



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 08:03 AM UTC

PDB ID : 7MQ8 / pdb_00007mq8
EMDB ID : EMD-23936
Title : Cryo-EM structure of the human SSU processome, state pre-A1
Authors : Vanden Broeck, A.; Singh, S.; Klinge, S.
Deposited on : 2021-05-05
Resolution : 3.60 Å(reported)
Based on initial models : 6G4S, 6ZOJ, 5FAI, 2IPX, 5WLC, 6ZQD, 2OZB, 6G18, 4JXM

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 EMD archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

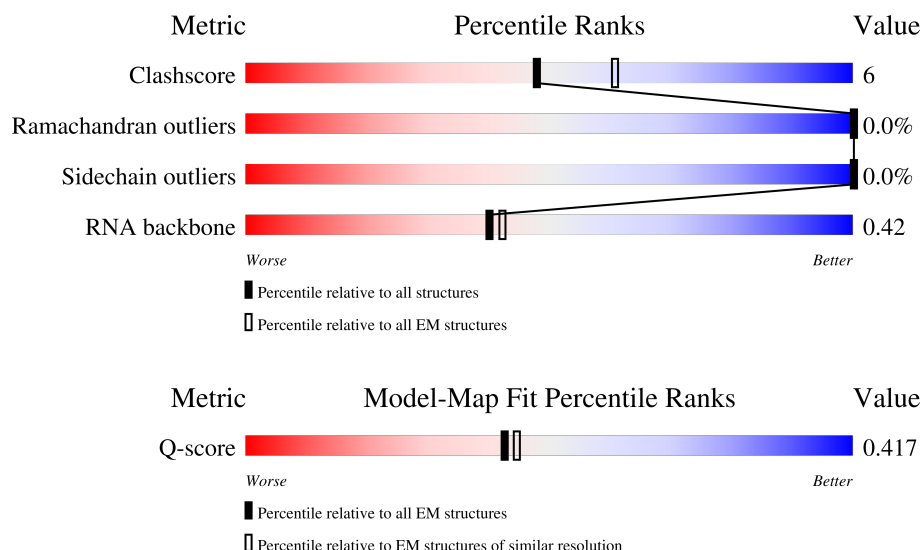
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

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

Mol	Chain	Length	Quality of chain
1	L0	3617	 93%
2	L1	1869	 38% 27% 30% 9%
3	L2	217	 18% 46% 44% 10%

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Mol	Chain	Length	Quality of chain
4	L3	116	
5	L4	263	
6	L5	204	
7	L6	249	
8	L7	194	
9	L8	208	
10	L9	194	
11	LA	132	
12	LC	146	
13	LD	158	
14	LF	133	
15	LG	69	
16	LH	830	
17	LI	678	
18	LJ	518	
19	LK	677	
19	LL	677	
20	LM	2144	
21	LN	686	
22	LO	919	
23	LP	597	
24	LQ	943	
25	LR	808	
26	LS	556	
27	LT	951	

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Mol	Chain	Length	Quality of chain
28	LU	445	
29	LW	610	
30	LZ	184	
31	N0	22	
32	NA	681	
33	NB	479	
34	NC	315	
35	ND	257	
36	NE	293	
37	NF	151	
38	NG	151	
39	NH	1146	
40	NI	280	
41	NJ	1025	
41	NK	1025	
42	NM	264	
43	NN	560	
44	NO	130	
45	NQ	84	
46	NR	861	
47	NT	156	
48	NU	135	
49	NW	688	
50	NY	381	
51	SA	594	

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Mol	Chain	Length	Quality of chain
52	SB	529	
53	SC	321	
53	SD	321	
54	SE	128	
54	SF	128	
55	SG	475	
56	SH	373	
57	SI	1282	
58	SJ	244	
58	SK	244	
59	SL	198	
60	SM	291	
61	SP	2785	
62	SQ	756	
63	SR	143	
64	SS	771	
65	ST	632	
66	SU	472	
67	SW	252	
68	Sx	38	
69	SX	273	
70	SY	253	
71	SZ	304	

2 Entry composition

There are 76 unique types of molecules in this entry. The entry contains 245114 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 5'ETS rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L0	242	Total	C	N	O	P	0	0
			5152	2289	908	1713	242		

- Molecule 2 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L1	1301	Total	C	N	O	P	0	0
			27777	12396	5002	9078	1301		

- Molecule 3 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L2	215	Total	C	N	O	P	0	0
			4589	2047	809	1518	215		

- Molecule 4 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L3	115	Total	C	N	O	S	0	0
			854	538	164	151	1		

- Molecule 5 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L4	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 6 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L5	190	Total	C	N	O	S	0	0
			1501	939	285	270	7		

- Molecule 7 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L6	223	Total	C	N	O	S	0	0
			1811	1133	361	311	6		

- Molecule 8 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L7	168	Total	C	N	O	S	0	0
			1346	862	239	244	1		

- Molecule 9 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L8	180	Total	C	N	O	S	0	0
			1474	925	294	250	5		

- Molecule 10 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L9	171	Total	C	N	O	S	0	0
			1425	908	284	232	1		

- Molecule 11 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LA	120	Total	C	N	O	S	0	0
			931	584	164	174	9		

- Molecule 12 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LC	139	Total	C	N	O	S	0	0
			1098	699	207	189	3		

- Molecule 13 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LD	147	Total	C	N	O	S	0	0
			1204	767	225	206	6		

- Molecule 14 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LF	104	Total	C	N	O	S	0	0
			851	543	158	145	5		

- Molecule 15 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LG	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 16 is a protein called WD repeat-containing protein 75.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LH	746	Total	C	N	O	S	0	0
			5987	3846	1005	1101	35		

- Molecule 17 is a protein called Nucleolar protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LI	537	Total	C	N	O	S	0	0
			3889	2508	654	706	21		

- Molecule 18 is a protein called U3 small nucleolar RNA-associated protein 15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LJ	469	Total	C	N	O	S	0	0
			3711	2372	637	688	14		

- Molecule 19 is a protein called WD repeat-containing protein 43.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LK	118	Total	C	N	O	S	0	0
			943	612	163	163	5		
19	LL	510	Total	C	N	O	S	0	0
			3982	2538	686	731	27		

- Molecule 20 is a protein called HEAT repeat-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LM	2005	Total	C	N	O	S	0	0
			15820	10259	2597	2883	81		

- Molecule 21 is a protein called U3 small nucleolar RNA-associated protein 4 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LN	671	Total	C	N	O	S	0	0
			5299	3394	925	956	24		

- Molecule 22 is a protein called Periodic tryptophan protein 2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LO	848	Total	C	N	O	S	0	0
			6676	4258	1151	1234	33		

- Molecule 23 is a protein called U3 small nucleolar RNA-associated protein 6 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LP	567	Total	C	N	O	S	0	0
			4705	3022	808	847	28		

- Molecule 24 is a protein called WD repeat-containing protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LQ	828	Total	C	N	O	S	0	0
			6438	4103	1108	1194	33		

- Molecule 25 is a protein called Transducin beta-like protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LR	773	Total	C	N	O	S	0	0
			6015	3789	1079	1116	31		

- Molecule 26 is a protein called U3 small nucleolar RNA-associated protein 18 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LS	453	Total	C	N	O	S	0	0
			3560	2235	631	671	23		

- Molecule 27 is a protein called WD repeat-containing protein 36.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LT	869	Total	C	N	O	S	0	0
			6756	4321	1158	1244	33		

- Molecule 28 is a protein called DDB1- and CUL4-associated factor 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LU	445	Total	C	N	O	S	0	0
			3611	2282	653	651	25		

- Molecule 29 is a protein called WD repeat-containing protein 46.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LW	453	Total	C	N	O	S	0	0
			3519	2221	637	646	15		

- Molecule 30 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LZ	183	Total	C	N	O	S	0	0
			1532	966	292	270	4		

- Molecule 31 is a RNA chain called 5'ETS rRNA.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	N0	22	Total	C	O	P	0	0
			264	110	132	22		

- Molecule 32 is a protein called U3 small nucleolar ribonucleoprotein protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	NA	249	Total	C	N	O	S	0	0
			2055	1299	359	391	6		

- Molecule 33 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	NB	73	Total	C	N	O	0	0
			617	379	140	98		

- Molecule 34 is a protein called Neuroguidin.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	NC	94	Total	C	N	O	S	0	0
			779	469	160	147	3		

- Molecule 35 is a protein called Nucleolar protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	ND	84	Total	C	N	O	S	0	0
			696	438	143	114	1		

- Molecule 36 is a protein called Uncharacterized protein C1orf131.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	NE	100	Total	C	N	O	S	0	0
			799	509	143	146	1		

- Molecule 37 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	NF	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 38 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	NG	116	Total	C	N	O	S	0	0
			861	531	159	165	6		

- Molecule 39 is a protein called Nucleolar protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	NH	1066	Total	C	N	O	S	0	0
			8374	5345	1491	1506	32		

- Molecule 40 is a protein called Ribosomal RNA-processing protein 7 homolog A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	NI	234	Total	C	N	O	S	0	0
			1840	1171	329	336	4		

- Molecule 41 is a protein called RNA cytidine acetyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	NJ	827	Total	C	N	O	S	0	0
			6526	4187	1126	1178	35		
41	NK	815	Total	C	N	O	S	0	0
			6419	4118	1109	1160	32		

- Molecule 42 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	NM	233	Total	C	N	O	S	0	0
			1873	1186	339	334	14		

- Molecule 43 is a protein called Protein AATF.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	NN	42	Total	C	N	O	S	0	0
			340	215	63	60	2		

- Molecule 44 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	NO	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 45 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	NQ	82	Total	C	N	O	S	0	0
			640	402	118	113	7		

- Molecule 46 is a protein called RRP12-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	NR	861	Total	C	N	O		0	0
			4305	2583	861	861			

- Molecule 47 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	NT	58	Total	C	N	O	S	0	0
			470	295	89	79	7		

- Molecule 48 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	NU	60	Total	C	N	O	S	0	0
			495	314	98	81	2		

- Molecule 49 is a protein called Nucleolar protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	NW	311	Total	C	N	O	S	0	0
			2498	1599	413	472	14		

- Molecule 50 is a protein called KRR1 small subunit processome component homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	NY	274	Total	C	N	O	S	0	0
			2222	1422	391	400	9		

- Molecule 51 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SA	396	Total	C	N	O	S	0	0
			3077	1948	542	575	12		

- Molecule 52 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SB	440	Total	C	N	O	S	0	0
			3439	2179	596	642	22		

- Molecule 53 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SC	229	Total	C	N	O	S	0	0
			1781	1129	322	323	7		
53	SD	237	Total	C	N	O	S	0	0
			1841	1163	337	334	7		

- Molecule 54 is a protein called NHP2-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SE	125	Total	C	N	O	S	0	0
			968	611	172	180	5		
54	SF	123	Total	C	N	O	S	0	0
			955	604	170	176	5		

- Molecule 55 is a protein called U3 small nucleolar RNA-interacting protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SG	389	Total	C	N	O	S	1	0
			2884	1809	534	528	13		

- Molecule 56 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SH	368	Total	C	N	O	S	0	0
			2832	1803	495	518	16		

- Molecule 57 is a protein called Ribosome biogenesis protein BMS1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SI	844	Total	C	N	O	S	0	0
			6803	4351	1230	1188	34		

- Molecule 58 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SJ	204	Total	C	N	O	S	0	0
			1579	1012	272	286	9		
58	SK	204	Total	C	N	O	S	0	0
			1579	1012	272	286	9		

- Molecule 59 is a protein called rRNA-processing protein FCF1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SL	192	Total	C	N	O	S	0	0
			1586	1006	290	275	15		

- Molecule 60 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SM	290	Total	C	N	O	S	0	0
			2369	1485	451	424	9		

- Molecule 61 is a protein called Small subunit processome component 20 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SP	1993	Total	C	N	O	S	0	0
			16078	10412	2689	2897	80		

- Molecule 62 is a protein called Deoxynucleotidyltransferase terminal-interacting protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SQ	187	Total	C	N	O	S	0	0
			1533	972	278	277	6		

- Molecule 63 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SR	108	Total	C	N	O	S	0	0
			816	521	153	140	2		

- Molecule 64 is a protein called U3 small nucleolar RNA-associated protein 14 homolog A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SS	197	Total	C	N	O	S	0	0
			1626	1039	301	285	1		

- Molecule 65 is a protein called Nucleolar protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	ST	568	Total	C	N	O	S	0	0
			4170	2634	760	755	21		

- Molecule 66 is a protein called Nucleolar complex protein 4 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SU	442	Total	C	N	O	S	0	0
			3154	2030	565	551	8		

- Molecule 67 is a protein called RNA-binding protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SW	180	Total	C	N	O	S	0	0
			1413	906	257	246	4		

- Molecule 68 is a protein called Unassigned peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
68	Sx	38	Total	C	N	O	0	0
			190	114	38	38		

- Molecule 69 is a protein called Unassigned peptides.

Mol	Chain	Residues	Atoms				AltConf	Trace
69	SX	139	Total	C	N	O	0	0
			695	417	139	139		

- Molecule 70 is a protein called Probable U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SY	238	Total	C	N	O	S	0	0
			2024	1280	385	353	6		

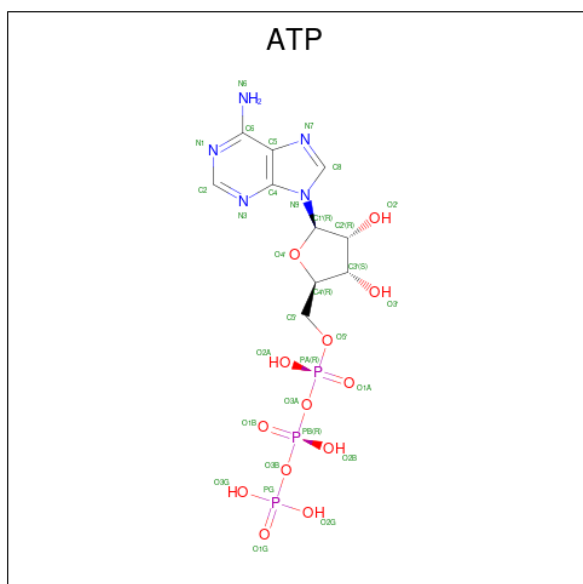
- Molecule 71 is a protein called Bystin.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SZ	290	Total	C	N	O	S	0	0
			2222	1438	392	383	9		

- Molecule 72 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
72	L1	19	Total	Mg	0
			19	19	
72	NH	1	Total	Mg	0
			1	1	
72	SI	1	Total	Mg	0
			1	1	
72	SL	1	Total	Mg	0
			1	1	

- Molecule 73 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



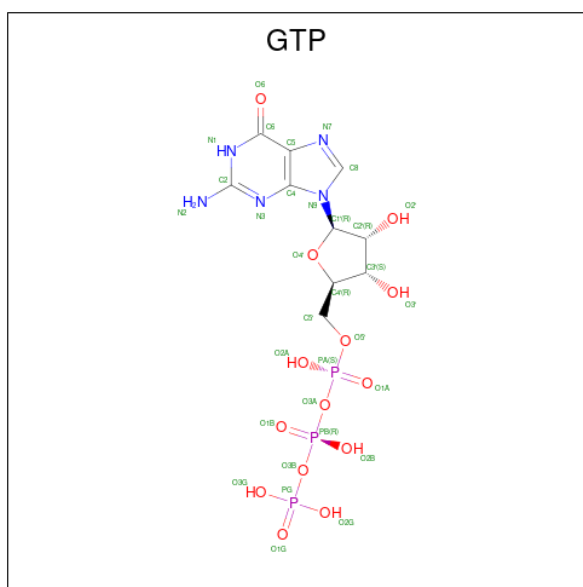
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Mol	Chain	Residues	Atoms					AltConf
73	NK	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 74 is ZINC ION (CCD ID: ZN) (formula: Zn).

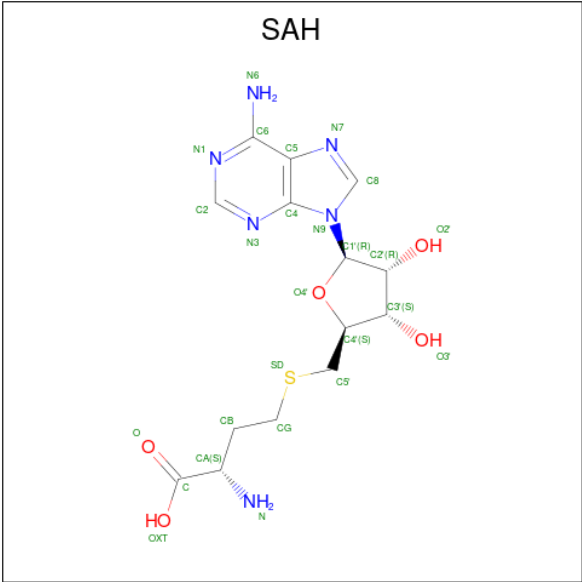
Mol	Chain	Residues	Atoms		AltConf
74	NQ	1	Total	Zn	0
			1	1	
74	NT	1	Total	Zn	0
			1	1	
74	SL	1	Total	Zn	0
			1	1	

- Molecule 75 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



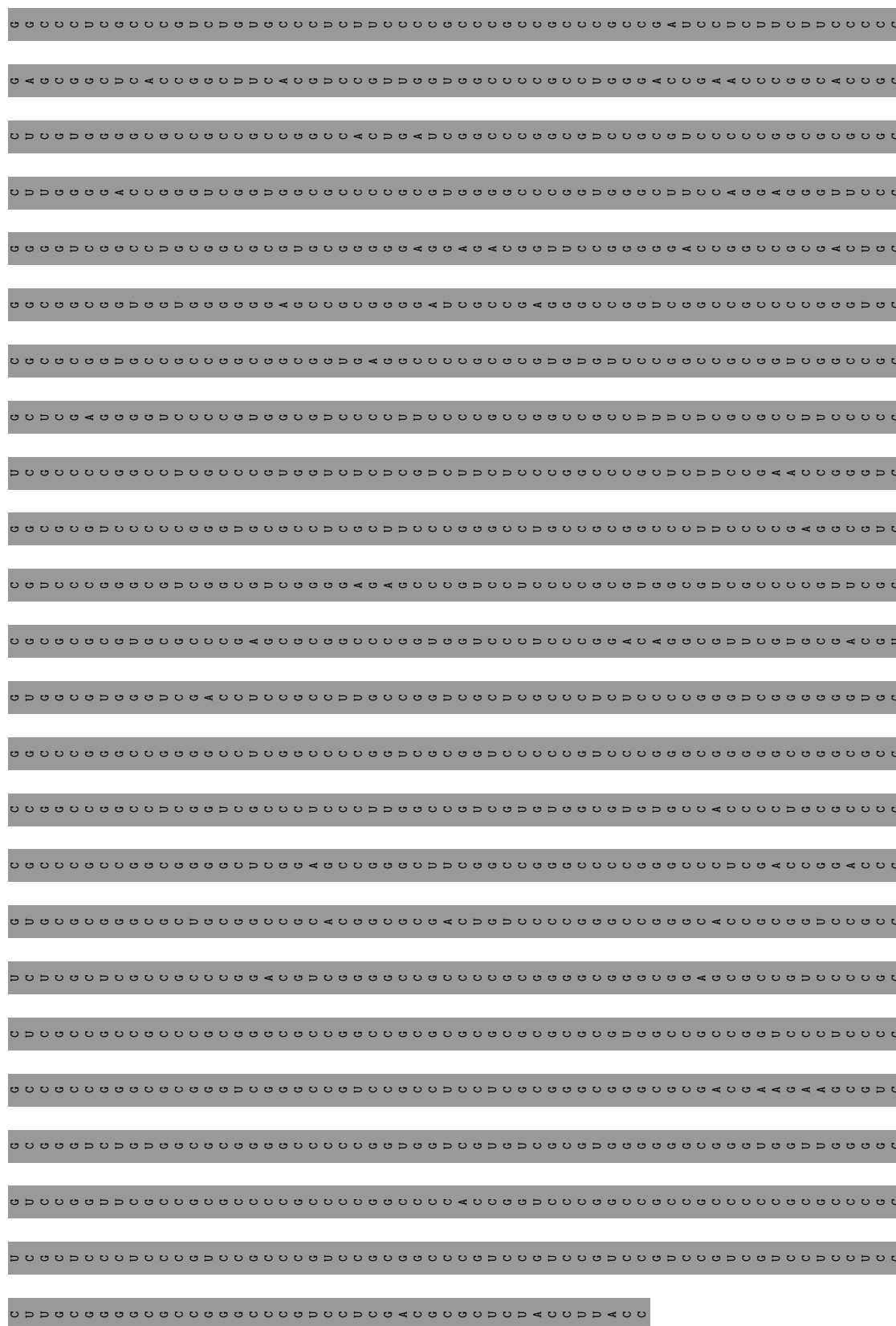
Mol	Chain	Residues	Atoms					AltConf
75	SI	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 76 is S-ADENOSYL-L-HOMOCYSTEINE (CCD ID: SAH) (formula: C₁₄H₂₀N₆O₅S).



Mol	Chain	Residues	Atoms					AltConf
76	SJ	1	Total	C	N	O	S	0
			26	14	6	5	1	
76	SK	1	Total	C	N	O	S	0
			26	14	6	5	1	

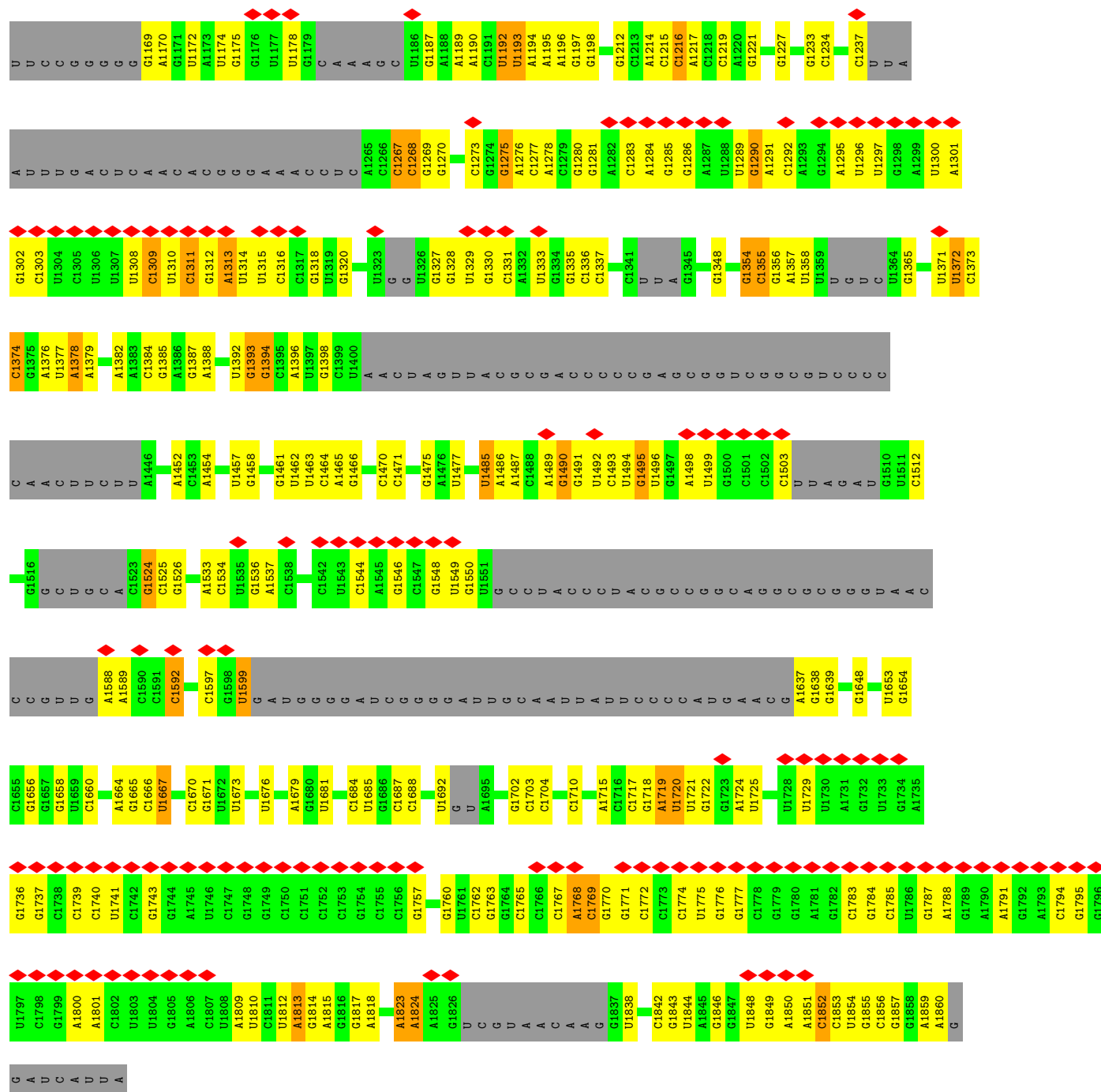




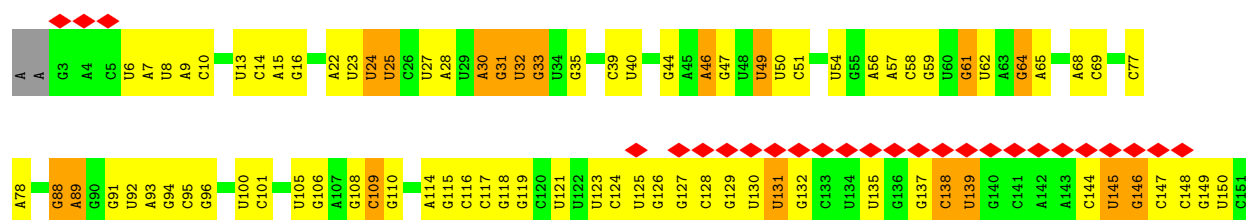
- Molecule 2: 18S rRNA

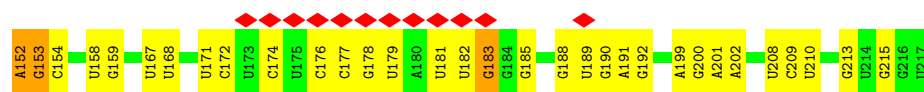




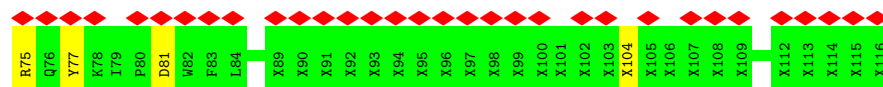
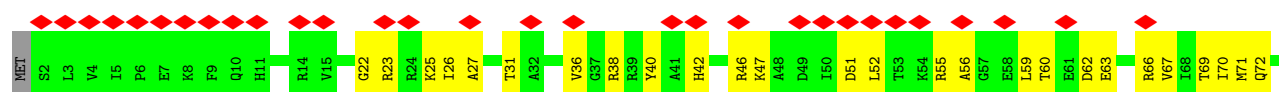
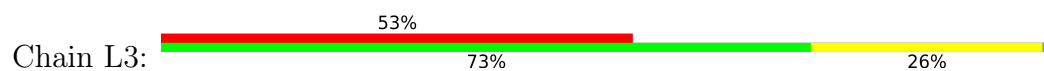


• Molecule 3: U3 snoRNA

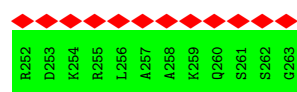
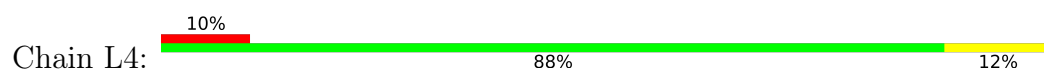




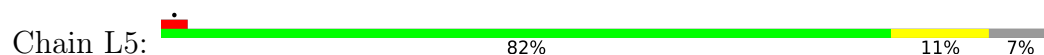
- Molecule 4: 40S ribosomal protein S18



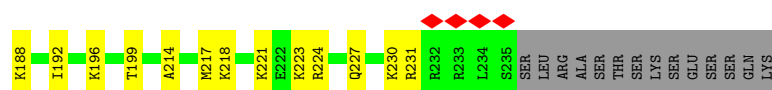
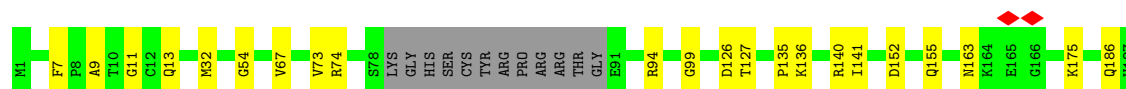
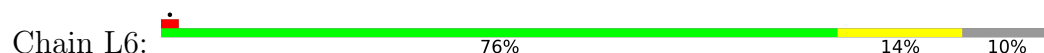
- Molecule 5: 40S ribosomal protein S4, X isoform



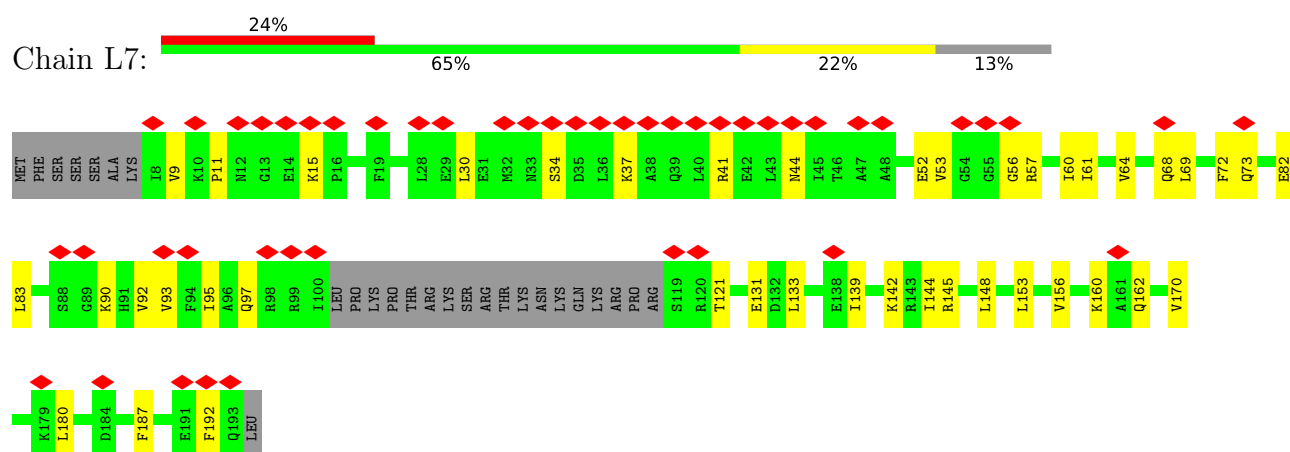
- Molecule 6: 40S ribosomal protein S5



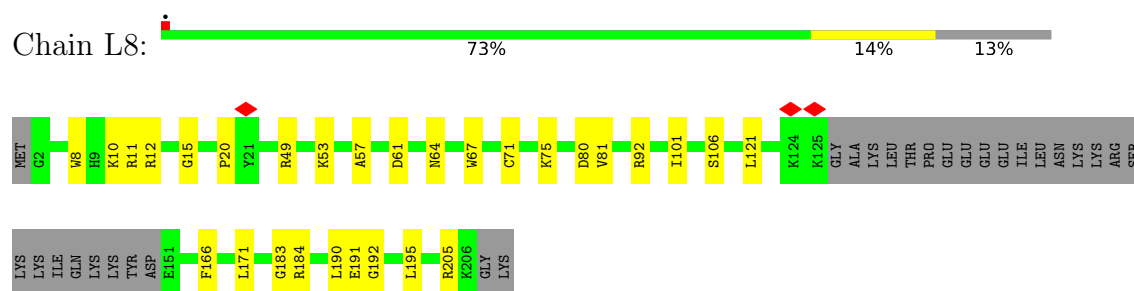
- Molecule 7: 40S ribosomal protein S6



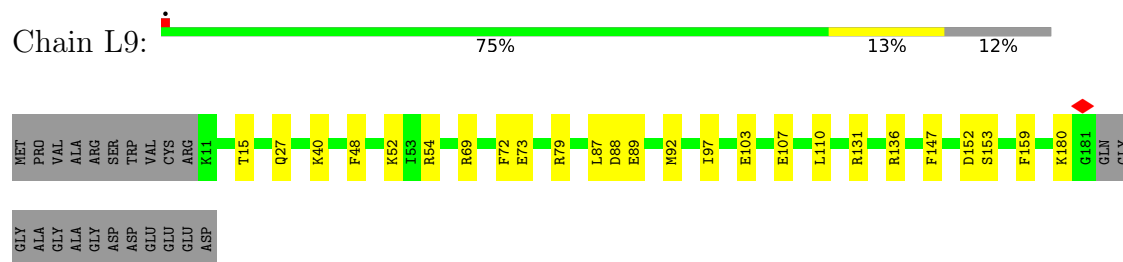
- Molecule 8: 40S ribosomal protein S7



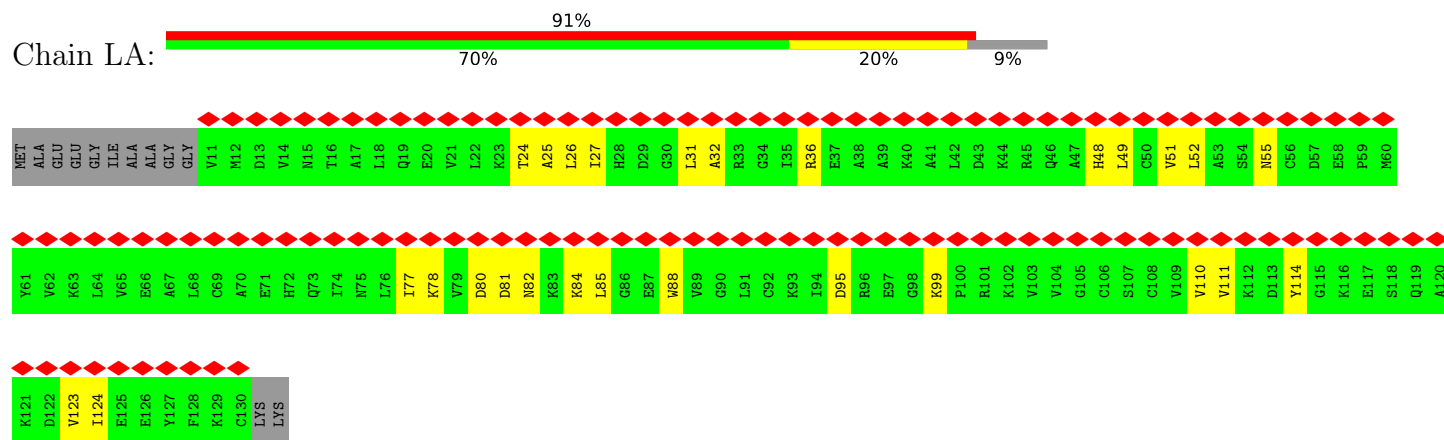
• Molecule 9: 40S ribosomal protein S8



• Molecule 10: 40S ribosomal protein S9

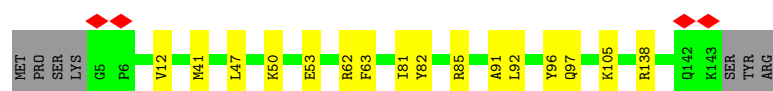


• Molecule 11: 40S ribosomal protein S12



• Molecule 12: 40S ribosomal protein S16

Chain LC: 



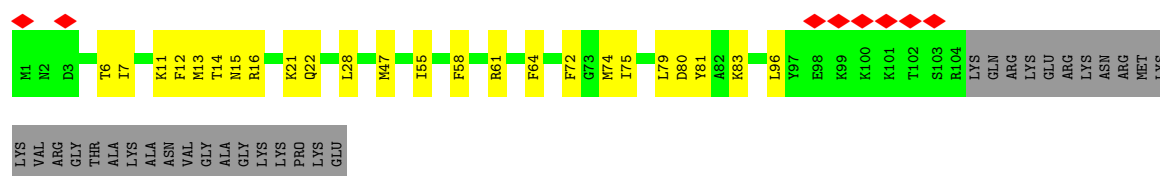
- Molecule 13: 40S ribosomal protein S11

Chain LD: 



- Molecule 14: 40S ribosomal protein S24

Chain LF: 



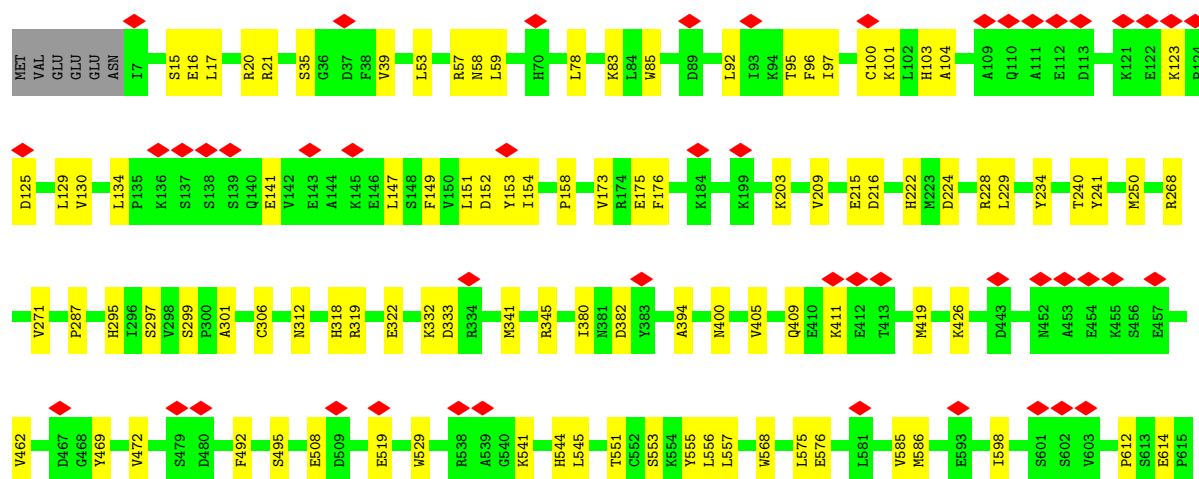
- Molecule 15: 40S ribosomal protein S28

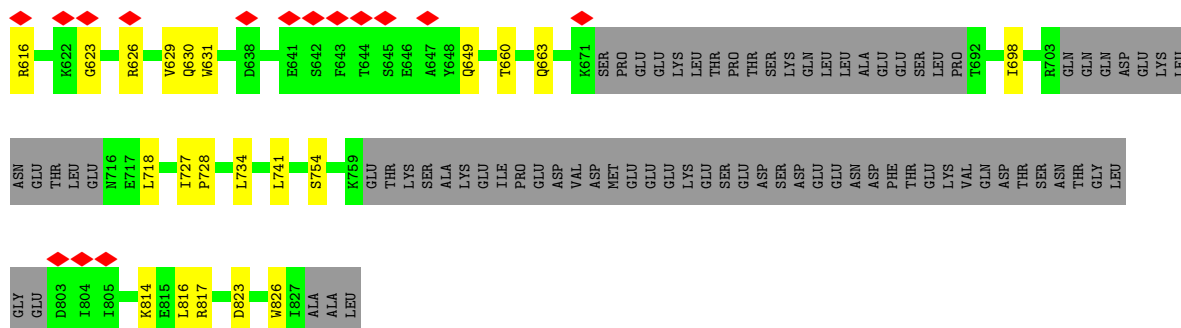
Chain LG: 



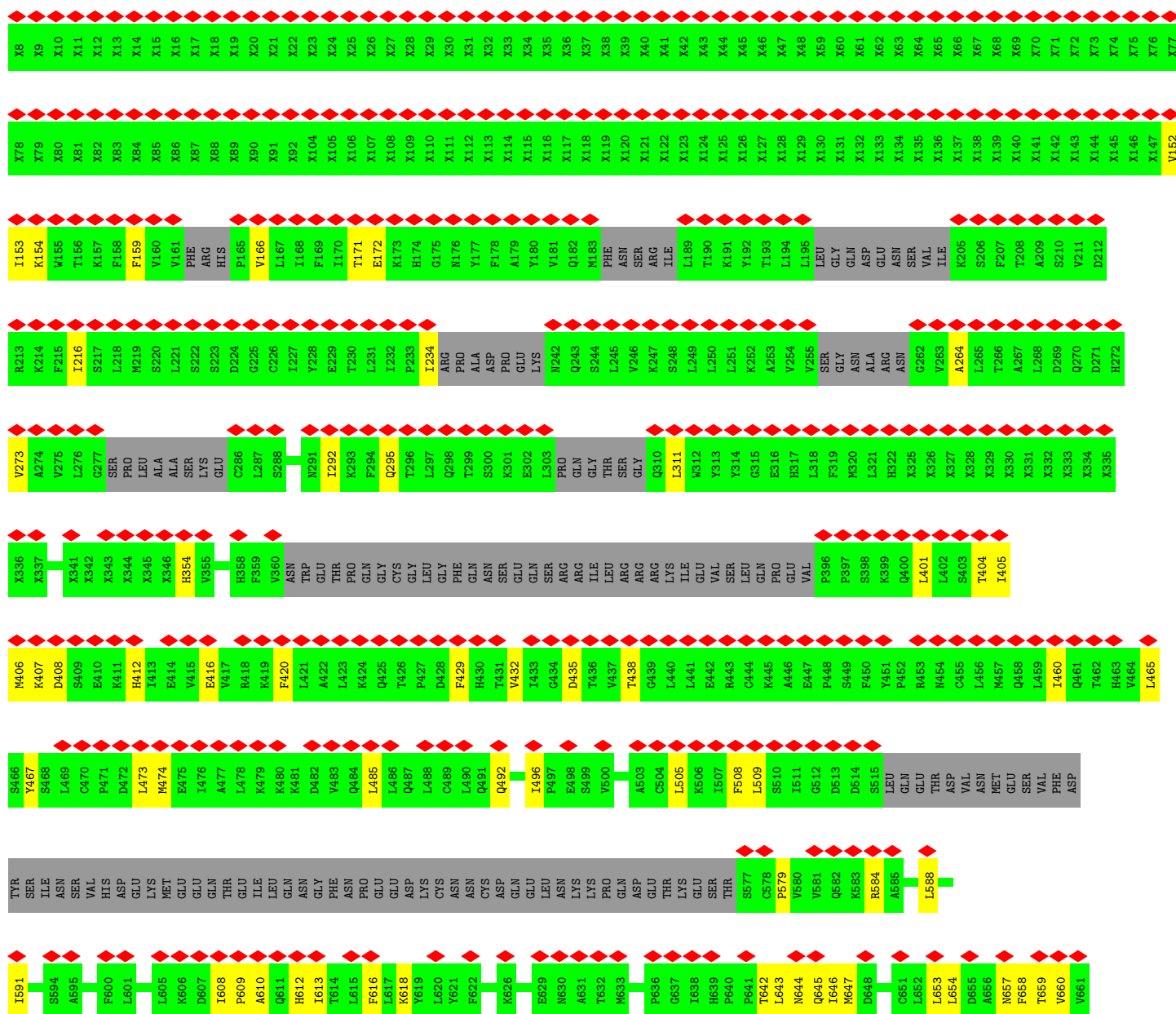
- Molecule 16: WD repeat-containing protein 75

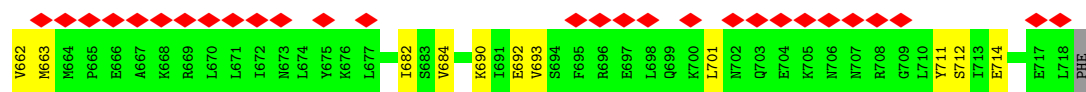
Chain LH: 



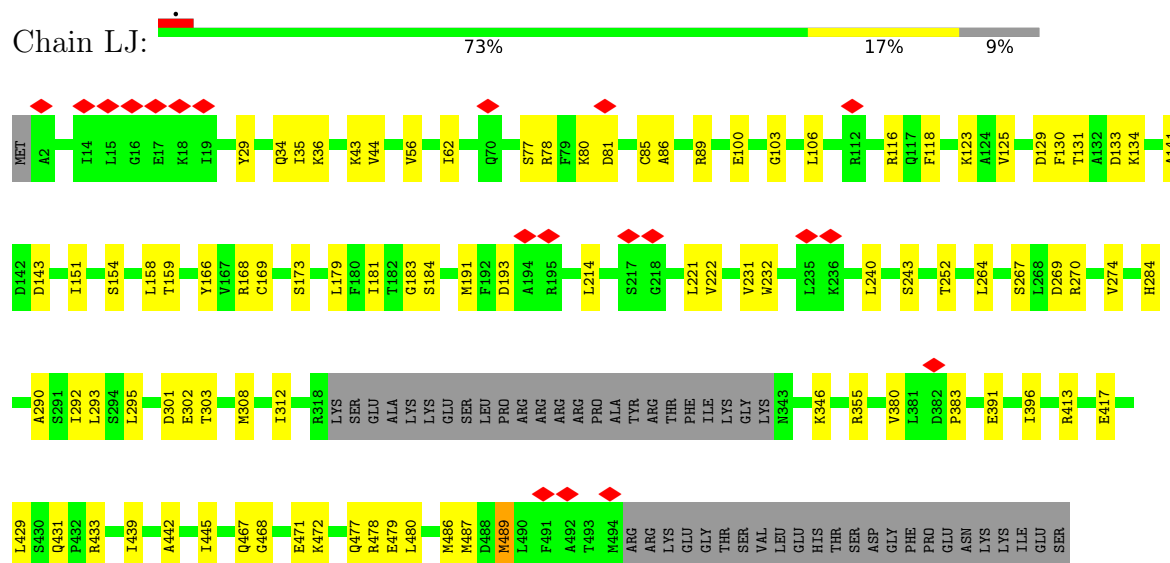


• Molecule 17: Nucleolar protein 11

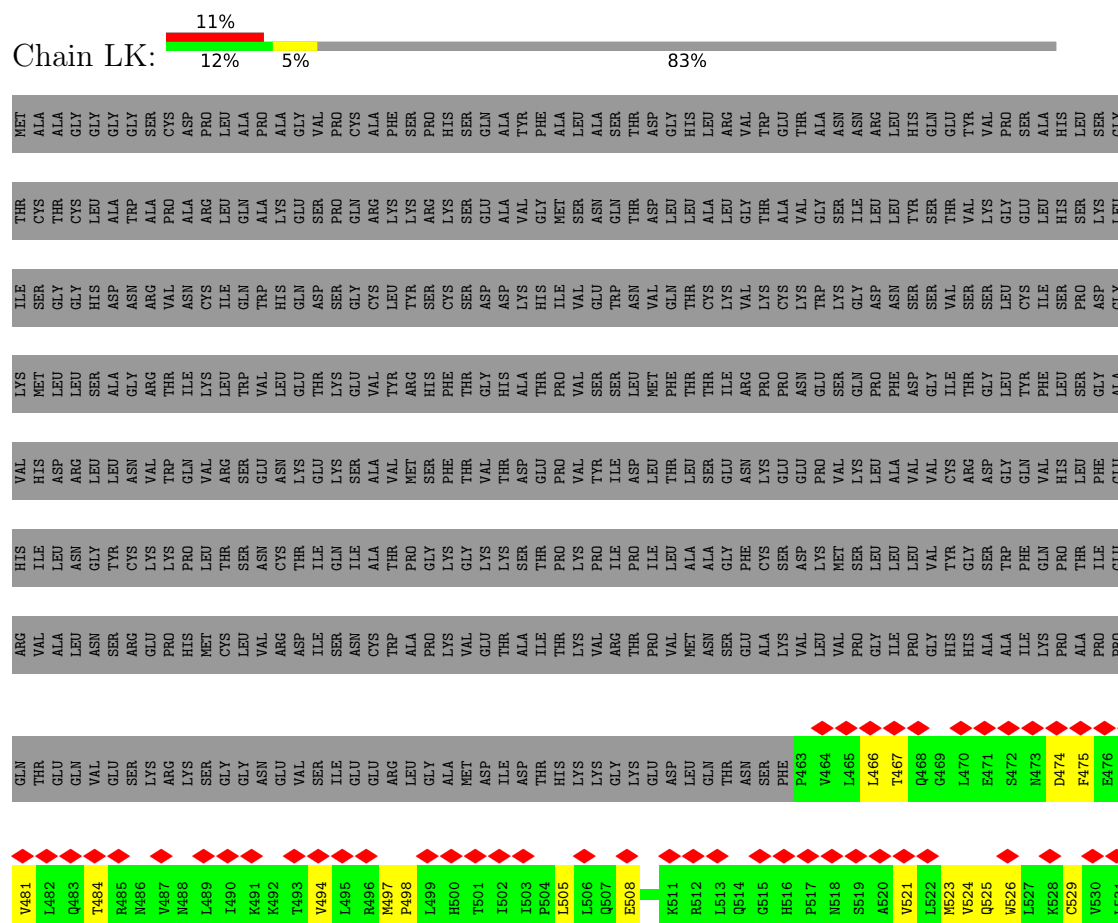


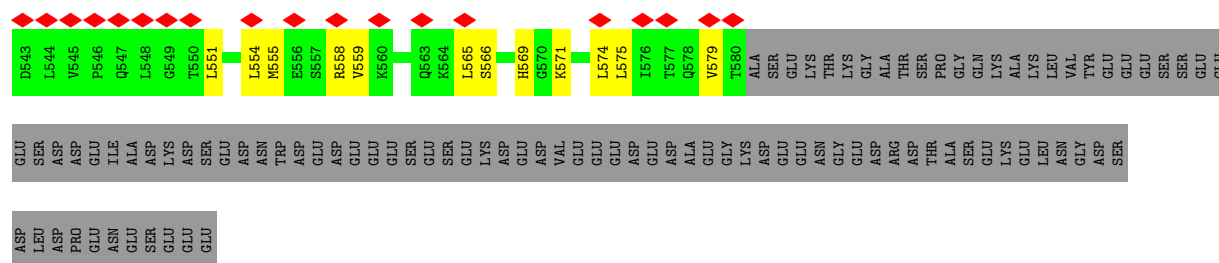


- Molecule 18: U3 small nucleolar RNA-associated protein 15 homolog

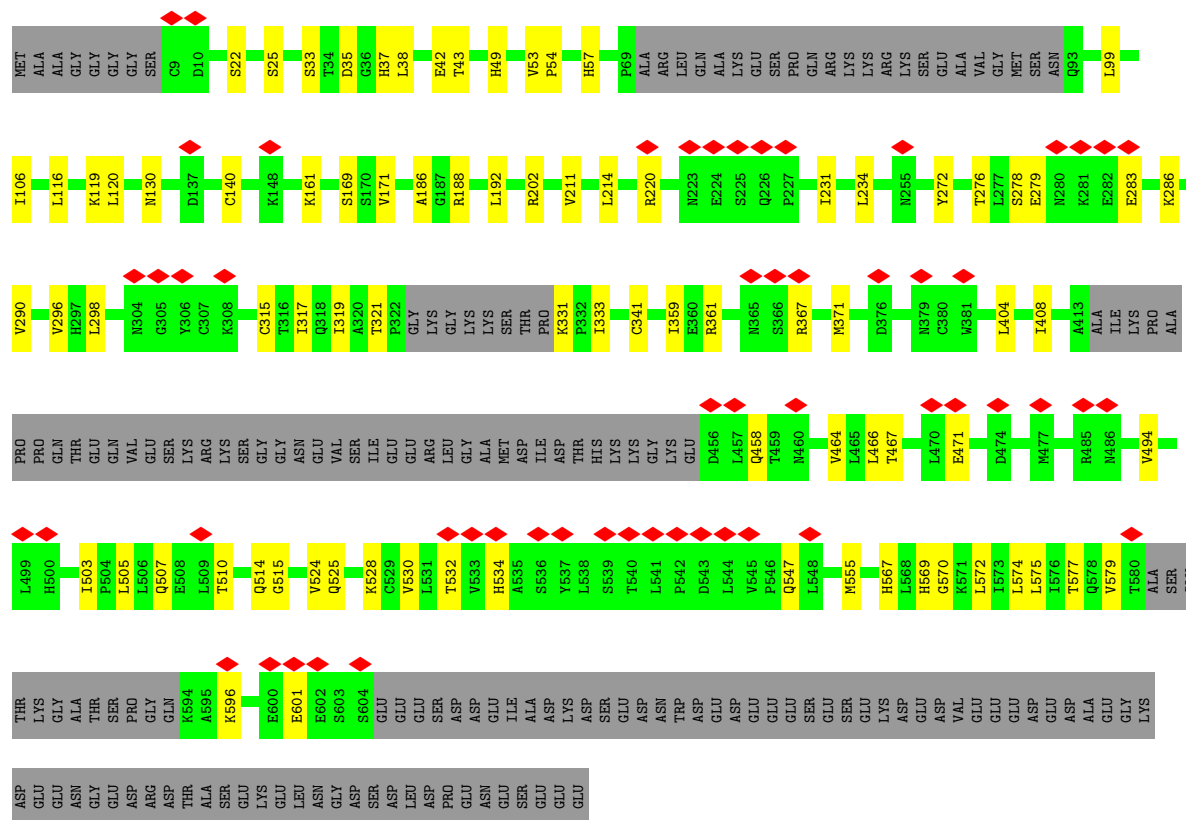


- Molecule 19: WD repeat-containing protein 43

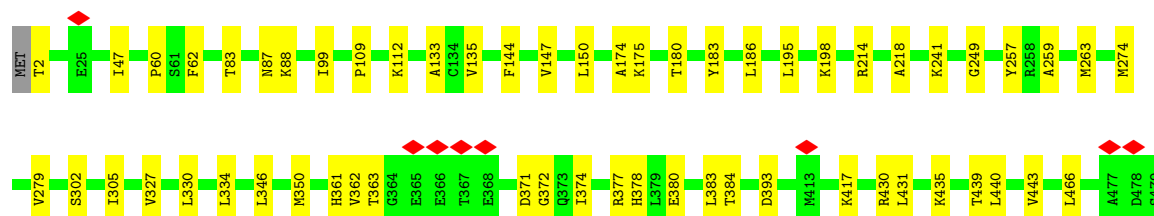
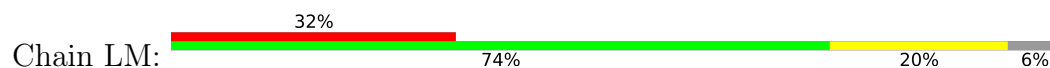




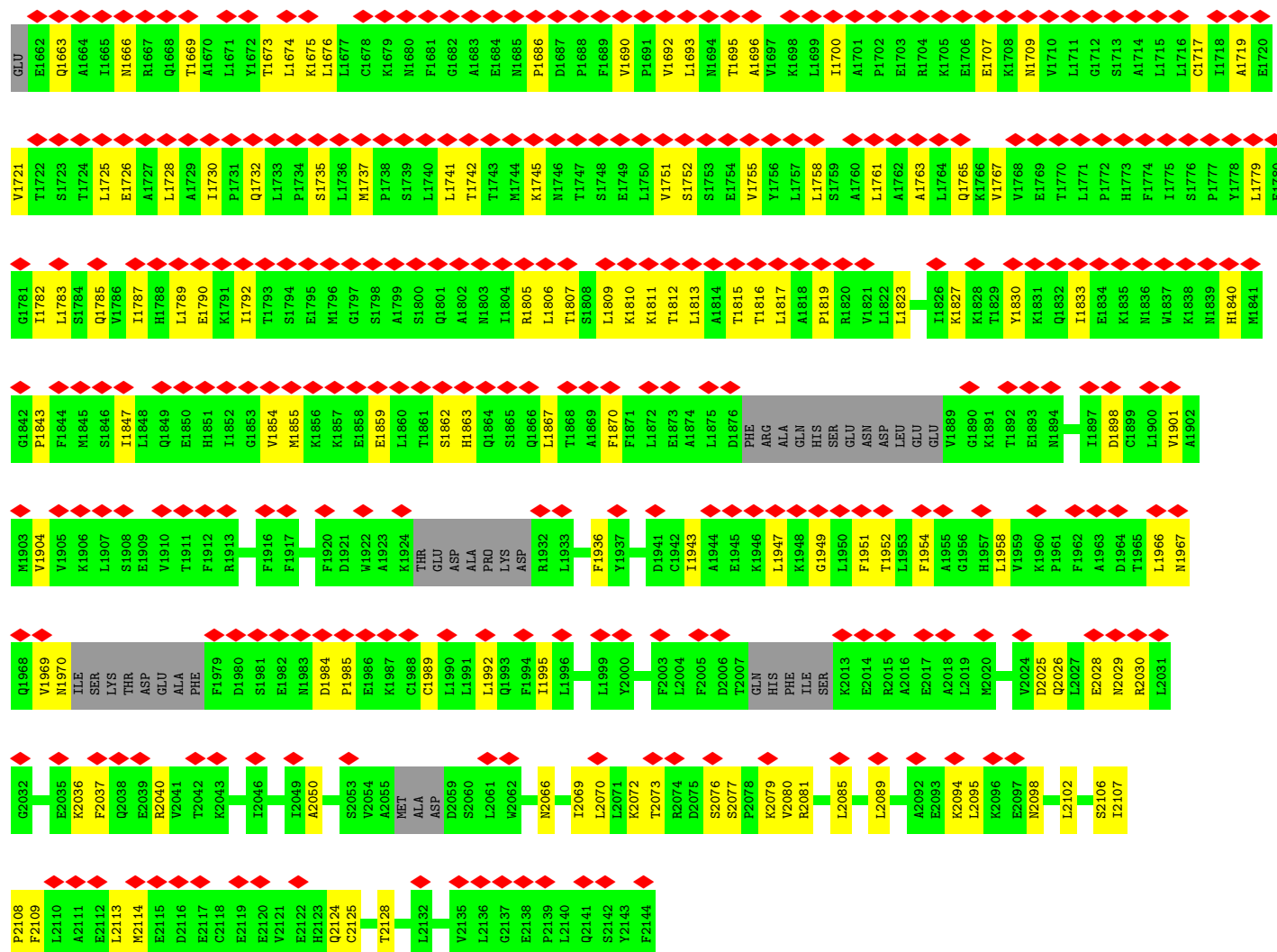
• Molecule 19: WD repeat-containing protein 43



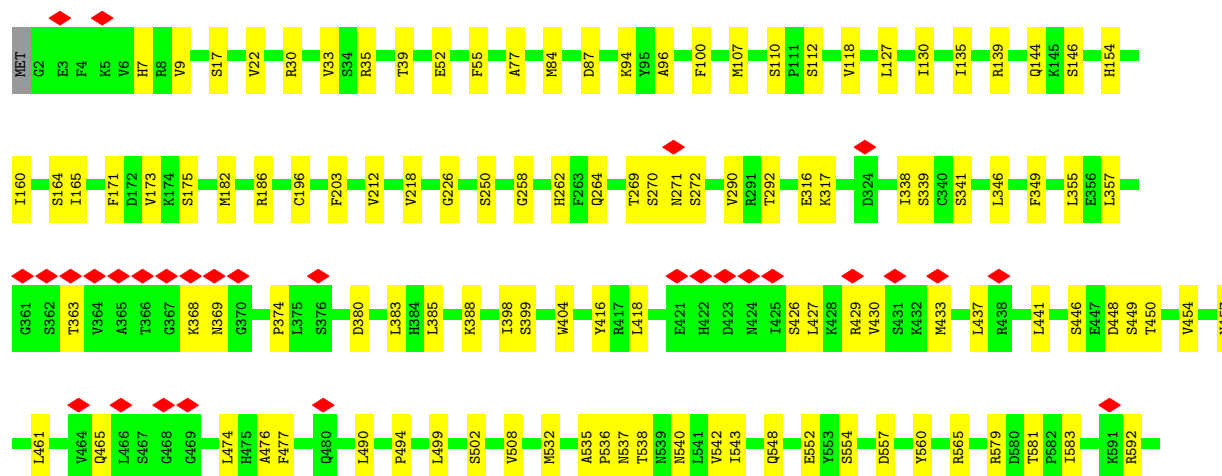
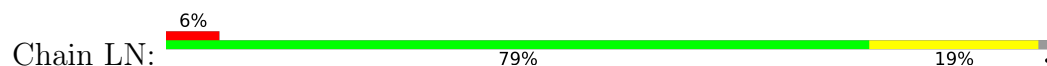
• Molecule 20: HEAT repeat-containing protein 1

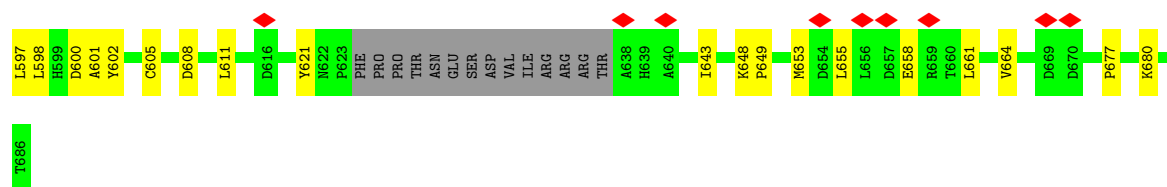




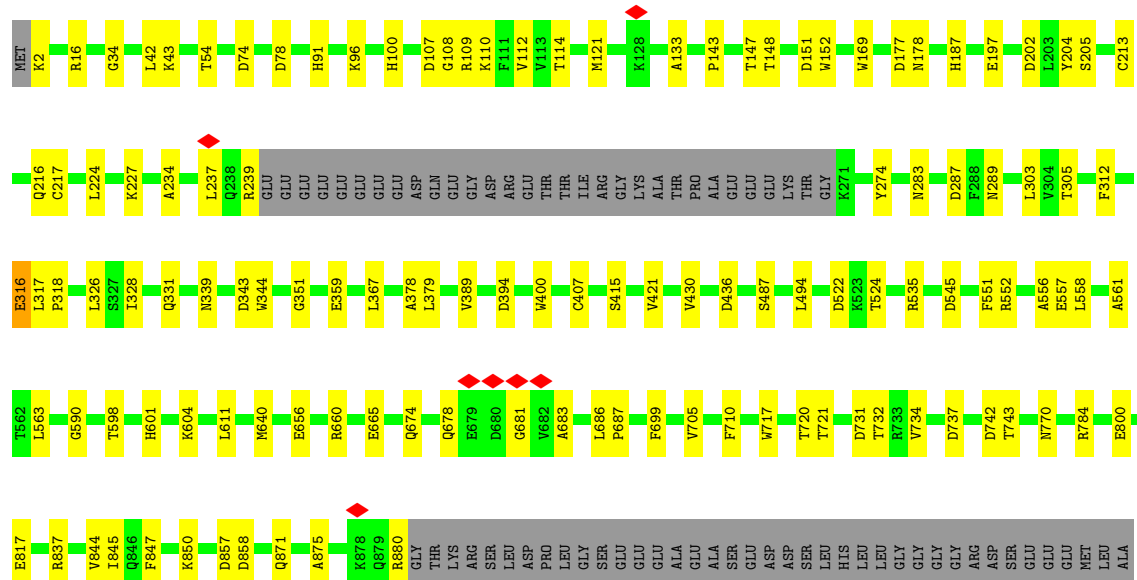
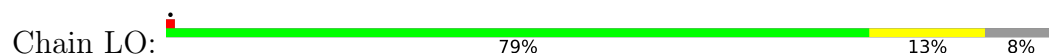


● Molecule 21: U3 small nucleolar RNA-associated protein 4 homolog

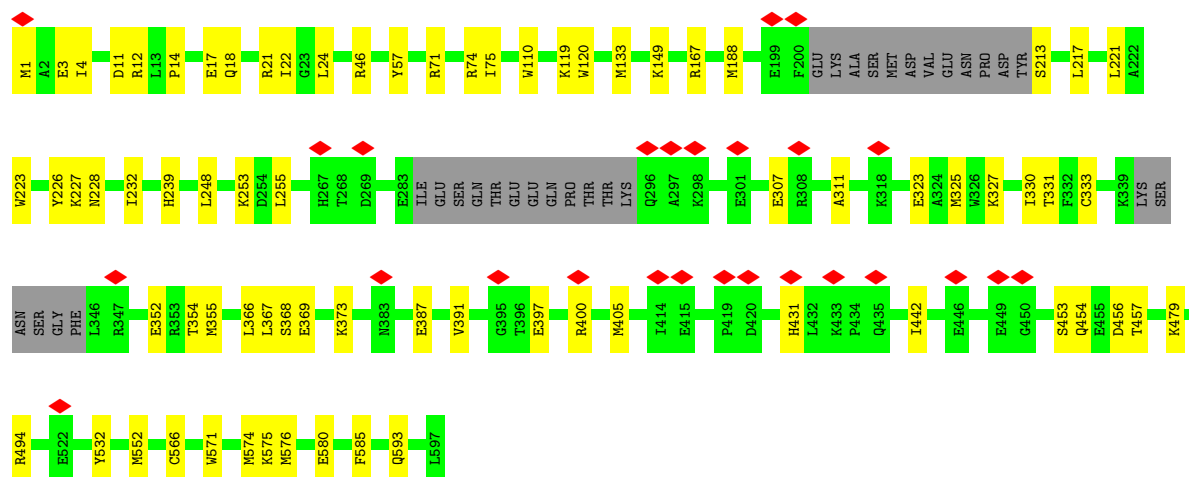
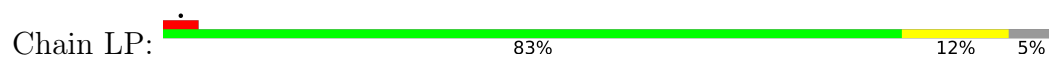




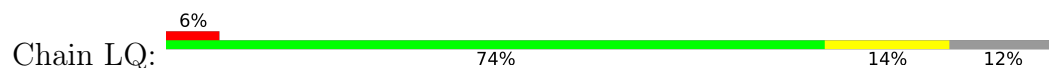
- Molecule 22: Periodic tryptophan protein 2 homolog

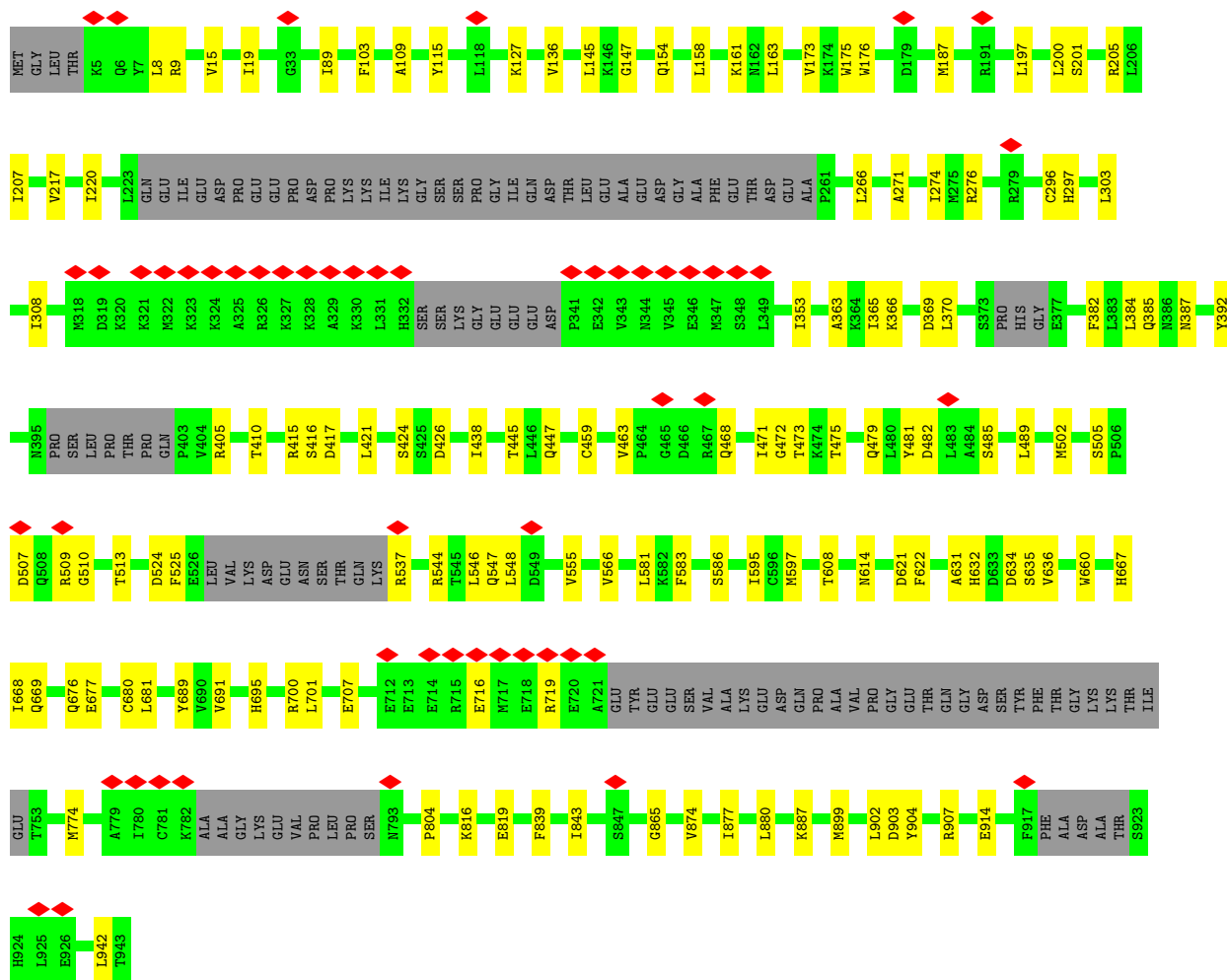


- Molecule 23: U3 small nucleolar RNA-associated protein 6 homolog



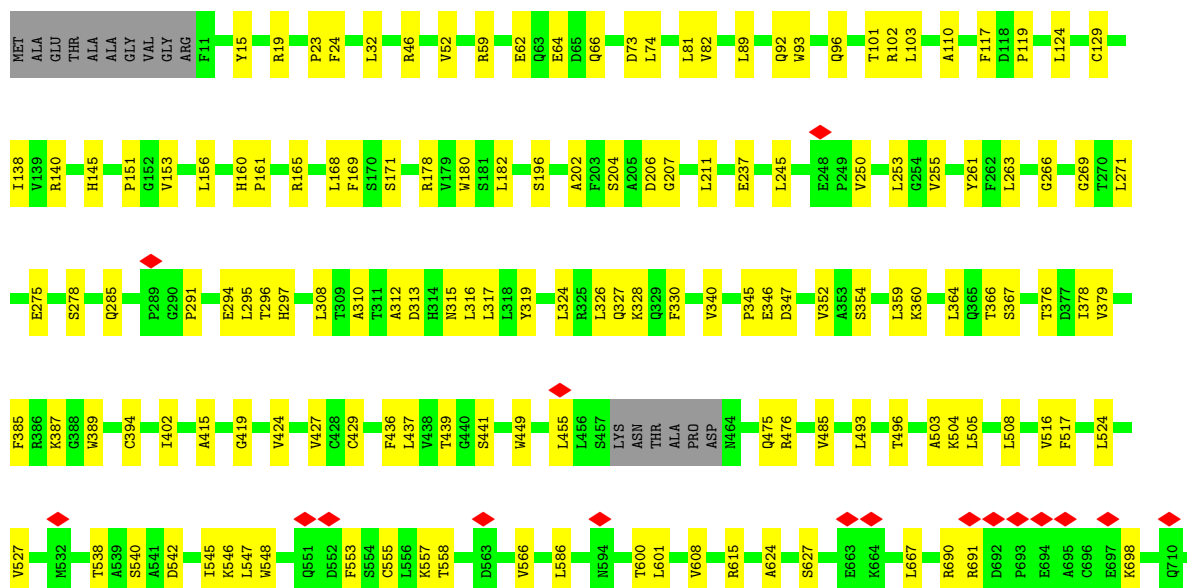
- Molecule 24: WD repeat-containing protein 3



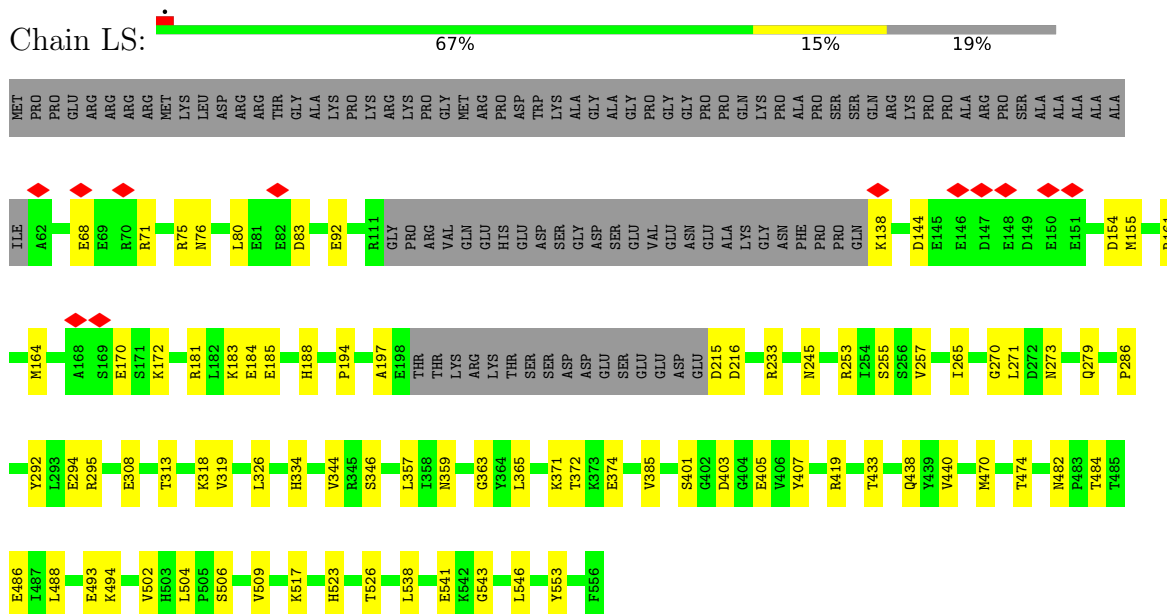


• Molecule 25: Transducin beta-like protein 3

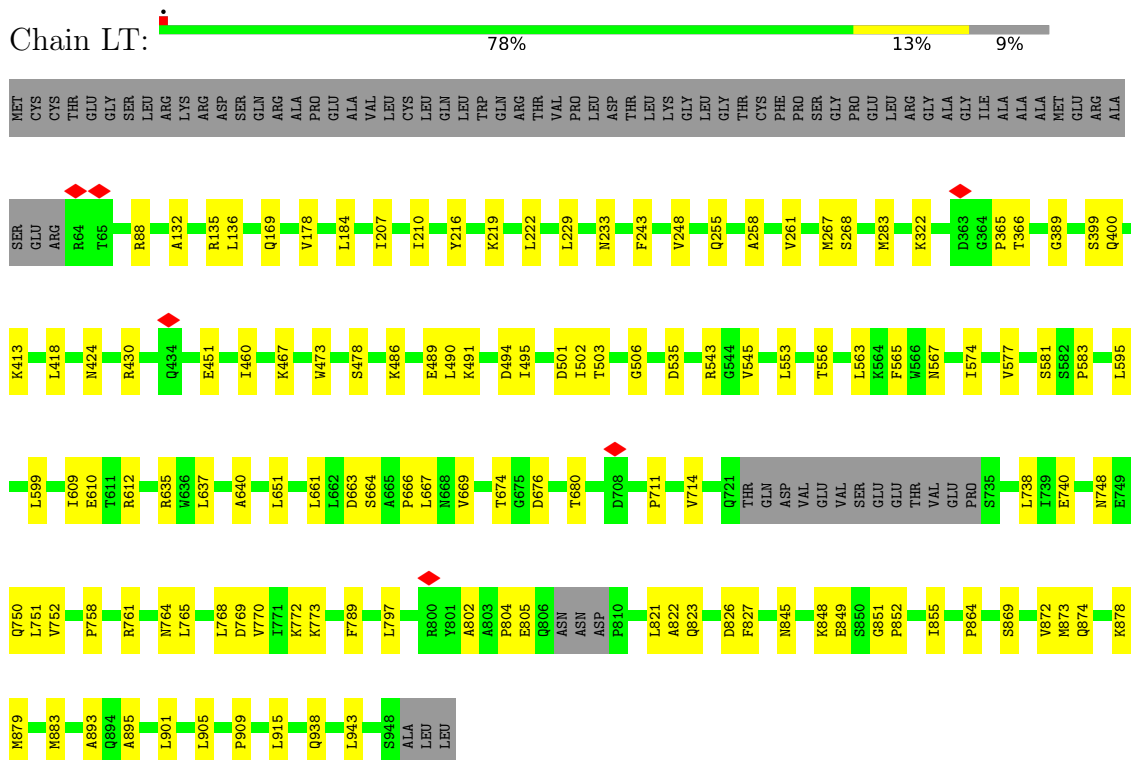
Chain LR:



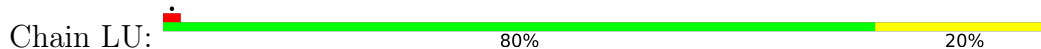
- Molecule 26: U3 small nucleolar RNA-associated protein 18 homolog

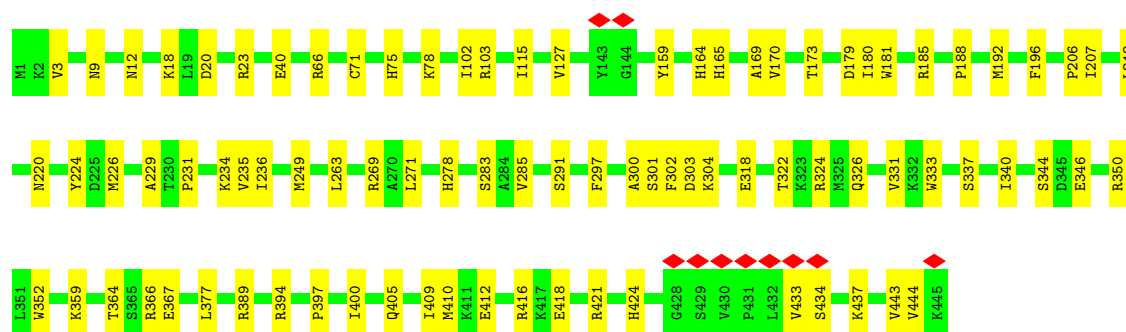


- Molecule 27: WD repeat-containing protein 36

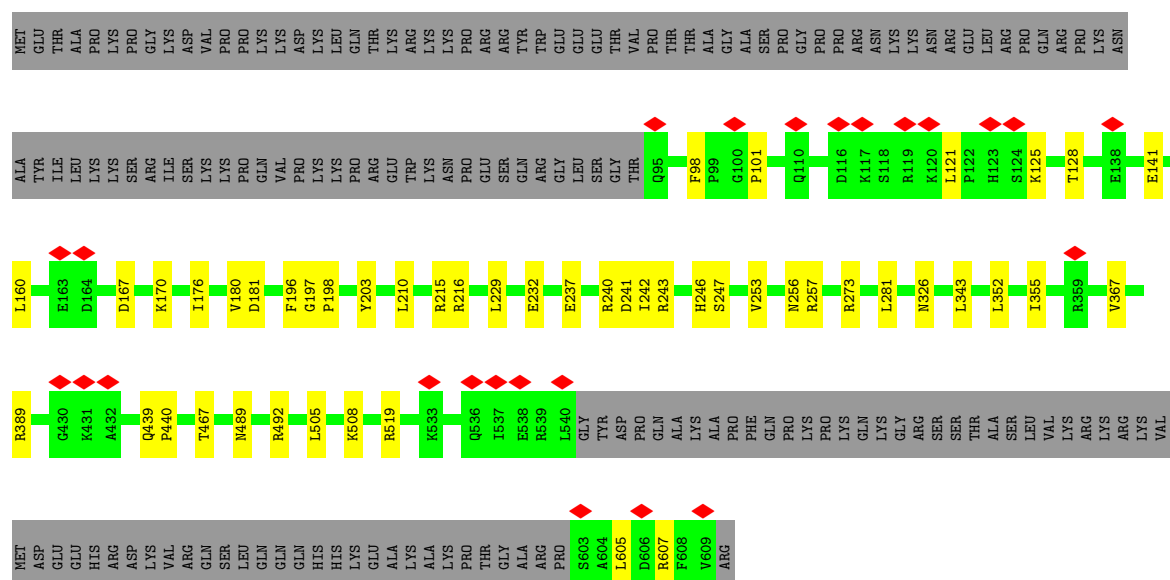


- Molecule 28: DDB1- and CUL4-associated factor 13





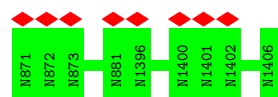
- Molecule 29: WD repeat-containing protein 46



- Molecule 30: U3 small nucleolar ribonucleoprotein protein IMP3

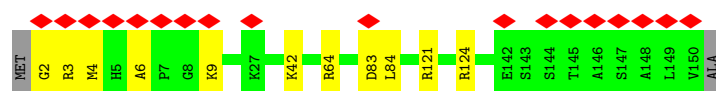
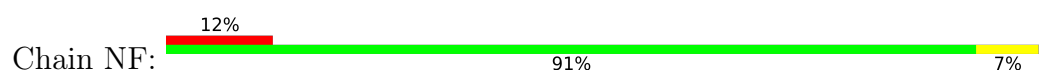


- Molecule 31: 5'ETS rRNA

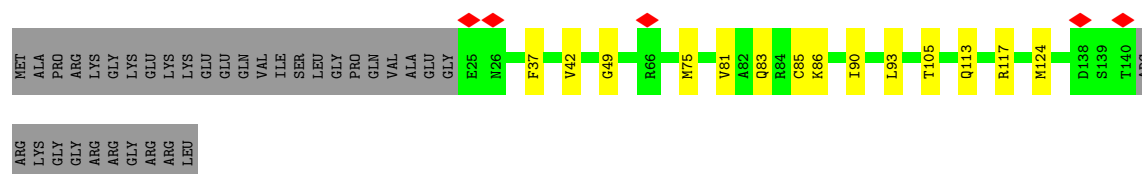


- Molecule 32: U3 small nucleolar ribonucleoprotein protein MPP10

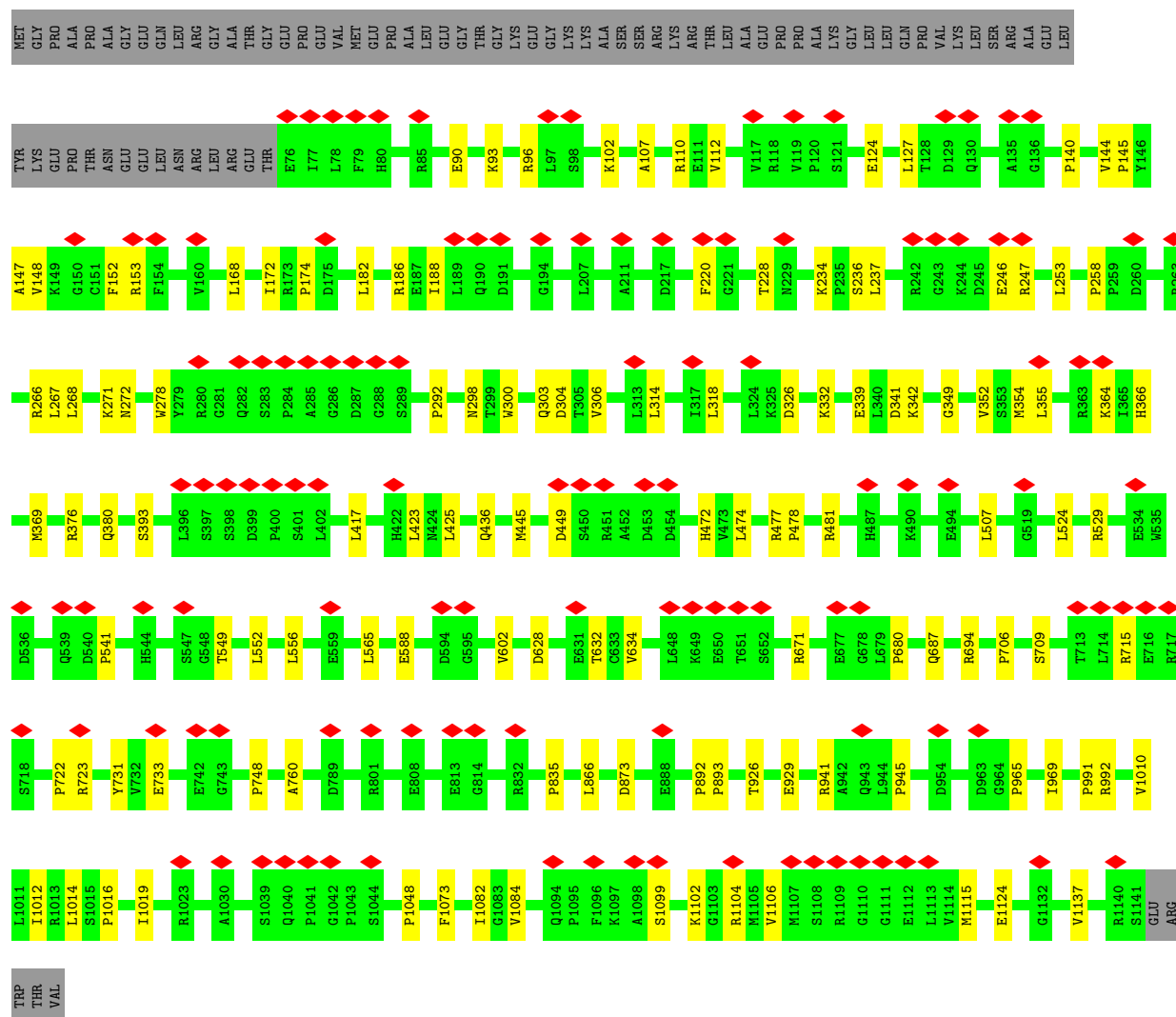
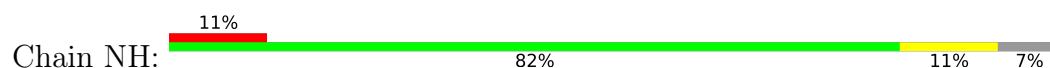


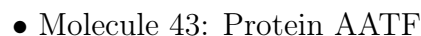
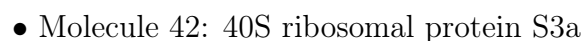


- Molecule 38: 40S ribosomal protein S14



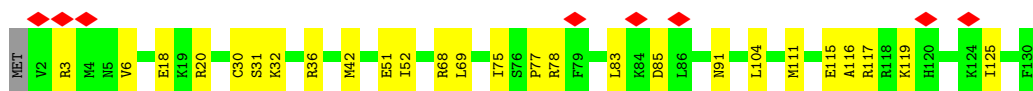
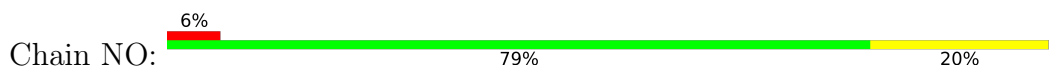
- Molecule 39: Nucleolar protein 6



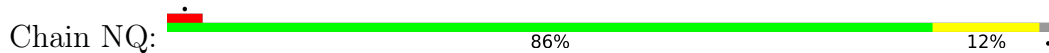


[illegible]

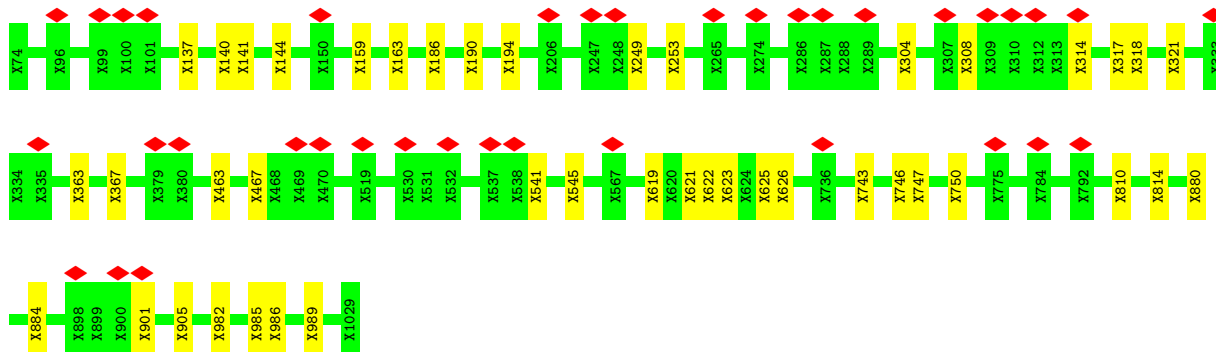
- Molecule 44: 40S ribosomal protein S15a



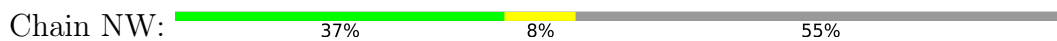
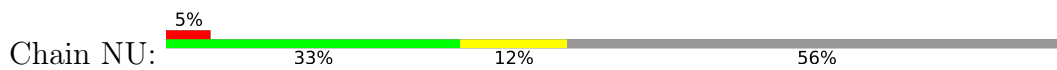
- Molecule 45: 40S ribosomal protein S27



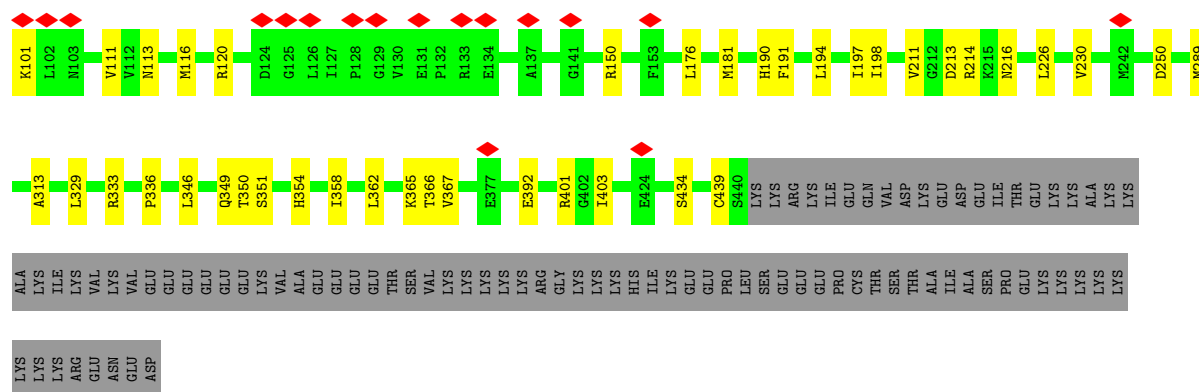
- Molecule 46: RRP12-like protein



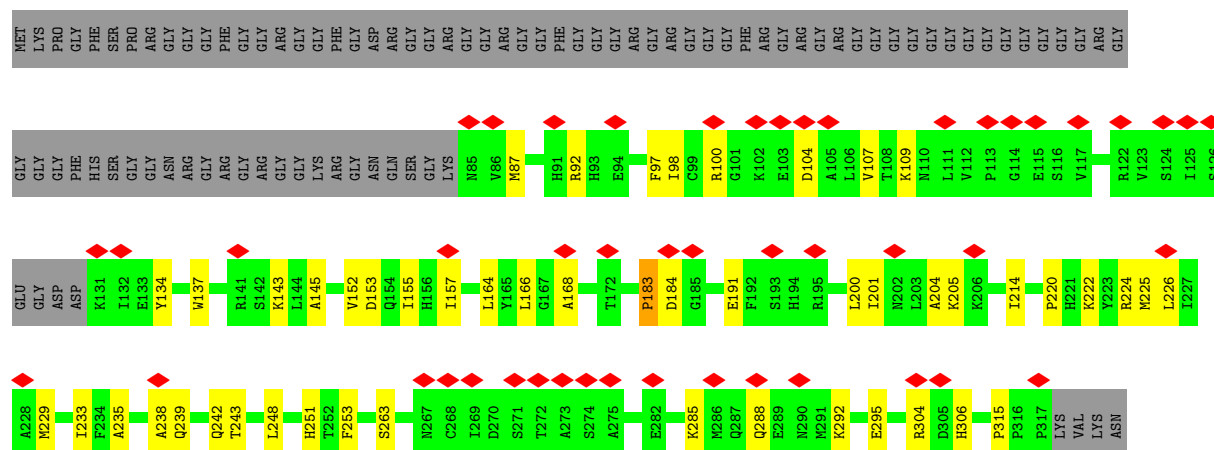
Chain NT:



Year	Publications
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1983	1
1984	1
1985	1
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1988	1
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2020	1



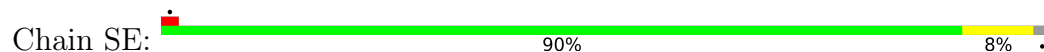
- Molecule 53: rRNA 2'-O-methyltransferase fibrillar



- Molecule 53: rRNA 2'-O-methyltransferase fibrillar

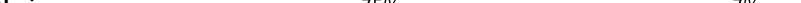


- Molecule 54: NHP2-like protein 1

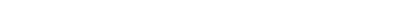


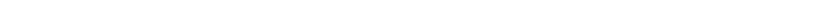
- Molecule 54: NHP2-like protein 1

MET THR GLU ALA ASP V6 K9 R36 I50 R84 R97 I106 V128

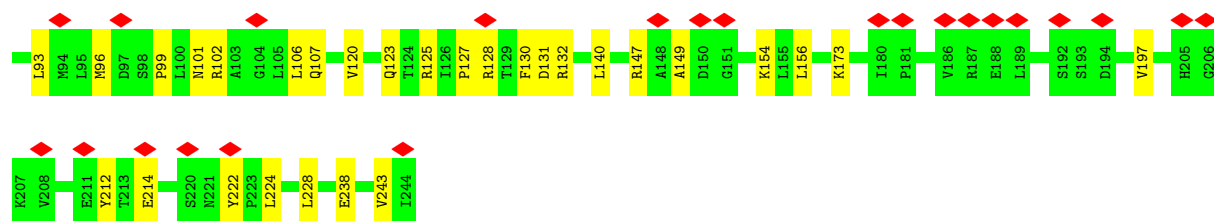
- Chain SG: 

[illegible]

- Chain SH:  86% 13%

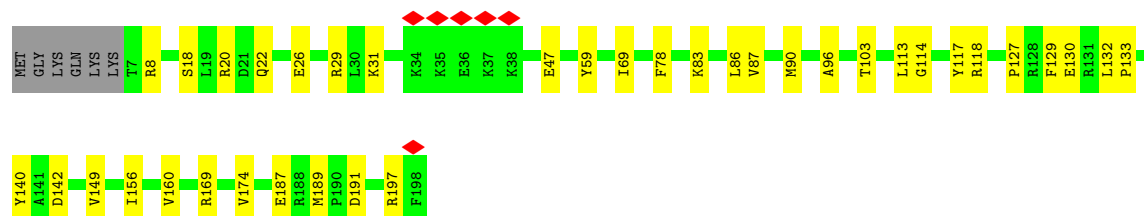
- Chain SI: 

[illegible]



- Molecule 59: rRNA-processing protein FCF1 homolog

Chain SL: 78% 19%



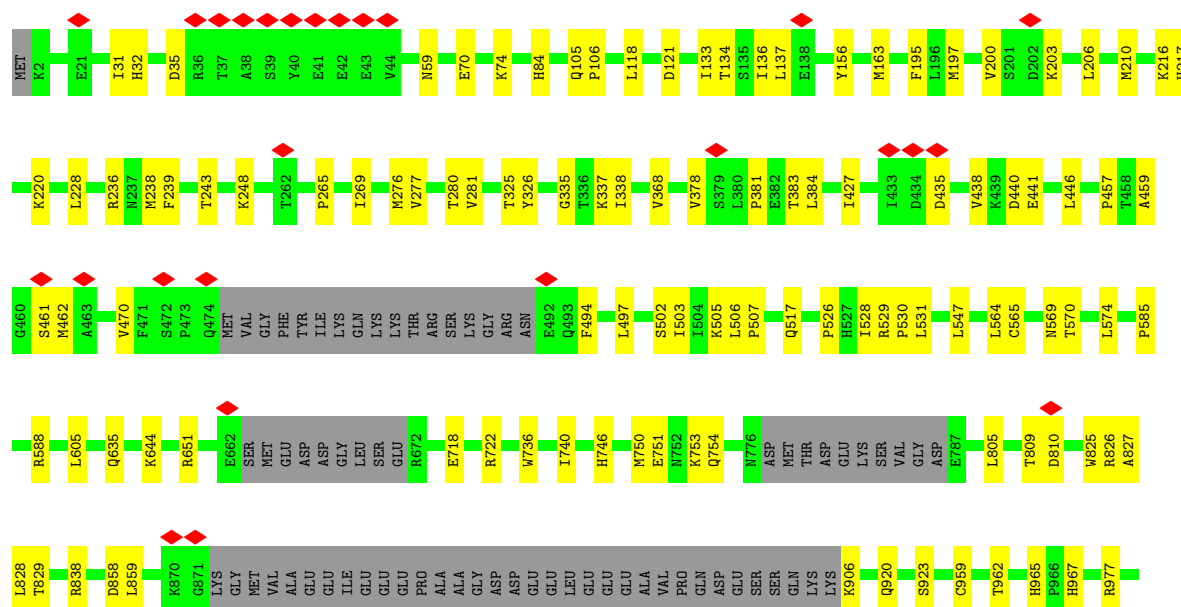
- Molecule 60: U3 small nucleolar ribonucleoprotein protein IMP4

Chain SM: 90% 10%



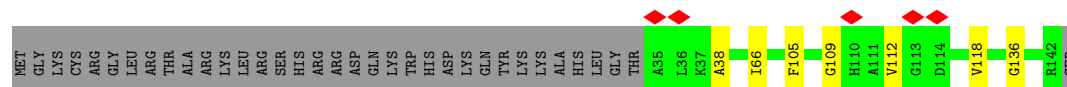
- Molecule 61: Small subunit processome component 20 homolog

Chain SP: 7% 59% 12% 28%

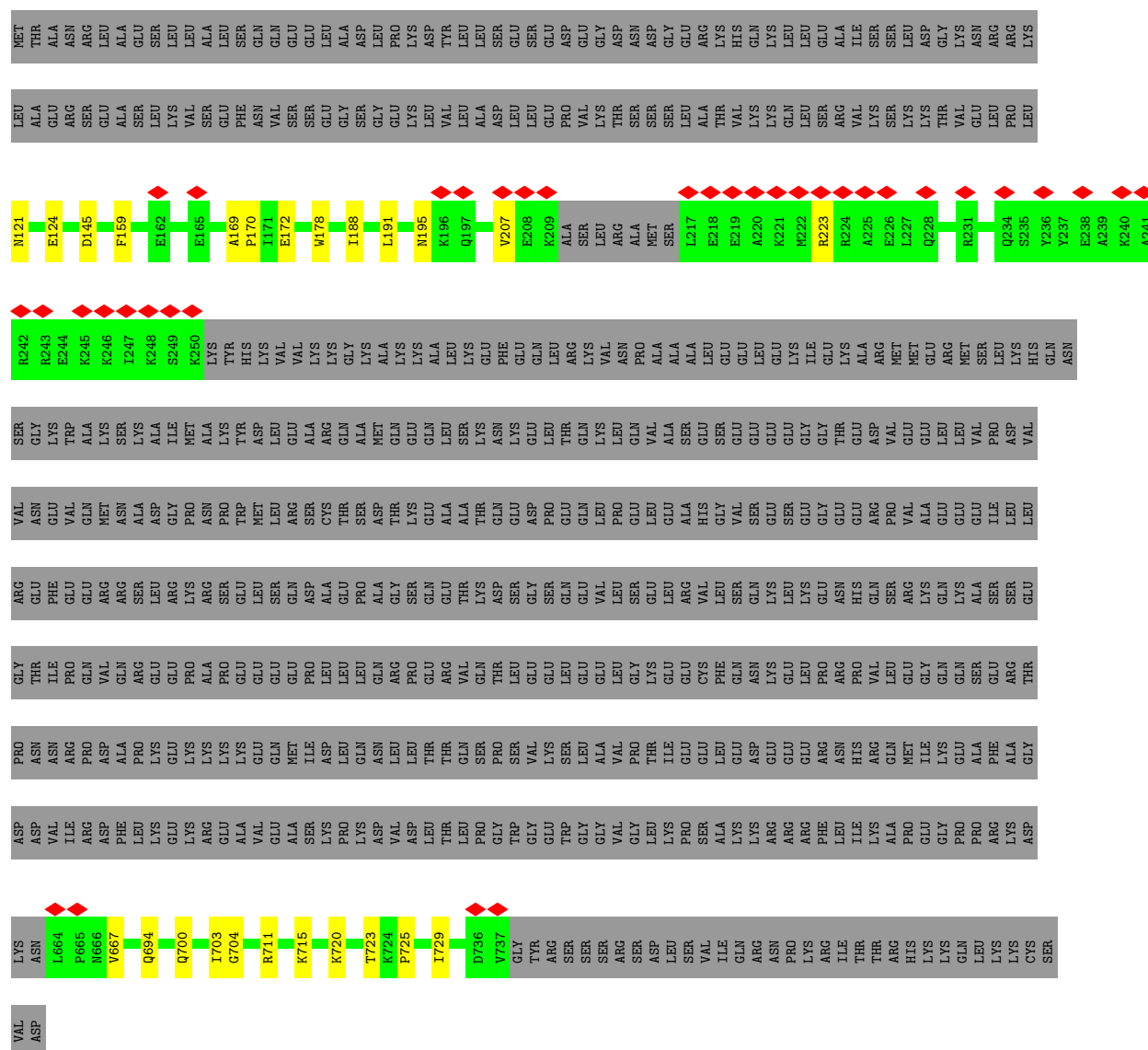




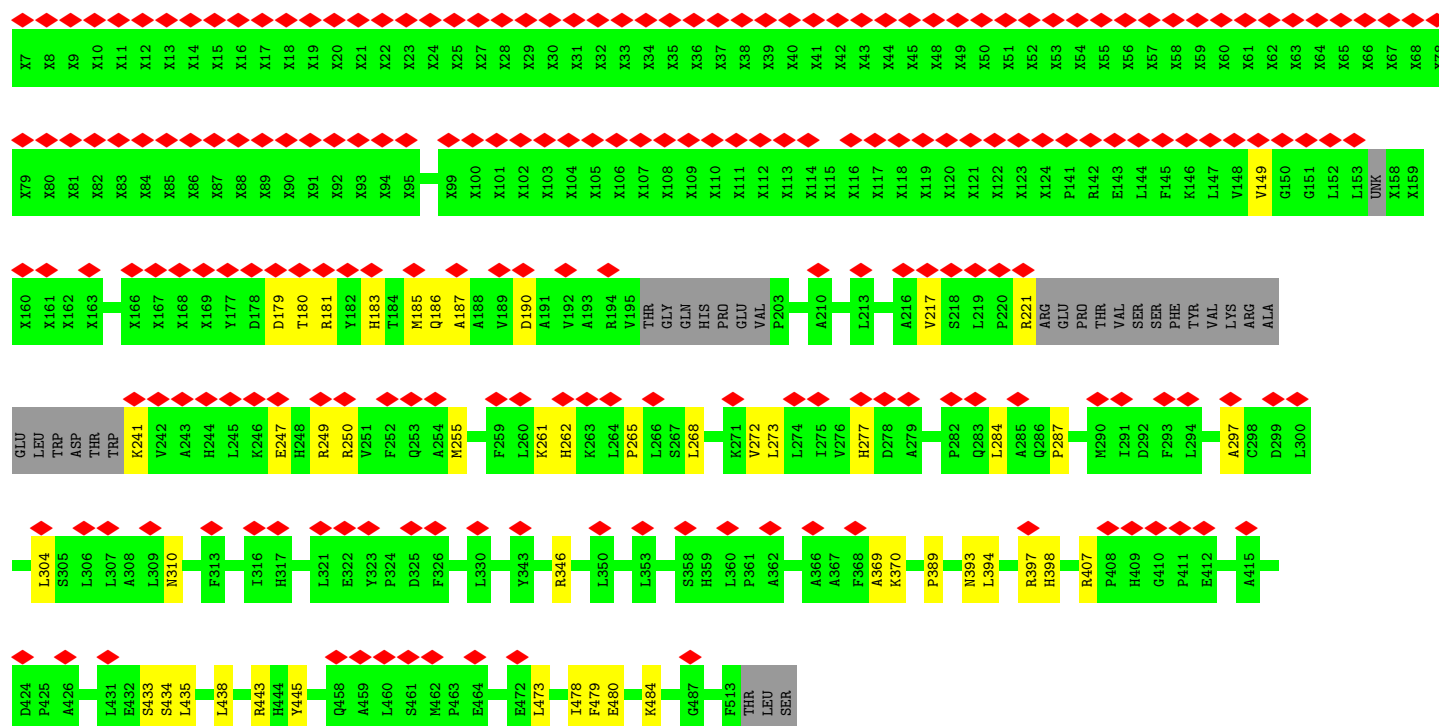
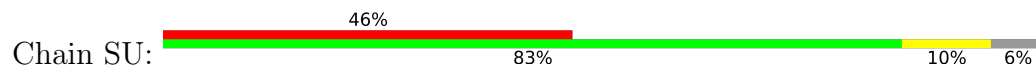
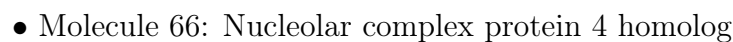
- Molecule 63: 40S ribosomal protein S23



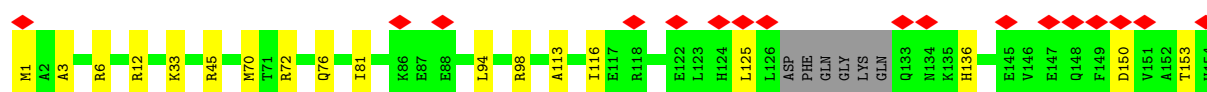
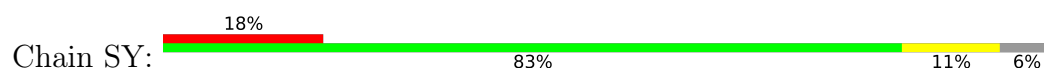
- Molecule 64: U3 small nucleolar RNA-associated protein 14 homolog A

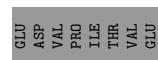


Chain ST:



Chain SW:





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	42142	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	58	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	20.935	Depositor
Minimum map value	-14.456	Depositor
Average map value	0.024	Depositor
Map value standard deviation	0.682	Depositor
Recommended contour level	2.68	Depositor
Map size (Å)	604.80005, 604.80005, 604.80005	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	Depositor

5 Model quality

5.1 Standard geometry

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

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	L0	0.11	0/5739	0.32	0/8931
2	L1	0.11	0/31039	0.31	1/48327 (0.0%)
3	L2	0.10	0/5130	0.29	0/7996
4	L3	0.17	0/720	0.42	0/970
5	L4	0.12	0/2118	0.36	0/2849
6	L5	0.16	0/1523	0.40	2/2048 (0.1%)
7	L6	0.16	0/1830	0.39	0/2434
8	L7	0.19	0/1365	0.44	0/1830
9	L8	0.13	0/1500	0.33	0/2002
10	L9	0.12	0/1447	0.31	0/1930
11	LA	0.19	0/941	0.45	0/1264
12	LC	0.14	0/1115	0.34	0/1494
13	LD	0.14	0/1225	0.39	0/1640
14	LF	0.12	0/868	0.32	0/1159
15	LG	0.10	0/490	0.31	0/656
16	LH	0.13	0/6127	0.36	0/8292
17	LI	0.15	0/3245	0.37	0/4386
18	LJ	0.16	0/3788	0.43	1/5128 (0.0%)
19	LK	0.21	0/959	0.55	1/1302 (0.1%)
19	LL	0.14	0/4072	0.38	0/5539
20	LM	0.17	0/16110	0.41	0/21817
21	LN	0.13	0/5438	0.36	0/7377
22	LO	0.14	0/6835	0.40	0/9256
23	LP	0.12	0/4806	0.32	0/6455
24	LQ	0.12	0/6548	0.34	0/8839
25	LR	0.13	0/6141	0.36	0/8348
26	LS	0.11	0/3621	0.32	0/4876
27	LT	0.12	0/6907	0.34	0/9359
28	LU	0.12	0/3695	0.35	0/4986
29	LW	0.19	1/3594 (0.0%)	0.39	3/4867 (0.1%)
30	LZ	0.13	0/1560	0.34	0/2104
32	NA	0.13	0/2084	0.35	0/2789

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	NB	0.12	0/622	0.32	0/816
34	NC	0.13	0/788	0.34	0/1049
35	ND	0.13	0/708	0.32	0/947
36	NE	0.11	0/807	0.29	0/1069
37	NF	0.11	0/1226	0.28	0/1649
38	NG	0.11	0/873	0.31	0/1177
39	NH	0.13	0/8580	0.32	0/11685
40	NI	0.12	0/1887	0.32	0/2558
41	NJ	0.14	0/6652	0.37	0/9006
41	NK	0.15	0/6545	0.38	1/8867 (0.0%)
42	NM	0.10	0/1899	0.30	0/2533
43	NN	0.13	0/346	0.38	0/462
44	NO	0.16	0/1051	0.44	0/1406
45	NQ	0.10	0/653	0.29	0/876
47	NT	0.18	0/479	0.53	1/635 (0.2%)
48	NU	0.15	0/501	0.38	0/667
49	NW	0.14	0/2556	0.43	2/3469 (0.1%)
50	NY	0.13	0/2265	0.32	0/3045
51	SA	0.10	0/3122	0.27	0/4208
52	SB	0.12	0/3491	0.33	0/4695
53	SC	0.19	0/1818	0.41	2/2463 (0.1%)
53	SD	0.10	0/1878	0.30	1/2540 (0.0%)
54	SE	0.12	0/980	0.33	0/1323
54	SF	0.13	0/967	0.34	0/1305
55	SG	0.11	0/2941	0.31	0/3988
56	SH	0.10	0/2882	0.30	0/3887
57	SI	0.12	0/6917	0.32	0/9297
58	SJ	0.14	0/1609	0.39	0/2181
58	SK	0.13	0/1609	0.38	0/2181
59	SL	0.13	0/1619	0.34	0/2174
60	SM	0.12	0/2420	0.34	0/3264
61	SP	0.14	0/16393	0.36	0/22173
62	SQ	0.11	0/1561	0.29	0/2083
63	SR	0.13	0/828	0.36	0/1110
64	SS	0.13	0/1663	0.34	0/2250
65	ST	0.18	0/3597	0.37	0/4836
66	SU	0.14	0/2634	0.36	0/3581
67	SW	0.19	0/1436	0.43	0/1936
70	SY	0.10	0/2051	0.29	0/2723
71	SZ	0.14	0/2043	0.40	0/2763
All	All	0.13	1/245477 (0.0%)	0.35	15/340127 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	L5	0	1
22	LO	0	1
67	SW	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	LW	101	PRO	CG-CD	-7.69	1.24	1.50

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	LW	101	PRO	N-CD-CG	-10.97	86.75	103.20
53	SC	183	PRO	CA-N-CD	-7.84	101.03	112.00
53	SC	183	PRO	N-CD-CG	-7.76	91.56	103.20
6	L5	136	ARG	CB-CG-CD	7.24	127.95	111.30
19	LK	542	PRO	CA-N-CD	-7.23	101.88	112.00
47	NT	122	PRO	CA-N-CD	-6.59	102.77	112.00
29	LW	101	PRO	CA-N-CD	-6.40	103.04	112.00
18	LJ	489	MET	CB-CG-SD	-5.85	95.16	112.70
41	NK	220	PRO	CA-N-CD	-5.70	104.02	112.00
29	LW	101	PRO	CA-CB-CG	-5.55	93.96	104.50
49	NW	71	GLY	CA-C-N	5.41	129.16	121.42
49	NW	71	GLY	C-N-CA	5.41	129.16	121.42
6	L5	136	ARG	CA-CB-CG	5.36	124.81	114.10
53	SD	155	ILE	N-CA-C	-5.35	108.29	113.53
2	L1	589	G	C2'-C3'-O3'	5.13	117.19	109.50

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	L5	136	ARG	Sidechain
22	LO	316	GLU	Peptide
67	SW	247	ARG	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L0	5152	0	2630	52	0
2	L1	27777	0	14063	253	0
3	L2	4589	0	2306	45	0
4	L3	854	0	774	25	0
5	L4	2076	0	2177	18	0
6	L5	1501	0	1557	16	0
7	L6	1811	0	1974	23	0
8	L7	1346	0	1410	31	0
9	L8	1474	0	1542	19	0
10	L9	1425	0	1541	17	0
11	LA	931	0	961	17	0
12	LC	1098	0	1168	11	0
13	LD	1204	0	1274	11	0
14	LF	851	0	894	18	0
15	LG	488	0	514	4	0
16	LH	5987	0	5953	77	0
17	LI	3889	0	3464	55	0
18	LJ	3711	0	3758	69	0
19	LK	943	0	1023	28	0
19	LL	3982	0	4031	55	0
20	LM	15820	0	16318	290	0
21	LN	5299	0	5269	80	0
22	LO	6676	0	6579	76	0
23	LP	4705	0	4720	57	0
24	LQ	6438	0	6400	78	0
25	LR	6015	0	5981	90	0
26	LS	3560	0	3570	56	0
27	LT	6756	0	6768	87	0
28	LU	3611	0	3618	64	0
29	LW	3519	0	3518	34	0
30	LZ	1532	0	1553	12	0
31	N0	264	0	178	0	0
32	NA	2055	0	2135	21	0
33	NB	617	0	685	8	0
34	NC	779	0	788	11	0
35	ND	696	0	729	10	0
36	NE	799	0	854	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	NF	1202	0	1289	10	0
38	NG	861	0	871	10	0
39	NH	8374	0	8456	80	0
40	NI	1840	0	1812	19	0
41	NJ	6526	0	6599	60	0
41	NK	6419	0	6480	91	0
42	NM	1873	0	1968	20	0
43	NN	340	0	345	3	0
44	NO	1034	0	1080	20	0
45	NQ	640	0	661	8	0
46	NR	4305	0	945	22	0
47	NT	470	0	474	14	0
48	NU	495	0	541	9	0
49	NW	2498	0	2456	34	0
50	NY	2222	0	2310	18	0
51	SA	3077	0	3139	32	0
52	SB	3439	0	3559	45	0
53	SC	1781	0	1803	37	0
53	SD	1841	0	1867	14	0
54	SE	968	0	1017	7	0
54	SF	955	0	1008	5	0
55	SG	2884	0	2751	17	0
56	SH	2832	0	2937	29	0
57	SI	6803	0	6966	68	0
58	SJ	1579	0	1646	29	0
58	SK	1579	0	1646	24	0
59	SL	1586	0	1641	31	0
60	SM	2369	0	2376	18	0
61	SP	16078	0	16633	216	0
62	SQ	1533	0	1579	9	0
63	SR	816	0	871	5	0
64	SS	1626	0	1677	20	0
65	ST	4170	0	3804	60	0
66	SU	3154	0	2736	35	0
67	SW	1413	0	1489	29	0
68	Sx	190	0	41	2	0
69	SX	695	0	151	0	0
70	SY	2024	0	2148	20	0
71	SZ	2222	0	2142	31	0
72	L1	19	0	0	0	0
72	NH	1	0	0	0	0
72	SI	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
72	SL	1	0	0	0	0
73	NH	31	0	12	2	0
73	NK	31	0	12	1	0
74	NQ	1	0	0	0	0
74	NT	1	0	0	0	0
74	SL	1	0	0	0	0
75	SI	32	0	12	0	0
76	SJ	26	0	19	3	0
76	SK	26	0	19	0	0
All	All	245114	0	224665	2688	0

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

All (2688) 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)
20:LM:1457:GLN:HE21	20:LM:1457:GLN:N	1.53	1.06
28:LU:66:ARG:HH12	59:SL:127:PRO:HD3	1.40	0.84
27:LT:748:ASN:HB3	27:LT:751:LEU:HD23	1.60	0.83
21:LN:461:LEU:HB2	21:LN:477:PHE:HB2	1.63	0.81
61:SP:1430:VAL:HG12	61:SP:1477:ASN:HD21	1.45	0.80
61:SP:2085:GLU:HB3	61:SP:2089:ARG:HH12	1.46	0.79
18:LJ:179:LEU:HD12	18:LJ:193:ASP:HB2	1.65	0.78
2:L1:1396:A:O2'	2:L1:1398:G:N7	2.15	0.78
61:SP:1885:LEU:HB3	61:SP:1927:ILE:HG21	1.64	0.77
5:L4:248:ILE:HG22	5:L4:251:GLU:HG2	1.67	0.77
20:LM:605:PRO:HA	20:LM:703:THR:HG21	1.66	0.77
19:LL:276:THR:HB	19:LL:286:LYS:HB2	1.68	0.76
32:NA:383:PRO:HG2	32:NA:386:LEU:HD13	1.68	0.75
2:L1:164:A:H3'	2:L1:165:G:H21	1.51	0.75
8:L7:53:VAL:O	8:L7:57:ARG:HB2	1.86	0.75
4:L3:36:VAL:HG23	4:L3:40:TYR:HD2	1.52	0.75
2:L1:1354:G:N2	2:L1:1357:A:OP2	2.19	0.75
20:LM:843:VAL:HG22	20:LM:846:ARG:HH21	1.51	0.75
1:L0:1434:U:H5'	51:SA:44:SER:HA	1.68	0.74
2:L1:97:U:H3	2:L1:434:G:H1	1.32	0.74
20:LM:688:ILE:HG12	20:LM:732:LEU:HD11	1.68	0.74
19:LL:596:LYS:NZ	21:LN:380:ASP:OD2	2.21	0.74
2:L1:1392:U:H2'	2:L1:1393:G:H8	1.53	0.73
20:LM:1761:LEU:HB3	20:LM:1805:ARG:HH21	1.53	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:LR:732:GLN:HE22	25:LR:764:THR:HG23	1.54	0.72
42:NM:139:CYS:HB2	42:NM:172:MET:HE1	1.71	0.72
24:LQ:668:ILE:HG22	24:LQ:669:GLN:HG3	1.72	0.72
52:SB:289:MET:HE1	52:SB:365:LYS:HB3	1.69	0.72
49:NW:151:PHE:HB2	49:NW:159:TYR:HB2	1.72	0.72
51:SA:217:ILE:HG21	51:SA:223:LEU:HD12	1.71	0.72
1:L0:668:U:H5'	35:ND:247:ARG:HD2	1.71	0.72
23:LP:333:CYS:HB3	23:LP:354:THR:HG22	1.71	0.72
20:LM:1457:GLN:N	20:LM:1457:GLN:NE2	2.34	0.71
5:L4:246:LEU:HD12	5:L4:247:THR:HG22	1.72	0.71
17:LI:608:ILE:HG23	17:LI:613:ILE:HD11	1.73	0.71
61:SP:565:CYS:HA	61:SP:605:LEU:HD12	1.72	0.71
4:L3:55:ARG:NH2	18:LJ:77:SER:O	2.24	0.70
19:LL:106:ILE:HB	19:LL:120:LEU:HB2	1.72	0.70
2:L1:368:U:OP2	43:NN:516:ARG:NH2	2.24	0.70
59:SL:69:ILE:HG22	59:SL:156:ILE:HB	1.72	0.70
17:LI:693:VAL:HB	19:LL:570:GLY:HA3	1.73	0.70
41:NK:160:LEU:HD23	41:NK:188:ILE:HD11	1.72	0.70
44:NO:91:ASN:O	59:SL:83:LYS:NZ	2.21	0.70
26:LS:68:GLU:HG2	26:LS:71:ARG:HH22	1.56	0.70
41:NK:779:LEU:HA	41:NK:783:PHE:HB2	1.74	0.69
22:LO:389:VAL:HG21	22:LO:430:VAL:HG21	1.74	0.69
25:LR:493:LEU:HD12	25:LR:505:LEU:HD11	1.73	0.69
41:NJ:283:THR:HG22	41:NJ:413:ILE:HD11	1.72	0.69
17:LI:657:ASN:HB3	17:LI:660:VAL:HB	1.73	0.69
22:LO:2:LYS:HD3	22:LO:640:MET:HE1	1.74	0.69
25:LR:168:LEU:HB3	25:LR:180:TRP:HB2	1.74	0.69
27:LT:864:PRO:HD3	27:LT:873:MET:HE1	1.73	0.69
26:LS:253:ARG:HH21	26:LS:271:LEU:HD21	1.58	0.69
56:SH:13:CYS:HB3	56:SH:35:ILE:HG23	1.73	0.69
2:L1:1130:G:N2	2:L1:1130:G:OP2	2.25	0.69
20:LM:1741:LEU:HD22	20:LM:1785:GLN:HG3	1.75	0.69
57:SI:881:ARG:HG2	57:SI:884:MET:HE3	1.74	0.69
16:LH:21:ARG:HG2	16:LH:295:HIS:HB3	1.75	0.69
26:LS:371:LYS:HG3	26:LS:372:THR:HG23	1.74	0.69
1:L0:679:A:O2'	54:SE:28:GLN:NE2	2.26	0.68
61:SP:1191:LEU:HG	61:SP:1238:ILE:HD11	1.75	0.68
41:NK:284:ALA:HB3	41:NK:290:LYS:HD3	1.75	0.68
61:SP:1538:GLN:HE22	61:SP:1619:THR:HG21	1.58	0.68
61:SP:59:ASN:HD22	61:SP:106:PRO:HG2	1.58	0.68
4:L3:104:UNK:HA	65:ST:796:HIS:HD2	1.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LA:80:ASP:OD1	11:LA:84:LYS:NZ	2.27	0.67
39:NH:393:SER:HA	39:NH:417:LEU:HB2	1.77	0.67
8:L7:57:ARG:HH22	8:L7:90:LYS:HA	1.58	0.67
61:SP:1609:LEU:HA	61:SP:1613:ILE:HD13	1.76	0.67
24:LQ:274:ILE:HG21	24:LQ:353:ILE:HD11	1.76	0.67
61:SP:1303:VAL:HG11	61:SP:1343:MET:HG3	1.77	0.67
20:LM:1349:THR:HA	20:LM:1352:MET:HE2	1.75	0.67
61:SP:1826:ALA:HA	61:SP:1829:LYS:HE3	1.76	0.67
66:SU:407:ARG:NH2	66:SU:433:SER:O	2.28	0.67
71:SZ:182:LEU:HG	71:SZ:186:ARG:HH12	1.59	0.67
19:LL:298:LEU:HB2	19:LL:315:CYS:HB2	1.74	0.67
20:LM:1989:CYS:SG	20:LM:2040:ARG:NH2	2.67	0.67
21:LN:212:VAL:HG12	21:LN:218:VAL:HG22	1.77	0.67
2:L1:134:C:O2'	61:SP:906:LYS:NZ	2.28	0.67
16:LH:85:TRP:HE1	16:LH:92:LEU:HD13	1.60	0.67
18:LJ:489:MET:HE2	19:LK:571:LYS:HA	1.77	0.67
19:LL:503:ILE:HG22	19:LL:507:GLN:HE22	1.60	0.67
53:SD:284:LYS:NZ	59:SL:130:GLU:OE1	2.28	0.67
25:LR:402:ILE:HG21	25:LR:455:LEU:HD21	1.77	0.67
49:NW:160:ARG:HD2	49:NW:172:LEU:HD23	1.76	0.67
44:NO:75:ILE:O	44:NO:78:ARG:NH1	2.27	0.67
58:SJ:96:MET:HA	58:SJ:101:ASN:HD22	1.60	0.67
61:SP:1260:LEU:HB3	61:SP:1338:LYS:HG3	1.75	0.67
6:L5:71:ARG:NH2	6:L5:148:ASN:OD1	2.28	0.66
23:LP:1:MET:SD	28:LU:366:ARG:NH2	2.68	0.66
41:NK:509:TYR:HB3	41:NK:696:LEU:HB2	1.77	0.66
2:L1:1192:U:H4'	2:L1:1193:U:H5'	1.77	0.66
6:L5:168:THR:OG1	6:L5:171:GLU:OE1	2.14	0.66
22:LO:880:ARG:HH22	27:LT:909:PRO:HB2	1.60	0.66
24:LQ:903:ASP:OD2	24:LQ:907:ARG:NH1	2.29	0.66
41:NK:309:ILE:HB	41:NK:368:ILE:HG22	1.78	0.66
49:NW:138:ARG:H	49:NW:153:GLY:HA2	1.61	0.66
23:LP:110:TRP:HB3	23:LP:133:MET:HE2	1.77	0.66
23:LP:552:MET:HE3	23:LP:566:CYS:HB3	1.78	0.66
2:L1:39:A:H61	2:L1:515:G:H1'	1.61	0.66
23:LP:149:LYS:NZ	62:SQ:564:ILE:O	2.29	0.66
41:NJ:277:ARG:HB3	41:NJ:458:ARG:HG2	1.75	0.66
61:SP:494:PHE:HB3	61:SP:497:LEU:HD13	1.78	0.66
9:L8:205:ARG:HH22	13:LD:8:ARG:HH21	1.44	0.66
20:LM:962:LYS:HB3	20:LM:965:GLU:HB2	1.76	0.66
59:SL:26:GLU:OE1	59:SL:29:ARG:NH1	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:LI:693:VAL:HG21	19:LL:567:HIS:HA	1.78	0.66
20:LM:688:ILE:HG23	20:LM:732:LEU:HD21	1.78	0.66
2:L1:1394:G:N2	2:L1:1475:G:O2'	2.26	0.66
39:NH:246:GLU:HG3	39:NH:247:ARG:HD3	1.77	0.66
41:NJ:501:LEU:HD11	41:NJ:638:MET:HG3	1.76	0.66
65:ST:708:PHE:HB3	65:ST:748:GLN:HE22	1.61	0.66
1:L0:1420:G:H1	3:L2:49:U:H3	1.42	0.66
10:L9:136:ARG:NH1	10:L9:159:PHE:O	2.29	0.66
19:LK:535:ALA:HB3	19:LL:577:THR:HG21	1.76	0.66
21:LN:494:PRO:HG2	21:LN:536:PRO:HA	1.76	0.66
52:SB:350:THR:HG21	52:SB:358:ILE:HG13	1.78	0.66
53:SD:195:ARG:NH2	54:SF:9:LYS:O	2.29	0.66
18:LJ:103:GLY:HA2	18:LJ:118:PHE:O	1.96	0.65
20:LM:542:GLU:O	20:LM:545:LYS:NZ	2.30	0.65
61:SP:1530:LEU:HD13	61:SP:1615:PRO:HG3	1.79	0.65
2:L1:1736:G:H2'	2:L1:1737:G:H8	1.59	0.65
41:NJ:821:ASP:HB3	41:NJ:841:MET:HE1	1.79	0.65
57:SI:178:LYS:NZ	57:SI:243:LYS:O	2.29	0.65
57:SI:1063:THR:HG22	57:SI:1096:VAL:HG12	1.76	0.65
61:SP:156:TYR:HA	61:SP:163:MET:HE1	1.78	0.65
16:LH:409:GLN:NE2	16:LH:411:LYS:O	2.29	0.65
61:SP:2204:LEU:HD23	61:SP:2231:ILE:HG13	1.76	0.65
18:LJ:181:ILE:HG21	18:LJ:221:LEU:HD11	1.77	0.65
39:NH:172:ILE:HG22	39:NH:174:PRO:HD2	1.79	0.65
20:LM:1765:GLN:NE2	20:LM:1805:ARG:O	2.30	0.65
41:NJ:310:PHE:HB2	41:NJ:385:VAL:HG22	1.79	0.65
1:L0:1414:A:N6	59:SL:18:SER:OG	2.29	0.65
2:L1:508:A:H3'	2:L1:509:G:H8	1.62	0.65
12:LC:62:ARG:O	12:LC:96:TYR:OH	2.14	0.65
4:L3:67:VAL:HG12	4:L3:71:MET:HE2	1.77	0.65
1:L0:852:G:N2	22:LO:287:ASP:O	2.30	0.64
20:LM:1863:HIS:HA	20:LM:1867:LEU:HB2	1.79	0.64
24:LQ:632:HIS:HD2	24:LQ:636:VAL:HG12	1.62	0.64
24:LQ:774:MET:HE1	24:LQ:804:PRO:HG3	1.79	0.64
18:LJ:467:GLN:NE2	18:LJ:471:GLU:OE2	2.31	0.64
27:LT:772:LYS:HG3	27:LT:773:LYS:HD2	1.78	0.64
60:SM:153:HIS:HB3	60:SM:157:GLY:HA3	1.79	0.64
22:LO:303:LEU:HB2	22:LO:317:LEU:HD11	1.79	0.64
51:SA:45:ILE:HG13	51:SA:46:VAL:HG23	1.78	0.64
67:SW:161:GLU:OE2	67:SW:222:ARG:NH1	2.30	0.64
18:LJ:264:LEU:HG	18:LJ:274:VAL:HG22	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:NK:386:VAL:HG22	41:NK:408:PHE:HB2	1.80	0.64
57:SI:90:PRO:HG2	57:SI:93:VAL:HB	1.78	0.64
71:SZ:308:VAL:HA	71:SZ:311:ILE:HD12	1.77	0.64
3:L2:159:G:OP2	54:SF:97:ARG:NH2	2.30	0.64
6:L5:124:ASP:OD1	6:L5:125:SER:N	2.30	0.64
56:SH:159:MET:HG3	56:SH:160:PRO:HD2	1.80	0.64
1:L0:858:C:OP2	30:LZ:53:ARG:NH2	2.28	0.64
2:L1:484:A:OP1	57:SI:215:LYS:NZ	2.30	0.64
5:L4:45:ILE:HG13	5:L4:61:VAL:HG21	1.79	0.64
25:LR:504:LYS:HG2	25:LR:516:VAL:HG12	1.80	0.64
23:LP:213:SER:OG	64:SS:195:ASN:ND2	2.30	0.64
3:L2:59:G:H5'	22:LO:598:THR:HG23	1.79	0.64
20:LM:652:LYS:O	20:LM:656:LEU:N	2.28	0.64
22:LO:857:ASP:OD1	22:LO:858:ASP:N	2.30	0.64
20:LM:1125:GLN:NE2	20:LM:1164:GLU:OE2	2.31	0.63
28:LU:318:GLU:HG3	28:LU:394:ARG:HE	1.62	0.63
20:LM:1004:LEU:HD12	20:LM:1034:LEU:HD21	1.80	0.63
2:L1:190:G:O2'	61:SP:1197:TYR:OH	2.16	0.63
4:L3:75:ARG:NH2	4:L3:81:ASP:OD2	2.29	0.63
10:L9:72:PHE:HB3	34:NC:205:VAL:HG11	1.80	0.63
23:LP:22:ILE:HD13	29:LW:98:PHE:HZ	1.62	0.63
28:LU:326:GLN:O	28:LU:344:SER:OG	2.17	0.63
40:NI:63:VAL:HB	40:NI:119:ALA:HB3	1.81	0.63
41:NJ:71:LYS:HA	41:NJ:74:ARG:HE	1.64	0.63
61:SP:1866:ARG:HG3	61:SP:1904:THR:HG23	1.80	0.63
65:ST:606:GLN:O	66:SU:443:ARG:NH2	2.31	0.63
2:L1:277:C:H5'	7:L6:231:ARG:HH21	1.63	0.63
16:LH:462:VAL:HG22	16:LH:472:VAL:HG22	1.80	0.63
16:LH:734:LEU:O	20:LM:175:LYS:NZ	2.32	0.63
20:LM:1289:VAL:HG22	20:LM:1326:ILE:HD11	1.81	0.63
41:NJ:285:ALA:HB2	41:NJ:413:ILE:HB	1.79	0.63
1:L0:715:G:H1	1:L0:755:C:H42	1.45	0.63
2:L1:687:C:HO3'	8:L7:121:THR:HG1	1.39	0.63
20:LM:554:ILE:HG21	20:LM:595:LEU:HD12	1.81	0.63
26:LS:363:GLY:HA2	26:LS:385:VAL:HG23	1.80	0.63
16:LH:823:ASP:O	16:LH:826:TRP:NE1	2.32	0.63
19:LL:186:ALA:HB1	19:LL:211:VAL:HB	1.79	0.63
39:NH:477:ARG:HD2	39:NH:992:ARG:HH21	1.64	0.63
41:NK:13:LEU:HD22	41:NK:198:LEU:HD13	1.81	0.63
48:NU:30:THR:HA	48:NU:33:ARG:HG2	1.81	0.63
1:L0:717:G:O6	1:L0:752:C:N4	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:NH:731:TYR:HE1	39:NH:733:GLU:HB2	1.64	0.62
3:L2:215:G:H4'	52:SB:401:ARG:HD2	1.79	0.62
28:LU:340:ILE:HB	28:LU:352:TRP:HB2	1.80	0.62
57:SI:143:LEU:HD21	57:SI:906:PRO:HG2	1.81	0.62
61:SP:1219:LEU:HA	61:SP:1231:ILE:HD11	1.81	0.62
61:SP:1820:ARG:HA	61:SP:1823:LEU:HD13	1.81	0.62
2:L1:1110:G:N7	40:NI:211:ARG:NH2	2.45	0.62
2:L1:1743:G:H1'	2:L1:1791:A:H61	1.64	0.62
17:LI:408:ASP:OD2	17:LI:412:HIS:ND1	2.31	0.62
17:LI:505:LEU:HD13	17:LI:591:ILE:HG21	1.81	0.62
22:LO:239:ARG:HD2	52:SB:439:CYS:HB2	1.81	0.62
61:SP:281:VAL:O	61:SP:337:LYS:NZ	2.31	0.62
18:LJ:44:VAL:HG22	18:LJ:56:VAL:HG22	1.82	0.62
21:LN:560:TYR:O	21:LN:565:ARG:NH1	2.33	0.62
6:L5:49:LEU:HD12	12:LC:50:LYS:HG2	1.82	0.62
7:L6:152:ASP:HB3	7:L6:155:GLN:HG3	1.82	0.62
19:LK:535:ALA:HA	19:LK:538:LEU:HD12	1.81	0.62
19:LL:494:VAL:HG21	19:LL:530:VAL:HG23	1.80	0.62
20:LM:1133:ASP:OD1	20:LM:1206:ARG:NH1	2.33	0.62
41:NK:290:LYS:NZ	41:NK:411:SER:O	2.33	0.62
2:L1:621:C:O4'	70:SY:12:ARG:NH2	2.32	0.62
16:LH:576:GLU:O	17:LI:354:HIS:N	2.32	0.62
29:LW:519:ARG:NH1	64:SS:700:GLN:OE1	2.33	0.62
65:ST:582:ILE:O	65:ST:644:ASN:ND2	2.32	0.62
28:LU:185:ARG:HA	61:SP:2169:LEU:HD22	1.80	0.62
20:LM:1331:GLY:O	20:LM:1335:MET:HB2	1.99	0.62
33:NB:448:ARG:O	33:NB:452:ARG:NH2	2.33	0.62
1:L0:604:C:H41	18:LJ:431:GLN:HB3	1.64	0.61
2:L1:1194:A:N6	24:LQ:614:ASN:OD1	2.33	0.61
61:SP:1475:MET:HB3	61:SP:1479:PHE:HE2	1.65	0.61
61:SP:1609:LEU:HD23	61:SP:1613:ILE:HD13	1.80	0.61
22:LO:151:ASP:OD1	22:LO:152:TRP:N	2.33	0.61
32:NA:523:GLU:OE2	32:NA:525:LYS:NZ	2.30	0.61
40:NI:201:GLU:O	45:NQ:80:ARG:NH1	2.33	0.61
2:L1:542:U:O2	57:SI:1234:LYS:NZ	2.31	0.61
20:LM:2:THR:N	22:LO:665:GLU:OE2	2.33	0.61
20:LM:688:ILE:HD13	20:LM:728:ARG:HB3	1.82	0.61
39:NH:706:PRO:HG3	39:NH:1048:PRO:HB3	1.82	0.61
65:ST:577:LEU:HD22	65:ST:611:GLU:HB3	1.82	0.61
71:SZ:275:ALA:O	71:SZ:279:ALA:N	2.33	0.61
20:LM:1602:PRO:HD3	20:LM:1640:ARG:HH12	1.64	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:LP:373:LYS:NZ	23:LP:405:MET:SD	2.68	0.61
60:SM:279:THR:HB	60:SM:282:ALA:HB2	1.83	0.61
20:LM:330:LEU:HD21	20:LM:350:MET:HE1	1.83	0.61
23:LP:74:ARG:NH1	26:LS:83:ASP:O	2.32	0.61
2:L1:412:G:H1	2:L1:430:C:H42	1.46	0.61
16:LH:250:MET:SD	16:LH:268:ARG:NH2	2.73	0.61
27:LT:804:PRO:HD2	27:LT:805:GLU:H	1.65	0.61
57:SI:923:GLN:HB2	57:SI:1016:ASP:HB2	1.80	0.61
21:LN:186:ARG:HA	21:LN:196:CYS:HB2	1.82	0.61
23:LP:226:TYR:OH	23:LP:239:HIS:NE2	2.34	0.61
18:LJ:413:ARG:HB3	18:LJ:417:GLU:HB2	1.82	0.61
24:LQ:438:ILE:HD11	24:LQ:471:ILE:HD13	1.82	0.61
2:L1:1702:G:OP2	2:L1:1702:G:N2	2.25	0.61
24:LQ:597:MET:HG2	24:LQ:608:THR:HG22	1.82	0.61
61:SP:70:GLU:O	61:SP:74:LYS:NZ	2.33	0.61
21:LN:357:LEU:HB3	21:LN:383:LEU:HB3	1.83	0.61
26:LS:488:LEU:HB2	26:LS:504:LEU:HD21	1.83	0.61
67:SW:247:ARG:NH2	67:SW:250:ASP:OD2	2.34	0.61
53:SC:152:VAL:HG11	53:SC:155:ILE:HD11	1.83	0.60
55:SG:364:ALA:O	55:SG:401:ARG:NH1	2.32	0.60
2:L1:1485:U:H3'	2:L1:1486:A:H8	1.67	0.60
20:LM:1761:LEU:HD21	20:LM:1806:LEU:HB2	1.83	0.60
20:LM:2107:ILE:HG13	20:LM:2108:PRO:HD3	1.82	0.60
22:LO:737:ASP:O	22:LO:770:ASN:ND2	2.25	0.60
25:LR:340:VAL:HG12	25:LR:352:VAL:HG12	1.83	0.60
39:NH:268:LEU:HB2	39:NH:271:LYS:HG2	1.82	0.60
49:NW:239:ASN:O	49:NW:243:THR:OG1	2.19	0.60
61:SP:326:TYR:HB3	61:SP:368:VAL:HG21	1.82	0.60
1:L0:818:G:H5''	26:LS:517:LYS:HZ1	1.65	0.60
20:LM:430:ARG:NH1	20:LM:466:LEU:O	2.31	0.60
24:LQ:8:LEU:O	24:LQ:669:GLN:NE2	2.34	0.60
28:LU:346:GLU:OE2	28:LU:350:ARG:NH1	2.33	0.60
41:NJ:6:VAL:HB	57:SI:352:VAL:HB	1.82	0.60
47:NT:92:LYS:HG3	47:NT:93:HIS:H	1.66	0.60
61:SP:1859:GLN:OE1	61:SP:1862:ARG:NH2	2.29	0.60
1:L0:454:C:OP1	21:LN:680:LYS:NZ	2.35	0.60
16:LH:814:LYS:HG2	16:LH:817:ARG:HH21	1.67	0.60
20:LM:1164:GLU:OE1	20:LM:1206:ARG:NH2	2.35	0.60
25:LR:263:LEU:HD21	25:LR:271:LEU:HD22	1.83	0.60
54:SE:95:VAL:HG12	54:SE:97:ARG:H	1.66	0.60
21:LN:110:SER:OG	21:LN:112:SER:O	2.18	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:LO:710:PHE:HD1	22:LO:717:TRP:HB3	1.66	0.60
61:SP:825:TRP:HA	61:SP:828:LEU:HD12	1.82	0.60
63:SR:112:VAL:HG11	63:SR:118:VAL:HG21	1.83	0.60
28:LU:263:LEU:HD21	28:LU:285:VAL:HG11	1.82	0.60
30:LZ:138:VAL:HG22	30:LZ:158:VAL:HG12	1.82	0.60
41:NK:374:ALA:HA	41:NK:397:LEU:HD11	1.83	0.60
57:SI:152:MET:HE1	57:SI:168:LEU:HG	1.84	0.60
20:LM:658:GLY:HA3	20:LM:765:VAL:HG13	1.84	0.60
20:LM:1406:LEU:HD13	20:LM:1411:PHE:HB3	1.83	0.60
2:L1:369:C:H5	49:NW:132:ARG:HB2	1.66	0.60
17:LI:642:THR:OG1	17:LI:644:ASN:OD1	2.17	0.60
51:SA:98:PRO:HA	51:SA:114:THR:HG21	1.84	0.60
61:SP:1294:ILE:HA	61:SP:1297:ARG:HD2	1.83	0.60
70:SY:237:GLU:HB3	70:SY:243:ALA:HB2	1.84	0.60
22:LO:331:GLN:HG3	22:LO:351:GLY:HA3	1.83	0.60
26:LS:154:ASP:HA	26:LS:172:LYS:HG2	1.84	0.60
20:LM:634:HIS:NE2	20:LM:683:MET:SD	2.68	0.59
20:LM:1280:GLU:O	20:LM:1318:LYS:NZ	2.34	0.59
25:LR:347:ASP:OD1	25:LR:615:ARG:NH1	2.35	0.59
50:NY:319:LYS:HA	50:NY:322:ILE:HD12	1.83	0.59
2:L1:286:U:H2'	2:L1:287:U:H4'	1.84	0.59
2:L1:1536:G:H2'	2:L1:1537:A:H8	1.66	0.59
19:LL:601:GLU:OE2	21:LN:429:ARG:NH1	2.34	0.59
20:LM:1045:ILE:HG23	20:LM:1095:LEU:HD21	1.84	0.59
25:LR:419:GLY:H	25:LR:449:TRP:HH2	1.49	0.59
57:SI:205:ARG:NH1	57:SI:208:THR:OG1	2.35	0.59
2:L1:454:U:H2'	2:L1:455:A:H8	1.66	0.59
2:L1:961:G:N2	50:NY:235:ARG:O	2.35	0.59
20:LM:1578:ARG:HH12	20:LM:1582:SER:HB3	1.66	0.59
64:SS:159:PHE:HB2	64:SS:723:THR:HG22	1.83	0.59
27:LT:229:LEU:HB2	27:LT:243:PHE:HB2	1.84	0.59
28:LU:206:PRO:HG2	28:LU:207:ILE:HD12	1.83	0.59
41:NK:507:LEU:HB3	41:NK:698:LEU:HD11	1.83	0.59
53:SC:243:THR:HG21	53:SC:285:LYS:HB3	1.84	0.59
57:SI:1106:ILE:HD12	57:SI:1107:PRO:HD2	1.84	0.59
60:SM:97:LEU:HD13	60:SM:141:GLU:HB3	1.83	0.59
61:SP:1457:THR:HA	61:SP:1460:ILE:HD12	1.85	0.59
61:SP:2181:VAL:HG22	61:SP:2223:THR:HG21	1.84	0.59
63:SR:105:PHE:HE2	63:SR:109:GLY:HA2	1.68	0.59
20:LM:2030:ARG:HH21	20:LM:2079:LYS:HB2	1.66	0.59
39:NH:760:ALA:HB2	40:NI:173:VAL:HG11	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:NW:318:VAL:HG23	49:NW:329:THR:HG22	1.84	0.59
57:SI:961:ASP:OD1	57:SI:967:ARG:NH1	2.36	0.59
25:LR:690:ARG:HB3	25:LR:691:ARG:HH21	1.68	0.59
41:NJ:779:LEU:HA	41:NJ:783:PHE:HB2	1.82	0.59
57:SI:382:THR:HG23	57:SI:385:ALA:H	1.67	0.59
58:SK:96:MET:HA	58:SK:101:ASN:HD22	1.68	0.59
61:SP:1360:LEU:HD23	61:SP:1365:ILE:HD11	1.85	0.59
65:ST:708:PHE:HB3	65:ST:748:GLN:NE2	2.18	0.59
1:L0:865:G:H1	1:L0:1412:U:H3	1.49	0.59
18:LJ:380:VAL:HG11	18:LJ:396:ILE:HG13	1.85	0.59
20:LM:1345:VAL:O	20:LM:1349:THR:OG1	2.16	0.59
20:LM:1674:LEU:HD13	20:LM:1692:VAL:HG13	1.83	0.59
20:LM:1707:GLU:HG3	20:LM:1709:ASN:H	1.67	0.59
22:LO:845:ILE:HG23	27:LT:943:LEU:HD22	1.85	0.59
25:LR:269:GLY:HA2	25:LR:295:LEU:HD23	1.84	0.59
40:NI:227:GLU:OE2	40:NI:230:ARG:NH2	2.35	0.59
52:SB:213:ASP:OD1	52:SB:214:ARG:N	2.36	0.59
8:L7:64:VAL:HB	8:L7:72:PHE:HE2	1.68	0.59
21:LN:250:SER:OG	21:LN:262:HIS:NE2	2.30	0.59
28:LU:235:VAL:HG21	28:LU:271:LEU:HB3	1.84	0.59
39:NH:1106:VAL:HG22	39:NH:1115:MET:HE1	1.83	0.59
41:NJ:429:GLN:HA	41:NJ:432:ARG:HD2	1.85	0.59
41:NK:12:ILE:HD12	41:NK:217:GLU:HB3	1.84	0.59
61:SP:502:SER:HA	61:SP:505:LYS:HD2	1.85	0.59
20:LM:1351:LYS:HG3	20:LM:1401:GLN:HE21	1.68	0.59
20:LM:1901:VAL:HA	20:LM:1904:VAL:HG22	1.83	0.59
24:LQ:9:ARG:NH1	24:LQ:707:GLU:OE1	2.36	0.59
27:LT:88:ARG:HD3	27:LT:132:ALA:HB1	1.84	0.59
61:SP:1525:LYS:HG3	61:SP:1526:LEU:N	2.18	0.59
16:LH:15:SER:O	16:LH:312:ASN:ND2	2.36	0.59
29:LW:489:ASN:HB3	29:LW:492:ARG:HB3	1.84	0.59
2:L1:1512:C:H4'	71:SZ:197:SER:HB3	1.85	0.58
20:LM:1311:VAL:O	20:LM:1315:PHE:N	2.29	0.58
61:SP:2159:LEU:O	61:SP:2163:LEU:N	2.27	0.58
20:LM:1787:ILE:HG12	20:LM:1840:HIS:HB3	1.84	0.58
28:LU:12:ASN:O	28:LU:23:ARG:NH1	2.35	0.58
30:LZ:120:MET:HE1	30:LZ:159:THR:HA	1.84	0.58
12:LC:82:TYR:HA	12:LC:85:ARG:HD3	1.84	0.58
41:NK:344:ILE:HD12	41:NK:357:ARG:HB3	1.85	0.58
3:L2:54:U:OP1	70:SY:72:ARG:NH2	2.35	0.58
13:LD:95:TYR:HE2	13:LD:97:ARG:HE	1.50	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:LK:536:SER:O	19:LK:539:SER:OG	2.19	0.58
30:LZ:64:ASP:O	36:NE:185:LYS:NZ	2.26	0.58
2:L1:102:A:OP2	2:L1:408:A:N6	2.37	0.58
2:L1:1762:C:H2'	2:L1:1763:G:C8	2.38	0.58
20:LM:1566:GLU:HG2	20:LM:1612:LEU:HD21	1.85	0.58
39:NH:474:LEU:HD23	39:NH:552:LEU:HD12	1.84	0.58
58:SJ:110:ILE:HB	58:SJ:118:ILE:HB	1.86	0.58
61:SP:2116:SER:HB2	61:SP:2151:LYS:HE2	1.84	0.58
2:L1:1004:U:H2'	2:L1:1005:G:H8	1.68	0.58
14:LF:14:THR:HG23	14:LF:21:LYS:HG2	1.85	0.58
21:LN:146:SER:OG	21:LN:164:SER:OG	2.21	0.58
24:LQ:158:LEU:HD12	24:LQ:163:LEU:HB2	1.86	0.58
26:LS:401:SER:OG	26:LS:403:ASP:OD1	2.22	0.58
41:NK:514:THR:HG21	41:NK:694:LEU:HA	1.85	0.58
41:NK:821:ASP:HB3	41:NK:841:MET:HE1	1.86	0.58
6:L5:138:ALA:HB3	15:LG:63:ARG:HH12	1.69	0.58
10:L9:103:GLU:O	10:L9:107:GLU:HG2	2.04	0.58
16:LH:15:SER:OG	16:LH:35:SER:OG	2.20	0.58
41:NJ:290:LYS:NZ	41:NJ:388:ASP:OD1	2.36	0.58
41:NK:123:LEU:HD23	41:NK:129:LEU:HD21	1.86	0.58
53:SC:225:MET:N	53:SC:225:MET:SD	2.74	0.58
57:SI:103:ILE:HG21	57:SI:111:LEU:HD12	1.86	0.58
47:NT:105:TYR:HD2	47:NT:131:PHE:HD2	1.50	0.58
53:SC:143:LYS:NZ	53:SC:263:SER:OG	2.37	0.58
20:LM:384:THR:HA	20:LM:435:LYS:HE3	1.85	0.58
20:LM:2030:ARG:NH2	20:LM:2077:SER:OG	2.37	0.58
39:NH:268:LEU:O	39:NH:298:ASN:ND2	2.37	0.58
16:LH:333:ASP:O	16:LH:663:GLN:NE2	2.37	0.58
18:LJ:222:VAL:HG12	18:LJ:231:VAL:HG22	1.86	0.58
20:LM:1413:TRP:HB3	20:LM:1462:SER:HA	1.85	0.58
20:LM:2076:SER:O	20:LM:2081:ARG:NH2	2.34	0.58
21:LN:22:VAL:H	21:LN:292:THR:HG21	1.68	0.58
61:SP:531:LEU:HD21	61:SP:574:LEU:HD22	1.85	0.58
1:L0:812:G:OP2	1:L0:812:G:N2	2.28	0.57
17:LI:509:LEU:HB3	17:LI:612:HIS:HD2	1.69	0.57
39:NH:474:LEU:HD11	39:NH:634:VAL:HG13	1.86	0.57
71:SZ:133:UNK:HA	71:SZ:303:ARG:HH12	1.69	0.57
2:L1:924:G:H5''	37:NF:4:MET:HE2	1.87	0.57
16:LH:555:TYR:HE1	16:LH:576:GLU:HG3	1.69	0.57
24:LQ:555:VAL:HG12	24:LQ:566:VAL:HG12	1.85	0.57
26:LS:144:ASP:OD1	27:LT:233:ASN:ND2	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LU:263:LEU:HB2	28:LU:278:HIS:HB2	1.86	0.57
39:NH:354:MET:HG3	39:NH:425:LEU:HD21	1.86	0.57
41:NK:310:PHE:HB2	41:NK:385:VAL:HG22	1.86	0.57
41:NK:808:LEU:HD12	41:NK:848:ILE:HG21	1.86	0.57
49:NW:162:ASN:HB2	49:NW:169:LEU:HG	1.86	0.57
61:SP:197:MET:O	61:SP:203:LYS:NZ	2.37	0.57
61:SP:1517:ILE:HG13	61:SP:1518:ILE:HG12	1.86	0.57
2:L1:319:C:H2'	2:L1:320:G:C8	2.39	0.57
4:L3:22:GLY:HA2	4:L3:56:ALA:HB3	1.87	0.57
18:LJ:131:THR:OG1	18:LJ:133:ASP:OD1	2.23	0.57
20:LM:1807:THR:HA	20:LM:1810:LYS:HD3	1.85	0.57
41:NK:470:ARG:NH2	73:NK:1101:ATP:O3'	2.37	0.57
20:LM:2073:THR:HB	20:LM:2113:LEU:HD11	1.87	0.57
26:LS:255:SER:H	26:LS:270:GLY:HA2	1.68	0.57
36:NE:227:GLU:HA	36:NE:230:ARG:HH11	1.68	0.57
41:NK:307:SER:HA	41:NK:366:GLN:HG2	1.84	0.57
44:NO:111:MET:HE3	44:NO:115:GLU:HG3	1.86	0.57
61:SP:277:VAL:HG21	61:SP:325:THR:HG23	1.87	0.57
2:L1:67:C:H41	7:L6:163:ASN:HA	1.70	0.57
2:L1:1392:U:H2'	2:L1:1393:G:C8	2.35	0.57
23:LP:221:LEU:HD11	64:SS:188:ILE:HG23	1.86	0.57
27:LT:553:LEU:HD11	27:LT:565:PHE:HB3	1.87	0.57
52:SB:197:ILE:HG23	52:SB:198:ILE:HG13	1.85	0.57
56:SH:306:THR:HG22	56:SH:337:ILE:HD13	1.86	0.57
16:LH:623:GLY:HA2	16:LH:626:ARG:HH22	1.69	0.57
18:LJ:477:GLN:HA	18:LJ:480:LEU:HD12	1.86	0.57
19:LL:404:LEU:HA	19:LL:408:ILE:HD11	1.86	0.57
19:LL:528:LYS:O	19:LL:532:THR:OG1	2.10	0.57
28:LU:333:TRP:HE1	28:LU:337:SER:HA	1.69	0.57
41:NJ:507:LEU:HD11	41:NJ:557:PHE:HB3	1.87	0.57
66:SU:370:LYS:NZ	66:SU:434:SER:O	2.34	0.57
18:LJ:36:LYS:HA	18:LJ:312:ILE:HG22	1.87	0.57
19:LL:42:GLU:OE2	19:LL:49:HIS:ND1	2.37	0.57
20:LM:1636:THR:O	20:LM:1640:ARG:HG3	2.05	0.57
61:SP:1853:LEU:HD23	61:SP:1865:ALA:HB2	1.86	0.57
5:L4:17:HIS:HB2	5:L4:108:ARG:HG3	1.86	0.57
20:LM:1967:ASN:HA	20:LM:1970:ASN:HD22	1.69	0.57
27:LT:772:LYS:HD3	67:SW:247:ARG:NH1	2.18	0.57
2:L1:1097:G:H4'	28:LU:410:MET:HE2	1.86	0.57
10:L9:15:THR:O	59:SL:197:ARG:NH1	2.34	0.57
19:LL:33:SER:OG	19:LL:35:ASP:OD1	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:LM:1690:VAL:HG21	20:LM:1728:LEU:HD22	1.85	0.57
21:LN:341:SER:HB3	21:LN:346:LEU:HB2	1.86	0.57
57:SI:1061:ILE:HG22	57:SI:1098:MET:HB3	1.86	0.57
70:SY:158:ALA:HB3	70:SY:161:LEU:HD13	1.86	0.57
2:L1:1525:C:H2'	2:L1:1526:G:H8	1.70	0.57
2:L1:1856:C:O3'	25:LR:140:ARG:NH2	2.38	0.57
19:LK:554:LEU:O	19:LK:558:ARG:HG2	2.05	0.57
26:LS:257:VAL:H	26:LS:526:THR:HG21	1.70	0.57
26:LS:502:VAL:HG22	26:LS:509:VAL:HG22	1.86	0.57
52:SB:4:LEU:HB2	52:SB:87:LEU:HD11	1.85	0.57
58:SK:128:ARG:H	58:SK:132:ARG:HH21	1.52	0.57
65:ST:609:ILE:HD13	65:ST:612:LEU:HB2	1.86	0.57
4:L3:60:THR:OG1	4:L3:62:ASP:OD1	2.21	0.56
7:L6:192:ILE:HG22	7:L6:196:LYS:HE3	1.86	0.56
21:LN:465:GLN:HB2	21:LN:474:LEU:HD21	1.85	0.56
41:NK:259:ASP:OD1	41:NK:260:GLN:N	2.38	0.56
58:SJ:42:ARG:HE	58:SJ:107:GLN:HB2	1.70	0.56
59:SL:103:THR:HG22	59:SL:132:LEU:HD11	1.87	0.56
2:L1:103:A:H4'	2:L1:104:A:C8	2.40	0.56
2:L1:925:G:OP1	37:NF:121:ARG:NH1	2.37	0.56
2:L1:1589:A:H1'	2:L1:1654:G:H4'	1.87	0.56
2:L1:1679:A:OP1	6:L5:60:ARG:NH2	2.38	0.56
18:LJ:181:ILE:HG13	18:LJ:191:MET:HG3	1.86	0.56
20:LM:1111:THR:H	20:LM:1114:PHE:HB3	1.70	0.56
20:LM:1819:PRO:HG3	20:LM:1855:MET:HG3	1.87	0.56
25:LR:503:ALA:HB3	25:LR:517:PHE:HB2	1.86	0.56
58:SJ:47:LEU:HD12	58:SJ:202:ALA:HB2	1.87	0.56
61:SP:335:GLY:HA3	61:SP:378:VAL:HB	1.87	0.56
2:L1:647:U:H2'	2:L1:648:A:H8	1.70	0.56
2:L1:1297:U:N3	2:L1:1300:U:OP2	2.36	0.56
3:L2:56:A:H2'	3:L2:57:A:C8	2.40	0.56
14:LF:61:ARG:HG2	34:NC:248:ARG:HH12	1.70	0.56
17:LI:509:LEU:HD23	17:LI:612:HIS:HB3	1.88	0.56
18:LJ:292:ILE:HG13	18:LJ:308:MET:HE1	1.86	0.56
18:LJ:355:ARG:HH21	26:LS:295:ARG:HG3	1.69	0.56
22:LO:784:ARG:HD3	27:LT:751:LEU:HD21	1.85	0.56
41:NJ:577:ILE:HG22	41:NJ:629:ILE:HG13	1.87	0.56
41:NK:857:LEU:HD12	41:NK:901:LYS:HB3	1.88	0.56
50:NY:76:TRP:HA	50:NY:79:VAL:HG12	1.88	0.56
51:SA:16:LEU:HB3	51:SA:50:ALA:HB3	1.87	0.56
51:SA:37:LEU:HD11	53:SD:256:ASN:HD22	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:SI:180:MET:HE1	57:SI:238:PHE:HB3	1.86	0.56
61:SP:967:HIS:ND1	61:SP:1007:ASP:OD2	2.38	0.56
61:SP:1427:ILE:HG13	61:SP:1470:TYR:HD1	1.69	0.56
19:LL:22:SER:OG	19:LL:25:SER:O	2.21	0.56
19:LL:503:ILE:O	19:LL:507:GLN:NE2	2.38	0.56
28:LU:102:ILE:HG22	28:LU:103:ARG:HG3	1.86	0.56
20:LM:1086:ILE:HD12	20:LM:1130:MET:HG3	1.87	0.56
21:LN:535:ALA:HB3	21:LN:540:ASN:H	1.69	0.56
24:LQ:546:LEU:HD12	24:LQ:581:LEU:HG	1.85	0.56
25:LR:275:GLU:HG3	25:LR:278:SER:H	1.69	0.56
29:LW:505:LEU:HB3	30:LZ:13:LEU:HD11	1.88	0.56
32:NA:533:ILE:HD12	32:NA:542:SER:HB2	1.88	0.56
36:NE:287:ASN:ND2	44:NO:85:ASP:OD2	2.36	0.56
58:SJ:146:VAL:HB	58:SJ:156:LEU:HB2	1.85	0.56
12:LC:12:VAL:HG21	12:LC:91:ALA:HA	1.86	0.56
15:LG:21:THR:HG22	15:LG:29:GLN:HG3	1.88	0.56
18:LJ:106:LEU:HD12	18:LJ:116:ARG:HB2	1.87	0.56
19:LL:220:ARG:NH2	19:LL:279:GLU:O	2.37	0.56
27:LT:169:GLN:HB2	27:LT:210:ILE:HD12	1.86	0.56
61:SP:1633:THR:O	61:SP:1637:THR:OG1	2.23	0.56
16:LH:16:GLU:OE1	16:LH:332:LYS:NZ	2.38	0.56
19:LK:474:ASP:HB3	19:LK:477:MET:HG2	1.87	0.56
20:LM:1511:ARG:HG2	20:LM:1583:LYS:HE3	1.88	0.56
49:NW:281:GLN:HE22	49:NW:283:SER:HB2	1.70	0.56
61:SP:547:LEU:HB3	61:SP:564:LEU:HD12	1.88	0.56
2:L1:389:A:OP1	49:NW:117:ARG:NH1	2.37	0.56
2:L1:923:G:OP1	37:NF:2:GLY:N	2.39	0.56
3:L2:131:U:O4	3:L2:138:C:N4	2.38	0.56
9:L8:11:ARG:NH1	9:L8:15:GLY:O	2.36	0.56
24:LQ:173:VAL:HB	24:LQ:187:MET:HB2	1.88	0.56
27:LT:821:LEU:O	27:LT:823:GLN:NE2	2.38	0.56
58:SJ:96:MET:SD	58:SJ:101:ASN:ND2	2.79	0.56
61:SP:506:LEU:HD12	61:SP:507:PRO:HD2	1.87	0.56
2:L1:925:G:H1	2:L1:1017:U:H3	1.53	0.56
2:L1:1311:C:H2'	2:L1:1312:G:C8	2.41	0.56
2:L1:1717:C:H2'	2:L1:1718:G:C8	2.41	0.56
18:LJ:116:ARG:NH1	18:LJ:154:SER:OG	2.39	0.56
20:LM:1751:VAL:HG11	20:LM:1792:ILE:HG12	1.86	0.56
25:LR:436:PHE:HZ	25:LR:508:LEU:HD21	1.70	0.56
57:SI:205:ARG:NH1	57:SI:209:GLU:OE2	2.39	0.56
57:SI:954:ILE:HG22	57:SI:1106:ILE:HD11	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:SP:526:PRO:HG3	61:SP:570:THR:HG23	1.87	0.56
61:SP:2111:LEU:HB3	61:SP:2145:LEU:HD21	1.87	0.56
20:LM:1402:LEU:HD23	20:LM:1415:LEU:HD13	1.87	0.56
24:LQ:15:VAL:HG22	24:LQ:700:ARG:HG2	1.88	0.56
51:SA:382:ILE:O	51:SA:386:SER:OG	2.22	0.56
53:SC:98:ILE:HG23	53:SC:100:ARG:HH12	1.71	0.56
59:SL:169:ARG:NH1	59:SL:187:GLU:OE1	2.39	0.56
3:L2:95:C:H2'	3:L2:96:G:H8	1.71	0.55
8:L7:93:VAL:HG21	8:L7:133:LEU:HD12	1.88	0.55
16:LH:405:VAL:HG22	16:LH:419:MET:HG3	1.87	0.55
20:LM:1280:GLU:HB3	20:LM:1318:LYS:HD2	1.89	0.55
21:LN:144:GLN:O	54:SE:125:ARG:NH2	2.39	0.55
28:LU:192:MET:HE2	28:LU:229:ALA:HA	1.87	0.55
56:SH:60:ASN:ND2	65:ST:79:LYS:O	2.40	0.55
59:SL:149:VAL:HG13	59:SL:174:VAL:HG21	1.88	0.55
61:SP:1530:LEU:HD12	61:SP:1531:LYS:HE3	1.88	0.55
2:L1:981:A:H2'	2:L1:982:G:C8	2.41	0.55
17:LI:153:ILE:HA	17:LI:171:THR:HG22	1.88	0.55
20:LM:1356:ALA:O	20:LM:1360:SER:HB3	2.05	0.55
25:LR:196:SER:HG	42:NM:51:ARG:HH21	1.52	0.55
27:LT:797:LEU:H	67:SW:251:ARG:HG2	1.71	0.55
28:LU:212:LEU:HB2	28:LU:224:TYR:HB2	1.88	0.55
51:SA:163:ARG:NH1	51:SA:386:SER:O	2.33	0.55
2:L1:126:G:H8	7:L6:199:THR:HG21	1.71	0.55
2:L1:170:A:OP2	7:L6:140:ARG:NH1	2.40	0.55
2:L1:1813:A:H2'	2:L1:1814:G:C8	2.40	0.55
18:LJ:35:ILE:O	18:LJ:312:ILE:HA	2.06	0.55
18:LJ:116:ARG:NH1	18:LJ:151:ILE:O	2.39	0.55
20:LM:1663:GLN:HB2	20:LM:1666:ASN:HD22	1.70	0.55
21:LN:154:HIS:HD2	21:LN:203:PHE:HE2	1.54	0.55
24:LQ:505:SER:OG	24:LQ:507:ASP:OD1	2.22	0.55
27:LT:389:GLY:HA2	27:LT:451:GLU:HG2	1.88	0.55
33:NB:473:LYS:HE2	59:SL:47:GLU:HG2	1.89	0.55
40:NI:94:PRO:HA	40:NI:118:VAL:HG21	1.88	0.55
59:SL:22:GLN:HA	59:SL:29:ARG:HE	1.71	0.55
61:SP:1669:ASN:HB3	61:SP:1672:LEU:HB3	1.87	0.55
66:SU:389:PRO:O	66:SU:393:ASN:ND2	2.39	0.55
18:LJ:89:ARG:NH1	18:LJ:134:LYS:O	2.39	0.55
41:NJ:765:ALA:HA	41:NJ:800:MET:HE1	1.88	0.55
51:SA:217:ILE:HG22	51:SA:227:LYS:HE3	1.88	0.55
56:SH:133:LYS:NZ	56:SH:152:LEU:O	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:SP:1167:GLU:O	61:SP:1214:ARG:NH1	2.40	0.55
61:SP:1311:SER:HB3	61:SP:1355:LEU:HD21	1.89	0.55
71:SZ:286:TRP:HH2	71:SZ:312:ILE:HG13	1.70	0.55
2:L1:1378:A:OP2	2:L1:1379:A:O2'	2.22	0.55
16:LH:380:ILE:HG22	16:LH:382:ASP:H	1.71	0.55
16:LH:718:LEU:HB2	26:LS:438:GLN:HE22	1.71	0.55
20:LM:615:GLU:O	20:LM:620:LYS:NZ	2.40	0.55
28:LU:173:THR:OG1	28:LU:181:TRP:NE1	2.40	0.55
39:NH:1124:GLU:HG2	40:NI:36:ALA:HB3	1.89	0.55
49:NW:288:LEU:HG	49:NW:297:MET:HG2	1.89	0.55
57:SI:941:PRO:HG3	57:SI:1129:MET:HG2	1.87	0.55
65:ST:43:ILE:HB	65:ST:46:ARG:HG2	1.88	0.55
6:L5:198:ARG:NH2	58:SK:214:GLU:OE2	2.39	0.55
20:LM:503:LYS:O	20:LM:506:MET:HB3	2.06	0.55
27:LT:501:ASP:OD1	27:LT:502:ILE:N	2.39	0.55
51:SA:375:LYS:HD3	51:SA:397:LEU:HD22	1.88	0.55
2:L1:613:G:N7	70:SY:45:ARG:NH2	2.43	0.55
20:LM:1334:VAL:O	20:LM:1338:ASP:N	2.40	0.55
24:LQ:502:MET:HG2	24:LQ:513:THR:HG22	1.88	0.55
40:NI:244:TRP:HA	40:NI:247:ARG:HG2	1.88	0.55
55:SG:332:LEU:HD23	55:SG:338:MET:HB3	1.87	0.55
60:SM:15:ARG:NH2	60:SM:68:THR:OG1	2.39	0.55
16:LH:698:ILE:HG22	26:LS:265:ILE:HD11	1.88	0.55
20:LM:1843:PRO:O	20:LM:1847:ILE:HG12	2.06	0.55
22:LO:731:ASP:HB3	22:LO:734:VAL:HG23	1.89	0.55
2:L1:1127:C:H4'	45:NQ:17:ARG:HH11	1.72	0.55
16:LH:59:LEU:HB3	16:LH:78:LEU:HD12	1.87	0.55
18:LJ:267:SER:OG	18:LJ:269:ASP:OD1	2.24	0.55
19:LL:278:SER:HB2	19:LL:283:GLU:HB3	1.89	0.55
20:LM:1419:LEU:HD22	20:LM:1447:TRP:HE1	1.72	0.55
21:LN:418:LEU:HA	21:LN:426:SER:O	2.06	0.55
51:SA:12:VAL:HG21	51:SA:137:THR:HG21	1.89	0.55
58:SK:173:LYS:HD2	58:SK:212:TYR:HD2	1.72	0.55
20:LM:1145:GLN:NE2	52:SB:84:HIS:O	2.40	0.54
22:LO:817:GLU:HG2	27:LT:752:VAL:HB	1.88	0.54
39:NH:1099:SER:O	39:NH:1102:LYS:NZ	2.40	0.54
41:NJ:356:ILE:HG23	41:NJ:370:TYR:HB3	1.88	0.54
41:NK:298:ILE:HD11	41:NK:386:VAL:HG21	1.89	0.54
52:SB:90:ALA:HB2	52:SB:116:MET:HE3	1.88	0.54
57:SI:1059:ALA:HB3	57:SI:1071:ILE:HD12	1.89	0.54
2:L1:1702:G:O2'	32:NA:560:ALA:O	2.24	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L3:38:ARG:O	4:L3:42:HIS:ND1	2.29	0.54
55:SG:223:ILE:HB	55:SG:237:PHE:HB2	1.89	0.54
61:SP:1645:LYS:HD3	61:SP:1685:HIS:HB3	1.89	0.54
61:SP:1857:ARG:O	61:SP:1862:ARG:NH1	2.40	0.54
16:LH:519:GLU:HA	16:LH:541:LYS:HA	1.89	0.54
21:LN:182:MET:HE3	21:LN:226:GLY:HA2	1.88	0.54
39:NH:90:GLU:HA	39:NH:93:LYS:HD3	1.87	0.54
39:NH:941:ARG:NH1	39:NH:945:PRO:O	2.36	0.54
2:L1:447:A:OP1	9:L8:49:ARG:NH1	2.39	0.54
58:SK:140:LEU:HD22	58:SK:156:LEU:HD13	1.90	0.54
66:SU:435:LEU:HB3	66:SU:438:LEU:HD23	1.90	0.54
2:L1:649:U:H2'	2:L1:650:A:C8	2.43	0.54
20:LM:1392:GLU:HA	20:LM:1395:ARG:HB2	1.88	0.54
21:LN:17:SER:O	21:LN:35:ARG:NH1	2.40	0.54
21:LN:621:TYR:HB2	21:LN:643:ILE:HD11	1.90	0.54
24:LQ:843:ILE:O	24:LQ:887:LYS:NZ	2.41	0.54
25:LR:204:SER:OG	25:LR:206:ASP:O	2.25	0.54
41:NJ:697:LYS:HB2	41:NJ:700:GLU:HG3	1.89	0.54
49:NW:152:VAL:HG21	49:NW:182:CYS:HB3	1.90	0.54
61:SP:1418:SER:HB3	61:SP:1428:THR:HG21	1.88	0.54
2:L1:1524:G:H21	65:ST:37:ASN:HD21	1.54	0.54
18:LJ:252:THR:H	18:LJ:267:SER:HA	1.71	0.54
46:NR:186:UNK:O	46:NR:190:UNK:N	2.41	0.54
47:NT:119:ARG:HG3	47:NT:132:MET:HG3	1.89	0.54
71:SZ:365:LEU:HA	71:SZ:404:LEU:HD21	1.90	0.54
4:L3:23:ARG:HH22	18:LJ:80:LYS:HA	1.72	0.54
20:LM:374:ILE:HG13	20:LM:378:HIS:CE1	2.43	0.54
20:LM:610:ASN:H	20:LM:619:MET:HE1	1.72	0.54
20:LM:1408:ALA:HA	20:LM:1411:PHE:HB2	1.90	0.54
21:LN:448:ASP:OD2	21:LN:450:THR:OG1	2.22	0.54
24:LQ:363:ALA:HB3	24:LQ:384:LEU:HD13	1.89	0.54
41:NJ:344:ILE:HD12	41:NJ:357:ARG:HG2	1.89	0.54
53:SC:220:PRO:HG3	53:SC:248:LEU:HB3	1.88	0.54
61:SP:239:PHE:HB3	61:SP:243:THR:HG21	1.89	0.54
16:LH:123:LYS:NZ	16:LH:125:ASP:OD2	2.40	0.54
20:LM:83:THR:O	20:LM:87:ASN:ND2	2.41	0.54
21:LN:127:LEU:HB3	21:LN:139:ARG:HG2	1.89	0.54
24:LQ:621:ASP:OD1	24:LQ:622:PHE:N	2.41	0.54
25:LR:15:TYR:HB2	25:LR:601:LEU:HD21	1.90	0.54
39:NH:722:PRO:HG2	40:NI:156:ILE:HG12	1.90	0.54
41:NJ:158:LYS:HB2	41:NJ:678:VAL:HG21	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:NJ:431:LEU:HB3	41:NJ:460:LEU:HD13	1.90	0.54
58:SJ:121:ASN:HB3	58:SJ:124:THR:HG23	1.90	0.54
20:LM:1351:LYS:HA	20:LM:1405:THR:HG21	1.89	0.54
24:LQ:421:LEU:HD21	24:LQ:691:VAL:HG12	1.89	0.54
26:LS:538:LEU:HD23	26:LS:546:LEU:HD12	1.89	0.54
61:SP:1482:LEU:HD13	61:SP:1541:TYR:HE1	1.72	0.54
2:L1:1762:C:H2'	2:L1:1763:G:H8	1.73	0.54
20:LM:47:ILE:HG12	62:SQ:600:LYS:HG3	1.90	0.54
20:LM:1011:PRO:HD2	20:LM:1014:ILE:HD12	1.90	0.54
24:LQ:595:ILE:HG23	32:NA:680:LYS:HD2	1.90	0.54
25:LR:129:CYS:HA	25:LR:153:VAL:HG23	1.90	0.54
28:LU:359:LYS:NZ	28:LU:367:GLU:OE2	2.41	0.54
2:L1:1702:G:H1	25:LR:725:SER:HG	1.55	0.53
17:LI:682:ILE:HG13	19:LK:569:HIS:CD2	2.43	0.53
20:LM:1320:LEU:O	20:LM:1323:ILE:HG22	2.07	0.53
21:LN:548:GLN:OE1	21:LN:579:ARG:NH2	2.41	0.53
20:LM:1827:LYS:HE2	20:LM:1870:PHE:HB2	1.90	0.53
25:LR:424:VAL:HG12	25:LR:441:SER:HB2	1.90	0.53
26:LS:164:MET:HE2	26:LS:185:GLU:HG3	1.89	0.53
26:LS:184:GLU:O	26:LS:188:HIS:ND1	2.41	0.53
26:LS:215:ASP:OD1	26:LS:216:ASP:N	2.40	0.53
61:SP:1303:VAL:HG13	61:SP:1339:ILE:HG23	1.90	0.53
3:L2:210:U:OP2	54:SE:44:LYS:NZ	2.34	0.53
14:LF:6:THR:HB	14:LF:28:LEU:HB2	1.91	0.53
49:NW:9:VAL:HG21	49:NW:307:THR:HB	1.91	0.53
61:SP:585:PRO:HG2	61:SP:588:ARG:HD3	1.89	0.53
65:ST:570:LEU:HD21	66:SU:445:TYR:HD2	1.74	0.53
20:LM:707:ILE:HA	20:LM:710:VAL:HG22	1.91	0.53
20:LM:1693:LEU:HB2	20:LM:1721:VAL:HG11	1.90	0.53
24:LQ:509:ARG:NH2	24:LQ:525:PHE:O	2.41	0.53
41:NK:280:VAL:HG22	41:NK:461:TYR:HD2	1.73	0.53
61:SP:1610:GLN:HA	61:SP:1614:MET:HE2	1.89	0.53
71:SZ:207:ILE:HD12	71:SZ:216:ILE:HG21	1.90	0.53
2:L1:1856:C:H2'	2:L1:1857:G:C8	2.44	0.53
4:L3:46:ARG:HH22	4:L3:52:LEU:HG	1.73	0.53
20:LM:334:LEU:HD21	20:LM:346:LEU:HD23	1.91	0.53
22:LO:732:THR:O	27:LT:635:ARG:NH2	2.38	0.53
40:NI:42:VAL:HB	40:NI:61:LEU:HD11	1.90	0.53
41:NK:468:SER:OG	41:NK:471:TYR:O	2.25	0.53
61:SP:1187:GLN:HB2	61:SP:1202:LEU:HD13	1.89	0.53
65:ST:767:THR:HG21	68:Sx:717:UNK:HA	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L1:1457:U:H2'	2:L1:1458:G:H8	1.72	0.53
8:L7:44:ASN:OD1	8:L7:68:GLN:NE2	2.42	0.53
8:L7:148:LEU:HA	44:NO:42:MET:HE2	1.91	0.53
18:LJ:302:GLU:OE1	18:LJ:303:THR:OG1	2.24	0.53
18:LJ:391:GLU:OE2	18:LJ:433:ARG:NH1	2.42	0.53
18:LJ:479:GLU:HB3	19:LL:524:VAL:HG11	1.90	0.53
20:LM:83:THR:HA	29:LW:181:ASP:HA	1.89	0.53
25:LR:540:SER:OG	25:LR:542:ASP:OD1	2.24	0.53
29:LW:273:ARG:NH2	30:LZ:30:GLU:OE2	2.41	0.53
32:NA:458:LEU:O	32:NA:462:HIS:ND1	2.41	0.53
32:NA:549:LEU:HB3	32:NA:554:ILE:HD11	1.91	0.53
56:SH:187:LYS:HD3	57:SI:759:VAL:HA	1.90	0.53
57:SI:956:LEU:HG	57:SI:1106:ILE:HD13	1.89	0.53
65:ST:635:VAL:HG23	65:ST:637:PRO:HD2	1.90	0.53
3:L2:46:A:H2'	3:L2:47:G:H8	1.73	0.53
20:LM:901:LEU:HD22	20:LM:945:LEU:HD21	1.91	0.53
24:LQ:297:HIS:CE1	24:LQ:365:ILE:HB	2.44	0.53
49:NW:195:THR:H	49:NW:233:ILE:HD12	1.73	0.53
56:SH:321:SER:HB2	56:SH:324:THR:HG23	1.91	0.53
58:SK:127:PRO:HB3	58:SK:132:ARG:HG3	1.90	0.53
61:SP:1512:LYS:HA	61:SP:1515:ARG:HH21	1.74	0.53
65:ST:51:ASP:OD1	65:ST:51:ASP:N	2.41	0.53
2:L1:1120:U:H5'	2:L1:1121:G:H5'	1.91	0.53
8:L7:69:LEU:O	8:L7:73:GLN:HG2	2.09	0.53
20:LM:1350:VAL:HB	20:LM:1401:GLN:HE22	1.74	0.53
25:LR:82:VAL:HG22	25:LR:92:GLN:HG3	1.90	0.53
27:LT:764:ASN:ND2	32:NA:540:PRO:O	2.40	0.53
28:LU:301:SER:OG	28:LU:303:ASP:OD2	2.25	0.53
39:NH:687:GLN:HB3	39:NH:835:PRO:HB3	1.89	0.53
45:NQ:42:LYS:HZ1	45:NQ:57:VAL:HB	1.74	0.53
58:SJ:173:LYS:HB2	58:SJ:213:THR:HA	1.90	0.53
65:ST:725:ASP:OD1	65:ST:726:CYS:N	2.42	0.53
1:L0:667:C:H5	35:ND:246:ARG:HG2	1.73	0.53
2:L1:546:G:H5'	33:NB:472:VAL:HG11	1.91	0.53
14:LF:61:ARG:HG2	34:NC:248:ARG:NH1	2.23	0.53
27:LT:135:ARG:HB2	27:LT:136:LEU:HD12	1.91	0.53
35:ND:178:LYS:HA	35:ND:178:LYS:HE3	1.91	0.53
61:SP:2178:HIS:O	61:SP:2182:ASN:ND2	2.41	0.53
1:L0:1431:C:H2'	1:L0:1432:G:H8	1.74	0.53
20:LM:2025:ASP:O	20:LM:2029:ASN:N	2.42	0.53
21:LN:537:ASN:OD1	21:LN:538:THR:N	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:SP:1068:LYS:HE3	61:SP:1118:LYS:HD2	1.91	0.53
4:L3:70:ILE:HA	4:L3:77:TYR:CE2	2.43	0.52
16:LH:175:GLU:HG3	16:LH:176:PHE:H	1.73	0.52
33:NB:431:ASN:HB3	33:NB:434:VAL:HG22	1.90	0.52
37:NF:3:ARG:HB2	37:NF:6:ALA:HB3	1.90	0.52
61:SP:826:ARG:O	61:SP:829:THR:OG1	2.27	0.52
1:L0:817:U:OP1	27:LT:424:ASN:ND2	2.38	0.52
3:L2:152:A:O2'	3:L2:153:G:OP1	2.27	0.52
16:LH:53:LEU:HD23	16:LH:85:TRP:CE3	2.44	0.52
18:LJ:169:CYS:O	18:LJ:183:GLY:N	2.42	0.52
20:LM:542:GLU:HB3	20:LM:582:ILE:HD11	1.91	0.52
20:LM:1392:GLU:HA	20:LM:1395:ARG:HE	1.74	0.52
20:LM:1649:LEU:HB3	20:LM:1695:THR:HG21	1.90	0.52
24:LQ:479:GLN:OE1	24:LQ:481:TYR:OH	2.24	0.52
25:LR:546:LYS:HG2	25:LR:558:THR:HG22	1.91	0.52
27:LT:874:GLN:O	27:LT:878:LYS:HG3	2.09	0.52
2:L1:45:A:N1	2:L1:480:G:O2'	2.40	0.52
5:L4:48:LEU:HD23	5:L4:61:VAL:HG13	1.90	0.52
20:LM:1419:LEU:HD13	20:LM:1447:TRP:CD1	2.44	0.52
20:LM:2070:LEU:O	20:LM:2073:THR:OG1	2.20	0.52
23:LP:307:GLU:O	23:LP:311:ALA:N	2.38	0.52
24:LQ:220:ILE:HD11	24:LQ:266:LEU:HD22	1.90	0.52
41:NJ:381:GLN:NE2	41:NK:369:GLN:OE1	2.42	0.52
51:SA:140:SER:HB3	51:SA:143:LYS:HE2	1.91	0.52
2:L1:559:G:O2'	2:L1:560:A:O5'	2.27	0.52
14:LF:11:LYS:HE3	34:NC:243:GLU:HB3	1.91	0.52
18:LJ:129:ASP:OD2	18:LJ:130:PHE:N	2.43	0.52
18:LJ:486:MET:HE3	19:LK:574:LEU:HB2	1.90	0.52
20:LM:1159:GLU:OE2	20:LM:1162:ARG:NH2	2.42	0.52
24:LQ:147:GLY:HA3	24:LQ:176:TRP:HH2	1.74	0.52
27:LT:283:MET:HE2	27:LT:322:LYS:HE3	1.90	0.52
42:NM:26:SER:O	42:NM:51:ARG:NH1	2.43	0.52
50:NY:281:GLU:HG2	50:NY:287:TYR:HB2	1.92	0.52
61:SP:1337:SER:O	61:SP:1341:LYS:NZ	2.41	0.52
2:L1:948:C:H2'	2:L1:949:G:H8	1.75	0.52
19:LL:290:VAL:HG22	19:LL:296:VAL:HG22	1.91	0.52
20:LM:1035:LEU:HD12	20:LM:1084:ILE:HD12	1.90	0.52
25:LR:424:VAL:HA	25:LR:441:SER:HA	1.91	0.52
61:SP:718:GLU:OE2	61:SP:722:ARG:NE	2.41	0.52
61:SP:1583:ILE:HA	61:SP:1586:ARG:HE	1.74	0.52
66:SU:473:LEU:HD13	66:SU:478:ILE:HD11	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:SZ:247:GLN:HG2	71:SZ:285:ALA:HA	1.90	0.52
20:LM:1305:LEU:HD21	20:LM:1345:VAL:HG13	1.92	0.52
20:LM:1936:PHE:HE2	20:LM:1958:LEU:HD21	1.75	0.52
23:LP:369:GLU:HG2	23:LP:373:LYS:HE2	1.91	0.52
25:LR:402:ILE:HD11	25:LR:437:LEU:HD11	1.91	0.52
27:LT:789:PHE:C	67:SW:199:ARG:HH22	2.17	0.52
41:NK:277:ARG:NH1	41:NK:405:TYR:O	2.43	0.52
45:NQ:37:CYS:HB3	45:NQ:63:LEU:HD21	1.92	0.52
61:SP:1399:SER:HB2	61:SP:1476:HIS:HB3	1.92	0.52
10:L9:79:ARG:HD2	10:L9:92:MET:HE1	1.90	0.52
20:LM:909:LYS:HB3	20:LM:948:VAL:HG21	1.91	0.52
20:LM:1732:GLN:OE1	20:LM:1735:SER:OG	2.28	0.52
32:NA:386:LEU:HD23	57:SI:939:ARG:HH12	1.74	0.52
41:NK:731:VAL:HG11	41:NK:749:LEU:HD12	1.92	0.52
61:SP:1374:LEU:HD22	61:SP:1413:VAL:HG21	1.92	0.52
20:LM:383:LEU:HB3	20:LM:431:LEU:HD22	1.92	0.52
53:SC:107:VAL:HB	53:SC:134:TYR:HB3	1.92	0.52
20:LM:133:ALA:HB1	20:LM:195:LEU:HD13	1.92	0.52
21:LN:583:ILE:HG12	21:LN:598:LEU:HD12	1.92	0.52
51:SA:297:SER:HB2	51:SA:302:GLU:HG3	1.91	0.52
61:SP:1780:GLN:HG3	61:SP:1834:LEU:HG	1.90	0.52
61:SP:1831:MET:HE2	61:SP:1839:MET:HA	1.91	0.52
17:LI:154:LYS:HD3	17:LI:172:GLU:HB3	1.92	0.52
22:LO:487:SER:HB2	22:LO:494:LEU:HD21	1.91	0.52
27:LT:768:LEU:C	27:LT:772:LYS:HZ2	2.18	0.52
53:SD:179:ASP:OD1	53:SD:207:ARG:NH1	2.35	0.52
61:SP:236:ARG:HB2	61:SP:238:MET:HE3	1.92	0.52
1:L0:710:G:H2'	1:L0:711:A:H8	1.75	0.51
2:L1:1227:G:OP1	65:ST:40:LYS:NZ	2.35	0.51
3:L2:77:C:H2'	3:L2:78:A:H8	1.75	0.51
16:LH:826:TRP:CD1	16:LH:826:TRP:H	2.26	0.51
20:LM:1403:VAL:HB	20:LM:1415:LEU:HD22	1.91	0.51
25:LR:46:ARG:HG2	25:LR:62:GLU:HB2	1.91	0.51
26:LS:255:SER:O	26:LS:526:THR:OG1	2.28	0.51
52:SB:25:VAL:HB	52:SB:111:VAL:HG12	1.92	0.51
1:L0:757:G:H1	1:L0:803:U:H3	1.56	0.51
20:LM:60:PRO:O	20:LM:62:PHE:N	2.43	0.51
20:LM:1984:ASP:OD1	20:LM:1985:PRO:HD3	2.10	0.51
21:LN:597:LEU:HD21	21:LN:653:MET:HE3	1.92	0.51
24:LQ:489:LEU:HD12	24:LQ:537:ARG:HH11	1.75	0.51
61:SP:335:GLY:HA2	61:SP:338:ILE:HD12	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:SQ:549:LEU:HD13	62:SQ:570:ILE:HG12	1.91	0.51
2:L1:530:U:H2'	2:L1:531:A:H8	1.75	0.51
2:L1:1787:G:H2'	2:L1:1788:A:C8	2.45	0.51
8:L7:145:ARG:NE	44:NO:51:GLU:OE1	2.43	0.51
13:LD:99:TYR:HB2	13:LD:101:ARG:HD2	1.91	0.51
19:LL:464:VAL:HA	19:LL:467:THR:HG22	1.91	0.51
19:LL:507:GLN:OE1	19:LL:547:GLN:NE2	2.43	0.51
28:LU:224:TYR:HA	28:LU:231:PRO:HA	1.90	0.51
38:NG:83:GLN:HA	38:NG:86:LYS:NZ	2.26	0.51
39:NH:96:ARG:NH2	39:NH:326:ASP:OD1	2.43	0.51
52:SB:31:GLU:HB3	52:SB:41:ILE:HG13	1.92	0.51
71:SZ:315:CYS:SG	71:SZ:316:SER:N	2.83	0.51
7:L6:136:LYS:NZ	7:L6:175:LYS:O	2.39	0.51
18:LJ:34:GLN:HE21	18:LJ:312:ILE:HD12	1.76	0.51
20:LM:1721:VAL:O	20:LM:1725:LEU:N	2.40	0.51
22:LO:187:HIS:NE2	22:LO:205:SER:OG	2.29	0.51
27:LT:761:ARG:NH2	27:LT:849:GLU:O	2.43	0.51
39:NH:549:THR:HG21	39:NH:991:PRO:HG2	1.92	0.51
39:NH:866:LEU:HB3	39:NH:1073:PHE:HB3	1.91	0.51
39:NH:1106:VAL:HG21	40:NI:20:PRO:HD3	1.92	0.51
41:NK:728:PHE:HB3	41:NK:748:MET:HB3	1.92	0.51
51:SA:97:ASP:HB3	51:SA:100:ILE:HG22	1.92	0.51
51:SA:196:HIS:O	51:SA:220:ARG:NH1	2.44	0.51
2:L1:190:G:HO2'	61:SP:1197:TYR:HH	1.45	0.51
2:L1:928:G:H2'	2:L1:929:G:C8	2.45	0.51
2:L1:1275:G:C6	71:SZ:277:LYS:HE3	2.46	0.51
4:L3:62:ASP:OD1	4:L3:63:GLU:N	2.43	0.51
18:LJ:468:GLY:O	18:LJ:472:LYS:HG3	2.09	0.51
21:LN:9:VAL:HB	21:LN:664:VAL:HA	1.92	0.51
39:NH:481:ARG:NH2	39:NH:628:ASP:O	2.41	0.51
57:SI:668:LYS:HA	57:SI:671:LEU:HG	1.93	0.51
58:SJ:73:LEU:HD12	58:SJ:78:ARG:HG3	1.92	0.51
60:SM:262:THR:HG22	60:SM:263:LEU:HD23	1.92	0.51
2:L1:1457:U:H2'	2:L1:1458:G:C8	2.46	0.51
8:L7:9:VAL:HG12	8:L7:11:PRO:HD3	1.91	0.51
21:LN:100:PHE:HZ	53:SC:288:GLN:HG3	1.75	0.51
24:LQ:424:SER:OG	24:LQ:426:ASP:O	2.28	0.51
25:LR:124:LEU:HB2	25:LR:138:ILE:HD11	1.93	0.51
25:LR:285:GLN:NE2	25:LR:319:TYR:OH	2.43	0.51
55:SG:298:VAL:HG12	55:SG:309:VAL:HG22	1.93	0.51
61:SP:1614:MET:HB3	61:SP:1618:MET:HG2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L0:830:G:H3'	1:L0:831:A:H5''	1.93	0.51
2:L1:1310:U:H4'	47:NT:143:LYS:HD3	1.91	0.51
2:L1:1546:G:O2'	2:L1:1670:C:O2'	2.23	0.51
13:LD:113:LEU:HD23	13:LD:142:VAL:HG21	1.92	0.51
19:LK:505:LEU:O	19:LK:508:GLU:HG3	2.10	0.51
20:LM:1686:PRO:HB2	20:LM:1725:LEU:HD21	1.93	0.51
23:LP:369:GLU:HG3	23:LP:405:MET:HE2	1.93	0.51
52:SB:211:VAL:HG13	52:SB:216:ASN:HB2	1.92	0.51
56:SH:230:MET:O	56:SH:235:SER:OG	2.27	0.51
61:SP:459:ALA:HB3	61:SP:462:MET:HG3	1.93	0.51
1:L0:666:U:H4'	1:L0:667:C:OP2	2.08	0.51
1:L0:1423:U:H2'	1:L0:1424:U:C6	2.46	0.51
2:L1:573:U:N3	2:L1:576:A:OP2	2.37	0.51
16:LH:53:LEU:HD23	16:LH:85:TRP:HE3	1.76	0.51
20:LM:1586:ASP:O	20:LM:1590:LYS:N	2.44	0.51
41:NK:135:ALA:HA	41:NK:481:LEU:HD21	1.92	0.51
53:SC:166:LEU:HB2	53:SC:235:ALA:HA	1.93	0.51
61:SP:1333:LEU:HD21	61:SP:1372:ASP:HB3	1.93	0.51
61:SP:1779:ILE:O	61:SP:1783:ILE:HG12	2.10	0.51
65:ST:443:UNK:O	65:ST:447:UNK:N	2.44	0.51
67:SW:150:LEU:HD12	67:SW:153:ILE:HD12	1.92	0.51
2:L1:1007:C:H2'	2:L1:1008:A:C8	2.45	0.51
2:L1:1597:C:H5''	4:L3:25:LYS:HD2	1.93	0.51
8:L7:144:ILE:HB	44:NO:52:ILE:HB	1.92	0.51
17:LI:644:ASN:OD1	17:LI:645:GLN:N	2.44	0.51
26:LS:433:THR:HG22	26:LS:440:VAL:HG22	1.91	0.51
28:LU:269:ARG:NH1	64:SS:145:ASP:OD1	2.38	0.51
28:LU:377:LEU:HD23	64:SS:703:ILE:HD11	1.93	0.51
29:LW:607:ARG:HH22	39:NH:748:PRO:HG3	1.75	0.51
39:NH:376:ARG:NH2	39:NH:449:ASP:OD1	2.44	0.51
48:NU:41:ILE:HG21	48:NU:47:ARG:HB2	1.93	0.51
61:SP:1573:ASP:OD1	61:SP:1576:GLU:N	2.40	0.51
2:L1:1118:C:O2'	42:NM:166:LYS:NZ	2.35	0.51
17:LI:692:GLU:HG3	19:LK:559:VAL:HG21	1.92	0.51
20:LM:955:ILE:HD13	20:LM:1003:LEU:HD21	1.92	0.51
20:LM:1256:LEU:HD22	20:LM:1303:HIS:HB3	1.93	0.51
22:LO:178:ASN:HD21	22:LO:224:LEU:HA	1.74	0.51
24:LQ:547:GLN:NE2	24:LQ:548:LEU:O	2.43	0.51
27:LT:503:THR:HG23	27:LT:506:GLY:H	1.76	0.51
56:SH:135:THR:HG21	56:SH:256:SER:HB3	1.93	0.51
56:SH:146:ASP:O	56:SH:174:ARG:NH2	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:SZ:399:GLU:HA	71:SZ:402:LEU:HD13	1.93	0.51
22:LO:100:HIS:ND1	22:LO:148:THR:O	2.44	0.50
25:LR:359:LEU:HD21	25:LR:379:VAL:HG11	1.93	0.50
25:LR:667:LEU:HD11	25:LR:698:LYS:HG3	1.93	0.50
26:LS:75:ARG:NH2	26:LS:76:ASN:OD1	2.44	0.50
39:NH:694:ARG:NH2	39:NH:873:ASP:OD2	2.43	0.50
41:NJ:808:LEU:HD11	41:NJ:848:ILE:HG21	1.93	0.50
41:NK:502:PRO:HA	41:NK:643:ARG:HD3	1.93	0.50
2:L1:674:C:H2'	2:L1:675:U:C6	2.46	0.50
2:L1:1842:C:H2'	2:L1:1843:G:C8	2.45	0.50
17:LI:654:LEU:HG	19:LK:575:LEU:HD11	1.93	0.50
41:NJ:60:LYS:HG3	41:NJ:61:LYS:HG3	1.91	0.50
41:NK:892:MET:HE2	41:NK:892:MET:HA	1.92	0.50
58:SJ:127:PRO:HB3	58:SJ:132:ARG:HE	1.76	0.50
61:SP:959:CYS:O	61:SP:962:THR:OG1	2.22	0.50
61:SP:1576:GLU:OE1	61:SP:1585:ARG:NH2	2.45	0.50
61:SP:1583:ILE:HG22	61:SP:1632:ILE:HD11	1.92	0.50
67:SW:233:PRO:HG2	67:SW:236:LYS:HE3	1.92	0.50
17:LI:643:LEU:HD21	17:LI:647:MET:HE3	1.94	0.50
19:LL:37:HIS:HD1	19:LL:53:VAL:HG22	1.75	0.50
22:LO:110:LYS:HD3	22:LO:121:MET:HE3	1.93	0.50
24:LQ:276:ARG:NE	24:LQ:296:CYS:SG	2.80	0.50
27:LT:640:ALA:HB1	27:LT:666:PRO:HG2	1.93	0.50
27:LT:748:ASN:ND2	27:LT:750:GLN:OE1	2.44	0.50
52:SB:60:PHE:O	52:SB:64:MET:HG2	2.11	0.50
2:L1:103:A:O4'	2:L1:356:C:N4	2.43	0.50
2:L1:1216:C:H42	60:SM:179:MET:HB2	1.76	0.50
2:L1:1599:U:OP2	18:LJ:78:ARG:NH2	2.45	0.50
24:LQ:303:LEU:HD13	24:LQ:382:PHE:HE2	1.77	0.50
26:LS:161:ARG:NH2	52:SB:434:SER:O	2.41	0.50
41:NJ:694:LEU:HG	41:NJ:695:LEU:HD12	1.92	0.50
41:NK:363:GLU:HG2	41:NK:364:HIS:ND1	2.27	0.50
44:NO:83:LEU:HD11	44:NO:117:ARG:HA	1.94	0.50
46:NR:743:UNK:O	46:NR:747:UNK:N	2.44	0.50
53:SD:125:ILE:HD13	62:SQ:691:GLY:HA3	1.92	0.50
56:SH:122:ASN:OD1	56:SH:157:ARG:NH1	2.44	0.50
67:SW:145:GLN:NE2	67:SW:147:GLU:OE1	2.40	0.50
18:LJ:487:MET:HE1	19:LL:555:MET:HG3	1.92	0.50
19:LK:475:PHE:O	19:LK:479:ASN:ND2	2.44	0.50
26:LS:170:GLU:OE1	26:LS:181:ARG:NH1	2.41	0.50
39:NH:182:LEU:HD11	39:NH:253:LEU:HD12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:NJ:635:TYR:HB3	41:NJ:640:TYR:HE2	1.76	0.50
44:NO:18:GLU:HG2	44:NO:69:LEU:HB3	1.91	0.50
2:L1:374:G:OP1	13:LD:59:LYS:NZ	2.45	0.50
5:L4:197:ASN:ND2	5:L4:199:GLU:OE2	2.43	0.50
7:L6:223:LYS:O	7:L6:227:GLN:HG2	2.11	0.50
16:LH:129:LEU:HB3	16:LH:151:LEU:HB2	1.94	0.50
19:LK:477:MET:O	19:LK:481:VAL:HG23	2.11	0.50
20:LM:1966:LEU:O	20:LM:1970:ASN:ND2	2.45	0.50
27:LT:758:PRO:HD2	27:LT:761:ARG:HD2	1.93	0.50
61:SP:1104:VAL:HG13	61:SP:1108:ILE:HD11	1.93	0.50
64:SS:121:ASN:N	64:SS:124:GLU:OE2	2.44	0.50
65:ST:577:LEU:HD21	65:ST:615:PHE:HB2	1.94	0.50
2:L1:166:A:H1'	7:L6:13:GLN:HE21	1.77	0.50
17:LI:643:LEU:HA	17:LI:646:ILE:HD12	1.92	0.50
19:LL:466:LEU:HD11	19:LL:505:LEU:HD21	1.93	0.50
20:LM:1289:VAL:HG13	20:LM:1326:ILE:HG12	1.93	0.50
21:LN:542:VAL:HG12	21:LN:552:GLU:HG3	1.93	0.50
24:LQ:89:ILE:HB	24:LQ:103:PHE:HB2	1.94	0.50
25:LR:202:ALA:HB3	25:LR:211:LEU:HB3	1.93	0.50
41:NJ:357:ARG:HD2	41:NJ:369:GLN:HG2	1.93	0.50
61:SP:1460:ILE:HA	61:SP:1463:MET:HE2	1.93	0.50
65:ST:688:LEU:HD11	65:ST:722:HIS:HE1	1.77	0.50
18:LJ:383:PRO:HG2	35:ND:251:ARG:HH12	1.77	0.50
20:LM:846:ARG:HA	20:LM:849:MET:HE2	1.93	0.50
20:LM:1555:LEU:HA	20:LM:1558:ILE:HG12	1.93	0.50
22:LO:216:GLN:NE2	22:LO:217:CYS:O	2.45	0.50
24:LQ:158:LEU:HD11	24:LQ:175:TRP:HZ3	1.75	0.50
25:LR:547:LEU:HD12	25:LR:557:LYS:HB2	1.94	0.50
38:NG:117:ARG:HH11	50:NY:45:PHE:HB2	1.77	0.50
41:NJ:403:GLY:O	41:NJ:458:ARG:NH1	2.44	0.50
41:NK:357:ARG:HD2	41:NK:369:GLN:HB2	1.92	0.50
46:NR:622:UNK:O	46:NR:626:UNK:N	2.45	0.50
49:NW:287:ILE:HD11	49:NW:300:LYS:HG3	1.94	0.50
51:SA:340:LYS:HD2	51:SA:353:HIS:HB2	1.94	0.50
57:SI:1243:GLU:O	57:SI:1247:LYS:N	2.39	0.50
58:SK:173:LYS:HG2	58:SK:197:VAL:HB	1.94	0.50
60:SM:7:ARG:NH1	60:SM:11:GLU:OE2	2.45	0.50
61:SP:826:ARG:NH1	61:SP:920:GLN:OE1	2.43	0.50
67:SW:126:ASP:OD2	67:SW:127:VAL:N	2.45	0.50
2:L1:444:G:N2	2:L1:447:A:OP2	2.44	0.50
4:L3:47:LYS:HE3	4:L3:77:TYR:HB3	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:L8:67:TRP:NE1	9:L8:191:GLU:OE2	2.40	0.50
20:LM:1204:TRP:CD2	20:LM:1248:MET:HE1	2.47	0.50
20:LM:1823:LEU:O	20:LM:1827:LYS:HG2	2.12	0.50
21:LN:87:ASP:HB2	21:LN:94:LYS:HG3	1.94	0.50
27:LT:661:LEU:HD23	27:LT:714:VAL:HG12	1.94	0.50
44:NO:68:ARG:HA	59:SL:118:ARG:HH22	1.77	0.50
57:SI:120:ILE:HG22	57:SI:335:VAL:HG22	1.94	0.50
3:L2:137:G:N2	3:L2:139:U:O2'	2.43	0.49
11:LA:49:LEU:HB3	11:LA:111:VAL:HB	1.94	0.49
24:LQ:874:VAL:HG22	25:LR:788:MET:HG2	1.92	0.49
25:LR:64:GLU:O	25:LR:66:GLN:NE2	2.45	0.49
44:NO:104:LEU:HD23	44:NO:125:ILE:HA	1.94	0.49
61:SP:1476:HIS:HA	61:SP:1479:PHE:HD2	1.77	0.49
61:SP:2085:GLU:HA	61:SP:2088:LEU:HD12	1.94	0.49
18:LJ:471:GLU:OE2	19:LL:569:HIS:NE2	2.45	0.49
20:LM:489:HIS:CE1	20:LM:491:LEU:HB2	2.47	0.49
20:LM:2070:LEU:HD21	20:LM:2106:SER:HA	1.94	0.49
25:LR:385:PHE:CE1	25:LR:429:CYS:HB3	2.47	0.49
41:NK:529:LEU:HD11	41:NK:576:VAL:HG21	1.92	0.49
41:NK:577:ILE:HG22	41:NK:629:ILE:HG13	1.93	0.49
52:SB:113:ASN:ND2	53:SC:251:HIS:CE1	2.80	0.49
55:SG:404:GLN:HB2	55:SG:415:LEU:HD21	1.95	0.49
16:LH:83:LYS:HG2	16:LH:95:THR:HG23	1.95	0.49
20:LM:541:PHE:HZ	20:LM:553:THR:HG22	1.76	0.49
20:LM:1065:GLY:HA2	20:LM:1109:LYS:HE2	1.92	0.49
24:LQ:19:ILE:HB	24:LQ:387:ASN:HB2	1.94	0.49
27:LT:822:ALA:HB3	67:SW:215:PHE:HZ	1.77	0.49
28:LU:300:ALA:HB2	28:LU:331:VAL:HG23	1.93	0.49
32:NA:496:ILE:HA	32:NA:499:MET:HG2	1.93	0.49
38:NG:37:PHE:HE2	38:NG:105:THR:HG21	1.76	0.49
52:SB:64:MET:HE2	53:SC:222:LYS:HA	1.94	0.49
61:SP:1188:ILE:HG12	61:SP:1231:ILE:HG22	1.94	0.49
61:SP:1393:PRO:HA	61:SP:1396:LYS:HG2	1.94	0.49
61:SP:2023:LEU:HD22	61:SP:2114:PHE:HE2	1.77	0.49
65:ST:525:MET:HE2	66:SU:479:PHE:CD2	2.47	0.49
71:SZ:362:PHE:HA	71:SZ:365:LEU:HG	1.94	0.49
8:L7:160:LYS:O	8:L7:162:GLN:N	2.45	0.49
16:LH:318:HIS:NE2	16:LH:322:GLU:HB3	2.28	0.49
20:LM:361:HIS:CG	20:LM:372:GLY:HA3	2.47	0.49
20:LM:1859:GLU:O	20:LM:1862:SER:HB3	2.12	0.49
20:LM:2028:GLU:HG2	20:LM:2072:LYS:HD2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:LQ:583:PHE:HZ	24:LQ:586:SER:HB2	1.77	0.49
28:LU:434:SER:HB3	28:LU:437:LYS:HG2	1.93	0.49
41:NK:485:LEU:HB2	41:NK:487:LEU:HG	1.95	0.49
9:L8:57:ALA:HB2	9:L8:183:GLY:HA2	1.95	0.49
21:LN:127:LEU:HD23	21:LN:139:ARG:HD3	1.93	0.49
22:LO:16:ARG:HB3	22:LO:34:GLY:H	1.77	0.49
23:LP:21:ARG:HH21	29:LW:98:PHE:HD2	1.61	0.49
27:LT:418:LEU:HD22	27:LT:478:SER:HA	1.94	0.49
41:NJ:235:LEU:HD13	41:NJ:258:LEU:HA	1.94	0.49
58:SJ:55:VAL:HG11	58:SJ:64:LEU:HD13	1.94	0.49
62:SQ:568:LEU:HD23	62:SQ:573:LEU:HD21	1.94	0.49
1:L0:740:G:H3'	1:L0:741:G:H5''	1.95	0.49
2:L1:141:A:H4'	2:L1:142:C:H5'	1.95	0.49
2:L1:454:U:H2'	2:L1:455:A:C8	2.45	0.49
2:L1:941:C:H2'	2:L1:942:G:H8	1.77	0.49
2:L1:1673:U:O2'	6:L5:84:GLY:O	2.24	0.49
4:L3:23:ARG:NH1	18:LJ:80:LYS:O	2.46	0.49
20:LM:1581:LEU:HB3	20:LM:1585:TYR:CE2	2.47	0.49
20:LM:2085:LEU:HD21	20:LM:2125:CYS:HA	1.93	0.49
23:LP:442:ILE:HD12	23:LP:479:LYS:HD2	1.95	0.49
24:LQ:510:GLY:HA2	24:LQ:524:ASP:HA	1.94	0.49
39:NH:1102:LYS:HB3	40:NI:116:PHE:HD2	1.78	0.49
41:NK:61:LYS:HA	41:NK:106:TYR:HE2	1.78	0.49
46:NR:619:UNK:O	46:NR:623:UNK:N	2.45	0.49
48:NU:7:LYS:HA	48:NU:10:LYS:HG2	1.94	0.49
71:SZ:286:TRP:CD1	71:SZ:290:ILE:HD13	2.47	0.49
2:L1:1842:C:H2'	2:L1:1843:G:H8	1.77	0.49
3:L2:46:A:H2'	3:L2:47:G:C8	2.47	0.49
16:LH:17:LEU:N	16:LH:312:ASN:OD1	2.44	0.49
16:LH:629:VAL:HG22	16:LH:660:THR:HG22	1.93	0.49
20:LM:1141:SER:HA	52:SB:84:HIS:HB3	1.93	0.49
22:LO:710:PHE:CD1	22:LO:717:TRP:HB3	2.47	0.49
25:LR:119:PRO:HG3	25:LR:161:PRO:HA	1.93	0.49
25:LR:316:LEU:HB2	25:LR:330:PHE:HB2	1.94	0.49
39:NH:147:ALA:O	39:NH:278:TRP:NE1	2.37	0.49
58:SK:123:GLN:HB3	65:ST:766:PHE:HD2	1.78	0.49
71:SZ:317:ILE:O	71:SZ:350:TYR:OH	2.24	0.49
1:L0:817:U:OP2	27:LT:430:ARG:NH2	2.46	0.49
19:LL:192:LEU:HB3	19:LL:202:ARG:HB2	1.94	0.49
20:LM:1136:VAL:HG12	20:LM:1209:LEU:HD12	1.95	0.49
28:LU:412:GLU:HG3	28:LU:416:ARG:HH12	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:NB:411:ILE:HA	57:SI:162:MET:HE2	1.95	0.49
39:NH:234:LYS:NZ	39:NH:304:ASP:OD1	2.35	0.49
39:NH:671:ARG:HH12	42:NM:37:ALA:HB1	1.78	0.49
39:NH:926:THR:HG22	39:NH:929:GLU:HG3	1.93	0.49
41:NJ:577:ILE:HD12	41:NJ:648:LEU:HD11	1.95	0.49
42:NM:47:THR:OG1	42:NM:65:ARG:NH1	2.46	0.49
46:NR:982:UNK:O	46:NR:986:UNK:N	2.46	0.49
51:SA:284:TYR:OH	52:SB:250:ASP:OD1	2.27	0.49
61:SP:1349:SER:HB3	61:SP:1384:CYS:HA	1.95	0.49
61:SP:1448:VAL:O	61:SP:1452:THR:OG1	2.28	0.49
61:SP:1475:MET:HB3	61:SP:1479:PHE:CE2	2.47	0.49
66:SU:149:VAL:HG11	66:SU:187:ALA:HB1	1.94	0.49
20:LM:1601:ILE:HA	20:LM:1604:ILE:HG22	1.95	0.49
22:LO:344:TRP:NE1	22:LO:359:GLU:OE1	2.39	0.49
25:LR:378:ILE:HD11	42:NM:19:LYS:HG2	1.95	0.49
39:NH:366:HIS:H	39:NH:369:MET:HE3	1.78	0.49
42:NM:90:ASP:OD2	42:NM:92:GLN:NE2	2.45	0.49
44:NO:3:ARG:HD3	44:NO:6:VAL:HG12	1.94	0.49
46:NR:314:UNK:O	46:NR:318:UNK:N	2.46	0.49
49:NW:51:MET:HG2	49:NW:71:GLY:HA3	1.93	0.49
56:SH:159:MET:HE1	56:SH:196:TYR:HE1	1.78	0.49
56:SH:175:LYS:NZ	57:SI:989:GLN:OE1	2.46	0.49
65:ST:834:LYS:O	65:ST:838:ASN:ND2	2.41	0.49
66:SU:369:ALA:HB2	66:SU:394:LEU:HD23	1.94	0.49
67:SW:91:ASN:HA	67:SW:94:LYS:HE2	1.94	0.49
2:L1:641:A:OP1	10:L9:40:LYS:NZ	2.42	0.49
4:L3:47:LYS:HG3	4:L3:70:ILE:HD13	1.95	0.49
14:LF:72:PHE:HE2	34:NC:248:ARG:HE	1.60	0.49
16:LH:341:MET:HE1	16:LH:394:ALA:HA	1.95	0.49
16:LH:727:ILE:HD13	16:LH:754:SER:HB3	1.93	0.49
19:LL:458:GLN:HE22	66:SU:262:HIS:HB3	1.78	0.49
20:LM:958:HIS:O	20:LM:961:SER:OG	2.27	0.49
20:LM:1073:SER:HA	20:LM:1076:ASN:HD22	1.77	0.49
23:LP:46:ARG:HD2	28:LU:20:ASP:HA	1.94	0.49
24:LQ:676:GLN:HB3	24:LQ:695:HIS:HB3	1.94	0.49
25:LR:545:ILE:HD11	25:LR:566:VAL:HG21	1.94	0.49
38:NG:93:LEU:HG	38:NG:124:MET:HE2	1.95	0.49
41:NJ:386:VAL:HG22	41:NJ:408:PHE:HB2	1.95	0.49
49:NW:51:MET:HG3	49:NW:52:PRO:HD2	1.95	0.49
53:SD:97:PHE:HB2	53:SD:107:VAL:HG23	1.95	0.49
56:SH:57:LYS:NZ	56:SH:86:GLU:O	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L1:1234:C:O2	65:ST:35:LYS:NZ	2.45	0.48
2:L1:1787:G:H2'	2:L1:1788:A:H8	1.77	0.48
3:L2:61:G:OP2	22:LO:660:ARG:NH1	2.40	0.48
7:L6:67:VAL:HG13	7:L6:99:GLY:HA2	1.95	0.48
14:LF:83:LYS:HE2	14:LF:96:LEU:HD12	1.95	0.48
17:LI:584:ARG:O	17:LI:588:LEU:HG	2.12	0.48
21:LN:605:CYS:HB2	21:LN:643:ILE:HG22	1.94	0.48
23:LP:119:LYS:HG2	23:LP:120:TRP:CD1	2.48	0.48
24:LQ:877:ILE:HA	24:LQ:880:LEU:HB2	1.94	0.48
25:LR:250:VAL:H	25:LR:255:VAL:HB	1.77	0.48
29:LW:326:ASN:HA	29:LW:367:VAL:HG21	1.95	0.48
39:NH:127:LEU:HB2	39:NH:148:VAL:HG21	1.95	0.48
42:NM:147:ASN:OD1	42:NM:148:ASN:N	2.46	0.48
42:NM:229:MET:HA	42:NM:229:MET:HE3	1.95	0.48
58:SJ:42:ARG:NH1	58:SJ:104:GLY:O	2.46	0.48
61:SP:210:MET:HE1	61:SP:228:LEU:HD21	1.94	0.48
61:SP:1674:VAL:HG21	61:SP:1819:VAL:HB	1.93	0.48
65:ST:738:SER:O	65:ST:741:THR:OG1	2.29	0.48
1:L0:604:C:H42	18:LJ:433:ARG:HE	1.61	0.48
2:L1:1536:G:H2'	2:L1:1537:A:C8	2.46	0.48
23:LP:24:LEU:HD22	23:LP:71:ARG:HB3	1.94	0.48
37:NF:2:GLY:HA2	37:NF:9:LYS:HG2	1.94	0.48
39:NH:127:LEU:HD23	39:NH:152:PHE:HB2	1.94	0.48
41:NK:29:VAL:HG12	41:NK:151:LEU:HD12	1.95	0.48
58:SJ:73:LEU:HD21	58:SJ:80:PRO:HA	1.95	0.48
59:SL:20:ARG:HH12	59:SL:31:LYS:HB3	1.78	0.48
65:ST:432:UNK:O	65:ST:436:UNK:N	2.46	0.48
66:SU:179:ASP:O	66:SU:183:HIS:ND1	2.41	0.48
4:L3:46:ARG:HH12	4:L3:52:LEU:HD11	1.76	0.48
11:LA:26:LEU:HB2	11:LA:31:LEU:HD13	1.95	0.48
11:LA:52:LEU:HD11	11:LA:78:LYS:HG3	1.95	0.48
20:LM:1342:SER:O	20:LM:1346:ILE:HG12	2.13	0.48
20:LM:1966:LEU:HD21	20:LM:1995:ILE:HG21	1.96	0.48
21:LN:579:ARG:NE	21:LN:600:ASP:OD2	2.45	0.48
23:LP:221:LEU:HD13	64:SS:191:LEU:HD23	1.95	0.48
25:LR:527:VAL:HG22	25:LR:538:THR:HG22	1.94	0.48
28:LU:75:HIS:HD2	28:LU:78:LYS:H	1.61	0.48
36:NE:189:ARG:O	36:NE:193:GLN:HG2	2.12	0.48
61:SP:805:LEU:O	61:SP:809:THR:OG1	2.28	0.48
61:SP:1902:THR:HG21	61:SP:1935:GLU:HB2	1.95	0.48
65:ST:545:VAL:HA	65:ST:548:TYR:HD1	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:SU:247:GLU:CD	66:SU:250:ARG:HH12	2.21	0.48
2:L1:1139:C:H2'	2:L1:1140:G:H8	1.78	0.48
2:L1:1859:A:H2'	2:L1:1860:A:C8	2.48	0.48
16:LH:345:ARG:NH2	16:LH:400:ASN:OD1	2.46	0.48
20:LM:1719:ALA:HB2	20:LM:1763:ALA:HA	1.94	0.48
25:LR:394:CYS:HB2	25:LR:424:VAL:HG23	1.96	0.48
27:LT:674:THR:OG1	27:LT:676:ASP:OD1	2.31	0.48
41:NK:30:GLY:HA2	41:NK:154:MET:HE2	1.96	0.48
50:NY:88:VAL:HG23	50:NY:103:THR:HA	1.94	0.48
58:SK:238:GLU:HB3	58:SK:243:VAL:HB	1.96	0.48
60:SM:232:HIS:HB3	60:SM:244:LEU:HD22	1.95	0.48
5:L4:22:LYS:HG3	5:L4:23:LEU:HG	1.96	0.48
18:LJ:270:ARG:HG2	18:LJ:290:ALA:C	2.39	0.48
20:LM:109:PRO:HA	20:LM:112:LYS:HD3	1.95	0.48
20:LM:174:ALA:HB2	52:SB:403:ILE:HG22	1.96	0.48
20:LM:764:PRO:HG2	20:LM:767:LEU:HB2	1.94	0.48
20:LM:1409:GLU:HA	20:LM:1458:HIS:CD2	2.49	0.48
20:LM:1815:THR:HG22	20:LM:1854:VAL:HG21	1.95	0.48
27:LT:543:ARG:NH1	27:LT:583:PRO:O	2.46	0.48
40:NI:20:PRO:HG2	40:NI:23:TYR:HB2	1.94	0.48
58:SJ:190:VAL:HG11	58:SJ:240:VAL:HG21	1.96	0.48
58:SK:93:LEU:HD11	58:SK:128:ARG:HG3	1.96	0.48
1:L0:459:G:H22	35:ND:245:LYS:NZ	2.12	0.48
2:L1:104:A:OP1	9:L8:12:ARG:NE	2.46	0.48
5:L4:129:ILE:HD11	5:L4:139:LEU:HD12	1.94	0.48
16:LH:97:ILE:HD11	16:LH:141:GLU:HG3	1.94	0.48
18:LJ:125:VAL:HA	18:LJ:141:ALA:HA	1.94	0.48
20:LM:836:MET:HA	20:LM:836:MET:HE3	1.96	0.48
23:LP:223:TRP:HB2	23:LP:255:LEU:HD11	1.94	0.48
25:LR:297:HIS:HB2	25:LR:310:ALA:HB3	1.95	0.48
27:LT:789:PHE:O	67:SW:199:ARG:NH2	2.36	0.48
44:NO:75:ILE:HG22	44:NO:77:PRO:HD2	1.96	0.48
60:SM:29:LYS:HA	60:SM:53:LEU:HD23	1.96	0.48
61:SP:967:HIS:HA	61:SP:1004:HIS:HD2	1.78	0.48
61:SP:1479:PHE:CD1	61:SP:1525:LYS:HD3	2.49	0.48
64:SS:207:VAL:HG21	64:SS:223:ARG:HH22	1.79	0.48
66:SU:179:ASP:OD1	66:SU:180:THR:N	2.47	0.48
5:L4:128:LYS:HB3	5:L4:140:VAL:HB	1.95	0.48
10:L9:54:ARG:NH2	59:SL:96:ALA:HB2	2.29	0.48
14:LF:14:THR:HG22	14:LF:16:ARG:HE	1.79	0.48
20:LM:1376:VAL:HG21	20:LM:1411:PHE:HD1	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:LM:1387:LEU:O	20:LM:1395:ARG:NH1	2.44	0.48
22:LO:674:GLN:HA	22:LO:699:PHE:CZ	2.48	0.48
24:LQ:217:VAL:HG13	24:LQ:271:ALA:HB3	1.95	0.48
24:LQ:410:THR:OG1	24:LQ:415:ARG:NH1	2.47	0.48
27:LT:769:ASP:OD1	27:LT:770:VAL:N	2.47	0.48
28:LU:235:VAL:HG22	28:LU:443:VAL:HG22	1.95	0.48
28:LU:410:MET:HE1	45:NQ:2:PRO:HA	1.94	0.48
32:NA:450:ASP:OD1	32:NA:451:ALA:N	2.45	0.48
47:NT:108:VAL:HG22	47:NT:114:ILE:HG12	1.95	0.48
2:L1:210:U:OP2	61:SP:1137:ARG:NH2	2.47	0.48
2:L1:597:G:H5''	70:SY:1:MET:HG3	1.96	0.48
12:LC:53:GLU:OE1	12:LC:85:ARG:NH2	2.33	0.48
18:LJ:29:TYR:OH	18:LJ:301:ASP:O	2.22	0.48
18:LJ:81:ASP:HB3	18:LJ:100:GLU:HG2	1.96	0.48
18:LJ:181:ILE:HD13	18:LJ:214:LEU:HD11	1.96	0.48
20:LM:374:ILE:HD12	20:LM:377:ARG:HE	1.79	0.48
21:LN:418:LEU:HB3	21:LN:427:LEU:HD23	1.96	0.48
28:LU:322:THR:HG22	28:LU:324:ARG:H	1.79	0.48
41:NJ:530:MET:HE2	41:NJ:545:LEU:HD12	1.94	0.48
41:NK:513:ASP:OD1	41:NK:514:THR:N	2.46	0.48
53:SC:168:ALA:N	53:SC:191:GLU:OE2	2.47	0.48
53:SD:107:VAL:HG12	53:SD:136:ALA:HA	1.96	0.48
56:SH:220:ILE:HG22	56:SH:222:ASP:H	1.79	0.48
61:SP:1192:GLY:HA2	61:SP:1238:ILE:HG12	1.96	0.48
66:SU:221:ARG:O	66:SU:249:ARG:NH2	2.47	0.48
17:LI:684:VAL:HG23	19:LK:524:VAL:HG21	1.95	0.48
20:LM:1558:ILE:HA	20:LM:1561:VAL:HG12	1.95	0.48
23:LP:188:MET:HE3	62:SQ:560:THR:HG21	1.95	0.48
24:LQ:109:ALA:HB3	24:LQ:127:LYS:HD2	1.96	0.48
26:LS:482:ASN:OD1	26:LS:484:THR:OG1	2.29	0.48
35:ND:176:ARG:HG2	35:ND:178:LYS:H	1.79	0.48
41:NK:360:VAL:HG23	41:NK:366:GLN:HB2	1.95	0.48
65:ST:565:VAL:C	65:ST:568:PRO:HD2	2.39	0.48
67:SW:176:LEU:HD21	67:SW:207:VAL:HG12	1.94	0.48
1:L0:827:C:C4	27:LT:413:LYS:HA	2.48	0.48
2:L1:382:C:H2'	2:L1:383:G:H8	1.78	0.48
3:L2:32:U:O2'	3:L2:33:G:O5'	2.28	0.48
3:L2:135:U:H3	3:L2:138:C:P	2.37	0.48
3:L2:139:U:OP2	20:LM:1752:SER:OG	2.19	0.48
18:LJ:166:TYR:HB3	18:LJ:168:ARG:HD2	1.96	0.48
20:LM:1693:LEU:HD21	20:LM:1732:GLN:HG2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:SG:308:ARG:NH1	55:SG:317:GLN:OE1	2.36	0.48
1:L0:811:G:C8	27:LT:486:LYS:HD2	2.49	0.47
2:L1:106:C:H2'	2:L1:107:A:H8	1.79	0.47
2:L1:1125:C:H2'	2:L1:1126:G:H8	1.79	0.47
7:L6:126:ASP:OD1	7:L6:127:THR:N	2.47	0.47
16:LH:173:VAL:HG21	16:LH:209:VAL:HB	1.96	0.47
17:LI:435:ASP:O	17:LI:438:THR:OG1	2.24	0.47
21:LN:581:THR:HG21	21:LN:601:ALA:HB3	1.96	0.47
40:NI:88:VAL:HG12	40:NI:121:VAL:HG23	1.96	0.47
41:NJ:691:LEU:HD21	57:SI:392:VAL:HA	1.95	0.47
42:NM:33:VAL:HA	42:NM:96:CYS:HB2	1.95	0.47
58:SJ:219:ILE:HG12	76:SJ:301:SAH:N1	2.29	0.47
65:ST:525:MET:HE2	66:SU:479:PHE:HD2	1.79	0.47
2:L1:219:U:H1'	9:L8:184:ARG:HD2	1.95	0.47
2:L1:1280:G:H2'	2:L1:1281:G:H8	1.79	0.47
8:L7:61:ILE:HG23	8:L7:95:ILE:HD13	1.95	0.47
20:LM:2095:LEU:HD12	20:LM:2098:ASN:HB2	1.96	0.47
21:LN:430:VAL:HG21	21:LN:433:MET:HE2	1.96	0.47
39:NH:124:GLU:OE2	39:NH:153:ARG:NH1	2.45	0.47
65:ST:77:ARG:HD3	65:ST:77:ARG:HA	1.72	0.47
2:L1:924:G:OP2	37:NF:3:ARG:NH2	2.42	0.47
3:L2:6:U:H2'	3:L2:7:A:C8	2.48	0.47
10:L9:88:ASP:OD1	10:L9:89:GLU:N	2.48	0.47
17:LI:152:VAL:O	17:LI:152:VAL:HG12	2.15	0.47
19:LK:494:VAL:HA	19:LK:497:MET:HE2	1.96	0.47
20:LM:1565:MET:HG3	20:LM:1581:LEU:HD11	1.95	0.47
24:LQ:366:LYS:HE2	24:LQ:385:GLN:HG3	1.97	0.47
39:NH:477:ARG:NH2	39:NH:632:THR:O	2.47	0.47
46:NR:190:UNK:O	46:NR:194:UNK:N	2.48	0.47
50:NY:132:ALA:O	50:NY:135:ILE:HG12	2.13	0.47
53:SD:100:ARG:NH1	53:SD:104:ASP:OD1	2.46	0.47
59:SL:87:VAL:HA	59:SL:90:MET:HE2	1.96	0.47
66:SU:265:PRO:HD2	66:SU:268:LEU:HD12	1.96	0.47
2:L1:919:A:OP2	37:NF:64:ARG:NH2	2.45	0.47
2:L1:1280:G:H2'	2:L1:1281:G:C8	2.50	0.47
3:L2:93:A:H2'	3:L2:94:G:C8	2.50	0.47
10:L9:48:PHE:CE2	10:L9:52:LYS:HE2	2.49	0.47
10:L9:152:ASP:OD2	10:L9:153:SER:N	2.47	0.47
20:LM:1742:THR:HG23	20:LM:1745:LYS:HE3	1.95	0.47
22:LO:177:ASP:HB2	22:LO:227:LYS:HA	1.96	0.47
41:NK:277:ARG:NE	41:NK:458:ARG:HG2	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SB:120:ARG:HG2	53:SC:229:MET:SD	2.54	0.47
58:SJ:44:ILE:HG13	58:SJ:107:GLN:HB3	1.96	0.47
58:SJ:67:ASP:OD2	58:SJ:68:LYS:N	2.47	0.47
71:SZ:326:MET:HA	71:SZ:329:ILE:HG22	1.97	0.47
71:SZ:364:PHE:HE2	71:SZ:385:LEU:HD22	1.80	0.47
2:L1:433:A:H2'	2:L1:434:G:C8	2.49	0.47
2:L1:511:U:H2'	2:L1:512:A:C8	2.49	0.47
7:L6:74:ARG:HB3	7:L6:94:ARG:HG2	1.96	0.47
17:LI:273:VAL:HB	17:LI:292:ILE:HD11	1.96	0.47
18:LJ:43:LYS:HD3	18:LJ:85:CYS:HA	1.97	0.47
18:LJ:123:LYS:HE2	18:LJ:143:ASP:HB3	1.96	0.47
18:LJ:181:ILE:HD13	18:LJ:214:LEU:HD21	1.96	0.47
20:LM:607:MET:SD	20:LM:625:LEU:HD23	2.55	0.47
20:LM:1813:LEU:HA	20:LM:1817:LEU:HD13	1.96	0.47
26:LS:493:GLU:O	26:LS:523:HIS:ND1	2.48	0.47
39:NH:332:LYS:HD3	39:NH:349:GLY:HA3	1.96	0.47
41:NJ:130:THR:HG23	41:NJ:133:LEU:H	1.80	0.47
41:NK:257:THR:HG21	41:NK:467:GLU:HB2	1.97	0.47
53:SC:87:MET:N	53:SC:87:MET:SD	2.87	0.47
57:SI:282:LEU:HD13	57:SI:909:LEU:HD11	1.95	0.47
57:SI:926:LEU:O	57:SI:978:CYS:N	2.46	0.47
58:SK:125:ARG:NH2	65:ST:765:LEU:O	2.47	0.47
61:SP:200:VAL:HG21	61:SP:206:LEU:HD22	1.95	0.47
61:SP:858:ASP:OD1	61:SP:859:LEU:N	2.47	0.47
61:SP:1552:PHE:HB3	61:SP:1555:GLN:HG2	1.94	0.47
61:SP:2005:ARG:O	61:SP:2008:THR:OG1	2.31	0.47
1:L0:1414:A:H5'	1:L0:1415:G:H5''	1.95	0.47
3:L2:64:G:H2'	3:L2:65:A:C8	2.49	0.47
7:L6:67:VAL:HG21	7:L6:73:VAL:HG21	1.97	0.47
8:L7:52:GLU:OE2	8:L7:56:GLY:N	2.42	0.47
14:LF:64:PHE:HB3	34:NC:224:ARG:HH22	1.80	0.47
16:LH:130:VAL:HG12	16:LH:149:PHE:HA	1.96	0.47
19:LL:317:ILE:HG12	19:LL:371:MET:HE2	1.96	0.47
20:LM:274:MET:HE2	20:LM:279:VAL:HG22	1.96	0.47
20:LM:702:VAL:HG12	20:LM:771:TYR:HE2	1.80	0.47
24:LQ:482:ASP:OD1	24:LQ:489:LEU:HD21	2.14	0.47
27:LT:663:ASP:OD1	27:LT:664:SER:N	2.48	0.47
28:LU:220:ASN:HB3	28:LU:236:ILE:HG12	1.95	0.47
29:LW:605:LEU:HB3	39:NH:680:PRO:HG2	1.96	0.47
39:NH:341:ASP:OD1	39:NH:341:ASP:N	2.48	0.47
41:NJ:210:SER:HB2	41:NJ:213:VAL:HG13	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:NJ:358:VAL:HB	41:NJ:368:ILE:HB	1.96	0.47
41:NK:602:GLY:HA2	41:NK:607:TRP:HE1	1.79	0.47
61:SP:1256:VAL:O	61:SP:1260:LEU:HG	2.15	0.47
2:L1:375:U:H2'	2:L1:376:A:C8	2.50	0.47
2:L1:650:A:H2'	2:L1:651:U:O4'	2.15	0.47
2:L1:996:A:H2'	2:L1:997:A:C8	2.49	0.47
2:L1:1592:C:H5''	6:L5:91:ARG:HH12	1.80	0.47
7:L6:214:ALA:O	7:L6:218:LYS:HG3	2.14	0.47
8:L7:131:GLU:HG3	8:L7:139:ILE:HD12	1.97	0.47
17:LI:658:PHE:CZ	18:LJ:489:MET:HB3	2.50	0.47
20:LM:758:MET:HA	20:LM:794:LYS:HD2	1.96	0.47
20:LM:1101:THR:HG22	20:LM:1103:GLN:H	1.80	0.47
20:LM:1525:LEU:HD22	20:LM:1594:LEU:HB3	1.96	0.47
24:LQ:392:TYR:OH	24:LQ:405:ARG:NH2	2.43	0.47
25:LR:586:LEU:HD12	25:LR:600:THR:HG22	1.95	0.47
41:NJ:499:CYS:SG	41:NJ:561:PRO:HB3	2.54	0.47
41:NK:44:LEU:HD22	41:NK:146:LEU:HG	1.97	0.47
41:NK:696:LEU:HD12	41:NK:700:GLU:HB2	1.96	0.47
49:NW:253:VAL:HG22	49:NW:275:ILE:HD13	1.97	0.47
52:SB:45:LYS:HE2	52:SB:79:ILE:HG23	1.96	0.47
52:SB:97:VAL:HG13	52:SB:101:LYS:NZ	2.29	0.47
57:SI:946:VAL:HG22	57:SI:993:PHE:HB2	1.97	0.47
58:SJ:101:ASN:HB2	58:SJ:106:LEU:HD12	1.97	0.47
58:SJ:127:PRO:HB3	58:SJ:132:ARG:NE	2.30	0.47
58:SK:99:PRO:HA	58:SK:102:ARG:HB2	1.96	0.47
61:SP:134:THR:HA	61:SP:137:LEU:HD13	1.96	0.47
61:SP:1583:ILE:HA	61:SP:1586:ARG:HH21	1.80	0.47
65:ST:259:UNK:HA	71:SZ:355:ARG:HH21	1.79	0.47
65:ST:621:TYR:O	65:ST:624:THR:OG1	2.30	0.47
66:SU:185:MET:HE1	66:SU:217:VAL:HG13	1.97	0.47
11:LA:85:LEU:HA	11:LA:88:TRP:HD1	1.79	0.47
20:LM:186:LEU:HB3	20:LM:241:LYS:HE3	1.97	0.47
20:LM:374:ILE:O	20:LM:378:HIS:ND1	2.36	0.47
20:LM:1726:GLU:O	20:LM:1730:ILE:HG13	2.15	0.47
22:LO:871:GLN:O	22:LO:875:ALA:N	2.48	0.47
23:LP:248:LEU:HD21	62:SQ:562:SER:HB3	1.97	0.47
25:LR:101:THR:HG23	25:LR:102:ARG:HG2	1.97	0.47
28:LU:291:SER:HA	28:LU:333:TRP:CD1	2.50	0.47
41:NK:715:LEU:HD22	41:NK:733:LEU:HD11	1.96	0.47
61:SP:644:LYS:NZ	61:SP:810:ASP:O	2.42	0.47
61:SP:1001:LYS:HD2	61:SP:1004:HIS:CE1	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:SP:1522:LEU:HD21	61:SP:1548:LEU:HD11	1.96	0.47
61:SP:1975:ASP:OD1	61:SP:1975:ASP:N	2.46	0.47
2:L1:1588:A:H2'	2:L1:1589:A:C8	2.49	0.47
9:L8:8:TRP:CZ3	9:L8:20:PRO:HB3	2.50	0.47
17:LI:401:LEU:HD11	17:LI:420:PHE:CG	2.49	0.47
18:LJ:429:LEU:HD11	18:LJ:439:ILE:HG13	1.97	0.47
20:LM:1649:LEU:HD21	20:LM:1692:VAL:HG22	1.96	0.47
21:LN:399:SER:HB3	21:LN:404:TRP:HB2	1.97	0.47
25:LR:117:PHE:CE1	25:LR:124:LEU:HD12	2.50	0.47
25:LR:313:ASP:O	25:LR:315:ASN:N	2.46	0.47
25:LR:485:VAL:HG12	25:LR:496:THR:HG22	1.97	0.47
25:LR:782:ASP:OD2	27:LT:938:GLN:NE2	2.47	0.47
36:NE:184:GLY:O	36:NE:188:GLU:N	2.41	0.47
50:NY:114:ILE:HG23	50:NY:117:ARG:HH12	1.80	0.47
57:SI:959:ILE:HB	57:SI:969:LEU:HD11	1.97	0.47
61:SP:133:ILE:HA	61:SP:136:ILE:HD12	1.97	0.47
2:L1:387:C:OP2	9:L8:10:LYS:NZ	2.48	0.47
2:L1:485:A:N6	57:SI:216:LEU:O	2.48	0.47
2:L1:589:G:O2'	2:L1:590:A:O5'	2.32	0.47
2:L1:1470:C:H2'	2:L1:1471:C:H6	1.79	0.47
3:L2:105:U:OP1	51:SA:337:ARG:NH1	2.47	0.47
16:LH:20:ARG:NH2	16:LH:103:HIS:O	2.48	0.47
17:LI:662:VAL:HG13	19:LK:579:VAL:HG22	1.96	0.47
19:LL:494:VAL:HG22	19:LL:534:HIS:CD2	2.49	0.47
20:LM:843:VAL:HG22	20:LM:846:ARG:NH2	2.26	0.47
20:LM:2070:LEU:HD23	20:LM:2109:PHE:CD2	2.50	0.47
22:LO:312:PHE:HE1	22:LO:328:ILE:HD11	1.78	0.47
27:LT:494:ASP:OD1	27:LT:495:ILE:N	2.48	0.47
39:NH:588:GLU:HB3	42:NM:249:LYS:HZ2	1.80	0.47
41:NK:179:VAL:HG12	41:NK:552:PRO:HD3	1.95	0.47
57:SI:1050:ALA:HB3	65:ST:800:PHE:HZ	1.80	0.47
65:ST:259:UNK:O	65:ST:263:UNK:N	2.48	0.47
1:L0:719:G:N2	1:L0:751:C:N3	2.63	0.46
2:L1:649:U:H2'	2:L1:650:A:H8	1.79	0.46
2:L1:1237:C:H42	65:ST:805:ARG:HH22	1.62	0.46
19:LL:116:LEU:HD21	19:LL:119:LYS:HG3	1.96	0.46
19:LL:169:SER:OG	19:LL:188:ARG:NH1	2.37	0.46
20:LM:835:MET:HE3	20:LM:835:MET:HB3	1.77	0.46
20:LM:1458:HIS:O	20:LM:1462:SER:OG	2.31	0.46
27:LT:823:GLN:O	67:SW:219:LYS:NZ	2.41	0.46
28:LU:179:ASP:HB3	28:LU:188:PRO:HB3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LU:364:THR:HG23	28:LU:367:GLU:H	1.80	0.46
29:LW:241:ASP:OD1	29:LW:242:ILE:N	2.48	0.46
41:NK:387:ILE:HB	41:NK:409:MET:HG2	1.98	0.46
46:NR:901:UNK:O	46:NR:905:UNK:N	2.49	0.46
60:SM:49:GLU:HG2	60:SM:52:ALA:HB3	1.96	0.46
1:L0:1433:A:N7	51:SA:40:GLY:HA3	2.30	0.46
2:L1:115:U:O2'	2:L1:381:C:O2	2.23	0.46
2:L1:388:U:H2'	2:L1:389:A:H8	1.80	0.46
2:L1:562:U:H2'	2:L1:563:G:C8	2.50	0.46
2:L1:617:G:H2'	2:L1:618:C:C6	2.51	0.46
2:L1:1823:A:H4'	2:L1:1824:A:O5'	2.14	0.46
3:L2:8:U:H2'	3:L2:9:A:C8	2.50	0.46
7:L6:7:PHE:CE2	7:L6:9:ALA:HB3	2.50	0.46
19:LL:38:LEU:HD22	19:LL:99:LEU:HD21	1.96	0.46
20:LM:2089:LEU:HD12	20:LM:2128:THR:HA	1.98	0.46
21:LN:441:LEU:HG	21:LN:457:ASN:HA	1.97	0.46
21:LN:532:MET:HG2	21:LN:543:ILE:HG12	1.97	0.46
41:NK:268:ILE:HD13	41:NK:271:ILE:HD12	1.96	0.46
50:NY:208:ASP:OD1	50:NY:213:ILE:HB	2.15	0.46
53:SD:246:VAL:HG11	53:SD:262:ILE:HD11	1.97	0.46
56:SH:211:SER:OG	56:SH:273:GLU:OE2	2.33	0.46
61:SP:528:ILE:HG22	61:SP:530:PRO:HD2	1.98	0.46
64:SS:159:PHE:HB3	64:SS:729:ILE:HG12	1.97	0.46
2:L1:1221:G:O2'	2:L1:1676:U:O2	2.33	0.46
3:L2:49:U:H2'	3:L2:50:U:C6	2.50	0.46
11:LA:123:VAL:HG13	11:LA:124:ILE:HD12	1.97	0.46
16:LH:585:VAL:HB	16:LH:598:ILE:HB	1.97	0.46
19:LK:467:THR:HG21	19:LK:498:PRO:HG2	1.98	0.46
20:LM:499:MET:HE3	20:LM:533:VAL:HG13	1.97	0.46
23:LP:323:GLU:HG3	23:LP:366:LEU:HB3	1.96	0.46
61:SP:1409:LEU:O	61:SP:1413:VAL:HG23	2.15	0.46
2:L1:1004:U:H2'	2:L1:1005:G:C8	2.49	0.46
17:LI:610:ALA:HA	17:LI:613:ILE:HD13	1.97	0.46
21:LN:437:LEU:HD22	21:LN:454:VAL:HG11	1.97	0.46
21:LN:446:SER:OG	21:LN:448:ASP:O	2.31	0.46
23:LP:253:LYS:O	23:LP:253:LYS:HD2	2.16	0.46
23:LP:330:ILE:HD13	23:LP:367:LEU:HD11	1.98	0.46
24:LQ:175:TRP:HE1	24:LQ:187:MET:HE3	1.80	0.46
24:LQ:899:MET:HE1	25:LR:764:THR:HG22	1.97	0.46
26:LS:233:ARG:NH1	26:LS:506:SER:OG	2.48	0.46
29:LW:241:ASP:OD2	29:LW:281:LEU:N	2.43	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:NH:237:LEU:HB3	39:NH:253:LEU:HB2	1.97	0.46
39:NH:1104:ARG:HD3	39:NH:1115:MET:HB3	1.97	0.46
41:NK:813:LEU:HD11	41:NK:822:LEU:HD21	1.97	0.46
52:SB:190:HIS:NE2	52:SB:213:ASP:OD1	2.45	0.46
61:SP:216:LYS:HD3	61:SP:216:LYS:HA	1.73	0.46
61:SP:1398:PHE:HD2	61:SP:1410:LEU:HD21	1.80	0.46
2:L1:942:G:H2'	2:L1:943:U:C6	2.50	0.46
2:L1:1309:C:OP1	47:NT:104:LYS:NZ	2.47	0.46
6:L5:38:TYR:OH	15:LG:54:ASP:OD1	2.30	0.46
17:LI:467:TYR:HB2	17:LI:496:ILE:HD13	1.97	0.46
20:LM:440:LEU:HA	20:LM:443:VAL:HG12	1.96	0.46
20:LM:1741:LEU:HD21	20:LM:1782:ILE:HG22	1.98	0.46
22:LO:522:ASP:OD1	22:LO:524:THR:OG1	2.27	0.46
22:LO:844:VAL:O	22:LO:847:PHE:HB3	2.15	0.46
23:LP:453:SER:OG	23:LP:456:ASP:OD2	2.33	0.46
25:LR:24:PHE:HZ	25:LR:330:PHE:HB3	1.81	0.46
39:NH:1010:VAL:HB	39:NH:1084:VAL:HB	1.97	0.46
40:NI:56:PRO:O	40:NI:60:THR:OG1	2.21	0.46
40:NI:104:ARG:HG2	40:NI:111:LYS:NZ	2.30	0.46
41:NJ:823:LYS:O	41:NJ:827:MET:HG2	2.15	0.46
41:NJ:881:GLU:HG3	41:NJ:888:SER:HB2	1.97	0.46
42:NM:173:THR:O	42:NM:177:GLN:HG2	2.16	0.46
58:SJ:224:LEU:HD22	58:SJ:228:LEU:HD22	1.98	0.46
61:SP:1670:GLN:HG3	61:SP:1819:VAL:HG21	1.98	0.46
1:L0:1429:A:H2'	1:L0:1430:G:C8	2.51	0.46
2:L1:75:G:H1'	2:L1:76:U:H2'	1.97	0.46
18:LJ:252:THR:HG21	18:LJ:293:LEU:HA	1.98	0.46
21:LN:368:LYS:HD2	21:LN:369:ASN:H	1.81	0.46
23:LP:11:ASP:OD2	64:SS:711:ARG:NH2	2.48	0.46
27:LT:610:GLU:O	27:LT:612:ARG:NH1	2.48	0.46
27:LT:768:LEU:HD21	27:LT:852:PRO:HB2	1.96	0.46
39:NH:306:VAL:HG11	39:NH:423:LEU:HD22	1.97	0.46
51:SA:21:GLU:HB2	64:SS:725:PRO:HG2	1.97	0.46
60:SM:255:LEU:HD21	60:SM:258:ILE:HD11	1.98	0.46
61:SP:1797:SER:O	61:SP:1820:ARG:NH1	2.48	0.46
61:SP:1861:ILE:HA	61:SP:1864:ILE:HG22	1.97	0.46
71:SZ:152:UNK:O	71:SZ:156:UNK:N	2.49	0.46
2:L1:1653:U:H3	2:L1:1671:G:H1	1.63	0.46
3:L2:59:G:N3	59:SL:8:ARG:NH1	2.63	0.46
7:L6:227:GLN:O	7:L6:230:LYS:HG2	2.15	0.46
8:L7:82:GLU:OE2	8:L7:83:LEU:HD22	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LH:229:LEU:O	16:LH:241:TYR:HA	2.15	0.46
19:LL:467:THR:O	19:LL:471:GLU:HG2	2.16	0.46
20:LM:214:ARG:NE	23:LP:593:GLN:O	2.45	0.46
22:LO:545:ASP:HB3	22:LO:563:LEU:HB2	1.98	0.46
25:LR:52:VAL:O	25:LR:328:LYS:HE2	2.14	0.46
33:NB:438:GLU:OE2	33:NB:441:ARG:NH2	2.42	0.46
55:SG:338:MET:HG2	55:SG:350:TRP:HB2	1.97	0.46
56:SH:210:ASP:N	56:SH:210:ASP:OD1	2.49	0.46
61:SP:1167:GLU:OE1	61:SP:1212:ASN:ND2	2.48	0.46
61:SP:1842:ASN:OD1	61:SP:1845:SER:OG	2.33	0.46
71:SZ:269:ASN:HB2	71:SZ:272:LEU:HD12	1.97	0.46
71:SZ:282:LYS:HD3	71:SZ:282:LYS:HA	1.80	0.46
2:L1:432:G:H2'	2:L1:433:A:C8	2.51	0.46
2:L1:615:C:H2'	2:L1:616:A:C8	2.50	0.46
2:L1:1739:C:H2'	2:L1:1740:C:H6	1.81	0.46
3:L2:57:A:H2'	3:L2:58:C:C6	2.50	0.46
10:L9:69:ARG:O	10:L9:73:GLU:HG2	2.16	0.46
18:LJ:355:ARG:N	26:LS:294:GLU:OE1	2.46	0.46
20:LM:362:VAL:HG12	20:LM:363:THR:HG23	1.98	0.46
22:LO:197:GLU:OE2	22:LO:204:TYR:OH	2.16	0.46
22:LO:400:TRP:HA	22:LO:407:CYS:HA	1.96	0.46
38:NG:85:CYS:HB3	38:NG:90:ILE:HB	1.97	0.46
41:NK:694:LEU:HG	41:NK:695:LEU:HG	1.97	0.46
52:SB:191:PHE:CD2	52:SB:194:LEU:HB2	2.51	0.46
52:SB:351:SER:OG	52:SB:354:HIS:ND1	2.43	0.46
53:SC:183:PRO:HD2	53:SC:184:ASP:H	1.80	0.46
57:SI:96:SER:HA	57:SI:99:ILE:HD12	1.98	0.46
61:SP:1370:GLU:CD	61:SP:1403:ASN:HD22	2.23	0.46
67:SW:214:SER:O	67:SW:218:ILE:HG12	2.16	0.46
1:L0:718:G:N2	1:L0:752:C:N3	2.64	0.46
9:L8:92:ARG:HH12	49:NW:138:ARG:NE	2.14	0.46
11:LA:32:ALA:HB3	11:LA:110:VAL:HB	1.98	0.46
13:LD:128:VAL:HG12	13:LD:142:VAL:HA	1.96	0.46
17:LI:509:LEU:HB3	17:LI:612:HIS:CD2	2.48	0.46
20:LM:803:PRO:HG2	20:LM:806:PHE:HB2	1.97	0.46
20:LM:1584:ALA:O	20:LM:1587:LEU:HB3	2.16	0.46
22:LO:74:ASP:OD1	22:LO:78:ASP:N	2.49	0.46
23:LP:575:LYS:HD3	52:SB:349:GLN:HB3	1.98	0.46
39:NH:352:VAL:HA	39:NH:355:LEU:HB2	1.98	0.46
39:NH:715:ARG:HH11	39:NH:715:ARG:HA	1.81	0.46
41:NJ:162:THR:HG21	41:NJ:171:TYR:HB2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:NK:323:PHE:HA	41:NK:326:VAL:HG12	1.98	0.46
61:SP:1863:ASP:OD1	61:SP:1866:ARG:NH1	2.47	0.46
65:ST:622:ILE:HG22	65:ST:648:LEU:H	1.81	0.46
65:ST:819:LEU:O	65:ST:823:MET:HG2	2.16	0.46
9:L8:67:TRP:O	9:L8:71:CYS:N	2.48	0.46
16:LH:104:ALA:HB2	16:LH:158:PRO:HG3	1.98	0.46
17:LI:579:PRO:HG3	17:LI:618:LYS:HG3	1.98	0.46
20:LM:1779:LEU:O	20:LM:1783:LEU:HG	2.16	0.46
20:LM:2029:ASN:O	20:LM:2037:PHE:HE2	1.99	0.46
21:LN:490:LEU:HD22	21:LN:499:LEU:HD11	1.97	0.46
23:LP:352:GLU:HA	23:LP:355:MET:HE2	1.97	0.46
25:LR:427:VAL:HG12	25:LR:439:THR:HG22	1.98	0.46
27:LT:802:ALA:HB2	27:LT:826:ASP:HB3	1.98	0.46
41:NJ:307:SER:HA	41:NJ:366:GLN:HG2	1.97	0.46
47:NT:123:SER:HB2	47:NT:126:CYS:HB2	1.98	0.46
51:SA:294:PRO:HB2	51:SA:391:SER:HB3	1.97	0.46
59:SL:86:LEU:O	59:SL:90:MET:HG3	2.16	0.46
70:SY:76:GLN:HB2	70:SY:81:ILE:HD13	1.97	0.46
17:LI:647:MET:HE1	19:LK:565:LEU:HD12	1.96	0.45
19:LL:341:CYS:SG	19:LL:361:ARG:NH1	2.89	0.45
20:LM:1330:MET:O	20:LM:1334:VAL:HG22	2.16	0.45
22:LO:552:ARG:NH1	22:LO:557:GLU:OE1	2.50	0.45
24:LQ:816:LYS:HB3	24:LQ:819:GLU:HG2	1.97	0.45
25:LR:110:ALA:HB1	25:LR:129:CYS:HB2	1.98	0.45
42:NM:76:ASN:OD1	42:NM:77:ASP:N	2.49	0.45
42:NM:164:ILE:O	42:NM:168:MET:HG3	2.17	0.45
61:SP:381:PRO:HG2	61:SP:384:LEU:HD23	1.98	0.45
61:SP:753:LYS:HD3	61:SP:838:ARG:HH12	1.81	0.45
61:SP:1513:ASP:O	61:SP:1517:ILE:HG12	2.16	0.45
61:SP:1965:TYR:CE2	61:SP:2003:THR:HG23	2.51	0.45
70:SY:165:VAL:HG23	70:SY:168:ARG:HH12	1.81	0.45
1:L0:445:C:H5''	26:LS:318:LYS:HD2	1.98	0.45
1:L0:857:C:OP1	30:LZ:50:GLN:NE2	2.50	0.45
2:L1:1687:C:H2'	2:L1:1688:C:H6	1.81	0.45
8:L7:60:ILE:HD13	8:L7:92:VAL:HG22	1.98	0.45
8:L7:192:PHE:HZ	45:NQ:12:PRO:HA	1.81	0.45
19:LL:231:ILE:HD12	19:LL:234:LEU:HD12	1.97	0.45
20:LM:384:THR:HG22	20:LM:431:LEU:HD11	1.97	0.45
20:LM:927:LEU:HD22	20:LM:966:ILE:HG21	1.98	0.45
20:LM:1322:ASN:O	20:LM:1326:ILE:HG13	2.17	0.45
20:LM:1811:LYS:HE2	20:LM:1815:THR:HG21	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:LP:71:ARG:NH2	26:LS:92:GLU:OE1	2.40	0.45
24:LQ:689:TYR:HB3	24:LQ:701:LEU:HD11	1.98	0.45
25:LR:387:LYS:HG3	25:LR:389:TRP:H	1.81	0.45
47:NT:104:LYS:HZ2	47:NT:118:ARG:HE	1.64	0.45
53:SC:225:MET:HG2	53:SC:226:LEU:HD22	1.98	0.45
61:SP:1775:THR:O	61:SP:1779:ILE:HG12	2.16	0.45
2:L1:1094:C:H4'	44:NO:20:ARG:NH2	2.32	0.45
3:L2:176:C:H2'	3:L2:177:C:C6	2.52	0.45
16:LH:568:TRP:HA	16:LH:575:LEU:HA	1.98	0.45
19:LK:521:VAL:O	19:LK:524:VAL:HB	2.16	0.45
20:LM:1565:MET:HE2	20:LM:1581:LEU:HD11	1.98	0.45
22:LO:343:ASP:OD2	67:SW:251:ARG:HD2	2.16	0.45
27:LT:489:GLU:HG3	27:LT:490:LEU:HD22	1.98	0.45
27:LT:661:LEU:HB2	27:LT:711:PRO:HG2	1.98	0.45
28:LU:433:VAL:HG23	28:LU:437:LYS:HZ2	1.81	0.45
29:LW:125:LYS:HB2	29:LW:128:THR:HG23	1.98	0.45
29:LW:439:GLN:HG3	29:LW:440:PRO:HD2	1.98	0.45
41:NJ:623:GLY:HA2	41:NJ:706:LEU:HG	1.98	0.45
41:NK:41:HIS:HA	41:NK:120:MET:HE1	1.99	0.45
43:NN:514:LYS:HA	43:NN:514:LYS:HD3	1.66	0.45
49:NW:333:THR:HG22	49:NW:335:LYS:H	1.80	0.45
52:SB:313:ALA:HA	52:SB:367:VAL:HG11	1.97	0.45
53:SD:284:LYS:HE3	59:SL:132:LEU:HA	1.98	0.45
61:SP:1504:LEU:HD13	61:SP:1517:ILE:HD12	1.99	0.45
61:SP:1653:MET:HA	61:SP:1656:LEU:HD12	1.97	0.45
2:L1:478:G:H2'	2:L1:479:C:C6	2.52	0.45
2:L1:1292:C:H1'	47:NT:140:TYR:CE1	2.51	0.45
17:LI:711:TYR:OH	21:LN:7:HIS:ND1	2.49	0.45
19:LK:481:VAL:O	19:LK:484:THR:HG23	2.17	0.45
20:LM:259:ALA:O	20:LM:263:MET:HG3	2.17	0.45
20:LM:668:LEU:HD12	20:LM:710:VAL:HG11	1.97	0.45
20:LM:1624:ASN:OD1	20:LM:1676:LEU:HD12	2.17	0.45
22:LO:107:ASP:OD1	22:LO:108:GLY:N	2.50	0.45
27:LT:765:LEU:HD12	27:LT:895:ALA:HB1	1.97	0.45
39:NH:339:GLU:O	39:NH:529:ARG:NH2	2.48	0.45
49:NW:341:ILE:HG22	49:NW:344:LEU:H	1.82	0.45
61:SP:1555:GLN:HE21	61:SP:1557:GLU:HB3	1.81	0.45
61:SP:1886:LYS:NZ	61:SP:1927:ILE:HD11	2.30	0.45
61:SP:2138:ILE:HD11	61:SP:2182:ASN:HB3	1.98	0.45
2:L1:157:U:O2'	2:L1:158:A:OP1	2.33	0.45
2:L1:1010:G:H2'	2:L1:1011:A:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:L7:170:VAL:HG13	8:L7:187:PHE:HB2	1.98	0.45
10:L9:87:LEU:HD11	10:L9:97:ILE:HG12	1.99	0.45
17:LI:508:PHE:O	17:LI:584:ARG:NH1	2.49	0.45
18:LJ:489:MET:CE	19:LK:571:LYS:HA	2.46	0.45
20:LM:740:LEU:O	20:LM:744:ILE:HG12	2.16	0.45
21:LN:30:ARG:NH1	21:LN:52:GLU:OE2	2.49	0.45
22:LO:316:GLU:OE1	22:LO:318:PRO:HD2	2.17	0.45
25:LR:745:GLU:HA	25:LR:748:LEU:HD12	1.98	0.45
39:NH:436:GLN:HG2	39:NH:524:LEU:HD21	1.98	0.45
41:NK:160:LEU:HD12	41:NK:163:VAL:HG21	1.99	0.45
57:SI:107:THR:HG23	57:SI:109:GLN:H	1.82	0.45
1:L0:863:C:N3	60:SM:11:GLU:HG2	2.32	0.45
2:L1:227:U:H4'	2:L1:228:C:O5'	2.16	0.45
2:L1:1311:C:H4'	71:SZ:241:LEU:HD11	1.99	0.45
21:LN:77:ALA:HB2	21:LN:107:MET:HE3	1.97	0.45
25:LR:165:ARG:HH22	25:LR:207:GLY:HA3	1.82	0.45
25:LR:475:GLN:NE2	25:LR:476:ARG:O	2.49	0.45
29:LW:121:LEU:HD13	64:SS:694:GLN:HG2	1.98	0.45
39:NH:234:LYS:HE2	39:NH:300:TRP:HB3	1.98	0.45
41:NJ:112:LYS:HB3	41:NJ:112:LYS:HE3	1.85	0.45
58:SK:101:ASN:HB2	58:SK:106:LEU:HD23	1.99	0.45
61:SP:1215:TYR:HA	61:SP:1218:LEU:HD13	1.98	0.45
2:L1:478:G:H2'	2:L1:479:C:H6	1.82	0.45
2:L1:975:G:O2'	38:NG:49:GLY:O	2.27	0.45
13:LD:48:LYS:O	13:LD:51:ILE:N	2.50	0.45
16:LH:630:GLN:HG3	16:LH:631:TRP:CD1	2.52	0.45
17:LI:159:PHE:CE1	17:LI:166:VAL:HB	2.52	0.45
18:LJ:346:LYS:HB2	26:LS:292:TYR:CE2	2.51	0.45
19:LK:497:MET:HG3	19:LK:498:PRO:HD2	1.98	0.45
19:LK:525:GLN:NE2	19:LK:529:CYS:SG	2.89	0.45
20:LM:417:LYS:HA	20:LM:417:LYS:HD3	1.73	0.45
20:LM:502:LEU:O	20:LM:506:MET:N	2.45	0.45
23:LP:46:ARG:NH1	28:LU:20:ASP:OD1	2.43	0.45
44:NO:30:CYS:SG	44:NO:31:SER:N	2.90	0.45
61:SP:1230:ASP:O	61:SP:1234:ASN:ND2	2.49	0.45
61:SP:1424:LEU:HB2	61:SP:1427:ILE:HD13	1.99	0.45
61:SP:1450:PHE:HA	61:SP:1453:PHE:CD2	2.52	0.45
2:L1:110:U:H2'	2:L1:111:A:C8	2.52	0.45
2:L1:639:C:H2'	2:L1:640:A:H8	1.82	0.45
2:L1:1373:C:H2'	2:L1:1374:C:C6	2.52	0.45
5:L4:55:ALA:HB1	5:L4:60:GLU:HG3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:L7:61:ILE:HD13	8:L7:180:LEU:HD11	1.99	0.45
16:LH:319:ARG:HG2	26:LS:374:GLU:HG2	1.99	0.45
17:LI:460:ILE:HG12	17:LI:465:LEU:HD23	1.99	0.45
17:LI:712:SER:OG	17:LI:714:GLU:OE2	2.34	0.45
20:LM:1966:LEU:HD22	20:LM:2026:GLN:HG3	1.99	0.45
21:LN:258:GLY:HA2	21:LN:290:VAL:HG23	1.98	0.45
24:LQ:463:VAL:HG11	24:LQ:468:GLN:HB2	1.98	0.45
24:LQ:473:THR:OG1	24:LQ:475:THR:O	2.23	0.45
27:LT:563:LEU:HB3	27:LT:577:VAL:HB	1.99	0.45
29:LW:242:ILE:HD13	29:LW:253:VAL:HG12	1.99	0.45
30:LZ:14:LYS:O	30:LZ:15:GLN:HG2	2.16	0.45
39:NH:1016:PRO:HA	39:NH:1019:ILE:HD12	1.99	0.45
46:NR:159:UNK:O	46:NR:163:UNK:N	2.50	0.45
61:SP:470:VAL:HG22	61:SP:529:ARG:HG3	1.99	0.45
61:SP:1783:ILE:HG13	61:SP:1834:LEU:HD21	1.99	0.45
61:SP:1845:SER:O	61:SP:1849:LYS:NZ	2.41	0.45
66:SU:181:ARG:O	66:SU:185:MET:HG2	2.15	0.45
2:L1:36:U:H2'	2:L1:37:C:C6	2.51	0.45
2:L1:191:A:N6	2:L1:208:G:O2'	2.48	0.45
2:L1:1844:U:H3	2:L1:1855:G:H1	1.65	0.45
2:L1:1852:C:H2'	2:L1:1853:C:C6	2.52	0.45
3:L2:31:G:H5''	3:L2:32:U:C2	2.52	0.45
16:LH:39:VAL:O	16:LH:53:LEU:HB2	2.17	0.45
17:LI:460:ILE:HG22	17:LI:492:GLN:HG3	1.99	0.45
18:LJ:478:ARG:NH1	18:LJ:479:GLU:OE2	2.50	0.45
20:LM:327:VAL:HG23	20:LM:330:LEU:HB2	1.97	0.45
21:LN:160:ILE:HB	21:LN:171:PHE:HB2	1.98	0.45
22:LO:601:HIS:HA	22:LO:604:LYS:HD3	1.99	0.45
23:LP:18:GLN:O	23:LP:22:ILE:HG12	2.16	0.45
23:LP:75:ILE:HD11	26:LS:80:LEU:HG	1.99	0.45
25:LR:253:LEU:HD21	25:LR:324:LEU:HD13	1.98	0.45
25:LR:436:PHE:CZ	25:LR:508:LEU:HD21	2.51	0.45
27:LT:216:TYR:HB3	27:LT:219:LYS:HB2	1.97	0.45
27:LT:535:ASP:OD1	27:LT:535:ASP:N	2.50	0.45
41:NK:266:LYS:HE3	41:NK:461:TYR:CG	2.52	0.45
48:NU:56:HIS:O	48:NU:60:ARG:HG2	2.17	0.45
49:NW:178:GLU:HB3	49:NW:196:ILE:HB	1.99	0.45
56:SH:94:GLY:HA2	56:SH:120:VAL:HG13	1.98	0.45
61:SP:427:ILE:HG21	61:SP:446:LEU:HD21	1.99	0.45
61:SP:1452:THR:O	61:SP:1456:ILE:HG12	2.16	0.45
65:ST:610:PRO:HD2	66:SU:445:TYR:HE1	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:ST:636:HIS:O	65:ST:639:ARG:NH1	2.50	0.45
2:L1:980:A:H2'	2:L1:981:A:C8	2.52	0.45
3:L2:30:A:O2'	3:L2:32:U:O4	2.30	0.45
19:LL:43:THR:HG23	19:LL:359:ILE:HG21	1.98	0.45
20:LM:1647:ASP:O	20:LM:1651:ILE:HG12	2.17	0.45
21:LN:461:LEU:O	21:LN:476:ALA:HA	2.17	0.45
27:LT:595:LEU:HB2	27:LT:609:ILE:HD11	1.99	0.45
27:LT:883:MET:HE2	27:LT:893:ALA:HB2	1.99	0.45
35:ND:240:ASN:HA	35:ND:243:ARG:HH21	1.82	0.45
40:NI:23:TYR:HE1	40:NI:43:ARG:HD3	1.82	0.45
46:NR:621:UNK:O	46:NR:625:UNK:N	2.50	0.45
56:SH:284:LEU:HA	56:SH:287:ILE:HD12	1.99	0.45
56:SH:368:LEU:O	57:SI:989:GLN:NE2	2.45	0.45
59:SL:189:MET:HE2	59:SL:191:ASP:HB2	1.99	0.45
62:SQ:682:ASP:OD1	62:SQ:683:GLY:N	2.50	0.45
2:L1:219:U:H2'	2:L1:220:U:C6	2.52	0.44
2:L1:618:C:H2'	2:L1:619:A:O4'	2.18	0.44
13:LD:82:MET:HE1	13:LD:87:VAL:HG23	1.99	0.44
16:LH:816:LEU:HB3	20:LM:933:GLU:HG2	1.97	0.44
19:LL:130:ASN:ND2	19:LL:171:VAL:O	2.47	0.44
23:LP:3:GLU:HG2	23:LP:4:ILE:HD12	1.99	0.44
23:LP:22:ILE:HD13	29:LW:98:PHE:CZ	2.49	0.44
25:LR:32:LEU:HG	25:LR:308:LEU:HD22	1.99	0.44
25:LR:151:PRO:HD3	25:LR:178:ARG:HH21	1.82	0.44
29:LW:229:LEU:HD21	29:LW:232:GLU:HB2	1.99	0.44
41:NK:28:VAL:HG12	41:NK:200:ILE:HG13	1.98	0.44
41:NK:284:ALA:HB2	41:NK:465:LEU:H	1.82	0.44
49:NW:167:ARG:HD3	50:NY:324:PRO:HG3	2.00	0.44
53:SC:92:ARG:HH11	70:SY:168:ARG:HG3	1.82	0.44
58:SJ:190:VAL:HG11	58:SJ:240:VAL:HG11	2.00	0.44
61:SP:1338:LYS:HD3	61:SP:1341:LYS:HZ3	1.81	0.44
61:SP:1649:TRP:CD1	61:SP:1778:ASN:HD21	2.35	0.44
1:L0:751:C:H2'	1:L0:752:C:C6	2.52	0.44
17:LI:406:MET:SD	17:LI:407:LYS:HG2	2.57	0.44
20:LM:135:VAL:HG22	20:LM:144:PHE:HD1	1.83	0.44
20:LM:1812:THR:O	20:LM:1816:THR:OG1	2.34	0.44
20:LM:1830:TYR:O	20:LM:1833:ILE:HG22	2.16	0.44
22:LO:217:CYS:HB3	22:LO:274:TYR:CE1	2.53	0.44
23:LP:213:SER:O	23:LP:217:LEU:HD23	2.17	0.44
25:LR:291:PRO:HD3	25:LR:376:THR:HG22	1.99	0.44
25:LR:294:GLU:HB2	25:LR:312:ALA:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:LS:319:VAL:HA	26:LS:334:HIS:HA	1.98	0.44
27:LT:851:GLY:O	27:LT:855:ILE:HG12	2.17	0.44
28:LU:192:MET:HE1	28:LU:226:MET:HA	1.99	0.44
28:LU:249:MET:HE3	28:LU:249:MET:HB3	1.83	0.44
34:NC:194:GLU:CD	34:NC:198:ARG:HE	2.25	0.44
41:NJ:866:LEU:HD21	41:NJ:895:PHE:HB2	1.99	0.44
50:NY:76:TRP:HZ3	50:NY:99:MET:HE3	1.82	0.44
57:SI:88:MET:HB3	57:SI:133:CYS:HB3	1.98	0.44
58:SK:44:ILE:HB	58:SK:197:VAL:HG22	1.99	0.44
61:SP:1543:THR:HA	61:SP:1579:LYS:HZ2	1.81	0.44
65:ST:571:VAL:HG11	66:SU:479:PHE:HB2	1.99	0.44
70:SY:33:LYS:HA	70:SY:33:LYS:HD3	1.86	0.44
2:L1:119:U:H2'	2:L1:120:U:H6	1.83	0.44
2:L1:1169:G:O6	57:SI:1256:LYS:NZ	2.32	0.44
3:L2:89:A:H5'	52:SB:336:PRO:HB3	1.99	0.44
8:L7:148:LEU:HD23	44:NO:42:MET:HE2	1.99	0.44
20:LM:1383:PHE:O	20:LM:1387:LEU:HG	2.18	0.44
20:LM:1422:GLN:O	20:LM:1426:LYS:HG2	2.17	0.44
20:LM:1573:THR:O	20:LM:1576:PHE:HB3	2.18	0.44
20:LM:1669:THR:O	20:LM:1673:THR:HG23	2.16	0.44
20:LM:1992:LEU:HD23	20:LM:1992:LEU:HA	1.88	0.44
24:LQ:660:TRP:CZ3	24:LQ:667:HIS:HB2	2.51	0.44
25:LR:81:LEU:O	25:LR:93:TRP:N	2.41	0.44
26:LS:346:SER:OG	26:LS:359:ASN:OD1	2.32	0.44
29:LW:243:ARG:HD3	29:LW:243:ARG:HA	1.82	0.44
34:NC:235:ASP:OD1	34:NC:259:ARG:NE	2.50	0.44
39:NH:186:ARG:HG2	39:NH:258:PRO:HG2	1.99	0.44
39:NH:892:PRO:HA	39:NH:893:PRO:HD3	1.89	0.44
41:NK:623:GLY:HA2	41:NK:706:LEU:HG	1.98	0.44
49:NW:282:ASP:OD1	49:NW:283:SER:N	2.49	0.44
56:SH:124:GLN:NE2	56:SH:260:ALA:O	2.42	0.44
58:SK:131:ASP:OD1	58:SK:132:ARG:N	2.49	0.44
61:SP:1399:SER:O	61:SP:1402:LYS:NZ	2.41	0.44
71:SZ:240:ASN:O	71:SZ:242:LYS:HG3	2.17	0.44
2:L1:103:A:H4'	2:L1:104:A:H8	1.81	0.44
2:L1:223:C:H2'	2:L1:224:A:H8	1.81	0.44
2:L1:498:C:H2'	2:L1:499:G:C8	2.53	0.44
2:L1:1355:C:H2'	2:L1:1356:G:O4'	2.17	0.44
9:L8:101:ILE:HD12	9:L8:190:LEU:HD11	1.99	0.44
16:LH:469:TYR:HD1	16:LH:495:SER:HB3	1.82	0.44
17:LI:474:MET:HE3	17:LI:496:ILE:HD12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:LM:1604:ILE:HD11	20:LM:1619:ALA:HA	1.98	0.44
20:LM:1951:PHE:HE1	20:LM:1954:PHE:HB2	1.82	0.44
21:LN:554:SER:HB3	21:LN:557:ASP:HB2	1.99	0.44
22:LO:54:THR:HG21	22:LO:74:ASP:HB3	2.00	0.44
22:LO:339:ASN:ND2	22:LO:343:ASP:OD1	2.39	0.44
39:NH:709:SER:O	39:NH:723:ARG:NH1	2.49	0.44
41:NJ:256:LYS:HD3	41:NJ:469:ILE:HG23	1.99	0.44
41:NK:131:PRO:HB3	41:NK:485:LEU:HD22	1.98	0.44
41:NK:425:LEU:HA	41:NK:428:ILE:HG22	2.00	0.44
57:SI:310:ILE:HD11	57:SI:886:VAL:HB	1.99	0.44
58:SJ:88:THR:O	58:SJ:92:LEU:HG	2.18	0.44
58:SK:56:LYS:O	65:ST:45:GLY:HA3	2.18	0.44
63:SR:66:ILE:HG23	65:ST:836:LEU:HD23	1.97	0.44
1:L0:799:C:O2'	1:L0:800:G:OP2	2.31	0.44
2:L1:337:C:H2'	2:L1:338:G:C8	2.52	0.44
5:L4:171:ASP:OD1	5:L4:171:ASP:N	2.49	0.44
7:L6:217:MET:HE3	7:L6:217:MET:HA	1.98	0.44
19:LL:575:LEU:O	19:LL:579:VAL:HG23	2.18	0.44
20:LM:1288:ILE:O	20:LM:1292:ILE:HG13	2.18	0.44
20:LM:1810:LYS:HE3	20:LM:1847:ILE:HD11	2.00	0.44
27:LT:460:ILE:HB	27:LT:473:TRP:HB2	1.99	0.44
27:LT:567:ASN:ND2	27:LT:574:ILE:HD11	2.33	0.44
29:LW:197:GLY:HA3	29:LW:215:ARG:HB3	2.00	0.44
29:LW:246:HIS:CG	29:LW:247:SER:H	2.35	0.44
38:NG:83:GLN:HA	38:NG:86:LYS:HZ3	1.82	0.44
39:NH:364:LYS:HE3	39:NH:364:LYS:HB3	1.81	0.44
41:NK:341:TYR:HB3	41:NK:360:VAL:HG12	1.99	0.44
41:NK:548:LEU:HD21	41:NK:556:LEU:HD11	2.00	0.44
42:NM:40:ASN:OD1	42:NM:41:ILE:N	2.51	0.44
45:NQ:33:MET:HE2	45:NQ:48:SER:HA	1.99	0.44
47:NT:104:LYS:HD3	47:NT:118:ARG:HH21	1.82	0.44
47:NT:133:ALA:HB3	47:NT:140:TYR:HB3	1.99	0.44
53:SC:224:ARG:HA	53:SC:253:PHE:CZ	2.53	0.44
60:SM:6:ALA:HB1	60:SM:10:ARG:HH12	1.82	0.44
61:SP:1656:LEU:O	61:SP:1660:ILE:HD12	2.18	0.44
2:L1:558:G:H2'	2:L1:559:G:C8	2.53	0.44
3:L2:144:C:H3'	3:L2:145:U:C5'	2.48	0.44
5:L4:48:LEU:HD21	5:L4:64:ILE:HG21	2.00	0.44
5:L4:248:ILE:HG23	5:L4:250:GLU:H	1.83	0.44
20:LM:586:GLU:HA	20:LM:633:LEU:HD11	2.00	0.44
20:LM:754:HIS:CD2	20:LM:755:ILE:HG23	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:LM:1423:TYR:OH	20:LM:1440:LEU:HG	2.17	0.44
26:LS:313:THR:OG1	26:LS:344:VAL:O	2.35	0.44
26:LS:405:GLU:HG2	26:LS:407:TYR:HE1	1.83	0.44
27:LT:826:ASP:OD1	27:LT:827:PHE:N	2.50	0.44
27:LT:869:SER:HB3	27:LT:872:VAL:HG23	2.00	0.44
28:LU:234:LYS:HB3	28:LU:444:VAL:HB	2.00	0.44
32:NA:532:ALA:HA	32:NA:548:LEU:HD13	2.00	0.44
35:ND:235:ILE:HG23	35:ND:236:GLN:HG2	1.99	0.44
39:NH:965:PRO:HA	39:NH:969:ILE:HD11	2.00	0.44
41:NK:721:LYS:HE2	41:NK:721:LYS:HB3	1.86	0.44
51:SA:123:ARG:NH2	53:SD:254:LEU:O	2.51	0.44
53:SC:164:LEU:HB3	53:SC:233:ILE:HG12	1.99	0.44
54:SE:64:GLU:HA	54:SE:67:LEU:HG	1.99	0.44
55:SG:171:ILE:HG12	55:SG:183:VAL:HG22	2.00	0.44
61:SP:217:HIS:HB2	61:SP:220:LYS:HE2	1.99	0.44
61:SP:1578:MET:HA	61:SP:1586:ARG:HG3	2.00	0.44
65:ST:528:MET:O	65:ST:532:ILE:HG13	2.17	0.44
67:SW:220:MET:HE2	67:SW:244:VAL:HG13	2.00	0.44
71:SZ:232:GLN:OE1	71:SZ:235:ARG:NE	2.43	0.44
2:L1:589:G:HO2'	2:L1:590:A:P	2.40	0.44
2:L1:1312:G:O6	11:LA:36:ARG:NH1	2.51	0.44
17:LI:429:PHE:O	17:LI:432:VAL:HB	2.17	0.44
18:LJ:232:TRP:CH2	18:LJ:240:LEU:HD12	2.52	0.44
20:LM:180:THR:HA	20:LM:183:TYR:CE2	2.53	0.44
20:LM:1696:ALA:O	20:LM:1700:ILE:HG12	2.17	0.44
20:LM:1806:LEU:O	20:LM:1809:LEU:HG	2.18	0.44
22:LO:234:ALA:HA	22:LO:237:LEU:HG	2.00	0.44
23:LP:24:LEU:O	23:LP:71:ARG:NH1	2.48	0.44
23:LP:397:GLU:HA	23:LP:400:ARG:HH22	1.83	0.44
24:LQ:145:LEU:HD12	24:LQ:176:TRP:CE3	2.53	0.44
24:LQ:904:TYR:CD1	27:LT:905:LEU:HD22	2.52	0.44
29:LW:237:GLU:OE1	29:LW:257:ARG:N	2.47	0.44
39:NH:272:ASN:ND2	39:NH:292:PRO:O	2.51	0.44
39:NH:1014:LEU:HD11	39:NH:1082:ILE:HG13	1.98	0.44
56:SH:242:GLY:HA2	56:SH:275:LEU:HD21	2.00	0.44
61:SP:1137:ARG:HA	61:SP:1140:ILE:HG12	2.00	0.44
67:SW:103:LEU:HB3	67:SW:129:ALA:HB1	2.00	0.44
1:L0:817:U:H4'	26:LS:517:LYS:HG2	1.99	0.44
2:L1:640:A:H2'	2:L1:641:A:C8	2.52	0.44
2:L1:1125:C:H2'	2:L1:1126:G:C8	2.53	0.44
11:LA:99:LYS:HE2	11:LA:99:LYS:HB3	1.75	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LF:7:ILE:HD12	14:LF:47:MET:HE1	2.00	0.44
17:LI:404:THR:HG21	17:LI:416:GLU:HG3	1.99	0.44
20:LM:1400:VAL:HG22	20:LM:1446:PHE:CZ	2.53	0.44
21:LN:130:ILE:HG12	21:LN:135:ILE:HG22	1.99	0.44
22:LO:109:ARG:HG3	22:LO:110:LYS:HG3	2.00	0.44
25:LR:73:ASP:OD2	25:LR:74:LEU:N	2.51	0.44
25:LR:402:ILE:HB	25:LR:415:ALA:HB3	1.99	0.44
27:LT:258:ALA:HB3	27:LT:261:VAL:HB	2.00	0.44
28:LU:66:ARG:NH1	59:SL:127:PRO:HD3	2.21	0.44
28:LU:180:ILE:HD13	28:LU:226:MET:HG3	1.99	0.44
29:LW:196:PHE:HA	29:LW:216:ARG:HH11	1.81	0.44
32:NA:480:LEU:HD13	32:NA:523:GLU:HG3	2.00	0.44
41:NJ:687:PRO:C	41:NJ:688:ARG:HE	2.25	0.44
41:NK:577:ILE:HD12	41:NK:648:LEU:HD22	1.99	0.44
46:NR:363:UNK:O	46:NR:367:UNK:N	2.50	0.44
50:NY:179:THR:HG21	50:NY:202:VAL:HG23	1.99	0.44
53:SC:104:ASP:O	70:SY:125:LEU:HD13	2.18	0.44
53:SD:284:LYS:HE3	59:SL:133:PRO:HD3	1.98	0.44
57:SI:1237:PHE:O	57:SI:1241:GLN:HG2	2.18	0.44
58:SJ:96:MET:HA	58:SJ:101:ASN:ND2	2.31	0.44
66:SU:261:LYS:HE3	66:SU:261:LYS:HB2	1.86	0.44
2:L1:615:C:H2'	2:L1:616:A:H8	1.82	0.44
16:LH:222:HIS:CE1	16:LH:228:ARG:HH11	2.36	0.44
20:LM:1663:GLN:HB2	20:LM:1666:ASN:ND2	2.33	0.44
21:LN:271:ASN:OD1	21:LN:272:SER:N	2.51	0.44
39:NH:112:VAL:HG22	39:NH:220:PHE:HE1	1.83	0.44
41:NK:365:ARG:HG3	57:SI:667:TRP:CD1	2.52	0.44
46:NR:140:UNK:O	46:NR:144:UNK:N	2.51	0.44
48:NU:5:ARG:HH11	48:NU:53:TYR:HD1	1.65	0.44
49:NW:74:LYS:O	49:NW:76:ARG:HG3	2.18	0.44
52:SB:150:ARG:NE	53:SC:214:ILE:O	2.51	0.44
55:SG:323:HIS:CE1	55:SG:342:ALA:HB2	2.53	0.44
61:SP:248:LYS:HA	61:SP:248:LYS:HD3	1.74	0.44
61:SP:740:ILE:HD12	61:SP:827:ALA:HB2	2.00	0.44
61:SP:1516:GLU:HA	61:SP:1520:ARG:HG2	2.00	0.44
67:SW:108:ARG:CZ	67:SW:119:ARG:HH22	2.31	0.44
1:L0:854:U:H4'	1:L0:855:G:O5'	2.17	0.43
2:L1:1109:C:H1'	28:LU:424:HIS:O	2.18	0.43
2:L1:1284:A:H4'	2:L1:1285:G:H5''	1.99	0.43
2:L1:1854:U:H2'	2:L1:1855:G:H8	1.82	0.43
14:LF:58:PHE:HE1	14:LF:74:MET:HE2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:LI:692:GLU:HG2	19:LK:555:MET:HB3	2.00	0.43
22:LO:96:LYS:HD2	22:LO:96:LYS:HA	1.86	0.43
26:LS:273:ASN:HB2	26:LS:292:TYR:CE1	2.53	0.43
28:LU:3:VAL:HG22	29:LW:160:LEU:HD13	1.99	0.43
36:NE:212:LYS:O	36:NE:216:GLU:HG2	2.18	0.43
41:NJ:132:ASN:HD21	41:NJ:543:ASN:HB2	1.81	0.43
56:SH:67:ASN:HB2	56:SH:72:THR:HG22	1.99	0.43
56:SH:123:ASP:OD1	56:SH:124:GLN:N	2.48	0.43
57:SI:381:SER:HB2	57:SI:386:LYS:HE3	2.00	0.43
61:SP:1398:PHE:CD2	61:SP:1410:LEU:HD21	2.53	0.43
66:SU:397:ARG:HG3	66:SU:398:HIS:ND1	2.32	0.43
2:L1:306:C:O2	9:L8:53:LYS:NZ	2.45	0.43
8:L7:64:VAL:O	8:L7:97:GLN:N	2.49	0.43
11:LA:24:THR:O	11:LA:27:ILE:HG22	2.18	0.43
12:LC:47:LEU:O	12:LC:50:LYS:HB2	2.18	0.43
12:LC:97:GLN:HB2	12:LC:105:LYS:HG3	1.99	0.43
20:LM:2066:ASN:HD22	20:LM:2102:LEU:HB3	1.82	0.43
22:LO:847:PHE:O	22:LO:850:LYS:HG3	2.18	0.43
23:LP:494:ARG:NH1	23:LP:532:TYR:OH	2.42	0.43
24:LQ:482:ASP:HB2	24:LQ:485:SER:HB2	2.00	0.43
25:LR:524:LEU:HA	25:LR:540:SER:HA	1.99	0.43
26:LS:245:ASN:ND2	26:LS:543:GLY:O	2.47	0.43
41:NJ:209:ILE:O	57:SI:382:THR:OG1	2.36	0.43
42:NM:224:GLU:OE1	42:NM:227:LYS:N	2.50	0.43
46:NR:746:UNK:O	46:NR:750:UNK:N	2.51	0.43
56:SH:124:GLN:O	57:SI:736:ARG:NH1	2.51	0.43
59:SL:86:LEU:HD23	59:SL:129:PHE:CZ	2.53	0.43
61:SP:31:ILE:HD11	61:SP:195:PHE:HB2	2.01	0.43
61:SP:1235:VAL:HA	61:SP:1238:ILE:HD12	1.99	0.43
61:SP:2088:LEU:HD13	61:SP:2132:GLY:HA3	2.00	0.43
65:ST:285:HIS:HA	65:ST:288:LYS:HZ3	1.84	0.43
2:L1:145:G:H2'	2:L1:146:G:C8	2.53	0.43
2:L1:979:C:H2'	2:L1:980:A:H8	1.82	0.43
4:L3:36:VAL:HG23	4:L3:40:TYR:CD2	2.41	0.43
5:L4:212:ASP:OD1	5:L4:216:ASN:N	2.51	0.43
8:L7:37:LYS:HG2	8:L7:41:ARG:HG3	2.00	0.43
11:LA:55:ASN:OD1	11:LA:81:ASP:HA	2.18	0.43
12:LC:138:ARG:HG3	22:LO:535:ARG:HG2	2.00	0.43
16:LH:318:HIS:HE2	16:LH:322:GLU:HB3	1.83	0.43
20:LM:302:SER:HA	20:LM:305:ILE:HD12	1.99	0.43
20:LM:1323:ILE:HD12	20:LM:1353:VAL:HG21	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:LQ:369:ASP:OD1	24:LQ:370:LEU:N	2.52	0.43
26:LS:407:TYR:CD1	26:LS:419:ARG:HG2	2.54	0.43
39:NH:140:PRO:HA	39:NH:541:PRO:HG3	2.00	0.43
41:NJ:290:LYS:HD3	41:NJ:410:ALA:HB1	2.00	0.43
48:NU:8:THR:HA	48:NU:11:LYS:NZ	2.33	0.43
50:NY:210:MET:HA	50:NY:210:MET:HE3	1.99	0.43
58:SJ:44:ILE:HB	58:SJ:197:VAL:HG22	2.00	0.43
58:SJ:102:ARG:NH2	58:SK:222:TYR:OH	2.51	0.43
61:SP:1670:GLN:HG2	61:SP:1816:GLU:HG3	2.00	0.43
61:SP:1976:GLN:NE2	61:SP:1979:LYS:HD2	2.33	0.43
2:L1:1336:C:H2'	2:L1:1337:C:C6	2.53	0.43
2:L1:1794:C:H2'	2:L1:1795:G:H8	1.84	0.43
10:L9:54:ARG:HH21	59:SL:96:ALA:HB2	1.84	0.43
16:LH:557:LEU:HD11	16:LH:612:PRO:HB3	2.00	0.43
20:LM:1520:PHE:HD2	20:LM:1521:MET:HE2	1.83	0.43
23:LP:227:LYS:HE3	23:LP:227:LYS:HB3	1.76	0.43
24:LQ:902:LEU:HD23	25:LR:761:LEU:HD22	2.01	0.43
27:LT:845:ASN:O	27:LT:848:LYS:HG2	2.19	0.43
28:LU:283:SER:HB3	28:LU:302:PHE:HB3	2.01	0.43
28:LU:418:GLU:OE1	28:LU:421:ARG:NH1	2.51	0.43
39:NH:445:MET:HE3	39:NH:445:MET:HB3	1.78	0.43
40:NI:42:VAL:HG12	40:NI:63:VAL:HG13	2.00	0.43
58:SJ:150:ASP:OD1	58:SJ:150:ASP:N	2.52	0.43
61:SP:118:LEU:HB3	61:SP:121:ASP:HB2	2.00	0.43
61:SP:276:MET:O	61:SP:280:THR:OG1	2.33	0.43
61:SP:457:PRO:HD2	61:SP:569:ASN:HD21	1.82	0.43
2:L1:318:A:H61	7:L6:186:GLN:HE22	1.67	0.43
2:L1:989:C:OP2	42:NM:155:TYR:OH	2.26	0.43
3:L2:88:G:O6	52:SB:333:ARG:NH1	2.51	0.43
6:L5:30:ILE:HG23	6:L5:117:ILE:HD11	2.01	0.43
8:L7:153:LEU:HD21	28:LU:196:PHE:CD2	2.54	0.43
20:LM:363:THR:HG22	20:LM:417:LYS:HD2	2.00	0.43
20:LM:1737:MET:HE1	20:LM:1767:VAL:HG11	2.01	0.43
20:LM:1790:GLU:OE1	20:LM:1806:LEU:HD22	2.18	0.43
26:LS:486:GLU:OE1	26:LS:553:TYR:OH	2.31	0.43
46:NR:810:UNK:O	46:NR:814:UNK:N	2.51	0.43
52:SB:64:MET:CE	53:SC:222:LYS:HA	2.48	0.43
61:SP:2186:CYS:HA	61:SP:2189:ILE:HD12	2.00	0.43
3:L2:50:U:H2'	3:L2:51:C:C6	2.54	0.43
4:L3:23:ARG:NH2	18:LJ:80:LYS:HA	2.34	0.43
16:LH:614:GLU:HG3	16:LH:616:ARG:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:LJ:264:LEU:HB3	18:LJ:295:LEU:HD21	1.99	0.43
20:LM:611:ASN:H	20:LM:619:MET:HE3	1.82	0.43
22:LO:590:GLY:HA2	22:LO:656:GLU:HA	2.00	0.43
24:LQ:200:LEU:HD22	24:LQ:308:ILE:HD13	2.00	0.43
41:NK:508:TYR:N	41:NK:558:CYS:O	2.51	0.43
48:NU:55:THR:HA	48:NU:58:MET:HB3	1.99	0.43
57:SI:956:LEU:HD22	57:SI:968:LEU:HD11	2.00	0.43
61:SP:977:ARG:NH1	61:SP:987:GLU:OE1	2.49	0.43
61:SP:1341:LYS:O	61:SP:1344:LYS:NZ	2.52	0.43
8:L7:30:LEU:O	8:L7:34:SER:HB3	2.18	0.43
8:L7:64:VAL:HB	8:L7:72:PHE:CE2	2.51	0.43
9:L8:61:ASP:OD2	9:L8:61:ASP:N	2.52	0.43
16:LH:345:ARG:HE	16:LH:426:LYS:NZ	2.16	0.43
17:LI:509:LEU:HD21	17:LI:616:PHE:HB2	2.01	0.43
17:LI:690:LYS:O	19:LL:569:HIS:ND1	2.50	0.43
20:LM:502:LEU:HD11	20:LM:518:ILE:HG12	2.01	0.43
20:LM:1518:VAL:HB	20:LM:1590:LYS:HD3	2.00	0.43
20:LM:1587:LEU:O	20:LM:1591:VAL:N	2.51	0.43
21:LN:363:THR:OG1	21:LN:374:PRO:O	2.37	0.43
21:LN:404:TRP:HE1	21:LN:449:SER:HB2	1.83	0.43
21:LN:502:SER:HB3	21:LN:508:VAL:HG22	2.01	0.43
25:LR:317:LEU:HD12	25:LR:326:LEU:HD11	2.01	0.43
25:LR:517:PHE:HE1	25:LR:553:PHE:HA	1.84	0.43
27:LT:248:VAL:HG11	27:LT:268:SER:H	1.84	0.43
39:NH:267:LEU:HD22	39:NH:298:ASN:HA	2.01	0.43
39:NH:477:ARG:HB2	39:NH:478:PRO:HD3	2.01	0.43
40:NI:63:VAL:O	40:NI:119:ALA:N	2.39	0.43
61:SP:1378:GLN:CD	61:SP:1413:VAL:HA	2.43	0.43
61:SP:1631:ASN:OD1	61:SP:1632:ILE:HD12	2.19	0.43
61:SP:1985:LYS:HG3	61:SP:2083:PHE:HE2	1.83	0.43
2:L1:285:U:H2'	2:L1:286:U:C6	2.54	0.43
2:L1:1387:G:H3'	2:L1:1388:A:H8	1.84	0.43
5:L4:54:TYR:O	14:LF:15:ASN:ND2	2.52	0.43
5:L4:176:ASP:OD1	5:L4:177:THR:N	2.51	0.43
9:L8:64:ASN:HA	9:L8:75:LYS:HA	2.01	0.43
9:L8:80:ASP:OD2	9:L8:81:VAL:N	2.52	0.43
20:LM:249:GLY:HA2	20:LM:257:TYR:CE2	2.54	0.43
20:LM:2114:MET:HE1	61:SP:32:HIS:HA	2.00	0.43
25:LR:524:LEU:HD23	25:LR:538:THR:HB	2.01	0.43
28:LU:9:ASN:HB2	28:LU:12:ASN:ND2	2.33	0.43
28:LU:164:HIS:CE1	28:LU:169:ALA:HA	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:LW:355:ILE:HG13	64:SS:667:VAL:HG13	2.00	0.43
41:NJ:330:PHE:HA	41:NJ:335:TYR:HD2	1.84	0.43
41:NK:285:ALA:HB3	41:NK:288:ARG:HE	1.84	0.43
41:NK:587:ARG:O	41:NK:590:ILE:HG22	2.19	0.43
50:NY:239:TRP:HA	50:NY:242:PHE:HD2	1.84	0.43
55:SG:349:LEU:HD11	55:SG:412:LEU:HD13	2.00	0.43
60:SM:97:LEU:HD22	60:SM:141:GLU:HG2	2.01	0.43
61:SP:635:GLN:HE21	61:SP:722:ARG:HE	1.65	0.43
61:SP:1204:LYS:O	61:SP:1208:ILE:HG12	2.19	0.43
66:SU:186:GLN:NE2	66:SU:190:ASP:OD1	2.51	0.43
66:SU:241:LYS:HB2	66:SU:247:GLU:HG3	2.00	0.43
12:LC:63:PHE:CZ	12:LC:92:LEU:HD22	2.54	0.43
16:LH:57:ARG:HD3	16:LH:57:ARG:HA	1.81	0.43
17:LI:658:PHE:HZ	18:LJ:489:MET:HB3	1.84	0.43
20:LM:558:LEU:HD11	20:LM:602:CYS:HB2	2.01	0.43
26:LS:170:GLU:CD	26:LS:181:ARG:HH12	2.25	0.43
26:LS:183:LYS:HB2	26:LS:183:LYS:HE2	1.82	0.43
26:LS:279:GLN:HB3	26:LS:286:PRO:HD2	2.00	0.43
29:LW:343:LEU:O	29:LW:352:LEU:N	2.44	0.43
48:NU:54:VAL:O	48:NU:58:MET:N	2.43	0.43
49:NW:119:ILE:HD11	49:NW:133:ILE:HB	2.01	0.43
50:NY:101:VAL:HG21	50:NY:116:ALA:HB1	2.01	0.43
59:SL:113:LEU:HB3	59:SL:117:TYR:CD1	2.53	0.43
66:SU:277:HIS:CE1	66:SU:346:ARG:HH22	2.36	0.43
66:SU:310:ASN:HD22	66:SU:346:ARG:NH2	2.17	0.43
70:SY:116:ILE:HG23	70:SY:202:LEU:HD11	2.01	0.43
2:L1:175:A:H2'	2:L1:176:U:C6	2.54	0.43
2:L1:219:U:H2'	2:L1:220:U:H6	1.84	0.43
2:L1:1289:U:H2'	2:L1:1290:G:C8	2.54	0.43
2:L1:1670:C:OP2	60:SM:91:ARG:NH1	2.52	0.43
7:L6:188:LYS:O	7:L6:192:ILE:HG12	2.19	0.43
9:L8:192:GLY:O	9:L8:195:LEU:N	2.51	0.43
10:L9:131:ARG:HA	10:L9:131:ARG:HD2	1.80	0.43
16:LH:152:ASP:OD1	16:LH:153:TYR:N	2.50	0.43
18:LJ:173:SER:OG	18:LJ:179:LEU:HB3	2.19	0.43
22:LO:705:VAL:HA	22:LO:721:THR:HG22	2.00	0.43
23:LP:12:ARG:NH2	23:LP:57:TYR:OH	2.52	0.43
23:LP:580:GLU:OE2	23:LP:580:GLU:N	2.42	0.43
24:LQ:680:CYS:SG	24:LQ:681:LEU:N	2.92	0.43
26:LS:357:LEU:HD11	26:LS:365:LEU:HB3	2.00	0.43
27:LT:267:MET:HE2	27:LT:267:MET:HB3	1.98	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:LT:491:LYS:HE2	27:LT:491:LYS:HB2	1.82	0.43
28:LU:234:LYS:HD2	28:LU:444:VAL:HG21	2.00	0.43
37:NF:83:ASP:OD1	37:NF:84:LEU:N	2.52	0.43
41:NJ:388:ASP:OD1	41:NJ:389:GLU:N	2.51	0.43
41:NK:612:GLN:HB3	41:NK:774:ARG:HH12	1.83	0.43
42:NM:52:THR:HG23	42:NM:57:ILE:HA	2.01	0.43
49:NW:143:HIS:CD2	49:NW:145:PRO:HD2	2.54	0.43
53:SC:155:ILE:HG22	53:SC:157:ILE:HG12	2.01	0.43
58:SJ:51:SER:OG	58:SJ:83:ALA:HA	2.19	0.43
58:SJ:124:THR:HG22	58:SJ:155:LEU:HB3	2.01	0.43
61:SP:1637:THR:HG23	61:SP:1676:LEU:HD23	2.01	0.43
64:SS:720:LYS:HE3	64:SS:720:LYS:HB3	1.92	0.43
66:SU:284:LEU:HD23	66:SU:287:PRO:HA	2.00	0.43
66:SU:297:ALA:HB1	66:SU:304:LEU:HD21	2.00	0.43
2:L1:980:A:H2'	2:L1:981:A:H8	1.84	0.42
2:L1:1384:C:H2'	2:L1:1385:G:C8	2.54	0.42
2:L1:1687:C:H2'	2:L1:1688:C:C6	2.54	0.42
8:L7:142:LYS:HE2	8:L7:156:VAL:HG22	2.00	0.42
14:LF:13:MET:SD	14:LF:22:GLN:NE2	2.85	0.42
14:LF:55:ILE:HG13	14:LF:75:ILE:HD13	2.01	0.42
16:LH:508:GLU:CD	16:LH:553:SER:HB2	2.44	0.42
17:LI:682:ILE:HD11	19:LK:566:SER:HA	2.01	0.42
19:LL:321:THR:HG1	19:LL:331:LYS:N	2.17	0.42
20:LM:1334:VAL:HB	20:LM:1339:ASP:HB3	2.01	0.42
20:LM:1396:LEU:O	20:LM:1400:VAL:HG23	2.19	0.42
21:LN:100:PHE:CZ	53:SC:288:GLN:HG3	2.53	0.42
24:LQ:445:THR:HG22	24:LQ:447:GLN:OE1	2.18	0.42
25:LR:345:PRO:HG2	25:LR:346:GLU:OE1	2.19	0.42
27:LT:207:ILE:HG12	27:LT:222:LEU:HD22	2.00	0.42
29:LW:198:PRO:HB3	29:LW:467:THR:HG22	2.01	0.42
39:NH:266:ARG:HD2	39:NH:266:ARG:HA	1.83	0.42
47:NT:99:LYS:HB2	47:NT:99:LYS:HE2	1.84	0.42
53:SC:97:PHE:CE1	53:SC:109:LYS:HE3	2.54	0.42
54:SF:36:ARG:HA	54:SF:36:ARG:HD2	1.81	0.42
61:SP:1390:PHE:C	61:SP:1393:PRO:HD2	2.44	0.42
61:SP:1398:PHE:HA	61:SP:1401:ILE:HG22	2.01	0.42
61:SP:1895:GLY:O	61:SP:1898:VAL:HG22	2.19	0.42
3:L2:178:G:H1'	3:L2:183:G:C2	2.54	0.42
4:L3:26:ILE:HD12	4:L3:59:LEU:HD11	2.00	0.42
14:LF:12:PHE:HZ	14:LF:21:LYS:HD3	1.83	0.42
16:LH:130:VAL:HG21	16:LH:147:LEU:HD12	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LH:297:SER:HB2	16:LH:306:CYS:SG	2.59	0.42
20:LM:1755:VAL:O	20:LM:1758:LEU:HG	2.18	0.42
20:LM:2085:LEU:HD23	20:LM:2124:GLN:HG3	2.01	0.42
21:LN:602:TYR:HA	21:LN:648:LYS:O	2.19	0.42
22:LO:742:ASP:OD1	22:LO:743:THR:N	2.51	0.42
23:LP:400:ARG:HG2	23:LP:431:HIS:HB3	2.02	0.42
28:LU:127:VAL:HG11	28:LU:159:TYR:HB2	2.01	0.42
30:LZ:2:VAL:HG23	30:LZ:3:ARG:H	1.84	0.42
52:SB:59:ALA:HA	52:SB:69:ASN:OD1	2.19	0.42
54:SF:50:ILE:HA	54:SF:106:ILE:HD12	2.01	0.42
55:SG:382:VAL:HG12	55:SG:393:THR:HG22	2.01	0.42
65:ST:548:TYR:O	65:ST:552:THR:HG23	2.19	0.42
2:L1:375:U:H2'	2:L1:376:A:H8	1.82	0.42
2:L1:993:G:OP1	2:L1:1131:G:N2	2.48	0.42
2:L1:1091:C:H2'	2:L1:1092:G:C8	2.54	0.42
2:L1:1387:G:C2	2:L1:1388:A:H1'	2.54	0.42
3:L2:9:A:H2'	3:L2:10:C:C6	2.53	0.42
3:L2:25:U:O4	28:LU:389:ARG:NH1	2.52	0.42
4:L3:66:ARG:O	4:L3:70:ILE:HG13	2.18	0.42
11:LA:51:VAL:HG22	11:LA:77:ILE:HG22	2.02	0.42
20:LM:99:ILE:HD11	20:LM:198:LYS:HE3	2.02	0.42
20:LM:1420:PHE:HB3	20:LM:1516:LEU:HD21	2.01	0.42
21:LN:39:THR:HA	21:LN:55:PHE:O	2.19	0.42
22:LO:202:ASP:OD1	22:LO:216:GLN:HA	2.20	0.42
25:LR:354:SER:OG	25:LR:360:LYS:NZ	2.52	0.42
39:NH:376:ARG:O	39:NH:380:GLN:HG3	2.19	0.42
41:NK:267:PHE:HZ	41:NK:282:LEU:HD11	1.84	0.42
46:NR:304:UNK:O	46:NR:308:UNK:N	2.52	0.42
47:NT:104:LYS:HE3	47:NT:105:TYR:CE1	2.54	0.42
49:NW:249:THR:HA	49:NW:274:PRO:HB3	2.01	0.42
53:SC:295:GLU:OE2	70:SY:136:HIS:NE2	2.52	0.42
54:SF:84:ARG:HB2	55:SG:375:GLN:HE21	1.84	0.42
56:SH:46:ASP:OD1	56:SH:47:PHE:N	2.52	0.42
56:SH:156:ARG:HG2	56:SH:166:GLU:HB3	2.01	0.42
3:L2:40:U:H5'	28:LU:18:LYS:HE3	2.01	0.42
8:L7:153:LEU:HD21	28:LU:196:PHE:HD2	1.84	0.42
16:LH:545:LEU:HD11	16:LH:556:LEU:HD21	2.01	0.42
17:LI:609:PRO:HB2	17:LI:612:HIS:ND1	2.34	0.42
18:LJ:240:LEU:HD21	18:LJ:243:SER:HB2	2.01	0.42
20:LM:1522:SER:HA	20:LM:1594:LEU:HD11	2.00	0.42
25:LR:237:GLU:OE1	25:LR:266:GLY:HA3	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:LT:210:ILE:HG22	27:LT:222:LEU:HD23	2.01	0.42
27:LT:901:LEU:O	27:LT:905:LEU:HB2	2.19	0.42
38:NG:42:VAL:HG13	38:NG:81:VAL:HG21	2.00	0.42
47:NT:121:CYS:HB3	47:NT:126:CYS:HB3	2.02	0.42
48:NU:5:ARG:HG2	48:NU:49:LYS:NZ	2.35	0.42
49:NW:73:TYR:O	49:NW:76:ARG:NH1	2.52	0.42
53:SC:239:GLN:O	53:SC:242:GLN:HG3	2.19	0.42
57:SI:930:ARG:NH1	63:SR:136:GLY:O	2.47	0.42
61:SP:383:THR:HG23	61:SP:384:LEU:HD22	2.01	0.42
61:SP:461:SER:H	61:SP:651:ARG:HH21	1.68	0.42
61:SP:1325:ASN:HD21	61:SP:1328:GLN:HG3	1.84	0.42
70:SY:164:ARG:HH21	70:SY:167:ASN:HB3	1.84	0.42
71:SZ:349:LYS:HB3	71:SZ:388:ARG:HD3	2.01	0.42
1:L0:856:C:H2'	1:L0:857:C:C6	2.54	0.42
2:L1:19:A:O2'	2:L1:20:G:O4'	2.37	0.42
11:LA:80:ASP:OD1	11:LA:80:ASP:N	2.53	0.42
19:LL:510:THR:O	19:LL:514:GLN:NE2	2.43	0.42
20:LM:698:LEU:HB2	20:LM:775:LEU:HD22	2.01	0.42
20:LM:1008:TYR:OH	20:LM:1033:GLN:O	2.37	0.42
20:LM:1508:LYS:HA	20:LM:1511:ARG:HE	1.84	0.42
20:LM:1789:LEU:HA	20:LM:1792:ILE:HG22	2.00	0.42
21:LN:404:TRP:NE1	21:LN:449:SER:HB2	2.35	0.42
22:LO:800:GLU:OE2	22:LO:837:ARG:NH2	2.39	0.42
24:LQ:544:ARG:HD2	24:LQ:544:ARG:HA	1.83	0.42
24:LQ:839:PHE:O	24:LQ:843:ILE:HG12	2.20	0.42
37:NF:42:LYS:HD2	37:NF:42:LYS:HA	1.76	0.42
39:NH:153:ARG:HE	39:NH:188:ILE:HG22	1.85	0.42
39:NH:303:GLN:HG3	73:NH:3000:ATP:C2	2.55	0.42
41:NJ:125:ASP:OD1	41:NJ:152:ARG:NH2	2.52	0.42
41:NJ:266:LYS:HD2	41:NJ:461:TYR:CG	2.54	0.42
41:NJ:617:ASP:OD1	41:NJ:618:PHE:N	2.52	0.42
41:NK:280:VAL:HA	41:NK:461:TYR:HB2	2.01	0.42
41:NK:859:LEU:HD22	41:NK:898:ILE:HG12	2.01	0.42
51:SA:249:ARG:HA	51:SA:249:ARG:HD3	1.92	0.42
57:SI:924:MET:HE3	57:SI:1014:VAL:HG22	2.00	0.42
65:ST:702:TYR:HB3	65:ST:705:LEU:HD12	2.01	0.42
2:L1:74:G:H1'	2:L1:76:U:OP1	2.20	0.42
2:L1:639:C:H2'	2:L1:640:A:C8	2.54	0.42
2:L1:1373:C:H2'	2:L1:1374:C:H6	1.85	0.42
6:L5:99:ILE:HD13	6:L5:171:GLU:HG3	2.00	0.42
8:L7:192:PHE:CZ	45:NQ:12:PRO:HA	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LA:95:ASP:OD1	11:LA:95:ASP:N	2.53	0.42
16:LH:96:PHE:CE1	16:LH:134:LEU:HB3	2.55	0.42
16:LH:271:VAL:HG13	16:LH:287:PRO:HA	2.02	0.42
16:LH:826:TRP:CZ3	20:LM:849:MET:HE1	2.54	0.42
17:LI:401:LEU:O	17:LI:405:ILE:HG13	2.19	0.42
20:LM:1265:LYS:HE2	20:LM:1265:LYS:HB3	1.76	0.42
23:LP:14:PRO:HA	23:LP:17:GLU:HG2	2.02	0.42
25:LR:160:HIS:HB2	25:LR:169:PHE:HE2	1.84	0.42
27:LT:669:VAL:HG23	27:LT:680:THR:HG22	2.02	0.42
28:LU:71:CYS:HB3	28:LU:115:ILE:HG22	2.01	0.42
36:NE:176:HIS:CE1	36:NE:180:ILE:HD11	2.55	0.42
39:NH:228:THR:HB	39:NH:236:SER:HB3	2.01	0.42
53:SC:137:TRP:CE2	53:SC:145:ALA:HB2	2.55	0.42
55:SG:168:CYS:HB2	55:SG:186:ARG:HB2	2.01	0.42
61:SP:746:HIS:O	61:SP:750:MET:HG2	2.19	0.42
65:ST:212:UNK:O	65:ST:216:UNK:N	2.52	0.42
67:SW:213:GLY:N	67:SW:218:ILE:HD11	2.34	0.42
2:L1:675:U:H2'	2:L1:676:C:C6	2.55	0.42
2:L1:951:C:H2'	2:L1:952:G:H8	1.84	0.42
20:LM:913:ALA:O	20:LM:950:SER:OG	2.25	0.42
20:LM:1283:PHE:HE2	20:LM:1285:VAL:HG22	1.83	0.42
20:LM:1296:GLU:C	20:LM:1297:MET:HE2	2.44	0.42
20:LM:1562:ALA:HB1	20:LM:1612:LEU:HD12	2.02	0.42
20:LM:1966:LEU:O	20:LM:2026:GLN:NE2	2.51	0.42
20:LM:2036:LYS:NZ	20:LM:2040:ARG:HB2	2.34	0.42
20:LM:2066:ASN:ND2	20:LM:2102:LEU:HB3	2.35	0.42
21:LN:677:PRO:HB3	35:ND:206:THR:O	2.19	0.42
22:LO:91:HIS:ND1	22:LO:133:ALA:HB2	2.34	0.42
24:LQ:154:GLN:HG2	24:LQ:197:LEU:HB3	2.02	0.42
26:LS:474:THR:HG21	26:LS:494:LYS:HB2	2.02	0.42
30:LZ:31:LEU:HD23	30:LZ:34:LEU:HD12	2.01	0.42
30:LZ:173:TYR:CD2	70:SY:70:MET:HE3	2.55	0.42
39:NH:102:LYS:HE3	39:NH:102:LYS:HB2	1.90	0.42
41:NK:635:TYR:HB3	41:NK:640:TYR:HE2	1.85	0.42
52:SB:194:LEU:HD12	52:SB:194:LEU:HA	1.93	0.42
53:SC:97:PHE:HB2	53:SC:107:VAL:HG23	2.02	0.42
55:SG:363:GLU:HG2	55:SG:376:PRO:HB3	2.01	0.42
57:SI:1235:GLU:HG3	57:SI:1238:ARG:HH21	1.84	0.42
58:SK:85:PRO:HG2	58:SK:130:PHE:HZ	1.84	0.42
61:SP:435:ASP:HB3	61:SP:438:VAL:HG12	2.01	0.42
61:SP:1906:HIS:HB2	61:SP:1960:LYS:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L2:46:A:O2'	59:SL:22:GLN:NE2	2.51	0.42
6:L5:26:ASP:OD1	6:L5:27:ASP:N	2.52	0.42
13:LD:80:MET:HA	13:LD:86:ILE:HG22	2.01	0.42
19:LL:169:SER:HG	19:LL:188:ARG:HH12	1.65	0.42
19:LL:272:TYR:HB3	19:LL:290:VAL:HB	2.01	0.42
19:LL:319:ILE:HG22	19:LL:333:ILE:HD12	2.01	0.42
20:LM:484:MET:HE2	20:LM:484:MET:HB3	1.81	0.42
20:LM:610:ASN:ND2	20:LM:702:VAL:HG21	2.35	0.42
20:LM:943:GLN:HG2	20:LM:960:ILE:HG23	2.02	0.42
20:LM:1279:ASP:HB3	20:LM:1282:LYS:HE2	2.02	0.42
20:LM:1376:VAL:O	20:LM:1380:ILE:HG12	2.19	0.42
21:LN:608:ASP:OD2	21:LN:611:LEU:N	2.50	0.42
24:LQ:201:SER:HB3	24:LQ:205:ARG:HG3	2.02	0.42
25:LR:19:ARG:NE	25:LR:364:LEU:O	2.41	0.42
34:NC:203:SER:O	34:NC:207:ARG:HG3	2.20	0.42
46:NR:317:UNK:O	46:NR:321:UNK:N	2.52	0.42
52:SB:63:LEU:O	52:SB:94:LEU:HD21	2.19	0.42
52:SB:346:LEU:HD12	52:SB:362:LEU:HD13	2.02	0.42
52:SB:362:LEU:O	52:SB:366:THR:OG1	2.24	0.42
70:SY:233:LYS:HG2	70:SY:245:TYR:HE1	1.84	0.42
1:L0:817:U:H4'	26:LS:517:LYS:HZ2	1.85	0.42
2:L1:1219:C:OP1	6:L5:127:ARG:NH2	2.48	0.42
4:L3:27:ALA:O	4:L3:31:THR:HG23	2.20	0.42
16:LH:529:TRP:CE3	16:LH:529:TRP:HA	2.55	0.42
16:LH:741:LEU:HD23	20:LM:218:ALA:HB1	2.01	0.42
19:LK:466:LEU:HD13	19:LK:481:VAL:HG11	2.01	0.42
20:LM:2069:ILE:O	20:LM:2073:THR:HG23	2.20	0.42
22:LO:552:ARG:HH21	22:LO:556:ALA:HB3	1.85	0.42
24:LQ:631:ALA:HA	24:LQ:660:TRP:CZ2	2.54	0.42
27:LT:667:LEU:HD23	27:LT:667:LEU:HA	1.87	0.42
28:LU:283:SER:HB2	28:LU:303:ASP:H	1.85	0.42
36:NE:282:ASP:O	36:NE:286:ILE:HG13	2.20	0.42
44:NO:111:MET:HE2	44:NO:116:ALA:HA	2.02	0.42
46:NR:880:UNK:O	46:NR:884:UNK:N	2.53	0.42
53:SC:292:LYS:HE2	53:SC:315:PRO:HG3	2.02	0.42
61:SP:751:GLU:OE1	61:SP:754:GLN:N	2.46	0.42
61:SP:1471:LEU:O	61:SP:1475:MET:HG2	2.19	0.42
61:SP:1580:HIS:CG	61:SP:1585:ARG:HD3	2.55	0.42
67:SW:220:MET:HE1	67:SW:245:ALA:HA	2.01	0.42
1:L0:453:U:H2'	1:L0:454:C:C6	2.55	0.42
2:L1:1214:A:O2'	2:L1:1216:C:OP1	2.32	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L1:1667:U:H5'	60:SM:142:HIS:HA	2.00	0.42
11:LA:82:ASN:HA	11:LA:85:LEU:HD12	2.02	0.42
20:LM:1949:GLY:O	20:LM:1952:THR:OG1	2.34	0.42
22:LO:674:GLN:O	22:LO:678:GLN:HG2	2.20	0.42
23:LP:325:MET:O	23:LP:325:MET:HE3	2.20	0.42
23:LP:571:TRP:HZ3	52:SB:392:GLU:HG2	1.84	0.42
25:LR:89:LEU:HD22	25:LR:103:LEU:HD21	2.01	0.42
27:LT:637:LEU:HB2	27:LT:651:LEU:HD11	2.02	0.42
29:LW:141:GLU:HG2	64:SS:715:LYS:HE2	2.02	0.42
36:NE:278:LEU:HB2	44:NO:77:PRO:HG2	2.01	0.42
41:NK:414:ASN:HB2	41:NK:488:ASP:HA	2.01	0.42
53:SC:92:ARG:NH2	53:SC:153:ASP:OD1	2.52	0.42
53:SC:304:ARG:O	53:SC:306:HIS:ND1	2.47	0.42
55:SG:125:LYS:H	55:SG:125:LYS:HD2	1.83	0.42
57:SI:1236:HIS:O	57:SI:1240:LYS:HG2	2.20	0.42
58:SK:224:LEU:HD23	58:SK:228:LEU:HG	2.00	0.42
59:SL:140:TYR:CZ	59:SL:142:ASP:HB2	2.55	0.42
61:SP:1610:GLN:HA	61:SP:1614:MET:CE	2.50	0.42
64:SS:169:ALA:HA	64:SS:170:PRO:HD3	1.86	0.42
67:SW:86:THR:OG1	67:SW:87:PRO:HD3	2.20	0.42
2:L1:29:G:H2'	2:L1:30:C:C6	2.55	0.41
2:L1:607:U:OP1	57:SI:1099:ARG:NH1	2.53	0.41
2:L1:1102:G:H2'	2:L1:1103:C:C6	2.55	0.41
17:LI:701:LEU:HD21	19:LL:574:LEU:HG	2.01	0.41
20:LM:850:LYS:O	20:LM:854:LYS:HG2	2.20	0.41
21:LN:592:ARG:NH2	21:LN:658:GLU:OE2	2.53	0.41
22:LO:42:LEU:HD11	22:LO:367:LEU:HB2	2.02	0.41
22:LO:112:VAL:HG22	22:LO:121:MET:HG3	2.02	0.41
22:LO:681:GLY:O	22:LO:683:ALA:N	2.49	0.41
24:LQ:459:CYS:O	24:LQ:472:GLY:N	2.47	0.41
27:LT:769:ASP:HA	27:LT:772:LYS:NZ	2.35	0.41
29:LW:240:ARG:NH2	29:LW:256:ASN:OD1	2.53	0.41
57:SI:260:ARG:HD3	57:SI:338:PRO:HB2	2.01	0.41
57:SI:1274:LEU:HA	57:SI:1274:LEU:HD12	1.87	0.41
59:SL:78:PHE:CD1	59:SL:160:VAL:HG21	2.55	0.41
61:SP:1395:ALA:HA	61:SP:1398:PHE:CE2	2.55	0.41
65:ST:579:LYS:O	65:ST:579:LYS:HG2	2.20	0.41
67:SW:89:LYS:HD3	67:SW:89:LYS:HA	1.89	0.41
67:SW:154:ARG:HG3	67:SW:155:LEU:HD12	2.02	0.41
2:L1:1267:C:H2'	2:L1:1268:C:C6	2.55	0.41
2:L1:1269:G:H2'	2:L1:1270:G:C8	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L1:1495:G:OP1	71:SZ:301:THR:OG1	2.26	0.41
3:L2:109:C:N4	33:NB:457:GLU:HG2	2.36	0.41
3:L2:145:U:O2'	3:L2:146:G:OP2	2.31	0.41
8:L7:15:LYS:HE2	8:L7:15:LYS:HB3	1.79	0.41
9:L8:106:SER:HB3	9:L8:171:LEU:HG	2.02	0.41
16:LH:240:THR:HG21	21:LN:264:GLN:HE22	1.85	0.41
17:LI:216:ILE:HD11	17:LI:234:ILE:HG13	2.01	0.41
19:LL:601:GLU:OE1	21:LN:416:TYR:OH	2.26	0.41
20:LM:374:ILE:HD12	20:LM:374:ILE:HA	1.94	0.41
20:LM:630:ILE:HD12	20:LM:630:ILE:H	1.86	0.41
24:LQ:115:TYR:HE1	24:LQ:136:VAL:HG21	1.86	0.41
24:LQ:207:ILE:HG13	24:LQ:217:VAL:HG23	2.01	0.41
28:LU:304:LYS:HG2	28:LU:326:GLN:HA	2.01	0.41
28:LU:397:PRO:HD2	28:LU:400:ILE:HD12	2.02	0.41
28:LU:405:GLN:O	28:LU:409:ILE:HG12	2.20	0.41
35:ND:194:ILE:HD12	35:ND:194:ILE:HA	1.88	0.41
41:NK:157:LEU:HB3	41:NK:188:ILE:HD13	2.02	0.41
44:NO:32:LYS:O	44:NO:36:ARG:HG3	2.21	0.41
52:SB:351:SER:HB3	62:SQ:617:HIS:CG	2.55	0.41
57:SI:922:VAL:HG22	57:SI:1017:LEU:HD23	2.02	0.41
57:SI:1131:THR:HG22	57:SI:1134:GLN:HG3	2.01	0.41
58:SK:149:ALA:HB2	65:ST:769:ARG:HA	2.01	0.41
61:SP:736:TRP:O	61:SP:740:ILE:HG12	2.20	0.41
1:L0:742:G:H3'	1:L0:743:G:H8	1.85	0.41
1:L0:858:C:P	30:LZ:53:ARG:HH22	2.43	0.41
2:L1:941:C:H2'	2:L1:942:G:C8	2.53	0.41
7:L6:221:LYS:HD2	7:L6:224:ARG:HH11	1.85	0.41
18:LJ:442:ALA:HA	18:LJ:445:ILE:HG12	2.02	0.41
20:LM:1082:LEU:HD21	20:LM:1126:LYS:HD3	2.01	0.41
20:LM:1326:ILE:HG23	20:LM:1330:MET:HE2	2.02	0.41
20:LM:1601:ILE:O	20:LM:1604:ILE:HG22	2.20	0.41
22:LO:114:THR:HB	22:LO:147:THR:OG1	2.20	0.41
22:LO:143:PRO:HG3	22:LO:169:TRP:CD1	2.55	0.41
22:LO:283:ASN:HD21	22:LO:289:ASN:HB3	1.84	0.41
23:LP:368:SER:OG	23:LP:369:GLU:N	2.53	0.41
24:LQ:716:GLU:HA	24:LQ:719:ARG:HD2	2.02	0.41
25:LR:156:LEU:HB3	25:LR:171:SER:HB3	2.01	0.41
27:LT:399:SER:OG	27:LT:400:GLN:N	2.54	0.41
27:LT:879:MET:O	27:LT:883:MET:HG3	2.21	0.41
34:NC:269:LEU:HD22	34:NC:272:LEU:HD11	2.02	0.41
36:NE:183:TYR:HB3	36:NE:187:LYS:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:NH:472:HIS:CE1	39:NH:556:LEU:HD11	2.55	0.41
53:SC:238:ALA:H	53:SC:242:GLN:HE21	1.68	0.41
54:SE:25:LEU:HD22	54:SE:119:ILE:HG13	2.02	0.41
61:SP:1356:LEU:HG	61:SP:1373:ILE:HG23	2.01	0.41
65:ST:570:LEU:HD11	66:SU:445:TYR:HB2	2.01	0.41
66:SU:255:MET:HE2	66:SU:255:MET:HB3	1.92	0.41
66:SU:261:LYS:HG2	66:SU:262:HIS:HD2	1.85	0.41
20:LM:523:LEU:HD23	20:LM:523:LEU:HA	1.88	0.41
20:LM:539:SER:O	20:LM:542:GLU:HG3	2.21	0.41
20:LM:1898:ASP:HA	20:LM:1901:VAL:HG22	2.02	0.41
21:LN:22:VAL:HG12	21:LN:33:VAL:HG22	2.02	0.41
21:LN:338:ILE:HG12	21:LN:349:PHE:CD1	2.55	0.41
22:LO:561:ALA:HB2	22:LO:611:LEU:HD11	2.01	0.41
25:LR:59:ARG:NH2	25:LR:96:GLN:O	2.53	0.41
28:LU:326:GLN:HE22	59:SL:114:GLY:HA2	1.85	0.41
29:LW:176:ILE:O	29:LW:180:VAL:HG23	2.20	0.41
41:NK:283:THR:HG22	41:NK:411:SER:HB2	2.02	0.41
41:NK:337:GLU:HA	41:NK:341:TYR:CZ	2.55	0.41
42:NM:62:LEU:HD12	42:NM:62:LEU:HA	1.92	0.41
51:SA:252:MET:HB3	53:SC:205:LYS:HG2	2.02	0.41
53:SC:200:LEU:O	53:SC:204:ALA:N	2.48	0.41
54:SE:20:LYS:HA	54:SE:20:LYS:HD2	1.91	0.41
55:SG:368:ARG:HB3	55:SG:377:PHE:CZ	2.55	0.41
56:SH:191:ILE:HB	56:SH:223:ILE:HG13	2.03	0.41
57:SI:391:ARG:HA	57:SI:402:GLY:HA3	2.02	0.41
57:SI:925:ARG:HB2	57:SI:1015:LEU:HD11	2.03	0.41
58:SK:173:LYS:HD2	58:SK:212:TYR:CD2	2.55	0.41
61:SP:74:LYS:HD2	61:SP:84:HIS:HB3	2.01	0.41
61:SP:1524:GLU:HG3	61:SP:1528:LYS:NZ	2.35	0.41
61:SP:1878:VAL:HG12	61:SP:1912:LEU:HD13	2.02	0.41
65:ST:726:CYS:SG	65:ST:728:HIS:NE2	2.92	0.41
70:SY:3:ALA:HA	70:SY:6:ARG:HE	1.85	0.41
2:L1:71:G:H2'	2:L1:72:C:O4'	2.20	0.41
2:L1:438:G:N2	49:NW:125:SER:OG	2.53	0.41
2:L1:1740:C:H2'	2:L1:1741:U:H6	1.85	0.41
6:L5:40:ALA:HB1	6:L5:45:TYR:CG	2.56	0.41
12:LC:81:ILE:O	12:LC:85:ARG:HG3	2.21	0.41
19:LL:54:PRO:HG2	19:LL:57:HIS:HB3	2.02	0.41
20:LM:665:ILE:HA	20:LM:710:VAL:HG12	2.03	0.41
22:LO:379:LEU:HD22	22:LO:720:THR:HG23	2.02	0.41
23:LP:576:MET:HE2	23:LP:576:MET:HB3	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:LQ:9:ARG:HA	24:LQ:669:GLN:NE2	2.35	0.41
25:LR:245:LEU:HD12	25:LR:261:TYR:HB3	2.02	0.41
26:LS:253:ARG:HB3	26:LS:271:LEU:HG	2.02	0.41
32:NA:418:THR:HG22	32:NA:421:THR:HG23	2.03	0.41
39:NH:425:LEU:HD12	73:NH:3000:ATP:N1	2.35	0.41
46:NR:249:UNK:O	46:NR:253:UNK:N	2.53	0.41
52:SB:11:TYR:HE1	52:SB:63:LEU:HD11	1.85	0.41
53:SD:312:VAL:HG13	53:SD:315:PRO:HG3	2.02	0.41
57:SI:320:PRO:HB3	57:SI:332:GLU:OE1	2.19	0.41
57:SI:1022:LYS:NZ	65:ST:78:ASP:OD2	2.53	0.41
58:SJ:172:MET:C	58:SJ:173:LYS:HD3	2.46	0.41
58:SK:147:ARG:HG2	58:SK:154:LYS:HD3	2.02	0.41
59:SL:132:LEU:HA	59:SL:133:PRO:HD3	1.90	0.41
60:SM:165:CYS:HB2	60:SM:252:GLU:HB2	2.01	0.41
1:L0:614:U:H2'	1:L0:615:C:C6	2.55	0.41
2:L1:373:G:H2'	2:L1:374:G:H8	1.85	0.41
2:L1:496:C:H2'	2:L1:497:C:H6	1.86	0.41
2:L1:979:C:H2'	2:L1:980:A:C8	2.56	0.41
2:L1:1702:G:N1	25:LR:725:SER:OG	2.51	0.41
14:LF:80:ASP:OD1	14:LF:81:TYR:N	2.52	0.41
16:LH:129:LEU:HB2	16:LH:154:ILE:HD13	2.03	0.41
18:LJ:158:LEU:HD23	18:LJ:159:THR:N	2.36	0.41
20:LM:794:LYS:HB3	20:LM:794:LYS:HE3	1.89	0.41
20:LM:827:HIS:CD2	20:LM:883:CYS:HB3	2.56	0.41
20:LM:1387:LEU:HD23	20:LM:1395:ARG:HD2	2.01	0.41
21:LN:316:GLU:HG2	21:LN:317:LYS:HG3	2.03	0.41
23:LP:167:ARG:HH21	64:SS:178:TRP:CG	2.39	0.41
23:LP:574:MET:HE3	23:LP:585:PHE:HD2	1.86	0.41
38:NG:75:MET:HE2	38:NG:75:MET:HB3	1.84	0.41
41:NJ:172:ARG:HE	41:NJ:172:ARG:HB3	1.76	0.41
41:NJ:884:ILE:HG22	41:NJ:886:LEU:H	1.85	0.41
41:NK:849:TYR:CZ	41:NK:859:LEU:HD12	2.55	0.41
52:SB:329:LEU:HD23	52:SB:329:LEU:HA	1.89	0.41
61:SP:965:HIS:CD2	61:SP:967:HIS:H	2.39	0.41
63:SR:38:ALA:O	65:ST:850:LEU:HD23	2.21	0.41
2:L1:1091:C:H2'	2:L1:1092:G:H8	1.86	0.41
2:L1:1313:A:H4'	2:L1:1314:U:O4'	2.20	0.41
3:L2:24:U:O4	29:LW:508:LYS:NZ	2.52	0.41
3:L2:100:U:H2'	3:L2:101:C:H6	1.85	0.41
3:L2:121:U:H1'	3:L2:153:G:N2	2.35	0.41
11:LA:25:ALA:HB3	11:LA:31:LEU:HD12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LF:79:LEU:HG	14:LF:83:LYS:HE3	2.01	0.41
15:LG:39:SER:HB3	24:LQ:865:GLY:HA3	2.03	0.41
16:LH:58:ASN:HD22	16:LH:78:LEU:HB2	1.85	0.41
16:LH:271:VAL:HG22	16:LH:287:PRO:HA	2.02	0.41
16:LH:551:THR:HB	17:LI:295:GLN:HE21	1.86	0.41
19:LL:367:ARG:H	19:LL:367:ARG:HD3	1.85	0.41
20:LM:1408:ALA:HB1	20:LM:1412:LEU:HB2	2.02	0.41
20:LM:1969:VAL:HG12	20:LM:2029:ASN:HD21	1.84	0.41
22:LO:43:LYS:HG3	67:SW:252:PHE:CE2	2.56	0.41
22:LO:551:PHE:CE1	22:LO:558:LEU:HD12	2.56	0.41
25:LR:608:VAL:HA	25:LR:624:ALA:HA	2.02	0.41
27:LT:255:GLN:NE2	27:LT:261:VAL:O	2.54	0.41
27:LT:797:LEU:HB2	67:SW:251:ARG:NE	2.35	0.41
32:NA:398:ASN:HB3	32:NA:401:LEU:HD12	2.02	0.41
49:NW:142:TYR:HD1	49:NW:149:LEU:HB2	1.85	0.41
49:NW:254:LEU:HG	49:NW:266:VAL:HG12	2.02	0.41
76:SJ:301:SAH:H8	76:SJ:301:SAH:SD	2.61	0.41
61:SP:1510:THR:HG23	61:SP:1513:ASP:H	1.86	0.41
61:SP:1876:LEU:HB3	61:SP:1880:PHE:CD2	2.55	0.41
61:SP:2096:LYS:HB2	61:SP:2139:TRP:CZ3	2.55	0.41
65:ST:463:ALA:HB3	65:ST:466:ASN:CG	2.46	0.41
70:SY:94:LEU:HG	70:SY:98:ARG:HE	1.84	0.41
71:SZ:361:VAL:HG12	71:SZ:365:LEU:HD23	2.02	0.41
1:L0:745:U:O2'	1:L0:746:G:H5''	2.20	0.41
1:L0:754:G:H2'	1:L0:755:C:C5	2.55	0.41
2:L1:110:U:H2'	2:L1:111:A:H8	1.86	0.41
2:L1:1296:U:H2'	2:L1:1297:U:O4'	2.21	0.41
2:L1:1768:A:H2'	2:L1:1769:C:H4'	2.03	0.41
4:L3:25:LYS:HA	4:L3:55:ARG:HA	2.02	0.41
7:L6:32:MET:SD	7:L6:54:GLY:HA2	2.61	0.41
13:LD:24:LEU:HD23	13:LD:24:LEU:HA	1.91	0.41
17:LI:473:LEU:HD21	17:LI:485:LEU:HD21	2.03	0.41
18:LJ:166:TYR:C	18:LJ:184:SER:HG	2.26	0.41
20:LM:380:GLU:O	20:LM:384:THR:HG23	2.20	0.41
20:LM:1310:THR:O	20:LM:1314:ILE:HG12	2.20	0.41
20:LM:2030:ARG:NH2	20:LM:2080:VAL:HG13	2.35	0.41
21:LN:269:THR:OG1	21:LN:271:ASN:OD1	2.29	0.41
22:LO:305:THR:O	22:LO:312:PHE:HA	2.21	0.41
24:LQ:416:SER:OG	24:LQ:417:ASP:N	2.53	0.41
26:LS:194:PRO:HG2	26:LS:197:ALA:HB2	2.03	0.41
27:LT:545:VAL:HG12	27:LT:556:THR:HG22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LU:75:HIS:HD2	28:LU:78:LYS:N	2.19	0.41
28:LU:263:LEU:HD13	28:LU:297:PHE:HE1	1.86	0.41
32:NA:592:LYS:HA	32:NA:595:ARG:NH1	2.35	0.41
41:NJ:502:PRO:HA	41:NJ:643:ARG:HD3	2.02	0.41
41:NK:833:VAL:HG23	41:NK:834:ASP:OD1	2.20	0.41
52:SB:44:LEU:HD23	52:SB:44:LEU:HA	1.80	0.41
76:SJ:301:SAH:HG2	76:SJ:301:SAH:H3'	2.03	0.41
1:L0:812:G:O6	27:LT:467:LYS:NZ	2.45	0.41
2:L1:22:A:H61	2:L1:652:U:H3	1.68	0.41
2:L1:1233:G:H2'	2:L1:1234:C:C6	2.56	0.41
3:L2:106:G:N2	3:L2:167:U:OP2	2.45	0.41
5:L4:141:THR:OG1	5:L4:143:ASP:OD1	2.32	0.41
7:L6:7:PHE:O	7:L6:11:GLY:N	2.53	0.41
7:L6:135:PRO:HG2	7:L6:141:ILE:HG12	2.03	0.41
9:L8:121:LEU:HD21	9:L8:166:PHE:CG	2.55	0.41
10:L9:110:LEU:HB2	10:L9:147:PHE:HB3	2.01	0.41
13:LD:13:GLN:NE2	13:LD:36:TYR:HB3	2.36	0.41
16:LH:203:LYS:H	16:LH:224:ASP:HB3	1.85	0.41
18:LJ:479:GLU:OE1	19:LL:525:GLN:NE2	2.54	0.41
19:LL:140:CYS:SG	19:LL:161:LYS:NZ	2.70	0.41
20:LM:147:VAL:HA	20:LM:150:LEU:HD12	2.03	0.41
20:LM:679:SER:O	20:LM:683:MET:HG2	2.20	0.41
20:LM:1151:PHE:CE2	20:LM:1213:LEU:HB3	2.56	0.41
20:LM:1335:MET:HE1	20:LM:1386:ALA:HB1	2.03	0.41
20:LM:1384:VAL:O	20:LM:1388:PRO:HD3	2.20	0.41
20:LM:1555:LEU:HD23	20:LM:1558:ILE:HD11	2.02	0.41
20:LM:1675:LYS:HG3	20:LM:1717:CYS:SG	2.61	0.41
20:LM:2050:ALA:HB1	20:LM:2094:LYS:HG3	2.02	0.41
20:LM:2077:SER:O	20:LM:2081:ARG:HG3	2.21	0.41
21:LN:139:ARG:NH2	21:LN:173:VAL:O	2.54	0.41
21:LN:165:ILE:H	21:LN:165:ILE:HD12	1.86	0.41
21:LN:339:SER:HB2	21:LN:398:ILE:HG22	2.03	0.41
21:LN:388:LYS:HE2	21:LN:388:LYS:HB2	1.78	0.41
22:LO:312:PHE:CE1	22:LO:326:LEU:HB2	2.55	0.41
22:LO:415:SER:OG	22:LO:436:ASP:OD1	2.27	0.41
23:LP:454:GLN:O	23:LP:457:THR:OG1	2.31	0.41
25:LR:23:PRO:HG3	25:LR:627:SER:OG	2.21	0.41
26:LS:470:MET:HE3	26:LS:470:MET:HB3	1.94	0.41
27:LT:178:VAL:HG22	27:LT:184:LEU:HD12	2.03	0.41
27:LT:738:LEU:HD13	27:LT:740:GLU:HG3	2.02	0.41
27:LT:770:VAL:HG12	32:NA:533:ILE:HB	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:LT:879:MET:HE2	27:LT:879:MET:HB3	1.94	0.41
27:LT:909:PRO:HA	27:LT:915:LEU:HD21	2.02	0.41
28:LU:40:GLU:OE2	64:SS:704:GLY:N	2.54	0.41
28:LU:165:HIS:N	28:LU:170:VAL:O	2.43	0.41
29:LW:167:ASP:HB3	29:LW:170:LYS:HE2	2.03	0.41
33:NB:465:LEU:HD12	53:SD:103:GLU:OE2	2.21	0.41
39:NH:107:ALA:HA	39:NH:110:ARG:HE	1.86	0.41
39:NH:314:LEU:HD12	39:NH:318:LEU:HD13	2.03	0.41
39:NH:507:LEU:HD23	39:NH:507:LEU:HA	1.90	0.41
41:NJ:234:GLU:HB2	41:NJ:258:LEU:HD22	2.03	0.41
41:NJ:843:PRO:HD3	41:NK:781:TYR:OH	2.20	0.41
41:NK:6:VAL:HG12	41:NK:204:LEU:HG	2.03	0.41
41:NK:25:LEU:HD23	41:NK:197:CYS:SG	2.61	0.41
41:NK:688:ARG:O	41:NK:691:LEU:HD22	2.21	0.41
41:NK:866:LEU:HD21	41:NK:895:PHE:HB2	2.02	0.41
44:NO:119:LYS:HA	44:NO:119:LYS:HD3	1.84	0.41
46:NR:541:UNK:O	46:NR:545:UNK:N	2.54	0.41
51:SA:197:PHE:CD2	51:SA:200:LEU:HB2	2.56	0.41
51:SA:365:LYS:HB2	51:SA:365:LYS:HE2	1.83	0.41
53:SC:201:ILE:HG22	53:SC:205:LYS:HE3	2.03	0.41
55:SG:130:GLU:OE1	55:SG:466:ARG:NH2	2.54	0.41
57:SI:1000:SER:HB2	57:SI:1125:THR:HA	2.03	0.41
61:SP:1609:LEU:HD22	61:SP:1643:ILE:HD12	2.03	0.41
61:SP:1925:LEU:HD23	61:SP:1976:GLN:HE21	1.85	0.41
61:SP:2112:ASP:HB3	61:SP:2113:PRO:HD3	2.02	0.41
66:SU:480:GLU:OE1	66:SU:484:LYS:NZ	2.48	0.41
67:SW:251:ARG:HD3	67:SW:251:ARG:O	2.21	0.41
2:L1:530:U:H2'	2:L1:531:A:C8	2.55	0.41
2:L1:596:U:H2'	2:L1:597:G:C8	2.56	0.41
2:L1:1336:C:H2'	2:L1:1337:C:H6	1.85	0.41
2:L1:1658:G:H2'	57:SI:1037:PHE:HB3	2.02	0.41
2:L1:1814:G:H2'	2:L1:1815:A:C8	2.56	0.41
4:L3:51:ASP:OD1	4:L3:51:ASP:N	2.53	0.41
12:LC:41:MET:HE3	12:LC:41:MET:HB3	1.97	0.41
16:LH:100:CYS:SG	16:LH:101:LYS:N	2.94	0.41
17:LI:616:PHE:HD2	17:LI:653:LEU:HD11	1.86	0.41
18:LJ:467:GLN:HA	19:LL:572:LEU:HD13	2.03	0.41
20:LM:1564:SER:O	20:LM:1567:ARG:HG2	2.21	0.41
20:LM:1741:LEU:HD23	20:LM:1741:LEU:HA	1.92	0.41
21:LN:84:MET:HG2	21:LN:96:ALA:HB2	2.04	0.41
22:LO:378:ALA:HB1	22:LO:421:VAL:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:LO:686:LEU:HD12	22:LO:687:PRO:HD2	2.03	0.41
23:LP:327:LYS:HA	23:LP:330:ILE:HG12	2.03	0.41
24:LQ:634:ASP:OD1	24:LQ:635:SER:N	2.46	0.41
29:LW:203:TYR:CE1	29:LW:210:LEU:HD12	2.56	0.41
39:NH:342:LYS:HA	39:NH:342:LYS:HD2	1.78	0.41
46:NR:463:UNK:O	46:NR:467:UNK:N	2.54	0.41
49:NW:170:ASN:HA	49:NW:171:PRO:HD3	1.95	0.41
51:SA:286:ARG:NH1	51:SA:302:GLU:OE1	2.54	0.41
51:SA:325:THR:HA	51:SA:328:ILE:HD12	2.03	0.41
52:SB:226:LEU:HD21	52:SB:230:VAL:HG12	2.03	0.41
57:SI:138:ASN:HB3	57:SI:950:ARG:HH12	1.86	0.41
58:SK:107:GLN:NE2	58:SK:120:VAL:O	2.53	0.41
60:SM:166:ASN:O	60:SM:251:PHE:HA	2.20	0.41
61:SP:105:GLN:HB3	61:SP:106:PRO:HD3	2.02	0.41
61:SP:923:SER:HG	61:SP:959:CYS:HG	1.61	0.41
61:SP:1858:ALA:HB3	61:SP:1861:ILE:HG12	2.03	0.41
65:ST:567:THR:OG1	65:ST:568:PRO:HD3	2.20	0.41
65:ST:570:LEU:HD21	66:SU:445:TYR:CD2	2.55	0.41
65:ST:614:ASN:HB3	65:ST:635:VAL:HG21	2.02	0.41
66:SU:272:VAL:HG13	66:SU:273:LEU:HD12	2.02	0.41
2:L1:115:U:H2'	2:L1:116:U:C6	2.56	0.40
2:L1:181:A:H2'	2:L1:182:C:C6	2.56	0.40
2:L1:543:C:OP2	57:SI:1233:ASN:ND2	2.53	0.40
2:L1:627:U:OP1	57:SI:1136:ARG:NH2	2.41	0.40
3:L2:177:C:H2'	3:L2:178:G:O4'	2.21	0.40
16:LH:299:SER:OG	16:LH:301:ALA:O	2.35	0.40
18:LJ:274:VAL:HB	18:LJ:284:HIS:HB3	2.02	0.40
21:LN:107:MET:HE2	21:LN:118:VAL:HG22	2.02	0.40
21:LN:648:LYS:HB2	21:LN:649:PRO:HD3	2.03	0.40
23:LP:228:ASN:O	23:LP:232:ILE:HG12	2.21	0.40
24:LQ:161:LYS:HE3	24:LQ:161:LYS:HB3	1.89	0.40
24:LQ:942:LEU:HD21	32:NA:451:ALA:HB2	2.03	0.40
25:LR:296:THR:HG23	25:LR:297:HIS:ND1	2.36	0.40
25:LR:366:THR:O	25:LR:367:SER:OG	2.30	0.40
27:LT:581:SER:HB3	27:LT:599:LEU:HB3	2.02	0.40
36:NE:171:ALA:HB1	50:NY:220:LYS:HG3	2.02	0.40
38:NG:113:GLN:HE21	38:NG:117:ARG:HH21	1.67	0.40
41:NJ:372:HIS:CG	41:NJ:373:PRO:HD2	2.56	0.40
41:NJ:739:ASP:OD1	41:NJ:739:ASP:N	2.53	0.40
41:NK:168:HIS:NE2	41:NK:550:ASP:OD2	2.52	0.40
49:NW:129:TYR:CE2	49:NW:131:THR:HB	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:NY:214:HIS:CE1	50:NY:216:ILE:HG12	2.56	0.40
51:SA:20:LYS:HB3	51:SA:20:LYS:HE2	1.72	0.40
61:SP:35:ASP:OD1	61:SP:35:ASP:N	2.45	0.40
61:SP:1925:LEU:HD22	61:SP:1976:GLN:HG3	2.02	0.40
65:ST:70:LEU:HD12	65:ST:813:PHE:CD2	2.57	0.40
65:ST:579:LYS:HE3	65:ST:579:LYS:HB3	1.87	0.40
71:SZ:240:ASN:O	71:SZ:241:LEU:HG	2.21	0.40
2:L1:12:U:H2'	2:L1:13:C:H6	1.86	0.40
2:L1:235:A:C4	2:L1:236:A:C8	3.09	0.40
2:L1:370:G:N7	43:NN:511:LYS:HE3	2.36	0.40
2:L1:1490:G:H2'	2:L1:1490:G:N3	2.36	0.40
5:L4:173:ILE:HD11	5:L4:235:TRP:CD2	2.56	0.40
17:LI:264:ALA:HB3	17:LI:311:LEU:HD13	2.03	0.40
18:LJ:62:ILE:HD13	18:LJ:86:ALA:HB2	2.04	0.40
20:LM:371:ASP:O	20:LM:374:ILE:HG22	2.21	0.40
20:LM:712:VAL:HG12	20:LM:795:LYS:HD2	2.02	0.40
20:LM:1819:PRO:O	20:LM:1823:LEU:HG	2.20	0.40
24:LQ:914:GLU:OE2	67:SW:242:ARG:NH2	2.54	0.40
32:NA:456:LYS:HE2	32:NA:456:LYS:HB2	1.85	0.40
39:NH:144:VAL:HB	39:NH:145:PRO:HD3	2.03	0.40
41:NJ:397:LEU:HD12	41:NJ:397:LEU:HA	1.94	0.40
41:NK:559:LEU:HD23	41:NK:644:ALA:HB2	2.02	0.40
41:NK:587:ARG:HG2	41:NK:587:ARG:HH11	1.86	0.40
46:NR:137:UNK:O	46:NR:141:UNK:N	2.54	0.40
46:NR:985:UNK:O	46:NR:989:UNK:N	2.55	0.40
52:SB:181:MET:HE2	52:SB:181:MET:HB2	1.93	0.40
57:SI:114:ILE:HA	57:SI:340:SER:OG	2.21	0.40
61:SP:503:ILE:HD13	61:SP:517:GLN:HB3	2.02	0.40
61:SP:1596:GLN:HB3	61:SP:1602:VAL:HG12	2.03	0.40
65:ST:630:GLN:CD	65:ST:630:GLN:H	2.29	0.40
71:SZ:243:GLU:O	71:SZ:247:GLN:HG3	2.21	0.40
1:L0:732:G:O2'	1:L0:733:C:OP1	2.34	0.40
2:L1:1023:A:OP2	37:NF:124:ARG:NH1	2.55	0.40
2:L1:1736:G:H2'	2:L1:1737:G:C8	2.49	0.40
10:L9:180:LYS:HE2	10:L9:180:LYS:HB3	1.69	0.40
11:LA:48:HIS:CE1	11:LA:114:TYR:HB2	2.55	0.40
14:LF:22:GLN:HB2	34:NC:246:MET:HE1	2.04	0.40
16:LH:333:ASP:N	16:LH:663:GLN:HE22	2.20	0.40
16:LH:727:ILE:HA	16:LH:728:PRO:HD3	1.97	0.40
19:LK:523:MET:O	19:LK:526:TRP:HB2	2.22	0.40
20:LM:393:ASP:HB3	20:LM:439:THR:HG21	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:LM:1320:LEU:HD11	20:LM:1357:LEU:HD11	2.02	0.40
20:LM:1423:TYR:HE1	20:LM:1439:ILE:HB	1.85	0.40
20:LM:2114:MET:HB3	20:LM:2114:MET:HE3	1.76	0.40
22:LO:394:ASP:N	22:LO:394:ASP:OD1	2.54	0.40
23:LP:330:ILE:HG13	23:LP:331:THR:N	2.36	0.40
23:LP:387:GLU:O	23:LP:391:VAL:HG23	2.21	0.40
25:LR:145:HIS:CE1	25:LR:182:LEU:HD12	2.57	0.40
25:LR:548:TRP:CZ3	25:LR:555:CYS:HB2	2.57	0.40
26:LS:138:LYS:HD3	26:LS:138:LYS:HA	1.87	0.40
26:LS:253:ARG:HG2	26:LS:541:GLU:HA	2.04	0.40
29:LW:389:ARG:HD3	29:LW:389:ARG:HA	1.78	0.40
32:NA:570:THR:OG1	32:NA:571:ALA:N	2.53	0.40
39:NH:565:LEU:HG	39:NH:602:VAL:HG22	2.03	0.40
51:SA:228:LEU:HD22	51:SA:245:LEU:HD13	2.02	0.40
51:SA:270:ARG:HA	51:SA:270:ARG:HH11	1.85	0.40
61:SP:1583:ILE:HD12	61:SP:1583:ILE:H	1.85	0.40
61:SP:1922:ASP:OD1	61:SP:1923:SER:N	2.54	0.40
70:SY:113:ALA:HA	70:SY:116:ILE:HD12	2.04	0.40
71:SZ:184:VAL:O	71:SZ:188:VAL:HG23	2.22	0.40
1:L0:433:U:O2'	1:L0:434:C:OP1	2.34	0.40
1:L0:604:C:H3'	19:LL:515:GLY:HA2	2.03	0.40
2:L1:276:G:H2'	2:L1:277:C:C6	2.56	0.40
2:L1:536:A:H3'	2:L1:537:C:H6	1.86	0.40
2:L1:962:A:H2'	2:L1:963:A:O4'	2.21	0.40
2:L1:1719:A:H2'	2:L1:1720:U:O4'	2.22	0.40
6:L5:136:ARG:HG3	6:L5:203:ASN:OD1	2.20	0.40
8:L7:44:ASN:H	8:L7:68:GLN:HE22	1.70	0.40
16:LH:215:GLU:HG2	16:LH:216:ASP:N	2.37	0.40
16:LH:472:VAL:HB	16:LH:492:PHE:HB3	2.03	0.40
17:LI:659:THR:O	17:LI:663:MET:HG2	2.21	0.40
20:LM:489:HIS:HE1	20:LM:491:LEU:HB2	1.85	0.40
20:LM:1414:ILE:H	20:LM:1414:ILE:HG13	1.78	0.40
20:LM:1742:THR:O	20:LM:1745:LYS:HG2	2.21	0.40
21:LN:355:LEU:HB2	21:LN:385:LEU:HG	2.03	0.40
24:LQ:677:GLU:OE2	24:LQ:677:GLU:N	2.52	0.40
25:LR:327:GLN:OE1	25:LR:327:GLN:N	2.54	0.40
26:LS:308:GLU:HB3	26:LS:326:LEU:HD23	2.04	0.40
27:LT:365:PRO:C	27:LT:366:THR:HG1	2.28	0.40
32:NA:397:GLU:HA	57:SI:1048:ASN:ND2	2.36	0.40
41:NK:869:GLY:HA3	41:NK:880:LEU:HD11	2.03	0.40
49:NW:157:GLU:OE2	49:NW:171:PRO:HB3	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SB:68:ILE:HD12	52:SB:101:LYS:HE3	2.04	0.40
53:SC:183:PRO:HD2	53:SC:184:ASP:N	2.37	0.40
58:SK:99:PRO:HB2	58:SK:238:GLU:OE1	2.22	0.40
61:SP:440:ASP:OD1	61:SP:441:GLU:N	2.55	0.40
61:SP:1062:GLU:OE2	61:SP:1065:ARG:NE	2.52	0.40
61:SP:1403:ASN:O	61:SP:1407:ARG:HG2	2.22	0.40
61:SP:1613:ILE:C	61:SP:1615:PRO:HD2	2.46	0.40
67:SW:233:PRO:HA	67:SW:234:PRO:HD3	1.96	0.40
68:Sx:702:UNK:O	68:Sx:706:UNK:N	2.55	0.40
70:SY:150:ASP:HB3	70:SY:153:THR:HB	2.02	0.40
2:L1:116:U:H3	2:L1:347:G:H1	1.69	0.40
2:L1:156:G:H1	2:L1:162:C:H42	1.69	0.40
2:L1:382:C:H2'	2:L1:383:G:C8	2.55	0.40
2:L1:1010:G:H2'	2:L1:1011:A:C8	2.56	0.40
2:L1:1290:G:H2'	2:L1:1291:A:C8	2.56	0.40
2:L1:1372:U:H2'	2:L1:1373:C:C6	2.55	0.40
4:L3:69:THR:O	4:L3:72:GLN:HG2	2.21	0.40
10:L9:27:GLN:HG3	59:SL:59:TYR:CZ	2.57	0.40
16:LH:234:TYR:CE1	21:LN:270:SER:HB2	2.56	0.40
16:LH:544:HIS:HB3	16:LH:586:MET:HE2	2.04	0.40
19:LK:551:LEU:O	19:LK:555:MET:HG3	2.22	0.40
19:LL:214:LEU:HD23	19:LL:214:LEU:HA	1.97	0.40
20:LM:88:LYS:HB3	20:LM:88:LYS:HE3	1.90	0.40
20:LM:1443:ASP:HB3	20:LM:1447:TRP:CZ2	2.56	0.40
20:LM:1943:ILE:HG23	20:LM:1947:LEU:HD13	2.03	0.40
21:LN:655:LEU:HD23	21:LN:661:LEU:HG	2.04	0.40
22:LO:205:SER:OG	22:LO:213:CYS:HB3	2.20	0.40
26:LS:155:MET:HE3	26:LS:155:MET:HB3	1.94	0.40
39:NH:168:LEU:HD23	39:NH:168:LEU:HA	1.92	0.40
39:NH:1012:ILE:HD12	39:NH:1137:VAL:HG22	2.03	0.40
41:NK:126:PHE:CD2	41:NK:160:LEU:HD11	2.56	0.40
41:NK:260:GLN:HG3	41:NK:293:ALA:HB2	2.03	0.40
50:NY:310:ILE:O	50:NY:314:GLN:HG2	2.21	0.40
51:SA:308:LEU:HD23	51:SA:308:LEU:HA	1.90	0.40
52:SB:176:LEU:HD12	52:SB:176:LEU:HA	1.96	0.40
56:SH:121:THR:HG23	56:SH:165:GLY:HA3	2.03	0.40
61:SP:265:PRO:O	61:SP:269:ILE:HG13	2.21	0.40
61:SP:1456:ILE:O	61:SP:1460:ILE:HG13	2.21	0.40
64:SS:170:PRO:O	64:SS:172:GLU:N	2.46	0.40
71:SZ:179:PRO:O	71:SZ:182:LEU:HB3	2.21	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	
4	L3	85/116 (73%)	84 (99%)	1 (1%)	0	100	100
5	L4	260/263 (99%)	259 (100%)	1 (0%)	0	100	100
6	L5	188/204 (92%)	182 (97%)	6 (3%)	0	100	100
7	L6	219/249 (88%)	218 (100%)	1 (0%)	0	100	100
8	L7	164/194 (84%)	160 (98%)	4 (2%)	0	100	100
9	L8	176/208 (85%)	174 (99%)	2 (1%)	0	100	100
10	L9	169/194 (87%)	168 (99%)	1 (1%)	0	100	100
11	LA	118/132 (89%)	111 (94%)	7 (6%)	0	100	100
12	LC	137/146 (94%)	136 (99%)	1 (1%)	0	100	100
13	LD	145/158 (92%)	141 (97%)	4 (3%)	0	100	100
14	LF	102/133 (77%)	102 (100%)	0	0	100	100
15	LG	60/69 (87%)	59 (98%)	1 (2%)	0	100	100
16	LH	738/830 (89%)	721 (98%)	17 (2%)	0	100	100
17	LI	374/678 (55%)	370 (99%)	4 (1%)	0	100	100
18	LJ	465/518 (90%)	448 (96%)	17 (4%)	0	100	100
19	LK	116/677 (17%)	113 (97%)	3 (3%)	0	100	100
19	LL	500/677 (74%)	483 (97%)	17 (3%)	0	100	100
20	LM	1977/2144 (92%)	1933 (98%)	44 (2%)	0	100	100
21	LN	667/686 (97%)	647 (97%)	19 (3%)	1 (0%)	48	79
22	LO	844/919 (92%)	826 (98%)	18 (2%)	0	100	100
23	LP	559/597 (94%)	556 (100%)	3 (0%)	0	100	100
24	LQ	810/943 (86%)	792 (98%)	18 (2%)	0	100	100
25	LR	769/808 (95%)	748 (97%)	21 (3%)	0	100	100
26	LS	447/556 (80%)	440 (98%)	7 (2%)	0	100	100
27	LT	863/951 (91%)	847 (98%)	16 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	LU	443/445 (100%)	435 (98%)	8 (2%)	0	100	100
29	LW	449/610 (74%)	436 (97%)	13 (3%)	0	100	100
30	LZ	181/184 (98%)	179 (99%)	2 (1%)	0	100	100
32	NA	243/681 (36%)	242 (100%)	1 (0%)	0	100	100
33	NB	71/479 (15%)	69 (97%)	2 (3%)	0	100	100
34	NC	92/315 (29%)	90 (98%)	2 (2%)	0	100	100
35	ND	82/257 (32%)	81 (99%)	1 (1%)	0	100	100
36	NE	94/293 (32%)	94 (100%)	0	0	100	100
37	NF	147/151 (97%)	145 (99%)	2 (1%)	0	100	100
38	NG	114/151 (76%)	113 (99%)	1 (1%)	0	100	100
39	NH	1064/1146 (93%)	1044 (98%)	20 (2%)	0	100	100
40	NI	232/280 (83%)	229 (99%)	3 (1%)	0	100	100
41	NJ	809/1025 (79%)	783 (97%)	26 (3%)	0	100	100
41	NK	801/1025 (78%)	782 (98%)	19 (2%)	0	100	100
42	NM	229/264 (87%)	226 (99%)	3 (1%)	0	100	100
43	NN	40/560 (7%)	39 (98%)	1 (2%)	0	100	100
44	NO	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
45	NQ	80/84 (95%)	79 (99%)	1 (1%)	0	100	100
47	NT	56/156 (36%)	55 (98%)	1 (2%)	0	100	100
48	NU	58/135 (43%)	57 (98%)	1 (2%)	0	100	100
49	NW	305/688 (44%)	293 (96%)	12 (4%)	0	100	100
50	NY	270/381 (71%)	270 (100%)	0	0	100	100
51	SA	390/594 (66%)	388 (100%)	2 (0%)	0	100	100
52	SB	438/529 (83%)	437 (100%)	1 (0%)	0	100	100
53	SC	225/321 (70%)	219 (97%)	6 (3%)	0	100	100
53	SD	233/321 (73%)	227 (97%)	6 (3%)	0	100	100
54	SE	123/128 (96%)	122 (99%)	1 (1%)	0	100	100
54	SF	121/128 (94%)	119 (98%)	2 (2%)	0	100	100
55	SG	383/475 (81%)	374 (98%)	9 (2%)	0	100	100
56	SH	366/373 (98%)	362 (99%)	4 (1%)	0	100	100
57	SI	825/1282 (64%)	812 (98%)	13 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
58	SJ	202/244 (83%)	200 (99%)	2 (1%)	0	100	100
58	SK	202/244 (83%)	200 (99%)	2 (1%)	0	100	100
59	SL	190/198 (96%)	186 (98%)	4 (2%)	0	100	100
60	SM	288/291 (99%)	280 (97%)	8 (3%)	0	100	100
61	SP	1967/2785 (71%)	1933 (98%)	34 (2%)	0	100	100
62	SQ	183/756 (24%)	182 (100%)	1 (0%)	0	100	100
63	SR	106/143 (74%)	104 (98%)	2 (2%)	0	100	100
64	SS	191/771 (25%)	187 (98%)	4 (2%)	0	100	100
65	ST	432/632 (68%)	424 (98%)	8 (2%)	0	100	100
66	SU	316/472 (67%)	311 (98%)	5 (2%)	0	100	100
67	SW	178/252 (71%)	175 (98%)	3 (2%)	0	100	100
70	SY	232/253 (92%)	230 (99%)	2 (1%)	0	100	100
71	SZ	244/304 (80%)	237 (97%)	7 (3%)	0	100	100
All	All	24774/33986 (73%)	24292 (98%)	481 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	LN	175	SER

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	L3	76/77 (99%)	76 (100%)	0	100	100
5	L4	224/225 (100%)	224 (100%)	0	100	100
6	L5	160/170 (94%)	160 (100%)	0	100	100
7	L6	195/218 (89%)	195 (100%)	0	100	100
8	L7	149/174 (86%)	149 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	L8	155/180 (86%)	155 (100%)	0	100	100
10	L9	152/168 (90%)	152 (100%)	0	100	100
11	LA	102/108 (94%)	102 (100%)	0	100	100
12	LC	114/121 (94%)	114 (100%)	0	100	100
13	LD	133/142 (94%)	133 (100%)	0	100	100
14	LF	92/115 (80%)	92 (100%)	0	100	100
15	LG	55/62 (89%)	55 (100%)	0	100	100
16	LH	670/748 (90%)	669 (100%)	1 (0%)	88	87
17	LI	368/497 (74%)	368 (100%)	0	100	100
18	LJ	412/456 (90%)	412 (100%)	0	100	100
19	LK	112/594 (19%)	112 (100%)	0	100	100
19	LL	456/594 (77%)	456 (100%)	0	100	100
20	LM	1783/1943 (92%)	1782 (100%)	1 (0%)	88	87
21	LN	582/597 (98%)	582 (100%)	0	100	100
22	LO	726/783 (93%)	726 (100%)	0	100	100
23	LP	499/527 (95%)	499 (100%)	0	100	100
24	LQ	690/828 (83%)	690 (100%)	0	100	100
25	LR	648/672 (96%)	648 (100%)	0	100	100
26	LS	393/476 (83%)	393 (100%)	0	100	100
27	LT	744/823 (90%)	744 (100%)	0	100	100
28	LU	399/399 (100%)	399 (100%)	0	100	100
29	LW	373/512 (73%)	373 (100%)	0	100	100
30	LZ	166/167 (99%)	166 (100%)	0	100	100
32	NA	229/626 (37%)	229 (100%)	0	100	100
33	NB	63/413 (15%)	63 (100%)	0	100	100
34	NC	87/282 (31%)	87 (100%)	0	100	100
35	ND	72/222 (32%)	72 (100%)	0	100	100
36	NE	86/253 (34%)	86 (100%)	0	100	100
37	NF	130/131 (99%)	130 (100%)	0	100	100
38	NG	92/119 (77%)	92 (100%)	0	100	100
39	NH	917/984 (93%)	917 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	NI	193/246 (78%)	193 (100%)	0	100	100
41	NJ	707/899 (79%)	706 (100%)	1 (0%)	88	87
41	NK	692/899 (77%)	692 (100%)	0	100	100
42	NM	207/231 (90%)	207 (100%)	0	100	100
43	NN	37/484 (8%)	37 (100%)	0	100	100
44	NO	112/113 (99%)	112 (100%)	0	100	100
45	NQ	74/76 (97%)	74 (100%)	0	100	100
47	NT	51/140 (36%)	51 (100%)	0	100	100
48	NU	53/122 (43%)	53 (100%)	0	100	100
49	NW	282/635 (44%)	281 (100%)	1 (0%)	84	81
50	NY	245/340 (72%)	245 (100%)	0	100	100
51	SA	334/511 (65%)	334 (100%)	0	100	100
52	SB	372/455 (82%)	372 (100%)	0	100	100
53	SC	192/234 (82%)	192 (100%)	0	100	100
53	SD	198/234 (85%)	198 (100%)	0	100	100
54	SE	108/111 (97%)	108 (100%)	0	100	100
54	SF	107/111 (96%)	107 (100%)	0	100	100
55	SG	287/382 (75%)	287 (100%)	0	100	100
56	SH	315/318 (99%)	315 (100%)	0	100	100
57	SI	738/1114 (66%)	738 (100%)	0	100	100
58	SJ	181/209 (87%)	181 (100%)	0	100	100
58	SK	181/209 (87%)	181 (100%)	0	100	100
59	SL	177/182 (97%)	177 (100%)	0	100	100
60	SM	253/254 (100%)	253 (100%)	0	100	100
61	SP	1822/2522 (72%)	1822 (100%)	0	100	100
62	SQ	165/676 (24%)	165 (100%)	0	100	100
63	SR	85/115 (74%)	85 (100%)	0	100	100
64	SS	177/686 (26%)	177 (100%)	0	100	100
65	ST	389/439 (89%)	389 (100%)	0	100	100
66	SU	269/303 (89%)	269 (100%)	0	100	100
67	SW	152/208 (73%)	152 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
70	SY	219/232 (94%)	219 (100%)	0	100	100
71	SZ	214/227 (94%)	214 (100%)	0	100	100
All	All	21892/29323 (75%)	21888 (100%)	4 (0%)	100	100

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	LH	649	GLN
20	LM	1457	GLN
41	NJ	430	GLN
49	NW	7	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (210) such sidechains are listed below:

Mol	Chain	Res	Type
4	L3	72	GLN
5	L4	17	HIS
6	L5	29	GLN
6	L5	65	GLN
8	L7	162	GLN
9	L8	52	ASN
9	L8	165	GLN
10	L9	156	HIS
13	LD	121	GLN
15	LG	29	GLN
16	LH	503	ASN
17	LI	176	ASN
18	LJ	10	GLN
18	LJ	34	GLN
18	LJ	246	ASN
18	LJ	317	HIS
18	LJ	455	GLN
19	LK	525	GLN
19	LL	46	ASN
19	LL	117	HIS
19	LL	458	GLN
19	LL	486	ASN
19	LL	500	HIS
19	LL	507	GLN
19	LL	547	GLN

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Mol	Chain	Res	Type
19	LL	553	GLN
20	LM	181	HIS
20	LM	373	GLN
20	LM	390	ASN
20	LM	488	ASN
20	LM	594	GLN
20	LM	827	HIS
20	LM	904	GLN
20	LM	907	GLN
20	LM	911	GLN
20	LM	943	GLN
20	LM	985	GLN
20	LM	1068	ASN
20	LM	1103	GLN
20	LM	1125	GLN
20	LM	1137	ASN
20	LM	1142	HIS
20	LM	1264	GLN
20	LM	1344	GLN
20	LM	1389	HIS
20	LM	1401	GLN
20	LM	1666	ASN
20	LM	1765	GLN
20	LM	1970	ASN
20	LM	2044	HIS
21	LN	144	GLN
21	LN	219	GLN
21	LN	442	GLN
21	LN	480	GLN
21	LN	519	HIS
22	LO	132	ASN
22	LO	283	ASN
22	LO	324	HIS
22	LO	601	HIS
22	LO	832	GLN
22	LO	849	GLN
23	LP	163	GLN
23	LP	172	HIS
23	LP	256	GLN
23	LP	267	HIS
23	LP	407	GLN
23	LP	478	ASN

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Mol	Chain	Res	Type
23	LP	565	ASN
23	LP	589	HIS
24	LQ	79	HIS
24	LQ	590	HIS
24	LQ	632	HIS
24	LQ	669	GLN
24	LQ	898	ASN
25	LR	141	HIS
25	LR	475	GLN
25	LR	510	GLN
25	LR	722	ASN
25	LR	732	GLN
26	LS	285	ASN
26	LS	503	HIS
26	LS	520	ASN
27	LT	567	ASN
27	LT	748	ASN
27	LT	924	GLN
28	LU	12	ASN
28	LU	75	HIS
28	LU	177	GLN
28	LU	348	ASN
29	LW	265	GLN
29	LW	382	GLN
30	LZ	123	HIS
32	NA	584	GLN
35	ND	236	GLN
36	NE	210	ASN
37	NF	58	HIS
39	NH	87	GLN
39	NH	130	GLN
39	NH	229	ASN
39	NH	303	GLN
39	NH	337	GLN
39	NH	438	GLN
39	NH	457	HIS
39	NH	635	HIS
39	NH	740	HIS
39	NH	865	GLN
39	NH	914	ASN
39	NH	953	GLN
39	NH	1018	HIS

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Mol	Chain	Res	Type
40	NI	34	GLN
41	NJ	111	HIS
41	NJ	430	GLN
41	NJ	578	GLN
41	NJ	796	GLN
41	NJ	873	GLN
41	NK	359	ASN
41	NK	372	HIS
41	NK	430	GLN
41	NK	537	HIS
41	NK	543	ASN
41	NK	612	GLN
41	NK	836	HIS
42	NM	158	HIS
42	NM	159	GLN
42	NM	202	GLN
44	NO	56	HIS
44	NO	90	GLN
45	NQ	9	HIS
47	NT	135	HIS
48	NU	26	ASN
49	NW	170	ASN
49	NW	188	HIS
49	NW	331	ASN
50	NY	86	HIS
50	NY	87	HIS
50	NY	218	ASN
51	SA	131	ASN
51	SA	263	ASN
51	SA	364	ASN
52	SB	113	ASN
52	SB	276	GLN
52	SB	421	HIS
53	SC	251	HIS
53	SC	259	HIS
53	SC	287	GLN
53	SC	288	GLN
53	SD	156	HIS
53	SD	242	GLN
53	SD	259	HIS
54	SE	27	GLN
54	SE	28	GLN

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Mol	Chain	Res	Type
54	SE	115	GLN
54	SF	120	GLN
55	SG	124	GLN
55	SG	425	ASN
56	SH	18	GLN
56	SH	181	GLN
56	SH	203	GLN
57	SI	61	GLN
57	SI	68	HIS
57	SI	727	HIS
57	SI	966	GLN
57	SI	1203	HIS
58	SJ	65	ASN
58	SJ	101	ASN
58	SJ	107	GLN
58	SK	90	GLN
58	SK	123	GLN
59	SL	58	GLN
59	SL	136	HIS
61	SP	80	GLN
61	SP	84	HIS
61	SP	90	GLN
61	SP	187	ASN
61	SP	237	ASN
61	SP	304	HIS
61	SP	624	GLN
61	SP	635	GLN
61	SP	655	HIS
61	SP	659	GLN
61	SP	950	GLN
61	SP	965	HIS
61	SP	1095	HIS
61	SP	1141	GLN
61	SP	1308	GLN
61	SP	1403	ASN
61	SP	1464	GLN
61	SP	1555	GLN
61	SP	1563	GLN
61	SP	1629	HIS
61	SP	1670	GLN
61	SP	1889	GLN
61	SP	1910	GLN

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Mol	Chain	Res	Type
61	SP	1976	GLN
61	SP	2081	HIS
61	SP	2182	ASN
62	SQ	679	ASN
64	SS	195	ASN
64	SS	666	ASN
64	SS	680	HIS
64	SS	708	ASN
65	ST	37	ASN
65	ST	722	HIS
65	ST	748	GLN
65	ST	796	HIS
65	ST	818	GLN
66	SU	262	HIS
66	SU	310	ASN
70	SY	248	GLN
71	SZ	271	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L0	234/3617 (6%)	101 (43%)	6 (2%)
2	L1	1275/1869 (68%)	346 (27%)	23 (1%)
3	L2	214/217 (98%)	80 (37%)	4 (1%)
31	N0	0/22	-	-
All	All	1723/5725 (30%)	527 (30%)	33 (1%)

All (527) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L0	434	C
1	L0	439	U
1	L0	442	U
1	L0	445	C
1	L0	446	G
1	L0	448	C
1	L0	449	G
1	L0	450	U
1	L0	459	G
1	L0	462	C
1	L0	599	G

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Mol	Chain	Res	Type
1	L0	602	C
1	L0	604	C
1	L0	605	G
1	L0	607	C
1	L0	608	C
1	L0	610	G
1	L0	613	C
1	L0	662	G
1	L0	664	C
1	L0	666	U
1	L0	667	C
1	L0	672	G
1	L0	678	G
1	L0	679	A
1	L0	680	C
1	L0	681	A
1	L0	685	C
1	L0	687	C
1	L0	688	G
1	L0	690	U
1	L0	691	G
1	L0	692	U
1	L0	694	G
1	L0	714	U
1	L0	716	C
1	L0	717	G
1	L0	718	G
1	L0	719	G
1	L0	720	C
1	L0	721	G
1	L0	723	C
1	L0	724	C
1	L0	725	C
1	L0	728	C
1	L0	732	G
1	L0	733	C
1	L0	734	G
1	L0	735	G
1	L0	736	C
1	L0	737	G
1	L0	738	G
1	L0	740	G

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Mol	Chain	Res	Type
1	L0	741	G
1	L0	742	G
1	L0	743	G
1	L0	744	G
1	L0	745	U
1	L0	746	G
1	L0	751	C
1	L0	752	C
1	L0	754	G
1	L0	755	C
1	L0	756	C
1	L0	761	C
1	L0	796	C
1	L0	797	G
1	L0	798	U
1	L0	800	G
1	L0	801	G
1	L0	803	U
1	L0	814	C
1	L0	818	G
1	L0	819	C
1	L0	820	G
1	L0	822	U
1	L0	823	G
1	L0	829	G
1	L0	831	A
1	L0	832	G
1	L0	833	C
1	L0	840	G
1	L0	843	U
1	L0	844	G
1	L0	855	G
1	L0	859	G
1	L0	860	A
1	L0	862	G
1	L0	863	C
1	L0	864	C
1	L0	865	G
1	L0	1414	A
1	L0	1415	G
1	L0	1418	A
1	L0	1419	A

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Mol	Chain	Res	Type
1	L0	1420	G
1	L0	1421	C
1	L0	1428	U
1	L0	1430	G
1	L0	1433	A
1	L0	1435	C
2	L1	5	U
2	L1	8	U
2	L1	9	U
2	L1	10	G
2	L1	17	C
2	L1	18	C
2	L1	20	G
2	L1	21	U
2	L1	23	G
2	L1	33	G
2	L1	46	A
2	L1	47	G
2	L1	50	A
2	L1	56	G
2	L1	59	U
2	L1	64	A
2	L1	65	C
2	L1	67	C
2	L1	68	A
2	L1	72	C
2	L1	73	C
2	L1	74	G
2	L1	75	G
2	L1	76	U
2	L1	92	A
2	L1	95	G
2	L1	96	C
2	L1	97	U
2	L1	98	C
2	L1	99	A
2	L1	100	U
2	L1	103	A
2	L1	104	A
2	L1	105	U
2	L1	113	G
2	L1	115	U

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Mol	Chain	Res	Type
2	L1	126	G
2	L1	127	C
2	L1	132	U
2	L1	134	C
2	L1	142	C
2	L1	143	U
2	L1	155	G
2	L1	158	A
2	L1	161	U
2	L1	162	C
2	L1	172	U
2	L1	173	A
2	L1	180	G
2	L1	182	C
2	L1	184	G
2	L1	185	G
2	L1	188	C
2	L1	190	G
2	L1	192	C
2	L1	195	C
2	L1	204	G
2	L1	205	G
2	L1	206	G
2	L1	210	U
2	L1	214	U
2	L1	215	G
2	L1	226	A
2	L1	227	U
2	L1	228	C
2	L1	229	A
2	L1	235	A
2	L1	238	C
2	L1	248	C
2	L1	269	G
2	L1	271	C
2	L1	272	G
2	L1	275	C
2	L1	279	G
2	L1	283	G
2	L1	285	U
2	L1	287	U
2	L1	288	G

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Mol	Chain	Res	Type
2	L1	306	C
2	L1	307	G
2	L1	308	G
2	L1	312	G
2	L1	319	C
2	L1	321	C
2	L1	322	C
2	L1	323	C
2	L1	325	C
2	L1	326	C
2	L1	328	U
2	L1	329	G
2	L1	332	G
2	L1	335	G
2	L1	347	G
2	L1	350	C
2	L1	362	C
2	L1	364	A
2	L1	368	U
2	L1	369	C
2	L1	370	G
2	L1	385	G
2	L1	386	C
2	L1	389	A
2	L1	391	C
2	L1	400	C
2	L1	405	G
2	L1	407	G
2	L1	408	A
2	L1	413	G
2	L1	415	A
2	L1	416	U
2	L1	417	C
2	L1	419	G
2	L1	420	G
2	L1	422	U
2	L1	423	U
2	L1	424	C
2	L1	427	U
2	L1	430	C
2	L1	431	G
2	L1	432	G

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Mol	Chain	Res	Type
2	L1	439	A
2	L1	447	A
2	L1	451	G
2	L1	452	G
2	L1	467	G
2	L1	471	G
2	L1	478	G
2	L1	480	G
2	L1	481	C
2	L1	482	G
2	L1	483	C
2	L1	484	A
2	L1	485	A
2	L1	486	A
2	L1	487	U
2	L1	488	U
2	L1	492	C
2	L1	496	C
2	L1	502	C
2	L1	514	U
2	L1	515	G
2	L1	516	A
2	L1	525	A
2	L1	528	A
2	L1	534	G
2	L1	535	G
2	L1	541	U
2	L1	544	G
2	L1	548	C
2	L1	550	C
2	L1	554	A
2	L1	555	A
2	L1	556	U
2	L1	559	G
2	L1	560	A
2	L1	564	A
2	L1	570	C
2	L1	588	G
2	L1	590	A
2	L1	591	U
2	L1	594	A
2	L1	606	G

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Mol	Chain	Res	Type
2	L1	611	G
2	L1	614	C
2	L1	622	C
2	L1	624	C
2	L1	627	U
2	L1	628	A
2	L1	643	A
2	L1	644	G
2	L1	651	U
2	L1	652	U
2	L1	653	A
2	L1	654	A
2	L1	655	A
2	L1	684	G
2	L1	920	A
2	L1	933	G
2	L1	938	A
2	L1	943	U
2	L1	955	A
2	L1	969	U
2	L1	970	G
2	L1	983	A
2	L1	990	A
2	L1	991	G
2	L1	992	A
2	L1	1017	U
2	L1	1023	A
2	L1	1027	A
2	L1	1093	A
2	L1	1094	C
2	L1	1096	G
2	L1	1100	A
2	L1	1111	U
2	L1	1114	U
2	L1	1115	U
2	L1	1121	G
2	L1	1133	A
2	L1	1137	U
2	L1	1144	A
2	L1	1145	A
2	L1	1147	C
2	L1	1148	A

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Mol	Chain	Res	Type
2	L1	1170	A
2	L1	1172	U
2	L1	1174	U
2	L1	1175	G
2	L1	1178	U
2	L1	1187	G
2	L1	1189	A
2	L1	1190	A
2	L1	1192	U
2	L1	1193	U
2	L1	1195	A
2	L1	1196	A
2	L1	1198	G
2	L1	1212	G
2	L1	1215	C
2	L1	1216	C
2	L1	1217	A
2	L1	1267	C
2	L1	1268	C
2	L1	1273	C
2	L1	1275	G
2	L1	1276	A
2	L1	1277	C
2	L1	1278	A
2	L1	1283	C
2	L1	1286	G
2	L1	1290	G
2	L1	1295	A
2	L1	1301	A
2	L1	1302	G
2	L1	1303	C
2	L1	1308	U
2	L1	1309	C
2	L1	1311	C
2	L1	1313	A
2	L1	1315	U
2	L1	1316	C
2	L1	1318	G
2	L1	1320	G
2	L1	1327	G
2	L1	1328	G
2	L1	1329	U

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Mol	Chain	Res	Type
2	L1	1330	G
2	L1	1331	C
2	L1	1333	U
2	L1	1335	G
2	L1	1348	G
2	L1	1354	G
2	L1	1355	C
2	L1	1358	U
2	L1	1365	G
2	L1	1371	U
2	L1	1372	U
2	L1	1374	C
2	L1	1376	A
2	L1	1377	U
2	L1	1378	A
2	L1	1382	A
2	L1	1394	G
2	L1	1452	A
2	L1	1454	A
2	L1	1461	G
2	L1	1462	U
2	L1	1463	U
2	L1	1464	C
2	L1	1465	A
2	L1	1466	G
2	L1	1477	U
2	L1	1485	U
2	L1	1487	A
2	L1	1489	A
2	L1	1490	G
2	L1	1491	G
2	L1	1492	U
2	L1	1493	C
2	L1	1494	U
2	L1	1495	G
2	L1	1496	U
2	L1	1498	A
2	L1	1499	U
2	L1	1503	C
2	L1	1524	G
2	L1	1533	A
2	L1	1534	C

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Mol	Chain	Res	Type
2	L1	1544	C
2	L1	1548	G
2	L1	1549	U
2	L1	1550	G
2	L1	1592	C
2	L1	1599	U
2	L1	1638	G
2	L1	1639	G
2	L1	1648	G
2	L1	1656	G
2	L1	1660	C
2	L1	1664	A
2	L1	1665	G
2	L1	1666	C
2	L1	1667	U
2	L1	1681	U
2	L1	1685	U
2	L1	1692	U
2	L1	1704	C
2	L1	1710	C
2	L1	1715	A
2	L1	1720	U
2	L1	1721	U
2	L1	1722	G
2	L1	1724	A
2	L1	1725	U
2	L1	1729	U
2	L1	1757	G
2	L1	1760	G
2	L1	1765	C
2	L1	1767	C
2	L1	1768	A
2	L1	1769	C
2	L1	1770	G
2	L1	1771	G
2	L1	1772	C
2	L1	1774	C
2	L1	1775	U
2	L1	1776	G
2	L1	1777	G
2	L1	1783	C
2	L1	1784	G

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Mol	Chain	Res	Type
2	L1	1785	C
2	L1	1800	A
2	L1	1801	A
2	L1	1809	A
2	L1	1810	U
2	L1	1812	U
2	L1	1813	A
2	L1	1818	A
2	L1	1824	A
2	L1	1838	U
2	L1	1846	G
2	L1	1848	U
2	L1	1849	G
2	L1	1850	A
2	L1	1851	A
2	L1	1852	C
3	L2	13	U
3	L2	14	C
3	L2	15	A
3	L2	16	G
3	L2	22	A
3	L2	23	U
3	L2	24	U
3	L2	25	U
3	L2	27	U
3	L2	28	A
3	L2	30	A
3	L2	31	G
3	L2	32	U
3	L2	33	G
3	L2	35	G
3	L2	39	C
3	L2	44	G
3	L2	46	A
3	L2	49	U
3	L2	61	G
3	L2	62	U
3	L2	64	G
3	L2	68	A
3	L2	69	C
3	L2	88	G
3	L2	89	A

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Mol	Chain	Res	Type
3	L2	91	G
3	L2	92	U
3	L2	108	G
3	L2	109	C
3	L2	110	G
3	L2	114	A
3	L2	115	G
3	L2	116	C
3	L2	117	C
3	L2	118	G
3	L2	119	G
3	L2	123	U
3	L2	124	C
3	L2	125	U
3	L2	126	G
3	L2	127	G
3	L2	128	C
3	L2	129	G
3	L2	130	U
3	L2	131	U
3	L2	132	G
3	L2	138	C
3	L2	139	U
3	L2	145	U
3	L2	146	G
3	L2	147	C
3	L2	148	C
3	L2	149	G
3	L2	150	U
3	L2	152	A
3	L2	153	G
3	L2	154	C
3	L2	158	U
3	L2	168	U
3	L2	171	U
3	L2	172	C
3	L2	174	C
3	L2	179	U
3	L2	181	U
3	L2	182	U
3	L2	183	G
3	L2	185	G

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Mol	Chain	Res	Type
3	L2	188	G
3	L2	189	U
3	L2	190	G
3	L2	191	A
3	L2	192	G
3	L2	199	A
3	L2	200	G
3	L2	201	A
3	L2	202	A
3	L2	208	U
3	L2	209	C
3	L2	213	G

All (33) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L0	433	U
1	L0	604	C
1	L0	666	U
1	L0	732	G
1	L0	799	C
1	L0	854	U
2	L1	157	U
2	L1	226	A
2	L1	227	U
2	L1	325	C
2	L1	368	U
2	L1	369	C
2	L1	423	U
2	L1	450	C
2	L1	466	G
2	L1	487	U
2	L1	589	G
2	L1	969	U
2	L1	1197	G
2	L1	1393	G
2	L1	1461	G
2	L1	1637	A
2	L1	1664	A
2	L1	1684	C
2	L1	1703	C
2	L1	1719	A

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Mol	Chain	Res	Type
2	L1	1765	C
2	L1	1817	G
2	L1	1823	A
3	L2	14	C
3	L2	145	U
3	L2	152	A
3	L2	188	G

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 30 ligands modelled in this entry, 25 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$
73	ATP	NK	1101	-	32,33,33	0.27	0	48,52,52	0.28	0
75	GTP	SI	2001	72	33,34,34	0.97	1 (3%)	50,54,54	1.64	9 (18%)
76	SAH	SK	301	-	27,28,28	1.09	4 (14%)	36,40,40	2.02	9 (25%)
76	SAH	SJ	301	-	27,28,28	1.09	4 (14%)	36,40,40	2.02	10 (27%)
73	ATP	NH	3000	72	32,33,33	0.28	0	48,52,52	0.36	0

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
73	ATP	NK	1101	-	-	9/22/38/38	0/3/3/3
75	GTP	SI	2001	72	-	7/22/38/38	0/3/3/3
76	SAH	SK	301	-	-	9/15/31/31	0/3/3/3
76	SAH	SJ	301	-	-	2/15/31/31	0/3/3/3
73	ATP	NH	3000	72	-	7/22/38/38	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
76	SK	301	SAH	C2-N1	2.57	1.38	1.33
76	SJ	301	SAH	C2-N1	2.55	1.38	1.33
76	SJ	301	SAH	C2-N3	2.53	1.38	1.33
76	SK	301	SAH	C2-N3	2.47	1.38	1.33
76	SK	301	SAH	OXT-C	-2.21	1.23	1.30
76	SJ	301	SAH	OXT-C	-2.21	1.23	1.30
75	SI	2001	GTP	C2-N3	2.14	1.38	1.33
76	SK	301	SAH	C8-N7	2.11	1.35	1.31
76	SJ	301	SAH	C8-N7	2.05	1.35	1.31

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
76	SK	301	SAH	N3-C2-N1	-5.51	120.25	128.58
76	SJ	301	SAH	N3-C2-N1	-5.50	120.25	128.58
75	SI	2001	GTP	C5-C4-N3	-5.48	119.66	128.39
75	SI	2001	GTP	C2-N3-C4	4.91	120.76	112.30
76	SJ	301	SAH	C5-C4-N3	-4.58	120.41	126.72
76	SK	301	SAH	C5-C4-N3	-4.43	120.61	126.72
76	SK	301	SAH	N9-C8-N7	-3.82	108.52	113.94
76	SJ	301	SAH	N9-C8-N7	-3.75	108.62	113.94
76	SK	301	SAH	C5'-SD-CG	-3.45	92.02	102.26
75	SI	2001	GTP	N9-C4-N3	3.41	132.77	125.95
76	SJ	301	SAH	C2-N3-C4	3.39	120.10	111.83
76	SK	301	SAH	C2-N3-C4	3.38	120.08	111.83
76	SJ	301	SAH	C5'-SD-CG	-3.35	92.33	102.26
76	SK	301	SAH	C5-N7-C8	3.31	108.66	103.45
76	SJ	301	SAH	C5-N7-C8	3.31	108.65	103.45
76	SJ	301	SAH	N3-C4-N9	3.12	132.47	127.17
76	SK	301	SAH	N3-C4-N9	2.89	132.09	127.17
75	SI	2001	GTP	C2-N1-C6	-2.81	120.02	125.11
76	SK	301	SAH	OXT-C-O	-2.69	117.99	124.08
75	SI	2001	GTP	C8-N7-C5	2.65	108.99	104.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
76	SJ	301	SAH	OXT-C-O	-2.64	118.09	124.08
75	SI	2001	GTP	N9-C8-N7	-2.55	108.67	113.40
75	SI	2001	GTP	C5-C6-N1	2.41	119.38	113.25
76	SK	301	SAH	C4-C5-N7	-2.33	107.92	110.58
75	SI	2001	GTP	O6-C6-C5	-2.29	120.48	126.53
75	SI	2001	GTP	C3'-C2'-C1'	2.24	105.69	101.46
76	SJ	301	SAH	C4-C5-N7	-2.23	108.03	110.58
76	SJ	301	SAH	C3'-C2'-C1'	2.01	105.27	101.46

There are no chirality outliers.

All (34) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
73	NH	3000	ATP	C5'-O5'-PA-O1A
73	NH	3000	ATP	C5'-O5'-PA-O3A
73	NK	1101	ATP	C5'-O5'-PA-O1A
73	NK	1101	ATP	C5'-O5'-PA-O3A
75	SI	2001	GTP	C5'-O5'-PA-O3A
75	SI	2001	GTP	C5'-O5'-PA-O1A
75	SI	2001	GTP	C5'-O5'-PA-O2A
76	SK	301	SAH	O4'-C4'-C5'-SD
76	SK	301	SAH	OXT-C-CA-CB
73	NH	3000	ATP	O4'-C4'-C5'-O5'
76	SK	301	SAH	C-CA-CB-CG
76	SK	301	SAH	O-C-CA-CB
73	NH	3000	ATP	C3'-C4'-C5'-O5'
76	SJ	301	SAH	OXT-C-CA-N
73	NK	1101	ATP	C4'-C5'-O5'-PA
76	SJ	301	SAH	CA-CB-CG-SD
76	SK	301	SAH	OXT-C-CA-N
73	NK	1101	ATP	PA-O3A-PB-O1B
76	SK	301	SAH	C3'-C4'-C5'-SD
76	SK	301	SAH	CB-CG-SD-C5'
73	NH	3000	ATP	C4'-C5'-O5'-PA
73	NK	1101	ATP	C5'-O5'-PA-O2A
73	NK	1101	ATP	O4'-C4'-C5'-O5'
75	SI	2001	GTP	PG-O3B-PB-O2B
75	SI	2001	GTP	PB-O3A-PA-O1A
76	SK	301	SAH	O-C-CA-N
75	SI	2001	GTP	PB-O3A-PA-O2A
73	NH	3000	ATP	PG-O3B-PB-O1B
73	NK	1101	ATP	PG-O3B-PB-O2B

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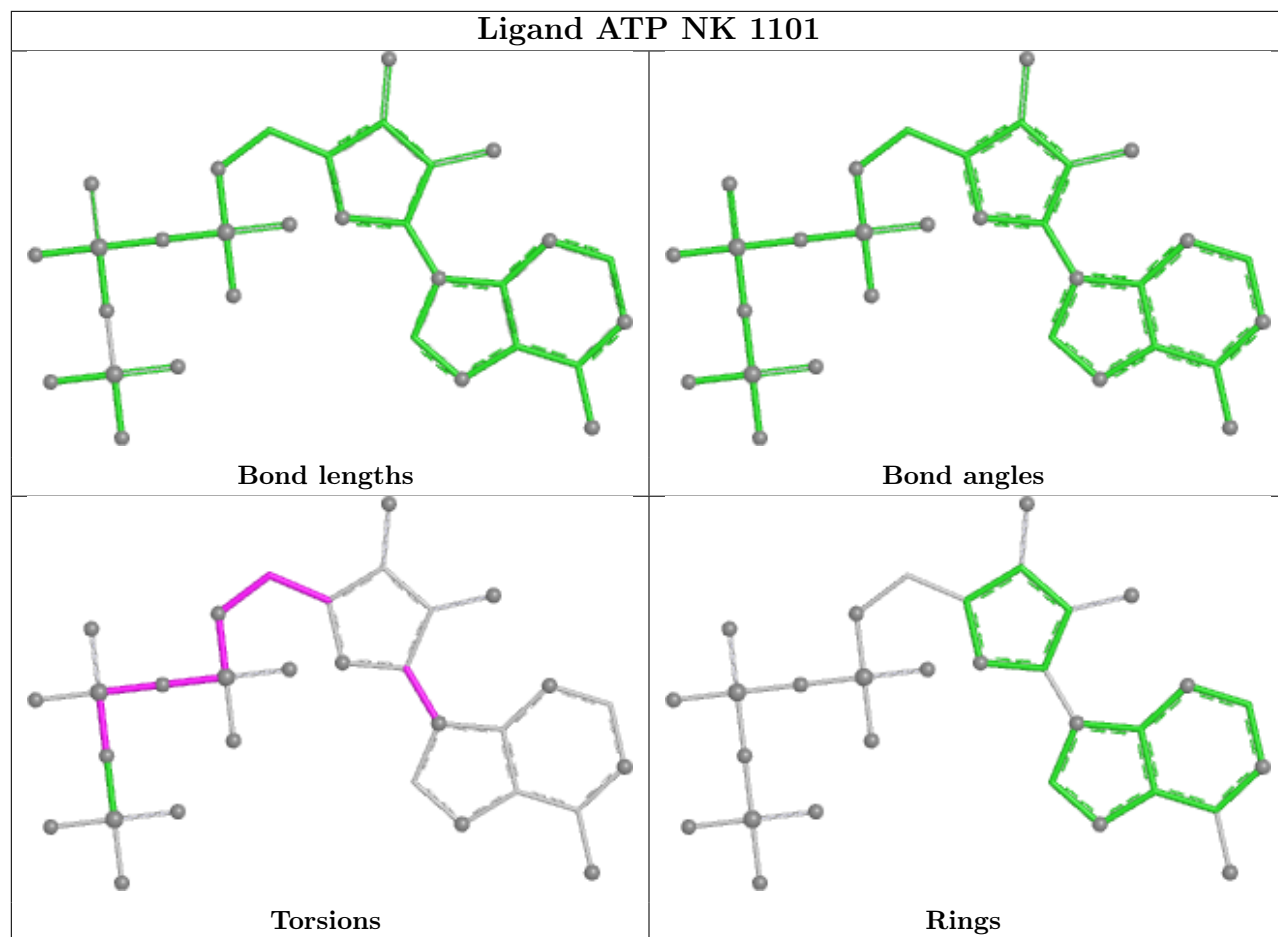
Mol	Chain	Res	Type	Atoms
75	SI	2001	GTP	PG-O3B-PB-O1B
73	NK	1101	ATP	O4'-C1'-N9-C8
76	SK	301	SAH	CA-CB-CG-SD
73	NH	3000	ATP	PG-O3B-PB-O2B
73	NK	1101	ATP	PB-O3A-PA-O2A

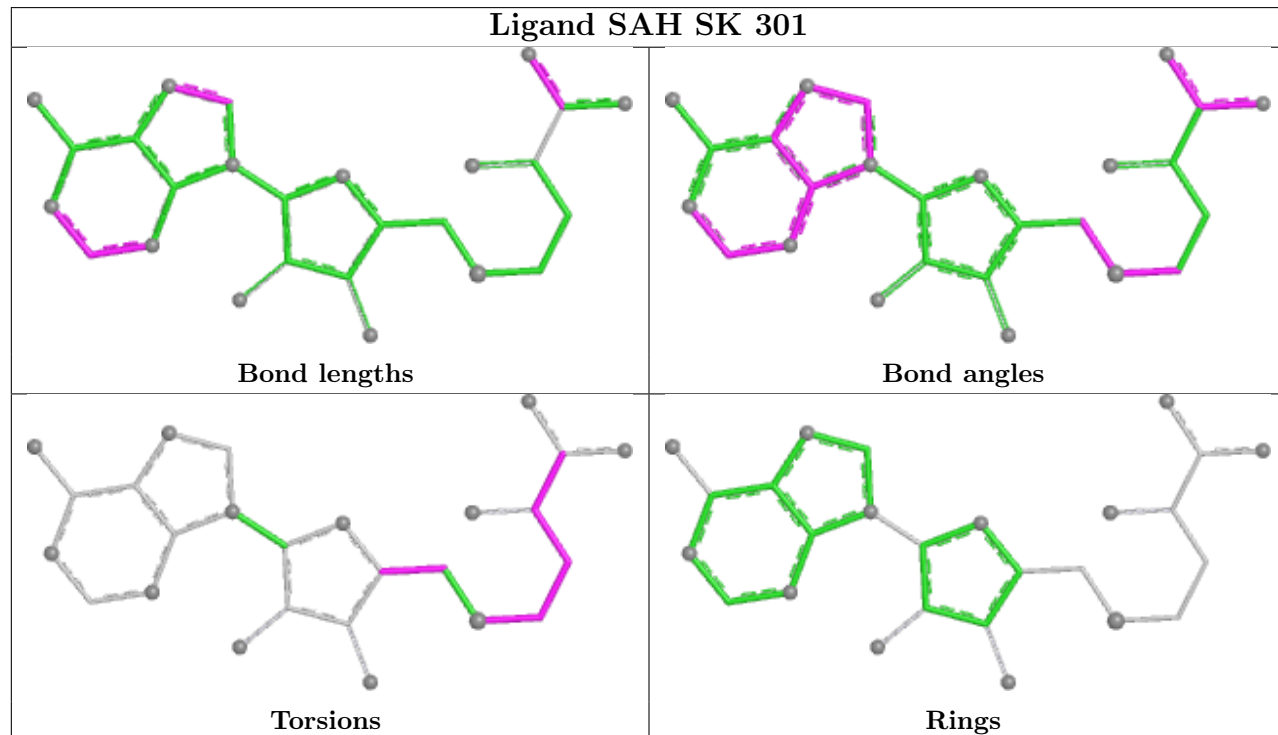
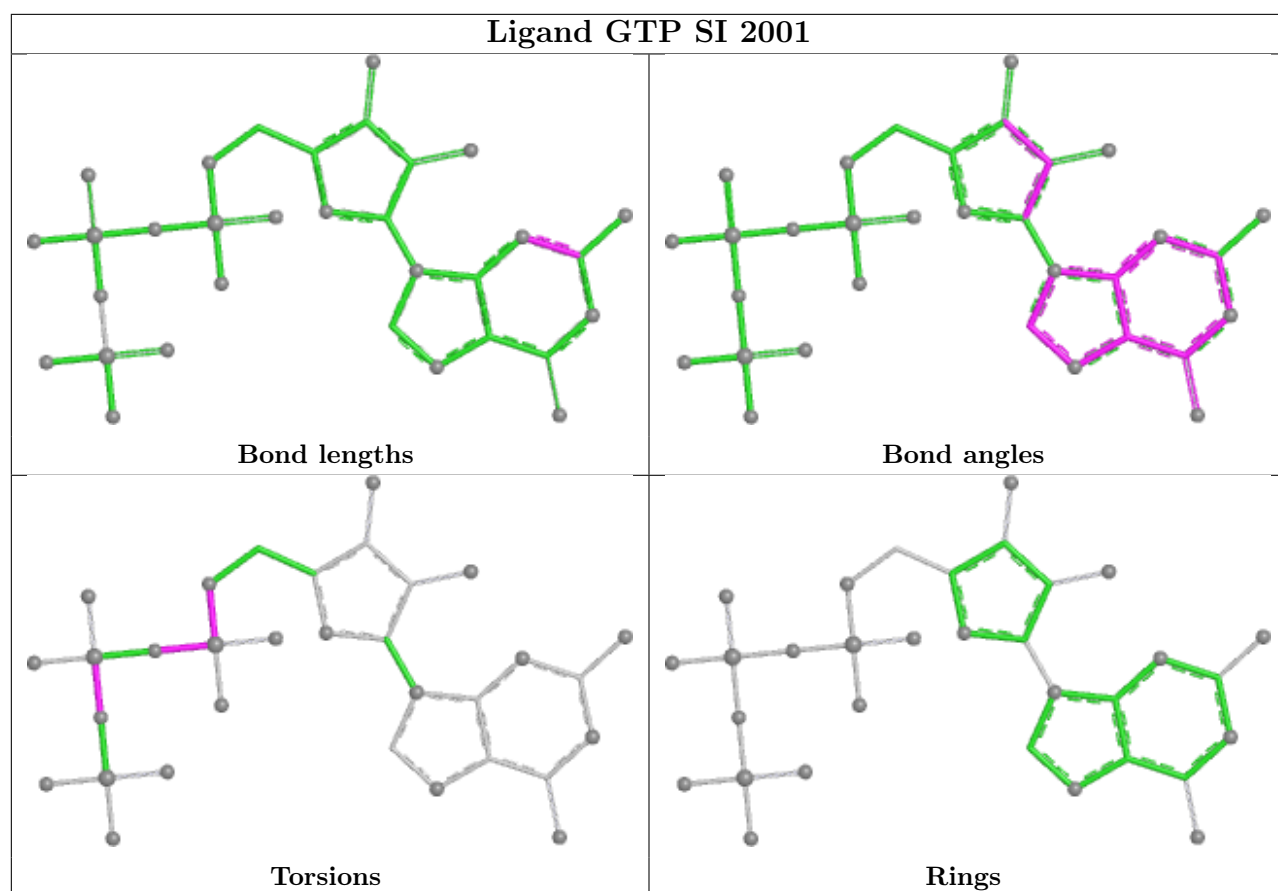
There are no ring outliers.

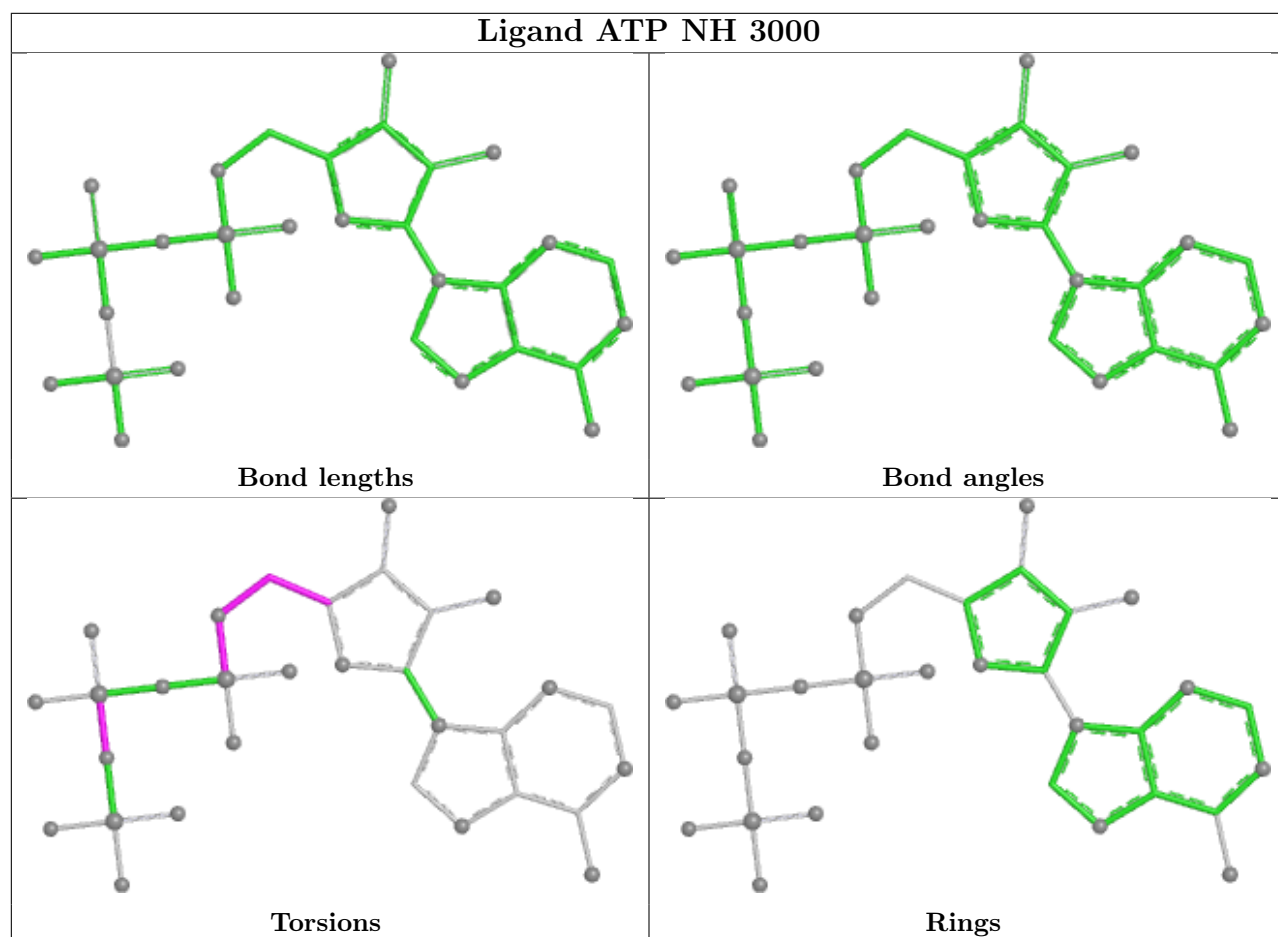
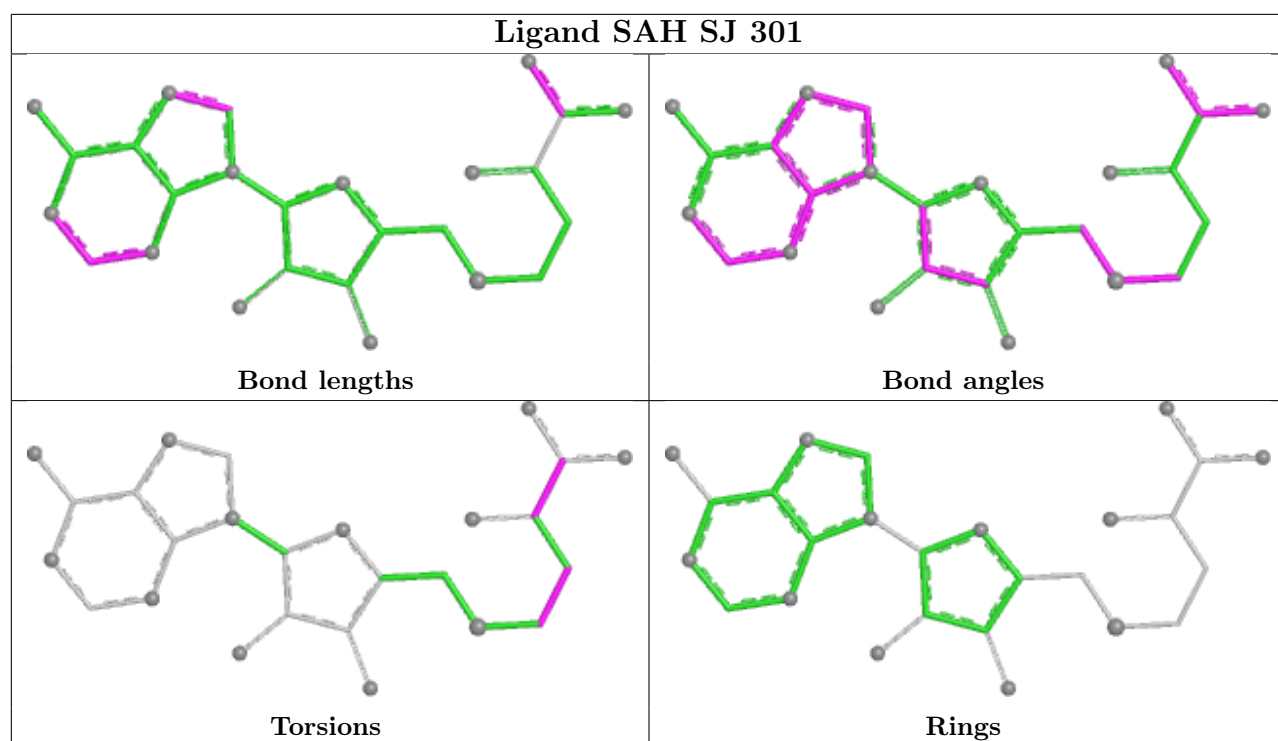
3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
73	NK	1101	ATP	1	0
76	SJ	301	SAH	3	0
73	NH	3000	ATP	2	0

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







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
46	NR	41
17	LI	5
66	SU	5
65	ST	3
31	N0	1
71	SZ	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	ST	298:LEU	C	414:UNK	N	52.49
1	ST	86:LYS	C	186:UNK	N	37.14
1	LI	48:UNK	C	59:UNK	N	26.45
1	ST	234:UNK	C	246:UNK	N	22.17
1	LI	92:UNK	C	104:UNK	N	18.16
1	NR	567:UNK	C	571:UNK	N	16.63
1	NR	310:UNK	C	312:UNK	N	16.61
1	NR	803:UNK	C	807:UNK	N	16.44
1	NR	131:UNK	C	134:UNK	N	15.65
1	N0	881:N	O3'	1396:N	P	15.50
1	LI	346:UNK	C	354:HIS	N	15.48
1	NR	358:UNK	C	361:UNK	N	15.11
1	NR	450:UNK	C	452:UNK	N	14.79
1	NR	976:UNK	C	980:UNK	N	14.36
1	NR	915:UNK	C	919:UNK	N	13.77
1	NR	496:UNK	C	498:UNK	N	13.11
1	NR	101:UNK	C	112:UNK	N	13.01
1	NR	647:UNK	C	651:UNK	N	12.81
1	NR	953:UNK	C	957:UNK	N	12.49
1	NR	613:UNK	C	616:UNK	N	12.32
1	NR	517:UNK	C	519:UNK	N	12.19
1	SU	68:UNK	C	78:UNK	N	12.19
1	LI	147:UNK	C	152:VAL	N	12.09
1	NR	688:UNK	C	692:UNK	N	12.06
1	NR	475:UNK	C	477:UNK	N	11.96

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	NR	426:UNK	C	428:UNK	N	11.89
1	NR	221:UNK	C	225:UNK	N	11.77
1	NR	870:UNK	C	874:UNK	N	11.74
1	NR	995:UNK	C	999:UNK	N	11.59
1	NR	335:UNK	C	339:UNK	N	11.11
1	NR	672:UNK	C	674:UNK	N	11.07
1	NR	713:UNK	C	717:UNK	N	10.68
1	NR	846:UNK	C	850:UNK	N	10.28
1	NR	934:UNK	C	936:UNK	N	10.24
1	NR	894:UNK	C	898:UNK	N	10.23
1	SZ	164:UNK	C	169:UNK	N	10.07
1	NR	631:UNK	C	633:UNK	N	9.93
1	NR	780:UNK	C	784:UNK	N	9.87
1	NR	590:UNK	C	592:UNK	N	9.00
1	NR	538:UNK	C	541:UNK	N	8.70
1	NR	824:UNK	C	828:UNK	N	8.69
1	NR	550:UNK	C	555:UNK	N	8.55
1	SU	169:UNK	C	177:TYR	N	8.34
1	SU	25:UNK	C	27:UNK	N	7.92
1	NR	1008:UNK	C	1010:UNK	N	7.73
1	NR	243:UNK	C	246:UNK	N	7.72
1	NR	262:UNK	C	264:UNK	N	7.28
1	NR	756:UNK	C	760:UNK	N	7.03
1	NR	734:UNK	C	736:UNK	N	6.94
1	NR	381:UNK	C	383:UNK	N	5.74
1	SU	45:UNK	C	48:UNK	N	5.53
1	NR	200:UNK	C	204:UNK	N	5.43
1	LI	322:HIS	C	325:UNK	N	5.34
1	SU	124:UNK	C	141:PRO	N	4.96
1	NR	289:UNK	C	291:UNK	N	4.86
1	NR	404:UNK	C	407:UNK	N	3.63

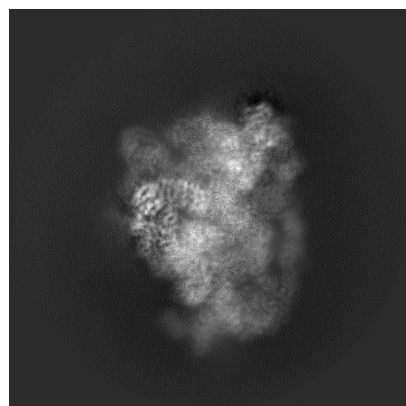
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23936. These allow visual inspection of the internal detail of the map and identification of artifacts.

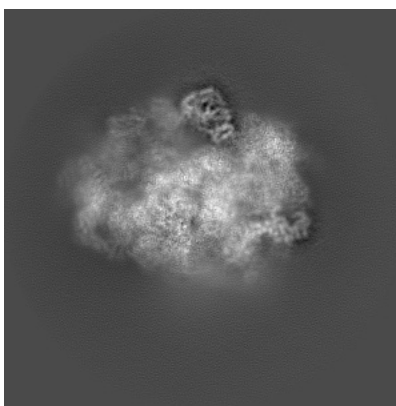
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

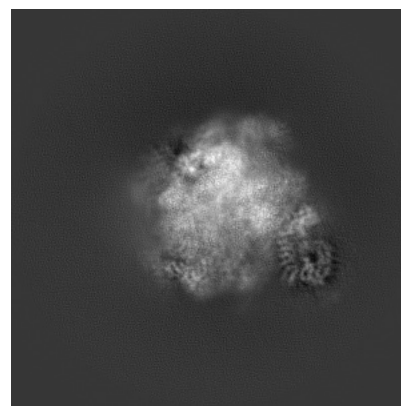
6.1.1 Primary map



X

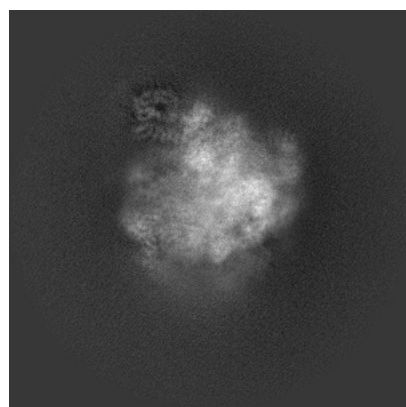


Y

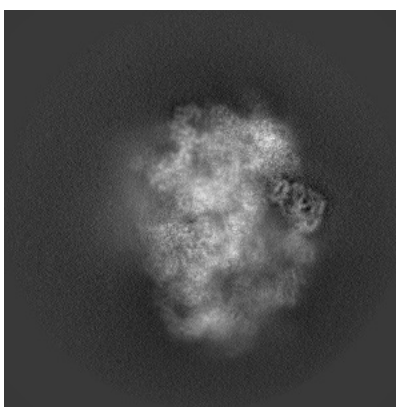


Z

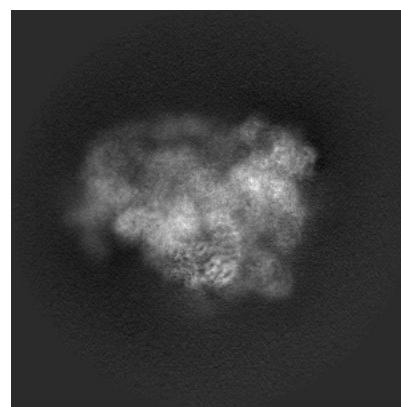
6.1.2 Raw map



X



Y

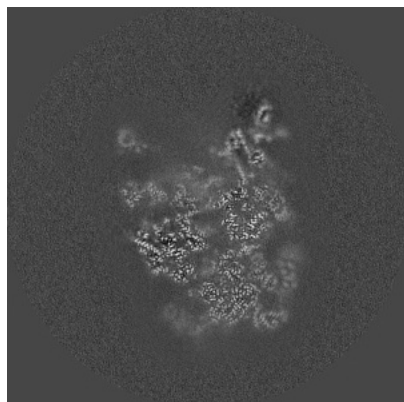


Z

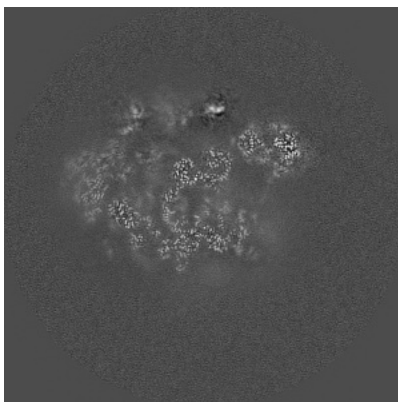
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

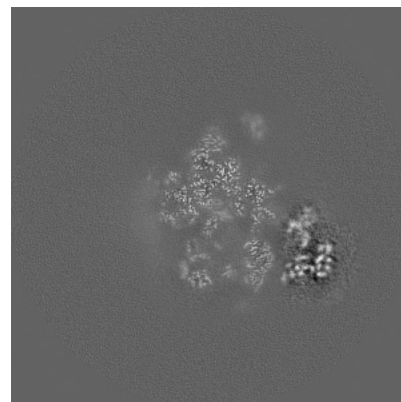
6.2.1 Primary map



X Index: 280

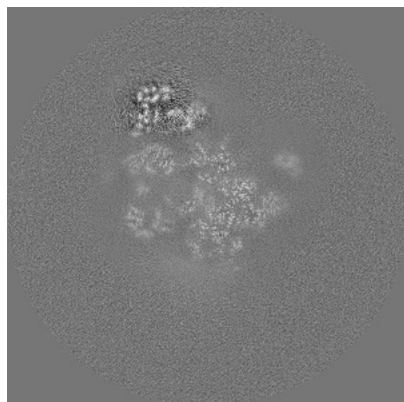


Y Index: 280

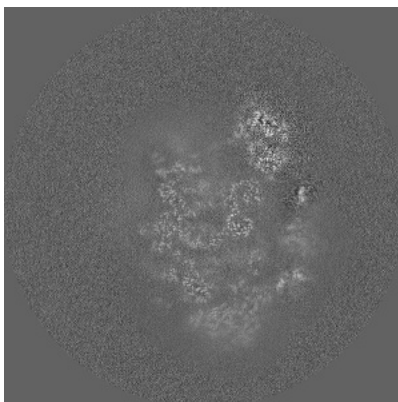


Z Index: 280

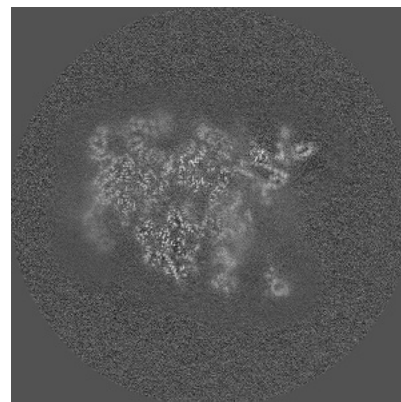
6.2.2 Raw map



X Index: 280



Y Index: 280

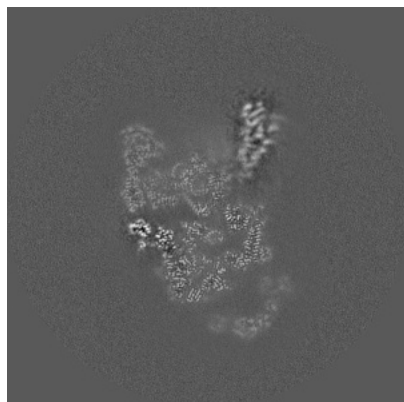


Z Index: 280

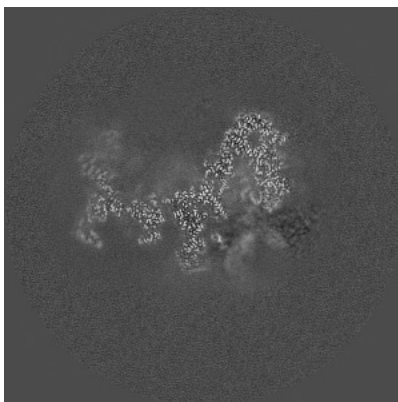
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

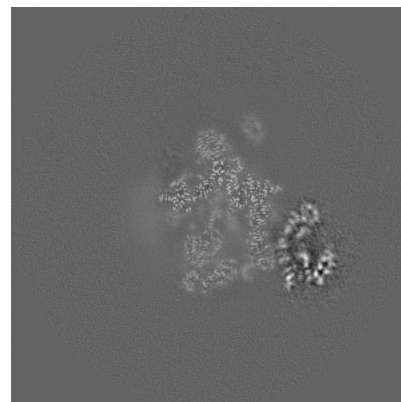
6.3.1 Primary map



X Index: 254

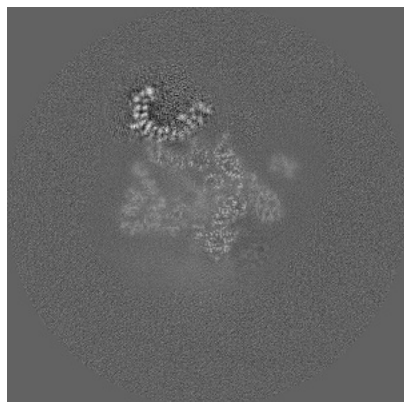


Y Index: 318

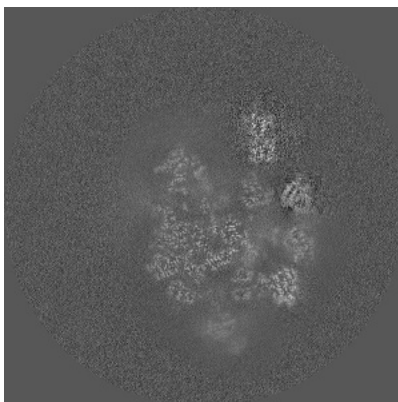


Z Index: 291

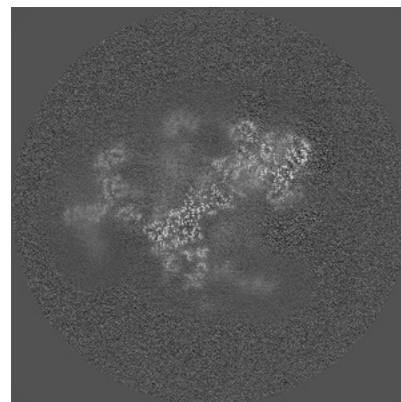
6.3.2 Raw map



X Index: 298



Y Index: 261

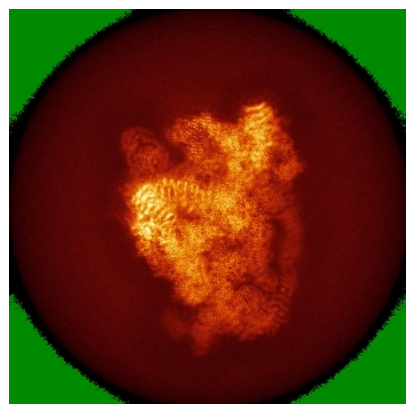


Z Index: 320

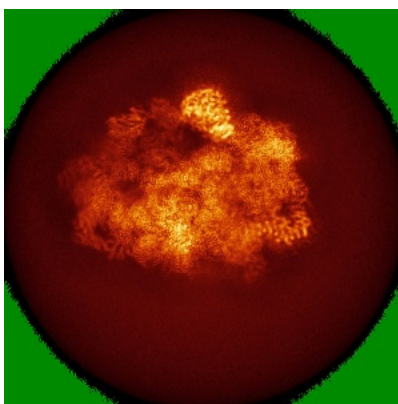
The images above show the largest variance slices of the map in three orthogonal directions.

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

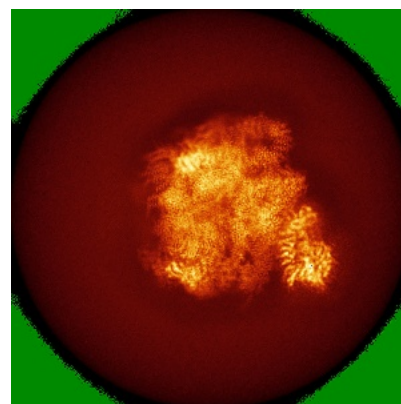
6.4.1 Primary map



X

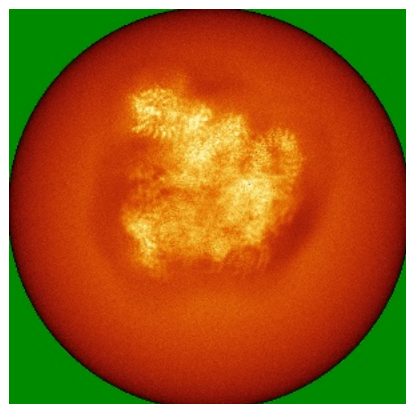


Y

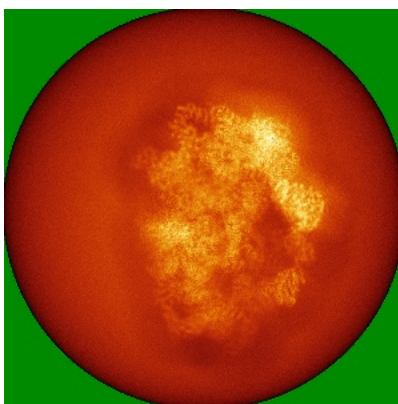


Z

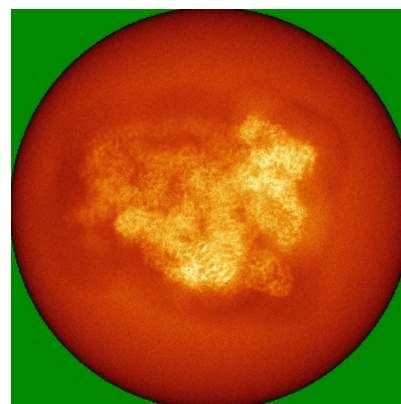
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

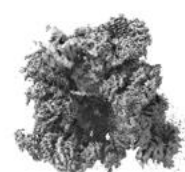
6.5.1 Primary map



X



Y



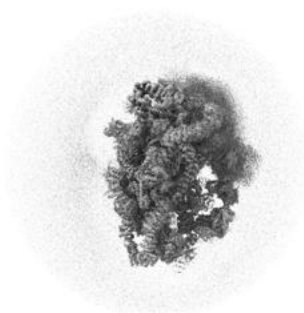
Z

The images above show the 3D surface view of the map at the recommended contour level 2.68. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

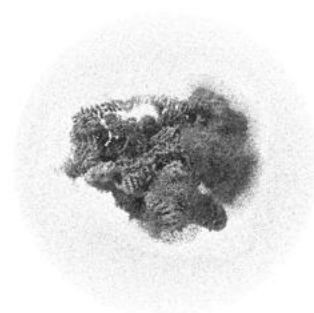
6.5.2 Raw map



X



Y



Z

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

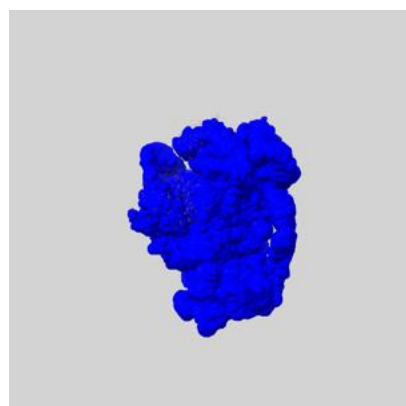
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

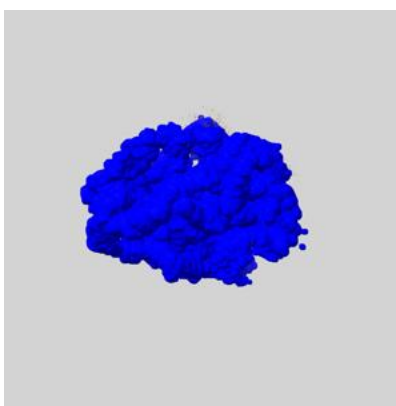
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

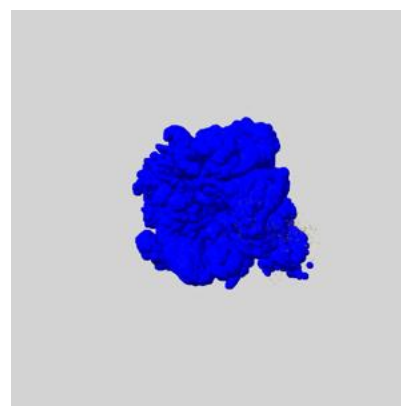
6.6.1 emd_23936_msk_1.map [i](#)



X



Y

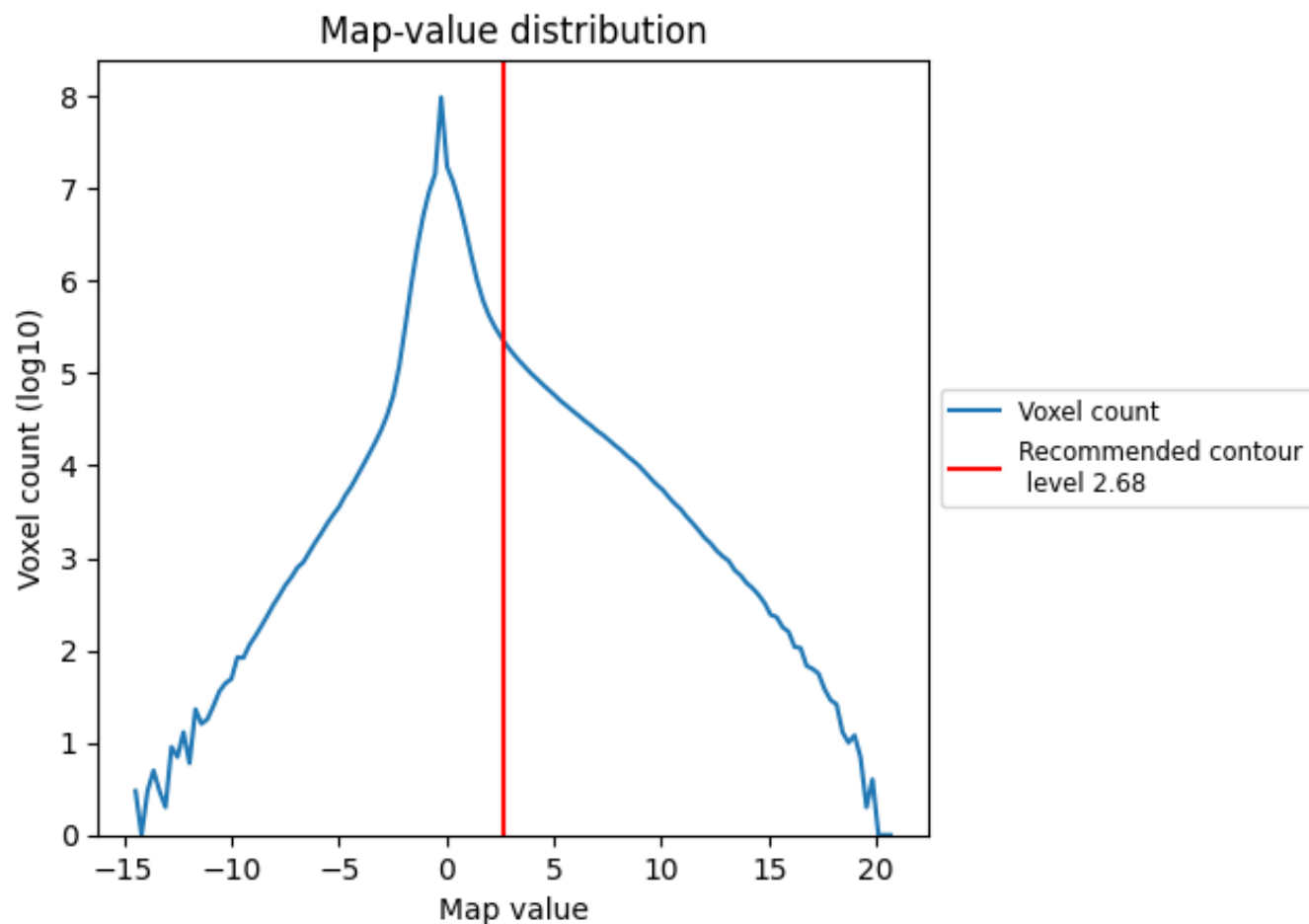


Z

7 Map analysis [i](#)

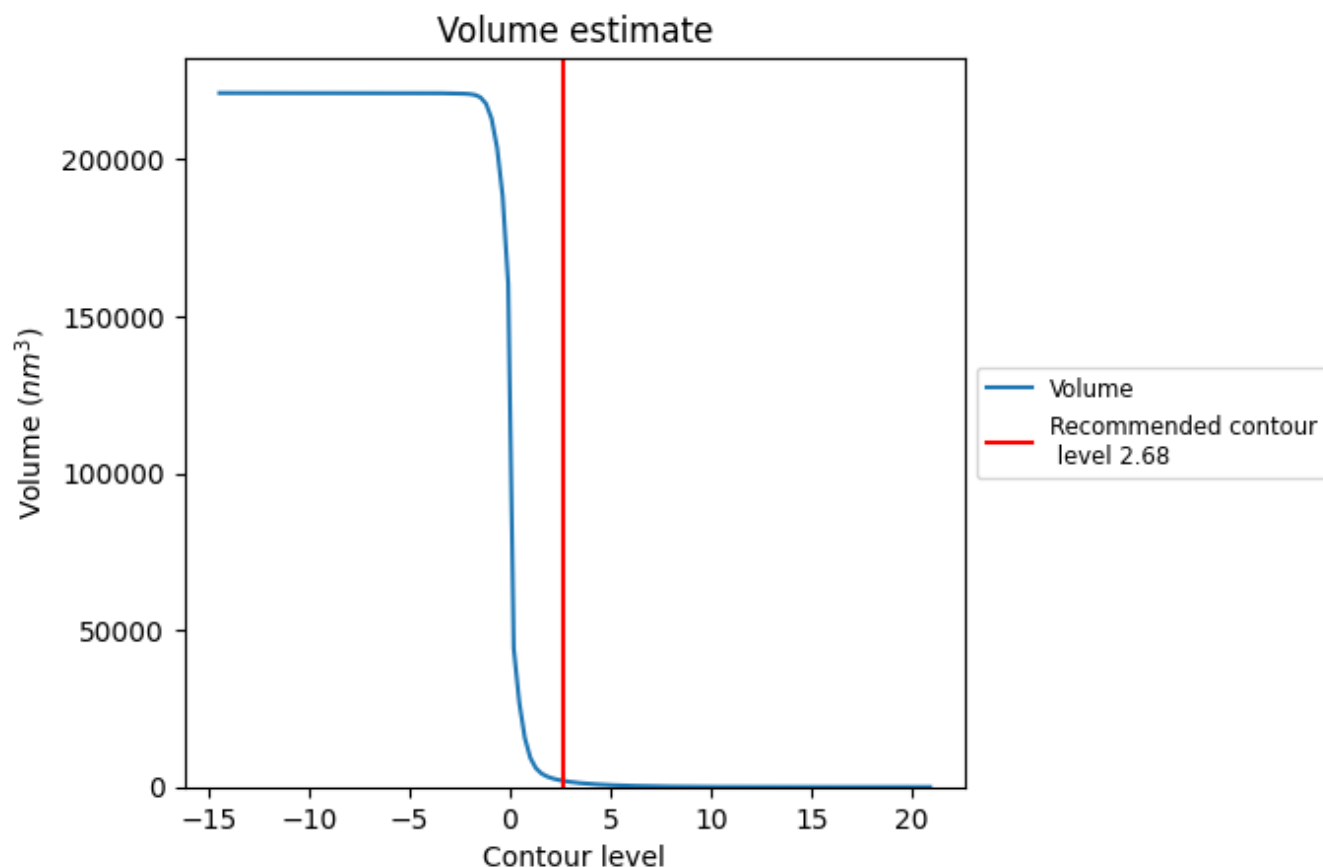
This section contains the results of statistical analysis of the map.

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.

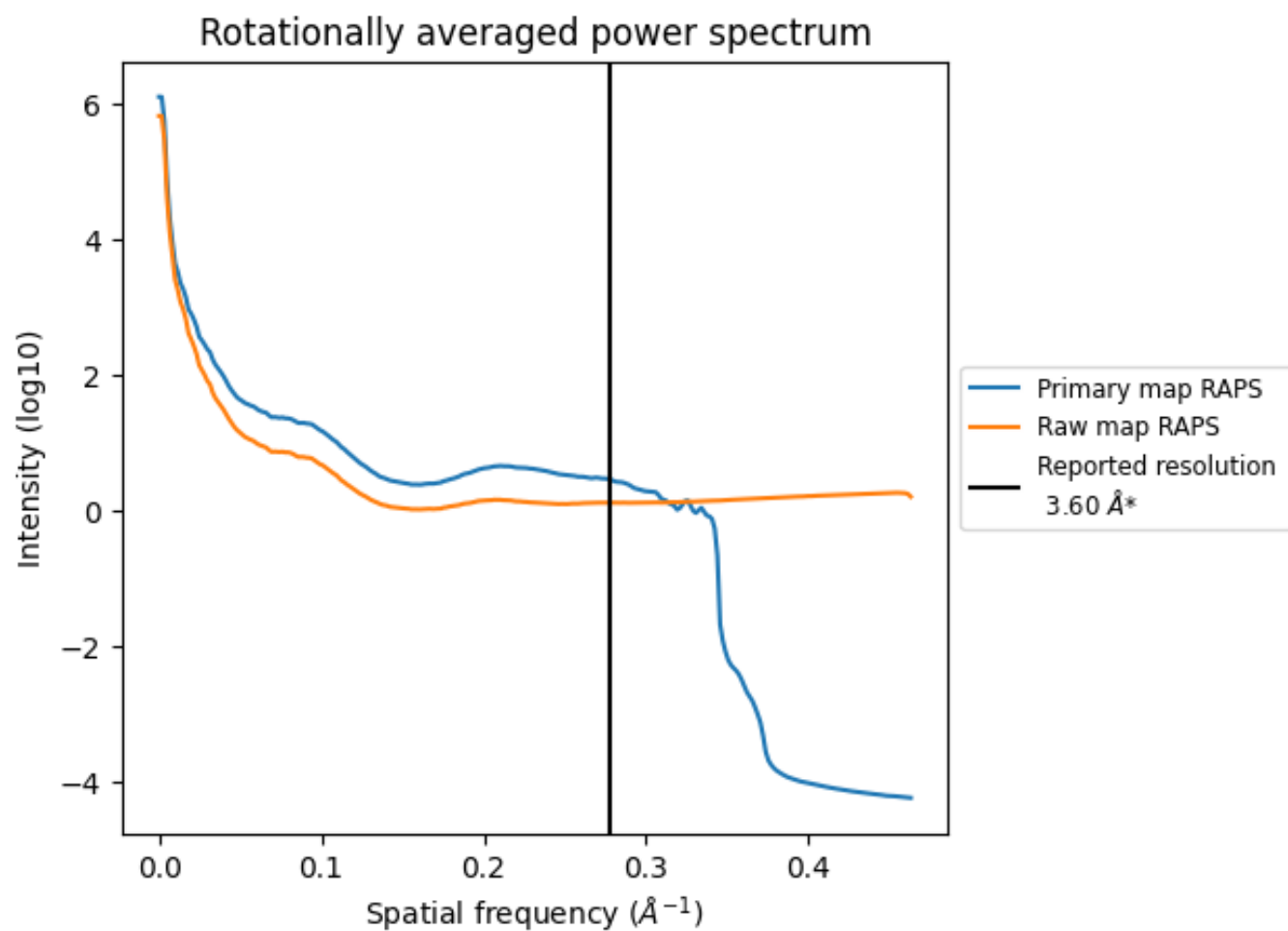
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1931 nm^3 ; this corresponds to an approximate mass of 1744 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 ⓘ

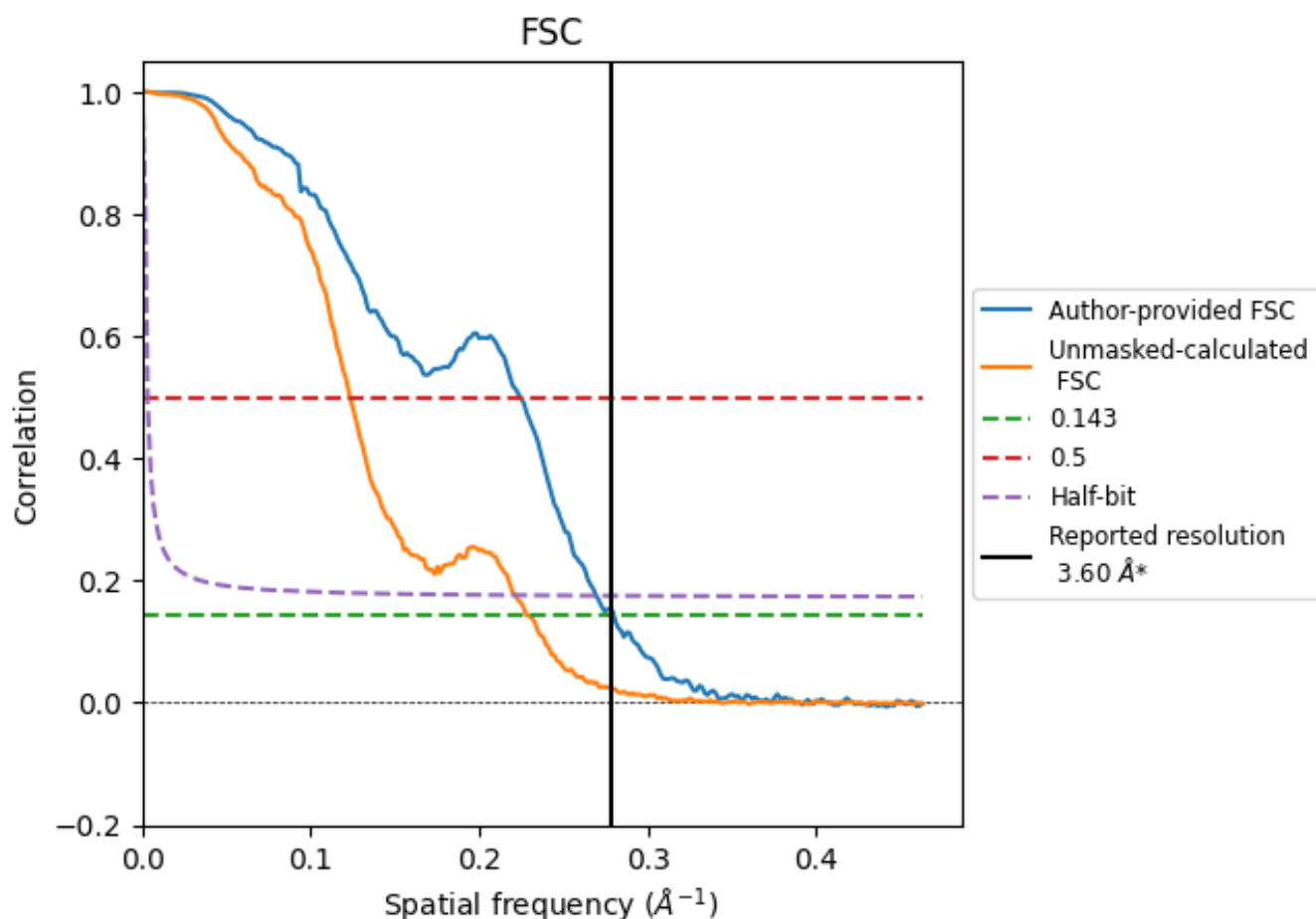


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.278 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

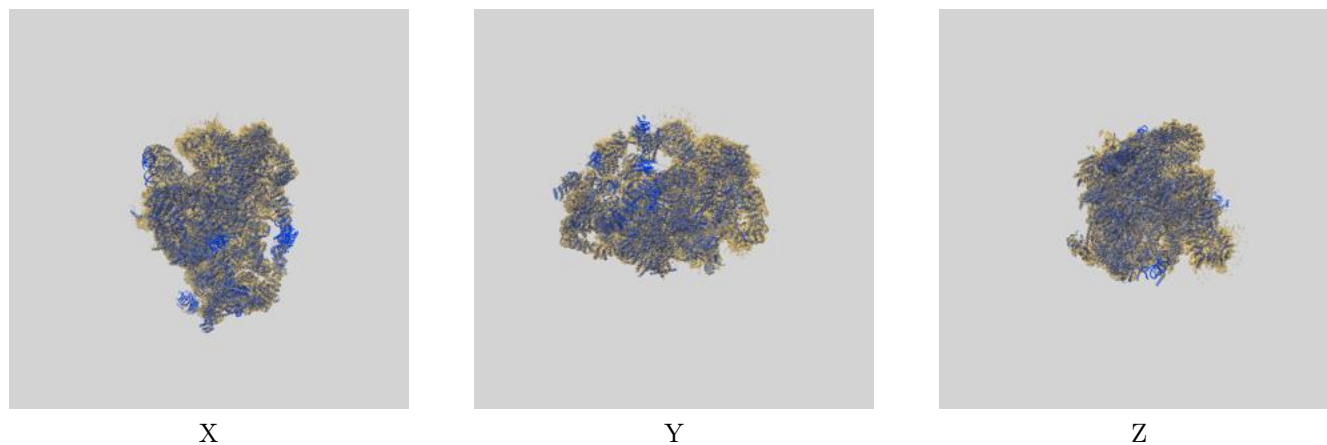
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.57	4.46	3.71
Unmasked-calculated*	4.38	8.10	4.52

*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 4.38 differs from the reported value 3.6 by more than 10 %

9 Map-model fit [i](#)

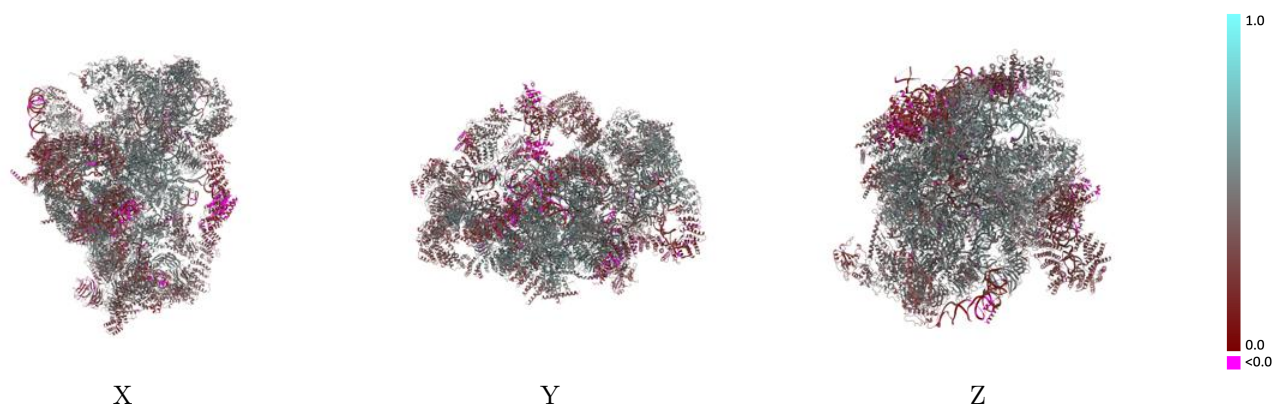
This section contains information regarding the fit between EMDB map EMD-23936 and PDB model 7MQ8. Per-residue inclusion information can be found in section 3 on page 19.

9.1 Map-model overlay [i](#)



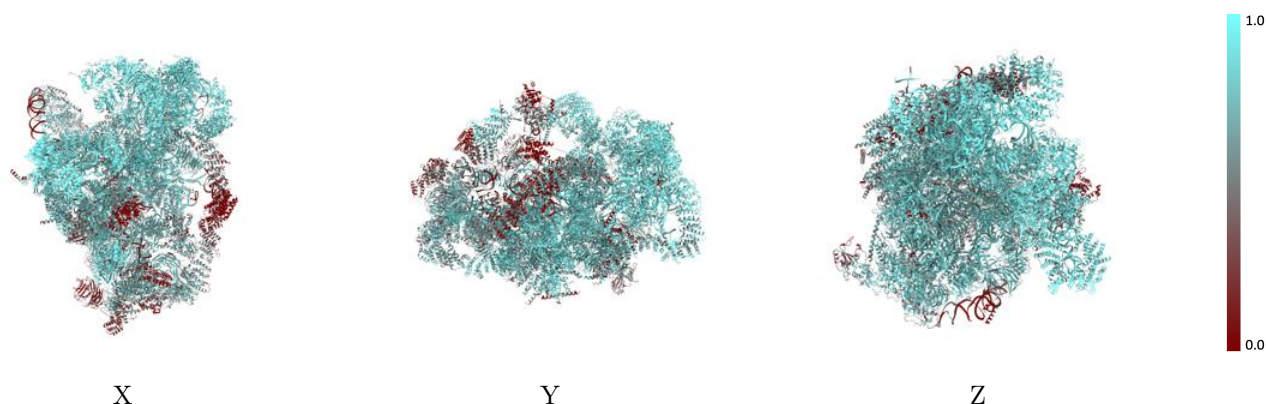
The images above show the 3D surface view of the map at the recommended contour level 2.68 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



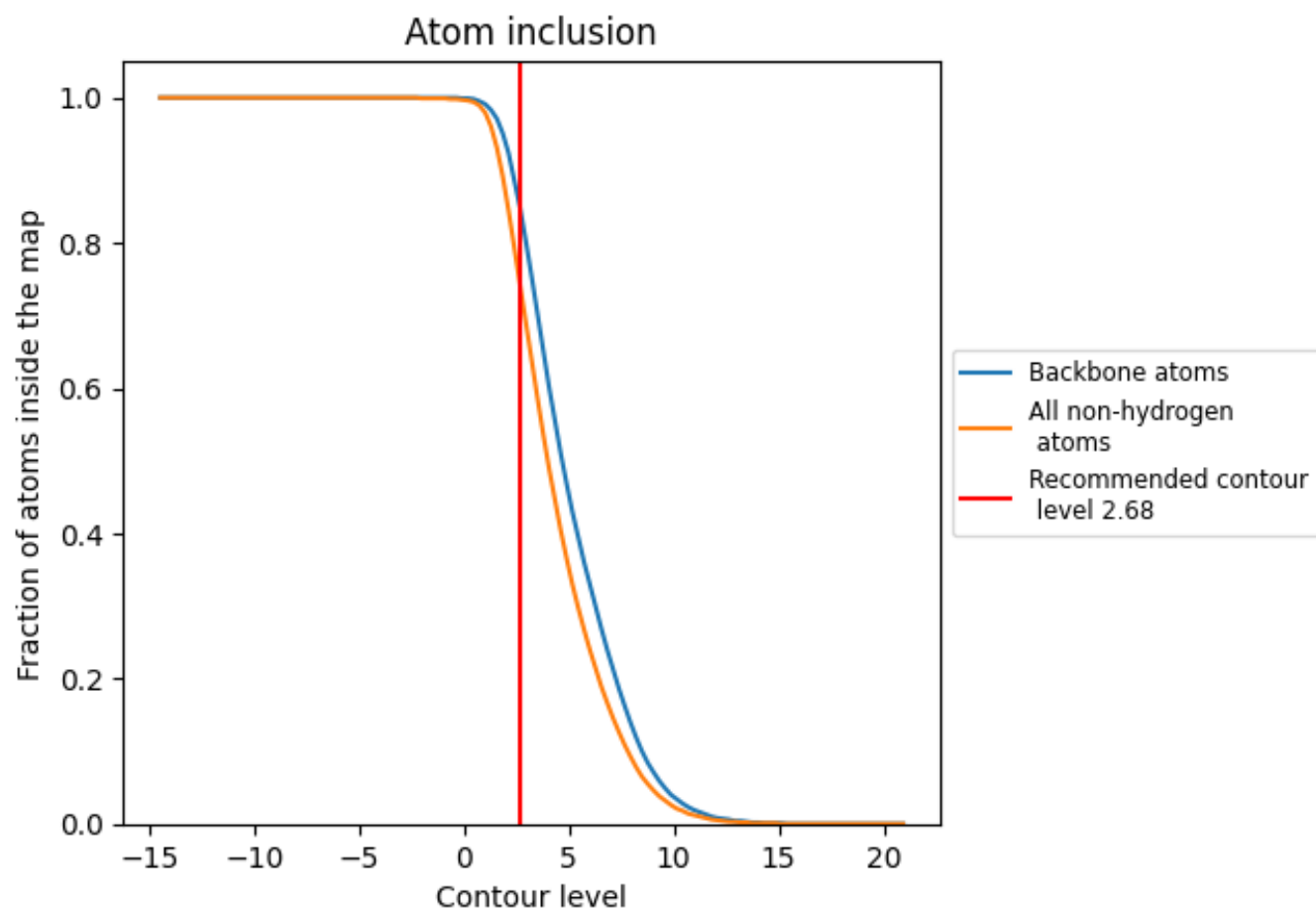
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2.68).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 74% 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 (2.68) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7440	 0.4170
L0	 0.5930	 0.3800
L1	 0.8240	 0.3850
L2	 0.7870	 0.4060
L3	 0.3730	 0.3330
L4	 0.8270	 0.4270
L5	 0.8640	 0.5070
L6	 0.8730	 0.4700
L7	 0.5340	 0.3320
L8	 0.9090	 0.4960
L9	 0.9010	 0.5360
LA	 0.0020	 0.0770
LC	 0.8590	 0.5180
LD	 0.8340	 0.4070
LF	 0.8150	 0.4490
LG	 0.8570	 0.5030
LH	 0.7380	 0.4450
LI	 0.1930	 0.2410
LJ	 0.7520	 0.4570
LK	 0.3240	 0.3190
LL	 0.7280	 0.4550
LM	 0.5090	 0.2910
LN	 0.7620	 0.4500
LO	 0.8740	 0.5190
LP	 0.7730	 0.4530
LQ	 0.7590	 0.4540
LR	 0.7840	 0.4430
LS	 0.8280	 0.5170
LT	 0.8670	 0.5220
LU	 0.8530	 0.5120
LW	 0.8220	 0.5080
LZ	 0.8780	 0.5340
N0	 0.5300	 0.3920
NA	 0.7890	 0.4960
NB	 0.9140	 0.5630



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Chain	Atom inclusion	Q-score
NC	 0.7540	 0.4330
ND	 0.6010	 0.4040
NE	 0.6560	 0.4580
NF	 0.6800	 0.4240
NG	 0.7670	 0.4680
NH	 0.6650	 0.3730
NI	 0.4700	 0.3110
NJ	 0.8630	 0.4660
NK	 0.8890	 0.4630
NM	 0.7030	 0.4550
NN	 0.8550	 0.4880
NO	 0.7100	 0.4780
NQ	 0.7710	 0.5090
NR	 0.9110	 0.2750
NT	 0.0350	 0.1220
NU	 0.7070	 0.2240
NW	 0.8850	 0.4900
NY	 0.6540	 0.4250
SA	 0.8380	 0.4900
SB	 0.7290	 0.4540
SC	 0.6170	 0.3780
SD	 0.9280	 0.5620
SE	 0.8620	 0.5220
SF	 0.8800	 0.5270
SG	 0.7850	 0.4290
SH	 0.8560	 0.5200
SI	 0.8630	 0.5100
SJ	 0.3440	 0.2800
SK	 0.5870	 0.4270
SL	 0.8710	 0.5300
SM	 0.8860	 0.5350
SP	 0.7810	 0.3450
SQ	 0.7580	 0.4580
SR	 0.8750	 0.5290
SS	 0.6780	 0.4560
ST	 0.7310	 0.3820
SU	 0.4610	 0.3320
SW	 0.8380	 0.3510
SX	 0.0010	 0.0460
SY	 0.6790	 0.4100
SZ	 0.5930	 0.2680
Sx	 0.3740	 0.2470