422	A
83	S1	434	U
83	S1	435	A
83	S1	456	A
83	S1	458	C
83	S1	459	C
83	S1	462	A
83	S1	474	A
83	S1	479	A
83	S1	481	C
83	S1	495	A
83	S1	504	C
83	S1	507	A
83	S1	519	A
83	S1	520	A
83	S1	525	C
83	S1	532	G

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Mol	Chain	Res	Type
83	S1	533	U
83	S1	540	U
83	S1	541	A
83	S1	542	U
83	S1	543	C
83	S1	546	U
83	S1	567	A
83	S1	568	U
83	S1	573	A
83	S1	576	C
83	S1	578	C
83	S1	582	U
83	S1	585	A
83	S1	590	A
83	S1	598	U
83	S1	599	U
83	S1	600	G
83	S1	601	C
83	S1	603	C
83	S1	604	A
83	S1	607	C
83	S1	610	U
83	S1	612	U
83	S1	614	C
83	S1	622	U
83	S1	624	C
83	S1	631	C
83	S1	636	A
83	S1	638	G
83	S1	643	C
83	S1	645	A
83	S1	646	C
83	S1	647	A
83	S1	648	A
83	S1	670	A
83	S1	679	A
83	S1	680	G
83	S1	685	A
83	S1	695	C
83	S1	696	A
83	S1	697	U
83	S1	706	A

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Mol	Chain	Res	Type
83	S1	709	A
83	S1	720	A
83	S1	723	U
83	S1	729	C
83	S1	730	C
83	S1	731	C
83	S1	732	A
83	S1	742	G
83	S1	743	A
83	S1	744	U
83	S1	745	A
83	S1	755	A
83	S1	768	G
83	S1	769	A
83	S1	770	A
83	S1	773	U
83	S1	783	A
83	S1	800	G
83	S1	823	A
83	S1	833	A
83	S1	835	A
83	S1	865	A
83	S1	867	A
83	S1	870	A
83	S1	874	U
83	S1	877	A
83	S1	878	C
83	S1	879	U
83	S1	885	C
83	S1	886	C
83	S1	888	U
83	S1	889	A
83	S1	890	C
83	S1	891	G
83	S1	892	C
83	S1	893	A
83	S1	894	U
83	S1	897	A
83	S1	910	A
83	S1	912	G
83	S1	915	G
83	S1	917	A

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Mol	Chain	Res	Type
83	S1	921	U
83	S1	935	G
83	S1	937	A
83	S1	947	G
83	S1	948	G
83	S1	952	A

All (20) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L1	33	C
1	L1	551	C
1	L1	575	A
1	L1	837	A
1	L1	860	A
1	L1	889	U
1	L1	929	U
1	L1	1235	A
1	L1	1319	G
1	L1	1371	U
83	S1	70	G
83	S1	374	U
83	S1	519	A
83	S1	542	U
83	S1	599	U
83	S1	611	A
83	S1	684	A
83	S1	768	G
83	S1	887	C
83	S1	890	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

Of 156 ligands modelled in this entry, 152 are monoatomic - leaving 4 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
85	T1C	L1	1705	-	45,45,45	1.16	4 (8%)	56,72,72	0.88	2 (3%)
85	T1C	L1	1706	84	45,45,45	1.13	4 (8%)	56,72,72	0.97	3 (5%)
85	T1C	S1	1034	84	45,45,45	1.18	3 (6%)	56,72,72	1.01	2 (3%)
87	GDP	Se	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.87	8 (17%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
85	T1C	L1	1705	-	-	6/22/80/80	0/4/4/4
85	T1C	L1	1706	84	-	10/22/80/80	0/4/4/4
85	T1C	S1	1034	84	-	10/22/80/80	0/4/4/4
87	GDP	Se	500	-	-	2/16/32/32	0/3/3/3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	S1	1034	T1C	C21-N21	5.06	1.48	1.33
85	L1	1706	T1C	C21-N21	5.00	1.47	1.33
85	L1	1705	T1C	C21-N21	4.95	1.47	1.33
87	Se	500	GDP	C5-C4	3.18	1.47	1.38
85	L1	1705	T1C	C4-N4	2.66	1.53	1.47
87	Se	500	GDP	C6-N1	-2.43	1.34	1.38
85	S1	1034	T1C	C4-N4	2.43	1.52	1.47
85	L1	1705	T1C	O11-C11	2.23	1.27	1.23
85	S1	1034	T1C	O11-C11	2.21	1.27	1.23
85	L1	1706	T1C	C4-N4	2.19	1.52	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	L1	1706	T1C	O11-C11	2.18	1.27	1.23
85	L1	1706	T1C	C7-N7	2.06	1.48	1.42
85	L1	1705	T1C	C7-N7	2.05	1.48	1.42
87	Se	500	GDP	C5-N7	-2.04	1.35	1.39

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
87	Se	500	GDP	C5-C4-N3	-6.57	117.94	128.39
87	Se	500	GDP	C2-N3-C4	5.34	121.49	112.30
87	Se	500	GDP	N9-C4-N3	5.04	136.03	125.95
85	S1	1034	T1C	C1-C1C-C12	3.95	114.52	109.88
85	S1	1034	T1C	C11-C1B-C12	3.70	121.73	118.80
85	L1	1706	T1C	O1C-C1C-C12	-3.09	105.19	110.14
87	Se	500	GDP	C6-C5-N7	2.95	135.66	130.29
85	L1	1705	T1C	O1C-C1C-C12	-2.92	105.48	110.14
85	L1	1706	T1C	C1C-C1-C2	2.91	120.37	115.75
85	L1	1705	T1C	C11-C1B-C12	2.80	121.02	118.80
87	Se	500	GDP	C3'-C2'-C1'	2.56	106.30	101.46
87	Se	500	GDP	C4-C5-N7	-2.41	106.85	110.67
85	L1	1706	T1C	C11-C1B-C12	2.35	120.66	118.80
87	Se	500	GDP	C2'-C1'-N9	-2.21	107.11	113.25
87	Se	500	GDP	O6-C6-C5	-2.15	120.84	126.53

There are no chirality outliers.

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
85	L1	1705	T1C	C41-C4-N4-C43
85	L1	1705	T1C	C3-C2-C21-O21
85	L1	1705	T1C	C3-C2-C21-N21
85	L1	1705	T1C	C1-C2-C21-O21
85	L1	1706	T1C	C92-C91-N9-C9
85	L1	1706	T1C	C41-C4-N4-C43
85	L1	1706	T1C	C3-C2-C21-O21
85	L1	1706	T1C	C3-C2-C21-N21
85	L1	1706	T1C	C1-C2-C21-O21
85	S1	1034	T1C	C92-C91-N9-C9
87	Se	500	GDP	O4'-C1'-N9-C8
87	Se	500	GDP	O4'-C1'-N9-C4
85	L1	1706	T1C	O91-C91-N9-C9
85	S1	1034	T1C	O91-C91-N9-C9

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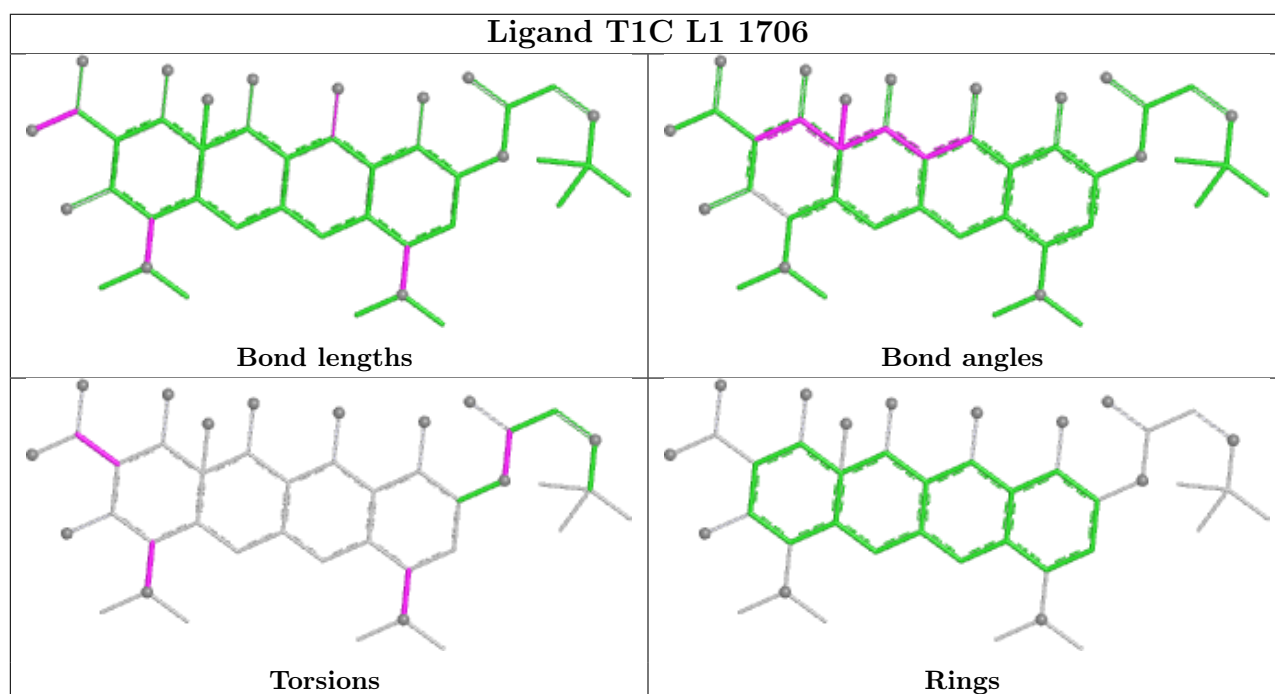
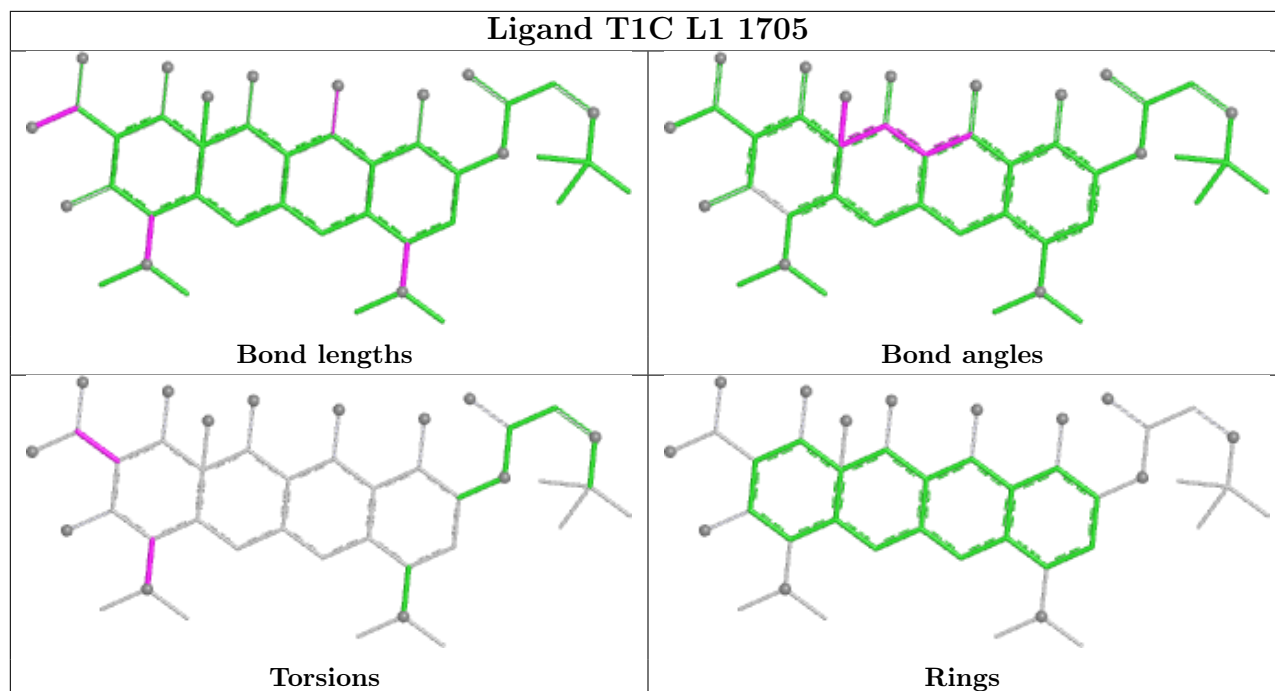
Mol	Chain	Res	Type	Atoms
85	L1	1706	T1C	C3-C4-N4-C42
85	S1	1034	T1C	C3-C2-C21-N21
85	S1	1034	T1C	C3-C2-C21-O21
85	L1	1705	T1C	C1-C2-C21-N21
85	L1	1706	T1C	C1-C2-C21-N21
85	S1	1034	T1C	C1-C2-C21-N21
85	S1	1034	T1C	N9-C91-C92-N92
85	S1	1034	T1C	O91-C91-C92-N92
85	L1	1706	T1C	C61-C7-N7-C71
85	S1	1034	T1C	C61-C7-N7-C72
85	L1	1705	T1C	C3-C4-N4-C43
85	S1	1034	T1C	C41-C4-N4-C42
85	L1	1706	T1C	C61-C7-N7-C72
85	S1	1034	T1C	C61-C7-N7-C71

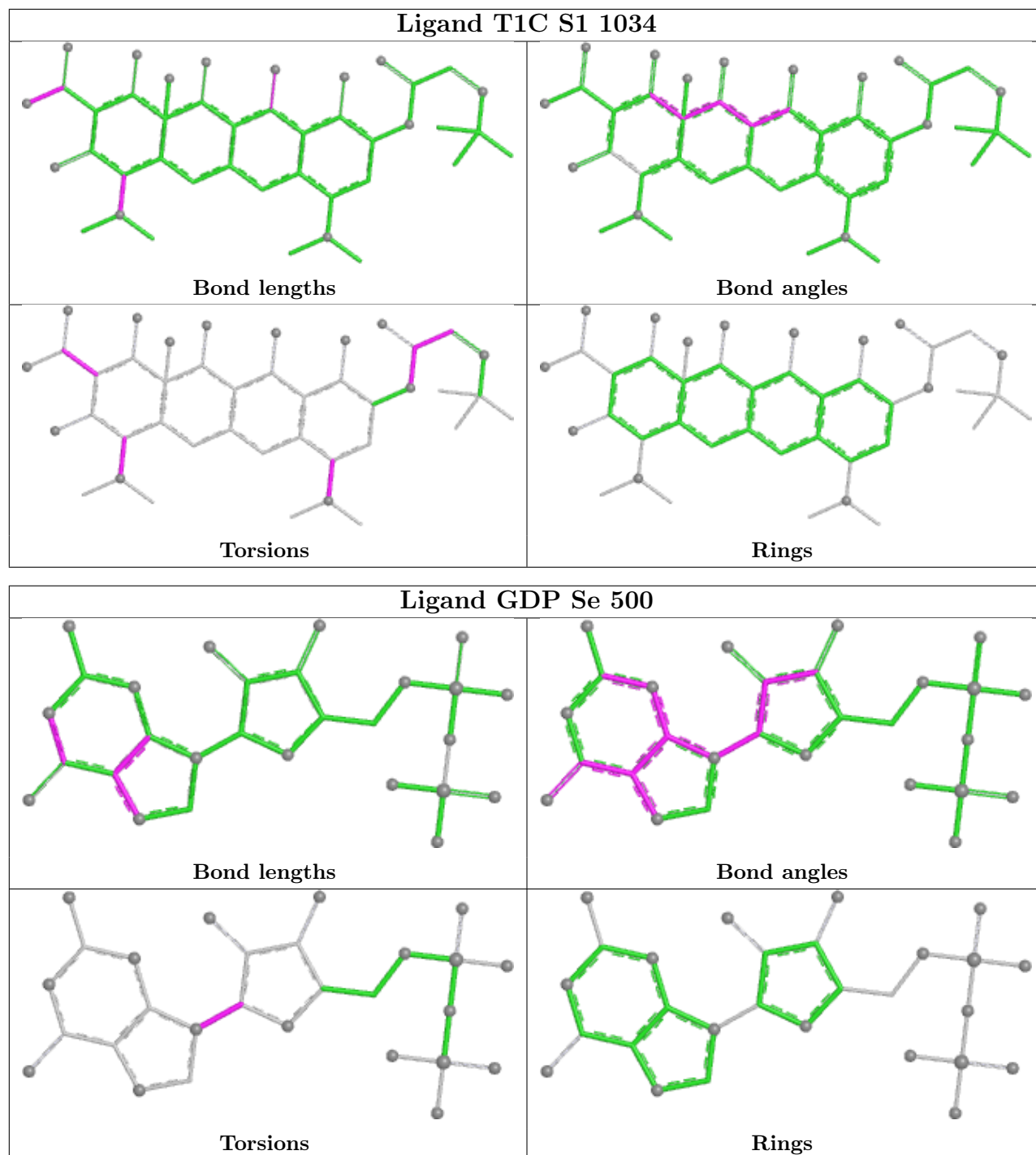
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
85	L1	1705	T1C	1	0
85	L1	1706	T1C	1	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

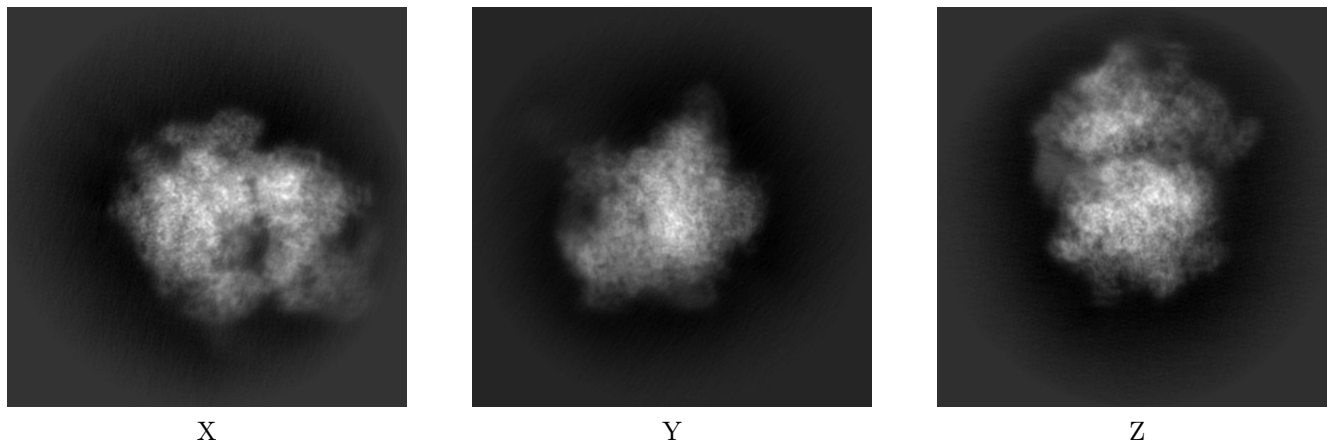
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38634. These allow visual inspection of the internal detail of the map and identification of artifacts.

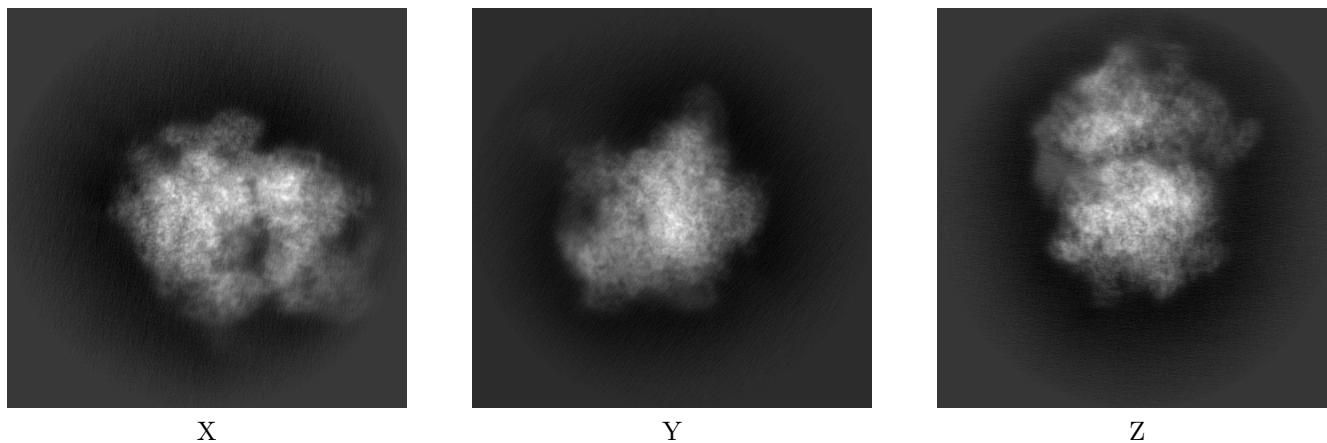
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



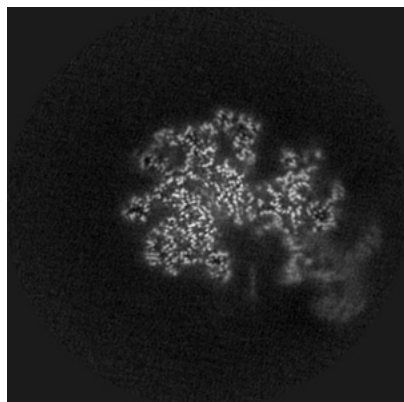
6.1.2 Raw map



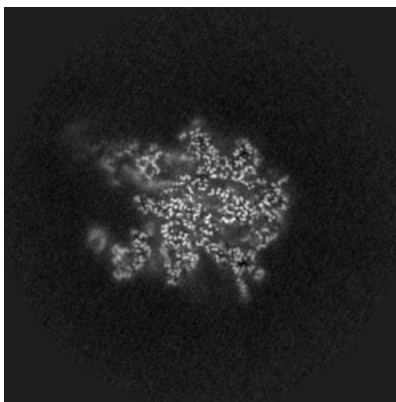
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

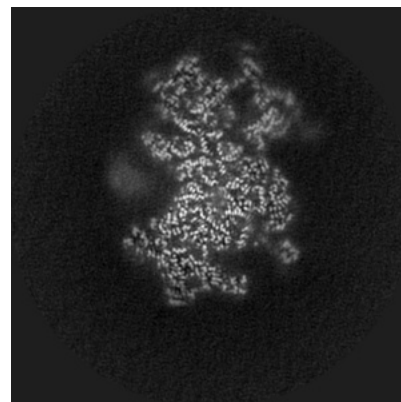
6.2.1 Primary map



X Index: 210

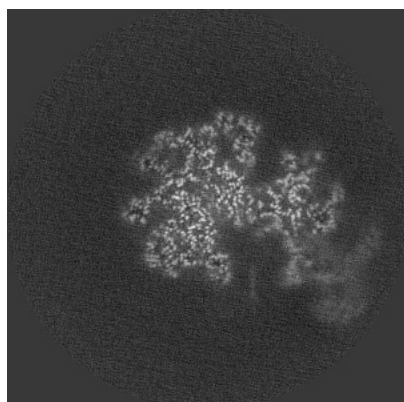


Y Index: 210

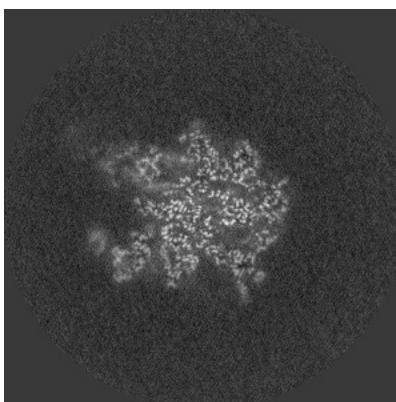


Z Index: 210

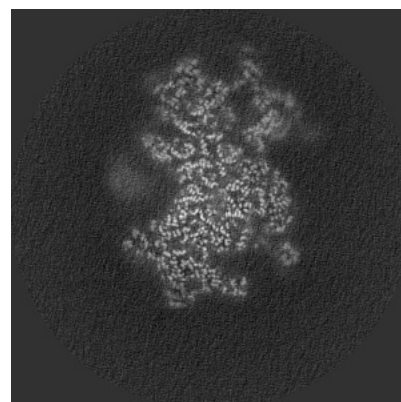
6.2.2 Raw map



X Index: 210



Y Index: 210

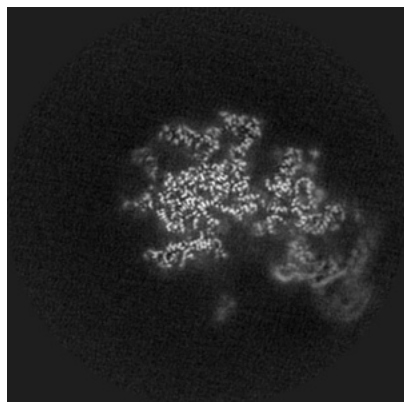


Z Index: 210

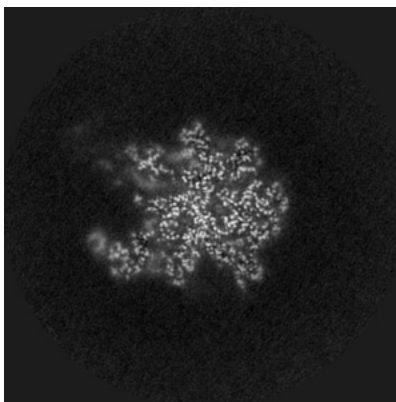
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

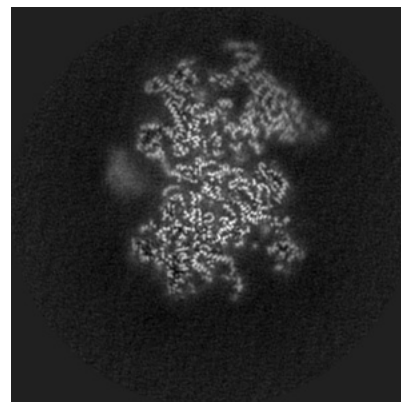
6.3.1 Primary map



X Index: 199

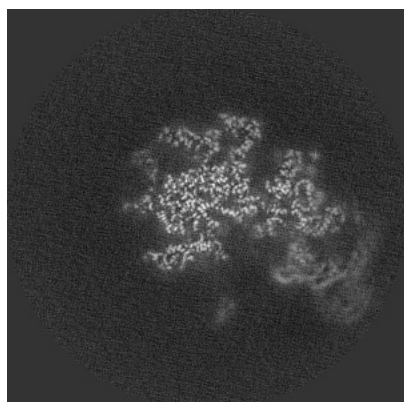


Y Index: 206

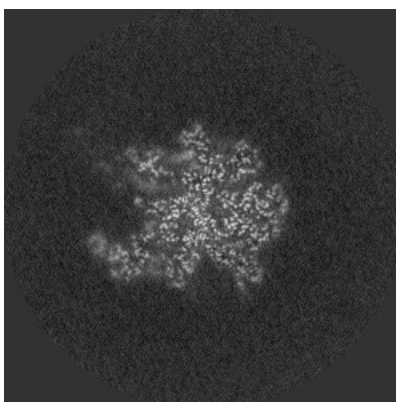


Z Index: 219

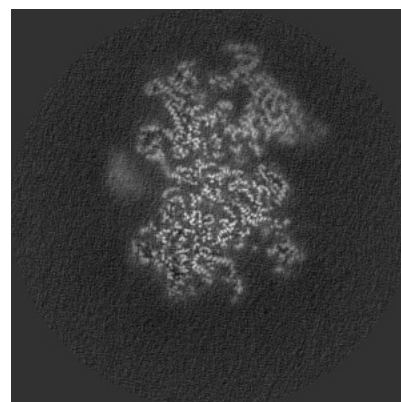
6.3.2 Raw map



X Index: 199



Y Index: 206

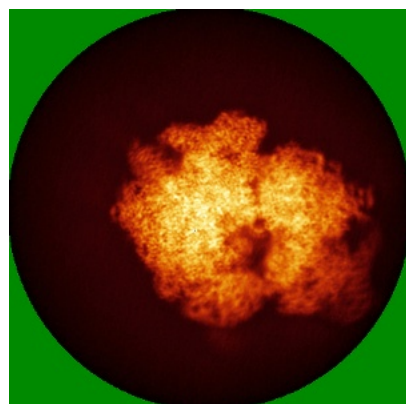


Z Index: 219

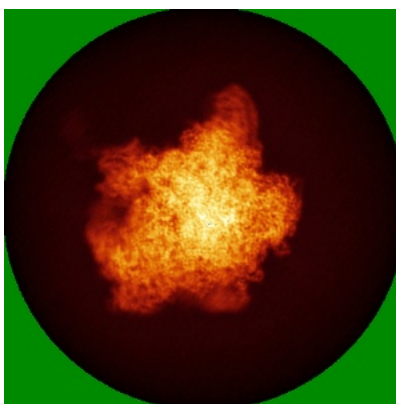
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

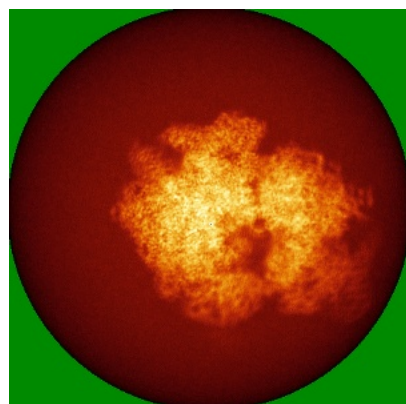


Y

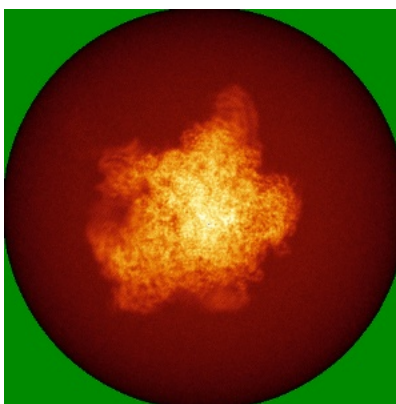


Z

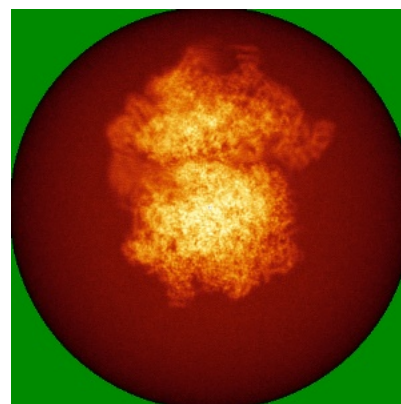
6.4.2 Raw map



X



Y

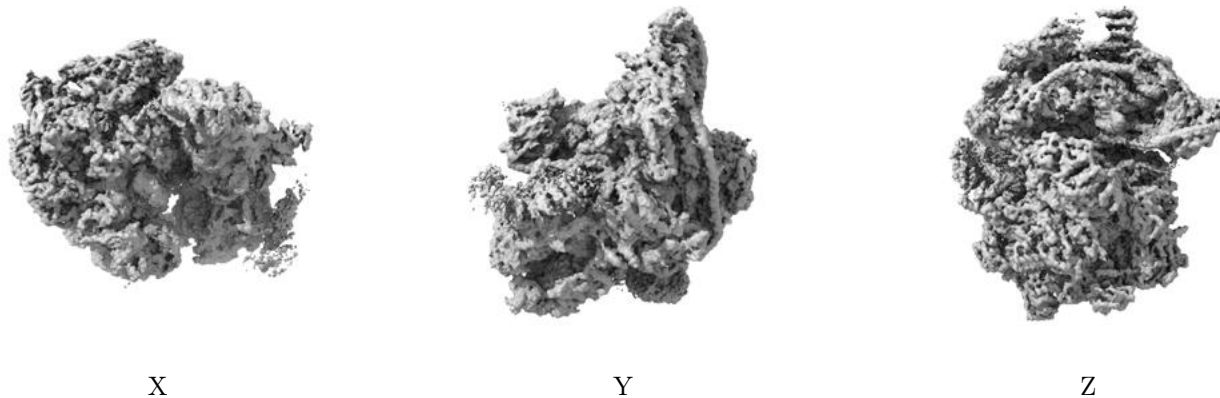


Z

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

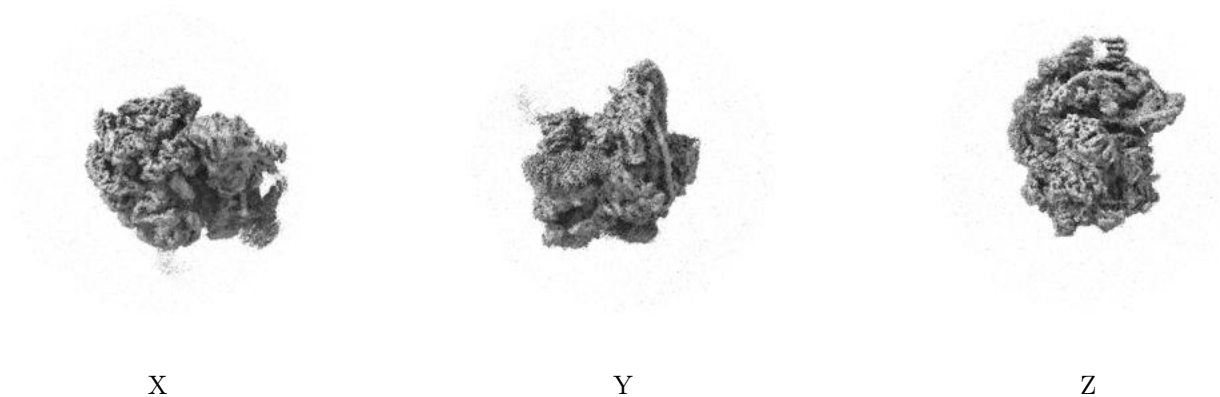
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

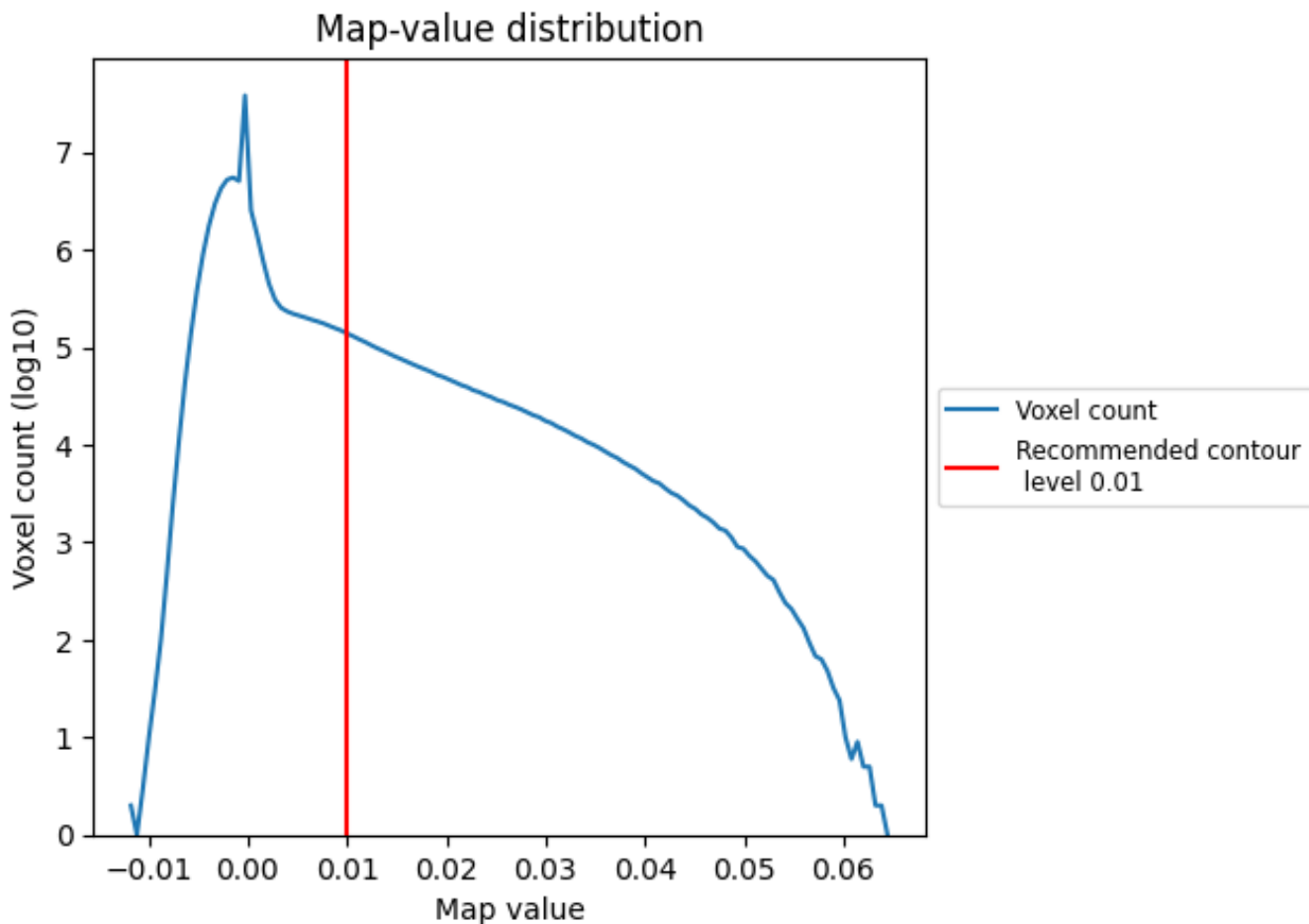
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

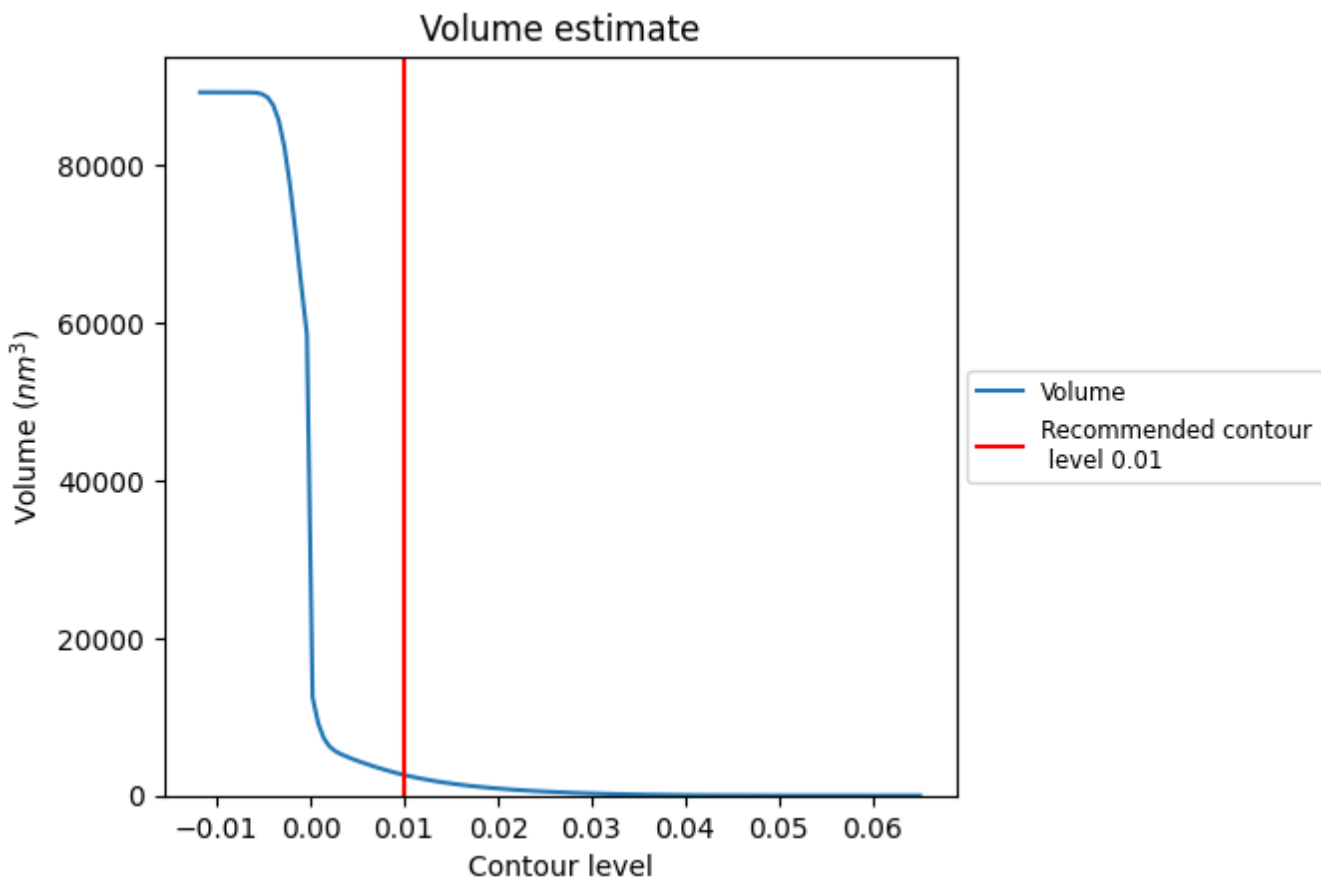
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

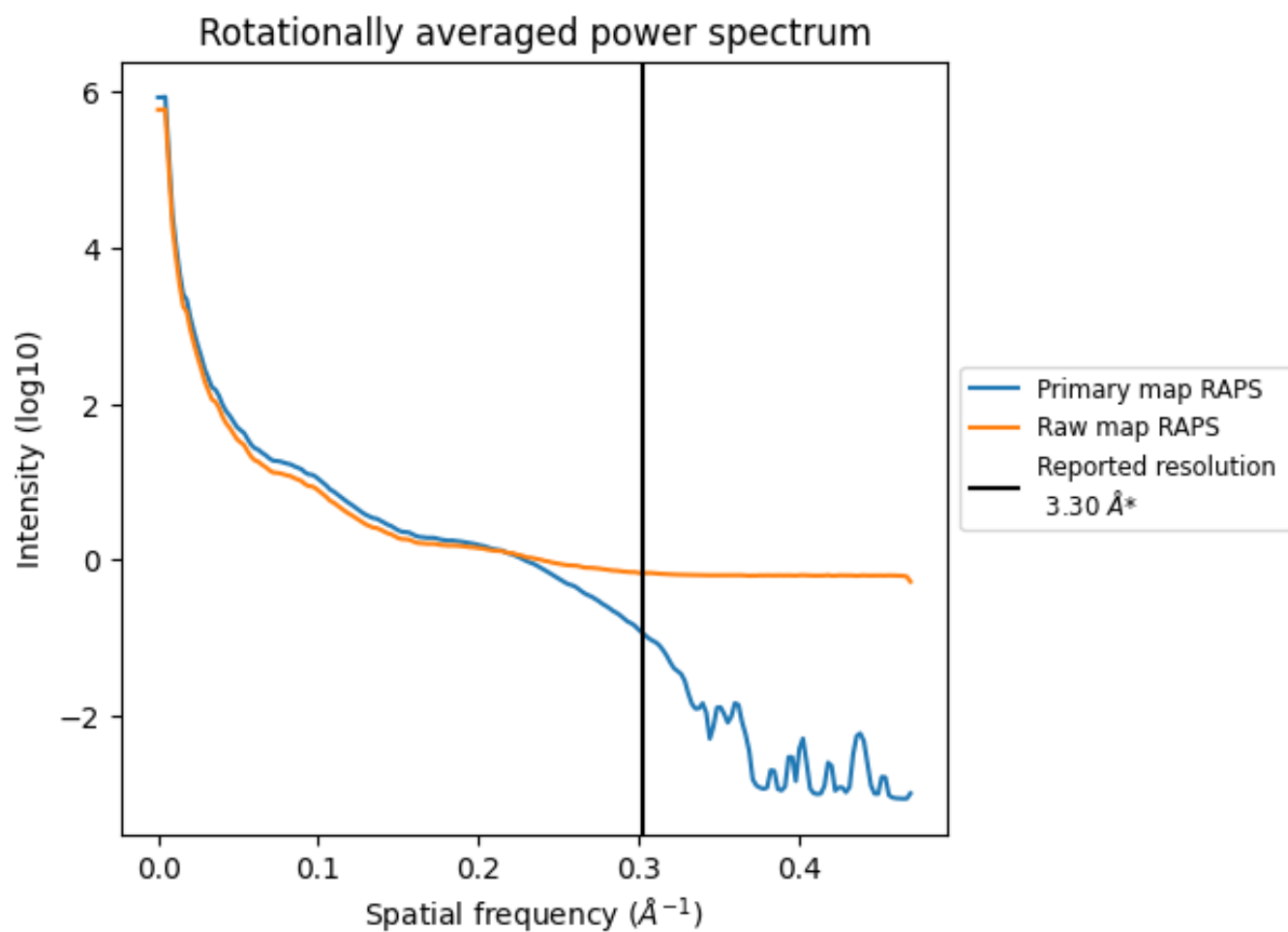
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2621 nm^3 ; this corresponds to an approximate mass of 2368 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

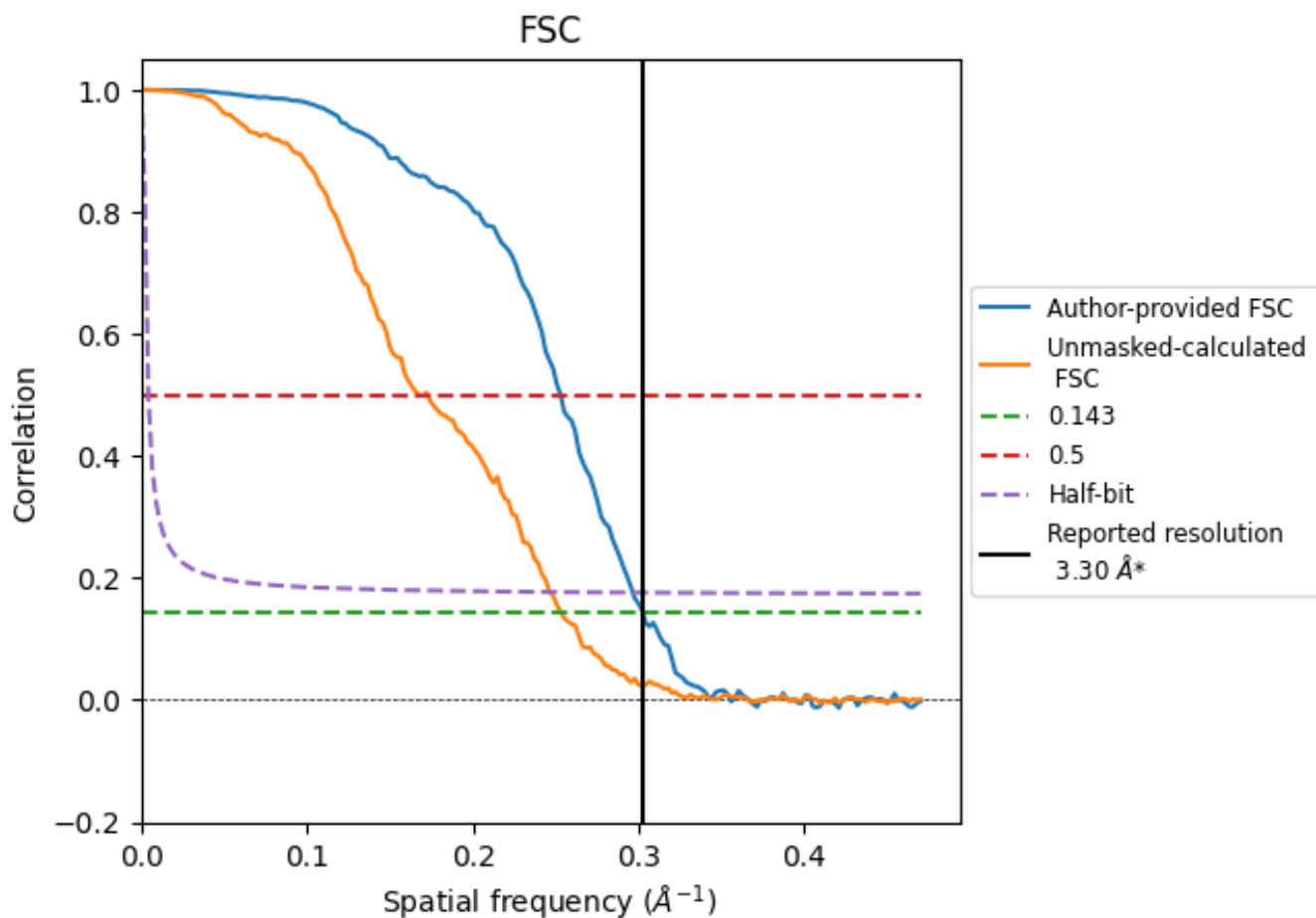


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 0.303 Å⁻¹

8.2 Resolution estimates [i](#)

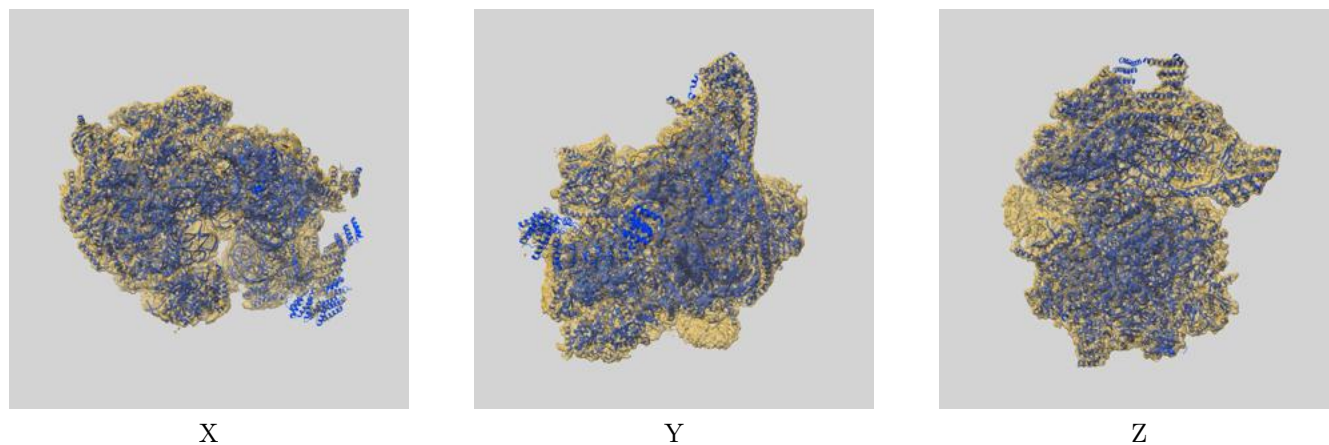
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.31	3.95	3.37
Unmasked-calculated*	3.95	5.98	4.06

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.95 differs from the reported value 3.3 by more than 10 %

9 Map-model fit [i](#)

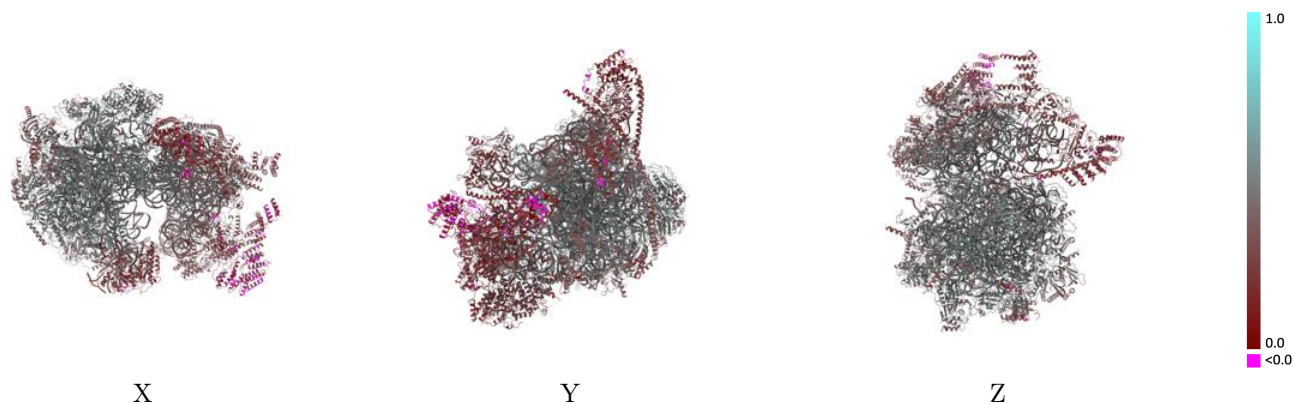
This section contains information regarding the fit between EMDB map EMD-38634 and PDB model 8XT2. Per-residue inclusion information can be found in section 3 on page 22.

9.1 Map-model overlay [i](#)



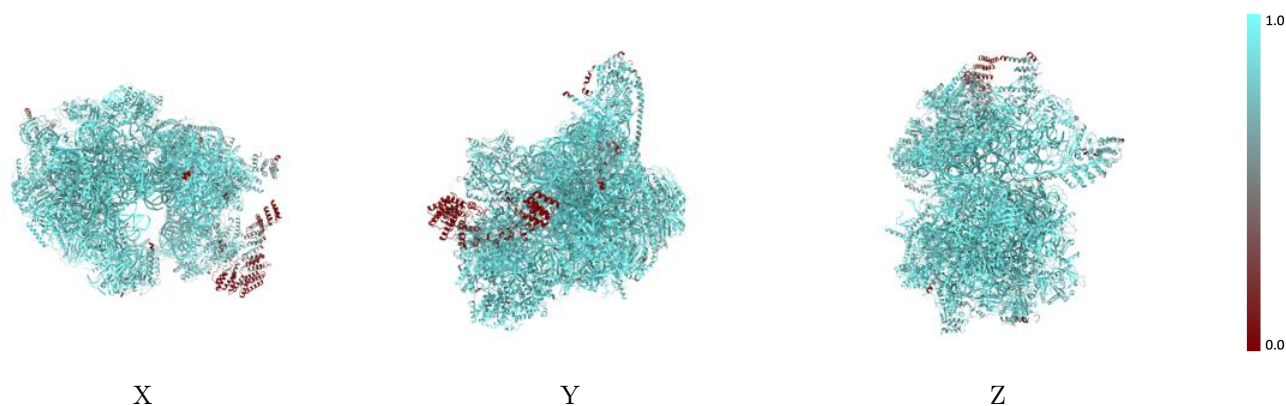
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



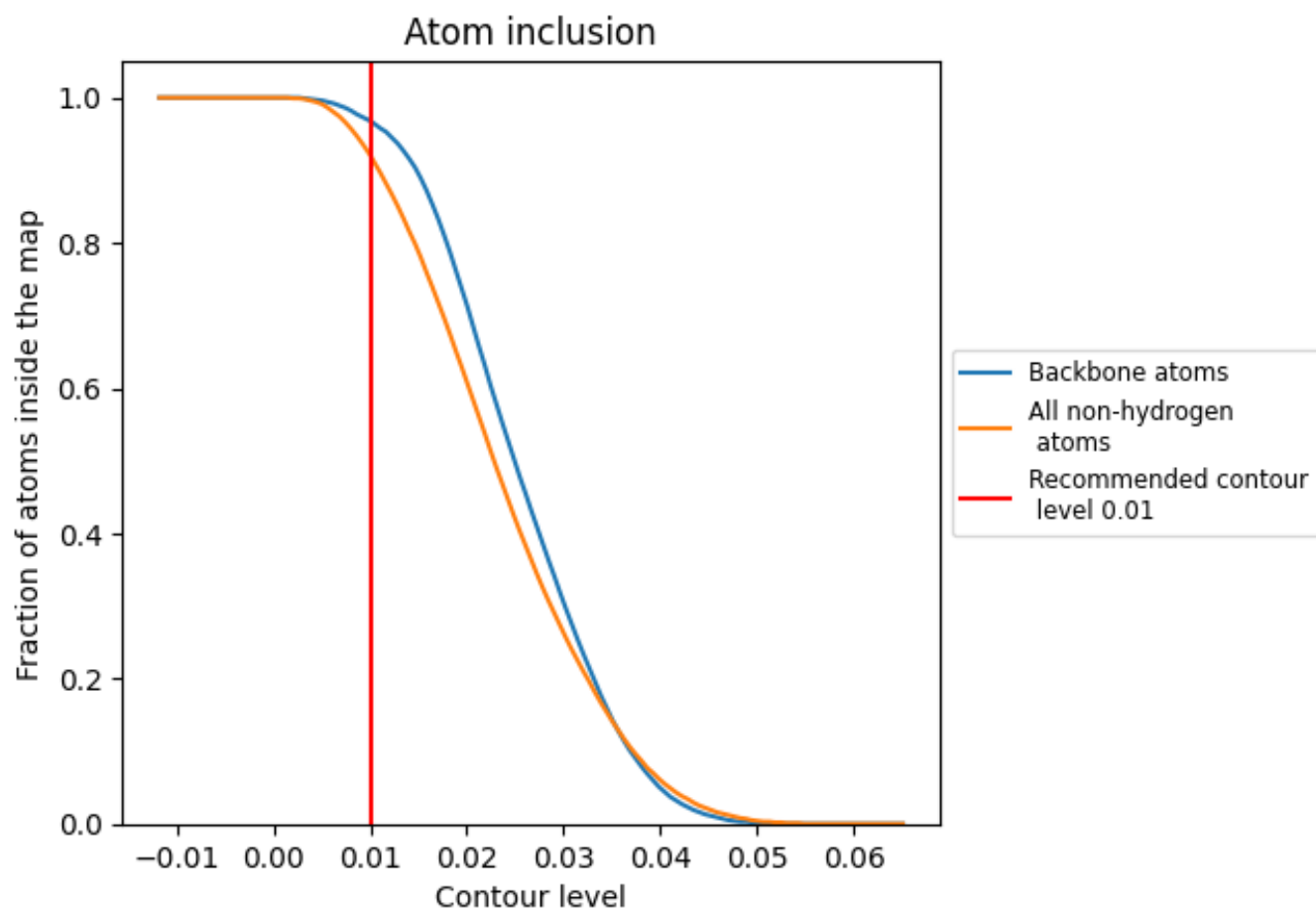
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).






































































9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 92% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9210	 0.4150
L1	 0.9980	 0.4930
L2	 0.9770	 0.3350
L3	 0.8870	 0.3250
L4	 0.8020	 0.2870
L5	 0.9660	 0.3440
L6	 0.9780	 0.5020
L7	 0.8990	 0.4170
L8	 0.8880	 0.4010
LB	 0.9850	 0.5190
LC	 0.9610	 0.4820
LD	 0.9570	 0.4940
LI	 0.9230	 0.4220
LJ	 0.8690	 0.3190
LK	 0.7710	 0.2390
LM	 0.9770	 0.4960
LN	 0.9800	 0.4880
LO	 0.9490	 0.4870
LP	 0.9680	 0.4780
LQ	 0.9610	 0.4820
LR	 0.9390	 0.4500
LS	 0.9480	 0.4640
LT	 0.9680	 0.4920
LU	 0.9510	 0.4900
LV	 0.9560	 0.5020
LW	 0.9200	 0.4680
LX	 0.8320	 0.4240
La	 0.9820	 0.5130
Lb	 0.9100	 0.4570
Ld	 0.9660	 0.5070
Lf	 0.9480	 0.4800
Lg	 0.9790	 0.4660
Lh	 1.0000	 0.5210
Li	 0.9860	 0.5240
Lj	 0.9880	 0.5100

















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Chain	Atom inclusion	Q-score
Lk	 0.9470	 0.4650
Ll	 0.9230	 0.4220
Lm	 0.8830	 0.4050
Ln	 0.8850	 0.2890
Lo	 0.8900	 0.4600
Lp	 0.9190	 0.4570
Lq	 0.9660	 0.4950
Lr	 0.9220	 0.4460
Ls	 0.7640	 0.3850
Lt	 0.8560	 0.2430
Lu	 0.9520	 0.4660
Lv	 0.8910	 0.3450
Lw	 0.9520	 0.4850
Lx	 0.7970	 0.4050
Ly	 0.9820	 0.5120
Lz	 0.9250	 0.4500
S1	 0.9960	 0.4300
SB	 0.9330	 0.4150
SE	 0.8990	 0.3840
SF	 0.9270	 0.4530
SG	 0.9370	 0.3640
SI	 0.9000	 0.3170
SJ	 0.9000	 0.2820
SK	 0.9610	 0.4450
SL	 0.9820	 0.4400
SN	 0.9310	 0.3030
SO	 0.9240	 0.4100
SP	 0.9220	 0.3330
SQ	 0.9690	 0.4580
SR	 0.9770	 0.4750
SS	 0.9040	 0.3310
ST	 0.9250	 0.4480
SW	 0.9630	 0.4600
SX	 0.7510	 0.2830
SY	 0.8640	 0.3650
SZ	 0.8960	 0.3160
Sa	 0.9280	 0.4060
Sb	 0.8760	 0.3220
Sc	 0.7770	 0.2020
Sd	 0.9010	 0.4120
Se	 0.9030	 0.3060
Sf	 0.9630	 0.4790

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Chain	Atom inclusion	Q-score
Sg	 0.7460	 0.2220
Si	 0.9070	 0.2600
Sj	 0.9010	 0.2740
Sk	 0.8370	 0.2340
Sm	 0.9350	 0.3930
Sn	 0.9850	 0.4690
So	 0.2830	 0.1160