



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 10:59 AM UTC

PDB ID : 6LQQ / pdb_00006lqq
EMDB ID : EMD-0950
Title : Cryo-EM structure of 90S small subunit preribosomes in transition states (State B)
Authors : Du, Y.; Ye, K.
Deposited on : 2020-01-14
Resolution : 4.10 Å(reported)
Based on initial model : 6LQP

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

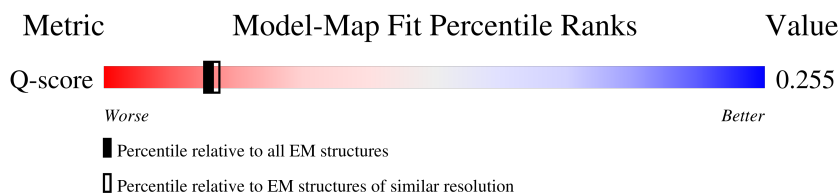
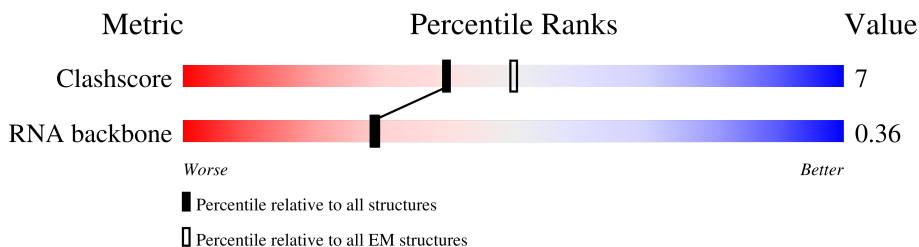
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.10 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	6458 (3.60 - 4.60)

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

Mol	Chain	Length	Quality of chain
1	3A	333	
2	5A	700	
3	SA	1808	
4	SC	255	
5	SF	261	

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Mol	Chain	Length	Quality of chain
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	573	
24	3G	126	
24	3H	126	
25	A4	776	
26	A5	643	
27	A8	713	
28	A9	575	

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Mol	Chain	Length	Quality of chain
29	AE	1769	
30	AF	513	
31	AG	896	
32	B1	923	
33	B2	943	
34	B3	817	
35	B8	594	
36	BE	939	
37	B6	440	
38	5B	214	
39	5C	554	
40	5D	250	
41	5E	593	
42	5F	183	
43	5G	290	
44	5H	610	
45	5I	489	
46	5J	217	
47	5K	189	
48	RA	707	
49	RB	357	
50	RC	316	
51	RD	1729	
52	RE	1237	
53	RF	297	

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Mol	Chain	Length	Quality of chain
54	RG	252	
54	RH	252	
55	RJ	1183	
56	RK	367	
57	RL	1056	
57	RM	1056	
58	RN	810	
59	RO	552	
60	RP	2493	
61	RQ	899	
62	RS	483	
63	RT	326	
64	RV	346	
65	RY	534	
66	X1	347	

2 Entry composition

There are 69 unique types of molecules in this entry. The entry contains 226161 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called U3 snoRNA.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5A	375	Total	C	N	O	P	0	0
			8009	3578	1426	2630	375		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SA	1323	Total	C	N	O	P	0	0
			28210	12608	5022	9257	1323		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 12 is a protein called 40S ribosomal protein 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	103	Total	C	N	O	S	0	0
			786	503	144	137	2		

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

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

- 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 fibrillarin.

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	369	Total	C	N	O	S	0	0
			2848	1811	489	540	8		

- Molecule 22 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	3E	431	Total	C	N	O	S	0	0
			3028	1888	543	588	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	3F	454	Total	C	N	O	S	0	0
			3643	2315	638	680	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	662	Total	C	N	O	S	0	0
			5226	3309	910	986	21		

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

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

- Molecule 27 is a protein called U3 small nucleolar RNA-associated protein 8.

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

- Molecule 28 is a protein called U3 small nucleolar RNA-associated protein 9.

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

- Molecule 29 is a protein called U3 small nucleolar RNA-associated protein 10.

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

- Molecule 30 is a protein called U3 small nucleolar RNA-associated protein 15.

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

- Molecule 31 is a protein called NET1-associated nuclear protein 1.

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

- Molecule 32 is a protein called Periodic tryptophan protein 2.

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

- Molecule 33 is a protein called U3 small nucleolar RNA-associated protein 12.

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

- Molecule 34 is a protein called U3 small nucleolar RNA-associated protein 13.

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

- Molecule 35 is a protein called U3 small nucleolar RNA-associated protein 18.

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

- Molecule 36 is a protein called U3 small nucleolar RNA-associated protein 21.

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

- Molecule 37 is a protein called U3 small nucleolar RNA-associated protein 6.

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

- Molecule 38 is a protein called Bud site selection protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	5B	60	Total	C	N	O		0	0
			495	310	101	84			

- Molecule 39 is a protein called U3 small nucleolar RNA-associated protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	5C	535	Total	C	N	O	S	0	0
			4237	2656	762	807	12		

- Molecule 40 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	5D	167	Total	C	N	O	S	0	0
			1396	862	266	263	5		

- Molecule 41 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	5E	204	Total	C	N	O	S	0	0
			1647	1021	294	328	4		

- Molecule 42 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	5F	182	Total	C	N	O	S	0	0
			1530	967	287	269	7		

- Molecule 43 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	5G	282	Total	C	N	O	S	0	0
			2296	1441	430	418	7		

- Molecule 44 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	5H	74	Total	C	N	O	S	0	0
			596	373	122	101			

- Molecule 45 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	5I	461	Total	C	N	O	S	0	0
			3765	2354	686	709	16		

- Molecule 46 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	5J	151	Total	C	N	O	S	0	0
			1280	807	240	228	5		

- Molecule 47 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	5K	175	Total	C	N	O	S	0	0
			1403	896	256	241	10		

- Molecule 48 is a protein called Ribosome biogenesis protein ENP2.

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

- Molecule 49 is a protein called U3 small nucleolar ribonucleoprotein protein LCP5.

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

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

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

- Molecule 51 is a protein called rRNA biogenesis protein RRP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	RD	316	Total	C	N	O	S	0	0
			2412	1541	414	452	5		

- Molecule 52 is a protein called U3 small nucleolar RNA-associated protein 22.

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

- Molecule 53 is a protein called Ribosomal RNA-processing protein 7.

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

- Molecule 54 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

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

- Molecule 55 is a protein called Ribosome biogenesis protein BMS1.

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

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

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

- Molecule 57 is a protein called RNA cytidine acetyltransferase.

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

- Molecule 58 is a protein called Nucleolar complex protein 14.

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

- Molecule 59 is a protein called Nucleolar complex protein 4.

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

- Molecule 60 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	RP	2108	Total	C	N	O	S	0	0
			12171	7483	2291	2381	16		

- Molecule 61 is a protein called U3 small nucleolar RNA-associated protein 14.

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

- Molecule 62 is a protein called Essential nuclear protein 1.

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

- Molecule 63 is a protein called Pno1.

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

- Molecule 64 is a protein called Protein FAF1.

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

- Molecule 65 is a protein called Protein BFR2.

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

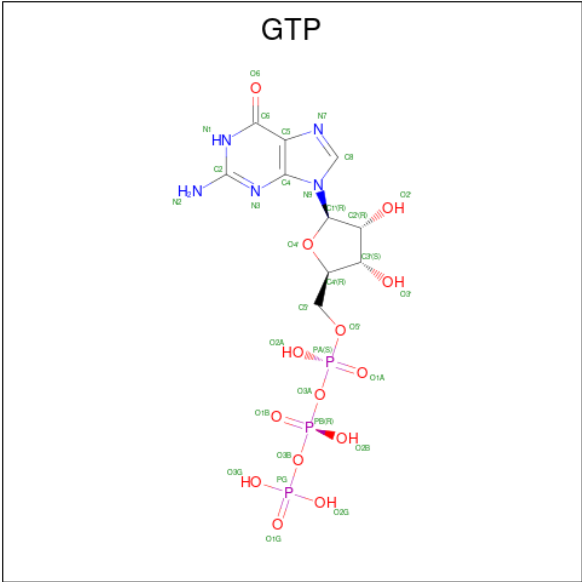
- Molecule 66 is a protein called Unassigned helices.

Mol	Chain	Residues	Atoms				AltConf	Trace
66	X1	75	Total	C	N	O	0	0
			375	225	75	75		

- Molecule 67 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
67	Sc	1	Total	Zn	0
			1	1	
67	5K	1	Total	Zn	0
			1	1	

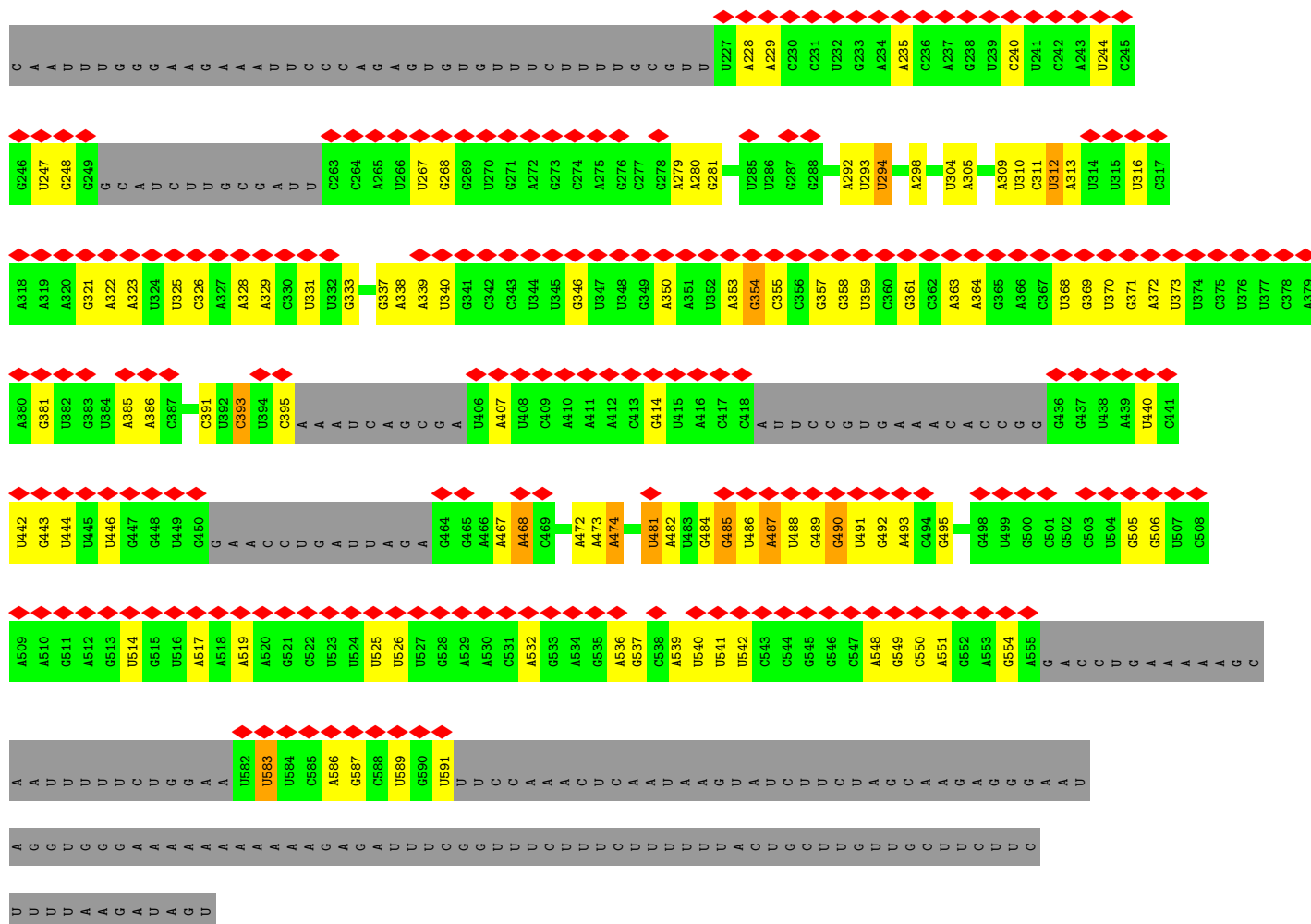
- Molecule 68 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



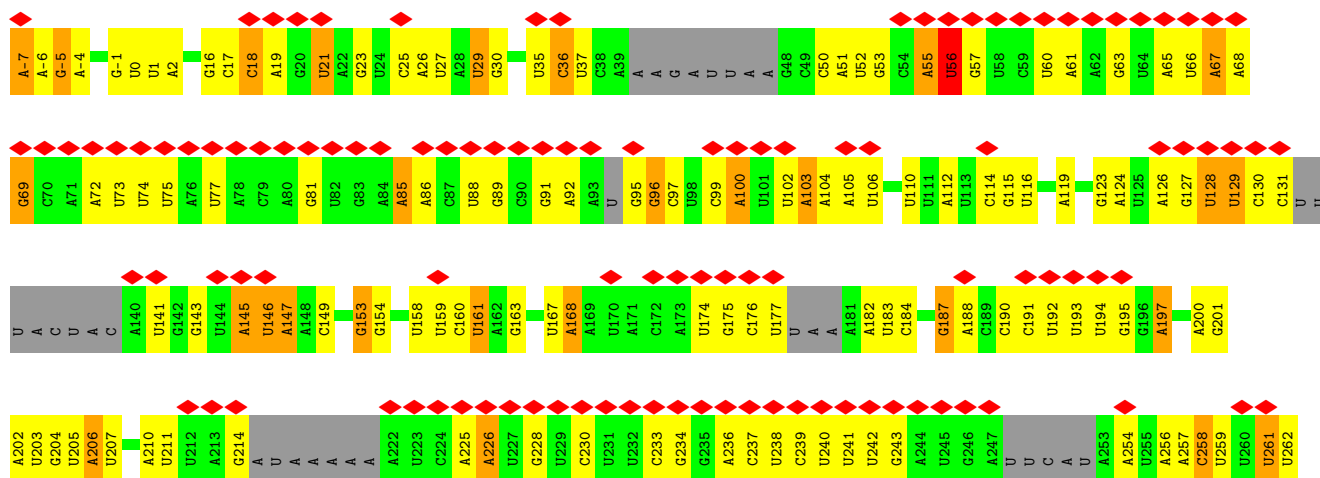
Mol	Chain	Residues	Atoms					AltConf
68	RJ	1	Total	C	N	O	P	0
			32	10	5	14	3	

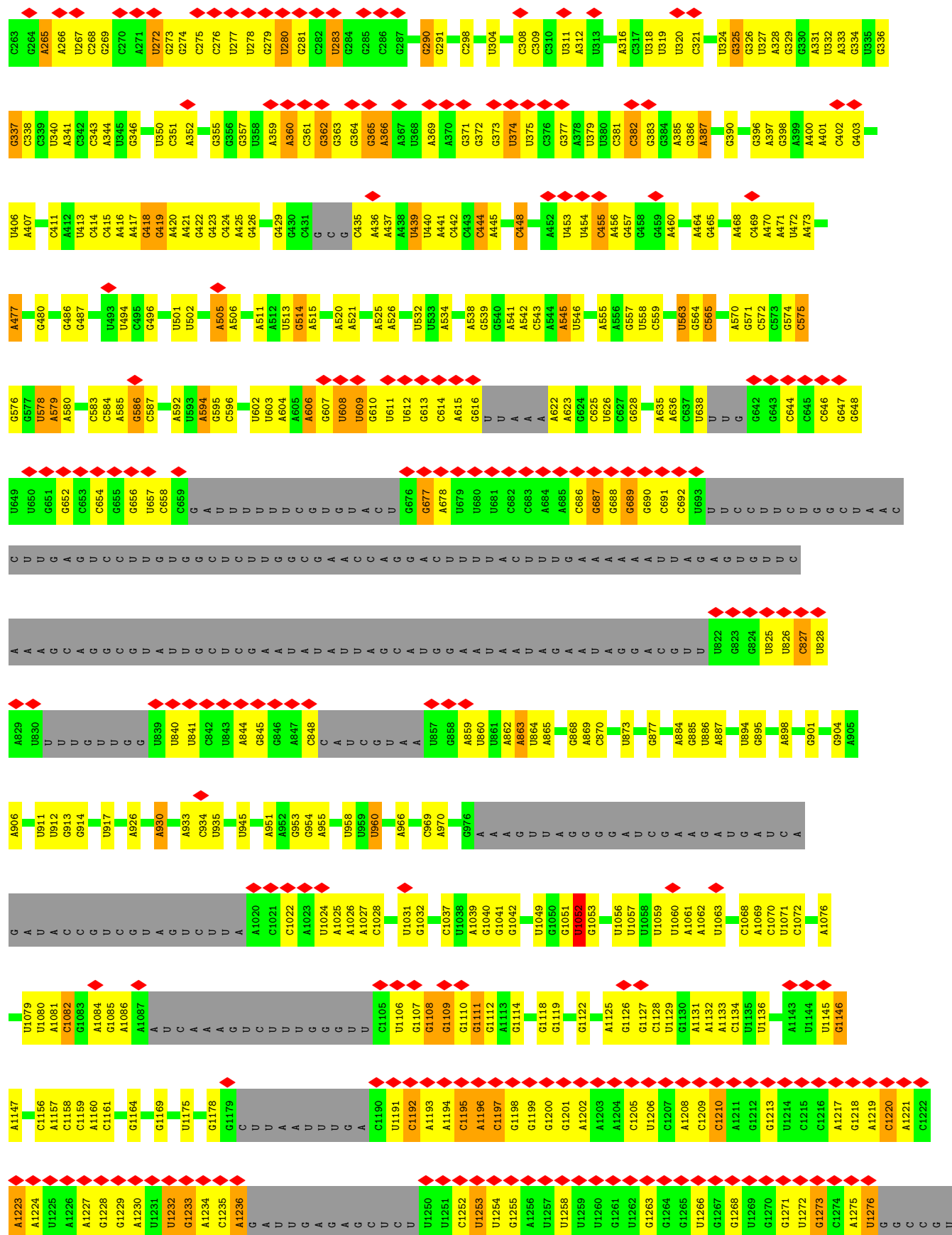
- Molecule 69 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

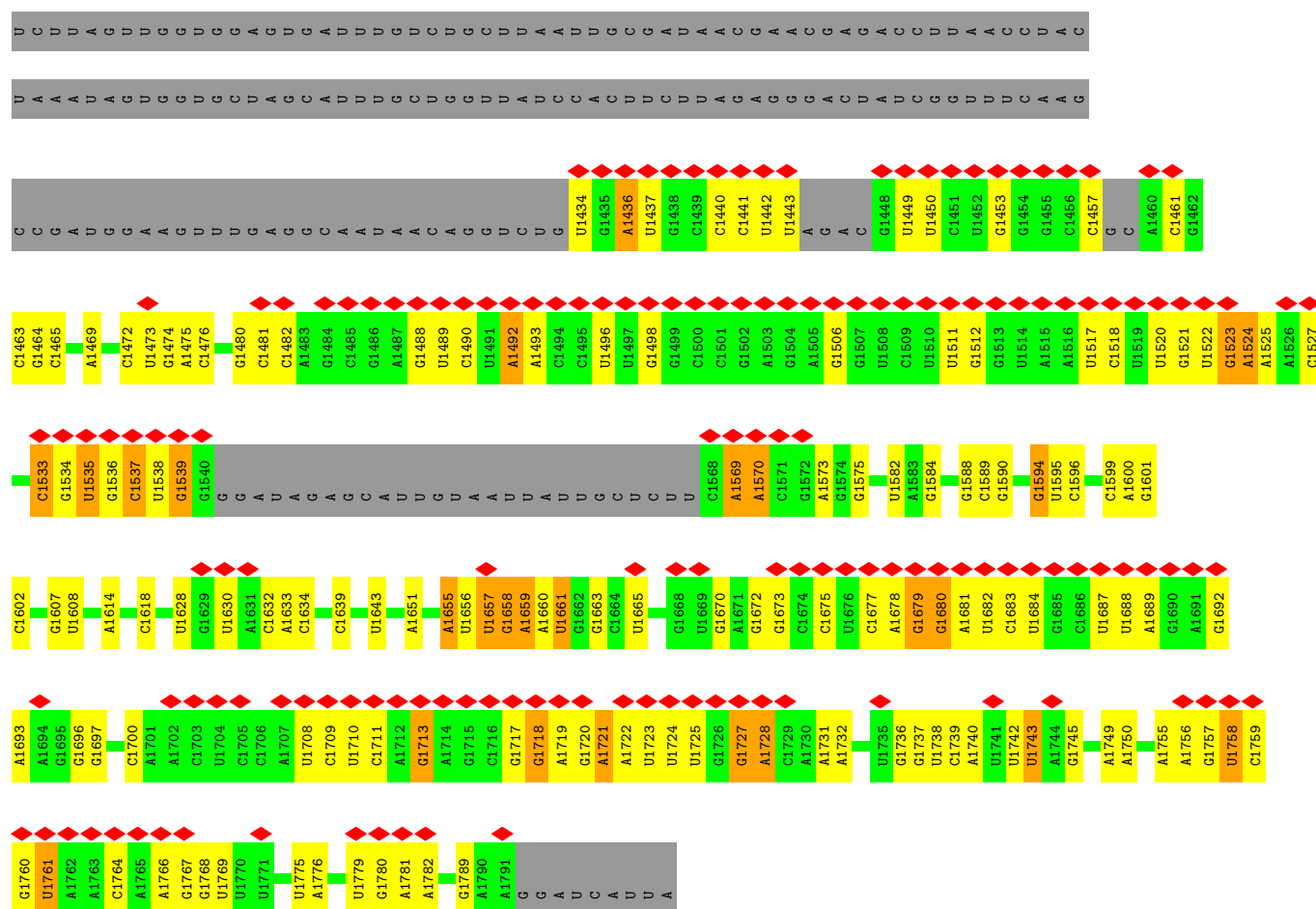
Mol	Chain	Residues	Atoms		AltConf
69	RJ	1	Total	Mg	0
			1	1	



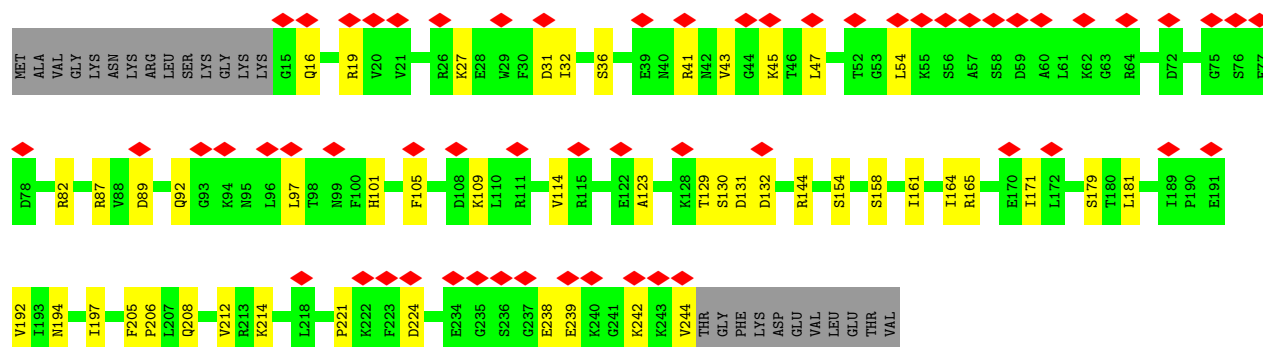
• Molecule 3: 18S pre-rRNA



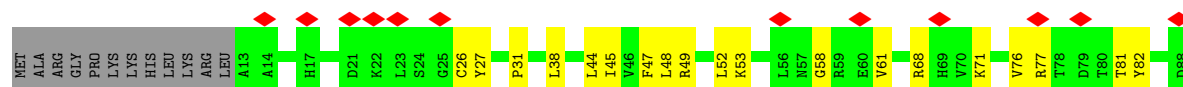


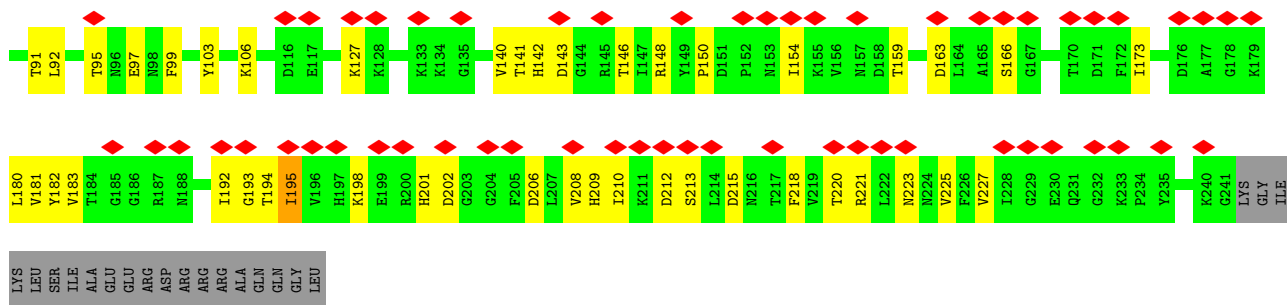


• Molecule 4: 40S ribosomal protein S1-A

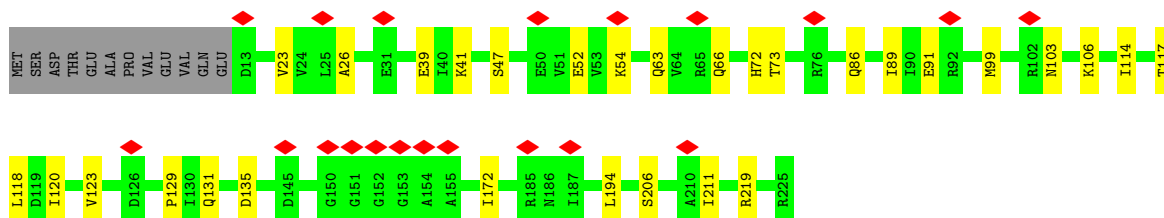
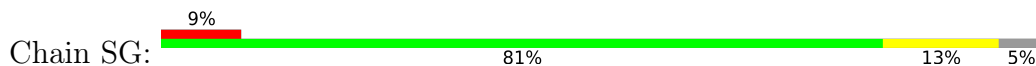


• Molecule 5: 40S ribosomal protein S4-A

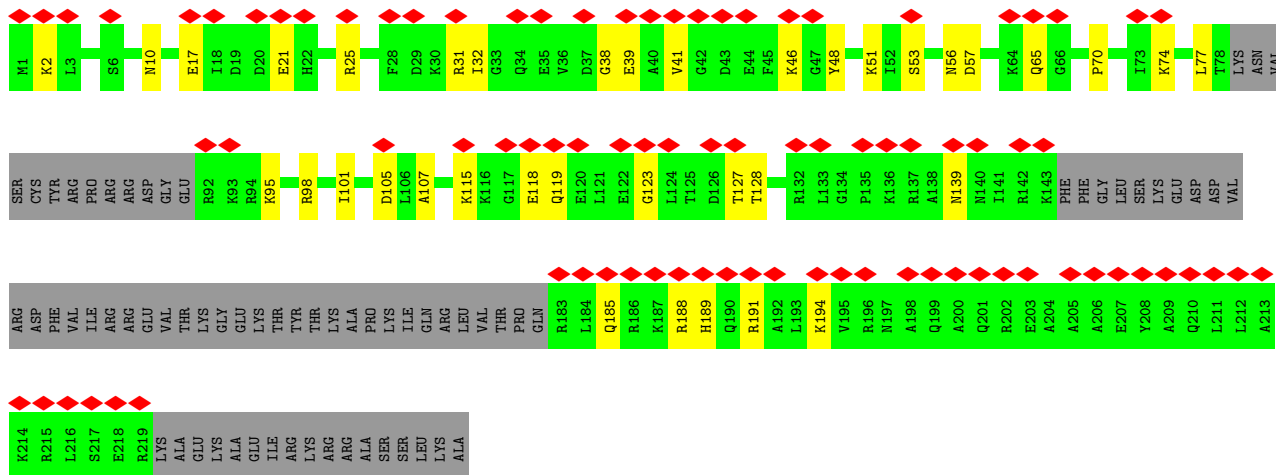




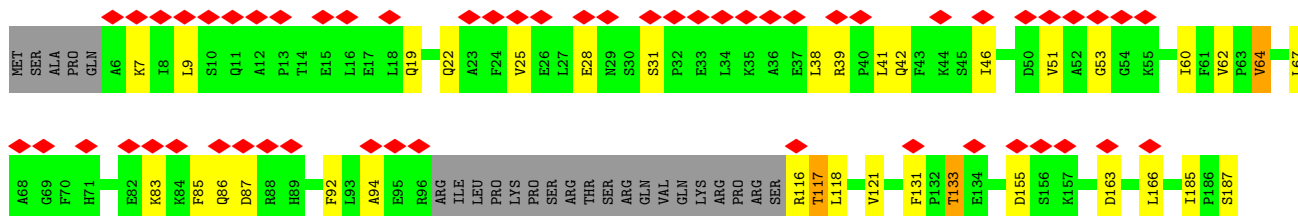
- Molecule 6: 40S ribosomal protein S5

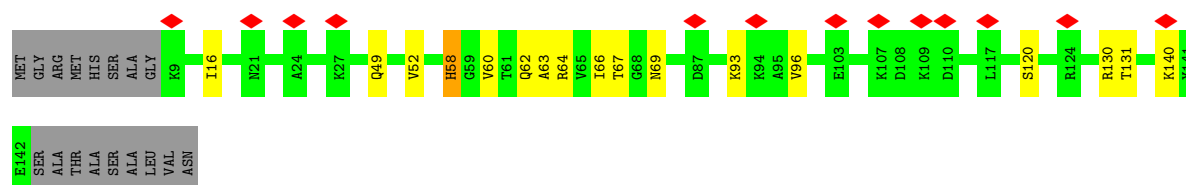
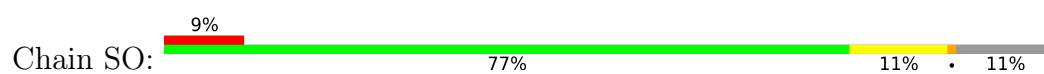


- Molecule 7: 40S ribosomal protein S6-A

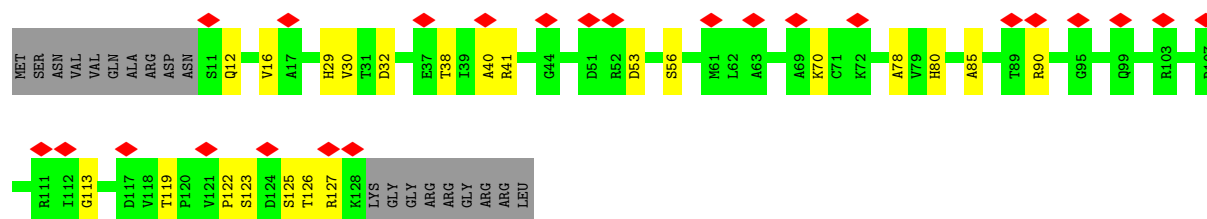


- Molecule 8: 40S ribosomal protein S7-A

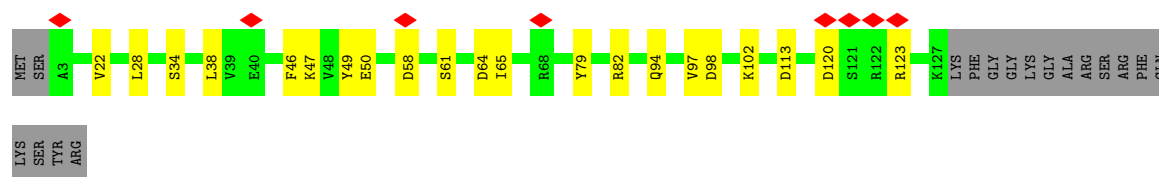
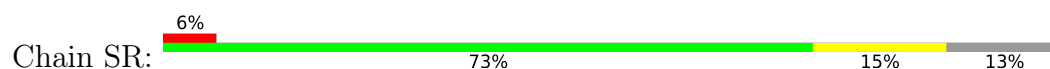




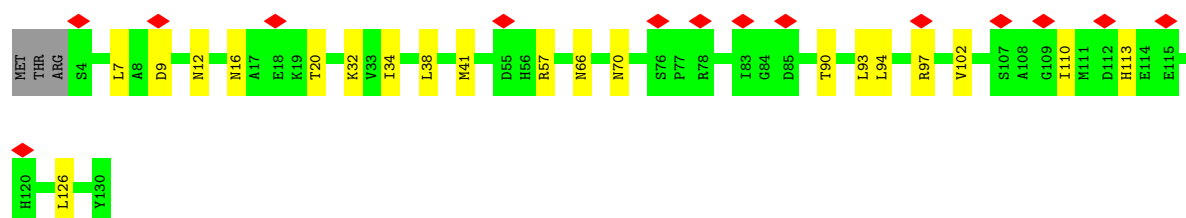
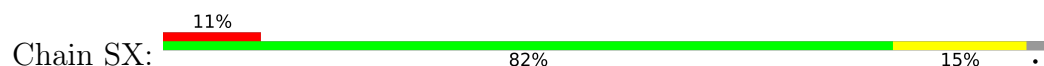
• Molecule 13: 40S ribosomal protein S14-A



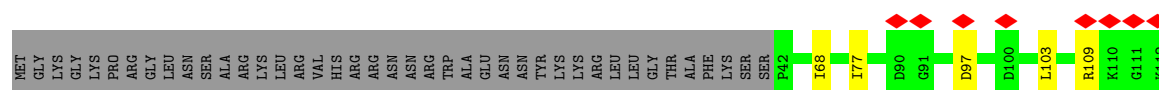
• Molecule 14: 40S ribosomal protein S16-A



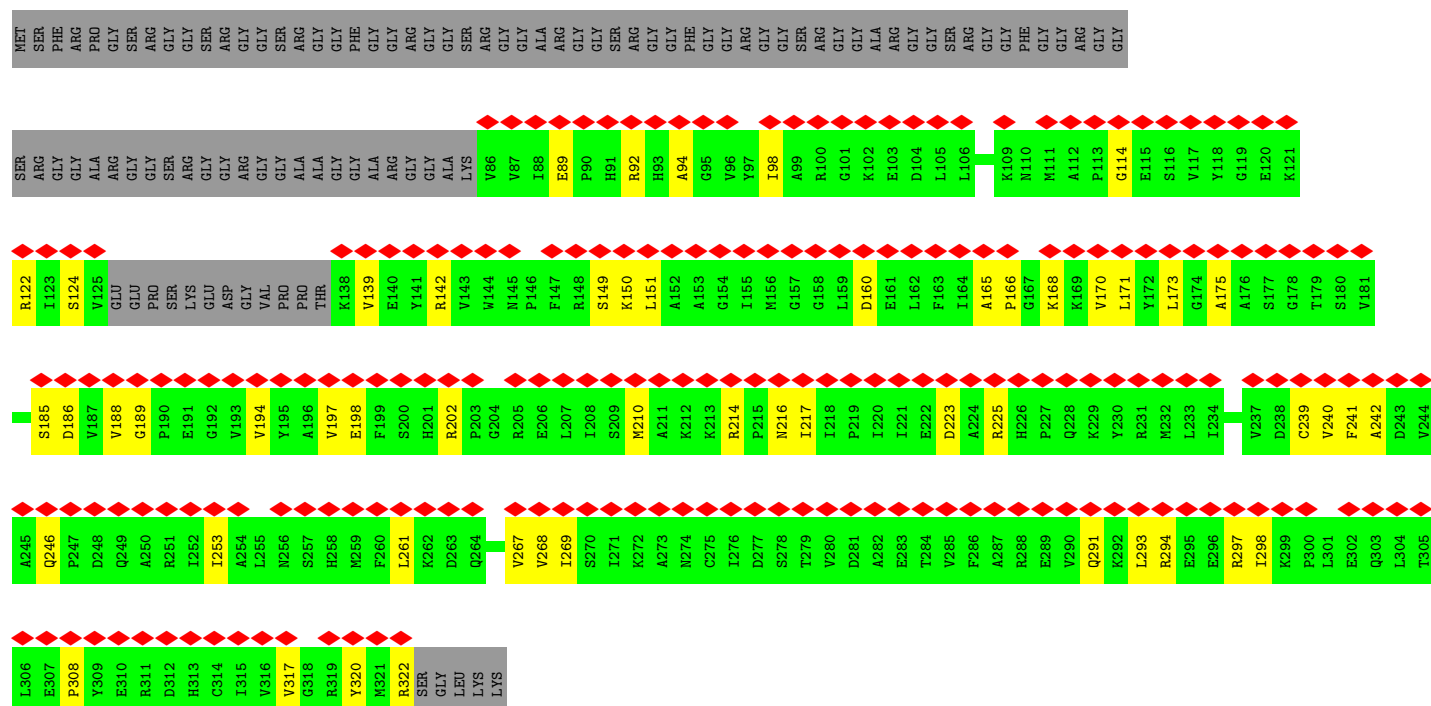
• Molecule 15: 40S ribosomal protein S22-B



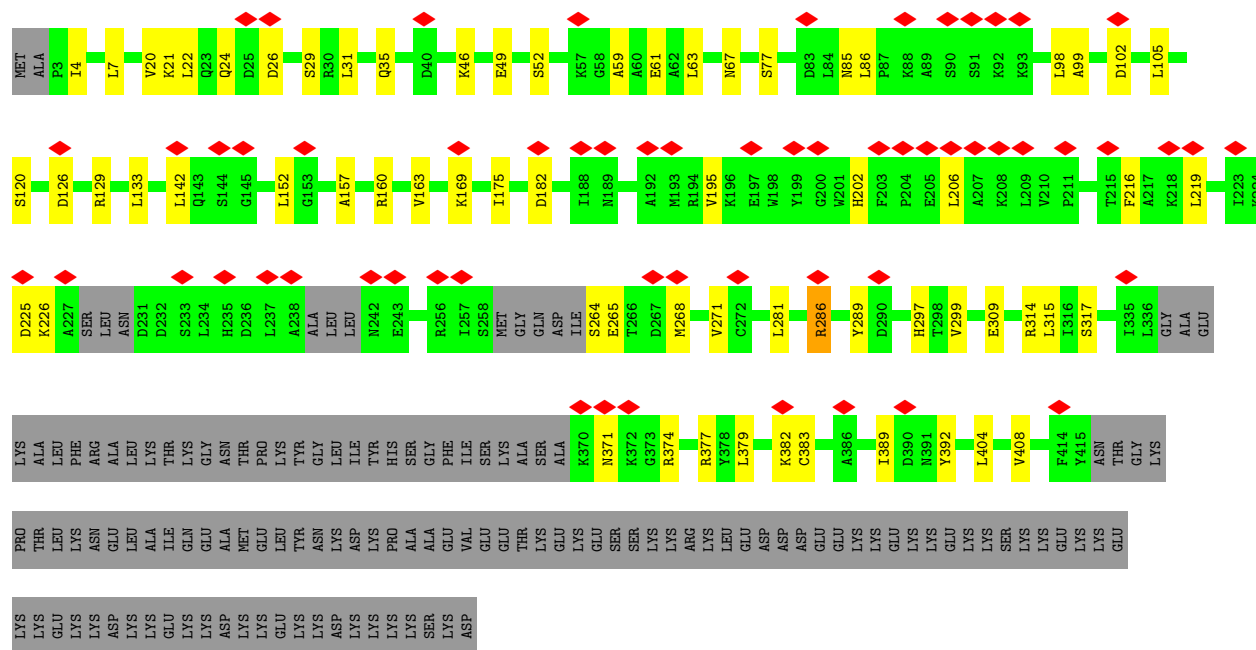
• Molecule 16: 40S ribosomal protein S23-A



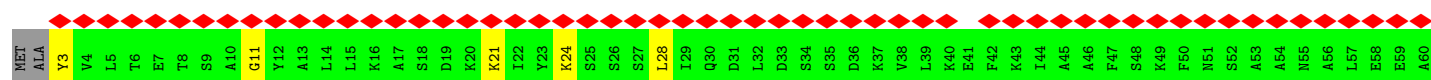


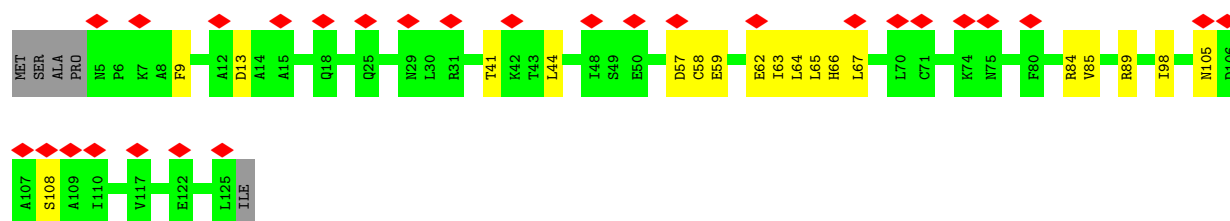
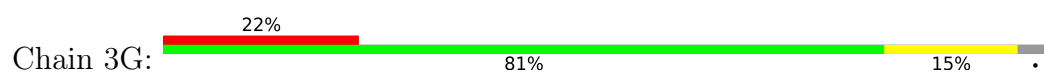


• Molecule 21: Nucleolar protein 56

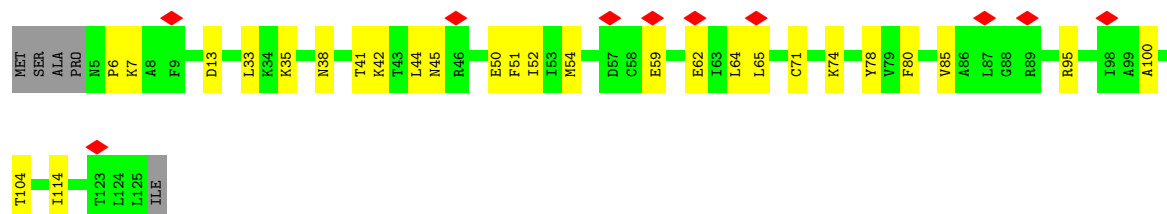
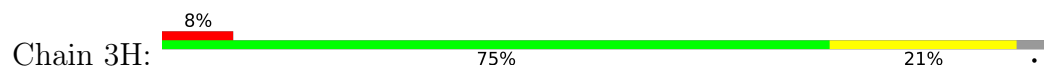


• Molecule 22: Nucleolar protein 58

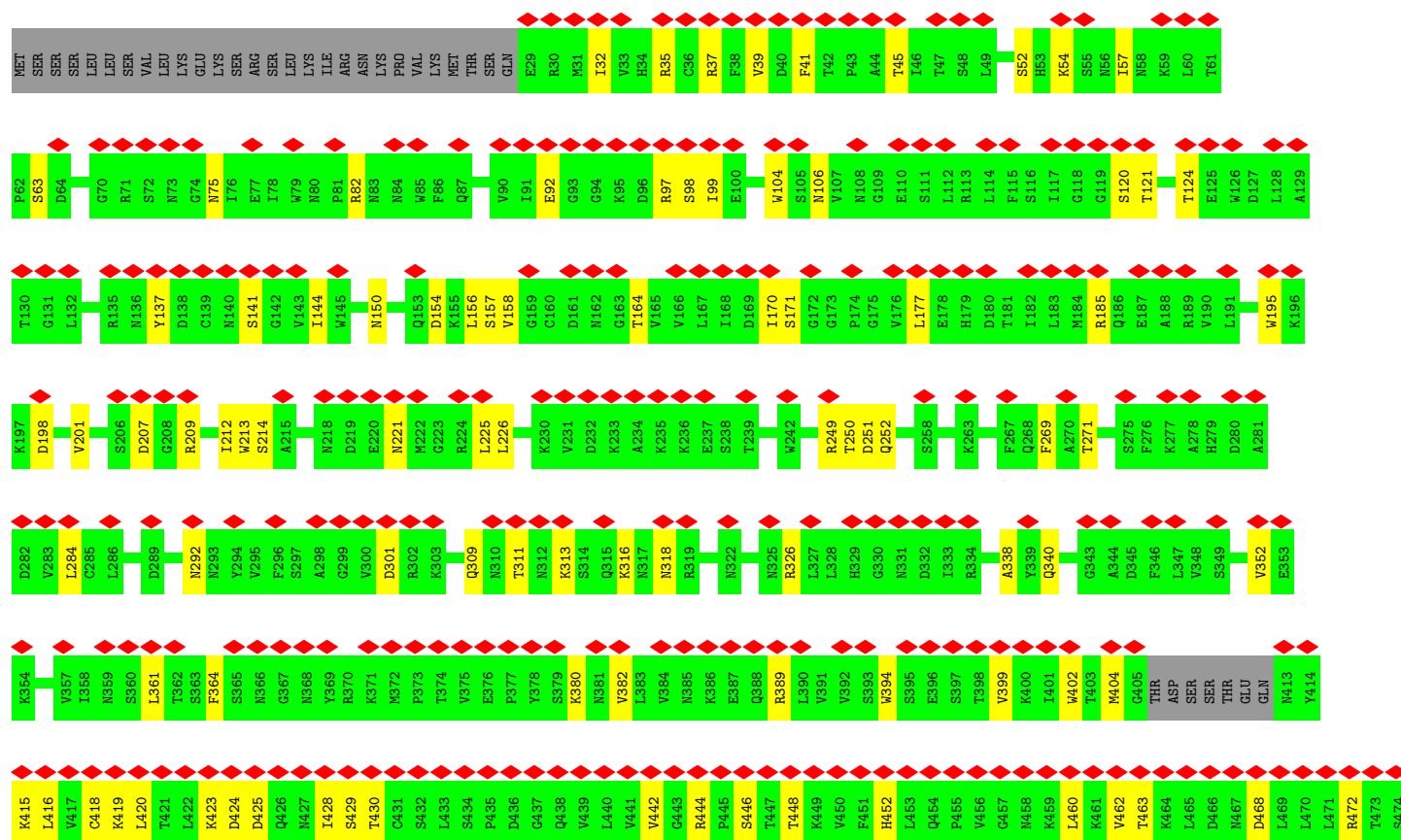


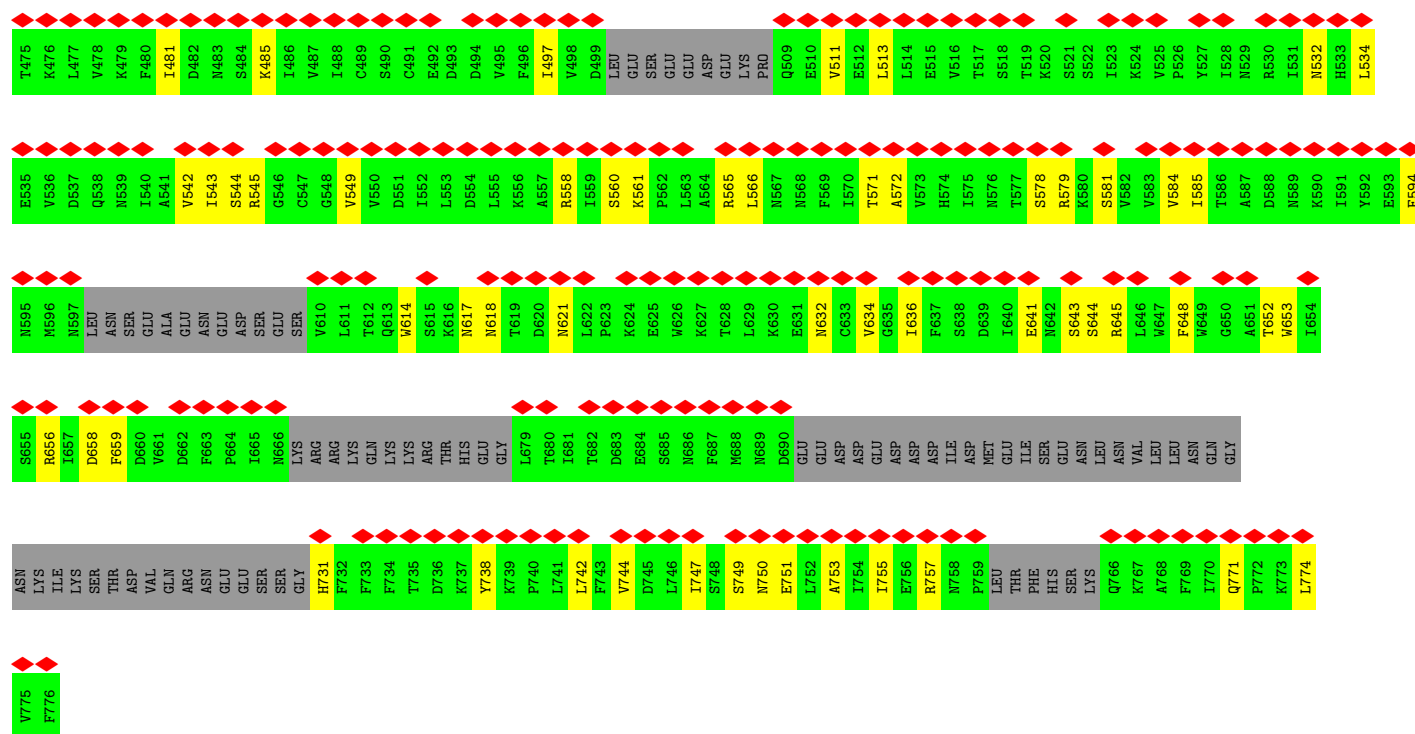


- Molecule 24: 13 kDa ribonucleoprotein-associated protein

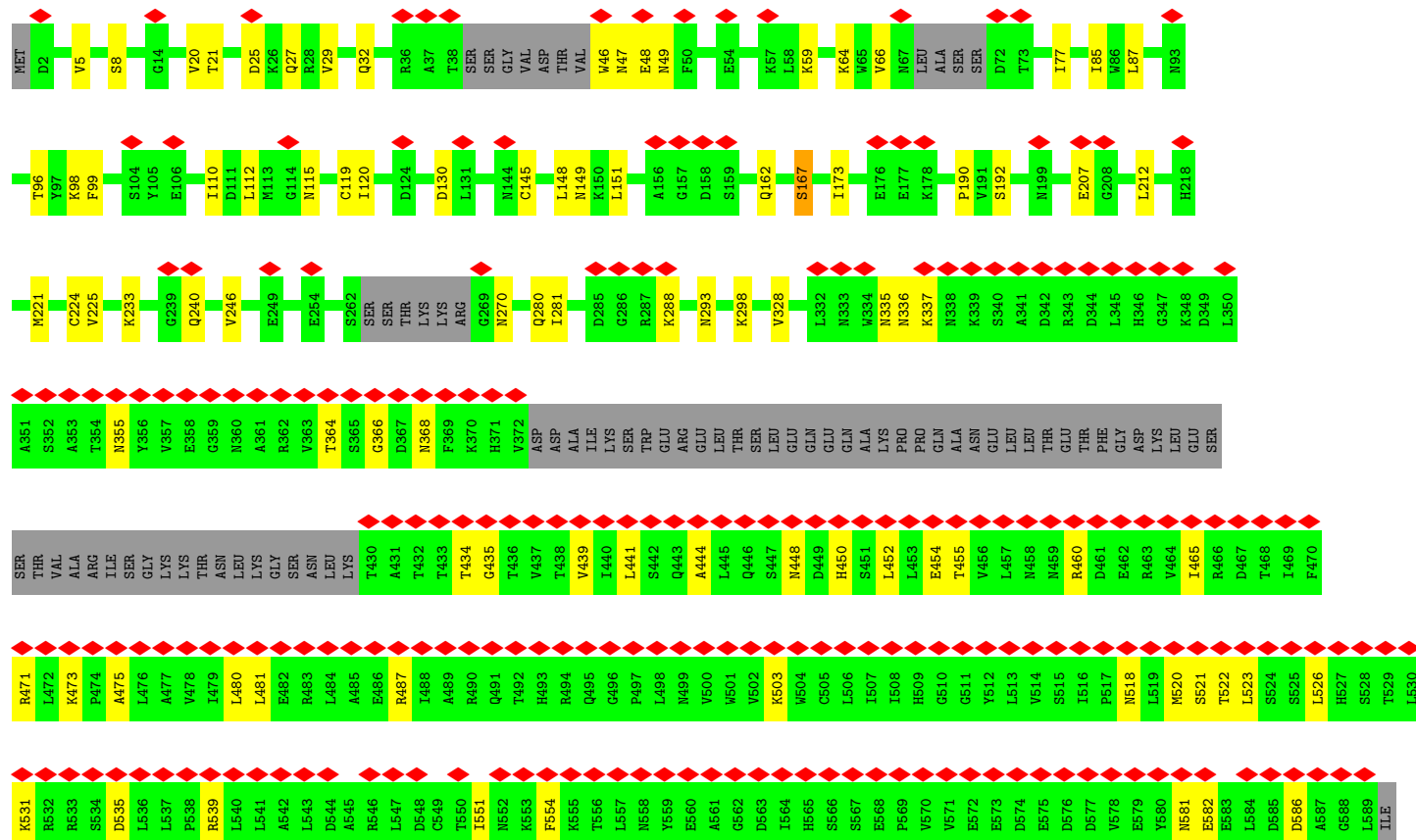
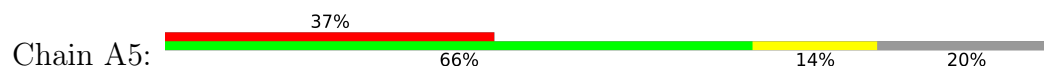


- Molecule 25: U3 small nucleolar RNA-associated protein 4





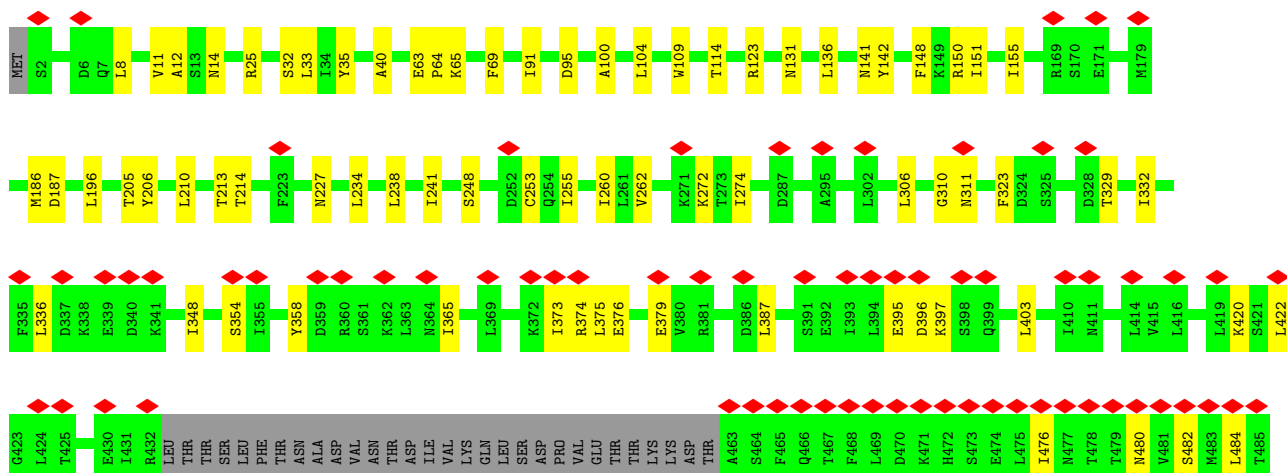
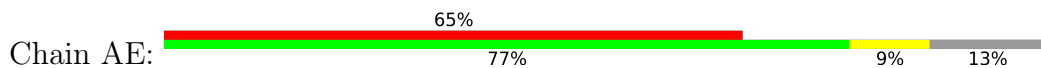
• Molecule 26: U3 small nucleolar RNA-associated protein 5



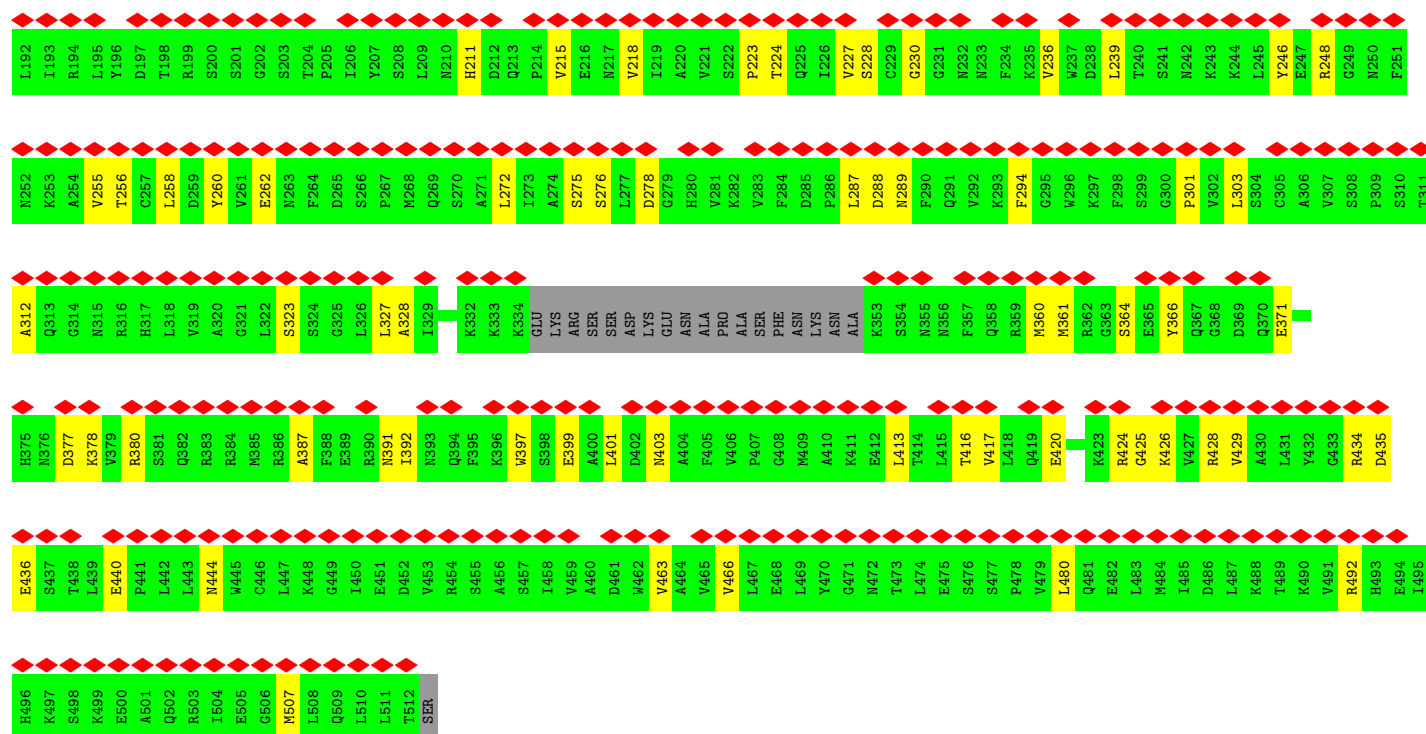
Chain A8:



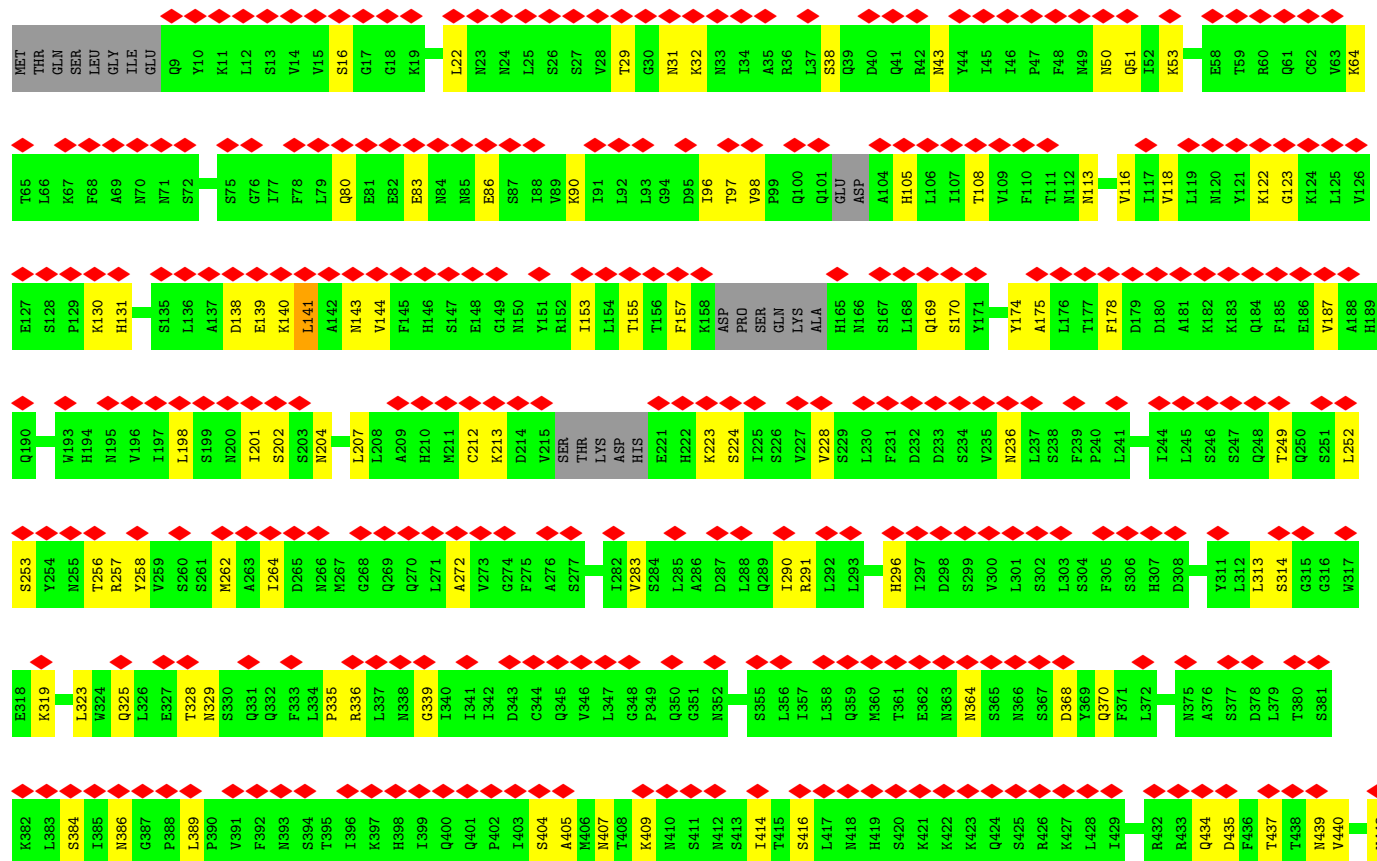
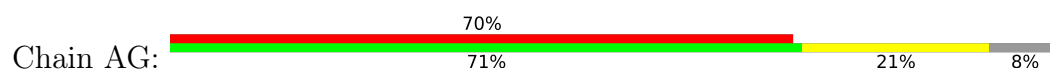
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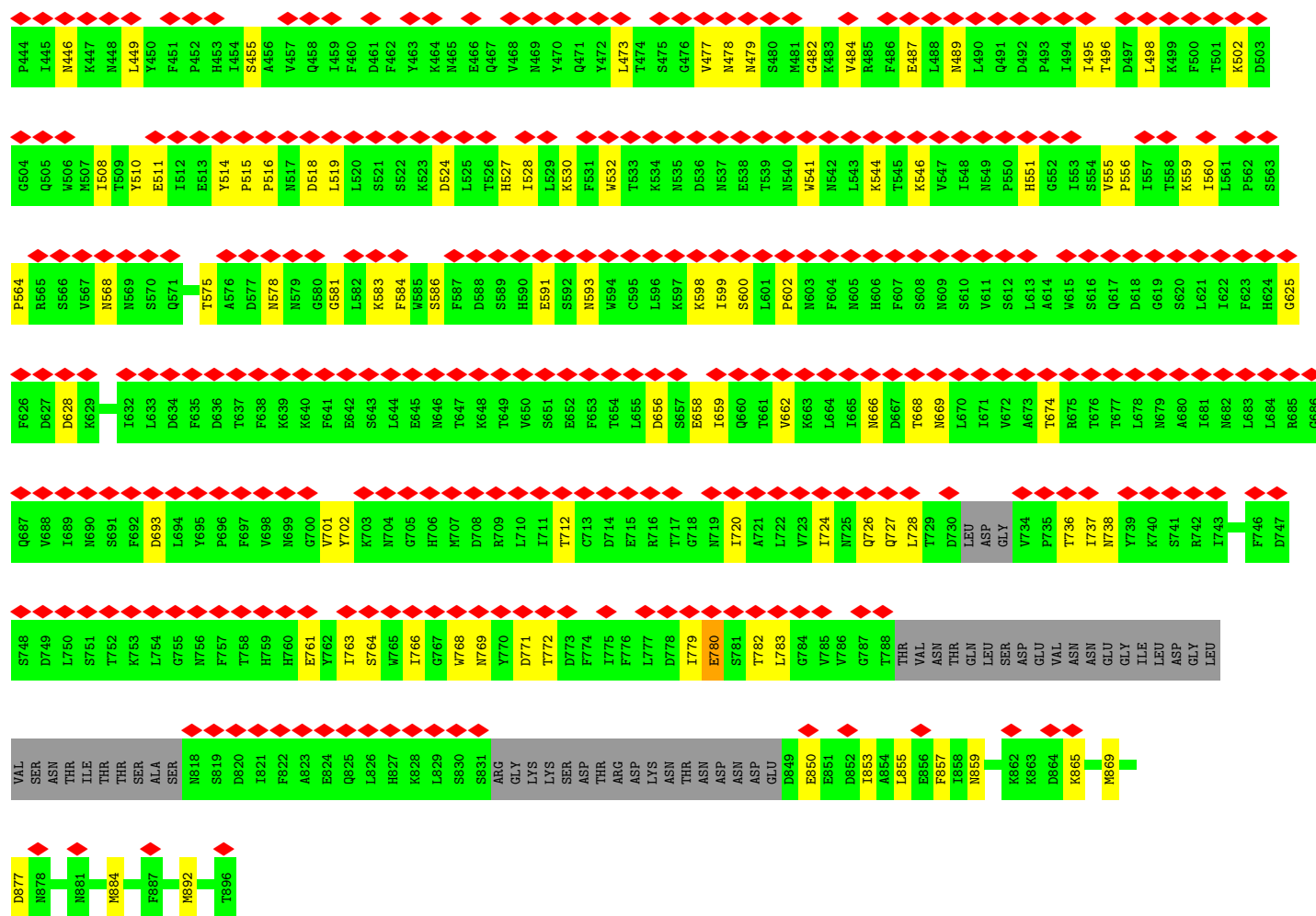




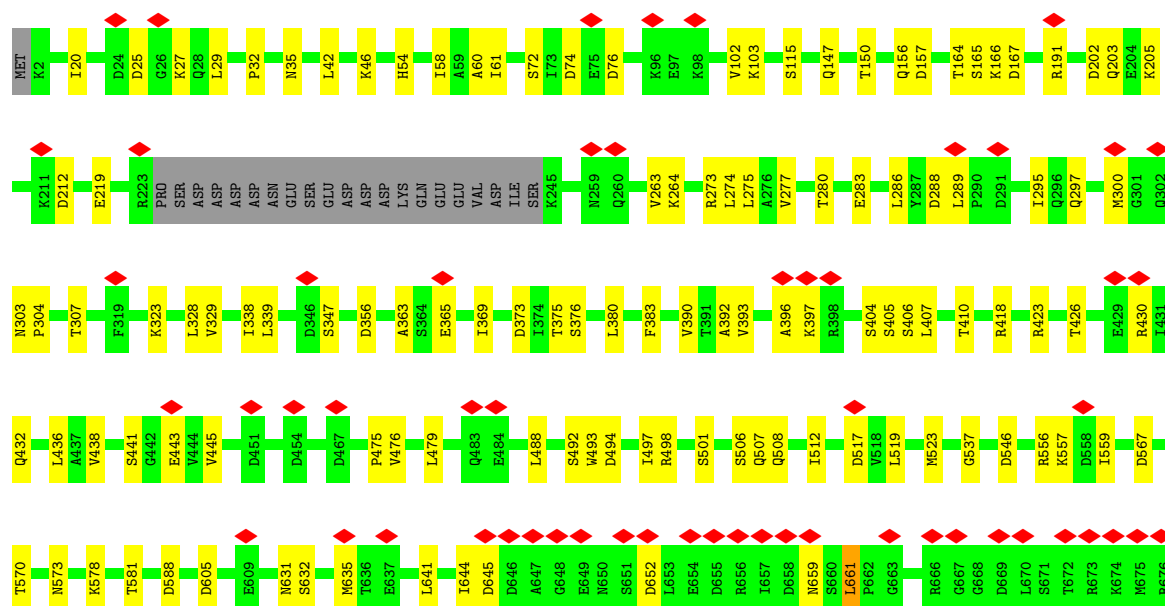
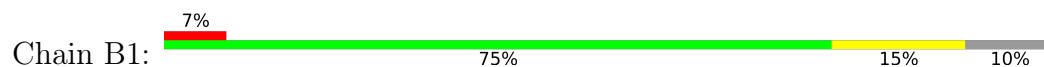


• Molecule 31: NET1-associated nuclear protein 1

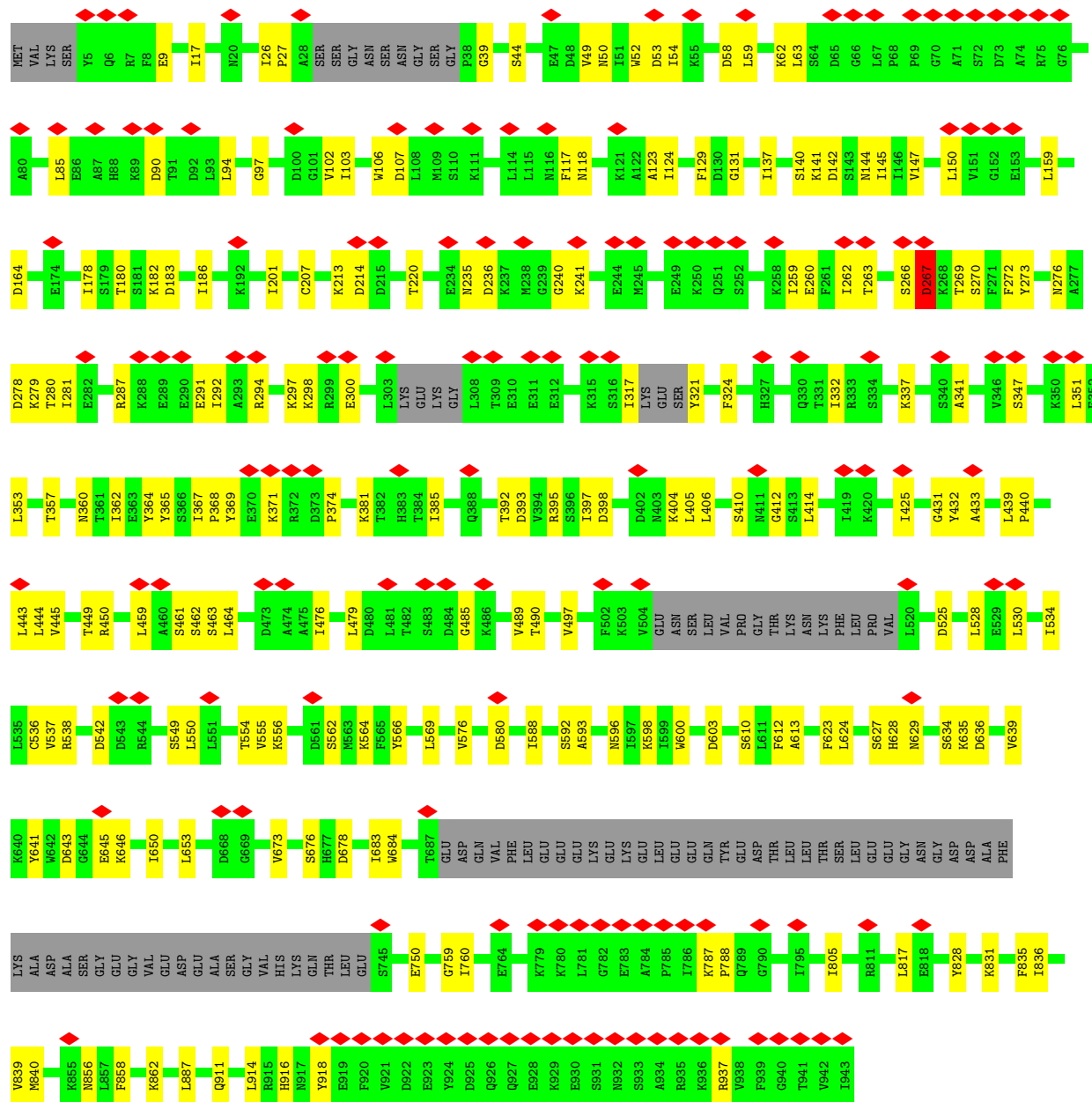




• Molecule 32: Periodic tryptophan protein 2



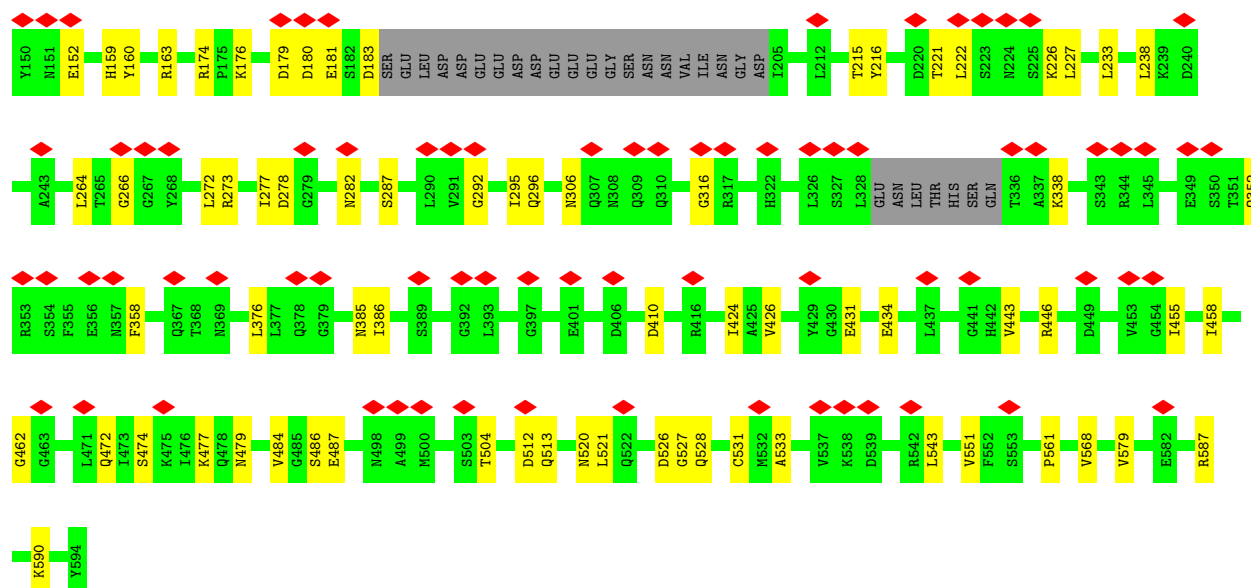
- Molecule 33: U3 small nucleolar RNA-associated protein 12



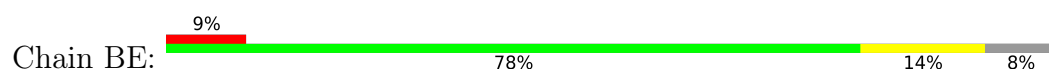
- Molecule 34: U3 small nucleolar RNA-associated protein 13



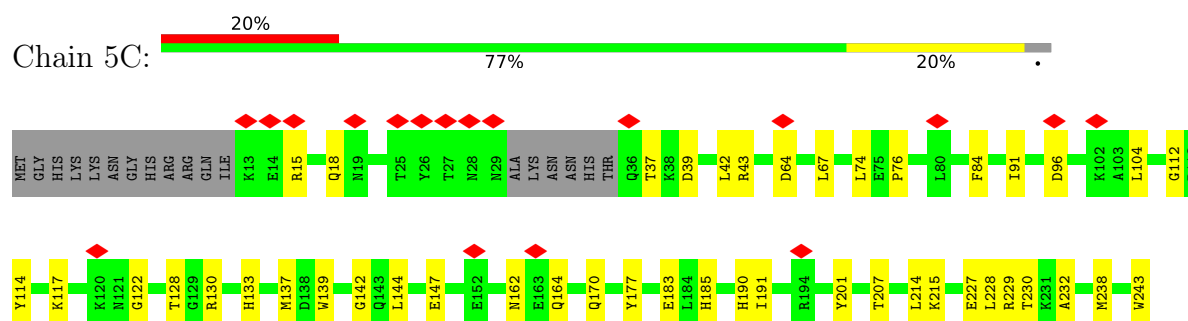
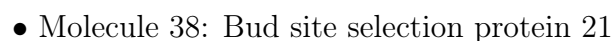




• Molecule 36: U3 small nucleolar RNA-associated protein 21



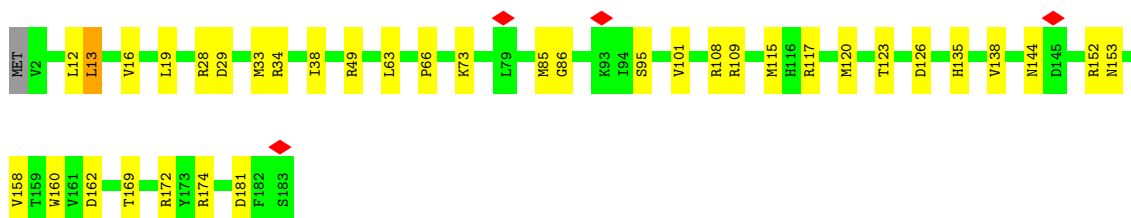
Chain B6:





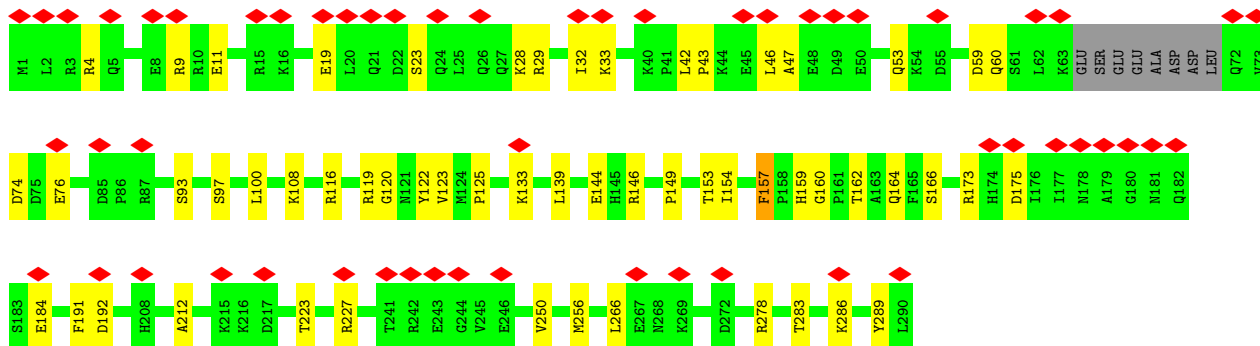
- Molecule 42: U3 small nucleolar ribonucleoprotein protein IMP3

Chain 5F: 80% 19%

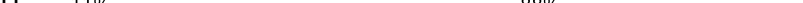


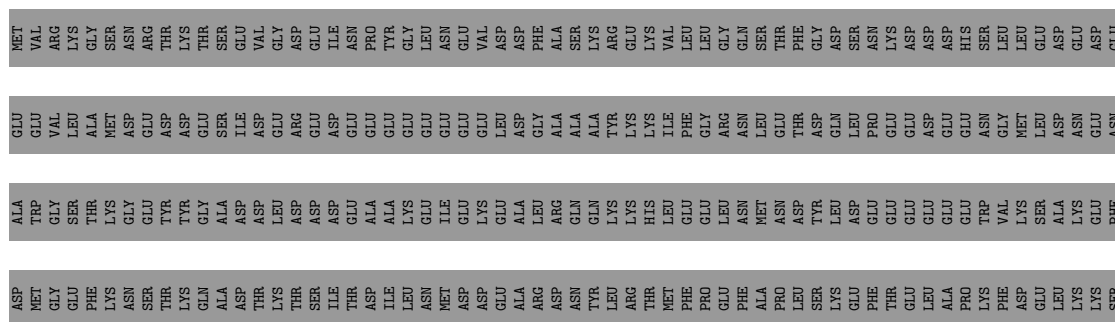
- Molecule 43: U3 small nucleolar ribonucleoprotein protein IMP4

Chain 5G: 



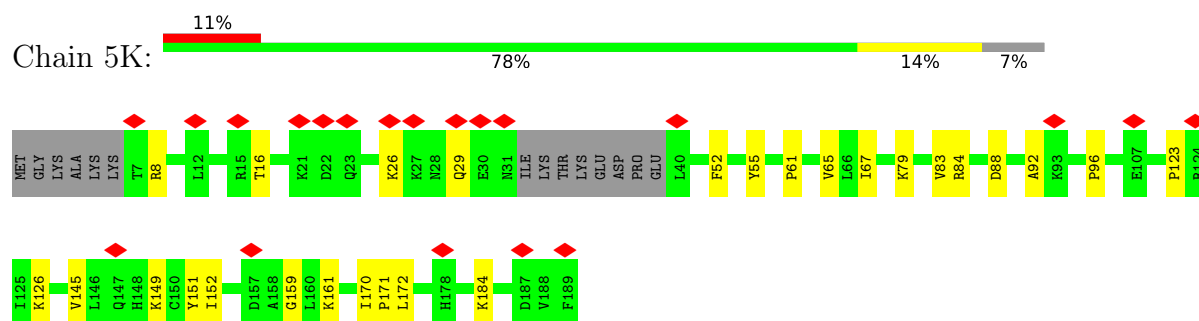
- Molecule 44: Something about silencing protein 10

Chain 5H:  11% 88%

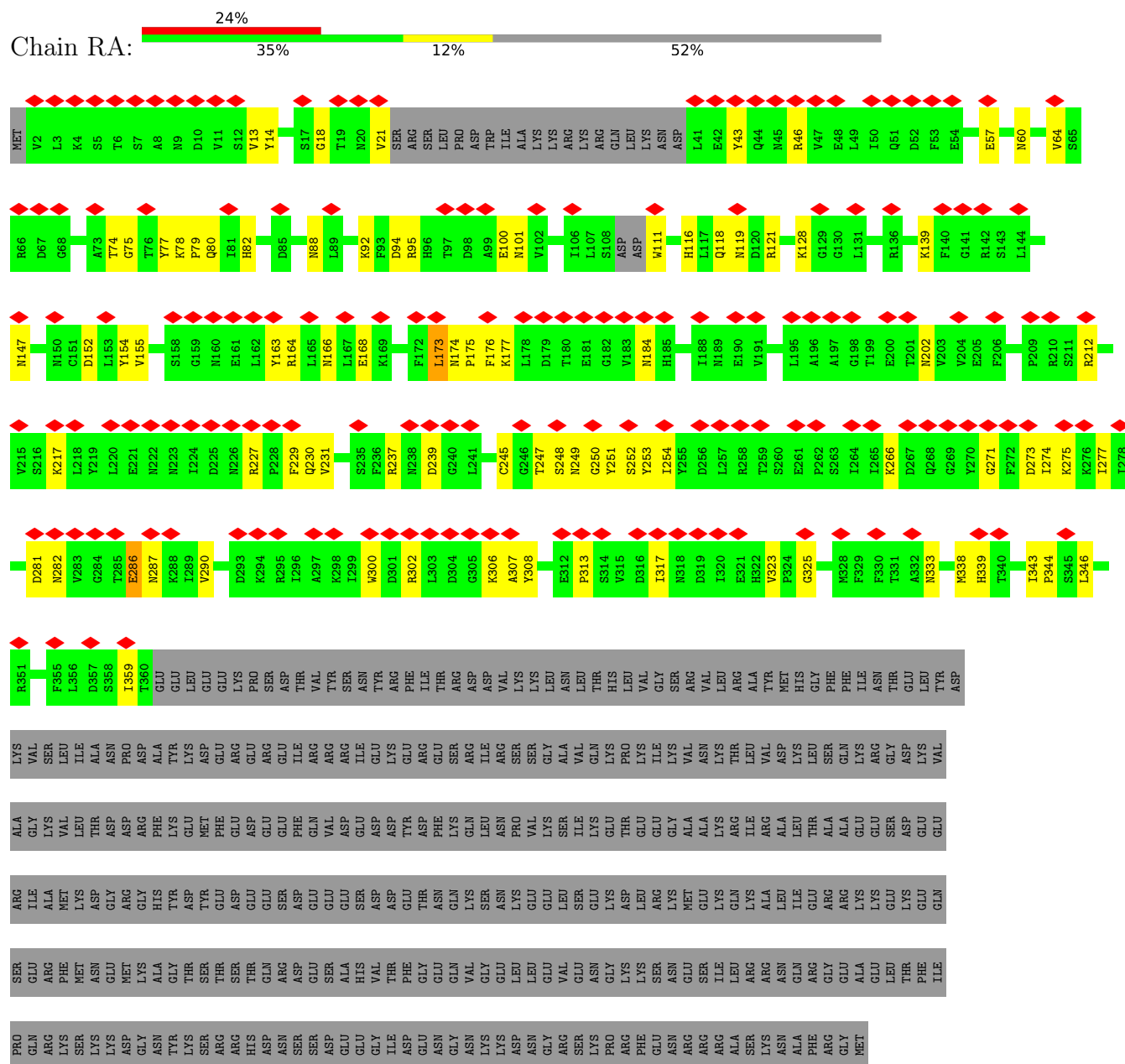




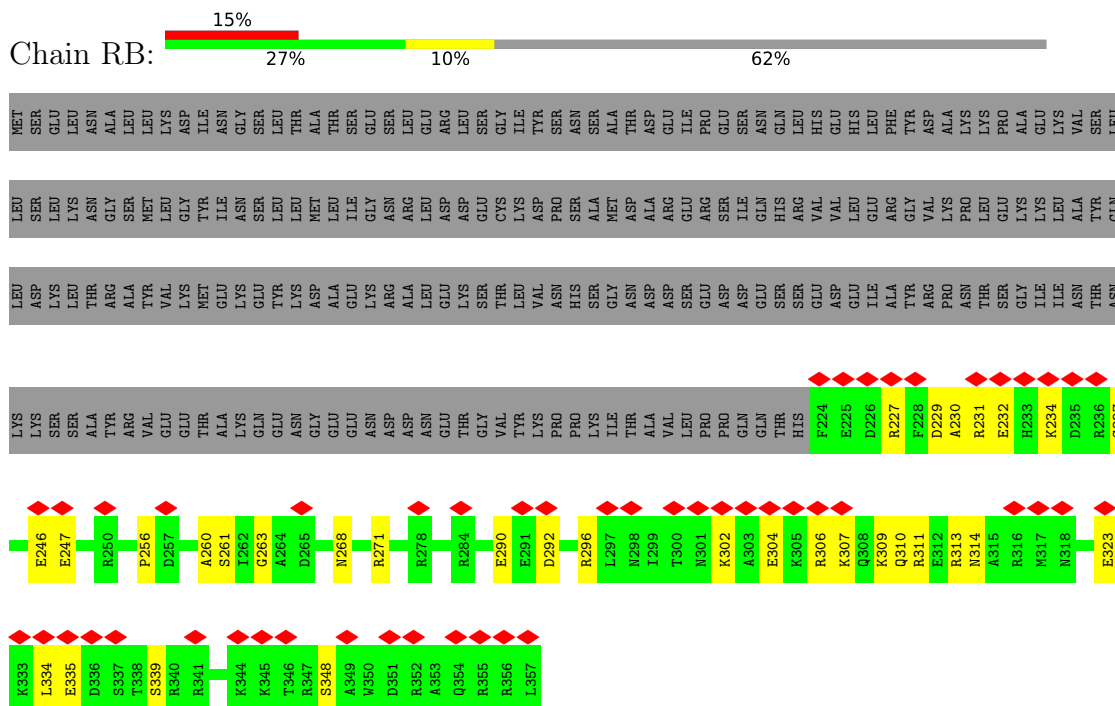
- Molecule 47: rRNA-processing protein FCF1



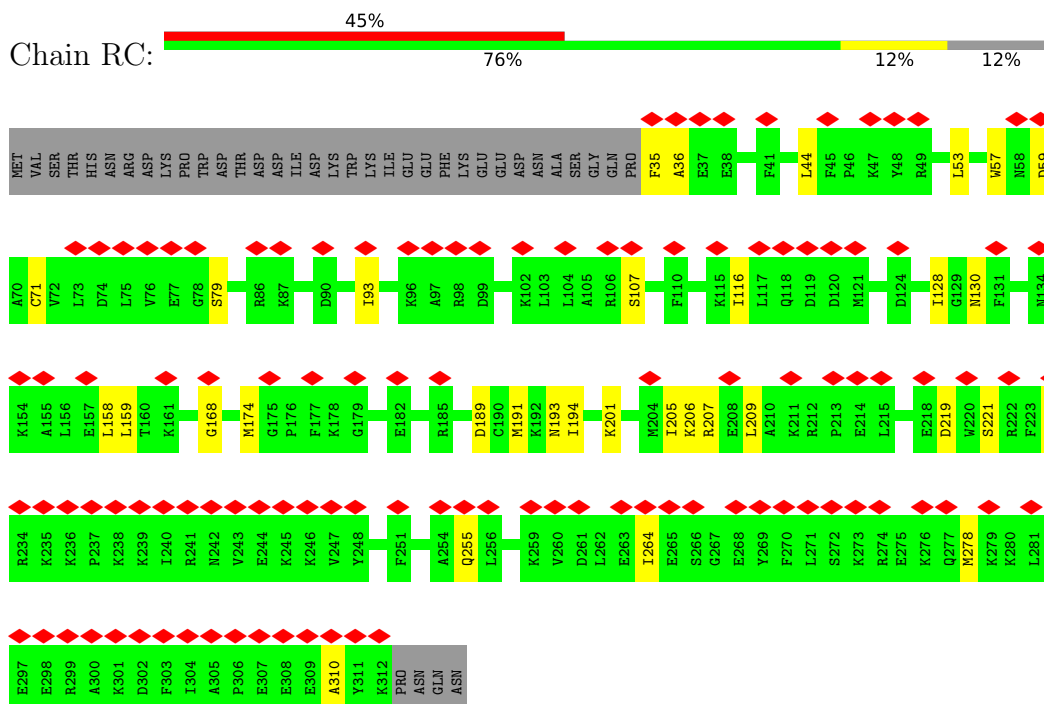
- Molecule 48: Ribosome biogenesis protein ENP2



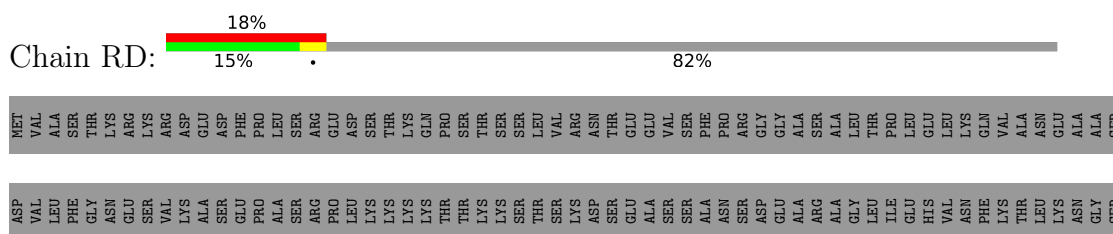
- Molecule 49: U3 small nucleolar ribonucleoprotein protein LCP5



- Molecule 50: KRR1 small subunit processome component

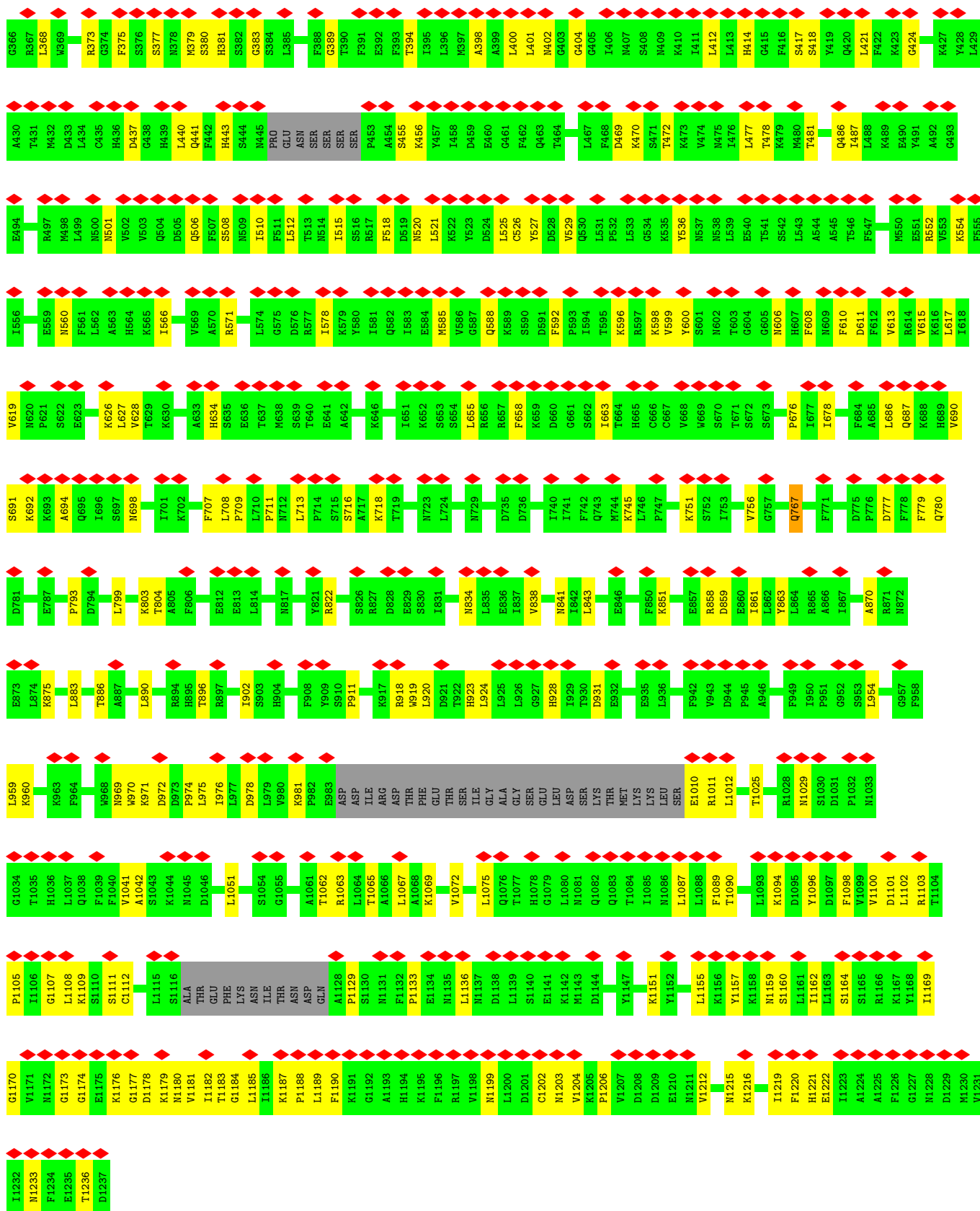


- Molecule 51: rRNA biogenesis protein RRP5

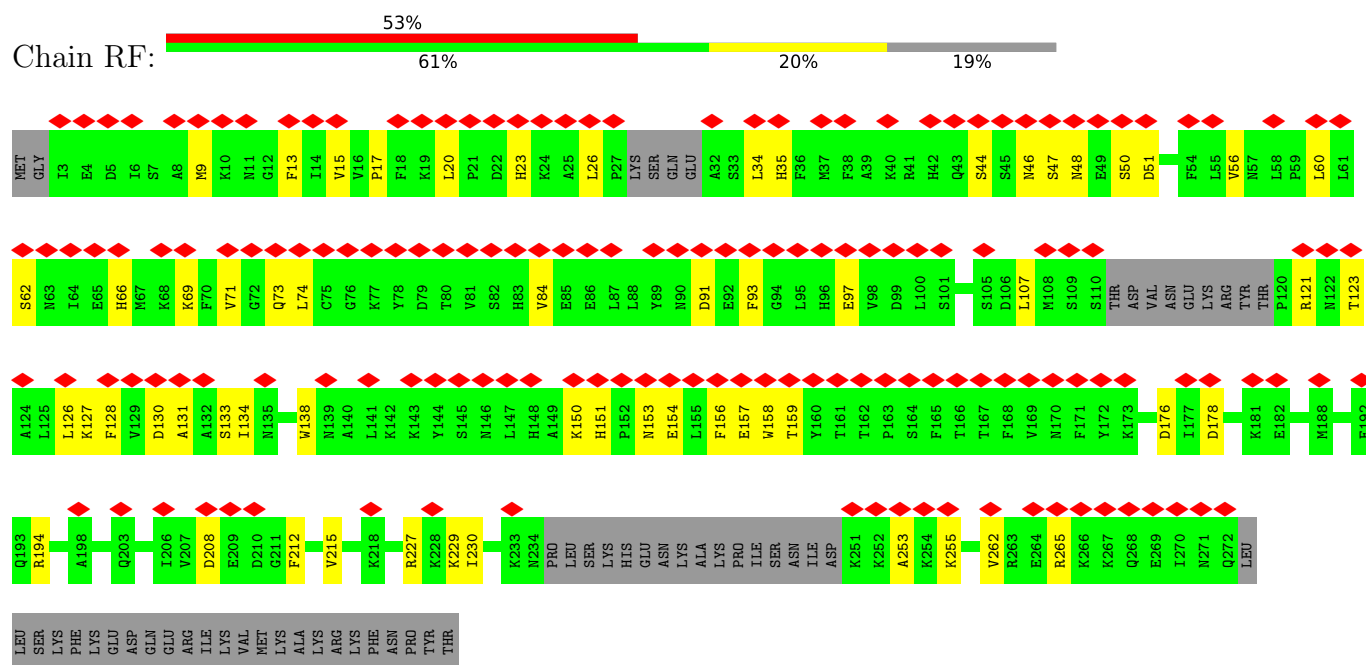




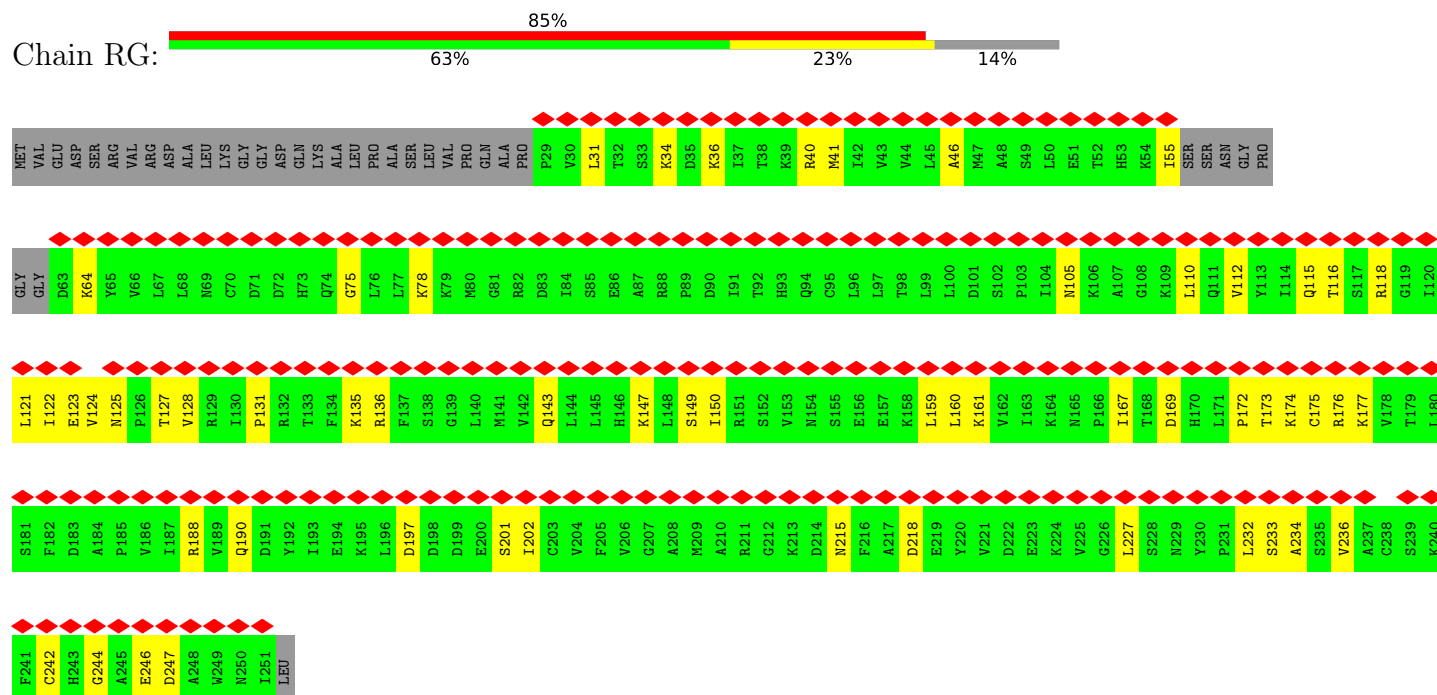




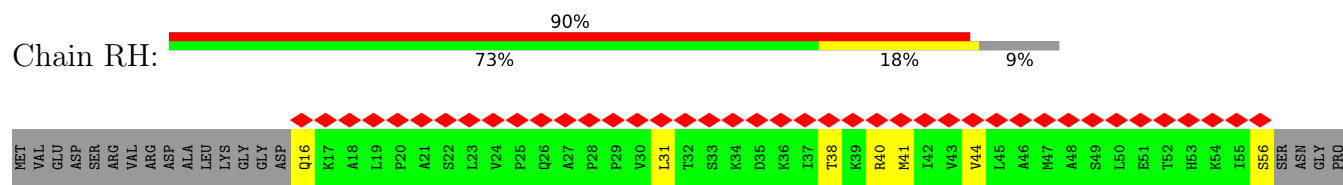
• Molecule 53: Ribosomal RNA-processing protein 7

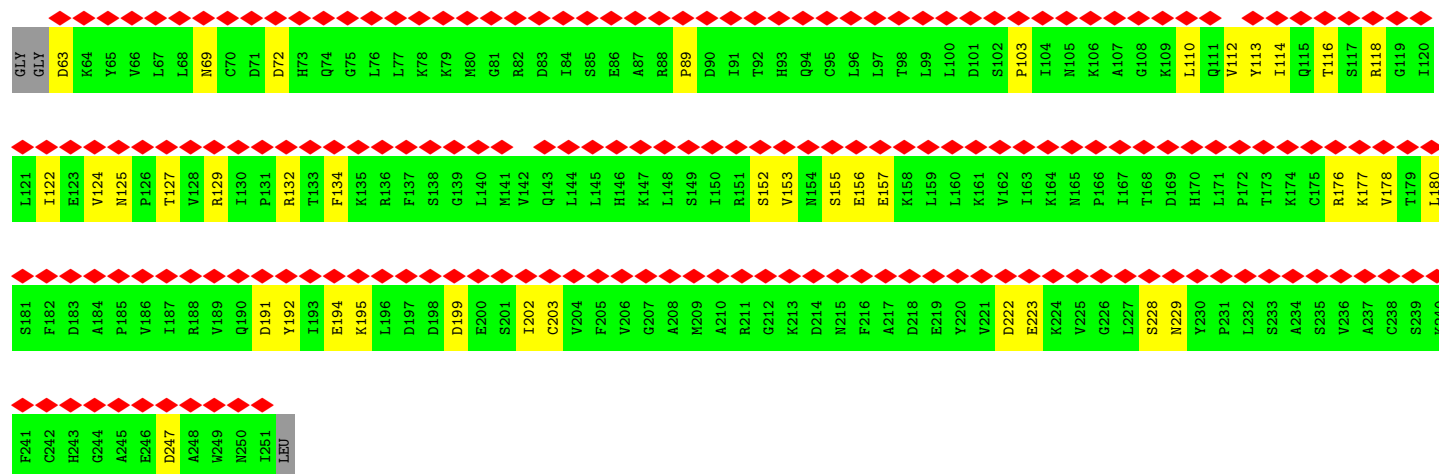


- Molecule 54: Ribosomal RNA small subunit methyltransferase NEP1

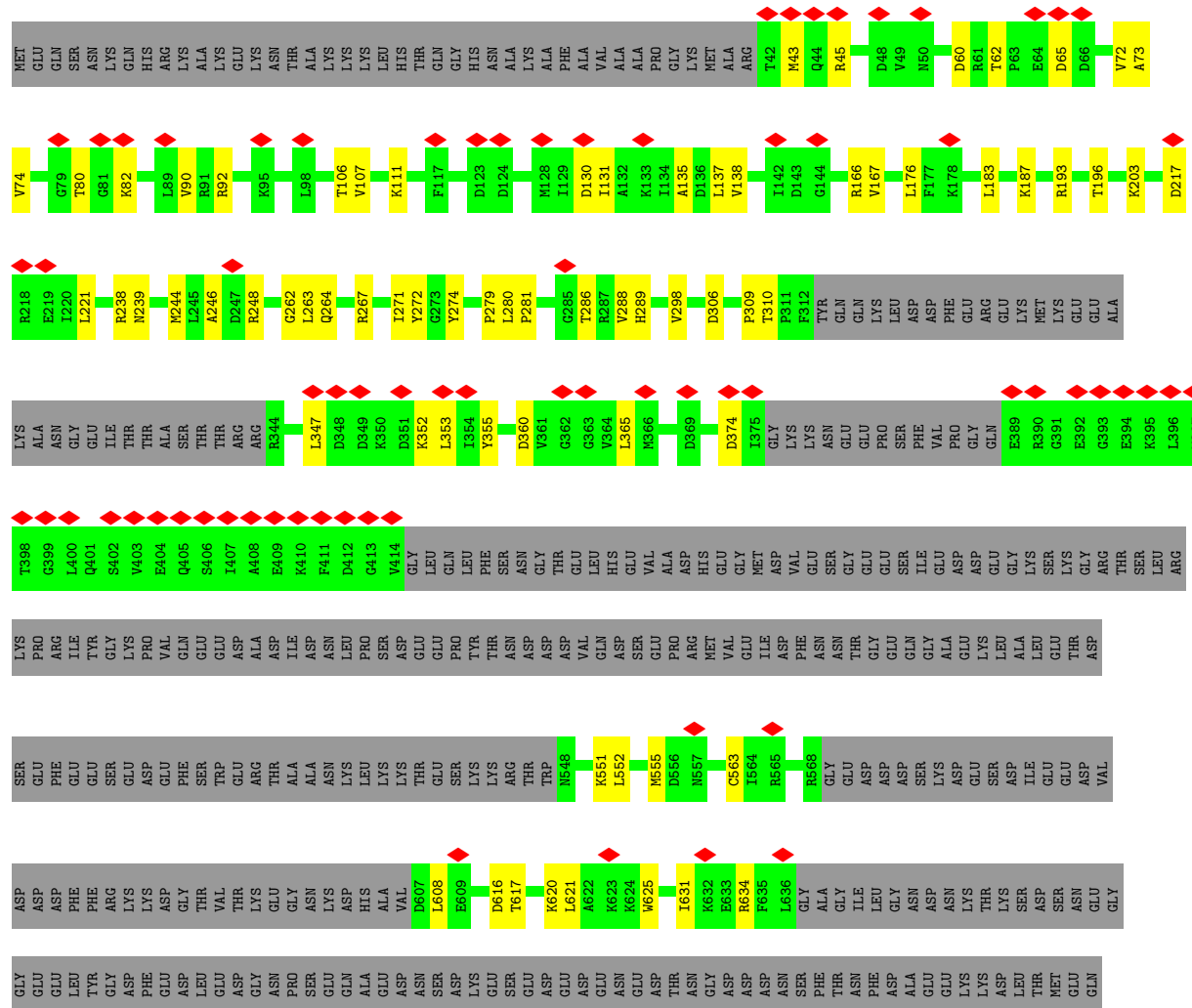


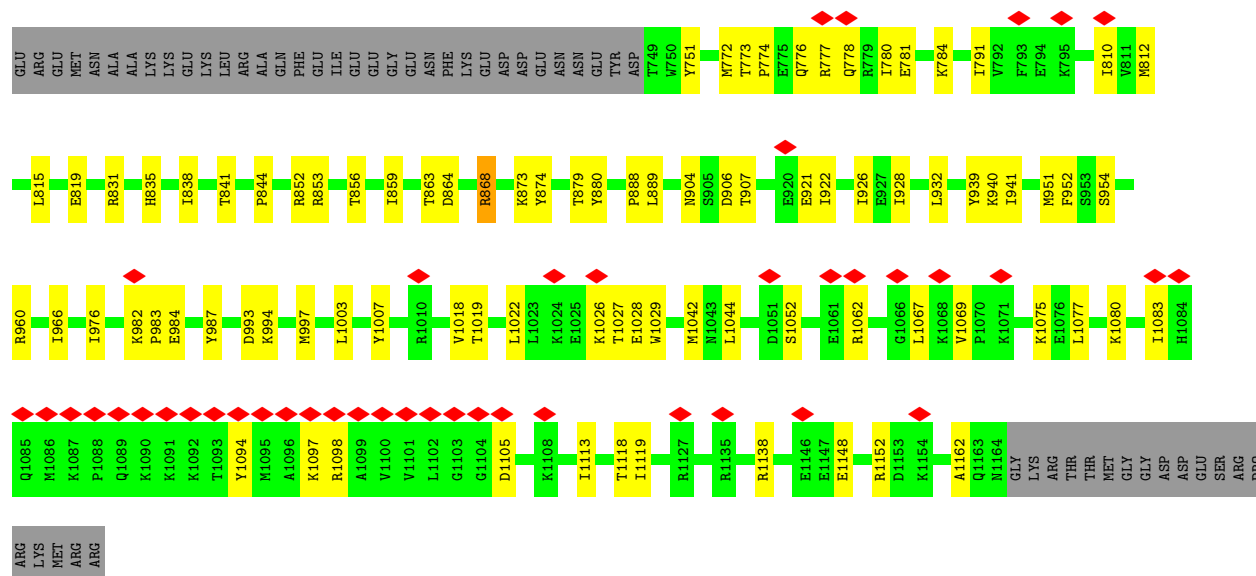
- Molecule 54: Ribosomal RNA small subunit methyltransferase NEP1



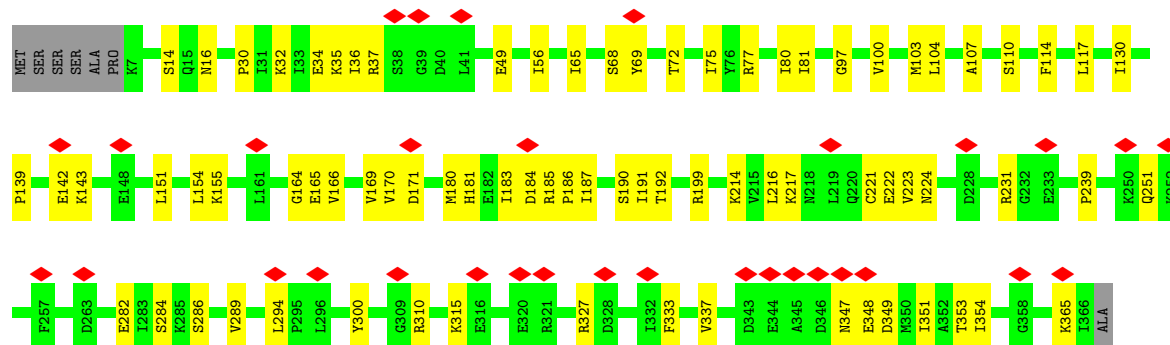
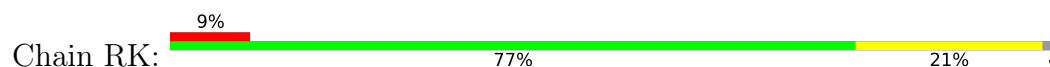


• Molecule 55: Ribosome biogenesis protein BMS1

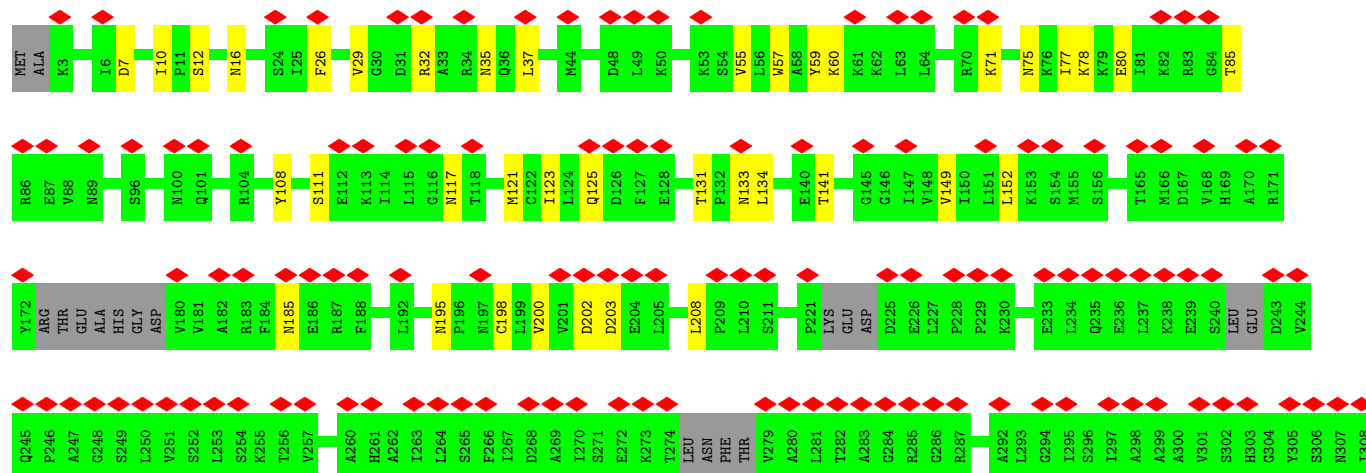
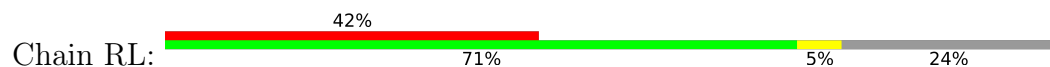


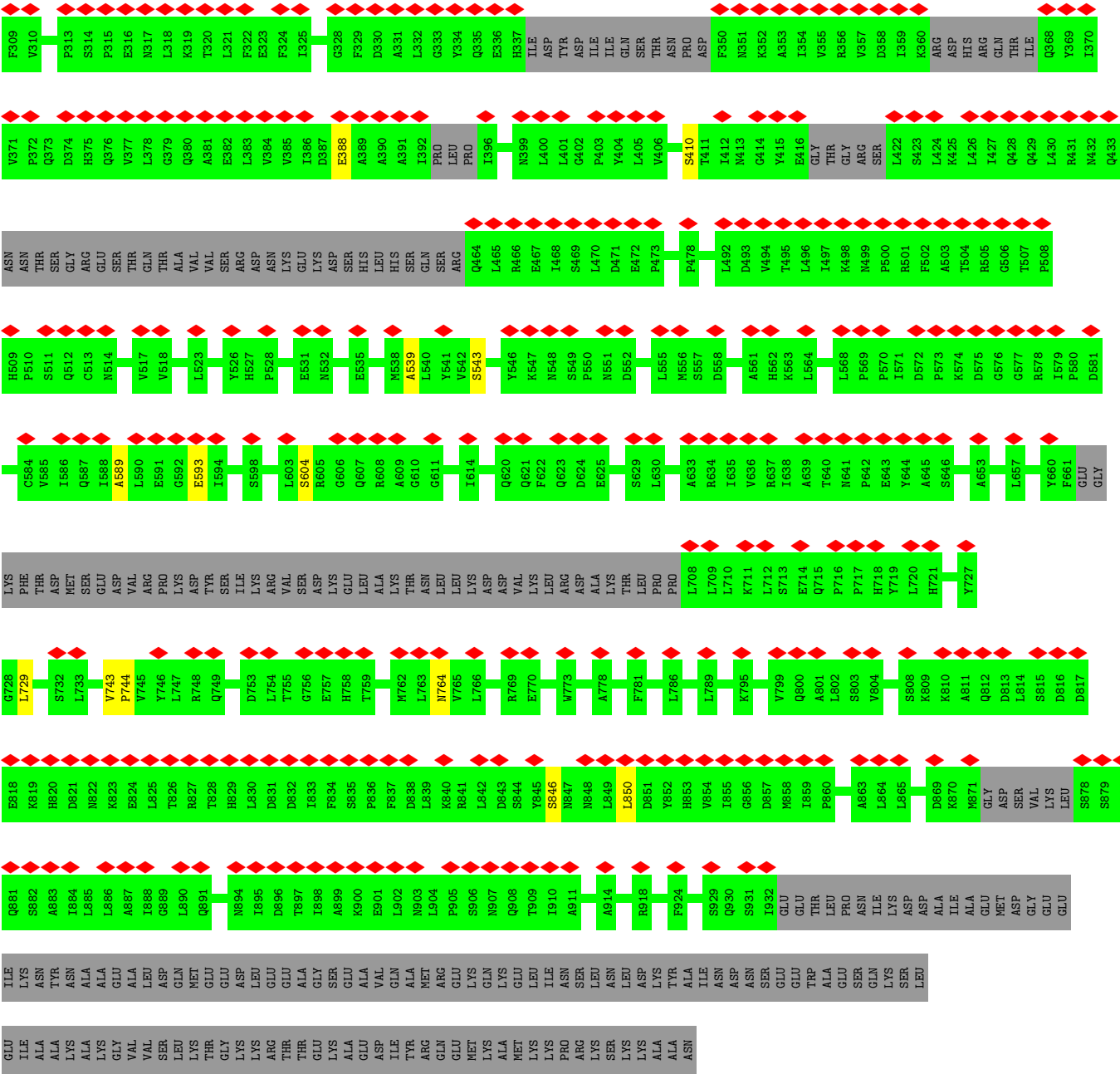


- Molecule 56: RNA 3'-terminal phosphate cyclase-like protein

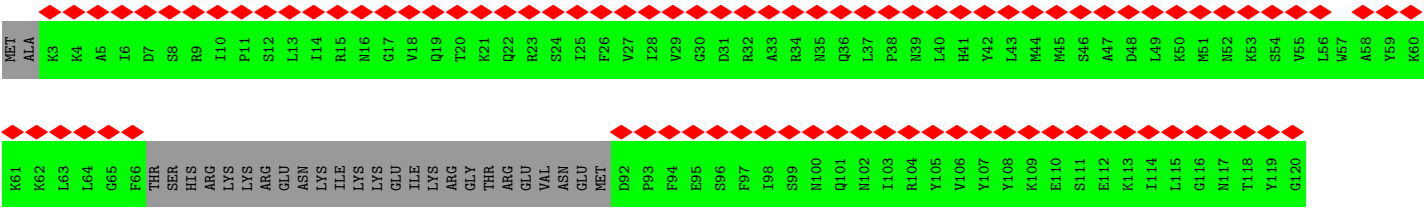
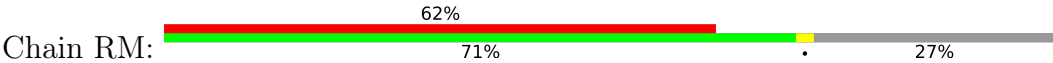


- Molecule 57: RNA cytidine acetyltransferase





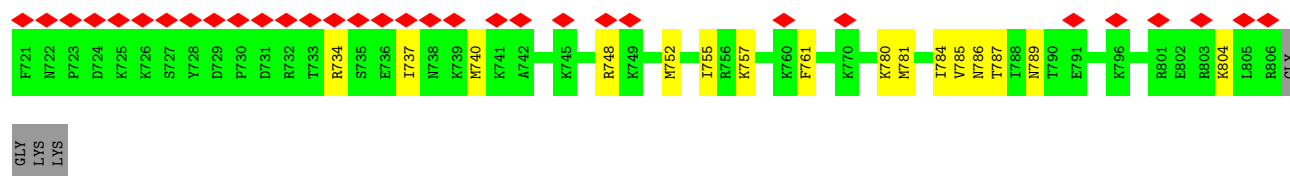
● Molecule 57: RNA cytidine acetyltransferase



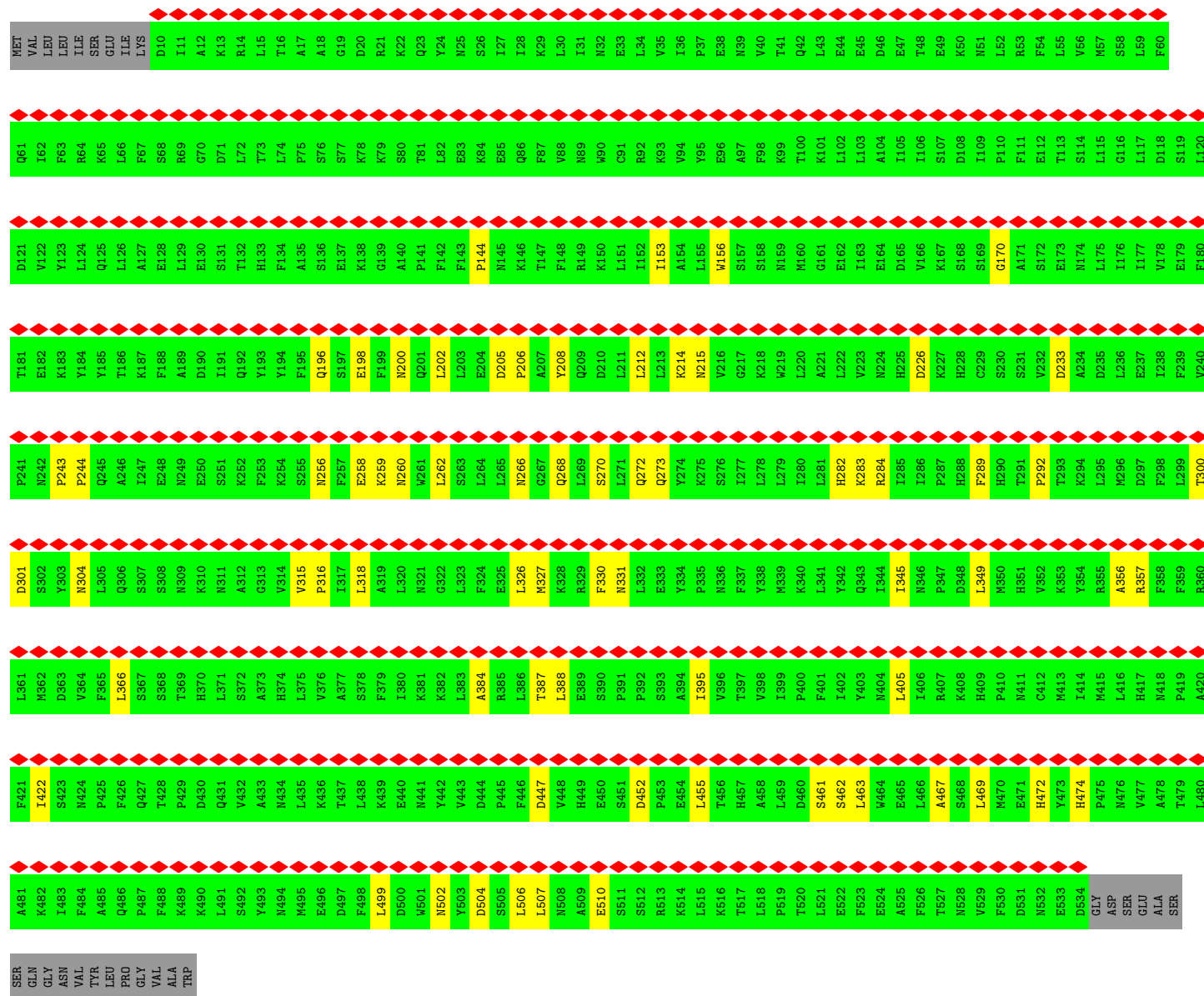
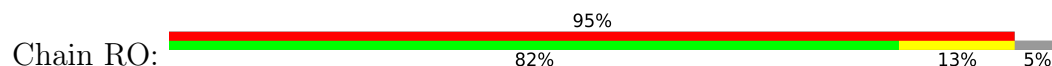


Chain RN:

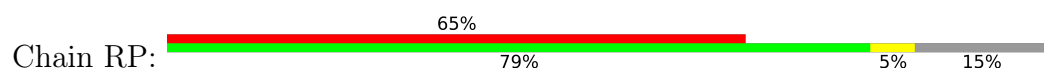




• Molecule 59: Nucleolar complex protein 4



• Molecule 60: U3 small nucleolar RNA-associated protein 20

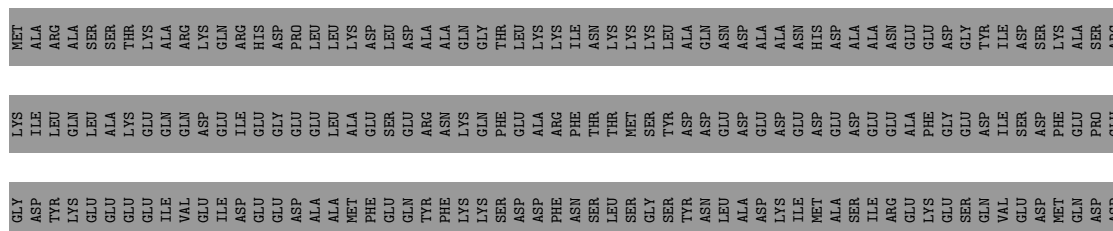


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A61	K62	P63	T64	E65	F66	A67	A68	E69	L70	E71	H72	T131	H73	L132	V74	T75	L77	P78	Q79	I80	L81	H82	H83	D84	K85	K86	I87	F88	N89	S90	L91	V92	S93	P94	I95	N96	F97	H98	D99	E100	F101	S102	L103	Q104	P105	L106	L107	D108	L109	L110	A111	Q112	F113	C114	H115	D116	L117	G118	P119	D120
F121	L122	K123	F124	Y125	E126	E127	A128	I129	F131	K130	T131	H132	L133	N134	L135	L136	D137	A138	A139	I140	E141	F142	E143	S144	S145	N146	V147	F148	E149	V150	G151	F152	L155	A156	Y157	I158	F159	K160	Y161	L162	S163	K164	F165	L166	V167	K168	L169	L170	V171	L172	T173	C174	D175	L176	L177	I178	P179	L180		
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T246	L247	H248	S249	A251	K252	A253	I254	M255	S256	V257	L258	L259	H260	E261	A262	L263	T264	K265	R266	S267	P268	E269	R270	S271	V272	S273	L274	D277	L278	W279	M280	N281	I282	S283	K284	Y285	A286	S287	I288	E289	S290	L291	K292	P293	V294	Y295	E296	V297	M298	Y299	Q300	D301	F302	N303	D304	S305	LEU			
ASP	ALA	THR	ASN	ASP	R313	I314	L315	K316	V317	L318	T319	T320	I321	V322	F323	S324	E325	SER	GLY	ARG	LYS	I330	P331	D332	W333	N334	K335	I336	T337	I338	L339	I340	E341	R342	I343	M344	SER	GLN	GLU	ASN	CYS	ALA	SER	L353	S354	Q355	D356	K357	V358	A359	F360	L361	F362	A363	L364	F365	I366			
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I746	W747	S748	K749	Y750	S751	T752	Q753	N754	T755	S756	I757	F758	S759	T760	T761	I762	E763	R764	R765	G766	N767	T768	T769	Y770	P771	I772	L773	I774	R775	N776	Q777	A778	L779	K780	W781	M782	I785	P786	A789	E790	N791	H792	F793	V794	A797	P798	F799	V800	Y801	N802	D803	K808	E811	D812						
M813	E814	N815	E816	I819	T820	G821	S822	L832	K833	T834	L835	S836	K837	F838	I841	V844	Y845	S846	A847	T848	E849	L850	H851	D852	H853	L854	L857	L858	R861	N862	T863	D864	V865	Q866	K867	L868	A869	L870	D871	A872	L873	L874	A875	Y876	K877	N878	P879	T880	L881	N882	K883	Y884	R885							

D886	N887	L888	K889	D893	L896	D899	E900	I901	T902	T903	F904	L905	T906	N908	G909	S910	Q911	S912	I913	K914	A915	E916	D917	E918	K919	V920	M921	P922	P923	Y924	I928	R932	A933	Q934	V935	P936	P937	T938	S939	G940	Q941	K942	R943	S944	R945	K946	I947	A948	V949	I950	S951	V952	L953						
P954	N955	I961	F964	F964	R971	Y974	N975	Y976	F977	F978	G979	S986	A989	T990	T993	I994	R995	T998	V1001	M1002	I1003	V1004	M1005	S1006	T1007	H1018	T1019	V1022	P1025	L1026	S1029	I1030	A1031	M1032	A1033	Y1034	Y1035	V1036	L1037	E1040	S1041	T1042	E1043	E1044	V1045	H1046													
L1047	R1048	K1049	M1050	A1051	R1055	Q1056	Q1057	K1060	C1061	L1062	S1063	S1064	V1065	F1066	F1068	F1073	D1074	W1075	S1076	T1077	S1078	Y1083	A1084	V1085	V1086	V1087	K1088	P1089	I1091	S1092	H1093	F1094	S1095	D1096	E1097	N1098	L1099	Q1100	S1103	S1104	L1105	L1108	F1109	L1110	Y1111	W1112	A1113	H1114	N1115	P1116	S1117								
L1118	Y1119	F1121	M1122	Y1123	Y1124	F1127	A1128	T1129	A1130	T1131	A1132	L1133	M1134	D1135	T1136	I1137	S1138	M1139	Q1140	H1141	V1142	K1143	E1144	A1145	V1146	I1147	G1148	P1149	I1150	I1151	E1152	A1153	A1154	D1155	S1156	I1157	I1158	R1159	M1160	P1161	V1162	M1163	D1164	D1165	H1166	Y1167	V1168	D1169	L1170	V1171	T1172	H1173	I1174	C1175	T1176	C1178			
L1179	K1180	I1181	L1182	P1183	S1184	L1185	Y1186	V1187	K1188	L1189	S1190	D1191	S1192	M1193	S1194	I1195	S1196	T1197	F1198	L1199	M1200	L1201	L1202	V1203	S1204	I1205	T1206	E1207	M1208	G1209	F1210	I1211	Q1212	D1213	D1214	H1215	V1216	R1217	S1218	R1219	L1220	I1221	S1222	S1223	L1224	I1225	S1226	I1227	L1228	K1229	G1230	K1231	L1232	K1233	K1234	L1235	Q1236	E1237	N1238
D1239	T1240	Q1241	K1242	L1243	L1244	K1245	L1246	L1247	K1248	L1249	L1250	V1251	F1252	N1253	Y1254	C1256	S1257	W1258	S1259	D1260	I1261	E1262	E1263	L1264	Y1265	T1266	T1267	I1268	S1269	L1270	L1271	F1272	K1273	T1274	F1275	D1276	E1277	R1278	N1279	L1280	R1281	V1282	S1283	L1284	T1285	E1286	L1287	F1288	I1289	E1290	L1291	G1292	R1293	K1294	E1297	L1298	E1299		
S1300	I1301	S1302	K1303	L1304	V1305	A1306	D1307	L1308	M1309	S1310	Y1311	S1312	S1313	S1314	R1315	M1316	H1317	E1318	Y1319	D1320	F1321	P1322	ARG	ILE	LEU	SER	THR	PHE	LYS	GLY	LEU	ILE	ASP	GLY	TYR	LYS	TYR	GLU	TRP	PRO	LEU	PHE	THR	PHE	LEU	HIS	PHE	ILE	ASN	LYS	GLN	GLU							
GLU	LEU	ALA	ARG	THR	ASN	ALA	HIS	ALA	ILE	MET	LYS	PHE	D1376	F1377	I1378	M1379	E1380	K1381	P1382	M1383	L1384	M1385	E1386	A1387	K1388	K1389	S1390	I1391	S1392	M1393	L1394	K1395	D1396	I1397	L1398	L1399	P1400	N1401	I1402	R1403	I1404	G1405	L1406	R1407	D1408	S1409	L1410	E1411	E1412	V1413	GLN	SER	GLU	THR	VAL	SER			
V1420	L1421	S1422	Y1423	M1424	V1425	K1426	N1427	T1428	K1429	Y1430	F1431	T1432	D1433	D1436	I1439	L1440	L1441	Y1442	M1443	G1444	D1445	E1446	E1447	A1448	D1449	PHE	PHE	THR	ASN	VAL	ASN	ASN	HIS	ILE	GLN	LEU	HIS	P1461	R1462	Q1463	R1464	A1465	I1466	K1467	E1471	H1472	A1473	L1474	Q1475	L1476	K1477	D1478	M1479	S1480	T1481	L1482	H1483		
Y1484	L1485	I1486	P1487	M1488	I1489	E1490	SER	H1491	Y1492	V1493	F1494	S1495	D1496	D1497	E1498	R1499	Y1500	R1501	M1502	I1503	G1504	N1505	E1506	T1507	Q1508	I1509	A1510	I1511	G1512	G1513	Q1516	H1517	M1518	S1519	V1520	N1521	Q1522	Y1523	K1524	A1525	L1526	L1527	R1528	L1529	Y1530	I1531	S1532	M1533	L1534	K1535	T1536	K1537	P1538	M1539	Q1540	M1541	K1542	Q1543	A1544
V1545	Q1546	L1547	I1548	VAL	GLN	LEU	SER	VAL	PRO	LEU	ARG	GLU	T1558	L1559	R1560	I1561	V1562	R1563	D1564	G1565	A1566	E1567	S1568	K1569	L1570	S1573	K1574	F1575	P1576	S1577	ASN	LEU	ASP	GLU	PRO	SER	ASN	PHE	ILE	LYS	GLN	LEU	TYR	PRO	THR	SER	LYS	ILE	GLY	THR	ARG	ASP	GLU	THR					
ILE	ILE	E1608	R1609	M1610	P1611	I1612	A1613	E1614	V1617	N1618	I1619	V1620	L1621	T1624	N1625	D1626	D1627	I1628	T1629	M1630	F1631	L1632	P1633	S1634	I1635	L1636	C1640	Q1641	V1642	L1643	R1644	S1645	K1646	S1647	E1648	E1649	L1650	R1651	D1652	V1653	V1654	R1655	Y1656	I1663	T1664	L1665	E1668	Y1669	L1670	V1671	F1672	H1673	T1674	K1675					
E1676	A1679	T1680	L1681	K1682	R1683	G1684	S1685	Q1686	I1687	H1688	V1689	L1690	S1691	Y1692	H1695	Y1696	M1701	H1702	G1703	V1704	L1705	K1706	H1707	S1708	D1709	L1710	D1711	T1712	S1713	M1716	K1719	I1720	I1721	H1722	E1723	N1724	I1725	F1726	G1727	F1728	A1729	G1730	E1731	E1732	K1733	D1734	S1735	E1736	N1737	Y1738	H1739	T1740	K1741	V1742					

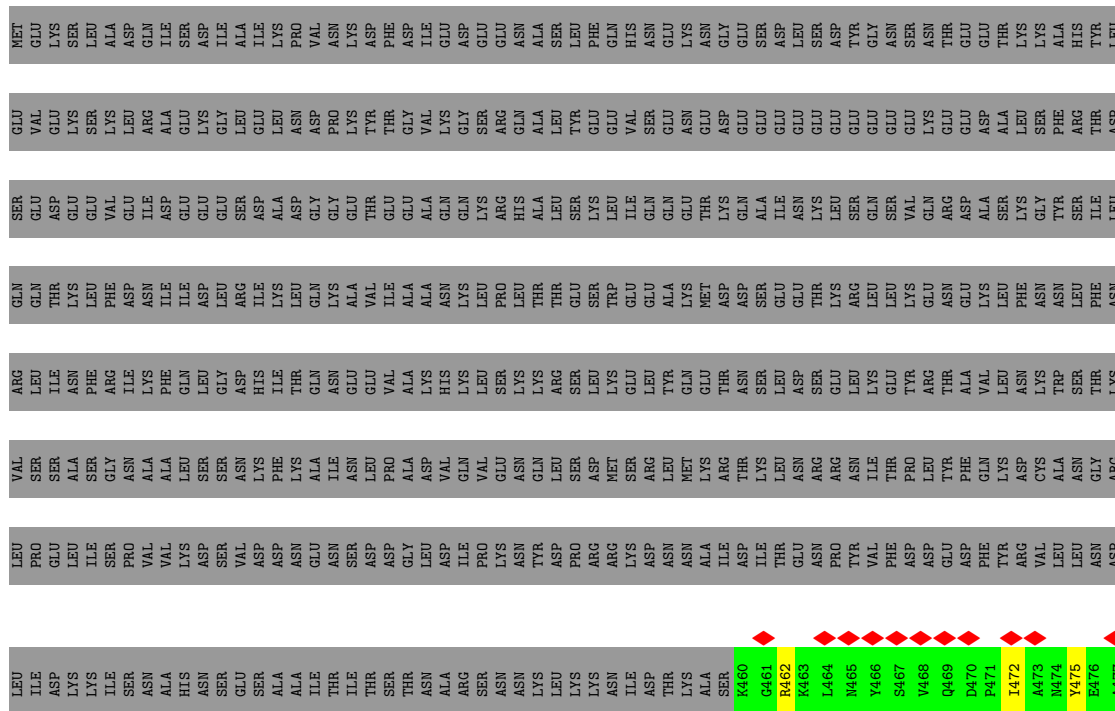
- Molecule 61: U3 small nucleolar RNA-associated protein 14







- Molecule 65: Protein BFR2



- Molecule 66: Unassigned helices





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	17924	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	0.126	Depositor
Minimum map value	-0.059	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	597.632, 597.632, 597.632	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.334, 1.334, 1.334	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	3A	0.45	0/4141	0.48	0/6433
2	5A	0.44	0/8952	0.47	1/13931 (0.0%)
3	SA	0.35	0/31535	0.47	5/49095 (0.0%)
4	SC	0.44	0/1856	0.77	3/2490 (0.1%)
5	SF	0.29	0/1854	0.66	0/2504
6	SG	0.49	0/1690	0.67	2/2285 (0.1%)
7	SH	0.24	0/1341	0.61	1/1789 (0.1%)
8	SI	0.32	0/1341	0.69	2/1806 (0.1%)
9	SJ	0.26	0/1347	0.60	0/1801
10	SK	0.44	0/1410	0.63	0/1888
11	SM	0.26	0/1020	0.64	0/1374
12	SO	0.39	0/1109	0.63	0/1495
13	SP	0.46	0/879	0.79	0/1186
14	SR	0.52	0/990	0.77	3/1335 (0.2%)
15	SX	0.46	0/1020	0.63	0/1371
16	SY	0.48	0/798	0.65	0/1065
17	SZ	0.36	0/822	0.73	0/1103
18	Sc	0.40	0/613	0.63	0/828
19	Sd	0.50	0/499	0.72	2/670 (0.3%)
20	3B	0.51	0/1901	0.66	1/2567 (0.0%)
20	3C	0.37	0/1796	0.66	0/2424
21	3D	0.40	0/2891	0.62	0/3895
22	3E	0.38	0/3059	0.62	0/4153
23	3F	0.36	0/3715	0.64	0/5001
24	3G	0.51	0/928	0.72	1/1262 (0.1%)
24	3H	0.45	0/928	0.70	0/1262
25	A4	0.43	0/5321	0.66	0/7207
26	A5	0.44	0/4044	0.65	0/5493
27	A8	0.23	0/3328	0.62	0/4565
28	A9	0.28	0/951	0.60	0/1287
29	AE	0.32	1/10049 (0.0%)	0.56	1/13737 (0.0%)
30	AF	0.48	0/3993	0.68	0/5413

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	AG	0.42	0/6699	0.64	3/9077 (0.0%)
32	B1	0.58	0/6780	0.69	0/9175
33	B2	0.39	0/6853	0.68	2/9256 (0.0%)
34	B3	0.35	0/6014	0.70	2/8137 (0.0%)
35	B8	0.55	0/3848	0.63	0/5218
36	BE	0.53	0/6948	0.64	2/9391 (0.0%)
37	B6	0.37	0/2849	0.60	0/3853
38	5B	0.31	0/499	0.62	0/659
39	5C	0.55	0/4321	0.66	2/5832 (0.0%)
40	5D	0.47	0/1417	0.73	0/1885
41	5E	0.44	0/1665	0.66	2/2233 (0.1%)
42	5F	0.64	0/1559	0.72	1/2097 (0.0%)
43	5G	0.52	0/2337	0.67	2/3148 (0.1%)
44	5H	0.47	0/601	0.59	0/789
45	5I	0.56	0/3844	0.68	0/5174
46	5J	0.36	0/1302	0.58	0/1728
47	5K	0.51	0/1426	0.66	0/1917
48	RA	0.27	0/2769	0.66	2/3753 (0.1%)
49	RB	0.37	0/1121	0.79	0/1487
50	RC	0.40	0/2245	0.60	0/3021
51	RD	0.26	0/2453	0.67	2/3308 (0.1%)
52	RE	0.33	0/8924	0.64	4/12070 (0.0%)
53	RF	0.28	0/2004	0.66	1/2697 (0.0%)
54	RG	0.32	0/1727	0.70	0/2329
54	RH	0.37	0/1828	0.59	0/2470
55	RJ	0.44	0/6514	0.61	0/8768
56	RK	0.39	0/2832	0.64	0/3825
57	RL	0.21	0/4549	0.51	1/6241 (0.0%)
57	RM	0.15	0/3765	0.44	1/5218 (0.0%)
58	RN	0.30	0/4591	0.63	1/6187 (0.0%)
59	RO	0.32	0/3849	0.63	0/5261
60	RP	0.21	0/12225	0.54	4/16812 (0.0%)
61	RQ	0.41	0/1678	0.63	1/2282 (0.0%)
62	RS	0.30	0/2104	0.70	0/2854
63	RT	0.38	0/1379	0.68	0/1853
64	RV	0.43	0/1456	0.60	1/1937 (0.1%)
65	RY	0.23	0/307	0.53	0/415
All	All	0.40	1/233403 (0.0%)	0.60	56/325072 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	SC	0	1
5	SF	0	2
8	SI	0	3
9	SJ	0	1
11	SM	0	1
12	SO	0	1
13	SP	0	1
17	SZ	0	1
18	Sc	0	1
21	3D	0	3
22	3E	0	1
23	3F	0	1
24	3G	0	2
24	3H	0	1
25	A4	0	1
26	A5	0	1
27	A8	0	4
31	AG	0	2
32	B1	0	3
33	B2	0	9
34	B3	0	11
36	BE	0	1
39	5C	0	2
40	5D	0	1
41	5E	0	1
42	5F	0	1
43	5G	0	1
45	5I	0	2
48	RA	0	2
49	RB	0	1
52	RE	0	1
53	RF	0	1
55	RJ	0	2
56	RK	0	1
57	RL	0	1
57	RM	0	1
58	RN	0	1
59	RO	0	1
60	RP	0	3
61	RQ	0	1
64	RV	0	2
All	All	0	78

All (1) bond length outliers are listed below:

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

All (56) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	RD	1223	PRO	N-CA-CB	8.04	111.69	103.25
52	RE	1105	PRO	O-C-N	-7.87	112.02	122.64
51	RD	1205	PRO	N-CA-CB	7.68	110.60	103.15
33	B2	267	ASP	CA-C-N	6.86	134.65	121.54
33	B2	267	ASP	C-N-CA	6.86	134.65	121.54
2	5A	312	U	P-O3'-C3'	6.82	130.43	120.20
60	RP	2033	LYS	CA-C-N	6.64	134.22	121.54
60	RP	2033	LYS	C-N-CA	6.64	134.22	121.54
42	5F	13	LEU	CA-CB-CG	6.47	138.96	116.30
53	RF	157	GLU	N-CA-C	6.11	116.34	108.34
57	RL	744	PRO	N-CA-C	6.07	124.97	112.47
43	5G	157	PHE	N-CA-C	6.02	123.11	109.81
57	RM	744	PRO	N-CA-C	5.99	124.81	112.47
31	AG	141	LEU	N-CA-C	5.92	117.83	110.91
24	3G	67	LEU	CA-CB-CG	5.86	136.82	116.30
60	RP	1745	ILE	CA-C-N	5.82	132.66	121.54
60	RP	1745	ILE	C-N-CA	5.82	132.66	121.54
8	SI	117	THR	CA-C-N	5.82	132.65	121.54
8	SI	117	THR	C-N-CA	5.82	132.65	121.54
36	BE	840	PHE	CA-C-N	5.67	130.10	121.03
36	BE	840	PHE	C-N-CA	5.67	130.10	121.03
3	SA	1052	U	O3'-P-O5'	5.66	112.49	104.00
64	RV	204	GLY	N-CA-C	5.63	126.52	113.18
14	SR	123	ARG	CA-C-N	5.59	140.41	127.00
14	SR	123	ARG	C-N-CA	5.59	140.41	127.00
4	SC	54	LEU	CA-CB-CG	5.58	135.85	116.30
52	RE	924	LEU	CA-CB-CG	5.49	135.50	116.30
48	RA	286	GLU	CA-C-N	5.46	131.98	121.54
48	RA	286	GLU	C-N-CA	5.46	131.98	121.54
41	5E	452	SER	CA-C-O	-5.46	110.17	118.91
61	RQ	313	PHE	N-CA-C	5.43	121.82	109.81
3	SA	579	A	P-O3'-C3'	5.38	128.27	120.20
29	AE	1589	ILE	N-CA-C	-5.35	107.61	112.96
4	SC	54	LEU	CA-C-N	5.31	131.68	121.54
4	SC	54	LEU	C-N-CA	5.31	131.68	121.54
3	SA	272	U	P-O3'-C3'	5.30	128.16	120.20
7	SH	41	VAL	N-CA-C	-5.24	107.72	112.96
52	RE	1105	PRO	CA-C-N	5.22	130.68	122.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	RE	1105	PRO	C-N-CA	5.22	130.68	122.33
41	5E	454	VAL	N-CA-C	5.18	120.11	109.34
14	SR	123	ARG	C-N-CD	-5.07	109.46	120.60
19	Sd	50	GLU	CA-C-N	5.05	131.19	121.54
19	Sd	50	GLU	C-N-CA	5.05	131.19	121.54
43	5G	120	GLY	N-CA-C	-5.05	101.21	113.18
39	5C	456	SER	CA-C-N	5.04	128.82	121.31
39	5C	456	SER	C-N-CA	5.04	128.82	121.31
3	SA	1594	G	C4'-C3'-O3'	5.04	116.95	109.40
31	AG	138	ASP	CA-C-N	5.03	128.22	120.82
31	AG	138	ASP	C-N-CA	5.03	128.22	120.82
3	SA	56	U	P-O3'-C3'	5.03	127.74	120.20
6	SG	99	MET	CA-C-N	5.01	131.12	121.54
6	SG	99	MET	C-N-CA	5.01	131.12	121.54
20	3B	306	LEU	CA-CB-CG	5.01	133.82	116.30
34	B3	471	PRO	CA-C-N	5.01	135.31	126.45
34	B3	471	PRO	C-N-CA	5.01	135.31	126.45
58	RN	592	ARG	CA-CB-CG	5.00	124.10	114.10

There are no chirality outliers.

All (78) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	3D	142	LEU	Peptide
21	3D	202	HIS	Peptide
21	3D	286	ARG	Peptide
22	3E	331	LYS	Peptide
23	3F	237	ASP	Peptide
24	3G	59	GLU	Peptide
24	3G	9	PHE	Peptide
24	3H	59	GLU	Peptide
39	5C	540	GLU	Peptide
39	5C	551	SER	Peptide
40	5D	138	ASP	Peptide
41	5E	453	SER	Peptide
42	5F	101	VAL	Peptide
43	5G	74	ASP	Peptide
45	5I	230	ASN	Peptide
45	5I	283	ASP	Peptide
25	A4	54	LYS	Peptide
26	A5	167	SER	Peptide
27	A8	257	SER	Peptide

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Mol	Chain	Res	Type	Group
27	A8	266	ILE	Peptide
27	A8	496	TYR	Peptide
27	A8	529	HIS	Peptide
31	AG	178	PHE	Peptide
31	AG	780	GLU	Peptide
32	B1	288	ASP	Peptide
32	B1	661	LEU	Peptide
32	B1	690	ALA	Peptide
33	B2	131	GLY	Peptide
33	B2	213	LYS	Peptide
33	B2	266	SER	Peptide
33	B2	267	ASP	Peptide
33	B2	278	ASP	Peptide
33	B2	44	SER	Peptide
33	B2	613	ALA	Peptide
33	B2	916	HIS	Peptide
33	B2	918	TYR	Peptide
34	B3	34	THR	Peptide
34	B3	435	ALA	Peptide
34	B3	473	ALA	Peptide
34	B3	479	ILE	Peptide
34	B3	480	ILE	Peptide
34	B3	585	ASN	Peptide
34	B3	593	CYS	Peptide
34	B3	594	GLY	Peptide
34	B3	627	ASN	Peptide
34	B3	89	HIS	Peptide
34	B3	90	LEU	Peptide
36	BE	94	TYR	Peptide
48	RA	111	TRP	Peptide
48	RA	173	LEU	Peptide
49	RB	261	SER	Peptide
52	RE	767	GLN	Peptide
53	RF	253	ALA	Peptide
55	RJ	1026	LYS	Peptide
55	RJ	868	ARG	Peptide
56	RK	333	PHE	Peptide
57	RL	743	VAL	Peptide
57	RM	743	VAL	Peptide
58	RN	286	SER	Peptide
59	RO	144	PRO	Peptide
60	RP	1746	LYS	Peptide

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Mol	Chain	Res	Type	Group
60	RP	2051	ASP	Peptide
60	RP	835	LEU	Peptide
61	RQ	313	PHE	Peptide
64	RV	203	ILE	Peptide
64	RV	261	GLY	Peptide
4	SC	238	GLU	Peptide
5	SF	193	GLY	Peptide
5	SF	195	ILE	Peptide
8	SI	133	THR	Peptide
8	SI	31	SER	Peptide
8	SI	64	VAL	Peptide
9	SJ	85	PRO	Peptide
11	SM	128	CYS	Peptide
12	SO	58	HIS	Peptide
13	SP	90	ARG	Peptide
17	SZ	76	TYR	Peptide
18	Sc	49	HIS	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	3A	3711	0	1882	21	0
2	5A	8009	0	4030	52	0
3	SA	28210	0	14226	240	0
4	SC	1830	0	1914	33	0
5	SF	1815	0	1870	45	0
6	SG	1669	0	1724	18	0
7	SH	1327	0	1403	30	0
8	SI	1321	0	1387	23	0
9	SJ	1324	0	1344	48	0
10	SK	1388	0	1467	32	0
11	SM	997	0	1048	34	0
12	SO	1087	0	1152	13	0
13	SP	868	0	894	14	0
14	SR	973	0	1029	14	0
15	SX	1003	0	1040	16	0
16	SY	786	0	843	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	SZ	809	0	842	15	0
18	Sc	603	0	623	9	0
19	Sd	497	0	535	3	0
20	3B	1865	0	1910	30	0
20	3C	1763	0	1805	34	0
21	3D	2848	0	2815	46	0
22	3E	3028	0	2813	62	0
23	3F	3643	0	3654	79	0
24	3G	916	0	964	11	0
24	3H	916	0	964	26	0
25	A4	5226	0	5199	96	0
26	A5	3976	0	3919	56	0
27	A8	3307	0	2316	39	0
28	A9	939	0	898	19	0
29	AE	9955	0	7968	103	0
30	AF	3911	0	3906	71	0
31	AG	6570	0	6473	127	0
32	B1	6635	0	6525	103	0
33	B2	6723	0	6698	121	0
34	B3	5919	0	6007	127	0
35	B8	3764	0	3757	58	0
36	BE	6810	0	6787	86	0
37	B6	2800	0	2517	35	0
38	5B	495	0	561	13	0
39	5C	4237	0	4239	85	0
40	5D	1396	0	1407	20	0
41	5E	1647	0	1678	30	0
42	5F	1530	0	1572	30	0
43	5G	2296	0	2325	41	0
44	5H	596	0	661	8	0
45	5I	3765	0	3714	73	0
46	5J	1280	0	1331	23	0
47	5K	1403	0	1484	19	0
48	RA	2709	0	2622	66	0
49	RB	1108	0	1087	27	0
50	RC	2207	0	2229	29	0
51	RD	2412	0	2263	40	0
52	RE	8716	0	8828	240	0
53	RF	1963	0	1942	45	0
54	RG	1701	0	1767	40	0
54	RH	1799	0	1872	29	0
55	RJ	6379	0	6506	110	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	RK	2781	0	2878	51	0
57	RL	4539	0	2874	29	0
57	RM	3779	0	1650	8	0
58	RN	4529	0	4262	69	0
59	RO	3766	0	3269	47	0
60	RP	12171	0	7749	76	0
61	RQ	1651	0	1450	28	0
62	RS	2051	0	2096	53	0
63	RT	1357	0	1426	15	0
64	RV	1448	0	1435	16	0
65	RY	299	0	275	6	0
66	X1	375	0	92	4	0
67	5K	1	0	0	0	0
67	Sc	1	0	0	0	0
68	RJ	32	0	12	2	0
69	RJ	1	0	0	0	0
All	All	226161	0	194704	2951	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (2951) 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)
52:RE:1203:ASN:HD22	52:RE:1219:ILE:CG2	1.50	1.22
52:RE:1102:LEU:HD23	52:RE:1180:ASN:O	1.40	1.20
52:RE:1216:LYS:NZ	52:RE:1236:THR:HG23	1.65	1.11
52:RE:518:PHE:CZ	52:RE:1075:LEU:HG	1.92	1.05
52:RE:1203:ASN:HD22	52:RE:1219:ILE:HG21	1.18	1.04
52:RE:1204:VAL:HB	52:RE:1212:VAL:HG11	1.35	1.04
27:A8:264:SER:O	27:A8:267:ILE:HA	1.61	1.01
33:B2:17:ILE:HG22	33:B2:52:TRP:CZ2	1.94	1.01
58:RN:527:GLN:O	58:RN:531:GLN:HB2	1.60	1.01
61:RQ:298:TRP:NE1	61:RQ:899:LYS:HG3	1.76	1.00
3:SA:36:C:H42	3:SA:472:U:H3	1.00	0.99
52:RE:1203:ASN:ND2	52:RE:1219:ILE:CG2	2.28	0.96
10:SK:65:LYS:HZ2	23:3F:59:PRO:CD	1.77	0.96
52:RE:518:PHE:HZ	52:RE:1075:LEU:HG	1.28	0.96
52:RE:1216:LYS:HZ1	52:RE:1236:THR:HG23	1.24	0.95
10:SK:65:LYS:HZ2	23:3F:59:PRO:CG	1.78	0.94
52:RE:1204:VAL:HB	52:RE:1212:VAL:CG1	1.97	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:RE:918:ARG:HE	52:RE:1089:PHE:HE2	1.12	0.94
52:RE:1203:ASN:ND2	52:RE:1219:ILE:HG21	1.83	0.93
10:SK:65:LYS:HZ2	23:3F:59:PRO:CB	1.82	0.92
52:RE:1098:PHE:HD2	52:RE:1184:GLY:H	1.12	0.91
52:RE:918:ARG:NE	52:RE:1089:PHE:HE2	1.68	0.91
3:SA:36:C:N4	3:SA:472:U:H3	1.70	0.89
10:SK:65:LYS:NZ	23:3F:59:PRO:CG	2.35	0.89
52:RE:1157:TYR:HE1	52:RE:1203:ASN:HD21	1.17	0.88
45:5I:231:GLU:OE2	61:RQ:899:LYS:HD3	1.74	0.87
51:RD:1473:ASN:HB3	51:RD:1509:GLU:OE2	1.72	0.87
34:B3:494:ILE:N	34:B3:510:SER:HG	1.71	0.87
52:RE:1203:ASN:HD22	52:RE:1219:ILE:HG22	1.37	0.87
52:RE:1065:THR:O	52:RE:1069:LYS:HG3	1.75	0.86
52:RE:1216:LYS:HZ1	52:RE:1236:THR:CG2	1.88	0.85
10:SK:65:LYS:NZ	23:3F:59:PRO:CD	2.38	0.85
57:RM:313:PRO:O	57:RM:372:PRO:HA	1.77	0.84
62:RS:424:PHE:O	62:RS:428:TYR:HB2	1.78	0.84
52:RE:919:TRP:CZ2	52:RE:1067:LEU:HD22	2.12	0.84
5:SF:213:SER:HG	23:3F:102:ASP:N	1.75	0.84
59:RO:502:ASN:O	59:RO:506:LEU:HB2	1.77	0.83
52:RE:1216:LYS:NZ	52:RE:1236:THR:CG2	2.42	0.82
51:RD:1509:GLU:HB3	51:RD:1512:GLU:HB2	1.60	0.82
61:RQ:346:LEU:O	61:RQ:350:ASN:HA	1.80	0.81
24:3H:44:LEU:HD22	24:3H:52:ILE:CD1	2.10	0.81
29:AE:151:ILE:O	29:AE:155:ILE:HB	1.81	0.81
57:RM:746:TYR:O	57:RM:765:VAL:HA	1.81	0.80
61:RQ:298:TRP:HE1	61:RQ:899:LYS:HG3	1.44	0.80
52:RE:1174:GLY:HA3	52:RE:1179:LYS:HE2	1.62	0.80
52:RE:1157:TYR:HE1	52:RE:1203:ASN:ND2	1.79	0.79
37:B6:319:TYR:O	37:B6:323:PHE:HB2	1.81	0.79
9:SJ:48:THR:O	9:SJ:52:ASN:HB2	1.83	0.79
51:RD:1470:GLY:O	52:RE:1189:LEU:HA	1.82	0.78
3:SA:825:U:H3	3:SA:845:G:H1	1.32	0.78
10:SK:65:LYS:NZ	23:3F:59:PRO:HD3	1.97	0.78
3:SA:1663:G:H1	3:SA:1738:U:H3	1.31	0.78
30:AF:224:THR:O	30:AF:239:LEU:HB2	1.83	0.78
3:SA:868:G:H1	3:SA:960:U:H3	1.30	0.78
52:RE:1169:ILE:HD12	52:RE:1177:GLY:O	1.84	0.77
52:RE:1098:PHE:HD2	52:RE:1184:GLY:N	1.80	0.77
3:SA:153:G:H1	3:SA:161:U:H3	1.33	0.77
3:SA:1688:U:H3	3:SA:1713:G:H1	1.34	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:SK:138:LYS:H	49:RB:263:GLY:HA3	1.51	0.75
3:SA:415:C:H1'	3:SA:419:G:H22	1.50	0.75
52:RE:1203:ASN:ND2	52:RE:1219:ILE:HG22	1.98	0.74
25:A4:614:TRP:O	25:A4:618:ASN:HB2	1.87	0.74
46:5J:114:ARG:O	46:5J:118:GLN:HB3	1.88	0.74
52:RE:1102:LEU:CD2	52:RE:1180:ASN:O	2.30	0.74
3:SA:1051:G:H21	45:5I:447:THR:HG21	1.54	0.73
52:RE:919:TRP:CH2	52:RE:1067:LEU:HD22	2.24	0.72
34:B3:216:ARG:HH11	34:B3:241:GLN:HE22	1.36	0.72
10:SK:65:LYS:HZ1	23:3F:59:PRO:HD3	1.55	0.72
10:SK:65:LYS:NZ	23:3F:59:PRO:CB	2.52	0.72
3:SA:505:A:H61	3:SA:586:G:H8	1.38	0.71
22:3E:397:ARG:HH21	22:3E:400:GLN:HE21	1.38	0.71
57:RL:29:VAL:HG12	57:RL:152:LEU:HD12	1.72	0.71
31:AG:435:ASP:HB2	31:AG:702:TYR:CD1	2.26	0.71
51:RD:1508:ARG:NH1	53:RF:97:GLU:HG2	2.06	0.70
51:RD:1518:ILE:HG12	51:RD:1552:LYS:HG2	1.73	0.70
52:RE:1189:LEU:HD23	52:RE:1189:LEU:C	2.16	0.70
5:SF:92:LEU:HB2	5:SF:97:GLU:HB2	1.74	0.70
6:SG:206:SER:H	6:SG:211:ILE:HD11	1.55	0.70
52:RE:1174:GLY:CA	52:RE:1179:LYS:HE2	2.22	0.70
52:RE:1108:LEU:O	52:RE:1112:CYS:HB2	1.91	0.69
32:B1:58:ILE:HA	32:B1:74:ASP:HA	1.74	0.69
2:5A:316:U:H5'	39:5C:364:ARG:HH22	1.58	0.69
52:RE:1204:VAL:CB	52:RE:1212:VAL:HG11	2.19	0.69
52:RE:441:GLN:O	52:RE:455:SER:HA	1.93	0.69
17:SZ:29:HIS:HB2	17:SZ:32:ARG:HB2	1.76	0.68
10:SK:65:LYS:NZ	23:3F:59:PRO:HB3	2.08	0.68
45:5I:345:THR:HG22	45:5I:347:ARG:H	1.58	0.68
51:RD:1512:GLU:HG2	52:RE:1199:ASN:HD21	1.57	0.68
3:SA:646:C:H2'	3:SA:647:G:H8	1.59	0.68
61:RQ:297:LYS:HB2	61:RQ:899:LYS:HB3	1.76	0.68
56:RK:192:THR:HA	56:RK:224:ASN:O	1.92	0.68
29:AE:692:ILE:HA	29:AE:695:TYR:HB3	1.76	0.68
60:RP:173:THR:O	60:RP:177:LEU:HB2	1.94	0.68
30:AF:86:SER:O	30:AF:98:ALA:HA	1.93	0.68
30:AF:211:HIS:HD1	30:AF:228:SER:HG	1.42	0.67
33:B2:17:ILE:HG22	33:B2:52:TRP:CH2	2.28	0.67
10:SK:65:LYS:NZ	23:3F:59:PRO:HG3	2.08	0.67
52:RE:918:ARG:NE	52:RE:1089:PHE:CE2	2.59	0.67
3:SA:1679:G:H1'	3:SA:1722:A:H61	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3F:443:LEU:HD21	23:3F:492:TRP:HE1	1.59	0.67
52:RE:1069:LYS:O	52:RE:1072:VAL:HG12	1.94	0.67
52:RE:1096:TYR:CZ	52:RE:1183:THR:OG1	2.46	0.67
36:BE:209:ILE:HG22	36:BE:225:THR:HG22	1.76	0.67
23:3F:185:LEU:H	23:3F:202:THR:HB	1.59	0.67
25:A4:645:ARG:HD2	25:A4:656:ARG:HD3	1.76	0.67
35:B8:513:GLN:HG3	35:B8:551:VAL:HG21	1.76	0.67
33:B2:536:CYS:HB3	33:B2:549:SER:HB3	1.77	0.67
3:SA:187:G:N2	3:SA:197:A:N7	2.43	0.66
17:SZ:51:GLU:HB2	17:SZ:54:ALA:HB3	1.76	0.66
32:B1:20:ILE:H	32:B1:307:THR:HG21	1.58	0.66
52:RE:235:LEU:O	52:RE:239:LEU:HB2	1.95	0.66
43:5G:123:VAL:HG12	43:5G:125:PRO:HD2	1.78	0.66
31:AG:435:ASP:HB3	31:AG:701:VAL:O	1.96	0.66
36:BE:209:ILE:HA	36:BE:225:THR:HA	1.76	0.66
16:SY:103:LEU:HB3	16:SY:126:LYS:HB2	1.76	0.66
20:3B:103:GLU:HG3	46:5J:134:ARG:HH12	1.60	0.66
11:SM:67:ARG:HH21	11:SM:129:ARG:H	1.44	0.66
55:RJ:248:ARG:HB3	55:RJ:272:TYR:HB2	1.78	0.66
31:AG:16:SER:HB2	31:AG:783:LEU:HB2	1.77	0.66
52:RE:756:VAL:HA	52:RE:896:THR:HG21	1.78	0.66
30:AF:52:PRO:HG2	30:AF:312:ALA:HA	1.77	0.65
34:B3:462:THR:HA	34:B3:484:GLU:HG2	1.77	0.65
36:BE:847:LEU:HD11	63:RT:266:VAL:HG23	1.78	0.65
57:RM:283:ALA:HA	57:RM:411:THR:O	1.96	0.65
3:SA:207:U:H3	3:SA:258:C:H42	1.45	0.65
52:RE:518:PHE:HE2	52:RE:1075:LEU:HB3	1.62	0.65
57:RM:311:THR:O	57:RM:370:ILE:HA	1.97	0.65
63:RT:222:THR:HG22	63:RT:235:GLY:HA3	1.79	0.65
25:A4:497:ILE:HD11	25:A4:511:VAL:HG23	1.78	0.65
27:A8:576:ARG:HG2	27:A8:578:LEU:H	1.61	0.65
33:B2:262:ILE:O	33:B2:270:SER:HA	1.97	0.65
1:3A:84:U:OP2	22:3E:361:ARG:NH2	2.30	0.65
39:5C:170:GLN:NE2	39:5C:177:TYR:OH	2.30	0.64
52:RE:1101:ASP:HB3	52:RE:1233:ASN:HB2	1.78	0.64
4:SC:132:ASP:HB2	4:SC:221:PRO:HB3	1.79	0.64
11:SM:87:ARG:HE	11:SM:104:HIS:HB2	1.62	0.64
23:3F:125:VAL:O	23:3F:128:GLN:NE2	2.30	0.64
51:RD:1525:ASN:HD22	51:RD:1556:ILE:HG22	1.62	0.64
54:RG:122:ILE:HA	54:RG:161:LYS:O	1.97	0.64
55:RJ:263:LEU:HD23	55:RJ:267:ARG:HH22	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:RO:472:HIS:HD2	59:RO:474:HIS:H	1.46	0.64
3:SA:1052:U:H5''	45:5I:449:LYS:HG2	1.78	0.64
10:SK:57:ARG:HE	47:5K:88:ASP:HB3	1.60	0.64
2:5A:487:A:H62	61:RQ:876:GLN:HE22	1.45	0.64
3:SA:415:C:H1'	3:SA:419:G:N2	2.12	0.64
3:SA:1727:G:N2	3:SA:1728:A:N7	2.46	0.64
32:B1:438:VAL:HG12	32:B1:445:VAL:HG23	1.79	0.64
41:5E:299:SER:HA	41:5E:302:LYS:HE2	1.80	0.64
33:B2:439:LEU:HB2	33:B2:444:LEU:HB3	1.79	0.64
34:B3:719:ILE:HD11	34:B3:762:CYS:HB3	1.78	0.64
36:BE:631:ASN:HB2	36:BE:644:THR:HB	1.80	0.64
42:5F:33:MET:HB2	42:5F:38:ILE:HB	1.79	0.64
16:SY:97:ASP:OD1	16:SY:97:ASP:N	2.31	0.64
35:B8:521:LEU:HA	35:B8:531:CYS:O	1.98	0.64
9:SJ:5:ARG:NH2	9:SJ:29:LEU:O	2.31	0.63
26:A5:145:CYS:HB2	26:A5:148:LEU:HD21	1.80	0.63
59:RO:318:LEU:HA	59:RO:357:ARG:HH12	1.62	0.63
24:3H:44:LEU:HD22	24:3H:52:ILE:HD11	1.80	0.63
48:RA:18:GLY:HA2	48:RA:339:HIS:HD2	1.62	0.63
3:SA:343:C:H2'	3:SA:344:A:H8	1.63	0.63
9:SJ:42:ARG:HD3	48:RA:57:GLU:HB3	1.80	0.63
17:SZ:20:ARG:HD2	17:SZ:74:LEU:HD12	1.79	0.63
55:RJ:831:ARG:NH2	55:RJ:835:HIS:O	2.30	0.63
25:A4:578:SER:HG	25:A4:643:SER:HG	1.46	0.63
23:3F:538:ARG:HA	23:3F:566:ALA:O	1.97	0.63
39:5C:386:PHE:O	45:5I:8:ARG:NH2	2.31	0.63
54:RH:192:TYR:HA	54:RH:195:LYS:HD2	1.81	0.63
2:5A:357:G:N7	39:5C:493:LYS:NZ	2.45	0.63
34:B3:244:GLU:HG2	34:B3:293:VAL:H	1.64	0.63
43:5G:32:ILE:HG22	43:5G:42:LEU:HD11	1.81	0.63
14:SR:94:GLN:HB2	14:SR:102:LYS:HG3	1.80	0.63
10:SK:65:LYS:HZ2	23:3F:59:PRO:HB3	1.64	0.63
25:A4:399:VAL:HG22	25:A4:420:LEU:HB2	1.80	0.63
29:AE:638:SER:HA	29:AE:641:LEU:HD12	1.80	0.63
34:B3:531:ASN:HD21	34:B3:568:MET:HE2	1.63	0.63
48:RA:247:THR:HG23	48:RA:249:ASN:H	1.64	0.63
8:SI:9:LEU:HD22	8:SI:42:GLN:HE22	1.63	0.62
54:RH:129:ARG:HH11	54:RH:132:ARG:HD3	1.63	0.62
22:3E:384:GLY:O	22:3E:388:LEU:HB2	1.99	0.62
27:A8:553:GLN:NE2	27:A8:557:THR:OG1	2.32	0.62
48:RA:287:ASN:HB2	48:RA:302:ARG:HB2	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:RJ:932:LEU:HD22	55:RJ:1007:TYR:HB2	1.80	0.62
40:5D:29:GLU:OE2	40:5D:37:ARG:NH1	2.31	0.62
59:RO:300:THR:O	59:RO:304:ASN:ND2	2.32	0.62
62:RS:379:LYS:HD2	62:RS:427:ARG:HE	1.64	0.62
37:B6:285:TYR:HD2	37:B6:308:THR:HG22	1.63	0.62
3:SA:146:U:H3	3:SA:168:A:N6	1.97	0.62
27:A8:530:PRO:HG2	27:A8:553:GLN:HE22	1.64	0.62
58:RN:482:GLN:HG2	59:RO:507:LEU:HD11	1.80	0.62
3:SA:1220:C:H2'	3:SA:1221:A:H8	1.64	0.62
3:SA:1655:A:N6	3:SA:1743:U:O4	2.32	0.62
26:A5:120:ILE:HB	26:A5:151:LEU:HD23	1.82	0.62
28:A9:432:LYS:HB3	28:A9:435:LEU:HB3	1.81	0.62
36:BE:733:THR:O	36:BE:737:LEU:HB3	2.00	0.62
3:SA:477:A:H5'	44:5H:560:ASN:HD22	1.64	0.62
62:RS:214:TYR:HB3	62:RS:249:THR:HG22	1.80	0.62
32:B1:303:ASN:ND2	32:B1:323:LYS:HD3	2.15	0.61
3:SA:1538:U:H2'	3:SA:1569:A:H61	1.65	0.61
30:AF:440:GLU:O	30:AF:444:ASN:HB2	2.00	0.61
52:RE:1096:TYR:OH	52:RE:1183:THR:HG21	2.00	0.61
58:RN:95:ARG:HH12	58:RN:757:LYS:HG3	1.64	0.61
24:3H:50:GLU:HG3	24:3H:104:THR:HG22	1.82	0.61
36:BE:471:CYS:SG	36:BE:514:ASN:ND2	2.74	0.61
3:SA:362:G:H22	3:SA:382:C:H1'	1.66	0.61
30:AF:428:ARG:NH2	31:AG:518:ASP:O	2.34	0.61
56:RK:155:LYS:HG2	56:RK:165:GLU:HG2	1.82	0.61
62:RS:423:THR:HA	62:RS:426:GLN:HG2	1.81	0.61
3:SA:521:A:N3	17:SZ:34:ASN:ND2	2.48	0.61
5:SF:95:THR:HG22	60:RP:59:LEU:HB3	1.83	0.61
5:SF:212:ASP:H	5:SF:215:ASP:HA	1.65	0.61
13:SP:16:VAL:HG12	13:SP:80:HIS:HB2	1.82	0.61
35:B8:424:ILE:HG12	35:B8:434:GLU:HG2	1.83	0.61
26:A5:162:GLN:HA	26:A5:173:ILE:O	2.01	0.61
30:AF:51:HIS:O	30:AF:53:HIS:ND1	2.30	0.61
54:RG:36:LYS:HB3	54:RG:172:PRO:HA	1.82	0.61
31:AG:335:PRO:HB2	31:AG:336:ARG:HD3	1.82	0.61
31:AG:769:ASN:ND2	31:AG:771:ASP:OD1	2.33	0.61
37:B6:286:ILE:HG22	37:B6:308:THR:HG21	1.83	0.61
52:RE:398:ALA:HA	52:RE:401:LEU:HD12	1.82	0.61
52:RE:779:PHE:HB3	52:RE:851:LYS:HG3	1.82	0.61
63:RT:224:ILE:HG12	63:RT:233:ILE:HG12	1.83	0.61
58:RN:511:SER:HA	58:RN:557:SER:HB2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:SP:80:HIS:HA	13:SP:113:GLY:O	2.01	0.60
20:3B:142:ARG:NH1	20:3B:186:ASP:OD2	2.34	0.60
23:3F:356:ARG:NH1	49:RB:260:ALA:O	2.34	0.60
26:A5:481:LEU:HD21	26:A5:526:LEU:HD22	1.82	0.60
60:RP:91:LEU:HD21	60:RP:110:LEU:HD12	1.83	0.60
20:3C:186:ASP:OD1	20:3C:214:ARG:NH1	2.34	0.60
55:RJ:60:ASP:O	55:RJ:239:ASN:ND2	2.34	0.60
3:SA:374:U:H5''	49:RB:331:LYS:HE3	1.83	0.60
34:B3:160:ILE:HG22	34:B3:162:LEU:HD13	1.82	0.60
37:B6:201:LYS:HZ1	46:5J:55:ILE:HG21	1.67	0.60
39:5C:529:ARG:HH21	39:5C:543:LYS:HZ1	1.49	0.60
45:5I:260:GLN:NE2	45:5I:289:TYR:OH	2.35	0.60
52:RE:923:HIS:CD2	52:RE:1067:LEU:HD11	2.35	0.60
54:RG:147:LYS:HD3	54:RG:150:ILE:HG22	1.83	0.60
54:RH:156:GLU:HG2	54:RH:157:GLU:HG2	1.81	0.60
59:RO:461:SER:OG	59:RO:462:SER:N	2.33	0.60
3:SA:435:C:H42	55:RJ:166:ARG:HH12	1.47	0.60
23:3F:328:ILE:HG13	23:3F:338:THR:HG22	1.82	0.60
25:A4:429:SER:HB3	25:A4:444:ARG:HA	1.83	0.60
41:5E:480:GLN:HG2	41:5E:482:LEU:H	1.66	0.60
50:RC:205:ILE:O	50:RC:209:LEU:HB2	2.01	0.60
58:RN:548:ARG:NH1	58:RN:638:ASN:OD1	2.34	0.60
59:RO:452:ASP:HB3	59:RO:455:LEU:HB2	1.84	0.60
3:SA:606:A:N3	3:SA:607:G:N1	2.50	0.60
5:SF:194:THR:HG23	5:SF:195:ILE:HG12	1.83	0.60
58:RN:649:THR:HG23	58:RN:650:VAL:HG23	1.82	0.60
10:SK:65:LYS:HZ2	23:3F:59:PRO:N	1.98	0.60
21:3D:29:SER:O	21:3D:35:GLN:NE2	2.34	0.60
33:B2:54:ILE:HD13	33:B2:364:TYR:HD2	1.66	0.60
34:B3:581:CYS:HA	34:B3:590:LEU:O	2.02	0.60
52:RE:363:THR:HG22	52:RE:394:THR:HG21	1.83	0.60
40:5D:22:ARG:NH1	55:RJ:997:MET:O	2.35	0.60
3:SA:85:A:H2'	3:SA:86:A:H8	1.65	0.60
48:RA:333:ASN:HD21	48:RA:338:MET:HA	1.67	0.60
3:SA:870:C:O2	18:Sc:51:GLN:NE2	2.35	0.59
29:AE:699:ARG:NH1	29:AE:702:TRP:O	2.35	0.59
30:AF:248:ARG:NH1	30:AF:289:ASN:O	2.35	0.59
52:RE:345:TYR:O	52:RE:349:LEU:HB3	2.02	0.59
56:RK:14:SER:HB2	56:RK:36:ILE:HG23	1.83	0.59
8:SI:118:LEU:HA	8:SI:121:VAL:HB	1.82	0.59
13:SP:40:ALA:HB2	13:SP:70:LYS:HD2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:AF:301:PRO:HG2	30:AF:323:SER:HB3	1.84	0.59
34:B3:189:HIS:NE2	34:B3:217:ASP:OD1	2.35	0.59
52:RE:1100:VAL:O	52:RE:1181:VAL:HG12	2.01	0.59
6:SG:131:GLN:NE2	6:SG:135:ASP:OD1	2.35	0.59
7:SH:70:PRO:HB3	7:SH:101:ILE:HB	1.84	0.59
21:3D:382:LYS:HD2	21:3D:404:LEU:HD22	1.83	0.59
30:AF:133:HIS:HD2	30:AF:135:GLN:H	1.50	0.59
52:RE:383:GLY:HA3	52:RE:585:MET:HG2	1.82	0.59
31:AG:90:LYS:HG2	31:AG:144:VAL:HG22	1.85	0.59
58:RN:614:ILE:HG22	58:RN:616:LEU:HB2	1.85	0.59
9:SJ:32:GLN:HG2	48:RA:79:PRO:HD2	1.84	0.59
18:Sc:73:LEU:HB2	53:RF:215:VAL:HG21	1.85	0.59
52:RE:344:ASN:HA	52:RE:347:LYS:HD2	1.84	0.59
60:RP:112:GLN:NE2	60:RP:116:ASP:OD2	2.36	0.59
52:RE:1111:SER:HA	52:RE:1129:PRO:HG3	1.85	0.59
60:RP:54:TRP:O	60:RP:58:ASN:ND2	2.35	0.59
21:3D:286:ARG:HA	21:3D:289:TYR:HB3	1.85	0.59
22:3E:210:LEU:HD23	22:3E:256:ASN:HD22	1.68	0.59
32:B1:497:ILE:HG23	32:B1:512:ILE:HB	1.84	0.59
37:B6:15:MET:HA	37:B6:18:LEU:HB3	1.85	0.59
39:5C:257:SER:OG	39:5C:259:TRP:NE1	2.36	0.59
5:SF:180:LEU:HA	5:SF:194:THR:HG21	1.85	0.59
15:SX:90:THR:O	15:SX:94:LEU:HB2	2.03	0.59
52:RE:525:LEU:HB2	52:RE:617:LEU:HB2	1.84	0.59
54:RG:125:ASN:ND2	54:RG:127:THR:OG1	2.36	0.59
58:RN:535:ASN:OD1	58:RN:539:ARG:NH1	2.36	0.59
3:SA:1028:C:N4	50:RC:193:ASN:O	2.36	0.58
12:SO:130:ARG:HB3	50:RC:264:ILE:HD12	1.85	0.58
20:3C:114:GLY:O	20:3C:122:ARG:NH1	2.35	0.58
31:AG:510:TYR:HH	31:AG:527:HIS:HD1	1.49	0.58
39:5C:190:HIS:HB3	39:5C:207:THR:HG21	1.84	0.58
52:RE:1096:TYR:OH	52:RE:1183:THR:CG2	2.51	0.58
19:Sd:65:ARG:NH2	33:B2:750:GLU:OE2	2.36	0.58
27:A8:533:PRO:HA	27:A8:559:PRO:HG2	1.85	0.58
31:AG:153:ILE:HG22	31:AG:174:TYR:HB2	1.85	0.58
52:RE:381:HIS:NE2	52:RE:478:THR:O	2.36	0.58
63:RT:110:ARG:NH2	63:RT:130:MET:SD	2.76	0.58
15:SX:97:ARG:HH11	47:5K:84:ARG:HH12	1.51	0.58
32:B1:300:MET:HE3	32:B1:328:LEU:HD13	1.85	0.58
52:RE:834:ASN:ND2	52:RE:863:TYR:OH	2.36	0.58
60:RP:1904:LEU:HD12	60:RP:1940:LYS:HE2	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:RV:232:GLU:O	64:RV:239:ARG:NH1	2.36	0.58
4:SC:92:GLN:HE21	4:SC:97:LEU:HD21	1.68	0.58
25:A4:380:LYS:NZ	25:A4:634:VAL:O	2.35	0.58
39:5C:76:PRO:HA	45:5I:1:MET:HE2	1.86	0.58
53:RF:91:ASP:O	53:RF:121:ARG:NH2	2.36	0.58
60:RP:144:SER:HB3	60:RP:147:VAL:HG12	1.86	0.58
3:SA:563:U:H4'	43:5G:278:ARG:HG3	1.85	0.58
25:A4:565:ARG:HD3	29:AE:633:GLU:HB2	1.86	0.58
31:AG:568:ASN:ND2	31:AG:586:SER:OG	2.35	0.58
33:B2:97:GLY:HA3	33:B2:124:ILE:HD11	1.84	0.58
34:B3:237:LEU:HD21	52:RE:663:ILE:HG21	1.86	0.58
45:5I:411:LYS:O	45:5I:415:ARG:HB2	2.02	0.58
52:RE:520:ASN:HD22	52:RE:959:LEU:HD12	1.68	0.58
1:3A:30:A:N6	45:5I:341:GLU:OE2	2.36	0.58
22:3E:11:GLY:HA2	22:3E:143:LEU:HD22	1.86	0.58
40:5D:37:ARG:NH2	55:RJ:994:LYS:O	2.36	0.58
60:RP:2030:ASN:O	60:RP:2036:ARG:NH2	2.35	0.58
60:RP:2036:ARG:HH12	60:RP:2074:SER:HB2	1.69	0.58
51:RD:1583:SER:HA	51:RD:1586:VAL:HG12	1.85	0.58
5:SF:44:LEU:HD13	5:SF:82:TYR:HB3	1.85	0.58
25:A4:269:PHE:O	35:B8:446:ARG:NH2	2.36	0.58
29:AE:248:SER:OG	29:AE:253:CYS:SG	2.62	0.58
31:AG:118:VAL:HB	31:AG:130:LYS:HB2	1.85	0.58
34:B3:494:ILE:N	34:B3:510:SER:OG	2.35	0.58
59:RO:202:LEU:HD22	59:RO:212:LEU:HD22	1.86	0.58
1:3A:251:G:H2'	23:3F:155:ASN:HD21	1.67	0.58
3:SA:126:A:N6	3:SA:291:G:O2'	2.37	0.58
31:AG:435:ASP:CB	31:AG:702:TYR:HA	2.34	0.58
33:B2:259:ILE:HA	33:B2:273:TYR:O	2.03	0.58
48:RA:75:GLY:HA3	48:RA:80:GLN:H	1.68	0.58
52:RE:412:LEU:HD21	52:RE:424:GLY:HA3	1.84	0.58
54:RH:44:VAL:HA	54:RH:113:TYR:O	2.03	0.58
20:3B:236:MET:HG3	21:3D:133:LEU:HA	1.84	0.58
31:AG:144:VAL:HG12	31:AG:153:ILE:HG13	1.86	0.58
31:AG:157:PHE:HB2	31:AG:170:SER:HB3	1.86	0.58
32:B1:432:GLN:HE22	41:5E:455:HIS:HA	1.69	0.58
32:B1:501:SER:HB2	32:B1:508:GLN:HB2	1.84	0.58
39:5C:185:HIS:NE2	42:5F:19:LEU:O	2.36	0.58
51:RD:1530:GLU:HA	51:RD:1533:LEU:HB2	1.85	0.58
34:B3:584:ILE:HD11	34:B3:599:ILE:HD11	1.85	0.57
39:5C:541:ASP:O	39:5C:542:HIS:ND1	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:RA:212:ARG:HH12	50:RC:310:ALA:H	1.52	0.57
52:RE:373:ARG:NH2	52:RE:510:ILE:O	2.37	0.57
59:RO:270:SER:H	59:RO:273:GLN:HE21	1.50	0.57
23:3F:241:THR:HG21	23:3F:285:SER:HA	1.86	0.57
24:3H:44:LEU:HD13	24:3H:52:ILE:HD11	1.86	0.57
29:AE:671:LEU:O	29:AE:675:ASN:HB3	2.04	0.57
30:AF:303:LEU:HD13	30:AF:323:SER:HB2	1.86	0.57
35:B8:221:THR:OG1	35:B8:222:LEU:N	2.38	0.57
36:BE:482:GLY:HA2	36:BE:505:VAL:HG23	1.86	0.57
39:5C:317:THR:HG23	39:5C:334:ARG:HB3	1.86	0.57
52:RE:443:HIS:HB3	52:RE:470:LYS:HB2	1.85	0.57
55:RJ:773:THR:HA	55:RJ:777:ARG:HH11	1.69	0.57
56:RK:114:PHE:HB2	56:RK:170:VAL:HG22	1.86	0.57
3:SA:1196:A:N3	54:RG:136:ARG:NH2	2.52	0.57
16:SY:109:ARG:NH2	16:SY:120:VAL:O	2.37	0.57
29:AE:186:MET:HE1	29:AE:234:LEU:HD12	1.86	0.57
33:B2:365:TYR:HA	33:B2:381:LYS:HA	1.85	0.57
38:5B:194:LYS:HD2	38:5B:199:ILE:HG13	1.86	0.57
54:RH:31:LEU:HD13	54:RH:40:ARG:HE	1.69	0.57
17:SZ:83:LYS:HD2	17:SZ:96:LEU:HD21	1.86	0.57
20:3C:267:VAL:HG21	20:3C:298:ILE:HD12	1.87	0.57
34:B3:744:ARG:HA	34:B3:785:ILE:HG21	1.86	0.57
35:B8:227:LEU:HB2	35:B8:528:GLN:HE22	1.67	0.57
36:BE:359:ALA:O	36:BE:421:ASN:ND2	2.38	0.57
41:5E:369:ILE:HG12	43:5G:223:THR:HG21	1.86	0.57
22:3E:339:TYR:HB3	22:3E:343:TYR:HB2	1.85	0.57
29:AE:559:ASN:HA	29:AE:592:ARG:HD3	1.85	0.57
39:5C:450:GLY:O	61:RQ:857:TYR:OH	2.21	0.57
57:RL:29:VAL:HG22	57:RL:202:ASP:HA	1.86	0.57
63:RT:217:GLU:HG2	63:RT:223:ARG:HA	1.86	0.57
5:SF:206:ASP:OD1	5:SF:206:ASP:N	2.38	0.57
9:SJ:167:ALA:HB2	9:SJ:183:ILE:HD12	1.87	0.57
26:A5:148:LEU:HD23	26:A5:167:SER:HB3	1.86	0.57
30:AF:24:GLN:O	30:AF:28:ARG:HB3	2.05	0.57
32:B1:264:LYS:HD3	32:B1:280:THR:HG22	1.87	0.57
32:B1:405:SER:HB3	32:B1:436:LEU:HD23	1.85	0.57
34:B3:392:ASN:H	34:B3:407:SER:HA	1.69	0.57
45:5I:87:SER:OG	45:5I:89:ASP:OD1	2.22	0.57
53:RF:134:ILE:O	53:RF:138:TRP:HB3	2.05	0.57
60:RP:2073:GLU:OE2	60:RP:2076:ARG:NH1	2.36	0.57
3:SA:205:U:H2'	3:SA:206:A:H8	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:1684:U:H3	3:SA:1718:G:H1	1.52	0.57
23:3F:442:ILE:HA	23:3F:472:PRO:HA	1.86	0.57
35:B8:146:LEU:O	35:B8:163:ARG:NH1	2.37	0.57
52:RE:440:LEU:HA	52:RE:456:LYS:O	2.05	0.57
52:RE:919:TRP:CZ2	52:RE:1067:LEU:CD2	2.87	0.57
2:5A:323:A:N6	32:B1:212:ASP:OD2	2.37	0.57
20:3C:142:ARG:NH1	20:3C:186:ASP:OD2	2.36	0.57
41:5E:312:GLU:O	41:5E:316:ASN:ND2	2.38	0.57
48:RA:152:ASP:HA	48:RA:166:ASN:HA	1.86	0.57
55:RJ:1042:MET:HG3	55:RJ:1044:LEU:HD13	1.86	0.57
2:5A:481:U:O2'	37:B6:102:LYS:NZ	2.37	0.57
3:SA:146:U:N3	3:SA:168:A:N6	2.51	0.57
3:SA:559:C:OP1	55:RJ:868:ARG:NH2	2.37	0.57
21:3D:264:SER:OG	21:3D:265:GLU:N	2.37	0.57
23:3F:142:ILE:HA	23:3F:568:ILE:HD11	1.86	0.57
26:A5:434:THR:HG23	59:RO:266:ASN:HD21	1.68	0.57
31:AG:86:GLU:OE1	31:AG:113:ASN:ND2	2.36	0.57
35:B8:129:ASP:OD1	36:BE:194:ARG:NH2	2.36	0.57
45:5I:81:ASN:ND2	45:5I:96:ASN:OD1	2.38	0.57
52:RE:1160:SER:O	52:RE:1187:LYS:HG2	2.04	0.57
57:RL:32:ARG:HE	57:RL:35:ASN:HD21	1.53	0.57
3:SA:112:A:O2'	11:SM:67:ARG:NH1	2.37	0.57
8:SI:187:SER:OG	8:SI:188:GLU:N	2.38	0.57
27:A8:536:ARG:NH1	27:A8:537:THR:OG1	2.38	0.57
27:A8:614:ILE:HD12	27:A8:634:LEU:HD13	1.86	0.57
36:BE:666:ARG:NH1	36:BE:706:ASP:OD2	2.38	0.57
45:5I:45:LEU:HD13	45:5I:410:ILE:HG22	1.86	0.57
52:RE:1170:GLY:HA3	52:RE:1177:GLY:HA2	1.87	0.57
60:RP:54:TRP:HA	60:RP:57:ILE:HG22	1.87	0.57
62:RS:209:LYS:HE3	62:RS:212:LYS:HG3	1.87	0.57
3:SA:1197:C:OP1	54:RG:136:ARG:NH1	2.38	0.56
23:3F:545:LYS:HG2	23:3F:561:ASN:HD21	1.70	0.56
26:A5:212:LEU:HD11	26:A5:246:VAL:HG11	1.87	0.56
32:B1:373:ASP:HB2	32:B1:380:LEU:HD21	1.86	0.56
47:5K:26:LYS:HD3	47:5K:29:GLN:HG3	1.87	0.56
2:5A:338:A:O2'	2:5A:340:U:O4	2.20	0.56
31:AG:473:LEU:HB2	31:AG:495:ILE:HD11	1.87	0.56
32:B1:54:HIS:NE2	32:B1:72:SER:OG	2.32	0.56
32:B1:479:LEU:HD12	32:B1:488:LEU:HD11	1.87	0.56
39:5C:493:LYS:O	39:5C:498:ARG:NH1	2.38	0.56
42:5F:66:PRO:HG3	64:RV:207:ARG:HH11	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5I:15:PRO:HB3	45:5I:20:GLN:HE21	1.70	0.56
57:RL:12:SER:O	57:RL:16:ASN:ND2	2.38	0.56
3:SA:439:U:H4'	3:SA:465:G:H22	1.69	0.56
3:SA:1680:G:N2	3:SA:1720:G:O6	2.38	0.56
27:A8:539:ASN:ND2	27:A8:560:ASN:O	2.38	0.56
30:AF:147:ARG:NH2	54:RH:16:GLN:O	2.39	0.56
33:B2:598:LYS:NZ	33:B2:610:SER:OG	2.38	0.56
48:RA:227:ARG:NH2	48:RA:248:SER:O	2.34	0.56
49:RB:230:ALA:O	49:RB:234:LYS:HB2	2.05	0.56
54:RG:41:MET:HG3	54:RG:202:ILE:HG23	1.88	0.56
56:RK:221:CYS:SG	56:RK:222:GLU:N	2.71	0.56
3:SA:337:G:N2	3:SA:340:U:OP2	2.39	0.56
22:3E:414:ARG:NH1	29:AE:187:ASP:OD2	2.36	0.56
28:A9:473:LYS:O	28:A9:477:LYS:NZ	2.39	0.56
16:SY:132:LEU:HA	16:SY:135:LEU:HB2	1.87	0.56
25:A4:32:ILE:O	25:A4:751:GLU:HA	2.06	0.56
25:A4:37:ARG:NH1	27:A8:704:PRO:O	2.38	0.56
32:B1:329:VAL:HG12	32:B1:339:LEU:HG	1.87	0.56
43:5G:108:LYS:HD2	43:5G:116:ARG:HB2	1.87	0.56
51:RD:1509:GLU:HG2	52:RE:1199:ASN:HB2	1.87	0.56
10:SK:78:ARG:NH2	49:RB:247:GLU:OE1	2.33	0.56
25:A4:301:ASP:O	25:A4:771:GLN:NE2	2.38	0.56
33:B2:145:ILE:HG23	33:B2:159:LEU:HB2	1.88	0.56
43:5G:144:GLU:HA	43:5G:149:PRO:HA	1.88	0.56
52:RE:228:ARG:HE	52:RE:296:ILE:HG12	1.71	0.56
52:RE:606:ASN:ND2	52:RE:608:PHE:O	2.39	0.56
52:RE:822:ARG:HE	52:RE:1136:LEU:HD21	1.71	0.56
57:RL:71:LYS:O	57:RL:75:ASN:ND2	2.38	0.56
2:5A:484:G:OP2	37:B6:3:LYS:NZ	2.39	0.56
4:SC:87:ARG:HH21	4:SC:101:HIS:HD2	1.52	0.56
52:RE:223:ARG:HA	52:RE:226:HIS:HB2	1.86	0.56
59:RO:170:GLY:O	59:RO:272:GLN:NE2	2.32	0.56
2:5A:5:G:N2	2:5A:8:A:OP2	2.39	0.56
20:3C:160:ASP:OD1	20:3C:160:ASP:N	2.37	0.56
26:A5:435:GLY:HA3	59:RO:262:LEU:HD11	1.88	0.56
33:B2:347:SER:O	33:B2:371:LYS:NZ	2.39	0.56
33:B2:461:SER:OG	33:B2:462:SER:N	2.38	0.56
53:RF:262:VAL:HA	53:RF:265:ARG:HG2	1.88	0.56
57:RL:7:ASP:HB2	57:RL:10:ILE:HG12	1.88	0.56
2:5A:329:A:OP1	39:5C:229:ARG:NH2	2.36	0.56
3:SA:143:G:OP2	7:SH:139:ASN:ND2	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:1657:U:OP1	3:SA:1658:G:O2'	2.23	0.56
9:SJ:104:ILE:O	9:SJ:164:ARG:HA	2.06	0.56
21:3D:389:ILE:HA	24:3H:62:GLU:HB2	1.87	0.56
26:A5:25:ASP:OD2	35:B8:590:LYS:NZ	2.37	0.56
26:A5:471:ARG:NH2	59:RO:301:ASP:OD2	2.39	0.56
47:5K:123:PRO:O	47:5K:126:LYS:NZ	2.39	0.56
48:RA:175:PRO:O	48:RA:177:LYS:NZ	2.36	0.56
52:RE:241:ILE:HA	52:RE:244:LYS:HD2	1.88	0.56
63:RT:109:LEU:O	63:RT:113:TRP:HB2	2.06	0.56
22:3E:136:LEU:HG	22:3E:139:MET:HE2	1.88	0.56
29:AE:272:LYS:NZ	29:AE:310:GLY:O	2.39	0.56
39:5C:541:ASP:N	39:5C:541:ASP:OD1	2.38	0.56
42:5F:29:ASP:N	42:5F:29:ASP:OD1	2.38	0.56
45:5I:73:ILE:HG12	45:5I:85:THR:HG22	1.88	0.56
52:RE:560:ASN:OD1	52:RE:560:ASN:N	2.39	0.56
56:RK:34:GLU:HG3	56:RK:35:LYS:HG2	1.88	0.56
56:RK:154:LEU:HB2	56:RK:165:GLU:HG3	1.88	0.56
58:RN:478:ILE:HD13	58:RN:520:PRO:HB2	1.88	0.56
58:RN:512:ASP:OD1	58:RN:512:ASP:N	2.38	0.56
65:RY:487:ASP:N	65:RY:487:ASP:OD1	2.36	0.56
3:SA:1490:C:OP1	55:RJ:1062:ARG:NH2	2.38	0.55
20:3C:320:TYR:OH	20:3C:322:ARG:NH2	2.39	0.55
23:3F:417:SER:OG	23:3F:418:ASP:N	2.37	0.55
26:A5:364:THR:OG1	26:A5:368:ASN:ND2	2.38	0.55
29:AE:95:ASP:HB2	29:AE:131:ASN:HD21	1.71	0.55
31:AG:435:ASP:HB3	31:AG:702:TYR:HA	1.88	0.55
34:B3:12:LEU:HG	34:B3:641:PHE:HB2	1.87	0.55
35:B8:181:GLU:HB3	36:BE:281:ARG:HH12	1.71	0.55
60:RP:67:ALA:O	60:RP:71:GLU:HB2	2.07	0.55
3:SA:448:C:OP2	5:SF:49:ARG:NH2	2.38	0.55
7:SH:46:LYS:HB3	7:SH:118:GLU:HG2	1.88	0.55
17:SZ:54:ALA:HB1	17:SZ:76:TYR:HB2	1.88	0.55
24:3H:41:THR:O	24:3H:45:ASN:ND2	2.39	0.55
26:A5:5:VAL:HA	26:A5:21:THR:HG22	1.89	0.55
33:B2:463:SER:OG	33:B2:464:LEU:N	2.39	0.55
33:B2:858:PHE:O	33:B2:862:LYS:HB2	2.06	0.55
46:5J:129:ALA:HB1	55:RJ:1119:ILE:HG22	1.89	0.55
48:RA:101:ASN:HA	48:RA:118:GLN:HA	1.88	0.55
3:SA:128:U:H3	60:RP:906:THR:H	1.53	0.55
39:5C:433:LEU:HG	42:5F:13:LEU:HD11	1.88	0.55
43:5G:60:GLN:OE1	64:RV:207:ARG:NH1	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:RE:578:ILE:HG22	52:RE:619:VAL:HG12	1.88	0.55
60:RP:1760:ASN:ND2	60:RP:1805:ASP:OD2	2.39	0.55
3:SA:396:G:O6	9:SJ:26:LYS:NZ	2.37	0.55
3:SA:1678:A:N6	3:SA:1723:U:O4	2.39	0.55
9:SJ:195:ARG:NH2	11:SM:11:ARG:O	2.39	0.55
33:B2:124:ILE:HA	33:B2:140:SER:HA	1.89	0.55
33:B2:142:ASP:OD2	33:B2:144:ASN:ND2	2.39	0.55
33:B2:267:ASP:OD1	33:B2:267:ASP:N	2.36	0.55
45:5I:26:ARG:NH1	61:RQ:867:GLN:O	2.40	0.55
45:5I:340:ARG:NH2	45:5I:377:SER:O	2.39	0.55
51:RD:1674:LEU:HD23	51:RD:1677:ARG:HD3	1.88	0.55
52:RE:707:PHE:O	52:RE:918:ARG:NH1	2.39	0.55
55:RJ:939:TYR:HA	55:RJ:997:MET:HE1	1.88	0.55
56:RK:139:PRO:HA	56:RK:142:GLU:HB2	1.89	0.55
58:RN:682:ARG:O	58:RN:686:ASN:ND2	2.40	0.55
60:RP:1981:TYR:OH	60:RP:1985:ARG:NH1	2.39	0.55
3:SA:207:U:H3	3:SA:258:C:N4	2.04	0.55
3:SA:444:C:O2	3:SA:460:A:N6	2.39	0.55
3:SA:453:U:O2'	3:SA:455:C:OP2	2.24	0.55
3:SA:862:A:OP2	12:SO:64:ARG:NH2	2.40	0.55
4:SC:192:VAL:HG21	52:RE:751:LYS:HA	1.88	0.55
20:3B:225:ARG:NH1	20:3B:248:ASP:OD2	2.38	0.55
20:3C:189:GLY:O	20:3C:216:ASN:ND2	2.39	0.55
20:3C:225:ARG:NH2	20:3C:246:GLN:OE1	2.38	0.55
23:3F:289:ARG:NH2	23:3F:332:ALA:O	2.39	0.55
23:3F:337:VAL:HG23	23:3F:407:MET:HE2	1.88	0.55
23:3F:552:TRP:HB3	24:3H:85:VAL:HG13	1.88	0.55
31:AG:262:MET:HA	31:AG:272:ALA:O	2.07	0.55
34:B3:366:PRO:HG2	34:B3:378:PRO:HB3	1.88	0.55
39:5C:162:ASN:HB3	39:5C:164:GLN:H	1.71	0.55
39:5C:369:MET:HE1	39:5C:404:PRO:HD2	1.88	0.55
45:5I:173:ILE:HG13	45:5I:174:ARG:HG2	1.87	0.55
45:5I:329:ILE:HG12	45:5I:343:TYR:HB2	1.89	0.55
52:RE:412:LEU:HD13	52:RE:421:LEU:HD12	1.89	0.55
55:RJ:279:PRO:HB3	55:RJ:784:LYS:HA	1.88	0.55
55:RJ:360:ASP:OD1	55:RJ:360:ASP:N	2.35	0.55
55:RJ:608:LEU:HB2	56:RK:16:ASN:HD22	1.72	0.55
55:RJ:921:GLU:HB2	56:RK:365:LYS:HG3	1.88	0.55
61:RQ:896:ALA:HB1	61:RQ:897:PRO:HD2	1.89	0.55
9:SJ:41:LYS:HE2	9:SJ:43:ILE:HD11	1.89	0.55
9:SJ:98:LYS:NZ	9:SJ:170:SER:O	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A4:57:ILE:HD13	25:A4:340:GLN:HG2	1.89	0.55
31:AG:583:LYS:HE2	31:AG:599:ILE:HD13	1.88	0.55
35:B8:526:ASP:OD1	35:B8:526:ASP:N	2.38	0.55
35:B8:561:PRO:O	35:B8:587:ARG:NH1	2.39	0.55
37:B6:278:MET:HA	37:B6:312:LEU:HD11	1.89	0.55
49:RB:304:GLU:OE1	49:RB:309:LYS:NZ	2.40	0.55
52:RE:1174:GLY:N	52:RE:1179:LYS:CE	2.70	0.55
61:RQ:898:PHE:N	61:RQ:898:PHE:CD1	2.73	0.55
3:SA:365:G:N7	49:RB:231:ARG:NH1	2.55	0.55
3:SA:545:A:O2'	3:SA:546:U:O4'	2.22	0.55
3:SA:1232:U:O4	3:SA:1234:A:N6	2.39	0.55
23:3F:293:ASP:N	23:3F:293:ASP:OD1	2.37	0.55
29:AE:1172:ASP:N	29:AE:1236:ASN:O	2.40	0.55
32:B1:418:ARG:HH22	41:5E:491:ALA:HA	1.72	0.55
33:B2:592:SER:OG	33:B2:593:ALA:N	2.40	0.55
34:B3:179:LYS:O	34:B3:181:LYS:NZ	2.38	0.55
52:RE:691:SER:OG	52:RE:692:LYS:N	2.40	0.55
62:RS:445:ARG:NH1	62:RS:445:ARG:O	2.40	0.55
10:SK:139:GLN:NE2	17:SZ:64:PHE:O	2.39	0.55
21:3D:21:LYS:HE2	21:3D:49:GLU:HB2	1.88	0.55
24:3G:57:ASP:O	24:3G:84:ARG:NH1	2.40	0.55
25:A4:641:GLU:OE2	25:A4:645:ARG:NH1	2.40	0.55
31:AG:51:GLN:HE21	31:AG:53:LYS:HD3	1.72	0.55
32:B1:356:ASP:HB2	32:B1:826:ARG:HG3	1.89	0.55
33:B2:787:LYS:NZ	33:B2:788:PRO:O	2.38	0.55
34:B3:5:THR:O	34:B3:611:LYS:NZ	2.39	0.55
42:5F:162:ASP:OD1	42:5F:162:ASP:N	2.40	0.55
45:5I:75:LYS:NZ	45:5I:356:TYR:O	2.34	0.55
48:RA:166:ASN:ND2	48:RA:168:GLU:O	2.40	0.55
52:RE:356:THR:HB	52:RE:414:HIS:HB2	1.89	0.55
55:RJ:130:ASP:OD2	55:RJ:853:ARG:NH2	2.40	0.55
56:RK:171:ASP:N	56:RK:171:ASP:OD1	2.39	0.55
63:RT:169:ASP:OD1	63:RT:169:ASP:N	2.39	0.55
3:SA:96:G:N2	3:SA:387:A:N1	2.55	0.55
3:SA:258:C:O2	9:SJ:178:ARG:NH2	2.40	0.55
3:SA:1758:U:O4	33:B2:937:ARG:NH2	2.40	0.55
5:SF:45:ILE:HG13	5:SF:61:VAL:HG11	1.88	0.55
12:SO:60:VAL:HG23	12:SO:66:ILE:HD12	1.88	0.55
26:A5:454:GLU:OE2	26:A5:487:ARG:NH1	2.40	0.55
29:AE:196:LEU:HD11	29:AE:213:THR:HG21	1.88	0.55
29:AE:636:ASP:OD1	29:AE:639:ARG:NH1	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B3:107:ILE:HD11	34:B3:147:ILE:HG22	1.88	0.55
52:RE:508:SER:HA	52:RE:512:LEU:HB2	1.89	0.55
56:RK:155:LYS:HG3	56:RK:164:GLY:HA2	1.89	0.55
58:RN:290:LYS:O	62:RS:458:ARG:NH1	2.40	0.55
3:SA:1684:U:O2	3:SA:1718:G:N2	2.40	0.55
7:SH:10:ASN:O	7:SH:128:THR:OG1	2.25	0.55
11:SM:125:VAL:HB	11:SM:137:PHE:HB3	1.89	0.55
13:SP:122:PRO:HB2	13:SP:125:SER:HB3	1.89	0.55
22:3E:280:MET:HG3	22:3E:288:THR:HG22	1.89	0.55
26:A5:531:LYS:O	26:A5:535:ASP:HB2	2.07	0.55
29:AE:12:ALA:HB2	39:5C:142:GLY:HA3	1.89	0.55
29:AE:558:VAL:O	29:AE:592:ARG:NH1	2.40	0.55
29:AE:652:MET:HE3	29:AE:683:SER:HB3	1.89	0.55
41:5E:299:SER:O	41:5E:303:GLN:NE2	2.40	0.55
44:5H:565:LYS:HA	44:5H:568:LYS:HG2	1.89	0.55
50:RC:69:ILE:HD11	50:RC:93:ILE:HG23	1.88	0.55
52:RE:190:ALA:O	52:RE:350:TYR:OH	2.25	0.55
52:RE:267:ILE:HD12	52:RE:293:ASN:HB3	1.89	0.55
55:RJ:289:HIS:HB2	55:RJ:815:LEU:HD21	1.89	0.55
2:5A:354:G:N1	39:5C:485:ASP:O	2.38	0.54
3:SA:332:U:OP1	9:SJ:31:ARG:NH2	2.37	0.54
9:SJ:8:ARG:HD2	9:SJ:22:ARG:HH11	1.72	0.54
21:3D:379:LEU:O	21:3D:383:CYS:HB2	2.07	0.54
30:AF:75:LYS:HD3	30:AF:113:PRO:HD3	1.89	0.54
30:AF:420:GLU:O	30:AF:424:ARG:HB3	2.07	0.54
32:B1:430:ARG:HD2	41:5E:460:PRO:HA	1.89	0.54
35:B8:176:LYS:O	35:B8:180:ASP:CB	2.55	0.54
39:5C:96:ASP:OD1	39:5C:96:ASP:N	2.35	0.54
41:5E:344:GLU:HA	55:RJ:960:ARG:HH21	1.71	0.54
41:5E:448:LEU:HD22	42:5F:85:MET:HE1	1.89	0.54
52:RE:536:TYR:OH	52:RE:552:ARG:NH1	2.40	0.54
52:RE:1189:LEU:HD23	52:RE:1189:LEU:O	2.07	0.54
55:RJ:551:LYS:O	55:RJ:555:MET:HB2	2.07	0.54
27:A8:666:VAL:HG22	28:A9:496:LEU:HB3	1.89	0.54
31:AG:727:GLN:OE1	31:AG:738:ASN:ND2	2.39	0.54
32:B1:375:THR:OG1	32:B1:376:SER:N	2.41	0.54
32:B1:641:LEU:HD23	32:B1:644:ILE:HD12	1.89	0.54
35:B8:176:LYS:O	35:B8:180:ASP:HB3	2.07	0.54
37:B6:187:LYS:HE3	46:5J:63:PRO:HB2	1.89	0.54
45:5I:402:GLU:O	45:5I:405:ARG:NH2	2.40	0.54
55:RJ:966:ILE:HD13	55:RJ:976:ILE:HG22	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:RO:345:ILE:HA	59:RO:349:LEU:HD13	1.89	0.54
29:AE:205:THR:HB	29:AE:210:LEU:HD21	1.89	0.54
31:AG:850:GLU:HA	31:AG:853:ILE:HD12	1.89	0.54
45:5I:133:GLN:NE2	45:5I:151:ASN:OD1	2.40	0.54
49:RB:335:GLU:HA	49:RB:339:SER:HB2	1.89	0.54
56:RK:37:ARG:NH2	56:RK:49:GLU:OE2	2.36	0.54
62:RS:319:LYS:HA	62:RS:323:PHE:HB2	1.89	0.54
14:SR:22:VAL:HG22	14:SR:65:ILE:HG23	1.89	0.54
21:3D:63:LEU:O	21:3D:67:ASN:ND2	2.40	0.54
25:A4:534:LEU:HA	25:A4:542:VAL:O	2.07	0.54
32:B1:202:ASP:N	32:B1:202:ASP:OD1	2.40	0.54
34:B3:537:TRP:N	34:B3:551:SER:O	2.37	0.54
48:RA:78:LYS:O	48:RA:80:GLN:NE2	2.41	0.54
49:RB:242:MET:HE2	49:RB:332:ARG:HE	1.73	0.54
55:RJ:1018:VAL:O	55:RJ:1029:TRP:NE1	2.41	0.54
59:RO:156:TRP:O	59:RO:215:ASN:ND2	2.40	0.54
25:A4:252:GLN:NE2	25:A4:318:ASN:OD1	2.40	0.54
27:A8:443:CYS:HA	31:AG:728:LEU:HD22	1.87	0.54
30:AF:215:VAL:HA	30:AF:230:GLY:HA3	1.90	0.54
34:B3:328:GLN:NE2	34:B3:329:VAL:O	2.41	0.54
35:B8:352:GLN:HE21	35:B8:385:ASN:HD22	1.54	0.54
36:BE:73:GLU:OE2	36:BE:74:LYS:NZ	2.40	0.54
36:BE:626:ASP:N	36:BE:626:ASP:OD1	2.35	0.54
42:5F:115:MET:HG3	42:5F:120:MET:HB3	1.89	0.54
54:RH:114:ILE:HG12	54:RH:122:ILE:HB	1.89	0.54
3:SA:103:A:OP1	9:SJ:18:ARG:NH1	2.40	0.54
21:3D:392:TYR:HB3	24:3H:65:LEU:HD22	1.90	0.54
29:AE:274:ILE:HD11	35:B8:215:THR:HG21	1.90	0.54
30:AF:360:MET:HE3	30:AF:361:MET:HE3	1.89	0.54
31:AG:64:LYS:NZ	31:AG:123:GLY:O	2.39	0.54
55:RJ:73:ALA:HB1	55:RJ:131:ILE:HD12	1.90	0.54
3:SA:511:A:OP2	10:SK:176:ASN:ND2	2.40	0.54
3:SA:1175:U:OP1	58:RN:748:ARG:NH1	2.41	0.54
5:SF:198:LYS:HG3	5:SF:208:VAL:HG23	1.89	0.54
6:SG:26:ALA:HB3	14:SR:28:LEU:HB3	1.89	0.54
14:SR:34:SER:HB2	14:SR:38:LEU:HD12	1.90	0.54
23:3F:398:CYS:O	23:3F:419:ASN:ND2	2.40	0.54
23:3F:414:ILE:HD11	23:3F:480:ALA:HB2	1.90	0.54
24:3G:13:ASP:OD1	24:3G:13:ASP:N	2.39	0.54
32:B1:396:ALA:HB2	32:B1:438:VAL:HG21	1.90	0.54
32:B1:645:ASP:OD1	32:B1:645:ASP:N	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:B2:287:ARG:NH1	33:B2:324:PHE:O	2.41	0.54
35:B8:486:SER:OG	35:B8:487:GLU:N	2.41	0.54
47:5K:145:VAL:HG23	47:5K:151:TYR:HB2	1.89	0.54
49:RB:310:GLN:O	49:RB:314:ASN:ND2	2.40	0.54
56:RK:347:ASN:ND2	56:RK:349:ASP:OD2	2.40	0.54
58:RN:515:HIS:HB3	58:RN:518:ILE:HG22	1.90	0.54
58:RN:780:LYS:HG2	58:RN:781:MET:HE2	1.90	0.54
64:RV:199:ASP:OD1	64:RV:199:ASP:N	2.40	0.54
20:3B:90:PRO:HD3	46:5J:106:LEU:HD12	1.90	0.54
20:3C:268:VAL:HG22	20:3C:317:VAL:HG12	1.89	0.54
23:3F:481:ILE:HD12	23:3F:486:VAL:HG13	1.90	0.54
31:AG:325:GLN:NE2	31:AG:328:THR:OG1	2.41	0.54
31:AG:368:ASP:OD1	31:AG:368:ASP:N	2.38	0.54
33:B2:317:ILE:O	33:B2:321:TYR:N	2.41	0.54
34:B3:510:SER:O	34:B3:514:THR:OG1	2.26	0.54
48:RA:64:VAL:HG21	48:RA:323:VAL:HG12	1.90	0.54
48:RA:121:ARG:HH22	65:RY:462:ARG:HD2	1.72	0.54
48:RA:250:GLY:HA2	48:RA:274:ILE:HG23	1.88	0.54
52:RE:174:TYR:HE2	52:RE:227:LYS:HB3	1.73	0.54
52:RE:578:ILE:HG21	52:RE:617:LEU:HD12	1.90	0.54
1:3A:258:U:O4	21:3D:377:ARG:NH2	2.41	0.54
3:SA:146:U:O4	3:SA:168:A:N7	2.41	0.54
3:SA:265:A:OP2	7:SH:194:LYS:NZ	2.37	0.54
20:3B:124:SER:HB3	46:5J:153:ILE:HD11	1.90	0.54
26:A5:20:VAL:HG22	26:A5:29:VAL:HG22	1.89	0.54
29:AE:519:LEU:HD23	29:AE:523:ILE:HD13	1.88	0.54
30:AF:387:ALA:O	30:AF:391:ASN:ND2	2.40	0.54
31:AG:510:TYR:OH	31:AG:527:HIS:ND1	2.35	0.54
31:AG:724:ILE:HD11	31:AG:763:ILE:HG22	1.90	0.54
33:B2:260:GLU:O	33:B2:272:PHE:HA	2.08	0.54
36:BE:430:ILE:HB	36:BE:443:TRP:HB2	1.89	0.54
36:BE:604:SER:OG	36:BE:606:ASP:OD1	2.25	0.54
52:RE:931:ASP:OD1	52:RE:931:ASP:N	2.37	0.54
55:RJ:954:SER:HA	55:RJ:984:GLU:HG3	1.89	0.54
2:5A:354:G:N2	39:5C:495:SER:O	2.41	0.54
3:SA:325:G:H2'	3:SA:326:G:H8	1.73	0.54
3:SA:1539:G:N1	3:SA:1569:A:OP2	2.41	0.54
21:3D:392:TYR:HB2	24:3H:62:GLU:HB3	1.90	0.54
22:3E:380:ARG:NH1	22:3E:382:ASP:OD1	2.40	0.54
23:3F:399:GLU:OE2	23:3F:417:SER:OG	2.26	0.54
24:3H:38:ASN:HA	24:3H:41:THR:HG22	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A4:207:ASP:OD2	25:A4:209:ARG:NH1	2.37	0.54
25:A4:641:GLU:HB3	25:A4:749:SER:HB3	1.90	0.54
32:B1:661:LEU:HD11	41:5E:450:VAL:HG12	1.90	0.54
36:BE:160:THR:OG1	36:BE:163:GLN:NE2	2.41	0.54
39:5C:449:ILE:HD11	45:5I:38:ALA:HA	1.89	0.54
52:RE:375:PHE:HZ	52:RE:487:ILE:HG23	1.73	0.54
55:RJ:1027:THR:HG23	55:RJ:1028:GLU:HG2	1.89	0.54
56:RK:214:LYS:O	56:RK:217:LYS:NZ	2.40	0.54
58:RN:605:ASP:OD1	58:RN:610:ARG:NH1	2.41	0.54
60:RP:1939:ARG:HG3	60:RP:1974:LEU:HD11	1.88	0.54
3:SA:1738:U:OP1	33:B2:279:LYS:NZ	2.40	0.53
8:SI:155:ASP:OD1	8:SI:155:ASP:N	2.41	0.53
9:SJ:184:LEU:HD23	9:SJ:189:LEU:HA	1.90	0.53
18:Sc:67:THR:OG1	18:Sc:70:LYS:O	2.26	0.53
25:A4:271:THR:HG21	35:B8:443:VAL:HG21	1.91	0.53
31:AG:157:PHE:O	31:AG:169:GLN:NE2	2.40	0.53
32:B1:635:MET:HE1	47:5K:8:ARG:HH11	1.73	0.53
33:B2:525:ASP:OD1	33:B2:525:ASP:N	2.41	0.53
45:5I:192:SER:HB2	45:5I:206:VAL:HG22	1.89	0.53
52:RE:227:LYS:HA	52:RE:230:VAL:HG12	1.90	0.53
10:SK:76:LEU:HB2	49:RB:328:PHE:CE1	2.43	0.53
31:AG:404:SER:OG	31:AG:405:ALA:N	2.40	0.53
52:RE:1183:THR:HG23	52:RE:1183:THR:O	2.07	0.53
54:RH:125:ASN:ND2	54:RH:127:THR:OG1	2.42	0.53
58:RN:96:LYS:HD2	58:RN:761:PHE:HZ	1.73	0.53
3:SA:396:G:N7	9:SJ:47:ARG:NH1	2.56	0.53
6:SG:73:THR:OG1	6:SG:91:GLU:OE1	2.27	0.53
25:A4:311:THR:HG22	25:A4:313:LYS:H	1.74	0.53
29:AE:651:LEU:HD21	29:AE:680:TYR:HB2	1.90	0.53
30:AF:173:THR:HG21	30:AF:218:VAL:H	1.74	0.53
32:B1:283:GLU:OE2	32:B1:297:GLN:NE2	2.42	0.53
4:SC:32:ILE:HB	4:SC:43:VAL:HG22	1.90	0.53
20:3B:230:TYR:OH	20:3B:256:ASN:OD1	2.25	0.53
27:A8:573:ILE:HG22	27:A8:575:ASN:H	1.72	0.53
29:AE:626:PHE:HB3	29:AE:629:GLU:HB2	1.90	0.53
34:B3:596:ASP:OD1	34:B3:596:ASP:N	2.42	0.53
39:5C:312:VAL:HG21	39:5C:353:PRO:HG2	1.90	0.53
51:RD:1473:ASN:CB	51:RD:1509:GLU:OE2	2.51	0.53
53:RF:107:LEU:HD12	53:RF:194:ARG:HG3	1.89	0.53
23:3F:357:LEU:HD22	49:RB:256:PRO:HB2	1.90	0.53
24:3H:45:ASN:HA	24:3H:74:LYS:HE2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:AG:291:ARG:HD2	31:AG:329:ASN:HD21	1.73	0.53
33:B2:412:GLY:HA2	33:B2:431:GLY:H	1.73	0.53
45:5I:349:GLN:O	45:5I:367:SER:OG	2.24	0.53
52:RE:179:LYS:HB2	52:RE:210:PRO:HG2	1.90	0.53
52:RE:1098:PHE:HE2	52:RE:1182:ILE:HG22	1.72	0.53
7:SH:48:TYR:OH	7:SH:119:GLN:O	2.27	0.53
11:SM:82:ARG:HA	11:SM:111:VAL:HG13	1.91	0.53
31:AG:213:LYS:HA	31:AG:223:LYS:HA	1.91	0.53
43:5G:93:SER:O	43:5G:119:ARG:NH2	2.41	0.53
52:RE:687:GLN:NE2	52:RE:694:ALA:O	2.41	0.53
54:RG:36:LYS:NZ	54:RG:169:ASP:O	2.40	0.53
56:RK:289:VAL:HG21	56:RK:294:LEU:HD13	1.90	0.53
57:RL:37:LEU:HD13	57:RL:123:ILE:HD13	1.90	0.53
3:SA:1108:G:O2'	3:SA:1109:G:N7	2.37	0.53
3:SA:1159:C:N4	43:5G:184:GLU:OE2	2.38	0.53
42:5F:108:ARG:O	42:5F:117:ARG:NH1	2.42	0.53
52:RE:969:ASN:ND2	52:RE:972:ASP:OD1	2.41	0.53
1:3A:256:G:OP1	21:3D:382:LYS:NZ	2.37	0.53
3:SA:513:U:H2'	3:SA:514:G:C8	2.44	0.53
3:SA:1209:C:N3	3:SA:1210:C:N4	2.56	0.53
5:SF:209:HIS:ND1	5:SF:218:PHE:O	2.41	0.53
22:3E:289:GLN:HE21	22:3E:388:LEU:HD13	1.74	0.53
26:A5:46:TRP:HD1	26:A5:48:GLU:HG3	1.74	0.53
27:A8:558:CYS:O	27:A8:585:ARG:NH2	2.42	0.53
31:AG:283:VAL:HG12	31:AG:290:ILE:HG22	1.91	0.53
33:B2:554:THR:OG1	33:B2:556:LYS:NZ	2.39	0.53
54:RG:188:ARG:NH2	54:RH:247:ASP:OD2	2.41	0.53
55:RJ:374:ASP:OD1	55:RJ:374:ASP:N	2.40	0.53
62:RS:437:ARG:NH2	62:RS:459:GLU:O	2.42	0.53
3:SA:647:G:H22	3:SA:687:G:H22	1.56	0.53
25:A4:35:ARG:HH11	25:A4:738:TYR:HD1	1.57	0.53
25:A4:420:LEU:HD23	26:A5:581:ASN:HA	1.91	0.53
28:A9:513:ARG:HH21	28:A9:515:ASP:HA	1.72	0.53
48:RA:202:ASN:ND2	48:RA:229:PHE:O	2.41	0.53
52:RE:417:SER:OG	52:RE:418:SER:N	2.42	0.53
54:RG:121:LEU:HD21	54:RG:167:ILE:HG13	1.89	0.53
55:RJ:844:PRO:HA	55:RJ:856:THR:O	2.08	0.53
59:RO:233:ASP:N	59:RO:233:ASP:OD1	2.42	0.53
21:3D:102:ASP:HB3	21:3D:105:LEU:HB3	1.91	0.53
29:AE:40:ALA:HB1	29:AE:123:ARG:HH12	1.73	0.53
32:B1:567:ASP:HB3	42:5F:144:ASN:HD21	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B1:812:GLU:HG3	32:B1:813:HIS:HD2	1.74	0.53
3:SA:1136:U:O2'	33:B2:596:ASN:ND2	2.43	0.52
11:SM:97:TYR:O	11:SM:99:ARG:NH1	2.42	0.52
29:AE:571:LEU:HD11	29:AE:582:VAL:HG11	1.91	0.52
35:B8:216:TYR:OH	36:BE:276:TYR:OH	2.27	0.52
39:5C:483:ILE:HG23	39:5C:516:VAL:HG22	1.90	0.52
48:RA:13:VAL:HG12	48:RA:343:ILE:HG12	1.89	0.52
52:RE:526:CYS:O	52:RE:698:ASN:ND2	2.42	0.52
60:RP:18:SER:OG	60:RP:19:PHE:N	2.42	0.52
3:SA:153:G:H2'	3:SA:154:G:H8	1.74	0.52
21:3D:157:ALA:O	37:B6:293:TYR:OH	2.26	0.52
22:3E:251:ASP:OD1	22:3E:251:ASP:N	2.42	0.52
23:3F:162:CYS:SG	23:3F:525:GLN:NE2	2.78	0.52
30:AF:87:ALA:HA	30:AF:97:CYS:O	2.08	0.52
48:RA:212:ARG:HH22	50:RC:310:ALA:HB3	1.74	0.52
52:RE:398:ALA:O	52:RE:402:ASN:ND2	2.43	0.52
52:RE:596:LYS:HZ2	52:RE:600:TYR:HD1	1.56	0.52
52:RE:1108:LEU:HB2	52:RE:1169:ILE:HD11	1.91	0.52
55:RJ:135:ALA:O	55:RJ:238:ARG:NH2	2.42	0.52
55:RJ:982:LYS:HG3	55:RJ:983:PRO:HD3	1.92	0.52
57:RL:131:THR:OG1	57:RL:133:ASN:ND2	2.42	0.52
61:RQ:298:TRP:HE1	61:RQ:899:LYS:CG	2.19	0.52
3:SA:258:C:H4'	9:SJ:75:LYS:HD2	1.91	0.52
29:AE:502:ILE:HG23	29:AE:542:ILE:HG13	1.90	0.52
34:B3:787:PRO:HB2	41:5E:492:PRO:HG3	1.89	0.52
43:5G:153:THR:HG23	43:5G:164:GLN:HG2	1.91	0.52
52:RE:443:HIS:HB3	52:RE:470:LYS:HE2	1.91	0.52
55:RJ:90:VAL:HG23	55:RJ:107:VAL:HG11	1.92	0.52
56:RK:97:GLY:HA2	56:RK:100:VAL:HG12	1.92	0.52
56:RK:180:MET:HE3	56:RK:181:HIS:H	1.75	0.52
58:RN:587:ASP:OD1	58:RN:587:ASP:N	2.42	0.52
3:SA:153:G:N2	7:SH:56:ASN:OD1	2.42	0.52
10:SK:67:PRO:HB2	49:RB:334:LEU:HD23	1.91	0.52
24:3H:54:MET:HE1	24:3H:78:TYR:HB2	1.90	0.52
25:A4:39:VAL:H	25:A4:755:ILE:HD11	1.75	0.52
25:A4:658:ASP:OD2	25:A4:731:HIS:N	2.42	0.52
26:A5:481:LEU:HD22	26:A5:523:LEU:HD22	1.92	0.52
33:B2:398:ASP:HB2	33:B2:406:LEU:HB3	1.92	0.52
36:BE:470:GLN:NE2	36:BE:512:GLY:O	2.42	0.52
52:RE:437:ASP:N	52:RE:437:ASP:OD1	2.42	0.52
5:SF:53:LYS:O	23:3F:120:ARG:NH2	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:SJ:191:PHE:O	9:SJ:195:ARG:NH1	2.41	0.52
34:B3:337:HIS:HD2	34:B3:363:ARG:HD3	1.74	0.52
36:BE:268:THR:HG22	36:BE:270:SER:H	1.75	0.52
42:5F:123:THR:HG23	42:5F:126:ASP:H	1.73	0.52
51:RD:1547:TYR:OH	51:RD:1583:SER:OG	2.27	0.52
52:RE:270:ILE:HB	52:RE:292:ILE:HG23	1.91	0.52
52:RE:518:PHE:CE2	52:RE:1075:LEU:HG	2.43	0.52
54:RH:116:THR:HG22	54:RH:118:ARG:H	1.73	0.52
3:SA:494:U:OP1	55:RJ:1138:ARG:NH2	2.32	0.52
3:SA:594:A:OP1	10:SK:38:ASN:ND2	2.43	0.52
20:3B:281:ASP:OD1	20:3B:281:ASP:N	2.41	0.52
21:3D:169:LYS:HA	21:3D:299:VAL:HG22	1.92	0.52
23:3F:284:LEU:O	23:3F:548:ARG:NH2	2.38	0.52
27:A8:566:LEU:HG	27:A8:582:ILE:HD11	1.92	0.52
29:AE:556:LYS:O	29:AE:592:ARG:NH2	2.42	0.52
50:RC:142:ARG:NH1	50:RC:168:GLY:O	2.40	0.52
52:RE:596:LYS:HG3	52:RE:598:LYS:H	1.74	0.52
53:RF:51:ASP:HB2	53:RF:134:ILE:HG21	1.91	0.52
54:RG:169:ASP:N	54:RG:169:ASP:OD1	2.40	0.52
56:RK:30:PRO:HB3	56:RK:77:ARG:HG3	1.90	0.52
60:RP:452:ASN:O	60:RP:456:GLU:N	2.43	0.52
3:SA:331:A:N3	9:SJ:5:ARG:NH1	2.57	0.52
3:SA:1436:A:H1'	62:RS:419:LYS:HD2	1.91	0.52
7:SH:105:ASP:OD1	7:SH:105:ASP:N	2.43	0.52
9:SJ:110:ARG:NH1	9:SJ:161:SER:O	2.43	0.52
28:A9:504:GLU:OE2	28:A9:507:ARG:NH1	2.43	0.52
31:AG:319:LYS:HD2	31:AG:339:GLY:H	1.74	0.52
36:BE:578:VAL:O	36:BE:579:ARG:NH1	2.42	0.52
36:BE:605:LEU:HD23	36:BE:628:VAL:HG11	1.92	0.52
52:RE:186:ILE:HD11	52:RE:206:LEU:HB2	1.91	0.52
53:RF:44:SER:H	53:RF:50:SER:HA	1.75	0.52
59:RO:258:GLU:HG3	59:RO:289:PHE:HD1	1.74	0.52
60:RP:1892:LEU:HA	60:RP:1895:PHE:HB2	1.92	0.52
62:RS:397:PHE:HD1	62:RS:407:GLU:HG2	1.75	0.52
2:5A:7:A:N7	31:AG:578:ASN:ND2	2.55	0.52
3:SA:862:A:H4'	15:SX:57:ARG:HG3	1.90	0.52
22:3E:426:ALA:HB2	36:BE:305:ASN:HD21	1.75	0.52
27:A8:563:LEU:HA	27:A8:566:LEU:HB2	1.92	0.52
34:B3:680:ASN:N	34:B3:680:ASN:OD1	2.42	0.52
36:BE:819:LYS:NZ	36:BE:823:GLU:OE2	2.40	0.52
43:5G:43:PRO:HG2	43:5G:46:LEU:HB2	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:5J:58:ASN:HA	46:5J:61:LYS:HG2	1.92	0.52
48:RA:147:ASN:ND2	48:RA:154:TYR:OH	2.43	0.52
52:RE:315:ILE:HG13	52:RE:329:THR:HG21	1.92	0.52
52:RE:529:VAL:HB	52:RE:613:VAL:HB	1.91	0.52
1:3A:198:U:O4	23:3F:151:ARG:NE	2.38	0.52
7:SH:39:GLU:HG3	7:SH:46:LYS:HG3	1.91	0.52
8:SI:163:ASP:HA	8:SI:166:LEU:HG	1.90	0.52
20:3C:297:ARG:HD3	20:3C:322:ARG:HA	1.92	0.52
26:A5:503:LYS:HD3	28:A9:508:ARG:HH22	1.75	0.52
27:A8:672:ASN:HB2	28:A9:486:LEU:HD22	1.92	0.52
30:AF:256:THR:N	30:AF:275:SER:O	2.39	0.52
33:B2:634:SER:OG	33:B2:635:LYS:N	2.41	0.52
36:BE:377:SER:HB2	36:BE:445:MET:HE1	1.92	0.52
55:RJ:72:VAL:HG22	55:RJ:137:LEU:HB3	1.91	0.52
55:RJ:246:ALA:HB3	55:RJ:810:ILE:HB	1.91	0.52
55:RJ:776:GLN:NE2	55:RJ:781:GLU:OE2	2.40	0.52
59:RO:356:ALA:HA	59:RO:499:LEU:HD22	1.91	0.52
60:RP:1880:ILE:HD11	60:RP:1892:LEU:HD21	1.91	0.52
3:SA:1533:C:OP2	30:AF:114:ARG:NH2	2.43	0.52
3:SA:1720:G:N7	3:SA:1721:A:N6	2.58	0.52
4:SC:164:ILE:HD11	4:SC:205:PHE:HB2	1.91	0.52
22:3E:3:TYR:N	22:3E:21:LYS:O	2.43	0.52
22:3E:359:ILE:HA	22:3E:362:VAL:HG12	1.92	0.52
33:B2:53:ASP:OD2	33:B2:58:ASP:OD1	2.27	0.52
37:B6:296:SER:HB3	37:B6:300:MET:HB2	1.91	0.52
55:RJ:193:ARG:NH2	55:RJ:196:THR:OG1	2.43	0.52
57:RL:589:ALA:HB3	57:RL:593:GLU:H	1.75	0.52
61:RQ:298:TRP:NE1	61:RQ:899:LYS:CG	2.62	0.52
62:RS:360:LEU:HD21	62:RS:393:TYR:HB2	1.92	0.52
64:RV:224:HIS:HD2	64:RV:226:ASP:H	1.57	0.52
3:SA:532:U:O2'	17:SZ:33:ALA:O	2.27	0.51
6:SG:120:ILE:HA	6:SG:123:VAL:HG12	1.92	0.51
22:3E:385:ASP:OD1	22:3E:385:ASP:N	2.42	0.51
33:B2:54:ILE:CD1	33:B2:364:TYR:CD2	2.93	0.51
39:5C:130:ARG:NH2	39:5C:379:GLU:OE2	2.42	0.51
39:5C:495:SER:O	39:5C:495:SER:OG	2.29	0.51
43:5G:53:GLN:HB3	64:RV:215:LEU:HD13	1.92	0.51
45:5I:319:GLU:OE2	45:5I:356:TYR:OH	2.27	0.51
45:5I:324:SER:OG	45:5I:326:ASP:OD1	2.23	0.51
52:RE:634:HIS:HB2	52:RE:655:LEU:HD11	1.91	0.51
53:RF:128:PHE:HD2	53:RF:134:ILE:HG22	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:RO:200:ASN:ND2	59:RO:256:ASN:O	2.43	0.51
61:RQ:298:TRP:CD1	61:RQ:899:LYS:HG3	2.44	0.51
2:5A:294:U:OP1	32:B1:631:ASN:ND2	2.43	0.51
3:SA:-5:G:N1	39:5C:39:ASP:OD1	2.36	0.51
3:SA:419:G:H5"	3:SA:419:G:H8	1.75	0.51
7:SH:74:LYS:HB2	48:RA:88:ASN:HD21	1.75	0.51
8:SI:83:LYS:O	8:SI:86:GLN:NE2	2.43	0.51
20:3B:277:ASP:N	20:3B:277:ASP:OD1	2.43	0.51
24:3H:44:LEU:HD22	24:3H:52:ILE:HD12	1.90	0.51
25:A4:63:SER:HA	25:A4:82:ARG:HH12	1.75	0.51
29:AE:659:LEU:HD13	29:AE:690:GLU:HB3	1.92	0.51
31:AG:736:THR:HG23	31:AG:738:ASN:H	1.74	0.51
32:B1:506:SER:OG	32:B1:507:GLN:N	2.43	0.51
33:B2:281:ILE:HB	33:B2:332:ILE:HG23	1.91	0.51
33:B2:362:ILE:HG12	33:B2:385:ILE:HB	1.92	0.51
39:5C:410:ASN:O	45:5I:27:ASN:ND2	2.43	0.51
52:RE:469:ASP:OD2	52:RE:472:THR:OG1	2.27	0.51
52:RE:1215:ASN:HD21	53:RF:35:HIS:HA	1.75	0.51
53:RF:227:ARG:HA	53:RF:230:ILE:HD12	1.91	0.51
55:RJ:864:ASP:OD1	55:RJ:864:ASP:N	2.44	0.51
20:3B:120:GLU:OE2	20:3B:142:ARG:NE	2.41	0.51
25:A4:481:ILE:HB	25:A4:485:LYS:HB2	1.91	0.51
27:A8:28:TYR:HA	27:A8:356:THR:HA	1.92	0.51
31:AG:407:ASN:ND2	31:AG:416:SER:OG	2.44	0.51
33:B2:759:GLY:HA3	33:B2:805:ILE:HD11	1.91	0.51
34:B3:679:THR:HG21	34:B3:723:GLU:HB2	1.93	0.51
41:5E:373:ILE:HG13	41:5E:378:PHE:HZ	1.75	0.51
43:5G:139:LEU:HD23	43:5G:266:LEU:HD12	1.92	0.51
49:RB:348:SER:HB2	60:RP:1728:PHE:HB3	1.93	0.51
52:RE:261:ASN:HB3	52:RE:379:MET:HB2	1.91	0.51
53:RF:71:VAL:HA	53:RF:74:LEU:HD12	1.92	0.51
55:RJ:616:ASP:HB2	55:RJ:621:LEU:HG	1.90	0.51
59:RO:214:LYS:O	59:RO:268:GLN:NE2	2.43	0.51
5:SF:201:HIS:H	5:SF:206:ASP:HB3	1.75	0.51
9:SJ:171:SER:HB3	9:SJ:180:ASP:H	1.74	0.51
21:3D:126:ASP:HA	21:3D:129:ARG:HG2	1.93	0.51
23:3F:136:PHE:HE1	23:3F:484:SER:HB2	1.74	0.51
57:RL:117:ASN:O	57:RL:141:THR:OG1	2.26	0.51
60:RP:85:LYS:NZ	60:RP:89:ASN:OD1	2.40	0.51
60:RP:1746:LYS:O	60:RP:1748:ASN:ND2	2.41	0.51
1:3A:319:G:OP1	20:3C:122:ARG:NH2	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5A:473:A:H5''	39:5C:164:GLN:HE22	1.76	0.51
8:SI:67:LEU:HD13	8:SI:94:ALA:HB2	1.93	0.51
21:3D:26:ASP:OD1	45:5I:98:SER:OG	2.29	0.51
22:3E:218:ALA:O	22:3E:236:LYS:NZ	2.41	0.51
25:A4:402:TRP:HB3	25:A4:416:LEU:HA	1.91	0.51
32:B1:329:VAL:HG13	32:B1:338:ILE:HB	1.92	0.51
36:BE:59:GLN:HG2	36:BE:71:VAL:HG22	1.91	0.51
45:5I:329:ILE:HG22	45:5I:351:VAL:HG11	1.93	0.51
52:RE:111:LEU:HA	52:RE:114:VAL:HG12	1.93	0.51
54:RG:105:ASN:HD21	54:RG:110:LEU:HD22	1.75	0.51
56:RK:315:LYS:HB2	56:RK:348:GLU:HB3	1.92	0.51
58:RN:661:ILE:HG22	58:RN:665:GLN:HG3	1.92	0.51
6:SG:118:LEU:HG	6:SG:129:PRO:HB2	1.92	0.51
9:SJ:100:ALA:O	9:SJ:168:CYS:HA	2.10	0.51
11:SM:18:HIS:HB2	11:SM:63:LEU:HD21	1.91	0.51
20:3B:91:HIS:HD2	20:3B:93:HIS:H	1.57	0.51
27:A8:712:ASP:OD1	27:A8:712:ASP:N	2.40	0.51
29:AE:558:VAL:HG13	29:AE:615:ASN:HA	1.93	0.51
32:B1:588:ASP:OD1	32:B1:588:ASP:N	2.43	0.51
34:B3:501:PRO:HG3	34:B3:543:GLN:HG3	1.91	0.51
36:BE:854:SER:HB2	36:BE:895:VAL:HG21	1.93	0.51
45:5I:122:ARG:HB2	45:5I:192:SER:HB3	1.93	0.51
45:5I:327:LYS:HG2	45:5I:350:HIS:H	1.76	0.51
48:RA:101:ASN:HD21	48:RA:116:HIS:HB3	1.76	0.51
52:RE:1202:CYS:SG	52:RE:1203:ASN:N	2.83	0.51
60:RP:1896:ILE:HG13	60:RP:1897:PRO:HD3	1.92	0.51
62:RS:229:LEU:HD11	62:RS:233:PHE:HD2	1.74	0.51
7:SH:70:PRO:HD3	7:SH:101:ILE:HD12	1.93	0.51
25:A4:420:LEU:HD11	25:A4:462:VAL:HG21	1.92	0.51
31:AG:434:GLN:OE1	31:AG:434:GLN:N	2.43	0.51
32:B1:722:THR:HG22	32:B1:724:HIS:H	1.75	0.51
33:B2:201:ILE:HG13	34:B3:663:VAL:HG11	1.92	0.51
34:B3:497:LEU:HA	34:B3:507:ALA:O	2.11	0.51
62:RS:263:THR:HA	62:RS:266:PHE:HB2	1.93	0.51
3:SA:898:A:N1	3:SA:911:U:O2'	2.41	0.51
9:SJ:67:TRP:NE1	9:SJ:70:GLU:OE1	2.42	0.51
20:3C:94:ALA:HB3	20:3C:166:PRO:HG3	1.92	0.51
30:AF:258:LEU:HD22	30:AF:272:LEU:HD21	1.93	0.51
32:B1:273:ARG:NH1	36:BE:763:SER:O	2.43	0.51
32:B1:392:ALA:O	32:B1:404:SER:HA	2.10	0.51
34:B3:414:VAL:HG23	34:B3:427:TYR:HB3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:5C:74:LEU:HD23	39:5C:404:PRO:HG2	1.93	0.51
46:5J:120:ASP:HB2	46:5J:173:ILE:HD12	1.92	0.51
52:RE:298:PHE:HB2	52:RE:340:SER:HA	1.93	0.51
52:RE:1162:ILE:HG23	52:RE:1187:LYS:NZ	2.26	0.51
53:RF:178:ASP:OD1	53:RF:178:ASP:N	2.43	0.51
54:RG:150:ILE:HD11	54:RG:160:LEU:HD23	1.92	0.51
57:RL:539:ALA:O	57:RL:543:SER:CB	2.59	0.51
2:5A:293:U:H3	32:B1:632:SER:HB3	1.75	0.51
3:SA:283:U:OP1	7:SH:191:ARG:NH1	2.40	0.51
3:SA:340:U:H2'	3:SA:341:A:H8	1.75	0.51
3:SA:647:G:H1	3:SA:687:G:H1	1.59	0.51
3:SA:1643:U:OP2	41:5E:530:ARG:NH1	2.44	0.51
13:SP:12:GLN:HE21	13:SP:78:ALA:HB2	1.76	0.51
20:3C:171:LEU:HD23	20:3C:240:VAL:HG12	1.92	0.51
27:A8:248:LEU:HA	27:A8:264:SER:HA	1.92	0.51
28:A9:471:LYS:HZ3	28:A9:474:HIS:H	1.59	0.51
29:AE:522:ARG:HH12	29:AE:561:PHE:HB2	1.76	0.51
34:B3:17:ALA:HB3	34:B3:35:PRO:HA	1.91	0.51
42:5F:86:GLY:HA3	42:5F:109:ARG:HD2	1.93	0.51
48:RA:282:ASN:HD21	48:RA:325:GLY:H	1.58	0.51
52:RE:777:ASP:O	52:RE:780:GLN:NE2	2.43	0.51
54:RH:178:VAL:HG12	54:RH:223:GLU:HB2	1.93	0.51
63:RT:107:THR:O	63:RT:111:ASN:ND2	2.44	0.51
1:3A:59:G:H5'	32:B1:570:THR:HG23	1.92	0.51
3:SA:29:U:H2'	3:SA:30:G:H8	1.74	0.51
3:SA:123:G:OP1	5:SF:77:ARG:NH2	2.40	0.51
3:SA:826:U:O2'	3:SA:827:C:O2	2.23	0.51
4:SC:36:SER:HA	4:SC:41:ARG:HD3	1.91	0.51
9:SJ:104:ILE:HD13	9:SJ:167:ALA:HB3	1.91	0.51
12:SO:63:ALA:O	12:SO:67:THR:OG1	2.24	0.51
17:SZ:86:GLU:OE2	17:SZ:90:ARG:NH1	2.43	0.51
22:3E:355:ASN:HB2	22:3E:401:LEU:HD13	1.93	0.51
26:A5:8:SER:OG	26:A5:293:ASN:ND2	2.43	0.51
26:A5:439:VAL:HG11	59:RO:300:THR:HG21	1.92	0.51
27:A8:570:LEU:HD21	27:A8:637:LEU:HD21	1.91	0.51
29:AE:586:LEU:O	29:AE:590:ALA:CB	2.58	0.51
32:B1:732:GLU:HG2	32:B1:734:GLN:HE22	1.76	0.51
36:BE:135:ASN:ND2	36:BE:165:GLY:O	2.42	0.51
52:RE:1107:GLY:HA3	52:RE:1176:LYS:HG2	1.93	0.51
52:RE:1189:LEU:HD22	52:RE:1190:PHE:CD2	2.46	0.51
55:RJ:776:GLN:HA	55:RJ:780:ILE:HG22	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:SC:27:LYS:HB3	4:SC:47:LEU:HD22	1.93	0.50
7:SH:21:GLU:OE2	7:SH:25:ARG:NH2	2.44	0.50
12:SO:120:SER:HB2	50:RC:255:GLN:HE22	1.75	0.50
20:3B:142:ARG:NH2	20:3B:182:SER:OG	2.44	0.50
31:AG:668:THR:OG1	31:AG:669:ASN:OD1	2.30	0.50
33:B2:562:SER:HB2	33:B2:564:LYS:HB2	1.93	0.50
33:B2:627:SER:OG	33:B2:628:HIS:N	2.45	0.50
39:5C:91:ILE:HG23	45:5I:3:ILE:HD11	1.92	0.50
41:5E:298:SER:OG	41:5E:299:SER:N	2.43	0.50
52:RE:404:GLY:H	52:RE:455:SER:HB3	1.76	0.50
54:RG:150:ILE:HG12	54:RG:160:LEU:HB2	1.93	0.50
57:RL:80:GLU:OE2	57:RL:85:THR:OG1	2.29	0.50
3:SA:290:G:H3'	3:SA:291:G:H8	1.76	0.50
3:SA:442:C:O2'	3:SA:525:A:N1	2.35	0.50
26:A5:192:SER:HB3	26:A5:207:GLU:HG3	1.93	0.50
31:AG:855:LEU:HD23	35:B8:477:LYS:HE3	1.93	0.50
34:B3:413:ILE:HG22	34:B3:429:LYS:HA	1.92	0.50
45:5I:54:PHE:O	45:5I:382:ARG:NH2	2.44	0.50
3:SA:304:U:OP1	11:SM:136:ARG:NH2	2.45	0.50
3:SA:340:U:H2'	3:SA:341:A:C8	2.47	0.50
3:SA:420:A:H8	3:SA:420:A:H3'	1.76	0.50
20:3C:223:ASP:OD2	20:3C:225:ARG:NH1	2.44	0.50
30:AF:401:LEU:HB3	30:AF:434:ARG:HH22	1.77	0.50
31:AG:207:LEU:HG	31:AG:264:ILE:HD12	1.93	0.50
36:BE:225:THR:OG1	36:BE:227:THR:O	2.29	0.50
36:BE:370:SER:OG	36:BE:372:ASP:OD1	2.20	0.50
37:B6:297:ASP:OD1	37:B6:297:ASP:N	2.44	0.50
39:5C:238:MET:HE3	39:5C:247:MET:HE2	1.92	0.50
52:RE:261:ASN:OD1	52:RE:588:GLN:NE2	2.42	0.50
54:RH:228:SER:OG	54:RH:229:ASN:N	2.44	0.50
1:3A:93:U:OP2	22:3E:302:HIS:ND1	2.42	0.50
2:5A:90:G:O2'	2:5A:91:U:O4'	2.25	0.50
3:SA:413:U:H2'	3:SA:414:C:H6	1.77	0.50
30:AF:224:THR:O	30:AF:239:LEU:CB	2.57	0.50
30:AF:378:LYS:NZ	35:B8:292:GLY:O	2.44	0.50
39:5C:434:LEU:HD11	42:5F:12:LEU:HD23	1.93	0.50
51:RD:1674:LEU:HA	51:RD:1677:ARG:HG2	1.93	0.50
55:RJ:634:ARG:HD2	56:RK:185:ARG:HH21	1.77	0.50
55:RJ:772:MET:HE3	55:RJ:773:THR:H	1.76	0.50
56:RK:65:ILE:HB	58:RN:112:VAL:HG12	1.94	0.50
56:RK:183:ILE:HG22	56:RK:351:ILE:HD13	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:RP:1873:LEU:HD22	60:RP:1917:ILE:HG13	1.93	0.50
5:SF:26:CYS:SG	5:SF:27:TYR:N	2.84	0.50
13:SP:85:ALA:H	13:SP:119:THR:HB	1.76	0.50
20:3B:111:MET:HB2	20:3B:186:ASP:HB3	1.92	0.50
22:3E:430:ASP:HA	36:BE:125:GLY:HA2	1.93	0.50
25:A4:382:VAL:HG11	25:A4:755:ILE:HG21	1.92	0.50
26:A5:355:ASN:OD1	31:AG:479:ASN:ND2	2.44	0.50
30:AF:399:GLU:O	30:AF:403:ASN:ND2	2.42	0.50
31:AG:249:THR:HG22	31:AG:256:THR:HB	1.93	0.50
52:RE:1096:TYR:CD2	52:RE:1185:LEU:HD12	2.47	0.50
54:RH:41:MET:O	54:RH:110:LEU:HA	2.11	0.50
54:RH:41:MET:HG3	54:RH:202:ILE:HG23	1.92	0.50
62:RS:322:LEU:HD21	62:RS:359:LEU:HD11	1.92	0.50
3:SA:420:A:H3'	3:SA:420:A:C8	2.47	0.50
3:SA:1134:C:H1'	33:B2:610:SER:HB2	1.94	0.50
11:SM:109:VAL:HG11	11:SM:139:VAL:HG13	1.94	0.50
20:3C:170:VAL:HG23	20:3C:194:VAL:HG13	1.93	0.50
27:A8:671:ARG:NH1	28:A9:447:ASN:O	2.45	0.50
29:AE:558:VAL:HG22	29:AE:615:ASN:HD22	1.76	0.50
30:AF:59:SER:OG	30:AF:60:SER:N	2.43	0.50
33:B2:102:VAL:HA	33:B2:118:ASN:HA	1.94	0.50
34:B3:182:CYS:SG	34:B3:183:LEU:N	2.84	0.50
36:BE:810:ARG:NH2	63:RT:183:GLU:OE2	2.45	0.50
38:5B:173:ARG:HE	40:5D:146:PHE:HA	1.76	0.50
42:5F:181:ASP:OD1	42:5F:181:ASP:N	2.42	0.50
47:5K:79:LYS:NZ	64:RV:308:ILE:O	2.40	0.50
50:RC:44:LEU:HA	50:RC:79:SER:HA	1.93	0.50
52:RE:177:ASN:ND2	52:RE:213:LEU:O	2.44	0.50
2:5A:20:C:H2'	2:5A:21:A:H8	1.77	0.50
2:5A:505:G:H2'	2:5A:506:G:C8	2.47	0.50
3:SA:1192:C:H1'	54:RG:131:PRO:HA	1.92	0.50
3:SA:1194:A:OP2	3:SA:1195:C:N4	2.40	0.50
20:3B:228:GLN:O	20:3B:231:ARG:NH2	2.43	0.50
31:AG:80:GLN:NE2	31:AG:83:GLU:OE1	2.44	0.50
50:RC:206:LYS:HE3	50:RC:224:LEU:HD21	1.93	0.50
52:RE:1062:THR:HG21	66:X1:310:UNK:HA	1.94	0.50
56:RK:114:PHE:O	56:RK:169:VAL:HA	2.12	0.50
60:RP:1769:LEU:HD21	60:RP:1797:LEU:HD22	1.94	0.50
5:SF:181:VAL:HA	5:SF:227:VAL:HA	1.94	0.50
25:A4:415:LYS:NZ	25:A4:416:LEU:O	2.45	0.50
31:AG:139:GLU:HB3	31:AG:155:THR:HB	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B3:407:SER:OG	34:B3:408:LYS:N	2.45	0.50
34:B3:455:LEU:HA	34:B3:464:LYS:O	2.12	0.50
39:5C:37:THR:O	39:5C:43:ARG:NH2	2.44	0.50
43:5G:192:ASP:OD2	43:5G:227:ARG:NH2	2.37	0.50
54:RG:175:CYS:SG	54:RG:201:SER:OG	2.67	0.50
59:RO:327:MET:O	59:RO:331:ASN:HA	2.11	0.50
62:RS:439:PHE:HA	62:RS:442:GLU:HG3	1.94	0.50
63:RT:216:ILE:O	63:RT:220:THR:OG1	2.29	0.50
65:RY:472:ILE:HA	65:RY:475:TYR:HB2	1.93	0.50
2:5A:293:U:H2'	32:B1:631:ASN:HA	1.93	0.50
2:5A:484:G:O6	61:RQ:872:ARG:NH1	2.45	0.50
3:SA:1588:G:H1	3:SA:1608:U:H3	1.60	0.50
8:SI:28:GLU:OE2	8:SI:39:ARG:NH2	2.45	0.50
9:SJ:80:GLY:O	9:SJ:103:GLN:NE2	2.45	0.50
18:Sc:78:SER:HB3	53:RF:212:PHE:HB3	1.94	0.50
25:A4:156:LEU:HD22	25:A4:170:ILE:HD11	1.93	0.50
25:A4:418:CYS:SG	25:A4:419:LYS:N	2.85	0.50
30:AF:48:ASN:ND2	30:AF:111:TYR:OH	2.45	0.50
30:AF:260:TYR:OH	30:AF:262:GLU:OE1	2.30	0.50
31:AG:370:GLN:NE2	31:AG:384:SER:OG	2.44	0.50
31:AG:877:ASP:N	31:AG:877:ASP:OD1	2.43	0.50
36:BE:587:ARG:HB3	36:BE:605:LEU:HD12	1.92	0.50
38:5B:186:ASP:HA	38:5B:189:THR:HG22	1.94	0.50
52:RE:345:TYR:O	52:RE:349:LEU:CB	2.59	0.50
55:RJ:852:ARG:HD2	55:RJ:888:PRO:HG3	1.94	0.50
3:SA:55:A:OP2	57:RL:78:LYS:NZ	2.43	0.49
4:SC:144:ARG:HB3	4:SC:206:PRO:HB2	1.93	0.49
11:SM:109:VAL:HG13	11:SM:138:ASN:HA	1.94	0.49
26:A5:115:ASN:ND2	26:A5:130:ASP:OD1	2.45	0.49
29:AE:306:LEU:HD22	29:AE:311:ASN:HA	1.94	0.49
33:B2:828:TYR:HA	33:B2:831:LYS:HG2	1.93	0.49
35:B8:410:ASP:OD1	35:B8:479:ASN:ND2	2.45	0.49
52:RE:138:ILE:HD11	52:RE:238:HIS:HB3	1.94	0.49
55:RJ:106:THR:HG23	55:RJ:355:TYR:HB3	1.94	0.49
55:RJ:138:VAL:HB	55:RJ:167:VAL:HG22	1.93	0.49
55:RJ:274:TYR:OH	55:RJ:306:ASP:OD1	2.29	0.49
60:RP:73:ASP:OD2	60:RP:83:HIS:ND1	2.45	0.49
2:5A:485:G:H4'	2:5A:486:U:H5'	1.94	0.49
3:SA:123:G:H21	5:SF:146:THR:HG21	1.76	0.49
23:3F:365:PRO:HB3	23:3F:397:PHE:HA	1.93	0.49
25:A4:452:HIS:HB3	25:A4:463:THR:HG23	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A4:566:LEU:HD11	25:A4:584:VAL:HG21	1.94	0.49
27:A8:533:PRO:HG2	31:AG:656:ASP:HA	1.94	0.49
31:AG:435:ASP:HB2	31:AG:702:TYR:HD1	1.75	0.49
34:B3:65:THR:HA	34:B3:80:SER:HA	1.94	0.49
35:B8:520:ASN:HB2	35:B8:533:ALA:HB3	1.94	0.49
48:RA:281:ASP:OD1	48:RA:281:ASP:N	2.45	0.49
52:RE:566:ILE:HD13	52:RE:690:VAL:HG21	1.94	0.49
52:RE:711:PRO:HG3	52:RE:767:GLN:HE21	1.76	0.49
55:RJ:1069:VAL:HG11	55:RJ:1083:ILE:HD13	1.93	0.49
63:RT:182:ILE:HA	63:RT:233:ILE:O	2.13	0.49
3:SA:268:C:H2'	3:SA:269:G:H8	1.76	0.49
32:B1:839:THR:HG22	36:BE:882:GLU:HG3	1.95	0.49
33:B2:90:ASP:N	33:B2:90:ASP:OD1	2.39	0.49
33:B2:476:ILE:HD11	33:B2:490:THR:HB	1.93	0.49
34:B3:22:VAL:O	34:B3:68:LYS:NZ	2.45	0.49
36:BE:118:VAL:HA	36:BE:132:THR:HA	1.94	0.49
39:5C:340:LEU:O	39:5C:368:TYR:N	2.43	0.49
40:5D:149:GLU:HB3	40:5D:153:ASN:HA	1.94	0.49
43:5G:153:THR:HG21	43:5G:266:LEU:HD21	1.93	0.49
48:RA:300:TRP:HB3	48:RA:307:ALA:HA	1.95	0.49
52:RE:606:ASN:ND2	52:RE:610:PHE:O	2.45	0.49
55:RJ:1094:TYR:HA	55:RJ:1097:LYS:HG2	1.94	0.49
60:RP:1473:ALA:O	60:RP:1477:LYS:CB	2.61	0.49
29:AE:387:LEU:HD21	29:AE:403:LEU:HD13	1.93	0.49
30:AF:133:HIS:HB2	30:AF:139:ILE:HG13	1.94	0.49
31:AG:584:PHE:HB3	31:AG:598:LYS:HB2	1.94	0.49
39:5C:84:PHE:HA	39:5C:369:MET:HA	1.95	0.49
48:RA:252:SER:HB2	48:RA:266:LYS:HB3	1.94	0.49
55:RJ:777:ARG:O	55:RJ:778:GLN:NE2	2.46	0.49
55:RJ:951:MET:SD	55:RJ:987:TYR:OH	2.63	0.49
56:RK:107:ALA:HB1	56:RK:170:VAL:HG21	1.94	0.49
58:RN:600:LEU:HD21	58:RN:636:LEU:HD13	1.94	0.49
58:RN:623:ASP:O	58:RN:627:HIS:HB3	2.13	0.49
9:SJ:70:GLU:OE2	9:SJ:117:TYR:OH	2.30	0.49
14:SR:58:ASP:OD1	14:SR:58:ASP:N	2.43	0.49
22:3E:164:ILE:HG12	22:3E:301:ALA:HA	1.93	0.49
24:3H:52:ILE:HG22	24:3H:54:MET:SD	2.52	0.49
33:B2:180:THR:OG1	33:B2:207:CYS:SG	2.62	0.49
33:B2:624:LEU:HD12	33:B2:629:ASN:HB2	1.93	0.49
34:B3:513:LYS:HG3	34:B3:532:HIS:HB2	1.95	0.49
39:5C:492:GLY:HA2	39:5C:495:SER:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5I:76:ASN:HA	45:5I:118:VAL:HG21	1.93	0.49
45:5I:140:SER:OG	45:5I:141:ASP:N	2.44	0.49
51:RD:1519:ALA:HA	51:RD:1522:ASN:HD22	1.78	0.49
52:RE:803:LYS:NZ	52:RE:859:ASP:OD2	2.43	0.49
52:RE:972:ASP:OD1	52:RE:972:ASP:N	2.45	0.49
54:RG:46:ALA:HA	54:RG:115:GLN:HG3	1.93	0.49
56:RK:180:MET:O	56:RK:181:HIS:ND1	2.45	0.49
58:RN:752:MET:HA	58:RN:755:ILE:HG12	1.93	0.49
60:RP:752:THR:O	60:RP:756:SER:CB	2.59	0.49
2:5A:323:A:OP1	32:B1:191:ARG:NH2	2.46	0.49
3:SA:622:A:H1'	3:SA:623:A:C8	2.48	0.49
22:3E:24:LYS:O	22:3E:28:LEU:CB	2.60	0.49
24:3H:7:LYS:HB3	24:3H:65:LEU:HD11	1.95	0.49
24:3H:54:MET:O	24:3H:80:PHE:HA	2.12	0.49
31:AG:96:ILE:HG12	31:AG:108:THR:HG21	1.95	0.49
31:AG:628:ASP:H	31:AG:658:GLU:HA	1.77	0.49
31:AG:736:THR:OG1	31:AG:737:ILE:N	2.45	0.49
32:B1:286:LEU:HD12	32:B1:295:ILE:HB	1.94	0.49
32:B1:406:SER:OG	32:B1:407:LEU:N	2.46	0.49
33:B2:337:LYS:O	33:B2:357:THR:OG1	2.25	0.49
33:B2:549:SER:OG	33:B2:576:VAL:O	2.28	0.49
33:B2:817:LEU:HD11	33:B2:856:ASN:HD21	1.77	0.49
34:B3:466:TRP:HZ3	34:B3:478:GLN:HA	1.77	0.49
37:B6:63:VAL:HG13	37:B6:88:ILE:HD11	1.94	0.49
39:5C:183:GLU:HB3	47:5K:16:THR:HG22	1.94	0.49
42:5F:174:ARG:NH2	55:RJ:1077:LEU:O	2.44	0.49
49:RB:268:ASN:HB3	49:RB:271:ARG:HB3	1.94	0.49
51:RD:1633:ASP:OD2	51:RD:1636:ARG:NH1	2.42	0.49
54:RH:38:THR:O	54:RH:40:ARG:NH1	2.45	0.49
54:RH:69:ASN:HD22	54:RH:72:ASP:HB3	1.77	0.49
55:RJ:176:LEU:HD12	55:RJ:183:LEU:HA	1.94	0.49
60:RP:1794:ARG:HH22	60:RP:1870:LYS:HD2	1.77	0.49
3:SA:1465:C:N3	43:5G:146:ARG:NH1	2.58	0.49
4:SC:158:SER:HA	4:SC:161:ILE:HB	1.94	0.49
7:SH:57:ASP:HA	7:SH:107:ALA:H	1.78	0.49
25:A4:338:ALA:HB1	25:A4:361:LEU:HD11	1.95	0.49
27:A8:541:LEU:HA	27:A8:544:LEU:HD13	1.93	0.49
29:AE:637:ILE:HA	29:AE:640:ILE:HG22	1.94	0.49
33:B2:397:ILE:HD11	33:B2:405:LEU:HD21	1.94	0.49
33:B2:862:LYS:HE2	34:B3:805:ILE:HD13	1.93	0.49
34:B3:80:SER:OG	34:B3:81:GLN:N	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:B8:43:ASP:N	35:B8:43:ASP:OD1	2.40	0.49
54:RH:112:VAL:O	54:RH:124:VAL:HB	2.12	0.49
1:3A:64:A:OP2	36:BE:392:ARG:NH2	2.46	0.49
24:3G:105:ASN:HB3	24:3G:108:SER:HB2	1.94	0.49
30:AF:276:SER:OG	30:AF:278:ASP:OD1	2.30	0.49
31:AG:31:ASN:HD21	31:AG:201:ILE:HB	1.78	0.49
31:AG:116:VAL:O	31:AG:131:HIS:HA	2.13	0.49
34:B3:343:MET:HE2	34:B3:622:ALA:HB1	1.95	0.49
35:B8:183:ASP:OD1	36:BE:281:ARG:NH2	2.45	0.49
36:BE:528:PHE:HZ	36:BE:570:ILE:HD11	1.78	0.49
45:5I:315:PRO:HG2	45:5I:360:SER:HB3	1.93	0.49
45:5I:421:GLN:HG3	45:5I:425:LYS:HD2	1.95	0.49
47:5K:65:VAL:HG22	47:5K:152:ILE:HB	1.94	0.49
55:RJ:262:GLY:O	55:RJ:264:GLN:NE2	2.44	0.49
58:RN:646:THR:HA	58:RN:649:THR:HG22	1.95	0.49
61:RQ:853:ASN:OD1	61:RQ:853:ASN:N	2.45	0.49
62:RS:388:ASP:HA	62:RS:391:VAL:HG22	1.93	0.49
5:SF:202:ASP:OD1	5:SF:202:ASP:N	2.41	0.49
20:3B:269:ILE:O	20:3B:315:ILE:HA	2.13	0.49
25:A4:389:ARG:HE	25:A4:404:MET:HB2	1.78	0.49
29:AE:1628:SER:O	29:AE:1632:PHE:CB	2.60	0.49
33:B2:440:PRO:HG3	33:B2:485:GLY:HA3	1.94	0.49
34:B3:198:ILE:HG12	34:B3:211:LEU:HD13	1.95	0.49
35:B8:233:LEU:HD11	35:B8:543:LEU:HD12	1.95	0.49
36:BE:274:ILE:HG23	36:BE:286:VAL:HG22	1.94	0.49
39:5C:507:ASN:HD22	50:RC:57:TRP:HE1	1.60	0.49
49:RB:230:ALA:O	49:RB:234:LYS:CB	2.61	0.49
50:RC:107:SER:O	50:RC:107:SER:OG	2.29	0.49
55:RJ:309:PRO:HD2	55:RJ:353:LEU:HD22	1.95	0.49
63:RT:96:SER:HA	63:RT:139:LEU:O	2.12	0.49
3:SA:895:G:H1	3:SA:917:U:H3	1.61	0.49
6:SG:219:ARG:NH2	54:RH:222:ASP:OD2	2.45	0.49
11:SM:109:VAL:HG21	11:SM:125:VAL:HG11	1.95	0.49
21:3D:297:HIS:NE2	21:3D:309:GLU:OE2	2.46	0.49
23:3F:305:ARG:HG2	23:3F:317:ILE:HD13	1.94	0.49
32:B1:441:SER:O	32:B1:443:GLU:N	2.43	0.49
36:BE:173:LEU:HD13	36:BE:219:ASP:HA	1.95	0.49
36:BE:469:SER:HB3	36:BE:510:LEU:HD23	1.95	0.49
36:BE:902:ASN:HB3	36:BE:905:ILE:HG22	1.95	0.49
45:5I:145:VAL:HB	45:5I:176:PHE:HB2	1.94	0.49
52:RE:858:ARG:HD2	52:RE:861:ILE:HD11	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:RE:1216:LYS:HZ2	52:RE:1236:THR:HG23	1.69	0.49
53:RF:23:HIS:HD2	53:RF:26:LEU:HG	1.78	0.49
54:RG:197:ASP:OD1	54:RG:197:ASP:N	2.45	0.49
3:SA:158:U:H3	3:SA:420:A:HO2'	1.59	0.48
10:SK:82:ARG:NH1	49:RB:323:GLU:OE2	2.46	0.48
22:3E:214:ILE:HD11	22:3E:252:LEU:HD22	1.94	0.48
24:3H:51:PHE:HE1	24:3H:114:ILE:HG23	1.78	0.48
26:A5:280:GLN:HB2	26:A5:288:LYS:HE2	1.95	0.48
27:A8:305:VAL:HA	27:A8:311:VAL:HA	1.95	0.48
30:AF:75:LYS:HD2	30:AF:111:TYR:HA	1.95	0.48
30:AF:428:ARG:HH21	31:AG:518:ASP:HB3	1.76	0.48
33:B2:263:THR:HA	33:B2:269:THR:O	2.13	0.48
34:B3:454:LEU:O	34:B3:465:LYS:HA	2.12	0.48
35:B8:462:GLY:HA2	35:B8:527:GLY:HA3	1.95	0.48
52:RE:1189:LEU:C	52:RE:1189:LEU:CD2	2.85	0.48
54:RG:190:GLN:HE22	54:RG:247:ASP:HB2	1.78	0.48
58:RN:786:ASN:HA	58:RN:789:ASN:HB2	1.95	0.48
3:SA:129:U:O2'	60:RP:903:THR:O	2.30	0.48
3:SA:1133:A:OP1	56:RK:231:ARG:NE	2.42	0.48
4:SC:129:THR:OG1	4:SC:179:SER:O	2.31	0.48
24:3H:54:MET:HB3	24:3H:64:LEU:HD13	1.93	0.48
26:A5:149:ASN:HD21	26:A5:190:PRO:HB3	1.77	0.48
31:AG:249:THR:O	31:AG:257:ARG:NH1	2.41	0.48
33:B2:291:GLU:HA	33:B2:294:ARG:HG2	1.94	0.48
38:5B:155:ILE:HD12	38:5B:158:LYS:HE3	1.95	0.48
39:5C:112:GLY:HA3	39:5C:130:ARG:HB3	1.94	0.48
39:5C:284:ARG:NH1	39:5C:408:GLU:OE1	2.39	0.48
47:5K:149:LYS:HD3	47:5K:170:ILE:HD11	1.95	0.48
53:RF:56:VAL:HG22	53:RF:123:THR:HG22	1.93	0.48
60:RP:393:PHE:O	60:RP:397:PHE:CB	2.60	0.48
60:RP:1802:HIS:HE1	60:RP:1882:ARG:HB2	1.77	0.48
17:SZ:52:LYS:O	17:SZ:94:TYR:OH	2.23	0.48
21:3D:225:ASP:OD1	21:3D:226:LYS:N	2.46	0.48
23:3F:421:ASN:HD22	23:3F:437:ARG:HA	1.78	0.48
29:AE:8:LEU:HD12	39:5C:144:LEU:HD23	1.96	0.48
29:AE:395:GLU:OE2	29:AE:397:LYS:NZ	2.44	0.48
29:AE:482:SER:HB2	29:AE:484:LEU:HG	1.94	0.48
33:B2:392:THR:HG21	33:B2:410:SER:HB3	1.93	0.48
36:BE:656:ASN:N	36:BE:656:ASN:OD1	2.46	0.48
37:B6:16:ASP:OD2	39:5C:15:ARG:NH2	2.46	0.48
37:B6:273:ILE:HA	37:B6:276:VAL:HG22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5I:260:GLN:NE2	45:5I:460:GLN:OE1	2.47	0.48
50:RC:59:ASP:OD1	50:RC:62:ARG:NH2	2.46	0.48
52:RE:146:LEU:HA	52:RE:149:VAL:HG12	1.94	0.48
52:RE:592:PHE:HB3	52:RE:599:VAL:HG22	1.95	0.48
56:RK:103:MET:O	56:RK:107:ALA:HB2	2.13	0.48
11:SM:132:SER:OG	11:SM:133:LYS:N	2.46	0.48
15:SX:70:ASN:N	15:SX:70:ASN:OD1	2.43	0.48
18:Sc:58:SER:OG	18:Sc:59:CYS:N	2.46	0.48
20:3C:170:VAL:HG12	20:3C:239:CYS:HB3	1.96	0.48
27:A8:561:LEU:HD13	27:A8:566:LEU:HD11	1.95	0.48
31:AG:771:ASP:OD1	31:AG:771:ASP:N	2.46	0.48
34:B3:536:LEU:HA	34:B3:552:SER:HA	1.96	0.48
34:B3:600:LYS:HA	34:B3:609:CYS:HA	1.95	0.48
47:5K:67:ILE:HD11	47:5K:96:PRO:HB2	1.95	0.48
52:RE:264:LEU:HD12	52:RE:265:LEU:HG	1.94	0.48
55:RJ:863:THR:O	55:RJ:863:THR:OG1	2.30	0.48
55:RJ:951:MET:HE1	55:RJ:1003:LEU:HB2	1.94	0.48
56:RK:130:ILE:HG23	56:RK:151:LEU:HD23	1.95	0.48
57:RM:716:PRO:O	57:RM:720:LEU:CB	2.61	0.48
59:RO:447:ASP:OD1	59:RO:447:ASP:N	2.46	0.48
3:SA:163:G:O2'	7:SH:53:SER:OG	2.30	0.48
3:SA:886:U:H2'	3:SA:887:A:H8	1.78	0.48
12:SO:131:THR:HG22	50:RC:264:ILE:HG21	1.94	0.48
24:3H:13:ASP:OD1	24:3H:13:ASP:N	2.42	0.48
25:A4:150:ASN:ND2	25:A4:198:ASP:OD1	2.37	0.48
32:B1:717:LEU:HD12	36:BE:578:VAL:HB	1.94	0.48
33:B2:643:ASP:HB3	33:B2:650:ILE:HD11	1.95	0.48
34:B3:44:ASP:OD1	34:B3:44:ASP:N	2.46	0.48
35:B8:148:THR:OG1	35:B8:152:GLU:OE2	2.31	0.48
35:B8:266:GLY:HA3	35:B8:295:ILE:HD11	1.95	0.48
35:B8:458:ILE:HG13	35:B8:484:VAL:HG22	1.95	0.48
36:BE:529:TYR:HA	36:BE:536:LEU:HA	1.95	0.48
36:BE:630:THR:N	36:BE:644:THR:O	2.44	0.48
50:RC:53:LEU:O	50:RC:57:TRP:HB2	2.13	0.48
52:RE:132:TYR:HA	52:RE:135:LEU:HG	1.95	0.48
55:RJ:634:ARG:NH2	56:RK:186:PRO:O	2.42	0.48
3:SA:364:G:N7	3:SA:366:A:N6	2.62	0.48
5:SF:223:ASN:OD1	5:SF:223:ASN:N	2.47	0.48
9:SJ:72:ILE:HG22	9:SJ:74:LYS:HG2	1.96	0.48
25:A4:424:ASP:N	25:A4:424:ASP:OD1	2.45	0.48
27:A8:496:TYR:OH	31:AG:693:ASP:OD1	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:B6:426:ASP:O	37:B6:430:TYR:N	2.47	0.48
41:5E:452:SER:O	41:5E:452:SER:OG	2.29	0.48
51:RD:1508:ARG:HH12	53:RF:97:GLU:HB3	1.78	0.48
52:RE:886:THR:HG23	52:RE:890:LEU:HD12	1.96	0.48
53:RF:97:GLU:OE2	53:RF:121:ARG:NH1	2.45	0.48
3:SA:647:G:H22	3:SA:687:G:H1	1.60	0.48
11:SM:90:TYR:H	11:SM:103:ARG:HB3	1.79	0.48
17:SZ:20:ARG:NH1	17:SZ:22:GLN:OE1	2.47	0.48
22:3E:225:GLU:HG2	22:3E:226:ILE:HG13	1.96	0.48
23:3F:448:PHE:HA	23:3F:451:ILE:HG22	1.95	0.48
25:A4:579:ARG:NH2	25:A4:644:SER:OG	2.47	0.48
30:AF:420:GLU:O	30:AF:424:ARG:CB	2.61	0.48
31:AG:105:HIS:HB2	31:AG:122:LYS:HG3	1.95	0.48
34:B3:167:ASP:OD1	34:B3:168:THR:N	2.47	0.48
49:RB:237:SER:O	49:RB:237:SER:OG	2.32	0.48
51:RD:1662:GLU:HG3	51:RD:1671:VAL:HG22	1.95	0.48
52:RE:373:ARG:HA	52:RE:515:ILE:HG12	1.96	0.48
52:RE:1174:GLY:N	52:RE:1179:LYS:HE2	2.28	0.48
55:RJ:298:VAL:HG23	55:RJ:791:ILE:HG23	1.94	0.48
57:RM:507:THR:H	65:RY:495:ALA:HB3	1.77	0.48
58:RN:734:ARG:HA	58:RN:737:ILE:HG12	1.95	0.48
59:RO:507:LEU:HA	59:RO:510:GLU:HB3	1.95	0.48
3:SA:895:G:H21	13:SP:38:THR:HG21	1.79	0.48
14:SR:120:ASP:OD1	14:SR:120:ASP:N	2.40	0.48
23:3F:477:SER:OG	23:3F:521:VAL:O	2.27	0.48
29:AE:684:TYR:HB2	29:AE:687:LEU:HD23	1.95	0.48
34:B3:161:TRP:HB3	34:B3:177:LEU:HG	1.96	0.48
35:B8:183:ASP:HB2	36:BE:242:ARG:HA	1.96	0.48
39:5C:538:ILE:HD12	39:5C:542:HIS:HE1	1.79	0.48
48:RA:313:PRO:HG3	48:RA:317:ILE:HD11	1.94	0.48
50:RC:159:LEU:O	50:RC:207:ARG:NH2	2.46	0.48
51:RD:1644:LEU:HD13	51:RD:1654:LEU:HD22	1.96	0.48
52:RE:1108:LEU:O	52:RE:1112:CYS:CB	2.60	0.48
59:RO:153:ILE:HD13	59:RO:202:LEU:HD21	1.94	0.48
60:RP:48:LEU:HG	60:RP:74:VAL:HG22	1.95	0.48
1:3A:332:G:H21	31:AG:869:MET:HE3	1.79	0.48
3:SA:153:G:N2	3:SA:161:U:O2	2.43	0.48
3:SA:464:A:H2'	3:SA:465:G:H8	1.78	0.48
7:SH:31:ARG:HE	48:RA:359:ILE:HD13	1.78	0.48
10:SK:136:VAL:HG12	10:SK:156:ILE:HG12	1.96	0.48
25:A4:560:SER:OG	25:A4:561:LYS:N	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:AE:336:LEU:HD22	29:AE:373:ILE:HG21	1.96	0.48
29:AE:484:LEU:HD13	29:AE:663:SER:HB3	1.95	0.48
30:AF:435:ASP:OD1	30:AF:435:ASP:N	2.45	0.48
33:B2:479:LEU:HA	33:B2:489:VAL:O	2.14	0.48
34:B3:271:ASP:OD1	34:B3:271:ASP:N	2.47	0.48
34:B3:301:GLN:HG2	34:B3:315:ASN:HA	1.95	0.48
39:5C:137:MET:HA	39:5C:144:LEU:HA	1.96	0.48
53:RF:66:HIS:HA	53:RF:69:LYS:HG3	1.94	0.48
57:RL:55:VAL:HG23	57:RL:121:MET:HB3	1.95	0.48
57:RL:388:GLU:HA	57:RL:410:SER:O	2.14	0.48
58:RN:560:TYR:OH	59:RO:388:LEU:O	2.30	0.48
60:RP:190:ARG:NH1	60:RP:194:GLU:OE2	2.46	0.48
3:SA:1041:G:H2'	3:SA:1042:G:C8	2.49	0.48
3:SA:1082:C:H5''	15:SX:20:THR:HA	1.96	0.48
21:3D:160:ARG:NH2	22:3E:243:MET:O	2.43	0.48
22:3E:207:ARG:HH11	22:3E:226:ILE:HG12	1.78	0.48
23:3F:523:LYS:O	23:3F:541:ALA:HA	2.13	0.48
31:AG:141:LEU:HD11	31:AG:153:ILE:HD11	1.96	0.48
48:RA:164:ARG:NH2	48:RA:174:ASN:OD1	2.46	0.48
52:RE:209:MET:HB2	52:RE:299:PRO:HD3	1.96	0.48
53:RF:9:MET:HB2	53:RF:13:PHE:HB2	1.96	0.48
53:RF:176:ASP:OD1	53:RF:176:ASP:N	2.37	0.48
54:RG:173:THR:OG1	54:RG:174:LYS:N	2.47	0.48
60:RP:1709:ASP:HA	60:RP:1758:ALA:HA	1.94	0.48
61:RQ:322:ASN:OD1	61:RQ:322:ASN:N	2.46	0.48
3:SA:124:A:O2'	5:SF:148:ARG:NH2	2.33	0.47
3:SA:336:G:H1	9:SJ:5:ARG:HB2	1.79	0.47
3:SA:351:C:N3	11:SM:102:LYS:NZ	2.52	0.47
3:SA:1511:U:H2'	3:SA:1512:G:C8	2.49	0.47
11:SM:124:THR:HG22	11:SM:141:LYS:HB3	1.96	0.47
15:SX:9:ASP:OD1	15:SX:9:ASP:N	2.45	0.47
25:A4:284:LEU:HD21	38:5B:206:LEU:HD21	1.95	0.47
25:A4:747:ILE:HD11	25:A4:753:ALA:HB2	1.96	0.47
26:A5:335:ASN:O	26:A5:337:LYS:NZ	2.47	0.47
29:AE:329:THR:HG21	29:AE:365:ILE:HG21	1.95	0.47
31:AG:440:VAL:HG11	31:AG:449:LEU:HD12	1.95	0.47
32:B1:205:LYS:HG2	32:B1:219:GLU:HG2	1.96	0.47
33:B2:118:ASN:OD1	33:B2:118:ASN:N	2.46	0.47
33:B2:404:LYS:HZ1	33:B2:425:ILE:HD11	1.78	0.47
34:B3:77:THR:HG22	34:B3:86:LYS:HB3	1.96	0.47
52:RE:1063:ARG:HD2	66:X1:305:UNK:CB	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:RG:232:LEU:HD21	54:RH:103:PRO:HG3	1.96	0.47
55:RJ:1105:ASP:N	55:RJ:1105:ASP:OD1	2.47	0.47
56:RK:282:GLU:O	56:RK:286:SER:HB3	2.14	0.47
57:RL:57:TRP:NE1	57:RL:125:GLN:OE1	2.39	0.47
60:RP:1778:MET:HG2	60:RP:1864:LEU:HD22	1.96	0.47
2:5A:517:A:OP2	60:RP:1939:ARG:NH1	2.46	0.47
3:SA:954:G:H2'	3:SA:955:A:C8	2.49	0.47
13:SP:16:VAL:O	13:SP:30:VAL:HA	2.14	0.47
25:A4:97:ARG:NE	38:5B:191:PRO:O	2.39	0.47
26:A5:460:ARG:HA	26:A5:465:ILE:HD11	1.96	0.47
29:AE:376:GLU:H	29:AE:379:GLU:HG3	1.79	0.47
30:AF:246:TYR:OH	30:AF:289:ASN:ND2	2.44	0.47
33:B2:54:ILE:CD1	33:B2:364:TYR:HD2	2.27	0.47
48:RA:250:GLY:HA3	48:RA:271:GLY:HA2	1.96	0.47
48:RA:273:ASP:O	48:RA:275:LYS:NZ	2.47	0.47
5:SF:143:ASP:OD1	5:SF:143:ASP:N	2.35	0.47
11:SM:112:SER:HB3	11:SM:139:VAL:HG23	1.95	0.47
25:A4:214:SER:OG	25:A4:221:ASN:O	2.28	0.47
26:A5:473:LYS:HE3	26:A5:475:ALA:HB3	1.96	0.47
30:AF:135:GLN:HE22	30:AF:178:PRO:HA	1.79	0.47
33:B2:137:ILE:HG22	33:B2:147:VAL:HG22	1.97	0.47
33:B2:530:LEU:HD13	33:B2:550:LEU:HD11	1.94	0.47
39:5C:333:SER:HB3	39:5C:381:LEU:HD11	1.95	0.47
42:5F:152:ARG:NH1	43:5G:11:GLU:OE2	2.46	0.47
52:RE:400:LEU:HB3	52:RE:412:LEU:HD12	1.95	0.47
52:RE:627:LEU:HD12	52:RE:628:VAL:HG23	1.96	0.47
52:RE:1025:THR:O	52:RE:1029:ASN:ND2	2.47	0.47
55:RJ:92:ARG:HH21	55:RJ:221:LEU:HG	1.79	0.47
55:RJ:111:LYS:O	55:RJ:310:THR:OG1	2.32	0.47
3:SA:280:U:H2'	7:SH:188:ARG:HH22	1.80	0.47
3:SA:1061:A:OP1	53:RF:229:LYS:NZ	2.46	0.47
6:SG:52:GLU:OE2	6:SG:54:LYS:NZ	2.48	0.47
10:SK:87:SER:OG	10:SK:89:ASP:OD1	2.33	0.47
31:AG:581:GLY:HA2	31:AG:602:PRO:HD2	1.97	0.47
33:B2:214:ASP:OD1	33:B2:214:ASP:N	2.45	0.47
39:5C:133:HIS:HE1	39:5C:147:GLU:HG3	1.79	0.47
47:5K:152:ILE:HG12	47:5K:171:PRO:HG2	1.95	0.47
57:RL:200:VAL:HG12	57:RL:208:LEU:HD13	1.97	0.47
4:SC:16:GLN:HB2	34:B3:358:ASN:HD22	1.80	0.47
5:SF:103:TYR:O	5:SF:182:TYR:OH	2.32	0.47
8:SI:64:VAL:HG23	8:SI:67:LEU:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:AE:141:ASN:ND2	29:AE:206:TYR:OH	2.46	0.47
31:AG:498:LEU:HA	31:AG:508:ILE:O	2.14	0.47
31:AG:855:LEU:O	31:AG:859:ASN:HB2	2.13	0.47
33:B2:9:GLU:O	33:B2:684:TRP:HA	2.14	0.47
33:B2:414:LEU:HD11	33:B2:445:VAL:HG11	1.94	0.47
34:B3:223:TRP:CD1	34:B3:230:LYS:HZ1	2.33	0.47
49:RB:290:GLU:OE2	49:RB:296:ARG:NH1	2.47	0.47
50:RC:189:ASP:HB3	50:RC:194:ILE:HD11	1.96	0.47
53:RF:17:PRO:HB2	53:RF:34:LEU:HD11	1.96	0.47
55:RJ:631:ILE:HG13	55:RJ:634:ARG:HB2	1.97	0.47
59:RO:198:GLU:O	59:RO:202:LEU:HB2	2.13	0.47
60:RP:1278:ARG:O	60:RP:1282:VAL:HA	2.15	0.47
61:RQ:835:VAL:HG13	61:RQ:837:LYS:HG3	1.96	0.47
3:SA:869:A:H61	3:SA:958:U:H3	1.62	0.47
22:3E:355:ASN:HA	22:3E:358:LYS:HB2	1.97	0.47
25:A4:157:SER:OG	25:A4:195:TRP:NE1	2.47	0.47
25:A4:744:VAL:HA	25:A4:753:ALA:O	2.15	0.47
32:B1:150:THR:N	32:B1:164:THR:O	2.45	0.47
52:RE:1103:ARG:HA	52:RE:1178:ASP:HB2	1.96	0.47
52:RE:1157:TYR:HE1	52:RE:1203:ASN:CG	2.22	0.47
54:RH:153:VAL:HA	58:RN:716:LYS:HB2	1.96	0.47
62:RS:258:VAL:HA	62:RS:261:GLU:HG2	1.97	0.47
64:RV:271:GLN:HA	64:RV:290:SER:HB3	1.96	0.47
3:SA:406:U:H2'	3:SA:407:A:C8	2.50	0.47
3:SA:576:G:OP2	55:RJ:873:LYS:NZ	2.36	0.47
7:SH:32:ILE:HD12	7:SH:65:GLN:HA	1.96	0.47
13:SP:53:ASP:O	13:SP:56:SER:OG	2.28	0.47
20:3C:173:LEU:HA	20:3C:197:VAL:HG13	1.97	0.47
22:3E:262:ILE:HA	22:3E:265:PHE:HB2	1.96	0.47
25:A4:534:LEU:HB3	25:A4:543:ILE:HG22	1.95	0.47
31:AG:175:ALA:O	31:AG:187:VAL:HA	2.15	0.47
32:B1:156:GLN:HB2	32:B1:203:GLN:HE21	1.79	0.47
32:B1:165:SER:OG	32:B1:166:LYS:N	2.48	0.47
32:B1:537:GLY:HA3	32:B1:556:ARG:HB3	1.96	0.47
33:B2:183:ASP:OD1	33:B2:183:ASP:N	2.42	0.47
34:B3:10:ILE:HG23	34:B3:643:PHE:HB2	1.95	0.47
34:B3:108:LEU:HG	34:B3:119:VAL:HG12	1.97	0.47
35:B8:238:LEU:HD11	35:B8:590:LYS:HB2	1.97	0.47
36:BE:207:ASP:N	36:BE:207:ASP:OD1	2.47	0.47
48:RA:80:GLN:HB2	48:RA:82:HIS:HD2	1.78	0.47
52:RE:159:SER:O	52:RE:256:TYR:OH	2.27	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:RE:253:GLN:NE2	52:RE:254:LEU:O	2.48	0.47
52:RE:348:TYR:HA	52:RE:351:LYS:HD3	1.97	0.47
53:RF:69:LYS:NZ	53:RF:159:THR:H	2.12	0.47
55:RJ:879:THR:OG1	55:RJ:880:TYR:N	2.48	0.47
61:RQ:341:LYS:HA	61:RQ:344:GLN:HE21	1.79	0.47
14:SR:50:GLU:OE2	14:SR:82:ARG:NH2	2.47	0.47
17:SZ:59:GLY:O	49:RB:296:ARG:NH2	2.44	0.47
22:3E:176:GLU:HA	22:3E:179:THR:HG22	1.97	0.47
22:3E:191:HIS:HD2	22:3E:246:GLU:HA	1.80	0.47
31:AG:22:LEU:HD12	31:AG:32:LYS:HB2	1.97	0.47
33:B2:235:ASN:ND2	33:B2:240:GLY:O	2.40	0.47
33:B2:367:ILE:HD12	33:B2:368:PRO:HD2	1.97	0.47
34:B3:19:SER:OG	34:B3:20:SER:N	2.48	0.47
34:B3:113:THR:OG1	34:B3:114:SER:N	2.48	0.47
34:B3:339:ILE:HG13	34:B3:358:ASN:HD21	1.80	0.47
34:B3:481:LYS:HE2	34:B3:522:ASN:HA	1.97	0.47
35:B8:568:VAL:HG23	35:B8:579:VAL:HG22	1.96	0.47
37:B6:14:GLU:OE2	37:B6:91:ARG:NH2	2.38	0.47
37:B6:122:ASN:OD1	37:B6:122:ASN:N	2.48	0.47
52:RE:1087:LEU:HA	52:RE:1090:THR:HG23	1.97	0.47
52:RE:1159:ASN:O	52:RE:1187:LYS:HG3	2.14	0.47
55:RJ:80:THR:O	68:RJ:1201:GTP:O2B	2.31	0.47
2:5A:69:U:O4	2:5A:70:A:N6	2.48	0.47
2:5A:414:G:N1	2:5A:442:U:O2	2.48	0.47
3:SA:158:U:N3	3:SA:420:A:O2'	2.46	0.47
3:SA:677:G:O2'	60:RP:1884:ARG:NH2	2.48	0.47
3:SA:1760:G:H5'	3:SA:1761:U:H5'	1.96	0.47
13:SP:123:SER:O	13:SP:123:SER:OG	2.29	0.47
23:3F:70:TYR:OH	49:RB:246:GLU:OE2	2.29	0.47
24:3G:57:ASP:HB3	24:3G:84:ARG:HG2	1.97	0.47
26:A5:366:GLY:O	31:AG:583:LYS:NZ	2.48	0.47
29:AE:136:LEU:HD21	29:AE:155:ILE:HG12	1.97	0.47
33:B2:393:ASP:OD1	33:B2:393:ASP:N	2.46	0.47
34:B3:139:SER:OG	34:B3:140:PHE:N	2.48	0.47
34:B3:245:SER:O	34:B3:245:SER:OG	2.32	0.47
42:5F:153:ASN:HB3	43:5G:4:ARG:HH22	1.80	0.47
45:5I:201:ILE:HD12	45:5I:225:LEU:HD21	1.97	0.47
50:RC:158:LEU:HD22	64:RV:195:ILE:HD13	1.96	0.47
52:RE:578:ILE:HA	52:RE:619:VAL:HA	1.96	0.47
53:RF:46:ASN:OD1	53:RF:46:ASN:N	2.39	0.47
55:RJ:347:LEU:O	55:RJ:352:LYS:NZ	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:RN:510:THR:HB	58:RN:518:ILE:HD13	1.96	0.47
2:5A:18:G:H2'	2:5A:19:A:C8	2.50	0.47
2:5A:485:G:H2'	21:3D:22:LEU:HD21	1.97	0.47
25:A4:511:VAL:HA	25:A4:558:ARG:HB3	1.96	0.47
27:A8:647:LEU:HG	28:A9:509:GLN:HE22	1.79	0.47
31:AG:443:ASN:ND2	31:AG:446:ASN:OD1	2.48	0.47
32:B1:115:SER:O	32:B1:115:SER:OG	2.33	0.47
33:B2:542:ASP:N	33:B2:542:ASP:OD1	2.45	0.47
33:B2:588:ILE:HG12	33:B2:600:TRP:HB2	1.97	0.47
34:B3:593:CYS:HB2	34:B3:620:LEU:HB3	1.95	0.47
34:B3:622:ALA:HB3	34:B3:636:ASP:H	1.78	0.47
36:BE:170:LEU:HG	36:BE:180:LEU:HD21	1.97	0.47
36:BE:430:ILE:HD11	36:BE:445:MET:HB2	1.97	0.47
51:RD:1592:LEU:HB3	51:RD:1597:GLU:HB2	1.97	0.47
52:RE:1174:GLY:CA	52:RE:1179:LYS:CE	2.91	0.47
62:RS:271:THR:OG1	62:RS:274:GLU:OE1	2.31	0.47
4:SC:19:ARG:HH21	34:B3:359:SER:HA	1.80	0.46
33:B2:360:ASN:OD1	33:B2:360:ASN:N	2.47	0.46
34:B3:352:LYS:HA	34:B3:365:ILE:O	2.15	0.46
34:B3:680:ASN:HA	34:B3:683:LEU:HG	1.96	0.46
34:B3:749:ASN:HB3	34:B3:751:LYS:H	1.81	0.46
41:5E:383:ARG:NH2	43:5G:212:ALA:O	2.48	0.46
52:RE:1063:ARG:CD	66:X1:305:UNK:CB	2.93	0.46
58:RN:451:THR:O	58:RN:455:LEU:HB2	2.15	0.46
60:RP:1721:ILE:HD11	60:RP:1751:TYR:HB2	1.96	0.46
2:5A:446:U:H5'	55:RJ:1118:THR:HB	1.96	0.46
3:SA:545:A:OP2	44:5H:542:TYR:OH	2.33	0.46
3:SA:1160:A:H2'	3:SA:1161:C:H6	1.80	0.46
5:SF:52:LEU:O	23:3F:120:ARG:NH1	2.48	0.46
5:SF:53:LYS:NZ	49:RB:292:ASP:OD2	2.38	0.46
29:AE:262:VAL:HG21	31:AG:892:MET:HE1	1.96	0.46
33:B2:676:SER:OG	33:B2:678:ASP:OD1	2.22	0.46
34:B3:476:ASP:N	34:B3:476:ASP:OD1	2.48	0.46
37:B6:185:TYR:HE2	61:RQ:338:LEU:HD21	1.81	0.46
38:5B:173:ARG:NH2	40:5D:144:ASN:O	2.48	0.46
40:5D:25:TYR:HD1	46:5J:213:ARG:HE	1.62	0.46
43:5G:173:ARG:HH21	43:5G:250:VAL:HG23	1.80	0.46
48:RA:245:CYS:HB3	48:RA:253:TYR:HB2	1.96	0.46
48:RA:251:TYR:HA	48:RA:266:LYS:O	2.16	0.46
49:RB:309:LYS:HB3	49:RB:313:ARG:HH11	1.80	0.46
51:RD:1183:ILE:CB	52:RE:718:LYS:NZ	2.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:RE:793:PRO:HG2	52:RE:799:LEU:HA	1.96	0.46
57:RL:729:LEU:HA	57:RL:764:ASN:HA	1.97	0.46
60:RP:1725:ILE:HD11	60:RP:1793:LEU:HD22	1.98	0.46
20:3C:194:VAL:HB	20:3C:217:ILE:HD13	1.97	0.46
25:A4:418:CYS:HB2	25:A4:460:LEU:HB2	1.97	0.46
25:A4:742:LEU:HD12	25:A4:757:ARG:HG3	1.96	0.46
29:AE:509:SER:HA	29:AE:512:LEU:HD12	1.98	0.46
31:AG:204:ASN:OD1	31:AG:204:ASN:N	2.47	0.46
31:AG:530:LYS:HG2	31:AG:546:LYS:HB3	1.97	0.46
33:B2:236:ASP:OD1	33:B2:236:ASP:N	2.46	0.46
34:B3:69:LEU:HD13	34:B3:109:ASP:HA	1.96	0.46
48:RA:286:GLU:HG3	48:RA:287:ASN:H	1.80	0.46
52:RE:209:MET:HB3	52:RE:213:LEU:HD21	1.98	0.46
52:RE:1189:LEU:HD22	52:RE:1190:PHE:CE2	2.51	0.46
53:RF:69:LYS:HZ1	53:RF:158:TRP:HA	1.79	0.46
55:RJ:187:LYS:HE3	55:RJ:187:LYS:HB2	1.75	0.46
56:RK:337:VAL:HG23	56:RK:354:ILE:HG12	1.98	0.46
58:RN:56:ASN:HD21	58:RN:59:GLU:HG3	1.81	0.46
59:RO:202:LEU:HD23	59:RO:208:TYR:HB3	1.98	0.46
60:RP:1756:ILE:HD13	60:RP:1800:LEU:HB3	1.98	0.46
2:5A:485:G:OP2	21:3D:46:LYS:NZ	2.39	0.46
13:SP:32:ASP:OD1	13:SP:32:ASP:N	2.47	0.46
17:SZ:45:ALA:HB2	17:SZ:55:VAL:HG11	1.97	0.46
23:3F:417:SER:HB3	23:3F:421:ASN:HB2	1.96	0.46
26:A5:518:ASN:O	26:A5:522:THR:OG1	2.32	0.46
27:A8:374:SER:HA	27:A8:408:LEU:HA	1.96	0.46
28:A9:505:MET:HB2	30:AF:507:MET:HE3	1.98	0.46
29:AE:374:ARG:NH1	29:AE:375:LEU:O	2.49	0.46
32:B1:32:PRO:HG3	32:B1:61:ILE:HG13	1.97	0.46
34:B3:189:HIS:HD2	34:B3:191:SER:H	1.62	0.46
35:B8:306:ASN:OD1	35:B8:306:ASN:N	2.43	0.46
52:RE:218:ASP:N	52:RE:218:ASP:OD1	2.46	0.46
54:RH:152:SER:OG	54:RH:155:SER:N	2.49	0.46
55:RJ:819:GLU:O	55:RJ:852:ARG:NH2	2.47	0.46
56:RK:282:GLU:O	56:RK:286:SER:CB	2.64	0.46
59:RO:196:GLN:OE1	59:RO:260:ASN:ND2	2.37	0.46
3:SA:1276:U:H3	3:SA:1434:U:H3	1.64	0.46
8:SI:62:VAL:HG12	8:SI:64:VAL:H	1.80	0.46
12:SO:16:ILE:HG23	12:SO:62:GLN:HE22	1.79	0.46
20:3C:308:PRO:HG3	40:5D:129:SER:HA	1.96	0.46
25:A4:326:ARG:NH2	25:A4:364:PHE:O	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A5:85:ILE:HB	26:A5:99:PHE:HB2	1.98	0.46
31:AG:212:CYS:HB2	31:AG:224:SER:HB3	1.98	0.46
31:AG:446:ASN:OD1	31:AG:446:ASN:N	2.46	0.46
32:B1:29:LEU:HD22	32:B1:42:LEU:HD11	1.96	0.46
32:B1:557:LYS:NZ	36:BE:426:GLU:OE1	2.44	0.46
34:B3:67:LEU:HD23	34:B3:68:LYS:H	1.80	0.46
34:B3:534:ARG:HH11	34:B3:535:GLY:H	1.63	0.46
34:B3:708:ARG:NH2	34:B3:720:PHE:O	2.49	0.46
35:B8:278:ASP:N	35:B8:278:ASP:OD1	2.46	0.46
38:5B:211:LEU:HD13	38:5B:213:LYS:HE3	1.96	0.46
52:RE:333:ASN:HA	52:RE:336:VAL:HG22	1.96	0.46
54:RG:112:VAL:HB	54:RG:124:VAL:HG22	1.97	0.46
55:RJ:360:ASP:HB3	55:RJ:365:LEU:HB2	1.98	0.46
59:RO:462:SER:OG	59:RO:463:LEU:N	2.48	0.46
62:RS:270:LEU:HB3	62:RS:278:PHE:HZ	1.80	0.46
3:SA:328:A:H2'	3:SA:329:G:C8	2.50	0.46
14:SR:113:ASP:N	14:SR:113:ASP:OD1	2.48	0.46
16:SY:113:ALA:HB3	16:SY:116:ASP:HB2	1.96	0.46
29:AE:568:ILE:HD11	29:AE:673:ASN:HD21	1.80	0.46
34:B3:591:ILE:HG23	34:B3:600:LYS:HZ1	1.81	0.46
35:B8:472:GLN:NE2	35:B8:474:SER:OG	2.49	0.46
45:5I:288:TYR:O	45:5I:298:LEU:N	2.42	0.46
52:RE:822:ARG:HB2	52:RE:843:LEU:HB2	1.96	0.46
54:RG:55:ILE:O	54:RG:64:LYS:HB2	2.16	0.46
56:RK:104:LEU:O	56:RK:300:TYR:OH	2.33	0.46
60:RP:104:GLN:HG3	60:RP:105:PRO:HD3	1.97	0.46
60:RP:1691:SER:HA	60:RP:1724:ASN:HD21	1.81	0.46
1:3A:56:A:O2'	40:5D:63:TYR:OH	2.34	0.46
2:5A:486:U:H4'	2:5A:487:A:H5''	1.98	0.46
3:SA:1111:G:C8	55:RJ:1162:ALA:HA	2.51	0.46
7:SH:17:GLU:N	57:RL:604:SER:O	2.47	0.46
9:SJ:48:THR:O	9:SJ:52:ASN:CB	2.58	0.46
25:A4:164:THR:HG22	25:A4:185:ARG:HG2	1.98	0.46
29:AE:583:LYS:HE2	29:AE:627:LEU:HA	1.98	0.46
30:AF:436:GLU:HG2	30:AF:480:LEU:HD23	1.98	0.46
33:B2:63:LEU:HD21	33:B2:106:TRP:CD2	2.50	0.46
33:B2:341:ALA:HB1	33:B2:353:LEU:HD11	1.96	0.46
36:BE:640:LEU:HD23	36:BE:655:THR:HG22	1.98	0.46
45:5I:255:THR:HG22	61:RQ:288:TYR:HD1	1.81	0.46
47:5K:83:VAL:HG12	47:5K:96:PRO:HG3	1.98	0.46
58:RN:547:VAL:HA	58:RN:550:VAL:HG12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:RN:554:GLN:HE21	58:RN:559:ARG:H	1.63	0.46
58:RN:804:LYS:HD3	58:RN:804:LYS:HA	1.75	0.46
59:RO:395:ILE:HG23	59:RO:469:LEU:HD21	1.98	0.46
62:RS:379:LYS:HA	62:RS:379:LYS:HD3	1.72	0.46
62:RS:392:TYR:HA	62:RS:395:MET:HB2	1.96	0.46
62:RS:413:LEU:O	62:RS:418:HIS:NE2	2.49	0.46
4:SC:129:THR:OG1	4:SC:130:SER:N	2.47	0.46
8:SI:7:LYS:O	8:SI:42:GLN:NE2	2.49	0.46
9:SJ:32:GLN:HE21	48:RA:78:LYS:HG2	1.81	0.46
21:3D:175:ILE:HD12	21:3D:317:SER:HA	1.98	0.46
21:3D:371:ASN:OD1	21:3D:374:ARG:NH1	2.48	0.46
32:B1:280:THR:HA	32:B1:304:PRO:HB3	1.98	0.46
34:B3:32:LEU:HD12	34:B3:68:LYS:HE2	1.97	0.46
36:BE:323:VAL:HB	36:BE:343:LEU:HD22	1.98	0.46
43:5G:97:SER:OG	43:5G:144:GLU:OE1	2.28	0.46
48:RA:164:ARG:HH12	48:RA:176:PHE:H	1.64	0.46
50:RC:201:LYS:NZ	64:RV:152:ASP:OD2	2.45	0.46
51:RD:1512:GLU:HG2	52:RE:1199:ASN:ND2	2.28	0.46
51:RD:1520:MET:HE3	51:RD:1536:VAL:HB	1.98	0.46
52:RE:377:SER:HB3	52:RE:389:GLY:HA3	1.97	0.46
57:RM:249:SER:O	57:RM:253:LEU:CB	2.63	0.46
1:3A:306:G:H2'	1:3A:307:G:H8	1.80	0.46
2:5A:86:C:N4	31:AG:482:GLY:O	2.45	0.46
3:SA:1273:G:H1	3:SA:1437:U:H2'	1.80	0.46
4:SC:144:ARG:HG3	4:SC:208:GLN:HB3	1.98	0.46
16:SY:137:LYS:HE2	16:SY:137:LYS:HB3	1.80	0.46
20:3B:261:LEU:O	21:3D:129:ARG:NH1	2.49	0.46
22:3E:392:ALA:O	22:3E:396:ASN:ND2	2.49	0.46
31:AG:143:ASN:OD1	31:AG:143:ASN:N	2.47	0.46
31:AG:253:SER:O	31:AG:256:THR:OG1	2.33	0.46
31:AG:296:HIS:NE2	31:AG:314:SER:OG	2.37	0.46
34:B3:195:GLY:O	34:B3:245:SER:OG	2.29	0.46
34:B3:625:THR:HG22	34:B3:633:VAL:HG13	1.97	0.46
38:5B:200:ARG:O	38:5B:204:ARG:HB3	2.15	0.46
45:5I:280:ALA:HB2	45:5I:311:VAL:HB	1.97	0.46
45:5I:281:ASN:ND2	45:5I:283:ASP:OD1	2.49	0.46
48:RA:300:TRP:HA	48:RA:308:TYR:H	1.80	0.46
52:RE:501:ASN:OD1	52:RE:501:ASN:N	2.49	0.46
62:RS:280:ASN:ND2	62:RS:320:GLY:O	2.46	0.46
62:RS:359:LEU:HB2	62:RS:372:ILE:HD11	1.97	0.46
3:SA:225:A:H2'	3:SA:226:A:H8	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A4:124:THR:HG21	38:5B:191:PRO:HG3	1.97	0.46
29:AE:495:LEU:HA	29:AE:498:PHE:HB2	1.97	0.46
30:AF:117:LEU:HD12	30:AF:117:LEU:HA	1.79	0.46
39:5C:335:GLY:HA2	39:5C:377:LYS:HG3	1.98	0.46
42:5F:115:MET:HB2	42:5F:115:MET:HE3	1.58	0.46
45:5I:283:ASP:OD2	45:5I:287:TYR:OH	2.30	0.46
56:RK:199:ARG:HB2	56:RK:239:PRO:HA	1.97	0.46
58:RN:495:ASN:HD22	58:RN:617:HIS:HB2	1.80	0.46
59:RO:366:LEU:HD13	59:RO:405:LEU:HD11	1.96	0.46
60:RP:1948:SER:O	60:RP:1985:ARG:NH2	2.48	0.46
3:SA:689:G:C6	3:SA:690:G:O6	2.69	0.45
9:SJ:83:TYR:HB3	9:SJ:101:ILE:HD11	1.98	0.45
9:SJ:103:GLN:HB3	9:SJ:164:ARG:HG2	1.98	0.45
19:Sd:35:ASP:N	19:Sd:35:ASP:OD1	2.45	0.45
22:3E:381:ASP:OD1	22:3E:381:ASP:N	2.49	0.45
25:A4:444:ARG:HG3	25:A4:446:SER:H	1.81	0.45
25:A4:545:ARG:HG3	25:A4:549:VAL:HB	1.98	0.45
25:A4:652:THR:HG23	25:A4:653:TRP:HD1	1.81	0.45
39:5C:541:ASP:HB2	39:5C:543:LYS:HG2	1.97	0.45
39:5C:542:HIS:O	39:5C:544:ASP:N	2.47	0.45
50:RC:135:LYS:HE2	50:RC:135:LYS:HB3	1.79	0.45
52:RE:521:LEU:HD22	52:RE:960:LYS:HG3	1.97	0.45
52:RE:928:HIS:HE1	52:RE:1164:SER:HB2	1.80	0.45
55:RJ:65:ASP:OD1	55:RJ:65:ASP:N	2.46	0.45
55:RJ:772:MET:HG3	55:RJ:774:PRO:HD2	1.98	0.45
1:3A:36:C:O2'	45:5I:389:ARG:NH1	2.48	0.45
2:5A:485:G:N2	45:5I:386:LYS:O	2.41	0.45
3:SA:381:C:H2'	3:SA:382:C:H4'	1.97	0.45
3:SA:420:A:C8	3:SA:420:A:C3'	2.98	0.45
5:SF:58:GLY:HA2	5:SF:61:VAL:HG12	1.99	0.45
5:SF:127:LYS:HB2	5:SF:140:VAL:HG23	1.99	0.45
11:SM:76:VAL:HG21	11:SM:87:ARG:HH11	1.81	0.45
36:BE:351:GLN:HG3	36:BE:372:ASP:HB3	1.97	0.45
36:BE:420:GLU:HG2	36:BE:470:GLN:HA	1.97	0.45
39:5C:15:ARG:HB2	39:5C:18:GLN:HG3	1.98	0.45
40:5D:48:LEU:HG	55:RJ:1067:LEU:HD11	1.98	0.45
45:5I:306:SER:HB3	45:5I:326:ASP:H	1.81	0.45
48:RA:60:ASN:ND2	48:RA:100:GLU:OE2	2.50	0.45
49:RB:229:ASP:HB3	49:RB:232:GLU:HG2	1.97	0.45
52:RE:380:SER:HB2	52:RE:481:THR:HG22	1.98	0.45
52:RE:626:LYS:HA	52:RE:626:LYS:HD3	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:397:A:H5''	9:SJ:50:GLY:HA2	1.98	0.45
3:SA:895:G:H22	3:SA:917:U:H3	1.64	0.45
3:SA:1463:C:H4'	58:RN:63:ALA:HB1	1.98	0.45
3:SA:1639:C:H41	34:B3:692:MET:HE1	1.82	0.45
26:A5:66:VAL:HG12	26:A5:112:LEU:HD21	1.97	0.45
27:A8:583:SER:HB2	27:A8:637:LEU:HD22	1.97	0.45
29:AE:11:VAL:HA	29:AE:14:ASN:HD22	1.80	0.45
29:AE:255:ILE:HD11	31:AG:884:MET:HB3	1.98	0.45
29:AE:1700:SER:O	29:AE:1703:GLU:N	2.49	0.45
30:AF:69:ARG:HG3	30:AF:70:THR:HG23	1.97	0.45
33:B2:760:ILE:HD11	33:B2:835:PHE:HB2	1.98	0.45
34:B3:343:MET:HB3	34:B3:355:LEU:HD23	1.98	0.45
39:5C:39:ASP:HB3	39:5C:42:LEU:HB3	1.97	0.45
39:5C:243:TRP:NE1	39:5C:304:ARG:HH22	2.15	0.45
42:5F:95:SER:OG	43:5G:59:ASP:OD2	2.32	0.45
43:5G:76:GLU:HG2	43:5G:160:GLY:HA2	1.98	0.45
52:RE:1157:TYR:CE1	52:RE:1203:ASN:ND2	2.59	0.45
54:RG:143:GLN:HE22	54:RG:149:SER:HA	1.81	0.45
58:RN:13:LEU:HD22	58:RN:16:ARG:HE	1.81	0.45
60:RP:971:ARG:O	60:RP:975:ASN:HA	2.16	0.45
62:RS:271:THR:H	62:RS:274:GLU:HB2	1.82	0.45
3:SA:1775:U:H2'	3:SA:1776:A:C8	2.51	0.45
4:SC:224:ASP:OD2	52:RE:981:LYS:NZ	2.43	0.45
4:SC:242:LYS:N	52:RE:655:LEU:O	2.48	0.45
21:3D:379:LEU:HD13	21:3D:408:VAL:HG21	1.98	0.45
25:A4:137:TYR:HB2	25:A4:177:LEU:HD12	1.99	0.45
26:A5:452:LEU:HA	26:A5:455:THR:HG22	1.98	0.45
26:A5:518:ASN:HB2	26:A5:521:SER:HB3	1.98	0.45
26:A5:539:ARG:NH1	31:AG:524:ASP:OD2	2.49	0.45
30:AF:171:VAL:HG22	30:AF:188:SER:HB3	1.99	0.45
33:B2:49:VAL:HG22	33:B2:63:LEU:HD22	1.98	0.45
41:5E:358:THR:HB	58:RN:89:GLN:HB3	1.97	0.45
51:RD:1675:PHE:HE1	51:RD:1691:PHE:HB3	1.82	0.45
53:RF:255:LYS:O	53:RF:265:ARG:NH1	2.45	0.45
54:RH:191:ASP:HA	54:RH:194:GLU:HG2	1.98	0.45
58:RN:600:LEU:HD22	58:RN:633:VAL:HG22	1.98	0.45
62:RS:399:ILE:O	62:RS:406:GLY:N	2.50	0.45
3:SA:385:A:OP1	9:SJ:25:ARG:NH2	2.46	0.45
6:SG:117:THR:HG21	6:SG:194:LEU:HD23	1.98	0.45
12:SO:69:ASN:OD1	12:SO:69:ASN:N	2.47	0.45
21:3D:195:VAL:HG12	21:3D:216:PHE:HE2	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:3G:58:CYS:HB3	24:3G:98:ILE:HD12	1.99	0.45
25:A4:249:ARG:HB2	25:A4:292:ASN:HD22	1.81	0.45
27:A8:662:ILE:HA	27:A8:665:GLN:HB2	1.97	0.45
29:AE:718:ARG:HA	29:AE:721:VAL:HG12	1.99	0.45
31:AG:364:ASN:OD1	31:AG:364:ASN:N	2.42	0.45
33:B2:103:ILE:HB	33:B2:117:PHE:HB2	1.99	0.45
33:B2:220:THR:HG22	33:B2:259:ILE:HD11	1.96	0.45
35:B8:264:LEU:HD11	35:B8:272:LEU:HD12	1.97	0.45
37:B6:186:VAL:HG12	37:B6:273:ILE:HG13	1.98	0.45
39:5C:507:ASN:ND2	50:RC:71:CYS:O	2.50	0.45
42:5F:63:LEU:HB3	64:RV:204:GLY:HA2	1.98	0.45
43:5G:19:GLU:O	43:5G:23:SER:HB2	2.17	0.45
48:RA:21:VAL:HG12	48:RA:46:ARG:HH12	1.81	0.45
50:RC:35:PHE:HB2	50:RC:36:ALA:H	1.62	0.45
52:RE:308:LEU:HG	52:RE:337:LEU:HD21	1.99	0.45
54:RH:56:SER:HA	54:RH:63:ASP:HB2	1.99	0.45
2:5A:550:C:H2'	2:5A:551:A:C8	2.52	0.45
3:SA:1537:C:N4	54:RH:155:SER:O	2.37	0.45
5:SF:150:PRO:HB2	5:SF:154:ILE:HG13	1.98	0.45
6:SG:39:GLU:OE2	6:SG:47:SER:OG	2.33	0.45
23:3F:164:GLN:HE21	23:3F:527:VAL:HG13	1.81	0.45
23:3F:452:SER:HB3	23:3F:460:ARG:HG2	1.99	0.45
29:AE:864:VAL:O	29:AE:868:LYS:CB	2.65	0.45
30:AF:31:THR:OG1	30:AF:32:SER:N	2.46	0.45
31:AG:726:GLN:NE2	31:AG:736:THR:O	2.42	0.45
31:AG:761:GLU:HG3	31:AG:779:ILE:HG22	1.99	0.45
36:BE:851:SER:O	36:BE:851:SER:OG	2.31	0.45
48:RA:14:TYR:HE2	48:RA:344:PRO:HG3	1.81	0.45
48:RA:164:ARG:HH12	48:RA:176:PHE:N	2.15	0.45
52:RE:151:SER:HA	52:RE:154:LYS:HB2	1.98	0.45
52:RE:1155:LEU:HD23	53:RF:93:PHE:HB3	1.98	0.45
60:RP:378:HIS:O	60:RP:382:PHE:CB	2.65	0.45
3:SA:67:A:H2'	3:SA:69:G:C8	2.52	0.45
3:SA:420:A:C8	3:SA:420:A:O5'	2.70	0.45
11:SM:92:HIS:HD2	11:SM:94:ILE:HG13	1.82	0.45
12:SO:49:GLN:HA	12:SO:52:VAL:HG12	1.99	0.45
21:3D:120:SER:O	21:3D:120:SER:OG	2.33	0.45
25:A4:468:ASP:OD2	25:A4:472:ARG:NH1	2.44	0.45
25:A4:636:ILE:HG23	25:A4:648:PHE:HD2	1.82	0.45
29:AE:583:LYS:HD3	29:AE:631:VAL:HG21	1.99	0.45
31:AG:600:SER:O	31:AG:600:SER:OG	2.33	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:B2:54:ILE:HD13	33:B2:364:TYR:CD2	2.48	0.45
33:B2:140:SER:OG	33:B2:142:ASP:OD1	2.31	0.45
34:B3:42:ILE:HD11	34:B3:379:LEU:HD13	1.97	0.45
35:B8:512:ASP:OD1	35:B8:512:ASP:N	2.48	0.45
39:5C:104:LEU:HD21	39:5C:139:TRP:HB2	1.99	0.45
51:RD:1628:GLU:HG3	51:RD:1640:LEU:HD22	1.99	0.45
57:RL:77:ILE:HD12	57:RL:77:ILE:HA	1.82	0.45
57:RL:846:SER:O	57:RL:850:LEU:CB	2.65	0.45
58:RN:423:GLY:O	58:RN:426:THR:OG1	2.31	0.45
60:RP:2006:LEU:HG	60:RP:2011:ILE:HD12	1.97	0.45
2:5A:514:U:OP2	60:RP:1975:LYS:NZ	2.37	0.45
3:SA:145:A:O2'	3:SA:146:U:O5'	2.33	0.45
3:SA:326:G:H4'	11:SM:82:ARG:HD2	1.98	0.45
3:SA:884:A:H2'	3:SA:885:G:C8	2.52	0.45
3:SA:1070:C:H5''	18:Sc:17:ARG:HH21	1.82	0.45
5:SF:159:THR:HB	5:SF:173:ILE:HB	1.99	0.45
11:SM:57:LYS:O	11:SM:138:ASN:ND2	2.50	0.45
20:3C:253:ILE:HD11	20:3C:293:LEU:HD21	1.99	0.45
27:A8:648:PHE:HD1	28:A9:509:GLN:HE21	1.64	0.45
29:AE:65:LYS:HB3	29:AE:104:LEU:HD11	1.99	0.45
30:AF:227:VAL:HG22	30:AF:236:VAL:HG12	1.99	0.45
31:AG:38:SER:OG	31:AG:43:ASN:O	2.35	0.45
32:B1:25:ASP:O	32:B1:27:LYS:N	2.49	0.45
32:B1:369:ILE:HD11	32:B1:390:VAL:HG11	1.99	0.45
34:B3:217:ASP:OD1	34:B3:217:ASP:N	2.48	0.45
34:B3:509:ALA:HB1	34:B3:515:CYS:HA	1.98	0.45
39:5C:311:SER:OG	39:5C:313:GLU:OE2	2.33	0.45
45:5I:94:TYR:OH	45:5I:134:ASN:ND2	2.41	0.45
48:RA:247:THR:HG21	48:RA:251:TYR:HB2	1.99	0.45
1:3A:12:U:H3	3:SA:1112:G:H1	1.65	0.45
3:SA:1223:A:H2'	3:SA:1224:A:C8	2.52	0.45
4:SC:242:LYS:HD2	4:SC:244:VAL:H	1.82	0.45
20:3B:88:ILE:HD11	20:3B:123:ILE:HG21	1.98	0.45
24:3H:33:LEU:HD23	24:3H:35:LYS:HE3	1.98	0.45
29:AE:348:ILE:HD13	29:AE:348:ILE:HA	1.87	0.45
32:B1:300:MET:HE2	32:B1:300:MET:HB3	1.78	0.45
32:B1:475:PRO:HD2	32:B1:493:TRP:HB2	1.99	0.45
45:5I:297:SER:OG	45:5I:299:ASN:O	2.33	0.45
46:5J:110:ASP:OD1	46:5J:110:ASP:N	2.36	0.45
51:RD:1670:LYS:HG2	51:RD:1674:LEU:HG	1.99	0.45
55:RJ:617:THR:HG23	55:RJ:620:LYS:HE2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:RP:465:PHE:HA	60:RP:468:ALA:HB3	1.98	0.45
62:RS:235:VAL:HG12	62:RS:238:SER:HB3	1.98	0.45
62:RS:429:LYS:HD2	62:RS:437:ARG:HH22	1.82	0.45
3:SA:1634:C:O2	32:B1:397:LYS:NZ	2.50	0.45
20:3C:175:ALA:N	20:3C:198:GLU:OE2	2.48	0.45
26:A5:582:GLU:O	26:A5:586:ASP:N	2.50	0.45
29:AE:659:LEU:HD21	29:AE:691:PHE:HA	1.98	0.45
30:AF:371:GLU:OE2	35:B8:273:ARG:NH2	2.50	0.45
39:5C:214:LEU:HD23	39:5C:228:LEU:HD12	1.99	0.45
39:5C:269:LYS:HB2	61:RQ:830:ILE:HG23	1.98	0.45
39:5C:460:ARG:HB3	61:RQ:847:VAL:HB	1.99	0.45
48:RA:231:VAL:HA	48:RA:247:THR:HA	1.98	0.45
51:RD:1708:ILE:HA	51:RD:1711:VAL:HG22	1.99	0.45
52:RE:173:ASN:O	52:RE:175:LYS:NZ	2.37	0.45
53:RF:71:VAL:HG21	53:RF:84:VAL:HB	1.98	0.45
56:RK:143:LYS:HE3	56:RK:143:LYS:HB2	1.75	0.45
62:RS:373:LYS:HG3	62:RS:420:ALA:HA	1.99	0.45
3:SA:930:A:H2'	4:SC:114:VAL:HG11	1.99	0.44
4:SC:31:ASP:HB3	4:SC:45:LYS:HG2	1.99	0.44
11:SM:46:LYS:HD3	11:SM:49:ILE:HD12	1.98	0.44
26:A5:87:LEU:O	26:A5:96:THR:N	2.50	0.44
27:A8:574:ARG:H	27:A8:576:ARG:NH1	2.16	0.44
29:AE:109:TRP:HA	29:AE:114:THR:HG21	2.00	0.44
31:AG:43:ASN:OD1	31:AG:43:ASN:N	2.48	0.44
33:B2:129:PHE:HE1	33:B2:150:LEU:HD11	1.82	0.44
33:B2:292:ILE:HG23	33:B2:324:PHE:HE2	1.83	0.44
33:B2:641:TYR:O	33:B2:650:ILE:N	2.49	0.44
36:BE:546:ILE:HG21	36:BE:560:LEU:HD22	1.99	0.44
43:5G:166:SER:O	43:5G:256:MET:HA	2.17	0.44
45:5I:210:LYS:HA	45:5I:210:LYS:HD3	1.69	0.44
51:RD:1483:ALA:HA	51:RD:1486:LEU:HB2	1.99	0.44
54:RG:135:LYS:HD3	54:RG:135:LYS:HA	1.87	0.44
55:RJ:1148:GLU:OE2	55:RJ:1152:ARG:NH1	2.49	0.44
60:RP:60:SER:HB3	60:RP:102:SER:HB3	1.99	0.44
2:5A:247:U:OP1	40:5D:82:ARG:NH1	2.50	0.44
3:SA:406:U:H2'	3:SA:407:A:H8	1.82	0.44
11:SM:94:ILE:HD12	11:SM:101:GLU:H	1.81	0.44
18:Sc:48:SER:OG	18:Sc:49:HIS:ND1	2.50	0.44
20:3B:104:ASP:OD1	20:3B:104:ASP:N	2.38	0.44
51:RD:1670:LYS:HA	51:RD:1673:ASP:HB2	1.98	0.44
52:RE:585:MET:HB3	52:RE:610:PHE:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:RJ:889:LEU:HD22	55:RJ:922:ILE:HB	2.00	0.44
57:RL:111:SER:HB3	57:RL:134:LEU:HD12	1.99	0.44
58:RN:737:ILE:HA	58:RN:740:MET:HG2	2.00	0.44
59:RO:282:HIS:CD2	59:RO:283:LYS:HG2	2.52	0.44
3:SA:1080:U:H5'	45:5I:425:LYS:HE2	1.99	0.44
8:SI:163:ASP:O	61:RQ:277:ARG:NH2	2.50	0.44
22:3E:372:ARG:HG3	24:3G:63:ILE:HA	2.00	0.44
23:3F:405:VAL:HG12	23:3F:415:THR:HG22	2.00	0.44
29:AE:763:LEU:HD12	29:AE:768:LYS:HD3	2.00	0.44
30:AF:51:HIS:O	30:AF:53:HIS:N	2.49	0.44
33:B2:566:TYR:OH	33:B2:603:ASP:O	2.33	0.44
33:B2:580:ASP:OD2	33:B2:623:PHE:N	2.40	0.44
34:B3:32:LEU:HD22	34:B3:76:LEU:HD12	2.00	0.44
34:B3:104:PRO:O	34:B3:122:THR:OG1	2.35	0.44
36:BE:921:ARG:O	36:BE:925:LEU:HB2	2.17	0.44
55:RJ:288:VAL:HG11	55:RJ:812:MET:HE2	1.98	0.44
60:RP:107:LEU:HD21	60:RP:150:TRP:HB3	1.98	0.44
2:5A:228:A:H2'	2:5A:229:A:C8	2.51	0.44
3:SA:362:G:H2'	3:SA:363:G:C8	2.52	0.44
3:SA:608:U:O2'	3:SA:609:U:O4'	2.34	0.44
3:SA:863:A:H4'	15:5X:57:ARG:HG2	1.99	0.44
3:SA:1146:G:H2'	3:SA:1147:A:H8	1.83	0.44
3:SA:1660:A:H2'	3:SA:1661:U:C6	2.52	0.44
11:SM:84:ILE:N	11:SM:109:VAL:O	2.47	0.44
20:3B:210:MET:HE2	20:3B:210:MET:HB3	1.79	0.44
21:3D:31:LEU:HD21	45:5I:59:VAL:HG13	1.99	0.44
25:A4:579:ARG:HH12	25:A4:659:PHE:HD1	1.65	0.44
32:B1:157:ASP:N	32:B1:157:ASP:OD1	2.50	0.44
34:B3:430:TYR:HD2	34:B3:454:LEU:HD23	1.82	0.44
34:B3:531:ASN:OD1	34:B3:531:ASN:N	2.49	0.44
39:5C:433:LEU:HD21	42:5F:16:VAL:HG11	1.99	0.44
44:5H:555:ASN:HB3	44:5H:558:ASN:HB2	1.98	0.44
49:RB:302:LYS:HB3	49:RB:306:ARG:HH22	1.81	0.44
52:RE:165:PRO:HD2	52:RE:222:PHE:HZ	1.83	0.44
52:RE:174:TYR:CE2	52:RE:227:LYS:HB3	2.53	0.44
52:RE:804:THR:HG21	52:RE:838:VAL:HB	1.99	0.44
53:RF:15:VAL:HG12	53:RF:17:PRO:HD3	1.98	0.44
53:RF:84:VAL:HG13	53:RF:126:LEU:HD11	1.99	0.44
56:RK:187:ILE:HB	56:RK:251:GLN:HE22	1.82	0.44
58:RN:443:LYS:HG3	58:RN:448:PHE:HE2	1.81	0.44
2:5A:554:G:H1	2:5A:583:U:H3	1.64	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:SG:63:GLN:HE22	6:SG:66:GLN:HB3	1.82	0.44
12:SO:93:LYS:HA	12:SO:96:VAL:HG12	1.99	0.44
20:3C:92:ARG:HH12	40:5D:151:PHE:HB2	1.81	0.44
21:3D:281:LEU:HD23	22:3E:261:GLN:HE21	1.82	0.44
25:A4:75:ASN:HB3	25:A4:92:GLU:HA	2.00	0.44
25:A4:201:VAL:HG13	25:A4:213:TRP:HB2	1.99	0.44
29:AE:488:GLY:HA2	29:AE:491:TYR:HB3	1.98	0.44
29:AE:729:LYS:HA	29:AE:733:MET:HG3	2.00	0.44
31:AG:414:ILE:HA	31:AG:414:ILE:HD12	1.80	0.44
33:B2:443:LEU:HG	33:B2:459:LEU:HD13	2.00	0.44
34:B3:467:ILE:H	34:B3:479:ILE:HD11	1.83	0.44
35:B8:358:PHE:HA	35:B8:376:LEU:O	2.17	0.44
36:BE:356:ILE:HG22	36:BE:633:LYS:HG3	2.00	0.44
39:5C:122:GLY:O	39:5C:139:TRP:NE1	2.34	0.44
48:RA:60:ASN:HB3	48:RA:74:THR:HB	2.00	0.44
50:RC:174:MET:HE2	50:RC:174:MET:HB3	1.78	0.44
52:RE:554:LYS:HA	52:RE:554:LYS:HD2	1.82	0.44
54:RG:242:CYS:O	54:RG:246:GLU:HG3	2.18	0.44
60:RP:70:ILE:HG21	60:RP:87:ILE:HG22	1.98	0.44
2:5A:20:C:H2'	2:5A:21:A:C8	2.52	0.44
3:SA:592:A:O2'	3:SA:596:C:OP1	2.35	0.44
3:SA:1234:A:O2'	3:SA:1236:A:N6	2.50	0.44
6:SG:86:GLN:HE22	32:B1:546:ASP:HB3	1.83	0.44
16:SY:77:ILE:HG22	55:RJ:751:TYR:HB2	1.99	0.44
20:3B:125:VAL:HG12	46:5J:150:GLY:HA3	2.00	0.44
20:3B:169:LYS:HA	20:3B:193:VAL:O	2.18	0.44
25:A4:120:SER:OG	25:A4:121:THR:N	2.50	0.44
31:AG:484:VAL:O	31:AG:487:GLU:N	2.51	0.44
32:B1:476:VAL:HA	32:B1:492:SER:HB3	1.98	0.44
32:B1:743:PHE:HZ	32:B1:778:ILE:HD13	1.83	0.44
34:B3:691:PRO:HD2	41:5E:516:SER:HB2	2.00	0.44
35:B8:27:PHE:HB3	37:B6:31:LEU:HD23	1.98	0.44
51:RD:1181:ASP:HA	51:RD:1191:GLY:HA2	1.98	0.44
52:RE:655:LEU:HD12	52:RE:655:LEU:HA	1.90	0.44
52:RE:1098:PHE:CD2	52:RE:1184:GLY:N	2.72	0.44
54:RH:199:ASP:OD1	54:RH:199:ASP:N	2.49	0.44
59:RO:259:LYS:HB3	59:RO:259:LYS:HE2	1.72	0.44
3:SA:398:G:OP2	9:SJ:47:ARG:NH2	2.40	0.44
5:SF:140:VAL:HG12	5:SF:146:THR:HG22	2.00	0.44
10:SK:38:ASN:HA	44:5H:565:LYS:HE2	1.99	0.44
11:SM:57:LYS:HG3	11:SM:110:HIS:CE1	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:SR:64:ASP:OD1	14:SR:64:ASP:N	2.50	0.44
20:3B:218:ILE:HD11	21:3D:152:LEU:HD22	1.98	0.44
22:3E:227:LEU:HG	22:3E:231:ILE:HB	2.00	0.44
29:AE:396:ASP:OD1	29:AE:396:ASP:N	2.47	0.44
30:AF:20:THR:HA	30:AF:24:GLN:HE21	1.83	0.44
31:AG:768:TRP:HE1	31:AG:772:THR:HA	1.83	0.44
34:B3:111:ASP:N	34:B3:111:ASP:OD1	2.48	0.44
42:5F:169:THR:HA	42:5F:172:ARG:HG2	1.99	0.44
43:5G:139:LEU:HB2	43:5G:157:PHE:CE2	2.53	0.44
45:5I:241:ASP:OD1	45:5I:241:ASP:N	2.39	0.44
48:RA:152:ASP:OD1	48:RA:152:ASP:N	2.51	0.44
53:RF:150:LYS:HG3	53:RF:151:HIS:ND1	2.33	0.44
53:RF:208:ASP:N	53:RF:212:PHE:O	2.41	0.44
55:RJ:841:THR:HB	55:RJ:859:ILE:HA	1.99	0.44
58:RN:314:MET:HA	58:RN:512:ASP:HA	2.00	0.44
60:RP:1183:PRO:O	60:RP:1187:VAL:CB	2.65	0.44
65:RY:489:GLN:O	65:RY:493:PHE:CB	2.66	0.44
4:SC:36:SER:OG	4:SC:41:ARG:NH1	2.50	0.44
9:SJ:66:SER:HA	9:SJ:73:SER:HA	1.99	0.44
21:3D:206:LEU:HD11	21:3D:219:LEU:HD11	2.00	0.44
25:A4:214:SER:HB3	25:A4:226:LEU:HD13	1.99	0.44
29:AE:63:GLU:HA	29:AE:64:PRO:HD3	1.88	0.44
33:B2:107:ASP:OD1	33:B2:107:ASP:N	2.46	0.44
45:5I:444:GLU:OE2	45:5I:448:ARG:NH2	2.37	0.44
48:RA:184:ASN:OD1	48:RA:230:GLN:NE2	2.51	0.44
52:RE:822:ARG:NH1	52:RE:1133:PRO:O	2.50	0.44
53:RF:131:ALA:HA	53:RF:134:ILE:HG12	1.99	0.44
54:RG:227:LEU:HA	54:RG:227:LEU:HD23	1.79	0.44
3:SA:1599:C:H2'	3:SA:1600:A:C8	2.53	0.44
4:SC:129:THR:HG23	4:SC:131:ASP:H	1.82	0.44
4:SC:194:ASN:HD21	4:SC:212:VAL:HG23	1.82	0.44
7:SH:65:GLN:NE2	48:RA:43:TYR:O	2.51	0.44
8:SI:38:LEU:HD12	8:SI:41:LEU:HD12	2.00	0.44
9:SJ:67:TRP:HD1	9:SJ:70:GLU:H	1.66	0.44
11:SM:36:LYS:HD2	11:SM:36:LYS:HA	1.74	0.44
15:SX:66:ASN:O	45:5I:325:TYR:OH	2.27	0.44
25:A4:45:THR:HB	25:A4:352:VAL:HA	1.99	0.44
25:A4:774:LEU:HD12	25:A4:774:LEU:HA	1.83	0.44
27:A8:638:LEU:HD21	27:A8:662:ILE:HD11	1.99	0.44
29:AE:238:LEU:HA	29:AE:241:ILE:HG22	1.99	0.44
29:AE:538:ALA:HA	29:AE:541:LEU:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:AG:228:VAL:HG23	31:AG:236:ASN:HB3	2.00	0.44
31:AG:510:TYR:HE1	31:AG:527:HIS:HB3	1.83	0.44
31:AG:532:TRP:HB3	31:AG:541:TRP:HB3	1.99	0.44
32:B1:35:ASN:HA	32:B1:58:ILE:HG23	1.99	0.44
32:B1:157:ASP:OD1	32:B1:203:GLN:NE2	2.38	0.44
32:B1:661:LEU:H	32:B1:661:LEU:HG	1.62	0.44
33:B2:59:LEU:HD21	33:B2:62:LYS:HE2	1.99	0.44
34:B3:188:GLU:O	34:B3:221:ASN:ND2	2.50	0.44
35:B8:277:ILE:HA	35:B8:282:ASN:HD22	1.83	0.44
36:BE:852:LEU:HD22	36:BE:860:GLU:HG2	2.00	0.44
39:5C:162:ASN:ND2	39:5C:429:GLU:OE1	2.51	0.44
41:5E:379:ASP:HB2	43:5G:191:PHE:HD2	1.83	0.44
52:RE:1160:SER:C	52:RE:1187:LYS:HG2	2.43	0.44
52:RE:1188:PRO:HG3	66:X1:308:UNK:CB	2.48	0.44
52:RE:1222:GLU:HG2	53:RF:60:LEU:HB2	2.00	0.44
54:RH:89:PRO:HG2	54:RH:134:PHE:HZ	1.83	0.44
57:RL:195:ASN:HB3	57:RL:198:CYS:HB3	1.99	0.44
61:RQ:284:ARG:HE	61:RQ:284:ARG:HB3	1.51	0.44
3:SA:257:A:O2'	9:SJ:73:SER:O	2.34	0.43
3:SA:415:C:O2'	3:SA:418:G:O6	2.36	0.43
26:A5:233:LYS:HA	26:A5:233:LYS:HD3	1.82	0.43
26:A5:520:MET:H	26:A5:520:MET:HG3	1.60	0.43
29:AE:100:ALA:HB1	35:B8:44:PHE:HZ	1.82	0.43
30:AF:288:ASP:OD1	30:AF:288:ASP:N	2.48	0.43
32:B1:356:ASP:OD1	32:B1:356:ASP:N	2.50	0.43
34:B3:652:ILE:HD12	34:B3:652:ILE:HA	1.92	0.43
36:BE:76:THR:OG1	36:BE:78:SER:O	2.29	0.43
39:5C:228:LEU:HD22	39:5C:264:PRO:HA	1.99	0.43
45:5I:139:CYS:HB3	45:5I:145:VAL:HG22	1.99	0.43
53:RF:50:SER:O	53:RF:127:LYS:NZ	2.51	0.43
54:RG:177:LYS:HE2	54:RG:177:LYS:HB3	1.68	0.43
55:RJ:203:LYS:HA	55:RJ:203:LYS:HD2	1.78	0.43
60:RP:103:LEU:HD11	60:RP:147:VAL:HG23	1.99	0.43
3:SA:328:A:H2'	3:SA:329:G:H8	1.83	0.43
4:SC:123:ALA:HB2	4:SC:165:ARG:HG3	2.00	0.43
4:SC:171:ILE:HD11	4:SC:197:ILE:HA	1.99	0.43
8:SI:87:ASP:OD1	60:RP:2031:HIS:NE2	2.49	0.43
11:SM:123:VAL:HG12	11:SM:142:VAL:HA	1.99	0.43
20:3B:221:ILE:HD13	21:3D:163:VAL:HB	2.00	0.43
25:A4:212:ILE:O	25:A4:226:LEU:N	2.50	0.43
25:A4:571:THR:HG21	25:A4:632:ASN:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A5:240:GLN:HE22	26:A5:298:LYS:HB3	1.83	0.43
31:AG:712:THR:HG23	31:AG:720:ILE:HD13	1.99	0.43
37:B6:5:ARG:HA	37:B6:5:ARG:HD2	1.80	0.43
42:5F:34:ARG:NH2	47:5K:16:THR:OG1	2.50	0.43
43:5G:119:ARG:NH1	43:5G:122:TYR:O	2.52	0.43
43:5G:283:THR:HG22	43:5G:286:LYS:HB2	2.00	0.43
51:RD:1479:MET:HE2	51:RD:1519:ALA:HB2	1.99	0.43
52:RE:518:PHE:HD1	52:RE:520:ASN:H	1.67	0.43
52:RE:976:ILE:HG22	52:RE:1042:ALA:HB3	2.00	0.43
52:RE:1221:HIS:CE1	53:RF:20:LEU:HB3	2.53	0.43
55:RJ:625:TRP:HZ2	56:RK:284:SER:HB3	1.83	0.43
57:RM:281:LEU:HA	57:RM:409:ALA:HB3	1.99	0.43
59:RO:292:PRO:HG2	59:RO:330:PHE:HE2	1.82	0.43
59:RO:315:VAL:HG23	59:RO:316:PRO:HD3	1.98	0.43
59:RO:472:HIS:CD2	59:RO:474:HIS:H	2.31	0.43
60:RP:1941:VAL:HA	60:RP:1944:ILE:HD12	1.99	0.43
3:SA:153:G:O3'	7:SH:2:LYS:NZ	2.41	0.43
3:SA:513:U:H2'	3:SA:514:G:H8	1.82	0.43
3:SA:1146:G:H2'	3:SA:1147:A:C8	2.53	0.43
5:SF:183:VAL:HB	5:SF:225:VAL:HG23	2.00	0.43
5:SF:194:THR:H	5:SF:210:ILE:HG23	1.82	0.43
8:SI:19:GLN:HB3	8:SI:85:PHE:HZ	1.83	0.43
9:SJ:74:LYS:HD3	9:SJ:74:LYS:HA	1.68	0.43
22:3E:330:LEU:HD13	40:5D:109:THR:HG21	2.00	0.43
25:A4:144:ILE:HD12	25:A4:158:VAL:HB	2.00	0.43
29:AE:641:LEU:O	29:AE:644:LYS:NZ	2.42	0.43
31:AG:516:PRO:HG2	31:AG:519:LEU:HD21	2.00	0.43
32:B1:605:ASP:OD1	32:B1:605:ASP:N	2.40	0.43
34:B3:28:ASN:OD1	34:B3:28:ASN:N	2.48	0.43
34:B3:34:THR:HG23	34:B3:68:LYS:HE3	2.00	0.43
40:5D:78:LEU:HA	40:5D:78:LEU:HD12	1.82	0.43
41:5E:524:ASP:OD2	41:5E:527:ARG:NH2	2.42	0.43
45:5I:306:SER:OG	45:5I:307:ALA:N	2.50	0.43
47:5K:171:PRO:HA	47:5K:184:LYS:HB2	2.00	0.43
60:RP:1756:ILE:HG21	60:RP:1800:LEU:HB3	2.01	0.43
60:RP:1782:ASN:OD1	60:RP:1782:ASN:N	2.44	0.43
5:SF:141:THR:OG1	5:SF:142:HIS:N	2.52	0.43
22:3E:206:ALA:HB2	22:3E:262:ILE:HD11	2.00	0.43
25:A4:572:ALA:HB3	25:A4:585:ILE:HD11	2.00	0.43
25:A4:750:ASN:N	25:A4:750:ASN:OD1	2.50	0.43
29:AE:655:ALA:O	29:AE:659:LEU:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:AF:24:GLN:HB2	30:AF:294:PHE:HD1	1.83	0.43
32:B1:369:ILE:HB	32:B1:383:PHE:HB2	1.99	0.43
34:B3:194:ARG:HD3	34:B3:243:VAL:HG13	1.99	0.43
39:5C:512:ARG:O	39:5C:516:VAL:HG23	2.18	0.43
45:5I:358:MET:HB3	61:RQ:890:VAL:HG23	2.00	0.43
46:5J:207:LYS:HE2	46:5J:207:LYS:HB3	1.88	0.43
52:RE:527:TYR:HB2	52:RE:615:VAL:HG13	2.00	0.43
52:RE:870:ALA:O	52:RE:875:LYS:NZ	2.51	0.43
55:RJ:904:ASN:HA	55:RJ:907:THR:HB	2.00	0.43
56:RK:68:SER:OG	56:RK:69:TYR:N	2.52	0.43
62:RS:221:LEU:HD22	62:RS:258:VAL:HG11	2.00	0.43
62:RS:373:LYS:HE2	62:RS:373:LYS:HB3	1.84	0.43
2:5A:467:A:N1	2:5A:468:A:N6	2.66	0.43
2:5A:489:G:O6	37:B6:120:ARG:NH1	2.51	0.43
3:SA:18:C:O2'	3:SA:21:U:O4'	2.37	0.43
3:SA:578:U:OP2	55:RJ:874:TYR:OH	2.29	0.43
8:SI:22:GLN:HA	8:SI:25:VAL:HG22	1.99	0.43
9:SJ:76:THR:OG1	9:SJ:77:ARG:N	2.52	0.43
10:SK:65:LYS:HZ2	23:3F:59:PRO:CA	2.27	0.43
15:SX:32:LYS:HB2	15:SX:32:LYS:HE3	1.81	0.43
16:SY:68:ILE:HD12	58:RN:785:VAL:HG23	2.00	0.43
20:3C:185:SER:HB3	20:3C:217:ILE:HD11	2.00	0.43
22:3E:191:HIS:HB2	22:3E:247:ILE:HG23	1.99	0.43
24:3G:62:GLU:HA	24:3G:65:LEU:HG	2.00	0.43
24:3H:95:ARG:HD2	24:3H:95:ARG:HA	1.87	0.43
31:AG:50:ASN:HD21	31:AG:782:THR:HG22	1.84	0.43
31:AG:252:LEU:HD23	31:AG:256:THR:HG21	2.00	0.43
32:B1:829:VAL:HG23	32:B1:830:ARG:HG2	2.01	0.43
33:B2:276:ASN:ND2	33:B2:280:THR:O	2.47	0.43
34:B3:41:ASN:OD1	34:B3:41:ASN:N	2.49	0.43
36:BE:606:ASP:OD1	36:BE:606:ASP:N	2.41	0.43
45:5I:8:ARG:HD3	45:5I:8:ARG:HA	1.80	0.43
47:5K:52:PHE:HB3	47:5K:55:TYR:HB3	2.01	0.43
47:5K:161:LYS:HG2	47:5K:172:LEU:HD21	1.99	0.43
51:RD:1472:PRO:HG2	52:RE:1189:LEU:HD12	2.00	0.43
52:RE:207:LEU:HB2	52:RE:296:ILE:HA	2.00	0.43
52:RE:1109:LYS:HZ1	52:RE:1170:GLY:H	1.66	0.43
55:RJ:80:THR:C	68:RJ:1201:GTP:O2B	2.61	0.43
58:RN:640:MET:HE2	58:RN:640:MET:HB3	1.81	0.43
60:RP:1610:MET:O	60:RP:1614:GLU:CB	2.67	0.43
62:RS:359:LEU:HD23	62:RS:362:LEU:HD12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:RT:186:GLU:HG3	63:RT:230:LYS:HG2	2.00	0.43
3:SA:526:A:OP1	17:SZ:93:ARG:NE	2.48	0.43
10:SK:155:HIS:NE2	23:3F:321:HIS:O	2.50	0.43
15:SX:38:LEU:HA	15:SX:41:MET:HG2	2.01	0.43
20:3C:261:LEU:O	22:3E:118:ARG:NH2	2.34	0.43
22:3E:372:ARG:O	22:3E:376:LEU:HB2	2.19	0.43
23:3F:303:LYS:HB3	23:3F:317:ILE:HD11	2.01	0.43
24:3H:52:ILE:HD12	24:3H:71:CYS:SG	2.58	0.43
26:A5:336:ASN:OD1	26:A5:336:ASN:N	2.49	0.43
33:B2:645:GLU:HG2	33:B2:646:LYS:HG3	1.99	0.43
36:BE:569:VAL:HB	36:BE:579:ARG:HB2	2.01	0.43
42:5F:138:VAL:HG12	42:5F:158:VAL:HG22	2.00	0.43
45:5I:6:ILE:HG21	45:5I:8:ARG:HH21	1.84	0.43
48:RA:155:VAL:HG13	48:RA:163:TYR:HB2	2.00	0.43
51:RD:1544:MET:HB2	51:RD:1544:MET:HE2	1.67	0.43
52:RE:257:SER:O	52:RE:266:PRO:HA	2.18	0.43
52:RE:611:ASP:OD1	52:RE:611:ASP:N	2.51	0.43
52:RE:745:LYS:HA	52:RE:745:LYS:HD2	1.83	0.43
56:RK:36:ILE:HB	56:RK:72:THR:HA	2.01	0.43
58:RN:590:ASN:OD1	58:RN:590:ASN:N	2.50	0.43
3:SA:646:C:H2'	3:SA:647:G:C8	2.47	0.43
4:SC:239:GLU:HG2	52:RE:658:PHE:HA	2.00	0.43
6:SG:89:ILE:HD11	6:SG:172:ILE:HD11	2.00	0.43
8:SI:46:ILE:HD12	8:SI:60:ILE:HG13	2.01	0.43
8:SI:185:ILE:HG13	8:SI:187:SER:HB3	2.01	0.43
20:3C:185:SER:HA	20:3C:188:VAL:HG12	2.01	0.43
29:AE:348:ILE:HG21	29:AE:373:ILE:HD11	2.00	0.43
29:AE:715:HIS:HA	29:AE:718:ARG:HG2	2.00	0.43
31:AG:140:LYS:HA	31:AG:140:LYS:HD3	1.78	0.43
34:B3:377:LEU:HA	34:B3:378:PRO:HD3	1.85	0.43
34:B3:519:ASN:HD22	34:B3:524:GLU:H	1.67	0.43
34:B3:678:TRP:HE3	34:B3:697:VAL:HG23	1.84	0.43
35:B8:35:GLU:O	35:B8:39:LYS:HB2	2.18	0.43
39:5C:64:ASP:HA	39:5C:67:LEU:HG	1.99	0.43
43:5G:28:LYS:HB2	43:5G:46:LEU:HD11	2.00	0.43
45:5I:133:GLN:HA	45:5I:150:ILE:O	2.18	0.43
55:RJ:280:LEU:HD12	55:RJ:281:PRO:HD2	2.01	0.43
58:RN:616:LEU:HB3	58:RN:619:LEU:HD13	2.01	0.43
58:RN:644:ASP:OD1	58:RN:687:LYS:NZ	2.51	0.43
64:RV:203:ILE:HG22	64:RV:204:GLY:H	1.84	0.43
64:RV:315:THR:HG23	64:RV:317:ASN:H	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:SF:163:ASP:OD2	5:SF:166:SER:N	2.51	0.43
6:SG:72:HIS:O	14:SR:79:TYR:OH	2.37	0.43
23:3F:209:LYS:HA	23:3F:209:LYS:HD2	1.82	0.43
23:3F:343:ASP:OD1	23:3F:343:ASP:N	2.46	0.43
23:3F:415:THR:OG1	23:3F:425:TRP:NE1	2.39	0.43
26:A5:281:ILE:HG12	26:A5:328:VAL:HB	2.01	0.43
28:A9:475:THR:HA	28:A9:478:ASN:HB2	1.99	0.43
30:AF:377:ASP:OD1	30:AF:377:ASP:N	2.51	0.43
30:AF:463:VAL:HA	30:AF:466:VAL:HG12	2.01	0.43
32:B1:847:ARG:O	32:B1:851:SER:OG	2.30	0.43
33:B2:596:ASN:HB3	33:B2:612:PHE:HA	1.99	0.43
35:B8:376:LEU:HG	35:B8:386:ILE:HG12	1.99	0.43
36:BE:24:PHE:HB3	36:BE:654:TRP:HB3	2.01	0.43
40:5D:145:GLU:OE1	40:5D:146:PHE:N	2.52	0.43
41:5E:335:ARG:HH22	55:RJ:952:PHE:HA	1.84	0.43
45:5I:344:HIS:NE2	45:5I:418:HIS:O	2.51	0.43
52:RE:911:PRO:HB2	52:RE:954:LEU:HD13	2.01	0.43
52:RE:1206:PRO:HB3	52:RE:1212:VAL:HG22	2.01	0.43
58:RN:700:LEU:HD21	59:RO:467:ALA:HB2	2.00	0.43
65:RY:489:GLN:O	65:RY:493:PHE:HB3	2.19	0.43
2:5A:474:A:OP2	39:5C:425:ARG:NH2	2.37	0.43
3:SA:1233:G:H1	3:SA:1253:U:H2'	1.83	0.43
4:SC:154:SER:O	4:SC:154:SER:OG	2.32	0.43
5:SF:182:TYR:CD2	5:SF:192:ILE:HD11	2.54	0.43
6:SG:103:ASN:HA	6:SG:106:LYS:HD2	2.01	0.43
8:SI:131:PHE:O	8:SI:133:THR:N	2.52	0.43
9:SJ:67:TRP:O	9:SJ:71:GLY:HA2	2.18	0.43
21:3D:52:SER:HB2	21:3D:85:ASN:HD21	1.84	0.43
22:3E:218:ALA:HA	22:3E:221:THR:HG22	2.00	0.43
22:3E:319:ILE:HD12	22:3E:326:LEU:HD22	2.01	0.43
23:3F:201:ILE:HG12	23:3F:538:ARG:HD3	2.00	0.43
25:A4:617:ASN:O	25:A4:621:ASN:HB2	2.19	0.43
27:A8:583:SER:HA	27:A8:586:ILE:HG22	2.00	0.43
31:AG:478:ASN:OD1	31:AG:478:ASN:N	2.51	0.43
32:B1:76:ASP:OD1	32:B1:76:ASP:N	2.51	0.43
33:B2:178:ILE:HD11	33:B2:186:ILE:HD11	2.01	0.43
34:B3:192:ALA:HB3	34:B3:216:ARG:HG3	2.00	0.43
35:B8:426:VAL:HG11	35:B8:455:ILE:HG21	2.01	0.43
36:BE:50:ILE:HD13	36:BE:311:VAL:HG11	2.01	0.43
39:5C:487:LYS:HD3	39:5C:490:VAL:HG11	2.00	0.43
43:5G:29:ARG:HD2	43:5G:59:ASP:HB3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:5G:33:LYS:HB2	43:5G:33:LYS:HE3	1.79	0.43
43:5G:100:LEU:HD13	43:5G:144:GLU:HB3	2.01	0.43
52:RE:208:THR:OG1	52:RE:209:MET:N	2.52	0.43
55:RJ:831:ARG:HD3	55:RJ:838:ILE:HD12	2.01	0.43
58:RN:484:ARG:HB3	58:RN:492:ALA:HB1	2.01	0.43
58:RN:669:SER:HA	58:RN:672:THR:HG22	2.01	0.43
60:RP:1741:LYS:HD3	60:RP:1741:LYS:HA	1.90	0.43
3:SA:200:A:H2'	3:SA:201:G:H8	1.84	0.43
3:SA:555:A:N6	3:SA:571:G:O2'	2.50	0.43
3:SA:628:G:OP1	12:SO:120:SER:OG	2.37	0.43
3:SA:1169:G:N1	3:SA:1575:G:OP2	2.44	0.43
9:SJ:31:ARG:HH12	9:SJ:48:THR:HB	1.84	0.43
15:SX:12:ASN:O	15:SX:16:ASN:ND2	2.52	0.43
25:A4:313:LYS:HA	25:A4:316:LYS:HG2	2.01	0.43
26:A5:110:ILE:HG22	26:A5:119:CYS:HB2	2.00	0.43
26:A5:448:ASN:OD1	26:A5:450:HIS:NE2	2.52	0.43
29:AE:586:LEU:O	29:AE:590:ALA:HB2	2.18	0.43
30:AF:413:LEU:HA	30:AF:416:THR:HG22	2.00	0.43
31:AG:202:SER:OG	31:AG:204:ASN:OD1	2.30	0.43
32:B1:493:TRP:HA	32:B1:517:ASP:HB2	2.01	0.43
34:B3:133:ASN:OD1	34:B3:133:ASN:N	2.51	0.43
36:BE:627:ASN:ND2	36:BE:647:THR:OG1	2.52	0.43
38:5B:164:LYS:HB3	38:5B:164:LYS:HE3	1.76	0.43
39:5C:268:VAL:HG13	61:RQ:831:ILE:HG12	2.00	0.43
39:5C:544:ASP:HB3	39:5C:547:GLU:HB3	2.00	0.43
40:5D:102:GLN:HE21	55:RJ:1098:ARG:NH1	2.17	0.43
47:5K:61:PRO:HB3	47:5K:92:ALA:HB1	2.01	0.43
50:RC:116:ILE:HD13	50:RC:174:MET:HE3	2.01	0.43
52:RE:224:CYS:O	52:RE:227:LYS:HG3	2.19	0.43
53:RF:130:ASP:HB2	53:RF:133:SER:HB2	2.01	0.43
54:RG:75:GLY:HA2	54:RG:78:LYS:HE3	2.01	0.43
55:RJ:1080:LYS:HA	55:RJ:1080:LYS:HD2	1.80	0.43
58:RN:475:ARG:HH22	58:RN:516:LEU:HB3	1.84	0.43
1:3A:62:C:O2'	36:BE:447:ASN:O	2.35	0.42
3:SA:200:A:O2'	60:RP:1061:CYS:O	2.36	0.42
3:SA:327:U:OP2	11:SM:57:LYS:NZ	2.38	0.42
5:SF:45:ILE:O	5:SF:49:ARG:HB3	2.19	0.42
15:SX:93:LEU:HD11	15:SX:102:VAL:HG22	2.01	0.42
22:3E:283:ILE:HD13	22:3E:283:ILE:HA	1.88	0.42
23:3F:414:ILE:HG13	23:3F:478:LEU:HD21	2.00	0.42
26:A5:441:LEU:HD11	26:A5:480:LEU:HD13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:AE:476:ILE:HG23	29:AE:515:PHE:HE2	1.84	0.42
33:B2:351:LEU:HB2	33:B2:367:ILE:HG23	2.00	0.42
33:B2:369:TYR:HA	33:B2:374:PRO:HA	2.01	0.42
36:BE:470:GLN:HB3	36:BE:553:ARG:NH1	2.34	0.42
39:5C:230:THR:HG22	39:5C:232:ALA:H	1.83	0.42
48:RA:95:ARG:NH2	48:RA:128:LYS:O	2.51	0.42
48:RA:254:ILE:HD12	48:RA:254:ILE:HA	1.84	0.42
51:RD:1592:LEU:HB2	51:RD:1601:ALA:HB2	2.01	0.42
55:RJ:1019:THR:HB	55:RJ:1022:LEU:HD12	2.01	0.42
55:RJ:1075:LYS:HE3	55:RJ:1075:LYS:HB2	1.84	0.42
59:RO:504:ASP:OD1	59:RO:504:ASP:N	2.48	0.42
62:RS:266:PHE:O	62:RS:270:LEU:HB3	2.18	0.42
62:RS:398:ARG:H	62:RS:406:GLY:HA3	1.83	0.42
62:RS:437:ARG:HH21	62:RS:463:GLY:HA3	1.84	0.42
6:SG:39:GLU:OE1	6:SG:41:LYS:NZ	2.45	0.42
22:3E:132:SER:OG	22:3E:134:ASN:OD1	2.34	0.42
23:3F:160:ILE:HG12	23:3F:542:SER:HB2	2.00	0.42
25:A4:106:ASN:OD1	25:A4:106:ASN:N	2.51	0.42
26:A5:270:ASN:OD1	26:A5:270:ASN:N	2.49	0.42
27:A8:120:LEU:HA	27:A8:132:ILE:HA	2.01	0.42
30:AF:424:ARG:HA	31:AG:477:VAL:HG11	2.01	0.42
31:AG:555:VAL:HA	31:AG:556:PRO:HD3	1.89	0.42
31:AG:857:PHE:HE2	35:B8:226:LYS:HB3	1.84	0.42
33:B2:123:ALA:HB3	33:B2:141:LYS:HD3	2.00	0.42
34:B3:260:THR:HG22	34:B3:269:LEU:HD13	2.01	0.42
36:BE:353:PRO:HA	36:BE:370:SER:HA	2.01	0.42
37:B6:72:LYS:HD2	37:B6:72:LYS:HA	1.78	0.42
41:5E:370:ARG:HA	41:5E:373:ILE:HG22	2.01	0.42
43:5G:28:LYS:HB2	43:5G:46:LEU:HD21	2.01	0.42
44:5H:550:LEU:HD23	44:5H:550:LEU:HA	1.88	0.42
48:RA:217:LYS:HE2	48:RA:217:LYS:HB3	1.87	0.42
48:RA:277:ILE:HA	48:RA:290:VAL:O	2.19	0.42
54:RG:34:LYS:HD3	54:RG:34:LYS:HA	1.84	0.42
58:RN:65:ASN:OD1	58:RN:65:ASN:N	2.50	0.42
59:RO:208:TYR:O	59:RO:212:LEU:HB2	2.19	0.42
62:RS:382:LEU:HD11	62:RS:428:TYR:CG	2.55	0.42
3:SA:274:G:N1	3:SA:283:U:O2'	2.50	0.42
3:SA:1739:C:H2'	3:SA:1740:A:C8	2.53	0.42
20:3B:198:GLU:O	20:3B:221:ILE:HA	2.18	0.42
22:3E:160:ASP:HB3	22:3E:283:ILE:HG21	2.01	0.42
25:A4:532:ASN:N	25:A4:544:SER:O	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A4:566:LEU:HA	25:A4:566:LEU:HD23	1.83	0.42
29:AE:323:PHE:CZ	29:AE:332:ILE:HD11	2.54	0.42
29:AE:354:SER:O	29:AE:358:TYR:HB2	2.20	0.42
29:AE:422:LEU:HD12	29:AE:422:LEU:HA	1.87	0.42
31:AG:437:THR:OG1	31:AG:764:SER:O	2.31	0.42
31:AG:551:HIS:HA	31:AG:583:LYS:HE3	2.00	0.42
32:B1:749:TYR:HE2	36:BE:705:ILE:HG13	1.84	0.42
33:B2:297:LYS:HA	33:B2:300:GLU:HB2	2.02	0.42
33:B2:636:ASP:OD1	33:B2:636:ASP:N	2.52	0.42
33:B2:673:VAL:HG23	33:B2:683:ILE:HD13	2.01	0.42
33:B2:840:MET:HE1	33:B2:887:LEU:HD13	2.02	0.42
34:B3:188:GLU:HB2	34:B3:223:TRP:HZ2	1.83	0.42
34:B3:572:GLU:HG3	34:B3:600:LYS:HD2	2.01	0.42
38:5B:213:LYS:HZ2	38:5B:213:LYS:HG3	1.69	0.42
41:5E:453:SER:O	41:5E:455:HIS:ND1	2.53	0.42
48:RA:306:LYS:HA	48:RA:306:LYS:HD2	1.83	0.42
51:RD:1472:PRO:CG	52:RE:1189:LEU:HD12	2.49	0.42
51:RD:1695:TRP:HE1	51:RD:1711:VAL:HG11	1.84	0.42
52:RE:902:ILE:HD13	52:RE:902:ILE:HA	1.90	0.42
52:RE:1151:LYS:HE3	52:RE:1151:LYS:HB2	1.92	0.42
3:SA:-7:A:N7	45:5I:292:ARG:NH1	2.68	0.42
7:SH:74:LYS:O	48:RA:88:ASN:ND2	2.52	0.42
10:SK:163:PRO:HB3	10:SK:169:PRO:HA	2.01	0.42
20:3B:272:LYS:HD3	20:3B:275:CYS:HB3	2.01	0.42
31:AG:780:GLU:O	31:AG:782:THR:N	2.49	0.42
33:B2:39:GLY:O	33:B2:54:ILE:HG13	2.20	0.42
33:B2:294:ARG:O	33:B2:298:LYS:NZ	2.44	0.42
33:B2:432:TYR:O	33:B2:450:ARG:N	2.48	0.42
33:B2:497:VAL:HG12	33:B2:528:LEU:HB3	2.01	0.42
39:5C:215:LYS:HG2	39:5C:227:GLU:HG2	2.00	0.42
45:5I:456:GLU:HA	45:5I:459:LYS:HE2	2.01	0.42
46:5J:106:LEU:O	46:5J:146:ARG:NH1	2.44	0.42
49:RB:307:LYS:O	49:RB:311:ARG:HB3	2.19	0.42
52:RE:713:LEU:HB2	52:RE:716:SER:HB2	2.01	0.42
56:RK:81:ILE:HG22	56:RK:110:SER:HB3	2.01	0.42
57:RL:203:ASP:OD1	57:RL:203:ASP:N	2.52	0.42
58:RN:108:LYS:HA	58:RN:108:LYS:HD2	1.85	0.42
3:SA:99:C:H2'	3:SA:100:A:C8	2.54	0.42
3:SA:147:A:N7	3:SA:167:U:O2	2.52	0.42
3:SA:1659:A:H2'	3:SA:1660:A:C8	2.53	0.42
8:SI:51:VAL:HG23	8:SI:53:GLY:H	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:SI:188:GLU:HG3	45:5I:465:VAL:HG22	2.00	0.42
21:3D:4:ILE:HG23	21:3D:20:VAL:HG21	2.01	0.42
32:B1:25:ASP:OD1	32:B1:25:ASP:N	2.50	0.42
32:B1:46:LYS:HE2	32:B1:46:LYS:HB3	1.87	0.42
32:B1:275:LEU:HD22	32:B1:289:LEU:HD13	2.02	0.42
33:B2:534:ILE:HD11	33:B2:537:VAL:HG12	2.01	0.42
33:B2:836:ILE:HA	33:B2:839:VAL:HG12	2.00	0.42
36:BE:27:PHE:HB2	36:BE:655:THR:HG23	2.00	0.42
46:5J:216:ARG:HA	46:5J:216:ARG:HD3	1.82	0.42
52:RE:919:TRP:HE3	52:RE:920:LEU:HD12	1.85	0.42
52:RE:976:ILE:HA	52:RE:1042:ALA:O	2.19	0.42
59:RO:395:ILE:HD12	59:RO:469:LEU:HD11	2.02	0.42
62:RS:210:VAL:HG23	62:RS:212:LYS:HG2	2.00	0.42
2:5A:532:A:O2'	61:RQ:332:ASP:OD2	2.37	0.42
5:SF:68:ARG:HH21	5:SF:76:VAL:HG11	1.85	0.42
6:SG:23:VAL:HG23	14:SR:61:SER:HB3	2.00	0.42
21:3D:61:GLU:OE2	21:3D:77:SER:OG	2.36	0.42
26:A5:221:MET:HE3	26:A5:221:MET:HB3	1.75	0.42
31:AG:511:GLU:HG2	31:AG:528:ILE:HB	2.00	0.42
36:BE:21:SER:OG	36:BE:621:ASP:OD2	2.28	0.42
36:BE:523:ASP:OD1	36:BE:523:ASP:N	2.38	0.42
43:5G:154:ILE:O	43:5G:162:THR:HA	2.20	0.42
45:5I:464:THR:HG21	45:5I:468:TYR:HE1	1.85	0.42
53:RF:153:ASN:HD22	53:RF:154:GLU:HG2	1.84	0.42
55:RJ:217:ASP:O	55:RJ:221:LEU:HB2	2.20	0.42
55:RJ:940:LYS:HB2	55:RJ:940:LYS:HE2	1.73	0.42
56:RK:310:ARG:HB3	56:RK:353:THR:HG22	2.01	0.42
58:RN:501:PHE:HB3	58:RN:549:ILE:HG21	2.02	0.42
60:RP:1945:ILE:HA	60:RP:1948:SER:HB2	2.01	0.42
62:RS:432:ILE:HG23	62:RS:436:GLN:HB2	2.00	0.42
63:RT:124:LEU:HG	63:RT:151:ALA:HB1	2.02	0.42
3:SA:341:A:OP1	48:RA:121:ARG:NH2	2.48	0.42
3:SA:1068:C:H2'	3:SA:1069:A:C8	2.55	0.42
4:SC:181:LEU:HA	4:SC:181:LEU:HD23	1.86	0.42
5:SF:71:LYS:N	5:SF:91:THR:O	2.52	0.42
6:SG:114:ILE:HA	6:SG:117:THR:HG22	2.02	0.42
11:SM:92:HIS:NE2	11:SM:101:GLU:O	2.52	0.42
22:3E:172:ASP:O	22:3E:176:GLU:HG2	2.20	0.42
29:AE:487:THR:HG22	29:AE:488:GLY:H	1.85	0.42
29:AE:539:LEU:HD12	29:AE:540:LYS:HG3	2.01	0.42
32:B1:60:ALA:HB1	32:B1:102:VAL:HG12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B1:380:LEU:HD12	41:5E:484:MET:HE2	2.01	0.42
34:B3:674:SER:OG	34:B3:675:LYS:N	2.52	0.42
36:BE:62:ASP:O	36:BE:66:LEU:N	2.48	0.42
41:5E:427:SER:O	41:5E:431:GLN:HB2	2.19	0.42
50:RC:278:MET:O	50:RC:282:ASN:ND2	2.38	0.42
51:RD:1597:GLU:HB3	51:RD:1600:GLU:HB3	2.00	0.42
52:RE:379:MET:HE3	52:RE:381:HIS:HB2	2.02	0.42
52:RE:918:ARG:HD3	52:RE:1089:PHE:CZ	2.54	0.42
52:RE:1216:LYS:HG2	52:RE:1220:PHE:CE2	2.55	0.42
53:RF:73:GLN:HE21	53:RF:156:PHE:HD2	1.65	0.42
54:RG:190:GLN:NE2	54:RG:244:GLY:HA2	2.34	0.42
1:3A:118:A:C5	23:3F:218:ALA:HB2	2.55	0.42
9:SJ:67:TRP:O	9:SJ:71:GLY:CA	2.68	0.42
10:SK:45:ILE:HD12	10:SK:48:GLN:HE21	1.84	0.42
11:SM:70:ILE:HA	11:SM:125:VAL:O	2.20	0.42
11:SM:115:PHE:CG	11:SM:142:VAL:HG21	2.55	0.42
20:3C:124:SER:HA	20:3C:139:VAL:O	2.19	0.42
23:3F:560:ARG:HE	23:3F:560:ARG:HB3	1.75	0.42
26:A5:27:GLN:HG3	26:A5:59:LYS:HA	2.02	0.42
29:AE:25:ARG:HH21	45:5I:16:VAL:HG22	1.83	0.42
31:AG:313:LEU:HD23	31:AG:323:LEU:HB3	2.01	0.42
31:AG:559:LYS:HE2	31:AG:559:LYS:HB2	1.79	0.42
34:B3:367:VAL:HG12	34:B3:643:PHE:HE2	1.85	0.42
35:B8:504:THR:O	35:B8:504:THR:OG1	2.35	0.42
43:5G:175:ASP:O	58:RN:64:ARG:NH2	2.53	0.42
50:RC:219:ASP:OD2	50:RC:221:SER:OG	2.35	0.42
52:RE:486:GLN:HE22	52:RE:571:ARG:HH22	1.68	0.42
52:RE:1178:ASP:OD1	52:RE:1178:ASP:N	2.52	0.42
56:RK:56:ILE:HD13	56:RK:56:ILE:HA	1.89	0.42
56:RK:216:LEU:HB3	56:RK:223:VAL:HG21	2.01	0.42
57:RL:37:LEU:HD22	57:RL:149:VAL:HG11	2.01	0.42
57:RL:59:TYR:O	57:RL:108:TYR:N	2.53	0.42
60:RP:1877:ARG:NH2	60:RP:1913:SER:O	2.51	0.42
62:RS:364:PHE:HE1	62:RS:417:TRP:HE1	1.67	0.42
62:RS:373:LYS:HA	62:RS:376:LEU:HG	2.02	0.42
62:RS:382:LEU:HD21	62:RS:428:TYR:CZ	2.53	0.42
3:SA:565:C:N4	55:RJ:993:ASP:HB3	2.35	0.42
3:SA:1656:U:H3	3:SA:1743:U:H3	1.67	0.42
5:SF:47:PHE:HD2	5:SF:48:LEU:HD12	1.84	0.42
5:SF:220:THR:OG1	5:SF:221:ARG:N	2.53	0.42
8:SI:116:ARG:HB3	8:SI:117:THR:H	1.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:SO:58:HIS:O	12:SO:60:VAL:N	2.49	0.42
18:Sc:50:ALA:O	18:Sc:52:THR:N	2.53	0.42
25:A4:313:LYS:HA	25:A4:316:LYS:HZ3	1.84	0.42
26:A5:98:LYS:HE3	26:A5:98:LYS:HB2	1.88	0.42
32:B1:274:LEU:HD11	32:B1:286:LEU:HD13	2.02	0.42
34:B3:516:LYS:HE2	34:B3:516:LYS:HB2	1.89	0.42
36:BE:361:SER:HA	36:BE:636:PRO:HB2	2.02	0.42
43:5G:43:PRO:O	43:5G:47:ALA:HB2	2.19	0.42
48:RA:164:ARG:NH2	48:RA:174:ASN:O	2.51	0.42
52:RE:209:MET:HE3	52:RE:213:LEU:HD11	2.02	0.42
54:RG:128:VAL:HG22	54:RG:159:LEU:HD22	2.01	0.42
54:RH:176:ARG:NH2	54:RH:192:TYR:OH	2.52	0.42
55:RJ:773:THR:HG23	55:RJ:777:ARG:HD3	2.02	0.42
56:RK:190:SER:OG	56:RK:191:ILE:N	2.51	0.42
58:RN:700:LEU:HD23	58:RN:702:LEU:HG	2.01	0.42
62:RS:437:ARG:HD2	62:RS:460:LEU:HG	2.02	0.42
3:SA:575:C:O2	55:RJ:1052:SER:OG	2.28	0.42
4:SC:109:LYS:HA	4:SC:109:LYS:HD2	1.88	0.42
5:SF:31:PRO:HA	5:SF:81:THR:HB	2.01	0.42
7:SH:77:LEU:HD12	7:SH:95:LYS:HD3	2.00	0.42
7:SH:101:ILE:H	7:SH:101:ILE:HG13	1.72	0.42
15:SX:7:LEU:HD13	15:SX:34:ILE:HG12	2.02	0.42
20:3B:107:VAL:HG13	20:3B:141:TYR:HB3	2.01	0.42
22:3E:117:TYR:HA	22:3E:120:ILE:HG12	2.01	0.42
23:3F:303:LYS:HE3	23:3F:319:TYR:HE2	1.85	0.42
25:A4:98:SER:OG	25:A4:99:ILE:N	2.53	0.42
25:A4:213:TRP:HA	25:A4:225:LEU:HA	2.02	0.42
26:A5:224:CYS:SG	26:A5:225:VAL:N	2.93	0.42
27:A8:632:THR:HG22	28:A9:492:ILE:HD13	2.01	0.42
29:AE:91:ILE:HD13	29:AE:91:ILE:HA	1.90	0.42
29:AE:420:LYS:HB2	29:AE:420:LYS:HE2	1.91	0.42
31:AG:502:LYS:HD2	31:AG:564:PRO:HA	2.02	0.42
32:B1:147:GLN:HB2	32:B1:167:ASP:H	1.85	0.42
33:B2:26:ILE:HA	33:B2:27:PRO:HD3	1.94	0.42
33:B2:405:LEU:HD11	33:B2:673:VAL:HG21	2.02	0.42
33:B2:555:VAL:HG22	33:B2:569:LEU:HB2	2.02	0.42
34:B3:303:PHE:HA	34:B3:312:GLN:O	2.20	0.42
39:5C:191:ILE:HD13	39:5C:191:ILE:HA	1.87	0.42
39:5C:369:MET:HB3	39:5C:369:MET:HE2	1.79	0.42
46:5J:134:ARG:HD2	46:5J:134:ARG:HA	1.83	0.42
50:RC:128:ILE:HD12	50:RC:191:MET:HE3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5A:490:G:H1'	2:5A:495:G:H5'	2.01	0.41
3:SA:318:U:O2	3:SA:346:G:O6	2.37	0.41
3:SA:1489:U:N3	46:5J:202:ARG:O	2.53	0.41
20:3C:149:SER:OG	20:3C:150:LYS:N	2.52	0.41
20:3C:291:GLN:HA	20:3C:294:ARG:HG2	2.01	0.41
22:3E:333:LYS:HD3	40:5D:103:ASP:HB3	2.02	0.41
23:3F:301:ASP:OD1	23:3F:301:ASP:N	2.51	0.41
23:3F:368:LEU:HB3	23:3F:396:PHE:HE2	1.83	0.41
24:3G:44:LEU:HD23	24:3G:44:LEU:HA	1.87	0.41
25:A4:423:LYS:NZ	38:5B:167:ARG:HH11	2.18	0.41
29:AE:755:ARG:O	29:AE:759:ILE:HG12	2.20	0.41
30:AF:105:VAL:HG21	30:AF:142:THR:HG21	2.02	0.41
43:5G:42:LEU:HD12	43:5G:43:PRO:HD2	2.02	0.41
45:5I:336:HIS:CE1	45:5I:338:HIS:HB2	2.55	0.41
52:RE:501:ASN:HD21	52:RE:506:GLN:HE22	1.66	0.41
52:RE:974:PRO:HB2	52:RE:976:ILE:HG23	2.02	0.41
52:RE:1072:VAL:HA	52:RE:1075:LEU:HB2	2.02	0.41
54:RG:215:ASN:HB2	54:RG:218:ASP:HB2	2.01	0.41
58:RN:611:SER:OG	58:RN:612:THR:N	2.52	0.41
58:RN:616:LEU:HD13	58:RN:619:LEU:HD22	2.01	0.41
60:RP:129:ILE:O	60:RP:133:ILE:HG12	2.20	0.41
60:RP:1975:LYS:HA	60:RP:1975:LYS:HD2	1.80	0.41
63:RT:263:LEU:HA	63:RT:266:VAL:HG12	2.02	0.41
2:5A:150:G:C6	30:AF:380:ARG:HG3	2.54	0.41
2:5A:298:A:OP2	36:BE:103:ARG:NH2	2.45	0.41
12:SO:140:LYS:HA	12:SO:140:LYS:HD3	1.88	0.41
21:3D:268:MET:HA	21:3D:271:VAL:HG12	2.02	0.41
23:3F:421:ASN:ND2	23:3F:437:ARG:HA	2.34	0.41
23:3F:476:THR:HG22	23:3F:491:SER:HA	2.02	0.41
29:AE:35:TYR:O	29:AE:150:ARG:NH1	2.53	0.41
29:AE:664:PRO:HB2	29:AE:716:PHE:HE2	1.85	0.41
30:AF:366:TYR:OH	30:AF:371:GLU:OE1	2.23	0.41
31:AG:625:GLY:HA3	31:AG:662:VAL:HG11	2.02	0.41
31:AG:659:ILE:HG22	31:AG:674:THR:HB	2.01	0.41
32:B1:300:MET:HG2	32:B1:328:LEU:HD22	2.02	0.41
32:B1:498:ARG:HH11	32:B1:498:ARG:HD3	1.72	0.41
33:B2:538:ARG:HD3	33:B2:580:ASP:HA	2.02	0.41
34:B3:506:PHE:CE1	34:B3:518:TRP:HB2	2.55	0.41
36:BE:517:MET:HE3	36:BE:517:MET:HB2	1.85	0.41
36:BE:635:SER:OG	36:BE:637:ASN:OD1	2.30	0.41
39:5C:201:TYR:OH	39:5C:415:GLU:OE1	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5F:73:LYS:HE2	42:5F:73:LYS:HB3	1.88	0.41
42:5F:135:HIS:HB3	42:5F:160:TRP:CD1	2.55	0.41
59:RO:243:PRO:HA	59:RO:244:PRO:HD3	1.81	0.41
60:RP:1756:ILE:HG22	60:RP:1760:ASN:HD21	1.85	0.41
62:RS:255:SER:HB3	62:RS:258:VAL:HG22	2.01	0.41
2:5A:244:U:H1'	40:5D:93:MET:HE1	2.02	0.41
3:SA:360:A:O2'	3:SA:362:G:N2	2.45	0.41
7:SH:123:GLY:O	7:SH:127:THR:OG1	2.39	0.41
10:SK:154:LYS:HE2	10:SK:154:LYS:HB3	1.88	0.41
19:Sd:43:ASN:OD1	19:Sd:43:ASN:N	2.53	0.41
20:3B:150:LYS:NZ	20:3B:310:GLU:OE2	2.44	0.41
20:3C:242:ALA:HB3	20:3C:269:ILE:HA	2.01	0.41
21:3D:206:LEU:HB3	21:3D:216:PHE:HE1	1.84	0.41
28:A9:451:LEU:HA	28:A9:451:LEU:HD13	1.83	0.41
29:AE:148:PHE:HA	29:AE:151:ILE:HG12	2.01	0.41
29:AE:480:ASN:HA	29:AE:518:THR:HG21	2.02	0.41
30:AF:177:ILE:HA	30:AF:178:PRO:HD3	1.84	0.41
32:B1:275:LEU:HB2	32:B1:289:LEU:HD22	2.02	0.41
32:B1:363:ALA:HB2	32:B1:393:VAL:HG13	2.01	0.41
32:B1:501:SER:O	32:B1:506:SER:OG	2.38	0.41
32:B1:721:VAL:O	36:BE:579:ARG:NH2	2.53	0.41
37:B6:106:ASP:OD1	37:B6:106:ASP:N	2.38	0.41
39:5C:357:SER:O	39:5C:357:SER:OG	2.39	0.41
43:5G:289:TYR:HD1	43:5G:289:TYR:HA	1.68	0.41
51:RD:1695:TRP:HD1	51:RD:1696:LEU:HD22	1.86	0.41
52:RE:1010:GLU:HG2	52:RE:1011:ARG:HG2	2.01	0.41
56:RK:80:ILE:HD13	56:RK:80:ILE:HA	1.90	0.41
1:3A:49:C:H42	2:5A:467:A:H61	1.67	0.41
3:SA:647:G:N2	3:SA:687:G:H22	2.17	0.41
3:SA:886:U:OP1	4:SC:214:LYS:NZ	2.54	0.41
3:SA:1049:U:H5''	18:Sc:70:LYS:HG3	2.01	0.41
7:SH:51:LYS:HE2	7:SH:51:LYS:HB3	1.91	0.41
14:SR:97:VAL:HG12	14:SR:98:ASP:H	1.83	0.41
22:3E:388:LEU:HD12	22:3E:388:LEU:HA	1.89	0.41
23:3F:132:VAL:HG21	23:3F:505:LEU:HD21	2.02	0.41
23:3F:260:LEU:HD21	23:3F:283:VAL:HG11	2.02	0.41
23:3F:304:ILE:HB	23:3F:318:LEU:HG	2.03	0.41
24:3G:64:LEU:O	24:3G:66:HIS:N	2.43	0.41
29:AE:559:ASN:HB2	29:AE:614:LEU:HD12	2.02	0.41
29:AE:682:SER:O	29:AE:682:SER:OG	2.33	0.41
30:AF:34:GLN:O	30:AF:328:ALA:HA	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:AG:258:TYR:CD1	31:AG:414:ILE:HD11	2.55	0.41
31:AG:386:ASN:HD21	31:AG:389:LEU:HD11	1.86	0.41
32:B1:347:SER:HB2	32:B1:365:GLU:HB3	2.03	0.41
32:B1:559:ILE:HG21	32:B1:578:LYS:HA	2.03	0.41
33:B2:50:ASN:HB3	33:B2:62:LYS:HG3	2.02	0.41
34:B3:195:GLY:HA3	34:B3:245:SER:H	1.85	0.41
34:B3:242:GLN:HA	34:B3:263:GLY:HA3	2.01	0.41
34:B3:264:ASP:HA	34:B3:289:PHE:HB2	2.03	0.41
35:B8:174:ARG:NE	35:B8:179:ASP:OD2	2.44	0.41
35:B8:278:ASP:H	35:B8:282:ASN:HD22	1.67	0.41
35:B8:296:GLN:HB3	35:B8:316:GLY:HA2	2.03	0.41
45:5I:58:PHE:HE1	45:5I:373:ARG:HB3	1.85	0.41
45:5I:107:LYS:NZ	45:5I:109:HIS:O	2.45	0.41
52:RE:477:LEU:HD23	52:RE:477:LEU:HA	1.94	0.41
52:RE:975:LEU:HG	52:RE:1041:VAL:HG23	2.01	0.41
52:RE:978:ASP:HB3	52:RE:1012:LEU:HG	2.02	0.41
55:RJ:244:MET:HE2	55:RJ:271:ILE:HG22	2.02	0.41
55:RJ:1042:MET:HE2	55:RJ:1042:MET:HB3	1.87	0.41
56:RK:32:LYS:HG2	56:RK:75:ILE:HG13	2.02	0.41
57:RL:26:PHE:O	57:RL:149:VAL:HA	2.20	0.41
58:RN:481:MET:HE3	58:RN:481:MET:HB2	1.92	0.41
60:RP:1752:ASP:HA	60:RP:1755:GLU:HG2	2.03	0.41
62:RS:355:ALA:HA	62:RS:358:TYR:CE2	2.55	0.41
2:5A:248:G:OP1	40:5D:82:ARG:NH2	2.53	0.41
5:SF:181:VAL:HG23	5:SF:227:VAL:HG22	2.02	0.41
13:SP:127:ARG:HE	50:RC:130:ASN:HD21	1.68	0.41
14:SR:46:PHE:HA	14:SR:49:TYR:HB2	2.02	0.41
20:3C:151:LEU:HD13	20:3C:241:PHE:HE1	1.86	0.41
22:3E:163:ILE:HD13	22:3E:163:ILE:HA	1.86	0.41
23:3F:488:ILE:HG22	23:3F:524:ILE:HD13	2.02	0.41
25:A4:39:VAL:HG12	25:A4:41:PHE:H	1.85	0.41
25:A4:171:SER:O	25:A4:171:SER:OG	2.32	0.41
26:A5:32:GLN:HE22	26:A5:47:ASN:HB3	1.85	0.41
29:AE:526:LEU:HA	29:AE:529:VAL:HG12	2.01	0.41
30:AF:392:ILE:HD11	30:AF:417:VAL:HG23	2.03	0.41
31:AG:97:THR:OG1	31:AG:98:VAL:N	2.54	0.41
31:AG:544:LYS:HD3	31:AG:544:LYS:HA	1.88	0.41
33:B2:433:ALA:HA	33:B2:449:THR:HA	2.03	0.41
43:5G:133:LYS:HE3	43:5G:133:LYS:HB3	1.85	0.41
48:RA:164:ARG:HB2	48:RA:173:LEU:HB2	2.03	0.41
52:RE:708:LEU:HA	52:RE:709:PRO:HD3	1.96	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:RJ:552:LEU:HD23	55:RJ:552:LEU:HA	1.92	0.41
56:RK:286:SER:OG	56:RK:289:VAL:O	2.33	0.41
58:RN:515:HIS:O	58:RN:519:THR:OG1	2.32	0.41
60:RP:1923:ARG:HA	60:RP:1923:ARG:HD3	1.71	0.41
61:RQ:313:PHE:HE2	61:RQ:883:ILE:HD12	1.84	0.41
3:SA:88:U:H2'	3:SA:89:G:H8	1.85	0.41
3:SA:110:U:OP1	49:RB:227:ARG:NH1	2.53	0.41
3:SA:1156:C:H2'	3:SA:1157:A:C8	2.54	0.41
3:SA:1523:G:H1'	3:SA:1524:A:H5'	2.02	0.41
3:SA:1534:G:O2'	3:SA:1535:U:O2	2.29	0.41
20:3C:89:GLU:HG2	20:3C:98:ILE:HB	2.03	0.41
25:A4:154:ASP:OD1	25:A4:154:ASP:N	2.49	0.41
25:A4:394:TRP:HB3	25:A4:399:VAL:HG12	2.03	0.41
26:A5:551:ILE:HA	26:A5:554:PHE:CE2	2.56	0.41
29:AE:109:TRP:HB2	29:AE:142:TYR:CZ	2.56	0.41
31:AG:31:ASN:OD1	31:AG:31:ASN:N	2.52	0.41
31:AG:712:THR:HG22	31:AG:766:ILE:HG23	2.01	0.41
32:B1:150:THR:OG1	32:B1:164:THR:OG1	2.31	0.41
32:B1:659:ASN:OD1	32:B1:659:ASN:N	2.54	0.41
33:B2:164:ASP:HB3	33:B2:182:LYS:HB3	2.02	0.41
34:B3:218:ASP:OD1	34:B3:218:ASP:N	2.52	0.41
35:B8:137:ILE:HD13	35:B8:137:ILE:HA	1.86	0.41
35:B8:159:HIS:O	35:B8:163:ARG:HG2	2.21	0.41
35:B8:278:ASP:H	35:B8:282:ASN:ND2	2.18	0.41
37:B6:35:LYS:HE3	37:B6:35:LYS:HB3	1.88	0.41
37:B6:268:ASP:OD1	37:B6:268:ASP:N	2.53	0.41
37:B6:311:TYR:O	37:B6:315:GLU:HG2	2.21	0.41
39:5C:244:ASN:HB3	39:5C:446:PRO:HG3	2.02	0.41
41:5E:465:LEU:HD12	41:5E:465:LEU:HA	1.96	0.41
43:5G:9:ARG:HD3	43:5G:159:HIS:CD2	2.56	0.41
44:5H:542:TYR:CZ	44:5H:546:LYS:HG3	2.56	0.41
52:RE:518:PHE:CE2	52:RE:1075:LEU:HB3	2.48	0.41
52:RE:1094:LYS:HB3	52:RE:1096:TYR:HD1	1.85	0.41
53:RF:9:MET:HE1	53:RF:15:VAL:HG23	2.02	0.41
54:RH:180:LEU:HD23	54:RH:180:LEU:HA	1.88	0.41
64:RV:147:GLU:HG2	64:RV:150:GLN:H	1.85	0.41
1:3A:113:G:O6	24:3H:42:LYS:NZ	2.44	0.41
7:SH:70:PRO:O	7:SH:98:ARG:NH2	2.54	0.41
7:SH:115:LYS:HB2	7:SH:115:LYS:HE3	1.76	0.41
11:SM:82:ARG:HD3	11:SM:110:HIS:CD2	2.55	0.41
11:SM:115:PHE:HB2	11:SM:142:VAL:HG11	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:3C:210:MET:HE2	20:3C:210:MET:HB2	1.97	0.41
22:3E:192:PHE:CD2	22:3E:195:LEU:HB2	2.56	0.41
23:3F:158:THR:HG23	23:3F:548:ARG:HB2	2.02	0.41
23:3F:321:HIS:CE1	23:3F:340:GLY:H	2.39	0.41
23:3F:502:SER:OG	23:3F:504:ASN:OD1	2.32	0.41
26:A5:64:LYS:HB3	26:A5:77:ILE:HG13	2.02	0.41
28:A9:416:ILE:O	28:A9:420:ILE:CB	2.69	0.41
29:AE:549:LYS:HD3	29:AE:549:LYS:HA	1.91	0.41
30:AF:255:VAL:HA	30:AF:276:SER:HA	2.03	0.41
32:B1:410:THR:HG22	32:B1:426:THR:HG22	2.01	0.41
32:B1:652:ASP:N	32:B1:652:ASP:OD1	2.52	0.41
34:B3:468:ILE:HA	34:B3:469:PRO:HD3	1.83	0.41
46:5J:117:VAL:HG11	46:5J:149:ILE:HG13	2.02	0.41
48:RA:94:ASP:OD1	48:RA:94:ASP:N	2.54	0.41
52:RE:356:THR:HG23	52:RE:359:PHE:HB2	2.02	0.41
52:RE:841:ASN:ND2	52:RE:851:LYS:HG2	2.35	0.41
54:RG:232:LEU:HB3	54:RG:236:VAL:HG13	2.02	0.41
58:RN:283:ALA:HA	62:RS:381:ALA:HB1	2.03	0.41
58:RN:784:ILE:HA	58:RN:787:THR:HG22	2.03	0.41
62:RS:264:LYS:HB2	62:RS:264:LYS:HE3	1.81	0.41
3:SA:200:A:H2'	3:SA:201:G:C8	2.56	0.41
9:SJ:35:ASN:HD21	48:RA:119:ASN:HD22	1.69	0.41
9:SJ:58:LEU:HD21	48:RA:77:TYR:HB2	2.02	0.41
10:SK:63:ASP:OD1	10:SK:63:ASP:N	2.46	0.41
21:3D:24:GLN:NE2	21:3D:126:ASP:OD1	2.48	0.41
25:A4:389:ARG:HG2	25:A4:747:ILE:HG21	2.02	0.41
25:A4:428:ILE:HD12	25:A4:444:ARG:HH21	1.85	0.41
26:A5:49:ASN:OD1	26:A5:49:ASN:N	2.49	0.41
27:A8:703:LEU:HA	27:A8:704:PRO:HD3	1.96	0.41
29:AE:32:SER:OG	29:AE:33:LEU:N	2.54	0.41
29:AE:33:LEU:HD11	29:AE:151:ILE:HG22	2.03	0.41
29:AE:69:PHE:HE2	29:AE:104:LEU:HD13	1.85	0.41
29:AE:572:ARG:NH2	29:AE:632:THR:O	2.40	0.41
29:AE:597:HIS:HB3	29:AE:615:ASN:HB3	2.03	0.41
31:AG:439:ASN:ND2	31:AG:496:THR:O	2.54	0.41
31:AG:514:TYR:HA	31:AG:515:PRO:HD3	1.94	0.41
34:B3:90:LEU:O	34:B3:92:THR:N	2.54	0.41
36:BE:870:GLN:HA	36:BE:873:LYS:HE3	2.03	0.41
39:5C:504:LYS:HD3	39:5C:504:LYS:HA	1.83	0.41
48:RA:237:ARG:NE	48:RA:239:ASP:OD2	2.46	0.41
52:RE:217:LYS:HD3	52:RE:217:LYS:HA	1.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:RE:360:VAL:O	52:RE:363:THR:OG1	2.30	0.41
53:RF:153:ASN:ND2	53:RF:154:GLU:HG2	2.36	0.41
54:RG:40:ARG:O	54:RG:201:SER:HA	2.20	0.41
57:RL:185:ASN:OD1	57:RL:185:ASN:N	2.52	0.41
59:RO:226:ASP:OD1	59:RO:284:ARG:NE	2.54	0.41
60:RP:2073:GLU:HA	60:RP:2076:ARG:HG2	2.03	0.41
62:RS:238:SER:O	62:RS:238:SER:OG	2.33	0.41
2:5A:18:G:H2'	2:5A:19:A:H8	1.85	0.41
2:5A:329:A:O2'	2:5A:331:U:OP2	2.39	0.41
3:SA:153:G:O6	3:SA:161:U:O4	2.39	0.41
3:SA:406:U:O2'	48:RA:92:LYS:O	2.38	0.41
3:SA:1538:U:H1'	3:SA:1570:A:H61	1.84	0.41
4:SC:82:ARG:HD3	4:SC:105:PHE:HE1	1.86	0.41
7:SH:185:GLN:O	7:SH:189:HIS:ND1	2.44	0.41
9:SJ:36:THR:O	9:SJ:96:LEU:N	2.52	0.41
9:SJ:49:ARG:HA	9:SJ:49:ARG:HD3	1.83	0.41
13:SP:125:SER:HB2	13:SP:126:THR:H	1.73	0.41
20:3B:116:SER:OG	20:3B:120:GLU:OE1	2.28	0.41
21:3D:7:LEU:HD12	21:3D:99:ALA:HB3	2.02	0.41
21:3D:157:ALA:HB2	37:B6:292:TYR:CZ	2.56	0.41
22:3E:311:LYS:HB3	22:3E:311:LYS:HE2	1.84	0.41
23:3F:457:GLU:HG3	23:3F:461:LYS:HE2	2.02	0.41
24:3G:85:VAL:O	24:3G:89:ARG:HG2	2.21	0.41
25:A4:52:SER:HA	25:A4:104:TRP:CG	2.56	0.41
25:A4:249:ARG:NH2	25:A4:309:GLN:OE1	2.49	0.41
25:A4:513:LEU:HD12	25:A4:513:LEU:HA	1.89	0.41
25:A4:581:SER:HA	25:A4:594:PHE:O	2.21	0.41
28:A9:475:THR:HA	28:A9:478:ASN:HD22	1.86	0.41
29:AE:214:THR:HG23	29:AE:260:ILE:HG13	2.03	0.41
29:AE:227:ASN:OD1	29:AE:227:ASN:N	2.53	0.41
30:AF:287:LEU:HD13	30:AF:287:LEU:HA	1.96	0.41
31:AG:455:SER:O	31:AG:455:SER:OG	2.34	0.41
31:AG:591:GLU:O	31:AG:593:ASN:N	2.54	0.41
31:AG:666:ASN:OD1	31:AG:666:ASN:N	2.54	0.41
32:B1:492:SER:OG	32:B1:494:ASP:OD1	2.28	0.41
33:B2:17:ILE:CG2	33:B2:52:TRP:CH2	3.01	0.41
34:B3:567:VAL:HG22	34:B3:568:MET:HG2	2.02	0.41
35:B8:338:LYS:HE3	35:B8:338:LYS:HB2	1.89	0.41
36:BE:724:SER:O	36:BE:728:ARG:NH2	2.39	0.41
37:B6:15:MET:HE2	37:B6:15:MET:HB3	1.67	0.41
39:5C:117:LYS:HD2	39:5C:117:LYS:HA	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:5C:491:LYS:HA	39:5C:491:LYS:HD3	1.94	0.41
45:5I:400:LEU:HD12	45:5I:400:LEU:HA	1.89	0.41
46:5J:119:ARG:HD3	55:RJ:1113:ILE:HG13	2.02	0.41
48:RA:139:LYS:HA	48:RA:139:LYS:HD2	1.89	0.41
51:RD:1457:ALA:HA	51:RD:1458:PRO:HD3	1.95	0.41
52:RE:566:ILE:HD11	52:RE:686:LEU:HD21	2.03	0.41
52:RE:970:TRP:HB2	52:RE:971:LYS:HD3	2.02	0.41
54:RG:31:LEU:HD23	54:RG:31:LEU:HA	1.86	0.41
54:RG:116:THR:HG22	54:RG:118:ARG:H	1.86	0.41
54:RG:123:GLU:HB2	54:RG:161:LYS:HB2	2.03	0.41
54:RG:233:SER:OG	54:RG:234:ALA:N	2.54	0.41
54:RH:177:LYS:HG2	54:RH:203:CYS:HB3	2.03	0.41
55:RJ:43:MET:N	55:RJ:43:MET:SD	2.94	0.41
55:RJ:906:ASP:OD1	55:RJ:906:ASP:N	2.45	0.41
55:RJ:926:ILE:HG12	55:RJ:928:ILE:HG23	2.01	0.41
56:RK:117:LEU:HA	56:RK:166:VAL:O	2.21	0.41
60:RP:76:THR:O	60:RP:79:GLN:N	2.54	0.41
60:RP:879:PRO:O	60:RP:882:ASN:C	2.64	0.41
62:RS:288:ARG:O	62:RS:292:GLU:HG2	2.21	0.41
62:RS:407:GLU:HB2	62:RS:411:ARG:HD2	2.03	0.41
2:5A:333:G:H5'	42:5F:49:ARG:HE	1.86	0.41
3:SA:27:U:H4'	55:RJ:45:ARG:HG3	2.02	0.41
3:SA:1492:A:N6	55:RJ:941:ILE:O	2.46	0.41
3:SA:1655:A:O2'	33:B2:395:ARG:NH1	2.53	0.41
3:SA:1776:A:O2'	34:B3:136:ILE:O	2.34	0.41
4:SC:31:ASP:HA	4:SC:45:LYS:HA	2.03	0.41
13:SP:29:HIS:CD2	13:SP:41:ARG:HB2	2.56	0.41
22:3E:201:ASP:HB3	22:3E:204:ALA:HB3	2.03	0.41
25:A4:425:ASP:OD2	25:A4:444:ARG:NH2	2.53	0.41
27:A8:532:PHE:HD1	27:A8:534:LEU:H	1.69	0.41
30:AF:136:ASP:OD1	30:AF:137:ASN:N	2.54	0.41
30:AF:364:SER:O	30:AF:364:SER:OG	2.26	0.41
30:AF:492:ARG:HD3	30:AF:492:ARG:HA	1.80	0.41
32:B1:263:VAL:HG13	32:B1:277:VAL:HG13	2.03	0.41
33:B2:241:LYS:HB2	33:B2:241:LYS:HE3	1.89	0.41
33:B2:911:GLN:HA	33:B2:914:LEU:HG	2.02	0.41
34:B3:410:ASN:OD1	34:B3:435:ALA:N	2.52	0.41
36:BE:83:LEU:HA	36:BE:91:TYR:O	2.21	0.41
37:B6:26:LYS:HA	37:B6:29:VAL:HG12	2.03	0.41
37:B6:306:LYS:HE3	37:B6:306:LYS:HB2	1.77	0.41
45:5I:225:LEU:HA	45:5I:225:LEU:HD23	1.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:RD:1622:ARG:NH1	51:RD:1626:GLN:HE21	2.19	0.41
52:RE:177:ASN:HB2	52:RE:213:LEU:HB2	2.03	0.41
58:RN:668:LEU:HD23	58:RN:671:TYR:HD2	1.86	0.41
60:RP:149:GLU:HA	60:RP:152:PHE:CD2	2.56	0.41
64:RV:229:ASN:OD1	64:RV:229:ASN:N	2.54	0.41
3:SA:304:U:H5''	11:SM:136:ARG:HH21	1.86	0.40
7:SH:38:GLY:N	7:SH:48:TYR:O	2.54	0.40
8:SI:60:ILE:HB	8:SI:92:PHE:HD1	1.86	0.40
15:SX:102:VAL:O	15:SX:113:HIS:N	2.54	0.40
22:3E:162:MET:HB3	22:3E:162:MET:HE2	1.86	0.40
23:3F:212:LYS:HB2	23:3F:212:LYS:HE3	1.88	0.40
25:A4:250:THR:OG1	25:A4:251:ASP:N	2.53	0.40
28:A9:432:LYS:HA	28:A9:432:LYS:HD3	1.85	0.40
29:AE:688:PHE:HB3	29:AE:730:GLN:HE21	1.86	0.40
30:AF:183:LEU:HD12	30:AF:183:LEU:HA	1.85	0.40
30:AF:397:TRP:CZ3	30:AF:425:GLY:HA3	2.56	0.40
32:B1:519:LEU:HD13	32:B1:581:THR:HG22	2.03	0.40
32:B1:523:MET:HE2	32:B1:523:MET:HB2	1.76	0.40
34:B3:678:TRP:CE3	34:B3:697:VAL:HG23	2.56	0.40
40:5D:70:ARG:HD3	40:5D:78:LEU:HD11	2.02	0.40
46:5J:77:LYS:HA	46:5J:77:LYS:HD2	1.84	0.40
52:RE:110:LEU:HD21	52:RE:368:LEU:HD23	2.03	0.40
52:RE:202:SER:OG	52:RE:203:ILE:N	2.54	0.40
52:RE:676:PRO:HB2	52:RE:678:ILE:HG22	2.03	0.40
52:RE:1173:GLY:CA	52:RE:1179:LYS:HB2	2.52	0.40
53:RF:62:SER:HA	53:RF:66:HIS:NE2	2.36	0.40
54:RG:176:ARG:HA	54:RG:176:ARG:HD2	1.91	0.40
56:RK:184:ASP:OD1	56:RK:185:ARG:N	2.53	0.40
58:RN:504:ILE:HA	58:RN:507:LEU:HG	2.03	0.40
2:5A:393:C:O4'	42:5F:28:ARG:NH2	2.54	0.40
3:SA:844:A:H2'	3:SA:845:G:C8	2.57	0.40
3:SA:1525:A:N3	3:SA:1589:C:O2'	2.53	0.40
3:SA:1672:G:H2'	3:SA:1673:G:C8	2.55	0.40
5:SF:97:GLU:HB3	5:SF:99:PHE:CE2	2.56	0.40
15:SX:110:ILE:HD12	15:SX:126:LEU:HD22	2.02	0.40
20:3B:248:ASP:OD1	20:3B:248:ASP:N	2.37	0.40
20:3C:202:ARG:HA	20:3C:202:ARG:HD2	1.96	0.40
22:3E:88:ILE:HA	22:3E:106:ASN:O	2.22	0.40
24:3G:41:THR:HG21	24:3G:66:HIS:CE1	2.55	0.40
24:3H:33:LEU:HD11	24:3H:100:ALA:HB1	2.02	0.40
25:A4:141:SER:O	25:A4:141:SER:OG	2.34	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:AF:57:VAL:HG21	30:AF:327:LEU:HD11	2.04	0.40
30:AF:426:LYS:HB3	30:AF:429:VAL:HB	2.03	0.40
32:B1:430:ARG:HH21	41:5E:458:PRO:HB2	1.85	0.40
33:B2:639:VAL:HG22	33:B2:653:LEU:HB2	2.03	0.40
34:B3:25:VAL:HG22	34:B3:294:LEU:HD13	2.03	0.40
34:B3:313:LEU:O	34:B3:330:THR:OG1	2.33	0.40
36:BE:265:SER:O	36:BE:265:SER:OG	2.39	0.40
36:BE:290:ILE:HG23	36:BE:291:HIS:CD2	2.56	0.40
37:B6:304:LEU:O	37:B6:308:THR:HG23	2.21	0.40
39:5C:340:LEU:HD22	39:5C:403:VAL:HG11	2.03	0.40
46:5J:106:LEU:HD23	46:5J:106:LEU:HA	1.95	0.40
46:5J:195:GLN:O	46:5J:199:THR:HG22	2.22	0.40
52:RE:1216:LYS:HZ2	52:RE:1236:THR:CG2	2.27	0.40
59:RO:422:ILE:HD13	59:RO:422:ILE:HA	1.93	0.40
60:RP:100:GLU:OE2	60:RP:146:ASN:ND2	2.54	0.40
62:RS:245:VAL:O	62:RS:249:THR:HG23	2.22	0.40
3:SA:16:G:H4'	47:5K:159:GLY:HA2	2.03	0.40
3:SA:268:C:H2'	3:SA:269:G:C8	2.56	0.40
3:SA:298:C:H5''	5:SF:38:LEU:HG	2.02	0.40
3:SA:625:C:H2'	3:SA:626:U:C6	2.57	0.40
5:SF:106:LYS:HE3	5:SF:106:LYS:HB3	1.88	0.40
10:SK:79:ARG:HE	10:SK:79:ARG:HB3	1.78	0.40
20:3C:165:ALA:HB3	20:3C:168:LYS:HD3	2.04	0.40
21:3D:182:ASP:OD1	21:3D:314:ARG:NH2	2.39	0.40
22:3E:248:THR:OG1	22:3E:251:ASP:OD1	2.29	0.40
22:3E:367:ALA:O	22:3E:371:LEU:HB3	2.22	0.40
22:3E:431:ALA:O	35:B8:160:TYR:OH	2.28	0.40
23:3F:263:TRP:HA	23:3F:269:SER:O	2.22	0.40
23:3F:465:GLN:HG2	24:3H:6:PRO:HG3	2.03	0.40
25:A4:429:SER:OG	25:A4:430:THR:N	2.52	0.40
31:AG:29:THR:HB	31:AG:198:LEU:HD11	2.03	0.40
31:AG:560:ILE:HG22	31:AG:575:THR:HG22	2.03	0.40
34:B3:415:TRP:HA	34:B3:425:ASP:O	2.20	0.40
35:B8:431:GLU:H	35:B8:431:GLU:HG2	1.71	0.40
37:B6:110:TRP:CD2	37:B6:136:LEU:HD13	2.56	0.40
39:5C:114:TYR:HA	39:5C:128:THR:O	2.22	0.40
39:5C:495:SER:OG	39:5C:523:GLU:OE2	2.27	0.40
41:5E:358:THR:HG22	58:RN:88:LYS:HB3	2.03	0.40
48:RA:343:ILE:HG22	48:RA:346:LEU:H	1.87	0.40
52:RE:310:PRO:HA	52:RE:333:ASN:HD21	1.87	0.40
52:RE:1204:VAL:HG23	52:RE:1204:VAL:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:RJ:60:ASP:OD2	55:RJ:62:THR:OG1	2.32	0.40
55:RJ:74:VAL:HG11	55:RJ:82:LYS:HA	2.03	0.40
55:RJ:563:CYS:SG	56:RK:327:ARG:NH2	2.95	0.40
57:RL:60:LYS:HB3	57:RL:108:TYR:CD2	2.56	0.40
58:RN:424:LYS:O	58:RN:428:VAL:HG23	2.20	0.40
62:RS:446:GLN:HG2	62:RS:447:ARG:HE	1.86	0.40
1:3A:253:G:OP2	24:3H:95:ARG:NH1	2.54	0.40
3:SA:259:U:O2'	3:SA:261:U:OP2	2.32	0.40
3:SA:514:G:H2'	3:SA:515:A:H8	1.87	0.40
3:SA:1463:C:H2'	3:SA:1464:G:O4'	2.22	0.40
3:SA:1464:G:H2'	3:SA:1465:C:C6	2.57	0.40
3:SA:1480:G:H2'	3:SA:1481:C:O4'	2.22	0.40
4:SC:87:ARG:NH1	4:SC:89:ASP:OD2	2.47	0.40
15:SX:66:ASN:OD1	15:SX:66:ASN:N	2.50	0.40
20:3B:227:PRO:HG2	20:3B:255:LEU:HB3	2.02	0.40
21:3D:86:LEU:HD21	21:3D:98:LEU:HD13	2.03	0.40
21:3D:315:LEU:HD12	21:3D:315:LEU:HA	1.90	0.40
22:3E:215:ARG:NH1	22:3E:244:GLY:O	2.54	0.40
22:3E:299:LEU:HD22	22:3E:320:LEU:HD23	2.03	0.40
22:3E:306:LEU:HG	22:3E:375:ALA:HB2	2.04	0.40
22:3E:359:ILE:HD13	22:3E:398:LEU:HD13	2.03	0.40
25:A4:442:VAL:O	25:A4:448:THR:OG1	2.26	0.40
30:AF:371:GLU:HG3	35:B8:287:SER:OG	2.21	0.40
31:AG:409:LYS:HG2	31:AG:489:ASN:HA	2.03	0.40
32:B1:423:ARG:HD3	32:B1:423:ARG:HA	1.88	0.40
34:B3:189:HIS:NE2	34:B3:215:GLY:HA3	2.37	0.40
34:B3:393:SER:OG	34:B3:394:LEU:N	2.53	0.40
36:BE:366:MET:HE3	36:BE:366:MET:HB2	1.80	0.40
36:BE:743:ARG:HB2	41:5E:475:SER:HA	2.02	0.40
50:RC:149:ASN:HD21	64:RV:274:LYS:HD3	1.86	0.40
53:RF:47:SER:OG	53:RF:48:ASN:N	2.54	0.40
53:RF:71:VAL:HG11	53:RF:84:VAL:HG21	2.03	0.40
58:RN:572:LEU:HB3	58:RN:667:LEU:HD13	2.04	0.40
58:RN:710:ILE:HD13	58:RN:710:ILE:HA	1.91	0.40
59:RO:205:ASP:HA	59:RO:206:PRO:HD3	1.89	0.40
59:RO:326:LEU:HA	59:RO:326:LEU:HD12	1.90	0.40
59:RO:384:ALA:HA	59:RO:387:THR:HG22	2.03	0.40
1:3A:59:G:OP1	32:B1:573:ASN:ND2	2.43	0.40
3:SA:56:U:O2	3:SA:91:G:N2	2.54	0.40
3:SA:1071:U:H2'	3:SA:1072:C:C6	2.56	0.40
9:SJ:191:PHE:HA	9:SJ:194:ARG:HE	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:SK:37:LYS:O	44:5H:561:SER:OG	2.39	0.40
14:SR:47:LYS:HD2	14:SR:47:LYS:HA	1.93	0.40
17:SZ:13:ILE:HD11	17:SZ:22:GLN:HE21	1.85	0.40
21:3D:59:ALA:HB1	37:B6:292:TYR:HE1	1.87	0.40
23:3F:68:LYS:HE3	23:3F:68:LYS:HB2	1.93	0.40
26:A5:444:ALA:HB2	26:A5:452:LEU:HD12	2.03	0.40
27:A8:642:LEU:HD12	28:A9:499:ILE:HG23	2.04	0.40
29:AE:677:SER:HA	29:AE:678:PRO:HD3	1.98	0.40
30:AF:178:PRO:HD2	30:AF:223:PRO:HA	2.02	0.40
31:AG:865:LYS:HE2	31:AG:865:LYS:HB3	1.81	0.40
32:B1:103:LYS:HB3	32:B1:103:LYS:HE3	1.92	0.40
32:B1:567:ASP:HB3	42:5F:144:ASN:ND2	2.36	0.40
33:B2:85:LEU:HD12	33:B2:94:LEU:HD11	2.04	0.40
34:B3:51:LYS:H	34:B3:51:LYS:HG2	1.66	0.40
34:B3:698:LEU:HD23	34:B3:698:LEU:HA	1.92	0.40
39:5C:258:LEU:O	39:5C:267:LEU:N	2.54	0.40
39:5C:307:LYS:HA	39:5C:307:LYS:HD3	1.89	0.40
42:5F:120:MET:HE3	42:5F:120:MET:HB2	1.98	0.40
46:5J:121:LEU:HD22	46:5J:141:TRP:HH2	1.87	0.40
52:RE:883:LEU:HD22	52:RE:1051:LEU:HA	2.03	0.40
55:RJ:286:THR:H	55:RJ:298:VAL:HG12	1.86	0.40
60:RP:2009:LYS:HD3	60:RP:2009:LYS:HA	1.88	0.40
62:RS:258:VAL:O	62:RS:262:ALA:CB	2.69	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	169/333 (50%)	44 (26%)	2 (1%)
2	5A	365/700 (52%)	104 (28%)	7 (1%)
3	SA	1303/1808 (72%)	494 (37%)	19 (1%)
All	All	1837/2841 (64%)	642 (34%)	28 (1%)

All (642) RNA backbone outliers are listed below:

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

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Mol	Chain	Res	Type
1	3A	311	G
1	3A	313	A
1	3A	314	C
1	3A	322	A
1	3A	324	U
1	3A	325	C
1	3A	328	A
1	3A	329	C
1	3A	332	G
2	5A	5	G
2	5A	6	A
2	5A	7	A
2	5A	8	A
2	5A	11	A
2	5A	13	U
2	5A	14	U
2	5A	15	G
2	5A	63	G
2	5A	64	U
2	5A	70	A
2	5A	82	A
2	5A	83	U
2	5A	86	C
2	5A	87	C
2	5A	90	G
2	5A	143	A
2	5A	144	C
2	5A	150	G
2	5A	151	U
2	5A	152	U
2	5A	156	U
2	5A	159	A
2	5A	161	A
2	5A	162	U
2	5A	163	G
2	5A	167	U
2	5A	168	G
2	5A	169	A
2	5A	235	A
2	5A	240	C
2	5A	267	U
2	5A	268	G

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Mol	Chain	Res	Type
2	5A	279	A
2	5A	280	A
2	5A	281	G
2	5A	292	A
2	5A	294	U
2	5A	304	U
2	5A	305	A
2	5A	309	A
2	5A	310	U
2	5A	311	C
2	5A	312	U
2	5A	313	A
2	5A	321	G
2	5A	322	A
2	5A	325	U
2	5A	326	C
2	5A	328	A
2	5A	337	G
2	5A	339	A
2	5A	346	G
2	5A	350	A
2	5A	353	A
2	5A	354	G
2	5A	355	C
2	5A	359	U
2	5A	361	G
2	5A	363	A
2	5A	364	A
2	5A	368	U
2	5A	369	G
2	5A	370	U
2	5A	371	G
2	5A	372	A
2	5A	373	U
2	5A	381	G
2	5A	385	A
2	5A	386	A
2	5A	391	C
2	5A	393	C
2	5A	395	C
2	5A	407	A
2	5A	440	U

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Mol	Chain	Res	Type
2	5A	443	G
2	5A	444	U
2	5A	468	A
2	5A	472	A
2	5A	474	A
2	5A	481	U
2	5A	482	A
2	5A	485	G
2	5A	487	A
2	5A	488	U
2	5A	490	G
2	5A	491	U
2	5A	493	A
2	5A	519	A
2	5A	525	U
2	5A	526	U
2	5A	536	A
2	5A	537	G
2	5A	539	A
2	5A	540	U
2	5A	541	U
2	5A	542	U
2	5A	548	A
2	5A	549	G
2	5A	583	U
2	5A	586	A
2	5A	587	G
2	5A	589	U
2	5A	591	U
3	SA	-6	A
3	SA	-5	G
3	SA	-4	A
3	SA	-1	G
3	SA	0	U
3	SA	1	U
3	SA	2	A
3	SA	17	C
3	SA	18	C
3	SA	19	A
3	SA	21	U
3	SA	23	G
3	SA	25	C

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Mol	Chain	Res	Type
3	SA	26	A
3	SA	29	U
3	SA	35	U
3	SA	36	C
3	SA	37	U
3	SA	50	C
3	SA	51	A
3	SA	52	U
3	SA	53	G
3	SA	55	A
3	SA	56	U
3	SA	57	G
3	SA	60	U
3	SA	61	A
3	SA	63	G
3	SA	65	A
3	SA	66	U
3	SA	67	A
3	SA	68	A
3	SA	69	G
3	SA	72	A
3	SA	73	U
3	SA	74	U
3	SA	75	U
3	SA	77	U
3	SA	81	G
3	SA	85	A
3	SA	92	A
3	SA	95	G
3	SA	96	G
3	SA	97	C
3	SA	100	A
3	SA	102	U
3	SA	103	A
3	SA	104	A
3	SA	105	A
3	SA	106	U
3	SA	114	C
3	SA	115	G
3	SA	116	U
3	SA	119	A
3	SA	127	G

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Mol	Chain	Res	Type
3	SA	128	U
3	SA	129	U
3	SA	130	C
3	SA	131	C
3	SA	141	U
3	SA	145	A
3	SA	146	U
3	SA	147	A
3	SA	149	C
3	SA	153	G
3	SA	159	U
3	SA	160	C
3	SA	161	U
3	SA	168	A
3	SA	174	U
3	SA	175	G
3	SA	176	C
3	SA	177	U
3	SA	182	A
3	SA	183	U
3	SA	184	C
3	SA	187	G
3	SA	188	A
3	SA	190	C
3	SA	191	C
3	SA	192	U
3	SA	193	U
3	SA	194	U
3	SA	195	G
3	SA	197	A
3	SA	202	A
3	SA	203	U
3	SA	204	G
3	SA	206	A
3	SA	210	A
3	SA	211	U
3	SA	214	G
3	SA	226	A
3	SA	228	G
3	SA	230	C
3	SA	233	C
3	SA	234	G

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Mol	Chain	Res	Type
3	SA	236	A
3	SA	237	C
3	SA	238	U
3	SA	239	C
3	SA	240	U
3	SA	241	U
3	SA	242	U
3	SA	243	G
3	SA	254	A
3	SA	256	A
3	SA	258	C
3	SA	261	U
3	SA	262	U
3	SA	265	A
3	SA	266	A
3	SA	267	U
3	SA	272	U
3	SA	273	G
3	SA	275	C
3	SA	276	C
3	SA	277	U
3	SA	278	U
3	SA	279	G
3	SA	280	U
3	SA	281	G
3	SA	283	U
3	SA	290	G
3	SA	308	C
3	SA	309	C
3	SA	311	U
3	SA	312	A
3	SA	316	A
3	SA	319	U
3	SA	320	U
3	SA	321	C
3	SA	324	U
3	SA	325	G
3	SA	333	A
3	SA	334	G
3	SA	337	G
3	SA	338	C
3	SA	350	U

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Mol	Chain	Res	Type
3	SA	352	A
3	SA	355	G
3	SA	357	G
3	SA	359	A
3	SA	360	A
3	SA	361	C
3	SA	362	G
3	SA	365	G
3	SA	366	A
3	SA	369	A
3	SA	371	G
3	SA	373	G
3	SA	374	U
3	SA	375	U
3	SA	377	G
3	SA	379	U
3	SA	382	C
3	SA	383	G
3	SA	386	G
3	SA	387	A
3	SA	390	G
3	SA	400	A
3	SA	401	A
3	SA	402	C
3	SA	403	G
3	SA	411	C
3	SA	416	A
3	SA	417	A
3	SA	418	G
3	SA	419	G
3	SA	421	A
3	SA	422	G
3	SA	423	G
3	SA	424	C
3	SA	425	A
3	SA	426	G
3	SA	429	G
3	SA	436	A
3	SA	437	A
3	SA	439	U
3	SA	440	U
3	SA	441	A

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Mol	Chain	Res	Type
3	SA	444	C
3	SA	445	A
3	SA	448	C
3	SA	454	U
3	SA	455	C
3	SA	456	A
3	SA	457	G
3	SA	468	A
3	SA	469	C
3	SA	470	A
3	SA	471	A
3	SA	473	A
3	SA	477	A
3	SA	480	G
3	SA	486	G
3	SA	487	G
3	SA	496	G
3	SA	501	U
3	SA	502	U
3	SA	505	A
3	SA	506	A
3	SA	514	G
3	SA	520	A
3	SA	534	A
3	SA	538	A
3	SA	539	G
3	SA	541	A
3	SA	542	A
3	SA	543	C
3	SA	545	A
3	SA	557	G
3	SA	558	U
3	SA	563	U
3	SA	564	G
3	SA	565	C
3	SA	570	A
3	SA	572	C
3	SA	574	G
3	SA	575	C
3	SA	578	U
3	SA	579	A
3	SA	580	A

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Mol	Chain	Res	Type
3	SA	583	C
3	SA	584	C
3	SA	585	A
3	SA	586	G
3	SA	587	C
3	SA	594	A
3	SA	595	G
3	SA	602	U
3	SA	603	U
3	SA	604	A
3	SA	606	A
3	SA	608	U
3	SA	609	U
3	SA	610	G
3	SA	611	U
3	SA	612	U
3	SA	613	G
3	SA	614	C
3	SA	615	A
3	SA	616	G
3	SA	635	A
3	SA	636	A
3	SA	638	U
3	SA	644	C
3	SA	648	G
3	SA	652	G
3	SA	654	C
3	SA	656	G
3	SA	657	U
3	SA	658	C
3	SA	677	G
3	SA	678	A
3	SA	686	C
3	SA	687	G
3	SA	688	G
3	SA	689	G
3	SA	691	C
3	SA	692	C
3	SA	827	C
3	SA	828	U
3	SA	840	U
3	SA	841	U

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Mol	Chain	Res	Type
3	SA	848	C
3	SA	859	A
3	SA	860	U
3	SA	863	A
3	SA	864	U
3	SA	865	A
3	SA	873	U
3	SA	877	G
3	SA	894	U
3	SA	901	G
3	SA	904	G
3	SA	906	A
3	SA	912	U
3	SA	913	G
3	SA	914	G
3	SA	926	A
3	SA	930	A
3	SA	933	A
3	SA	934	C
3	SA	935	U
3	SA	945	U
3	SA	951	A
3	SA	953	G
3	SA	960	U
3	SA	966	A
3	SA	969	C
3	SA	970	A
3	SA	1022	C
3	SA	1024	U
3	SA	1025	A
3	SA	1026	A
3	SA	1027	A
3	SA	1031	U
3	SA	1032	G
3	SA	1037	C
3	SA	1039	A
3	SA	1040	G
3	SA	1052	U
3	SA	1053	G
3	SA	1056	U
3	SA	1057	U
3	SA	1059	U

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Mol	Chain	Res	Type
3	SA	1060	U
3	SA	1062	A
3	SA	1063	U
3	SA	1076	A
3	SA	1079	U
3	SA	1081	A
3	SA	1082	C
3	SA	1084	A
3	SA	1085	G
3	SA	1086	A
3	SA	1106	U
3	SA	1107	G
3	SA	1108	G
3	SA	1109	G
3	SA	1110	G
3	SA	1111	G
3	SA	1114	G
3	SA	1118	G
3	SA	1119	G
3	SA	1122	G
3	SA	1125	A
3	SA	1126	G
3	SA	1127	G
3	SA	1128	C
3	SA	1129	U
3	SA	1131	A
3	SA	1132	A
3	SA	1145	U
3	SA	1146	G
3	SA	1158	C
3	SA	1164	G
3	SA	1178	G
3	SA	1191	U
3	SA	1192	C
3	SA	1193	A
3	SA	1195	C
3	SA	1196	A
3	SA	1197	C
3	SA	1198	G
3	SA	1199	G
3	SA	1200	G
3	SA	1201	G

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Mol	Chain	Res	Type
3	SA	1202	A
3	SA	1205	C
3	SA	1206	U
3	SA	1208	A
3	SA	1210	C
3	SA	1213	G
3	SA	1217	A
3	SA	1218	G
3	SA	1219	A
3	SA	1220	C
3	SA	1223	A
3	SA	1227	A
3	SA	1228	G
3	SA	1229	G
3	SA	1230	A
3	SA	1232	U
3	SA	1233	G
3	SA	1235	C
3	SA	1236	A
3	SA	1252	C
3	SA	1253	U
3	SA	1254	U
3	SA	1255	G
3	SA	1258	U
3	SA	1263	G
3	SA	1266	U
3	SA	1268	G
3	SA	1271	G
3	SA	1272	U
3	SA	1273	G
3	SA	1275	A
3	SA	1276	U
3	SA	1436	A
3	SA	1440	C
3	SA	1441	C
3	SA	1442	U
3	SA	1443	U
3	SA	1449	U
3	SA	1450	U
3	SA	1453	G
3	SA	1457	C
3	SA	1461	C

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Mol	Chain	Res	Type
3	SA	1469	A
3	SA	1472	C
3	SA	1473	U
3	SA	1474	G
3	SA	1475	A
3	SA	1476	C
3	SA	1482	C
3	SA	1488	G
3	SA	1492	A
3	SA	1493	A
3	SA	1496	U
3	SA	1498	G
3	SA	1506	G
3	SA	1517	U
3	SA	1518	C
3	SA	1520	U
3	SA	1521	G
3	SA	1522	U
3	SA	1523	G
3	SA	1524	A
3	SA	1527	C
3	SA	1533	C
3	SA	1535	U
3	SA	1536	G
3	SA	1537	C
3	SA	1539	G
3	SA	1569	A
3	SA	1570	A
3	SA	1573	A
3	SA	1582	U
3	SA	1584	G
3	SA	1590	G
3	SA	1594	G
3	SA	1595	U
3	SA	1596	C
3	SA	1601	G
3	SA	1602	C
3	SA	1607	G
3	SA	1614	A
3	SA	1618	C
3	SA	1628	U
3	SA	1630	U

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Mol	Chain	Res	Type
3	SA	1633	A
3	SA	1651	A
3	SA	1655	A
3	SA	1657	U
3	SA	1658	G
3	SA	1659	A
3	SA	1661	U
3	SA	1665	U
3	SA	1670	G
3	SA	1675	C
3	SA	1677	C
3	SA	1679	G
3	SA	1680	G
3	SA	1681	A
3	SA	1682	U
3	SA	1683	C
3	SA	1687	U
3	SA	1689	A
3	SA	1692	G
3	SA	1693	A
3	SA	1696	G
3	SA	1697	G
3	SA	1700	C
3	SA	1708	U
3	SA	1709	C
3	SA	1710	U
3	SA	1711	C
3	SA	1713	G
3	SA	1717	G
3	SA	1718	G
3	SA	1719	A
3	SA	1721	A
3	SA	1724	U
3	SA	1725	U
3	SA	1727	G
3	SA	1728	A
3	SA	1731	A
3	SA	1732	A
3	SA	1736	G
3	SA	1737	G
3	SA	1742	U
3	SA	1743	U

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Mol	Chain	Res	Type
3	SA	1745	G
3	SA	1749	A
3	SA	1750	A
3	SA	1755	A
3	SA	1756	A
3	SA	1757	G
3	SA	1758	U
3	SA	1759	C
3	SA	1761	U
3	SA	1764	C
3	SA	1766	A
3	SA	1767	G
3	SA	1768	G
3	SA	1769	U
3	SA	1779	U
3	SA	1780	G
3	SA	1781	A
3	SA	1782	A
3	SA	1789	G

All (28) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	3A	198	U
1	3A	248	G
2	5A	312	U
2	5A	358	G
2	5A	363	A
2	5A	368	U
2	5A	487	A
2	5A	492	G
2	5A	536	A
3	SA	-7	A
3	SA	0	U
3	SA	56	U
3	SA	68	A
3	SA	272	U
3	SA	372	G
3	SA	401	A
3	SA	417	A
3	SA	538	A
3	SA	542	A

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Mol	Chain	Res	Type
3	SA	579	A
3	SA	602	U
3	SA	1031	U
3	SA	1052	U
3	SA	1084	A
3	SA	1197	C
3	SA	1521	G
3	SA	1594	G
3	SA	1632	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [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	$\# Z > 2$
68	GTP	RJ	1201	69	33,34,34	0.56	0	50,54,54	0.72	1 (2%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
68	GTP	RJ	1201	69	-	3/22/38/38	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

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

There are no chirality outliers.

All (3) torsion outliers are listed below:

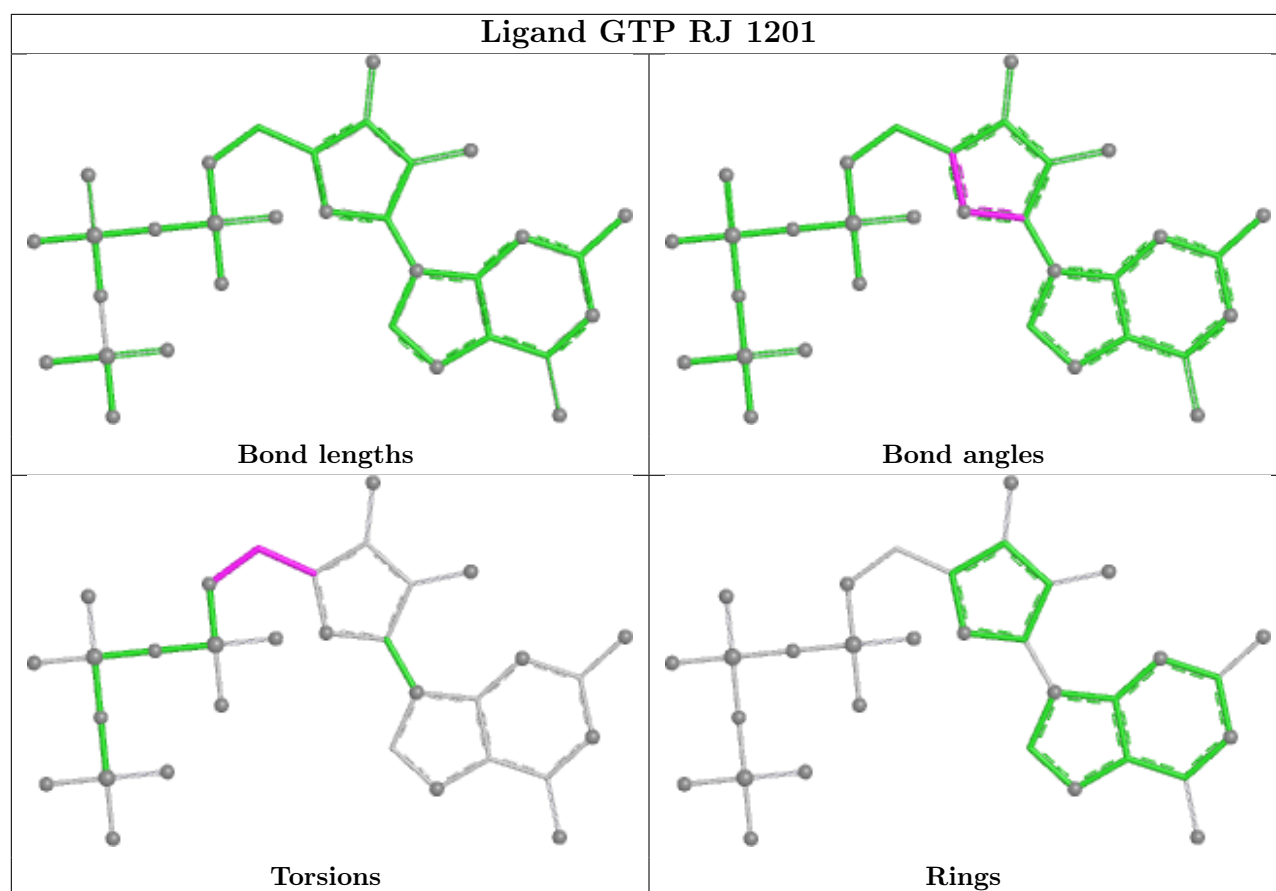
Mol	Chain	Res	Type	Atoms
68	RJ	1201	GTP	O4'-C4'-C5'-O5'
68	RJ	1201	GTP	C3'-C4'-C5'-O5'
68	RJ	1201	GTP	C4'-C5'-O5'-PA

There are no ring outliers.

1 monomer is involved in 2 short contacts:

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

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

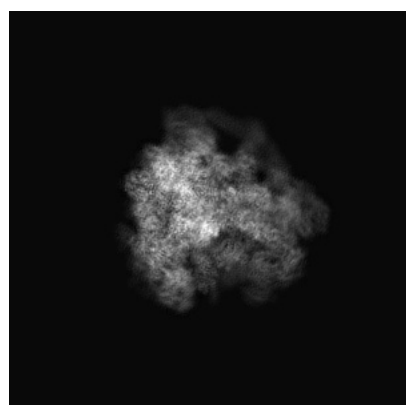
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0950. These allow visual inspection of the internal detail of the map and identification of artifacts.

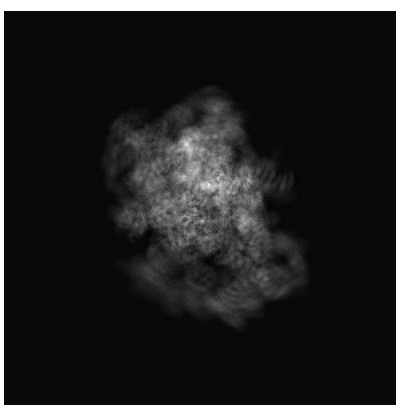
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

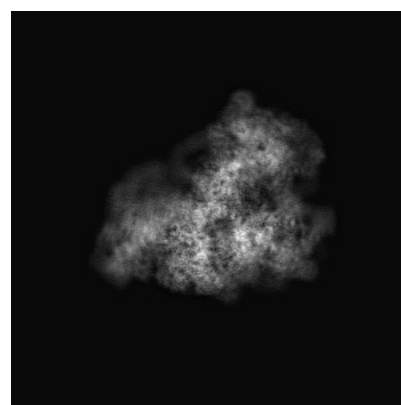
6.1.1 Primary map



X



Y

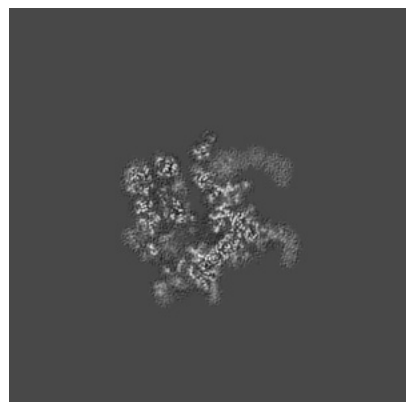


Z

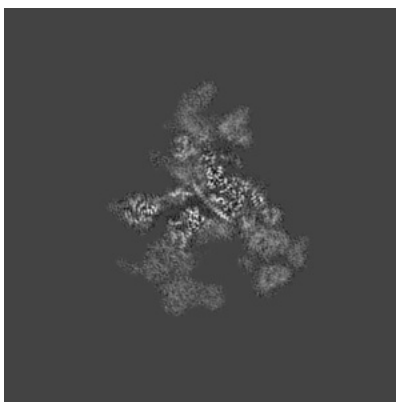
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

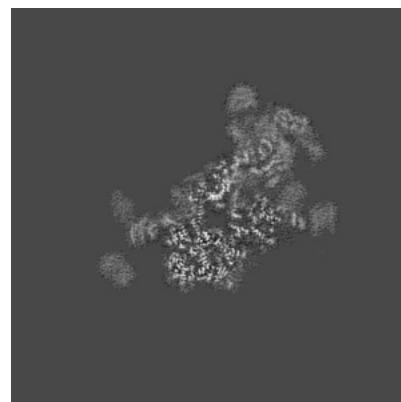
6.2.1 Primary map



X Index: 224



Y Index: 224

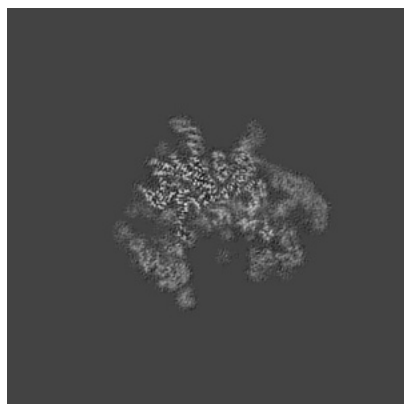


Z Index: 224

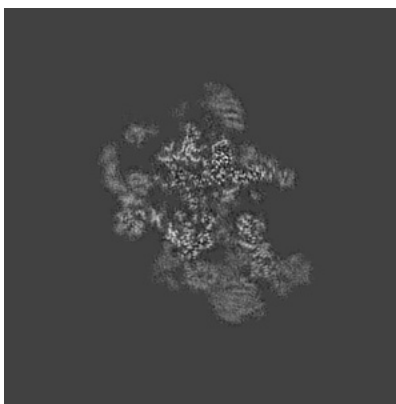
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

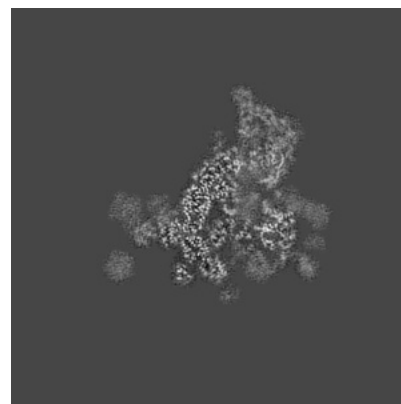
6.3.1 Primary map



X Index: 253



Y Index: 197

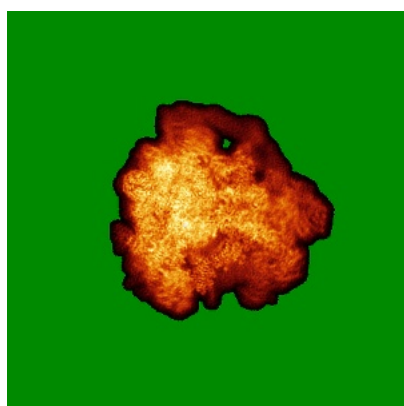


Z Index: 208

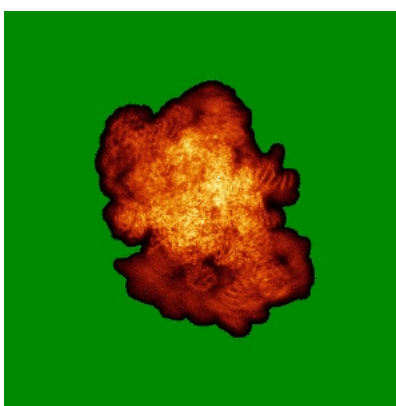
The images above show the largest variance slices of the map in three orthogonal directions.

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

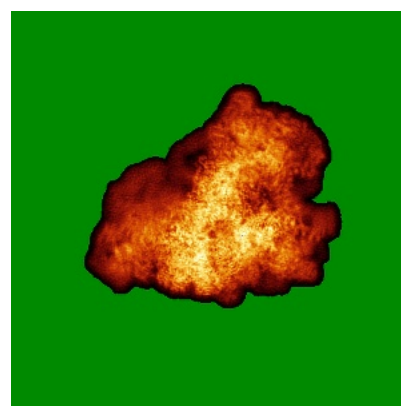
6.4.1 Primary map



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

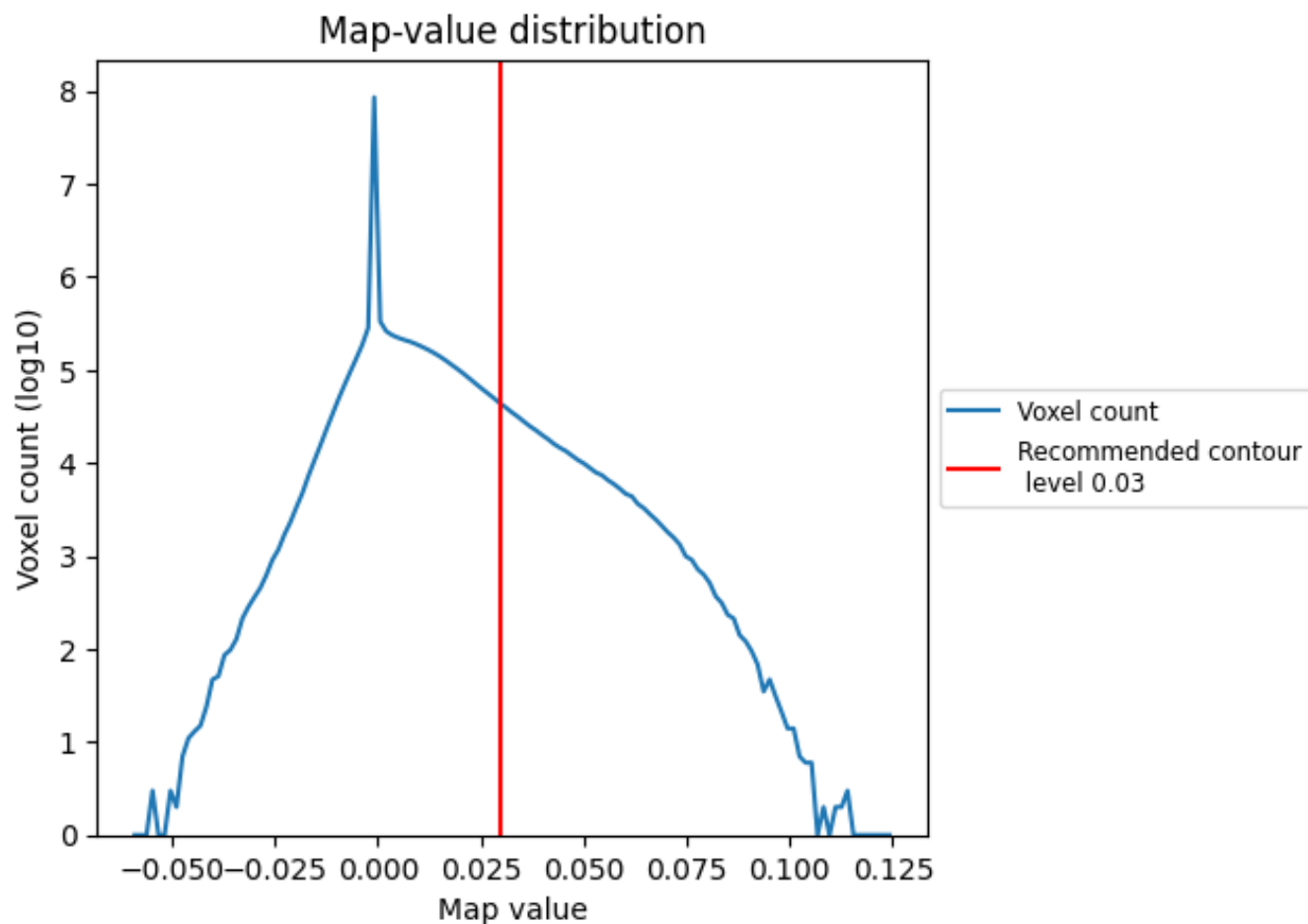
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

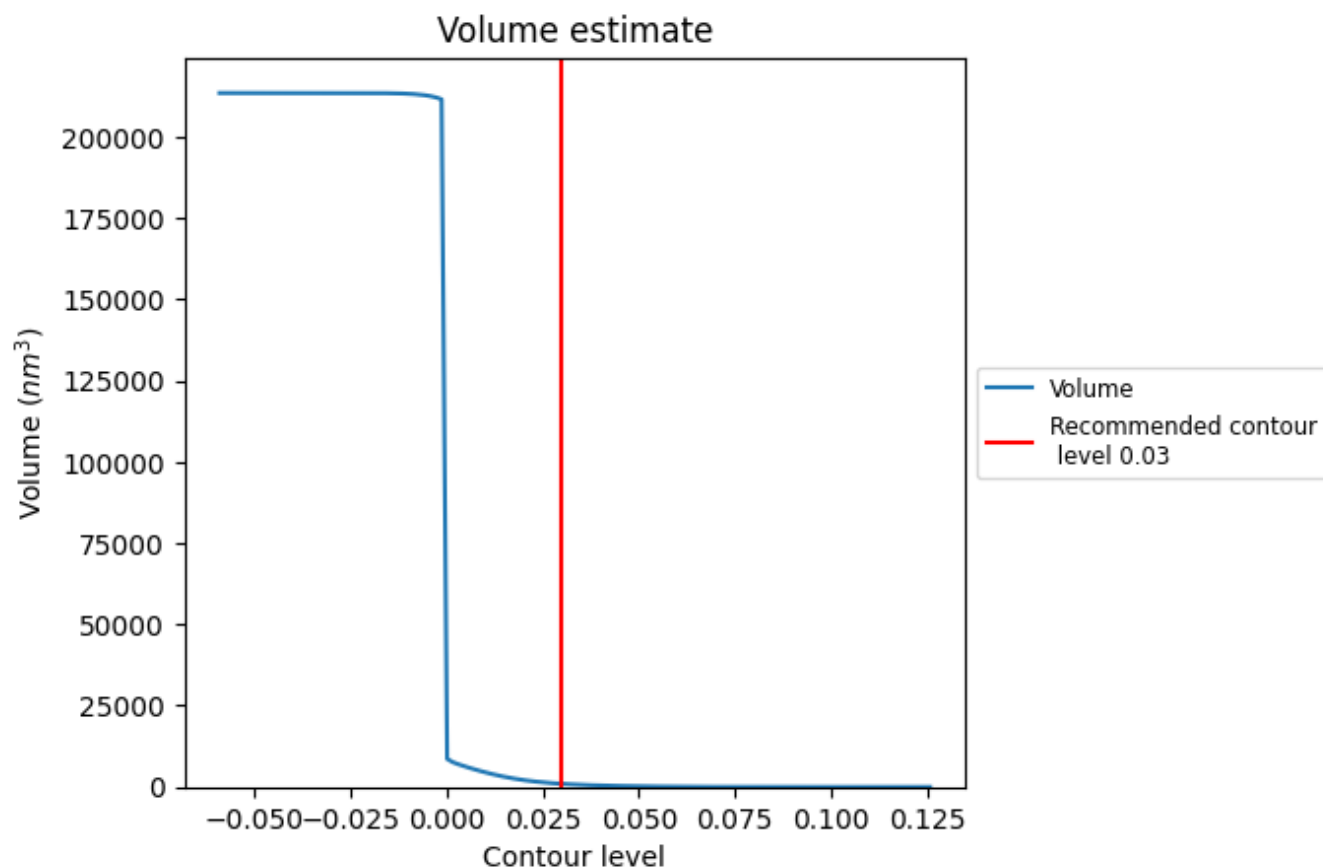
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

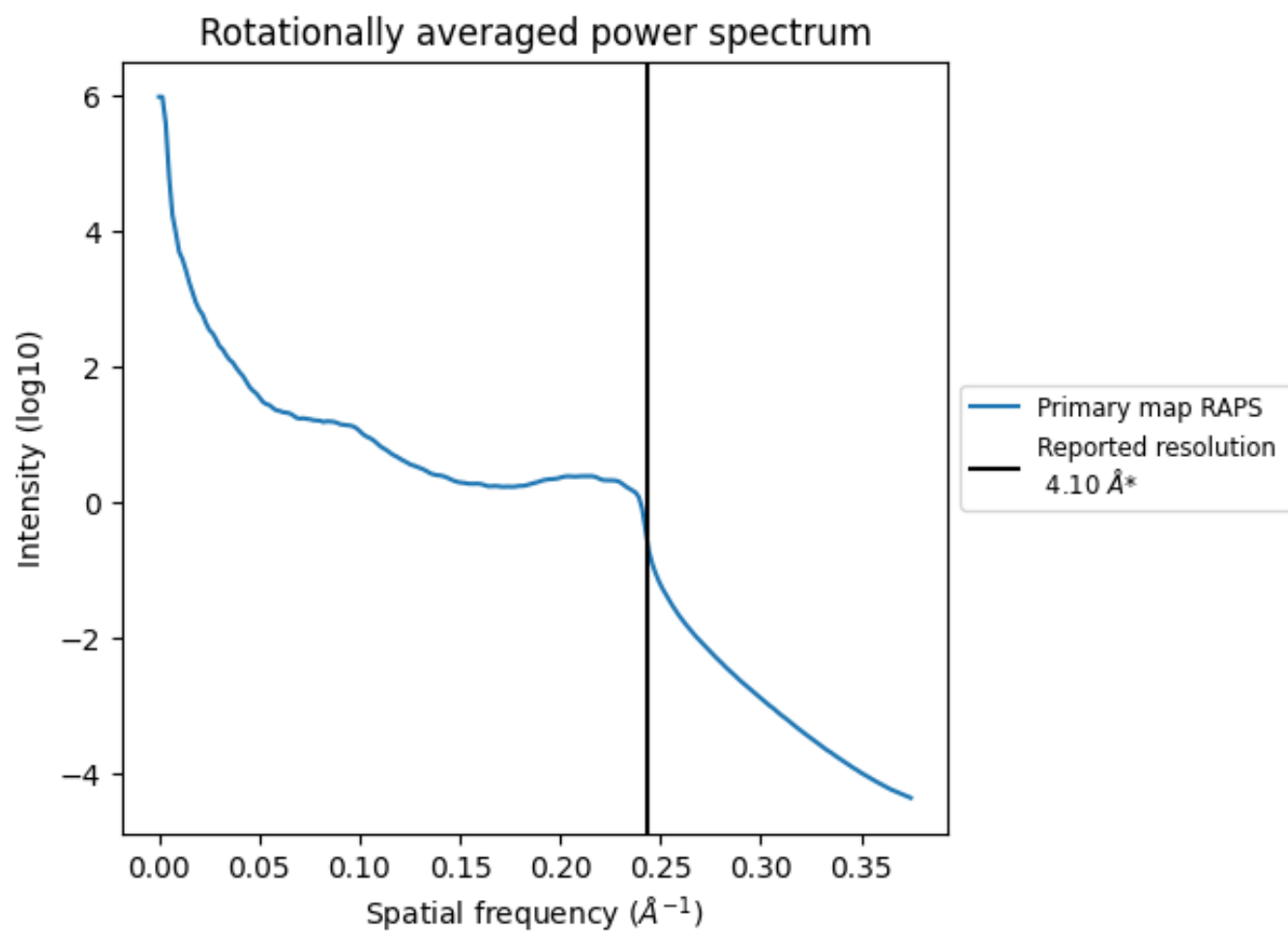
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 963 nm^3 ; this corresponds to an approximate mass of 870 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 0.244 Å⁻¹

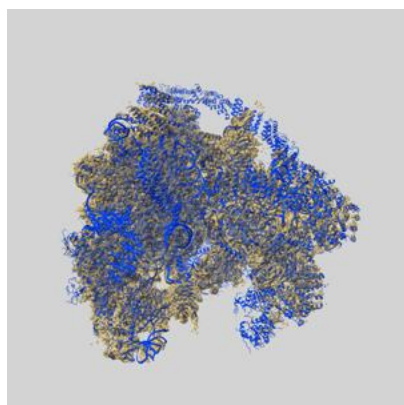
8 Fourier-Shell correlation

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

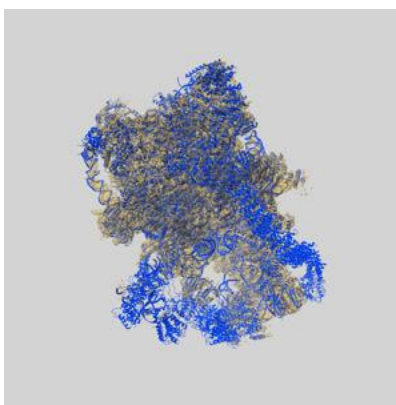
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0950 and PDB model 6LQQ. Per-residue inclusion information can be found in section 3 on page 17.

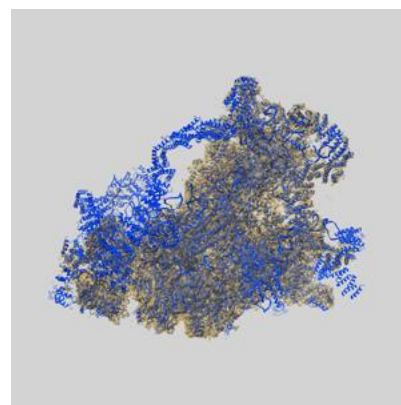
9.1 Map-model overlay [i](#)



X



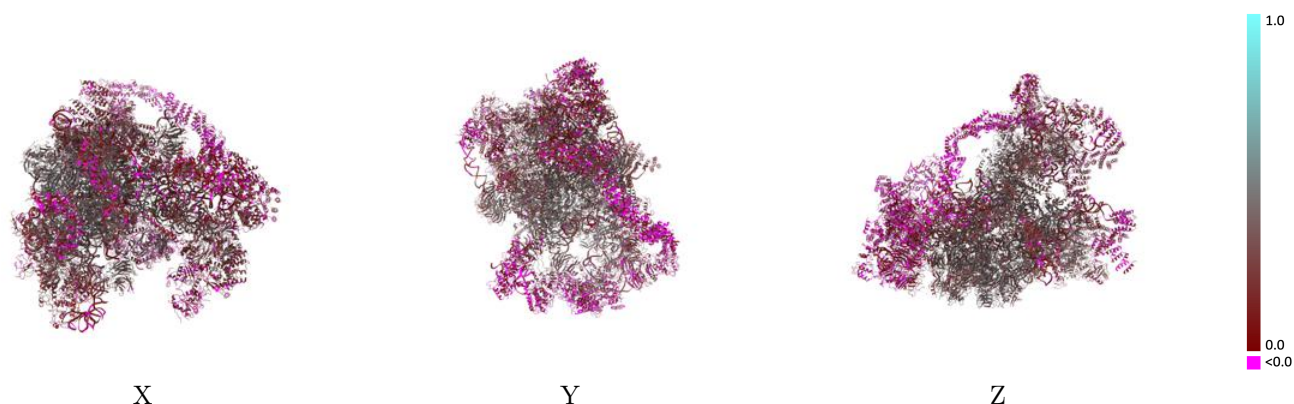
Y



Z

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

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

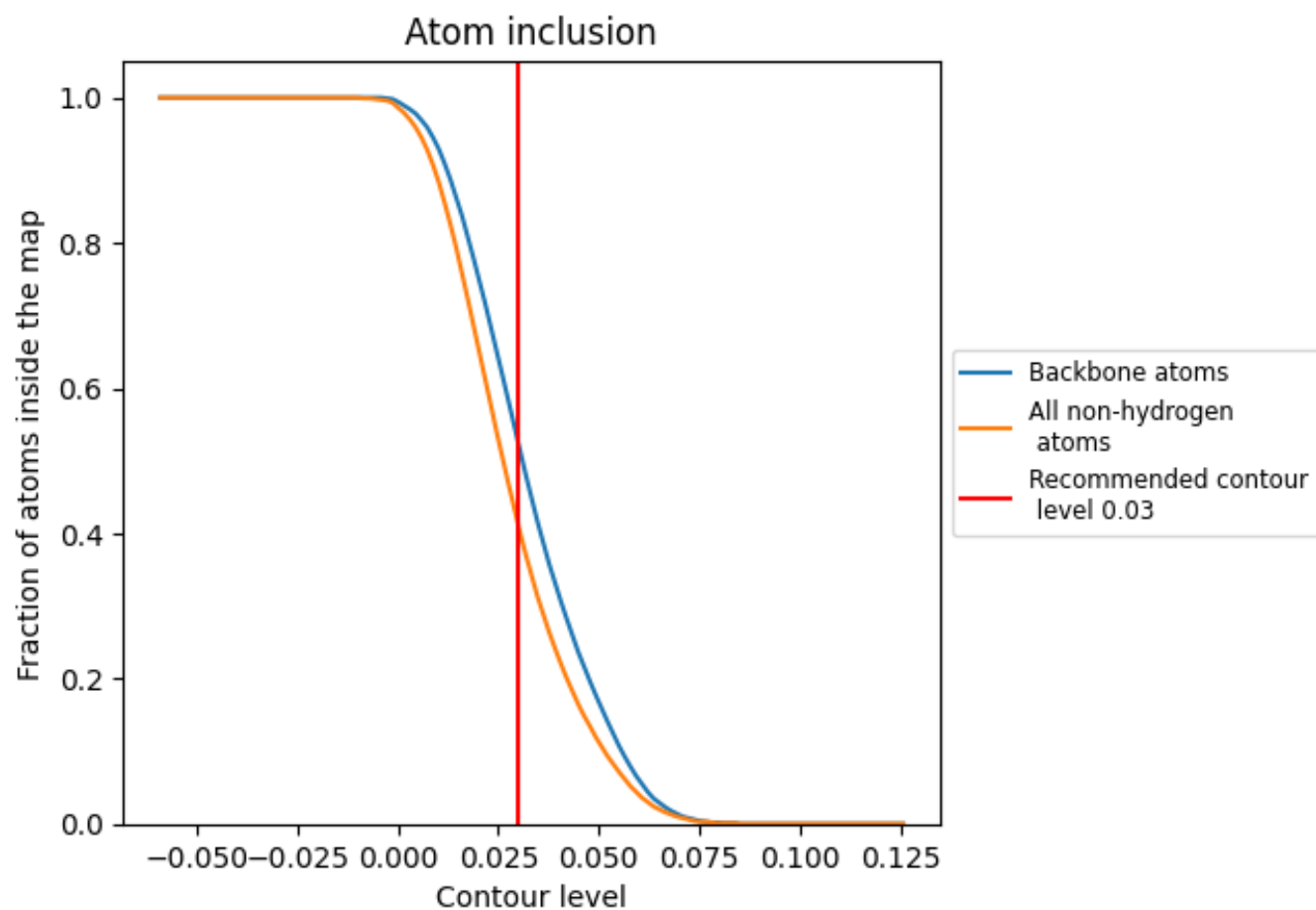


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 52% of all backbone atoms, 41% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4110	 0.2550
3A	 0.6470	 0.2880
3B	 0.6400	 0.3850
3C	 0.1330	 0.1640
3D	 0.5950	 0.3190
3E	 0.4170	 0.2480
3F	 0.5760	 0.3330
3G	 0.5180	 0.2880
3H	 0.6120	 0.3680
5A	 0.2360	 0.2060
5B	 0.0290	 0.1290
5C	 0.5690	 0.3810
5D	 0.2920	 0.2640
5E	 0.5310	 0.3520
5F	 0.6520	 0.3990
5G	 0.5730	 0.3840
5H	 0.6500	 0.3910
5I	 0.6900	 0.4090
5J	 0.3860	 0.2600
5K	 0.6320	 0.4030
A4	 0.2650	 0.1750
A5	 0.4090	 0.2640
A8	 0.0170	 0.0350
A9	 0.0500	 0.0530
AE	 0.2040	 0.1300
AF	 0.1830	 0.1930
AG	 0.2310	 0.1370
B1	 0.6490	 0.4020
B2	 0.5870	 0.3260
B3	 0.4860	 0.2820
B6	 0.5520	 0.2760
B8	 0.5770	 0.3310
BE	 0.6500	 0.3950
RA	 0.4000	 0.2630
RB	 0.4710	 0.2910



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Chain	Atom inclusion	Q-score
RC	 0.3940	 0.3180
RD	 0.0020	 0.0240
RE	 0.3440	 0.2480
RF	 0.2870	 0.2400
RG	 0.0150	 0.1160
RH	 0.0410	 0.1740
RJ	 0.5980	 0.3620
RK	 0.6270	 0.3690
RL	 0.4210	 0.2740
RM	 0.1620	 0.1440
RN	 0.0760	 0.1140
RO	 0.0000	 0.0830
RP	 0.2500	 0.1580
RQ	 0.4550	 0.3130
RS	 0.0020	 0.0210
RT	 0.2210	 0.3060
RV	 0.3570	 0.3440
RY	 0.3040	 0.2060
SA	 0.5390	 0.2470
SC	 0.5380	 0.3630
SF	 0.4940	 0.2910
SG	 0.6060	 0.3600
SH	 0.3660	 0.2430
SI	 0.4620	 0.2910
SJ	 0.3960	 0.2340
SK	 0.6400	 0.3810
SM	 0.2530	 0.1500
SO	 0.5920	 0.3670
SP	 0.5510	 0.3690
SR	 0.6340	 0.3890
SX	 0.5970	 0.3850
SY	 0.6040	 0.4080
SZ	 0.5550	 0.3210
Sc	 0.5900	 0.3860
Sd	 0.5950	 0.3980
X1	 0.0830	 0.1700