



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 09:15 AM UTC

PDB ID : 8K2A / pdb_00008k2a
EMDB ID : EMD-36836
Title : Cryo-EM structure of the human 55S mitoribosome with Tigecycline
Authors : Li, X.; Wang, M.; Cheng, J.
Deposited on : 2023-07-12
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

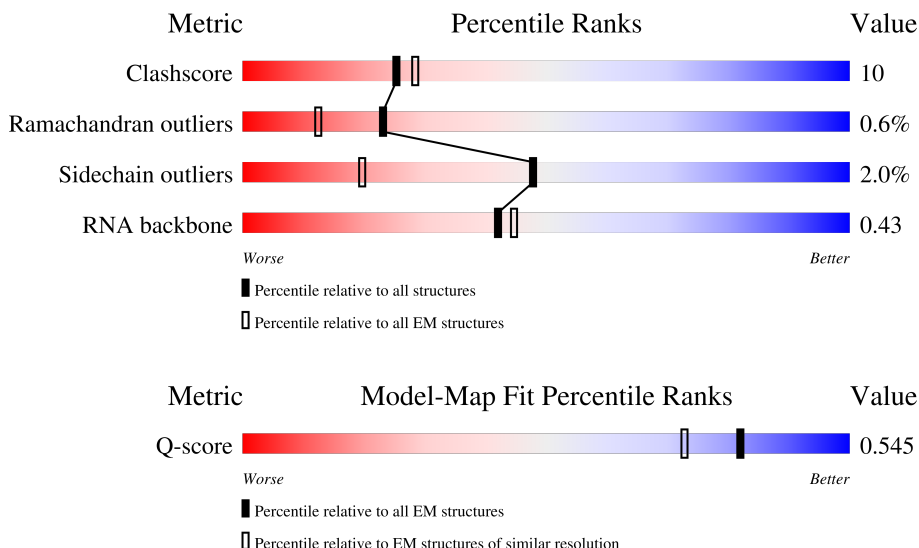
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 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.



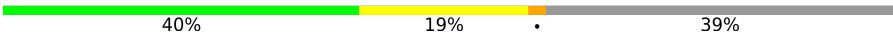
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	59% 32% 5% .
2	L2	69	48% 32% . 19%
3	LB	305	68% 10% 22%

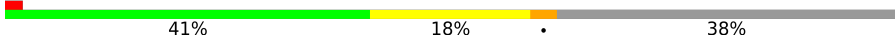
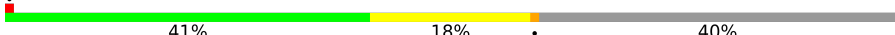
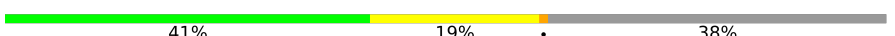
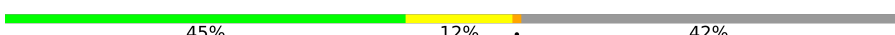
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Mol	Chain	Length	Quality of chain
4	LC	348	
5	LD	311	
6	LI	267	
7	LJ	261	
8	LK	192	
9	LM	178	
10	LN	145	
11	LO	296	
12	LP	251	
13	LQ	175	
14	LR	179	
15	LS	292	
16	LT	149	
17	LU	205	
18	LV	212	
19	LW	153	
20	LX	216	
21	La	148	
22	Lb	256	
23	Lu	250	
24	Ld	161	
25	Lf	188	
26	Lg	65	
27	Lh	92	
28	Li	188	

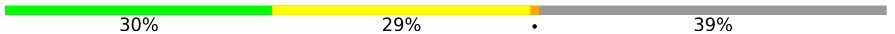
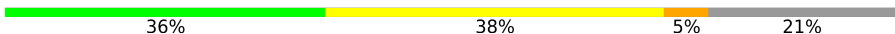
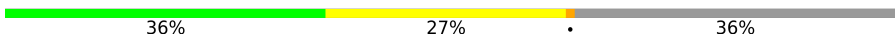
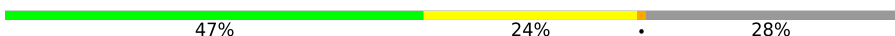
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Mol	Chain	Length	Quality of chain
29	Lj	103	
30	Lk	423	
31	Ll	380	
32	Lm	338	
33	Ln	206	
34	Lo	137	
35	Lp	142	
36	Lq	215	
37	Lr	332	
38	Ls	306	
39	Lt	279	
40	Lv	212	
41	Lw	166	
42	Lx	158	
43	Ly	128	
44	Lz	123	
45	L3	112	
46	L4	138	
47	L5	128	
48	L6	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	
55	SE	430	
56	SF	125	
57	SG	242	
58	SI	396	
59	SJ	201	
60	SK	194	
61	SL	138	
62	SN	128	
63	SO	257	
64	SP	137	
65	SQ	130	
66	SS	258	
67	ST	142	
68	SW	87	
69	SX	360	
70	SY	190	
71	Sa	173	
72	Sb	205	
73	Sc	414	
74	Sd	187	
75	Se	398	
76	Sg	395	
77	Si	106	
78	Sj	218	

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Mol	Chain	Length	Quality of chain
79	Sk	323	44%33%21%
80	Sm	118	69%29%
81	Sn	199	26%9%65%
82	So	689	18%67%21%11%
83	S1	954	58%34%5%

2 Entry composition

There are 87 unique types of molecules in this entry. The entry contains 165285 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
1	L1	1500	Total	C	N	O	P	0	0
			31847	14290	5750	10307	1500		

- Molecule 2 is a RNA chain called Val tRNA.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
35	Lp	97	Total	C	N	O	S	0	0
			815	514	147	149	5		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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		

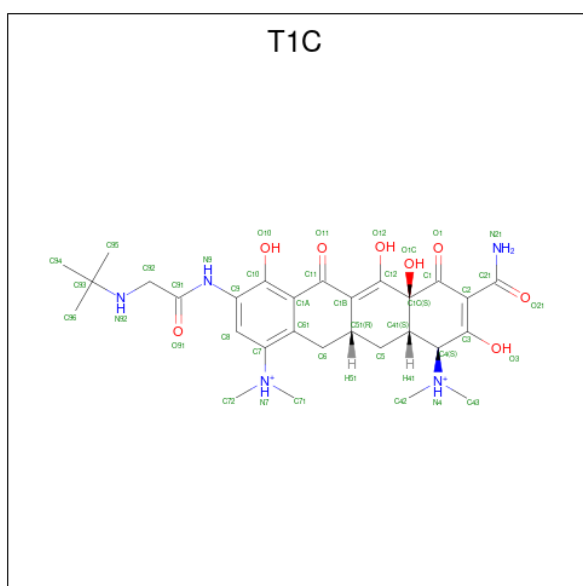
- Molecule 83 is a RNA chain called 12S rRNA.

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

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

Mol	Chain	Residues	Atoms		AltConf
84	L1	105	Total	Mg	0
			105	105	
84	LB	3	Total	Mg	0
			3	3	
84	LC	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).



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

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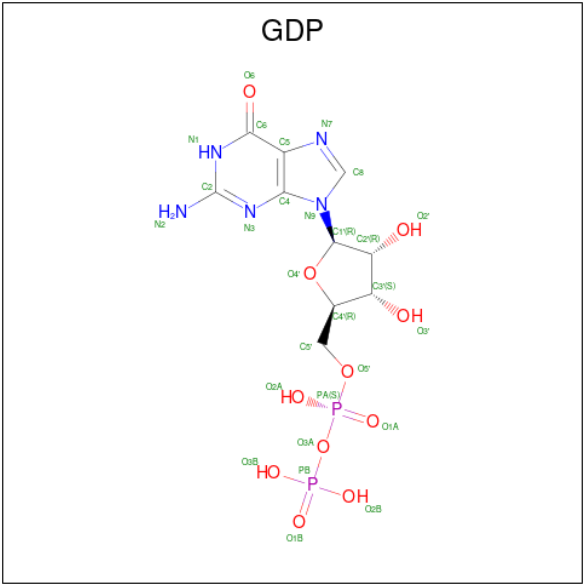
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Mol	Chain	Residues	Atoms				AltConf
85	S1	1	Total	C	N	O	0
			42	29	5	8	
85	S1	1	Total	C	N	O	0
			42	29	5	8	

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

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

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

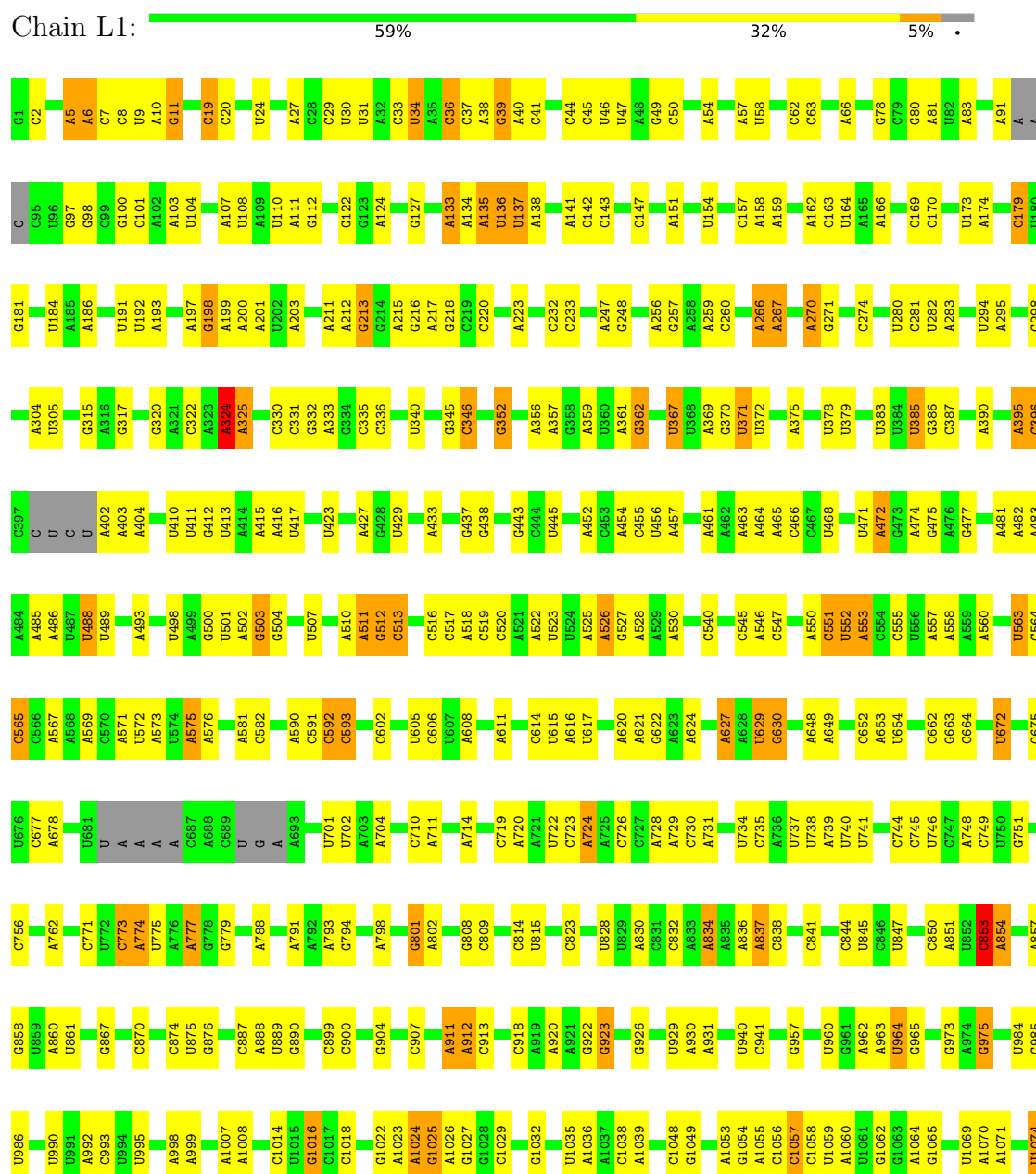


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
87	Se	1	28	10	5	11	2	0

3 Residue-property plots

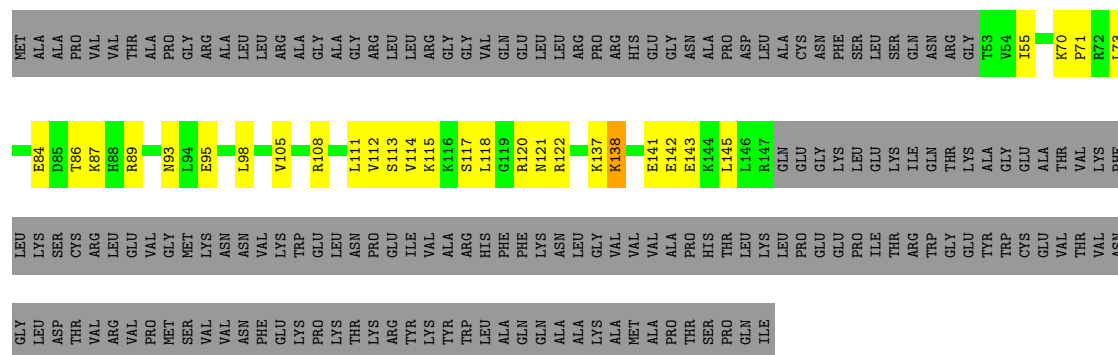
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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

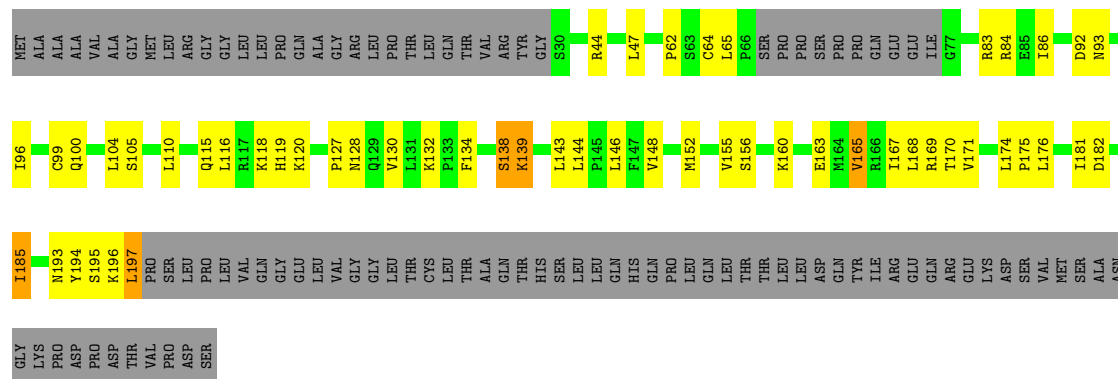


L248	F72	LEU	MET
M253	V77	GLN	
H266	D81	PRO	
Q257	L82	VAL	
V260	F87	ARG	
T262	L93	ALA	
V266	H97	ARG	
L273	Q98	ALA	
L274	V99	TRP	
M275	K113	LEU	
Q276	R121	ARG	
D277	R125	GLY	
S278	R138	GLN	
R279	H138	LEU	
R281	W146	SER	
P282	G157	SER	
L283	P158	LEU	
Y284	G173	ALA	
Y290	L174	ALA	
S291	K175	ARG	
D292	M190	ALA	
P293	D191	GLU	
P294	S192	THR	
ARG	L193	ASN	
PRO	E194	PRO	
HIS	L195	GLU	
THR	P196	VAL	
THR	Q201	ALA	
GLN	Y202	SER	
PRO	E205	GLU	
ALA	Y209	GLY	
ALA	R210	LEU	
ALA	R211	PRO	
THR	D214	THR	
PRO	H223	E45	
THR	M226	R49	
PRO	V231	K90	
PRO	L237	P56	
TYR	L241	R59	
HIS		V62	
CYS		W65	
		L69	
		R70	
		G74	

Chain LI:

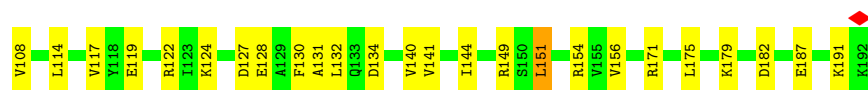


Chain LJ: 40% 19% 39%



Chain LK: 65% 24% .. 9%





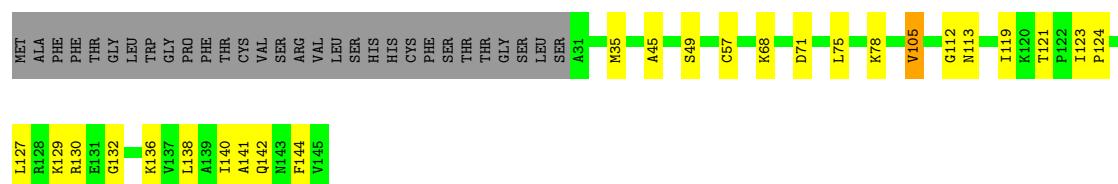
- Molecule 9: Large ribosomal subunit protein uL13m

Chain LM: 81% 17% ..



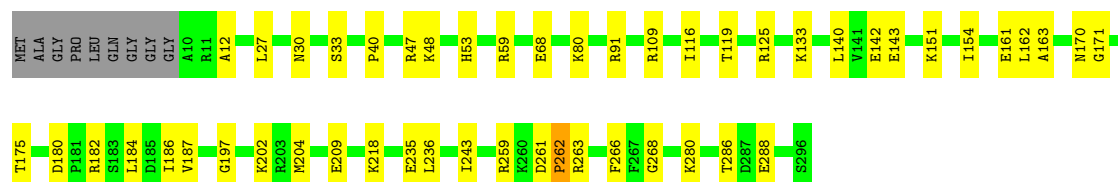
- Molecule 10: Large ribosomal subunit protein uL14m

Chain LN: 62% 17% 21%



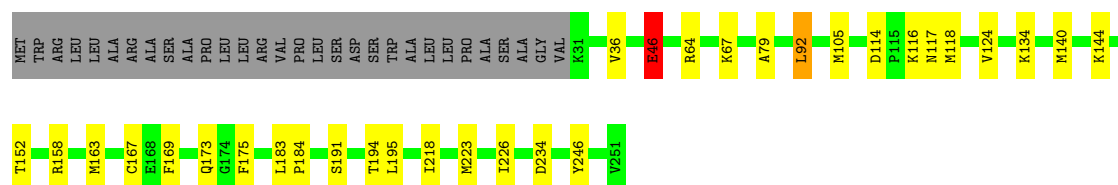
- Molecule 11: Large ribosomal subunit protein uL15m

Chain LO: 80% 17%



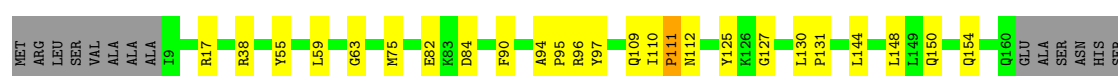
- Molecule 12: Large ribosomal subunit protein uL16m

Chain LP: 75% 12% 12%



- Molecule 13: Large ribosomal subunit protein bL17m

Chain LQ: 73% 14% 13%



SER
HIS
THR
ALA
GLN
THR
PRO
GLY
ILE

- Molecule 14: Mitochondrial ribosomal protein L18, isoform CRA_b

Chain LR:



MET ALA LEU ARG SER GLN PHE TRP GLY PHE SER PHE VAL CYS ARG ASN PRO GLY CYS ARG PHE ALA ALA LEU ARG LEU THR SER CYS GLU PRO ALA ALA LYS PRO E34 V43 N49 R50 N51 P52 R53 E56 R62 R65 E75 F76 W77 H78 R79 L80 I83 E90 A91

L32 V33 V101 V102 S105 T106 R107 A110 I111 H114 L115 A123 I127 L131 A132 Q133 R134 C135 L136 E137 M143 Q146 D155 S156 R159 L160 V169 V170 E179

- Molecule 15: Large ribosomal subunit protein bL19m

Chain LS:



MET ALA ALA CYS ASP ILE LYS HIS ARG PRO VAL HIS TRP PHE MET ARG GLY LEU GLY ARG SER PHE GLN ALA ALA ARG LEU THR LEU PRO PRO PRO ALA SER LEU ILE CYS ARG VAL HIS ALA GLY VAL ARG VAL GLN SER THR GLY PRO SER GLU PRO C248 L249 T250 E251 Q252 Q253 M254 K255 E256 K259

VAL ILE VAL ASP LYS HIS ARG PRO VAL HIS TRP PHE MET ARG GLY LEU GLY ARG SER PHE GLN ALA ALA ARG LEU THR LEU PRO PRO PRO ALA SER LEU ILE CYS ARG VAL HIS ALA GLY VAL ARG VAL GLN SER THR GLY PRO SER GLU PRO C248 L249 T250 E251 Q252 Q253 M254 K255 E256 K259

M269 I282 E285 I286 S292

- Molecule 16: Large ribosomal subunit protein bL20m

Chain LT:



MET VAL PHE LEU THR ALA GLN LEU TRP L10 R11 R17 I21 Q22 E23 K26 K35 K40 R40 R57 Y58 L59 K60 K61 N89 D104 Y108 R122 R123 E126 I141 H149

- Molecule 17: Large ribosomal subunit protein bL21m

Chain LU:



MET ALA ALA SER VAL LEU THR VAL THR LEU GLY ARG LEU ALA SER ASN CYS SER HIS SER ILE LEU ARG PRO SER GLY PRO GLY ALA ALA SER LEU TRP SER ALA SER ARG ARG PHE ASN SER GLN THR S45 V51 P52 K53 E71 E72 T73 R74 K82 R94 L95 F96

K107 E111 E119 C124 G125 L130 A138 L143 L144 L153 V156 V160 M179 P189 C203 L204 LEU

- Molecule 18: 39S ribosomal protein L22, mitochondrial

Chain LV:



MET ALA ALA VAL LEU GLY GLN LEU GLY LEU TRP ILE HIS ASN LEU ARG SER ARG GLY LYS LEU ALA LEU GLY LEU LEU SER PHE HIS SER VAL LEU PRO GLN SER TYR THR HIS THR ALA SER LEU ASP I47 K50 N55 R69 Y74 K81 Y82 M87



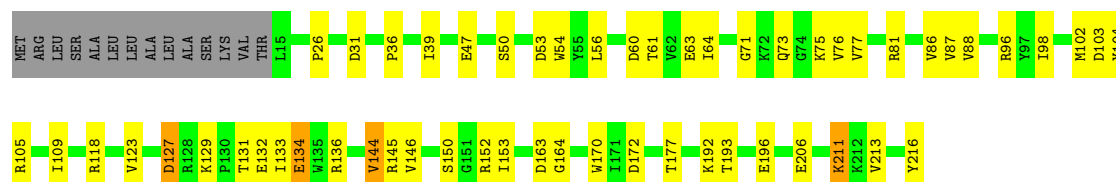
- Molecule 19: Large ribosomal subunit protein uL23m

Chain LW: 73% 20% 7%



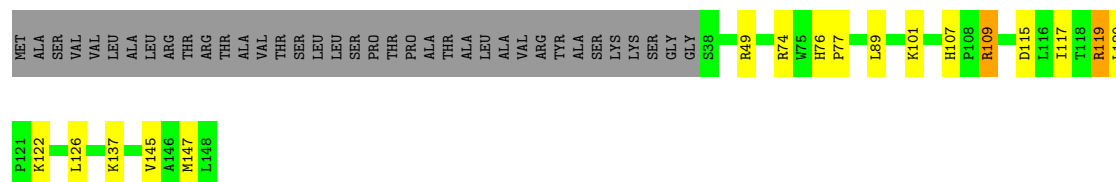
- Molecule 20: Large ribosomal subunit protein uL24m

Chain LX: 68% 24% 6%



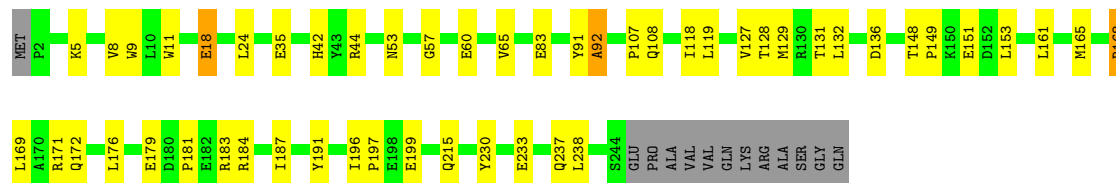
- Molecule 21: Large ribosomal subunit protein bL27m

Chain La: 64% 10% 25%



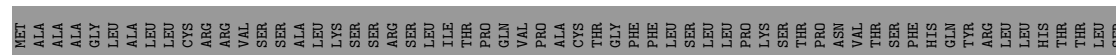
- Molecule 22: Large ribosomal subunit protein bL28m

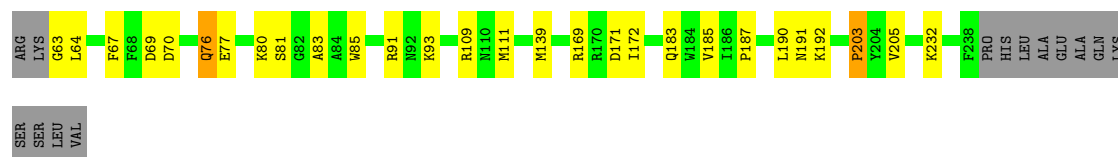
Chain Lb: 75% 19% 5%



- Molecule 23: Large ribosomal subunit protein uL29m

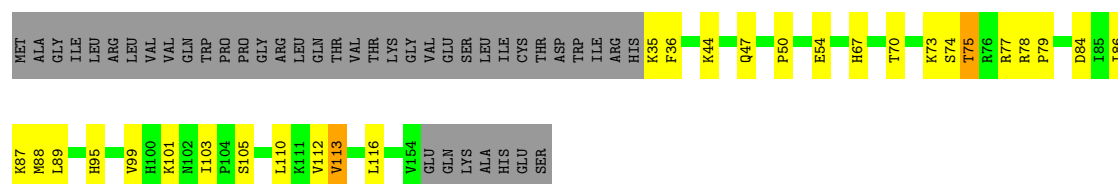
Chain Lu: 59% 10% 30%





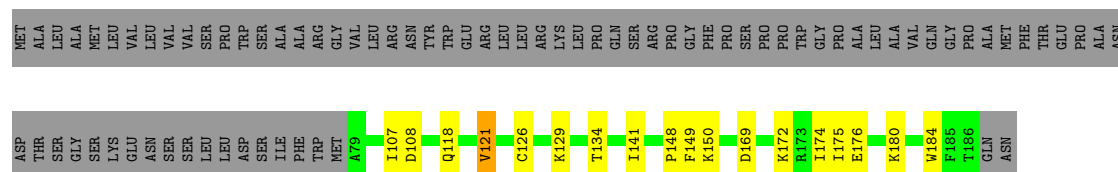
- Molecule 24: Large ribosomal subunit protein uL30m

Chain Ld: 57% 16% 25%



- Molecule 25: Large ribosomal subunit protein bL32m

Chain Lf: 48% 9% 43%



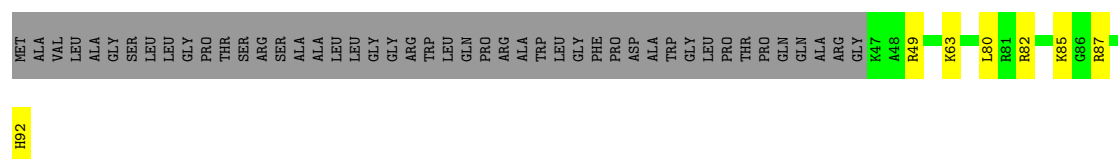
- Molecule 26: Large ribosomal subunit protein bL33m

Chain Lg: 54% 26% 20%



- Molecule 27: Large ribosomal subunit protein bL34m

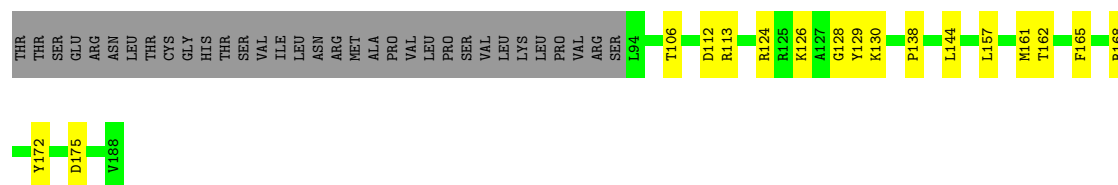
Chain Lh: 42% 8% 50%



- Molecule 28: Large ribosomal subunit protein bL35m

Chain Li: 41% 9% 49%

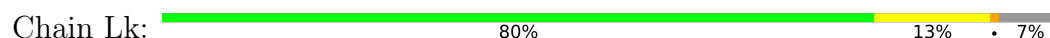




- Molecule 29: Large ribosomal subunit protein bL36m



- Molecule 30: Large ribosomal subunit protein mL37

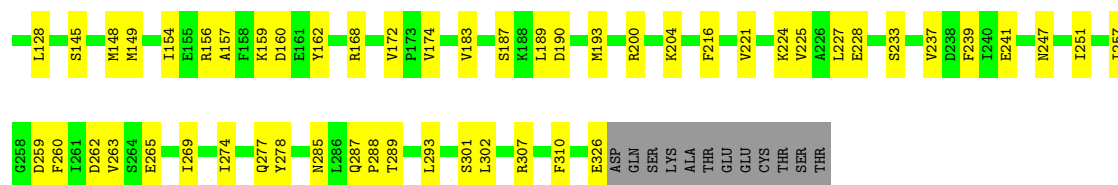


- Molecule 31: Large ribosomal subunit protein mL38



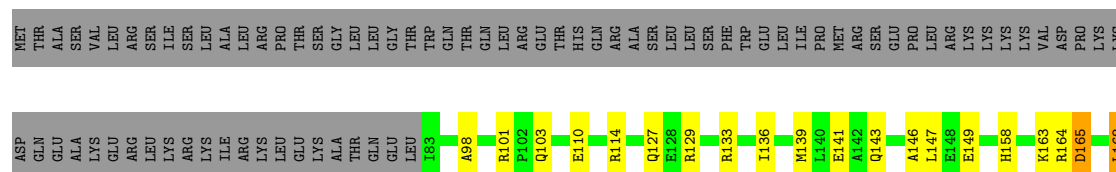
- Molecule 32: Large ribosomal subunit protein mL39





- Molecule 33: Large ribosomal subunit protein mL40

Chain Ln: 35% 11% 52%



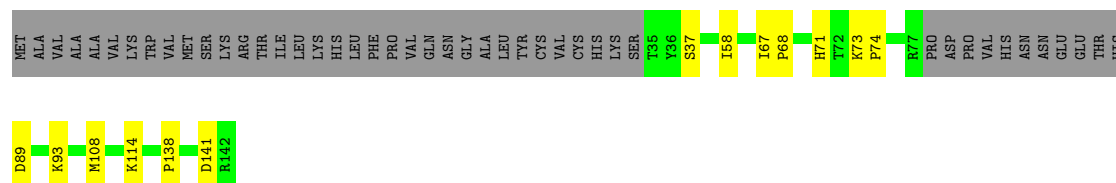
- Molecule 34: Large ribosomal subunit protein mL41

Chain Lo: 75% 15% 9%



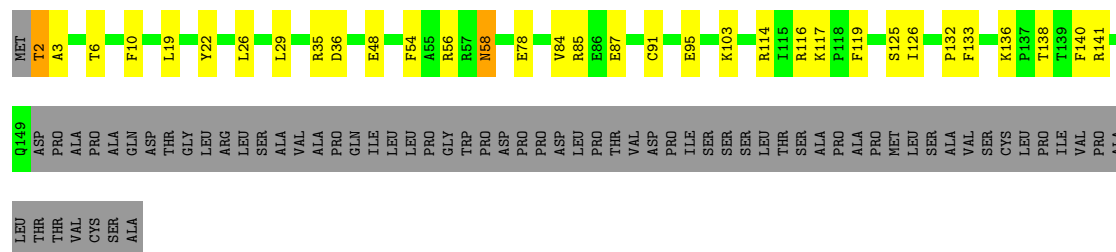
- Molecule 35: Large ribosomal subunit protein mL42

Chain Lp: 59% 9% 32%



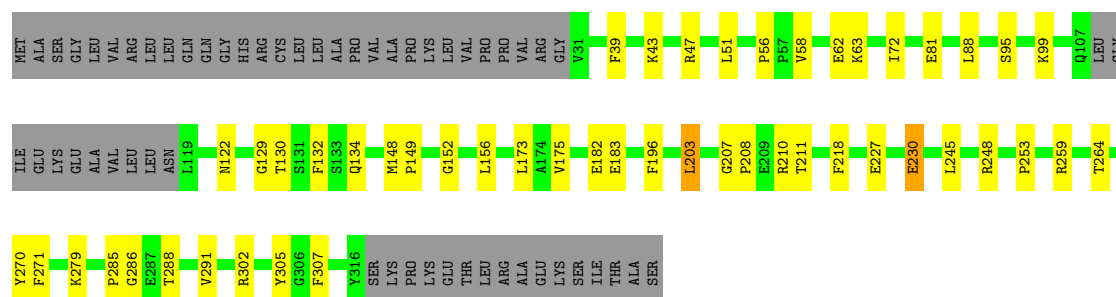
- Molecule 36: Large ribosomal subunit protein mL43

Chain Lq: 53% 14% 31%



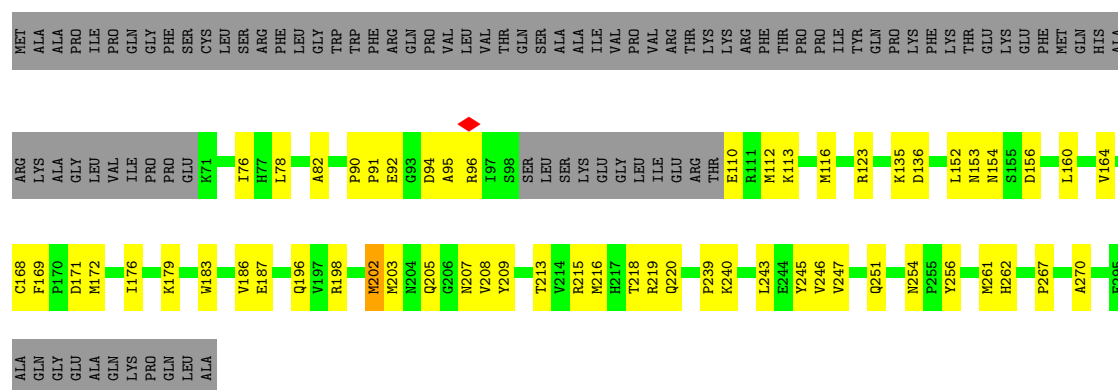
- Molecule 37: Large ribosomal subunit protein mL44

Chain Lr:  68% 14% 17%



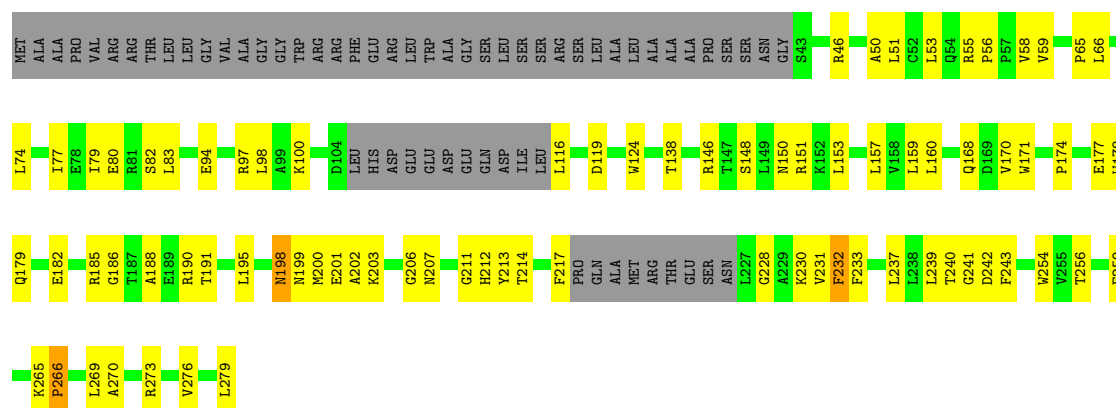
• Molecule 38: Large ribosomal subunit protein mL45

Chain Ls:  51% 19% 30%

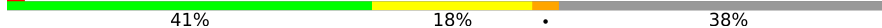


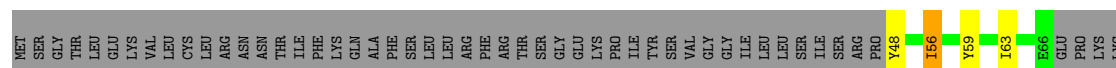
• Molecule 39: Large ribosomal subunit protein mL46

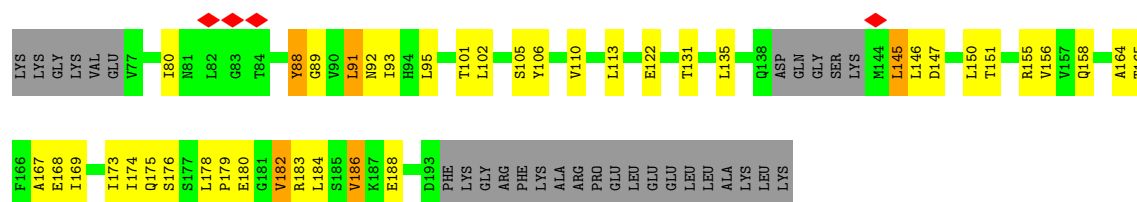
Chain Lt:  49% 28% 22%



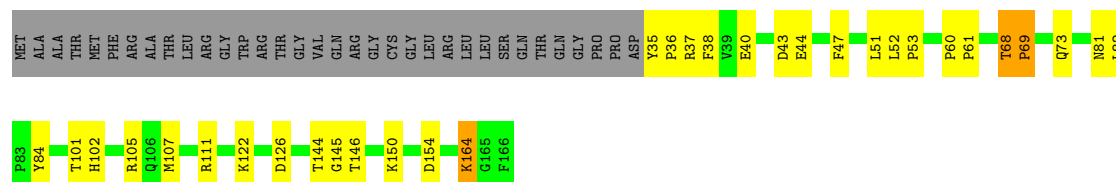
• Molecule 40: Large ribosomal subunit protein mL48

Chain Lv:  41% 18% 38%

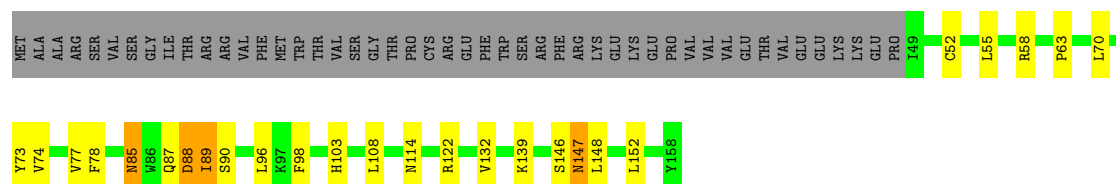




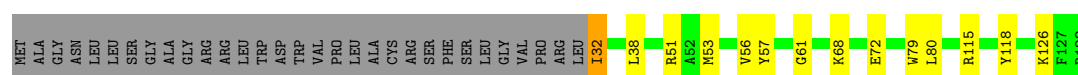
- Molecule 41: Large ribosomal subunit protein mL49



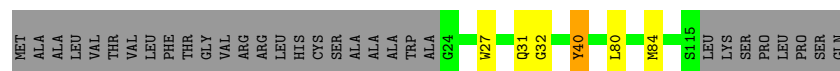
- Molecule 42: Large ribosomal subunit protein mL50



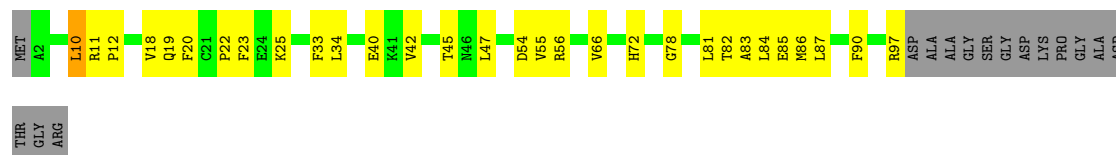
- Molecule 43: Large ribosomal subunit protein mL51

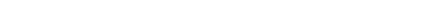


- Molecule 44: 39S ribosomal protein L52, mitochondrial



- Molecule 45: Large ribosomal subunit protein mL53



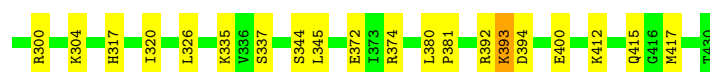
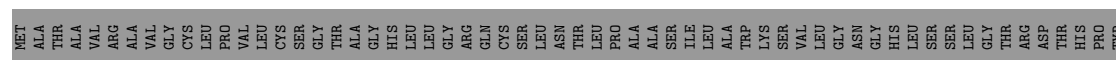
- Chain L4:  41% 18% 40%





- Molecule 55: Small ribosomal subunit protein uS5m

Chain SE: 61% 12% 26%



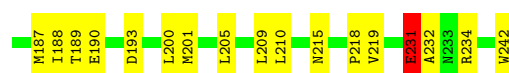
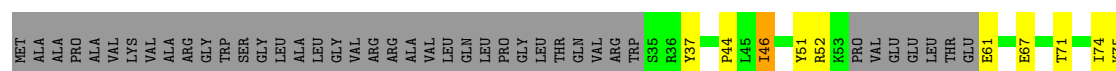
- Molecule 56: Small ribosomal subunit protein bS6m

Chain SF: 76% 22%



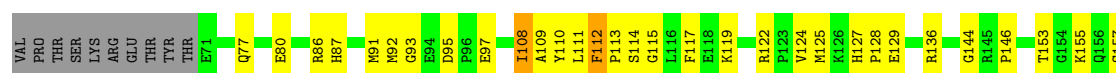
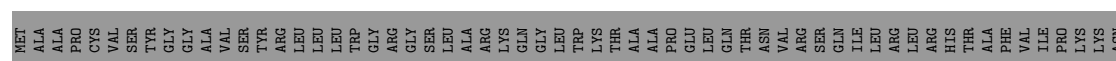
- Molecule 57: Small ribosomal subunit protein uS7m

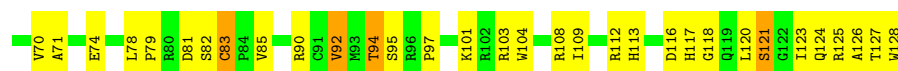
Chain SG: 57% 25% 17%



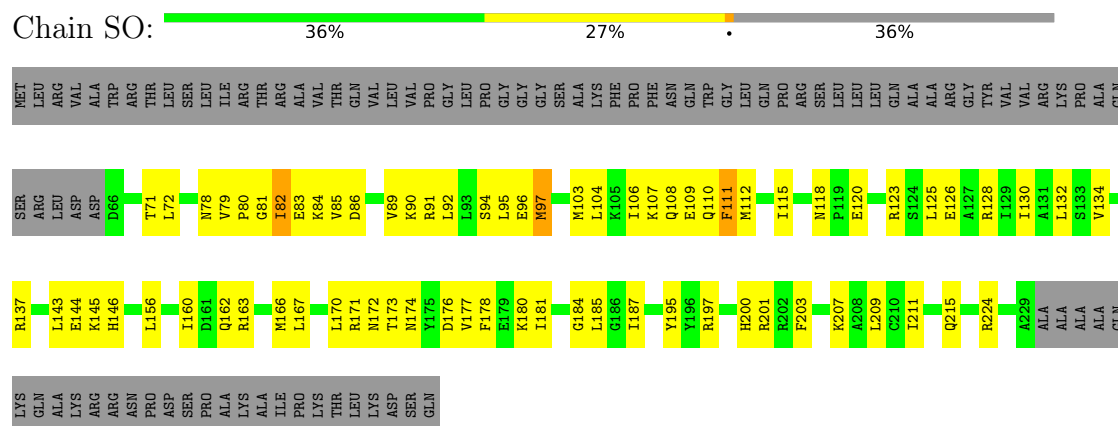
- Molecule 58: Small ribosomal subunit protein uS9m

Chain SI: 54% 21% 23%

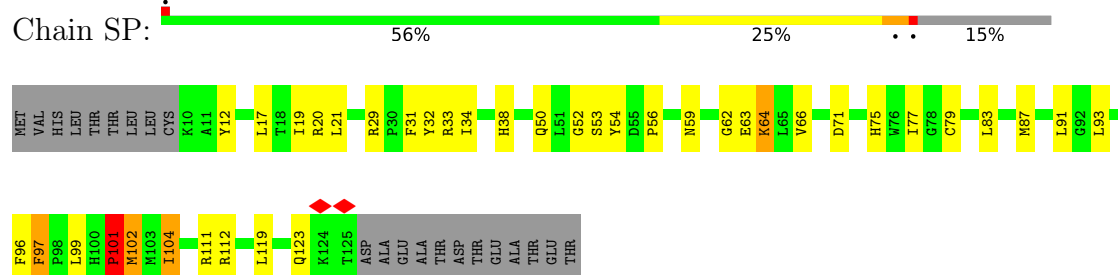




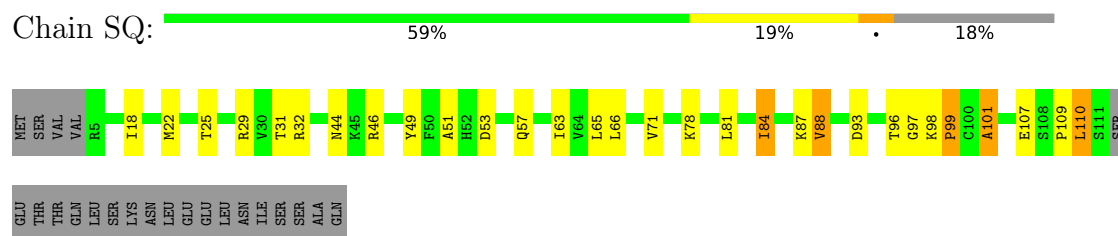
- Molecule 63: Small ribosomal subunit protein uS15m



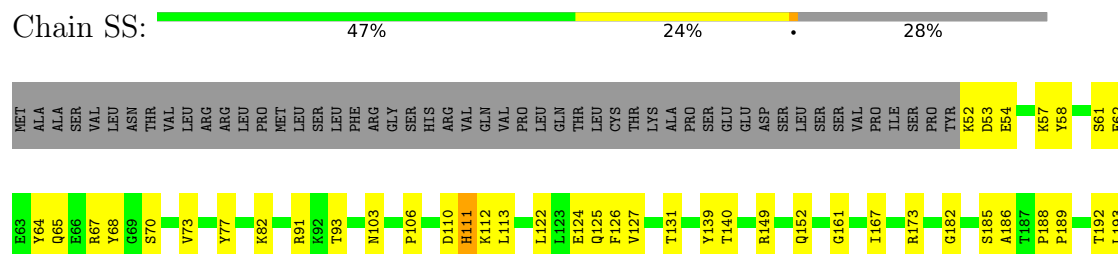
- Molecule 64: Small ribosomal subunit protein bS16m

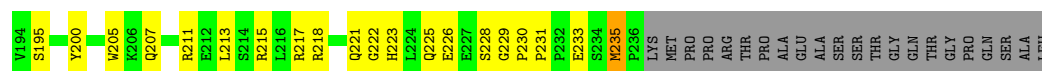


- Molecule 65: Small ribosomal subunit protein uS17m

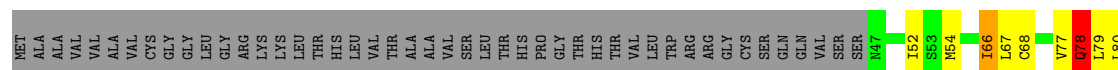


- Molecule 66: Small ribosomal subunit protein mS40

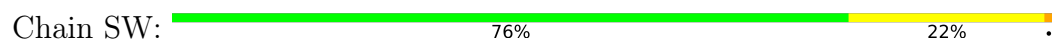




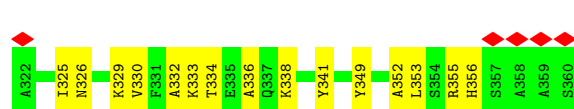
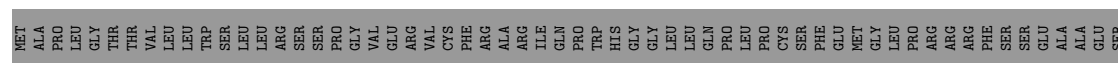
- Molecule 67: Small ribosomal subunit protein bS18m



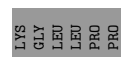
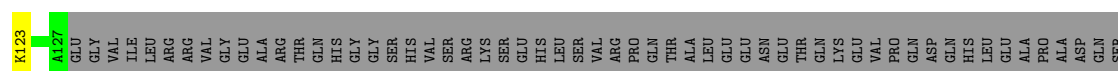
- Molecule 68: Small ribosomal subunit protein bS21m



- Molecule 69: Small ribosomal subunit protein mS22

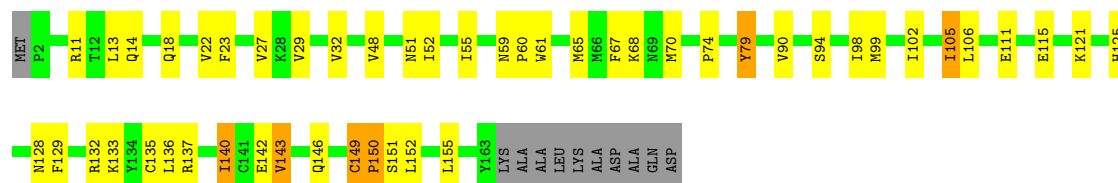


- Molecule 70: Small ribosomal subunit protein mS23



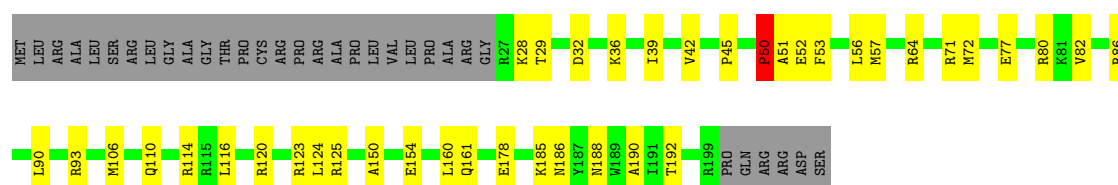
- Molecule 71: Small ribosomal subunit protein mS25

Chain Sa: 



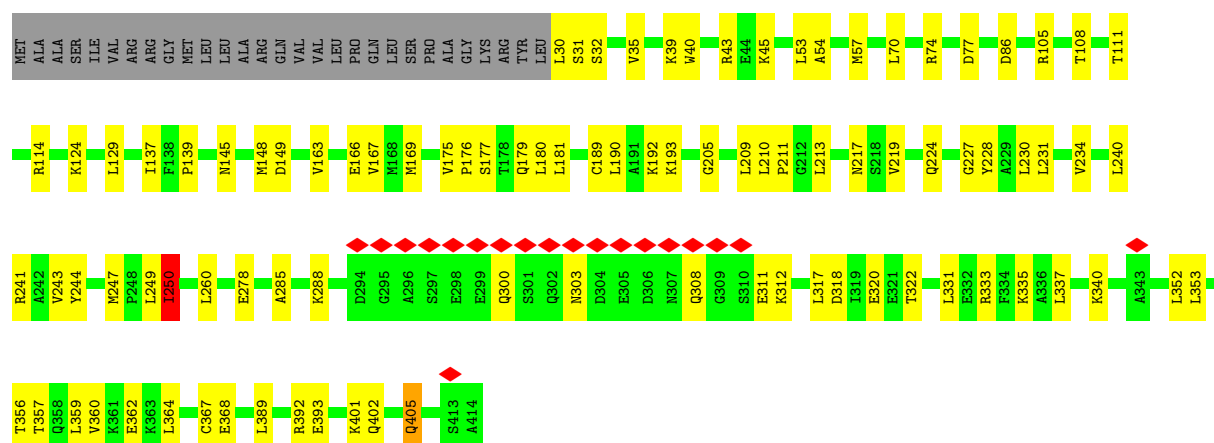
- Molecule 72: Small ribosomal subunit protein mS26

Chain Sb: 

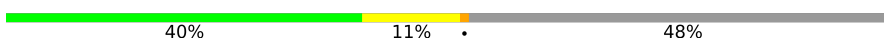


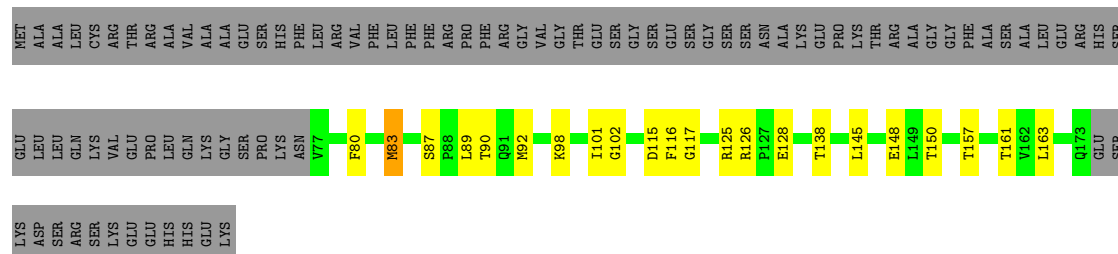
- Molecule 73: Small ribosomal subunit protein mS27

Chain Sc: 



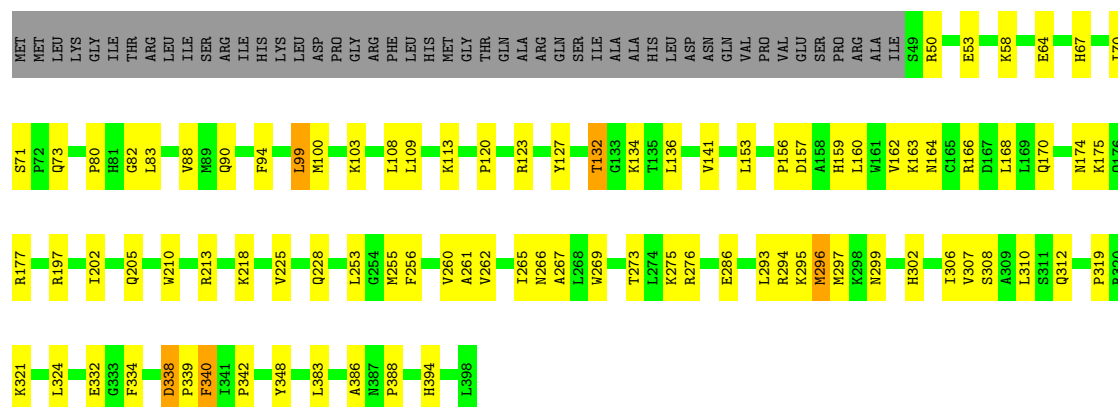
- Molecule 74: Small ribosomal subunit protein bS1m

Chain Sd: 



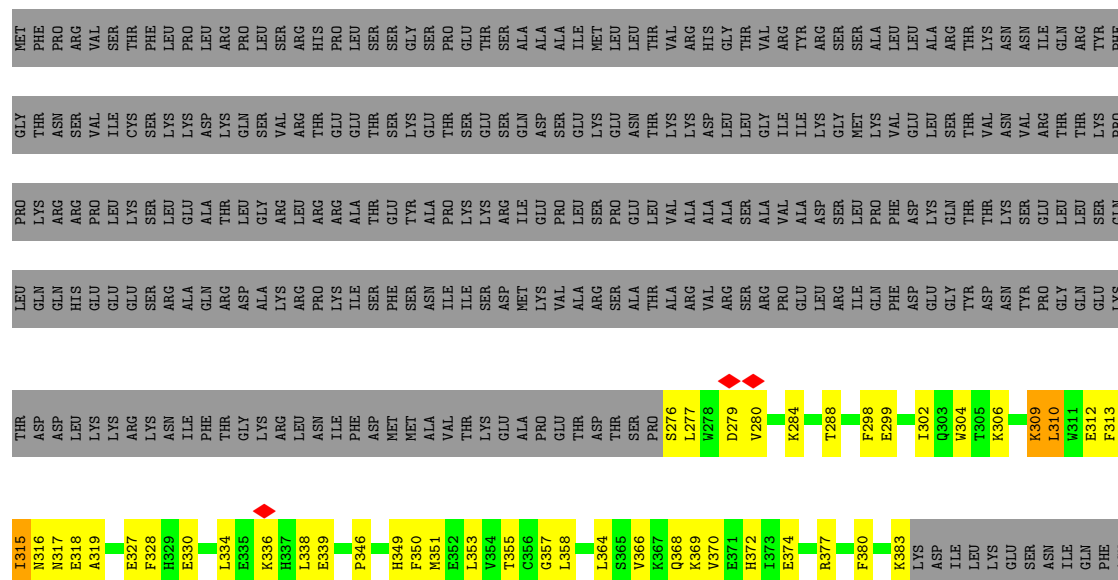
• Molecule 75: Small ribosomal subunit protein mS29

Chain Se:  66% 21% 12%

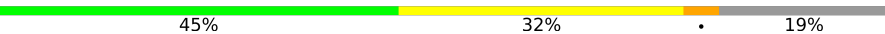


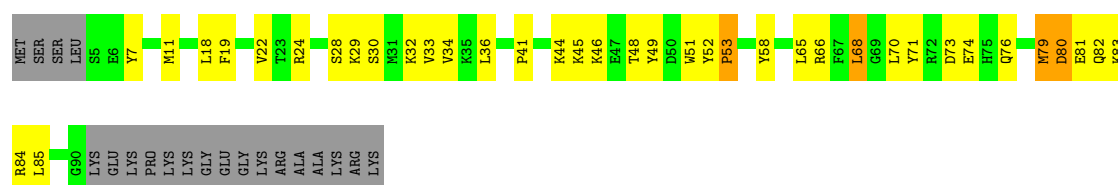
• Molecule 76: Small ribosomal subunit protein mS31

Chain Sg:  16% 11% 73%



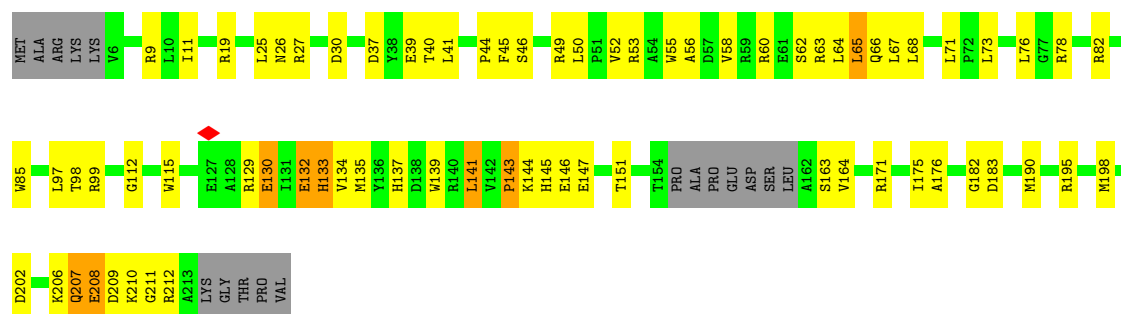
• Molecule 77: Small ribosomal subunit protein mS33

Chain Si:  45% 32% 19%

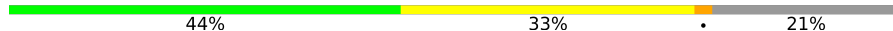


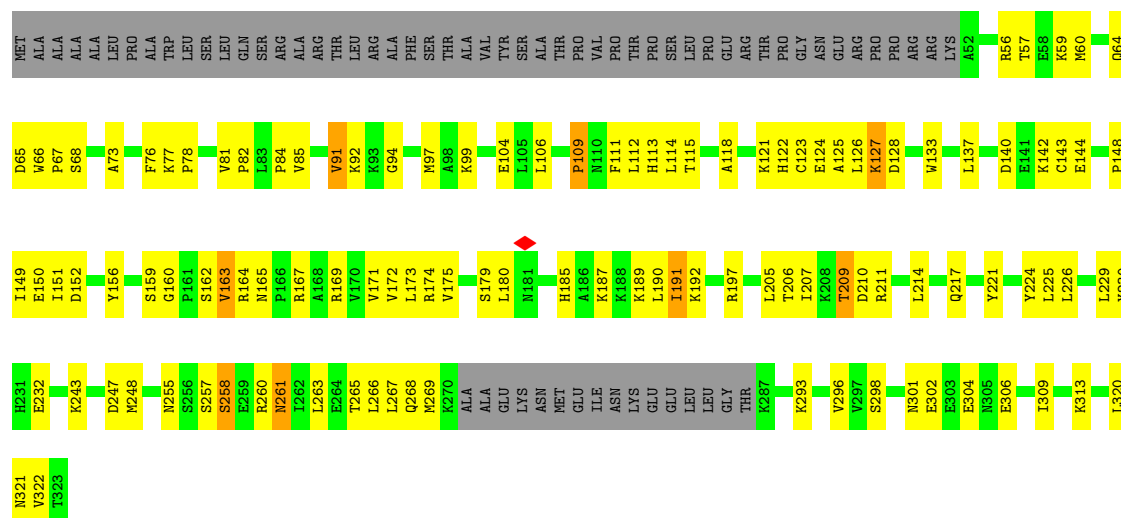
• Molecule 78: Small ribosomal subunit protein mS34

Chain Sj: 



- Molecule 79: Small ribosomal subunit protein mS35

Chain Sk: 



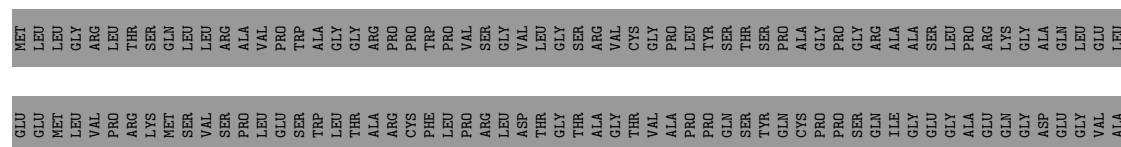
- Molecule 80: Small ribosomal subunit protein mS37

Chain Sm: 



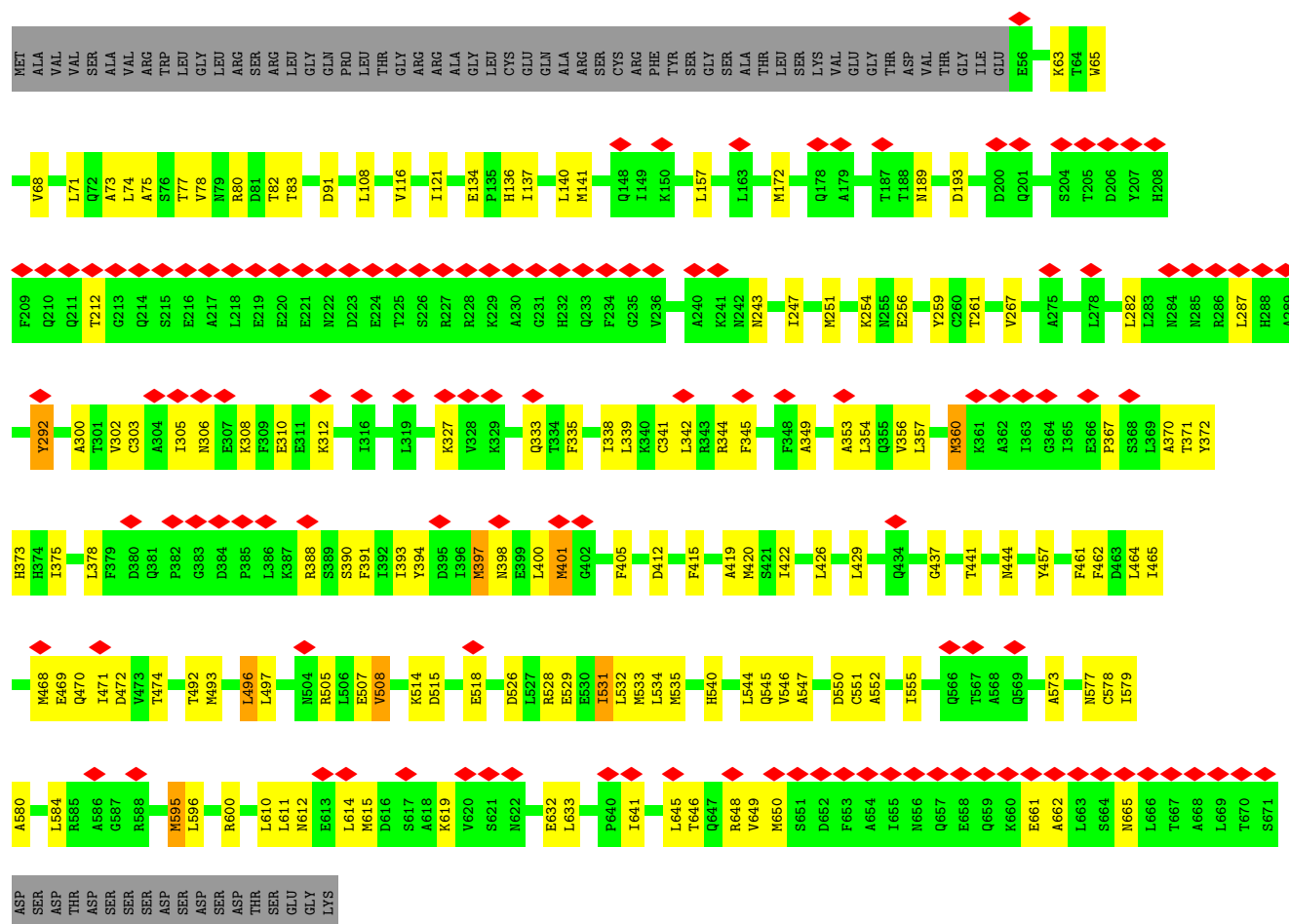
- Molecule 81: Small ribosomal subunit protein mS38

Chain Sn: 

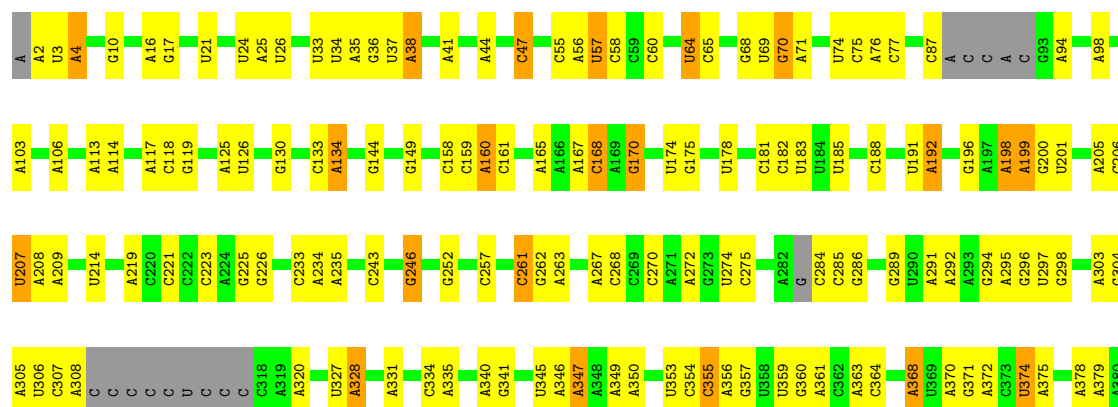




• Molecule 82: Small ribosomal subunit protein mS39



• Molecule 83: 12S rRNA



G381	A507	U610	A706	C782	A883	G381
G382	G508	A611	A706	A783	C884	G382
G383	U612	U612	A709	A786	C885	G383
G384	A514	A613	A709	A787	C886	G384
C385	A515	C614	U712		C887	C385
U386		C618	U712	A791	U888	U386
U387	A519	A619	G713	A792	A889	U387
U388	A520	U620	G714	A793	C890	U388
		C621	A720	A794	C891	
U395	C525	U622	A720	A795	C892	U395
C396	G532	U623	U721	U796	A893	C396
U397	U533	C624	U722	U797	U894	U397
A402	U537	A625	U723	A798	A897	A402
				A799		
C405	U540	C631	U726	G800	A910	C405
G410	A541	C632	A727		A911	G410
C418	U542	C633	C728	U805	G912	C418
C419	C543		C729	A806		C419
	C544	A636	C730	G807	G915	
A422	C545	U637	C731	U808	U916	A422
	U546	G638	A732	U809	A917	
U434	C547		G733		A918	U434
A443	U548	C643	A734	G817		A443
C451	A549	U644	A735	C818	U921	C451
A456	A573	A645	A736	C819	G922	A456
A457		C646	A		G923	A457
C458	C576	A647	C	A823		C458
C459	C577	A648	U	A824	U930	C459
C461	C578		A	G825	A931	C461
A462	C579	G654	C741		C932	A462
A463	G580	U654	G742	A831	G935	A463
		C655	U743	C832	A936	
U468	C583	U656	U744	C833	A937	U468
A	C586	A662	A745	C834	A938	A
A		C663		C835	G939	A
U	A590	C667	U751		U940	U
C473	C591		A752	C841	G941	C473
A474	C592	C683	U753	U841	G942	A474
	A593	A684	G754	U843	A943	
A479		A685	A755			A479
A480	U598		A756	C847	G947	A480
C481	U599	A686	A757	C848	U849	C481
	G600	C689	C			
C489	C601	C694	U	C864		C489
U497	U602	C695	U760	A865	A952	U497
A498	A604	C696	A679	A866	A953	A498
		U697	G680	A867	C954	
C504	C607	G700	G689	A870		C504
		G701		U874		
					A877	
					C878	
					U880	
					A881	
					A882	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	143725	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	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.669	Depositor
Minimum map value	-0.297	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	499.80002, 499.80002, 499.80002	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.19, 1.19, 1.19	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, T1C, ZN, GDP

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	0.34	0/35628	0.51	5/55448 (0.0%)
2	L2	0.18	0/1328	0.36	0/2056
3	LB	0.53	0/1888	0.83	0/2538
4	LC	0.61	0/2462	1.00	6/3340 (0.2%)
5	LD	0.55	0/2071	0.92	4/2817 (0.1%)
6	LI	0.46	0/798	0.84	1/1073 (0.1%)
7	LJ	0.66	2/1308 (0.2%)	1.18	6/1761 (0.3%)
8	LK	0.43	0/1340	0.81	3/1802 (0.2%)
9	LM	0.53	0/1495	0.88	1/2029 (0.0%)
10	LN	0.61	0/904	0.93	1/1218 (0.1%)
11	LO	0.51	0/2359	0.85	3/3185 (0.1%)
12	LP	0.51	0/1826	0.82	2/2458 (0.1%)
13	LQ	0.53	0/1269	0.90	2/1708 (0.1%)
14	LR	0.56	0/1215	0.92	1/1645 (0.1%)
15	LS	0.40	0/1863	0.71	3/2509 (0.1%)
16	LT	0.45	0/1174	0.81	0/1572
17	LU	0.55	1/1311 (0.1%)	0.87	2/1778 (0.1%)
18	LV	0.53	0/1402	0.88	3/1886 (0.2%)
19	LW	0.31	0/1217	0.61	0/1644
20	LX	0.52	0/1697	0.91	0/2302
21	La	0.61	0/893	0.94	3/1204 (0.2%)
22	Lb	0.45	0/2090	0.91	3/2825 (0.1%)
23	Lu	0.47	0/1552	0.83	4/2079 (0.2%)
24	Ld	0.63	0/1003	1.03	4/1354 (0.3%)
25	Lf	0.61	0/895	0.94	0/1201
26	Lg	0.53	0/438	0.89	0/583
27	Lh	0.56	0/382	0.92	0/507
28	Li	0.35	0/852	0.68	0/1136
29	Lj	0.57	0/349	0.97	2/461 (0.4%)
30	Lk	0.43	0/3305	0.75	6/4502 (0.1%)
31	Ll	0.58	0/3042	0.95	10/4140 (0.2%)
32	Lm	0.42	0/2439	0.78	2/3299 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Ln	0.60	0/855	1.08	3/1152 (0.3%)
34	Lo	0.56	0/1025	0.90	3/1379 (0.2%)
35	Lp	0.40	0/839	0.82	2/1136 (0.2%)
36	Lq	0.62	0/1202	0.87	0/1626
37	Lr	0.61	0/2264	1.05	6/3059 (0.2%)
38	Ls	0.49	0/1800	0.85	2/2436 (0.1%)
39	Lt	0.36	0/1797	0.78	1/2422 (0.0%)
40	Lv	0.60	0/1051	1.01	2/1422 (0.1%)
41	Lw	0.57	0/1134	1.00	3/1547 (0.2%)
42	Lx	0.65	0/918	1.00	0/1249
43	Ly	0.51	0/849	0.89	1/1135 (0.1%)
44	Lz	0.48	0/747	0.85	1/1005 (0.1%)
45	L3	0.59	0/754	1.21	3/1017 (0.3%)
46	L4	0.58	0/722	1.09	0/978
47	L5	0.58	0/379	0.97	0/510
48	L6	0.52	0/818	0.85	0/1097
49	L7	0.55	0/1071	0.98	4/1433 (0.3%)
50	L8	0.39	0/1107	0.74	4/1498 (0.3%)
51	SR	0.47	0/1238	0.81	0/1676
52	Sf	0.53	0/3114	0.87	4/4225 (0.1%)
53	SB	0.61	0/1811	1.05	6/2451 (0.2%)
54	SZ	0.50	0/1112	0.99	2/1505 (0.1%)
55	SE	0.41	0/2590	0.80	6/3477 (0.2%)
56	SF	0.34	0/989	0.68	0/1335
57	SG	0.47	0/1708	0.87	5/2291 (0.2%)
58	SI	0.46	0/2555	0.85	0/3424
59	SJ	0.49	0/1019	1.10	4/1379 (0.3%)
60	SK	0.47	0/1031	0.79	0/1390
61	SL	0.68	0/854	1.11	6/1148 (0.5%)
62	SN	0.65	1/879 (0.1%)	1.17	2/1182 (0.2%)
63	SO	0.63	0/1406	1.13	3/1878 (0.2%)
64	SP	0.60	0/941	1.05	2/1265 (0.2%)
65	SQ	0.67	0/864	1.03	1/1169 (0.1%)
66	SS	0.55	0/1580	0.95	6/2150 (0.3%)
67	ST	0.66	0/791	1.08	4/1062 (0.4%)
68	SW	0.61	0/752	1.08	5/1001 (0.5%)
69	SX	0.46	0/2452	0.96	4/3310 (0.1%)
70	SY	0.52	0/1069	0.89	0/1441
71	Sa	0.58	0/1361	0.97	1/1829 (0.1%)
72	Sb	0.46	0/1474	0.82	1/1976 (0.1%)
73	Sc	0.33	0/3177	0.72	1/4292 (0.0%)
74	Sd	0.72	0/778	1.24	5/1048 (0.5%)
75	Se	0.36	0/2908	0.75	5/3936 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Sg	0.53	0/931	1.03	1/1259 (0.1%)
77	Si	0.54	0/748	1.05	3/1000 (0.3%)
78	Sj	0.51	0/1723	1.00	8/2334 (0.3%)
79	Sk	0.55	0/2113	1.06	8/2863 (0.3%)
80	Sm	0.43	0/939	0.84	2/1256 (0.2%)
81	Sn	0.46	0/621	0.89	0/820
82	So	0.33	0/5093	0.70	9/6891 (0.1%)
83	S1	0.26	0/22053	0.44	2/34324 (0.0%)
All	All	0.45	4/173801 (0.0%)	0.77	218/246748 (0.1%)

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
76	Sg	0	1
All	All	0	3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	LJ	115	GLN	C-O	6.71	1.32	1.24
62	SN	59	LYS	CA-CB	5.59	1.60	1.52
7	LJ	144	LEU	C-N	5.46	1.38	1.33
17	LU	160	VAL	C-O	-5.06	1.19	1.24

All (218) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	Lb	18	GLU	CA-C-N	-11.58	108.06	122.19
22	Lb	18	GLU	C-N-CA	-11.58	108.06	122.19
45	L3	45	THR	N-CA-C	-11.02	102.06	114.62
78	Sj	209	ASP	N-CA-C	-10.17	100.90	113.20
53	SB	148	ASN	CB-CA-C	-9.62	94.99	110.86
55	SE	281	TYR	CB-CA-C	-8.96	98.33	110.79
53	SB	61	LYS	N-CA-C	-8.79	103.68	114.75
62	SN	94	THR	CB-CA-C	8.54	123.36	111.23
1	L1	837	A	C2'-C3'-O3'	8.23	126.04	113.70
79	Sk	124	GLU	N-CA-C	-8.18	102.32	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	LD	77	VAL	N-CA-C	-8.11	105.42	113.20
37	Lr	230	GLU	N-CA-C	-8.07	103.57	113.50
37	Lr	63	LYS	CB-CA-C	8.00	122.58	109.46
21	La	109	ARG	N-CA-C	-7.82	104.89	114.75
33	Ln	169	PHE	CA-CB-CG	-7.72	106.08	113.80
7	LJ	139	LYS	CA-C-N	-7.71	111.34	122.06
7	LJ	139	LYS	C-N-CA	-7.71	111.34	122.06
29	Lj	76	CYS	CB-CA-C	-7.71	93.13	111.65
4	LC	197	HIS	N-CA-C	-7.59	103.09	111.36
35	Lp	138	PRO	N-CA-C	7.37	118.47	110.58
4	LC	281	ASN	CB-CA-C	7.36	121.72	111.86
76	Sg	350	PHE	CA-CB-CG	7.24	121.03	113.80
30	Lk	53	PRO	CB-CA-C	-7.18	102.04	111.23
37	Lr	175	VAL	N-CA-C	-7.14	105.82	112.96
13	LQ	75	MET	CB-CG-SD	-7.11	91.38	112.70
24	Ld	75	THR	N-CA-C	-7.04	104.57	113.72
79	Sk	127	LYS	CA-C-N	-6.95	110.97	120.28
79	Sk	127	LYS	C-N-CA	-6.95	110.97	120.28
4	LC	317	PRO	N-CA-C	-6.94	98.17	112.47
9	LM	152	PRO	N-CA-C	6.90	122.88	113.98
41	Lw	73	GLN	CA-C-N	6.90	124.63	119.66
41	Lw	73	GLN	C-N-CA	6.90	124.63	119.66
38	Ls	176	ILE	N-CA-C	-6.85	106.55	113.47
50	L8	145	LYS	CB-CG-CD	6.84	127.04	111.30
53	SB	62	ILE	N-CA-C	-6.84	106.33	112.90
69	SX	295	ASP	N-CA-C	-6.81	103.92	111.82
24	Ld	75	THR	CB-CA-C	6.75	120.90	109.55
4	LC	328	LEU	N-CA-C	6.71	117.32	109.60
40	Lv	188	GLU	CA-CB-CG	6.65	127.41	114.10
52	Sf	271	LEU	N-CA-C	-6.60	98.03	109.58
82	So	397	MET	CA-CB-CG	6.58	127.26	114.10
39	Lt	185	ARG	N-CA-C	-6.56	104.12	111.28
37	Lr	122	ASN	CB-CA-C	-6.54	98.24	110.01
82	So	134	GLU	CA-C-O	-6.49	113.52	119.62
24	Ld	112	VAL	N-CA-C	-6.46	106.69	112.90
55	SE	249	ASN	N-CA-C	-6.45	98.68	109.07
59	SJ	155	VAL	N-CA-C	-6.45	106.53	111.62
64	SP	101	PRO	N-CA-CB	-6.43	96.50	103.25
30	Lk	141	ASP	N-CA-C	-6.41	104.29	111.28
83	S1	611	A	C4'-C3'-O3'	6.39	118.98	109.40
31	L1	289	PRO	N-CA-C	-6.38	103.07	112.26
59	SJ	156	TYR	CB-CA-C	-6.33	100.42	110.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	So	397	MET	CB-CG-SD	6.33	131.68	112.70
55	SE	140	LEU	CB-CA-C	6.32	117.58	109.80
14	LR	77	TRP	N-CA-C	-6.28	104.33	112.68
75	Se	83	LEU	CA-C-N	6.26	124.17	119.66
75	Se	83	LEU	C-N-CA	6.26	124.17	119.66
24	Ld	67	HIS	CA-CB-CG	6.23	120.03	113.80
1	L1	593	C	C4'-C3'-O3'	-6.23	103.66	113.00
18	LV	93	LEU	CA-C-N	-6.19	115.83	121.65
18	LV	93	LEU	C-N-CA	-6.19	115.83	121.65
59	SJ	90	SER	N-CA-C	-6.15	104.50	111.14
68	SW	78	LYS	N-CA-C	-6.14	106.05	112.93
53	SB	75	VAL	N-CA-C	-6.13	105.75	112.80
83	S1	542	U	C2'-C3'-O3'	6.10	118.66	109.50
5	LD	214	ASP	N-CA-C	-6.04	105.91	113.28
49	L7	188	LEU	N-CA-C	-6.00	106.60	114.04
77	Si	53	PRO	N-CA-C	-5.99	101.76	110.80
52	Sf	283	PHE	CA-CB-CG	5.99	119.79	113.80
73	Sc	405	GLN	CA-CB-CG	5.98	126.06	114.10
63	SO	224	ARG	CB-CG-CD	5.95	124.98	111.30
31	L1	348	PRO	N-CA-C	5.87	117.86	110.70
15	LS	89	PRO	CA-C-N	5.84	128.11	120.28
15	LS	89	PRO	C-N-CA	5.84	128.11	120.28
74	Sd	145	LEU	N-CA-C	-5.83	106.82	114.04
82	So	508	VAL	CA-C-N	5.82	124.98	120.33
82	So	508	VAL	C-N-CA	5.82	124.98	120.33
74	Sd	90	THR	N-CA-C	-5.82	106.03	114.12
62	SN	56	SER	N-CA-C	-5.82	104.85	111.07
31	L1	51	TYR	CB-CA-C	-5.80	100.30	109.80
75	Se	88	VAL	N-CA-C	-5.79	104.71	110.62
7	LJ	194	TYR	N-CA-C	-5.79	106.26	113.15
75	Se	296	MET	CB-CG-SD	5.79	130.07	112.70
29	Lj	66	PHE	CA-CB-CG	5.75	119.55	113.80
30	Lk	140	VAL	N-CA-C	-5.75	107.66	113.47
35	Lp	138	PRO	N-CA-CB	-5.75	100.23	103.22
78	Sj	41	LEU	CA-C-N	-5.74	115.01	123.05
78	Sj	41	LEU	C-N-CA	-5.74	115.01	123.05
53	SB	150	GLN	N-CA-C	-5.74	106.32	113.38
30	Lk	143	PRO	CA-N-CD	-5.74	103.97	112.00
66	SS	70	SER	CA-C-N	5.72	133.16	121.48
66	SS	70	SER	C-N-CA	5.72	133.16	121.48
1	L1	853	C	C4'-C3'-O3'	5.68	117.92	109.40
82	So	531	ILE	CA-CB-CG1	5.65	120.01	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	SG	124	GLU	N-CA-C	-5.65	105.12	111.28
79	Sk	268	GLN	N-CA-CB	5.65	119.25	110.44
79	Sk	115	THR	CB-CA-C	5.64	117.54	108.91
45	L3	23	PHE	N-CA-C	-5.63	104.99	113.89
78	Sj	132	GLU	CB-CA-C	-5.63	101.16	114.16
66	SS	189	PRO	CA-C-N	5.62	129.19	120.60
66	SS	189	PRO	C-N-CA	5.62	129.19	120.60
55	SE	248	GLY	O-C-N	5.62	127.54	123.27
5	LD	158	PRO	N-CA-C	-5.61	101.72	111.32
69	SX	261	LEU	CA-C-N	-5.60	114.20	122.83
69	SX	261	LEU	C-N-CA	-5.60	114.20	122.83
31	Ll	347	PRO	CA-C-O	-5.58	116.88	120.90
49	L7	121	ILE	N-CA-C	-5.58	107.35	113.43
21	La	119	ARG	N-CA-C	-5.58	106.37	114.12
68	SW	79	ASN	N-CA-C	-5.56	106.70	112.93
17	LU	179	ASN	CA-C-N	-5.54	115.40	122.77
17	LU	179	ASN	C-N-CA	-5.54	115.40	122.77
21	La	145	VAL	N-CA-C	-5.53	108.11	113.53
31	Ll	346	ARG	CB-CA-C	5.53	116.83	108.86
8	LK	33	PRO	N-CA-C	5.50	117.42	110.70
50	L8	145	LYS	N-CA-CB	5.48	118.18	110.12
80	Sm	49	MET	N-CA-C	-5.46	105.32	111.28
82	So	401	MET	CG-SD-CE	-5.45	88.91	100.90
67	ST	78	GLN	N-CA-C	-5.44	99.22	110.80
57	SG	231	GLU	CA-C-O	-5.44	115.11	120.82
71	Sa	133	LYS	N-CA-C	-5.42	106.80	113.41
49	L7	189	ARG	N-CA-C	-5.42	106.70	113.15
79	Sk	258	SER	CA-C-O	-5.41	115.13	120.70
37	Lr	56	PRO	CB-CA-C	-5.40	104.33	110.92
13	LQ	84	ASP	N-CA-C	-5.39	106.54	113.23
68	SW	7	PHE	N-CA-C	5.39	116.91	110.44
69	SX	287	ASP	N-CA-C	-5.39	105.48	111.36
65	SQ	84	ILE	CA-C-O	-5.39	117.94	122.63
72	Sb	50	PRO	N-CA-C	5.39	123.57	112.47
54	SZ	115	ASN	N-CA-C	-5.38	106.50	112.57
11	LO	170	ASN	N-CA-C	-5.37	106.23	112.89
53	SB	59	ASN	N-CA-C	-5.37	106.80	113.19
11	LO	133	LYS	N-CA-C	-5.37	106.60	112.72
67	ST	133	PRO	CB-CA-C	-5.32	104.79	111.71
74	Sd	157	THR	N-CA-C	-5.32	106.95	113.50
33	Ln	103	GLN	CA-CB-CG	5.31	124.72	114.10
32	Lm	310	PHE	CA-CB-CG	5.31	119.11	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	L8	133	VAL	CA-C-N	-5.31	112.32	121.66
50	L8	133	VAL	C-N-CA	-5.31	112.32	121.66
61	SL	89	ARG	CA-C-N	-5.31	115.62	123.05
61	SL	89	ARG	C-N-CA	-5.31	115.62	123.05
34	Lo	114	LEU	N-CA-C	-5.30	106.59	113.16
78	Sj	208	GLU	N-CA-C	-5.30	106.66	113.23
64	SP	102	MET	CA-CB-CG	-5.29	103.53	114.10
61	SL	87	THR	N-CA-C	-5.28	106.73	114.39
79	Sk	255	ASN	CB-CA-C	-5.28	101.04	111.91
31	Ll	348	PRO	CB-CA-C	-5.26	104.50	110.92
1	L1	325	A	C4'-C3'-O3'	-5.26	105.11	113.00
44	Lz	40	TYR	CA-CB-CG	5.25	123.35	113.90
15	LS	237	ASN	N-CA-C	-5.25	107.54	114.31
4	LC	170	LEU	CA-C-N	5.24	123.48	119.66
4	LC	170	LEU	C-N-CA	5.24	123.48	119.66
63	SO	160	ILE	N-CA-C	-5.22	105.29	110.62
5	LD	158	PRO	CB-CA-C	5.20	118.19	110.85
54	SZ	147	TYR	CA-CB-CG	5.20	123.26	113.90
77	Si	79	MET	CA-CB-CG	5.19	124.49	114.10
7	LJ	139	LYS	N-CA-CB	-5.19	108.25	114.17
63	SO	110	GLN	N-CA-C	-5.19	105.27	111.03
68	SW	76	MET	N-CA-C	-5.19	106.92	113.20
78	Sj	143	PRO	N-CA-C	5.19	119.46	111.57
23	Lu	172	ILE	N-CA-C	-5.19	106.25	113.00
34	Lo	135	PHE	CA-CB-CG	5.18	118.98	113.80
30	Lk	60	PHE	CA-CB-CG	5.17	118.97	113.80
52	Sf	253	LEU	CA-C-O	-5.17	115.51	121.19
59	SJ	84	ASP	CA-CB-CG	5.16	117.76	112.60
77	Si	30	SER	N-CA-C	-5.15	107.55	113.88
57	SG	111	MET	CB-CG-SD	-5.14	97.27	112.70
38	Ls	202	MET	CB-CG-SD	5.14	128.13	112.70
49	L7	190	GLN	N-CA-C	-5.14	107.07	113.19
18	LV	203	LEU	N-CA-C	-5.14	106.27	112.54
41	Lw	164	LYS	N-CA-C	-5.13	106.87	113.23
30	Lk	38	THR	N-CA-C	-5.13	107.06	113.72
67	ST	130	LEU	N-CA-C	-5.13	106.23	113.20
57	SG	118	VAL	N-CA-C	-5.12	105.71	110.53
68	SW	8	ILE	N-CA-C	-5.12	107.57	111.62
79	Sk	104	GLU	N-CA-C	-5.12	105.39	111.69
40	Lv	56	ILE	N-CA-C	-5.12	106.58	112.98
23	Lu	76	GLN	CA-C-N	5.11	131.29	121.54
23	Lu	76	GLN	C-N-CA	5.11	131.29	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	Ln	169	PHE	CA-C-O	-5.11	114.23	119.08
82	So	496	LEU	N-CA-C	-5.10	106.15	112.38
11	LO	262	PRO	CA-C-O	-5.10	115.77	121.23
32	Lm	216	PHE	CA-CB-CG	5.10	118.90	113.80
45	L3	25	LYS	CB-CG-CD	5.09	123.01	111.30
12	LP	116	LYS	N-CA-C	-5.09	107.75	114.31
55	SE	393	LYS	CB-CG-CD	5.09	123.00	111.30
78	Sj	211	GLY	CA-C-N	-5.08	113.65	120.87
78	Sj	211	GLY	C-N-CA	-5.08	113.65	120.87
80	Sm	71	GLN	CA-CB-CG	5.08	124.26	114.10
31	Ll	93	PRO	N-CA-C	5.07	116.88	110.70
7	LJ	127	PRO	CB-CA-C	-5.06	104.91	111.39
61	SL	56	PRO	N-CA-CB	-5.06	97.94	103.25
23	Lu	203	PRO	N-CA-C	5.06	122.89	112.47
57	SG	46	ILE	CB-CG1-CD1	5.06	124.42	113.80
31	Ll	211	GLY	O-C-N	5.05	128.46	122.50
61	SL	60	GLY	CA-C-N	-5.05	116.09	123.06
61	SL	60	GLY	C-N-CA	-5.05	116.09	123.06
7	LJ	130	VAL	N-CA-C	-5.05	107.91	112.96
10	LN	112	GLY	N-CA-C	-5.05	108.03	114.85
75	Se	340	PHE	CA-CB-CG	5.05	118.85	113.80
43	Ly	126	LYS	N-CA-C	-5.04	107.67	113.88
66	SS	233	GLU	CA-C-N	-5.04	115.30	122.77
66	SS	233	GLU	C-N-CA	-5.04	115.30	122.77
74	Sd	117	GLY	CA-C-N	-5.04	115.60	121.85
74	Sd	117	GLY	C-N-CA	-5.04	115.60	121.85
1	Ll	324	A	C4'-C3'-O3'	-5.04	105.44	113.00
31	Ll	328	THR	N-CA-C	-5.04	105.79	111.28
82	So	595	MET	CG-SD-CE	-5.03	89.84	100.90
22	Lb	237	GLN	CA-CB-CG	5.03	124.15	114.10
34	Lo	109	PHE	N-CA-C	-5.02	101.56	109.25
31	Ll	349	PRO	CA-C-O	-5.02	115.66	122.08
37	Lr	203	LEU	N-CA-C	-5.02	105.70	111.07
6	LI	138	LYS	CB-CG-CD	5.02	122.84	111.30
52	Sf	271	LEU	CA-C-O	-5.01	114.60	119.51
55	SE	344	SER	N-CA-C	-5.01	107.83	114.04
12	LP	92	LEU	N-CA-C	-5.01	106.48	112.59
8	LK	134	ASP	CA-C-N	-5.00	112.87	122.13
8	LK	134	ASP	C-N-CA	-5.00	112.87	122.13
67	ST	135	VAL	N-CA-C	-5.00	108.40	113.20

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	LJ	138	SER	Peptide
8	LK	58	LYS	Peptide
76	Sg	327	GLU	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L1	31847	0	16179	216	0
2	L2	1191	0	607	9	0
3	LB	1851	0	1909	25	0
4	LC	2393	0	2398	59	0
5	LD	2013	0	2044	49	0
6	LI	784	0	832	22	0
7	LJ	1283	0	1370	41	0
8	LK	1323	0	1400	38	0
9	LM	1451	0	1448	31	0
10	LN	889	0	941	22	0
11	LO	2305	0	2378	45	0
12	LP	1779	0	1808	33	0
13	LQ	1245	0	1283	15	0
14	LR	1189	0	1180	42	0
15	LS	1822	0	1859	29	0
16	LT	1153	0	1214	14	0
17	LU	1284	0	1354	18	0
18	LV	1368	0	1410	24	0
19	LW	1188	0	1180	27	0
20	LX	1652	0	1658	54	0
21	La	871	0	898	15	0
22	Lb	2035	0	2054	44	0
23	Lu	1517	0	1561	23	0
24	Ld	978	0	1030	25	0
25	Lf	880	0	902	17	0
26	Lg	433	0	475	29	0
27	Lh	376	0	406	6	0
28	Li	831	0	883	13	0
29	Lj	341	0	361	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	Lk	3210	0	3206	42	0
31	Ll	2947	0	2841	79	0
32	Lm	2382	0	2393	56	0
33	Ln	836	0	844	37	0
34	Lo	997	0	987	20	0
35	Lp	815	0	792	12	0
36	Lq	1178	0	1180	31	0
37	Lr	2217	0	2220	39	0
38	Ls	1754	0	1732	69	0
39	Lt	1762	0	1767	67	0
40	Lv	1035	0	1040	56	0
41	Lw	1097	0	1085	26	0
42	Lx	895	0	881	24	0
43	Ly	827	0	857	15	0
44	Lz	732	0	730	6	0
45	L3	743	0	758	25	0
46	L4	703	0	693	29	0
47	L5	372	0	387	23	0
48	L6	797	0	804	23	0
49	L7	1058	0	1083	43	0
50	L8	1076	0	1049	25	0
51	SR	1203	0	1219	28	0
52	Sf	3036	0	3022	42	0
53	SB	1768	0	1765	61	0
54	SZ	1082	0	1088	44	0
55	SE	2540	0	2574	35	0
56	SF	972	0	1001	29	0
57	SG	1668	0	1716	53	0
58	SI	2501	0	2486	79	0
59	SJ	999	0	1024	79	0
60	SK	1011	0	1052	48	0
61	SL	838	0	887	23	0
62	SN	861	0	885	78	0
63	SO	1382	0	1472	85	0
64	SP	920	0	951	43	0
65	SQ	846	0	908	35	0
66	SS	1528	0	1488	57	0
67	ST	774	0	801	22	0
68	SW	740	0	754	25	0
69	SX	2405	0	2425	72	0
70	SY	1042	0	1037	45	0
71	Sa	1330	0	1342	51	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
72	Sb	1454	0	1464	53	0
73	Sc	3116	0	3069	83	0
74	Sd	766	0	785	16	0
75	Se	2836	0	2828	62	0
76	Sg	903	0	843	44	0
77	Si	731	0	734	84	0
78	Sj	1680	0	1674	66	0
79	Sk	2068	0	2087	148	0
80	Sm	925	0	962	25	0
81	Sn	610	0	682	20	0
82	So	4981	0	4959	181	0
83	S1	19716	0	10015	188	0
84	L1	105	0	0	1	0
84	L6	1	0	0	0	0
84	LB	3	0	0	0	0
84	LC	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	1	0
85	S1	84	0	76	1	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	165285	0	140514	3173	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 10.

All (3173) 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)
79:Sk:113:HIS:CD2	79:Sk:114:LEU:HG	1.43	1.50
73:Sc:180:LEU:HD12	73:Sc:181:LEU:N	1.27	1.49
40:Lv:146:LEU:HD23	40:Lv:147:ASP:N	1.19	1.47
40:Lv:146:LEU:CD2	40:Lv:147:ASP:H	1.25	1.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:Sk:320:LEU:HD13	79:Sk:321:ASN:N	1.33	1.41
77:Si:51:TRP:HD1	77:Si:52:TYR:CE1	1.40	1.40
20:LX:127:ASP:OD1	20:LX:129:LYS:HB2	1.19	1.33
72:Sb:71:ARG:NH1	72:Sb:72:MET:HE1	1.01	1.31
77:Si:51:TRP:CD1	77:Si:52:TYR:CE1	2.19	1.30
77:Si:51:TRP:HD1	77:Si:52:TYR:CD1	1.48	1.29
72:Sb:71:ARG:NH1	72:Sb:72:MET:CE	1.96	1.28
82:So:515:ASP:HA	82:So:518:GLU:OE2	1.31	1.27
60:SK:75:TRP:HB3	60:SK:146:HIS:CD2	1.69	1.24
79:Sk:66:TRP:HH2	79:Sk:82:PRO:CD	1.50	1.24
77:Si:7:TYR:CE1	77:Si:11:MET:HG2	1.71	1.23
77:Si:7:TYR:HE1	77:Si:11:MET:CG	1.49	1.23
82:So:420:MET:HE3	82:So:457:TYR:CD2	1.75	1.22
59:SJ:91:TYR:CE1	59:SJ:165:PRO:HD3	1.77	1.20
77:Si:79:MET:O	77:Si:83:LYS:HG2	1.41	1.17
4:LC:135:LYS:HE2	4:LC:141:LYS:HA	1.18	1.17
77:Si:46:LYS:HA	77:Si:49:TYR:CE1	1.79	1.17
59:SJ:136:MET:HE1	62:SN:104:TRP:HZ2	1.09	1.16
73:Sc:356:THR:O	73:Sc:360:VAL:HG23	1.41	1.16
40:Lv:131:THR:HG22	40:Lv:151:THR:HG22	1.25	1.16
59:SJ:148:LEU:HG	59:SJ:152:THR:CG2	1.74	1.15
32:Lm:285:ASN:ND2	32:Lm:293:LEU:HD21	1.62	1.15
77:Si:51:TRP:CD1	77:Si:52:TYR:HE1	1.60	1.15
31:Ll:306:LYS:HG3	31:Ll:307:HIS:CD2	1.81	1.15
54:SZ:63:ALA:HB3	62:SN:124:GLN:NE2	1.62	1.14
79:Sk:269:MET:HE3	79:Sk:269:MET:HA	1.19	1.13
30:Lk:274:LYS:HA	30:Lk:274:LYS:HE2	1.20	1.12
40:Lv:135:LEU:HD12	40:Lv:135:LEU:O	1.48	1.12
77:Si:7:TYR:HE1	77:Si:11:MET:HG2	0.95	1.11
83:S1:77:C:N4	83:S1:103:A:H61	1.47	1.11
82:So:420:MET:CE	82:So:457:TYR:CE2	2.34	1.11
83:S1:77:C:H42	83:S1:103:A:N6	1.47	1.11
21:La:120:LEU:HD11	21:La:126:LEU:HD13	1.20	1.10
58:SI:87:HIS:O	58:SI:91:MET:SD	2.09	1.10
59:SJ:148:LEU:HG	59:SJ:152:THR:HG21	1.27	1.10
69:SX:182:ARG:HB3	69:SX:182:ARG:NH1	1.65	1.10
81:Sn:173:LEU:HD12	81:Sn:191:THR:HG23	1.34	1.10
49:L7:98:LYS:HD3	49:L7:138:GLU:OE2	1.52	1.10
82:So:514:LYS:O	82:So:518:GLU:HG3	1.51	1.09
78:Sj:163:SER:OG	78:Sj:190:MET:SD	2.09	1.09
58:SI:292:ARG:HB2	58:SI:292:ARG:HH11	1.13	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:Sk:113:HIS:CD2	79:Sk:114:LEU:CG	2.35	1.09
79:Sk:66:TRP:CH2	79:Sk:82:PRO:CD	2.36	1.09
65:SQ:65:LEU:HD22	71:Sa:79:TYR:CD2	1.88	1.08
59:SJ:136:MET:HE1	62:SN:104:TRP:CZ2	1.88	1.07
12:LP:223:MET:HE3	48:L6:42:GLU:HG2	1.35	1.07
14:LR:102:VAL:HG23	14:LR:131:LEU:HD11	1.38	1.06
32:Lm:187:SER:HA	32:Lm:190:ASP:OD1	1.56	1.06
33:Ln:139:MET:HE2	40:Lv:169:ILE:HG23	1.37	1.06
39:Lt:212:HIS:CE1	39:Lt:232:PHE:CE1	2.44	1.06
76:Sg:364:LEU:HD22	76:Sg:368:GLN:OE1	1.55	1.06
79:Sk:113:HIS:NE2	79:Sk:114:LEU:HG	1.71	1.06
82:So:420:MET:HE1	82:So:457:TYR:CE1	1.90	1.06
47:L5:55:LEU:CD1	47:L5:63:THR:OG1	2.03	1.06
82:So:580:ALA:HA	82:So:595:MET:CE	1.86	1.05
73:Sc:180:LEU:CD1	73:Sc:181:LEU:N	2.19	1.05
77:Si:51:TRP:CD1	77:Si:52:TYR:CD1	2.38	1.05
54:SZ:63:ALA:HB3	62:SN:124:GLN:HE22	1.00	1.05
82:So:420:MET:HE1	82:So:457:TYR:CD1	1.90	1.05
20:LX:98:ILE:HD12	20:LX:109:ILE:HD13	1.38	1.04
20:LX:98:ILE:CD1	20:LX:109:ILE:HD13	1.88	1.04
39:Lt:212:HIS:NE2	39:Lt:232:PHE:CE1	2.25	1.04
55:SE:176:ARG:HH22	77:Si:84:ARG:HD3	1.17	1.04
14:LR:90:GLU:HG2	14:LR:105:SER:HB3	1.36	1.03
82:So:420:MET:CE	82:So:457:TYR:CD2	2.40	1.03
65:SQ:31:THR:HG22	65:SQ:44:ASN:HD22	1.24	1.03
47:L5:55:LEU:HD12	47:L5:63:THR:OG1	1.56	1.02
38:Ls:196:GLN:NE2	38:Ls:198:ARG:NH2	2.07	1.02
60:SK:75:TRP:HB3	60:SK:146:HIS:HD2	1.20	1.02
72:Sb:45:PRO:HB2	78:Sj:53:ARG:HH21	1.18	1.02
63:SO:167:LEU:HD11	63:SO:187:ILE:HD12	1.41	1.02
77:Si:7:TYR:CE1	77:Si:11:MET:CG	2.35	1.02
38:Ls:203:MET:SD	38:Ls:203:MET:O	2.17	1.01
40:Lv:88:TYR:HE1	40:Lv:164:ALA:HA	1.23	1.01
78:Sj:163:SER:OG	78:Sj:190:MET:HG3	1.60	1.01
58:SI:292:ARG:HB2	58:SI:292:ARG:NH1	1.75	1.01
76:Sg:328:PHE:HE1	79:Sk:221:TYR:HD1	1.04	1.01
55:SE:95:ALA:HB2	77:Si:74:GLU:HB3	1.43	1.00
76:Sg:353:LEU:O	77:Si:34:VAL:HG22	1.61	1.00
71:Sa:125:HIS:HB3	71:Sa:128:ASN:OD1	1.60	1.00
82:So:615:MET:HE2	82:So:645:LEU:HD22	1.43	1.00
79:Sk:189:LYS:NZ	79:Sk:232:GLU:O	1.93	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:Lv:131:THR:HG22	40:Lv:151:THR:CG2	1.92	0.99
60:SK:60:PHE:CE2	68:SW:15:GLN:HB2	1.98	0.99
73:Sc:180:LEU:CD1	73:Sc:181:LEU:H	1.74	0.99
73:Sc:180:LEU:HD11	73:Sc:181:LEU:HG	1.44	0.99
82:So:515:ASP:CA	82:So:518:GLU:OE2	2.11	0.99
73:Sc:402:GLN:HA	73:Sc:405:GLN:HE22	1.25	0.98
79:Sk:66:TRP:HH2	79:Sk:82:PRO:HD3	1.25	0.98
67:ST:113:ARG:HG2	67:ST:117:MET:HE3	1.42	0.98
33:Ln:129:ARG:NH1	33:Ln:133:ARG:HG3	1.78	0.98
71:Sa:143:VAL:HG23	71:Sa:146:GLN:HG3	1.44	0.97
82:So:580:ALA:HA	82:So:595:MET:HE1	1.45	0.97
59:SJ:81:LYS:HD2	59:SJ:170:MET:CE	1.95	0.97
79:Sk:320:LEU:HD12	79:Sk:322:VAL:HG12	1.45	0.97
79:Sk:320:LEU:CD1	79:Sk:321:ASN:N	2.27	0.97
79:Sk:269:MET:HA	79:Sk:269:MET:CE	1.93	0.96
33:Ln:129:ARG:HH11	33:Ln:133:ARG:HG3	1.26	0.96
62:SN:90:ARG:HH21	62:SN:97:PRO:HG3	1.30	0.96
79:Sk:269:MET:HE3	79:Sk:269:MET:CA	1.95	0.96
69:SX:128:MET:HE1	69:SX:269:GLY:HA3	1.44	0.96
78:Sj:163:SER:OG	78:Sj:190:MET:CG	2.14	0.96
82:So:420:MET:CE	82:So:457:TYR:CZ	2.48	0.96
65:SQ:65:LEU:HD22	71:Sa:79:TYR:HD2	1.27	0.95
73:Sc:356:THR:O	73:Sc:360:VAL:CG2	2.12	0.95
24:Ld:103:ILE:HG23	44:Lz:84:MET:HE3	1.44	0.95
20:LX:127:ASP:OD1	20:LX:129:LYS:CB	2.15	0.95
76:Sg:339:GLU:HB3	76:Sg:377:ARG:NH1	1.82	0.95
39:Lt:200:MET:HE1	39:Lt:242:ASP:C	1.91	0.94
70:SY:73:LYS:HE2	70:SY:114:GLU:OE2	1.65	0.94
56:SF:35:ILE:HD12	63:SO:97:MET:CE	1.98	0.94
30:Lk:139:LEU:HD22	30:Lk:423:ALA:HB3	1.48	0.94
53:SB:102:MET:HE2	53:SB:224:ASP:O	1.66	0.94
79:Sk:66:TRP:HH2	79:Sk:82:PRO:HD2	1.31	0.94
77:Si:29:LYS:H	77:Si:29:LYS:HE2	1.33	0.93
77:Si:7:TYR:O	77:Si:7:TYR:HD1	1.50	0.93
65:SQ:31:THR:H	71:Sa:65:MET:HE3	1.34	0.93
4:LC:135:LYS:HE2	4:LC:141:LYS:CA	1.97	0.93
38:Ls:90:PRO:HB3	38:Ls:245:TYR:HE2	1.34	0.93
73:Sc:180:LEU:CD1	73:Sc:181:LEU:HG	1.99	0.93
75:Se:265:ILE:HD11	75:Se:269:TRP:HZ3	1.32	0.92
81:Sn:173:LEU:HD12	81:Sn:191:THR:CG2	1.99	0.92
77:Si:11:MET:O	77:Si:11:MET:HE3	1.70	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:Ls:196:GLN:CG	38:Ls:198:ARG:HH22	1.83	0.92
69:SX:70:PHE:HD1	69:SX:71:MET:CE	1.83	0.92
76:Sg:328:PHE:HE1	79:Sk:221:TYR:CD1	1.86	0.91
57:SG:159:VAL:CG2	57:SG:172:VAL:HG11	2.01	0.91
40:Lv:135:LEU:O	40:Lv:135:LEU:CD1	2.18	0.91
79:Sk:64:GLN:NE2	82:So:83:THR:OG1	2.03	0.91
82:So:533:MET:N	82:So:533:MET:HE3	1.85	0.90
79:Sk:320:LEU:HD13	79:Sk:321:ASN:H	1.08	0.90
32:Lm:285:ASN:HD21	32:Lm:293:LEU:HD21	1.33	0.90
60:SK:79:LYS:N	60:SK:82:GLU:OE2	2.05	0.90
70:SY:74:PHE:CD2	70:SY:99:PHE:CD2	2.61	0.89
78:Sj:56:ALA:O	78:Sj:60:ARG:HG3	1.71	0.89
72:Sb:71:ARG:HH12	72:Sb:72:MET:HE1	1.17	0.89
30:Lk:133:PRO:HG2	30:Lk:136:VAL:HG23	1.52	0.89
20:LX:177:THR:HG22	34:Lo:71:LYS:H	1.38	0.89
51:SR:39:VAL:CG2	51:SR:52:ARG:NH1	2.35	0.89
71:Sa:121:LYS:HA	71:Sa:121:LYS:HE3	1.53	0.89
20:LX:150:SER:HB2	20:LX:152:ARG:NH2	1.88	0.89
79:Sk:320:LEU:CD1	79:Sk:322:VAL:H	1.86	0.89
62:SN:33:ARG:HB3	62:SN:90:ARG:NH1	1.87	0.88
21:La:120:LEU:HD11	21:La:126:LEU:CD1	2.02	0.88
46:L4:112:PRO:HA	46:L4:117:TYR:CD2	2.08	0.88
79:Sk:66:TRP:CH2	79:Sk:82:PRO:HD2	2.07	0.88
70:SY:77:VAL:HG13	70:SY:78:TYR:H	1.39	0.88
38:Ls:209:TYR:CE1	38:Ls:251:GLN:HG3	2.09	0.87
21:La:120:LEU:CD1	21:La:126:LEU:HD13	2.02	0.87
79:Sk:266:LEU:HD12	79:Sk:267:LEU:N	1.89	0.87
63:SO:132:LEU:HD12	63:SO:166:MET:HE1	1.56	0.87
31:Ll:281:PHE:HE1	31:Ll:307:HIS:HD1	1.22	0.87
26:Lg:16:ILE:HD12	26:Lg:61:LYS:HG3	1.56	0.87
70:SY:74:PHE:HD2	70:SY:99:PHE:CD2	1.93	0.87
77:Si:28:SER:OG	77:Si:29:LYS:NZ	2.07	0.87
39:Lt:198:ASN:HB2	39:Lt:200:MET:SD	2.15	0.87
39:Lt:200:MET:HE1	39:Lt:243:PHE:N	1.90	0.87
14:LR:90:GLU:HG2	14:LR:105:SER:CB	2.05	0.86
72:Sb:71:ARG:HH11	72:Sb:72:MET:CE	1.72	0.86
82:So:137:ILE:H	82:So:141:MET:HE1	1.39	0.86
32:Lm:187:SER:CA	32:Lm:190:ASP:OD1	2.23	0.86
59:SJ:91:TYR:OH	59:SJ:164:LEU:HA	1.75	0.86
56:SF:23:LYS:O	56:SF:27:GLU:HG3	1.74	0.86
73:Sc:311:GLU:OE2	78:Sj:60:ARG:NH1	2.08	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:Si:45:LYS:O	77:Si:49:TYR:HD1	1.57	0.86
75:Se:265:ILE:HD11	75:Se:269:TRP:CZ3	2.09	0.86
60:SK:172:VAL:CG2	68:SW:19:VAL:HG22	2.05	0.86
82:So:420:MET:HE3	82:So:457:TYR:CE2	2.05	0.86
54:SZ:63:ALA:CB	62:SN:124:GLN:HE22	1.88	0.86
59:SJ:148:LEU:HG	59:SJ:152:THR:HG22	1.58	0.85
69:SX:182:ARG:HB3	69:SX:182:ARG:HH11	1.37	0.85
4:LC:329:PRO:HD2	4:LC:332:LEU:HD11	1.58	0.85
20:LX:26:PRO:HA	20:LX:31:ASP:OD2	1.77	0.85
59:SJ:98:ALA:O	59:SJ:102:LEU:HG	1.74	0.85
67:ST:77:VAL:HG13	67:ST:120:MET:HE2	1.58	0.85
37:Lr:227:GLU:HG2	37:Lr:230:GLU:CD	2.00	0.85
56:SF:35:ILE:CD1	63:SO:97:MET:HE2	2.05	0.85
77:Si:80:ASP:HA	77:Si:83:LYS:HE3	1.56	0.85
76:Sg:364:LEU:CD2	76:Sg:368:GLN:OE1	2.23	0.85
79:Sk:320:LEU:HD12	79:Sk:322:VAL:H	1.40	0.85
1:L1:1125:U:H1'	22:Lb:108:GLN:HG2	1.57	0.85
38:Ls:196:GLN:NE2	38:Ls:198:ARG:HH21	1.74	0.85
38:Ls:203:MET:HE2	38:Ls:203:MET:HA	1.58	0.85
82:So:580:ALA:CA	82:So:595:MET:HE1	2.07	0.84
26:Lg:55:LEU:H	50:L8:128:MET:CE	1.90	0.84
24:Ld:103:ILE:CG2	44:Lz:84:MET:HE3	2.06	0.84
31:Ll:172:PRO:HD2	31:Ll:207:GLU:OE2	1.77	0.84
59:SJ:148:LEU:CG	59:SJ:152:THR:CG2	2.54	0.84
8:LK:128:GLU:O	8:LK:132:LEU:HD23	1.76	0.84
59:SJ:148:LEU:CG	59:SJ:152:THR:HG22	2.07	0.84
62:SN:35:TRP:HA	62:SN:38:VAL:HG12	1.59	0.84
41:Lw:105:ARG:O	41:Lw:107:MET:HE2	1.77	0.84
69:SX:182:ARG:HH11	69:SX:182:ARG:CB	1.90	0.84
76:Sg:328:PHE:CE1	79:Sk:221:TYR:HD1	1.94	0.84
22:Lb:127:VAL:HB	22:Lb:131:THR:CG2	2.08	0.83
40:Lv:175:GLN:OE1	40:Lv:176:SER:N	2.11	0.83
31:Ll:330:ILE:HG23	31:Ll:334:LEU:HD12	1.58	0.83
39:Lt:58:VAL:CG1	39:Lt:153:LEU:HD22	2.09	0.83
64:SP:34:ILE:H	64:SP:34:ILE:HD12	1.43	0.83
22:Lb:127:VAL:HB	22:Lb:131:THR:HG21	1.59	0.82
64:SP:77:ILE:HD13	64:SP:83:LEU:HD11	1.61	0.82
76:Sg:339:GLU:HB3	76:Sg:377:ARG:HH12	1.40	0.82
40:Lv:146:LEU:HD23	40:Lv:147:ASP:CA	2.09	0.82
52:Sf:362:THR:HG22	52:Sf:364:GLY:H	1.42	0.82
82:So:580:ALA:CA	82:So:595:MET:CE	2.57	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:So:420:MET:CE	82:So:457:TYR:CG	2.62	0.82
60:SK:75:TRP:CB	60:SK:146:HIS:HD2	1.91	0.82
37:Lr:227:GLU:HG2	37:Lr:230:GLU:OE2	1.79	0.82
63:SO:92:LEU:HD23	72:Sb:160:LEU:HD11	1.62	0.82
32:Lm:148:MET:CE	32:Lm:257:ILE:HG12	2.10	0.82
78:Sj:115:TRP:HA	78:Sj:130:GLU:HA	1.60	0.82
47:L5:55:LEU:HD13	47:L5:63:THR:OG1	1.80	0.81
72:Sb:90:LEU:HD23	72:Sb:93:ARG:HH11	1.44	0.81
82:So:612:ASN:HA	82:So:615:MET:SD	2.20	0.81
51:SR:39:VAL:HG21	51:SR:52:ARG:NH1	1.94	0.81
36:Lq:2:THR:O	36:Lq:6:THR:HG23	1.80	0.81
51:SR:39:VAL:CG2	51:SR:52:ARG:HH12	1.92	0.81
56:SF:35:ILE:HD12	63:SO:97:MET:HE2	1.62	0.81
59:SJ:158:GLU:HB2	76:Sg:314:PRO:HD3	1.62	0.81
79:Sk:123:CYS:HA	79:Sk:126:LEU:HB2	1.62	0.81
53:SB:76:LYS:HB3	53:SB:126:GLN:HE22	1.43	0.81
69:SX:253:ILE:O	69:SX:257:GLY:HA2	1.80	0.81
70:SY:73:LYS:HZ2	70:SY:73:LYS:HB3	1.45	0.81
63:SO:178:PHE:O	63:SO:181:ILE:HG22	1.81	0.81
73:Sc:180:LEU:HD12	73:Sc:181:LEU:CA	2.10	0.80
77:Si:11:MET:HE3	77:Si:11:MET:C	2.06	0.80
50:L8:128:MET:HE3	50:L8:132:ILE:HD11	1.63	0.80
60:SK:60:PHE:CD2	68:SW:15:GLN:OE1	2.33	0.80
21:La:101:LYS:HG2	40:Lv:56:ILE:HG21	1.63	0.80
79:Sk:320:LEU:CD1	79:Sk:321:ASN:H	1.90	0.80
62:SN:90:ARG:NH2	62:SN:97:PRO:HG3	1.94	0.80
77:Si:80:ASP:HA	77:Si:83:LYS:CE	2.11	0.80
1:L1:136:U:H4'	1:L1:137:U:H5'	1.64	0.80
26:Lg:16:ILE:HD11	26:Lg:18:VAL:CG1	2.12	0.80
72:Sb:29:THR:N	72:Sb:32:ASP:OD2	2.15	0.80
82:So:420:MET:HE1	82:So:457:TYR:CG	2.17	0.80
38:Ls:207:ASN:HD22	38:Ls:251:GLN:NE2	1.80	0.80
54:SZ:63:ALA:CB	62:SN:124:GLN:NE2	2.45	0.80
11:LO:142:GLU:OE1	11:LO:142:GLU:N	2.12	0.79
32:Lm:187:SER:C	32:Lm:190:ASP:OD1	2.25	0.79
77:Si:46:LYS:HA	77:Si:49:TYR:HE1	1.43	0.79
38:Ls:196:GLN:HE21	38:Ls:198:ARG:NH2	1.78	0.79
40:Lv:146:LEU:CG	40:Lv:147:ASP:H	1.96	0.79
62:SN:41:ARG:NH1	77:Si:52:TYR:CE1	2.49	0.79
26:Lg:16:ILE:CD1	26:Lg:18:VAL:CG1	2.61	0.79
77:Si:51:TRP:CD1	77:Si:52:TYR:HD1	1.98	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:LC:145:LEU:HD12	4:LC:181:ILE:HD13	1.65	0.79
82:So:420:MET:HE1	82:So:457:TYR:CZ	2.16	0.79
79:Sk:125:ALA:HB1	82:So:73:ALA:HB1	1.65	0.79
49:L7:41:SER:O	49:L7:47:LYS:HE3	1.82	0.79
22:Lb:129:MET:HE2	22:Lb:132:LEU:HD12	1.63	0.78
12:LP:79:ALA:HB3	12:LP:158:ARG:HE	1.48	0.78
49:L7:98:LYS:HZ2	49:L7:98:LYS:HB3	1.48	0.78
57:SG:159:VAL:HG23	57:SG:172:VAL:HG11	1.63	0.78
61:SL:58:LEU:HD22	61:SL:85:LEU:HB3	1.65	0.78
59:SJ:91:TYR:CE1	59:SJ:165:PRO:CD	2.65	0.78
31:Ll:281:PHE:HE1	31:Ll:307:HIS:ND1	1.80	0.78
40:Lv:146:LEU:CD2	40:Lv:147:ASP:O	2.31	0.78
38:Ls:112:MET:H	38:Ls:112:MET:HE3	1.48	0.78
63:SO:144:GLU:OE1	63:SO:144:GLU:HA	1.83	0.78
1:L1:438:G:O2'	12:LP:140:MET:HE1	1.83	0.78
14:LR:83:ILE:HD11	14:LR:92:LEU:HD12	1.66	0.78
72:Sb:90:LEU:HD23	72:Sb:93:ARG:NH1	1.98	0.78
69:SX:70:PHE:CD1	69:SX:71:MET:CE	2.66	0.78
77:Si:45:LYS:O	77:Si:49:TYR:CD1	2.36	0.78
78:Sj:64:LEU:O	78:Sj:68:LEU:HB3	1.83	0.78
26:Lg:54:VAL:HB	50:L8:128:MET:HE2	1.64	0.77
31:Ll:306:LYS:CG	31:Ll:307:HIS:CD2	2.66	0.77
9:LM:90:VAL:HG22	9:LM:94:GLN:HB2	1.66	0.77
25:Lf:180:LYS:H	25:Lf:180:LYS:HD3	1.48	0.77
62:SN:57:LEU:O	62:SN:57:LEU:HD23	1.84	0.77
69:SX:182:ARG:NH1	69:SX:182:ARG:CB	2.46	0.77
70:SY:70:ILE:HD11	70:SY:100:VAL:HB	1.67	0.77
35:Lp:67:ILE:H	35:Lp:67:ILE:HD12	1.49	0.77
62:SN:33:ARG:HB3	62:SN:90:ARG:HH12	1.48	0.77
30:Lk:133:PRO:HG2	30:Lk:136:VAL:CG2	2.14	0.77
63:SO:85:VAL:HG12	72:Sb:161:GLN:HE21	1.50	0.77
38:Ls:196:GLN:CD	38:Ls:198:ARG:NH2	2.42	0.77
77:Si:7:TYR:O	77:Si:7:TYR:CD1	2.36	0.77
82:So:420:MET:HE2	82:So:457:TYR:CZ	2.19	0.77
12:LP:114:ASP:OD2	12:LP:117:ASN:OD1	2.03	0.77
46:L4:107:LEU:HD21	46:L4:124:GLN:OE1	1.84	0.77
79:Sk:66:TRP:CH2	79:Sk:82:PRO:HD3	2.10	0.77
82:So:420:MET:CE	82:So:457:TYR:CE1	2.68	0.77
82:So:615:MET:CE	82:So:645:LEU:HD22	2.14	0.77
30:Lk:274:LYS:HD3	30:Lk:275:ASN:N	2.00	0.76
32:Lm:285:ASN:HD22	32:Lm:293:LEU:HD21	1.47	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:SN:56:SER:HB3	77:Si:36:LEU:HD22	1.64	0.76
82:So:394:TYR:HA	82:So:397:MET:SD	2.25	0.76
2:L2:39:A:OP1	14:LR:156:SER:OG	2.03	0.76
59:SJ:81:LYS:HD3	59:SJ:140:TYR:HE1	1.50	0.76
53:SB:164:GLU:OE1	53:SB:164:GLU:HA	1.85	0.76
64:SP:77:ILE:CD1	64:SP:83:LEU:HD11	2.15	0.76
70:SY:74:PHE:CE2	70:SY:99:PHE:HD2	2.04	0.76
82:So:580:ALA:HA	82:So:595:MET:HE3	1.65	0.76
51:SR:39:VAL:HG22	51:SR:52:ARG:NH1	2.01	0.76
82:So:420:MET:HE2	82:So:457:TYR:CE2	2.19	0.76
9:LM:140:ASN:HD21	37:Lr:264:THR:H	1.34	0.76
10:LN:123:ILE:HD11	10:LN:144:PHE:CE2	2.20	0.76
28:Li:129:TYR:CZ	28:Li:130:LYS:HD2	2.20	0.76
77:Si:7:TYR:CE1	77:Si:11:MET:HG3	2.19	0.76
57:SG:46:ILE:HD13	58:Sl:315:PHE:HZ	1.51	0.75
62:SN:57:LEU:HD23	62:SN:57:LEU:C	2.11	0.75
20:LX:134:GLU:OE1	20:LX:136:ARG:HG3	1.85	0.75
31:Ll:306:LYS:HG3	31:Ll:307:HIS:HD2	1.50	0.75
60:SK:78:LYS:HB3	60:SK:82:GLU:HG2	1.67	0.75
20:LX:150:SER:HB2	20:LX:152:ARG:HH21	1.51	0.75
79:Sk:60:MET:HE1	79:Sk:66:TRP:CE3	2.22	0.75
64:SP:54:TYR:CD1	64:SP:66:VAL:HG22	2.21	0.75
79:Sk:320:LEU:HD13	79:Sk:320:LEU:C	2.11	0.75
38:Ls:152:LEU:CD1	38:Ls:160:LEU:HD11	2.17	0.75
67:ST:141:ARG:HH11	67:ST:141:ARG:HG3	1.51	0.75
57:SG:82:THR:HG22	57:SG:84:SER:H	1.52	0.74
80:Sm:40:LYS:HE2	80:Sm:40:LYS:H	1.52	0.74
46:L4:76:ASN:HD22	46:L4:82:GLN:H	1.35	0.74
38:Ls:187:GLU:OE2	38:Ls:219:ARG:NE	2.19	0.74
54:SZ:138:TYR:CE1	54:SZ:142:LEU:HD12	2.22	0.74
31:Ll:179:VAL:O	31:Ll:183:ASP:HB2	1.86	0.74
65:SQ:99:PRO:HG2	65:SQ:107:GLU:HB2	1.70	0.74
31:Ll:35:MET:HG3	31:Ll:36:PRO:HD2	1.69	0.74
81:Sn:173:LEU:CD1	81:Sn:191:THR:HG23	2.16	0.74
62:SN:128:TRP:HZ2	83:S1:805:U:H5"	1.52	0.74
77:Si:79:MET:C	77:Si:83:LYS:HE2	2.13	0.74
79:Sk:113:HIS:HD2	79:Sk:114:LEU:N	1.85	0.74
30:Lk:274:LYS:HE2	30:Lk:274:LYS:CA	2.02	0.74
32:Lm:148:MET:HE1	32:Lm:257:ILE:HG12	1.69	0.74
49:L7:98:LYS:HB3	49:L7:98:LYS:NZ	2.00	0.74
4:LC:106:MET:HE2	4:LC:118:VAL:HG22	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:SN:37:ASP:OD2	77:Si:52:TYR:OH	2.05	0.74
78:Sj:175:ILE:HD12	78:Sj:176:ALA:N	2.03	0.74
5:LD:275:TRP:O	5:LD:279:ARG:HB2	1.88	0.73
38:Ls:196:GLN:CG	38:Ls:198:ARG:NH2	2.51	0.73
64:SP:54:TYR:HD1	64:SP:66:VAL:HG22	1.52	0.73
74:Sd:89:LEU:HD12	74:Sd:92:MET:HE2	1.70	0.73
31:Ll:187:VAL:HG13	31:Ll:319:PHE:HB3	1.70	0.73
59:SJ:81:LYS:HG2	59:SJ:140:TYR:CD1	2.23	0.73
59:SJ:91:TYR:CZ	59:SJ:165:PRO:HD3	2.22	0.73
64:SP:33:ARG:HB3	64:SP:50:GLN:HE21	1.51	0.73
59:SJ:76:LEU:HD13	59:SJ:175:THR:HG22	1.70	0.73
77:Si:29:LYS:H	77:Si:29:LYS:CE	2.02	0.73
18:LV:157:ARG:HB2	18:LV:167:MET:HG3	1.70	0.73
39:Lt:212:HIS:NE2	39:Lt:232:PHE:CD1	2.56	0.73
62:SN:123:ILE:H	62:SN:123:ILE:HD12	1.54	0.73
70:SY:77:VAL:HG13	70:SY:78:TYR:CD1	2.22	0.73
12:LP:223:MET:HE3	48:L6:42:GLU:CG	2.14	0.73
19:LW:46:MET:HE1	19:LW:72:VAL:HG13	1.71	0.73
26:Lg:20:MET:HE1	26:Lg:41:LEU:O	1.89	0.73
40:Lv:88:TYR:CE1	40:Lv:164:ALA:HA	2.15	0.73
75:Se:269:TRP:CD1	75:Se:332:GLU:OE1	2.42	0.73
61:SL:38:ARG:HG2	61:SL:38:ARG:HH11	1.53	0.73
65:SQ:31:THR:CG2	65:SQ:44:ASN:HD22	2.02	0.73
65:SQ:65:LEU:HD22	71:Sa:79:TYR:CE2	2.23	0.73
4:LC:135:LYS:CE	4:LC:141:LYS:HA	2.11	0.73
7:LJ:84:ARG:NH2	46:L4:113:GLU:OE1	2.19	0.73
57:SG:159:VAL:HG23	57:SG:172:VAL:CG1	2.19	0.73
70:SY:88:PHE:HZ	74:Sd:115:ASP:HB3	1.54	0.73
82:So:531:ILE:O	82:So:535:MET:HB3	1.87	0.73
12:LP:79:ALA:CB	12:LP:158:ARG:HH21	2.02	0.73
32:Lm:79:PHE:HB3	32:Lm:81:MET:HE3	1.71	0.73
60:SK:172:VAL:CG2	68:SW:19:VAL:CG2	2.67	0.73
32:Lm:154:ILE:HG21	32:Lm:183:VAL:HG21	1.70	0.72
49:L7:80:TYR:OH	49:L7:147:LEU:HD22	1.89	0.72
40:Lv:131:THR:CG2	40:Lv:151:THR:HG22	2.15	0.72
59:SJ:135:GLU:HG3	62:SN:124:GLN:HB2	1.72	0.72
1:L1:501:U:C2	1:L1:503:G:H4'	2.24	0.72
65:SQ:65:LEU:CD2	71:Sa:79:TYR:HD2	2.00	0.72
30:Lk:281:GLU:CD	30:Lk:281:GLU:H	1.97	0.72
63:SO:109:GLU:HA	63:SO:112:MET:HB2	1.71	0.72
1:L1:468:U:H5''	24:Ld:73:LYS:HE2	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:LD:72:PHE:CE2	42:Lx:52:CYS:HB2	2.25	0.72
12:LP:163:MET:HE1	12:LP:175:PHE:CE2	2.25	0.72
19:LW:129:MET:HG3	38:Ls:82:ALA:HB2	1.70	0.72
57:SG:145:PHE:HA	57:SG:209:LEU:HD11	1.72	0.72
9:LM:160:GLN:O	9:LM:164:ASP:OD1	2.08	0.72
26:Lg:16:ILE:HD11	26:Lg:18:VAL:HG11	1.72	0.72
39:Lt:58:VAL:HG11	39:Lt:153:LEU:HD22	1.71	0.72
62:SN:43:MET:SD	62:SN:82:SER:HB3	2.29	0.72
1:L1:324:A:H5'	1:L1:324:A:H8	1.54	0.71
24:Ld:44:LYS:HA	24:Ld:47:GLN:OE1	1.90	0.71
63:SO:92:LEU:CD2	72:Sb:160:LEU:HD11	2.20	0.71
64:SP:34:ILE:HD13	64:SP:52:GLY:C	2.14	0.71
69:SX:330:VAL:HA	69:SX:333:LYS:HE3	1.71	0.71
53:SB:82:ARG:HD3	74:Sd:83:MET:HE1	1.72	0.71
57:SG:51:TYR:O	57:SG:52:ARG:HG3	1.90	0.71
58:SI:91:MET:HG3	79:Sk:66:TRP:CG	2.25	0.71
33:Ln:139:MET:CE	40:Lv:169:ILE:HG23	2.15	0.71
59:SJ:104:ILE:HG21	59:SJ:148:LEU:HD12	1.72	0.71
75:Se:342:PRO:HD2	79:Sk:313:LYS:HD3	1.73	0.71
4:LC:244:ALA:HB1	4:LC:248:ILE:HD11	1.72	0.71
26:Lg:16:ILE:CD1	26:Lg:18:VAL:HG13	2.20	0.71
53:SB:65:GLU:HA	53:SB:68:LYS:NZ	2.04	0.71
72:Sb:71:ARG:HH11	72:Sb:72:MET:HE1	0.90	0.71
1:L1:746:U:OP2	52:Sf:165:ARG:NH2	2.23	0.71
1:L1:746:U:H4'	34:Lo:52:GLN:HB3	1.73	0.71
33:Ln:129:ARG:NH1	33:Ln:133:ARG:CG	2.53	0.71
59:SJ:145:LEU:HD21	59:SJ:156:TYR:HE2	1.53	0.71
82:So:600:ARG:NH2	82:So:632:GLU:CD	2.49	0.71
26:Lg:55:LEU:H	50:L8:128:MET:HE1	1.52	0.71
60:SK:74:ARG:HD3	60:SK:78:LYS:O	1.91	0.71
82:So:136:HIS:CE1	82:So:141:MET:HE2	2.26	0.71
18:LV:197:LYS:NZ	18:LV:197:LYS:HB3	2.05	0.71
75:Se:261:ALA:HA	75:Se:307:VAL:O	1.89	0.71
78:Sj:63:ARG:HE	78:Sj:66:GLN:HB3	1.56	0.71
62:SN:127:THR:OG1	83:S1:662:A:H1'	1.89	0.71
75:Se:157:ASP:HB3	75:Se:160:LEU:HB2	1.73	0.71
70:SY:67:GLU:O	70:SY:70:ILE:HG13	1.91	0.70
59:SJ:136:MET:CE	62:SN:104:TRP:HZ2	1.98	0.70
20:LX:152:ARG:HE	20:LX:152:ARG:H	1.39	0.70
58:SI:292:ARG:C	58:SI:293:ILE:HD13	2.16	0.70
62:SN:54:ILE:HG23	62:SN:71:ALA:HB1	1.71	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Lm:233:SER:O	32:Lm:237:VAL:HG23	1.91	0.70
47:L5:70:GLU:HG3	47:L5:72:ARG:HG3	1.73	0.70
82:So:646:THR:O	82:So:650:MET:HE2	1.92	0.70
78:Sj:133:HIS:O	78:Sj:139:TRP:NE1	2.24	0.70
79:Sk:113:HIS:NE2	79:Sk:114:LEU:CG	2.45	0.70
7:LJ:119:HIS:HB3	7:LJ:160:LYS:HD3	1.74	0.70
20:LX:133:ILE:HD13	20:LX:145:ARG:HG2	1.71	0.70
63:SO:173:THR:CG2	65:SQ:101:ALA:HB1	2.21	0.70
71:Sa:14:GLN:O	71:Sa:18:GLN:HB2	1.92	0.70
32:Lm:145:SER:O	32:Lm:149:MET:HG3	1.91	0.70
82:So:464:LEU:HD23	82:So:468:MET:SD	2.31	0.70
12:LP:79:ALA:HB2	12:LP:158:ARG:HH21	1.56	0.70
69:SX:106:MET:HB2	69:SX:110:GLN:HB2	1.71	0.70
74:Sd:126:ARG:HH11	74:Sd:126:ARG:HG3	1.55	0.70
79:Sk:64:GLN:NE2	82:So:83:THR:CG2	2.55	0.70
4:LC:106:MET:HE3	4:LC:287:GLY:O	1.92	0.70
66:SS:67:ARG:HD3	66:SS:68:TYR:CE1	2.27	0.70
66:SS:73:VAL:HB	66:SS:125:GLN:OE1	1.92	0.70
77:Si:11:MET:HE3	77:Si:11:MET:CA	2.20	0.70
6:LI:93:ASN:OD1	6:LI:114:VAL:O	2.09	0.70
71:Sa:105:ILE:HG22	71:Sa:106:LEU:HG	1.74	0.70
75:Se:166:ARG:NH2	83:S1:734:A:O2'	2.24	0.70
76:Sg:277:LEU:HD23	82:So:193:ASP:HB3	1.73	0.70
33:Ln:168:LEU:HD22	39:Lt:206:GLY:HA2	1.74	0.69
71:Sa:143:VAL:CG2	71:Sa:146:GLN:HG3	2.21	0.69
1:L1:163:C:OP2	36:Lq:114:ARG:NH2	2.25	0.69
30:Lk:274:LYS:HA	30:Lk:274:LYS:CE	2.06	0.69
47:L5:55:LEU:HD12	47:L5:63:THR:CB	2.22	0.69
62:SN:120:LEU:HB3	62:SN:123:ILE:HD13	1.72	0.69
3:LB:218:ARG:NH1	3:LB:218:ARG:HB2	2.07	0.69
65:SQ:31:THR:HG23	65:SQ:46:ARG:HG3	1.75	0.69
56:SF:112:PRO:HG2	80:Sm:7:ARG:HH22	1.55	0.69
63:SO:132:LEU:HD12	63:SO:166:MET:CE	2.22	0.69
69:SX:182:ARG:HB3	69:SX:182:ARG:CZ	2.23	0.69
75:Se:293:LEU:O	75:Se:297:MET:HE2	1.92	0.69
79:Sk:64:GLN:HE22	82:So:83:THR:CB	2.05	0.69
82:So:468:MET:N	82:So:468:MET:HE3	2.06	0.69
61:SL:38:ARG:HG2	61:SL:38:ARG:NH1	2.08	0.69
63:SO:209:LEU:HD11	81:Sn:177:TRP:HE1	1.57	0.69
1:L1:37:C:O2	30:Lk:80:ARG:NH2	2.25	0.69
22:Lb:161:LEU:O	22:Lb:165:MET:HG3	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:Lk:139:LEU:HD22	30:Lk:423:ALA:CB	2.23	0.69
65:SQ:63:ILE:HD12	71:Sa:67:PHE:CZ	2.27	0.69
73:Sc:180:LEU:HD12	73:Sc:181:LEU:H	0.87	0.69
82:So:137:ILE:N	82:So:141:MET:HE1	2.07	0.69
1:L1:973:G:O2'	1:L1:975:G:OP2	2.10	0.69
10:LN:129:LYS:HD3	15:LS:125:TYR:OH	1.93	0.69
63:SO:173:THR:HG23	65:SQ:101:ALA:HB1	1.73	0.69
73:Sc:278:GLU:HG3	73:Sc:352:LEU:HD13	1.75	0.69
80:Sm:40:LYS:HE2	80:Sm:40:LYS:N	2.08	0.69
14:LR:49:ASN:ND2	14:LR:51:ASN:H	1.91	0.69
16:LT:122:ARG:NH2	17:LU:72:GLU:OE2	2.26	0.69
62:SN:92:VAL:HG22	77:Si:53:PRO:HD3	1.75	0.69
1:L1:468:U:OP1	24:Ld:73:LYS:NZ	2.23	0.68
60:SK:75:TRP:CB	60:SK:146:HIS:CD2	2.60	0.68
70:SY:73:LYS:HB3	70:SY:73:LYS:NZ	2.06	0.68
7:LJ:134:PHE:O	7:LJ:138:SER:OG	2.11	0.68
79:Sk:60:MET:HE1	79:Sk:66:TRP:CZ3	2.29	0.68
78:Sj:44:PRO:C	78:Sj:46:SER:H	2.02	0.68
1:L1:500:G:OP2	8:LK:21:ARG:NH2	2.26	0.68
7:LJ:100:GLN:OE1	45:L3:34:LEU:HD23	1.92	0.68
62:SN:43:MET:HE1	62:SN:79:PRO:HB2	1.75	0.68
33:Ln:149:GLU:HB2	39:Lt:212:HIS:ND1	2.08	0.68
39:Lt:58:VAL:HG12	39:Lt:153:LEU:HD22	1.74	0.68
82:So:335:PHE:CD1	82:So:360:MET:HE1	2.29	0.68
38:Ls:160:LEU:HD22	38:Ls:169:PHE:CD1	2.28	0.68
56:SF:32:ARG:HH22	56:SF:81:HIS:HB2	1.58	0.68
79:Sk:180:LEU:HD11	79:Sk:230:TYR:HE1	1.57	0.68
1:L1:520:C:OP2	46:L4:120:ARG:NH1	2.25	0.68
40:Lv:88:TYR:HE1	40:Lv:164:ALA:CA	2.04	0.68
58:SI:317:PHE:HE2	58:SI:348:MET:HE3	1.57	0.68
73:Sc:402:GLN:HA	73:Sc:405:GLN:NE2	2.05	0.68
77:Si:7:TYR:CD1	77:Si:7:TYR:C	2.70	0.68
79:Sk:66:TRP:HZ3	79:Sk:82:PRO:HG3	1.58	0.68
79:Sk:140:ASP:O	79:Sk:144:GLU:HG3	1.93	0.68
79:Sk:320:LEU:HD13	79:Sk:321:ASN:CA	2.24	0.68
39:Lt:212:HIS:CE1	39:Lt:232:PHE:HE1	2.07	0.68
1:L1:256:A:OP1	3:LB:78:LYS:HE2	1.94	0.68
14:LR:49:ASN:HD22	14:LR:50:ARG:N	1.92	0.68
37:Lr:227:GLU:HG3	37:Lr:230:GLU:HB2	1.76	0.68
62:SN:121:SER:O	62:SN:123:ILE:HD12	1.93	0.68
5:LD:113:LYS:HG3	5:LD:157:GLY:H	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:SL:61:VAL:HG23	61:SL:107:ILE:HD13	1.76	0.67
73:Sc:39:LYS:HZ3	73:Sc:39:LYS:H	1.42	0.67
73:Sc:392:ARG:NH2	83:S1:878:C:OP1	2.27	0.67
79:Sk:68:SER:HA	82:So:78:VAL:HG23	1.77	0.67
37:Lr:58:VAL:CG1	37:Lr:62:GLU:OE1	2.42	0.67
62:SN:35:TRP:HA	62:SN:38:VAL:CG1	2.24	0.67
83:S1:77:C:N3	83:S1:103:A:N1	2.43	0.67
1:L1:1182:C:H5	26:Lg:32:THR:HG21	1.60	0.67
14:LR:102:VAL:HG23	14:LR:131:LEU:CD1	2.22	0.67
38:Ls:90:PRO:HB3	38:Ls:245:TYR:CE2	2.24	0.67
47:L5:55:LEU:CD1	47:L5:63:THR:CG2	2.73	0.67
53:SB:210:ARG:HH11	53:SB:214:LYS:HD2	1.59	0.67
69:SX:128:MET:HE1	69:SX:269:GLY:CA	2.23	0.67
22:Lb:230:TYR:HD1	22:Lb:233:GLU:OE1	1.77	0.67
56:SF:103:LYS:HE2	56:SF:103:LYS:H	1.59	0.67
64:SP:75:HIS:CE1	64:SP:79:CYS:SG	2.87	0.67
73:Sc:209:LEU:HD23	73:Sc:228:TYR:N	2.09	0.67
40:Lv:80:ILE:HG22	40:Lv:89:GLY:HA2	1.77	0.67
59:SJ:126:ILE:HG13	59:SJ:127:TYR:CE1	2.29	0.67
73:Sc:209:LEU:HD23	73:Sc:227:GLY:C	2.20	0.67
11:LO:142:GLU:H	11:LO:142:GLU:CD	1.97	0.67
5:LD:201:GLN:HG2	5:LD:205:GLU:OE2	1.95	0.67
63:SO:115:ILE:HD11	63:SO:184:GLY:HA3	1.76	0.67
82:So:420:MET:CE	82:So:457:TYR:CD1	2.75	0.67
82:So:533:MET:HE2	82:So:578:CYS:SG	2.35	0.67
26:Lg:16:ILE:CD1	26:Lg:61:LYS:HG3	2.24	0.67
78:Sj:85:TRP:CH2	78:Sj:139:TRP:CH2	2.83	0.67
66:SS:211:ARG:NE	66:SS:215:ARG:HH21	1.93	0.66
71:Sa:137:ARG:HH11	71:Sa:137:ARG:HG3	1.60	0.66
73:Sc:54:ALA:HA	73:Sc:57:MET:CE	2.24	0.66
9:LM:25:MET:HE3	9:LM:149:ARG:NH2	2.10	0.66
79:Sk:66:TRP:CZ3	79:Sk:82:PRO:HG3	2.30	0.66
79:Sk:122:HIS:CD2	82:So:77:THR:HG21	2.30	0.66
1:L1:133:A:H2	1:L1:136:U:H5"	1.60	0.66
22:Lb:230:TYR:CD1	22:Lb:233:GLU:OE1	2.49	0.66
62:SN:59:LYS:HE2	77:Si:32:LYS:HE3	1.77	0.66
79:Sk:64:GLN:NE2	82:So:83:THR:HG21	2.09	0.66
52:Sf:243:ILE:HD12	52:Sf:245:LYS:O	1.95	0.66
66:SS:82:LYS:HE2	83:S1:21:U:H5"	1.76	0.66
72:Sb:110:GLN:HB3	72:Sb:114:ARG:HH21	1.60	0.66
82:So:141:MET:N	82:So:141:MET:SD	2.69	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:So:580:ALA:CB	82:So:595:MET:HE3	2.26	0.66
7:LJ:168:LEU:CD1	7:LJ:176:LEU:HB2	2.26	0.66
52:Sf:212:ARG:HD2	52:Sf:379:LEU:HB3	1.78	0.66
54:SZ:40:ALA:HB3	54:SZ:59:PRO:HD3	1.76	0.66
68:SW:50:ARG:NH2	83:S1:948:G:O6	2.29	0.66
79:Sk:64:GLN:HE22	82:So:83:THR:CG2	2.08	0.66
1:L1:608:A:OP1	43:Ly:51:ARG:NH1	2.29	0.66
23:Lu:109:ARG:HD3	23:Lu:139:MET:HE2	1.78	0.66
53:SB:207:VAL:O	53:SB:211:ASP:OD1	2.13	0.66
56:SF:27:GLU:O	56:SF:31:ASP:CG	2.38	0.66
60:SK:172:VAL:HG21	68:SW:19:VAL:CG2	2.26	0.66
73:Sc:54:ALA:HA	73:Sc:57:MET:HE2	1.77	0.66
1:L1:133:A:C2	1:L1:136:U:H5''	2.30	0.66
1:L1:438:G:N7	12:LP:67:LYS:NZ	2.44	0.66
6:LI:115:LYS:O	6:LI:118:LEU:O	2.14	0.66
38:Ls:215:ARG:HG3	38:Ls:245:TYR:CE1	2.30	0.66
59:SJ:113:ARG:HD2	59:SJ:115:ILE:HD11	1.77	0.66
58:SI:262:TYR:CE1	58:SI:268:ALA:HB2	2.31	0.66
64:SP:75:HIS:O	64:SP:79:CYS:SG	2.54	0.66
11:LO:140:LEU:CD2	11:LO:163:ALA:HB1	2.26	0.66
19:LW:18:ARG:HH21	20:LX:206:GLU:HG2	1.60	0.65
71:Sa:121:LYS:HE3	71:Sa:121:LYS:CA	2.23	0.65
13:LQ:150:GLN:OE1	13:LQ:154:GLN:NE2	2.29	0.65
59:SJ:111:PRO:HB2	59:SJ:140:TYR:HB2	1.77	0.65
1:L1:433:A:HO2'	24:Ld:35:LYS:N	1.95	0.65
40:Lv:92:ASN:ND2	40:Lv:158:GLN:HG3	2.11	0.65
59:SJ:81:LYS:HD2	59:SJ:170:MET:HE2	1.78	0.65
20:LX:98:ILE:HD11	20:LX:109:ILE:HD13	1.74	0.65
41:Lw:150:LYS:NZ	48:L6:79:THR:O	2.29	0.65
68:SW:25:THR:O	68:SW:29:ILE:HD12	1.96	0.65
76:Sg:353:LEU:HD23	77:Si:22:VAL:HG11	1.78	0.65
32:Lm:285:ASN:HD22	32:Lm:293:LEU:HD11	1.59	0.65
37:Lr:245:LEU:HD12	37:Lr:253:PRO:HD3	1.78	0.65
59:SJ:81:LYS:HG2	59:SJ:140:TYR:HD1	1.60	0.65
69:SX:70:PHE:CD1	69:SX:71:MET:HE3	2.31	0.65
4:LC:80:LEU:HA	4:LC:84:PRO:HG3	1.78	0.65
11:LO:288:GLU:OE1	11:LO:288:GLU:HA	1.96	0.65
12:LP:169:PHE:O	12:LP:173:GLN:HB2	1.96	0.65
32:Lm:285:ASN:ND2	32:Lm:293:LEU:CD2	2.52	0.65
63:SO:174:ASN:HB3	63:SO:177:VAL:CG2	2.27	0.65
1:L1:629:U:H5''	1:L1:630:G:H5''	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:L5:74:MET:HE3	47:L5:75:LEU:C	2.22	0.65
68:SW:15:GLN:HG2	68:SW:16:GLU:HG2	1.77	0.65
79:Sk:320:LEU:CD1	79:Sk:322:VAL:N	2.58	0.65
1:L1:611:A:OP1	48:L6:100:LYS:NZ	2.27	0.65
14:LR:62:ARG:NH2	21:La:137:LYS:O	2.30	0.65
77:Si:7:TYR:CD1	77:Si:11:MET:HG2	2.30	0.65
77:Si:18:LEU:HD21	79:Sk:229:LEU:HD22	1.78	0.65
82:So:529:GLU:O	82:So:533:MET:SD	2.54	0.65
10:LN:119:ILE:HG13	10:LN:140:ILE:HD12	1.77	0.65
79:Sk:298:SER:O	79:Sk:302:GLU:HB3	1.97	0.65
63:SO:167:LEU:HD21	63:SO:187:ILE:CD1	2.26	0.64
82:So:393:ILE:HG13	82:So:422:ILE:HG21	1.79	0.64
82:So:515:ASP:HA	82:So:518:GLU:CD	2.20	0.64
8:LK:149:ARG:HH12	46:L4:104:PRO:HD3	1.62	0.64
33:Ln:143:GLN:OE1	40:Lv:165:THR:HB	1.96	0.64
53:SB:76:LYS:CB	53:SB:126:GLN:HE22	2.10	0.64
57:SG:46:ILE:HD13	58:SI:315:PHE:CZ	2.31	0.64
58:SI:87:HIS:O	58:SI:91:MET:CE	2.44	0.64
79:Sk:113:HIS:CD2	79:Sk:114:LEU:N	2.65	0.64
82:So:580:ALA:CA	82:So:595:MET:HE3	2.26	0.64
32:Lm:148:MET:HE2	32:Lm:257:ILE:HG12	1.79	0.64
82:So:514:LYS:O	82:So:518:GLU:CG	2.38	0.64
9:LM:142:VAL:HG11	36:Lq:133:PHE:HE1	1.61	0.64
19:LW:153:LEU:HD11	38:Ls:240:LYS:HB2	1.79	0.64
32:Lm:187:SER:HA	32:Lm:190:ASP:CG	2.22	0.64
60:SK:79:LYS:HB2	60:SK:82:GLU:OE2	1.98	0.64
63:SO:167:LEU:CD1	63:SO:187:ILE:HD12	2.23	0.64
10:LN:129:LYS:HD3	15:LS:125:TYR:CZ	2.33	0.64
40:Lv:135:LEU:HD22	40:Lv:145:LEU:HD13	1.80	0.64
58:SI:317:PHE:CE2	58:SI:348:MET:HE3	2.31	0.64
20:LX:131:THR:OG1	20:LX:132:GLU:N	2.30	0.64
30:Lk:125:LYS:HA	30:Lk:253:LEU:HD11	1.79	0.64
65:SQ:31:THR:HG22	65:SQ:44:ASN:ND2	2.07	0.64
69:SX:275:PHE:O	69:SX:279:LYS:HA	1.98	0.64
72:Sb:53:PHE:HE1	72:Sb:57:MET:SD	2.21	0.64
32:Lm:247:ASN:ND2	32:Lm:251:ILE:O	2.31	0.64
59:SJ:91:TYR:HE1	59:SJ:165:PRO:HD3	1.56	0.64
64:SP:34:ILE:HD13	64:SP:53:SER:N	2.13	0.64
67:ST:113:ARG:CG	67:ST:117:MET:HE3	2.25	0.64
79:Sk:298:SER:O	79:Sk:301:ASN:O	2.16	0.64
1:L1:324:A:H5'	1:L1:324:A:C8	2.33	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Lq:78:GLU:HG2	36:Lq:84:VAL:HG22	1.80	0.64
37:Lr:259:ARG:HB2	37:Lr:271:PHE:HB2	1.78	0.64
67:ST:113:ARG:HG2	67:ST:117:MET:CE	2.23	0.64
73:Sc:175:VAL:HG22	73:Sc:177:SER:H	1.61	0.64
7:LJ:44:ARG:NH2	12:LP:234:ASP:OD2	2.30	0.64
8:LK:73:LYS:O	8:LK:76:ARG:N	2.31	0.64
25:Lf:174:ILE:HG22	25:Lf:176:GLU:OE1	1.97	0.64
40:Lv:146:LEU:HD23	40:Lv:147:ASP:H	0.48	0.64
57:SG:105:VAL:CG2	57:SG:106:LEU:N	2.61	0.64
76:Sg:299:GLU:HA	76:Sg:302:ILE:HG12	1.80	0.64
19:LW:18:ARG:NH1	34:Lo:59:GLU:OE2	2.30	0.63
64:SP:77:ILE:HD11	64:SP:83:LEU:HD21	1.79	0.63
70:SY:68:ASP:HA	70:SY:71:ARG:HB2	1.80	0.63
71:Sa:129:PHE:CZ	71:Sa:140:ILE:HG22	2.32	0.63
75:Se:153:LEU:HB3	75:Se:260:VAL:HG12	1.80	0.63
39:Lt:200:MET:CE	39:Lt:242:ASP:C	2.68	0.63
56:SF:35:ILE:HD12	63:SO:97:MET:HE1	1.77	0.63
6:LI:87:LYS:HE2	22:Lb:108:GLN:HG3	1.79	0.63
22:Lb:118:ILE:O	22:Lb:176:LEU:HD13	1.99	0.63
31:Ll:306:LYS:HD3	31:Ll:307:HIS:NE2	2.13	0.63
61:SL:95:ILE:HD13	61:SL:102:LEU:HD22	1.80	0.63
79:Sk:306:GLU:HA	79:Sk:309:ILE:HG22	1.79	0.63
58:SI:198:ARG:HH12	58:SI:246:ARG:HB2	1.63	0.63
59:SJ:148:LEU:CD1	59:SJ:152:THR:HG22	2.28	0.63
60:SK:60:PHE:CZ	68:SW:15:GLN:HB2	2.33	0.63
75:Se:260:VAL:HG11	75:Se:296:MET:SD	2.38	0.63
14:LR:83:ILE:N	14:LR:83:ILE:HD12	2.13	0.63
1:L1:169:C:H5"	9:LM:115:ASN:HB2	1.80	0.63
49:L7:98:LYS:HD2	49:L7:136:THR:HG21	1.81	0.63
49:L7:189:ARG:HD2	49:L7:189:ARG:O	1.98	0.63
75:Se:312:GLN:NE2	75:Se:319:PRO:O	2.30	0.63
5:LD:72:PHE:CD2	42:Lx:52:CYS:SG	2.92	0.63
9:LM:6:ARG:HH11	9:LM:6:ARG:HG3	1.64	0.63
47:L5:59:GLN:OE1	47:L5:78:PRO:C	2.42	0.63
54:SZ:91:PHE:CE2	77:Si:58:TYR:HD1	2.16	0.63
64:SP:54:TYR:CD1	64:SP:66:VAL:CG2	2.81	0.63
77:Si:7:TYR:HD1	77:Si:7:TYR:C	2.07	0.63
82:So:420:MET:HE3	82:So:457:TYR:CG	2.25	0.63
1:L1:563:U:C2	4:LC:248:ILE:HG22	2.33	0.63
25:Lf:148:PRO:O	25:Lf:150:LYS:HG2	1.98	0.62
63:SO:71:THR:HG22	63:SO:72:LEU:H	1.63	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:SG:158:LEU:HD13	57:SG:169:GLN:HB3	1.81	0.62
59:SJ:66:SER:OG	59:SJ:67:ASP:N	2.28	0.62
60:SK:62:ILE:HG21	67:ST:141:ARG:HD3	1.82	0.62
1:L1:523:U:H3	1:L1:526:A:H2	1.47	0.62
9:LM:60:MET:HE2	9:LM:133:ILE:HD11	1.81	0.62
22:Lb:8:VAL:O	22:Lb:11:TRP:HB2	1.99	0.62
46:L4:107:LEU:CD1	46:L4:117:TYR:HE1	2.13	0.62
14:LR:79:ARG:HH11	14:LR:146:GLN:HE22	1.47	0.62
30:Lk:139:LEU:CD2	30:Lk:423:ALA:HB3	2.25	0.62
56:Sf:15:ARG:NH2	72:Sb:178:GLU:OE1	2.32	0.62
62:SN:123:ILE:HD12	62:SN:123:ILE:N	2.14	0.62
64:SP:54:TYR:HD1	64:SP:66:VAL:CG2	2.11	0.62
77:Si:18:LEU:HD21	79:Sk:229:LEU:CD2	2.29	0.62
77:Si:46:LYS:CA	77:Si:49:TYR:CE1	2.71	0.62
32:Lm:187:SER:O	32:Lm:190:ASP:OD1	2.18	0.62
64:SP:20:ARG:NH2	64:SP:38:HIS:O	2.32	0.62
17:LU:51:VAL:HG12	51:SR:76:ASN:O	1.99	0.62
61:SL:99:GLY:O	61:SL:127:ARG:NH2	2.33	0.62
84:L1:1705:MG:MG	85:L1:1707:T1C:O12	1.43	0.62
3:LB:218:ARG:HB2	3:LB:218:ARG:CZ	2.29	0.62
50:L8:48:PRO:HB3	50:L8:50:TRP:CD1	2.35	0.62
72:Sb:64:ARG:NH2	83:S1:198:A:OP1	2.33	0.62
82:So:600:ARG:NH2	82:So:632:GLU:OE2	2.32	0.62
82:So:641:ILE:HD13	82:So:645:LEU:HD11	1.81	0.62
83:S1:782:C:H4'	83:S1:783:A:H5'	1.81	0.62
11:LO:119:THR:HG21	41:Lw:51:LEU:HD23	1.80	0.62
33:Ln:178:TYR:HB3	47:L5:63:THR:HG23	1.80	0.62
38:Ls:215:ARG:HG3	38:Ls:245:TYR:HE1	1.65	0.62
52:Sf:271:LEU:O	52:Sf:272:PRO:C	2.42	0.62
57:SG:105:VAL:HG23	57:SG:106:LEU:N	2.15	0.62
73:Sc:53:LEU:O	73:Sc:57:MET:HE2	1.99	0.62
65:SQ:18:ILE:HD11	65:SQ:29:ARG:HB2	1.81	0.62
14:LR:106:THR:HG23	14:LR:127:ILE:HD11	1.82	0.62
24:Ld:78:ARG:HD2	24:Ld:116:LEU:HD21	1.82	0.62
37:Lr:148:MET:HE2	37:Lr:305:TYR:HB3	1.81	0.62
49:L7:128:ASN:ND2	49:L7:132:GLU:OE2	2.33	0.62
54:SZ:75:ASN:OD1	62:SN:104:TRP:NE1	2.29	0.62
79:Sk:173:LEU:O	79:Sk:206:THR:HA	2.00	0.62
46:L4:95:TRP:HA	46:L4:98:GLU:HG2	1.82	0.61
32:Lm:200:ARG:HH21	32:Lm:204:LYS:HZ1	1.48	0.61
63:SO:209:LEU:HD13	81:Sn:173:LEU:HD13	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:SS:65:GLN:N	66:SS:65:GLN:OE1	2.33	0.61
70:SY:69:ARG:HG2	70:SY:69:ARG:NH1	2.14	0.61
50:L8:84:GLU:OE1	50:L8:84:GLU:HA	1.99	0.61
39:Lt:50:ALA:HA	39:Lt:174:PRO:O	1.99	0.61
56:SF:35:ILE:CD1	63:SO:97:MET:CE	2.69	0.61
73:Sc:308:GLN:O	73:Sc:312:LYS:HB2	2.00	0.61
74:Sd:126:ARG:HG3	74:Sd:126:ARG:NH1	2.12	0.61
74:Sd:161:THR:HG22	74:Sd:163:LEU:H	1.63	0.61
5:LD:70:ARG:HA	5:LD:196:PRO:HD3	1.81	0.61
20:LX:76:VAL:HA	20:LX:88:VAL:HA	1.81	0.61
49:L7:128:ASN:OD1	49:L7:129:ARG:N	2.33	0.61
59:SJ:148:LEU:CD1	59:SJ:152:THR:CG2	2.78	0.61
82:So:137:ILE:O	82:So:141:MET:SD	2.59	0.61
82:So:533:MET:CE	82:So:578:CYS:SG	2.89	0.61
5:LD:72:PHE:HD2	42:Lx:52:CYS:HG	1.46	0.61
33:Ln:127:GLN:OE1	33:Ln:127:GLN:HA	2.00	0.61
46:L4:112:PRO:O	46:L4:117:TYR:HD2	1.82	0.61
66:SS:173:ARG:NH1	69:SX:236:GLU:OE2	2.33	0.61
82:So:251:MET:HE1	82:So:254:LYS:HG2	1.82	0.61
1:L1:564:C:HO2'	1:L1:1018:C:HO2'	1.49	0.61
7:LJ:165:VAL:HG13	7:LJ:169:ARG:HE	1.62	0.61
16:LT:17:ARG:O	16:LT:21:ILE:HG12	2.00	0.61
45:L3:82:THR:HG22	45:L3:85:GLU:HB2	1.83	0.61
52:Sf:177:LEU:HD23	52:Sf:238:ASN:HD22	1.65	0.61
56:SF:40:GLU:OE1	72:Sb:185:LYS:HD3	2.00	0.61
25:Lf:180:LYS:H	25:Lf:180:LYS:CD	2.12	0.61
66:SS:188:PRO:O	78:Sj:171:ARG:NH2	2.33	0.61
66:SS:215:ARG:HG3	66:SS:218:ARG:HH21	1.66	0.61
4:LC:279:LYS:HE2	4:LC:330:GLU:OE2	2.00	0.61
7:LJ:119:HIS:CD2	7:LJ:163:GLU:HG2	2.35	0.61
20:LX:152:ARG:H	20:LX:152:ARG:NE	1.98	0.61
52:Sf:251:VAL:HG22	52:Sf:252:PRO:HD2	1.82	0.61
59:SJ:92:GLU:HB2	59:SJ:141:ARG:HD3	1.83	0.61
66:SS:167:ILE:HD13	69:SX:226:ASP:HB3	1.83	0.61
70:SY:73:LYS:CE	70:SY:114:GLU:OE2	2.45	0.61
79:Sk:66:TRP:CZ3	79:Sk:82:PRO:CG	2.83	0.61
19:LW:11:ARG:HH21	20:LX:213:VAL:HA	1.65	0.61
63:SO:167:LEU:HD21	63:SO:187:ILE:HD11	1.82	0.61
79:Sk:243:LYS:HE3	79:Sk:247:ASP:HB3	1.82	0.61
8:LK:39:LEU:HB3	8:LK:44:VAL:HB	1.82	0.60
47:L5:55:LEU:HD12	47:L5:63:THR:CG2	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:SQ:98:LYS:HG2	65:SQ:107:GLU:O	2.01	0.60
69:SX:352:ALA:HA	69:SX:355:ARG:HD2	1.83	0.60
76:Sg:330:GLU:HB3	76:Sg:366:VAL:HG21	1.81	0.60
19:LW:64:PRO:HB2	19:LW:100:ALA:HB3	1.83	0.60
73:Sc:357:THR:HA	73:Sc:360:VAL:CG2	2.31	0.60
83:S1:592:C:H2'	83:S1:593:A:H8	1.66	0.60
1:L1:719:C:H5''	30:Lk:301:PRO:HB3	1.82	0.60
1:L1:1441:A:H5'	4:LC:266:ARG:NH2	2.16	0.60
7:LJ:62:PRO:HA	7:LJ:65:LEU:HB2	1.82	0.60
71:Sa:111:GLU:O	71:Sa:115:GLU:HG3	2.01	0.60
72:Sb:42:VAL:HA	78:Sj:49:ARG:NH2	2.17	0.60
5:LD:237:LEU:O	50:L8:25:TYR:N	2.34	0.60
22:Lb:128:THR:H	22:Lb:131:THR:HG22	1.66	0.60
70:SY:69:ARG:HG2	70:SY:69:ARG:HH11	1.65	0.60
4:LC:187:ILE:HG22	4:LC:191:THR:HG21	1.84	0.60
6:LI:115:LYS:O	6:LI:118:LEU:C	2.45	0.60
21:La:115:ASP:O	21:La:119:ARG:HD3	2.02	0.60
58:SI:91:MET:HG3	79:Sk:66:TRP:CD2	2.35	0.60
63:SO:174:ASN:CG	63:SO:177:VAL:HG22	2.25	0.60
71:Sa:51:ASN:HB3	71:Sa:99:MET:HE3	1.84	0.60
78:Sj:99:ARG:HB2	78:Sj:115:TRP:HB2	1.82	0.60
81:Sn:166:GLN:HG3	81:Sn:170:GLU:OE2	2.02	0.60
1:L1:179:C:OP2	11:LO:53:HIS:NE2	2.35	0.60
38:Ls:154:ASN:HD21	38:Ls:156:ASP:HB2	1.66	0.60
76:Sg:349:HIS:CG	77:Si:24:ARG:HH12	2.20	0.60
77:Si:29:LYS:HE2	77:Si:29:LYS:N	2.13	0.60
79:Sk:66:TRP:CH2	79:Sk:82:PRO:CG	2.84	0.60
11:LO:12:ALA:HB2	48:L6:88:ILE:HD12	1.83	0.60
30:Lk:67:VAL:HG12	30:Lk:70:LEU:HB2	1.83	0.60
57:SG:166:ARG:NH1	83:S1:347:A:O2'	2.34	0.60
58:SI:292:ARG:HH11	58:SI:292:ARG:CB	2.03	0.60
60:SK:136:ALA:HB1	60:SK:170:LEU:HD13	1.83	0.60
66:SS:182:GLY:O	69:SX:183:LYS:NZ	2.34	0.60
78:Sj:64:LEU:O	78:Sj:68:LEU:CB	2.49	0.60
79:Sk:113:HIS:NE2	79:Sk:114:LEU:CD1	2.65	0.60
81:Sn:160:GLY:HA2	81:Sn:163:ARG:NH1	2.17	0.60
1:L1:1182:C:C5	26:Lg:32:THR:HG21	2.36	0.60
9:LM:25:MET:HB2	9:LM:151:ILE:HD11	1.84	0.60
12:LP:163:MET:HE1	12:LP:175:PHE:CZ	2.36	0.60
30:Lk:142:ASP:CG	30:Lk:144:ARG:HH21	2.10	0.60
54:SZ:123:VAL:O	54:SZ:157:THR:HA	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:SE:178:GLU:OE2	55:SE:182:LYS:HE3	2.01	0.60
60:SK:172:VAL:HG21	68:SW:19:VAL:HG22	1.84	0.60
76:Sg:319:ALA:O	79:Sk:164:ARG:NH2	2.35	0.60
22:Lb:119:LEU:HD22	30:Lk:53:PRO:HG2	1.83	0.60
55:SE:279:LEU:O	70:SY:6:LEU:HD11	2.02	0.60
58:SI:328:VAL:HG12	58:SI:329:THR:N	2.14	0.60
64:SP:71:ASP:OD1	64:SP:71:ASP:N	2.35	0.60
79:Sk:174:ARG:HG2	79:Sk:206:THR:HG22	1.83	0.60
82:So:532:LEU:C	82:So:533:MET:HE3	2.26	0.60
82:So:533:MET:N	82:So:533:MET:CE	2.64	0.60
5:LD:223:HIS:HA	5:LD:226:MET:HE2	1.83	0.59
25:Lf:180:LYS:HD3	25:Lf:180:LYS:N	2.16	0.59
62:SN:52:LEU:HD13	77:Si:41:PRO:HB3	1.84	0.59
63:SO:145:LYS:HD2	63:SO:146:HIS:CD2	2.37	0.59
71:Sa:23:PHE:HB3	71:Sa:27:VAL:HG11	1.83	0.59
1:L1:482:A:H5'	48:L6:38:ARG:HH21	1.67	0.59
20:LX:98:ILE:CD1	20:LX:109:ILE:CD1	2.74	0.59
30:Lk:394:LYS:C	30:Lk:395:ARG:HD2	2.26	0.59
73:Sc:357:THR:HA	73:Sc:360:VAL:HG23	1.82	0.59
14:LR:133:GLN:O	14:LR:137:GLU:HG3	2.02	0.59
34:Lo:109:PHE:HE2	34:Lo:111:PRO:HB3	1.66	0.59
53:SB:102:MET:HE2	53:SB:224:ASP:C	2.28	0.59
62:SN:40:ARG:NE	62:SN:81:ASP:OD1	2.35	0.59
79:Sk:113:HIS:HE2	79:Sk:114:LEU:CD1	2.14	0.59
4:LC:221:ARG:HA	4:LC:261:MET:SD	2.43	0.59
52:Sf:304:ASP:OD1	52:Sf:307:ARG:NH1	2.36	0.59
1:L1:1179:G:OP1	26:Lg:14:LYS:NZ	2.34	0.59
38:Ls:186:VAL:HG21	38:Ls:239:PRO:HB3	1.85	0.59
39:Lt:82:SER:OG	39:Lt:83:LEU:N	2.36	0.59
54:SZ:76:LEU:HD23	59:SJ:138:THR:HG22	1.84	0.59
67:ST:142:GLU:H	68:SW:28:ARG:HH21	1.49	0.59
73:Sc:30:LEU:HD12	73:Sc:149:ASP:HB2	1.85	0.59
79:Sk:64:GLN:HE22	82:So:83:THR:HG21	1.67	0.59
1:L1:777:A:OP1	52:Sf:59:ARG:NH1	2.35	0.59
31:Ll:133:ASP:OD1	31:Ll:133:ASP:N	2.36	0.59
31:Ll:288:SER:HB2	31:Ll:289:PRO:HD3	1.84	0.59
53:SB:102:MET:SD	53:SB:229:PRO:HG3	2.43	0.59
73:Sc:240:LEU:HA	73:Sc:243:VAL:HG12	1.85	0.59
1:L1:1343:G:HO2'	29:Lj:66:PHE:N	2.00	0.59
59:SJ:84:ASP:HB3	59:SJ:168:VAL:HG21	1.83	0.59
59:SJ:148:LEU:HD11	59:SJ:152:THR:HG22	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:Sb:45:PRO:HB2	78:Sj:53:ARG:NH2	2.03	0.59
75:Se:70:ILE:HD11	75:Se:99:LEU:HD12	1.83	0.59
1:L1:845:U:O2'	3:LB:282:ALA:O	2.20	0.59
38:Ls:152:LEU:HD21	38:Ls:172:MET:HG3	1.84	0.59
62:SN:128:TRP:CZ2	83:S1:805:U:H5''	2.36	0.59
72:Sb:53:PHE:CE1	72:Sb:57:MET:SD	2.96	0.59
76:Sg:334:LEU:HB2	76:Sg:355:THR:HG23	1.85	0.59
28:Li:106:THR:HG23	28:Li:162:THR:HA	1.85	0.59
59:SJ:83:HIS:H	59:SJ:168:VAL:HG23	1.67	0.59
75:Se:334:PHE:HE1	75:Se:340:PHE:HE2	1.50	0.59
38:Ls:196:GLN:CD	38:Ls:198:ARG:HH22	2.08	0.59
43:Ly:72:GLU:OE1	50:L8:33:ARG:NH1	2.36	0.59
63:SO:201:ARG:NH2	83:S1:504:C:OP2	2.35	0.59
73:Sc:209:LEU:O	73:Sc:209:LEU:HD13	2.03	0.59
33:Ln:136:ILE:HD11	40:Lv:173:ILE:HG13	1.85	0.58
40:Lv:146:LEU:HD23	40:Lv:147:ASP:O	2.00	0.58
57:SG:91:ILE:HG23	57:SG:111:MET:HE2	1.85	0.58
67:ST:141:ARG:HG3	67:ST:141:ARG:NH1	2.14	0.58
71:Sa:137:ARG:HG3	71:Sa:137:ARG:NH1	2.17	0.58
30:Lk:166:THR:O	52:Sf:287:LYS:NZ	2.35	0.58
32:Lm:107:LEU:HD13	32:Lm:128:LEU:HD11	1.84	0.58
54:SZ:140:GLU:OE2	54:SZ:152:ARG:HA	2.03	0.58
64:SP:56:PRO:O	64:SP:64:LYS:HE2	2.03	0.58
68:SW:6:LYS:HZ1	83:S1:359:U:H5''	1.68	0.58
69:SX:75:VAL:HG23	69:SX:303:LEU:HD11	1.84	0.58
73:Sc:30:LEU:HD11	73:Sc:181:LEU:HD11	1.85	0.58
73:Sc:148:MET:HA	73:Sc:148:MET:HE3	1.84	0.58
82:So:611:LEU:HB3	82:So:615:MET:HE1	1.85	0.58
83:S1:174:U:H2'	83:S1:175:G:H8	1.68	0.58
38:Ls:160:LEU:HD22	38:Ls:169:PHE:CE1	2.38	0.58
40:Lv:95:LEU:HD21	40:Lv:106:TYR:HD2	1.68	0.58
64:SP:32:TYR:CE2	83:S1:191:U:H4'	2.38	0.58
75:Se:253:LEU:HB3	75:Se:255:MET:HE1	1.84	0.58
83:S1:712:U:H2'	83:S1:713:G:H8	1.68	0.58
10:LN:124:PRO:HD2	10:LN:127:LEU:HD12	1.83	0.58
15:LS:88:ASP:OD1	15:LS:89:PRO:HD2	2.03	0.58
38:Ls:196:GLN:NE2	38:Ls:198:ARG:HH22	1.95	0.58
53:SB:165:TYR:CE2	58:SI:146:PRO:HG2	2.39	0.58
54:SZ:165:LYS:HE2	54:SZ:167:LEU:HD21	1.84	0.58
1:L1:488:U:OP1	51:SR:182:ARG:NH2	2.36	0.58
53:SB:210:ARG:NH1	53:SB:214:LYS:HD2	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:SN:90:ARG:HH21	62:SN:97:PRO:CG	2.13	0.58
5:LD:190:MET:HG3	5:LD:260:VAL:HG13	1.84	0.58
15:LS:96:ARG:NH1	15:LS:285:GLU:OE1	2.36	0.58
22:Lb:119:LEU:HD23	22:Lb:168:ARG:HD2	1.85	0.58
58:SI:392:THR:OG1	58:SI:393:TRP:N	2.36	0.58
72:Sb:53:PHE:HE2	83:S1:198:A:C2	2.21	0.58
77:Si:84:ARG:HE	77:Si:85:LEU:HG	1.68	0.58
3:LB:126:VAL:O	3:LB:160:GLY:N	2.35	0.58
41:Lw:68:THR:HG22	41:Lw:69:PRO:HD2	1.85	0.58
45:L3:78:GLY:HA2	45:L3:81:LEU:HB2	1.86	0.58
51:SR:39:VAL:O	51:SR:49:ILE:HA	2.03	0.58
66:SS:124:GLU:HA	66:SS:127:VAL:HG12	1.85	0.58
75:Se:348:TYR:HB2	75:Se:386:ALA:HB1	1.86	0.58
6:LI:93:ASN:OD1	6:LI:114:VAL:C	2.47	0.58
20:LX:98:ILE:HD11	20:LX:109:ILE:CD1	2.34	0.58
32:Lm:162:TYR:CD2	32:Lm:189:LEU:HD11	2.39	0.58
36:Lq:132:PRO:O	36:Lq:136:LYS:HE2	2.03	0.58
55:SE:412:LYS:HG2	55:SE:417:MET:HG3	1.85	0.58
62:SN:112:ARG:NH2	83:S1:618:C:OP1	2.37	0.58
66:SS:64:TYR:OH	66:SS:125:GLN:NE2	2.37	0.58
69:SX:258:LYS:HB2	69:SX:261:LEU:HB2	1.86	0.58
9:LM:73:GLU:OE2	51:SR:149:ARG:NH2	2.32	0.58
32:Lm:59:THR:HG21	32:Lm:84:ASN:HB2	1.86	0.58
66:SS:185:SER:OG	66:SS:186:ALA:N	2.33	0.58
78:Sj:71:LEU:HD11	78:Sj:141:LEU:HD21	1.86	0.58
79:Sk:173:LEU:HD21	79:Sk:226:LEU:HD22	1.86	0.58
1:L1:1016:G:H5'	1:L1:1434:U:H4'	1.84	0.58
3:LB:217:LEU:HD11	3:LB:227:GLN:HB2	1.84	0.58
12:LP:124:VAL:HG13	12:LP:152:THR:HG21	1.84	0.58
20:LX:136:ARG:HH21	20:LX:146:VAL:CG1	2.17	0.58
30:Lk:274:LYS:HD3	30:Lk:275:ASN:H	1.67	0.58
31:Ll:214:TRP:HA	31:Ll:275:GLN:HG3	1.86	0.58
32:Lm:159:LYS:NZ	35:Lp:89:ASP:O	2.36	0.58
38:Ls:218:THR:OG1	38:Ls:219:ARG:N	2.37	0.58
74:Sd:89:LEU:CD1	74:Sd:92:MET:HE2	2.34	0.58
82:So:256:GLU:HG2	82:So:287:LEU:HB3	1.84	0.58
82:So:303:CYS:SG	82:So:344:ARG:NH1	2.76	0.58
37:Lr:208:PRO:HA	37:Lr:211:THR:HG22	1.85	0.57
31:Ll:306:LYS:CD	31:Ll:307:HIS:NE2	2.67	0.57
70:SY:113:ASP:O	70:SY:117:LEU:HD23	2.04	0.57
11:LO:162:LEU:HD11	49:L7:144:PHE:HB3	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LR:123:ALA:O	14:LR:127:ILE:HG12	2.05	0.57
38:Ls:209:TYR:HE1	38:Ls:251:GLN:HG3	1.69	0.57
54:SZ:113:ARG:HD3	59:SJ:166:GLU:HG2	1.86	0.57
57:SG:187:MET:HE1	57:SG:219:VAL:HG21	1.85	0.57
64:SP:34:ILE:CD1	64:SP:53:SER:N	2.68	0.57
81:Sn:138:MET:HE2	81:Sn:142:LYS:HG3	1.85	0.57
14:LR:53:ARG:NH1	31:Ll:155:TYR:OH	2.37	0.57
40:Lv:135:LEU:HD13	40:Lv:145:LEU:HD22	1.84	0.57
47:L5:55:LEU:CD1	47:L5:63:THR:HG21	2.34	0.57
59:SJ:117:ARG:HD2	62:SN:128:TRP:CE3	2.39	0.57
64:SP:21:LEU:HB3	64:SP:32:TYR:HB3	1.86	0.57
83:S1:533:U:OP1	83:S1:923:G:N2	2.36	0.57
83:S1:760:U:H1'	83:S1:798:G:H21	1.69	0.57
20:LX:36:PRO:HD2	20:LX:39:ILE:HB	1.87	0.57
26:Lg:57:VAL:HG13	26:Lg:59:LYS:HE2	1.85	0.57
48:L6:12:ILE:HG13	48:L6:23:ARG:HB2	1.87	0.57
64:SP:29:ARG:HH22	71:Sa:140:ILE:HG12	1.68	0.57
71:Sa:29:VAL:HB	71:Sa:79:TYR:HB2	1.85	0.57
76:Sg:276:SER:N	76:Sg:279:ASP:OD2	2.37	0.57
82:So:661:GLU:OE1	82:So:662:ALA:N	2.38	0.57
59:SJ:149:THR:HG1	79:Sk:133:TRP:CD1	2.22	0.57
8:LK:171:ARG:HE	8:LK:175:LEU:HG	1.70	0.57
11:LO:151:LYS:CG	11:LO:171:GLY:O	2.53	0.57
20:LX:50:SER:HB2	20:LX:53:ASP:OD1	2.04	0.57
40:Lv:146:LEU:CD2	40:Lv:147:ASP:N	2.08	0.57
52:Sf:73:ALA:O	52:Sf:79:LYS:NZ	2.36	0.57
62:SN:37:ASP:HB3	77:Si:52:TYR:OH	2.04	0.57
73:Sc:43:ARG:NH2	73:Sc:77:ASP:OD1	2.35	0.57
4:LC:234:THR:O	4:LC:236:THR:N	2.38	0.57
6:LI:108:ARG:NH1	6:LI:143:GLU:OE2	2.37	0.57
63:SO:96:GLU:HG2	63:SO:97:MET:HG2	1.86	0.57
64:SP:34:ILE:CD1	64:SP:52:GLY:C	2.77	0.57
78:Sj:85:TRP:CH2	78:Sj:139:TRP:HH2	2.22	0.57
82:So:373:HIS:HB2	82:So:415:PHE:HA	1.87	0.57
82:So:547:ALA:HA	82:So:550:ASP:OD2	2.04	0.57
48:L6:47:TYR:O	48:L6:51:MET:HE2	2.05	0.57
58:SI:91:MET:CG	79:Sk:66:TRP:CD2	2.88	0.57
62:SN:36:ARG:HG3	62:SN:40:ARG:HH22	1.70	0.57
73:Sc:331:LEU:HD22	73:Sc:335:LYS:HE3	1.87	0.57
74:Sd:80:PHE:HA	74:Sd:83:MET:HG3	1.87	0.57
3:LB:218:ARG:CZ	3:LB:218:ARG:CB	2.81	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:LD:214:ASP:OD1	5:LD:257:GLN:CD	2.48	0.57
17:LU:111:GLU:HG2	36:Lq:19:LEU:HD21	1.85	0.57
38:Ls:196:GLN:HG2	38:Ls:198:ARG:NH2	2.19	0.57
38:Ls:251:GLN:OE1	38:Ls:254:ASN:HB2	2.05	0.57
43:Ly:79:TRP:O	43:Ly:80:LEU:HD23	2.04	0.57
45:L3:19:GLN:HA	45:L3:54:ASP:HB3	1.86	0.57
46:L4:76:ASN:ND2	46:L4:80:GLU:O	2.37	0.57
55:SE:155:GLN:HE21	82:So:108:LEU:HD13	1.70	0.57
58:SI:157:SER:HB3	58:SI:209:LEU:HD22	1.87	0.57
63:SO:125:LEU:HD23	63:SO:128:ARG:NH2	2.20	0.57
63:SO:126:GLU:O	63:SO:130:ILE:HD12	2.05	0.57
4:LC:202:GLN:NE2	4:LC:301:ASP:OD1	2.38	0.56
14:LR:90:GLU:CG	14:LR:105:SER:HB3	2.25	0.56
23:Lu:80:LYS:HG2	23:Lu:81:SER:H	1.70	0.56
52:Sf:296:HIS:HE1	52:Sf:425:LEU:HA	1.68	0.56
75:Se:123:ARG:HD2	75:Se:299:ASN:HB3	1.86	0.56
82:So:632:GLU:CD	82:So:632:GLU:C	2.72	0.56
6:LI:142:GLU:HA	6:LI:145:LEU:HG	1.87	0.56
22:Lb:129:MET:CE	22:Lb:132:LEU:HD12	2.33	0.56
40:Lv:146:LEU:HD21	40:Lv:147:ASP:O	2.05	0.56
63:SO:103:MET:CE	63:SO:104:LEU:HD23	2.34	0.56
73:Sc:359:LEU:HA	73:Sc:362:GLU:HB2	1.87	0.56
75:Se:170:GLN:NE2	75:Se:174:ASN:O	2.36	0.56
75:Se:276:ARG:NH2	75:Se:286:GLU:OE1	2.38	0.56
4:LC:107:MET:HE2	15:LS:95:GLU:HG2	1.87	0.56
8:LK:30:MET:N	8:LK:30:MET:HE2	2.20	0.56
9:LM:140:ASN:ND2	37:Lr:264:THR:OG1	2.38	0.56
20:LX:177:THR:HG21	23:Lu:85:TRP:HZ2	1.70	0.56
55:SE:176:ARG:NH2	77:Si:84:ARG:HD3	2.02	0.56
58:SI:266:GLY:C	58:SI:267:MET:HE2	2.30	0.56
63:SO:82:ILE:HD12	63:SO:83:GLU:N	2.20	0.56
64:SP:91:LEU:HD22	64:SP:96:PHE:HB3	1.87	0.56
79:Sk:137:LEU:HD12	79:Sk:142:LYS:HG3	1.88	0.56
79:Sk:211:ARG:NH1	79:Sk:221:TYR:OH	2.39	0.56
82:So:615:MET:HE2	82:So:645:LEU:CD2	2.28	0.56
5:LD:175:LYS:HG2	5:LD:273:LEU:HD13	1.87	0.56
20:LX:177:THR:HG21	23:Lu:85:TRP:CZ2	2.40	0.56
31:Ll:79:GLY:O	31:Ll:81:LYS:NZ	2.38	0.56
60:SK:74:ARG:HD3	60:SK:79:LYS:HA	1.87	0.56
79:Sk:266:LEU:HD12	79:Sk:266:LEU:C	2.31	0.56
82:So:580:ALA:N	82:So:595:MET:HE1	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LP:218:ILE:HG23	12:LP:223:MET:HB2	1.86	0.56
32:Lm:224:LYS:O	32:Lm:228:GLU:HG3	2.06	0.56
58:SI:80:GLU:HG3	79:Sk:84:PRO:HG3	1.87	0.56
82:So:615:MET:HB3	82:So:648:ARG:NE	2.19	0.56
10:LN:124:PRO:HD2	10:LN:127:LEU:CD1	2.36	0.56
14:LR:56:GLU:OE2	14:LR:78:HIS:HE1	1.88	0.56
38:Ls:152:LEU:CD1	38:Ls:160:LEU:CD1	2.84	0.56
38:Ls:207:ASN:HD22	38:Ls:251:GLN:HE22	1.52	0.56
60:SK:166:ILE:HD11	60:SK:172:VAL:HG22	1.87	0.56
61:SL:34:ASN:O	61:SL:38:ARG:HG3	2.04	0.56
65:SQ:31:THR:N	71:Sa:65:MET:HE3	2.14	0.56
66:SS:185:SER:O	69:SX:183:LYS:NZ	2.39	0.56
71:Sa:48:VAL:HA	71:Sa:52:ILE:HG13	1.88	0.56
73:Sc:392:ARG:NH1	83:S1:877:A:OP2	2.39	0.56
79:Sk:150:GLU:OE1	79:Sk:174:ARG:NH2	2.38	0.56
79:Sk:156:TYR:O	79:Sk:165:ASN:ND2	2.38	0.56
1:L1:672:U:H5'	19:LW:78:LYS:HB2	1.88	0.56
5:LD:231:VAL:HG13	50:L8:26:ARG:HD3	1.88	0.56
15:LS:256:GLU:HA	15:LS:259:LYS:HD2	1.87	0.56
55:SE:176:ARG:HH12	77:Si:84:ARG:CZ	2.18	0.56
62:SN:35:TRP:CA	62:SN:38:VAL:HG12	2.33	0.56
63:SO:174:ASN:ND2	63:SO:176:ASP:OD1	2.39	0.56
33:Ln:165:ASP:HB2	39:Lt:207:ASN:HB2	1.88	0.56
35:Lp:67:ILE:HD12	35:Lp:67:ILE:N	2.20	0.56
38:Ls:152:LEU:HD11	38:Ls:160:LEU:HD11	1.87	0.56
45:L3:20:PHE:C	45:L3:22:PRO:HD3	2.31	0.56
53:SB:152:SER:O	53:SB:156:GLU:HG3	2.06	0.56
58:SI:328:VAL:CG1	58:SI:329:THR:N	2.68	0.56
64:SP:59:ASN:HB2	64:SP:62:GLY:H	1.70	0.56
1:L1:346:C:OP2	11:LO:59:ARG:NH1	2.39	0.56
1:L1:1074:U:O2'	1:L1:1076:U:O4	2.20	0.56
31:Ll:173:LEU:HD11	31:Ll:204:VAL:HG13	1.87	0.56
33:Ln:164:ARG:O	33:Ln:165:ASP:C	2.49	0.56
69:SX:349:TYR:CZ	69:SX:353:LEU:HD21	2.41	0.56
73:Sc:337:LEU:HA	73:Sc:340:LYS:HG2	1.87	0.56
15:LS:248:CYS:C	15:LS:249:LEU:HD23	2.30	0.56
56:SF:103:LYS:H	56:SF:103:LYS:CE	2.19	0.56
58:SI:125:MET:HA	58:SI:125:MET:HE3	1.88	0.56
61:SL:95:ILE:CD1	61:SL:102:LEU:HD22	2.36	0.56
1:L1:627:A:H5'	16:LT:40:ARG:HH22	1.70	0.55
2:L2:58:U:H2'	2:L2:59:G:H8	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LO:140:LEU:HD23	11:LO:163:ALA:HB1	1.88	0.55
19:LW:1:MET:HE3	34:Lo:58:PRO:HG2	1.88	0.55
31:Ll:174:HIS:HB2	31:Ll:205:THR:OG1	2.07	0.55
31:Ll:329:TYR:CE1	31:Ll:333:GLN:HB2	2.42	0.55
31:Ll:375:PRO:O	49:L7:141:ARG:NH2	2.39	0.55
32:Lm:278:TYR:CD1	32:Lm:301:SER:HB2	2.41	0.55
46:L4:109:GLU:OE1	46:L4:109:GLU:N	2.38	0.55
55:SE:335:LYS:HE2	83:S1:2:A:H5''	1.88	0.55
60:SK:152:LYS:HG3	60:SK:180:PRO:HD3	1.88	0.55
79:Sk:59:LYS:HZ3	82:So:83:THR:HB	1.71	0.55
1:L1:995:U:OP2	13:LQ:17:ARG:HD2	2.06	0.55
11:LO:286:THR:OG1	41:Lw:37:ARG:HB2	2.07	0.55
37:Lr:148:MET:HG3	37:Lr:149:PRO:HD2	1.89	0.55
45:L3:40:GLU:N	45:L3:40:GLU:OE1	2.39	0.55
53:SB:81:VAL:HG13	53:SB:118:LEU:HB3	1.87	0.55
55:SE:372:GLU:OE2	55:SE:374:ARG:HG2	2.06	0.55
62:SN:60:ASN:HB3	77:Si:33:VAL:CG2	2.36	0.55
71:Sa:11:ARG:HH21	83:S1:285:C:H5	1.53	0.55
72:Sb:186:ASN:OD1	72:Sb:188:ASN:HB2	2.06	0.55
76:Sg:328:PHE:CE1	79:Sk:221:TYR:CD1	2.79	0.55
1:L1:216:G:H1	43:Ly:61:GLY:HA3	1.70	0.55
49:L7:78:ILE:HG12	49:L7:101:VAL:HG22	1.86	0.55
66:SS:111:HIS:CD2	66:SS:112:LYS:HG2	2.41	0.55
70:SY:88:PHE:HE2	74:Sd:102:GLY:HA2	1.72	0.55
82:So:63:LYS:HG3	82:So:65:TRP:HE1	1.71	0.55
14:LR:90:GLU:HG3	14:LR:107:ARG:NH2	2.21	0.55
33:Ln:101:ARG:HG2	39:Lt:80:GLU:HA	1.88	0.55
39:Lt:200:MET:HE1	39:Lt:242:ASP:CA	2.36	0.55
49:L7:100:GLU:OE2	49:L7:134:ILE:HG23	2.06	0.55
78:Sj:175:ILE:HD12	78:Sj:175:ILE:C	2.32	0.55
79:Sk:60:MET:HE1	79:Sk:66:TRP:HE3	1.70	0.55
82:So:515:ASP:N	82:So:518:GLU:OE2	2.40	0.55
18:LV:82:TYR:HD2	18:LV:87:MET:HG2	1.71	0.55
53:SB:65:GLU:HA	53:SB:68:LYS:HZ1	1.68	0.55
58:SI:136:ARG:HH11	58:SI:210:VAL:HB	1.71	0.55
59:SJ:73:TYR:HE1	59:SJ:177:LEU:HD22	1.71	0.55
76:Sg:358:LEU:HB3	76:Sg:369:LYS:HG2	1.88	0.55
77:Si:81:GLU:HG3	77:Si:84:ARG:NH2	2.20	0.55
83:S1:178:U:O4	83:S1:181:C:N3	2.40	0.55
38:Ls:164:VAL:HG13	38:Ls:168:CYS:HB3	1.89	0.55
73:Sc:70:LEU:HD11	73:Sc:389:LEU:HB3	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:Sk:298:SER:O	79:Sk:301:ASN:C	2.49	0.55
80:Sm:95:GLU:OE1	80:Sm:98:SER:OG	2.18	0.55
7:LJ:167:ILE:O	7:LJ:170:THR:OG1	2.23	0.55
33:Ln:172:GLU:HG2	40:Lv:183:ARG:HH21	1.72	0.55
39:Lt:97:ARG:HA	39:Lt:100:LYS:HE2	1.87	0.55
39:Lt:178:TRP:NE1	39:Lt:182:GLU:O	2.39	0.55
63:SO:143:LEU:HD12	63:SO:156:LEU:HD22	1.88	0.55
64:SP:19:ILE:HG22	64:SP:87:MET:HG3	1.89	0.55
77:Si:82:GLN:NE2	83:S1:689:G:H5''	2.22	0.55
83:S1:226:G:N3	83:S1:274:U:O2'	2.39	0.55
5:LD:248:LEU:HG	5:LD:253:MET:HE2	1.87	0.55
38:Ls:196:GLN:HG3	38:Ls:198:ARG:HH22	1.71	0.55
47:L5:55:LEU:HD12	47:L5:63:THR:HG21	1.89	0.55
49:L7:111:ILE:HB	49:L7:116:ARG:HG3	1.88	0.55
63:SO:180:LYS:NZ	63:SO:180:LYS:HB3	2.22	0.55
63:SO:209:LEU:HD22	81:Sn:173:LEU:HD22	1.87	0.55
77:Si:18:LEU:CD2	79:Sk:229:LEU:HD21	2.36	0.55
1:L1:853:C:H4'	1:L1:854:A:OP1	2.07	0.55
1:L1:1070:A:H2'	1:L1:1071:A:C8	2.42	0.55
79:Sk:65:ASP:O	79:Sk:68:SER:OG	2.19	0.55
83:S1:881:A:H2'	83:S1:882:A:H8	1.71	0.55
1:L1:801:G:H5''	10:LN:35:MET:O	2.07	0.55
4:LC:135:LYS:HE2	4:LC:141:LYS:C	2.31	0.55
11:LO:262:PRO:HB2	49:L7:43:TYR:O	2.07	0.55
32:Lm:148:MET:HE2	32:Lm:260:PHE:HD2	1.71	0.55
40:Lv:95:LEU:HD21	40:Lv:106:TYR:CD2	2.42	0.55
64:SP:112:ARG:HH22	66:SS:229:GLY:HA3	1.72	0.55
69:SX:128:MET:CE	69:SX:269:GLY:HA3	2.27	0.55
75:Se:324:LEU:HD13	79:Sk:304:GLU:HB2	1.88	0.55
78:Sj:144:LYS:HA	78:Sj:147:GLU:HB2	1.89	0.55
83:S1:205:A:H3'	83:S1:206:C:H6	1.71	0.55
1:L1:875:U:H5''	1:L1:876:G:H5'	1.88	0.54
11:LO:180:ASP:HB2	11:LO:204:MET:HB2	1.87	0.54
20:LX:47:GLU:OE1	20:LX:118:ARG:NH1	2.40	0.54
37:Lr:72:ILE:HG23	37:Lr:88:LEU:HD23	1.88	0.54
57:SG:231:GLU:HA	57:SG:234:ARG:HG3	1.88	0.54
8:LK:187:GLU:HG3	8:LK:191:LYS:HE3	1.89	0.54
24:Ld:103:ILE:HG23	44:Lz:84:MET:CE	2.30	0.54
46:L4:107:LEU:CD2	46:L4:124:GLN:OE1	2.53	0.54
49:L7:80:TYR:CE1	49:L7:143:GLN:HB2	2.42	0.54
55:SE:300:ARG:NH1	83:S1:474:A:OP1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:SG:187:MET:CE	57:SG:219:VAL:HG21	2.37	0.54
1:L1:474:A:OP1	16:LT:57:ARG:NH1	2.41	0.54
1:L1:911:A:O2'	1:L1:912:A:N7	2.39	0.54
8:LK:48:GLN:NE2	8:LK:52:GLU:OE2	2.40	0.54
60:SK:184:ASN:ND2	83:S1:368:A:OP1	2.39	0.54
66:SS:192:THR:O	66:SS:195:SER:C	2.51	0.54
7:LJ:132:LYS:NZ	7:LJ:148:VAL:HG12	2.23	0.54
33:Ln:101:ARG:NH1	39:Lt:79:ILE:O	2.41	0.54
33:Ln:141:GLU:OE1	33:Ln:141:GLU:HA	2.07	0.54
59:SJ:81:LYS:CD	59:SJ:140:TYR:HE1	2.19	0.54
69:SX:252:ASP:OD1	69:SX:256:ARG:NH1	2.41	0.54
78:Sj:78:ARG:HH21	78:Sj:143:PRO:HA	1.71	0.54
82:So:372:TYR:HA	82:So:375:ILE:HD11	1.90	0.54
82:So:600:ARG:NH2	82:So:632:GLU:OE1	2.39	0.54
83:S1:841:C:H2'	83:S1:842:G:C8	2.43	0.54
7:LJ:118:LYS:C	7:LJ:120:LYS:H	2.15	0.54
14:LR:111:ILE:HG22	14:LR:115:LEU:HD23	1.89	0.54
16:LT:23:GLU:OE1	16:LT:26:LYS:HE2	2.08	0.54
31:Ll:326:SER:O	31:Ll:330:ILE:HG13	2.08	0.54
49:L7:111:ILE:HG22	49:L7:115:VAL:HG23	1.88	0.54
54:SZ:99:THR:O	54:SZ:101:PRO:HD3	2.06	0.54
57:SG:187:MET:HE2	57:SG:219:VAL:HG11	1.89	0.54
11:LO:116:ILE:HB	11:LO:154:ILE:HD12	1.89	0.54
20:LX:56:LEU:HG	20:LX:86:VAL:HG11	1.89	0.54
21:La:122:LYS:NZ	31:Ll:56:ARG:HD2	2.21	0.54
31:Ll:255:LEU:HD12	31:Ll:256:PRO:HD2	1.89	0.54
73:Sc:177:SER:O	73:Sc:180:LEU:HG	2.07	0.54
73:Sc:364:LEU:HD12	73:Sc:368:GLU:HG3	1.89	0.54
82:So:397:MET:HE2	82:So:401:MET:CE	2.38	0.54
82:So:420:MET:SD	82:So:461:PHE:HB2	2.47	0.54
19:LW:48:MET:HE2	19:LW:53:LEU:HA	1.90	0.54
52:Sf:113:VAL:HG23	52:Sf:392:ILE:HG23	1.89	0.54
53:SB:148:ASN:HD21	53:SB:197:HIS:CD2	2.24	0.54
55:SE:400:GLU:OE1	55:SE:400:GLU:N	2.36	0.54
75:Se:50:ARG:HG2	75:Se:67:HIS:HB2	1.90	0.54
78:Sj:163:SER:CB	78:Sj:190:MET:SD	2.95	0.54
82:So:342:LEU:HD13	82:So:378:LEU:HD22	1.89	0.54
5:LD:291:SER:HA	41:Lw:52:LEU:HD23	1.89	0.54
13:LQ:59:LEU:HA	15:LS:269:MET:HE1	1.89	0.54
37:Lr:130:THR:O	37:Lr:134:GLN:HG2	2.08	0.54
37:Lr:182:GLU:HG3	37:Lr:183:GLU:HG3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:Lw:144:THR:O	41:Lw:146:THR:HG22	2.07	0.54
46:L4:76:ASN:ND2	46:L4:82:GLN:H	2.05	0.54
73:Sc:180:LEU:CD1	73:Sc:181:LEU:CG	2.81	0.54
78:Sj:39:GLU:OE1	78:Sj:39:GLU:N	2.40	0.54
82:So:308:LYS:HG3	82:So:310:GLU:H	1.72	0.54
83:S1:583:C:N4	83:S1:799:A:O2'	2.40	0.54
17:LU:95:LEU:HD23	17:LU:138:ALA:HB2	1.89	0.54
33:Ln:129:ARG:HH11	33:Ln:133:ARG:CG	2.10	0.54
46:L4:120:ARG:O	46:L4:124:GLN:HG3	2.07	0.54
65:SQ:22:MET:HE3	65:SQ:25:THR:HB	1.89	0.54
66:SS:228:SER:HB3	72:Sb:51:ALA:HB3	1.90	0.54
70:SY:12:ILE:O	70:SY:16:THR:OG1	2.22	0.54
82:So:573:ALA:O	82:So:577:ASN:ND2	2.38	0.54
1:L1:1088:G:OP1	6:LI:122:ARG:NH2	2.39	0.54
23:Lu:109:ARG:HD3	23:Lu:139:MET:CE	2.38	0.54
30:Lk:40:LYS:HD3	30:Lk:41:SER:H	1.73	0.54
54:SZ:76:LEU:O	62:SN:103:ARG:NH2	2.41	0.54
31:LI:217:LEU:HD13	31:LI:236:LEU:HD13	1.89	0.53
53:SB:158:MET:O	53:SB:162:CYS:SG	2.58	0.53
70:SY:77:VAL:HG13	70:SY:78:TYR:N	2.15	0.53
82:So:619:LYS:HG3	82:So:648:ARG:HH21	1.73	0.53
4:LC:329:PRO:HD2	4:LC:332:LEU:CD1	2.35	0.53
9:LM:174:GLU:HG2	51:SR:56:THR:HG21	1.90	0.53
59:SJ:176:GLN:HE21	79:Sk:174:ARG:HH21	1.56	0.53
82:So:540:HIS:O	82:So:545:GLN:NE2	2.40	0.53
23:Lu:69:ASP:OD1	23:Lu:70:ASP:N	2.38	0.53
39:Lt:214:THR:HB	39:Lt:230:LYS:HD2	1.90	0.53
45:L3:72:HIS:CE1	45:L3:97:ARG:CZ	2.90	0.53
59:SJ:101:GLU:OE1	79:Sk:123:CYS:HB3	2.08	0.53
60:SK:79:LYS:CA	60:SK:82:GLU:OE2	2.55	0.53
60:SK:136:ALA:HA	60:SK:170:LEU:HD21	1.90	0.53
66:SS:161:GLY:O	69:SX:223:ARG:NH2	2.41	0.53
71:Sa:142:GLU:O	71:Sa:143:VAL:C	2.51	0.53
83:S1:786:A:H3'	83:S1:787:A:H8	1.73	0.53
1:L1:247:A:OP1	27:Lh:63:LYS:HE3	2.08	0.53
8:LK:20:ILE:HD11	8:LK:42:ARG:HG2	1.90	0.53
40:Lv:105:SER:HB2	47:L5:41:THR:HG21	1.89	0.53
50:L8:71:VAL:O	50:L8:74:SER:OG	2.27	0.53
59:SJ:165:PRO:HG3	79:Sk:111:PHE:HZ	1.73	0.53
72:Sb:28:LYS:HB3	72:Sb:32:ASP:OD2	2.08	0.53
80:Sm:52:MET:HG3	80:Sm:70:ILE:HG13	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:L4:107:LEU:HD12	46:L4:117:TYR:HE1	1.74	0.53
75:Se:260:VAL:HG21	75:Se:296:MET:HE1	1.91	0.53
76:Sg:346:PRO:HA	76:Sg:349:HIS:CD2	2.43	0.53
79:Sk:113:HIS:HE2	79:Sk:114:LEU:HD12	1.74	0.53
14:LR:90:GLU:OE1	14:LR:92:LEU:HG	2.08	0.53
32:Lm:51:GLU:HG3	32:Lm:225:VAL:HG11	1.90	0.53
51:SR:101:PRO:HG2	51:SR:104:ILE:HD13	1.91	0.53
62:SN:55:ASN:O	62:SN:58:ARG:HB3	2.09	0.53
69:SX:333:LYS:HD2	69:SX:334:THR:HG23	1.91	0.53
76:Sg:338:LEU:O	76:Sg:377:ARG:NH1	2.42	0.53
21:La:117:ILE:HG23	31:Ll:57:TYR:CG	2.44	0.53
28:Li:157:LEU:O	28:Li:161:MET:HG3	2.09	0.53
55:SE:392:ARG:NH1	55:SE:394:ASP:OD1	2.34	0.53
58:SI:292:ARG:O	58:SI:293:ILE:HD13	2.08	0.53
83:S1:68:G:H1'	83:S1:170:G:H5'	1.91	0.53
1:L1:143:C:O2	43:Ly:32:ILE:HG21	2.09	0.53
1:L1:468:U:H5''	24:Ld:73:LYS:CE	2.38	0.53
1:L1:565:C:H5''	48:L6:9:ARG:HD3	1.91	0.53
5:LD:291:SER:N	41:Lw:53:PRO:O	2.38	0.53
10:LN:113:ASN:ND2	10:LN:136:LYS:HE2	2.24	0.53
57:SG:129:ALA:HB3	57:SG:134:GLN:HG3	1.91	0.53
70:SY:74:PHE:CE2	70:SY:99:PHE:CD2	2.86	0.53
71:Sa:135:CYS:C	71:Sa:136:LEU:HD12	2.33	0.53
79:Sk:320:LEU:HD13	79:Sk:322:VAL:H	1.73	0.53
80:Sm:36:ARG:NH2	80:Sm:91:GLU:OE1	2.42	0.53
81:Sn:128:LYS:NZ	83:S1:460:U:O4	2.41	0.53
83:S1:805:U:H2'	83:S1:806:A:C8	2.43	0.53
1:L1:791:A:H4'	4:LC:235:LYS:HB3	1.91	0.53
31:Ll:281:PHE:CE1	31:Ll:307:HIS:CE1	2.97	0.53
32:Lm:162:TYR:CG	32:Lm:189:LEU:HD11	2.43	0.53
45:L3:18:VAL:HG21	45:L3:34:LEU:HD13	1.90	0.53
55:SE:393:LYS:HA	55:SE:393:LYS:HE3	1.90	0.53
59:SJ:136:MET:CE	62:SN:104:TRP:CZ2	2.79	0.53
60:SK:88:ILE:HB	60:SK:151:VAL:HG12	1.91	0.53
81:Sn:171:LYS:NZ	83:S1:894:U:OP1	2.42	0.53
5:LD:241:ASN:ND2	5:LD:256:HIS:NE2	2.48	0.53
7:LJ:99:CYS:HB3	7:LJ:152:MET:HE3	1.91	0.53
31:Ll:268:LEU:CD1	31:Ll:321:CYS:HB2	2.39	0.53
31:Ll:281:PHE:CE1	31:Ll:307:HIS:ND1	2.70	0.53
39:Lt:146:ARG:HA	39:Lt:151:ARG:HD3	1.91	0.53
53:SB:141:ILE:HB	53:SB:190:PRO:HA	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:SJ:81:LYS:HD2	59:SJ:170:MET:HE3	1.87	0.53
60:SK:172:VAL:HG23	68:SW:19:VAL:HG22	1.88	0.53
64:SP:29:ARG:HH22	71:Sa:140:ILE:CG1	2.21	0.53
10:LN:141:ALA:HB3	10:LN:144:PHE:CZ	2.44	0.52
39:Lt:74:LEU:HD23	39:Lt:77:ILE:HD11	1.90	0.52
47:L5:51:LEU:HB3	47:L5:67:ARG:HB3	1.89	0.52
54:SZ:136:VAL:O	54:SZ:140:GLU:HB2	2.09	0.52
58:SI:119:LYS:HA	58:SI:122:ARG:HE	1.74	0.52
61:SL:68:ARG:HH21	61:SL:92:VAL:HG11	1.73	0.52
4:LC:45:SER:O	32:Lm:307:ARG:NH2	2.42	0.52
4:LC:293:LYS:HE3	15:LS:87:THR:OG1	2.09	0.52
30:Lk:146:HIS:CE1	30:Lk:412:ARG:HD3	2.43	0.52
39:Lt:199:ASN:O	39:Lt:241:GLY:HA3	2.09	0.52
39:Lt:200:MET:CE	39:Lt:242:ASP:CA	2.87	0.52
45:L3:22:PRO:CG	45:L3:55:VAL:HG13	2.39	0.52
59:SJ:102:LEU:HB3	59:SJ:104:ILE:HD13	1.91	0.52
64:SP:102:MET:HE3	83:S1:199:A:O5'	2.09	0.52
71:Sa:98:ILE:O	71:Sa:102:ILE:HG12	2.09	0.52
83:S1:160:A:H8	83:S1:161:C:H41	1.56	0.52
1:L1:282:U:H2'	1:L1:283:A:C8	2.44	0.52
8:LK:130:PHE:CD1	8:LK:130:PHE:N	2.77	0.52
24:Ld:75:THR:O	24:Ld:78:ARG:HB2	2.10	0.52
55:SE:317:HIS:HD2	83:S1:4:A:H5'	1.75	0.52
62:SN:126:ALA:HB1	62:SN:128:TRP:CZ3	2.44	0.52
66:SS:77:TYR:CD2	66:SS:106:PRO:HD3	2.44	0.52
70:SY:75:TYR:CE1	74:Sd:98:LYS:HE2	2.44	0.52
79:Sk:209:THR:HB	79:Sk:221:TYR:HD2	1.75	0.52
82:So:462:PHE:CE2	82:So:496:LEU:HD22	2.45	0.52
1:L1:648:A:H2'	1:L1:649:A:C8	2.44	0.52
6:LI:120:ARG:NH1	22:Lb:136:ASP:OD2	2.35	0.52
9:LM:6:ARG:HD2	37:Lr:230:GLU:OE2	2.09	0.52
10:LN:45:ALA:O	10:LN:49:SER:HB2	2.09	0.52
26:Lg:16:ILE:HD12	26:Lg:18:VAL:CG1	2.39	0.52
31:Ll:268:LEU:HD13	31:Ll:321:CYS:HB2	1.91	0.52
32:Lm:157:ALA:O	35:Lp:93:LYS:HG3	2.09	0.52
52:Sf:235:ASP:OD2	52:Sf:331:SER:OG	2.25	0.52
53:SB:148:ASN:O	53:SB:149:ARG:HB2	2.10	0.52
53:SB:239:ASN:ND2	53:SB:242:SER:OG	2.42	0.52
66:SS:211:ARG:CD	66:SS:215:ARG:HH21	2.22	0.52
75:Se:163:LYS:HG3	75:Se:164:ASN:HD22	1.74	0.52
78:Sj:137:HIS:HB2	83:S1:58:C:H5	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:So:552:ALA:HA	82:So:555:ILE:HD12	1.92	0.52
83:S1:442:U:H2'	83:S1:443:A:H8	1.75	0.52
83:S1:592:C:H2'	83:S1:593:A:C8	2.45	0.52
4:LC:87:ILE:HG23	4:LC:317:PRO:HG2	1.91	0.52
31:Ll:241:PRO:HG2	31:Ll:247:GLU:HB2	1.91	0.52
31:Ll:306:LYS:C	31:Ll:307:HIS:HD2	2.17	0.52
59:SJ:121:LEU:HD11	59:SJ:128:LYS:HG3	1.91	0.52
64:SP:29:ARG:NH2	71:Sa:140:ILE:HD11	2.25	0.52
13:LQ:144:LEU:HD23	32:Lm:302:LEU:HD23	1.91	0.52
14:LR:83:ILE:CD1	14:LR:92:LEU:HD12	2.38	0.52
31:Ll:207:GLU:CD	31:Ll:207:GLU:H	2.17	0.52
56:SF:78:MET:HE3	56:SF:82:LEU:HG	1.92	0.52
59:SJ:102:LEU:HD23	79:Sk:123:CYS:SG	2.49	0.52
59:SJ:115:ILE:HA	59:SJ:136:MET:O	2.09	0.52
63:SO:130:ILE:O	63:SO:134:VAL:HG23	2.10	0.52
71:Sa:140:ILE:H	71:Sa:140:ILE:HD13	1.73	0.52
6:LI:105:VAL:HG13	6:LI:112:VAL:HG21	1.90	0.52
54:SZ:119:ILE:HB	54:SZ:153:LEU:HG	1.92	0.52
57:SG:122:GLN:HB3	57:SG:139:ARG:HG2	1.91	0.52
69:SX:281:ILE:O	69:SX:285:LEU:HD22	2.09	0.52
1:L1:411:U:H2'	1:L1:412:G:C8	2.44	0.52
8:LK:70:ILE:HG23	8:LK:80:ILE:HG13	1.91	0.52
19:LW:129:MET:SD	38:Ls:78:LEU:HD22	2.50	0.52
50:L8:37:PRO:HG3	50:L8:68:SER:HA	1.92	0.52
66:SS:205:TRP:CZ2	66:SS:207:GLN:HB2	2.45	0.52
73:Sc:300:GLN:O	73:Sc:303:ASN:ND2	2.43	0.52
73:Sc:357:THR:CA	73:Sc:360:VAL:HG23	2.40	0.52
82:So:302:VAL:HG21	82:So:341:CYS:HB3	1.91	0.52
1:L1:122:G:OP2	27:Lh:85:LYS:NZ	2.42	0.52
1:L1:1070:A:N3	1:L1:1251:A:O2'	2.36	0.52
8:LK:108:VAL:O	8:LK:171:ARG:NH1	2.43	0.52
14:LR:79:ARG:HD3	14:LR:146:GLN:NE2	2.25	0.52
52:Sf:354:PRO:HB3	52:Sf:373:GLN:HE21	1.74	0.52
82:So:390:SER:HB3	82:So:426:LEU:HD11	1.92	0.52
82:So:584:LEU:HD11	82:So:614:LEU:HG	1.90	0.52
1:L1:502:A:H4'	1:L1:511:A:H4'	1.92	0.52
8:LK:48:GLN:HA	8:LK:51:LYS:HD2	1.92	0.52
14:LR:43:VAL:HG12	31:Ll:225:LEU:HB3	1.91	0.52
31:Ll:185:MET:SD	49:L7:189:ARG:HB2	2.50	0.52
37:Lr:58:VAL:HG13	37:Lr:62:GLU:OE1	2.10	0.52
39:Lt:198:ASN:CB	39:Lt:200:MET:SD	2.96	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:Lv:92:ASN:HD22	40:Lv:92:ASN:N	2.08	0.52
41:Lw:84:TYR:OH	41:Lw:164:LYS:HE2	2.10	0.52
42:Lx:85:ASN:HB2	42:Lx:88:ASP:HB2	1.91	0.52
49:L7:80:TYR:HH	49:L7:147:LEU:HD22	1.73	0.52
63:SO:163:ARG:HA	63:SO:166:MET:CE	2.40	0.52
63:SO:174:ASN:HB3	63:SO:177:VAL:HG22	1.92	0.52
82:So:400:LEU:HD22	82:So:405:PHE:HZ	1.75	0.52
82:So:580:ALA:HB2	82:So:595:MET:HE3	1.92	0.52
7:LJ:105:SER:N	45:L3:40:GLU:OE2	2.32	0.51
29:Lj:90:VAL:HB	29:Lj:100:GLN:HB2	1.91	0.51
55:SE:225:VAL:HG22	55:SE:243:VAL:HG12	1.92	0.51
62:SN:41:ARG:NH1	77:Si:52:TYR:CZ	2.79	0.51
65:SQ:51:ALA:HB2	65:SQ:66:LEU:HD13	1.91	0.51
69:SX:157:VAL:HG22	69:SX:174:VAL:HG13	1.92	0.51
75:Se:273:THR:O	75:Se:275:LYS:NZ	2.42	0.51
79:Sk:169:ARG:NH1	79:Sk:210:ASP:O	2.43	0.51
82:So:259:TYR:HB3	82:So:282:LEU:HD12	1.92	0.51
20:LX:192:LYS:HE2	20:LX:196:GLU:HB3	1.91	0.51
22:Lb:128:THR:O	22:Lb:131:THR:HG22	2.11	0.51
53:SB:65:GLU:HA	53:SB:68:LYS:HZ3	1.73	0.51
54:SZ:99:THR:C	54:SZ:101:PRO:HD3	2.35	0.51
63:SO:197:ARG:HD3	83:S1:134:A:H62	1.75	0.51
72:Sb:52:GLU:O	72:Sb:56:LEU:HB2	2.10	0.51
80:Sm:75:ASP:HB3	80:Sm:79:ARG:HH22	1.75	0.51
82:So:465:ILE:O	82:So:469:GLU:HB2	2.11	0.51
83:S1:767:C:H3'	83:S1:768:G:C8	2.46	0.51
83:S1:805:U:H2'	83:S1:806:A:H8	1.75	0.51
1:L1:622:G:O2'	16:LT:11:ARG:O	2.23	0.51
46:L4:135:ASN:O	46:L4:136:LYS:C	2.53	0.51
58:SI:229:LEU:HG	58:SI:241:VAL:HG11	1.92	0.51
65:SQ:31:THR:HB	71:Sa:65:MET:HE2	1.93	0.51
78:Sj:206:LYS:NZ	78:Sj:208:GLU:HB2	2.24	0.51
79:Sk:225:LEU:O	79:Sk:229:LEU:HB2	2.09	0.51
1:L1:266:A:H4'	1:L1:267:A:N7	2.25	0.51
32:Lm:148:MET:HE2	32:Lm:257:ILE:CD1	2.40	0.51
37:Lr:227:GLU:OE2	37:Lr:230:GLU:HG3	2.11	0.51
38:Ls:187:GLU:OE2	38:Ls:219:ARG:CZ	2.58	0.51
70:SY:77:VAL:CG1	70:SY:78:TYR:CD1	2.92	0.51
77:Si:52:TYR:CD1	77:Si:52:TYR:N	2.78	0.51
4:LC:200:PRO:HD3	4:LC:276:ILE:HD12	1.92	0.51
9:LM:177:ARG:HH21	51:SR:38:VAL:HB	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:LW:125:ASP:OD2	38:Ls:205:GLN:NE2	2.44	0.51
30:Lk:281:GLU:CD	30:Lk:281:GLU:N	2.66	0.51
39:Lt:168:GLN:HB3	39:Lt:170:VAL:HG22	1.91	0.51
47:L5:55:LEU:CD1	47:L5:63:THR:CB	2.86	0.51
57:SG:181:PHE:CD1	57:SG:181:PHE:C	2.89	0.51
63:SO:107:LYS:O	63:SO:111:PHE:HB2	2.10	0.51
79:Sk:269:MET:CE	79:Sk:269:MET:CA	2.70	0.51
83:S1:327:U:O2'	83:S1:328:A:N7	2.38	0.51
83:S1:751:U:H2'	83:S1:752:A:H8	1.76	0.51
2:L2:8:U:O2	2:L2:15:A:N6	2.44	0.51
10:LN:68:LYS:N	10:LN:71:ASP:OD2	2.37	0.51
38:Ls:135:LYS:NZ	38:Ls:136:ASP:OD1	2.43	0.51
53:SB:94:LYS:HG3	74:Sd:148:GLU:CD	2.35	0.51
62:SN:60:ASN:HB3	77:Si:33:VAL:HG21	1.93	0.51
62:SN:83:CYS:HB2	62:SN:85:VAL:HG12	1.93	0.51
63:SO:82:ILE:HD12	63:SO:83:GLU:H	1.76	0.51
63:SO:197:ARG:HD3	83:S1:134:A:N6	2.26	0.51
1:L1:457:A:H4'	1:L1:581:A:C5	2.46	0.51
9:LM:59:ILE:HB	9:LM:127:LEU:HD23	1.93	0.51
22:Lb:183:ARG:O	22:Lb:187:ILE:HG13	2.11	0.51
22:Lb:238:LEU:HD11	34:Lo:101:GLU:HG2	1.93	0.51
38:Ls:164:VAL:HG22	38:Ls:261:MET:HB3	1.92	0.51
64:SP:34:ILE:HD12	64:SP:34:ILE:N	2.20	0.51
76:Sg:316:ASN:C	76:Sg:318:GLU:H	2.19	0.51
83:S1:864:C:H3'	83:S1:865:A:H5''	1.92	0.51
3:LB:218:ARG:HH11	3:LB:218:ARG:CG	2.24	0.51
12:LP:64:ARG:NH1	12:LP:144:LYS:O	2.43	0.51
58:SI:267:MET:HE2	58:SI:267:MET:N	2.26	0.51
63:SO:163:ARG:HA	63:SO:166:MET:HE2	1.93	0.51
70:SY:99:PHE:O	70:SY:99:PHE:HD1	1.94	0.51
70:SY:111:GLU:HB3	70:SY:117:LEU:HD21	1.93	0.51
79:Sk:78:PRO:HB2	79:Sk:99:LYS:HE3	1.93	0.51
83:S1:37:U:H2'	83:S1:38:A:H8	1.74	0.51
3:LB:86:ASP:OD2	3:LB:92:ARG:NH1	2.43	0.51
20:LX:53:ASP:OD1	20:LX:53:ASP:N	2.43	0.51
33:Ln:169:PHE:O	33:Ln:171:PHE:N	2.44	0.51
33:Ln:177:HIS:N	33:Ln:177:HIS:ND1	2.57	0.51
58:SI:164:ASP:O	58:SI:168:MET:HG3	2.11	0.51
66:SS:225:GLN:HG2	66:SS:226:GLU:H	1.75	0.51
82:So:71:LEU:HD23	82:So:74:LEU:HD12	1.93	0.51
82:So:398:ASN:HA	82:So:401:MET:HE1	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:S1:451:C:OP1	83:S1:504:C:N4	2.44	0.51
1:L1:122:G:N7	27:Lh:87:ARG:NH2	2.59	0.51
23:Lu:187:PRO:HD2	23:Lu:190:LEU:HD12	1.91	0.51
36:Lq:140:PHE:CD1	36:Lq:141:ARG:HG2	2.46	0.51
42:Lx:70:LEU:O	42:Lx:74:VAL:HG12	2.11	0.51
66:SS:91:ARG:HH22	66:SS:103:ASN:HB3	1.75	0.51
17:LU:125:GLY:N	17:LU:160:VAL:O	2.44	0.50
38:Ls:213:THR:HG23	38:Ls:247:VAL:HG22	1.93	0.50
49:L7:98:LYS:CG	49:L7:136:THR:HG23	2.41	0.50
52:Sf:113:VAL:HG21	52:Sf:257:VAL:HG11	1.93	0.50
53:SB:255:THR:O	53:SB:259:ARG:HG3	2.10	0.50
61:SL:58:LEU:CD2	61:SL:85:LEU:HB3	2.36	0.50
75:Se:82:GLY:HA2	75:Se:156:PRO:HB3	1.92	0.50
75:Se:338:ASP:HB3	75:Se:339:PRO:HD3	1.93	0.50
77:Si:11:MET:CA	77:Si:11:MET:CE	2.89	0.50
8:LK:30:MET:C	8:LK:32:GLY:H	2.19	0.50
12:LP:79:ALA:HB3	12:LP:158:ARG:NE	2.23	0.50
31:Ll:213:LEU:HB3	31:Ll:275:GLN:OE1	2.12	0.50
33:Ln:168:LEU:HA	39:Lt:203:LYS:HE2	1.93	0.50
34:Lo:109:PHE:CE2	34:Lo:111:PRO:HA	2.46	0.50
40:Lv:106:TYR:O	40:Lv:110:VAL:HG23	2.11	0.50
46:L4:64:ASP:HB3	46:L4:67:GLN:CB	2.41	0.50
49:L7:98:LYS:CD	49:L7:136:THR:HG21	2.41	0.50
53:SB:102:MET:SD	53:SB:223:VAL:HG12	2.52	0.50
69:SX:253:ILE:HG13	69:SX:258:LYS:H	1.75	0.50
75:Se:205:GLN:HA	75:Se:218:LYS:HE2	1.93	0.50
1:L1:356:A:H2'	1:L1:357:A:C8	2.47	0.50
33:Ln:169:PHE:CE1	40:Lv:91:LEU:HD22	2.45	0.50
42:Lx:78:PHE:HE1	42:Lx:96:LEU:HB3	1.75	0.50
53:SB:233:THR:HG22	70:SY:44:PRO:HG3	1.92	0.50
54:SZ:145:TYR:CD2	82:So:121:ILE:HD13	2.46	0.50
57:SG:114:THR:HG21	57:SG:205:LEU:HD22	1.92	0.50
70:SY:69:ARG:HH11	70:SY:69:ARG:CG	2.25	0.50
75:Se:310:LEU:HD23	75:Se:310:LEU:H	1.77	0.50
76:Sg:328:PHE:HZ	79:Sk:224:TYR:CD2	2.30	0.50
30:Lk:284:PRO:HG2	52:Sf:148:ASP:OD2	2.11	0.50
39:Lt:186:GLY:O	39:Lt:190:ARG:HG2	2.12	0.50
39:Lt:213:TYR:HB2	39:Lt:233:PHE:HE2	1.76	0.50
49:L7:98:LYS:HD2	49:L7:136:THR:CG2	2.42	0.50
78:Sj:73:LEU:HD23	78:Sj:76:LEU:HB2	1.94	0.50
82:So:136:HIS:NE2	82:So:141:MET:HE2	2.25	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:So:372:TYR:O	82:So:375:ILE:HD12	2.11	0.50
83:S1:174:U:H2'	83:S1:175:G:C8	2.45	0.50
83:S1:356:A:H2'	83:S1:357:G:H8	1.76	0.50
1:L1:266:A:H4'	1:L1:267:A:C8	2.46	0.50
1:L1:504:G:H4'	8:LK:151:LEU:CD1	2.42	0.50
1:L1:517:C:H2'	1:L1:518:A:C8	2.47	0.50
5:LD:277:ASP:N	5:LD:277:ASP:OD1	2.44	0.50
6:LI:95:GLU:OE1	6:LI:113:SER:OG	2.25	0.50
8:LK:117:VAL:HG22	8:LK:141:VAL:HG23	1.94	0.50
30:Lk:201:ARG:NH1	30:Lk:418:TYR:O	2.29	0.50
31:Ll:173:LEU:C	31:Ll:173:LEU:HD12	2.36	0.50
37:Lr:47:ARG:O	37:Lr:51:LEU:HD22	2.10	0.50
39:Lt:211:GLY:O	39:Lt:212:HIS:HD2	1.94	0.50
57:SG:44:PRO:HD3	57:SG:75:LYS:HG2	1.93	0.50
73:Sc:356:THR:C	73:Sc:360:VAL:HG23	2.30	0.50
82:So:531:ILE:O	82:So:535:MET:CB	2.59	0.50
83:S1:378:A:H2'	83:S1:379:A:C8	2.45	0.50
1:L1:1183:A:N7	26:Lg:53:ARG:HD3	2.27	0.50
22:Lb:91:TYR:O	22:Lb:92:ALA:C	2.54	0.50
26:Lg:20:MET:HE3	26:Lg:58:GLU:HB2	1.92	0.50
31:Ll:307:HIS:CD2	31:Ll:307:HIS:N	2.79	0.50
39:Lt:94:GLU:HB3	39:Lt:116:LEU:HD12	1.93	0.50
65:SQ:96:THR:HG21	65:SQ:109:PRO:HB3	1.94	0.50
70:SY:74:PHE:HE2	70:SY:99:PHE:HD2	1.56	0.50
7:LJ:84:ARG:NH1	46:L4:113:GLU:OE1	2.45	0.50
9:LM:25:MET:HE3	9:LM:149:ARG:HH22	1.74	0.50
10:LN:142:GLN:OE1	10:LN:142:GLN:N	2.45	0.50
20:LX:102:MET:HG3	20:LX:103:ASP:H	1.77	0.50
31:Ll:257:PRO:HB3	31:Ll:268:LEU:HD21	1.93	0.50
37:Lr:203:LEU:HD13	37:Lr:211:THR:HG21	1.94	0.50
39:Lt:58:VAL:HG13	39:Lt:59:VAL:HG23	1.94	0.50
39:Lt:201:GLU:HG3	39:Lt:239:LEU:HD23	1.92	0.50
53:SB:214:LYS:HE2	83:S1:633:C:H5''	1.94	0.50
73:Sc:86:ASP:OD1	73:Sc:124:LYS:NZ	2.45	0.50
74:Sd:148:GLU:HG2	74:Sd:150:THR:HG23	1.94	0.50
83:S1:514:A:H2'	83:S1:515:A:H8	1.77	0.50
83:S1:824:A:H2'	83:S1:825:G:C8	2.46	0.50
3:LB:157:MET:HE2	3:LB:163:ILE:HG21	1.94	0.50
3:LB:222:GLY:O	3:LB:238:GLU:HG2	2.12	0.50
27:Lh:82:ARG:NH2	27:Lh:87:ARG:HD2	2.27	0.50
31:Ll:136:ARG:NH1	31:Ll:140:GLU:OE2	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Ll:281:PHE:HE1	31:Ll:307:HIS:CE1	2.29	0.50
38:Ls:154:ASN:OD1	38:Ls:156:ASP:HB2	2.11	0.50
56:SF:96:HIS:HB3	56:SF:99:THR:HG23	1.94	0.50
58:SI:117:PHE:HE2	62:SN:124:GLN:OE1	1.95	0.50
59:SJ:77:SER:HA	59:SJ:144:GLU:HA	1.94	0.50
61:SL:114:ARG:HG3	61:SL:116:GLN:HG3	1.94	0.50
71:Sa:23:PHE:HB3	71:Sa:27:VAL:CG1	2.42	0.50
71:Sa:55:ILE:O	71:Sa:59:ASN:ND2	2.45	0.50
73:Sc:231:LEU:HA	73:Sc:234:VAL:HG12	1.93	0.50
83:S1:355:C:H2'	83:S1:356:A:H8	1.77	0.50
1:L1:563:U:N3	4:LC:248:ILE:HG22	2.27	0.50
7:LJ:96:ILE:HA	7:LJ:155:VAL:HG12	1.94	0.50
24:Ld:73:LYS:HG3	24:Ld:74:SER:H	1.77	0.50
63:SO:200:HIS:H	63:SO:200:HIS:CD2	2.28	0.50
78:Sj:25:LEU:HD21	83:S1:884:C:H2'	1.92	0.50
14:LR:83:ILE:HD11	14:LR:92:LEU:CD1	2.40	0.49
30:Lk:216:GLU:OE2	30:Lk:367:ASN:ND2	2.44	0.49
32:Lm:285:ASN:HD22	32:Lm:293:LEU:CD2	2.22	0.49
45:L3:10:LEU:HD21	45:L3:42:VAL:HB	1.93	0.49
72:Sb:45:PRO:HB3	78:Sj:52:VAL:HG21	1.93	0.49
81:Sn:138:MET:HE2	81:Sn:142:LYS:CG	2.42	0.49
83:S1:294:G:C6	83:S1:462:A:C5	3.00	0.49
4:LC:123:GLN:HG3	4:LC:282:ILE:HD13	1.93	0.49
6:LI:117:SER:O	6:LI:121:ASN:OD1	2.31	0.49
8:LK:33:PRO:O	8:LK:34:PRO:C	2.55	0.49
8:LK:75:ASP:OD1	8:LK:75:ASP:N	2.42	0.49
30:Lk:208:THR:HA	30:Lk:224:GLY:O	2.11	0.49
31:Ll:95:PRO:HD3	31:Ll:170:ARG:HD3	1.94	0.49
58:SI:365:ARG:HB2	58:SI:370:LEU:HD12	1.94	0.49
75:Se:53:GLU:HG2	75:Se:58:LYS:HD2	1.93	0.49
20:LX:163:ASP:OD1	20:LX:164:GLY:N	2.46	0.49
22:Lb:24:LEU:HD23	22:Lb:215:GLN:HG3	1.93	0.49
25:Lf:174:ILE:HG22	25:Lf:176:GLU:CD	2.37	0.49
31:Ll:173:LEU:HD22	31:Ll:272:LEU:HB2	1.94	0.49
37:Lr:286:GLY:HA3	37:Lr:291:VAL:HG23	1.94	0.49
38:Ls:168:CYS:HB2	38:Ls:262:HIS:O	2.12	0.49
45:L3:20:PHE:O	45:L3:22:PRO:HD3	2.12	0.49
61:SL:38:ARG:HH11	61:SL:38:ARG:CG	2.23	0.49
64:SP:102:MET:HE1	83:S1:199:A:H4'	1.94	0.49
10:LN:57:CYS:HA	10:LN:75:LEU:HD23	1.94	0.49
33:Ln:127:GLN:OE1	33:Ln:127:GLN:CA	2.61	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:Ls:152:LEU:HD12	38:Ls:160:LEU:CD1	2.42	0.49
38:Ls:203:MET:HE2	38:Ls:203:MET:CA	2.36	0.49
40:Lv:175:GLN:C	40:Lv:175:GLN:CD	2.80	0.49
69:SX:122:ALA:O	69:SX:126:LEU:HB2	2.11	0.49
77:Si:18:LEU:CD2	79:Sk:229:LEU:CD2	2.90	0.49
1:L1:372:U:O2'	11:LO:68:GLU:HG2	2.12	0.49
12:LP:79:ALA:HB3	12:LP:158:ARG:HH21	1.76	0.49
22:Lb:35:GLU:OE1	22:Lb:35:GLU:N	2.46	0.49
38:Ls:196:GLN:HG2	38:Ls:198:ARG:HH22	1.67	0.49
41:Lw:81:ASN:O	41:Lw:82:LEU:HD12	2.11	0.49
42:Lx:148:LEU:HD22	42:Lx:152:LEU:HD23	1.93	0.49
56:SF:112:PRO:HG2	80:Sm:7:ARG:NH2	2.25	0.49
62:SN:113:HIS:CE1	62:SN:117:HIS:CE1	3.00	0.49
65:SQ:57:GLN:HB2	65:SQ:84:ILE:HD11	1.95	0.49
82:So:546:VAL:O	82:So:550:ASP:OD2	2.30	0.49
20:LX:60:ASP:OD1	20:LX:61:THR:N	2.45	0.49
54:SZ:145:TYR:HE1	82:So:140:LEU:HD22	1.77	0.49
64:SP:20:ARG:HB2	83:S1:192:A:H5'	1.95	0.49
79:Sk:152:ASP:O	79:Sk:171:VAL:HA	2.13	0.49
82:So:526:ASP:OD1	82:So:526:ASP:N	2.43	0.49
83:S1:793:G:H2'	83:S1:794:A:C8	2.48	0.49
31:Ll:257:PRO:HB3	31:Ll:268:LEU:CD2	2.42	0.49
37:Lr:152:GLY:O	37:Lr:156:LEU:HD13	2.12	0.49
39:Lt:55:ARG:HD3	39:Lt:157:LEU:HD23	1.95	0.49
53:SB:131:PHE:O	53:SB:135:MET:HG2	2.13	0.49
59:SJ:158:GLU:OE1	76:Sg:313:PHE:HB3	2.12	0.49
65:SQ:93:ASP:HB3	65:SQ:96:THR:O	2.12	0.49
69:SX:70:PHE:HD1	69:SX:71:MET:HE3	1.67	0.49
78:Sj:202:ASP:OD1	78:Sj:202:ASP:N	2.45	0.49
1:L1:320:G:OP1	3:LB:269:ARG:NH1	2.37	0.49
9:LM:154:ARG:HG2	51:SR:127:LEU:HA	1.94	0.49
40:Lv:92:ASN:ND2	40:Lv:92:ASN:N	2.60	0.49
42:Lx:78:PHE:CE1	42:Lx:96:LEU:HB3	2.48	0.49
49:L7:70:ASP:N	49:L7:70:ASP:OD1	2.45	0.49
53:SB:155:ILE:HD12	53:SB:196:LEU:HD12	1.95	0.49
58:SI:234:GLY:O	58:SI:238:GLU:HG2	2.13	0.49
66:SS:58:TYR:CD1	66:SS:64:TYR:HB2	2.48	0.49
69:SX:209:ILE:HD12	69:SX:214:ASN:HB3	1.93	0.49
83:S1:726:U:H2'	83:S1:727:A:C8	2.47	0.49
1:L1:844:C:H2'	1:L1:845:U:H6	1.77	0.49
1:L1:1330:A:H2'	1:L1:1331:G:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:L3:20:PHE:HZ	45:L3:34:LEU:HB2	1.77	0.49
53:SB:219:THR:HG22	53:SB:232:ILE:HG23	1.93	0.49
54:SZ:91:PHE:CE2	77:Si:58:TYR:CD1	3.00	0.49
69:SX:185:SER:O	69:SX:189:ARG:HB2	2.13	0.49
78:Sj:195:ARG:O	78:Sj:195:ARG:NE	2.43	0.49
79:Sk:73:ALA:HB2	79:Sk:113:HIS:CE1	2.48	0.49
82:So:370:ALA:N	82:So:412:ASP:OD1	2.46	0.49
82:So:579:ILE:C	82:So:595:MET:HE1	2.37	0.49
83:S1:940:U:H2'	83:S1:941:G:H8	1.78	0.49
4:LC:145:LEU:CD1	4:LC:181:ILE:HD13	2.39	0.49
18:LV:123:GLU:O	18:LV:127:MET:HG2	2.12	0.49
30:Lk:105:TYR:CZ	30:Lk:262:ILE:HD13	2.48	0.49
63:SO:120:GLU:N	63:SO:120:GLU:OE1	2.45	0.49
78:Sj:44:PRO:O	78:Sj:46:SER:N	2.45	0.49
78:Sj:207:GLN:HA	78:Sj:210:LYS:HB2	1.95	0.49
4:LC:201:GLY:N	4:LC:273:VAL:O	2.43	0.48
11:LO:140:LEU:HG	11:LO:163:ALA:HB1	1.95	0.48
51:SR:40:GLU:HA	51:SR:49:ILE:HG22	1.94	0.48
54:SZ:145:TYR:HD2	82:So:121:ILE:HG21	1.78	0.48
60:SK:136:ALA:HA	60:SK:170:LEU:CD2	2.43	0.48
63:SO:90:LYS:O	63:SO:94:SER:HB3	2.13	0.48
64:SP:31:PHE:CZ	64:SP:53:SER:HB2	2.48	0.48
65:SQ:53:ASP:OD1	65:SQ:53:ASP:O	2.30	0.48
69:SX:338:LYS:HG3	69:SX:341:TYR:HB2	1.95	0.48
79:Sk:320:LEU:CD1	79:Sk:320:LEU:C	2.80	0.48
83:S1:191:U:H2'	83:S1:192:A:H8	1.78	0.48
83:S1:262:G:H2'	83:S1:263:A:H8	1.78	0.48
83:S1:930:U:H2'	83:S1:931:A:C8	2.47	0.48
1:L1:547:C:OP1	7:LJ:128:ASN:OD1	2.31	0.48
1:L1:1543:A:H2'	1:L1:1544:C:C6	2.49	0.48
5:LD:72:PHE:CE2	42:Lx:52:CYS:CB	2.96	0.48
11:LO:30:ASN:O	11:LO:33:SER:OG	2.24	0.48
40:Lv:146:LEU:HD23	40:Lv:147:ASP:C	2.36	0.48
42:Lx:132:VAL:O	42:Lx:132:VAL:CG1	2.61	0.48
49:L7:98:LYS:CD	49:L7:136:THR:CG2	2.91	0.48
65:SQ:32:ARG:NH2	65:SQ:49:TYR:OH	2.46	0.48
66:SS:149:ARG:HA	66:SS:152:GLN:OE1	2.13	0.48
69:SX:167:HIS:O	69:SX:189:ARG:NH1	2.44	0.48
79:Sk:214:LEU:HB2	79:Sk:217:GLN:HE21	1.77	0.48
82:So:464:LEU:O	82:So:468:MET:SD	2.71	0.48
1:L1:1184:U:H4'	28:Li:138:PRO:HG2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:LB:218:ARG:HE	3:LB:225:ILE:HD12	1.78	0.48
17:LU:130:LEU:HB2	17:LU:156:VAL:HB	1.95	0.48
31:Ll:329:TYR:HD1	31:Ll:333:GLN:HG2	1.79	0.48
33:Ln:110:GLU:OE1	33:Ln:114:ARG:NH1	2.46	0.48
38:Ls:154:ASN:ND2	38:Ls:156:ASP:HB2	2.27	0.48
40:Lv:101:THR:HG22	47:L5:41:THR:HG22	1.94	0.48
53:SB:98:ARG:HG3	53:SB:225:THR:HG23	1.95	0.48
53:SB:220:VAL:HG22	53:SB:234:TYR:HB2	1.96	0.48
63:SO:81:GLY:HA2	63:SO:84:LYS:HZ3	1.78	0.48
63:SO:108:GLN:O	63:SO:112:MET:HB2	2.12	0.48
66:SS:173:ARG:HH21	69:SX:193:ILE:HG21	1.77	0.48
69:SX:70:PHE:CD1	69:SX:71:MET:HE1	2.47	0.48
69:SX:314:ALA:O	69:SX:318:LYS:HD3	2.13	0.48
72:Sb:42:VAL:HA	78:Sj:49:ARG:HH22	1.76	0.48
73:Sc:129:LEU:HD12	73:Sc:166:GLU:CD	2.38	0.48
73:Sc:320:GLU:OE1	73:Sc:320:GLU:N	2.47	0.48
7:LJ:143:LEU:HD22	7:LJ:146:LEU:HD22	1.95	0.48
37:Lr:132:PHE:CE2	37:Lr:211:THR:HG23	2.48	0.48
37:Lr:288:THR:H	37:Lr:291:VAL:HG22	1.78	0.48
40:Lv:93:ILE:HG12	40:Lv:186:VAL:HG12	1.96	0.48
49:L7:98:LYS:HG3	49:L7:138:GLU:HG2	1.95	0.48
49:L7:135:LEU:HD11	49:L7:157:MET:HE3	1.93	0.48
51:SR:39:VAL:HG21	51:SR:52:ARG:HH12	1.59	0.48
65:SQ:96:THR:O	65:SQ:98:LYS:N	2.38	0.48
73:Sc:105:ARG:HB2	73:Sc:108:THR:HG22	1.95	0.48
77:Si:81:GLU:HG3	77:Si:84:ARG:HH21	1.78	0.48
80:Sm:39:GLU:HA	80:Sm:40:LYS:NZ	2.28	0.48
1:Ll:411:U:H1'	24:Ld:105:SER:OG	2.13	0.48
3:LB:218:ARG:HH11	3:LB:218:ARG:HG3	1.78	0.48
4:LC:135:LYS:CD	4:LC:140:GLY:O	2.62	0.48
4:LC:142:MET:HE3	4:LC:180:ASN:HB3	1.94	0.48
9:LM:140:ASN:ND2	37:Lr:264:THR:H	2.07	0.48
14:LR:170:VAL:HG21	49:L7:180:ILE:HD13	1.95	0.48
15:LS:252:GLN:OE1	15:LS:252:GLN:O	2.32	0.48
18:LV:195:HIS:ND1	35:Lp:108:MET:HE3	2.27	0.48
37:Lr:148:MET:HE1	37:Lr:307:PHE:HB2	1.96	0.48
39:Lt:46:ARG:N	39:Lt:228:GLY:O	2.42	0.48
45:L3:83:ALA:O	45:L3:87:LEU:HD12	2.13	0.48
49:L7:113:GLU:N	49:L7:114:PRO:HD2	2.28	0.48
55:SE:89:PHE:HA	55:SE:92:LYS:HG2	1.95	0.48
55:SE:171:ASP:O	55:SE:175:GLN:HG3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:S1:24:U:H2'	83:S1:25:A:H8	1.78	0.48
1:L1:39:G:H4'	23:Lu:192:LYS:HG3	1.96	0.48
1:L1:141:A:H4'	18:LV:50:LYS:HD2	1.96	0.48
1:L1:1086:C:H2'	1:L1:1087:A:C8	2.48	0.48
4:LC:106:MET:CE	4:LC:287:GLY:O	2.61	0.48
15:LS:250:THR:HG23	15:LS:253:GLN:H	1.79	0.48
30:Lk:68:PRO:HG2	30:Lk:69:TRP:CE3	2.49	0.48
30:Lk:329:TYR:HD2	30:Lk:336:LEU:HD22	1.79	0.48
32:Lm:148:MET:HE2	32:Lm:257:ILE:CG1	2.41	0.48
38:Ls:152:LEU:HD11	38:Ls:172:MET:HG2	1.94	0.48
54:SZ:91:PHE:CD2	77:Si:58:TYR:HD1	2.31	0.48
58:SI:155:LYS:NZ	58:SI:217:ASP:OD2	2.43	0.48
58:SI:293:ILE:HD12	58:SI:328:VAL:HB	1.96	0.48
63:SO:167:LEU:HD11	63:SO:187:ILE:CD1	2.27	0.48
73:Sc:190:LEU:HD12	73:Sc:352:LEU:HD11	1.95	0.48
79:Sk:60:MET:CE	79:Sk:66:TRP:CZ3	2.97	0.48
81:Sn:174:ARG:HA	81:Sn:177:TRP:CE3	2.49	0.48
83:S1:35:A:H2'	83:S1:36:G:H8	1.78	0.48
83:S1:694:C:H5''	83:S1:695:C:H4'	1.94	0.48
5:LD:72:PHE:HD1	5:LD:72:PHE:H	1.62	0.48
11:LO:175:THR:HG21	11:LO:259:ARG:HD2	1.94	0.48
12:LP:191:SER:H	12:LP:194:THR:HG1	1.59	0.48
20:LX:64:ILE:O	20:LX:71:GLY:N	2.46	0.48
20:LX:118:ARG:HD2	20:LX:118:ARG:N	2.29	0.48
56:SF:17:GLU:OE1	56:SF:17:GLU:N	2.46	0.48
72:Sb:29:THR:HG22	83:S1:64:U:OP2	2.14	0.48
75:Se:269:TRP:CZ2	75:Se:294:ARG:HG2	2.49	0.48
82:So:397:MET:O	82:So:400:LEU:N	2.47	0.48
83:S1:842:G:H2'	83:S1:843:U:H6	1.79	0.48
8:LK:140:VAL:O	8:LK:144:ILE:HG12	2.14	0.48
11:LO:184:LEU:HA	11:LO:187:VAL:HG12	1.96	0.48
24:Ld:84:ASP:HA	24:Ld:87:LYS:HE2	1.96	0.48
24:Ld:86:ILE:HG12	24:Ld:113:VAL:HG21	1.95	0.48
38:Ls:202:MET:HA	38:Ls:208:VAL:HG22	1.95	0.48
39:Lt:174:PRO:HB3	39:Lt:195:LEU:HD21	1.96	0.48
39:Lt:201:GLU:H	39:Lt:241:GLY:HA3	1.79	0.48
41:Lw:38:PHE:HE1	41:Lw:40:GLU:HG3	1.78	0.48
53:SB:223:VAL:HG13	53:SB:227:CYS:HB2	1.96	0.48
58:SI:318:HIS:ND1	58:SI:318:HIS:O	2.46	0.48
58:SI:344:ILE:HG22	58:SI:348:MET:SD	2.54	0.48
70:SY:99:PHE:HD1	70:SY:99:PHE:C	2.22	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:Sj:11:ILE:HB	83:S1:159:C:C2	2.48	0.48
78:Sj:58:VAL:HA	78:Sj:137:HIS:HD2	1.79	0.48
82:So:339:LEU:HA	82:So:342:LEU:HG	1.95	0.48
83:S1:611:A:N7	83:S1:683:C:H5''	2.29	0.48
83:S1:755:A:H3'	83:S1:756:A:H8	1.78	0.48
1:L1:551:C:O2'	1:L1:553:A:N6	2.47	0.48
1:L1:1035:U:OP2	9:LM:119:ARG:NH2	2.40	0.48
1:L1:1087:A:H5'	6:LI:122:ARG:NH2	2.29	0.48
1:L1:1397:U:OP1	4:LC:234:THR:OG1	2.30	0.48
7:LJ:193:ASN:C	7:LJ:195:SER:H	2.20	0.48
11:LO:197:GLY:HA3	50:L8:62:ALA:HB2	1.95	0.48
15:LS:251:GLU:N	15:LS:251:GLU:OE1	2.47	0.48
19:LW:74:HIS:HB2	34:Lo:24:LYS:HE3	1.95	0.48
23:Lu:83:ALA:N	34:Lo:74:VAL:O	2.47	0.48
39:Lt:212:HIS:HA	39:Lt:231:VAL:O	2.13	0.48
45:L3:66:VAL:HG11	45:L3:90:PHE:HE1	1.78	0.48
50:L8:48:PRO:CB	50:L8:50:TRP:CD1	2.97	0.48
61:SL:42:PRO:HD3	83:S1:284:C:C2	2.47	0.48
62:SN:126:ALA:HB1	62:SN:128:TRP:HZ3	1.79	0.48
68:SW:30:LEU:HD22	68:SW:35:LEU:HD22	1.95	0.48
69:SX:237:PRO:HA	69:SX:242:TYR:CG	2.49	0.48
5:LD:138:HIS:CD2	5:LD:146:TRP:HE1	2.31	0.48
5:LD:214:ASP:OD1	5:LD:257:GLN:OE1	2.32	0.48
6:LI:84:GLU:OE1	22:Lb:44:ARG:NH2	2.47	0.48
9:LM:94:GLN:O	9:LM:98:ARG:HG3	2.14	0.48
18:LV:197:LYS:HB3	18:LV:197:LYS:HZ1	1.78	0.48
21:La:119:ARG:NH2	40:Lv:63:ILE:HD12	2.29	0.48
31:Ll:329:TYR:CD1	31:Ll:333:GLN:HG2	2.49	0.48
32:Lm:239:PHE:HZ	32:Lm:265:GLU:HG2	1.79	0.48
51:SR:58:LYS:HE3	51:SR:58:LYS:HB3	1.68	0.48
52:Sf:239:ASN:HB2	52:Sf:299:PHE:HB2	1.94	0.48
54:SZ:61:TYR:HB3	54:SZ:65:ARG:HB2	1.94	0.48
62:SN:103:ARG:HB3	62:SN:104:TRP:CE3	2.49	0.48
66:SS:58:TYR:CE2	66:SS:112:LYS:HB2	2.49	0.48
70:SY:85:PHE:O	74:Sd:101:ILE:HD12	2.13	0.48
73:Sc:364:LEU:HD12	73:Sc:364:LEU:C	2.38	0.48
81:Sn:142:LYS:HZ2	83:S1:842:G:H5''	1.78	0.48
83:S1:942:C:H2'	83:S1:943:A:C8	2.49	0.48
58:SI:361:VAL:HG23	58:SI:364:MET:HE2	1.95	0.47
62:SN:41:ARG:CD	77:Si:48:THR:O	2.62	0.47
73:Sc:169:MET:HE1	73:Sc:247:MET:HB2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:So:63:LYS:HG3	82:So:65:TRP:NE1	2.29	0.47
82:So:462:PHE:HE2	82:So:496:LEU:HD22	1.78	0.47
17:LU:94:ARG:HG3	36:Lq:126:ILE:HD13	1.96	0.47
34:Lo:109:PHE:CE2	34:Lo:111:PRO:CA	2.97	0.47
53:SB:196:LEU:HD23	53:SB:196:LEU:HA	1.79	0.47
62:SN:57:LEU:C	62:SN:57:LEU:CD2	2.83	0.47
63:SO:109:GLU:CA	63:SO:112:MET:HB2	2.43	0.47
63:SO:211:ILE:O	63:SO:215:GLN:HG2	2.14	0.47
67:ST:67:LEU:HD21	67:ST:79:LEU:HD11	1.96	0.47
75:Se:210:TRP:CD1	75:Se:228:GLN:HG2	2.49	0.47
79:Sk:56:ARG:HA	79:Sk:59:LYS:HB3	1.95	0.47
79:Sk:148:PRO:HB3	79:Sk:179:SER:OG	2.13	0.47
82:So:464:LEU:O	82:So:468:MET:CE	2.62	0.47
4:LC:219:MET:SD	4:LC:238:ARG:HG2	2.55	0.47
8:LK:127:ASP:OD1	8:LK:128:GLU:N	2.47	0.47
30:Lk:146:HIS:O	30:Lk:194:LYS:NZ	2.48	0.47
36:Lq:140:PHE:CE1	36:Lq:141:ARG:HG2	2.49	0.47
39:Lt:124:TRP:CE2	47:L5:72:ARG:HG2	2.49	0.47
52:Sf:257:VAL:HG21	52:Sf:392:ILE:HD12	1.97	0.47
66:SS:205:TRP:CZ3	66:SS:230:PRO:HB3	2.48	0.47
70:SY:97:GLN:HA	70:SY:100:VAL:HG12	1.96	0.47
72:Sb:36:LYS:O	72:Sb:39:ILE:HG22	2.14	0.47
83:S1:334:C:H2'	83:S1:335:A:H8	1.79	0.47
83:S1:554:A:H2'	83:S1:555:G:C8	2.49	0.47
1:L1:1371:U:H4'	1:L1:1372:U:OP1	2.15	0.47
1:L1:1384:G:H2'	1:L1:1385:U:C6	2.49	0.47
1:L1:1480:U:H2'	1:L1:1481:A:C8	2.50	0.47
4:LC:248:ILE:HD12	4:LC:248:ILE:O	2.15	0.47
6:LI:138:LYS:HA	6:LI:141:GLU:HG3	1.96	0.47
7:LJ:64:CYS:SG	51:SR:73:CYS:SG	3.12	0.47
14:LR:79:ARG:CD	14:LR:146:GLN:NE2	2.78	0.47
18:LV:195:HIS:CE1	35:Lp:108:MET:HE3	2.50	0.47
20:LX:144:VAL:HG13	20:LX:153:ILE:HG23	1.96	0.47
31:Ll:187:VAL:HG11	31:Ll:270:PHE:HE2	1.78	0.47
37:Lr:39:PHE:CZ	37:Lr:43:LYS:HE3	2.50	0.47
45:L3:33:PHE:HD2	45:L3:86:MET:HE3	1.80	0.47
60:SK:145:ILE:HG22	60:SK:146:HIS:ND1	2.30	0.47
62:SN:37:ASP:HB3	77:Si:52:TYR:CE2	2.49	0.47
75:Se:334:PHE:CE1	75:Se:340:PHE:HE2	2.32	0.47
82:So:75:ALA:O	82:So:78:VAL:O	2.32	0.47
82:So:615:MET:HB3	82:So:648:ARG:CZ	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:S1:356:A:H2'	83:S1:357:G:C8	2.50	0.47
1:L1:39:G:H5'	23:Lu:192:LYS:HE3	1.97	0.47
1:L1:335:C:H2'	1:L1:336:C:C6	2.50	0.47
1:L1:371:U:H2'	1:L1:372:U:C6	2.49	0.47
1:L1:1339:C:O2'	1:L1:1445:U:OP1	2.28	0.47
5:LD:282:PRO:O	5:LD:290:TYR:OH	2.18	0.47
8:LK:171:ARG:O	8:LK:175:LEU:HB2	2.15	0.47
13:LQ:63:GLY:HA2	13:LQ:90:PHE:CE1	2.50	0.47
25:Lf:169:ASP:HA	25:Lf:172:LYS:HD2	1.96	0.47
38:Ls:152:LEU:HD21	38:Ls:172:MET:CG	2.45	0.47
40:Lv:135:LEU:HB2	40:Lv:145:LEU:HB2	1.96	0.47
57:SG:193:ASP:OD1	57:SG:193:ASP:N	2.47	0.47
58:SI:87:HIS:C	58:SI:91:MET:HE1	2.40	0.47
66:SS:211:ARG:NH1	73:Sc:317:LEU:HD11	2.29	0.47
68:SW:35:LEU:O	68:SW:39:ILE:HG13	2.14	0.47
69:SX:161:ILE:O	69:SX:170:ARG:NH2	2.30	0.47
72:Sb:150:ALA:O	72:Sb:154:GLU:HG2	2.15	0.47
77:Si:71:TYR:HE2	77:Si:73:ASP:HB3	1.79	0.47
1:L1:283:A:O2'	1:L1:793:A:OP1	2.30	0.47
10:LN:130:ARG:C	10:LN:132:GLY:N	2.71	0.47
12:LP:105:MET:HE2	12:LP:183:LEU:HD21	1.96	0.47
33:Ln:149:GLU:CB	39:Lt:212:HIS:ND1	2.77	0.47
40:Lv:122:GLU:N	40:Lv:158:GLN:O	2.48	0.47
42:Lx:63:PRO:HG2	42:Lx:108:LEU:HD22	1.97	0.47
52:Sf:113:VAL:HG22	52:Sf:392:ILE:HD13	1.97	0.47
58:SI:91:MET:CG	79:Sk:66:TRP:CG	2.96	0.47
66:SS:192:THR:O	66:SS:195:SER:O	2.32	0.47
69:SX:242:TYR:CZ	69:SX:246:HIS:CE1	3.02	0.47
82:So:533:MET:HE3	82:So:533:MET:CA	2.43	0.47
83:S1:191:U:H2'	83:S1:192:A:C8	2.49	0.47
1:L1:108:U:C5	5:LD:121:ARG:HD3	2.49	0.47
1:L1:395:A:C5	21:La:74:ARG:HD2	2.50	0.47
1:L1:501:U:N3	1:L1:503:G:H4'	2.28	0.47
1:L1:722:U:H2'	1:L1:724:A:H62	1.79	0.47
1:L1:1007:A:H2'	1:L1:1008:A:C8	2.50	0.47
1:L1:1078:A:H2'	1:L1:1079:A:C8	2.50	0.47
8:LK:87:VAL:HG22	8:LK:124:LYS:HE3	1.95	0.47
13:LQ:55:TYR:CD1	15:LS:269:MET:HB2	2.50	0.47
13:LQ:55:TYR:HD1	15:LS:269:MET:HB2	1.78	0.47
16:LT:59:LEU:HD12	16:LT:59:LEU:HA	1.70	0.47
22:Lb:169:LEU:HD21	22:Lb:191:TYR:O	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Ld:84:ASP:O	24:Ld:88:MET:HG3	2.14	0.47
26:Lg:16:ILE:HG13	26:Lg:16:ILE:O	2.14	0.47
26:Lg:54:VAL:CB	50:L8:128:MET:HE2	2.40	0.47
28:Li:157:LEU:HG	28:Li:161:MET:HE2	1.95	0.47
32:Lm:289:THR:HG23	32:Lm:293:LEU:HD13	1.95	0.47
35:Lp:73:LYS:HG2	35:Lp:74:PRO:HD2	1.97	0.47
39:Lt:212:HIS:NE2	39:Lt:232:PHE:CZ	2.75	0.47
42:Lx:77:VAL:HG12	42:Lx:78:PHE:HD1	1.80	0.47
45:L3:72:HIS:CE1	45:L3:97:ARG:NH2	2.83	0.47
49:L7:72:PRO:HB2	49:L7:75:ARG:HB2	1.96	0.47
49:L7:113:GLU:OE1	49:L7:113:GLU:HA	2.13	0.47
49:L7:118:LYS:NZ	49:L7:118:LYS:HB2	2.30	0.47
55:SE:241:ILE:HG21	55:SE:264:ARG:HG3	1.96	0.47
57:SG:231:GLU:O	57:SG:234:ARG:HG3	2.15	0.47
58:SI:108:ILE:O	58:SI:109:ALA:C	2.58	0.47
66:SS:217:ARG:HH12	73:Sc:318:ASP:HB2	1.80	0.47
69:SX:338:LYS:HE3	69:SX:341:TYR:HB2	1.96	0.47
73:Sc:163:VAL:O	73:Sc:167:VAL:HG23	2.14	0.47
78:Sj:65:LEU:HG	78:Sj:112:GLY:H	1.80	0.47
82:So:267:VAL:HG22	82:So:300:ALA:HB2	1.96	0.47
82:So:312:LYS:HD2	82:So:345:PHE:HZ	1.79	0.47
82:So:470:GLN:HE22	82:So:472:ASP:HB2	1.79	0.47
83:S1:205:A:H3'	83:S1:206:C:C6	2.49	0.47
32:Lm:156:ARG:HH12	32:Lm:259:ASP:HB2	1.79	0.47
32:Lm:168:ARG:NH2	32:Lm:326:GLU:OE2	2.46	0.47
36:Lq:48:GLU:HG2	42:Lx:139:LYS:HE2	1.95	0.47
37:Lr:129:GLY:HA3	37:Lr:196:PHE:O	2.14	0.47
37:Lr:227:GLU:OE1	37:Lr:302:ARG:NH1	2.47	0.47
50:L8:40:PRO:HG3	50:L8:51:GLN:HB3	1.96	0.47
59:SJ:111:PRO:HA	59:SJ:112:PRO:HD3	1.75	0.47
60:SK:79:LYS:CB	60:SK:82:GLU:OE2	2.61	0.47
71:Sa:60:PRO:HG2	71:Sa:61:TRP:CD1	2.50	0.47
1:L1:751:G:H5''	34:Lo:24:LYS:HG2	1.96	0.47
3:LB:218:ARG:NH1	3:LB:218:ARG:CB	2.78	0.47
4:LC:129:VAL:HG12	4:LC:189:PRO:HA	1.96	0.47
5:LD:281:ARG:HG3	11:LO:125:ARG:HD3	1.96	0.47
31:Ll:329:TYR:HE1	31:Ll:333:GLN:HB2	1.79	0.47
36:Lq:114:ARG:HH21	36:Lq:116:ARG:HG2	1.79	0.47
40:Lv:145:LEU:HD12	40:Lv:145:LEU:H	1.80	0.47
44:Lz:32:GLY:O	44:Lz:40:TYR:OH	2.29	0.47
49:L7:189:ARG:O	49:L7:189:ARG:CD	2.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:SG:92:SER:O	57:SG:96:ASN:ND2	2.48	0.47
67:ST:138:ILE:HD13	67:ST:140:TYR:CZ	2.49	0.47
71:Sa:136:LEU:HD12	71:Sa:136:LEU:N	2.30	0.47
79:Sk:56:ARG:NH1	82:So:91:ASP:HB3	2.30	0.47
82:So:441:THR:OG1	82:So:444:ASN:ND2	2.47	0.47
83:S1:35:A:H2'	83:S1:36:G:C8	2.50	0.47
83:S1:226:G:H1'	83:S1:274:U:H1'	1.97	0.47
1:L1:19:C:H5''	22:Lb:5:LYS:HG2	1.97	0.47
1:L1:437:G:H5''	12:LP:144:LYS:HD2	1.97	0.47
1:L1:1022:G:O6	1:L1:1025:G:H5''	2.14	0.47
4:LC:107:MET:HE3	4:LC:121:LEU:HD11	1.97	0.47
9:LM:28:PRO:HG3	9:LM:65:ILE:HD12	1.96	0.47
29:Lj:72:LEU:HD22	29:Lj:100:GLN:HB3	1.97	0.47
57:SG:147:GLN:OE1	57:SG:151:ASN:ND2	2.48	0.47
59:SJ:65:ILE:H	59:SJ:65:ILE:HD12	1.80	0.47
63:SO:82:ILE:O	63:SO:85:VAL:HG22	2.15	0.47
63:SO:106:ILE:HA	63:SO:109:GLU:HG3	1.96	0.47
69:SX:349:TYR:O	69:SX:353:LEU:HG	2.14	0.47
70:SY:99:PHE:C	70:SY:99:PHE:CD1	2.92	0.47
72:Sb:45:PRO:CB	78:Sj:53:ARG:HH21	2.07	0.47
75:Se:159:HIS:CD2	75:Se:267:ALA:HB2	2.49	0.47
82:So:335:PHE:CG	82:So:360:MET:SD	3.08	0.47
15:LS:250:THR:O	15:LS:254:MET:HG2	2.15	0.46
17:LU:71:GLU:OE1	17:LU:74:ARG:NH2	2.48	0.46
22:Lb:9:TRP:CD1	22:Lb:9:TRP:H	2.31	0.46
32:Lm:193:MET:HE1	32:Lm:285:ASN:OD1	2.16	0.46
37:Lr:81:GLU:OE1	37:Lr:210:ARG:HD2	2.14	0.46
41:Lw:154:ASP:OD1	41:Lw:154:ASP:N	2.46	0.46
46:L4:107:LEU:CD1	46:L4:117:TYR:CE1	2.95	0.46
53:SB:183:PHE:CB	53:SB:187:VAL:HG11	2.45	0.46
55:SE:249:ASN:OD1	55:SE:253:ALA:HB3	2.14	0.46
69:SX:167:HIS:HA	69:SX:170:ARG:HH11	1.81	0.46
69:SX:276:VAL:HG22	69:SX:281:ILE:HG21	1.97	0.46
73:Sc:241:ARG:HA	73:Sc:244:TYR:CE1	2.50	0.46
78:Sj:19:ARG:NH1	83:S1:161:C:OP1	2.48	0.46
80:Sm:104:LEU:HD23	80:Sm:104:LEU:HA	1.82	0.46
83:S1:514:A:H2'	83:S1:515:A:C8	2.50	0.46
5:LD:69:LEU:HB3	5:LD:195:LEU:HD23	1.95	0.46
7:LJ:168:LEU:HD22	7:LJ:174:LEU:HD23	1.97	0.46
8:LK:42:ARG:HB3	8:LK:44:VAL:HG23	1.97	0.46
8:LK:127:ASP:O	8:LK:131:ALA:HB2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:LX:63:GLU:OE1	20:LX:73:GLN:NE2	2.48	0.46
20:LX:73:GLN:OE1	20:LX:123:VAL:HG11	2.14	0.46
30:Lk:115:GLU:HB2	30:Lk:119:GLN:HB2	1.96	0.46
39:Lt:51:LEU:HD13	39:Lt:188:ALA:HB1	1.97	0.46
43:Ly:32:ILE:HD13	43:Ly:32:ILE:HA	1.76	0.46
49:L7:152:GLN:OE1	49:L7:152:GLN:O	2.33	0.46
63:SO:172:ASN:O	63:SO:172:ASN:OD1	2.33	0.46
82:So:507:GLU:HA	82:So:544:LEU:HD11	1.97	0.46
83:S1:817:G:H21	83:S1:819:C:H42	1.62	0.46
1:L1:773:C:H5'	1:L1:774:A:C5	2.50	0.46
1:L1:1280:U:H2'	1:L1:1281:A:H8	1.81	0.46
4:LC:187:ILE:CG2	4:LC:191:THR:HG21	2.46	0.46
11:LO:202:LYS:HB2	11:LO:263:ARG:HG3	1.97	0.46
13:LQ:97:TYR:OH	13:LQ:125:TYR:HB3	2.15	0.46
39:Lt:53:LEU:HD12	39:Lt:254:TRP:HH2	1.81	0.46
50:L8:129:PRO:O	50:L8:133:VAL:HG13	2.15	0.46
60:SK:172:VAL:O	68:SW:14:VAL:HG21	2.15	0.46
61:SL:62:VAL:HA	61:SL:83:VAL:HG22	1.97	0.46
79:Sk:92:LYS:HE3	83:S1:655:C:OP2	2.15	0.46
83:S1:817:G:H21	83:S1:819:C:N4	2.14	0.46
1:L1:1199:A:P	28:Li:124:ARG:HH22	2.39	0.46
1:L1:1534:C:H5''	1:L1:1534:C:H6	1.80	0.46
31:Ll:233:LEU:HB2	31:Ll:298:PHE:HB2	1.97	0.46
32:Lm:81:MET:HE1	32:Lm:94:HIS:CD2	2.51	0.46
32:Lm:160:ASP:OD1	32:Lm:160:ASP:N	2.48	0.46
36:Lq:3:ALA:HB1	36:Lq:114:ARG:HH11	1.80	0.46
36:Lq:48:GLU:OE2	48:L6:101:TRP:NE1	2.48	0.46
38:Ls:95:ALA:HB2	38:Ls:243:LEU:HD22	1.97	0.46
57:SG:46:ILE:O	57:SG:46:ILE:HG22	2.15	0.46
60:SK:74:ARG:CD	60:SK:78:LYS:O	2.61	0.46
69:SX:128:MET:HE3	69:SX:128:MET:HB3	1.67	0.46
69:SX:172:ILE:HD13	69:SX:189:ARG:HG2	1.97	0.46
70:SY:102:LYS:O	70:SY:105:GLU:HB3	2.15	0.46
79:Sk:174:ARG:HA	79:Sk:205:LEU:O	2.16	0.46
82:So:646:THR:C	82:So:650:MET:HE2	2.40	0.46
2:L2:41:G:H2'	2:L2:42:A:C8	2.51	0.46
12:LP:169:PHE:O	12:LP:173:GLN:CB	2.62	0.46
14:LR:49:ASN:HD22	14:LR:50:ARG:H	1.63	0.46
20:LX:211:LYS:H	20:LX:211:LYS:HG2	1.41	0.46
24:Ld:101:LYS:HE3	44:Lz:80:LEU:HD22	1.97	0.46
31:Ll:233:LEU:HD21	31:Ll:236:LEU:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:Lr:248:ARG:HE	37:Lr:248:ARG:HB3	1.49	0.46
42:Lx:132:VAL:O	42:Lx:132:VAL:HG13	2.15	0.46
55:SE:295:SER:HB3	55:SE:304:LYS:HE3	1.97	0.46
59:SJ:119:THR:OG1	59:SJ:133:GLN:HG2	2.15	0.46
62:SN:57:LEU:O	62:SN:60:ASN:OD1	2.34	0.46
63:SO:92:LEU:CD2	72:Sb:160:LEU:HD21	2.45	0.46
65:SQ:96:THR:C	65:SQ:98:LYS:H	2.22	0.46
67:ST:125:LYS:O	67:ST:126:ASP:C	2.59	0.46
67:ST:126:ASP:HB3	67:ST:129:TYR:CD2	2.50	0.46
81:Sn:141:HIS:HE1	83:S1:938:A:H62	1.62	0.46
81:Sn:142:LYS:NZ	83:S1:842:G:H5''	2.31	0.46
83:S1:16:A:H2'	83:S1:17:G:C8	2.50	0.46
83:S1:160:A:H1'	83:S1:161:C:H5	1.79	0.46
83:S1:397:U:OP1	83:S1:463:A:O2'	2.33	0.46
83:S1:586:C:H1'	83:S1:755:A:H61	1.80	0.46
1:L1:416:A:H2'	1:L1:417:U:C6	2.51	0.46
1:L1:452:A:H5'	24:Ld:77:ARG:HG3	1.97	0.46
5:LD:201:GLN:O	5:LD:205:GLU:OE1	2.34	0.46
13:LQ:96:ARG:HD3	13:LQ:127:GLY:HA3	1.97	0.46
14:LR:49:ASN:HD22	14:LR:49:ASN:C	2.23	0.46
16:LT:104:ASP:OD1	18:LV:212:LEU:HG	2.15	0.46
26:Lg:33:LYS:HB3	26:Lg:65:LEU:HD21	1.96	0.46
37:Lr:227:GLU:CG	37:Lr:230:GLU:CD	2.82	0.46
38:Ls:207:ASN:HB3	38:Ls:251:GLN:HE21	1.80	0.46
48:L6:48:TRP:CE3	48:L6:51:MET:HE1	2.51	0.46
50:L8:141:GLU:HB3	50:L8:145:LYS:NZ	2.30	0.46
54:SZ:60:HIS:HA	62:SN:125:ARG:HG3	1.97	0.46
71:Sa:74:PRO:HB2	71:Sa:90:VAL:HG23	1.98	0.46
71:Sa:151:SER:OG	83:S1:37:U:O2'	2.32	0.46
76:Sg:309:LYS:HA	82:So:137:ILE:HD13	1.96	0.46
79:Sk:60:MET:CE	79:Sk:66:TRP:HZ3	2.27	0.46
83:S1:543:C:H2'	83:S1:544:C:H6	1.80	0.46
1:L1:198:G:H2'	11:LO:40:PRO:HG3	1.97	0.46
11:LO:80:LYS:HG3	28:Li:113:ARG:HG2	1.96	0.46
66:SS:221:GLN:H	66:SS:221:GLN:HG2	1.61	0.46
69:SX:86:ASN:OD1	69:SX:86:ASN:C	2.58	0.46
70:SY:117:LEU:O	70:SY:121:THR:HG22	2.15	0.46
79:Sk:113:HIS:CD2	79:Sk:113:HIS:C	2.92	0.46
80:Sm:85:LYS:N	80:Sm:85:LYS:HE2	2.30	0.46
1:L1:19:C:N4	22:Lb:18:GLU:OE1	2.49	0.46
4:LC:220:LYS:HG2	4:LC:261:MET:HE1	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:LJ:168:LEU:HD11	7:LJ:176:LEU:HD23	1.97	0.46
11:LO:80:LYS:HE3	28:Li:112:ASP:HB3	1.97	0.46
21:La:147:MET:HG2	31:Ll:338:ARG:HH21	1.80	0.46
22:Lb:151:GLU:CD	22:Lb:151:GLU:H	2.22	0.46
43:Ly:57:TYR:OH	50:L8:28:ARG:O	2.25	0.46
45:L3:22:PRO:HG3	45:L3:55:VAL:HG13	1.96	0.46
45:L3:72:HIS:ND1	45:L3:97:ARG:CZ	2.79	0.46
57:SG:105:VAL:CG2	57:SG:106:LEU:H	2.28	0.46
57:SG:146:HIS:O	57:SG:150:LYS:HG2	2.16	0.46
59:SJ:148:LEU:C	59:SJ:148:LEU:HD23	2.41	0.46
62:SN:41:ARG:HD3	77:Si:48:THR:O	2.16	0.46
70:SY:77:VAL:HG13	70:SY:78:TYR:HD1	1.75	0.46
76:Sg:366:VAL:O	76:Sg:370:VAL:HG13	2.16	0.46
79:Sk:56:ARG:HH12	82:So:91:ASP:HB3	1.79	0.46
83:S1:831:A:N1	83:S1:918:A:O2'	2.45	0.46
1:L1:385:U:H2'	1:L1:386:G:H8	1.81	0.46
3:LB:260:ALA:O	3:LB:264:ARG:HG2	2.16	0.46
6:LI:55:ILE:HD11	6:LI:86:THR:HG23	1.97	0.46
8:LK:154:ARG:NH2	46:L4:101:LEU:O	2.46	0.46
23:Lu:91:ARG:NH1	34:Lo:83:GLU:OE1	2.40	0.46
26:Lg:16:ILE:HD12	26:Lg:18:VAL:HG13	1.96	0.46
39:Lt:138:THR:OG1	39:Lt:150:ASN:O	2.23	0.46
43:Ly:68:LYS:HE3	43:Ly:68:LYS:HB3	1.81	0.46
63:SO:170:LEU:HD11	63:SO:177:VAL:HG23	1.97	0.46
63:SO:173:THR:HG22	65:SQ:101:ALA:HB1	1.95	0.46
68:SW:10:ARG:HG2	68:SW:30:LEU:HD21	1.98	0.46
69:SX:168:ARG:HA	69:SX:189:ARG:HH12	1.80	0.46
77:Si:71:TYR:CE2	77:Si:73:ASP:HB3	2.49	0.46
78:Sj:143:PRO:HG2	78:Sj:146:GLU:OE1	2.15	0.46
79:Sk:67:PRO:HG3	79:Sk:118:ALA:HB2	1.98	0.46
79:Sk:91:VAL:HG23	79:Sk:94:GLY:HA3	1.98	0.46
81:Sn:155:ARG:O	81:Sn:159:GLU:HG2	2.15	0.46
82:So:335:PHE:HA	82:So:338:ILE:HD12	1.98	0.46
1:L1:122:G:O2'	5:LD:125:ARG:NH1	2.48	0.46
1:L1:575:A:H2'	51:SR:189:ARG:HE	1.81	0.46
1:L1:1534:C:H5''	1:L1:1534:C:C6	2.51	0.46
7:LJ:167:ILE:O	7:LJ:168:LEU:C	2.59	0.46
11:LO:182:ARG:O	11:LO:186:ILE:HG12	2.16	0.46
19:LW:75:GLY:HA3	19:LW:90:PRO:O	2.16	0.46
19:LW:137:ARG:HH11	20:LX:104:TYR:HE1	1.62	0.46
22:Lb:8:VAL:HA	22:Lb:11:TRP:CG	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Lu:205:VAL:HG22	27:Lh:80:LEU:HD11	1.98	0.46
37:Lr:270:TYR:O	37:Lr:285:PRO:HA	2.16	0.46
39:Lt:273:ARG:HA	39:Lt:276:VAL:HG12	1.98	0.46
57:SG:92:SER:HA	57:SG:95:THR:OG1	2.16	0.46
65:SQ:78:LYS:HE3	65:SQ:78:LYS:HB2	1.75	0.46
73:Sc:74:ARG:NH2	73:Sc:393:GLU:OE2	2.50	0.46
79:Sk:113:HIS:CD2	79:Sk:114:LEU:CB	2.96	0.46
1:L1:340:U:OP2	43:Ly:115:ARG:NH1	2.46	0.45
1:L1:1441:A:H5'	4:LC:266:ARG:HH21	1.81	0.45
3:LB:62:ASN:OD1	3:LB:62:ASN:N	2.48	0.45
5:LD:72:PHE:N	5:LD:72:PHE:CD1	2.84	0.45
8:LK:132:LEU:H	8:LK:132:LEU:CD2	2.29	0.45
12:LP:195:LEU:HD12	12:LP:195:LEU:HA	1.83	0.45
28:Li:172:TYR:HB2	28:Li:175:ASP:HB2	1.97	0.45
66:SS:68:TYR:CD2	66:SS:73:VAL:HA	2.51	0.45
73:Sc:177:SER:O	73:Sc:180:LEU:CD1	2.64	0.45
76:Sg:351:MET:HE3	76:Sg:351:MET:HA	1.98	0.45
78:Sj:208:GLU:C	78:Sj:210:LYS:H	2.23	0.45
82:So:632:GLU:OE1	82:So:633:LEU:N	2.48	0.45
83:S1:334:C:H2'	83:S1:335:A:C8	2.51	0.45
83:S1:410:G:H4'	83:S1:931:A:H4'	1.98	0.45
1:L1:211:A:OP2	41:Lw:111:ARG:NH2	2.49	0.45
1:L1:867:G:O2'	1:L1:964:U:OP2	2.29	0.45
1:L1:1269:C:H2'	1:L1:1270:A:C8	2.51	0.45
5:LD:72:PHE:HD2	42:Lx:52:CYS:SG	2.33	0.45
14:LR:93:VAL:HG21	14:LR:135:CYS:SG	2.56	0.45
18:LV:87:MET:HG3	18:LV:172:CYS:SG	2.56	0.45
18:LV:94:ILE:HG22	18:LV:94:ILE:O	2.17	0.45
22:Lb:53:ASN:O	22:Lb:57:GLY:N	2.49	0.45
22:Lb:179:GLU:OE1	22:Lb:179:GLU:N	2.47	0.45
37:Lr:95:SER:O	37:Lr:99:LYS:HG3	2.17	0.45
42:Lx:73:TYR:CE1	42:Lx:103:HIS:HB3	2.51	0.45
52:Sf:271:LEU:O	52:Sf:273:LEU:N	2.49	0.45
53:SB:75:VAL:HA	53:SB:78:LEU:HD12	1.98	0.45
77:Si:68:LEU:HB3	77:Si:70:LEU:HD12	1.98	0.45
79:Sk:122:HIS:HD2	82:So:77:THR:HG21	1.78	0.45
80:Sm:18:LYS:HB2	80:Sm:18:LYS:HE2	1.53	0.45
82:So:429:LEU:HA	82:So:464:LEU:HD21	1.97	0.45
1:L1:481:A:H2'	1:L1:482:A:C8	2.52	0.45
1:L1:552:U:H2'	1:L1:553:A:N3	2.31	0.45
4:LC:218:VAL:HB	4:LC:224:PHE:CD2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:LC:316:PHE:HB3	4:LC:317:PRO:HD3	1.99	0.45
9:LM:24:LYS:O	9:LM:25:MET:HB2	2.17	0.45
11:LO:161:GLU:HG2	11:LO:236:LEU:HD21	1.99	0.45
14:LR:155:ASP:O	14:LR:159:ARG:HG2	2.15	0.45
15:LS:99:MET:HE2	15:LS:144:GLY:HA2	1.98	0.45
17:LU:96:PHE:HD1	36:Lq:126:ILE:HD12	1.82	0.45
17:LU:119:GLU:HG2	17:LU:189:PRO:HB2	1.99	0.45
26:Lg:20:MET:HE3	26:Lg:58:GLU:CA	2.46	0.45
54:SZ:81:HIS:O	54:SZ:84:GLU:OE1	2.34	0.45
63:SO:86:ASP:N	63:SO:86:ASP:OD1	2.48	0.45
63:SO:162:GLN:O	63:SO:166:MET:HE2	2.16	0.45
65:SQ:98:LYS:HB2	65:SQ:98:LYS:HE2	1.75	0.45
66:SS:113:LEU:HD12	66:SS:122:LEU:HD12	1.99	0.45
75:Se:100:MET:HE2	75:Se:100:MET:HB3	1.72	0.45
75:Se:334:PHE:HE1	75:Se:340:PHE:CE2	2.32	0.45
76:Sg:339:GLU:HB3	76:Sg:377:ARG:HH11	1.75	0.45
77:Si:19:PHE:O	79:Sk:211:ARG:NH1	2.48	0.45
82:So:397:MET:HE2	82:So:401:MET:HE1	1.97	0.45
1:L1:1364:U:H2'	1:L1:1365:C:C6	2.51	0.45
5:LD:56:PRO:HB2	5:LD:59:ARG:HG3	1.99	0.45
8:LK:29:ALA:C	8:LK:30:MET:SD	2.99	0.45
11:LO:161:GLU:CG	11:LO:236:LEU:HD21	2.46	0.45
16:LT:122:ARG:NH1	16:LT:126:GLU:OE2	2.47	0.45
20:LX:134:GLU:OE1	20:LX:134:GLU:O	2.34	0.45
36:Lq:95:GLU:OE1	36:Lq:95:GLU:N	2.50	0.45
39:Lt:159:LEU:HD12	39:Lt:174:PRO:HG3	1.99	0.45
43:Ly:79:TRP:CD1	43:Ly:80:LEU:HG	2.51	0.45
52:Sf:308:ARG:HG3	52:Sf:320:ILE:HD13	1.99	0.45
66:SS:221:GLN:O	66:SS:223:HIS:N	2.50	0.45
68:SW:16:GLU:OE1	68:SW:16:GLU:HA	2.16	0.45
79:Sk:123:CYS:SG	79:Sk:123:CYS:O	2.75	0.45
79:Sk:152:ASP:HB2	79:Sk:172:VAL:HG22	1.99	0.45
5:LD:97:HIS:HD2	11:LO:27:LEU:HB3	1.81	0.45
31:Ll:55:ASP:O	31:Ll:59:ARG:HG3	2.16	0.45
60:SK:146:HIS:CE1	60:SK:171:GLU:OE1	2.69	0.45
61:SL:66:PHE:HZ	61:SL:92:VAL:CG1	2.30	0.45
63:SO:167:LEU:HD21	63:SO:187:ILE:HD12	1.96	0.45
65:SQ:109:PRO:HG2	72:Sb:124:LEU:HD13	1.99	0.45
69:SX:251:GLU:OE2	69:SX:274:TYR:OH	2.32	0.45
73:Sc:53:LEU:C	73:Sc:57:MET:HE2	2.42	0.45
76:Sg:338:LEU:O	76:Sg:377:ARG:NH2	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:LC:293:LYS:CE	15:LS:87:THR:OG1	2.64	0.45
11:LO:91:ARG:NH2	11:LO:209:GLU:OE2	2.37	0.45
12:LP:118:MET:HG2	12:LP:167:CYS:SG	2.56	0.45
20:LX:177:THR:HG23	34:Lo:73:TYR:O	2.16	0.45
32:Lm:148:MET:CE	32:Lm:260:PHE:HD2	2.29	0.45
35:Lp:114:LYS:HE2	35:Lp:114:LYS:HB3	1.76	0.45
53:SB:73:PHE:O	53:SB:259:ARG:NH2	2.50	0.45
54:SZ:138:TYR:CZ	54:SZ:142:LEU:HD12	2.52	0.45
58:SI:206:GLU:OE2	58:SI:212:LYS:NZ	2.49	0.45
62:SN:64:PRO:HD2	62:SN:67:LEU:HD22	1.97	0.45
64:SP:101:PRO:O	64:SP:104:ILE:HG12	2.16	0.45
69:SX:170:ARG:O	69:SX:189:ARG:NH2	2.49	0.45
72:Sb:120:ARG:HG2	72:Sb:123:ARG:NH1	2.30	0.45
73:Sc:260:LEU:HD13	73:Sc:333:ARG:HD2	1.98	0.45
78:Sj:37:ASP:OD1	78:Sj:40:THR:OG1	2.32	0.45
78:Sj:50:LEU:HD23	78:Sj:50:LEU:HA	1.83	0.45
83:S1:24:U:H2'	83:S1:25:A:C8	2.52	0.45
1:L1:352:G:N2	1:L1:602:C:H1'	2.32	0.45
1:L1:516:C:H2'	1:L1:517:C:C6	2.51	0.45
1:L1:1064:A:H2'	1:L1:1065:G:H8	1.82	0.45
5:LD:280:TYR:CD1	11:LO:125:ARG:HD2	2.52	0.45
10:LN:75:LEU:HD11	10:LN:105:VAL:HG11	1.99	0.45
11:LO:266:PHE:HD1	41:Lw:51:LEU:HD21	1.82	0.45
20:LX:170:TRP:HD1	34:Lo:77:LEU:HG	1.81	0.45
33:Ln:179:THR:HG23	47:L5:63:THR:HG22	1.99	0.45
49:L7:188:LEU:C	49:L7:190:GLN:H	2.23	0.45
49:L7:189:ARG:C	49:L7:191:LYS:H	2.24	0.45
59:SJ:134:TYR:OH	62:SN:116:ASP:OD1	2.30	0.45
61:SL:85:LEU:C	61:SL:87:THR:H	2.25	0.45
69:SX:141:VAL:HG13	69:SX:180:THR:HG23	1.98	0.45
77:Si:46:LYS:CA	77:Si:49:TYR:HE1	2.22	0.45
78:Sj:9:ARG:HD2	83:S1:158:C:H5	1.82	0.45
82:So:464:LEU:O	82:So:468:MET:HE1	2.16	0.45
83:S1:753:U:O2'	83:S1:797:A:N3	2.46	0.45
83:S1:791:A:H2'	83:S1:792:A:H8	1.82	0.45
1:L1:1531:A:H2'	1:L1:1532:U:O4'	2.17	0.45
19:LW:63:VAL:HG22	23:Lu:63:GLY:HA2	1.98	0.45
23:Lu:76:GLN:O	23:Lu:77:GLU:HG2	2.16	0.45
31:Ll:233:LEU:HD13	31:Ll:286:ARG:HE	1.81	0.45
37:Lr:208:PRO:HA	37:Lr:211:THR:CG2	2.46	0.45
38:Ls:267:PRO:HG2	38:Ls:270:ALA:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:L8:150:LYS:HA	50:L8:150:LYS:HD2	1.79	0.45
55:SE:216:GLU:OE1	55:SE:216:GLU:N	2.45	0.45
57:SG:71:THR:O	58:SI:253:LYS:NZ	2.36	0.45
60:SK:74:ARG:CZ	60:SK:79:LYS:HG2	2.46	0.45
63:SO:181:ILE:HG13	63:SO:185:LEU:HD12	1.99	0.45
75:Se:174:ASN:HD22	75:Se:177:ARG:HE	1.65	0.45
76:Sg:298:PHE:CE2	82:So:74:LEU:HB3	2.52	0.45
78:Sj:30:ASP:OD1	78:Sj:30:ASP:N	2.50	0.45
79:Sk:164:ARG:HD3	79:Sk:164:ARG:HA	1.68	0.45
82:So:136:HIS:CD2	82:So:141:MET:HE2	2.52	0.45
82:So:641:ILE:O	82:So:645:LEU:HG	2.17	0.45
1:L1:828:U:H2'	1:L1:834:A:N6	2.31	0.45
2:L2:62:C:H2'	2:L2:63:G:H8	1.81	0.45
33:Ln:147:LEU:HD13	33:Ln:147:LEU:H	1.82	0.45
52:Sf:219:ARG:HE	52:Sf:219:ARG:HB3	1.67	0.45
58:SI:392:THR:HG21	83:S1:714:G:H4'	1.99	0.45
66:SS:211:ARG:HH11	73:Sc:317:LEU:HD11	1.82	0.45
83:S1:196:G:C2	83:S1:198:A:H5''	2.52	0.45
16:LT:23:GLU:OE1	16:LT:23:GLU:HA	2.17	0.45
31:Ll:99:ARG:HA	31:Ll:99:ARG:HD2	1.88	0.45
31:Ll:177:TYR:O	31:Ll:184:LEU:HA	2.16	0.45
32:Lm:277:GLN:O	32:Lm:301:SER:HA	2.16	0.45
36:Lq:54:PHE:O	36:Lq:58:ASN:ND2	2.41	0.45
38:Ls:76:ILE:HG22	38:Ls:78:LEU:HG	1.97	0.45
41:Lw:36:PRO:HD2	50:L8:73:GLY:O	2.17	0.45
48:L6:69:GLU:OE1	48:L6:69:GLU:N	2.50	0.45
51:SR:39:VAL:HG23	51:SR:50:GLU:HG3	1.98	0.45
52:Sf:419:LEU:HD23	52:Sf:419:LEU:HA	1.77	0.45
53:SB:183:PHE:HB2	53:SB:187:VAL:HG11	1.99	0.45
57:SG:84:SER:HA	58:SI:318:HIS:CD2	2.52	0.45
59:SJ:73:TYR:CD1	59:SJ:177:LEU:HB3	2.52	0.45
59:SJ:126:ILE:C	59:SJ:127:TYR:CD1	2.95	0.45
60:SK:187:ARG:O	83:S1:419:C:O2'	2.34	0.45
61:SL:78:ARG:HB2	61:SL:118:LEU:HD11	1.98	0.45
62:SN:85:VAL:HG23	83:S1:797:A:C5	2.52	0.45
64:SP:112:ARG:HH22	66:SS:229:GLY:CA	2.30	0.45
73:Sc:247:MET:SD	73:Sc:249:LEU:HB2	2.57	0.45
77:Si:41:PRO:O	77:Si:45:LYS:NZ	2.49	0.45
82:So:157:LEU:HB2	82:So:172:MET:HE1	1.98	0.45
1:L1:1058:C:H2'	1:L1:1059:U:H6	1.82	0.44
4:LC:199:ARG:NH2	4:LC:328:LEU:HD21	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:LD:262:THR:O	5:LD:266:VAL:HG23	2.16	0.44
15:LS:95:GLU:O	15:LS:99:MET:HG3	2.17	0.44
18:LV:108:PHE:CD2	25:Lf:107:ILE:HD12	2.53	0.44
20:LX:213:VAL:HG21	23:Lu:183:GLN:HE21	1.83	0.44
30:Lk:60:PHE:CZ	30:Lk:73:PRO:HD2	2.52	0.44
33:Ln:143:GLN:O	33:Ln:146:ALA:HB3	2.17	0.44
34:Lo:109:PHE:CZ	34:Lo:111:PRO:HA	2.52	0.44
38:Ls:91:PRO:HG2	38:Ls:94:ASP:HB2	1.99	0.44
38:Ls:218:THR:HG21	38:Ls:220:GLN:NE2	2.32	0.44
51:SR:71:PRO:HD2	51:SR:107:LEU:HD23	1.98	0.44
51:SR:79:HIS:HB3	51:SR:184:ASN:HA	1.98	0.44
57:SG:132:GLU:O	57:SG:133:GLU:C	2.60	0.44
58:SI:87:HIS:O	58:SI:91:MET:HE1	2.17	0.44
60:SK:85:ILE:HD11	60:SK:148:ARG:HH21	1.82	0.44
63:SO:174:ASN:CB	63:SO:177:VAL:HG22	2.47	0.44
66:SS:67:ARG:CD	66:SS:110:ASP:OD2	2.66	0.44
71:Sa:125:HIS:CB	71:Sa:128:ASN:OD1	2.48	0.44
72:Sb:53:PHE:C	72:Sb:53:PHE:CD1	2.95	0.44
82:So:535:MET:HE1	82:So:551:CYS:HB2	1.99	0.44
83:S1:225:G:H2'	83:S1:226:G:C8	2.52	0.44
83:S1:767:C:H3'	83:S1:768:G:H8	1.81	0.44
83:S1:847:C:H2'	83:S1:848:C:C6	2.52	0.44
1:L1:663:G:H2'	1:L1:664:C:C6	2.52	0.44
1:L1:1481:A:H4'	15:LS:146:GLY:O	2.17	0.44
12:LP:46:GLU:OE1	12:LP:46:GLU:HA	2.17	0.44
19:LW:1:MET:HB3	19:LW:24:PHE:CE2	2.52	0.44
20:LX:216:TYR:HE2	23:Lu:191:ASN:HD22	1.64	0.44
27:Lh:49:ARG:HA	27:Lh:49:ARG:HD2	1.68	0.44
35:Lp:68:PRO:HD2	35:Lp:71:HIS:HB2	1.98	0.44
40:Lv:88:TYR:HD1	40:Lv:88:TYR:H	1.66	0.44
55:SE:172:MET:HE2	55:SE:172:MET:HB2	1.77	0.44
58:SI:202:LYS:HG3	58:SI:218:TYR:HB2	1.98	0.44
58:SI:227:LYS:HE2	58:SI:227:LYS:HB3	1.82	0.44
58:SI:358:GLU:HA	58:SI:361:VAL:HG12	1.98	0.44
60:SK:85:ILE:HG12	68:SW:7:PHE:CZ	2.51	0.44
62:SN:113:HIS:O	62:SN:117:HIS:CD2	2.70	0.44
73:Sc:209:LEU:HD21	73:Sc:228:TYR:CG	2.53	0.44
83:S1:304:G:H2'	83:S1:305:A:H8	1.81	0.44
1:L1:333:A:OP2	1:L1:1064:A:O2'	2.30	0.44
1:L1:1522:C:OP1	51:SR:132:ARG:NH2	2.45	0.44
6:LI:71:PRO:HG3	22:Lb:65:VAL:HG13	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LR:143:MET:HE3	14:LR:169:VAL:CG1	2.46	0.44
22:Lb:128:THR:N	22:Lb:131:THR:HG22	2.30	0.44
30:Lk:132:LEU:HG	30:Lk:377:ASP:HB2	1.99	0.44
33:Ln:147:LEU:H	33:Ln:147:LEU:CD1	2.30	0.44
42:Lx:114:ASN:OD1	42:Lx:114:ASN:N	2.50	0.44
57:SG:110:LEU:HD13	57:SG:201:MET:HG2	1.99	0.44
59:SJ:177:LEU:HD12	59:SJ:179:GLN:NE2	2.32	0.44
60:SK:74:ARG:HD3	60:SK:74:ARG:HA	1.81	0.44
61:SL:40:GLY:O	61:SL:41:PRO:C	2.59	0.44
64:SP:102:MET:CE	83:S1:199:A:O5'	2.65	0.44
66:SS:205:TRP:CG	66:SS:231:PRO:HD2	2.52	0.44
69:SX:237:PRO:HA	69:SX:242:TYR:CD1	2.52	0.44
79:Sk:73:ALA:HB2	79:Sk:113:HIS:ND1	2.31	0.44
79:Sk:92:LYS:NZ	83:S1:655:C:P	2.90	0.44
80:Sm:7:ARG:HB2	80:Sm:7:ARG:HH11	1.82	0.44
82:So:648:ARG:HH11	82:So:649:VAL:HG22	1.81	0.44
83:S1:34:U:H2'	83:S1:35:A:H8	1.83	0.44
83:S1:55:C:H2'	83:S1:56:A:O4'	2.17	0.44
83:S1:355:C:H2'	83:S1:356:A:C8	2.52	0.44
1:L1:738:U:H2'	1:L1:739:A:C8	2.52	0.44
1:L1:844:C:H2'	1:L1:845:U:C6	2.53	0.44
5:LD:211:ARG:HD2	42:Lx:58:ARG:HD2	1.99	0.44
7:LJ:168:LEU:HD12	7:LJ:176:LEU:HB2	1.97	0.44
9:LM:18:TRP:HB2	9:LM:140:ASN:O	2.16	0.44
10:LN:78:LYS:HE2	10:LN:78:LYS:HB3	1.84	0.44
10:LN:130:ARG:C	10:LN:132:GLY:H	2.25	0.44
24:Ld:50:PRO:O	24:Ld:54:GLU:HG2	2.17	0.44
25:Lf:180:LYS:CD	25:Lf:180:LYS:N	2.80	0.44
30:Lk:274:LYS:CD	30:Lk:275:ASN:N	2.78	0.44
38:Ls:92:GLU:OE2	38:Ls:96:ARG:NH1	2.50	0.44
40:Lv:178:LEU:HD22	40:Lv:182:VAL:O	2.17	0.44
42:Lx:77:VAL:HG12	42:Lx:78:PHE:CD1	2.52	0.44
53:SB:65:GLU:N	53:SB:66:PRO:HD2	2.32	0.44
59:SJ:67:ASP:OD1	59:SJ:68:GLU:N	2.50	0.44
78:Sj:164:VAL:N	78:Sj:190:MET:SD	2.90	0.44
82:So:397:MET:O	82:So:401:MET:SD	2.74	0.44
82:So:580:ALA:CB	82:So:595:MET:CE	2.95	0.44
1:L1:169:C:H2'	1:L1:170:C:C6	2.53	0.44
11:LO:218:LYS:NZ	11:LO:235:GLU:OE1	2.51	0.44
15:LS:148:THR:HG22	15:LS:165:GLU:HG2	1.98	0.44
52:Sf:178:ASP:OD1	52:Sf:178:ASP:N	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:SB:137:TYR:CD1	53:SB:137:TYR:C	2.95	0.44
59:SJ:84:ASP:CG	59:SJ:87:VAL:HG23	2.43	0.44
66:SS:126:PHE:CE1	66:SS:140:THR:HG21	2.53	0.44
69:SX:294:ILE:HG13	69:SX:349:TYR:OH	2.16	0.44
71:Sa:94:SER:O	71:Sa:98:ILE:HG13	2.17	0.44
76:Sg:351:MET:N	76:Sg:351:MET:SD	2.91	0.44
77:Si:44:LYS:HA	77:Si:44:LYS:HD2	1.80	0.44
78:Sj:26:ASN:HD21	83:S1:885:C:H5	1.65	0.44
78:Sj:206:LYS:HZ2	78:Sj:208:GLU:HB2	1.82	0.44
1:L1:27:A:O2'	1:L1:34:U:OP2	2.34	0.44
1:L1:36:C:H1'	19:LW:9:LEU:HD11	1.98	0.44
1:L1:551:C:HO2'	1:L1:553:A:N6	2.16	0.44
1:L1:1087:A:H5'	6:LI:122:ARG:HH21	1.82	0.44
1:L1:1408:C:H2'	1:L1:1409:G:C8	2.53	0.44
10:LN:119:ILE:HG13	10:LN:140:ILE:CD1	2.46	0.44
11:LO:266:PHE:CD1	41:Lw:51:LEU:HD21	2.53	0.44
12:LP:223:MET:HE3	48:L6:42:GLU:CB	2.48	0.44
22:Lb:127:VAL:CB	22:Lb:131:THR:HG21	2.41	0.44
30:Lk:246:GLU:OE1	30:Lk:246:GLU:C	2.61	0.44
57:SG:90:VAL:HG13	57:SG:184:MET:HE2	1.99	0.44
59:SJ:126:ILE:HG13	59:SJ:127:TYR:CD1	2.52	0.44
63:SO:85:VAL:HG12	72:Sb:161:GLN:NE2	2.26	0.44
63:SO:125:LEU:CD2	63:SO:128:ARG:NH2	2.80	0.44
65:SQ:87:LYS:O	65:SQ:88:VAL:C	2.60	0.44
66:SS:213:LEU:HD21	72:Sb:50:PRO:HB2	1.99	0.44
67:ST:142:GLU:H	68:SW:28:ARG:NH2	2.14	0.44
69:SX:182:ARG:HH11	69:SX:182:ARG:HB2	1.79	0.44
71:Sa:149:CYS:O	71:Sa:150:PRO:C	2.60	0.44
76:Sg:357:GLY:N	77:Si:34:VAL:HG13	2.33	0.44
1:L1:748:A:H2'	1:L1:749:C:H6	1.83	0.44
4:LC:135:LYS:HD2	4:LC:140:GLY:O	2.18	0.44
6:LI:98:LEU:HD11	6:LI:105:VAL:HG12	2.00	0.44
10:LN:140:ILE:HD12	10:LN:140:ILE:O	2.17	0.44
17:LU:143:LEU:HD13	17:LU:153:LEU:HD21	1.99	0.44
18:LV:167:MET:HE3	18:LV:167:MET:HB3	1.76	0.44
29:Lj:97:ARG:HG3	29:Lj:98:HIS:CD2	2.52	0.44
32:Lm:89:TYR:O	32:Lm:93:MET:HG3	2.18	0.44
32:Lm:269:ILE:HD12	32:Lm:274:ILE:HB	2.00	0.44
39:Lt:265:LYS:HB2	39:Lt:266:PRO:HD3	2.00	0.44
41:Lw:84:TYR:OH	41:Lw:164:LYS:CE	2.65	0.44
42:Lx:78:PHE:HE2	42:Lx:89:ILE:HB	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:Lx:146:SER:O	42:Lx:148:LEU:N	2.50	0.44
52:Sf:318:ASP:OD2	52:Sf:319:GLN:HG2	2.18	0.44
58:SI:113:PRO:HB2	59:SJ:87:VAL:HG22	1.98	0.44
58:SI:328:VAL:CG1	58:SI:330:CYS:SG	3.05	0.44
59:SJ:81:LYS:HG2	59:SJ:140:TYR:CE1	2.53	0.44
59:SJ:124:VAL:HG12	62:SN:109:ILE:HG21	2.00	0.44
59:SJ:128:LYS:HG2	59:SJ:131:ARG:NH2	2.33	0.44
63:SO:203:PHE:CZ	63:SO:207:LYS:HD2	2.53	0.44
69:SX:242:TYR:O	69:SX:246:HIS:CD2	2.71	0.44
75:Se:64:GLU:HG3	75:Se:103:LYS:HD3	1.99	0.44
75:Se:127:TYR:HB3	75:Se:310:LEU:HD21	2.00	0.44
79:Sk:197:ARG:NH1	79:Sk:207:ILE:HD13	2.32	0.44
79:Sk:258:SER:C	79:Sk:260:ARG:H	2.26	0.44
5:LD:293:PHE:HA	5:LD:294:PRO:HD2	1.83	0.44
14:LR:146:GLN:HE21	14:LR:146:GLN:HB2	1.63	0.44
19:LW:141:ASP:HB3	19:LW:144:ARG:HG2	1.99	0.44
20:LX:54:TRP:CD1	20:LX:81:ARG:HD3	2.53	0.44
22:Lb:181:PRO:HA	22:Lb:184:ARG:HB3	1.98	0.44
23:Lu:93:LYS:HE2	34:Lo:70:LEU:HD11	2.00	0.44
30:Lk:113:LEU:HD12	30:Lk:311:ALA:HB1	2.00	0.44
32:Lm:39:GLU:HA	32:Lm:42:GLU:OE1	2.17	0.44
32:Lm:93:MET:HE2	32:Lm:93:MET:HB3	1.88	0.44
32:Lm:221:VAL:O	32:Lm:251:ILE:HA	2.18	0.44
45:L3:54:ASP:O	45:L3:56:ARG:HG2	2.18	0.44
52:Sf:150:LEU:HG	52:Sf:176:PHE:CE1	2.53	0.44
53:SB:90:HIS:CE1	53:SB:91:LEU:HD13	2.53	0.44
57:SG:90:VAL:HG12	57:SG:145:PHE:HE2	1.82	0.44
57:SG:94:PHE:CE1	57:SG:188:ILE:HG13	2.53	0.44
59:SJ:176:GLN:HA	79:Sk:151:ILE:O	2.18	0.44
71:Sa:22:VAL:HA	71:Sa:59:ASN:OD1	2.18	0.44
72:Sb:52:GLU:O	72:Sb:56:LEU:CB	2.65	0.44
72:Sb:71:ARG:NH1	83:S1:87:C:O3'	2.50	0.44
73:Sc:213:LEU:HA	73:Sc:224:GLN:HE21	1.82	0.44
75:Se:134:LYS:NZ	75:Se:310:LEU:O	2.42	0.44
76:Sg:284:LYS:O	76:Sg:288:THR:HG23	2.17	0.44
83:S1:780:A:H2'	83:S1:781:G:C8	2.52	0.44
1:L1:97:G:OP2	23:Lu:232:LYS:NZ	2.36	0.44
1:L1:1488:A:H2'	1:L1:1489:A:C8	2.53	0.44
5:LD:191:ASP:OD1	5:LD:192:SER:N	2.46	0.44
9:LM:117:HIS:O	9:LM:121:MET:HG3	2.18	0.44
31:Ll:173:LEU:HD11	31:Ll:204:VAL:CG1	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Lq:26:LEU:HD21	36:Lq:29:LEU:HG	2.00	0.44
39:Lt:199:ASN:O	39:Lt:241:GLY:CA	2.66	0.44
46:L4:64:ASP:HB3	46:L4:67:GLN:HB2	1.99	0.44
52:Sf:63:ILE:HD13	52:Sf:66:TRP:HE1	1.82	0.44
55:SE:279:LEU:O	70:SY:6:LEU:CD1	2.66	0.44
57:SG:51:TYR:O	57:SG:52:ARG:CG	2.62	0.44
57:SG:67:GLU:O	57:SG:71:THR:HG23	2.18	0.44
62:SN:37:ASP:CG	77:Si:52:TYR:HH	2.14	0.44
62:SN:37:ASP:CB	77:Si:52:TYR:OH	2.66	0.44
64:SP:75:HIS:ND1	64:SP:79:CYS:SG	2.91	0.44
67:ST:120:MET:HE3	67:ST:120:MET:HB2	1.70	0.44
69:SX:285:LEU:HD13	69:SX:300:LEU:HD23	2.00	0.44
74:Sd:125:ARG:HD2	74:Sd:125:ARG:HA	1.74	0.44
83:S1:386:U:H2'	83:S1:387:U:C6	2.53	0.44
83:S1:700:G:H2'	83:S1:701:G:C8	2.53	0.44
1:L1:143:C:H2'	43:Ly:32:ILE:HG13	2.00	0.43
5:LD:62:VAL:HG23	5:LD:82:LEU:HB2	1.98	0.43
7:LJ:84:ARG:HH12	46:L4:113:GLU:CD	2.26	0.43
7:LJ:163:GLU:O	7:LJ:167:ILE:HG12	2.17	0.43
8:LK:119:GLU:HA	8:LK:122:ARG:HG3	2.00	0.43
8:LK:171:ARG:HA	8:LK:171:ARG:HD2	1.77	0.43
16:LT:108:TYR:HD1	36:Lq:125:SER:HB2	1.84	0.43
24:Ld:89:LEU:HD13	24:Ld:110:LEU:HD23	1.98	0.43
25:Lf:149:PHE:C	25:Lf:150:LYS:HG2	2.43	0.43
26:Lg:20:MET:CE	26:Lg:41:LEU:O	2.62	0.43
31:Ll:194:THR:OG1	31:Ll:196:THR:OG1	2.33	0.43
32:Lm:287:GLN:HB2	32:Lm:288:PRO:HD3	2.00	0.43
41:Lw:122:LYS:HG2	41:Lw:126:ASP:OD2	2.18	0.43
45:L3:22:PRO:CD	45:L3:55:VAL:HG13	2.48	0.43
55:SE:127:ASN:ND2	77:Si:74:GLU:OE2	2.51	0.43
57:SG:174:LEU:HD22	57:SG:178:ARG:HG2	1.99	0.43
58:SI:115:GLY:HA3	59:SJ:84:ASP:CG	2.43	0.43
65:SQ:110:LEU:HD22	72:Sb:124:LEU:HB3	1.99	0.43
66:SS:167:ILE:HG21	69:SX:230:LEU:HD12	2.00	0.43
76:Sg:374:GLU:HA	76:Sg:377:ARG:HB2	2.00	0.43
80:Sm:67:ARG:HA	80:Sm:67:ARG:HD3	1.89	0.43
82:So:514:LYS:C	82:So:518:GLU:OE2	2.61	0.43
1:L1:181:G:H2'	1:L1:1023:A:N7	2.33	0.43
1:L1:213:G:OP2	11:LO:109:ARG:NH2	2.46	0.43
5:LD:72:PHE:CE1	5:LD:202:TYR:HE1	2.36	0.43
7:LJ:86:ILE:HD13	7:LJ:134:PHE:CG	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LO:243:ILE:H	11:LO:243:ILE:HD12	1.83	0.43
11:LO:268:GLY:HA3	41:Lw:47:PHE:CG	2.53	0.43
14:LR:143:MET:HE3	14:LR:169:VAL:HG11	2.00	0.43
19:LW:146:GLY:O	38:Ls:179:LYS:NZ	2.51	0.43
20:LX:60:ASP:OD1	20:LX:60:ASP:C	2.61	0.43
22:Lb:128:THR:H	22:Lb:131:THR:CG2	2.31	0.43
31:Ll:207:GLU:O	31:Ll:207:GLU:HG2	2.18	0.43
35:Lp:67:ILE:H	35:Lp:67:ILE:CD1	2.26	0.43
53:SB:148:ASN:CG	53:SB:151:PHE:HD2	2.26	0.43
58:SI:86:ARG:HH22	58:SI:95:ASP:C	2.26	0.43
58:SI:228:LEU:HD23	58:SI:228:LEU:HA	1.88	0.43
64:SP:91:LEU:HB3	64:SP:97:PHE:HB2	2.00	0.43
66:SS:53:ASP:OD1	66:SS:54:GLU:N	2.52	0.43
66:SS:139:TYR:CD1	66:SS:139:TYR:C	2.96	0.43
75:Se:123:ARG:HH21	75:Se:339:PRO:HD2	1.82	0.43
75:Se:202:ILE:HG12	75:Se:256:PHE:HE2	1.83	0.43
76:Sg:306:LYS:HE3	82:So:68:VAL:HG21	2.00	0.43
78:Sj:44:PRO:C	78:Sj:46:SER:N	2.65	0.43
83:S1:625:A:N1	83:S1:656:G:O2'	2.46	0.43
1:L1:191:U:H2'	1:L1:192:U:H6	1.82	0.43
1:L1:802:A:H5''	10:LN:35:MET:HE3	2.00	0.43
4:LC:145:LEU:HD11	4:LC:187:ILE:H	1.83	0.43
5:LD:201:GLN:O	5:LD:205:GLU:CD	2.62	0.43
10:LN:45:ALA:O	10:LN:49:SER:CB	2.67	0.43
17:LU:124:CYS:HB3	36:Lq:22:TYR:CZ	2.53	0.43
31:Ll:39:ASP:OD1	31:Ll:39:ASP:N	2.40	0.43
40:Lv:167:ALA:O	40:Lv:168:GLU:C	2.61	0.43
54:SZ:145:TYR:HD2	82:So:121:ILE:HD13	1.83	0.43
58:SI:393:TRP:CE3	58:SI:393:TRP:C	2.96	0.43
64:SP:34:ILE:H	64:SP:34:ILE:CD1	2.20	0.43
69:SX:288:GLN:OE1	69:SX:297:ALA:HA	2.18	0.43
72:Sb:53:PHE:CE2	83:S1:198:A:C2	3.04	0.43
75:Se:123:ARG:NH2	75:Se:339:PRO:HD2	2.33	0.43
78:Sj:163:SER:C	78:Sj:190:MET:SD	3.02	0.43
79:Sk:298:SER:O	79:Sk:302:GLU:CB	2.65	0.43
82:So:429:LEU:HB2	82:So:468:MET:SD	2.58	0.43
82:So:661:GLU:OE2	82:So:665:ASN:ND2	2.51	0.43
83:S1:795:G:H22	83:S1:800:G:H22	1.67	0.43
1:L1:1078:A:H2'	1:L1:1079:A:H8	1.84	0.43
1:L1:1199:A:N7	31:Ll:360:ARG:NH1	2.66	0.43
9:LM:135:GLU:O	9:LM:139:LYS:HG3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LO:151:LYS:HG3	11:LO:171:GLY:O	2.19	0.43
19:LW:81:ASP:HB3	19:LW:87:ILE:HD11	1.99	0.43
22:Lb:42:HIS:CE1	22:Lb:83:GLU:HG3	2.53	0.43
22:Lb:149:PRO:O	22:Lb:153:LEU:HB2	2.19	0.43
36:Lq:133:PHE:HB3	37:Lr:259:ARG:HH11	1.82	0.43
53:SB:164:GLU:OE1	53:SB:164:GLU:CA	2.58	0.43
57:SG:61:GLU:OE1	57:SG:61:GLU:N	2.51	0.43
58:SI:110:TYR:O	58:SI:111:LEU:C	2.61	0.43
59:SJ:135:GLU:CG	62:SN:124:GLN:HB2	2.44	0.43
69:SX:289:ILE:O	69:SX:290:GLN:C	2.60	0.43
69:SX:325:ILE:HG12	69:SX:329:LYS:HE3	2.00	0.43
71:Sa:32:VAL:HG21	71:Sa:52:ILE:HD11	2.00	0.43
73:Sc:364:LEU:CD1	73:Sc:368:GLU:HG3	2.48	0.43
76:Sg:280:VAL:O	76:Sg:284:LYS:HG3	2.18	0.43
82:So:189:ASN:HD22	82:So:189:ASN:HA	1.68	0.43
82:So:388:ARG:HA	82:So:391:PHE:CD2	2.53	0.43
83:S1:359:U:H2'	83:S1:360:G:C8	2.54	0.43
1:L1:356:A:H2'	1:L1:357:A:H8	1.82	0.43
1:L1:1077:U:H2'	1:L1:1078:A:C8	2.53	0.43
8:LK:42:ARG:HA	8:LK:42:ARG:HD3	1.71	0.43
8:LK:132:LEU:N	8:LK:132:LEU:HD22	2.34	0.43
20:LX:75:LYS:HB2	20:LX:75:LYS:HE3	1.78	0.43
21:La:107:HIS:ND1	21:La:109:ARG:HB2	2.33	0.43
30:Lk:201:ARG:HG2	30:Lk:232:THR:HG22	2.00	0.43
38:Ls:112:MET:O	38:Ls:116:MET:HB2	2.19	0.43
38:Ls:154:ASN:OD1	38:Ls:154:ASN:C	2.61	0.43
38:Ls:160:LEU:HB3	38:Ls:169:PHE:HE1	1.83	0.43
46:L4:70:THR:O	46:L4:86:LEU:HD23	2.18	0.43
53:SB:210:ARG:HH11	53:SB:210:ARG:HG2	1.83	0.43
53:SB:222:ILE:HD13	53:SB:236:VAL:HB	2.00	0.43
54:SZ:85:ARG:HH21	79:Sk:160:GLY:HA3	1.82	0.43
58:SI:91:MET:HG2	79:Sk:66:TRP:CD2	2.53	0.43
58:SI:285:VAL:HG13	58:SI:328:VAL:HG22	2.00	0.43
60:SK:84:PRO:HG2	60:SK:144:VAL:HG22	2.00	0.43
62:SN:103:ARG:HD3	62:SN:104:TRP:CZ2	2.53	0.43
68:SW:12:VAL:HG11	68:SW:25:THR:HG22	2.01	0.43
71:Sa:68:LYS:O	71:Sa:70:MET:HG3	2.18	0.43
75:Se:260:VAL:HG23	75:Se:306:ILE:HA	2.01	0.43
78:Sj:132:GLU:O	78:Sj:133:HIS:C	2.61	0.43
79:Sk:191:ILE:O	79:Sk:192:LYS:C	2.62	0.43
79:Sk:320:LEU:HD13	79:Sk:322:VAL:N	2.29	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:So:327:LYS:HB2	82:So:327:LYS:HE2	1.76	0.43
82:So:335:PHE:HD2	82:So:356:VAL:HG13	1.83	0.43
82:So:518:GLU:HG3	82:So:518:GLU:H	1.66	0.43
83:S1:37:U:H2'	83:S1:38:A:C8	2.52	0.43
83:S1:207:U:H2'	83:S1:208:A:C8	2.53	0.43
83:S1:267:A:H2'	83:S1:268:C:C6	2.53	0.43
1:L1:738:U:H2'	1:L1:739:A:H8	1.83	0.43
5:LD:209:TYR:HA	42:Lx:55:LEU:HD12	2.00	0.43
8:LK:103:GLN:HB3	8:LK:106:LYS:HD2	2.01	0.43
11:LO:143:GLU:HG3	31:Ll:377:TYR:HD2	1.83	0.43
34:Lo:41:ILE:HB	34:Lo:57:VAL:HG22	2.00	0.43
39:Lt:55:ARG:HH12	39:Lt:153:LEU:HD23	1.84	0.43
39:Lt:190:ARG:HG2	39:Lt:190:ARG:H	1.58	0.43
48:L6:57:GLU:H	48:L6:57:GLU:CD	2.27	0.43
50:L8:119:GLN:O	50:L8:123:GLU:HG2	2.18	0.43
53:SB:188:ARG:HE	58:SI:144:GLY:HA3	1.84	0.43
56:SF:54:HIS:CD2	56:SF:86:ILE:HA	2.53	0.43
58:SI:224:LEU:HD12	58:SI:224:LEU:HA	1.90	0.43
58:SI:379:ARG:O	58:SI:381:LYS:NZ	2.40	0.43
64:SP:119:LEU:O	64:SP:123:GLN:HG2	2.18	0.43
67:ST:78:GLN:HE21	72:Sb:190:ALA:HB2	1.83	0.43
69:SX:256:ARG:HB2	69:SX:258:LYS:HE3	2.01	0.43
70:SY:70:ILE:C	70:SY:70:ILE:HD12	2.43	0.43
72:Sb:71:ARG:CZ	83:S1:87:C:O3'	2.67	0.43
78:Sj:62:SER:HB2	78:Sj:67:LEU:HD11	2.00	0.43
1:L1:992:A:OP1	1:L1:1489:A:O2'	2.27	0.43
5:LD:65:TRP:HZ3	42:Lx:98:PHE:CD1	2.36	0.43
9:LM:6:ARG:CG	9:LM:6:ARG:NH1	2.81	0.43
11:LO:266:PHE:CD1	41:Lw:51:LEU:CD2	3.02	0.43
23:Lu:111:MET:HE3	23:Lu:111:MET:HB3	1.84	0.43
31:Ll:243:ASN:O	31:Ll:245:VAL:HG23	2.19	0.43
35:Lp:141:ASP:HB3	36:Lq:10:PHE:CG	2.54	0.43
39:Lt:56:PRO:HG3	39:Lt:237:LEU:HD21	2.00	0.43
40:Lv:174:ILE:HD12	40:Lv:184:LEU:HD11	1.99	0.43
53:SB:158:MET:HE3	53:SB:158:MET:HB3	1.88	0.43
56:SF:27:GLU:HA	56:SF:30:MET:HE3	2.01	0.43
59:SJ:81:LYS:CG	59:SJ:140:TYR:CE1	3.02	0.43
63:SO:103:MET:HB3	63:SO:103:MET:HE2	1.80	0.43
63:SO:137:ARG:HH11	63:SO:137:ARG:HG3	1.83	0.43
66:SS:226:GLU:O	72:Sb:50:PRO:HD3	2.18	0.43
78:Sj:64:LEU:HB2	78:Sj:139:TRP:CD1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:Sm:7:ARG:HB2	80:Sm:7:ARG:NH1	2.34	0.43
82:So:193:ASP:HA	82:So:261:THR:HG21	1.99	0.43
83:S1:25:A:H2'	83:S1:26:U:C6	2.54	0.43
83:S1:460:U:H5'	83:S1:461:C:H5	1.84	0.43
83:S1:670:A:H3'	83:S1:671:A:H8	1.83	0.43
1:L1:1280:U:H2'	1:L1:1281:A:C8	2.54	0.43
3:LB:155:GLU:HA	3:LB:248:SER:HA	2.01	0.43
4:LC:150:LYS:O	4:LC:173:LYS:HA	2.18	0.43
4:LC:300:LYS:HB2	4:LC:300:LYS:HE3	1.79	0.43
7:LJ:193:ASN:C	7:LJ:195:SER:N	2.77	0.43
18:LV:74:TYR:CZ	18:LV:177:LYS:HD2	2.54	0.43
18:LV:97:MET:HE1	18:LV:105:GLN:HG3	2.00	0.43
31:Ll:151:LEU:HD13	31:Ll:189:CYS:HB3	2.00	0.43
37:Lr:279:LYS:HA	37:Lr:279:LYS:HD2	1.69	0.43
40:Lv:93:ILE:O	40:Lv:156:VAL:HA	2.18	0.43
46:L4:66:VAL:HG22	46:L4:70:THR:HG23	2.00	0.43
53:SB:223:VAL:CG1	53:SB:227:CYS:HB2	2.49	0.43
54:SZ:81:HIS:HB2	54:SZ:85:ARG:NH1	2.32	0.43
56:SF:122:LYS:NZ	80:Sm:116:TYR:CE2	2.82	0.43
58:SI:111:LEU:HD22	79:Sk:112:LEU:HD23	1.99	0.43
58:SI:352:LEU:O	58:SI:356:VAL:HG12	2.19	0.43
63:SO:79:VAL:HA	63:SO:80:PRO:HD2	1.89	0.43
63:SO:118:ASN:C	63:SO:120:GLU:H	2.26	0.43
65:SQ:63:ILE:HD12	71:Sa:67:PHE:CE1	2.54	0.43
76:Sg:315:ILE:HG21	79:Sk:163:VAL:HG11	2.01	0.43
78:Sj:9:ARG:HH21	83:S1:159:C:H4'	1.84	0.43
79:Sk:92:LYS:HE2	83:S1:654:G:OP1	2.19	0.43
83:S1:360:G:H2'	83:S1:361:A:C8	2.53	0.43
83:S1:762:A:H2'	83:S1:763:G:C8	2.53	0.43
1:L1:2:C:O2'	18:LV:149:ARG:O	2.29	0.43
1:L1:402:A:H2'	1:L1:403:A:C8	2.54	0.43
1:L1:1354:U:H2'	1:L1:1355:A:C8	2.53	0.43
4:LC:94:SER:HB3	4:LC:184:ASN:HD21	1.83	0.43
6:LI:111:LEU:HD11	6:LI:137:LYS:HZ2	1.84	0.43
8:LK:179:LYS:HA	8:LK:182:ASP:OD2	2.19	0.43
36:Lq:114:ARG:NH2	36:Lq:116:ARG:HG2	2.33	0.43
46:L4:64:ASP:HB3	46:L4:67:GLN:HB3	2.00	0.43
54:SZ:91:PHE:CD2	77:Si:58:TYR:CD1	3.07	0.43
57:SG:37:TYR:CE1	57:SG:75:LYS:HB2	2.53	0.43
69:SX:66:LYS:HB3	69:SX:66:LYS:HE3	1.76	0.43
73:Sc:180:LEU:HD12	73:Sc:181:LEU:HG	1.95	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:Sk:56:ARG:HB3	79:Sk:59:LYS:NZ	2.34	0.43
82:So:397:MET:HE2	82:So:401:MET:HE3	1.99	0.43
1:L1:472:A:C2	1:L1:592:C:H2'	2.54	0.43
5:LD:93:LEU:HD22	48:L6:92:LEU:HD23	2.01	0.43
6:LI:73:LEU:HD21	22:Lb:65:VAL:HG11	2.01	0.43
7:LJ:139:LYS:O	7:LJ:139:LYS:HD2	2.19	0.43
14:LR:90:GLU:HG3	14:LR:107:ARG:HH22	1.82	0.43
18:LV:199:TYR:CE2	18:LV:203:LEU:HD11	2.54	0.43
32:Lm:262:ASP:OD1	32:Lm:263:VAL:N	2.52	0.43
33:Ln:147:LEU:CD1	33:Ln:147:LEU:N	2.82	0.43
38:Ls:216:MET:HE1	38:Ls:246:VAL:HG21	2.01	0.43
39:Lt:202:ALA:HA	39:Lt:239:LEU:H	1.84	0.43
52:Sf:118:LEU:HD22	52:Sf:420:GLN:NE2	2.33	0.43
56:SF:26:ILE:HG22	56:SF:30:MET:HE2	2.00	0.43
56:SF:35:ILE:HG13	63:SO:91:ARG:HH21	1.84	0.43
57:SG:46:ILE:CD1	58:SI:315:PHE:HZ	2.26	0.43
57:SG:94:PHE:HE1	57:SG:188:ILE:HG13	1.84	0.43
60:SK:74:ARG:CD	60:SK:78:LYS:C	2.92	0.43
66:SS:211:ARG:HE	66:SS:215:ARG:HH21	1.67	0.43
67:ST:80:LEU:HD22	67:ST:111:ILE:HG13	2.01	0.43
69:SX:353:LEU:HA	69:SX:356:HIS:CE1	2.54	0.43
80:Sm:40:LYS:N	80:Sm:40:LYS:CE	2.81	0.43
82:So:354:LEU:HA	82:So:357:LEU:HG	2.01	0.43
83:S1:297:U:H2'	83:S1:298:G:C8	2.54	0.43
1:L1:1302:A:H5''	12:LP:184:PRO:HA	2.01	0.42
4:LC:328:LEU:HA	4:LC:329:PRO:HD3	1.84	0.42
7:LJ:83:ARG:HG2	7:LJ:83:ARG:HH11	1.83	0.42
9:LM:6:ARG:HH11	9:LM:6:ARG:CG	2.27	0.42
12:LP:36:VAL:HG23	46:L4:128:ARG:HD2	2.00	0.42
12:LP:163:MET:HE1	12:LP:175:PHE:HE2	1.77	0.42
13:LQ:38:ARG:NH2	13:LQ:82:GLU:OE1	2.51	0.42
15:LS:214:LYS:H	15:LS:214:LYS:HG3	1.62	0.42
15:LS:245:PHE:HA	15:LS:248:CYS:HG	1.84	0.42
17:LU:107:LYS:HD3	18:LV:212:LEU:HD11	2.01	0.42
18:LV:55:ASN:CG	18:LV:74:TYR:H	2.27	0.42
38:Ls:203:MET:O	38:Ls:203:MET:CG	2.67	0.42
52:Sf:51:MET:HE2	52:Sf:51:MET:HB2	1.88	0.42
62:SN:56:SER:C	62:SN:58:ARG:N	2.77	0.42
64:SP:112:ARG:NH2	66:SS:229:GLY:HA3	2.33	0.42
67:ST:85:SER:HA	67:ST:86:PRO:HD2	1.85	0.42
73:Sc:40:TRP:HE1	73:Sc:111:THR:HG22	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:So:471:ILE:HG21	82:So:505:ARG:HG3	2.01	0.42
83:S1:765:G:H2'	83:S1:766:U:O4'	2.19	0.42
83:S1:865:A:H4'	83:S1:866:A:H3'	2.01	0.42
1:L1:83:A:OP1	43:Ly:118:TYR:OH	2.23	0.42
1:L1:1133:A:H2'	1:L1:1134:A:O4'	2.19	0.42
1:L1:1141:G:H2'	1:L1:1142:U:H6	1.84	0.42
4:LC:144:THR:HB	4:LC:178:ILE:HG23	2.00	0.42
4:LC:293:LYS:HZ3	4:LC:293:LYS:HB2	1.84	0.42
5:LD:99:VAL:HG21	5:LD:173:GLY:HA3	2.01	0.42
20:LX:152:ARG:HE	20:LX:152:ARG:N	2.13	0.42
22:Lb:148:THR:HB	22:Lb:153:LEU:HD13	2.01	0.42
26:Lg:20:MET:CE	26:Lg:58:GLU:N	2.81	0.42
38:Ls:254:ASN:OD1	38:Ls:256:TYR:N	2.51	0.42
40:Lv:175:GLN:OE1	40:Lv:176:SER:CA	2.66	0.42
53:SB:151:PHE:O	53:SB:155:ILE:HG12	2.18	0.42
53:SB:175:MET:HE3	53:SB:182:LEU:HD23	2.01	0.42
53:SB:224:ASP:OD1	53:SB:225:THR:N	2.48	0.42
53:SB:230:CYS:SG	70:SY:46:PHE:HA	2.59	0.42
55:SE:184:LYS:HA	55:SE:184:LYS:HD3	1.82	0.42
59:SJ:176:GLN:NE2	79:Sk:152:ASP:OD1	2.52	0.42
69:SX:242:TYR:CE1	69:SX:246:HIS:CE1	3.07	0.42
69:SX:276:VAL:HG12	69:SX:307:LEU:HD23	2.00	0.42
70:SY:75:TYR:CD1	74:Sd:98:LYS:HE2	2.54	0.42
73:Sc:367:CYS:O	73:Sc:368:GLU:C	2.62	0.42
74:Sd:128:GLU:H	74:Sd:128:GLU:CD	2.26	0.42
75:Se:338:ASP:O	75:Se:340:PHE:N	2.52	0.42
83:S1:793:G:H2'	83:S1:794:A:H8	1.83	0.42
8:LK:132:LEU:CD2	8:LK:132:LEU:N	2.81	0.42
14:LR:114:HIS:ND1	31:Ll:131:PRO:HD2	2.34	0.42
20:LX:134:GLU:OE1	20:LX:134:GLU:C	2.63	0.42
24:Ld:101:LYS:HB3	24:Ld:103:ILE:HG23	2.01	0.42
39:Lt:239:LEU:HG	39:Lt:240:THR:HG22	2.01	0.42
43:Ly:53:MET:HE3	43:Ly:53:MET:HB3	1.68	0.42
50:L8:81:GLN:O	50:L8:85:LEU:HD13	2.19	0.42
53:SB:142:ILE:HB	53:SB:164:GLU:HG3	2.01	0.42
56:SF:103:LYS:HE2	56:SF:103:LYS:HB2	1.70	0.42
57:SG:126:TYR:HB2	57:SG:139:ARG:HD3	2.00	0.42
58:SI:317:PHE:HB3	58:SI:323:LEU:HA	2.01	0.42
58:SI:391:PHE:HB3	58:SI:392:THR:H	1.71	0.42
60:SK:75:TRP:HB3	60:SK:146:HIS:NE2	2.23	0.42
67:ST:126:ASP:HB3	67:ST:129:TYR:HD2	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:Sc:137:ILE:HG22	73:Sc:139:PRO:HD3	2.02	0.42
75:Se:197:ARG:H	75:Se:197:ARG:HG3	1.56	0.42
75:Se:210:TRP:HZ2	75:Se:225:VAL:HG13	1.84	0.42
78:Sj:62:SER:HB2	78:Sj:67:LEU:HD21	2.01	0.42
80:Sm:95:GLU:HB2	80:Sm:100:LEU:HD23	2.01	0.42
82:So:353:ALA:HB1	82:So:375:ILE:HG22	2.01	0.42
83:S1:69:U:H2'	83:S1:70:G:C8	2.54	0.42
83:S1:497:U:H2'	83:S1:498:A:H8	1.84	0.42
83:S1:848:C:H2'	83:S1:849:U:C6	2.54	0.42
1:L1:395:A:H1'	1:L1:396:C:C6	2.54	0.42
1:L1:395:A:OP1	40:Lv:48:TYR:N	2.53	0.42
4:LC:157:LYS:HA	4:LC:157:LYS:HD2	1.81	0.42
14:LR:56:GLU:OE2	14:LR:78:HIS:CE1	2.71	0.42
26:Lg:60:LYS:HA	26:Lg:60:LYS:HD2	1.77	0.42
33:Ln:178:TYR:HB2	40:Lv:180:GLU:OE2	2.20	0.42
39:Lt:177:GLU:O	39:Lt:190:ARG:NH2	2.52	0.42
41:Lw:144:THR:O	41:Lw:146:THR:N	2.52	0.42
49:L7:107:THR:O	49:L7:107:THR:OG1	2.34	0.42
52:Sf:109:PHE:O	52:Sf:212:ARG:HD3	2.18	0.42
53:SB:102:MET:SD	53:SB:223:VAL:CG1	3.07	0.42
54:SZ:92:LEU:HD11	54:SZ:143:LEU:HG	2.01	0.42
56:SF:3:ARG:HB3	56:SF:99:THR:HG21	2.00	0.42
58:SI:360:GLU:HA	58:SI:363:TRP:HB2	2.00	0.42
60:SK:173:ILE:HA	68:SW:14:VAL:HG22	2.01	0.42
66:SS:131:THR:HG23	69:SX:97:GLU:HA	2.00	0.42
79:Sk:142:LYS:HD2	79:Sk:142:LYS:HA	1.86	0.42
82:So:75:ALA:O	82:So:78:VAL:C	2.62	0.42
82:So:292:TYR:HD1	82:So:333:GLN:HE22	1.67	0.42
82:So:391:PHE:CD1	82:So:394:TYR:HE2	2.37	0.42
82:So:619:LYS:HG3	82:So:648:ARG:NH2	2.35	0.42
1:L1:135:A:OP2	20:LX:96:ARG:HD3	2.19	0.42
1:L1:483:A:H2'	48:L6:30:ARG:NH2	2.35	0.42
4:LC:129:VAL:HB	4:LC:191:THR:HG22	2.01	0.42
15:LS:127:SER:O	15:LS:128:GLY:C	2.61	0.42
20:LX:150:SER:OG	20:LX:152:ARG:NE	2.52	0.42
31:Ll:214:TRP:N	31:Ll:275:GLN:OE1	2.52	0.42
39:Lt:269:LEU:HD23	39:Lt:269:LEU:HA	1.86	0.42
54:SZ:73:THR:HG21	79:Sk:159:SER:HB3	2.00	0.42
54:SZ:152:ARG:HG2	76:Sg:304:TRP:HH2	1.85	0.42
57:SG:110:LEU:HD11	83:S1:722:U:O4'	2.19	0.42
57:SG:151:ASN:HB3	57:SG:215:ASN:HD21	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:SO:166:MET:HE3	63:SO:166:MET:HB2	1.67	0.42
65:SQ:98:LYS:CG	65:SQ:107:GLU:O	2.67	0.42
67:ST:102:LYS:HE3	67:ST:103:LYS:HE2	2.01	0.42
71:Sa:121:LYS:CA	71:Sa:121:LYS:CE	2.94	0.42
73:Sc:190:LEU:HA	73:Sc:193:LYS:HG2	2.00	0.42
73:Sc:285:ALA:HA	73:Sc:288:LYS:HG3	2.01	0.42
75:Se:321:LYS:HB2	75:Se:321:LYS:HE2	1.80	0.42
76:Sg:380:PHE:HA	76:Sg:383:LYS:HZ3	1.84	0.42
82:So:372:TYR:HA	82:So:375:ILE:CD1	2.50	0.42
83:S1:548:U:H2'	83:S1:549:A:C8	2.55	0.42
83:S1:618:C:H2'	83:S1:619:A:H8	1.84	0.42
1:L1:191:U:H2'	1:L1:192:U:C6	2.54	0.42
2:L2:42:A:OP1	31:L1:114:ARG:NH2	2.41	0.42
4:LC:179:PHE:CZ	4:LC:298:LYS:HG3	2.55	0.42
11:LO:266:PHE:HB3	41:Lw:51:LEU:HD11	2.01	0.42
17:LU:153:LEU:HD12	17:LU:203:CYS:HB2	2.00	0.42
18:LV:211:THR:O	36:Lq:117:LYS:HD2	2.19	0.42
25:Lf:126:CYS:HA	25:Lf:129:LYS:HE3	2.01	0.42
25:Lf:141:ILE:HG12	25:Lf:175:ILE:HG12	2.02	0.42
25:Lf:169:ASP:HA	25:Lf:172:LYS:CD	2.50	0.42
62:SN:54:ILE:O	62:SN:57:LEU:HB3	2.18	0.42
64:SP:31:PHE:HZ	64:SP:53:SER:HB2	1.83	0.42
67:ST:66:ILE:H	67:ST:66:ILE:HG12	1.63	0.42
67:ST:134:LYS:NZ	67:ST:138:ILE:O	2.49	0.42
73:Sc:205:GLY:HA3	73:Sc:230:LEU:HD22	2.01	0.42
75:Se:262:VAL:HB	75:Se:308:SER:HB2	2.02	0.42
79:Sk:140:ASP:OD1	79:Sk:144:GLU:OE2	2.37	0.42
79:Sk:258:SER:C	79:Sk:260:ARG:N	2.77	0.42
82:So:437:GLY:O	82:So:441:THR:HG23	2.19	0.42
1:L1:5:A:H2'	1:L1:6:A:C8	2.55	0.42
12:LP:92:LEU:O	12:LP:246:TYR:HB3	2.20	0.42
12:LP:114:ASP:O	12:LP:118:MET:HB2	2.19	0.42
17:LU:82:LYS:HB2	17:LU:82:LYS:HE3	1.88	0.42
24:Ld:73:LYS:HG3	24:Ld:74:SER:N	2.35	0.42
28:Li:165:PHE:O	28:Li:168:ARG:HG2	2.20	0.42
33:Ln:98:ALA:HA	39:Lt:83:LEU:HB2	2.01	0.42
37:Lr:173:LEU:HD11	37:Lr:218:PHE:CE1	2.55	0.42
39:Lt:119:ASP:OD1	75:Se:213:ARG:NH2	2.53	0.42
40:Lv:88:TYR:CD1	40:Lv:88:TYR:N	2.88	0.42
51:SR:83:TYR:HB3	51:SR:121:MET:HE3	2.01	0.42
55:SE:141:TRP:HB3	55:SE:142:PRO:HD2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:SK:74:ARG:CD	60:SK:79:LYS:HA	2.48	0.42
61:SL:96:PRO:HG3	61:SL:124:THR:HG23	2.01	0.42
63:SO:92:LEU:HD23	72:Sb:160:LEU:HD21	2.01	0.42
63:SO:171:ARG:HG3	63:SO:178:PHE:CE2	2.55	0.42
73:Sc:189:CYS:HA	73:Sc:192:LYS:HD2	2.01	0.42
73:Sc:231:LEU:HD22	73:Sc:243:VAL:HG23	2.02	0.42
75:Se:67:HIS:CE1	75:Se:100:MET:HG3	2.55	0.42
75:Se:132:THR:HA	75:Se:388:PRO:HD2	2.01	0.42
80:Sm:9:ARG:NH2	83:S1:374:U:OP2	2.49	0.42
80:Sm:25:LYS:HE3	83:S1:952:A:C6	2.55	0.42
82:So:492:THR:O	82:So:493:MET:C	2.62	0.42
83:S1:57:U:OP1	83:S1:198:A:N6	2.53	0.42
83:S1:370:A:OP2	83:S1:371:G:O2'	2.29	0.42
4:LC:151:THR:HG23	4:LC:171:PRO:HB2	2.02	0.42
7:LJ:86:ILE:HD13	7:LJ:134:PHE:CD2	2.54	0.42
9:LM:25:MET:CE	9:LM:149:ARG:HH22	2.33	0.42
26:Lg:33:LYS:CB	26:Lg:65:LEU:HD21	2.49	0.42
30:Lk:337:GLU:H	30:Lk:337:GLU:CD	2.26	0.42
31:Ll:306:LYS:CD	31:Ll:307:HIS:CD2	3.02	0.42
36:Lq:103:LYS:HE3	36:Lq:103:LYS:HB3	1.85	0.42
57:SG:94:PHE:CD2	57:SG:145:PHE:CZ	3.08	0.42
66:SS:61:SER:OG	66:SS:62:GLU:N	2.51	0.42
69:SX:231:CYS:SG	69:SX:246:HIS:CD2	3.12	0.42
76:Sg:377:ARG:HA	76:Sg:377:ARG:HD3	1.82	0.42
78:Sj:115:TRP:CE2	78:Sj:130:GLU:HB3	2.54	0.42
79:Sk:248:MET:H	79:Sk:248:MET:HE2	1.84	0.42
79:Sk:261:ASN:HD22	79:Sk:261:ASN:HA	1.67	0.42
80:Sm:52:MET:HE2	80:Sm:52:MET:HB3	1.95	0.42
82:So:305:ILE:HG22	82:So:306:ASN:ND2	2.35	0.42
82:So:528:ARG:O	82:So:531:ILE:HD12	2.19	0.42
1:L1:362:G:O2'	1:L1:1195:C:O2	2.27	0.42
1:L1:1064:A:H2'	1:L1:1065:G:C8	2.55	0.42
15:LS:282:ILE:O	15:LS:286:ILE:HG13	2.20	0.42
30:Lk:215:ARG:NH2	30:Lk:367:ASN:OD1	2.52	0.42
31:Ll:110:ILE:HD13	31:Ll:110:ILE:HA	1.86	0.42
31:Ll:241:PRO:HB2	31:Ll:242:GLY:H	1.63	0.42
31:Ll:253:PRO:HG3	31:Ll:288:SER:O	2.20	0.42
38:Ls:110:GLU:OE2	38:Ls:113:LYS:HE2	2.20	0.42
43:Ly:38:LEU:HD23	43:Ly:38:LEU:HA	1.92	0.42
51:SR:86:VAL:O	51:SR:90:SER:HB2	2.20	0.42
53:SB:59:ASN:C	53:SB:61:LYS:H	2.28	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:SB:264:ARG:NE	53:SB:268:GLU:OE2	2.47	0.42
63:SO:108:GLN:HB2	63:SO:134:VAL:HG21	2.00	0.42
66:SS:73:VAL:CB	66:SS:125:GLN:OE1	2.63	0.42
67:ST:54:MET:HE2	67:ST:54:MET:HB3	1.90	0.42
73:Sc:209:LEU:HD13	73:Sc:209:LEU:C	2.45	0.42
76:Sg:336:LYS:HE3	76:Sg:336:LYS:HB3	1.88	0.42
79:Sk:229:LEU:HD22	79:Sk:229:LEU:HA	1.67	0.42
83:S1:680:G:H5''	85:S1:1034:T1C:O12	2.20	0.42
83:S1:930:U:H2'	83:S1:931:A:H8	1.84	0.42
1:L1:270:A:H2'	1:L1:271:G:H8	1.85	0.42
1:L1:728:A:H2'	1:L1:729:A:O4'	2.19	0.42
1:L1:1349:G:O2'	1:L1:1455:A:N1	2.48	0.42
7:LJ:196:LYS:O	7:LJ:197:LEU:C	2.63	0.42
9:LM:74:GLN:HE22	51:SR:175:PRO:HD2	1.85	0.42
11:LO:140:LEU:CG	11:LO:163:ALA:HB1	2.49	0.42
13:LQ:94:ALA:HB3	13:LQ:95:PRO:HD3	2.01	0.42
14:LR:65:ARG:HG2	14:LR:75:GLU:HG3	2.02	0.42
18:LV:90:LEU:HD11	18:LV:111:LYS:HD3	2.01	0.42
19:LW:144:ARG:HA	19:LW:144:ARG:HD2	1.83	0.42
26:Lg:44:LEU:HD12	26:Lg:44:LEU:HA	1.81	0.42
41:Lw:60:PRO:HA	41:Lw:61:PRO:HD3	1.97	0.42
54:SZ:138:TYR:O	54:SZ:142:LEU:HB2	2.20	0.42
55:SE:320:ILE:HD11	55:SE:345:LEU:HD11	2.02	0.42
56:SF:75:VAL:HG13	56:SF:93:ILE:HG21	2.02	0.42
58:SI:364:MET:HE3	58:SI:370:LEU:HD21	2.00	0.42
62:SN:54:ILE:HG13	62:SN:74:GLU:OE1	2.20	0.42
71:Sa:79:TYR:N	71:Sa:79:TYR:CD1	2.87	0.42
75:Se:295:LYS:HB2	75:Se:295:LYS:HE2	1.81	0.42
82:So:71:LEU:HA	82:So:74:LEU:HB2	2.02	0.42
82:So:596:LEU:HD11	82:So:614:LEU:HD13	2.01	0.42
83:S1:541:A:C2	83:S1:781:G:H2'	2.55	0.42
83:S1:543:C:H2'	83:S1:544:C:C6	2.55	0.42
1:L1:475:G:H3'	16:LT:61:LYS:HE3	2.02	0.41
1:L1:1058:C:H2'	1:L1:1059:U:C6	2.55	0.41
4:LC:162:LEU:HD23	4:LC:162:LEU:HA	1.81	0.41
15:LS:245:PHE:HA	15:LS:248:CYS:SG	2.60	0.41
34:Lo:109:PHE:HE2	34:Lo:111:PRO:CB	2.31	0.41
36:Lq:58:ASN:ND2	36:Lq:58:ASN:N	2.68	0.41
49:L7:120:ALA:O	49:L7:124:LYS:HG2	2.20	0.41
55:SE:380:LEU:HD12	55:SE:381:PRO:HD2	2.00	0.41
57:SG:242:TRP:O	80:Sm:84:ARG:NH1	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:SL:78:ARG:NH1	83:S1:246:G:N7	2.67	0.41
62:SN:78:LEU:HD22	62:SN:79:PRO:HD2	2.02	0.41
68:SW:6:LYS:NZ	83:S1:359:U:H5"	2.33	0.41
70:SY:111:GLU:HB3	70:SY:117:LEU:CD2	2.49	0.41
76:Sg:304:TRP:HE3	76:Sg:310:LEU:HD12	1.85	0.41
76:Sg:351:MET:HG3	76:Sg:377:ARG:HH21	1.85	0.41
78:Sj:182:GLY:O	78:Sj:183:ASP:C	2.62	0.41
81:Sn:150:THR:O	81:Sn:154:ARG:HG3	2.20	0.41
82:So:342:LEU:HB2	82:So:349:ALA:HB1	2.02	0.41
83:S1:791:A:H2'	83:S1:792:A:C8	2.55	0.41
1:L1:847:U:OP1	3:LB:287:ARG:NH1	2.53	0.41
1:L1:1057:C:H2'	1:L1:1058:C:C6	2.55	0.41
5:LD:214:ASP:OD1	5:LD:214:ASP:N	2.39	0.41
7:LJ:47:LEU:HD22	12:LP:226:ILE:HG12	2.02	0.41
10:LN:138:LEU:CD2	10:LN:144:PHE:HE2	2.33	0.41
13:LQ:130:LEU:HD22	25:Lf:134:THR:HG23	2.01	0.41
31:Ll:243:ASN:O	31:Ll:245:VAL:CG2	2.68	0.41
39:Lt:160:LEU:HG	39:Lt:171:TRP:HB3	2.02	0.41
41:Lw:35:TYR:HE1	50:L8:74:SER:HB3	1.84	0.41
49:L7:80:TYR:CD1	49:L7:143:GLN:HB2	2.55	0.41
54:SZ:105:ALA:HB3	54:SZ:122:VAL:HG13	2.02	0.41
63:SO:125:LEU:HD23	63:SO:125:LEU:HA	1.95	0.41
63:SO:171:ARG:HG3	63:SO:178:PHE:CD2	2.55	0.41
64:SP:17:LEU:HD23	64:SP:17:LEU:HA	1.89	0.41
72:Sb:116:LEU:O	72:Sb:120:ARG:HG3	2.20	0.41
73:Sc:31:SER:O	73:Sc:35:VAL:HG23	2.20	0.41
73:Sc:401:LYS:O	73:Sc:405:GLN:OE1	2.38	0.41
75:Se:109:LEU:O	75:Se:113:LYS:HG3	2.20	0.41
75:Se:383:LEU:HB3	75:Se:394:HIS:CD2	2.54	0.41
76:Sg:302:ILE:HD12	82:So:68:VAL:HG13	2.02	0.41
83:S1:554:A:H2'	83:S1:555:G:H8	1.84	0.41
83:S1:632:C:H2'	83:S1:633:C:C6	2.55	0.41
1:L1:485:A:H2'	1:L1:486:A:C8	2.56	0.41
1:L1:525:A:P	46:L4:119:ARG:HH12	2.44	0.41
4:LC:202:GLN:HG2	4:LC:203:TYR:N	2.36	0.41
13:LQ:148:LEU:CD1	32:Lm:174:VAL:HG12	2.50	0.41
15:LS:88:ASP:OD1	15:LS:89:PRO:CD	2.68	0.41
18:LV:81:LYS:HA	18:LV:81:LYS:HD2	1.88	0.41
23:Lu:64:LEU:H	23:Lu:64:LEU:HG	1.70	0.41
23:Lu:169:ARG:HH22	30:Lk:64:MET:HE2	1.85	0.41
25:Lf:118:GLN:HB3	25:Lf:121:VAL:HG23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:L3:84:LEU:HD12	45:L3:84:LEU:O	2.20	0.41
49:L7:98:LYS:CG	49:L7:136:THR:CG2	2.98	0.41
57:SG:74:ILE:HG13	58:SI:366:GLN:HA	2.02	0.41
58:SI:113:PRO:HG2	79:Sk:109:PRO:HB2	2.02	0.41
59:SJ:128:LYS:HE3	83:S1:580:G:OP1	2.21	0.41
62:SN:101:LYS:HG2	62:SN:104:TRP:HZ3	1.86	0.41
63:SO:106:ILE:O	63:SO:109:GLU:HG3	2.20	0.41
65:SQ:31:THR:H	71:Sa:65:MET:CE	2.19	0.41
71:Sa:152:LEU:HD23	71:Sa:152:LEU:HA	1.90	0.41
72:Sb:71:ARG:HH12	72:Sb:72:MET:CE	1.98	0.41
79:Sk:127:LYS:O	79:Sk:128:ASP:C	2.61	0.41
83:S1:662:A:H2'	83:S1:663:C:C6	2.56	0.41
1:L1:80:G:H2'	1:L1:81:A:C8	2.56	0.41
1:L1:788:A:O2'	4:LC:215:PHE:O	2.27	0.41
6:LI:70:LYS:HD2	6:LI:70:LYS:HA	1.73	0.41
12:LP:183:LEU:HD23	12:LP:183:LEU:HA	1.86	0.41
14:LR:80:LEU:HD21	14:LR:160:LEU:HD21	2.03	0.41
19:LW:67:ALA:HB3	19:LW:98:GLN:HB2	2.03	0.41
20:LX:77:VAL:N	20:LX:87:VAL:O	2.45	0.41
21:La:77:PRO:HG3	21:La:89:LEU:HD21	2.03	0.41
26:Lg:20:MET:HE3	26:Lg:58:GLU:N	2.36	0.41
36:Lq:36:ASP:HA	48:L6:100:LYS:HB3	2.02	0.41
39:Lt:151:ARG:NH1	39:Lt:254:TRP:O	2.39	0.41
47:L5:56:LEU:HD23	47:L5:64:ILE:HD11	2.03	0.41
52:Sf:143:ARG:NH2	52:Sf:415:ASP:OD2	2.28	0.41
54:SZ:91:PHE:HE2	77:Si:58:TYR:HD1	1.66	0.41
57:SG:231:GLU:O	57:SG:232:ALA:C	2.63	0.41
58:SI:282:GLU:HB2	58:SI:331:THR:HG22	2.03	0.41
59:SJ:74:LYS:HZ1	59:SJ:146:GLU:HB2	1.86	0.41
59:SJ:148:LEU:HD11	59:SJ:152:THR:CG2	2.48	0.41
61:SL:103:GLN:HB2	61:SL:106:GLN:HG3	2.01	0.41
64:SP:63:GLU:HB3	69:SX:157:VAL:HG23	2.01	0.41
72:Sb:186:ASN:OD1	72:Sb:188:ASN:N	2.46	0.41
75:Se:168:LEU:HD12	75:Se:168:LEU:HA	1.86	0.41
82:So:80:ARG:HH21	82:So:82:THR:HA	1.84	0.41
83:S1:304:G:H2'	83:S1:305:A:C8	2.55	0.41
1:L1:461:A:P	48:L6:23:ARG:HH22	2.43	0.41
7:LJ:84:ARG:CZ	46:L4:113:GLU:OE1	2.69	0.41
15:LS:241:LYS:HE2	15:LS:241:LYS:HB3	1.86	0.41
17:LU:96:PHE:CD1	36:Lq:126:ILE:HD12	2.56	0.41
22:Lb:196:ILE:HG12	22:Lb:197:PRO:HD2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Lm:114:ASP:HB2	32:Lm:117:LYS:HB2	2.01	0.41
33:Ln:169:PHE:CZ	40:Lv:91:LEU:HB3	2.56	0.41
40:Lv:150:LEU:HD23	40:Lv:150:LEU:HA	1.92	0.41
40:Lv:178:LEU:HD23	40:Lv:179:PRO:CD	2.50	0.41
45:L3:11:ARG:H	45:L3:12:PRO:HD2	1.85	0.41
53:SB:148:ASN:OD1	53:SB:197:HIS:CE1	2.73	0.41
54:SZ:81:HIS:HB2	54:SZ:85:ARG:HH12	1.86	0.41
54:SZ:127:LEU:HB2	54:SZ:132:TYR:CE1	2.55	0.41
55:SE:272:LYS:O	55:SE:276:VAL:HG22	2.20	0.41
58:SI:86:ARG:NH2	58:SI:97:GLU:HA	2.34	0.41
66:SS:228:SER:HB3	72:Sb:51:ALA:CB	2.50	0.41
71:Sa:67:PHE:HB3	71:Sa:70:MET:SD	2.60	0.41
72:Sb:82:VAL:HG12	72:Sb:86:ARG:HH21	1.86	0.41
78:Sj:27:ARG:HD3	78:Sj:212:ARG:HH22	1.85	0.41
82:So:243:ASN:O	82:So:247:ILE:HG12	2.20	0.41
82:So:577:ASN:HA	82:So:610:LEU:HD22	2.03	0.41
83:S1:753:U:H2'	83:S1:754:G:C8	2.55	0.41
2:L2:42:A:P	31:Ll:114:ARG:HH22	2.44	0.41
7:LJ:93:ASN:HB3	7:LJ:156:SER:C	2.45	0.41
18:LV:161:ARG:HB3	18:LV:162:GLY:H	1.73	0.41
39:Lt:146:ARG:HH12	39:Lt:259:GLU:HB3	1.84	0.41
47:L5:77:MET:HA	47:L5:78:PRO:HD3	1.84	0.41
51:SR:89:LEU:HB3	51:SR:119:VAL:HG22	2.03	0.41
59:SJ:120:LEU:HD23	62:SN:108:ARG:HA	2.02	0.41
62:SN:43:MET:SD	62:SN:81:ASP:C	3.03	0.41
62:SN:85:VAL:HG21	83:S1:756:A:H62	1.86	0.41
63:SO:130:ILE:HG13	63:SO:181:ILE:HD11	2.02	0.41
66:SS:228:SER:CB	72:Sb:51:ALA:HB3	2.49	0.41
66:SS:235:MET:HE2	66:SS:235:MET:HB3	1.85	0.41
69:SX:313:SER:HA	69:SX:334:THR:HG21	2.02	0.41
73:Sc:176:PRO:HA	73:Sc:179:GLN:HB2	2.01	0.41
78:Sj:144:LYS:O	78:Sj:145:HIS:C	2.64	0.41
79:Sk:149:ILE:HG22	79:Sk:175:VAL:HG23	2.03	0.41
82:So:497:LEU:HB3	82:So:534:LEU:CD1	2.50	0.41
82:So:646:THR:HB	82:So:650:MET:HE2	2.02	0.41
83:S1:442:U:H2'	83:S1:443:A:C8	2.54	0.41
83:S1:620:U:H2'	83:S1:621:C:C6	2.55	0.41
1:L1:410:U:H3'	1:L1:411:U:H6	1.86	0.41
1:L1:992:A:H2'	1:L1:993:C:C6	2.56	0.41
3:LB:126:VAL:HA	3:LB:142:VAL:HG12	2.02	0.41
5:LD:284:TYR:O	5:LD:290:TYR:OH	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:LJ:118:LYS:C	7:LJ:120:LYS:N	2.78	0.41
7:LJ:128:ASN:OD1	7:LJ:128:ASN:N	2.53	0.41
19:LW:37:GLU:H	19:LW:37:GLU:HG2	1.62	0.41
22:Lb:83:GLU:HG2	22:Lb:107:PRO:HB3	2.03	0.41
23:Lu:64:LEU:HA	23:Lu:67:PHE:HD2	1.84	0.41
24:Ld:36:PHE:HE2	24:Ld:79:PRO:HG3	1.85	0.41
32:Lm:227:LEU:HD11	32:Lm:241:GLU:OE2	2.20	0.41
37:Lr:207:GLY:O	37:Lr:211:THR:HG22	2.21	0.41
52:Sf:62:ARG:HG2	52:Sf:65:ARG:HH21	1.86	0.41
55:SE:248:GLY:HA3	55:SE:326:LEU:HB3	2.02	0.41
60:SK:82:GLU:N	60:SK:82:GLU:CD	2.79	0.41
60:SK:140:LYS:HB3	60:SK:140:LYS:HE2	1.88	0.41
79:Sk:77:LYS:O	79:Sk:81:VAL:HG23	2.21	0.41
80:Sm:26:PRO:HB2	80:Sm:28:ILE:HD12	2.03	0.41
82:So:419:ALA:HA	82:So:422:ILE:HG12	2.03	0.41
83:S1:262:G:H2'	83:S1:263:A:C8	2.54	0.41
1:L1:280:U:H2'	1:L1:281:C:C6	2.55	0.41
1:L1:445:U:H1'	1:L1:1144:G:O6	2.21	0.41
1:L1:940:U:H2'	1:L1:941:C:C6	2.56	0.41
1:L1:1156:G:OP1	21:La:49:ARG:HD3	2.20	0.41
7:LJ:65:LEU:HD23	7:LJ:65:LEU:HA	1.95	0.41
14:LR:111:ILE:O	14:LR:115:LEU:HD23	2.21	0.41
17:LU:53:LYS:HD2	17:LU:53:LYS:HA	1.82	0.41
31:Ll:214:TRP:CA	31:Ll:275:GLN:HG3	2.49	0.41
31:Ll:233:LEU:HD11	31:Ll:236:LEU:HD22	2.02	0.41
33:Ln:147:LEU:HG	33:Ln:158:HIS:HE1	1.85	0.41
34:Lo:68:PHE:CE2	34:Lo:70:LEU:HB2	2.56	0.41
37:Lr:47:ARG:O	37:Lr:51:LEU:CD2	2.69	0.41
38:Ls:153:ASN:HD21	38:Ls:183:TRP:H	1.69	0.41
44:Lz:27:TRP:O	44:Lz:31:GLN:HG2	2.21	0.41
50:L8:108:LEU:HD23	50:L8:108:LEU:HA	1.93	0.41
52:Sf:85:LYS:HG3	52:Sf:86:MET:HG2	2.02	0.41
52:Sf:273:LEU:HD12	52:Sf:273:LEU:HA	1.95	0.41
53:SB:142:ILE:O	53:SB:164:GLU:HB3	2.21	0.41
55:SE:206:PRO:HA	55:SE:272:LYS:HD2	2.02	0.41
55:SE:220:THR:HG22	55:SE:247:VAL:HG13	2.02	0.41
66:SS:110:ASP:C	66:SS:112:LYS:N	2.79	0.41
69:SX:332:ALA:HA	69:SX:336:ALA:HB3	2.03	0.41
71:Sa:155:LEU:HD12	71:Sa:155:LEU:HA	1.82	0.41
78:Sj:65:LEU:HG	78:Sj:112:GLY:N	2.36	0.41
82:So:302:VAL:HA	82:So:312:LYS:HD3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:So:342:LEU:HA	82:So:345:PHE:HB2	2.03	0.41
83:S1:766:U:H2'	83:S1:767:C:O4'	2.21	0.41
1:L1:10:A:H5'	1:L1:11:G:OP2	2.20	0.41
1:L1:294:U:H2'	1:L1:295:A:C8	2.56	0.41
1:L1:468:U:OP1	24:Ld:73:LYS:CE	2.69	0.41
1:L1:605:U:H2'	1:L1:606:C:C6	2.56	0.41
1:L1:740:U:H2'	1:L1:741:U:H6	1.86	0.41
1:L1:1077:U:H2'	1:L1:1078:A:H8	1.84	0.41
2:L2:21:A:H2'	2:L2:22:G:C8	2.56	0.41
3:LB:172:MET:HE2	56:SF:86:ILE:H	1.85	0.41
4:LC:109:LEU:HD21	4:LC:337:VAL:HG22	2.03	0.41
14:LR:101:VAL:HG12	14:LR:102:VAL:HG13	2.03	0.41
19:LW:133:GLU:OE1	19:LW:137:ARG:NH2	2.54	0.41
22:Lb:153:LEU:HD12	22:Lb:153:LEU:HA	1.93	0.41
28:Li:128:GLY:O	28:Li:144:LEU:HD13	2.21	0.41
31:Ll:306:LYS:C	31:Ll:307:HIS:CD2	2.98	0.41
33:Ln:143:GLN:O	33:Ln:147:LEU:HD13	2.21	0.41
38:Ls:207:ASN:HD22	38:Ls:251:GLN:HE21	1.62	0.41
38:Ls:216:MET:CE	38:Ls:246:VAL:HG21	2.51	0.41
47:L5:57:VAL:HG22	47:L5:74:MET:HE1	2.03	0.41
51:SR:101:PRO:O	51:SR:105:THR:HG23	2.21	0.41
52:Sf:108:TYR:CD2	52:Sf:264:ILE:HG12	2.56	0.41
52:Sf:414:ASN:OD1	52:Sf:416:ASP:HB2	2.21	0.41
53:SB:167:HIS:CE1	58:SI:153:THR:HA	2.55	0.41
54:SZ:124:LEU:HD23	54:SZ:158:VAL:HG12	2.03	0.41
55:SE:234:LYS:HE2	55:SE:234:LYS:HB3	1.72	0.41
56:SF:30:MET:HE3	56:SF:30:MET:HB2	1.93	0.41
58:SI:127:HIS:ND1	58:SI:129:GLU:HB3	2.35	0.41
60:SK:172:VAL:HG21	68:SW:19:VAL:CG1	2.51	0.41
61:SL:57:GLN:HG3	61:SL:111:GLU:HG3	2.03	0.41
62:SN:123:ILE:H	62:SN:123:ILE:CD1	2.30	0.41
63:SO:195:TYR:OH	83:S1:134:A:OP2	2.37	0.41
66:SS:52:LYS:HD3	66:SS:57:LYS:HB2	2.02	0.41
66:SS:213:LEU:CD2	72:Sb:50:PRO:HB2	2.50	0.41
70:SY:85:PHE:HB3	70:SY:87:LEU:HD23	2.03	0.41
73:Sc:40:TRP:CD1	73:Sc:114:ARG:HG3	2.56	0.41
73:Sc:353:LEU:HD12	73:Sc:353:LEU:HA	1.92	0.41
75:Se:99:LEU:HD21	75:Se:136:LEU:HB3	2.02	0.41
75:Se:159:HIS:HA	75:Se:162:VAL:HG12	2.02	0.41
78:Sj:78:ARG:HB3	78:Sj:97:LEU:HD12	2.03	0.41
78:Sj:198:MET:HE2	78:Sj:198:MET:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:Sk:263:LEU:HA	79:Sk:266:LEU:HG	2.02	0.41
80:Sm:51:VAL:HG23	80:Sm:69:GLU:HG3	2.03	0.41
80:Sm:56:TRP:HE1	80:Sm:70:ILE:HD11	1.85	0.41
83:S1:47:C:H2'	83:S1:168:C:H41	1.86	0.41
83:S1:387:U:H2'	83:S1:388:U:H6	1.85	0.41
83:S1:700:G:H2'	83:S1:701:G:H8	1.86	0.41
83:S1:808:U:H2'	83:S1:809:U:C6	2.56	0.41
1:L1:367:U:H4'	1:L1:370:G:N1	2.36	0.41
1:L1:512:G:H2'	1:L1:513:C:C6	2.55	0.41
1:L1:1167:A:H2'	1:L1:1168:A:N3	2.36	0.41
7:LJ:181:ILE:O	7:LJ:182:ASP:C	2.64	0.41
7:LJ:185:ILE:H	7:LJ:185:ILE:HG12	1.69	0.41
8:LK:64:ILE:HA	8:LK:64:ILE:HD13	1.81	0.41
14:LR:106:THR:CG2	14:LR:127:ILE:HD11	2.50	0.41
20:LX:50:SER:O	20:LX:53:ASP:OD1	2.39	0.41
20:LX:98:ILE:HD12	20:LX:109:ILE:HG21	2.03	0.41
20:LX:105:ARG:HH22	38:Ls:171:ASP:HB3	1.86	0.41
32:Lm:285:ASN:HD22	32:Lm:293:LEU:CD1	2.30	0.41
33:Ln:147:LEU:HG	33:Ln:158:HIS:CE1	2.56	0.41
34:Lo:136:LEU:HD23	34:Lo:136:LEU:HA	1.92	0.41
36:Lq:85:ARG:HE	36:Lq:87:GLU:CD	2.29	0.41
41:Lw:43:ASP:OD1	41:Lw:44:GLU:OE1	2.38	0.41
41:Lw:101:THR:HG23	41:Lw:102:HIS:ND1	2.36	0.41
45:L3:33:PHE:CD2	45:L3:86:MET:HE3	2.55	0.41
56:SF:40:GLU:HB2	56:SF:65:LEU:HB2	2.03	0.41
58:SI:293:ILE:HD13	58:SI:293:ILE:N	2.36	0.41
60:SK:172:VAL:CG2	68:SW:19:VAL:HG21	2.49	0.41
61:SL:97:GLY:HA3	61:SL:127:ARG:NH1	2.36	0.41
69:SX:341:TYR:HD1	69:SX:341:TYR:O	2.04	0.41
70:SY:73:LYS:NZ	70:SY:73:LYS:CB	2.75	0.41
73:Sc:43:ARG:HH22	73:Sc:45:LYS:HE2	1.86	0.41
73:Sc:250:ILE:H	73:Sc:250:ILE:HG13	1.52	0.41
75:Se:260:VAL:HG21	75:Se:296:MET:SD	2.61	0.41
79:Sk:167:ARG:H	79:Sk:167:ARG:HG2	1.61	0.41
83:S1:34:U:H2'	83:S1:35:A:C8	2.56	0.41
83:S1:246:G:O2'	83:S1:261:C:O2'	2.34	0.41
1:L1:192:U:H2'	1:L1:193:A:C8	2.56	0.40
1:L1:378:U:H2'	1:L1:379:U:C6	2.57	0.40
1:L1:1134:A:H2'	1:L1:1135:A:C8	2.56	0.40
3:LB:218:ARG:NE	3:LB:225:ILE:HD12	2.36	0.40
8:LK:130:PHE:H	8:LK:130:PHE:HD1	1.66	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LO:47:ARG:HB3	11:LO:48:LYS:H	1.74	0.40
24:Ld:103:ILE:HD12	48:L6:59:GLU:OE1	2.21	0.40
26:Lg:16:ILE:HG13	26:Lg:18:VAL:HG13	2.03	0.40
31:Ll:351:HIS:HA	31:Ll:352:PRO:HD2	1.97	0.40
39:Lt:83:LEU:O	47:L5:49:ALA:HA	2.21	0.40
39:Lt:188:ALA:O	39:Lt:191:THR:OG1	2.31	0.40
46:L4:99:MET:HE3	46:L4:99:MET:HB2	1.66	0.40
53:SB:210:ARG:NH1	53:SB:210:ARG:HG2	2.37	0.40
54:SZ:62:ILE:HD11	62:SN:118:GLY:HA3	2.03	0.40
54:SZ:142:LEU:HD23	54:SZ:142:LEU:HA	1.94	0.40
59:SJ:128:LYS:HZ3	59:SJ:131:ARG:NH2	2.18	0.40
59:SJ:163:ASN:OD1	79:Sk:114:LEU:HD11	2.21	0.40
63:SO:95:LEU:HD23	63:SO:95:LEU:HA	1.93	0.40
63:SO:209:LEU:HD11	81:Sn:177:TRP:NE1	2.30	0.40
73:Sc:364:LEU:HD11	73:Sc:368:GLU:OE2	2.21	0.40
75:Se:120:PRO:HA	75:Se:302:HIS:HB3	2.03	0.40
75:Se:266:ASN:OD1	75:Se:266:ASN:N	2.53	0.40
77:Si:46:LYS:HD3	77:Si:49:TYR:OH	2.20	0.40
79:Sk:64:GLN:NE2	82:So:83:THR:CB	2.75	0.40
79:Sk:92:LYS:NZ	83:S1:655:C:OP1	2.54	0.40
79:Sk:121:LYS:HG2	82:So:77:THR:HG23	2.03	0.40
82:So:367:PRO:HB3	82:So:371:THR:HG21	2.03	0.40
83:S1:55:C:OP1	83:S1:201:U:O2'	2.39	0.40
1:L1:1024:A:C6	1:L1:1315:C:H1'	2.56	0.40
1:L1:1272:C:H2'	1:L1:1273:G:H8	1.85	0.40
2:L2:62:C:H2'	2:L2:63:G:C8	2.56	0.40
3:LB:192:LEU:HD23	3:LB:192:LEU:HA	1.89	0.40
5:LD:49:ARG:NH1	5:LD:81:ASP:O	2.54	0.40
7:LJ:165:VAL:HG11	7:LJ:169:ARG:HH21	1.86	0.40
14:LR:110:ALA:HA	31:Ll:138:GLU:OE2	2.22	0.40
16:LT:89:ASN:HB3	16:LT:123:ARG:HB3	2.03	0.40
19:LW:49:THR:HG22	19:LW:51:VAL:H	1.85	0.40
30:Lk:276:ASP:OD1	52:Sf:158:ARG:NH1	2.54	0.40
30:Lk:284:PRO:HG2	52:Sf:148:ASP:CG	2.45	0.40
39:Lt:58:VAL:HG13	39:Lt:59:VAL:N	2.36	0.40
45:L3:86:MET:HE2	45:L3:86:MET:HB2	1.87	0.40
48:L6:65:VAL:O	48:L6:69:GLU:OE1	2.39	0.40
49:L7:113:GLU:O	49:L7:114:PRO:C	2.63	0.40
54:SZ:85:ARG:NH2	79:Sk:160:GLY:HA3	2.37	0.40
58:SI:112:PHE:CE1	79:Sk:85:VAL:HG21	2.56	0.40
62:SN:58:ARG:CZ	62:SN:58:ARG:HB2	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:Sc:145:ASN:ND2	73:Sc:177:SER:OG	2.53	0.40
75:Se:175:LYS:HA	75:Se:175:LYS:HD3	1.90	0.40
82:So:661:GLU:OE1	82:So:661:GLU:C	2.64	0.40
83:S1:113:A:N1	83:S1:133:C:O2'	2.49	0.40
83:S1:931:A:H2'	83:S1:932:C:C6	2.56	0.40
1:L1:481:A:O3'	48:L6:38:ARG:NH2	2.54	0.40
3:LB:213:CYS:SG	3:LB:246:ARG:HD2	2.61	0.40
9:LM:142:VAL:HG11	36:Lq:133:PHE:CE1	2.49	0.40
11:LO:161:GLU:OE2	11:LO:236:LEU:HD21	2.21	0.40
13:LQ:131:PRO:HB3	25:Lf:184:TRP:HZ3	1.86	0.40
15:LS:252:GLN:OE1	15:LS:252:GLN:C	2.64	0.40
18:LV:130:ARG:NH1	18:LV:131:ASP:OD2	2.54	0.40
22:Lb:199:GLU:H	22:Lb:199:GLU:CD	2.29	0.40
25:Lf:184:TRP:CD1	25:Lf:184:TRP:H	2.38	0.40
32:Lm:148:MET:HE2	32:Lm:257:ILE:HD11	2.02	0.40
33:Ln:129:ARG:HD3	33:Ln:129:ARG:O	2.22	0.40
36:Lq:56:ARG:NH2	42:Lx:147:ASN:O	2.54	0.40
40:Lv:146:LEU:CG	40:Lv:147:ASP:N	2.63	0.40
47:L5:57:VAL:HG22	47:L5:76:ALA:HA	2.03	0.40
50:L8:30:PRO:HA	50:L8:31:PRO:HD3	1.93	0.40
55:SE:415:GLN:HE21	71:Sa:13:LEU:HB2	1.87	0.40
57:SG:210:LEU:HD13	57:SG:210:LEU:HA	1.96	0.40
59:SJ:165:PRO:HG3	79:Sk:111:PHE:CZ	2.56	0.40
70:SY:113:ASP:HB3	70:SY:116:LYS:HD3	2.02	0.40
70:SY:119:VAL:O	70:SY:123:LYS:HG2	2.21	0.40
77:Si:80:ASP:N	77:Si:83:LYS:HE2	2.37	0.40
78:Sj:52:VAL:HA	78:Sj:55:TRP:CD1	2.57	0.40
78:Sj:190:MET:HE2	78:Sj:190:MET:HA	2.03	0.40
82:So:470:GLN:O	82:So:474:THR:HG23	2.22	0.40
82:So:552:ALA:HB1	82:So:579:ILE:HG23	2.04	0.40
1:L1:259:A:H2'	1:L1:260:C:C6	2.56	0.40
1:L1:677:C:H2'	1:L1:678:A:C8	2.56	0.40
1:L1:899:C:H3'	1:L1:923:G:C8	2.57	0.40
8:LK:114:LEU:HA	8:LK:117:VAL:HG12	2.04	0.40
9:LM:71:LYS:HG2	51:SR:174:MET:SD	2.62	0.40
19:LW:11:ARG:NH2	23:Lu:185:VAL:HA	2.37	0.40
24:Ld:70:THR:HG23	24:Ld:95:HIS:HA	2.04	0.40
28:Li:129:TYR:CZ	28:Li:130:LYS:CD	3.00	0.40
31:Ll:330:ILE:HG13	31:Ll:330:ILE:H	1.65	0.40
36:Lq:35:ARG:HG3	48:L6:101:TRP:HB2	2.04	0.40
39:Lt:179:GLN:HG2	39:Lt:190:ARG:HH12	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:L7:98:LYS:HG3	49:L7:136:THR:CG2	2.52	0.40
49:L7:100:GLU:OE1	49:L7:102:ARG:HD2	2.20	0.40
52:Sf:66:TRP:O	52:Sf:69:THR:OG1	2.29	0.40
53:SB:61:LYS:O	53:SB:65:GLU:HB2	2.21	0.40
53:SB:263:LYS:O	53:SB:267:VAL:HG23	2.20	0.40
56:SF:113:LEU:HD12	56:SF:113:LEU:HA	1.92	0.40
57:SG:190:GLU:HG2	57:SG:218:PRO:HB2	2.03	0.40
58:SI:257:ILE:HD11	58:SI:361:VAL:HG11	2.04	0.40
58:SI:262:TYR:CD1	58:SI:268:ALA:HB2	2.56	0.40
58:SI:393:TRP:CE3	58:SI:393:TRP:O	2.74	0.40
60:SK:150:VAL:HG22	60:SK:176:THR:HB	2.03	0.40
72:Sb:77:GLU:OE1	72:Sb:80:ARG:NH2	2.53	0.40
73:Sc:210:LEU:HB3	73:Sc:211:PRO:HD3	2.02	0.40
75:Se:90:GLN:O	75:Se:94:PHE:HB2	2.22	0.40
77:Si:65:LEU:HD23	77:Si:65:LEU:HA	1.97	0.40
78:Sj:82:ARG:HB3	78:Sj:85:TRP:CD2	2.56	0.40
1:L1:49:G:H2'	1:L1:50:C:H6	1.86	0.40
1:L1:438:G:H5''	12:LP:134:LYS:HG3	2.03	0.40
1:L1:616:A:H2'	1:L1:617:U:C6	2.57	0.40
1:L1:858:G:OP1	3:LB:135:ARG:NH2	2.45	0.40
1:L1:998:A:H2'	1:L1:999:A:C8	2.57	0.40
5:LD:50:LYS:HB3	5:LD:50:LYS:HE3	1.87	0.40
5:LD:82:LEU:HB3	5:LD:87:PHE:CD2	2.57	0.40
13:LQ:148:LEU:HD12	32:Lm:174:VAL:HG12	2.04	0.40
15:LS:193:ALA:HA	15:LS:224:MET:HA	2.04	0.40
16:LT:141:ILE:H	16:LT:141:ILE:HG12	1.66	0.40
17:LU:144:LEU:HB2	35:Lp:58:ILE:HB	2.04	0.40
21:La:76:HIS:HA	21:La:77:PRO:HD3	1.91	0.40
22:Lb:171:ARG:O	22:Lb:172:GLN:C	2.64	0.40
28:Li:126:LYS:HB3	28:Li:126:LYS:HE3	1.80	0.40
31:Ll:217:LEU:HA	31:Ll:235:TRP:O	2.22	0.40
39:Lt:58:VAL:CG1	39:Lt:59:VAL:N	2.84	0.40
43:Ly:53:MET:HE3	43:Ly:56:VAL:HG21	2.02	0.40
48:L6:10:GLY:HA3	51:SR:167:PRO:HG3	2.03	0.40
49:L7:110:TRP:CD1	49:L7:110:TRP:H	2.38	0.40
52:Sf:107:GLN:HG3	52:Sf:329:ILE:HD13	2.03	0.40
52:Sf:300:HIS:HB2	52:Sf:361:ILE:HG12	2.03	0.40
54:SZ:138:TYR:OH	77:Si:65:LEU:HD13	2.22	0.40
58:SI:77:GLN:C	58:SI:128:PRO:HG2	2.46	0.40
59:SJ:74:LYS:HZ2	59:SJ:74:LYS:HG3	1.73	0.40
60:SK:75:TRP:CG	60:SK:146:HIS:HD2	2.38	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:SK:88:ILE:HG13	60:SK:97:ILE:HG23	2.03	0.40
63:SO:86:ASP:OD1	63:SO:89:VAL:HB	2.21	0.40
63:SO:109:GLU:HA	63:SO:112:MET:CB	2.46	0.40
63:SO:145:LYS:HD2	63:SO:146:HIS:NE2	2.36	0.40
70:SY:74:PHE:CD1	70:SY:74:PHE:C	2.99	0.40
73:Sc:217:ASN:OD1	73:Sc:219:VAL:N	2.52	0.40
75:Se:108:LEU:HD13	75:Se:141:VAL:HG21	2.04	0.40
77:Si:80:ASP:CA	77:Si:83:LYS:CE	2.93	0.40
77:Si:84:ARG:CZ	77:Si:84:ARG:HB3	2.48	0.40
81:Sn:173:LEU:HD12	81:Sn:191:THR:HG21	1.96	0.40
83:S1:349:A:H2'	83:S1:350:A:C8	2.56	0.40
83:S1:792:A:H2'	83:S1:793:G:C8	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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%)	224 (95%)	9 (4%)	2 (1%)	14	41
4	LC	302/348 (87%)	275 (91%)	25 (8%)	2 (1%)	18	48
5	LD	248/311 (80%)	233 (94%)	15 (6%)	0	100	100
6	LI	93/267 (35%)	83 (89%)	10 (11%)	0	100	100
7	LJ	154/261 (59%)	132 (86%)	19 (12%)	3 (2%)	6	23
8	LK	173/192 (90%)	156 (90%)	15 (9%)	2 (1%)	10	34
9	LM	175/178 (98%)	164 (94%)	10 (6%)	1 (1%)	21	51
10	LN	113/145 (78%)	103 (91%)	10 (9%)	0	100	100
11	LO	285/296 (96%)	274 (96%)	10 (4%)	1 (0%)	30	59
12	LP	219/251 (87%)	214 (98%)	4 (2%)	1 (0%)	24	54

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	LQ	150/175 (86%)	141 (94%)	8 (5%)	1 (1%)	18	48
14	LR	144/179 (80%)	138 (96%)	6 (4%)	0	100	100
15	LS	217/292 (74%)	206 (95%)	11 (5%)	0	100	100
16	LT	138/149 (93%)	135 (98%)	3 (2%)	0	100	100
17	LU	158/205 (77%)	150 (95%)	7 (4%)	1 (1%)	21	51
18	LV	164/212 (77%)	151 (92%)	12 (7%)	1 (1%)	21	51
19	LW	139/153 (91%)	138 (99%)	1 (1%)	0	100	100
20	LX	200/216 (93%)	184 (92%)	16 (8%)	0	100	100
21	La	109/148 (74%)	104 (95%)	5 (5%)	0	100	100
22	Lb	241/256 (94%)	225 (93%)	15 (6%)	1 (0%)	30	59
23	Lu	174/250 (70%)	167 (96%)	6 (3%)	1 (1%)	21	51
24	Ld	118/161 (73%)	111 (94%)	7 (6%)	0	100	100
25	Lf	106/188 (56%)	101 (95%)	5 (5%)	0	100	100
26	Lg	50/65 (77%)	49 (98%)	1 (2%)	0	100	100
27	Lh	44/92 (48%)	42 (96%)	2 (4%)	0	100	100
28	Li	93/188 (50%)	90 (97%)	3 (3%)	0	100	100
29	Lj	36/103 (35%)	36 (100%)	0	0	100	100
30	Lk	392/423 (93%)	375 (96%)	17 (4%)	0	100	100
31	Ll	352/380 (93%)	323 (92%)	26 (7%)	3 (1%)	14	41
32	Lm	291/338 (86%)	278 (96%)	12 (4%)	1 (0%)	36	65
33	Ln	97/206 (47%)	81 (84%)	14 (14%)	2 (2%)	5	21
34	Lo	122/137 (89%)	115 (94%)	6 (5%)	1 (1%)	16	44
35	Lp	93/142 (66%)	89 (96%)	4 (4%)	0	100	100
36	Lq	146/215 (68%)	133 (91%)	13 (9%)	0	100	100
37	Lr	271/332 (82%)	261 (96%)	10 (4%)	0	100	100
38	Ls	210/306 (69%)	200 (95%)	10 (5%)	0	100	100
39	Lt	211/279 (76%)	186 (88%)	23 (11%)	2 (1%)	14	41
40	Lv	125/212 (59%)	114 (91%)	10 (8%)	1 (1%)	16	44
41	Lw	130/166 (78%)	121 (93%)	8 (6%)	1 (1%)	16	44
42	Lx	108/158 (68%)	103 (95%)	4 (4%)	1 (1%)	14	41
43	Ly	95/128 (74%)	90 (95%)	5 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	Lz	90/123 (73%)	84 (93%)	6 (7%)	0	100	100
45	L3	94/112 (84%)	79 (84%)	14 (15%)	1 (1%)	11	36
46	L4	81/138 (59%)	73 (90%)	6 (7%)	2 (2%)	4	17
47	L5	43/128 (34%)	38 (88%)	4 (9%)	1 (2%)	5	19
48	L6	92/102 (90%)	90 (98%)	2 (2%)	0	100	100
49	L7	119/206 (58%)	114 (96%)	5 (4%)	0	100	100
50	L8	126/222 (57%)	124 (98%)	2 (2%)	0	100	100
51	SR	140/196 (71%)	134 (96%)	6 (4%)	0	100	100
52	Sf	366/439 (83%)	345 (94%)	19 (5%)	2 (0%)	24	54
53	SB	215/296 (73%)	200 (93%)	15 (7%)	0	100	100
54	SZ	130/167 (78%)	111 (85%)	18 (14%)	1 (1%)	16	44
55	SE	314/430 (73%)	289 (92%)	24 (8%)	1 (0%)	36	65
56	SF	120/125 (96%)	118 (98%)	2 (2%)	0	100	100
57	SG	197/242 (81%)	192 (98%)	4 (2%)	1 (0%)	24	54
58	SI	300/396 (76%)	267 (89%)	28 (9%)	5 (2%)	7	26
59	SJ	120/201 (60%)	101 (84%)	18 (15%)	1 (1%)	16	44
60	SK	134/194 (69%)	126 (94%)	8 (6%)	0	100	100
61	SL	106/138 (77%)	90 (85%)	12 (11%)	4 (4%)	2	10
62	SN	99/128 (77%)	86 (87%)	12 (12%)	1 (1%)	12	39
63	SO	162/257 (63%)	148 (91%)	12 (7%)	2 (1%)	10	34
64	SP	114/137 (83%)	105 (92%)	7 (6%)	2 (2%)	6	25
65	SQ	105/130 (81%)	91 (87%)	10 (10%)	4 (4%)	2	10
66	SS	183/258 (71%)	156 (85%)	24 (13%)	3 (2%)	7	27
67	ST	94/142 (66%)	89 (95%)	4 (4%)	1 (1%)	11	36
68	SW	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
69	SX	293/360 (81%)	274 (94%)	19 (6%)	0	100	100
70	SY	124/190 (65%)	115 (93%)	7 (6%)	2 (2%)	7	27
71	Sa	160/173 (92%)	143 (89%)	14 (9%)	3 (2%)	6	23
72	Sb	171/205 (83%)	168 (98%)	2 (1%)	1 (1%)	21	51
73	Sc	383/414 (92%)	364 (95%)	18 (5%)	1 (0%)	36	65
74	Sd	95/187 (51%)	85 (90%)	9 (10%)	1 (1%)	11	36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
75	Se	348/398 (87%)	333 (96%)	13 (4%)	2 (1%)	21	51
76	Sg	106/395 (27%)	98 (92%)	7 (7%)	1 (1%)	14	41
77	Si	84/106 (79%)	78 (93%)	6 (7%)	0	100	100
78	Sj	197/218 (90%)	161 (82%)	31 (16%)	5 (2%)	4	17
79	Sk	252/323 (78%)	217 (86%)	33 (13%)	2 (1%)	16	44
80	Sm	114/118 (97%)	107 (94%)	6 (5%)	1 (1%)	14	41
81	Sn	67/199 (34%)	65 (97%)	2 (3%)	0	100	100
82	So	614/689 (89%)	595 (97%)	19 (3%)	0	100	100
All	All	13557/17977 (75%)	12631 (93%)	846 (6%)	80 (1%)	23	51

All (80) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	LC	82	ASP
13	LQ	111	PRO
22	Lb	92	ALA
39	Lt	266	PRO
39	Lt	270	ALA
46	L4	88	PRO
58	SI	92	MET
61	SL	56	PRO
63	SO	78	ASN
71	Sa	143	VAL
74	Sd	116	PHE
76	Sg	317	ASN
7	LJ	104	LEU
11	LO	280	LYS
17	LU	179	ASN
31	LI	241	PRO
42	Lx	147	ASN
45	L3	47	LEU
58	SI	114	SER
61	SL	117	ASP
62	SN	95	SER
65	SQ	88	VAL
65	SQ	101	ALA
78	Sj	45	PHE
78	Sj	151	THR
79	Sk	76	PHE

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Mol	Chain	Res	Type
3	LB	195	ASN
8	LK	34	PRO
12	LP	46	GLU
32	Lm	60	PRO
47	L5	72	ARG
52	Sf	250	PHE
52	Sf	272	PRO
57	SG	129	ALA
61	SL	70	PRO
61	SL	72	LYS
63	SO	123	ARG
64	SP	12	TYR
66	SS	222	GLY
67	ST	78	GLN
72	Sb	50	PRO
75	Se	80	PRO
78	Sj	98	THR
80	Sm	64	ASP
9	LM	151	ILE
41	Lw	145	GLY
46	L4	136	LYS
54	SZ	155	LEU
58	SI	93	GLY
58	SI	392	THR
71	Sa	132	ARG
78	Sj	133	HIS
3	LB	67	LYS
4	LC	317	PRO
7	LJ	92	ASP
34	Lo	121	PRO
40	Lv	59	TYR
31	Ll	287	PRO
33	Ln	165	ASP
33	Ln	170	PRO
64	SP	64	LYS
66	SS	111	HIS
31	Ll	36	PRO
65	SQ	97	GLY
66	SS	200	TYR
75	Se	338	ASP
8	LK	31	PRO
65	SQ	99	PRO

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Mol	Chain	Res	Type
71	Sa	105	ILE
73	Sc	250	ILE
79	Sk	191	ILE
70	SY	110	GLY
7	LJ	175	PRO
18	LV	69	ARG
70	SY	77	VAL
78	Sj	134	VAL
23	Lu	203	PRO
55	SE	142	PRO
58	SI	295	VAL
59	SJ	167	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	LB	191/245 (78%)	191 (100%)	0	100	100
4	LC	258/290 (89%)	254 (98%)	4 (2%)	55	83
5	LD	217/262 (83%)	216 (100%)	1 (0%)	81	93
6	LI	86/228 (38%)	85 (99%)	1 (1%)	63	86
7	LJ	145/232 (62%)	139 (96%)	6 (4%)	27	61
8	LK	137/150 (91%)	131 (96%)	6 (4%)	25	59
9	LM	155/156 (99%)	154 (99%)	1 (1%)	78	93
10	LN	98/124 (79%)	96 (98%)	2 (2%)	48	78
11	LO	245/249 (98%)	244 (100%)	1 (0%)	84	94
12	LP	188/211 (89%)	187 (100%)	1 (0%)	81	93
13	LQ	133/150 (89%)	129 (97%)	4 (3%)	36	70
14	LR	128/154 (83%)	128 (100%)	0	100	100
15	LS	201/256 (78%)	200 (100%)	1 (0%)	81	93
16	LT	118/126 (94%)	116 (98%)	2 (2%)	53	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	LU	145/180 (81%)	145 (100%)	0	100	100
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%)	174 (97%)	6 (3%)	33	67
21	La	91/119 (76%)	91 (100%)	0	100	100
22	Lb	219/229 (96%)	217 (99%)	2 (1%)	70	90
23	Lu	159/223 (71%)	158 (99%)	1 (1%)	78	93
24	Ld	111/147 (76%)	109 (98%)	2 (2%)	51	80
25	Lf	97/164 (59%)	95 (98%)	2 (2%)	47	77
26	Lg	49/60 (82%)	49 (100%)	0	100	100
27	Lh	40/72 (56%)	39 (98%)	1 (2%)	42	74
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%)	350 (99%)	3 (1%)	73	90
31	Ll	313/332 (94%)	309 (99%)	4 (1%)	61	86
32	Lm	269/303 (89%)	268 (100%)	1 (0%)	84	94
33	Ln	91/190 (48%)	88 (97%)	3 (3%)	33	67
34	Lo	104/112 (93%)	103 (99%)	1 (1%)	68	89
35	Lp	93/133 (70%)	92 (99%)	1 (1%)	65	88
36	Lq	130/186 (70%)	125 (96%)	5 (4%)	29	64
37	Lr	241/288 (84%)	241 (100%)	0	100	100
38	Ls	196/274 (72%)	195 (100%)	1 (0%)	81	93
39	Lt	188/236 (80%)	179 (95%)	9 (5%)	23	55
40	Lv	116/188 (62%)	108 (93%)	8 (7%)	14	41
41	Lw	122/148 (82%)	120 (98%)	2 (2%)	55	83
42	Lx	104/148 (70%)	98 (94%)	6 (6%)	18	49
43	Ly	86/110 (78%)	85 (99%)	1 (1%)	63	86
44	Lz	73/97 (75%)	73 (100%)	0	100	100
45	L3	81/90 (90%)	80 (99%)	1 (1%)	63	86
46	L4	78/116 (67%)	77 (99%)	1 (1%)	61	86
47	L5	40/113 (35%)	38 (95%)	2 (5%)	22	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	L6	80/87 (92%)	79 (99%)	1 (1%)	61	86
49	L7	117/181 (65%)	116 (99%)	1 (1%)	70	90
50	L8	110/178 (62%)	110 (100%)	0	100	100
51	SR	133/169 (79%)	132 (99%)	1 (1%)	73	90
52	Sf	326/381 (86%)	322 (99%)	4 (1%)	63	86
53	SB	191/249 (77%)	188 (98%)	3 (2%)	55	83
54	SZ	115/143 (80%)	107 (93%)	8 (7%)	14	40
55	SE	267/357 (75%)	260 (97%)	7 (3%)	40	73
56	SF	104/107 (97%)	102 (98%)	2 (2%)	50	79
57	SG	178/209 (85%)	174 (98%)	4 (2%)	45	77
58	SI	263/342 (77%)	251 (95%)	12 (5%)	24	57
59	SJ	112/180 (62%)	109 (97%)	3 (3%)	39	73
60	SK	104/147 (71%)	103 (99%)	1 (1%)	68	89
61	SL	93/118 (79%)	90 (97%)	3 (3%)	34	68
62	SN	91/113 (80%)	80 (88%)	11 (12%)	5	16
63	SO	152/226 (67%)	149 (98%)	3 (2%)	48	78
64	SP	95/113 (84%)	89 (94%)	6 (6%)	16	45
65	SQ	93/115 (81%)	90 (97%)	3 (3%)	34	68
66	SS	166/230 (72%)	163 (98%)	3 (2%)	51	80
67	ST	87/123 (71%)	84 (97%)	3 (3%)	32	66
68	SW	78/79 (99%)	77 (99%)	1 (1%)	61	86
69	SX	263/318 (83%)	258 (98%)	5 (2%)	50	79
70	SY	109/164 (66%)	104 (95%)	5 (5%)	24	57
71	Sa	150/157 (96%)	146 (97%)	4 (3%)	39	73
72	Sb	148/174 (85%)	145 (98%)	3 (2%)	48	78
73	Sc	338/364 (93%)	335 (99%)	3 (1%)	70	90
74	Sd	84/158 (53%)	81 (96%)	3 (4%)	31	65
75	Se	310/351 (88%)	306 (99%)	4 (1%)	61	86
76	Sg	97/357 (27%)	92 (95%)	5 (5%)	21	52
77	Si	79/95 (83%)	75 (95%)	4 (5%)	21	53
78	Sj	175/190 (92%)	169 (97%)	6 (3%)	32	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
79	Sk	235/291 (81%)	218 (93%)	17 (7%)	13	39
80	Sm	99/101 (98%)	91 (92%)	8 (8%)	11	33
81	Sn	63/166 (38%)	62 (98%)	1 (2%)	55	83
82	So	548/609 (90%)	543 (99%)	5 (1%)	70	90
All	All	12121/15564 (78%)	11875 (98%)	246 (2%)	48	78

All (246) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	LC	78	CYS
4	LC	127	CYS
4	LC	187	ILE
4	LC	189	PRO
5	LD	194	GLU
6	LI	89	ARG
7	LJ	110	LEU
7	LJ	116	LEU
7	LJ	165	VAL
7	LJ	171	VAL
7	LJ	185	ILE
7	LJ	197	LEU
8	LK	19	VAL
8	LK	34	PRO
8	LK	38	VAL
8	LK	87	VAL
8	LK	151	LEU
8	LK	156	VAL
9	LM	149	ARG
10	LN	105	VAL
10	LN	121	THR
11	LO	261	ASP
12	LP	46	GLU
13	LQ	109	GLN
13	LQ	110	ILE
13	LQ	111	PRO
13	LQ	112	ASN
15	LS	241	LYS
16	LT	35	LYS
16	LT	149	HIS
20	LX	127	ASP
20	LX	134	GLU

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Mol	Chain	Res	Type
20	LX	144	VAL
20	LX	172	ASP
20	LX	193	THR
20	LX	211	LYS
22	Lb	60	GLU
22	Lb	168	ARG
23	Lu	171	ASP
24	Ld	99	VAL
24	Ld	113	VAL
25	Lf	108	ASP
25	Lf	121	VAL
27	Lh	92	HIS
30	Lk	49	VAL
30	Lk	67	VAL
30	Lk	393	LYS
31	Ll	50	LYS
31	Ll	241	PRO
31	Ll	279	ILE
31	Ll	321	CYS
32	Lm	172	VAL
33	Ln	163	LYS
33	Ln	168	LEU
33	Ln	177	HIS
34	Lo	123	GLN
35	Lp	37	SER
36	Lq	2	THR
36	Lq	58	ASN
36	Lq	91	CYS
36	Lq	119	PHE
36	Lq	138	THR
38	Ls	123	ARG
39	Lt	65	PRO
39	Lt	66	LEU
39	Lt	98	LEU
39	Lt	148	SER
39	Lt	198	ASN
39	Lt	217	PHE
39	Lt	232	PHE
39	Lt	256	THR
39	Lt	279	LEU
40	Lv	88	TYR
40	Lv	91	LEU

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Mol	Chain	Res	Type
40	Lv	102	LEU
40	Lv	113	LEU
40	Lv	145	LEU
40	Lv	155	ARG
40	Lv	182	VAL
40	Lv	186	VAL
41	Lw	68	THR
41	Lw	69	PRO
42	Lx	85	ASN
42	Lx	87	GLN
42	Lx	88	ASP
42	Lx	89	ILE
42	Lx	90	SER
42	Lx	122	ARG
43	Ly	32	ILE
45	L3	10	LEU
46	L4	73	MET
47	L5	69	ARG
47	L5	73	ARG
48	L6	101	TRP
49	L7	95	VAL
51	SR	108	CYS
52	Sf	240	GLN
52	Sf	251	VAL
52	Sf	256	SER
52	Sf	271	LEU
53	SB	109	SER
53	SB	207	VAL
53	SB	219	THR
54	SZ	51	VAL
54	SZ	54	GLU
54	SZ	92	LEU
54	SZ	108	LEU
54	SZ	111	LYS
54	SZ	118	GLU
54	SZ	143	LEU
54	SZ	158	VAL
55	SE	91	THR
55	SE	146	VAL
55	SE	214	THR
55	SE	228	VAL
55	SE	240	SER

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Mol	Chain	Res	Type
55	SE	276	VAL
55	SE	337	SER
56	SF	72	THR
56	SF	109	VAL
57	SG	123	PHE
57	SG	189	THR
57	SG	200	LEU
57	SG	231	GLU
58	SI	108	ILE
58	SI	112	PHE
58	SI	124	VAL
58	SI	210	VAL
58	SI	228	LEU
58	SI	229	LEU
58	SI	232	GLN
58	SI	258	GLU
58	SI	261	GLN
58	SI	262	TYR
58	SI	298	ILE
58	SI	357	THR
59	SJ	62	VAL
59	SJ	158	GLU
59	SJ	160	ILE
60	SK	81	GLU
61	SL	56	PRO
61	SL	104	GLU
61	SL	117	ASP
62	SN	29	TYR
62	SN	31	ASP
62	SN	62	ILE
62	SN	63	LEU
62	SN	65	LYS
62	SN	67	LEU
62	SN	70	VAL
62	SN	83	CYS
62	SN	92	VAL
62	SN	94	THR
62	SN	121	SER
63	SO	82	ILE
63	SO	97	MET
63	SO	111	PHE
64	SP	93	LEU

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Mol	Chain	Res	Type
64	SP	97	PHE
64	SP	99	LEU
64	SP	101	PRO
64	SP	104	ILE
64	SP	111	ARG
65	SQ	71	VAL
65	SQ	81	LEU
65	SQ	110	LEU
66	SS	93	THR
66	SS	193	LEU
66	SS	235	MET
67	ST	52	ILE
67	ST	66	ILE
67	ST	68	CYS
68	SW	56	SER
69	SX	82	MET
69	SX	154	THR
69	SX	273	TRP
69	SX	289	ILE
69	SX	326	ASN
70	SY	80	SER
70	SY	87	LEU
70	SY	89	ASN
70	SY	94	SER
70	SY	108	LYS
71	Sa	79	TYR
71	Sa	140	ILE
71	Sa	149	CYS
71	Sa	150	PRO
72	Sb	106	MET
72	Sb	125	ARG
72	Sb	192	THR
73	Sc	32	SER
73	Sc	250	ILE
73	Sc	322	THR
74	Sd	83	MET
74	Sd	87	SER
74	Sd	138	THR
75	Se	71	SER
75	Se	73	GLN
75	Se	99	LEU
75	Se	132	THR

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Mol	Chain	Res	Type
76	Sg	309	LYS
76	Sg	310	LEU
76	Sg	312	GLU
76	Sg	315	ILE
76	Sg	372	HIS
77	Si	66	ARG
77	Si	68	LEU
77	Si	76	GLN
77	Si	80	ASP
78	Sj	65	LEU
78	Sj	129	ARG
78	Sj	130	GLU
78	Sj	135	MET
78	Sj	141	LEU
78	Sj	207	GLN
79	Sk	57	THR
79	Sk	91	VAL
79	Sk	97	MET
79	Sk	106	LEU
79	Sk	109	PRO
79	Sk	143	CYS
79	Sk	162	SER
79	Sk	163	VAL
79	Sk	185	HIS
79	Sk	187	LYS
79	Sk	190	LEU
79	Sk	209	THR
79	Sk	257	SER
79	Sk	261	ASN
79	Sk	265	THR
79	Sk	293	LYS
79	Sk	296	VAL
80	Sm	33	VAL
80	Sm	50	SER
80	Sm	53	MET
80	Sm	57	LYS
80	Sm	58	GLN
80	Sm	66	CYS
80	Sm	70	ILE
80	Sm	107	LEU
81	Sn	144	ARG
82	So	116	VAL

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Mol	Chain	Res	Type
82	So	212	THR
82	So	292	TYR
82	So	360	MET
82	So	508	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (149) such sidechains are listed below:

Mol	Chain	Res	Type
3	LB	128	GLN
3	LB	156	ASN
3	LB	195	ASN
3	LB	235	GLN
4	LC	125	GLN
4	LC	280	HIS
5	LD	188	HIS
5	LD	241	ASN
6	LI	126	GLN
7	LJ	115	GLN
7	LJ	119	HIS
7	LJ	193	ASN
8	LK	168	GLN
8	LK	178	GLN
9	LM	9	GLN
9	LM	117	HIS
9	LM	140	ASN
9	LM	147	GLN
10	LN	59	HIS
10	LN	80	GLN
10	LN	113	ASN
11	LO	170	ASN
12	LP	237	HIS
13	LQ	154	GLN
14	LR	49	ASN
14	LR	146	GLN
15	LS	203	ASN
15	LS	239	ASN
16	LT	94	GLN
17	LU	76	HIS
17	LU	84	ASN
20	LX	18	HIS
20	LX	78	GLN
21	La	72	HIS

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Mol	Chain	Res	Type
23	Lu	117	GLN
23	Lu	183	GLN
24	Ld	107	ASN
28	Li	185	ASN
30	Lk	94	HIS
30	Lk	269	ASN
30	Lk	275	ASN
30	Lk	280	GLN
31	Ll	266	HIS
32	Lm	231	GLN
33	Ln	144	GLN
33	Ln	158	HIS
35	Lp	111	GLN
36	Lq	129	GLN
37	Lr	65	ASN
37	Lr	73	GLN
37	Lr	134	GLN
37	Lr	222	GLN
38	Ls	119	GLN
38	Ls	205	GLN
38	Ls	251	GLN
39	Lt	75	GLN
39	Lt	248	ASN
40	Lv	92	ASN
40	Lv	94	HIS
40	Lv	138	GLN
40	Lv	153	HIS
41	Lw	46	GLN
42	Lx	110	HIS
44	Lz	89	GLN
45	L3	46	ASN
46	L4	76	ASN
49	L7	104	HIS
49	L7	176	HIS
52	Sf	339	GLN
52	Sf	386	ASN
52	Sf	387	ASN
52	Sf	420	GLN
53	SB	64	ASN
53	SB	126	GLN
53	SB	167	HIS
55	SE	130	GLN

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Mol	Chain	Res	Type
55	SE	280	HIS
55	SE	369	HIS
56	SF	59	ASN
56	SF	92	ASN
57	SG	122	GLN
57	SG	151	ASN
57	SG	169	GLN
57	SG	197	GLN
57	SG	215	ASN
58	SI	82	ASN
58	SI	101	GLN
58	SI	176	GLN
58	SI	232	GLN
59	SJ	161	GLN
59	SJ	176	GLN
60	SK	146	HIS
61	SL	74	ASN
62	SN	117	HIS
62	SN	124	GLN
63	SO	174	ASN
63	SO	218	GLN
65	SQ	44	ASN
66	SS	146	GLN
66	SS	160	HIS
66	SS	225	GLN
67	ST	71	HIS
67	ST	78	GLN
68	SW	53	GLN
68	SW	79	ASN
69	SX	246	HIS
69	SX	315	GLN
69	SX	350	GLN
70	SY	89	ASN
70	SY	97	GLN
71	Sa	54	GLN
71	Sa	56	GLN
72	Sb	43	ASN
72	Sb	109	ASN
72	Sb	131	GLN
72	Sb	133	GLN
72	Sb	135	GLN
72	Sb	161	GLN

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Mol	Chain	Res	Type
72	Sb	188	ASN
73	Sc	246	ASN
73	Sc	358	GLN
73	Sc	381	GLN
73	Sc	405	GLN
74	Sd	86	HIS
75	Se	54	ASN
75	Se	66	GLN
75	Se	90	GLN
75	Se	159	HIS
75	Se	358	GLN
75	Se	367	GLN
76	Sg	329	HIS
76	Sg	331	HIS
76	Sg	372	HIS
77	Si	55	HIS
78	Sj	88	GLN
78	Sj	137	HIS
79	Sk	64	GLN
79	Sk	217	GLN
79	Sk	321	ASN
80	Sm	59	ASN
81	Sn	141	HIS
81	Sn	158	GLN
82	So	136	HIS
82	So	189	ASN
82	So	243	ASN
82	So	255	ASN
82	So	436	HIS
82	So	444	ASN
82	So	452	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L1	1491/1559 (95%)	384 (25%)	27 (1%)
2	L2	52/69 (75%)	13 (25%)	0
83	S1	921/954 (96%)	208 (22%)	16 (1%)
All	All	2464/2582 (95%)	605 (24%)	43 (1%)

All (605) 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	36	C
1	L1	38	A
1	L1	39	G
1	L1	40	A
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	62	C
1	L1	63	C
1	L1	66	A
1	L1	78	G
1	L1	91	A
1	L1	98	G
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

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Mol	Chain	Res	Type
1	L1	136	U
1	L1	137	U
1	L1	138	A
1	L1	142	C
1	L1	147	C
1	L1	151	A
1	L1	154	U
1	L1	157	C
1	L1	158	A
1	L1	159	A
1	L1	162	A
1	L1	164	U
1	L1	166	A
1	L1	173	U
1	L1	174	A
1	L1	179	C
1	L1	184	U
1	L1	186	A
1	L1	197	A
1	L1	198	G
1	L1	199	A
1	L1	200	A
1	L1	201	A
1	L1	203	A
1	L1	212	A
1	L1	213	G
1	L1	215	A
1	L1	217	A
1	L1	218	G
1	L1	220	C
1	L1	223	A
1	L1	232	C
1	L1	233	C
1	L1	248	G
1	L1	257	G
1	L1	266	A
1	L1	267	A
1	L1	270	A
1	L1	274	C
1	L1	298	G
1	L1	304	A
1	L1	305	U

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Mol	Chain	Res	Type
1	L1	315	G
1	L1	317	G
1	L1	322	C
1	L1	324	A
1	L1	325	A
1	L1	330	C
1	L1	331	C
1	L1	332	G
1	L1	345	G
1	L1	346	C
1	L1	352	G
1	L1	359	A
1	L1	361	A
1	L1	362	G
1	L1	367	U
1	L1	369	A
1	L1	371	U
1	L1	375	A
1	L1	383	U
1	L1	385	U
1	L1	387	C
1	L1	390	A
1	L1	395	A
1	L1	396	C
1	L1	404	A
1	L1	413	U
1	L1	415	A
1	L1	423	U
1	L1	427	A
1	L1	429	U
1	L1	443	G
1	L1	454	A
1	L1	455	C
1	L1	456	U
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

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Mol	Chain	Res	Type
1	L1	489	U
1	L1	493	A
1	L1	498	U
1	L1	503	G
1	L1	507	U
1	L1	510	A
1	L1	511	A
1	L1	512	G
1	L1	513	C
1	L1	519	C
1	L1	522	A
1	L1	527	G
1	L1	528	A
1	L1	530	A
1	L1	540	C
1	L1	545	C
1	L1	546	A
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	560	A
1	L1	563	U
1	L1	565	C
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	582	C
1	L1	590	A
1	L1	591	C
1	L1	592	C
1	L1	593	C
1	L1	614	C
1	L1	615	U
1	L1	620	A

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Mol	Chain	Res	Type
1	L1	621	A
1	L1	624	A
1	L1	627	A
1	L1	629	U
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	701	U
1	L1	702	U
1	L1	704	A
1	L1	711	A
1	L1	714	A
1	L1	720	A
1	L1	723	C
1	L1	724	A
1	L1	726	C
1	L1	730	C
1	L1	731	A
1	L1	734	U
1	L1	735	C
1	L1	737	U
1	L1	744	C
1	L1	745	C
1	L1	756	C
1	L1	762	A
1	L1	771	C
1	L1	773	C
1	L1	774	A
1	L1	775	U
1	L1	777	A
1	L1	779	G
1	L1	794	G
1	L1	798	A
1	L1	801	G
1	L1	808	G
1	L1	809	C
1	L1	814	C
1	L1	815	U

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Mol	Chain	Res	Type
1	L1	823	C
1	L1	830	A
1	L1	832	C
1	L1	834	A
1	L1	836	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
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	918	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	957	G
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	984	U

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Mol	Chain	Res	Type
1	L1	985	G
1	L1	986	U
1	L1	990	U
1	L1	1014	C
1	L1	1016	G
1	L1	1024	A
1	L1	1025	G
1	L1	1026	A
1	L1	1027	G
1	L1	1029	C
1	L1	1032	G
1	L1	1036	A
1	L1	1038	C
1	L1	1039	A
1	L1	1048	C
1	L1	1049	G
1	L1	1053	A
1	L1	1054	G
1	L1	1055	A
1	L1	1056	C
1	L1	1057	C
1	L1	1060	A
1	L1	1062	G
1	L1	1069	U
1	L1	1074	U
1	L1	1075	A
1	L1	1087	A
1	L1	1088	G
1	L1	1089	U
1	L1	1134	A
1	L1	1140	G
1	L1	1161	G
1	L1	1162	A
1	L1	1163	A
1	L1	1174	G
1	L1	1177	C
1	L1	1184	U
1	L1	1185	G
1	L1	1191	A
1	L1	1194	U
1	L1	1195	C
1	L1	1222	A

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Mol	Chain	Res	Type
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	1245	C
1	L1	1246	G
1	L1	1247	G
1	L1	1248	A
1	L1	1249	A
1	L1	1250	C
1	L1	1252	A
1	L1	1256	A
1	L1	1257	C
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
1	L1	1304	A
1	L1	1305	G
1	L1	1307	G
1	L1	1308	U
1	L1	1309	U
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	1323	U
1	L1	1324	U
1	L1	1335	A
1	L1	1337	C
1	L1	1346	G
1	L1	1351	C
1	L1	1352	G
1	L1	1372	U

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Mol	Chain	Res	Type
1	L1	1379	U
1	L1	1383	A
1	L1	1384	G
1	L1	1386	C
1	L1	1390	C
1	L1	1393	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	1443	A
1	L1	1444	U
1	L1	1452	U
1	L1	1461	G
1	L1	1465	A
1	L1	1469	G
1	L1	1479	C
1	L1	1480	U
1	L1	1482	C
1	L1	1485	C
1	L1	1487	C
1	L1	1488	A
1	L1	1490	A
1	L1	1491	G
1	L1	1492	C
1	L1	1498	C
1	L1	1499	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

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Mol	Chain	Res	Type
1	L1	1540	C
1	L1	1542	C
1	L1	1547	A
1	L1	1548	A
1	L1	1550	A
2	L2	4	A
2	L2	7	G
2	L2	8	U
2	L2	9	A
2	L2	10	G
2	L2	13	U
2	L2	14	A
2	L2	40	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	10	G
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
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	118	C
83	S1	119	G
83	S1	125	A

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Mol	Chain	Res	Type
83	S1	126	U
83	S1	130	G
83	S1	134	A
83	S1	144	G
83	S1	149	G
83	S1	160	A
83	S1	165	A
83	S1	167	A
83	S1	168	C
83	S1	170	G
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	200	G
83	S1	207	U
83	S1	209	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	243	C
83	S1	246	G
83	S1	252	G
83	S1	257	C
83	S1	261	C
83	S1	270	C
83	S1	272	A
83	S1	275	C
83	S1	286	G
83	S1	289	G
83	S1	291	A
83	S1	292	A
83	S1	295	A
83	S1	296	G
83	S1	303	A

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Mol	Chain	Res	Type
83	S1	306	U
83	S1	307	C
83	S1	308	A
83	S1	320	A
83	S1	328	A
83	S1	331	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	363	A
83	S1	364	C
83	S1	368	A
83	S1	372	A
83	S1	374	U
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	451	C
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	489	C
83	S1	497	U
83	S1	504	C
83	S1	507	A
83	S1	508	G

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Mol	Chain	Res	Type
83	S1	519	A
83	S1	520	A
83	S1	525	C
83	S1	532	G
83	S1	533	U
83	S1	537	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	580	G
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	611	A
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	667	C
83	S1	670	A
83	S1	676	G

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Mol	Chain	Res	Type
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
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	745	A
83	S1	755	A
83	S1	756	A
83	S1	768	G
83	S1	769	A
83	S1	770	A
83	S1	773	U
83	S1	783	A
83	S1	794	A
83	S1	797	A
83	S1	800	G
83	S1	823	A
83	S1	833	A
83	S1	834	C
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	879	U
83	S1	885	C
83	S1	888	U
83	S1	889	A
83	S1	890	C
83	S1	891	G

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Mol	Chain	Res	Type
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
83	S1	918	A
83	S1	921	U
83	S1	935	G
83	S1	937	A
83	S1	943	A
83	S1	947	G
83	S1	948	G
83	S1	952	A

All (43) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L1	33	C
1	L1	133	A
1	L1	200	A
1	L1	304	A
1	L1	324	A
1	L1	395	A
1	L1	427	A
1	L1	465	A
1	L1	510	A
1	L1	511	A
1	L1	526	A
1	L1	528	A
1	L1	551	C
1	L1	575	A
1	L1	592	C
1	L1	710	C
1	L1	773	C
1	L1	814	C
1	L1	837	A
1	L1	853	C
1	L1	860	A
1	L1	889	U

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Mol	Chain	Res	Type
1	L1	929	U
1	L1	1055	A
1	L1	1235	A
1	L1	1319	G
1	L1	1371	U
83	S1	70	G
83	S1	117	A
83	S1	374	U
83	S1	383	G
83	S1	507	A
83	S1	519	A
83	S1	542	U
83	S1	599	U
83	S1	600	G
83	S1	611	A
83	S1	684	A
83	S1	722	U
83	S1	768	G
83	S1	864	C
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 [i](#)

Of 157 ligands modelled in this entry, 152 are monoatomic - leaving 5 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	1706	84	45,45,45	1.13	4 (8%)	56,72,72	0.86	2 (3%)
85	T1C	L1	1707	84	45,45,45	1.15	4 (8%)	56,72,72	0.97	4 (7%)
85	T1C	S1	1034	84	45,45,45	1.18	4 (8%)	56,72,72	0.98	2 (3%)
87	GDP	Se	500	-	29,30,30	1.16	3 (10%)	45,47,47	1.86	7 (15%)
85	T1C	S1	1035	-	45,45,45	1.13	4 (8%)	56,72,72	1.09	5 (8%)

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	1706	84	-	10/22/80/80	0/4/4/4
85	T1C	L1	1707	84	-	9/22/80/80	0/4/4/4
85	T1C	S1	1034	84	-	10/22/80/80	0/4/4/4
87	GDP	Se	500	-	-	3/16/32/32	0/3/3/3
85	T1C	S1	1035	-	-	7/22/80/80	0/4/4/4

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	S1	1034	T1C	C21-N21	5.02	1.47	1.33
85	L1	1707	T1C	C21-N21	5.00	1.47	1.33
85	S1	1035	T1C	C21-N21	4.99	1.47	1.33
85	L1	1706	T1C	C21-N21	4.90	1.47	1.33
87	Se	500	GDP	C5-C4	3.19	1.47	1.38
85	S1	1034	T1C	C4-N4	2.52	1.52	1.47
87	Se	500	GDP	C6-N1	-2.50	1.34	1.38
85	L1	1707	T1C	C4-N4	2.31	1.52	1.47
85	S1	1034	T1C	O11-C11	2.30	1.28	1.23
85	S1	1035	T1C	O11-C11	2.28	1.28	1.23
85	S1	1035	T1C	C4-N4	2.24	1.52	1.47
85	L1	1706	T1C	O11-C11	2.24	1.27	1.23
85	L1	1706	T1C	C4-N4	2.23	1.52	1.47
85	L1	1707	T1C	O11-C11	2.13	1.27	1.23
87	Se	500	GDP	C5-N7	-2.11	1.34	1.39
85	S1	1035	T1C	C7-N7	2.11	1.48	1.42
85	S1	1034	T1C	C7-N7	2.08	1.48	1.42
85	L1	1706	T1C	C7-N7	2.08	1.48	1.42
85	L1	1707	T1C	C7-N7	2.07	1.48	1.42

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
87	Se	500	GDP	C5-C4-N3	-6.57	117.93	128.39
87	Se	500	GDP	C2-N3-C4	5.33	121.48	112.30
87	Se	500	GDP	N9-C4-N3	5.01	135.96	125.95
85	S1	1035	T1C	C11-C1B-C12	4.06	122.01	118.80
85	S1	1034	T1C	C1-C1C-C12	3.83	114.37	109.88
85	S1	1034	T1C	C11-C1B-C12	3.48	121.56	118.80
85	S1	1035	T1C	C1-C1C-C12	3.42	113.90	109.88
87	Se	500	GDP	C6-C5-N7	3.01	135.76	130.29
85	L1	1707	T1C	C1C-C1-C2	2.87	120.31	115.75
85	L1	1707	T1C	O1C-C1C-C12	-2.75	105.74	110.14
85	L1	1707	T1C	C11-C1B-C12	2.74	120.96	118.80
85	L1	1706	T1C	C11-C1B-C12	2.73	120.96	118.80
87	Se	500	GDP	C3'-C2'-C1'	2.48	106.14	101.46
87	Se	500	GDP	C4-C5-N7	-2.45	106.78	110.67
85	S1	1035	T1C	C1C-C41-C4	2.37	114.88	111.64
85	S1	1035	T1C	O1C-C1C-C12	-2.23	106.57	110.14
85	L1	1706	T1C	C1C-C1-C2	2.23	119.29	115.75
87	Se	500	GDP	O6-C6-C5	-2.17	120.81	126.53
85	L1	1707	T1C	C1C-C41-C4	2.07	114.47	111.64
85	S1	1035	T1C	C5-C41-C4	-2.01	110.83	113.73

There are no chirality outliers.

All (39) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
85	L1	1706	T1C	C41-C4-N4-C43
85	L1	1706	T1C	C3-C4-N4-C43
85	L1	1706	T1C	C3-C4-N4-C42
85	L1	1707	T1C	C41-C4-N4-C43
85	L1	1707	T1C	C3-C4-N4-C43
85	L1	1707	T1C	C3-C4-N4-C42
85	S1	1034	T1C	C92-C91-N9-C9
85	S1	1035	T1C	C3-C2-C21-O21
87	Se	500	GDP	O4'-C1'-N9-C8
87	Se	500	GDP	O4'-C1'-N9-C4
85	S1	1034	T1C	O91-C91-N9-C9
85	L1	1707	T1C	C92-C91-N9-C9
85	S1	1035	T1C	C92-C91-N9-C9
85	L1	1707	T1C	O91-C91-N9-C9
85	S1	1035	T1C	O91-C91-N9-C9
85	L1	1707	T1C	N9-C91-C92-N92

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Mol	Chain	Res	Type	Atoms
85	L1	1706	T1C	O91-C91-C92-N92
85	L1	1706	T1C	N9-C91-C92-N92
85	L1	1707	T1C	O91-C91-C92-N92
85	L1	1706	T1C	C41-C4-N4-C42
85	L1	1706	T1C	C3-C2-C21-N21
85	L1	1707	T1C	C3-C2-C21-N21
85	S1	1034	T1C	C3-C2-C21-N21
85	S1	1035	T1C	C3-C2-C21-N21
85	L1	1706	T1C	C3-C2-C21-O21
85	S1	1034	T1C	C3-C2-C21-O21
85	L1	1706	T1C	C1-C2-C21-N21
85	L1	1707	T1C	C1-C2-C21-N21
85	S1	1034	T1C	C1-C2-C21-N21
85	S1	1035	T1C	C1-C2-C21-N21
85	S1	1035	T1C	N9-C91-C92-N92
85	S1	1034	T1C	N9-C91-C92-N92
85	S1	1035	T1C	O91-C91-C92-N92
85	S1	1034	T1C	O91-C91-C92-N92
85	L1	1706	T1C	C10-C9-N9-C91
87	Se	500	GDP	O4'-C4'-C5'-O5'
85	S1	1034	T1C	C61-C7-N7-C72
85	S1	1034	T1C	C41-C4-N4-C42
85	S1	1034	T1C	C61-C7-N7-C71

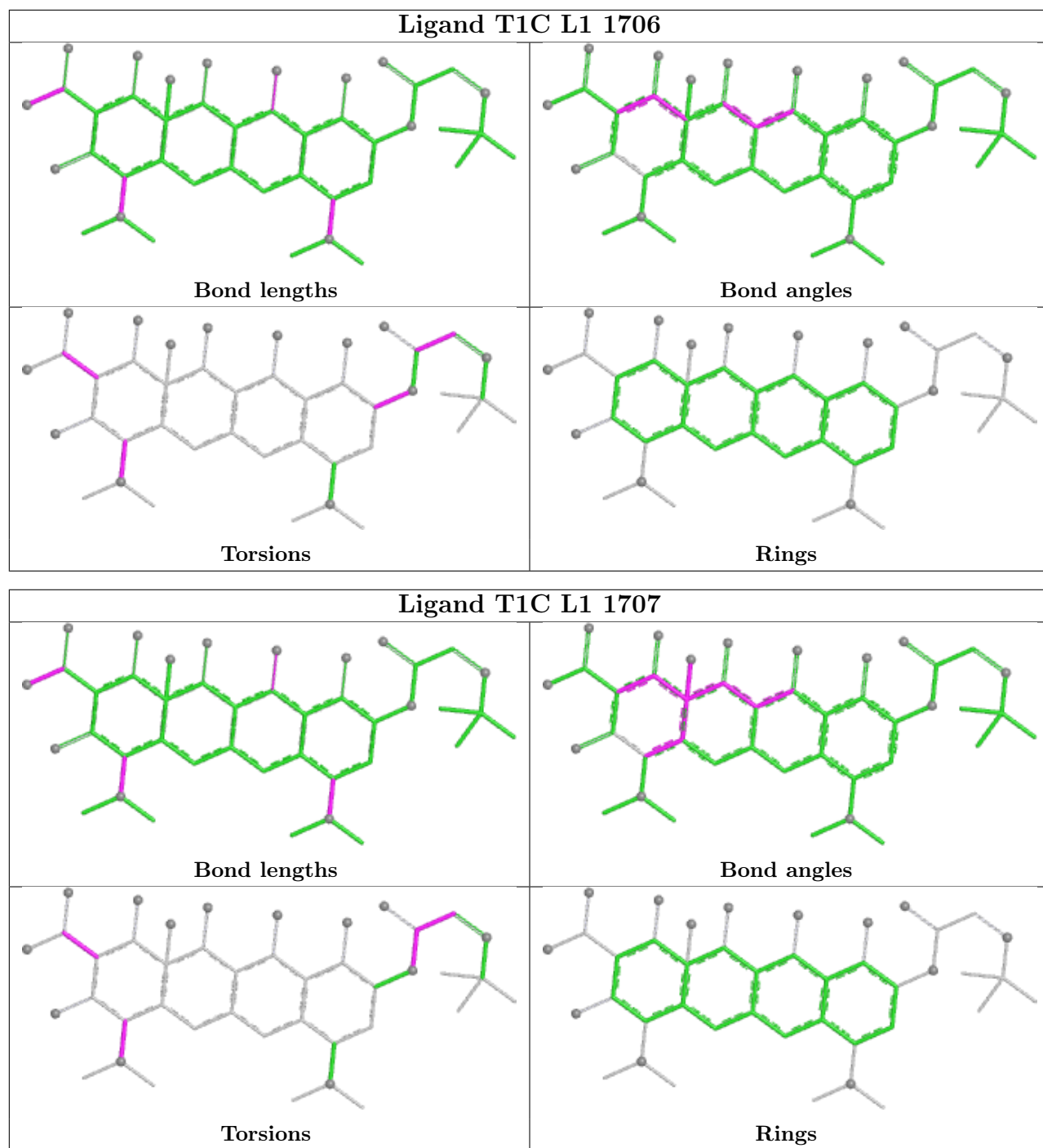
There are no ring outliers.

2 monomers are involved in 2 short contacts:

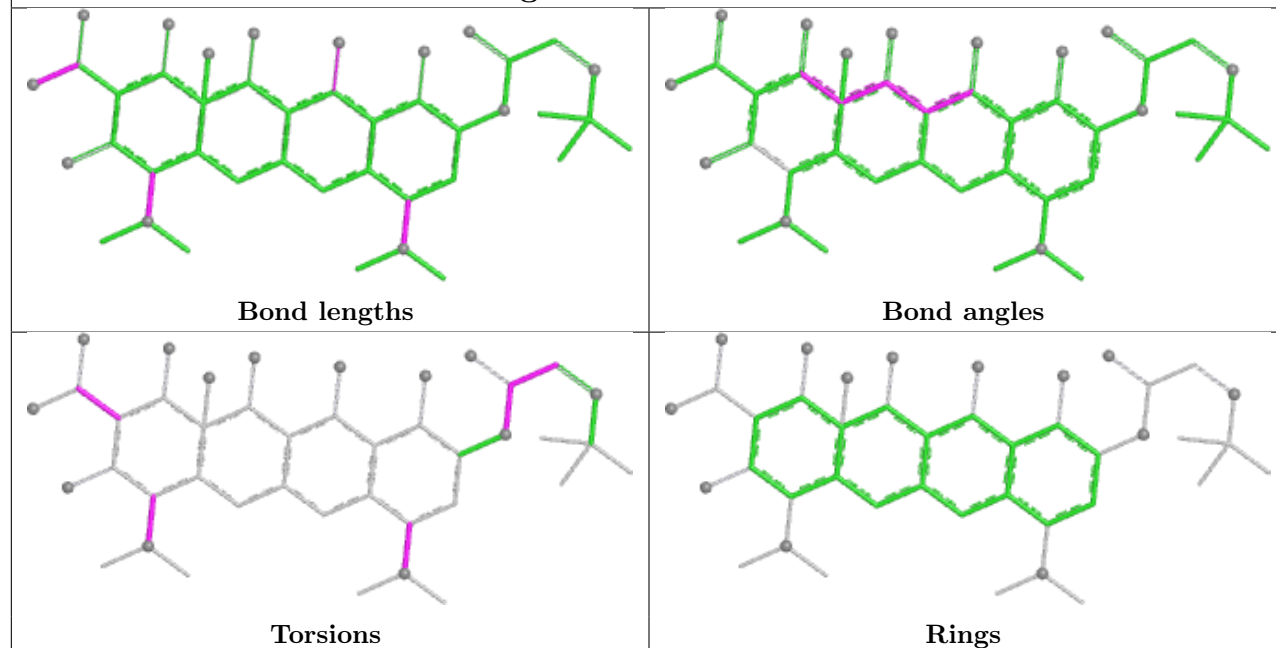
Mol	Chain	Res	Type	Clashes	Symm-Clashes
85	L1	1707	T1C	1	0
85	S1	1034	T1C	1	0

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

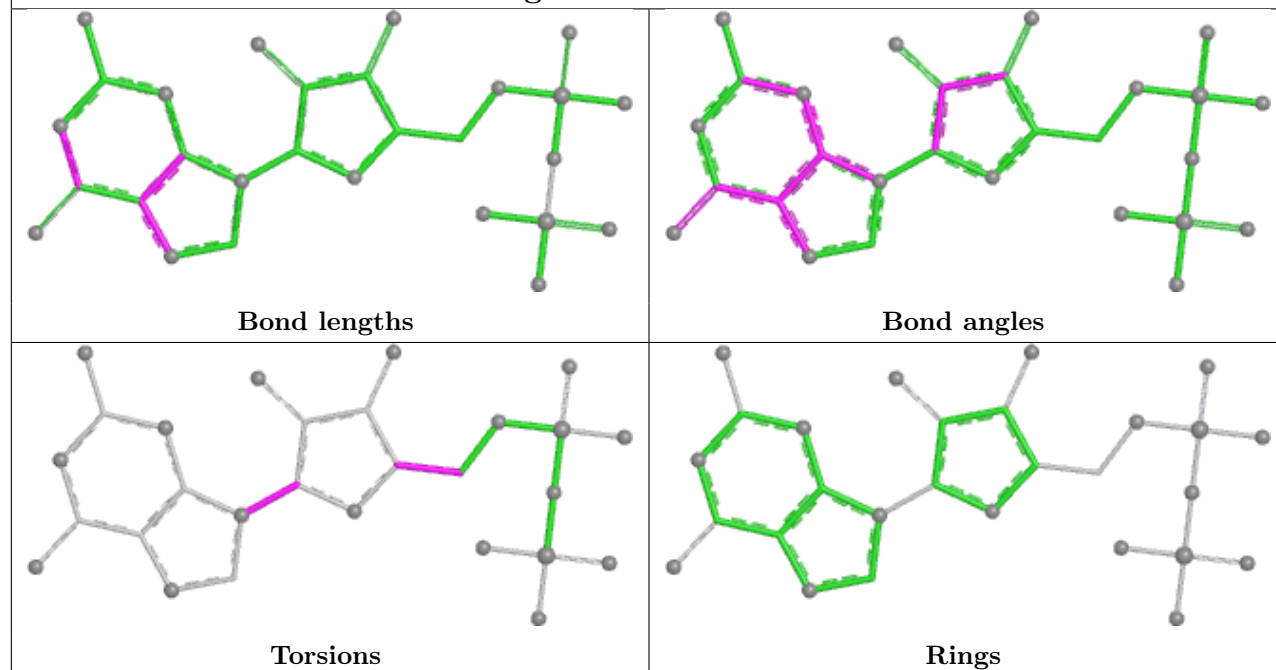
equivalents in the CSD to analyse the geometry.

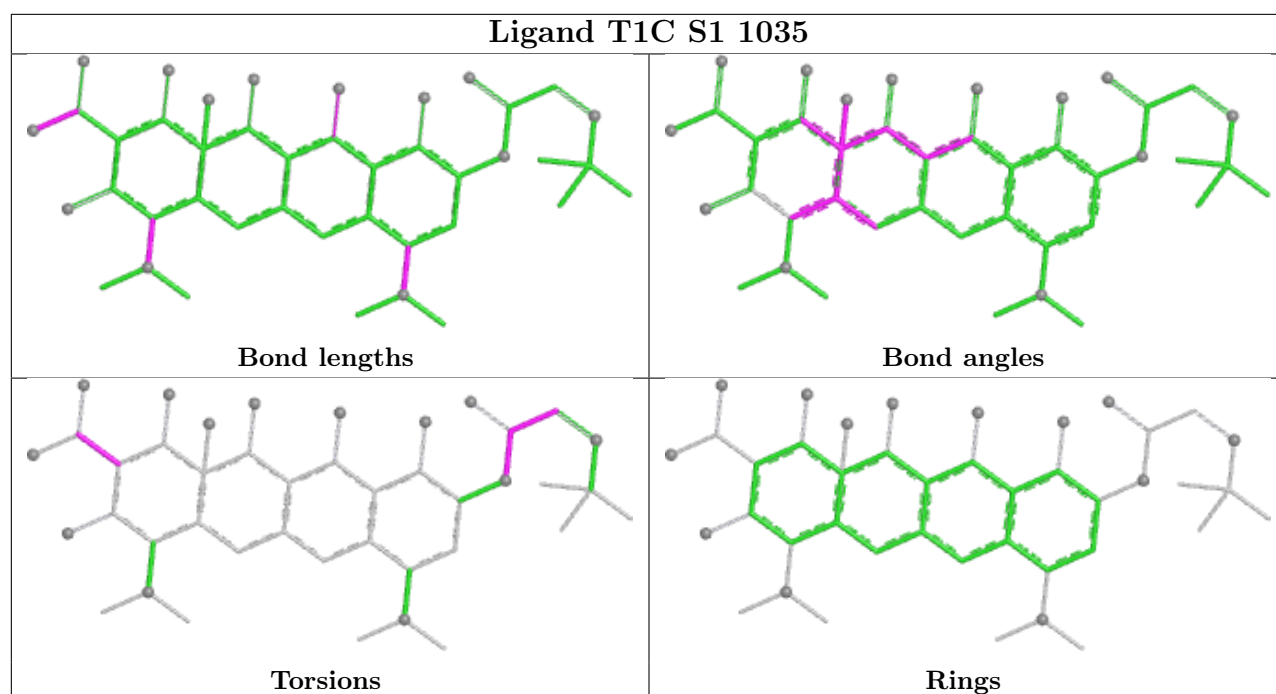


Ligand T1C S1 1034



Ligand GDP Se 500





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.

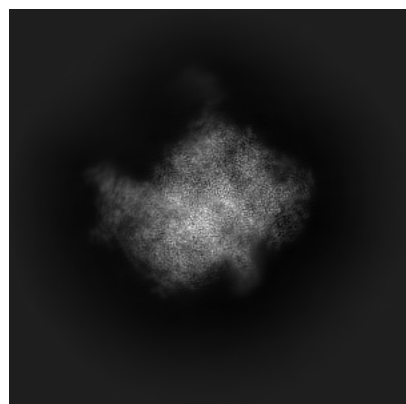
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-36836. These allow visual inspection of the internal detail of the map and identification of artifacts.

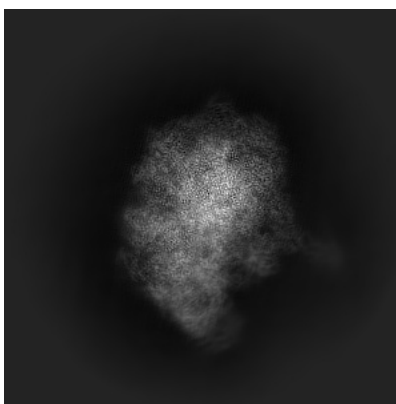
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

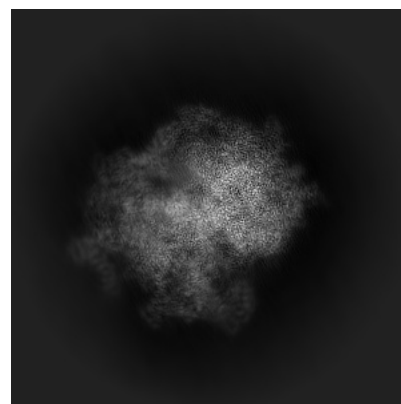
6.1.1 Primary map



X

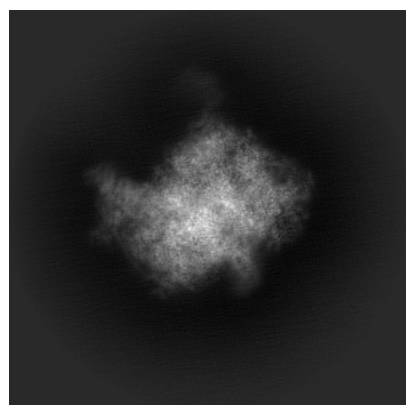


Y

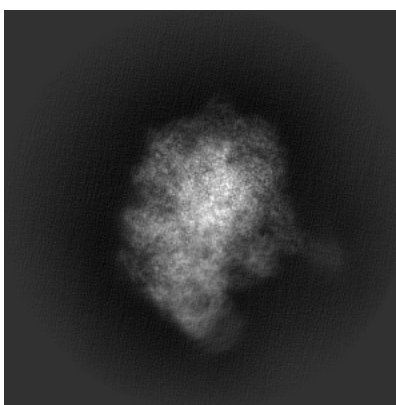


Z

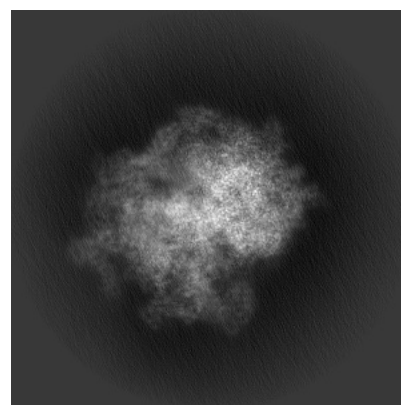
6.1.2 Raw map



X



Y

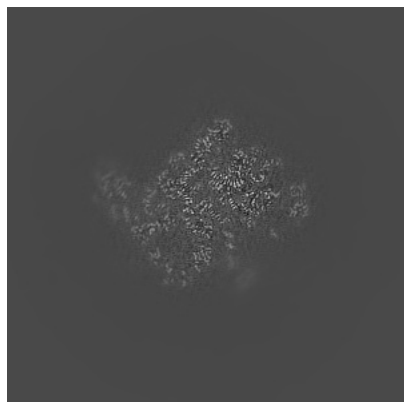


Z

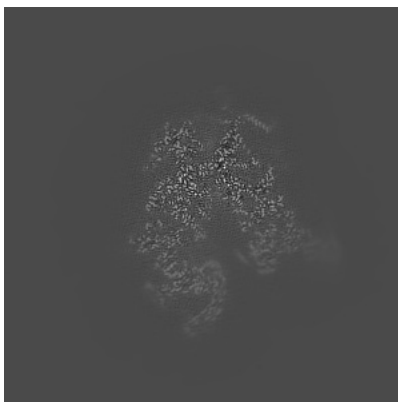
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

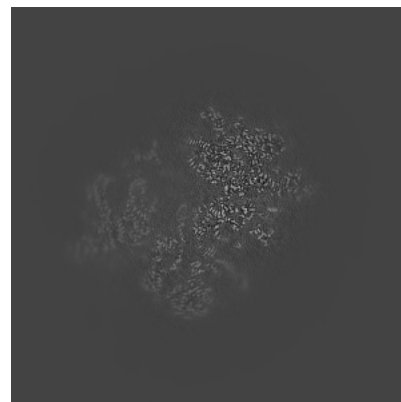
6.2.1 Primary map



X Index: 210

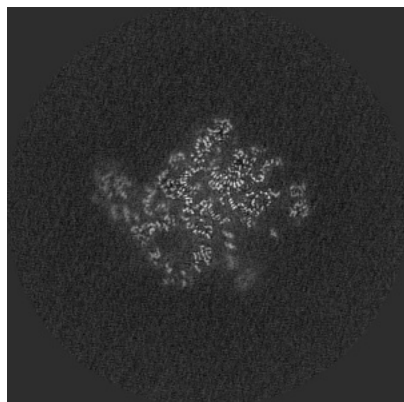


Y Index: 210

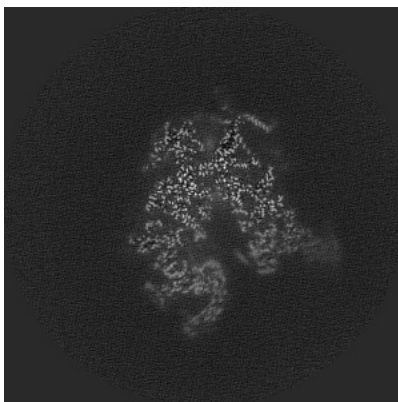


Z Index: 210

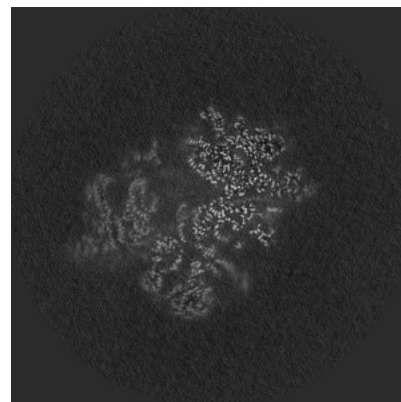
6.2.2 Raw map



X Index: 210



Y Index: 210

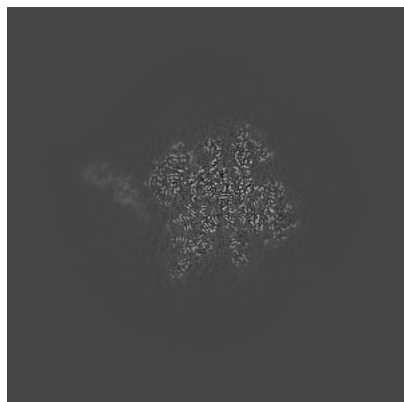


Z Index: 210

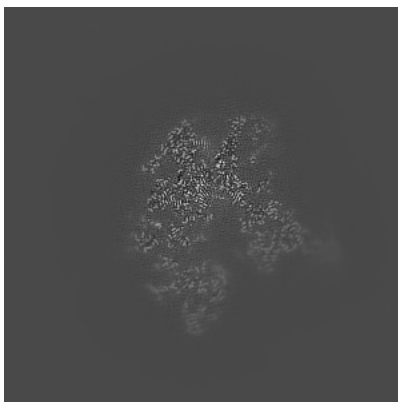
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

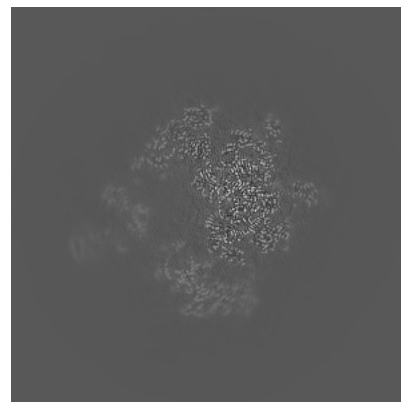
6.3.1 Primary map



X Index: 236

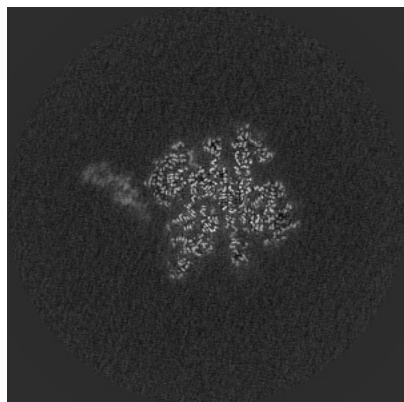


Y Index: 206

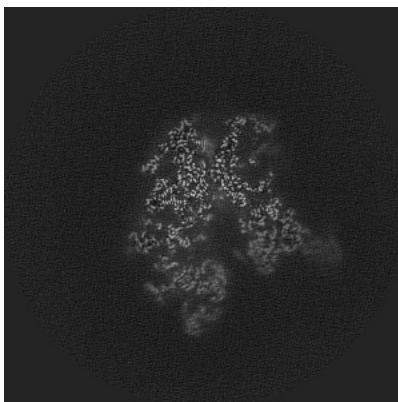


Z Index: 230

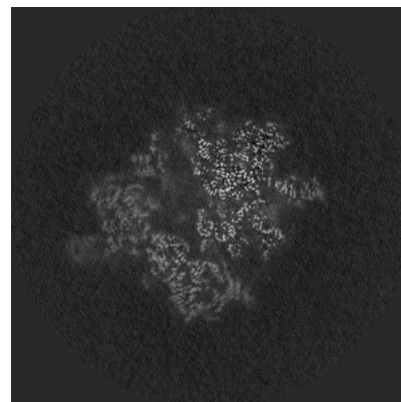
6.3.2 Raw map



X Index: 236



Y Index: 207

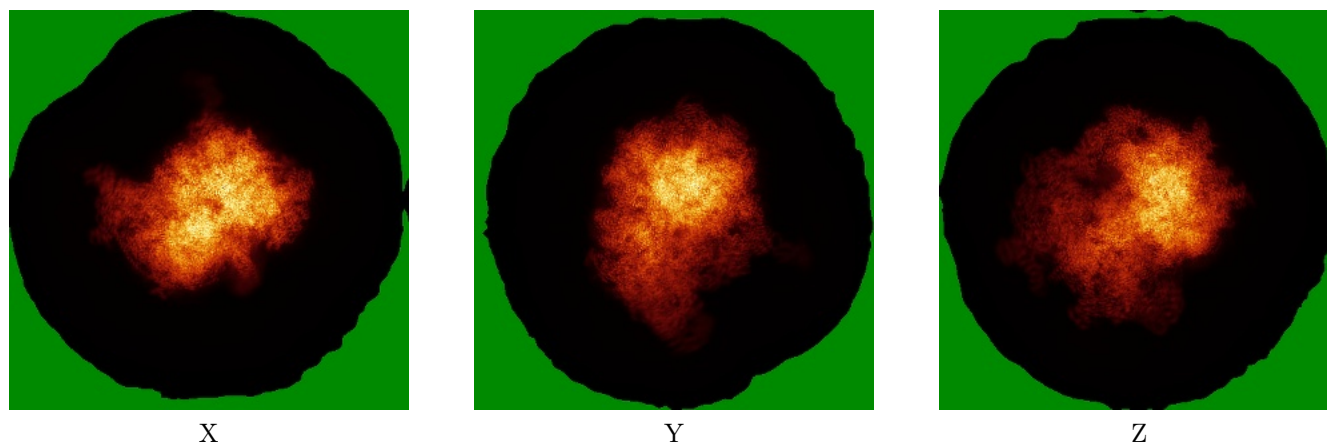


Z Index: 218

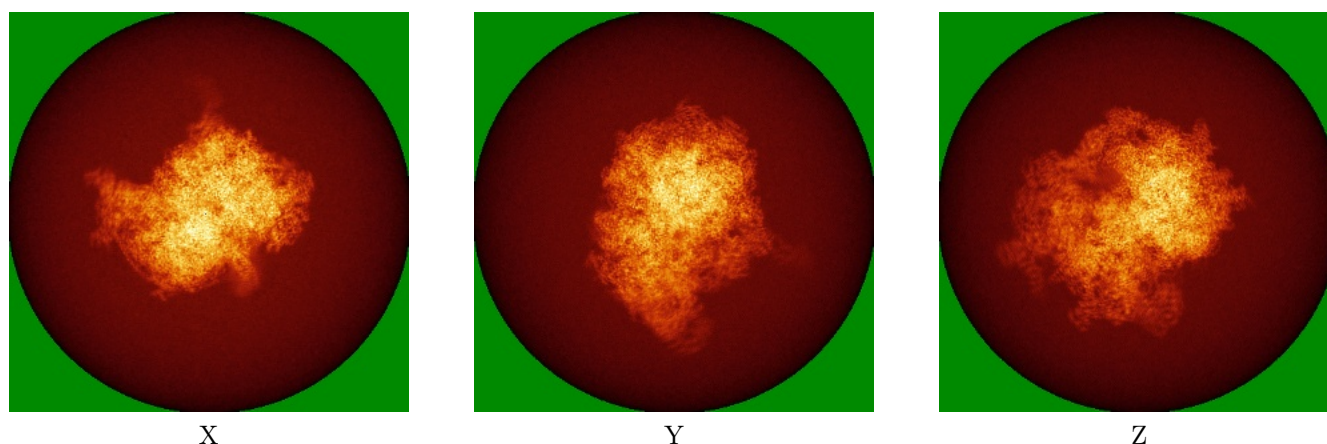
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

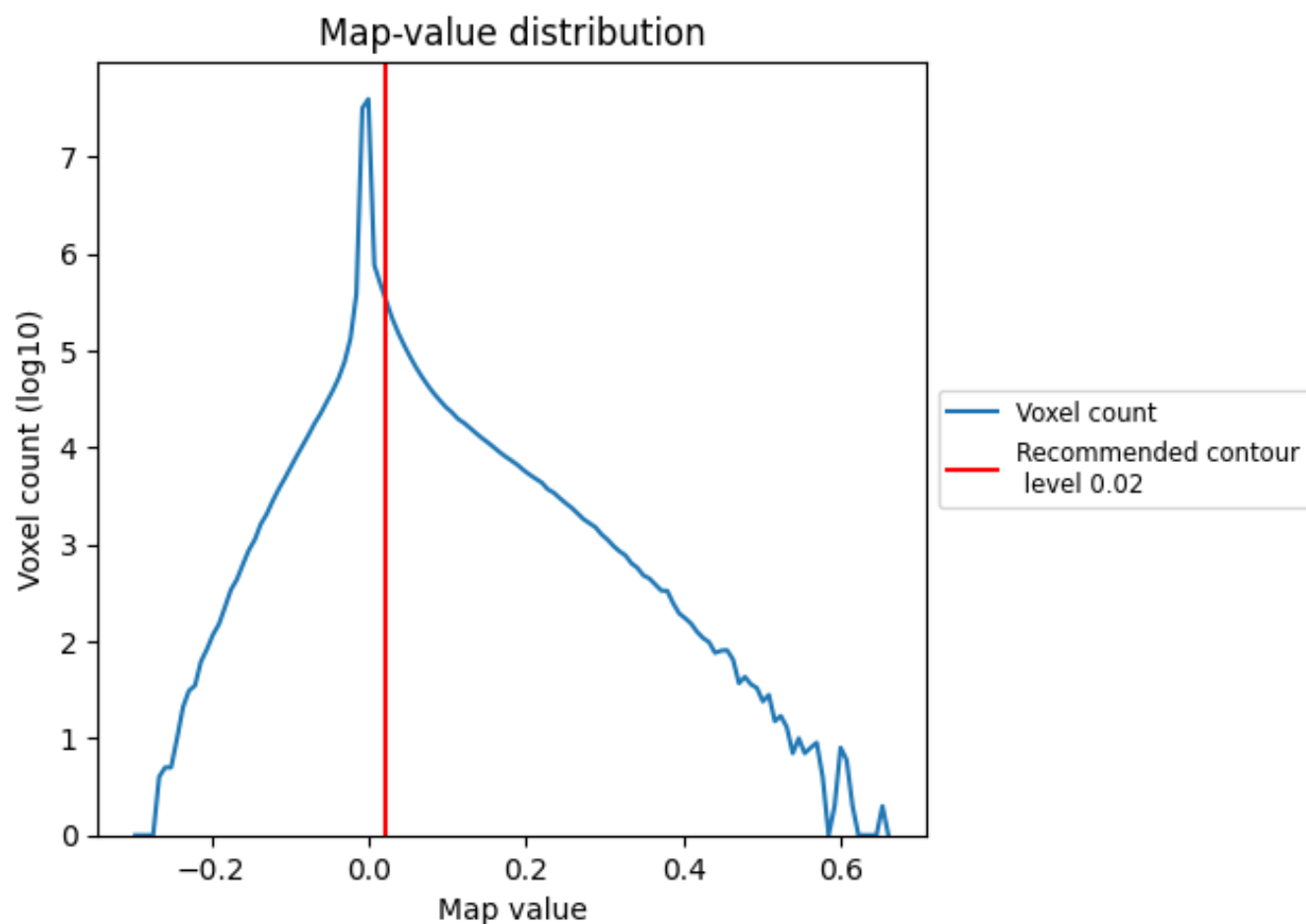
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

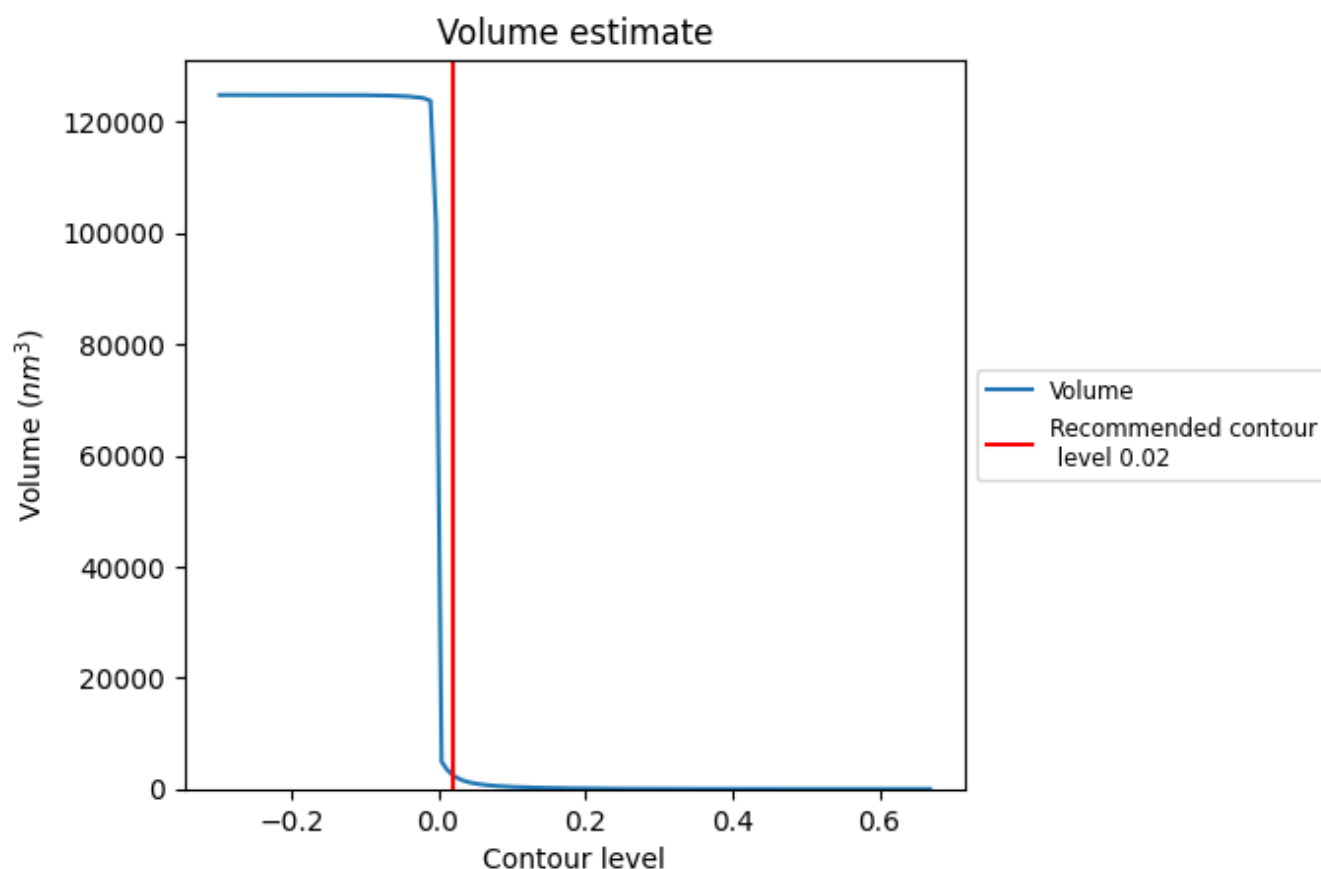
This section contains the results of statistical analysis of the map.

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.

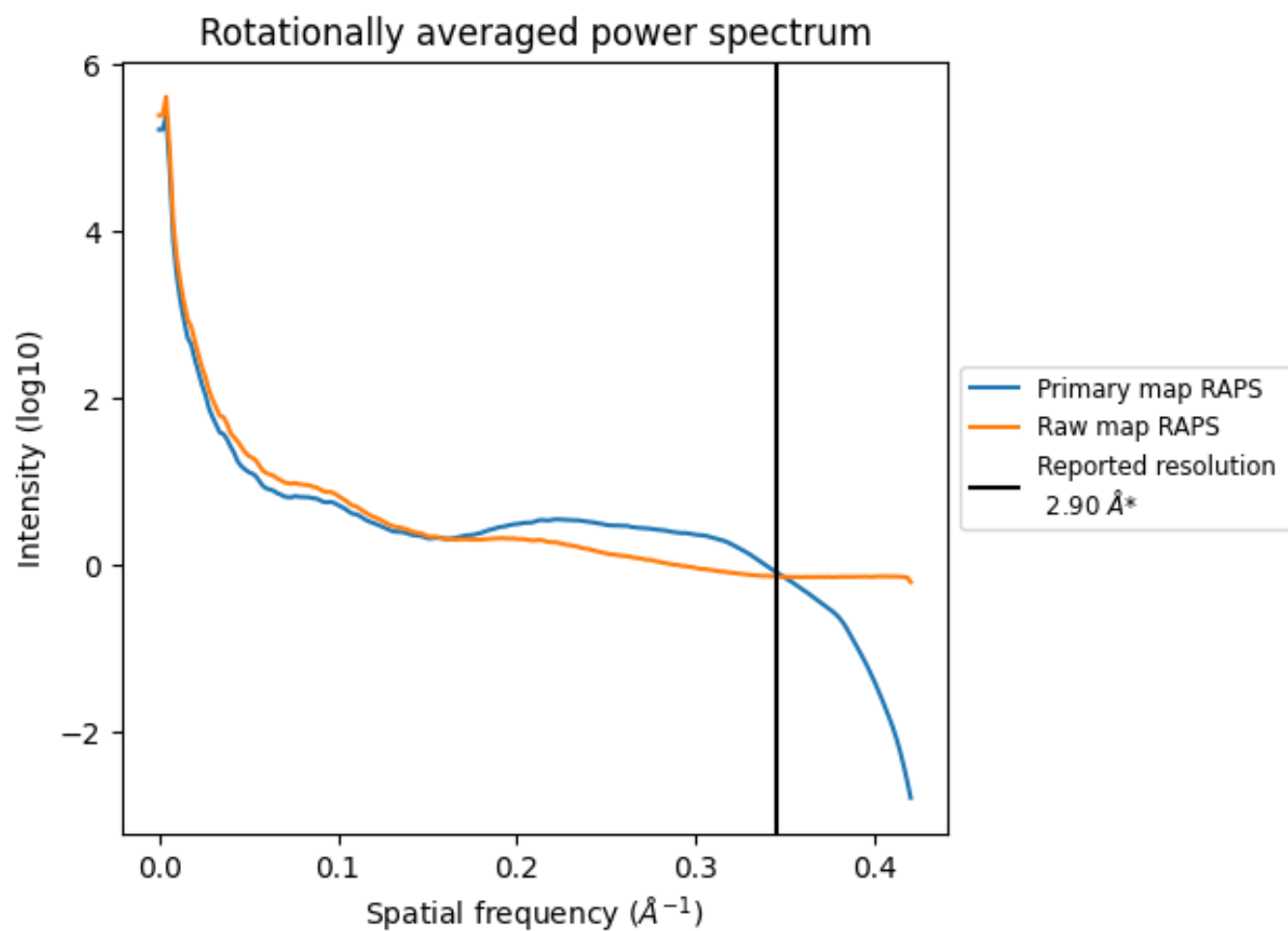
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2486 nm^3 ; this corresponds to an approximate mass of 2246 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

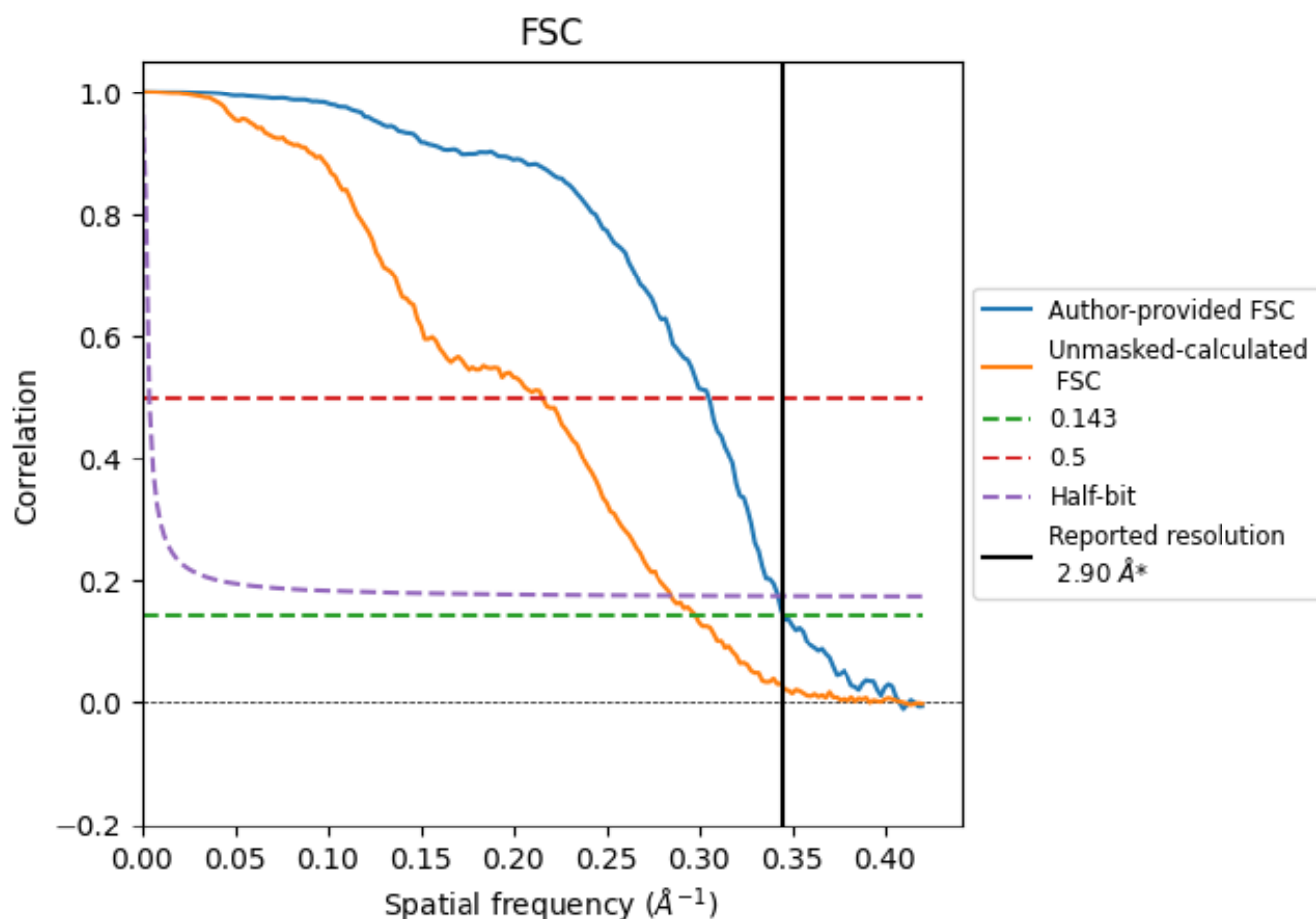


*Reported resolution corresponds to spatial frequency of 0.345 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.345 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.90	3.28	2.92
Unmasked-calculated*	3.35	4.64	3.51

*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 3.35 differs from the reported value 2.9 by more than 10 %

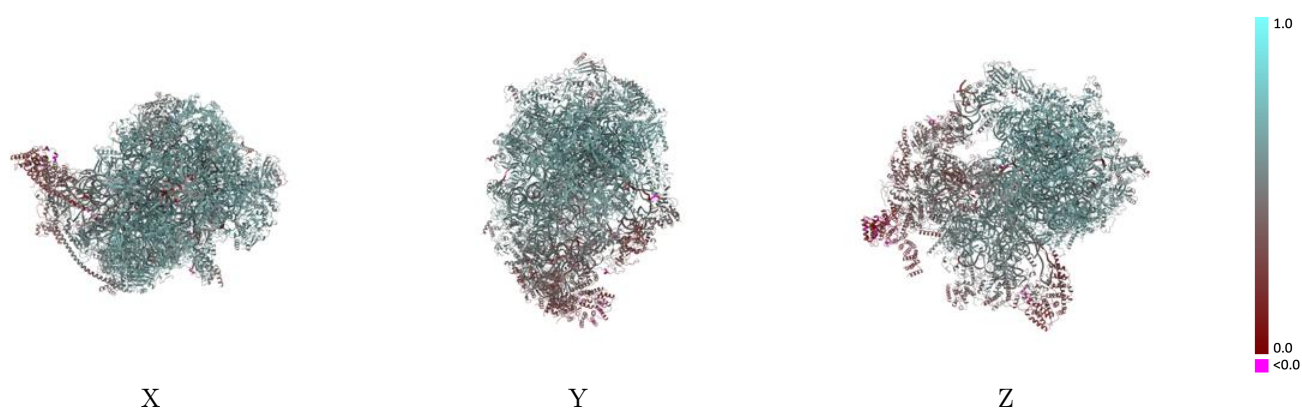
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-36836 and PDB model 8K2A. Per-residue inclusion information can be found in section 3 on page 22.

9.1 Map-model overlay [i](#)

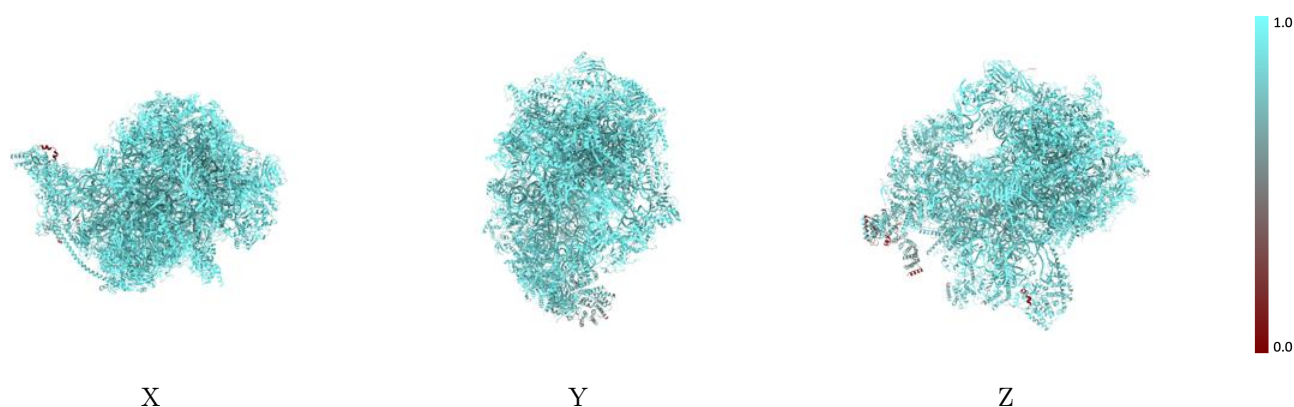
This section was not generated.

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



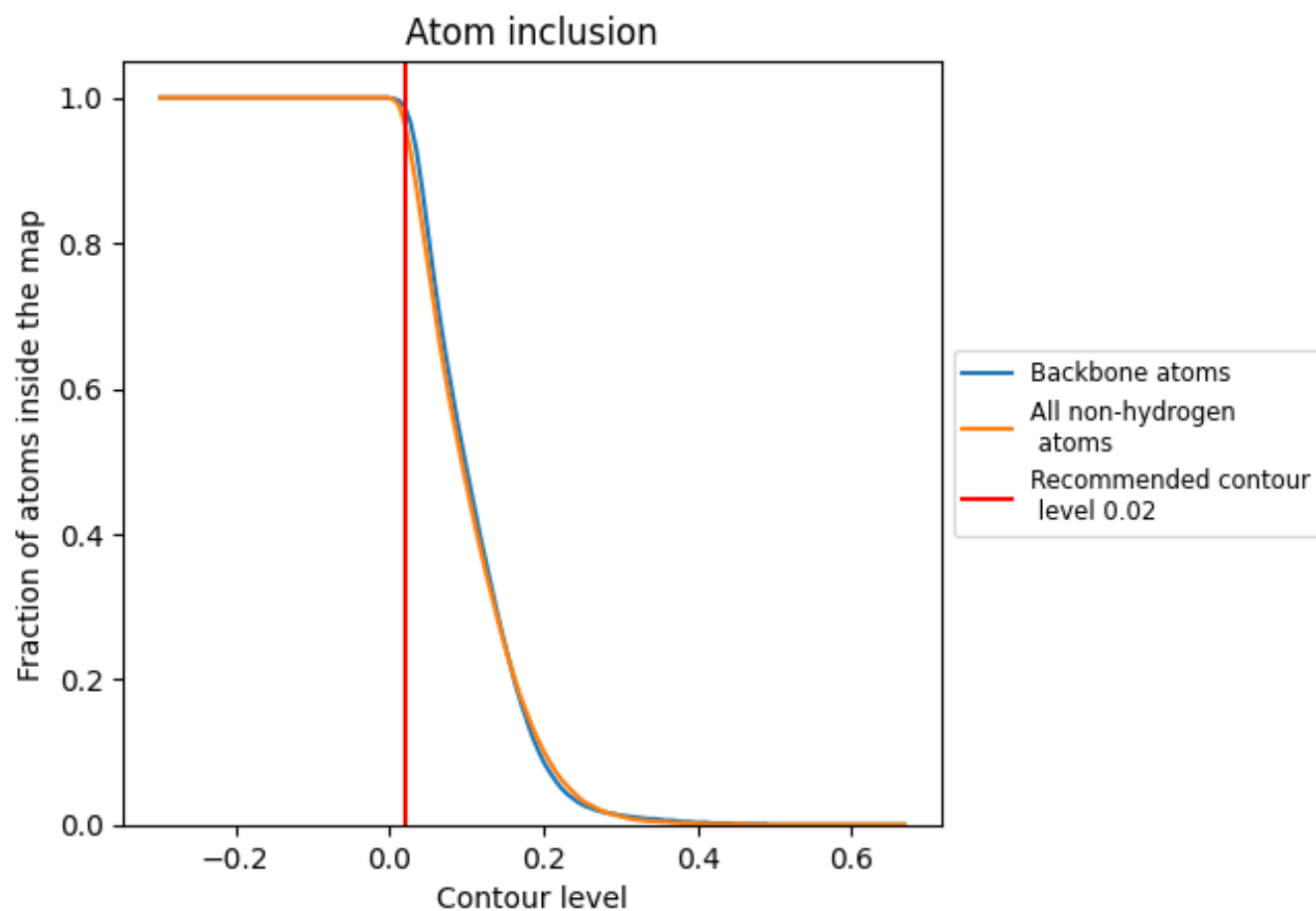
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 96% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9640	 0.5450
L1	 0.9940	 0.6210
L2	 0.9920	 0.4300
L3	 0.9790	 0.4960
L4	 0.9110	 0.4000
L5	 0.9770	 0.4960
L6	 0.9960	 0.6560
L7	 0.9800	 0.5540
L8	 0.9730	 0.5510
LB	 0.9970	 0.6540
LC	 0.9850	 0.6220
LD	 0.9940	 0.6350
LI	 0.9880	 0.5600
LJ	 0.9590	 0.4850
LK	 0.8890	 0.3380
LM	 0.9900	 0.6470
LN	 0.9900	 0.6190
LO	 0.9930	 0.6340
LP	 0.9910	 0.6270
LQ	 0.9930	 0.6220
LR	 0.9750	 0.5880
LS	 0.9830	 0.5990
LT	 0.9860	 0.6500
LU	 0.9920	 0.6370
LV	 0.9960	 0.6440
LW	 0.9670	 0.6010
LX	 0.9760	 0.5600
La	 0.9910	 0.6450
Lb	 0.9820	 0.5910
Ld	 0.9920	 0.6440
Lf	 0.9840	 0.6230
Lg	 0.9930	 0.6170
Lh	 1.0000	 0.6760
Li	 0.9950	 0.6690
Lj	 0.9970	 0.6350



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Chain	Atom inclusion	Q-score
Lk	 0.9890	 0.6040
Ll	 0.9720	 0.5620
Lm	 0.9780	 0.5630
Ln	 0.9200	 0.4040
Lo	 0.9750	 0.5920
Lp	 0.9710	 0.5990
Lq	 0.9970	 0.6450
Lr	 0.9860	 0.5970
Ls	 0.9450	 0.5230
Lt	 0.8990	 0.3610
Lu	 0.9930	 0.6220
Lv	 0.9400	 0.4860
Lw	 0.9840	 0.6130
Lx	 0.9650	 0.5410
Ly	 0.9930	 0.6520
Lz	 0.9520	 0.5870
S1	 0.9960	 0.5510
SB	 0.9770	 0.5590
SE	 0.9630	 0.5260
SF	 0.9880	 0.5940
SG	 0.9580	 0.4690
SI	 0.9380	 0.4620
SJ	 0.9430	 0.4340
SK	 0.9900	 0.5760
SL	 0.9830	 0.5490
SN	 0.9490	 0.4350
SO	 0.9760	 0.5270
SP	 0.9580	 0.4970
SQ	 0.9960	 0.5790
SR	 0.9900	 0.6140
SS	 0.9560	 0.4790
ST	 0.9840	 0.5890
SW	 0.9890	 0.5990
SX	 0.9060	 0.4160
SY	 0.9540	 0.5130
SZ	 0.9670	 0.4840
Sa	 0.9730	 0.5360
Sb	 0.9540	 0.4660
Sc	 0.8410	 0.2790
Sd	 0.9770	 0.5540
Se	 0.9250	 0.4040
Sf	 0.9930	 0.6210

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Chain	Atom inclusion	Q-score
Sg	 0.8670	 0.3230
Si	 0.9610	 0.3830
Sj	 0.9370	 0.3810
Sk	 0.8790	 0.3470
Sm	 0.9680	 0.5280
Sn	 0.9970	 0.6020
So	 0.6390	 0.1880