



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 02:04 PM UTC

PDB ID : 7SUK / pdb_00007suk
EMDB ID : EMD-25441
Title : Structure of Bfr2-Lcp5 Complex Observed in the Small Subunit Processome
Isolated from R2TP-depleted Yeast Cells
Authors : Rai, J.; Zhao, Y.; Li, H.
Deposited on : 2021-11-17
Resolution : 3.99 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

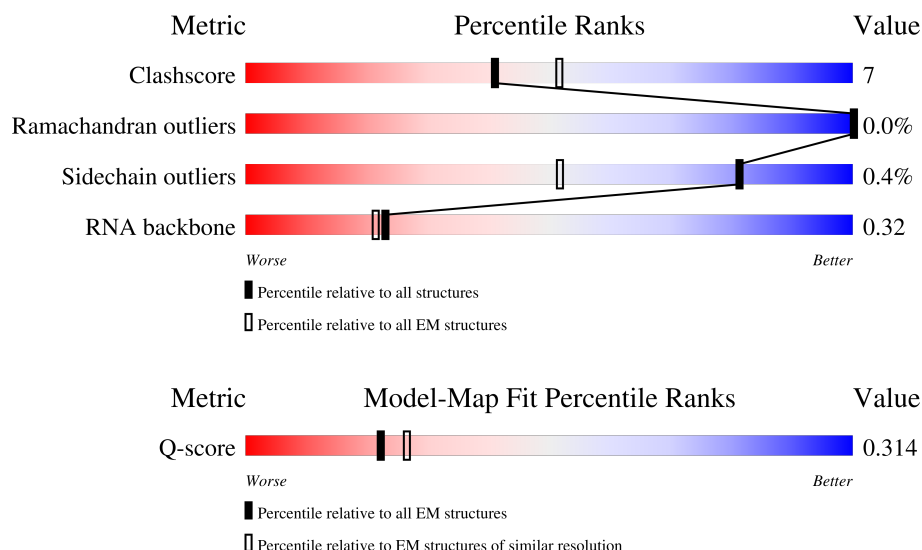
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.99 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.



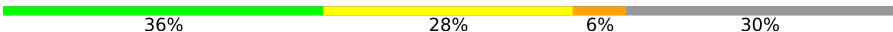
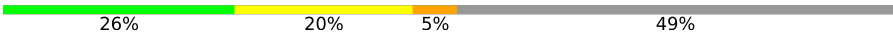
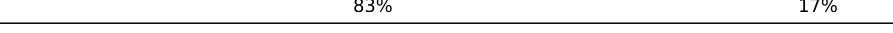
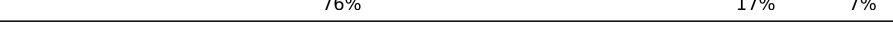
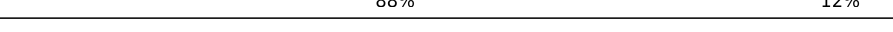
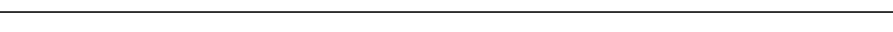
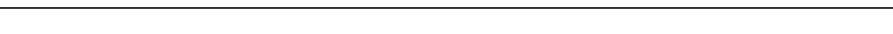
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7463 (3.49 - 4.49)

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	NA	245	
2	SA	413	
3	NB	180	

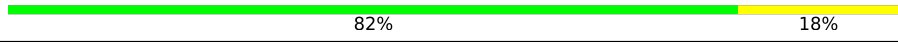
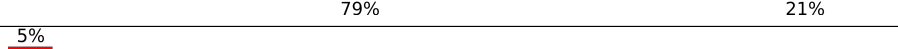
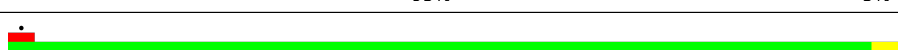
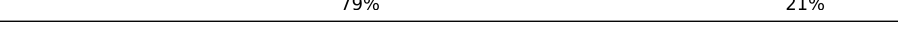
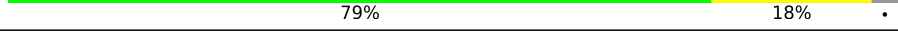
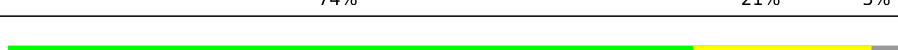
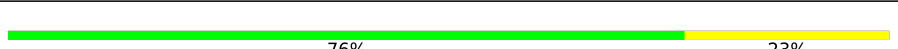
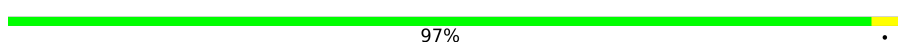
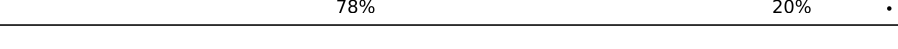
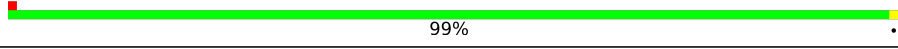
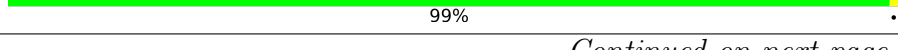
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Mol	Chain	Length	Quality of chain
4	L0	700	
5	L2	333	
6	L3	127	
7	L4	228	
8	L5	213	
9	L7	190	
10	L8	200	
11	L9	175	
12	LC	125	
13	LD	156	
14	LE	127	
15	LF	90	
16	LG	63	
17	LH	896	
18	LJ	513	
19	LK	123	
20	LL	555	
21	LM	431	
22	LN	748	
23	LO	855	
24	LP	420	
25	LQ	939	
26	LS	594	
27	LT	921	
28	LU	465	

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Mol	Chain	Length	Quality of chain
29	LV	362	
30	LW	438	
31	LZ	182	
32	NG	111	
33	NK	175	
34	SC	247	
34	SD	247	
35	SE	121	
35	SF	121	
36	SG	464	
37	SH	360	
38	SI	1123	
39	SJ	236	
39	SK	236	
40	SL	183	
41	SM	290	
42	SN	247	
43	SO	179	
44	SQ	167	
45	SR	104	
46	SS	197	
47	ST	806	
48	SY	248	
49	SZ	261	
50	NJ	265	

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Mol	Chain	Length	Quality of chain
51	NH	1141	
52	NI	187	
53	8	1807	
54	SU	513	
55	LI	687	
56	ND	60	
57	LR	811	
58	NE	240	
59	SB	436	
60	SV	92	
61	SP	2418	
62	LX	923	
62	LY	923	
63	L6	219	
64	NF	124	
65	5	534	
66	6	357	

2 Entry composition

There are 66 unique types of molecules in this entry. The entry contains 213241 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 protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	NA	207	Total	C	N	O	S	0	0
			1667	1034	297	332	4		

- Molecule 2 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	SA	370	Total	C	N	O	S	0	0
			2854	1815	490	541	8		

- Molecule 3 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	NB	142	Total	C	N	O		0	0
			1098	677	218	203			

- Molecule 4 is a RNA chain called 5' ETS.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L0	488	Total	C	N	O	P	0	0
			10405	4650	1838	3429	488		

- Molecule 5 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L2	169	Total	C	N	O	P	0	0
			3585	1605	629	1182	169		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L2	200	C	G	conflict	GB 751247007

- Molecule 6 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L3	113	Total	C	N	O	S	0	0
			901	569	168	162	2		

- Molecule 7 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L4	228	Total	C	N	O	S	0	0
			1810	1158	330	319	3		

- Molecule 8 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L5	213	Total	C	N	O	S	0	0
			1669	1045	307	314	3		

- Molecule 9 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L7	165	Total	C	N	O	S	0	0
			1321	854	227	240			

- Molecule 10 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L8	170	Total	C	N	O	S	0	0
			1349	839	267	241	2		

- Molecule 11 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L9	175	Total	C	N	O	S	0	0
			1415	895	273	246	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LC	125	Total	C	N	O	S	0	0
			973	625	174	174			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LD	127	Total	C	N	O	S	0	0
			1027	660	194	170	3		

- Molecule 14 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LE	127	Total	C	N	O	S	0	0
			1003	640	183	177	3		

- Molecule 15 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LF	90	Total	C	N	O	S	0	0
			715	458	131	126			

- Molecule 16 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LG	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 17 is a protein called NET1-associated nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LH	834	Total	C	N	O	S	0	0
			6633	4215	1121	1278	19		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LJ	493	Total	C	N	O	S	0	0
			3911	2462	702	735	12		

- Molecule 19 is a protein called U3 small nucleolar RNA-associated protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LK	123	Total	C	N	O	S	0	0
			898	567	166	163	2		

- Molecule 20 is a protein called U3 small nucleolar RNA-associated protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LL	475	Total	C	N	O	S	0	0
			3772	2400	649	710	13		

- Molecule 21 is a protein called U3 small nucleolar RNA-associated protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LM	431	Total	C	N	O	S	0	0
			3443	2224	566	641	12		

- Molecule 22 is a protein called U3 small nucleolar RNA-associated protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LN	678	Total	C	N	O	S	0	0
			5344	3384	930	1009	21		

- Molecule 23 is a protein called Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LO	834	Total	C	N	O	S	0	0
			6635	4223	1140	1253	19		

- Molecule 24 is a protein called U3 small nucleolar RNA-associated protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LP	359	Total	C	N	O	S	0	0
			2709	1723	486	488	12		

- Molecule 25 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LQ	848	Total	C	N	O	S	0	0
			6640	4244	1116	1253	27		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LS	481	Total	C	N	O	S	0	0
			3791	2399	668	714	10		

- Molecule 27 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LT	850	Total	C	N	O	S	0	0
			6697	4253	1154	1269	21		

- Molecule 28 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LU	457	Total	C	N	O	S	0	0
			3725	2328	679	702	16		

- Molecule 29 is a protein called Ribosome biogenesis protein ENP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LV	362	Total	C	N	O	S	0	0
			2840	1789	487	555	9		

- Molecule 30 is a protein called U3 small nucleolar RNA-associated protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LW	438	Total	C	N	O	S	0	0
			3428	2163	601	652	12		

- Molecule 31 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LZ	182	Total	C	N	O	S	0	0
			1530	967	287	269	7		

- Molecule 32 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	NG	111	Total	C	N	O	0	0
			543	321	111	111		

- Molecule 33 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	NK	175	Total	C	N	O	0	0
			868	518	175	175		

- Molecule 34 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	SC	242	Total	C	N	O	S	0	0
			1881	1193	338	340	10		
34	SD	228	Total	C	N	O	S	0	0
			1782	1131	320	321	10		

- Molecule 35 is a protein called Ribonucloprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	SE	121	Total	C	N	O	S	0	0
			916	583	158	171	4		
35	SF	121	Total	C	N	O	S	0	0
			916	583	158	171	4		

- Molecule 36 is a protein called RRP9 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	SG	429	Total	C	N	O	S	0	0
			3428	2185	596	637	10		

- Molecule 37 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	SH	360	Total	C	N	O	S	0	0
			2781	1781	473	516	11		

- Molecule 38 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	SI	802	Total	C	N	O	S	0	0
			6412	4108	1142	1133	29		

- Molecule 39 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	SJ	216	Total	C	N	O	S	0	0
			1701	1079	296	315	11		
39	SK	230	Total	C	N	O	S	0	0
			1799	1142	313	333	11		

- Molecule 40 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	SL	174	Total	C	N	O	S	0	0
			1395	890	255	240	10		

- Molecule 41 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	SM	282	Total	C	N	O	S	0	0
			2296	1441	430	418	7		

- Molecule 42 is a protein called Ribosome biogenesis protein UTP30.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	SN	247	Total	C	N	O	S	0	0
			2006	1284	356	358	8		

- Molecule 43 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	SO	179	Total	C	N	O	S	0	0
			998	606	199	192	1		

- Molecule 44 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	SQ	135	Total	C	N	O	S	0	0
			1137	721	211	201	4		

- Molecule 45 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	SR	104	Total	C	N	O	S	0	0
			792	506	145	139	2		

- Molecule 46 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	SS	197	Total	C	N	O	S	0	0
			1466	905	282	277	2		

- Molecule 47 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	ST	599	Total	C	N	O	S	0	0
			4473	2830	809	823	11		

- Molecule 48 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SY	241	Total	C	N	O	S	0	0
			2016	1251	388	370	7		

- Molecule 49 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	SZ	261	Total	C	N	O	0	0
			1295	773	261	261		

- Molecule 50 is a protein called rRNA biogenesis protein RRP5.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	NJ	265	Total	C	N	O	0	0
			1314	784	265	265		

- Molecule 51 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	NH	1082	Total	C	N	O	0	0
			5362	3198	1082	1082		

- Molecule 52 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	NI	169	Total	C	N	O	0	0
			841	503	169	169		

- Molecule 53 is a RNA chain called 18S pre-rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	8	1192	Total	C	N	O	P	0	0
			25439	11367	4542	8338	1192		

- Molecule 54 is a protein called Nucleolar complex protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SU	481	Total	C	N	O	S	0	0
			3650	2355	611	672	12		

- Molecule 55 is a protein called U3 small nucleolar RNA-associated protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	LI	441	Total	C	N	O	S	0	0
			2690	1672	492	523	3		

- Molecule 56 is a protein called Bud site selection protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	ND	60	Total	C	N	O		0	0
			495	310	101	84			

- Molecule 57 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	LR	762	Total	C	N	O	S	0	0
			5957	3779	1006	1144	28		

- Molecule 58 is a protein called Protein FAF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	NE	163	Total	C	N	O	S	0	0
			1235	759	252	221	3		

- Molecule 59 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SB	435	Total	C	N	O	S	0	0
			2985	1852	543	582	8		

- Molecule 60 is a protein called Regulator of rDNA transcription protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SV	63	Total	C	N	O		0	0
			381	234	69	78			

- Molecule 61 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms				AltConf	Trace
61	SP	2234	Total	C	N	O	0	0
			11108	6640	2234	2234		

- Molecule 62 is a protein called RNA cytidine acetyltransferase.

Mol	Chain	Residues	Atoms				AltConf	Trace	
62	LY	835	Total	C	N	O	0	0	
			4132	2462	835	835			
62	LX	812	Total	C	N	O	S	0	0
			5892	3727	1041	1099	25		

- Molecule 63 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	L6	167	Total	C	N	O	S	0	0
			1327	834	256	235	2		

- Molecule 64 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms				AltConf	Trace
64	NF	124	Total	C	N	O	0	0
			614	367	123	124		

- Molecule 65 is a protein called Protein BFR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	5	296	Total	C	N	O	S	0	0
			2389	1496	422	467	4		

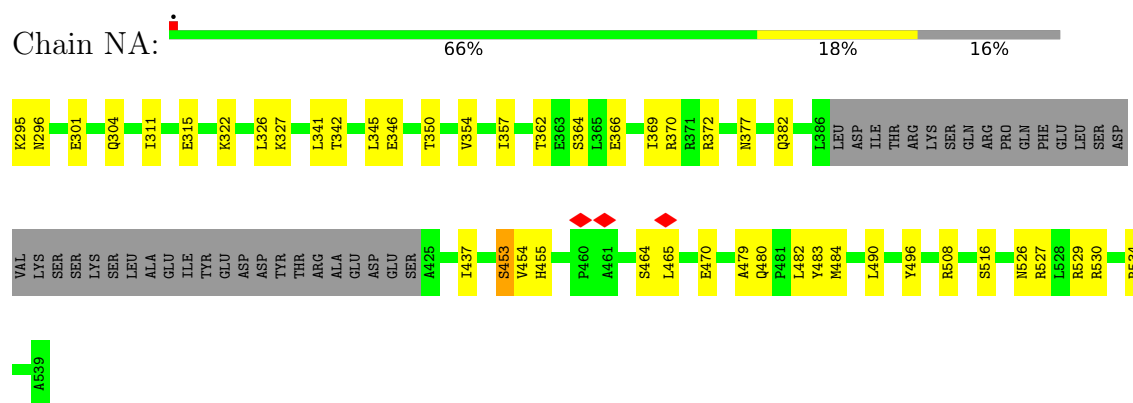
- Molecule 66 is a protein called U3 small nucleolar ribonucleoprotein protein LCP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	6	277	Total	C	N	O	S	0	0
			2244	1371	426	438	9		

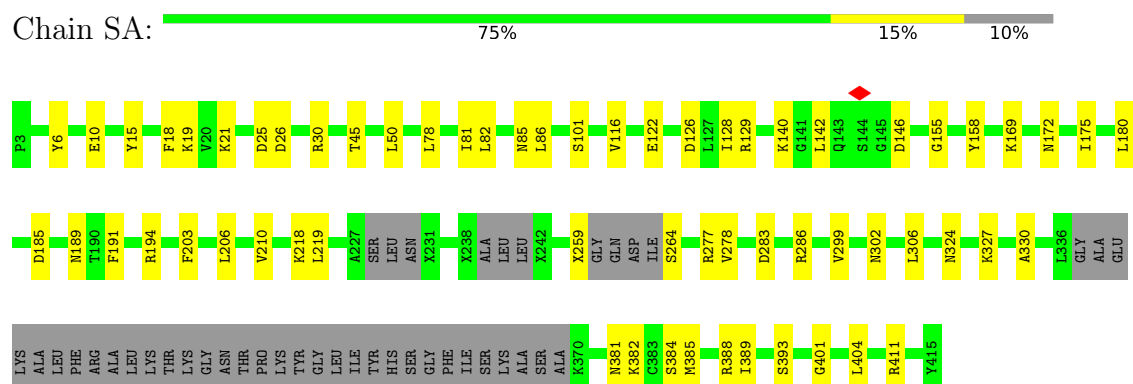
3 Residue-property plots

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

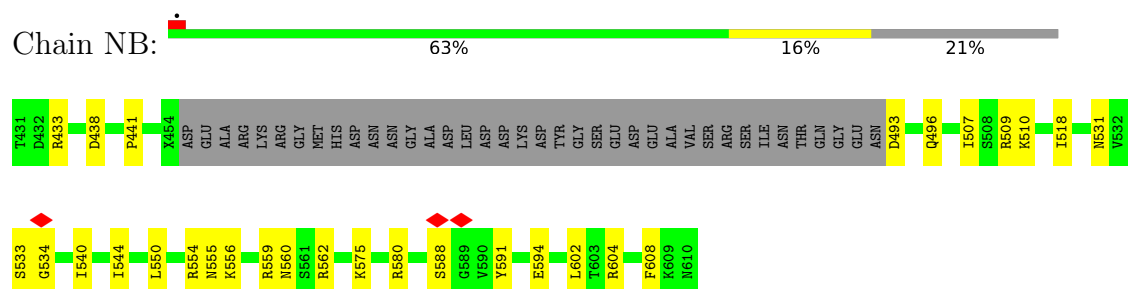
- Molecule 1: U3 small nucleolar RNA-associated protein MPP10



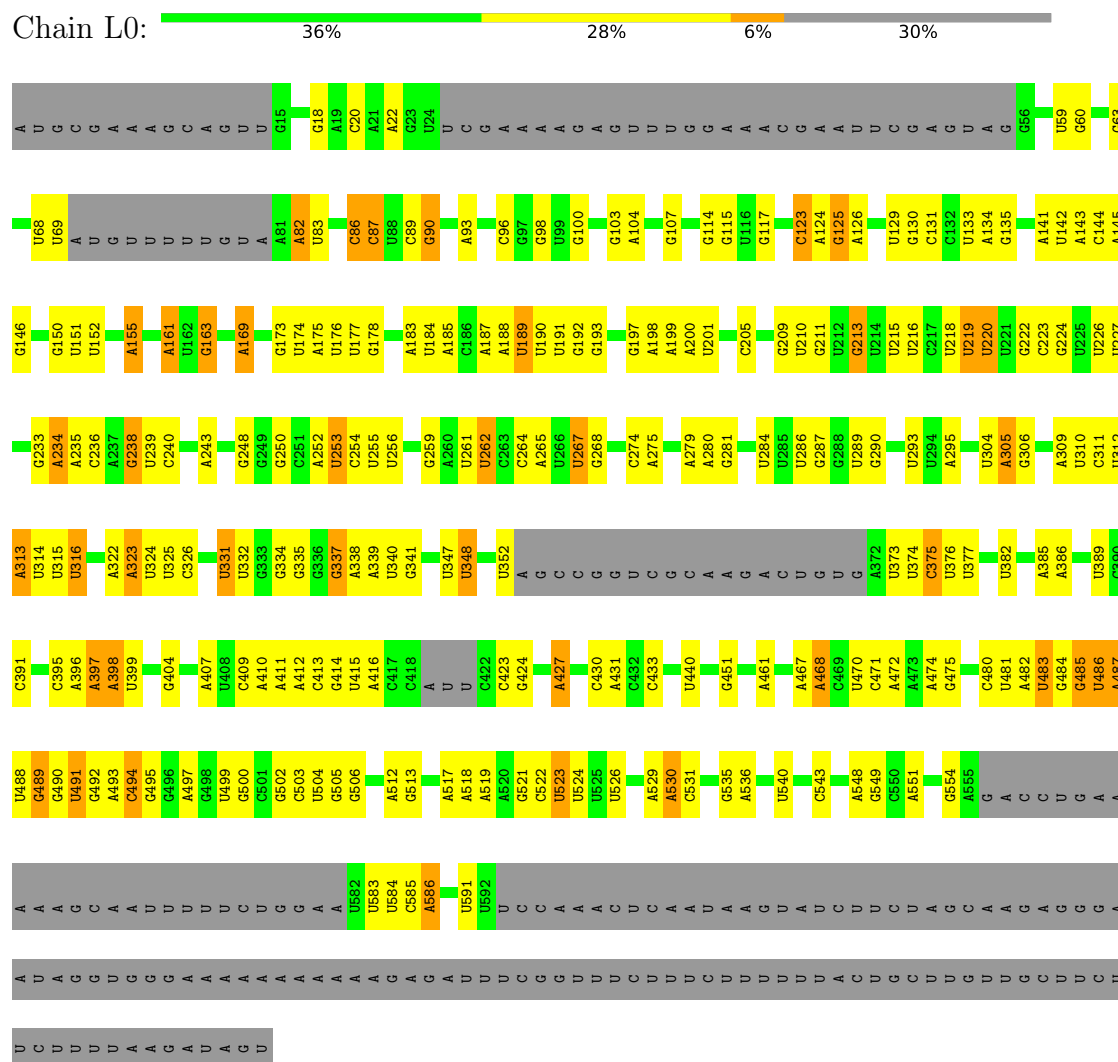
- Molecule 2: Nucleolar protein 56



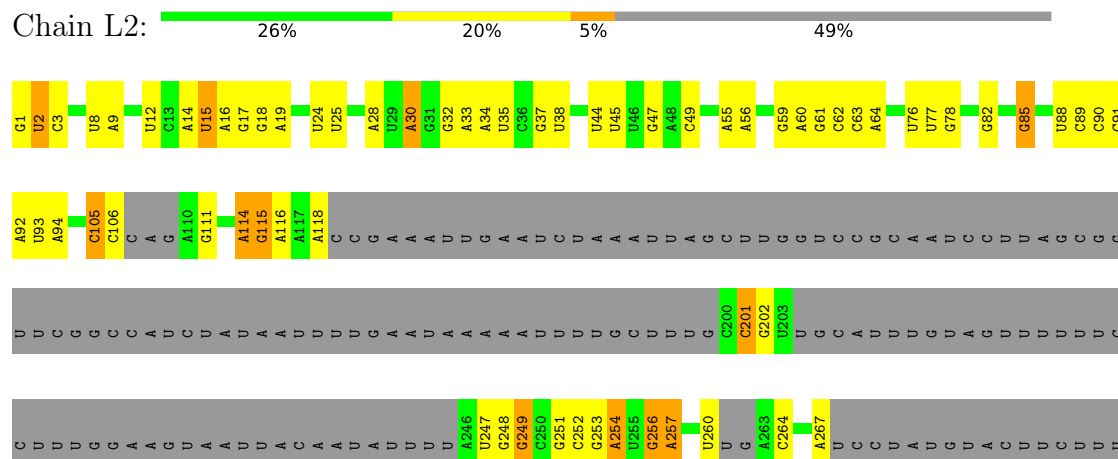
- Molecule 3: Something about silencing protein 10

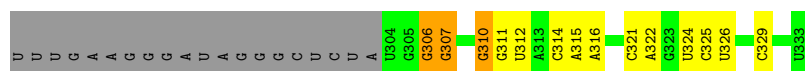


● Molecule 4: 5' ETS

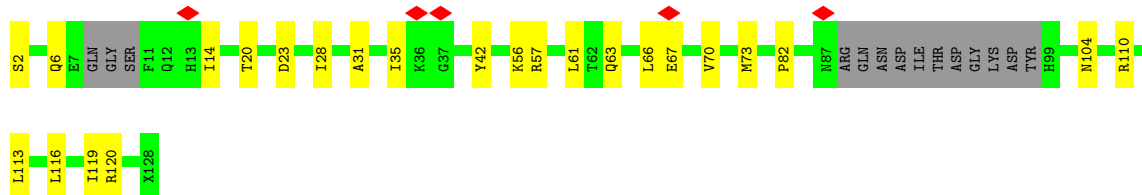


● Molecule 5: U3 snoRNA

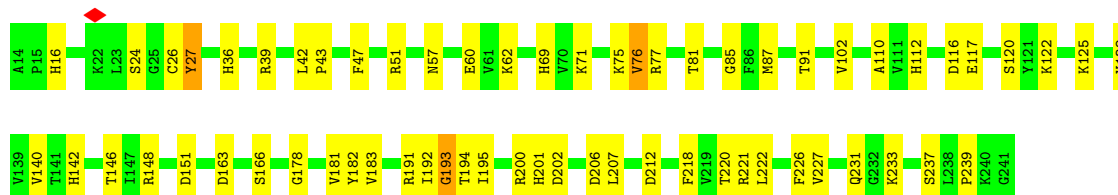




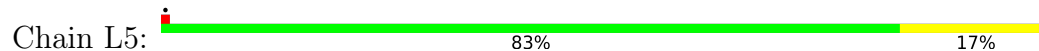
- Molecule 6: 40S ribosomal protein S18-A



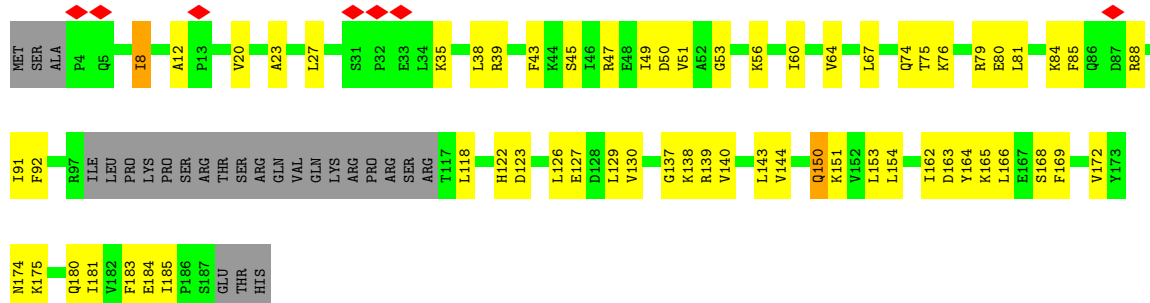
- Molecule 7: 40S ribosomal protein S4-A



- Molecule 8: 40S ribosomal protein S5

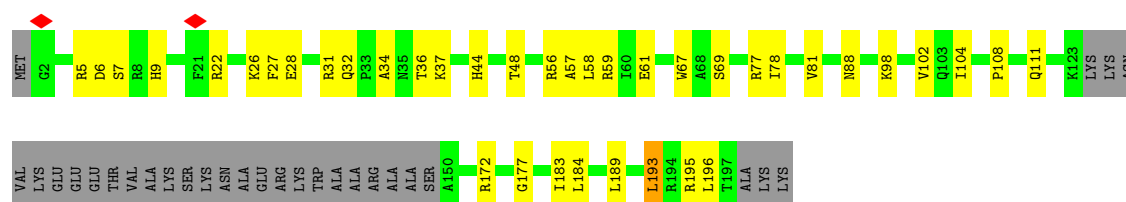


- Molecule 9: 40S ribosomal protein S7-A



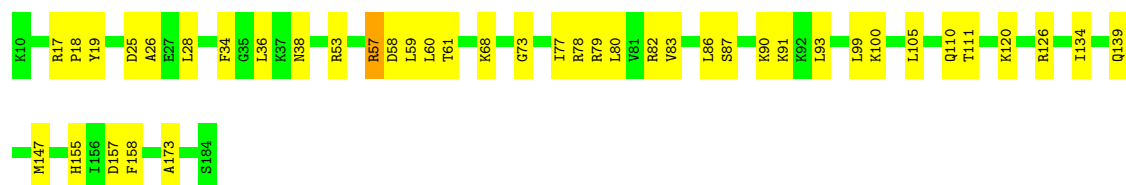
- Molecule 10: 40S ribosomal protein S8-A

Chain L8: 



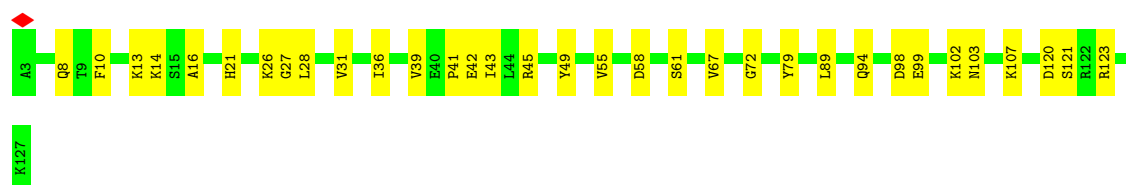
- Molecule 11: 40S ribosomal protein S9-A

Chain L9: 



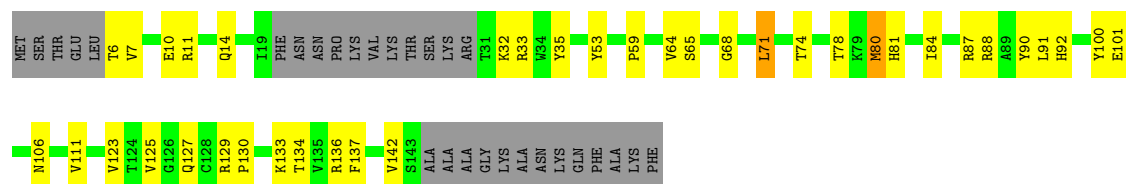
- Molecule 12: 40S ribosomal protein S16-A

Chain LC: 



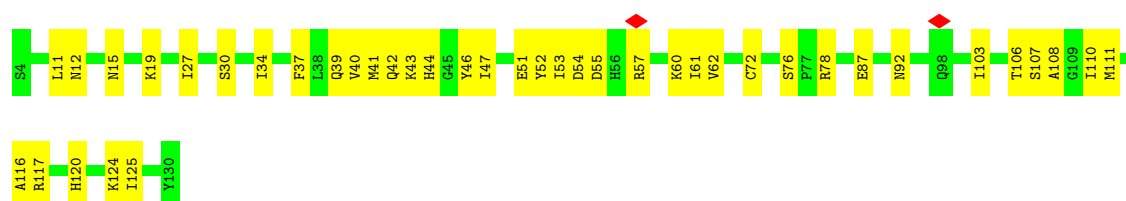
- Molecule 13: 40S ribosomal protein S11-A

Chain LD: 



- Molecule 14: 40S ribosomal protein S22-A

Chain LE: 



- Molecule 15: 40S ribosomal protein S24-A

Chain LF:  68% 32%



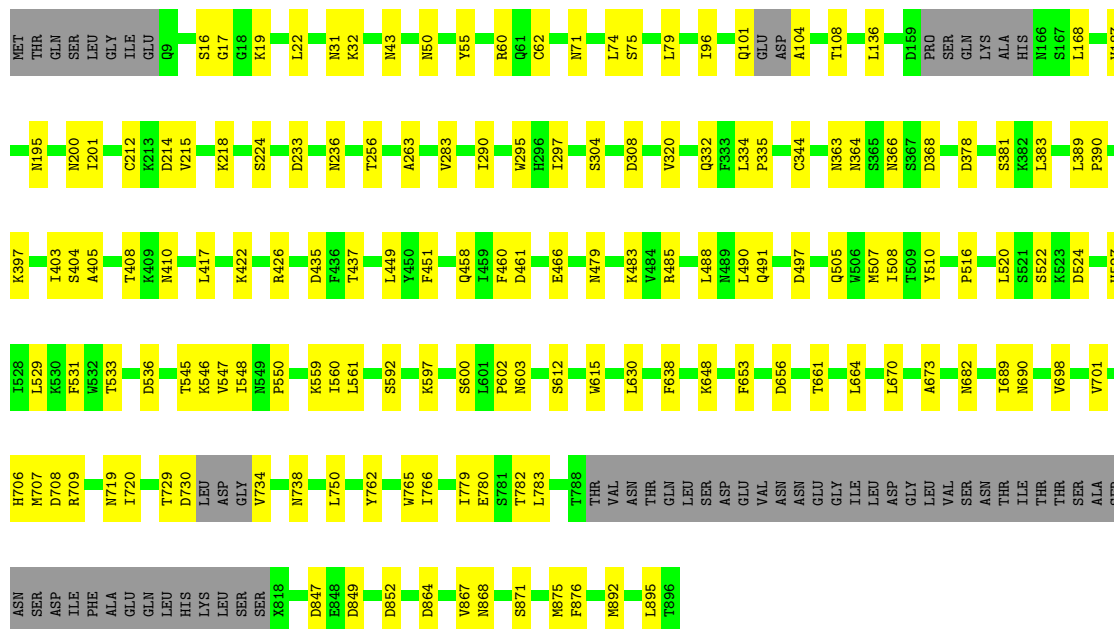
- Molecule 16: 40S ribosomal protein S28-A

Chain LG:  83% 17%



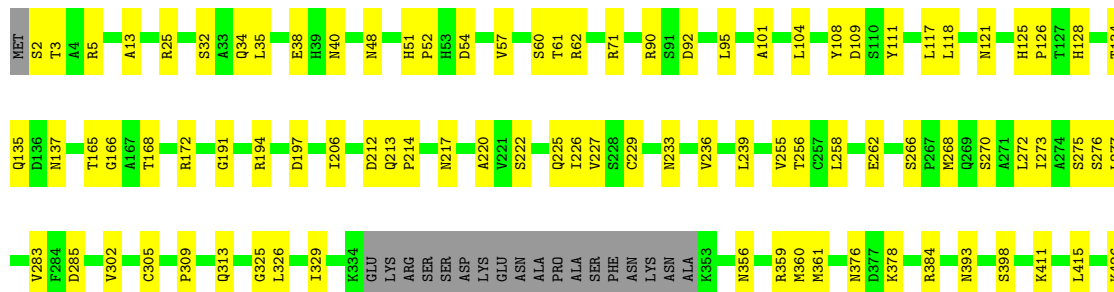
- Molecule 17: NET1-associated nuclear protein 1

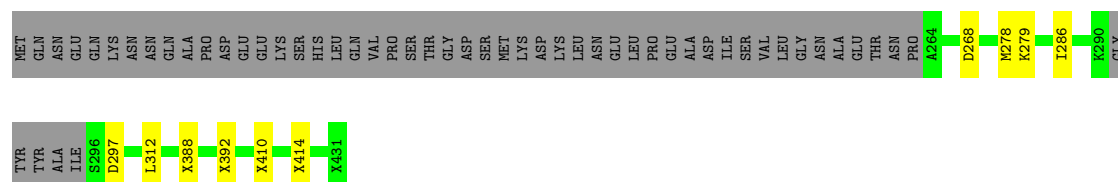
Chain LH:  76% 17% 7%



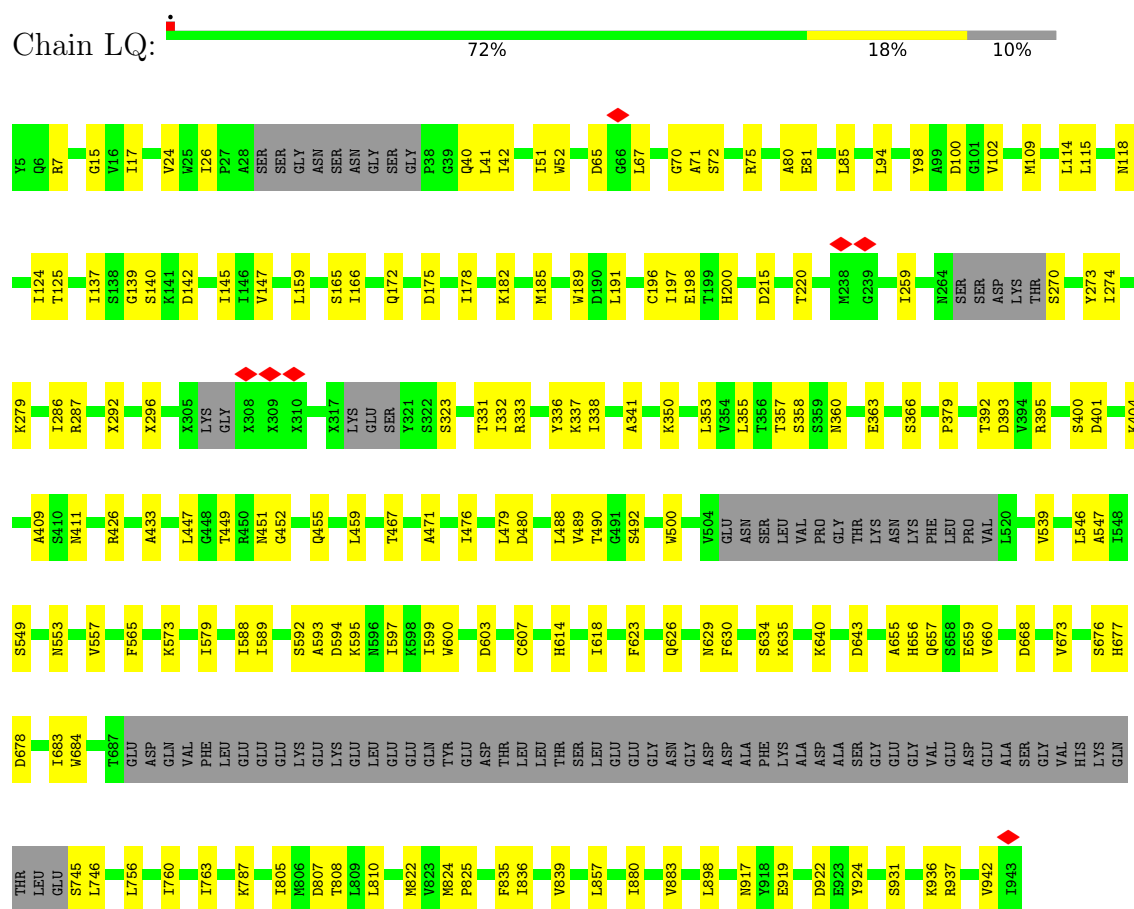
- Molecule 18: U3 small nucleolar RNA-associated protein 15

Chain LJ:  75% 21% .

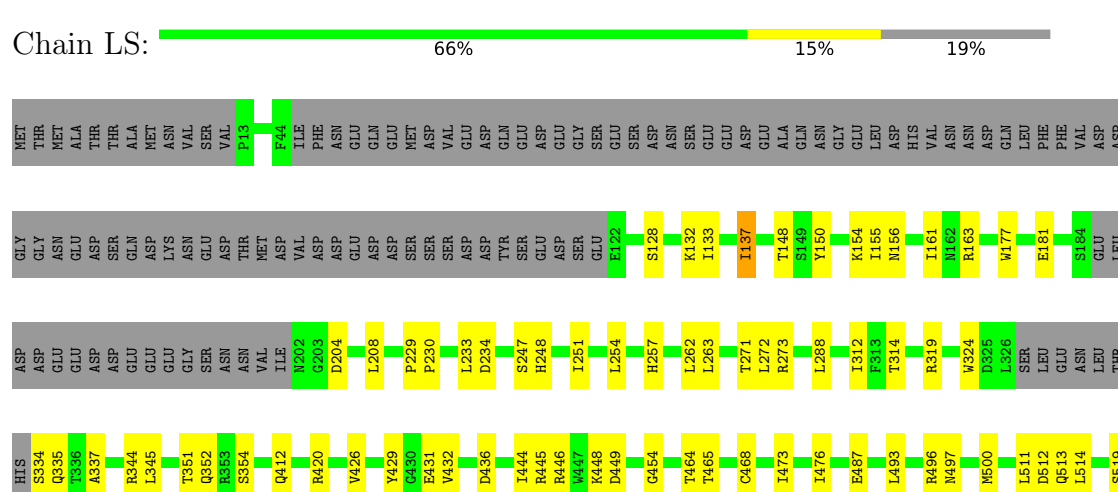




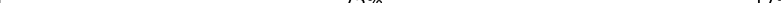
• Molecule 25: U3 small nucleolar RNA-associated protein 12

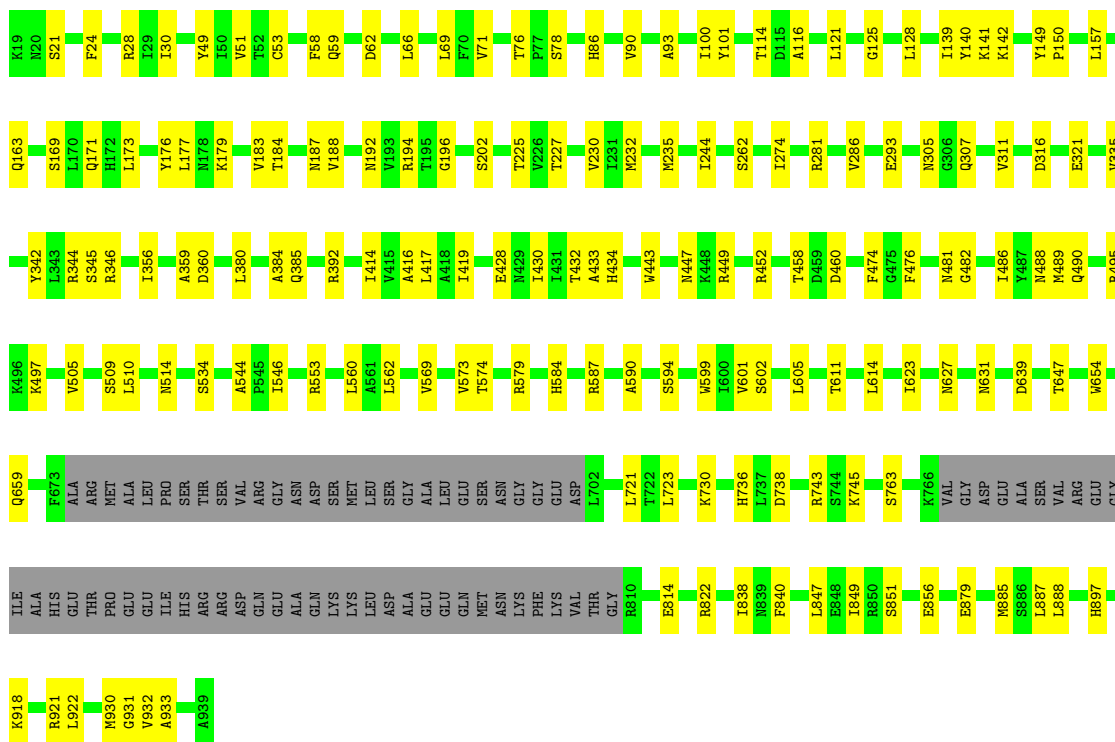


• Molecule 26: U3 small nucleolar RNA-associated protein 18



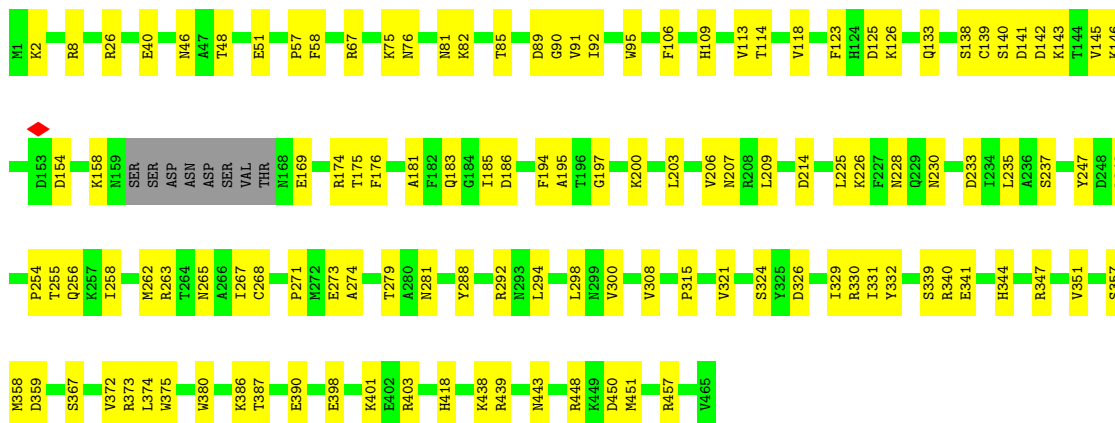
- Molecule 27: U3 small nucleolar RNA-associated protein 21

Chain LT:  75% 17% 8%



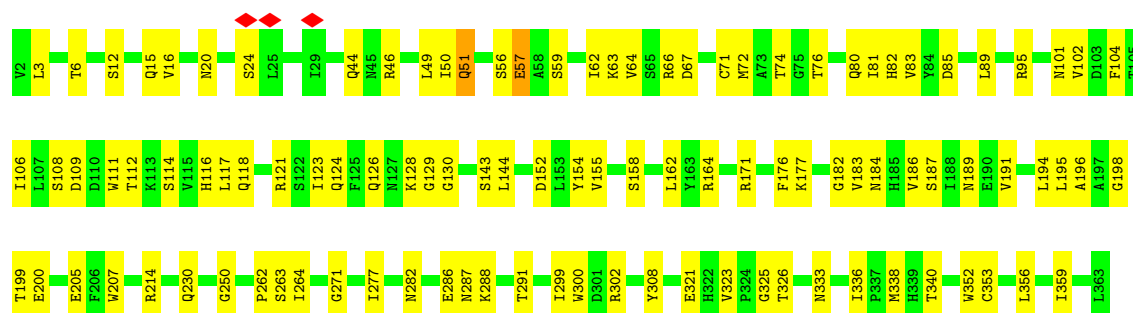
- Molecule 28: Protein SOF1

Chain LU: 72% 26%



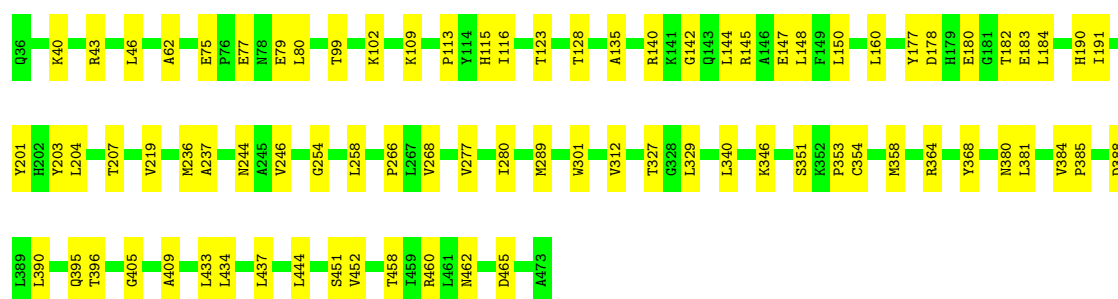
- Molecule 29: Ribosome biogenesis protein ENP2

Chain LV:



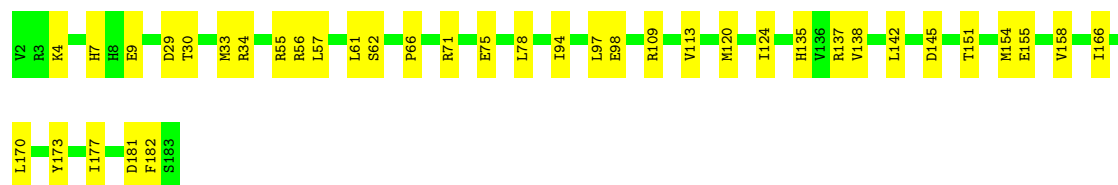
- Molecule 30: U3 small nucleolar RNA-associated protein 7

Chain LW: 82% 18%



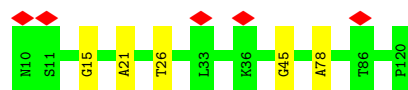
- Molecule 31: U3 small nucleolar ribonucleoprotein protein IMP3

Chain LZ: 79% 21%



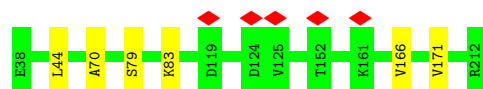
- Molecule 32: 40S ribosomal protein S14-B

Chain NG: 5% 95% 5%



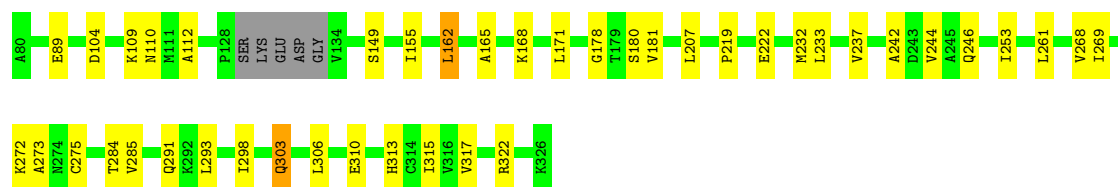
- Molecule 33: KRR1 small subunit processome component

Chain NK: 97%



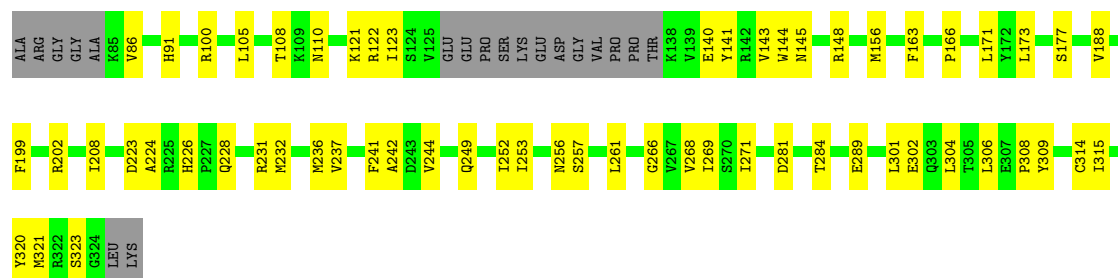
- Molecule 34: rRNA 2'-O-methyltransferase fibrillarin

Chain SC:  81% 16% ..



• Molecule 34: rRNA 2'-O-methyltransferase fibrillar

Chain SD:  68% 24% 8%



• Molecule 35: Ribonucloprotein

Chain SE:  77% 23%



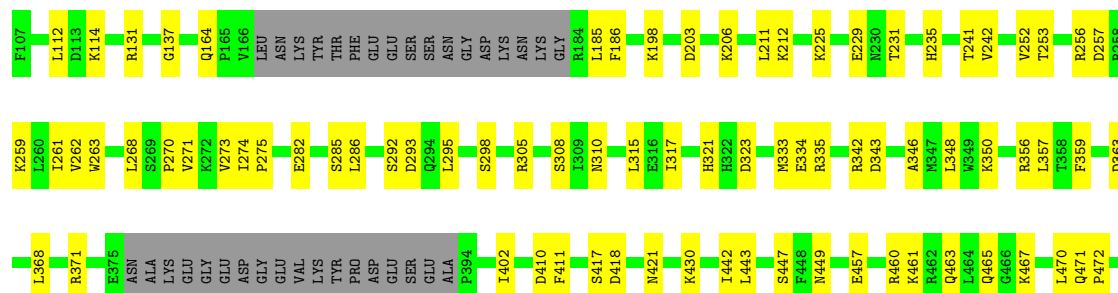
• Molecule 35: Ribonucloprotein

Chain SF:  79% 21%



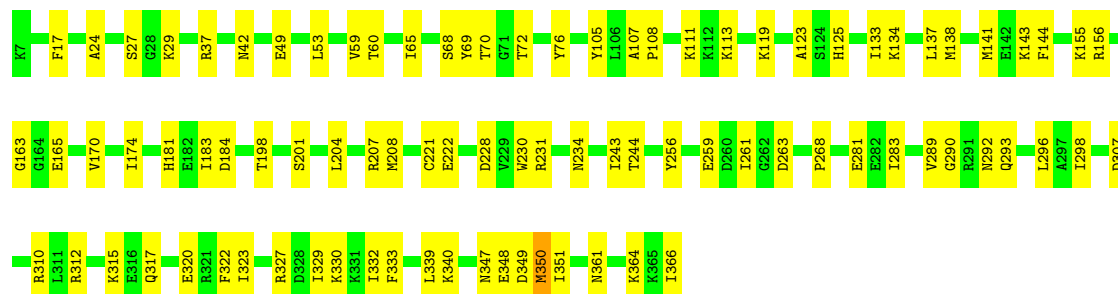
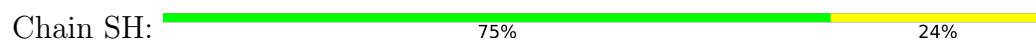
• Molecule 36: RRP9 isoform 1

Chain SG:  69% 24% 8%

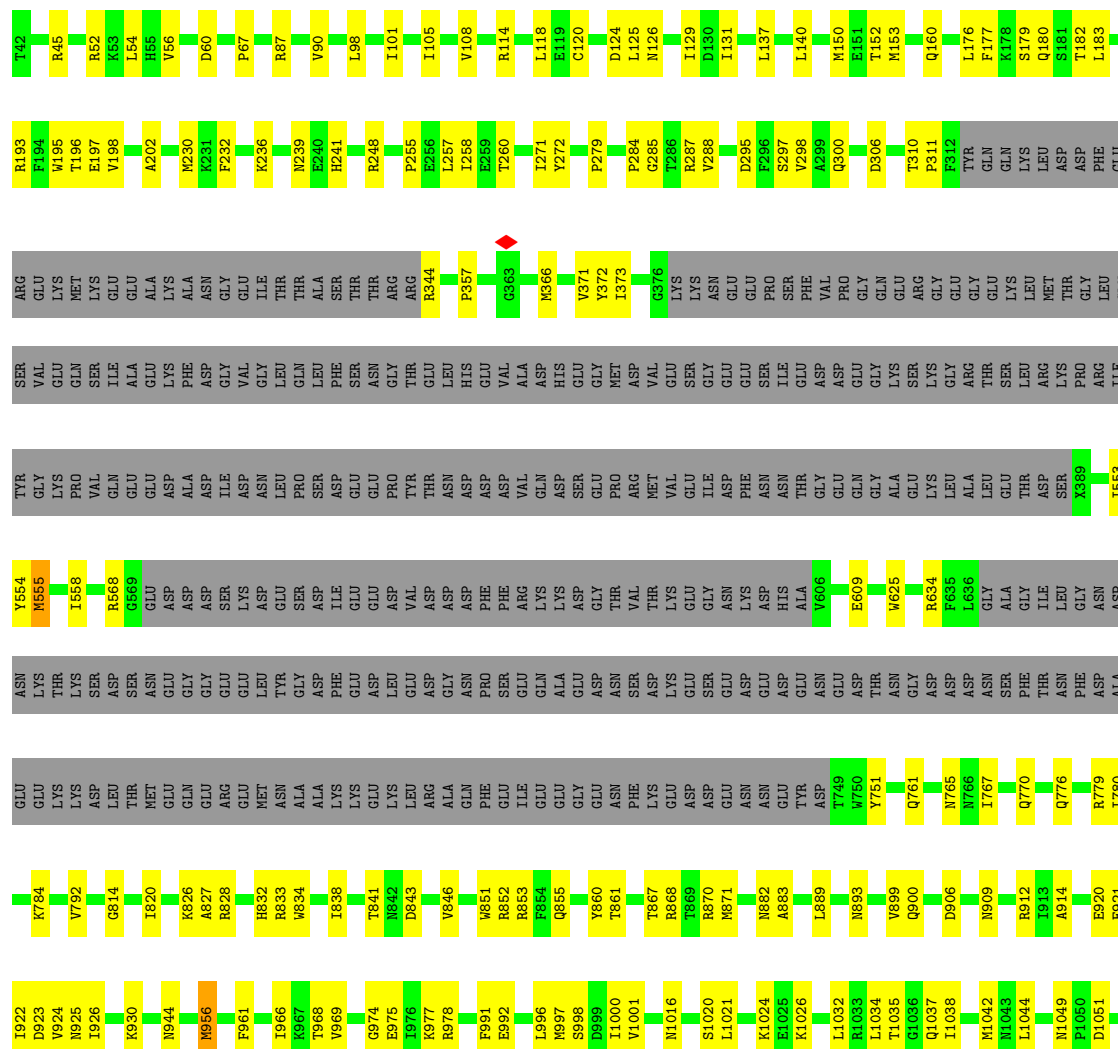




- Molecule 37: RNA 3'-terminal phosphate cyclase-like protein



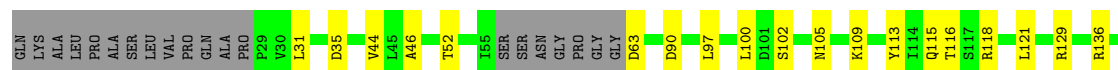
- Molecule 38: Ribosome biogenesis protein BMS1





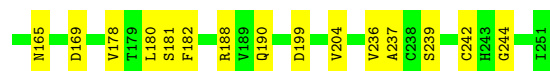
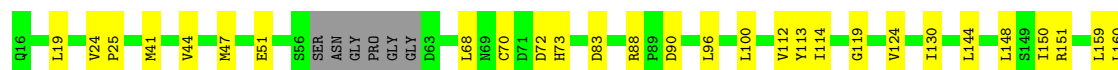
- Molecule 39: Ribosomal RNA small subunit methyltransferase NEP1

Chain SJ: 75% 17% 8%



- Molecule 39: Ribosomal RNA small subunit methyltransferase NEP1

Chain SK: 79% 18% .



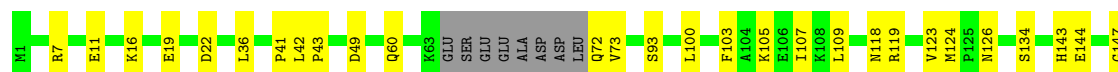
- Molecule 40: rRNA-processing protein FCF1

Chain SL: 74% 21% 5%



- Molecule 41: U3 small nucleolar ribonucleoprotein protein IMP4

Chain SM: 77% 20% .



- Molecule 42: Ribosome biogenesis protein UTP30

Chain SN: 76% 23%





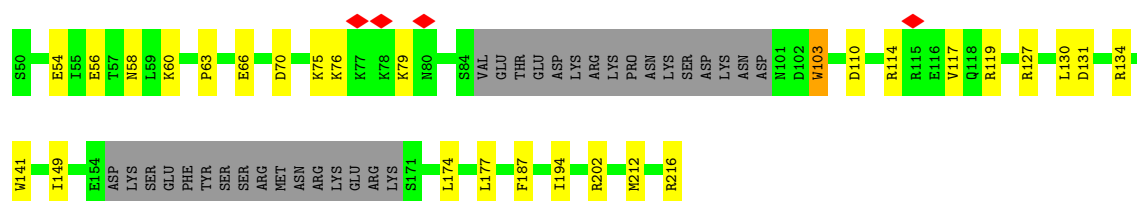
- Molecule 43: Pre-rRNA-processing protein PNO1

Chain SO: 97%



- Molecule 44: rRNA-processing protein FCF2

Chain SQ: 64% 16% 19%



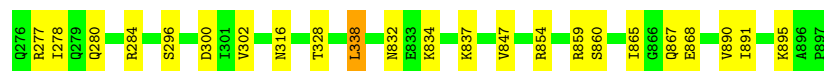
- Molecule 45: 40S ribosomal protein S23-A

Chain SR: 78% 20%



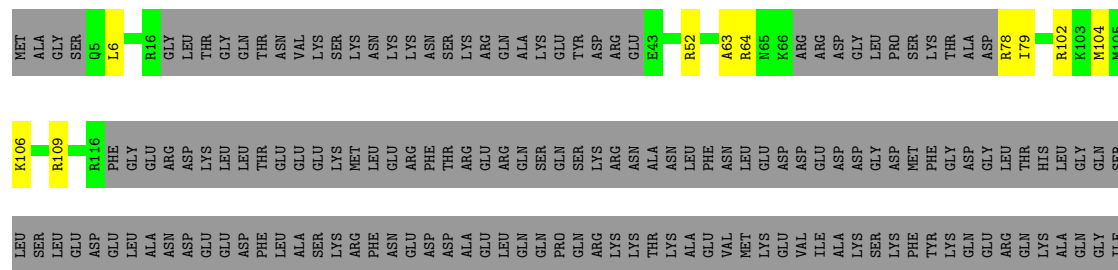
- Molecule 46: U3 small nucleolar RNA-associated protein 14

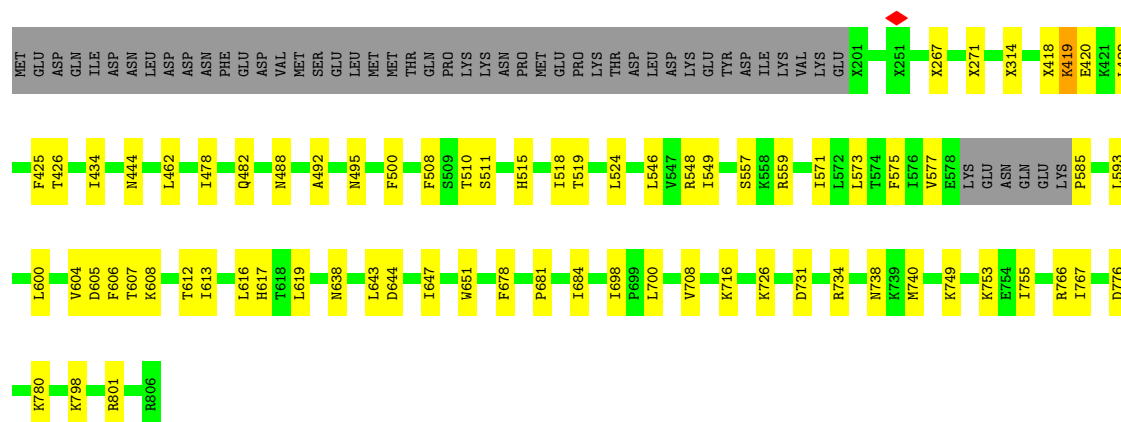
Chain SS: 88% 11%



- Molecule 47: Nucleolar complex protein 14

Chain ST: 64% 10% 26%





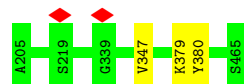
- Molecule 48: U3 small nucleolar RNA-associated protein 11

Chain SY: 81% 16% .



- Molecule 49: Essential nuclear protein 1

Chain SZ: 99% .



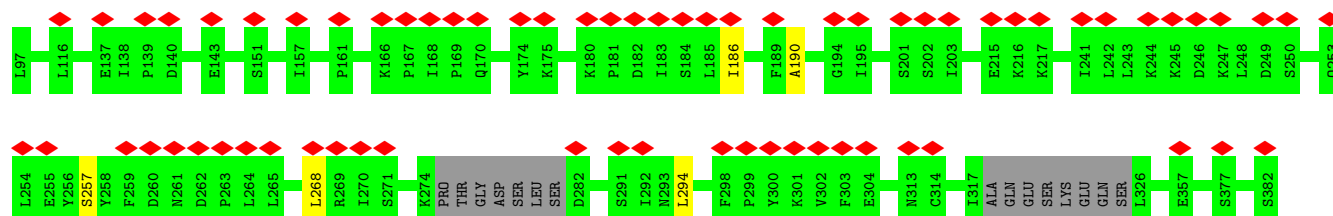
- Molecule 50: rRNA biogenesis protein RRP5

Chain NJ: 99% .

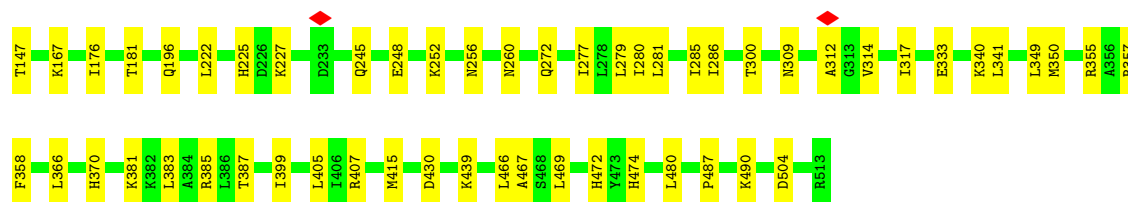


- Molecule 51: U3 small nucleolar RNA-associated protein 22

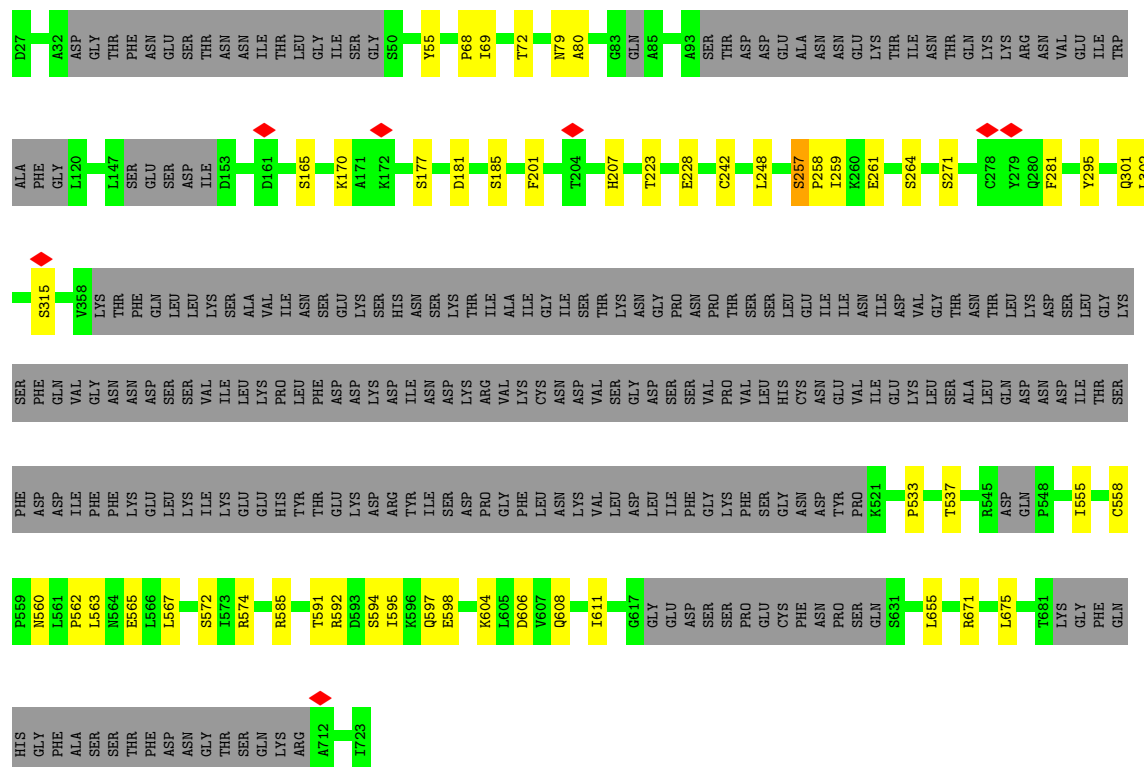
Chain NH: 33% 92% 5% .



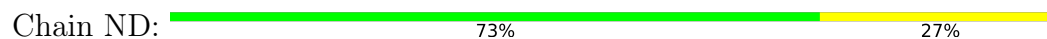




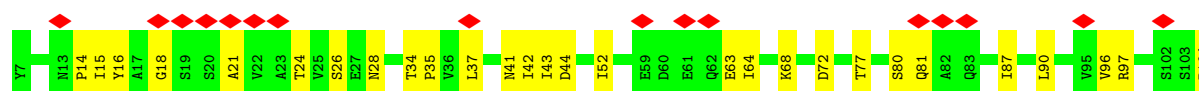
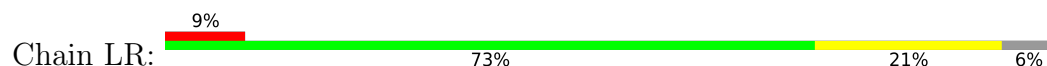
• Molecule 55: U3 small nucleolar RNA-associated protein 8

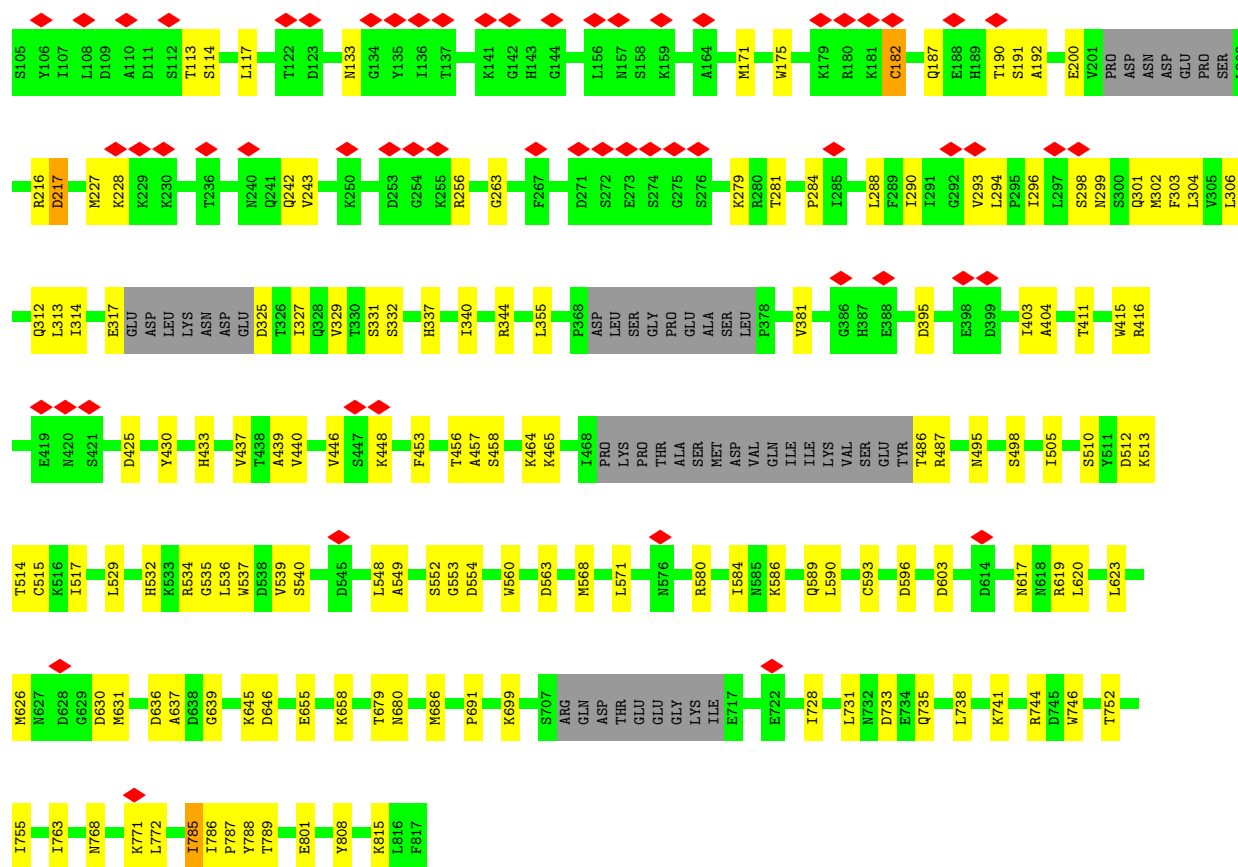


• Molecule 56: Bud site selection protein 21

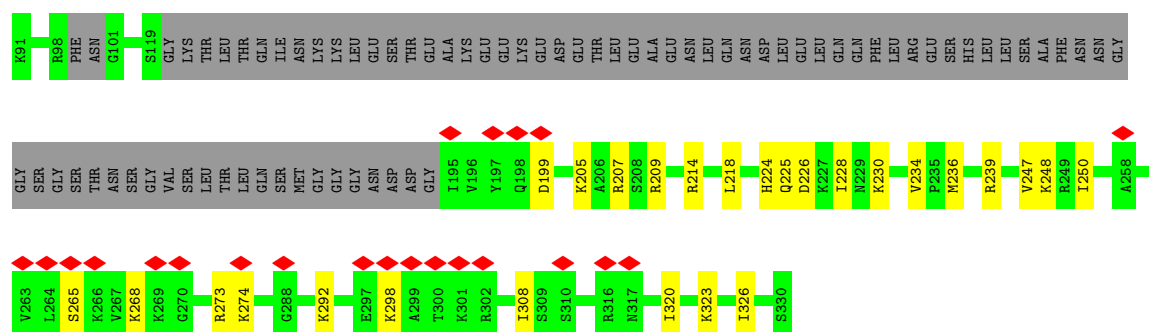


• Molecule 57: U3 small nucleolar RNA-associated protein 13

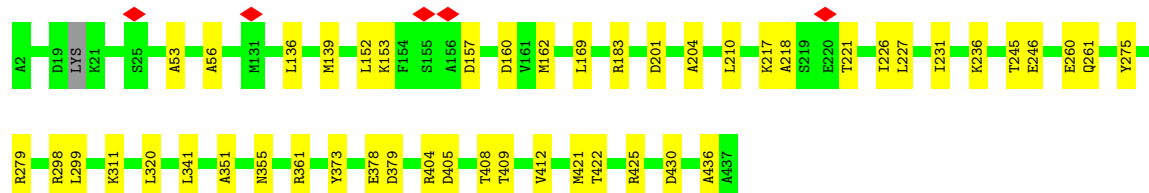




• Molecule 58: Protein FAF1

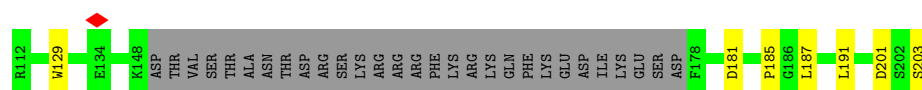


• Molecule 59: Nucleolar protein 58



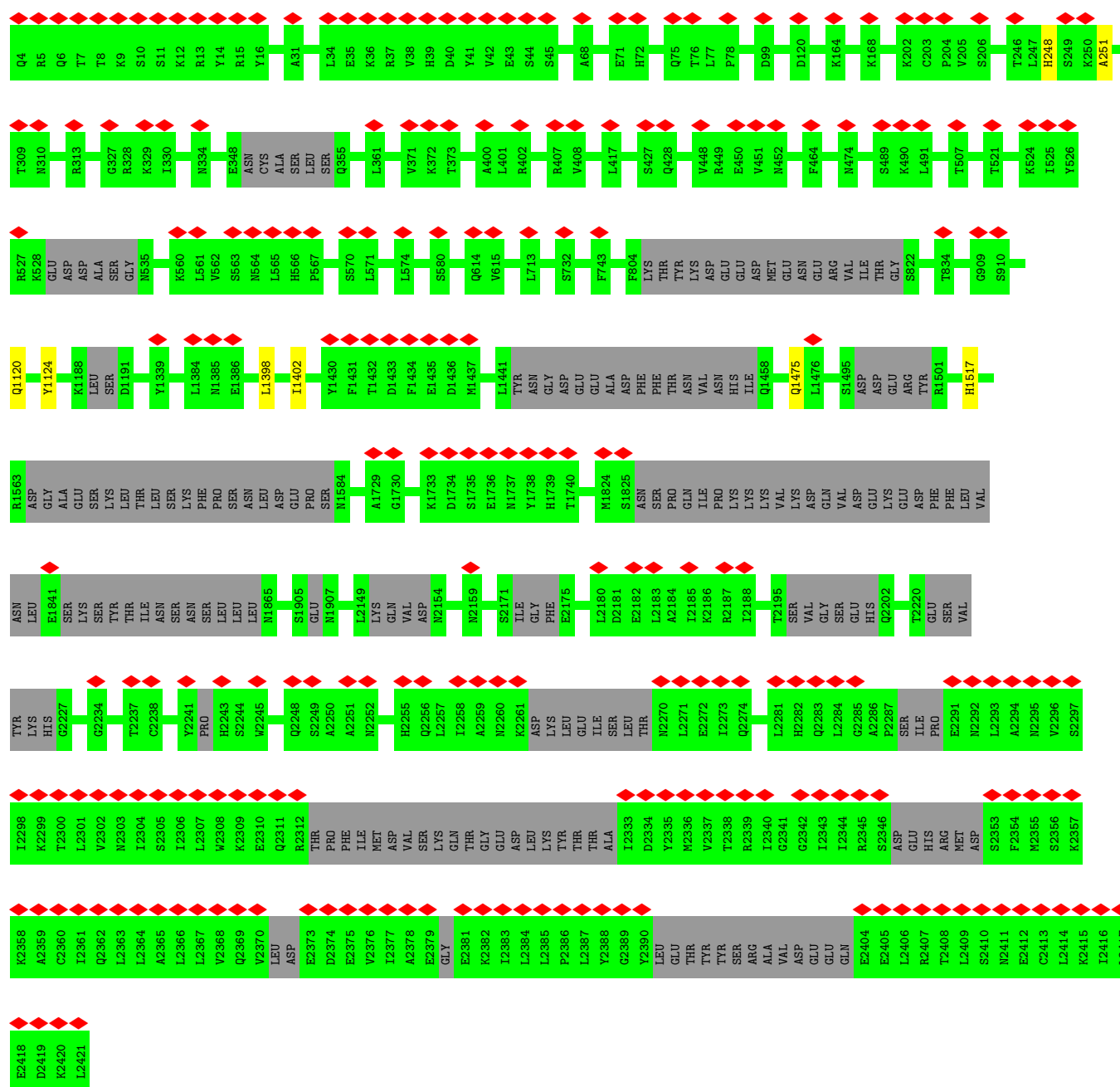
- Molecule 60: Regulator of rDNA transcription protein 14

Chain SV:  61% 8% 32%

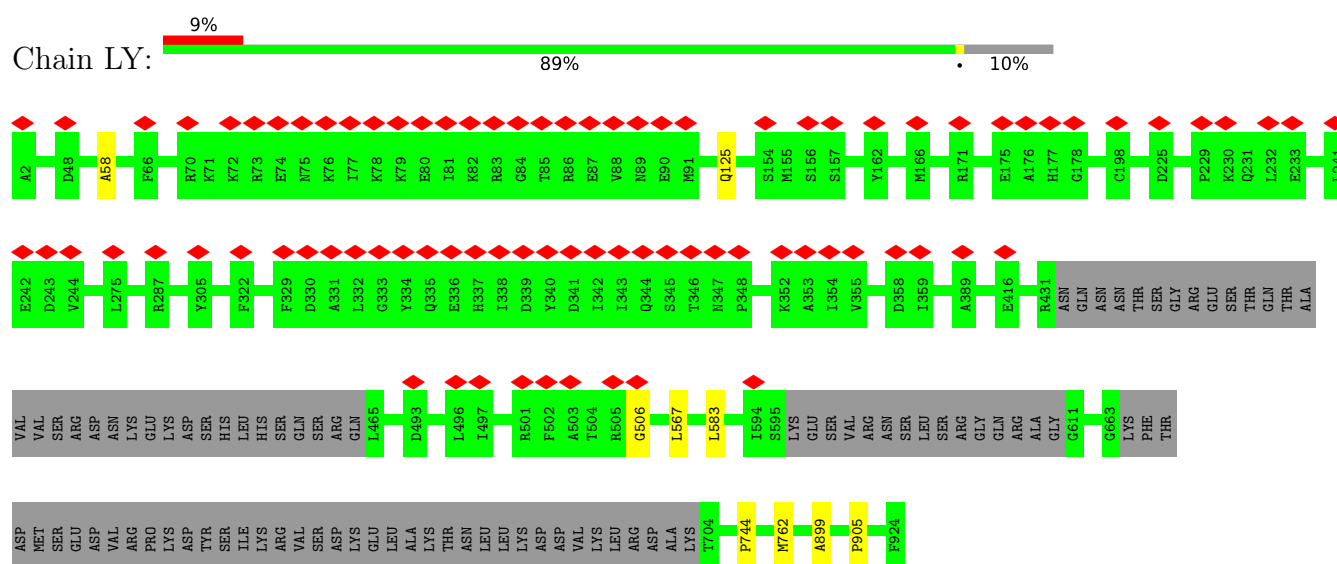


- Molecule 61: U3 small nucleolar RNA-associated protein 20

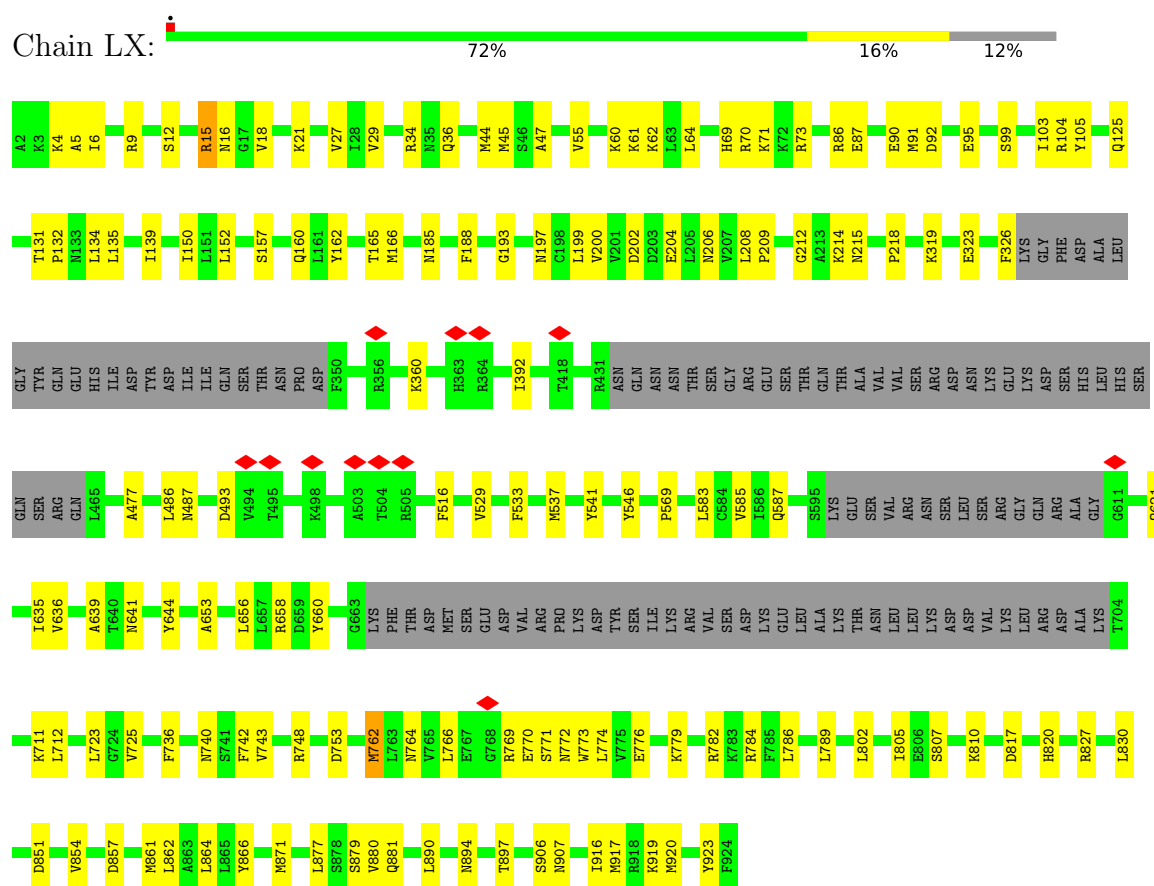
Chain SP:  10% 92% 8%



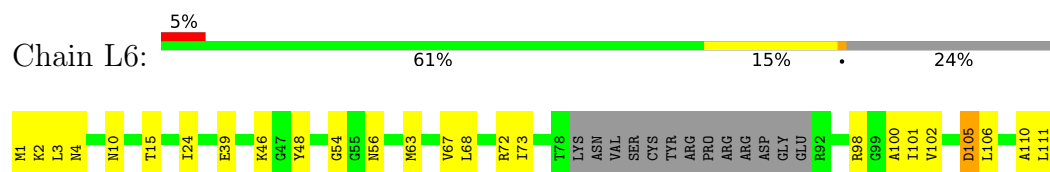
- Molecule 62: RNA cytidine acetyltransferase

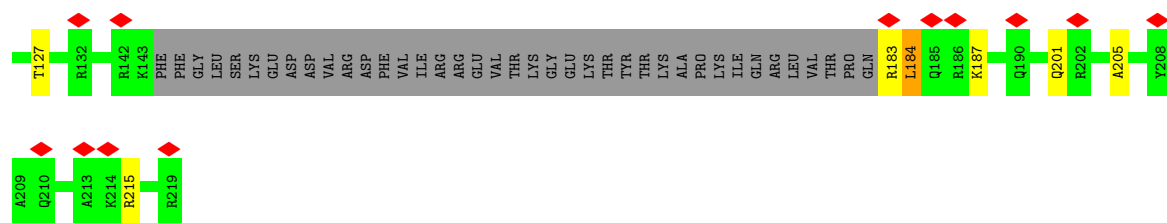


• Molecule 62: RNA cytidine acetyltransferase



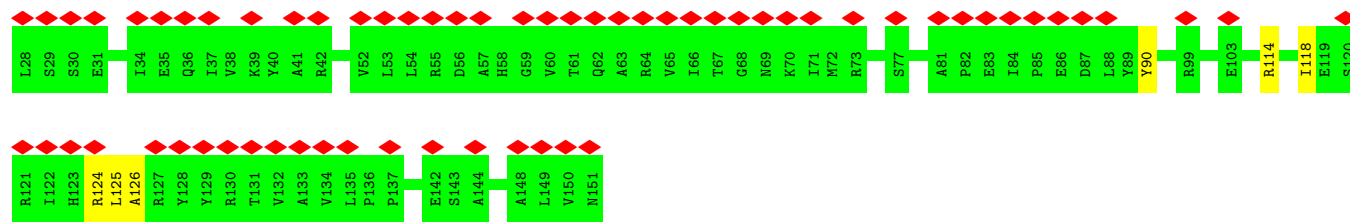
• Molecule 63: 40S ribosomal protein S6-A





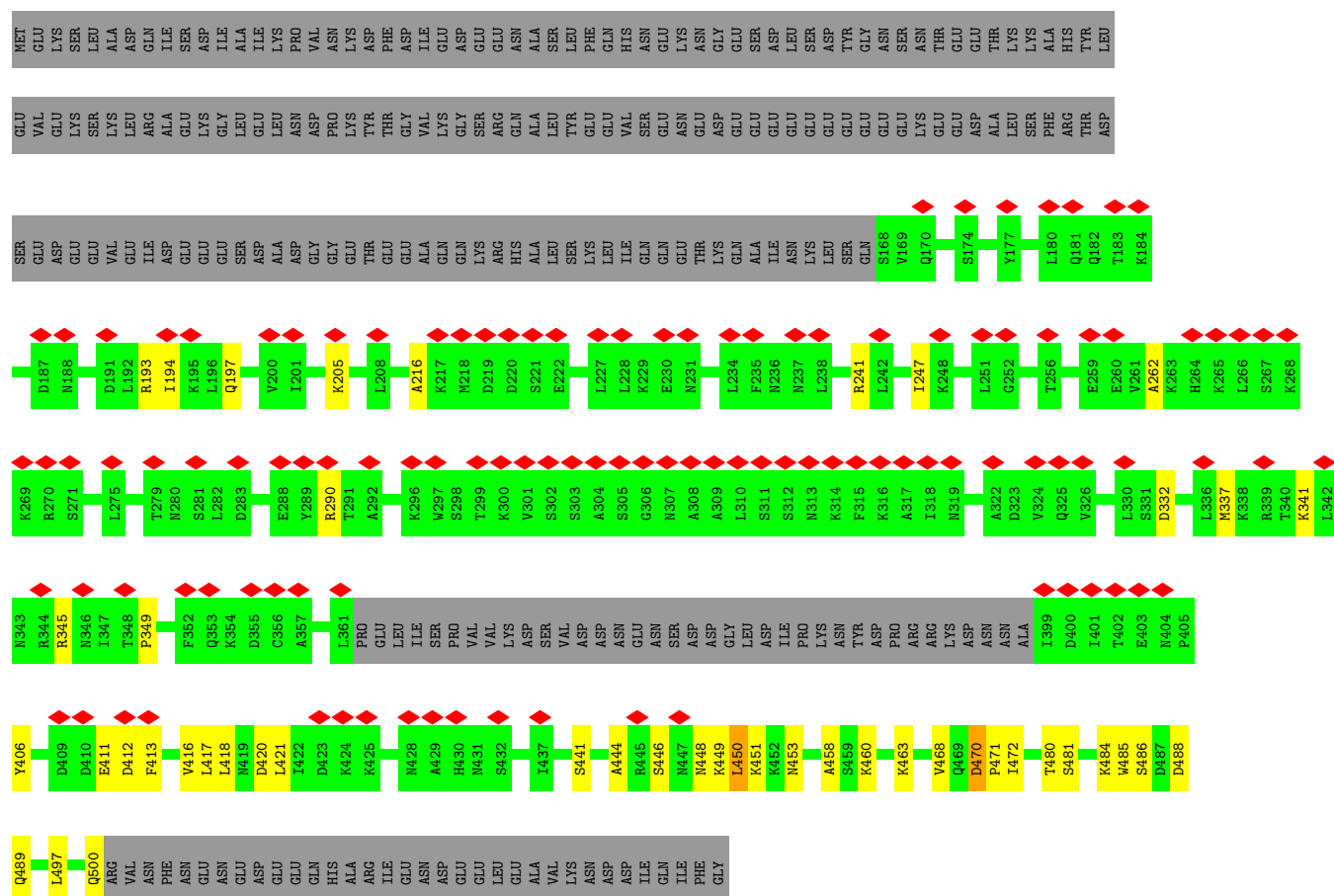
- Molecule 64: 40S ribosomal protein S13

Chain NF: 51% 95% 5%

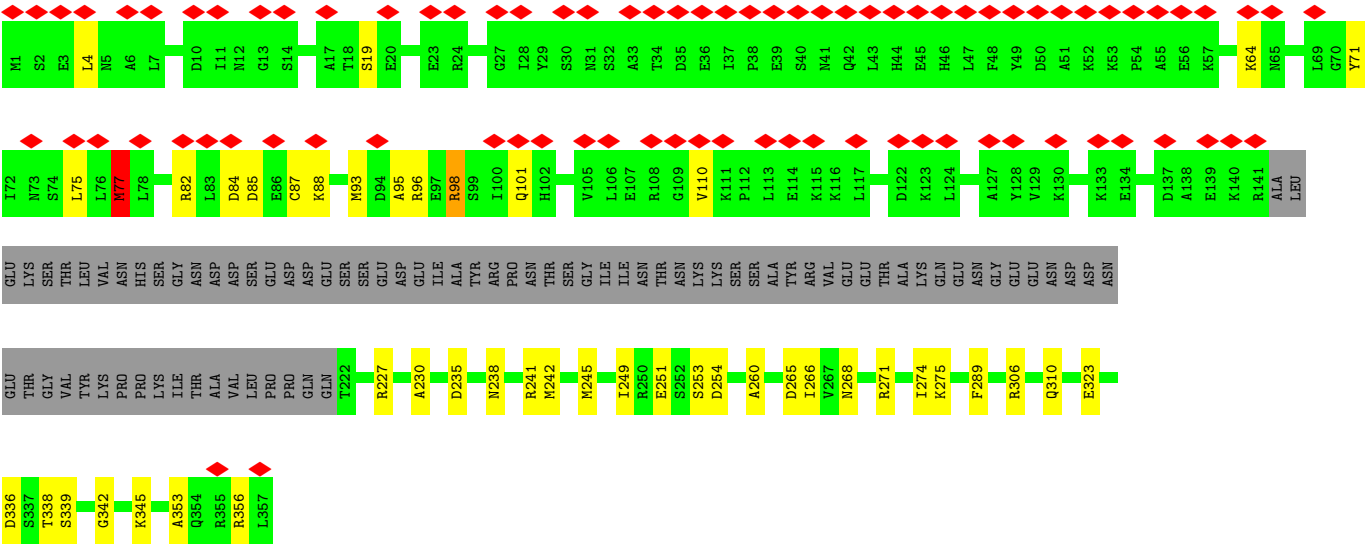


- Molecule 65: Protein BFR2

Chain 5: 21% 47% 8% 45%



- Molecule 66: U3 small nucleolar ribonucleoprotein protein LCP5



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	199534	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 ($e^-/\text{\AA}^2$)	1.074	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.065	Depositor
Minimum map value	-0.009	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.007	Depositor
Map size (Å)	463.968, 463.968, 463.968	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.074, 1.074, 1.074	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	NA	0.20	0/1685	0.53	1/2261 (0.0%)
2	SA	0.17	0/2769	0.42	0/3728
3	NB	0.22	0/1042	0.56	1/1377 (0.1%)
4	L0	0.19	0/11634	0.39	0/18120
5	L2	0.20	0/4001	0.38	0/6215
6	L3	0.18	0/871	0.55	0/1171
7	L4	0.23	0/1849	0.62	0/2497
8	L5	0.21	0/1690	0.54	0/2285
9	L7	0.28	0/1342	0.77	1/1807 (0.1%)
10	L8	0.25	0/1372	0.67	2/1834 (0.1%)
11	L9	0.28	0/1437	0.71	2/1924 (0.1%)
12	LC	0.30	0/990	0.80	2/1335 (0.1%)
13	LD	0.24	0/1050	0.68	2/1415 (0.1%)
14	LE	0.24	0/1020	0.68	0/1371
15	LF	0.29	0/727	0.79	1/977 (0.1%)
16	LG	0.34	0/499	0.89	2/670 (0.3%)
17	LH	0.18	0/6694	0.48	1/9070 (0.0%)
18	LJ	0.20	0/3993	0.49	1/5413 (0.0%)
19	LK	0.17	0/735	0.46	0/987
20	LL	0.19	0/3840	0.46	0/5208
21	LM	0.19	0/3470	0.44	0/4694
22	LN	0.19	0/5369	0.48	0/7272
23	LO	0.23	0/6780	0.49	1/9175 (0.0%)
24	LP	0.19	0/2281	0.45	0/3059
25	LQ	0.18	0/6574	0.49	1/8881 (0.0%)
26	LS	0.21	0/3875	0.43	0/5254
27	LT	0.21	0/6834	0.47	1/9238 (0.0%)
28	LU	0.21	0/3802	0.52	0/5118
29	LV	0.24	0/2902	0.65	2/3941 (0.1%)
30	LW	0.21	0/3505	0.44	0/4748
31	LZ	0.29	0/1559	0.72	2/2097 (0.1%)
32	NG	0.13	0/542	0.41	0/750
33	NK	0.11	0/867	0.33	0/1208
34	SC	0.23	0/1917	0.53	0/2588

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	SD	0.23	0/1815	0.60	0/2448
35	SE	0.30	0/928	0.69	0/1262
35	SF	0.32	0/928	0.75	2/1262 (0.2%)
36	SG	0.17	0/3498	0.49	1/4712 (0.0%)
37	SH	0.20	0/2832	0.46	1/3825 (0.0%)
38	SI	0.22	0/6403	0.55	4/8616 (0.0%)
39	SJ	0.17	0/1727	0.47	0/2329
39	SK	0.20	0/1828	0.50	0/2470
40	SL	0.23	0/1418	0.59	0/1906
41	SM	0.24	0/2337	0.61	6/3148 (0.2%)
42	SN	0.24	0/2041	0.59	1/2745 (0.0%)
43	SO	0.15	0/1003	0.45	0/1381
44	SQ	0.22	0/1156	0.56	1/1536 (0.1%)
45	SR	0.29	0/804	0.80	2/1074 (0.2%)
46	SS	0.22	0/1230	0.61	0/1660
47	ST	0.16	0/3826	0.48	2/5125 (0.0%)
48	SY	0.20	0/2042	0.49	0/2704
49	SZ	0.11	0/1294	0.33	0/1804
50	NJ	0.08	0/1313	0.29	0/1830
51	NH	0.10	0/5357	0.31	1/7463 (0.0%)
52	NI	0.11	0/838	0.32	0/1166
53	8	0.75	5/28439 (0.0%)	0.39	0/44273
54	SU	0.19	1/3736 (0.0%)	0.50	3/5086 (0.1%)
55	LI	0.17	0/2703	0.50	0/3703
56	ND	0.23	0/499	0.60	0/659
57	LR	0.19	1/6058 (0.0%)	0.51	4/8201 (0.0%)
58	NE	0.19	0/1240	0.50	0/1645
59	SB	0.18	0/3012	0.47	1/4091 (0.0%)
60	SV	0.32	0/385	0.67	2/529 (0.4%)
61	SP	0.09	0/11085	0.32	0/15445
62	LX	0.19	0/5994	0.52	4/8139 (0.0%)
62	LY	0.11	0/4128	0.34	0/5747
63	L6	2.81	1/1341 (0.1%)	0.80	5/1789 (0.3%)
64	NF	0.15	0/613	0.48	1/853 (0.1%)
65	5	0.19	0/2422	0.55	1/3257 (0.0%)
66	6	0.21	0/2271	0.59	2/3029 (0.1%)
All	All	0.39	8/218061 (0.0%)	0.48	67/304600 (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
1	NA	0	1
7	L4	0	2
9	L7	0	1
11	L9	0	1
15	LF	0	2
22	LN	0	1
29	LV	0	2
34	SD	0	1
35	SE	0	2
35	SF	0	1
38	SI	0	1
55	LI	0	1
57	LR	0	1
63	L6	0	1
65	5	0	1
66	6	0	1
All	All	0	20

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
63	L6	184	LEU	CA-CB	102.58	3.16	1.53
53	8	140	A	N9-C8	60.03	2.57	1.37
53	8	140	A	N7-C5	56.11	2.51	1.39
53	8	140	A	N9-C4	55.70	2.49	1.37
53	8	140	A	C8-N7	54.60	2.40	1.31
53	8	140	A	C5-C4	47.47	2.33	1.38
57	LR	104	PRO	CG-CD	-5.79	1.31	1.50
54	SU	286	ILE	C-N	5.44	1.38	1.33

All (67) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	LR	104	PRO	CA-N-CD	-12.17	94.96	112.00
63	L6	184	LEU	CA-CB-CG	10.93	154.55	116.30
16	LG	6	PRO	CA-N-CD	-10.75	96.95	112.00
11	L9	18	PRO	CA-N-CD	-9.90	98.14	112.00
57	LR	104	PRO	N-CD-CG	-9.21	89.38	103.20
63	L6	184	LEU	CB-CA-C	8.99	126.14	110.85
41	SM	41	PRO	CA-N-CD	-8.89	99.56	112.00
62	LX	762	MET	CB-CG-SD	7.72	135.86	112.70
29	LV	286	GLU	CA-CB-CG	7.60	129.31	114.10
41	SM	41	PRO	CA-C-N	7.56	139.99	122.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	SM	41	PRO	C-N-CA	7.56	139.99	122.31
51	NH	1207	VAL	N-CA-C	-7.47	105.72	111.62
63	L6	184	LEU	N-CA-C	-7.45	103.24	111.36
12	LC	43	ILE	N-CA-C	-7.33	106.35	113.53
57	LR	785	ILE	CA-C-N	7.16	124.75	120.24
57	LR	785	ILE	C-N-CA	7.16	124.75	120.24
18	LJ	313	GLN	CA-CB-CG	6.58	127.26	114.10
45	SR	98	GLU	CA-CB-CG	6.45	127.00	114.10
63	L6	184	LEU	N-CA-CB	6.41	119.65	110.16
62	LX	209	PRO	CA-N-CD	-6.37	103.08	112.00
54	SU	314	VAL	CA-C-N	6.37	124.25	120.24
54	SU	314	VAL	C-N-CA	6.37	124.25	120.24
27	LT	489	MET	CB-CG-SD	6.34	131.72	112.70
60	SV	185	PRO	CA-N-CD	-6.06	103.51	112.00
23	LO	741	MET	CA-CB-CG	6.04	126.18	114.10
63	L6	63	MET	CB-CG-SD	5.93	130.49	112.70
66	6	77	MET	CB-CG-SD	5.91	130.44	112.70
35	SF	31	ARG	CA-CB-CG	5.91	125.91	114.10
11	L9	147	MET	CB-CG-SD	5.89	130.36	112.70
12	LC	107	LYS	CB-CG-CD	5.87	124.81	111.30
38	SI	555	MET	CB-CG-SD	5.86	130.28	112.70
42	SN	156	MET	CB-CG-SD	5.85	130.24	112.70
54	SU	314	VAL	N-CA-C	-5.82	106.07	113.22
35	SF	50	GLU	CA-CB-CG	5.75	125.61	114.10
62	LX	15	ARG	CA-CB-CG	5.66	125.42	114.10
41	SM	124	MET	CB-CG-SD	5.65	129.64	112.70
3	NB	550	LEU	CA-CB-CG	5.64	136.03	116.30
9	L7	8	ILE	CA-CB-CG2	5.63	120.07	110.50
60	SV	185	PRO	N-CD-CG	-5.54	94.89	103.20
15	LF	18	LEU	CA-CB-CG	5.51	135.58	116.30
37	SH	350	MET	CB-CG-SD	5.49	129.18	112.70
10	L8	193	LEU	CA-CB-CG	5.46	135.43	116.30
44	SQ	216	ARG	CA-CB-CG	5.45	124.99	114.10
1	NA	382	GLN	CA-CB-CG	5.44	124.98	114.10
47	ST	104	MET	CB-CG-SD	5.42	128.96	112.70
47	ST	740	MET	CA-CB-CG	5.41	124.91	114.10
13	LD	71	LEU	CA-CB-CG	5.37	135.10	116.30
38	SI	956	MET	CB-CG-SD	5.35	128.76	112.70
17	LH	507	MET	CB-CG-SD	5.29	128.56	112.70
16	LG	6	PRO	N-CD-CG	-5.25	95.32	103.20
25	LQ	185	MET	CB-CG-SD	5.17	128.22	112.70
45	SR	101	GLU	CA-CB-CG	5.17	124.44	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	L8	61	GLU	CA-CB-CG	5.17	124.44	114.10
41	SM	268	ASN	CA-C-N	5.17	129.68	122.08
41	SM	268	ASN	C-N-CA	5.17	129.68	122.08
64	NF	124	ARG	N-CA-C	5.16	120.50	114.62
38	SI	236	LYS	CB-CG-CD	5.16	123.16	111.30
36	SG	114	LYS	CA-CB-CG	5.15	124.40	114.10
31	LZ	181	ASP	CA-C-N	5.15	129.72	122.46
31	LZ	181	ASP	C-N-CA	5.15	129.72	122.46
65	5	470	ASP	N-CA-C	5.13	121.16	109.81
13	LD	80	MET	CB-CG-SD	5.11	128.03	112.70
62	LX	15	ARG	CB-CG-CD	5.09	123.02	111.30
38	SI	230	MET	CB-CG-SD	5.06	127.88	112.70
59	SB	421	MET	CB-CG-SD	5.05	127.86	112.70
66	6	98	ARG	CB-CG-CD	5.05	122.91	111.30
29	LV	262	PRO	CA-N-CD	-5.00	105.00	112.00

There are no chirality outliers.

All (20) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
65	5	450	LEU	Peptide
66	6	338	THR	Peptide
7	L4	193	GLY	Peptide
7	L4	195	ILE	Peptide
63	L6	68	LEU	Peptide
9	L7	12	ALA	Peptide
11	L9	57	ARG	Sidechain
15	LF	31	ASN	Peptide
15	LF	51	GLU	Peptide
55	LI	257	SER	Peptide
22	LN	30	ARG	Sidechain
57	LR	626	MET	Peptide
29	LV	51	GLN	Peptide
29	LV	57	GLU	Peptide
1	NA	453	SER	Peptide
34	SD	321	MET	Peptide
35	SE	89	ARG	Sidechain
35	SE	9	PHE	Peptide
35	SF	9	PHE	Peptide
38	SI	198	VAL	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	NA	1667	0	1701	37	0
2	SA	2854	0	2792	43	0
3	NB	1098	0	1102	24	0
4	L0	10405	0	5231	97	0
5	L2	3585	0	1819	34	0
6	L3	901	0	907	16	0
7	L4	1810	0	1865	42	0
8	L5	1669	0	1724	24	0
9	L7	1321	0	1390	43	0
10	L8	1349	0	1372	25	0
11	L9	1415	0	1497	30	0
12	LC	973	0	1029	25	0
13	LD	1027	0	1084	25	0
14	LE	1003	0	1040	28	0
15	LF	715	0	744	14	0
16	LG	497	0	535	6	0
17	LH	6633	0	6510	103	0
18	LJ	3911	0	3906	70	0
19	LK	898	0	811	11	0
20	LL	3772	0	3806	55	0
21	LM	3443	0	3559	42	0
22	LN	5344	0	5301	101	0
23	LO	6635	0	6525	119	0
24	LP	2709	0	2371	30	0
25	LQ	6640	0	6503	109	0
26	LS	3791	0	3772	59	0
27	LT	6697	0	6676	105	0
28	LU	3725	0	3679	94	0
29	LV	2840	0	2685	71	0
30	LW	3428	0	3407	55	0
31	LZ	1530	0	1572	26	0
32	NG	543	0	277	3	0
33	NK	868	0	379	3	0
34	SC	1881	0	1928	29	0
34	SD	1782	0	1826	37	0
35	SE	916	0	964	19	0
35	SF	916	0	964	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	SG	3428	0	3446	76	0
37	SH	2781	0	2878	62	0
38	SI	6412	0	6498	128	0
39	SJ	1701	0	1767	29	0
39	SK	1799	0	1872	33	0
40	SL	1395	0	1476	29	0
41	SM	2296	0	2325	44	0
42	SN	2006	0	2118	40	0
43	SO	998	0	631	5	0
44	SQ	1137	0	1188	20	0
45	SR	792	0	847	22	0
46	SS	1466	0	1257	23	0
47	ST	4473	0	4057	54	0
48	SY	2016	0	2093	32	0
49	SZ	1295	0	571	3	0
50	NJ	1314	0	610	1	0
51	NH	5362	0	2295	13	0
52	NI	841	0	365	4	0
53	8	25439	0	12823	274	0
54	SU	3650	0	3365	41	0
55	LI	2690	0	1931	33	0
56	ND	495	0	561	13	0
57	LR	5957	0	5992	112	0
58	NE	1235	0	1243	21	0
59	SB	2985	0	2703	34	0
60	SV	381	0	255	6	0
61	SP	11108	0	4748	4	0
62	LX	5892	0	5420	92	0
62	LY	4132	0	1819	5	0
63	L6	1327	0	1403	39	0
64	NF	614	0	279	7	0
65	5	2389	0	2411	36	0
66	6	2244	0	2245	39	0
All	All	213241	0	176745	2615	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 7.

All (2615) 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)
53:8:140:A:C4	53:8:140:A:C5	2.33	1.17
53:8:140:A:C4	63:L6:184:LEU:HA	1.94	1.02
45:SR:41:SER:N	53:8:600:U:HO2'	1.68	0.91
53:8:140:A:C8	53:8:140:A:N7	2.40	0.88
53:8:140:A:C8	63:L6:184:LEU:CB	2.59	0.86
53:8:140:A:C5	63:L6:184:LEU:HB2	2.10	0.85
53:8:140:A:N9	63:L6:184:LEU:HB3	1.92	0.83
53:8:140:A:C5	63:L6:184:LEU:CB	2.64	0.81
53:8:140:A:C4	53:8:140:A:N9	2.49	0.80
53:8:140:A:C4	63:L6:184:LEU:CB	2.65	0.80
53:8:140:A:C5	53:8:140:A:N7	2.51	0.79
53:8:140:A:N9	63:L6:184:LEU:CB	2.48	0.76
53:8:140:A:C8	63:L6:184:LEU:CA	2.70	0.74
53:8:1695:G:N2	53:8:1706:C:C2	2.56	0.74
53:8:140:A:N7	63:L6:184:LEU:CB	2.51	0.73
53:8:140:A:C4	63:L6:184:LEU:CA	2.72	0.73
53:8:140:A:C8	53:8:140:A:N9	2.57	0.73
53:8:984:G:H1	53:8:1017:U:H3	1.36	0.72
53:8:1588:G:H1	53:8:1608:U:H3	1.39	0.70
53:8:140:A:C5	63:L6:184:LEU:CA	2.74	0.70
27:LT:584:HIS:HE2	27:LT:602:SER:HG	1.39	0.70
5:L2:85:G:N7	59:SB:361:ARG:NH1	2.41	0.68
46:SS:316:ASN:HD21	46:SS:895:LYS:H	1.42	0.68
29:LV:64:VAL:HG11	29:LV:323:VAL:HG22	1.76	0.67
31:LZ:109:ARG:HH22	31:LZ:155:GLU:HB2	1.59	0.67
62:LX:60:LYS:HG3	62:LX:61:LYS:HG2	1.76	0.67
25:LQ:137:ILE:HG23	25:LQ:147:VAL:HG22	1.75	0.66
53:8:140:A:N9	63:L6:184:LEU:CA	2.59	0.66
18:LJ:108:TYR:HB3	18:LJ:117:LEU:H	1.60	0.66
17:LH:630:LEU:HB2	17:LH:653:PHE:HB2	1.77	0.66
37:SH:315:LYS:HD2	37:SH:348:GLU:HB2	1.77	0.66
2:SA:191:PHE:HB3	2:SA:278:VAL:HG22	1.78	0.66
17:LH:17:GLY:HA2	17:LH:50:ASN:HD21	1.59	0.66
53:8:314:C:H42	53:8:354:C:H42	1.44	0.66
7:L4:71:LYS:HG2	7:L4:91:THR:HB	1.77	0.66
22:LN:265:TRP:HA	22:LN:272:LEU:HA	1.78	0.66
62:LX:27:VAL:HG23	62:LX:150:ILE:HB	1.78	0.66
2:SA:10:GLU:HB2	34:SC:232:MET:HE1	1.77	0.66
27:LT:723:LEU:HD22	27:LT:879:GLU:HB2	1.76	0.65
53:8:140:A:C4	63:L6:184:LEU:HB2	2.30	0.65
39:SJ:44:VAL:HG12	39:SJ:113:TYR:HB2	1.78	0.65
57:LR:495:ASN:H	57:LR:510:SER:HA	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:L7:43:PHE:HB2	9:L7:60:ILE:HD11	1.77	0.65
25:LQ:588:ILE:HB	25:LQ:600:TRP:HB2	1.77	0.65
25:LQ:594:ASP:HB2	53:8:1137:A:H1'	1.78	0.65
37:SH:141:MET:HA	37:SH:144:PHE:HB2	1.78	0.65
37:SH:181:HIS:HB3	37:SH:310:ARG:HH21	1.61	0.65
39:SK:51:GLU:HG2	39:SK:68:LEU:HD23	1.79	0.65
1:NA:516:SER:HB2	57:LR:691:PRO:HD2	1.79	0.65
10:L8:22:ARG:HH12	53:8:384:G:H5''	1.62	0.65
42:SN:63:LYS:HG2	42:SN:185:LYS:HB2	1.79	0.65
41:SM:100:LEU:HA	41:SM:103:PHE:HB3	1.79	0.65
7:L4:151:ASP:HA	63:L6:215:ARG:HH12	1.62	0.64
53:8:151:G:H22	53:8:163:G:H1	1.44	0.64
14:LE:51:GLU:HB2	14:LE:62:VAL:HB	1.79	0.64
25:LQ:392:THR:HG21	25:LQ:411:ASN:H	1.61	0.64
22:LN:482:ASP:HB2	22:LN:485:LYS:HB2	1.78	0.64
47:ST:647:ILE:HA	47:ST:651:TRP:HB2	1.80	0.64
17:LH:892:MET:HE1	21:LM:262:VAL:HG11	1.80	0.64
35:SE:58:CYS:HA	35:SE:84:ARG:HD3	1.80	0.64
34:SD:171:LEU:HB2	34:SD:237:VAL:HG11	1.78	0.64
10:L8:44:HIS:HB3	10:L8:56:ARG:HB2	1.81	0.63
38:SI:828:ARG:NH1	45:SR:94:ASN:O	2.28	0.63
1:NA:484:MET:SD	23:LO:359:ARG:NH1	2.71	0.63
53:8:273:G:H1	53:8:284:G:H1'	1.64	0.63
53:8:1711:C:N4	53:8:1713:G:N7	2.46	0.63
5:L2:12:U:H3	53:8:1112:G:H1	1.46	0.63
39:SK:44:VAL:HG22	39:SK:113:TYR:HB2	1.78	0.63
20:LL:281:ILE:HG12	20:LL:328:VAL:HB	1.80	0.63
23:LO:717:LEU:HD23	23:LO:744:ARG:HG2	1.80	0.63
38:SI:924:VAL:O	47:ST:109:ARG:NH1	2.30	0.63
30:LW:434:LEU:HD11	31:LZ:9:GLU:HB2	1.80	0.63
34:SC:149:SER:HB2	34:SC:180:SER:HB2	1.80	0.63
62:LX:641:ASN:HB3	62:LX:644:TYR:HB2	1.81	0.63
7:L4:206:ASP:HB2	7:L4:222:LEU:HB3	1.78	0.63
23:LO:20:ILE:H	23:LO:307:THR:HG21	1.62	0.63
65:5:337:MET:SD	65:5:341:LYS:NZ	2.72	0.63
55:LI:604:LYS:HG3	55:LI:608:GLN:HE22	1.64	0.63
28:LU:315:PRO:HB2	46:SS:891:ILE:HD11	1.80	0.63
9:L7:140:VAL:HG12	9:L7:150:GLN:HB3	1.81	0.62
11:L9:60:LEU:HD21	11:L9:93:LEU:HB3	1.80	0.62
38:SI:52:ARG:HH22	53:8:28:A:H4'	1.64	0.62
9:L7:150:GLN:HE22	9:L7:181:ILE:HD13	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:LR:395:ASP:HB3	57:LR:404:ALA:HB3	1.81	0.62
29:LV:50:ILE:HG22	29:LV:51:GLN:HG3	1.81	0.62
36:SG:333:MET:HG3	36:SG:335:ARG:HG2	1.80	0.62
45:SR:98:GLU:OE2	45:SR:99:ASN:ND2	2.33	0.62
53:8:140:A:N7	63:L6:184:LEU:CA	2.63	0.62
4:L0:551:A:N1	4:L0:586:A:N6	2.47	0.61
22:LN:139:CYS:SG	22:LN:140:ASN:N	2.72	0.61
27:LT:885:MET:HA	27:LT:888:LEU:HB2	1.83	0.61
48:SY:10:LYS:NZ	53:8:552:G:N7	2.48	0.61
57:LR:548:LEU:HB3	57:LR:560:TRP:HB2	1.81	0.61
57:LR:728:ILE:HA	57:LR:731:LEU:HD12	1.82	0.61
63:L6:72:ARG:HA	63:L6:98:ARG:HA	1.80	0.61
1:NA:346:GLU:HB2	47:ST:766:ARG:HH12	1.65	0.61
6:L3:14:ILE:HG22	6:L3:23:ASP:HA	1.80	0.61
23:LO:162:LEU:HB3	23:LO:172:ILE:HG12	1.83	0.61
27:LT:587:ARG:HH21	27:LT:605:LEU:HD11	1.65	0.61
30:LW:190:HIS:HD1	30:LW:207:THR:HG1	1.44	0.61
38:SI:944:ASN:ND2	38:SI:991:PHE:O	2.33	0.61
42:SN:42:THR:H	42:SN:195:ASN:HB2	1.64	0.61
14:LE:41:MET:HG2	14:LE:47:ILE:HG12	1.83	0.61
62:LX:786:LEU:HA	62:LX:890:LEU:HD21	1.82	0.61
18:LJ:213:GLN:NE2	18:LJ:233:ASN:OD1	2.34	0.61
40:SL:27:LYS:NZ	40:SL:28:ASN:OD1	2.33	0.61
62:LY:899:ALA:HB1	62:LY:905:PRO:HA	1.83	0.61
2:SA:155:GLY:HA2	34:SC:233:LEU:HD23	1.83	0.61
4:L0:123:C:N4	54:SU:134:PHE:O	2.34	0.61
22:LN:247:LEU:HD23	22:LN:292:ASN:HB3	1.83	0.61
27:LT:28:ARG:HH11	27:LT:30:ILE:HD13	1.66	0.61
27:LT:509:SER:OG	27:LT:510:LEU:N	2.34	0.61
22:LN:186:GLN:NE2	22:LN:205:CYS:SG	2.74	0.61
25:LQ:26:ILE:HB	25:LQ:40:GLN:HB2	1.83	0.61
39:SK:24:VAL:HG12	54:SU:487:PRO:HB2	1.81	0.61
4:L0:135:G:O2'	20:LL:494:ARG:NH1	2.33	0.60
9:L7:162:ILE:HA	9:L7:165:LYS:HG2	1.83	0.60
35:SE:17:THR:HA	35:SE:20:ILE:HG22	1.83	0.60
18:LJ:197:ASP:HB2	18:LJ:206:ILE:HD11	1.84	0.60
21:LM:194:SER:HB2	27:LT:335:VAL:HG11	1.81	0.60
26:LS:448:LYS:NZ	26:LS:449:ASP:O	2.34	0.60
27:LT:311:VAL:HG22	27:LT:321:GLU:HG2	1.83	0.60
29:LV:288:LYS:HB3	29:LV:299:ILE:HD11	1.83	0.60
9:L7:166:LEU:HD13	9:L7:183:PHE:HB2	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:LO:673:ARG:HG3	23:LO:675:MET:H	1.67	0.60
53:8:185:U:H3'	53:8:186:C:H4'	1.83	0.60
57:LR:64:ILE:HA	57:LR:80:SER:HA	1.82	0.60
66:6:238:ASN:OD1	66:6:241:ARG:NH2	2.35	0.60
4:L0:219:U:H5'	56:ND:204:ARG:HH12	1.66	0.60
12:LC:98:ASP:OD2	27:LT:488:ASN:ND2	2.35	0.60
23:LO:440:PRO:HG3	23:LO:483:GLN:HA	1.84	0.60
42:SN:103:VAL:HG11	42:SN:131:VAL:HG21	1.82	0.60
21:LM:366:ILE:HA	21:LM:369:LEU:HB2	1.84	0.60
62:LX:621:GLN:HB3	62:LX:784:ARG:HH12	1.66	0.60
29:LV:263:SER:OG	29:LV:264:ILE:N	2.35	0.60
47:ST:700:LEU:HD21	54:SU:467:ALA:HB2	1.84	0.60
57:LR:171:MET:HB3	57:LR:187:GLN:HA	1.84	0.60
17:LH:497:ASP:HB2	17:LH:510:TYR:HB3	1.83	0.59
23:LO:10:LEU:HD13	23:LO:702:LEU:HD23	1.84	0.59
36:SG:235:HIS:HA	36:SG:259:LYS:HZ1	1.67	0.59
57:LR:540:SER:HB2	57:LR:549:ALA:HB3	1.84	0.59
2:SA:385:MET:HG2	35:SF:63:ILE:HB	1.83	0.59
57:LR:290:ILE:HA	57:LR:306:LEU:HA	1.84	0.59
4:L0:174:U:O2'	4:L0:222:G:N2	2.35	0.59
36:SG:368:LEU:HD23	36:SG:371:ARG:HD3	1.83	0.59
36:SG:481:ILE:HD13	36:SG:486:VAL:HG13	1.84	0.59
36:SG:541:ALA:HB3	36:SG:564:TYR:HB3	1.84	0.59
38:SI:925:ASN:OD1	47:ST:109:ARG:NH1	2.35	0.59
15:LF:83:LYS:HE3	15:LF:91:LEU:HD12	1.85	0.59
44:SQ:131:ASP:HB3	44:SQ:134:ARG:HG2	1.85	0.59
5:L2:82:G:N7	35:SE:38:ASN:ND2	2.47	0.59
12:LC:121:SER:OG	12:LC:123:ARG:NH1	2.36	0.59
28:LU:226:LYS:HG2	28:LU:268:CYS:HA	1.85	0.59
28:LU:332:TYR:HB3	28:LU:339:SER:HA	1.83	0.59
38:SI:1122:ALA:HB2	44:SQ:194:ILE:HD12	1.83	0.59
13:LD:87:ARG:HH21	13:LD:106:ASN:HD21	1.50	0.59
28:LU:133:GLN:HE22	28:LU:169:GLU:HG2	1.67	0.59
4:L0:87:C:O2	17:LH:332:GLN:NE2	2.36	0.59
13:LD:33:ARG:NH2	13:LD:53:TYR:O	2.36	0.59
18:LJ:275:SER:HB3	18:LJ:305:CYS:HB3	1.84	0.59
22:LN:470:LEU:HD11	22:LN:498:VAL:HG11	1.85	0.59
23:LO:347:SER:HB2	23:LO:365:GLU:H	1.68	0.59
15:LF:54:ALA:HB2	15:LF:79:VAL:HG12	1.84	0.58
23:LO:79:ALA:HB3	23:LO:93:PHE:HB3	1.85	0.58
29:LV:121:ARG:HH12	53:8:340:U:H5''	1.66	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:NA:370:ARG:HH22	47:ST:52:ARG:HD3	1.69	0.58
2:SA:185:ASP:O	2:SA:189:ASN:ND2	2.36	0.58
4:L0:335:G:H1	4:L0:389:U:H3	1.51	0.58
5:L2:256:G:N7	35:SF:38:ASN:ND2	2.51	0.58
22:LN:489:CYS:HB2	22:LN:534:LEU:HD11	1.85	0.58
27:LT:128:LEU:HB3	27:LT:140:TYR:HB2	1.85	0.58
36:SG:198:LYS:HE2	36:SG:212:LYS:HB2	1.84	0.58
2:SA:277:ARG:NH2	59:SB:261:GLN:OE1	2.36	0.58
17:LH:320:VAL:HG22	17:LH:335:PRO:HA	1.84	0.58
22:LN:166:VAL:HG22	22:LN:182:ILE:HG12	1.85	0.58
57:LR:439:ALA:HB3	57:LR:457:ALA:HB3	1.85	0.58
63:L6:67:VAL:H	63:L6:100:ALA:HB2	1.68	0.58
11:L9:57:ARG:NH2	40:SL:87:MET:O	2.36	0.58
35:SF:22:ASP:O	35:SF:26:GLN:NE2	2.36	0.58
62:LX:585:VAL:HB	62:LX:639:ALA:HB3	1.85	0.58
9:L7:163:ASP:OD1	9:L7:163:ASP:N	2.34	0.58
28:LU:114:THR:HG1	28:LU:139:CYS:HG	1.51	0.58
36:SG:333:MET:SD	36:SG:350:LYS:NZ	2.76	0.58
36:SG:442:ILE:HA	36:SG:472:PRO:HA	1.84	0.58
41:SM:123:VAL:HG23	41:SM:126:ASN:HB2	1.86	0.58
63:L6:105:ASP:OD2	63:L6:105:ASP:N	2.35	0.58
10:L8:98:LYS:HD2	10:L8:172:ARG:HG2	1.84	0.58
29:LV:162:LEU:HB3	29:LV:176:PHE:HB2	1.85	0.58
1:NA:366:GLU:HA	1:NA:369:ILE:HD12	1.86	0.58
38:SI:1059:ARG:NH1	48:SY:33:ASP:OD2	2.35	0.58
62:LX:12:SER:O	62:LX:16:ASN:ND2	2.37	0.58
66:6:64:LYS:HB2	66:6:110:VAL:HG11	1.85	0.58
4:L0:471:C:OP1	21:LM:27:LYS:NZ	2.37	0.58
22:LN:384:VAL:HG23	22:LN:391:VAL:HG12	1.86	0.58
30:LW:354:CYS:SG	30:LW:364:ARG:NH2	2.77	0.58
37:SH:289:VAL:O	37:SH:317:GLN:NE2	2.36	0.58
37:SH:339:LEU:HB3	37:SH:350:MET:HE2	1.85	0.58
1:NA:470:GLU:HG3	1:NA:490:LEU:HB2	1.86	0.58
25:LQ:447:LEU:HB3	25:LQ:455:GLN:HB2	1.86	0.58
54:SU:350:MET:O	54:SU:355:ARG:NH1	2.37	0.58
65:5:337:MET:O	66:6:96:ARG:NH2	2.37	0.58
8:L5:76:ARG:NH1	12:LC:120:ASP:OD2	2.37	0.58
26:LS:254:LEU:HD22	26:LS:263:LEU:HD11	1.86	0.58
42:SN:93:THR:HG22	42:SN:177:ARG:HB2	1.86	0.58
57:LR:440:VAL:HG12	57:LR:456:THR:HG22	1.85	0.58
34:SD:105:LEU:HD21	48:SY:124:GLN:HA	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:8:538:A:H5'	53:8:543:C:H41	1.68	0.57
9:L7:74:GLN:HG2	9:L7:92:PHE:HD2	1.68	0.57
26:LS:568:VAL:HG23	26:LS:579:VAL:HG22	1.87	0.57
45:SR:41:SER:N	53:8:600:U:O2'	2.36	0.57
53:8:376:C:O2'	53:8:378:A:N7	2.36	0.57
53:8:965:U:H5''	64:NF:126:ALA:HB2	1.86	0.57
65:5:193:ARG:HH11	66:6:75:LEU:HD13	1.69	0.57
1:NA:483:TYR:OH	27:LT:736:HIS:ND1	2.37	0.57
25:LQ:196:CYS:SG	25:LQ:197:ILE:N	2.76	0.57
36:SG:402:ILE:HA	36:SG:417:SER:HA	1.86	0.57
38:SI:761:GLN:O	38:SI:765:ASN:ND2	2.38	0.57
44:SQ:110:ASP:O	44:SQ:114:ARG:NH2	2.38	0.57
48:SY:140:ARG:NH1	56:ND:166:LEU:O	2.37	0.57
48:SY:154:THR:HA	48:SY:168:LYS:HG3	1.86	0.57
53:8:1161:C:H1'	53:8:1619:C:H41	1.69	0.57
9:L7:151:LYS:HE2	9:L7:184:GLU:HB3	1.86	0.57
22:LN:583:VAL:HG22	22:LN:593:GLU:HG3	1.86	0.57
27:LT:28:ARG:HH21	27:LT:71:VAL:HG11	1.69	0.57
37:SH:123:ALA:HB1	37:SH:261:ILE:HG21	1.85	0.57
44:SQ:202:ARG:O	53:8:1489:U:N3	2.37	0.57
47:ST:478:ILE:HG12	47:ST:524:LEU:HD13	1.86	0.57
61:SP:1475:GLN:HA	61:SP:1517:HIS:HA	1.85	0.57
10:L8:98:LYS:HB3	53:8:329:G:H5''	1.87	0.57
17:LH:602:PRO:HB3	55:LI:591:THR:HB	1.87	0.57
26:LS:312:ILE:HB	26:LS:324:TRP:HB3	1.87	0.57
29:LV:56:SER:HA	29:LV:336:ILE:HA	1.86	0.57
35:SF:22:ASP:OD2	36:SG:342:ARG:NH2	2.37	0.57
40:SL:171:PRO:HA	40:SL:184:LYS:HB2	1.86	0.57
57:LR:786:ILE:HG13	57:LR:787:PRO:HD3	1.86	0.57
65:5:444:ALA:O	65:5:448:ASN:ND2	2.38	0.57
1:NA:326:LEU:O	38:SI:930:LYS:NZ	2.32	0.57
18:LJ:48:ASN:ND2	18:LJ:51:HIS:O	2.38	0.57
21:LM:123:ARG:O	21:LM:126:GLN:NE2	2.37	0.57
25:LQ:760:ILE:HA	25:LQ:763:ILE:HB	1.85	0.57
29:LV:72:MET:HE1	29:LV:83:VAL:HG22	1.86	0.57
53:8:966:A:OP2	64:NF:126:ALA:N	2.26	0.57
3:NB:507:ILE:HG22	3:NB:510:LYS:HE3	1.87	0.57
4:L0:337:G:OP1	58:NE:209:ARG:NH2	2.38	0.57
8:L5:60:ASP:HA	8:L5:65:ARG:HH22	1.70	0.57
25:LQ:756:LEU:HD22	25:LQ:824:MET:HE1	1.87	0.57
26:LS:538:LYS:HE2	26:LS:563:GLY:HA2	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:SM:282:ARG:NH2	53:8:560:U:OP2	2.37	0.57
57:LR:313:LEU:HB3	57:LR:331:SER:HB3	1.86	0.57
28:LU:298:LEU:O	28:LU:457:ARG:NH1	2.38	0.57
53:8:579:A:H4'	53:8:580:A:H5'	1.87	0.57
55:LI:165:SER:HA	55:LI:181:ASP:HA	1.85	0.57
7:L4:200:ARG:NH1	7:L4:206:ASP:OD1	2.37	0.57
17:LH:867:VAL:HG22	17:LH:895:LEU:HD21	1.87	0.57
25:LQ:114:LEU:HG	25:LQ:115:LEU:HG	1.85	0.57
62:LX:104:ARG:NH1	62:LX:105:TYR:O	2.38	0.57
20:LL:516:ILE:HD12	20:LL:517:PRO:HD2	1.87	0.56
24:LP:15:MET:HE3	24:LP:29:VAL:HB	1.87	0.56
38:SI:1062:ARG:NH2	53:8:1490:C:OP1	2.38	0.56
14:LE:15:ASN:ND2	14:LE:72:CYS:O	2.38	0.56
23:LO:726:THR:HA	23:LO:741:MET:HE1	1.86	0.56
25:LQ:433:ALA:HA	25:LQ:449:THR:HA	1.87	0.56
29:LV:66:ARG:HH12	29:LV:108:SER:HB2	1.68	0.56
35:SE:24:VAL:HG12	35:SE:102:ILE:HD11	1.85	0.56
39:SK:190:GLN:NE2	39:SK:244:GLY:O	2.38	0.56
4:L0:293:U:H3	23:LO:632:SER:HB3	1.70	0.56
22:LN:481:ILE:HA	22:LN:536:VAL:HG21	1.87	0.56
28:LU:344:HIS:NE2	28:LU:418:HIS:O	2.39	0.56
37:SH:281:GLU:OE1	38:SI:625:TRP:NE1	2.38	0.56
41:SM:93:SER:O	41:SM:119:ARG:NH1	2.39	0.56
53:8:140:A:C5	63:L6:184:LEU:HA	2.41	0.56
53:8:312:A:H2	53:8:315:A:H5'	1.71	0.56
63:L6:10:ASN:ND2	63:L6:127:THR:O	2.37	0.56
1:NA:480:GLN:O	27:LT:743:ARG:NH2	2.39	0.56
4:L0:274:C:H2'	4:L0:275:A:H8	1.70	0.56
11:L9:77:ILE:HG21	11:L9:91:LYS:HA	1.87	0.56
15:LF:15:ASN:HB3	15:LF:20:ARG:HB2	1.87	0.56
17:LH:536:ASP:N	17:LH:536:ASP:OD1	2.38	0.56
28:LU:258:ILE:HD12	28:LU:294:LEU:HB3	1.86	0.56
28:LU:358:MET:HE1	46:SS:890:VAL:HA	1.87	0.56
53:8:877:G:O2'	53:8:942:G:N2	2.39	0.56
9:L7:20:VAL:HA	9:L7:23:ALA:HB3	1.86	0.56
17:LH:559:LYS:HG2	17:LH:612:SER:HA	1.86	0.56
31:LZ:151:THR:HB	31:LZ:154:MET:HB2	1.87	0.56
42:SN:74:LEU:HD23	42:SN:100:ILE:HD12	1.88	0.56
45:SR:65:ASN:HB3	45:SR:90:ASP:HB2	1.88	0.56
28:LU:262:MET:O	28:LU:281:ASN:ND2	2.39	0.56
30:LW:178:ASP:HB2	30:LW:184:LEU:HD21	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:SG:523:LYS:NZ	36:SG:524:ILE:O	2.38	0.56
55:LI:555:ILE:O	55:LI:585:ARG:NH1	2.39	0.56
4:L0:375:C:OP2	46:SS:834:LYS:NZ	2.39	0.56
7:L4:24:SER:HB2	66:6:289:PHE:HZ	1.69	0.56
11:L9:79:ARG:HD2	66:6:323:GLU:HB3	1.87	0.56
17:LH:682:ASN:HB2	17:LH:689:ILE:HD11	1.88	0.56
39:SK:83:ASP:OD1	39:SK:83:ASP:N	2.39	0.56
40:SL:163:ARG:HD2	53:8:15:U:H4'	1.88	0.56
62:LX:917:MET:HA	62:LX:920:MET:HE1	1.87	0.56
9:L7:150:GLN:NE2	9:L7:180:GLN:O	2.38	0.56
10:L8:67:TRP:HA	10:L8:183:ILE:HG22	1.88	0.56
26:LS:272:LEU:HD12	26:LS:288:LEU:HD23	1.87	0.56
27:LT:432:THR:OG1	27:LT:443:TRP:NE1	2.37	0.56
27:LT:510:LEU:O	27:LT:553:ARG:NH1	2.39	0.56
37:SH:256:TYR:HD1	37:SH:283:ILE:HG12	1.69	0.56
42:SN:56:ILE:HD13	42:SN:183:ILE:HG13	1.88	0.56
53:8:1468:U:H2'	53:8:1469:A:H8	1.71	0.56
5:L2:34:A:N7	31:LZ:7:HIS:ND1	2.51	0.56
9:L7:164:TYR:HD2	46:SS:278:ILE:HD13	1.69	0.56
29:LV:126:GLN:NE2	29:LV:129:GLY:O	2.39	0.56
37:SH:111:LYS:NZ	38:SI:921:GLU:OE2	2.37	0.56
57:LR:416:ARG:H	57:LR:425:ASP:HB2	1.71	0.56
17:LH:690:ASN:HD22	17:LH:750:LEU:HB2	1.70	0.56
36:SG:356:ARG:NH1	66:6:260:ALA:O	2.38	0.56
37:SH:330:LYS:NZ	38:SI:554:TYR:O	2.39	0.56
41:SM:42:LEU:HD12	58:NE:218:LEU:HB3	1.88	0.56
15:LF:5:VAL:O	15:LF:43:LYS:NZ	2.38	0.55
20:LL:167:SER:O	20:LL:168:HIS:ND1	2.39	0.55
47:ST:616:LEU:HB3	47:ST:619:LEU:HB2	1.86	0.55
4:L0:169:A:N7	22:LN:236:LYS:NZ	2.53	0.55
11:L9:17:ARG:NH2	53:8:22:A:OP1	2.40	0.55
14:LE:41:MET:SD	14:LE:41:MET:N	2.70	0.55
28:LU:90:GLY:HA2	28:LU:113:VAL:HG23	1.89	0.55
28:LU:457:ARG:NH2	53:8:1:U:O4	2.39	0.55
34:SD:320:TYR:OH	34:SD:323:SER:OG	2.24	0.55
57:LR:513:LYS:HG2	57:LR:535:GLY:HA2	1.88	0.55
57:LR:596:ASP:OD1	57:LR:596:ASP:N	2.39	0.55
23:LO:88:ASN:ND2	27:LT:659:GLN:O	2.40	0.55
47:ST:482:GLN:HB2	47:ST:524:LEU:HD11	1.87	0.55
53:8:235:G:N2	53:8:236:A:N7	2.53	0.55
57:LR:296:ILE:HG22	57:LR:298:SER:H	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:LR:679:THR:OG1	57:LR:680:ASN:N	2.39	0.55
39:SK:70:CYS:SG	53:8:1192:C:N4	2.79	0.55
57:LR:227:MET:N	57:LR:227:MET:SD	2.78	0.55
4:L0:89:C:OP1	26:LS:319:ARG:NH1	2.39	0.55
23:LO:411:VAL:HG23	23:LO:425:PHE:HB2	1.89	0.55
23:LO:624:ASN:ND2	23:LO:676:ARG:O	2.39	0.55
34:SD:314:CYS:SG	34:SD:315:ILE:N	2.79	0.55
53:8:911:U:OP1	57:LR:534:ARG:NE	2.38	0.55
1:NA:534:ARG:NH2	53:8:1641:C:OP2	2.39	0.55
3:NB:544:ILE:O	38:SI:193:ARG:NH2	2.40	0.55
17:LH:71:ASN:HD22	17:LH:74:LEU:HG	1.70	0.55
17:LH:368:ASP:HB3	17:LH:389:LEU:HD13	1.88	0.55
20:LL:110:ILE:HD12	20:LL:119:CYS:HB3	1.88	0.55
28:LU:85:THR:OG1	28:LU:95:TRP:NE1	2.35	0.55
34:SC:171:LEU:HB2	34:SC:237:VAL:HG11	1.88	0.55
47:ST:422:LEU:HA	47:ST:425:PHE:HB3	1.87	0.55
19:LK:496:LEU:HA	19:LK:499:ILE:HD12	1.89	0.55
22:LN:542:VAL:HG23	22:LN:552:ILE:HG13	1.88	0.55
30:LW:40:LYS:HA	30:LW:43:ARG:HG2	1.89	0.55
36:SG:164:GLN:NE2	36:SG:528:GLU:O	2.40	0.55
39:SJ:100:LEU:O	39:SJ:105:ASN:ND2	2.38	0.55
39:SK:144:LEU:HB2	39:SK:150:ILE:HD11	1.88	0.55
47:ST:548:ARG:NH2	47:ST:638:ASN:OD1	2.39	0.55
58:NE:265:SER:O	58:NE:273:ARG:NH1	2.40	0.55
10:L8:81:VAL:HA	10:L8:102:VAL:HA	1.87	0.55
12:LC:31:VAL:HG22	12:LC:67:VAL:HB	1.88	0.55
29:LV:152:ASP:OD1	29:LV:152:ASP:N	2.40	0.55
38:SI:855:GLN:HE21	38:SI:1016:ASN:HD22	1.55	0.55
47:ST:734:ARG:O	47:ST:738:ASN:ND2	2.39	0.55
5:L2:15:U:OP2	58:NE:224:HIS:NE2	2.38	0.55
9:L7:162:ILE:O	9:L7:166:LEU:N	2.39	0.55
14:LE:11:LEU:HD21	14:LE:37:PHE:HE1	1.72	0.55
21:LM:196:LEU:HD11	21:LM:213:THR:HG21	1.89	0.55
23:LO:556:ARG:NH2	23:LO:575:GLU:OE1	2.40	0.55
28:LU:228:ASN:ND2	28:LU:230:ASN:O	2.39	0.55
39:SJ:168:THR:HA	39:SJ:171:LEU:HB2	1.89	0.55
4:L0:391:C:O2	31:LZ:55:ARG:NH1	2.40	0.55
8:L5:92:ARG:NH2	8:L5:169:ASN:OD1	2.40	0.55
20:LL:203:ILE:HD11	20:LL:212:LEU:HB3	1.89	0.55
21:LM:166:ASN:ND2	59:SB:408:THR:O	2.40	0.55
25:LQ:338:ILE:HG22	25:LQ:355:LEU:HD21	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:SD:242:ALA:HB2	34:SD:253:ILE:HD11	1.89	0.55
36:SG:460:ARG:HA	36:SG:463:GLN:HB2	1.89	0.55
48:SY:140:ARG:NH2	56:ND:169:ASP:OD1	2.40	0.55
4:L0:489:G:O6	24:LP:120:ARG:NH1	2.40	0.54
9:L7:64:VAL:HG13	9:L7:67:LEU:HB2	1.89	0.54
14:LE:27:ILE:HB	14:LE:61:ILE:HB	1.89	0.54
14:LE:78:ARG:HH21	14:LE:124:LYS:HG3	1.71	0.54
18:LJ:90:ARG:HH21	18:LJ:137:ASN:HB3	1.72	0.54
19:LK:456:LEU:HD23	55:LI:675:LEU:HD22	1.89	0.54
20:LL:469:ILE:HG21	20:LL:505:CYS:HA	1.89	0.54
21:LM:245:LEU:HB3	21:LM:257:ALA:HB2	1.89	0.54
26:LS:177:TRP:HZ3	27:LT:232:MET:HE1	1.73	0.54
28:LU:265:ASN:ND2	28:LU:308:VAL:O	2.39	0.54
28:LU:438:LYS:NZ	53:8:0:U:OP1	2.40	0.54
48:SY:234:VAL:HG22	48:SY:240:ILE:HG22	1.89	0.54
18:LJ:90:ARG:NH2	18:LJ:137:ASN:O	2.40	0.54
30:LW:115:HIS:HB3	30:LW:128:THR:HB	1.89	0.54
31:LZ:62:SER:O	58:NE:207:ARG:NH1	2.40	0.54
53:8:523:G:H21	53:8:529:A:H62	1.54	0.54
53:8:966:A:OP2	64:NF:125:LEU:N	2.40	0.54
7:L4:43:PRO:HB3	7:L4:81:THR:HA	1.90	0.54
28:LU:450:ASP:OD1	28:LU:450:ASP:N	2.40	0.54
31:LZ:170:LEU:HA	48:SY:67:MET:HE3	1.88	0.54
38:SI:60:ASP:O	38:SI:239:ASN:ND2	2.40	0.54
54:SU:181:THR:HB	54:SU:225:HIS:HE1	1.71	0.54
55:LI:301:GLN:HA	55:LI:315:SER:HA	1.89	0.54
57:LR:15:ILE:HG12	57:LR:43:ILE:HD13	1.89	0.54
17:LH:19:LYS:HE2	17:LH:366:ASN:HD21	1.71	0.54
34:SD:91:HIS:NE2	48:SY:163:GLU:O	2.37	0.54
35:SF:13:ASP:O	35:SF:17:THR:OG1	2.24	0.54
53:8:1670:G:O2'	53:8:1731:A:N6	2.39	0.54
55:LI:207:HIS:HA	55:LI:223:THR:HA	1.89	0.54
4:L0:238:G:N2	4:L0:274:C:O2	2.37	0.54
26:LS:556:PRO:HB2	26:LS:560:THR:HG21	1.90	0.54
36:SG:137:GLY:HA3	36:SG:500:LYS:HD2	1.89	0.54
36:SG:498:VAL:HG23	36:SG:511:LEU:HB2	1.90	0.54
47:ST:488:ASN:HB2	47:ST:492:ALA:HB2	1.90	0.54
53:8:126:A:H61	53:8:290:G:H1	1.55	0.54
57:LR:593:CYS:HB2	57:LR:620:LEU:HG	1.89	0.54
10:L8:88:ASN:OD1	10:L8:88:ASN:N	2.41	0.54
17:LH:529:LEU:HB3	17:LH:547:VAL:HB	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:LL:189:SER:HB2	20:LL:206:ALA:HB1	1.89	0.54
26:LS:128:SER:O	26:LS:132:LYS:NZ	2.40	0.54
34:SD:173:LEU:HB3	34:SD:242:ALA:HA	1.90	0.54
37:SH:156:ARG:HH21	37:SH:230:TRP:HE1	1.54	0.54
57:LR:763:ILE:HG23	57:LR:772:LEU:HD13	1.90	0.54
17:LH:437:THR:OG1	17:LH:706:HIS:ND1	2.41	0.54
21:LM:59:LEU:HD21	21:LM:114:THR:HG22	1.90	0.54
28:LU:123:PHE:HA	28:LU:207:ASN:HD21	1.73	0.54
29:LV:112:THR:HA	29:LV:128:LYS:HD3	1.89	0.54
29:LV:353:CYS:HB3	29:LV:356:LEU:HB2	1.89	0.54
30:LW:289:MET:HG2	30:LW:301:TRP:HB2	1.90	0.54
38:SI:344:ARG:NH1	53:8:426:G:O6	2.41	0.54
39:SJ:116:THR:HG22	39:SJ:118:ARG:H	1.72	0.54
39:SK:88:ARG:NH1	53:8:1191:U:O2	2.40	0.54
39:SK:199:ASP:N	39:SK:199:ASP:OD1	2.39	0.54
4:L0:146:G:N2	20:LL:360:ASN:OD1	2.38	0.54
11:L9:53:ARG:NH2	11:L9:99:LEU:O	2.40	0.54
23:LO:99:CYS:HB3	23:LO:113:LEU:HD11	1.90	0.54
23:LO:112:ALA:HB1	23:LO:119:LEU:HD11	1.88	0.54
28:LU:82:LYS:NZ	28:LU:154:ASP:OD2	2.40	0.54
4:L0:83:U:H2'	22:LN:327:LEU:HD22	1.90	0.54
10:L8:31:ARG:HH21	10:L8:48:THR:HG22	1.73	0.54
17:LH:664:LEU:HB3	17:LH:670:LEU:HD12	1.88	0.54
22:LN:122:VAL:HB	56:ND:192:PRO:HG3	1.90	0.54
22:LN:590:LYS:NZ	22:LN:619:THR:O	2.41	0.54
25:LQ:109:MET:N	25:LQ:109:MET:SD	2.80	0.54
30:LW:451:SER:OG	30:LW:452:VAL:N	2.41	0.54
39:SJ:35:ASP:OD1	39:SJ:35:ASP:N	2.41	0.54
66:6:336:ASP:OD1	66:6:336:ASP:N	2.40	0.54
7:L4:221:ARG:NH1	53:8:111:U:OP1	2.41	0.54
8:L5:51:VAL:HG11	8:L5:130:ILE:HG12	1.90	0.54
9:L7:138:LYS:NZ	9:L7:139:ARG:O	2.41	0.54
13:LD:80:MET:HE2	13:LD:81:HIS:H	1.73	0.54
17:LH:404:SER:OG	17:LH:405:ALA:N	2.40	0.54
21:LM:124:ARG:NH1	21:LM:124:ARG:O	2.41	0.54
28:LU:340:ARG:NH1	28:LU:341:GLU:OE1	2.41	0.54
29:LV:67:ASP:OD1	29:LV:67:ASP:N	2.40	0.54
34:SD:122:ARG:NH1	34:SD:140:GLU:OE2	2.41	0.54
39:SJ:183:ASP:N	39:SJ:183:ASP:OD1	2.41	0.54
7:L4:57:ASN:ND2	53:8:446:A:OP1	2.41	0.53
26:LS:148:THR:OG1	26:LS:163:ARG:NH2	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:LT:342:TYR:HH	27:LT:345:SER:HG	1.56	0.53
36:SG:305:ARG:HG2	36:SG:317:ILE:HG23	1.90	0.53
37:SH:155:LYS:NZ	37:SH:163:GLY:O	2.40	0.53
42:SN:181:ARG:NH1	60:SV:203:SER:O	2.41	0.53
62:LX:131:THR:HG22	62:LX:134:LEU:H	1.73	0.53
1:NA:530:ARG:HH12	53:8:1642:G:H5"	1.73	0.53
7:L4:182:TYR:N	7:L4:226:PHE:O	2.40	0.53
17:LH:708:ASP:OD1	17:LH:708:ASP:N	2.41	0.53
22:LN:345:ASP:HB2	22:LN:361:LEU:HB2	1.89	0.53
27:LT:392:ARG:HE	27:LT:449:ARG:HH22	1.55	0.53
53:8:627:C:N4	53:8:970:A:OP2	2.41	0.53
54:SU:407:ARG:NH2	54:SU:490:LYS:O	2.41	0.53
15:LF:10:ARG:HH22	15:LF:26:ASP:HB2	1.73	0.53
20:LL:112:LEU:HD11	20:LL:131:LEU:HD11	1.89	0.53
23:LO:828:ILE:HG21	27:LT:930:MET:HB2	1.89	0.53
26:LS:436:ASP:OD1	26:LS:436:ASP:N	2.40	0.53
30:LW:258:LEU:HB2	30:LW:268:VAL:HG22	1.90	0.53
35:SF:58:CYS:HA	35:SF:84:ARG:HD3	1.91	0.53
38:SI:828:ARG:NH1	45:SR:94:ASN:OD1	2.41	0.53
41:SM:220:ARG:NH1	41:SM:235:GLN:OE1	2.42	0.53
54:SU:466:LEU:HA	54:SU:469:LEU:HD12	1.90	0.53
55:LI:567:LEU:HD21	55:LI:595:ILE:HD11	1.90	0.53
62:LX:736:PHE:O	62:LX:740:ASN:ND2	2.42	0.53
4:L0:334:G:OP1	31:LZ:56:ARG:NH2	2.41	0.53
8:L5:57:SER:OG	8:L5:167:ARG:NH1	2.39	0.53
14:LE:87:GLU:OE1	14:LE:117:ARG:NH2	2.37	0.53
18:LJ:134:THR:OG1	18:LJ:135:GLN:OE1	2.25	0.53
23:LO:36:ARG:NH2	23:LO:53:GLU:OE1	2.39	0.53
23:LO:597:ASN:HA	23:LO:680:ARG:HB2	1.90	0.53
26:LS:465:THR:HG23	26:LS:468:CYS:H	1.72	0.53
37:SH:340:LYS:HG3	37:SH:351:ILE:HB	1.90	0.53
45:SR:97:ASP:N	45:SR:97:ASP:OD1	2.40	0.53
6:L3:110:ARG:HH22	6:L3:113:LEU:HD12	1.73	0.53
7:L4:87:MET:O	7:L4:122:LYS:NZ	2.42	0.53
23:LO:567:ASP:OD1	23:LO:576:ARG:NH2	2.40	0.53
23:LO:598:ASN:ND2	23:LO:600:SER:OG	2.41	0.53
27:LT:346:ARG:NH1	27:LT:384:ALA:O	2.42	0.53
38:SI:67:PRO:O	38:SI:114:ARG:NH2	2.41	0.53
62:LX:635:ILE:HB	62:LX:725:VAL:HG12	1.90	0.53
63:L6:98:ARG:NH2	63:L6:105:ASP:OD2	2.34	0.53
1:NA:311:ILE:HB	38:SI:1032:LEU:HD13	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L0:313:A:N6	30:LW:79:GLU:OE1	2.40	0.53
12:LC:42:GLU:OE2	12:LC:45:ARG:NH1	2.41	0.53
17:LH:461:ASP:OD1	17:LH:461:ASP:N	2.41	0.53
23:LO:834:GLU:HA	23:LO:837:ASN:HB2	1.89	0.53
29:LV:109:ASP:OD1	29:LV:109:ASP:N	2.41	0.53
29:LV:189:ASN:HB3	29:LV:194:LEU:H	1.73	0.53
29:LV:205:GLU:OE1	29:LV:207:TRP:NE1	2.41	0.53
34:SD:166:PRO:HA	34:SD:188:VAL:HA	1.91	0.53
35:SF:6:PRO:HB3	36:SG:465:GLN:HE21	1.72	0.53
38:SI:870:ARG:NH2	53:8:573:C:O2'	2.41	0.53
42:SN:58:PRO:HA	42:SN:186:ASN:HD22	1.74	0.53
47:ST:314:UNK:O	47:ST:559:ARG:NH2	2.42	0.53
54:SU:245:GLN:HB3	54:SU:248:GLU:HG2	1.90	0.53
28:LU:183:GLN:N	28:LU:197:GLY:O	2.38	0.53
36:SG:484:SER:OG	36:SG:485:ASN:N	2.42	0.53
38:SI:124:ASP:OD1	38:SI:124:ASP:N	2.35	0.53
39:SJ:63:ASP:N	39:SJ:63:ASP:OD1	2.40	0.53
41:SM:281:ILE:HD11	53:8:564:G:H4'	1.90	0.53
53:8:378:A:O2'	66:6:306:ARG:NH2	2.42	0.53
53:8:1052:U:H3	53:8:1066:C:H42	1.55	0.53
57:LR:325:ASP:OD1	57:LR:325:ASP:N	2.41	0.53
17:LH:297:ILE:O	17:LH:485:ARG:NH2	2.42	0.53
23:LO:828:ILE:HA	23:LO:832:ALA:HB3	1.91	0.53
27:LT:230:VAL:HB	27:LT:244:ILE:HB	1.91	0.53
28:LU:357:SER:OG	28:LU:358:MET:N	2.42	0.53
31:LZ:137:ARG:HA	31:LZ:142:LEU:HA	1.91	0.53
37:SH:29:LYS:NZ	37:SH:332:ILE:O	2.42	0.53
42:SN:33:ASP:OD1	42:SN:33:ASP:N	2.42	0.53
53:8:110:U:H4'	66:6:227:ARG:HH21	1.74	0.53
53:8:364:G:H1	53:8:380:U:H3	1.57	0.53
53:8:964:U:O2'	64:NF:125:LEU:O	2.27	0.53
20:LL:448:ASN:OD1	20:LL:483:ARG:NH1	2.42	0.53
22:LN:589:ASN:OD1	22:LN:632:ASN:ND2	2.42	0.53
24:LP:12:ILE:HG21	30:LW:62:ALA:HB1	1.90	0.53
53:8:956:C:H2'	53:8:957:G:C8	2.44	0.53
55:LI:261:GLU:HA	55:LI:271:SER:HA	1.90	0.53
62:LX:879:SER:OG	62:LX:880:VAL:N	2.42	0.53
3:NB:433:ARG:O	39:SJ:211:ARG:NH1	2.42	0.53
14:LE:92:ASN:O	40:SL:79:LYS:NZ	2.42	0.53
23:LO:156:GLN:NE2	23:LO:200:SER:O	2.42	0.53
30:LW:266:PRO:O	46:SS:832:ASN:ND2	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:LZ:145:ASP:OD1	31:LZ:145:ASP:N	2.38	0.53
39:SK:165:ASN:ND2	53:8:1576:A:OP1	2.42	0.53
47:ST:434:ILE:HD11	47:ST:500:PHE:HB2	1.91	0.53
54:SU:281:LEU:HA	54:SU:285:ILE:HB	1.91	0.53
55:LI:558:CYS:O	55:LI:585:ARG:NH2	2.41	0.53
57:LR:631:MET:HB2	57:LR:645:LYS:HG3	1.91	0.53
62:LX:44:MET:H	62:LX:44:MET:HE3	1.73	0.53
11:L9:59:LEU:HD21	11:L9:73:GLY:HA2	1.90	0.52
17:LH:16:SER:HB3	17:LH:783:LEU:HB2	1.91	0.52
17:LH:55:TYR:HB3	17:LH:383:LEU:HD11	1.90	0.52
20:LL:56:SER:O	20:LL:59:LYS:NZ	2.41	0.52
22:LN:66:ARG:NH1	22:LN:80:ASN:OD1	2.42	0.52
25:LQ:480:ASP:HB3	25:LQ:539:VAL:HG23	1.91	0.52
28:LU:330:ARG:NH1	28:LU:339:SER:OG	2.39	0.52
29:LV:46:ARG:NH1	29:LV:46:ARG:O	2.42	0.52
30:LW:144:LEU:HD21	30:LW:147:GLU:HB2	1.91	0.52
40:SL:157:ASP:OD2	40:SL:157:ASP:N	2.40	0.52
53:8:1083:G:N2	53:8:1095:U:OP2	2.41	0.52
53:8:1484:G:N2	53:8:1606:C:O2	2.42	0.52
62:LX:166:MET:N	62:LX:166:MET:SD	2.82	0.52
66:6:77:MET:HG2	66:6:95:ALA:HB2	1.90	0.52
6:L3:104:ASN:OD1	6:L3:104:ASN:N	2.40	0.52
11:L9:57:ARG:HH12	40:SL:88:ASP:HA	1.75	0.52
23:LO:491:ALA:HB2	23:LO:521:LEU:HB2	1.92	0.52
25:LQ:100:ASP:OD2	25:LQ:100:ASP:N	2.37	0.52
25:LQ:165:SER:OG	25:LQ:166:ILE:N	2.42	0.52
28:LU:26:ARG:HH21	46:SS:868:GLU:HA	1.74	0.52
35:SE:29:ASN:ND2	48:SY:244:TRP:O	2.42	0.52
37:SH:37:ARG:NH2	37:SH:49:GLU:OE2	2.37	0.52
53:8:364:G:N2	53:8:380:U:O2	2.40	0.52
53:8:1044:U:H3	53:8:1074:G:H1	1.57	0.52
6:L3:20:THR:HG21	6:L3:35:ILE:HG23	1.91	0.52
8:L5:63:GLN:HE22	8:L5:66:GLN:HE21	1.58	0.52
18:LJ:415:LEU:HD11	18:LJ:458:ILE:HD13	1.91	0.52
22:LN:585:ILE:HG12	22:LN:633:CYS:HB3	1.92	0.52
25:LQ:595:LYS:HA	25:LQ:618:ILE:HG13	1.90	0.52
28:LU:146:LYS:HG2	28:LU:175:THR:HG22	1.91	0.52
30:LW:116:ILE:O	30:LW:380:ASN:ND2	2.42	0.52
38:SI:287:ARG:HH21	38:SI:297:SER:HB2	1.73	0.52
42:SN:177:ARG:NH2	60:SV:201:ASP:O	2.39	0.52
53:8:23:G:H1	53:8:602:U:H2'	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L4:183:VAL:HG21	7:L4:220:THR:HG21	1.92	0.52
13:LD:91:LEU:HB3	13:LD:100:TYR:HB3	1.91	0.52
24:LP:120:ARG:HH21	24:LP:123:GLN:HB3	1.75	0.52
25:LQ:172:GLN:HE22	25:LQ:178:ILE:HG13	1.74	0.52
25:LQ:807:ASP:HA	25:LQ:810:LEU:HD13	1.91	0.52
36:SG:335:ARG:HD3	36:SG:348:LEU:HD21	1.91	0.52
42:SN:156:MET:HE3	42:SN:176:VAL:HG11	1.92	0.52
53:8:183:U:O2	53:8:203:U:N3	2.41	0.52
53:8:884:A:H61	53:8:927:C:H42	1.58	0.52
53:8:929:A:OP2	53:8:931:C:N4	2.42	0.52
54:SU:317:ILE:HD11	54:SU:349:LEU:HD22	1.90	0.52
1:NA:496:TYR:O	57:LR:788:TYR:OH	2.28	0.52
18:LJ:229:CYS:HB2	18:LJ:258:LEU:HD13	1.92	0.52
23:LO:29:LEU:HD21	23:LO:327:LEU:HD21	1.92	0.52
23:LO:453:PHE:HB3	23:LO:475:PRO:HA	1.92	0.52
34:SD:281:ASP:HB2	34:SD:284:THR:HG23	1.92	0.52
36:SG:286:LEU:HD23	36:SG:295:LEU:HD11	1.91	0.52
45:SR:103:LEU:HB2	45:SR:126:LYS:HB2	1.92	0.52
53:8:593:U:H5''	53:8:594:A:H5'	1.90	0.52
53:8:1274:C:H2'	53:8:1275:A:H8	1.75	0.52
57:LR:568:MET:N	57:LR:568:MET:SD	2.82	0.52
65:5:345:ARG:NH2	65:5:411:GLU:OE1	2.41	0.52
3:NB:580:ARG:NH1	40:SL:51:LEU:O	2.42	0.52
3:NB:588:SER:O	35:SF:46:ARG:NH1	2.42	0.52
9:L7:118:LEU:O	9:L7:122:HIS:ND1	2.42	0.52
11:L9:19:TYR:OH	53:8:20:G:N1	2.42	0.52
12:LC:16:ALA:HB2	12:LC:72:GLY:HA3	1.91	0.52
18:LJ:356:ASN:OD1	18:LJ:359:ARG:NH2	2.43	0.52
20:LL:155:PRO:HD3	20:LL:196:VAL:HG11	1.92	0.52
26:LS:137:ILE:HD12	26:LS:155:ILE:HD12	1.92	0.52
35:SF:25:GLN:NE2	36:SG:323:ASP:OD1	2.40	0.52
37:SH:207:ARG:HE	37:SH:268:PRO:HG2	1.73	0.52
38:SI:956:MET:HE2	47:ST:755:ILE:HD12	1.90	0.52
41:SM:49:ASP:OD1	41:SM:49:ASP:N	2.42	0.52
45:SR:49:ALA:HB3	45:SR:104:LEU:HB2	1.90	0.52
4:L0:491:U:H4'	24:LP:83:LEU:HD13	1.92	0.52
8:L5:156:ARG:NH1	8:L5:157:ARG:O	2.43	0.52
11:L9:100:LYS:NZ	40:SL:59:ILE:O	2.43	0.52
26:LS:204:ASP:OD1	26:LS:204:ASP:N	2.41	0.52
27:LT:274:ILE:HG12	27:LT:286:VAL:HG12	1.92	0.52
28:LU:145:VAL:HB	28:LU:176:PHE:HB2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LU:254:PRO:HG2	46:SS:284:ARG:HE	1.74	0.52
38:SI:160:GLN:NE2	38:SI:197:GLU:O	2.42	0.52
39:SJ:102:SER:HA	39:SK:236:VAL:HG21	1.91	0.52
39:SJ:188:ARG:HG2	39:SJ:191:ASP:H	1.75	0.52
62:LX:91:MET:SD	62:LX:91:MET:N	2.83	0.52
1:NA:496:TYR:OH	1:NA:508:ARG:NH2	2.41	0.52
4:L0:68:U:OP2	17:LH:426:ARG:NH1	2.42	0.52
22:LN:520:LYS:O	22:LN:524:LYS:NZ	2.43	0.52
23:LO:303:ASN:HD21	23:LO:324:LEU:HD12	1.75	0.52
23:LO:471:GLY:O	23:LO:498:ARG:NH2	2.39	0.52
25:LQ:479:LEU:HD22	25:LQ:490:THR:HG22	1.92	0.52
29:LV:116:HIS:HB2	29:LV:124:GLN:HB2	1.92	0.52
36:SG:242:VAL:HG23	36:SG:253:THR:HG22	1.92	0.52
47:ST:573:LEU:HB3	47:ST:593:LEU:HD11	1.91	0.52
47:ST:612:THR:OG1	47:ST:613:ILE:N	2.40	0.52
53:8:505:A:H61	53:8:585:A:H2'	1.75	0.52
53:8:992:A:OP2	53:8:993:A:N6	2.37	0.52
53:8:1170:G:N2	53:8:1571:C:O3'	2.42	0.52
62:LX:193:GLY:HA2	62:LX:212:GLY:H	1.75	0.52
2:SA:210:VAL:HG11	2:SA:219:LEU:HD12	1.92	0.52
26:LS:464:THR:HG21	26:LS:476:ILE:HA	1.92	0.52
27:LT:93:ALA:HB2	27:LT:121:LEU:HD22	1.91	0.52
27:LT:430:ILE:HB	27:LT:443:TRP:HB2	1.91	0.52
30:LW:135:ALA:HB1	30:LW:144:LEU:HD11	1.91	0.52
30:LW:244:ASN:HB3	30:LW:246:VAL:HG22	1.91	0.52
36:SG:241:THR:HG21	36:SG:285:SER:HA	1.91	0.52
39:SK:96:LEU:HD11	39:SK:114:ILE:HD11	1.91	0.52
65:5:412:ASP:N	65:5:412:ASP:OD1	2.42	0.52
66:6:268:ASN:HD21	66:6:271:ARG:HB2	1.75	0.52
3:NB:562:ARG:NH1	53:8:476:U:OP2	2.42	0.52
4:L0:323:A:OP1	23:LO:191:ARG:NH1	2.43	0.52
22:LN:589:ASN:ND2	22:LN:629:LEU:O	2.42	0.52
26:LS:161:ILE:HD13	27:LT:177:LEU:HB2	1.92	0.52
27:LT:460:ASP:O	27:LT:481:ASN:ND2	2.43	0.52
38:SI:923:ASP:N	38:SI:923:ASP:OD1	2.43	0.52
47:ST:510:THR:HA	47:ST:518:ILE:HD13	1.91	0.52
47:ST:515:HIS:O	47:ST:519:THR:OG1	2.28	0.52
47:ST:678:PHE:HB3	47:ST:681:PRO:HD2	1.91	0.52
57:LR:699:LYS:HD3	57:LR:755:ILE:HD11	1.92	0.52
62:LX:326:PHE:HA	62:LX:360:LYS:HA	1.92	0.52
2:SA:21:LYS:NZ	2:SA:45:THR:O	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L2:314:C:H2'	5:L2:315:A:H8	1.75	0.51
21:LM:262:VAL:HG13	21:LM:301:LYS:HG2	1.93	0.51
36:SG:203:ASP:O	36:SG:538:ARG:NH2	2.43	0.51
36:SG:308:SER:HB3	36:SG:315:LEU:HD21	1.92	0.51
38:SI:366:MET:SD	38:SI:366:MET:N	2.83	0.51
40:SL:138:ASP:HB3	40:SL:160:LEU:HD13	1.92	0.51
42:SN:76:THR:OG1	42:SN:77:LYS:N	2.43	0.51
53:8:538:A:N3	53:8:540:G:N2	2.59	0.51
1:NA:370:ARG:NH2	41:SM:246:GLU:OE1	2.43	0.51
11:L9:36:LEU:HD11	11:L9:105:LEU:HD21	1.92	0.51
15:LF:29:HIS:HB2	15:LF:67:GLY:HA2	1.91	0.51
25:LQ:15:GLY:O	25:LQ:360:ASN:ND2	2.43	0.51
25:LQ:393:ASP:OD1	25:LQ:393:ASP:N	2.44	0.51
41:SM:36:LEU:O	58:NE:214:ARG:NH2	2.43	0.51
53:8:598:U:H2'	53:8:599:A:H8	1.74	0.51
62:LX:9:ARG:HH22	62:LX:214:LYS:HA	1.75	0.51
6:L3:57:ARG:NH1	18:LJ:61:THR:OG1	2.41	0.51
7:L4:181:VAL:HA	7:L4:227:VAL:HA	1.93	0.51
23:LO:27:LYS:HD3	23:LO:43:ILE:HG13	1.91	0.51
23:LO:269:HIS:NE2	23:LO:312:GLN:O	2.43	0.51
23:LO:434:ASN:HD21	23:LO:450:LEU:HD23	1.74	0.51
28:LU:292:ARG:NH1	46:SS:296:SER:OG	2.44	0.51
31:LZ:66:PRO:HA	31:LZ:71:ARG:HH11	1.76	0.51
34:SC:310:GLU:OE1	34:SC:313:HIS:ND1	2.44	0.51
35:SE:33:LEU:HD11	35:SE:100:ALA:HB1	1.91	0.51
38:SI:1156:LYS:HD2	53:8:18:C:H5'	1.92	0.51
39:SK:90:ASP:OD1	39:SK:90:ASP:N	2.43	0.51
41:SM:19:GLU:HA	41:SM:22:ASP:HB2	1.91	0.51
47:ST:616:LEU:HD13	47:ST:619:LEU:HD12	1.93	0.51
51:NH:862:LEU:HA	51:NH:866:ALA:HB3	1.93	0.51
53:8:887:A:C2	53:8:925:G:N1	2.79	0.51
59:SB:404:ARG:NH1	59:SB:405:ASP:O	2.43	0.51
62:LX:802:LEU:HD23	62:LX:805:ILE:HD11	1.92	0.51
65:5:450:LEU:O	65:5:453:ASN:N	2.41	0.51
13:LD:6:THR:OG1	13:LD:7:VAL:N	2.42	0.51
18:LJ:212:ASP:OD1	18:LJ:212:ASP:N	2.43	0.51
20:LL:440:ILE:HG12	20:LL:452:LEU:HD21	1.93	0.51
25:LQ:635:LYS:HA	25:LQ:659:GLU:HG2	1.92	0.51
27:LT:730:LYS:NZ	27:LT:838:ILE:O	2.41	0.51
28:LU:140:SER:OG	28:LU:141:ASP:N	2.43	0.51
42:SN:242:ILE:HG13	42:SN:254:ILE:HG13	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:ST:102:ARG:O	47:ST:106:LYS:NZ	2.41	0.51
53:8:1208:A:N6	53:8:1454:G:N1	2.58	0.51
53:8:1220:C:H42	53:8:1263:G:H1	1.58	0.51
57:LR:34:THR:HG23	57:LR:41:ASN:HB2	1.91	0.51
57:LR:42:ILE:HG21	57:LR:90:LEU:HD11	1.91	0.51
62:LX:62:LYS:O	62:LX:125:GLN:NE2	2.43	0.51
5:L2:326:U:OP1	35:SE:46:ARG:NH2	2.37	0.51
9:L7:51:VAL:HG23	9:L7:53:GLY:H	1.76	0.51
17:LH:709:ARG:HB2	17:LH:765:TRP:HD1	1.76	0.51
18:LJ:266:SER:OG	18:LJ:268:MET:O	2.28	0.51
22:LN:232:ASP:OD1	22:LN:232:ASP:N	2.44	0.51
22:LN:345:ASP:OD1	22:LN:345:ASP:N	2.42	0.51
22:LN:597:ASN:N	22:LN:597:ASN:OD1	2.43	0.51
23:LO:300:MET:SD	23:LO:326:GLN:NE2	2.83	0.51
25:LQ:337:LYS:HB3	25:LQ:358:SER:HB3	1.91	0.51
26:LS:133:ILE:HD12	27:LT:194:ARG:HH12	1.75	0.51
26:LS:511:LEU:HD13	26:LS:544:VAL:HG11	1.92	0.51
27:LT:125:GLY:HA2	59:SB:430:ASP:HA	1.92	0.51
28:LU:448:ARG:HG2	28:LU:451:MET:HE3	1.92	0.51
34:SC:284:THR:HG22	40:SL:64:GLN:HE22	1.75	0.51
40:SL:18:ASN:HB3	40:SL:21:LYS:HB3	1.92	0.51
57:LR:498:SER:OG	57:LR:539:VAL:O	2.29	0.51
3:NB:438:ASP:OD1	3:NB:438:ASP:N	2.42	0.51
4:L0:163:G:H4'	26:LS:354:SER:HB2	1.92	0.51
6:L3:56:LYS:HE2	6:L3:61:LEU:HG	1.93	0.51
20:LL:443:GLN:NE2	54:SU:333:GLU:O	2.43	0.51
23:LO:849:LEU:HD22	27:LT:897:HIS:HB2	1.93	0.51
25:LQ:922:ASP:OD1	25:LQ:922:ASP:N	2.40	0.51
26:LS:412:GLN:OE1	26:LS:420:ARG:NH2	2.44	0.51
26:LS:473:ILE:HA	26:LS:476:ILE:HD12	1.92	0.51
27:LT:627:ASN:ND2	27:LT:647:THR:OG1	2.37	0.51
28:LU:67:ARG:HH21	40:SL:122:ASP:HA	1.75	0.51
29:LV:59:SER:HG	29:LV:74:THR:HG1	1.57	0.51
38:SI:1089:GLN:HB3	48:SY:82:ARG:HH21	1.75	0.51
38:SI:1150:SER:OG	38:SI:1154:LYS:NZ	2.44	0.51
47:ST:605:ASP:OD1	47:ST:605:ASP:N	2.44	0.51
50:NJ:1574:ALA:HA	50:NJ:1578:GLY:HA3	1.93	0.51
57:LR:563:ASP:OD1	57:LR:563:ASP:N	2.42	0.51
62:LX:753:ASP:OD1	62:LX:753:ASP:N	2.43	0.51
66:6:353:ALA:O	66:6:356:ARG:NH1	2.43	0.51
4:L0:161:A:C4	18:LJ:361:MET:HE1	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L0:183:A:N6	4:L0:213:G:O6	2.44	0.51
35:SE:42:LYS:HD2	35:SE:46:ARG:HH12	1.74	0.51
36:SG:185:LEU:HD21	36:SG:527:VAL:HG11	1.92	0.51
38:SI:288:VAL:HG23	38:SI:814:GLY:HA2	1.91	0.51
38:SI:767:ILE:O	38:SI:770:GLN:NE2	2.42	0.51
38:SI:968:THR:HG22	38:SI:1001:VAL:HG12	1.92	0.51
38:SI:974:GLY:HA3	38:SI:991:PHE:HD1	1.75	0.51
52:NI:15:VAL:HA	52:NI:38:PHE:HA	1.92	0.51
57:LR:505:ILE:HB	57:LR:517:ILE:HD11	1.92	0.51
1:NA:341:LEU:O	6:L3:120:ARG:NH2	2.44	0.51
2:SA:172:ASN:HA	2:SA:175:ILE:HD12	1.92	0.51
4:L0:467:A:H61	5:L2:49:C:H42	1.59	0.51
26:LS:493:LEU:HD21	26:LS:530:LEU:HD22	1.92	0.51
29:LV:57:GLU:O	29:LV:76:THR:OG1	2.29	0.51
31:LZ:120:MET:HA	48:SY:62:GLU:HA	1.92	0.51
34:SC:89:GLU:OE1	44:SQ:141:TRP:NE1	2.41	0.51
34:SD:110:ASN:ND2	34:SD:141:TYR:O	2.44	0.51
37:SH:119:LYS:HB3	37:SH:165:GLU:HB3	1.92	0.51
37:SH:201:SER:HB3	37:SH:204:LEU:HD13	1.93	0.51
37:SH:361:ASN:HD22	37:SH:364:LYS:HD2	1.76	0.51
2:SA:86:LEU:HD13	2:SA:116:VAL:HG21	1.93	0.51
4:L0:248:G:OP2	48:SY:82:ARG:NH2	2.44	0.51
23:LO:450:LEU:HA	23:LO:475:PRO:HB3	1.92	0.51
23:LO:525:PRO:HG2	23:LO:587:PHE:HA	1.92	0.51
25:LQ:488:LEU:HB3	25:LQ:500:TRP:HB2	1.91	0.51
28:LU:367:SER:HB3	28:LU:373:ARG:HH12	1.75	0.51
34:SD:301:LEU:HD23	34:SD:302:GLU:HB2	1.93	0.51
36:SG:525:GLN:HB2	36:SG:540:LEU:HB2	1.93	0.51
36:SG:546:GLU:OE2	36:SG:551:ARG:NH1	2.44	0.51
38:SI:846:VAL:HG22	38:SI:855:GLN:HB3	1.93	0.51
54:SU:167:LYS:O	54:SU:272:GLN:NE2	2.43	0.51
9:L7:50:ASP:HA	9:L7:56:LYS:HG3	1.92	0.51
10:L8:9:HIS:NE2	53:8:321:C:N3	2.50	0.51
11:L9:87:SER:HB3	11:L9:90:LYS:HG3	1.92	0.51
13:LD:64:VAL:HG12	13:LD:129:ARG:HH11	1.76	0.51
22:LN:370:ARG:NH2	22:LN:630:LYS:O	2.44	0.51
27:LT:307:GLN:NE2	59:SB:422:THR:O	2.39	0.51
27:LT:590:ALA:HB3	27:LT:631:ASN:HA	1.92	0.51
28:LU:403:ARG:NH2	46:SS:860:SER:O	2.44	0.51
29:LV:300:TRP:HA	29:LV:308:TYR:H	1.76	0.51
30:LW:113:PRO:HA	30:LW:395:GLN:HA	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:SD:257:SER:HA	34:SD:261:LEU:HD23	1.92	0.51
39:SJ:167:ILE:HG13	39:SJ:171:LEU:HG	1.92	0.51
39:SK:151:ARG:HB2	47:ST:716:LYS:HE3	1.93	0.51
53:8:883:C:O2	53:8:946:U:N3	2.44	0.51
57:LR:580:ARG:HG2	57:LR:623:LEU:HB3	1.93	0.51
5:L2:59:G:H5'	23:LO:570:THR:HG23	1.93	0.50
7:L4:140:VAL:HG12	7:L4:146:THR:HG22	1.92	0.50
11:L9:110:GLN:OE1	11:L9:126:ARG:NH1	2.41	0.50
11:L9:155:HIS:NE2	36:SG:321:HIS:O	2.45	0.50
11:L9:157:ASP:OD2	11:L9:158:PHE:N	2.44	0.50
13:LD:11:ARG:NH2	53:8:342:C:O2'	2.43	0.50
17:LH:490:LEU:HD11	18:LJ:426:LYS:HD2	1.93	0.50
23:LO:660:SER:HA	23:LO:672:THR:HA	1.93	0.50
24:LP:297:ASP:OD1	24:LP:297:ASP:N	2.43	0.50
36:SG:262:VAL:HG13	36:SG:271:VAL:HG23	1.91	0.50
38:SI:125:LEU:HD21	38:SI:899:VAL:HG21	1.93	0.50
38:SI:826:LYS:NZ	38:SI:923:ASP:OD2	2.44	0.50
41:SM:187:PRO:HB3	41:SM:220:ARG:HE	1.75	0.50
2:SA:158:TYR:OH	34:SC:222:GLU:OE1	2.28	0.50
17:LH:531:PHE:HD2	17:LH:545:THR:HB	1.76	0.50
20:LL:64:LYS:HB3	20:LL:77:ILE:HD12	1.92	0.50
23:LO:78:ARG:NH1	23:LO:94:ASN:OD1	2.43	0.50
23:LO:354:SER:OG	23:LO:356:ASP:OD1	2.27	0.50
25:LQ:137:ILE:HG12	25:LQ:147:VAL:HG13	1.92	0.50
25:LQ:336:TYR:HB2	25:LQ:357:THR:HB	1.93	0.50
25:LQ:350:LYS:HD2	25:LQ:366:SER:HB3	1.91	0.50
38:SI:248:ARG:HG2	38:SI:272:TYR:HB2	1.93	0.50
57:LR:26:SER:OG	57:LR:28:ASN:OD1	2.30	0.50
9:L7:143:LEU:O	14:LE:42:GLN:NE2	2.45	0.50
14:LE:54:ASP:OD1	14:LE:54:ASP:N	2.45	0.50
18:LJ:40:ASN:HB2	18:LJ:60:SER:HB3	1.94	0.50
20:LL:231:ASP:N	20:LL:231:ASP:OD1	2.43	0.50
23:LO:30:LEU:HD11	23:LO:63:LEU:HD22	1.93	0.50
26:LS:257:HIS:HB2	26:LS:262:LEU:HB2	1.94	0.50
57:LR:18:GLY:HA2	57:LR:37:LEU:HG	1.92	0.50
62:LX:877:LEU:HD21	62:LX:919:LYS:HD3	1.93	0.50
10:L8:108:PRO:HA	10:L8:111:GLN:HB2	1.93	0.50
17:LH:136:LEU:HD13	17:LH:187:VAL:HB	1.93	0.50
17:LH:215:VAL:HG21	17:LH:224:SER:HB3	1.92	0.50
18:LJ:217:ASN:HB3	18:LJ:229:CYS:HB3	1.93	0.50
22:LN:417:VAL:HG11	22:LN:460:LEU:HD13	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:LQ:426:ARG:NH2	25:LQ:459:LEU:O	2.44	0.50
27:LT:738:ASP:OD1	27:LT:738:ASP:N	2.44	0.50
27:LT:851:SER:OG	43:SO:241:ARG:NH2	2.43	0.50
29:LV:184:ASN:ND2	29:LV:198:GLY:O	2.43	0.50
53:8:1491:U:H4'	53:8:1492:A:H5'	1.93	0.50
57:LR:96:VAL:HG12	57:LR:97:ARG:HD2	1.92	0.50
62:LX:215:ASN:N	62:LX:215:ASN:OD1	2.42	0.50
2:SA:330:ALA:HB1	2:SA:381:ASN:HA	1.94	0.50
19:LK:453:PRO:HB3	55:LI:675:LEU:HD11	1.94	0.50
28:LU:8:ARG:HH22	30:LW:409:ALA:HA	1.76	0.50
37:SH:283:ILE:O	38:SI:634:ARG:NH1	2.45	0.50
38:SI:285:GLY:H	38:SI:298:VAL:HG23	1.75	0.50
40:SL:165:ARG:NH1	53:8:19:A:N1	2.60	0.50
53:8:992:A:H3'	53:8:993:A:C8	2.47	0.50
57:LR:44:ASP:N	57:LR:44:ASP:OD1	2.39	0.50
59:SB:299:LEU:HD22	59:SB:320:LEU:HD23	1.94	0.50
4:L0:316:U:OP1	30:LW:364:ARG:NH2	2.44	0.50
5:L2:306:G:H2'	5:L2:307:G:C8	2.47	0.50
9:L7:139:ARG:NH2	14:LE:52:TYR:O	2.44	0.50
10:L8:77:ARG:NH1	10:L8:78:ILE:O	2.44	0.50
22:LN:466:ASP:OD1	22:LN:466:ASP:N	2.42	0.50
25:LQ:65:ASP:HB2	25:LQ:67:LEU:HD22	1.94	0.50
34:SD:199:PHE:HE2	34:SD:223:ASP:HB2	1.75	0.50
56:ND:185:GLN:NE2	56:ND:186:ASP:OD2	2.45	0.50
57:LR:446:VAL:HG13	57:LR:448:LYS:H	1.76	0.50
1:NA:453:SER:O	1:NA:455:HIS:N	2.45	0.50
10:L8:193:LEU:HA	10:L8:196:LEU:HB2	1.93	0.50
25:LQ:7:ARG:NH2	25:LQ:70:GLY:O	2.45	0.50
25:LQ:655:ALA:HB2	25:LQ:684:TRP:HZ2	1.75	0.50
25:LQ:760:ILE:HD11	25:LQ:835:PHE:HB2	1.94	0.50
29:LV:89:LEU:HD12	63:L6:73:ILE:HG12	1.93	0.50
38:SI:287:ARG:HD2	38:SI:820:ILE:HD13	1.92	0.50
42:SN:39:ILE:HG12	42:SN:243:PHE:HB2	1.93	0.50
66:6:71:TYR:HD1	66:6:75:LEU:HD11	1.76	0.50
7:L4:16:HIS:HE2	66:6:230:ALA:HA	1.77	0.50
20:LL:438:THR:HG21	20:LL:471:ARG:HB3	1.93	0.50
22:LN:226:LEU:O	22:LN:227:HIS:ND1	2.45	0.50
23:LO:853:ASP:N	23:LO:853:ASP:OD1	2.44	0.50
24:LP:166:ASN:HD22	46:SS:328:THR:HA	1.77	0.50
25:LQ:102:VAL:HG12	25:LQ:118:ASN:HB3	1.94	0.50
25:LQ:547:ALA:HA	25:LQ:557:VAL:HA	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:LT:573:VAL:HG13	27:LT:574:THR:HG23	1.93	0.50
37:SH:184:ASP:N	37:SH:184:ASP:OD1	2.45	0.50
39:SJ:129:ARG:O	53:8:1194:A:N6	2.41	0.50
62:LX:920:MET:HA	62:LX:923:TYR:HB3	1.93	0.50
1:NA:479:ALA:O	23:LO:341:GLN:NE2	2.44	0.50
5:L2:253:G:OP2	35:SF:95:ARG:NH1	2.45	0.50
8:L5:189:THR:OG1	8:L5:192:GLU:OE1	2.30	0.50
13:LD:14:GLN:OE1	13:LD:14:GLN:N	2.45	0.50
20:LL:439:VAL:HG11	54:SU:300:THR:HG21	1.92	0.50
25:LQ:880:ILE:HA	25:LQ:883:VAL:HG12	1.93	0.50
25:LQ:917:ASN:ND2	25:LQ:919:GLU:OE2	2.44	0.50
28:LU:200:LYS:HE3	28:LU:214:ASP:HB3	1.94	0.50
36:SG:539:ILE:HB	36:SG:566:ALA:HB3	1.94	0.50
37:SH:327:ARG:NH2	38:SI:555:MET:O	2.36	0.50
38:SI:120:CYS:HB2	38:SI:131:ILE:HD13	1.92	0.50
47:ST:798:LYS:O	47:ST:801:ARG:NH2	2.45	0.50
57:LR:571:LEU:HD11	57:LR:590:LEU:HD23	1.94	0.50
57:LR:584:ILE:HG13	57:LR:586:LYS:H	1.77	0.50
62:LX:743:VAL:HG11	62:LX:774:LEU:HG	1.94	0.50
66:6:85:ASP:OD1	66:6:85:ASP:N	2.45	0.50
2:SA:129:ARG:NH1	34:SC:261:LEU:O	2.44	0.49
3:NB:554:ARG:NH2	53:8:547:U:OP2	2.44	0.49
4:L0:485:G:H1	28:LU:386:LYS:H	1.61	0.49
14:LE:76:SER:HB2	58:NE:320:ILE:HG12	1.94	0.49
17:LH:22:LEU:HD21	17:LH:32:LYS:HD3	1.93	0.49
18:LJ:285:ASP:OD1	18:LJ:285:ASP:N	2.42	0.49
22:LN:35:ARG:HA	22:LN:754:ILE:HB	1.94	0.49
22:LN:529:ASN:O	22:LN:545:ARG:NH1	2.39	0.49
28:LU:40:GLU:OE2	46:SS:865:ILE:N	2.43	0.49
28:LU:273:GLU:HA	46:SS:302:VAL:HG21	1.94	0.49
39:SJ:239:SER:HG	39:SK:239:SER:HG	1.59	0.49
41:SM:281:ILE:HB	41:SM:284:ALA:HB2	1.94	0.49
51:NH:443:HIS:HA	51:NH:471:SER:H	1.76	0.49
57:LR:344:ARG:NH2	57:LR:395:ASP:OD1	2.42	0.49
4:L0:499:U:H2'	4:L0:500:G:H8	1.77	0.49
17:LH:214:ASP:N	17:LH:214:ASP:OD1	2.43	0.49
18:LJ:453:VAL:HG11	20:LL:532:ARG:HE	1.76	0.49
21:LM:12:ALA:HB2	30:LW:142:GLY:HA3	1.94	0.49
23:LO:528:LYS:O	23:LO:543:ASN:ND2	2.44	0.49
23:LO:650:ASN:ND2	23:LO:655:ASP:OD2	2.42	0.49
25:LQ:634:SER:OG	25:LQ:635:LYS:N	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:LV:187:SER:HB3	29:LV:196:ALA:HB3	1.93	0.49
29:LV:200:GLU:HA	29:LV:230:GLN:HB3	1.92	0.49
30:LW:177:TYR:HE1	30:LW:183:GLU:HG2	1.77	0.49
34:SD:249:GLN:HB3	34:SD:269:ILE:HD11	1.94	0.49
36:SG:348:LEU:HB3	36:SG:357:LEU:HB2	1.93	0.49
42:SN:126:VAL:HG22	42:SN:154:ILE:HG12	1.95	0.49
42:SN:148:LYS:HG2	42:SN:149:LYS:HD2	1.94	0.49
53:8:223:U:H3	53:8:243:G:H22	1.59	0.49
55:LI:295:TYR:HA	55:LI:302:LEU:HA	1.94	0.49
1:NA:527:ARG:NH1	53:8:1641:C:OP1	2.39	0.49
4:L0:331:U:H2'	30:LW:191:ILE:HD12	1.93	0.49
4:L0:348:U:OP2	4:L0:377:U:N3	2.45	0.49
14:LE:53:ILE:N	14:LE:60:LYS:O	2.43	0.49
17:LH:520:LEU:HD11	20:LL:542:ALA:HB1	1.93	0.49
23:LO:303:ASN:HA	23:LO:323:LYS:HE3	1.93	0.49
24:LP:2:SER:OG	24:LP:3:LYS:N	2.45	0.49
34:SD:100:ARG:NH2	60:SV:129:TRP:O	2.45	0.49
38:SI:279:PRO:HB3	38:SI:784:LYS:HA	1.94	0.49
41:SM:118:ASN:OD1	41:SM:118:ASN:N	2.45	0.49
53:8:140:A:C8	63:L6:184:LEU:N	2.80	0.49
53:8:863:A:H8	53:8:865:A:H4'	1.77	0.49
5:L2:64:A:OP2	27:LT:392:ARG:NH1	2.46	0.49
7:L4:116:ASP:OD1	7:L4:116:ASP:N	2.46	0.49
21:LM:281:THR:HG21	26:LS:208:LEU:HB2	1.93	0.49
22:LN:102:LEU:HD23	22:LN:116:SER:HB2	1.94	0.49
22:LN:383:LEU:HD22	22:LN:394:TRP:HZ3	1.78	0.49
25:LQ:215:ASP:OD1	25:LQ:215:ASP:N	2.38	0.49
26:LS:345:LEU:HD11	26:LS:352:GLN:HE21	1.77	0.49
29:LV:85:ASP:OD1	29:LV:85:ASP:N	2.41	0.49
36:SG:256:ARG:NH1	36:SG:282:GLU:OE1	2.45	0.49
38:SI:1024:LYS:O	38:SI:1026:LYS:NZ	2.45	0.49
41:SM:193:ASN:HB3	41:SM:226:ASN:HB3	1.95	0.49
42:SN:71:ASN:HB2	42:SN:123:ASP:H	1.77	0.49
53:8:965:U:H3'	64:NF:125:LEU:H	1.77	0.49
58:NE:224:HIS:ND1	58:NE:226:ASP:OD1	2.46	0.49
65:5:194:ILE:O	65:5:197:GLN:NE2	2.45	0.49
24:LP:11:CYS:HB2	24:LP:33:MET:HE1	1.93	0.49
24:LP:187:LYS:HE2	44:SQ:63:PRO:HB2	1.95	0.49
25:LQ:807:ASP:N	25:LQ:807:ASP:OD1	2.41	0.49
27:LT:53:CYS:HA	27:LT:58:PHE:HA	1.94	0.49
29:LV:291:THR:HG23	29:LV:300:TRP:HE1	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:SC:109:LYS:NZ	44:SQ:103:TRP:O	2.40	0.49
36:SG:252:VAL:HA	36:SG:262:VAL:HA	1.94	0.49
37:SH:329:ILE:HG23	37:SH:333:PHE:HD2	1.78	0.49
38:SI:867:THR:OG1	38:SI:868:ARG:NH1	2.45	0.49
42:SN:243:PHE:HB3	42:SN:251:SER:HB2	1.93	0.49
53:8:487:G:H2'	53:8:488:G:H8	1.76	0.49
57:LR:537:TRP:HD1	57:LR:553:GLY:HA2	1.76	0.49
61:SP:1120:GLN:O	61:SP:1124:TYR:N	2.45	0.49
5:L2:76:U:OP2	26:LS:513:GLN:NE2	2.45	0.49
18:LJ:431:LEU:HD21	18:LJ:466:VAL:HG22	1.93	0.49
22:LN:302:ARG:NH1	22:LN:330:GLY:O	2.45	0.49
22:LN:574:HIS:HE2	22:LN:638:SER:HG	1.61	0.49
23:LO:252:LYS:NZ	23:LO:253:LYS:O	2.44	0.49
42:SN:60:THR:HG23	42:SN:61:LYS:HG2	1.94	0.49
53:8:479:C:O2	53:8:510:G:N2	2.45	0.49
53:8:1057:U:O2'	53:8:1058:U:O2	2.31	0.49
55:LI:271:SER:O	55:LI:281:PHE:N	2.44	0.49
7:L4:163:ASP:OD2	7:L4:166:SER:OG	2.31	0.49
25:LQ:836:ILE:HA	25:LQ:839:VAL:HG12	1.94	0.49
26:LS:576:LEU:HD13	26:LS:588:LEU:HD21	1.94	0.49
27:LT:49:TYR:OH	27:LT:86:HIS:O	2.30	0.49
36:SG:443:LEU:HD12	36:SG:471:GLN:HB2	1.93	0.49
36:SG:491:SER:OG	36:SG:492:TRP:N	2.46	0.49
37:SH:312:ARG:NH2	37:SH:349:ASP:OD2	2.46	0.49
38:SI:45:ARG:NE	53:8:28:A:OP1	2.44	0.49
45:SR:89:ASN:HD22	48:SY:4:LEU:HB3	1.76	0.49
53:8:1506:G:H2'	53:8:1507:G:H8	1.78	0.49
59:SB:136:LEU:HA	59:SB:139:MET:HE3	1.94	0.49
7:L4:117:GLU:O	7:L4:120:SER:OG	2.31	0.49
13:LD:92:HIS:N	13:LD:101:GLU:O	2.43	0.49
17:LH:524:ASP:OD1	17:LH:524:ASP:N	2.42	0.49
21:LM:130:LYS:HA	21:LM:130:LYS:HD2	1.66	0.49
23:LO:258:ALA:HB1	23:LO:261:ALA:HB3	1.94	0.49
29:LV:3:LEU:HD22	29:LV:15:GLN:H	1.78	0.49
36:SG:285:SER:N	36:SG:298:SER:OG	2.44	0.49
41:SM:183:SER:HB3	41:SM:220:ARG:HD3	1.95	0.49
55:LI:606:ASP:OD1	55:LI:606:ASP:N	2.42	0.49
62:LX:827:ARG:HA	62:LX:830:LEU:HD12	1.94	0.49
3:NB:493:ASP:OD1	3:NB:496:GLN:NE2	2.45	0.49
14:LE:103:ILE:HB	14:LE:110:ILE:HD11	1.93	0.49
18:LJ:411:LYS:NZ	18:LJ:448:LYS:O	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:LL:78:LEU:HB2	20:LL:86:TRP:HB2	1.95	0.49
38:SI:1049:ASN:OD1	38:SI:1049:ASN:N	2.42	0.49
38:SI:1113:ILE:HG13	44:SQ:119:ARG:HD2	1.95	0.49
53:8:901:G:H3'	53:8:902:G:H8	1.77	0.49
54:SU:350:MET:HA	54:SU:355:ARG:HB3	1.95	0.49
1:NA:372:ARG:NH2	1:NA:377:ASN:O	2.41	0.49
1:NA:484:MET:HB3	23:LO:359:ARG:HH12	1.78	0.49
8:L5:97:LEU:HD23	8:L5:176:THR:HG23	1.95	0.49
23:LO:470:SER:OG	41:SM:134:SER:O	2.29	0.49
27:LT:24:PHE:HB3	27:LT:654:TRP:HB3	1.94	0.49
27:LT:569:VAL:HB	27:LT:579:ARG:HB2	1.94	0.49
28:LU:140:SER:OG	28:LU:142:ASP:OD1	2.30	0.49
29:LV:287:ASN:HB3	29:LV:302:ARG:HG2	1.95	0.49
31:LZ:78:LEU:HD22	31:LZ:97:LEU:HD11	1.95	0.49
34:SC:155:ILE:HD11	34:SC:162:LEU:HD13	1.92	0.49
36:SG:256:ARG:NH2	36:SG:549:LEU:O	2.46	0.49
53:8:199:G:O2'	53:8:201:G:N2	2.45	0.49
53:8:1049:U:O4	53:8:1067:C:N4	2.46	0.49
57:LR:515:CYS:HB2	57:LR:536:LEU:HD22	1.95	0.49
6:L3:6:GLN:OE1	6:L3:6:GLN:N	2.46	0.48
10:L8:5:ARG:NH2	10:L8:27:PHE:O	2.46	0.48
17:LH:101:GLN:OE1	17:LH:104:ALA:N	2.46	0.48
18:LJ:453:VAL:HG21	20:LL:532:ARG:HG2	1.95	0.48
27:LT:188:VAL:H	27:LT:202:SER:HB3	1.78	0.48
27:LT:476:PHE:HD1	27:LT:486:ILE:HG12	1.78	0.48
30:LW:201:TYR:HB3	30:LW:437:LEU:HD23	1.95	0.48
38:SI:255:PRO:HA	38:SI:258:ILE:HD12	1.95	0.48
41:SM:143:HIS:HB2	41:SM:151:SER:HB3	1.94	0.48
53:8:897:C:H2'	53:8:914:G:H22	1.76	0.48
53:8:1193:A:OP2	53:8:1195:C:N4	2.45	0.48
57:LR:686:MET:HG2	57:LR:735:GLN:HB3	1.94	0.48
62:LX:9:ARG:NH1	62:LX:214:LYS:O	2.46	0.48
27:LT:62:ASP:HB2	27:LT:69:LEU:HD21	1.95	0.48
28:LU:76:ASN:HA	28:LU:118:VAL:HG21	1.94	0.48
30:LW:160:LEU:HD22	30:LW:219:VAL:HG11	1.96	0.48
30:LW:358:MET:N	30:LW:358:MET:SD	2.86	0.48
34:SD:309:TYR:OH	48:SY:127:PHE:O	2.27	0.48
36:SG:467:LYS:HA	36:SG:470:LEU:HD12	1.95	0.48
37:SH:156:ARG:NH2	37:SH:228:ASP:OD2	2.44	0.48
37:SH:323:ILE:HG23	38:SI:553:ILE:HG23	1.95	0.48
3:NB:556:LYS:HD3	3:NB:559:ARG:HD3	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L2:201:C:O2	5:L2:249:G:N1	2.43	0.48
22:LN:156:LEU:HG	22:LN:170:ILE:HD11	1.96	0.48
23:LO:367:GLY:HA2	23:LO:390:VAL:HG23	1.95	0.48
24:LP:187:LYS:NZ	44:SQ:66:GLU:OE2	2.46	0.48
25:LQ:476:ILE:HD12	25:LQ:479:LEU:HD21	1.94	0.48
35:SF:11:LEU:HA	35:SF:80:PHE:HB2	1.94	0.48
38:SI:87:ARG:NE	38:SI:98:LEU:O	2.42	0.48
38:SI:176:LEU:HD23	38:SI:177:PHE:HB3	1.94	0.48
38:SI:827:ALA:O	38:SI:883:ALA:N	2.38	0.48
39:SJ:31:LEU:HD12	39:SJ:109:LYS:HA	1.95	0.48
47:ST:508:PHE:HB3	47:ST:518:ILE:HD11	1.95	0.48
53:8:461:G:H2'	53:8:462:G:H8	1.78	0.48
62:LX:776:GLU:OE2	62:LX:820:HIS:NE2	2.46	0.48
65:5:417:LEU:O	65:5:421:LEU:N	2.45	0.48
1:NA:350:THR:HG21	38:SI:975:GLU:HG2	1.95	0.48
10:L8:58:LEU:O	10:L8:59:ARG:NH1	2.41	0.48
13:LD:123:VAL:HG12	13:LD:142:VAL:HA	1.95	0.48
23:LO:559:ILE:HG21	23:LO:578:LYS:HA	1.95	0.48
25:LQ:805:ILE:O	25:LQ:808:THR:OG1	2.31	0.48
25:LQ:836:ILE:HD12	25:LQ:857:LEU:HD13	1.95	0.48
27:LT:721:LEU:HD13	27:LT:922:LEU:HD23	1.95	0.48
29:LV:191:VAL:HG23	65:5:484:LYS:HE2	1.96	0.48
34:SC:207:LEU:HG	34:SC:219:PRO:HB3	1.94	0.48
34:SD:208:ILE:HD12	59:SB:152:LEU:HD22	1.96	0.48
46:SS:300:ASP:OD2	46:SS:300:ASP:N	2.45	0.48
47:ST:63:ALA:HB1	53:8:1463:C:H4'	1.95	0.48
47:ST:64:ARG:HA	47:ST:78:ARG:HG2	1.95	0.48
51:NH:257:SER:HA	51:NH:592:PHE:H	1.78	0.48
51:NH:976:ILE:HA	51:NH:1042:ALA:HB3	1.95	0.48
53:8:875:G:N2	53:8:953:G:N3	2.61	0.48
54:SU:104:ALA:HB1	54:SU:115:LEU:HD21	1.95	0.48
58:NE:268:LYS:HD2	58:NE:298:LYS:HZ1	1.78	0.48
62:LX:789:LEU:HD23	62:LX:890:LEU:HD23	1.95	0.48
5:L2:115:G:O2'	5:L2:257:A:N3	2.44	0.48
11:L9:58:ASP:OD1	11:L9:58:ASP:N	2.45	0.48
22:LN:282:ASP:OD1	22:LN:282:ASP:N	2.37	0.48
25:LQ:273:TYR:OH	25:LQ:341:ALA:O	2.32	0.48
25:LQ:549:SER:HB3	25:LQ:579:ILE:HD11	1.96	0.48
27:LT:176:TYR:HB3	27:LT:179:LYS:HB2	1.93	0.48
28:LU:89:ASP:HB2	28:LU:91:VAL:HG12	1.96	0.48
30:LW:388:ASP:OD1	30:LW:388:ASP:N	2.40	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:SM:42:LEU:HD23	41:SM:43:PRO:HD2	1.94	0.48
62:LX:487:ASN:HD21	62:LX:493:ASP:HB2	1.78	0.48
63:L6:39:GLU:HG3	63:L6:46:LYS:HG3	1.94	0.48
28:LU:138:SER:OG	28:LU:139:CYS:N	2.47	0.48
29:LV:118:GLN:OE1	29:LV:124:GLN:NE2	2.47	0.48
38:SI:126:ASN:OD1	38:SI:126:ASN:N	2.47	0.48
42:SN:87:LEU:O	42:SN:93:THR:OG1	2.31	0.48
48:SY:13:HIS:O	53:8:554:C:O2'	2.31	0.48
52:NI:39:ALA:HA	52:NI:55:LEU:HA	1.95	0.48
57:LR:619:ARG:O	57:LR:637:ALA:N	2.42	0.48
62:LX:537:MET:O	62:LX:541:TYR:N	2.46	0.48
2:SA:306:LEU:HD13	2:SA:404:LEU:HB3	1.96	0.48
9:L7:174:ASN:OD1	9:L7:174:ASN:N	2.46	0.48
11:L9:38:ASN:N	11:L9:38:ASN:OD1	2.47	0.48
18:LJ:168:THR:OG1	18:LJ:194:ARG:NH2	2.47	0.48
25:LQ:565:PHE:O	37:SH:207:ARG:NH2	2.46	0.48
25:LQ:597:ILE:HD13	25:LQ:630:PHE:HE2	1.79	0.48
38:SI:826:LYS:HE3	38:SI:926:ILE:HG22	1.95	0.48
48:SY:241:SER:OG	48:SY:242:PHE:N	2.46	0.48
53:8:1514:U:H2'	53:8:1515:A:H8	1.78	0.48
53:8:1541:G:H21	53:8:1569:A:H62	1.60	0.48
62:LX:34:ARG:NH1	62:LX:64:LEU:O	2.46	0.48
62:LX:769:ARG:NH1	62:LX:770:GLU:O	2.47	0.48
65:5:290:ARG:HH12	66:6:101:GLN:HE21	1.61	0.48
65:5:446:SER:HA	65:5:449:LYS:HZ1	1.79	0.48
65:5:471:PRO:HD2	65:5:472:ILE:HD12	1.94	0.48
7:L4:191:ARG:HH22	7:L4:218:PHE:HB3	1.78	0.48
8:L5:124:LEU:HD11	18:LJ:117:LEU:HD21	1.96	0.48
15:LF:55:VAL:HG23	15:LF:75:VAL:HB	1.96	0.48
18:LJ:35:LEU:HD23	18:LJ:326:LEU:HD13	1.96	0.48
20:LL:80:MET:HB2	20:LL:80:MET:HE3	1.61	0.48
23:LO:23:SER:OG	23:LO:24:ASP:N	2.46	0.48
25:LQ:745:SER:OG	25:LQ:746:LEU:N	2.46	0.48
29:LV:338:MET:N	29:LV:338:MET:SD	2.86	0.48
36:SG:259:LYS:HB2	36:SG:259:LYS:HE3	1.71	0.48
54:SU:123:TYR:OH	54:SU:147:THR:O	2.31	0.48
56:ND:190:LEU:HD12	56:ND:191:PRO:HD2	1.95	0.48
59:SB:227:LEU:HD23	59:SB:231:ILE:HG22	1.95	0.48
65:5:480:THR:OG1	65:5:481:SER:N	2.44	0.48
2:SA:25:ASP:OD1	2:SA:25:ASP:N	2.47	0.48
8:L5:72:HIS:O	12:LC:79:TYR:OH	2.32	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:LH:656:ASP:OD1	17:LH:656:ASP:N	2.43	0.48
18:LJ:220:ALA:HA	18:LJ:226:ILE:HG22	1.94	0.48
22:LN:106:ASN:H	22:LN:153:GLN:HG2	1.79	0.48
23:LO:130:ASP:N	23:LO:130:ASP:OD1	2.42	0.48
23:LO:296:GLN:NE2	23:LO:332:TRP:O	2.47	0.48
28:LU:329:ILE:HD11	28:LU:351:VAL:HG21	1.95	0.48
37:SH:228:ASP:OD2	37:SH:230:TRP:NE1	2.47	0.48
40:SL:130:CYS:HB2	40:SL:132:HIS:CE1	2.49	0.48
48:SY:168:LYS:HA	48:SY:171:LEU:HG	1.96	0.48
53:8:1003:A:H1'	53:8:1005:A:H62	1.79	0.48
53:8:1512:G:H2'	53:8:1513:G:H8	1.79	0.48
59:SB:162:MET:SD	59:SB:275:TYR:OH	2.66	0.48
59:SB:217:LYS:O	59:SB:221:THR:OG1	2.31	0.48
62:LX:723:LEU:O	62:LX:764:ASN:N	2.47	0.48
1:NA:322:LYS:HE3	1:NA:327:LYS:HG2	1.96	0.48
2:SA:306:LEU:HD21	2:SA:382:LYS:HB3	1.96	0.48
4:L0:484:G:OP2	24:LP:3:LYS:NZ	2.44	0.48
8:L5:16:VAL:HG21	27:LT:534:SER:HB3	1.95	0.48
17:LH:849:ASP:H	17:LH:852:ASP:HB2	1.78	0.48
17:LH:864:ASP:OD1	17:LH:864:ASP:N	2.47	0.48
18:LJ:125:HIS:NE2	39:SK:19:LEU:O	2.45	0.48
20:LL:66:VAL:HG22	20:LL:112:LEU:HD22	1.96	0.48
31:LZ:138:VAL:HG22	31:LZ:158:VAL:HG12	1.96	0.48
36:SG:417:SER:HB3	36:SG:421:ASN:HB2	1.95	0.48
40:SL:22:ASP:OD1	40:SL:22:ASP:N	2.40	0.48
41:SM:268:ASN:OD1	48:SY:56:LYS:NZ	2.44	0.48
53:8:261:U:O2'	53:8:262:U:O4'	2.31	0.48
53:8:375:U:H5''	53:8:376:C:H5'	1.95	0.48
57:LR:279:LYS:NZ	57:LR:317:GLU:O	2.47	0.48
57:LR:619:ARG:NH1	57:LR:620:LEU:O	2.47	0.48
57:LR:630:ASP:HB3	57:LR:646:ASP:HB2	1.96	0.48
62:LX:771:SER:HB2	62:LX:773:TRP:CE2	2.49	0.48
7:L4:110:ALA:HB1	36:SG:112:LEU:HD23	1.96	0.47
17:LH:479:ASN:HD22	18:LJ:3:THR:HG21	1.79	0.47
25:LQ:72:SER:HA	25:LQ:75:ARG:HH22	1.79	0.47
26:LS:334:SER:OG	26:LS:335:GLN:N	2.47	0.47
29:LV:95:ARG:NH2	29:LV:129:GLY:O	2.47	0.47
33:NK:70:ALA:HB3	33:NK:83:LYS:H	1.78	0.47
34:SC:110:ASN:ND2	34:SC:112:ALA:O	2.47	0.47
35:SE:102:ILE:HG21	35:SE:114:ILE:HD11	1.96	0.47
39:SK:119:GLY:O	39:SK:165:ASN:ND2	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:8:513:U:H2'	53:8:514:G:C8	2.49	0.47
62:LX:29:VAL:HA	62:LX:152:LEU:HB3	1.96	0.47
62:LX:157:SER:HA	62:LX:160:GLN:HB2	1.96	0.47
1:NA:301:GLU:OE2	1:NA:304:GLN:NE2	2.47	0.47
8:L5:26:ALA:N	12:LC:27:GLY:O	2.44	0.47
17:LH:435:ASP:OD1	17:LH:435:ASP:N	2.41	0.47
21:LM:81:LEU:O	21:LM:124:ARG:NH2	2.47	0.47
22:LN:490:SER:OG	22:LN:491:CYS:N	2.46	0.47
26:LS:272:LEU:HD11	26:LS:314:THR:HG21	1.96	0.47
27:LT:128:LEU:HB2	27:LT:150:PRO:HG2	1.96	0.47
29:LV:154:TYR:HB3	29:LV:164:ARG:HA	1.94	0.47
36:SG:346:ALA:HB3	36:SG:359:PHE:HB2	1.95	0.47
37:SH:208:MET:HB3	37:SH:243:ILE:HD12	1.96	0.47
47:ST:726:LYS:NZ	53:8:1461:C:OP2	2.44	0.47
57:LR:21:ALA:HB3	57:LR:35:PRO:HG3	1.96	0.47
2:SA:26:ASP:OD2	28:LU:81:ASN:ND2	2.43	0.47
2:SA:126:ASP:OD1	34:SC:322:ARG:NH2	2.47	0.47
2:SA:142:LEU:HA	24:LP:105:GLN:HE21	1.79	0.47
2:SA:169:LYS:HA	2:SA:299:VAL:HG22	1.96	0.47
4:L0:490:G:H21	4:L0:495:G:H1'	1.78	0.47
18:LJ:191:GLY:H	18:LJ:214:PRO:HA	1.78	0.47
18:LJ:227:VAL:HG23	18:LJ:236:VAL:HG12	1.95	0.47
20:LL:488:ILE:HG13	20:LL:529:THR:HG21	1.96	0.47
22:LN:66:ARG:HH21	22:LN:528:ILE:HD11	1.79	0.47
22:LN:468:ASP:OD1	22:LN:468:ASP:N	2.45	0.47
22:LN:510:GLU:O	22:LN:558:ARG:NH1	2.42	0.47
27:LT:21:SER:HB2	27:LT:623:ILE:HG12	1.97	0.47
28:LU:380:TRP:NE1	28:LU:398:GLU:OE2	2.46	0.47
38:SI:125:LEU:HD22	38:SI:912:ARG:HD2	1.96	0.47
41:SM:105:LYS:NZ	53:8:1581:C:OP2	2.43	0.47
42:SN:41:ASN:ND2	53:8:1499:G:O2'	2.47	0.47
45:SR:126:LYS:HG2	45:SR:131:SER:HA	1.96	0.47
65:5:488:ASP:OD1	65:5:488:ASP:N	2.42	0.47
3:NB:531:ASN:O	38:SI:909:ASN:ND2	2.47	0.47
3:NB:555:ASN:OD1	3:NB:555:ASN:N	2.48	0.47
7:L4:138:TYR:HA	7:L4:148:ARG:HA	1.96	0.47
9:L7:144:VAL:HG23	28:LU:181:ALA:HB3	1.95	0.47
13:LD:68:GLY:HA3	13:LD:127:GLN:HE21	1.79	0.47
13:LD:134:THR:OG1	53:8:325:G:OP1	2.32	0.47
23:LO:496:THR:HA	23:LO:513:GLU:HA	1.96	0.47
23:LO:713:ASP:OD1	23:LO:713:ASP:N	2.40	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:LT:51:VAL:HG21	27:LT:90:VAL:HG21	1.97	0.47
28:LU:125:ASP:OD1	28:LU:125:ASP:N	2.46	0.47
51:NH:755:PRO:HA	51:NH:782:VAL:HA	1.95	0.47
57:LR:190:THR:OG1	57:LR:217:ASP:OD2	2.32	0.47
64:NF:114:ARG:O	64:NF:118:ILE:N	2.48	0.47
12:LC:42:GLU:HA	12:LC:45:ARG:HH12	1.79	0.47
13:LD:65:SER:OG	53:8:115:G:OP2	2.33	0.47
14:LE:41:MET:HB2	14:LE:46:TYR:HB2	1.96	0.47
17:LH:195:ASN:N	17:LH:195:ASN:OD1	2.47	0.47
18:LJ:32:SER:O	18:LJ:71:ARG:NH2	2.39	0.47
22:LN:149:ILE:HD12	22:LN:153:GLN:HG3	1.95	0.47
28:LU:308:VAL:HA	28:LU:324:SER:HA	1.94	0.47
36:SG:348:LEU:HD22	36:SG:357:LEU:HD12	1.95	0.47
38:SI:56:VAL:HG23	45:SR:52:ILE:HD11	1.97	0.47
42:SN:190:ILE:HD12	42:SN:191:PRO:HD2	1.96	0.47
51:NH:631:GLY:N	51:NH:665:HIS:O	2.46	0.47
53:8:1203:A:O2'	53:8:1209:C:O2'	2.27	0.47
55:LI:594:SER:HA	55:LI:597:GLN:HE22	1.79	0.47
57:LR:344:ARG:HE	57:LR:395:ASP:HA	1.78	0.47
57:LR:746:TRP:O	57:LR:752:THR:OG1	2.32	0.47
58:NE:323:LYS:HA	58:NE:326:ILE:HD12	1.96	0.47
59:SB:160:ASP:N	59:SB:160:ASP:OD1	2.43	0.47
3:NB:602:LEU:HG	3:NB:604:ARG:HG2	1.96	0.47
7:L4:71:LYS:HB2	7:L4:76:VAL:HA	1.97	0.47
18:LJ:398:SER:O	18:LJ:434:ARG:NH2	2.39	0.47
20:LL:338:ASN:OD1	26:LS:337:ALA:N	2.48	0.47
20:LL:513:LEU:HD21	20:LL:523:LEU:HD11	1.97	0.47
25:LQ:41:LEU:HD23	25:LQ:52:TRP:HE1	1.80	0.47
27:LT:458:THR:OG1	27:LT:497:LYS:NZ	2.41	0.47
27:LT:849:ILE:HD12	27:LT:887:LEU:HD23	1.97	0.47
34:SD:145:ASN:OD1	34:SD:148:ARG:NH1	2.47	0.47
34:SD:308:PRO:HG3	48:SY:129:SER:HA	1.96	0.47
38:SI:54:LEU:HD21	45:SR:77:ILE:HB	1.95	0.47
53:8:9:U:O2'	58:NE:239:ARG:NH1	2.47	0.47
53:8:300:A:H2'	53:8:301:A:C8	2.49	0.47
53:8:897:C:OP2	53:8:914:G:N2	2.47	0.47
57:LR:290:ILE:HG22	57:LR:306:LEU:HG	1.97	0.47
1:NA:464:SER:OG	1:NA:465:LEU:N	2.48	0.47
3:NB:540:ILE:HD13	38:SI:150:MET:HG3	1.97	0.47
4:L0:503:C:H2'	4:L0:504:U:H6	1.79	0.47
7:L4:42:LEU:HD21	7:L4:47:PHE:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:L5:26:ALA:HB3	12:LC:28:LEU:HB3	1.97	0.47
12:LC:55:VAL:HG21	12:LC:89:LEU:HD21	1.97	0.47
16:LG:62:GLU:HB3	16:LG:64:ARG:HH21	1.80	0.47
19:LK:475:THR:HA	19:LK:478:ASN:HB2	1.97	0.47
22:LN:31:MET:HE2	22:LN:31:MET:HB3	1.82	0.47
22:LN:566:LEU:HD23	22:LN:570:ILE:HG12	1.96	0.47
22:LN:594:PHE:HA	22:LN:611:LEU:HA	1.95	0.47
23:LO:296:GLN:OE1	23:LO:330:TYR:OH	2.32	0.47
23:LO:412:ARG:NH2	25:LQ:942:VAL:O	2.48	0.47
23:LO:541:ILE:HD13	23:LO:606:VAL:HG13	1.97	0.47
25:LQ:476:ILE:HA	25:LQ:492:SER:HA	1.96	0.47
25:LQ:603:ASP:N	25:LQ:603:ASP:OD1	2.44	0.47
27:LT:194:ARG:HD3	59:SB:436:ALA:HB2	1.96	0.47
28:LU:185:ILE:HD11	28:LU:194:PHE:HD2	1.79	0.47
29:LV:277:ILE:HG12	29:LV:291:THR:HG22	1.97	0.47
30:LW:329:LEU:HD11	30:LW:340:LEU:HB3	1.96	0.47
38:SI:978:ARG:NH1	53:8:1600:A:OP1	2.48	0.47
38:SI:1034:LEU:HB2	38:SI:1037:GLN:HG3	1.97	0.47
39:SJ:90:ASP:N	39:SJ:90:ASP:OD1	2.47	0.47
41:SM:149:PRO:HG2	41:SM:170:VAL:HG21	1.95	0.47
42:SN:128:ASP:OD1	42:SN:128:ASP:N	2.47	0.47
47:ST:749:LYS:NZ	53:8:1175:U:OP2	2.38	0.47
48:SY:135:ILE:HG23	56:ND:178:VAL:HG22	1.97	0.47
53:8:239:C:O2'	53:8:241:U:OP1	2.32	0.47
57:LR:337:HIS:HB3	57:LR:340:ILE:HD11	1.96	0.47
59:SB:351:ALA:HB1	59:SB:355:ASN:HB3	1.97	0.47
4:L0:293:U:H2'	23:LO:631:ASN:HA	1.97	0.47
18:LJ:222:SER:HB3	18:LJ:225:GLN:HB2	1.96	0.47
18:LJ:258:LEU:HD21	18:LJ:272:LEU:HD11	1.97	0.47
25:LQ:24:VAL:HG12	25:LQ:42:ILE:HB	1.95	0.47
25:LQ:629:ASN:HD22	25:LQ:643:ASP:HA	1.80	0.47
27:LT:510:LEU:HD21	27:LT:514:ASN:HA	1.95	0.47
27:LT:601:VAL:HG12	27:LT:611:THR:HG22	1.96	0.47
29:LV:191:VAL:HG23	65:5:484:LYS:HB2	1.97	0.47
36:SG:333:MET:SD	36:SG:334:GLU:N	2.88	0.47
37:SH:327:ARG:NH2	38:SI:558:ILE:O	2.36	0.47
38:SI:300:GLN:HG3	38:SI:792:VAL:HG22	1.96	0.47
38:SI:1042:MET:HG3	38:SI:1044:LEU:HD13	1.95	0.47
42:SN:153:MET:HG3	60:SV:191:LEU:HD22	1.96	0.47
54:SU:317:ILE:HG23	54:SU:358:PHE:HB2	1.97	0.47
57:LR:510:SER:OG	57:LR:512:ASP:OD1	2.33	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:LX:569:PRO:HD3	62:LX:583:LEU:HG	1.97	0.47
1:NA:295:LYS:HB3	1:NA:296:ASN:H	1.52	0.47
4:L0:267:U:H3	12:LC:21:HIS:CG	2.32	0.47
7:L4:151:ASP:OD1	63:L6:215:ARG:NH2	2.48	0.47
14:LE:106:THR:HG23	14:LE:108:ALA:H	1.79	0.47
20:LL:151:LEU:HD11	20:LL:163:LEU:HD22	1.97	0.47
22:LN:288:THR:HG22	22:LN:295:VAL:HG23	1.96	0.47
22:LN:620:ASP:OD1	22:LN:620:ASP:N	2.48	0.47
23:LO:273:ARG:NH1	27:LT:763:SER:O	2.45	0.47
27:LT:414:ILE:HA	27:LT:434:HIS:HA	1.97	0.47
29:LV:85:ASP:O	29:LV:89:LEU:N	2.42	0.47
36:SG:186:PHE:HE1	36:SG:211:LEU:HD13	1.79	0.47
38:SI:1135:ARG:NH1	53:8:495:C:OP2	2.48	0.47
51:NH:186:ILE:HA	51:NH:190:ALA:HB2	1.96	0.47
54:SU:279:LEU:HA	54:SU:357:ARG:HH12	1.79	0.47
59:SB:379:ASP:OD1	59:SB:379:ASP:N	2.40	0.47
62:LX:45:MET:SD	62:LX:45:MET:N	2.88	0.47
62:LX:87:GLU:HB3	62:LX:90:GLU:HB2	1.96	0.47
1:NA:526:ASN:OD1	1:NA:529:ARG:NH2	2.47	0.47
8:L5:157:ARG:HB2	8:L5:224:ASN:HD21	1.80	0.47
9:L7:27:LEU:HG	9:L7:38:LEU:HD11	1.97	0.47
17:LH:233:ASP:OD1	17:LH:236:ASN:ND2	2.47	0.47
17:LH:510:TYR:HE1	17:LH:527:HIS:HB3	1.80	0.47
20:LL:281:ILE:HB	20:LL:291:ILE:HD11	1.97	0.47
23:LO:159:ARG:NH1	23:LO:179:GLU:OE2	2.48	0.47
24:LP:278:MET:HB2	24:LP:312:LEU:HD13	1.96	0.47
30:LW:327:THR:OG1	30:LW:405:GLY:O	2.32	0.47
53:8:894:U:O2'	53:8:919:A:N6	2.48	0.47
53:8:1743:U:H2'	53:8:1744:A:H8	1.79	0.47
54:SU:399:ILE:HG21	54:SU:480:LEU:HB3	1.96	0.47
62:LX:817:ASP:OD1	62:LX:817:ASP:N	2.48	0.47
62:LX:894:ASN:O	62:LX:897:THR:OG1	2.30	0.47
4:L0:145:A:H2'	4:L0:146:G:H8	1.80	0.46
4:L0:413:C:H2'	4:L0:414:G:H8	1.79	0.46
16:LG:10:ALA:HB1	16:LG:30:VAL:HB	1.97	0.46
17:LH:408:THR:HG21	17:LH:488:LEU:HB2	1.97	0.46
18:LJ:376:ASN:OD1	18:LJ:376:ASN:N	2.47	0.46
19:LK:462:LEU:HD11	20:LL:556:THR:HG21	1.96	0.46
22:LN:624:LYS:HD3	22:LN:624:LYS:HA	1.72	0.46
24:LP:54:ILE:HG12	24:LP:112:MET:HE1	1.97	0.46
24:LP:268:ASP:N	24:LP:268:ASP:OD1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:LW:178:ASP:OD2	40:SL:24:ARG:NH1	2.48	0.46
36:SG:488:ILE:HG12	36:SG:498:VAL:HG12	1.96	0.46
37:SH:105:TYR:HE2	37:SH:296:LEU:HA	1.80	0.46
37:SH:298:ILE:HG13	37:SH:322:PHE:HE1	1.79	0.46
37:SH:366:ILE:HD11	38:SI:920:GLU:HA	1.96	0.46
38:SI:248:ARG:HB3	38:SI:357:PRO:HG2	1.98	0.46
39:SJ:113:TYR:HB3	39:SJ:121:LEU:HD11	1.96	0.46
40:SL:101:CYS:SG	40:SL:102:VAL:N	2.89	0.46
53:8:239:C:O2	53:8:244:A:N6	2.49	0.46
57:LR:332:SER:OG	57:LR:381:VAL:O	2.32	0.46
57:LR:464:LYS:HA	57:LR:487:ARG:H	1.80	0.46
65:5:485:TRP:CD1	65:5:489:GLN:HE21	2.32	0.46
2:SA:203:PHE:HB3	2:SA:206:LEU:HD13	1.97	0.46
4:L0:125:G:H2'	4:L0:126:A:H8	1.80	0.46
10:L8:6:ASP:HB2	10:L8:28:GLU:HG3	1.97	0.46
11:L9:34:PHE:HD2	11:L9:111:THR:HG21	1.80	0.46
11:L9:58:ASP:HA	11:L9:61:THR:HG22	1.97	0.46
13:LD:130:PRO:HB3	13:LD:136:ARG:HA	1.97	0.46
17:LH:215:VAL:HA	17:LH:218:LYS:HB2	1.96	0.46
18:LJ:172:ARG:HH12	54:SU:370:HIS:HA	1.79	0.46
20:LL:191:VAL:HA	20:LL:206:ALA:HA	1.97	0.46
22:LN:82:ARG:NH1	22:LN:726:UNK:O	2.48	0.46
22:LN:550:VAL:HG23	22:LN:563:LEU:HB2	1.98	0.46
23:LO:805:ALA:HA	57:LR:815:LYS:HE2	1.97	0.46
26:LS:534:SER:HB3	26:LS:540:ALA:HB1	1.96	0.46
27:LT:416:ALA:HB3	27:LT:433:ALA:HB3	1.96	0.46
28:LU:439:ARG:O	28:LU:443:ASN:ND2	2.48	0.46
32:NG:45:GLY:N	53:8:900:A:OP1	2.47	0.46
37:SH:59:VAL:HG23	37:SH:60:THR:HG23	1.95	0.46
39:SK:100:LEU:HD11	39:SK:112:VAL:HG11	1.96	0.46
48:SY:5:VAL:HG21	48:SY:10:LYS:HE3	1.96	0.46
57:LR:97:ARG:HH22	57:LR:133:ASN:HA	1.80	0.46
62:LX:725:VAL:HG22	62:LX:762:MET:HB2	1.97	0.46
62:LX:807:SER:HA	62:LX:810:LYS:HE2	1.96	0.46
63:L6:48:TYR:OH	63:L6:119:GLN:O	2.33	0.46
3:NB:608:PHE:HE2	34:SC:303:GLN:HB3	1.79	0.46
4:L0:90:G:OP1	18:LJ:378:LYS:NZ	2.42	0.46
4:L0:220:U:H5''	56:ND:200:ARG:HH21	1.80	0.46
7:L4:62:LYS:NZ	53:8:454:U:OP2	2.44	0.46
22:LN:476:LYS:HG3	22:LN:491:CYS:HA	1.96	0.46
24:LP:278:MET:SD	24:LP:278:MET:N	2.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:LQ:259:ILE:HG12	25:LQ:274:ILE:HG23	1.97	0.46
26:LS:454:GLY:O	26:LS:487:GLU:N	2.48	0.46
28:LU:2:LYS:HB2	30:LW:75:GLU:HB2	1.98	0.46
29:LV:333:ASN:OD1	29:LV:333:ASN:N	2.43	0.46
38:SI:1148:GLU:HB3	38:SI:1152:ARG:HH12	1.80	0.46
39:SJ:228:SER:HB3	39:SJ:232:LEU:HD21	1.96	0.46
39:SK:100:LEU:HD13	39:SK:130:ILE:HD11	1.97	0.46
39:SK:178:VAL:HG23	39:SK:204:VAL:HG22	1.97	0.46
53:8:35:U:H1'	53:8:474:A:H61	1.80	0.46
53:8:1695:G:H2'	53:8:1696:G:C8	2.50	0.46
54:SU:196:GLN:OE1	54:SU:260:ASN:ND2	2.47	0.46
4:L0:93:A:OP2	18:LJ:384:ARG:NH2	2.42	0.46
5:L2:254:A:C8	35:SF:35:LYS:HE2	2.50	0.46
12:LC:103:ASN:HD21	23:LO:554:ASP:HB2	1.80	0.46
25:LQ:489:VAL:HG21	25:LQ:546:LEU:HD11	1.96	0.46
32:NG:15:GLY:N	32:NG:78:ALA:O	2.48	0.46
34:SC:293:LEU:HD22	34:SC:298:ILE:HD12	1.98	0.46
57:LR:738:LEU:HA	57:LR:741:LYS:HE2	1.97	0.46
61:SP:248:HIS:H	61:SP:251:ALA:HB3	1.80	0.46
2:SA:6:TYR:HD2	2:SA:86:LEU:HD23	1.80	0.46
2:SA:283:ASP:OD1	2:SA:286:ARG:NH2	2.47	0.46
4:L0:348:U:N3	4:L0:376:U:O2	2.49	0.46
4:L0:475:G:O3'	31:LZ:4:LYS:NZ	2.46	0.46
6:L3:82:PRO:HB3	42:SN:68:ARG:HB2	1.97	0.46
19:LK:505:MET:O	19:LK:509:GLN:N	2.34	0.46
22:LN:649:TRP:NE1	22:LN:744:VAL:O	2.49	0.46
24:LP:67:ARG:NH2	24:LP:84:SER:OG	2.49	0.46
26:LS:519:SER:HB3	26:LS:535:ARG:HG2	1.98	0.46
27:LT:918:LYS:O	27:LT:921:ARG:NE	2.45	0.46
29:LV:282:ASN:OD1	29:LV:325:GLY:N	2.36	0.46
35:SE:32:GLN:NE2	35:SE:103:THR:O	2.41	0.46
35:SF:35:LYS:HD2	35:SF:91:CYS:SG	2.55	0.46
53:8:1684:U:H2'	53:8:1685:G:H8	1.79	0.46
62:LX:742:PHE:HB3	62:LX:762:MET:HE2	1.97	0.46
62:LX:871:MET:N	62:LX:871:MET:SD	2.89	0.46
63:L6:98:ARG:NH1	63:L6:101:ILE:O	2.49	0.46
17:LH:508:ILE:HD11	17:LH:560:ILE:HG21	1.97	0.46
22:LN:251:ASP:OD1	22:LN:251:ASP:N	2.48	0.46
22:LN:330:GLY:HA3	22:LN:353:GLU:HG3	1.98	0.46
25:LQ:392:THR:OG1	25:LQ:393:ASP:N	2.48	0.46
25:LQ:614:HIS:H	25:LQ:640:LYS:HZ1	1.60	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:SD:271:ILE:HG12	34:SD:289:GLU:HG3	1.97	0.46
36:SG:198:LYS:HD3	36:SG:268:LEU:HD13	1.97	0.46
39:SK:180:LEU:HD23	39:SK:237:ALA:HB1	1.97	0.46
53:8:329:G:H2'	53:8:330:G:H8	1.80	0.46
56:ND:160:ARG:HA	56:ND:163:LEU:HB3	1.97	0.46
57:LR:72:ASP:OD1	57:LR:72:ASP:N	2.46	0.46
57:LR:299:ASN:HB2	57:LR:301:GLN:HG2	1.98	0.46
65:5:241:ARG:NH2	66:6:19:SER:O	2.49	0.46
3:NB:559:ARG:HA	53:8:545:A:H62	1.79	0.46
17:LH:334:LEU:HD22	18:LJ:2:SER:HB2	1.97	0.46
23:LO:530:VAL:HG23	23:LO:544:ILE:HG12	1.97	0.46
25:LQ:165:SER:HB3	25:LQ:182:LYS:HB2	1.98	0.46
25:LQ:198:GLU:OE1	25:LQ:200:HIS:ND1	2.42	0.46
25:LQ:592:SER:OG	25:LQ:593:ALA:N	2.47	0.46
26:LS:233:LEU:O	26:LS:554:ASN:ND2	2.41	0.46
28:LU:387:THR:HG23	28:LU:390:GLU:H	1.81	0.46
30:LW:236:MET:HE2	30:LW:236:MET:HB3	1.83	0.46
34:SD:228:GLN:HA	34:SD:231:ARG:HB2	1.98	0.46
36:SG:131:ARG:HE	36:SG:411:PHE:HE2	1.62	0.46
36:SG:447:SER:OG	36:SG:449:ASN:OD1	2.34	0.46
37:SH:65:ILE:HG12	37:SH:76:TYR:HD1	1.80	0.46
37:SH:221:CYS:SG	37:SH:222:GLU:N	2.88	0.46
38:SI:861:THR:N	38:SI:882:ASN:O	2.44	0.46
38:SI:1051:ASP:OD1	38:SI:1051:ASP:N	2.48	0.46
48:SY:207:ARG:NH1	48:SY:210:GLN:OE1	2.49	0.46
66:6:306:ARG:O	66:6:310:GLN:NE2	2.49	0.46
4:L0:226:U:C2	22:LN:236:LYS:HE3	2.51	0.46
7:L4:233:LYS:HB3	7:L4:233:LYS:HE2	1.80	0.46
13:LD:125:VAL:HB	13:LD:137:PHE:HB3	1.97	0.46
18:LJ:104:LEU:HB2	18:LJ:121:ASN:HA	1.98	0.46
20:LL:349:ASP:O	20:LL:352:SER:OG	2.34	0.46
21:LM:387:LEU:HD12	21:LM:407:PHE:HE2	1.79	0.46
25:LQ:118:ASN:N	25:LQ:118:ASN:OD1	2.48	0.46
27:LT:76:THR:OG1	27:LT:78:SER:O	2.34	0.46
27:LT:232:MET:HB3	27:LT:232:MET:HE2	1.56	0.46
31:LZ:29:ASP:OD1	31:LZ:29:ASP:N	2.45	0.46
34:SD:224:ALA:O	34:SD:256:ASN:ND2	2.39	0.46
36:SG:263:TRP:HA	36:SG:270:PRO:HA	1.98	0.46
36:SG:417:SER:OG	36:SG:418:ASP:N	2.48	0.46
37:SH:183:ILE:HD13	37:SH:310:ARG:HH12	1.81	0.46
53:8:362:G:H2'	53:8:363:G:H8	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:SU:366:LEU:HB3	54:SU:405:LEU:HD21	1.97	0.46
57:LR:216:ARG:NE	57:LR:243:VAL:O	2.43	0.46
65:5:205:LYS:HA	65:5:349:PRO:HA	1.98	0.46
4:L0:411:A:H2'	4:L0:412:A:H8	1.81	0.46
10:L8:7:SER:OG	53:8:336:G:N2	2.49	0.46
10:L8:36:THR:OG1	10:L8:37:LYS:N	2.49	0.46
12:LC:36:ILE:HG23	12:LC:49:TYR:HE1	1.80	0.46
13:LD:35:TYR:OH	53:8:247:A:O3'	2.33	0.46
17:LH:200:ASN:HD22	17:LH:263:ALA:HA	1.80	0.46
17:LH:720:ILE:HD11	17:LH:766:ILE:HG21	1.98	0.46
17:LH:868:ASN:O	17:LH:871:SER:OG	2.33	0.46
18:LJ:52:PRO:HB3	18:LJ:309:PRO:HD2	1.97	0.46
20:LL:333:ASN:OD1	20:LL:333:ASN:N	2.49	0.46
20:LL:441:LEU:HB2	20:LL:456:VAL:HG11	1.98	0.46
21:LM:284:SER:O	21:LM:326:LYS:NZ	2.43	0.46
25:LQ:331:THR:OG1	25:LQ:333:ARG:NH1	2.48	0.46
27:LT:163:GLN:O	27:LT:187:ASN:ND2	2.44	0.46
27:LT:359:ALA:HA	27:LT:419:ILE:HD13	1.98	0.46
34:SD:108:THR:OG1	34:SD:144:TRP:NE1	2.48	0.46
35:SE:70:LEU:HD13	59:SB:311:LYS:HD2	1.98	0.46
36:SG:137:GLY:H	36:SG:485:ASN:HD21	1.63	0.46
51:NH:268:LEU:H	51:NH:294:LEU:H	1.64	0.46
53:8:1576:A:H3'	53:8:1577:A:H8	1.81	0.46
54:SU:381:LYS:HB2	54:SU:415:MET:HE1	1.96	0.46
55:LI:537:THR:HB	55:LI:560:ASN:HB2	1.97	0.46
56:ND:183:THR:OG1	56:ND:186:ASP:OD2	2.33	0.46
8:L5:218:GLU:O	8:L5:222:LYS:N	2.46	0.46
12:LC:58:ASP:O	12:LC:61:SER:OG	2.31	0.46
14:LE:106:THR:OG1	14:LE:107:SER:N	2.49	0.46
17:LH:762:TYR:HB3	17:LH:779:ILE:HG12	1.98	0.46
18:LJ:273:ILE:HG22	18:LJ:283:VAL:HG23	1.98	0.46
20:LL:166:ALA:HB2	20:LL:170:ILE:HG23	1.98	0.46
25:LQ:145:ILE:HB	25:LQ:159:LEU:HB2	1.98	0.46
27:LT:546:ILE:HG23	27:LT:560:LEU:HB3	1.98	0.46
31:LZ:173:TYR:OH	38:SI:1082:GLN:OE1	2.33	0.46
34:SC:306:LEU:HD23	34:SC:315:ILE:HG12	1.96	0.46
35:SE:62:GLU:HG2	59:SB:373:TYR:HA	1.97	0.46
37:SH:347:ASN:ND2	37:SH:349:ASP:OD2	2.49	0.46
38:SI:295:ASP:OD2	38:SI:852:ARG:NH2	2.49	0.46
42:SN:181:ARG:NH1	60:SV:201:ASP:O	2.48	0.46
55:LI:55:TYR:HA	55:LI:72:THR:HA	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:LI:185:SER:HA	55:LI:201:PHE:HA	1.97	0.46
57:LR:302:MET:N	57:LR:302:MET:SD	2.89	0.46
62:LX:660:TYR:HB2	62:LX:712:LEU:HD21	1.97	0.46
66:6:235:ASP:OD1	66:6:235:ASP:N	2.48	0.46
16:LG:10:ALA:N	16:LG:54:LEU:O	2.49	0.45
18:LJ:440:GLU:O	18:LJ:444:ASN:ND2	2.45	0.45
25:LQ:124:ILE:HA	25:LQ:140:SER:HA	1.98	0.45
28:LU:58:PHE:HA	28:LU:375:TRP:CD1	2.51	0.45
28:LU:359:ASP:OD1	28:LU:359:ASP:N	2.49	0.45
34:SC:273:ALA:HA	34:SC:285:VAL:HG11	1.97	0.45
40:SL:149:LYS:HG2	40:SL:170:ILE:HD11	1.97	0.45
41:SM:7:ARG:NH1	41:SM:11:GLU:OE2	2.49	0.45
41:SM:72:GLN:NE2	41:SM:73:VAL:O	2.48	0.45
55:LI:257:SER:O	55:LI:259:ILE:N	2.49	0.45
63:L6:1:MET:HE3	63:L6:2:LYS:H	1.81	0.45
9:L7:137:GLY:HA3	9:L7:153:LEU:HD23	1.97	0.45
17:LH:875:MET:N	17:LH:875:MET:SD	2.89	0.45
20:LL:252:SER:OG	20:LL:253:LEU:N	2.50	0.45
24:LP:44:ASN:OD1	24:LP:98:ARG:NH1	2.50	0.45
25:LQ:400:SER:OG	25:LQ:401:ASP:N	2.47	0.45
29:LV:207:TRP:CE2	29:LV:214:ARG:HB3	2.51	0.45
29:LV:323:VAL:O	29:LV:326:THR:OG1	2.31	0.45
30:LW:340:LEU:O	30:LW:368:TYR:N	2.45	0.45
31:LZ:30:THR:HG23	31:LZ:34:ARG:HH21	1.82	0.45
36:SG:261:ILE:HG23	36:SG:273:VAL:HG12	1.99	0.45
38:SI:372:TYR:HD1	62:LX:5:ALA:HA	1.80	0.45
39:SK:112:VAL:HG13	39:SK:124:VAL:HB	1.98	0.45
53:8:1486:G:O6	53:8:1487:A:N6	2.49	0.45
53:8:1662:G:H2'	53:8:1663:G:H8	1.81	0.45
57:LR:340:ILE:HD12	57:LR:355:LEU:HD22	1.98	0.45
57:LR:786:ILE:O	57:LR:789:THR:OG1	2.30	0.45
65:5:413:PHE:O	65:5:417:LEU:N	2.43	0.45
17:LH:96:ILE:H	17:LH:108:THR:HG21	1.81	0.45
22:LN:55:SER:HB2	22:LN:290:THR:HB	1.98	0.45
26:LS:426:VAL:HG23	26:LS:432:VAL:HG22	1.98	0.45
27:LT:192:ASN:O	27:LT:196:GLY:N	2.49	0.45
27:LT:639:ASP:OD1	27:LT:639:ASP:N	2.47	0.45
28:LU:321:VAL:HG23	28:LU:331:ILE:HG12	1.98	0.45
29:LV:63:LYS:HD2	29:LV:63:LYS:HA	1.80	0.45
34:SC:268:VAL:HG22	34:SC:317:VAL:HG13	1.98	0.45
44:SQ:54:GLU:O	44:SQ:58:ASN:ND2	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:SR:89:ASN:O	45:SR:91:GLY:N	2.49	0.45
54:SU:430:ASP:OD1	54:SU:430:ASP:N	2.49	0.45
57:LR:191:SER:HB3	57:LR:216:ARG:H	1.82	0.45
57:LR:281:THR:HG22	57:LR:327:ILE:HB	1.97	0.45
58:NE:274:LYS:HA	58:NE:274:LYS:HD3	1.79	0.45
4:L0:253:U:H3	42:SN:78:ASP:HB2	1.81	0.45
4:L0:427:A:O2'	48:SY:185:MET:SD	2.71	0.45
10:L8:57:ALA:HB2	10:L8:177:GLY:HA2	1.98	0.45
15:LF:78:SER:OG	15:LF:81:GLU:OE2	2.34	0.45
22:LN:579:ARG:NH1	22:LN:593:GLU:OE2	2.41	0.45
27:LT:851:SER:HB3	43:SO:242:MET:HE1	1.99	0.45
28:LU:273:GLU:OE1	28:LU:288:TYR:OH	2.34	0.45
38:SI:900:GLN:HG2	38:SI:914:ALA:HB2	1.97	0.45
41:SM:287:LYS:NZ	53:8:562:G:OP1	2.39	0.45
42:SN:228:LYS:HE3	42:SN:228:LYS:HB3	1.68	0.45
53:8:312:A:H62	53:8:352:A:H1'	1.82	0.45
53:8:1511:U:H2'	53:8:1512:G:C8	2.52	0.45
53:8:1541:G:N2	53:8:1569:A:N7	2.64	0.45
4:L0:487:A:H62	24:LP:3:LYS:HG3	1.80	0.45
5:L2:105:C:O2'	5:L2:106:C:O4'	2.32	0.45
11:L9:134:ILE:HA	11:L9:158:PHE:HA	1.98	0.45
17:LH:212:CYS:SG	17:LH:224:SER:OG	2.74	0.45
17:LH:397:LYS:NZ	17:LH:738:ASN:OD1	2.50	0.45
17:LH:516:PRO:O	17:LH:522:SER:OG	2.35	0.45
17:LH:719:ASN:OD1	17:LH:719:ASN:N	2.50	0.45
22:LN:120:SER:OG	22:LN:121:THR:N	2.40	0.45
22:LN:298:ALA:HB2	22:LN:336:ILE:HG13	1.99	0.45
22:LN:495:VAL:HB	22:LN:511:VAL:HB	1.98	0.45
23:LO:356:ASP:OD1	23:LO:356:ASP:N	2.39	0.45
23:LO:568:ARG:HD3	23:LO:568:ARG:HA	1.71	0.45
23:LO:777:ARG:HA	23:LO:777:ARG:HD2	1.80	0.45
25:LQ:17:ILE:HB	25:LQ:360:ASN:HB3	1.99	0.45
25:LQ:125:THR:N	25:LQ:139:GLY:O	2.50	0.45
26:LS:177:TRP:CD1	27:LT:262:SER:HG	2.34	0.45
27:LT:594:SER:HB2	27:LT:599:TRP:HB2	1.98	0.45
28:LU:329:ILE:HG13	28:LU:375:TRP:HZ3	1.80	0.45
29:LV:24:SER:O	29:LV:44:GLN:NE2	2.50	0.45
29:LV:62:ILE:HG23	29:LV:321:GLU:HB2	1.97	0.45
34:SD:223:ASP:OD2	34:SD:226:HIS:ND1	2.47	0.45
39:SK:25:PRO:HB2	47:ST:708:VAL:HG23	1.99	0.45
39:SK:96:LEU:HB3	39:SK:130:ILE:HD13	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:ST:546:LEU:HD23	47:ST:549:ILE:HD12	1.99	0.45
49:SZ:347:VAL:N	53:8:1220:C:OP1	2.50	0.45
53:8:327:U:H2'	53:8:328:A:H8	1.82	0.45
53:8:590:C:H2'	53:8:591:A:H8	1.82	0.45
59:SB:298:ARG:HB3	59:SB:341:LEU:HD21	1.98	0.45
2:SA:81:ILE:O	2:SA:85:ASN:ND2	2.50	0.45
2:SA:259:UNK:O	2:SA:264:SER:N	2.49	0.45
5:L2:8:U:H2'	5:L2:9:A:H8	1.82	0.45
6:L3:28:ILE:HA	6:L3:31:ALA:HB3	1.97	0.45
8:L5:224:ASN:OD1	8:L5:224:ASN:N	2.48	0.45
9:L7:49:ILE:HG23	9:L7:175:LYS:HD3	1.98	0.45
18:LJ:165:THR:OG1	18:LJ:166:GLY:N	2.49	0.45
18:LJ:378:LYS:HZ3	18:LJ:378:LYS:HG2	1.50	0.45
22:LN:240:LEU:H	22:LN:258:SER:HB3	1.80	0.45
24:LP:40:GLU:OE2	24:LP:91:ARG:NH2	2.45	0.45
24:LP:92:ILE:HA	24:LP:95:ILE:HD12	1.98	0.45
25:LQ:85:LEU:HB2	25:LQ:94:LEU:HD11	1.98	0.45
28:LU:225:LEU:HA	28:LU:237:SER:HA	1.98	0.45
28:LU:357:SER:OG	28:LU:359:ASP:OD1	2.27	0.45
29:LV:117:LEU:HD12	29:LV:123:ILE:HD11	1.99	0.45
34:SC:242:ALA:HB2	34:SC:253:ILE:HD11	1.98	0.45
34:SD:236:MET:SD	34:SD:236:MET:N	2.90	0.45
36:SG:229:GLU:HB2	36:SG:231:THR:HG23	1.99	0.45
38:SI:306:ASP:OD1	38:SI:306:ASP:N	2.42	0.45
51:NH:765:LEU:HA	51:NH:914:ARG:HA	1.99	0.45
53:8:319:U:H1'	53:8:323:A:C8	2.51	0.45
53:8:396:G:H21	53:8:398:G:H3'	1.81	0.45
53:8:1629:G:O2'	53:8:1630:U:O4'	2.33	0.45
54:SU:415:MET:HE3	54:SU:415:MET:HB2	1.88	0.45
57:LR:620:LEU:HA	57:LR:636:ASP:HA	1.99	0.45
57:LR:744:ARG:HG3	57:LR:785:ILE:HG12	1.98	0.45
62:LY:58:ALA:HB3	62:LY:125:GLN:H	1.82	0.45
62:LX:851:ASP:HB3	62:LX:854:VAL:HG23	1.99	0.45
65:5:216:ALA:HB1	66:6:4:LEU:HD22	1.99	0.45
9:L7:35:LYS:O	9:L7:39:ARG:NH1	2.50	0.45
22:LN:399:VAL:HB	22:LN:420:LEU:HD12	1.98	0.45
23:LO:446:CYS:HB3	23:LO:457:VAL:HG12	1.98	0.45
23:LO:563:ARG:HH11	23:LO:630:LEU:HD12	1.82	0.45
25:LQ:614:HIS:HB2	25:LQ:618:ILE:HG12	1.98	0.45
27:LT:360:ASP:N	27:LT:360:ASP:OD1	2.49	0.45
28:LU:46:ASN:ND2	30:LW:434:LEU:O	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LU:58:PHE:HD1	28:LU:375:TRP:HE1	1.65	0.45
30:LW:99:THR:HA	30:LW:102:LYS:HB2	1.99	0.45
36:SG:292:SER:OG	36:SG:293:ASP:N	2.50	0.45
38:SI:996:LEU:HB3	38:SI:998:SER:H	1.81	0.45
39:SK:124:VAL:HG22	39:SK:160:LEU:HD22	1.98	0.45
39:SK:181:SER:OG	39:SK:182:PHE:N	2.49	0.45
41:SM:144:GLU:OE1	41:SM:147:GLY:N	2.47	0.45
51:NH:403:GLY:HA2	51:NH:411:ILE:H	1.82	0.45
53:8:878:G:H2'	53:8:879:G:H8	1.81	0.45
4:L0:472:A:OP1	30:LW:145:ARG:NH1	2.48	0.45
7:L4:26:CYS:SG	7:L4:27:TYR:N	2.89	0.45
25:LQ:80:ALA:HB1	25:LQ:98:TYR:HB3	1.99	0.45
28:LU:225:LEU:HD12	28:LU:235:LEU:HD11	1.99	0.45
31:LZ:113:VAL:HG22	31:LZ:124:ILE:HD11	1.99	0.45
37:SH:234:ASN:OD1	37:SH:234:ASN:N	2.49	0.45
53:8:1157:A:O2'	53:8:1159:C:OP2	2.30	0.45
53:8:1693:A:H2'	53:8:1694:A:C4	2.52	0.45
66:6:88:LYS:HA	66:6:88:LYS:HD3	1.75	0.45
3:NB:533:SER:OG	3:NB:534:GLY:N	2.49	0.45
4:L0:100:G:N7	18:LJ:25:ARG:NH1	2.56	0.45
4:L0:548:A:H2'	4:L0:549:G:C8	2.52	0.45
5:L2:114:A:H61	5:L2:256:G:H1'	1.81	0.45
8:L5:95:ASN:O	53:8:1611:A:O2'	2.30	0.45
14:LE:11:LEU:O	14:LE:15:ASN:ND2	2.49	0.45
17:LH:437:THR:HB	17:LH:709:ARG:HD2	1.98	0.45
18:LJ:255:VAL:HG12	18:LJ:276:SER:HA	1.99	0.45
22:LN:303:LYS:HD3	22:LN:305:PHE:HE1	1.82	0.45
25:LQ:81:GLU:OE1	25:LQ:657:GLN:NE2	2.50	0.45
26:LS:177:TRP:CZ3	27:LT:232:MET:HE1	2.52	0.45
28:LU:67:ARG:NH1	28:LU:89:ASP:OD2	2.41	0.45
28:LU:347:ARG:O	28:LU:373:ARG:NH2	2.50	0.45
38:SI:196:THR:HG23	38:SI:197:GLU:HG3	1.98	0.45
41:SM:285:ASN:HD22	47:ST:767:ILE:HD12	1.82	0.45
47:ST:511:SER:HA	47:ST:557:SER:HB3	1.98	0.45
54:SU:252:LYS:O	54:SU:256:ASN:ND2	2.50	0.45
63:L6:4:ASN:O	63:L6:111:LEU:N	2.46	0.45
4:L0:86:C:H5'	17:LH:295:TRP:HZ2	1.82	0.45
5:L2:62:C:O2'	27:LT:447:ASN:O	2.35	0.45
9:L7:127:GLU:HA	9:L7:130:VAL:HG22	1.98	0.45
17:LH:31:ASN:HD21	17:LH:201:ILE:HD12	1.81	0.45
17:LH:60:ARG:NH1	17:LH:381:SER:O	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:LH:283:VAL:HB	17:LH:290:ILE:HG22	1.98	0.45
17:LH:403:ILE:HG12	17:LH:417:LEU:HD21	1.99	0.45
26:LS:271:THR:OG1	26:LS:273:ARG:NH1	2.50	0.45
26:LS:351:THR:OG1	26:LS:352:GLN:N	2.50	0.45
26:LS:514:LEU:O	48:SY:248:ARG:NH2	2.50	0.45
30:LW:237:ALA:HB1	30:LW:280:ILE:HG12	1.99	0.45
7:L4:39:ARG:HA	7:L4:39:ARG:HD3	1.87	0.44
13:LD:71:LEU:HD21	13:LD:88:ARG:HG3	1.99	0.44
17:LH:707:MET:N	17:LH:707:MET:SD	2.91	0.44
17:LH:729:THR:O	17:LH:734:VAL:N	2.50	0.44
18:LJ:13:ALA:HB2	18:LJ:454:ARG:HG3	1.99	0.44
27:LT:66:LEU:HD12	27:LT:344:ARG:HB3	1.98	0.44
28:LU:230:ASN:ND2	28:LU:271:PRO:O	2.50	0.44
36:SG:206:LYS:HD2	36:SG:206:LYS:HA	1.77	0.44
38:SI:826:LYS:HB2	38:SI:921:GLU:HB3	1.98	0.44
38:SI:906:ASP:OD1	38:SI:906:ASP:N	2.43	0.44
41:SM:188:HIS:HB2	41:SM:221:VAL:HG12	1.99	0.44
53:8:29:U:H2'	53:8:30:G:H8	1.82	0.44
53:8:1502:G:N2	53:8:1505:A:OP2	2.42	0.44
57:LR:312:GLN:HB3	57:LR:329:VAL:HG21	1.99	0.44
62:LX:55:VAL:HG13	62:LX:103:ILE:HG23	1.99	0.44
4:L0:337:G:OP2	58:NE:205:LYS:NZ	2.39	0.44
17:LH:876:PHE:HZ	21:LM:180:ILE:HD11	1.82	0.44
19:LK:507:ARG:HB3	55:LI:655:LEU:HD23	1.99	0.44
23:LO:5:PHE:HA	23:LO:706:THR:HG22	1.99	0.44
23:LO:7:PHE:HD2	23:LO:51:GLU:HA	1.82	0.44
23:LO:825:GLN:HA	23:LO:828:ILE:HG22	1.98	0.44
27:LT:139:ILE:HD11	27:LT:157:LEU:HD12	1.99	0.44
29:LV:16:VAL:HG23	29:LV:340:THR:HG23	1.99	0.44
29:LV:106:ILE:HD11	29:LV:111:TRP:HA	1.98	0.44
38:SI:195:TRP:NE1	38:SI:202:ALA:O	2.38	0.44
39:SJ:232:LEU:HB3	39:SJ:237:ALA:HB2	2.00	0.44
41:SM:217:ASP:OD1	41:SM:217:ASP:N	2.45	0.44
42:SN:223:LEU:HB3	42:SN:235:ILE:HD12	1.98	0.44
48:SY:6:HIS:H	48:SY:9:GLN:HB3	1.82	0.44
54:SU:222:LEU:O	54:SU:225:HIS:NE2	2.46	0.44
57:LR:113:THR:OG1	57:LR:114:SER:N	2.49	0.44
57:LR:465:LYS:H	57:LR:486:THR:HA	1.82	0.44
59:SB:430:ASP:OD1	59:SB:430:ASP:N	2.49	0.44
61:SP:1398:LEU:O	61:SP:1402:ILE:N	2.48	0.44
62:LY:567:LEU:O	62:LY:583:LEU:N	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:6:265:ASP:HB2	66:6:275:LYS:HB2	1.99	0.44
7:L4:212:ASP:OD1	7:L4:212:ASP:N	2.45	0.44
8:L5:71:ALA:HB1	8:L5:91:GLU:HA	2.00	0.44
13:LD:78:THR:HA	13:LD:84:ILE:HG22	1.98	0.44
17:LH:550:PRO:HA	20:LL:366:GLY:HA3	2.00	0.44
17:LH:561:LEU:HD21	17:LH:615:TRP:HB2	1.99	0.44
18:LJ:95:LEU:HD11	18:LJ:117:LEU:HD22	1.99	0.44
22:LN:258:SER:HA	22:LN:282:ASP:HB3	1.98	0.44
22:LN:258:SER:HB2	56:ND:205:TRP:HZ2	1.83	0.44
23:LO:311:ASN:HD22	23:LO:316:TRP:HB2	1.81	0.44
26:LS:181:GLU:HB3	27:LT:281:ARG:HH21	1.82	0.44
27:LT:114:THR:HG22	27:LT:116:ALA:H	1.82	0.44
34:SC:244:VAL:HG22	34:SC:246:GLN:HG2	1.99	0.44
38:SI:90:VAL:HG11	38:SI:105:ILE:HD12	2.00	0.44
38:SI:833:ARG:NH2	45:SR:141:GLU:OE2	2.51	0.44
42:SN:74:LEU:HD13	42:SN:154:ILE:HD11	2.00	0.44
53:8:473:A:H1'	66:6:271:ARG:HD2	1.99	0.44
62:LX:36:GLN:HE21	62:LX:204:GLU:H	1.64	0.44
62:LX:162:TYR:O	62:LX:165:THR:OG1	2.32	0.44
66:6:266:ILE:HG22	66:6:274:ILE:HA	1.99	0.44
5:L2:47:G:O2'	30:LW:180:GLU:OE1	2.30	0.44
15:LF:38:ASP:OD1	15:LF:41:ARG:NH1	2.50	0.44
17:LH:71:ASN:HB3	17:LH:74:LEU:HB2	1.99	0.44
17:LH:597:LYS:HA	17:LH:597:LYS:HD3	1.71	0.44
17:LH:661:THR:HB	17:LH:673:ALA:HB3	2.00	0.44
20:LL:370:LYS:H	20:LL:372:VAL:HG23	1.82	0.44
21:LM:317:SER:OG	21:LM:321:LYS:NZ	2.50	0.44
22:LN:530:ARG:HD3	22:LN:530:ARG:HA	1.76	0.44
23:LO:593:VAL:HG11	23:LO:684:VAL:HG11	1.98	0.44
23:LO:760:ILE:HA	23:LO:763:ILE:HD12	1.99	0.44
28:LU:158:LYS:HA	28:LU:158:LYS:HD3	1.71	0.44
29:LV:143:SER:HB3	29:LV:186:VAL:HG12	1.98	0.44
37:SH:323:ILE:HG12	38:SI:553:ILE:HG12	1.99	0.44
38:SI:843:ASP:OD1	38:SI:1035:THR:OG1	2.36	0.44
47:ST:731:ASP:HB3	47:ST:734:ARG:HB2	1.99	0.44
48:SY:3:LYS:HA	48:SY:3:LYS:HD2	1.81	0.44
48:SY:29:GLU:OE2	48:SY:37:ARG:NH1	2.50	0.44
53:8:327:U:H2'	53:8:328:A:C8	2.52	0.44
54:SU:277:ILE:HA	54:SU:280:ILE:HD12	1.99	0.44
54:SU:340:LYS:HD2	54:SU:340:LYS:HA	1.79	0.44
58:NE:234:VAL:HG23	58:NE:239:ARG:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:L6:54:GLY:O	63:L6:110:ALA:N	2.39	0.44
2:SA:101:SER:HB3	2:SA:128:ILE:HG21	1.99	0.44
4:L0:289:U:H2'	4:L0:290:G:H8	1.81	0.44
13:LD:133:LYS:NZ	53:8:324:U:OP1	2.45	0.44
23:LO:624:ASN:HB2	23:LO:678:GLU:HA	1.99	0.44
30:LW:460:ARG:HB3	46:SS:847:VAL:HB	1.99	0.44
30:LW:462:ASN:HB2	30:LW:465:ASP:H	1.82	0.44
31:LZ:30:THR:HA	31:LZ:33:MET:HB2	1.99	0.44
34:SD:241:PHE:HA	34:SD:268:VAL:HB	2.00	0.44
37:SH:42:ASN:OD1	37:SH:42:ASN:N	2.50	0.44
53:8:468:A:H2	53:8:471:A:H62	1.64	0.44
53:8:1726:G:H2'	53:8:1727:G:C8	2.53	0.44
57:LR:14:PRO:HG3	57:LR:639:GLY:HA3	2.00	0.44
60:SV:181:ASP:HB2	60:SV:187:LEU:HD22	2.00	0.44
62:LX:861:MET:HA	62:LX:864:LEU:HD12	2.00	0.44
1:NA:364:SER:HB2	41:SM:227:ARG:HH22	1.82	0.44
2:SA:30:ARG:NH1	2:SA:122:GLU:OE2	2.50	0.44
4:L0:494:C:H2'	4:L0:495:G:H8	1.81	0.44
6:L3:67:GLU:HA	6:L3:70:VAL:HG12	2.00	0.44
14:LE:78:ARG:NH2	14:LE:125:ILE:O	2.51	0.44
16:LG:60:GLU:N	16:LG:60:GLU:OE2	2.50	0.44
21:LM:2:SER:OG	21:LM:3:SER:N	2.51	0.44
22:LN:116:SER:HB3	22:LN:126:TRP:HE1	1.82	0.44
22:LN:429:SER:OG	22:LN:430:THR:N	2.46	0.44
23:LO:61:ILE:HG23	23:LO:70:LEU:HD11	2.00	0.44
23:LO:295:ILE:HG22	23:LO:296:GLN:HG3	2.00	0.44
30:LW:381:LEU:HD12	30:LW:390:LEU:HD12	2.00	0.44
35:SE:34:LYS:HD3	35:SE:34:LYS:HA	1.84	0.44
37:SH:107:ALA:HB1	37:SH:170:VAL:HG21	2.00	0.44
38:SI:889:LEU:HD22	38:SI:922:ILE:HG23	1.98	0.44
41:SM:219:GLU:HB3	47:ST:6:LEU:HD13	2.00	0.44
47:ST:698:ILE:HG12	54:SU:439:LYS:HD2	2.00	0.44
53:8:101:U:O5'	53:8:383:G:N2	2.51	0.44
57:LR:617:ASN:OD1	57:LR:617:ASN:N	2.51	0.44
58:NE:225:GLN:HA	58:NE:228:ILE:HG12	1.98	0.44
59:SB:245:THR:OG1	59:SB:246:GLU:N	2.51	0.44
62:LX:16:ASN:HD21	62:LX:218:PRO:HA	1.81	0.44
62:LX:771:SER:OG	62:LX:772:ASN:N	2.49	0.44
66:6:242:MET:HB3	66:6:245:MET:HE2	2.00	0.44
1:NA:342:THR:HG22	6:L3:119:ILE:HG21	1.99	0.44
4:L0:499:U:H2'	4:L0:500:G:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L2:77:U:H2'	5:L2:78:G:H8	1.83	0.44
7:L4:51:ARG:HH22	7:L4:110:ALA:HA	1.82	0.44
7:L4:102:VAL:N	7:L4:110:ALA:O	2.47	0.44
17:LH:55:TYR:HA	17:LH:62:CYS:HA	1.98	0.44
17:LH:55:TYR:OH	17:LH:466:GLU:OE1	2.31	0.44
17:LH:364:ASN:ND2	17:LH:410:ASN:OD1	2.46	0.44
17:LH:483:LYS:HD3	17:LH:488:LEU:HA	1.98	0.44
18:LJ:38:GLU:N	18:LJ:325:GLY:O	2.45	0.44
18:LJ:449:GLY:O	18:LJ:455:SER:OG	2.36	0.44
21:LM:364:ASN:OD1	21:LM:364:ASN:N	2.49	0.44
23:LO:266:VAL:HG12	23:LO:277:VAL:HA	2.00	0.44
25:LQ:355:LEU:HB3	25:LQ:363:GLU:HB2	1.99	0.44
27:LT:305:ASN:ND2	59:SB:425:ARG:O	2.46	0.44
28:LU:300:VAL:HG22	53:8:-1:G:C6	2.53	0.44
29:LV:20:ASN:OD1	29:LV:20:ASN:N	2.50	0.44
29:LV:182:GLY:HA3	29:LV:199:THR:HA	1.99	0.44
38:SI:893:ASN:HD21	45:SR:98:GLU:HB3	1.83	0.44
44:SQ:56:GLU:O	44:SQ:60:LYS:NZ	2.45	0.44
47:ST:776:ASP:OD1	47:ST:780:LYS:NZ	2.48	0.44
51:NH:780:GLN:H	51:NH:850:PHE:HA	1.83	0.44
53:8:1592:A:H2'	53:8:1593:A:H8	1.82	0.44
57:LR:302:MET:HE2	57:LR:314:ILE:HG23	1.98	0.44
63:L6:115:LYS:HE3	63:L6:115:LYS:HB2	1.84	0.44
66:6:84:ASP:HB3	66:6:87:CYS:HB2	1.99	0.44
5:L2:17:G:H2'	5:L2:18:G:C8	2.52	0.44
11:L9:139:GLN:HB3	66:6:266:ILE:HD11	2.00	0.44
12:LC:94:GLN:HB3	12:LC:102:LYS:HG3	2.00	0.44
16:LG:52:ASP:OD1	16:LG:52:ASP:N	2.51	0.44
17:LH:304:SER:OG	17:LH:344:CYS:O	2.31	0.44
18:LJ:5:ARG:NH1	18:LJ:393:ASN:OD1	2.51	0.44
18:LJ:500:GLU:OE2	18:LJ:503:ARG:NH1	2.51	0.44
21:LM:122:VAL:HA	21:LM:127:ILE:HG12	1.99	0.44
22:LN:57:ILE:HG22	22:LN:340:GLN:HB3	2.00	0.44
22:LN:561:LYS:HD3	22:LN:561:LYS:HA	1.88	0.44
25:LQ:42:ILE:HG12	25:LQ:51:ILE:HB	1.98	0.44
25:LQ:455:GLN:HG2	25:LQ:467:THR:HB	2.00	0.44
29:LV:356:LEU:HD23	29:LV:359:ILE:HD11	1.99	0.44
34:SD:86:VAL:HG11	34:SD:123:ILE:HG21	2.00	0.44
37:SH:108:PRO:HB2	37:SH:174:ILE:HG12	2.00	0.44
37:SH:320:GLU:HA	37:SH:323:ILE:HD12	2.00	0.44
53:8:148:A:N6	53:8:166:C:N3	2.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:8:225:A:H2'	53:8:226:A:H4'	1.99	0.44
53:8:1592:A:H2'	53:8:1593:A:C8	2.53	0.44
53:8:1702:A:N6	53:8:1703:C:O2	2.51	0.44
54:SU:309:ASN:HB3	54:SU:312:ALA:HB3	1.98	0.44
55:LI:228:GLU:O	55:LI:242:CYS:N	2.51	0.44
57:LR:293:VAL:HG12	57:LR:304:LEU:HG	2.00	0.44
62:LX:779:LYS:HA	62:LX:782:ARG:HE	1.83	0.44
65:5:193:ARG:O	65:5:193:ARG:NE	2.49	0.44
5:L2:1:G:N2	53:8:1124:A:H1'	2.33	0.44
8:L5:89:ILE:HD12	8:L5:137:ILE:HD12	2.00	0.44
9:L7:75:THR:O	9:L7:79:ARG:NH1	2.51	0.44
11:L9:78:ARG:HH12	66:6:251:GLU:HG2	1.82	0.44
12:LC:99:GLU:HB2	12:LC:102:LYS:HE3	2.00	0.44
20:LL:253:LEU:HD21	20:LL:301:LEU:HD11	2.00	0.44
25:LQ:452:GLY:O	25:LQ:471:ALA:N	2.51	0.44
25:LQ:588:ILE:O	25:LQ:600:TRP:N	2.46	0.44
29:LV:71:CYS:SG	29:LV:72:MET:N	2.91	0.44
29:LV:250:GLY:HA3	29:LV:271:GLY:HA2	2.00	0.44
34:SD:156:MET:HE2	34:SD:156:MET:HB2	1.84	0.44
47:ST:604:VAL:HG13	47:ST:606:PHE:H	1.82	0.44
53:8:153:G:OP1	63:L6:15:THR:OG1	2.33	0.44
53:8:933:A:H4'	53:8:934:C:H5'	1.99	0.44
53:8:1506:G:H2'	53:8:1507:G:C8	2.53	0.44
57:LR:242:GLN:HE21	57:LR:263:GLY:HA3	1.83	0.44
6:L3:2:SER:OG	54:SU:370:HIS:O	2.36	0.43
7:L4:201:HIS:HB2	7:L4:207:LEU:HG	2.00	0.43
14:LE:30:SER:HA	14:LE:34:ILE:HD11	2.00	0.43
18:LJ:426:LYS:HB2	18:LJ:429:VAL:HG23	1.99	0.43
20:LL:494:ARG:HE	20:LL:498:LEU:HD11	1.83	0.43
21:LM:249:LYS:HE3	21:LM:249:LYS:HB3	1.87	0.43
21:LM:336:LEU:HD22	21:LM:373:ILE:HD13	2.00	0.43
22:LN:67:LEU:HD23	22:LN:81:PRO:HG3	1.99	0.43
22:LN:313:LYS:HD2	22:LN:313:LYS:HA	1.78	0.43
23:LO:261:ALA:HB1	23:LO:279:PHE:HB3	2.00	0.43
24:LP:279:LYS:HA	24:LP:279:LYS:HD2	1.86	0.43
25:LQ:937:ARG:HD2	25:LQ:937:ARG:HA	1.78	0.43
27:LT:931:GLY:N	57:LR:801:GLU:OE2	2.51	0.43
37:SH:290:GLY:HA3	37:SH:293:GLN:HG3	2.00	0.43
38:SI:992:GLU:OE1	53:8:564:G:O2'	2.32	0.43
51:NH:675:GLU:HA	51:NH:702:LYS:HA	1.99	0.43
57:LR:513:LYS:HE2	57:LR:513:LYS:HB3	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L0:189:U:H3	4:L0:209:G:H22	1.66	0.43
4:L0:331:U:H3	23:LO:656:ARG:HH12	1.64	0.43
21:LM:218:ILE:HD12	21:LM:263:VAL:HB	2.00	0.43
21:LM:276:LEU:HD23	21:LM:276:LEU:HA	1.90	0.43
23:LO:516:SER:HB3	23:LO:536:LYS:HD3	1.99	0.43
34:SD:242:ALA:HB3	34:SD:269:ILE:HA	1.99	0.43
37:SH:68:SER:OG	37:SH:69:TYR:N	2.49	0.43
37:SH:156:ARG:HD2	37:SH:198:THR:HG21	2.00	0.43
38:SI:179:SER:OG	38:SI:182:THR:OG1	2.35	0.43
42:SN:41:ASN:OD1	42:SN:41:ASN:N	2.51	0.43
49:SZ:380:TYR:HA	53:8:1220:C:H4'	1.99	0.43
53:8:52:U:H2'	53:8:53:G:C8	2.52	0.43
53:8:154:G:N3	63:L6:56:ASN:ND2	2.67	0.43
53:8:262:U:H2'	53:8:263:C:H4'	2.00	0.43
53:8:406:U:H2'	53:8:407:A:C8	2.53	0.43
53:8:1655:A:H2	53:8:1745:G:H22	1.66	0.43
54:SU:472:HIS:HD1	54:SU:474:HIS:H	1.65	0.43
57:LR:548:LEU:N	57:LR:560:TRP:O	2.49	0.43
57:LR:655:GLU:HA	57:LR:658:LYS:HB2	2.00	0.43
4:L0:82:A:N7	17:LH:256:THR:OG1	2.46	0.43
4:L0:114:G:H2'	4:L0:115:G:H8	1.82	0.43
4:L0:529:A:H2'	4:L0:530:A:C8	2.53	0.43
7:L4:57:ASN:N	7:L4:60:GLU:OE2	2.51	0.43
8:L5:185:ARG:NH2	53:8:1472:C:OP1	2.50	0.43
9:L7:35:LYS:HA	9:L7:38:LEU:HB2	1.98	0.43
12:LC:14:LYS:NZ	53:8:1610:G:N7	2.66	0.43
22:LN:130:THR:HG23	22:LN:132:LEU:H	1.81	0.43
27:LT:30:ILE:HG13	27:LT:380:LEU:HD23	1.99	0.43
28:LU:85:THR:HG21	28:LU:372:VAL:HG21	2.01	0.43
28:LU:114:THR:OG1	28:LU:139:CYS:SG	2.66	0.43
34:SC:253:ILE:HD13	34:SC:253:ILE:HA	1.89	0.43
53:8:164:A:H2'	53:8:165:G:C8	2.54	0.43
53:8:927:C:O2'	53:8:928:U:O4'	2.34	0.43
57:LR:433:HIS:HE1	57:LR:437:VAL:HB	1.83	0.43
62:LX:9:ARG:HH21	62:LX:199:LEU:HD21	1.83	0.43
62:LX:748:ARG:HD3	62:LX:748:ARG:HA	1.80	0.43
65:5:332:ASP:OD1	65:5:332:ASP:N	2.46	0.43
65:5:418:LEU:HD13	65:5:441:SER:HB2	2.01	0.43
5:L2:1:G:H2'	5:L2:2:U:C6	2.53	0.43
11:L9:26:ALA:HA	40:SL:55:TYR:HE2	1.83	0.43
13:LD:59:PRO:HA	13:LD:64:VAL:HG23	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:LN:249:ARG:NH2	22:LN:309:GLN:OE1	2.51	0.43
22:LN:635:GLY:HA3	22:LN:649:TRP:CE2	2.53	0.43
23:LO:147:GLN:HB3	23:LO:166:LYS:HB2	2.00	0.43
25:LQ:668:ASP:OD1	25:LQ:668:ASP:N	2.52	0.43
35:SF:21:LEU:HA	35:SF:24:VAL:HG22	1.99	0.43
36:SG:457:GLU:OE2	36:SG:461:LYS:NZ	2.51	0.43
37:SH:17:PHE:N	38:SI:609:GLU:OE2	2.52	0.43
38:SI:751:TYR:HB2	45:SR:77:ILE:HG22	2.00	0.43
48:SY:229:SER:HB2	48:SY:245:LYS:HB2	1.99	0.43
53:8:1049:U:H2'	53:8:1050:G:C8	2.53	0.43
53:8:1274:C:H2'	53:8:1275:A:C8	2.53	0.43
57:LR:554:ASP:OD1	57:LR:554:ASP:N	2.49	0.43
62:LX:73:ARG:HH22	62:LX:99:SER:HA	1.83	0.43
62:LX:587:GLN:O	62:LX:636:VAL:N	2.48	0.43
66:6:98:ARG:HH22	66:6:101:GLN:HG2	1.83	0.43
66:6:339:SER:O	66:6:345:LYS:NZ	2.51	0.43
7:L4:112:HIS:CD2	7:L4:239:PRO:HG3	2.53	0.43
10:L8:184:LEU:HG	10:L8:189:LEU:HG	1.99	0.43
11:L9:82:ARG:NH1	66:6:323:GLU:OE1	2.49	0.43
15:LF:45:ALA:HA	15:LF:50:ALA:HB3	1.99	0.43
18:LJ:117:LEU:HD23	18:LJ:118:LEU:HB2	2.00	0.43
20:LL:518:ASN:OD1	20:LL:518:ASN:N	2.50	0.43
21:LM:166:ASN:HD21	59:SB:409:THR:HG22	1.83	0.43
21:LM:304:GLN:HA	21:LM:346:LYS:HD2	2.01	0.43
25:LQ:392:THR:HG23	25:LQ:409:ALA:HB1	2.01	0.43
25:LQ:539:VAL:HG22	25:LQ:546:LEU:HD12	2.00	0.43
26:LS:497:ASN:HA	26:LS:500:MET:HE2	2.01	0.43
30:LW:109:LYS:HD3	30:LW:396:THR:HB	2.00	0.43
30:LW:312:VAL:HG21	30:LW:353:PRO:HG2	2.00	0.43
41:SM:241:THR:OG1	41:SM:244:GLY:O	2.34	0.43
42:SN:180:LEU:HA	42:SN:183:ILE:HG22	2.01	0.43
66:6:249:ILE:O	66:6:253:SER:OG	2.31	0.43
4:L0:133:U:H2'	4:L0:134:A:H8	1.84	0.43
7:L4:148:ARG:HH12	53:8:125:U:H5'	1.83	0.43
9:L7:80:GLU:O	9:L7:84:LYS:NZ	2.50	0.43
17:LH:363:ASN:ND2	17:LH:390:PRO:O	2.50	0.43
19:LK:439:LYS:HA	19:LK:439:LYS:HD2	1.83	0.43
20:LL:104:SER:O	20:LL:104:SER:OG	2.33	0.43
21:LM:201:LYS:HE2	21:LM:201:LYS:HB3	1.85	0.43
22:LN:382:VAL:HG11	22:LN:755:ILE:HD13	2.00	0.43
26:LS:512:ASP:OD1	26:LS:512:ASP:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LU:174:ARG:HD2	28:LU:209:LEU:HD21	2.00	0.43
40:SL:16:THR:OG1	40:SL:17:LEU:N	2.49	0.43
42:SN:113:SER:O	42:SN:116:THR:OG1	2.37	0.43
53:8:109:G:O3'	66:6:227:ARG:NH2	2.51	0.43
53:8:878:G:H2'	53:8:879:G:C8	2.53	0.43
62:LX:92:ASP:HB3	62:LX:95:GLU:H	1.83	0.43
62:LX:139:ILE:HG13	62:LX:486:LEU:HD13	2.00	0.43
1:NA:315:GLU:HG2	38:SI:1038:ILE:HG21	2.01	0.43
4:L0:423:C:H2'	4:L0:424:G:H8	1.83	0.43
5:L2:8:U:H2'	5:L2:9:A:C8	2.54	0.43
7:L4:193:GLY:H	7:L4:194:THR:HG23	1.84	0.43
20:LL:80:MET:SD	20:LL:86:TRP:NE1	2.91	0.43
20:LL:302:ASN:HD21	20:LL:314:PHE:HB3	1.84	0.43
25:LQ:175:ASP:HA	25:LQ:191:LEU:HB2	1.99	0.43
25:LQ:189:TRP:HA	25:LQ:196:CYS:HA	2.01	0.43
26:LS:444:ILE:HG22	26:LS:445:ARG:HG2	2.01	0.43
29:LV:104:PHE:HE1	29:LV:114:SER:HB2	1.84	0.43
33:NK:44:LEU:HA	33:NK:79:SER:HA	2.01	0.43
34:SC:242:ALA:HB3	34:SC:269:ILE:HA	1.99	0.43
36:SG:476:THR:HG22	36:SG:491:SER:HA	2.00	0.43
37:SH:292:ASN:OD1	37:SH:292:ASN:N	2.51	0.43
38:SI:108:VAL:HA	38:SI:114:ARG:HB3	2.00	0.43
38:SI:373:ILE:HB	62:LX:6:ILE:HD11	2.01	0.43
41:SM:60:GLN:OE1	58:NE:207:ARG:NH2	2.51	0.43
41:SM:190:ILE:HB	41:SM:223:THR:HA	2.01	0.43
42:SN:231:GLN:N	42:SN:231:GLN:OE1	2.51	0.43
47:ST:444:ASN:OD1	47:ST:444:ASN:N	2.52	0.43
53:8:590:C:H2'	53:8:591:A:C8	2.54	0.43
57:LR:314:ILE:HD13	57:LR:329:VAL:HA	2.00	0.43
57:LR:437:VAL:HA	57:LR:458:SER:HA	2.01	0.43
57:LR:733:ASP:OD1	57:LR:733:ASP:N	2.43	0.43
58:NE:248:LYS:HE2	58:NE:248:LYS:HB2	1.93	0.43
62:LX:857:ASP:OD1	62:LX:857:ASP:N	2.50	0.43
1:NA:341:LEU:HD22	6:L3:116:LEU:HD11	2.00	0.43
1:NA:354:VAL:HG21	41:SM:168:HIS:HB2	2.01	0.43
1:NA:362:THR:HG22	41:SM:234:ARG:HH12	1.84	0.43
4:L0:486:U:H4'	4:L0:487:A:H5''	2.01	0.43
7:L4:202:ASP:OD1	7:L4:202:ASP:N	2.52	0.43
12:LC:39:VAL:HG12	12:LC:41:PRO:HD2	2.00	0.43
12:LC:98:ASP:HA	27:LT:490:GLN:HG3	2.00	0.43
14:LE:12:ASN:OD1	14:LE:12:ASN:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:LF:20:ARG:HG2	15:LF:76:TYR:HE2	1.84	0.43
18:LJ:226:ILE:HG23	18:LJ:239:LEU:HD11	1.99	0.43
18:LJ:494:GLU:HG3	20:LL:540:LEU:HD13	2.01	0.43
21:LM:382:LEU:HD23	21:LM:382:LEU:HA	1.90	0.43
23:LO:192:ASP:HB2	23:LO:212:ASP:HB3	2.00	0.43
25:LQ:449:THR:OG1	25:LQ:451:ASN:O	2.37	0.43
29:LV:171:ARG:HG2	65:5:468:VAL:HA	2.00	0.43
36:SG:495:SER:HB2	36:SG:513:GLU:HG3	2.00	0.43
37:SH:70:THR:HG23	37:SH:72:THR:H	1.84	0.43
39:SK:169:ASP:OD1	39:SK:169:ASP:N	2.51	0.43
49:SZ:379:LYS:O	53:8:1220:C:O2'	2.32	0.43
57:LR:77:THR:HG21	57:LR:117:LEU:HG	2.00	0.43
58:NE:247:VAL:HA	58:NE:250:ILE:HB	2.01	0.43
62:LX:392:ILE:O	62:LX:546:TYR:OH	2.34	0.43
5:L2:17:G:H2'	5:L2:18:G:H8	1.84	0.43
5:L2:47:G:O2'	40:SL:15:ARG:NH2	2.52	0.43
17:LH:43:ASN:OD1	17:LH:43:ASN:N	2.52	0.43
22:LN:744:VAL:HG13	22:LN:752:LEU:HD11	2.00	0.43
23:LO:211:LYS:HE3	23:LO:262:LYS:HD3	1.99	0.43
27:LT:169:SER:HG	27:LT:171:GLN:HE21	1.64	0.43
38:SI:1021:LEU:HA	38:SI:1026:LYS:HG2	2.01	0.43
39:SK:41:MET:HE1	39:SK:242:CYS:HA	2.00	0.43
40:SL:78:LYS:HE3	40:SL:177:GLY:H	1.83	0.43
41:SM:107:ILE:HD13	41:SM:107:ILE:HA	1.90	0.43
53:8:1499:G:H1	53:8:1508:U:H3	1.66	0.43
53:8:1694:A:H2'	53:8:1695:G:C5	2.54	0.43
62:LY:506:GLY:HA3	65:5:489:GLN:HB2	2.01	0.43
63:L6:1:MET:HG2	63:L6:24:ILE:HD13	2.00	0.43
65:5:497:LEU:HB3	65:5:500:GLN:HB3	1.99	0.43
2:SA:194:ARG:HD2	59:SB:169:LEU:HD12	2.01	0.43
4:L0:397:A:H2'	4:L0:398:A:C8	2.54	0.43
12:LC:8:GLN:HE21	12:LC:10:PHE:HE1	1.67	0.43
23:LO:3:SER:HB2	23:LO:612:LEU:HD13	2.01	0.43
23:LO:559:ILE:HG23	23:LO:598:ASN:HD22	1.83	0.43
25:LQ:7:ARG:HH21	25:LQ:71:ALA:HA	1.84	0.43
30:LW:109:LYS:HB2	30:LW:109:LYS:HE2	1.79	0.43
30:LW:346:LYS:HZ3	30:LW:351:SER:HG	1.63	0.43
35:SF:17:THR:HG23	35:SF:81:VAL:HG12	2.01	0.43
47:ST:577:VAL:HG23	47:ST:585:PRO:HG3	2.00	0.43
53:8:868:G:H21	64:NF:90:TYR:H	1.66	0.43
62:LX:529:VAL:O	62:LX:533:PHE:N	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:LX:920:MET:HE3	62:LX:920:MET:H	1.84	0.43
4:L0:295:A:OP2	27:LT:385:GLN:NE2	2.45	0.42
6:L3:63:GLN:HA	6:L3:66:LEU:HB2	2.01	0.42
17:LH:437:THR:HG21	17:LH:706:HIS:HB3	2.00	0.42
17:LH:451:PHE:HB2	17:LH:458:GLN:HB3	2.01	0.42
18:LJ:34:GLN:HE21	18:LJ:329:ILE:HD12	1.83	0.42
21:LM:103:LEU:HD23	21:LM:103:LEU:HA	1.92	0.42
21:LM:250:SER:OG	21:LM:253:CYS:SG	2.69	0.42
23:LO:477:SER:N	23:LO:491:ALA:O	2.41	0.42
23:LO:746:ASN:OD1	23:LO:777:ARG:NE	2.49	0.42
25:LQ:270:SER:OG	25:LQ:286:ILE:O	2.34	0.42
25:LQ:287:ARG:NH1	25:LQ:323:SER:O	2.51	0.42
25:LQ:673:VAL:HG22	25:LQ:683:ILE:HG12	2.00	0.42
26:LS:429:TYR:CD1	26:LS:448:LYS:HE2	2.54	0.42
26:LS:431:GLU:HB3	26:LS:446:ARG:HH21	1.83	0.42
27:LT:100:ILE:HD13	27:LT:149:TYR:HB2	2.01	0.42
31:LZ:75:GLU:HG3	31:LZ:94:ILE:HG12	2.00	0.42
33:NK:166:VAL:HA	33:NK:171:VAL:HA	2.01	0.42
34:SD:121:LYS:HG2	34:SD:143:VAL:HG11	2.01	0.42
35:SF:73:ASP:OD1	35:SF:73:ASP:N	2.52	0.42
36:SG:363:ASP:N	36:SG:363:ASP:OD1	2.43	0.42
36:SG:501:ILE:HG22	36:SG:508:PHE:HB3	2.01	0.42
53:8:22:A:O2'	53:8:23:G:O4'	2.37	0.42
55:LI:69:ILE:HA	55:LI:79:ASN:HA	2.01	0.42
57:LR:175:TRP:HA	57:LR:182:CYS:HA	2.01	0.42
57:LR:403:ILE:HD12	57:LR:415:TRP:HB2	2.00	0.42
57:LR:510:SER:OG	57:LR:514:THR:OG1	2.31	0.42
57:LR:589:GLN:HA	57:LR:603:ASP:HA	2.01	0.42
58:NE:230:LYS:HD3	58:NE:230:LYS:HA	1.79	0.42
62:LX:21:LYS:HB3	62:LX:477:ALA:HB2	2.01	0.42
2:SA:146:ASP:N	2:SA:146:ASP:OD1	2.48	0.42
5:L2:30:A:C5	28:LU:57:PRO:HG2	2.55	0.42
9:L7:85:PHE:HB3	9:L7:88:ARG:HB2	2.00	0.42
17:LH:868:ASN:OD1	17:LH:868:ASN:N	2.49	0.42
22:LN:262:ILE:HD11	22:LN:283:VAL:HG11	2.00	0.42
22:LN:580:LYS:HG3	22:LN:596:MET:HB2	2.00	0.42
23:LO:336:SER:HA	27:LT:745:LYS:HA	2.00	0.42
24:LP:286:ILE:HD13	24:LP:286:ILE:HA	1.93	0.42
28:LU:143:LYS:HE2	28:LU:143:LYS:HB2	1.84	0.42
34:SC:272:LYS:HA	34:SC:313:HIS:HD2	1.84	0.42
37:SH:143:LYS:HD2	37:SH:143:LYS:HA	1.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:SQ:79:LYS:HA	44:SQ:79:LYS:HD2	1.80	0.42
47:ST:607:THR:OG1	47:ST:608:LYS:N	2.53	0.42
53:8:487:G:H2'	53:8:488:G:C8	2.54	0.42
53:8:939:A:H61	53:8:975:C:H1'	1.84	0.42
53:8:1130:G:H3'	53:8:1131:A:H4'	2.00	0.42
54:SU:130:GLU:HG2	54:SU:134:PHE:HB2	2.01	0.42
55:LI:563:LEU:HD13	55:LI:598:GLU:HG3	2.02	0.42
57:LR:24:THR:HG21	57:LR:68:LYS:HD3	2.01	0.42
57:LR:294:LEU:HB2	57:LR:303:PHE:HB2	2.01	0.42
62:LX:86:ARG:HH21	62:LX:91:MET:HA	1.84	0.42
62:LX:653:ALA:HA	62:LX:656:LEU:HB2	2.00	0.42
2:SA:393:SER:N	35:SF:62:GLU:OE2	2.52	0.42
3:NB:509:ARG:NE	53:8:1504:G:OP1	2.52	0.42
4:L0:409:C:H5''	38:SI:1089:GLN:HE21	1.85	0.42
13:LD:84:ILE:HG12	13:LD:111:VAL:HB	2.01	0.42
17:LH:449:LEU:N	17:LH:460:PHE:O	2.52	0.42
25:LQ:822:MET:HE3	25:LQ:822:MET:HB2	1.81	0.42
26:LS:229:PRO:HA	26:LS:230:PRO:HD3	1.91	0.42
26:LS:571:SER:OG	26:LS:575:GLY:N	2.52	0.42
27:LT:141:LYS:NZ	27:LT:142:LYS:O	2.45	0.42
28:LU:2:LYS:HZ2	30:LW:77:GLU:HG3	1.83	0.42
28:LU:230:ASN:HB2	28:LU:274:ALA:HB2	2.01	0.42
29:LV:6:THR:HG22	29:LV:12:SER:HA	2.00	0.42
29:LV:101:ASN:HA	29:LV:118:GLN:HG3	2.00	0.42
44:SQ:119:ARG:HG2	44:SQ:174:LEU:HD22	2.01	0.42
57:LR:228:LYS:HD2	57:LR:228:LYS:HA	1.78	0.42
1:NA:480:GLN:HG3	1:NA:482:LEU:H	1.83	0.42
2:SA:381:ASN:O	2:SA:384:SER:OG	2.34	0.42
4:L0:210:U:H2'	4:L0:211:G:C8	2.54	0.42
11:L9:120:LYS:HB2	11:L9:120:LYS:HE3	1.80	0.42
22:LN:116:SER:OG	22:LN:117:ILE:N	2.53	0.42
23:LO:522:SER:HB3	23:LO:583:ILE:HG22	2.02	0.42
27:LT:428:GLU:OE2	27:LT:452:ARG:NH1	2.52	0.42
29:LV:101:ASN:OD1	29:LV:118:GLN:NE2	2.51	0.42
38:SI:284:PRO:HD3	38:SI:779:ARG:HH22	1.84	0.42
38:SI:371:VAL:HG13	62:LX:6:ILE:HD12	2.01	0.42
41:SM:268:ASN:HD22	41:SM:271:ALA:HB2	1.83	0.42
44:SQ:75:LYS:NZ	44:SQ:76:LYS:O	2.51	0.42
44:SQ:130:LEU:HA	44:SQ:187:PHE:HZ	1.84	0.42
47:ST:419:LYS:HE3	47:ST:419:LYS:HB2	1.75	0.42
53:8:443:C:O2'	53:8:525:A:N1	2.47	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:LX:69:HIS:CE1	62:LX:71:LYS:HB2	2.53	0.42
14:LE:117:ARG:O	14:LE:120:HIS:ND1	2.51	0.42
21:LM:175:THR:OG1	21:LM:176:ALA:N	2.52	0.42
22:LN:111:SER:HA	22:LN:524:LYS:HA	2.01	0.42
22:LN:325:ASN:OD1	22:LN:325:ASN:N	2.50	0.42
23:LO:99:CYS:HA	23:LO:115:SER:HA	2.01	0.42
23:LO:335:GLU:O	25:LQ:924:TYR:OH	2.37	0.42
23:LO:478:CYS:SG	23:LO:479:LEU:N	2.93	0.42
24:LP:169:GLN:HE22	46:SS:338:LEU:HD22	1.83	0.42
27:LT:482:GLY:HA2	27:LT:505:VAL:HG23	2.01	0.42
27:LT:930:MET:HA	27:LT:933:ALA:HB3	2.02	0.42
29:LV:59:SER:OG	29:LV:74:THR:OG1	2.28	0.42
29:LV:352:TRP:CD1	29:LV:352:TRP:H	2.38	0.42
37:SH:53:LEU:HD22	37:SH:65:ILE:HD13	2.02	0.42
48:SY:223:GLU:HA	48:SY:226:LYS:HE3	2.02	0.42
59:SB:201:ASP:HB3	59:SB:204:ALA:HB3	2.02	0.42
59:SB:218:ALA:O	59:SB:236:LYS:NZ	2.46	0.42
62:LX:202:ASP:OD2	62:LX:206:ASN:ND2	2.53	0.42
65:5:290:ARG:NH1	66:6:101:GLN:HE21	2.17	0.42
11:L9:25:ASP:HA	11:L9:28:LEU:HB3	2.00	0.42
11:L9:80:LEU:HA	11:L9:83:VAL:HG22	2.00	0.42
22:LN:207:ASP:HB3	22:LN:209:ARG:HE	1.84	0.42
22:LN:481:ILE:HB	22:LN:485:LYS:HB3	2.00	0.42
23:LO:221:THR:OG1	23:LO:222:LYS:N	2.48	0.42
24:LP:115:ASN:ND2	44:SQ:70:ASP:OD1	2.53	0.42
26:LS:234:ASP:OD2	26:LS:234:ASP:N	2.41	0.42
27:LT:579:ARG:NE	27:LT:614:LEU:O	2.52	0.42
34:SD:177:SER:OG	34:SD:202:ARG:NH1	2.53	0.42
37:SH:138:MET:HG2	37:SH:141:MET:HE1	2.02	0.42
38:SI:853:ARG:HH21	38:SI:1020:SER:HB3	1.85	0.42
39:SJ:136:ARG:NH2	53:8:1196:A:N3	2.58	0.42
39:SK:51:GLU:OE2	39:SK:51:GLU:N	2.52	0.42
53:8:1049:U:H2'	53:8:1050:G:H8	1.84	0.42
62:LX:516:PHE:HD1	62:LX:711:LYS:HA	1.85	0.42
2:SA:218:LYS:HA	2:SA:218:LYS:HD2	1.65	0.42
9:L7:8:ILE:HD12	9:L7:8:ILE:HG23	1.85	0.42
10:L8:26:LYS:HE3	10:L8:26:LYS:HB3	1.82	0.42
11:L9:68:LYS:HB2	11:L9:68:LYS:HE2	1.84	0.42
18:LJ:54:ASP:OD2	18:LJ:111:TYR:OH	2.33	0.42
19:LK:471:LYS:HZ2	19:LK:474:HIS:H	1.67	0.42
20:LL:85:ILE:HB	20:LL:99:PHE:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:LN:422:LEU:HD13	22:LN:444:ARG:HH22	1.83	0.42
25:LQ:332:ILE:HG12	25:LQ:379:PRO:HG3	2.01	0.42
25:LQ:931:SER:O	25:LQ:936:LYS:NZ	2.45	0.42
26:LS:496:ARG:HA	26:LS:496:ARG:HD2	1.86	0.42
36:SG:310:ASN:N	36:SG:310:ASN:OD1	2.52	0.42
36:SG:481:ILE:H	36:SG:481:ILE:HD12	1.84	0.42
39:SK:148:LEU:HD11	53:8:1575:G:H21	1.84	0.42
41:SM:285:ASN:OD1	41:SM:285:ASN:N	2.48	0.42
44:SQ:177:LEU:HD12	44:SQ:177:LEU:HA	1.93	0.42
53:8:126:A:N6	53:8:290:G:H1	2.17	0.42
53:8:399:A:H1'	53:8:401:A:H5'	2.02	0.42
57:LR:453:PHE:HB2	57:LR:465:LYS:HD2	2.01	0.42
62:LX:69:HIS:HE1	62:LX:71:LYS:HB2	1.84	0.42
14:LE:55:ASP:OD2	14:LE:57:ARG:NH1	2.53	0.42
17:LH:308:ASP:OD1	17:LH:308:ASP:N	2.46	0.42
17:LH:603:ASN:O	55:LI:592:ARG:NH2	2.52	0.42
23:LO:172:ILE:HD11	23:LO:206:ILE:HG12	2.01	0.42
23:LO:431:ILE:HG21	23:LO:452:ASN:HB2	2.02	0.42
24:LP:388:UNK:O	24:LP:392:UNK:N	2.53	0.42
25:LQ:626:GLN:NE2	25:LQ:668:ASP:O	2.44	0.42
34:SC:165:ALA:HB3	34:SC:168:LYS:HB2	2.01	0.42
36:SG:442:ILE:HD12	36:SG:470:LEU:HD22	2.01	0.42
38:SI:966:ILE:HD11	38:SI:1001:VAL:HB	2.01	0.42
38:SI:1153:ASP:HA	38:SI:1156:LYS:HE3	2.00	0.42
42:SN:35:ASP:OD1	42:SN:35:ASP:N	2.43	0.42
53:8:199:G:N3	53:8:201:G:N2	2.68	0.42
53:8:362:G:H2'	53:8:363:G:C8	2.55	0.42
56:ND:181:LEU:HD23	56:ND:181:LEU:HA	1.89	0.42
57:LR:63:GLU:O	57:LR:81:GLN:N	2.53	0.42
59:SB:157:ASP:HA	59:SB:279:ARG:HH21	1.85	0.42
62:LX:185:ASN:OD1	62:LX:185:ASN:N	2.53	0.42
2:SA:389:ILE:HG22	35:SF:62:GLU:HB3	2.02	0.42
18:LJ:499:LYS:HB3	18:LJ:503:ARG:HH12	1.84	0.42
22:LN:645:ARG:HD3	22:LN:656:ARG:HH22	1.84	0.42
23:LO:69:LEU:HD23	23:LO:69:LEU:HA	1.92	0.42
23:LO:317:LEU:HD12	23:LO:332:TRP:HB3	2.02	0.42
25:LQ:279:LYS:HE2	25:LQ:279:LYS:HB2	1.91	0.42
27:LT:90:VAL:HG13	27:LT:101:TYR:HB2	2.01	0.42
27:LT:316:ASP:OD1	27:LT:316:ASP:N	2.51	0.42
38:SI:150:MET:HA	38:SI:153:MET:HB3	2.00	0.42
39:SJ:52:THR:HG21	39:SJ:146:HIS:CE1	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:SK:72:ASP:OD2	39:SK:73:HIS:ND1	2.41	0.42
41:SM:109:LEU:HD12	41:SM:109:LEU:HA	1.90	0.42
53:8:322:G:C8	65:5:460:LYS:HE3	2.54	0.42
55:LI:562:PRO:HB2	55:LI:565:GLU:HB2	2.01	0.42
57:LR:16:TYR:OH	57:LR:21:ALA:O	2.31	0.42
57:LR:43:ILE:HG22	57:LR:52:ILE:HA	2.02	0.42
4:L0:234:A:C5	18:LJ:360:MET:HE1	2.54	0.42
4:L0:415:U:H2'	4:L0:416:A:H8	1.85	0.42
15:LF:20:ARG:HG2	15:LF:76:TYR:CE2	2.55	0.42
17:LH:378:ASP:O	26:LS:344:ARG:NH1	2.53	0.42
18:LJ:492:ARG:HH21	18:LJ:495:ILE:HD12	1.85	0.42
22:LN:631:GLU:HG2	22:LN:651:ALA:HB3	2.02	0.42
28:LU:174:ARG:NH2	28:LU:206:VAL:O	2.49	0.42
28:LU:448:ARG:HE	53:8:1050:G:H21	1.68	0.42
30:LW:254:GLY:HA2	30:LW:277:VAL:HG23	2.02	0.42
35:SE:111:LYS:HA	35:SE:111:LYS:HD2	1.78	0.42
36:SG:257:ASP:HB2	36:SG:259:LYS:HE2	2.02	0.42
37:SH:231:ARG:HA	37:SH:231:ARG:HD3	1.90	0.42
42:SN:44:LYS:HD2	42:SN:236:LYS:HB2	2.00	0.42
44:SQ:117:VAL:HG23	44:SQ:149:ILE:HD11	2.01	0.42
53:8:243:G:H2'	53:8:244:A:H8	1.84	0.42
53:8:591:A:H2'	53:8:592:A:C8	2.55	0.42
53:8:1659:A:H2'	53:8:1660:A:C8	2.54	0.42
53:8:1661:U:H2'	53:8:1662:G:H8	1.85	0.42
54:SU:227:LYS:HA	54:SU:227:LYS:HD2	1.75	0.42
58:NE:199:ASP:N	58:NE:199:ASP:OD1	2.48	0.42
62:LX:18:VAL:HG11	62:LX:44:MET:HB2	2.00	0.42
62:LX:906:SER:OG	62:LX:907:ASN:N	2.53	0.42
3:NB:575:LYS:NZ	53:8:490:C:OP1	2.44	0.41
4:L0:264:C:H2'	4:L0:265:A:C8	2.55	0.41
5:L2:18:G:H2'	5:L2:19:A:H8	1.85	0.41
9:L7:49:ILE:HG12	9:L7:172:VAL:HG12	2.01	0.41
17:LH:60:ARG:HB2	20:LL:341:ALA:HB1	2.02	0.41
18:LJ:109:ASP:OD1	18:LJ:109:ASP:N	2.51	0.41
19:LK:447:ASN:O	55:LI:671:ARG:NH2	2.51	0.41
20:LL:110:ILE:HD11	20:LL:117:LEU:HD21	2.02	0.41
20:LL:212:LEU:HB2	20:LL:226:LEU:HB2	2.02	0.41
23:LO:30:LEU:HD22	23:LO:39:VAL:HG22	2.02	0.41
25:LQ:553:ASN:HD22	25:LQ:573:LYS:H	1.66	0.41
25:LQ:659:GLU:O	25:LQ:677:HIS:N	2.49	0.41
28:LU:75:LYS:H	28:LU:75:LYS:HG2	1.70	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:LV:144:LEU:HB2	29:LV:155:VAL:HG22	2.02	0.41
36:SG:430:LYS:H	66:6:254:ASP:HB2	1.85	0.41
36:SG:523:LYS:HD2	36:SG:523:LYS:HA	1.85	0.41
38:SI:137:LEU:HD22	38:SI:232:PHE:HE1	1.84	0.41
38:SI:257:LEU:HA	38:SI:260:THR:HG22	2.01	0.41
42:SN:227:SER:OG	42:SN:228:LYS:N	2.52	0.41
47:ST:753:LYS:HA	47:ST:753:LYS:HD2	1.79	0.41
53:8:329:G:H2'	53:8:330:G:C8	2.55	0.41
53:8:523:G:N2	53:8:529:A:H62	2.17	0.41
53:8:1690:G:H2'	53:8:1691:A:H8	1.84	0.41
62:LX:197:ASN:OD1	62:LX:197:ASN:N	2.52	0.41
3:NB:560:ASN:ND2	53:8:477:A:OP1	2.53	0.41
8:L5:133:VAL:HG22	8:L5:198:LEU:HD13	2.01	0.41
12:LC:94:GLN:HE22	31:LZ:182:PHE:HB3	1.84	0.41
14:LE:39:GLN:O	14:LE:43:LYS:N	2.46	0.41
17:LH:491:GLN:H	17:LH:491:GLN:HG2	1.65	0.41
17:LH:698:VAL:HA	17:LH:701:VAL:HG22	2.01	0.41
19:LK:506:LEU:HB3	55:LI:655:LEU:HD21	2.02	0.41
20:LL:150:LYS:HD2	20:LL:150:LYS:HA	1.89	0.41
22:LN:741:LEU:HA	22:LN:756:GLU:HA	2.02	0.41
27:LT:932:VAL:HG22	57:LR:808:TYR:HB2	2.02	0.41
28:LU:195:ALA:HB2	28:LU:203:LEU:HD12	2.01	0.41
30:LW:46:LEU:HD13	46:SS:859:ARG:HH12	1.84	0.41
30:LW:123:THR:OG1	30:LW:140:ARG:NH2	2.53	0.41
37:SH:125:HIS:NE2	37:SH:263:ASP:OD1	2.45	0.41
38:SI:140:LEU:HD11	38:SI:152:THR:HB	2.01	0.41
38:SI:1135:ARG:HH11	53:8:494:U:H3'	1.85	0.41
40:SL:18:ASN:HD22	40:SL:21:LYS:HD2	1.84	0.41
40:SL:67:ILE:HG23	40:SL:71:PHE:HD2	1.85	0.41
41:SM:288:ASP:OD1	41:SM:288:ASP:N	2.51	0.41
43:SO:242:MET:HE2	43:SO:266:VAL:HG11	2.02	0.41
53:8:972:G:H2'	53:8:973:A:H8	1.85	0.41
53:8:1672:G:H2'	53:8:1673:G:C8	2.55	0.41
54:SU:341:LEU:HD23	54:SU:341:LEU:HA	1.93	0.41
55:LI:68:PRO:O	55:LI:80:ALA:N	2.50	0.41
62:LX:916:ILE:HA	62:LX:919:LYS:HD2	2.02	0.41
65:5:458:ALA:HB2	65:5:463:LYS:HE3	2.02	0.41
1:NA:345:LEU:HD11	38:SI:961:PHE:HZ	1.85	0.41
5:L2:63:C:H2'	5:L2:64:A:H8	1.85	0.41
7:L4:178:GLY:O	7:L4:231:GLN:NE2	2.49	0.41
8:L5:79:ASN:OD1	53:8:1583:A:O2'	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:L7:123:ASP:HA	9:L7:126:LEU:HG	2.02	0.41
9:L7:163:ASP:HA	9:L7:166:LEU:HD23	2.02	0.41
10:L8:195:ARG:NH2	13:LD:10:GLU:O	2.54	0.41
12:LC:13:LYS:HD2	12:LC:13:LYS:HA	1.89	0.41
17:LH:168:LEU:HD23	17:LH:168:LEU:HA	1.94	0.41
17:LH:592:SER:O	17:LH:592:SER:OG	2.31	0.41
22:LN:71:ARG:HB2	22:LN:75:ASN:HB2	2.02	0.41
23:LO:538:GLN:HG3	23:LO:554:ASP:HA	2.01	0.41
25:LQ:656:HIS:CE1	25:LQ:660:VAL:HG22	2.55	0.41
27:LT:293:GLU:OE1	27:LT:293:GLU:N	2.52	0.41
28:LU:48:THR:HA	28:LU:51:GLU:HG2	2.02	0.41
29:LV:158:SER:H	29:LV:183:VAL:HG12	1.86	0.41
34:SC:272:LYS:HG2	34:SC:275:CYS:H	1.85	0.41
39:SJ:97:LEU:HD23	39:SJ:97:LEU:HA	1.94	0.41
39:SJ:115:GLN:HB3	39:SJ:121:LEU:HD13	2.02	0.41
39:SJ:229:ASN:OD1	39:SJ:229:ASN:N	2.53	0.41
51:NH:1098:PHE:H	51:NH:1184:GLY:HA3	1.84	0.41
53:8:1208:A:N6	53:8:1454:G:C6	2.88	0.41
57:LR:548:LEU:O	57:LR:560:TRP:N	2.44	0.41
63:L6:102:VAL:HG23	63:L6:106:LEU:HG	2.02	0.41
4:L0:145:A:H2'	4:L0:146:G:C8	2.54	0.41
12:LC:26:LYS:H	12:LC:26:LYS:HG2	1.73	0.41
17:LH:730:ASP:HB3	17:LH:734:VAL:HG22	2.02	0.41
17:LH:847:ASP:N	17:LH:847:ASP:OD1	2.53	0.41
21:LM:160:LEU:HD23	59:SB:412:VAL:HG11	2.02	0.41
22:LN:474:SER:OG	22:LN:475:THR:N	2.52	0.41
23:LO:11:LEU:HD11	23:LO:372:TRP:HB3	2.03	0.41
25:LQ:220:THR:HB	25:LQ:259:ILE:HD11	2.02	0.41
27:LT:417:LEU:HG	27:LT:432:THR:HG22	2.01	0.41
29:LV:80:GLN:HB3	29:LV:82:HIS:CD2	2.56	0.41
31:LZ:135:HIS:HB3	31:LZ:166:ILE:HG21	2.02	0.41
34:SD:244:VAL:HG11	34:SD:252:ILE:HG21	2.02	0.41
35:SF:24:VAL:HG12	35:SF:102:ILE:HD11	2.03	0.41
36:SG:410:ASP:OD1	36:SG:410:ASP:N	2.53	0.41
37:SH:133:ILE:HG23	37:SH:137:LEU:HD12	2.03	0.41
63:L6:3:LEU:HD12	63:L6:111:LEU:HD11	2.01	0.41
2:SA:6:TYR:HE1	2:SA:19:LYS:HD2	1.86	0.41
2:SA:302:ASN:OD1	2:SA:401:GLY:N	2.53	0.41
4:L0:89:C:H5''	4:L0:90:G:H5'	2.02	0.41
4:L0:192:G:H2'	4:L0:193:G:C8	2.56	0.41
9:L7:45:SER:OG	9:L7:47:ARG:NH1	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:L7:165:LYS:HE2	9:L7:169:PHE:HZ	1.85	0.41
13:LD:90:TYR:O	13:LD:92:HIS:ND1	2.54	0.41
17:LH:648:LYS:HE2	17:LH:648:LYS:HB2	1.88	0.41
18:LJ:262:GLU:HG3	18:LJ:270:SER:HB3	2.02	0.41
21:LM:316:PRO:HD2	21:LM:319:ILE:HD12	2.03	0.41
22:LN:143:VAL:HB	56:ND:198:ILE:HD13	2.02	0.41
23:LO:641:LEU:HD12	23:LO:641:LEU:HA	1.93	0.41
23:LO:728:GLU:HA	23:LO:731:ARG:HD2	2.01	0.41
25:LQ:142:ASP:OD1	25:LQ:142:ASP:N	2.39	0.41
25:LQ:676:SER:OG	25:LQ:678:ASP:OD1	2.27	0.41
26:LS:251:ILE:HG12	26:LS:584:GLY:HA2	2.03	0.41
28:LU:233:ASP:HB3	28:LU:249:LEU:HB2	2.01	0.41
28:LU:267:ILE:HG22	28:LU:279:THR:HG22	2.03	0.41
29:LV:80:GLN:HB3	29:LV:82:HIS:HD2	1.85	0.41
30:LW:203:TYR:HE2	30:LW:433:LEU:HA	1.85	0.41
34:SC:291:GLN:HE21	40:SL:128:LEU:HB2	1.85	0.41
34:SD:231:ARG:HB3	34:SD:232:MET:HE2	2.03	0.41
38:SI:98:LEU:HB2	38:SI:101:ILE:HD11	2.02	0.41
38:SI:841:THR:HG22	38:SI:860:TYR:H	1.84	0.41
39:SJ:46:ALA:HA	39:SJ:115:GLN:HG2	2.01	0.41
40:SL:185:LEU:HD23	40:SL:186:PRO:HD2	2.02	0.41
46:SS:837:LYS:HD3	46:SS:837:LYS:HA	1.89	0.41
53:8:415:C:OP1	62:LX:70:ARG:NH1	2.52	0.41
53:8:1131:A:O2'	53:8:1136:U:O4	2.34	0.41
54:SU:130:GLU:HB3	54:SU:144:PRO:HG3	2.02	0.41
54:SU:136:SER:O	54:SU:136:SER:OG	2.36	0.41
55:LI:608:GLN:HA	55:LI:611:ILE:HG12	2.03	0.41
57:LR:513:LYS:NZ	57:LR:532:HIS:O	2.52	0.41
62:LX:15:ARG:HH21	62:LX:47:ALA:HB2	1.84	0.41
1:NA:437:ILE:HD11	31:LZ:61:LEU:HG	2.03	0.41
4:L0:68:U:O4	17:LH:422:LYS:NZ	2.53	0.41
4:L0:96:C:O2	4:L0:155:A:O2'	2.37	0.41
7:L4:69:HIS:HD2	15:LF:17:LEU:HB2	1.85	0.41
9:L7:81:LEU:HD23	9:L7:81:LEU:HA	1.87	0.41
17:LH:96:ILE:HG12	17:LH:108:THR:HG21	2.02	0.41
22:LN:497:ILE:HD11	22:LN:555:LEU:HD13	2.02	0.41
26:LS:154:LYS:HB3	26:LS:154:LYS:HE2	1.83	0.41
26:LS:247:SER:OG	26:LS:248:HIS:N	2.54	0.41
27:LT:474:PHE:HE1	27:LT:495:ARG:HG3	1.86	0.41
38:SI:54:LEU:HD23	45:SR:50:LYS:HB2	2.03	0.41
38:SI:568:ARG:HA	38:SI:568:ARG:HD3	1.80	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:SI:1123:LYS:HE2	38:SI:1123:LYS:HB2	1.91	0.41
39:SJ:152:SER:O	39:SJ:155:SER:OG	2.28	0.41
44:SQ:60:LYS:H	44:SQ:60:LYS:HG2	1.70	0.41
45:SR:58:GLY:HA3	45:SR:69:ARG:HA	2.02	0.41
47:ST:267:UNK:O	47:ST:271:UNK:N	2.53	0.41
53:8:140:A:N9	63:L6:184:LEU:N	2.69	0.41
53:8:144:U:H2'	53:8:145:A:H4'	2.02	0.41
53:8:890:C:H2'	53:8:891:A:C8	2.55	0.41
55:LI:170:LYS:HA	55:LI:177:SER:HA	2.03	0.41
55:LI:248:LEU:HA	55:LI:264:SER:HA	2.02	0.41
59:SB:153:LYS:HE3	59:SB:378:GLU:HB2	2.02	0.41
1:NA:357:ILE:HD13	41:SM:234:ARG:HH21	1.86	0.41
2:SA:180:LEU:HD13	59:SB:183:ARG:HG2	2.03	0.41
2:SA:388:ARG:HB3	35:SF:63:ILE:HA	2.02	0.41
4:L0:411:A:H2'	4:L0:412:A:C8	2.56	0.41
4:L0:489:G:H22	24:LP:125:SER:H	1.69	0.41
10:L8:32:GLN:HE22	10:L8:34:ALA:HB2	1.84	0.41
17:LH:31:ASN:OD1	17:LH:31:ASN:N	2.53	0.41
17:LH:505:GLN:O	17:LH:533:THR:OG1	2.33	0.41
20:LL:20:VAL:HG12	20:LL:29:VAL:HG22	2.03	0.41
22:LN:287:THR:HG21	22:LN:337:CYS:HA	2.03	0.41
23:LO:557:LYS:HD3	23:LO:557:LYS:HA	1.88	0.41
26:LS:150:TYR:HE1	30:LW:80:LEU:HA	1.86	0.41
26:LS:529:ILE:HD12	26:LS:591:LEU:HD13	2.02	0.41
27:LT:184:THR:OG1	27:LT:187:ASN:OD1	2.32	0.41
28:LU:255:THR:OG1	28:LU:256:GLN:N	2.53	0.41
28:LU:401:LYS:HE3	28:LU:401:LYS:HB2	1.79	0.41
29:LV:81:ILE:HD12	29:LV:81:ILE:HA	1.96	0.41
30:LW:148:LEU:HD23	30:LW:148:LEU:HA	1.96	0.41
30:LW:182:THR:HG22	40:SL:15:ARG:HG2	2.02	0.41
30:LW:204:LEU:HD12	30:LW:204:LEU:HA	1.93	0.41
30:LW:384:VAL:HA	30:LW:385:PRO:HD3	1.92	0.41
38:SI:776:GLN:HA	38:SI:780:ILE:HG22	2.01	0.41
46:SS:277:ARG:HA	46:SS:280:GLN:HG2	2.03	0.41
48:SY:125:LEU:HD12	48:SY:125:LEU:HA	1.93	0.41
53:8:283:U:O2'	53:8:284:G:OP1	2.38	0.41
53:8:999:U:N3	53:8:1002:G:OP1	2.42	0.41
54:SU:383:LEU:O	54:SU:387:THR:OG1	2.28	0.41
54:SU:504:ASP:OD1	54:SU:504:ASP:N	2.51	0.41
62:LY:744:PRO:HA	62:LY:762:MET:HA	2.03	0.41
62:LX:4:LYS:NZ	62:LX:5:ALA:O	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:LX:132:PRO:HA	62:LX:135:LEU:HD12	2.02	0.41
65:5:406:TYR:O	66:6:82:ARG:NH2	2.54	0.41
65:5:470:ASP:OD1	65:5:471:PRO:HD3	2.20	0.41
2:SA:140:LYS:NZ	4:L0:483:U:O4	2.48	0.41
2:SA:324:ASN:HA	2:SA:327:LYS:HB2	2.03	0.41
4:L0:289:U:H2'	4:L0:290:G:C8	2.56	0.41
4:L0:409:C:H2'	4:L0:410:A:C8	2.56	0.41
6:L3:42:TYR:HE2	6:L3:73:MET:HE1	1.85	0.41
9:L7:165:LYS:O	9:L7:168:SER:OG	2.36	0.41
10:L8:32:GLN:H	10:L8:32:GLN:HG3	1.70	0.41
13:LD:32:LYS:HE2	13:LD:32:LYS:HB2	1.82	0.41
17:LH:690:ASN:ND2	17:LH:750:LEU:O	2.54	0.41
22:LN:105:SER:O	22:LN:105:SER:OG	2.34	0.41
24:LP:410:UNK:O	24:LP:414:UNK:N	2.54	0.41
25:LQ:400:SER:HB3	25:LQ:404:LYS:HB3	2.03	0.41
25:LQ:824:MET:HA	25:LQ:825:PRO:HD3	1.94	0.41
27:LT:187:ASN:OD1	27:LT:187:ASN:N	2.51	0.41
28:LU:26:ARG:NH2	46:SS:867:GLN:O	2.54	0.41
28:LU:142:ASP:OD1	28:LU:142:ASP:N	2.48	0.41
28:LU:254:PRO:HG2	46:SS:284:ARG:NE	2.36	0.41
29:LV:126:GLN:HE21	29:LV:130:GLY:HA2	1.86	0.41
31:LZ:57:LEU:HA	31:LZ:57:LEU:HD12	1.85	0.41
36:SG:553:ILE:HD12	36:SG:553:ILE:HA	1.99	0.41
38:SI:838:ILE:HD11	53:8:578:U:C4	2.56	0.41
38:SI:969:VAL:HG12	38:SI:1000:ILE:H	1.85	0.41
52:NI:41:ARG:HA	52:NI:53:LEU:HA	2.02	0.41
53:8:600:U:H2'	53:8:601:A:C8	2.55	0.41
53:8:1110:G:O2'	53:8:1111:G:O4'	2.37	0.41
53:8:1661:U:H2'	53:8:1662:G:C8	2.56	0.41
2:SA:15:TYR:CZ	2:SA:78:LEU:HB2	2.55	0.41
4:L0:114:G:H2'	4:L0:115:G:C8	2.56	0.41
4:L0:223:C:H2'	4:L0:224:G:C8	2.56	0.41
7:L4:36:HIS:CE1	7:L4:85:GLY:HA3	2.56	0.41
7:L4:125:LYS:HB3	7:L4:142:HIS:HD2	1.85	0.41
8:L5:196:GLU:OE2	8:L5:200:ASN:ND2	2.45	0.41
9:L7:56:LYS:HB2	9:L7:88:ARG:HH12	1.86	0.41
9:L7:91:ILE:HG21	9:L7:129:LEU:HD12	2.03	0.41
10:L8:67:TRP:NE1	10:L8:69:SER:OG	2.53	0.41
11:L9:173:ALA:HB2	53:8:511:A:H5'	2.03	0.41
14:LE:19:LYS:HD3	14:LE:19:LYS:HA	1.83	0.41
17:LH:780:GLU:O	17:LH:782:THR:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:LJ:90:ARG:HG3	18:LJ:92:ASP:H	1.85	0.41
21:LM:284:SER:OG	21:LM:285:ASN:N	2.53	0.41
23:LO:397:LYS:HZ2	23:LO:442:GLY:H	1.69	0.41
23:LO:482:SER:OG	23:LO:486:SER:N	2.53	0.41
23:LO:791:HIS:O	23:LO:795:ASN:ND2	2.54	0.41
26:LS:156:ASN:OD1	26:LS:156:ASN:N	2.54	0.41
27:LT:59:GLN:HG2	27:LT:71:VAL:HG12	2.02	0.41
27:LT:173:LEU:HD23	27:LT:173:LEU:HA	1.90	0.41
28:LU:247:TYR:HD1	28:LU:254:PRO:HB3	1.86	0.41
29:LV:102:VAL:HG23	29:LV:117:LEU:HD23	2.03	0.41
35:SE:21:LEU:HA	35:SE:24:VAL:HG22	2.02	0.41
35:SE:37:ALA:HA	35:SE:99:ALA:HB3	2.03	0.41
36:SG:274:ILE:HA	36:SG:275:PRO:HD3	1.89	0.41
36:SG:343:ASP:OD1	36:SG:343:ASP:N	2.47	0.41
36:SG:523:LYS:NZ	36:SG:525:GLN:OE1	2.41	0.41
37:SH:24:ALA:HA	37:SH:27:SER:HB3	2.03	0.41
37:SH:134:LYS:HB3	37:SH:134:LYS:HE2	1.90	0.41
37:SH:298:ILE:HD13	37:SH:298:ILE:HA	1.95	0.41
38:SI:153:MET:HE2	38:SI:153:MET:HB2	1.98	0.41
38:SI:780:ILE:HD12	38:SI:780:ILE:HA	1.92	0.41
39:SK:88:ARG:HE	39:SK:88:ARG:HB3	1.64	0.41
39:SK:188:ARG:HG2	39:SK:190:GLN:HB2	2.03	0.41
42:SN:242:ILE:HG12	42:SN:255:TYR:HB3	2.03	0.41
45:SR:104:LEU:HD13	45:SR:104:LEU:HA	1.92	0.41
47:ST:495:ASN:ND2	47:ST:617:HIS:O	2.53	0.41
47:ST:575:PHE:HD1	47:ST:600:LEU:HB2	1.84	0.41
52:NI:40:LYS:O	52:NI:54:PHE:N	2.53	0.41
53:8:9:U:H5'	58:NE:292:LYS:HE2	2.01	0.41
53:8:107:C:H2'	53:8:108:A:H8	1.86	0.41
53:8:116:U:H2'	53:8:117:U:C6	2.56	0.41
53:8:222:A:H5'	53:8:246:G:C2	2.56	0.41
53:8:312:A:H4'	53:8:313:U:H5'	2.03	0.41
53:8:477:A:H2'	53:8:478:A:H8	1.85	0.41
53:8:911:U:H5'	57:LR:534:ARG:HB2	2.02	0.41
53:8:1783:C:H2'	53:8:1784:C:C6	2.56	0.41
55:LI:572:SER:HB3	55:LI:574:ARG:NH1	2.36	0.41
55:LI:604:LYS:HB2	55:LI:604:LYS:HE2	1.86	0.41
57:LR:87:ILE:HG12	57:LR:97:ARG:HB2	2.03	0.41
57:LR:284:PRO:HB2	57:LR:288:LEU:HD23	2.03	0.41
63:L6:201:GLN:O	63:L6:205:ALA:N	2.50	0.41
66:6:342:GLY:O	66:6:345:LYS:NZ	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:SA:18:PHE:HD1	2:SA:50:LEU:HA	1.86	0.41
2:SA:411:ARG:HA	2:SA:411:ARG:HD3	1.94	0.41
3:NB:559:ARG:HE	53:8:545:A:H8	1.67	0.41
3:NB:604:ARG:NH1	53:8:498:G:O3'	2.50	0.41
4:L0:467:A:N1	4:L0:468:A:N6	2.69	0.41
11:L9:77:ILE:HG23	11:L9:86:LEU:HD23	2.03	0.41
12:LC:39:VAL:O	12:LC:45:ARG:NH2	2.54	0.41
14:LE:40:VAL:O	14:LE:44:HIS:ND1	2.40	0.41
14:LE:111:MET:HE1	14:LE:116:ALA:HB2	2.02	0.41
16:LG:21:SER:OG	16:LG:25:VAL:O	2.28	0.41
18:LJ:101:ALA:HA	18:LJ:126:PRO:HB3	2.03	0.41
20:LL:198:THR:HG23	20:LL:200:GLU:H	1.86	0.41
22:LN:112:LEU:HD11	22:LN:525:VAL:HG22	2.02	0.41
22:LN:197:LYS:HA	22:LN:197:LYS:HD3	1.76	0.41
22:LN:393:SER:OG	22:LN:394:TRP:N	2.54	0.41
23:LO:539:ILE:HB	23:LO:553:ILE:HG13	2.02	0.41
26:LS:541:LEU:O	26:LS:542:ARG:NH1	2.42	0.41
28:LU:186:ASP:HB2	28:LU:225:LEU:HG	2.03	0.41
35:SE:106:ASP:OD1	35:SE:106:ASP:N	2.54	0.41
36:SG:461:LYS:HA	36:SG:461:LYS:HD3	1.92	0.41
38:SI:118:LEU:HD23	38:SI:131:ILE:HD11	2.01	0.41
47:ST:426:THR:HG22	47:ST:462:LEU:HD13	2.02	0.41
57:LR:768:ASN:HB3	57:LR:771:LYS:HE3	2.03	0.41
65:5:486:SER:OG	65:5:488:ASP:OD1	2.29	0.41
3:NB:518:ILE:HD13	3:NB:518:ILE:HA	1.91	0.40
4:L0:409:C:H2'	4:L0:410:A:H8	1.87	0.40
7:L4:75:LYS:HB2	7:L4:77:ARG:HG2	2.02	0.40
9:L7:76:LYS:HA	9:L7:76:LYS:HD2	1.89	0.40
13:LD:74:THR:O	13:LD:87:ARG:N	2.54	0.40
17:LH:75:SER:HA	17:LH:79:LEU:HB2	2.02	0.40
17:LH:600:SER:HB2	17:LH:638:PHE:HB3	2.03	0.40
29:LV:24:SER:H	29:LV:49:LEU:HD21	1.86	0.40
29:LV:177:LYS:HA	29:LV:177:LYS:HD2	1.81	0.40
34:SC:104:ASP:OD1	44:SQ:127:ARG:NH1	2.54	0.40
34:SD:304:LEU:HD23	34:SD:306:LEU:HD12	2.04	0.40
38:SI:129:ILE:HD11	38:SI:853:ARG:HD2	2.03	0.40
39:SJ:174:LYS:HG2	39:SJ:199:ASP:HB3	2.03	0.40
39:SJ:175:CYS:SG	39:SJ:176:ARG:N	2.94	0.40
41:SM:263:LEU:HD12	41:SM:263:LEU:HA	1.91	0.40
42:SN:125:VAL:HG13	42:SN:151:PRO:HA	2.02	0.40
53:8:340:U:H2'	53:8:341:A:H8	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:8:922:G:H2'	53:8:923:A:C8	2.56	0.40
53:8:1695:G:C2	53:8:1706:C:C2	3.08	0.40
59:SB:53:ALA:HB3	59:SB:56:ALA:HB3	2.03	0.40
59:SB:210:LEU:HD11	59:SB:260:GLU:HB3	2.03	0.40
59:SB:299:LEU:HD23	59:SB:341:LEU:HD23	2.03	0.40
2:SA:82:LEU:HD23	2:SA:82:LEU:HA	1.81	0.40
4:L0:250:G:H1	4:L0:262:U:H3	1.70	0.40
4:L0:523:U:H5''	28:LU:126:LYS:HA	2.02	0.40
9:L7:166:LEU:HA	9:L7:169:PHE:CD1	2.56	0.40
15:LF:59:GLY:HA3	15:LF:72:PHE:HB3	2.03	0.40
20:LL:516:ILE:HG23	20:LL:519:LEU:HD21	2.04	0.40
23:LO:526:ASP:HA	23:LO:815:TYR:CZ	2.57	0.40
25:LQ:292:UNK:O	25:LQ:296:UNK:N	2.54	0.40
27:LT:225:THR:OG1	27:LT:227:THR:O	2.36	0.40
27:LT:847:LEU:O	27:LT:851:SER:OG	2.31	0.40
28:LU:58:PHE:HE1	28:LU:373:ARG:HG2	1.86	0.40
28:LU:92:ILE:HG13	28:LU:106:PHE:HB2	2.02	0.40
28:LU:109:HIS:CG	28:LU:140:SER:HB2	2.55	0.40
28:LU:263:ARG:O	28:LU:281:ASN:ND2	2.54	0.40
30:LW:458:THR:HA	46:SS:854:ARG:HD3	2.02	0.40
32:NG:21:ALA:HA	32:NG:26:THR:HA	2.02	0.40
36:SG:225:LYS:HE3	36:SG:225:LYS:HB3	1.92	0.40
37:SH:244:THR:HG23	37:SH:259:GLU:HB3	2.02	0.40
37:SH:307:ASP:OD1	38:SI:765:ASN:ND2	2.46	0.40
43:SO:263:LEU:HA	43:SO:266:VAL:HG22	2.02	0.40
45:SR:130:VAL:HG13	45:SR:135:LEU:HD21	2.02	0.40
46:SS:278:ILE:H	46:SS:278:ILE:HD12	1.86	0.40
53:8:1733:C:H2'	53:8:1734:U:H6	1.87	0.40
57:LR:200:GLU:O	57:LR:256:ARG:NH2	2.54	0.40
62:LX:658:ARG:HD3	62:LX:766:LEU:HD13	2.04	0.40
65:5:416:VAL:O	65:5:420:ASP:N	2.45	0.40
3:NB:591:TYR:OH	3:NB:594:GLU:O	2.32	0.40
4:L0:286:U:H2'	4:L0:287:G:H8	1.86	0.40
4:L0:494:C:H2'	4:L0:495:G:C8	2.56	0.40
5:L2:45:U:O2'	40:SL:23:GLN:OE1	2.28	0.40
5:L2:310:G:H2'	5:L2:311:G:C8	2.55	0.40
9:L7:154:LEU:HD12	9:L7:185:ILE:HG22	2.03	0.40
10:L8:78:ILE:HA	10:L8:104:ILE:HG22	2.02	0.40
17:LH:546:LYS:HE2	17:LH:548:ILE:HD11	2.02	0.40
18:LJ:256:THR:HG21	18:LJ:277:LEU:HD13	2.03	0.40
21:LM:31:ALA:HB1	21:LM:154:ILE:HG23	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:LM:83:ARG:HE	21:LM:91:ILE:HD11	1.86	0.40
21:LM:124:ARG:HA	21:LM:124:ARG:HD2	1.87	0.40
23:LO:425:PHE:HB3	23:LO:458:TRP:CD1	2.56	0.40
23:LO:496:THR:HG22	23:LO:513:GLU:HB3	2.03	0.40
23:LO:612:LEU:HD23	23:LO:612:LEU:HA	1.90	0.40
27:LT:814:GLU:OE1	27:LT:822:ARG:NH1	2.55	0.40
27:LT:856:GLU:HB2	43:SO:252:LEU:HD11	2.03	0.40
31:LZ:55:ARG:HG2	31:LZ:98:GLU:HG2	2.03	0.40
34:SD:163:PHE:CG	34:SD:266:GLY:HA3	2.56	0.40
35:SE:68:PRO:HA	35:SE:71:CYS:HB2	2.02	0.40
37:SH:113:LYS:HE3	37:SH:113:LYS:HB3	1.94	0.40
38:SI:180:GLN:HA	38:SI:183:LEU:HB3	2.03	0.40
38:SI:310:THR:HA	38:SI:311:PRO:HD3	1.96	0.40
38:SI:832:HIS:CD2	38:SI:834:TRP:HB2	2.56	0.40
39:SJ:150:ILE:HD12	39:SJ:160:LEU:HD12	2.02	0.40
47:ST:643:LEU:HD23	47:ST:684:ILE:HD13	2.03	0.40
53:8:1210:C:H2'	53:8:1211:A:C8	2.56	0.40
59:SB:226:ILE:HG13	59:SB:227:LEU:HD12	2.03	0.40
62:LX:62:LYS:HA	62:LX:62:LYS:HD3	1.80	0.40
62:LX:200:VAL:HG22	62:LX:208:LEU:HD12	2.03	0.40
62:LX:881:GLN:H	62:LX:881:GLN:HG2	1.67	0.40
65:5:194:ILE:HD11	65:5:421:LEU:HD11	2.03	0.40
4:L0:192:G:H2'	4:L0:193:G:H8	1.85	0.40
4:L0:305:A:H2'	4:L0:306:G:C8	2.57	0.40
4:L0:480:C:O2	24:LP:46:ARG:NH1	2.54	0.40
7:L4:112:HIS:NE2	7:L4:237:SER:O	2.55	0.40
18:LJ:62:ARG:HE	18:LJ:62:ARG:HB3	1.76	0.40
18:LJ:128:HIS:CE1	18:LJ:172:ARG:HH21	2.40	0.40
21:LM:131:ASN:OD1	21:LM:131:ASN:N	2.48	0.40
21:LM:218:ILE:HG23	21:LM:263:VAL:HG11	2.02	0.40
22:LN:394:TRP:HB3	22:LN:399:VAL:HG13	2.02	0.40
22:LN:639:ASP:OD2	22:LN:647:TRP:NE1	2.52	0.40
25:LQ:589:ILE:HG12	25:LQ:599:ILE:HG12	2.03	0.40
28:LU:326:ASP:OD1	28:LU:326:ASP:N	2.46	0.40
29:LV:195:LEU:HD13	29:LV:207:TRP:HB2	2.04	0.40
35:SE:20:ILE:HD13	35:SE:79:VAL:HG21	2.04	0.40
38:SI:977:LYS:NZ	53:8:1598:U:OP2	2.41	0.40
47:ST:571:ILE:HD13	47:ST:571:ILE:HA	1.89	0.40
47:ST:573:LEU:HD23	47:ST:573:LEU:HA	1.93	0.40
48:SY:40:ASP:O	48:SY:44:LYS:NZ	2.48	0.40
53:8:631:G:O6	53:8:968:U:O4	2.39	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:8:1512:G:H2'	53:8:1513:G:C8	2.56	0.40
57:LR:299:ASN:O	57:LR:301:GLN:NE2	2.41	0.40
57:LR:536:LEU:HA	57:LR:552:SER:HA	2.04	0.40
4:L0:505:G:H2'	4:L0:506:G:C8	2.56	0.40
20:LL:469:ILE:HB	20:LL:508:ILE:HD12	2.04	0.40
21:LM:6:ASP:OD1	21:LM:6:ASP:N	2.54	0.40
22:LN:758:ASN:HB2	22:LN:763:HIS:CD2	2.57	0.40
23:LO:162:LEU:HD13	23:LO:197:ALA:HB3	2.04	0.40
23:LO:750:LEU:HD23	23:LO:750:LEU:HA	1.84	0.40
25:LQ:341:ALA:HB1	25:LQ:353:LEU:HD11	2.03	0.40
25:LQ:395:ARG:HA	25:LQ:395:ARG:HD3	1.85	0.40
27:LT:544:ALA:HB3	27:LT:562:LEU:HD22	2.02	0.40
34:SC:178:GLY:HA2	34:SC:181:VAL:HG12	2.02	0.40
34:SD:253:ILE:HD13	34:SD:253:ILE:HA	1.94	0.40
38:SI:241:HIS:HB3	38:SI:851:TRP:HE1	1.86	0.40
38:SI:833:ARG:HH12	45:SR:141:GLU:HG3	1.86	0.40
39:SJ:136:ARG:HD3	53:8:1195:C:C2	2.56	0.40
41:SM:16:LYS:HE2	41:SM:16:LYS:HB2	1.95	0.40
42:SN:223:LEU:HD12	42:SN:235:ILE:HG13	2.03	0.40
47:ST:418:UNK:O	47:ST:420:GLU:N	2.53	0.40
47:ST:644:ASP:HB3	47:ST:684:ILE:HG12	2.04	0.40
53:8:33:U:H2'	53:8:34:G:C2	2.57	0.40
54:SU:381:LYS:HE3	54:SU:385:ARG:HH21	1.85	0.40
57:LR:192:ALA:O	57:LR:216:ARG:NH1	2.54	0.40
57:LR:411:THR:OG1	57:LR:430:TYR:O	2.33	0.40
62:LX:185:ASN:HA	62:LX:188:PHE:HB3	2.04	0.40
62:LX:319:LYS:O	62:LX:323:GLU:N	2.53	0.40
62:LX:862:LEU:O	62:LX:866:TYR:N	2.54	0.40
63:L6:183:ARG:O	63:L6:187:LYS:N	2.52	0.40
65:5:247:ILE:HG23	65:5:262:ALA:HB1	2.03	0.40
66:6:242:MET:HG3	66:6:245:MET:HG2	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	NA	203/245 (83%)	194 (96%)	8 (4%)	1 (0%)	24	60
2	SA	338/413 (82%)	332 (98%)	6 (2%)	0	100	100
3	NB	126/180 (70%)	118 (94%)	7 (6%)	1 (1%)	16	52
6	L3	100/127 (79%)	91 (91%)	9 (9%)	0	100	100
7	L4	226/228 (99%)	202 (89%)	24 (11%)	0	100	100
8	L5	211/213 (99%)	194 (92%)	17 (8%)	0	100	100
9	L7	161/190 (85%)	142 (88%)	19 (12%)	0	100	100
10	L8	166/200 (83%)	156 (94%)	10 (6%)	0	100	100
11	L9	173/175 (99%)	159 (92%)	14 (8%)	0	100	100
12	LC	123/125 (98%)	113 (92%)	10 (8%)	0	100	100
13	LD	123/156 (79%)	109 (89%)	14 (11%)	0	100	100
14	LE	125/127 (98%)	115 (92%)	10 (8%)	0	100	100
15	LF	88/90 (98%)	74 (84%)	13 (15%)	1 (1%)	11	44
16	LG	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
17	LH	810/896 (90%)	754 (93%)	56 (7%)	0	100	100
18	LJ	489/513 (95%)	461 (94%)	28 (6%)	0	100	100
19	LK	86/123 (70%)	84 (98%)	2 (2%)	0	100	100
20	LL	465/555 (84%)	435 (94%)	30 (6%)	0	100	100
21	LM	424/431 (98%)	407 (96%)	17 (4%)	0	100	100
22	LN	654/748 (87%)	610 (93%)	43 (7%)	1 (0%)	43	75
23	LO	830/855 (97%)	777 (94%)	53 (6%)	0	100	100
24	LP	259/420 (62%)	257 (99%)	2 (1%)	0	100	100
25	LQ	798/939 (85%)	739 (93%)	58 (7%)	1 (0%)	48	81
26	LS	473/594 (80%)	448 (95%)	25 (5%)	0	100	100
27	LT	844/921 (92%)	805 (95%)	39 (5%)	0	100	100
28	LU	453/465 (97%)	415 (92%)	38 (8%)	0	100	100
29	LV	360/362 (99%)	324 (90%)	36 (10%)	0	100	100
30	LW	436/438 (100%)	409 (94%)	27 (6%)	0	100	100
31	LZ	180/182 (99%)	170 (94%)	10 (6%)	0	100	100
32	NG	109/111 (98%)	97 (89%)	12 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	NK	173/175 (99%)	165 (95%)	8 (5%)	0	100	100
34	SC	238/247 (96%)	227 (95%)	11 (5%)	0	100	100
34	SD	224/247 (91%)	207 (92%)	17 (8%)	0	100	100
35	SE	119/121 (98%)	110 (92%)	9 (8%)	0	100	100
35	SF	119/121 (98%)	107 (90%)	12 (10%)	0	100	100
36	SG	423/464 (91%)	401 (95%)	22 (5%)	0	100	100
37	SH	358/360 (99%)	342 (96%)	16 (4%)	0	100	100
38	SI	763/1123 (68%)	727 (95%)	36 (5%)	0	100	100
39	SJ	212/236 (90%)	205 (97%)	7 (3%)	0	100	100
39	SK	226/236 (96%)	221 (98%)	5 (2%)	0	100	100
40	SL	170/183 (93%)	160 (94%)	10 (6%)	0	100	100
41	SM	278/290 (96%)	260 (94%)	18 (6%)	0	100	100
42	SN	245/247 (99%)	232 (95%)	13 (5%)	0	100	100
43	SO	177/179 (99%)	163 (92%)	14 (8%)	0	100	100
44	SQ	129/167 (77%)	124 (96%)	5 (4%)	0	100	100
45	SR	102/104 (98%)	91 (89%)	10 (10%)	1 (1%)	12	45
46	SS	142/197 (72%)	132 (93%)	10 (7%)	0	100	100
47	ST	448/806 (56%)	425 (95%)	22 (5%)	1 (0%)	43	75
48	SY	237/248 (96%)	222 (94%)	15 (6%)	0	100	100
49	SZ	259/261 (99%)	237 (92%)	22 (8%)	0	100	100
50	NJ	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
51	NH	1072/1141 (94%)	1025 (96%)	47 (4%)	0	100	100
52	NI	163/187 (87%)	157 (96%)	6 (4%)	0	100	100
54	SU	471/513 (92%)	447 (95%)	24 (5%)	0	100	100
55	LI	423/687 (62%)	376 (89%)	45 (11%)	2 (0%)	24	60
56	ND	58/60 (97%)	58 (100%)	0	0	100	100
57	LR	750/811 (92%)	693 (92%)	57 (8%)	0	100	100
58	NE	157/240 (65%)	139 (88%)	18 (12%)	0	100	100
59	SB	431/436 (99%)	401 (93%)	30 (7%)	0	100	100
60	SV	59/92 (64%)	56 (95%)	3 (5%)	0	100	100
61	SP	2189/2418 (90%)	2132 (97%)	57 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	LX	802/923 (87%)	745 (93%)	57 (7%)	0	100	100
62	LY	827/923 (90%)	774 (94%)	53 (6%)	0	100	100
63	L6	161/219 (74%)	150 (93%)	11 (7%)	0	100	100
64	NF	122/124 (98%)	112 (92%)	10 (8%)	0	100	100
65	5	292/534 (55%)	269 (92%)	22 (8%)	1 (0%)	36	70
66	6	273/357 (76%)	259 (95%)	14 (5%)	0	100	100
All	All	23449/27027 (87%)	22060 (94%)	1379 (6%)	10 (0%)	100	100

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	NA	454	VAL
3	NB	441	PRO
45	SR	90	ASP
65	5	451	LYS
22	LN	666	ASN
47	ST	419	LYS
55	LI	533	PRO
55	LI	258	PRO
15	LF	32	ARG
25	LQ	787	LYS

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	
1	NA	187/223 (84%)	187 (100%)	0	100	100
2	SA	296/328 (90%)	296 (100%)	0	100	100
3	NB	108/139 (78%)	108 (100%)	0	100	100
6	L3	96/108 (89%)	96 (100%)	0	100	100
7	L4	196/196 (100%)	193 (98%)	3 (2%)	57	70
8	L5	180/180 (100%)	179 (99%)	1 (1%)	78	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	L7	146/170 (86%)	145 (99%)	1 (1%)	76	79
10	L8	138/161 (86%)	138 (100%)	0	100	100
11	L9	150/150 (100%)	150 (100%)	0	100	100
12	LC	105/105 (100%)	105 (100%)	0	100	100
13	LD	114/137 (83%)	114 (100%)	0	100	100
14	LE	108/108 (100%)	108 (100%)	0	100	100
15	LF	76/76 (100%)	75 (99%)	1 (1%)	61	72
16	LG	56/56 (100%)	55 (98%)	1 (2%)	51	68
17	LH	758/813 (93%)	758 (100%)	0	100	100
18	LJ	437/454 (96%)	435 (100%)	2 (0%)	81	82
19	LK	83/83 (100%)	83 (100%)	0	100	100
20	LL	428/497 (86%)	426 (100%)	2 (0%)	81	82
21	LM	391/391 (100%)	391 (100%)	0	100	100
22	LN	604/671 (90%)	601 (100%)	3 (0%)	81	82
23	LO	730/751 (97%)	727 (100%)	3 (0%)	84	84
24	LP	248/302 (82%)	247 (100%)	1 (0%)	84	84
25	LQ	717/794 (90%)	714 (100%)	3 (0%)	84	84
26	LS	424/529 (80%)	423 (100%)	1 (0%)	87	87
27	LT	745/802 (93%)	741 (100%)	4 (0%)	81	82
28	LU	412/420 (98%)	411 (100%)	1 (0%)	87	87
29	LV	307/326 (94%)	307 (100%)	0	100	100
30	LW	373/373 (100%)	371 (100%)	2 (0%)	81	82
31	LZ	171/171 (100%)	170 (99%)	1 (1%)	78	81
34	SC	202/206 (98%)	200 (99%)	2 (1%)	68	76
34	SD	192/206 (93%)	192 (100%)	0	100	100
35	SE	100/100 (100%)	100 (100%)	0	100	100
35	SF	100/100 (100%)	99 (99%)	1 (1%)	68	76
36	SG	373/402 (93%)	373 (100%)	0	100	100
37	SH	307/307 (100%)	307 (100%)	0	100	100
38	SI	684/965 (71%)	681 (100%)	3 (0%)	84	84
39	SJ	195/209 (93%)	195 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	SK	206/209 (99%)	204 (99%)	2 (1%)	68	76
40	SL	156/165 (94%)	155 (99%)	1 (1%)	78	81
41	SM	251/258 (97%)	250 (100%)	1 (0%)	84	84
42	SN	230/230 (100%)	226 (98%)	4 (2%)	53	68
43	SO	33/156 (21%)	33 (100%)	0	100	100
44	SQ	124/156 (80%)	122 (98%)	2 (2%)	55	70
45	SR	86/86 (100%)	86 (100%)	0	100	100
46	SS	135/135 (100%)	134 (99%)	1 (1%)	76	79
47	ST	417/604 (69%)	416 (100%)	1 (0%)	87	87
48	SY	226/233 (97%)	226 (100%)	0	100	100
54	SU	360/473 (76%)	358 (99%)	2 (1%)	78	81
55	LI	150/634 (24%)	150 (100%)	0	100	100
56	ND	57/57 (100%)	57 (100%)	0	100	100
57	LR	665/713 (93%)	662 (100%)	3 (0%)	81	82
58	NE	119/210 (57%)	117 (98%)	2 (2%)	53	68
59	SB	244/359 (68%)	244 (100%)	0	100	100
60	SV	22/87 (25%)	22 (100%)	0	100	100
62	LX	549/822 (67%)	549 (100%)	0	100	100
63	L6	139/188 (74%)	138 (99%)	1 (1%)	76	79
65	5	267/482 (55%)	267 (100%)	0	100	100
66	6	244/315 (78%)	242 (99%)	2 (1%)	73	77
All	All	15617/18581 (84%)	15559 (100%)	58 (0%)	81	84

All (58) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	L4	27	TYR
7	L4	76	VAL
7	L4	192	ILE
8	L5	98	MET
9	L7	150	GLN
15	LF	57	VAL
16	LG	36	THR
18	LJ	57	VAL
18	LJ	302	VAL

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Mol	Chain	Res	Type
20	LL	214	VAL
20	LL	222	THR
22	LN	90	VAL
22	LN	231	VAL
22	LN	597	ASN
23	LO	293	THR
23	LO	635	MET
23	LO	721	VAL
24	LP	107	LEU
25	LQ	607	CYS
25	LQ	623	PHE
25	LQ	898	LEU
26	LS	137	ILE
27	LT	183	VAL
27	LT	235	MET
27	LT	356	ILE
27	LT	840	PHE
28	LU	374	LEU
30	LW	150	LEU
30	LW	444	LEU
31	LZ	177	ILE
34	SC	162	LEU
34	SC	303	GLN
35	SF	85	VAL
38	SI	271	ILE
38	SI	871	MET
38	SI	997	MET
39	SK	47	MET
39	SK	159	LEU
40	SL	150	CYS
41	SM	176	ILE
42	SN	53	ILE
42	SN	117	GLN
42	SN	134	LEU
42	SN	203	TYR
44	SQ	103	TRP
44	SQ	212	MET
46	SS	338	LEU
47	ST	79	ILE
54	SU	123	TYR
54	SU	176	ILE
57	LR	182	CYS

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Mol	Chain	Res	Type
57	LR	217	ASP
57	LR	529	LEU
58	NE	236	MET
58	NE	308	ILE
63	L6	105	ASP
66	6	77	MET
66	6	93	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (164) such sidechains are listed below:

Mol	Chain	Res	Type
1	NA	382	GLN
1	NA	431	GLN
2	SA	183	GLN
2	SA	189	ASN
2	SA	276	GLN
6	L3	25	ASN
7	L4	130	GLN
8	L5	66	GLN
8	L5	139	ASN
8	L5	186	ASN
9	L7	11	GLN
9	L7	89	HIS
9	L7	150	GLN
10	L8	20	GLN
10	L8	32	GLN
10	L8	111	GLN
10	L8	159	GLN
12	LC	94	GLN
13	LD	118	GLN
14	LE	15	ASN
17	LH	71	ASN
17	LH	112	ASN
17	LH	331	GLN
17	LH	345	GLN
17	LH	407	ASN
17	LH	412	ASN
17	LH	489	ASN
17	LH	542	ASN
17	LH	606	HIS
17	LH	679	ASN
17	LH	690	ASN

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Mol	Chain	Res	Type
17	LH	699	ASN
17	LH	870	ASN
18	LJ	18	GLN
18	LJ	34	GLN
18	LJ	280	HIS
20	LL	143	ASN
20	LL	149	ASN
20	LL	336	ASN
21	LM	51	ASN
21	LM	128	HIS
22	LN	153	GLN
22	LN	317	ASN
22	LN	381	ASN
22	LN	438	GLN
22	LN	483	ASN
22	LN	529	ASN
22	LN	539	ASN
22	LN	599	ASN
22	LN	632	ASN
23	LO	17	GLN
23	LO	44	ASN
23	LO	57	ASN
23	LO	142	HIS
23	LO	312	GLN
23	LO	349	ASN
23	LO	452	ASN
23	LO	598	ASN
23	LO	734	GLN
23	LO	795	ASN
23	LO	811	ASN
24	LP	27	ASN
24	LP	58	ASN
24	LP	81	ASN
24	LP	105	GLN
24	LP	122	ASN
24	LP	287	ASN
25	LQ	116	ASN
25	LQ	251	GLN
25	LQ	264	ASN
25	LQ	390	GLN
25	LQ	524	HIS
25	LQ	608	HIS

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Mol	Chain	Res	Type
25	LQ	620	ASN
25	LQ	791	ASN
25	LQ	913	ASN
25	LQ	917	ASN
25	LQ	927	GLN
26	LS	352	GLN
26	LS	440	ASN
26	LS	497	ASN
26	LS	520	ASN
27	LT	171	GLN
27	LT	631	ASN
27	LT	715	GLN
27	LT	853	ASN
27	LT	875	ASN
27	LT	911	ASN
28	LU	120	GLN
28	LU	133	GLN
28	LU	265	ASN
28	LU	281	ASN
28	LU	443	ASN
29	LV	88	ASN
29	LV	116	HIS
29	LV	126	GLN
29	LV	226	ASN
30	LW	52	GLN
30	LW	202	HIS
30	LW	244	ASN
30	LW	278	ASN
30	LW	361	ASN
31	LZ	74	HIS
34	SC	145	ASN
34	SC	226	HIS
34	SC	264	GLN
34	SC	291	GLN
35	SF	19	GLN
35	SF	38	ASN
35	SF	75	ASN
36	SG	147	GLN
37	SH	12	GLN
38	SI	239	ASN
38	SI	261	GLN
38	SI	548	ASN

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Mol	Chain	Res	Type
38	SI	909	ASN
38	SI	1016	ASN
38	SI	1089	GLN
39	SK	190	GLN
39	SK	250	ASN
40	SL	73	ASN
41	SM	236	HIS
42	SN	117	GLN
42	SN	186	ASN
42	SN	256	GLN
44	SQ	58	ASN
45	SR	99	ASN
46	SS	276	GLN
46	SS	331	GLN
46	SS	875	HIS
47	ST	5	GLN
47	ST	94	GLN
47	ST	452	GLN
47	ST	479	ASN
47	ST	488	ASN
47	ST	658	ASN
47	ST	738	ASN
47	ST	765	GLN
47	ST	789	ASN
48	SY	65	HIS
48	SY	180	ASN
48	SY	215	GLN
54	SU	174	ASN
54	SU	245	GLN
54	SU	256	ASN
55	LI	529	HIS
55	LI	608	GLN
57	LR	351	ASN
57	LR	410	ASN
57	LR	667	GLN
58	NE	216	ASN
59	SB	271	GLN
59	SB	350	GLN
62	LX	69	HIS
62	LX	125	GLN
62	LX	206	ASN
62	LX	487	ASN

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Mol	Chain	Res	Type
62	LX	512	GLN
62	LX	519	ASN
62	LX	800	GLN
63	L6	201	GLN
65	5	236	ASN
65	5	264	HIS
65	5	469	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	L0	483/700 (69%)	164 (33%)	3 (0%)
5	L2	163/333 (48%)	56 (34%)	0
53	8	1169/1807 (64%)	527 (45%)	17 (1%)
All	All	1815/2840 (63%)	747 (41%)	20 (1%)

All (747) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	L0	18	G
4	L0	20	C
4	L0	22	A
4	L0	59	U
4	L0	60	G
4	L0	63	G
4	L0	69	U
4	L0	82	A
4	L0	86	C
4	L0	87	C
4	L0	90	G
4	L0	98	G
4	L0	103	G
4	L0	104	A
4	L0	107	G
4	L0	117	G
4	L0	123	C
4	L0	124	A
4	L0	125	G
4	L0	129	U
4	L0	130	G
4	L0	131	C

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Mol	Chain	Res	Type
4	L0	141	A
4	L0	142	U
4	L0	143	A
4	L0	144	C
4	L0	150	G
4	L0	151	U
4	L0	152	U
4	L0	155	A
4	L0	161	A
4	L0	163	G
4	L0	169	A
4	L0	173	G
4	L0	175	A
4	L0	176	U
4	L0	177	U
4	L0	178	G
4	L0	184	U
4	L0	185	A
4	L0	187	A
4	L0	188	A
4	L0	189	U
4	L0	190	U
4	L0	191	U
4	L0	197	G
4	L0	198	A
4	L0	199	A
4	L0	200	A
4	L0	201	U
4	L0	205	C
4	L0	213	G
4	L0	215	U
4	L0	216	U
4	L0	218	U
4	L0	219	U
4	L0	220	U
4	L0	227	U
4	L0	233	G
4	L0	234	A
4	L0	235	A
4	L0	236	C
4	L0	238	G
4	L0	239	U

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Mol	Chain	Res	Type
4	L0	240	C
4	L0	243	A
4	L0	252	A
4	L0	253	U
4	L0	254	C
4	L0	255	U
4	L0	256	U
4	L0	259	G
4	L0	261	U
4	L0	262	U
4	L0	267	U
4	L0	268	G
4	L0	279	A
4	L0	280	A
4	L0	281	G
4	L0	284	U
4	L0	304	U
4	L0	305	A
4	L0	309	A
4	L0	310	U
4	L0	311	C
4	L0	312	U
4	L0	313	A
4	L0	314	U
4	L0	315	U
4	L0	316	U
4	L0	322	A
4	L0	323	A
4	L0	324	U
4	L0	325	U
4	L0	326	C
4	L0	331	U
4	L0	332	U
4	L0	337	G
4	L0	338	A
4	L0	339	A
4	L0	340	U
4	L0	341	G
4	L0	347	U
4	L0	348	U
4	L0	352	U
4	L0	373	U

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Mol	Chain	Res	Type
4	L0	374	U
4	L0	375	C
4	L0	382	U
4	L0	385	A
4	L0	386	A
4	L0	395	C
4	L0	396	A
4	L0	397	A
4	L0	398	A
4	L0	399	U
4	L0	404	G
4	L0	407	A
4	L0	427	A
4	L0	430	C
4	L0	431	A
4	L0	433	C
4	L0	440	U
4	L0	451	G
4	L0	461	A
4	L0	468	A
4	L0	470	U
4	L0	474	A
4	L0	481	U
4	L0	482	A
4	L0	483	U
4	L0	485	G
4	L0	486	U
4	L0	487	A
4	L0	488	U
4	L0	489	G
4	L0	491	U
4	L0	492	G
4	L0	493	A
4	L0	494	C
4	L0	497	A
4	L0	502	G
4	L0	512	A
4	L0	513	G
4	L0	517	A
4	L0	518	A
4	L0	519	A
4	L0	521	G

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Mol	Chain	Res	Type
4	L0	522	C
4	L0	523	U
4	L0	524	U
4	L0	526	U
4	L0	530	A
4	L0	531	C
4	L0	535	G
4	L0	536	A
4	L0	540	U
4	L0	543	C
4	L0	554	G
4	L0	583	U
4	L0	584	U
4	L0	585	C
4	L0	586	A
4	L0	591	U
5	L2	2	U
5	L2	3	C
5	L2	14	A
5	L2	15	U
5	L2	16	A
5	L2	24	U
5	L2	25	U
5	L2	28	A
5	L2	30	A
5	L2	32	G
5	L2	33	A
5	L2	35	U
5	L2	37	G
5	L2	38	U
5	L2	44	U
5	L2	55	A
5	L2	56	A
5	L2	60	A
5	L2	61	G
5	L2	85	G
5	L2	88	U
5	L2	89	C
5	L2	90	C
5	L2	91	C
5	L2	92	A
5	L2	93	U

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Mol	Chain	Res	Type
5	L2	94	A
5	L2	105	C
5	L2	111	G
5	L2	114	A
5	L2	115	G
5	L2	116	A
5	L2	118	A
5	L2	201	C
5	L2	202	G
5	L2	247	U
5	L2	248	G
5	L2	249	G
5	L2	251	G
5	L2	252	C
5	L2	254	A
5	L2	256	G
5	L2	257	A
5	L2	260	U
5	L2	264	C
5	L2	267	A
5	L2	306	G
5	L2	307	G
5	L2	310	G
5	L2	312	U
5	L2	316	A
5	L2	321	C
5	L2	322	A
5	L2	324	U
5	L2	325	C
5	L2	329	C
53	8	-5	G
53	8	-4	A
53	8	-3	U
53	8	-2	A
53	8	-1	G
53	8	0	U
53	8	1	U
53	8	8	U
53	8	9	U
53	8	16	G
53	8	18	C
53	8	19	A

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Mol	Chain	Res	Type
53	8	20	G
53	8	21	U
53	8	22	A
53	8	23	G
53	8	26	A
53	8	28	A
53	8	33	U
53	8	34	G
53	8	35	U
53	8	36	C
53	8	37	U
53	8	39	A
53	8	50	C
53	8	51	A
53	8	53	G
53	8	55	A
53	8	99	C
53	8	102	U
53	8	103	A
53	8	104	A
53	8	109	G
53	8	110	U
53	8	111	U
53	8	112	A
53	8	113	U
53	8	114	C
53	8	115	G
53	8	116	U
53	8	119	A
53	8	122	U
53	8	126	A
53	8	127	G
53	8	140	A
53	8	141	U
53	8	142	G
53	8	143	G
53	8	144	U
53	8	145	A
53	8	146	U
53	8	147	A
53	8	150	U
53	8	153	G

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Mol	Chain	Res	Type
53	8	159	U
53	8	160	C
53	8	161	U
53	8	162	A
53	8	180	A
53	8	181	A
53	8	185	U
53	8	186	C
53	8	188	A
53	8	190	C
53	8	191	C
53	8	192	U
53	8	194	U
53	8	195	G
53	8	196	G
53	8	197	A
53	8	199	G
53	8	200	A
53	8	201	G
53	8	204	G
53	8	205	U
53	8	207	U
53	8	210	A
53	8	211	U
53	8	212	U
53	8	213	A
53	8	214	G
53	8	223	U
53	8	226	A
53	8	227	U
53	8	228	G
53	8	233	C
53	8	234	G
53	8	235	G
53	8	236	A
53	8	237	C
53	8	239	C
53	8	240	U
53	8	241	U
53	8	242	U
53	8	245	U
53	8	246	G

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Mol	Chain	Res	Type
53	8	257	A
53	8	258	C
53	8	261	U
53	8	262	U
53	8	263	C
53	8	264	G
53	8	265	A
53	8	266	A
53	8	267	U
53	8	269	G
53	8	271	A
53	8	273	G
53	8	278	U
53	8	280	U
53	8	281	G
53	8	282	C
53	8	283	U
53	8	284	G
53	8	285	G
53	8	286	C
53	8	287	G
53	8	289	U
53	8	298	C
53	8	300	A
53	8	301	A
53	8	305	C
53	8	306	U
53	8	307	G
53	8	308	C
53	8	312	A
53	8	313	U
53	8	315	A
53	8	316	A
53	8	319	U
53	8	320	U
53	8	321	C
53	8	322	G
53	8	323	A
53	8	325	G
53	8	336	G
53	8	337	G
53	8	338	C

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Mol	Chain	Res	Type
53	8	345	U
53	8	346	G
53	8	347	G
53	8	348	U
53	8	351	C
53	8	352	A
53	8	355	G
53	8	359	A
53	8	360	A
53	8	361	C
53	8	362	G
53	8	366	A
53	8	368	U
53	8	369	A
53	8	371	G
53	8	372	G
53	8	373	G
53	8	374	U
53	8	376	C
53	8	377	G
53	8	378	A
53	8	379	U
53	8	382	C
53	8	383	G
53	8	390	G
53	8	396	G
53	8	398	G
53	8	400	A
53	8	401	A
53	8	402	C
53	8	404	G
53	8	407	A
53	8	412	A
53	8	414	C
53	8	417	A
53	8	418	G
53	8	420	A
53	8	421	A
53	8	423	G
53	8	431	C
53	8	440	U
53	8	442	C

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Mol	Chain	Res	Type
53	8	444	C
53	8	448	C
53	8	449	C
53	8	452	A
53	8	453	U
53	8	454	U
53	8	455	C
53	8	456	A
53	8	459	G
53	8	460	A
53	8	461	G
53	8	465	G
53	8	466	U
53	8	468	A
53	8	469	C
53	8	470	A
53	8	471	A
53	8	477	A
53	8	480	G
53	8	485	A
53	8	486	G
53	8	487	G
53	8	493	U
53	8	495	C
53	8	496	G
53	8	501	U
53	8	502	U
53	8	504	U
53	8	505	A
53	8	506	A
53	8	507	U
53	8	511	A
53	8	514	G
53	8	515	A
53	8	520	A
53	8	527	A
53	8	529	A
53	8	530	C
53	8	532	U
53	8	533	U
53	8	534	A
53	8	535	A

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Mol	Chain	Res	Type
53	8	536	C
53	8	538	A
53	8	539	G
53	8	540	G
53	8	542	A
53	8	543	C
53	8	544	A
53	8	545	A
53	8	546	U
53	8	553	G
53	8	562	G
53	8	563	U
53	8	565	C
53	8	570	A
53	8	572	C
53	8	573	C
53	8	574	G
53	8	576	G
53	8	579	A
53	8	580	A
53	8	581	U
53	8	582	U
53	8	584	C
53	8	585	A
53	8	586	G
53	8	587	C
53	8	594	A
53	8	595	G
53	8	600	U
53	8	603	U
53	8	624	G
53	8	627	C
53	8	629	U
53	8	630	A
53	8	632	U
53	8	633	U
53	8	636	A
53	8	637	C
53	8	638	U
53	8	860	U
53	8	861	U
53	8	862	A

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Mol	Chain	Res	Type
53	8	863	A
53	8	864	U
53	8	865	A
53	8	866	G
53	8	870	C
53	8	871	G
53	8	872	G
53	8	877	G
53	8	880	C
53	8	881	A
53	8	882	U
53	8	886	U
53	8	887	A
53	8	892	A
53	8	894	U
53	8	895	G
53	8	896	U
53	8	897	C
53	8	898	A
53	8	899	G
53	8	900	A
53	8	904	G
53	8	905	A
53	8	906	A
53	8	908	U
53	8	911	U
53	8	912	U
53	8	913	G
53	8	914	G
53	8	916	U
53	8	917	U
53	8	918	U
53	8	919	A
53	8	920	U
53	8	921	U
53	8	924	A
53	8	925	G
53	8	929	A
53	8	931	C
53	8	932	U
53	8	933	A
53	8	934	C

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Mol	Chain	Res	Type
53	8	935	U
53	8	939	A
53	8	940	A
53	8	942	G
53	8	945	U
53	8	947	U
53	8	948	G
53	8	950	C
53	8	952	A
53	8	955	A
53	8	959	U
53	8	961	U
53	8	962	C
53	8	963	A
53	8	964	U
53	8	965	U
53	8	966	A
53	8	967	A
53	8	969	C
53	8	972	G
53	8	975	C
53	8	976	G
53	8	978	A
53	8	979	A
53	8	980	G
53	8	981	U
53	8	983	A
53	8	984	G
53	8	988	A
53	8	992	A
53	8	993	A
53	8	994	G
53	8	995	A
53	8	996	U
53	8	997	G
53	8	998	A
53	8	999	U
53	8	1001	A
53	8	1002	G
53	8	1003	A
53	8	1004	U
53	8	1005	A

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Mol	Chain	Res	Type
53	8	1006	C
53	8	1007	C
53	8	1009	U
53	8	1010	C
53	8	1011	G
53	8	1012	U
53	8	1014	G
53	8	1015	U
53	8	1016	C
53	8	1017	U
53	8	1019	A
53	8	1036	A
53	8	1038	U
53	8	1039	A
53	8	1040	G
53	8	1042	G
53	8	1043	A
53	8	1053	G
53	8	1054	U
53	8	1057	U
53	8	1058	U
53	8	1060	U
53	8	1061	A
53	8	1062	A
53	8	1063	U
53	8	1064	G
53	8	1072	C
53	8	1076	A
53	8	1083	G
53	8	1084	A
53	8	1085	G
53	8	1086	A
53	8	1088	A
53	8	1089	U
53	8	1090	C
53	8	1091	A
53	8	1092	A
53	8	1093	A
53	8	1094	G
53	8	1095	U
53	8	1096	C
53	8	1097	U

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Mol	Chain	Res	Type
53	8	1098	U
53	8	1099	U
53	8	1100	G
53	8	1104	U
53	8	1106	U
53	8	1107	G
53	8	1108	G
53	8	1109	G
53	8	1110	G
53	8	1112	G
53	8	1113	A
53	8	1116	A
53	8	1118	G
53	8	1119	G
53	8	1126	G
53	8	1127	G
53	8	1131	A
53	8	1132	A
53	8	1134	C
53	8	1135	U
53	8	1144	U
53	8	1146	G
53	8	1149	G
53	8	1158	C
53	8	1159	C
53	8	1160	A
53	8	1164	G
53	8	1174	C
53	8	1191	U
53	8	1192	C
53	8	1193	A
53	8	1197	C
53	8	1198	G
53	8	1200	G
53	8	1202	A
53	8	1204	A
53	8	1206	U
53	8	1212	G
53	8	1213	G
53	8	1214	U
53	8	1216	C
53	8	1218	G

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Mol	Chain	Res	Type
53	8	1223	A
53	8	1224	A
53	8	1226	A
53	8	1259	U
53	8	1262	U
53	8	1266	U
53	8	1267	G
53	8	1268	G
53	8	1270	G
53	8	1272	U
53	8	1273	G
53	8	1276	U
53	8	1434	U
53	8	1436	A
53	8	1437	U
53	8	1438	G
53	8	1443	U
53	8	1449	U
53	8	1471	A
53	8	1473	U
53	8	1474	G
53	8	1477	G
53	8	1479	A
53	8	1483	A
53	8	1484	G
53	8	1486	G
53	8	1488	G
53	8	1489	U
53	8	1492	A
53	8	1493	A
53	8	1498	G
53	8	1504	G
53	8	1506	G
53	8	1509	C
53	8	1531	G
53	8	1533	C
53	8	1534	G
53	8	1573	A
53	8	1574	G
53	8	1575	G
53	8	1576	A
53	8	1583	A

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Mol	Chain	Res	Type
53	8	1584	G
53	8	1590	G
53	8	1595	U
53	8	1596	C
53	8	1597	A
53	8	1600	A
53	8	1602	C
53	8	1614	A
53	8	1618	C
53	8	1628	U
53	8	1629	G
53	8	1630	U
53	8	1632	C
53	8	1639	C
53	8	1640	C
53	8	1645	G
53	8	1652	C
53	8	1653	C
53	8	1657	U
53	8	1658	G
53	8	1666	U
53	8	1670	G
53	8	1678	A
53	8	1680	G
53	8	1681	A
53	8	1682	U
53	8	1683	C
53	8	1684	U
53	8	1693	A
53	8	1697	G
53	8	1703	C
53	8	1704	U
53	8	1711	C
53	8	1712	A
53	8	1713	G
53	8	1717	G
53	8	1726	G
53	8	1727	G
53	8	1730	A
53	8	1736	G
53	8	1742	U
53	8	1744	A

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Mol	Chain	Res	Type
53	8	1747	G
53	8	1748	G
53	8	1771	U
53	8	1773	C
53	8	1774	G
53	8	1775	U
53	8	1780	G
53	8	1781	A
53	8	1783	C
53	8	1785	U
53	8	1791	A

All (20) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	L0	199	A
4	L0	314	U
4	L0	522	C
53	8	-3	U
53	8	0	U
53	8	22	A
53	8	199	G
53	8	240	U
53	8	283	U
53	8	322	G
53	8	372	G
53	8	876	G
53	8	880	C
53	8	919	A
53	8	997	G
53	8	1057	U
53	8	1094	G
53	8	1573	A
53	8	1638	G
53	8	1790	A

5.4 Non-standard residues in protein, DNA, RNA chains

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](#)

There are no ligands in this entry.

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	SS	2
22	LN	2
47	ST	2
24	LP	2
19	LK	2
38	SI	1
17	LH	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	SS	408:UNK	C	828:ASN	N	85.72
1	SI	417:UNK	C	548:ASN	N	63.03
1	LN	730:UNK	C	731:HIS	N	39.41
1	ST	316:UNK	C	382:UNK	N	38.49
1	LH	831:UNK	C	846:ASN	N	26.10
1	LN	716:UNK	C	717:UNK	N	21.45
1	LP	416:UNK	C	418:UNK	N	15.60
1	ST	252:UNK	C	264:UNK	N	14.89
1	LP	369:UNK	C	379:UNK	N	11.71
1	LK	426:UNK	C	428:ASP	N	11.33
1	SS	363:UNK	C	369:UNK	N	10.71
1	LK	402:UNK	C	404:UNK	N	4.30

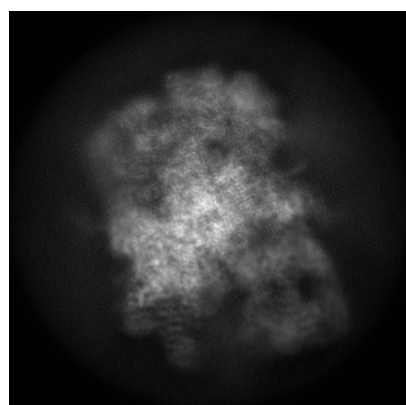
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25441. These allow visual inspection of the internal detail of the map and identification of artifacts.

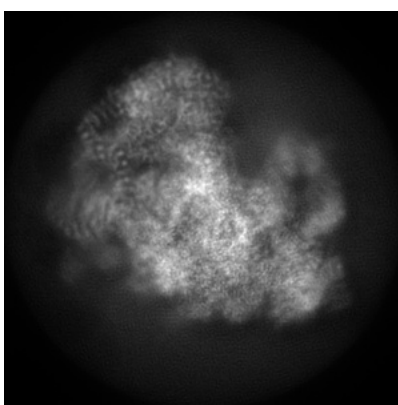
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

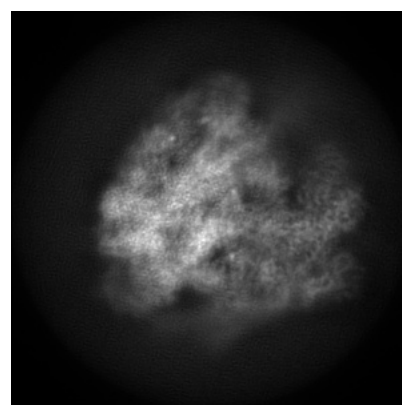
6.1.1 Primary map



X



Y

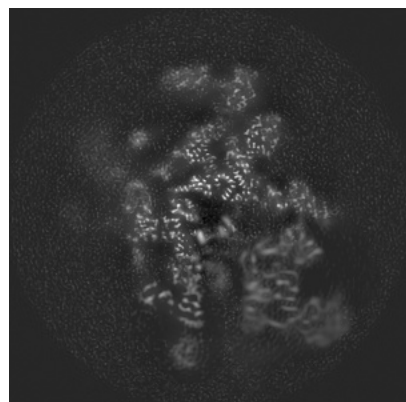


Z

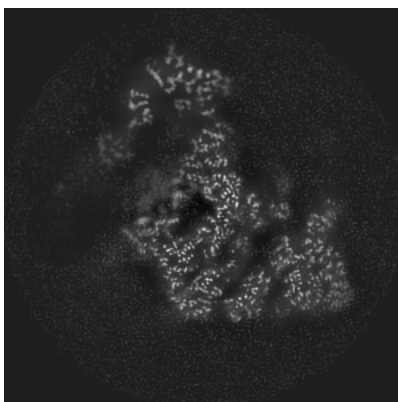
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

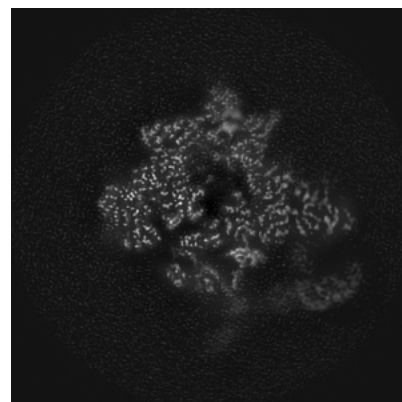
6.2.1 Primary map



X Index: 216



Y Index: 216

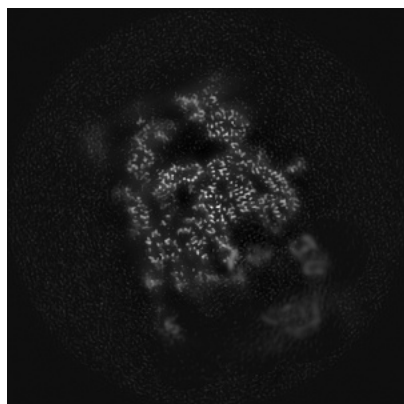


Z Index: 216

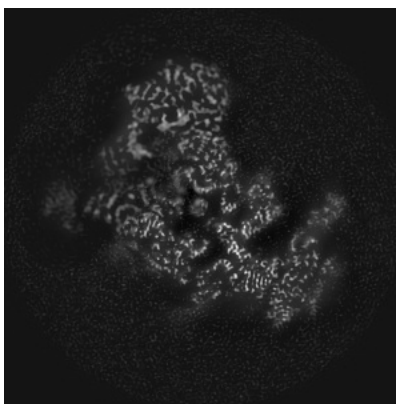
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

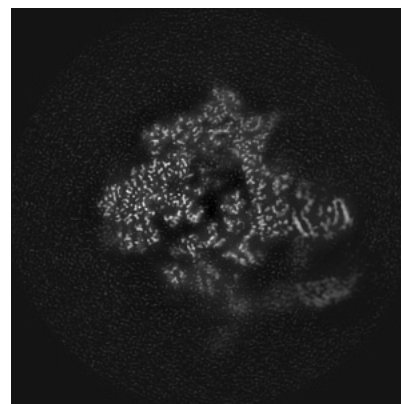
6.3.1 Primary map



X Index: 182



Y Index: 199

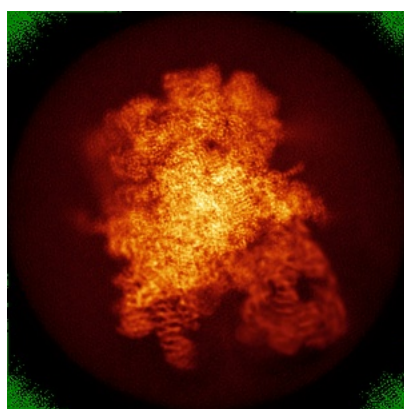


Z Index: 219

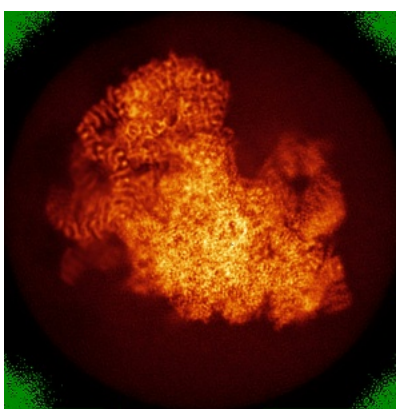
The images above show the largest variance slices of the map in three orthogonal directions.

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

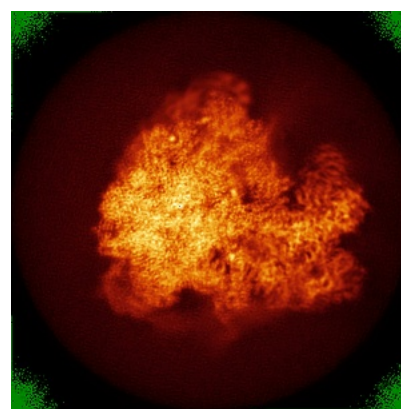
6.4.1 Primary map



X



Y

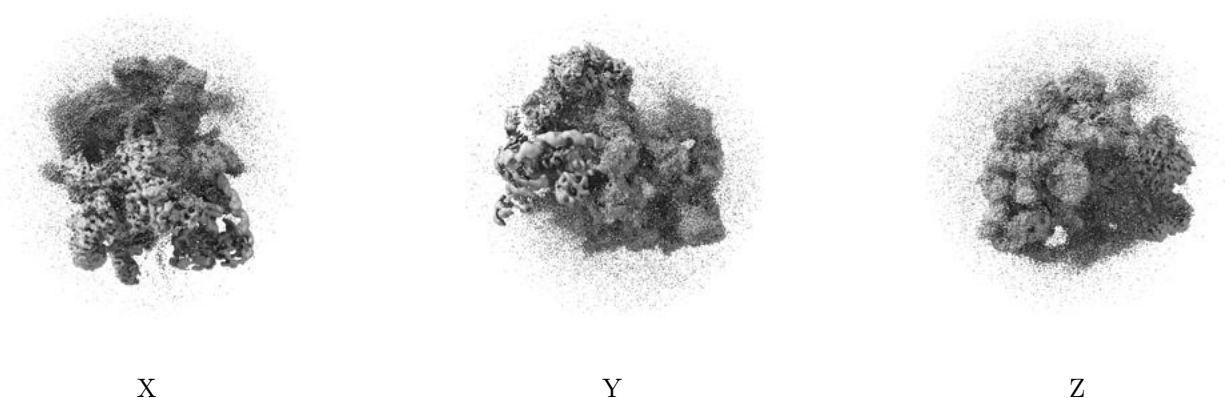


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.007. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

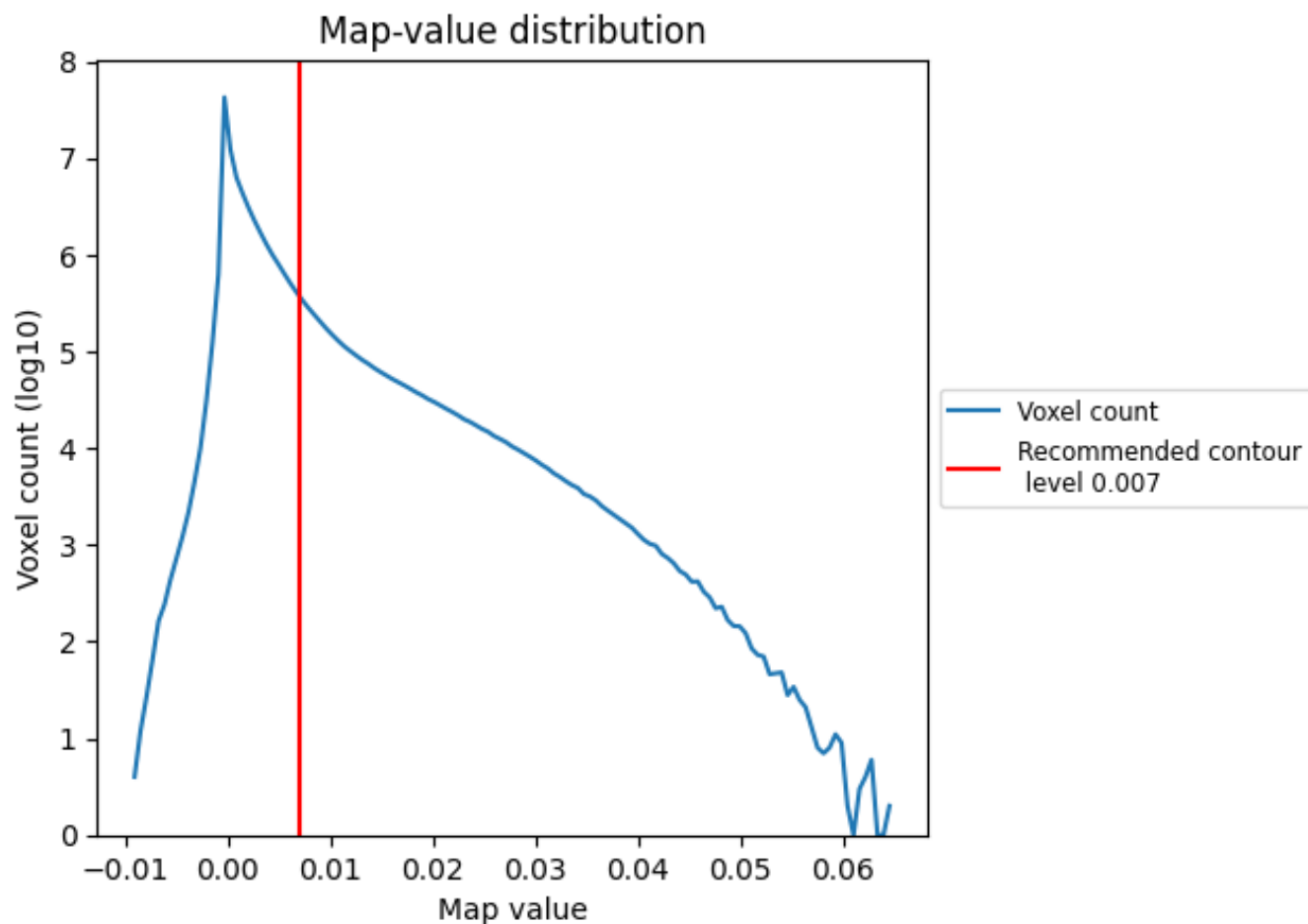
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

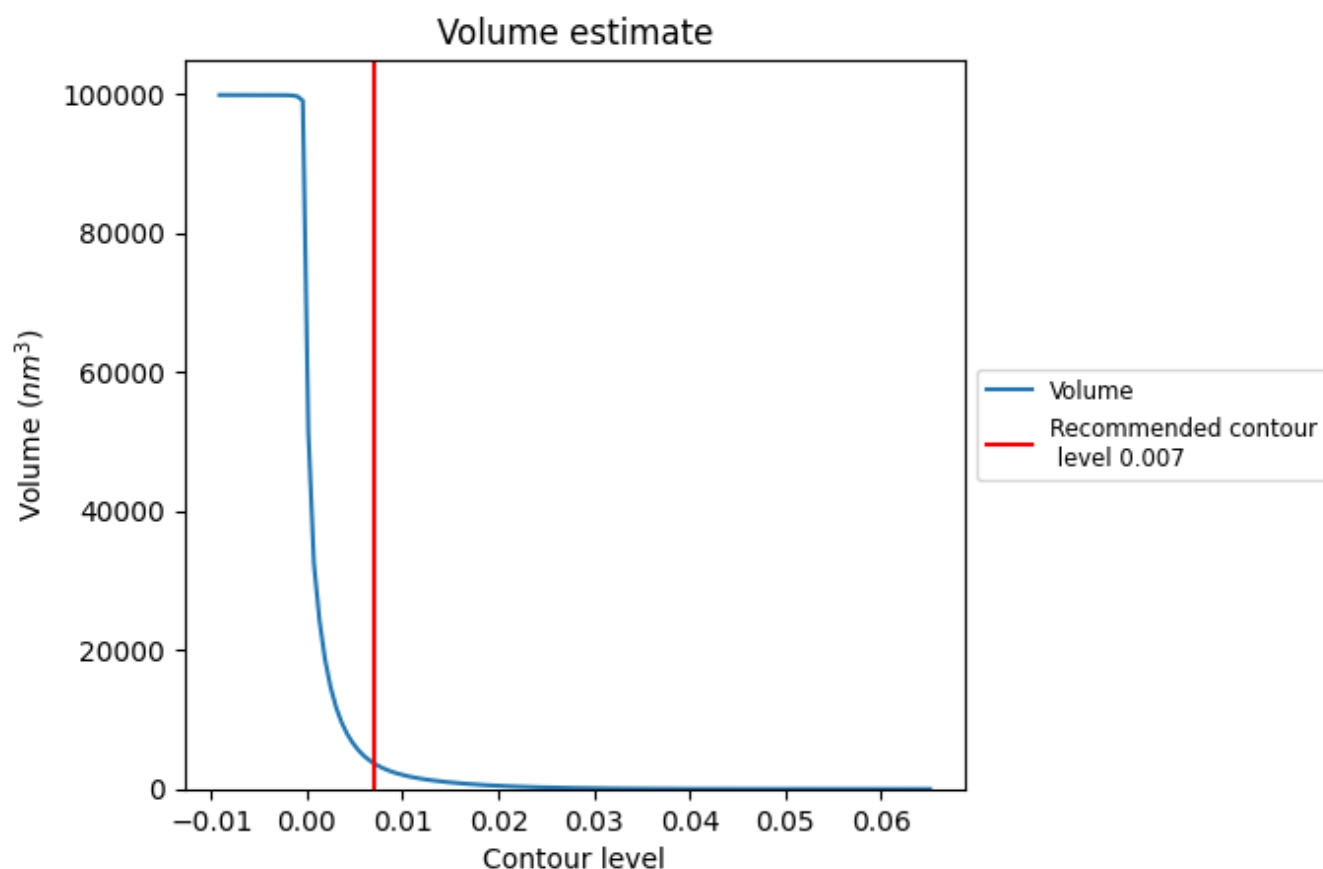
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

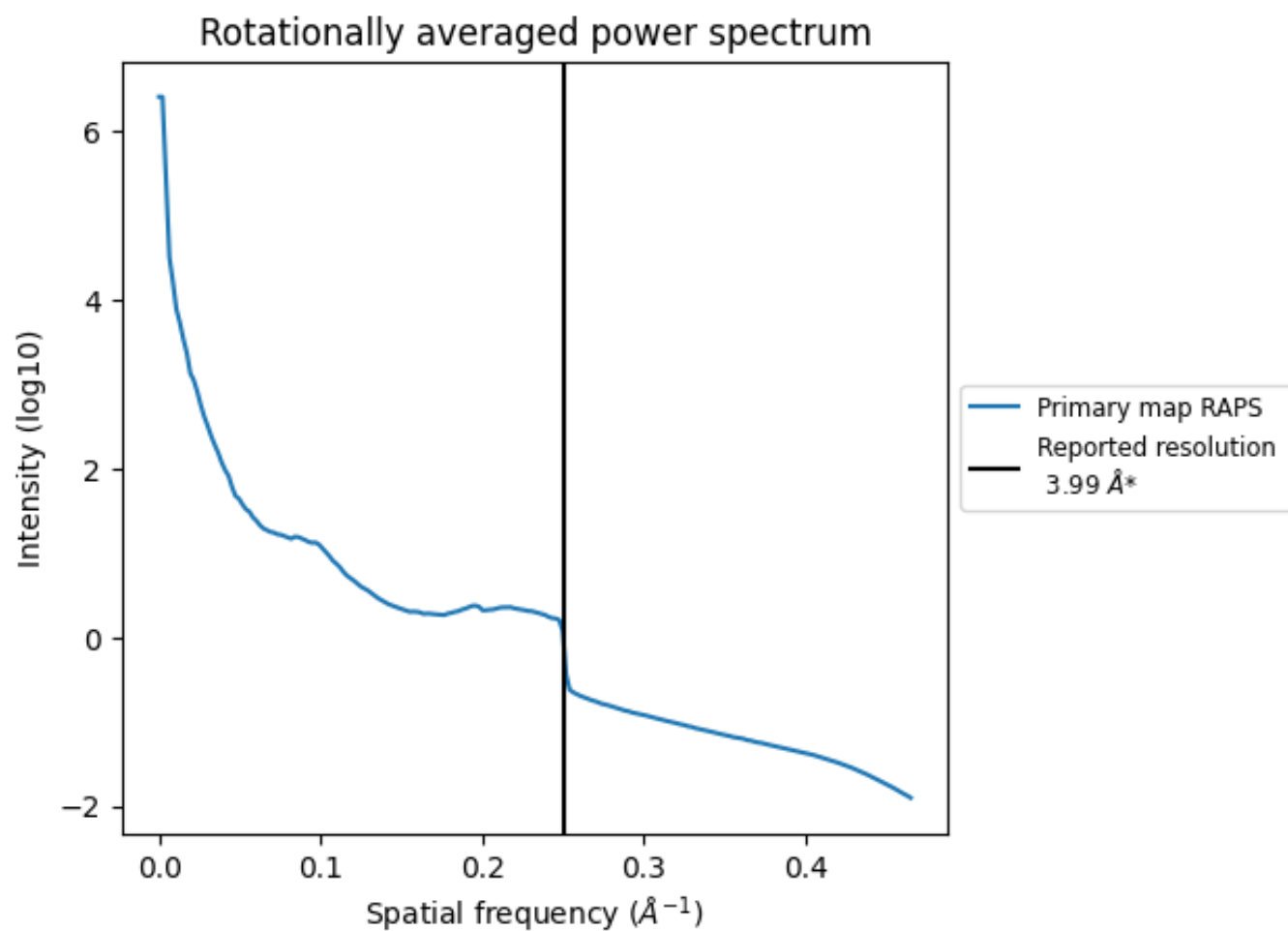
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3693 nm^3 ; this corresponds to an approximate mass of 3336 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 0.251 Å⁻¹

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

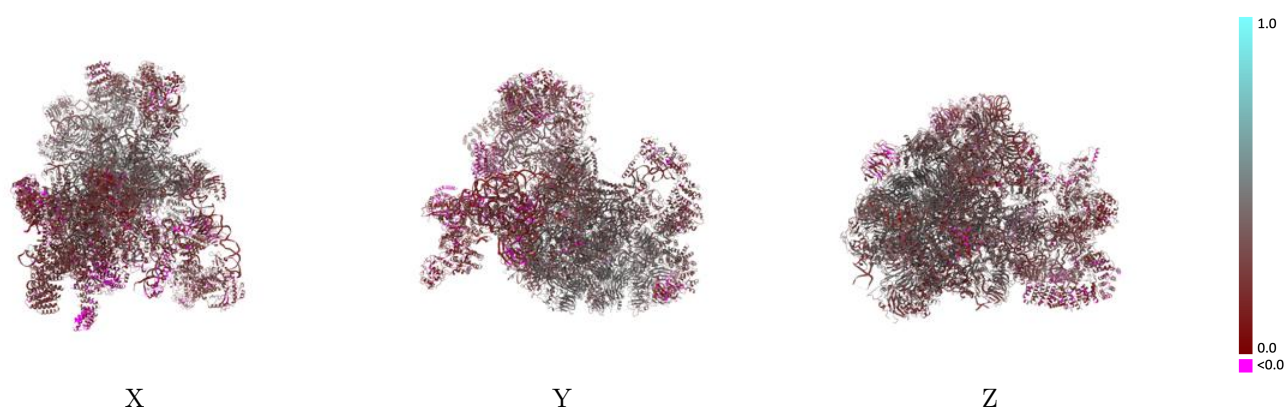
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-25441 and PDB model 7SUK. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)

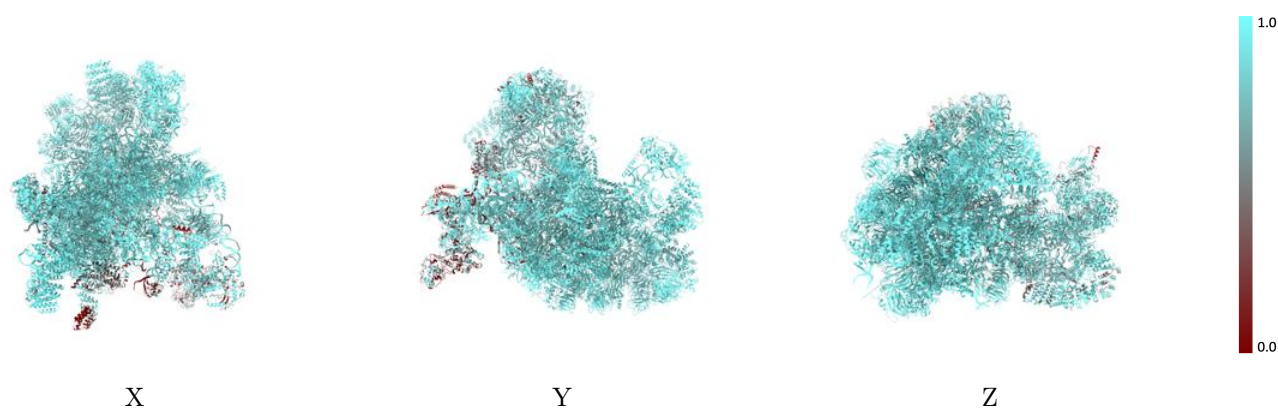
This section was not generated.

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



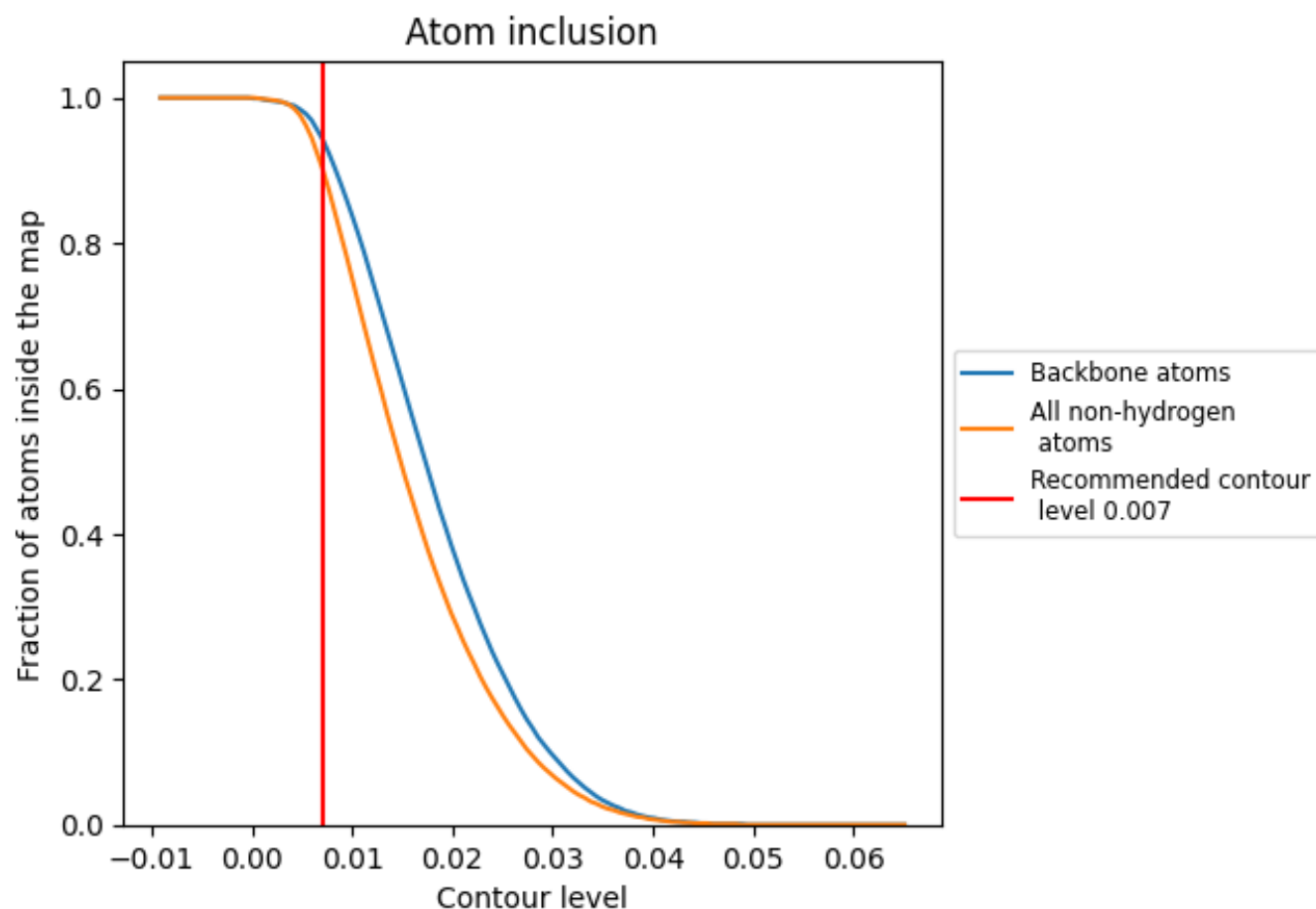
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.007).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.007) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9040	 0.3140
5	 0.5200	 0.1000
6	 0.6050	 0.1570
8	 0.9090	 0.2630
L0	 0.9890	 0.3530
L2	 0.9880	 0.3600
L3	 0.8400	 0.3230
L4	 0.8350	 0.2260
L5	 0.9450	 0.4070
L6	 0.7430	 0.1750
L7	 0.7720	 0.2040
L8	 0.8670	 0.2410
L9	 0.9360	 0.3690
LC	 0.9570	 0.4350
LD	 0.8710	 0.2350
LE	 0.8460	 0.2520
LF	 0.9020	 0.2620
LG	 0.9810	 0.4260
LH	 0.9480	 0.3750
LI	 0.9290	 0.2260
LJ	 0.9540	 0.3970
LK	 0.9810	 0.3210
LL	 0.9530	 0.3990
LM	 0.9460	 0.3870
LN	 0.9490	 0.3700
LO	 0.9520	 0.4190
LP	 0.9710	 0.3330
LQ	 0.9530	 0.3300
LR	 0.8190	 0.1640
LS	 0.9550	 0.4190
LT	 0.9600	 0.4180
LU	 0.9370	 0.3700
LV	 0.8430	 0.2340
LW	 0.9490	 0.4130
LX	 0.8470	 0.2280



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Chain	Atom inclusion	Q-score
LY	 0.8620	 0.2620
LZ	 0.9480	 0.4160
NA	 0.9010	 0.3710
NB	 0.9340	 0.3810
ND	 0.9270	 0.3450
NE	 0.7280	 0.2910
NF	 0.4850	 0.0300
NG	 0.9010	 0.2330
NH	 0.6270	 0.1930
NI	 0.3470	 0.1710
NJ	 0.9320	 0.2520
NK	 0.9510	 0.2180
SA	 0.9440	 0.3620
SB	 0.9440	 0.3510
SC	 0.9430	 0.4130
SD	 0.9390	 0.3550
SE	 0.9240	 0.3920
SF	 0.9500	 0.3550
SG	 0.9530	 0.3100
SH	 0.9470	 0.3710
SI	 0.9330	 0.3620
SJ	 0.9480	 0.3210
SK	 0.9610	 0.3840
SL	 0.9550	 0.4140
SM	 0.9260	 0.4050
SN	 0.9590	 0.3740
SO	 0.9890	 0.3240
SP	 0.8630	 0.2240
SQ	 0.8950	 0.3950
SR	 0.9210	 0.3730
SS	 0.9320	 0.3350
ST	 0.9440	 0.3160
SU	 0.9440	 0.2940
SV	 0.9070	 0.3540
SY	 0.9420	 0.3970
SZ	 0.9610	 0.2440