



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 02:11 PM UTC

PDB ID : 6LQP / pdb_00006lqp
EMDB ID : EMD-0949
Title : Cryo-EM structure of 90S small subunit preribosomes in transition states (State A)
Authors : Du, Y.; Ye, K.
Deposited on : 2020-01-14
Resolution : 3.20 Å(reported)
Based on initial model : 6KE6

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

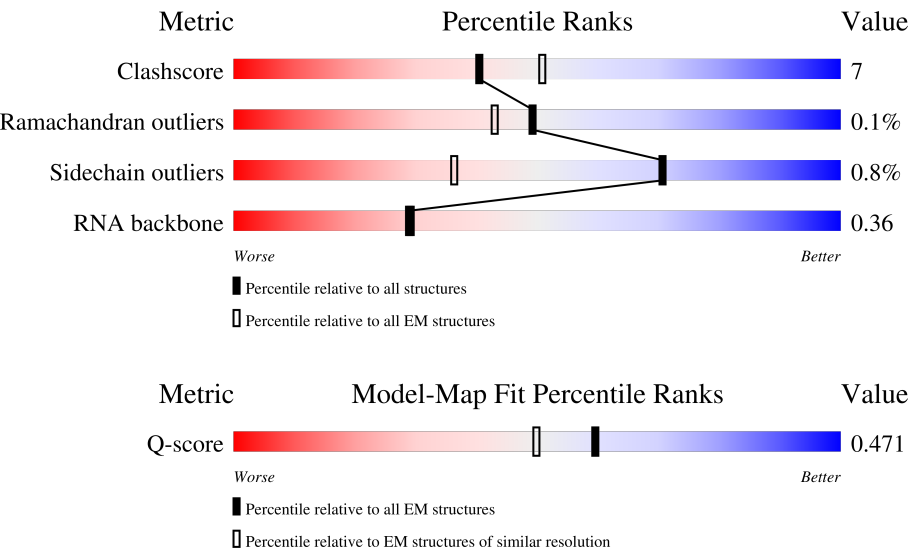
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.20 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.



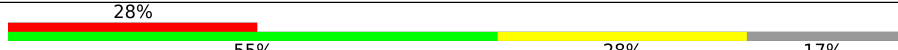
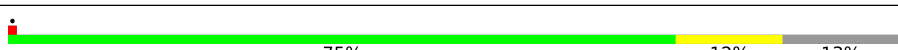
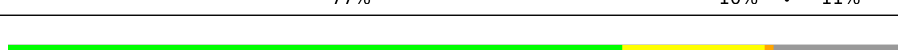
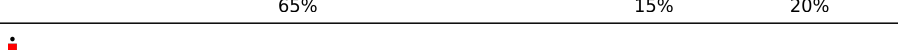
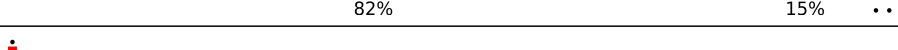
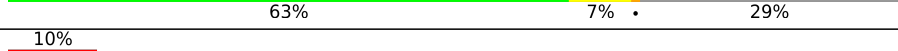
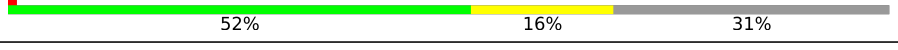
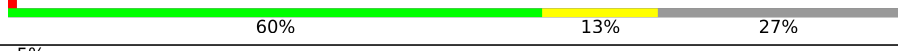
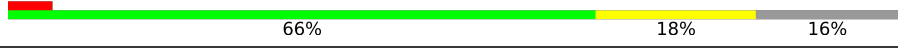
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	3A	333	
2	5A	700	
3	SA	1808	

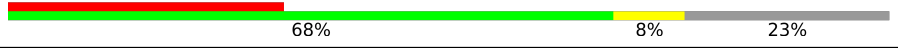
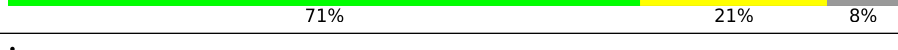
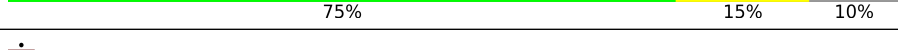
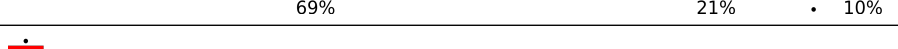
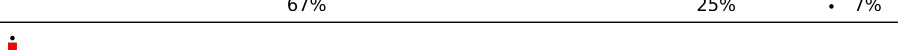
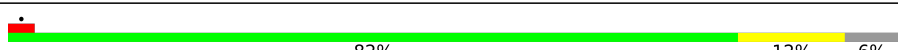
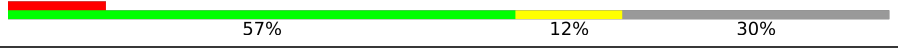
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Mol	Chain	Length	Quality of chain
4	SC	255	
5	SF	261	
6	SG	225	
7	SH	236	
8	SI	190	
9	SJ	200	
10	SK	197	
11	SM	156	
12	SN	143	
13	SO	151	
14	SP	137	
15	SR	143	
16	ST	146	
17	SX	130	
18	SY	145	
19	SZ	135	
20	Sc	82	
21	Sd	67	
22	3B	327	
22	3C	327	
23	3D	504	
24	3E	511	
25	3F	573	
26	3G	126	
26	3H	126	

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Mol	Chain	Length	Quality of chain
27	A4	776	
28	A5	643	
29	A8	713	
30	A9	575	
31	AE	1769	
32	AF	513	
33	AG	896	
34	B1	923	
35	B2	943	
36	B3	817	
37	B8	594	
38	BE	939	
39	B6	440	
40	5B	214	
41	5C	554	
42	5D	250	
43	5E	593	
44	5F	183	
45	5G	290	
46	5H	610	
47	5I	489	
48	5J	217	
49	5K	189	
50	RA	707	
51	RB	357	

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Mol	Chain	Length	Quality of chain
52	RC	316	
53	RE	1237	
54	RF	297	
55	RG	252	
55	RH	252	
56	RI	274	
57	RJ	1183	
58	RK	367	
59	RL	1056	
59	RM	1056	
60	RN	810	
61	RO	552	
62	RP	2493	
63	RQ	899	
64	RS	483	
65	RT	326	
66	RV	346	
67	RW	206	
68	RY	534	
69	X1	347	

2 Entry composition

There are 72 unique types of molecules in this entry. The entry contains 232186 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3A	175	Total	C	N	O	P	0	0
			3711	1661	648	1227	175		

- Molecule 2 is a RNA chain called 5' ETS.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5A	523	Total	C	N	O	P	0	0
			11163	4988	1984	3668	523		

- Molecule 3 is a RNA chain called 18S pre-rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SA	1325	Total	C	N	O	P	0	0
			28258	12629	5035	9269	1325		

- Molecule 4 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SC	230	Total	C	N	O	S	0	0
			1830	1156	335	335	4		

- Molecule 5 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SF	229	Total	C	N	O	S	0	0
			1815	1161	331	320	3		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SI	165	Total	C	N	O	S	0	0
			1321	853	226	242			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SJ	166	Total	C	N	O	S	0	0
			1324	824	262	236	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SK	171	Total	C	N	O	S	0	0
			1388	879	268	240	1		

- Molecule 11 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SM	123	Total	C	N	O	S	0	0
			997	641	189	164	3		

- Molecule 12 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SN	119	Total	C	N	O	S	0	0
			865	545	151	167	2		

- Molecule 13 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SO	134	Total	C	N	O	S	0	0
			1087	698	202	186	1		

- Molecule 14 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SP	118	Total	C	N	O	S	0	0
			868	536	164	165	3		

- Molecule 15 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SR	125	Total	C	N	O		0	0
			973	625	174	174			

- Molecule 16 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	ST	117	Total	C	N	O	S	0	0
			964	610	184	168	2		

- Molecule 17 is a protein called 40S ribosomal protein S22-B.

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

- Molecule 18 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SY	103	Total	C	N	O	S	0	0
			786	503	144	137	2		

- Molecule 19 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SZ	102	Total	C	N	O		0	0
			809	517	148	144			

- Molecule 20 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Sc	80	Total	C	N	O	S	0	0
			603	377	109	112	5		

- Molecule 21 is a protein called 40S ribosomal protein S28-A.

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

- Molecule 22 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	3B	240	Total	C	N	O	S	0	0
			1865	1184	333	338	10		
22	3C	225	Total	C	N	O	S	0	0
			1763	1120	316	317	10		

- Molecule 23 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	3D	369	Total	C	N	O	S	0	0
			2848	1811	489	540	8		

- Molecule 24 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	3E	431	Total	C	N	O	S	0	0
			3028	1888	543	588	9		

- Molecule 25 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	3F	454	Total	C	N	O	S	0	0
			3643	2315	638	680	10		

- Molecule 26 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	3G	121	Total	C	N	O	S	0	0
			916	583	158	171	4		
26	3H	121	Total	C	N	O	S	0	0
			916	583	158	171	4		

- Molecule 27 is a protein called U3 small nucleolar RNA-associated protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A4	662	Total	C	N	O	S	0	0
			5226	3309	910	986	21		

- Molecule 28 is a protein called U3 small nucleolar RNA-associated protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	A5	514	Total	C	N	O	S	0	0
			3976	2520	688	755	13		

- Molecule 29 is a protein called U3 small nucleolar RNA-associated protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	A8	548	Total	C	N	O	S	0	0
			3307	2054	608	642	3		

- Molecule 30 is a protein called U3 small nucleolar RNA-associated protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	A9	128	Total	C	N	O	S	0	0
			939	594	173	170	2		

- Molecule 31 is a protein called U3 small nucleolar RNA-associated protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AE	1534	Total	C	N	O	S	0	0
			9955	6242	1771	1923	19		

- Molecule 32 is a protein called U3 small nucleolar RNA-associated protein 15.

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

- Molecule 33 is a protein called NET1-associated nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AG	826	Total	C	N	O	S	0	0
			6570	4181	1111	1259	19		

- Molecule 34 is a protein called Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	B1	834	Total	C	N	O	S	0	0
			6635	4223	1140	1253	19		

- Molecule 35 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	B2	851	Total	C	N	O	S	0	0
			6723	4294	1133	1269	27		

- Molecule 36 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	B3	757	Total	C	N	O	S	0	0
			5919	3769	993	1130	27		

- Molecule 37 is a protein called U3 small nucleolar RNA-associated protein 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	B8	477	Total	C	N	O	S	0	0
			3764	2387	662	705	10		

- Molecule 38 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BE	865	Total	C	N	O	S	0	0
			6810	4322	1175	1292	21		

- Molecule 39 is a protein called U3 small nucleolar RNA-associated protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	B6	374	Total	C	N	O	S	0	0
			2800	1782	501	505	12		

- Molecule 40 is a protein called Bud site selection protein 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	5B	60	Total	C	N	O	0	0
			495	310	101	84		

- Molecule 41 is a protein called U3 small nucleolar RNA-associated protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	5C	535	Total	C	N	O	S	0	0
			4237	2656	762	807	12		

- Molecule 42 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	5D	235	Total	C	N	O	S	0	0
			1972	1226	380	359	7		

- Molecule 43 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	5E	204	Total	C	N	O	S	0	0
			1647	1021	294	328	4		

- Molecule 44 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	5F	182	Total	C	N	O	S	0	0
			1530	967	287	269	7		

- Molecule 45 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	5G	282	Total	C	N	O	S	0	0
			2296	1441	430	418	7		

- Molecule 46 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	5H	136	Total	C	N	O		0	0
			1065	658	211	196			

- Molecule 47 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	5I	461	Total	C	N	O	S	0	0
			3765	2354	686	709	16		

- Molecule 48 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	5J	151	Total	C	N	O	S	0	0
			1280	807	240	228	5		

- Molecule 49 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	5K	175	Total	C	N	O	S	0	0
			1403	896	256	241	10		

- Molecule 50 is a protein called Ribosome biogenesis protein ENP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	RA	338	Total	C	N	O	S	0	0
			2709	1713	463	524	9		

- Molecule 51 is a protein called U3 small nucleolar ribonucleoprotein protein LCP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	RB	134	Total	C	N	O	S	0	0
			1108	664	227	214	3		

- Molecule 52 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	RC	278	Total	C	N	O	S	0	0
			2207	1408	391	395	13		

- Molecule 53 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	RE	1079	Total	C	N	O	S	0	0
			8716	5666	1437	1589	24		

- Molecule 54 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	RF	241	Total	C	N	O	S	0	0
			1963	1253	335	367	8		

- Molecule 55 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	RG	216	Total	C	N	O	S	0	0
			1701	1079	296	315	11		
55	RH	230	Total	C	N	O	S	0	0
			1799	1142	313	333	11		

- Molecule 56 is a protein called Ribosome biogenesis protein UTP30.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	RI	252	Total	C	N	O	S	0	0
			2045	1309	362	366	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
57	RJ	796	Total	C	N	O	S	0	0
			6379	4086	1136	1128	29		

- Molecule 58 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

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

- Molecule 59 is a protein called RNA cytidine acetyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	RL	805	Total	C	N	O	S	0	0
			4539	2760	885	887	7		
59	RM	766	Total	C	N	O		0	0
			3779	2247	766	766			

- Molecule 60 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	RN	607	Total	C	N	O	S	0	0
			4529	2861	820	837	11		

- Molecule 61 is a protein called Nucleolar complex protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	RO	525	Total	C	N	O	S	0	0
			3766	2412	646	696	12		

- Molecule 62 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	RP	2109	Total	C	N	O	S	0	0
			12176	7486	2292	2382	16		

- Molecule 63 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	RQ	226	Total	C	N	O	S	0	0
			1651	1023	313	313	2		

- Molecule 64 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	RS	251	Total	C	N	O	S	0	0
			2051	1340	349	359	3		

- Molecule 65 is a protein called Pno1.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	RT	171	Total	C	N	O	S	0	0
			1357	864	249	240	4		

- Molecule 66 is a protein called Protein FAF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	RV	190	Total	C	N	O	S	0	0
			1448	891	290	264	3		

- Molecule 67 is a protein called Regulator of rDNA transcription protein 14.

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

- Molecule 68 is a protein called Protein BFR2.

Mol	Chain	Residues	Atoms				AltConf	Trace
68	RY	37	Total	C	N	O	0	0
			299	191	48	60		

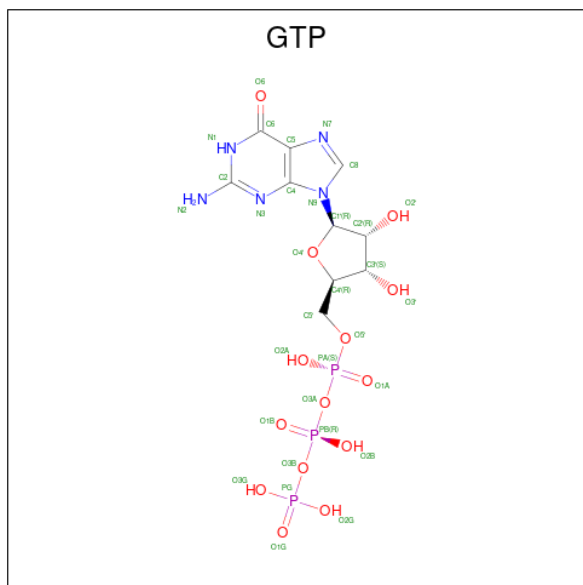
- Molecule 69 is a protein called Unassigned helices.

Mol	Chain	Residues	Atoms				AltConf	Trace
69	X1	61	Total	C	N	O	0	0
			305	183	61	61		

- Molecule 70 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
70	Sc	1	Total	Zn	0
			1	1	
70	5K	1	Total	Zn	0
			1	1	

- Molecule 71 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

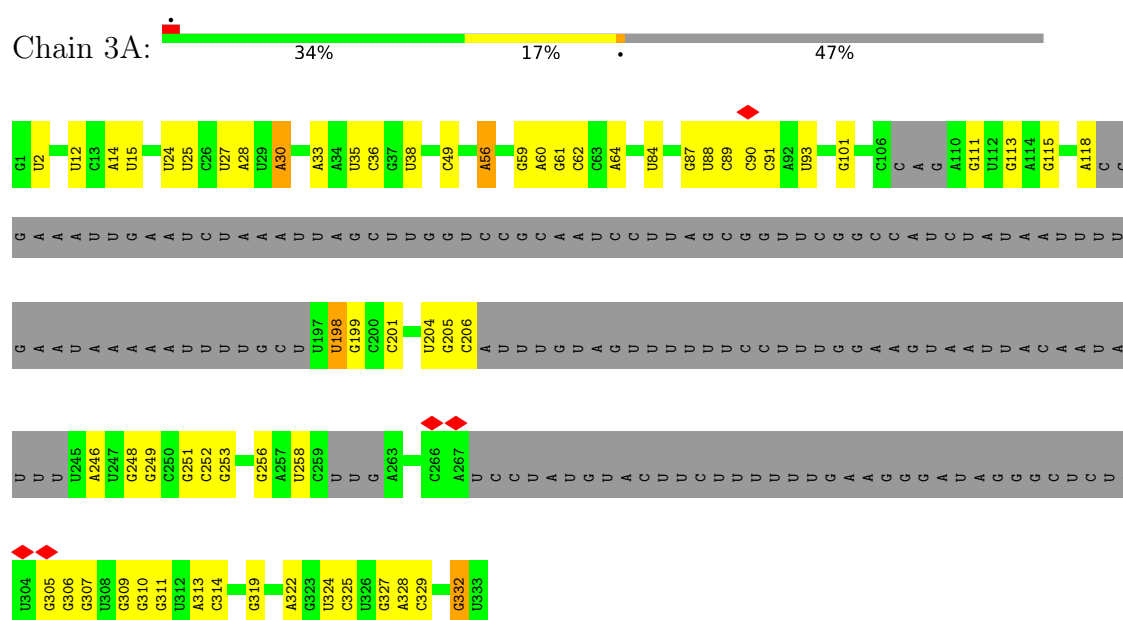
- Molecule 72 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
72	RJ	1	Total	Mg	0
			1	1	

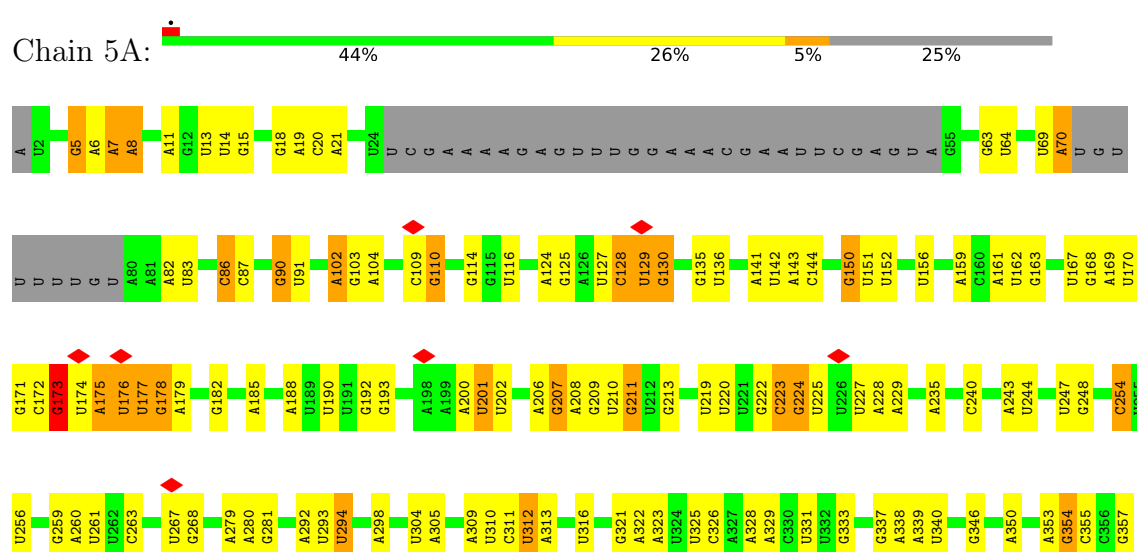
3 Residue-property plots [i](#)

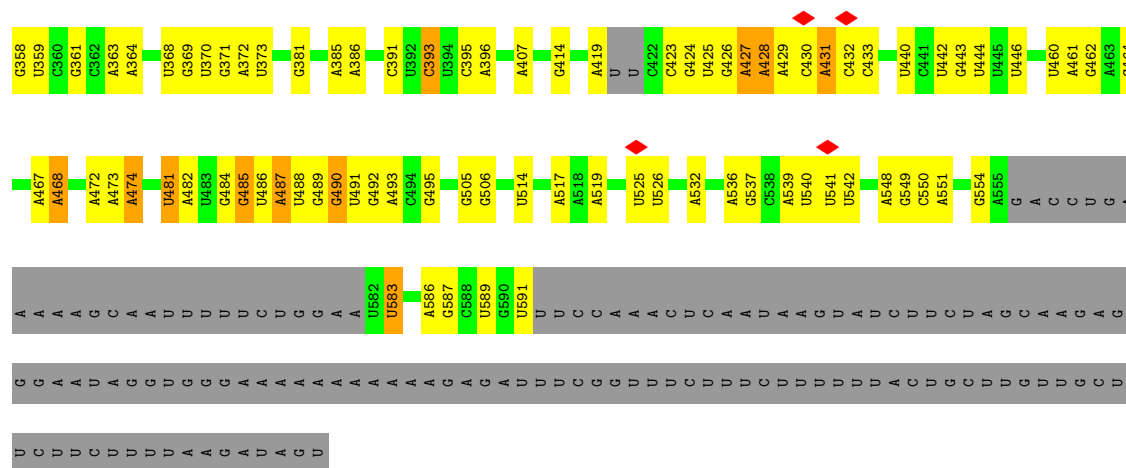
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: U3 snoRNA

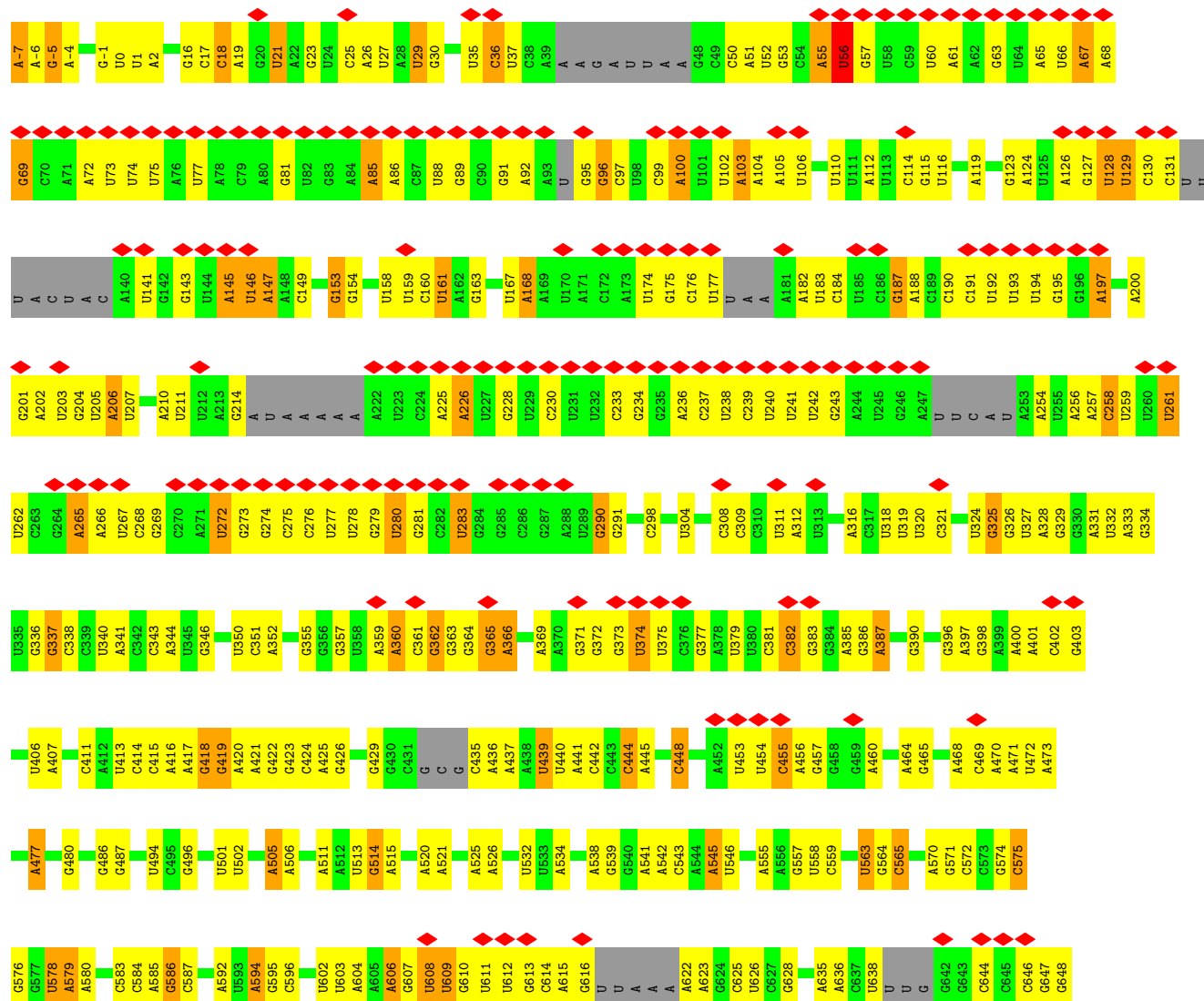


• Molecule 2: 5' ETS

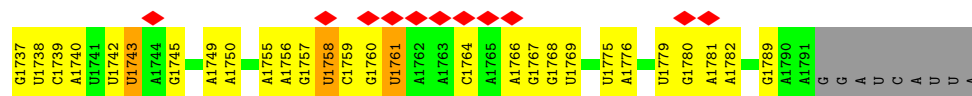




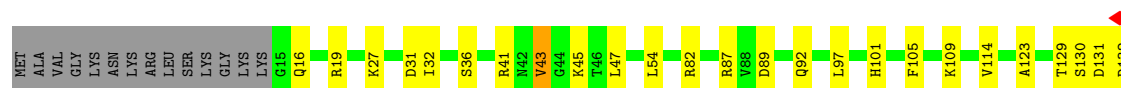
• Molecule 3: 18S pre-rRNA



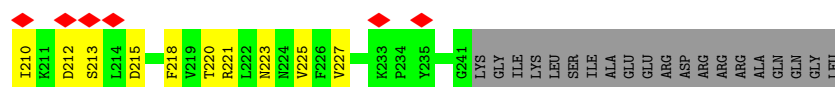
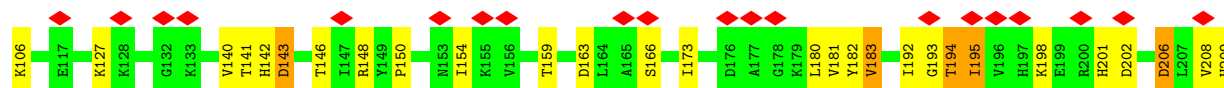




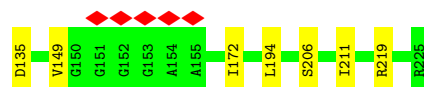
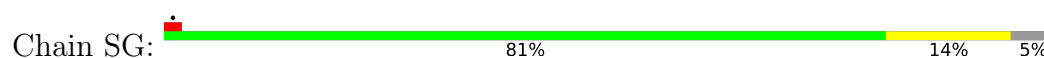
- Molecule 4: 40S ribosomal protein S1-A



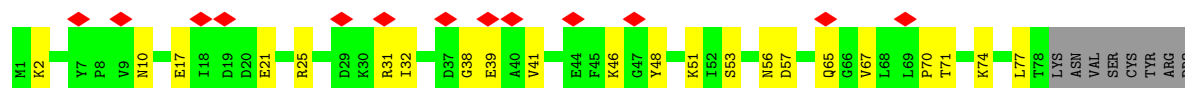
- Molecule 5: 40S ribosomal protein S4-A

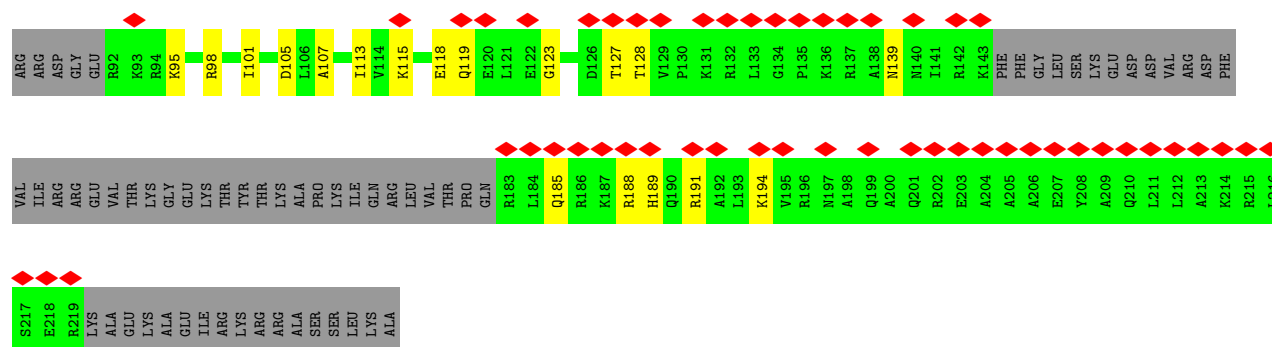


- Molecule 6: 40S ribosomal protein S5

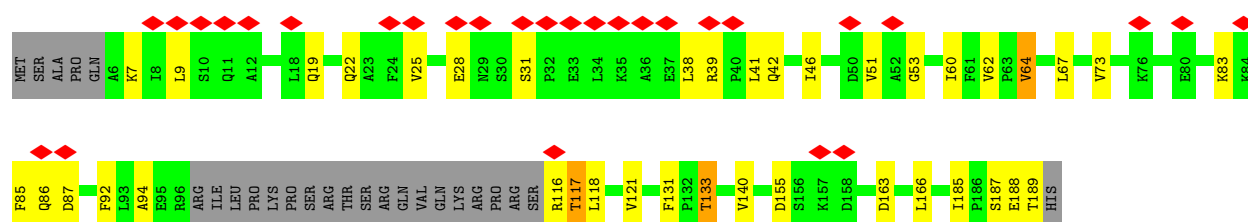


- Molecule 7: 40S ribosomal protein S6-A

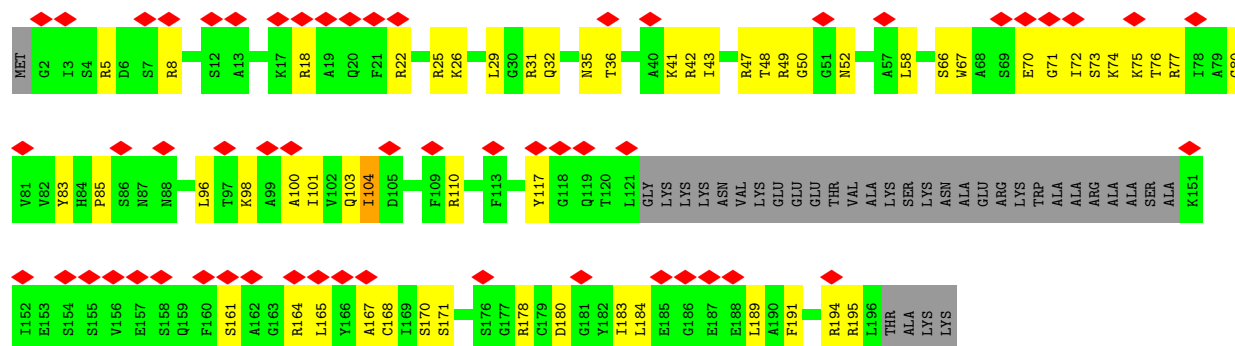




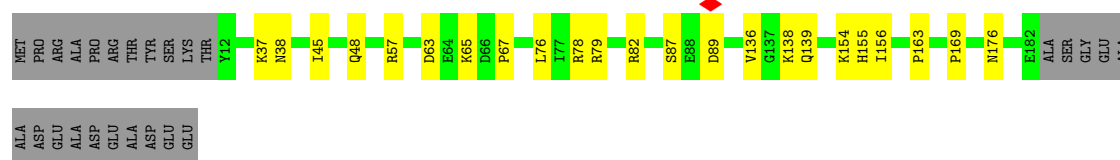
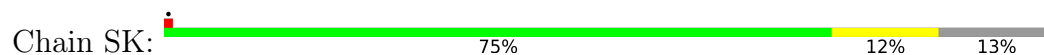
• Molecule 8: 40S ribosomal protein S7-A



• Molecule 9: 40S ribosomal protein S8-A

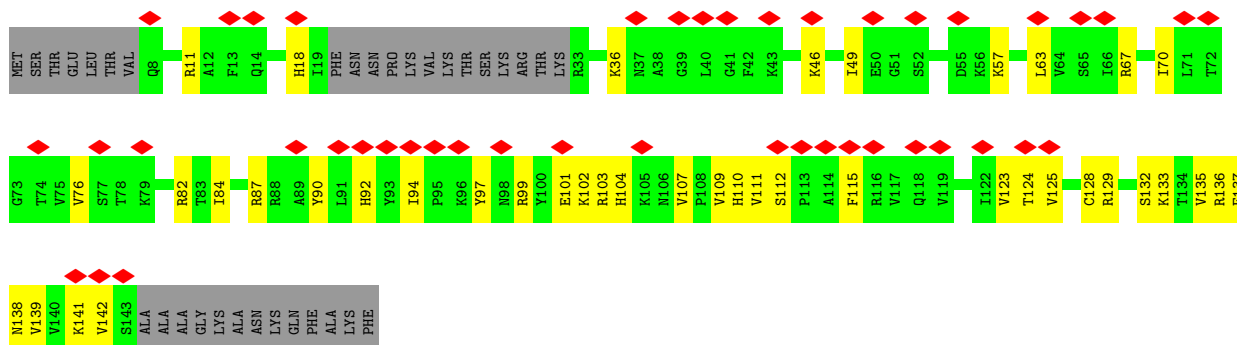


• Molecule 10: 40S ribosomal protein S9-A

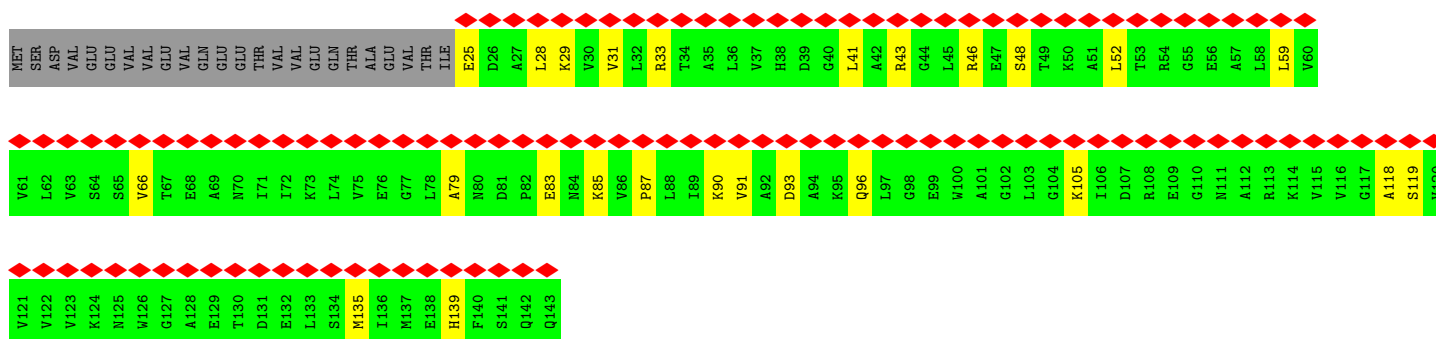
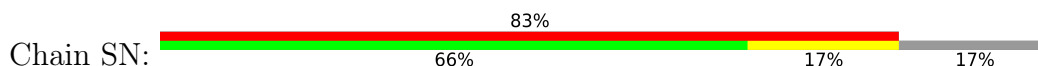


• Molecule 11: 40S ribosomal protein S11-A

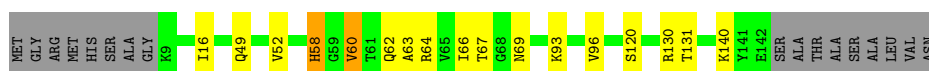
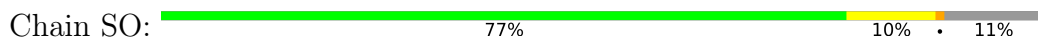




• Molecule 12: 40S ribosomal protein S12



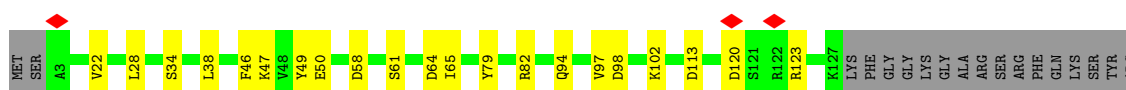
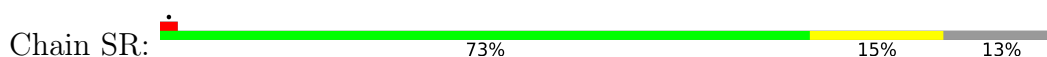
• Molecule 13: 40S ribosomal protein S13



• Molecule 14: 40S ribosomal protein S14-A

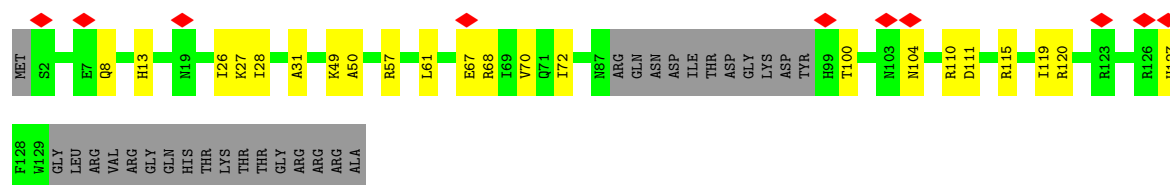


• Molecule 15: 40S ribosomal protein S16-A



• Molecule 16: 40S ribosomal protein S18-A





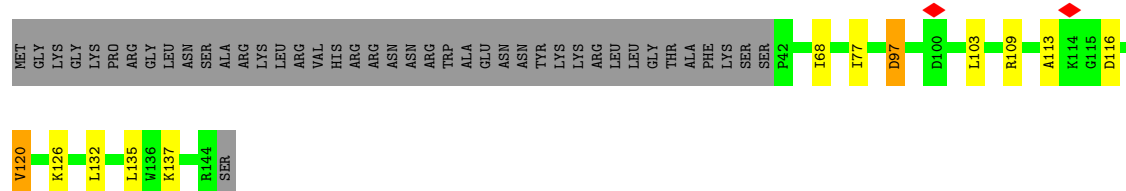
- Molecule 17: 40S ribosomal protein S22-B

Chain SX: 82% 15% ..



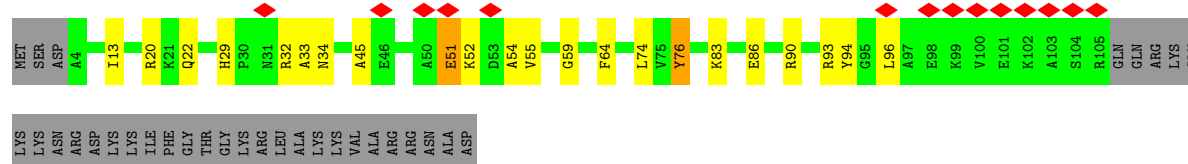
- Molecule 18: 40S ribosomal protein S23-A

Chain SY: 63% 7% 29%



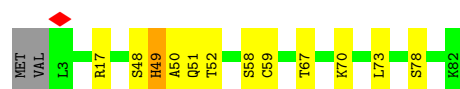
- Molecule 19: 40S ribosomal protein S24-A

Chain SZ: 10% 59% 15% 24%



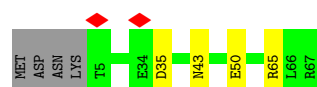
- Molecule 20: 40S ribosomal protein S27-A

Chain Sc: 83% 13% ..



- Molecule 21: 40S ribosomal protein S28-A

Chain Sd: 88% 6% 6%



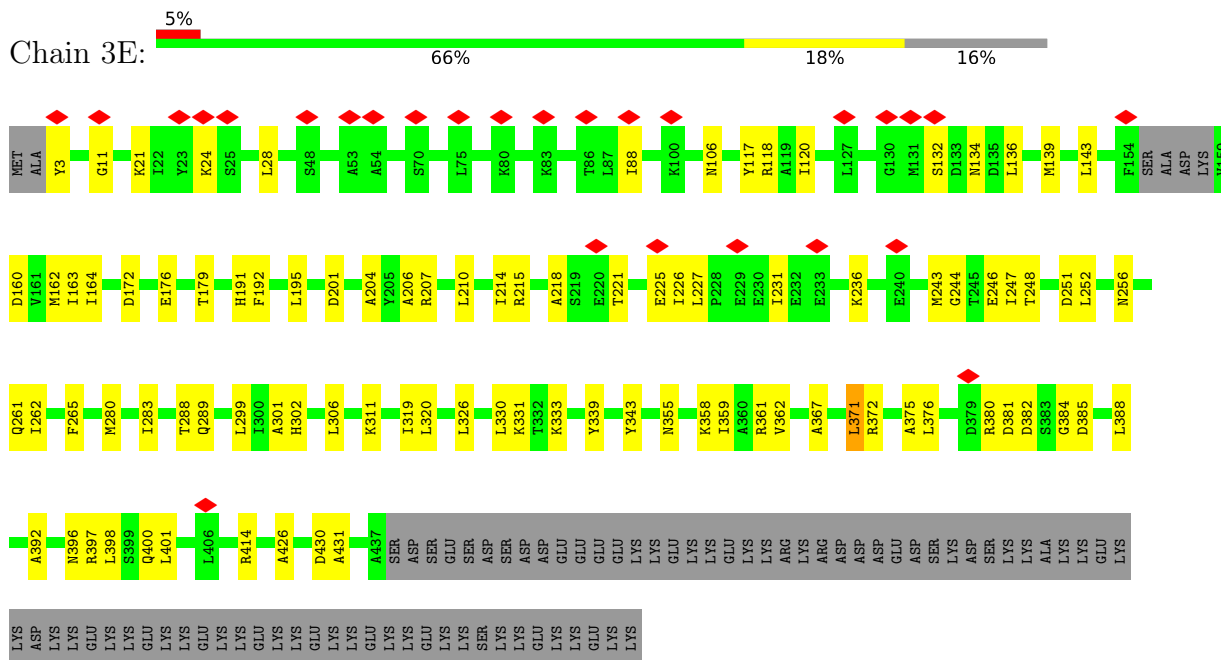
[illegible][illegible]

Chain 3D:

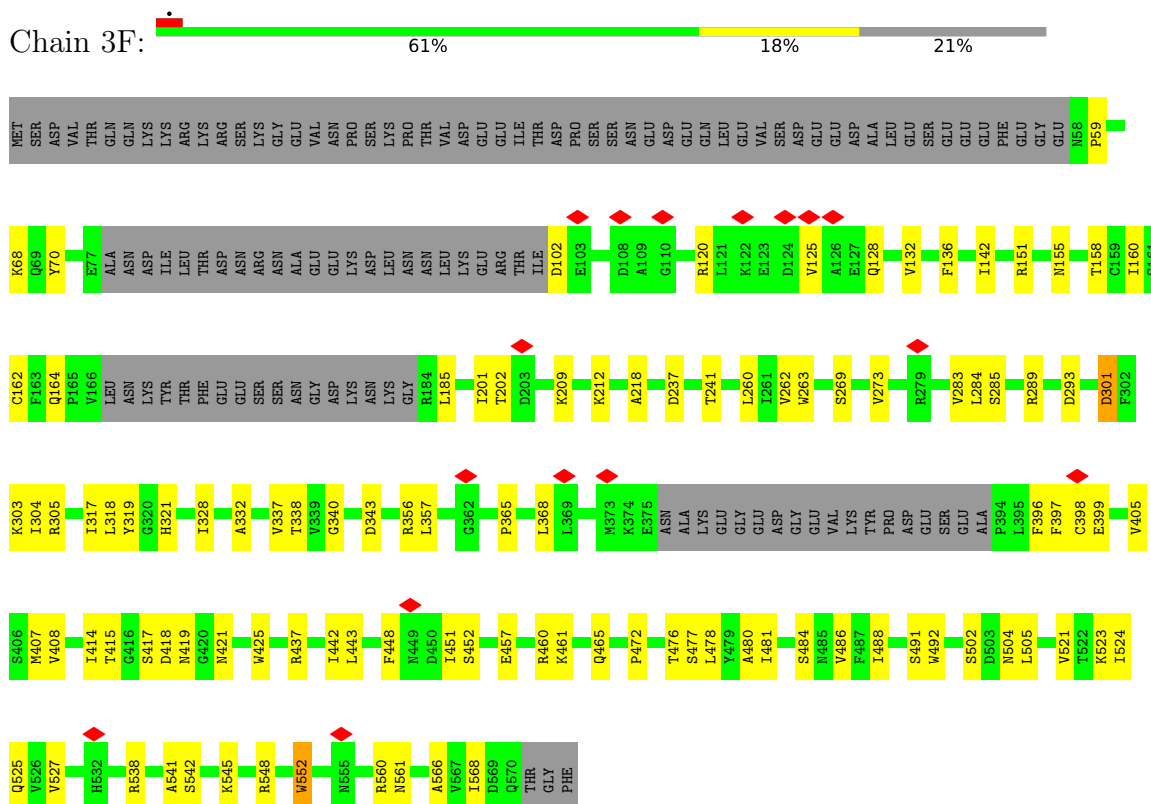
60% 13% 27%

MET ALA P3 I4 L7 V20 K21 L22 Q23 Q24 D25 D26 S29 E30 L31 Q35 K46 E49 S52 A59 A60 E61 A62 L63 N67 S77 N85 L86 L98 A99 D102 L105 S120 D126 R129 L133 L142 Q143 S144 L152 A157 R150 V163 K169 I175 D182 V195 Y199 H202 L206 P211 F216 L219 D225 K226 A227 SER LEU ASN D231 A238 ALA LEU LEU TYR LEU HIS N242 E243 R250 S258 MET GLY GLN ASP ILE S264 E265 T266 D267 M268 V271 L281 R286 Y289 H297 T296 V299 E309 R314 L315 S317 L336 GLY ALA GLU ASN LYS LEU ALA LEU PHE ARG ALA LEU MET LYS THR LYS THR PRO LYS TYR GLY LEU ALA GLU VAL GLU THR LYS PHE SER LYS SER ALA SER ALA K370 K371 R374 R377 Y378 L379 K382 C383 I389 Y392 L404 V408 Y415 ASN THR GLY LYS PRO THR LEU LYS ASN GLU ASP LYS ALA THR GLN GLU ASP MET LYS GLU LEU TYR ASN ASP LYS ASP LYS PRO LYS ALA SER SER LYS ARG LYS LEU GLU ASP ASP ASP GLU LYS

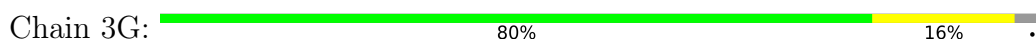
- Molecule 24: Nucleolar protein 58

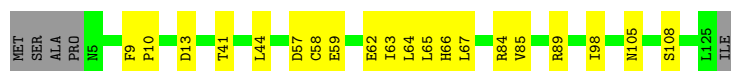


- Molecule 25: Ribosomal RNA-processing protein 9



- Molecule 26: 13 kDa ribonucleoprotein-associated protein





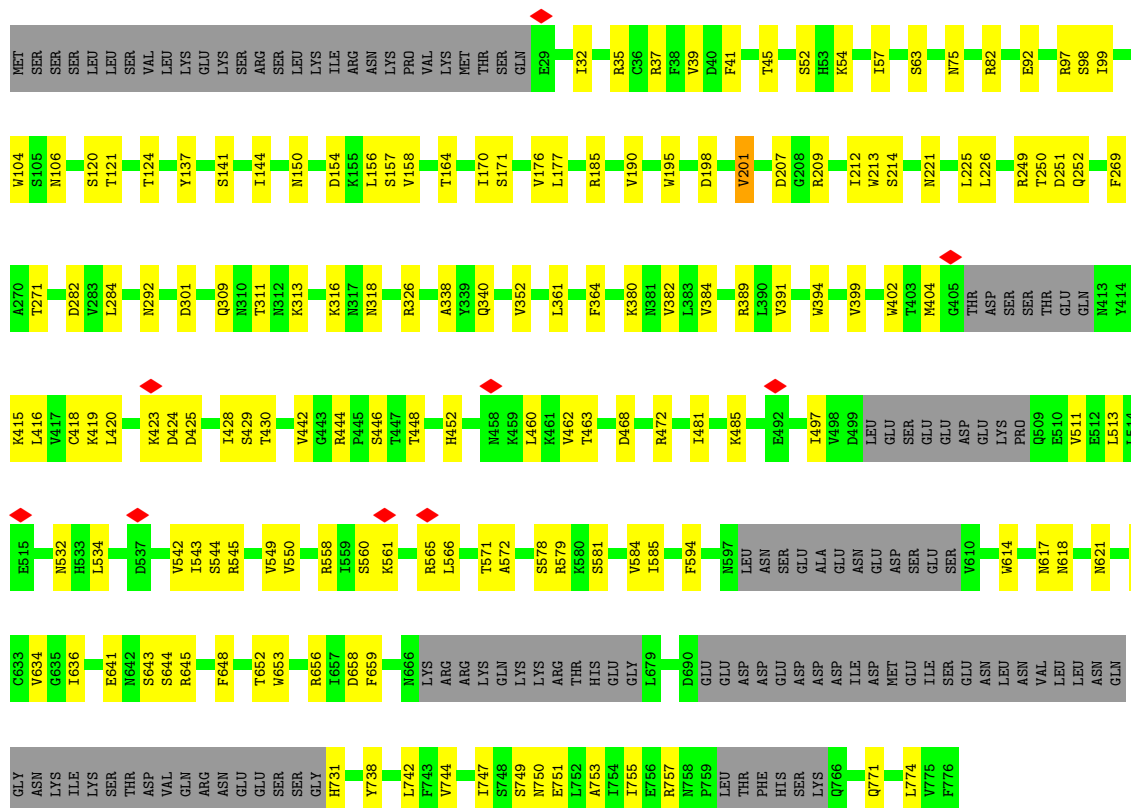
- Molecule 26: 13 kDa ribonucleoprotein-associated protein

Chain 3H: 75% 21% .



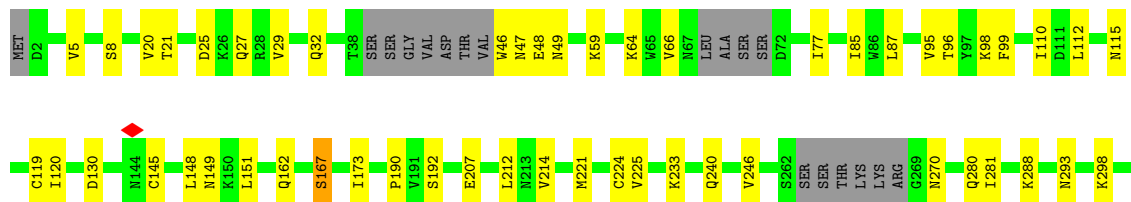
- Molecule 27: U3 small nucleolar RNA-associated protein 4

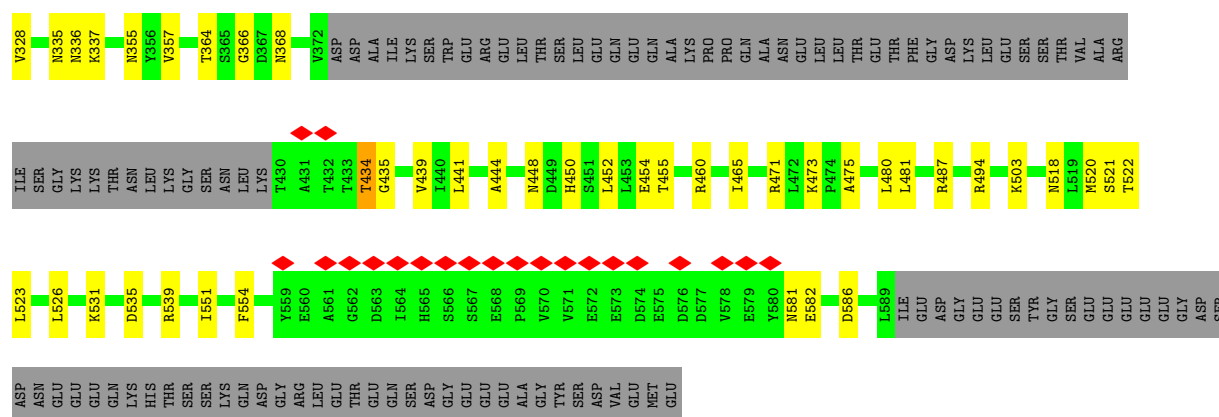
Chain A4: 65% 20% 15%



- Molecule 28: U3 small nucleolar RNA-associated protein 5

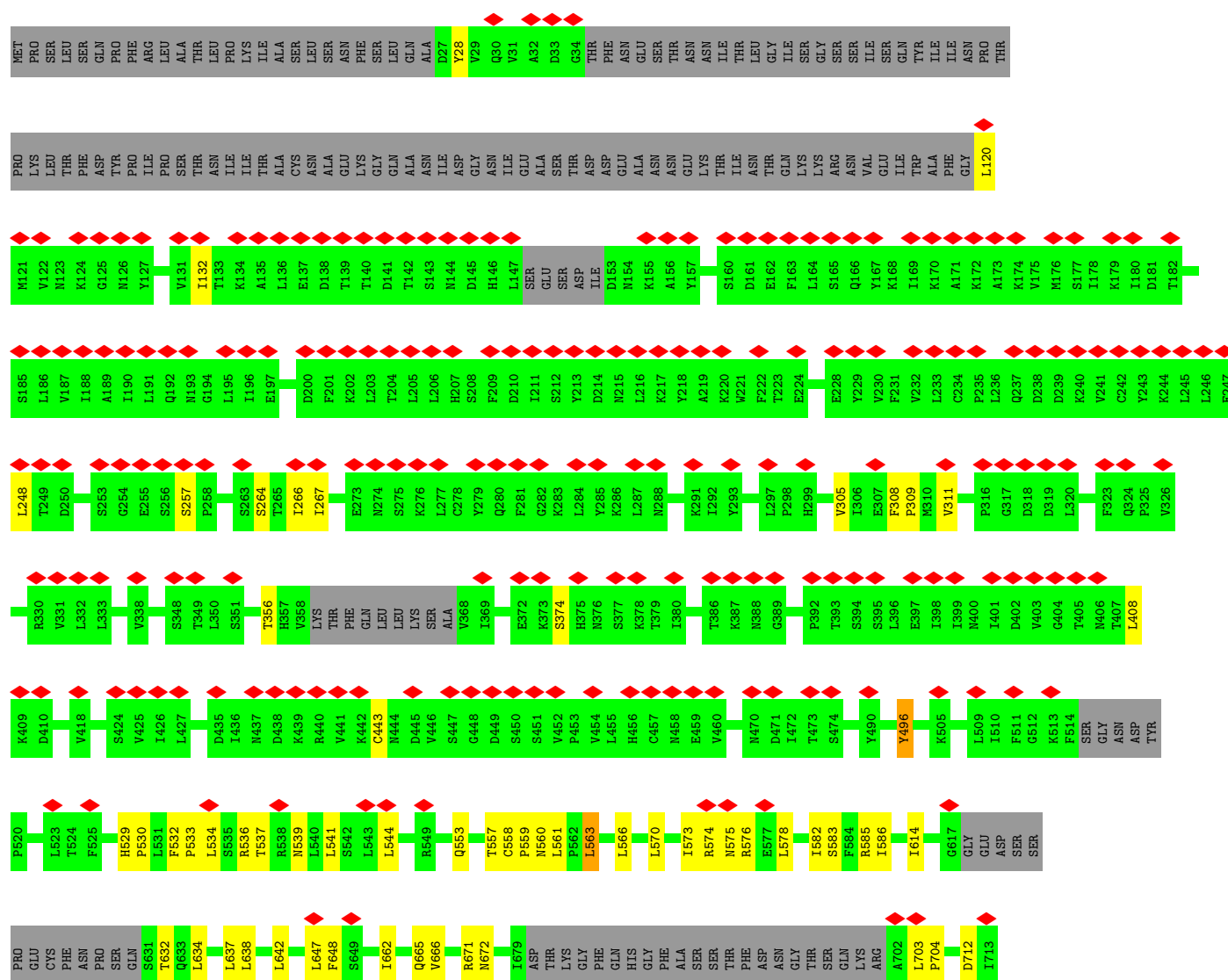
Chain A5: 65% 14% 20%



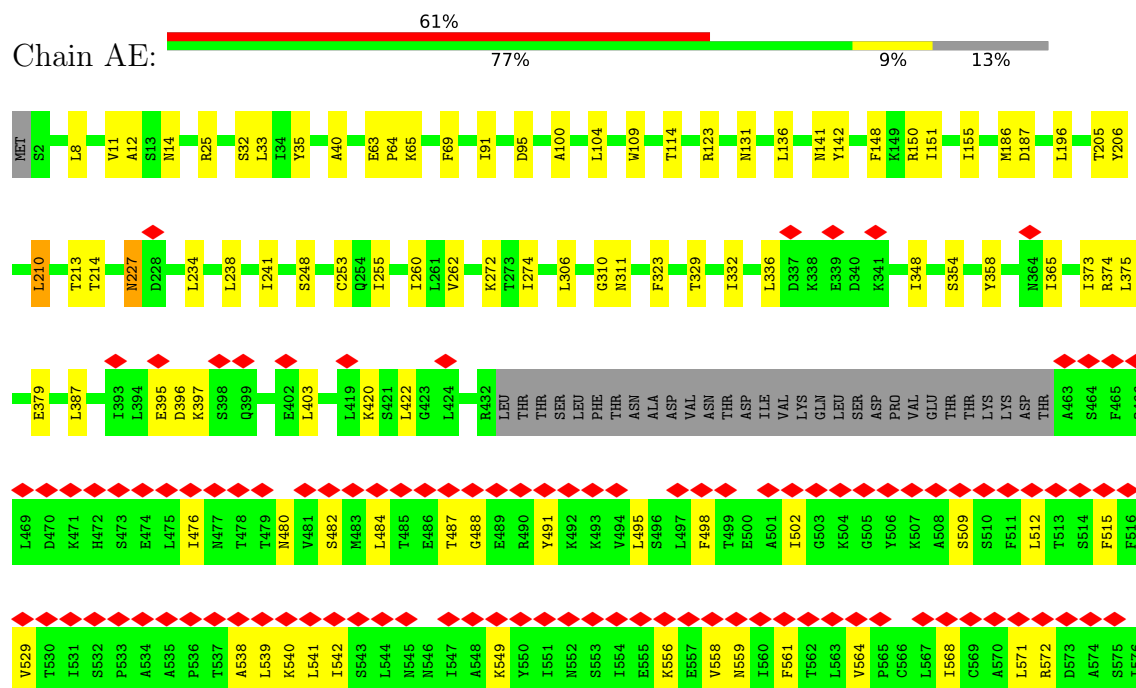


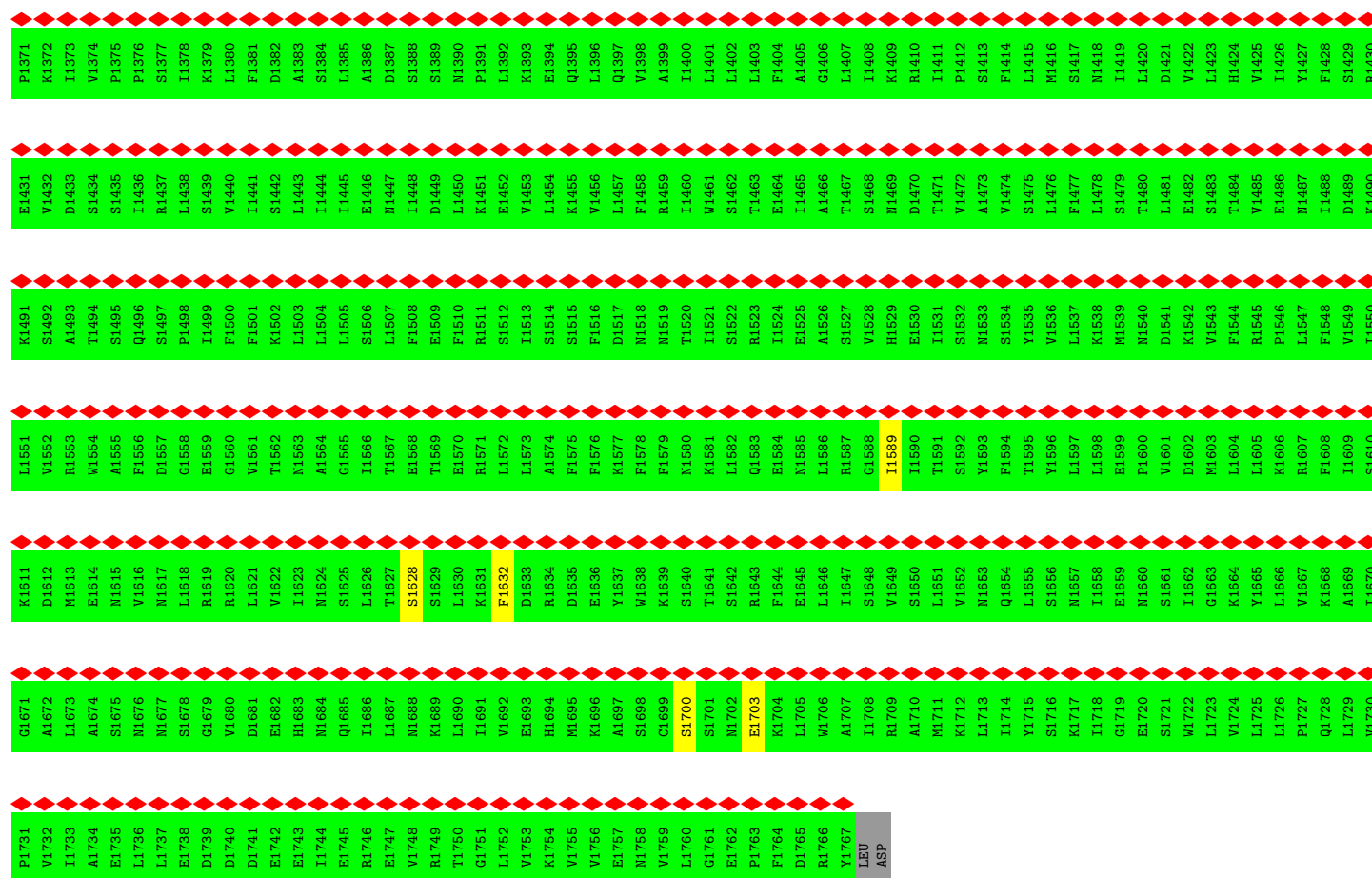
• Molecule 29: U3 small nucleolar RNA-associated protein 8

Chain A8: 31% 68% 8% 23%



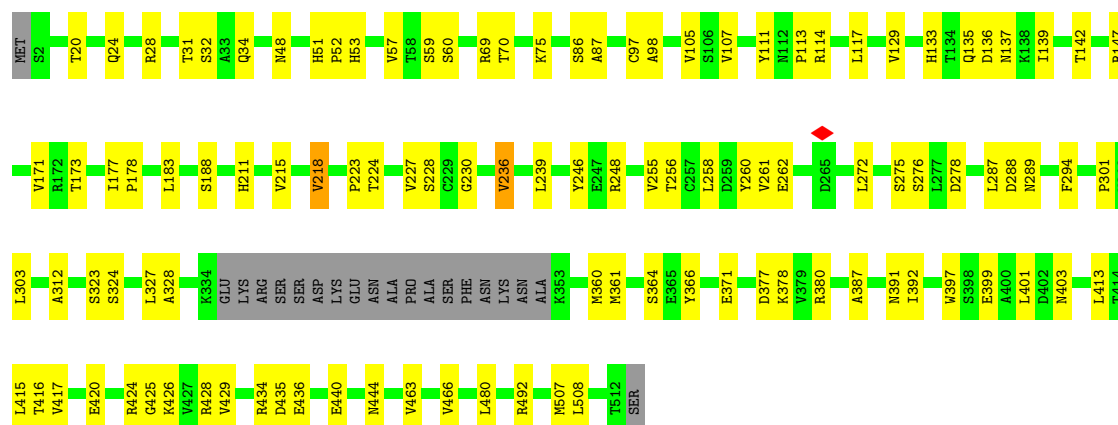
• Molecule 30: U3 small nucleolar RNA-associated protein 9





• Molecule 32: U3 small nucleolar RNA-associated protein 15

Chain AF: 75% 21% .



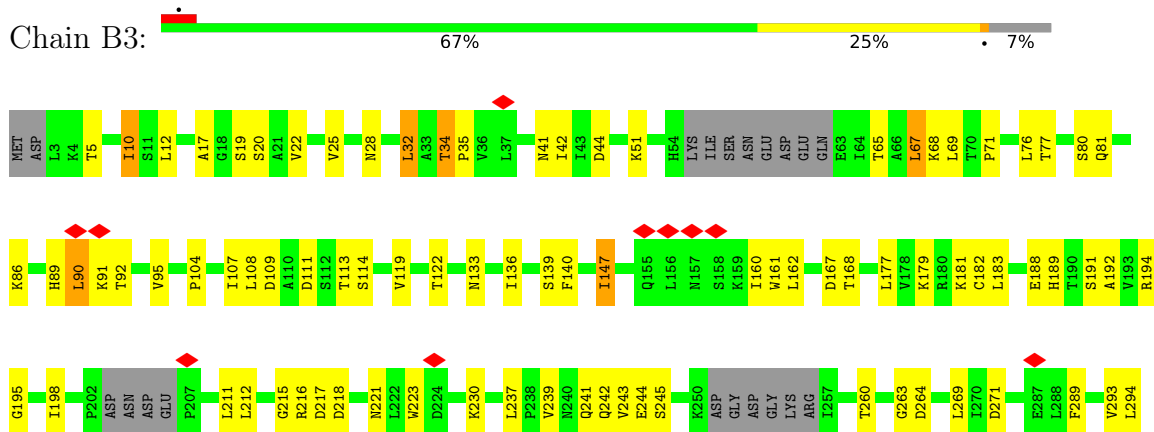
• Molecule 33: NET1-associated nuclear protein 1

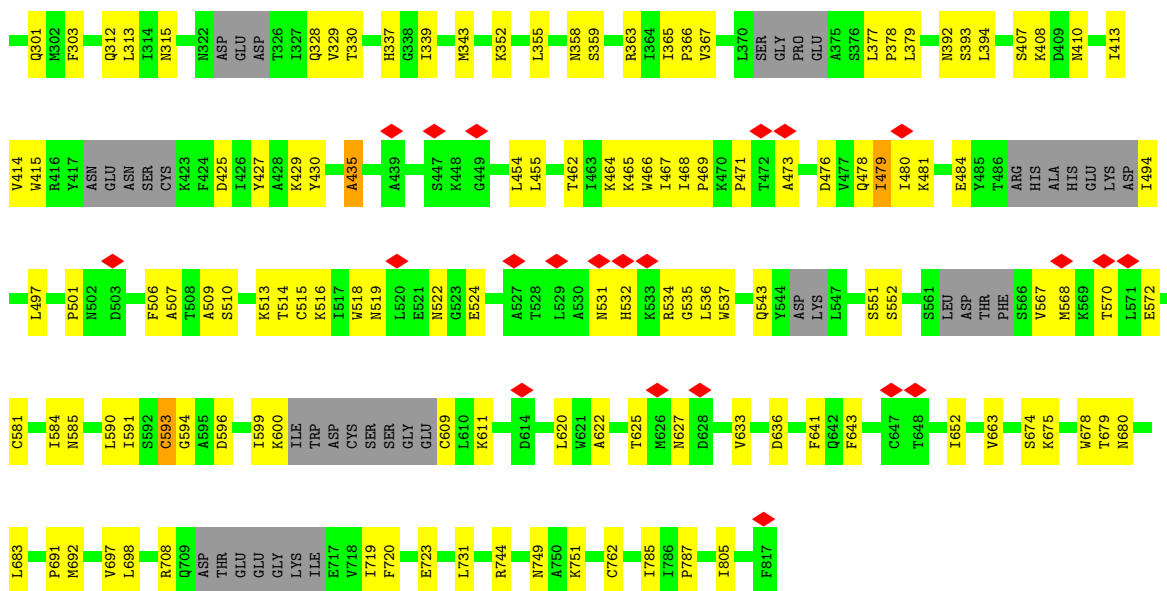
Chain AG: 71% 21% 8%

Chain B2:

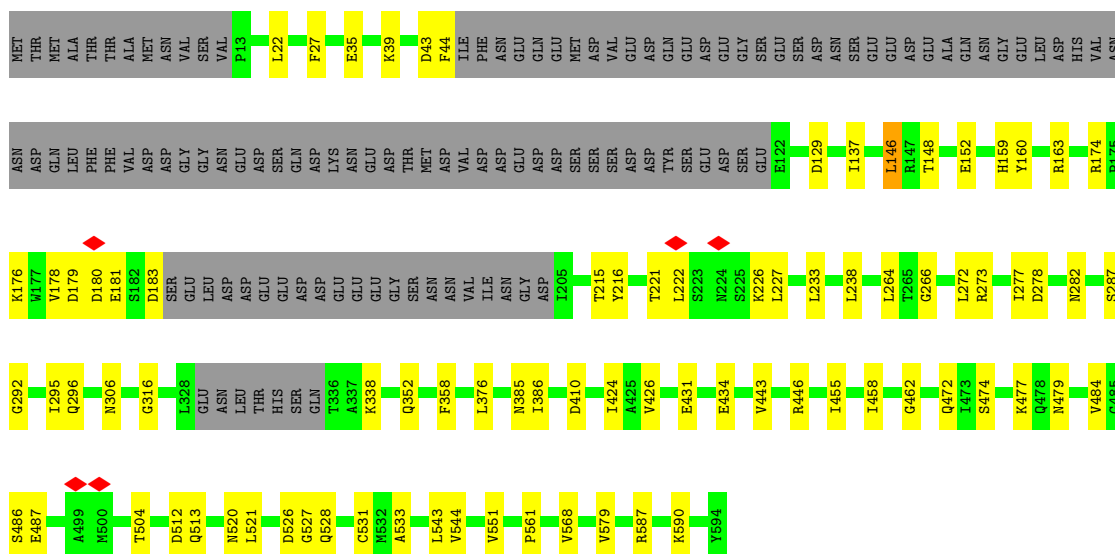


Chain B3:

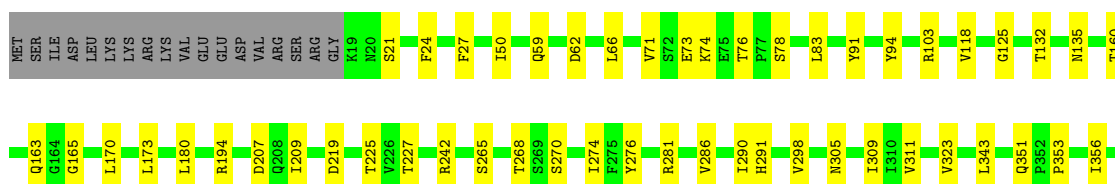
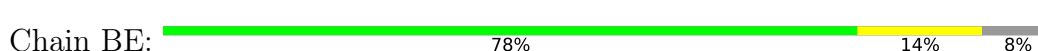


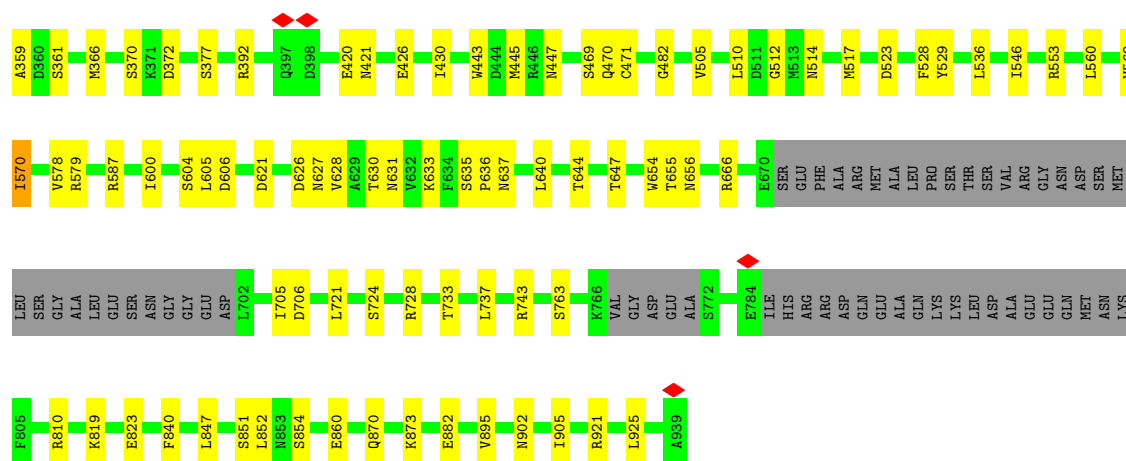


- Molecule 37: U3 small nucleolar RNA-associated protein 18

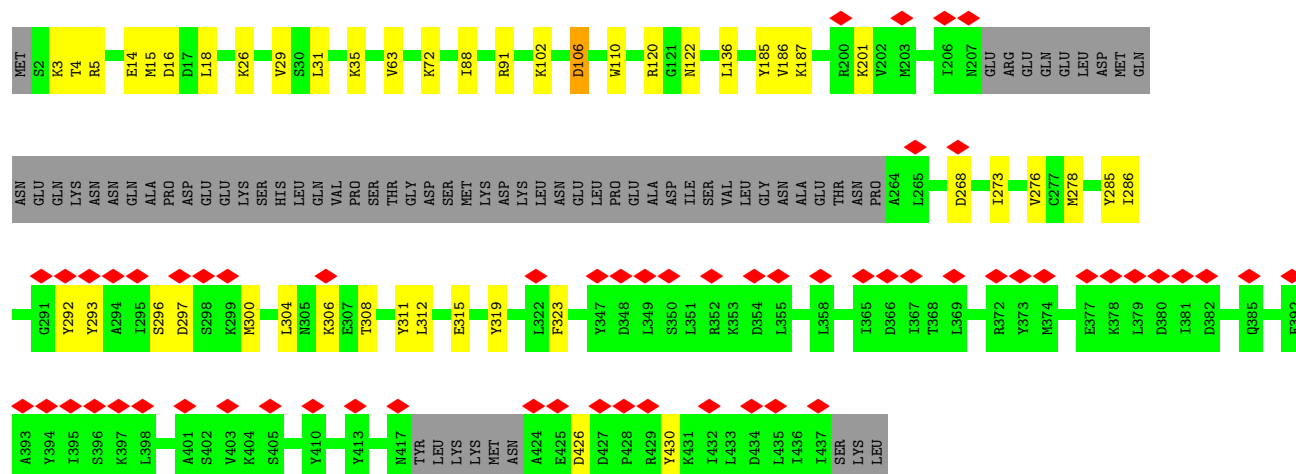
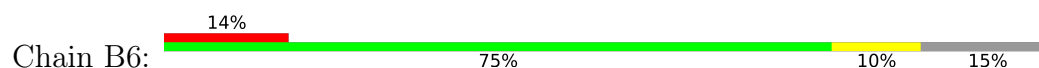


- Molecule 38: U3 small nucleolar RNA-associated protein 21

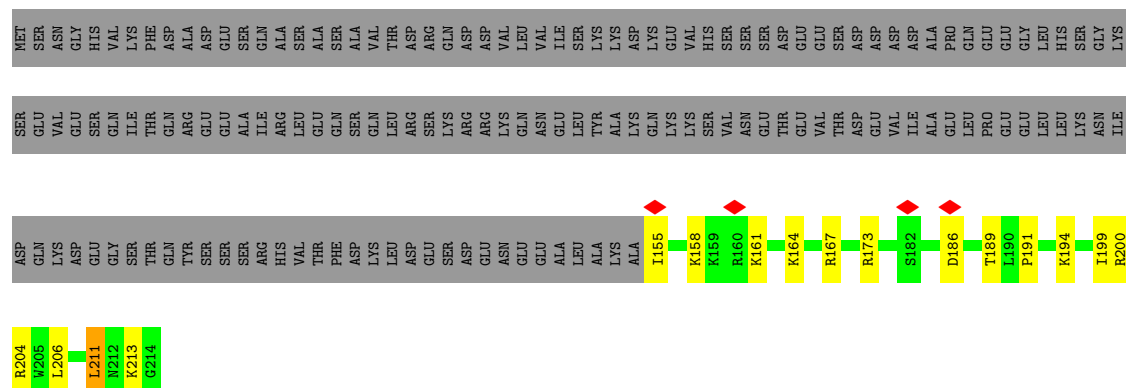




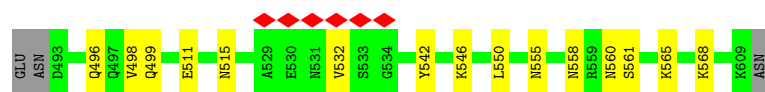
- Molecule 39: U3 small nucleolar RNA-associated protein 6



- Molecule 40: Bud site selection protein 21

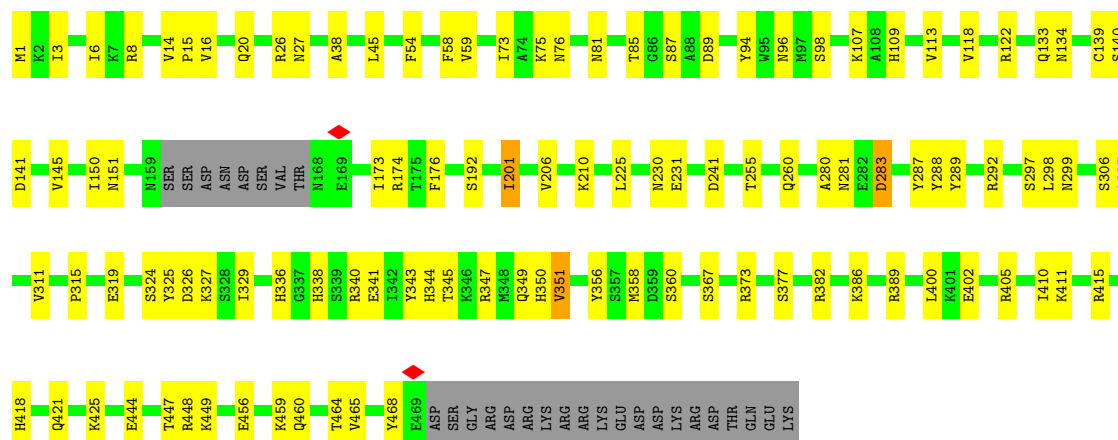


- Molecule 41: U3 small nucleolar RNA-associated protein 7



• Molecule 47: Protein SOF1

Chain 5I: 72% 22% 6%



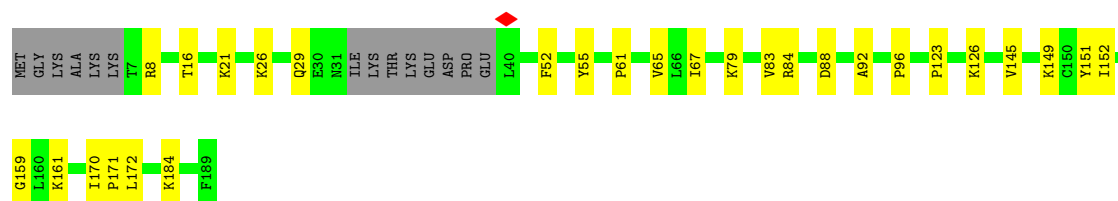
• Molecule 48: rRNA-processing protein FCF2

Chain 5J: 11% 57% 12% 30%



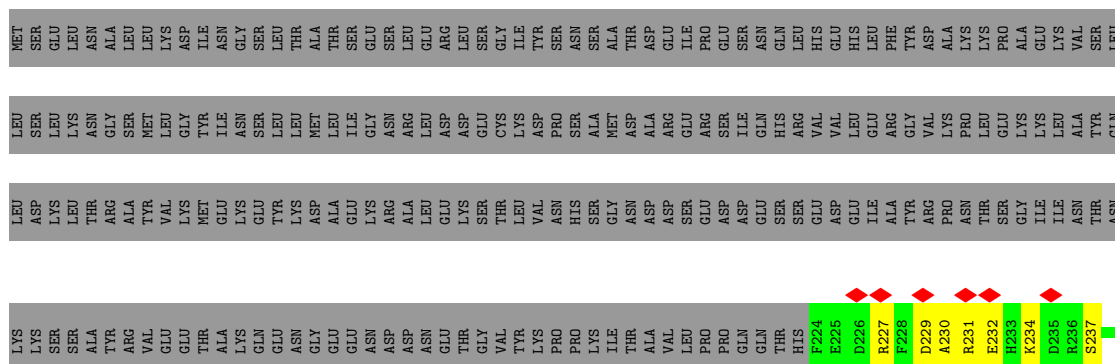
• Molecule 49: rRNA-processing protein FCF1

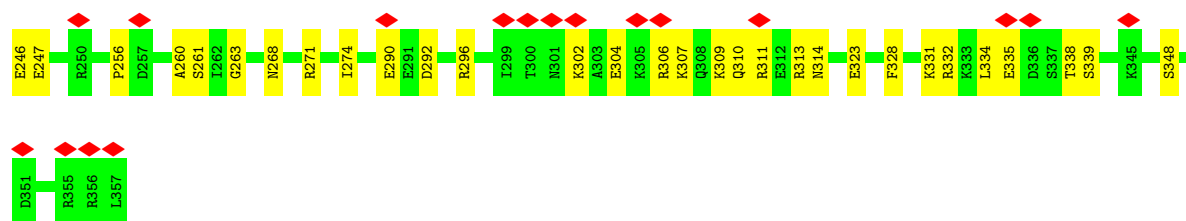
Chain 5K: 78% 15% 7%



• Molecule 50: Ribosome biogenesis protein ENP2

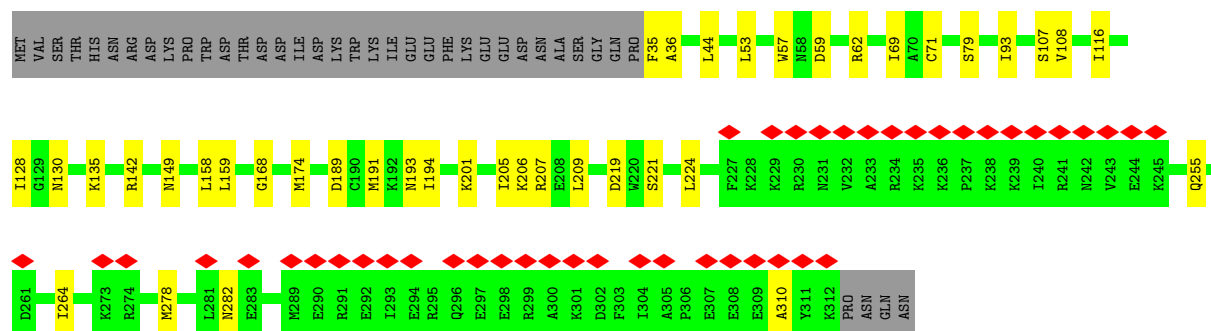
Chain RA: 12% 35% 12% 52%





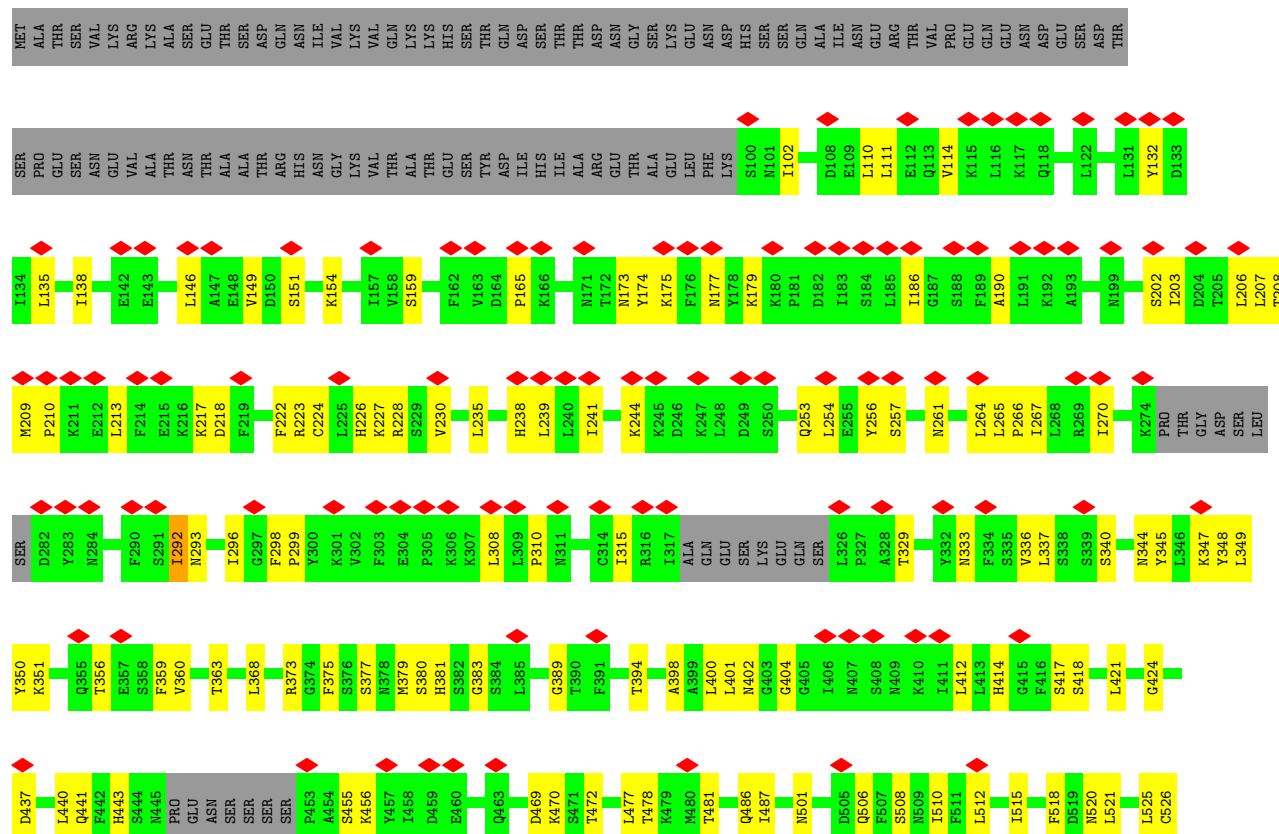
- Molecule 52: KRR1 small subunit processome component

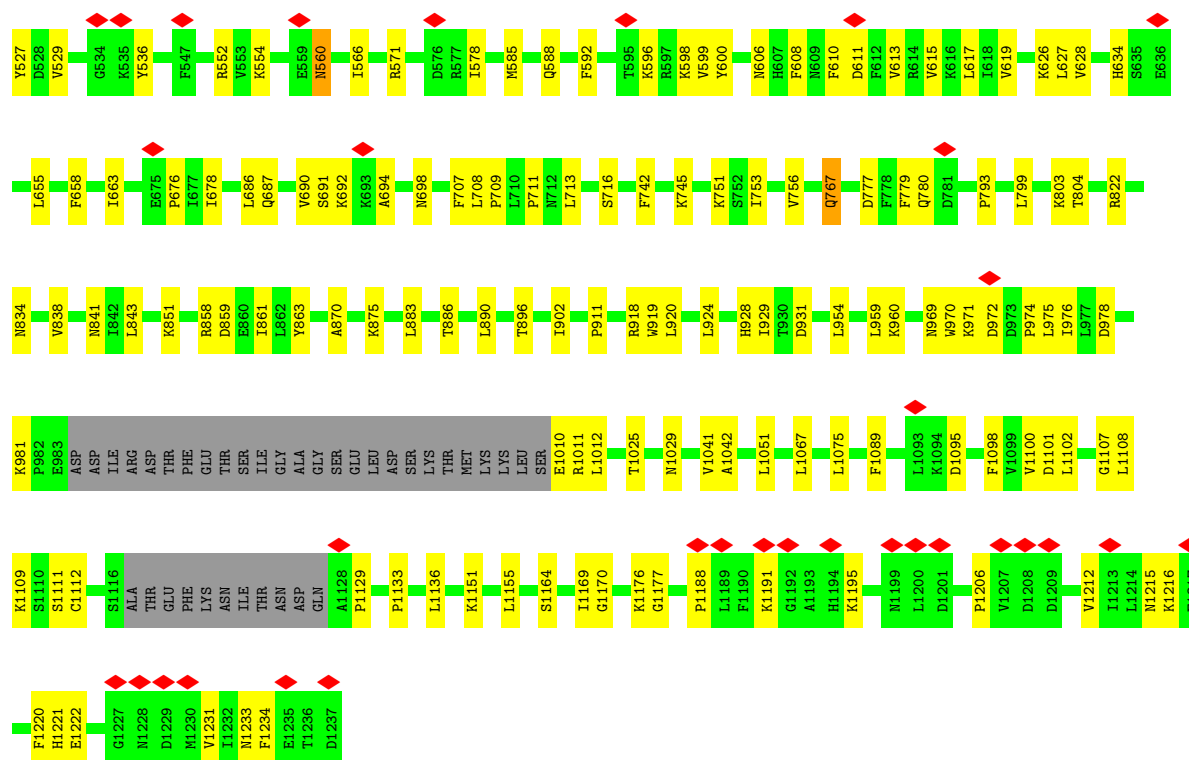
Chain RC: 14% 75% 13% 12%



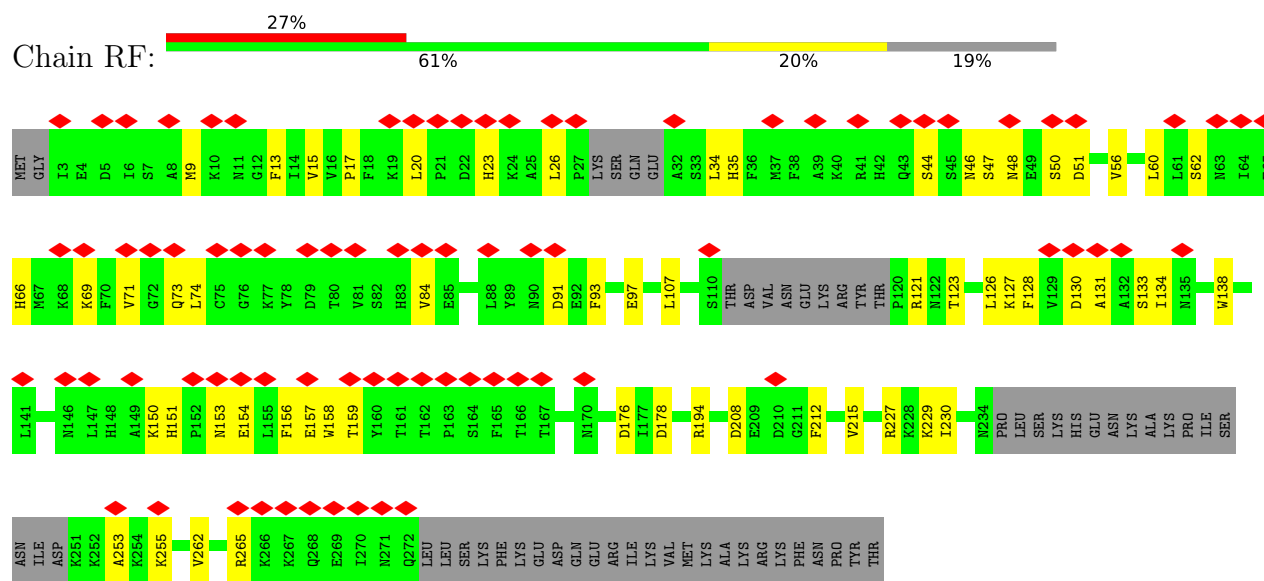
- Molecule 53: U3 small nucleolar RNA-associated protein 22

Chain RE: 11% 66% 21% 13%

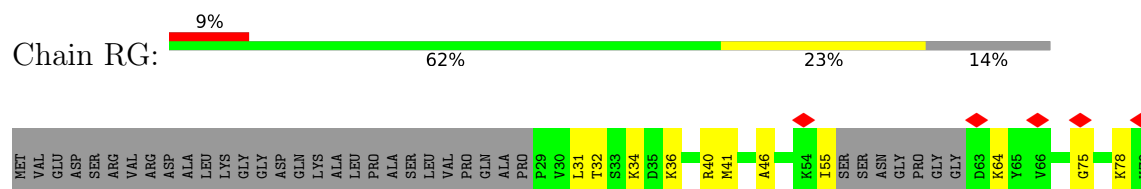




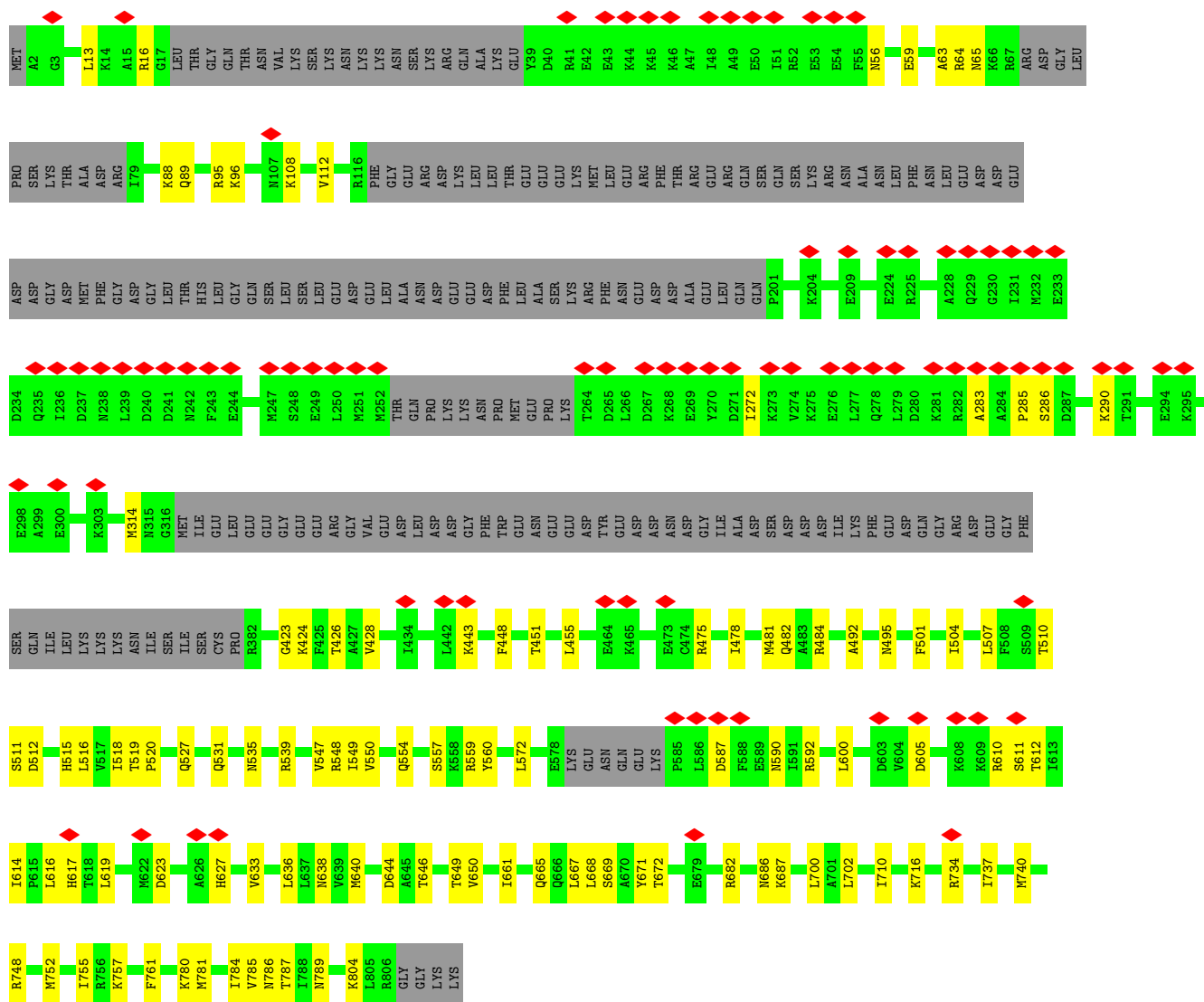
• Molecule 54: Ribosomal RNA-processing protein 7



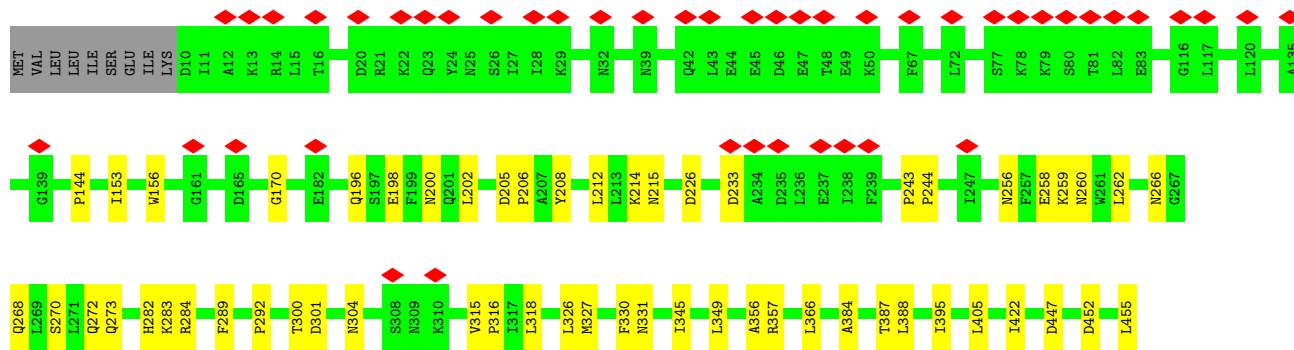
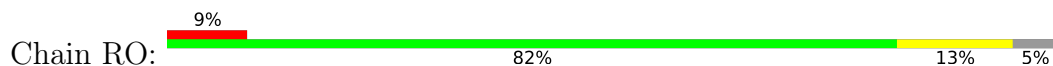
• Molecule 55: Ribosomal RNA small subunit methyltransferase NEP1

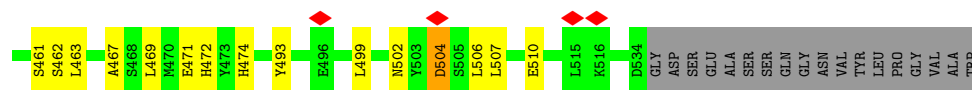




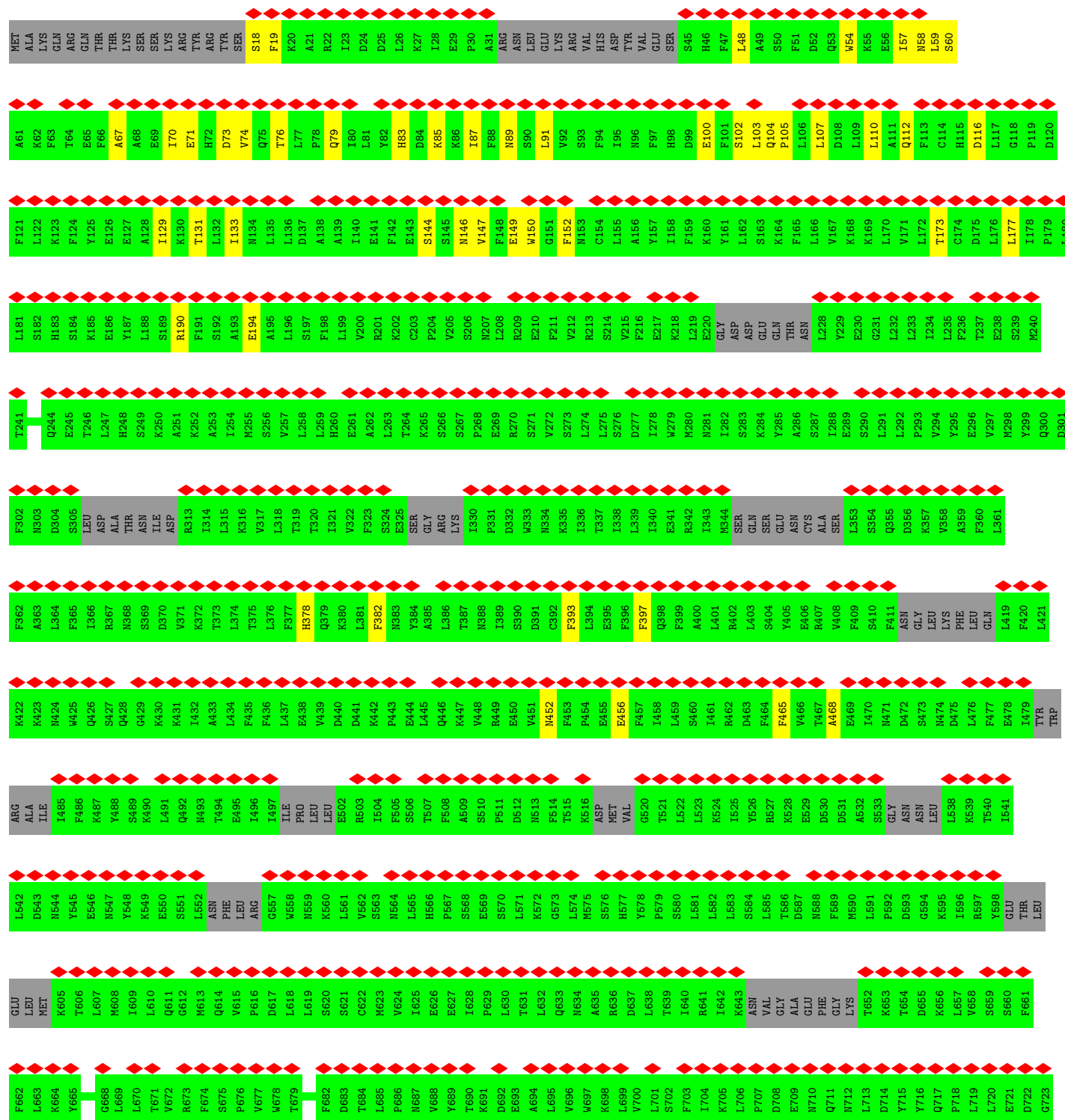
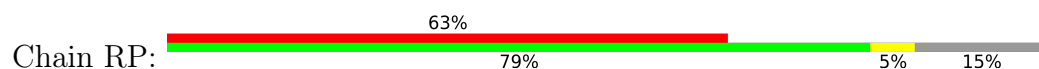


• Molecule 61: Nucleolar complex protein 4





- Molecule 62: U3 small nucleolar RNA-associated protein 20



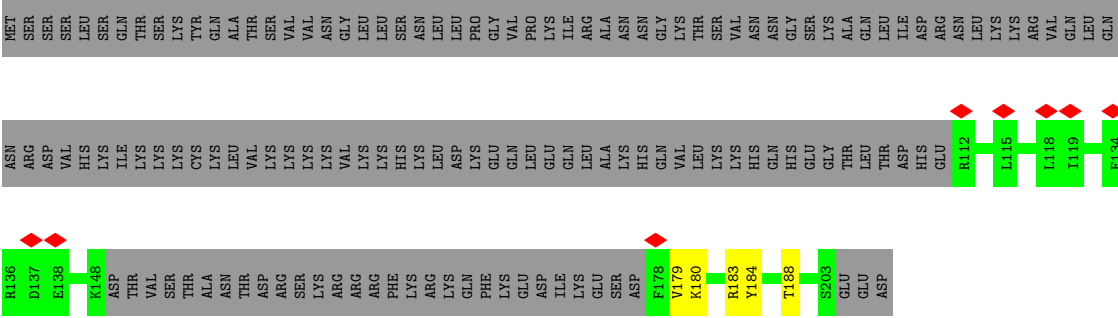
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K726	E790	H851	Q911	S981	Q1057	Q1121	I1181	Q1241	S1302	ALA	H1483	Y1500	H1483	Y1500
V727	E791	D852	Q912	H982	G1058	L1122	L1182	K1242	K1303	LEU	Y1484	R1501	Y1484	R1501
L728	H792	H853	I913	Q983	L1059	Y1123	P1183	L1243	L1304	THR	I1485	I1502	I1485	I1502
W729	F793	L854	I914	Q984	K1060	Y1124	S1184	L1244	V1305	ASN	L1486	G1504	L1486	G1504
D730	D794	M955	A915	N985	C1061	D1125	L1185	K1245	A1306	ALA	K1487	N1506	K1487	N1506
S731	V795	V956	E916	S986	L1062	E1126	Y1186	I1246	D1307	HIS	M1488	E1506	M1488	E1506
W732	I796	L857	D917	S987	S1063	F1127	V1187	K1247	L1308	ILE	T1428	I1507	T1428	I1507
V733	A797	L858	E918	K988	S1064	A1128	L1188	L1248	M1309	ALA	K1429	Q1508	K1429	Q1508
V734	P798	G959	K919	A989	S1065	T1129	L1189	L1249	S1310	LYS	H1491	I1509	H1491	I1509
R735	F799	S860	V920	T990	F1066	A1130	S1190	I1250	Y1311	PHE	D1431	D1521	D1431	D1521
L736	V800	R861	V921	L991	V1069	T1131	D1191	T1251	S1312	ILE	D1432	I1439	D1432	I1439
R737	N862	N862	H922	R995	G1070	A1132	S1192	F1252	S1313	D1376	D1433	L1440	D1433	L1440
D738	N803	T863	P923	T998	T1072	L1133	M1193	N1253	S1314	F1377	F1434	L1441	F1434	L1441
T739	D804	D864	Y924	G999	F1073	M1134	S1194	Y1254	R1315	I1378	D1435	I1442	D1435	I1442
I740	K805	V965	I928	F1000	D1074	T1135	I1195	C1256	M1316	N1379	D1436	I1443	D1436	I1443
F743	Y807	K867	I928	V1001	W1075	I1137	S1196	S1257	H1317	E1380	I1439	I1443	I1439	I1443
S744	K808	L868	G931	V1002	T1076	N1139	T1197	W1258	E1318	K1381	L1440	I1444	K1381	L1440
H745	D809	A969	R932	I1003	S1077	Q1140	F1198	I1259	Y1319	P1382	R1501	I1445	P1382	R1501
I746	E810	L870	A933	V1004	S1078	H1141	M1200	D1260	D1320	N1383	I1502	I1446	N1383	I1502
W747	E911	D871	Q934	N1005	D1081	V1142	L1201	I1261	F1321	L1384	G1504	E1446	L1384	G1504
S748	D812	A872	V935	S1006	A1084	K1143	L1202	E1262	P1322	E1386	I1505	E1447	E1386	I1505
T752	E814	L874	P936	T1007	V1087	E1144	S1204	L1264	ILE	A1387	I1506	E1448	A1387	I1506
Q753	N815	A875	P937	V1010	K1068	V1146	I1205	Y1265	LEU	S1388	Q1508	A1448	S1388	Q1508
N754	E816	K877	S939	V1022	P1089	I1147	T1206	T1266	THR	K1389	I1509	D1449	K1389	I1509
T755	R817	N878	G940	Q1023	R1090	G1148	E1207	T1267	PHE	I1391	PHE	I1510	I1391	PHE
S756	V818	P879	Q941	Q1024	I1091	P1149	M1208	I1268	GLY	S1392	THR	I1511	S1392	THR
I757	I819	T880	K942	Q1025	S1092	I1150	G1209	S1269	ILE	M1393	ASN	I1512	M1393	ASN
I758	T820	L881	V943	P1025	F1094	I1151	F1210	S1270	GLU	L1394	VAL	G1513	L1394	VAL
S759	G821	N882	R944	S1029	E1094	E1152	I1211	L1271	ASP	K1395	ASN	A1514	K1395	ASN
T760	S822	K883	R945	I1030	F1095	A1153	Q1212	F1272	TYR	D1396	HIS	I1515	D1396	HIS
T761	E825	Y884	K946	A1031	D1096	A1154	D1213	K1273	LYS	I1397	GLN	I1516	I1397	GLN
I762	V826	R885	I947	M1032	E1097	D1155	D1214	T1274	SER	L1398	LEU	I1517	L1398	LEU
E763	D827	D886	A948	A1033	N1098	S1156	H1215	F1275	TYR	L1399	HIS	I1518	L1399	HIS
R764	R828	L888	V949	Y1034	L1099	I1157	V1216	D1276	SER	P1400	I1519	S1519	P1400	I1519
R765	N829	K889	I950	Y1035	L1099	I1158	R1217	E1277	LEU	L1401	W1520	W1520	L1401	W1520
R766	N830	V830	V951	V1036	Q1100	I1159	S1218	R1278	GLU	I1402	N1521	N1521	I1402	N1521
W767	F831	L891	V952	L1037	Q1101	R1159	R1219	N1279	TRP	R1403	R1464	R1464	R1403	R1464
Y770	L832	L892	L953	D1038	P1102	N1160	L1220	L1280	LEU	I1404	A1465	I1466	I1404	A1465
I772	K833	D894	P954	T1039	S1103	P1161	I1221	L1284	PRO	G1405	I1466	I1466	G1405	I1466
L773	T834	T895	N955	E1040	S1104	V1162	S1222	V1282	LEU	L1406	K1467	K1467	L1406	K1467
L774	L835	L896	I961	S1041	L1105	N1163	S1223	S1283	PHE	R1407	L1468	L1468	R1407	L1468
I775	S836	F897	F964	T1042	L1106	D1164	L1224	L1284	THR	D1408	L1469	L1469	D1408	L1469
R776	K837	K898	S969	E1043	R1107	D1165	I1225	T1285	PHE	S1409	G1470	G1470	S1409	G1470
Q777	F838	D899	E970	E1044	F1109	H1166	S1226	E1286	HIS	L1410	E1471	E1471	L1410	HIS
A778	N840	E900	E970	H1046	Y1111	Y1167	I1227	L1287	PHE	E1411	A1472	A1472	E1411	PHE
L779	K842	I901	R971	L1047	W1112	D1169	L1228	F1288	ASN	E1412	H1473	H1473	E1412	ASN
W781	N843	T902	D973	R1048	W1113	T1170	G1230	I1289	LYS	L1413	I1474	I1474	L1413	LYS
T782	V844	T903	Y974	M1050	H1114	V1171	K1231	E1290	GLU	GLN	Q1475	Q1475	GLN	GLN
W783	Y845	F904	Y976	M1051	H1115	T1172	L1232	R1293	SER	SER	L1476	L1476	SER	SER
L783	S846	F784	F977	S1052	P1116	L1173	K1233	K1294	THR	GLU	K1477	K1477	THR	GLU
I785	A847	T906	F978	N1053	S1117	C1175	L1235	P1296	VAL	VAL	D1478	D1478	VAL	VAL
F786	T848	E907	F978	L1054	L1118	T1176	Q1236	E1297	GLU	SER	N1479	N1479	SER	SER
Q787						C1178	E1237	E1299			M1541	M1541		





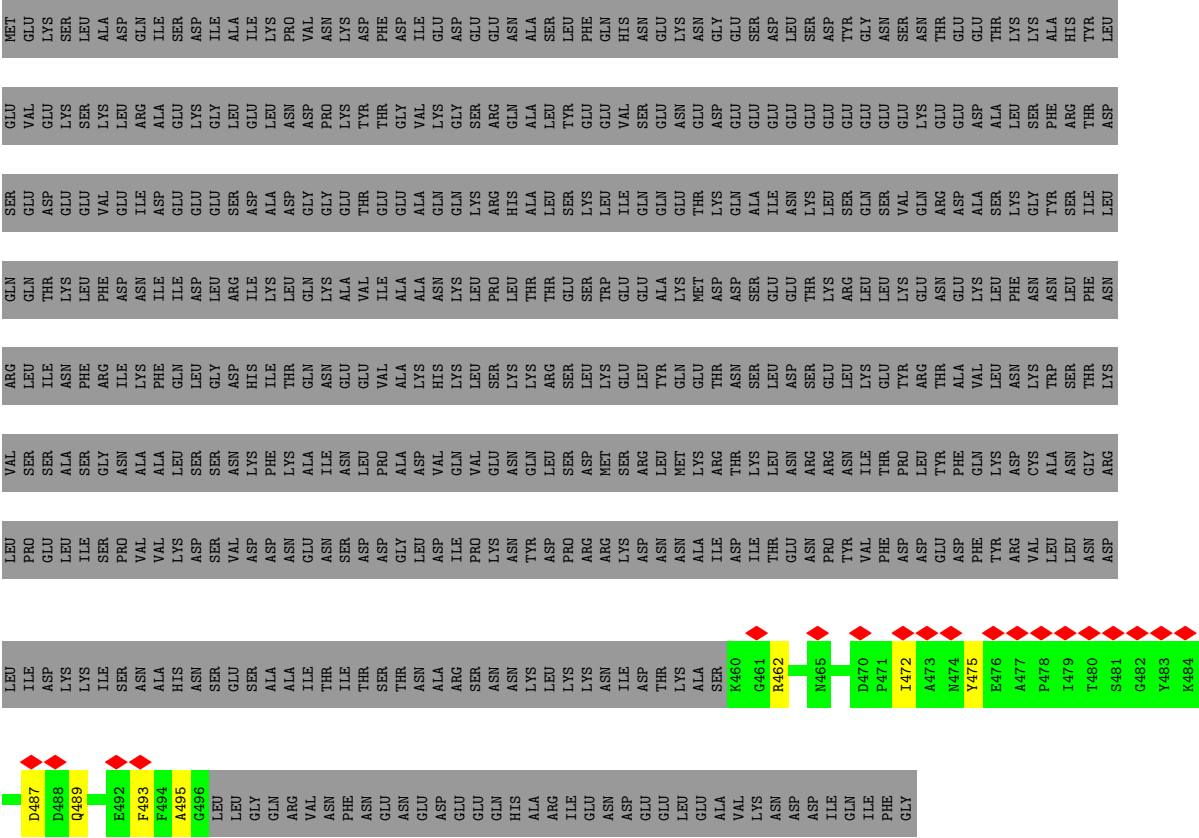
• Molecule 67: Regulator of rDNA transcription protein 14

Chain RW: 28% 69%



• Molecule 68: Protein BFR2

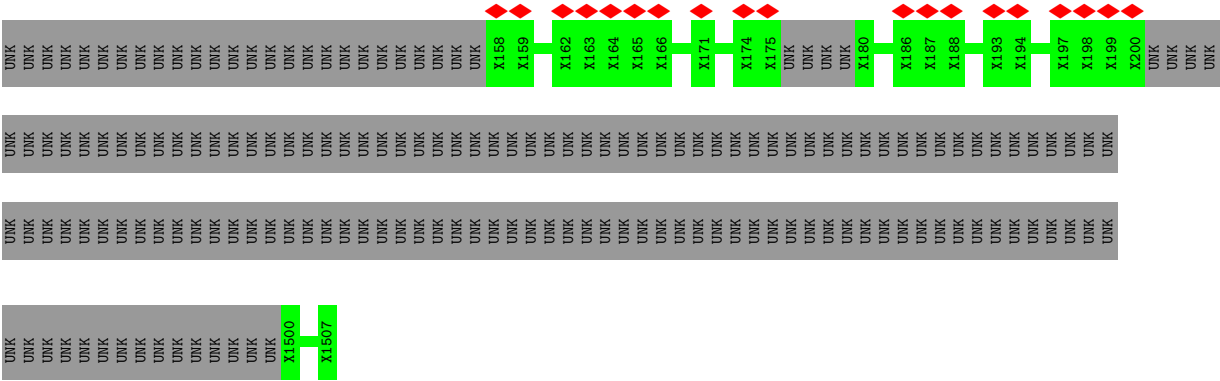
Chain RY: 6% 93%



• Molecule 69: Unassigned helices

Chain X1: 5% 18% 82%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	71230	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.246	Depositor
Minimum map value	-0.115	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	597.632, 597.632, 597.632	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.334, 1.334, 1.334	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	3A	0.45	0/4141	0.48	0/6433
2	5A	0.41	0/12485	0.47	2/19449 (0.0%)
3	SA	0.35	0/31590	0.46	5/49182 (0.0%)
4	SC	0.44	0/1856	0.77	3/2490 (0.1%)
5	SF	0.29	0/1854	0.66	0/2504
6	SG	0.49	0/1690	0.67	2/2285 (0.1%)
7	SH	0.24	0/1341	0.61	1/1789 (0.1%)
8	SI	0.32	0/1341	0.69	2/1806 (0.1%)
9	SJ	0.26	0/1347	0.60	0/1801
10	SK	0.44	0/1410	0.63	0/1888
11	SM	0.26	0/1020	0.64	0/1374
12	SN	0.29	0/873	0.78	0/1185
13	SO	0.39	0/1109	0.63	0/1495
14	SP	0.46	0/879	0.79	0/1186
15	SR	0.52	0/990	0.77	3/1335 (0.2%)
16	ST	0.30	0/980	0.65	0/1319
17	SX	0.46	0/1020	0.63	0/1371
18	SY	0.48	0/798	0.65	0/1065
19	SZ	0.36	0/822	0.73	0/1103
20	Sc	0.40	0/613	0.63	0/828
21	Sd	0.50	0/499	0.72	2/670 (0.3%)
22	3B	0.51	0/1901	0.66	1/2567 (0.0%)
22	3C	0.37	0/1796	0.66	0/2424
23	3D	0.40	0/2891	0.62	0/3895
24	3E	0.38	0/3059	0.62	0/4153
25	3F	0.36	0/3715	0.64	0/5001
26	3G	0.51	0/928	0.72	1/1262 (0.1%)
26	3H	0.45	0/928	0.70	0/1262
27	A4	0.43	0/5321	0.66	0/7207
28	A5	0.44	0/4044	0.65	0/5493
29	A8	0.23	0/3328	0.62	0/4565
30	A9	0.28	0/951	0.60	0/1287

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	AE	0.32	1/10049 (0.0%)	0.56	1/13737 (0.0%)
32	AF	0.48	0/3993	0.68	0/5413
33	AG	0.42	0/6699	0.64	3/9077 (0.0%)
34	B1	0.58	0/6780	0.69	0/9175
35	B2	0.39	0/6853	0.68	2/9256 (0.0%)
36	B3	0.35	0/6014	0.70	2/8137 (0.0%)
37	B8	0.55	0/3848	0.63	0/5218
38	BE	0.53	0/6948	0.64	2/9391 (0.0%)
39	B6	0.37	0/2849	0.60	0/3853
40	5B	0.31	0/499	0.62	0/659
41	5C	0.55	0/4321	0.66	2/5832 (0.0%)
42	5D	0.46	0/1998	0.70	0/2644
43	5E	0.44	0/1665	0.66	2/2233 (0.1%)
44	5F	0.64	0/1559	0.72	1/2097 (0.0%)
45	5G	0.52	0/2337	0.67	2/3148 (0.1%)
46	5H	0.40	0/1074	0.57	0/1422
47	5I	0.56	0/3844	0.68	0/5174
48	5J	0.36	0/1302	0.58	0/1728
49	5K	0.51	0/1426	0.66	0/1917
50	RA	0.27	0/2769	0.66	2/3753 (0.1%)
51	RB	0.37	0/1121	0.79	0/1487
52	RC	0.40	0/2245	0.60	0/3021
53	RE	0.30	0/8924	0.60	1/12070 (0.0%)
54	RF	0.28	0/2004	0.66	1/2697 (0.0%)
55	RG	0.32	0/1727	0.70	0/2329
55	RH	0.37	0/1828	0.59	0/2470
56	RI	0.41	0/2080	0.65	0/2797
57	RJ	0.44	0/6514	0.61	0/8768
58	RK	0.39	0/2832	0.64	0/3825
59	RL	0.21	0/4549	0.51	1/6241 (0.0%)
59	RM	0.15	0/3765	0.44	1/5218 (0.0%)
60	RN	0.30	0/4591	0.63	1/6187 (0.0%)
61	RO	0.32	0/3849	0.63	0/5261
62	RP	0.21	0/12230	0.54	4/16819 (0.0%)
63	RQ	0.41	0/1678	0.63	1/2282 (0.0%)
64	RS	0.30	0/2104	0.70	0/2854
65	RT	0.38	0/1379	0.68	0/1853
66	RV	0.43	0/1456	0.60	1/1937 (0.1%)
67	RW	0.26	0/385	0.49	0/529
68	RY	0.23	0/307	0.53	0/415
All	All	0.39	1/239915 (0.0%)	0.60	52/334598 (0.0%)

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

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	SC	0	1
5	SF	0	2
8	SI	0	3
9	SJ	0	1
11	SM	0	1
13	SO	0	1
14	SP	0	1
16	ST	0	1
19	SZ	0	1
20	Sc	0	1
23	3D	0	3
24	3E	0	1
25	3F	0	1
26	3G	0	2
26	3H	0	1
27	A4	0	1
28	A5	0	1
29	A8	0	4
33	AG	0	2
34	B1	0	3
35	B2	0	9
36	B3	0	11
38	BE	0	1
41	5C	0	2
42	5D	0	1
43	5E	0	1
44	5F	0	1
45	5G	0	1
47	5I	0	2
50	RA	0	2
51	RB	0	1
53	RE	0	1
54	RF	0	1
57	RJ	0	2
58	RK	0	1
59	RL	0	1
59	RM	0	1
60	RN	0	1
61	RO	0	1
62	RP	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
63	RQ	0	1
66	RV	0	2
All	All	0	79

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	AE	564	VAL	C-N	5.39	1.40	1.34

All (52) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	B2	267	ASP	CA-C-N	6.86	134.65	121.54
35	B2	267	ASP	C-N-CA	6.86	134.65	121.54
2	5A	312	U	P-O3'-C3'	6.82	130.43	120.20
62	RP	2033	LYS	CA-C-N	6.64	134.22	121.54
62	RP	2033	LYS	C-N-CA	6.64	134.22	121.54
44	5F	13	LEU	CA-CB-CG	6.47	138.96	116.30
54	RF	157	GLU	N-CA-C	6.11	116.34	108.34
59	RL	744	PRO	N-CA-C	6.07	124.97	112.47
45	5G	157	PHE	N-CA-C	6.02	123.11	109.81
59	RM	744	PRO	N-CA-C	5.99	124.81	112.47
33	AG	141	LEU	N-CA-C	5.92	117.83	110.91
26	3G	67	LEU	CA-CB-CG	5.86	136.82	116.30
62	RP	1745	ILE	CA-C-N	5.82	132.66	121.54
62	RP	1745	ILE	C-N-CA	5.82	132.66	121.54
8	SI	117	THR	CA-C-N	5.82	132.65	121.54
8	SI	117	THR	C-N-CA	5.82	132.65	121.54
38	BE	840	PHE	CA-C-N	5.67	130.10	121.03
38	BE	840	PHE	C-N-CA	5.67	130.10	121.03
3	SA	1052	U	O3'-P-O5'	5.66	112.49	104.00
66	RV	204	GLY	N-CA-C	5.63	126.52	113.18
15	SR	123	ARG	CA-C-N	5.59	140.41	127.00
15	SR	123	ARG	C-N-CA	5.59	140.41	127.00
4	SC	54	LEU	CA-CB-CG	5.58	135.85	116.30
53	RE	924	LEU	CA-CB-CG	5.49	135.50	116.30
50	RA	286	GLU	CA-C-N	5.46	131.98	121.54
50	RA	286	GLU	C-N-CA	5.46	131.98	121.54
43	5E	452	SER	CA-C-O	-5.46	110.17	118.91
63	RQ	313	PHE	N-CA-C	5.43	121.82	109.81
3	SA	579	A	P-O3'-C3'	5.38	128.27	120.20
31	AE	1589	ILE	N-CA-C	-5.35	107.61	112.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5A	173	G	P-O3'-C3'	5.32	128.18	120.20
4	SC	54	LEU	CA-C-N	5.31	131.68	121.54
4	SC	54	LEU	C-N-CA	5.31	131.68	121.54
3	SA	272	U	P-O3'-C3'	5.30	128.16	120.20
7	SH	41	VAL	N-CA-C	-5.24	107.72	112.96
43	5E	454	VAL	N-CA-C	5.18	120.11	109.34
15	SR	123	ARG	C-N-CD	-5.07	109.46	120.60
21	Sd	50	GLU	CA-C-N	5.05	131.19	121.54
21	Sd	50	GLU	C-N-CA	5.05	131.19	121.54
45	5G	120	GLY	N-CA-C	-5.05	101.21	113.18
41	5C	456	SER	CA-C-N	5.04	128.82	121.31
41	5C	456	SER	C-N-CA	5.04	128.82	121.31
3	SA	1594	G	C4'-C3'-O3'	5.04	116.95	109.40
33	AG	138	ASP	CA-C-N	5.03	128.22	120.82
33	AG	138	ASP	C-N-CA	5.03	128.22	120.82
3	SA	56	U	P-O3'-C3'	5.03	127.74	120.20
6	SG	99	MET	CA-C-N	5.01	131.12	121.54
6	SG	99	MET	C-N-CA	5.01	131.12	121.54
22	3B	306	LEU	CA-CB-CG	5.01	133.82	116.30
36	B3	471	PRO	CA-C-N	5.01	135.31	126.45
36	B3	471	PRO	C-N-CA	5.01	135.31	126.45
60	RN	592	ARG	CA-CB-CG	5.00	124.10	114.10

There are no chirality outliers.

All (79) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
23	3D	142	LEU	Peptide
23	3D	202	HIS	Peptide
23	3D	286	ARG	Peptide
24	3E	331	LYS	Peptide
25	3F	237	ASP	Peptide
26	3G	59	GLU	Peptide
26	3G	9	PHE	Peptide
26	3H	59	GLU	Peptide
41	5C	540	GLU	Peptide
41	5C	551	SER	Peptide
42	5D	138	ASP	Peptide
43	5E	453	SER	Peptide
44	5F	101	VAL	Peptide
45	5G	74	ASP	Peptide
47	5I	230	ASN	Peptide

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Mol	Chain	Res	Type	Group
47	5I	283	ASP	Peptide
27	A4	54	LYS	Peptide
28	A5	167	SER	Peptide
29	A8	257	SER	Peptide
29	A8	266	ILE	Peptide
29	A8	496	TYR	Peptide
29	A8	529	HIS	Peptide
33	AG	178	PHE	Peptide
33	AG	780	GLU	Peptide
34	B1	288	ASP	Peptide
34	B1	661	LEU	Peptide
34	B1	690	ALA	Peptide
35	B2	131	GLY	Peptide
35	B2	213	LYS	Peptide
35	B2	266	SER	Peptide
35	B2	267	ASP	Peptide
35	B2	278	ASP	Peptide
35	B2	44	SER	Peptide
35	B2	613	ALA	Peptide
35	B2	916	HIS	Peptide
35	B2	918	TYR	Peptide
36	B3	34	THR	Peptide
36	B3	435	ALA	Peptide
36	B3	473	ALA	Peptide
36	B3	479	ILE	Peptide
36	B3	480	ILE	Peptide
36	B3	585	ASN	Peptide
36	B3	593	CYS	Peptide
36	B3	594	GLY	Peptide
36	B3	627	ASN	Peptide
36	B3	89	HIS	Peptide
36	B3	90	LEU	Peptide
38	BE	94	TYR	Peptide
50	RA	111	TRP	Peptide
50	RA	173	LEU	Peptide
51	RB	261	SER	Peptide
53	RE	767	GLN	Peptide
54	RF	253	ALA	Peptide
57	RJ	1026	LYS	Peptide
57	RJ	868	ARG	Peptide
58	RK	333	PHE	Peptide
59	RL	743	VAL	Peptide

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Mol	Chain	Res	Type	Group
59	RM	743	VAL	Peptide
60	RN	286	SER	Peptide
61	RO	144	PRO	Peptide
62	RP	1746	LYS	Peptide
62	RP	2051	ASP	Peptide
62	RP	835	LEU	Peptide
63	RQ	313	PHE	Peptide
66	RV	203	ILE	Peptide
66	RV	261	GLY	Peptide
4	SC	238	GLU	Peptide
5	SF	193	GLY	Peptide
5	SF	195	ILE	Peptide
8	SI	133	THR	Peptide
8	SI	31	SER	Peptide
8	SI	64	VAL	Peptide
9	SJ	85	PRO	Peptide
11	SM	128	CYS	Peptide
13	SO	58	HIS	Peptide
14	SP	90	ARG	Peptide
16	ST	13	HIS	Peptide
19	SZ	76	TYR	Peptide
20	Sc	49	HIS	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	3A	3711	0	1882	22	0
2	5A	11163	0	5611	84	0
3	SA	28258	0	14249	250	0
4	SC	1830	0	1914	33	0
5	SF	1815	0	1870	45	0
6	SG	1669	0	1724	18	0
7	SH	1327	0	1403	30	0
8	SI	1321	0	1387	23	0
9	SJ	1324	0	1344	48	0
10	SK	1388	0	1467	32	0
11	SM	997	0	1048	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	SN	865	0	874	16	0
13	SO	1087	0	1152	13	0
14	SP	868	0	894	14	0
15	SR	973	0	1029	14	0
16	ST	964	0	991	16	0
17	SX	1003	0	1040	16	0
18	SY	786	0	843	8	0
19	SZ	809	0	842	15	0
20	Sc	603	0	623	9	0
21	Sd	497	0	535	3	0
22	3B	1865	0	1910	30	0
22	3C	1763	0	1805	34	0
23	3D	2848	0	2815	46	0
24	3E	3028	0	2813	62	0
25	3F	3643	0	3654	79	0
26	3G	916	0	964	11	0
26	3H	916	0	964	26	0
27	A4	5226	0	5199	96	0
28	A5	3976	0	3919	58	0
29	A8	3307	0	2316	39	0
30	A9	939	0	898	19	0
31	AE	9955	0	7968	103	0
32	AF	3911	0	3906	73	0
33	AG	6570	0	6473	127	0
34	B1	6635	0	6525	103	0
35	B2	6723	0	6698	121	0
36	B3	5919	0	6007	127	0
37	B8	3764	0	3757	59	0
38	BE	6810	0	6787	86	0
39	B6	2800	0	2517	35	0
40	5B	495	0	561	14	0
41	5C	4237	0	4239	85	0
42	5D	1972	0	2054	28	0
43	5E	1647	0	1678	33	0
44	5F	1530	0	1572	30	0
45	5G	2296	0	2325	42	0
46	5H	1065	0	1097	17	0
47	5I	3765	0	3714	73	0
48	5J	1280	0	1331	23	0
49	5K	1403	0	1484	20	0
50	RA	2709	0	2622	66	0
51	RB	1108	0	1087	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	RC	2207	0	2229	29	0
53	RE	8716	0	8828	168	0
54	RF	1963	0	1942	43	0
55	RG	1701	0	1767	40	0
55	RH	1799	0	1872	32	0
56	RI	2045	0	2162	38	0
57	RJ	6379	0	6506	111	0
58	RK	2781	0	2878	51	0
59	RL	4539	0	2874	29	0
59	RM	3779	0	1650	8	0
60	RN	4529	0	4262	71	0
61	RO	3766	0	3269	47	0
62	RP	12176	0	7751	76	0
63	RQ	1651	0	1450	28	0
64	RS	2051	0	2096	54	0
65	RT	1357	0	1426	15	0
66	RV	1448	0	1435	16	0
67	RW	381	0	255	4	0
68	RY	299	0	275	6	0
69	X1	305	0	73	0	0
70	5K	1	0	0	0	0
70	Sc	1	0	0	0	0
71	RJ	32	0	12	2	0
72	RJ	1	0	0	0	0
All	All	232186	0	199393	2963	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 (2963) 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)
29:A8:264:SER:O	29:A8:267:ILE:HA	1.61	1.01
35:B2:17:ILE:HG22	35:B2:52:TRP:CZ2	1.94	1.01
60:RN:527:GLN:O	60:RN:531:GLN:HB2	1.60	1.01
63:RQ:298:TRP:NE1	63:RQ:899:LYS:HG3	1.76	1.00
3:SA:36:C:H42	3:SA:472:U:H3	1.00	0.99
10:SK:65:LYS:HZ2	25:3F:59:PRO:CD	1.77	0.96
10:SK:65:LYS:HZ2	25:3F:59:PRO:CG	1.78	0.94
10:SK:65:LYS:HZ2	25:3F:59:PRO:CB	1.82	0.92
3:SA:36:C:N4	3:SA:472:U:H3	1.70	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:SK:65:LYS:NZ	25:3F:59:PRO:CG	2.35	0.89
47:5I:231:GLU:OE2	63:RQ:899:LYS:HD3	1.74	0.87
36:B3:494:ILE:N	36:B3:510:SER:HG	1.71	0.87
10:SK:65:LYS:NZ	25:3F:59:PRO:CD	2.38	0.85
59:RM:313:PRO:O	59:RM:372:PRO:HA	1.77	0.84
64:RS:424:PHE:O	64:RS:428:TYR:HB2	1.78	0.84
5:SF:213:SER:HG	25:3F:102:ASP:N	1.75	0.84
61:RO:502:ASN:O	61:RO:506:LEU:HB2	1.77	0.83
63:RQ:346:LEU:O	63:RQ:350:ASN:HA	1.80	0.81
26:3H:44:LEU:HD22	26:3H:52:ILE:CD1	2.10	0.81
31:AE:151:ILE:O	31:AE:155:ILE:HB	1.81	0.81
59:RM:746:TYR:O	59:RM:765:VAL:HA	1.81	0.80
63:RQ:298:TRP:HE1	63:RQ:899:LYS:HG3	1.44	0.80
39:B6:319:TYR:O	39:B6:323:PHE:HB2	1.81	0.79
9:SJ:48:THR:O	9:SJ:52:ASN:HB2	1.83	0.79
10:SK:65:LYS:NZ	25:3F:59:PRO:HD3	1.97	0.78
3:SA:1663:G:H1	3:SA:1738:U:H3	1.31	0.78
32:AF:224:THR:O	32:AF:239:LEU:HB2	1.83	0.78
3:SA:868:G:H1	3:SA:960:U:H3	1.30	0.78
3:SA:153:G:H1	3:SA:161:U:H3	1.33	0.77
3:SA:1688:U:H3	3:SA:1713:G:H1	1.34	0.76
10:SK:138:LYS:H	51:RB:263:GLY:HA3	1.51	0.75
3:SA:415:C:H1'	3:SA:419:G:H22	1.50	0.75
27:A4:614:TRP:O	27:A4:618:ASN:HB2	1.87	0.74
48:5J:114:ARG:O	48:5J:118:GLN:HB3	1.88	0.74
3:SA:1051:G:H21	47:5I:447:THR:HG21	1.54	0.73
36:B3:216:ARG:HH11	36:B3:241:GLN:HE22	1.36	0.72
10:SK:65:LYS:HZ1	25:3F:59:PRO:HD3	1.55	0.72
10:SK:65:LYS:NZ	25:3F:59:PRO:CB	2.52	0.72
3:SA:505:A:H61	3:SA:586:G:H8	1.38	0.71
24:3E:397:ARG:HH21	24:3E:400:GLN:HE21	1.38	0.71
59:RL:29:VAL:HG12	59:RL:152:LEU:HD12	1.72	0.71
33:AG:435:ASP:HB2	33:AG:702:TYR:CD1	2.26	0.71
5:SF:92:LEU:HB2	5:SF:97:GLU:HB2	1.74	0.70
6:SG:206:SER:H	6:SG:211:ILE:HD11	1.55	0.70
56:RI:77:LYS:HD2	56:RI:130:ARG:HH11	1.57	0.70
53:RE:1108:LEU:O	53:RE:1112:CYS:HB2	1.91	0.69
34:B1:58:ILE:HA	34:B1:74:ASP:HA	1.74	0.69
2:5A:135:G:H4'	28:A5:494:ARG:HD3	1.74	0.69
2:5A:316:U:H5'	41:5C:364:ARG:HH22	1.58	0.69
53:RE:441:GLN:O	53:RE:455:SER:HA	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:SZ:29:HIS:HB2	19:SZ:32:ARG:HB2	1.76	0.68
10:SK:65:LYS:NZ	25:3F:59:PRO:HB3	2.08	0.68
47:5I:345:THR:HG22	47:5I:347:ARG:H	1.58	0.68
3:SA:646:C:H2'	3:SA:647:G:H8	1.59	0.68
63:RQ:297:LYS:HB2	63:RQ:899:LYS:HB3	1.76	0.68
58:RK:192:THR:HA	58:RK:224:ASN:O	1.92	0.68
31:AE:692:ILE:HA	31:AE:695:TYR:HB3	1.76	0.68
62:RP:173:THR:O	62:RP:177:LEU:HB2	1.94	0.68
32:AF:86:SER:O	32:AF:98:ALA:HA	1.93	0.68
32:AF:211:HIS:HD1	32:AF:228:SER:HG	1.42	0.67
35:B2:17:ILE:HG22	35:B2:52:TRP:CH2	2.28	0.67
10:SK:65:LYS:NZ	25:3F:59:PRO:HG3	2.08	0.67
3:SA:1679:G:H1'	3:SA:1722:A:H61	1.59	0.67
25:3F:443:LEU:HD21	25:3F:492:TRP:HE1	1.59	0.67
38:BE:209:ILE:HG22	38:BE:225:THR:HG22	1.76	0.67
25:3F:185:LEU:H	25:3F:202:THR:HB	1.59	0.67
27:A4:645:ARG:HD2	27:A4:656:ARG:HD3	1.76	0.67
37:B8:513:GLN:HG3	37:B8:551:VAL:HG21	1.76	0.67
35:B2:536:CYS:HB3	35:B2:549:SER:HB3	1.77	0.67
3:SA:187:G:N2	3:SA:197:A:N7	2.43	0.66
19:SZ:51:GLU:HB2	19:SZ:54:ALA:HB3	1.76	0.66
34:B1:20:ILE:H	34:B1:307:THR:HG21	1.58	0.66
53:RE:235:LEU:O	53:RE:239:LEU:HB2	1.95	0.66
45:5G:123:VAL:HG12	45:5G:125:PRO:HD2	1.78	0.66
33:AG:435:ASP:HB3	33:AG:701:VAL:O	1.96	0.66
38:BE:209:ILE:HA	38:BE:225:THR:HA	1.76	0.66
18:SY:103:LEU:HB3	18:SY:126:LYS:HB2	1.76	0.66
22:3B:103:GLU:HG3	48:5J:134:ARG:HH12	1.60	0.66
11:SM:67:ARG:HH21	11:SM:129:ARG:H	1.44	0.66
57:RJ:248:ARG:HB3	57:RJ:272:TYR:HB2	1.78	0.66
33:AG:16:SER:HB2	33:AG:783:LEU:HB2	1.77	0.66
53:RE:756:VAL:HA	53:RE:896:THR:HG21	1.78	0.66
32:AF:52:PRO:HG2	32:AF:312:ALA:HA	1.77	0.65
36:B3:462:THR:HA	36:B3:484:GLU:HG2	1.77	0.65
38:BE:847:LEU:HD11	65:RT:266:VAL:HG23	1.78	0.65
59:RM:283:ALA:HA	59:RM:411:THR:O	1.96	0.65
3:SA:207:U:H3	3:SA:258:C:H42	1.45	0.65
59:RM:311:THR:O	59:RM:370:ILE:HA	1.97	0.65
65:RT:222:THR:HG22	65:RT:235:GLY:HA3	1.79	0.65
27:A4:497:ILE:HD11	27:A4:511:VAL:HG23	1.78	0.65
29:A8:576:ARG:HG2	29:A8:578:LEU:H	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:B2:262:ILE:O	35:B2:270:SER:HA	1.97	0.65
1:3A:84:U:OP2	24:3E:361:ARG:NH2	2.30	0.65
41:5C:170:GLN:NE2	41:5C:177:TYR:OH	2.30	0.64
4:SC:132:ASP:HB2	4:SC:221:PRO:HB3	1.79	0.64
11:SM:87:ARG:HE	11:SM:104:HIS:HB2	1.62	0.64
25:3F:125:VAL:O	25:3F:128:GLN:NE2	2.30	0.64
55:RG:122:ILE:HA	55:RG:161:LYS:O	1.97	0.64
57:RJ:263:LEU:HD23	57:RJ:267:ARG:HH22	1.63	0.64
61:RO:472:HIS:HD2	61:RO:474:HIS:H	1.46	0.64
3:SA:1052:U:H5''	47:5I:449:LYS:HG2	1.78	0.64
10:SK:57:ARG:HE	49:5K:88:ASP:HB3	1.60	0.64
2:5A:487:A:H62	63:RQ:876:GLN:HE22	1.45	0.64
3:SA:415:C:H1'	3:SA:419:G:N2	2.12	0.64
3:SA:1727:G:N2	3:SA:1728:A:N7	2.46	0.64
34:B1:438:VAL:HG12	34:B1:445:VAL:HG23	1.79	0.64
43:5E:299:SER:HA	43:5E:302:LYS:HE2	1.80	0.64
35:B2:439:LEU:HB2	35:B2:444:LEU:HB3	1.79	0.64
36:B3:719:ILE:HD11	36:B3:762:CYS:HB3	1.78	0.64
38:BE:631:ASN:HB2	38:BE:644:THR:HB	1.80	0.64
44:5F:33:MET:HB2	44:5F:38:ILE:HB	1.79	0.64
18:SY:97:ASP:OD1	18:SY:97:ASP:N	2.31	0.64
37:B8:521:LEU:HA	37:B8:531:CYS:O	1.98	0.64
2:5A:173:G:N7	2:5A:175:A:N6	2.46	0.64
9:SJ:5:ARG:NH2	9:SJ:29:LEU:O	2.31	0.63
28:A5:145:CYS:HB2	28:A5:148:LEU:HD21	1.80	0.63
61:RO:318:LEU:HA	61:RO:357:ARG:HH12	1.62	0.63
26:3H:44:LEU:HD22	26:3H:52:ILE:HD11	1.80	0.63
50:RA:18:GLY:HA2	50:RA:339:HIS:HD2	1.62	0.63
3:SA:343:C:H2'	3:SA:344:A:H8	1.63	0.63
9:SJ:42:ARG:HD3	50:RA:57:GLU:HB3	1.80	0.63
19:SZ:20:ARG:HD2	19:SZ:74:LEU:HD12	1.79	0.63
57:RJ:831:ARG:NH2	57:RJ:835:HIS:O	2.30	0.63
27:A4:578:SER:HG	27:A4:643:SER:HG	1.46	0.63
25:3F:538:ARG:HA	25:3F:566:ALA:O	1.97	0.63
41:5C:386:PHE:O	47:5I:8:ARG:NH2	2.31	0.63
55:RH:192:TYR:HA	55:RH:195:LYS:HD2	1.81	0.63
2:5A:357:G:N7	41:5C:493:LYS:NZ	2.45	0.63
36:B3:244:GLU:HG2	36:B3:293:VAL:H	1.64	0.63
45:5G:32:ILE:HG22	45:5G:42:LEU:HD11	1.81	0.63
15:SR:94:GLN:HB2	15:SR:102:LYS:HG3	1.80	0.63
10:SK:65:LYS:HZ2	25:3F:59:PRO:HB3	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A4:399:VAL:HG22	27:A4:420:LEU:HB2	1.80	0.63
31:AE:638:SER:HA	31:AE:641:LEU:HD12	1.80	0.63
36:B3:531:ASN:HD21	36:B3:568:MET:HE2	1.63	0.63
50:RA:247:THR:HG23	50:RA:249:ASN:H	1.64	0.63
8:SI:9:LEU:HD22	8:SI:42:GLN:HE22	1.63	0.62
55:RH:129:ARG:HH11	55:RH:132:ARG:HD3	1.63	0.62
24:3E:384:GLY:O	24:3E:388:LEU:HB2	1.99	0.62
29:A8:553:GLN:NE2	29:A8:557:THR:OG1	2.32	0.62
50:RA:287:ASN:HB2	50:RA:302:ARG:HB2	1.80	0.62
57:RJ:932:LEU:HD22	57:RJ:1007:TYR:HB2	1.80	0.62
42:5D:29:GLU:OE2	42:5D:37:ARG:NH1	2.31	0.62
61:RO:300:THR:O	61:RO:304:ASN:ND2	2.32	0.62
64:RS:379:LYS:HD2	64:RS:427:ARG:HE	1.64	0.62
39:B6:285:TYR:HD2	39:B6:308:THR:HG22	1.63	0.62
3:SA:146:U:H3	3:SA:168:A:N6	1.97	0.62
29:A8:530:PRO:HG2	29:A8:553:GLN:HE22	1.64	0.62
60:RN:482:GLN:HG2	61:RO:507:LEU:HD11	1.80	0.62
3:SA:1220:C:H2'	3:SA:1221:A:H8	1.64	0.62
3:SA:1655:A:N6	3:SA:1743:U:O4	2.32	0.62
28:A5:120:ILE:HB	28:A5:151:LEU:HD23	1.82	0.62
30:A9:432:LYS:HB3	30:A9:435:LEU:HB3	1.81	0.62
38:BE:733:THR:O	38:BE:737:LEU:HB3	2.00	0.62
3:SA:477:A:H5'	46:5H:560:ASN:HD22	1.64	0.62
64:RS:214:TYR:HB3	64:RS:249:THR:HG22	1.80	0.62
34:B1:303:ASN:ND2	34:B1:323:LYS:HD3	2.15	0.61
3:SA:1538:U:H2'	3:SA:1569:A:H61	1.65	0.61
32:AF:440:GLU:O	32:AF:444:ASN:HB2	2.00	0.61
60:RN:95:ARG:HH12	60:RN:757:LYS:HG3	1.64	0.61
26:3H:50:GLU:HG3	26:3H:104:THR:HG22	1.82	0.61
38:BE:471:CYS:SG	38:BE:514:ASN:ND2	2.74	0.61
3:SA:362:G:H22	3:SA:382:C:H1'	1.66	0.61
32:AF:428:ARG:NH2	33:AG:518:ASP:O	2.34	0.61
58:RK:155:LYS:HG2	58:RK:165:GLU:HG2	1.82	0.61
64:RS:423:THR:HA	64:RS:426:GLN:HG2	1.81	0.61
3:SA:521:A:N3	19:SZ:34:ASN:ND2	2.48	0.61
5:SF:95:THR:HG22	62:RP:59:LEU:HB3	1.83	0.61
3:SA:1512:G:H5''	56:RI:148:LYS:HD2	1.83	0.61
5:SF:212:ASP:H	5:SF:215:ASP:HA	1.65	0.61
14:SP:16:VAL:HG12	14:SP:80:HIS:HB2	1.82	0.61
37:B8:424:ILE:HG12	37:B8:434:GLU:HG2	1.83	0.61
28:A5:162:GLN:HA	28:A5:173:ILE:O	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:AF:51:HIS:O	32:AF:53:HIS:ND1	2.30	0.61
55:RG:36:LYS:HB3	55:RG:172:PRO:HA	1.82	0.61
33:AG:335:PRO:HB2	33:AG:336:ARG:HD3	1.82	0.61
33:AG:769:ASN:ND2	33:AG:771:ASP:OD1	2.33	0.61
39:B6:286:ILE:HG22	39:B6:308:THR:HG21	1.83	0.61
53:RE:398:ALA:HA	53:RE:401:LEU:HD12	1.82	0.61
53:RE:779:PHE:HB3	53:RE:851:LYS:HG3	1.82	0.61
65:RT:224:ILE:HG12	65:RT:233:ILE:HG12	1.83	0.61
60:RN:511:SER:HA	60:RN:557:SER:HB2	1.82	0.61
14:SP:80:HIS:HA	14:SP:113:GLY:O	2.01	0.60
22:3B:142:ARG:NH1	22:3B:186:ASP:OD2	2.34	0.60
25:3F:356:ARG:NH1	51:RB:260:ALA:O	2.34	0.60
28:A5:481:LEU:HD21	28:A5:526:LEU:HD22	1.82	0.60
62:RP:91:LEU:HD21	62:RP:110:LEU:HD12	1.83	0.60
22:3C:186:ASP:OD1	22:3C:214:ARG:NH1	2.34	0.60
57:RJ:60:ASP:O	57:RJ:239:ASN:ND2	2.34	0.60
3:SA:374:U:H5''	51:RB:331:LYS:HE3	1.83	0.60
36:B3:160:ILE:HG22	36:B3:162:LEU:HD13	1.82	0.60
39:B6:201:LYS:HZ1	48:5J:55:ILE:HG21	1.67	0.60
41:5C:529:ARG:HH21	41:5C:543:LYS:HZ1	1.49	0.60
47:5I:260:GLN:NE2	47:5I:289:TYR:OH	2.35	0.60
55:RG:147:LYS:HD3	55:RG:150:ILE:HG22	1.83	0.60
55:RH:156:GLU:HG2	55:RH:157:GLU:HG2	1.81	0.60
61:RO:461:SER:OG	61:RO:462:SER:N	2.33	0.60
3:SA:435:C:H42	57:RJ:166:ARG:HH12	1.47	0.60
25:3F:328:ILE:HG13	25:3F:338:THR:HG22	1.82	0.60
27:A4:429:SER:HB3	27:A4:444:ARG:HA	1.83	0.60
43:5E:480:GLN:HG2	43:5E:482:LEU:H	1.66	0.60
52:RC:205:ILE:O	52:RC:209:LEU:HB2	2.01	0.60
60:RN:548:ARG:NH1	60:RN:638:ASN:OD1	2.34	0.60
61:RO:452:ASP:HB3	61:RO:455:LEU:HB2	1.84	0.60
3:SA:606:A:N3	3:SA:607:G:N1	2.50	0.60
5:SF:194:THR:HG23	5:SF:195:ILE:HG12	1.83	0.60
60:RN:649:THR:HG23	60:RN:650:VAL:HG23	1.82	0.60
10:SK:65:LYS:HZ2	25:3F:59:PRO:N	1.98	0.60
23:3D:29:SER:O	23:3D:35:GLN:NE2	2.34	0.60
35:B2:54:ILE:HD13	35:B2:364:TYR:HD2	1.66	0.60
36:B3:581:CYS:HA	36:B3:590:LEU:O	2.02	0.60
53:RE:363:THR:HG22	53:RE:394:THR:HG21	1.83	0.60
42:5D:22:ARG:NH1	57:RJ:997:MET:O	2.35	0.60
3:SA:85:A:H2'	3:SA:86:A:H8	1.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:5H:434:PHE:HA	55:RH:129:ARG:HH12	1.67	0.60
50:RA:333:ASN:HD21	50:RA:338:MET:HA	1.67	0.60
3:SA:870:C:O2	20:Sc:51:GLN:NE2	2.35	0.59
31:AE:699:ARG:NH1	31:AE:702:TRP:O	2.35	0.59
32:AF:248:ARG:NH1	32:AF:289:ASN:O	2.35	0.59
53:RE:345:TYR:O	53:RE:349:LEU:HB3	2.02	0.59
58:RK:14:SER:HB2	58:RK:36:ILE:HG23	1.83	0.59
8:SI:118:LEU:HA	8:SI:121:VAL:HB	1.82	0.59
14:SP:40:ALA:HB2	14:SP:70:LYS:HD2	1.84	0.59
32:AF:301:PRO:HG2	32:AF:323:SER:HB3	1.84	0.59
36:B3:189:HIS:NE2	36:B3:217:ASP:OD1	2.35	0.59
6:SG:131:GLN:NE2	6:SG:135:ASP:OD1	2.35	0.59
7:SH:70:PRO:HB3	7:SH:101:ILE:HB	1.84	0.59
23:3D:382:LYS:HD2	23:3D:404:LEU:HD22	1.83	0.59
32:AF:133:HIS:HD2	32:AF:135:GLN:H	1.50	0.59
53:RE:383:GLY:HA3	53:RE:585:MET:HG2	1.82	0.59
33:AG:90:LYS:HG2	33:AG:144:VAL:HG22	1.85	0.59
60:RN:614:ILE:HG22	60:RN:616:LEU:HB2	1.85	0.59
9:SJ:32:GLN:HG2	50:RA:79:PRO:HD2	1.84	0.59
20:Sc:73:LEU:HB2	54:RF:215:VAL:HG21	1.85	0.59
53:RE:344:ASN:HA	53:RE:347:LYS:HD2	1.84	0.59
62:RP:112:GLN:NE2	62:RP:116:ASP:OD2	2.36	0.59
53:RE:1111:SER:HA	53:RE:1129:PRO:HG3	1.85	0.59
62:RP:54:TRP:O	62:RP:58:ASN:ND2	2.35	0.59
23:3D:286:ARG:HA	23:3D:289:TYR:HB3	1.85	0.59
24:3E:210:LEU:HD23	24:3E:256:ASN:HD22	1.68	0.59
34:B1:497:ILE:HG23	34:B1:512:ILE:HB	1.84	0.59
39:B6:15:MET:HA	39:B6:18:LEU:HB3	1.85	0.59
41:5C:257:SER:OG	41:5C:259:TRP:NE1	2.36	0.59
5:SF:180:LEU:HA	5:SF:194:THR:HG21	1.85	0.59
17:SX:90:THR:O	17:SX:94:LEU:HB2	2.03	0.59
53:RE:525:LEU:HB2	53:RE:617:LEU:HB2	1.84	0.59
55:RG:125:ASN:ND2	55:RG:127:THR:OG1	2.36	0.59
60:RN:535:ASN:OD1	60:RN:539:ARG:NH1	2.36	0.59
3:SA:1028:C:N4	52:RC:193:ASN:O	2.36	0.58
13:SO:130:ARG:HB3	52:RC:264:ILE:HD12	1.85	0.58
22:3C:114:GLY:O	22:3C:122:ARG:NH1	2.35	0.58
33:AG:510:TYR:HH	33:AG:527:HIS:HD1	1.49	0.58
41:5C:190:HIS:HB3	41:5C:207:THR:HG21	1.84	0.58
2:5A:425:U:H3	2:5A:431:A:H61	1.51	0.58
21:Sd:65:ARG:NH2	35:B2:750:GLU:OE2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A8:533:PRO:HA	29:A8:559:PRO:HG2	1.85	0.58
33:AG:153:ILE:HG22	33:AG:174:TYR:HB2	1.85	0.58
53:RE:381:HIS:NE2	53:RE:478:THR:O	2.36	0.58
65:RT:110:ARG:NH2	65:RT:130:MET:SD	2.76	0.58
17:SX:97:ARG:HH11	49:5K:84:ARG:HH12	1.51	0.58
34:B1:300:MET:HE3	34:B1:328:LEU:HD13	1.85	0.58
53:RE:834:ASN:ND2	53:RE:863:TYR:OH	2.36	0.58
62:RP:1904:LEU:HD12	62:RP:1940:LYS:HE2	1.85	0.58
66:RV:232:GLU:O	66:RV:239:ARG:NH1	2.36	0.58
4:SC:92:GLN:HE21	4:SC:97:LEU:HD21	1.68	0.58
27:A4:380:LYS:NZ	27:A4:634:VAL:O	2.35	0.58
41:5C:76:PRO:HA	47:5I:1:MET:HE2	1.86	0.58
54:RF:91:ASP:O	54:RF:121:ARG:NH2	2.36	0.58
62:RP:144:SER:HB3	62:RP:147:VAL:HG12	1.86	0.58
3:SA:563:U:H4'	45:5G:278:ARG:HG3	1.85	0.58
27:A4:565:ARG:HD3	31:AE:633:GLU:HB2	1.86	0.58
33:AG:568:ASN:ND2	33:AG:586:SER:OG	2.35	0.58
35:B2:97:GLY:HA3	35:B2:124:ILE:HD11	1.84	0.58
36:B3:237:LEU:HD21	53:RE:663:ILE:HG21	1.86	0.58
47:5I:411:LYS:O	47:5I:415:ARG:HB2	2.02	0.58
53:RE:520:ASN:HD22	53:RE:959:LEU:HD12	1.68	0.58
1:3A:30:A:N6	47:5I:341:GLU:OE2	2.36	0.58
24:3E:11:GLY:HA2	24:3E:143:LEU:HD22	1.86	0.58
42:5D:37:ARG:NH2	57:RJ:994:LYS:O	2.36	0.58
62:RP:2030:ASN:O	62:RP:2036:ARG:NH2	2.35	0.58
62:RP:2036:ARG:HH12	62:RP:2074:SER:HB2	1.69	0.58
5:SF:44:LEU:HD13	5:SF:82:TYR:HB3	1.85	0.58
27:A4:269:PHE:O	37:B8:446:ARG:NH2	2.36	0.58
31:AE:248:SER:OG	31:AE:253:CYS:SG	2.62	0.58
33:AG:118:VAL:HB	33:AG:130:LYS:HB2	1.85	0.58
36:B3:494:ILE:N	36:B3:510:SER:OG	2.35	0.58
61:RO:202:LEU:HD22	61:RO:212:LEU:HD22	1.86	0.58
1:3A:251:G:H2'	25:3F:155:ASN:HD21	1.67	0.58
3:SA:126:A:N6	3:SA:291:G:O2'	2.37	0.58
33:AG:435:ASP:CB	33:AG:702:TYR:HA	2.34	0.58
35:B2:259:ILE:HA	35:B2:273:TYR:O	2.03	0.58
50:RA:75:GLY:HA3	50:RA:80:GLN:H	1.68	0.58
53:RE:412:LEU:HD21	53:RE:424:GLY:HA3	1.84	0.58
55:RH:44:VAL:HA	55:RH:113:TYR:O	2.03	0.58
3:SA:1498:G:HO2'	56:RI:251:SER:HG	1.51	0.58
22:3B:236:MET:HG3	23:3D:133:LEU:HA	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:AG:144:VAL:HG12	33:AG:153:ILE:HG13	1.86	0.58
33:AG:157:PHE:HB2	33:AG:170:SER:HB3	1.86	0.58
34:B1:432:GLN:HE22	43:5E:455:HIS:HA	1.69	0.58
34:B1:501:SER:HB2	34:B1:508:GLN:HB2	1.84	0.58
41:5C:185:HIS:NE2	44:5F:19:LEU:O	2.36	0.58
36:B3:584:ILE:HD11	36:B3:599:ILE:HD11	1.85	0.57
41:5C:541:ASP:O	41:5C:542:HIS:ND1	2.37	0.57
46:5H:532:VAL:HA	57:RJ:909:ASN:HD21	1.69	0.57
50:RA:212:ARG:HH12	52:RC:310:ALA:H	1.52	0.57
53:RE:373:ARG:NH2	53:RE:510:ILE:O	2.37	0.57
61:RO:270:SER:H	61:RO:273:GLN:HE21	1.50	0.57
25:3F:241:THR:HG21	25:3F:285:SER:HA	1.86	0.57
26:3H:44:LEU:HD13	26:3H:52:ILE:HD11	1.86	0.57
31:AE:671:LEU:O	31:AE:675:ASN:HB3	2.04	0.57
32:AF:303:LEU:HD13	32:AF:323:SER:HB2	1.86	0.57
37:B8:221:THR:OG1	37:B8:222:LEU:N	2.38	0.57
38:BE:482:GLY:HA2	38:BE:505:VAL:HG23	1.86	0.57
41:5C:317:THR:HG23	41:5C:334:ARG:HB3	1.86	0.57
53:RE:443:HIS:HB3	53:RE:470:LYS:HB2	1.85	0.57
57:RJ:773:THR:HA	57:RJ:777:ARG:HH11	1.69	0.57
58:RK:114:PHE:HB2	58:RK:170:VAL:HG22	1.86	0.57
3:SA:1196:A:N3	55:RG:136:ARG:NH2	2.52	0.57
18:SY:109:ARG:NH2	18:SY:120:VAL:O	2.37	0.57
31:AE:186:MET:HE1	31:AE:234:LEU:HD12	1.86	0.57
35:B2:365:TYR:HA	35:B2:381:LYS:HA	1.85	0.57
40:5B:194:LYS:HD2	40:5B:199:ILE:HG13	1.86	0.57
55:RH:31:LEU:HD13	55:RH:40:ARG:HE	1.69	0.57
2:5A:177:U:O2'	2:5A:178:G:N7	2.35	0.57
19:SZ:83:LYS:HD2	19:SZ:96:LEU:HD21	1.86	0.57
22:3C:267:VAL:HG21	22:3C:298:ILE:HD12	1.87	0.57
36:B3:744:ARG:HA	36:B3:785:ILE:HG21	1.86	0.57
37:B8:227:LEU:HB2	37:B8:528:GLN:HE22	1.67	0.57
38:BE:359:ALA:O	38:BE:421:ASN:ND2	2.38	0.57
42:5D:111:ARG:HH11	42:5D:212:LYS:HD2	1.69	0.57
43:5E:369:ILE:HG12	45:5G:223:THR:HG21	1.86	0.57
24:3E:339:TYR:HB3	24:3E:343:TYR:HB2	1.85	0.57
31:AE:559:ASN:HA	31:AE:592:ARG:HD3	1.85	0.57
41:5C:450:GLY:O	63:RQ:857:TYR:OH	2.21	0.57
59:RL:29:VAL:HG22	59:RL:202:ASP:HA	1.86	0.57
65:RT:217:GLU:HG2	65:RT:223:ARG:HA	1.86	0.57
5:SF:206:ASP:OD1	5:SF:206:ASP:N	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:SJ:167:ALA:HB2	9:SJ:183:ILE:HD12	1.87	0.57
28:A5:148:LEU:HD23	28:A5:167:SER:HB3	1.86	0.57
32:AF:24:GLN:O	32:AF:28:ARG:HB3	2.05	0.57
34:B1:264:LYS:HD3	34:B1:280:THR:HG22	1.87	0.57
34:B1:405:SER:HB3	34:B1:436:LEU:HD23	1.85	0.57
36:B3:392:ASN:H	36:B3:407:SER:HA	1.69	0.57
47:5I:87:SER:OG	47:5I:89:ASP:OD1	2.22	0.57
54:RF:134:ILE:O	54:RF:138:TRP:HB3	2.05	0.57
62:RP:2073:GLU:OE2	62:RP:2076:ARG:NH1	2.36	0.57
3:SA:205:U:H2'	3:SA:206:A:H8	1.68	0.57
3:SA:1684:U:H3	3:SA:1718:G:H1	1.52	0.57
25:3F:442:ILE:HA	25:3F:472:PRO:HA	1.86	0.57
37:B8:146:LEU:O	37:B8:163:ARG:NH1	2.37	0.57
46:5H:498:VAL:HG21	56:RI:253:PRO:HD3	1.86	0.57
53:RE:440:LEU:HA	53:RE:456:LYS:O	2.05	0.57
2:5A:323:A:N6	34:B1:212:ASP:OD2	2.37	0.57
22:3C:142:ARG:NH1	22:3C:186:ASP:OD2	2.36	0.57
43:5E:312:GLU:O	43:5E:316:ASN:ND2	2.38	0.57
50:RA:152:ASP:HA	50:RA:166:ASN:HA	1.86	0.57
57:RJ:1042:MET:HG3	57:RJ:1044:LEU:HD13	1.86	0.57
2:5A:481:U:O2'	39:B6:102:LYS:NZ	2.37	0.57
3:SA:146:U:N3	3:SA:168:A:N6	2.51	0.57
3:SA:559:C:OP1	57:RJ:868:ARG:NH2	2.37	0.57
23:3D:264:SER:OG	23:3D:265:GLU:N	2.37	0.57
25:3F:142:ILE:HA	25:3F:568:ILE:HD11	1.86	0.57
28:A5:434:THR:HG23	61:RO:266:ASN:HD21	1.68	0.57
33:AG:86:GLU:OE1	33:AG:113:ASN:ND2	2.36	0.57
37:B8:129:ASP:OD1	38:BE:194:ARG:NH2	2.36	0.57
46:5H:438:ASP:OD1	46:5H:438:ASP:N	2.38	0.57
47:5I:81:ASN:ND2	47:5I:96:ASN:OD1	2.38	0.57
59:RL:32:ARG:HE	59:RL:35:ASN:HD21	1.53	0.57
3:SA:112:A:O2'	11:SM:67:ARG:NH1	2.37	0.57
8:SI:187:SER:OG	8:SI:188:GLU:N	2.38	0.57
29:A8:536:ARG:NH1	29:A8:537:THR:OG1	2.38	0.57
29:A8:614:ILE:HD12	29:A8:634:LEU:HD13	1.86	0.57
38:BE:666:ARG:NH1	38:BE:706:ASP:OD2	2.38	0.57
47:5I:45:LEU:HD13	47:5I:410:ILE:HG22	1.86	0.57
62:RP:54:TRP:HA	62:RP:57:ILE:HG22	1.87	0.57
64:RS:209:LYS:HE3	64:RS:212:LYS:HG3	1.87	0.57
3:SA:1197:C:OP1	55:RG:136:ARG:NH1	2.38	0.56
25:3F:545:LYS:HG2	25:3F:561:ASN:HD21	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:A5:212:LEU:HD11	28:A5:246:VAL:HG11	1.87	0.56
34:B1:373:ASP:HB2	34:B1:380:LEU:HD21	1.86	0.56
49:5K:26:LYS:HD3	49:5K:29:GLN:HG3	1.87	0.56
2:5A:338:A:O2'	2:5A:340:U:O4	2.20	0.56
33:AG:473:LEU:HB2	33:AG:495:ILE:HD11	1.87	0.56
34:B1:54:HIS:NE2	34:B1:72:SER:OG	2.32	0.56
34:B1:479:LEU:HD12	34:B1:488:LEU:HD11	1.87	0.56
41:5C:493:LYS:O	41:5C:498:ARG:NH1	2.38	0.56
44:5F:66:PRO:HG3	66:RV:207:ARG:HH11	1.70	0.56
47:5I:15:PRO:HB3	47:5I:20:GLN:HE21	1.70	0.56
59:RL:12:SER:O	59:RL:16:ASN:ND2	2.38	0.56
2:5A:173:G:N2	2:5A:224:G:O2'	2.38	0.56
3:SA:439:U:H4'	3:SA:465:G:H22	1.69	0.56
3:SA:1680:G:N2	3:SA:1720:G:O6	2.38	0.56
29:A8:539:ASN:ND2	29:A8:560:ASN:O	2.38	0.56
32:AF:147:ARG:NH2	55:RH:16:GLN:O	2.39	0.56
35:B2:598:LYS:NZ	35:B2:610:SER:OG	2.38	0.56
50:RA:227:ARG:NH2	50:RA:248:SER:O	2.34	0.56
51:RB:230:ALA:O	51:RB:234:LYS:HB2	2.05	0.56
55:RG:41:MET:HG3	55:RG:202:ILE:HG23	1.88	0.56
58:RK:221:CYS:SG	58:RK:222:GLU:N	2.71	0.56
3:SA:337:G:N2	3:SA:340:U:OP2	2.39	0.56
16:ST:27:LYS:HA	16:ST:57:ARG:HA	1.88	0.56
24:3E:414:ARG:NH1	31:AE:187:ASP:OD2	2.36	0.56
30:A9:473:LYS:O	30:A9:477:LYS:NZ	2.39	0.56
18:SY:132:LEU:HA	18:SY:135:LEU:HB2	1.87	0.56
27:A4:32:ILE:O	27:A4:751:GLU:HA	2.06	0.56
27:A4:37:ARG:NH1	29:A8:704:PRO:O	2.38	0.56
34:B1:329:VAL:HG12	34:B1:339:LEU:HG	1.87	0.56
45:5G:108:LYS:HD2	45:5G:116:ARG:HB2	1.87	0.56
56:RI:33:ASP:N	56:RI:33:ASP:OD1	2.37	0.56
10:SK:78:ARG:NH2	51:RB:247:GLU:OE1	2.33	0.56
27:A4:301:ASP:O	27:A4:771:GLN:NE2	2.38	0.56
35:B2:145:ILE:HG23	35:B2:159:LEU:HB2	1.88	0.56
45:5G:144:GLU:HA	45:5G:149:PRO:HA	1.88	0.56
53:RE:228:ARG:HE	53:RE:296:ILE:HG12	1.71	0.56
53:RE:606:ASN:ND2	53:RE:608:PHE:O	2.39	0.56
53:RE:822:ARG:HE	53:RE:1136:LEU:HD21	1.71	0.56
59:RL:71:LYS:O	59:RL:75:ASN:ND2	2.38	0.56
2:5A:484:G:OP2	39:B6:3:LYS:NZ	2.39	0.56
4:SC:87:ARG:HH21	4:SC:101:HIS:HD2	1.52	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:RE:223:ARG:HA	53:RE:226:HIS:HB2	1.86	0.56
61:RO:170:GLY:O	61:RO:272:GLN:NE2	2.32	0.56
2:5A:5:G:N2	2:5A:8:A:OP2	2.39	0.56
22:3C:160:ASP:OD1	22:3C:160:ASP:N	2.37	0.56
28:A5:435:GLY:HA3	61:RO:262:LEU:HD11	1.88	0.56
35:B2:347:SER:O	35:B2:371:LYS:NZ	2.39	0.56
35:B2:461:SER:OG	35:B2:462:SER:N	2.38	0.56
54:RF:262:VAL:HA	54:RF:265:ARG:HG2	1.88	0.56
59:RL:7:ASP:HB2	59:RL:10:ILE:HG12	1.88	0.56
2:5A:329:A:OP1	41:5C:229:ARG:NH2	2.36	0.56
3:SA:143:G:OP2	7:SH:139:ASN:ND2	2.38	0.56
3:SA:1657:U:OP1	3:SA:1658:G:O2'	2.23	0.56
9:SJ:104:ILE:O	9:SJ:164:ARG:HA	2.06	0.56
16:ST:8:GLN:NE2	32:AF:324:SER:O	2.39	0.56
23:3D:389:ILE:HA	26:3H:62:GLU:HB2	1.87	0.56
28:A5:25:ASP:OD2	37:B8:590:LYS:NZ	2.37	0.56
28:A5:471:ARG:NH2	61:RO:301:ASP:OD2	2.39	0.56
49:5K:123:PRO:O	49:5K:126:LYS:NZ	2.39	0.56
50:RA:175:PRO:O	50:RA:177:LYS:NZ	2.36	0.56
53:RE:241:ILE:HA	53:RE:244:LYS:HD2	1.88	0.56
65:RT:109:LEU:O	65:RT:113:TRP:HB2	2.06	0.56
24:3E:136:LEU:HG	24:3E:139:MET:HE2	1.88	0.56
31:AE:272:LYS:NZ	31:AE:310:GLY:O	2.39	0.56
41:5C:541:ASP:N	41:5C:541:ASP:OD1	2.38	0.56
44:5F:29:ASP:N	44:5F:29:ASP:OD1	2.38	0.56
47:5I:73:ILE:HG12	47:5I:85:THR:HG22	1.88	0.56
53:RE:560:ASN:OD1	53:RE:560:ASN:N	2.39	0.56
58:RK:34:GLU:HG3	58:RK:35:LYS:HG2	1.88	0.56
58:RK:154:LEU:HB2	58:RK:165:GLU:HG3	1.88	0.56
60:RN:478:ILE:HD13	60:RN:520:PRO:HB2	1.88	0.56
60:RN:512:ASP:OD1	60:RN:512:ASP:N	2.38	0.56
68:RY:487:ASP:N	68:RY:487:ASP:OD1	2.36	0.56
3:SA:1490:C:OP1	57:RJ:1062:ARG:NH2	2.38	0.55
22:3C:320:TYR:OH	22:3C:322:ARG:NH2	2.39	0.55
25:3F:417:SER:OG	25:3F:418:ASP:N	2.37	0.55
28:A5:364:THR:OG1	28:A5:368:ASN:ND2	2.38	0.55
31:AE:95:ASP:HB2	31:AE:131:ASN:HD21	1.71	0.55
33:AG:435:ASP:HB3	33:AG:702:TYR:HA	1.88	0.55
36:B3:12:LEU:HG	36:B3:641:PHE:HB2	1.87	0.55
37:B8:181:GLU:HB3	38:BE:281:ARG:HH12	1.71	0.55
62:RP:67:ALA:O	62:RP:71:GLU:HB2	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:448:C:OP2	5:SF:49:ARG:NH2	2.38	0.55
3:SA:1542:G:O6	3:SA:1568:C:N4	2.36	0.55
7:SH:46:LYS:HB3	7:SH:118:GLU:HG2	1.88	0.55
19:SZ:54:ALA:HB1	19:SZ:76:TYR:HB2	1.88	0.55
26:3H:41:THR:O	26:3H:45:ASN:ND2	2.39	0.55
28:A5:5:VAL:HA	28:A5:21:THR:HG22	1.89	0.55
35:B2:463:SER:OG	35:B2:464:LEU:N	2.39	0.55
35:B2:858:PHE:O	35:B2:862:LYS:HB2	2.06	0.55
48:5J:129:ALA:HB1	57:RJ:1119:ILE:HG22	1.89	0.55
50:RA:101:ASN:HA	50:RA:118:GLN:HA	1.88	0.55
3:SA:128:U:H3	62:RP:906:THR:H	1.53	0.55
41:5C:433:LEU:HG	44:5F:13:LEU:HD11	1.88	0.55
45:5G:60:GLN:OE1	66:RV:207:ARG:NH1	2.39	0.55
53:RE:578:ILE:HG22	53:RE:619:VAL:HG12	1.88	0.55
62:RP:1760:ASN:ND2	62:RP:1805:ASP:OD2	2.39	0.55
3:SA:396:G:O6	9:SJ:26:LYS:NZ	2.37	0.55
3:SA:1678:A:N6	3:SA:1723:U:O4	2.39	0.55
9:SJ:195:ARG:NH2	11:SM:11:ARG:O	2.39	0.55
35:B2:124:ILE:HA	35:B2:140:SER:HA	1.89	0.55
35:B2:142:ASP:OD2	35:B2:144:ASN:ND2	2.39	0.55
35:B2:267:ASP:OD1	35:B2:267:ASP:N	2.36	0.55
47:5I:26:ARG:NH1	63:RQ:867:GLN:O	2.40	0.55
47:5I:340:ARG:NH2	47:5I:377:SER:O	2.39	0.55
53:RE:707:PHE:O	53:RE:918:ARG:NH1	2.39	0.55
57:RJ:939:TYR:HA	57:RJ:997:MET:HE1	1.88	0.55
58:RK:139:PRO:HA	58:RK:142:GLU:HB2	1.89	0.55
60:RN:682:ARG:O	60:RN:686:ASN:ND2	2.40	0.55
62:RP:1981:TYR:OH	62:RP:1985:ARG:NH1	2.39	0.55
3:SA:207:U:H3	3:SA:258:C:N4	2.04	0.55
3:SA:444:C:O2	3:SA:460:A:N6	2.39	0.55
3:SA:453:U:O2'	3:SA:455:C:OP2	2.24	0.55
3:SA:862:A:OP2	13:SO:64:ARG:NH2	2.40	0.55
4:SC:192:VAL:HG21	53:RE:751:LYS:HA	1.88	0.55
22:3B:225:ARG:NH1	22:3B:248:ASP:OD2	2.38	0.55
22:3C:189:GLY:O	22:3C:216:ASN:ND2	2.39	0.55
22:3C:225:ARG:NH2	22:3C:246:GLN:OE1	2.38	0.55
25:3F:289:ARG:NH2	25:3F:332:ALA:O	2.39	0.55
25:3F:337:VAL:HG23	25:3F:407:MET:HE2	1.88	0.55
25:3F:552:TRP:HB3	26:3H:85:VAL:HG13	1.88	0.55
33:AG:262:MET:HA	33:AG:272:ALA:O	2.07	0.55
36:B3:366:PRO:HG2	36:B3:378:PRO:HB3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:5C:162:ASN:HB3	41:5C:164:GLN:H	1.71	0.55
41:5C:369:MET:HE1	41:5C:404:PRO:HD2	1.88	0.55
47:5I:173:ILE:HG13	47:5I:174:ARG:HG2	1.87	0.55
47:5I:329:ILE:HG12	47:5I:343:TYR:HB2	1.89	0.55
53:RE:412:LEU:HD13	53:RE:421:LEU:HD12	1.89	0.55
57:RJ:279:PRO:HB3	57:RJ:784:LYS:HA	1.88	0.55
57:RJ:360:ASP:OD1	57:RJ:360:ASP:N	2.35	0.55
57:RJ:608:LEU:HB2	58:RK:16:ASN:HD22	1.72	0.55
57:RJ:921:GLU:HB2	58:RK:365:LYS:HG3	1.88	0.55
63:RQ:896:ALA:HB1	63:RQ:897:PRO:HD2	1.89	0.55
9:SJ:41:LYS:HE2	9:SJ:43:ILE:HD11	1.89	0.55
9:SJ:98:LYS:NZ	9:SJ:170:SER:O	2.36	0.55
12:SN:90:LYS:HE3	12:SN:91:VAL:HG12	1.88	0.55
27:A4:57:ILE:HD13	27:A4:340:GLN:HG2	1.89	0.55
33:AG:583:LYS:HE2	33:AG:599:ILE:HD13	1.88	0.55
37:B8:526:ASP:OD1	37:B8:526:ASP:N	2.38	0.55
37:B8:561:PRO:O	37:B8:587:ARG:NH1	2.39	0.55
39:B6:278:MET:HA	39:B6:312:LEU:HD11	1.89	0.55
51:RB:304:GLU:OE1	51:RB:309:LYS:NZ	2.40	0.55
63:RQ:898:PHE:N	63:RQ:898:PHE:CD1	2.73	0.55
3:SA:365:G:N7	51:RB:231:ARG:NH1	2.55	0.55
3:SA:545:A:O2'	3:SA:546:U:O4'	2.22	0.55
3:SA:1232:U:O4	3:SA:1234:A:N6	2.39	0.55
25:3F:293:ASP:N	25:3F:293:ASP:OD1	2.37	0.55
31:AE:1172:ASP:N	31:AE:1236:ASN:O	2.40	0.55
34:B1:418:ARG:HH22	43:5E:491:ALA:HA	1.72	0.55
35:B2:592:SER:OG	35:B2:593:ALA:N	2.40	0.55
36:B3:179:LYS:O	36:B3:181:LYS:NZ	2.38	0.55
53:RE:691:SER:OG	53:RE:692:LYS:N	2.40	0.55
64:RS:445:ARG:NH1	64:RS:445:ARG:O	2.40	0.55
2:5A:243:A:H4'	42:5D:224:LEU:HD21	1.89	0.55
10:SK:139:GLN:NE2	19:SZ:64:PHE:O	2.39	0.55
23:3D:21:LYS:HE2	23:3D:49:GLU:HB2	1.88	0.55
26:3G:57:ASP:O	26:3G:84:ARG:NH1	2.40	0.55
27:A4:641:GLU:OE2	27:A4:645:ARG:NH1	2.40	0.55
33:AG:51:GLN:HE21	33:AG:53:LYS:HD3	1.72	0.55
34:B1:356:ASP:HB2	34:B1:826:ARG:HG3	1.89	0.55
35:B2:787:LYS:NZ	35:B2:788:PRO:O	2.38	0.55
36:B3:5:THR:O	36:B3:611:LYS:NZ	2.39	0.55
44:5F:162:ASP:OD1	44:5F:162:ASP:N	2.40	0.55
47:5I:75:LYS:NZ	47:5I:356:TYR:O	2.34	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:RA:166:ASN:ND2	50:RA:168:GLU:O	2.40	0.55
53:RE:356:THR:HB	53:RE:414:HIS:HB2	1.89	0.55
57:RJ:130:ASP:OD2	57:RJ:853:ARG:NH2	2.40	0.55
58:RK:171:ASP:N	58:RK:171:ASP:OD1	2.39	0.55
65:RT:169:ASP:OD1	65:RT:169:ASP:N	2.39	0.55
3:SA:96:G:N2	3:SA:387:A:N1	2.55	0.55
3:SA:258:C:O2	9:SJ:178:ARG:NH2	2.40	0.55
3:SA:1758:U:O4	35:B2:937:ARG:NH2	2.40	0.55
5:SF:45:ILE:HG13	5:SF:61:VAL:HG11	1.88	0.55
13:SO:60:VAL:HG23	13:SO:66:ILE:HD12	1.88	0.55
28:A5:454:GLU:OE2	28:A5:487:ARG:NH1	2.40	0.55
31:AE:196:LEU:HD11	31:AE:213:THR:HG21	1.88	0.55
31:AE:636:ASP:OD1	31:AE:639:ARG:NH1	2.40	0.55
36:B3:107:ILE:HD11	36:B3:147:ILE:HG22	1.88	0.55
46:5H:432:ASP:O	55:RH:129:ARG:NH2	2.39	0.55
53:RE:508:SER:HA	53:RE:512:LEU:HB2	1.89	0.55
58:RK:155:LYS:HG3	58:RK:164:GLY:HA2	1.89	0.55
60:RN:290:LYS:O	64:RS:458:ARG:NH1	2.40	0.55
3:SA:1684:U:O2	3:SA:1718:G:N2	2.40	0.55
7:SH:10:ASN:O	7:SH:128:THR:OG1	2.25	0.55
11:SM:125:VAL:HB	11:SM:137:PHE:HB3	1.89	0.55
14:SP:122:PRO:HB2	14:SP:125:SER:HB3	1.89	0.55
24:3E:280:MET:HG3	24:3E:288:THR:HG22	1.89	0.55
28:A5:531:LYS:O	28:A5:535:ASP:HB2	2.07	0.55
31:AE:12:ALA:HB2	41:5C:142:GLY:HA3	1.89	0.55
31:AE:558:VAL:O	31:AE:592:ARG:NH1	2.40	0.55
31:AE:652:MET:HE3	31:AE:683:SER:HB3	1.89	0.55
43:5E:299:SER:O	43:5E:303:GLN:NE2	2.40	0.55
46:5H:565:LYS:HA	46:5H:568:LYS:HG2	1.89	0.55
52:RC:69:ILE:HD11	52:RC:93:ILE:HG23	1.88	0.55
53:RE:190:ALA:O	53:RE:350:TYR:OH	2.25	0.55
53:RE:267:ILE:HD12	53:RE:293:ASN:HB3	1.89	0.55
57:RJ:289:HIS:HB2	57:RJ:815:LEU:HD21	1.89	0.55
2:5A:354:G:N1	41:5C:485:ASP:O	2.38	0.54
3:SA:332:U:OP1	9:SJ:31:ARG:NH2	2.37	0.54
3:SA:1533:C:OP1	16:ST:27:LYS:NZ	2.40	0.54
9:SJ:8:ARG:HD2	9:SJ:22:ARG:HH11	1.72	0.54
23:3D:379:LEU:O	23:3D:383:CYS:HB2	2.07	0.54
32:AF:75:LYS:HD3	32:AF:113:PRO:HD3	1.89	0.54
32:AF:420:GLU:O	32:AF:424:ARG:HB3	2.07	0.54
34:B1:430:ARG:HD2	43:5E:460:PRO:HA	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:B8:176:LYS:O	37:B8:180:ASP:CB	2.55	0.54
41:5C:96:ASP:OD1	41:5C:96:ASP:N	2.35	0.54
43:5E:344:GLU:HA	57:RJ:960:ARG:HH21	1.71	0.54
43:5E:448:LEU:HD22	44:5F:85:MET:HE1	1.89	0.54
53:RE:536:TYR:OH	53:RE:552:ARG:NH1	2.40	0.54
57:RJ:551:LYS:O	57:RJ:555:MET:HB2	2.07	0.54
29:A8:666:VAL:HG22	30:A9:496:LEU:HB3	1.89	0.54
33:AG:727:GLN:OE1	33:AG:738:ASN:ND2	2.39	0.54
34:B1:375:THR:OG1	34:B1:376:SER:N	2.41	0.54
34:B1:641:LEU:HD23	34:B1:644:ILE:HD12	1.89	0.54
37:B8:176:LYS:O	37:B8:180:ASP:HB3	2.07	0.54
39:B6:187:LYS:HE3	48:5J:63:PRO:HB2	1.89	0.54
47:5I:402:GLU:O	47:5I:405:ARG:NH2	2.40	0.54
57:RJ:966:ILE:HD13	57:RJ:976:ILE:HG22	1.88	0.54
61:RO:345:ILE:HA	61:RO:349:LEU:HD13	1.89	0.54
3:SA:846:G:N2	3:SA:846:G:OP2	2.40	0.54
31:AE:205:THR:HB	31:AE:210:LEU:HD21	1.89	0.54
33:AG:850:GLU:HA	33:AG:853:ILE:HD12	1.89	0.54
47:5I:133:GLN:NE2	47:5I:151:ASN:OD1	2.40	0.54
51:RB:335:GLU:HA	51:RB:339:SER:HB2	1.89	0.54
58:RK:37:ARG:NH2	58:RK:49:GLU:OE2	2.36	0.54
64:RS:319:LYS:HA	64:RS:323:PHE:HB2	1.89	0.54
15:SR:22:VAL:HG22	15:SR:65:ILE:HG23	1.89	0.54
23:3D:63:LEU:O	23:3D:67:ASN:ND2	2.40	0.54
27:A4:534:LEU:HA	27:A4:542:VAL:O	2.07	0.54
34:B1:202:ASP:N	34:B1:202:ASP:OD1	2.40	0.54
36:B3:537:TRP:N	36:B3:551:SER:O	2.37	0.54
50:RA:78:LYS:O	50:RA:80:GLN:NE2	2.41	0.54
51:RB:242:MET:HE2	51:RB:332:ARG:HE	1.73	0.54
57:RJ:1018:VAL:O	57:RJ:1029:TRP:NE1	2.41	0.54
61:RO:156:TRP:O	61:RO:215:ASN:ND2	2.40	0.54
27:A4:252:GLN:NE2	27:A4:318:ASN:OD1	2.40	0.54
29:A8:443:CYS:HA	33:AG:728:LEU:HD22	1.87	0.54
32:AF:215:VAL:HA	32:AF:230:GLY:HA3	1.90	0.54
36:B3:328:GLN:NE2	36:B3:329:VAL:O	2.41	0.54
37:B8:352:GLN:HE21	37:B8:385:ASN:HD22	1.54	0.54
38:BE:73:GLU:OE2	38:BE:74:LYS:NZ	2.40	0.54
38:BE:626:ASP:N	38:BE:626:ASP:OD1	2.35	0.54
44:5F:115:MET:HG3	44:5F:120:MET:HB3	1.89	0.54
53:RE:1101:ASP:HB3	53:RE:1233:ASN:HB3	1.88	0.54
55:RH:114:ILE:HG12	55:RH:122:ILE:HB	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:103:A:OP1	9:SJ:18:ARG:NH1	2.40	0.54
23:3D:392:TYR:HB3	26:3H:65:LEU:HD22	1.90	0.54
31:AE:274:ILE:HD11	37:B8:215:THR:HG21	1.90	0.54
32:AF:360:MET:HE3	32:AF:361:MET:HE3	1.89	0.54
33:AG:64:LYS:NZ	33:AG:123:GLY:O	2.39	0.54
57:RJ:73:ALA:HB1	57:RJ:131:ILE:HD12	1.90	0.54
3:SA:511:A:OP2	10:SK:176:ASN:ND2	2.40	0.54
3:SA:1175:U:OP1	60:RN:748:ARG:NH1	2.41	0.54
5:SF:198:LYS:HG3	5:SF:208:VAL:HG23	1.89	0.54
6:SG:26:ALA:HB3	15:SR:28:LEU:HB3	1.89	0.54
15:SR:34:SER:HB2	15:SR:38:LEU:HD12	1.90	0.54
25:3F:398:CYS:O	25:3F:419:ASN:ND2	2.40	0.54
25:3F:414:ILE:HD11	25:3F:480:ALA:HB2	1.90	0.54
26:3G:13:ASP:OD1	26:3G:13:ASP:N	2.39	0.54
34:B1:396:ALA:HB2	34:B1:438:VAL:HG21	1.90	0.54
34:B1:645:ASP:OD1	34:B1:645:ASP:N	2.39	0.54
35:B2:287:ARG:NH1	35:B2:324:PHE:O	2.41	0.54
37:B8:486:SER:OG	37:B8:487:GLU:N	2.41	0.54
49:5K:145:VAL:HG23	49:5K:151:TYR:HB2	1.89	0.54
51:RB:310:GLN:O	51:RB:314:ASN:ND2	2.40	0.54
58:RK:347:ASN:ND2	58:RK:349:ASP:OD2	2.40	0.54
60:RN:515:HIS:HB3	60:RN:518:ILE:HG22	1.90	0.54
60:RN:780:LYS:HG2	60:RN:781:MET:HE2	1.90	0.54
66:RV:199:ASP:OD1	66:RV:199:ASP:N	2.40	0.54
2:5A:175:A:N6	2:5A:177:U:O2	2.40	0.54
22:3B:90:PRO:HD3	48:5J:106:LEU:HD12	1.90	0.54
22:3C:268:VAL:HG22	22:3C:317:VAL:HG12	1.89	0.54
25:3F:481:ILE:HD12	25:3F:486:VAL:HG13	1.90	0.54
33:AG:325:GLN:NE2	33:AG:328:THR:OG1	2.41	0.54
33:AG:368:ASP:OD1	33:AG:368:ASP:N	2.38	0.54
35:B2:317:ILE:O	35:B2:321:TYR:N	2.41	0.54
36:B3:510:SER:O	36:B3:514:THR:OG1	2.26	0.54
50:RA:64:VAL:HG21	50:RA:323:VAL:HG12	1.90	0.54
50:RA:121:ARG:HH22	68:RY:462:ARG:HD2	1.72	0.54
50:RA:250:GLY:HA2	50:RA:274:ILE:HG23	1.88	0.54
53:RE:174:TYR:HE2	53:RE:227:LYS:HB3	1.73	0.54
53:RE:578:ILE:HG21	53:RE:617:LEU:HD12	1.90	0.54
1:3A:258:U:O4	23:3D:377:ARG:NH2	2.41	0.54
3:SA:146:U:O4	3:SA:168:A:N7	2.41	0.54
3:SA:265:A:OP2	7:SH:194:LYS:NZ	2.37	0.54
22:3B:124:SER:HB3	48:5J:153:ILE:HD11	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:A5:20:VAL:HG22	28:A5:29:VAL:HG22	1.89	0.54
31:AE:519:LEU:HD23	31:AE:523:ILE:HD13	1.88	0.54
32:AF:387:ALA:O	32:AF:391:ASN:ND2	2.40	0.54
33:AG:510:TYR:OH	33:AG:527:HIS:ND1	2.35	0.54
33:AG:724:ILE:HD11	33:AG:763:ILE:HG22	1.90	0.54
35:B2:260:GLU:O	35:B2:272:PHE:HA	2.08	0.54
38:BE:430:ILE:HB	38:BE:443:TRP:HB2	1.89	0.54
38:BE:604:SER:OG	38:BE:606:ASP:OD1	2.25	0.54
53:RE:931:ASP:OD1	53:RE:931:ASP:N	2.37	0.54
57:RJ:954:SER:HA	57:RJ:984:GLU:HG3	1.89	0.54
2:5A:354:G:N2	41:5C:495:SER:O	2.41	0.54
3:SA:325:G:H2'	3:SA:326:G:H8	1.73	0.54
3:SA:1539:G:N1	3:SA:1569:A:OP2	2.41	0.54
23:3D:392:TYR:HB2	26:3H:62:GLU:HB3	1.90	0.54
24:3E:380:ARG:NH1	24:3E:382:ASP:OD1	2.40	0.54
25:3F:399:GLU:OE2	25:3F:417:SER:OG	2.26	0.54
26:3H:38:ASN:HA	26:3H:41:THR:HG22	1.90	0.54
27:A4:207:ASP:OD2	27:A4:209:ARG:NH1	2.37	0.54
27:A4:641:GLU:HB3	27:A4:749:SER:HB3	1.90	0.54
34:B1:661:LEU:HD11	43:5E:450:VAL:HG12	1.90	0.54
38:BE:160:THR:OG1	38:BE:163:GLN:NE2	2.41	0.54
41:5C:449:ILE:HD11	47:5I:38:ALA:HA	1.89	0.54
53:RE:375:PHE:HZ	53:RE:487:ILE:HG23	1.73	0.54
57:RJ:1027:THR:HG23	57:RJ:1028:GLU:HG2	1.89	0.54
58:RK:214:LYS:O	58:RK:217:LYS:NZ	2.40	0.54
60:RN:605:ASP:OD1	60:RN:610:ARG:NH1	2.41	0.54
62:RP:1939:ARG:HG3	62:RP:1974:LEU:HD11	1.88	0.54
3:SA:1738:U:OP1	35:B2:279:LYS:NZ	2.40	0.53
8:SI:155:ASP:OD1	8:SI:155:ASP:N	2.41	0.53
9:SJ:184:LEU:HD23	9:SJ:189:LEU:HA	1.90	0.53
20:Sc:67:THR:OG1	20:Sc:70:LYS:O	2.26	0.53
27:A4:271:THR:HG21	37:B8:443:VAL:HG21	1.91	0.53
33:AG:157:PHE:O	33:AG:169:GLN:NE2	2.40	0.53
34:B1:635:MET:HE1	49:5K:8:ARG:HH11	1.73	0.53
35:B2:525:ASP:OD1	35:B2:525:ASP:N	2.41	0.53
47:5I:192:SER:HB2	47:5I:206:VAL:HG22	1.89	0.53
53:RE:227:LYS:HA	53:RE:230:VAL:HG12	1.90	0.53
10:SK:76:LEU:HB2	51:RB:328:PHE:CE1	2.43	0.53
12:SN:105:LYS:HA	64:RS:350:LEU:HD22	1.91	0.53
33:AG:404:SER:OG	33:AG:405:ALA:N	2.40	0.53
55:RH:125:ASN:ND2	55:RH:127:THR:OG1	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:RN:96:LYS:HD2	60:RN:761:PHE:HZ	1.73	0.53
3:SA:396:G:N7	9:SJ:47:ARG:NH1	2.56	0.53
6:SG:73:THR:OG1	6:SG:91:GLU:OE1	2.27	0.53
27:A4:311:THR:HG22	27:A4:313:LYS:H	1.74	0.53
31:AE:651:LEU:HD21	31:AE:680:TYR:HB2	1.90	0.53
32:AF:173:THR:HG21	32:AF:218:VAL:H	1.74	0.53
34:B1:283:GLU:OE2	34:B1:297:GLN:NE2	2.42	0.53
4:SC:32:ILE:HB	4:SC:43:VAL:HG22	1.90	0.53
22:3B:230:TYR:OH	22:3B:256:ASN:OD1	2.25	0.53
29:A8:573:ILE:HG22	29:A8:575:ASN:H	1.72	0.53
31:AE:626:PHE:HB3	31:AE:629:GLU:HB2	1.90	0.53
36:B3:596:ASP:OD1	36:B3:596:ASP:N	2.42	0.53
41:5C:312:VAL:HG21	41:5C:353:PRO:HG2	1.90	0.53
54:RF:107:LEU:HD12	54:RF:194:ARG:HG3	1.89	0.53
25:3F:357:LEU:HD22	51:RB:256:PRO:HB2	1.90	0.53
26:3H:45:ASN:HA	26:3H:74:LYS:HE2	1.90	0.53
33:AG:291:ARG:HD2	33:AG:329:ASN:HD21	1.73	0.53
35:B2:412:GLY:HA2	35:B2:431:GLY:H	1.73	0.53
46:5H:511:GLU:O	46:5H:515:ASN:ND2	2.40	0.53
47:5I:349:GLN:O	47:5I:367:SER:OG	2.24	0.53
53:RE:179:LYS:HB2	53:RE:210:PRO:HG2	1.90	0.53
56:RI:83:TYR:O	56:RI:87:LEU:HB2	2.08	0.53
7:SH:48:TYR:OH	7:SH:119:GLN:O	2.27	0.53
11:SM:82:ARG:HA	11:SM:111:VAL:HG13	1.91	0.53
33:AG:213:LYS:HA	33:AG:223:LYS:HA	1.91	0.53
45:5G:93:SER:O	45:5G:119:ARG:NH2	2.41	0.53
53:RE:687:GLN:NE2	53:RE:694:ALA:O	2.41	0.53
55:RG:36:LYS:NZ	55:RG:169:ASP:O	2.40	0.53
56:RI:83:TYR:OH	56:RI:169:GLU:OE1	2.27	0.53
58:RK:289:VAL:HG21	58:RK:294:LEU:HD13	1.90	0.53
59:RL:37:LEU:HD13	59:RL:123:ILE:HD13	1.90	0.53
3:SA:1108:G:O2'	3:SA:1109:G:N7	2.37	0.53
3:SA:1159:C:N4	45:5G:184:GLU:OE2	2.38	0.53
44:5F:108:ARG:O	44:5F:117:ARG:NH1	2.42	0.53
53:RE:969:ASN:ND2	53:RE:972:ASP:OD1	2.41	0.53
1:3A:256:G:OP1	23:3D:382:LYS:NZ	2.37	0.53
3:SA:513:U:H2'	3:SA:514:G:C8	2.44	0.53
3:SA:1209:C:N3	3:SA:1210:C:N4	2.56	0.53
5:SF:209:HIS:ND1	5:SF:218:PHE:O	2.41	0.53
24:3E:289:GLN:HE21	24:3E:388:LEU:HD13	1.74	0.53
28:A5:46:TRP:HD1	28:A5:48:GLU:HG3	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A8:558:CYS:O	29:A8:585:ARG:NH2	2.42	0.53
33:AG:283:VAL:HG12	33:AG:290:ILE:HG22	1.91	0.53
35:B2:554:THR:OG1	35:B2:556:LYS:NZ	2.39	0.53
55:RG:188:ARG:NH2	55:RH:247:ASP:OD2	2.41	0.53
56:RI:231:GLN:NE2	67:RW:188:THR:O	2.42	0.53
57:RJ:374:ASP:OD1	57:RJ:374:ASP:N	2.40	0.53
64:RS:437:ARG:NH2	64:RS:459:GLU:O	2.42	0.53
3:SA:647:G:H22	3:SA:687:G:H22	1.56	0.53
27:A4:35:ARG:HH11	27:A4:738:TYR:HD1	1.57	0.53
27:A4:420:LEU:HD23	28:A5:581:ASN:HA	1.91	0.53
30:A9:513:ARG:HH21	30:A9:515:ASP:HA	1.72	0.53
50:RA:202:ASN:ND2	50:RA:229:PHE:O	2.41	0.53
53:RE:417:SER:OG	53:RE:418:SER:N	2.42	0.53
55:RG:121:LEU:HD21	55:RG:167:ILE:HG13	1.89	0.53
57:RJ:844:PRO:HA	57:RJ:856:THR:O	2.08	0.53
61:RO:233:ASP:N	61:RO:233:ASP:OD1	2.42	0.53
23:3D:102:ASP:HB3	23:3D:105:LEU:HB3	1.91	0.53
31:AE:40:ALA:HB1	31:AE:123:ARG:HH12	1.73	0.53
34:B1:567:ASP:HB3	44:5F:144:ASN:HD21	1.74	0.53
34:B1:812:GLU:HG3	34:B1:813:HIS:HD2	1.74	0.53
2:5A:135:G:O3'	28:A5:494:ARG:NH1	2.42	0.52
3:SA:1136:U:O2'	35:B2:596:ASN:ND2	2.43	0.52
11:SM:97:TYR:O	11:SM:99:ARG:NH1	2.42	0.52
31:AE:571:LEU:HD11	31:AE:582:VAL:HG11	1.91	0.52
37:B8:216:TYR:OH	38:BE:276:TYR:OH	2.27	0.52
41:5C:483:ILE:HG23	41:5C:516:VAL:HG22	1.90	0.52
50:RA:13:VAL:HG12	50:RA:343:ILE:HG12	1.89	0.52
53:RE:526:CYS:O	53:RE:698:ASN:ND2	2.42	0.52
62:RP:18:SER:OG	62:RP:19:PHE:N	2.42	0.52
3:SA:153:G:H2'	3:SA:154:G:H8	1.74	0.52
23:3D:157:ALA:O	39:B6:293:TYR:OH	2.26	0.52
24:3E:251:ASP:OD1	24:3E:251:ASP:N	2.42	0.52
25:3F:162:CYS:SG	25:3F:525:GLN:NE2	2.78	0.52
32:AF:87:ALA:HA	32:AF:97:CYS:O	2.08	0.52
50:RA:212:ARG:HH22	52:RC:310:ALA:HB3	1.74	0.52
53:RE:398:ALA:O	53:RE:402:ASN:ND2	2.43	0.52
53:RE:596:LYS:HZ2	53:RE:600:TYR:HD1	1.56	0.52
53:RE:1108:LEU:HB2	53:RE:1169:ILE:HD11	1.91	0.52
56:RI:135:LEU:HD22	56:RI:139:LEU:HD13	1.91	0.52
57:RJ:135:ALA:O	57:RJ:238:ARG:NH2	2.42	0.52
57:RJ:982:LYS:HG3	57:RJ:983:PRO:HD3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:RL:131:THR:OG1	59:RL:133:ASN:ND2	2.42	0.52
63:RQ:298:TRP:HE1	63:RQ:899:LYS:CG	2.19	0.52
3:SA:258:C:H4'	9:SJ:75:LYS:HD2	1.91	0.52
31:AE:502:ILE:HG23	31:AE:542:ILE:HG13	1.90	0.52
36:B3:787:PRO:HB2	43:5E:492:PRO:HG3	1.89	0.52
45:5G:153:THR:HG23	45:5G:164:GLN:HG2	1.91	0.52
53:RE:443:HIS:HB3	53:RE:470:LYS:HE2	1.91	0.52
56:RI:233:GLY:O	56:RI:236:LYS:NZ	2.41	0.52
57:RJ:90:VAL:HG23	57:RJ:107:VAL:HG11	1.92	0.52
58:RK:97:GLY:HA2	58:RK:100:VAL:HG12	1.92	0.52
58:RK:180:MET:HE3	58:RK:181:HIS:H	1.75	0.52
60:RN:587:ASP:OD1	60:RN:587:ASP:N	2.42	0.52
2:5A:254:C:H2'	67:RW:183:ARG:HH21	1.74	0.52
3:SA:153:G:N2	7:SH:56:ASN:OD1	2.42	0.52
10:SK:67:PRO:HB2	51:RB:334:LEU:HD23	1.91	0.52
26:3H:54:MET:HE1	26:3H:78:TYR:HB2	1.90	0.52
27:A4:39:VAL:H	27:A4:755:ILE:HD11	1.75	0.52
27:A4:658:ASP:OD2	27:A4:731:HIS:N	2.42	0.52
28:A5:481:LEU:HD22	28:A5:523:LEU:HD22	1.92	0.52
35:B2:398:ASP:HB2	35:B2:406:LEU:HB3	1.92	0.52
38:BE:470:GLN:NE2	38:BE:512:GLY:O	2.42	0.52
53:RE:437:ASP:N	53:RE:437:ASP:OD1	2.42	0.52
5:SF:53:LYS:O	25:3F:120:ARG:NH2	2.42	0.52
9:SJ:191:PHE:O	9:SJ:195:ARG:NH1	2.41	0.52
36:B3:337:HIS:HD2	36:B3:363:ARG:HD3	1.74	0.52
38:BE:268:THR:HG22	38:BE:270:SER:H	1.75	0.52
44:5F:123:THR:HG23	44:5F:126:ASP:H	1.73	0.52
53:RE:270:ILE:HB	53:RE:292:ILE:HG23	1.91	0.52
55:RH:116:THR:HG22	55:RH:118:ARG:H	1.73	0.52
3:SA:494:U:OP1	57:RJ:1138:ARG:NH2	2.32	0.52
3:SA:594:A:OP1	10:SK:38:ASN:ND2	2.43	0.52
22:3B:281:ASP:OD1	22:3B:281:ASP:N	2.41	0.52
23:3D:169:LYS:HA	23:3D:299:VAL:HG22	1.92	0.52
25:3F:284:LEU:O	25:3F:548:ARG:NH2	2.38	0.52
29:A8:566:LEU:HG	29:A8:582:ILE:HD11	1.92	0.52
31:AE:556:LYS:O	31:AE:592:ARG:NH2	2.42	0.52
52:RC:142:ARG:NH1	52:RC:168:GLY:O	2.40	0.52
53:RE:596:LYS:HG3	53:RE:598:LYS:H	1.74	0.52
54:RF:51:ASP:HB2	54:RF:134:ILE:HG21	1.91	0.52
55:RG:169:ASP:N	55:RG:169:ASP:OD1	2.40	0.52
58:RK:30:PRO:HB3	58:RK:77:ARG:HG3	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:RP:452:ASN:O	62:RP:456:GLU:N	2.43	0.52
3:SA:331:A:N3	9:SJ:5:ARG:NH1	2.57	0.52
3:SA:1436:A:H1'	64:RS:419:LYS:HD2	1.91	0.52
7:SH:105:ASP:OD1	7:SH:105:ASP:N	2.43	0.52
9:SJ:110:ARG:NH1	9:SJ:161:SER:O	2.43	0.52
30:A9:504:GLU:OE2	30:A9:507:ARG:NH1	2.43	0.52
33:AG:319:LYS:HD2	33:AG:339:GLY:H	1.74	0.52
38:BE:578:VAL:O	38:BE:579:ARG:NH1	2.42	0.52
38:BE:605:LEU:HD23	38:BE:628:VAL:HG11	1.92	0.52
53:RE:186:ILE:HD11	53:RE:206:LEU:HB2	1.91	0.52
54:RF:44:SER:H	54:RF:50:SER:HA	1.75	0.52
56:RI:155:ARG:O	56:RI:179:GLN:NE2	2.42	0.52
61:RO:258:GLU:HG3	61:RO:289:PHE:HD1	1.74	0.52
62:RP:1892:LEU:HA	62:RP:1895:PHE:HB2	1.92	0.52
64:RS:397:PHE:HD1	64:RS:407:GLU:HG2	1.75	0.52
2:5A:7:A:N7	33:AG:578:ASN:ND2	2.55	0.52
3:SA:862:A:H4'	17:SX:57:ARG:HG3	1.90	0.52
24:3E:426:ALA:HB2	38:BE:305:ASN:HD21	1.75	0.52
29:A8:563:LEU:HA	29:A8:566:LEU:HB2	1.92	0.52
36:B3:680:ASN:N	36:B3:680:ASN:OD1	2.42	0.52
38:BE:819:LYS:NZ	38:BE:823:GLU:OE2	2.40	0.52
45:5G:43:PRO:HG2	45:5G:46:LEU:HB2	1.90	0.52
48:5J:58:ASN:HA	48:5J:61:LYS:HG2	1.92	0.52
50:RA:147:ASN:ND2	50:RA:154:TYR:OH	2.43	0.52
53:RE:315:ILE:HG13	53:RE:329:THR:HG21	1.92	0.52
53:RE:529:VAL:HB	53:RE:613:VAL:HB	1.91	0.52
53:RE:1095:ASP:OD1	53:RE:1095:ASP:N	2.42	0.52
1:3A:198:U:O4	25:3F:151:ARG:NE	2.38	0.52
7:SH:39:GLU:HG3	7:SH:46:LYS:HG3	1.91	0.52
8:SI:163:ASP:HA	8:SI:166:LEU:HG	1.90	0.52
22:3C:297:ARG:HD3	22:3C:322:ARG:HA	1.92	0.52
28:A5:503:LYS:HD3	30:A9:508:ARG:HH22	1.75	0.52
29:A8:672:ASN:HB2	30:A9:486:LEU:HD22	1.92	0.52
32:AF:256:THR:N	32:AF:275:SER:O	2.39	0.52
35:B2:634:SER:OG	35:B2:635:LYS:N	2.41	0.52
38:BE:377:SER:HB2	38:BE:445:MET:HE1	1.92	0.52
57:RJ:72:VAL:HG22	57:RJ:137:LEU:HB3	1.91	0.52
57:RJ:246:ALA:HB3	57:RJ:810:ILE:HB	1.91	0.52
57:RJ:776:GLN:NE2	57:RJ:781:GLU:OE2	2.40	0.52
61:RO:356:ALA:HA	61:RO:499:LEU:HD22	1.91	0.52
62:RP:1880:ILE:HD11	62:RP:1892:LEU:HD21	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:1533:C:OP2	32:AF:114:ARG:NH2	2.43	0.52
3:SA:1720:G:N7	3:SA:1721:A:N6	2.58	0.52
4:SC:164:ILE:HD11	4:SC:205:PHE:HB2	1.91	0.52
24:3E:3:TYR:N	24:3E:21:LYS:O	2.43	0.52
24:3E:359:ILE:HA	24:3E:362:VAL:HG12	1.92	0.52
35:B2:53:ASP:OD2	35:B2:58:ASP:OD1	2.27	0.52
39:B6:296:SER:HB3	39:B6:300:MET:HB2	1.91	0.52
57:RJ:193:ARG:NH2	57:RJ:196:THR:OG1	2.43	0.52
59:RL:589:ALA:HB3	59:RL:593:GLU:H	1.75	0.52
63:RQ:298:TRP:NE1	63:RQ:899:LYS:CG	2.62	0.52
64:RS:360:LEU:HD21	64:RS:393:TYR:HB2	1.92	0.52
66:RV:224:HIS:HD2	66:RV:226:ASP:H	1.57	0.52
3:SA:532:U:O2'	19:SZ:33:ALA:O	2.27	0.51
6:SG:120:ILE:HA	6:SG:123:VAL:HG12	1.92	0.51
24:3E:385:ASP:OD1	24:3E:385:ASP:N	2.42	0.51
35:B2:54:ILE:CD1	35:B2:364:TYR:CD2	2.93	0.51
41:5C:130:ARG:NH2	41:5C:379:GLU:OE2	2.42	0.51
41:5C:495:SER:O	41:5C:495:SER:OG	2.29	0.51
45:5G:53:GLN:HB3	66:RV:215:LEU:HD13	1.92	0.51
47:5I:319:GLU:OE2	47:5I:356:TYR:OH	2.27	0.51
47:5I:324:SER:OG	47:5I:326:ASP:OD1	2.23	0.51
53:RE:634:HIS:HB2	53:RE:655:LEU:HD11	1.91	0.51
54:RF:128:PHE:HD2	54:RF:134:ILE:HG22	1.76	0.51
61:RO:200:ASN:ND2	61:RO:256:ASN:O	2.43	0.51
63:RQ:298:TRP:CD1	63:RQ:899:LYS:HG3	2.44	0.51
2:5A:294:U:OP1	34:B1:631:ASN:ND2	2.43	0.51
3:SA:-5:G:N1	41:5C:39:ASP:OD1	2.36	0.51
3:SA:419:G:H5''	3:SA:419:G:H8	1.75	0.51
7:SH:74:LYS:HB2	50:RA:88:ASN:HD21	1.75	0.51
8:SI:83:LYS:O	8:SI:86:GLN:NE2	2.43	0.51
16:ST:28:ILE:HD13	16:ST:61:LEU:HD11	1.92	0.51
22:3B:277:ASP:N	22:3B:277:ASP:OD1	2.43	0.51
26:3H:44:LEU:HD22	26:3H:52:ILE:HD12	1.90	0.51
27:A4:63:SER:HA	27:A4:82:ARG:HH12	1.75	0.51
31:AE:659:LEU:HD13	31:AE:690:GLU:HB3	1.92	0.51
33:AG:736:THR:HG23	33:AG:738:ASN:H	1.74	0.51
34:B1:506:SER:OG	34:B1:507:GLN:N	2.43	0.51
35:B2:281:ILE:HB	35:B2:332:ILE:HG23	1.91	0.51
35:B2:362:ILE:HG12	35:B2:385:ILE:HB	1.92	0.51
41:5C:410:ASN:O	47:5I:27:ASN:ND2	2.43	0.51
53:RE:469:ASP:OD2	53:RE:472:THR:OG1	2.27	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:RE:1215:ASN:HD21	54:RF:35:HIS:HA	1.75	0.51
54:RF:227:ARG:HA	54:RF:230:ILE:HD12	1.91	0.51
57:RJ:864:ASP:OD1	57:RJ:864:ASP:N	2.44	0.51
16:ST:67:GLU:HA	16:ST:70:VAL:HG12	1.91	0.51
22:3B:120:GLU:OE2	22:3B:142:ARG:NE	2.41	0.51
27:A4:481:ILE:HB	27:A4:485:LYS:HB2	1.91	0.51
29:A8:28:TYR:HA	29:A8:356:THR:HA	1.92	0.51
33:AG:407:ASN:ND2	33:AG:416:SER:OG	2.44	0.51
35:B2:759:GLY:HA3	35:B2:805:ILE:HD11	1.91	0.51
36:B3:679:THR:HG21	36:B3:723:GLU:HB2	1.93	0.51
43:5E:373:ILE:HG13	43:5E:378:PHE:HZ	1.75	0.51
45:5G:139:LEU:HD23	45:5G:266:LEU:HD12	1.92	0.51
51:RB:348:SER:HB2	62:RP:1728:PHE:HB3	1.93	0.51
53:RE:261:ASN:HB3	53:RE:379:MET:HB2	1.91	0.51
54:RF:71:VAL:HA	54:RF:74:LEU:HD12	1.92	0.51
57:RJ:616:ASP:HB2	57:RJ:621:LEU:HG	1.90	0.51
61:RO:214:LYS:O	61:RO:268:GLN:NE2	2.43	0.51
5:SF:201:HIS:H	5:SF:206:ASP:HB3	1.75	0.51
9:SJ:171:SER:HB3	9:SJ:180:ASP:H	1.74	0.51
23:3D:126:ASP:HA	23:3D:129:ARG:HG2	1.93	0.51
25:3F:136:PHE:HE1	25:3F:484:SER:HB2	1.74	0.51
59:RL:117:ASN:O	59:RL:141:THR:OG1	2.26	0.51
62:RP:85:LYS:NZ	62:RP:89:ASN:OD1	2.40	0.51
62:RP:1746:LYS:O	62:RP:1748:ASN:ND2	2.41	0.51
1:3A:319:G:OP1	22:3C:122:ARG:NH2	2.44	0.51
2:5A:426:G:C2	2:5A:428:A:H5''	2.46	0.51
2:5A:473:A:H5''	41:5C:164:GLN:HE22	1.76	0.51
8:SI:67:LEU:HD13	8:SI:94:ALA:HB2	1.93	0.51
23:3D:26:ASP:OD1	47:5I:98:SER:OG	2.29	0.51
24:3E:218:ALA:O	24:3E:236:LYS:NZ	2.41	0.51
27:A4:402:TRP:HB3	27:A4:416:LEU:HA	1.91	0.51
34:B1:329:VAL:HG13	34:B1:338:ILE:HB	1.92	0.51
38:BE:59:GLN:HG2	38:BE:71:VAL:HG22	1.91	0.51
47:5I:329:ILE:HG22	47:5I:351:VAL:HG11	1.93	0.51
53:RE:111:LEU:HA	53:RE:114:VAL:HG12	1.93	0.51
55:RG:105:ASN:HD21	55:RG:110:LEU:HD22	1.75	0.51
58:RK:315:LYS:HB2	58:RK:348:GLU:HB3	1.92	0.51
60:RN:661:ILE:HG22	60:RN:665:GLN:HG3	1.92	0.51
2:5A:176:U:O2'	2:5A:178:G:OP2	2.23	0.51
6:SG:118:LEU:HG	6:SG:129:PRO:HB2	1.92	0.51
9:SJ:100:ALA:O	9:SJ:168:CYS:HA	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:SM:18:HIS:HB2	11:SM:63:LEU:HD21	1.91	0.51
22:3B:91:HIS:HD2	22:3B:93:HIS:H	1.57	0.51
29:A8:712:ASP:OD1	29:A8:712:ASP:N	2.40	0.51
31:AE:558:VAL:HG13	31:AE:615:ASN:HA	1.93	0.51
34:B1:588:ASP:OD1	34:B1:588:ASP:N	2.43	0.51
36:B3:501:PRO:HG3	36:B3:543:GLN:HG3	1.91	0.51
38:BE:854:SER:HB2	38:BE:895:VAL:HG21	1.93	0.51
47:5I:122:ARG:HB2	47:5I:192:SER:HB3	1.93	0.51
47:5I:327:LYS:HG2	47:5I:350:HIS:H	1.76	0.51
50:RA:101:ASN:HD21	50:RA:116:HIS:HB3	1.76	0.51
62:RP:1896:ILE:HG13	62:RP:1897:PRO:HD3	1.92	0.51
64:RS:229:LEU:HD11	64:RS:233:PHE:HD2	1.74	0.51
7:SH:70:PRO:HD3	7:SH:101:ILE:HD12	1.93	0.51
27:A4:420:LEU:HD11	27:A4:462:VAL:HG21	1.92	0.51
33:AG:434:GLN:OE1	33:AG:434:GLN:N	2.43	0.51
34:B1:722:THR:HG22	34:B1:724:HIS:H	1.75	0.51
35:B2:201:ILE:HG13	36:B3:663:VAL:HG11	1.92	0.51
36:B3:497:LEU:HA	36:B3:507:ALA:O	2.11	0.51
64:RS:263:THR:HA	64:RS:266:PHE:HB2	1.93	0.51
3:SA:898:A:N1	3:SA:911:U:O2'	2.41	0.51
9:SJ:67:TRP:NE1	9:SJ:70:GLU:OE1	2.42	0.51
12:SN:48:SER:O	12:SN:52:LEU:HB2	2.10	0.51
16:ST:120:ARG:NH2	43:5E:341:LEU:O	2.44	0.51
22:3C:94:ALA:HB3	22:3C:166:PRO:HG3	1.92	0.51
32:AF:258:LEU:HD22	32:AF:272:LEU:HD21	1.93	0.51
34:B1:273:ARG:NH1	38:BE:763:SER:O	2.43	0.51
34:B1:392:ALA:O	34:B1:404:SER:HA	2.10	0.51
36:B3:414:VAL:HG23	36:B3:427:TYR:HB3	1.92	0.51
41:5C:74:LEU:HD23	41:5C:404:PRO:HG2	1.93	0.51
48:5J:120:ASP:HB2	48:5J:173:ILE:HD12	1.92	0.51
53:RE:298:PHE:HB2	53:RE:340:SER:HA	1.93	0.51
54:RF:178:ASP:OD1	54:RF:178:ASP:N	2.43	0.51
55:RG:150:ILE:HD11	55:RG:160:LEU:HD23	1.92	0.51
56:RI:107:ARG:HB3	56:RI:138:VAL:HG13	1.93	0.51
59:RL:539:ALA:O	59:RL:543:SER:CB	2.59	0.51
2:5A:293:U:H3	34:B1:632:SER:HB3	1.75	0.51
3:SA:283:U:OP1	7:SH:191:ARG:NH1	2.40	0.51
3:SA:340:U:H2'	3:SA:341:A:H8	1.75	0.51
3:SA:647:G:H1	3:SA:687:G:H1	1.59	0.51
3:SA:1643:U:OP2	43:5E:530:ARG:NH1	2.44	0.51
14:SP:12:GLN:HE21	14:SP:78:ALA:HB2	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:3C:171:LEU:HD23	22:3C:240:VAL:HG12	1.92	0.51
29:A8:248:LEU:HA	29:A8:264:SER:HA	1.92	0.51
30:A9:471:LYS:HZ3	30:A9:474:HIS:H	1.59	0.51
31:AE:522:ARG:HH12	31:AE:561:PHE:HB2	1.76	0.51
36:B3:17:ALA:HB3	36:B3:35:PRO:HA	1.91	0.51
44:5F:86:GLY:HA3	44:5F:109:ARG:HD2	1.93	0.51
50:RA:282:ASN:HD21	50:RA:325:GLY:H	1.58	0.51
53:RE:777:ASP:O	53:RE:780:GLN:NE2	2.43	0.51
55:RH:178:VAL:HG12	55:RH:223:GLU:HB2	1.93	0.51
56:RI:84:ARG:NH1	56:RI:100:ILE:O	2.42	0.51
65:RT:107:THR:O	65:RT:111:ASN:ND2	2.44	0.51
1:3A:59:G:H5'	34:B1:570:THR:HG23	1.92	0.51
3:SA:29:U:H2'	3:SA:30:G:H8	1.74	0.51
3:SA:123:G:OP1	5:SF:77:ARG:NH2	2.40	0.51
4:SC:36:SER:HA	4:SC:41:ARG:HD3	1.91	0.51
9:SJ:104:ILE:HD13	9:SJ:167:ALA:HB3	1.91	0.51
13:SO:63:ALA:O	13:SO:67:THR:OG1	2.24	0.51
19:SZ:86:GLU:OE2	19:SZ:90:ARG:NH1	2.43	0.51
24:3E:355:ASN:HB2	24:3E:401:LEU:HD13	1.93	0.51
28:A5:8:SER:OG	28:A5:293:ASN:ND2	2.43	0.51
28:A5:439:VAL:HG11	61:RO:300:THR:HG21	1.92	0.51
29:A8:570:LEU:HD21	29:A8:637:LEU:HD21	1.91	0.51
31:AE:586:LEU:O	31:AE:590:ALA:CB	2.58	0.51
34:B1:732:GLU:HG2	34:B1:734:GLN:HE22	1.76	0.51
38:BE:135:ASN:ND2	38:BE:165:GLY:O	2.42	0.51
46:5H:496:GLN:HA	46:5H:499:GLN:HE21	1.75	0.51
53:RE:1107:GLY:HA3	53:RE:1176:LYS:HG2	1.93	0.51
57:RJ:776:GLN:HA	57:RJ:780:ILE:HG22	1.93	0.51
4:SC:27:LYS:HB3	4:SC:47:LEU:HD22	1.93	0.50
7:SH:21:GLU:OE2	7:SH:25:ARG:NH2	2.44	0.50
12:SN:93:ASP:HB3	12:SN:96:GLN:HG3	1.93	0.50
13:SO:120:SER:HB2	52:RC:255:GLN:HE22	1.75	0.50
22:3B:142:ARG:NH2	22:3B:182:SER:OG	2.44	0.50
33:AG:668:THR:OG1	33:AG:669:ASN:OD1	2.30	0.50
35:B2:562:SER:HB2	35:B2:564:LYS:HB2	1.93	0.50
35:B2:627:SER:OG	35:B2:628:HIS:N	2.45	0.50
41:5C:91:ILE:HG23	47:5I:3:ILE:HD11	1.92	0.50
43:5E:298:SER:OG	43:5E:299:SER:N	2.43	0.50
53:RE:404:GLY:H	53:RE:455:SER:HB3	1.76	0.50
55:RG:150:ILE:HG12	55:RG:160:LEU:HB2	1.93	0.50
59:RL:80:GLU:OE2	59:RL:85:THR:OG1	2.29	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5A:427:A:H2'	2:5A:428:A:H4'	1.93	0.50
3:SA:290:G:H3'	3:SA:291:G:H8	1.76	0.50
3:SA:442:C:O2'	3:SA:525:A:N1	2.35	0.50
28:A5:192:SER:HB3	28:A5:207:GLU:HG3	1.93	0.50
33:AG:855:LEU:HD23	37:B8:477:LYS:HE3	1.93	0.50
36:B3:413:ILE:HG22	36:B3:429:LYS:HA	1.92	0.50
47:5I:54:PHE:O	47:5I:382:ARG:NH2	2.44	0.50
3:SA:304:U:OP1	11:SM:136:ARG:NH2	2.45	0.50
3:SA:340:U:H2'	3:SA:341:A:C8	2.47	0.50
3:SA:420:A:H8	3:SA:420:A:H3'	1.76	0.50
22:3C:223:ASP:OD2	22:3C:225:ARG:NH1	2.44	0.50
32:AF:401:LEU:HB3	32:AF:434:ARG:HH22	1.77	0.50
33:AG:207:LEU:HG	33:AG:264:ILE:HD12	1.93	0.50
38:BE:225:THR:OG1	38:BE:227:THR:O	2.29	0.50
38:BE:370:SER:OG	38:BE:372:ASP:OD1	2.20	0.50
39:B6:297:ASP:OD1	39:B6:297:ASP:N	2.44	0.50
41:5C:238:MET:HE3	41:5C:247:MET:HE2	1.92	0.50
53:RE:261:ASN:OD1	53:RE:588:GLN:NE2	2.42	0.50
55:RH:228:SER:OG	55:RH:229:ASN:N	2.44	0.50
56:RI:173:PRO:HA	56:RI:176:VAL:HG12	1.93	0.50
1:3A:93:U:OP2	24:3E:302:HIS:ND1	2.42	0.50
2:5A:90:G:O2'	2:5A:91:U:O4'	2.25	0.50
3:SA:413:U:H2'	3:SA:414:C:H6	1.77	0.50
32:AF:224:THR:O	32:AF:239:LEU:CB	2.57	0.50
32:AF:378:LYS:NZ	37:B8:292:GLY:O	2.44	0.50
41:5C:434:LEU:HD11	44:5F:12:LEU:HD23	1.93	0.50
57:RJ:634:ARG:HD2	58:RK:185:ARG:HH21	1.77	0.50
57:RJ:772:MET:HE3	57:RJ:773:THR:H	1.76	0.50
58:RK:65:ILE:HB	60:RN:112:VAL:HG12	1.94	0.50
58:RK:183:ILE:HG22	58:RK:351:ILE:HD13	1.94	0.50
62:RP:1873:LEU:HD22	62:RP:1917:ILE:HG13	1.93	0.50
3:SA:1512:G:O6	56:RI:145:HIS:NE2	2.42	0.50
5:SF:26:CYS:SG	5:SF:27:TYR:N	2.84	0.50
14:SP:85:ALA:H	14:SP:119:THR:HB	1.76	0.50
16:ST:49:LYS:HG3	16:ST:72:ILE:HD13	1.94	0.50
22:3B:111:MET:HB2	22:3B:186:ASP:HB3	1.92	0.50
24:3E:430:ASP:HA	38:BE:125:GLY:HA2	1.93	0.50
27:A4:382:VAL:HG11	27:A4:755:ILE:HG21	1.92	0.50
28:A5:355:ASN:OD1	33:AG:479:ASN:ND2	2.44	0.50
32:AF:399:GLU:O	32:AF:403:ASN:ND2	2.42	0.50
33:AG:249:THR:HG22	33:AG:256:THR:HB	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:B8:512:ASP:O	42:5D:248:ARG:NH1	2.42	0.50
55:RH:41:MET:O	55:RH:110:LEU:HA	2.11	0.50
55:RH:41:MET:HG3	55:RH:202:ILE:HG23	1.92	0.50
64:RS:322:LEU:HD21	64:RS:359:LEU:HD11	1.92	0.50
3:SA:420:A:H3'	3:SA:420:A:C8	2.47	0.50
3:SA:1134:C:H1'	35:B2:610:SER:HB2	1.94	0.50
3:SA:1499:G:N2	56:RI:194:ASP:OD2	2.44	0.50
11:SM:109:VAL:HG11	11:SM:139:VAL:HG13	1.94	0.50
22:3C:170:VAL:HG23	22:3C:194:VAL:HG13	1.93	0.50
29:A8:671:ARG:NH1	30:A9:447:ASN:O	2.45	0.50
31:AE:558:VAL:HG22	31:AE:615:ASN:HD22	1.76	0.50
32:AF:59:SER:OG	32:AF:60:SER:N	2.43	0.50
35:B2:102:VAL:HA	35:B2:118:ASN:HA	1.94	0.50
36:B3:182:CYS:SG	36:B3:183:LEU:N	2.84	0.50
38:BE:810:ARG:NH2	65:RT:183:GLU:OE2	2.45	0.50
40:5B:173:ARG:HE	42:5D:146:PHE:HA	1.76	0.50
44:5F:181:ASP:OD1	44:5F:181:ASP:N	2.42	0.50
49:5K:79:LYS:NZ	66:RV:308:ILE:O	2.40	0.50
52:RC:44:LEU:HA	52:RC:79:SER:HA	1.93	0.50
53:RE:177:ASN:ND2	53:RE:213:LEU:O	2.44	0.50
2:5A:20:C:H2'	2:5A:21:A:H8	1.77	0.50
2:5A:505:G:H2'	2:5A:506:G:C8	2.47	0.50
3:SA:1192:C:H1'	55:RG:131:PRO:HA	1.92	0.50
3:SA:1194:A:OP2	3:SA:1195:C:N4	2.40	0.50
22:3B:228:GLN:O	22:3B:231:ARG:NH2	2.43	0.50
33:AG:80:GLN:NE2	33:AG:83:GLU:OE1	2.44	0.50
52:RC:206:LYS:HE3	52:RC:224:LEU:HD21	1.93	0.50
58:RK:114:PHE:O	58:RK:169:VAL:HA	2.12	0.50
62:RP:1769:LEU:HD21	62:RP:1797:LEU:HD22	1.94	0.50
5:SF:181:VAL:HA	5:SF:227:VAL:HA	1.94	0.50
12:SN:33:ARG:HH12	60:RN:272:ILE:HA	1.76	0.50
27:A4:415:LYS:NZ	27:A4:416:LEU:O	2.45	0.50
33:AG:139:GLU:HB3	33:AG:155:THR:HB	1.94	0.50
36:B3:407:SER:OG	36:B3:408:LYS:N	2.45	0.50
36:B3:455:LEU:HA	36:B3:464:LYS:O	2.12	0.50
41:5C:37:THR:O	41:5C:43:ARG:NH2	2.44	0.50
45:5G:192:ASP:OD2	45:5G:227:ARG:NH2	2.37	0.50
55:RG:175:CYS:SG	55:RG:201:SER:OG	2.67	0.50
61:RO:327:MET:O	61:RO:331:ASN:HA	2.11	0.50
64:RS:439:PHE:HA	64:RS:442:GLU:HG3	1.94	0.50
65:RT:216:ILE:O	65:RT:220:THR:OG1	2.29	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:RY:472:ILE:HA	68:RY:475:TYR:HB2	1.93	0.50
2:5A:293:U:H2'	34:B1:631:ASN:HA	1.93	0.50
2:5A:484:G:O6	63:RQ:872:ARG:NH1	2.45	0.50
3:SA:1588:G:H1	3:SA:1608:U:H3	1.60	0.50
8:SI:28:GLU:OE2	8:SI:39:ARG:NH2	2.45	0.50
9:SJ:80:GLY:O	9:SJ:103:GLN:NE2	2.45	0.50
20:Sc:78:SER:HB3	54:RF:212:PHE:HB3	1.94	0.50
27:A4:156:LEU:HD22	27:A4:170:ILE:HD11	1.93	0.50
27:A4:418:CYS:SG	27:A4:419:LYS:N	2.85	0.50
32:AF:48:ASN:ND2	32:AF:111:TYR:OH	2.45	0.50
32:AF:260:TYR:OH	32:AF:262:GLU:OE1	2.30	0.50
33:AG:370:GLN:NE2	33:AG:384:SER:OG	2.44	0.50
33:AG:877:ASP:N	33:AG:877:ASP:OD1	2.43	0.50
38:BE:587:ARG:HB3	38:BE:605:LEU:HD12	1.92	0.50
40:5B:186:ASP:HA	40:5B:189:THR:HG22	1.94	0.50
53:RE:345:TYR:O	53:RE:349:LEU:CB	2.59	0.50
57:RJ:852:ARG:HD2	57:RJ:888:PRO:HG3	1.94	0.50
3:SA:55:A:OP2	59:RL:78:LYS:NZ	2.43	0.49
4:SC:144:ARG:HB3	4:SC:206:PRO:HB2	1.93	0.49
11:SM:109:VAL:HG13	11:SM:138:ASN:HA	1.94	0.49
28:A5:115:ASN:ND2	28:A5:130:ASP:OD1	2.45	0.49
31:AE:306:LEU:HD22	31:AE:311:ASN:HA	1.94	0.49
35:B2:828:TYR:HA	35:B2:831:LYS:HG2	1.93	0.49
37:B8:410:ASP:OD1	37:B8:479:ASN:ND2	2.45	0.49
53:RE:138:ILE:HD11	53:RE:238:HIS:HB3	1.94	0.49
56:RI:38:ILE:HA	56:RI:243:PHE:O	2.12	0.49
57:RJ:106:THR:HG23	57:RJ:355:TYR:HB3	1.94	0.49
57:RJ:138:VAL:HB	57:RJ:167:VAL:HG22	1.93	0.49
57:RJ:274:TYR:OH	57:RJ:306:ASP:OD1	2.29	0.49
62:RP:73:ASP:OD2	62:RP:83:HIS:ND1	2.45	0.49
2:5A:485:G:H4'	2:5A:486:U:H5'	1.94	0.49
3:SA:123:G:H21	5:SF:146:THR:HG21	1.76	0.49
25:3F:365:PRO:HB3	25:3F:397:PHE:HA	1.93	0.49
27:A4:452:HIS:HB3	27:A4:463:THR:HG23	1.94	0.49
27:A4:566:LEU:HD11	27:A4:584:VAL:HG21	1.94	0.49
29:A8:533:PRO:HG2	33:AG:656:ASP:HA	1.94	0.49
33:AG:435:ASP:HB2	33:AG:702:TYR:HD1	1.75	0.49
36:B3:65:THR:HA	36:B3:80:SER:HA	1.94	0.49
37:B8:520:ASN:HB2	37:B8:533:ALA:HB3	1.94	0.49
50:RA:281:ASP:OD1	50:RA:281:ASP:N	2.45	0.49
53:RE:566:ILE:HD13	53:RE:690:VAL:HG21	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:RE:711:PRO:HG3	53:RE:767:GLN:HE21	1.76	0.49
56:RI:211:GLU:O	56:RI:215:ASN:ND2	2.44	0.49
57:RJ:1069:VAL:HG11	57:RJ:1083:ILE:HD13	1.93	0.49
65:RT:182:ILE:HA	65:RT:233:ILE:O	2.13	0.49
3:SA:268:C:H2'	3:SA:269:G:H8	1.76	0.49
34:B1:839:THR:HG22	38:BE:882:GLU:HG3	1.95	0.49
35:B2:90:ASP:N	35:B2:90:ASP:OD1	2.39	0.49
35:B2:476:ILE:HD11	35:B2:490:THR:HB	1.93	0.49
36:B3:22:VAL:O	36:B3:68:LYS:NZ	2.45	0.49
38:BE:118:VAL:HA	38:BE:132:THR:HA	1.94	0.49
41:5C:340:LEU:O	41:5C:368:TYR:N	2.43	0.49
42:5D:149:GLU:HB3	42:5D:153:ASN:HA	1.94	0.49
45:5G:153:THR:HG21	45:5G:266:LEU:HD21	1.93	0.49
50:RA:300:TRP:HB3	50:RA:307:ALA:HA	1.95	0.49
53:RE:606:ASN:ND2	53:RE:610:PHE:O	2.45	0.49
56:RI:98:LYS:NZ	56:RI:121:ASP:OD1	2.38	0.49
57:RJ:1094:TYR:HA	57:RJ:1097:LYS:HG2	1.94	0.49
62:RP:1473:ALA:O	62:RP:1477:LYS:CB	2.61	0.49
31:AE:387:LEU:HD21	31:AE:403:LEU:HD13	1.93	0.49
32:AF:133:HIS:HB2	32:AF:139:ILE:HG13	1.94	0.49
33:AG:584:PHE:HB3	33:AG:598:LYS:HB2	1.94	0.49
41:5C:84:PHE:HA	41:5C:369:MET:HA	1.95	0.49
50:RA:252:SER:HB2	50:RA:266:LYS:HB3	1.94	0.49
57:RJ:777:ARG:O	57:RJ:778:GLN:NE2	2.46	0.49
57:RJ:951:MET:SD	57:RJ:987:TYR:OH	2.63	0.49
58:RK:107:ALA:HB1	58:RK:170:VAL:HG21	1.94	0.49
60:RN:600:LEU:HD21	60:RN:636:LEU:HD13	1.94	0.49
60:RN:623:ASP:O	60:RN:627:HIS:HB3	2.13	0.49
9:SJ:70:GLU:OE2	9:SJ:117:TYR:OH	2.30	0.49
15:SR:58:ASP:OD1	15:SR:58:ASP:N	2.43	0.49
16:ST:111:ASP:OD1	16:ST:115:ARG:NH1	2.46	0.49
24:3E:164:ILE:HG12	24:3E:301:ALA:HA	1.93	0.49
26:3H:52:ILE:HG22	26:3H:54:MET:SD	2.52	0.49
35:B2:180:THR:OG1	35:B2:207:CYS:SG	2.62	0.49
35:B2:624:LEU:HD12	35:B2:629:ASN:HB2	1.93	0.49
36:B3:513:LYS:HG3	36:B3:532:HIS:HB2	1.95	0.49
41:5C:492:GLY:HA2	41:5C:495:SER:HB2	1.94	0.49
47:5I:76:ASN:HA	47:5I:118:VAL:HG21	1.93	0.49
47:5I:140:SER:OG	47:5I:141:ASP:N	2.44	0.49
53:RE:803:LYS:NZ	53:RE:859:ASP:OD2	2.43	0.49
53:RE:972:ASP:OD1	53:RE:972:ASP:N	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:RG:46:ALA:HA	55:RG:115:GLN:HG3	1.93	0.49
58:RK:180:MET:O	58:RK:181:HIS:ND1	2.45	0.49
60:RN:752:MET:HA	60:RN:755:ILE:HG12	1.93	0.49
62:RP:752:THR:O	62:RP:756:SER:CB	2.59	0.49
2:5A:323:A:OP1	34:B1:191:ARG:NH2	2.46	0.49
3:SA:622:A:H1'	3:SA:623:A:C8	2.48	0.49
24:3E:24:LYS:O	24:3E:28:LEU:CB	2.60	0.49
26:3H:7:LYS:HB3	26:3H:65:LEU:HD11	1.95	0.49
26:3H:54:MET:O	26:3H:80:PHE:HA	2.12	0.49
33:AG:96:ILE:HG12	33:AG:108:THR:HG21	1.95	0.49
33:AG:628:ASP:H	33:AG:658:GLU:HA	1.77	0.49
33:AG:736:THR:OG1	33:AG:737:ILE:N	2.45	0.49
34:B1:286:LEU:HD12	34:B1:295:ILE:HB	1.94	0.49
34:B1:406:SER:OG	34:B1:407:LEU:N	2.46	0.49
35:B2:337:LYS:O	35:B2:357:THR:OG1	2.25	0.49
35:B2:549:SER:OG	35:B2:576:VAL:O	2.28	0.49
35:B2:817:LEU:HD11	35:B2:856:ASN:HD21	1.77	0.49
36:B3:466:TRP:HZ3	36:B3:478:GLN:HA	1.77	0.49
39:B6:63:VAL:HG13	39:B6:88:ILE:HD11	1.94	0.49
41:5C:183:GLU:HB3	49:5K:16:THR:HG22	1.94	0.49
44:5F:174:ARG:NH2	57:RJ:1077:LEU:O	2.44	0.49
51:RB:268:ASN:HB3	51:RB:271:ARG:HB3	1.94	0.49
55:RH:38:THR:O	55:RH:40:ARG:NH1	2.45	0.49
55:RH:69:ASN:HD22	55:RH:72:ASP:HB3	1.77	0.49
57:RJ:176:LEU:HD12	57:RJ:183:LEU:HA	1.94	0.49
62:RP:1794:ARG:HH22	62:RP:1870:LYS:HD2	1.77	0.49
3:SA:1465:C:N3	45:5G:146:ARG:NH1	2.58	0.49
4:SC:158:SER:HA	4:SC:161:ILE:HB	1.94	0.49
7:SH:57:ASP:HA	7:SH:107:ALA:H	1.78	0.49
27:A4:338:ALA:HB1	27:A4:361:LEU:HD11	1.95	0.49
29:A8:541:LEU:HA	29:A8:544:LEU:HD13	1.93	0.49
31:AE:637:ILE:HA	31:AE:640:ILE:HG22	1.94	0.49
35:B2:397:ILE:HD11	35:B2:405:LEU:HD21	1.94	0.49
35:B2:862:LYS:HE2	36:B3:805:ILE:HD13	1.93	0.49
36:B3:80:SER:OG	36:B3:81:GLN:N	2.46	0.49
37:B8:43:ASP:N	37:B8:43:ASP:OD1	2.40	0.49
42:5D:111:ARG:HE	42:5D:212:LYS:HB2	1.77	0.49
55:RH:112:VAL:O	55:RH:124:VAL:HB	2.12	0.49
1:3A:64:A:OP2	38:BE:392:ARG:NH2	2.46	0.49
26:3G:105:ASN:HB3	26:3G:108:SER:HB2	1.94	0.49
32:AF:276:SER:OG	32:AF:278:ASP:OD1	2.30	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:AG:31:ASN:HD21	33:AG:201:ILE:HB	1.78	0.49
33:AG:116:VAL:O	33:AG:131:HIS:HA	2.13	0.49
36:B3:343:MET:HE2	36:B3:622:ALA:HB1	1.95	0.49
37:B8:183:ASP:OD1	38:BE:281:ARG:NH2	2.45	0.49
38:BE:528:PHE:HZ	38:BE:570:ILE:HD11	1.78	0.49
47:5I:315:PRO:HG2	47:5I:360:SER:HB3	1.93	0.49
47:5I:421:GLN:HG3	47:5I:425:LYS:HD2	1.95	0.49
49:5K:65:VAL:HG22	49:5K:152:ILE:HB	1.94	0.49
56:RI:125:VAL:O	56:RI:151:PRO:HA	2.12	0.49
56:RI:155:ARG:NH1	56:RI:175:TYR:OH	2.46	0.49
57:RJ:262:GLY:O	57:RJ:264:GLN:NE2	2.44	0.49
60:RN:646:THR:HA	60:RN:649:THR:HG22	1.95	0.49
63:RQ:853:ASN:OD1	63:RQ:853:ASN:N	2.45	0.49
64:RS:388:ASP:HA	64:RS:391:VAL:HG22	1.93	0.49
5:SF:202:ASP:OD1	5:SF:202:ASP:N	2.41	0.49
12:SN:28:LEU:HA	12:SN:31:VAL:HG12	1.94	0.49
22:3B:269:ILE:O	22:3B:315:ILE:HA	2.13	0.49
27:A4:389:ARG:HE	27:A4:404:MET:HB2	1.78	0.49
31:AE:1628:SER:O	31:AE:1632:PHE:CB	2.60	0.49
35:B2:440:PRO:HG3	35:B2:485:GLY:HA3	1.94	0.49
36:B3:198:ILE:HG12	36:B3:211:LEU:HD13	1.95	0.49
37:B8:233:LEU:HD11	37:B8:543:LEU:HD12	1.95	0.49
38:BE:274:ILE:HG23	38:BE:286:VAL:HG22	1.94	0.49
41:5C:507:ASN:HD22	52:RC:57:TRP:HE1	1.60	0.49
51:RB:230:ALA:O	51:RB:234:LYS:CB	2.61	0.49
52:RC:107:SER:O	52:RC:107:SER:OG	2.29	0.49
56:RI:13:ALA:HA	56:RI:254:ILE:HG12	1.95	0.49
57:RJ:309:PRO:HD2	57:RJ:353:LEU:HD22	1.95	0.49
65:RT:96:SER:HA	65:RT:139:LEU:O	2.12	0.49
3:SA:895:G:H1	3:SA:917:U:H3	1.61	0.49
6:SG:219:ARG:NH2	55:RH:222:ASP:OD2	2.45	0.49
11:SM:109:VAL:HG21	11:SM:125:VAL:HG11	1.95	0.49
23:3D:297:HIS:NE2	23:3D:309:GLU:OE2	2.46	0.49
25:3F:305:ARG:HG2	25:3F:317:ILE:HD13	1.94	0.49
34:B1:441:SER:O	34:B1:443:GLU:N	2.43	0.49
38:BE:173:LEU:HD13	38:BE:219:ASP:HA	1.95	0.49
38:BE:469:SER:HB3	38:BE:510:LEU:HD23	1.95	0.49
38:BE:902:ASN:HB3	38:BE:905:ILE:HG22	1.95	0.49
47:5I:145:VAL:HB	47:5I:176:PHE:HB2	1.94	0.49
53:RE:858:ARG:HD2	53:RE:861:ILE:HD11	1.95	0.49
54:RF:23:HIS:HD2	54:RF:26:LEU:HG	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:RG:197:ASP:OD1	55:RG:197:ASP:N	2.45	0.49
3:SA:158:U:H3	3:SA:420:A:HO2'	1.59	0.48
10:SK:82:ARG:NH1	51:RB:323:GLU:OE2	2.46	0.48
24:3E:214:ILE:HD11	24:3E:252:LEU:HD22	1.94	0.48
26:3H:51:PHE:HE1	26:3H:114:ILE:HG23	1.78	0.48
28:A5:280:GLN:HB2	28:A5:288:LYS:HE2	1.95	0.48
29:A8:305:VAL:HA	29:A8:311:VAL:HA	1.95	0.48
32:AF:75:LYS:HD2	32:AF:111:TYR:HA	1.95	0.48
32:AF:428:ARG:HH21	33:AG:518:ASP:HB3	1.76	0.48
35:B2:263:THR:HA	35:B2:269:THR:O	2.13	0.48
36:B3:454:LEU:O	36:B3:465:LYS:HA	2.12	0.48
37:B8:462:GLY:HA2	37:B8:527:GLY:HA3	1.95	0.48
55:RG:190:GLN:HE22	55:RG:247:ASP:HB2	1.78	0.48
60:RN:786:ASN:HA	60:RN:789:ASN:HB2	1.95	0.48
3:SA:129:U:O2'	62:RP:903:THR:O	2.30	0.48
3:SA:1133:A:OP1	58:RK:231:ARG:NE	2.42	0.48
4:SC:129:THR:OG1	4:SC:179:SER:O	2.31	0.48
26:3H:54:MET:HB3	26:3H:64:LEU:HD13	1.93	0.48
28:A5:149:ASN:HD21	28:A5:190:PRO:HB3	1.77	0.48
33:AG:249:THR:O	33:AG:257:ARG:NH1	2.41	0.48
35:B2:291:GLU:HA	35:B2:294:ARG:HG2	1.94	0.48
40:5B:155:ILE:HD12	40:5B:158:LYS:HE3	1.95	0.48
41:5C:112:GLY:HA3	41:5C:130:ARG:HB3	1.94	0.48
41:5C:284:ARG:NH1	41:5C:408:GLU:OE1	2.39	0.48
49:5K:149:LYS:HD3	49:5K:170:ILE:HD11	1.95	0.48
54:RF:56:VAL:HG22	54:RF:123:THR:HG22	1.93	0.48
62:RP:393:PHE:O	62:RP:397:PHE:CB	2.60	0.48
62:RP:1802:HIS:HE1	62:RP:1882:ARG:HB2	1.77	0.48
19:SZ:52:LYS:O	19:SZ:94:TYR:OH	2.23	0.48
23:3D:225:ASP:OD1	23:3D:226:LYS:N	2.46	0.48
25:3F:421:ASN:HD22	25:3F:437:ARG:HA	1.78	0.48
31:AE:8:LEU:HD12	41:5C:144:LEU:HD23	1.96	0.48
31:AE:395:GLU:OE2	31:AE:397:LYS:NZ	2.44	0.48
31:AE:482:SER:HB2	31:AE:484:LEU:HG	1.94	0.48
35:B2:392:THR:HG21	35:B2:410:SER:HB3	1.93	0.48
38:BE:656:ASN:N	38:BE:656:ASN:OD1	2.46	0.48
39:B6:16:ASP:OD2	41:5C:15:ARG:NH2	2.46	0.48
39:B6:273:ILE:HA	39:B6:276:VAL:HG22	1.95	0.48
47:5I:260:GLN:NE2	47:5I:460:GLN:OE1	2.47	0.48
52:RC:59:ASP:OD1	52:RC:62:ARG:NH2	2.46	0.48
53:RE:146:LEU:HA	53:RE:149:VAL:HG12	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:RE:592:PHE:HB3	53:RE:599:VAL:HG22	1.95	0.48
58:RK:103:MET:O	58:RK:107:ALA:HB2	2.13	0.48
11:SM:132:SER:OG	11:SM:133:LYS:N	2.46	0.48
17:SX:70:ASN:N	17:SX:70:ASN:OD1	2.43	0.48
20:Sc:58:SER:OG	20:Sc:59:CYS:N	2.46	0.48
22:3C:170:VAL:HG12	22:3C:239:CYS:HB3	1.96	0.48
29:A8:561:LEU:HD13	29:A8:566:LEU:HD11	1.95	0.48
33:AG:771:ASP:OD1	33:AG:771:ASP:N	2.46	0.48
36:B3:536:LEU:HA	36:B3:552:SER:HA	1.96	0.48
36:B3:600:LYS:HA	36:B3:609:CYS:HA	1.95	0.48
49:5K:67:ILE:HD11	49:5K:96:PRO:HB2	1.95	0.48
53:RE:264:LEU:HD12	53:RE:265:LEU:HG	1.94	0.48
57:RJ:863:THR:O	57:RJ:863:THR:OG1	2.30	0.48
57:RJ:951:MET:HE1	57:RJ:1003:LEU:HB2	1.94	0.48
58:RK:130:ILE:HG23	58:RK:151:LEU:HD23	1.95	0.48
59:RM:716:PRO:O	59:RM:720:LEU:CB	2.61	0.48
61:RO:447:ASP:OD1	61:RO:447:ASP:N	2.46	0.48
3:SA:163:G:O2'	7:SH:53:SER:OG	2.30	0.48
3:SA:886:U:H2'	3:SA:887:A:H8	1.78	0.48
13:SO:131:THR:HG22	52:RC:264:ILE:HG21	1.94	0.48
26:3H:13:ASP:OD1	26:3H:13:ASP:N	2.42	0.48
27:A4:150:ASN:ND2	27:A4:198:ASP:OD1	2.37	0.48
34:B1:717:LEU:HD12	38:BE:578:VAL:HB	1.94	0.48
35:B2:643:ASP:HB3	35:B2:650:ILE:HD11	1.95	0.48
36:B3:44:ASP:OD1	36:B3:44:ASP:N	2.46	0.48
37:B8:148:THR:OG1	37:B8:152:GLU:OE2	2.31	0.48
37:B8:266:GLY:HA3	37:B8:295:ILE:HD11	1.95	0.48
37:B8:458:ILE:HG13	37:B8:484:VAL:HG22	1.95	0.48
38:BE:529:TYR:HA	38:BE:536:LEU:HA	1.95	0.48
38:BE:630:THR:N	38:BE:644:THR:O	2.44	0.48
52:RC:53:LEU:O	52:RC:57:TRP:HB2	2.13	0.48
53:RE:132:TYR:HA	53:RE:135:LEU:HG	1.95	0.48
57:RJ:634:ARG:NH2	58:RK:186:PRO:O	2.42	0.48
3:SA:364:G:N7	3:SA:366:A:N6	2.62	0.48
5:SF:223:ASN:OD1	5:SF:223:ASN:N	2.47	0.48
9:SJ:72:ILE:HG22	9:SJ:74:LYS:HG2	1.96	0.48
27:A4:424:ASP:N	27:A4:424:ASP:OD1	2.45	0.48
29:A8:496:TYR:OH	33:AG:693:ASP:OD1	2.28	0.48
39:B6:426:ASP:O	39:B6:430:TYR:N	2.47	0.48
43:5E:452:SER:O	43:5E:452:SER:OG	2.29	0.48
53:RE:886:THR:HG23	53:RE:890:LEU:HD12	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:RF:97:GLU:OE2	54:RF:121:ARG:NH1	2.45	0.48
3:SA:647:G:H22	3:SA:687:G:H1	1.60	0.48
11:SM:90:TYR:H	11:SM:103:ARG:HB3	1.79	0.48
19:SZ:20:ARG:NH1	19:SZ:22:GLN:OE1	2.47	0.48
24:3E:225:GLU:HG2	24:3E:226:ILE:HG13	1.96	0.48
25:3F:448:PHE:HA	25:3F:451:ILE:HG22	1.95	0.48
27:A4:579:ARG:NH2	27:A4:644:SER:OG	2.47	0.48
32:AF:420:GLU:O	32:AF:424:ARG:CB	2.61	0.48
33:AG:105:HIS:HB2	33:AG:122:LYS:HG3	1.95	0.48
36:B3:167:ASP:OD1	36:B3:168:THR:N	2.47	0.48
51:RB:237:SER:O	51:RB:237:SER:OG	2.32	0.48
53:RE:373:ARG:HA	53:RE:515:ILE:HG12	1.96	0.48
57:RJ:298:VAL:HG23	57:RJ:791:ILE:HG23	1.94	0.48
59:RM:507:THR:H	68:RY:495:ALA:HB3	1.77	0.48
60:RN:734:ARG:HA	60:RN:737:ILE:HG12	1.95	0.48
61:RO:507:LEU:HA	61:RO:510:GLU:HB3	1.95	0.48
3:SA:895:G:H21	14:SP:38:THR:HG21	1.79	0.48
15:SR:120:ASP:OD1	15:SR:120:ASP:N	2.40	0.48
25:3F:477:SER:OG	25:3F:521:VAL:O	2.27	0.48
31:AE:684:TYR:HB2	31:AE:687:LEU:HD23	1.95	0.48
36:B3:161:TRP:HB3	36:B3:177:LEU:HG	1.96	0.48
37:B8:183:ASP:HB2	38:BE:242:ARG:HA	1.96	0.48
41:5C:538:ILE:HD12	41:5C:542:HIS:HE1	1.79	0.48
50:RA:313:PRO:HG3	50:RA:317:ILE:HD11	1.94	0.48
52:RC:159:LEU:O	52:RC:207:ARG:NH2	2.46	0.48
53:RE:1108:LEU:O	53:RE:1112:CYS:CB	2.60	0.48
61:RO:153:ILE:HD13	61:RO:202:LEU:HD21	1.94	0.48
62:RP:48:LEU:HG	62:RP:74:VAL:HG22	1.95	0.48
1:3A:332:G:H21	33:AG:869:MET:HE3	1.79	0.48
3:SA:153:G:N2	3:SA:161:U:O2	2.43	0.48
3:SA:464:A:H2'	3:SA:465:G:H8	1.78	0.48
7:SH:31:ARG:HE	50:RA:359:ILE:HD13	1.78	0.48
10:SK:136:VAL:HG12	10:SK:156:ILE:HG12	1.96	0.48
27:A4:560:SER:OG	27:A4:561:LYS:N	2.47	0.48
31:AE:336:LEU:HD22	31:AE:373:ILE:HG21	1.96	0.48
31:AE:484:LEU:HD13	31:AE:663:SER:HB3	1.95	0.48
32:AF:435:ASP:OD1	32:AF:435:ASP:N	2.45	0.48
35:B2:479:LEU:HA	35:B2:489:VAL:O	2.14	0.48
36:B3:271:ASP:OD1	36:B3:271:ASP:N	2.47	0.48
36:B3:301:GLN:HG2	36:B3:315:ASN:HA	1.95	0.48
41:5C:137:MET:HA	41:5C:144:LEU:HA	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:RF:66:HIS:HA	54:RF:69:LYS:HG3	1.94	0.48
59:RL:55:VAL:HG23	59:RL:121:MET:HB3	1.95	0.48
59:RL:388:GLU:HA	59:RL:410:SER:O	2.14	0.48
60:RN:560:TYR:OH	61:RO:388:LEU:O	2.30	0.48
62:RP:190:ARG:NH1	62:RP:194:GLU:OE2	2.46	0.48
3:SA:1041:G:H2'	3:SA:1042:G:C8	2.49	0.48
3:SA:1082:C:H5''	17:SX:20:THR:HA	1.96	0.48
23:3D:160:ARG:NH2	24:3E:243:MET:O	2.43	0.48
24:3E:207:ARG:HH11	24:3E:226:ILE:HG12	1.78	0.48
25:3F:523:LYS:O	25:3F:541:ALA:HA	2.13	0.48
33:AG:141:LEU:HD11	33:AG:153:ILE:HD11	1.96	0.48
50:RA:164:ARG:NH2	50:RA:174:ASN:OD1	2.46	0.48
53:RE:209:MET:HB2	53:RE:299:PRO:HD3	1.96	0.48
54:RF:9:MET:HB2	54:RF:13:PHE:HB2	1.96	0.48
54:RF:176:ASP:OD1	54:RF:176:ASP:N	2.37	0.48
55:RG:173:THR:OG1	55:RG:174:LYS:N	2.47	0.48
62:RP:1709:ASP:HA	62:RP:1758:ALA:HA	1.94	0.48
63:RQ:322:ASN:OD1	63:RQ:322:ASN:N	2.46	0.48
2:5A:201:U:H2'	2:5A:202:U:H6	1.78	0.47
3:SA:124:A:O2'	5:SF:148:ARG:NH2	2.33	0.47
3:SA:336:G:H1	9:SJ:5:ARG:HB2	1.79	0.47
3:SA:351:C:N3	11:SM:102:LYS:NZ	2.52	0.47
3:SA:1511:U:H2'	3:SA:1512:G:C8	2.49	0.47
11:SM:124:THR:HG22	11:SM:141:LYS:HB3	1.96	0.47
17:SX:9:ASP:OD1	17:SX:9:ASP:N	2.45	0.47
27:A4:284:LEU:HD21	40:5B:206:LEU:HD21	1.95	0.47
27:A4:747:ILE:HD11	27:A4:753:ALA:HB2	1.96	0.47
28:A5:335:ASN:O	28:A5:337:LYS:NZ	2.47	0.47
31:AE:329:THR:HG21	31:AE:365:ILE:HG21	1.95	0.47
33:AG:440:VAL:HG11	33:AG:449:LEU:HD12	1.95	0.47
34:B1:205:LYS:HG2	34:B1:219:GLU:HG2	1.96	0.47
35:B2:118:ASN:OD1	35:B2:118:ASN:N	2.46	0.47
35:B2:404:LYS:HZ1	35:B2:425:ILE:HD11	1.78	0.47
36:B3:77:THR:HG22	36:B3:86:LYS:HB3	1.96	0.47
55:RG:232:LEU:HD21	55:RH:103:PRO:HG3	1.96	0.47
57:RJ:1105:ASP:N	57:RJ:1105:ASP:OD1	2.47	0.47
58:RK:282:GLU:O	58:RK:286:SER:HB3	2.14	0.47
59:RL:57:TRP:NE1	59:RL:125:GLN:OE1	2.39	0.47
62:RP:1778:MET:HG2	62:RP:1864:LEU:HD22	1.96	0.47
2:5A:517:A:OP2	62:RP:1939:ARG:NH1	2.46	0.47
3:SA:954:G:H2'	3:SA:955:A:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:SP:16:VAL:O	14:SP:30:VAL:HA	2.14	0.47
27:A4:97:ARG:NE	40:5B:191:PRO:O	2.39	0.47
28:A5:460:ARG:HA	28:A5:465:ILE:HD11	1.96	0.47
31:AE:376:GLU:H	31:AE:379:GLU:HG3	1.79	0.47
32:AF:246:TYR:OH	32:AF:289:ASN:ND2	2.44	0.47
35:B2:54:ILE:CD1	35:B2:364:TYR:HD2	2.27	0.47
50:RA:250:GLY:HA3	50:RA:271:GLY:HA2	1.96	0.47
50:RA:273:ASP:O	50:RA:275:LYS:NZ	2.47	0.47
2:5A:116:U:H3	2:5A:130:G:H1	1.61	0.47
5:SF:143:ASP:OD1	5:SF:143:ASP:N	2.35	0.47
11:SM:112:SER:HB3	11:SM:139:VAL:HG23	1.95	0.47
27:A4:214:SER:OG	27:A4:221:ASN:O	2.28	0.47
28:A5:473:LYS:HE3	28:A5:475:ALA:HB3	1.96	0.47
32:AF:135:GLN:HE22	32:AF:178:PRO:HA	1.79	0.47
35:B2:137:ILE:HG22	35:B2:147:VAL:HG22	1.97	0.47
35:B2:530:LEU:HD13	35:B2:550:LEU:HD11	1.94	0.47
41:5C:333:SER:HB3	41:5C:381:LEU:HD11	1.95	0.47
44:5F:152:ARG:NH1	45:5G:11:GLU:OE2	2.46	0.47
53:RE:400:LEU:HB3	53:RE:412:LEU:HD12	1.95	0.47
53:RE:627:LEU:HD12	53:RE:628:VAL:HG23	1.96	0.47
53:RE:1025:THR:O	53:RE:1029:ASN:ND2	2.47	0.47
56:RI:105:ASN:HA	56:RI:108:ARG:HB3	1.96	0.47
57:RJ:92:ARG:HH21	57:RJ:221:LEU:HG	1.79	0.47
57:RJ:111:LYS:O	57:RJ:310:THR:OG1	2.32	0.47
3:SA:280:U:H2'	7:SH:188:ARG:HH22	1.80	0.47
3:SA:1061:A:OP1	54:RF:229:LYS:NZ	2.46	0.47
6:SG:52:GLU:OE2	6:SG:54:LYS:NZ	2.48	0.47
10:SK:87:SER:OG	10:SK:89:ASP:OD1	2.33	0.47
33:AG:581:GLY:HA2	33:AG:602:PRO:HD2	1.97	0.47
35:B2:214:ASP:OD1	35:B2:214:ASP:N	2.45	0.47
41:5C:133:HIS:HE1	41:5C:147:GLU:HG3	1.79	0.47
49:5K:152:ILE:HG12	49:5K:171:PRO:HG2	1.95	0.47
59:RL:200:VAL:HG12	59:RL:208:LEU:HD13	1.97	0.47
4:SC:16:GLN:HB2	36:B3:358:ASN:HD22	1.80	0.47
5:SF:103:TYR:O	5:SF:182:TYR:OH	2.32	0.47
8:SI:64:VAL:HG23	8:SI:67:LEU:HB3	1.96	0.47
31:AE:141:ASN:ND2	31:AE:206:TYR:OH	2.46	0.47
33:AG:498:LEU:HA	33:AG:508:ILE:O	2.14	0.47
33:AG:855:LEU:O	33:AG:859:ASN:HB2	2.13	0.47
35:B2:9:GLU:O	35:B2:684:TRP:HA	2.14	0.47
35:B2:414:LEU:HD11	35:B2:445:VAL:HG11	1.94	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:B3:223:TRP:CD1	36:B3:230:LYS:HZ1	2.33	0.47
51:RB:290:GLU:OE2	51:RB:296:ARG:NH1	2.47	0.47
52:RC:189:ASP:HB3	52:RC:194:ILE:HD11	1.96	0.47
53:RE:1188:PRO:HA	53:RE:1191:LYS:HE2	1.96	0.47
54:RF:17:PRO:HB2	54:RF:34:LEU:HD11	1.96	0.47
57:RJ:631:ILE:HG13	57:RJ:634:ARG:HB2	1.97	0.47
61:RO:198:GLU:O	61:RO:202:LEU:HB2	2.13	0.47
62:RP:1278:ARG:O	62:RP:1282:VAL:HA	2.15	0.47
63:RQ:835:VAL:HG13	63:RQ:837:LYS:HG3	1.96	0.47
3:SA:869:A:H61	3:SA:958:U:H3	1.62	0.47
3:SA:1179:G:H3'	16:ST:127:HIS:HB2	1.96	0.47
24:3E:355:ASN:HA	24:3E:358:LYS:HB2	1.97	0.47
27:A4:157:SER:OG	27:A4:195:TRP:NE1	2.47	0.47
27:A4:744:VAL:HA	27:A4:753:ALA:O	2.15	0.47
34:B1:150:THR:N	34:B1:164:THR:O	2.45	0.47
55:RH:153:VAL:HA	60:RN:716:LYS:HB2	1.96	0.47
64:RS:258:VAL:HA	64:RS:261:GLU:HG2	1.97	0.47
66:RV:271:GLN:HA	66:RV:290:SER:HB3	1.96	0.47
3:SA:406:U:H2'	3:SA:407:A:C8	2.50	0.47
3:SA:576:G:OP2	57:RJ:873:LYS:NZ	2.36	0.47
7:SH:32:ILE:HD12	7:SH:65:GLN:HA	1.96	0.47
14:SP:53:ASP:O	14:SP:56:SER:OG	2.28	0.47
22:3C:173:LEU:HA	22:3C:197:VAL:HG13	1.97	0.47
24:3E:262:ILE:HA	24:3E:265:PHE:HB2	1.96	0.47
27:A4:534:LEU:HB3	27:A4:543:ILE:HG22	1.95	0.47
33:AG:175:ALA:O	33:AG:187:VAL:HA	2.15	0.47
34:B1:156:GLN:HB2	34:B1:203:GLN:HE21	1.79	0.47
34:B1:165:SER:OG	34:B1:166:LYS:N	2.48	0.47
34:B1:537:GLY:HA3	34:B1:556:ARG:HB3	1.96	0.47
35:B2:183:ASP:OD1	35:B2:183:ASP:N	2.42	0.47
36:B3:10:ILE:HG23	36:B3:643:PHE:HB2	1.95	0.47
36:B3:108:LEU:HG	36:B3:119:VAL:HG12	1.97	0.47
37:B8:238:LEU:HD11	37:B8:590:LYS:HB2	1.97	0.47
38:BE:207:ASP:N	38:BE:207:ASP:OD1	2.47	0.47
46:5H:434:PHE:H	55:RH:129:ARG:HH22	1.63	0.47
50:RA:80:GLN:HB2	50:RA:82:HIS:HD2	1.78	0.47
53:RE:159:SER:O	53:RE:256:TYR:OH	2.27	0.47
53:RE:253:GLN:NE2	53:RE:254:LEU:O	2.48	0.47
53:RE:348:TYR:HA	53:RE:351:LYS:HD3	1.97	0.47
54:RF:69:LYS:NZ	54:RF:159:THR:H	2.12	0.47
57:RJ:879:THR:OG1	57:RJ:880:TYR:N	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:RQ:341:LYS:HA	63:RQ:344:GLN:HE21	1.79	0.47
2:5A:207:G:H2'	2:5A:208:A:H8	1.80	0.47
15:SR:50:GLU:OE2	15:SR:82:ARG:NH2	2.47	0.47
19:SZ:59:GLY:O	51:RB:296:ARG:NH2	2.44	0.47
24:3E:176:GLU:HA	24:3E:179:THR:HG22	1.97	0.47
24:3E:191:HIS:HD2	24:3E:246:GLU:HA	1.80	0.47
33:AG:22:LEU:HD12	33:AG:32:LYS:HB2	1.97	0.47
35:B2:235:ASN:ND2	35:B2:240:GLY:O	2.40	0.47
35:B2:367:ILE:HD12	35:B2:368:PRO:HD2	1.97	0.47
36:B3:19:SER:OG	36:B3:20:SER:N	2.48	0.47
36:B3:113:THR:OG1	36:B3:114:SER:N	2.48	0.47
36:B3:339:ILE:HG13	36:B3:358:ASN:HD21	1.80	0.47
36:B3:481:LYS:HE2	36:B3:522:ASN:HA	1.97	0.47
37:B8:568:VAL:HG23	37:B8:579:VAL:HG22	1.96	0.47
39:B6:14:GLU:OE2	39:B6:91:ARG:NH2	2.38	0.47
39:B6:122:ASN:OD1	39:B6:122:ASN:N	2.48	0.47
57:RJ:80:THR:O	71:RJ:1201:GTP:O2B	2.31	0.47
2:5A:69:U:O4	2:5A:70:A:N6	2.48	0.47
2:5A:414:G:N1	2:5A:442:U:O2	2.48	0.47
3:SA:158:U:N3	3:SA:420:A:O2'	2.46	0.47
3:SA:677:G:O2'	62:RP:1884:ARG:NH2	2.48	0.47
3:SA:1760:G:H5'	3:SA:1761:U:H5'	1.96	0.47
14:SP:123:SER:O	14:SP:123:SER:OG	2.29	0.47
25:3F:70:TYR:OH	51:RB:246:GLU:OE2	2.29	0.47
26:3G:57:ASP:HB3	26:3G:84:ARG:HG2	1.97	0.47
28:A5:366:GLY:O	33:AG:583:LYS:NZ	2.48	0.47
31:AE:136:LEU:HD21	31:AE:155:ILE:HG12	1.97	0.47
35:B2:393:ASP:OD1	35:B2:393:ASP:N	2.46	0.47
36:B3:139:SER:OG	36:B3:140:PHE:N	2.48	0.47
36:B3:245:SER:O	36:B3:245:SER:OG	2.32	0.47
44:5F:153:ASN:HB3	45:5G:4:ARG:HH22	1.80	0.47
47:5I:201:ILE:HD12	47:5I:225:LEU:HD21	1.97	0.47
52:RC:158:LEU:HD22	66:RV:195:ILE:HD13	1.96	0.47
53:RE:578:ILE:HA	53:RE:619:VAL:HA	1.96	0.47
54:RF:46:ASN:OD1	54:RF:46:ASN:N	2.39	0.47
57:RJ:347:LEU:O	57:RJ:352:LYS:NZ	2.48	0.47
60:RN:510:THR:HB	60:RN:518:ILE:HD13	1.96	0.47
2:5A:18:G:H2'	2:5A:19:A:C8	2.50	0.47
2:5A:485:G:H2'	23:3D:22:LEU:HD21	1.97	0.47
27:A4:511:VAL:HA	27:A4:558:ARG:HB3	1.96	0.47
29:A8:647:LEU:HG	30:A9:509:GLN:HE22	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:AG:443:ASN:ND2	33:AG:446:ASN:OD1	2.48	0.47
34:B1:115:SER:O	34:B1:115:SER:OG	2.33	0.47
35:B2:542:ASP:N	35:B2:542:ASP:OD1	2.45	0.47
35:B2:588:ILE:HG12	35:B2:600:TRP:HB2	1.97	0.47
36:B3:593:CYS:HB2	36:B3:620:LEU:HB3	1.95	0.47
36:B3:622:ALA:HB3	36:B3:636:ASP:H	1.78	0.47
38:BE:170:LEU:HG	38:BE:180:LEU:HD21	1.97	0.47
38:BE:430:ILE:HD11	38:BE:445:MET:HB2	1.97	0.47
64:RS:271:THR:OG1	64:RS:274:GLU:OE1	2.31	0.47
4:SC:19:ARG:HH21	36:B3:359:SER:HA	1.80	0.46
35:B2:360:ASN:OD1	35:B2:360:ASN:N	2.47	0.46
36:B3:352:LYS:HA	36:B3:365:ILE:O	2.15	0.46
36:B3:680:ASN:HA	36:B3:683:LEU:HG	1.96	0.46
36:B3:749:ASN:HB3	36:B3:751:LYS:H	1.81	0.46
43:5E:383:ARG:NH2	45:5G:212:ALA:O	2.48	0.46
60:RN:451:THR:O	60:RN:455:LEU:HB2	2.15	0.46
62:RP:1721:ILE:HD11	62:RP:1751:TYR:HB2	1.96	0.46
2:5A:446:U:H5'	57:RJ:1118:THR:HB	1.96	0.46
3:SA:545:A:OP2	46:5H:542:TYR:OH	2.33	0.46
3:SA:1160:A:H2'	3:SA:1161:C:H6	1.80	0.46
3:SA:1228:G:H22	12:SN:119:SER:HB2	1.79	0.46
5:SF:52:LEU:O	25:3F:120:ARG:NH1	2.48	0.46
5:SF:53:LYS:NZ	51:RB:292:ASP:OD2	2.38	0.46
31:AE:262:VAL:HG21	33:AG:892:MET:HE1	1.96	0.46
35:B2:676:SER:OG	35:B2:678:ASP:OD1	2.22	0.46
36:B3:476:ASP:N	36:B3:476:ASP:OD1	2.48	0.46
39:B6:185:TYR:HE2	63:RQ:338:LEU:HD21	1.81	0.46
40:5B:173:ARG:NH2	42:5D:144:ASN:O	2.48	0.46
42:5D:25:TYR:HD1	48:5J:213:ARG:HE	1.62	0.46
45:5G:173:ARG:HH21	45:5G:250:VAL:HG23	1.80	0.46
50:RA:245:CYS:HB3	50:RA:253:TYR:HB2	1.96	0.46
50:RA:251:TYR:HA	50:RA:266:LYS:O	2.16	0.46
51:RB:309:LYS:HB3	51:RB:313:ARG:HH11	1.80	0.46
53:RE:793:PRO:HG2	53:RE:799:LEU:HA	1.96	0.46
56:RI:59:LEU:HD22	56:RI:215:ASN:HB2	1.97	0.46
59:RL:729:LEU:HA	59:RL:764:ASN:HA	1.97	0.46
62:RP:1725:ILE:HD11	62:RP:1793:LEU:HD22	1.98	0.46
2:5A:128:C:H5''	2:5A:129:U:H4'	1.98	0.46
22:3C:194:VAL:HB	22:3C:217:ILE:HD13	1.97	0.46
27:A4:418:CYS:HB2	27:A4:460:LEU:HB2	1.97	0.46
27:A4:742:LEU:HD12	27:A4:757:ARG:HG3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:AE:509:SER:HA	31:AE:512:LEU:HD12	1.98	0.46
33:AG:204:ASN:OD1	33:AG:204:ASN:N	2.47	0.46
33:AG:530:LYS:HG2	33:AG:546:LYS:HB3	1.97	0.46
35:B2:236:ASP:OD1	35:B2:236:ASP:N	2.46	0.46
36:B3:69:LEU:HD13	36:B3:109:ASP:HA	1.96	0.46
50:RA:286:GLU:HG3	50:RA:287:ASN:H	1.80	0.46
53:RE:209:MET:HB3	53:RE:213:LEU:HD21	1.98	0.46
54:RF:69:LYS:HZ1	54:RF:158:TRP:HA	1.79	0.46
57:RJ:187:LYS:HE3	57:RJ:187:LYS:HB2	1.75	0.46
58:RK:337:VAL:HG23	58:RK:354:ILE:HG12	1.98	0.46
60:RN:56:ASN:HD21	60:RN:59:GLU:HG3	1.81	0.46
61:RO:202:LEU:HD23	61:RO:208:TYR:HB3	1.98	0.46
62:RP:1756:ILE:HD13	62:RP:1800:LEU:HB3	1.98	0.46
2:5A:188:A:H61	2:5A:209:G:H1	1.63	0.46
2:5A:485:G:OP2	23:3D:46:LYS:NZ	2.39	0.46
14:SP:32:ASP:OD1	14:SP:32:ASP:N	2.47	0.46
19:SZ:45:ALA:HB2	19:SZ:55:VAL:HG11	1.97	0.46
25:3F:417:SER:HB3	25:3F:421:ASN:HB2	1.96	0.46
28:A5:518:ASN:O	28:A5:522:THR:OG1	2.32	0.46
29:A8:374:SER:HA	29:A8:408:LEU:HA	1.96	0.46
30:A9:505:MET:HB2	32:AF:507:MET:HE3	1.98	0.46
31:AE:374:ARG:NH1	31:AE:375:LEU:O	2.49	0.46
34:B1:32:PRO:HG3	34:B1:61:ILE:HG13	1.97	0.46
36:B3:189:HIS:HD2	36:B3:191:SER:H	1.62	0.46
37:B8:306:ASN:OD1	37:B8:306:ASN:N	2.43	0.46
53:RE:218:ASP:N	53:RE:218:ASP:OD1	2.46	0.46
55:RH:152:SER:OG	55:RH:155:SER:N	2.49	0.46
56:RI:55:ARG:HD2	56:RI:191:PRO:HD3	1.98	0.46
57:RJ:819:GLU:O	57:RJ:852:ARG:NH2	2.47	0.46
58:RK:282:GLU:O	58:RK:286:SER:CB	2.64	0.46
61:RO:196:GLN:OE1	61:RO:260:ASN:ND2	2.37	0.46
2:5A:396:A:H62	45:5G:11:GLU:HG2	1.81	0.46
3:SA:1276:U:H3	3:SA:1434:U:H3	1.64	0.46
8:SI:62:VAL:HG12	8:SI:64:VAL:H	1.80	0.46
13:SO:16:ILE:HG23	13:SO:62:GLN:HE22	1.79	0.46
22:3C:308:PRO:HG3	42:5D:129:SER:HA	1.96	0.46
27:A4:326:ARG:NH2	27:A4:364:PHE:O	2.49	0.46
28:A5:85:ILE:HB	28:A5:99:PHE:HB2	1.98	0.46
33:AG:212:CYS:HB2	33:AG:224:SER:HB3	1.98	0.46
33:AG:446:ASN:OD1	33:AG:446:ASN:N	2.46	0.46
34:B1:29:LEU:HD22	34:B1:42:LEU:HD11	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B1:557:LYS:NZ	38:BE:426:GLU:OE1	2.44	0.46
36:B3:67:LEU:HD23	36:B3:68:LYS:H	1.80	0.46
36:B3:534:ARG:HH11	36:B3:535:GLY:H	1.63	0.46
36:B3:708:ARG:NH2	36:B3:720:PHE:O	2.49	0.46
37:B8:278:ASP:N	37:B8:278:ASP:OD1	2.46	0.46
40:5B:211:LEU:HD13	40:5B:213:LYS:HE3	1.96	0.46
53:RE:333:ASN:HA	53:RE:336:VAL:HG22	1.96	0.46
55:RG:112:VAL:HB	55:RG:124:VAL:HG22	1.97	0.46
57:RJ:360:ASP:HB3	57:RJ:365:LEU:HB2	1.98	0.46
61:RO:462:SER:OG	61:RO:463:LEU:N	2.48	0.46
64:RS:270:LEU:HB3	64:RS:278:PHE:HZ	1.80	0.46
3:SA:328:A:H2'	3:SA:329:G:C8	2.50	0.46
12:SN:25:GLU:OE2	12:SN:29:LYS:NZ	2.43	0.46
15:SR:113:ASP:N	15:SR:113:ASP:OD1	2.48	0.46
18:SY:113:ALA:HB3	18:SY:116:ASP:HB2	1.96	0.46
31:AE:568:ILE:HD11	31:AE:673:ASN:HD21	1.80	0.46
36:B3:591:ILE:HG23	36:B3:600:LYS:HZ1	1.81	0.46
37:B8:472:GLN:NE2	37:B8:474:SER:OG	2.49	0.46
47:5I:288:TYR:O	47:5I:298:LEU:N	2.42	0.46
53:RE:822:ARG:HB2	53:RE:843:LEU:HB2	1.96	0.46
55:RG:55:ILE:O	55:RG:64:LYS:HB2	2.16	0.46
58:RK:104:LEU:O	58:RK:300:TYR:OH	2.33	0.46
62:RP:104:GLN:HG3	62:RP:105:PRO:HD3	1.97	0.46
62:RP:1691:SER:HA	62:RP:1724:ASN:HD21	1.81	0.46
1:3A:56:A:O2'	42:5D:63:TYR:OH	2.34	0.46
2:5A:116:U:O2	2:5A:130:G:N2	2.43	0.46
2:5A:426:G:H21	2:5A:428:A:H8	1.64	0.46
2:5A:486:U:H4'	2:5A:487:A:H5''	1.98	0.46
3:SA:1111:G:C8	57:RJ:1162:ALA:HA	2.51	0.46
7:SH:17:GLU:N	59:RL:604:SER:O	2.47	0.46
9:SJ:48:THR:O	9:SJ:52:ASN:CB	2.58	0.46
27:A4:164:THR:HG22	27:A4:185:ARG:HG2	1.98	0.46
31:AE:583:LYS:HE2	31:AE:627:LEU:HA	1.98	0.46
32:AF:436:GLU:HG2	32:AF:480:LEU:HD23	1.98	0.46
35:B2:63:LEU:HD21	35:B2:106:TRP:CD2	2.50	0.46
35:B2:341:ALA:HB1	35:B2:353:LEU:HD11	1.96	0.46
38:BE:640:LEU:HD23	38:BE:655:THR:HG22	1.98	0.46
47:5I:255:THR:HG22	63:RQ:288:TYR:HD1	1.81	0.46
49:5K:83:VAL:HG12	49:5K:96:PRO:HG3	1.98	0.46
60:RN:547:VAL:HA	60:RN:550:VAL:HG12	1.97	0.46
60:RN:554:GLN:HE21	60:RN:559:ARG:H	1.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:RN:804:LYS:HD3	60:RN:804:LYS:HA	1.75	0.46
61:RO:395:ILE:HG23	61:RO:469:LEU:HD21	1.98	0.46
64:RS:379:LYS:HA	64:RS:379:LYS:HD3	1.72	0.46
64:RS:392:TYR:HA	64:RS:395:MET:HB2	1.96	0.46
64:RS:413:LEU:O	64:RS:418:HIS:NE2	2.49	0.46
3:SA:1542:G:H2'	3:SA:1543:A:C4	2.51	0.46
4:SC:129:THR:OG1	4:SC:130:SER:N	2.47	0.46
8:SI:7:LYS:O	8:SI:42:GLN:NE2	2.49	0.46
9:SJ:32:GLN:HE21	50:RA:78:LYS:HG2	1.81	0.46
23:3D:175:ILE:HD12	23:3D:317:SER:HA	1.98	0.46
23:3D:371:ASN:OD1	23:3D:374:ARG:NH1	2.48	0.46
34:B1:280:THR:HA	34:B1:304:PRO:HB3	1.98	0.46
36:B3:32:LEU:HD12	36:B3:68:LYS:HE2	1.97	0.46
38:BE:323:VAL:HB	38:BE:343:LEU:HD22	1.98	0.46
45:5G:97:SER:OG	45:5G:144:GLU:OE1	2.28	0.46
50:RA:164:ARG:HH12	50:RA:176:PHE:H	1.64	0.46
52:RC:201:LYS:NZ	66:RV:152:ASP:OD2	2.45	0.46
53:RE:377:SER:HB3	53:RE:389:GLY:HA3	1.97	0.46
59:RM:249:SER:O	59:RM:253:LEU:CB	2.63	0.46
1:3A:306:G:H2'	1:3A:307:G:H8	1.80	0.46
2:5A:86:C:N4	33:AG:482:GLY:O	2.45	0.46
3:SA:1273:G:H1	3:SA:1437:U:H2'	1.80	0.46
4:SC:144:ARG:HG3	4:SC:208:GLN:HB3	1.98	0.46
18:SY:137:LYS:HE2	18:SY:137:LYS:HB3	1.80	0.46
22:3B:261:LEU:O	23:3D:129:ARG:NH1	2.49	0.46
24:3E:392:ALA:O	24:3E:396:ASN:ND2	2.49	0.46
33:AG:143:ASN:OD1	33:AG:143:ASN:N	2.47	0.46
33:AG:253:SER:O	33:AG:256:THR:OG1	2.33	0.46
33:AG:296:HIS:NE2	33:AG:314:SER:OG	2.37	0.46
36:B3:195:GLY:O	36:B3:245:SER:OG	2.29	0.46
36:B3:625:THR:HG22	36:B3:633:VAL:HG13	1.97	0.46
40:5B:200:ARG:O	40:5B:204:ARG:HB3	2.15	0.46
47:5I:280:ALA:HB2	47:5I:311:VAL:HB	1.97	0.46
47:5I:281:ASN:ND2	47:5I:283:ASP:OD1	2.49	0.46
50:RA:300:TRP:HA	50:RA:308:TYR:H	1.80	0.46
53:RE:501:ASN:OD1	53:RE:501:ASN:N	2.49	0.46
56:RI:20:LEU:HD11	56:RI:245:LYS:HA	1.97	0.46
64:RS:280:ASN:ND2	64:RS:320:GLY:O	2.46	0.46
64:RS:359:LEU:HB2	64:RS:372:ILE:HD11	1.97	0.46
3:SA:225:A:H2'	3:SA:226:A:H8	1.79	0.46
27:A4:124:THR:HG21	40:5B:191:PRO:HG3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:AE:495:LEU:HA	31:AE:498:PHE:HB2	1.97	0.46
32:AF:117:LEU:HD12	32:AF:117:LEU:HA	1.79	0.46
41:5C:335:GLY:HA2	41:5C:377:LYS:HG3	1.98	0.46
44:5F:115:MET:HB2	44:5F:115:MET:HE3	1.58	0.46
47:5I:283:ASP:OD2	47:5I:287:TYR:OH	2.30	0.46
58:RK:199:ARG:HB2	58:RK:239:PRO:HA	1.97	0.46
60:RN:495:ASN:HD22	60:RN:617:HIS:HB2	1.80	0.46
61:RO:366:LEU:HD13	61:RO:405:LEU:HD11	1.96	0.46
62:RP:1948:SER:O	62:RP:1985:ARG:NH2	2.48	0.46
3:SA:689:G:C6	3:SA:690:G:O6	2.69	0.45
9:SJ:83:TYR:HB3	9:SJ:101:ILE:HD11	1.98	0.45
9:SJ:103:GLN:HB3	9:SJ:164:ARG:HG2	1.98	0.45
21:Sd:35:ASP:N	21:Sd:35:ASP:OD1	2.45	0.45
24:3E:381:ASP:OD1	24:3E:381:ASP:N	2.49	0.45
27:A4:444:ARG:HG3	27:A4:446:SER:H	1.81	0.45
27:A4:545:ARG:HG3	27:A4:549:VAL:HB	1.98	0.45
27:A4:652:THR:HG23	27:A4:653:TRP:HD1	1.81	0.45
41:5C:541:ASP:HB2	41:5C:543:LYS:HG2	1.97	0.45
41:5C:542:HIS:O	41:5C:544:ASP:N	2.47	0.45
52:RC:135:LYS:HE2	52:RC:135:LYS:HB3	1.79	0.45
53:RE:521:LEU:HD22	53:RE:960:LYS:HG3	1.97	0.45
53:RE:928:HIS:HE1	53:RE:1164:SER:HB2	1.80	0.45
56:RI:114:LYS:HE3	56:RI:114:LYS:HB3	1.83	0.45
57:RJ:65:ASP:OD1	57:RJ:65:ASP:N	2.46	0.45
57:RJ:772:MET:HG3	57:RJ:774:PRO:HD2	1.98	0.45
1:3A:36:C:O2'	47:5I:389:ARG:NH1	2.48	0.45
2:5A:192:G:H21	42:5D:155:THR:HG21	1.81	0.45
2:5A:485:G:N2	47:5I:386:LYS:O	2.41	0.45
3:SA:381:C:H2'	3:SA:382:C:H4'	1.97	0.45
3:SA:420:A:C8	3:SA:420:A:C3'	2.98	0.45
5:SF:58:GLY:HA2	5:SF:61:VAL:HG12	1.99	0.45
5:SF:127:LYS:HB2	5:SF:140:VAL:HG23	1.99	0.45
11:SM:76:VAL:HG21	11:SM:87:ARG:HH11	1.81	0.45
38:BE:351:GLN:HG3	38:BE:372:ASP:HB3	1.97	0.45
38:BE:420:GLU:HG2	38:BE:470:GLN:HA	1.97	0.45
41:5C:15:ARG:HB2	41:5C:18:GLN:HG3	1.98	0.45
42:5D:48:LEU:HG	57:RJ:1067:LEU:HD11	1.98	0.45
47:5I:306:SER:HB3	47:5I:326:ASP:H	1.81	0.45
50:RA:60:ASN:ND2	50:RA:100:GLU:OE2	2.50	0.45
51:RB:229:ASP:HB3	51:RB:232:GLU:HG2	1.97	0.45
53:RE:380:SER:HB2	53:RE:481:THR:HG22	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:RE:626:LYS:HA	53:RE:626:LYS:HD3	1.80	0.45
3:SA:397:A:H5''	9:SJ:50:GLY:HA2	1.98	0.45
3:SA:895:G:H22	3:SA:917:U:H3	1.64	0.45
3:SA:1228:G:N2	12:SN:118:ALA:O	2.48	0.45
3:SA:1463:C:H4'	60:RN:63:ALA:HB1	1.98	0.45
3:SA:1639:C:H41	36:B3:692:MET:HE1	1.82	0.45
28:A5:66:VAL:HG12	28:A5:112:LEU:HD21	1.97	0.45
29:A8:583:SER:HB2	29:A8:637:LEU:HD22	1.97	0.45
31:AE:11:VAL:HA	31:AE:14:ASN:HD22	1.80	0.45
31:AE:255:ILE:HD11	33:AG:884:MET:HB3	1.98	0.45
31:AE:1700:SER:O	31:AE:1703:GLU:N	2.49	0.45
32:AF:69:ARG:HG3	32:AF:70:THR:HG23	1.97	0.45
35:B2:760:ILE:HD11	35:B2:835:PHE:HB2	1.98	0.45
36:B3:343:MET:HB3	36:B3:355:LEU:HD23	1.98	0.45
41:5C:39:ASP:HB3	41:5C:42:LEU:HB3	1.97	0.45
41:5C:243:TRP:NE1	41:5C:304:ARG:HH22	2.15	0.45
44:5F:95:SER:OG	45:5G:59:ASP:OD2	2.32	0.45
45:5G:76:GLU:HG2	45:5G:160:GLY:HA2	1.98	0.45
55:RG:143:GLN:HE22	55:RG:149:SER:HA	1.81	0.45
60:RN:13:LEU:HD22	60:RN:16:ARG:HE	1.81	0.45
62:RP:971:ARG:O	62:RP:975:ASN:HA	2.16	0.45
64:RS:271:THR:H	64:RS:274:GLU:HB2	1.82	0.45
3:SA:1775:U:H2'	3:SA:1776:A:C8	2.51	0.45
4:SC:224:ASP:OD2	53:RE:981:LYS:NZ	2.43	0.45
4:SC:242:LYS:N	53:RE:655:LEU:O	2.48	0.45
23:3D:379:LEU:HD13	23:3D:408:VAL:HG21	1.98	0.45
27:A4:137:TYR:HB2	27:A4:177:LEU:HD12	1.99	0.45
28:A5:452:LEU:HA	28:A5:455:THR:HG22	1.98	0.45
28:A5:518:ASN:HB2	28:A5:521:SER:HB3	1.98	0.45
28:A5:539:ARG:NH1	33:AG:524:ASP:OD2	2.49	0.45
32:AF:171:VAL:HG22	32:AF:188:SER:HB3	1.99	0.45
35:B2:49:VAL:HG22	35:B2:63:LEU:HD22	1.98	0.45
43:5E:358:THR:HB	60:RN:89:GLN:HB3	1.97	0.45
54:RF:255:LYS:O	54:RF:265:ARG:NH1	2.45	0.45
55:RH:191:ASP:HA	55:RH:194:GLU:HG2	1.98	0.45
60:RN:600:LEU:HD22	60:RN:633:VAL:HG22	1.98	0.45
64:RS:399:ILE:O	64:RS:406:GLY:N	2.50	0.45
3:SA:385:A:OP1	9:SJ:25:ARG:NH2	2.46	0.45
6:SG:117:THR:HG21	6:SG:194:LEU:HD23	1.98	0.45
13:SO:69:ASN:OD1	13:SO:69:ASN:N	2.47	0.45
23:3D:195:VAL:HG12	23:3D:216:PHE:HE2	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:3G:58:CYS:HB3	26:3G:98:ILE:HD12	1.99	0.45
27:A4:249:ARG:HB2	27:A4:292:ASN:HD22	1.81	0.45
29:A8:662:ILE:HA	29:A8:665:GLN:HB2	1.97	0.45
31:AE:718:ARG:HA	31:AE:721:VAL:HG12	1.99	0.45
33:AG:364:ASN:OD1	33:AG:364:ASN:N	2.42	0.45
35:B2:103:ILE:HB	35:B2:117:PHE:HB2	1.99	0.45
35:B2:220:THR:HG22	35:B2:259:ILE:HD11	1.96	0.45
37:B8:264:LEU:HD11	37:B8:272:LEU:HD12	1.97	0.45
39:B6:186:VAL:HG12	39:B6:273:ILE:HG13	1.98	0.45
41:5C:507:ASN:ND2	52:RC:71:CYS:O	2.50	0.45
44:5F:63:LEU:HB3	66:RV:204:GLY:HA2	1.98	0.45
45:5G:19:GLU:O	45:5G:23:SER:HB2	2.17	0.45
50:RA:21:VAL:HG12	50:RA:46:ARG:HH12	1.81	0.45
52:RC:35:PHE:HB2	52:RC:36:ALA:H	1.62	0.45
53:RE:308:LEU:HG	53:RE:337:LEU:HD21	1.99	0.45
55:RH:56:SER:HA	55:RH:63:ASP:HB2	1.99	0.45
2:5A:550:C:H2'	2:5A:551:A:C8	2.52	0.45
3:SA:1537:C:N4	55:RH:155:SER:O	2.37	0.45
5:SF:150:PRO:HB2	5:SF:154:ILE:HG13	1.98	0.45
6:SG:39:GLU:OE2	6:SG:47:SER:OG	2.33	0.45
25:3F:164:GLN:HE21	25:3F:527:VAL:HG13	1.81	0.45
25:3F:452:SER:HB3	25:3F:460:ARG:HG2	1.99	0.45
31:AE:864:VAL:O	31:AE:868:LYS:CB	2.65	0.45
32:AF:31:THR:OG1	32:AF:32:SER:N	2.46	0.45
33:AG:726:GLN:NE2	33:AG:736:THR:O	2.42	0.45
33:AG:761:GLU:HG3	33:AG:779:ILE:HG22	1.99	0.45
38:BE:851:SER:O	38:BE:851:SER:OG	2.31	0.45
50:RA:14:TYR:HE2	50:RA:344:PRO:HG3	1.81	0.45
50:RA:164:ARG:HH12	50:RA:176:PHE:N	2.15	0.45
53:RE:151:SER:HA	53:RE:154:LYS:HB2	1.98	0.45
53:RE:1155:LEU:HD23	54:RF:93:PHE:HB3	1.98	0.45
62:RP:378:HIS:O	62:RP:382:PHE:CB	2.65	0.45
3:SA:67:A:H2'	3:SA:69:G:C8	2.52	0.45
3:SA:420:A:C8	3:SA:420:A:O5'	2.70	0.45
3:SA:1509:C:O2'	56:RI:192:ASN:ND2	2.50	0.45
11:SM:92:HIS:HD2	11:SM:94:ILE:HG13	1.82	0.45
13:SO:49:GLN:HA	13:SO:52:VAL:HG12	1.99	0.45
23:3D:120:SER:O	23:3D:120:SER:OG	2.33	0.45
27:A4:468:ASP:OD2	27:A4:472:ARG:NH1	2.44	0.45
27:A4:636:ILE:HG23	27:A4:648:PHE:HD2	1.82	0.45
31:AE:583:LYS:HD3	31:AE:631:VAL:HG21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:AG:600:SER:O	33:AG:600:SER:OG	2.33	0.45
35:B2:54:ILE:HD13	35:B2:364:TYR:CD2	2.48	0.45
35:B2:140:SER:OG	35:B2:142:ASP:OD1	2.31	0.45
36:B3:42:ILE:HD11	36:B3:379:LEU:HD13	1.97	0.45
37:B8:512:ASP:OD1	37:B8:512:ASP:N	2.48	0.45
41:5C:104:LEU:HD21	41:5C:139:TRP:HB2	1.99	0.45
59:RL:77:ILE:HD12	59:RL:77:ILE:HA	1.82	0.45
59:RL:846:SER:O	59:RL:850:LEU:CB	2.65	0.45
60:RN:423:GLY:O	60:RN:426:THR:OG1	2.31	0.45
62:RP:2006:LEU:HG	62:RP:2011:ILE:HD12	1.97	0.45
2:5A:102:A:H61	32:AF:415:LEU:HD22	1.81	0.45
2:5A:514:U:OP2	62:RP:1975:LYS:NZ	2.37	0.45
3:SA:145:A:O2'	3:SA:146:U:O5'	2.33	0.45
3:SA:326:G:H4'	11:SM:82:ARG:HD2	1.98	0.45
3:SA:884:A:H2'	3:SA:885:G:C8	2.52	0.45
3:SA:1070:C:H5''	20:Sc:17:ARG:HH21	1.82	0.45
5:SF:159:THR:HB	5:SF:173:ILE:HB	1.99	0.45
11:SM:57:LYS:O	11:SM:138:ASN:ND2	2.50	0.45
22:3C:253:ILE:HD11	22:3C:293:LEU:HD21	1.99	0.45
29:A8:648:PHE:HD1	30:A9:509:GLN:HE21	1.64	0.45
31:AE:65:LYS:HB3	31:AE:104:LEU:HD11	1.99	0.45
32:AF:227:VAL:HG22	32:AF:236:VAL:HG12	1.99	0.45
33:AG:38:SER:OG	33:AG:43:ASN:O	2.35	0.45
34:B1:25:ASP:O	34:B1:27:LYS:N	2.49	0.45
34:B1:369:ILE:HD11	34:B1:390:VAL:HG11	1.99	0.45
36:B3:217:ASP:OD1	36:B3:217:ASP:N	2.48	0.45
36:B3:509:ALA:HB1	36:B3:515:CYS:HA	1.98	0.45
41:5C:311:SER:OG	41:5C:313:GLU:OE2	2.33	0.45
47:5I:94:TYR:OH	47:5I:134:ASN:ND2	2.41	0.45
50:RA:247:THR:HG21	50:RA:251:TYR:HB2	1.99	0.45
1:3A:12:U:H3	3:SA:1112:G:H1	1.65	0.45
3:SA:1223:A:H2'	3:SA:1224:A:C8	2.52	0.45
4:SC:242:LYS:HD2	4:SC:244:VAL:H	1.82	0.45
22:3B:88:ILE:HD11	22:3B:123:ILE:HG21	1.98	0.45
26:3H:33:LEU:HD23	26:3H:35:LYS:HE3	1.98	0.45
31:AE:348:ILE:HD13	31:AE:348:ILE:HA	1.87	0.45
34:B1:300:MET:HE2	34:B1:300:MET:HB3	1.78	0.45
34:B1:475:PRO:HD2	34:B1:493:TRP:HB2	1.99	0.45
47:5I:297:SER:OG	47:5I:299:ASN:O	2.33	0.45
48:5J:110:ASP:OD1	48:5J:110:ASP:N	2.36	0.45
57:RJ:617:THR:HG23	57:RJ:620:LYS:HE2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:RP:465:PHE:HA	62:RP:468:ALA:HB3	1.98	0.45
64:RS:235:VAL:HG12	64:RS:238:SER:HB3	1.98	0.45
64:RS:429:LYS:HD2	64:RS:437:ARG:HH22	1.82	0.45
2:5A:254:C:OP2	67:RW:184:TYR:OH	2.31	0.45
3:SA:1634:C:O2	34:B1:397:LYS:NZ	2.50	0.45
22:3C:175:ALA:N	22:3C:198:GLU:OE2	2.48	0.45
28:A5:582:GLU:O	28:A5:586:ASP:N	2.50	0.45
31:AE:659:LEU:HD21	31:AE:691:PHE:HA	1.98	0.45
32:AF:371:GLU:OE2	37:B8:273:ARG:NH2	2.50	0.45
41:5C:214:LEU:HD23	41:5C:228:LEU:HD12	1.99	0.45
41:5C:269:LYS:HB2	63:RQ:830:ILE:HG23	1.98	0.45
41:5C:460:ARG:HB3	63:RQ:847:VAL:HB	1.99	0.45
50:RA:231:VAL:HA	50:RA:247:THR:HA	1.98	0.45
53:RE:173:ASN:O	53:RE:175:LYS:NZ	2.37	0.45
54:RF:71:VAL:HG21	54:RF:84:VAL:HB	1.98	0.45
58:RK:143:LYS:HE3	58:RK:143:LYS:HB2	1.75	0.45
64:RS:373:LYS:HG3	64:RS:420:ALA:HA	1.99	0.45
3:SA:930:A:H2'	4:SC:114:VAL:HG11	1.99	0.44
4:SC:31:ASP:HB3	4:SC:45:LYS:HG2	1.99	0.44
11:SM:46:LYS:HD3	11:SM:49:ILE:HD12	1.98	0.44
12:SN:41:LEU:HB3	12:SN:43:ARG:HG3	1.99	0.44
28:A5:87:LEU:O	28:A5:96:THR:N	2.50	0.44
29:A8:574:ARG:H	29:A8:576:ARG:NH1	2.16	0.44
31:AE:109:TRP:HA	31:AE:114:THR:HG21	2.00	0.44
33:AG:43:ASN:OD1	33:AG:43:ASN:N	2.48	0.44
35:B2:129:PHE:HE1	35:B2:150:LEU:HD11	1.82	0.44
35:B2:292:ILE:HG23	35:B2:324:PHE:HE2	1.83	0.44
35:B2:641:TYR:O	35:B2:650:ILE:N	2.49	0.44
38:BE:546:ILE:HG21	38:BE:560:LEU:HD22	1.99	0.44
45:5G:166:SER:O	45:5G:256:MET:HA	2.17	0.44
47:5I:210:LYS:HA	47:5I:210:LYS:HD3	1.69	0.44
55:RG:135:LYS:HD3	55:RG:135:LYS:HA	1.87	0.44
57:RJ:1148:GLU:OE2	57:RJ:1152:ARG:NH1	2.49	0.44
62:RP:60:SER:HB3	62:RP:102:SER:HB3	1.99	0.44
2:5A:110:G:N2	2:5A:136:U:O2	2.49	0.44
2:5A:247:U:OP1	42:5D:82:ARG:NH1	2.50	0.44
3:SA:406:U:H2'	3:SA:407:A:H8	1.82	0.44
11:SM:94:ILE:HD12	11:SM:101:GLU:H	1.81	0.44
20:Sc:48:SER:OG	20:Sc:49:HIS:ND1	2.50	0.44
22:3B:104:ASP:OD1	22:3B:104:ASP:N	2.38	0.44
53:RE:585:MET:HB3	53:RE:610:PHE:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:RJ:889:LEU:HD22	57:RJ:922:ILE:HB	2.00	0.44
59:RL:111:SER:HB3	59:RL:134:LEU:HD12	1.99	0.44
60:RN:737:ILE:HA	60:RN:740:MET:HG2	2.00	0.44
61:RO:282:HIS:CD2	61:RO:283:LYS:HG2	2.52	0.44
3:SA:1080:U:H5'	47:5I:425:LYS:HE2	1.99	0.44
8:SI:163:ASP:O	63:RQ:277:ARG:NH2	2.50	0.44
16:ST:50:ALA:O	16:ST:68:ARG:NH1	2.51	0.44
24:3E:372:ARG:HG3	26:3G:63:ILE:HA	2.00	0.44
25:3F:405:VAL:HG12	25:3F:415:THR:HG22	2.00	0.44
31:AE:763:LEU:HD12	31:AE:768:LYS:HD3	2.00	0.44
32:AF:51:HIS:O	32:AF:53:HIS:N	2.49	0.44
35:B2:566:TYR:OH	35:B2:603:ASP:O	2.33	0.44
35:B2:580:ASP:OD2	35:B2:623:PHE:N	2.40	0.44
36:B3:32:LEU:HD22	36:B3:76:LEU:HD12	2.00	0.44
36:B3:104:PRO:O	36:B3:122:THR:OG1	2.35	0.44
38:BE:921:ARG:O	38:BE:925:LEU:HB2	2.17	0.44
57:RJ:288:VAL:HG11	57:RJ:812:MET:HE2	1.98	0.44
62:RP:107:LEU:HD21	62:RP:150:TRP:HB3	1.98	0.44
2:5A:228:A:H2'	2:5A:229:A:C8	2.51	0.44
3:SA:362:G:H2'	3:SA:363:G:C8	2.52	0.44
3:SA:608:U:O2'	3:SA:609:U:O4'	2.34	0.44
3:SA:863:A:H4'	17:5X:57:ARG:HG2	1.99	0.44
3:SA:1146:G:H2'	3:SA:1147:A:H8	1.83	0.44
3:SA:1660:A:H2'	3:SA:1661:U:C6	2.52	0.44
11:SM:84:ILE:N	11:SM:109:VAL:O	2.47	0.44
22:3B:210:MET:HE2	22:3B:210:MET:HB3	1.79	0.44
23:3D:31:LEU:HD21	47:5I:59:VAL:HG13	1.99	0.44
27:A4:579:ARG:HH12	27:A4:659:PHE:HD1	1.65	0.44
34:B1:157:ASP:N	34:B1:157:ASP:OD1	2.50	0.44
36:B3:430:TYR:HD2	36:B3:454:LEU:HD23	1.82	0.44
36:B3:531:ASN:OD1	36:B3:531:ASN:N	2.49	0.44
41:5C:433:LEU:HD21	44:5F:16:VAL:HG11	1.99	0.44
46:5H:555:ASN:HB3	46:5H:558:ASN:HB2	1.98	0.44
51:RB:302:LYS:HB3	51:RB:306:ARG:HH22	1.81	0.44
53:RE:165:PRO:HD2	53:RE:222:PHE:HZ	1.83	0.44
53:RE:174:TYR:CE2	53:RE:227:LYS:HB3	2.53	0.44
53:RE:804:THR:HG21	53:RE:838:VAL:HB	1.99	0.44
54:RF:15:VAL:HG12	54:RF:17:PRO:HD3	1.98	0.44
54:RF:84:VAL:HG13	54:RF:126:LEU:HD11	1.99	0.44
58:RK:187:ILE:HB	58:RK:251:GLN:HE22	1.82	0.44
60:RN:443:LYS:HG3	60:RN:448:PHE:HE2	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5A:554:G:H1	2:5A:583:U:H3	1.64	0.44
6:SG:63:GLN:HE22	6:SG:66:GLN:HB3	1.82	0.44
13:SO:93:LYS:HA	13:SO:96:VAL:HG12	1.99	0.44
22:3C:92:ARG:HH12	42:5D:151:PHE:HB2	1.81	0.44
23:3D:281:LEU:HD23	24:3E:261:GLN:HE21	1.82	0.44
27:A4:75:ASN:HB3	27:A4:92:GLU:HA	2.00	0.44
27:A4:201:VAL:HG13	27:A4:213:TRP:HB2	1.99	0.44
31:AE:488:GLY:HA2	31:AE:491:TYR:HB3	1.98	0.44
31:AE:729:LYS:HA	31:AE:733:MET:HG3	2.00	0.44
33:AG:414:ILE:HA	33:AG:414:ILE:HD12	1.80	0.44
35:B2:443:LEU:HG	35:B2:459:LEU:HD13	2.00	0.44
36:B3:467:ILE:H	36:B3:479:ILE:HD11	1.83	0.44
37:B8:358:PHE:HA	37:B8:376:LEU:O	2.17	0.44
38:BE:356:ILE:HG22	38:BE:633:LYS:HG3	2.00	0.44
41:5C:122:GLY:O	41:5C:139:TRP:NE1	2.34	0.44
50:RA:60:ASN:HB3	50:RA:74:THR:HB	2.00	0.44
52:RC:174:MET:HE2	52:RC:174:MET:HB3	1.78	0.44
53:RE:554:LYS:HA	53:RE:554:LYS:HD2	1.82	0.44
55:RG:242:CYS:O	55:RG:246:GLU:HG3	2.18	0.44
56:RI:129:TYR:HB2	56:RI:153:MET:HE2	1.99	0.44
62:RP:70:ILE:HG21	62:RP:87:ILE:HG22	1.98	0.44
2:5A:20:C:H2'	2:5A:21:A:C8	2.52	0.44
3:SA:592:A:O2'	3:SA:596:C:OP1	2.35	0.44
3:SA:1234:A:O2'	3:SA:1236:A:N6	2.50	0.44
6:SG:86:GLN:HE22	34:B1:546:ASP:HB3	1.83	0.44
18:SY:77:ILE:HG22	57:RJ:751:TYR:HB2	1.99	0.44
22:3B:125:VAL:HG12	48:5J:150:GLY:HA3	2.00	0.44
22:3B:169:LYS:HA	22:3B:193:VAL:O	2.18	0.44
27:A4:120:SER:OG	27:A4:121:THR:N	2.50	0.44
33:AG:484:VAL:O	33:AG:487:GLU:N	2.51	0.44
34:B1:476:VAL:HA	34:B1:492:SER:HB3	1.98	0.44
34:B1:743:PHE:HZ	34:B1:778:ILE:HD13	1.83	0.44
36:B3:691:PRO:HD2	43:5E:516:SER:HB2	2.00	0.44
37:B8:27:PHE:HB3	39:B6:31:LEU:HD23	1.98	0.44
53:RE:655:LEU:HD12	53:RE:655:LEU:HA	1.90	0.44
55:RH:199:ASP:OD1	55:RH:199:ASP:N	2.49	0.44
61:RO:259:LYS:HB3	61:RO:259:LYS:HE2	1.72	0.44
2:5A:207:G:H2'	2:5A:208:A:C8	2.52	0.44
3:SA:398:G:OP2	9:SJ:47:ARG:NH2	2.40	0.44
5:SF:140:VAL:HG12	5:SF:146:THR:HG22	2.00	0.44
10:SK:38:ASN:HA	46:5H:565:LYS:HE2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:SM:57:LYS:HG3	11:SM:110:HIS:CE1	2.53	0.44
15:SR:64:ASP:OD1	15:SR:64:ASP:N	2.50	0.44
22:3B:218:ILE:HD11	23:3D:152:LEU:HD22	1.98	0.44
24:3E:227:LEU:HG	24:3E:231:ILE:HB	2.00	0.44
31:AE:396:ASP:OD1	31:AE:396:ASP:N	2.47	0.44
32:AF:20:THR:HA	32:AF:24:GLN:HE21	1.83	0.44
33:AG:768:TRP:HE1	33:AG:772:THR:HA	1.83	0.44
36:B3:111:ASP:N	36:B3:111:ASP:OD1	2.48	0.44
44:5F:169:THR:HA	44:5F:172:ARG:HG2	1.99	0.44
45:5G:139:LEU:HB2	45:5G:157:PHE:CE2	2.53	0.44
47:5I:241:ASP:OD1	47:5I:241:ASP:N	2.39	0.44
50:RA:152:ASP:OD1	50:RA:152:ASP:N	2.51	0.44
54:RF:150:LYS:HG3	54:RF:151:HIS:ND1	2.33	0.44
54:RF:208:ASP:N	54:RF:212:PHE:O	2.41	0.44
57:RJ:841:THR:HB	57:RJ:859:ILE:HA	1.99	0.44
60:RN:314:MET:HA	60:RN:512:ASP:HA	2.00	0.44
62:RP:1183:PRO:O	62:RP:1187:VAL:CB	2.65	0.44
68:RY:489:GLN:O	68:RY:493:PHE:CB	2.66	0.44
4:SC:36:SER:OG	4:SC:41:ARG:NH1	2.50	0.44
9:SJ:66:SER:HA	9:SJ:73:SER:HA	1.99	0.44
23:3D:206:LEU:HD11	23:3D:219:LEU:HD11	2.00	0.44
27:A4:214:SER:HB3	27:A4:226:LEU:HD13	1.99	0.44
31:AE:63:GLU:HA	31:AE:64:PRO:HD3	1.88	0.44
35:B2:107:ASP:OD1	35:B2:107:ASP:N	2.46	0.44
47:5I:444:GLU:OE2	47:5I:448:ARG:NH2	2.37	0.44
50:RA:184:ASN:OD1	50:RA:230:GLN:NE2	2.51	0.44
53:RE:822:ARG:NH1	53:RE:1133:PRO:O	2.50	0.44
54:RF:131:ALA:HA	54:RF:134:ILE:HG12	1.99	0.44
55:RG:227:LEU:HA	55:RG:227:LEU:HD23	1.79	0.44
3:SA:1599:C:H2'	3:SA:1600:A:C8	2.53	0.44
4:SC:129:THR:HG23	4:SC:131:ASP:H	1.82	0.44
4:SC:194:ASN:HD21	4:SC:212:VAL:HG23	1.82	0.44
7:SH:65:GLN:NE2	50:RA:43:TYR:O	2.51	0.44
8:SI:38:LEU:HD12	8:SI:41:LEU:HD12	2.00	0.44
9:SJ:67:TRP:HD1	9:SJ:70:GLU:H	1.66	0.44
11:SM:36:LYS:HD2	11:SM:36:LYS:HA	1.74	0.44
17:SX:66:ASN:O	47:5I:325:TYR:OH	2.27	0.44
27:A4:45:THR:HB	27:A4:352:VAL:HA	1.99	0.44
27:A4:774:LEU:HD12	27:A4:774:LEU:HA	1.83	0.44
29:A8:638:LEU:HD21	29:A8:662:ILE:HD11	1.99	0.44
31:AE:238:LEU:HA	31:AE:241:ILE:HG22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:AE:538:ALA:HA	31:AE:541:LEU:HB2	2.00	0.44
33:AG:228:VAL:HG23	33:AG:236:ASN:HB3	2.00	0.44
33:AG:510:TYR:HE1	33:AG:527:HIS:HB3	1.83	0.44
33:AG:532:TRP:HB3	33:AG:541:TRP:HB3	1.99	0.44
34:B1:35:ASN:HA	34:B1:58:ILE:HG23	1.99	0.44
34:B1:157:ASP:OD1	34:B1:203:GLN:NE2	2.38	0.44
34:B1:661:LEU:H	34:B1:661:LEU:HG	1.62	0.44
35:B2:59:LEU:HD21	35:B2:62:LYS:HE2	1.99	0.44
36:B3:188:GLU:O	36:B3:221:ASN:ND2	2.50	0.44
37:B8:277:ILE:HA	37:B8:282:ASN:HD22	1.83	0.44
38:BE:852:LEU:HD22	38:BE:860:GLU:HG2	2.00	0.44
41:5C:162:ASN:ND2	41:5C:429:GLU:OE1	2.51	0.44
43:5E:379:ASP:HB2	45:5G:191:PHE:HD2	1.83	0.44
53:RE:1222:GLU:HG2	54:RF:60:LEU:HB2	2.00	0.44
55:RH:89:PRO:HG2	55:RH:134:PHE:HZ	1.83	0.44
59:RL:195:ASN:HB3	59:RL:198:CYS:HB3	1.99	0.44
63:RQ:284:ARG:HE	63:RQ:284:ARG:HB3	1.51	0.44
1:3A:327:G:OP1	42:5D:222:ARG:NH2	2.44	0.43
3:SA:257:A:O2'	9:SJ:73:SER:O	2.34	0.43
3:SA:415:C:O2'	3:SA:418:G:O6	2.36	0.43
28:A5:233:LYS:HA	28:A5:233:LYS:HD3	1.82	0.43
28:A5:520:MET:H	28:A5:520:MET:HG3	1.60	0.43
31:AE:100:ALA:HB1	37:B8:44:PHE:HZ	1.82	0.43
32:AF:288:ASP:OD1	32:AF:288:ASP:N	2.48	0.43
34:B1:356:ASP:OD1	34:B1:356:ASP:N	2.50	0.43
36:B3:652:ILE:HD12	36:B3:652:ILE:HA	1.92	0.43
38:BE:76:THR:OG1	38:BE:78:SER:O	2.29	0.43
41:5C:228:LEU:HD22	41:5C:264:PRO:HA	1.99	0.43
47:5I:139:CYS:HB3	47:5I:145:VAL:HG22	1.99	0.43
54:RF:50:SER:O	54:RF:127:LYS:NZ	2.51	0.43
55:RG:177:LYS:HE2	55:RG:177:LYS:HB3	1.68	0.43
57:RJ:203:LYS:HA	57:RJ:203:LYS:HD2	1.78	0.43
62:RP:103:LEU:HD11	62:RP:147:VAL:HG23	1.99	0.43
3:SA:328:A:H2'	3:SA:329:G:H8	1.83	0.43
4:SC:123:ALA:HB2	4:SC:165:ARG:HG3	2.00	0.43
4:SC:171:ILE:HD11	4:SC:197:ILE:HA	1.99	0.43
8:SI:87:ASP:OD1	62:RP:2031:HIS:NE2	2.49	0.43
11:SM:123:VAL:HG12	11:SM:142:VAL:HA	1.99	0.43
22:3B:221:ILE:HD13	23:3D:163:VAL:HB	2.00	0.43
27:A4:212:ILE:O	27:A4:226:LEU:N	2.50	0.43
27:A4:571:THR:HG21	27:A4:632:ASN:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:A5:240:GLN:HE22	28:A5:298:LYS:HB3	1.83	0.43
33:AG:712:THR:HG23	33:AG:720:ILE:HD13	1.99	0.43
39:B6:5:ARG:HA	39:B6:5:ARG:HD2	1.80	0.43
44:5F:34:ARG:NH2	49:5K:16:THR:OG1	2.50	0.43
45:5G:119:ARG:NH1	45:5G:122:TYR:O	2.52	0.43
45:5G:283:THR:HG22	45:5G:286:LYS:HB2	2.00	0.43
53:RE:518:PHE:HD1	53:RE:520:ASN:H	1.67	0.43
53:RE:976:ILE:HG22	53:RE:1042:ALA:HB3	2.00	0.43
53:RE:1221:HIS:CE1	54:RF:20:LEU:HB3	2.53	0.43
57:RJ:625:TRP:HZ2	58:RK:284:SER:HB3	1.83	0.43
59:RM:281:LEU:HA	59:RM:409:ALA:HB3	1.99	0.43
61:RO:292:PRO:HG2	61:RO:330:PHE:HE2	1.82	0.43
61:RO:315:VAL:HG23	61:RO:316:PRO:HD3	1.98	0.43
61:RO:472:HIS:CD2	61:RO:474:HIS:H	2.31	0.43
62:RP:1941:VAL:HA	62:RP:1944:ILE:HD12	1.99	0.43
3:SA:153:G:O3'	7:SH:2:LYS:NZ	2.41	0.43
3:SA:513:U:H2'	3:SA:514:G:H8	1.82	0.43
3:SA:1146:G:H2'	3:SA:1147:A:C8	2.53	0.43
5:SF:183:VAL:HB	5:SF:225:VAL:HG23	2.00	0.43
5:SF:194:THR:H	5:SF:210:ILE:HG23	1.82	0.43
8:SI:19:GLN:HB3	8:SI:85:PHE:HZ	1.83	0.43
9:SJ:74:LYS:HD3	9:SJ:74:LYS:HA	1.68	0.43
24:3E:330:LEU:HD13	42:5D:109:THR:HG21	2.00	0.43
27:A4:144:ILE:HD12	27:A4:158:VAL:HB	2.00	0.43
31:AE:641:LEU:O	31:AE:644:LYS:NZ	2.42	0.43
33:AG:516:PRO:HG2	33:AG:519:LEU:HD21	2.00	0.43
34:B1:605:ASP:OD1	34:B1:605:ASP:N	2.40	0.43
36:B3:28:ASN:OD1	36:B3:28:ASN:N	2.48	0.43
36:B3:34:THR:HG23	36:B3:68:LYS:HE3	2.00	0.43
42:5D:78:LEU:HA	42:5D:78:LEU:HD12	1.82	0.43
43:5E:524:ASP:OD2	43:5E:527:ARG:NH2	2.42	0.43
47:5I:306:SER:OG	47:5I:307:ALA:N	2.50	0.43
49:5K:171:PRO:HA	49:5K:184:LYS:HB2	2.00	0.43
62:RP:1756:ILE:HG21	62:RP:1800:LEU:HB3	2.01	0.43
62:RP:1782:ASN:OD1	62:RP:1782:ASN:N	2.44	0.43
5:SF:141:THR:OG1	5:SF:142:HIS:N	2.52	0.43
16:ST:110:ARG:NH1	60:RN:740:MET:HB2	2.33	0.43
24:3E:206:ALA:HB2	24:3E:262:ILE:HD11	2.00	0.43
27:A4:572:ALA:HB3	27:A4:585:ILE:HD11	2.00	0.43
27:A4:750:ASN:N	27:A4:750:ASN:OD1	2.50	0.43
31:AE:655:ALA:O	31:AE:659:LEU:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:AF:24:GLN:HB2	32:AF:294:PHE:HD1	1.83	0.43
34:B1:369:ILE:HB	34:B1:383:PHE:HB2	1.99	0.43
36:B3:194:ARG:HD3	36:B3:243:VAL:HG13	1.99	0.43
41:5C:512:ARG:O	41:5C:516:VAL:HG23	2.18	0.43
42:5D:194:LYS:HA	42:5D:194:LYS:HD3	1.83	0.43
47:5I:358:MET:HB3	63:RQ:890:VAL:HG23	2.00	0.43
48:5J:207:LYS:HE2	48:5J:207:LYS:HB3	1.88	0.43
53:RE:527:TYR:HB2	53:RE:615:VAL:HG13	2.00	0.43
53:RE:870:ALA:O	53:RE:875:LYS:NZ	2.51	0.43
56:RI:208:SER:OG	56:RI:209:ILE:N	2.52	0.43
57:RJ:904:ASN:HA	57:RJ:907:THR:HB	2.00	0.43
58:RK:68:SER:OG	58:RK:69:TYR:N	2.52	0.43
64:RS:221:LEU:HD22	64:RS:258:VAL:HG11	2.00	0.43
64:RS:373:LYS:HE2	64:RS:373:LYS:HB3	1.84	0.43
2:5A:467:A:N1	2:5A:468:A:N6	2.66	0.43
2:5A:489:G:O6	39:B6:120:ARG:NH1	2.51	0.43
3:SA:18:C:O2'	3:SA:21:U:O4'	2.37	0.43
3:SA:578:U:OP2	57:RJ:874:TYR:OH	2.29	0.43
8:SI:22:GLN:HA	8:SI:25:VAL:HG22	1.99	0.43
9:SJ:76:THR:OG1	9:SJ:77:ARG:N	2.52	0.43
10:SK:65:LYS:HZ2	25:3F:59:PRO:CA	2.27	0.43
17:SX:32:LYS:HB2	17:SX:32:LYS:HE3	1.81	0.43
18:SY:68:ILE:HD12	60:RN:785:VAL:HG23	2.00	0.43
22:3C:185:SER:HB3	22:3C:217:ILE:HD11	2.00	0.43
24:3E:191:HIS:HB2	24:3E:247:ILE:HG23	1.99	0.43
26:3G:62:GLU:HA	26:3G:65:LEU:HG	2.00	0.43
26:3H:95:ARG:HD2	26:3H:95:ARG:HA	1.87	0.43
33:AG:50:ASN:HD21	33:AG:782:THR:HG22	1.84	0.43
33:AG:252:LEU:HD23	33:AG:256:THR:HG21	2.00	0.43
34:B1:829:VAL:HG23	34:B1:830:ARG:HG2	2.01	0.43
35:B2:276:ASN:ND2	35:B2:280:THR:O	2.47	0.43
36:B3:41:ASN:OD1	36:B3:41:ASN:N	2.49	0.43
38:BE:606:ASP:OD1	38:BE:606:ASP:N	2.41	0.43
47:5I:8:ARG:HD3	47:5I:8:ARG:HA	1.80	0.43
49:5K:52:PHE:HB3	49:5K:55:TYR:HB3	2.01	0.43
49:5K:161:LYS:HG2	49:5K:172:LEU:HD21	1.99	0.43
53:RE:207:LEU:HB2	53:RE:296:ILE:HA	2.00	0.43
53:RE:1109:LYS:HZ1	53:RE:1170:GLY:H	1.66	0.43
56:RI:123:ASP:OD1	56:RI:123:ASP:N	2.49	0.43
57:RJ:80:THR:C	71:RJ:1201:GTP:O2B	2.61	0.43
60:RN:640:MET:HE2	60:RN:640:MET:HB3	1.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:RP:1610:MET:O	62:RP:1614:GLU:CB	2.67	0.43
64:RS:359:LEU:HD23	64:RS:362:LEU:HD12	2.00	0.43
65:RT:186:GLU:HG3	65:RT:230:LYS:HG2	2.00	0.43
3:SA:526:A:OP1	19:SZ:93:ARG:NE	2.48	0.43
10:SK:155:HIS:NE2	25:3F:321:HIS:O	2.50	0.43
17:SX:38:LEU:HA	17:SX:41:MET:HG2	2.01	0.43
22:3C:261:LEU:O	24:3E:118:ARG:NH2	2.34	0.43
24:3E:372:ARG:O	24:3E:376:LEU:HB2	2.19	0.43
25:3F:303:LYS:HB3	25:3F:317:ILE:HD11	2.01	0.43
26:3H:52:ILE:HD12	26:3H:71:CYS:SG	2.58	0.43
28:A5:336:ASN:OD1	28:A5:336:ASN:N	2.49	0.43
35:B2:645:GLU:HG2	35:B2:646:LYS:HG3	1.99	0.43
38:BE:569:VAL:HB	38:BE:579:ARG:HB2	2.01	0.43
44:5F:138:VAL:HG12	44:5F:158:VAL:HG22	2.00	0.43
47:5I:6:ILE:HG21	47:5I:8:ARG:HH21	1.84	0.43
50:RA:155:VAL:HG13	50:RA:163:TYR:HB2	2.00	0.43
53:RE:257:SER:O	53:RE:266:PRO:HA	2.18	0.43
53:RE:611:ASP:OD1	53:RE:611:ASP:N	2.51	0.43
53:RE:745:LYS:HA	53:RE:745:LYS:HD2	1.83	0.43
58:RK:36:ILE:HB	58:RK:72:THR:HA	2.01	0.43
60:RN:590:ASN:OD1	60:RN:590:ASN:N	2.50	0.43
3:SA:646:C:H2'	3:SA:647:G:C8	2.47	0.43
4:SC:239:GLU:HG2	53:RE:658:PHE:HA	2.00	0.43
6:SG:89:ILE:HD11	6:SG:172:ILE:HD11	2.00	0.43
8:SI:46:ILE:HD12	8:SI:60:ILE:HG13	2.01	0.43
8:SI:185:ILE:HG13	8:SI:187:SER:HB3	2.01	0.43
16:ST:119:ILE:HD13	43:5E:342:THR:HG22	2.00	0.43
22:3C:185:SER:HA	22:3C:188:VAL:HG12	2.01	0.43
31:AE:348:ILE:HG21	31:AE:373:ILE:HD11	2.00	0.43
31:AE:715:HIS:HA	31:AE:718:ARG:HG2	2.00	0.43
33:AG:140:LYS:HA	33:AG:140:LYS:HD3	1.78	0.43
36:B3:377:LEU:HA	36:B3:378:PRO:HD3	1.85	0.43
36:B3:519:ASN:HD22	36:B3:524:GLU:H	1.67	0.43
36:B3:678:TRP:HE3	36:B3:697:VAL:HG23	1.84	0.43
37:B8:35:GLU:O	37:B8:39:LYS:HB2	2.18	0.43
41:5C:64:ASP:HA	41:5C:67:LEU:HG	1.99	0.43
45:5G:28:LYS:HB2	45:5G:46:LEU:HD11	2.00	0.43
47:5I:133:GLN:HA	47:5I:150:ILE:O	2.18	0.43
57:RJ:280:LEU:HD12	57:RJ:281:PRO:HD2	2.01	0.43
60:RN:616:LEU:HB3	60:RN:619:LEU:HD13	2.01	0.43
60:RN:644:ASP:OD1	60:RN:687:LYS:NZ	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:RV:203:ILE:HG22	66:RV:204:GLY:H	1.84	0.43
66:RV:315:THR:HG23	66:RV:317:ASN:H	1.83	0.43
5:SF:163:ASP:OD2	5:SF:166:SER:N	2.51	0.43
6:SG:72:HIS:O	15:SR:79:TYR:OH	2.37	0.43
25:3F:209:LYS:HA	25:3F:209:LYS:HD2	1.82	0.43
25:3F:343:ASP:OD1	25:3F:343:ASP:N	2.46	0.43
25:3F:415:THR:OG1	25:3F:425:TRP:NE1	2.39	0.43
28:A5:281:ILE:HG12	28:A5:328:VAL:HB	2.01	0.43
30:A9:475:THR:HA	30:A9:478:ASN:HB2	1.99	0.43
32:AF:377:ASP:OD1	32:AF:377:ASP:N	2.51	0.43
32:AF:463:VAL:HA	32:AF:466:VAL:HG12	2.01	0.43
34:B1:847:ARG:O	34:B1:851:SER:OG	2.30	0.43
35:B2:596:ASN:HB3	35:B2:612:PHE:HA	1.99	0.43
37:B8:376:LEU:HG	37:B8:386:ILE:HG12	1.99	0.43
38:BE:24:PHE:HB3	38:BE:654:TRP:HB3	2.01	0.43
42:5D:145:GLU:OE1	42:5D:146:PHE:N	2.52	0.43
43:5E:335:ARG:HH22	57:RJ:952:PHE:HA	1.84	0.43
47:5I:344:HIS:NE2	47:5I:418:HIS:O	2.51	0.43
53:RE:911:PRO:HB2	53:RE:954:LEU:HD13	2.01	0.43
53:RE:1170:GLY:HA3	53:RE:1177:GLY:HA2	2.01	0.43
53:RE:1195:LYS:HE2	53:RE:1195:LYS:HB3	1.91	0.43
53:RE:1206:PRO:HB3	53:RE:1212:VAL:HG22	2.01	0.43
60:RN:700:LEU:HD21	61:RO:467:ALA:HB2	2.00	0.43
68:RY:489:GLN:O	68:RY:493:PHE:HB3	2.19	0.43
2:5A:474:A:OP2	41:5C:425:ARG:NH2	2.37	0.43
3:SA:1233:G:H1	3:SA:1253:U:H2'	1.83	0.43
4:SC:154:SER:O	4:SC:154:SER:OG	2.32	0.43
5:SF:182:TYR:CD2	5:SF:192:ILE:HD11	2.54	0.43
6:SG:103:ASN:HA	6:SG:106:LYS:HD2	2.01	0.43
8:SI:131:PHE:O	8:SI:133:THR:N	2.52	0.43
9:SJ:67:TRP:O	9:SJ:71:GLY:HA2	2.18	0.43
16:ST:120:ARG:NH1	43:5E:344:GLU:OE2	2.50	0.43
23:3D:52:SER:HB2	23:3D:85:ASN:HD21	1.84	0.43
24:3E:218:ALA:HA	24:3E:221:THR:HG22	2.00	0.43
24:3E:319:ILE:HD12	24:3E:326:LEU:HD22	2.01	0.43
25:3F:201:ILE:HG12	25:3F:538:ARG:HD3	2.00	0.43
27:A4:617:ASN:O	27:A4:621:ASN:HB2	2.19	0.43
29:A8:583:SER:HA	29:A8:586:ILE:HG22	2.00	0.43
33:AG:478:ASN:OD1	33:AG:478:ASN:N	2.51	0.43
34:B1:76:ASP:OD1	34:B1:76:ASP:N	2.51	0.43
35:B2:178:ILE:HD11	35:B2:186:ILE:HD11	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:B3:192:ALA:HB3	36:B3:216:ARG:HG3	2.00	0.43
37:B8:426:VAL:HG11	37:B8:455:ILE:HG21	2.01	0.43
38:BE:50:ILE:HD13	38:BE:311:VAL:HG11	2.01	0.43
41:5C:487:LYS:HD3	41:5C:490:VAL:HG11	2.00	0.43
45:5G:29:ARG:HD2	45:5G:59:ASP:HB3	2.01	0.43
45:5G:33:LYS:HB2	45:5G:33:LYS:HE3	1.79	0.43
45:5G:100:LEU:HD13	45:5G:144:GLU:HB3	2.01	0.43
53:RE:208:THR:OG1	53:RE:209:MET:N	2.52	0.43
57:RJ:831:ARG:HD3	57:RJ:838:ILE:HD12	2.01	0.43
60:RN:484:ARG:HB3	60:RN:492:ALA:HB1	2.01	0.43
60:RN:669:SER:HA	60:RN:672:THR:HG22	2.01	0.43
62:RP:1741:LYS:HD3	62:RP:1741:LYS:HA	1.90	0.43
3:SA:200:A:H2'	3:SA:201:G:H8	1.84	0.43
3:SA:555:A:N6	3:SA:571:G:O2'	2.50	0.43
3:SA:628:G:OP1	13:SO:120:SER:OG	2.37	0.43
3:SA:1169:G:N1	3:SA:1575:G:OP2	2.44	0.43
9:SJ:31:ARG:HH12	9:SJ:48:THR:HB	1.84	0.43
17:SX:12:ASN:O	17:SX:16:ASN:ND2	2.52	0.43
27:A4:313:LYS:HA	27:A4:316:LYS:HG2	2.01	0.43
28:A5:110:ILE:HG22	28:A5:119:CYS:HB2	2.00	0.43
28:A5:448:ASN:OD1	28:A5:450:HIS:NE2	2.52	0.43
31:AE:586:LEU:O	31:AE:590:ALA:HB2	2.18	0.43
32:AF:413:LEU:HA	32:AF:416:THR:HG22	2.00	0.43
33:AG:202:SER:OG	33:AG:204:ASN:OD1	2.30	0.43
34:B1:493:TRP:HA	34:B1:517:ASP:HB2	2.01	0.43
36:B3:133:ASN:OD1	36:B3:133:ASN:N	2.51	0.43
38:BE:627:ASN:ND2	38:BE:647:THR:OG1	2.52	0.43
40:5B:164:LYS:HB3	40:5B:164:LYS:HE3	1.76	0.43
41:5C:268:VAL:HG13	63:RQ:831:ILE:HG12	2.00	0.43
41:5C:544:ASP:HB3	41:5C:547:GLU:HB3	2.00	0.43
42:5D:102:GLN:HE21	57:RJ:1098:ARG:NH1	2.17	0.43
49:5K:61:PRO:HB3	49:5K:92:ALA:HB1	2.01	0.43
52:RC:116:ILE:HD13	52:RC:174:MET:HE3	2.01	0.43
53:RE:224:CYS:O	53:RE:227:LYS:HG3	2.19	0.43
54:RF:130:ASP:HB2	54:RF:133:SER:HB2	2.01	0.43
55:RG:75:GLY:HA2	55:RG:78:LYS:HE3	2.01	0.43
57:RJ:1080:LYS:HA	57:RJ:1080:LYS:HD2	1.80	0.43
60:RN:475:ARG:HH22	60:RN:516:LEU:HB3	1.84	0.43
1:3A:62:C:O2'	38:BE:447:ASN:O	2.35	0.42
3:SA:200:A:O2'	62:RP:1061:CYS:O	2.36	0.42
3:SA:327:U:OP2	11:SM:57:LYS:NZ	2.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:SF:45:ILE:O	5:SF:49:ARG:HB3	2.19	0.42
12:SN:79:ALA:HA	12:SN:85:LYS:HD2	2.01	0.42
17:SX:93:LEU:HD11	17:SX:102:VAL:HG22	2.01	0.42
24:3E:283:ILE:HD13	24:3E:283:ILE:HA	1.88	0.42
25:3F:414:ILE:HG13	25:3F:478:LEU:HD21	2.00	0.42
28:A5:441:LEU:HD11	28:A5:480:LEU:HD13	2.01	0.42
31:AE:476:ILE:HG23	31:AE:515:PHE:HE2	1.84	0.42
35:B2:351:LEU:HB2	35:B2:367:ILE:HG23	2.00	0.42
35:B2:369:TYR:HA	35:B2:374:PRO:HA	2.01	0.42
38:BE:470:GLN:HB3	38:BE:553:ARG:NH1	2.34	0.42
41:5C:230:THR:HG22	41:5C:232:ALA:H	1.83	0.42
46:5H:496:GLN:HA	46:5H:499:GLN:HG2	2.00	0.42
50:RA:95:ARG:NH2	50:RA:128:LYS:O	2.51	0.42
50:RA:254:ILE:HD12	50:RA:254:ILE:HA	1.84	0.42
57:RJ:1019:THR:HB	57:RJ:1022:LEU:HD12	2.01	0.42
57:RJ:1075:LYS:HE3	57:RJ:1075:LYS:HB2	1.84	0.42
61:RO:504:ASP:OD1	61:RO:504:ASP:N	2.48	0.42
64:RS:266:PHE:O	64:RS:270:LEU:HB3	2.18	0.42
64:RS:398:ARG:H	64:RS:406:GLY:HA3	1.83	0.42
64:RS:437:ARG:HH21	64:RS:463:GLY:HA3	1.84	0.42
2:5A:192:G:H2'	2:5A:193:G:C8	2.53	0.42
6:SG:39:GLU:OE1	6:SG:41:LYS:NZ	2.45	0.42
24:3E:132:SER:OG	24:3E:134:ASN:OD1	2.34	0.42
25:3F:160:ILE:HG12	25:3F:542:SER:HB2	2.00	0.42
27:A4:106:ASN:OD1	27:A4:106:ASN:N	2.51	0.42
28:A5:270:ASN:OD1	28:A5:270:ASN:N	2.49	0.42
29:A8:120:LEU:HA	29:A8:132:ILE:HA	2.01	0.42
32:AF:424:ARG:HA	33:AG:477:VAL:HG11	2.01	0.42
33:AG:555:VAL:HA	33:AG:556:PRO:HD3	1.89	0.42
33:AG:857:PHE:HE2	37:B8:226:LYS:HB3	1.84	0.42
35:B2:123:ALA:HB3	35:B2:141:LYS:HD3	2.00	0.42
36:B3:260:THR:HG22	36:B3:269:LEU:HD13	2.01	0.42
38:BE:353:PRO:HA	38:BE:370:SER:HA	2.01	0.42
39:B6:72:LYS:HD2	39:B6:72:LYS:HA	1.78	0.42
43:5E:370:ARG:HA	43:5E:373:ILE:HG22	2.01	0.42
45:5G:28:LYS:HB2	45:5G:46:LEU:HD21	2.01	0.42
46:5H:550:LEU:HD23	46:5H:550:LEU:HA	1.88	0.42
50:RA:217:LYS:HE2	50:RA:217:LYS:HB3	1.87	0.42
50:RA:277:ILE:HA	50:RA:290:VAL:O	2.19	0.42
55:RG:34:LYS:HD3	55:RG:34:LYS:HA	1.84	0.42
60:RN:65:ASN:OD1	60:RN:65:ASN:N	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:RO:208:TYR:O	61:RO:212:LEU:HB2	2.19	0.42
64:RS:382:LEU:HD11	64:RS:428:TYR:CG	2.55	0.42
3:SA:274:G:N1	3:SA:283:U:O2'	2.50	0.42
3:SA:1739:C:H2'	3:SA:1740:A:C8	2.53	0.42
22:3B:198:GLU:O	22:3B:221:ILE:HA	2.18	0.42
24:3E:160:ASP:HB3	24:3E:283:ILE:HG21	2.01	0.42
27:A4:532:ASN:N	27:A4:544:SER:O	2.50	0.42
27:A4:566:LEU:HA	27:A4:566:LEU:HD23	1.83	0.42
31:AE:323:PHE:CZ	31:AE:332:ILE:HD11	2.54	0.42
31:AE:354:SER:O	31:AE:358:TYR:HB2	2.20	0.42
31:AE:422:LEU:HD12	31:AE:422:LEU:HA	1.87	0.42
33:AG:437:THR:OG1	33:AG:764:SER:O	2.31	0.42
33:AG:551:HIS:HA	33:AG:583:LYS:HE3	2.00	0.42
34:B1:749:TYR:HE2	38:BE:705:ILE:HG13	1.84	0.42
35:B2:297:LYS:HA	35:B2:300:GLU:HB2	2.02	0.42
35:B2:636:ASP:OD1	35:B2:636:ASP:N	2.52	0.42
35:B2:673:VAL:HG23	35:B2:683:ILE:HD13	2.01	0.42
35:B2:840:MET:HE1	35:B2:887:LEU:HD13	2.02	0.42
36:B3:188:GLU:HB2	36:B3:223:TRP:HZ2	1.83	0.42
36:B3:572:GLU:HG3	36:B3:600:LYS:HD2	2.01	0.42
40:5B:213:LYS:HZ2	40:5B:213:LYS:HG3	1.69	0.42
43:5E:453:SER:O	43:5E:455:HIS:ND1	2.53	0.42
50:RA:306:LYS:HA	50:RA:306:LYS:HD2	1.83	0.42
53:RE:902:ILE:HD13	53:RE:902:ILE:HA	1.90	0.42
53:RE:1151:LYS:HE3	53:RE:1151:LYS:HB2	1.92	0.42
3:SA:-7:A:N7	47:5I:292:ARG:NH1	2.68	0.42
7:SH:74:LYS:O	50:RA:88:ASN:ND2	2.52	0.42
10:SK:163:PRO:HB3	10:SK:169:PRO:HA	2.01	0.42
22:3B:272:LYS:HD3	22:3B:275:CYS:HB3	2.01	0.42
33:AG:780:GLU:O	33:AG:782:THR:N	2.49	0.42
35:B2:39:GLY:O	35:B2:54:ILE:HG13	2.20	0.42
35:B2:294:ARG:O	35:B2:298:LYS:NZ	2.44	0.42
35:B2:432:TYR:O	35:B2:450:ARG:N	2.48	0.42
35:B2:497:VAL:HG12	35:B2:528:LEU:HB3	2.01	0.42
41:5C:215:LYS:HG2	41:5C:227:GLU:HG2	2.00	0.42
47:5I:456:GLU:HA	47:5I:459:LYS:HE2	2.01	0.42
48:5J:106:LEU:O	48:5J:146:ARG:NH1	2.44	0.42
51:RB:307:LYS:O	51:RB:311:ARG:HB3	2.19	0.42
53:RE:713:LEU:HB2	53:RE:716:SER:HB2	2.01	0.42
58:RK:81:ILE:HG22	58:RK:110:SER:HB3	2.01	0.42
59:RL:203:ASP:OD1	59:RL:203:ASP:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:RN:108:LYS:HA	60:RN:108:LYS:HD2	1.85	0.42
3:SA:99:C:H2'	3:SA:100:A:C8	2.54	0.42
3:SA:147:A:N7	3:SA:167:U:O2	2.52	0.42
3:SA:1659:A:H2'	3:SA:1660:A:C8	2.53	0.42
8:SI:51:VAL:HG23	8:SI:53:GLY:H	1.84	0.42
8:SI:188:GLU:HG3	47:5I:465:VAL:HG22	2.00	0.42
23:3D:4:ILE:HG23	23:3D:20:VAL:HG21	2.01	0.42
34:B1:25:ASP:OD1	34:B1:25:ASP:N	2.50	0.42
34:B1:46:LYS:HE2	34:B1:46:LYS:HB3	1.87	0.42
34:B1:275:LEU:HD22	34:B1:289:LEU:HD13	2.02	0.42
35:B2:534:ILE:HD11	35:B2:537:VAL:HG12	2.01	0.42
35:B2:836:ILE:HA	35:B2:839:VAL:HG12	2.00	0.42
38:BE:27:PHE:HB2	38:BE:655:THR:HG23	2.00	0.42
48:5J:216:ARG:HA	48:5J:216:ARG:HD3	1.82	0.42
53:RE:919:TRP:HE3	53:RE:920:LEU:HD12	1.85	0.42
53:RE:976:ILE:HA	53:RE:1042:ALA:O	2.19	0.42
53:RE:1102:LEU:HG	53:RE:1231:VAL:HA	2.02	0.42
61:RO:395:ILE:HD12	61:RO:469:LEU:HD11	2.02	0.42
64:RS:210:VAL:HG23	64:RS:212:LYS:HG2	2.00	0.42
2:5A:192:G:H2'	2:5A:193:G:H8	1.85	0.42
2:5A:532:A:O2'	63:RQ:332:ASP:OD2	2.37	0.42
5:SF:68:ARG:HH21	5:SF:76:VAL:HG11	1.85	0.42
6:SG:23:VAL:HG23	15:SR:61:SER:HB3	2.00	0.42
23:3D:61:GLU:OE2	23:3D:77:SER:OG	2.36	0.42
28:A5:221:MET:HE3	28:A5:221:MET:HB3	1.75	0.42
33:AG:511:GLU:HG2	33:AG:528:ILE:HB	2.00	0.42
38:BE:21:SER:OG	38:BE:621:ASP:OD2	2.28	0.42
38:BE:523:ASP:OD1	38:BE:523:ASP:N	2.38	0.42
45:5G:154:ILE:O	45:5G:162:THR:HA	2.20	0.42
47:5I:464:THR:HG21	47:5I:468:TYR:HE1	1.85	0.42
53:RE:1100:VAL:HG22	53:RE:1234:PHE:HD1	1.85	0.42
54:RF:153:ASN:HD22	54:RF:154:GLU:HG2	1.84	0.42
57:RJ:217:ASP:O	57:RJ:221:LEU:HB2	2.20	0.42
57:RJ:940:LYS:HB2	57:RJ:940:LYS:HE2	1.73	0.42
58:RK:310:ARG:HB3	58:RK:353:THR:HG22	2.01	0.42
60:RN:501:PHE:HB3	60:RN:549:ILE:HG21	2.02	0.42
62:RP:1945:ILE:HA	62:RP:1948:SER:HB2	2.01	0.42
64:RS:432:ILE:HG23	64:RS:436:GLN:HB2	2.00	0.42
65:RT:124:LEU:HG	65:RT:151:ALA:HB1	2.02	0.42
3:SA:341:A:OP1	50:RA:121:ARG:NH2	2.48	0.42
3:SA:1068:C:H2'	3:SA:1069:A:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:SC:181:LEU:HA	4:SC:181:LEU:HD23	1.86	0.42
5:SF:71:LYS:N	5:SF:91:THR:O	2.52	0.42
6:SG:114:ILE:HA	6:SG:117:THR:HG22	2.02	0.42
11:SM:92:HIS:NE2	11:SM:101:GLU:O	2.52	0.42
24:3E:172:ASP:O	24:3E:176:GLU:HG2	2.20	0.42
31:AE:487:THR:HG22	31:AE:488:GLY:H	1.85	0.42
31:AE:539:LEU:HD12	31:AE:540:LYS:HG3	2.01	0.42
34:B1:60:ALA:HB1	34:B1:102:VAL:HG12	2.02	0.42
34:B1:380:LEU:HD12	43:5E:484:MET:HE2	2.01	0.42
36:B3:674:SER:OG	36:B3:675:LYS:N	2.52	0.42
38:BE:62:ASP:O	38:BE:66:LEU:N	2.48	0.42
43:5E:427:SER:O	43:5E:431:GLN:HB2	2.19	0.42
52:RC:278:MET:O	52:RC:282:ASN:ND2	2.38	0.42
53:RE:379:MET:HE3	53:RE:381:HIS:HB2	2.02	0.42
53:RE:1216:LYS:HG2	53:RE:1220:PHE:CE2	2.55	0.42
54:RF:73:GLN:HE21	54:RF:156:PHE:HD2	1.65	0.42
55:RG:190:GLN:NE2	55:RG:244:GLY:HA2	2.34	0.42
67:RW:180:LYS:HE2	67:RW:180:LYS:HB2	1.83	0.42
1:3A:118:A:C5	25:3F:218:ALA:HB2	2.55	0.42
9:SJ:67:TRP:O	9:SJ:71:GLY:CA	2.68	0.42
10:SK:45:ILE:HD12	10:SK:48:GLN:HE21	1.84	0.42
11:SM:70:ILE:HA	11:SM:125:VAL:O	2.20	0.42
11:SM:115:PHE:CG	11:SM:142:VAL:HG21	2.55	0.42
16:ST:100:THR:O	16:ST:104:ASN:ND2	2.53	0.42
22:3C:124:SER:HA	22:3C:139:VAL:O	2.19	0.42
25:3F:560:ARG:HE	25:3F:560:ARG:HB3	1.75	0.42
28:A5:27:GLN:HG3	28:A5:59:LYS:HA	2.02	0.42
31:AE:25:ARG:HH21	47:5I:16:VAL:HG22	1.83	0.42
33:AG:313:LEU:HD23	33:AG:323:LEU:HB3	2.01	0.42
33:AG:559:LYS:HE2	33:AG:559:LYS:HB2	1.79	0.42
36:B3:367:VAL:HG12	36:B3:643:PHE:HE2	1.85	0.42
37:B8:504:THR:O	37:B8:504:THR:OG1	2.35	0.42
45:5G:175:ASP:O	60:RN:64:ARG:NH2	2.53	0.42
52:RC:219:ASP:OD2	52:RC:221:SER:OG	2.35	0.42
53:RE:486:GLN:HE22	53:RE:571:ARG:HH22	1.68	0.42
58:RK:56:ILE:HD13	58:RK:56:ILE:HA	1.89	0.42
58:RK:216:LEU:HB3	58:RK:223:VAL:HG21	2.01	0.42
59:RL:37:LEU:HD22	59:RL:149:VAL:HG11	2.01	0.42
59:RL:59:TYR:O	59:RL:108:TYR:N	2.53	0.42
62:RP:1877:ARG:NH2	62:RP:1913:SER:O	2.51	0.42
64:RS:364:PHE:HE1	64:RS:417:TRP:HE1	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:RS:373:LYS:HA	64:RS:376:LEU:HG	2.02	0.42
64:RS:382:LEU:HD21	64:RS:428:TYR:CZ	2.53	0.42
3:SA:565:C:N4	57:RJ:993:ASP:HB3	2.35	0.42
3:SA:1229:G:O6	12:SN:46:ARG:NH1	2.52	0.42
3:SA:1656:U:H3	3:SA:1743:U:H3	1.67	0.42
5:SF:47:PHE:HD2	5:SF:48:LEU:HD12	1.84	0.42
5:SF:220:THR:OG1	5:SF:221:ARG:N	2.53	0.42
8:SI:116:ARG:HB3	8:SI:117:THR:H	1.55	0.42
13:SO:58:HIS:O	13:SO:60:VAL:N	2.49	0.42
20:Sc:50:ALA:O	20:Sc:52:THR:N	2.53	0.42
27:A4:313:LYS:HA	27:A4:316:LYS:HZ3	1.84	0.42
28:A5:98:LYS:HE3	28:A5:98:LYS:HB2	1.88	0.42
34:B1:274:LEU:HD11	34:B1:286:LEU:HD13	2.02	0.42
36:B3:516:LYS:HE2	36:B3:516:LYS:HB2	1.89	0.42
38:BE:361:SER:HA	38:BE:636:PRO:HB2	2.02	0.42
45:5G:43:PRO:O	45:5G:47:ALA:HB2	2.19	0.42
50:RA:164:ARG:NH2	50:RA:174:ASN:O	2.51	0.42
53:RE:209:MET:HE3	53:RE:213:LEU:HD11	2.02	0.42
55:RG:128:VAL:HG22	55:RG:159:LEU:HD22	2.01	0.42
55:RH:176:ARG:NH2	55:RH:192:TYR:OH	2.52	0.42
57:RJ:773:THR:HG23	57:RJ:777:ARG:HD3	2.02	0.42
58:RK:190:SER:OG	58:RK:191:ILE:N	2.51	0.42
60:RN:700:LEU:HD23	60:RN:702:LEU:HG	2.01	0.42
64:RS:437:ARG:HD2	64:RS:460:LEU:HG	2.02	0.42
3:SA:575:C:O2	57:RJ:1052:SER:OG	2.28	0.42
4:SC:109:LYS:HA	4:SC:109:LYS:HD2	1.88	0.42
5:SF:31:PRO:HA	5:SF:81:THR:HB	2.01	0.42
7:SH:77:LEU:HD12	7:SH:95:LYS:HD3	2.00	0.42
7:SH:101:ILE:H	7:SH:101:ILE:HG13	1.72	0.42
16:ST:27:LYS:O	16:ST:31:ALA:HB2	2.19	0.42
17:SX:7:LEU:HD13	17:SX:34:ILE:HG12	2.02	0.42
22:3B:107:VAL:HG13	22:3B:141:TYR:HB3	2.01	0.42
24:3E:117:TYR:HA	24:3E:120:ILE:HG12	2.01	0.42
25:3F:303:LYS:HE3	25:3F:319:TYR:HE2	1.85	0.42
27:A4:98:SER:OG	27:A4:99:ILE:N	2.53	0.42
27:A4:213:TRP:HA	27:A4:225:LEU:HA	2.02	0.42
28:A5:224:CYS:SG	28:A5:225:VAL:N	2.93	0.42
29:A8:632:THR:HG22	30:A9:492:ILE:HD13	2.01	0.42
31:AE:91:ILE:HD13	31:AE:91:ILE:HA	1.90	0.42
31:AE:420:LYS:HB2	31:AE:420:LYS:HE2	1.91	0.42
33:AG:502:LYS:HD2	33:AG:564:PRO:HA	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B1:147:GLN:HB2	34:B1:167:ASP:H	1.85	0.42
35:B2:26:ILE:HA	35:B2:27:PRO:HD3	1.94	0.42
35:B2:405:LEU:HD11	35:B2:673:VAL:HG21	2.02	0.42
35:B2:555:VAL:HG22	35:B2:569:LEU:HB2	2.02	0.42
36:B3:303:PHE:HA	36:B3:312:GLN:O	2.20	0.42
41:5C:191:ILE:HD13	41:5C:191:ILE:HA	1.87	0.42
41:5C:369:MET:HB3	41:5C:369:MET:HE2	1.79	0.42
48:5J:134:ARG:HD2	48:5J:134:ARG:HA	1.83	0.42
52:RC:128:ILE:HD12	52:RC:191:MET:HE3	2.02	0.42
56:RI:85:GLU:OE2	56:RI:89:LYS:NZ	2.43	0.42
56:RI:105:ASN:N	56:RI:105:ASN:OD1	2.48	0.42
2:5A:490:G:H1'	2:5A:495:G:H5'	2.01	0.41
3:SA:318:U:O2	3:SA:346:G:O6	2.37	0.41
3:SA:1489:U:N3	48:5J:202:ARG:O	2.53	0.41
12:SN:59:LEU:HB2	12:SN:87:PRO:HG2	2.02	0.41
22:3C:149:SER:OG	22:3C:150:LYS:N	2.52	0.41
22:3C:291:GLN:HA	22:3C:294:ARG:HG2	2.01	0.41
24:3E:333:LYS:HD3	42:5D:103:ASP:HB3	2.02	0.41
25:3F:301:ASP:OD1	25:3F:301:ASP:N	2.51	0.41
25:3F:368:LEU:HB3	25:3F:396:PHE:HE2	1.83	0.41
26:3G:44:LEU:HD23	26:3G:44:LEU:HA	1.87	0.41
27:A4:423:LYS:NZ	40:5B:167:ARG:HH11	2.18	0.41
31:AE:755:ARG:O	31:AE:759:ILE:HG12	2.20	0.41
32:AF:105:VAL:HG21	32:AF:142:THR:HG21	2.02	0.41
45:5G:42:LEU:HD12	45:5G:43:PRO:HD2	2.02	0.41
47:5I:336:HIS:CE1	47:5I:338:HIS:HB2	2.55	0.41
53:RE:501:ASN:HD21	53:RE:506:GLN:HE22	1.66	0.41
53:RE:974:PRO:HB2	53:RE:976:ILE:HG23	2.02	0.41
55:RG:215:ASN:HB2	55:RG:218:ASP:HB2	2.01	0.41
60:RN:611:SER:OG	60:RN:612:THR:N	2.52	0.41
60:RN:616:LEU:HD13	60:RN:619:LEU:HD22	2.01	0.41
62:RP:129:ILE:O	62:RP:133:ILE:HG12	2.20	0.41
62:RP:1975:LYS:HA	62:RP:1975:LYS:HD2	1.80	0.41
65:RT:263:LEU:HA	65:RT:266:VAL:HG12	2.02	0.41
2:5A:150:G:C6	32:AF:380:ARG:HG3	2.54	0.41
2:5A:298:A:OP2	38:BE:103:ARG:NH2	2.45	0.41
13:SO:140:LYS:HA	13:SO:140:LYS:HD3	1.88	0.41
23:3D:268:MET:HA	23:3D:271:VAL:HG12	2.02	0.41
25:3F:421:ASN:ND2	25:3F:437:ARG:HA	2.34	0.41
25:3F:476:THR:HG22	25:3F:491:SER:HA	2.02	0.41
31:AE:35:TYR:O	31:AE:150:ARG:NH1	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:AE:664:PRO:HB2	31:AE:716:PHE:HE2	1.85	0.41
32:AF:366:TYR:OH	32:AF:371:GLU:OE1	2.23	0.41
33:AG:625:GLY:HA3	33:AG:662:VAL:HG11	2.02	0.41
33:AG:659:ILE:HG22	33:AG:674:THR:HB	2.01	0.41
34:B1:300:MET:HG2	34:B1:328:LEU:HD22	2.02	0.41
34:B1:498:ARG:HH11	34:B1:498:ARG:HD3	1.72	0.41
35:B2:538:ARG:HD3	35:B2:580:ASP:HA	2.02	0.41
36:B3:506:PHE:CE1	36:B3:518:TRP:HB2	2.55	0.41
38:BE:517:MET:HE3	38:BE:517:MET:HB2	1.85	0.41
38:BE:635:SER:OG	38:BE:637:ASN:OD1	2.30	0.41
41:5C:201:TYR:OH	41:5C:415:GLU:OE1	2.29	0.41
44:5F:73:LYS:HE2	44:5F:73:LYS:HB3	1.88	0.41
44:5F:135:HIS:HB3	44:5F:160:TRP:CD1	2.55	0.41
56:RI:192:ASN:OD1	56:RI:192:ASN:N	2.53	0.41
61:RO:243:PRO:HA	61:RO:244:PRO:HD3	1.81	0.41
62:RP:1756:ILE:HG22	62:RP:1760:ASN:HD21	1.85	0.41
64:RS:255:SER:HB3	64:RS:258:VAL:HG22	2.01	0.41
2:5A:223:C:O2	2:5A:224:G:O2'	2.38	0.41
2:5A:244:U:H1'	42:5D:93:MET:HE1	2.02	0.41
3:SA:360:A:O2'	3:SA:362:G:N2	2.45	0.41
7:SH:123:GLY:O	7:SH:127:THR:OG1	2.39	0.41
10:SK:154:LYS:HE2	10:SK:154:LYS:HB3	1.88	0.41
21:Sd:43:ASN:OD1	21:Sd:43:ASN:N	2.53	0.41
22:3B:150:LYS:NZ	22:3B:310:GLU:OE2	2.44	0.41
22:3C:242:ALA:HB3	22:3C:269:ILE:HA	2.01	0.41
23:3D:206:LEU:HB3	23:3D:216:PHE:HE1	1.84	0.41
30:A9:451:LEU:HA	30:A9:451:LEU:HD13	1.83	0.41
31:AE:148:PHE:HA	31:AE:151:ILE:HG12	2.01	0.41
31:AE:480:ASN:HA	31:AE:518:THR:HG21	2.02	0.41
32:AF:177:ILE:HA	32:AF:178:PRO:HD3	1.84	0.41
34:B1:275:LEU:HB2	34:B1:289:LEU:HD22	2.02	0.41
34:B1:363:ALA:HB2	34:B1:393:VAL:HG13	2.01	0.41
34:B1:501:SER:O	34:B1:506:SER:OG	2.38	0.41
34:B1:721:VAL:O	38:BE:579:ARG:NH2	2.53	0.41
39:B6:106:ASP:OD1	39:B6:106:ASP:N	2.38	0.41
41:5C:357:SER:O	41:5C:357:SER:OG	2.39	0.41
45:5G:289:TYR:HD1	45:5G:289:TYR:HA	1.68	0.41
53:RE:1010:GLU:HG2	53:RE:1011:ARG:HG2	2.01	0.41
58:RK:80:ILE:HD13	58:RK:80:ILE:HA	1.90	0.41
1:3A:49:C:H42	2:5A:467:A:H61	1.67	0.41
3:SA:647:G:N2	3:SA:687:G:H22	2.17	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:886:U:OP1	4:SC:214:LYS:NZ	2.54	0.41
3:SA:1049:U:H5''	20:Sc:70:LYS:HG3	2.01	0.41
7:SH:51:LYS:HE2	7:SH:51:LYS:HB3	1.91	0.41
15:SR:97:VAL:HG12	15:SR:98:ASP:H	1.83	0.41
24:3E:388:LEU:HD12	24:3E:388:LEU:HA	1.89	0.41
25:3F:132:VAL:HG21	25:3F:505:LEU:HD21	2.02	0.41
25:3F:260:LEU:HD21	25:3F:283:VAL:HG11	2.02	0.41
25:3F:304:ILE:HB	25:3F:318:LEU:HG	2.03	0.41
26:3G:64:LEU:O	26:3G:66:HIS:N	2.43	0.41
31:AE:559:ASN:HB2	31:AE:614:LEU:HD12	2.02	0.41
31:AE:682:SER:O	31:AE:682:SER:OG	2.33	0.41
32:AF:34:GLN:O	32:AF:328:ALA:HA	2.21	0.41
33:AG:258:TYR:CD1	33:AG:414:ILE:HD11	2.55	0.41
33:AG:386:ASN:HD21	33:AG:389:LEU:HD11	1.86	0.41
34:B1:347:SER:HB2	34:B1:365:GLU:HB3	2.03	0.41
34:B1:559:ILE:HG21	34:B1:578:LYS:HA	2.03	0.41
35:B2:50:ASN:HB3	35:B2:62:LYS:HG3	2.02	0.41
36:B3:195:GLY:HA3	36:B3:245:SER:H	1.85	0.41
36:B3:242:GLN:HA	36:B3:263:GLY:HA3	2.01	0.41
36:B3:264:ASP:HA	36:B3:289:PHE:HB2	2.03	0.41
37:B8:174:ARG:NE	37:B8:179:ASP:OD2	2.44	0.41
37:B8:278:ASP:H	37:B8:282:ASN:HD22	1.67	0.41
37:B8:296:GLN:HB3	37:B8:316:GLY:HA2	2.03	0.41
47:5I:58:PHE:HE1	47:5I:373:ARG:HB3	1.85	0.41
47:5I:107:LYS:NZ	47:5I:109:HIS:O	2.45	0.41
53:RE:477:LEU:HD23	53:RE:477:LEU:HA	1.94	0.41
53:RE:975:LEU:HG	53:RE:1041:VAL:HG23	2.01	0.41
53:RE:978:ASP:HB3	53:RE:1012:LEU:HG	2.02	0.41
56:RI:114:LYS:H	56:RI:114:LYS:HG2	1.72	0.41
56:RI:215:ASN:HA	56:RI:218:ASP:HB2	2.03	0.41
57:RJ:244:MET:HE2	57:RJ:271:ILE:HG22	2.02	0.41
57:RJ:1042:MET:HE2	57:RJ:1042:MET:HB3	1.87	0.41
58:RK:32:LYS:HG2	58:RK:75:ILE:HG13	2.02	0.41
59:RL:26:PHE:O	59:RL:149:VAL:HA	2.20	0.41
60:RN:481:MET:HE3	60:RN:481:MET:HB2	1.92	0.41
62:RP:1752:ASP:HA	62:RP:1755:GLU:HG2	2.03	0.41
64:RS:355:ALA:HA	64:RS:358:TYR:CE2	2.55	0.41
2:5A:248:G:OP1	42:5D:82:ARG:NH2	2.53	0.41
5:SF:181:VAL:HG23	5:SF:227:VAL:HG22	2.02	0.41
14:SP:127:ARG:HE	52:RC:130:ASN:HD21	1.68	0.41
15:SR:46:PHE:HA	15:SR:49:TYR:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:3C:151:LEU:HD13	22:3C:241:PHE:HE1	1.86	0.41
24:3E:163:ILE:HD13	24:3E:163:ILE:HA	1.86	0.41
25:3F:488:ILE:HG22	25:3F:524:ILE:HD13	2.02	0.41
27:A4:39:VAL:HG12	27:A4:41:PHE:H	1.85	0.41
27:A4:171:SER:O	27:A4:171:SER:OG	2.32	0.41
28:A5:32:GLN:HE22	28:A5:47:ASN:HB3	1.85	0.41
31:AE:526:LEU:HA	31:AE:529:VAL:HG12	2.01	0.41
32:AF:392:ILE:HD11	32:AF:417:VAL:HG23	2.03	0.41
33:AG:97:THR:OG1	33:AG:98:VAL:N	2.54	0.41
33:AG:544:LYS:HD3	33:AG:544:LYS:HA	1.88	0.41
35:B2:433:ALA:HA	35:B2:449:THR:HA	2.03	0.41
45:5G:133:LYS:HE3	45:5G:133:LYS:HB3	1.85	0.41
50:RA:164:ARG:HB2	50:RA:173:LEU:HB2	2.03	0.41
53:RE:708:LEU:HA	53:RE:709:PRO:HD3	1.96	0.41
57:RJ:552:LEU:HD23	57:RJ:552:LEU:HA	1.92	0.41
58:RK:286:SER:OG	58:RK:289:VAL:O	2.33	0.41
60:RN:515:HIS:O	60:RN:519:THR:OG1	2.32	0.41
62:RP:1923:ARG:HA	62:RP:1923:ARG:HD3	1.71	0.41
63:RQ:313:PHE:HE2	63:RQ:883:ILE:HD12	1.84	0.41
3:SA:88:U:H2'	3:SA:89:G:H8	1.85	0.41
3:SA:110:U:OP1	51:RB:227:ARG:NH1	2.53	0.41
3:SA:1156:C:H2'	3:SA:1157:A:C8	2.54	0.41
3:SA:1523:G:H1'	3:SA:1524:A:H5'	2.02	0.41
3:SA:1534:G:O2'	3:SA:1535:U:O2	2.29	0.41
22:3C:89:GLU:HG2	22:3C:98:ILE:HB	2.03	0.41
27:A4:154:ASP:OD1	27:A4:154:ASP:N	2.49	0.41
27:A4:394:TRP:HB3	27:A4:399:VAL:HG12	2.03	0.41
28:A5:551:ILE:HA	28:A5:554:PHE:CE2	2.56	0.41
31:AE:109:TRP:HB2	31:AE:142:TYR:CZ	2.56	0.41
33:AG:31:ASN:OD1	33:AG:31:ASN:N	2.52	0.41
33:AG:712:THR:HG22	33:AG:766:ILE:HG23	2.01	0.41
34:B1:150:THR:OG1	34:B1:164:THR:OG1	2.31	0.41
34:B1:659:ASN:OD1	34:B1:659:ASN:N	2.54	0.41
35:B2:164:ASP:HB3	35:B2:182:LYS:HB3	2.02	0.41
36:B3:218:ASP:OD1	36:B3:218:ASP:N	2.52	0.41
37:B8:137:ILE:HD13	37:B8:137:ILE:HA	1.86	0.41
37:B8:159:HIS:O	37:B8:163:ARG:HG2	2.21	0.41
37:B8:278:ASP:H	37:B8:282:ASN:ND2	2.18	0.41
39:B6:35:LYS:HE3	39:B6:35:LYS:HB3	1.88	0.41
39:B6:268:ASP:OD1	39:B6:268:ASP:N	2.53	0.41
39:B6:311:TYR:O	39:B6:315:GLU:HG2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:5C:244:ASN:HB3	41:5C:446:PRO:HG3	2.02	0.41
43:5E:465:LEU:HD12	43:5E:465:LEU:HA	1.96	0.41
45:5G:9:ARG:HD3	45:5G:159:HIS:CD2	2.56	0.41
46:5H:542:TYR:CZ	46:5H:546:LYS:HG3	2.56	0.41
54:RF:9:MET:HE1	54:RF:15:VAL:HG23	2.02	0.41
55:RH:180:LEU:HD23	55:RH:180:LEU:HA	1.88	0.41
66:RV:147:GLU:HG2	66:RV:150:GLN:H	1.85	0.41
1:3A:113:G:O6	26:3H:42:LYS:NZ	2.44	0.41
7:SH:70:PRO:O	7:SH:98:ARG:NH2	2.54	0.41
7:SH:115:LYS:HB2	7:SH:115:LYS:HE3	1.76	0.41
11:SM:82:ARG:HD3	11:SM:110:HIS:CD2	2.55	0.41
11:SM:115:PHE:HB2	11:SM:142:VAL:HG11	2.03	0.41
22:3C:210:MET:HE2	22:3C:210:MET:HB2	1.97	0.41
24:3E:192:PHE:CD2	24:3E:195:LEU:HB2	2.56	0.41
25:3F:158:THR:HG23	25:3F:548:ARG:HB2	2.02	0.41
25:3F:321:HIS:CE1	25:3F:340:GLY:H	2.39	0.41
25:3F:502:SER:OG	25:3F:504:ASN:OD1	2.32	0.41
28:A5:64:LYS:HB3	28:A5:77:ILE:HG13	2.02	0.41
30:A9:416:ILE:O	30:A9:420:ILE:CB	2.69	0.41
31:AE:549:LYS:HD3	31:AE:549:LYS:HA	1.91	0.41
32:AF:255:VAL:HA	32:AF:276:SER:HA	2.03	0.41
34:B1:410:THR:HG22	34:B1:426:THR:HG22	2.01	0.41
34:B1:652:ASP:N	34:B1:652:ASP:OD1	2.52	0.41
36:B3:468:ILE:HA	36:B3:469:PRO:HD3	1.83	0.41
48:5J:117:VAL:HG11	48:5J:149:ILE:HG13	2.02	0.41
50:RA:94:ASP:OD1	50:RA:94:ASP:N	2.54	0.41
53:RE:356:THR:HG23	53:RE:359:PHE:HB2	2.02	0.41
53:RE:841:ASN:ND2	53:RE:851:LYS:HG2	2.35	0.41
55:RG:232:LEU:HB3	55:RG:236:VAL:HG13	2.02	0.41
60:RN:283:ALA:HA	64:RS:381:ALA:HB1	2.03	0.41
60:RN:784:ILE:HA	60:RN:787:THR:HG22	2.03	0.41
64:RS:264:LYS:HB2	64:RS:264:LYS:HE3	1.81	0.41
2:5A:210:U:H2'	2:5A:211:G:C8	2.56	0.41
2:5A:211:G:OP1	40:5B:161:LYS:NZ	2.54	0.41
3:SA:200:A:H2'	3:SA:201:G:C8	2.56	0.41
9:SJ:35:ASN:HD21	50:RA:119:ASN:HD22	1.69	0.41
9:SJ:58:LEU:HD21	50:RA:77:TYR:HB2	2.02	0.41
10:SK:63:ASP:OD1	10:SK:63:ASP:N	2.46	0.41
12:SN:135:MET:HG3	12:SN:139:HIS:CE1	2.55	0.41
16:ST:26:ILE:HG13	16:ST:31:ALA:HB2	2.03	0.41
23:3D:24:GLN:NE2	23:3D:126:ASP:OD1	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A4:389:ARG:HG2	27:A4:747:ILE:HG21	2.02	0.41
27:A4:428:ILE:HD12	27:A4:444:ARG:HH21	1.85	0.41
28:A5:49:ASN:OD1	28:A5:49:ASN:N	2.49	0.41
29:A8:703:LEU:HA	29:A8:704:PRO:HD3	1.96	0.41
31:AE:32:SER:OG	31:AE:33:LEU:N	2.54	0.41
31:AE:33:LEU:HD11	31:AE:151:ILE:HG22	2.03	0.41
31:AE:69:PHE:HE2	31:AE:104:LEU:HD13	1.85	0.41
31:AE:572:ARG:NH2	31:AE:632:THR:O	2.40	0.41
31:AE:597:HIS:HB3	31:AE:615:ASN:HB3	2.03	0.41
33:AG:439:ASN:ND2	33:AG:496:THR:O	2.54	0.41
33:AG:514:TYR:HA	33:AG:515:PRO:HD3	1.94	0.41
36:B3:90:LEU:O	36:B3:92:THR:N	2.54	0.41
38:BE:870:GLN:HA	38:BE:873:LYS:HE3	2.03	0.41
41:5C:504:LYS:HD3	41:5C:504:LYS:HA	1.83	0.41
50:RA:237:ARG:NE	50:RA:239:ASP:OD2	2.46	0.41
53:RE:217:LYS:HD3	53:RE:217:LYS:HA	1.83	0.41
53:RE:360:VAL:O	53:RE:363:THR:OG1	2.30	0.41
54:RF:153:ASN:ND2	54:RF:154:GLU:HG2	2.36	0.41
55:RG:40:ARG:O	55:RG:201:SER:HA	2.20	0.41
59:RL:185:ASN:OD1	59:RL:185:ASN:N	2.52	0.41
61:RO:226:ASP:OD1	61:RO:284:ARG:NE	2.54	0.41
62:RP:2073:GLU:HA	62:RP:2076:ARG:HG2	2.03	0.41
64:RS:238:SER:O	64:RS:238:SER:OG	2.33	0.41
2:5A:18:G:H2'	2:5A:19:A:H8	1.85	0.41
2:5A:329:A:O2'	2:5A:331:U:OP2	2.39	0.41
3:SA:153:G:O6	3:SA:161:U:O4	2.39	0.41
3:SA:406:U:O2'	50:RA:92:LYS:O	2.38	0.41
3:SA:1538:U:H1'	3:SA:1570:A:H61	1.84	0.41
4:SC:82:ARG:HD3	4:SC:105:PHE:HE1	1.86	0.41
7:SH:185:GLN:O	7:SH:189:HIS:ND1	2.44	0.41
9:SJ:36:THR:O	9:SJ:96:LEU:N	2.52	0.41
9:SJ:49:ARG:HA	9:SJ:49:ARG:HD3	1.83	0.41
12:SN:83:GLU:HG3	12:SN:85:LYS:HB2	2.03	0.41
14:SP:125:SER:HB2	14:SP:126:THR:H	1.73	0.41
22:3B:116:SER:OG	22:3B:120:GLU:OE1	2.28	0.41
23:3D:7:LEU:HD12	23:3D:99:ALA:HB3	2.02	0.41
23:3D:157:ALA:HB2	39:B6:292:TYR:CZ	2.56	0.41
24:3E:311:LYS:HB3	24:3E:311:LYS:HE2	1.84	0.41
25:3F:457:GLU:HG3	25:3F:461:LYS:HE2	2.02	0.41
26:3G:85:VAL:O	26:3G:89:ARG:HG2	2.21	0.41
27:A4:52:SER:HA	27:A4:104:TRP:CG	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A4:249:ARG:NH2	27:A4:309:GLN:OE1	2.49	0.41
27:A4:513:LEU:HD12	27:A4:513:LEU:HA	1.89	0.41
27:A4:581:SER:HA	27:A4:594:PHE:O	2.21	0.41
30:A9:475:THR:HA	30:A9:478:ASN:HD22	1.86	0.41
31:AE:214:THR:HG23	31:AE:260:ILE:HG13	2.03	0.41
31:AE:227:ASN:OD1	31:AE:227:ASN:N	2.53	0.41
32:AF:287:LEU:HD13	32:AF:287:LEU:HA	1.96	0.41
33:AG:455:SER:O	33:AG:455:SER:OG	2.34	0.41
33:AG:591:GLU:O	33:AG:593:ASN:N	2.54	0.41
33:AG:666:ASN:OD1	33:AG:666:ASN:N	2.54	0.41
34:B1:492:SER:OG	34:B1:494:ASP:OD1	2.28	0.41
35:B2:17:ILE:CG2	35:B2:52:TRP:CH2	3.01	0.41
36:B3:567:VAL:HG22	36:B3:568:MET:HG2	2.02	0.41
37:B8:338:LYS:HE3	37:B8:338:LYS:HB2	1.89	0.41
38:BE:724:SER:O	38:BE:728:ARG:NH2	2.39	0.41
39:B6:15:MET:HE2	39:B6:15:MET:HB3	1.67	0.41
41:5C:117:LYS:HD2	41:5C:117:LYS:HA	1.85	0.41
41:5C:491:LYS:HA	41:5C:491:LYS:HD3	1.94	0.41
47:5I:400:LEU:HD12	47:5I:400:LEU:HA	1.89	0.41
48:5J:119:ARG:HD3	57:RJ:1113:ILE:HG13	2.02	0.41
50:RA:139:LYS:HA	50:RA:139:LYS:HD2	1.89	0.41
53:RE:566:ILE:HD11	53:RE:686:LEU:HD21	2.03	0.41
53:RE:970:TRP:HB2	53:RE:971:LYS:HD3	2.02	0.41
55:RG:31:LEU:HD23	55:RG:31:LEU:HA	1.86	0.41
55:RG:116:THR:HG22	55:RG:118:ARG:H	1.86	0.41
55:RG:123:GLU:HB2	55:RG:161:LYS:HB2	2.03	0.41
55:RG:233:SER:OG	55:RG:234:ALA:N	2.54	0.41
55:RH:177:LYS:HG2	55:RH:203:CYS:HB3	2.03	0.41
57:RJ:43:MET:N	57:RJ:43:MET:SD	2.94	0.41
57:RJ:906:ASP:OD1	57:RJ:906:ASP:N	2.45	0.41
57:RJ:926:ILE:HG12	57:RJ:928:ILE:HG23	2.01	0.41
58:RK:117:LEU:HA	58:RK:166:VAL:O	2.21	0.41
62:RP:76:THR:O	62:RP:79:GLN:N	2.54	0.41
62:RP:879:PRO:O	62:RP:882:ASN:C	2.64	0.41
64:RS:288:ARG:O	64:RS:292:GLU:HG2	2.21	0.41
64:RS:407:GLU:HB2	64:RS:411:ARG:HD2	2.03	0.41
2:5A:333:G:H5'	44:5F:49:ARG:HE	1.86	0.41
2:5A:460:U:OP1	49:5K:21:LYS:NZ	2.42	0.41
3:SA:27:U:H4'	57:RJ:45:ARG:HG3	2.02	0.41
3:SA:1492:A:N6	57:RJ:941:ILE:O	2.46	0.41
3:SA:1655:A:O2'	35:B2:395:ARG:NH1	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:1776:A:O2'	36:B3:136:ILE:O	2.34	0.41
4:SC:31:ASP:HA	4:SC:45:LYS:HA	2.03	0.41
14:SP:29:HIS:CD2	14:SP:41:ARG:HB2	2.56	0.41
24:3E:201:ASP:HB3	24:3E:204:ALA:HB3	2.03	0.41
27:A4:425:ASP:OD2	27:A4:444:ARG:NH2	2.53	0.41
29:A8:532:PHE:HD1	29:A8:534:LEU:H	1.69	0.41
32:AF:136:ASP:OD1	32:AF:137:ASN:N	2.54	0.41
32:AF:364:SER:O	32:AF:364:SER:OG	2.26	0.41
32:AF:492:ARG:HD3	32:AF:492:ARG:HA	1.80	0.41
34:B1:263:VAL:HG13	34:B1:277:VAL:HG13	2.03	0.41
35:B2:241:LYS:HB2	35:B2:241:LYS:HE3	1.89	0.41
35:B2:911:GLN:HA	35:B2:914:LEU:HG	2.02	0.41
36:B3:410:ASN:OD1	36:B3:435:ALA:N	2.52	0.41
38:BE:83:LEU:HA	38:BE:91:TYR:O	2.21	0.41
39:B6:26:LYS:HA	39:B6:29:VAL:HG12	2.03	0.41
39:B6:306:LYS:HE3	39:B6:306:LYS:HB2	1.77	0.41
47:5I:225:LEU:HA	47:5I:225:LEU:HD23	1.87	0.41
53:RE:177:ASN:HB2	53:RE:213:LEU:HB2	2.03	0.41
53:RE:1098:PHE:HE1	53:RE:1216:LYS:HE2	1.86	0.41
60:RN:668:LEU:HD23	60:RN:671:TYR:HD2	1.86	0.41
62:RP:149:GLU:HA	62:RP:152:PHE:CD2	2.56	0.41
66:RV:229:ASN:OD1	66:RV:229:ASN:N	2.54	0.41
2:5A:423:C:H2'	2:5A:424:G:H8	1.86	0.40
3:SA:304:U:H5''	11:SM:136:ARG:HH21	1.86	0.40
7:SH:38:GLY:N	7:SH:48:TYR:O	2.54	0.40
8:SI:60:ILE:HB	8:SI:92:PHE:HD1	1.86	0.40
17:SX:102:VAL:O	17:SX:113:HIS:N	2.54	0.40
24:3E:162:MET:HB3	24:3E:162:MET:HE2	1.86	0.40
25:3F:212:LYS:HB2	25:3F:212:LYS:HE3	1.88	0.40
27:A4:250:THR:OG1	27:A4:251:ASP:N	2.53	0.40
30:A9:432:LYS:HA	30:A9:432:LYS:HD3	1.85	0.40
31:AE:688:PHE:HB3	31:AE:730:GLN:HE21	1.86	0.40
32:AF:183:LEU:HD12	32:AF:183:LEU:HA	1.85	0.40
32:AF:397:TRP:CZ3	32:AF:425:GLY:HA3	2.56	0.40
34:B1:519:LEU:HD13	34:B1:581:THR:HG22	2.03	0.40
34:B1:523:MET:HE2	34:B1:523:MET:HB2	1.76	0.40
36:B3:678:TRP:CE3	36:B3:697:VAL:HG23	2.56	0.40
42:5D:70:ARG:HD3	42:5D:78:LEU:HD11	2.02	0.40
48:5J:77:LYS:HA	48:5J:77:LYS:HD2	1.84	0.40
53:RE:110:LEU:HD21	53:RE:368:LEU:HD23	2.03	0.40
53:RE:202:SER:OG	53:RE:203:ILE:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:RE:676:PRO:HB2	53:RE:678:ILE:HG22	2.03	0.40
54:RF:62:SER:HA	54:RF:66:HIS:NE2	2.36	0.40
55:RG:176:ARG:HA	55:RG:176:ARG:HD2	1.91	0.40
58:RK:184:ASP:OD1	58:RK:185:ARG:N	2.53	0.40
60:RN:504:ILE:HA	60:RN:507:LEU:HG	2.03	0.40
2:5A:393:C:O4'	44:5F:28:ARG:NH2	2.54	0.40
3:SA:1525:A:N3	3:SA:1589:C:O2'	2.53	0.40
3:SA:1672:G:H2'	3:SA:1673:G:C8	2.55	0.40
5:SF:97:GLU:HB3	5:SF:99:PHE:CE2	2.56	0.40
17:SX:110:ILE:HD12	17:SX:126:LEU:HD22	2.02	0.40
22:3B:248:ASP:OD1	22:3B:248:ASP:N	2.37	0.40
22:3C:202:ARG:HA	22:3C:202:ARG:HD2	1.96	0.40
24:3E:88:ILE:HA	24:3E:106:ASN:O	2.22	0.40
26:3G:41:THR:HG21	26:3G:66:HIS:CE1	2.55	0.40
26:3H:33:LEU:HD11	26:3H:100:ALA:HB1	2.02	0.40
27:A4:141:SER:O	27:A4:141:SER:OG	2.34	0.40
32:AF:57:VAL:HG21	32:AF:327:LEU:HD11	2.04	0.40
32:AF:426:LYS:HB3	32:AF:429:VAL:HB	2.03	0.40
34:B1:430:ARG:HH21	43:5E:458:PRO:HB2	1.85	0.40
35:B2:639:VAL:HG22	35:B2:653:LEU:HB2	2.03	0.40
36:B3:25:VAL:HG22	36:B3:294:LEU:HD13	2.03	0.40
36:B3:313:LEU:O	36:B3:330:THR:OG1	2.33	0.40
38:BE:265:SER:O	38:BE:265:SER:OG	2.39	0.40
38:BE:290:ILE:HG23	38:BE:291:HIS:CD2	2.56	0.40
39:B6:304:LEU:O	39:B6:308:THR:HG23	2.21	0.40
41:5C:340:LEU:HD22	41:5C:403:VAL:HG11	2.03	0.40
48:5J:106:LEU:HD23	48:5J:106:LEU:HA	1.95	0.40
48:5J:195:GLN:O	48:5J:199:THR:HG22	2.22	0.40
56:RI:85:GLU:O	56:RI:89:LYS:HG2	2.22	0.40
56:RI:220:ILE:O	56:RI:224:THR:HG22	2.21	0.40
61:RO:422:ILE:HD13	61:RO:422:ILE:HA	1.93	0.40
62:RP:100:GLU:OE2	62:RP:146:ASN:ND2	2.54	0.40
64:RS:245:VAL:O	64:RS:249:THR:HG23	2.22	0.40
3:SA:16:G:H4'	49:5K:159:GLY:HA2	2.03	0.40
3:SA:268:C:H2'	3:SA:269:G:C8	2.56	0.40
3:SA:298:C:H5''	5:SF:38:LEU:HG	2.02	0.40
3:SA:625:C:H2'	3:SA:626:U:C6	2.57	0.40
5:SF:106:LYS:HE3	5:SF:106:LYS:HB3	1.88	0.40
10:SK:79:ARG:HE	10:SK:79:ARG:HB3	1.78	0.40
22:3C:165:ALA:HB3	22:3C:168:LYS:HD3	2.04	0.40
23:3D:182:ASP:OD1	23:3D:314:ARG:NH2	2.39	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:3E:248:THR:OG1	24:3E:251:ASP:OD1	2.29	0.40
24:3E:367:ALA:O	24:3E:371:LEU:HB3	2.22	0.40
24:3E:431:ALA:O	37:B8:160:TYR:OH	2.28	0.40
25:3F:263:TRP:HA	25:3F:269:SER:O	2.22	0.40
25:3F:465:GLN:HG2	26:3H:6:PRO:HG3	2.03	0.40
27:A4:429:SER:OG	27:A4:430:THR:N	2.52	0.40
33:AG:29:THR:HB	33:AG:198:LEU:HD11	2.03	0.40
33:AG:560:ILE:HG22	33:AG:575:THR:HG22	2.03	0.40
36:B3:415:TRP:HA	36:B3:425:ASP:O	2.20	0.40
37:B8:431:GLU:H	37:B8:431:GLU:HG2	1.71	0.40
39:B6:110:TRP:CD2	39:B6:136:LEU:HD13	2.56	0.40
41:5C:114:TYR:HA	41:5C:128:THR:O	2.22	0.40
41:5C:495:SER:OG	41:5C:523:GLU:OE2	2.27	0.40
43:5E:358:THR:HG22	60:RN:88:LYS:HB3	2.03	0.40
50:RA:343:ILE:HG22	50:RA:346:LEU:H	1.87	0.40
53:RE:310:PRO:HA	53:RE:333:ASN:HD21	1.87	0.40
53:RE:518:PHE:CZ	53:RE:1075:LEU:HB3	2.56	0.40
57:RJ:60:ASP:OD2	57:RJ:62:THR:OG1	2.32	0.40
57:RJ:74:VAL:HG11	57:RJ:82:LYS:HA	2.03	0.40
57:RJ:563:CYS:SG	58:RK:327:ARG:NH2	2.95	0.40
59:RL:60:LYS:HB3	59:RL:108:TYR:CD2	2.56	0.40
60:RN:424:LYS:O	60:RN:428:VAL:HG23	2.20	0.40
64:RS:446:GLN:HG2	64:RS:447:ARG:HE	1.86	0.40
1:3A:253:G:OP2	26:3H:95:ARG:NH1	2.54	0.40
3:SA:259:U:O2'	3:SA:261:U:OP2	2.32	0.40
3:SA:514:G:H2'	3:SA:515:A:H8	1.87	0.40
3:SA:1463:C:H2'	3:SA:1464:G:O4'	2.22	0.40
3:SA:1464:G:H2'	3:SA:1465:C:C6	2.57	0.40
3:SA:1480:G:H2'	3:SA:1481:C:O4'	2.22	0.40
4:SC:87:ARG:NH1	4:SC:89:ASP:OD2	2.47	0.40
12:SN:90:LYS:HD2	12:SN:90:LYS:HA	1.80	0.40
17:SX:66:ASN:OD1	17:SX:66:ASN:N	2.50	0.40
22:3B:227:PRO:HG2	22:3B:255:LEU:HB3	2.02	0.40
23:3D:86:LEU:HD21	23:3D:98:LEU:HD13	2.03	0.40
23:3D:315:LEU:HD12	23:3D:315:LEU:HA	1.90	0.40
24:3E:215:ARG:NH1	24:3E:244:GLY:O	2.54	0.40
24:3E:299:LEU:HD22	24:3E:320:LEU:HD23	2.03	0.40
24:3E:306:LEU:HG	24:3E:375:ALA:HB2	2.04	0.40
24:3E:359:ILE:HD13	24:3E:398:LEU:HD13	2.03	0.40
27:A4:442:VAL:O	27:A4:448:THR:OG1	2.26	0.40
32:AF:371:GLU:HG3	37:B8:287:SER:OG	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:AG:409:LYS:HG2	33:AG:489:ASN:HA	2.03	0.40
34:B1:423:ARG:HD3	34:B1:423:ARG:HA	1.88	0.40
36:B3:189:HIS:NE2	36:B3:215:GLY:HA3	2.37	0.40
36:B3:393:SER:OG	36:B3:394:LEU:N	2.53	0.40
38:BE:366:MET:HE3	38:BE:366:MET:HB2	1.80	0.40
38:BE:743:ARG:HB2	43:5E:475:SER:HA	2.02	0.40
42:5D:218:MET:HE3	42:5D:218:MET:HB2	1.85	0.40
52:RC:149:ASN:HD21	66:RV:274:LYS:HD3	1.86	0.40
53:RE:918:ARG:HD3	53:RE:1089:PHE:HE2	1.86	0.40
54:RF:47:SER:OG	54:RF:48:ASN:N	2.54	0.40
54:RF:71:VAL:HG11	54:RF:84:VAL:HG21	2.03	0.40
60:RN:572:LEU:HB3	60:RN:667:LEU:HD13	2.04	0.40
60:RN:710:ILE:HD13	60:RN:710:ILE:HA	1.91	0.40
61:RO:205:ASP:HA	61:RO:206:PRO:HD3	1.89	0.40
61:RO:326:LEU:HA	61:RO:326:LEU:HD12	1.90	0.40
61:RO:384:ALA:HA	61:RO:387:THR:HG22	2.03	0.40
1:3A:59:G:OP1	34:B1:573:ASN:ND2	2.43	0.40
3:SA:56:U:O2	3:SA:91:G:N2	2.54	0.40
3:SA:1071:U:H2'	3:SA:1072:C:C6	2.56	0.40
9:SJ:191:PHE:HA	9:SJ:194:ARG:HE	1.85	0.40
10:SK:37:LYS:O	46:5H:561:SER:OG	2.39	0.40
15:SR:47:LYS:HD2	15:SR:47:LYS:HA	1.93	0.40
19:SZ:13:ILE:HD11	19:SZ:22:GLN:HE21	1.85	0.40
23:3D:59:ALA:HB1	39:B6:292:TYR:HE1	1.87	0.40
25:3F:68:LYS:HE3	25:3F:68:LYS:HB2	1.93	0.40
28:A5:444:ALA:HB2	28:A5:452:LEU:HD12	2.03	0.40
29:A8:642:LEU:HD12	30:A9:499:ILE:HG23	2.04	0.40
31:AE:677:SER:HA	31:AE:678:PRO:HD3	1.98	0.40
32:AF:178:PRO:HD2	32:AF:223:PRO:HA	2.02	0.40
33:AG:865:LYS:HE2	33:AG:865:LYS:HB3	1.81	0.40
34:B1:103:LYS:HB3	34:B1:103:LYS:HE3	1.92	0.40
34:B1:567:ASP:HB3	44:5F:144:ASN:ND2	2.36	0.40
35:B2:85:LEU:HD12	35:B2:94:LEU:HD11	2.04	0.40
36:B3:51:LYS:H	36:B3:51:LYS:HG2	1.66	0.40
36:B3:698:LEU:HD23	36:B3:698:LEU:HA	1.92	0.40
41:5C:258:LEU:O	41:5C:267:LEU:N	2.54	0.40
41:5C:307:LYS:HA	41:5C:307:LYS:HD3	1.89	0.40
44:5F:120:MET:HE3	44:5F:120:MET:HB2	1.98	0.40
48:5J:121:LEU:HD22	48:5J:141:TRP:HH2	1.87	0.40
53:RE:883:LEU:HD22	53:RE:1051:LEU:HA	2.03	0.40
57:RJ:286:THR:H	57:RJ:298:VAL:HG12	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:RP:2009:LYS:HD3	62:RP:2009:LYS:HA	1.88	0.40
64:RS:258:VAL:O	64:RS:262:ALA:CB	2.69	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	SC	228/255 (89%)	196 (86%)	32 (14%)	0	100	100
5	SF	227/261 (87%)	197 (87%)	29 (13%)	1 (0%)	30	62
6	SG	211/225 (94%)	195 (92%)	16 (8%)	0	100	100
7	SH	161/236 (68%)	143 (89%)	18 (11%)	0	100	100
8	SI	161/190 (85%)	143 (89%)	18 (11%)	0	100	100
9	SJ	162/200 (81%)	140 (86%)	22 (14%)	0	100	100
10	SK	169/197 (86%)	163 (96%)	6 (4%)	0	100	100
11	SM	119/156 (76%)	103 (87%)	16 (13%)	0	100	100
12	SN	117/143 (82%)	89 (76%)	28 (24%)	0	100	100
13	SO	132/151 (87%)	123 (93%)	9 (7%)	0	100	100
14	SP	116/137 (85%)	99 (85%)	16 (14%)	1 (1%)	14	47
15	SR	123/143 (86%)	112 (91%)	11 (9%)	0	100	100
16	ST	113/146 (77%)	103 (91%)	10 (9%)	0	100	100
17	SX	125/130 (96%)	119 (95%)	6 (5%)	0	100	100
18	SY	101/145 (70%)	90 (89%)	11 (11%)	0	100	100
19	SZ	100/135 (74%)	87 (87%)	12 (12%)	1 (1%)	12	45
20	Sc	78/82 (95%)	69 (88%)	9 (12%)	0	100	100
21	Sd	61/67 (91%)	57 (93%)	4 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	3B	236/327 (72%)	222 (94%)	14 (6%)	0	100	100
22	3C	221/327 (68%)	207 (94%)	14 (6%)	0	100	100
23	3D	359/504 (71%)	346 (96%)	13 (4%)	0	100	100
24	3E	427/511 (84%)	387 (91%)	40 (9%)	0	100	100
25	3F	446/573 (78%)	403 (90%)	42 (9%)	1 (0%)	43	73
26	3G	119/126 (94%)	107 (90%)	11 (9%)	1 (1%)	16	50
26	3H	119/126 (94%)	111 (93%)	8 (7%)	0	100	100
27	A4	648/776 (84%)	590 (91%)	58 (9%)	0	100	100
28	A5	504/643 (78%)	465 (92%)	39 (8%)	0	100	100
29	A8	534/713 (75%)	398 (74%)	134 (25%)	2 (0%)	30	62
30	A9	126/575 (22%)	115 (91%)	11 (9%)	0	100	100
31	AE	1496/1769 (85%)	1367 (91%)	129 (9%)	0	100	100
32	AF	489/513 (95%)	442 (90%)	47 (10%)	0	100	100
33	AG	812/896 (91%)	731 (90%)	80 (10%)	1 (0%)	48	79
34	B1	830/923 (90%)	767 (92%)	63 (8%)	0	100	100
35	B2	839/943 (89%)	749 (89%)	88 (10%)	2 (0%)	43	73
36	B3	733/817 (90%)	606 (83%)	125 (17%)	2 (0%)	36	68
37	B8	469/594 (79%)	439 (94%)	30 (6%)	0	100	100
38	BE	857/939 (91%)	803 (94%)	54 (6%)	0	100	100
39	B6	368/440 (84%)	341 (93%)	27 (7%)	0	100	100
40	5B	58/214 (27%)	55 (95%)	3 (5%)	0	100	100
41	5C	531/554 (96%)	487 (92%)	43 (8%)	1 (0%)	43	73
42	5D	231/250 (92%)	204 (88%)	27 (12%)	0	100	100
43	5E	200/593 (34%)	183 (92%)	16 (8%)	1 (0%)	24	59
44	5F	180/183 (98%)	172 (96%)	8 (4%)	0	100	100
45	5G	278/290 (96%)	256 (92%)	22 (8%)	0	100	100
46	5H	132/610 (22%)	123 (93%)	9 (7%)	0	100	100
47	5I	457/489 (94%)	421 (92%)	36 (8%)	0	100	100
48	5J	147/217 (68%)	136 (92%)	11 (8%)	0	100	100
49	5K	171/189 (90%)	166 (97%)	5 (3%)	0	100	100
50	RA	332/707 (47%)	276 (83%)	56 (17%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	RB	132/357 (37%)	117 (89%)	14 (11%)	1 (1%)	16	50
52	RC	276/316 (87%)	259 (94%)	17 (6%)	0	100	100
53	RE	1067/1237 (86%)	999 (94%)	68 (6%)	0	100	100
54	RF	233/297 (78%)	203 (87%)	30 (13%)	0	100	100
55	RG	212/252 (84%)	182 (86%)	30 (14%)	0	100	100
55	RH	226/252 (90%)	219 (97%)	7 (3%)	0	100	100
56	RI	250/274 (91%)	233 (93%)	17 (7%)	0	100	100
57	RJ	784/1183 (66%)	721 (92%)	62 (8%)	1 (0%)	48	79
58	RK	358/367 (98%)	341 (95%)	17 (5%)	0	100	100
59	RL	781/1056 (74%)	664 (85%)	115 (15%)	2 (0%)	36	68
59	RM	738/1056 (70%)	625 (85%)	109 (15%)	4 (0%)	24	59
60	RN	593/810 (73%)	545 (92%)	47 (8%)	1 (0%)	43	73
61	RO	523/552 (95%)	455 (87%)	68 (13%)	0	100	100
62	RP	2043/2493 (82%)	1815 (89%)	227 (11%)	1 (0%)	100	100
63	RQ	220/899 (24%)	199 (90%)	21 (10%)	0	100	100
64	RS	247/483 (51%)	225 (91%)	22 (9%)	0	100	100
65	RT	165/326 (51%)	150 (91%)	15 (9%)	0	100	100
66	RV	184/346 (53%)	165 (90%)	19 (10%)	0	100	100
67	RW	59/206 (29%)	54 (92%)	5 (8%)	0	100	100
68	RY	35/534 (7%)	29 (83%)	6 (17%)	0	100	100
All	All	24979/33626 (74%)	22503 (90%)	2452 (10%)	24 (0%)	49	79

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
43	5E	454	VAL
59	RL	744	PRO
59	RM	744	PRO
59	RM	905	PRO
19	SZ	51	GLU
57	RJ	82	LYS
29	A8	309	PRO
33	AG	434	GLN
35	B2	132	THR
36	B3	91	LYS

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Mol	Chain	Res	Type
59	RM	904	LEU
60	RN	285	PRO
25	3F	552	TRP
5	SF	194	THR
29	A8	308	PHE
35	B2	118	ASN
51	RB	274	ILE
59	RL	743	VAL
59	RM	743	VAL
14	SP	123	SER
36	B3	71	PRO
41	5C	16	GLU
62	RP	2052	GLN
26	3G	10	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	SC	203/224 (91%)	201 (99%)	2 (1%)	68	80
5	SF	196/222 (88%)	193 (98%)	3 (2%)	57	76
6	SG	180/191 (94%)	179 (99%)	1 (1%)	78	84
7	SH	139/201 (69%)	136 (98%)	3 (2%)	45	71
8	SI	146/170 (86%)	143 (98%)	3 (2%)	47	71
9	SJ	136/161 (84%)	134 (98%)	2 (2%)	57	76
10	SK	147/166 (89%)	147 (100%)	0	100	100
11	SM	110/137 (80%)	108 (98%)	2 (2%)	51	74
12	SN	88/119 (74%)	87 (99%)	1 (1%)	65	79
13	SO	117/128 (91%)	116 (99%)	1 (1%)	70	81
14	SP	90/105 (86%)	89 (99%)	1 (1%)	65	79
15	SR	105/119 (88%)	105 (100%)	0	100	100
16	ST	105/129 (81%)	105 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	SX	108/111 (97%)	106 (98%)	2 (2%)	50	73
18	SY	85/120 (71%)	83 (98%)	2 (2%)	43	70
19	SZ	85/113 (75%)	85 (100%)	0	100	100
20	Sc	69/71 (97%)	69 (100%)	0	100	100
21	Sd	56/60 (93%)	56 (100%)	0	100	100
22	3B	201/240 (84%)	201 (100%)	0	100	100
22	3C	190/240 (79%)	188 (99%)	2 (1%)	65	79
23	3D	296/435 (68%)	295 (100%)	1 (0%)	86	88
24	3E	262/433 (60%)	261 (100%)	1 (0%)	84	86
25	3F	396/503 (79%)	392 (99%)	4 (1%)	68	80
26	3G	100/104 (96%)	100 (100%)	0	100	100
26	3H	100/104 (96%)	100 (100%)	0	100	100
27	A4	591/713 (83%)	584 (99%)	7 (1%)	63	79
28	A5	433/574 (75%)	429 (99%)	4 (1%)	70	81
29	A8	174/657 (26%)	173 (99%)	1 (1%)	78	84
30	A9	89/533 (17%)	89 (100%)	0	100	100
31	AE	708/1633 (43%)	705 (100%)	3 (0%)	84	86
32	AF	437/454 (96%)	431 (99%)	6 (1%)	59	77
33	AG	750/826 (91%)	739 (98%)	11 (2%)	57	76
34	B1	730/812 (90%)	720 (99%)	10 (1%)	59	77
35	B2	736/832 (88%)	729 (99%)	7 (1%)	68	80
36	B3	665/719 (92%)	656 (99%)	9 (1%)	59	77
37	B8	421/529 (80%)	417 (99%)	4 (1%)	68	80
38	BE	757/819 (92%)	752 (99%)	5 (1%)	76	83
39	B6	251/414 (61%)	249 (99%)	2 (1%)	73	82
40	5B	57/196 (29%)	56 (98%)	1 (2%)	51	74
41	5C	465/480 (97%)	463 (100%)	2 (0%)	84	86
42	5D	221/234 (94%)	221 (100%)	0	100	100
43	5E	185/535 (35%)	185 (100%)	0	100	100
44	5F	171/172 (99%)	168 (98%)	3 (2%)	51	74
45	5G	251/258 (97%)	246 (98%)	5 (2%)	48	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	5H	107/538 (20%)	107 (100%)	0	100	100
47	5I	416/443 (94%)	412 (99%)	4 (1%)	68	80
48	5J	140/200 (70%)	140 (100%)	0	100	100
49	5K	157/169 (93%)	157 (100%)	0	100	100
50	RA	303/636 (48%)	299 (99%)	4 (1%)	61	78
51	RB	117/315 (37%)	116 (99%)	1 (1%)	70	81
52	RC	231/289 (80%)	230 (100%)	1 (0%)	84	86
53	RE	984/1125 (88%)	977 (99%)	7 (1%)	76	83
54	RF	221/274 (81%)	221 (100%)	0	100	100
55	RG	195/222 (88%)	193 (99%)	2 (1%)	68	80
55	RH	206/222 (93%)	205 (100%)	1 (0%)	81	85
56	RI	235/256 (92%)	234 (100%)	1 (0%)	84	86
57	RJ	683/1039 (66%)	678 (99%)	5 (1%)	76	83
58	RK	307/312 (98%)	304 (99%)	3 (1%)	68	80
59	RL	164/934 (18%)	164 (100%)	0	100	100
60	RN	422/732 (58%)	422 (100%)	0	100	100
61	RO	329/506 (65%)	326 (99%)	3 (1%)	70	81
62	RP	499/2307 (22%)	496 (99%)	3 (1%)	78	84
63	RQ	148/808 (18%)	145 (98%)	3 (2%)	48	72
64	RS	225/424 (53%)	224 (100%)	1 (0%)	84	86
65	RT	148/282 (52%)	148 (100%)	0	100	100
66	RV	141/304 (46%)	141 (100%)	0	100	100
67	RW	22/192 (12%)	21 (96%)	1 (4%)	24	58
68	RY	31/482 (6%)	31 (100%)	0	100	100
All	All	18233/29007 (63%)	18082 (99%)	151 (1%)	70	82

All (151) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	SC	43	VAL
4	SC	172	LEU
5	SF	143	ASP
5	SF	183	VAL
5	SF	206	ASP

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Mol	Chain	Res	Type
6	SG	149	VAL
7	SH	67	VAL
7	SH	71	THR
7	SH	113	ILE
8	SI	73	VAL
8	SI	140	VAL
8	SI	189	THR
9	SJ	104	ILE
9	SJ	165	LEU
11	SM	107	VAL
11	SM	135	VAL
12	SN	66	VAL
13	SO	60	VAL
14	SP	42	VAL
17	SX	11	LEU
17	SX	70	ASN
18	SY	97	ASP
18	SY	120	VAL
22	3C	197	VAL
22	3C	237	VAL
23	3D	219	LEU
24	3E	371	LEU
25	3F	262	VAL
25	3F	273	VAL
25	3F	301	ASP
25	3F	408	VAL
27	A4	176	VAL
27	A4	190	VAL
27	A4	201	VAL
27	A4	282	ASP
27	A4	384	VAL
27	A4	391	VAL
27	A4	550	VAL
28	A5	95	VAL
28	A5	214	VAL
28	A5	357	VAL
28	A5	434	THR
29	A8	563	LEU
31	AE	210	LEU
31	AE	227	ASN
31	AE	734	ILE
32	AF	107	VAL

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Mol	Chain	Res	Type
32	AF	129	VAL
32	AF	218	VAL
32	AF	236	VAL
32	AF	261	VAL
32	AF	508	LEU
33	AG	109	VAL
33	AG	141	LEU
33	AG	259	VAL
33	AG	368	ASP
33	AG	391	VAL
33	AG	434	GLN
33	AG	435	ASP
33	AG	436	PHE
33	AG	508	ILE
33	AG	547	VAL
33	AG	650	VAL
34	B1	89	VAL
34	B1	141	VAL
34	B1	164	THR
34	B1	215	VAL
34	B1	351	LEU
34	B1	497	ILE
34	B1	519	LEU
34	B1	530	VAL
34	B1	661	LEU
34	B1	745	LEU
35	B2	47	GLU
35	B2	49	VAL
35	B2	144	ASN
35	B2	212	VAL
35	B2	332	ILE
35	B2	576	VAL
35	B2	588	ILE
36	B3	10	ILE
36	B3	32	LEU
36	B3	67	LEU
36	B3	95	VAL
36	B3	147	ILE
36	B3	212	LEU
36	B3	239	VAL
36	B3	570	THR
36	B3	731	LEU

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Mol	Chain	Res	Type
37	B8	22	LEU
37	B8	146	LEU
37	B8	178	VAL
37	B8	544	VAL
38	BE	298	VAL
38	BE	309	ILE
38	BE	570	ILE
38	BE	600	ILE
38	BE	721	LEU
39	B6	4	THR
39	B6	106	ASP
40	5B	211	LEU
41	5C	153	THR
41	5C	392	VAL
44	5F	32	VAL
44	5F	102	THR
44	5F	159	THR
45	5G	176	ILE
45	5G	209	LEU
45	5G	222	ILE
45	5G	239	VAL
45	5G	245	VAL
47	5I	14	VAL
47	5I	113	VAL
47	5I	201	ILE
47	5I	351	VAL
50	RA	76	THR
50	RA	155	VAL
50	RA	231	VAL
50	RA	264	ILE
51	RB	338	THR
52	RC	108	VAL
53	RE	102	ILE
53	RE	292	ILE
53	RE	560	ASN
53	RE	742	PHE
53	RE	753	ILE
53	RE	929	ILE
53	RE	1067	LEU
55	RG	32	THR
55	RG	100	LEU
55	RH	31	LEU

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Mol	Chain	Res	Type
56	RI	17	LEU
57	RJ	288	VAL
57	RJ	859	ILE
57	RJ	869	THR
57	RJ	976	ILE
57	RJ	1069	VAL
58	RK	26	LEU
58	RK	90	CYS
58	RK	335	THR
61	RO	471	GLU
61	RO	493	TYR
61	RO	504	ASP
62	RP	131	THR
62	RP	1770	LEU
62	RP	1896	ILE
63	RQ	330	THR
63	RQ	898	PHE
63	RQ	899	LYS
64	RS	326	VAL
67	RW	179	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (436) such sidechains are listed below:

Mol	Chain	Res	Type
4	SC	74	GLN
4	SC	92	GLN
4	SC	101	HIS
4	SC	194	ASN
6	SG	63	GLN
6	SG	66	GLN
6	SG	131	GLN
6	SG	169	ASN
7	SH	119	GLN
7	SH	140	ASN
8	SI	29	ASN
8	SI	42	GLN
8	SI	74	GLN
8	SI	122	HIS
8	SI	170	GLN
8	SI	174	ASN
8	SI	180	GLN
9	SJ	32	GLN

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Mol	Chain	Res	Type
9	SJ	103	GLN
9	SJ	159	GLN
10	SK	48	GLN
10	SK	142	ASN
11	SM	8	GLN
11	SM	81	HIS
11	SM	98	ASN
11	SM	106	ASN
13	SO	36	GLN
13	SO	58	HIS
14	SP	12	GLN
14	SP	24	ASN
15	SR	74	HIS
16	ST	13	HIS
16	ST	103	ASN
16	ST	104	ASN
17	SX	12	ASN
17	SX	16	ASN
17	SX	120	HIS
18	SY	48	HIS
20	Sc	5	GLN
20	Sc	19	HIS
20	Sc	42	ASN
22	3B	91	HIS
22	3B	228	GLN
22	3C	264	GLN
23	3D	39	ASN
23	3D	85	ASN
23	3D	168	GLN
23	3D	172	ASN
23	3D	183	GLN
23	3D	213	ASN
23	3D	324	ASN
23	3D	398	ASN
24	3E	191	HIS
24	3E	256	ASN
24	3E	286	ASN
24	3E	289	GLN
24	3E	396	ASN
24	3E	400	GLN
25	3F	129	GLN
25	3F	155	ASN

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Mol	Chain	Res	Type
25	3F	156	ASN
25	3F	164	GLN
25	3F	195	GLN
25	3F	226	HIS
25	3F	525	GLN
25	3F	561	ASN
26	3G	29	ASN
26	3H	5	ASN
26	3H	18	GLN
26	3H	45	ASN
27	A4	140	ASN
27	A4	279	HIS
27	A4	292	ASN
27	A4	317	ASN
27	A4	331	ASN
27	A4	438	GLN
27	A4	467	ASN
27	A4	483	ASN
27	A4	529	ASN
27	A4	574	HIS
27	A4	589	ASN
27	A4	621	ASN
27	A4	731	HIS
28	A5	32	GLN
28	A5	67	ASN
28	A5	103	ASN
28	A5	133	GLN
28	A5	139	HIS
28	A5	302	ASN
28	A5	308	ASN
28	A5	316	ASN
28	A5	333	ASN
28	A5	527	HIS
29	A8	553	GLN
29	A8	609	ASN
29	A8	636	GLN
30	A9	478	ASN
30	A9	509	GLN
31	AE	14	ASN
31	AE	96	ASN
31	AE	141	ASN
31	AE	166	ASN

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Mol	Chain	Res	Type
31	AE	224	ASN
31	AE	258	HIS
31	AE	304	GLN
31	AE	477	ASN
31	AE	480	ASN
31	AE	545	ASN
31	AE	673	ASN
31	AE	698	ASN
31	AE	730	GLN
32	AF	18	GLN
32	AF	48	ASN
32	AF	125	HIS
32	AF	133	HIS
32	AF	135	GLN
32	AF	137	ASN
32	AF	156	ASN
32	AF	217	ASN
32	AF	250	ASN
32	AF	269	GLN
32	AF	289	ASN
32	AF	419	GLN
32	AF	481	GLN
32	AF	496	HIS
33	AG	50	ASN
33	AG	105	HIS
33	AG	131	HIS
33	AG	166	ASN
33	AG	184	GLN
33	AG	190	GLN
33	AG	266	ASN
33	AG	269	GLN
33	AG	289	GLN
33	AG	325	GLN
33	AG	332	GLN
33	AG	370	GLN
33	AG	393	ASN
33	AG	407	ASN
33	AG	410	ASN
33	AG	418	ASN
33	AG	453	HIS
33	AG	467	GLN
33	AG	489	ASN

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Mol	Chain	Res	Type
33	AG	535	ASN
33	AG	568	ASN
33	AG	579	ASN
33	AG	603	ASN
33	AG	669	ASN
33	AG	706	HIS
33	AG	719	ASN
33	AG	880	GLN
34	B1	57	ASN
34	B1	92	HIS
34	B1	142	HIS
34	B1	188	ASN
34	B1	201	HIS
34	B1	254	HIS
34	B1	297	GLN
34	B1	303	ASN
34	B1	349	ASN
34	B1	386	HIS
34	B1	432	GLN
34	B1	452	ASN
34	B1	456	HIS
34	B1	461	GLN
34	B1	483	GLN
34	B1	549	GLN
34	B1	552	ASN
34	B1	650	ASN
34	B1	707	ASN
34	B1	734	GLN
34	B1	752	ASN
34	B1	813	HIS
34	B1	837	ASN
34	B1	842	ASN
35	B2	172	GLN
35	B2	327	HIS
35	B2	390	GLN
35	B2	455	GLN
35	B2	523	HIS
35	B2	524	HIS
35	B2	656	HIS
35	B2	657	GLN
35	B2	770	ASN
35	B2	856	ASN

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Mol	Chain	Res	Type
35	B2	871	GLN
35	B2	881	ASN
36	B3	81	GLN
36	B3	187	GLN
36	B3	241	GLN
36	B3	309	GLN
36	B3	312	GLN
36	B3	337	HIS
36	B3	358	ASN
36	B3	387	HIS
36	B3	478	GLN
36	B3	495	ASN
36	B3	519	ASN
36	B3	522	ASN
36	B3	642	GLN
36	B3	667	GLN
36	B3	735	GLN
36	B3	747	ASN
36	B3	753	HIS
36	B3	767	HIS
36	B3	792	HIS
37	B8	151	ASN
37	B8	162	ASN
37	B8	167	GLN
37	B8	224	ASN
37	B8	276	HIS
37	B8	282	ASN
37	B8	308	ASN
37	B8	322	HIS
37	B8	352	GLN
37	B8	472	GLN
37	B8	492	ASN
37	B8	498	ASN
37	B8	528	GLN
37	B8	592	ASN
37	B8	593	HIS
38	BE	32	ASN
38	BE	64	ASN
38	BE	120	HIS
38	BE	163	GLN
38	BE	248	GLN
38	BE	289	ASN

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Mol	Chain	Res	Type
38	BE	305	ASN
38	BE	349	HIS
38	BE	362	GLN
38	BE	447	ASN
38	BE	481	ASN
38	BE	501	HIS
38	BE	514	ASN
38	BE	627	ASN
38	BE	708	ASN
38	BE	736	HIS
38	BE	826	GLN
38	BE	877	ASN
38	BE	911	ASN
39	B6	62	ASN
39	B6	64	ASN
39	B6	90	GLN
39	B6	115	ASN
39	B6	166	ASN
39	B6	169	GLN
39	B6	287	ASN
39	B6	289	HIS
40	5B	207	ASN
41	5C	101	ASN
41	5C	124	HIS
41	5C	133	HIS
41	5C	143	GLN
41	5C	151	ASN
41	5C	155	HIS
41	5C	164	GLN
41	5C	170	GLN
41	5C	308	GLN
41	5C	371	HIS
41	5C	394	HIS
41	5C	468	GLN
41	5C	517	GLN
41	5C	525	ASN
42	5D	42	HIS
42	5D	144	ASN
42	5D	153	ASN
43	5E	303	GLN
43	5E	316	ASN
43	5E	526	ASN

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Mol	Chain	Res	Type
44	5F	7	HIS
44	5F	10	GLN
44	5F	99	ASN
44	5F	125	GLN
44	5F	135	HIS
44	5F	144	ASN
45	5G	18	GLN
45	5G	102	GLN
45	5G	121	ASN
45	5G	143	HIS
45	5G	159	HIS
45	5G	168	HIS
45	5G	236	HIS
46	5H	499	GLN
46	5H	513	HIS
46	5H	515	ASN
46	5H	560	ASN
47	5I	20	GLN
47	5I	46	ASN
47	5I	81	ASN
47	5I	109	HIS
47	5I	242	ASN
47	5I	260	GLN
47	5I	276	ASN
47	5I	281	ASN
47	5I	336	HIS
47	5I	371	ASN
47	5I	406	HIS
47	5I	418	HIS
47	5I	421	GLN
47	5I	427	GLN
48	5J	53	GLN
48	5J	135	HIS
48	5J	184	ASN
48	5J	192	ASN
48	5J	195	GLN
49	5K	29	GLN
50	RA	60	ASN
50	RA	82	HIS
50	RA	96	HIS
50	RA	118	GLN
50	RA	119	ASN

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Mol	Chain	Res	Type
50	RA	147	ASN
50	RA	230	GLN
50	RA	268	GLN
50	RA	282	ASN
51	RB	314	ASN
51	RB	318	ASN
52	RC	112	GLN
52	RC	149	ASN
52	RC	151	ASN
52	RC	255	GLN
53	RE	136	GLN
53	RE	170	GLN
53	RE	237	HIS
53	RE	293	ASN
53	RE	342	HIS
53	RE	344	ASN
53	RE	402	ASN
53	RE	409	ASN
53	RE	506	GLN
53	RE	520	ASN
53	RE	537	ASN
53	RE	568	ASN
53	RE	602	ASN
53	RE	683	ASN
53	RE	729	ASN
53	RE	767	GLN
53	RE	834	ASN
53	RE	841	ASN
53	RE	869	ASN
53	RE	956	ASN
53	RE	969	ASN
53	RE	1029	ASN
53	RE	1081	ASN
53	RE	1215	ASN
53	RE	1228	ASN
54	RF	23	HIS
54	RF	73	GLN
54	RF	135	ASN
54	RF	136	ASN
54	RF	187	HIS
54	RF	197	GLN
54	RF	261	GLN

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Mol	Chain	Res	Type
55	RG	105	ASN
55	RG	125	ASN
55	RH	69	ASN
55	RH	74	GLN
55	RH	105	ASN
55	RH	125	ASN
55	RH	250	ASN
56	RI	52	ASN
56	RI	117	GLN
56	RI	186	ASN
56	RI	193	ASN
56	RI	215	ASN
56	RI	221	ASN
56	RI	248	ASN
57	RJ	126	ASN
57	RJ	157	ASN
57	RJ	254	HIS
57	RJ	289	HIS
57	RJ	761	GLN
57	RJ	778	GLN
57	RJ	909	ASN
57	RJ	944	ASN
57	RJ	1082	GLN
57	RJ	1151	GLN
58	RK	16	ASN
58	RK	61	ASN
58	RK	317	GLN
58	RK	334	ASN
59	RL	16	ASN
59	RL	75	ASN
59	RL	117	ASN
59	RL	133	ASN
60	RN	8	ASN
60	RN	56	ASN
60	RN	432	HIS
60	RN	495	ASN
60	RN	531	GLN
60	RN	683	ASN
60	RN	686	ASN
60	RN	703	GLN
60	RN	705	HIS
60	RN	713	HIS

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Mol	Chain	Res	Type
60	RN	771	ASN
60	RN	797	ASN
61	RO	192	GLN
61	RO	249	ASN
61	RO	266	ASN
61	RO	268	GLN
61	RO	273	GLN
61	RO	290	HIS
61	RO	304	ASN
61	RO	306	GLN
61	RO	343	GLN
61	RO	434	ASN
61	RO	449	HIS
61	RO	472	HIS
61	RO	474	HIS
62	RP	58	ASN
62	RP	153	ASN
62	RP	1686	GLN
62	RP	1702	HIS
62	RP	1707	HIS
62	RP	1785	ASN
62	RP	1802	HIS
62	RP	1803	ASN
62	RP	1816	HIS
62	RP	2045	GLN
63	RQ	344	GLN
63	RQ	836	ASN
63	RQ	867	GLN
64	RS	241	ASN
64	RS	276	GLN
64	RS	300	ASN
65	RT	111	ASN
65	RT	127	GLN
65	RT	218	ASN
65	RT	232	HIS
66	RV	151	ASN
66	RV	222	ASN
66	RV	225	GLN
66	RV	237	HIS
68	RY	469	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	169/333 (50%)	44 (26%)	2 (1%)
2	5A	518/700 (74%)	161 (31%)	11 (2%)
3	SA	1305/1808 (72%)	499 (38%)	19 (1%)
All	All	1992/2841 (70%)	704 (35%)	32 (1%)

All (704) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3A	2	U
1	3A	14	A
1	3A	15	U
1	3A	24	U
1	3A	25	U
1	3A	27	U
1	3A	28	A
1	3A	30	A
1	3A	33	A
1	3A	35	U
1	3A	38	U
1	3A	56	A
1	3A	60	A
1	3A	61	G
1	3A	87	G
1	3A	88	U
1	3A	89	C
1	3A	90	C
1	3A	91	C
1	3A	101	G
1	3A	111	G
1	3A	115	G
1	3A	198	U
1	3A	199	G
1	3A	201	C
1	3A	204	U
1	3A	205	G
1	3A	206	C
1	3A	246	A
1	3A	248	G
1	3A	249	G
1	3A	252	C
1	3A	305	G
1	3A	309	G
1	3A	310	G

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Mol	Chain	Res	Type
1	3A	311	G
1	3A	313	A
1	3A	314	C
1	3A	322	A
1	3A	324	U
1	3A	325	C
1	3A	328	A
1	3A	329	C
1	3A	332	G
2	5A	5	G
2	5A	6	A
2	5A	7	A
2	5A	8	A
2	5A	11	A
2	5A	13	U
2	5A	14	U
2	5A	15	G
2	5A	63	G
2	5A	64	U
2	5A	70	A
2	5A	82	A
2	5A	83	U
2	5A	86	C
2	5A	87	C
2	5A	90	G
2	5A	102	A
2	5A	103	G
2	5A	104	A
2	5A	109	C
2	5A	110	G
2	5A	114	G
2	5A	124	A
2	5A	125	G
2	5A	127	U
2	5A	128	C
2	5A	129	U
2	5A	130	G
2	5A	141	A
2	5A	142	U
2	5A	143	A
2	5A	144	C
2	5A	150	G

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Mol	Chain	Res	Type
2	5A	151	U
2	5A	152	U
2	5A	156	U
2	5A	159	A
2	5A	161	A
2	5A	162	U
2	5A	163	G
2	5A	167	U
2	5A	168	G
2	5A	169	A
2	5A	170	U
2	5A	171	G
2	5A	172	C
2	5A	173	G
2	5A	174	U
2	5A	175	A
2	5A	176	U
2	5A	177	U
2	5A	178	G
2	5A	179	A
2	5A	182	G
2	5A	185	A
2	5A	190	U
2	5A	200	A
2	5A	201	U
2	5A	206	A
2	5A	207	G
2	5A	211	G
2	5A	213	G
2	5A	219	U
2	5A	220	U
2	5A	222	G
2	5A	223	C
2	5A	224	G
2	5A	225	U
2	5A	227	U
2	5A	235	A
2	5A	240	C
2	5A	254	C
2	5A	256	U
2	5A	259	G
2	5A	260	A

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Mol	Chain	Res	Type
2	5A	261	U
2	5A	263	C
2	5A	267	U
2	5A	268	G
2	5A	279	A
2	5A	280	A
2	5A	281	G
2	5A	292	A
2	5A	294	U
2	5A	304	U
2	5A	305	A
2	5A	309	A
2	5A	310	U
2	5A	311	C
2	5A	312	U
2	5A	313	A
2	5A	321	G
2	5A	322	A
2	5A	325	U
2	5A	326	C
2	5A	328	A
2	5A	337	G
2	5A	339	A
2	5A	346	G
2	5A	350	A
2	5A	353	A
2	5A	354	G
2	5A	355	C
2	5A	359	U
2	5A	361	G
2	5A	363	A
2	5A	364	A
2	5A	368	U
2	5A	369	G
2	5A	370	U
2	5A	371	G
2	5A	372	A
2	5A	373	U
2	5A	381	G
2	5A	385	A
2	5A	386	A
2	5A	391	C

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Mol	Chain	Res	Type
2	5A	393	C
2	5A	395	C
2	5A	407	A
2	5A	419	A
2	5A	427	A
2	5A	428	A
2	5A	429	A
2	5A	430	C
2	5A	431	A
2	5A	432	C
2	5A	433	C
2	5A	440	U
2	5A	443	G
2	5A	444	U
2	5A	461	A
2	5A	462	G
2	5A	464	G
2	5A	468	A
2	5A	472	A
2	5A	474	A
2	5A	481	U
2	5A	482	A
2	5A	485	G
2	5A	487	A
2	5A	488	U
2	5A	490	G
2	5A	491	U
2	5A	493	A
2	5A	519	A
2	5A	525	U
2	5A	526	U
2	5A	536	A
2	5A	537	G
2	5A	539	A
2	5A	540	U
2	5A	541	U
2	5A	542	U
2	5A	548	A
2	5A	549	G
2	5A	583	U
2	5A	586	A
2	5A	587	G

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Mol	Chain	Res	Type
2	5A	589	U
2	5A	591	U
3	SA	-6	A
3	SA	-5	G
3	SA	-4	A
3	SA	-1	G
3	SA	0	U
3	SA	1	U
3	SA	2	A
3	SA	17	C
3	SA	18	C
3	SA	19	A
3	SA	21	U
3	SA	23	G
3	SA	25	C
3	SA	26	A
3	SA	29	U
3	SA	35	U
3	SA	36	C
3	SA	37	U
3	SA	50	C
3	SA	51	A
3	SA	52	U
3	SA	53	G
3	SA	55	A
3	SA	56	U
3	SA	57	G
3	SA	60	U
3	SA	61	A
3	SA	63	G
3	SA	65	A
3	SA	66	U
3	SA	67	A
3	SA	68	A
3	SA	69	G
3	SA	72	A
3	SA	73	U
3	SA	74	U
3	SA	75	U
3	SA	77	U
3	SA	81	G
3	SA	85	A

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Mol	Chain	Res	Type
3	SA	92	A
3	SA	95	G
3	SA	96	G
3	SA	97	C
3	SA	100	A
3	SA	102	U
3	SA	103	A
3	SA	104	A
3	SA	105	A
3	SA	106	U
3	SA	114	C
3	SA	115	G
3	SA	116	U
3	SA	119	A
3	SA	127	G
3	SA	128	U
3	SA	129	U
3	SA	130	C
3	SA	131	C
3	SA	141	U
3	SA	145	A
3	SA	146	U
3	SA	147	A
3	SA	149	C
3	SA	153	G
3	SA	159	U
3	SA	160	C
3	SA	161	U
3	SA	168	A
3	SA	174	U
3	SA	175	G
3	SA	176	C
3	SA	177	U
3	SA	182	A
3	SA	183	U
3	SA	184	C
3	SA	187	G
3	SA	188	A
3	SA	190	C
3	SA	191	C
3	SA	192	U
3	SA	193	U

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Mol	Chain	Res	Type
3	SA	194	U
3	SA	195	G
3	SA	197	A
3	SA	202	A
3	SA	203	U
3	SA	204	G
3	SA	206	A
3	SA	210	A
3	SA	211	U
3	SA	214	G
3	SA	226	A
3	SA	228	G
3	SA	230	C
3	SA	233	C
3	SA	234	G
3	SA	236	A
3	SA	237	C
3	SA	238	U
3	SA	239	C
3	SA	240	U
3	SA	241	U
3	SA	242	U
3	SA	243	G
3	SA	254	A
3	SA	256	A
3	SA	258	C
3	SA	261	U
3	SA	262	U
3	SA	265	A
3	SA	266	A
3	SA	267	U
3	SA	272	U
3	SA	273	G
3	SA	275	C
3	SA	276	C
3	SA	277	U
3	SA	278	U
3	SA	279	G
3	SA	280	U
3	SA	281	G
3	SA	283	U
3	SA	290	G

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Mol	Chain	Res	Type
3	SA	308	C
3	SA	309	C
3	SA	311	U
3	SA	312	A
3	SA	316	A
3	SA	319	U
3	SA	320	U
3	SA	321	C
3	SA	324	U
3	SA	325	G
3	SA	333	A
3	SA	334	G
3	SA	337	G
3	SA	338	C
3	SA	350	U
3	SA	352	A
3	SA	355	G
3	SA	357	G
3	SA	359	A
3	SA	360	A
3	SA	361	C
3	SA	362	G
3	SA	365	G
3	SA	366	A
3	SA	369	A
3	SA	371	G
3	SA	373	G
3	SA	374	U
3	SA	375	U
3	SA	377	G
3	SA	379	U
3	SA	382	C
3	SA	383	G
3	SA	386	G
3	SA	387	A
3	SA	390	G
3	SA	400	A
3	SA	401	A
3	SA	402	C
3	SA	403	G
3	SA	411	C
3	SA	416	A

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Mol	Chain	Res	Type
3	SA	417	A
3	SA	418	G
3	SA	419	G
3	SA	421	A
3	SA	422	G
3	SA	423	G
3	SA	424	C
3	SA	425	A
3	SA	426	G
3	SA	429	G
3	SA	436	A
3	SA	437	A
3	SA	439	U
3	SA	440	U
3	SA	441	A
3	SA	444	C
3	SA	445	A
3	SA	448	C
3	SA	454	U
3	SA	455	C
3	SA	456	A
3	SA	457	G
3	SA	468	A
3	SA	469	C
3	SA	470	A
3	SA	471	A
3	SA	473	A
3	SA	477	A
3	SA	480	G
3	SA	486	G
3	SA	487	G
3	SA	496	G
3	SA	501	U
3	SA	502	U
3	SA	505	A
3	SA	506	A
3	SA	514	G
3	SA	520	A
3	SA	534	A
3	SA	538	A
3	SA	539	G
3	SA	541	A

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Mol	Chain	Res	Type
3	SA	542	A
3	SA	543	C
3	SA	545	A
3	SA	557	G
3	SA	558	U
3	SA	563	U
3	SA	564	G
3	SA	565	C
3	SA	570	A
3	SA	572	C
3	SA	574	G
3	SA	575	C
3	SA	578	U
3	SA	579	A
3	SA	580	A
3	SA	583	C
3	SA	584	C
3	SA	585	A
3	SA	586	G
3	SA	587	C
3	SA	594	A
3	SA	595	G
3	SA	602	U
3	SA	603	U
3	SA	604	A
3	SA	606	A
3	SA	608	U
3	SA	609	U
3	SA	610	G
3	SA	611	U
3	SA	612	U
3	SA	613	G
3	SA	614	C
3	SA	615	A
3	SA	616	G
3	SA	635	A
3	SA	636	A
3	SA	638	U
3	SA	644	C
3	SA	648	G
3	SA	652	G
3	SA	654	C

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Mol	Chain	Res	Type
3	SA	656	G
3	SA	657	U
3	SA	658	C
3	SA	677	G
3	SA	678	A
3	SA	686	C
3	SA	687	G
3	SA	688	G
3	SA	689	G
3	SA	691	C
3	SA	692	C
3	SA	823	G
3	SA	827	C
3	SA	844	A
3	SA	845	G
3	SA	848	C
3	SA	859	A
3	SA	860	U
3	SA	863	A
3	SA	864	U
3	SA	865	A
3	SA	873	U
3	SA	877	G
3	SA	894	U
3	SA	901	G
3	SA	904	G
3	SA	906	A
3	SA	912	U
3	SA	913	G
3	SA	914	G
3	SA	926	A
3	SA	930	A
3	SA	933	A
3	SA	934	C
3	SA	935	U
3	SA	945	U
3	SA	951	A
3	SA	953	G
3	SA	960	U
3	SA	966	A
3	SA	969	C
3	SA	970	A

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Mol	Chain	Res	Type
3	SA	1022	C
3	SA	1024	U
3	SA	1025	A
3	SA	1026	A
3	SA	1027	A
3	SA	1031	U
3	SA	1032	G
3	SA	1037	C
3	SA	1039	A
3	SA	1040	G
3	SA	1052	U
3	SA	1053	G
3	SA	1056	U
3	SA	1057	U
3	SA	1059	U
3	SA	1060	U
3	SA	1062	A
3	SA	1063	U
3	SA	1076	A
3	SA	1079	U
3	SA	1081	A
3	SA	1082	C
3	SA	1084	A
3	SA	1085	G
3	SA	1086	A
3	SA	1106	U
3	SA	1107	G
3	SA	1108	G
3	SA	1109	G
3	SA	1110	G
3	SA	1111	G
3	SA	1114	G
3	SA	1118	G
3	SA	1119	G
3	SA	1122	G
3	SA	1125	A
3	SA	1126	G
3	SA	1127	G
3	SA	1128	C
3	SA	1129	U
3	SA	1131	A
3	SA	1132	A

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Mol	Chain	Res	Type
3	SA	1145	U
3	SA	1146	G
3	SA	1158	C
3	SA	1164	G
3	SA	1178	G
3	SA	1191	U
3	SA	1192	C
3	SA	1193	A
3	SA	1195	C
3	SA	1196	A
3	SA	1197	C
3	SA	1198	G
3	SA	1199	G
3	SA	1200	G
3	SA	1201	G
3	SA	1202	A
3	SA	1205	C
3	SA	1206	U
3	SA	1208	A
3	SA	1210	C
3	SA	1213	G
3	SA	1217	A
3	SA	1218	G
3	SA	1219	A
3	SA	1220	C
3	SA	1223	A
3	SA	1227	A
3	SA	1228	G
3	SA	1229	G
3	SA	1230	A
3	SA	1232	U
3	SA	1233	G
3	SA	1235	C
3	SA	1236	A
3	SA	1252	C
3	SA	1253	U
3	SA	1254	U
3	SA	1255	G
3	SA	1258	U
3	SA	1263	G
3	SA	1266	U
3	SA	1268	G

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Mol	Chain	Res	Type
3	SA	1271	G
3	SA	1272	U
3	SA	1273	G
3	SA	1275	A
3	SA	1276	U
3	SA	1436	A
3	SA	1440	C
3	SA	1441	C
3	SA	1442	U
3	SA	1443	U
3	SA	1449	U
3	SA	1450	U
3	SA	1453	G
3	SA	1457	C
3	SA	1461	C
3	SA	1469	A
3	SA	1472	C
3	SA	1473	U
3	SA	1474	G
3	SA	1475	A
3	SA	1476	C
3	SA	1482	C
3	SA	1488	G
3	SA	1492	A
3	SA	1493	A
3	SA	1496	U
3	SA	1498	G
3	SA	1506	G
3	SA	1517	U
3	SA	1518	C
3	SA	1520	U
3	SA	1521	G
3	SA	1522	U
3	SA	1523	G
3	SA	1524	A
3	SA	1527	C
3	SA	1533	C
3	SA	1535	U
3	SA	1536	G
3	SA	1537	C
3	SA	1539	G
3	SA	1541	G

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Mol	Chain	Res	Type
3	SA	1543	A
3	SA	1544	U
3	SA	1567	U
3	SA	1568	C
3	SA	1569	A
3	SA	1570	A
3	SA	1573	A
3	SA	1582	U
3	SA	1584	G
3	SA	1590	G
3	SA	1594	G
3	SA	1595	U
3	SA	1596	C
3	SA	1601	G
3	SA	1602	C
3	SA	1607	G
3	SA	1614	A
3	SA	1618	C
3	SA	1628	U
3	SA	1630	U
3	SA	1633	A
3	SA	1651	A
3	SA	1655	A
3	SA	1657	U
3	SA	1658	G
3	SA	1659	A
3	SA	1661	U
3	SA	1665	U
3	SA	1670	G
3	SA	1675	C
3	SA	1677	C
3	SA	1679	G
3	SA	1680	G
3	SA	1681	A
3	SA	1682	U
3	SA	1683	C
3	SA	1687	U
3	SA	1689	A
3	SA	1692	G
3	SA	1693	A
3	SA	1696	G
3	SA	1697	G

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Mol	Chain	Res	Type
3	SA	1700	C
3	SA	1708	U
3	SA	1709	C
3	SA	1710	U
3	SA	1711	C
3	SA	1713	G
3	SA	1717	G
3	SA	1718	G
3	SA	1719	A
3	SA	1721	A
3	SA	1724	U
3	SA	1725	U
3	SA	1727	G
3	SA	1728	A
3	SA	1731	A
3	SA	1732	A
3	SA	1736	G
3	SA	1737	G
3	SA	1742	U
3	SA	1743	U
3	SA	1745	G
3	SA	1749	A
3	SA	1750	A
3	SA	1755	A
3	SA	1756	A
3	SA	1757	G
3	SA	1758	U
3	SA	1759	C
3	SA	1761	U
3	SA	1764	C
3	SA	1766	A
3	SA	1767	G
3	SA	1768	G
3	SA	1769	U
3	SA	1779	U
3	SA	1780	G
3	SA	1781	A
3	SA	1782	A
3	SA	1789	G

All (32) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	3A	198	U
1	3A	248	G
2	5A	169	A
2	5A	172	C
2	5A	173	G
2	5A	224	G
2	5A	312	U
2	5A	358	G
2	5A	363	A
2	5A	368	U
2	5A	487	A
2	5A	492	G
2	5A	536	A
3	SA	-7	A
3	SA	0	U
3	SA	56	U
3	SA	68	A
3	SA	272	U
3	SA	372	G
3	SA	401	A
3	SA	417	A
3	SA	538	A
3	SA	542	A
3	SA	579	A
3	SA	602	U
3	SA	1031	U
3	SA	1052	U
3	SA	1084	A
3	SA	1197	C
3	SA	1521	G
3	SA	1594	G
3	SA	1632	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
71	GTP	RJ	1201	72	33,34,34	0.56	0	50,54,54	0.72	1 (2%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
71	GTP	RJ	1201	72	-	3/22/38/38	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
71	RJ	1201	GTP	C4'-O4'-C1'	-2.15	104.72	109.47

There are no chirality outliers.

All (3) torsion outliers are listed below:

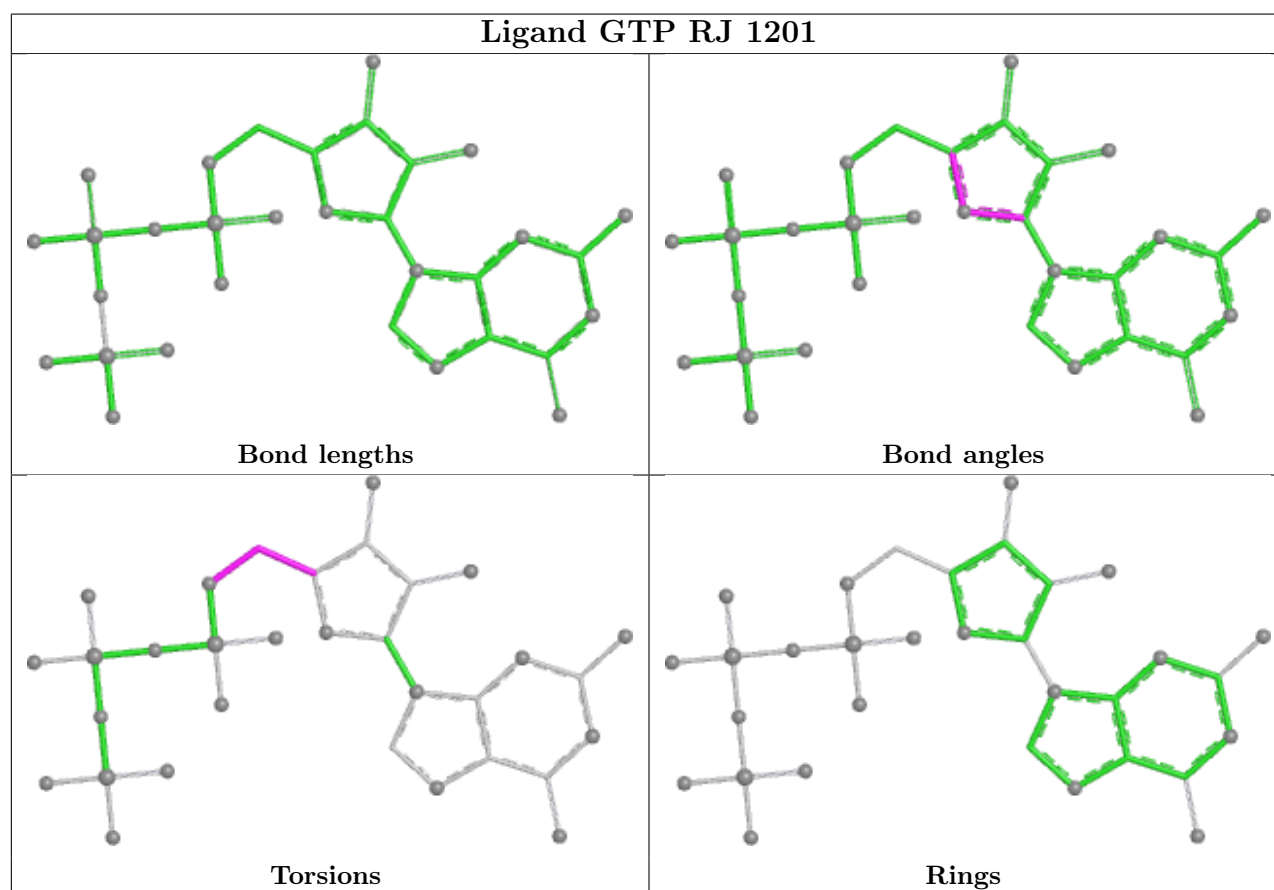
Mol	Chain	Res	Type	Atoms
71	RJ	1201	GTP	O4'-C4'-C5'-O5'
71	RJ	1201	GTP	C3'-C4'-C5'-O5'
71	RJ	1201	GTP	C4'-C5'-O5'-PA

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
71	RJ	1201	GTP	2	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

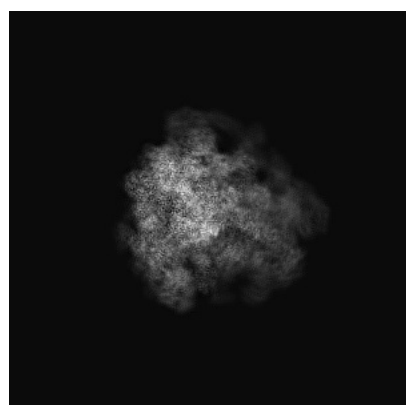
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0949. These allow visual inspection of the internal detail of the map and identification of artifacts.

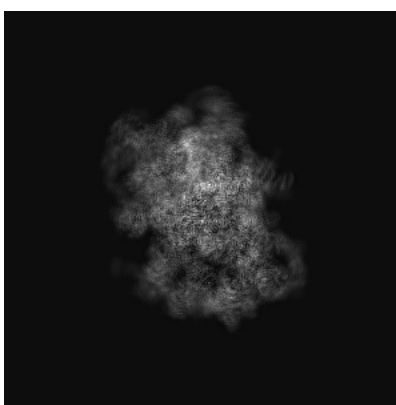
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

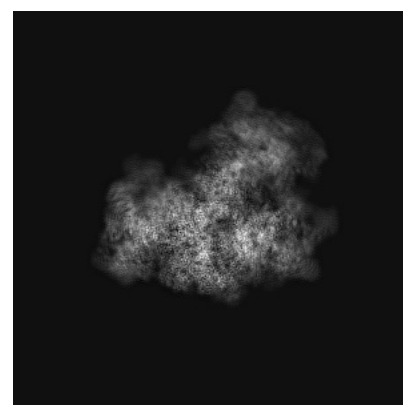
6.1.1 Primary map



X



Y

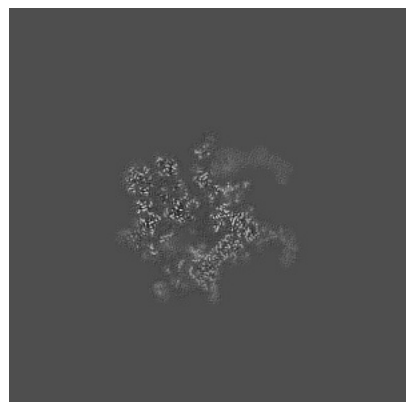


Z

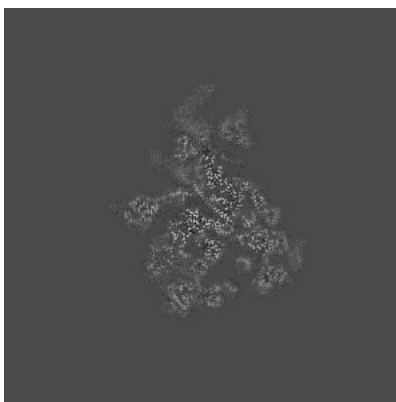
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

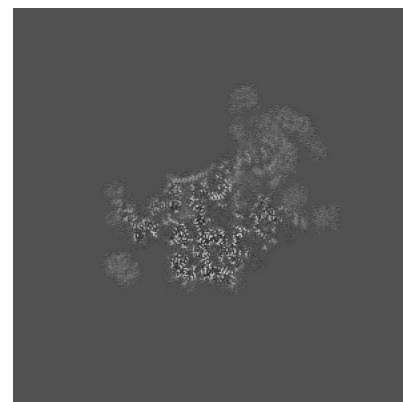
6.2.1 Primary map



X Index: 224



Y Index: 224



Z Index: 224

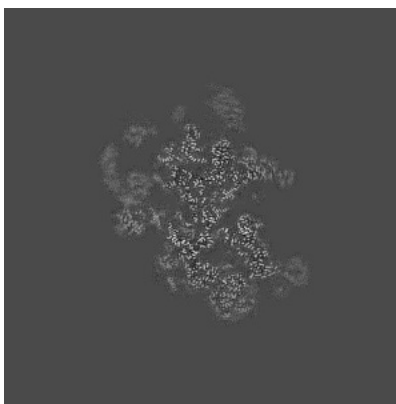
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

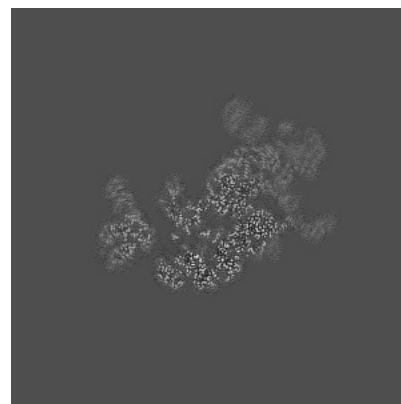
6.3.1 Primary map



X Index: 212



Y Index: 196

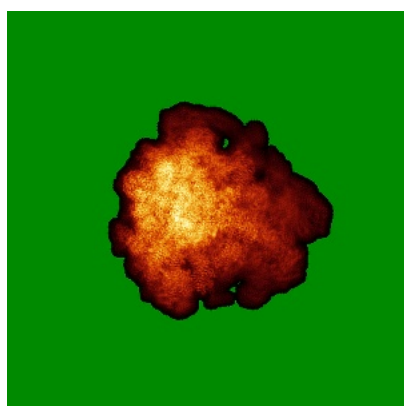


Z Index: 242

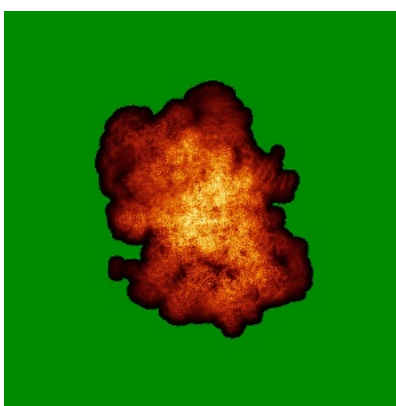
The images above show the largest variance slices of the map in three orthogonal directions.

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

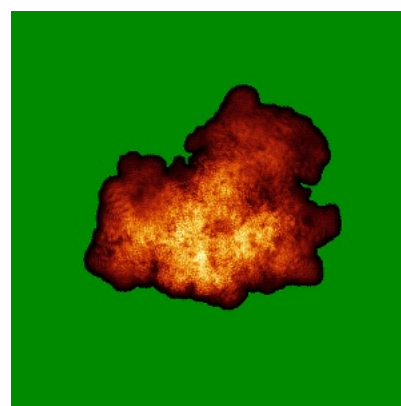
6.4.1 Primary map



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 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

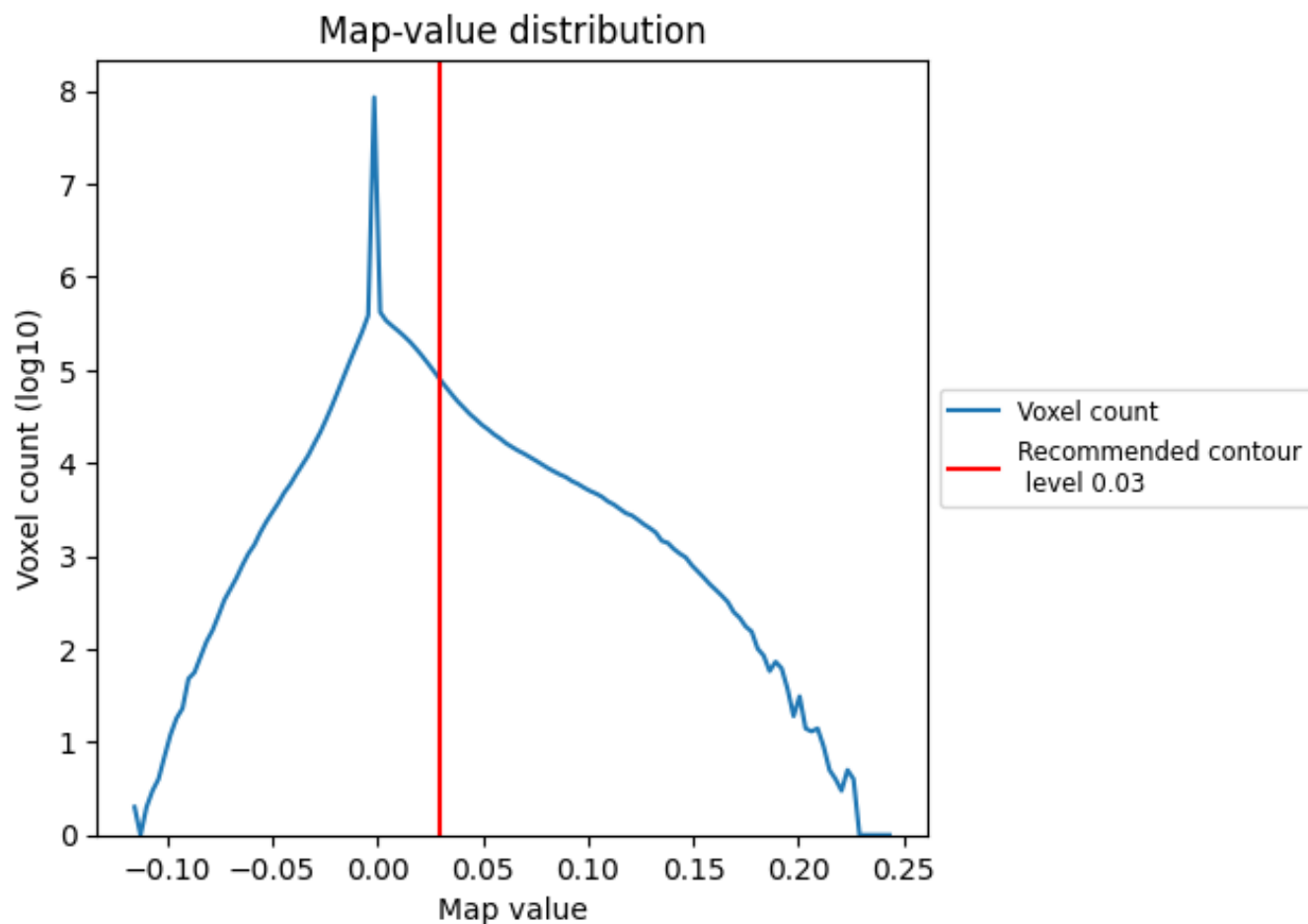
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

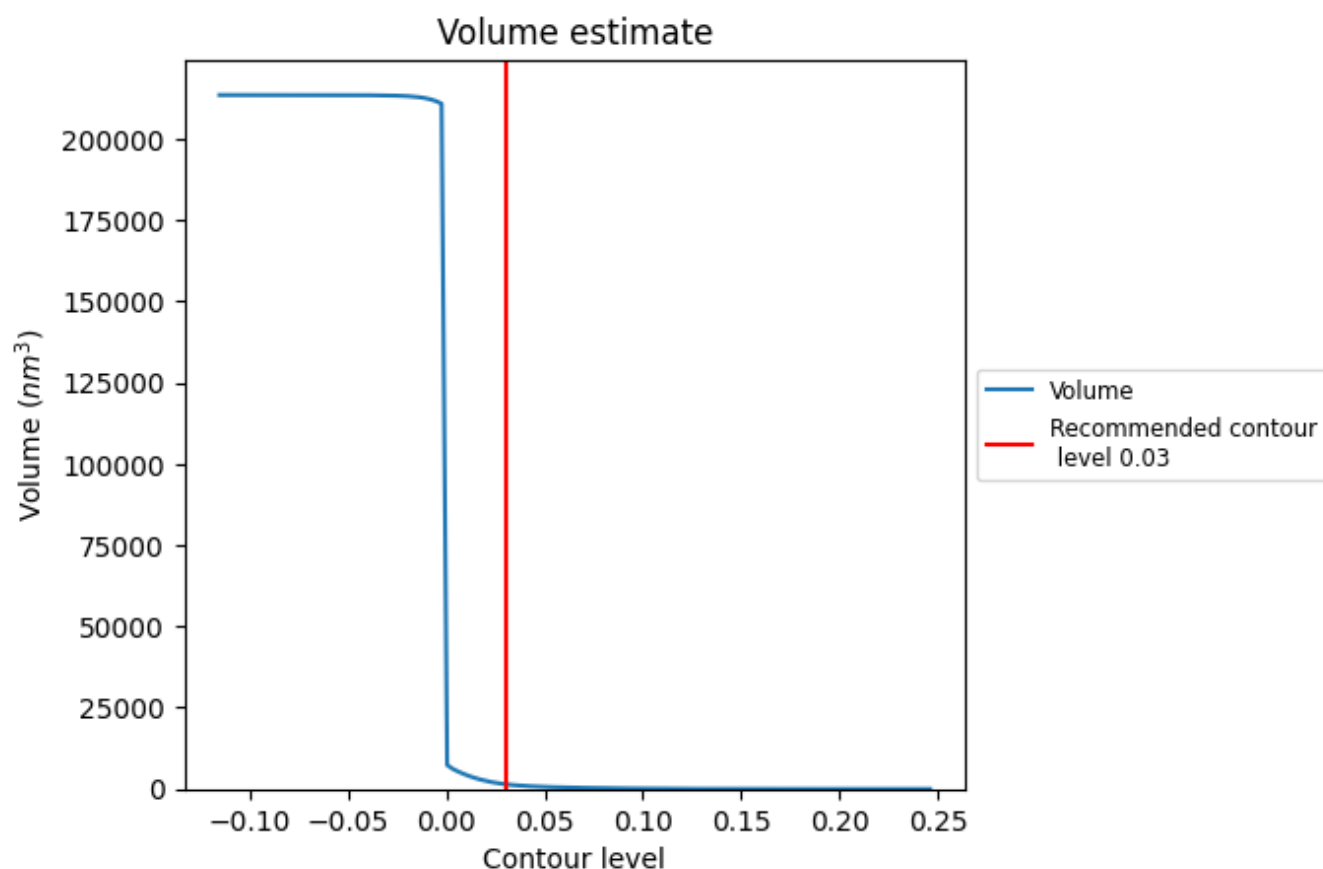
This section contains the results of statistical analysis of the map.

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.

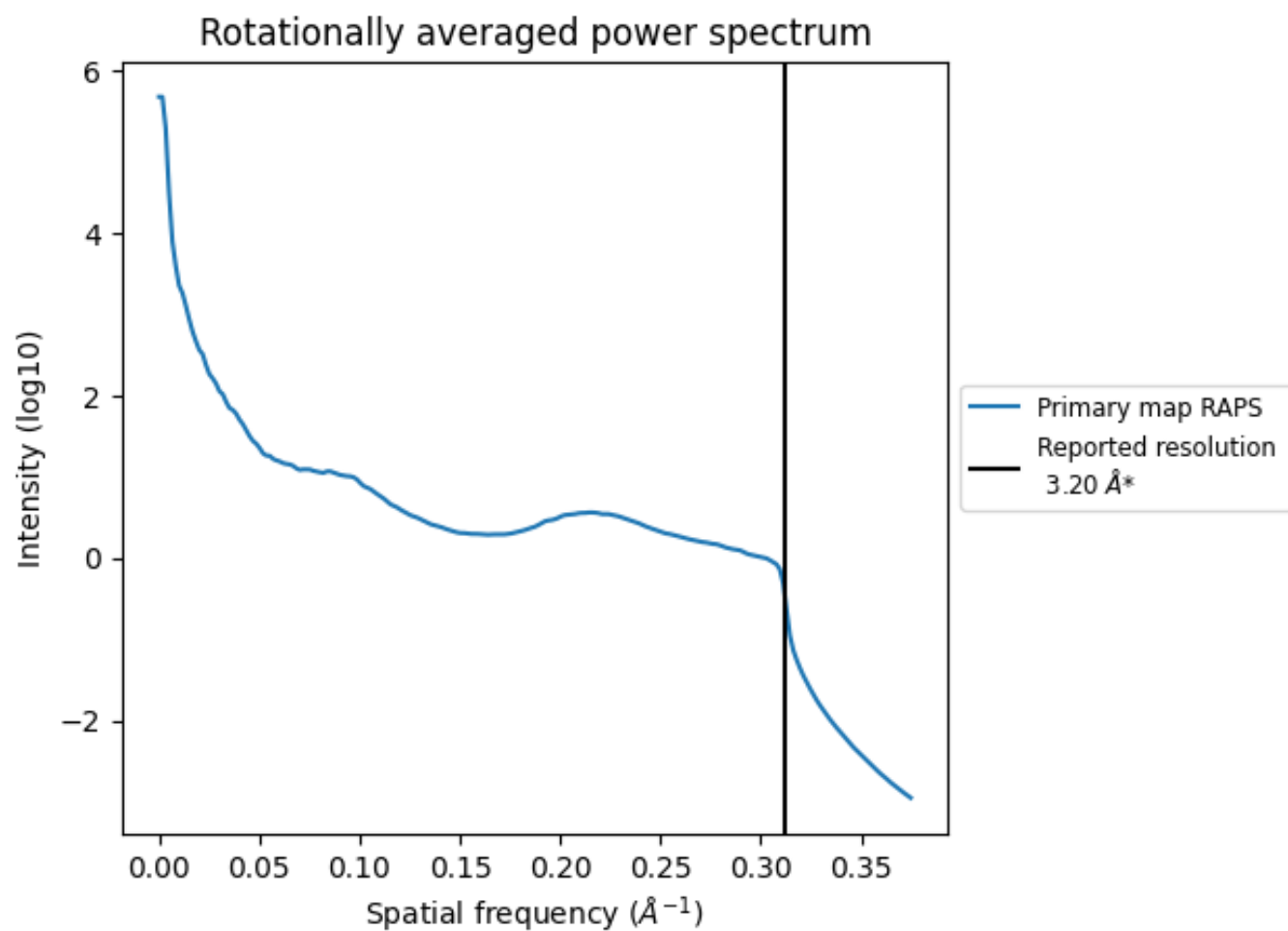
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1466 nm^3 ; this corresponds to an approximate mass of 1324 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 ⓘ

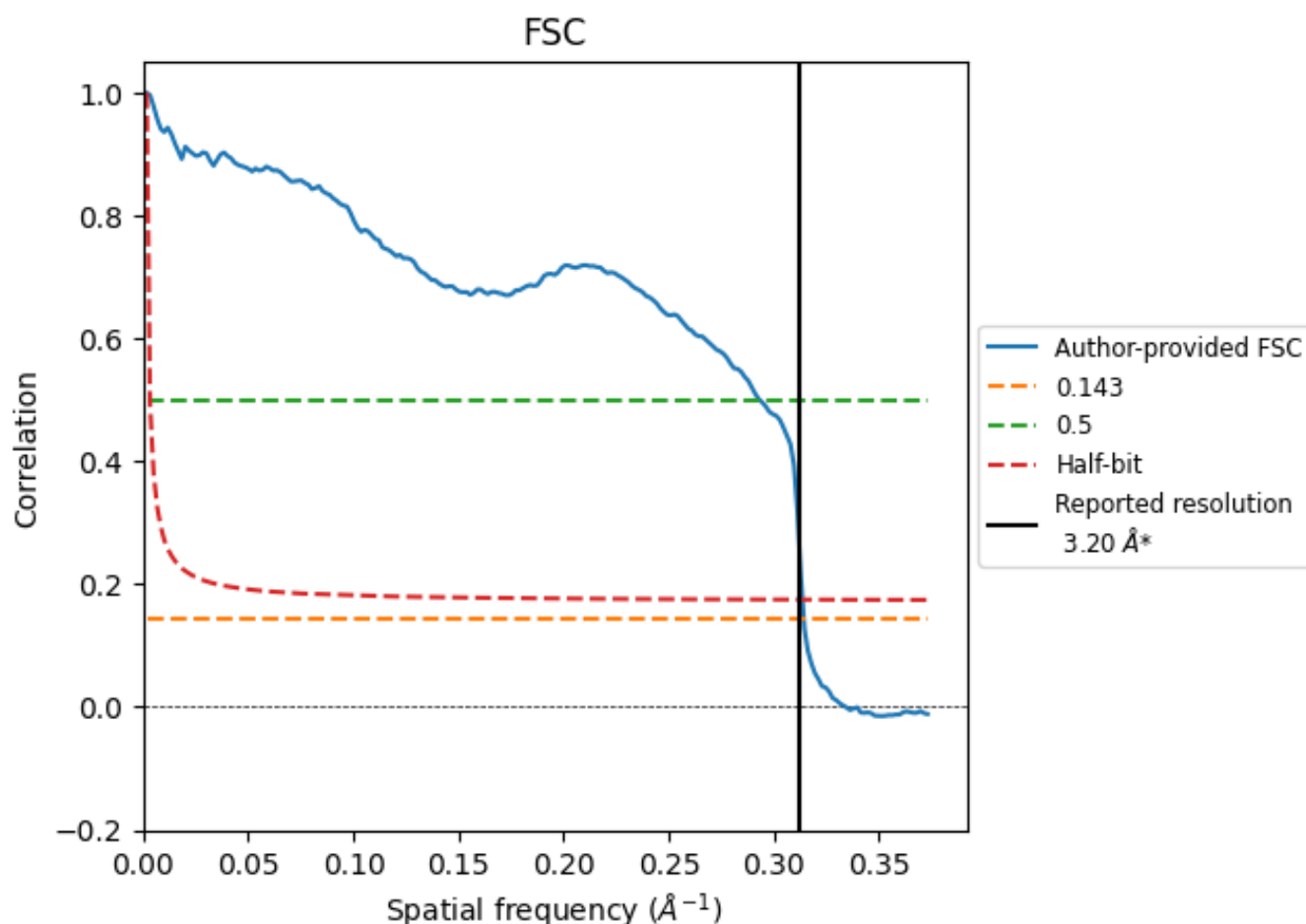


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

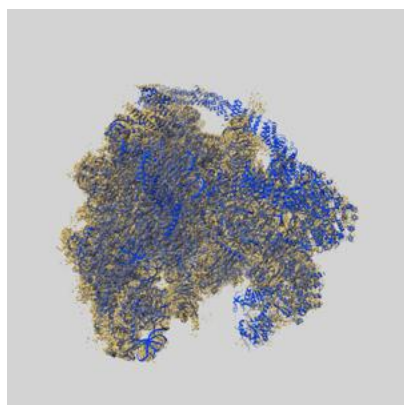
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.18	3.41	3.19
Unmasked-calculated*	-	-	-

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

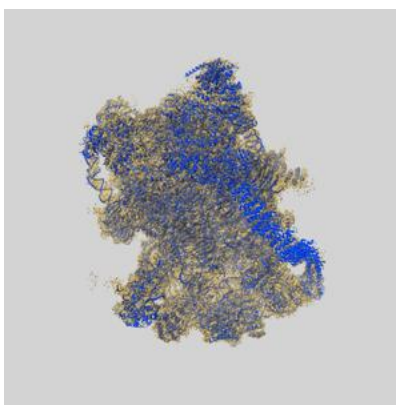
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0949 and PDB model 6LQP. Per-residue inclusion information can be found in section 3 on page 17.

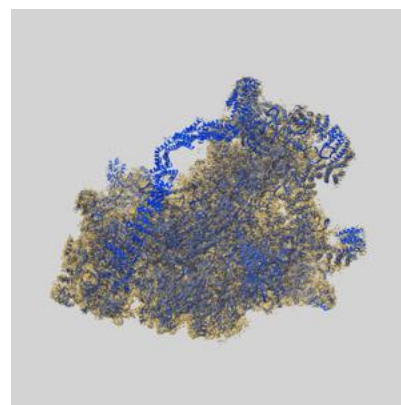
9.1 Map-model overlay [i](#)



X



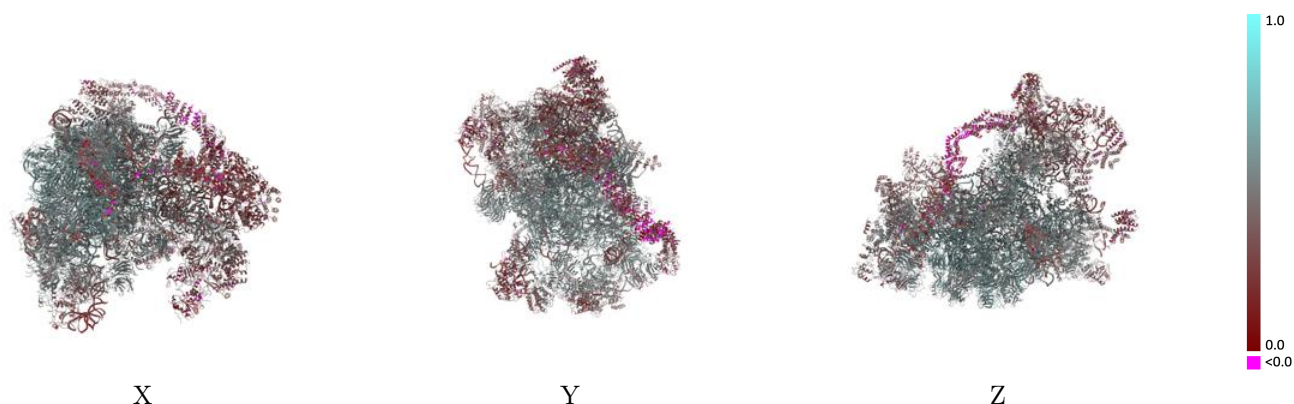
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

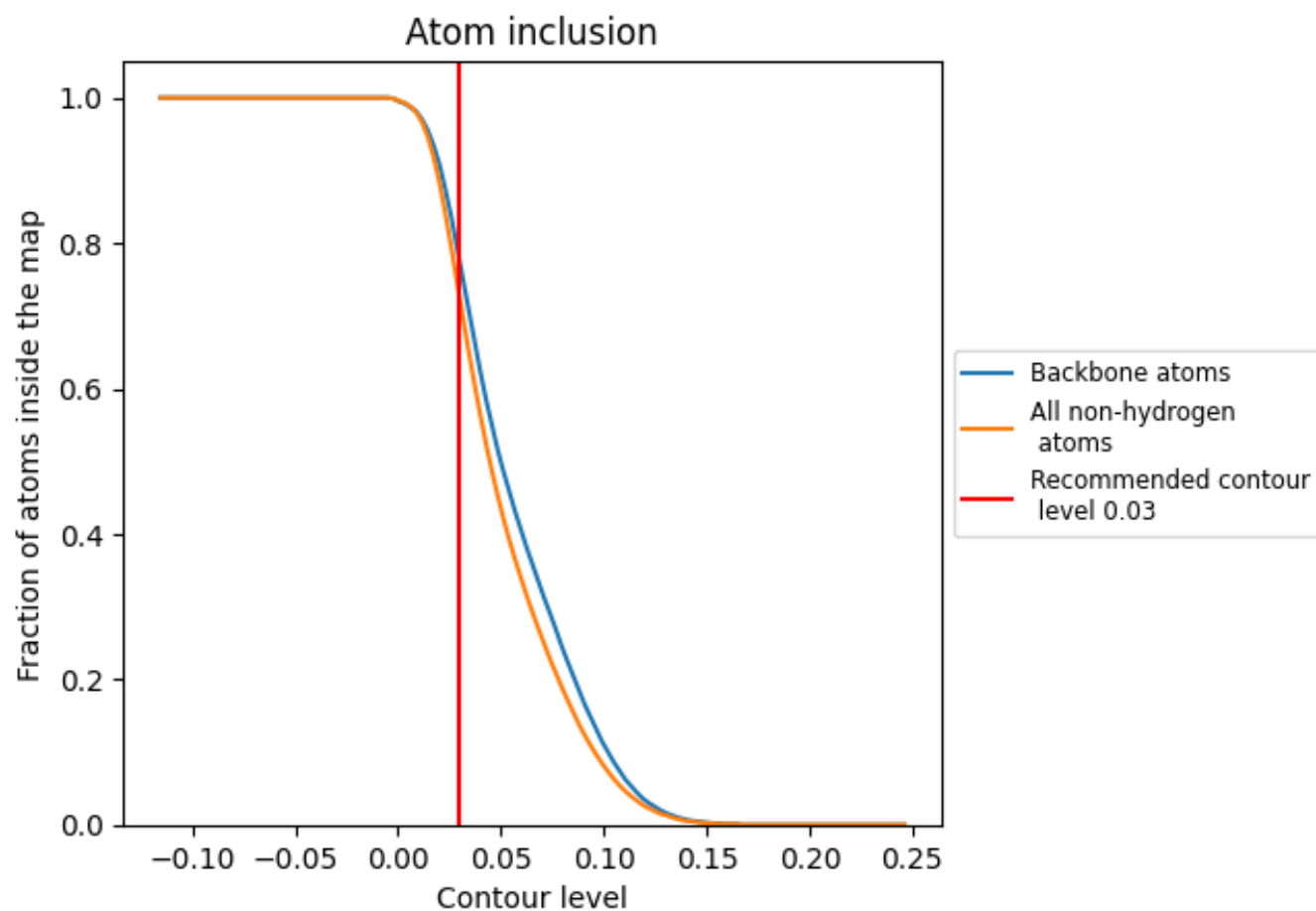


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 72% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7240	 0.4710
3A	 0.9050	 0.5090
3B	 0.8850	 0.5680
3C	 0.7980	 0.5000
3D	 0.8130	 0.5140
3E	 0.7920	 0.4870
3F	 0.7810	 0.4970
3G	 0.8710	 0.5540
3H	 0.8270	 0.5340
5A	 0.8940	 0.4880
5B	 0.7230	 0.4830
5C	 0.8960	 0.5750
5D	 0.8260	 0.5310
5E	 0.8190	 0.5440
5F	 0.9230	 0.5830
5G	 0.8720	 0.5680
5H	 0.8170	 0.5270
5I	 0.8990	 0.5770
5J	 0.7060	 0.5110
5K	 0.8810	 0.5670
A4	 0.8400	 0.5160
A5	 0.8530	 0.5350
A8	 0.5490	 0.3710
A9	 0.7580	 0.4200
AE	 0.3280	 0.3250
AF	 0.8920	 0.5540
AG	 0.8330	 0.5210
B1	 0.9100	 0.5770
B2	 0.8170	 0.5040
B3	 0.7660	 0.4720
B6	 0.7450	 0.4690
B8	 0.8980	 0.5670
BE	 0.9110	 0.5760
RA	 0.5410	 0.4120
RB	 0.6400	 0.4590



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Chain	Atom inclusion	Q-score
RC	 0.7470	 0.5120
RE	 0.6650	 0.4410
RF	 0.5400	 0.4040
RG	 0.6890	 0.4530
RH	 0.8230	 0.5330
RI	 0.8460	 0.5290
RJ	 0.8370	 0.5370
RK	 0.8320	 0.5310
RL	 0.5790	 0.4100
RM	 0.2390	 0.3000
RN	 0.6800	 0.4410
RO	 0.7590	 0.4580
RP	 0.3010	 0.3170
RQ	 0.7450	 0.5040
RS	 0.3360	 0.2730
RT	 0.8270	 0.5200
RV	 0.8290	 0.5350
RW	 0.7040	 0.4960
RY	 0.4400	 0.3860
SA	 0.7270	 0.4210
SC	 0.8170	 0.5370
SF	 0.6230	 0.4190
SG	 0.8590	 0.5590
SH	 0.4570	 0.4220
SI	 0.6410	 0.4510
SJ	 0.5160	 0.3740
SK	 0.8580	 0.5550
SM	 0.4930	 0.3660
SN	 0.0400	 0.2760
SO	 0.8530	 0.5380
SP	 0.8680	 0.5470
SR	 0.8980	 0.5690
ST	 0.6950	 0.4700
SX	 0.8400	 0.5470
SY	 0.8750	 0.5630
SZ	 0.6750	 0.4650
Sc	 0.8620	 0.5520
Sd	 0.8600	 0.5610
X1	 0.6560	 0.4480