



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 05:52 AM UTC

PDB ID : 6LQT / pdb_00006lqt
EMDB ID : EMD-0953
Title : Cryo-EM structure of 90S small subunit preribosomes in transition states (State E)
Authors : Du, Y.; Ye, K.
Deposited on : 2020-01-14
Resolution : 4.90 Å(reported)
Based on initial model : 6LQS

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

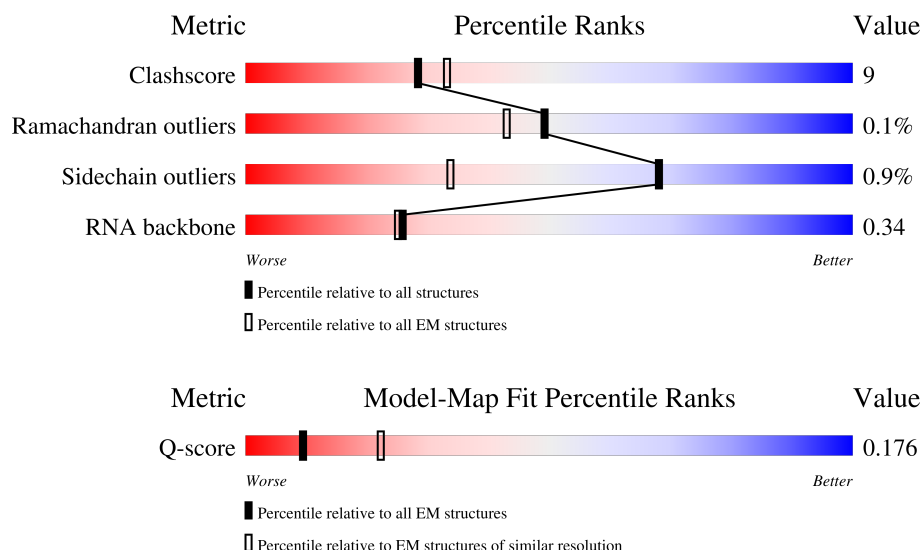
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.90 Å.

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



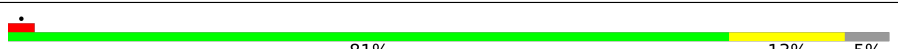
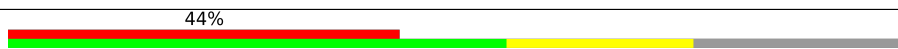
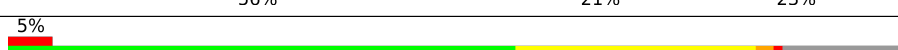
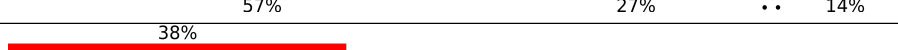
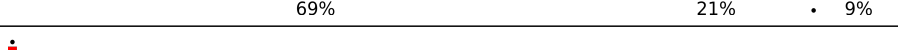
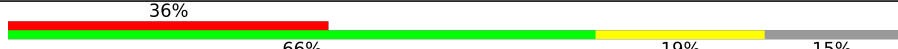
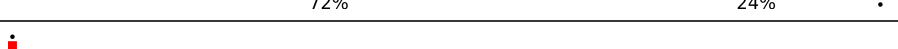
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	1274 (4.40 - 5.40)

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

Mol	Chain	Length	Quality of chain
1	3A	333	
2	5A	700	
3	SA	1809	

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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	SO	151	
13	SP	137	
14	SR	143	
15	SX	130	
16	SY	145	
17	SZ	135	
18	Sc	82	
19	Sd	67	
20	3B	327	
20	3C	327	
21	3D	504	
22	3E	511	
23	3F	572	
24	3G	126	
24	3H	126	
25	A4	776	
26	A5	643	

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Mol	Chain	Length	Quality of chain
27	A9	575	
28	AE	1769	
29	AF	513	
30	AG	896	
31	B1	923	
32	B2	943	
33	B3	817	
34	B8	594	
35	BE	939	
36	B6	440	
37	5C	554	
38	5D	250	
39	5E	593	
40	5F	183	
41	5G	290	
42	5H	610	
43	5I	489	
44	5J	217	
45	5K	189	
46	RD	1729	
47	RE	1237	
48	RF	297	
49	RH	252	
50	RJ	1183	
51	RK	367	

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Mol	Chain	Length	Quality of chain
52	RN	810	
53	RP	2493	
54	RQ	899	
55	RT	326	
56	X1	347	

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 175869 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	194	Total	C	N	O	P	0	0
			4114	1841	716	1363	194		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5A	152	Total	C	N	O	P	0	0
			3260	1455	593	1060	152		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SA	1155	Total	C	N	O	P	0	0
			24609	11001	4356	8097	1155		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SC	232	Total	C	N	O	S	0	0
			1848	1168	339	337	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SF	250	Total	C	N	O	S	0	0
			1930	1232	354	341	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	182	Total	C	N	O	S	0	0
			1457	917	273	266	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SI	164	Total	C	N	O	S	0	0
			1310	847	222	241			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SJ	140	Total	C	N	O	S	0	0
			1104	689	211	202	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	137	Total	C	N	O	S	0	0
			1113	715	212	183	3		

- Molecule 12 is a protein called 40S ribosomal protein S13.

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

- Molecule 13 is a protein called 40S ribosomal protein S14-A.

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

- Molecule 14 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 15 is a protein called 40S ribosomal protein S22-B.

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

- Molecule 16 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SY	106	Total	C	N	O	S	0	0
			807	515	148	142	2		

- Molecule 17 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	SZ	123	Total	C	N	O	0	0
			986	626	188	172		

- Molecule 18 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 19 is a protein called 40S ribosomal protein S28-A.

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

- Molecule 20 is a protein called rRNA 2'-O-methyltransferase fibrillar.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	3B	240	Total	C	N	O	S	0	0
			1865	1184	333	338	10		
20	3C	225	Total	C	N	O	S	0	0
			1763	1120	316	317	10		

- Molecule 21 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	3D	378	Total	C	N	O	S	0	0
			2974	1886	511	568	9		

- Molecule 22 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	3E	432	Total	C	N	O	S	0	0
			3041	1895	545	592	9		

- Molecule 23 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	3F	437	Total	C	N	O	S	0	0
			3498	2227	609	652	10		

- Molecule 24 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	3G	121	Total	C	N	O	S	0	0
			916	583	158	171	4		
24	3H	121	Total	C	N	O	S	0	0
			916	583	158	171	4		

- Molecule 25 is a protein called U3 small nucleolar RNA-associated protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	A4	664	Total	C	N	O	S	0	0
			5243	3320	912	990	21		

- Molecule 26 is a protein called U3 small nucleolar RNA-associated protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	A5	372	Total	C	N	O	S	0	0
			2943	1869	494	569	11		

- Molecule 27 is a protein called U3 small nucleolar RNA-associated protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A9	37	Total	C	N	O	S	0	0
			299	186	60	51	2		

- Molecule 28 is a protein called U3 small nucleolar RNA-associated protein 10.

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

- Molecule 29 is a protein called U3 small nucleolar RNA-associated protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AF	479	Total	C	N	O	S	0	0
			3807	2395	685	715	12		

- Molecule 30 is a protein called NET1-associated nuclear protein 1.

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

- Molecule 31 is a protein called Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	B1	806	Total	C	N	O	S	0	0
			6427	4104	1099	1205	19		

- Molecule 32 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B2	825	Total	C	N	O	S	0	0
			6502	4156	1096	1223	27		

- Molecule 33 is a protein called U3 small nucleolar RNA-associated protein 13.

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

- Molecule 34 is a protein called U3 small nucleolar RNA-associated protein 18.

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

- Molecule 35 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BE	823	Total	C	N	O	S	0	0
			6475	4107	1119	1228	21		

- Molecule 36 is a protein called U3 small nucleolar RNA-associated protein 6.

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

- Molecule 37 is a protein called U3 small nucleolar RNA-associated protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	5C	458	Total	C	N	O	S	0	0
			3612	2276	636	689	11		

- Molecule 38 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	5D	70	Total	C	N	O	S	0	0
			609	377	126	105	1		

- Molecule 39 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	5E	193	Total	C	N	O	S	0	0
			1564	970	280	310	4		

- Molecule 40 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	5F	182	Total	C	N	O	S	0	0
			1530	967	287	269	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	5G	216	Total	C	N	O	S	0	0
			1732	1093	321	312	6		

- Molecule 42 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	5H	74	Total	C	N	O	0	0
			596	373	122	101		

- Molecule 43 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	5I	460	Total	C	N	O	S	0	0
			3756	2349	685	706	16		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
44	5J	134	Total	C	N	O	S	0	0
			1127	712	205	207	3		

- Molecule 45 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	5K	166	Total	C	N	O	S	0	0
			1323	849	238	226	10		

- Molecule 46 is a protein called rRNA biogenesis protein RRP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	RD	316	Total	C	N	O	S	0	0
			2413	1541	415	452	5		

- Molecule 47 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	RE	1090	Total	C	N	O	S	0	0
			8805	5720	1452	1609	24		

- Molecule 48 is a protein called Ribosomal RNA-processing protein 7.

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

- Molecule 49 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	RH	219	Total	C	N	O	S	0	0
			1719	1090	299	319	11		

- Molecule 50 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	RJ	731	Total	C	N	O	S	0	0
			5935	3812	1051	1046	26		

- Molecule 51 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

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

- Molecule 52 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	RN	53	Total	C	N	O	S	0	0
			450	273	88	88	1		

- Molecule 53 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	RP	2180	Total	C	N	O	S	0	0
			12716	7827	2389	2484	16		

- Molecule 54 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	RQ	226	Total	C	N	O	S	0	0
			1655	1026	314	313	2		

- Molecule 55 is a protein called Pno1.

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

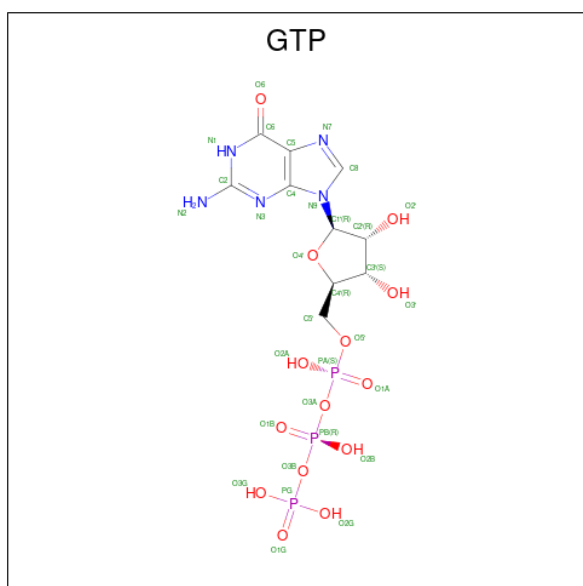
- Molecule 56 is a protein called Unassigned helices.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	X1	80	Total	C	N	O	0	0
			400	240	80	80		

- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
57	Sc	1	Total	Zn	0
			1	1	
57	5K	1	Total	Zn	0
			1	1	

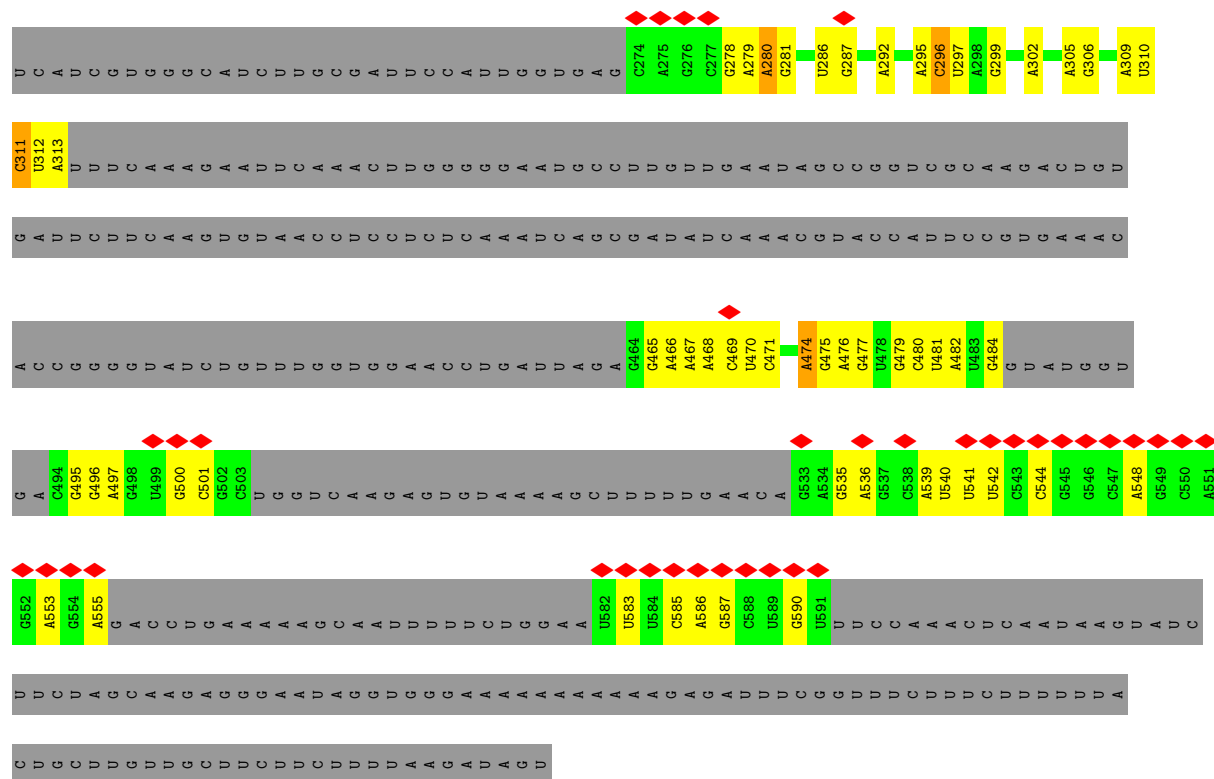
- Molecule 58 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



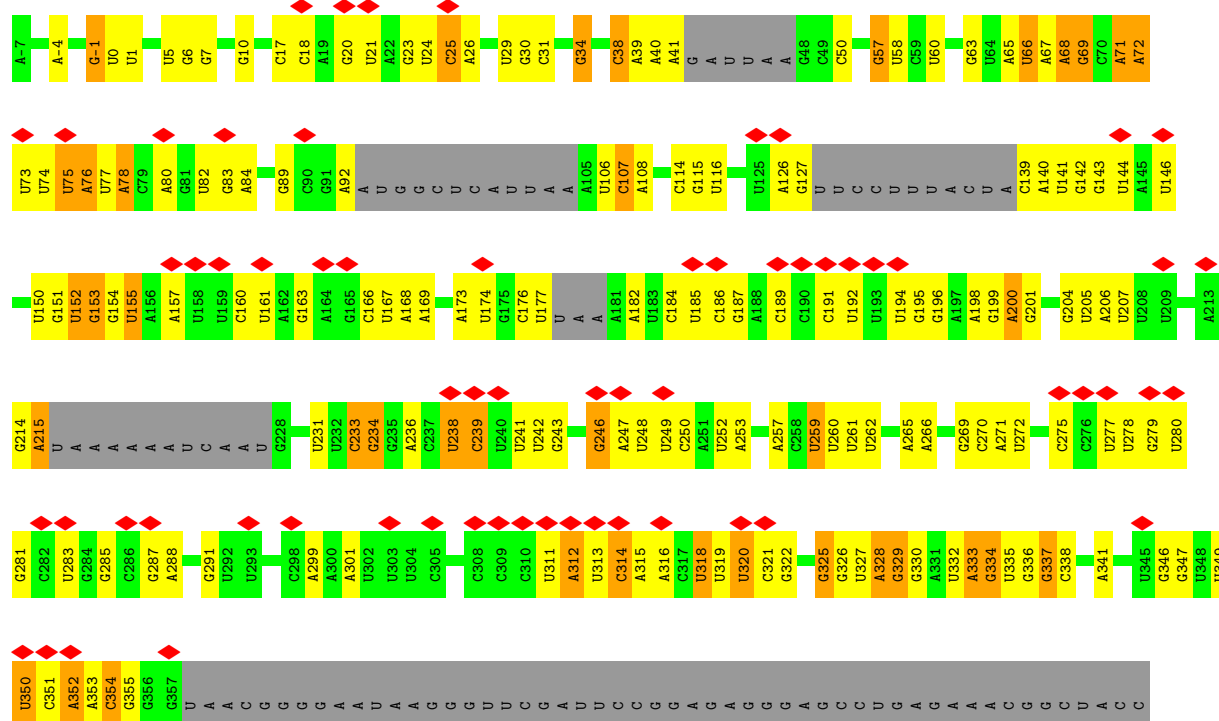
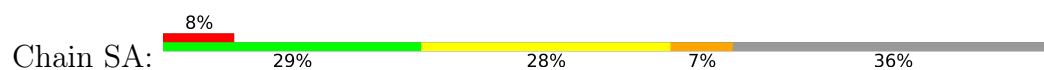
Mol	Chain	Residues	Atoms					AltConf
58	RJ	1	Total	C	N	O	P	0
			32	10	5	14	3	

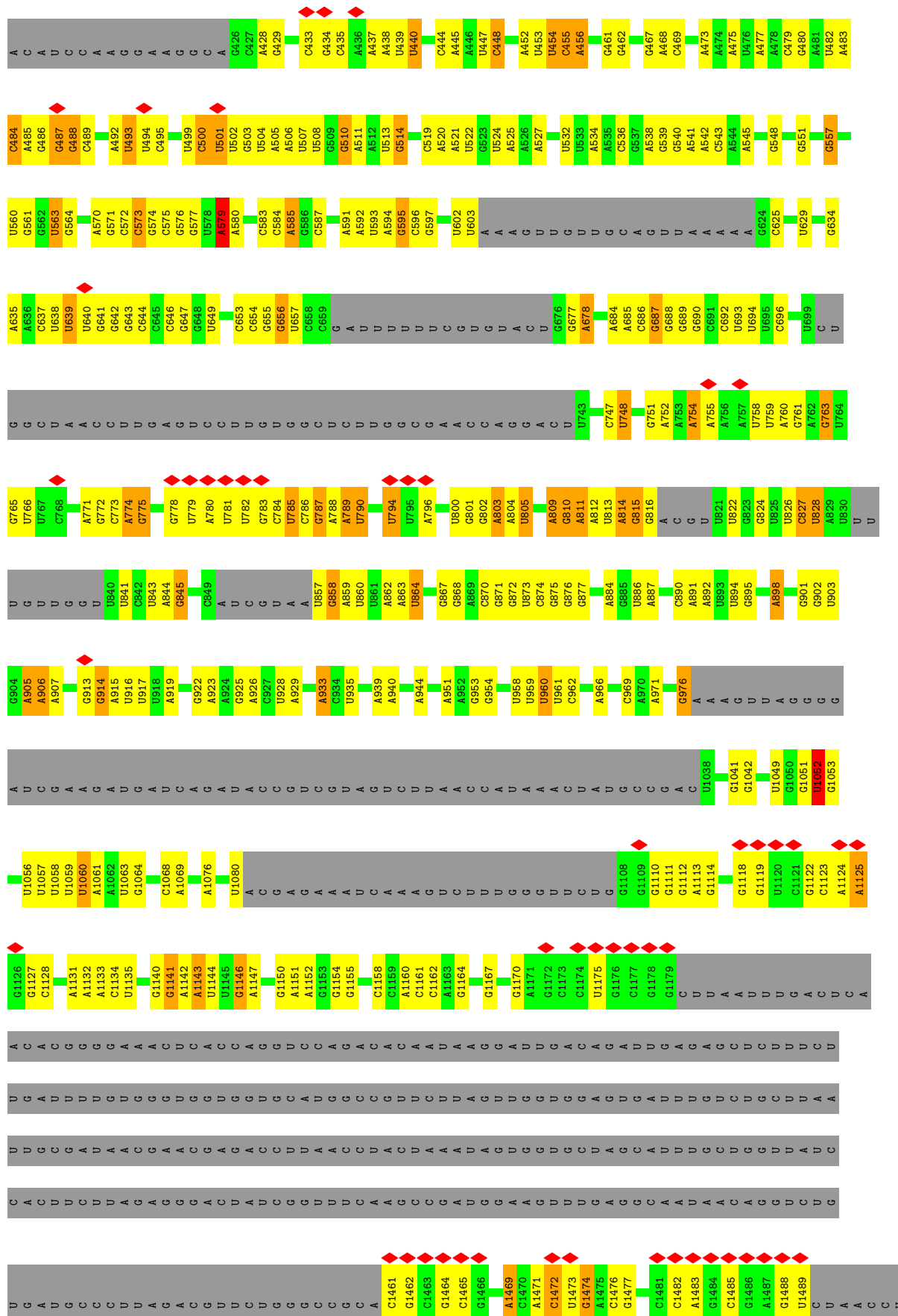
- Molecule 59 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

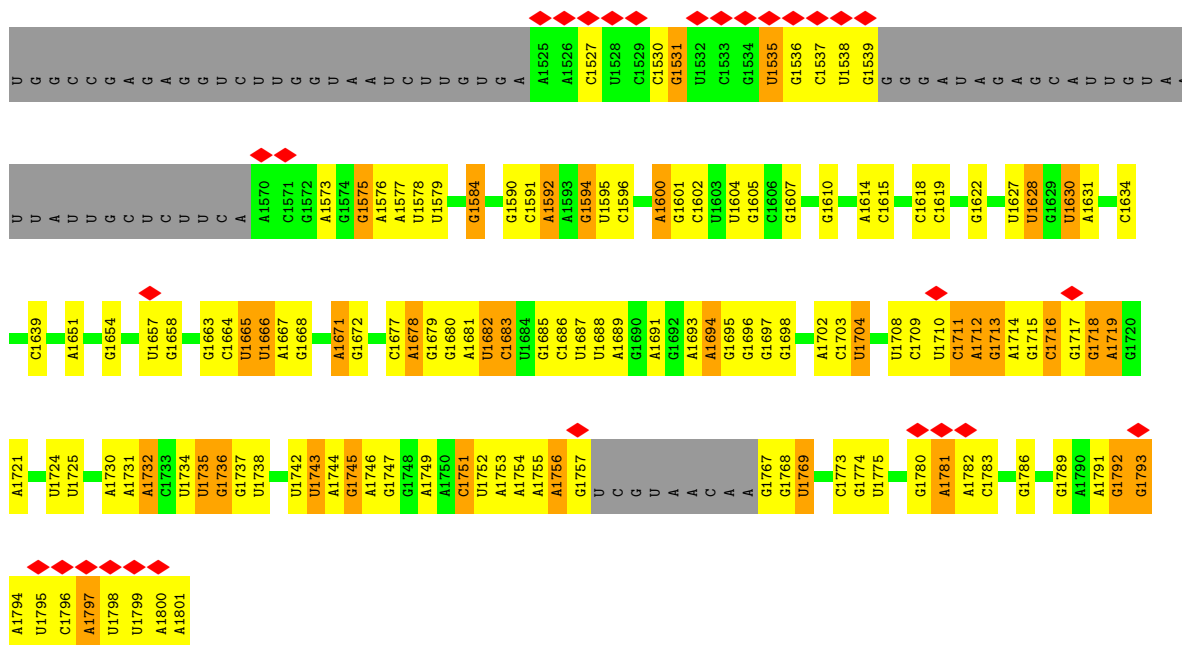
Mol	Chain	Residues	Atoms		AltConf
59	RJ	1	Total	Mg	0
			1	1	



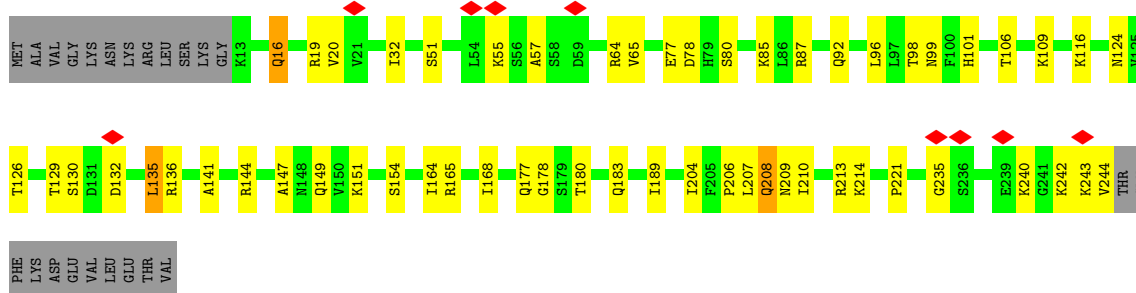
• Molecule 3: 18S pre-rRNA



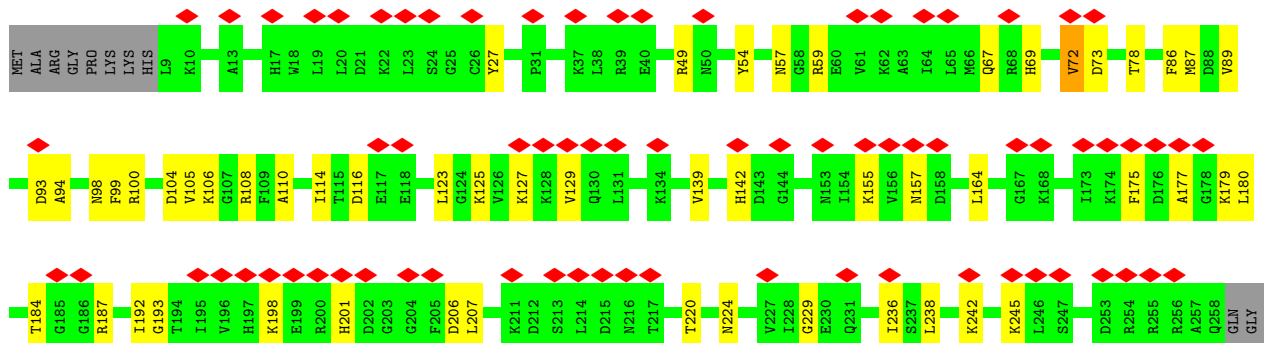
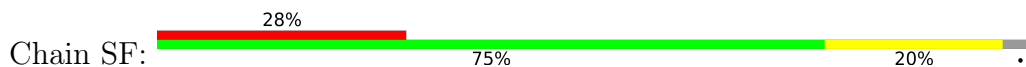




- Molecule 4: 40S ribosomal protein S1-A

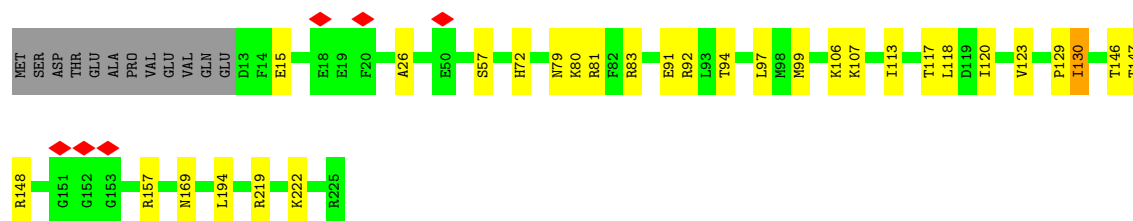


- Molecule 5: 40S ribosomal protein S4-A



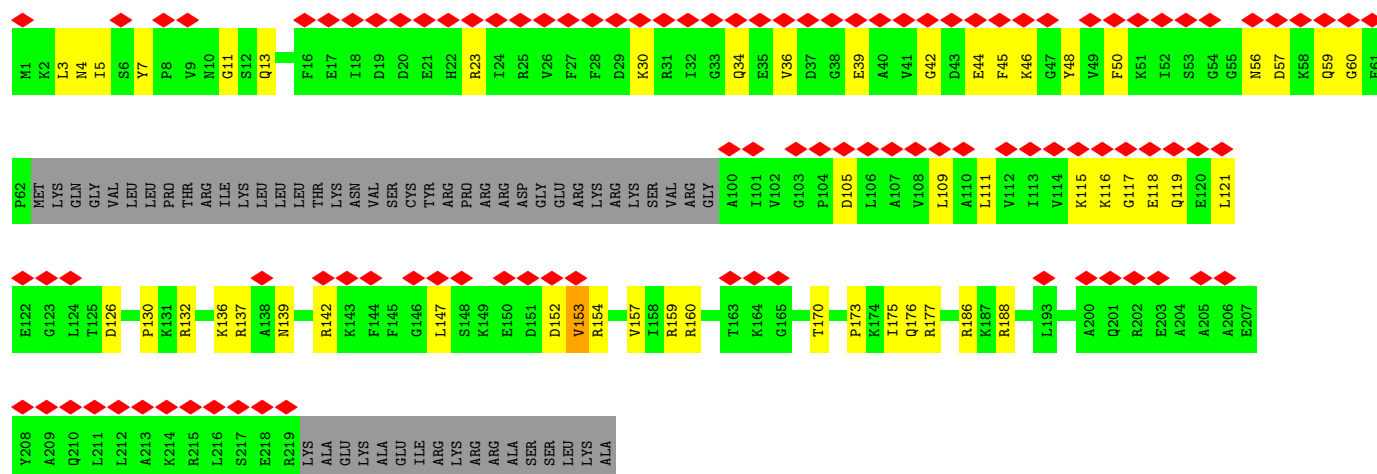
- Molecule 6: 40S ribosomal protein S5

Chain SG: 



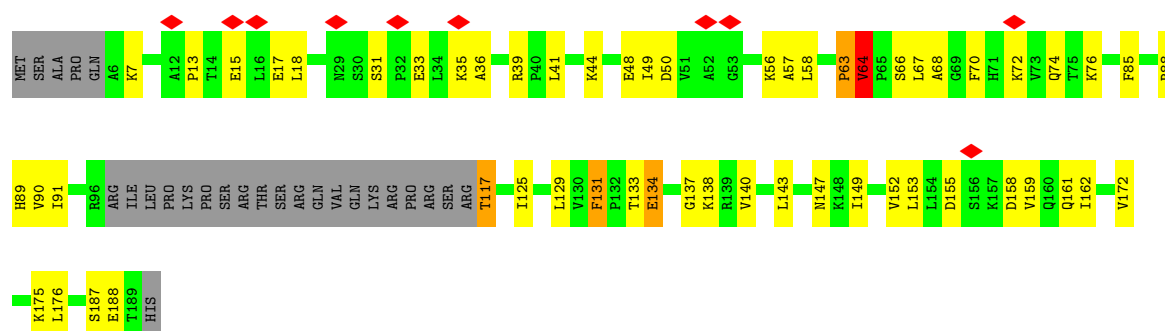
• Molecule 7: 40S ribosomal protein S6-A

Chain SH: 

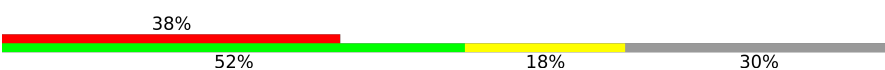


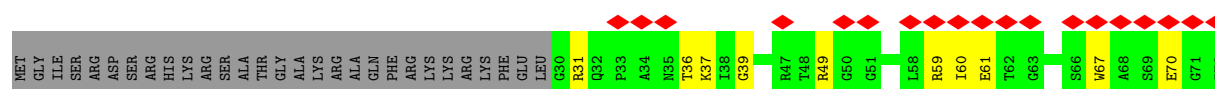
• Molecule 8: 40S ribosomal protein S7-A

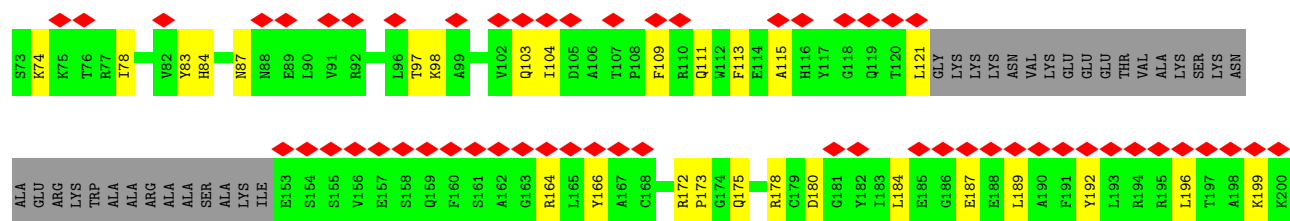
Chain SI: 



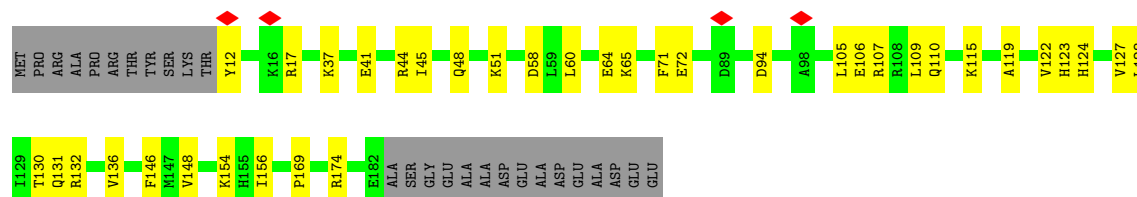
• Molecule 9: 40S ribosomal protein S8-A

Chain SJ: 

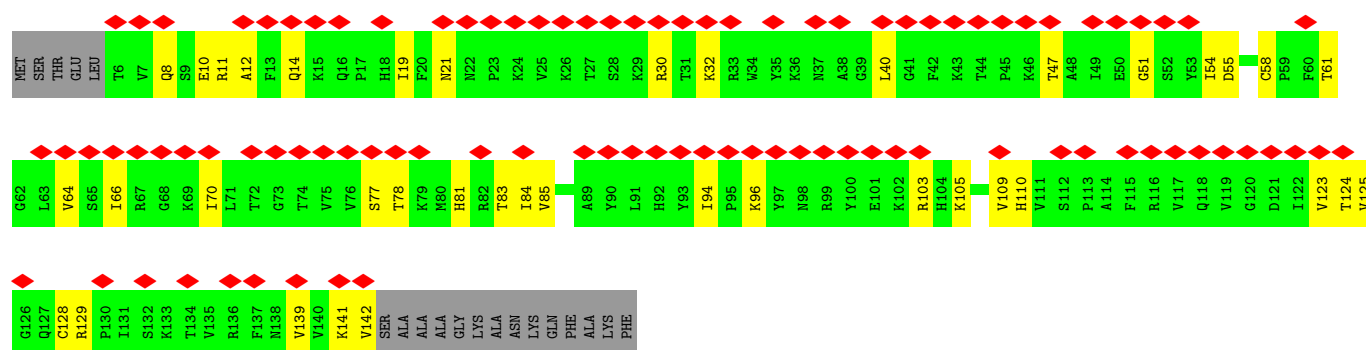




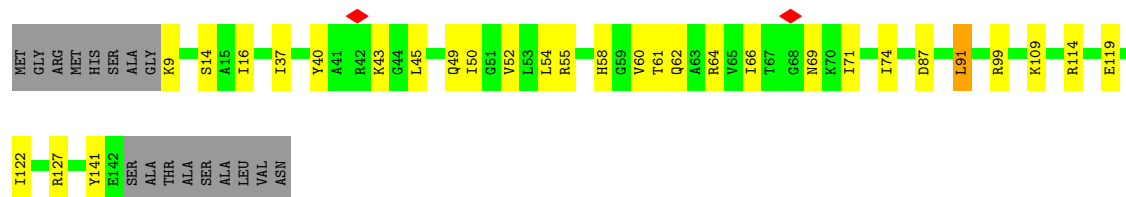
• Molecule 10: 40S ribosomal protein S9-A



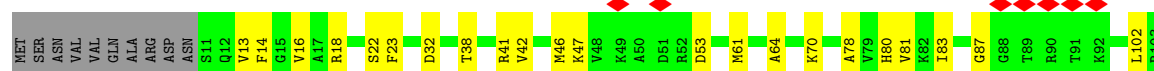
• Molecule 11: 40S ribosomal protein S11-A

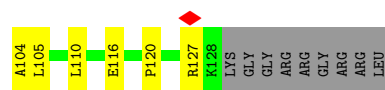


• Molecule 12: 40S ribosomal protein S13

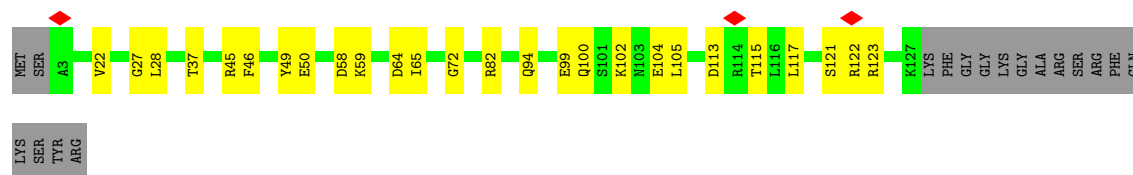


• Molecule 13: 40S ribosomal protein S14-A

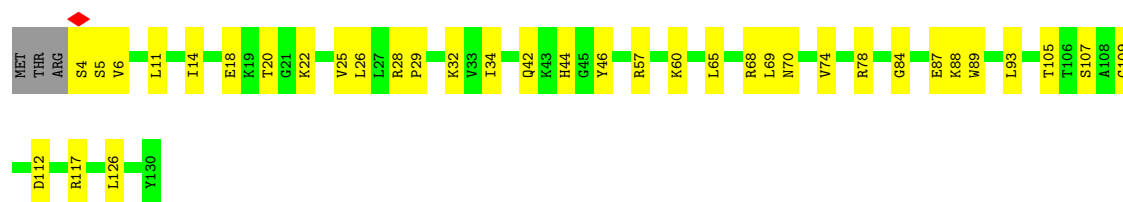




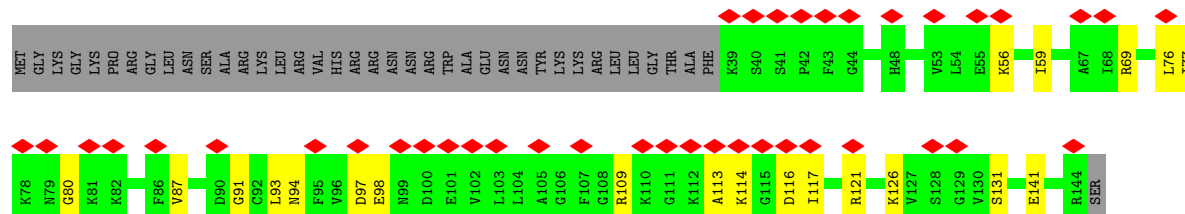
- Molecule 14: 40S ribosomal protein S16-A



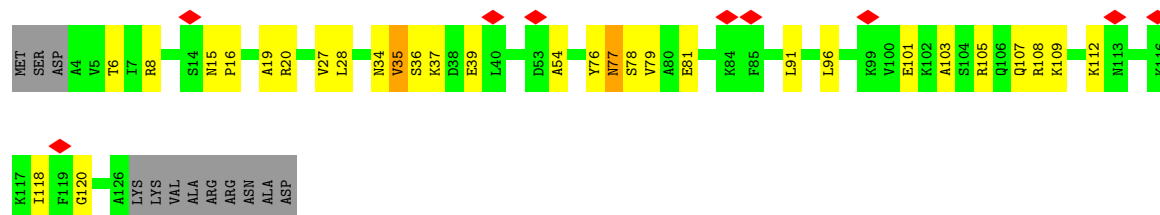
- Molecule 15: 40S ribosomal protein S22-B



- Molecule 16: 40S ribosomal protein S23-A

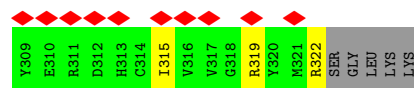


- Molecule 17: 40S ribosomal protein S24-A

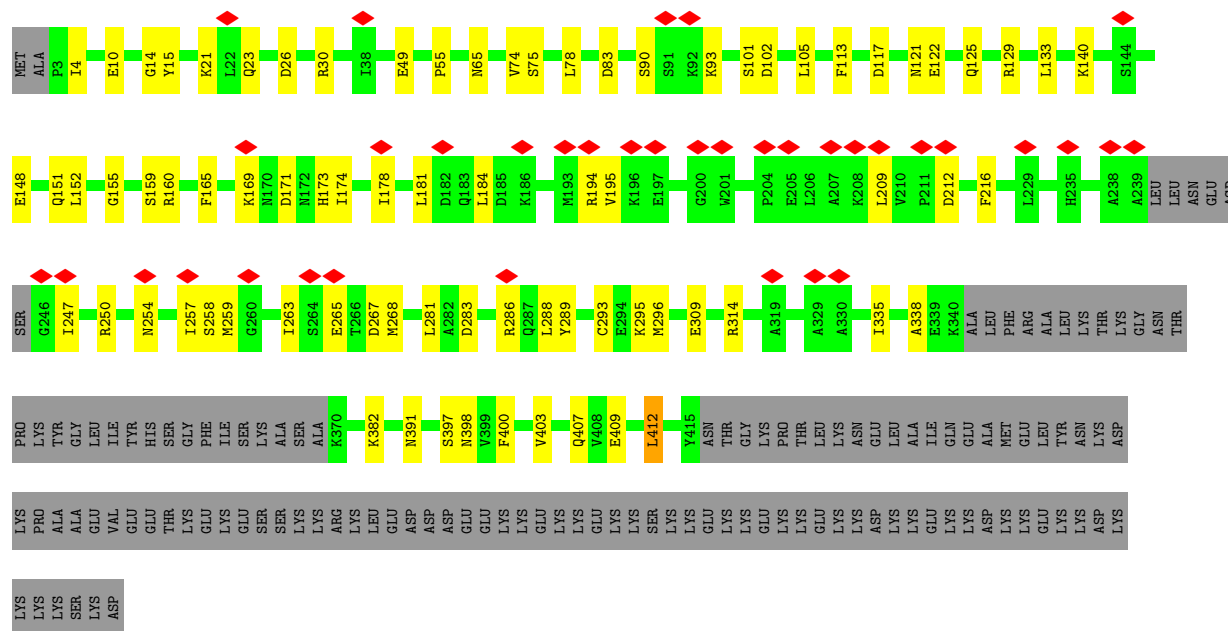


- Molecule 18: 40S ribosomal protein S27-A

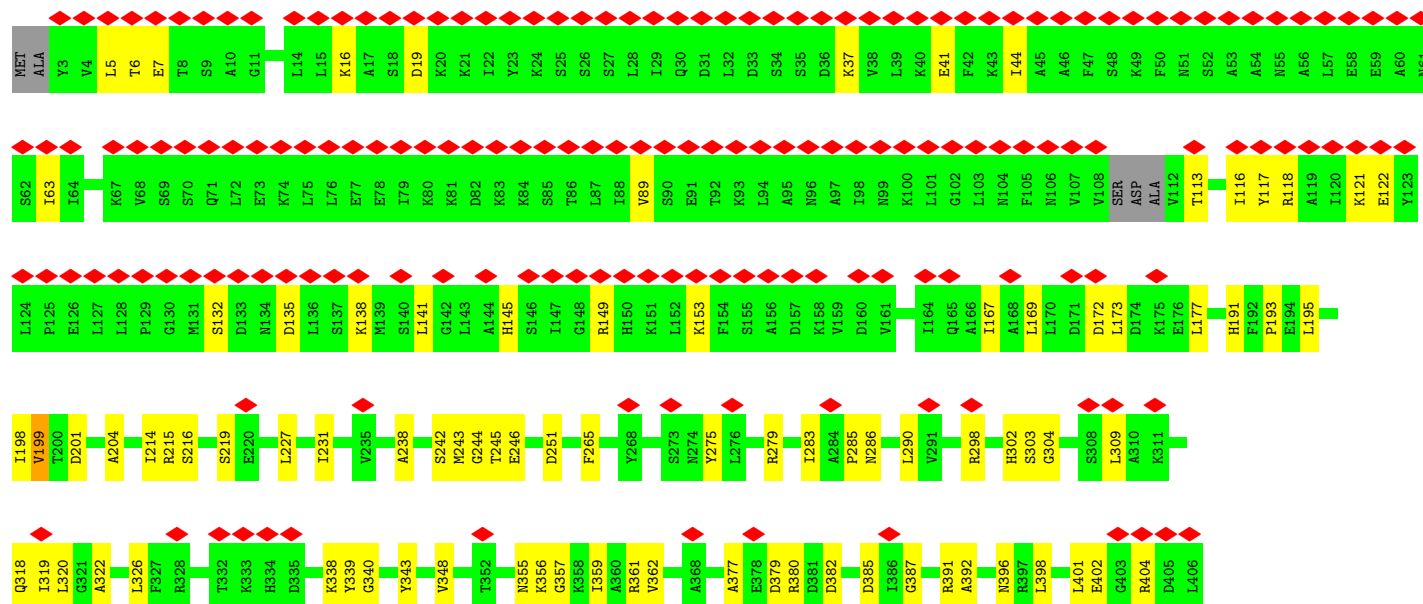




• Molecule 21: Nucleolar protein 56



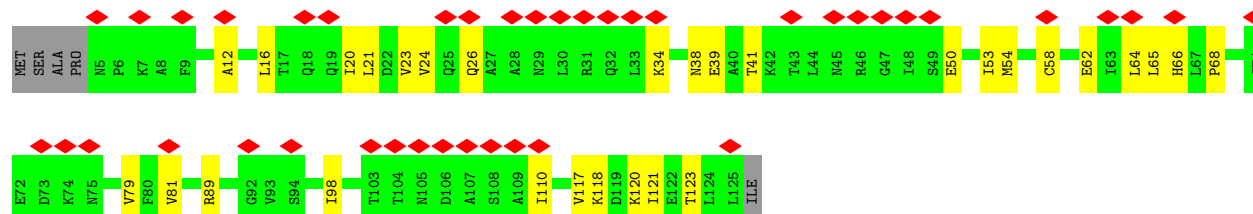
• Molecule 22: Nucleolar protein 58



- Molecule 23: Ribosomal RNA-processing protein 9

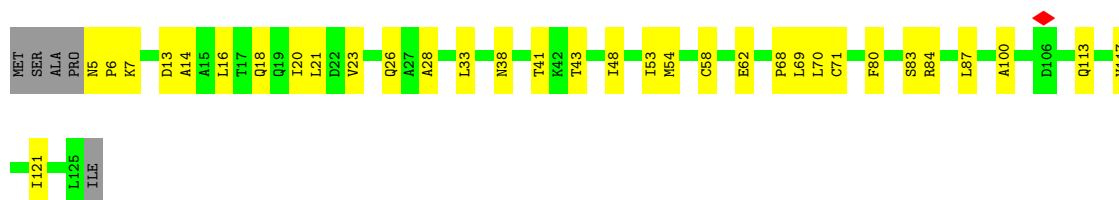


- Molecule 24: 13 kDa ribonucleoprotein-associated protein

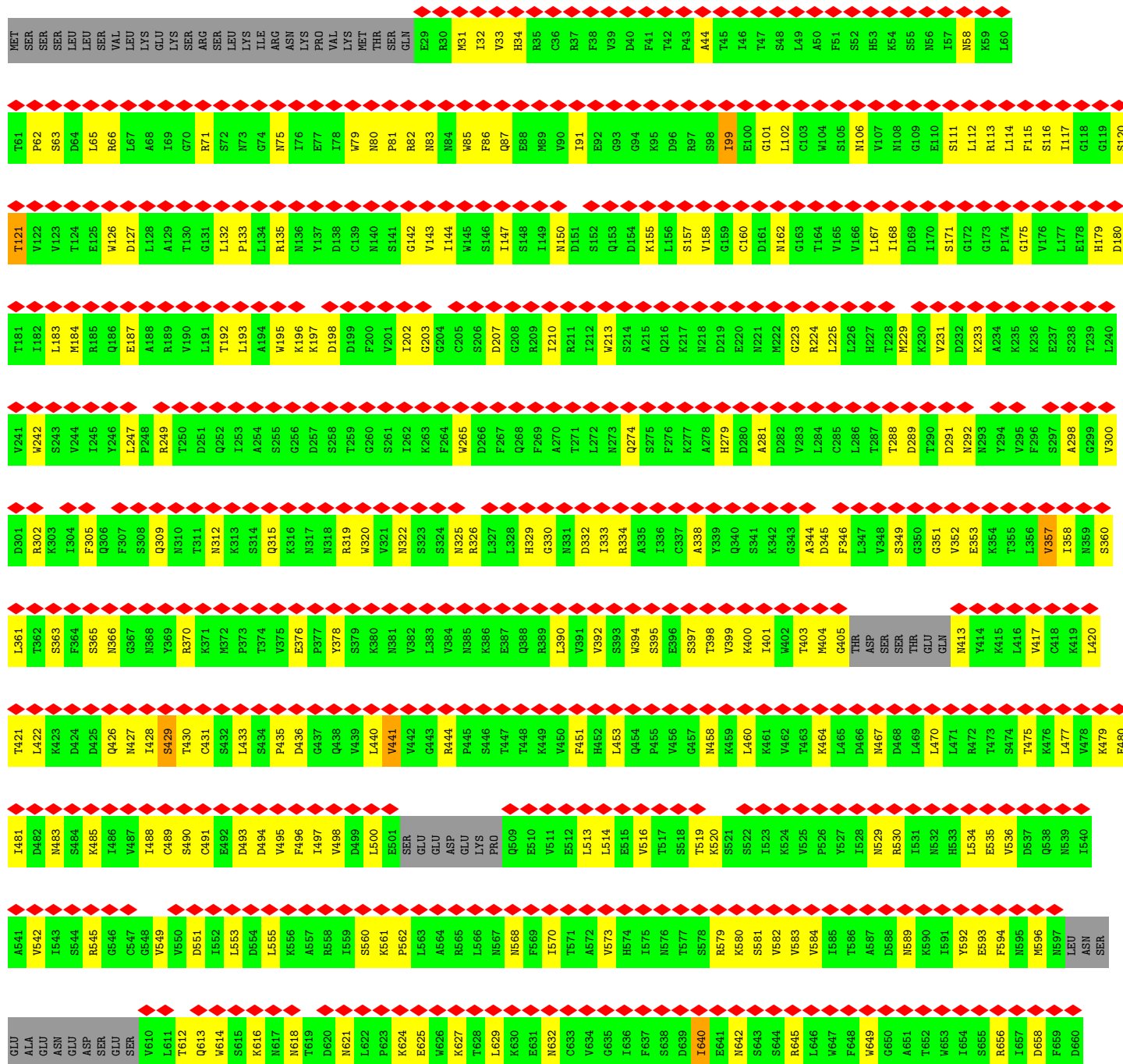
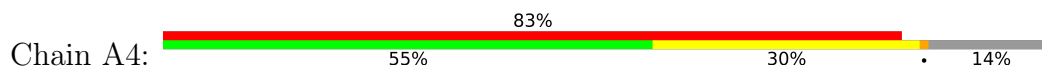


- Molecule 24: 13 kDa ribonucleoprotein-associated protein

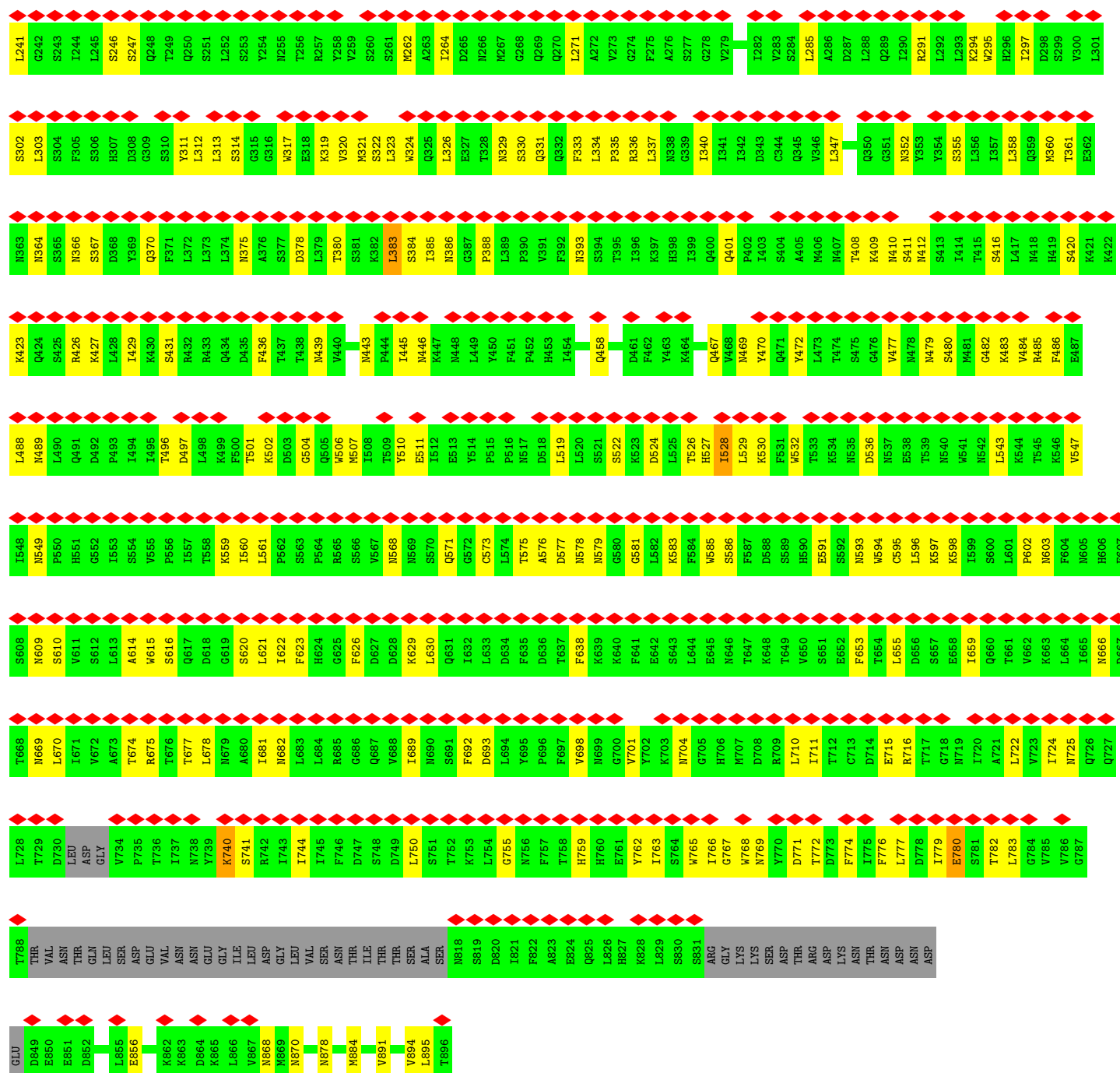


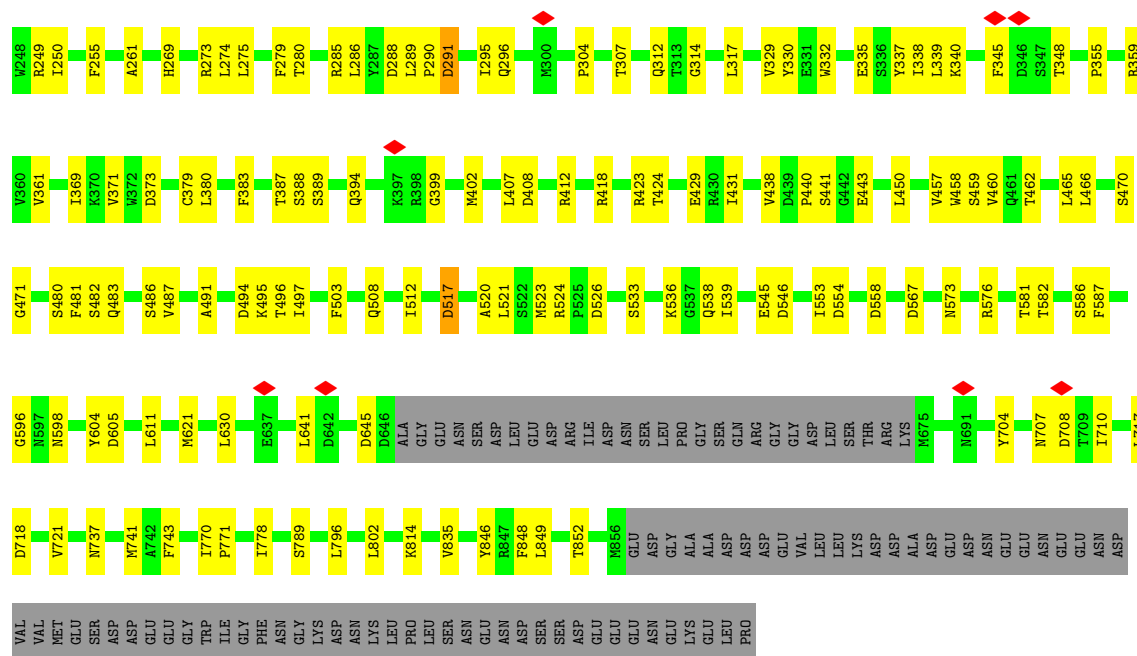


• Molecule 25: U3 small nucleolar RNA-associated protein 4

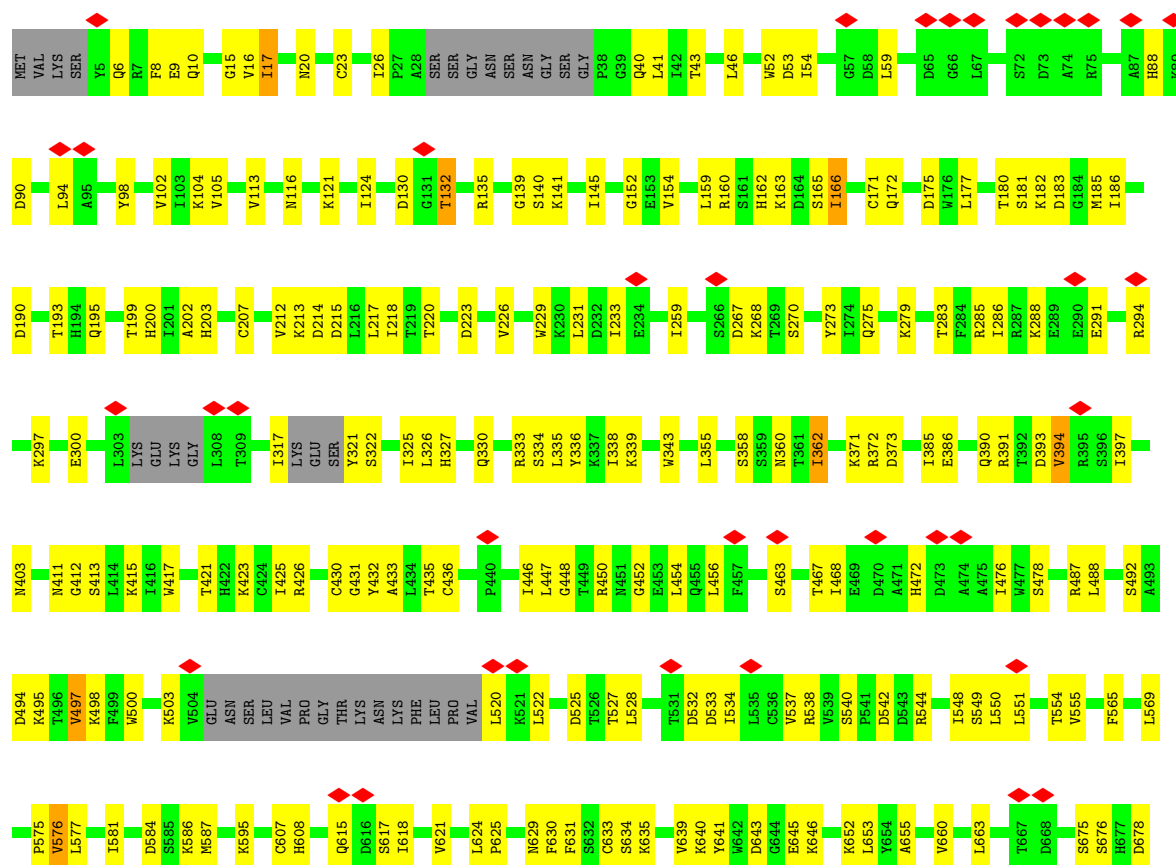


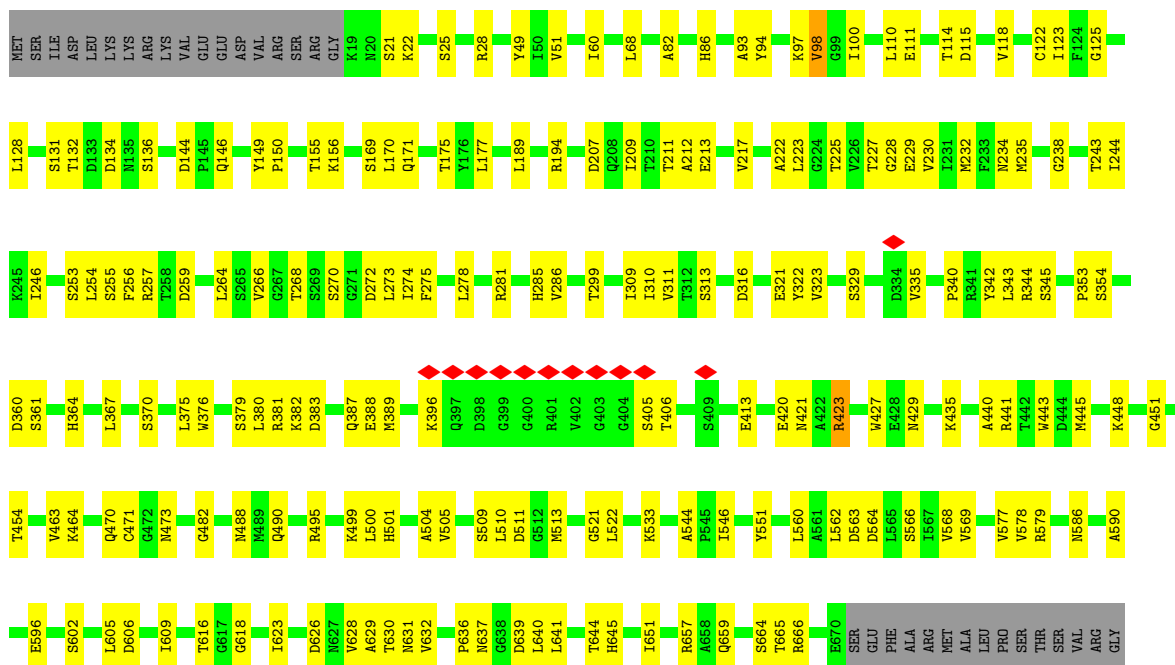


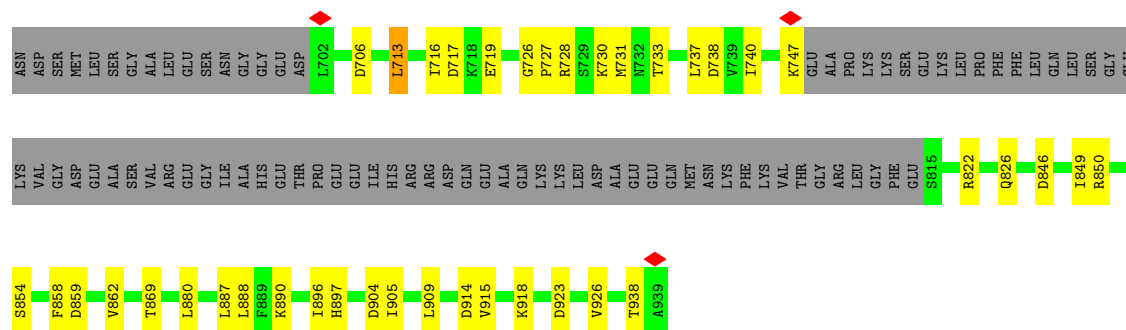




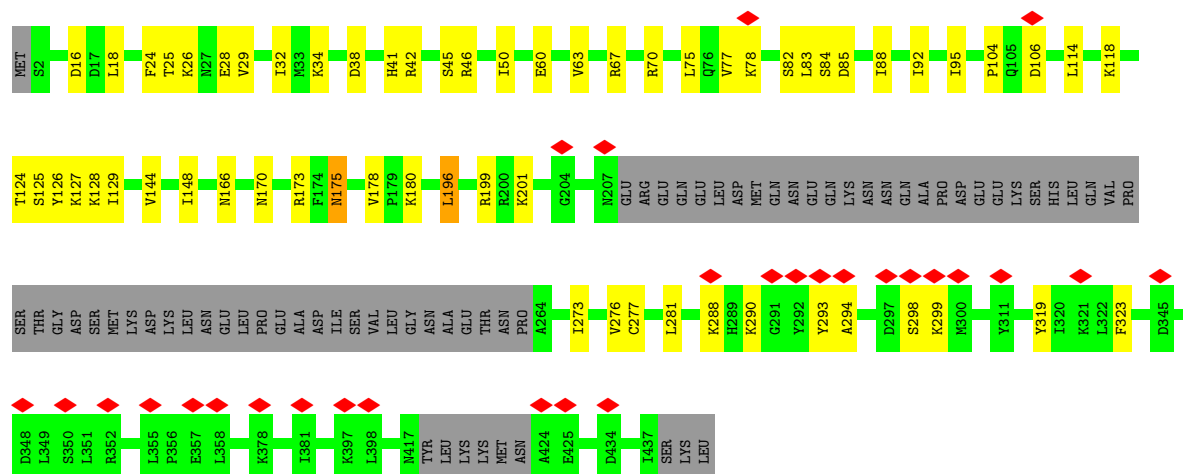
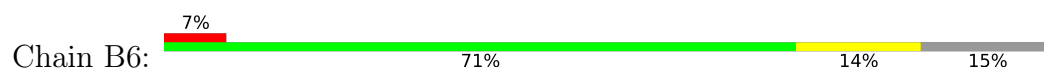
• Molecule 32: U3 small nucleolar RNA-associated protein 12



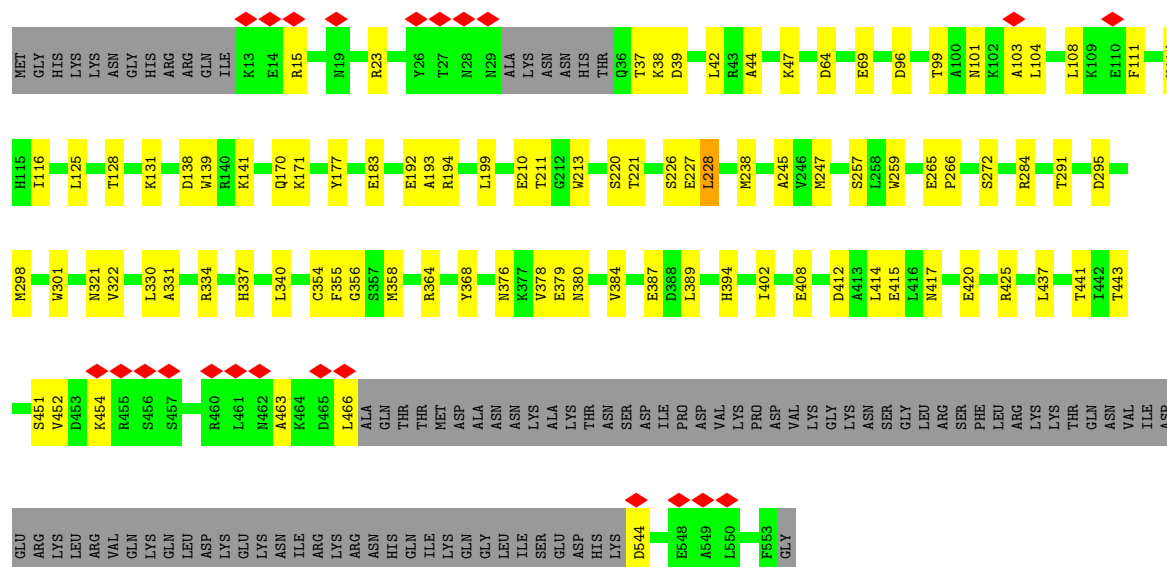




• Molecule 36: U3 small nucleolar RNA-associated protein 6

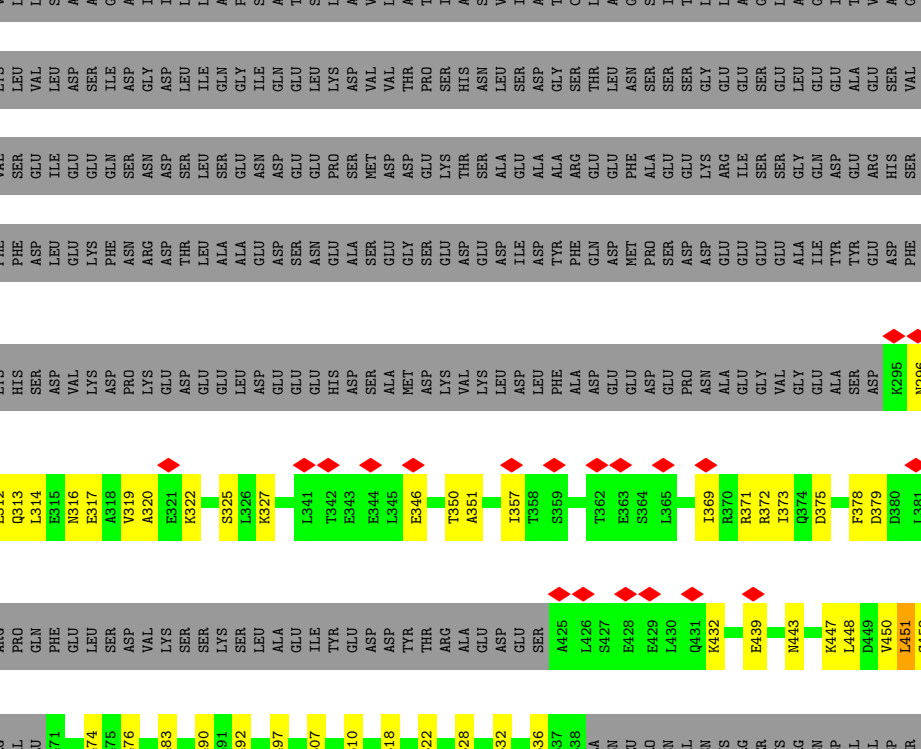


• Molecule 37: U3 small nucleolar RNA-associated protein 7



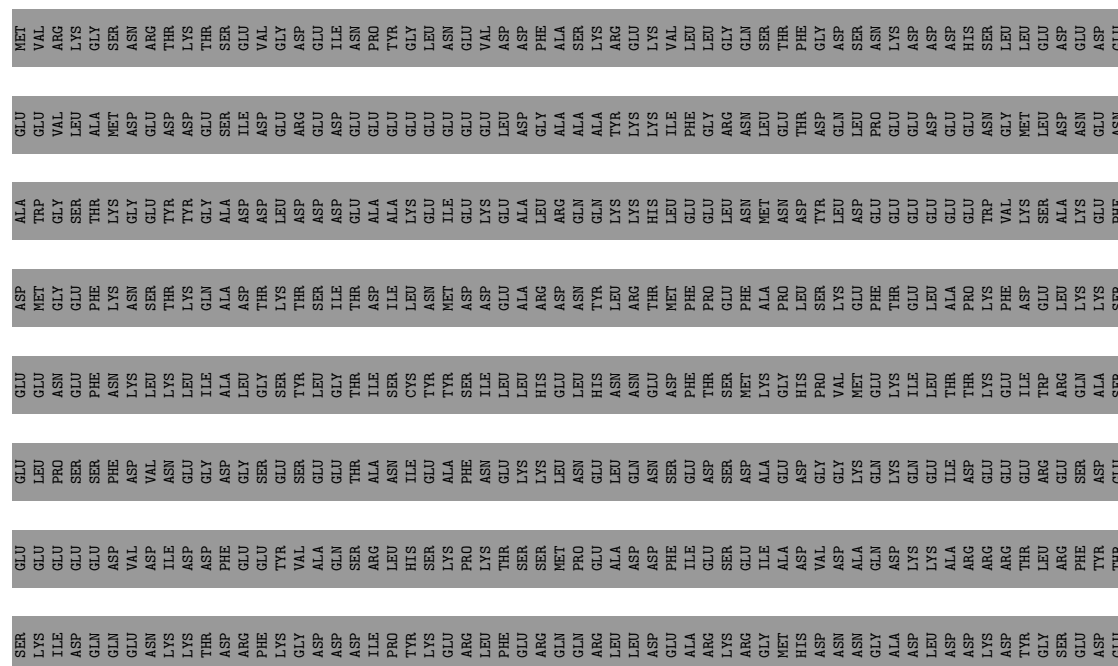
- [illegible]

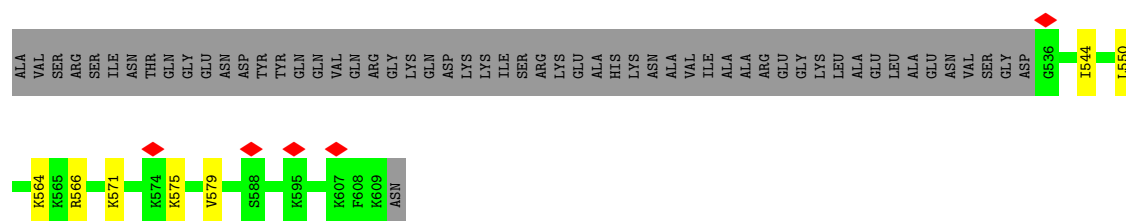
- Chain 5E:  24%  67%



Position	Amino Acid	Frequency (bits)
1	LEU	0.02
2	LYS	0.02
3	ASN	0.02
4	THR	0.02
5	ILE	0.02
6	THR	0.02
7	LEU	0.02
8	SER	0.02
9	THR	0.02
10	ILE	0.02
11	GLN	0.02
12	ARG	0.02
13	VAL	0.02
14	GLY	0.02
15	THR	0.02
16	GLU	0.02
17	THR	0.02
18	GLN	0.02
19	THR	0.02
20	GLY	0.02
21	THR	0.02
22	GLN	0.02
23	THR	0.02
24	GLY	0.02
25	THR	0.02
26	GLN	0.02
27	THR	0.02
28	GLN	0.02
29	THR	0.02
30	GLN	0.02
31	THR	0.02
32	GLN	0.02
33	THR	0.02
34	GLN	0.02
35	THR	0.02
36	GLN	0.02
37	THR	0.02
38	GLN	0.02
39	THR	0.02
40	GLN	0.02
41	THR	0.02
42	GLN	0.02
43	THR	0.02
44	GLN	0.02
45	THR	0.02
46	GLN	0.02
47	THR	0.02
48	GLN	0.02
49	THR	0.02
50	GLN	0.02
51	THR	0.02
52	GLN	0.02
53	THR	0.02
54	GLN	0.02
55	THR	0.02
56	GLN	0.02
57	THR	0.02
58	GLN	0.02
59	THR	0.02
60	GLN	0.02
61	THR	0.02
62	GLN	0.02
63	THR	0.02
64	GLN	0.02
65	THR	0.02
66	GLN	0.02
67	THR	0.02
68	GLN	0.02
69	THR	0.02
70	GLN	0.02
71	THR	0.02
72	GLN	0.02
73	THR	0.02
74	GLN	0.02
75	THR	0.02
76	GLN	0.02
77	THR	0.02
78	GLN	0.02
79	THR	0.02
80	GLN	0.02
81	THR	0.02
82	GLN	0.02
83	THR	0.02
84	GLN	0.02
85	THR	0.02
86	GLN	0.02
87	THR	0.02
88	GLN	0.02
89	THR	0.02
90	GLN	0.02
91	THR	0.02
92	GLN	0.02
93	THR	0.02
94	GLN	0.02
95	THR	0.02
96	GLN	0.02
97	THR	0.02
98	GLN	0.02
99	THR	0.02
100	GLN	0.02

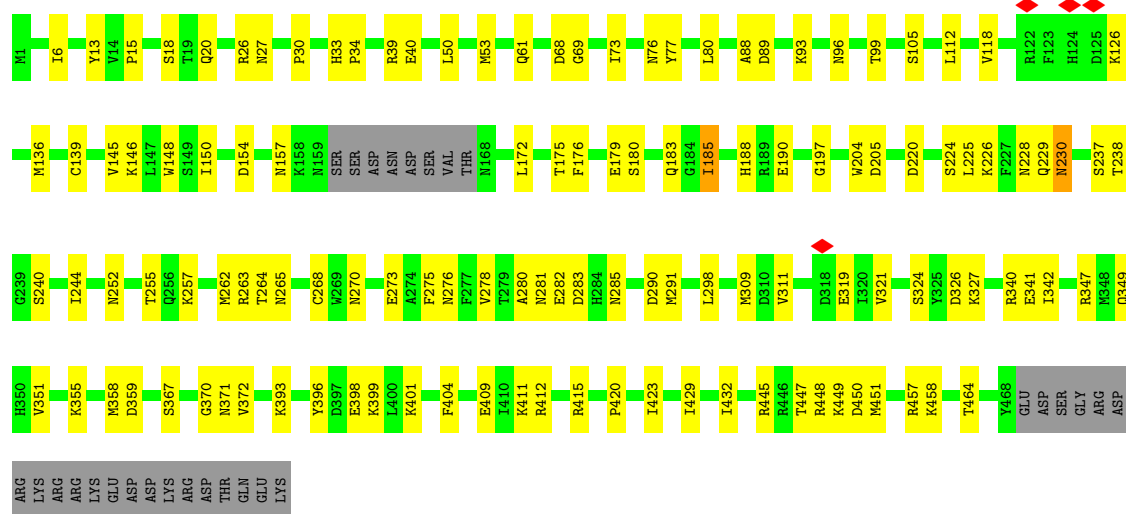
- Chain 5F: 76% 23%





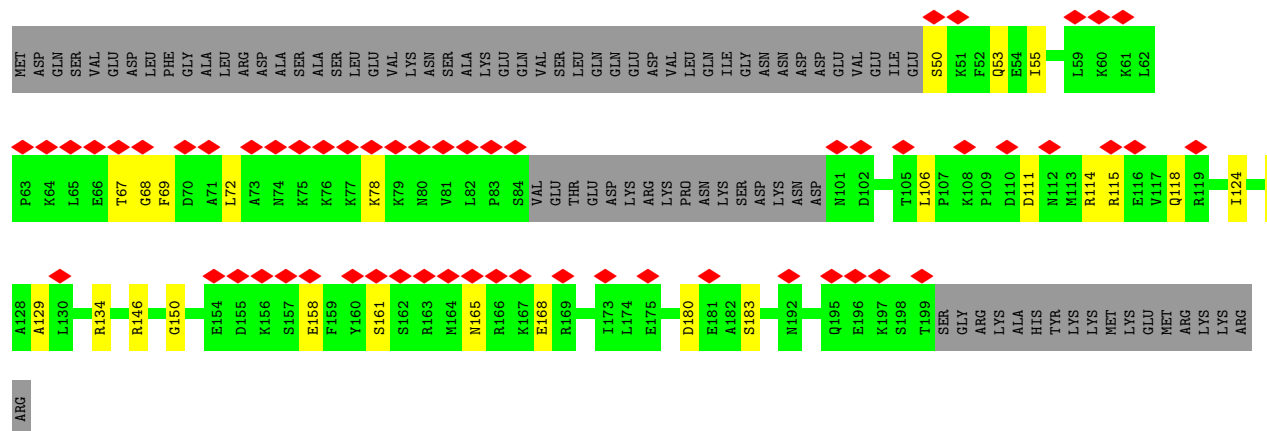
• Molecule 43: Protein SOF1

Chain 5I: 68% 25% 6%



• Molecule 44: rRNA-processing protein FCF2

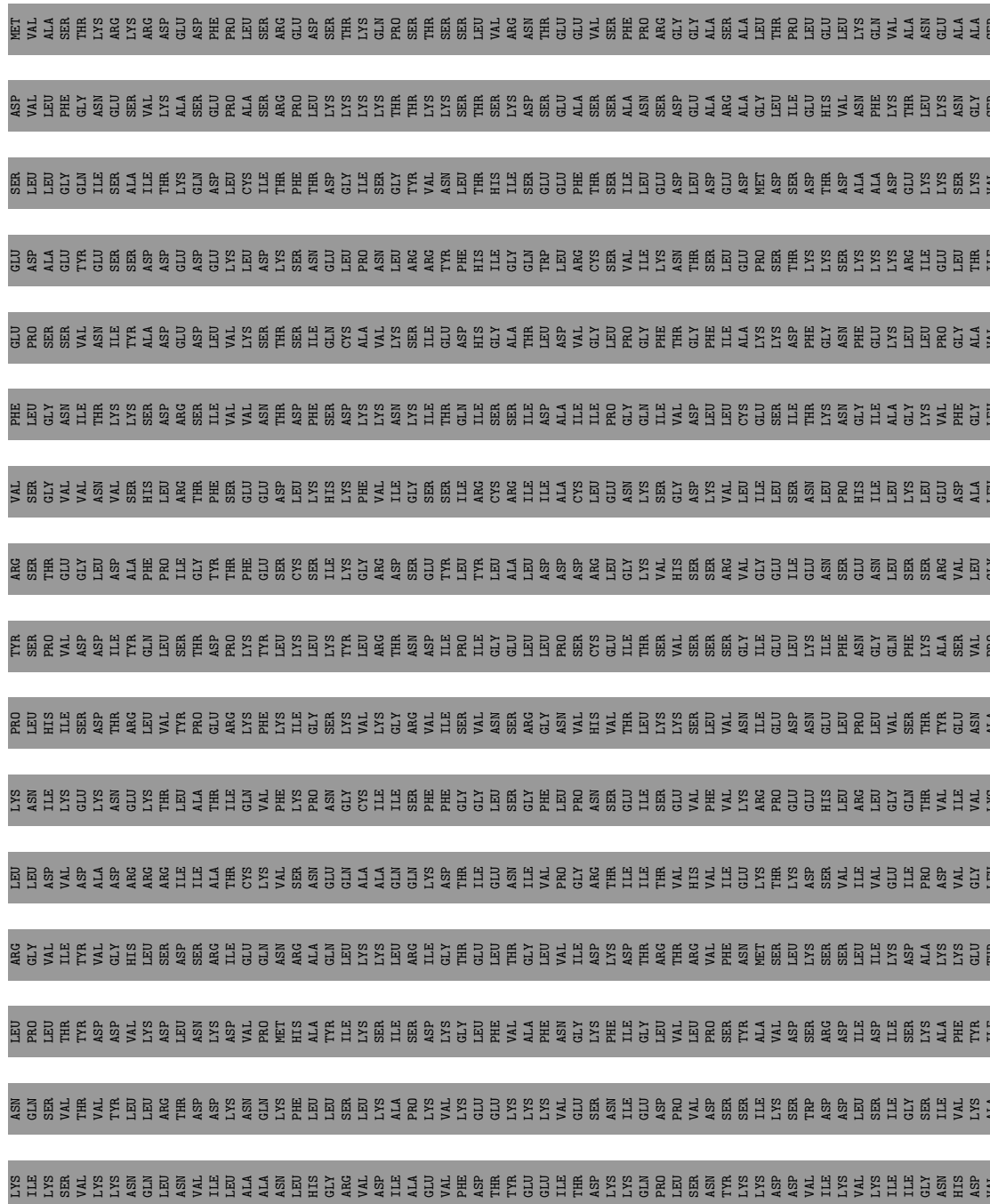
Chain 5J: 26% 50% 12% 38%

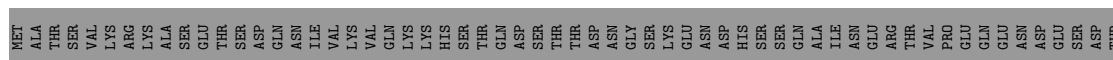


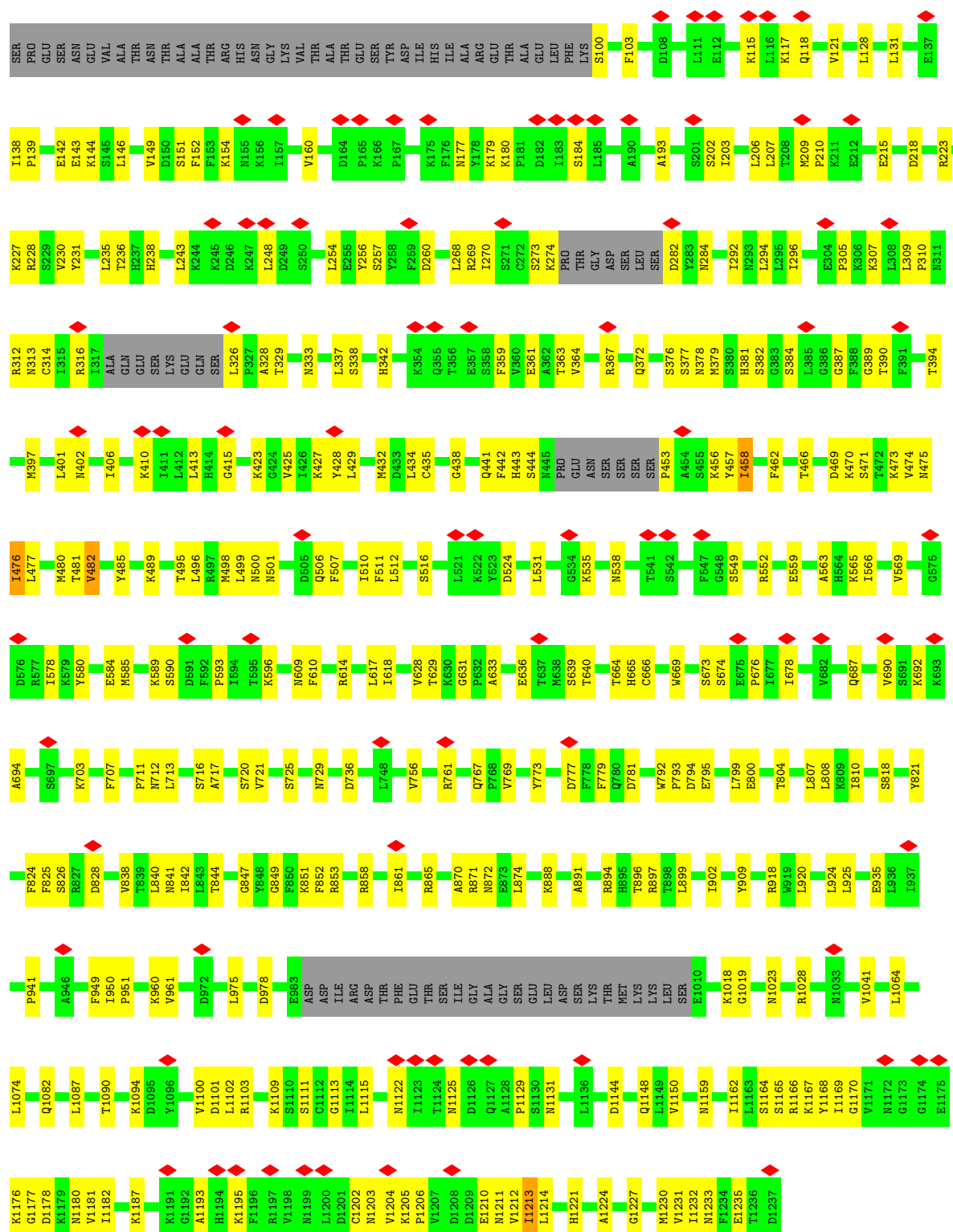
• Molecule 45: rRNA-processing protein FCF1

Chain 5K: 72% 16% 12%



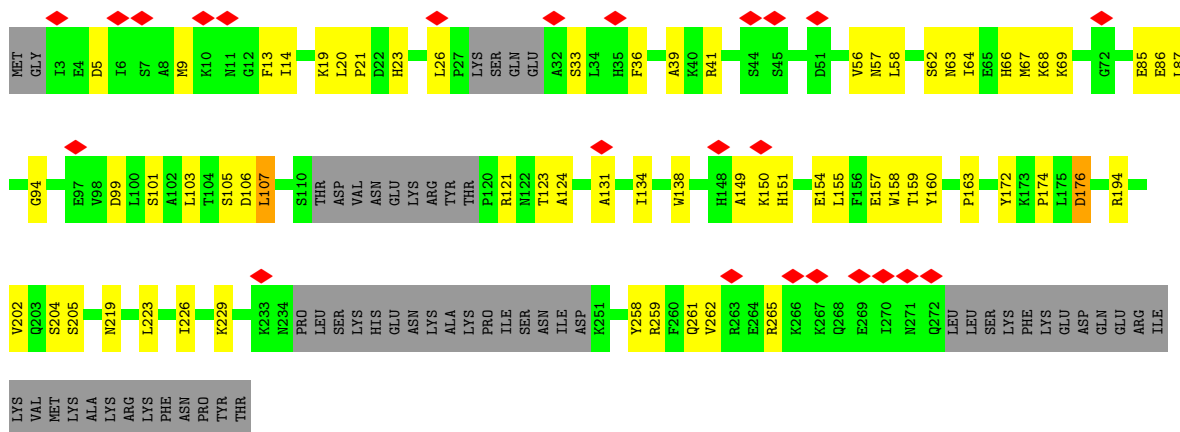




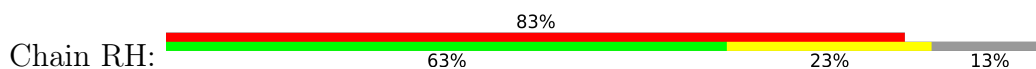


• Molecule 48: Ribosomal RNA-processing protein 7

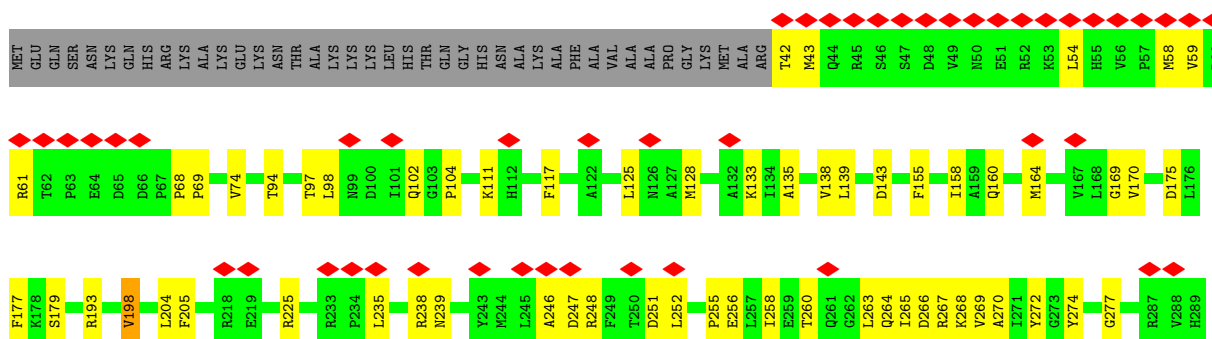




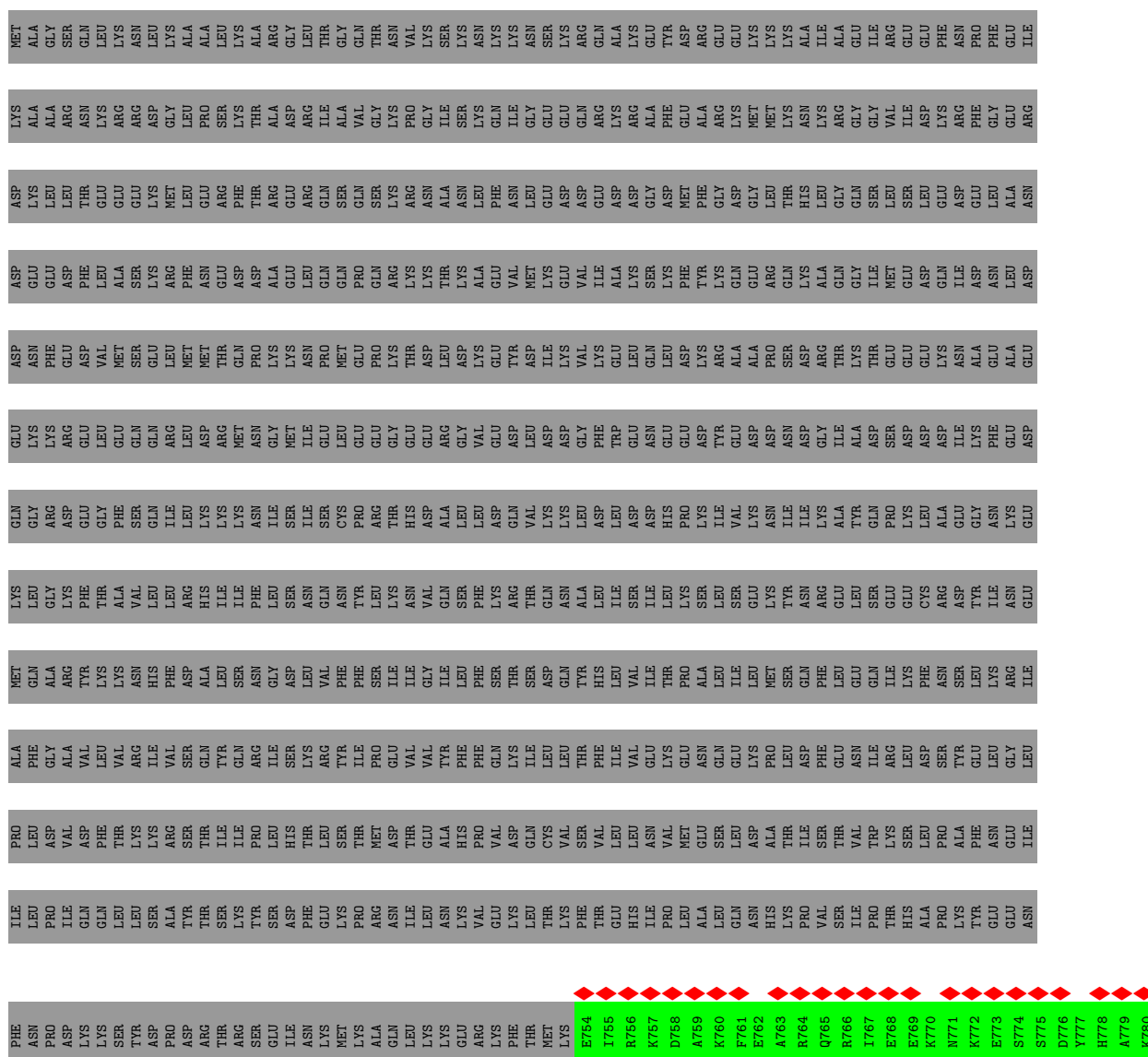
- Molecule 49: Ribosomal RNA small subunit methyltransferase NEP1



- Molecule 50: Ribosome biogenesis protein BMS1

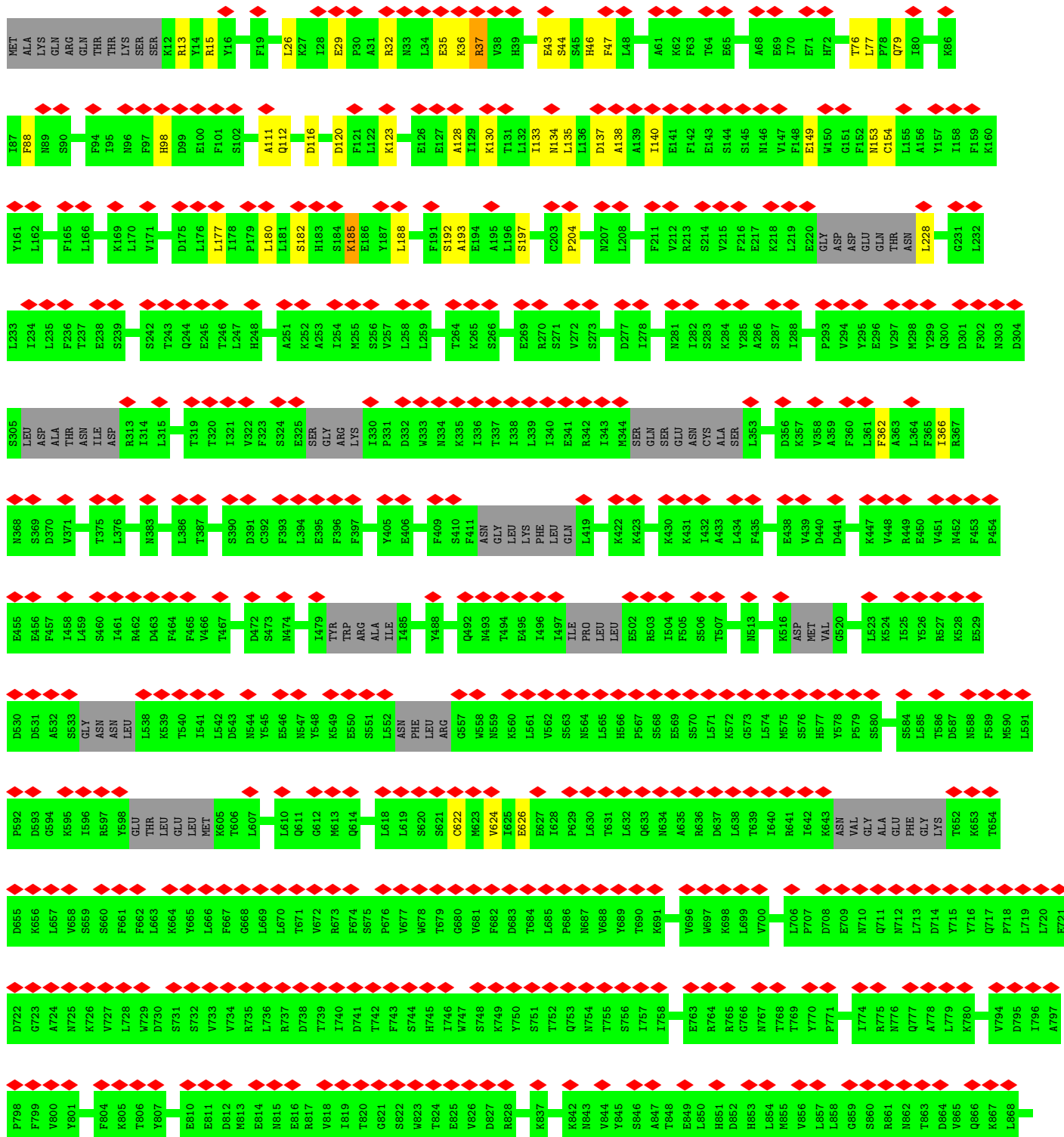
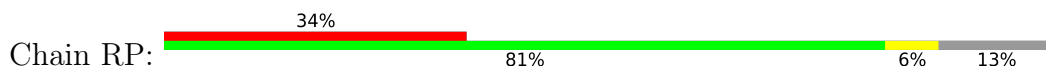


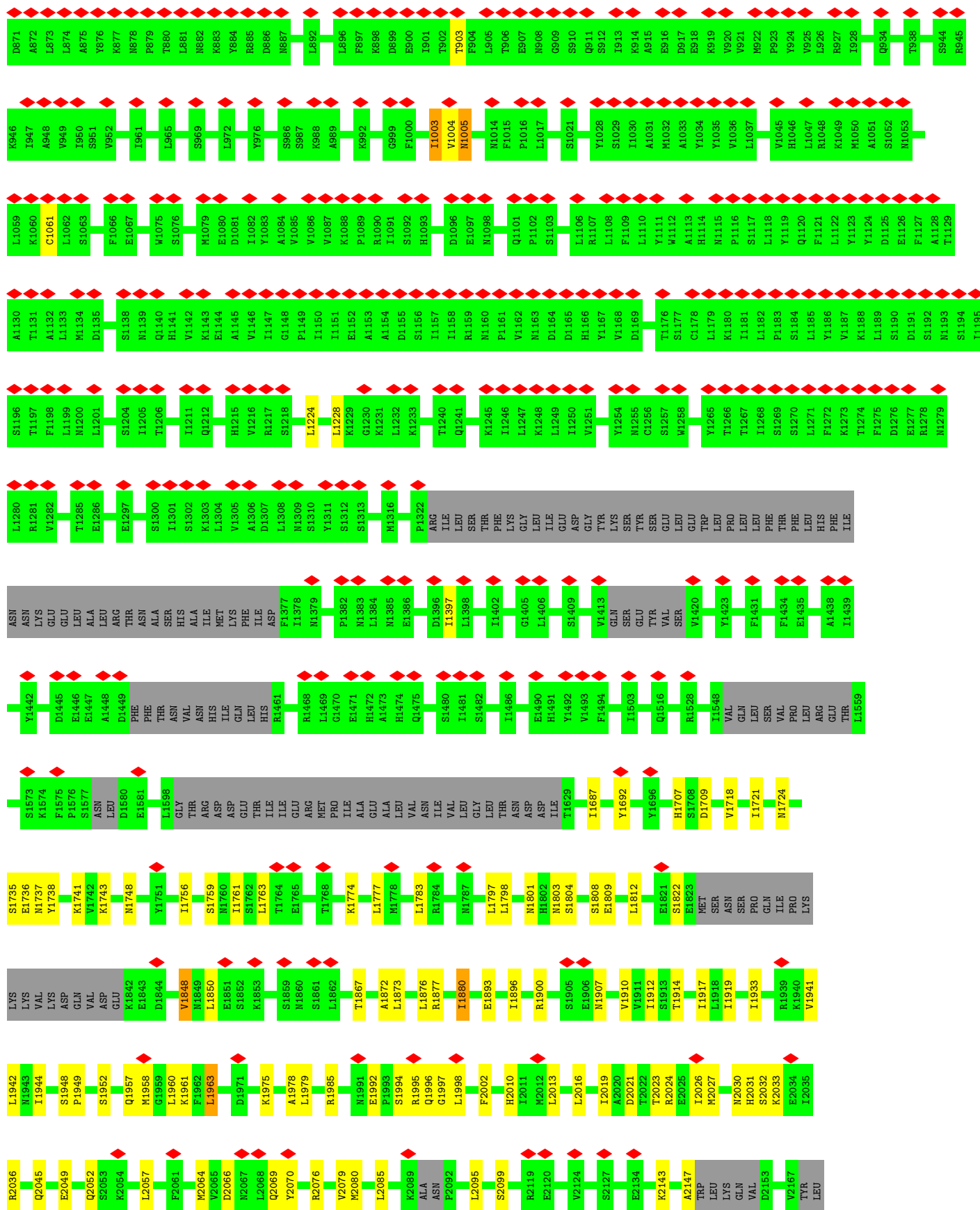
- Molecule 52: Nucleolar complex protein 14



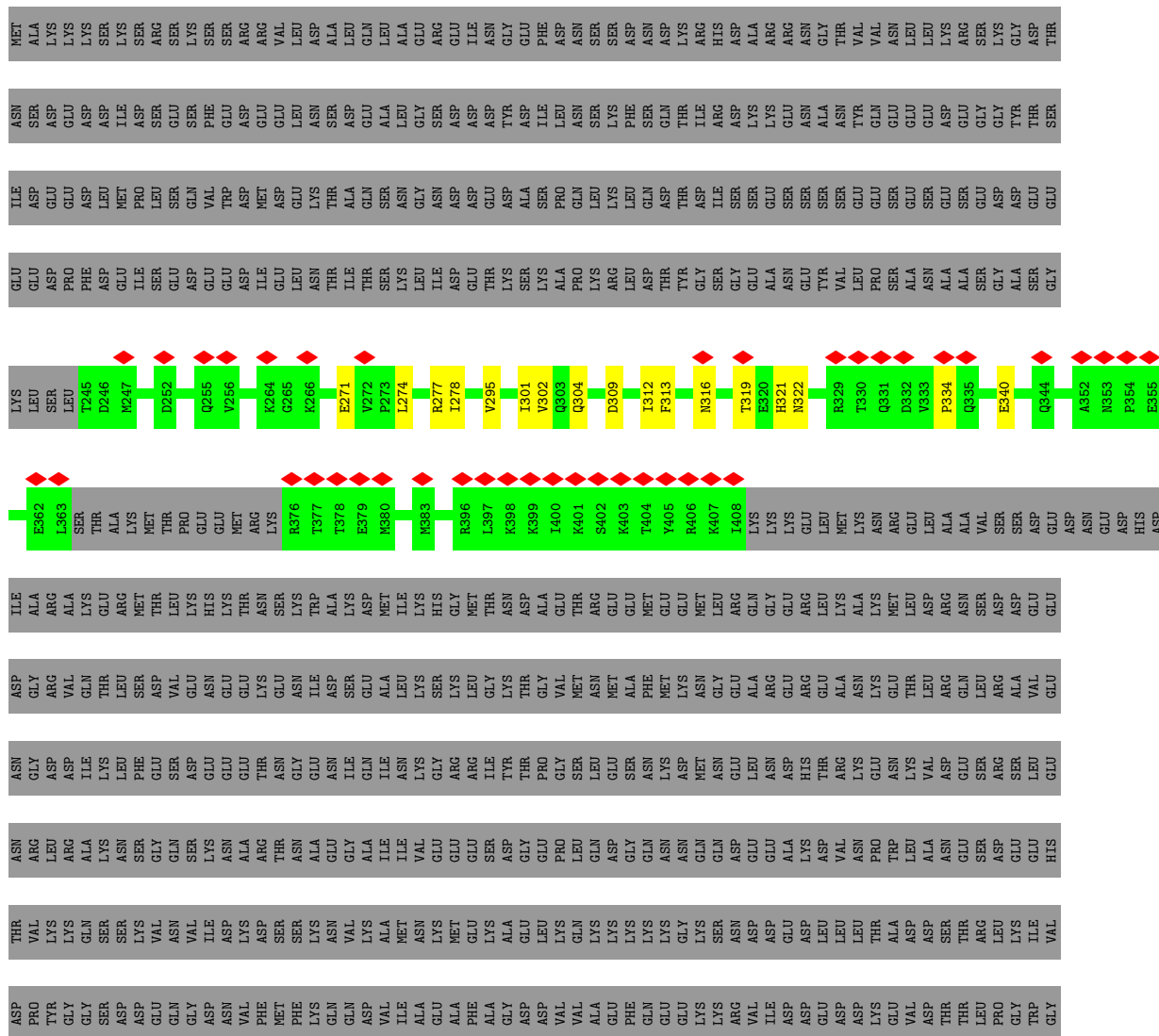


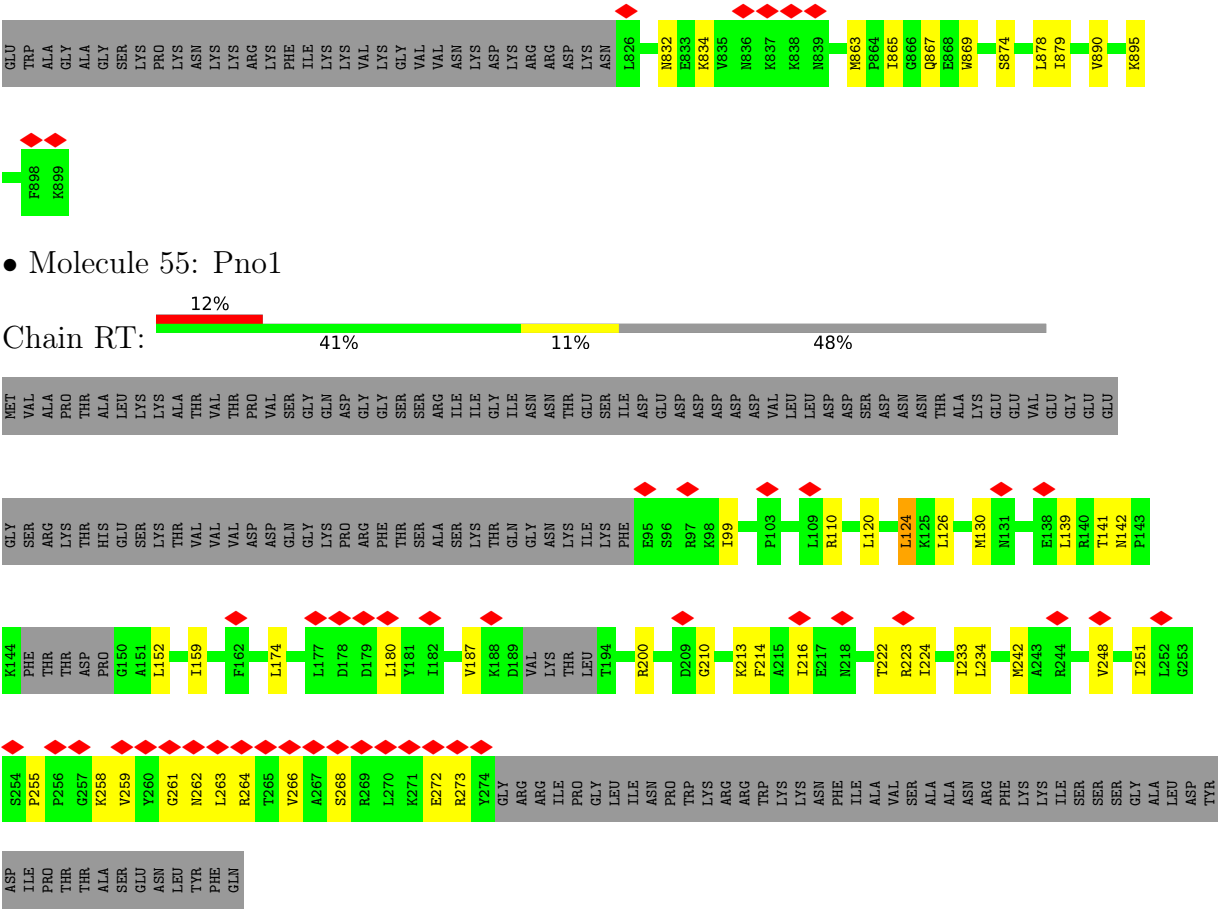
• Molecule 53: U3 small nucleolar RNA-associated protein 20



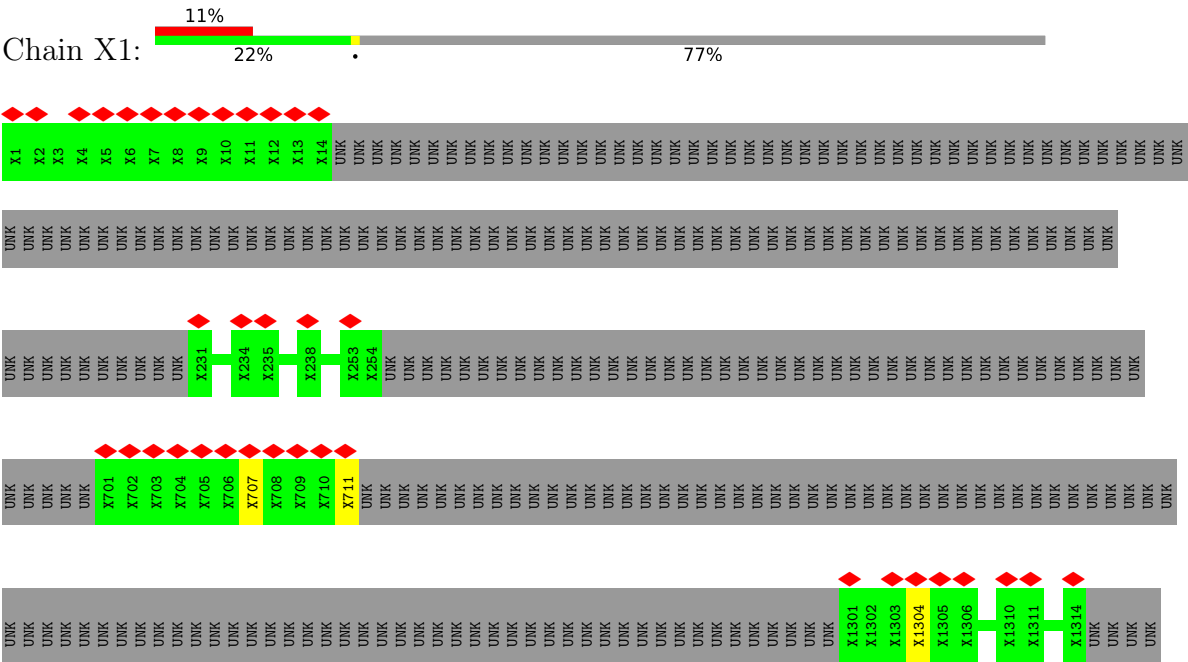


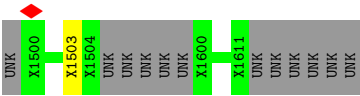
- Molecule 54: U3 small nucleolar RNA-associated protein 14





• Molecule 56: Unassigned helices





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	14475	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	0.086	Depositor
Minimum map value	-0.035	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.018	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	0.35	0/4592	0.49	1/7138 (0.0%)
2	5A	0.27	0/3643	0.46	1/5663 (0.0%)
3	SA	0.33	0/27506	0.47	4/42818 (0.0%)
4	SC	0.43	0/1874	0.81	3/2512 (0.1%)
5	SF	0.36	0/1969	0.78	3/2661 (0.1%)
6	SG	0.41	0/1690	0.67	0/2285
7	SH	0.24	0/1477	0.59	0/1977
8	SI	0.36	0/1330	0.77	5/1792 (0.3%)
9	SJ	0.25	0/1124	0.66	0/1510
10	SK	0.48	0/1410	0.69	0/1888
11	SM	0.25	0/1139	0.60	0/1535
12	SO	0.41	0/1109	0.72	0/1495
13	SP	0.37	0/879	0.68	1/1186 (0.1%)
14	SR	0.48	0/990	0.77	0/1335
15	SX	0.45	0/1020	0.70	0/1371
16	SY	0.38	0/819	0.69	0/1093
17	SZ	0.43	0/1000	0.72	0/1334
18	Sc	0.43	0/613	0.77	0/828
19	Sd	0.47	0/499	0.80	0/670
20	3B	0.50	0/1901	0.71	0/2567
20	3C	0.31	0/1796	0.69	0/2424
21	3D	0.41	0/3020	0.67	0/4066
22	3E	0.35	0/3072	0.62	0/4169
23	3F	0.46	0/3569	0.73	0/4806
24	3G	0.37	0/928	0.75	0/1262
24	3H	0.51	0/928	0.74	0/1262
25	A4	0.32	0/5338	0.69	3/7230 (0.0%)
26	A5	0.44	0/2995	0.65	0/4060
27	A9	0.28	0/301	0.68	0/398
28	AE	0.41	0/3500	0.65	0/4736
29	AF	0.26	0/3885	0.63	2/5261 (0.0%)
30	AG	0.28	0/6699	0.63	1/9077 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	B1	0.51	0/6570	0.70	2/8892 (0.0%)
32	B2	0.38	0/6628	0.70	2/8954 (0.0%)
33	B3	0.34	0/6014	0.77	2/8137 (0.0%)
34	B8	0.40	0/3848	0.66	2/5218 (0.0%)
35	BE	0.51	0/6606	0.71	0/8935
36	B6	0.38	0/2849	0.64	0/3853
37	5C	0.50	0/3690	0.68	0/4991
38	5D	0.31	0/621	0.58	0/823
39	5E	0.35	0/1580	0.72	0/2115
40	5F	0.47	0/1559	0.72	0/2097
41	5G	0.47	0/1768	0.72	0/2392
42	5H	0.41	0/601	0.69	0/789
43	5I	0.59	0/3835	0.75	0/5162
44	5J	0.32	0/1147	0.60	0/1531
45	5K	0.47	0/1346	0.66	0/1812
46	RD	0.25	0/2454	0.63	1/3310 (0.0%)
47	RE	0.31	0/9015	0.65	0/12195
48	RF	0.29	0/2004	0.67	0/2697
49	RH	0.24	0/1746	0.62	1/2357 (0.0%)
50	RJ	0.40	0/6067	0.66	3/8170 (0.0%)
51	RK	0.35	0/2832	0.66	0/3825
52	RN	0.25	0/454	0.61	0/600
53	RP	0.25	0/12777	0.58	6/17558 (0.0%)
54	RQ	0.39	0/1682	0.68	1/2286 (0.0%)
55	RT	0.29	0/1379	0.67	0/1853
All	All	0.37	0/181687	0.64	44/252961 (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	4
7	SH	0	1
8	SI	0	4
12	SO	0	1
18	Sc	0	2
19	Sd	0	1
20	3C	0	1
23	3F	0	1
26	A5	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
29	AF	0	1
30	AG	0	5
31	B1	0	1
32	B2	0	2
33	B3	0	5
39	5E	0	1
43	5I	0	3
47	RE	0	3
48	RF	0	3
49	RH	0	1
50	RJ	0	1
51	RK	0	1
53	RP	0	11
54	RQ	0	2
55	RT	0	1
All	All	0	57

There are no bond length outliers.

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	B3	584	ILE	CA-C-N	6.54	134.03	121.54
33	B3	584	ILE	C-N-CA	6.54	134.03	121.54
46	RD	1187	VAL	N-CA-C	-6.43	106.54	111.62
25	A4	480	PHE	N-CA-C	6.27	118.25	110.91
5	SF	193	GLY	N-CA-C	5.92	127.21	113.18
3	SA	1052	U	C2'-C3'-O3'	5.81	118.22	109.50
25	A4	435	PRO	CA-C-N	5.48	131.16	122.61
25	A4	435	PRO	C-N-CA	5.48	131.16	122.61
34	B8	224	ASN	CA-C-N	5.48	132.00	121.54
34	B8	224	ASN	C-N-CA	5.48	132.00	121.54
13	SP	127	ARG	N-CA-C	-5.43	105.95	113.18
2	5A	311	C	P-O3'-C3'	5.37	128.26	120.20
4	SC	207	LEU	N-CA-C	5.32	117.14	110.91
8	SI	64	VAL	N-CA-C	5.30	120.33	108.88
8	SI	117	THR	CA-C-N	5.29	131.65	121.54
8	SI	117	THR	C-N-CA	5.29	131.65	121.54
1	3A	248	G	C2'-C3'-O3'	5.27	117.40	109.50
54	RQ	313	PHE	N-CA-C	5.24	121.40	109.81
31	B1	345	PHE	CA-C-N	5.24	131.54	121.54
31	B1	345	PHE	C-N-CA	5.24	131.54	121.54
53	RP	2033	LYS	CA-C-N	5.23	131.53	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	RP	2033	LYS	C-N-CA	5.23	131.53	121.54
8	SI	63	PRO	CA-C-N	5.20	131.74	122.13
8	SI	63	PRO	C-N-CA	5.20	131.74	122.13
53	RP	1397	ILE	CA-C-N	5.19	131.46	121.54
53	RP	1397	ILE	C-N-CA	5.19	131.46	121.54
49	RH	88	ARG	N-CA-C	5.15	116.18	108.76
3	SA	287	G	O4'-C1'-N9	5.15	115.92	108.20
3	SA	579	A	P-O3'-C3'	5.15	127.93	120.20
3	SA	484	C	C2'-C3'-O3'	5.13	121.39	113.70
53	RP	1687	ILE	CA-C-N	5.12	131.33	121.54
53	RP	1687	ILE	C-N-CA	5.12	131.33	121.54
30	AG	383	LEU	CA-CB-CG	5.11	134.18	116.30
50	RJ	949	LYS	CA-C-N	5.11	129.37	122.07
50	RJ	949	LYS	C-N-CA	5.11	129.37	122.07
4	SC	147	ALA	CA-C-N	5.10	135.10	125.66
4	SC	147	ALA	C-N-CA	5.10	135.10	125.66
32	B2	542	ASP	CA-C-N	5.07	131.23	121.54
32	B2	542	ASP	C-N-CA	5.07	131.23	121.54
5	SF	72	VAL	CA-C-N	5.03	131.15	121.54
5	SF	72	VAL	C-N-CA	5.03	131.15	121.54
50	RJ	198	VAL	N-CA-C	-5.02	98.89	109.34
29	AF	60	SER	CA-C-N	5.00	130.41	122.61
29	AF	60	SER	C-N-CA	5.00	130.41	122.61

There are no chirality outliers.

All (57) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
20	3C	246	GLN	Peptide
23	3F	173	GLU	Peptide
39	5E	483	TYR	Peptide
43	5I	185	ILE	Peptide
43	5I	230	ASN	Peptide
43	5I	283	ASP	Peptide
26	A5	166	ALA	Peptide
29	AF	289	ASN	Peptide
30	AG	140	LYS	Peptide
30	AG	386	ASN	Peptide
30	AG	502	LYS	Peptide
30	AG	740	LYS	Peptide
30	AG	780	GLU	Peptide
31	B1	348	THR	Peptide

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Mol	Chain	Res	Type	Group
32	B2	212	VAL	Peptide
32	B2	213	LYS	Peptide
33	B3	34	THR	Peptide
33	B3	410	ASN	Peptide
33	B3	445	ILE	Peptide
33	B3	473	ALA	Peptide
33	B3	593	CYS	Peptide
47	RE	1028	ARG	Peptide
47	RE	1168	TYR	Peptide
47	RE	458	ILE	Peptide
48	RF	107	LEU	Peptide
48	RF	155	LEU	Peptide
48	RF	157	GLU	Peptide
49	RH	232	LEU	Peptide
50	RJ	783	PHE	Peptide
51	RK	259	GLU	Peptide
53	RP	1003	ILE	Peptide
53	RP	1005	ASN	Peptide
53	RP	13	ARG	Peptide
53	RP	1707	HIS	Peptide
53	RP	1804	SER	Peptide
53	RP	1848	VAL	Peptide
53	RP	185	LYS	Peptide
53	RP	1907	ASN	Peptide
53	RP	1996	GLN	Peptide
53	RP	36	LYS	Peptide
53	RP	903	THR	Peptide
54	RQ	271	GLU	Peptide
54	RQ	312	ILE	Peptide
55	RT	124	LEU	Peptide
4	SC	135	LEU	Peptide
4	SC	16	GLN	Peptide
4	SC	177	GLN	Peptide
4	SC	208	GLN	Peptide
7	SH	152	ASP	Peptide
8	SI	131	PHE	Peptide
8	SI	134	GLU	Peptide
8	SI	31	SER	Peptide
8	SI	64	VAL	Peptide
12	SO	58	HIS	Peptide
18	Sc	49	HIS	Peptide
18	Sc	74	SER	Peptide

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Mol	Chain	Res	Type	Group
19	Sd	51	ASN	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	3A	4114	0	2083	42	0
2	5A	3260	0	1643	36	0
3	SA	24609	0	12403	302	0
4	SC	1848	0	1940	40	0
5	SF	1930	0	1950	32	0
6	SG	1669	0	1724	25	0
7	SH	1457	0	1504	39	0
8	SI	1310	0	1374	36	0
9	SJ	1104	0	1107	28	0
10	SK	1388	0	1467	28	0
11	SM	1113	0	1181	28	0
12	SO	1087	0	1152	27	0
13	SP	868	0	894	20	0
14	SR	973	0	1029	20	0
15	SX	1003	0	1040	25	0
16	SY	807	0	865	16	0
17	SZ	986	0	1042	19	0
18	Sc	603	0	621	14	0
19	Sd	497	0	535	5	0
20	3B	1865	0	1910	46	0
20	3C	1763	0	1805	47	0
21	3D	2974	0	3001	57	0
22	3E	3041	0	2831	72	0
23	3F	3498	0	3515	80	0
24	3G	916	0	964	17	0
24	3H	916	0	964	24	0
25	A4	5243	0	5216	183	0
26	A5	2943	0	2928	61	0
27	A9	299	0	328	7	0
28	AE	3443	0	3564	61	0
29	AF	3807	0	3791	91	0
30	AG	6570	0	6473	188	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	B1	6427	0	6329	131	0
32	B2	6502	0	6493	154	0
33	B3	5919	0	6007	151	0
34	B8	3764	0	3757	82	0
35	BE	6475	0	6453	160	0
36	B6	2800	0	2517	43	0
37	5C	3612	0	3578	69	0
38	5D	609	0	616	8	0
39	5E	1564	0	1592	41	0
40	5F	1530	0	1572	31	0
41	5G	1732	0	1744	36	0
42	5H	596	0	661	8	0
43	5I	3756	0	3708	92	0
44	5J	1127	0	1150	17	0
45	5K	1323	0	1401	20	0
46	RD	2413	0	2264	29	0
47	RE	8805	0	8911	200	0
48	RF	1963	0	1942	43	0
49	RH	1719	0	1783	40	0
50	RJ	5935	0	6100	136	0
51	RK	2781	0	2878	79	0
52	RN	450	0	447	3	0
53	RP	12716	0	8235	94	0
54	RQ	1655	0	1461	22	0
55	RT	1357	0	1426	22	0
56	X1	400	0	99	3	0
57	5K	1	0	0	0	0
57	Sc	1	0	0	0	0
58	RJ	32	0	12	0	0
59	RJ	1	0	0	0	0
All	All	175869	0	155980	3094	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 9.

All (3094) 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)
25:A4:741:LEU:HD11	25:A4:744:VAL:CG2	1.48	1.42
25:A4:740:PRO:O	25:A4:756:GLU:HG2	1.44	1.16
25:A4:741:LEU:HD11	25:A4:744:VAL:HG21	1.16	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A4:741:LEU:HD21	25:A4:744:VAL:HG23	1.39	1.04
25:A4:741:LEU:CD1	25:A4:744:VAL:CG2	2.39	1.00
3:SA:1170:G:H1	3:SA:1469:A:N6	1.62	0.97
3:SA:656:G:H1	3:SA:678:A:H2	1.00	0.96
3:SA:142:G:N1	3:SA:173:A:C2	2.33	0.96
3:SA:656:G:N1	3:SA:678:A:C2	2.34	0.94
3:SA:902:G:H21	3:SA:907:A:H62	1.01	0.93
3:SA:69:G:H1	3:SA:82:U:H3	1.12	0.91
3:SA:1697:G:H1	3:SA:1704:U:H3	0.98	0.90
49:RH:44:VAL:HA	49:RH:113:TYR:O	1.72	0.89
3:SA:142:G:H1	3:SA:173:A:H2	0.92	0.89
3:SA:1688:U:H3	3:SA:1713:G:H1	0.89	0.88
3:SA:1170:G:H1	3:SA:1469:A:H61	0.90	0.87
35:BE:360:ASP:O	35:BE:636:PRO:HG2	1.73	0.87
1:3A:12:U:H3	3:SA:1112:G:H1	0.89	0.87
3:SA:142:G:N1	3:SA:173:A:H2	1.68	0.87
25:A4:739:LYS:HB2	25:A4:740:PRO:HD3	1.54	0.86
51:RK:114:PHE:O	51:RK:169:VAL:HA	1.75	0.86
3:SA:902:G:N2	3:SA:907:A:H62	1.75	0.84
25:A4:739:LYS:HE2	25:A4:739:LYS:HA	1.60	0.82
25:A4:740:PRO:O	25:A4:756:GLU:CG	2.26	0.82
44:5J:114:ARG:O	44:5J:118:GLN:HB3	1.79	0.82
3:SA:656:G:N1	3:SA:678:A:H2	1.74	0.82
28:AE:3:SER:O	28:AE:7:GLN:HB2	1.79	0.82
25:A4:741:LEU:CD2	25:A4:744:VAL:HG23	2.09	0.81
12:SO:40:TYR:HB3	12:SO:45:LEU:HD12	1.62	0.81
32:B2:322:SER:O	32:B2:326:LEU:HB2	1.78	0.81
3:SA:902:G:H21	3:SA:907:A:N6	1.78	0.81
23:3F:263:TRP:HZ3	23:3F:270:PRO:HD3	1.45	0.81
25:A4:741:LEU:HD11	25:A4:744:VAL:HG22	1.61	0.80
36:B6:319:TYR:O	36:B6:323:PHE:HB2	1.81	0.80
34:B8:311:ASN:HA	34:B8:324:TRP:O	1.80	0.79
23:3F:263:TRP:CZ3	23:3F:270:PRO:HG3	2.18	0.79
47:RE:442:PHE:O	47:RE:469:ASP:HA	1.82	0.78
37:5C:116:ILE:H	37:5C:380:ASN:HD21	1.30	0.78
25:A4:741:LEU:CD1	25:A4:744:VAL:HG21	2.07	0.78
41:5G:131:CYS:HG	41:5G:136:THR:HG1	1.32	0.77
25:A4:739:LYS:HE2	25:A4:739:LYS:CA	2.15	0.76
32:B2:386:GLU:HA	32:B2:391:ARG:HH22	1.50	0.76
35:BE:361:SER:HA	35:BE:636:PRO:CB	2.15	0.76
29:AF:86:SER:O	29:AF:98:ALA:HA	1.85	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:AE:309:GLN:HG2	34:B8:224:ASN:HD22	1.51	0.76
34:B8:435:PHE:HB3	34:B8:443:VAL:HA	1.69	0.74
1:3A:67:G:H1	2:5A:286:U:H3	1.35	0.74
3:SA:311:U:H3	3:SA:355:G:H1	1.33	0.74
51:RK:103:MET:O	51:RK:107:ALA:HB2	1.88	0.74
47:RE:438:GLY:HA2	47:RE:458:ILE:O	1.88	0.73
34:B8:357:ASN:HB2	34:B8:378:GLN:HG2	1.71	0.72
3:SA:174:U:H3	3:SA:266:A:H62	1.38	0.72
50:RJ:1034:LEU:H	50:RJ:1037:GLN:HE21	1.37	0.71
37:5C:265:GLU:OE1	54:RQ:834:LYS:HD2	1.89	0.71
25:A4:741:LEU:HD11	25:A4:744:VAL:HG23	1.66	0.71
31:B1:71:ILE:HD11	31:B1:102:VAL:HG21	1.73	0.70
29:AF:222:SER:HB2	29:AF:225:GLN:H	1.57	0.70
16:SY:97:ASP:HB3	50:RJ:828:ARG:HH22	1.57	0.70
50:RJ:235:LEU:O	50:RJ:239:ASN:HB2	1.92	0.70
3:SA:1051:G:H21	43:5I:447:THR:HG21	1.57	0.69
30:AG:585:TRP:HB3	30:AG:594:TRP:HE1	1.57	0.69
25:A4:739:LYS:HB2	25:A4:740:PRO:CD	2.22	0.69
35:BE:209:ILE:HA	35:BE:225:THR:HA	1.73	0.69
23:3F:263:TRP:HZ3	23:3F:270:PRO:CD	2.05	0.69
23:3F:426:SER:HB3	23:3F:433:ILE:HD11	1.74	0.68
46:RD:1612:LEU:HD21	46:RD:1616:ASN:HB2	1.76	0.68
32:B2:10:GLN:HE22	32:B2:682:ARG:HB2	1.59	0.68
25:A4:353:GLU:HA	25:A4:766:GLN:HE22	1.59	0.68
33:B3:561:SER:HG	33:B3:566:SER:N	1.92	0.68
8:SI:58:LEU:HB2	8:SI:90:VAL:HG12	1.76	0.68
25:A4:741:LEU:HD21	25:A4:744:VAL:CG2	2.21	0.68
33:B3:496:ALA:O	33:B3:508:THR:HA	1.94	0.68
10:SK:127:VAL:HG22	10:SK:131:GLN:HE22	1.60	0.67
21:3D:254:ASN:HA	21:3D:257:ILE:HG22	1.75	0.67
3:SA:656:G:O6	3:SA:678:A:N1	2.27	0.67
22:3E:286:ASN:HD22	22:3E:387:GLY:H	1.40	0.67
24:3G:53:ILE:HD11	24:3G:81:VAL:HG13	1.75	0.67
3:SA:68:A:H5'	7:SH:160:ARG:HH22	1.60	0.67
23:3F:545:LYS:HG2	23:3F:561:ASN:HD21	1.60	0.67
26:A5:8:SER:HB2	26:A5:17:LEU:HD11	1.76	0.67
3:SA:1167:G:H1	3:SA:1578:U:H3	1.42	0.67
17:SZ:20:ARG:HA	17:SZ:76:TYR:HB3	1.77	0.66
34:B8:455:ILE:HA	34:B8:486:SER:HA	1.78	0.66
1:3A:250:C:H41	23:3F:560:ARG:HH12	1.42	0.66
53:RP:137:ASP:HA	53:RP:140:ILE:HD12	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:RE:584:GLU:O	47:RE:614:ARG:HB2	1.95	0.66
53:RP:2045:GLN:O	53:RP:2049:GLU:HB2	1.96	0.66
30:AG:682:ASN:HB2	30:AG:689:ILE:HD11	1.78	0.66
30:AG:715:GLU:HG3	30:AG:716:ARG:HG2	1.77	0.66
28:AE:248:SER:HG	28:AE:253:CYS:HG	1.43	0.66
33:B3:461:LEU:HB3	33:B3:484:GLU:HB3	1.78	0.66
25:A4:741:LEU:C	25:A4:741:LEU:HD23	2.21	0.65
43:5I:76:ASN:HA	43:5I:118:VAL:HG21	1.77	0.65
32:B2:217:LEU:HB3	32:B2:229:TRP:HB2	1.77	0.65
22:3E:6:THR:O	22:3E:16:LYS:HA	1.96	0.65
33:B3:548:LEU:O	33:B3:559:ILE:HA	1.96	0.65
3:SA:349:U:H4'	3:SA:353:A:H1'	1.78	0.65
32:B2:160:ARG:HH21	39:5E:522:ARG:HD2	1.62	0.65
33:B3:513:LYS:H	33:B3:535:GLY:HA2	1.59	0.65
47:RE:498:MET:O	47:RE:506:GLN:NE2	2.28	0.65
51:RK:114:PHE:HB2	51:RK:170:VAL:HG22	1.78	0.65
25:A4:614:TRP:O	25:A4:618:ASN:HB2	1.97	0.65
3:SA:1663:G:H1	3:SA:1738:U:H3	1.42	0.65
22:3E:149:ARG:O	22:3E:153:LYS:HB2	1.97	0.65
30:AG:741:SER:HB2	30:AG:759:HIS:HB3	1.77	0.65
47:RE:179:LYS:HB2	47:RE:210:PRO:HG2	1.79	0.65
3:SA:763:G:H21	3:SA:774:A:H62	1.44	0.65
24:3G:54:MET:HB3	24:3G:64:LEU:HD21	1.79	0.65
44:5J:111:ASP:O	44:5J:115:ARG:NH2	2.30	0.65
48:RF:5:ASP:HA	48:RF:149:ALA:HB1	1.79	0.64
3:SA:656:G:C6	3:SA:678:A:N1	2.66	0.64
20:3C:94:ALA:HB3	20:3C:166:PRO:HG3	1.78	0.64
35:BE:504:ALA:HB3	35:BE:522:LEU:HD12	1.78	0.64
47:RE:1101:ASP:HB2	47:RE:1233:ASN:HB3	1.80	0.64
25:A4:453:LEU:HB3	25:A4:460:LEU:HD22	1.78	0.64
3:SA:142:G:O6	3:SA:173:A:N1	2.31	0.64
33:B3:665:GLN:HE22	33:B3:688:LEU:HD21	1.62	0.64
34:B8:386:ILE:HD13	34:B8:437:LEU:HD12	1.79	0.64
33:B3:350:LEU:HB3	33:B3:626:MET:HE3	1.79	0.64
47:RE:441:GLN:HE21	47:RE:456:LYS:HB2	1.61	0.64
30:AG:507:MET:HB2	30:AG:532:TRP:HB2	1.80	0.64
32:B2:338:ILE:HB	32:B2:355:LEU:HD11	1.78	0.64
3:SA:1688:U:O2	3:SA:1713:G:N2	2.28	0.64
22:3E:169:LEU:O	22:3E:173:LEU:HB2	1.98	0.64
23:3F:171:THR:OG1	23:3F:172:PHE:N	2.31	0.64
30:AG:320:VAL:HG12	30:AG:335:PRO:HA	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:B3:464:LYS:HZ2	33:B3:481:LYS:HB2	1.62	0.64
55:RT:126:LEU:HB3	55:RT:139:LEU:HD12	1.80	0.64
3:SA:573:C:O2'	50:RJ:870:ARG:NH2	2.30	0.64
13:SP:87:GLY:HA3	13:SP:120:PRO:HD2	1.79	0.64
33:B3:443:PRO:HA	33:B3:499:VAL:HG11	1.79	0.63
25:A4:117:ILE:HD11	25:A4:147:ILE:HG12	1.79	0.63
47:RE:149:VAL:HA	47:RE:152:PHE:HB3	1.80	0.63
24:3H:33:LEU:HD11	24:3H:100:ALA:HB1	1.81	0.63
43:5I:148:TRP:HE1	43:5I:172:LEU:HD13	1.62	0.63
47:RE:1170:GLY:HA3	47:RE:1177:GLY:HA2	1.81	0.63
3:SA:205:U:H2'	3:SA:206:A:H8	1.64	0.63
34:B8:511:LEU:HB2	34:B8:513:GLN:HE22	1.64	0.63
5:SF:177:ALA:HA	5:SF:198:LYS:HE2	1.80	0.63
34:B8:521:LEU:HA	34:B8:531:CYS:O	1.99	0.63
35:BE:268:THR:HG22	35:BE:270:SER:H	1.64	0.63
49:RH:116:THR:HG22	49:RH:118:ARG:H	1.64	0.63
30:AG:581:GLY:HA2	30:AG:602:PRO:HD2	1.80	0.63
23:3F:211:LEU:HB3	23:3F:212:LYS:HD2	1.81	0.63
29:AF:84:VAL:HA	29:AF:100:ASP:HA	1.80	0.63
28:AE:241:ILE:O	28:AE:245:LEU:HB2	1.99	0.63
3:SA:870:C:O2	18:Sc:51:GLN:NE2	2.32	0.62
9:SJ:109:PHE:O	9:SJ:113:PHE:HB2	1.99	0.62
3:SA:1175:U:H3	3:SA:1464:G:H22	1.46	0.62
13:SP:16:VAL:HA	13:SP:80:HIS:O	1.97	0.62
32:B2:268:LYS:HG2	32:B2:288:LYS:HG2	1.81	0.62
53:RP:1724:ASN:HD22	53:RP:1748:ASN:HB2	1.64	0.62
29:AF:273:ILE:HD11	29:AF:306:ALA:HA	1.81	0.62
23:3F:230:ASN:ND2	23:3F:236:TYR:OH	2.32	0.62
23:3F:405:VAL:HG13	23:3F:415:THR:HG22	1.82	0.62
21:3D:4:ILE:H	21:3D:23:GLN:HE22	1.48	0.62
29:AF:45:ILE:HD11	29:AF:306:ALA:HB3	1.81	0.62
48:RF:202:VAL:HG22	48:RF:223:LEU:HD12	1.81	0.62
50:RJ:1071:LYS:HA	50:RJ:1074:GLN:HG2	1.81	0.62
50:RJ:1103:GLY:HA2	50:RJ:1107:LYS:HD3	1.82	0.62
8:SI:57:ALA:HA	8:SI:89:HIS:O	1.99	0.62
35:BE:28:ARG:NH2	35:BE:383:ASP:OD2	2.32	0.62
4:SC:144:ARG:HB2	4:SC:208:GLN:H	1.65	0.62
8:SI:125:ILE:O	8:SI:129:LEU:HB2	2.00	0.62
29:AF:6:PRO:HD2	30:AG:480:SER:HB3	1.82	0.62
32:B2:452:GLY:HA3	32:B2:472:HIS:H	1.65	0.62
3:SA:475:A:H5'	10:SK:130:THR:HG21	1.80	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:487:G:H1	50:RJ:1119:ILE:HG23	1.64	0.61
20:3B:171:LEU:HB3	20:3B:240:VAL:HG12	1.81	0.61
30:AG:320:VAL:HA	30:AG:334:LEU:O	2.00	0.61
33:B3:669:LEU:HD13	33:B3:684:LEU:HB3	1.81	0.61
34:B8:585:LYS:HE3	34:B8:587:ARG:HH21	1.63	0.61
41:5G:188:HIS:HB2	41:5G:221:VAL:HG12	1.82	0.61
7:SH:56:ASN:HB3	7:SH:60:GLY:HA2	1.83	0.61
21:3D:160:ARG:HG3	21:3D:165:PHE:HB3	1.81	0.61
25:A4:656:ARG:HB3	25:A4:733:PHE:HB3	1.82	0.61
47:RE:307:LYS:HA	47:RE:312:ARG:HG3	1.83	0.61
50:RJ:616:ASP:N	50:RJ:616:ASP:OD1	2.31	0.61
53:RP:1761:ILE:HG22	53:RP:1763:LEU:H	1.63	0.61
1:3A:206:C:N3	1:3A:243:U:O4	2.33	0.61
20:3B:261:LEU:O	21:3D:129:ARG:NH1	2.33	0.61
25:A4:398:THR:HG23	25:A4:421:THR:HG22	1.83	0.61
40:5F:115:MET:HG3	40:5F:120:MET:HB3	1.83	0.61
55:RT:110:ARG:NH1	55:RT:130:MET:SD	2.73	0.61
34:B8:450:GLN:NE2	34:B8:505:PRO:O	2.33	0.61
35:BE:361:SER:HA	35:BE:636:PRO:CG	2.30	0.61
47:RE:1122:ASN:HA	47:RE:1125:ASN:HB2	1.82	0.61
48:RF:176:ASP:N	48:RF:176:ASP:OD1	2.33	0.61
3:SA:748:U:H3	3:SA:801:G:H1	1.46	0.61
3:SA:886:U:H2'	3:SA:887:A:H8	1.65	0.61
3:SA:1731:A:OP2	3:SA:1732:A:N6	2.32	0.61
30:AG:583:LYS:HD3	30:AG:596:LEU:HD13	1.82	0.61
31:B1:581:THR:HG22	31:B1:596:GLY:HA2	1.83	0.61
35:BE:321:GLU:OE1	35:BE:344:ARG:NH1	2.34	0.61
24:3G:23:VAL:HG11	24:3G:117:VAL:HG21	1.81	0.61
25:A4:279:HIS:HD2	25:A4:281:ALA:H	1.47	0.61
25:A4:589:ASN:HD21	25:A4:632:ASN:HA	1.66	0.61
30:AG:701:VAL:HG11	30:AG:724:ILE:HG21	1.82	0.61
20:3C:172:TYR:HH	20:3C:180:SER:HG	1.49	0.61
32:B2:175:ASP:N	32:B2:175:ASP:OD1	2.33	0.61
33:B3:403:ILE:O	33:B3:414:VAL:HA	2.00	0.61
37:5C:265:GLU:OE2	54:RQ:832:ASN:ND2	2.33	0.61
47:RE:713:LEU:HB2	47:RE:716:SER:HB3	1.83	0.61
48:RF:258:TYR:HB2	48:RF:261:GLN:HG3	1.83	0.61
51:RK:60:THR:HG22	51:RK:81:ILE:HG22	1.81	0.61
7:SH:44:GLU:O	7:SH:119:GLN:NE2	2.34	0.61
14:SR:122:ARG:NH1	14:SR:123:ARG:O	2.34	0.61
25:A4:642:ASN:HB3	25:A4:645:ARG:HB2	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B2:9:GLU:O	32:B2:684:TRP:HA	2.01	0.61
32:B2:537:VAL:HG12	32:B2:548:ILE:HG22	1.83	0.61
55:RT:259:VAL:HA	55:RT:262:ASN:HD22	1.64	0.61
28:AE:14:ASN:HB3	37:5C:101:ASN:HD21	1.66	0.61
32:B2:760:ILE:HG13	32:B2:831:LYS:HB2	1.83	0.61
35:BE:727:PRO:HG2	35:BE:730:LYS:HG3	1.83	0.61
51:RK:282:GLU:O	51:RK:286:SER:HB3	2.01	0.61
8:SI:172:VAL:O	8:SI:176:LEU:HB2	2.01	0.60
21:3D:65:ASN:ND2	21:3D:75:SER:OG	2.34	0.60
3:SA:647:G:H1	3:SA:687:G:H22	1.48	0.60
23:3F:201:ILE:HG12	23:3F:540:LEU:HD11	1.82	0.60
25:A4:656:ARG:NH1	25:A4:731:HIS:O	2.33	0.60
30:AG:630:LEU:HB3	30:AG:653:PHE:HB2	1.82	0.60
17:SZ:77:ASN:N	17:SZ:77:ASN:OD1	2.33	0.60
20:3B:238:ASP:HB3	20:3B:262:LYS:HD3	1.83	0.60
29:AF:248:ARG:NH1	29:AF:290:PHE:O	2.35	0.60
37:5C:226:SER:HB3	37:5C:228:LEU:HD13	1.83	0.60
46:RD:1518:ILE:HG12	46:RD:1552:LYS:HG2	1.82	0.60
3:SA:895:G:H22	3:SA:917:U:H3	1.48	0.60
29:AF:499:LYS:HB3	29:AF:503:ARG:HH21	1.67	0.60
30:AG:439:ASN:ND2	30:AG:496:THR:O	2.34	0.60
36:B6:148:ILE:HG22	44:5J:67:THR:HG22	1.82	0.60
43:5I:273:GLU:HA	54:RQ:302:VAL:HG21	1.83	0.60
33:B3:261:ALA:HB3	33:B3:268:GLN:HB2	1.83	0.60
4:SC:19:ARG:HG3	4:SC:20:VAL:HG12	1.84	0.60
15:SX:14:ILE:HG22	15:SX:25:VAL:HG21	1.84	0.60
23:3F:328:ILE:HG13	23:3F:338:THR:HG22	1.83	0.60
47:RE:466:THR:HG22	47:RE:475:ASN:HD21	1.65	0.60
3:SA:959:U:H5''	12:SO:14:SER:HB2	1.83	0.60
3:SA:1691:A:N6	3:SA:1711:C:O2'	2.34	0.60
20:3C:253:ILE:HD12	20:3C:269:ILE:HG12	1.83	0.60
31:B1:423:ARG:NH2	31:B1:460:VAL:O	2.35	0.60
32:B2:607:CYS:SG	32:B2:608:HIS:N	2.75	0.60
41:5G:128:VAL:HG11	41:5G:267:GLU:HB2	1.83	0.60
53:RP:111:ALA:HB2	53:RP:154:CYS:HB2	1.83	0.60
3:SA:789:A:N6	10:SK:72:GLU:OE2	2.34	0.60
12:SO:16:ILE:O	15:SX:57:ARG:NH2	2.34	0.60
22:3E:5:LEU:O	22:3E:89:VAL:HA	2.00	0.60
36:B6:26:LYS:HA	36:B6:29:VAL:HG12	1.83	0.60
49:RH:75:GLY:HA2	49:RH:78:LYS:HE3	1.82	0.60
3:SA:327:U:H1'	11:SM:10:GLU:HG2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:3C:225:ARG:NH1	20:3C:248:ASP:OD2	2.35	0.60
30:AG:598:LYS:HD2	30:AG:638:PHE:HB2	1.84	0.60
43:5I:61:GLN:OE1	43:5I:371:ASN:ND2	2.35	0.60
51:RK:141:MET:HG2	51:RK:300:TYR:HE2	1.67	0.60
3:SA:259:U:H1'	9:SJ:178:ARG:HH12	1.65	0.60
3:SA:1162:C:OP1	6:SG:148:ARG:NH2	2.35	0.60
30:AG:510:TYR:HB2	30:AG:529:LEU:HG	1.84	0.60
23:3F:263:TRP:CZ3	23:3F:270:PRO:CD	2.84	0.59
35:BE:309:ILE:HG22	35:BE:323:VAL:HG23	1.83	0.59
21:3D:293:CYS:HA	21:3D:309:GLU:HG2	1.85	0.59
25:A4:740:PRO:C	25:A4:756:GLU:HG2	2.24	0.59
26:A5:116:GLN:OE1	26:A5:118:TRP:NE1	2.36	0.59
30:AG:610:SER:HB3	30:AG:704:ASN:HB2	1.84	0.59
30:AG:766:ILE:HD11	30:AG:774:PHE:HB3	1.84	0.59
49:RH:32:THR:OG1	49:RH:125:ASN:ND2	2.35	0.59
3:SA:115:G:H5'	11:SM:129:ARG:HH11	1.67	0.59
30:AG:30:GLY:HA3	30:AG:200:ASN:HA	1.84	0.59
32:B2:629:ASN:HD22	32:B2:643:ASP:HA	1.66	0.59
47:RE:429:LEU:O	47:RE:489:LYS:NZ	2.35	0.59
20:3B:228:GLN:NE2	21:3D:101:SER:O	2.35	0.59
32:B2:362:ILE:HG12	32:B2:385:ILE:HB	1.85	0.59
35:BE:118:VAL:HA	35:BE:132:THR:HA	1.85	0.59
51:RK:24:ALA:HB2	51:RK:31:ILE:HD12	1.84	0.59
3:SA:551:G:N7	38:5D:2:ALA:N	2.50	0.59
31:B1:524:ARG:NH1	31:B1:526:ASP:OD2	2.36	0.59
47:RE:312:ARG:HH11	47:RE:314:CYS:H	1.50	0.59
47:RE:1148:GLN:NE2	48:RF:172:TYR:OH	2.35	0.59
49:RH:54:LYS:HA	49:RH:65:TYR:HA	1.85	0.59
52:RN:802:GLU:O	52:RN:806:ARG:NH1	2.35	0.59
55:RT:99:ILE:HD13	55:RT:159:ILE:HD11	1.84	0.59
32:B2:203:HIS:NE2	32:B2:220:THR:O	2.36	0.59
32:B2:317:ILE:O	32:B2:321:TYR:N	2.36	0.59
33:B3:38:ASP:N	33:B3:38:ASP:OD1	2.35	0.59
43:5I:319:GLU:OE2	43:5I:340:ARG:NH1	2.35	0.59
53:RP:2066:ASP:O	53:RP:2069:GLN:NE2	2.34	0.59
30:AG:43:ASN:HA	30:AG:55:TYR:O	2.01	0.59
32:B2:446:ILE:HG21	32:B2:488:LEU:HD11	1.85	0.59
44:5J:106:LEU:O	44:5J:146:ARG:NH1	2.35	0.59
55:RT:268:SER:O	55:RT:272:GLU:HB2	2.03	0.59
4:SC:16:GLN:HB2	33:B3:390:LEU:HD21	1.84	0.59
13:SP:16:VAL:HG12	13:SP:80:HIS:HB2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:3D:267:ASP:HB3	22:3E:275:TYR:HE1	1.68	0.59
30:AG:445:ILE:HG12	30:AG:504:GLY:HA3	1.85	0.59
31:B1:389:SER:HB3	31:B1:407:LEU:HD13	1.85	0.59
33:B3:702:LEU:HD21	33:B3:758:ARG:HD3	1.84	0.59
35:BE:747:LYS:H	39:5E:474:ILE:HD12	1.67	0.59
48:RF:23:HIS:HB3	48:RF:26:LEU:HB2	1.85	0.59
1:3A:76:U:O2'	30:AG:868:ASN:ND2	2.36	0.59
7:SH:23:ARG:HD3	7:SH:42:GLY:HA2	1.84	0.59
11:SM:125:VAL:HG12	11:SM:139:VAL:HA	1.85	0.59
22:3E:283:ILE:O	22:3E:380:ARG:NH2	2.36	0.59
29:AF:245:LEU:HD12	29:AF:246:TYR:HB2	1.85	0.59
32:B2:430:CYS:SG	32:B2:431:GLY:N	2.76	0.59
40:5F:69:PRO:HA	40:5F:72:ARG:HG2	1.84	0.59
47:RE:629:THR:HG22	47:RE:669:TRP:HE1	1.67	0.59
51:RK:89:ILE:HA	51:RK:119:LYS:HB2	1.85	0.59
3:SA:868:G:H1	3:SA:960:U:H3	1.49	0.59
15:SX:44:HIS:NE2	15:SX:112:ASP:OD2	2.36	0.59
25:A4:649:TRP:NE1	25:A4:744:VAL:O	2.35	0.59
26:A5:123:SER:O	26:A5:141:ARG:NH2	2.35	0.59
31:B1:440:PRO:HG3	31:B1:483:GLN:HA	1.85	0.59
35:BE:98:VAL:HG23	35:BE:110:LEU:HB2	1.84	0.59
37:5C:265:GLU:OE2	54:RQ:832:ASN:CG	2.46	0.59
47:RE:243:LEU:HD22	47:RE:248:LEU:HD21	1.84	0.59
51:RK:339:LEU:HD12	51:RK:350:MET:HB3	1.83	0.59
3:SA:532:U:OP1	10:SK:132:ARG:NH2	2.36	0.58
12:SO:40:TYR:CB	12:SO:45:LEU:HD12	2.31	0.58
20:3C:277:ASP:OD1	25:A4:162:ASN:ND2	2.36	0.58
30:AG:86:GLU:OE1	30:AG:113:ASN:ND2	2.35	0.58
33:B3:288:LEU:HB3	33:B3:307:SER:HB3	1.85	0.58
33:B3:355:LEU:HB3	33:B3:363:ARG:O	2.03	0.58
47:RE:363:THR:HG21	47:RE:394:THR:HG22	1.83	0.58
49:RH:175:CYS:HA	49:RH:201:SER:O	2.03	0.58
14:SR:50:GLU:OE2	14:SR:82:ARG:NH1	2.36	0.58
23:3F:263:TRP:CZ3	23:3F:270:PRO:CG	2.86	0.58
25:A4:426:GLN:H	25:A4:444:ARG:HH11	1.49	0.58
26:A5:281:ILE:HG12	26:A5:328:VAL:HB	1.84	0.58
26:A5:355:ASN:OD1	30:AG:479:ASN:ND2	2.36	0.58
30:AG:526:THR:HG22	30:AG:549:ASN:HD21	1.66	0.58
3:SA:151:G:N3	7:SH:13:GLN:NE2	2.51	0.58
3:SA:1627:U:H5''	3:SA:1628:U:H5'	1.85	0.58
25:A4:741:LEU:CD1	25:A4:744:VAL:HG23	2.29	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:AG:467:GLN:NE2	30:AG:469:ASN:O	2.36	0.58
3:SA:862:A:OP2	12:SO:64:ARG:NH2	2.37	0.58
3:SA:1775:U:O2	3:SA:1786:G:N2	2.35	0.58
11:SM:103:ARG:HH21	11:SM:105:LYS:HD3	1.69	0.58
22:3E:348:VAL:HG12	22:3E:359:ILE:HG23	1.85	0.58
26:A5:20:VAL:HG22	26:A5:29:VAL:HG22	1.84	0.58
33:B3:269:LEU:HB2	33:B3:279:LYS:HB2	1.86	0.58
15:SX:87:GLU:OE2	15:SX:117:ARG:NH2	2.37	0.58
16:SY:141:GLU:HB2	50:RJ:833:ARG:HH12	1.68	0.58
29:AF:216:GLU:N	29:AF:229:CYS:O	2.34	0.58
30:AG:527:HIS:O	30:AG:549:ASN:ND2	2.37	0.58
32:B2:26:ILE:HB	32:B2:40:GLN:HB2	1.85	0.58
47:RE:828:ASP:OD2	47:RE:888:LYS:NZ	2.37	0.58
50:RJ:1018:VAL:O	50:RJ:1029:TRP:NE1	2.36	0.58
51:RK:251:GLN:HE21	51:RK:252:LYS:HE3	1.68	0.58
53:RP:2064:MET:HE3	53:RP:2079:VAL:HG13	1.84	0.58
5:SF:106:LYS:HD2	5:SF:108:ARG:HE	1.69	0.58
7:SH:36:VAL:HB	7:SH:50:PHE:HB2	1.86	0.58
28:AE:336:LEU:O	28:AE:341:LYS:NZ	2.36	0.58
33:B3:231:CYS:SG	33:B3:232:LYS:N	2.76	0.58
50:RJ:553:ILE:HG21	51:RK:326:LEU:HD23	1.86	0.58
20:3B:90:PRO:HD3	44:5J:106:LEU:HD12	1.85	0.58
22:3E:339:TYR:HB3	22:3E:343:TYR:HB2	1.84	0.58
33:B3:294:LEU:HB2	33:B3:303:PHE:HB2	1.84	0.58
43:5I:324:SER:OG	43:5I:326:ASP:OD1	2.22	0.58
47:RE:1205:LYS:O	47:RE:1212:VAL:HA	2.04	0.58
23:3F:417:SER:OG	23:3F:418:ASP:N	2.34	0.58
26:A5:168:HIS:H	26:A5:191:VAL:HG23	1.69	0.58
30:AG:88:ILE:HA	30:AG:111:THR:HA	1.85	0.58
32:B2:94:LEU:O	32:B2:105:VAL:HA	2.04	0.58
46:RD:1659:VAL:HG21	46:RD:1678:ILE:HD11	1.86	0.58
51:RK:68:SER:HB2	51:RK:73:THR:HG22	1.86	0.58
3:SA:57:G:OP1	17:SZ:112:LYS:NZ	2.37	0.58
29:AF:256:THR:N	29:AF:275:SER:O	2.37	0.58
47:RE:496:LEU:O	47:RE:500:ASN:ND2	2.37	0.58
47:RE:1205:LYS:HB2	47:RE:1213:ILE:O	2.03	0.58
3:SA:886:U:OP1	4:SC:214:LYS:NZ	2.37	0.58
8:SI:56:LYS:HB2	8:SI:88:ARG:HD3	1.86	0.58
32:B2:20:ASN:HA	32:B2:339:LYS:HD3	1.86	0.58
33:B3:559:ILE:HB	33:B3:569:LYS:HB2	1.85	0.58
34:B8:180:ASP:OD2	35:BE:281:ARG:NH2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:BE:144:ASP:C	35:BE:146:GLN:H	2.12	0.58
47:RE:975:LEU:HD22	47:RE:1041:VAL:HG12	1.83	0.58
20:3B:165:ALA:HB3	20:3B:168:LYS:HG2	1.86	0.57
22:3E:199:VAL:HG11	22:3E:227:LEU:HD22	1.85	0.57
25:A4:312:ASN:HA	25:A4:315:GLN:HE21	1.68	0.57
32:B2:390:GLN:O	32:B2:411:ASN:ND2	2.37	0.57
47:RE:793:PRO:HG2	47:RE:799:LEU:HA	1.85	0.57
53:RP:1741:LYS:NZ	53:RP:1743:LYS:O	2.37	0.57
22:3E:430:ASP:HA	35:BE:125:GLY:HA2	1.86	0.57
29:AF:466:VAL:O	29:AF:470:TYR:HB2	2.04	0.57
33:B3:267:PHE:H	33:B3:281:THR:HG22	1.69	0.57
2:5A:86:C:O2'	29:AF:5:ARG:NH1	2.37	0.57
3:SA:332:U:OP1	9:SJ:31:ARG:NE	2.37	0.57
26:A5:55:ASP:N	26:A5:55:ASP:OD1	2.37	0.57
30:AG:321:MET:HB3	30:AG:334:LEU:HB3	1.86	0.57
31:B1:119:LEU:HD22	31:B1:163:THR:HG21	1.85	0.57
36:B6:38:ASP:OD2	36:B6:42:ARG:NH1	2.36	0.57
37:5C:183:GLU:OE2	40:5F:41:ARG:NH2	2.37	0.57
39:5E:351:ALA:HA	41:5G:285:ASN:HB3	1.86	0.57
53:RP:1948:SER:O	53:RP:1985:ARG:NH2	2.37	0.57
3:SA:318:U:O2	3:SA:346:G:O6	2.23	0.57
16:SY:121:ARG:NH2	52:RN:795:GLU:OE2	2.38	0.57
20:3B:125:VAL:HG12	44:5J:150:GLY:HA3	1.86	0.57
20:3B:253:ILE:HD13	20:3B:269:ILE:HD12	1.85	0.57
29:AF:283:VAL:H	29:AF:292:VAL:HG23	1.69	0.57
32:B2:448:GLY:HA3	32:B2:476:ILE:HD11	1.86	0.57
33:B3:30:LYS:HA	33:B3:42:ILE:O	2.04	0.57
33:B3:337:HIS:HD2	33:B3:363:ARG:HE	1.51	0.57
37:5C:114:TYR:HA	37:5C:128:THR:O	2.04	0.57
37:5C:415:GLU:OE2	43:5I:33:HIS:ND1	2.34	0.57
3:SA:5:U:O2	3:SA:7:G:N2	2.37	0.57
3:SA:901:G:H3'	3:SA:902:G:H8	1.70	0.57
10:SK:58:ASP:N	10:SK:58:ASP:OD1	2.36	0.57
20:3B:244:VAL:O	20:3B:249:GLN:NE2	2.37	0.57
23:3F:333:MET:SD	23:3F:335:ARG:NH1	2.76	0.57
26:A5:547:LEU:HD11	29:AF:487:LEU:HD21	1.87	0.57
45:5K:145:VAL:HG11	45:5K:170:ILE:HD13	1.87	0.57
47:RE:792:TRP:HE3	47:RE:793:PRO:HD2	1.69	0.57
48:RF:262:VAL:HA	48:RF:265:ARG:HG2	1.86	0.57
49:RH:168:THR:HA	49:RH:171:LEU:HG	1.84	0.57
20:3B:306:LEU:HD11	20:3B:313:HIS:HB2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:3D:14:GLY:HA3	21:3D:55:PRO:HA	1.87	0.57
47:RE:218:ASP:HA	47:RE:223:ARG:HH12	1.70	0.57
54:RQ:316:ASN:HD21	54:RQ:895:LYS:H	1.52	0.57
22:3E:303:SER:HB2	22:3E:309:LEU:HB3	1.87	0.57
28:AE:424:LEU:HG	28:AE:426:GLY:H	1.69	0.57
29:AF:33:ALA:HA	29:AF:329:ILE:O	2.05	0.57
32:B2:17:ILE:HG12	32:B2:360:ASN:HB2	1.87	0.57
33:B3:15:ILE:HG21	33:B3:379:LEU:HD11	1.87	0.57
34:B8:311:ASN:ND2	34:B8:325:ASP:OD1	2.38	0.57
37:5C:356:GLY:O	37:5C:364:ARG:NH1	2.37	0.57
39:5E:302:LYS:HA	39:5E:305:ILE:HG12	1.87	0.57
2:5A:480:C:O2	36:B6:46:ARG:NH2	2.38	0.57
3:SA:953:G:H2'	3:SA:954:G:H8	1.69	0.57
8:SI:147:ASN:ND2	43:5I:180:SER:OG	2.37	0.57
26:A5:284:LYS:NZ	26:A5:330:ILE:O	2.37	0.57
28:AE:413:ASP:HA	28:AE:416:LEU:HB2	1.86	0.57
30:AG:616:SER:HB3	30:AG:621:LEU:HG	1.87	0.57
32:B2:259:ILE:HA	32:B2:273:TYR:O	2.04	0.57
36:B6:175:ASN:OD1	36:B6:175:ASN:N	2.37	0.57
51:RK:89:ILE:HG22	51:RK:119:LYS:HG3	1.86	0.57
20:3C:171:LEU:HB2	20:3C:237:VAL:HG11	1.87	0.57
22:3E:355:ASN:ND2	22:3E:402:GLU:OE2	2.38	0.57
31:B1:520:ALA:HB3	31:B1:533:SER:HB3	1.87	0.57
35:BE:429:ASN:HD22	35:BE:445:MET:HB3	1.69	0.57
46:RD:1674:LEU:HA	46:RD:1677:ARG:HG2	1.87	0.57
51:RK:361:ASN:O	51:RK:364:LYS:NZ	2.37	0.57
3:SA:67:A:N6	3:SA:83:G:O2'	2.37	0.57
3:SA:207:U:O2	9:SJ:178:ARG:NH1	2.38	0.57
8:SI:187:SER:OG	8:SI:188:GLU:N	2.38	0.57
23:3F:475:ILE:HA	23:3F:491:SER:HB3	1.87	0.57
25:A4:497:ILE:HD11	25:A4:555:LEU:HD12	1.86	0.57
25:A4:621:ASN:ND2	25:A4:663:PHE:O	2.37	0.57
38:5D:37:ARG:NH2	50:RJ:994:LYS:O	2.38	0.57
47:RE:756:VAL:O	47:RE:761:ARG:NH2	2.37	0.57
47:RE:1166:ARG:HG3	47:RE:1181:VAL:HG22	1.87	0.57
48:RF:85:GLU:HG2	48:RF:86:GLU:HG3	1.87	0.57
49:RH:50:LEU:O	49:RH:118:ARG:NH1	2.38	0.57
50:RJ:169:GLY:O	50:RJ:204:LEU:HA	2.05	0.57
51:RK:161:LEU:HB2	51:RK:238:SER:HB2	1.86	0.57
3:SA:283:U:H5''	7:SH:188:ARG:HD3	1.87	0.56
25:A4:75:ASN:HA	25:A4:91:ILE:O	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:B1:209:VAL:HG22	31:B1:215:VAL:HG22	1.87	0.56
31:B1:558:ASP:N	31:B1:558:ASP:OD1	2.37	0.56
32:B2:897:ASP:OD2	33:B3:758:ARG:NH1	2.38	0.56
37:5C:257:SER:OG	37:5C:259:TRP:NE1	2.33	0.56
1:3A:95:A:H61	1:3A:321:C:H42	1.52	0.56
25:A4:739:LYS:HE2	25:A4:739:LYS:N	2.20	0.56
30:AG:59:THR:O	30:AG:61:GLN:NE2	2.38	0.56
31:B1:737:ASN:O	31:B1:741:MET:HB2	2.04	0.56
46:RD:1583:SER:HA	46:RD:1586:VAL:HG22	1.86	0.56
47:RE:1162:ILE:HG23	47:RE:1187:LYS:HZ1	1.70	0.56
1:3A:329:C:H2'	1:3A:330:A:H8	1.70	0.56
3:SA:447:U:O2'	5:SF:27:TYR:O	2.23	0.56
5:SF:100:ARG:HH11	5:SF:236:ILE:HG23	1.70	0.56
32:B2:655:ALA:O	32:B2:682:ARG:NH1	2.39	0.56
47:RE:423:LYS:HG2	47:RE:427:LYS:HE2	1.86	0.56
47:RE:1109:LYS:HZ2	47:RE:1170:GLY:H	1.53	0.56
48:RF:14:ILE:HB	48:RF:39:ALA:HB3	1.87	0.56
50:RJ:864:ASP:OD2	50:RJ:868:ARG:NH2	2.38	0.56
11:SM:128:CYS:SG	11:SM:129:ARG:N	2.79	0.56
22:3E:430:ASP:OD2	34:B8:142:LYS:NZ	2.39	0.56
28:AE:218:ILE:HG22	28:AE:263:VAL:HG11	1.87	0.56
32:B2:795:ILE:O	32:B2:798:ASN:ND2	2.39	0.56
37:5C:358:MET:HE3	37:5C:364:ARG:HH22	1.71	0.56
47:RE:377:SER:HB3	47:RE:389:GLY:HA3	1.86	0.56
3:SA:1170:G:N2	3:SA:1469:A:N1	2.51	0.56
23:3F:162:CYS:HA	23:3F:187:ALA:HA	1.88	0.56
24:3H:7:LYS:NZ	24:3H:62:GLU:OE2	2.34	0.56
30:AG:75:SER:HB2	30:AG:79:LEU:HG	1.88	0.56
53:RP:182:SER:HG	53:RP:228:LEU:N	2.04	0.56
54:RQ:874:SER:O	54:RQ:878:LEU:HB2	2.06	0.56
3:SA:564:G:O6	38:5D:42:HIS:NE2	2.39	0.56
25:A4:488:ILE:O	25:A4:495:VAL:HA	2.06	0.56
31:B1:379:CYS:SG	31:B1:380:LEU:N	2.78	0.56
32:B2:171:CYS:SG	32:B2:172:GLN:N	2.79	0.56
33:B3:9:GLY:HA2	33:B3:644:TRP:HA	1.87	0.56
46:RD:1607:ASN:HD22	46:RD:1610:LYS:HZ3	1.53	0.56
48:RF:69:LYS:NZ	48:RF:159:THR:OG1	2.39	0.56
50:RJ:831:ARG:NH1	50:RJ:877:GLU:O	2.38	0.56
53:RP:1798:LEU:HD12	53:RP:1801:ASN:HD22	1.70	0.56
2:5A:20:C:H2'	2:5A:21:A:H8	1.70	0.56
3:SA:505:A:OP1	3:SA:585:A:N6	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A4:579:ARG:NH2	25:A4:612:THR:OG1	2.39	0.56
26:A5:253:LEU:HB2	26:A5:291:ILE:HD11	1.87	0.56
30:AG:154:LEU:HD11	30:AG:171:TYR:HB3	1.87	0.56
33:B3:42:ILE:HG22	33:B3:49:SER:HA	1.88	0.56
37:5C:378:VAL:HG12	37:5C:394:HIS:HB3	1.88	0.56
48:RF:101:SER:O	48:RF:105:SER:CB	2.54	0.56
50:RJ:300:GLN:HE21	50:RJ:792:VAL:HG21	1.70	0.56
26:A5:299:ASP:HA	26:A5:319:TRP:HE3	1.70	0.56
38:5D:29:GLU:OE2	38:5D:37:ARG:NH1	2.39	0.56
41:5G:93:SER:O	41:5G:119:ARG:NH2	2.38	0.56
50:RJ:135:ALA:O	50:RJ:238:ARG:NH1	2.39	0.56
3:SA:1688:U:O4	3:SA:1713:G:O6	2.23	0.56
5:SF:127:LYS:HZ3	5:SF:142:HIS:HB3	1.70	0.56
6:SG:57:SER:HA	19:Sd:53:ILE:HG13	1.88	0.56
10:SK:94:ASP:N	10:SK:94:ASP:OD1	2.37	0.56
10:SK:169:PRO:O	10:SK:174:ARG:NH2	2.39	0.56
20:3C:142:ARG:NH1	20:3C:186:ASP:OD2	2.39	0.56
26:A5:210:ARG:NH1	35:BE:563:ASP:OD2	2.37	0.56
31:B1:152:LEU:HD11	31:B1:161:ILE:HD11	1.88	0.56
31:B1:789:SER:O	35:BE:728:ARG:NH2	2.39	0.56
32:B2:162:HIS:O	39:5E:522:ARG:NH2	2.39	0.56
45:5K:103:MET:SD	45:5K:127:ARG:NH1	2.79	0.56
47:RE:410:LYS:HZ3	47:RE:413:LEU:HB2	1.71	0.56
3:SA:246:G:N2	11:SM:66:ILE:O	2.38	0.56
3:SA:576:G:H4'	39:5E:327:LYS:HE2	1.87	0.56
3:SA:857:U:OP2	48:RF:259:ARG:NH2	2.39	0.56
25:A4:479:LYS:NZ	25:A4:535:GLU:OE1	2.39	0.56
26:A5:2:ASP:HB3	34:B8:281:THR:HG21	1.88	0.56
28:AE:35:TYR:O	28:AE:150:ARG:NH1	2.39	0.56
28:AE:171:GLU:OE2	28:AE:172:LYS:NZ	2.39	0.56
35:BE:733:THR:O	35:BE:737:LEU:HB3	2.06	0.56
39:5E:312:GLU:O	39:5E:316:ASN:ND2	2.38	0.56
47:RE:804:THR:HG22	47:RE:838:VAL:HG22	1.87	0.56
11:SM:47:THR:O	11:SM:51:GLY:HA3	2.06	0.55
20:3C:92:ARG:NH1	20:3C:160:ASP:O	2.39	0.55
29:AF:48:ASN:ND2	29:AF:51:HIS:O	2.39	0.55
37:5C:257:SER:HG	37:5C:259:TRP:HE1	1.53	0.55
47:RE:118:GLN:HA	47:RE:121:VAL:HG12	1.88	0.55
51:RK:109:PHE:HA	51:RK:361:ASN:HD22	1.70	0.55
3:SA:65:A:H2	3:SA:84:A:H62	1.54	0.55
21:3D:254:ASN:O	21:3D:258:SER:HB3	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:BE:738:ASP:N	35:BE:738:ASP:OD1	2.38	0.55
50:RJ:263:LEU:O	50:RJ:264:GLN:NE2	2.40	0.55
51:RK:340:LYS:HB2	51:RK:351:ILE:HB	1.89	0.55
3:SA:1472:C:N4	3:SA:1535:U:OP2	2.39	0.55
3:SA:1576:A:H5''	49:RH:165:ASN:HB2	1.89	0.55
22:3E:359:ILE:HA	22:3E:362:VAL:HG12	1.89	0.55
53:RP:149:GLU:O	53:RP:153:ASN:HB2	2.07	0.55
7:SH:3:LEU:HA	7:SH:109:LEU:O	2.06	0.55
10:SK:60:LEU:HD22	53:RP:1848:VAL:HG11	1.89	0.55
20:3B:277:ASP:N	20:3B:277:ASP:OD1	2.37	0.55
22:3E:385:ASP:N	22:3E:385:ASP:OD1	2.39	0.55
25:A4:491:CYS:O	25:A4:530:ARG:NH2	2.39	0.55
26:A5:85:ILE:HB	26:A5:99:PHE:HB2	1.88	0.55
26:A5:366:GLY:O	30:AG:583:LYS:NZ	2.39	0.55
26:A5:548:ASP:O	26:A5:552:ASN:ND2	2.40	0.55
34:B8:448:LYS:NZ	34:B8:449:ASP:O	2.37	0.55
40:5F:33:MET:HB2	40:5F:38:ILE:HB	1.88	0.55
53:RP:1721:ILE:HA	53:RP:1748:ASN:HD21	1.72	0.55
20:3C:199:PHE:HB2	20:3C:223:ASP:HA	1.87	0.55
21:3D:174:ILE:HD13	21:3D:296:MET:HG2	1.89	0.55
33:B3:94:LYS:HB2	55:RT:273:ARG:HH21	1.71	0.55
33:B3:466:TRP:HA	33:B3:479:ILE:HG12	1.88	0.55
33:B3:732:ASN:ND2	33:B3:734:GLU:OE2	2.40	0.55
41:5G:123:VAL:HG12	41:5G:125:PRO:HD2	1.87	0.55
50:RJ:255:PRO:HA	50:RJ:258:ILE:HG22	1.88	0.55
29:AF:184:VAL:O	29:AF:195:LEU:HA	2.07	0.55
30:AG:510:TYR:HE1	30:AG:527:HIS:HB3	1.72	0.55
31:B1:361:VAL:HG11	31:B1:402:MET:HE3	1.89	0.55
47:RE:228:ARG:HG3	47:RE:296:ILE:HD11	1.88	0.55
50:RJ:133:LYS:O	50:RJ:238:ARG:NH2	2.40	0.55
33:B3:303:PHE:HA	33:B3:312:GLN:O	2.06	0.55
44:5J:124:ILE:HA	44:5J:127:ARG:HG3	1.88	0.55
4:SC:144:ARG:HB3	4:SC:206:PRO:HB2	1.89	0.55
9:SJ:78:ILE:HA	9:SJ:104:ILE:HG23	1.89	0.55
12:SO:71:ILE:HA	12:SO:74:ILE:HG12	1.89	0.55
23:3F:263:TRP:CH2	23:3F:270:PRO:HG3	2.42	0.55
24:3G:118:LYS:HA	24:3G:121:ILE:HD12	1.88	0.55
25:A4:274:GLN:HE22	25:A4:320:TRP:H	1.53	0.55
25:A4:583:VAL:HA	25:A4:592:TYR:O	2.05	0.55
29:AF:467:LEU:HD22	29:AF:484:MET:HE2	1.89	0.55
39:5E:314:LEU:HA	39:5E:317:GLU:HB2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:RK:18:ARG:NH2	51:RK:101:GLU:OE1	2.39	0.55
3:SA:215:A:N6	3:SA:242:U:OP2	2.39	0.55
3:SA:1663:G:N2	3:SA:1738:U:O2	2.29	0.55
3:SA:1671:A:N6	3:SA:1730:A:O2'	2.40	0.55
13:SP:64:ALA:HB1	13:SP:105:LEU:HG	1.89	0.55
14:SR:99:GLU:HB3	35:BE:490:GLN:HE22	1.72	0.55
23:3F:471:GLN:HG3	24:3H:83:SER:HB2	1.88	0.55
28:AE:186:MET:N	28:AE:186:MET:SD	2.80	0.55
30:AG:561:LEU:O	30:AG:573:CYS:HA	2.07	0.55
35:BE:846:ASP:OD2	35:BE:850:ARG:NH2	2.40	0.55
36:B6:41:HIS:O	36:B6:45:SER:HB3	2.07	0.55
41:5G:88:ILE:O	41:5G:114:ALA:HA	2.07	0.55
41:5G:91:THR:O	41:5G:141:VAL:HA	2.06	0.55
50:RJ:634:ARG:NH2	51:RK:256:TYR:OH	2.40	0.55
2:5A:85:G:H21	2:5A:86:C:H41	1.55	0.55
3:SA:269:G:OP2	7:SH:186:ARG:NH2	2.37	0.55
6:SG:117:THR:HG21	6:SG:194:LEU:HD23	1.89	0.55
22:3E:219:SER:OG	36:B6:288:LYS:NZ	2.40	0.55
25:A4:111:SER:OG	25:A4:113:ARG:NH1	2.40	0.55
30:AG:388:PRO:HA	30:AG:458:GLN:HE22	1.72	0.55
32:B2:454:LEU:O	32:B2:467:THR:HA	2.07	0.55
47:RE:142:GLU:O	47:RE:144:LYS:NZ	2.40	0.55
51:RK:53:LEU:HD23	51:RK:65:ILE:HG21	1.89	0.55
3:SA:142:G:C6	3:SA:173:A:N1	2.74	0.54
11:SM:21:ASN:OD1	11:SM:30:ARG:NH2	2.40	0.54
26:A5:242:ASP:OD1	26:A5:242:ASP:N	2.34	0.54
31:B1:412:ARG:NH1	31:B1:424:THR:OG1	2.40	0.54
47:RE:376:SER:OG	47:RE:378:ASN:ND2	2.40	0.54
48:RF:226:ILE:HA	48:RF:229:LYS:HG2	1.89	0.54
3:SA:1634:C:OP1	31:B1:418:ARG:NH1	2.41	0.54
12:SO:99:ARG:NH2	12:SO:119:GLU:OE2	2.40	0.54
23:3F:303:LYS:HD3	23:3F:317:ILE:HD11	1.89	0.54
29:AF:233:ASN:ND2	29:AF:247:GLU:OE1	2.40	0.54
33:B3:454:LEU:O	33:B3:465:LYS:HA	2.07	0.54
46:RD:1633:ASP:OD2	46:RD:1636:ARG:NH1	2.40	0.54
21:3D:335:ILE:HD12	21:3D:338:ALA:HB3	1.89	0.54
25:A4:116:SER:HB3	25:A4:126:TRP:HE1	1.72	0.54
29:AF:314:GLY:O	29:AF:332:LYS:NZ	2.40	0.54
34:B8:217:ASN:OD1	34:B8:217:ASN:N	2.41	0.54
36:B6:290:LYS:HD2	36:B6:294:ALA:HA	1.87	0.54
43:5I:228:ASN:ND2	43:5I:230:ASN:O	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:RJ:246:ALA:HB3	50:RJ:810:ILE:HG13	1.89	0.54
3:SA:152:U:O2	7:SH:4:ASN:ND2	2.41	0.54
3:SA:916:U:O4	13:SP:41:ARG:NH2	2.40	0.54
7:SH:50:PHE:HB3	7:SH:111:LEU:HD22	1.90	0.54
16:SY:76:LEU:O	16:SY:80:GLY:CA	2.55	0.54
20:3C:301:LEU:HD11	20:3C:319:ARG:HG2	1.87	0.54
25:A4:397:SER:H	25:A4:428:ILE:HB	1.71	0.54
30:AG:319:LYS:HG3	30:AG:482:GLY:HA2	1.90	0.54
33:B3:242:GLN:HE21	33:B3:245:SER:HB2	1.73	0.54
35:BE:209:ILE:HG22	35:BE:225:THR:HG22	1.90	0.54
35:BE:511:ASP:OD1	35:BE:551:TYR:OH	2.24	0.54
47:RE:1102:LEU:HB3	47:RE:1230:MET:HE3	1.88	0.54
3:SA:454:U:OP1	3:SA:455:C:N4	2.41	0.54
3:SA:1665:U:O2	3:SA:1736:G:O6	2.25	0.54
5:SF:73:ASP:HB2	5:SF:164:LEU:HD11	1.89	0.54
8:SI:50:ASP:HA	8:SI:56:LYS:HA	1.89	0.54
20:3B:238:ASP:OD1	20:3B:238:ASP:N	2.40	0.54
22:3E:251:ASP:N	22:3E:251:ASP:OD1	2.39	0.54
26:A5:162:GLN:HA	26:A5:173:ILE:O	2.08	0.54
29:AF:227:VAL:HG12	29:AF:236:VAL:HG12	1.89	0.54
31:B1:708:ASP:OD1	31:B1:708:ASP:N	2.40	0.54
32:B2:334:SER:OG	32:B2:335:LEU:N	2.40	0.54
32:B2:540:SER:HB2	32:B2:544:ARG:H	1.72	0.54
32:B2:565:PHE:O	51:RK:207:ARG:NH2	2.36	0.54
47:RE:443:HIS:HB3	47:RE:470:LYS:HB2	1.88	0.54
51:RK:315:LYS:HZ3	51:RK:348:GLU:H	1.55	0.54
53:RP:1797:LEU:HD13	53:RP:1877:ARG:HB3	1.90	0.54
3:SA:319:U:H5'	3:SA:320:U:H5''	1.88	0.54
8:SI:155:ASP:OD1	8:SI:155:ASP:N	2.36	0.54
25:A4:433:LEU:HD13	25:A4:440:LEU:HB2	1.90	0.54
26:A5:10:TYR:OH	26:A5:302:ASN:ND2	2.40	0.54
28:AE:396:ASP:OD1	28:AE:396:ASP:N	2.41	0.54
30:AG:370:GLN:HE22	30:AG:384:SER:HB2	1.72	0.54
32:B2:500:TRP:HB3	32:B2:522:LEU:HD12	1.90	0.54
33:B3:182:CYS:SG	33:B3:183:LEU:N	2.80	0.54
33:B3:336:ASN:O	33:B3:363:ARG:NH2	2.40	0.54
33:B3:411:THR:HG22	33:B3:431:ILE:HA	1.89	0.54
35:BE:342:TYR:OH	35:BE:345:SER:OG	2.24	0.54
47:RE:1193:ALA:HA	47:RE:1212:VAL:O	2.07	0.54
53:RP:1735:SER:OG	53:RP:1736:GLU:N	2.39	0.54
3:SA:71:A:H8	3:SA:72:A:H5''	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:SH:45:PHE:HA	7:SH:119:GLN:HG2	1.89	0.54
22:3E:392:ALA:O	22:3E:396:ASN:ND2	2.40	0.54
26:A5:255:ILE:HG23	26:A5:277:LYS:HB2	1.89	0.54
31:B1:279:PHE:HE2	31:B1:285:ARG:HG3	1.73	0.54
32:B2:98:TYR:HD2	32:B2:102:VAL:HG13	1.73	0.54
35:BE:82:ALA:O	35:BE:93:ALA:HB3	2.08	0.54
39:5E:316:ASN:O	39:5E:320:ALA:HB2	2.08	0.54
47:RE:160:VAL:HG21	47:RE:230:VAL:HG12	1.90	0.54
47:RE:313:ASN:HB2	47:RE:328:ALA:HA	1.89	0.54
47:RE:1195:LYS:HA	47:RE:1210:GLU:O	2.08	0.54
53:RP:1873:LEU:HG	53:RP:1910:VAL:HG22	1.89	0.54
8:SI:15:GLU:HA	8:SI:18:LEU:HD12	1.89	0.54
9:SJ:113:PHE:HE2	9:SJ:121:LEU:HB3	1.72	0.54
25:A4:739:LYS:CA	25:A4:739:LYS:CE	2.85	0.54
32:B2:803:GLN:NE2	32:B2:807:ASP:OD1	2.40	0.54
35:BE:49:TYR:OH	35:BE:86:HIS:O	2.26	0.54
35:BE:375:LEU:HD22	35:BE:389:MET:HG3	1.90	0.54
50:RJ:164:MET:HE3	50:RJ:198:VAL:HG23	1.90	0.54
50:RJ:270:ALA:HA	50:RJ:791:ILE:O	2.08	0.54
50:RJ:993:ASP:N	50:RJ:993:ASP:OD1	2.39	0.54
4:SC:19:ARG:HH11	33:B3:338:GLY:HA3	1.73	0.54
6:SG:91:GLU:HA	6:SG:94:THR:HG22	1.90	0.54
11:SM:8:GLN:NE2	11:SM:12:ALA:O	2.41	0.54
20:3C:264:GLN:OE1	20:3C:319:ARG:NH2	2.40	0.54
25:A4:329:HIS:ND1	25:A4:353:GLU:OE2	2.37	0.54
28:AE:395:GLU:OE2	28:AE:397:LYS:NZ	2.38	0.54
30:AG:302:SER:O	30:AG:314:SER:HA	2.08	0.54
31:B1:497:ILE:HG23	31:B1:512:ILE:HB	1.89	0.54
32:B2:181:SER:OG	32:B2:183:ASP:OD1	2.23	0.54
33:B3:213:SER:OG	33:B3:221:ASN:ND2	2.39	0.54
46:RD:1530:GLU:HA	46:RD:1533:LEU:HB2	1.90	0.54
53:RP:1692:TYR:HA	53:RP:1743:LYS:HD2	1.90	0.54
4:SC:243:LYS:NZ	33:B3:232:LYS:O	2.34	0.54
7:SH:159:ARG:NH1	7:SH:170:THR:OG1	2.40	0.54
14:SR:59:LYS:HD3	14:SR:105:LEU:HD21	1.89	0.54
21:3D:117:ASP:OD1	43:5I:157:ASN:ND2	2.41	0.54
23:3F:398:CYS:SG	23:3F:399:GLU:N	2.72	0.54
29:AF:5:ARG:O	29:AF:7:ARG:NH1	2.40	0.54
31:B1:247:SER:O	31:B1:249:ARG:NH1	2.41	0.54
34:B8:524:SER:OG	34:B8:527:GLY:N	2.38	0.54
34:B8:581:ASN:HD21	34:B8:585:LYS:HG3	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:816:G:OP1	3:SA:858:G:N2	2.40	0.53
8:SI:158:ASP:OD2	8:SI:161:GLN:NE2	2.40	0.53
14:SR:99:GLU:HG2	14:SR:102:LYS:HE3	1.90	0.53
20:3C:96:VAL:HG21	20:3C:155:ILE:HG21	1.89	0.53
25:A4:99:ILE:HD11	25:A4:102:LEU:HB3	1.90	0.53
31:B1:25:ASP:OD1	31:B1:25:ASP:N	2.40	0.53
32:B2:426:ARG:NH1	32:B2:463:SER:OG	2.40	0.53
34:B8:445:ARG:HH11	34:B8:503:SER:H	1.57	0.53
35:BE:310:ILE:O	35:BE:321:GLU:HA	2.08	0.53
40:5F:136:VAL:HA	40:5F:160:TRP:HA	1.90	0.53
50:RJ:59:VAL:O	50:RJ:239:ASN:ND2	2.40	0.53
1:3A:2:U:O4	3:SA:1123:C:N3	2.40	0.53
23:3F:257:ASP:OD1	23:3F:257:ASP:N	2.36	0.53
25:A4:213:TRP:HA	25:A4:225:LEU:HA	1.90	0.53
25:A4:573:VAL:HG22	25:A4:584:VAL:HG23	1.90	0.53
28:AE:4:LEU:HD13	37:5C:108:LEU:HD11	1.90	0.53
28:AE:161:PHE:HD1	28:AE:182:LEU:HD11	1.73	0.53
30:AG:322:SER:OG	30:AG:331:GLN:NE2	2.39	0.53
32:B2:639:VAL:HG23	32:B2:653:LEU:HB2	1.90	0.53
41:5G:272:ASP:OD1	41:5G:272:ASP:N	2.41	0.53
50:RJ:841:THR:HG22	50:RJ:860:TYR:H	1.73	0.53
53:RP:1877:ARG:HA	53:RP:1880:ILE:HG13	1.89	0.53
2:5A:295:A:N7	35:BE:381:ARG:NH1	2.55	0.53
22:3E:290:LEU:O	22:3E:391:ARG:NH2	2.41	0.53
23:3F:194:LEU:HD21	23:3F:237:ASP:HA	1.90	0.53
28:AE:142:TYR:O	28:AE:145:THR:OG1	2.24	0.53
30:AG:573:CYS:O	30:AG:585:TRP:HB2	2.08	0.53
35:BE:209:ILE:HD12	35:BE:223:LEU:HD12	1.90	0.53
36:B6:63:VAL:HG13	36:B6:88:ILE:HD11	1.89	0.53
41:5G:164:GLN:NE2	41:5G:260:GLU:OE1	2.41	0.53
1:3A:255:U:O4	24:3H:84:ARG:NH1	2.42	0.53
16:SY:141:GLU:OE1	50:RJ:833:ARG:NH2	2.41	0.53
17:SZ:54:ALA:HB2	17:SZ:79:VAL:HG12	1.90	0.53
21:3D:258:SER:OG	21:3D:259:MET:N	2.42	0.53
31:B1:645:ASP:OD1	31:B1:645:ASP:N	2.39	0.53
33:B3:223:TRP:HA	33:B3:232:LYS:HA	1.89	0.53
33:B3:505:ILE:HB	33:B3:517:ILE:HG22	1.90	0.53
33:B3:584:ILE:HG13	33:B3:588:LYS:HG3	1.91	0.53
35:BE:666:ARG:NH1	35:BE:706:ASP:OD2	2.41	0.53
43:5I:136:MET:HE2	43:5I:150:ILE:HD11	1.90	0.53
43:5I:448:ARG:NH1	43:5I:451:MET:SD	2.81	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3A:197:U:OP2	23:3F:207:ARG:NH1	2.42	0.53
3:SA:629:U:OP1	12:SO:127:ARG:NH2	2.34	0.53
3:SA:1781:A:O2'	3:SA:1783:C:N4	2.39	0.53
32:B2:291:GLU:HA	32:B2:294:ARG:HG2	1.90	0.53
47:RE:807:LEU:HA	47:RE:810:ILE:HG22	1.91	0.53
53:RP:1876:LEU:HD13	53:RP:1914:THR:HG22	1.90	0.53
1:3A:12:U:O4	50:RJ:1158:LYS:NZ	2.39	0.53
5:SF:93:ASP:N	5:SF:93:ASP:OD1	2.40	0.53
14:SR:94:GLN:HG3	14:SR:102:LYS:HE2	1.90	0.53
20:3C:163:PHE:HZ	20:3C:319:ARG:HD2	1.72	0.53
24:3G:20:ILE:HA	24:3G:23:VAL:HG12	1.91	0.53
26:A5:79:GLY:HA3	26:A5:107:ILE:HD11	1.89	0.53
32:B2:534:ILE:HD13	32:B2:548:ILE:HB	1.90	0.53
33:B3:107:ILE:HD11	33:B3:147:ILE:HG23	1.90	0.53
35:BE:364:HIS:HB2	35:BE:381:ARG:HH21	1.72	0.53
35:BE:440:ALA:HB2	35:BE:463:VAL:HG21	1.89	0.53
36:B6:82:SER:OG	36:B6:83:LEU:N	2.42	0.53
37:5C:284:ARG:NH1	37:5C:408:GLU:OE2	2.41	0.53
47:RE:707:PHE:O	47:RE:918:ARG:NH1	2.41	0.53
47:RE:1103:ARG:HB2	47:RE:1232:ILE:HD12	1.91	0.53
2:5A:535:G:H5''	36:B6:127:LYS:HE3	1.89	0.53
3:SA:493:U:H4'	50:RJ:1138:ARG:HH12	1.73	0.53
11:SM:94:ILE:HG12	11:SM:96:LYS:H	1.74	0.53
15:SX:89:TRP:O	15:SX:93:LEU:HB3	2.09	0.53
29:AF:71:ARG:HD3	29:AF:331:THR:HG21	1.91	0.53
30:AG:409:LYS:HG2	30:AG:489:ASN:HD22	1.74	0.53
33:B3:410:ASN:ND2	33:B3:433:HIS:O	2.42	0.53
40:5F:66:PRO:O	40:5F:72:ARG:NH2	2.42	0.53
51:RK:12:GLN:NE2	51:RK:34:GLU:OE1	2.32	0.53
3:SA:106:U:H3'	3:SA:107:C:H4'	1.91	0.53
3:SA:200:A:O2'	53:RP:1061:CYS:O	2.26	0.53
3:SA:906:A:H3'	3:SA:907:A:H8	1.74	0.53
4:SC:98:THR:OG1	4:SC:99:ASN:N	2.42	0.53
20:3B:104:ASP:OD1	20:3B:104:ASP:N	2.39	0.53
20:3C:277:ASP:OD2	20:3C:288:ARG:NH2	2.41	0.53
23:3F:531:LYS:HE2	23:3F:534:LYS:HB2	1.91	0.53
29:AF:101:ALA:HA	29:AF:126:PRO:HB3	1.91	0.53
30:AG:393:ASN:HB2	30:AG:436:PHE:HA	1.90	0.53
35:BE:609:ILE:HG23	35:BE:623:ILE:HB	1.90	0.53
3:SA:760:A:H2'	3:SA:761:G:H8	1.73	0.53
3:SA:805:U:OP1	15:SX:32:LYS:NZ	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:SF:98:ASN:ND2	5:SF:114:ILE:O	2.39	0.53
20:3B:271:ILE:O	20:3B:313:HIS:HA	2.09	0.53
21:3D:83:ASP:OD2	36:B6:173:ARG:NH2	2.41	0.53
28:AE:54:LYS:NZ	44:5J:78:LYS:O	2.42	0.53
30:AG:519:LEU:HB3	30:AG:522:SER:HB3	1.91	0.53
32:B2:175:ASP:O	32:B2:190:ASP:HA	2.09	0.53
32:B2:640:LYS:HE2	32:B2:652:LYS:HE2	1.90	0.53
47:RE:406:ILE:HG13	47:RE:457:TYR:HB3	1.91	0.53
50:RJ:125:LEU:HA	50:RJ:128:MET:HB3	1.91	0.53
53:RP:2143:LYS:O	53:RP:2147:ALA:HB2	2.09	0.53
16:SY:91:GLY:O	16:SY:94:ASN:ND2	2.42	0.53
21:3D:93:LYS:NZ	54:RQ:319:THR:OG1	2.40	0.53
23:3F:152:VAL:HG12	23:3F:562:GLY:HA2	1.89	0.53
24:3G:120:LYS:NZ	25:A4:187:GLU:OE1	2.42	0.53
29:AF:319:VAL:HG12	29:AF:329:ILE:HG12	1.90	0.53
29:AF:443:LEU:HG	29:AF:480:LEU:HD21	1.90	0.53
30:AG:16:SER:HB2	30:AG:783:LEU:HB2	1.91	0.53
31:B1:394:GLN:HE21	31:B1:438:VAL:HG12	1.74	0.53
32:B2:124:ILE:HA	32:B2:140:SER:HA	1.91	0.53
33:B3:65:THR:HA	33:B3:80:SER:HB2	1.91	0.53
34:B8:348:HIS:HD2	34:B8:350:SER:H	1.56	0.53
34:B8:545:HIS:HD2	34:B8:548:SER:HB3	1.73	0.53
41:5G:88:ILE:HG12	41:5G:138:ASP:HB2	1.90	0.53
43:5I:448:ARG:HD2	43:5I:451:MET:HG3	1.91	0.53
46:RD:1510:GLU:HA	46:RD:1513:LYS:HE3	1.89	0.53
47:RE:824:PHE:HB2	48:RF:174:PRO:HB3	1.91	0.53
50:RJ:749:THR:OG1	50:RJ:750:TRP:N	2.42	0.53
53:RP:116:ASP:N	53:RP:116:ASP:OD1	2.39	0.53
1:3A:93:U:O4	22:3E:298:ARG:NH1	2.40	0.52
23:3F:439:ALA:O	23:3F:497:LYS:NZ	2.37	0.52
25:A4:399:VAL:HG12	25:A4:420:LEU:HB2	1.91	0.52
32:B2:180:THR:OG1	32:B2:207:CYS:SG	2.63	0.52
33:B3:352:LYS:HA	33:B3:365:ILE:O	2.08	0.52
37:5C:334:ARG:HB2	37:5C:337:HIS:HB2	1.91	0.52
47:RE:202:SER:OG	47:RE:203:ILE:N	2.37	0.52
53:RP:2070:TYR:O	53:RP:2076:ARG:NE	2.42	0.52
4:SC:78:ASP:OD1	4:SC:78:ASP:N	2.43	0.52
24:3G:62:GLU:HA	24:3G:65:LEU:HG	1.90	0.52
25:A4:773:LYS:NZ	25:A4:774:LEU:O	2.42	0.52
29:AF:463:VAL:HA	29:AF:466:VAL:HG12	1.91	0.52
32:B2:193:THR:O	32:B2:195:GLN:NE2	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:B3:24:THR:HG21	33:B3:69:LEU:HA	1.91	0.52
33:B3:96:VAL:O	33:B3:97:ARG:NH1	2.42	0.52
33:B3:779:VAL:HA	33:B3:782:VAL:HG12	1.91	0.52
35:BE:413:GLU:O	35:BE:435:LYS:N	2.43	0.52
47:RE:151:SER:HA	47:RE:154:LYS:HE2	1.91	0.52
51:RK:47:ASP:OD1	51:RK:47:ASP:N	2.39	0.52
55:RT:187:VAL:HG13	55:RT:251:ILE:HD12	1.90	0.52
10:SK:106:GLU:OE2	10:SK:115:LYS:NZ	2.42	0.52
10:SK:119:ALA:O	10:SK:124:HIS:ND1	2.32	0.52
23:3F:114:LYS:HA	23:3F:117:ILE:HD12	1.89	0.52
23:3F:286:LEU:HB3	23:3F:295:LEU:HD11	1.91	0.52
23:3F:409:ASP:OD1	23:3F:412:HIS:N	2.41	0.52
28:AE:370:LEU:HD13	28:AE:407:PHE:HZ	1.74	0.52
35:BE:361:SER:HA	35:BE:636:PRO:HG2	1.90	0.52
37:5C:451:SER:OG	37:5C:452:VAL:N	2.42	0.52
46:RD:1514:LEU:HA	46:RD:1544:MET:HE1	1.91	0.52
47:RE:673:SER:N	47:RE:717:ALA:O	2.43	0.52
50:RJ:555:MET:O	51:RK:327:ARG:NH2	2.42	0.52
50:RJ:1105:ASP:HA	50:RJ:1108:LYS:HG2	1.91	0.52
51:RK:214:LYS:HA	51:RK:217:LYS:HE3	1.91	0.52
13:SP:14:PHE:HA	13:SP:78:ALA:O	2.09	0.52
20:3B:228:GLN:O	20:3B:231:ARG:NH2	2.41	0.52
20:3B:239:CYS:SG	20:3B:240:VAL:N	2.83	0.52
23:3F:241:THR:HG21	23:3F:285:SER:HA	1.91	0.52
33:B3:217:ASP:OD1	33:B3:217:ASP:N	2.42	0.52
34:B8:378:GLN:HA	34:B8:384:ILE:HG22	1.91	0.52
35:BE:859:ASP:OD1	35:BE:859:ASP:N	2.41	0.52
40:5F:104:SER:OG	40:5F:108:ARG:NH1	2.43	0.52
47:RE:511:PHE:HB2	47:RE:512:LEU:HD22	1.91	0.52
50:RJ:158:ILE:HG13	50:RJ:913:ILE:HD11	1.90	0.52
3:SA:871:G:H2'	3:SA:872:G:C8	2.44	0.52
5:SF:238:LEU:HD12	5:SF:242:LYS:HG3	1.92	0.52
8:SI:70:PHE:O	8:SI:74:GLN:NE2	2.42	0.52
14:SR:100:GLN:HB3	35:BE:488:ASN:HD21	1.74	0.52
23:3F:224:SER:O	23:3F:226:HIS:ND1	2.32	0.52
24:3H:58:CYS:HA	24:3H:84:ARG:HD3	1.90	0.52
37:5C:64:ASP:OD1	37:5C:64:ASP:N	2.42	0.52
39:5E:371:ARG:NH1	39:5E:375:ASP:OD2	2.39	0.52
43:5I:270:ASN:ND2	43:5I:273:GLU:OE1	2.42	0.52
47:RE:316:ARG:NH1	47:RE:549:SER:OG	2.42	0.52
53:RP:2010:HIS:NE2	53:RP:2049:GLU:O	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:25:C:N4	10:SK:12:TYR:OH	2.43	0.52
14:SR:100:GLN:HE21	14:SR:104:GLU:HG3	1.74	0.52
25:A4:477:LEU:H	25:A4:489:CYS:HB3	1.73	0.52
33:B3:17:ALA:HB3	33:B3:35:PRO:HA	1.92	0.52
35:BE:904:ASP:N	35:BE:904:ASP:OD1	2.39	0.52
36:B6:85:ASP:N	36:B6:85:ASP:OD1	2.40	0.52
47:RE:589:LYS:O	47:RE:609:ASN:ND2	2.41	0.52
49:RH:49:SER:HA	49:RH:116:THR:HG23	1.92	0.52
3:SA:41:A:N6	3:SA:467:G:C2	2.78	0.52
3:SA:479:C:O2	3:SA:510:G:N2	2.42	0.52
15:SX:26:LEU:HB2	18:Sc:7:LEU:HD21	1.92	0.52
23:3F:539:ILE:O	23:3F:565:SER:HA	2.10	0.52
25:A4:493:ASP:HB3	25:A4:513:LEU:HD11	1.92	0.52
26:A5:536:LEU:O	26:A5:540:LEU:N	2.36	0.52
31:B1:19:ASN:HA	31:B1:307:THR:HG21	1.92	0.52
31:B1:58:ILE:HA	31:B1:74:ASP:HA	1.91	0.52
35:BE:225:THR:OG1	35:BE:227:THR:O	2.28	0.52
47:RE:215:GLU:OE2	47:RE:223:ARG:NH1	2.42	0.52
47:RE:844:THR:O	47:RE:847:GLY:N	2.37	0.52
50:RJ:803:ASN:ND2	50:RJ:1023:LEU:O	2.43	0.52
50:RJ:905:SER:N	50:RJ:1028:GLU:OE2	2.43	0.52
3:SA:563:U:OP2	41:5G:287:LYS:NZ	2.38	0.52
3:SA:754:A:O4'	5:SF:187:ARG:NH2	2.43	0.52
9:SJ:180:ASP:OD1	9:SJ:180:ASP:N	2.43	0.52
14:SR:64:ASP:N	14:SR:64:ASP:OD1	2.43	0.52
21:3D:26:ASP:HB2	43:5I:80:LEU:HD23	1.91	0.52
21:3D:212:ASP:O	21:3D:216:PHE:HB2	2.09	0.52
29:AF:90:ARG:NH1	29:AF:137:ASN:O	2.42	0.52
32:B2:8:PHE:HA	32:B2:685:GLU:O	2.10	0.52
32:B2:633:CYS:HB3	32:B2:663:LEU:HD22	1.92	0.52
43:5I:226:LYS:HD3	43:5I:268:CYS:HA	1.91	0.52
46:RD:1466:ARG:HH12	46:RD:1470:GLY:HA3	1.73	0.52
46:RD:1525:ASN:HD22	46:RD:1556:ILE:HG12	1.73	0.52
47:RE:676:PRO:HB2	47:RE:678:ILE:HG22	1.92	0.52
49:RH:167:ILE:HG22	49:RH:171:LEU:HD23	1.91	0.52
51:RK:249:SER:O	51:RK:253:GLY:N	2.43	0.52
53:RP:2032:SER:O	53:RP:2036:ARG:NE	2.39	0.52
5:SF:175:PHE:HA	5:SF:179:LYS:HD2	1.91	0.52
14:SR:58:ASP:OD1	14:SR:58:ASP:N	2.40	0.52
20:3C:263:ASP:OD1	22:3E:118:ARG:NH2	2.42	0.52
21:3D:181:LEU:HA	21:3D:184:LEU:HG	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A4:62:PRO:HG2	25:A4:65:LEU:HD21	1.92	0.52
26:A5:537:LEU:HD21	29:AF:498:SER:HB2	1.90	0.52
29:AF:194:ARG:HG3	29:AF:205:PRO:HG3	1.92	0.52
30:AG:324:TRP:HA	30:AG:330:SER:O	2.10	0.52
33:B3:438:THR:HG21	33:B3:495:ASN:HA	1.91	0.52
45:5K:69:THR:HG22	45:5K:106:LEU:HB2	1.91	0.52
47:RE:495:THR:O	47:RE:499:LEU:HB2	2.09	0.52
3:SA:939:A:OP1	12:SO:114:ARG:NH2	2.42	0.52
13:SP:42:VAL:HA	13:SP:46:MET:HE2	1.91	0.52
21:3D:102:ASP:OD2	21:3D:105:LEU:N	2.39	0.52
22:3E:145:HIS:O	22:3E:149:ARG:NE	2.35	0.52
30:AG:133:LYS:NZ	30:AG:137:ALA:O	2.36	0.52
30:AG:246:SER:OG	30:AG:247:SER:N	2.43	0.52
31:B1:586:SER:OG	31:B1:587:PHE:N	2.42	0.52
32:B2:397:ILE:HD12	32:B2:675:SER:HB3	1.92	0.52
33:B3:171:MET:HA	33:B3:186:LEU:O	2.08	0.52
33:B3:788:TYR:O	33:B3:792:HIS:ND1	2.43	0.52
35:BE:268:THR:HB	35:BE:272:ASP:HB2	1.92	0.52
37:5C:194:ARG:NE	37:5C:210:GLU:OE2	2.43	0.52
43:5I:96:ASN:ND2	43:5I:99:THR:OG1	2.43	0.52
50:RJ:251:ASP:HB2	50:RJ:267:ARG:HH21	1.73	0.52
50:RJ:1039:ARG:HH11	50:RJ:1046:THR:HG22	1.75	0.52
3:SA:34:G:N1	3:SA:475:A:C6	2.78	0.51
3:SA:152:U:N3	3:SA:163:G:N7	2.58	0.51
3:SA:522:U:H5"	17:SZ:37:LYS:HE3	1.92	0.51
10:SK:136:VAL:HG12	10:SK:156:ILE:HG12	1.91	0.51
23:3F:175:SER:OG	23:3F:176:SER:N	2.40	0.51
25:A4:739:LYS:N	25:A4:739:LYS:CE	2.73	0.51
31:B1:718:ASP:N	31:B1:718:ASP:OD1	2.43	0.51
32:B2:285:ARG:NH2	32:B2:371:LYS:O	2.42	0.51
47:RE:720:SER:OG	47:RE:721:VAL:N	2.41	0.51
48:RF:9:MET:HB2	48:RF:13:PHE:HB2	1.93	0.51
1:3A:264:C:O2	1:3A:307:G:N2	2.39	0.51
5:SF:207:LEU:HD22	5:SF:220:THR:H	1.75	0.51
21:3D:171:ASP:OD1	21:3D:171:ASP:N	2.40	0.51
24:3G:38:ASN:N	24:3G:38:ASN:OD1	2.39	0.51
24:3H:43:THR:OG1	24:3H:48:ILE:O	2.29	0.51
25:A4:80:ASN:HD21	25:A4:82:ARG:HH11	1.58	0.51
25:A4:405:GLY:O	25:A4:413:ASN:N	2.43	0.51
30:AG:211:MET:HG2	30:AG:225:ILE:HG12	1.92	0.51
32:B2:166:ILE:HA	32:B2:181:SER:HA	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:B3:557:VAL:HB	33:B3:572:GLU:HB2	1.92	0.51
35:BE:228:GLY:O	35:BE:246:ILE:HB	2.11	0.51
35:BE:275:PHE:HE2	35:BE:340:PRO:HG3	1.75	0.51
36:B6:166:ASN:O	36:B6:170:ASN:ND2	2.42	0.51
41:5G:154:ILE:O	41:5G:162:THR:HA	2.10	0.51
43:5I:445:ARG:NH2	43:5I:451:MET:O	2.43	0.51
51:RK:66:GLU:H	51:RK:75:ILE:HG22	1.76	0.51
53:RP:46:HIS:O	53:RP:112:GLN:NE2	2.43	0.51
7:SH:30:LYS:HD3	7:SH:34:GLN:HB2	1.93	0.51
32:B2:285:ARG:HB3	32:B2:327:HIS:HB3	1.91	0.51
35:BE:144:ASP:HB3	35:BE:146:GLN:HG3	1.91	0.51
35:BE:316:ASP:OD1	35:BE:316:ASP:N	2.34	0.51
35:BE:630:THR:N	35:BE:644:THR:O	2.43	0.51
53:RP:1809:GLU:HA	53:RP:1812:LEU:HB2	1.92	0.51
3:SA:805:U:O3'	15:SX:78:ARG:NH2	2.42	0.51
3:SA:1483:A:HO2'	3:SA:1607:G:HO2'	1.57	0.51
7:SH:46:LYS:HG2	7:SH:119:GLN:HB2	1.93	0.51
18:Sc:53:ALA:HB1	18:Sc:62:ILE:HD11	1.92	0.51
19:Sd:43:ASN:OD1	19:Sd:43:ASN:N	2.42	0.51
25:A4:62:PRO:O	25:A4:82:ARG:NH2	2.43	0.51
28:AE:328:ASP:OD1	28:AE:328:ASP:N	2.43	0.51
30:AG:366:ASN:OD1	30:AG:366:ASN:N	2.43	0.51
30:AG:769:ASN:ND2	30:AG:771:ASP:OD1	2.43	0.51
32:B2:909:LYS:O	32:B2:913:ASN:ND2	2.44	0.51
33:B3:188:GLU:OE2	33:B3:221:ASN:ND2	2.43	0.51
33:B3:787:PRO:HB2	39:5E:492:PRO:HG3	1.92	0.51
35:BE:122:CYS:SG	35:BE:123:ILE:N	2.83	0.51
46:RD:1466:ARG:NH1	46:RD:1466:ARG:O	2.40	0.51
47:RE:379:MET:HE3	47:RE:381:HIS:HB2	1.92	0.51
47:RE:563:ALA:HB2	47:RE:585:MET:HE1	1.93	0.51
51:RK:22:VAL:HG23	51:RK:106:LEU:HD12	1.91	0.51
3:SA:326:G:O6	3:SA:337:G:O6	2.29	0.51
3:SA:500:C:H4'	3:SA:501:U:H3'	1.93	0.51
25:A4:63:SER:O	25:A4:82:ARG:NH1	2.43	0.51
25:A4:142:GLY:HA3	25:A4:160:CYS:HB3	1.92	0.51
25:A4:210:ILE:HG23	25:A4:229:MET:HB2	1.92	0.51
25:A4:249:ARG:NH2	25:A4:309:GLN:OE1	2.44	0.51
30:AG:511:GLU:HG2	30:AG:528:ILE:HG23	1.92	0.51
32:B2:621:VAL:HA	32:B2:631:PHE:O	2.11	0.51
35:BE:562:LEU:HD12	35:BE:566:SER:HB2	1.91	0.51
43:5I:183:GLN:N	43:5I:197:GLY:O	2.34	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:RH:215:ASN:ND2	49:RH:218:ASP:OD2	2.43	0.51
3:SA:521:A:N3	17:SZ:34:ASN:ND2	2.57	0.51
3:SA:557:G:N2	3:SA:571:G:O2'	2.43	0.51
20:3C:171:LEU:HB3	20:3C:240:VAL:HG12	1.92	0.51
25:A4:102:LEU:HD12	25:A4:114:LEU:HD12	1.92	0.51
28:AE:46:ASP:OD1	28:AE:46:ASP:N	2.44	0.51
28:AE:243:ALA:HB2	34:B8:208:LEU:HD23	1.91	0.51
29:AF:84:VAL:HG12	29:AF:100:ASP:HB3	1.92	0.51
31:B1:361:VAL:HG22	31:B1:371:VAL:HG22	1.91	0.51
32:B2:104:LYS:HD2	32:B2:113:VAL:HG21	1.92	0.51
37:5C:193:ALA:O	37:5C:194:ARG:NH1	2.40	0.51
39:5E:372:ARG:HH11	39:5E:378:PHE:HA	1.75	0.51
50:RJ:1042:MET:HG3	50:RJ:1044:LEU:HD13	1.90	0.51
50:RJ:1049:ASN:ND2	50:RJ:1051:ASP:OD1	2.43	0.51
3:SA:141:U:O2'	3:SA:266:A:N3	2.36	0.51
7:SH:46:LYS:NZ	7:SH:118:GLU:OE1	2.43	0.51
15:SX:84:GLY:O	15:SX:88:LYS:NZ	2.44	0.51
23:3F:151:ARG:HD2	23:3F:560:ARG:HE	1.74	0.51
25:A4:291:ASP:OD1	25:A4:291:ASP:N	2.39	0.51
25:A4:363:SER:HB2	25:A4:366:ASN:HB3	1.93	0.51
32:B2:165:SER:O	32:B2:182:LYS:N	2.44	0.51
34:B8:426:VAL:HG12	34:B8:432:VAL:HG12	1.93	0.51
43:5I:450:ASP:OD1	43:5I:450:ASP:N	2.44	0.51
3:SA:579:A:OP2	50:RJ:837:LYS:NZ	2.39	0.51
4:SC:77:GLU:O	4:SC:80:SER:OG	2.29	0.51
20:3B:170:VAL:HB	20:3B:194:VAL:HG22	1.93	0.51
23:3F:343:ASP:OD1	23:3F:343:ASP:N	2.43	0.51
25:A4:302:ARG:NH2	25:A4:330:GLY:O	2.44	0.51
28:AE:34:ILE:HG12	28:AE:119:GLU:HG3	1.92	0.51
28:AE:83:ARG:NH1	28:AE:125:PHE:O	2.43	0.51
31:B1:835:VAL:HA	35:BE:731:MET:HE1	1.93	0.51
44:5J:158:GLU:OE2	44:5J:161:SER:OG	2.28	0.51
47:RE:139:PRO:HD2	47:RE:238:HIS:HE1	1.75	0.51
47:RE:1019:GLY:O	47:RE:1023:ASN:ND2	2.44	0.51
48:RF:101:SER:O	48:RF:105:SER:HB2	2.11	0.51
5:SF:180:LEU:N	5:SF:229:GLY:O	2.44	0.51
25:A4:395:SER:HB2	25:A4:398:THR:HB	1.93	0.51
30:AG:173:LEU:HB2	30:AG:191:ALA:HB3	1.92	0.51
30:AG:677:THR:OG1	30:AG:678:LEU:N	2.44	0.51
31:B1:42:LEU:HD23	31:B1:338:ILE:HG21	1.93	0.51
33:B3:5:THR:HB	33:B3:611:LYS:HG2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:B3:440:VAL:HG12	33:B3:456:THR:HG22	1.93	0.51
35:BE:726:GLY:O	35:BE:728:ARG:NH1	2.44	0.51
43:5I:154:ASP:OD1	43:5I:154:ASP:N	2.40	0.51
46:RD:1695:TRP:HD1	46:RD:1696:LEU:HD22	1.74	0.51
47:RE:139:PRO:HD2	47:RE:238:HIS:CE1	2.46	0.51
47:RE:236:THR:HG21	47:RE:256:TYR:HE1	1.75	0.51
47:RE:773:TYR:OH	47:RE:1131:ASN:O	2.29	0.51
50:RJ:266:ASP:HB3	50:RJ:795:LYS:HA	1.92	0.51
50:RJ:754:GLN:HA	50:RJ:757:LYS:HD2	1.92	0.51
2:5A:2:U:H2'	2:5A:3:G:H8	1.76	0.51
3:SA:1697:G:O6	3:SA:1704:U:O4	2.29	0.51
25:A4:207:ASP:O	25:A4:233:LYS:NZ	2.44	0.51
25:A4:394:TRP:HB3	25:A4:399:VAL:HG23	1.93	0.51
25:A4:582:VAL:O	25:A4:593:GLU:HA	2.11	0.51
26:A5:56:SER:O	26:A5:59:LYS:NZ	2.44	0.51
30:AG:96:ILE:HG12	30:AG:108:THR:HG21	1.93	0.51
31:B1:645:ASP:OD2	37:5C:171:LYS:NZ	2.44	0.51
33:B3:280:ARG:NH1	33:B3:281:THR:O	2.44	0.51
37:5C:322:VAL:HA	37:5C:331:ALA:O	2.11	0.51
47:RE:257:SER:OG	47:RE:269:ARG:NH1	2.44	0.51
49:RH:43:VAL:HG21	49:RH:99:LEU:HD13	1.92	0.51
3:SA:814:A:O2'	3:SA:815:G:O4'	2.27	0.50
3:SA:826:U:O2'	3:SA:827:C:O2	2.22	0.50
10:SK:110:GLN:HE21	10:SK:122:VAL:HG12	1.75	0.50
15:SX:6:VAL:HG22	15:SX:34:ILE:HD11	1.93	0.50
25:A4:741:LEU:HD23	25:A4:743:PHE:N	2.25	0.50
30:AG:225:ILE:HG13	30:AG:241:LEU:HD22	1.92	0.50
30:AG:659:ILE:HA	30:AG:674:THR:HA	1.93	0.50
32:B2:497:VAL:HG13	32:B2:528:LEU:HB2	1.92	0.50
33:B3:279:LYS:NZ	33:B3:326:THR:OG1	2.44	0.50
33:B3:544:TYR:OH	33:B3:628:ASP:OD2	2.29	0.50
35:BE:155:THR:OG1	35:BE:156:LYS:N	2.44	0.50
37:5C:199:LEU:HD23	37:5C:245:ALA:HB1	1.92	0.50
37:5C:544:ASP:N	37:5C:544:ASP:OD1	2.43	0.50
47:RE:274:LYS:O	47:RE:284:ASN:ND2	2.44	0.50
49:RH:112:VAL:HB	49:RH:124:VAL:HB	1.93	0.50
50:RJ:629:ASP:OD1	50:RJ:629:ASP:N	2.42	0.50
51:RK:30:PRO:HB3	51:RK:77:ARG:HG3	1.91	0.50
53:RP:120:ASP:O	53:RP:123:LYS:NZ	2.44	0.50
53:RP:1912:ILE:HG13	53:RP:1958:MET:HG2	1.93	0.50
3:SA:1483:A:O2'	3:SA:1607:G:O2'	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15: SX:46: TYR: HB3	15: SX:69: LEU: HD12	1.93	0.50
24: 3G:58: CYS: HB2	24: 3G:98: ILE: HD12	1.92	0.50
25: A4:481: ILE: HD11	25: A4:536: VAL: HG22	1.93	0.50
28: AE:272: LYS: NZ	28: AE:310: GLY: O	2.44	0.50
29: AF:377: ASP: OD1	29: AF:377: ASP: N	2.44	0.50
30: AG:48: PHE: HB2	30: AG:51: GLN: H	1.75	0.50
31: B1:470: SER: OG	31: B1:471: GLY: N	2.45	0.50
32: B2:297: LYS: HA	32: B2:300: GLU: HB2	1.92	0.50
32: B2:425: ILE: HG22	32: B2:426: ARG: HG2	1.94	0.50
33: B3:553: GLY: HA2	33: B3:577: ALA: HA	1.92	0.50
35: BE:234: ASN: O	35: BE:238: GLY: N	2.45	0.50
35: BE:380: LEU: HD11	35: BE:640: LEU: HD13	1.93	0.50
35: BE:606: ASP: OD1	35: BE:606: ASP: N	2.44	0.50
37: 5C:354: CYS: SG	37: 5C:355: PHE: N	2.78	0.50
43: 5I:220: ASP: N	43: 5I:220: ASP: OD1	2.44	0.50
3: SA:154: G: H21	7: SH:60: GLY: HA3	1.76	0.50
20: 3B:123: ILE: HG23	20: 3B:141: TYR: HB2	1.94	0.50
26: A5:130: ASP: OD1	26: A5:130: ASP: N	2.45	0.50
29: AF:288: ASP: OD1	29: AF:288: ASP: N	2.45	0.50
31: B1:35: ASN: OD1	31: B1:35: ASN: N	2.37	0.50
33: B3:139: SER: OG	33: B3:140: PHE: N	2.44	0.50
33: B3:496: ALA: HB2	33: B3:538: ASP: HA	1.94	0.50
34: B8:382: GLY: O	34: B8:399: LYS: HA	2.10	0.50
43: 5I:398: GLU: HA	43: 5I:401: LYS: HE2	1.93	0.50
47: RE:578: ILE: HG21	47: RE:617: LEU: HD12	1.93	0.50
3: SA:238: U: O2'	3: SA:239: C: O4'	2.30	0.50
3: SA:312: A: H62	3: SA:352: A: H1'	1.77	0.50
3: SA:473: A: OP1	10: SK:44: ARG: NH1	2.38	0.50
3: SA:976: G: OP1	12: SO:109: LYS: NZ	2.45	0.50
21: 3D:148: GLU: HA	21: 3D:151: GLN: HE21	1.77	0.50
30: AG:765: TRP: HE1	30: AG:777: LEU: HD13	1.76	0.50
31: B1:275: LEU: HD13	31: B1:289: LEU: HD22	1.93	0.50
35: BE:94: TYR: HE1	35: BE:97: LYS: HE2	1.75	0.50
43: 5I:290: ASP: OD1	43: 5I:291: MET: N	2.41	0.50
47: RE:305: PRO: HB2	47: RE:473: LYS: HD2	1.92	0.50
47: RE:1074: LEU: HD11	47: RE:1087: LEU: HD23	1.93	0.50
50: RJ:895: PRO: HA	50: RJ:918: ILE: HA	1.94	0.50
51: RK:124: SER: OG	51: RK:125: HIS: N	2.43	0.50
51: RK:247: ALA: O	51: RK:255: SER: HA	2.12	0.50
3: SA:347: G: OP1	11: SM:77: SER: OG	2.29	0.50
9: SJ:39: GLY: HA2	9: SJ:61: GLU: HG3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:SY:98:GLU:HG3	51:RK:366:ILE:HG23	1.94	0.50
17:SZ:103:ALA:O	17:SZ:108:ARG:NH1	2.45	0.50
28:AE:254:GLN:NE2	28:AE:285:ASN:O	2.41	0.50
29:AF:33:ALA:HB2	29:AF:330:ARG:HE	1.76	0.50
43:5I:263:ARG:NH2	43:5I:282:GLU:OE2	2.45	0.50
1:3A:18:G:H2'	1:3A:19:A:H8	1.76	0.50
5:SF:104:ASP:HB3	5:SF:110:ALA:HB2	1.94	0.50
7:SH:115:LYS:NZ	7:SH:116:LYS:O	2.42	0.50
8:SI:125:ILE:O	8:SI:129:LEU:CB	2.60	0.50
8:SI:138:LYS:HG2	8:SI:152:VAL:HG12	1.93	0.50
17:SZ:78:SER:OG	17:SZ:81:GLU:OE2	2.29	0.50
25:A4:127:ASP:OD1	25:A4:132:LEU:N	2.43	0.50
25:A4:642:ASN:HD22	25:A4:645:ARG:HG3	1.75	0.50
30:AG:17:GLY:HA2	30:AG:50:ASN:HD22	1.76	0.50
32:B2:54:ILE:HA	32:B2:385:ILE:HD11	1.94	0.50
33:B3:128:VAL:HB	33:B3:138:HIS:HB2	1.92	0.50
47:RE:402:ASN:ND2	47:RE:453:PRO:O	2.44	0.50
48:RF:99:ASP:O	48:RF:103:LEU:HB2	2.10	0.50
48:RF:105:SER:OG	48:RF:106:ASP:N	2.44	0.50
51:RK:185:ARG:HH11	51:RK:312:ARG:HH12	1.60	0.50
53:RP:1949:PRO:HA	53:RP:1985:ARG:HH21	1.76	0.50
55:RT:126:LEU:HD21	55:RT:152:LEU:HA	1.93	0.50
3:SA:925:G:H2'	3:SA:926:A:H8	1.75	0.50
3:SA:1738:U:H5''	32:B2:333:ARG:HH21	1.75	0.50
20:3B:155:ILE:HD11	20:3B:162:LEU:HD11	1.94	0.50
20:3C:236:MET:HG3	22:3E:122:GLU:HB3	1.94	0.50
20:3C:297:ARG:HH12	20:3C:322:ARG:HH21	1.60	0.50
22:3E:167:ILE:HD11	22:3E:298:ARG:HG3	1.94	0.50
25:A4:168:ILE:HA	25:A4:179:HIS:HA	1.94	0.50
26:A5:247:THR:HG21	26:A5:293:ASN:H	1.77	0.50
28:AE:92:LYS:O	28:AE:96:ASN:ND2	2.45	0.50
30:AG:744:ILE:HA	30:AG:755:GLY:O	2.12	0.50
31:B1:55:ARG:HB3	31:B1:621:MET:HE1	1.93	0.50
31:B1:457:VAL:HG23	31:B1:466:LEU:HB3	1.94	0.50
32:B2:503:LYS:O	32:B2:520:LEU:N	2.44	0.50
35:BE:367:LEU:HD23	35:BE:375:LEU:HD21	1.94	0.50
40:5F:109:ARG:NH2	40:5F:155:GLU:OE2	2.44	0.50
42:5H:579:VAL:HG12	45:5K:47:VAL:HG21	1.93	0.50
55:RT:222:THR:OG1	55:RT:223:ARG:N	2.45	0.50
6:SG:148:ARG:HA	6:SG:157:ARG:HG3	1.94	0.50
22:3E:201:ASP:HB3	22:3E:204:ALA:HB3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A4:553:LEU:HA	25:A4:560:SER:HA	1.93	0.50
30:AG:200:ASN:HD22	30:AG:262:MET:HG3	1.76	0.50
30:AG:313:LEU:HD23	30:AG:323:LEU:HB3	1.94	0.50
35:BE:637:ASN:ND2	35:BE:639:ASP:OD2	2.45	0.50
39:5E:296:ASN:O	50:RJ:264:GLN:NE2	2.45	0.50
43:5I:26:ARG:NH1	54:RQ:867:GLN:O	2.36	0.50
47:RE:428:TYR:O	47:RE:432:MET:HB2	2.12	0.50
51:RK:246:VAL:HA	51:RK:256:TYR:O	2.11	0.50
53:RP:1961:LYS:HB2	53:RP:1998:LEU:HD23	1.94	0.50
4:SC:242:LYS:HD2	33:B3:237:LEU:HD21	1.92	0.50
8:SI:143:LEU:O	15:SX:42:GLN:NE2	2.45	0.50
15:SX:4:SER:OG	15:SX:5:SER:N	2.45	0.50
24:3G:21:LEU:HA	24:3G:24:VAL:HG12	1.93	0.50
25:A4:542:VAL:HA	25:A4:551:ASP:O	2.11	0.50
26:A5:128:GLN:HB2	26:A5:138:GLN:H	1.76	0.50
29:AF:390:ARG:HB2	29:AF:394:GLN:HE22	1.77	0.50
32:B2:645:GLU:HG2	32:B2:646:LYS:HG3	1.93	0.50
34:B8:384:ILE:HD12	34:B8:423:LEU:HD21	1.93	0.50
34:B8:516:THR:HG21	34:B8:536:ALA:HB3	1.94	0.50
36:B6:178:VAL:HG22	36:B6:180:LYS:H	1.77	0.50
39:5E:357:ILE:HG12	41:5G:169:ASN:HD22	1.77	0.50
51:RK:19:LEU:HA	51:RK:22:VAL:HG12	1.94	0.50
51:RK:285:LYS:HG3	51:RK:316:GLU:HB3	1.93	0.50
51:RK:289:VAL:HG21	51:RK:294:LEU:HD13	1.94	0.50
3:SA:315:A:N6	3:SA:350:U:O4'	2.44	0.49
12:SO:61:THR:OG1	12:SO:62:GLN:N	2.43	0.49
25:A4:288:THR:OG1	25:A4:289:ASP:N	2.44	0.49
32:B2:270:SER:HB3	32:B2:286:ILE:HG13	1.94	0.49
34:B8:358:PHE:HA	34:B8:376:LEU:O	2.12	0.49
34:B8:391:SER:OG	34:B8:392:GLY:N	2.44	0.49
35:BE:128:LEU:HB2	35:BE:150:PRO:HG2	1.93	0.49
39:5E:379:ASP:OD1	39:5E:379:ASP:N	2.42	0.49
47:RE:138:ILE:O	47:RE:180:LYS:NZ	2.44	0.49
47:RE:361:GLU:HA	47:RE:364:VAL:HG12	1.94	0.49
47:RE:481:THR:OG1	47:RE:482:VAL:N	2.41	0.49
50:RJ:74:VAL:HG22	50:RJ:139:LEU:HD21	1.94	0.49
2:5A:278:G:N2	34:B8:558:SER:O	2.44	0.49
3:SA:593:U:H4'	3:SA:595:G:H4'	1.94	0.49
25:A4:126:TRP:HA	25:A4:133:PRO:HA	1.94	0.49
25:A4:614:TRP:NE1	25:A4:658:ASP:O	2.44	0.49
27:A9:502:ARG:HH11	29:AF:510:LEU:HB2	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:AF:285:ASP:N	29:AF:285:ASP:OD1	2.41	0.49
32:B2:215:ASP:OD1	32:B2:215:ASP:N	2.45	0.49
32:B2:403:ASN:OD1	32:B2:403:ASN:N	2.44	0.49
32:B2:446:ILE:HD13	32:B2:456:LEU:HD12	1.94	0.49
34:B8:465:THR:OG1	34:B8:466:THR:N	2.45	0.49
35:BE:21:SER:OG	35:BE:22:LYS:N	2.43	0.49
35:BE:737:LEU:HA	35:BE:740:ILE:HB	1.94	0.49
45:5K:183:GLU:HG2	45:5K:184:LYS:HG3	1.94	0.49
47:RE:725:SER:O	47:RE:729:ASN:ND2	2.45	0.49
47:RE:818:SER:O	47:RE:818:SER:OG	2.30	0.49
51:RK:300:TYR:HA	51:RK:303:ILE:HG22	1.93	0.49
53:RP:1774:LYS:HA	53:RP:1777:LEU:HB2	1.95	0.49
2:5A:474:A:OP2	37:5C:425:ARG:NH2	2.43	0.49
3:SA:919:A:H5'	13:SP:18:ARG:HH12	1.78	0.49
4:SC:129:THR:OG1	4:SC:130:SER:N	2.45	0.49
12:SO:91:LEU:HD22	12:SO:122:ILE:HG12	1.93	0.49
20:3C:96:VAL:HG23	20:3C:106:LEU:HD21	1.94	0.49
20:3C:165:ALA:HB3	20:3C:168:LYS:HB2	1.94	0.49
25:A4:360:SER:HG	25:A4:363:SER:HG	1.56	0.49
25:A4:444:ARG:O	25:A4:475:THR:OG1	2.30	0.49
25:A4:560:SER:OG	25:A4:561:LYS:N	2.45	0.49
33:B3:673:MET:HE3	33:B3:693:ARG:HG2	1.93	0.49
37:5C:414:LEU:HB2	43:5I:26:ARG:HH22	1.78	0.49
43:5I:224:SER:OG	43:5I:225:LEU:N	2.44	0.49
50:RJ:94:THR:HG21	50:RJ:354:ILE:HB	1.94	0.49
54:RQ:322:ASN:N	54:RQ:322:ASN:OD1	2.45	0.49
7:SH:7:TYR:O	7:SH:11:GLY:CA	2.61	0.49
10:SK:109:LEU:HB2	10:SK:146:PHE:HB3	1.94	0.49
25:A4:485:LYS:HA	25:A4:498:VAL:O	2.12	0.49
29:AF:48:ASN:HB3	29:AF:52:PRO:HA	1.93	0.49
29:AF:312:ALA:HB3	29:AF:316:ARG:HE	1.76	0.49
29:AF:390:ARG:O	29:AF:394:GLN:NE2	2.45	0.49
32:B2:634:SER:OG	32:B2:635:LYS:N	2.45	0.49
33:B3:387:HIS:CG	33:B3:407:SER:HB3	2.46	0.49
49:RH:222:ASP:OD1	49:RH:222:ASP:N	2.44	0.49
53:RP:362:PHE:O	53:RP:366:ILE:CB	2.61	0.49
2:5A:87:C:N4	30:AG:333:PHE:O	2.45	0.49
7:SH:39:GLU:HG2	7:SH:46:LYS:HA	1.93	0.49
9:SJ:67:TRP:HD1	9:SJ:70:GLU:H	1.59	0.49
13:SP:53:ASP:OD1	13:SP:53:ASP:N	2.43	0.49
20:3B:127:GLU:OE1	20:3B:137:THR:OG1	2.29	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:3E:37:LYS:O	22:3E:41:GLU:CB	2.60	0.49
24:3H:26:GLN:NE2	24:3H:113:GLN:OE1	2.45	0.49
25:A4:171:SER:O	25:A4:171:SER:OG	2.30	0.49
29:AF:308:SER:HB2	29:AF:316:ARG:HD3	1.94	0.49
30:AG:591:GLU:HG3	30:AG:593:ASN:HB3	1.93	0.49
32:B2:15:GLY:O	32:B2:360:ASN:ND2	2.46	0.49
33:B3:107:ILE:HD12	33:B3:150:LEU:HD22	1.93	0.49
33:B3:163:LEU:N	33:B3:175:TRP:O	2.45	0.49
37:5C:376:ASN:OD1	37:5C:376:ASN:N	2.43	0.49
43:5I:77:TYR:HE2	43:5I:229:GLN:HE21	1.59	0.49
48:RF:63:ASN:HD21	48:RF:163:PRO:HB2	1.78	0.49
48:RF:107:LEU:HD21	48:RF:194:ARG:HD3	1.94	0.49
3:SA:329:G:H2'	3:SA:330:G:H8	1.78	0.49
22:3E:245:THR:OG1	22:3E:246:GLU:N	2.45	0.49
31:B1:536:LYS:O	31:B1:538:GLN:N	2.46	0.49
33:B3:397:THR:HB	33:B3:399:ASP:H	1.78	0.49
47:RE:777:ASP:OD1	47:RE:777:ASP:N	2.39	0.49
47:RE:842:ILE:O	47:RE:849:GLY:HA2	2.13	0.49
50:RJ:258:ILE:HD13	50:RJ:265:ILE:HG12	1.93	0.49
50:RJ:295:ASP:OD1	50:RJ:295:ASP:N	2.44	0.49
50:RJ:779:ARG:NH1	51:RK:336:GLU:OE1	2.46	0.49
50:RJ:1105:ASP:N	50:RJ:1105:ASP:OD1	2.45	0.49
55:RT:216:ILE:HD13	55:RT:263:LEU:HD21	1.94	0.49
11:SM:123:VAL:HG12	11:SM:142:VAL:HG23	1.93	0.49
20:3C:236:MET:HE1	22:3E:118:ARG:HD2	1.94	0.49
29:AF:284:PHE:HB3	29:AF:290:PHE:HA	1.95	0.49
30:AG:207:LEU:HD23	30:AG:264:ILE:HD12	1.94	0.49
31:B1:69:LEU:HD23	31:B1:127:VAL:HG22	1.93	0.49
33:B3:509:ALA:HB1	33:B3:536:LEU:HB2	1.93	0.49
37:5C:37:THR:OG1	37:5C:38:LYS:N	2.44	0.49
43:5I:73:ILE:HG22	43:5I:355:LYS:HD2	1.94	0.49
47:RE:1100:VAL:HB	47:RE:1182:ILE:HB	1.95	0.49
51:RK:137:LEU:HD23	51:RK:296:LEU:HD13	1.95	0.49
2:5A:495:G:H2'	2:5A:496:G:C8	2.48	0.49
3:SA:29:U:H2'	3:SA:30:G:H8	1.78	0.49
3:SA:500:C:OP1	3:SA:501:U:N3	2.46	0.49
12:SO:55:ARG:NH2	18:Sc:51:GLN:OE1	2.40	0.49
22:3E:303:SER:OG	22:3E:304:GLY:N	2.45	0.49
23:3F:298:SER:OG	23:3F:325:VAL:O	2.24	0.49
23:3F:374:LYS:HG3	23:3F:375:GLU:HG3	1.95	0.49
25:A4:394:TRP:HA	25:A4:399:VAL:HA	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:AG:586:SER:O	30:AG:597:LYS:NZ	2.46	0.49
31:B1:70:LEU:HD22	31:B1:84:PHE:HD1	1.77	0.49
40:5F:29:ASP:N	40:5F:29:ASP:OD1	2.46	0.49
47:RE:359:PHE:HZ	47:RE:401:LEU:HD11	1.77	0.49
47:RE:840:LEU:HD23	47:RE:852:PHE:HD2	1.77	0.49
47:RE:1150:VAL:HG21	47:RE:1165:SER:HB2	1.94	0.49
47:RE:1206:PRO:HD2	48:RF:36:PHE:HD2	1.77	0.49
49:RH:111:GLN:NE2	49:RH:123:GLU:OE1	2.45	0.49
1:3A:8:U:H2'	1:3A:9:A:H8	1.78	0.49
5:SF:57:ASN:N	5:SF:57:ASN:OD1	2.45	0.49
9:SJ:36:THR:OG1	9:SJ:59:ARG:N	2.45	0.49
20:3C:303:GLN:HA	20:3C:315:ILE:O	2.12	0.49
25:A4:397:SER:OG	25:A4:426:GLN:O	2.30	0.49
25:A4:514:LEU:HD21	25:A4:562:PRO:HG3	1.95	0.49
28:AE:186:MET:HA	28:AE:189:LEU:HB2	1.94	0.49
30:AG:559:LYS:O	30:AG:576:ALA:HB3	2.13	0.49
32:B2:763:ILE:HD13	32:B2:838:THR:HG21	1.95	0.49
32:B2:861:ILE:HD11	33:B3:805:ILE:HG13	1.94	0.49
35:BE:471:CYS:SG	35:BE:473:ASN:ND2	2.77	0.49
47:RE:1193:ALA:HB1	47:RE:1211:ASN:HB3	1.94	0.49
50:RJ:775:GLU:O	50:RJ:780:ILE:N	2.45	0.49
3:SA:688:G:H2'	3:SA:689:G:H8	1.78	0.49
11:SM:141:LYS:NZ	11:SM:142:VAL:O	2.46	0.49
17:SZ:103:ALA:HB1	17:SZ:107:GLN:HB2	1.95	0.49
20:3B:228:GLN:HE21	21:3D:102:ASP:HB3	1.78	0.49
21:3D:90:SER:H	54:RQ:321:HIS:CE1	2.31	0.49
22:3E:356:LYS:HA	22:3E:359:ILE:HG22	1.95	0.49
22:3E:408:THR:O	28:AE:166:ASN:ND2	2.46	0.49
26:A5:212:LEU:HB2	26:A5:226:LEU:HB2	1.95	0.49
29:AF:145:ASP:OD1	29:AF:172:ARG:NE	2.46	0.49
36:B6:29:VAL:HA	36:B6:32:ILE:HG12	1.95	0.49
41:5G:81:SER:OG	41:5G:82:GLY:N	2.46	0.49
43:5I:420:PRO:HD2	43:5I:423:ILE:HD12	1.95	0.49
47:RE:384:SER:HA	47:RE:584:GLU:HG3	1.95	0.49
47:RE:444:SER:N	47:RE:471:SER:OG	2.40	0.49
49:RH:47:MET:HG2	49:RH:117:SER:HB3	1.94	0.49
50:RJ:143:ASP:OD1	50:RJ:143:ASP:N	2.46	0.49
50:RJ:170:VAL:HG12	50:RJ:205:PHE:HB2	1.94	0.49
50:RJ:847:LEU:O	50:RJ:853:ARG:HA	2.13	0.49
3:SA:155:U:H4'	7:SH:59:GLN:HG3	1.96	0.48
3:SA:1665:U:O2	3:SA:1736:G:C6	2.66	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:SC:64:ARG:NH2	13:SP:32:ASP:OD2	2.46	0.48
18:Sc:6:ASP:HB2	43:5I:262:MET:HG2	1.95	0.48
21:3D:74:VAL:HG13	21:3D:78:LEU:HD22	1.93	0.48
22:3E:215:ARG:NH1	22:3E:242:SER:OG	2.46	0.48
22:3E:422:THR:OG1	22:3E:423:GLU:N	2.46	0.48
23:3F:355:THR:OG1	23:3F:356:ARG:N	2.43	0.48
26:A5:362:ARG:NH1	30:AG:591:GLU:OE2	2.46	0.48
30:AG:73:LEU:O	30:AG:131:HIS:NE2	2.46	0.48
30:AG:175:ALA:HB3	30:AG:188:ALA:HB3	1.95	0.48
30:AG:501:THR:OG1	30:AG:506:TRP:N	2.46	0.48
32:B2:279:LYS:HD3	32:B2:336:TYR:HA	1.95	0.48
33:B3:519:ASN:ND2	33:B3:526:GLU:OE2	2.45	0.48
34:B8:144:LYS:HB2	34:B8:147:ARG:HH21	1.78	0.48
35:BE:255:SER:OG	35:BE:256:PHE:N	2.45	0.48
35:BE:329:SER:O	35:BE:329:SER:OG	2.31	0.48
41:5G:196:THR:HG23	41:5G:199:GLY:H	1.77	0.48
47:RE:397:MET:HG2	47:RE:425:VAL:HG21	1.95	0.48
49:RH:227:LEU:HD23	49:RH:240:LYS:HE2	1.95	0.48
51:RK:193:GLY:O	51:RK:225:ILE:HA	2.13	0.48
6:SG:120:ILE:HA	6:SG:123:VAL:HG12	1.95	0.48
25:A4:147:ILE:HG22	25:A4:158:VAL:HA	1.94	0.48
34:B8:450:GLN:HE21	34:B8:507:PRO:HD3	1.78	0.48
39:5E:346:GLU:O	50:RJ:1005:SER:OG	2.29	0.48
43:5I:252:ASN:ND2	53:RP:1949:PRO:O	2.43	0.48
46:RD:1542:GLN:OE1	47:RE:872:ASN:ND2	2.45	0.48
50:RJ:300:GLN:HG2	50:RJ:792:VAL:HB	1.95	0.48
3:SA:142:G:C2	3:SA:173:A:H2	2.31	0.48
20:3B:189:GLY:O	20:3B:216:ASN:ND2	2.46	0.48
22:3E:138:LYS:HD3	22:3E:141:LEU:HD21	1.95	0.48
25:A4:741:LEU:CD2	25:A4:741:LEU:C	2.85	0.48
26:A5:66:VAL:HG12	26:A5:112:LEU:HD21	1.96	0.48
30:AG:427:LYS:O	30:AG:431:SER:OG	2.28	0.48
30:AG:763:ILE:HD11	30:AG:776:PHE:HB2	1.95	0.48
32:B2:6:GLN:NE2	32:B2:686:GLU:OE1	2.45	0.48
32:B2:140:SER:OG	32:B2:141:LYS:N	2.44	0.48
32:B2:435:THR:HG21	32:B2:478:SER:HA	1.94	0.48
34:B8:445:ARG:NH2	34:B8:499:ALA:O	2.42	0.48
35:BE:51:VAL:HG12	35:BE:60:ILE:HG12	1.95	0.48
35:BE:169:SER:OG	35:BE:170:LEU:N	2.46	0.48
37:5C:414:LEU:HD22	43:5I:26:ARG:HH12	1.76	0.48
43:5I:275:PHE:HB3	54:RQ:295:VAL:HG11	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:RF:66:HIS:HB2	48:RF:158:TRP:HE1	1.78	0.48
1:3A:85:G:N7	22:3E:361:ARG:NH1	2.61	0.48
3:SA:867:G:OP1	12:SO:9:LYS:NZ	2.36	0.48
5:SF:54:TYR:O	17:SZ:15:ASN:ND2	2.46	0.48
9:SJ:83:TYR:OH	11:SM:11:ARG:O	2.30	0.48
18:Sc:64:CYS:HB3	18:Sc:73:LEU:HD23	1.96	0.48
26:A5:5:VAL:HA	26:A5:21:THR:HG22	1.95	0.48
26:A5:84:GLU:OE1	26:A5:86:TRP:NE1	2.31	0.48
30:AG:595:CYS:SG	30:AG:596:LEU:N	2.86	0.48
43:5I:40:GLU:HG3	43:5I:404:PHE:HE2	1.78	0.48
46:RD:1518:ILE:HG23	46:RD:1552:LYS:HE2	1.95	0.48
47:RE:794:ASP:OD1	47:RE:865:ARG:NH2	2.42	0.48
47:RE:1166:ARG:O	47:RE:1180:ASN:ND2	2.37	0.48
53:RP:185:LYS:HB3	53:RP:188:LEU:HD12	1.95	0.48
2:5A:296:C:O2'	35:BE:68:LEU:O	2.24	0.48
3:SA:513:U:H2'	3:SA:514:G:C8	2.49	0.48
3:SA:1527:C:OP1	6:SG:106:LYS:NZ	2.37	0.48
6:SG:80:LYS:NZ	31:B1:545:GLU:O	2.45	0.48
22:3E:7:GLU:O	22:3E:117:TYR:OH	2.31	0.48
23:3F:256:ARG:HD3	23:3F:282:GLU:HG2	1.94	0.48
25:A4:429:SER:OG	25:A4:430:THR:N	2.46	0.48
30:AG:762:TYR:HB3	30:AG:779:ILE:HG12	1.96	0.48
32:B2:492:SER:OG	32:B2:494:ASP:OD1	2.27	0.48
35:BE:222:ALA:HB2	35:BE:232:MET:HE3	1.96	0.48
35:BE:569:VAL:HB	35:BE:579:ARG:HB2	1.95	0.48
37:5C:384:VAL:HB	37:5C:389:LEU:O	2.13	0.48
45:5K:153:VAL:O	45:5K:172:LEU:HA	2.13	0.48
51:RK:142:GLU:O	51:RK:147:ARG:NH2	2.40	0.48
53:RP:1919:ILE:HD13	53:RP:1961:LYS:HD3	1.96	0.48
3:SA:448:C:OP2	5:SF:49:ARG:NH1	2.47	0.48
8:SI:137:GLY:O	8:SI:153:LEU:HB2	2.14	0.48
22:3E:379:ASP:N	22:3E:379:ASP:OD1	2.46	0.48
26:A5:82:ASN:OD1	26:A5:82:ASN:N	2.46	0.48
29:AF:282:LYS:HZ2	29:AF:292:VAL:HG21	1.79	0.48
31:B1:4:ASP:OD1	31:B1:4:ASP:N	2.42	0.48
31:B1:64:ASN:N	31:B1:64:ASN:OD1	2.46	0.48
31:B1:210:SER:OG	31:B1:211:LYS:N	2.45	0.48
32:B2:285:ARG:HH22	32:B2:372:ARG:HD2	1.79	0.48
33:B3:15:ILE:HG13	33:B3:33:ALA:HB3	1.96	0.48
33:B3:245:SER:OG	33:B3:262:GLY:N	2.41	0.48
33:B3:469:PRO:HG2	33:B3:475:MET:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:B3:513:LYS:HB2	33:B3:532:HIS:HB2	1.95	0.48
34:B8:364:GLN:HG3	34:B8:371:VAL:HG22	1.95	0.48
35:BE:132:THR:OG1	35:BE:134:ASP:OD1	2.32	0.48
35:BE:207:ASP:N	35:BE:207:ASP:OD1	2.45	0.48
35:BE:270:SER:O	35:BE:270:SER:OG	2.31	0.48
37:5C:128:THR:O	37:5C:128:THR:OG1	2.32	0.48
43:5I:188:HIS:HD1	43:5I:190:GLU:H	1.60	0.48
47:RE:559:GLU:HB2	47:RE:585:MET:HE3	1.96	0.48
50:RJ:776:GLN:HA	50:RJ:780:ILE:HG22	1.95	0.48
2:5A:495:G:H2'	2:5A:496:G:H8	1.78	0.48
3:SA:66:U:OP2	7:SH:136:LYS:NZ	2.46	0.48
3:SA:844:A:H2'	3:SA:845:G:H8	1.77	0.48
3:SA:874:C:H2'	3:SA:875:G:C8	2.49	0.48
3:SA:1041:G:H2'	3:SA:1042:G:C8	2.48	0.48
3:SA:1685:G:N2	3:SA:1716:C:O2'	2.45	0.48
6:SG:79:ASN:O	31:B1:508:GLN:NE2	2.46	0.48
6:SG:219:ARG:NH2	49:RH:222:ASP:OD2	2.43	0.48
13:SP:81:VAL:HG21	13:SP:102:LEU:HD12	1.94	0.48
21:3D:160:ARG:NH1	36:B6:293:TYR:OH	2.45	0.48
21:3D:194:ARG:NH2	22:3E:172:ASP:OD2	2.47	0.48
25:A4:192:THR:O	25:A4:203:GLY:HA2	2.14	0.48
30:AG:623:PHE:HE2	30:AG:670:LEU:HD11	1.79	0.48
37:5C:138:ASP:OD2	37:5C:141:LYS:NZ	2.44	0.48
37:5C:340:LEU:O	37:5C:368:TYR:N	2.46	0.48
40:5F:54:ILE:HD11	40:5F:101:VAL:HG21	1.95	0.48
40:5F:169:THR:HA	40:5F:172:ARG:HG2	1.96	0.48
48:RF:204:SER:OG	48:RF:205:SER:N	2.47	0.48
2:5A:8:A:H5''	27:A9:487:ARG:HH22	1.79	0.48
3:SA:760:A:N1	3:SA:790:U:C4	2.82	0.48
5:SF:87:MET:HE2	5:SF:123:LEU:HG	1.96	0.48
7:SH:142:ARG:HA	7:SH:147:LEU:HD23	1.96	0.48
23:3F:168:ASN:N	23:3F:174:GLU:O	2.47	0.48
23:3F:398:CYS:H	24:3H:14:ALA:HB1	1.78	0.48
26:A5:156:ALA:HB3	26:A5:159:SER:HB2	1.96	0.48
30:AG:335:PRO:HB2	30:AG:336:ARG:HD3	1.95	0.48
33:B3:148:SER:OG	33:B3:149:SER:N	2.38	0.48
34:B8:512:ASP:OD1	34:B8:512:ASP:N	2.47	0.48
55:RT:210:GLY:O	55:RT:214:PHE:HB2	2.13	0.48
1:3A:266:C:O2'	1:3A:267:A:O4'	2.32	0.48
3:SA:65:A:N6	3:SA:84:A:OP2	2.46	0.48
3:SA:884:A:OP1	4:SC:136:ARG:NH2	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:SC:65:VAL:HG21	4:SC:85:LYS:HE2	1.95	0.48
17:SZ:91:LEU:HD22	17:SZ:96:LEU:HD21	1.96	0.48
20:3C:100:ARG:HA	20:3C:104:ASP:HA	1.95	0.48
25:A4:613:GLN:HA	25:A4:616:LYS:HB3	1.95	0.48
30:AG:710:LEU:HG	30:AG:711:ILE:HG23	1.96	0.48
32:B2:476:ILE:HA	32:B2:492:SER:HA	1.95	0.48
43:5I:205:ASP:OD1	43:5I:205:ASP:N	2.43	0.48
45:5K:155:THR:OG1	45:5K:156:ASN:N	2.47	0.48
47:RE:826:SER:OG	47:RE:841:ASN:ND2	2.46	0.48
49:RH:189:VAL:HA	49:RH:192:TYR:HB3	1.95	0.48
53:RP:133:ILE:HD13	53:RP:180:LEU:HG	1.95	0.48
53:RP:193:ALA:O	53:RP:197:SER:HB3	2.13	0.48
8:SI:134:GLU:HB3	8:SI:155:ASP:HB3	1.96	0.48
16:SY:59:ILE:O	16:SY:69:ARG:NH2	2.42	0.48
20:3C:91:HIS:HB3	20:3C:96:VAL:HG13	1.95	0.48
22:3E:215:ARG:NH2	22:3E:244:GLY:O	2.47	0.48
24:3G:26:GLN:HB3	24:3G:110:ILE:HG21	1.95	0.48
25:A4:417:VAL:HG11	25:A4:460:LEU:HD12	1.96	0.48
29:AF:215:VAL:HA	29:AF:230:GLY:HA3	1.94	0.48
30:AG:378:ASP:O	34:B8:344:ARG:NH2	2.47	0.48
31:B1:261:ALA:HB1	31:B1:279:PHE:HB3	1.95	0.48
31:B1:387:THR:OG1	31:B1:388:SER:N	2.47	0.48
31:B1:538:GLN:HG2	31:B1:554:ASP:HA	1.96	0.48
53:RP:43:GLU:HG3	53:RP:44:SER:H	1.79	0.48
1:3A:206:C:N3	1:3A:243:U:C4	2.82	0.47
2:5A:295:A:C6	35:BE:381:ARG:HD2	2.49	0.47
3:SA:315:A:N1	3:SA:349:U:O2'	2.39	0.47
16:SY:76:LEU:O	16:SY:80:GLY:HA2	2.13	0.47
20:3B:236:MET:HG2	21:3D:133:LEU:HA	1.95	0.47
20:3C:118:TYR:OH	20:3C:178:GLY:O	2.30	0.47
24:3H:13:ASP:OD1	24:3H:13:ASP:N	2.46	0.47
25:A4:102:LEU:HA	25:A4:115:PHE:O	2.14	0.47
25:A4:305:PHE:HB3	25:A4:325:ASN:HA	1.96	0.47
30:AG:692:PHE:HE1	30:AG:750:LEU:HB3	1.79	0.47
33:B3:690:HIS:NE2	39:5E:518:GLU:OE2	2.47	0.47
35:BE:405:SER:OG	35:BE:406:THR:N	2.47	0.47
36:B6:67:ARG:NH1	36:B6:84:SER:OG	2.44	0.47
39:5E:316:ASN:O	39:5E:320:ALA:CB	2.62	0.47
41:5G:217:ASP:OD1	41:5G:217:ASP:N	2.44	0.47
41:5G:236:HIS:HA	41:5G:249:GLU:HA	1.95	0.47
43:5I:230:ASN:OD1	43:5I:230:ASN:N	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:RJ:268:LYS:HB3	50:RJ:794:GLU:HG3	1.94	0.47
1:3A:325:C:N4	22:3E:318:GLN:OE1	2.30	0.47
3:SA:486:G:N3	3:SA:500:C:N4	2.61	0.47
3:SA:524:U:N3	3:SA:527:A:OP2	2.46	0.47
3:SA:596:C:H2'	3:SA:597:G:H8	1.79	0.47
4:SC:92:GLN:NE2	4:SC:235:GLY:O	2.46	0.47
4:SC:209:ASN:OD1	4:SC:209:ASN:N	2.46	0.47
15:SX:6:VAL:HG23	15:SX:29:PRO:HD2	1.95	0.47
25:A4:62:PRO:HD2	25:A4:65:LEU:HD11	1.94	0.47
25:A4:378:TYR:OH	25:A4:632:ASN:ND2	2.47	0.47
26:A5:336:ASN:OD1	26:A5:336:ASN:N	2.47	0.47
26:A5:541:LEU:HG	29:AF:495:ILE:HD11	1.95	0.47
28:AE:56:LEU:HD22	28:AE:74:PHE:HD2	1.79	0.47
28:AE:191:LEU:O	28:AE:194:SER:OG	2.29	0.47
30:AG:138:ASP:OD1	30:AG:140:LYS:NZ	2.38	0.47
35:BE:134:ASP:OD1	35:BE:136:SER:OG	2.32	0.47
35:BE:323:VAL:HB	35:BE:343:LEU:HD22	1.96	0.47
37:5C:170:GLN:NE2	37:5C:177:TYR:OH	2.47	0.47
40:5F:137:ARG:NH2	40:5F:139:GLY:O	2.42	0.47
47:RE:379:MET:HE2	47:RE:382:SER:HB3	1.96	0.47
53:RP:1893:GLU:HA	53:RP:1896:ILE:HD12	1.96	0.47
53:RP:1957:GLN:NE2	53:RP:1995:ARG:O	2.47	0.47
53:RP:1998:LEU:H	53:RP:1998:LEU:HD12	1.79	0.47
3:SA:214:G:H4'	3:SA:242:U:H3	1.80	0.47
3:SA:1744:A:N6	3:SA:1746:A:N7	2.62	0.47
6:SG:57:SER:HB3	19:Sd:9:LEU:HD11	1.96	0.47
18:Sc:58:SER:OG	18:Sc:59:CYS:N	2.45	0.47
23:3F:342:ARG:HH12	24:3H:21:LEU:HB3	1.79	0.47
23:3F:492:TRP:HB3	23:3F:520:VAL:HG22	1.96	0.47
29:AF:238:ASP:OD2	29:AF:241:SER:OG	2.32	0.47
31:B1:36:ARG:NH2	31:B1:53:GLU:OE2	2.46	0.47
32:B2:139:GLY:HA3	32:B2:166:ILE:HD11	1.96	0.47
33:B3:536:LEU:HA	33:B3:552:SER:HB2	1.95	0.47
35:BE:361:SER:HA	35:BE:636:PRO:HB3	1.95	0.47
39:5E:310:GLN:HA	39:5E:313:GLN:HG2	1.96	0.47
39:5E:474:ILE:HG12	39:5E:476:MET:H	1.79	0.47
41:5G:131:CYS:SG	41:5G:136:THR:OG1	2.58	0.47
43:5I:244:ILE:O	43:5I:257:LYS:HA	2.14	0.47
49:RH:77:LEU:HD21	49:RH:84:ILE:HA	1.96	0.47
49:RH:232:LEU:HD11	49:RH:240:LYS:HZ2	1.79	0.47
53:RP:1914:THR:HA	53:RP:1917:ILE:HD12	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5A:84:G:H4'	30:AG:295:TRP:HA	1.95	0.47
30:AG:408:THR:HG21	30:AG:488:LEU:HD13	1.96	0.47
31:B1:369:ILE:HB	31:B1:383:PHE:HB2	1.96	0.47
35:BE:509:SER:OG	35:BE:510:LEU:N	2.47	0.47
38:5D:18:GLN:HB2	38:5D:28:LEU:H	1.80	0.47
53:RP:35:GLU:O	53:RP:37:ARG:NH2	2.48	0.47
1:3A:59:G:OP1	31:B1:573:ASN:ND2	2.46	0.47
2:5A:2:U:H2'	2:5A:3:G:C8	2.49	0.47
3:SA:29:U:H2'	3:SA:30:G:C8	2.49	0.47
4:SC:149:GLN:HE22	4:SC:154:SER:HB3	1.80	0.47
11:SM:64:VAL:HG12	11:SM:129:ARG:HE	1.79	0.47
16:SY:56:LYS:HE2	16:SY:97:ASP:HA	1.95	0.47
16:SY:76:LEU:O	16:SY:80:GLY:N	2.47	0.47
20:3C:166:PRO:HA	20:3C:188:VAL:HA	1.96	0.47
30:AG:317:TRP:HA	30:AG:340:ILE:HG23	1.97	0.47
31:B1:5:PHE:HB3	31:B1:704:TYR:HB3	1.97	0.47
33:B3:34:THR:OG1	33:B3:35:PRO:O	2.28	0.47
33:B3:741:LYS:HG2	33:B3:781:ILE:HD11	1.97	0.47
34:B8:129:ASP:HA	34:B8:132:LYS:HE3	1.97	0.47
34:B8:178:VAL:HG11	35:BE:217:VAL:HG11	1.96	0.47
35:BE:862:VAL:HG21	35:BE:904:ASP:HB2	1.95	0.47
49:RH:154:ASN:ND2	49:RH:156:GLU:OE2	2.48	0.47
3:SA:828:U:N3	3:SA:843:U:O2	2.48	0.47
3:SA:1756:A:H62	39:5E:532:LEU:HB2	1.78	0.47
5:SF:206:ASP:OD1	5:SF:206:ASP:N	2.47	0.47
8:SI:48:GLU:HG2	8:SI:56:LYS:HB3	1.97	0.47
14:SR:113:ASP:N	14:SR:113:ASP:OD1	2.45	0.47
15:SX:105:THR:O	15:SX:105:THR:OG1	2.31	0.47
20:3C:90:PRO:HA	20:3C:97:TYR:HD1	1.80	0.47
21:3D:212:ASP:O	21:3D:216:PHE:CB	2.62	0.47
23:3F:411:PHE:HA	23:3F:427:LEU:HD23	1.97	0.47
24:3H:16:LEU:HD21	24:3H:121:ILE:HG22	1.96	0.47
25:A4:101:GLY:HA3	25:A4:117:ILE:HD12	1.96	0.47
32:B2:171:CYS:HB2	32:B2:177:LEU:HD12	1.95	0.47
33:B3:410:ASN:HA	33:B3:435:ALA:HA	1.97	0.47
37:5C:265:GLU:HG3	37:5C:265:GLU:O	2.14	0.47
43:5I:411:LYS:O	43:5I:415:ARG:HB2	2.15	0.47
44:5J:165:ASN:ND2	44:5J:168:GLU:OE1	2.48	0.47
1:3A:30:A:N6	43:5I:342:ILE:O	2.36	0.47
3:SA:252:U:H2'	3:SA:253:A:H8	1.79	0.47
4:SC:149:GLN:HE21	4:SC:151:LYS:HG2	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:SY:109:ARG:NH2	16:SY:117:ILE:O	2.43	0.47
18:Sc:54:VAL:HG13	18:Sc:63:LEU:HB2	1.97	0.47
20:3B:218:ILE:HD12	21:3D:152:LEU:HA	1.96	0.47
20:3B:283:GLU:HG2	45:5K:150:CYS:HB3	1.97	0.47
21:3D:286:ARG:HA	21:3D:289:TYR:HB3	1.97	0.47
25:A4:121:THR:HA	25:A4:144:ILE:HG22	1.97	0.47
28:AE:259:THR:HG23	30:AG:891:VAL:HG11	1.96	0.47
29:AF:307:VAL:HA	29:AF:318:LEU:HA	1.97	0.47
30:AG:529:LEU:HB2	30:AG:547:VAL:HG23	1.96	0.47
30:AG:768:TRP:HE1	30:AG:772:THR:HA	1.79	0.47
31:B1:848:PHE:O	31:B1:852:THR:OG1	2.32	0.47
32:B2:218:ILE:HD11	32:B2:226:VAL:HB	1.95	0.47
32:B2:595:LYS:HD2	32:B2:615:GLN:HA	1.97	0.47
33:B3:12:LEU:HD23	33:B3:643:PHE:HE2	1.78	0.47
33:B3:151:LYS:H	33:B3:164:ALA:HB3	1.80	0.47
33:B3:393:SER:OG	33:B3:394:LEU:N	2.45	0.47
34:B8:253:SER:HB2	34:B8:297:THR:HA	1.96	0.47
35:BE:896:ILE:HG23	35:BE:905:ILE:HD12	1.95	0.47
36:B6:196:LEU:HA	36:B6:199:ARG:HB3	1.97	0.47
37:5C:69:GLU:OE1	43:5I:13:TYR:OH	2.32	0.47
37:5C:103:ALA:HB2	37:5C:402:ILE:HD11	1.96	0.47
44:5J:50:SER:O	44:5J:53:GLN:NE2	2.48	0.47
47:RE:891:ALA:HA	47:RE:894:ARG:HH11	1.80	0.47
47:RE:1087:LEU:O	47:RE:1090:THR:OG1	2.31	0.47
48:RF:64:ILE:HA	48:RF:87:LEU:HD13	1.97	0.47
48:RF:131:ALA:HA	48:RF:134:ILE:HG22	1.97	0.47
49:RH:191:ASP:HA	49:RH:194:GLU:HB3	1.97	0.47
51:RK:302:VAL:HG11	51:RK:329:ILE:HD11	1.96	0.47
53:RP:47:PHE:HA	53:RP:112:GLN:HG2	1.97	0.47
3:SA:455:C:H5'	5:SF:59:ARG:HH22	1.79	0.47
3:SA:461:G:H2'	3:SA:462:G:H8	1.78	0.47
3:SA:867:G:N2	12:SO:87:ASP:OD2	2.48	0.47
3:SA:1060:U:H2'	3:SA:1061:A:H8	1.79	0.47
8:SI:56:LYS:HE2	53:RP:2031:HIS:HE1	1.80	0.47
14:SR:37:THR:O	14:SR:45:ARG:NE	2.47	0.47
23:3F:120:ARG:HH11	53:RP:79:GLN:HA	1.79	0.47
34:B8:149:SER:HB3	34:B8:152:GLU:HG2	1.96	0.47
43:5I:126:LYS:NZ	43:5I:127:LYS:O	2.38	0.47
47:RE:639:SER:OG	47:RE:640:THR:N	2.47	0.47
50:RJ:552:LEU:HD21	50:RJ:566:ARG:HH11	1.80	0.47
3:SA:625:C:O2'	3:SA:939:A:N3	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:SJ:196:LEU:HA	9:SJ:199:LYS:HZ3	1.80	0.47
13:SP:22:SER:OG	13:SP:23:PHE:N	2.47	0.47
20:3B:144:TRP:CE2	20:3B:152:ALA:HB2	2.49	0.47
22:3E:227:LEU:HD13	22:3E:231:ILE:HB	1.97	0.47
25:A4:198:ASP:OD1	25:A4:198:ASP:N	2.43	0.47
25:A4:516:VAL:HG11	25:A4:529:ASN:HB3	1.96	0.47
26:A5:213:ASN:ND2	26:A5:215:TYR:OH	2.48	0.47
30:AG:352:ASN:OD1	30:AG:352:ASN:N	2.48	0.47
30:AG:420:SER:HA	30:AG:423:LYS:HE2	1.96	0.47
30:AG:443:ASN:ND2	30:AG:446:ASN:OD1	2.47	0.47
30:AG:868:ASN:N	30:AG:868:ASN:OD1	2.44	0.47
31:B1:314:GLY:O	31:B1:332:TRP:NE1	2.39	0.47
33:B3:25:VAL:HG12	33:B3:294:LEU:HD22	1.96	0.47
33:B3:340:ILE:HG12	33:B3:357:THR:HG22	1.97	0.47
33:B3:575:THR:OG1	33:B3:576:ASN:N	2.48	0.47
3:SA:763:G:H1'	3:SA:787:G:H1'	1.96	0.47
3:SA:1160:A:H2'	3:SA:1161:C:H6	1.80	0.47
3:SA:1751:C:H2'	3:SA:1752:U:C6	2.49	0.47
7:SH:130:PRO:HB3	53:RP:624:VAL:HA	1.97	0.47
28:AE:32:SER:OG	28:AE:35:TYR:O	2.32	0.47
32:B2:273:TYR:HE2	32:B2:275:GLN:HG3	1.80	0.47
32:B2:412:GLY:HA2	32:B2:431:GLY:H	1.80	0.47
33:B3:12:LEU:HG	33:B3:641:PHE:HB2	1.96	0.47
33:B3:211:LEU:O	33:B3:222:LEU:HA	2.15	0.47
33:B3:219:ILE:HB	33:B3:235:LYS:HE3	1.96	0.47
36:B6:126:TYR:HA	36:B6:129:ILE:HB	1.96	0.47
41:5G:236:HIS:CE1	41:5G:249:GLU:HB3	2.50	0.47
47:RE:870:ALA:HB2	48:RF:103:LEU:HD21	1.96	0.47
50:RJ:771:GLU:O	50:RJ:777:ARG:NH2	2.47	0.47
50:RJ:1061:GLU:OE1	50:RJ:1063:HIS:NE2	2.47	0.47
51:RK:196:TYR:HA	51:RK:228:ASP:O	2.14	0.47
3:SA:252:U:H2'	3:SA:253:A:C8	2.51	0.46
3:SA:429:G:H21	50:RJ:225:ARG:HH12	1.63	0.46
3:SA:922:G:H2'	3:SA:923:A:H8	1.80	0.46
8:SI:48:GLU:HA	8:SI:57:ALA:O	2.15	0.46
22:3E:338:LYS:HD3	22:3E:357:GLY:HA3	1.96	0.46
22:3E:355:ASN:HB2	22:3E:401:LEU:HD13	1.97	0.46
25:A4:298:ALA:HB1	25:A4:333:ILE:HG13	1.97	0.46
25:A4:344:ALA:HB2	25:A4:682:THR:HA	1.97	0.46
25:A4:545:ARG:HG2	25:A4:549:VAL:HB	1.98	0.46
28:AE:39:THR:O	28:AE:43:GLN:NE2	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:AF:398:SER:O	29:AF:434:ARG:NH2	2.47	0.46
30:AG:524:ASP:OD1	30:AG:524:ASP:N	2.47	0.46
31:B1:295:ILE:HG22	31:B1:296:GLN:HG2	1.96	0.46
31:B1:605:ASP:OD1	31:B1:605:ASP:N	2.42	0.46
32:B2:186:ILE:HG12	32:B2:202:ALA:HB2	1.96	0.46
35:BE:171:GLN:NE2	35:BE:212:ALA:O	2.48	0.46
35:BE:376:TRP:NE1	35:BE:388:GLU:OE1	2.48	0.46
35:BE:664:SER:OG	35:BE:665:THR:N	2.48	0.46
37:5C:183:GLU:HG2	45:5K:16:THR:HG22	1.97	0.46
43:5I:88:ALA:HB1	43:5I:112:LEU:HD23	1.96	0.46
47:RE:184:SER:HB3	47:RE:206:LEU:HB3	1.97	0.46
49:RH:44:VAL:HG22	49:RH:113:TYR:HB2	1.96	0.46
50:RJ:991:PHE:CG	50:RJ:995:ILE:HD11	2.50	0.46
3:SA:903:U:O2'	3:SA:905:A:N7	2.43	0.46
25:A4:147:ILE:HA	25:A4:157:SER:O	2.15	0.46
31:B1:517:ASP:OD1	31:B1:517:ASP:N	2.35	0.46
31:B1:567:ASP:OD1	31:B1:567:ASP:N	2.47	0.46
32:B2:23:CYS:HB2	32:B2:43:THR:HG22	1.97	0.46
32:B2:584:ASP:N	32:B2:584:ASP:OD1	2.46	0.46
33:B3:215:GLY:N	33:B3:242:GLN:OE1	2.48	0.46
35:BE:299:THR:OG1	35:BE:313:SER:O	2.30	0.46
35:BE:914:ASP:O	35:BE:918:LYS:NZ	2.43	0.46
43:5I:359:ASP:N	43:5I:359:ASP:OD1	2.48	0.46
47:RE:692:LYS:HE2	47:RE:692:LYS:HB2	1.81	0.46
49:RH:192:TYR:HA	49:RH:195:LYS:HE2	1.96	0.46
51:RK:126:ASN:OD1	51:RK:126:ASN:N	2.47	0.46
1:3A:247:U:O4	23:3F:151:ARG:NH1	2.49	0.46
10:SK:107:ARG:NH2	10:SK:148:VAL:O	2.41	0.46
12:SO:43:LYS:HB2	12:SO:43:LYS:HE3	1.74	0.46
22:3E:355:ASN:OD1	22:3E:355:ASN:N	2.48	0.46
25:A4:274:GLN:HE22	25:A4:319:ARG:HA	1.79	0.46
26:A5:96:THR:OG1	26:A5:97:TYR:N	2.48	0.46
26:A5:231:ASP:O	26:A5:249:GLU:N	2.47	0.46
30:AG:291:ARG:NH1	30:AG:326:LEU:O	2.48	0.46
30:AG:579:ASN:HD21	30:AG:603:ASN:HA	1.80	0.46
30:AG:655:LEU:HD13	30:AG:659:ILE:HG21	1.95	0.46
32:B2:498:LYS:HG3	32:B2:527:THR:HA	1.96	0.46
34:B8:268:TYR:OH	34:B8:296:GLN:NE2	2.48	0.46
35:BE:322:TYR:HE1	35:BE:342:TYR:HD1	1.62	0.46
35:BE:353:PRO:HA	35:BE:370:SER:HA	1.97	0.46
35:BE:719:GLU:OE1	35:BE:719:GLU:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:B6:144:VAL:HG11	36:B6:178:VAL:HG11	1.97	0.46
43:5I:291:MET:HE1	54:RQ:295:VAL:HG21	1.98	0.46
51:RK:280:LEU:HD13	51:RK:283:ILE:HD11	1.96	0.46
53:RP:135:LEU:HD13	53:RP:138:ALA:HB3	1.97	0.46
8:SI:33:GLU:O	8:SI:35:LYS:NZ	2.39	0.46
21:3D:169:LYS:NZ	21:3D:391:ASN:O	2.49	0.46
23:3F:160:ILE:HG12	23:3F:542:SER:HB3	1.97	0.46
26:A5:344:ASP:OD1	26:A5:348:LYS:N	2.40	0.46
29:AF:104:LEU:HA	29:AF:121:ASN:HA	1.97	0.46
30:AG:57:VAL:HG12	30:AG:383:LEU:HD21	1.96	0.46
30:AG:358:LEU:HB3	30:AG:370:GLN:HB3	1.96	0.46
31:B1:329:VAL:HG13	31:B1:338:ILE:HB	1.97	0.46
32:B2:433:ALA:HB1	32:B2:447:LEU:HD11	1.97	0.46
34:B8:238:LEU:HD13	34:B8:279:GLY:HA2	1.97	0.46
35:BE:626:ASP:N	35:BE:626:ASP:OD1	2.47	0.46
37:5C:23:ARG:HH22	54:RQ:869:TRP:HB3	1.80	0.46
37:5C:387:GLU:HG3	43:5I:6:ILE:HD11	1.96	0.46
43:5I:311:VAL:HA	43:5I:321:VAL:O	2.15	0.46
45:5K:185:LEU:HD12	45:5K:186:PRO:HD2	1.98	0.46
47:RE:462:PHE:HB2	47:RE:466:THR:HG21	1.97	0.46
47:RE:870:ALA:HA	48:RF:103:LEU:HD11	1.98	0.46
47:RE:924:LEU:HG	47:RE:1164:SER:HB3	1.96	0.46
53:RP:2023:THR:HA	53:RP:2026:ILE:HG12	1.97	0.46
1:3A:35:U:O2	43:5I:393:LYS:NZ	2.48	0.46
3:SA:488:G:H1	3:SA:499:U:H3	1.62	0.46
3:SA:592:A:O2'	3:SA:596:C:OP1	2.34	0.46
8:SI:72:LYS:O	8:SI:76:LYS:NZ	2.49	0.46
9:SJ:111:GLN:O	9:SJ:115:ALA:HB3	2.16	0.46
20:3B:219:PRO:O	21:3D:159:SER:OG	2.28	0.46
20:3C:111:MET:HG3	20:3C:216:ASN:HD22	1.81	0.46
22:3E:238:ALA:O	22:3E:242:SER:HB3	2.15	0.46
26:A5:23:ALA:HB1	34:B8:261:PRO:HG3	1.98	0.46
27:A9:477:LYS:HA	27:A9:480:LYS:HE2	1.96	0.46
30:AG:408:THR:OG1	30:AG:409:LYS:N	2.49	0.46
32:B2:495:LYS:HA	32:B2:533:ASP:HA	1.98	0.46
33:B3:686:MET:HE1	33:B3:731:LEU:HD22	1.98	0.46
40:5F:24:ASP:OD2	40:5F:27:HIS:NE2	2.49	0.46
47:RE:1233:ASN:ND2	47:RE:1235:GLU:OE2	2.49	0.46
50:RJ:61:ARG:NE	50:RJ:277:GLY:O	2.49	0.46
50:RJ:951:MET:SD	50:RJ:987:TYR:OH	2.70	0.46
53:RP:1759:SER:O	53:RP:1759:SER:OG	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:RT:174:LEU:HA	55:RT:180:LEU:HD21	1.97	0.46
3:SA:862:A:H3'	12:SO:16:ILE:HD11	1.97	0.46
3:SA:898:A:H62	3:SA:914:G:N2	2.13	0.46
7:SH:157:VAL:HB	7:SH:175:ILE:HD11	1.98	0.46
12:SO:49:GLN:HA	12:SO:52:VAL:HG12	1.97	0.46
19:Sd:35:ASP:OD1	19:Sd:35:ASP:N	2.40	0.46
20:3C:232:MET:HE1	22:3E:63:ILE:HA	1.98	0.46
28:AE:376:GLU:CD	28:AE:377:ARG:H	2.24	0.46
31:B1:191:ARG:HH12	31:B1:255:PHE:HE2	1.64	0.46
34:B8:426:VAL:HB	34:B8:455:ILE:HD11	1.98	0.46
35:BE:311:VAL:HG22	35:BE:321:GLU:HG2	1.98	0.46
40:5F:120:MET:HE3	40:5F:120:MET:HB2	1.77	0.46
45:5K:52:PHE:HB3	45:5K:55:TYR:HB3	1.96	0.46
50:RJ:138:VAL:HG11	50:RJ:155:PHE:HE2	1.79	0.46
53:RP:1876:LEU:HD23	53:RP:1876:LEU:HA	1.73	0.46
1:3A:18:G:H2'	1:3A:19:A:C8	2.51	0.46
2:5A:87:C:H41	30:AG:334:LEU:HA	1.81	0.46
3:SA:327:U:O3'	11:SM:14:GLN:NE2	2.48	0.46
6:SG:72:HIS:CE1	6:SG:107:LYS:HD3	2.51	0.46
12:SO:99:ARG:HH12	12:SO:141:TYR:HE2	1.64	0.46
21:3D:121:ASN:O	21:3D:125:GLN:NE2	2.49	0.46
29:AF:31:THR:OG1	29:AF:32:SER:N	2.45	0.46
30:AG:46:ILE:HD13	30:AG:385:ILE:HG21	1.96	0.46
30:AG:364:ASN:ND2	30:AG:409:LYS:O	2.49	0.46
30:AG:626:PHE:HB3	30:AG:629:LYS:HG3	1.96	0.46
32:B2:393:ASP:OD1	32:B2:393:ASP:N	2.46	0.46
39:5E:452:SER:O	39:5E:452:SER:OG	2.28	0.46
41:5G:233:VAL:HG21	41:5G:256:MET:HE3	1.96	0.46
47:RE:1204:VAL:HG12	48:RF:57:ASN:HD22	1.79	0.46
22:3E:279:ARG:HA	22:3E:279:ARG:HD2	1.81	0.46
23:3F:240:LEU:HB2	23:3F:255:GLY:HA2	1.97	0.46
25:A4:121:THR:HB	25:A4:143:VAL:HA	1.97	0.46
25:A4:180:ASP:OD1	25:A4:180:ASP:N	2.49	0.46
30:AG:201:ILE:HD12	30:AG:208:LEU:HB3	1.97	0.46
30:AG:722:LEU:HD13	30:AG:763:ILE:HD13	1.98	0.46
32:B2:917:ASN:OD1	32:B2:917:ASN:N	2.46	0.46
34:B8:206:ASN:O	34:B8:209:THR:OG1	2.30	0.46
35:BE:235:MET:HE2	35:BE:235:MET:HB3	1.79	0.46
36:B6:298:SER:OG	36:B6:299:LYS:N	2.45	0.46
46:RD:1644:LEU:HD21	46:RD:1654:LEU:HD22	1.97	0.46
50:RJ:618:PHE:HA	50:RJ:621:LEU:HD12	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:RJ:770:GLN:HA	50:RJ:777:ARG:HH12	1.80	0.46
1:3A:265:C:O2	1:3A:307:G:N2	2.49	0.46
3:SA:34:G:O6	3:SA:475:A:N6	2.48	0.46
3:SA:163:G:OP2	3:SA:163:G:N2	2.39	0.46
3:SA:482:U:H2'	3:SA:483:A:H8	1.81	0.46
3:SA:1731:A:H3'	3:SA:1732:A:H8	1.80	0.46
3:SA:1735:U:H2'	3:SA:1736:G:C8	2.51	0.46
8:SI:44:LYS:HG3	8:SI:63:PRO:HG3	1.98	0.46
21:3D:382:LYS:HD3	21:3D:382:LYS:HA	1.78	0.46
30:AG:34:ILE:HD12	30:AG:91:ILE:HG13	1.98	0.46
34:B8:464:THR:HG21	34:B8:476:ILE:HG13	1.98	0.46
43:5I:225:LEU:HA	43:5I:237:SER:HA	1.98	0.46
50:RJ:848:SER:O	50:RJ:848:SER:OG	2.34	0.46
53:RP:2095:LEU:O	53:RP:2099:SER:CB	2.64	0.46
3:SA:1530:C:N4	3:SA:1531:G:O6	2.49	0.46
8:SI:13:PRO:HB2	8:SI:17:GLU:HB3	1.98	0.46
13:SP:32:ASP:N	13:SP:32:ASP:OD1	2.45	0.46
25:A4:33:VAL:HG22	25:A4:752:LEU:HD13	1.98	0.46
25:A4:79:TRP:HA	25:A4:87:GLN:HA	1.98	0.46
25:A4:740:PRO:O	25:A4:756:GLU:CB	2.64	0.46
29:AF:68:SER:O	29:AF:315:ASN:ND2	2.40	0.46
31:B1:185:THR:OG1	31:B1:186:THR:N	2.49	0.46
31:B1:337:TYR:OH	39:5E:476:MET:SD	2.60	0.46
31:B1:482:SER:OG	31:B1:487:VAL:N	2.49	0.46
32:B2:555:VAL:HG23	32:B2:576:VAL:HG11	1.98	0.46
35:BE:211:THR:HG21	35:BE:253:SER:HA	1.97	0.46
36:B6:25:THR:OG1	36:B6:28:GLU:OE1	2.33	0.46
39:5E:439:GLU:O	39:5E:443:ASN:ND2	2.49	0.46
41:5G:169:ASN:HB2	41:5G:255:GLU:HG2	1.98	0.46
43:5I:265:ASN:N	43:5I:280:ALA:O	2.48	0.46
45:5K:100:ASP:OD1	45:5K:100:ASP:N	2.48	0.46
47:RE:631:GLY:N	47:RE:665:HIS:O	2.47	0.46
47:RE:711:PRO:HG3	47:RE:767:GLN:HB3	1.97	0.46
53:RP:622:CYS:O	53:RP:626:GLU:N	2.41	0.46
53:RP:1900:ARG:HE	53:RP:1933:ILE:HG12	1.81	0.46
6:SG:99:MET:HE3	6:SG:99:MET:HB3	1.78	0.45
11:SM:58:CYS:SG	11:SM:61:THR:OG1	2.69	0.45
11:SM:83:THR:HA	11:SM:110:HIS:HA	1.97	0.45
20:3B:164:ILE:HG23	20:3B:170:VAL:HG21	1.98	0.45
29:AF:422:ARG:HD2	29:AF:458:ILE:HD11	1.97	0.45
30:AG:767:GLY:O	30:AG:774:PHE:HA	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:AG:771:ASP:OD1	30:AG:771:ASP:N	2.42	0.45
33:B3:97:ARG:HD3	33:B3:97:ARG:HA	1.73	0.45
34:B8:264:LEU:HB2	34:B8:300:PHE:HE1	1.81	0.45
49:RH:123:GLU:OE2	49:RH:161:LYS:NZ	2.39	0.45
50:RJ:755:LYS:HD3	50:RJ:758:ILE:HD11	1.98	0.45
3:SA:168:A:O3'	7:SH:176:GLN:NE2	2.39	0.45
3:SA:454:U:H5''	3:SA:455:C:C4	2.51	0.45
3:SA:629:U:H5''	12:SO:127:ARG:HH12	1.80	0.45
10:SK:123:HIS:CD2	42:5H:566:ARG:HD2	2.51	0.45
21:3D:30:ARG:HH11	21:3D:122:GLU:HG3	1.82	0.45
23:3F:308:SER:OG	23:3F:310:ASN:OD1	2.34	0.45
24:3H:38:ASN:HA	24:3H:41:THR:HG22	1.97	0.45
25:A4:106:ASN:HB3	25:A4:112:LEU:HG	1.97	0.45
25:A4:349:SER:HB3	25:A4:357:VAL:HG22	1.97	0.45
29:AF:139:ILE:HD11	29:AF:151:LEU:HB3	1.99	0.45
30:AG:313:LEU:HD22	30:AG:321:MET:HE2	1.99	0.45
32:B2:163:LYS:HD3	32:B2:163:LYS:HA	1.69	0.45
32:B2:532:ASP:HB3	32:B2:550:LEU:HD23	1.97	0.45
35:BE:887:LEU:HA	35:BE:890:LYS:HZ3	1.80	0.45
48:RF:19:LYS:HE3	48:RF:160:TYR:H	1.81	0.45
2:5A:296:C:OP2	31:B1:94:ASN:ND2	2.46	0.45
3:SA:150:U:O4'	7:SH:132:ARG:NH1	2.49	0.45
9:SJ:111:GLN:O	9:SJ:115:ALA:CB	2.65	0.45
25:A4:33:VAL:HA	25:A4:752:LEU:HB3	1.98	0.45
28:AE:266:THR:HG21	30:AG:895:LEU:HD11	1.99	0.45
30:AG:152:ARG:NH1	30:AG:230:LEU:O	2.49	0.45
30:AG:175:ALA:O	30:AG:187:VAL:HA	2.16	0.45
30:AG:496:THR:OG1	30:AG:497:ASP:N	2.49	0.45
32:B2:130:ASP:OD2	32:B2:135:ARG:NE	2.49	0.45
32:B2:421:THR:HG22	32:B2:423:LYS:HG2	1.99	0.45
33:B3:24:THR:HB	33:B3:32:LEU:HD13	1.98	0.45
33:B3:138:HIS:CE1	33:B3:177:LEU:HB2	2.51	0.45
33:B3:362:LEU:HD22	33:B3:405:THR:HG21	1.98	0.45
35:BE:546:ILE:HG21	35:BE:560:LEU:HD23	1.97	0.45
35:BE:616:THR:HG23	35:BE:618:GLY:H	1.81	0.45
44:5J:129:ALA:HB2	50:RJ:1123:LYS:HD3	1.99	0.45
47:RE:128:LEU:HA	47:RE:131:LEU:HB2	1.98	0.45
47:RE:795:GLU:OE2	48:RF:101:SER:OG	2.30	0.45
50:RJ:610:LYS:NZ	50:RJ:612:VAL:O	2.48	0.45
50:RJ:852:ARG:HD2	50:RJ:888:PRO:HG3	1.98	0.45
51:RK:312:ARG:NH2	51:RK:349:ASP:OD2	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:RQ:301:ILE:HA	54:RQ:304:GLN:HG2	1.99	0.45
3:SA:493:U:OP2	50:RJ:1138:ARG:NH1	2.49	0.45
7:SH:126:ASP:OD1	7:SH:126:ASP:N	2.41	0.45
9:SJ:74:LYS:HA	9:SJ:74:LYS:HD2	1.78	0.45
12:SO:69:ASN:OD1	12:SO:69:ASN:N	2.49	0.45
17:SZ:6:THR:HG23	17:SZ:28:LEU:HB2	1.98	0.45
17:SZ:118:ILE:HG22	17:SZ:120:GLY:H	1.81	0.45
24:3G:120:LYS:O	24:3G:123:THR:OG1	2.34	0.45
25:A4:519:THR:OG1	25:A4:520:LYS:N	2.48	0.45
29:AF:123:SER:HG	29:AF:144:SER:HG	1.59	0.45
30:AG:85:ASN:O	30:AG:112:ASN:ND2	2.50	0.45
31:B1:459:SER:OG	31:B1:462:THR:O	2.28	0.45
33:B3:669:LEU:HD23	33:B3:693:ARG:HH21	1.82	0.45
35:BE:97:LYS:HG3	35:BE:111:GLU:HA	1.98	0.45
35:BE:232:MET:HE2	35:BE:232:MET:HB3	1.84	0.45
35:BE:854:SER:HB3	35:BE:858:PHE:HD1	1.81	0.45
39:5E:316:ASN:HA	39:5E:319:VAL:HG12	1.97	0.45
39:5E:350:THR:HG21	50:RJ:975:GLU:HB2	1.98	0.45
41:5G:233:VAL:HB	41:5G:254:PHE:HB2	1.97	0.45
43:5I:53:MET:HE3	43:5I:53:MET:HB2	1.71	0.45
51:RK:143:LYS:NZ	51:RK:180:MET:SD	2.89	0.45
1:3A:294:U:H2'	1:3A:295:A:C8	2.52	0.45
5:SF:201:HIS:H	5:SF:206:ASP:HB3	1.82	0.45
6:SG:118:LEU:HB2	6:SG:129:PRO:HB2	1.98	0.45
7:SH:46:LYS:H	7:SH:119:GLN:HB2	1.81	0.45
8:SI:49:ILE:HG12	8:SI:175:LYS:HE3	1.98	0.45
15:SX:18:GLU:HB3	15:SX:65:LEU:HD11	1.98	0.45
15:SX:68:ARG:NH1	43:5I:68:ASP:OD1	2.47	0.45
20:3B:269:ILE:O	20:3B:315:ILE:HA	2.17	0.45
21:3D:83:ASP:HB3	21:3D:113:PHE:HE1	1.81	0.45
23:3F:529:SER:OG	23:3F:530:GLY:N	2.50	0.45
25:A4:477:LEU:HD22	25:A4:534:LEU:H	1.82	0.45
25:A4:489:CYS:HB2	25:A4:534:LEU:HD23	1.98	0.45
32:B2:121:LYS:HD3	32:B2:121:LYS:HA	1.79	0.45
50:RJ:138:VAL:HG11	50:RJ:155:PHE:CE2	2.52	0.45
50:RJ:1051:ASP:OD1	50:RJ:1051:ASP:N	2.45	0.45
3:SA:126:A:H62	3:SA:291:G:H21	1.65	0.45
3:SA:794:U:H5''	3:SA:796:A:H62	1.80	0.45
25:A4:488:ILE:HB	25:A4:496:PHE:HB2	1.98	0.45
28:AE:295:ALA:HA	28:AE:298:THR:HG22	1.98	0.45
30:AG:110:PHE:HE1	30:AG:116:VAL:HG13	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:B1:802:LEU:HD23	31:B1:802:LEU:HA	1.79	0.45
33:B3:461:LEU:HD13	33:B3:485:TYR:HB2	1.99	0.45
35:BE:114:THR:OG1	35:BE:115:ASP:N	2.50	0.45
36:B6:201:LYS:HD2	44:5J:55:ILE:HG21	1.99	0.45
43:5I:18:SER:O	43:5I:18:SER:OG	2.29	0.45
43:5I:309:MET:H	43:5I:324:SER:HA	1.82	0.45
44:5J:134:ARG:HA	44:5J:134:ARG:HD2	1.86	0.45
47:RE:925:LEU:HD22	47:RE:1064:LEU:HD12	1.98	0.45
49:RH:186:VAL:HG23	49:RH:227:LEU:HA	1.99	0.45
50:RJ:761:GLN:O	50:RJ:765:ASN:HB2	2.16	0.45
50:RJ:1027:THR:OG1	50:RJ:1028:GLU:N	2.47	0.45
50:RJ:1106:GLU:HG3	50:RJ:1110:ARG:HH12	1.81	0.45
51:RK:97:GLY:HA2	51:RK:100:VAL:HG12	1.99	0.45
53:RP:1963:LEU:HD22	53:RP:2002:PHE:HE1	1.82	0.45
1:3A:329:C:H2'	1:3A:330:A:C8	2.49	0.45
2:5A:70:A:P	30:AG:426:ARG:HH22	2.40	0.45
3:SA:748:U:H3	3:SA:801:G:H22	1.64	0.45
7:SH:3:LEU:HB3	7:SH:5:ILE:HD11	1.97	0.45
9:SJ:60:ILE:HD11	9:SJ:173:PRO:HB3	1.99	0.45
20:3B:175:ALA:HB1	20:3B:181:VAL:HG21	1.99	0.45
20:3B:294:ARG:HH21	20:3B:300:PRO:HG2	1.82	0.45
20:3C:225:ARG:HG2	20:3C:252:ILE:HG12	1.99	0.45
23:3F:522:THR:OG1	23:3F:542:SER:OG	2.32	0.45
25:A4:625:GLU:O	25:A4:629:LEU:HB2	2.17	0.45
31:B1:576:ARG:HG2	40:5F:142:LEU:HD22	1.99	0.45
31:B1:710:ILE:HG13	35:BE:596:GLU:HG2	1.98	0.45
32:B2:16:VAL:HG21	32:B2:46:LEU:HG	1.99	0.45
32:B2:487:ARG:HA	32:B2:500:TRP:O	2.16	0.45
33:B3:439:ALA:HB3	33:B3:497:LEU:HB3	1.98	0.45
34:B8:390:THR:OG1	34:B8:391:SER:N	2.49	0.45
35:BE:421:ASN:ND2	35:BE:429:ASN:HD21	2.15	0.45
35:BE:590:ALA:O	35:BE:602:SER:HA	2.16	0.45
39:5E:298:SER:OG	39:5E:299:SER:N	2.50	0.45
47:RE:673:SER:OG	47:RE:674:SER:N	2.49	0.45
47:RE:1227:GLY:O	47:RE:1231:VAL:N	2.41	0.45
3:SA:677:G:H2'	3:SA:678:A:C8	2.52	0.45
3:SA:689:G:H2'	3:SA:690:G:H8	1.81	0.45
3:SA:960:U:H5'	12:SO:55:ARG:HD3	1.98	0.45
4:SC:178:GLY:HA2	47:RE:897:ARG:HH12	1.81	0.45
9:SJ:37:LYS:HB2	9:SJ:59:ARG:HG2	1.98	0.45
15:SX:70:ASN:N	15:SX:70:ASN:OD1	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:SX:89:TRP:O	15:SX:93:LEU:CB	2.64	0.45
20:3B:90:PRO:HA	20:3B:97:TYR:HD1	1.82	0.45
20:3B:92:ARG:NH1	20:3B:159:LEU:O	2.49	0.45
20:3C:242:ALA:HB3	20:3C:269:ILE:HG23	1.99	0.45
20:3C:281:ASP:O	20:3C:284:THR:OG1	2.27	0.45
21:3D:173:HIS:NE2	22:3E:251:ASP:OD2	2.50	0.45
22:3E:132:SER:HB2	22:3E:135:ASP:HB3	1.99	0.45
23:3F:156:ASN:HD21	23:3F:545:LYS:HG3	1.82	0.45
30:AG:80:GLN:NE2	30:AG:83:GLU:O	2.44	0.45
33:B3:175:TRP:HD1	33:B3:182:CYS:HA	1.80	0.45
35:BE:568:VAL:HG13	35:BE:577:VAL:HG13	1.99	0.45
37:5C:437:LEU:HD21	43:5I:39:ARG:HG3	1.98	0.45
43:5I:68:ASP:HB2	43:5I:89:ASP:HB3	1.99	0.45
43:5I:291:MET:HB3	43:5I:291:MET:HE2	1.84	0.45
44:5J:68:GLY:O	44:5J:72:LEU:HB2	2.15	0.45
47:RE:858:ARG:HD2	47:RE:861:ILE:HD11	1.99	0.45
50:RJ:864:ASP:OD1	50:RJ:864:ASP:N	2.45	0.45
51:RK:109:PHE:HB3	51:RK:361:ASN:HB3	1.99	0.45
53:RP:1952:SER:O	53:RP:1952:SER:OG	2.34	0.45
55:RT:224:ILE:HG22	55:RT:233:ILE:HG23	1.98	0.45
1:3A:30:A:N6	43:5I:341:GLU:OE2	2.49	0.45
3:SA:1068:C:H2'	3:SA:1069:A:C8	2.52	0.45
20:3C:205:ARG:HA	22:3E:153:LYS:HZ3	1.81	0.45
22:3E:359:ILE:HD12	22:3E:398:LEU:HD13	1.99	0.45
24:3H:20:ILE:HD12	24:3H:53:ILE:HD12	1.99	0.45
24:3H:28:ALA:HB2	24:3H:33:LEU:HD23	1.99	0.45
25:A4:184:MET:HB2	25:A4:224:ARG:HA	1.99	0.45
30:AG:484:VAL:HG12	30:AG:485:ARG:H	1.82	0.45
30:AG:870:ASN:OD1	30:AG:870:ASN:N	2.50	0.45
32:B2:322:SER:HA	32:B2:325:ILE:HG12	1.98	0.45
33:B3:340:ILE:HG21	33:B3:355:LEU:HG	1.98	0.45
43:5I:93:LYS:HG2	43:5I:105:SER:HB2	1.98	0.45
43:5I:358:MET:HB3	54:RQ:890:VAL:HG23	1.99	0.45
43:5I:396:TYR:HE1	54:RQ:865:ILE:HG13	1.82	0.45
43:5I:409:GLU:HA	43:5I:412:ARG:HG2	1.98	0.45
43:5I:458:LYS:HE3	43:5I:458:LYS:HB2	1.81	0.45
47:RE:736:ASP:OD1	47:RE:821:TYR:OH	2.35	0.45
47:RE:1169:ILE:HG22	47:RE:1180:ASN:HD22	1.81	0.45
49:RH:189:VAL:HG13	49:RH:227:LEU:HD13	1.98	0.45
50:RJ:752:GLU:HA	50:RJ:755:LYS:HB2	1.99	0.45
53:RP:1822:SER:O	53:RP:1822:SER:OG	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:RP:1975:LYS:HB3	53:RP:1978:ALA:HB3	1.99	0.45
3:SA:-1:G:O6	43:5I:457:ARG:NE	2.40	0.45
3:SA:144:U:O4	7:SH:137:ARG:NH1	2.50	0.45
3:SA:890:C:H2'	3:SA:891:A:H8	1.82	0.45
20:3B:116:SER:OG	20:3B:120:GLU:OE1	2.35	0.45
20:3B:142:ARG:NH2	20:3B:182:SER:OG	2.47	0.45
23:3F:224:SER:OG	23:3F:227:GLU:OE1	2.35	0.45
25:A4:458:ASN:N	25:A4:458:ASN:OD1	2.50	0.45
28:AE:148:PHE:HA	28:AE:151:ILE:HG22	1.98	0.45
31:B1:83:ASN:H	31:B1:90:LEU:HD23	1.81	0.45
32:B2:152:GLY:HA3	32:B2:154:VAL:HG12	1.99	0.45
34:B8:532:MET:O	34:B8:541:LEU:HA	2.17	0.45
36:B6:24:PHE:HE1	36:B6:70:ARG:HD3	1.82	0.45
40:5F:174:ARG:NH2	50:RJ:1077:LEU:O	2.50	0.45
47:RE:434:LEU:O	47:RE:466:THR:OG1	2.34	0.45
47:RE:687:GLN:NE2	47:RE:694:ALA:O	2.40	0.45
48:RF:123:THR:O	48:RF:123:THR:OG1	2.35	0.45
48:RF:151:HIS:HD2	48:RF:154:GLU:H	1.65	0.45
51:RK:263:ASP:O	51:RK:266:SER:OG	2.31	0.45
3:SA:1677:C:H2'	3:SA:1678:A:C8	2.52	0.44
3:SA:1775:U:H3	3:SA:1786:G:H1	1.65	0.44
5:SF:89:VAL:HA	5:SF:99:PHE:O	2.18	0.44
5:SF:127:LYS:HD3	5:SF:127:LYS:HA	1.77	0.44
6:SG:97:LEU:HD21	6:SG:113:ILE:HD11	1.98	0.44
12:SO:60:VAL:HB	12:SO:66:ILE:HD12	1.98	0.44
20:3B:118:TYR:OH	20:3B:148:ARG:NH2	2.50	0.44
24:3G:12:ALA:HB1	24:3G:16:LEU:HG	1.99	0.44
31:B1:74:ASP:OD1	31:B1:74:ASP:N	2.38	0.44
35:BE:274:ILE:HG13	35:BE:286:VAL:HG23	1.99	0.44
35:BE:441:ARG:HA	35:BE:454:THR:HA	1.99	0.44
35:BE:495:ARG:HA	35:BE:495:ARG:HD3	1.75	0.44
41:5G:93:SER:OG	41:5G:94:ARG:N	2.50	0.44
43:5I:327:LYS:HE3	43:5I:349:GLN:HG2	1.99	0.44
43:5I:351:VAL:HA	43:5I:367:SER:HA	1.98	0.44
46:RD:1672:GLU:HG2	46:RD:1695:TRP:HH2	1.81	0.44
47:RE:337:LEU:HD12	47:RE:337:LEU:HA	1.85	0.44
53:RP:29:GLU:HB3	53:RP:32:ARG:HB2	1.98	0.44
53:RP:130:LYS:O	53:RP:134:ASN:ND2	2.50	0.44
55:RT:248:VAL:HA	55:RT:251:ILE:HG12	1.99	0.44
1:3A:331:A:H2'	1:3A:332:G:C8	2.52	0.44
2:5A:88:U:H2'	2:5A:89:C:C2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:SF:69:HIS:HE1	5:SF:94:ALA:HB3	1.82	0.44
10:SK:48:GLN:HA	10:SK:51:LYS:HG2	1.99	0.44
23:3F:450:ASP:OD1	23:3F:450:ASP:N	2.50	0.44
24:3G:34:LYS:HB3	24:3G:39:GLU:HG2	1.98	0.44
24:3H:23:VAL:HA	24:3H:26:GLN:HE21	1.82	0.44
26:A5:226:LEU:HD13	26:A5:273:LYS:HB2	2.00	0.44
30:AG:669:ASN:HA	30:AG:681:ILE:O	2.17	0.44
33:B3:76:LEU:HG	33:B3:87:ILE:HB	1.99	0.44
33:B3:417:TYR:HA	33:B3:424:PHE:HD1	1.81	0.44
33:B3:433:HIS:HD2	33:B3:436:ALA:HB2	1.83	0.44
33:B3:542:CYS:HB3	33:B3:547:LEU:HB2	1.99	0.44
35:BE:100:ILE:HD13	35:BE:149:TYR:HB2	1.98	0.44
36:B6:34:LYS:HE3	36:B6:34:LYS:HB2	1.86	0.44
37:5C:111:PHE:HD1	37:5C:131:LYS:HB2	1.81	0.44
47:RE:507:PHE:HA	47:RE:510:ILE:HG22	2.00	0.44
49:RH:76:LEU:HA	49:RH:79:LYS:HG2	1.99	0.44
50:RJ:251:ASP:HA	50:RJ:269:VAL:HG22	1.98	0.44
2:5A:69:U:H2'	2:5A:70:A:C4	2.52	0.44
5:SF:129:VAL:HG12	5:SF:139:VAL:HA	2.00	0.44
11:SM:14:GLN:HB3	11:SM:54:ILE:HG21	1.99	0.44
23:3F:416:GLY:HA3	23:3F:475:ILE:HD11	1.99	0.44
25:A4:231:VAL:HG22	25:A4:265:TRP:HZ2	1.82	0.44
25:A4:326:ARG:HH11	25:A4:365:SER:HA	1.83	0.44
26:A5:356:TYR:HB2	30:AG:472:TYR:HB2	2.00	0.44
29:AF:27:TRP:HH2	29:AF:268:MET:HB3	1.81	0.44
30:AG:206:LYS:HB3	30:AG:206:LYS:HE2	1.82	0.44
30:AG:401:GLN:HB3	30:AG:411:SER:HB2	1.99	0.44
31:B1:156:GLN:H	31:B1:203:GLN:HE21	1.65	0.44
31:B1:329:VAL:HG12	31:B1:339:LEU:HG	2.00	0.44
33:B3:622:ALA:HB3	33:B3:636:ASP:HB3	1.99	0.44
33:B3:705:SER:OG	33:B3:719:ILE:O	2.29	0.44
41:5G:173:ARG:HE	41:5G:173:ARG:HB2	1.67	0.44
43:5I:15:PRO:HB3	43:5I:20:GLN:HG2	1.99	0.44
43:5I:69:GLY:HA2	43:5I:370:GLY:HA2	1.98	0.44
47:RE:218:ASP:O	47:RE:223:ARG:NH2	2.51	0.44
47:RE:309:LEU:HD12	47:RE:310:PRO:HD2	1.99	0.44
47:RE:549:SER:HA	47:RE:552:ARG:HG2	1.99	0.44
50:RJ:856:THR:OG1	50:RJ:857:LEU:N	2.47	0.44
53:RP:1960:LEU:HD23	53:RP:1960:LEU:HA	1.87	0.44
55:RT:261:GLY:HA2	55:RT:264:ARG:HE	1.82	0.44
4:SC:132:ASP:HB2	4:SC:221:PRO:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:SF:116:ASP:OD1	5:SF:116:ASP:N	2.50	0.44
7:SH:48:TYR:HD1	7:SH:117:GLY:H	1.64	0.44
9:SJ:97:THR:OG1	9:SJ:98:LYS:N	2.50	0.44
14:SR:22:VAL:HG22	14:SR:65:ILE:HG12	2.00	0.44
20:3B:267:VAL:HG21	20:3B:298:ILE:HD13	1.99	0.44
20:3C:146:PRO:HG2	20:3C:156:MET:HE2	1.99	0.44
21:3D:155:GLY:O	21:3D:159:SER:OG	2.36	0.44
23:3F:263:TRP:CZ3	23:3F:270:PRO:HD3	2.36	0.44
29:AF:464:ALA:O	29:AF:468:GLU:HB2	2.17	0.44
31:B1:359:ARG:HA	31:B1:373:ASP:HA	1.98	0.44
32:B2:218:ILE:HG23	32:B2:259:ILE:HD12	1.99	0.44
33:B3:296:ILE:HB	33:B3:301:GLN:HB2	2.00	0.44
42:5H:564:LYS:HE3	42:5H:564:LYS:HB2	1.75	0.44
43:5I:278:VAL:HG11	43:5I:311:VAL:HG21	1.98	0.44
47:RE:151:SER:HA	47:RE:154:LYS:HB2	1.99	0.44
3:SA:1792:G:O2'	3:SA:1793:G:O4'	2.35	0.44
4:SC:51:SER:HA	4:SC:57:ALA:HB3	2.00	0.44
6:SG:26:ALA:N	14:SR:27:GLY:O	2.50	0.44
22:3E:377:ALA:HB3	22:3E:380:ARG:HD2	1.98	0.44
30:AG:427:LYS:O	30:AG:431:SER:CB	2.66	0.44
30:AG:725:ASN:H	30:AG:740:LYS:HE2	1.81	0.44
31:B1:60:ALA:HB3	31:B1:73:ILE:HB	2.00	0.44
31:B1:337:TYR:HD2	31:B1:340:LYS:HD3	1.82	0.44
32:B2:214:ASP:OD1	32:B2:214:ASP:N	2.50	0.44
32:B2:267:ASP:OD1	32:B2:267:ASP:N	2.44	0.44
33:B3:539:VAL:HG22	33:B3:550:THR:HA	1.99	0.44
33:B3:593:CYS:HB2	33:B3:620:LEU:HB2	2.00	0.44
33:B3:672:TYR:HB3	33:B3:681:ALA:HB2	1.99	0.44
35:BE:379:SER:OG	35:BE:382:LYS:O	2.36	0.44
39:5E:373:ILE:HD12	39:5E:373:ILE:HA	1.86	0.44
40:5F:91:LYS:HE2	40:5F:91:LYS:HB2	1.90	0.44
50:RJ:906:ASP:OD1	50:RJ:906:ASP:N	2.51	0.44
51:RK:154:LEU:HD13	51:RK:165:GLU:HB3	1.98	0.44
51:RK:245:LEU:O	51:RK:257:PHE:HA	2.18	0.44
53:RP:177:LEU:HD22	53:RP:180:LEU:HD12	1.99	0.44
3:SA:689:G:H2'	3:SA:690:G:C8	2.53	0.44
3:SA:1052:U:H5''	43:5I:449:LYS:HE2	2.00	0.44
3:SA:1666:U:H2'	3:SA:1667:A:H8	1.83	0.44
4:SC:106:THR:OG1	13:SP:116:GLU:OE1	2.31	0.44
6:SG:146:THR:OG1	6:SG:147:THR:N	2.48	0.44
7:SH:57:ASP:HB2	7:SH:105:ASP:HB3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:3D:21:LYS:HD2	21:3D:49:GLU:HB2	1.98	0.44
25:A4:451:PHE:HD1	25:A4:464:LYS:HA	1.82	0.44
26:A5:213:ASN:OD1	26:A5:213:ASN:N	2.50	0.44
26:A5:222:THR:HG21	35:BE:586:ASN:HD21	1.82	0.44
31:B1:274:LEU:HD11	31:B1:286:LEU:HB2	2.00	0.44
33:B3:283:LYS:HD2	33:B3:284:PRO:HD2	2.00	0.44
34:B8:133:ILE:HD13	35:BE:194:ARG:HH22	1.82	0.44
34:B8:229:PRO:HA	34:B8:230:PRO:HD3	1.92	0.44
34:B8:310:GLN:HB3	34:B8:326:LEU:HG	2.00	0.44
35:BE:629:ALA:HA	35:BE:645:HIS:HA	1.99	0.44
35:BE:869:THR:HG23	35:BE:915:VAL:HG11	1.98	0.44
37:5C:23:ARG:NH1	54:RQ:863:MET:SD	2.91	0.44
40:5F:120:MET:HG3	40:5F:160:TRP:CZ2	2.52	0.44
47:RE:585:MET:HB3	47:RE:610:PHE:HB2	2.00	0.44
47:RE:756:VAL:HA	47:RE:896:THR:HG21	1.99	0.44
47:RE:1167:LYS:HB2	47:RE:1167:LYS:HE3	1.82	0.44
51:RK:8:TYR:CG	51:RK:30:PRO:HG2	2.52	0.44
1:3A:73:A:H2'	1:3A:74:A:C8	2.52	0.44
2:5A:20:C:H2'	2:5A:21:A:C8	2.52	0.44
3:SA:482:U:H2'	3:SA:483:A:C8	2.53	0.44
3:SA:961:U:H2'	3:SA:962:C:C6	2.53	0.44
4:SC:180:THR:O	4:SC:183:GLN:N	2.51	0.44
15:SX:11:LEU:HD22	15:SX:74:VAL:HG13	1.99	0.44
15:SX:28:ARG:HB3	15:SX:60:LYS:HG2	2.00	0.44
20:3C:194:VAL:HB	20:3C:217:ILE:HD13	1.99	0.44
22:3E:319:ILE:HD12	22:3E:326:LEU:HD22	2.00	0.44
23:3F:252:VAL:HA	23:3F:261:ILE:O	2.17	0.44
25:A4:167:LEU:HD23	25:A4:183:LEU:HD13	2.00	0.44
30:AG:140:LYS:HE2	30:AG:157:PHE:HE1	1.82	0.44
31:B1:102:VAL:HG23	31:B1:113:LEU:HB3	1.99	0.44
31:B1:796:LEU:HD23	31:B1:796:LEU:HA	1.82	0.44
33:B3:158:SER:OG	33:B3:159:LYS:N	2.45	0.44
34:B8:263:LEU:HB2	34:B8:277:ILE:HD13	2.00	0.44
35:BE:175:THR:O	35:BE:175:THR:OG1	2.32	0.44
35:BE:254:LEU:HG	35:BE:266:VAL:HG12	1.99	0.44
35:BE:443:TRP:HA	35:BE:451:GLY:H	1.82	0.44
51:RK:141:MET:HG2	51:RK:300:TYR:CE2	2.50	0.44
51:RK:309:GLY:O	51:RK:353:THR:HA	2.18	0.44
53:RP:2080:MET:HE3	53:RP:2080:MET:HB3	1.87	0.44
55:RT:242:MET:HB3	55:RT:266:VAL:HG21	2.00	0.44
3:SA:58:U:OP1	3:SA:456:A:O2'	2.35	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:82:U:OP1	53:RP:15:ARG:NH1	2.48	0.44
3:SA:1160:A:H2'	3:SA:1161:C:C6	2.52	0.44
4:SC:164:ILE:HD11	4:SC:204:ILE:HB	2.00	0.44
20:3C:157:GLY:HA3	20:3C:304:LEU:HD11	2.00	0.44
25:A4:427:ASN:OD1	25:A4:427:ASN:N	2.48	0.44
25:A4:490:SER:OG	25:A4:494:ASP:N	2.50	0.44
30:AG:46:ILE:HG23	30:AG:53:LYS:HB2	2.00	0.44
33:B3:680:ASN:N	33:B3:680:ASN:OD1	2.50	0.44
34:B8:388:HIS:HB3	34:B8:392:GLY:H	1.82	0.44
35:BE:227:THR:OG1	35:BE:229:GLU:OE1	2.34	0.44
39:5E:322:LYS:HD2	39:5E:327:LYS:HB2	2.00	0.44
40:5F:57:LEU:HD22	40:5F:78:LEU:HD22	1.98	0.44
40:5F:114:ILE:HD13	40:5F:150:VAL:HG21	1.99	0.44
41:5G:166:SER:O	41:5G:256:MET:HA	2.18	0.44
46:RD:1607:ASN:HD22	46:RD:1610:LYS:NZ	2.16	0.44
47:RE:535:LYS:H	47:RE:538:ASN:HB3	1.82	0.44
47:RE:1176:LYS:HD3	47:RE:1178:ASP:HB2	2.00	0.44
51:RK:192:THR:HA	51:RK:224:ASN:O	2.17	0.44
56:X1:707:UNK:O	56:X1:711:UNK:CB	2.66	0.44
3:SA:329:G:H2'	3:SA:330:G:C8	2.52	0.44
3:SA:1682:U:O2'	3:SA:1683:C:O4'	2.31	0.44
3:SA:1773:C:H2'	3:SA:1774:G:H8	1.83	0.44
14:SR:117:LEU:HD23	14:SR:117:LEU:HA	1.85	0.44
18:Sc:34:ASP:O	18:Sc:79:PHE:HA	2.18	0.44
20:3C:231:ARG:HA	20:3C:260:PHE:HZ	1.83	0.44
23:3F:301:ASP:O	23:3F:303:LYS:NZ	2.44	0.44
25:A4:167:LEU:HD13	25:A4:167:LEU:HA	1.87	0.44
25:A4:431:CYS:HA	25:A4:441:VAL:O	2.18	0.44
25:A4:453:LEU:HD12	25:A4:460:LEU:HB3	2.00	0.44
29:AF:23:GLU:HG3	29:AF:267:PRO:HB2	1.99	0.44
31:B1:495:LYS:HA	31:B1:517:ASP:HA	2.00	0.44
31:B1:846:TYR:HE1	35:BE:909:LEU:HB3	1.82	0.44
32:B2:586:LYS:HG3	32:B2:587:MET:HB2	1.99	0.44
33:B3:239:VAL:HG12	47:RE:636:GLU:HG2	1.99	0.44
35:BE:713:LEU:HD11	35:BE:716:ILE:HG13	2.00	0.44
39:5E:325:SER:O	39:5E:325:SER:OG	2.36	0.44
47:RE:372:GLN:O	47:RE:516:SER:OG	2.33	0.44
51:RK:221:CYS:SG	51:RK:222:GLU:N	2.91	0.44
53:RP:1224:LEU:O	53:RP:1228:LEU:CB	2.66	0.44
3:SA:577:G:H5''	50:RJ:1047:PRO:HG2	2.00	0.43
3:SA:1140:G:H2'	3:SA:1141:G:H8	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:SP:61:MET:HB2	13:SP:104:ALA:HB2	2.00	0.43
16:SY:126:LYS:HG2	16:SY:131:SER:HA	2.00	0.43
20:3C:241:PHE:HA	20:3C:268:VAL:O	2.18	0.43
20:3C:252:ILE:HA	20:3C:252:ILE:HD12	1.75	0.43
23:3F:253:THR:HG22	23:3F:261:ILE:HB	2.00	0.43
25:A4:120:SER:OG	25:A4:121:THR:N	2.49	0.43
25:A4:157:SER:OG	25:A4:195:TRP:NE1	2.51	0.43
25:A4:346:PHE:HA	25:A4:360:SER:HA	2.00	0.43
30:AG:337:LEU:HD23	30:AG:337:LEU:HA	1.87	0.43
32:B2:186:ILE:O	32:B2:199:THR:HA	2.17	0.43
35:BE:25:SER:HB2	35:BE:657:ARG:HH21	1.82	0.43
35:BE:132:THR:OG1	35:BE:136:SER:OG	2.35	0.43
39:5E:497:ASN:OD1	39:5E:497:ASN:N	2.49	0.43
46:RD:1181:ASP:HA	46:RD:1191:GLY:HA2	2.00	0.43
47:RE:949:PHE:O	47:RE:960:LYS:NZ	2.51	0.43
48:RF:58:LEU:HD21	48:RF:124:ALA:H	1.83	0.43
49:RH:174:LYS:HD2	49:RH:174:LYS:HA	1.74	0.43
50:RJ:998:SER:O	50:RJ:998:SER:OG	2.33	0.43
54:RQ:309:ASP:N	54:RQ:309:ASP:OD1	2.48	0.43
4:SC:136:ARG:HE	4:SC:136:ARG:HB3	1.61	0.43
5:SF:125:LYS:HE2	5:SF:157:ASN:HD22	1.83	0.43
9:SJ:166:TYR:HB3	9:SJ:184:LEU:HD21	2.00	0.43
9:SJ:172:ARG:HB2	9:SJ:175:GLN:HB2	1.99	0.43
11:SM:124:THR:O	11:SM:124:THR:OG1	2.37	0.43
25:A4:420:LEU:HB3	25:A4:422:LEU:HD23	1.99	0.43
29:AF:211:HIS:CE1	29:AF:235:LYS:HD3	2.53	0.43
30:AG:140:LYS:HE2	30:AG:157:PHE:CE1	2.53	0.43
30:AG:294:LYS:HB2	30:AG:294:LYS:HE3	1.79	0.43
31:B1:355:PRO:HD2	31:B1:399:GLY:HA2	2.00	0.43
32:B2:676:SER:OG	32:B2:678:ASP:OD1	2.28	0.43
32:B2:912:TRP:CD2	33:B3:779:VAL:HG21	2.53	0.43
33:B3:362:LEU:HG	33:B3:384:TYR:HB2	1.99	0.43
33:B3:662:GLN:HA	33:B3:665:GLN:HE21	1.83	0.43
34:B8:541:LEU:HD22	34:B8:562:LEU:HD21	2.00	0.43
35:BE:544:ALA:HB3	35:BE:562:LEU:HD22	1.99	0.43
36:B6:273:ILE:HA	36:B6:276:VAL:HG22	2.00	0.43
37:5C:272:SER:OG	37:5C:301:TRP:NE1	2.51	0.43
41:5G:107:ILE:HD11	41:5G:254:PHE:HZ	1.82	0.43
45:5K:97:LEU:HD23	45:5K:128:LEU:HD11	2.00	0.43
46:RD:1522:ASN:HD22	46:RD:1556:ILE:HD11	1.83	0.43
46:RD:1686:LYS:HB2	46:RD:1686:LYS:HE3	1.71	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:RE:1159:ASN:OD1	47:RE:1159:ASN:N	2.47	0.43
49:RH:130:ILE:HD12	49:RH:131:PRO:HD2	1.99	0.43
50:RJ:102:GLN:NE2	50:RJ:358:MET:O	2.47	0.43
53:RP:180:LEU:HD13	53:RP:192:SER:HB3	2.00	0.43
53:RP:1777:LEU:HB3	53:RP:1867:THR:HG22	2.00	0.43
1:3A:47:G:H2'	1:3A:48:A:C8	2.52	0.43
21:3D:15:TYR:CZ	21:3D:78:LEU:HD12	2.53	0.43
21:3D:263:ILE:HG22	21:3D:265:GLU:HB2	2.01	0.43
23:3F:162:CYS:N	23:3F:525:GLN:OE1	2.47	0.43
29:AF:212:ASP:OD1	29:AF:235:LYS:NZ	2.52	0.43
29:AF:302:VAL:HA	29:AF:322:LEU:HG	2.00	0.43
30:AG:71:ASN:HB3	30:AG:73:LEU:HB2	1.99	0.43
32:B2:116:ASN:OD1	32:B2:116:ASN:N	2.50	0.43
33:B3:485:TYR:CZ	33:B3:514:THR:HB	2.53	0.43
35:BE:880:LEU:HA	35:BE:880:LEU:HD23	1.78	0.43
37:5C:114:TYR:N	37:5C:379:GLU:OE2	2.50	0.43
37:5C:295:ASP:OD1	37:5C:295:ASP:N	2.48	0.43
47:RE:498:MET:HE3	47:RE:510:ILE:HG13	1.98	0.43
47:RE:703:LYS:HD3	47:RE:1082:GLN:HG2	1.99	0.43
50:RJ:104:PRO:HA	50:RJ:117:PHE:O	2.18	0.43
2:5A:286:U:H2'	2:5A:287:G:H8	1.83	0.43
3:SA:327:U:H2'	3:SA:328:A:C8	2.53	0.43
3:SA:591:A:H2'	3:SA:592:A:C8	2.53	0.43
3:SA:688:G:H2'	3:SA:689:G:C8	2.53	0.43
21:3D:173:HIS:HD2	21:3D:295:LYS:HE2	1.82	0.43
23:3F:185:LEU:H	23:3F:202:THR:HB	1.82	0.43
23:3F:245:SER:OG	23:3F:247:ASP:OD1	2.26	0.43
25:A4:400:LYS:NZ	25:A4:401:ILE:O	2.52	0.43
30:AG:616:SER:OG	30:AG:620:SER:N	2.39	0.43
31:B1:60:ALA:HB1	31:B1:102:VAL:HG12	2.00	0.43
32:B2:185:MET:HA	32:B2:200:HIS:O	2.18	0.43
32:B2:231:LEU:HD12	32:B2:233:ILE:HD11	2.01	0.43
32:B2:633:CYS:HA	32:B2:639:VAL:HG12	2.00	0.43
33:B3:16:TYR:OH	33:B3:21:ALA:O	2.31	0.43
35:BE:822:ARG:O	35:BE:826:GLN:NE2	2.52	0.43
36:B6:106:ASP:OD1	36:B6:106:ASP:N	2.39	0.43
38:5D:29:GLU:OE1	50:RJ:1062:ARG:NH1	2.51	0.43
43:5I:146:LYS:HG2	43:5I:175:THR:HG23	2.00	0.43
47:RE:307:LYS:HG2	47:RE:312:ARG:HG3	2.00	0.43
47:RE:909:TYR:OH	47:RE:935:GLU:O	2.36	0.43
49:RH:227:LEU:HB3	49:RH:240:LYS:HE2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:RK:45:LEU:HG	51:RK:49:GLU:HG3	2.00	0.43
51:RK:171:ASP:N	51:RK:171:ASP:OD1	2.49	0.43
3:SA:454:U:H2'	3:SA:455:C:C2	2.53	0.43
3:SA:488:G:H2'	3:SA:489:C:C6	2.53	0.43
4:SC:32:ILE:HG12	4:SC:96:LEU:HD12	2.00	0.43
8:SI:36:ALA:HA	8:SI:39:ARG:HH21	1.83	0.43
9:SJ:103:GLN:NE2	9:SJ:166:TYR:OH	2.52	0.43
23:3F:160:ILE:HD13	23:3F:160:ILE:HA	1.93	0.43
26:A5:231:ASP:HB3	26:A5:249:GLU:HB2	2.01	0.43
28:AE:48:ILE:HG13	28:AE:120:TRP:HD1	1.84	0.43
28:AE:194:SER:HB3	35:BE:335:VAL:HG11	2.00	0.43
31:B1:604:TYR:HD1	31:B1:611:LEU:HA	1.84	0.43
32:B2:339:LYS:HE3	32:B2:358:SER:HA	2.01	0.43
32:B2:390:GLN:HG2	32:B2:394:VAL:HB	2.01	0.43
32:B2:551:LEU:HA	32:B2:575:PRO:HB3	2.00	0.43
34:B8:146:LEU:HD12	34:B8:163:ARG:HB3	1.99	0.43
36:B6:92:ILE:HA	36:B6:95:ILE:HD12	2.00	0.43
37:5C:412:ASP:OD1	43:5I:27:ASN:N	2.50	0.43
37:5C:454:LYS:HD3	37:5C:454:LYS:HA	1.78	0.43
49:RH:100:LEU:O	49:RH:106:LYS:NZ	2.39	0.43
50:RJ:175:ASP:OD1	50:RJ:175:ASP:N	2.50	0.43
53:RP:1709:ASP:OD1	53:RP:1803:ASN:ND2	2.51	0.43
54:RQ:334:PRO:HB3	54:RQ:340:GLU:HB3	2.00	0.43
3:SA:803:A:O2'	15:SX:107:SER:O	2.37	0.43
3:SA:898:A:H62	3:SA:914:G:H21	1.65	0.43
3:SA:933:A:OP1	4:SC:116:LYS:NZ	2.49	0.43
3:SA:1068:C:H2'	3:SA:1069:A:H8	1.83	0.43
4:SC:165:ARG:HA	4:SC:168:ILE:HG22	2.00	0.43
11:SM:78:THR:HA	11:SM:84:ILE:HG22	2.01	0.43
20:3C:259:MET:HE3	20:3C:259:MET:HB2	1.94	0.43
22:3E:214:ILE:HG22	22:3E:216:SER:H	1.83	0.43
25:A4:32:ILE:HG23	25:A4:751:GLU:HA	2.00	0.43
25:A4:83:ASN:HB3	25:A4:86:PHE:HE2	1.83	0.43
25:A4:500:LEU:HD12	25:A4:500:LEU:HA	1.90	0.43
28:AE:101:TYR:HE2	28:AE:118:THR:HG23	1.83	0.43
28:AE:134:MET:O	28:AE:138:SER:HB3	2.19	0.43
30:AG:144:VAL:HA	30:AG:153:ILE:HA	2.01	0.43
31:B1:280:THR:HA	31:B1:304:PRO:HB3	2.01	0.43
32:B2:624:LEU:HA	32:B2:625:PRO:HD3	1.85	0.43
37:5C:23:ARG:HH21	43:5I:30:PRO:HG3	1.83	0.43
37:5C:96:ASP:OD1	37:5C:96:ASP:N	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:5C:417:ASN:HB3	37:5C:420:GLU:HB2	2.00	0.43
37:5C:441:THR:O	37:5C:441:THR:OG1	2.33	0.43
39:5E:448:LEU:HA	39:5E:451:LEU:HD23	2.00	0.43
51:RK:14:SER:O	51:RK:14:SER:OG	2.35	0.43
3:SA:1474:G:N2	3:SA:1535:U:O4	2.40	0.43
4:SC:240:LYS:HD2	4:SC:240:LYS:HA	1.75	0.43
10:SK:41:GLU:HA	10:SK:44:ARG:HE	1.82	0.43
10:SK:124:HIS:HA	10:SK:127:VAL:HG12	2.00	0.43
14:SR:121:SER:OG	14:SR:122:ARG:N	2.52	0.43
18:Sc:18:LYS:HB3	18:Sc:18:LYS:HE2	1.87	0.43
22:3E:193:PRO:HB2	22:3E:243:MET:HE3	2.01	0.43
25:A4:433:LEU:HB2	25:A4:440:LEU:HD12	2.01	0.43
29:AF:266:SER:OG	29:AF:268:MET:O	2.36	0.43
30:AG:90:LYS:HE2	30:AG:144:VAL:HB	2.00	0.43
30:AG:271:LEU:HD23	30:AG:285:LEU:HD21	1.99	0.43
31:B1:190:HIS:HD2	31:B1:210:SER:HB2	1.84	0.43
31:B1:621:MET:N	31:B1:621:MET:SD	2.91	0.43
32:B2:415:LYS:HB2	32:B2:417:TRP:HE1	1.83	0.43
32:B2:746:LEU:HD12	32:B2:750:GLU:HG3	2.00	0.43
43:5I:265:ASN:HD22	43:5I:309:MET:HA	1.84	0.43
45:5K:69:THR:HG23	45:5K:102:VAL:HG22	2.01	0.43
47:RE:1018:LYS:HD3	47:RE:1018:LYS:HA	1.68	0.43
47:RE:1205:LYS:HA	47:RE:1205:LYS:HD2	1.78	0.43
50:RJ:863:THR:HB	50:RJ:866:ARG:HA	2.00	0.43
51:RK:95:PRO:HG3	51:RK:124:SER:HB3	2.00	0.43
3:SA:1630:U:O4	39:5E:510:LYS:NZ	2.40	0.43
11:SM:77:SER:HB3	11:SM:85:VAL:HB	1.99	0.43
20:3B:135:PRO:HA	20:3B:136:PRO:HD3	1.86	0.43
21:3D:209:LEU:HD22	21:3D:250:ARG:HH12	1.84	0.43
21:3D:281:LEU:HD12	21:3D:281:LEU:HA	1.87	0.43
30:AG:670:LEU:HB3	30:AG:681:ILE:HB	2.01	0.43
31:B1:203:GLN:HB2	56:X1:1503:UNK:HA	2.01	0.43
31:B1:330:TYR:OH	31:B1:335:GLU:OE2	2.33	0.43
32:B2:163:LYS:HD3	39:5E:522:ARG:HH21	1.83	0.43
34:B8:546:LEU:HA	34:B8:549:CYS:H	1.82	0.43
35:BE:257:ARG:NE	35:BE:259:ASP:OD1	2.51	0.43
37:5C:321:ASN:ND2	37:5C:379:GLU:O	2.52	0.43
43:5I:399:LYS:HG2	54:RQ:879:ILE:HG22	2.01	0.43
47:RE:1202:CYS:SG	47:RE:1203:ASN:N	2.88	0.43
50:RJ:256:GLU:O	50:RJ:260:THR:OG1	2.31	0.43
50:RJ:1145:MET:HE3	50:RJ:1145:MET:HB2	1.80	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3A:206:C:O2	1:3A:243:U:N3	2.52	0.43
2:5A:309:A:OP2	22:3E:426:ALA:N	2.45	0.43
3:SA:560:U:H2'	3:SA:561:G:H8	1.84	0.43
3:SA:891:A:H2'	3:SA:892:A:H8	1.83	0.43
3:SA:1049:U:H5''	18:Sc:70:LYS:HG3	2.00	0.43
3:SA:1615:C:N4	6:SG:80:LYS:O	2.52	0.43
5:SF:184:THR:OG1	5:SF:224:ASN:O	2.36	0.43
9:SJ:84:HIS:ND1	9:SJ:87:ASN:O	2.39	0.43
14:SR:46:PHE:HA	14:SR:49:TYR:HB2	1.99	0.43
26:A5:4:PRO:HD2	26:A5:306:LEU:HD22	2.01	0.43
28:AE:225:SER:OG	28:AE:226:ASN:N	2.52	0.43
30:AG:360:MET:HE2	30:AG:360:MET:HB3	1.73	0.43
31:B1:212:ASP:OD1	31:B1:212:ASP:N	2.52	0.43
32:B2:373:ASP:N	32:B2:373:ASP:OD1	2.48	0.43
33:B3:679:THR:HG21	33:B3:723:GLU:HB2	2.00	0.43
35:BE:423:ARG:HD3	35:BE:427:TRP:CZ2	2.54	0.43
35:BE:564:ASP:OD1	35:BE:564:ASP:N	2.47	0.43
37:5C:330:LEU:O	37:5C:340:LEU:HA	2.18	0.43
43:5I:290:ASP:HB2	43:5I:298:LEU:HD23	1.99	0.43
46:RD:1511:ALA:HA	46:RD:1514:LEU:HD12	2.00	0.43
47:RE:1144:ASP:OD1	47:RE:1144:ASP:N	2.51	0.43
50:RJ:68:PRO:HB3	50:RJ:274:TYR:HE1	1.83	0.43
50:RJ:964:ALA:HB3	50:RJ:976:ILE:HD11	2.00	0.43
2:5A:68:U:H3'	30:AG:426:ARG:HH12	1.84	0.43
3:SA:89:G:H21	3:SA:452:A:H5''	1.84	0.43
3:SA:953:G:H2'	3:SA:954:G:C8	2.52	0.43
3:SA:1482:C:O2'	14:SR:72:GLY:O	2.32	0.43
3:SA:1615:C:OP1	6:SG:81:ARG:NH2	2.49	0.43
3:SA:1666:U:H2'	3:SA:1667:A:C8	2.53	0.43
17:SZ:8:ARG:NH2	23:3F:316:GLU:OE1	2.48	0.43
23:3F:168:ASN:H	23:3F:174:GLU:HA	1.84	0.43
25:A4:106:ASN:OD1	25:A4:106:ASN:N	2.51	0.43
25:A4:390:LEU:HB3	25:A4:403:THR:HG22	2.01	0.43
28:AE:102:LEU:HD23	28:AE:102:LEU:HA	1.89	0.43
28:AE:135:LEU:HD21	28:AE:151:ILE:HD11	2.01	0.43
30:AG:75:SER:O	30:AG:79:LEU:HB2	2.18	0.43
32:B2:549:SER:HA	32:B2:555:VAL:HG22	2.00	0.43
32:B2:630:PHE:O	32:B2:641:TYR:HA	2.19	0.43
37:5C:213:TRP:HZ3	37:5C:227:GLU:HB3	1.84	0.43
37:5C:238:MET:HE2	37:5C:247:MET:HE2	2.01	0.43
43:5I:50:LEU:HD23	43:5I:50:LEU:HA	1.86	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:5I:179:GLU:HB3	53:RP:1783:LEU:HD23	2.01	0.43
47:RE:260:ASP:HB3	47:RE:378:ASN:HA	2.01	0.43
47:RE:270:ILE:HB	47:RE:292:ILE:HG13	2.00	0.43
47:RE:580:TYR:HB2	47:RE:618:ILE:HD11	2.01	0.43
47:RE:871:ARG:HB3	47:RE:874:LEU:HD12	2.01	0.43
50:RJ:69:PRO:HD2	50:RJ:274:TYR:CE1	2.54	0.43
50:RJ:629:ASP:HA	50:RJ:632:LYS:HB2	2.01	0.43
51:RK:243:ILE:HG23	51:RK:275:VAL:HG21	1.99	0.43
3:SA:844:A:H2'	3:SA:845:G:C8	2.53	0.42
3:SA:895:G:H21	13:SP:38:THR:HG21	1.84	0.42
20:3B:241:PHE:HE2	20:3B:243:ASP:HB2	1.85	0.42
25:A4:135:ARG:NH1	25:A4:175:GLY:O	2.47	0.42
25:A4:338:ALA:HB1	25:A4:361:LEU:HD11	2.00	0.42
25:A4:645:ARG:NE	25:A4:656:ARG:HH21	2.17	0.42
26:A5:214:VAL:HG23	26:A5:224:CYS:H	1.83	0.42
26:A5:548:ASP:HA	26:A5:551:ILE:HG22	2.01	0.42
29:AF:252:ASN:HB2	29:AF:278:ASP:HB3	2.01	0.42
30:AG:52:ILE:HB	30:AG:66:LEU:HB2	2.00	0.42
30:AG:303:LEU:HD22	30:AG:312:LEU:HD11	2.00	0.42
30:AG:536:ASP:OD1	30:AG:536:ASP:N	2.50	0.42
31:B1:109:ARG:HG3	31:B1:110:LEU:HG	2.01	0.42
31:B1:743:PHE:HZ	31:B1:778:ILE:HD13	1.84	0.42
32:B2:525:ASP:OD1	32:B2:525:ASP:N	2.50	0.42
32:B2:821:LEU:HB2	32:B2:860:ILE:HD11	2.01	0.42
34:B8:485:GLY:HA3	34:B8:518:ILE:HD11	2.01	0.42
36:B6:50:ILE:HD13	36:B6:50:ILE:HA	1.84	0.42
41:5G:153:THR:HG21	41:5G:266:LEU:HD13	2.01	0.42
41:5G:200:LYS:HA	41:5G:203:VAL:HG12	2.00	0.42
43:5I:146:LYS:HB3	43:5I:148:TRP:NE1	2.34	0.42
43:5I:264:THR:HA	43:5I:281:ASN:HB3	2.01	0.42
47:RE:115:LYS:HD3	47:RE:117:LYS:HE3	2.01	0.42
47:RE:338:SER:O	47:RE:342:HIS:ND1	2.51	0.42
50:RJ:940:LYS:HB3	50:RJ:947:PHE:HB2	2.01	0.42
51:RK:185:ARG:HD2	51:RK:312:ARG:HH12	1.82	0.42
51:RK:244:THR:O	51:RK:244:THR:OG1	2.36	0.42
51:RK:249:SER:HB2	51:RK:251:GLN:HE22	1.84	0.42
53:RP:88:PHE:HZ	53:RP:128:ALA:HB2	1.83	0.42
53:RP:1718:VAL:HA	53:RP:1721:ILE:HD12	2.01	0.42
53:RP:1797:LEU:HD23	53:RP:1797:LEU:HA	1.84	0.42
1:3A:47:G:H2'	1:3A:48:A:H8	1.84	0.42
1:3A:204:U:H3'	1:3A:205:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:233:C:O2	3:SA:234:G:N2	2.52	0.42
3:SA:429:G:H21	50:RJ:225:ARG:NH1	2.16	0.42
3:SA:1112:G:O6	50:RJ:1158:LYS:NZ	2.52	0.42
3:SA:1693:A:H3'	3:SA:1694:A:C8	2.54	0.42
20:3B:198:GLU:OE2	20:3B:199:PHE:N	2.52	0.42
21:3D:268:MET:HE2	21:3D:268:MET:HB3	1.76	0.42
25:A4:58:ASN:OD1	25:A4:58:ASN:N	2.42	0.42
26:A5:46:TRP:HE1	26:A5:48:GLU:HG3	1.83	0.42
28:AE:11:VAL:HA	28:AE:14:ASN:HB2	2.01	0.42
30:AG:423:LYS:O	30:AG:427:LYS:HB2	2.19	0.42
30:AG:674:THR:OG1	30:AG:675:ARG:N	2.49	0.42
31:B1:190:HIS:CD2	31:B1:210:SER:HB2	2.54	0.42
33:B3:228:LYS:HA	33:B3:228:LYS:HD3	1.80	0.42
33:B3:303:PHE:HE1	33:B3:313:LEU:HD12	1.84	0.42
34:B8:175:PRO:HD2	35:BE:217:VAL:HG23	2.00	0.42
36:B6:78:LYS:HA	36:B6:78:LYS:HD3	1.80	0.42
36:B6:114:LEU:O	36:B6:118:LYS:HG2	2.19	0.42
36:B6:319:TYR:O	36:B6:323:PHE:CB	2.62	0.42
47:RE:254:LEU:HD11	47:RE:268:LEU:HB3	2.01	0.42
47:RE:593:PRO:HD2	47:RE:596:LYS:HB2	2.00	0.42
47:RE:633:ALA:HA	47:RE:664:THR:HA	2.00	0.42
49:RH:119:GLY:O	49:RH:165:ASN:ND2	2.47	0.42
50:RJ:1049:ASN:HA	50:RJ:1050:PRO:HD3	1.93	0.42
51:RK:255:SER:O	51:RK:293:GLN:NE2	2.50	0.42
9:SJ:187:GLU:H	11:SM:30:ARG:NE	2.17	0.42
21:3D:195:VAL:HG12	21:3D:216:PHE:HE2	1.84	0.42
21:3D:283:ASP:OD1	21:3D:286:ARG:NH1	2.51	0.42
22:3E:113:THR:HA	22:3E:116:ILE:HG12	2.01	0.42
23:3F:156:ASN:HD22	23:3F:544:ALA:HB1	1.84	0.42
25:A4:31:MET:HG2	25:A4:752:LEU:HD12	2.01	0.42
30:AG:347:LEU:HD22	30:AG:355:SER:HB3	2.00	0.42
30:AG:412:ASN:ND2	30:AG:416:SER:O	2.52	0.42
30:AG:878:ASN:OD1	30:AG:878:ASN:N	2.51	0.42
32:B2:436:CYS:HB3	32:B2:447:LEU:HD12	2.00	0.42
32:B2:468:ILE:HD11	32:B2:522:LEU:HB2	2.01	0.42
40:5F:71:ARG:NH1	40:5F:75:GLU:OE2	2.52	0.42
46:RD:1592:LEU:HB3	46:RD:1597:GLU:HB2	2.00	0.42
47:RE:853:ARG:CZ	47:RE:888:LYS:HE2	2.49	0.42
48:RF:23:HIS:HD2	48:RF:26:LEU:HG	1.84	0.42
53:RP:2021:ASP:OD1	53:RP:2024:ARG:NH1	2.53	0.42
55:RT:141:THR:OG1	55:RT:142:ASN:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3A:50:U:O2'	2:5A:467:A:N6	2.46	0.42
3:SA:789:A:H61	10:SK:71:PHE:HB3	1.85	0.42
3:SA:1154:G:H2'	3:SA:1155:G:H8	1.84	0.42
3:SA:1695:G:H2'	3:SA:1696:G:H8	1.84	0.42
3:SA:1751:C:H2'	3:SA:1752:U:H6	1.83	0.42
10:SK:127:VAL:O	10:SK:131:GLN:NE2	2.52	0.42
23:3F:481:ILE:HD11	23:3F:526:VAL:HG21	2.02	0.42
29:AF:139:ILE:HG12	29:AF:151:LEU:HD22	2.01	0.42
30:AG:311:TYR:HD2	30:AG:323:LEU:HD12	1.83	0.42
31:B1:9:ASN:OD1	31:B1:10:LEU:N	2.53	0.42
33:B3:4:LYS:HA	33:B3:649:GLU:HG3	2.01	0.42
33:B3:126:ILE:HD11	33:B3:147:ILE:HG12	2.02	0.42
35:BE:343:LEU:HD12	35:BE:343:LEU:HA	1.87	0.42
35:BE:387:GLN:HE21	35:BE:448:LYS:HD2	1.84	0.42
39:5E:369:ILE:HD11	41:5G:190:ILE:HD13	2.02	0.42
39:5E:507:ILE:HD11	39:5E:528:LEU:HD13	2.01	0.42
40:5F:61:LEU:HD23	40:5F:61:LEU:HA	1.87	0.42
40:5F:114:ILE:HA	40:5F:117:ARG:HB3	2.01	0.42
43:5I:270:ASN:HB2	43:5I:276:ASN:O	2.19	0.42
47:RE:282:ASP:N	47:RE:282:ASP:OD1	2.50	0.42
1:3A:331:A:O2'	22:3E:404:ARG:NH2	2.52	0.42
2:5A:66:C:H2'	2:5A:67:G:H8	1.84	0.42
3:SA:914:G:H4'	3:SA:915:A:H8	1.84	0.42
3:SA:922:G:H2'	3:SA:923:A:C8	2.54	0.42
3:SA:1578:U:H2'	3:SA:1579:U:C6	2.54	0.42
3:SA:1796:C:H1'	3:SA:1797:A:H5'	2.01	0.42
5:SF:67:GLN:HB3	5:SF:69:HIS:HB2	2.02	0.42
8:SI:64:VAL:HB	8:SI:67:LEU:HD22	2.01	0.42
12:SO:45:LEU:HB2	12:SO:50:ILE:CG2	2.49	0.42
16:SY:114:LYS:HB2	16:SY:114:LYS:HE3	1.85	0.42
25:A4:568:ASN:OD1	25:A4:568:ASN:N	2.53	0.42
25:A4:624:LYS:HD3	25:A4:627:LYS:HD2	2.01	0.42
30:AG:224:SER:HA	30:AG:240:PRO:HA	2.01	0.42
31:B1:54:HIS:NE2	31:B1:72:SER:OG	2.45	0.42
33:B3:279:LYS:NZ	33:B3:326:THR:O	2.48	0.42
33:B3:625:THR:HG22	33:B3:633:VAL:HG23	2.02	0.42
35:BE:171:GLN:HE22	35:BE:213:GLU:HA	1.84	0.42
37:5C:298:MET:HE2	37:5C:298:MET:HB3	1.95	0.42
43:5I:145:VAL:HB	43:5I:176:PHE:HB2	2.01	0.42
43:5I:185:ILE:HA	43:5I:185:ILE:HD13	1.84	0.42
50:RJ:824:ILE:HD13	50:RJ:926:ILE:HG12	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:RK:154:LEU:HD11	51:RK:167:HIS:HB2	2.00	0.42
53:RP:1942:LEU:HD21	53:RP:1978:ALA:HB1	2.02	0.42
3:SA:75:U:N3	3:SA:76:A:N3	2.47	0.42
3:SA:958:U:H2'	12:SO:14:SER:HB3	2.02	0.42
3:SA:1767:G:OP2	55:RT:200:ARG:NH1	2.53	0.42
6:SG:222:LYS:HE3	6:SG:222:LYS:HB3	1.84	0.42
10:SK:45:ILE:HD11	10:SK:105:LEU:HD23	2.02	0.42
12:SO:45:LEU:HB2	12:SO:50:ILE:HG22	2.01	0.42
18:Sc:48:SER:OG	18:Sc:49:HIS:ND1	2.35	0.42
20:3C:188:VAL:HG22	20:3C:192:GLY:HA3	2.01	0.42
23:3F:353:ASP:OD1	23:3F:353:ASP:N	2.49	0.42
24:3H:20:ILE:HG22	24:3H:117:VAL:HG13	2.01	0.42
24:3H:54:MET:O	24:3H:80:PHE:HA	2.19	0.42
26:A5:148:LEU:HD22	26:A5:165:VAL:HG12	2.01	0.42
28:AE:280:GLU:HB3	28:AE:319:ILE:HD12	2.01	0.42
30:AG:530:LYS:HB2	30:AG:543:LEU:HD11	2.02	0.42
32:B2:52:TRP:CD1	32:B2:59:LEU:HA	2.54	0.42
32:B2:180:THR:HB	32:B2:186:ILE:HD13	2.01	0.42
41:5G:107:ILE:HD13	41:5G:107:ILE:HA	1.87	0.42
47:RE:590:SER:O	47:RE:590:SER:OG	2.31	0.42
1:3A:8:U:H2'	1:3A:9:A:C8	2.54	0.42
3:SA:174:U:O4	3:SA:266:A:N7	2.53	0.42
3:SA:1736:G:H2'	3:SA:1737:G:C8	2.55	0.42
6:SG:92:ARG:NH1	6:SG:169:ASN:OD1	2.45	0.42
7:SH:121:LEU:HD23	7:SH:121:LEU:HA	1.85	0.42
8:SI:7:LYS:HG3	8:SI:41:LEU:HD21	2.02	0.42
8:SI:159:VAL:HA	8:SI:162:ILE:HB	2.02	0.42
22:3E:427:TYR:OH	22:3E:432:ASP:OD1	2.35	0.42
25:A4:322:ASN:O	30:AG:329:ASN:ND2	2.53	0.42
25:A4:580:LYS:HG3	25:A4:596:MET:HB2	2.01	0.42
26:A5:166:ALA:HB2	26:A5:170:ILE:HG23	2.01	0.42
28:AE:44:ASP:OD1	28:AE:45:TYR:N	2.49	0.42
28:AE:236:PRO:HA	34:B8:212:LEU:HD21	2.01	0.42
30:AG:408:THR:HG23	30:AG:411:SER:H	1.84	0.42
30:AG:669:ASN:OD1	30:AG:669:ASN:N	2.53	0.42
31:B1:273:ARG:HD2	31:B1:290:PRO:HG2	2.02	0.42
31:B1:849:LEU:HG	35:BE:897:HIS:HB2	2.02	0.42
32:B2:411:ASN:ND2	32:B2:413:SER:OG	2.53	0.42
33:B3:457:ALA:HB2	33:B3:497:LEU:HD22	2.01	0.42
36:B6:148:ILE:HD13	36:B6:148:ILE:HA	1.88	0.42
40:5F:64:LEU:HD23	40:5F:64:LEU:HA	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5H:544:ILE:HD13	50:RJ:834:TRP:CD2	2.55	0.42
43:5I:285:ASN:N	43:5I:285:ASN:OD1	2.50	0.42
47:RE:899:LEU:HA	47:RE:902:ILE:HG22	2.02	0.42
47:RE:920:LEU:HG	47:RE:925:LEU:HB2	2.01	0.42
47:RE:1187:LYS:HA	47:RE:1187:LYS:HD3	1.80	0.42
50:RJ:302:GLU:HB2	50:RJ:790:ARG:HG2	2.01	0.42
50:RJ:798:MET:HB2	50:RJ:798:MET:HE3	1.78	0.42
50:RJ:827:ALA:HA	50:RJ:920:GLU:H	1.85	0.42
51:RK:55:LEU:HD12	51:RK:88:HIS:CD2	2.54	0.42
53:RP:2069:GLN:H	53:RP:2069:GLN:HG3	1.71	0.42
3:SA:890:C:H2'	3:SA:891:A:C8	2.55	0.42
3:SA:1146:G:H2'	3:SA:1147:A:C8	2.55	0.42
3:SA:1752:U:H2'	3:SA:1753:A:C8	2.55	0.42
4:SC:124:ASN:OD1	4:SC:124:ASN:N	2.51	0.42
5:SF:105:VAL:HG13	5:SF:245:LYS:HB3	2.02	0.42
10:SK:123:HIS:CD2	42:5H:566:ARG:HH21	2.38	0.42
11:SM:40:LEU:HD21	11:SM:70:ILE:HG12	2.02	0.42
13:SP:70:LYS:HA	13:SP:70:LYS:HD2	1.79	0.42
25:A4:167:LEU:HD11	25:A4:195:TRP:HZ2	1.85	0.42
25:A4:332:ASP:HB2	25:A4:352:VAL:HG12	2.02	0.42
26:A5:120:ILE:HD11	26:A5:148:LEU:HB3	2.00	0.42
30:AG:86:GLU:OE2	30:AG:111:THR:OG1	2.31	0.42
30:AG:408:THR:HG23	30:AG:410:ASN:H	1.85	0.42
30:AG:891:VAL:HA	30:AG:894:VAL:HG12	2.01	0.42
33:B3:407:SER:OG	33:B3:409:ASP:OD1	2.28	0.42
34:B8:284:LEU:HD21	34:B8:287:SER:HB3	2.01	0.42
34:B8:526:ASP:OD1	34:B8:526:ASP:N	2.46	0.42
35:BE:354:SER:O	35:BE:631:ASN:ND2	2.52	0.42
36:B6:75:LEU:HB3	36:B6:77:VAL:HG22	2.02	0.42
37:5C:463:ALA:HA	37:5C:466:LEU:HD23	2.01	0.42
45:5K:70:ASN:HD21	45:5K:157:ASP:HB2	1.85	0.42
45:5K:139:ASP:HA	45:5K:142:VAL:HG12	2.02	0.42
47:RE:524:ASP:HB3	47:RE:618:ILE:HA	2.02	0.42
50:RJ:879:THR:OG1	50:RJ:880:TYR:N	2.53	0.42
50:RJ:1104:GLY:H	50:RJ:1107:LYS:HG2	1.84	0.42
51:RK:319:ASP:N	51:RK:319:ASP:OD1	2.52	0.42
53:RP:98:HIS:CG	53:RP:135:LEU:HD11	2.55	0.42
3:SA:314:C:H42	3:SA:354:C:H42	1.68	0.42
3:SA:1465:C:O2	41:5G:146:ARG:NH2	2.53	0.42
4:SC:106:THR:HG23	4:SC:109:LYS:H	1.85	0.42
5:SF:155:LYS:HA	5:SF:155:LYS:HD3	1.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:SP:83:ILE:HD11	13:SP:102:LEU:HD13	2.02	0.42
22:3E:322:ALA:H	22:3E:340:GLY:HA2	1.85	0.42
25:A4:649:TRP:CD1	25:A4:744:VAL:HB	2.55	0.42
28:AE:328:ASP:O	28:AE:331:SER:OG	2.36	0.42
28:AE:390:LEU:HA	28:AE:393:ILE:HG22	2.02	0.42
29:AF:458:ILE:HD12	29:AF:458:ILE:HA	1.83	0.42
30:AG:615:TRP:CD1	30:AG:622:ILE:HG12	2.55	0.42
31:B1:480:SER:OG	31:B1:523:MET:SD	2.69	0.42
31:B1:718:ASP:O	35:BE:579:ARG:NH1	2.47	0.42
32:B2:799:LYS:HE2	32:B2:799:LYS:HB2	1.86	0.42
32:B2:836:ILE:HA	32:B2:839:VAL:HG12	2.01	0.42
34:B8:534:SER:OG	34:B8:535:ARG:N	2.53	0.42
35:BE:501:HIS:CD2	35:BE:521:GLY:HA3	2.55	0.42
35:BE:513:MET:HB3	35:BE:513:MET:HE2	1.82	0.42
47:RE:329:THR:O	47:RE:333:ASN:ND2	2.52	0.42
47:RE:413:LEU:HG	47:RE:415:GLY:H	1.85	0.42
47:RE:495:THR:HA	47:RE:498:MET:HG2	2.01	0.42
47:RE:808:LEU:HD12	47:RE:825:PHE:CZ	2.55	0.42
48:RF:219:ASN:OD1	48:RF:219:ASN:N	2.53	0.42
49:RH:105:ASN:HD22	49:RH:110:LEU:HD23	1.85	0.42
50:RJ:42:THR:OG1	50:RJ:43:MET:N	2.53	0.42
50:RJ:97:THR:OG1	50:RJ:98:LEU:N	2.51	0.42
50:RJ:247:ASP:OD1	50:RJ:247:ASP:N	2.52	0.42
51:RK:228:ASP:OD2	51:RK:230:TRP:NE1	2.43	0.42
55:RT:255:PRO:HB2	55:RT:258:LYS:HD3	2.01	0.42
2:5A:84:G:O2'	30:AG:295:TRP:O	2.36	0.42
3:SA:34:G:C6	3:SA:475:A:C6	3.08	0.42
3:SA:333:A:OP1	9:SJ:49:ARG:NH1	2.52	0.42
3:SA:939:A:H2'	3:SA:940:A:C8	2.55	0.42
3:SA:1112:G:H2'	3:SA:1113:A:H8	1.85	0.42
3:SA:1150:G:H2'	3:SA:1151:A:C8	2.55	0.42
16:SY:77:ILE:HB	50:RJ:54:LEU:HD13	2.02	0.42
20:3B:229:LYS:HB3	20:3B:229:LYS:HE2	1.66	0.42
24:3H:20:ILE:HA	24:3H:23:VAL:HG12	2.01	0.42
24:3H:53:ILE:HG22	24:3H:87:LEU:HD11	2.02	0.42
24:3H:68:PRO:HA	24:3H:71:CYS:SG	2.60	0.42
25:A4:183:LEU:HG	25:A4:223:GLY:HA2	2.01	0.42
25:A4:581:SER:HA	25:A4:594:PHE:O	2.20	0.42
26:A5:233:LYS:HD3	26:A5:233:LYS:HA	1.85	0.42
28:AE:151:ILE:O	28:AE:155:ILE:HB	2.20	0.42
30:AG:559:LYS:HD2	30:AG:559:LYS:HA	1.75	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:B3:686:MET:HE3	33:B3:735:GLN:HB3	2.01	0.42
37:5C:39:ASP:HB3	37:5C:42:LEU:HB3	2.01	0.42
39:5E:432:LYS:HD2	39:5E:432:LYS:HA	1.81	0.42
46:RD:1513:LYS:HA	46:RD:1516:ILE:HG22	2.02	0.42
46:RD:1549:ILE:HD13	46:RD:1549:ILE:HA	1.91	0.42
47:RE:1224:ALA:HB1	47:RE:1231:VAL:HG11	2.02	0.42
49:RH:90:ASP:OD1	49:RH:90:ASP:N	2.49	0.42
53:RP:1003:ILE:O	53:RP:1005:ASN:N	2.53	0.42
53:RP:1808:SER:O	53:RP:1808:SER:OG	2.33	0.42
3:SA:1731:A:H3'	3:SA:1732:A:C8	2.55	0.41
4:SC:141:ALA:HB2	4:SC:210:ILE:HG23	2.01	0.41
20:3B:202:ARG:HB3	24:3H:69:LEU:HD12	2.01	0.41
21:3D:247:ILE:HG12	21:3D:250:ARG:HH21	1.85	0.41
23:3F:194:LEU:O	23:3F:215:LYS:HA	2.20	0.41
23:3F:488:ILE:HG22	23:3F:498:VAL:HG22	2.02	0.41
25:A4:150:ASN:HD22	25:A4:155:LYS:HB2	1.84	0.41
25:A4:334:ARG:H	25:A4:351:GLY:HA2	1.84	0.41
29:AF:165:THR:N	29:AF:202:GLY:O	2.53	0.41
30:AG:506:TRP:HA	30:AG:532:TRP:O	2.18	0.41
30:AG:577:ASP:OD1	30:AG:578:ASN:N	2.53	0.41
31:B1:44:ASN:O	31:B1:46:LYS:N	2.53	0.41
32:B2:413:SER:OG	32:B2:413:SER:O	2.33	0.41
33:B3:258:ILE:HG23	33:B3:269:LEU:HD12	2.02	0.41
36:B6:277:CYS:O	36:B6:281:LEU:HB2	2.20	0.41
41:5G:106:GLU:OE1	41:5G:172:MET:HB2	2.20	0.41
47:RE:781:ASP:HA	47:RE:851:LYS:HB2	2.01	0.41
50:RJ:980:LEU:HD23	50:RJ:980:LEU:HA	1.88	0.41
53:RP:2027:MET:HE2	53:RP:2027:MET:HB3	1.92	0.41
3:SA:1712:A:H8	3:SA:1713:G:H4'	1.86	0.41
3:SA:1769:U:O2	55:RT:213:LYS:NZ	2.48	0.41
3:SA:1773:C:H2'	3:SA:1774:G:C8	2.55	0.41
8:SI:140:VAL:HA	8:SI:149:ILE:O	2.20	0.41
10:SK:154:LYS:HD3	23:3F:322:HIS:CE1	2.55	0.41
25:A4:345:ASP:N	25:A4:345:ASP:OD1	2.52	0.41
28:AE:19:ALA:HB3	28:AE:25:ARG:HH11	1.86	0.41
28:AE:363:LEU:HD23	28:AE:403:LEU:HD21	2.02	0.41
29:AF:34:GLN:OE1	29:AF:71:ARG:NH1	2.53	0.41
29:AF:49:PRO:HG2	29:AF:91:SER:HA	2.02	0.41
29:AF:182:HIS:ND1	29:AF:197:ASP:OD1	2.53	0.41
29:AF:193:ILE:HB	29:AF:209:LEU:HB2	2.02	0.41
30:AG:340:ILE:HG13	30:AG:361:THR:HG22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:AG:698:VAL:HG12	30:AG:724:ILE:HB	2.02	0.41
31:B1:286:LEU:HG	31:B1:296:GLN:HB2	2.02	0.41
31:B1:441:SER:O	31:B1:443:GLU:N	2.53	0.41
32:B2:432:TYR:HB3	32:B2:450:ARG:HD2	2.01	0.41
32:B2:747:LYS:HE3	32:B2:747:LYS:HB2	1.80	0.41
47:RE:978:ASP:OD1	47:RE:978:ASP:N	2.48	0.41
48:RF:20:LEU:N	48:RF:33:SER:OG	2.52	0.41
50:RJ:58:MET:HE2	50:RJ:58:MET:HB3	1.98	0.41
50:RJ:556:ASP:OD1	50:RJ:556:ASP:N	2.43	0.41
3:SA:23:G:H2'	3:SA:24:U:C6	2.55	0.41
3:SA:925:G:H2'	3:SA:926:A:C8	2.54	0.41
4:SC:189:ILE:HD13	4:SC:189:ILE:HA	1.91	0.41
15:SX:105:THR:HG23	15:SX:126:LEU:HB2	2.01	0.41
18:Sc:62:ILE:HD12	18:Sc:62:ILE:HA	1.79	0.41
19:Sd:42:ARG:HE	19:Sd:42:ARG:HB3	1.73	0.41
21:3D:181:LEU:HB3	21:3D:288:LEU:HD23	2.01	0.41
22:3E:191:HIS:CE1	22:3E:246:GLU:HA	2.55	0.41
22:3E:279:ARG:O	22:3E:283:ILE:HG12	2.20	0.41
25:A4:81:PRO:HA	25:A4:85:TRP:HA	2.02	0.41
25:A4:85:TRP:HZ3	25:A4:376:GLU:HG2	1.86	0.41
25:A4:467:ASN:HB2	25:A4:470:LEU:HB3	2.02	0.41
25:A4:485:LYS:HD3	25:A4:497:ILE:HG23	2.02	0.41
26:A5:22:VAL:HG13	34:B8:278:ASP:HB2	2.01	0.41
28:AE:81:LEU:HD11	28:AE:86:GLN:HE22	1.85	0.41
30:AG:383:LEU:HD13	30:AG:385:ILE:HD11	2.02	0.41
30:AG:568:ASN:HB3	30:AG:571:GLN:HB2	2.02	0.41
30:AG:614:ALA:HB3	30:AG:623:PHE:HB2	2.01	0.41
31:B1:641:LEU:HD23	31:B1:641:LEU:HA	1.88	0.41
32:B2:41:LEU:HD13	32:B2:54:ILE:HG21	2.01	0.41
33:B3:147:ILE:HD12	33:B3:167:ASP:HA	2.01	0.41
36:B6:16:ASP:OD2	37:5C:15:ARG:NH1	2.43	0.41
43:5I:347:ARG:HG2	45:5K:108:LYS:HG3	2.00	0.41
47:RE:100:SER:HA	47:RE:103:PHE:HE1	1.85	0.41
47:RE:193:ALA:O	47:RE:367:ARG:NH2	2.54	0.41
48:RF:64:ILE:HD11	48:RF:68:LYS:HE3	2.03	0.41
50:RJ:996:LEU:HD23	50:RJ:996:LEU:HA	1.89	0.41
1:3A:61:G:O6	31:B1:630:LEU:N	2.43	0.41
2:5A:476:A:H2'	2:5A:477:G:C8	2.55	0.41
3:SA:142:G:N7	7:SH:177:ARG:NH1	2.68	0.41
3:SA:325:G:H21	11:SM:81:HIS:CD2	2.39	0.41
3:SA:334:G:C8	3:SA:335:U:H5	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:656:G:C2	3:SA:678:A:H2	2.36	0.41
3:SA:800:U:H2'	3:SA:801:G:C8	2.56	0.41
3:SA:1594:G:O2'	3:SA:1600:A:N6	2.40	0.41
8:SI:67:LEU:HD23	8:SI:68:ALA:H	1.85	0.41
17:SZ:105:ARG:O	17:SZ:109:LYS:HB2	2.20	0.41
20:3B:155:ILE:HD13	20:3B:155:ILE:HA	1.85	0.41
21:3D:140:LYS:HD2	36:B6:104:PRO:HD2	2.02	0.41
22:3E:285:PRO:HG3	22:3E:382:ASP:HA	2.01	0.41
25:A4:312:ASN:HA	25:A4:315:GLN:HG2	2.02	0.41
25:A4:741:LEU:CG	25:A4:744:VAL:CG2	2.98	0.41
28:AE:6:ASP:N	28:AE:6:ASP:OD1	2.41	0.41
28:AE:377:ARG:HH11	30:AG:856:GLU:HG3	1.85	0.41
30:AG:124:LYS:HA	30:AG:124:LYS:HD2	1.72	0.41
31:B1:11:LEU:HA	31:B1:11:LEU:HD23	1.82	0.41
31:B1:291:ASP:N	31:B1:291:ASP:OD1	2.51	0.41
31:B1:598:ASN:OD1	31:B1:598:ASN:N	2.49	0.41
32:B2:159:LEU:HD12	32:B2:159:LEU:HA	1.88	0.41
34:B8:380:ASN:OD1	34:B8:380:ASN:N	2.52	0.41
37:5C:192:GLU:OE2	37:5C:211:THR:N	2.41	0.41
47:RE:628:VAL:HG13	47:RE:666:CYS:HB2	2.02	0.41
47:RE:800:GLU:O	47:RE:804:THR:HG23	2.21	0.41
47:RE:1094:LYS:HD3	56:X1:1304:UNK:HA	2.03	0.41
47:RE:1111:SER:HA	47:RE:1129:PRO:HD3	2.02	0.41
47:RE:1221:HIS:NE2	48:RF:21:PRO:O	2.52	0.41
48:RF:150:LYS:HE2	48:RF:150:LYS:HB3	1.74	0.41
49:RH:39:LYS:HB2	49:RH:198:ASP:HA	2.02	0.41
50:RJ:871:MET:HE2	50:RJ:871:MET:HB3	1.98	0.41
51:RK:151:LEU:HD13	51:RK:168:LEU:HB3	2.01	0.41
51:RK:177:PRO:HD2	51:RK:304:GLY:HA2	2.01	0.41
1:3A:204:U:N3	1:3A:245:U:O2	2.54	0.41
1:3A:249:G:H2'	1:3A:250:C:H6	1.84	0.41
3:SA:1461:C:H2'	3:SA:1462:G:H8	1.85	0.41
3:SA:1742:U:H2'	3:SA:1743:U:H4'	2.03	0.41
7:SH:139:ASN:HA	7:SH:142:ARG:HB2	2.03	0.41
11:SM:54:ILE:HG23	11:SM:55:ASP:H	1.85	0.41
22:3E:19:ASP:HA	22:3E:44:ILE:HA	2.02	0.41
30:AG:25:LEU:HB3	30:AG:28:VAL:HB	2.02	0.41
30:AG:483:LYS:HA	30:AG:483:LYS:HD3	1.85	0.41
31:B1:68:THR:HB	31:B1:127:VAL:HG21	2.02	0.41
31:B1:288:ASP:HB2	31:B1:295:ILE:HD11	2.02	0.41
32:B2:53:ASP:OD1	32:B2:53:ASP:N	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B2:750:GLU:HA	32:B2:753:MET:HB3	2.03	0.41
33:B3:496:ALA:HB3	33:B3:509:ALA:HB3	2.03	0.41
33:B3:683:LEU:HD23	33:B3:683:LEU:HA	1.92	0.41
34:B8:168:PHE:HA	34:B8:171:ILE:HG22	2.02	0.41
34:B8:239:LYS:HE2	34:B8:243:ALA:HB3	2.03	0.41
34:B8:439:LYS:HG3	34:B8:442:HIS:HE1	1.85	0.41
35:BE:632:VAL:HG13	35:BE:641:LEU:HD11	2.02	0.41
40:5F:34:ARG:NH2	45:5K:16:THR:O	2.50	0.41
47:RE:712:ASN:N	47:RE:1113:GLY:O	2.47	0.41
47:RE:769:VAL:HG11	47:RE:1113:GLY:HA3	2.03	0.41
48:RF:41:ARG:HD2	48:RF:138:TRP:HB2	2.02	0.41
50:RJ:839:LEU:HD23	50:RJ:839:LEU:HA	1.91	0.41
55:RT:120:LEU:HD12	55:RT:124:LEU:HB3	2.02	0.41
3:SA:153:G:H2'	3:SA:154:G:C8	2.56	0.41
3:SA:428:A:O2'	3:SA:440:U:O2'	2.28	0.41
3:SA:1575:G:H2'	3:SA:1576:A:C8	2.56	0.41
20:3C:89:GLU:HB3	20:3C:98:ILE:HB	2.03	0.41
20:3C:185:SER:HA	20:3C:188:VAL:HG12	2.03	0.41
21:3D:382:LYS:NZ	21:3D:407:GLN:OE1	2.42	0.41
21:3D:400:PHE:HA	21:3D:403:VAL:HG12	2.03	0.41
23:3F:419:ASN:HA	23:3F:472:PRO:HG3	2.02	0.41
24:3H:5:ASN:OD1	24:3H:5:ASN:N	2.52	0.41
24:3H:70:LEU:HA	24:3H:70:LEU:HD23	1.86	0.41
25:A4:87:GLN:HB3	25:A4:378:TYR:CD2	2.56	0.41
26:A5:169:SER:O	26:A5:169:SER:OG	2.38	0.41
29:AF:108:TYR:HE2	29:AF:113:PRO:HA	1.86	0.41
30:AG:884:MET:HE3	30:AG:884:MET:HB3	1.85	0.41
31:B1:19:ASN:OD1	31:B1:19:ASN:N	2.53	0.41
31:B1:458:TRP:CD1	31:B1:465:LEU:HA	2.55	0.41
32:B2:660:VAL:HA	32:B2:676:SER:HA	2.03	0.41
33:B3:210:ASN:HD22	33:B3:222:LEU:HD21	1.86	0.41
33:B3:280:ARG:HH12	33:B3:283:LYS:H	1.67	0.41
35:BE:420:GLU:HG3	35:BE:470:GLN:HA	2.01	0.41
35:BE:605:LEU:HD23	35:BE:628:VAL:HG11	2.02	0.41
36:B6:60:GLU:HA	36:B6:63:VAL:HG12	2.03	0.41
36:B6:75:LEU:HD12	36:B6:75:LEU:HA	1.94	0.41
45:5K:164:ILE:HD12	45:5K:170:ILE:HD11	2.02	0.41
46:RD:1489:SER:O	46:RD:1489:SER:OG	2.32	0.41
47:RE:146:LEU:HD12	47:RE:146:LEU:HA	1.90	0.41
47:RE:207:LEU:HD11	47:RE:294:LEU:HD12	2.02	0.41
47:RE:209:MET:SD	47:RE:227:LYS:NZ	2.82	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:RE:227:LYS:O	47:RE:231:TYR:HB2	2.21	0.41
47:RE:377:SER:O	47:RE:377:SER:OG	2.37	0.41
47:RE:950:ILE:HA	47:RE:951:PRO:HD3	1.93	0.41
50:RJ:930:LYS:HE3	50:RJ:930:LYS:HB2	1.87	0.41
3:SA:891:A:H2'	3:SA:892:A:C8	2.56	0.41
3:SA:1485:C:N3	3:SA:1592:A:H1'	2.36	0.41
3:SA:1745:G:O2'	3:SA:1746:A:O4'	2.39	0.41
9:SJ:184:LEU:HD22	9:SJ:192:TYR:HD2	1.86	0.41
20:3B:247:PRO:HA	20:3B:276:ILE:HD13	2.02	0.41
21:3D:409:GLU:HA	21:3D:412:LEU:HD22	2.03	0.41
22:3E:195:LEU:HA	22:3E:198:ILE:HG12	2.02	0.41
23:3F:310:ASN:OD1	23:3F:310:ASN:N	2.53	0.41
25:A4:44:ALA:HB3	25:A4:71:ARG:HB3	2.03	0.41
26:A5:308:ASN:HB2	26:A5:311:MET:HG2	2.03	0.41
27:A9:502:ARG:HG2	29:AF:510:LEU:HD22	2.03	0.41
28:AE:414:LEU:HD23	28:AE:414:LEU:HA	1.88	0.41
29:AF:278:ASP:OD1	29:AF:278:ASP:N	2.53	0.41
30:AG:560:ILE:HD13	30:AG:575:THR:HG22	2.01	0.41
30:AG:678:LEU:HD12	30:AG:678:LEU:HA	1.91	0.41
33:B3:548:LEU:HB3	33:B3:560:TRP:HB2	2.02	0.41
33:B3:597:GLY:O	33:B3:613:LEU:HB2	2.20	0.41
33:B3:678:TRP:HB3	33:B3:697:VAL:HG22	2.01	0.41
35:BE:131:SER:HB3	35:BE:170:LEU:HD21	2.02	0.41
37:5C:220:SER:OG	37:5C:221:THR:N	2.54	0.41
38:5D:18:GLN:OE1	38:5D:19:LEU:N	2.53	0.41
47:RE:565:LYS:HD3	47:RE:690:VAL:HG12	2.02	0.41
50:RJ:860:TYR:HA	50:RJ:883:ALA:HA	2.02	0.41
2:5A:280:A:O2'	34:B8:554:ASN:O	2.35	0.41
3:SA:38:C:H2'	3:SA:39:A:C4	2.56	0.41
3:SA:1604:U:H2'	3:SA:1605:G:H8	1.86	0.41
6:SG:15:GLU:HG2	35:BE:499:LYS:HB3	2.03	0.41
11:SM:19:ILE:HG22	11:SM:32:LYS:HG3	2.03	0.41
12:SO:37:ILE:HG21	12:SO:74:ILE:HD11	2.02	0.41
14:SR:113:ASP:HB2	14:SR:115:THR:HG22	2.01	0.41
17:SZ:16:PRO:HA	17:SZ:19:ALA:HA	2.02	0.41
20:3C:228:GLN:O	20:3C:231:ARG:NE	2.34	0.41
29:AF:75:LYS:HE3	29:AF:75:LYS:HB3	1.93	0.41
31:B1:31:SER:HA	31:B1:32:PRO:HD3	1.91	0.41
31:B1:247:SER:O	31:B1:247:SER:OG	2.38	0.41
31:B1:486:SER:HB3	31:B1:503:PHE:HE2	1.86	0.41
31:B1:539:ILE:HG23	31:B1:553:ILE:HB	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:B1:707:ASN:OD1	31:B1:707:ASN:N	2.52	0.41
31:B1:721:VAL:HG23	31:B1:741:MET:HG2	2.02	0.41
31:B1:814:LYS:NZ	35:BE:938:THR:O	2.53	0.41
32:B2:88:HIS:CE1	32:B2:90:ASP:HB2	2.55	0.41
33:B3:377:LEU:O	33:B3:379:LEU:N	2.54	0.41
35:BE:229:GLU:HA	35:BE:244:ILE:O	2.21	0.41
40:5F:60:LYS:HA	40:5F:60:LYS:HD2	1.89	0.41
40:5F:128:VAL:O	40:5F:132:GLU:HB2	2.20	0.41
45:5K:84:ARG:HG2	53:RP:1850:LEU:HD11	2.03	0.41
47:RE:235:LEU:HA	47:RE:235:LEU:HD23	1.85	0.41
47:RE:1169:ILE:HG13	47:RE:1170:GLY:H	1.85	0.41
50:RJ:248:ARG:HB3	50:RJ:272:TYR:HB2	2.02	0.41
50:RJ:552:LEU:HD23	50:RJ:552:LEU:HA	1.84	0.41
50:RJ:775:GLU:HA	50:RJ:779:ARG:HG2	2.03	0.41
53:RP:1979:LEU:HD12	53:RP:2013:LEU:HD11	2.02	0.41
53:RP:2085:LEU:HA	53:RP:2085:LEU:HD12	1.85	0.41
54:RQ:274:LEU:H	54:RQ:274:LEU:HG	1.70	0.41
2:5A:6:A:H5'	30:AG:609:ASN:HD21	1.85	0.41
3:SA:560:U:H2'	3:SA:561:G:C8	2.56	0.41
3:SA:639:U:OP1	8:SI:117:THR:N	2.54	0.41
3:SA:810:G:H2'	3:SA:811:A:C8	2.56	0.41
3:SA:864:U:H6	3:SA:864:U:H2'	1.74	0.41
3:SA:1718:G:H2'	3:SA:1719:A:C4	2.55	0.41
3:SA:1752:U:H2'	3:SA:1753:A:H8	1.85	0.41
4:SC:19:ARG:HH22	33:B3:359:SER:N	2.18	0.41
4:SC:55:LYS:HA	4:SC:55:LYS:HD2	1.96	0.41
9:SJ:39:GLY:O	9:SJ:59:ARG:HB3	2.21	0.41
9:SJ:164:ARG:HD3	9:SJ:164:ARG:HA	1.88	0.41
10:SK:64:GLU:HG3	10:SK:65:LYS:HG3	2.03	0.41
11:SM:109:VAL:HG21	11:SM:125:VAL:HG11	2.02	0.41
13:SP:110:LEU:HD12	13:SP:110:LEU:HA	1.91	0.41
15:SX:109:GLY:HA2	53:RP:1737:ASN:HD22	1.86	0.41
16:SY:113:ALA:HB3	16:SY:116:ASP:HB2	2.01	0.41
17:SZ:101:GLU:OE1	17:SZ:108:ARG:NH2	2.54	0.41
20:3C:236:MET:HG2	22:3E:121:LYS:HB3	2.02	0.41
23:3F:142:ILE:HD13	23:3F:142:ILE:HA	1.97	0.41
23:3F:342:ARG:HA	23:3F:342:ARG:HD3	1.84	0.41
23:3F:400:GLY:HA2	24:3H:18:GLN:CD	2.46	0.41
24:3G:89:ARG:HH22	34:B8:492:ASN:HD21	1.69	0.41
25:A4:281:ALA:HB1	25:A4:300:VAL:HG23	2.03	0.41
25:A4:436:ASP:OD1	25:A4:483:ASN:ND2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A4:774:LEU:HD11	30:AG:297:ILE:HD12	2.03	0.41
26:A5:306:LEU:HD23	26:A5:310:THR:HA	2.03	0.41
26:A5:546:ARG:HA	26:A5:549:CYS:HB3	2.03	0.41
27:A9:502:ARG:HA	29:AF:507:MET:HE1	2.03	0.41
29:AF:46:SER:OG	29:AF:47:PHE:N	2.53	0.41
29:AF:103:GLY:HA2	29:AF:127:THR:HG22	2.03	0.41
29:AF:234:PHE:CE1	29:AF:248:ARG:HB2	2.55	0.41
29:AF:436:GLU:HA	29:AF:439:LEU:HB2	2.02	0.41
30:AG:90:LYS:HD2	30:AG:144:VAL:H	1.86	0.41
30:AG:426:ARG:HA	30:AG:429:ILE:HB	2.03	0.41
31:B1:480:SER:OG	31:B1:481:PHE:N	2.53	0.41
31:B1:491:ALA:HB2	31:B1:521:LEU:HD12	2.03	0.41
34:B8:231:LYS:O	34:B8:553:SER:OG	2.39	0.41
34:B8:233:LEU:HD23	34:B8:552:PHE:CG	2.56	0.41
34:B8:258:PRO:HB3	34:B8:469:PRO:HG2	2.01	0.41
35:BE:396:LYS:HE2	35:BE:396:LYS:HB3	1.83	0.41
35:BE:918:LYS:HE2	35:BE:918:LYS:HB2	1.87	0.41
35:BE:923:ASP:HA	35:BE:926:VAL:HG12	2.03	0.41
36:B6:128:LYS:HB2	36:B6:128:LYS:HE2	1.89	0.41
37:5C:96:ASP:OD1	37:5C:99:THR:OG1	2.26	0.41
39:5E:447:LYS:HA	39:5E:450:VAL:HG12	2.03	0.41
40:5F:183:SER:O	40:5F:183:SER:OG	2.33	0.41
46:RD:1642:GLU:HA	46:RD:1645:VAL:HG22	2.02	0.41
46:RD:1674:LEU:O	46:RD:1678:ILE:HG13	2.21	0.41
47:RE:387:GLY:HA3	47:RE:480:MET:HB3	2.03	0.41
47:RE:566:ILE:HA	47:RE:569:VAL:HG22	2.03	0.41
47:RE:712:ASN:HA	47:RE:1115:LEU:HD23	2.03	0.41
48:RF:62:SER:HA	48:RF:66:HIS:CE1	2.55	0.41
49:RH:35:ASP:OD1	49:RH:35:ASP:N	2.54	0.41
50:RJ:69:PRO:HD2	50:RJ:274:TYR:CZ	2.56	0.41
50:RJ:824:ILE:HD12	50:RJ:1011:VAL:HG11	2.03	0.41
50:RJ:1151:GLN:HA	50:RJ:1154:LYS:HE3	2.02	0.41
51:RK:307:ASP:O	51:RK:355:LYS:HA	2.20	0.41
51:RK:364:LYS:HB2	51:RK:364:LYS:HE2	1.82	0.41
53:RP:1738:TYR:HE2	53:RP:1741:LYS:HE3	1.86	0.41
53:RP:1941:VAL:HA	53:RP:1944:ILE:HD12	2.03	0.41
54:RQ:277:ARG:HG3	54:RQ:278:ILE:HD12	2.02	0.41
55:RT:263:LEU:HA	55:RT:266:VAL:HG12	2.03	0.41
1:3A:43:C:H2'	1:3A:44:U:H6	1.86	0.41
3:SA:775:G:H1	3:SA:785:U:H2'	1.86	0.41
3:SA:1146:G:H2'	3:SA:1147:A:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:SC:87:ARG:HH21	4:SC:101:HIS:HD2	1.69	0.41
4:SC:126:THR:HA	4:SC:135:LEU:O	2.21	0.41
5:SF:86:PHE:CE2	5:SF:87:MET:HG2	2.56	0.41
6:SG:83:ARG:HH12	31:B1:546:ASP:HA	1.85	0.41
7:SH:147:LEU:HG	7:SH:153:VAL:HG12	2.03	0.41
8:SI:175:LYS:HB2	8:SI:175:LYS:HE2	1.86	0.41
22:3E:193:PRO:HG2	22:3E:243:MET:HG3	2.03	0.41
25:A4:196:LYS:HG2	25:A4:197:LYS:HG3	2.03	0.41
25:A4:358:ILE:HB	25:A4:370:ARG:HB3	2.03	0.41
28:AE:193:THR:HG22	28:AE:241:ILE:HD13	2.03	0.41
29:AF:402:ASP:OD1	29:AF:434:ARG:NH2	2.43	0.41
29:AF:426:LYS:NZ	30:AG:486:PHE:O	2.43	0.41
30:AG:367:SER:O	30:AG:367:SER:OG	2.38	0.41
31:B1:195:MET:HB3	31:B1:195:MET:HE2	1.77	0.41
32:B2:181:SER:OG	32:B2:183:ASP:O	2.39	0.41
32:B2:223:ASP:OD1	32:B2:223:ASP:N	2.52	0.41
32:B2:550:LEU:HD13	32:B2:554:THR:HG23	2.03	0.41
33:B3:117:LEU:HB2	33:B3:131:ILE:HD11	2.03	0.41
35:BE:264:LEU:HB2	35:BE:278:LEU:HD11	2.02	0.41
39:5E:448:LEU:HD11	40:5F:81:LYS:HE3	2.03	0.41
41:5G:192:ASP:HB3	41:5G:225:ALA:HA	2.02	0.41
47:RE:858:ARG:HD2	47:RE:858:ARG:HA	1.94	0.41
50:RJ:111:LYS:HA	50:RJ:311:PRO:HG2	2.02	0.41
50:RJ:177:PHE:HB3	50:RJ:179:SER:H	1.86	0.41
50:RJ:568:ARG:HA	50:RJ:568:ARG:HD2	1.85	0.41
1:3A:1:G:N2	3:SA:1125:A:O3'	2.53	0.40
3:SA:1123:C:H2'	3:SA:1124:A:C8	2.56	0.40
3:SA:1584:G:O2'	3:SA:1610:G:O6	2.34	0.40
3:SA:1591:C:H2'	3:SA:1592:A:C8	2.56	0.40
8:SI:58:LEU:HD11	8:SI:85:PHE:HE2	1.86	0.40
8:SI:131:PHE:CD2	8:SI:133:THR:HG23	2.56	0.40
8:SI:162:ILE:HD13	8:SI:162:ILE:HA	1.88	0.40
15:SX:20:THR:OG1	15:SX:22:LYS:NZ	2.52	0.40
20:3B:193:VAL:HA	20:3B:216:ASN:O	2.21	0.40
22:3E:173:LEU:O	22:3E:177:LEU:HB2	2.21	0.40
23:3F:168:ASN:O	23:3F:170:TYR:N	2.54	0.40
24:3G:50:GLU:OE2	24:3G:118:LYS:NZ	2.41	0.40
25:A4:71:ARG:HB2	25:A4:75:ASN:OD1	2.21	0.40
27:A9:477:LYS:HA	27:A9:480:LYS:HB3	2.04	0.40
30:AG:666:ASN:OD1	30:AG:666:ASN:N	2.52	0.40
30:AG:780:GLU:O	30:AG:782:THR:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:B1:269:HIS:NE2	31:B1:312:GLN:O	2.37	0.40
31:B1:387:THR:OG1	31:B1:408:ASP:OD1	2.34	0.40
31:B1:418:ARG:NH2	39:5E:490:LEU:O	2.54	0.40
34:B8:226:LYS:HA	34:B8:226:LYS:HD2	1.83	0.40
34:B8:244:SER:OG	34:B8:245:HIS:N	2.54	0.40
34:B8:439:LYS:HB3	34:B8:439:LYS:HE2	1.75	0.40
35:BE:273:LEU:HD12	35:BE:273:LEU:HA	1.93	0.40
35:BE:285:HIS:ND1	35:BE:286:VAL:O	2.54	0.40
35:BE:464:LYS:HD2	35:BE:504:ALA:HB1	2.03	0.40
35:BE:533:LYS:HE2	35:BE:533:LYS:HB2	1.93	0.40
36:B6:124:THR:OG1	36:B6:125:SER:N	2.49	0.40
41:5G:149:PRO:HG2	41:5G:170:VAL:HG11	2.04	0.40
43:5I:449:LYS:HD3	43:5I:449:LYS:HA	1.82	0.40
47:RE:390:THR:O	47:RE:394:THR:HG23	2.21	0.40
47:RE:435:CYS:HB2	47:RE:485:TYR:CD2	2.56	0.40
53:RP:1872:ALA:HB3	53:RP:1910:VAL:HG21	2.02	0.40
53:RP:2052:GLN:HB3	53:RP:2057:LEU:HD12	2.02	0.40
53:RP:2070:TYR:HB3	53:RP:2076:ARG:HG3	2.03	0.40
2:5A:88:U:H3	34:B8:344:ARG:CZ	2.34	0.40
3:SA:78:A:H1'	7:SH:175:ILE:HG12	2.03	0.40
3:SA:809:A:C6	3:SA:810:G:H1'	2.57	0.40
3:SA:1143:A:H2'	3:SA:1144:U:O4'	2.21	0.40
9:SJ:184:LEU:HD13	9:SJ:189:LEU:HA	2.03	0.40
10:SK:17:ARG:HA	10:SK:17:ARG:HD2	1.88	0.40
10:SK:37:LYS:HE3	10:SK:37:LYS:HB2	1.76	0.40
18:Sc:37:CYS:HA	18:Sc:38:PRO:HD3	1.90	0.40
22:3E:177:LEU:HD21	22:3E:265:PHE:HB3	2.04	0.40
23:3F:142:ILE:HG21	23:3F:512:GLY:HA3	2.03	0.40
25:A4:66:ARG:HH12	25:A4:82:ARG:HH12	1.68	0.40
25:A4:193:LEU:HA	25:A4:202:ILE:O	2.21	0.40
25:A4:247:LEU:HD12	25:A4:292:ASN:HB3	2.03	0.40
25:A4:640:ILE:HG21	25:A4:749:SER:HA	2.03	0.40
28:AE:227:ASN:HB3	28:AE:230:LYS:HB3	2.03	0.40
29:AF:142:THR:O	29:AF:149:THR:OG1	2.29	0.40
29:AF:198:THR:HG23	29:AF:199:ARG:HD3	2.04	0.40
30:AG:23:ASN:HB2	30:AG:32:LYS:HA	2.03	0.40
30:AG:693:ASP:OD1	30:AG:693:ASP:N	2.53	0.40
31:B1:494:ASP:C	31:B1:496:THR:HG1	2.27	0.40
32:B2:145:ILE:O	32:B2:159:LEU:HB3	2.21	0.40
32:B2:268:LYS:HD3	32:B2:268:LYS:HA	1.94	0.40
32:B2:283:THR:OG1	32:B2:330:GLN:O	2.39	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B2:538:ARG:HG2	32:B2:581:ILE:HD12	2.03	0.40
33:B3:350:LEU:HD12	33:B3:350:LEU:HA	1.84	0.40
33:B3:402:TRP:HA	33:B3:415:TRP:O	2.20	0.40
33:B3:432:GLY:O	33:B3:433:HIS:ND1	2.54	0.40
34:B8:545:HIS:HB2	34:B8:552:PHE:CZ	2.56	0.40
35:BE:230:VAL:O	35:BE:243:THR:HA	2.21	0.40
35:BE:482:GLY:HA2	35:BE:505:VAL:HG23	2.03	0.40
35:BE:846:ASP:HA	35:BE:849:ILE:HG22	2.03	0.40
42:5H:571:LYS:O	42:5H:575:LYS:N	2.55	0.40
43:5I:429:ILE:HA	43:5I:432:ILE:HG12	2.03	0.40
47:RE:273:SER:O	47:RE:284:ASN:ND2	2.45	0.40
47:RE:476:ILE:H	47:RE:476:ILE:HG13	1.57	0.40
47:RE:779:PHE:HB3	47:RE:851:LYS:HG3	2.03	0.40
48:RF:66:HIS:HD2	48:RF:67:MET:HE2	1.85	0.40
53:RP:2026:ILE:O	53:RP:2030:ASN:HB2	2.20	0.40
3:SA:646:C:H2'	3:SA:647:G:C8	2.57	0.40
3:SA:1151:A:H2'	3:SA:1152:A:H8	1.85	0.40
20:3B:231:ARG:NE	21:3D:10:GLU:OE2	2.33	0.40
20:3C:112:ALA:HA	20:3C:113:PRO:HD3	1.93	0.40
20:3C:212:LYS:HE2	20:3C:212:LYS:HB2	1.85	0.40
21:3D:397:SER:OG	21:3D:398:ASN:N	2.54	0.40
22:3E:419:VAL:HG21	35:BE:323:VAL:HG21	2.03	0.40
25:A4:464:LYS:HB3	25:A4:464:LYS:HE2	1.82	0.40
29:AF:146:ASP:OD1	29:AF:146:ASP:N	2.39	0.40
29:AF:424:ARG:HA	30:AG:477:VAL:HG21	2.03	0.40
31:B1:176:ASP:OD1	31:B1:176:ASP:N	2.53	0.40
31:B1:317:LEU:O	31:B1:329:VAL:HA	2.21	0.40
32:B2:884:LYS:HE3	32:B2:884:LYS:HB3	1.83	0.40
34:B8:345:LEU:HD23	34:B8:345:LEU:HA	1.88	0.40
37:5C:104:LEU:HD21	37:5C:139:TRP:HB2	2.03	0.40
37:5C:116:ILE:HG23	37:5C:125:LEU:HD11	2.03	0.40
37:5C:259:TRP:CE2	37:5C:266:PRO:HB3	2.56	0.40
42:5H:544:ILE:O	50:RJ:193:ARG:NH1	2.33	0.40
47:RE:143:GLU:HB2	47:RE:177:ASN:ND2	2.36	0.40
47:RE:326:LEU:HD23	47:RE:326:LEU:HA	1.92	0.40
49:RH:240:LYS:O	49:RH:243:HIS:ND1	2.54	0.40
53:RP:177:LEU:HA	53:RP:177:LEU:HD23	1.90	0.40
53:RP:1992:GLU:OE2	53:RP:1994:SER:OG	2.28	0.40
53:RP:2016:LEU:HA	53:RP:2019:ILE:HB	2.02	0.40
2:5A:14:U:H5''	2:5A:15:G:H5''	2.02	0.40
2:5A:309:A:N3	34:B8:145:LYS:NZ	2.47	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:1756:A:C8	39:5E:536:ARG:HD3	2.56	0.40
4:SC:242:LYS:HG3	4:SC:244:VAL:HG12	2.03	0.40
6:SG:130:ILE:H	6:SG:130:ILE:HG12	1.65	0.40
7:SH:48:TYR:CZ	7:SH:119:GLN:HB3	2.57	0.40
17:SZ:27:VAL:HG21	17:SZ:35:VAL:HG21	2.04	0.40
21:3D:178:ILE:HG12	21:3D:314:ARG:HD2	2.03	0.40
24:3G:41:THR:HG21	24:3G:66:HIS:CE1	2.56	0.40
25:A4:34:HIS:ND1	25:A4:404:MET:SD	2.90	0.40
25:A4:192:THR:OG1	25:A4:242:TRP:O	2.26	0.40
29:AF:27:TRP:HZ2	29:AF:264:PHE:HZ	1.69	0.40
29:AF:375:HIS:CD2	34:B8:339:ILE:HD11	2.56	0.40
29:AF:391:ASN:O	29:AF:396:LYS:N	2.43	0.40
29:AF:474:LEU:HD12	29:AF:474:LEU:HA	1.90	0.40
30:AG:79:LEU:HA	30:AG:79:LEU:HD23	1.89	0.40
30:AG:375:ASN:OD1	30:AG:380:THR:N	2.54	0.40
30:AG:467:GLN:HE22	30:AG:470:TYR:HD2	1.70	0.40
30:AG:678:LEU:N	30:AG:692:PHE:O	2.54	0.40
31:B1:717:LEU:HD12	35:BE:578:VAL:HB	2.02	0.40
32:B2:478:SER:HB3	32:B2:537:VAL:H	1.86	0.40
35:BE:717:ASP:OD1	35:BE:717:ASP:N	2.54	0.40
37:5C:44:ALA:HA	37:5C:47:LYS:HG2	2.04	0.40
38:5D:17:SER:OG	38:5D:18:GLN:N	2.53	0.40
40:5F:65:PRO:HA	40:5F:66:PRO:HD3	1.94	0.40
40:5F:181:ASP:OD1	40:5F:181:ASP:N	2.54	0.40
42:5H:550:LEU:HD12	42:5H:550:LEU:HA	1.95	0.40
43:5I:139:CYS:SG	43:5I:185:ILE:HG12	2.61	0.40
44:5J:111:ASP:OD1	44:5J:111:ASP:N	2.42	0.40
47:RE:585:MET:HE2	47:RE:585:MET:HB2	1.98	0.40
47:RE:941:PRO:HG3	47:RE:961:VAL:HG22	2.03	0.40
47:RE:1101:ASP:OD2	47:RE:1233:ASN:ND2	2.54	0.40
48:RF:94:GLY:HA3	48:RF:121:ARG:HH12	1.87	0.40
51:RK:104:LEU:HD11	51:RK:138:MET:HE1	2.03	0.40
3:SA:246:G:H2'	3:SA:247:A:C8	2.56	0.40
3:SA:1695:G:H2'	3:SA:1696:G:C8	2.57	0.40
4:SC:87:ARG:HD3	4:SC:101:HIS:CD2	2.57	0.40
6:SG:26:ALA:HB3	14:SR:28:LEU:HB3	2.03	0.40
13:SP:47:LYS:HA	13:SP:47:LYS:HD3	1.81	0.40
17:SZ:36:SER:O	17:SZ:39:GLU:N	2.55	0.40
22:3E:302:HIS:ND1	22:3E:320:LEU:O	2.54	0.40
26:A5:191:VAL:HA	26:A5:206:ALA:HA	2.03	0.40
27:A9:505:MET:HG2	27:A9:508:ARG:NH1	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:AE:115:LEU:HD12	28:AE:115:LEU:HA	1.86	0.40
29:AF:235:LYS:HG3	29:AF:247:GLU:HG2	2.03	0.40
31:B1:88:ASN:ND2	35:BE:659:GLN:HG2	2.36	0.40
31:B1:429:GLU:HG2	31:B1:431:ILE:HG23	2.02	0.40
31:B1:770:ILE:HA	31:B1:771:PRO:HD3	1.98	0.40
32:B2:88:HIS:NE2	32:B2:132:THR:OG1	2.42	0.40
32:B2:617:SER:OG	32:B2:618:ILE:O	2.38	0.40
33:B3:340:ILE:H	33:B3:340:ILE:HG13	1.46	0.40
41:5G:285:ASN:OD1	41:5G:285:ASN:N	2.50	0.40
43:5I:240:SER:O	43:5I:240:SER:OG	2.39	0.40
44:5J:180:ASP:O	44:5J:183:SER:OG	2.37	0.40
47:RE:501:ASN:HD21	47:RE:506:GLN:HE22	1.69	0.40
50:RJ:841:THR:HB	50:RJ:859:ILE:HD12	2.04	0.40
51:RK:198:THR:OG1	51:RK:235:SER:O	2.40	0.40
51:RK:357:ILE:H	51:RK:357:ILE:HG12	1.70	0.40
52:RN:781:MET:HE3	52:RN:781:MET:HB2	1.93	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	230/255 (90%)	190 (83%)	39 (17%)	1 (0%)	30	67
5	SF	248/261 (95%)	211 (85%)	37 (15%)	0	100	100
6	SG	211/225 (94%)	194 (92%)	17 (8%)	0	100	100
7	SH	178/236 (75%)	158 (89%)	17 (10%)	3 (2%)	7	35
8	SI	160/190 (84%)	136 (85%)	24 (15%)	0	100	100
9	SJ	136/200 (68%)	113 (83%)	23 (17%)	0	100	100
10	SK	169/197 (86%)	155 (92%)	14 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	SM	135/156 (86%)	119 (88%)	16 (12%)	0	100	100
12	SO	132/151 (87%)	119 (90%)	13 (10%)	0	100	100
13	SP	116/137 (85%)	103 (89%)	13 (11%)	0	100	100
14	SR	123/143 (86%)	110 (89%)	13 (11%)	0	100	100
15	SX	125/130 (96%)	114 (91%)	11 (9%)	0	100	100
16	SY	104/145 (72%)	91 (88%)	13 (12%)	0	100	100
17	SZ	121/135 (90%)	104 (86%)	17 (14%)	0	100	100
18	Sc	78/82 (95%)	66 (85%)	12 (15%)	0	100	100
19	Sd	61/67 (91%)	56 (92%)	5 (8%)	0	100	100
20	3B	236/327 (72%)	222 (94%)	14 (6%)	0	100	100
20	3C	221/327 (68%)	204 (92%)	17 (8%)	0	100	100
21	3D	372/504 (74%)	343 (92%)	29 (8%)	0	100	100
22	3E	428/511 (84%)	389 (91%)	39 (9%)	0	100	100
23	3F	431/572 (75%)	365 (85%)	65 (15%)	1 (0%)	43	77
24	3G	119/126 (94%)	109 (92%)	10 (8%)	0	100	100
24	3H	119/126 (94%)	112 (94%)	6 (5%)	1 (1%)	16	52
25	A4	650/776 (84%)	583 (90%)	67 (10%)	0	100	100
26	A5	362/643 (56%)	333 (92%)	29 (8%)	0	100	100
27	A9	35/575 (6%)	34 (97%)	1 (3%)	0	100	100
28	AE	429/1769 (24%)	410 (96%)	19 (4%)	0	100	100
29	AF	473/513 (92%)	427 (90%)	46 (10%)	0	100	100
30	AG	812/896 (91%)	694 (86%)	118 (14%)	0	100	100
31	B1	800/923 (87%)	720 (90%)	80 (10%)	0	100	100
32	B2	813/943 (86%)	731 (90%)	82 (10%)	0	100	100
33	B3	733/817 (90%)	608 (83%)	123 (17%)	2 (0%)	36	71
34	B8	469/594 (79%)	423 (90%)	45 (10%)	1 (0%)	43	77
35	BE	817/939 (87%)	746 (91%)	71 (9%)	0	100	100
36	B6	368/440 (84%)	343 (93%)	25 (7%)	0	100	100
37	5C	452/554 (82%)	400 (88%)	52 (12%)	0	100	100
38	5D	68/250 (27%)	57 (84%)	10 (15%)	1 (2%)	8	38
39	5E	187/593 (32%)	173 (92%)	14 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	5F	180/183 (98%)	165 (92%)	15 (8%)	0	100	100
41	5G	214/290 (74%)	196 (92%)	18 (8%)	0	100	100
42	5H	72/610 (12%)	63 (88%)	9 (12%)	0	100	100
43	5I	456/489 (93%)	422 (92%)	33 (7%)	1 (0%)	43	77
44	5J	130/217 (60%)	121 (93%)	9 (7%)	0	100	100
45	5K	162/189 (86%)	149 (92%)	13 (8%)	0	100	100
46	RD	310/1729 (18%)	278 (90%)	32 (10%)	0	100	100
47	RE	1080/1237 (87%)	996 (92%)	84 (8%)	0	100	100
48	RF	233/297 (78%)	203 (87%)	30 (13%)	0	100	100
49	RH	215/252 (85%)	198 (92%)	17 (8%)	0	100	100
50	RJ	719/1183 (61%)	649 (90%)	69 (10%)	1 (0%)	48	83
51	RK	358/367 (98%)	335 (94%)	23 (6%)	0	100	100
52	RN	51/810 (6%)	51 (100%)	0	0	100	100
53	RP	2112/2493 (85%)	1903 (90%)	203 (10%)	6 (0%)	36	71
54	RQ	220/899 (24%)	197 (90%)	23 (10%)	0	100	100
55	RT	165/326 (51%)	152 (92%)	13 (8%)	0	100	100
All	All	18398/27999 (66%)	16543 (90%)	1837 (10%)	18 (0%)	49	83

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
34	B8	226	LYS
24	3H	6	PRO
53	RP	37	ARG
53	RP	1004	VAL
4	SC	213	ARG
7	SH	173	PRO
23	3F	270	PRO
33	B3	71	PRO
33	B3	474	SER
53	RP	77	LEU
53	RP	204	PRO
7	SH	154	ARG
38	5D	11	LYS
50	RJ	900	GLN
53	RP	76	THR

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Mol	Chain	Res	Type
53	RP	1997	GLY
7	SH	153	VAL
43	5I	34	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	205/224 (92%)	205 (100%)	0	100	100
5	SF	199/222 (90%)	196 (98%)	3 (2%)	57	71
6	SG	180/191 (94%)	179 (99%)	1 (1%)	78	81
7	SH	153/201 (76%)	153 (100%)	0	100	100
8	SI	145/170 (85%)	143 (99%)	2 (1%)	59	72
9	SJ	114/161 (71%)	114 (100%)	0	100	100
10	SK	147/166 (89%)	146 (99%)	1 (1%)	76	79
11	SM	124/137 (90%)	124 (100%)	0	100	100
12	SO	117/128 (91%)	115 (98%)	2 (2%)	53	68
13	SP	90/105 (86%)	89 (99%)	1 (1%)	65	74
14	SR	105/119 (88%)	105 (100%)	0	100	100
15	SX	108/111 (97%)	108 (100%)	0	100	100
16	SY	88/120 (73%)	86 (98%)	2 (2%)	44	63
17	SZ	103/113 (91%)	101 (98%)	2 (2%)	50	66
18	Sc	69/71 (97%)	65 (94%)	4 (6%)	18	40
19	Sd	56/60 (93%)	56 (100%)	0	100	100
20	3B	201/240 (84%)	199 (99%)	2 (1%)	68	76
20	3C	190/240 (79%)	186 (98%)	4 (2%)	47	65
21	3D	322/435 (74%)	321 (100%)	1 (0%)	86	84
22	3E	265/433 (61%)	264 (100%)	1 (0%)	84	83
23	3F	382/502 (76%)	372 (97%)	10 (3%)	40	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	3G	100/104 (96%)	98 (98%)	2 (2%)	48	66
24	3H	100/104 (96%)	100 (100%)	0	100	100
25	A4	593/713 (83%)	585 (99%)	8 (1%)	61	72
26	A5	334/574 (58%)	332 (99%)	2 (1%)	78	81
27	A9	34/533 (6%)	34 (100%)	0	100	100
28	AE	391/1633 (24%)	390 (100%)	1 (0%)	86	84
29	AF	424/454 (93%)	421 (99%)	3 (1%)	76	79
30	AG	750/826 (91%)	747 (100%)	3 (0%)	84	83
31	B1	707/812 (87%)	699 (99%)	8 (1%)	65	74
32	B2	712/832 (86%)	702 (99%)	10 (1%)	59	72
33	B3	665/719 (92%)	659 (99%)	6 (1%)	70	77
34	B8	421/529 (80%)	413 (98%)	8 (2%)	50	66
35	BE	721/819 (88%)	713 (99%)	8 (1%)	65	74
36	B6	251/414 (61%)	248 (99%)	3 (1%)	63	74
37	5C	394/480 (82%)	391 (99%)	3 (1%)	73	78
38	5D	65/234 (28%)	65 (100%)	0	100	100
39	5E	175/535 (33%)	174 (99%)	1 (1%)	78	81
40	5F	171/172 (99%)	171 (100%)	0	100	100
41	5G	191/258 (74%)	189 (99%)	2 (1%)	68	76
42	5H	63/538 (12%)	63 (100%)	0	100	100
43	5I	415/443 (94%)	410 (99%)	5 (1%)	63	74
44	5J	124/200 (62%)	123 (99%)	1 (1%)	73	78
45	5K	148/169 (88%)	148 (100%)	0	100	100
46	RD	226/1544 (15%)	225 (100%)	1 (0%)	84	83
47	RE	994/1125 (88%)	987 (99%)	7 (1%)	76	79
48	RF	221/274 (81%)	219 (99%)	2 (1%)	70	77
49	RH	197/222 (89%)	197 (100%)	0	100	100
50	RJ	649/1039 (62%)	643 (99%)	6 (1%)	70	77
51	RK	307/312 (98%)	302 (98%)	5 (2%)	55	69
52	RN	47/732 (6%)	47 (100%)	0	100	100
53	RP	550/2307 (24%)	546 (99%)	4 (1%)	76	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	RQ	149/808 (18%)	149 (100%)	0	100	100
55	RT	148/282 (52%)	147 (99%)	1 (1%)	76	79
All	All	14800/24889 (60%)	14664 (99%)	136 (1%)	68	77

All (136) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	SF	72	VAL
5	SF	78	THR
5	SF	192	ILE
6	SG	130	ILE
8	SI	66	SER
8	SI	91	ILE
10	SK	128	LEU
12	SO	54	LEU
12	SO	91	LEU
13	SP	13	VAL
16	SY	87	VAL
16	SY	93	LEU
17	SZ	35	VAL
17	SZ	77	ASN
18	Sc	8	LEU
18	Sc	65	THR
18	Sc	67	THR
18	Sc	77	THR
20	3B	117	VAL
20	3B	285	VAL
20	3C	96	VAL
20	3C	197	VAL
20	3C	237	VAL
20	3C	268	VAL
21	3D	412	LEU
22	3E	199	VAL
23	3F	160	ILE
23	3F	197	THR
23	3F	231	THR
23	3F	242	VAL
23	3F	262	VAL
23	3F	405	VAL
23	3F	425	TRP
23	3F	524	ILE

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Mol	Chain	Res	Type
23	3F	546	GLU
23	3F	553	ILE
24	3G	68	PRO
24	3G	79	VAL
25	A4	99	ILE
25	A4	121	THR
25	A4	357	VAL
25	A4	392	VAL
25	A4	429	SER
25	A4	441	VAL
25	A4	570	ILE
25	A4	640	ILE
26	A5	167	SER
26	A5	240	GLN
28	AE	87	THR
29	AF	73	VAL
29	AF	255	VAL
29	AF	481	GLN
30	AG	197	ILE
30	AG	235	VAL
30	AG	528	ILE
31	B1	119	LEU
31	B1	127	VAL
31	B1	161	ILE
31	B1	250	ILE
31	B1	291	ASP
31	B1	450	LEU
31	B1	517	ASP
31	B1	582	THR
32	B2	17	ILE
32	B2	132	THR
32	B2	166	ILE
32	B2	343	TRP
32	B2	362	ILE
32	B2	394	VAL
32	B2	497	VAL
32	B2	569	LEU
32	B2	576	VAL
32	B2	577	LEU
33	B3	346	VAL
33	B3	403	ILE
33	B3	438	THR

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Mol	Chain	Res	Type
33	B3	442	LEU
33	B3	698	LEU
33	B3	769	ILE
34	B8	254	LEU
34	B8	286	THR
34	B8	406	ASP
34	B8	432	VAL
34	B8	511	LEU
34	B8	534	SER
34	B8	541	LEU
34	B8	586	VAL
35	BE	98	VAL
35	BE	177	LEU
35	BE	189	LEU
35	BE	423	ARG
35	BE	500	LEU
35	BE	651	ILE
35	BE	713	LEU
35	BE	888	LEU
36	B6	18	LEU
36	B6	175	ASN
36	B6	196	LEU
37	5C	228	LEU
37	5C	291	THR
37	5C	443	THR
39	5E	451	LEU
41	5G	89	ILE
41	5G	185	VAL
43	5I	204	TRP
43	5I	238	THR
43	5I	255	THR
43	5I	372	VAL
43	5I	464	THR
44	5J	69	PHE
46	RD	1683	ILE
47	RE	474	VAL
47	RE	476	ILE
47	RE	477	LEU
47	RE	482	VAL
47	RE	531	LEU
47	RE	1213	ILE
47	RE	1214	LEU

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Mol	Chain	Res	Type
48	RF	56	VAL
48	RF	176	ASP
50	RJ	160	GLN
50	RJ	252	LEU
50	RJ	290	ILE
50	RJ	616	ASP
50	RJ	902	VAL
50	RJ	1021	LEU
51	RK	8	TYR
51	RK	244	THR
51	RK	246	VAL
51	RK	326	LEU
51	RK	354	ILE
53	RP	26	LEU
53	RP	1756	ILE
53	RP	1880	ILE
53	RP	1963	LEU
55	RT	234	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (285) such sidechains are listed below:

Mol	Chain	Res	Type
4	SC	74	GLN
4	SC	101	HIS
4	SC	199	ASN
5	SF	69	HIS
5	SF	157	ASN
5	SF	188	ASN
6	SG	35	GLN
6	SG	104	ASN
6	SG	131	GLN
7	SH	4	ASN
8	SI	11	GLN
8	SI	22	GLN
8	SI	147	ASN
8	SI	174	ASN
9	SJ	103	GLN
9	SJ	119	GLN
10	SK	74	ASN
10	SK	123	HIS
10	SK	131	GLN
11	SM	14	GLN

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Mol	Chain	Res	Type
11	SM	22	ASN
11	SM	81	HIS
11	SM	127	GLN
12	SO	58	HIS
14	SR	100	GLN
15	SX	12	ASN
16	SY	79	ASN
17	SZ	29	HIS
17	SZ	31	ASN
18	Sc	5	GLN
18	Sc	9	HIS
18	Sc	19	HIS
19	Sd	51	ASN
20	3B	228	GLN
20	3C	201	HIS
21	3D	23	GLN
21	3D	24	GLN
21	3D	39	ASN
21	3D	65	ASN
21	3D	85	ASN
21	3D	125	GLN
21	3D	151	GLN
21	3D	156	HIS
21	3D	168	GLN
21	3D	213	ASN
22	3E	254	ASN
22	3E	261	GLN
22	3E	286	ASN
22	3E	396	ASN
23	3F	128	GLN
23	3F	156	ASN
23	3F	230	ASN
23	3F	322	HIS
23	3F	366	GLN
23	3F	561	ASN
24	3G	5	ASN
24	3G	18	GLN
24	3H	5	ASN
24	3H	26	GLN
25	A4	53	HIS
25	A4	140	ASN
25	A4	179	HIS

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Mol	Chain	Res	Type
25	A4	274	GLN
25	A4	315	GLN
25	A4	317	ASN
25	A4	340	GLN
25	A4	589	ASN
25	A4	632	ASN
25	A4	642	ASN
25	A4	766	GLN
26	A5	7	GLN
26	A5	138	GLN
26	A5	302	ASN
26	A5	308	ASN
26	A5	316	ASN
26	A5	552	ASN
27	A9	500	GLN
28	AE	7	GLN
28	AE	14	ASN
28	AE	96	ASN
28	AE	128	HIS
28	AE	208	ASN
28	AE	209	GLN
28	AE	224	ASN
28	AE	258	HIS
29	AF	44	HIS
29	AF	50	GLN
29	AF	161	GLN
29	AF	263	ASN
29	AF	289	ASN
29	AF	394	GLN
29	AF	419	GLN
29	AF	472	ASN
30	AG	50	ASN
30	AG	113	ASN
30	AG	166	ASN
30	AG	331	GLN
30	AG	370	GLN
30	AG	393	ASN
30	AG	401	GLN
30	AG	418	ASN
30	AG	453	HIS
30	AG	467	GLN
30	AG	489	ASN

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Mol	Chain	Res	Type
30	AG	549	ASN
30	AG	568	ASN
30	AG	569	ASN
30	AG	579	ASN
30	AG	690	ASN
30	AG	756	ASN
30	AG	883	GLN
31	B1	88	ASN
31	B1	92	HIS
31	B1	296	GLN
31	B1	394	GLN
31	B1	400	GLN
31	B1	456	HIS
31	B1	734	GLN
31	B1	752	ASN
31	B1	795	ASN
31	B1	837	ASN
31	B1	842	ASN
32	B2	10	GLN
32	B2	195	GLN
32	B2	383	HIS
32	B2	620	ASN
32	B2	657	GLN
32	B2	677	HIS
32	B2	770	ASN
32	B2	798	ASN
32	B2	847	HIS
32	B2	856	ASN
32	B2	881	ASN
32	B2	913	ASN
32	B2	916	HIS
33	B3	81	GLN
33	B3	210	ASN
33	B3	322	ASN
33	B3	337	HIS
33	B3	444	ASN
33	B3	478	GLN
33	B3	543	GLN
33	B3	589	GLN
33	B3	616	HIS
33	B3	665	GLN
33	B3	696	ASN

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Mol	Chain	Res	Type
33	B3	735	GLN
33	B3	767	HIS
33	B3	798	ASN
34	B8	162	ASN
34	B8	167	GLN
34	B8	296	GLN
34	B8	308	ASN
34	B8	311	ASN
34	B8	362	HIS
34	B8	385	ASN
34	B8	427	ASN
34	B8	440	ASN
34	B8	450	GLN
34	B8	513	GLN
34	B8	545	HIS
34	B8	581	ASN
35	BE	67	HIS
35	BE	86	HIS
35	BE	171	GLN
35	BE	172	HIS
35	BE	263	HIS
35	BE	351	GLN
35	BE	387	GLN
35	BE	421	ASN
35	BE	429	ASN
35	BE	473	ASN
35	BE	481	ASN
35	BE	490	GLN
35	BE	586	ASN
35	BE	627	ASN
35	BE	631	ASN
35	BE	916	HIS
36	B6	10	GLN
36	B6	64	ASN
36	B6	115	ASN
36	B6	166	ASN
36	B6	207	ASN
37	5C	36	GLN
37	5C	88	GLN
37	5C	151	ASN
37	5C	170	GLN
37	5C	217	HIS

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Mol	Chain	Res	Type
37	5C	240	GLN
37	5C	310	HIS
37	5C	337	HIS
37	5C	394	HIS
37	5C	424	GLN
37	5C	435	ASN
38	5D	45	GLN
39	5E	303	GLN
39	5E	310	GLN
39	5E	316	ASN
39	5E	443	ASN
40	5F	39	GLN
41	5G	102	GLN
41	5G	118	ASN
41	5G	145	HIS
41	5G	169	ASN
42	5H	573	GLN
43	5I	46	ASN
43	5I	96	ASN
43	5I	207	ASN
43	5I	276	ASN
43	5I	293	ASN
43	5I	353	GLN
43	5I	371	ASN
43	5I	392	ASN
44	5J	126	HIS
44	5J	135	HIS
44	5J	165	ASN
45	5K	43	ASN
45	5K	148	HIS
45	5K	178	HIS
46	RD	1515	ASN
46	RD	1522	ASN
46	RD	1525	ASN
46	RD	1542	GLN
46	RD	1607	ASN
46	RD	1616	ASN
46	RD	1656	ASN
46	RD	1687	GLN
47	RE	136	GLN
47	RE	170	GLN
47	RE	221	ASN

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Mol	Chain	Res	Type
47	RE	261	ASN
47	RE	313	ASN
47	RE	441	GLN
47	RE	475	ASN
47	RE	530	GLN
47	RE	564	HIS
47	RE	568	ASN
47	RE	582	GLN
47	RE	588	GLN
47	RE	607	HIS
47	RE	665	HIS
47	RE	743	GLN
47	RE	872	ASN
47	RE	1023	ASN
47	RE	1148	GLN
47	RE	1172	ASN
47	RE	1194	HIS
47	RE	1203	ASN
48	RF	57	ASN
48	RF	66	HIS
48	RF	146	ASN
48	RF	187	HIS
48	RF	232	ASN
48	RF	268	GLN
48	RF	272	GLN
49	RH	105	ASN
49	RH	125	ASN
49	RH	215	ASN
50	RJ	99	ASN
50	RJ	222	ASN
50	RJ	300	GLN
50	RJ	766	ASN
50	RJ	770	GLN
50	RJ	803	ASN
50	RJ	1037	GLN
50	RJ	1049	ASN
51	RK	88	HIS
51	RK	206	ASN
51	RK	251	GLN
52	RN	786	ASN
52	RN	789	ASN
52	RN	797	ASN

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Mol	Chain	Res	Type
53	RP	33	ASN
53	RP	89	ASN
53	RP	115	HIS
53	RP	146	ASN
53	RP	1688	HIS
53	RP	1801	ASN
53	RP	1802	HIS
53	RP	1996	GLN
54	RQ	316	ASN
54	RQ	331	GLN
55	RT	127	GLN
55	RT	218	ASN
55	RT	262	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	189/333 (56%)	77 (40%)	3 (1%)
2	5A	144/700 (20%)	62 (43%)	2 (1%)
3	SA	1137/1809 (62%)	413 (36%)	20 (1%)
All	All	1470/2842 (51%)	552 (37%)	25 (1%)

All (552) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3A	4	G
1	3A	12	U
1	3A	15	U
1	3A	24	U
1	3A	25	U
1	3A	28	A
1	3A	30	A
1	3A	31	G
1	3A	33	A
1	3A	34	A
1	3A	35	U
1	3A	37	G
1	3A	38	U
1	3A	39	C
1	3A	46	U
1	3A	47	G

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Mol	Chain	Res	Type
1	3A	49	C
1	3A	51	C
1	3A	53	U
1	3A	54	C
1	3A	56	A
1	3A	59	G
1	3A	61	G
1	3A	67	G
1	3A	81	U
1	3A	82	G
1	3A	87	G
1	3A	88	U
1	3A	89	C
1	3A	90	C
1	3A	91	C
1	3A	92	A
1	3A	93	U
1	3A	94	A
1	3A	95	A
1	3A	101	G
1	3A	103	A
1	3A	104	C
1	3A	105	C
1	3A	107	C
1	3A	108	A
1	3A	109	G
1	3A	110	A
1	3A	111	G
1	3A	114	A
1	3A	115	G
1	3A	116	A
1	3A	198	U
1	3A	199	G
1	3A	203	U
1	3A	204	U
1	3A	205	G
1	3A	206	C
1	3A	207	A
1	3A	243	U
1	3A	247	U
1	3A	248	G
1	3A	249	G

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Mol	Chain	Res	Type
1	3A	252	C
1	3A	255	U
1	3A	256	G
1	3A	261	U
1	3A	262	G
1	3A	263	A
1	3A	265	C
1	3A	266	C
1	3A	267	A
1	3A	268	U
1	3A	270	C
1	3A	311	G
1	3A	313	A
1	3A	314	C
1	3A	315	A
1	3A	320	G
1	3A	324	U
1	3A	325	C
1	3A	329	C
2	5A	4	C
2	5A	6	A
2	5A	7	A
2	5A	8	A
2	5A	9	G
2	5A	10	C
2	5A	11	A
2	5A	12	G
2	5A	14	U
2	5A	15	G
2	5A	59	U
2	5A	63	G
2	5A	64	U
2	5A	83	U
2	5A	86	C
2	5A	87	C
2	5A	88	U
2	5A	89	C
2	5A	90	G
2	5A	279	A
2	5A	280	A
2	5A	281	G
2	5A	292	A

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Mol	Chain	Res	Type
2	5A	296	C
2	5A	297	U
2	5A	299	G
2	5A	302	A
2	5A	305	A
2	5A	306	G
2	5A	310	U
2	5A	311	C
2	5A	312	U
2	5A	313	A
2	5A	465	G
2	5A	466	A
2	5A	468	A
2	5A	469	C
2	5A	470	U
2	5A	471	C
2	5A	474	A
2	5A	475	G
2	5A	479	G
2	5A	481	U
2	5A	482	A
2	5A	484	G
2	5A	497	A
2	5A	500	G
2	5A	501	C
2	5A	536	A
2	5A	539	A
2	5A	540	U
2	5A	541	U
2	5A	542	U
2	5A	544	C
2	5A	548	A
2	5A	553	A
2	5A	555	A
2	5A	583	U
2	5A	585	C
2	5A	586	A
2	5A	587	G
2	5A	590	G
3	SA	-4	A
3	SA	-1	G
3	SA	0	U

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Mol	Chain	Res	Type
3	SA	1	U
3	SA	6	G
3	SA	10	G
3	SA	17	C
3	SA	18	C
3	SA	20	G
3	SA	21	U
3	SA	25	C
3	SA	26	A
3	SA	31	C
3	SA	34	G
3	SA	38	C
3	SA	40	A
3	SA	50	C
3	SA	57	G
3	SA	60	U
3	SA	63	G
3	SA	66	U
3	SA	68	A
3	SA	69	G
3	SA	71	A
3	SA	72	A
3	SA	73	U
3	SA	74	U
3	SA	75	U
3	SA	76	A
3	SA	77	U
3	SA	78	A
3	SA	80	A
3	SA	92	A
3	SA	107	C
3	SA	108	A
3	SA	114	C
3	SA	116	U
3	SA	127	G
3	SA	140	A
3	SA	143	G
3	SA	146	U
3	SA	152	U
3	SA	153	G
3	SA	155	U
3	SA	157	A

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Mol	Chain	Res	Type
3	SA	160	C
3	SA	161	U
3	SA	166	C
3	SA	167	U
3	SA	169	A
3	SA	176	C
3	SA	177	U
3	SA	182	A
3	SA	184	C
3	SA	185	U
3	SA	186	C
3	SA	187	G
3	SA	189	C
3	SA	191	C
3	SA	192	U
3	SA	194	U
3	SA	195	G
3	SA	196	G
3	SA	198	A
3	SA	199	G
3	SA	200	A
3	SA	201	G
3	SA	204	G
3	SA	215	A
3	SA	231	U
3	SA	233	C
3	SA	234	G
3	SA	236	A
3	SA	238	U
3	SA	239	C
3	SA	241	U
3	SA	243	G
3	SA	246	G
3	SA	248	U
3	SA	249	U
3	SA	250	C
3	SA	257	A
3	SA	259	U
3	SA	260	U
3	SA	261	U
3	SA	262	U
3	SA	265	A

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Mol	Chain	Res	Type
3	SA	270	C
3	SA	271	A
3	SA	272	U
3	SA	275	C
3	SA	277	U
3	SA	278	U
3	SA	279	G
3	SA	281	G
3	SA	285	G
3	SA	288	A
3	SA	299	A
3	SA	301	A
3	SA	312	A
3	SA	313	U
3	SA	314	C
3	SA	316	A
3	SA	318	U
3	SA	320	U
3	SA	321	C
3	SA	322	G
3	SA	325	G
3	SA	328	A
3	SA	329	G
3	SA	333	A
3	SA	334	G
3	SA	336	G
3	SA	337	G
3	SA	338	C
3	SA	341	A
3	SA	350	U
3	SA	351	C
3	SA	352	A
3	SA	354	C
3	SA	433	C
3	SA	434	G
3	SA	435	C
3	SA	437	A
3	SA	438	A
3	SA	439	U
3	SA	440	U
3	SA	444	C
3	SA	445	A

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Mol	Chain	Res	Type
3	SA	448	C
3	SA	453	U
3	SA	454	U
3	SA	455	C
3	SA	456	A
3	SA	468	A
3	SA	469	C
3	SA	477	A
3	SA	480	G
3	SA	484	C
3	SA	485	A
3	SA	487	G
3	SA	488	G
3	SA	492	A
3	SA	493	U
3	SA	494	U
3	SA	495	C
3	SA	500	C
3	SA	501	U
3	SA	502	U
3	SA	504	U
3	SA	506	A
3	SA	507	U
3	SA	508	U
3	SA	510	G
3	SA	511	A
3	SA	514	G
3	SA	519	C
3	SA	520	A
3	SA	525	A
3	SA	534	A
3	SA	536	C
3	SA	538	A
3	SA	539	G
3	SA	540	G
3	SA	541	A
3	SA	542	A
3	SA	543	C
3	SA	545	A
3	SA	548	G
3	SA	557	G
3	SA	563	U

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Mol	Chain	Res	Type
3	SA	570	A
3	SA	572	C
3	SA	573	C
3	SA	574	G
3	SA	575	C
3	SA	579	A
3	SA	580	A
3	SA	583	C
3	SA	584	C
3	SA	585	A
3	SA	587	C
3	SA	594	A
3	SA	595	G
3	SA	602	U
3	SA	603	U
3	SA	634	G
3	SA	635	A
3	SA	638	U
3	SA	639	U
3	SA	640	U
3	SA	641	G
3	SA	642	G
3	SA	643	G
3	SA	644	C
3	SA	649	U
3	SA	653	C
3	SA	654	C
3	SA	655	G
3	SA	656	G
3	SA	657	U
3	SA	678	A
3	SA	684	A
3	SA	685	A
3	SA	686	C
3	SA	687	G
3	SA	692	C
3	SA	693	U
3	SA	694	U
3	SA	696	C
3	SA	747	C
3	SA	748	U
3	SA	751	G

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Mol	Chain	Res	Type
3	SA	752	A
3	SA	754	A
3	SA	755	A
3	SA	758	U
3	SA	759	U
3	SA	763	G
3	SA	765	G
3	SA	766	U
3	SA	771	A
3	SA	772	G
3	SA	774	A
3	SA	775	G
3	SA	778	G
3	SA	779	U
3	SA	780	A
3	SA	781	U
3	SA	782	U
3	SA	783	G
3	SA	784	C
3	SA	785	U
3	SA	786	C
3	SA	787	G
3	SA	788	A
3	SA	789	A
3	SA	790	U
3	SA	794	U
3	SA	802	G
3	SA	803	A
3	SA	804	A
3	SA	805	U
3	SA	809	A
3	SA	810	G
3	SA	811	A
3	SA	812	A
3	SA	813	U
3	SA	814	A
3	SA	815	G
3	SA	822	U
3	SA	824	G
3	SA	827	C
3	SA	828	U
3	SA	841	U

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Mol	Chain	Res	Type
3	SA	845	G
3	SA	858	G
3	SA	859	A
3	SA	860	U
3	SA	863	A
3	SA	864	U
3	SA	873	U
3	SA	876	G
3	SA	877	G
3	SA	894	U
3	SA	898	A
3	SA	905	A
3	SA	906	A
3	SA	913	G
3	SA	914	G
3	SA	928	U
3	SA	929	A
3	SA	933	A
3	SA	935	U
3	SA	944	A
3	SA	951	A
3	SA	960	U
3	SA	966	A
3	SA	969	C
3	SA	971	A
3	SA	976	G
3	SA	1052	U
3	SA	1053	G
3	SA	1056	U
3	SA	1057	U
3	SA	1058	U
3	SA	1059	U
3	SA	1060	U
3	SA	1063	U
3	SA	1064	G
3	SA	1076	A
3	SA	1080	U
3	SA	1110	G
3	SA	1111	G
3	SA	1114	G
3	SA	1118	G
3	SA	1119	G

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Mol	Chain	Res	Type
3	SA	1122	G
3	SA	1125	A
3	SA	1127	G
3	SA	1128	C
3	SA	1131	A
3	SA	1132	A
3	SA	1133	A
3	SA	1134	C
3	SA	1135	U
3	SA	1141	G
3	SA	1142	A
3	SA	1143	A
3	SA	1146	G
3	SA	1158	C
3	SA	1164	G
3	SA	1469	A
3	SA	1471	A
3	SA	1472	C
3	SA	1473	U
3	SA	1474	G
3	SA	1476	C
3	SA	1477	G
3	SA	1488	G
3	SA	1489	U
3	SA	1531	G
3	SA	1535	U
3	SA	1536	G
3	SA	1537	C
3	SA	1538	U
3	SA	1539	G
3	SA	1573	A
3	SA	1575	G
3	SA	1577	A
3	SA	1584	G
3	SA	1590	G
3	SA	1592	A
3	SA	1595	U
3	SA	1596	C
3	SA	1600	A
3	SA	1601	G
3	SA	1602	C
3	SA	1614	A

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Mol	Chain	Res	Type
3	SA	1618	C
3	SA	1619	C
3	SA	1622	G
3	SA	1628	U
3	SA	1630	U
3	SA	1631	A
3	SA	1639	C
3	SA	1651	A
3	SA	1654	G
3	SA	1657	U
3	SA	1658	G
3	SA	1664	C
3	SA	1665	U
3	SA	1666	U
3	SA	1668	G
3	SA	1671	A
3	SA	1672	G
3	SA	1678	A
3	SA	1679	G
3	SA	1680	G
3	SA	1681	A
3	SA	1682	U
3	SA	1683	C
3	SA	1686	C
3	SA	1687	U
3	SA	1689	A
3	SA	1694	A
3	SA	1698	G
3	SA	1702	A
3	SA	1703	C
3	SA	1704	U
3	SA	1708	U
3	SA	1709	C
3	SA	1710	U
3	SA	1711	C
3	SA	1712	A
3	SA	1713	G
3	SA	1714	A
3	SA	1715	G
3	SA	1716	C
3	SA	1717	G
3	SA	1718	G

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Mol	Chain	Res	Type
3	SA	1719	A
3	SA	1721	A
3	SA	1724	U
3	SA	1725	U
3	SA	1732	A
3	SA	1734	U
3	SA	1735	U
3	SA	1736	G
3	SA	1743	U
3	SA	1745	G
3	SA	1747	G
3	SA	1749	A
3	SA	1751	C
3	SA	1755	A
3	SA	1756	A
3	SA	1757	G
3	SA	1768	G
3	SA	1769	U
3	SA	1780	G
3	SA	1781	A
3	SA	1782	A
3	SA	1789	G
3	SA	1791	A
3	SA	1792	G
3	SA	1793	G
3	SA	1794	A
3	SA	1795	U
3	SA	1797	A
3	SA	1798	U
3	SA	1799	U
3	SA	1800	A
3	SA	1801	A

All (25) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	3A	102	U
1	3A	107	C
1	3A	248	G
2	5A	6	A
2	5A	311	C
3	SA	0	U

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Mol	Chain	Res	Type
3	SA	68	A
3	SA	139	C
3	SA	278	U
3	SA	280	U
3	SA	454	U
3	SA	484	C
3	SA	503	G
3	SA	542	A
3	SA	579	A
3	SA	602	U
3	SA	637	C
3	SA	685	A
3	SA	773	C
3	SA	781	U
3	SA	1052	U
3	SA	1063	U
3	SA	1471	A
3	SA	1594	G
3	SA	1754	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 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
58	GTP	RJ	1201	59	33,34,34	0.85	1 (3%)	50,54,54	1.63	9 (18%)

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
58	GTP	RJ	1201	59	-	1/22/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	RJ	1201	GTP	C2-N3	2.01	1.38	1.33

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	RJ	1201	GTP	C5-C4-N3	-5.13	120.23	128.39
58	RJ	1201	GTP	C2-N3-C4	4.71	120.41	112.30
58	RJ	1201	GTP	C2-N1-C6	-3.20	119.31	125.11
58	RJ	1201	GTP	N9-C4-N3	3.14	132.23	125.95
58	RJ	1201	GTP	N9-C8-N7	-2.91	108.00	113.40
58	RJ	1201	GTP	C5-C6-N1	2.71	120.16	113.25
58	RJ	1201	GTP	C8-N7-C5	2.67	109.02	104.26
58	RJ	1201	GTP	O6-C6-C5	-2.36	120.29	126.53
58	RJ	1201	GTP	C3'-C2'-C1'	2.04	105.32	101.46

There are no chirality outliers.

All (1) torsion outliers are listed below:

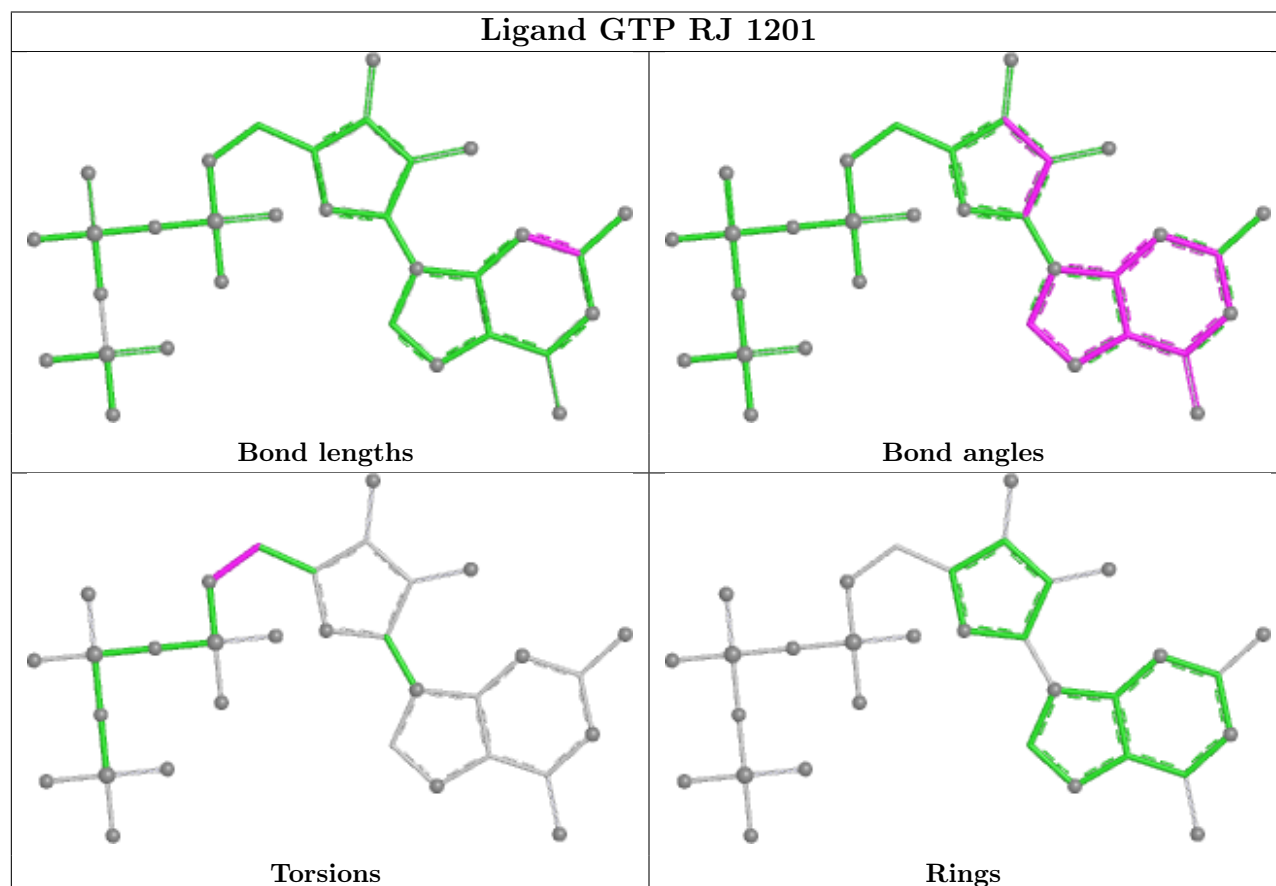
Mol	Chain	Res	Type	Atoms
58	RJ	1201	GTP	C4'-C5'-O5'-PA

There are no ring outliers.

No monomer is involved in short contacts.

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.

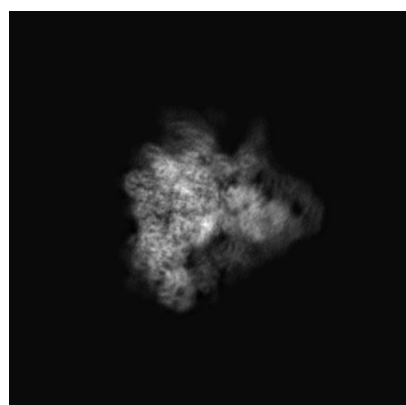
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0953. These allow visual inspection of the internal detail of the map and identification of artifacts.

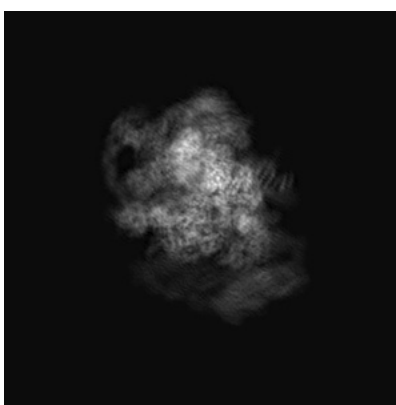
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

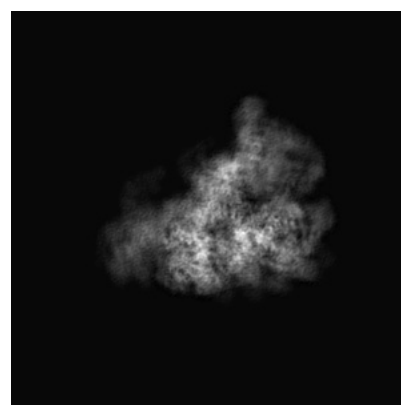
6.1.1 Primary map



X



Y

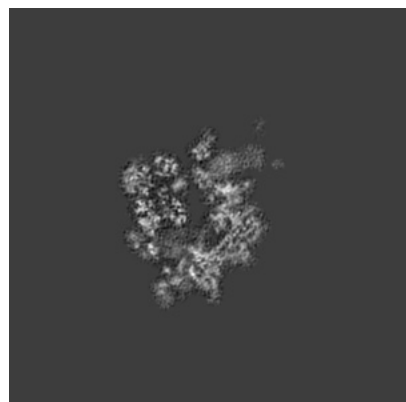


Z

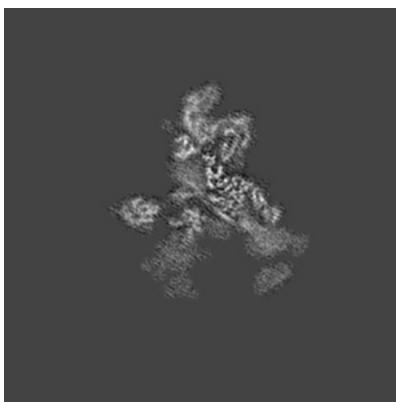
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 224



Y Index: 224

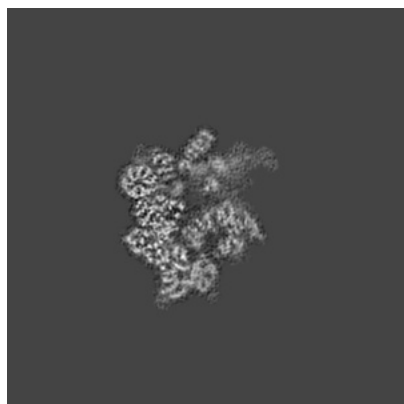


Z Index: 224

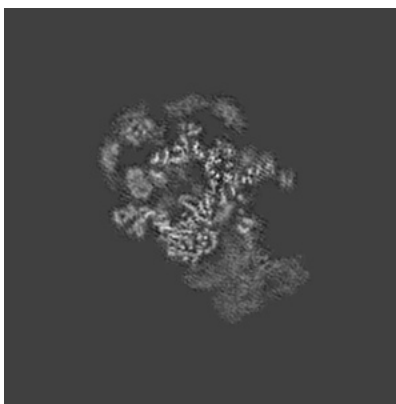
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

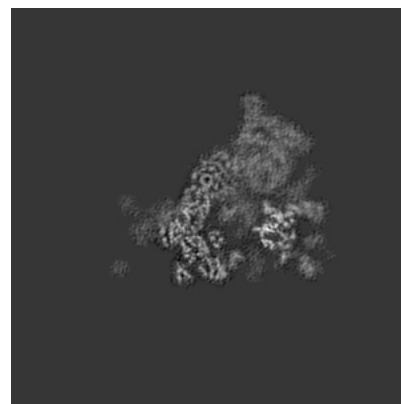
6.3.1 Primary map



X Index: 215



Y Index: 190

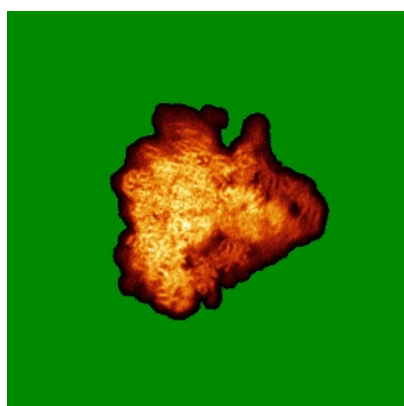


Z Index: 208

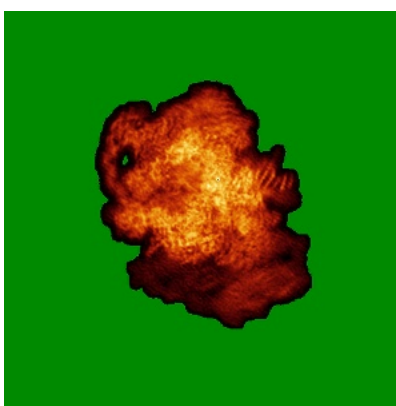
The images above show the largest variance slices of the map in three orthogonal directions.

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

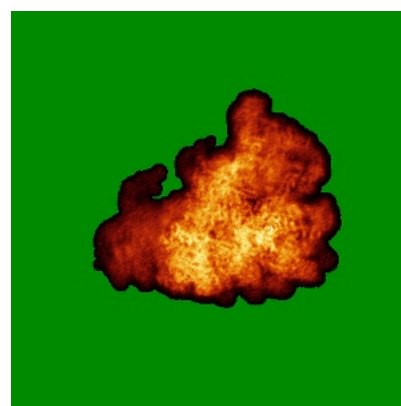
6.4.1 Primary map



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

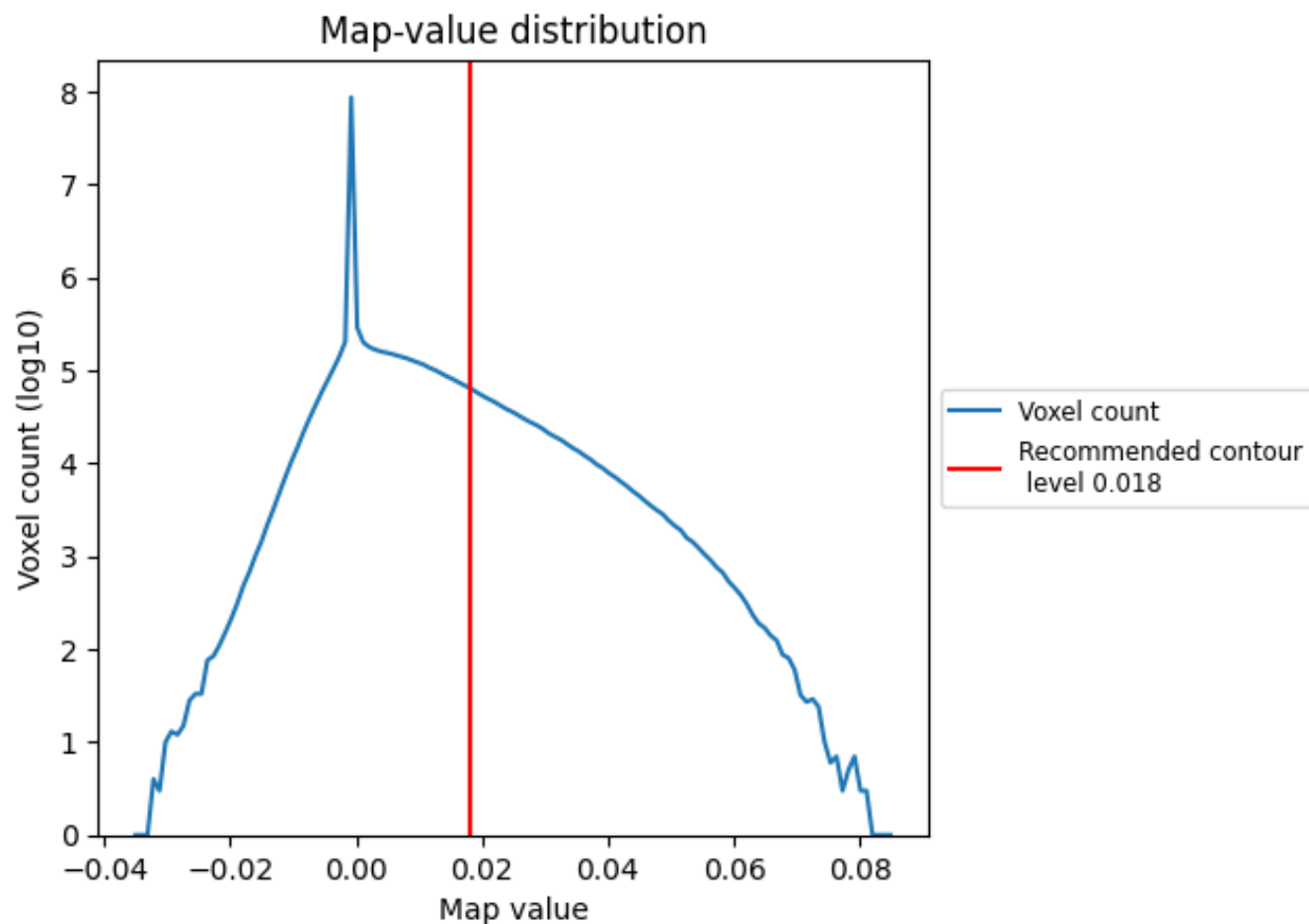
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

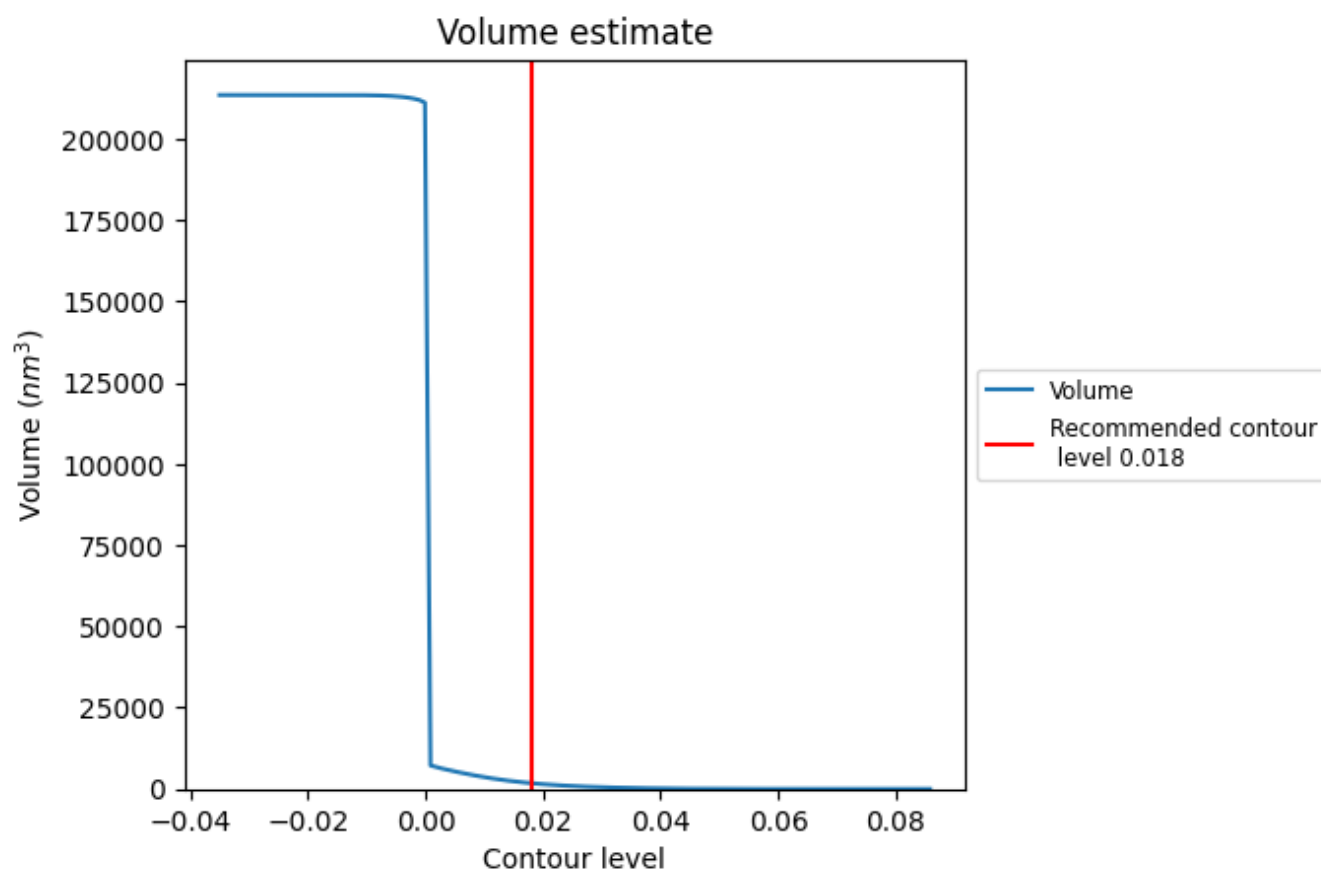
This section contains the results of statistical analysis of the map.

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.

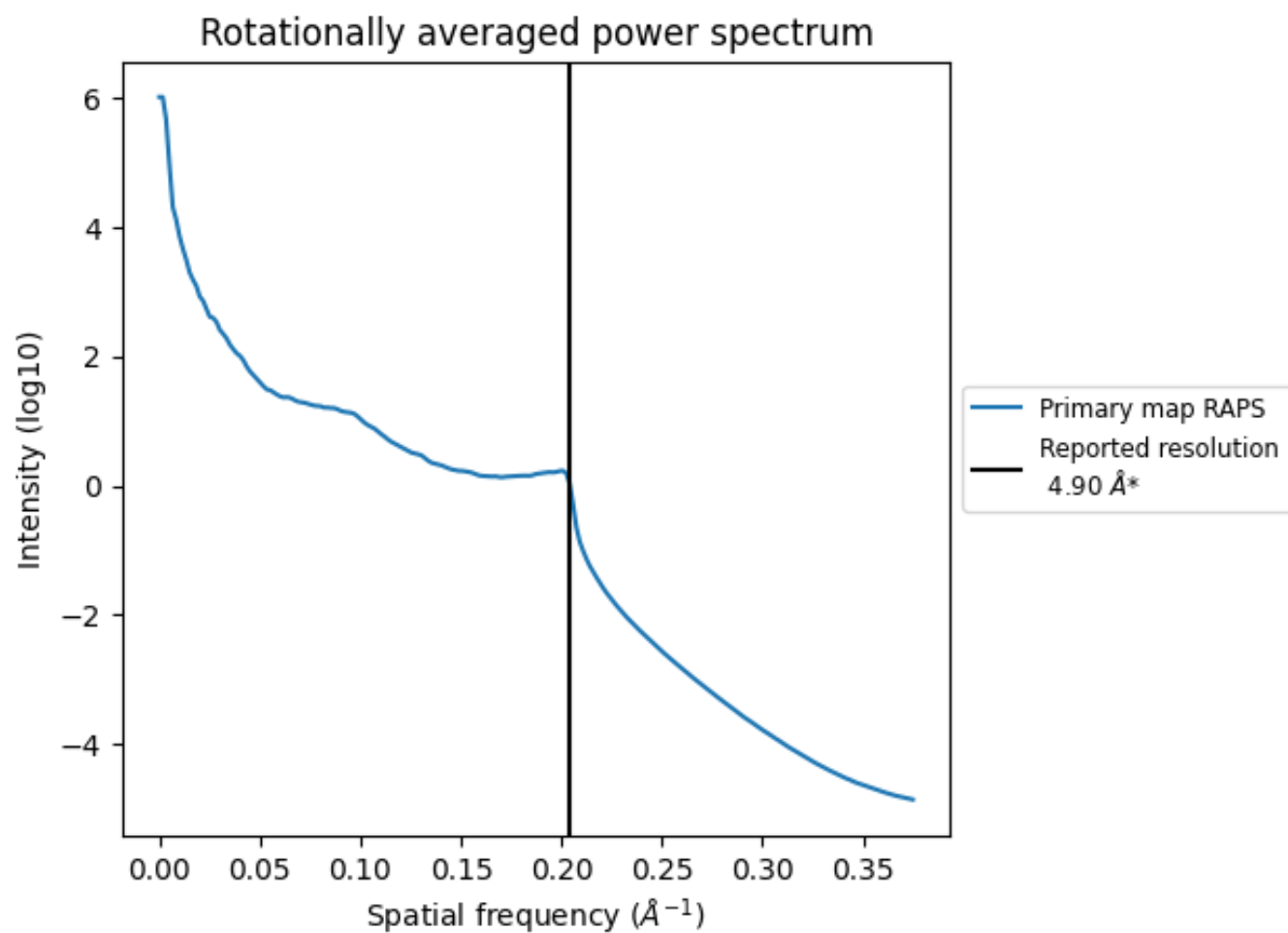
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1775 nm^3 ; this corresponds to an approximate mass of 1603 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 0.204 Å⁻¹

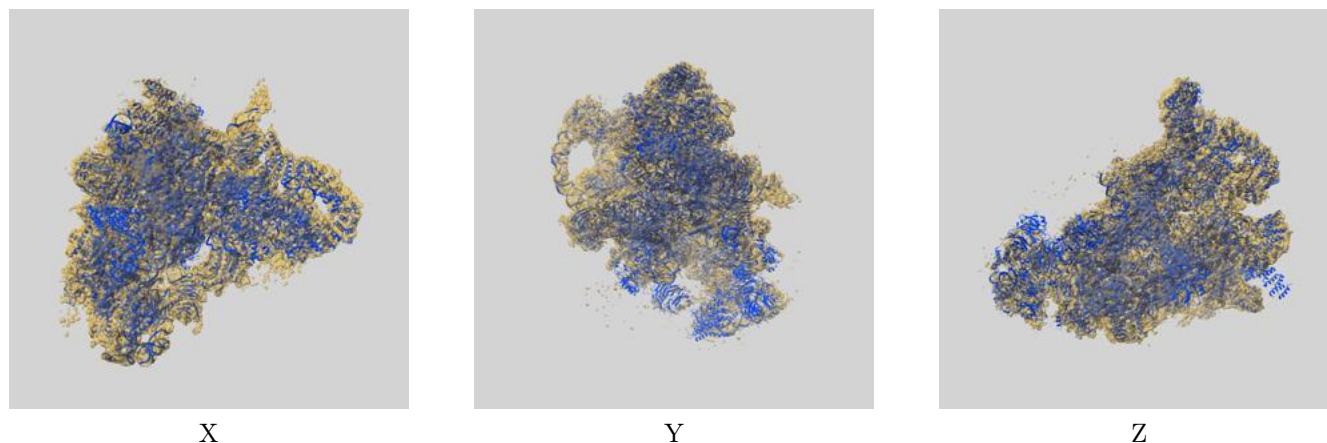
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

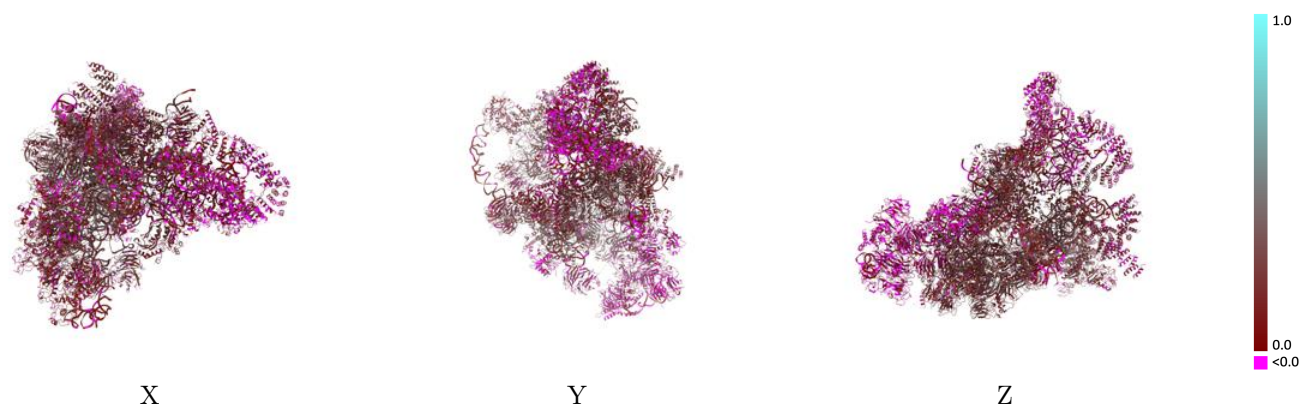
This section contains information regarding the fit between EMDB map EMD-0953 and PDB model 6LQT. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



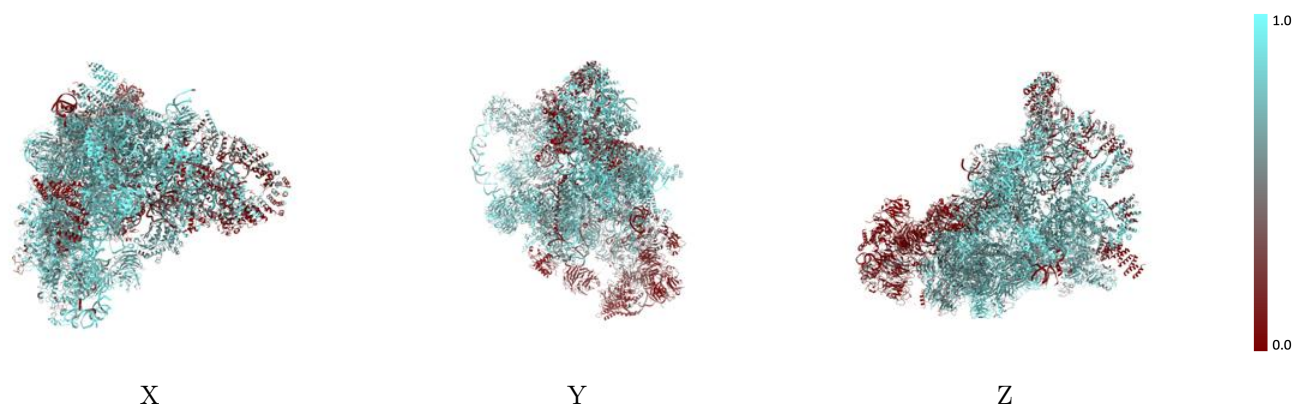
The images above show the 3D surface view of the map at the recommended contour level 0.018 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



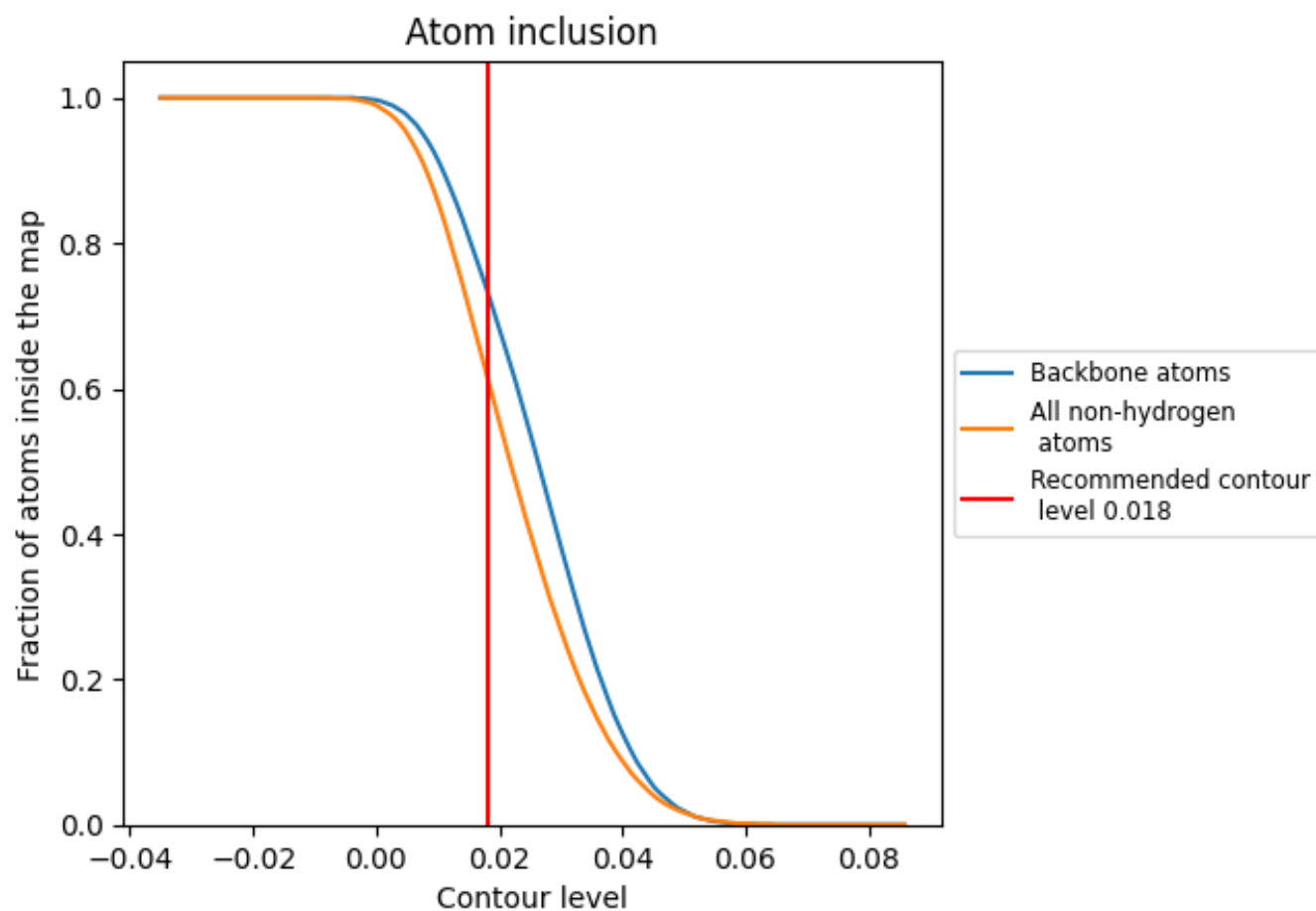
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.018).

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 62% 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 (0.018) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6170	 0.1760
3A	 0.7220	 0.1730
3B	 0.7350	 0.2510
3C	 0.2290	 0.0270
3D	 0.7200	 0.2100
3E	 0.5210	 0.1280
3F	 0.7380	 0.1990
3G	 0.5690	 0.0750
3H	 0.7190	 0.2500
5A	 0.4470	 0.1260
5C	 0.7510	 0.2720
5D	 0.4040	 0.1920
5E	 0.6550	 0.2140
5F	 0.7150	 0.2580
5G	 0.5840	 0.2170
5H	 0.7250	 0.2260
5I	 0.7840	 0.2810
5J	 0.4590	 0.1630
5K	 0.7250	 0.2770
A4	 0.0530	 0.0370
A5	 0.5280	 0.1980
A9	 0.0340	 -0.0100
AE	 0.6560	 0.2260
AF	 0.0570	 0.0650
AG	 0.1490	 0.0500
B1	 0.7890	 0.2790
B2	 0.7740	 0.1980
B3	 0.8130	 0.1990
B6	 0.7470	 0.2190
B8	 0.6200	 0.1640
BE	 0.7970	 0.2680
RD	 0.1150	 0.0930
RE	 0.7000	 0.1860
RF	 0.6930	 0.1820
RH	 0.0450	 0.0060



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Chain	Atom inclusion	Q-score
RJ	 0.6150	 0.1880
RK	 0.6710	 0.1890
RN	 0.1260	 0.1140
RP	 0.5610	 0.1180
RQ	 0.6330	 0.2320
RT	 0.5970	 0.1850
SA	 0.7860	 0.1830
SC	 0.7430	 0.2580
SF	 0.5820	 0.0960
SG	 0.7470	 0.2420
SH	 0.3820	 0.0560
SI	 0.6830	 0.2190
SJ	 0.4120	 0.0390
SK	 0.7420	 0.2280
SM	 0.2760	 0.0230
SO	 0.7900	 0.2440
SP	 0.7420	 0.2350
SR	 0.7600	 0.2490
SX	 0.7770	 0.2820
SY	 0.4970	 0.1920
SZ	 0.7190	 0.1340
Sc	 0.7700	 0.2800
Sd	 0.7710	 0.2780
X1	 0.5020	 0.1910