



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 11:41 AM UTC

PDB ID : 6KE6 / pdb_00006ke6
EMDB ID : EMD-9964
Title : 3.4 angstrom cryo-EM structure of yeast 90S small subunit preribosome
Authors : Du, Y.; Ye, K.; An, W.
Deposited on : 2019-07-03
Resolution : 3.40 Å(reported)
Based on initial models : 5WYJ, 5WLC

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:

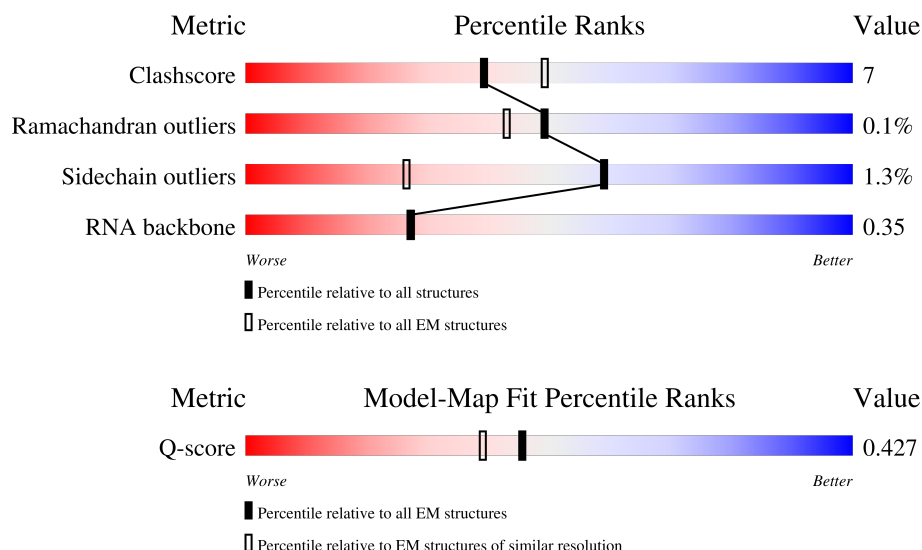
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.40 Å.

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



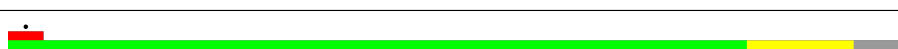
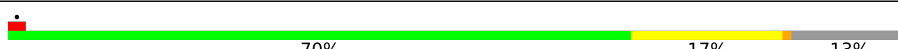
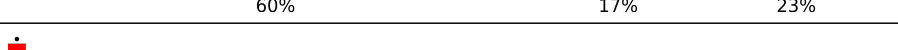
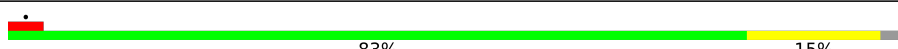
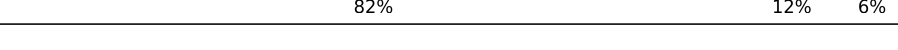
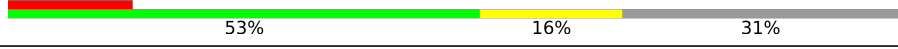
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	1807	

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

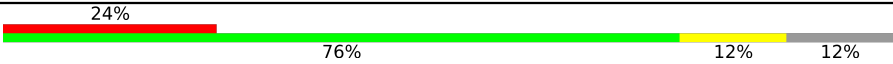
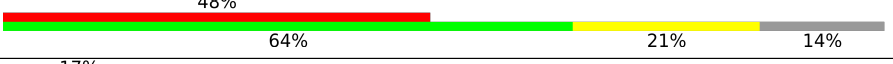
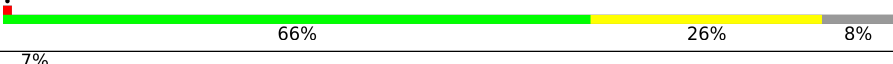
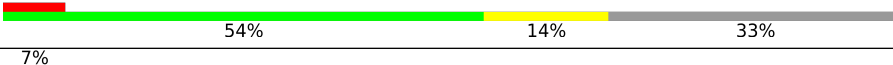
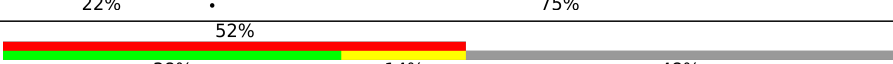
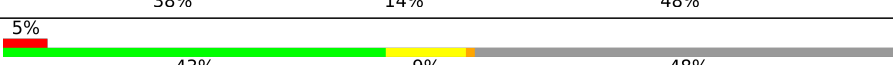
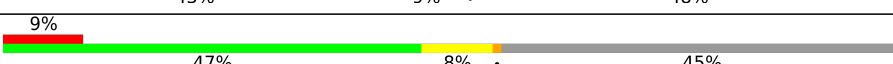
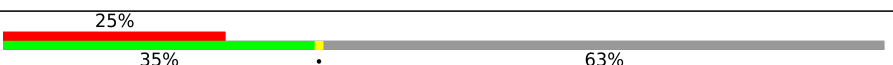
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Mol	Chain	Length	Quality of chain
27	A4	776	
28	A5	643	
29	A8	713	
30	A9	575	
31	AE	1769	
32	AF	513	
33	AG	896	
34	B1	923	
35	B2	943	
36	B3	817	
37	B8	594	
38	BE	939	
39	B6	440	
40	5B	214	
41	5C	554	
42	5D	250	
43	5E	593	
44	5F	183	
45	5G	290	
46	5H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

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

2 Entry composition

There are 70 unique types of molecules in this entry. The entry contains 224791 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	522	Total	C	N	O	P	0	0
			11143	4979	1982	3660	522		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SA	1310	Total	C	N	O	P	0	0
			27940	12487	4981	9162	1310		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SC	219	Total	C	N	O	S	0	0
			1751	1109	321	317	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	112	Total	C	N	O	S	0	0
			879	562	155	160	2		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	ST	113	Total	C	N	O	S	0	0
			918	578	174	164	2		

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 23 is a protein called Nucleolar protein 56.

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

- Molecule 24 is a protein called Nucleolar protein 58.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	3F	434	Total	C	N	O	S	0	0
			3473	2211	603	649	10		

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AE	777	Total	C	N	O	S	0	0
			6197	3998	1014	1166	19		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 47 is a protein called Protein SOF1.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
48	5J	144	Total	C	N	O	S	0	0
			1219	769	230	215	5		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 59 is a protein called RNA cytidine acetyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	RL	805	Total	C	N	O	S	0	0
			4539	2760	885	887	7		
59	RM	765	Total	C	N	O		0	0
			3774	2244	765	765			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	RN	587	Total	C	N	O	S	0	0
			4363	2758	791	803	11		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
62	RP	2052	Total	C	N	O		0	0
			10202	6098	2052	2052			

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

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

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

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

- Molecule 65 is a protein called Pre-rRNA-processing protein PNO1.

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

- Molecule 66 is a protein called Protein FAF1.

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

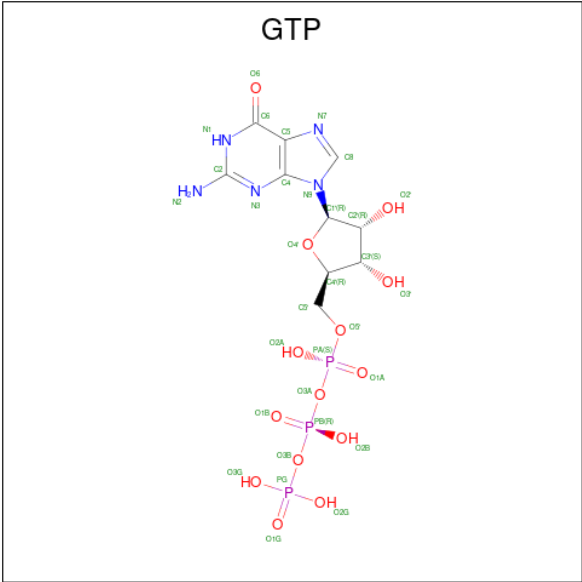
- Molecule 67 is a protein called Unassigned helices.

Mol	Chain	Residues	Atoms				AltConf	Trace
67	X1	127	Total	C	N	O	0	0
			635	381	127	127		

- Molecule 68 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
68	Sc	1	Total	Zn	0
			1	1	
68	5K	1	Total	Zn	0
			1	1	

- Molecule 69 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).

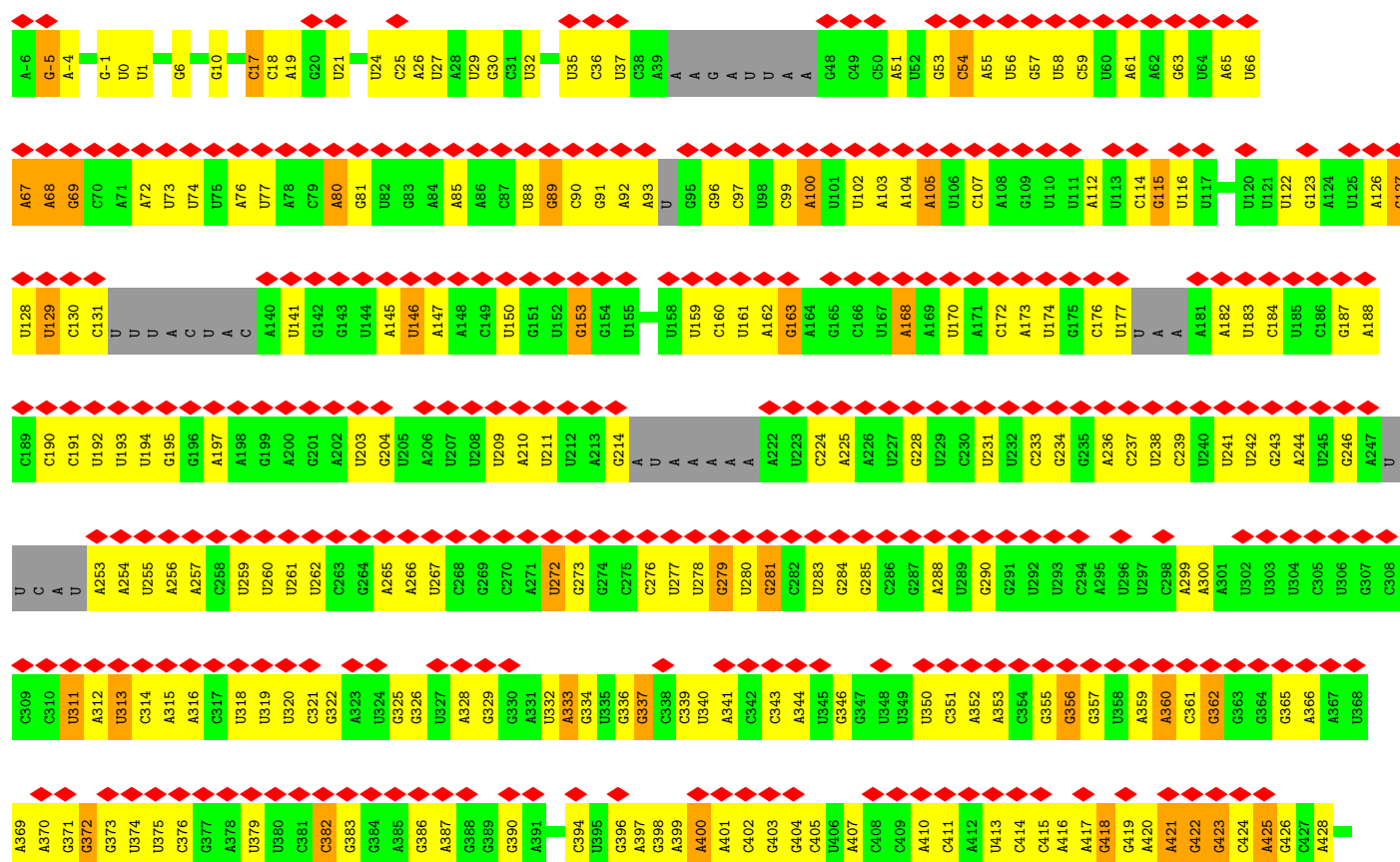


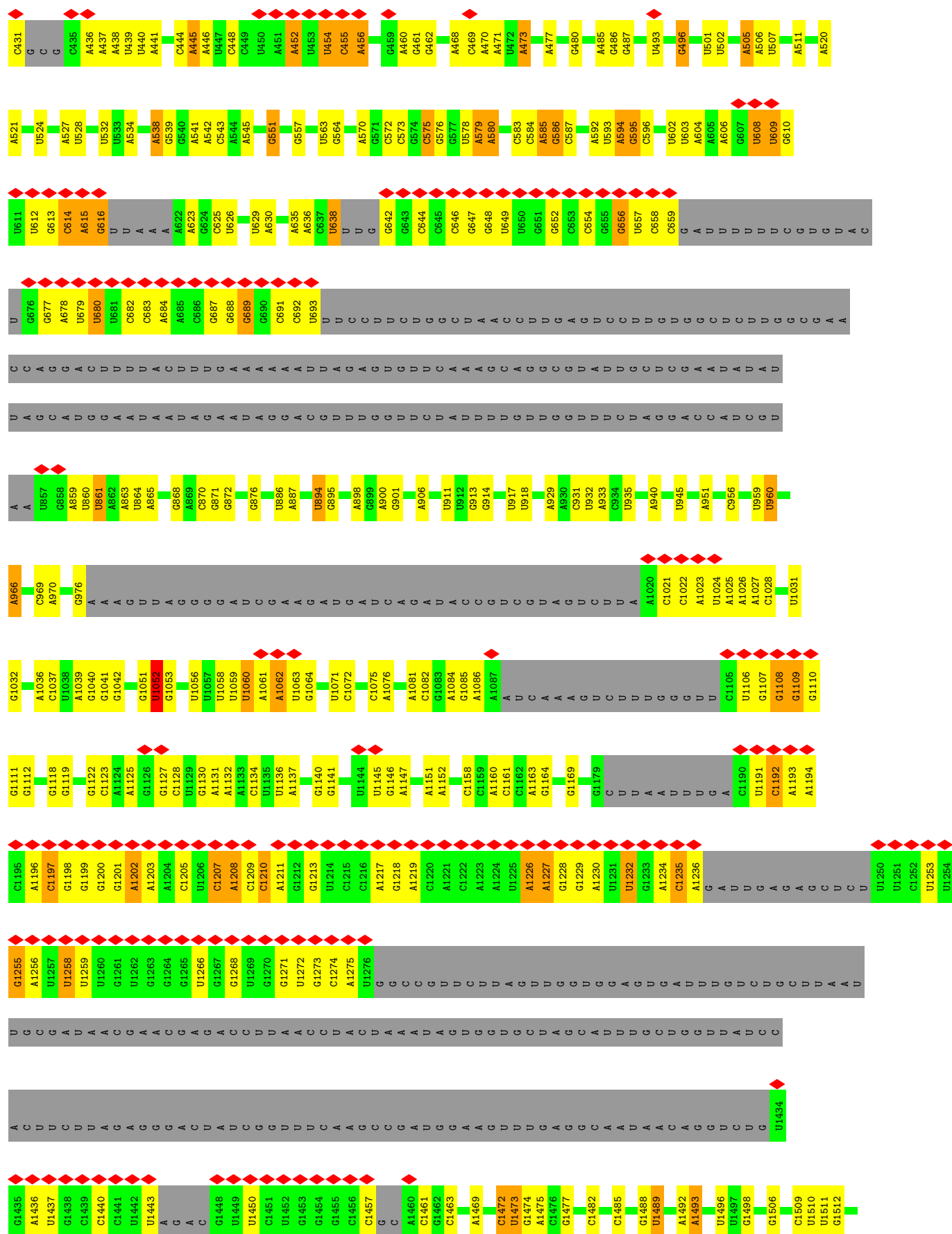
Mol	Chain	Residues	Atoms					AltConf
69	RJ	1	Total	C	N	O	P	0
			32	10	5	14	3	

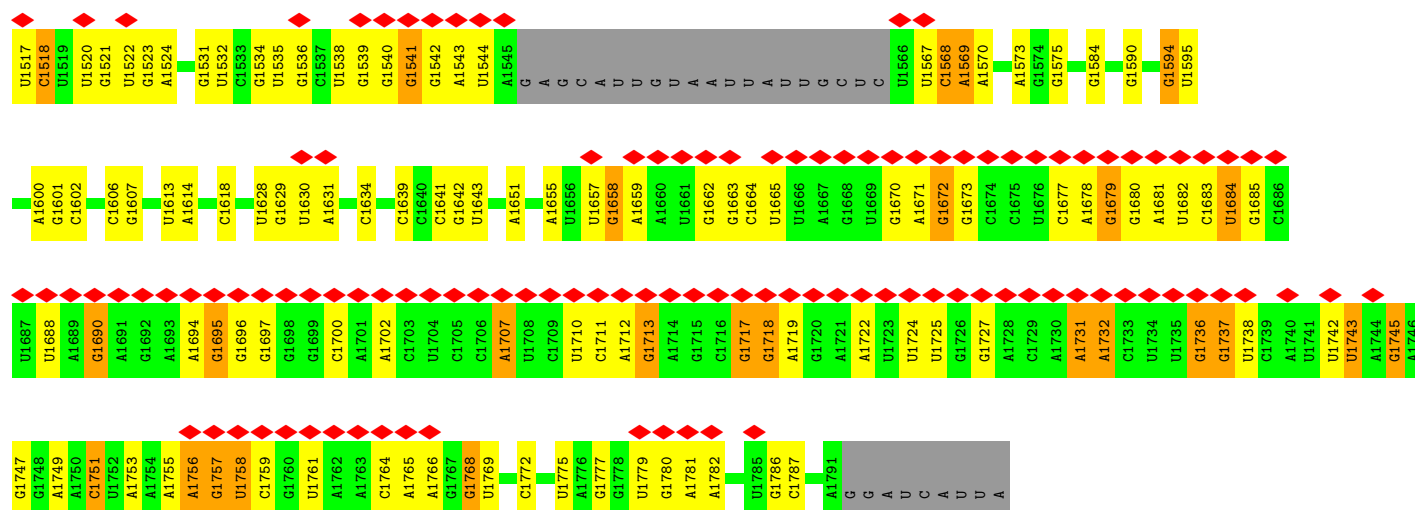
- Molecule 70 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

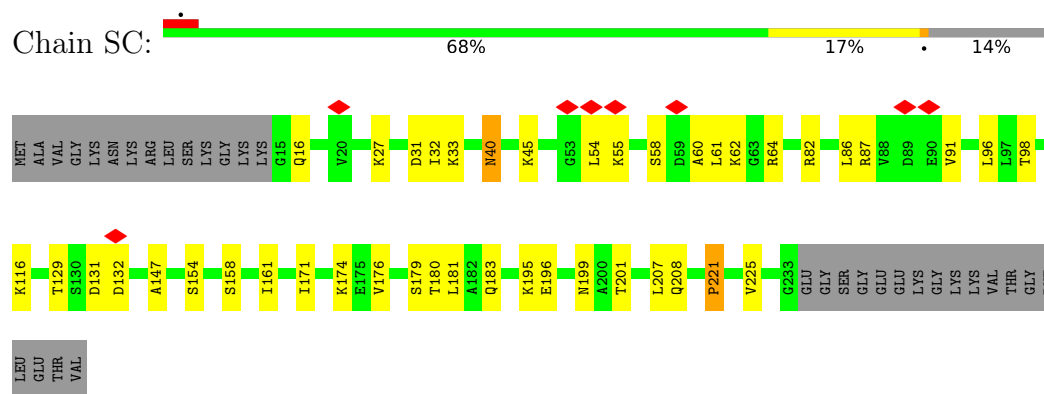
- Molecule 3: 18S rRNA



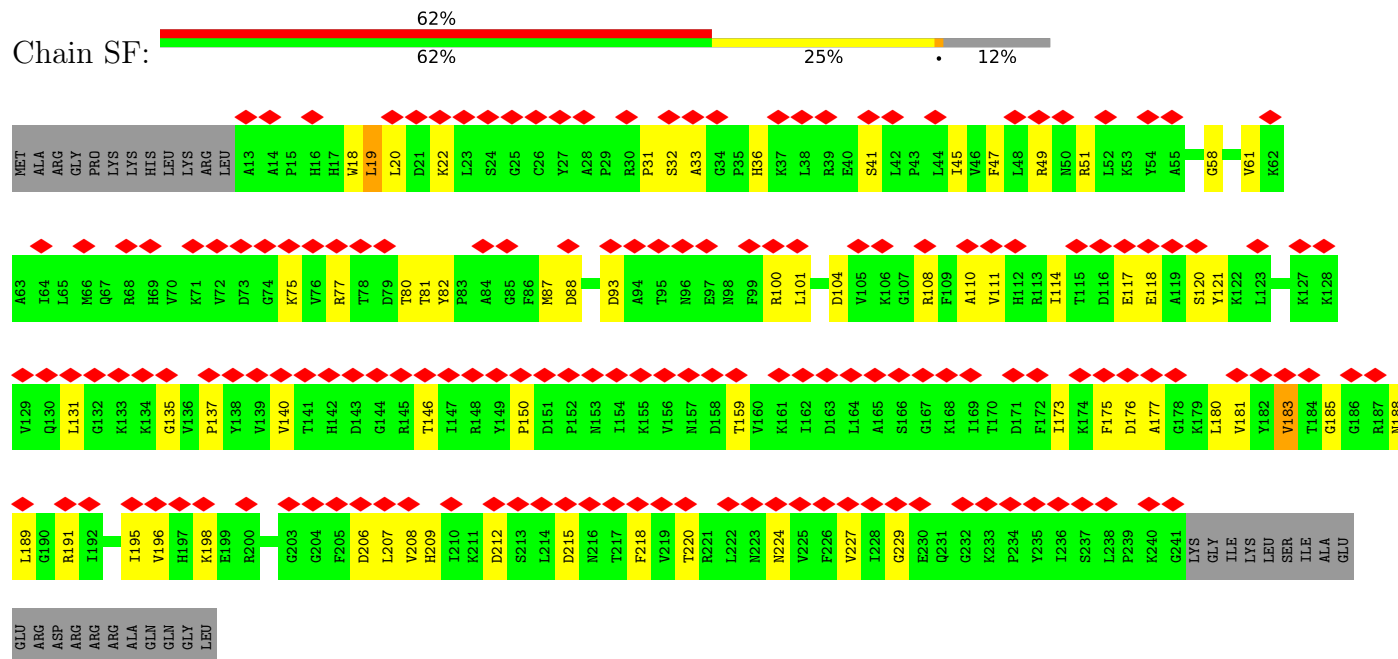




• Molecule 4: 40S ribosomal protein S1-A



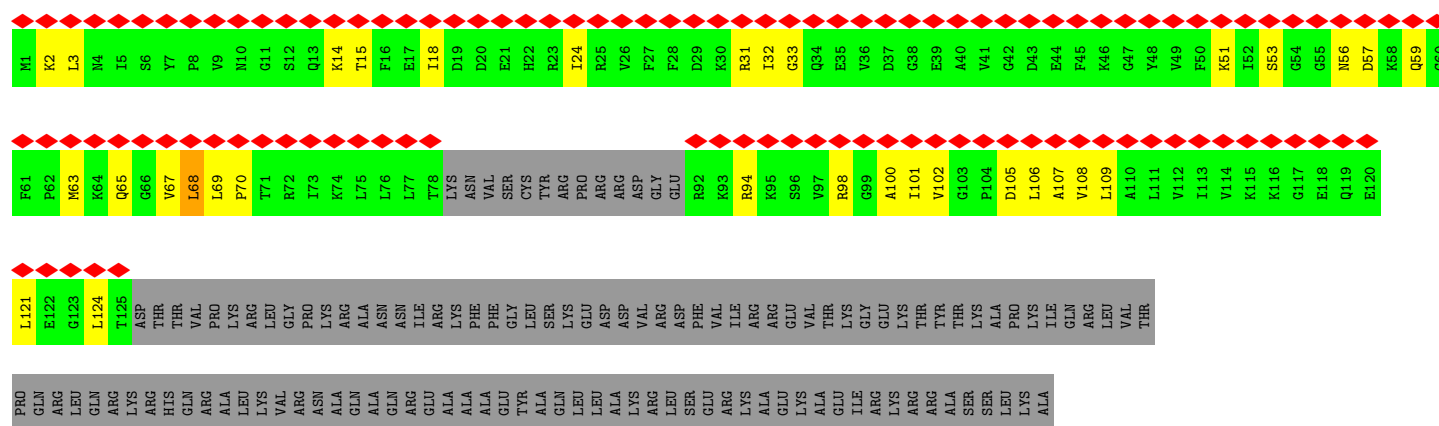
• Molecule 5: 40S ribosomal protein S4-A



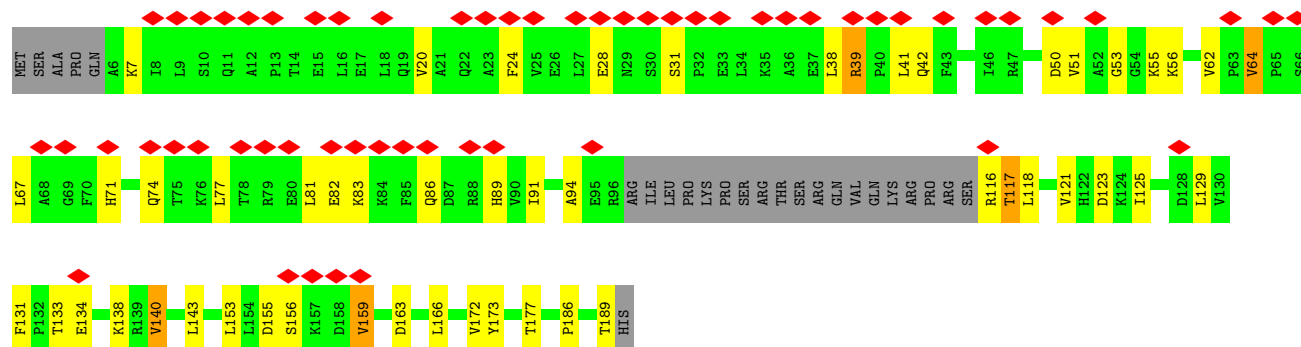
Bar chart showing the number of mutations for various amino acids. The y-axis represents the number of mutations (0 to 16). The x-axis lists amino acids. The bars are colored yellow, green, or grey. Red diamonds indicate specific mutations.

Amino Acid	Number of Mutations	Color	Specific Mutation
MET	16	Grey	
SER	1	Yellow	
ASP	1	Green	R135
THR	1	Yellow	
GLU	1	Yellow	
ALA	1	Yellow	
PRO	1	Yellow	
VAL	1	Yellow	
VAL	1	Green	
GLN	1	Yellow	
GLU	1	Green	
D13	1	Green	
A26	1	Yellow	
L58	1	Yellow	
Q63	1	Yellow	
Q66	1	Yellow	
T73	1	Yellow	
N79	1	Yellow	
R83	1	Yellow	
E91	1	Yellow	
R92	1	Yellow	
N99	1	Yellow	
N100	1	Yellow	
G101	1	Green	G101
N104	1	Yellow	
L108	1	Yellow	
I114	1	Yellow	
T117	1	Yellow	
L118	1	Yellow	
V123	1	Yellow	
L124	1	Green	
T125	1	Yellow	
D126	1	Yellow	
Q127	1	Yellow	
N128	1	Green	
P129	1	Yellow	
G151	1	Green	G151
G152	1	Green	G152
G153	1	Green	G153
A154	1	Green	A154
A155	1	Green	A155
N169	1	Yellow	

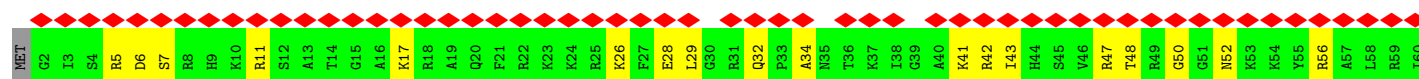
Chain SH:

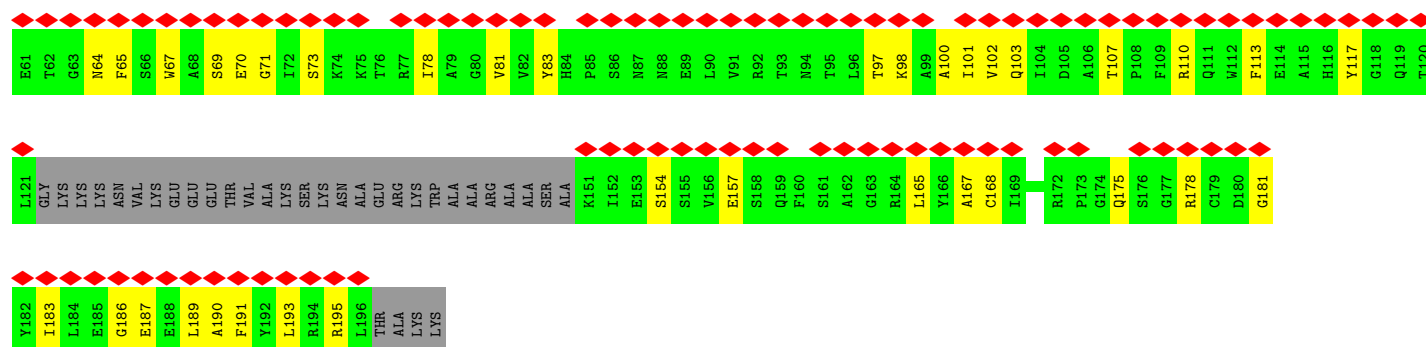


Chain SI:

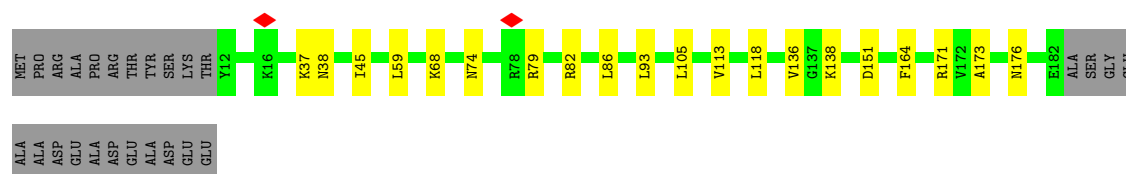
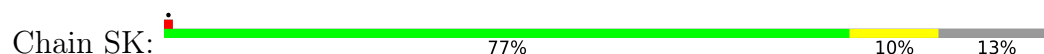


Chain SJ:

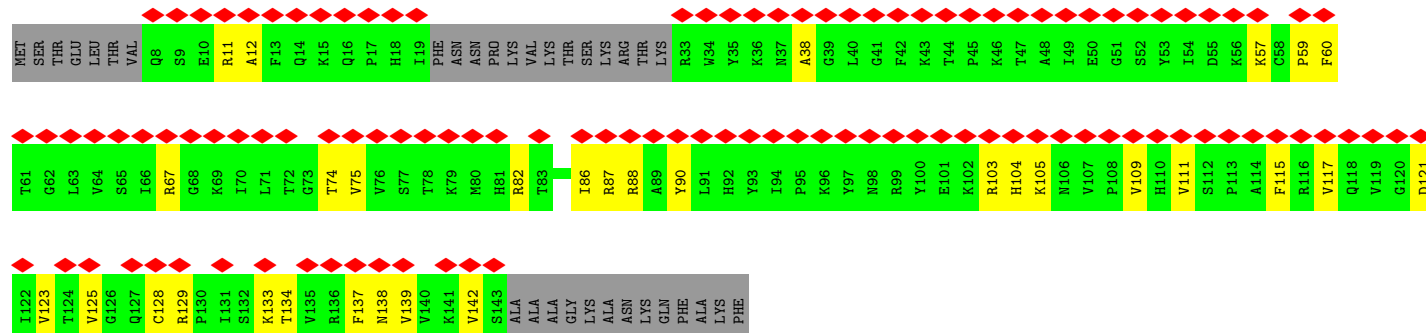
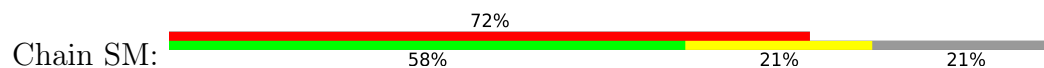




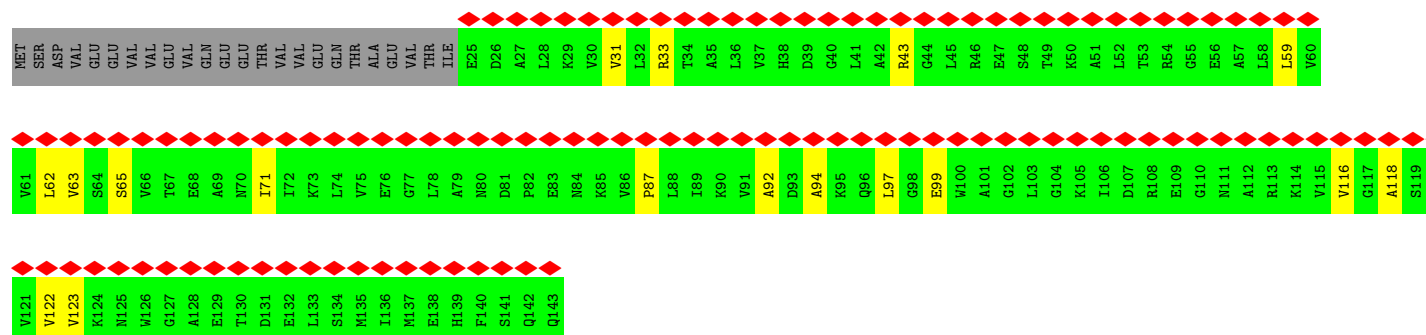
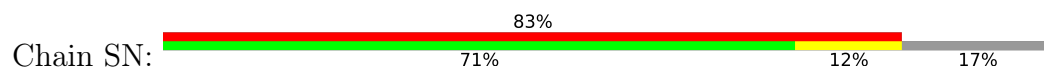
• Molecule 10: 40S ribosomal protein S9-A



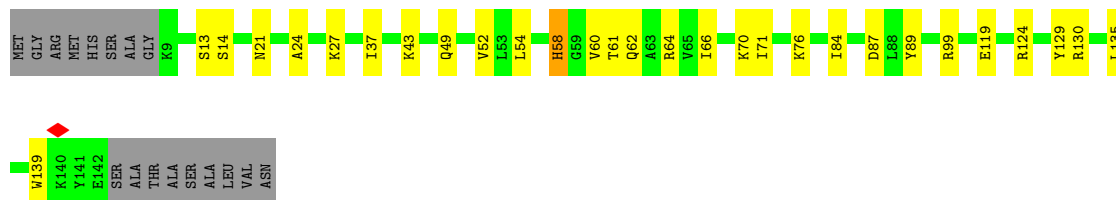
• Molecule 11: 40S ribosomal protein S11-A



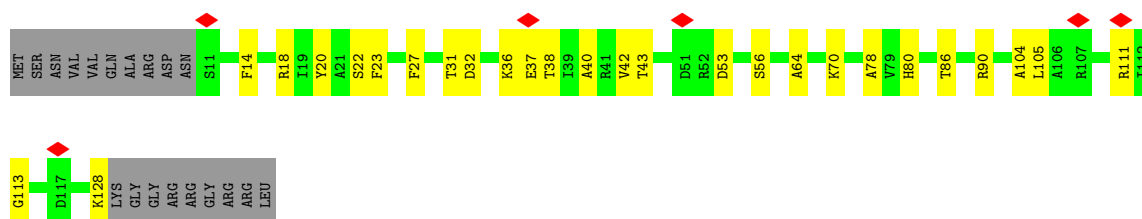
• Molecule 12: 40S ribosomal protein S12



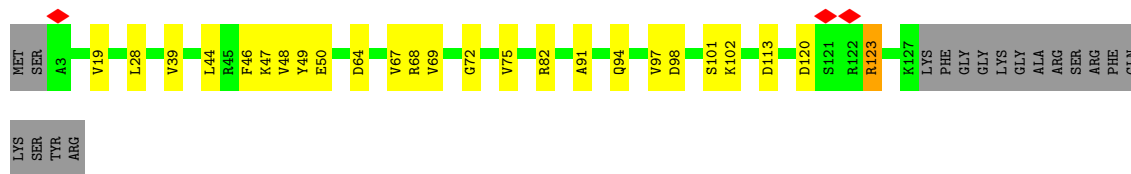
• Molecule 13: 40S ribosomal protein S13

Chain SO: 

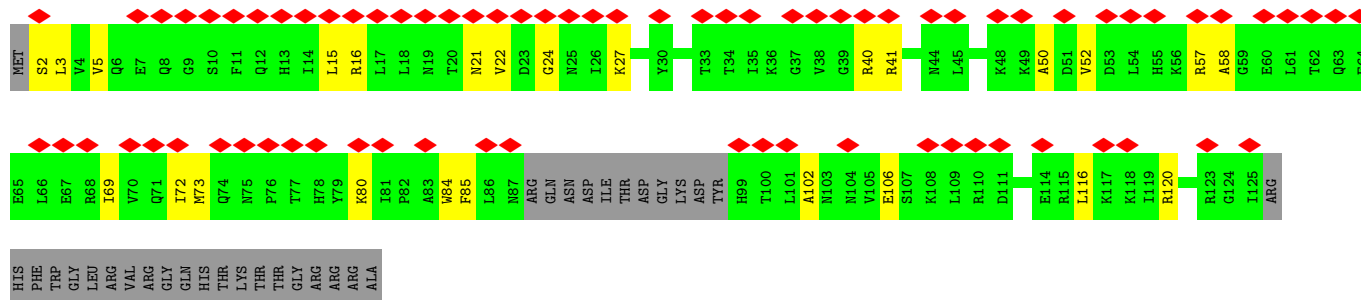
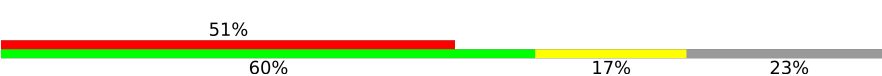
• Molecule 14: 40S ribosomal protein S14-A

Chain SP: 

• Molecule 15: 40S ribosomal protein S16-A

Chain SR: 

• Molecule 16: 40S ribosomal protein S18-A

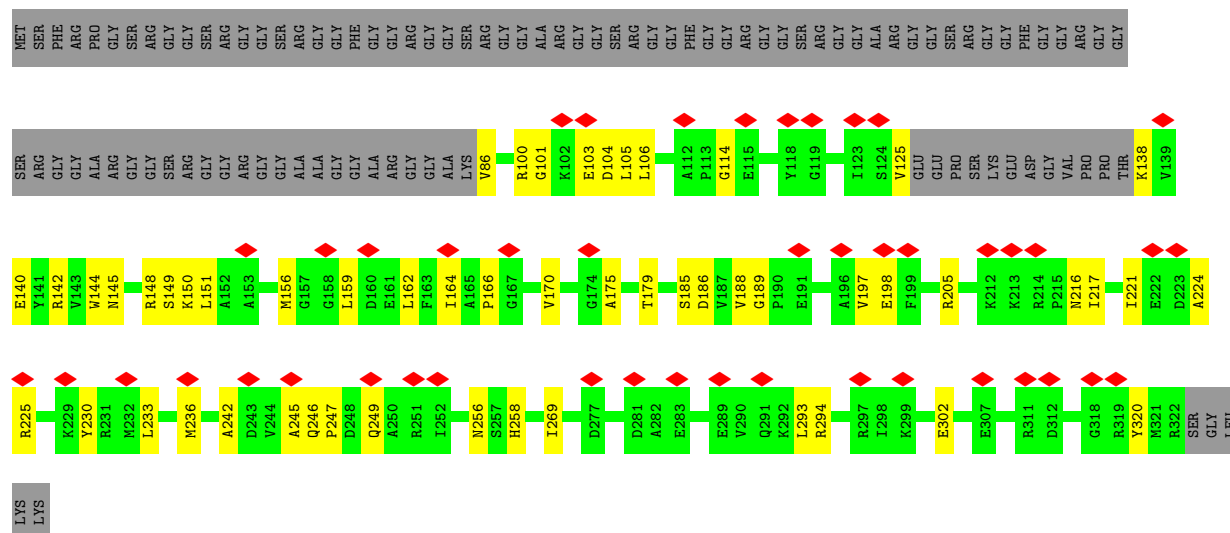
Chain ST: 

• Molecule 17: 40S ribosomal protein S22-B

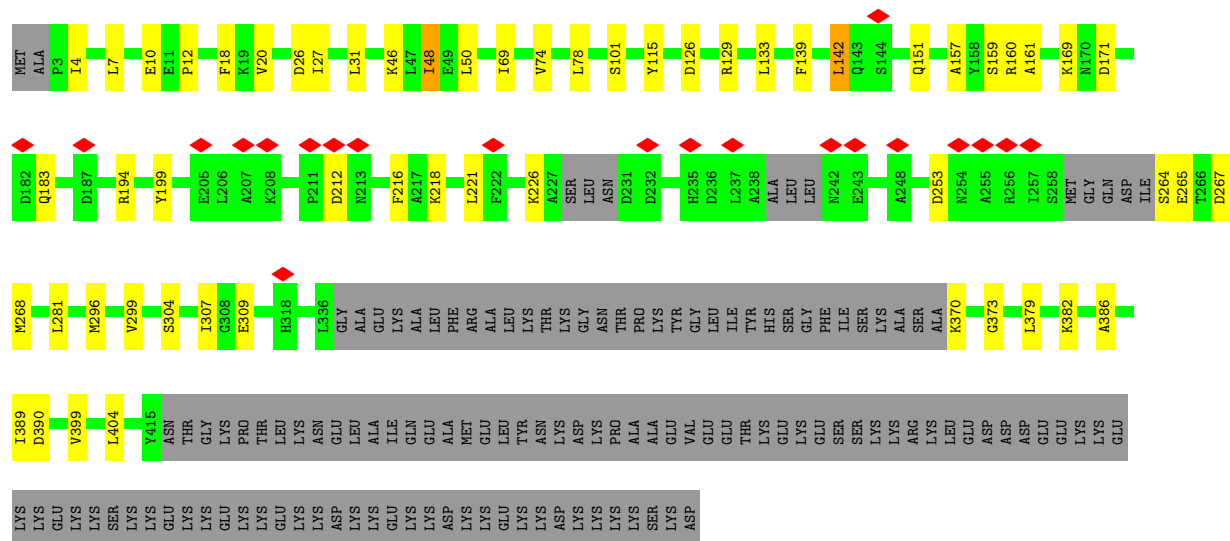
Chain SX: 



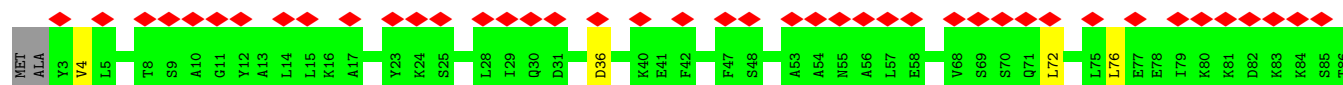
• Molecule 22: rRNA 2'-O-methyltransferase fibrillar

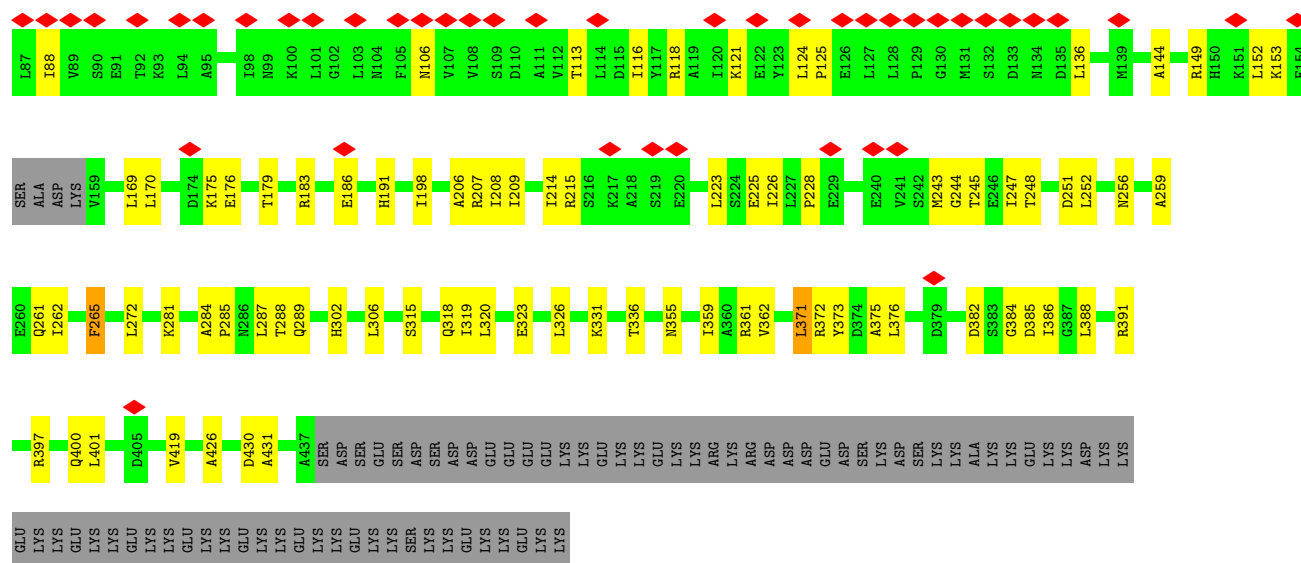


• Molecule 23: Nucleolar protein 56

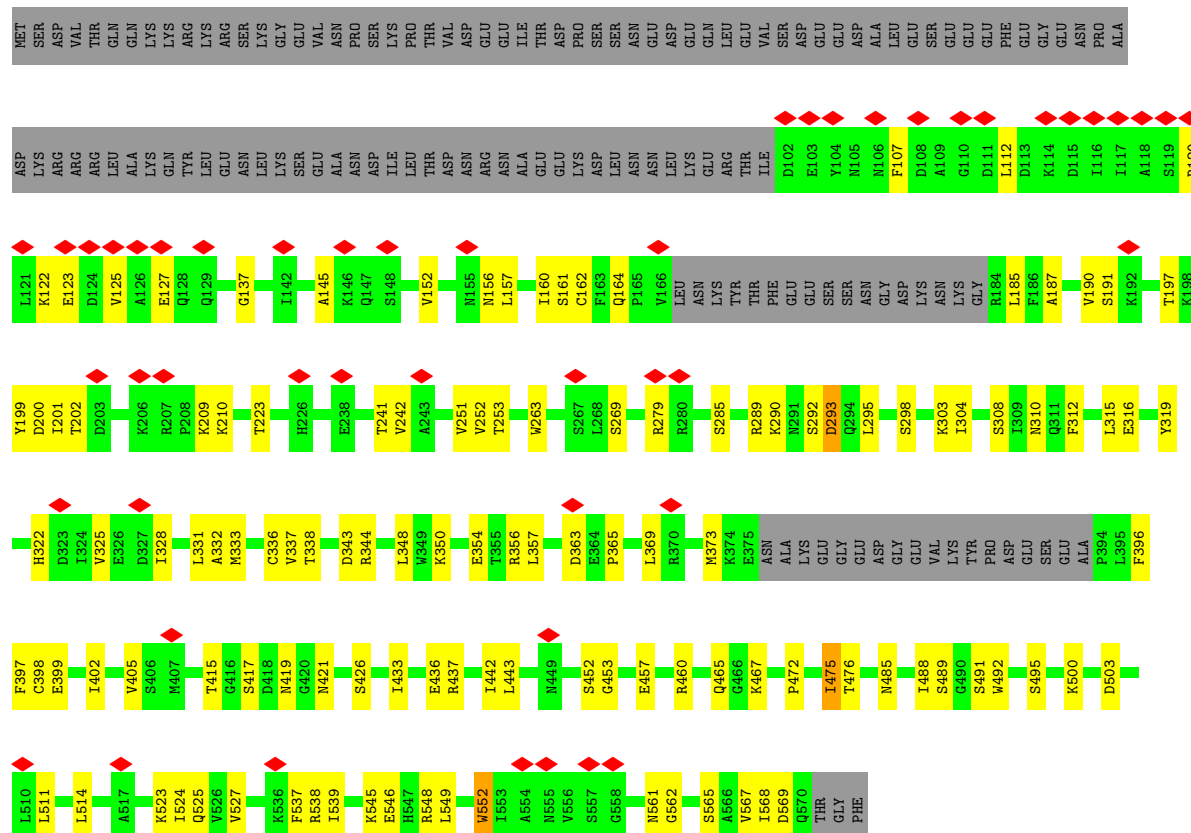


• Molecule 24: Nucleolar protein 58

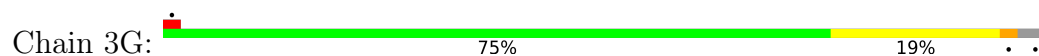


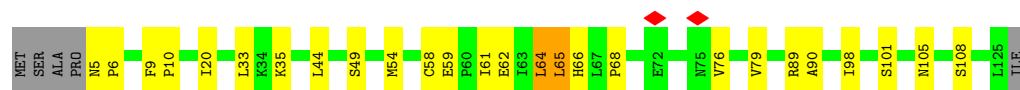


• Molecule 25: Ribosomal RNA-processing protein 9



• Molecule 26: 13 kDa ribonucleoprotein-associated protein

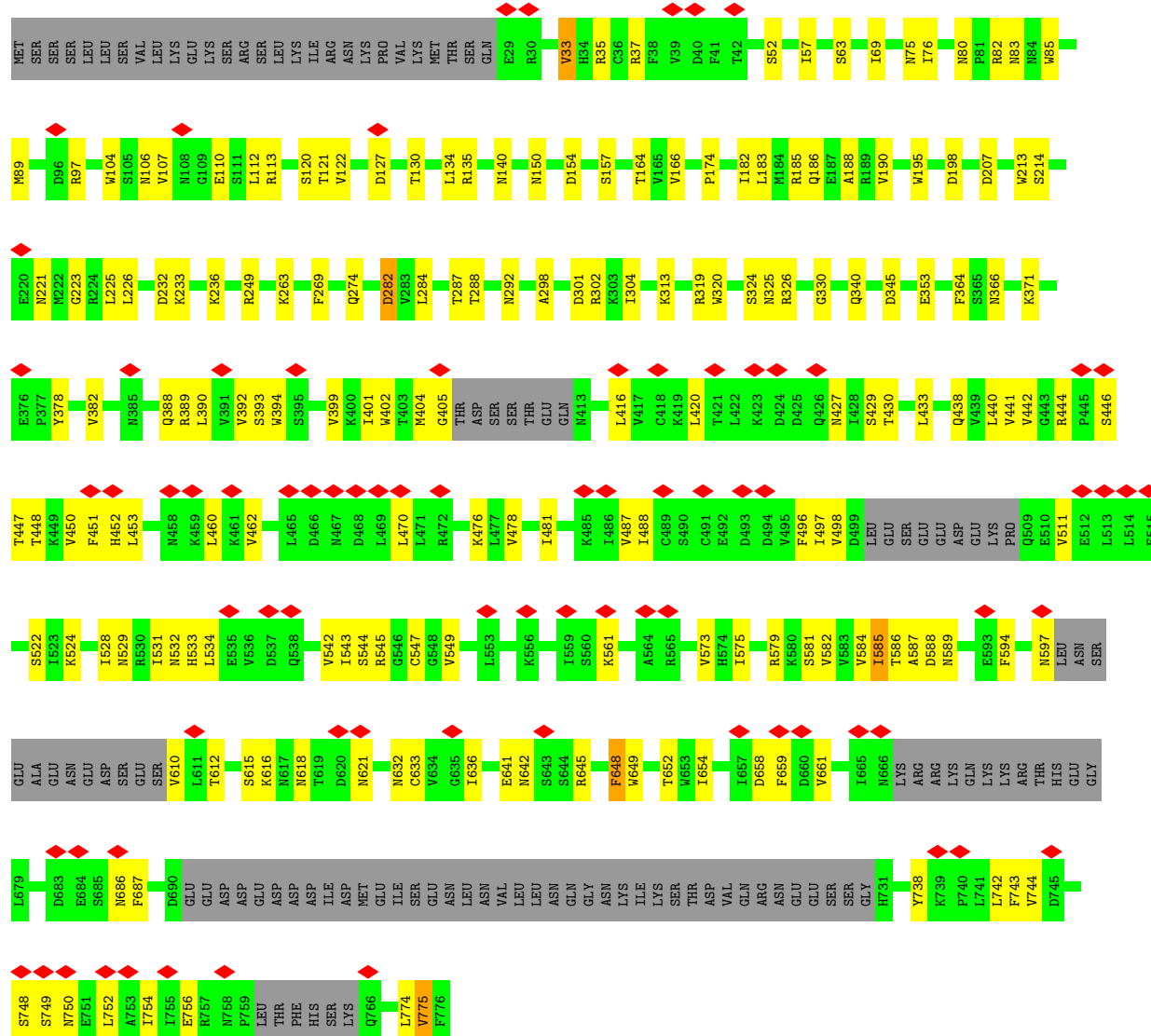




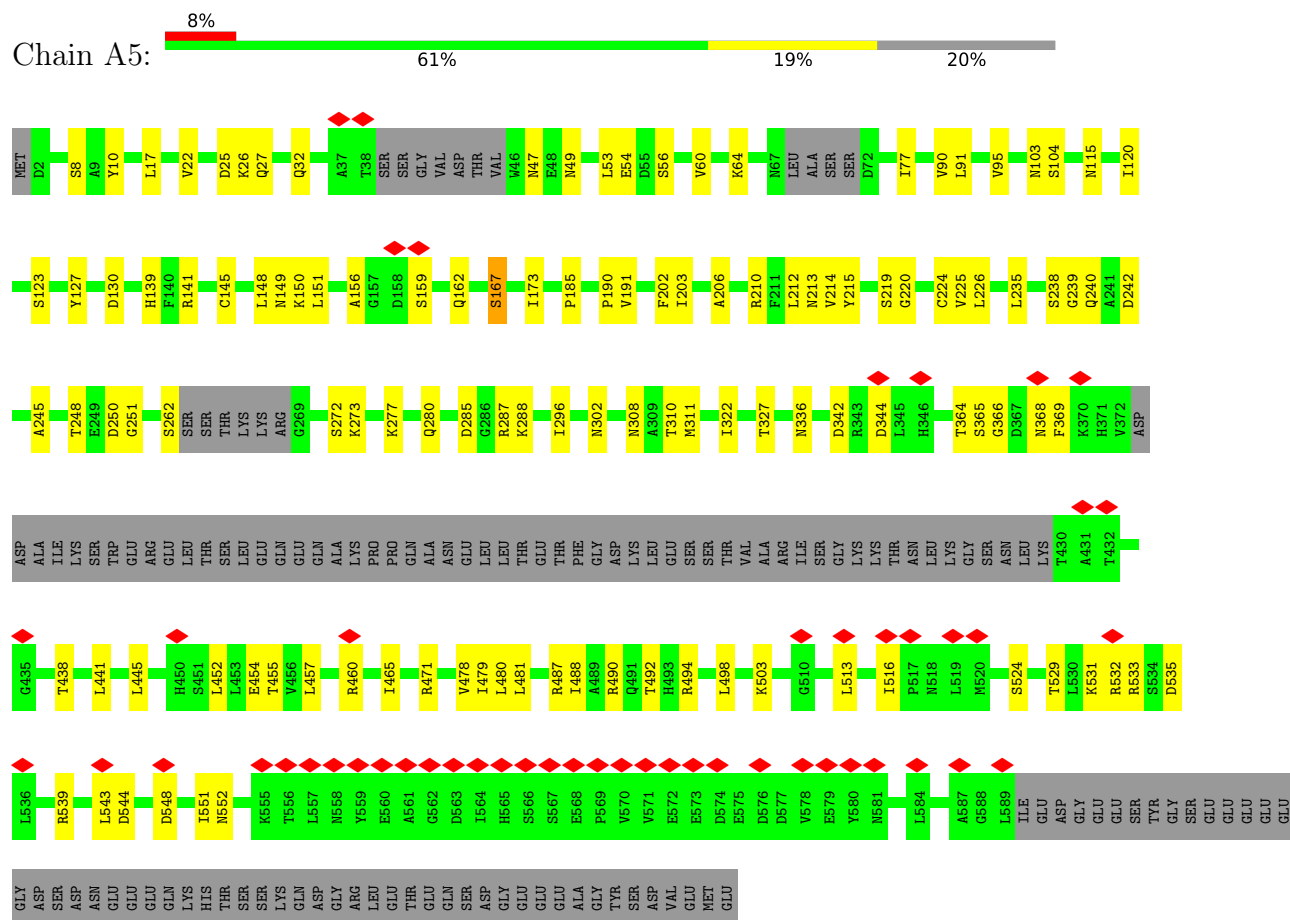
- Molecule 26: 13 kDa ribonucleoprotein-associated protein



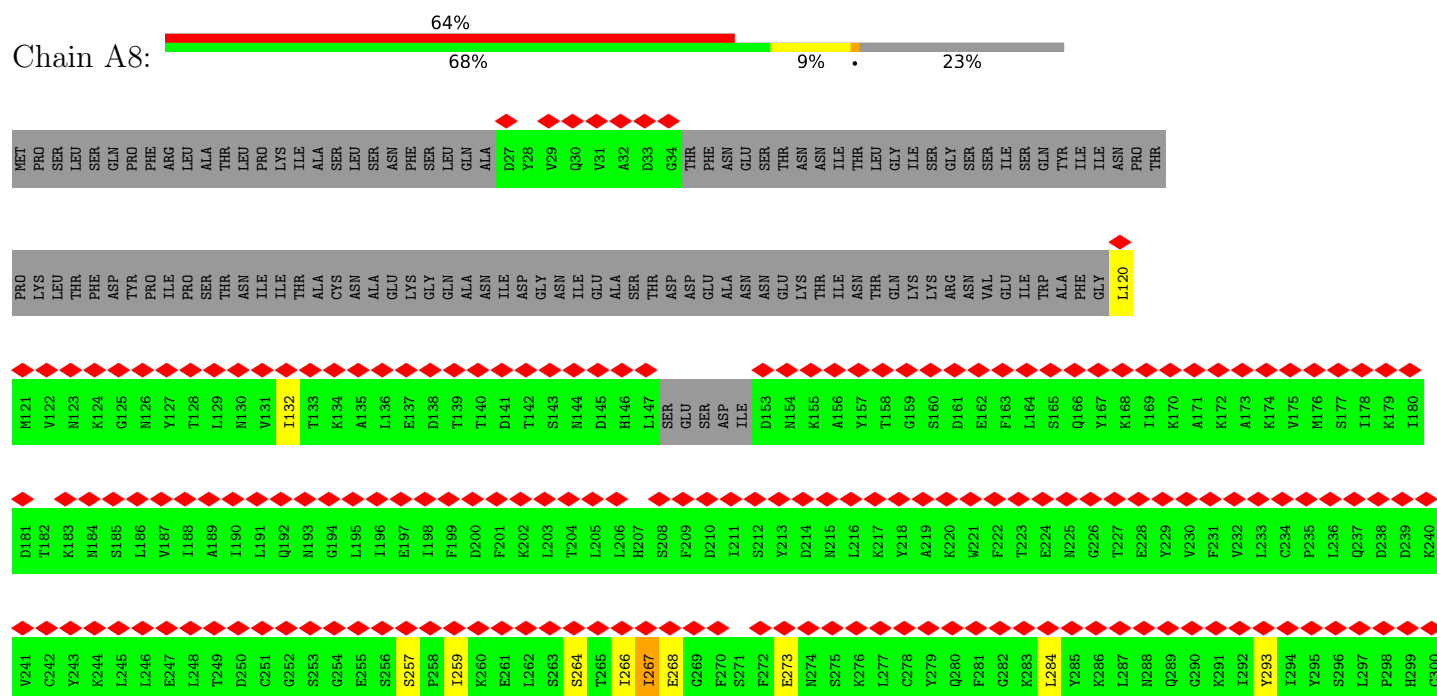
- Molecule 27: U3 small nucleolar RNA-associated protein 4

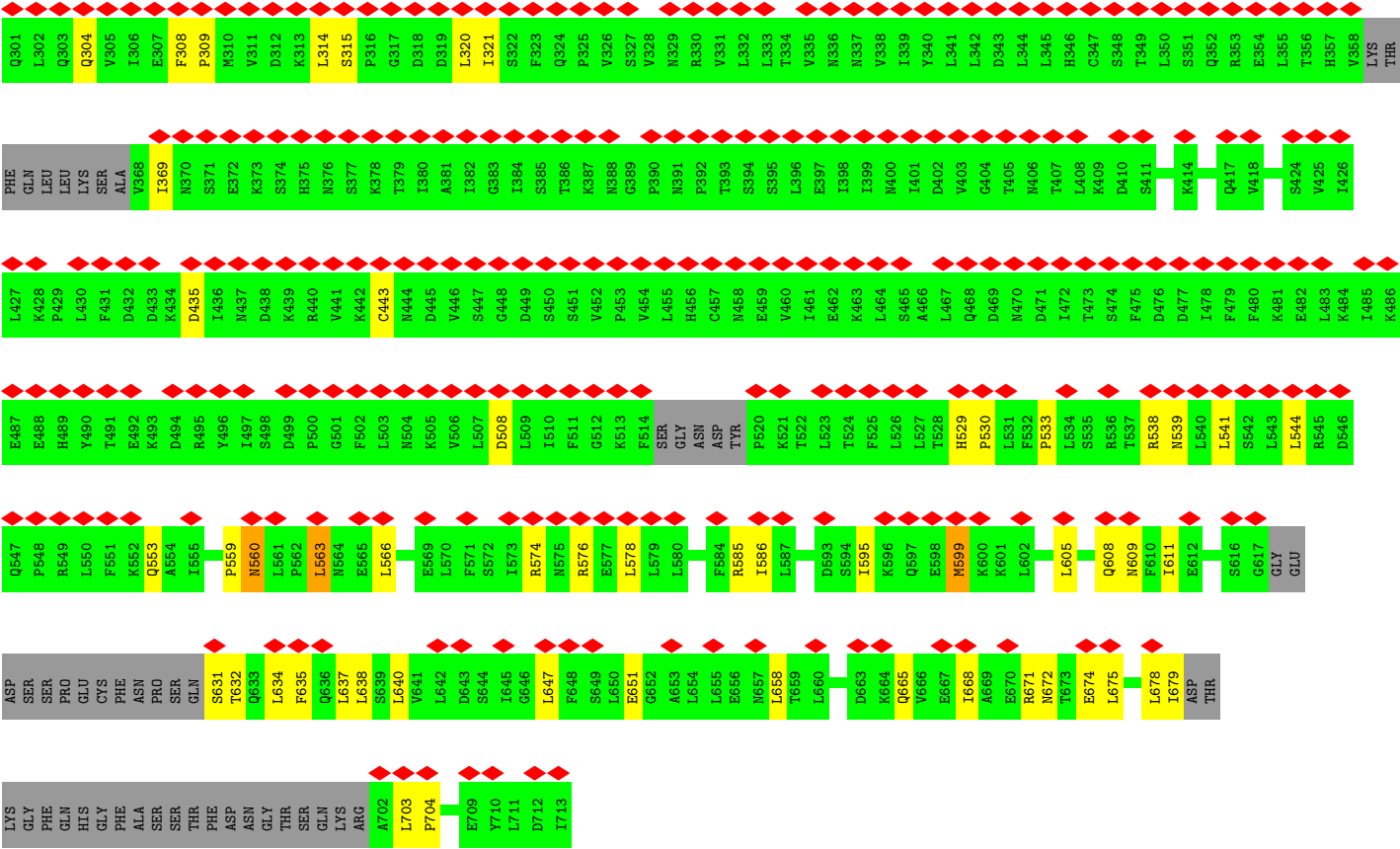


Chain A5:

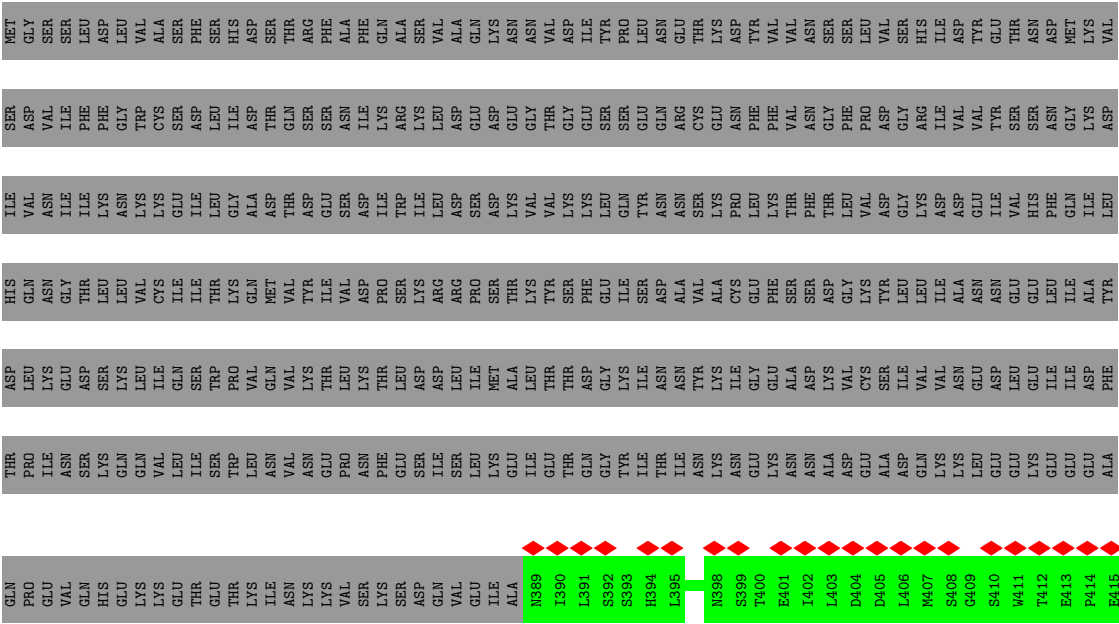


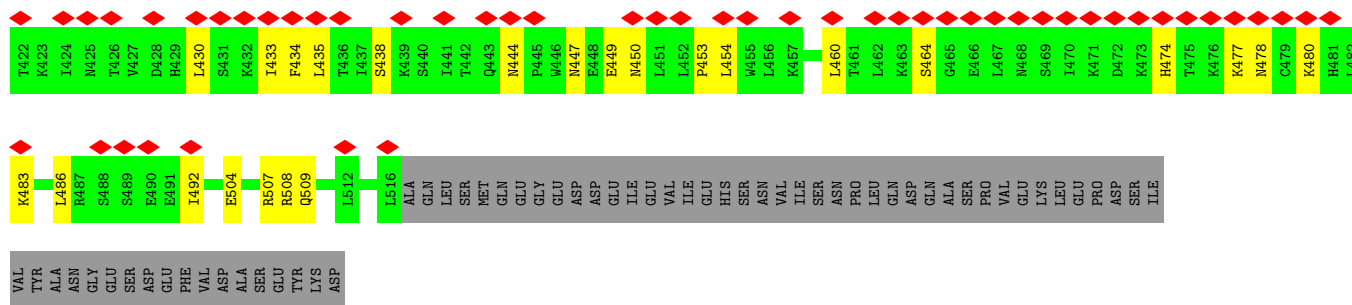
Chain A8:



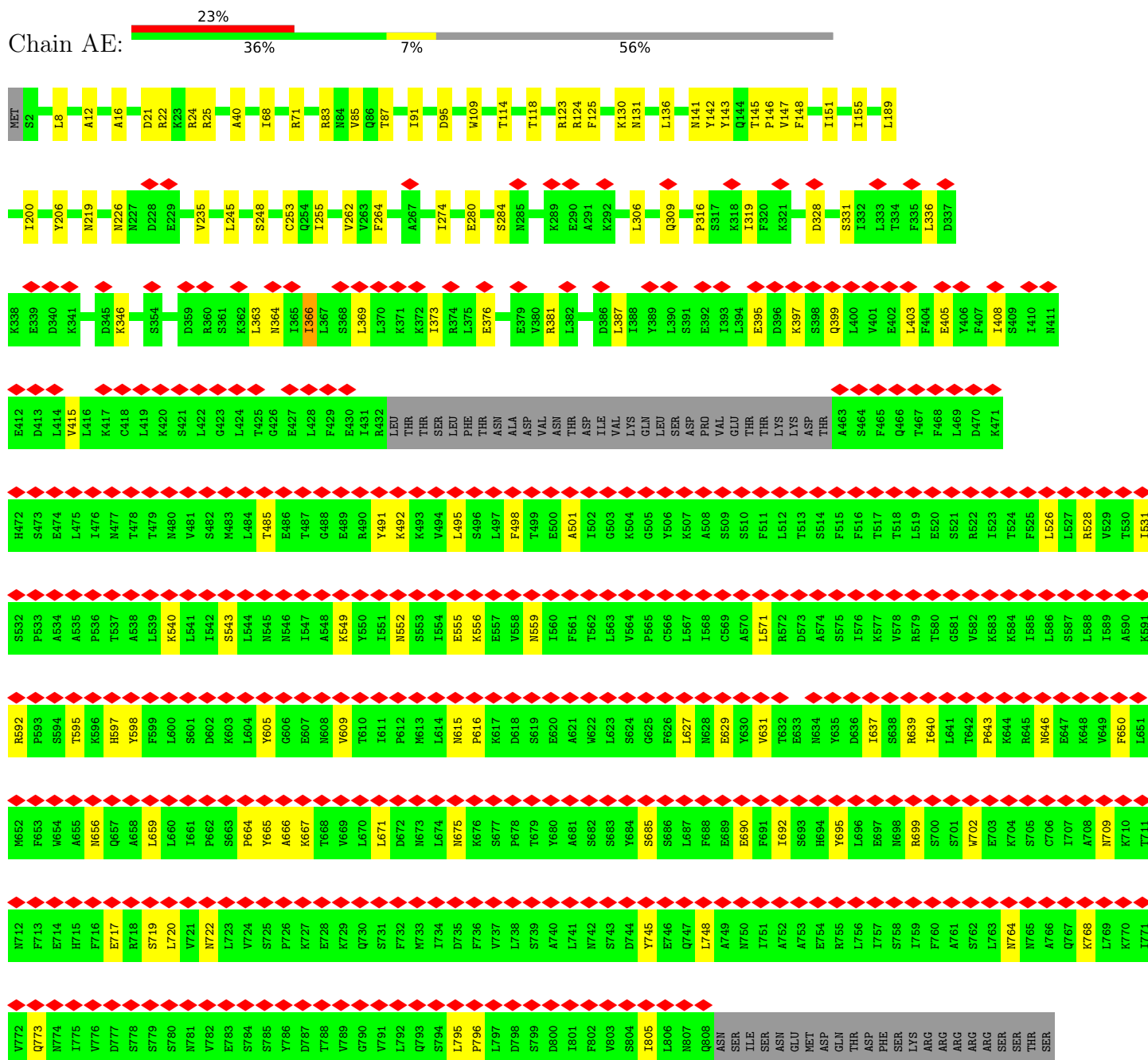


● Molecule 30: U3 small nucleolar RNA-associated protein 9



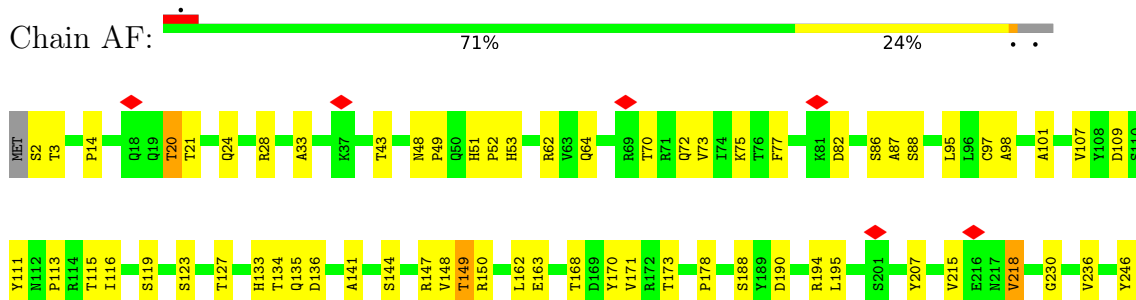


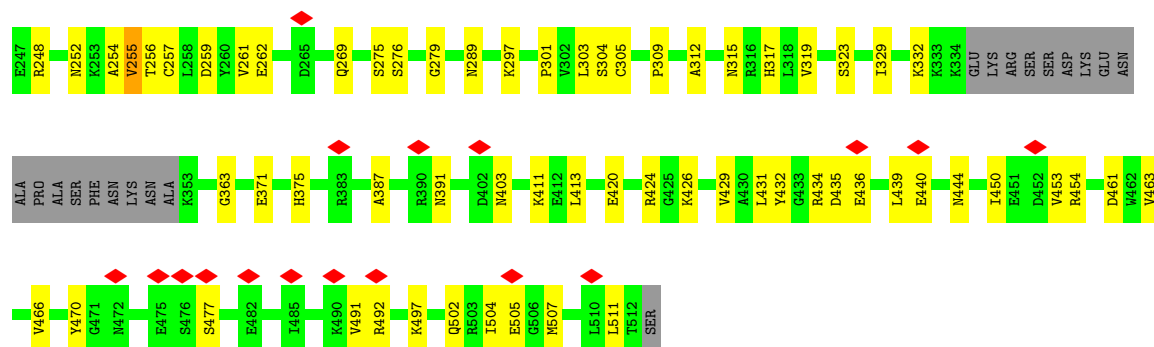
• Molecule 31: U3 small nucleolar RNA-associated protein 10



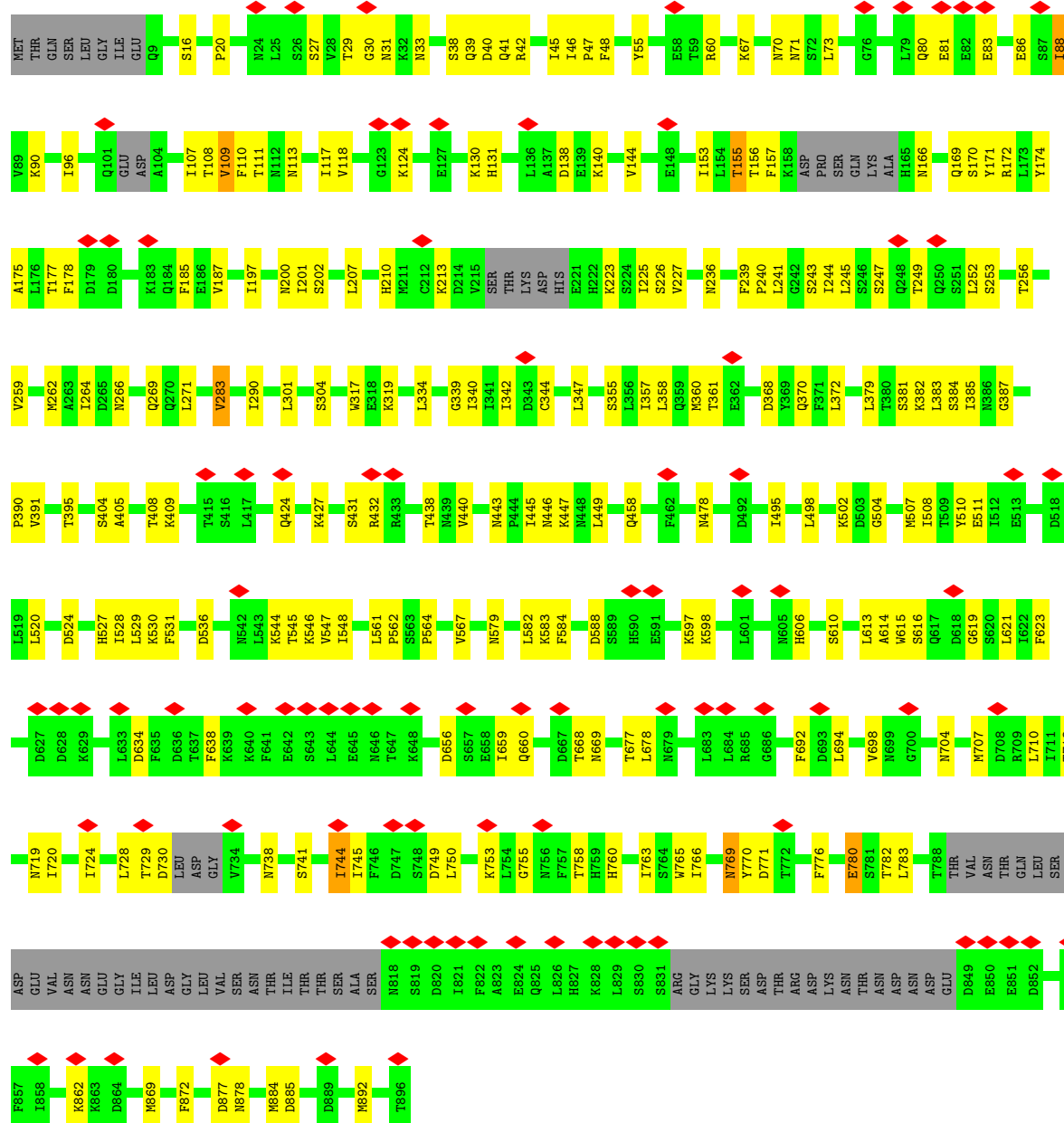
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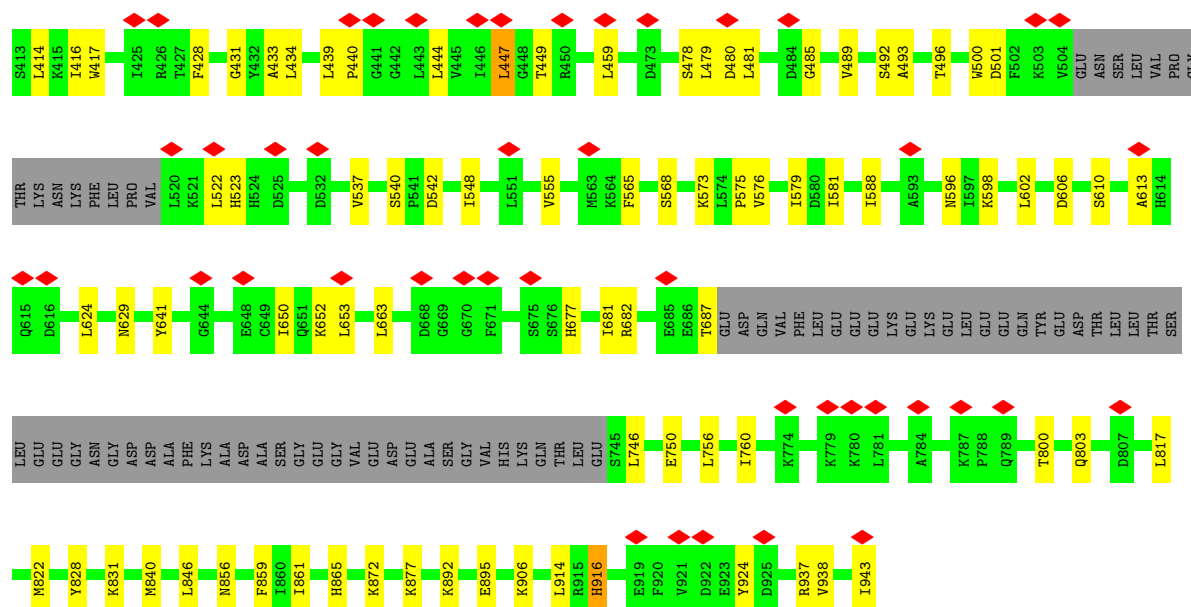
- Molecule 32: U3 small nucleolar RNA-associated protein 15



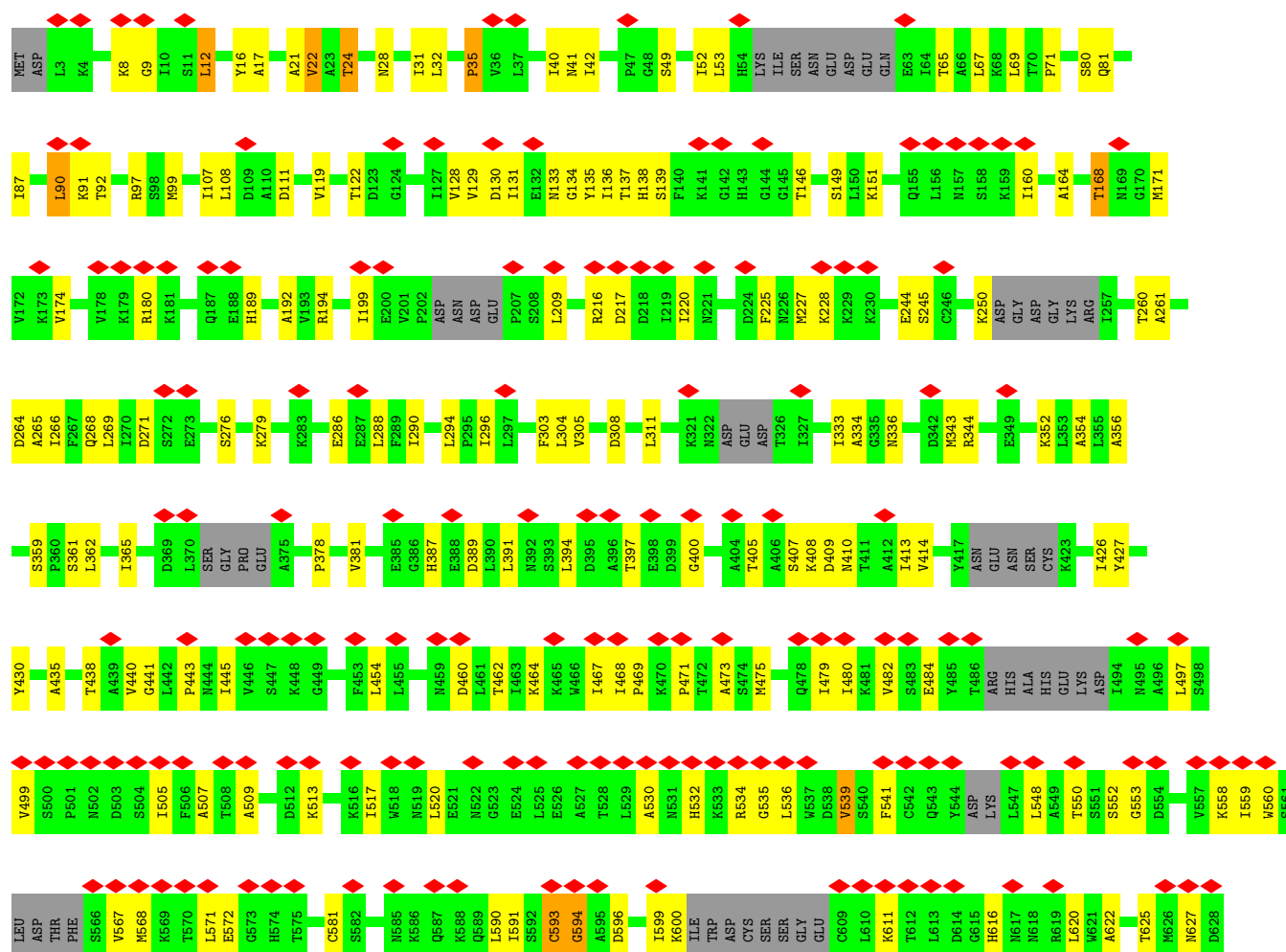


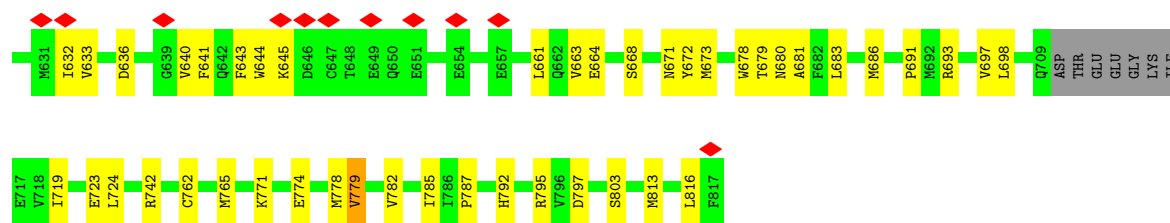
• Molecule 33: NET1-associated nuclear protein 1





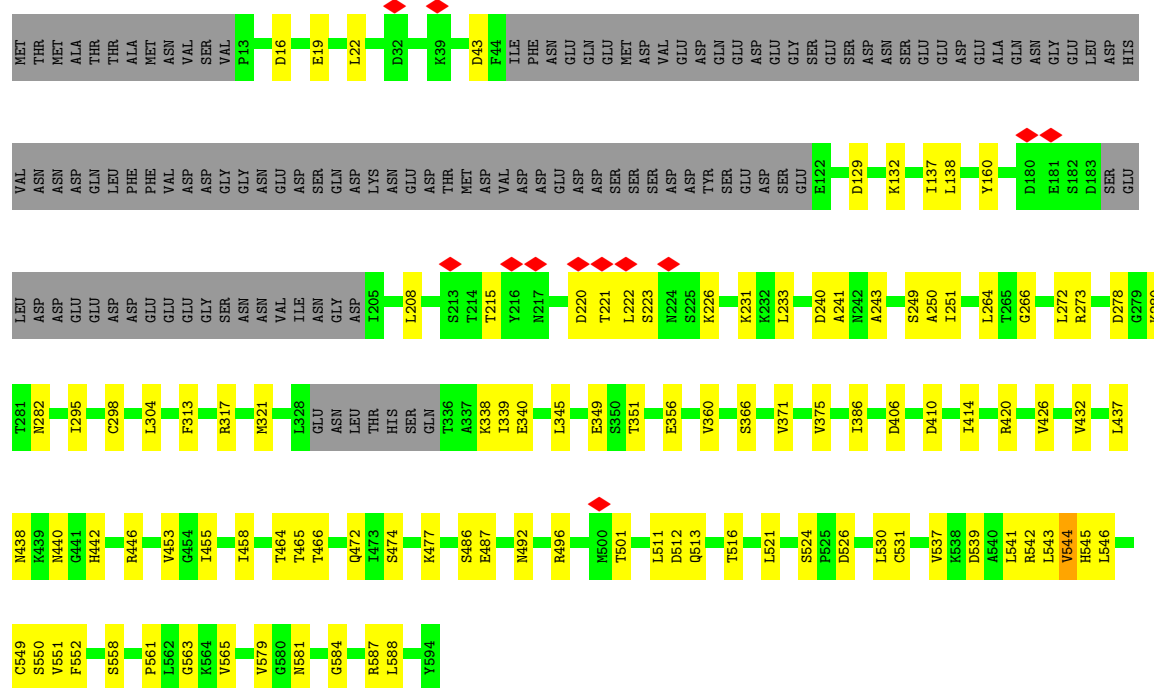
• Molecule 36: U3 small nucleolar RNA-associated protein 13





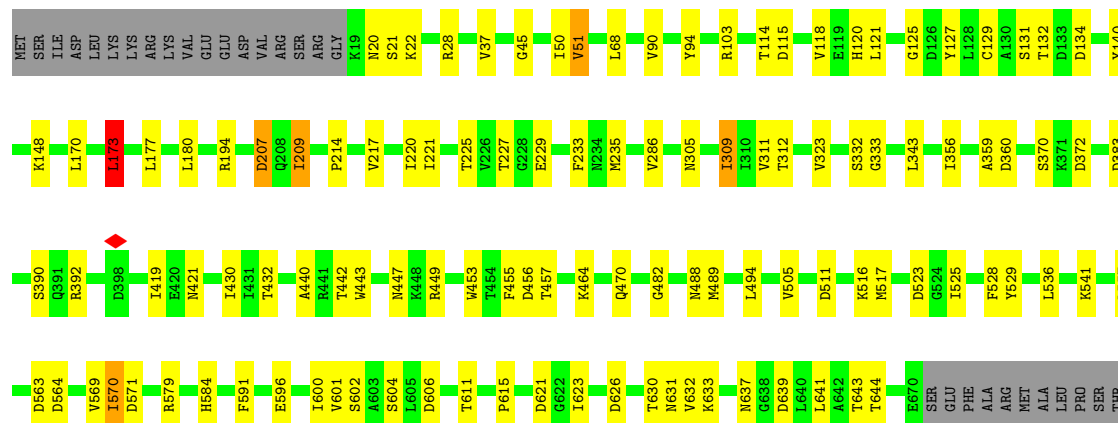
• Molecule 37: U3 small nucleolar RNA-associated protein 18

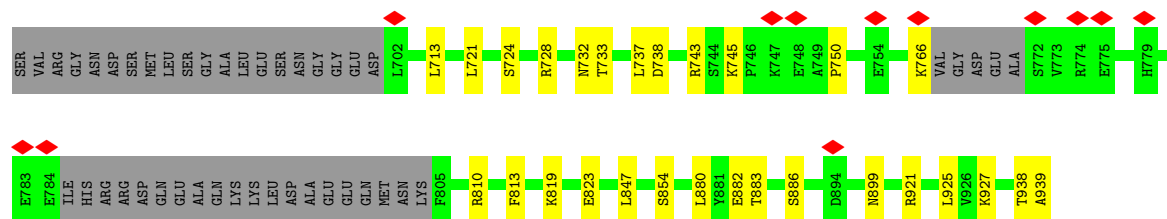
Chain B8: 63% 17% 20%



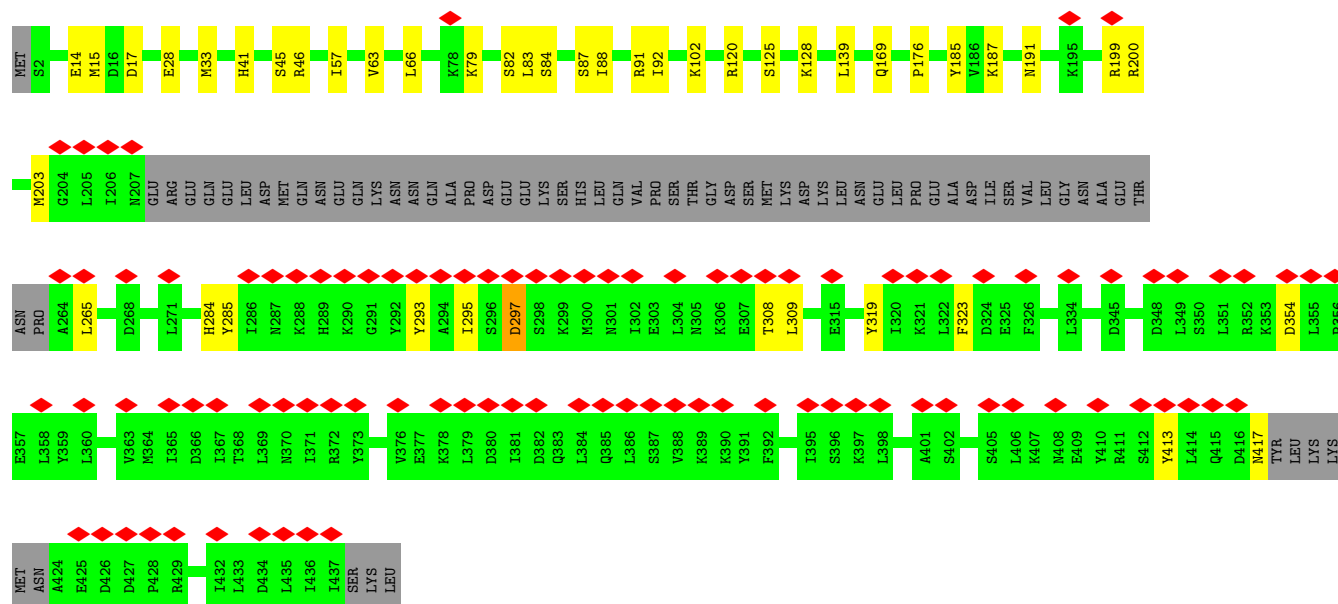
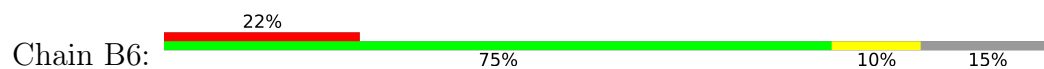
• Molecule 38: U3 small nucleolar RNA-associated protein 21

Chain BE: 77% 15% 8%

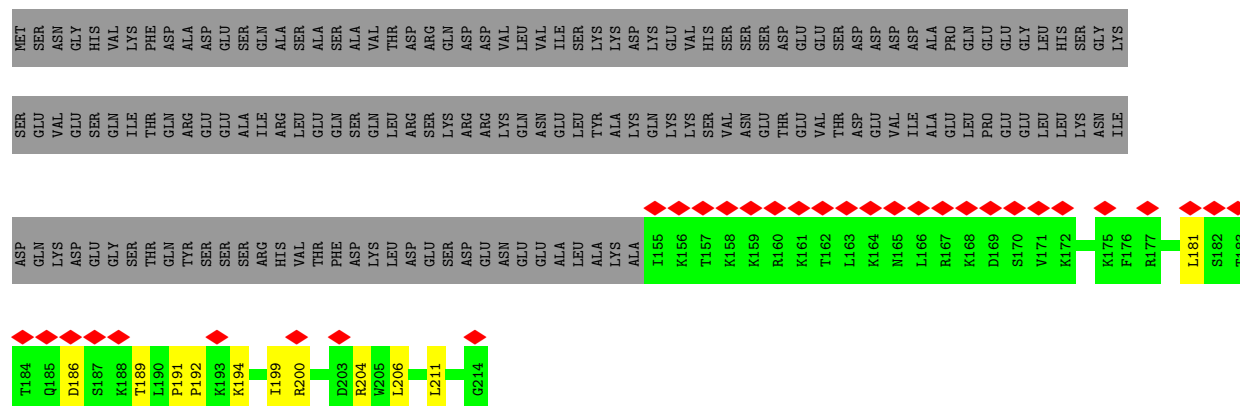




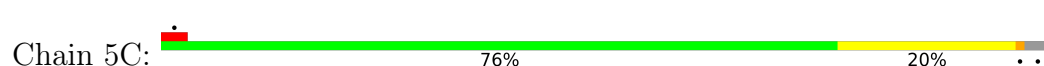
• Molecule 39: U3 small nucleolar RNA-associated protein 6



• Molecule 40: Bud site selection protein 21



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



- Molecule 44: U3 small nucleolar ribonucleoprotein protein IMP3

MET V2	L13	V16	L19	Q25	R28 D29	M33 R34	I38	L61	S62 L63	P66	E75	L78	M85	V101	C107 R108	M115 H116 R117	I131	H135	V136	R137	V138	G139	D145 P146		V158 T159	W160	S164	F180	S182
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MET	VAL	ARG	ARG	GLY	SER	ASN	ARG	THR	LYS	THR	SER	GLU	VAL	GLY	ASP	GLU	ILE	ASN	PRO	TYR	GLY	LEU	ASN	GLU	VAL	ASP	PHE	ALA	SER	LYS	ARG	GLU	GLN	VAL	LEU	LEU	GLY	GLN	SER	THR	PHE	GLY	ASP	SER	ASN	LYS	ASP	ASP	HIS	SER	LEU	LEU	GLU	ASP	GLU	ASP	GLN
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GLU GLU VAL VAL LEU LEU ALA ALA MET MET ASP ASP GLU GLU ASP ASP ASP ASP GLU GLU SER SER ILE ILE ASP ASP GLU GLU ARG ARG GLU GLU ASP ASP GLU GLU GLU GLU GLU GLU GLU GLU LEU LEU ASP ASP GLY GLY ALA ALA ALA ALA TYR TYR LYS LYS ILE ILE PHE PHE GLY GLY ARG ARG ASN ASN LEU LEU GLU GLU THR THR ASP ASP GLN GLN PRO PRO GLU GLU GLU GLU GLU GLU GLY GLY MET MET LEU LEU ASP ASP ASN ASN GLU GLU CYS CYS

ALA	TRP	GLY	GLY	THR	THR	LYS	GLY	GLU	TYR	TYR	GLY	ALA	ALA	ASP	ASP	ASP	ASP	ASP	ASP	GLU	GLU	ALA	ALA	ALA	LYS	LYS	ILE	GLU	GLY	LYS	GLU	GLU	LEU	ALA	LEU	ARG	GLN	GLN	GLN	LYS	LYS	HIS	LEU	GLU	GLU	GLU	LEU	LEU	ASN	ASN	ASN	ASP	TYR	LEU	LEU	ASP	GLU	GLU	GLU	GLU	GLU	TRP	TRP	VAL	LYS	SER	ALA	ALA	LYS	LYS	GLU	GLU	PRO
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ASP	MET	GLY	GLU	PHE	LYS	ASN	SER	THR	LYS	GLN	ALA	ASP	THR	LYS	SER	THR	ILE	THR	ASP	LEU	ILE	LEU	ASN	ASP	ASP	GLU	ALA	ALA	ARG	ASP	ASN	ASP	TYR	LEU	ARG	THR	MET	PHE	PRO	GLU	PHE	THR	GLU	ALA	PRO	PRO	LEU	SER	LYS	GLU	PHE	THR	GLU	LEU	ALA	PRO	LYS	PHE	ASP	GLU	LEU	LYS	LYS	SER
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GLU	GLU	ASN	GLU	PHE	ASN	LYS	LEU	LEU	ALA	LEU	GLY	SER	TYR	LEU	GLY	THR	ILE	SER	CYS	TYR	TYR	SER	ILE	LEU	LEU	HIS	HIS	ASN	ASN	GLU	ASP	PHE	THR	SER	SER	MET	LYS	GLY	HIS	GLY	PRO	VAL	MET	MET	GLU	LYS	LEU	THR	THR	LYS	GLU	GLU	ILE	LEU	THR	THR	THR	TRP	ARG	GLN	ALA	SER
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GLU LEU PRO SER SER PHE ASP VAL ASN GLN GLY ASP GLY SER GLU SER SER GLU THR ALA ASN ILE LYS LYS LEU ASN GLU GLN GLN ASN SER SER ASP GLU ASP GLY GLY LYS LYS LEU ARG GLU GLU ASP

GLU GLU GLU GLU GLU GLU GLU VAL ASP ASP ASP ASP ASP PHE PHE GLU GLU TYR VAL VAL GLN SER ARG ARG HIS HIS SER SER LYS PRO PRO LYS THR THR SER SER MET MET PRO PRO GLU GLU ALA ALA ASP ASP ASP ASP PHE PHE ILE ILE GLU GLU SER SER GLU GLU ILE ILE ALA ALA VAL VAL ASP ASP ALA ALA GLN GLN ASP ASP LYS LYS LYS LYS ALA ALA ARG ARG ARG ARG THR THR LEU LEU PHE PHE TYR TYR THR THR

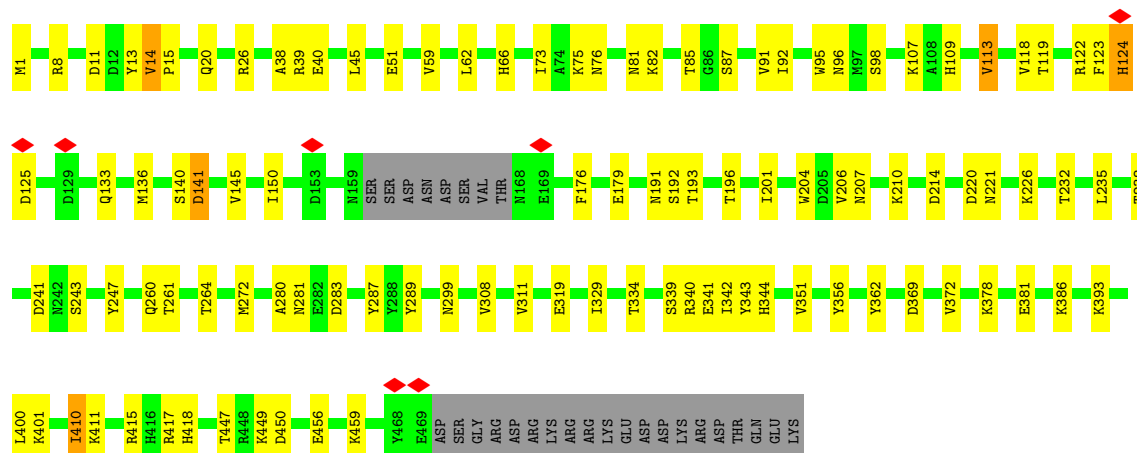
SER	LYS	ILE	ASP	GLN	GLN	GLU	ASN	LYS	LYS	T431	D432	R433	F434	K435	G436	D437	D438	D439	I440	P441	Y442	K443	E444	R445	L446	F447	E448	R449	GLN	GLN	ARG	LEU	LEU	LEU	ASP	GLU	ALA	ARG	LYS	ARG	GLY	MET	HIS	ASP	ASN	ASN	GLY	ALA	ASP	LEU	ASP	ASP	LYS	ASP	TYR	GLY	SER	GLU	ASP	GLU
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[illegible]



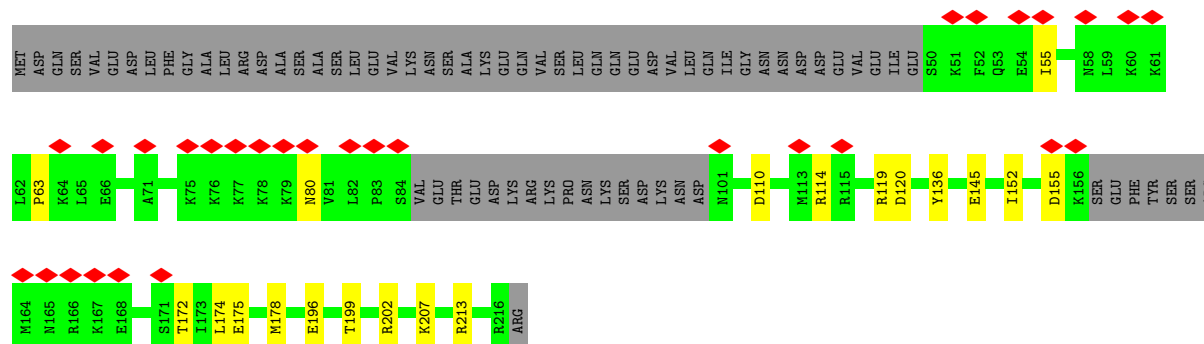
• Molecule 47: Protein SOF1

Chain 5I: 73% 21% 6%



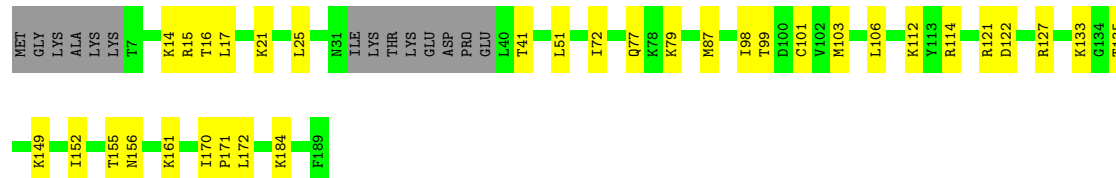
• Molecule 48: rRNA-processing protein FCF2

Chain 5J: 14% 57% 9% 34%



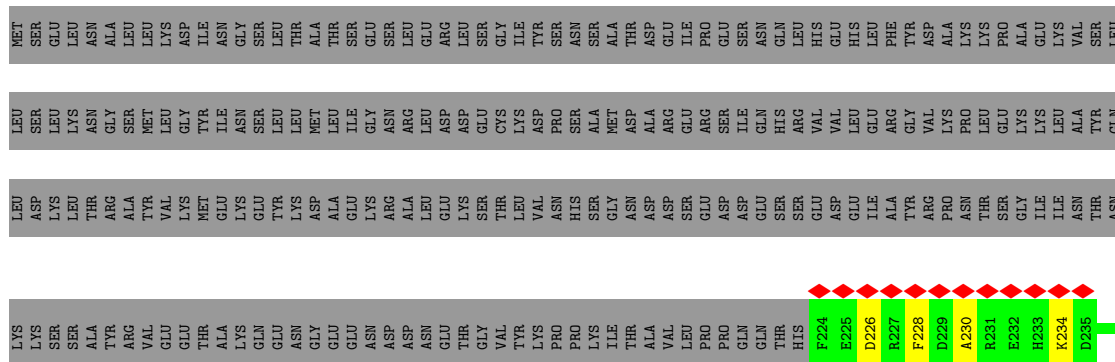
• Molecule 49: rRNA-processing protein FCF1

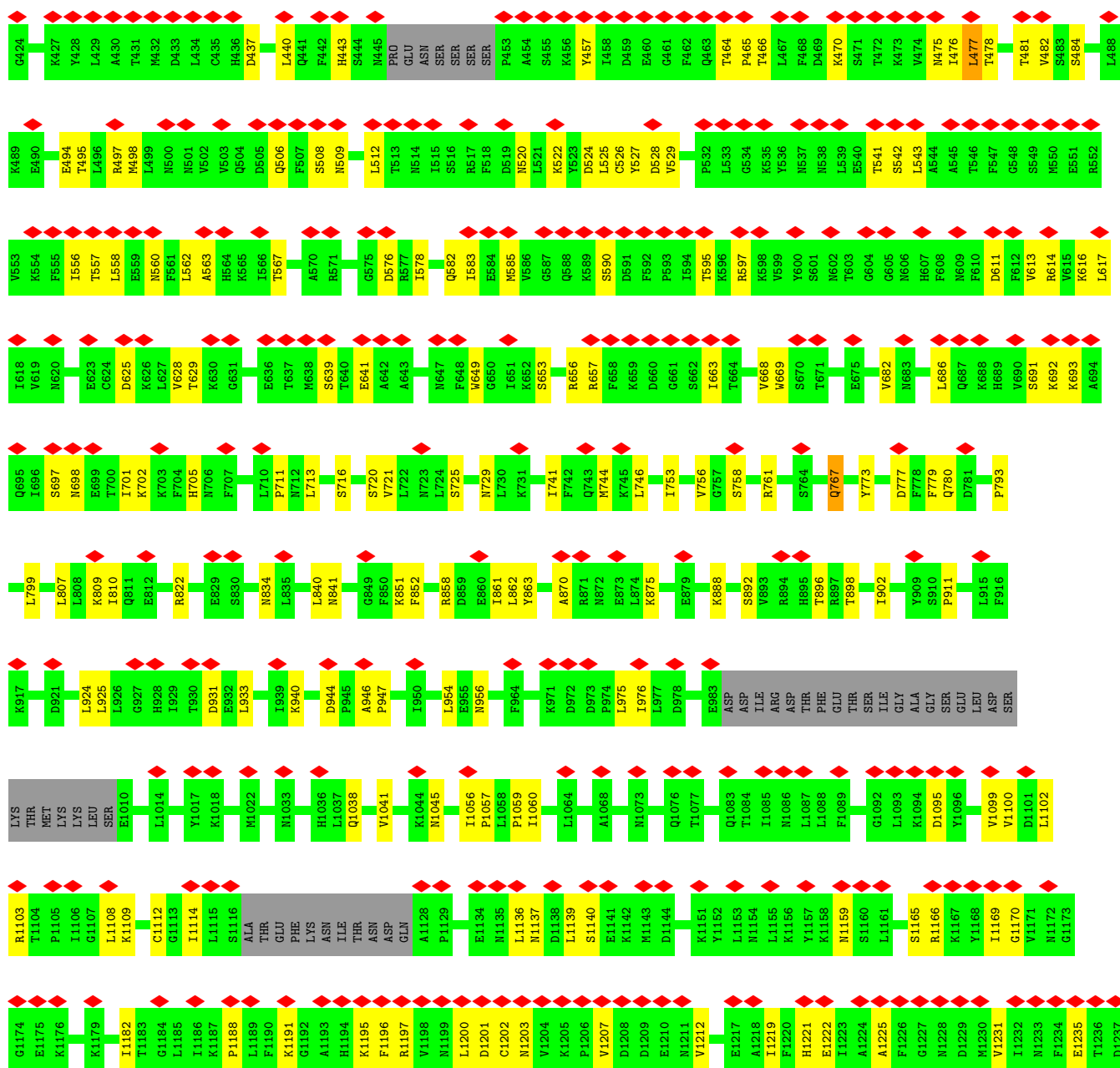
Chain 5K: 75% 17% 7%



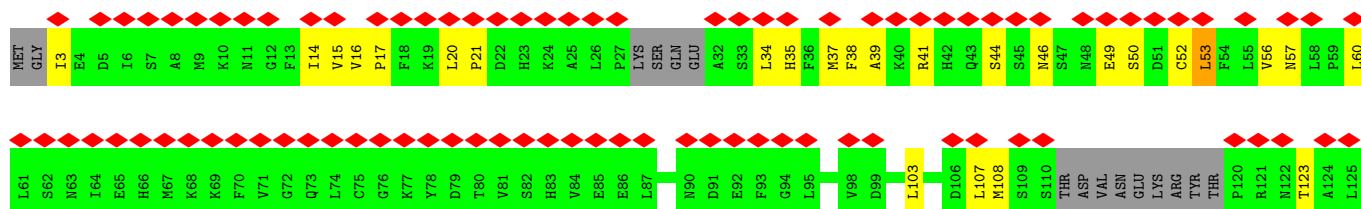
• Molecule 50: Ribosome biogenesis protein ENP2

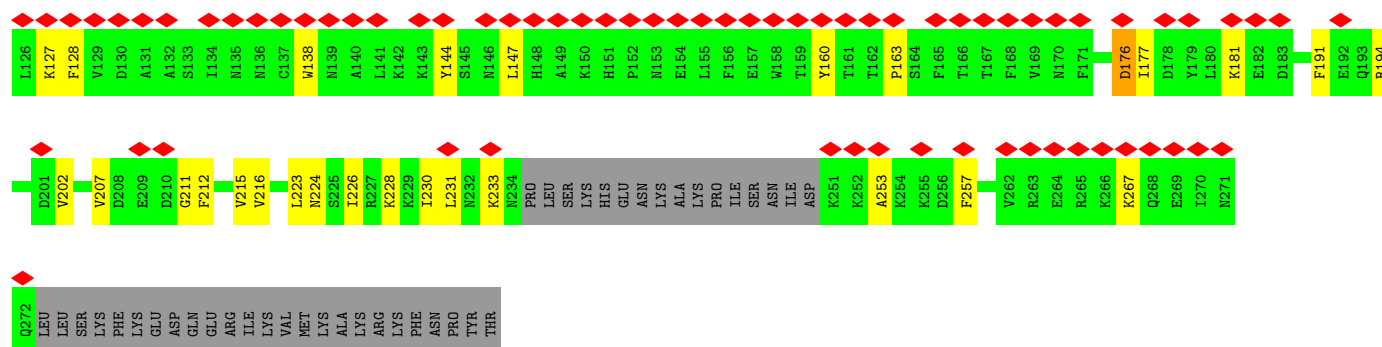
Chain RA: 47% 32% 15% 52%



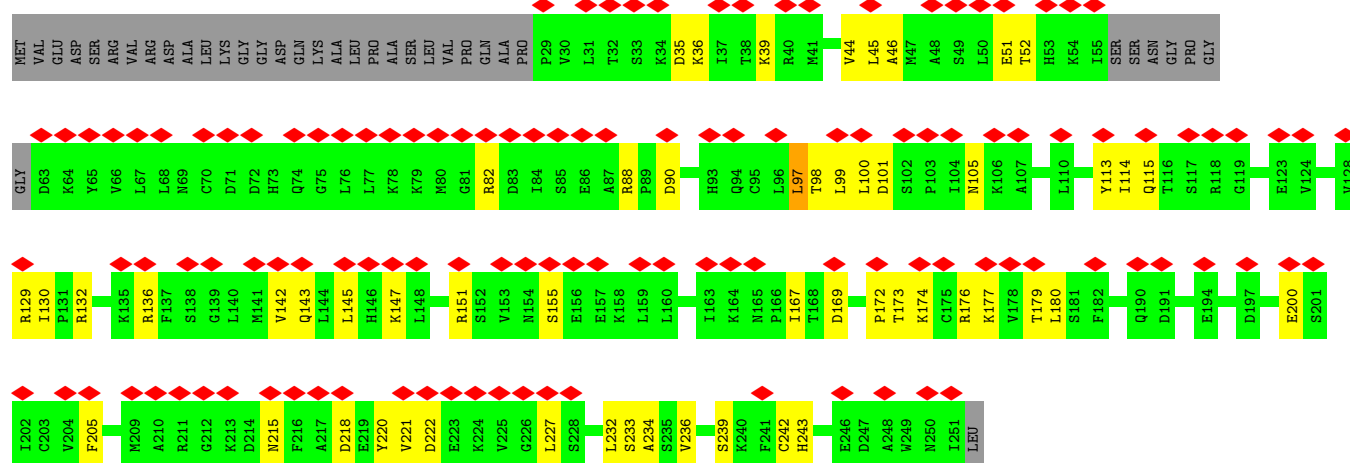


• Molecule 54: Ribosomal RNA-processing protein 7

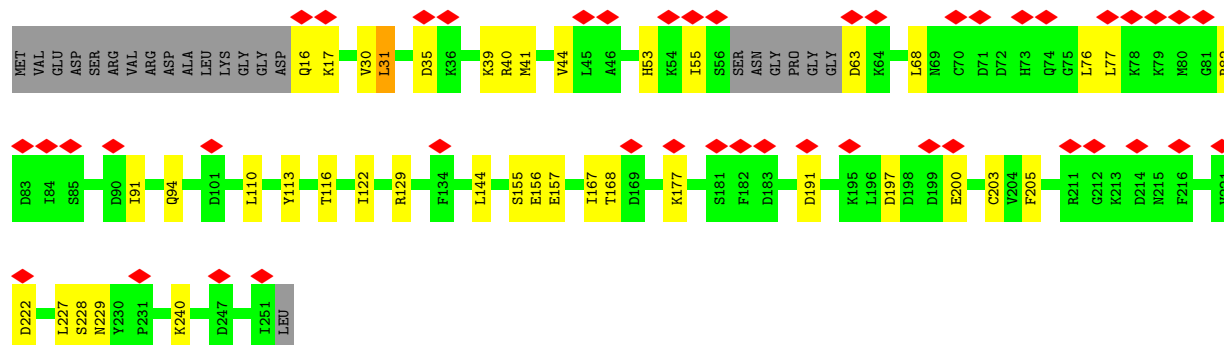
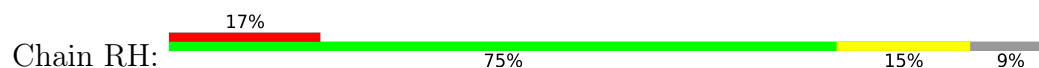




• Molecule 55: Ribosomal RNA small subunit methyltransferase NEP1

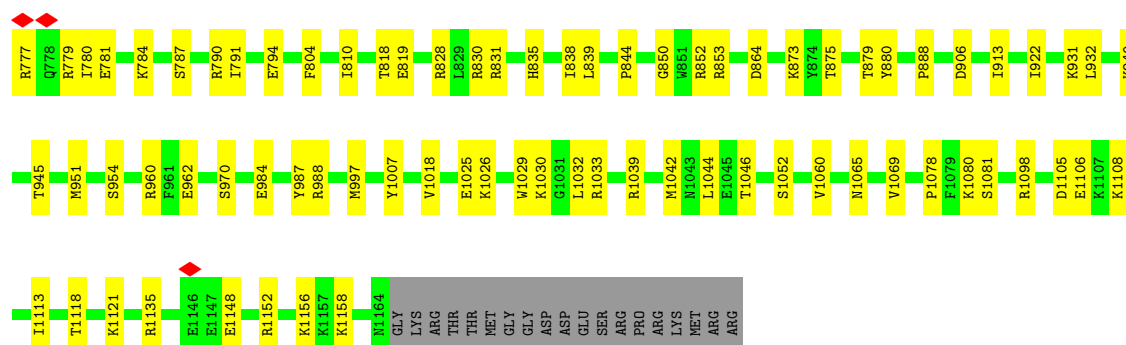


• Molecule 55: Ribosomal RNA small subunit methyltransferase NEP1

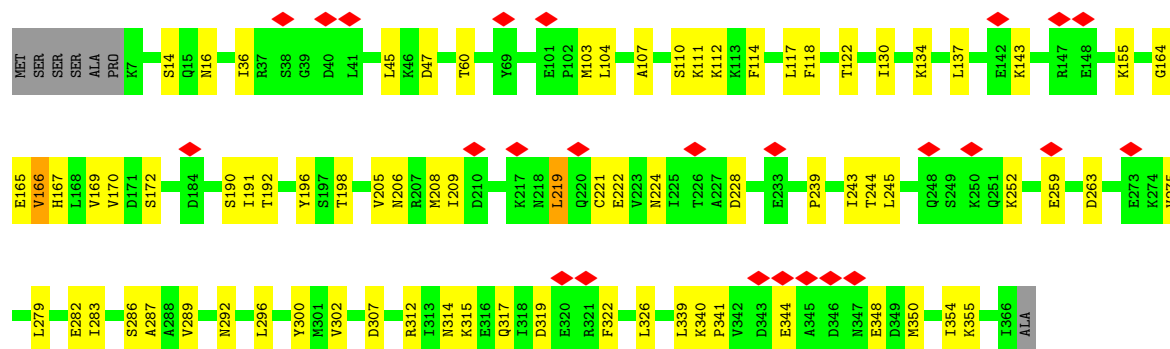
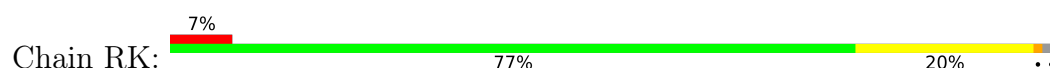


• Molecule 56: Ribosome biogenesis protein UTP30

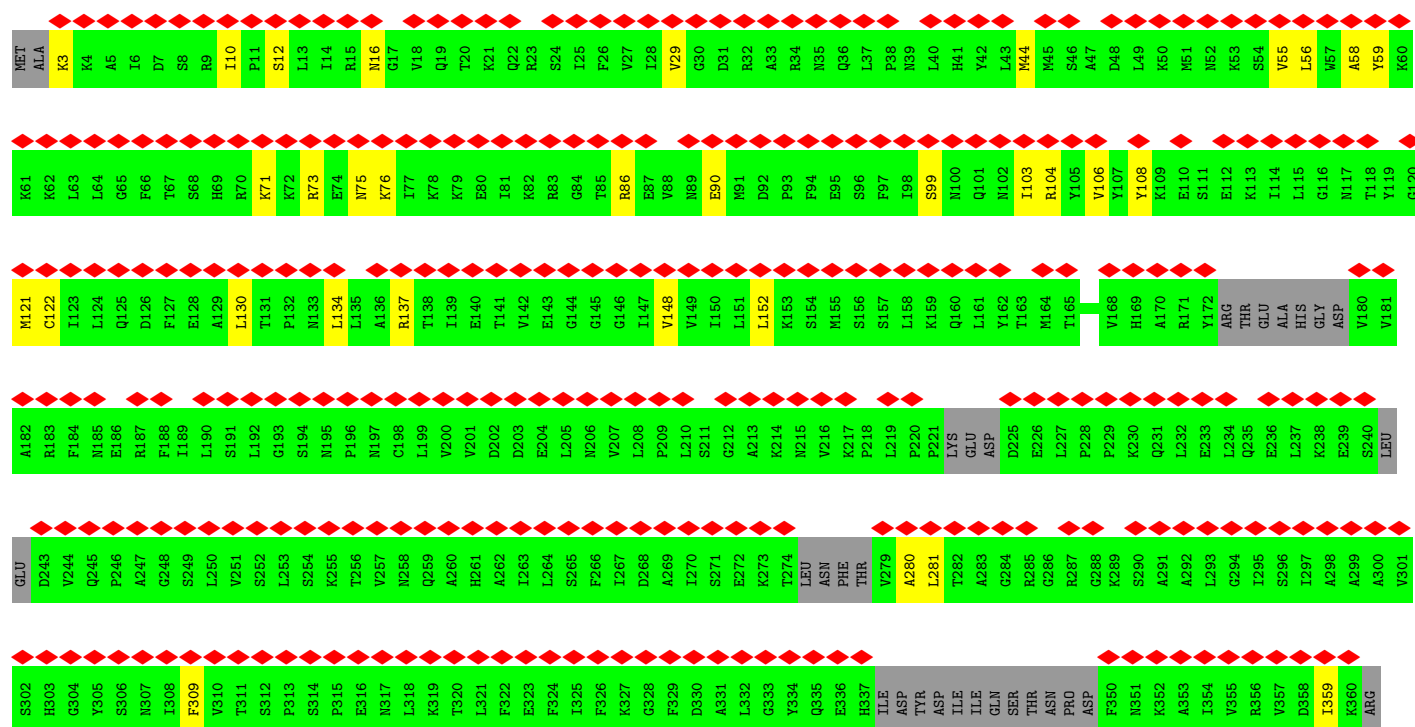
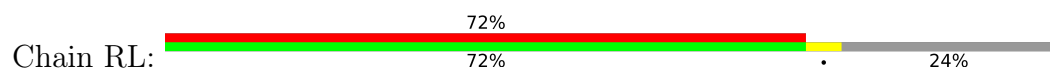


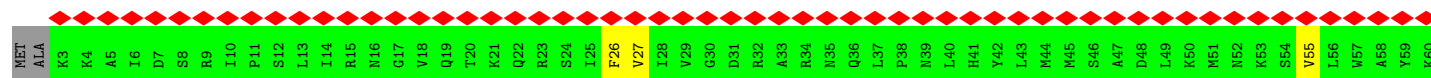


• Molecule 58: RNA 3'-terminal phosphate cyclase-like protein

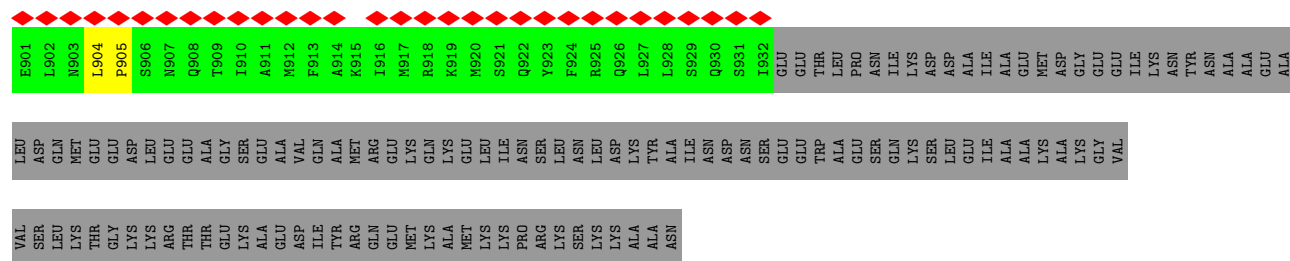


• Molecule 59: RNA cytidine acetyltransferase

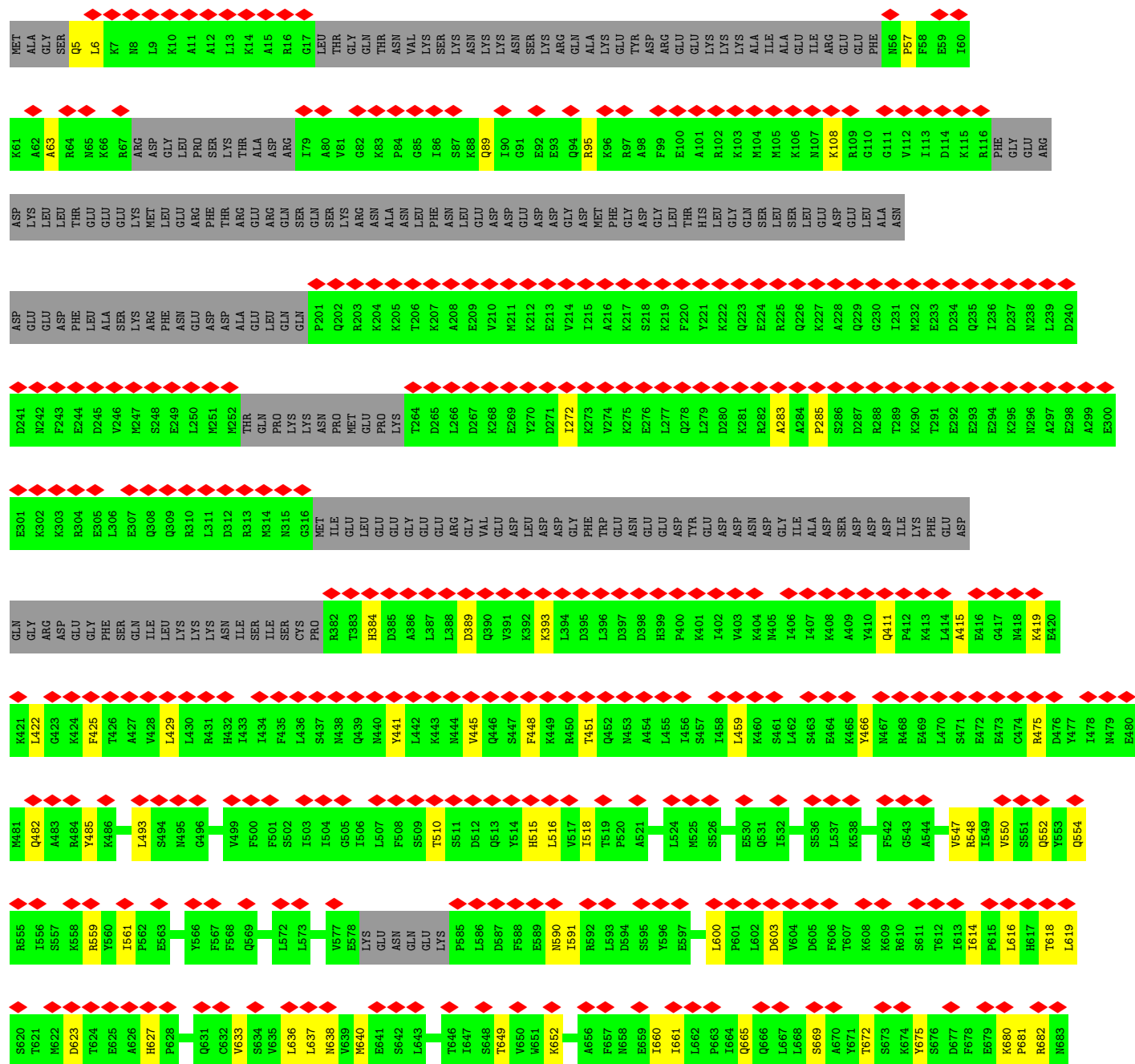




K61	K62	L63	L64	G65	F66	THR	SER	HIS	ARG	LYS	LYS	ARG	GLU	ASN	LYS	ILE	LYS	LYS	GLY	THR	ARG	GLU	VAL	ASN	GLU	MET	D92	P93	F94	E95	S96	F97	I98	S99	N100	Q101	N102	I103	R104	Y105	V106	Y107	Y108	K109	E110	S111	E112	K113	I114	L115	G116	N117	T118	Y119	G120					
M121	C122	I123	L124	Q125	D126	F127	E128	A129	L130	T131	P132	L133	L134	L135	A136	R137	T138	I139	E140	T141	V142	E143	G144	G145	G146	I147	V148	V149	I150	L151	L152	K153	S154	M155	S156	S157	L158	K159	Q160	L161	Y162	T163	T165	E166	D167	V168	H169	A170	R171	Y172	ARG	THR	GLU	ALA	HIS	GLY	ASP	V180		
V181	A182	R183	F184	N185	E186	R187	F188	I189	L190	S191	L192	G193	S194	N195	P196	N197	C198	L199	V200	V201	D202	D203	E204	L205	N206	V207	L208	P209	L210	S211	Q212	K213	K214	N215	V216	K217	PRO	LEU	A280	L281	T282	A283	G284	R285	G286	R287	Q288	K289	S290	A291	A292	L293	Q294	I295	S296	L297	A298	A299	SER	
LEU	D243	V244	Q245	P246	A247	G248	S249	L250	V251	S252	L253	S254	K255	T256	V257	N258	Q259	A260	H261	A262	I263	L264	S265	F266	I267	D268	A269	I270	S271	E272	K273	T274	LEU	ASN	PHE	THR	V279	A280	L281	T282	A283	G284	R285	G286	R287	Q288	K289	S290	A291	A292	L293	Q294	I295	S296	L297	A298	A299	A300		
V301	S302	H303	G304	Y305	S306	N307	I308	F309	V310	T311	S312	S314	P315	E316	N317	L318	K319	T320	L321	F322	E323	F324	I325	F326	K327	G328	F329	D330	A331	L332	G333	V334	Q335	E336	H337	ILE	ASP	TYR	ASP	ILE	ILE	G1N	THR	ASN	PRO	PHE	ASN	LYS	ALA	I354	V355	R356	V357	D358	I359	K360				
ARG	ASP	HIS	ARG	GLN	THR	ILE	Q368	Y369	I370	V371	P372	Q373	D374	H375	Q376	V377	L378	G379	Q380	A381	E382	L383	V384	V385	I386	D387	E388	A389	A390	A391	I392	PRO	LEU	PRO	I396	V397	K398	N399	L400	L401	G402	P403	Y404	L405	V406	F407	M408	A409	S410	T411	I412	M413	G414	TVR	GLU	GLY	THR	GLY	ARG	
SER	L422	S423	L424	K425	L426	I427	Q428	Q429	L430	R431	M432	Q433	ASN	ASN	THR	SER	GLY	ARG	GLU	SER	THR	GLN	THR	ALA	VAL	SER	ASP	ASN	LYS	LYS	ASP	HIS	LEU	HIS	SER	GLN	SER	ARG	GLN	LEU	ARG	E467	I468	S469	L470	D471	E472	P473	I474	R475	Y476	A477	P478	G479	D480					
P481	I482	E483	K484	W485	L486	N487	K488	L489	L490	C491	L492	D493	V494	L495	L496	S557	I497	K498	N499	P500	R501	F502	A503	T504	R505	G506	T507	P508	H509	P510	S511	Q512	C513	N514	L515	F516	V517	V518	N519	R520	D521	T522	L523	F524	S525	Y526	H527	P528	V529	S530	E531	N532	F533	L534	E535	K536	M537	M538	A539	L540
Y541	V542	S543	S544	H545	Y546	K547	N548	S549	P550	N551	D552	L553	Q554	L555	M556	S557	D558	A559	P560	A561	H562	K563	L564	F565	V566	L567	L568	P569	L570	P570	L571	D572	P573	K574	D575	G576	G577	R578	L579	P580	D581	P582	L583	C584	V585	T586	Q587	L588	A589	LEU	G592	E593	L594	S595	K596	E597	S598	V599	R600	
N601	S602	L603	S604	R605	G606	Q607	N608	A609	G610	G611	D612	L613	T614	P615	W616	L617	T618	S619	Q620	Q621	F622	Q623	D624	E625	F626	F627	A628	S629	L630	S631	G632	A633	R634	L635	W636	R637	T638	A639	T640	N641	P642	E643	Y644	A645	S646	M647	G648	Y649	G650	S651	R652	A653	T654	E655	L656	L657	R658	D659	Y660	
F661	GLU	GLY	LYS	PHE	THR	ASP	MET	GLU	ASP	PRO	LYS	ASP	TYR	SER	ILE	LYS	ARG	VAL	SER	ASP	LYS	GLU	ALA	LYS	THR	ASN	LEU	LYS	ASP	VAL	LYS	LEU	ARG	ASP	ALA	LYS	THR	LEU	PRO	L708	L709	L710	K711	L712	S713	E714	Q715	P716	P717	H718	W719	L720								
H721	Y722	L723	G724	W725	S726	Y727	G728	L729	W730	Q731	S732	L733	H734	K735	F736	W737	K738	N739	W740	S741	F742	W743	P744	Y745	Y746	L747	R748	Q749	K810	W750	A751	N752	D753	L754	T755	G756	E757	H758	T759	G760	W761	N762	L763	W764	W765	L766	E767	G768	R769	E770	S771	W772	W773	L774	W775	E776	F777	A778	K779	D780
F781	R782	K783	R784	W785	L786	S787	L788	L789	W790	Y791	D792	F793	H794	K795	F796	T797	A798	W799	Q800	A801	L802	S803	W804	L805	E806	S807	S808	K809	K810	A811	Q812	D813	L814	S815	D816	D817	E818	K819	H820	S882	A883	N884	L885	L886	A887	T888	G889	H829	Q891	R892	K893	N894	I895	D896	T897	R898	A899	K900		
L842	D843	S844	Y845	S846	W847	N848	L849	L850	D851	Y852	H853	W854	I855	G856	D857	M858	W859	P860	M861	L862	A863	L864	L865	Y866	F867	G868	D869	K870	A871	GLY	SER	VAL	LYS	LEU	S878	S879	V880	Q881	A883	L884	L885	A887	T888	G889	L890	Q891	R892	K893	N894	I895	D896	T897	R898	A899	K900					

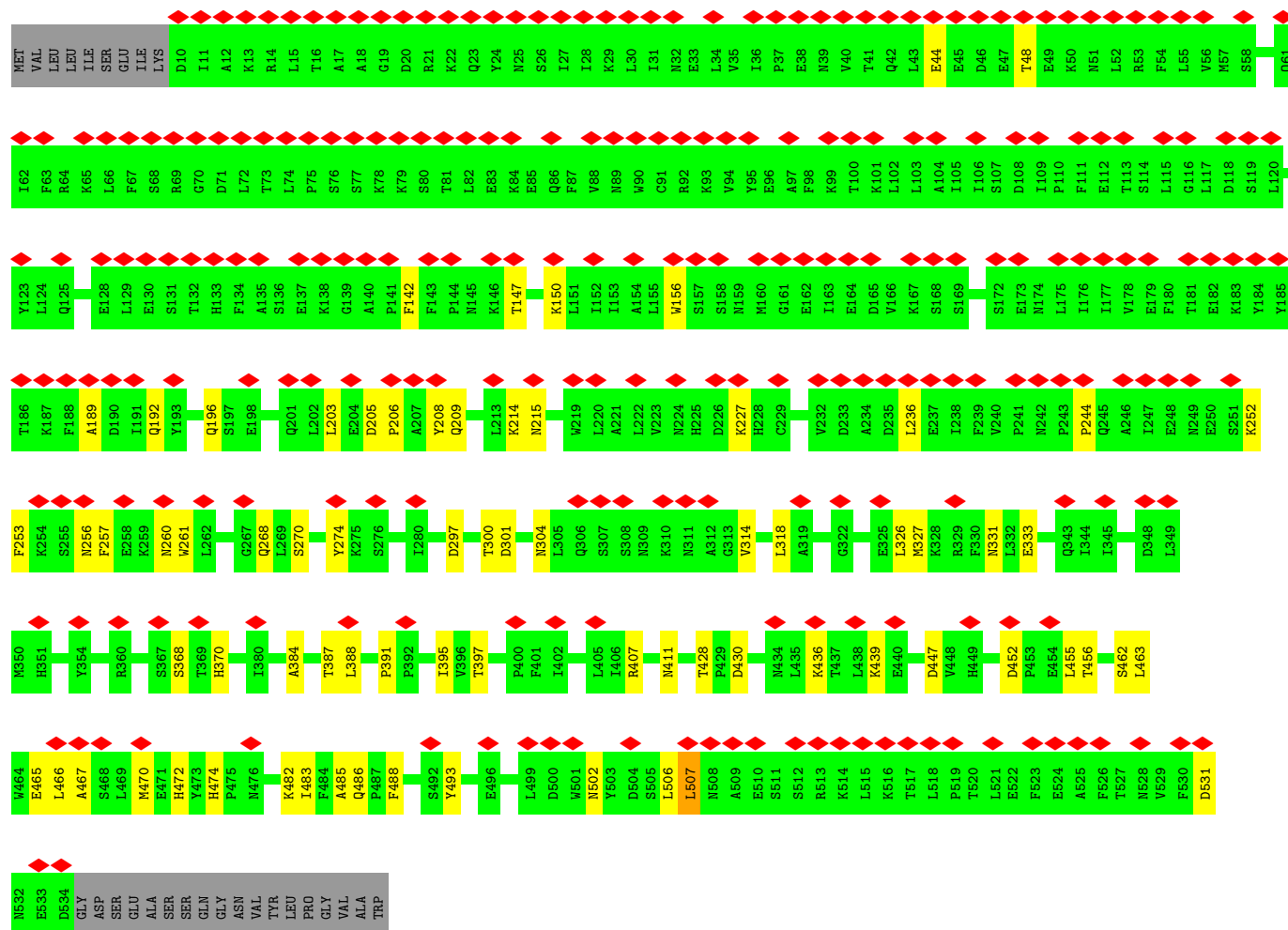
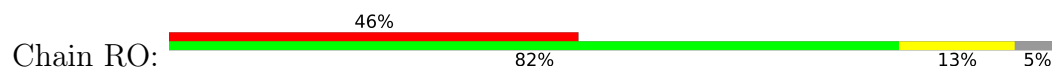


● Molecule 60: Nucleolar complex protein 14

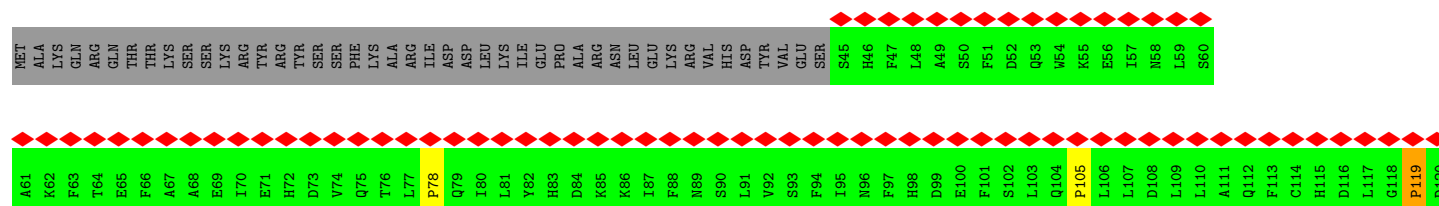
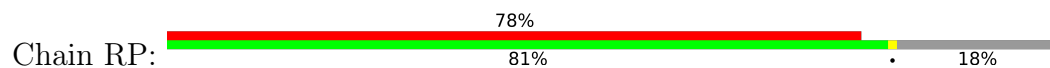




• Molecule 61: Nucleolar complex protein 4

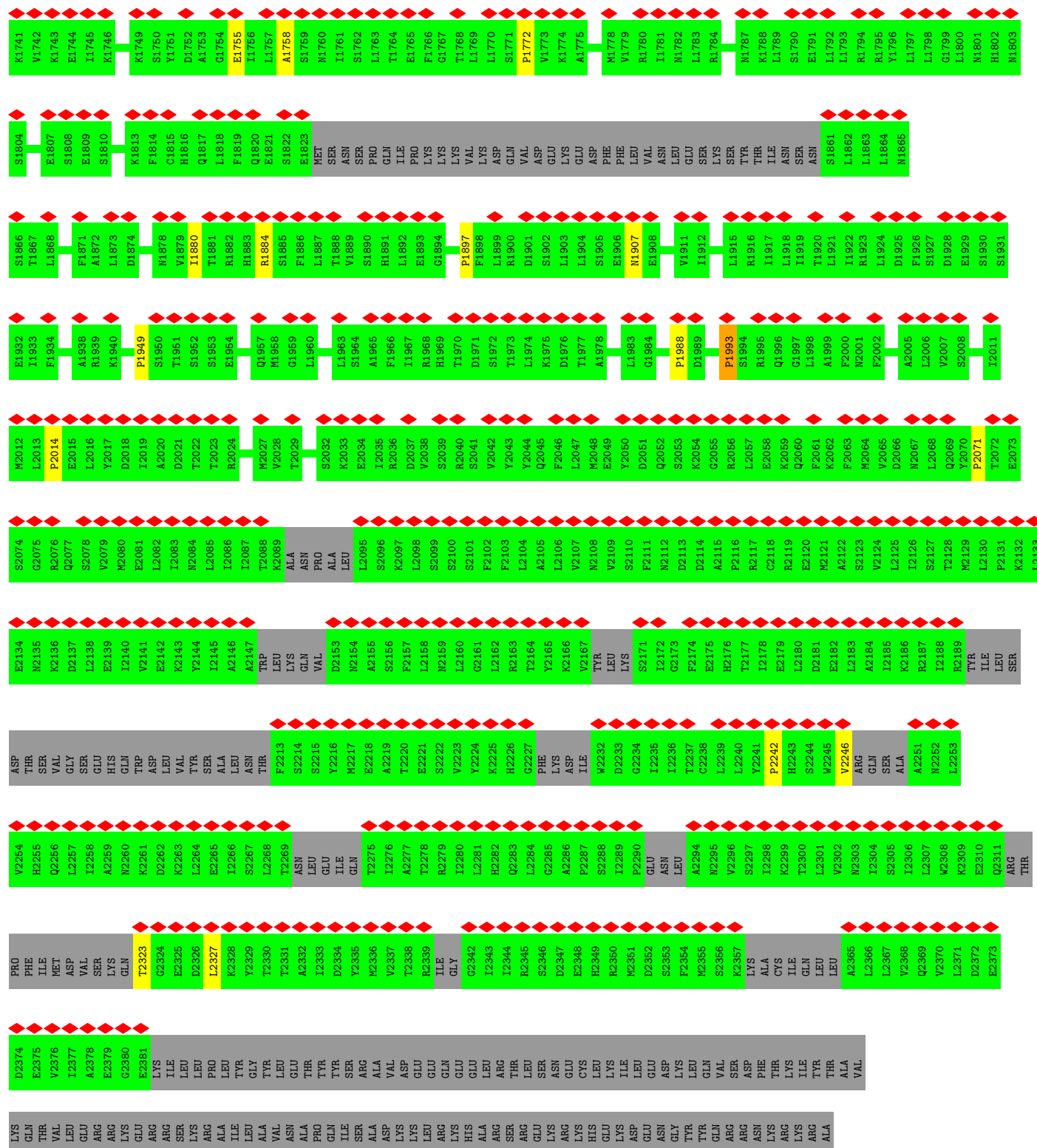


• Molecule 62: U3 small nucleolar RNA-associated protein 20



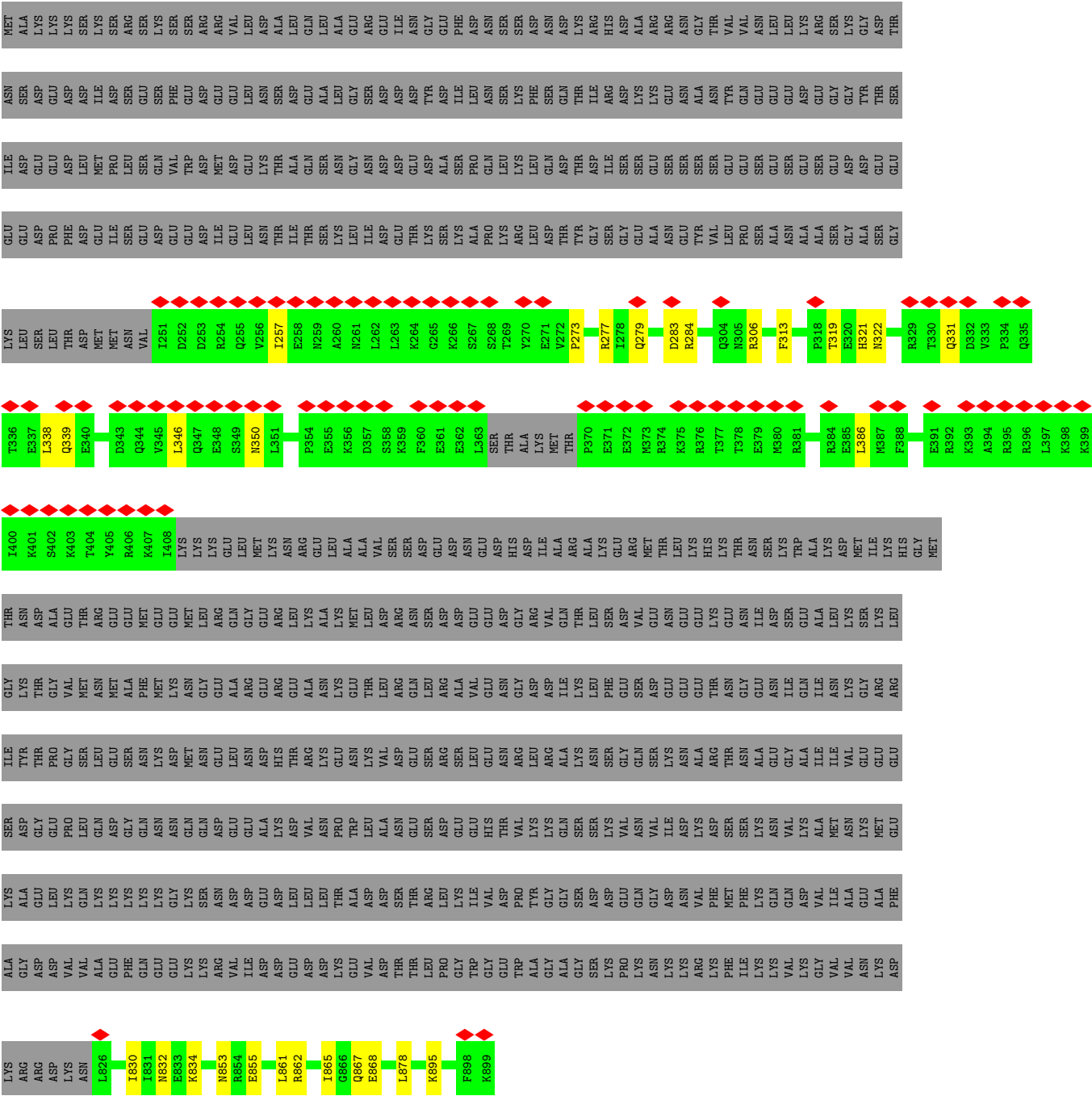
F121	L181	T241	D301	L361	L421	TRP	I541	F661	E721	V781	I841	I901
L122	S182	S242	F302	F362	K422	ARG	L542	F662	D722	H782	K842	T902
K123	H183	T243	N303	A363	K423	ALA	D543	L663	G723	L783	N843	T903
F124	S184	Q244	D304	L364	N424	ILE	N544	K664	A724	S784	V844	F904
Y125	K185	E245	S305	F365	N425	I485	Y545	L665	M725	T785	Y845	L905
E126	E186	T246	LEU	I366	Q426	F486	E546	L666	K726	T786	S846	T906
E127	Y187	L247	ASP	R367	S427	K487	N547	F667	V727	Q787	A847	E907
A128	L188	H248	ALA	N368	Q428	Y488	Y548	G668	L728	V788	T848	N908
I129	S189	T249	THR	S369	Q429	S489	K549	L669	W729	A789	E849	G909
K130	R190	K250	ASN	D370	K430	K490	E550	L670	L730	E790	L850	S910
T131	F191	A251	ILE	D371	K431	L491	S551	T671	S731	M791	H851	Q911
L132	S192	K252	ASP	V371	I432	Q492	L552	V672	W732	H792	D852	S912
I133	A193	E253	R313	K372	I433	N493	ASN	F673	V733	F793	H853	I913
N134	E194	I254	I314	T373	A433	T494	PHE	F674	W734	V794	L854	K914
L135	A195	M255	L315	L374	L434	E495	LEU	S675	V735	W795	M855	A915
L136	L196	S256	K316	T375	F435	L496	ARG	P676	L736	I796	V856	E916
D137	S197	V257	V317	L376	F436	I497	G557	V677	L737	A797	L857	D917
A138	F198	L258	T319	F377	L437	ILE	W558	V678	D738	T798	L858	E918
A139	L199	L259	T320	H378	E438	PRO	N559	W679	T739	F799	G859	K919
I140	V200	H260	I321	K380	V439	LEU	K560	T679	S739	W800	S860	V920
E141	R201	E261	V322	L381	D440	E502	L561	G680	I740	Y801	H861	V921
F142	K202	A262	F323	F382	K441	R503	V562	V681	D741	N802	N862	M922
E143	C203	L263	S324	N383	P443	I504	S563	D683	F743	D803	T863	P923
S144	P204	T264	E325	Y384	E444	F505	N564	T684	S744	F804	D864	Y924
S145	V205	K265	SER	A385	L445	S506	L565	L685	H745	K805	V865	V925
N146	S206	S266	GLY	L386	Q446	T507	H566	E686	I746	T806	Q866	L926
V147	N207	S267	ARG	T387	K447	F508	P567	V687	W747	Y807	K867	R927
F148	L208	P268	LYS	N388	V448	A509	S568	W688	S748	K808	L868	I928
E149	R209	E269	P331	I389	R449	S510	E569	Y689	K749	D809	A869	F929
W150	E210	R270	D332	S390	E450	P511	S570	T690	W750	E810	L870	P930
G151	F211	S271	W333	D391	V451	D512	L571	T691	S751	E811	D871	Q931
F152	V212	V272	N334	C392	N452	N513	K572	K691	D752	D812	T752	R932
C154	S214	L274	K335	F393	F453	F514	L574	E693	Q753	M813	Q753	A933
L155	V215	L275	I336	L394	P454	T515	M575	A694	N754	E814	L754	Q934
A156	F216	S276	T337	E395	E455	K516	S576	L695	T755	N815	A875	V935
Y157	E217	D277	I338	F396	E456	ASP	H577	V696	S756	E816	Y876	P936
I158	K218	I278	L339	F397	F457	MET	Y578	W697	I757	R817	K877	P937
F159	L219	W279	I340	Q398	L458	VAL	P579	K698	L758	V818	L878	S938
K160	E220	M280	E341	F399	L459	G520	S580	L699	S759	I819	P879	S939
Y161	GLY	N281	R342	A400	S460	L522	L581	V700	T760	T820	T880	Q940
L162	ASP	N282	I343	L401	L461	L523	L582	L701	T761	G821	L881	Q941
S163	ASP	I282	N344	R402	I462	K524	L583	L642	W762	S822	N882	K942
K164	GLN	S283	SER	L403	D463	L525	S584	ASN	E763	W823	K883	R943
F165	THR	K284	GLU	S404	F464	V526	L585	VAL	R764	T824	Y884	S944
L166	ASN	Y285	ASN	Y405	F465	R527	T586	GLY	K765	E825	R885	R945
V167	L228	A286	CYS	A406	V466	K528	W587	GLU	L706	W826	D886	K946
K168	Y229	S287	ALA	R407	T467	E529	N588	PHE	P707	D827	L887	I947
K169	E230	I288	SER	V408	A468	D530	F589	GLY	D708	T828	L888	A948
L170	Q231	E289	L353	F409	E469	A532	N590	LYS	E709	W830	K889	V949
V171	L232	L291	Q355	S410	N471	S533	L591	T652	W710	V831	L891	I950
L172	L233	L292	D356	F411	D472	GLY	P592	K653	Q711	F831	L892	S951
T173	I234	L293	K357	ASN	S473	ASN	D593	T654	N712	L832	L893	V952
C174	L235	P293	L358	LEU	N474	LEU	G594	D655	L713	K833	D893	L953
D175	F236	V294	V358	LYS	D475	LEU	K595	K656	D714	T834	D894	P954
L176	T237	Y295	A359	PHE	D476	L538	T596	L657	Y715	L835	T895	N955
L177	E238	E296	F360	LEU	L476	K539	S597	V658	Y716	N836	L896	P956
I178	S239	V297	L419	GLN	F477	T540	Y598	G659	Q717	K837	F897	K957
P179	M240	M298	L419	F420	E478		THR	S660	L719	F838	L898	P958
L180	Q300	Y299			I479						E900	V960

L1681	K1682	G1622	L1621	I1561	R1501	L1441	K1381	F1321	I1261	L1201	H1141	D1081	S1021	I961
K1682	G1622	G1622	G1622	V1562	N1502	Y1442	P1382	P1322	E1262	L1202	V1142	I1082	V1022	N962
G1683	L1623	L1623	L1623	R1563	I1503	G1443	N1383	ARG	E1263	V1203	K1143	Y1083	L1023	D963
G1684	T1624	G1624	L1384	D1564	G1504	G1444	L1384	ILE	L1264	S1204	E1144	A1084	Q1024	F964
S1685	N1625	G1565	E1385	G1565	N1505	D1445	L1385	LEU	Y1265	I1205	A1145	V1085	P1025	L965
Q1686	D1626	A1566	E1386	A1566	E1506	E1446	E1386	THR	T1266	T1206	V1146	V1086	L1026	S966
I1687	D1627	E1447	A1387	E1447	T1507	E1447	E1387	PHE	T1267	E1207	I1147	V1087	I1027	L967
H1688	I1628	S1568	S1388	S1568	Q1508	A1448	S1388	GLY	L1268	M1208	K1148	K1088	Y1028	A968
V1689	T1629	K1569	K1389	K1569	I1509	D1449	K1389	LEU	S1269	G1209	P1149	P1089	S1029	S969
L1690	M1630	L1570	S1390	L1570	A1510	PHE	S1390	ILE	S1270	F1210	I1150	R1090	I1030	E970
S1691	F1631	T1571	I1391	T1571	I1511	THR	I1391	ASP	L1271	I1211	I1151	I1091	A1031	R971
V1692	L1632	L1572	S1392	G1512	G1512	ASN	S1392	GLY	F1272	Q1212	E1152	S1092	M1032	L972
T1693	P1633	S1573	M1393	G1513	G1513	VAL	M1393	TYR	K1273	D1213	A1153	H1093	D973	D973
V1694	S1634	K1574	L1394	L1514	L1514	HIS	L1394	SER	T1274	D1214	A1154	F1094	Y1034	Y974
I1695	L1635	F1575	K1395	A1515	A1515	ILE	K1395	TYR	F1275	H1215	D1155	S1095	Y1035	N975
Y1696	L1636	P1576	D1396	Q1516	Q1516	GLN	D1396	SER	D1276	V1216	S1156	D1096	V1036	Y976
I1697	T1637	S1577	I1397	H1517	H1517	LEU	I1397	GLU	E1277	R1217	I1157	E1097	L1037	F977
L1698	N1638	ASN	L1398	M1518	M1518	HIS	L1398	LEU	R1278	S1218	I1158	M1098	D1038	F978
K1699	I1639	LEU	L1399	S1519	S1519	GLU	L1399	GLU	M1279	R1219	L1159	L1099	T1039	G979
S1700	G1640	ASP	P1400	W1520	W1520	R1462	P1400	TRP	L1280	L1220	N1160	Q1100	E1040	N980
M1701	Q1641	GLU	L1401	M1521	M1521	Q1463	L1401	PRO	R1281	I1221	P1161	Q1101	S1041	S981
H1702	V1642	SER	I1402	Q1522	Q1522	R1464	I1402	LEU	V1282	S1222	V1162	P1102	T1042	H982
G1703	L1643	ASN	R1403	Y1523	Y1523	A1465	R1403	PHE	S1283	S1223	M1163	S1103	E1043	Q983
R1644	R1644	PHE	I1404	K1524	K1524	I1466	I1404	THR	L1284	L1224	D1164	S1104	E1044	L984
L1705	S1645	ILE	G1405	L1525	L1525	K1467	G1405	PHE	T1285	I1225	D1165	L1105	V1045	N985
K1706	K1646	GLN	L1406	A1526	A1526	R1468	L1406	LEU	E1286	S1226	H1166	L1106	H1046	S986
H1707	S1647	LEU	R1407	L1527	L1527	L1469	R1407	PHE	L1287	I1227	Y1167	R1107	L1047	S987
S1708	E1648	TYR	D1408	R1528	R1528	G1470	D1408	ILE	F1288	L1228	V1168	L1108	K1048	K988
D1709	E1649	PRO	S1409	W1529	W1529	E1471	S1409	ASN	I1289	K1229	D1169	F1109	K1049	A989
L1710	L1650	THR	L1410	Y1530	Y1530	H1472	L1410	LYS	E1290	G1230	L1170	L1110	M1050	T990
R1651	L1651	LEU	E1411	I1531	I1531	H1474	E1411	GLU	L1291	K1231	V1171	Y1111	A1051	L991
T1712	D1652	LYS	E1412	S1532	S1532	H1474	E1412	GLU	G1292	L1232	T1172	Y1112	S1052	K992
S1713	A1653	ILE	V1413	M1533	M1533	Q1475	V1413	LEU	R1293	K1233	L1173	A1113	N1053	T993
S1714	V1654	LEU	GLN	L1534	L1534	L1476	GLN	LEU	K1294	K1234	I1174	H1114	L1054	L994
S1715	R1655	GLY	SER	K1535	K1535	K1477	SER	ARG	V1295	ARG	C1178	L1118	G1058	T998
M1716	V1656	THR	GLU	T1536	T1536	D1478	GLU	THR	P1296	Q1236	T1176	P1116	Q1056	R995
V1717	T1657	ARG	TVR	K1537	K1537	T1479	TVR	ASN	E1297	E1237	S1177	S1117	K1056	R996
K1718	L1658	ASP	VAL	Q1537	Q1537	S1480	VAL	SER	L1298	M1238	C1178	L1118	Q1057	R997
G1719	G1659	THR	SER	P1538	P1538	I1481	SER	HIS	L1299	N1238	L1178	L1118	G1058	T998
I1720	K1660	GLU	Y1430	M1539	M1539	I1481	V1420	ALA	E1299	D1239	K1179	Y1119	L1059	G999
I1721	I1661	Q1540	F1431	Q1540	Q1540	S1482	L1421	ILE	S1300	T1240	K1180	Q1120	K1060	F1000
N1722	S1662	H1483	T1432	S1422	S1422	H1483	S1422	MET	I1301	Q1241	I1181	F1121	C1061	V1001
E1723	I1663	Y1484	D1433	Y1423	Y1423	Y1484	Y1423	LYS	S1302	K1242	L1182	L1122	C1061	V1001
M1724	I1664	L1485	E1435	M1424	M1424	L1485	M1424	PHE	K1303	L1243	P1183	Y1123	L1062	N1002
I1725	L1665	I1486	D1436	V1425	V1425	I1486	V1425	ILE	L1304	L1244	S1184	Y1124	S1063	I1003
F1726	G1666	P1487	E1436	K1426	K1426	P1487	K1426	D1376	V1305	K1245	S1185	D1125	S1064	V1004
G1727	A1667	M1488	M1437	T1427	T1427	I1488	T1427	F1377	A1306	K1245	S1185	D1125	V1065	N1005
E1668	A1667	L1489	M1436	N1428	N1428	I1489	N1428	I1378	A1306	I1246	Y1186	E1126	F1066	N1005
F1728	E1668	L1547	M1437	T1428	T1428	E1490	T1428	N1379	A1307	L1247	V1187	F1127	E1067	S1006
A1729	I1669	I1548	K1429	K1429	K1429	E1490	K1429	E1380	D1307	K1248	K1188	A1128	E1067	T1007
L1670	V1671	VAL	Y1430	Y1430	Y1430	H1491	Y1430	M1309	L1308	L1249	L1189	T1129	V1069	L1008
E1731	V1671	GLN	F1431	GLN	GLN	V1492	F1431	N1309	S1309	I1250	S1190	A1130	V1069	S1009
F1732	V1672	LEU	T1432	LEU	LEU	V1493	T1432	S1310	S1310	V1251	S1190	A1130	G1070	V1010
K1733	F1673	SER	D1433	SER	SER	F1494	D1433	Y1311	Y1311	F1251	D1191	T1131	N1071	L1011
D1734	I1674	VAL	F1434	PRO	PRO	S1495	F1434	S1312	S1312	F1252	S1192	A1132	T1072	R1012
S1735	K1675	LEU	E1435	LEU	LEU	D1496	E1435	S1313	S1313	N1253	M1193	L1133	F1073	T1013
E1736	E1676	ARG	D1436	ARG	ARG	D1497	D1436	Y1254	S1314	Y1254	S1194	M1134	D1074	N1014
N1737	E1677	GLU	M1437	GLU	GLU	E1498	M1437	R1315	I1195	C1255	I1195	D1135	W1075	F1015
V1738	L1677	T1558	A1438	T1558	T1558	E1498	A1438	H1317	M1316	C1256	S1196	T1136	S1076	P1016
H1739	A1679	L1559	E1439	L1559	L1559	R1499	E1439	H1317	H1317	S1257	T1197	T1137	T1077	L1017
T1740	T1680	R1560	L1440	R1560	R1560	Y1500	L1440	Y1319	E1318	W1258	F1198	S1138	S1079	H1018

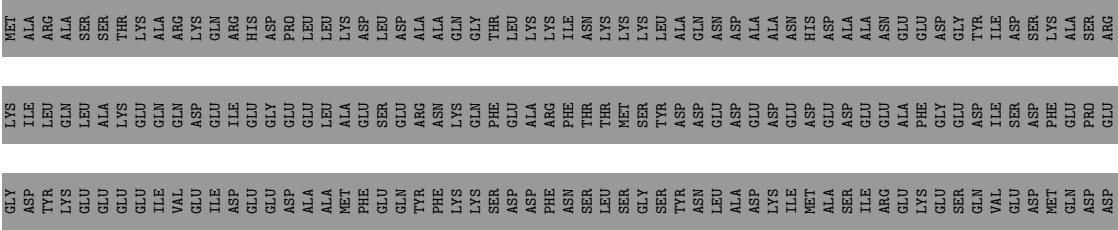
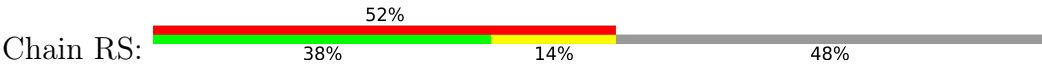


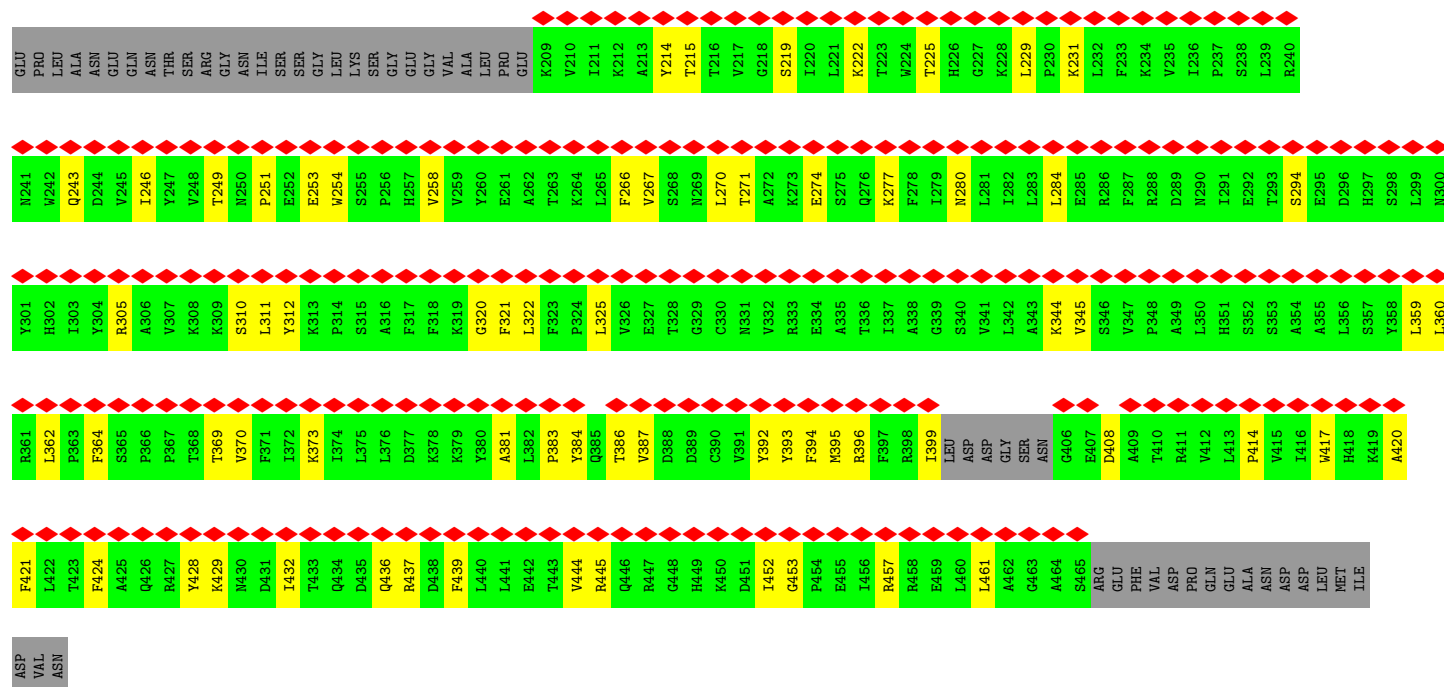
• Molecule 63: U3 small nucleolar RNA-associated protein 14



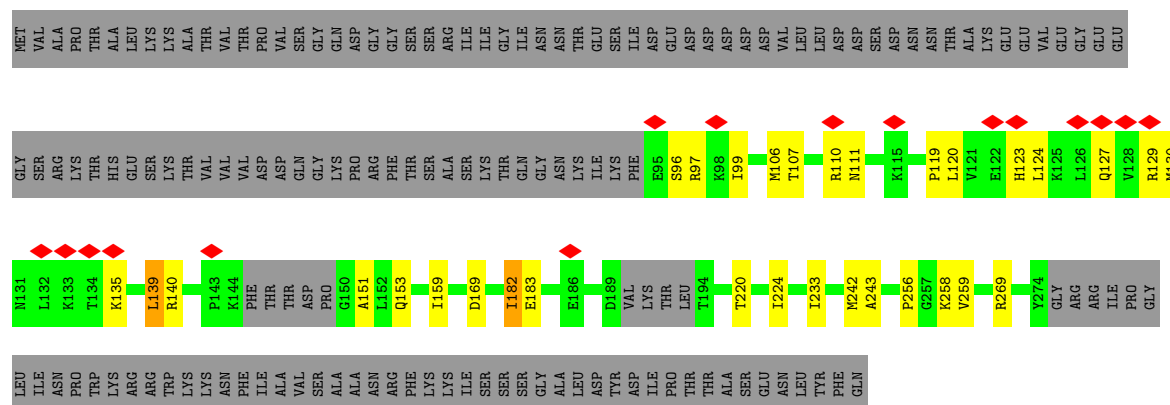
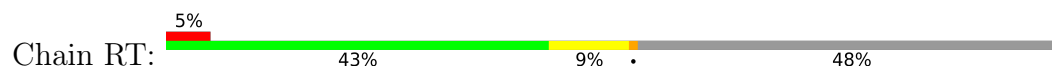


● Molecule 64: Essential nuclear protein 1

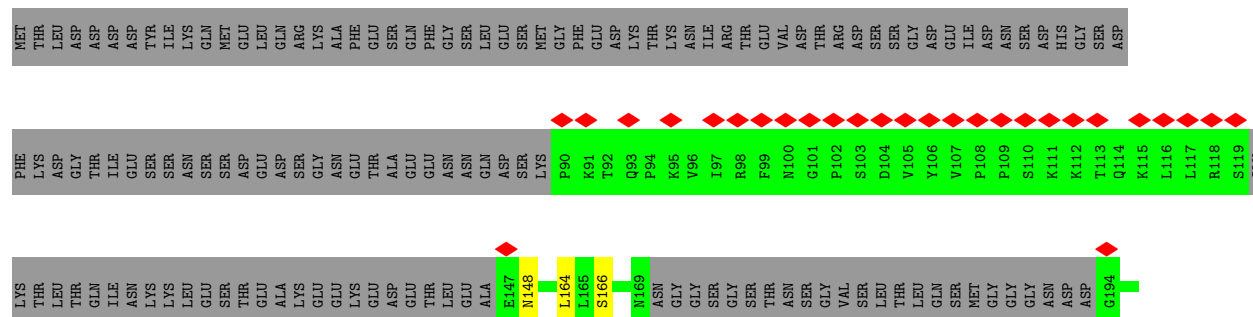




• Molecule 65: Pre-rRNA-processing protein PNO1



• Molecule 66: Protein FAF1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	121139	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	25000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.130	Depositor
Minimum map value	-0.073	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.016	Depositor
Map size (Å)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.61	0/4141	0.54	0/6433
2	5A	0.55	0/12462	0.53	5/19411 (0.0%)
3	SA	0.42	0/31237	0.50	5/48637 (0.0%)
4	SC	0.54	0/1777	0.82	5/2388 (0.2%)
5	SF	0.31	0/1854	0.75	0/2504
6	SG	0.66	0/1690	0.71	0/2285
7	SH	0.31	0/890	0.72	0/1189
8	SI	0.42	1/1341 (0.1%)	0.79	2/1806 (0.1%)
9	SJ	0.28	0/1347	0.65	0/1801
10	SK	0.58	0/1410	0.70	0/1888
11	SM	0.34	0/1020	0.73	0/1374
12	SN	0.27	0/873	0.71	0/1185
13	SO	0.46	0/1109	0.70	0/1495
14	SP	0.51	0/879	0.77	0/1186
15	SR	0.78	0/990	0.90	3/1335 (0.2%)
16	ST	0.32	0/930	0.67	0/1251
17	SX	0.59	0/1020	0.72	0/1371
18	SY	0.60	0/798	0.77	0/1065
19	SZ	0.36	0/822	0.74	0/1103
20	Sc	0.50	0/613	0.72	0/828
21	Sd	0.66	0/499	0.82	0/670
22	3B	0.74	0/1901	0.78	0/2567
22	3C	0.40	0/1796	0.70	0/2424
23	3D	0.52	0/2891	0.69	0/3895
24	3E	0.49	0/3059	0.69	0/4153
25	3F	0.42	0/3544	0.74	0/4775
26	3G	0.70	0/928	0.79	1/1262 (0.1%)
26	3H	0.54	0/928	0.75	0/1262
27	A4	0.46	0/5321	0.72	2/7207 (0.0%)
28	A5	0.55	0/4044	0.75	0/5493
29	A8	0.28	0/3328	0.74	3/4565 (0.1%)
30	A9	0.30	0/951	0.65	0/1287

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	AE	0.45	0/6308	0.71	0/8543
32	AF	0.50	0/3993	0.73	0/5413
33	AG	0.43	0/6699	0.71	0/9077
34	B1	0.82	0/6780	0.81	2/9175 (0.0%)
35	B2	0.42	0/6853	0.76	7/9256 (0.1%)
36	B3	0.42	0/6014	0.78	4/8137 (0.0%)
37	B8	0.70	0/3848	0.75	0/5218
38	BE	0.72	0/6948	0.74	3/9391 (0.0%)
39	B6	0.47	0/2849	0.68	0/3853
40	5B	0.35	0/499	0.74	0/659
41	5C	0.76	0/4321	0.78	0/5832
42	5D	0.63	0/1998	0.78	0/2644
43	5E	0.55	0/1665	0.71	1/2233 (0.0%)
44	5F	0.92	0/1559	0.86	1/2097 (0.0%)
45	5G	0.68	0/2337	0.78	3/3148 (0.1%)
46	5H	0.56	0/1074	0.65	0/1422
47	5I	0.74	0/3844	0.81	0/5174
48	5J	0.54	0/1238	0.69	0/1641
49	5K	0.73	0/1426	0.79	1/1917 (0.1%)
50	RA	0.32	0/2769	0.73	4/3753 (0.1%)
51	RB	0.38	0/1121	0.79	0/1487
52	RC	0.51	0/2245	0.67	1/3021 (0.0%)
53	RE	0.33	0/8924	0.67	4/12070 (0.0%)
54	RF	0.31	0/2004	0.70	1/2697 (0.0%)
55	RG	0.33	0/1727	0.75	0/2329
55	RH	0.40	0/1828	0.67	0/2470
56	RI	0.51	0/2080	0.72	0/2797
57	RJ	0.55	0/6514	0.69	0/8768
58	RK	0.41	0/2832	0.67	0/3825
59	RL	0.25	0/4549	0.60	2/6241 (0.0%)
59	RM	0.21	0/3760	0.53	1/5211 (0.0%)
60	RN	0.32	0/4423	0.68	3/5965 (0.1%)
61	RO	0.34	0/3849	0.68	0/5261
62	RP	0.23	0/10172	0.61	11/14158 (0.1%)
63	RQ	0.48	0/1678	0.68	1/2282 (0.0%)
64	RS	0.32	0/2104	0.76	0/2854
65	RT	0.41	0/1379	0.70	0/1853
66	RV	0.59	0/1456	0.72	1/1937 (0.1%)
All	All	0.50	1/232060 (0.0%)	0.68	77/323904 (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	1
6	SG	0	1
7	SH	0	1
8	SI	0	2
11	SM	0	1
12	SN	0	1
13	SO	0	1
14	SP	0	1
19	SZ	0	1
20	Sc	0	1
22	3B	0	1
23	3D	0	1
24	3E	0	2
26	3G	0	3
26	3H	0	1
28	A5	0	2
29	A8	0	4
33	AG	0	3
34	B1	0	3
35	B2	0	9
36	B3	0	8
37	B8	0	3
38	BE	0	3
39	B6	0	1
41	5C	0	3
42	5D	0	1
43	5E	0	1
44	5F	0	1
47	5I	0	1
49	5K	0	2
51	RB	0	1
53	RE	0	1
54	RF	0	1
56	RI	0	1
57	RJ	0	2
59	RL	0	1
59	RM	0	1
62	RP	0	1
63	RQ	0	1
66	RV	0	1
All	All	0	76

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	SI	39	ARG	C-N	6.54	1.38	1.33

All (77) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	RP	1897	PRO	N-CA-CB	10.22	109.66	102.81
35	B2	343	TRP	N-CA-C	7.40	117.78	108.45
15	SR	123	ARG	C-N-CD	-7.33	104.48	120.60
62	RP	2071	PRO	N-CA-CB	7.18	110.16	103.41
62	RP	1949	PRO	N-CA-CB	7.12	110.98	102.72
62	RP	2014	PRO	N-CA-CB	7.10	110.06	103.46
44	5F	13	LEU	CA-CB-CG	6.91	140.47	116.30
36	B3	779	VAL	N-CA-C	-6.81	106.86	113.53
36	B3	471	PRO	CA-C-N	6.80	135.20	123.91
36	B3	471	PRO	C-N-CA	6.80	135.20	123.91
15	SR	123	ARG	CA-C-N	6.78	143.27	127.00
15	SR	123	ARG	C-N-CA	6.78	143.27	127.00
2	5A	312	U	P-O3'-C3'	6.74	130.31	120.20
59	RL	359	ILE	N-CA-C	-6.50	106.80	113.10
62	RP	179	PRO	N-CA-CB	6.48	110.06	103.25
62	RP	78	PRO	N-CA-CB	6.47	110.16	103.23
62	RP	119	PRO	N-CA-CB	6.47	110.04	103.25
45	5G	157	PHE	N-CA-C	6.44	124.05	109.81
60	RN	591	ILE	N-CA-C	-6.32	107.71	113.71
62	RP	105	PRO	N-CA-CB	6.30	109.98	103.23
62	RP	1993	PRO	N-CA-CB	6.21	109.77	103.25
63	RQ	313	PHE	N-CA-C	6.10	123.30	109.81
35	B2	267	ASP	CA-C-N	6.09	133.18	121.54
35	B2	267	ASP	C-N-CA	6.09	133.18	121.54
59	RL	744	PRO	N-CA-C	5.95	124.72	112.47
62	RP	1988	PRO	N-CA-CB	5.88	110.03	103.44
53	RE	303	PHE	N-CA-C	5.85	116.14	108.07
59	RM	744	PRO	N-CA-C	5.80	124.41	112.47
8	SI	117	THR	CA-C-N	5.77	132.56	121.54
8	SI	117	THR	C-N-CA	5.77	132.56	121.54
62	RP	1772	PRO	N-CA-CB	5.70	109.82	103.44
2	5A	173	G	P-O3'-C3'	5.66	128.69	120.20
50	RA	149	VAL	CA-C-N	5.63	131.40	122.61
50	RA	149	VAL	C-N-CA	5.63	131.40	122.61
38	BE	37	VAL	N-CA-C	-5.61	103.80	109.02
66	RV	204	GLY	N-CA-C	5.53	126.29	113.18
50	RA	56	SER	CA-C-N	5.52	132.09	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	RA	56	SER	C-N-CA	5.52	132.09	121.54
38	BE	177	LEU	CA-C-N	5.50	130.21	122.46
38	BE	177	LEU	C-N-CA	5.50	130.21	122.46
3	SA	1052	U	O3'-P-O5'	5.48	112.22	104.00
43	5E	454	VAL	N-CA-C	5.42	120.62	109.34
53	RE	303	PHE	CA-C-N	5.42	137.76	122.21
53	RE	303	PHE	C-N-CA	5.42	137.76	122.21
34	B1	520	ALA	N-CA-C	5.37	117.19	110.91
4	SC	54	LEU	CA-CB-CG	5.36	135.05	116.30
3	SA	579	A	C2'-C3'-O3'	5.33	117.49	109.50
2	5A	312	U	O4'-C1'-N1	5.31	116.17	108.20
26	3G	65	LEU	CA-CB-CG	5.28	134.78	116.30
4	SC	147	ALA	CA-C-N	5.27	134.19	124.82
4	SC	147	ALA	C-N-CA	5.27	134.19	124.82
54	RF	257	PHE	N-CA-CB	-5.23	108.21	114.17
53	RE	924	LEU	CA-CB-CG	5.20	134.51	116.30
60	RN	384	HIS	CA-C-N	5.20	131.46	121.54
60	RN	384	HIS	C-N-CA	5.20	131.46	121.54
3	SA	272	U	P-O3'-C3'	5.17	127.96	120.20
2	5A	312	U	N1-C1'-C2'	5.17	121.75	114.00
35	B2	370	GLU	CA-C-N	5.14	131.36	121.54
35	B2	370	GLU	C-N-CA	5.14	131.36	121.54
35	B2	285	ARG	CA-C-N	-5.13	116.48	123.10
35	B2	285	ARG	C-N-CA	-5.13	116.48	123.10
49	5K	122	ASP	N-CA-C	-5.13	101.22	109.58
34	B1	33	VAL	N-CA-C	-5.12	104.42	110.21
3	SA	579	A	P-O3'-C3'	5.12	127.88	120.20
29	A8	369	ILE	N-CA-C	-5.12	107.31	112.17
4	SC	208	GLN	CA-C-N	5.08	131.25	121.54
4	SC	208	GLN	C-N-CA	5.08	131.25	121.54
52	RC	114	VAL	CB-CA-C	-5.08	102.97	111.29
36	B3	594	GLY	N-CA-C	-5.07	101.17	113.18
45	5G	192	ASP	CA-C-N	5.06	129.60	122.46
45	5G	192	ASP	C-N-CA	5.06	129.60	122.46
2	5A	358	G	P-O3'-C3'	5.04	127.77	120.20
27	A4	301	ASP	CA-C-N	5.04	129.49	122.08
27	A4	301	ASP	C-N-CA	5.04	129.49	122.08
29	A8	560	ASN	CA-C-N	-5.02	116.74	122.26
29	A8	560	ASN	C-N-CA	-5.02	116.74	122.26
3	SA	1594	G	C4'-C3'-O3'	5.01	116.91	109.40

There are no chirality outliers.

All (76) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
22	3B	176	ALA	Peptide
23	3D	142	LEU	Peptide
24	3E	228	PRO	Peptide
24	3E	36	ASP	Peptide
26	3G	59	GLU	Peptide
26	3G	64	LEU	Peptide
26	3G	9	PHE	Peptide
26	3H	59	GLU	Peptide
41	5C	111	PHE	Peptide
41	5C	140	ARG	Peptide
41	5C	540	GLU	Peptide
42	5D	84	GLY	Peptide
43	5E	453	SER	Peptide
44	5F	101	VAL	Peptide
47	5I	141	ASP	Peptide
49	5K	25	LEU	Peptide
49	5K	51	LEU	Peptide
28	A5	167	SER	Peptide
28	A5	457	LEU	Peptide
29	A8	257	SER	Peptide
29	A8	266	ILE	Peptide
29	A8	529	HIS	Peptide
29	A8	599	MET	Peptide
33	AG	178	PHE	Peptide
33	AG	769	ASN	Peptide
33	AG	780	GLU	Peptide
34	B1	288	ASP	Peptide
34	B1	661	LEU	Peptide
34	B1	733	LYS	Peptide
35	B2	131	GLY	Peptide
35	B2	266	SER	Peptide
35	B2	267	ASP	Peptide
35	B2	359	SER	Peptide
35	B2	52	TRP	Peptide
35	B2	575	PRO	Peptide
35	B2	613	ALA	Peptide
35	B2	653	LEU	Peptide
35	B2	916	HIS	Peptide
36	B3	35	PRO	Peptide
36	B3	473	ALA	Peptide
36	B3	480	ILE	Peptide
36	B3	530	ALA	Peptide

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Mol	Chain	Res	Type	Group
36	B3	593	CYS	Peptide
36	B3	594	GLY	Peptide
36	B3	785	ILE	Peptide
36	B3	90	LEU	Peptide
39	B6	354	ASP	Peptide
37	B8	366	SER	Peptide
37	B8	438	ASN	Peptide
37	B8	501	THR	Peptide
38	BE	173	LEU	Peptide
38	BE	899	ASN	Peptide
38	BE	94	TYR	Peptide
51	RB	273	GLY	Peptide
53	RE	767	GLN	Peptide
54	RF	253	ALA	Peptide
56	RI	50	ARG	Peptide
57	RJ	1026	LYS	Peptide
57	RJ	81	GLY	Peptide
59	RL	743	VAL	Peptide
59	RM	743	VAL	Peptide
62	RP	1907	ASN	Peptide
63	RQ	257	ILE	Peptide
66	RV	203	ILE	Peptide
4	SC	40	ASN	Peptide
5	SF	195	ILE	Peptide
6	SG	58	LEU	Peptide
7	SH	68	LEU	Peptide
8	SI	31	SER	Peptide
8	SI	64	VAL	Peptide
11	SM	128	CYS	Peptide
12	SN	99	GLU	Peptide
13	SO	24	ALA	Peptide
14	SP	90	ARG	Peptide
19	SZ	76	TYR	Peptide
20	Sc	74	SER	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	32	0
2	5A	11143	0	5602	93	0
3	SA	27940	0	14087	248	0
4	SC	1751	0	1834	25	0
5	SF	1815	0	1870	45	0
6	SG	1669	0	1724	17	0
7	SH	879	0	922	22	0
8	SI	1321	0	1387	34	0
9	SJ	1324	0	1344	40	0
10	SK	1388	0	1467	15	0
11	SM	997	0	1048	21	0
12	SN	865	0	874	11	0
13	SO	1087	0	1152	17	0
14	SP	868	0	894	18	0
15	SR	973	0	1029	20	0
16	ST	918	0	952	19	0
17	SX	1003	0	1040	18	0
18	SY	786	0	843	13	0
19	SZ	809	0	842	16	0
20	Sc	603	0	623	8	0
21	Sd	497	0	535	4	0
22	3B	1865	0	1910	33	0
22	3C	1763	0	1805	36	0
23	3D	2848	0	2815	40	0
24	3E	3028	0	2813	61	0
25	3F	3473	0	3477	82	0
26	3G	916	0	964	16	0
26	3H	916	0	964	26	0
27	A4	5226	0	5199	113	0
28	A5	3976	0	3919	80	0
29	A8	3307	0	2316	39	0
30	A9	939	0	898	16	0
31	AE	6197	0	6365	92	0
32	AF	3911	0	3906	94	0
33	AG	6570	0	6473	156	0
34	B1	6635	0	6525	107	0
35	B2	6723	0	6698	140	0
36	B3	5919	0	6007	145	0
37	B8	3764	0	3757	71	0
38	BE	6810	0	6787	99	0
39	B6	2800	0	2517	35	0
40	5B	495	0	561	10	0
41	5C	4237	0	4239	81	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	5D	1972	0	2054	30	0
43	5E	1647	0	1678	42	0
44	5F	1530	0	1572	25	0
45	5G	2296	0	2325	31	0
46	5H	1065	0	1097	16	0
47	5I	3765	0	3714	74	0
48	5J	1219	0	1278	17	0
49	5K	1403	0	1484	24	0
50	RA	2709	0	2622	75	0
51	RB	1108	0	1087	23	0
52	RC	2207	0	2229	25	0
53	RE	8716	0	8828	155	0
54	RF	1963	0	1942	37	0
55	RG	1701	0	1767	34	0
55	RH	1799	0	1872	25	0
56	RI	2045	0	2162	46	0
57	RJ	6379	0	6506	109	0
58	RK	2781	0	2878	46	0
59	RL	4539	0	2874	24	0
59	RM	3774	0	1649	16	0
60	RN	4363	0	4100	51	0
61	RO	3766	0	3269	44	0
62	RP	10202	0	4350	14	0
63	RQ	1651	0	1450	22	0
64	RS	2051	0	2096	39	0
65	RT	1357	0	1426	20	0
66	RV	1448	0	1435	22	0
67	X1	635	0	147	3	0
68	5K	1	0	0	0	0
68	Sc	1	0	0	0	0
69	RJ	32	0	12	0	0
70	RJ	1	0	0	0	0
All	All	224791	0	192769	2979	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 (2979) 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)
3:SA:356:G:N2	3:SA:357:G:H22	1.43	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:356:G:N2	3:SA:357:G:N2	1.95	1.14
3:SA:1663:G:H1	3:SA:1738:U:H3	1.06	0.92
3:SA:1775:U:H3	3:SA:1786:G:H1	1.15	0.90
39:B6:319:TYR:O	39:B6:323:PHE:HB2	1.70	0.90
2:5A:182:G:H1	2:5A:215:U:H3	1.16	0.90
51:RB:230:ALA:O	51:RB:234:LYS:HB2	1.72	0.88
2:5A:116:U:H3	2:5A:130:G:H1	1.15	0.87
9:SJ:48:THR:O	9:SJ:52:ASN:HB2	1.75	0.86
9:SJ:113:PHE:O	9:SJ:117:TYR:HB2	1.79	0.83
58:RK:282:GLU:O	58:RK:286:SER:HB2	1.78	0.82
32:AF:420:GLU:O	32:AF:424:ARG:HB3	1.78	0.82
31:AE:151:ILE:O	31:AE:155:ILE:HB	1.80	0.81
33:AG:175:ALA:O	33:AG:187:VAL:HA	1.82	0.80
60:RN:411:GLN:O	60:RN:415:ALA:HB2	1.82	0.80
61:RO:502:ASN:O	61:RO:506:LEU:HB2	1.83	0.79
3:SA:356:G:C2	3:SA:357:G:N2	2.51	0.79
27:A4:534:LEU:HA	27:A4:542:VAL:O	1.81	0.79
58:RK:103:MET:O	58:RK:107:ALA:HB2	1.84	0.78
3:SA:356:G:H22	3:SA:357:G:H22	1.31	0.78
59:RL:281:LEU:HA	59:RL:409:ALA:O	1.84	0.78
3:SA:153:G:H1	3:SA:161:U:H3	1.30	0.78
3:SA:868:G:H1	3:SA:960:U:H3	1.31	0.77
16:ST:102:ALA:O	16:ST:106:GLU:HB2	1.86	0.76
26:3H:62:GLU:HA	26:3H:65:LEU:HB2	1.68	0.76
3:SA:1606:C:OP2	45:5G:94:ARG:NH1	2.20	0.74
59:RL:309:PHE:O	59:RL:368:GLN:HA	1.88	0.73
2:5A:173:G:N7	2:5A:175:A:N6	2.36	0.73
35:B2:97:GLY:HA3	35:B2:124:ILE:HD11	1.68	0.73
57:RJ:248:ARG:HB3	57:RJ:272:TYR:HB2	1.72	0.72
1:3A:63:C:H5"	38:BE:449:ARG:HD3	1.71	0.72
10:SK:138:LYS:H	51:RB:263:GLY:HA3	1.54	0.72
3:SA:146:U:H3	3:SA:168:A:H62	1.32	0.72
36:B3:632:ILE:HA	36:B3:644:TRP:O	1.89	0.72
3:SA:146:U:C2	3:SA:168:A:N6	2.58	0.71
31:AE:142:TYR:O	31:AE:148:PHE:HB2	1.90	0.71
32:AF:86:SER:O	32:AF:98:ALA:HA	1.90	0.71
51:RB:242:MET:HE2	51:RB:332:ARG:HE	1.56	0.70
64:RS:399:ILE:HA	64:RS:408:ASP:HB2	1.71	0.70
33:AG:724:ILE:HD11	33:AG:763:ILE:HG22	1.74	0.70
36:B3:581:CYS:HA	36:B3:590:LEU:O	1.92	0.70
14:SP:14:PHE:HA	14:SP:78:ALA:O	1.92	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:SG:221:ALA:O	6:SG:225:ARG:HB2	1.91	0.70
37:B8:521:LEU:HA	37:B8:531:CYS:O	1.92	0.70
8:SI:62:VAL:HG12	8:SI:64:VAL:H	1.57	0.69
35:B2:581:ILE:HA	35:B2:588:ILE:HG22	1.72	0.69
66:RV:224:HIS:HD2	66:RV:226:ASP:H	1.40	0.69
2:5A:554:G:H1	2:5A:583:U:H3	1.39	0.69
14:SP:80:HIS:HA	14:SP:113:GLY:O	1.93	0.69
29:A8:632:THR:HB	30:A9:492:ILE:HG21	1.75	0.69
54:RF:202:VAL:HG22	54:RF:223:LEU:HD12	1.74	0.69
29:A8:599:MET:HE1	29:A8:640:LEU:HB3	1.74	0.69
33:AG:447:LYS:HE3	33:AG:770:TYR:HB2	1.74	0.68
55:RH:44:VAL:HA	55:RH:113:TYR:O	1.94	0.68
39:B6:169:GLN:HB3	63:RQ:339:GLN:HE21	1.58	0.68
53:RE:254:LEU:HG	53:RE:268:LEU:HD12	1.76	0.68
3:SA:336:G:H1	9:SJ:5:ARG:HB2	1.58	0.68
59:RM:55:VAL:O	59:RM:103:ILE:HA	1.94	0.68
64:RS:424:PHE:O	64:RS:428:TYR:HB2	1.94	0.68
25:3F:405:VAL:HG12	25:3F:415:THR:HG22	1.76	0.67
57:RJ:1018:VAL:O	57:RJ:1029:TRP:NE1	2.27	0.67
3:SA:343:C:H2'	3:SA:344:A:H8	1.60	0.67
35:B2:260:GLU:O	35:B2:272:PHE:HA	1.95	0.67
31:AE:665:TYR:HB2	31:AE:709:ASN:HD21	1.60	0.67
32:AF:133:HIS:HD2	32:AF:135:GLN:H	1.42	0.67
42:5D:161:ARG:NH1	42:5D:164:ASN:O	2.28	0.67
49:5K:161:LYS:HG2	49:5K:172:LEU:HD21	1.77	0.67
64:RS:432:ILE:HG23	64:RS:436:GLN:HB2	1.77	0.67
27:A4:429:SER:HB3	27:A4:444:ARG:HA	1.77	0.67
3:SA:1655:A:N6	3:SA:1743:U:O4	2.28	0.66
36:B3:362:LEU:HD21	36:B3:405:THR:HG21	1.76	0.66
2:5A:169:A:N6	27:A4:236:LYS:O	2.29	0.66
3:SA:146:U:H3	3:SA:168:A:N6	1.92	0.66
27:A4:80:ASN:O	27:A4:85:TRP:HA	1.95	0.66
58:RK:192:THR:HA	58:RK:224:ASN:O	1.96	0.66
58:RK:302:VAL:HG22	58:RK:354:ILE:HG21	1.77	0.66
3:SA:1695:G:H5''	53:RE:306:LYS:HE3	1.77	0.66
9:SJ:167:ALA:HB2	9:SJ:183:ILE:HD12	1.77	0.66
53:RE:508:SER:HA	53:RE:512:LEU:HB2	1.76	0.66
11:SM:59:PRO:HG3	11:SM:138:ASN:HB3	1.78	0.66
37:B8:278:ASP:O	37:B8:282:ASN:ND2	2.29	0.66
53:RE:146:LEU:HA	53:RE:149:VAL:HG12	1.78	0.65
50:RA:183:VAL:HG12	50:RA:199:THR:HG22	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:RI:181:ARG:O	56:RI:185:LYS:HB2	1.95	0.65
3:SA:146:U:N3	3:SA:168:A:N6	2.42	0.65
22:3B:253:ILE:HD13	22:3B:269:ILE:HD12	1.77	0.65
31:AE:364:ASN:HB3	31:AE:399:GLN:HE22	1.61	0.65
33:AG:510:TYR:HH	33:AG:527:HIS:HD1	1.44	0.65
5:SF:188:ASN:HD22	5:SF:191:ARG:HH12	1.44	0.65
34:B1:661:LEU:HD11	43:5E:450:VAL:HG13	1.78	0.65
29:A8:264:SER:O	29:A8:267:ILE:HA	1.97	0.65
37:B8:426:VAL:HG23	37:B8:432:VAL:HG22	1.78	0.65
24:3E:287:LEU:HD13	24:3E:371:LEU:HB2	1.79	0.65
26:3G:89:ARG:HH22	37:B8:492:ASN:HD21	1.42	0.65
32:AF:301:PRO:HG2	32:AF:323:SER:HB3	1.77	0.65
35:B2:416:ILE:HG21	35:B2:459:LEU:HD11	1.79	0.65
58:RK:198:THR:O	58:RK:239:PRO:HA	1.96	0.65
44:5F:33:MET:HB2	44:5F:38:ILE:HB	1.78	0.64
32:AF:147:ARG:NH2	55:RH:16:GLN:O	2.29	0.64
3:SA:870:C:O2	20:Sc:51:GLN:NE2	2.29	0.64
34:B1:76:ASP:N	34:B1:76:ASP:OD1	2.30	0.64
57:RJ:776:GLN:HA	57:RJ:780:ILE:HG22	1.79	0.64
28:A5:503:LYS:HD3	30:A9:508:ARG:HH22	1.63	0.64
31:AE:764:ASN:O	31:AE:768:LYS:HB2	1.98	0.64
53:RE:177:ASN:HB2	53:RE:213:LEU:HB2	1.79	0.64
3:SA:172:C:OP2	3:SA:173:A:N6	2.31	0.64
3:SA:1489:U:N3	48:5J:202:ARG:O	2.31	0.64
56:RI:155:ARG:O	56:RI:179:GLN:NE2	2.29	0.64
3:SA:396:G:O6	9:SJ:26:LYS:NZ	2.31	0.64
3:SA:656:G:H22	3:SA:679:U:H3	1.46	0.64
40:5B:200:ARG:O	40:5B:204:ARG:HB3	1.97	0.64
53:RE:629:THR:HG22	53:RE:669:TRP:HE1	1.63	0.64
44:5F:135:HIS:HD2	44:5F:164:SER:HB2	1.63	0.64
36:B3:719:ILE:HD11	36:B3:762:CYS:HB3	1.80	0.64
3:SA:445:A:H61	3:SA:462:G:H1'	1.64	0.63
34:B1:842:ASN:ND2	38:BE:886:SER:OG	2.30	0.63
3:SA:362:G:H22	3:SA:382:C:H1'	1.63	0.63
9:SJ:67:TRP:O	9:SJ:71:GLY:N	2.30	0.63
57:RJ:60:ASP:O	57:RJ:239:ASN:ND2	2.31	0.63
61:RO:205:ASP:HB3	61:RO:208:TYR:HB2	1.81	0.63
27:A4:444:ARG:HG3	27:A4:446:SER:H	1.63	0.63
33:AG:744:ILE:HA	33:AG:755:GLY:O	1.98	0.63
47:5I:260:GLN:NE2	47:5I:289:TYR:OH	2.31	0.63
5:SF:212:ASP:H	5:SF:215:ASP:HA	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:AE:597:HIS:HB3	31:AE:615:ASN:HB2	1.81	0.63
38:BE:127:TYR:HA	38:BE:140:TYR:O	1.98	0.63
53:RE:1109:LYS:HZ1	53:RE:1169:ILE:HG23	1.63	0.63
60:RN:623:ASP:O	60:RN:627:HIS:HB3	1.99	0.63
29:A8:611:ILE:HD11	29:A8:658:LEU:HB2	1.80	0.63
32:AF:391:ASN:ND2	32:AF:403:ASN:OD1	2.32	0.63
33:AG:55:TYR:HB3	33:AG:383:LEU:HD11	1.80	0.63
65:RT:182:ILE:HA	65:RT:233:ILE:O	1.99	0.63
24:3E:384:GLY:O	24:3E:388:LEU:HB2	1.99	0.63
25:3F:357:LEU:HD22	51:RB:256:PRO:HB2	1.79	0.63
41:5C:386:PHE:HB3	47:5I:8:ARG:HH22	1.64	0.63
55:RH:55:ILE:HD11	55:RH:76:LEU:HD11	1.80	0.63
3:SA:505:A:H5'	3:SA:585:A:H62	1.64	0.63
3:SA:1052:U:H5''	47:5I:449:LYS:HG2	1.80	0.63
36:B3:467:ILE:H	36:B3:479:ILE:HD11	1.64	0.63
57:RJ:561:GLU:OE1	57:RJ:565:ARG:NH2	2.32	0.63
34:B1:497:ILE:HG23	34:B1:512:ILE:HB	1.80	0.62
7:SH:67:VAL:H	7:SH:100:ALA:HB2	1.64	0.62
18:SY:132:LEU:HA	18:SY:135:LEU:HB2	1.81	0.62
27:A4:186:GLN:NE2	27:A4:188:ALA:O	2.32	0.62
60:RN:661:ILE:HG22	60:RN:665:GLN:HG3	1.78	0.62
14:SP:111:ARG:NH1	52:RC:37:GLU:OE2	2.32	0.62
22:3C:142:ARG:NH1	22:3C:186:ASP:OD2	2.32	0.62
34:B1:20:ILE:H	34:B1:307:THR:HG21	1.63	0.62
65:RT:97:ARG:NH2	65:RT:153:GLN:OE1	2.32	0.62
1:3A:15:U:O4	3:SA:17:C:N3	2.32	0.62
3:SA:311:U:O2	3:SA:355:G:N2	2.32	0.62
31:AE:25:ARG:NH2	47:5I:11:ASP:OD1	2.32	0.62
63:RQ:346:LEU:O	63:RQ:350:ASN:HA	2.00	0.62
33:AG:200:ASN:ND2	33:AG:262:MET:O	2.33	0.62
34:B1:356:ASP:HB2	34:B1:826:ARG:HG3	1.82	0.62
19:SZ:32:ARG:NH1	19:SZ:34:ASN:O	2.32	0.62
45:5G:187:PRO:HB3	45:5G:220:ARG:HE	1.64	0.62
65:RT:124:LEU:HD23	65:RT:151:ALA:HB1	1.82	0.62
22:3B:236:MET:HG3	23:3D:133:LEU:HA	1.81	0.62
28:A5:548:ASP:O	28:A5:552:ASN:ND2	2.33	0.62
36:B3:513:LYS:HG2	36:B3:532:HIS:HB2	1.81	0.62
52:RC:85:THR:HG23	52:RC:87:LYS:H	1.65	0.62
54:RF:107:LEU:HD12	54:RF:194:ARG:HG3	1.80	0.62
60:RN:441:TYR:HB2	60:RN:618:THR:HG21	1.82	0.62
41:5C:17:ASN:ND2	41:5C:64:ASP:OD2	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5A:490:G:O6	39:B6:120:ARG:NH2	2.33	0.62
3:SA:1684:U:N3	3:SA:1718:G:N1	2.48	0.62
3:SA:1688:U:O2	3:SA:1713:G:N2	2.32	0.62
27:A4:533:HIS:O	27:A4:543:ILE:HA	1.99	0.62
27:A4:654:ILE:HD11	27:A4:744:VAL:HG11	1.81	0.62
47:5I:26:ARG:NH1	63:RQ:867:GLN:O	2.33	0.62
57:RJ:852:ARG:HD2	57:RJ:888:PRO:HG3	1.80	0.62
57:RJ:631:ILE:HG12	58:RK:283:ILE:HG22	1.82	0.61
45:5G:44:LYS:NZ	45:5G:48:GLU:OE2	2.31	0.61
9:SJ:186:GLY:H	9:SJ:189:LEU:HD12	1.63	0.61
39:B6:187:LYS:HE2	48:5J:63:PRO:HB2	1.83	0.61
60:RN:548:ARG:NH1	60:RN:638:ASN:OD1	2.33	0.61
22:3C:86:VAL:N	22:3C:100:ARG:O	2.33	0.61
34:B1:423:ARG:NH2	34:B1:461:GLN:O	2.33	0.61
50:RA:333:ASN:HD21	50:RA:338:MET:HA	1.64	0.61
3:SA:1051:G:H21	47:5I:447:THR:HG21	1.66	0.61
17:SX:35:ILE:O	17:SX:39:GLN:HB2	1.99	0.61
33:AG:769:ASN:ND2	33:AG:771:ASP:OD1	2.32	0.61
64:RS:360:LEU:HD11	64:RS:393:TYR:HB2	1.82	0.61
65:RT:110:ARG:NH2	65:RT:130:MET:SD	2.73	0.61
2:5A:425:U:H3	2:5A:431:A:H61	1.47	0.61
11:SM:67:ARG:HH21	11:SM:129:ARG:H	1.46	0.61
33:AG:177:THR:O	33:AG:185:PHE:HA	2.00	0.61
36:B3:627:ASN:ND2	36:B3:632:ILE:O	2.33	0.61
50:RA:164:ARG:HG2	50:RA:173:LEU:HB2	1.83	0.61
53:RE:558:LEU:O	53:RE:562:LEU:HB2	2.00	0.61
55:RG:100:LEU:HD22	55:RG:132:ARG:HH22	1.65	0.61
3:SA:27:U:H5'	57:RJ:45:ARG:HH21	1.63	0.61
3:SA:1663:G:N2	3:SA:1738:U:O2	2.29	0.61
61:RO:206:PRO:HA	61:RO:209:GLN:HG2	1.82	0.61
5:SF:45:ILE:O	5:SF:49:ARG:HB3	2.01	0.61
36:B3:497:LEU:HA	36:B3:507:ALA:O	2.00	0.61
60:RN:554:GLN:HG3	60:RN:561:ILE:HD11	1.83	0.61
1:3A:62:C:H4'	38:BE:447:ASN:HD22	1.65	0.61
22:3C:106:LEU:HB2	22:3C:156:MET:HE2	1.83	0.61
49:5K:149:LYS:HA	49:5K:170:ILE:HD11	1.81	0.61
3:SA:1600:A:H61	57:RJ:945:THR:HG21	1.65	0.61
32:AF:48:ASN:ND2	32:AF:111:TYR:OH	2.33	0.61
34:B1:58:ILE:HA	34:B1:74:ASP:HA	1.83	0.61
38:BE:392:ARG:O	38:BE:449:ARG:NH1	2.33	0.61
41:5C:483:ILE:HG23	41:5C:516:VAL:HG22	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:5K:98:ILE:HG21	49:5K:103:MET:HE2	1.83	0.60
66:RV:282:ASP:OD2	66:RV:285:ARG:NH2	2.34	0.60
35:B2:295:GLY:HA2	35:B2:298:LYS:HD3	1.83	0.60
35:B2:361:THR:HG23	35:B2:386:GLU:HB3	1.84	0.60
37:B8:512:ASP:O	42:5D:248:ARG:NH1	2.34	0.60
45:5G:108:LYS:HD2	45:5G:116:ARG:HB2	1.81	0.60
60:RN:729:ASP:O	60:RN:732:ARG:NH1	2.33	0.60
8:SI:50:ASP:HB3	8:SI:56:LYS:HE2	1.82	0.60
29:A8:293:TYR:HA	29:A8:304:GLN:HA	1.83	0.60
34:B1:728:GLU:OE1	34:B1:731:ARG:NH2	2.34	0.60
35:B2:877:LYS:HE2	36:B3:813:MET:HB3	1.82	0.60
64:RS:251:PRO:O	64:RS:254:TRP:NE1	2.34	0.60
28:A5:454:GLU:OE2	28:A5:494:ARG:NH2	2.33	0.60
3:SA:312:A:H2	3:SA:353:A:H62	1.48	0.60
3:SA:1694:A:H2	3:SA:1707:A:H61	1.47	0.60
3:SA:538:A:OP2	10:SK:171:ARG:NH1	2.35	0.60
7:SH:98:ARG:NH1	7:SH:105:ASP:OD1	2.32	0.60
31:AE:145:THR:HB	31:AE:146:PRO:HD2	1.84	0.60
34:B1:621:MET:HG2	34:B1:627:LEU:HD11	1.83	0.60
36:B3:42:ILE:HG22	36:B3:49:SER:HA	1.84	0.60
27:A4:645:ARG:HG2	27:A4:658:ASP:HA	1.84	0.60
32:AF:371:GLU:OE2	37:B8:273:ARG:NH2	2.34	0.60
35:B2:7:ARG:HH12	35:B2:72:SER:HA	1.64	0.60
35:B2:50:ASN:HB2	35:B2:59:LEU:HD11	1.84	0.60
47:5I:281:ASN:ND2	47:5I:283:ASP:OD1	2.34	0.60
60:RN:510:THR:HB	60:RN:518:ILE:HD13	1.83	0.60
64:RS:445:ARG:NH1	64:RS:445:ARG:O	2.34	0.60
3:SA:1655:A:N1	3:SA:1745:G:O6	2.34	0.60
5:SF:19:LEU:HG	5:SF:108:ARG:HG2	1.83	0.60
25:3F:156:ASN:ND2	25:3F:546:GLU:OE1	2.32	0.60
28:A5:224:CYS:SG	28:A5:273:LYS:NZ	2.69	0.60
31:AE:659:LEU:HD13	31:AE:690:GLU:HG2	1.84	0.60
46:5H:565:LYS:HA	46:5H:568:LYS:HG2	1.83	0.60
49:5K:112:LYS:NZ	66:RV:303:GLU:O	2.34	0.60
53:RE:186:ILE:HD11	53:RE:206:LEU:HB2	1.82	0.60
55:RG:44:VAL:HA	55:RG:113:TYR:O	2.01	0.60
66:RV:323:LYS:HA	66:RV:326:ILE:HD12	1.82	0.60
2:5A:121:G:O2'	2:5A:124:A:N6	2.34	0.60
33:AG:249:THR:HA	33:AG:252:LEU:HD12	1.84	0.60
41:5C:96:ASP:OD1	41:5C:96:ASP:N	2.31	0.60
41:5C:317:THR:HG23	41:5C:334:ARG:HB3	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:RE:308:LEU:HB3	53:RE:337:LEU:HD21	1.84	0.60
16:ST:2:SER:N	61:RO:370:HIS:O	2.35	0.60
16:ST:41:ARG:NH2	56:RI:94:SER:O	2.35	0.60
27:A4:37:ARG:NH1	29:A8:704:PRO:O	2.35	0.60
33:AG:197:ILE:HD11	33:AG:213:LYS:HD2	1.83	0.60
37:B8:241:ALA:HB2	37:B8:588:LEU:HD13	1.84	0.60
50:RA:145:VAL:HG22	50:RA:186:VAL:HG13	1.82	0.60
64:RS:229:LEU:O	64:RS:231:LYS:NZ	2.35	0.60
22:3C:100:ARG:HG2	22:3C:104:ASP:HB3	1.84	0.59
22:3C:233:LEU:HD21	24:3E:144:ALA:HB2	1.83	0.59
37:B8:249:SER:OG	37:B8:250:ALA:N	2.33	0.59
61:RO:470:MET:O	61:RO:482:LYS:NZ	2.32	0.59
25:3F:162:CYS:SG	25:3F:525:GLN:NE2	2.75	0.59
29:A8:671:ARG:NH1	30:A9:449:GLU:O	2.35	0.59
57:RJ:128:MET:HG3	57:RJ:155:PHE:HD1	1.66	0.59
25:3F:328:ILE:HG13	25:3F:338:THR:HG22	1.83	0.59
29:A8:435:ASP:H	33:AG:753:LYS:HE3	1.67	0.59
33:AG:16:SER:HB2	33:AG:783:LEU:HB2	1.84	0.59
41:5C:343:ASP:HB3	41:5C:346:LYS:HE2	1.84	0.59
52:RC:226:MET:O	52:RC:228:LYS:NZ	2.35	0.59
2:5A:116:U:O2	2:5A:130:G:N2	2.32	0.59
2:5A:485:G:OP2	23:3D:46:LYS:NZ	2.35	0.59
3:SA:1473:U:O4	6:SG:100:ASN:ND2	2.35	0.59
4:SC:132:ASP:HB3	4:SC:221:PRO:HB3	1.84	0.59
23:3D:386:ALA:O	23:3D:390:ASP:HB2	2.01	0.59
25:3F:442:ILE:HA	25:3F:472:PRO:HA	1.84	0.59
35:B2:102:VAL:HA	35:B2:118:ASN:HA	1.83	0.59
37:B8:233:LEU:HD11	37:B8:543:LEU:HD12	1.84	0.59
42:5D:29:GLU:OE2	42:5D:37:ARG:NH1	2.35	0.59
45:5G:153:THR:HG23	45:5G:164:GLN:HG2	1.83	0.59
53:RE:520:ASN:ND2	53:RE:526:CYS:SG	2.75	0.59
2:5A:326:C:OP2	34:B1:191:ARG:NH2	2.35	0.59
31:AE:226:ASN:ND2	33:AG:869:MET:SD	2.76	0.59
38:BE:732:ASN:HB3	43:5E:483:TYR:HE1	1.66	0.59
56:RI:107:ARG:HB3	56:RI:138:VAL:HG13	1.83	0.59
3:SA:415:C:H1'	3:SA:419:G:H22	1.67	0.59
11:SM:115:PHE:HB3	11:SM:142:VAL:HG21	1.84	0.59
33:AG:202:SER:OG	33:AG:266:ASN:ND2	2.36	0.59
35:B2:352:GLU:HB2	35:B2:364:TYR:HE1	1.66	0.59
51:RB:245:MET:HG3	51:RB:338:THR:HG21	1.84	0.59
62:RP:752:THR:O	62:RP:756:SER:CB	2.51	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:505:A:N6	3:SA:585:A:O2'	2.36	0.59
3:SA:894:U:O2	14:SP:36:LYS:NZ	2.35	0.59
7:SH:121:LEU:HD13	7:SH:124:LEU:HD13	1.84	0.59
25:3F:152:VAL:HG22	25:3F:562:GLY:HA2	1.85	0.59
4:SC:201:THR:HG21	4:SC:207:LEU:HD22	1.85	0.59
29:A8:574:ARG:H	29:A8:576:ARG:HH11	1.51	0.59
34:B1:35:ASN:ND2	34:B1:53:GLU:OE2	2.36	0.59
34:B1:329:VAL:HG12	34:B1:339:LEU:HG	1.85	0.59
38:BE:631:ASN:HB2	38:BE:644:THR:HB	1.84	0.59
47:5I:26:ARG:HH12	63:RQ:868:GLU:HA	1.67	0.59
9:SJ:154:SER:HA	9:SJ:157:GLU:HB2	1.84	0.59
27:A4:420:LEU:HD21	27:A4:462:VAL:HG11	1.85	0.59
43:5E:480:GLN:HG2	43:5E:482:LEU:H	1.67	0.59
47:5I:140:SER:OG	47:5I:141:ASP:N	2.34	0.59
53:RE:383:GLY:HA3	53:RE:585:MET:HG2	1.83	0.59
24:3E:225:GLU:HG2	24:3E:226:ILE:HG13	1.85	0.59
33:AG:157:PHE:O	33:AG:169:GLN:NE2	2.36	0.59
52:RC:69:ILE:HD11	52:RC:93:ILE:HG23	1.85	0.59
59:RL:58:ALA:HA	59:RL:106:VAL:O	2.03	0.59
2:5A:268:G:N2	42:5D:90:SER:OG	2.35	0.58
22:3C:189:GLY:O	22:3C:216:ASN:ND2	2.36	0.58
27:A4:478:VAL:HG12	27:A4:488:ILE:HG12	1.85	0.58
32:AF:319:VAL:HG22	32:AF:329:ILE:HG23	1.84	0.58
33:AG:71:ASN:HD22	33:AG:73:LEU:HD22	1.68	0.58
33:AG:157:PHE:HB2	33:AG:170:SER:HB2	1.86	0.58
36:B3:53:LEU:HD13	36:B3:87:ILE:HG13	1.85	0.58
38:BE:733:THR:O	38:BE:737:LEU:HB3	2.03	0.58
54:RF:38:PHE:HB2	54:RF:56:VAL:HB	1.85	0.58
54:RF:176:ASP:OD1	54:RF:176:ASP:N	2.35	0.58
3:SA:1061:A:H5''	54:RF:233:LYS:HE2	1.85	0.58
3:SA:1756:A:H5'	43:5E:536:ARG:HB2	1.85	0.58
4:SC:180:THR:H	4:SC:183:GLN:HB2	1.69	0.58
22:3C:205:ARG:HG3	24:3E:152:LEU:HD21	1.85	0.58
42:5D:107:VAL:HG21	42:5D:218:MET:HE1	1.83	0.58
61:RO:156:TRP:O	61:RO:215:ASN:ND2	2.36	0.58
64:RS:429:LYS:O	64:RS:437:ARG:NH2	2.36	0.58
2:5A:489:G:O6	39:B6:120:ARG:NH1	2.37	0.58
3:SA:646:C:H2'	3:SA:647:G:H8	1.69	0.58
27:A4:641:GLU:OE2	27:A4:645:ARG:NH1	2.36	0.58
46:5H:540:ILE:HD12	57:RJ:148:PHE:HB3	1.84	0.58
53:RE:756:VAL:HA	53:RE:896:THR:HG21	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:153:G:N2	7:SH:56:ASN:OD1	2.35	0.58
35:B2:405:LEU:HB2	35:B2:417:TRP:HB2	1.85	0.58
36:B3:17:ALA:HB3	36:B3:35:PRO:HA	1.85	0.58
37:B8:345:LEU:HB2	37:B8:349:GLU:HG3	1.85	0.58
54:RF:17:PRO:HB2	54:RF:34:LEU:HD11	1.85	0.58
60:RN:419:LYS:NZ	60:RN:466:TYR:OH	2.36	0.58
24:3E:372:ARG:O	24:3E:376:LEU:HB2	2.03	0.58
38:BE:557:LEU:HD23	38:BE:571:ASP:HB3	1.85	0.58
39:B6:199:ARG:NH2	63:RQ:386:LEU:O	2.37	0.58
41:5C:329:LEU:HD22	41:5C:406:ALA:HB2	1.84	0.58
3:SA:1657:U:OP1	3:SA:1658:G:O2'	2.22	0.58
13:SO:60:VAL:HG23	13:SO:66:ILE:HD12	1.85	0.58
27:A4:83:ASN:ND2	27:A4:588:ASP:OD1	2.37	0.58
31:AE:40:ALA:O	31:AE:123:ARG:NH2	2.36	0.58
38:BE:810:ARG:NH2	65:RT:183:GLU:OE2	2.36	0.58
47:5I:235:LEU:HB3	47:5I:247:TYR:HB2	1.86	0.58
24:3E:306:LEU:HG	24:3E:375:ALA:HB2	1.84	0.58
41:5C:492:GLY:HA2	41:5C:495:SER:HB2	1.85	0.58
57:RJ:1105:ASP:N	57:RJ:1105:ASP:OD1	2.37	0.58
60:RN:600:LEU:HD21	60:RN:636:LEU:HD13	1.84	0.58
27:A4:326:ARG:NH2	27:A4:364:PHE:O	2.36	0.58
27:A4:585:ILE:HD13	27:A4:633:CYS:HB3	1.85	0.58
29:A8:530:PRO:HG2	29:A8:553:GLN:HE22	1.67	0.58
33:AG:31:ASN:HD21	33:AG:201:ILE:HB	1.68	0.58
54:RF:56:VAL:HG22	54:RF:123:THR:HG22	1.86	0.58
57:RJ:1042:MET:HG3	57:RJ:1044:LEU:HD13	1.86	0.58
3:SA:1028:C:OP1	52:RC:140:LYS:NZ	2.33	0.58
3:SA:1688:U:H3	3:SA:1713:G:H1	1.52	0.58
25:3F:161:SER:HB2	25:3F:242:VAL:HG13	1.86	0.58
34:B1:69:LEU:HD13	34:B1:81:LEU:HD11	1.85	0.58
52:RC:268:GLU:HG2	52:RC:276:LYS:HE2	1.85	0.58
58:RK:289:VAL:O	58:RK:317:GLN:NE2	2.37	0.58
1:3A:112:U:OP1	26:3H:46:ARG:NH1	2.35	0.58
3:SA:1679:G:H1'	3:SA:1722:A:H61	1.68	0.58
6:SG:219:ARG:NH2	55:RH:222:ASP:OD2	2.36	0.58
11:SM:11:ARG:HE	11:SM:12:ALA:H	1.51	0.58
45:5G:81:SER:OG	45:5G:82:GLY:N	2.37	0.58
53:RE:443:HIS:HB3	53:RE:470:LYS:HE2	1.85	0.58
55:RG:88:ARG:NH1	55:RG:90:ASP:OD2	2.36	0.58
13:SO:130:ARG:NH1	13:SO:139:TRP:O	2.37	0.57
22:3B:110:ASN:OD1	22:3B:142:ARG:NH1	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:B2:44:SER:HB3	35:B2:85:LEU:HD11	1.86	0.57
38:BE:819:LYS:NZ	38:BE:823:GLU:OE2	2.37	0.57
3:SA:318:U:O2	3:SA:346:G:O6	2.22	0.57
3:SA:340:U:OP1	50:RA:136:ARG:NH1	2.37	0.57
11:SM:82:ARG:HA	11:SM:111:VAL:HG13	1.86	0.57
27:A4:269:PHE:O	37:B8:446:ARG:NH2	2.35	0.57
27:A4:618:ASN:HA	27:A4:621:ASN:HB2	1.85	0.57
32:AF:387:ALA:O	32:AF:391:ASN:ND2	2.37	0.57
35:B2:124:ILE:HA	35:B2:140:SER:HA	1.85	0.57
37:B8:530:LEU:HB3	37:B8:544:VAL:HG22	1.86	0.57
38:BE:604:SER:OG	38:BE:606:ASP:OD1	2.22	0.57
60:RN:475:ARG:HH12	60:RN:516:LEU:HD23	1.68	0.57
3:SA:54:C:OP2	57:RJ:346:ARG:NH2	2.37	0.57
10:SK:113:VAL:HG13	10:SK:118:LEU:HB2	1.86	0.57
28:A5:10:TYR:OH	28:A5:302:ASN:ND2	2.38	0.57
34:B1:329:VAL:HG13	34:B1:338:ILE:HB	1.85	0.57
58:RK:114:PHE:HB2	58:RK:170:VAL:HG22	1.85	0.57
1:3A:12:U:H3	3:SA:1112:G:H1	1.53	0.57
1:3A:35:U:O2	47:5I:393:LYS:NZ	2.37	0.57
27:A4:127:ASP:HB2	27:A4:134:LEU:HB3	1.86	0.57
35:B2:439:LEU:HB2	35:B2:444:LEU:HB3	1.87	0.57
49:5K:152:ILE:HG12	49:5K:171:PRO:HG2	1.85	0.57
50:RA:101:ASN:ND2	50:RA:118:GLN:OE1	2.35	0.57
53:RE:1195:LYS:HE2	53:RE:1197:ARG:HE	1.69	0.57
61:RO:270:SER:O	61:RO:274:TYR:HB2	2.04	0.57
8:SI:55:LYS:HD2	63:RQ:273:PRO:HG2	1.85	0.57
31:AE:21:ASP:OD1	31:AE:21:ASP:N	2.36	0.57
31:AE:556:LYS:O	31:AE:592:ARG:NH2	2.38	0.57
35:B2:175:ASP:N	35:B2:175:ASP:OD1	2.38	0.57
64:RS:370:VAL:HA	64:RS:373:LYS:HD2	1.86	0.57
3:SA:1136:U:O2'	35:B2:596:ASN:ND2	2.38	0.57
3:SA:1509:C:O2'	56:RI:192:ASN:ND2	2.37	0.57
3:SA:1538:U:H2'	3:SA:1569:A:H61	1.70	0.57
31:AE:143:TYR:HA	31:AE:148:PHE:CD2	2.39	0.57
33:AG:86:GLU:OE2	33:AG:111:THR:OG1	2.22	0.57
35:B2:393:ASP:OD2	35:B2:395:ARG:NH1	2.36	0.57
36:B3:12:LEU:HD22	36:B3:378:PRO:HD2	1.85	0.57
56:RI:125:VAL:O	56:RI:151:PRO:HA	2.04	0.57
35:B2:480:ASP:OD1	35:B2:480:ASP:N	2.35	0.57
53:RE:1188:PRO:HA	53:RE:1191:LYS:HE2	1.85	0.57
57:RJ:610:LYS:NZ	57:RJ:612:VAL:O	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:1232:U:O4	3:SA:1234:A:N6	2.36	0.57
25:3F:369:LEU:O	25:3F:373:MET:HB2	2.03	0.57
27:A4:214:SER:OG	27:A4:221:ASN:O	2.23	0.57
50:RA:152:ASP:N	50:RA:152:ASP:OD1	2.35	0.57
5:SF:100:ARG:NH2	5:SF:121:TYR:O	2.37	0.57
11:SM:88:ARG:HB2	11:SM:105:LYS:HB2	1.86	0.57
24:3E:289:GLN:O	24:3E:391:ARG:NH1	2.37	0.57
25:3F:322:HIS:HB3	25:3F:343:ASP:HB3	1.87	0.57
25:3F:545:LYS:HG2	25:3F:561:ASN:HD21	1.69	0.57
28:A5:445:LEU:HD22	28:A5:479:ILE:HG13	1.85	0.57
37:B8:563:GLY:HA3	37:B8:581:ASN:HD22	1.67	0.57
44:5F:29:ASP:N	44:5F:29:ASP:OD1	2.34	0.57
3:SA:511:A:OP2	10:SK:176:ASN:ND2	2.38	0.57
22:3C:164:ILE:HG23	22:3C:170:VAL:HG21	1.84	0.57
27:A4:249:ARG:NH2	27:A4:292:ASN:O	2.34	0.57
31:AE:637:ILE:HA	31:AE:640:ILE:HG22	1.86	0.57
35:B2:201:ILE:HG13	36:B3:663:VAL:HG11	1.86	0.57
41:5C:547:GLU:OE2	53:RE:809:LYS:NZ	2.38	0.57
50:RA:64:VAL:HG11	50:RA:323:VAL:HG12	1.85	0.57
57:RJ:879:THR:OG1	57:RJ:880:TYR:N	2.38	0.57
15:SR:98:ASP:N	15:SR:98:ASP:OD1	2.36	0.56
16:ST:16:ARG:HG2	16:ST:21:ASN:HD22	1.70	0.56
28:A5:471:ARG:NH2	61:RO:301:ASP:OD1	2.38	0.56
33:AG:118:VAL:HB	33:AG:130:LYS:HB2	1.87	0.56
33:AG:615:TRP:HE1	33:AG:619:GLY:HA2	1.69	0.56
35:B2:588:ILE:HG23	35:B2:602:LEU:HD11	1.87	0.56
57:RJ:309:PRO:HD2	57:RJ:353:LEU:HD22	1.87	0.56
33:AG:502:LYS:HD2	33:AG:564:PRO:HA	1.85	0.56
41:5C:486:VAL:HG23	41:5C:523:GLU:HB2	1.86	0.56
43:5E:373:ILE:HG13	43:5E:378:PHE:HZ	1.70	0.56
51:RB:243:GLN:O	51:RB:247:GLU:HB2	2.05	0.56
53:RE:701:ILE:O	53:RE:705:HIS:ND1	2.39	0.56
64:RS:453:GLY:O	64:RS:457:ARG:HB2	2.06	0.56
5:SF:114:ILE:HB	5:SF:118:GLU:HB2	1.87	0.56
5:SF:209:HIS:ND1	5:SF:218:PHE:O	2.38	0.56
25:3F:289:ARG:NH2	25:3F:332:ALA:O	2.38	0.56
25:3F:365:PRO:HB3	25:3F:397:PHE:HA	1.87	0.56
31:AE:22:ARG:NH2	47:5I:20:GLN:O	2.36	0.56
31:AE:68:ILE:HG22	31:AE:71:ARG:HH12	1.70	0.56
33:AG:536:ASP:OD1	33:AG:536:ASP:N	2.39	0.56
34:B1:441:SER:O	34:B1:443:GLU:N	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:B3:462:THR:HA	36:B3:484:GLU:HG2	1.87	0.56
37:B8:410:ASP:OD2	37:B8:496:ARG:NH2	2.38	0.56
41:5C:121:ASN:OD1	41:5C:121:ASN:N	2.38	0.56
53:RE:524:ASP:OD1	53:RE:956:ASN:ND2	2.38	0.56
57:RJ:246:ALA:HB3	57:RJ:810:ILE:HB	1.87	0.56
58:RK:137:LEU:HG	58:RK:296:LEU:HD21	1.87	0.56
35:B2:126:LEU:HD11	35:B2:168:GLY:HA2	1.88	0.56
41:5C:541:ASP:HB2	41:5C:543:LYS:HG2	1.87	0.56
53:RE:466:THR:HG23	53:RE:475:ASN:HD21	1.69	0.56
2:5A:504:U:H4'	63:RQ:321:HIS:HD2	1.70	0.56
10:SK:79:ARG:HH11	51:RB:247:GLU:HG3	1.71	0.56
27:A4:378:TYR:OH	27:A4:632:ASN:ND2	2.39	0.56
34:B1:30:LEU:HG	34:B1:39:VAL:HG22	1.87	0.56
34:B1:152:LEU:HD23	34:B1:161:ILE:HD11	1.88	0.56
37:B8:278:ASP:N	37:B8:278:ASP:OD1	2.37	0.56
41:5C:241:ASN:ND2	41:5C:244:ASN:OD1	2.39	0.56
50:RA:144:LEU:HD13	50:RA:153:LEU:HD21	1.87	0.56
53:RE:542:SER:HB2	53:RE:693:LYS:HE2	1.86	0.56
59:RL:12:SER:O	59:RL:16:ASN:ND2	2.38	0.56
61:RO:147:THR:HA	61:RO:150:LYS:HE2	1.88	0.56
4:SC:16:GLN:NE2	36:B3:391:LEU:O	2.36	0.56
5:SF:177:ALA:HA	5:SF:198:LYS:HZ2	1.70	0.56
6:SG:100:ASN:O	6:SG:104:ASN:ND2	2.39	0.56
7:SH:57:ASP:HA	7:SH:107:ALA:H	1.70	0.56
22:3C:247:PRO:O	27:A4:140:ASN:ND2	2.38	0.56
33:AG:239:PHE:HE1	33:AG:244:ILE:HD11	1.70	0.56
36:B3:572:GLU:HG3	36:B3:600:LYS:HD2	1.88	0.56
50:RA:250:GLY:HA3	50:RA:271:GLY:HA2	1.88	0.56
52:RC:273:LYS:HA	52:RC:276:LYS:HB2	1.88	0.56
2:5A:485:G:N2	47:5I:386:LYS:O	2.38	0.56
3:SA:329:G:H5''	9:SJ:98:LYS:HB3	1.86	0.56
19:SZ:29:HIS:HB2	19:SZ:32:ARG:HB2	1.86	0.56
23:3D:212:ASP:O	23:3D:216:PHE:HB2	2.06	0.56
26:3G:90:ALA:HB2	37:B8:453:VAL:HG21	1.88	0.56
32:AF:502:GLN:NE2	32:AF:505:GLU:OE1	2.39	0.56
33:AG:81:GLU:HA	33:AG:760:HIS:HB3	1.87	0.56
45:5G:74:ASP:OD1	45:5G:74:ASP:N	2.37	0.56
1:3A:324:U:N3	24:3E:323:GLU:OE2	2.39	0.56
3:SA:163:G:OP1	7:SH:53:SER:OG	2.24	0.56
15:SR:50:GLU:OE2	15:SR:82:ARG:NH2	2.37	0.56
15:SR:120:ASP:OD1	15:SR:120:ASP:N	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:A5:8:SER:HB3	28:A5:17:LEU:HD11	1.88	0.56
32:AF:52:PRO:HG2	32:AF:312:ALA:HA	1.88	0.56
35:B2:124:ILE:HG22	35:B2:140:SER:HB3	1.88	0.56
35:B2:187:LYS:HG2	35:B2:199:THR:HG22	1.87	0.56
35:B2:259:ILE:HG12	35:B2:274:ILE:HG12	1.88	0.56
38:BE:430:ILE:HB	38:BE:443:TRP:HB2	1.88	0.56
46:5H:511:GLU:O	46:5H:515:ASN:ND2	2.38	0.56
57:RJ:217:ASP:OD1	57:RJ:217:ASP:N	2.37	0.56
66:RV:239:ARG:NH2	66:RV:286:ARG:O	2.39	0.56
3:SA:505:A:H61	3:SA:586:G:H8	1.54	0.56
6:SG:26:ALA:HB3	15:SR:28:LEU:HB3	1.88	0.56
25:3F:137:GLY:HA3	25:3F:485:ASN:HD22	1.70	0.56
26:3H:38:ASN:HA	26:3H:41:THR:HG22	1.88	0.56
42:5D:149:GLU:HA	42:5D:152:PHE:HB2	1.87	0.56
55:RG:151:ARG:HE	55:RG:155:SER:HB3	1.71	0.56
55:RH:41:MET:O	55:RH:110:LEU:HA	2.06	0.56
56:RI:71:ASN:ND2	56:RI:123:ASP:OD2	2.39	0.56
57:RJ:962:GLU:OE2	60:RN:756:ARG:NH1	2.37	0.56
3:SA:693:U:O4	8:SI:116:ARG:NH2	2.36	0.56
9:SJ:56:ARG:NH2	50:RA:77:TYR:OH	2.39	0.56
22:3B:189:GLY:O	22:3B:216:ASN:ND2	2.39	0.56
25:3F:356:ARG:NH2	51:RB:259:SER:OG	2.39	0.56
28:A5:149:ASN:HD21	28:A5:190:PRO:HB3	1.71	0.56
32:AF:426:LYS:HD3	32:AF:429:VAL:HG23	1.87	0.56
34:B1:165:SER:OG	34:B1:166:LYS:N	2.38	0.56
34:B1:406:SER:OG	34:B1:407:LEU:N	2.37	0.56
2:5A:393:C:O4'	44:5F:28:ARG:NH2	2.39	0.55
3:SA:551:G:N7	42:5D:2:ALA:N	2.54	0.55
22:3C:185:SER:HB3	22:3C:217:ILE:HD11	1.88	0.55
32:AF:147:ARG:HH11	61:RO:411:ASN:HD21	1.54	0.55
37:B8:129:ASP:HA	37:B8:132:LYS:HE2	1.89	0.55
37:B8:240:ASP:HB2	37:B8:243:ALA:HB2	1.89	0.55
38:BE:511:ASP:HB2	38:BE:516:LYS:HG3	1.89	0.55
56:RI:148:LYS:HG3	56:RI:149:LYS:HG2	1.88	0.55
29:A8:259:ILE:HA	29:A8:273:GLU:HA	1.88	0.55
29:A8:533:PRO:HA	29:A8:559:PRO:HG2	1.89	0.55
31:AE:387:LEU:HD21	31:AE:403:LEU:HD23	1.88	0.55
34:B1:645:ASP:OD1	34:B1:645:ASP:N	2.36	0.55
38:BE:207:ASP:N	38:BE:207:ASP:OD1	2.37	0.55
51:RB:230:ALA:O	51:RB:234:LYS:CB	2.52	0.55
53:RE:202:SER:OG	53:RE:293:ASN:ND2	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:SC:195:LYS:O	4:SC:199:ASN:ND2	2.34	0.55
22:3C:149:SER:OG	22:3C:150:LYS:N	2.38	0.55
23:3D:370:LYS:HG3	23:3D:373:GLY:H	1.72	0.55
24:3E:208:ILE:HG13	24:3E:223:LEU:HD11	1.88	0.55
26:3G:58:CYS:HB3	26:3G:98:ILE:HD12	1.87	0.55
35:B2:264:ASN:ND2	35:B2:348:SER:OG	2.39	0.55
36:B3:464:LYS:NZ	36:B3:479:ILE:O	2.32	0.55
37:B8:561:PRO:O	37:B8:587:ARG:NH1	2.39	0.55
47:5I:281:ASN:HD21	47:5I:287:TYR:HE2	1.53	0.55
63:RQ:279:GLN:NE2	63:RQ:283:ASP:OD1	2.40	0.55
3:SA:521:A:N3	19:SZ:34:ASN:ND2	2.55	0.55
22:3C:125:VAL:O	22:3C:138:LYS:N	2.39	0.55
27:A4:561:LYS:NZ	27:A4:597:ASN:OD1	2.39	0.55
27:A4:748:SER:OG	27:A4:749:SER:N	2.39	0.55
36:B3:414:VAL:HG23	36:B3:427:TYR:HB3	1.89	0.55
46:5H:560:ASN:HB3	46:5H:563:VAL:HG12	1.88	0.55
47:5I:81:ASN:ND2	47:5I:96:ASN:OD1	2.39	0.55
53:RE:223:ARG:HA	53:RE:226:HIS:HB2	1.88	0.55
53:RE:834:ASN:ND2	53:RE:863:TYR:OH	2.39	0.55
3:SA:1512:G:H5''	56:RI:148:LYS:HD2	1.88	0.55
19:SZ:54:ALA:HB1	19:SZ:76:TYR:HB2	1.87	0.55
24:3E:215:ARG:NH1	24:3E:244:GLY:O	2.39	0.55
32:AF:21:THR:HG23	32:AF:24:GLN:H	1.71	0.55
32:AF:190:ASP:OD2	32:AF:194:ARG:NH1	2.39	0.55
35:B2:171:CYS:SG	35:B2:172:GLN:N	2.79	0.55
39:B6:293:TYR:HB2	39:B6:295:ILE:HG22	1.89	0.55
44:5F:137:ARG:NH2	44:5F:139:GLY:O	2.40	0.55
47:5I:280:ALA:HB1	47:5I:308:VAL:HG12	1.87	0.55
61:RO:300:THR:O	61:RO:304:ASN:ND2	2.39	0.55
3:SA:153:G:H4'	7:SH:15:THR:HG21	1.89	0.55
3:SA:1786:G:H1'	36:B3:135:TYR:HB3	1.88	0.55
10:SK:59:LEU:HB3	10:SK:93:LEU:HD21	1.89	0.55
11:SM:133:LYS:HG2	11:SM:134:THR:HG23	1.89	0.55
28:A5:145:CYS:HB2	28:A5:148:LEU:HD21	1.88	0.55
41:5C:415:GLU:OE2	47:5I:39:ARG:NH2	2.38	0.55
50:RA:192:ASN:O	50:RA:210:ARG:NH1	2.40	0.55
53:RE:656:ARG:HG2	67:X1:1241:UNK:HA	1.89	0.55
58:RK:312:ARG:NH2	58:RK:344:GLU:OE1	2.40	0.55
59:RM:311:THR:O	59:RM:370:ILE:HA	2.07	0.55
61:RO:447:ASP:N	61:RO:447:ASP:OD1	2.37	0.55
64:RS:222:LYS:HD3	64:RS:253:GLU:HB2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:103:A:OP2	3:SA:360:A:N6	2.35	0.55
8:SI:51:VAL:HG23	8:SI:53:GLY:H	1.71	0.55
25:3F:336:CYS:SG	25:3F:337:VAL:N	2.79	0.55
58:RK:36:ILE:HG21	58:RK:45:LEU:HD23	1.88	0.55
2:5A:278:G:N2	37:B8:539:ASP:OD2	2.35	0.55
3:SA:284:G:N2	3:SA:285:G:O6	2.40	0.55
20:Sc:67:THR:OG1	20:Sc:70:LYS:O	2.23	0.55
22:3C:175:ALA:N	22:3C:198:GLU:OE2	2.36	0.55
24:3E:179:THR:O	24:3E:183:ARG:NH1	2.39	0.55
35:B2:351:LEU:HB2	35:B2:367:ILE:HG23	1.89	0.55
36:B3:65:THR:HA	36:B3:80:SER:HA	1.87	0.55
53:RE:711:PRO:HG3	53:RE:767:GLN:HE21	1.71	0.55
3:SA:325:G:H2'	3:SA:326:G:H8	1.72	0.55
23:3D:304:SER:HB2	23:3D:309:GLU:HG3	1.89	0.55
24:3E:397:ARG:HH21	24:3E:400:GLN:HE21	1.53	0.55
35:B2:414:LEU:HD12	35:B2:447:LEU:HD13	1.88	0.55
36:B3:67:LEU:HD13	36:B3:107:ILE:HA	1.89	0.55
37:B8:513:GLN:HG3	37:B8:551:VAL:HG21	1.89	0.55
50:RA:85:ASP:HB3	50:RA:88:ASN:HB2	1.87	0.55
3:SA:370:A:H3'	3:SA:370:A:N3	2.22	0.55
13:SO:13:SER:OG	13:SO:14:SER:N	2.40	0.55
26:3H:33:LEU:HD11	26:3H:100:ALA:HB1	1.89	0.55
53:RE:1222:GLU:HB3	54:RF:60:LEU:HD22	1.89	0.55
2:5A:474:A:OP2	41:5C:425:ARG:NH2	2.34	0.54
9:SJ:5:ARG:H	9:SJ:28:GLU:HG2	1.72	0.54
34:B1:449:SER:OG	34:B1:451:ASP:OD1	2.24	0.54
37:B8:317:ARG:NE	37:B8:356:GLU:OE2	2.34	0.54
41:5C:449:ILE:HD11	47:5I:38:ALA:HA	1.89	0.54
53:RE:114:VAL:O	53:RE:117:LYS:NZ	2.34	0.54
53:RE:221:ASN:HD21	53:RE:316:ARG:HH21	1.54	0.54
53:RE:713:LEU:HB2	53:RE:716:SER:HB3	1.90	0.54
53:RE:1159:ASN:HD22	53:RE:1201:ASP:HB3	1.72	0.54
60:RN:283:ALA:HA	64:RS:381:ALA:HB1	1.89	0.54
2:5A:173:G:N2	2:5A:224:G:O2'	2.40	0.54
3:SA:127:G:OP1	3:SA:127:G:N2	2.41	0.54
5:SF:185:GLY:HA3	5:SF:224:ASN:HD22	1.72	0.54
8:SI:67:LEU:HD22	8:SI:94:ALA:HB2	1.89	0.54
29:A8:541:LEU:HB2	29:A8:544:LEU:HB3	1.88	0.54
32:AF:64:GLN:HE21	32:AF:73:VAL:HG21	1.73	0.54
35:B2:330:GLN:NE2	35:B2:376:SER:O	2.41	0.54
41:5C:185:HIS:NE2	44:5F:19:LEU:O	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:5H:544:ILE:O	57:RJ:193:ARG:NH1	2.40	0.54
50:RA:316:ASP:OD1	50:RA:316:ASP:N	2.38	0.54
53:RE:498:MET:O	53:RE:506:GLN:NE2	2.39	0.54
55:RH:227:LEU:O	55:RH:240:LYS:NZ	2.41	0.54
57:RJ:262:GLY:O	57:RJ:264:GLN:NE2	2.40	0.54
58:RK:60:THR:O	60:RN:108:LYS:NZ	2.40	0.54
2:5A:460:U:OP1	49:5K:21:LYS:NZ	2.40	0.54
4:SC:87:ARG:HH21	4:SC:101:HIS:HD2	1.55	0.54
9:SJ:64:ASN:ND2	9:SJ:73:SER:OG	2.40	0.54
28:A5:280:GLN:O	28:A5:327:THR:HA	2.07	0.54
31:AE:248:SER:OG	31:AE:253:CYS:SG	2.66	0.54
33:AG:340:ILE:O	33:AG:358:LEU:HA	2.08	0.54
34:B1:449:SER:OG	34:B1:450:LEU:N	2.37	0.54
35:B2:10:GLN:OE1	35:B2:682:ARG:NH1	2.41	0.54
35:B2:433:ALA:HA	35:B2:449:THR:HA	1.89	0.54
37:B8:360:VAL:HG22	37:B8:375:VAL:HG12	1.89	0.54
37:B8:544:VAL:HG12	37:B8:551:VAL:HG22	1.89	0.54
41:5C:194:ARG:NE	41:5C:210:GLU:OE2	2.41	0.54
53:RE:556:ILE:H	53:RE:560:ASN:HD21	1.55	0.54
1:3A:113:G:O6	26:3H:42:LYS:NZ	2.40	0.54
2:5A:513:G:N2	47:5I:124:HIS:O	2.39	0.54
23:3D:226:LYS:HE2	23:3D:253:ASP:HA	1.89	0.54
25:3F:241:THR:HG21	25:3F:285:SER:HA	1.89	0.54
32:AF:173:THR:HG21	32:AF:218:VAL:H	1.72	0.54
32:AF:190:ASP:N	32:AF:190:ASP:OD1	2.40	0.54
35:B2:828:TYR:HA	35:B2:831:LYS:HG2	1.89	0.54
36:B3:558:LYS:HG2	36:B3:571:LEU:HD22	1.89	0.54
38:BE:626:ASP:N	38:BE:626:ASP:OD1	2.41	0.54
38:BE:721:LEU:HD13	38:BE:921:ARG:HH12	1.71	0.54
39:B6:14:GLU:OE1	39:B6:87:SER:OG	2.24	0.54
58:RK:315:LYS:HB2	58:RK:348:GLU:HB3	1.89	0.54
61:RO:483:ILE:HA	61:RO:486:GLN:HB2	1.88	0.54
3:SA:1634:C:OP1	34:B1:418:ARG:NH1	2.41	0.54
5:SF:185:GLY:HA3	5:SF:224:ASN:HB3	1.88	0.54
8:SI:117:THR:OG1	8:SI:118:LEU:N	2.33	0.54
10:SK:164:PHE:O	25:3F:279:ARG:NH2	2.40	0.54
19:SZ:20:ARG:HD2	19:SZ:74:LEU:HD12	1.88	0.54
22:3B:252:ILE:O	22:3B:256:ASN:ND2	2.41	0.54
36:B3:680:ASN:N	36:B3:680:ASN:OD1	2.40	0.54
38:BE:209:ILE:HA	38:BE:225:THR:HA	1.88	0.54
38:BE:227:THR:OG1	38:BE:229:GLU:OE1	2.26	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:B6:200:ARG:HG2	39:B6:203:MET:HE2	1.89	0.54
55:RG:115:GLN:HE22	55:RG:215:ASN:HD21	1.55	0.54
22:3B:240:VAL:HG23	22:3B:261:LEU:HD13	1.89	0.54
23:3D:157:ALA:O	39:B6:293:TYR:OH	2.26	0.54
23:3D:218:LYS:HD2	23:3D:221:LEU:HD21	1.90	0.54
32:AF:463:VAL:HA	32:AF:466:VAL:HG12	1.90	0.54
33:AG:616:SER:HG	33:AG:621:LEU:H	1.55	0.54
33:AG:713:CYS:HA	33:AG:719:ASN:HA	1.89	0.54
41:5C:25:THR:OG1	41:5C:26:TYR:N	2.40	0.54
49:5K:103:MET:HG2	49:5K:127:ARG:HH12	1.72	0.54
54:RF:16:VAL:HB	54:RF:37:MET:HB2	1.89	0.54
59:RL:71:LYS:O	59:RL:75:ASN:ND2	2.41	0.54
2:5A:546:G:H22	2:5A:591:U:H2'	1.72	0.54
3:SA:1532:U:O2'	16:ST:40:ARG:NH1	2.40	0.54
8:SI:163:ASP:HA	8:SI:166:LEU:HG	1.90	0.54
25:3F:120:ARG:O	25:3F:122:LYS:NZ	2.40	0.54
28:A5:203:ILE:HD12	28:A5:214:VAL:HB	1.90	0.54
31:AE:83:ARG:NH1	31:AE:125:PHE:O	2.38	0.54
33:AG:153:ILE:HG22	33:AG:174:TYR:HB2	1.90	0.54
34:B1:335:GLU:OE1	35:B2:924:TYR:OH	2.23	0.54
35:B2:171:CYS:O	35:B2:172:GLN:NE2	2.41	0.54
50:RA:152:ASP:HB2	50:RA:164:ARG:HD2	1.90	0.54
50:RA:247:THR:HG23	50:RA:249:ASN:H	1.72	0.54
53:RE:368:LEU:HA	53:RE:371:GLN:HE21	1.73	0.54
55:RG:99:LEU:O	55:RG:105:ASN:ND2	2.40	0.54
4:SC:31:ASP:HA	4:SC:45:LYS:HA	1.90	0.54
47:5I:107:LYS:NZ	47:5I:109:HIS:O	2.39	0.54
53:RE:167:PRO:HB2	53:RE:172:THR:HG21	1.89	0.54
55:RG:169:ASP:OD1	55:RG:169:ASP:N	2.37	0.54
57:RJ:94:THR:HG21	57:RJ:354:ILE:HD12	1.89	0.54
59:RL:76:LYS:O	59:RL:76:LYS:NZ	2.41	0.54
65:RT:169:ASP:OD1	65:RT:169:ASP:N	2.35	0.54
32:AF:461:ASP:HB3	33:AG:520:LEU:HB2	1.88	0.54
34:B1:755:TYR:OH	34:B1:795:ASN:ND2	2.40	0.54
35:B2:360:ASN:OD1	35:B2:360:ASN:N	2.41	0.54
35:B2:412:GLY:HA2	35:B2:431:GLY:H	1.72	0.54
38:BE:630:THR:N	38:BE:644:THR:O	2.40	0.54
59:RL:387:ASP:O	59:RL:409:ALA:HA	2.08	0.54
60:RN:95:ARG:HH11	60:RN:758:ASP:HB3	1.72	0.54
65:RT:127:GLN:HB2	65:RT:140:ARG:HG3	1.90	0.54
3:SA:112:A:O2'	11:SM:67:ARG:NH1	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:SG:118:LEU:HG	6:SG:129:PRO:HB2	1.90	0.54
22:3C:225:ARG:NH2	22:3C:246:GLN:OE1	2.41	0.54
27:A4:97:ARG:NE	40:5B:191:PRO:O	2.39	0.54
27:A4:427:ASN:OD1	27:A4:427:ASN:N	2.40	0.54
35:B2:145:ILE:HG23	35:B2:159:LEU:HB2	1.90	0.54
36:B3:513:LYS:H	36:B3:535:GLY:HA2	1.73	0.54
38:BE:21:SER:OG	38:BE:22:LYS:N	2.39	0.54
44:5F:135:HIS:HB3	44:5F:160:TRP:HD1	1.73	0.54
50:RA:142:ARG:NH1	50:RA:200:GLU:OE2	2.41	0.54
58:RK:205:VAL:HA	58:RK:208:MET:HE3	1.88	0.54
3:SA:396:G:N1	3:SA:399:A:OP2	2.40	0.53
8:SI:118:LEU:HA	8:SI:121:VAL:HB	1.89	0.53
22:3C:145:ASN:HD22	22:3C:148:ARG:HB2	1.73	0.53
26:3H:41:THR:O	26:3H:45:ASN:ND2	2.41	0.53
27:A4:529:ASN:ND2	27:A4:547:CYS:SG	2.81	0.53
28:A5:148:LEU:HD23	28:A5:167:SER:HB3	1.90	0.53
29:A8:566:LEU:HD21	29:A8:585:ARG:HG2	1.90	0.53
35:B2:479:LEU:HA	35:B2:489:VAL:O	2.08	0.53
38:BE:225:THR:OG1	38:BE:227:THR:O	2.25	0.53
41:5C:482:ASP:OD1	41:5C:515:ARG:NH2	2.41	0.53
42:5D:120:LYS:O	42:5D:124:GLN:NE2	2.41	0.53
57:RJ:775:GLU:HG3	57:RJ:779:ARG:HE	1.72	0.53
1:3A:37:G:N2	41:5C:428:GLN:OE1	2.41	0.53
20:Sc:73:LEU:HB2	54:RF:215:VAL:HG21	1.89	0.53
24:3E:215:ARG:NH1	24:3E:245:THR:O	2.42	0.53
24:3E:223:LEU:HD12	24:3E:226:ILE:HD12	1.90	0.53
24:3E:431:ALA:O	37:B8:160:TYR:OH	2.25	0.53
25:3F:503:ASP:N	25:3F:503:ASP:OD1	2.41	0.53
31:AE:773:GLN:HE22	31:AE:805:ILE:HG23	1.72	0.53
32:AF:51:HIS:O	32:AF:53:HIS:ND1	2.38	0.53
33:AG:584:PHE:HB3	33:AG:598:LYS:HB2	1.88	0.53
57:RJ:280:LEU:HD12	57:RJ:281:PRO:HD2	1.89	0.53
60:RN:660:ILE:HG12	61:RO:388:LEU:HD13	1.89	0.53
11:SM:75:VAL:HG12	11:SM:86:ILE:HG12	1.91	0.53
26:3G:44:LEU:HD21	26:3G:76:VAL:HG11	1.90	0.53
26:3H:29:ASN:O	26:3H:31:ARG:NH2	2.41	0.53
31:AE:309:GLN:NE2	37:B8:223:SER:O	2.41	0.53
33:AG:530:LYS:HG2	33:AG:546:LYS:HB3	1.90	0.53
34:B1:28:GLN:HA	34:B1:40:PHE:O	2.08	0.53
35:B2:943:ILE:HB	43:5E:462:SER:HB2	1.91	0.53
36:B3:443:PRO:HG2	36:B3:445:ILE:HG12	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:5C:220:SER:HB2	44:5F:16:VAL:HG22	1.90	0.53
53:RE:464:THR:O	53:RE:466:THR:OG1	2.26	0.53
53:RE:1203:ASN:OD1	54:RF:57:ASN:ND2	2.41	0.53
57:RJ:73:ALA:HB1	57:RJ:131:ILE:HD12	1.89	0.53
2:5A:207:G:H2'	2:5A:208:A:H8	1.72	0.53
5:SF:183:VAL:HG21	5:SF:220:THR:HG21	1.90	0.53
8:SI:71:HIS:HA	8:SI:74:GLN:HB2	1.89	0.53
13:SO:84:ILE:HG23	13:SO:89:TYR:HB2	1.91	0.53
25:3F:187:ALA:HB2	25:3F:201:ILE:HD13	1.90	0.53
28:A5:366:GLY:O	33:AG:583:LYS:NZ	2.40	0.53
35:B2:325:ILE:HG23	35:B2:326:LEU:HD13	1.91	0.53
41:5C:463:ALA:HA	41:5C:466:LEU:HB2	1.89	0.53
50:RA:65:SER:OG	50:RA:69:GLN:O	2.26	0.53
52:RC:142:ARG:NH1	52:RC:168:GLY:O	2.38	0.53
8:SI:38:LEU:HD12	8:SI:41:LEU:HD12	1.91	0.53
24:3E:207:ARG:HE	24:3E:226:ILE:HG12	1.73	0.53
25:3F:157:LEU:HD23	25:3F:191:SER:HB3	1.89	0.53
27:A4:522:SER:HA	27:A4:528:ILE:HD11	1.89	0.53
33:AG:46:ILE:HG21	33:AG:385:ILE:HD13	1.90	0.53
35:B2:107:ASP:OD2	35:B2:110:SER:OG	2.27	0.53
35:B2:501:ASP:HB2	35:B2:523:HIS:HB3	1.89	0.53
36:B3:591:ILE:HG23	36:B3:600:LYS:HZ3	1.73	0.53
37:B8:221:THR:OG1	37:B8:222:LEU:N	2.41	0.53
41:5C:170:GLN:NE2	41:5C:177:TYR:OH	2.40	0.53
61:RO:428:THR:HG22	61:RO:430:ASP:H	1.74	0.53
3:SA:1753:A:OP1	43:5E:525:LYS:NZ	2.39	0.53
10:SK:37:LYS:HG3	46:5H:562:ARG:HB2	1.90	0.53
27:A4:585:ILE:HD11	27:A4:589:ASN:HD22	1.73	0.53
28:A5:213:ASN:ND2	28:A5:215:TYR:OH	2.41	0.53
32:AF:2:SER:OG	32:AF:3:THR:N	2.40	0.53
44:5F:66:PRO:HG3	66:RV:207:ARG:HH11	1.72	0.53
53:RE:925:LEU:HD22	53:RE:1060:ILE:HG23	1.90	0.53
2:5A:481:U:O2'	39:B6:102:LYS:NZ	2.41	0.53
3:SA:311:U:H3	3:SA:355:G:H1	1.57	0.53
5:SF:206:ASP:OD1	5:SF:206:ASP:N	2.42	0.53
13:SO:61:THR:OG1	13:SO:62:GLN:N	2.41	0.53
28:A5:438:THR:N	61:RO:297:ASP:OD2	2.40	0.53
31:AE:699:ARG:NH1	31:AE:702:TRP:O	2.42	0.53
32:AF:248:ARG:NH2	32:AF:289:ASN:O	2.42	0.53
33:AG:529:LEU:HB3	33:AG:547:VAL:HG23	1.91	0.53
41:5C:257:SER:OG	41:5C:259:TRP:NE1	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:5C:480:ASN:HD22	41:5C:483:ILE:HG13	1.73	0.53
50:RA:183:VAL:HA	50:RA:199:THR:HA	1.91	0.53
53:RE:494:GLU:OE2	53:RE:497:ARG:NH2	2.42	0.53
55:RH:53:HIS:HB2	55:RH:68:LEU:HD11	1.91	0.53
55:RH:55:ILE:O	55:RH:63:ASP:N	2.42	0.53
28:A5:454:GLU:OE2	28:A5:487:ARG:NH1	2.41	0.53
29:A8:647:LEU:O	30:A9:509:GLN:NE2	2.42	0.53
34:B1:697:SER:OG	34:B1:698:THR:N	2.41	0.53
36:B3:80:SER:OG	36:B3:81:GLN:N	2.42	0.53
57:RJ:308:CYS:HB2	57:RJ:355:TYR:HB2	1.90	0.53
59:RM:609:ALA:O	59:RM:613:LEU:CB	2.57	0.53
2:5A:102:A:OP2	28:A5:490:ARG:NH2	2.41	0.53
5:SF:47:PHE:HE1	5:SF:111:VAL:HG11	1.74	0.53
8:SI:7:LYS:O	8:SI:42:GLN:NE2	2.42	0.53
15:SR:46:PHE:HA	15:SR:49:TYR:HB2	1.91	0.53
16:ST:50:ALA:HB2	16:ST:72:ILE:HD12	1.91	0.53
19:SZ:8:ARG:NH1	25:3F:316:GLU:OE2	2.40	0.53
27:A4:35:ARG:NH1	27:A4:756:GLU:OE2	2.42	0.53
33:AG:33:ASN:HB2	33:AG:357:ILE:HD11	1.91	0.53
35:B2:161:SER:O	35:B2:187:LYS:NZ	2.41	0.53
36:B3:129:VAL:HG12	36:B3:136:ILE:HG13	1.91	0.53
41:5C:28:ASN:ND2	63:RQ:855:GLU:OE1	2.42	0.53
49:5K:72:ILE:HD12	49:5K:106:LEU:HD11	1.91	0.53
53:RE:628:VAL:HG22	53:RE:668:VAL:HG12	1.91	0.53
53:RE:725:SER:O	53:RE:729:ASN:ND2	2.42	0.53
57:RJ:106:THR:HG23	57:RJ:355:TYR:HB3	1.91	0.53
59:RL:86:ARG:NH1	59:RL:90:GLU:O	2.42	0.53
3:SA:1482:C:O2'	15:SR:72:GLY:O	2.24	0.53
3:SA:1643:U:OP2	43:5E:530:ARG:NH1	2.41	0.53
5:SF:36:HIS:NE2	5:SF:88:ASP:OD1	2.42	0.53
31:AE:274:ILE:HD11	37:B8:215:THR:HG21	1.90	0.53
32:AF:246:TYR:OH	32:AF:289:ASN:ND2	2.39	0.53
33:AG:368:ASP:OD1	33:AG:368:ASP:N	2.42	0.53
36:B3:108:LEU:HG	36:B3:119:VAL:HG12	1.89	0.53
36:B3:194:ARG:HG3	36:B3:244:GLU:H	1.73	0.53
36:B3:343:MET:HA	36:B3:354:ALA:O	2.09	0.53
36:B3:787:PRO:HB2	43:5E:492:PRO:HG3	1.91	0.53
38:BE:921:ARG:O	38:BE:925:LEU:HB2	2.09	0.53
43:5E:344:GLU:HA	57:RJ:960:ARG:HH21	1.74	0.53
51:RB:310:GLN:HA	51:RB:313:ARG:HG2	1.91	0.53
56:RI:128:ASP:OD2	56:RI:130:ARG:NH1	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:RJ:932:LEU:HD22	57:RJ:1007:TYR:HB2	1.90	0.53
2:5A:153:U:O4	33:AG:544:LYS:NZ	2.42	0.52
2:5A:297:U:O2	38:BE:103:ARG:NH1	2.42	0.52
3:SA:1463:C:H4'	60:RN:63:ALA:HB1	1.91	0.52
14:SP:64:ALA:HB1	14:SP:105:LEU:HG	1.91	0.52
18:SY:103:LEU:HB3	18:SY:126:LYS:HB2	1.90	0.52
27:A4:107:VAL:HG23	27:A4:110:GLU:HB2	1.91	0.52
28:A5:250:ASP:OD1	28:A5:250:ASP:N	2.42	0.52
28:A5:364:THR:HG23	33:AG:547:VAL:HG12	1.90	0.52
36:B3:622:ALA:HB3	36:B3:636:ASP:H	1.73	0.52
65:RT:119:PRO:HA	65:RT:123:HIS:HB3	1.91	0.52
1:3A:49:C:H42	2:5A:467:A:H61	1.57	0.52
2:5A:182:G:N2	2:5A:215:U:O2	2.32	0.52
2:5A:333:G:O6	44:5F:25:GLN:NE2	2.43	0.52
5:SF:32:SER:OG	5:SF:33:ALA:N	2.43	0.52
31:AE:376:GLU:OE2	33:AG:862:LYS:NZ	2.39	0.52
33:AG:510:TYR:HE1	33:AG:527:HIS:HB3	1.74	0.52
33:AG:510:TYR:OH	33:AG:527:HIS:ND1	2.38	0.52
34:B1:300:MET:HE3	34:B1:328:LEU:HD13	1.91	0.52
34:B1:492:SER:OG	34:B1:494:ASP:OD1	2.27	0.52
36:B3:31:ILE:HG23	36:B3:42:ILE:HG13	1.90	0.52
36:B3:803:SER:O	36:B3:803:SER:OG	2.24	0.52
54:RF:14:ILE:HB	54:RF:39:ALA:HB3	1.90	0.52
60:RN:389:ASP:O	60:RN:393:LYS:CB	2.56	0.52
62:RP:238:GLU:O	62:RP:242:SER:CB	2.58	0.52
65:RT:129:ARG:NH2	65:RT:130:MET:O	2.42	0.52
1:3A:3:C:H2'	1:3A:4:G:H8	1.74	0.52
33:AG:668:THR:OG1	33:AG:669:ASN:N	2.42	0.52
34:B1:420:ARG:NH2	43:5E:489:SER:O	2.42	0.52
34:B1:524:ARG:HD2	34:B1:529:GLU:HB2	1.91	0.52
55:RG:52:THR:HG21	55:RG:145:LEU:HD11	1.91	0.52
55:RH:91:ILE:HA	55:RH:94:GLN:HG2	1.91	0.52
9:SJ:34:ALA:HB3	9:SJ:56:ARG:HG2	1.91	0.52
13:SO:99:ARG:NH2	13:SO:119:GLU:OE2	2.43	0.52
24:3E:355:ASN:HB2	24:3E:401:LEU:HD13	1.92	0.52
27:A4:150:ASN:ND2	27:A4:154:ASP:OD1	2.42	0.52
28:A5:531:LYS:O	28:A5:535:ASP:HB2	2.09	0.52
36:B3:16:TYR:OH	36:B3:21:ALA:O	2.27	0.52
47:5I:329:ILE:HG12	47:5I:343:TYR:HB2	1.91	0.52
64:RS:364:PHE:HB2	64:RS:396:ARG:HH21	1.74	0.52
2:5A:307:C:O2'	2:5A:311:C:OP1	2.28	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5A:461:A:N6	49:5K:14:LYS:O	2.40	0.52
3:SA:105:A:OP2	3:SA:107:C:N4	2.43	0.52
3:SA:895:G:H1	3:SA:917:U:H3	1.57	0.52
5:SF:176:ASP:N	5:SF:176:ASP:OD1	2.41	0.52
19:SZ:51:GLU:HB3	19:SZ:54:ALA:HB3	1.91	0.52
25:3F:539:ILE:O	25:3F:565:SER:HA	2.09	0.52
27:A4:282:ASP:OD1	27:A4:282:ASP:N	2.41	0.52
35:B2:238:MET:HE1	36:B3:668:SER:HA	1.91	0.52
35:B2:641:TYR:O	35:B2:650:ILE:N	2.43	0.52
37:B8:524:SER:OG	37:B8:526:ASP:OD1	2.26	0.52
53:RE:132:TYR:HA	53:RE:135:LEU:HG	1.90	0.52
56:RI:119:TYR:O	56:RI:149:LYS:NZ	2.42	0.52
57:RJ:65:ASP:OD1	57:RJ:65:ASP:N	2.41	0.52
57:RJ:906:ASP:OD2	57:RJ:1030:LYS:NZ	2.36	0.52
3:SA:918:U:O3'	14:SP:18:ARG:NH1	2.42	0.52
3:SA:1665:U:O2	3:SA:1736:G:O6	2.28	0.52
9:SJ:107:THR:HA	9:SJ:110:ARG:HB2	1.91	0.52
26:3G:64:LEU:O	26:3G:66:HIS:N	2.41	0.52
28:A5:285:ASP:HB2	28:A5:287:ARG:HG3	1.91	0.52
33:AG:109:VAL:HG13	33:AG:117:ILE:HB	1.92	0.52
35:B2:394:VAL:HG21	35:B2:681:ILE:HD11	1.92	0.52
55:RG:45:LEU:HD12	55:RG:114:ILE:HG12	1.91	0.52
60:RN:429:LEU:HD11	60:RN:459:LEU:HD13	1.92	0.52
17:SX:95:PRO:HB3	66:RV:308:ILE:HD12	1.91	0.52
26:3H:59:GLU:OE2	26:3H:84:ARG:NH2	2.43	0.52
27:A4:122:VAL:HG11	40:5B:192:PRO:HD2	1.92	0.52
30:A9:460:LEU:O	30:A9:464:SER:OG	2.22	0.52
33:AG:443:ASN:ND2	33:AG:446:ASN:OD1	2.38	0.52
36:B3:107:ILE:HG12	36:B3:149:SER:HA	1.92	0.52
53:RE:381:HIS:NE2	53:RE:478:THR:O	2.42	0.52
53:RE:975:LEU:HB3	53:RE:1041:VAL:HA	1.91	0.52
61:RO:327:MET:O	61:RO:331:ASN:HA	2.10	0.52
3:SA:362:G:N2	3:SA:382:C:O2	2.43	0.52
16:ST:5:VAL:H	61:RO:368:SER:HG	1.57	0.52
22:3B:314:CYS:SG	22:3B:315:ILE:N	2.83	0.52
32:AF:141:ALA:HA	32:AF:150:ARG:O	2.08	0.52
33:AG:561:LEU:HD12	33:AG:562:PRO:HD2	1.92	0.52
35:B2:259:ILE:HA	35:B2:273:TYR:O	2.09	0.52
36:B3:548:LEU:O	36:B3:559:ILE:HA	2.10	0.52
43:5E:448:LEU:HD22	44:5F:85:MET:HE1	1.91	0.52
48:5J:110:ASP:OD1	48:5J:110:ASP:N	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:RA:155:VAL:HG13	50:RA:163:TYR:HB2	1.91	0.52
17:SX:62:VAL:HG11	20:Sc:8:LEU:HD22	1.91	0.52
25:3F:426:SER:HB3	25:3F:433:ILE:HD11	1.91	0.52
28:A5:123:SER:O	28:A5:141:ARG:NH1	2.43	0.52
41:5C:254:GLY:HA2	41:5C:277:VAL:HG23	1.92	0.52
53:RE:576:ASP:OD1	53:RE:576:ASP:N	2.43	0.52
55:RH:228:SER:OG	55:RH:229:ASN:N	2.41	0.52
57:RJ:364:VAL:HG12	57:RJ:373:ILE:HG12	1.92	0.52
2:5A:177:U:O2'	2:5A:178:G:N7	2.41	0.52
21:Sd:65:ARG:NH2	35:B2:750:GLU:OE2	2.43	0.52
22:3B:277:ASP:N	22:3B:277:ASP:OD1	2.43	0.52
31:AE:235:VAL:HG22	31:AE:264:PHE:HE2	1.75	0.52
33:AG:395:THR:OG1	33:AG:424:GLN:NE2	2.42	0.52
33:AG:678:LEU:HD12	33:AG:694:LEU:HD11	1.92	0.52
36:B3:24:THR:HG21	36:B3:69:LEU:HA	1.92	0.52
37:B8:541:LEU:O	37:B8:542:ARG:NH1	2.42	0.52
53:RE:649:TRP:HB2	53:RE:653:SER:HB2	1.92	0.52
53:RE:940:LYS:HG3	53:RE:975:LEU:HD11	1.93	0.52
55:RH:156:GLU:HG2	55:RH:157:GLU:HG2	1.92	0.52
57:RJ:818:THR:HG23	57:RJ:819:GLU:HG3	1.91	0.52
59:RL:391:ALA:HB2	59:RL:414:GLY:H	1.75	0.52
1:3A:64:A:OP2	38:BE:392:ARG:NH2	2.43	0.51
3:SA:76:A:O2'	3:SA:80:A:N6	2.43	0.51
8:SI:129:LEU:HD13	8:SI:173:TYR:HD1	1.75	0.51
14:SP:53:ASP:OD1	14:SP:56:SER:OG	2.28	0.51
27:A4:345:ASP:N	27:A4:345:ASP:OD1	2.44	0.51
55:RG:239:SER:O	55:RG:243:HIS:ND1	2.35	0.51
7:SH:94:ARG:NH2	50:RA:91:LEU:O	2.37	0.51
22:3C:236:MET:HE1	24:3E:118:ARG:HE	1.74	0.51
25:3F:343:ASP:OD1	25:3F:343:ASP:N	2.43	0.51
30:A9:430:LEU:HD13	30:A9:433:ILE:HG22	1.93	0.51
33:AG:67:LYS:HB2	33:AG:70:ASN:HB2	1.92	0.51
35:B2:180:THR:OG1	35:B2:207:CYS:SG	2.63	0.51
35:B2:267:ASP:OD1	35:B2:267:ASP:N	2.41	0.51
36:B3:616:HIS:HD2	36:B3:640:VAL:HG13	1.75	0.51
38:BE:743:ARG:NH1	43:5E:480:GLN:O	2.42	0.51
50:RA:80:GLN:HA	50:RA:95:ARG:O	2.10	0.51
55:RH:31:LEU:HD13	55:RH:40:ARG:HE	1.74	0.51
3:SA:593:U:H4'	3:SA:595:G:H4'	1.93	0.51
18:SY:68:ILE:HD12	60:RN:785:VAL:HG23	1.92	0.51
19:SZ:60:PHE:O	19:SZ:61:ARG:NH1	2.39	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:AF:70:THR:O	32:AF:72:GLN:NE2	2.42	0.51
36:B3:593:CYS:HB2	36:B3:620:LEU:HB3	1.92	0.51
57:RJ:279:PRO:HB3	57:RJ:784:LYS:HA	1.92	0.51
2:5A:243:A:H4'	42:5D:224:LEU:HD21	1.92	0.51
2:5A:296:C:OP2	34:B1:94:ASN:ND2	2.42	0.51
2:5A:354:G:N2	41:5C:495:SER:O	2.39	0.51
2:5A:535:G:H4'	2:5A:536:A:H5'	1.92	0.51
3:SA:445:A:H2'	3:SA:446:A:H8	1.75	0.51
4:SC:129:THR:HG23	4:SC:131:ASP:H	1.75	0.51
7:SH:18:ILE:HG22	7:SH:24:ILE:HD11	1.92	0.51
17:SX:66:ASN:OD1	17:SX:66:ASN:N	2.42	0.51
23:3D:74:VAL:HG13	23:3D:78:LEU:HD22	1.91	0.51
41:5C:340:LEU:O	41:5C:368:TYR:N	2.43	0.51
42:5D:158:MET:HE2	42:5D:166:LEU:HB2	1.92	0.51
50:RA:80:GLN:HB2	50:RA:82:HIS:CD2	2.45	0.51
52:RC:206:LYS:HE3	52:RC:224:LEU:HD21	1.91	0.51
59:RM:746:TYR:O	59:RM:765:VAL:HA	2.11	0.51
29:A8:508:ASP:OD2	29:A8:538:ARG:NH2	2.44	0.51
33:AG:81:GLU:O	33:AG:738:ASN:ND2	2.42	0.51
47:5I:192:SER:HB2	47:5I:206:VAL:HG22	1.91	0.51
55:RG:179:THR:HB	55:RG:221:VAL:HG11	1.93	0.51
55:RH:191:ASP:OD1	55:RH:191:ASP:N	2.36	0.51
60:RN:640:MET:HE1	60:RN:681:PRO:HD3	1.93	0.51
3:SA:68:A:H62	3:SA:150:U:H5'	1.75	0.51
3:SA:1207:C:H5''	3:SA:1208:A:H8	1.75	0.51
9:SJ:7:SER:O	9:SJ:7:SER:OG	2.29	0.51
12:SN:63:VAL:HG21	12:SN:94:ALA:HB2	1.91	0.51
19:SZ:54:ALA:HB2	19:SZ:79:VAL:HG12	1.93	0.51
35:B2:160:ARG:NH2	43:5E:523:GLU:OE2	2.43	0.51
36:B3:552:SER:OG	36:B3:553:GLY:N	2.44	0.51
47:5I:136:MET:HE2	47:5I:150:ILE:HD11	1.92	0.51
50:RA:97:THR:HG21	50:RA:101:ASN:HD21	1.76	0.51
53:RE:1102:LEU:O	53:RE:1103:ARG:NH1	2.44	0.51
57:RJ:922:ILE:O	58:RK:111:LYS:NZ	2.36	0.51
3:SA:1227:A:O2'	12:SN:43:ARG:O	2.23	0.51
3:SA:1758:U:O4	35:B2:937:ARG:NH2	2.43	0.51
4:SC:129:THR:OG1	4:SC:179:SER:O	2.27	0.51
7:SH:2:LYS:HB2	7:SH:108:VAL:HG22	1.92	0.51
31:AE:531:ILE:HD11	31:AE:666:ALA:HB2	1.93	0.51
32:AF:303:LEU:HD22	32:AF:323:SER:HB2	1.91	0.51
33:AG:408:THR:OG1	33:AG:409:LYS:N	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:RA:19:THR:HG21	50:RA:314:SER:HB2	1.93	0.51
55:RG:97:LEU:O	55:RG:101:ASP:HB2	2.10	0.51
3:SA:638:U:O2	8:SI:116:ARG:N	2.43	0.51
3:SA:1230:A:O2'	3:SA:1258:U:O2	2.29	0.51
3:SA:1510:U:OP1	56:RI:50:ARG:NH2	2.37	0.51
5:SF:137:PRO:HB2	5:SF:150:PRO:HD2	1.92	0.51
8:SI:20:VAL:HG13	8:SI:81:LEU:HD11	1.92	0.51
14:SP:32:ASP:OD1	14:SP:32:ASP:N	2.44	0.51
35:B2:40:GLN:HA	35:B2:53:ASP:HA	1.93	0.51
50:RA:162:LEU:HB3	50:RA:176:PHE:HB2	1.92	0.51
53:RE:398:ALA:O	53:RE:402:ASN:ND2	2.44	0.51
53:RE:888:LYS:O	53:RE:892:SER:OG	2.25	0.51
3:SA:1662:G:H2'	3:SA:1663:G:H8	1.75	0.51
8:SI:134:GLU:OE2	13:SO:21:ASN:ND2	2.44	0.51
14:SP:31:THR:HG22	14:SP:38:THR:HA	1.93	0.51
14:SP:40:ALA:HB2	14:SP:70:LYS:HD2	1.91	0.51
25:3F:443:LEU:HD11	25:3F:492:TRP:HE1	1.75	0.51
27:A4:63:SER:OG	27:A4:687:PHE:O	2.28	0.51
31:AE:255:ILE:HD11	33:AG:884:MET:HB3	1.93	0.51
32:AF:215:VAL:HA	32:AF:230:GLY:HA3	1.93	0.51
36:B3:541:PHE:HB3	36:B3:548:LEU:HA	1.93	0.51
37:B8:43:ASP:N	37:B8:43:ASP:OD1	2.42	0.51
57:RJ:135:ALA:O	57:RJ:238:ARG:NH2	2.43	0.51
17:SX:12:ASN:O	17:SX:16:ASN:ND2	2.44	0.51
22:3C:198:GLU:O	22:3C:221:ILE:HA	2.11	0.51
31:AE:571:LEU:HD21	31:AE:631:VAL:HA	1.93	0.51
34:B1:25:ASP:OD1	34:B1:25:ASP:N	2.43	0.51
35:B2:872:LYS:HE3	36:B3:816:LEU:HG	1.93	0.51
36:B3:596:ASP:OD1	36:B3:596:ASP:N	2.44	0.51
45:5G:143:HIS:O	45:5G:150:THR:N	2.38	0.51
53:RE:215:GLU:OE2	53:RE:223:ARG:NH1	2.44	0.51
55:RG:142:VAL:HG22	55:RG:147:LYS:HB2	1.92	0.51
57:RJ:113:ARG:HH22	57:RJ:230:MET:H	1.59	0.51
58:RK:122:THR:HG23	58:RK:130:ILE:HG13	1.93	0.51
1:3A:322:A:OP1	24:3E:331:LYS:NZ	2.44	0.50
3:SA:614:C:O4'	3:SA:1108:G:N2	2.44	0.50
23:3D:26:ASP:O	47:5I:98:SER:OG	2.23	0.50
24:3E:426:ALA:HB2	38:BE:305:ASN:HD21	1.76	0.50
26:3H:13:ASP:OD1	26:3H:13:ASP:N	2.38	0.50
32:AF:363:GLY:HA3	37:B8:249:SER:HB2	1.93	0.50
33:AG:729:THR:OG1	33:AG:730:ASP:N	2.39	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B1:157:ASP:OD1	34:B1:157:ASP:N	2.44	0.50
35:B2:540:SER:OG	35:B2:542:ASP:OD1	2.23	0.50
36:B3:779:VAL:HA	36:B3:782:VAL:HG22	1.93	0.50
38:BE:591:PHE:HD2	38:BE:600:ILE:HD11	1.76	0.50
50:RA:278:ILE:HD13	50:RA:322:HIS:HB3	1.93	0.50
51:RB:349:ALA:HA	51:RB:352:ARG:HE	1.76	0.50
53:RE:1197:ARG:H	53:RE:1200:LEU:HD23	1.75	0.50
53:RE:1203:ASN:HD22	53:RE:1219:ILE:HG22	1.75	0.50
53:RE:1221:HIS:CE1	54:RF:20:LEU:HB3	2.46	0.50
55:RG:35:ASP:OD1	55:RG:35:ASP:N	2.42	0.50
57:RJ:608:LEU:HB2	58:RK:16:ASN:HD22	1.76	0.50
3:SA:259:U:H1'	9:SJ:178:ARG:HH12	1.77	0.50
3:SA:372:G:O6	51:RB:243:GLN:N	2.44	0.50
22:3B:261:LEU:O	23:3D:129:ARG:NH1	2.33	0.50
25:3F:298:SER:O	25:3F:298:SER:OG	2.29	0.50
25:3F:538:ARG:HB3	25:3F:567:VAL:HG22	1.93	0.50
31:AE:381:ARG:NE	33:AG:856:GLU:OE2	2.44	0.50
33:AG:381:SER:O	33:AG:381:SER:OG	2.29	0.50
34:B1:366:ASP:OD1	34:B1:366:ASP:N	2.37	0.50
58:RK:340:LYS:NZ	58:RK:341:PRO:O	2.44	0.50
62:RP:2323:THR:O	62:RP:2327:LEU:CB	2.60	0.50
64:RS:373:LYS:HE3	64:RS:420:ALA:HB2	1.93	0.50
3:SA:340:U:H2'	3:SA:341:A:C8	2.46	0.50
3:SA:1061:A:H2'	3:SA:1062:A:C4	2.46	0.50
8:SI:173:TYR:O	8:SI:177:THR:OG1	2.28	0.50
25:3F:421:ASN:ND2	25:3F:437:ARG:O	2.42	0.50
29:A8:675:LEU:HD11	30:A9:453:PRO:HB3	1.94	0.50
33:AG:245:LEU:HD22	33:AG:249:THR:HG21	1.94	0.50
33:AG:780:GLU:O	33:AG:782:THR:N	2.44	0.50
34:B1:202:ASP:N	34:B1:202:ASP:OD1	2.43	0.50
43:5E:298:SER:OG	43:5E:299:SER:N	2.42	0.50
43:5E:315:GLU:OE2	57:RJ:1033:ARG:NH1	2.43	0.50
43:5E:507:ILE:HD11	43:5E:517:LYS:HE2	1.93	0.50
50:RA:277:ILE:HA	50:RA:290:VAL:O	2.12	0.50
60:RN:614:ILE:HG22	60:RN:616:LEU:HB2	1.92	0.50
3:SA:1028:C:N4	52:RC:193:ASN:O	2.44	0.50
3:SA:1472:C:N3	3:SA:1534:G:N2	2.53	0.50
3:SA:1717:G:H3'	3:SA:1718:G:H8	1.77	0.50
8:SI:50:ASP:OD1	8:SI:50:ASP:N	2.39	0.50
8:SI:83:LYS:O	8:SI:86:GLN:NE2	2.43	0.50
27:A4:366:ASN:OD1	33:AG:247:SER:N	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:A5:548:ASP:HA	28:A5:551:ILE:HB	1.94	0.50
31:AE:492:LYS:HA	31:AE:495:LEU:HD12	1.93	0.50
33:AG:301:LEU:HD23	33:AG:342:ILE:HG22	1.93	0.50
36:B3:672:TYR:HB3	36:B3:681:ALA:HB2	1.94	0.50
37:B8:16:ASP:HB3	37:B8:19:GLU:HB3	1.93	0.50
37:B8:220:ASP:N	37:B8:220:ASP:OD1	2.41	0.50
43:5E:452:SER:O	43:5E:452:SER:OG	2.29	0.50
47:5I:125:ASP:OD1	47:5I:125:ASP:N	2.44	0.50
53:RE:173:ASN:OD1	53:RE:175:LYS:NZ	2.44	0.50
53:RE:528:ASP:HB2	53:RE:697:SER:HB3	1.94	0.50
54:RF:177:ILE:O	54:RF:181:LYS:HB2	2.11	0.50
55:RG:46:ALA:HA	55:RG:115:GLN:HG3	1.93	0.50
56:RI:57:ILE:HB	56:RI:187:THR:HG23	1.94	0.50
58:RK:228:ASP:N	58:RK:228:ASP:OD1	2.43	0.50
60:RN:554:GLN:OE1	60:RN:559:ARG:N	2.40	0.50
3:SA:89:G:N3	3:SA:452:A:N6	2.58	0.50
3:SA:328:A:H2'	3:SA:329:G:H8	1.77	0.50
3:SA:585:A:H3'	3:SA:586:G:H3'	1.94	0.50
27:A4:353:GLU:OE2	27:A4:371:LYS:NZ	2.42	0.50
32:AF:24:GLN:O	32:AF:28:ARG:HB3	2.11	0.50
33:AG:96:ILE:HG12	33:AG:108:THR:HG21	1.92	0.50
35:B2:141:LYS:HA	35:B2:165:SER:HB2	1.94	0.50
35:B2:278:ASP:OD1	35:B2:278:ASP:N	2.43	0.50
36:B3:12:LEU:HG	36:B3:641:PHE:HB2	1.94	0.50
36:B3:260:THR:HA	36:B3:268:GLN:O	2.11	0.50
43:5E:474:ILE:HD11	43:5E:486:ASN:HB3	1.93	0.50
47:5I:133:GLN:HA	47:5I:150:ILE:O	2.12	0.50
53:RE:506:GLN:O	53:RE:509:ASN:N	2.45	0.50
53:RE:526:CYS:O	53:RE:698:ASN:ND2	2.45	0.50
53:RE:541:THR:O	53:RE:692:LYS:NZ	2.41	0.50
57:RJ:287:ARG:HH11	57:RJ:297:SER:HB2	1.77	0.50
65:RT:224:ILE:HG12	65:RT:233:ILE:HG12	1.92	0.50
3:SA:1696:G:H2'	3:SA:1697:G:H8	1.76	0.50
6:SG:63:GLN:HE22	6:SG:66:GLN:HB3	1.76	0.50
25:3F:569:ASP:N	25:3F:569:ASP:OD1	2.45	0.50
29:A8:595:ILE:HG22	29:A8:599:MET:HE2	1.92	0.50
33:AG:669:ASN:ND2	33:AG:749:ASP:OD2	2.43	0.50
35:B2:42:ILE:HG23	35:B2:51:ILE:HG12	1.93	0.50
41:5C:116:ILE:HD12	41:5C:398:ILE:HG23	1.94	0.50
42:5D:44:LYS:NZ	57:RJ:1065:ASN:O	2.44	0.50
45:5G:237:VAL:HB	60:RN:6:LEU:HD12	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:RA:83:VAL:HG23	50:RA:92:LYS:HB2	1.93	0.50
53:RE:269:ARG:HA	53:RE:292:ILE:O	2.10	0.50
61:RO:463:LEU:HD21	61:RO:466:LEU:HD13	1.94	0.50
3:SA:116:U:O3'	3:SA:333:A:O2'	2.28	0.50
3:SA:575:C:OP1	57:RJ:931:LYS:NZ	2.39	0.50
3:SA:1756:A:O2'	3:SA:1757:G:N2	2.44	0.50
4:SC:27:LYS:NZ	14:SP:37:GLU:OE1	2.41	0.50
25:3F:127:GLU:HA	25:3F:333:MET:HG3	1.94	0.50
28:A5:26:LYS:NZ	28:A5:54:GLU:O	2.44	0.50
28:A5:532:ARG:HG3	32:AF:453:VAL:HG11	1.93	0.50
33:AG:885:ASP:OD1	33:AG:885:ASP:N	2.41	0.50
35:B2:220:THR:HG22	35:B2:259:ILE:HD11	1.94	0.50
35:B2:358:SER:OG	35:B2:359:SER:N	2.44	0.50
41:5C:106:LEU:HD11	41:5C:137:MET:HE1	1.93	0.50
9:SJ:42:ARG:NH2	50:RA:57:GLU:O	2.44	0.50
11:SM:87:ARG:HE	11:SM:104:HIS:HB2	1.77	0.50
27:A4:392:VAL:HG12	27:A4:401:ILE:HB	1.93	0.50
29:A8:576:ARG:HE	29:A8:578:LEU:HB2	1.76	0.50
36:B3:413:ILE:HD12	36:B3:426:ILE:HD13	1.93	0.50
36:B3:509:ALA:HB3	36:B3:539:VAL:HG11	1.93	0.50
47:5I:220:ASP:OD1	47:5I:220:ASP:N	2.41	0.50
47:5I:319:GLU:OE2	47:5I:356:TYR:OH	2.29	0.50
49:5K:99:THR:OG1	49:5K:101:CYS:SG	2.69	0.50
54:RF:20:LEU:HD21	54:RF:35:HIS:HB2	1.94	0.50
1:3A:59:G:H5'	34:B1:570:THR:HG23	1.93	0.50
9:SJ:6:ASP:OD1	9:SJ:6:ASP:N	2.44	0.50
24:3E:4:VAL:HA	24:3E:88:ILE:O	2.12	0.50
25:3F:548:ARG:HG3	25:3F:549:LEU:HG	1.94	0.50
27:A4:446:SER:OG	27:A4:447:THR:N	2.44	0.50
28:A5:149:ASN:OD1	28:A5:149:ASN:N	2.42	0.50
28:A5:460:ARG:HA	28:A5:465:ILE:HD11	1.93	0.50
28:A5:539:ARG:NH1	33:AG:524:ASP:OD2	2.45	0.50
31:AE:8:LEU:HD12	41:5C:144:LEU:HD23	1.94	0.50
50:RA:274:ILE:HA	50:RA:293:ASP:HA	1.94	0.50
50:RA:315:VAL:HG11	50:RA:335:SER:HB2	1.94	0.50
54:RF:108:MET:HE3	54:RF:191:PHE:HB2	1.94	0.50
1:3A:325:C:N4	24:3E:318:GLN:OE1	2.36	0.49
2:5A:316:U:H5'	41:5C:364:ARG:HH22	1.76	0.49
3:SA:1600:A:OP2	57:RJ:988:ARG:NH2	2.45	0.49
31:AE:498:PHE:HA	31:AE:501:ALA:HB3	1.93	0.49
32:AF:88:SER:OG	32:AF:97:CYS:SG	2.70	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:AF:440:GLU:O	32:AF:444:ASN:HB2	2.12	0.49
35:B2:276:ASN:HD21	35:B2:282:GLU:HG3	1.77	0.49
37:B8:304:LEU:HB2	37:B8:371:VAL:HG21	1.94	0.49
37:B8:464:THR:HG23	37:B8:477:LYS:H	1.77	0.49
46:5H:587:GLN:NE2	46:5H:589:GLY:O	2.41	0.49
50:RA:57:GLU:HA	50:RA:336:ILE:HG13	1.94	0.49
62:RP:1006:SER:O	62:RP:1010:VAL:CB	2.59	0.49
28:A5:32:GLN:HE22	28:A5:47:ASN:H	1.60	0.49
33:AG:40:ASP:O	33:AG:42:ARG:N	2.45	0.49
58:RK:114:PHE:O	58:RK:169:VAL:HA	2.12	0.49
22:3C:166:PRO:HA	22:3C:188:VAL:HA	1.94	0.49
27:A4:581:SER:HA	27:A4:594:PHE:O	2.13	0.49
31:AE:526:LEU:HD22	31:AE:543:SER:HB2	1.94	0.49
31:AE:719:SER:O	31:AE:722:ASN:ND2	2.45	0.49
33:AG:660:GLN:HE21	33:AG:704:ASN:HA	1.77	0.49
36:B3:192:ALA:HB3	36:B3:216:ARG:HG3	1.94	0.49
37:B8:486:SER:OG	37:B8:487:GLU:N	2.45	0.49
41:5C:74:LEU:HD23	41:5C:404:PRO:HG2	1.94	0.49
50:RA:65:SER:OG	50:RA:67:ASP:OD1	2.30	0.49
53:RE:611:ASP:OD1	53:RE:611:ASP:N	2.42	0.49
53:RE:898:THR:HG21	53:RE:1045:ASN:HD21	1.77	0.49
57:RJ:237:TRP:O	57:RJ:241:HIS:HB2	2.12	0.49
58:RK:339:LEU:HB3	58:RK:350:MET:HG2	1.92	0.49
11:SM:74:THR:O	11:SM:87:ARG:N	2.46	0.49
15:SR:98:ASP:OD2	38:BE:488:ASN:ND2	2.45	0.49
18:SY:52:ILE:HG23	18:SY:99:ASN:HA	1.94	0.49
28:A5:494:ARG:HE	28:A5:498:LEU:HD11	1.77	0.49
31:AE:395:GLU:OE2	31:AE:397:LYS:NZ	2.46	0.49
33:AG:370:GLN:HE21	33:AG:384:SER:HG	1.58	0.49
33:AG:707:MET:HA	33:AG:710:LEU:HD12	1.94	0.49
42:5D:162:SER:O	42:5D:162:SER:OG	2.30	0.49
50:RA:162:LEU:HB2	50:RA:178:LEU:HD21	1.93	0.49
1:3A:254:A:OP1	1:3A:255:U:O2'	2.23	0.49
2:5A:547:C:H2'	2:5A:548:A:H8	1.78	0.49
5:SF:77:ARG:NH1	5:SF:82:TYR:OH	2.46	0.49
7:SH:63:MET:HE2	7:SH:98:ARG:HD3	1.95	0.49
15:SR:120:ASP:OD2	15:SR:123:ARG:NH2	2.43	0.49
32:AF:150:ARG:HG2	32:AF:163:GLU:HG3	1.95	0.49
36:B3:352:LYS:HA	36:B3:365:ILE:O	2.12	0.49
41:5C:386:PHE:O	47:5I:8:ARG:NH2	2.45	0.49
58:RK:307:ASP:O	58:RK:355:LYS:HA	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:RT:106:MET:HE1	65:RT:135:LYS:HD2	1.94	0.49
3:SA:209:U:O4	3:SA:210:A:N6	2.46	0.49
3:SA:592:A:O2'	3:SA:596:C:OP1	2.31	0.49
3:SA:1130:G:O2'	3:SA:1137:A:N6	2.45	0.49
9:SJ:78:ILE:HG23	9:SJ:102:VAL:HG11	1.95	0.49
28:A5:248:THR:OG1	28:A5:250:ASP:OD1	2.24	0.49
33:AG:156:THR:HA	33:AG:170:SER:O	2.11	0.49
35:B2:265:SER:OG	35:B2:266:SER:N	2.45	0.49
36:B3:199:ILE:O	36:B3:209:LEU:HA	2.13	0.49
38:BE:637:ASN:O	38:BE:639:ASP:N	2.43	0.49
43:5E:359:SER:OG	60:RN:89:GLN:OE1	2.29	0.49
43:5E:470:GLU:HB2	43:5E:490:LEU:HD12	1.94	0.49
45:5G:100:LEU:HD22	45:5G:144:GLU:HB3	1.95	0.49
57:RJ:864:ASP:OD1	57:RJ:864:ASP:N	2.43	0.49
57:RJ:954:SER:HA	57:RJ:984:GLU:HG3	1.94	0.49
66:RV:225:GLN:HE21	66:RV:229:ASN:HD21	1.61	0.49
3:SA:1662:G:H2'	3:SA:1663:G:C8	2.48	0.49
10:SK:68:LYS:HA	51:RB:334:LEU:HD23	1.93	0.49
12:SN:31:VAL:HG22	12:SN:123:VAL:HG21	1.95	0.49
27:A4:750:ASN:N	27:A4:750:ASN:OD1	2.45	0.49
33:AG:495:ILE:HD13	33:AG:511:GLU:HB3	1.95	0.49
34:B1:829:VAL:HG23	34:B1:830:ARG:HG2	1.95	0.49
35:B2:161:SER:OG	35:B2:187:LYS:NZ	2.45	0.49
36:B3:137:THR:OG1	36:B3:180:ARG:NH2	2.45	0.49
36:B3:304:LEU:O	36:B3:311:LEU:HA	2.13	0.49
44:5F:34:ARG:NH2	49:5K:16:THR:OG1	2.46	0.49
50:RA:192:ASN:N	50:RA:192:ASN:OD1	2.43	0.49
51:RB:310:GLN:O	51:RB:314:ASN:ND2	2.45	0.49
52:RC:43:THR:HG22	52:RC:101:ILE:HD12	1.94	0.49
57:RJ:374:ASP:OD1	59:RL:3:LYS:N	2.46	0.49
3:SA:337:G:N2	3:SA:340:U:OP2	2.45	0.49
3:SA:615:A:H2'	3:SA:616:G:H4'	1.95	0.49
11:SM:90:TYR:H	11:SM:103:ARG:HB3	1.77	0.49
23:3D:7:LEU:HB3	23:3D:18:PHE:HB2	1.93	0.49
25:3F:263:TRP:HA	25:3F:269:SER:O	2.13	0.49
28:A5:115:ASN:ND2	28:A5:130:ASP:OD1	2.45	0.49
31:AE:141:ASN:ND2	31:AE:206:TYR:OH	2.46	0.49
32:AF:257:CYS:SG	32:AF:305:CYS:N	2.84	0.49
33:AG:582:LEU:HD11	33:AG:613:LEU:HD21	1.94	0.49
33:AG:712:THR:HG22	33:AG:766:ILE:HG23	1.94	0.49
34:B1:107:ASP:OD2	34:B1:109:ARG:NE	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B1:410:THR:HG21	34:B1:412:ARG:HH21	1.77	0.49
36:B3:217:ASP:OD1	36:B3:217:ASP:N	2.44	0.49
50:RA:63:LYS:HG3	50:RA:321:GLU:HG3	1.95	0.49
50:RA:178:LEU:HD13	50:RA:183:VAL:HG13	1.94	0.49
58:RK:14:SER:HB2	58:RK:36:ILE:HG23	1.94	0.49
64:RS:384:TYR:HA	64:RS:387:VAL:HG22	1.95	0.49
3:SA:623:A:H62	3:SA:976:G:H21	1.61	0.49
3:SA:886:U:H2'	3:SA:887:A:H8	1.78	0.49
25:3F:200:ASP:HB3	25:3F:209:LYS:HG2	1.94	0.49
35:B2:63:LEU:HD12	35:B2:111:LYS:HG2	1.95	0.49
35:B2:134:THR:HA	35:B2:150:LEU:HB2	1.94	0.49
35:B2:248:PHE:HB3	35:B2:322:SER:HB2	1.95	0.49
36:B3:245:SER:HA	36:B3:261:ALA:HA	1.95	0.49
36:B3:679:THR:HG22	36:B3:724:LEU:HB2	1.95	0.49
38:BE:632:VAL:HG13	38:BE:641:LEU:HD11	1.95	0.49
45:5G:81:SER:HB2	45:5G:208:HIS:HE1	1.77	0.49
53:RE:134:ILE:HG23	53:RE:242:LEU:HD13	1.94	0.49
53:RE:582:GLN:HB3	53:RE:616:LYS:HE3	1.95	0.49
57:RJ:270:ALA:HA	57:RJ:791:ILE:O	2.13	0.49
58:RK:243:ILE:HG23	58:RK:275:VAL:HG21	1.95	0.49
61:RO:252:LYS:O	61:RO:256:ASN:ND2	2.46	0.49
62:RP:1755:GLU:HA	62:RP:1758:ALA:HB3	1.95	0.49
2:5A:176:U:O2'	2:5A:178:G:OP2	2.27	0.49
3:SA:455:C:O2'	3:SA:456:A:O4'	2.30	0.49
25:3F:303:LYS:HE3	25:3F:319:TYR:HE1	1.78	0.49
25:3F:475:ILE:HD13	25:3F:489:SER:HB2	1.95	0.49
27:A4:324:SER:OG	27:A4:325:ASN:N	2.38	0.49
27:A4:402:TRP:HB3	27:A4:416:LEU:HA	1.94	0.49
27:A4:586:THR:OG1	27:A4:587:ALA:N	2.46	0.49
31:AE:745:TYR:HB3	31:AE:748:LEU:HB3	1.94	0.49
34:B1:668:GLY:H	43:5E:450:VAL:HG23	1.78	0.49
38:BE:170:LEU:HG	38:BE:180:LEU:HD21	1.93	0.49
56:RI:250:THR:OG1	56:RI:251:SER:N	2.46	0.49
65:RT:99:ILE:HD12	65:RT:139:LEU:HD11	1.95	0.49
3:SA:122:U:H4'	5:SF:77:ARG:HH12	1.78	0.48
3:SA:257:A:H1'	9:SJ:73:SER:HB3	1.94	0.48
5:SF:117:GLU:O	5:SF:120:SER:OG	2.31	0.48
7:SH:101:ILE:HG21	50:RA:355:PHE:HE2	1.78	0.48
23:3D:389:ILE:HA	26:3H:62:GLU:HB2	1.94	0.48
24:3E:359:ILE:HA	24:3E:362:VAL:HG12	1.95	0.48
24:3E:385:ASP:OD1	24:3E:385:ASP:N	2.35	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:A5:104:SER:O	28:A5:104:SER:OG	2.29	0.48
32:AF:20:THR:HA	32:AF:24:GLN:HE21	1.78	0.48
33:AG:253:SER:O	33:AG:256:THR:OG1	2.31	0.48
34:B1:526:ASP:OD1	34:B1:526:ASP:N	2.33	0.48
50:RA:75:GLY:HA3	50:RA:80:GLN:H	1.78	0.48
60:RN:448:PHE:HA	60:RN:451:THR:HG22	1.95	0.48
3:SA:1192:C:OP1	55:RG:132:ARG:NE	2.39	0.48
3:SA:1600:A:N6	57:RJ:945:THR:HG21	2.28	0.48
5:SF:45:ILE:O	5:SF:49:ARG:CB	2.62	0.48
8:SI:163:ASP:O	63:RQ:277:ARG:NH2	2.46	0.48
15:SR:94:GLN:HB2	15:SR:102:LYS:HG3	1.93	0.48
27:A4:429:SER:OG	27:A4:430:THR:N	2.46	0.48
33:AG:446:ASN:OD1	33:AG:446:ASN:N	2.43	0.48
34:B1:652:ASP:OD1	34:B1:652:ASP:N	2.46	0.48
34:B1:760:ILE:HA	34:B1:763:ILE:HG12	1.94	0.48
35:B2:606:ASP:OD1	35:B2:606:ASP:N	2.43	0.48
36:B3:397:THR:OG1	36:B3:400:GLY:O	2.31	0.48
36:B3:797:ASP:OD1	38:BE:927:LYS:NZ	2.39	0.48
41:5C:180:GLU:OE2	49:5K:15:ARG:NH1	2.46	0.48
47:5I:76:ASN:HA	47:5I:118:VAL:HG21	1.95	0.48
48:5J:120:ASP:OD1	48:5J:120:ASP:N	2.46	0.48
52:RC:44:LEU:HA	52:RC:79:SER:HA	1.95	0.48
53:RE:227:LYS:HA	53:RE:230:VAL:HG22	1.95	0.48
2:5A:338:A:O2'	2:5A:340:U:O4	2.22	0.48
2:5A:365:G:H2'	2:5A:366:A:H8	1.79	0.48
3:SA:396:G:N7	9:SJ:47:ARG:NH1	2.61	0.48
18:SY:97:ASP:HB3	57:RJ:828:ARG:HH22	1.78	0.48
24:3E:285:PRO:HG3	24:3E:382:ASP:HA	1.96	0.48
25:3F:552:TRP:HB3	26:3H:85:VAL:HG13	1.93	0.48
32:AF:168:THR:OG1	32:AF:190:ASP:OD2	2.30	0.48
32:AF:420:GLU:O	32:AF:424:ARG:CB	2.57	0.48
33:AG:38:SER:OG	33:AG:39:GLN:N	2.46	0.48
39:B6:185:TYR:HE2	63:RQ:338:LEU:HD21	1.78	0.48
47:5I:264:THR:HA	47:5I:281:ASN:HB3	1.95	0.48
58:RK:191:ILE:HD11	58:RK:245:LEU:HD23	1.96	0.48
60:RN:552:GLN:HG2	61:RO:531:ASP:HA	1.95	0.48
1:3A:33:A:OP1	49:5K:133:LYS:NZ	2.46	0.48
3:SA:1641:C:OP2	43:5E:534:ARG:NH2	2.43	0.48
9:SJ:67:TRP:HD1	9:SJ:70:GLU:H	1.62	0.48
26:3H:7:LYS:NZ	26:3H:62:GLU:OE2	2.46	0.48
31:AE:528:ARG:HA	31:AE:531:ILE:HG22	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B1:64:ASN:N	34:B1:64:ASN:OD1	2.39	0.48
34:B1:157:ASP:OD1	34:B1:203:GLN:NE2	2.42	0.48
34:B1:517:ASP:OD1	34:B1:517:ASP:N	2.43	0.48
35:B2:624:LEU:HD12	35:B2:629:ASN:HB2	1.95	0.48
35:B2:906:LYS:HB3	35:B2:906:LYS:HE2	1.68	0.48
48:5J:119:ARG:HD2	48:5J:174:LEU:HD22	1.96	0.48
53:RE:777:ASP:O	53:RE:780:GLN:NE2	2.46	0.48
59:RM:325:ILE:O	59:RM:329:PHE:CB	2.62	0.48
61:RO:384:ALA:HB1	61:RO:465:GLU:HB2	1.95	0.48
63:RQ:853:ASN:OD1	63:RQ:853:ASN:N	2.45	0.48
66:RV:199:ASP:OD1	66:RV:199:ASP:N	2.42	0.48
32:AF:432:TYR:O	32:AF:470:TYR:OH	2.32	0.48
33:AG:207:LEU:HG	33:AG:264:ILE:HD12	1.95	0.48
36:B3:97:ARG:NH2	36:B3:131:ILE:O	2.47	0.48
38:BE:569:VAL:HB	38:BE:579:ARG:HB2	1.94	0.48
41:5C:287:TYR:HD2	41:5C:304:ARG:HE	1.61	0.48
41:5C:369:MET:HE1	41:5C:404:PRO:HD2	1.95	0.48
44:5F:131:ILE:HD11	44:5F:146:PRO:HA	1.94	0.48
45:5G:9:ARG:HH21	45:5G:159:HIS:HD2	1.61	0.48
46:5H:436:GLY:HA2	55:RH:129:ARG:HE	1.79	0.48
56:RI:228:LYS:O	56:RI:232:GLY:N	2.44	0.48
66:RV:309:SER:OG	66:RV:310:SER:N	2.44	0.48
3:SA:394:C:OP1	50:RA:78:LYS:NZ	2.40	0.48
3:SA:1028:C:OP2	52:RC:144:ARG:NH2	2.46	0.48
15:SR:39:VAL:HG11	15:SR:48:VAL:HG21	1.95	0.48
22:3B:269:ILE:HG13	22:3B:293:LEU:HD11	1.94	0.48
31:AE:363:LEU:HD23	31:AE:403:LEU:HD22	1.95	0.48
31:AE:559:ASN:HD22	31:AE:592:ARG:HH11	1.62	0.48
35:B2:317:ILE:O	35:B2:321:TYR:N	2.46	0.48
36:B3:410:ASN:HA	36:B3:435:ALA:H	1.79	0.48
43:5E:437:ILE:HD12	44:5F:61:LEU:HD13	1.96	0.48
51:RB:268:ASN:HB3	51:RB:271:ARG:HB3	1.95	0.48
53:RE:625:ASP:OD2	53:RE:720:SER:OG	2.25	0.48
58:RK:219:LEU:HD13	58:RK:221:CYS:HB3	1.96	0.48
59:RM:585:VAL:HA	59:RM:632:GLY:HA2	1.96	0.48
60:RN:616:LEU:HB3	60:RN:619:LEU:HD13	1.95	0.48
61:RO:256:ASN:O	61:RO:260:ASN:ND2	2.47	0.48
9:SJ:67:TRP:NE1	9:SJ:69:SER:OG	2.46	0.48
10:SK:45:ILE:HD13	10:SK:105:LEU:HB3	1.95	0.48
26:3H:43:THR:OG1	26:3H:48:ILE:O	2.31	0.48
27:A4:214:SER:HB3	27:A4:226:LEU:HD13	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:AE:87:THR:HA	41:5C:96:ASP:HA	1.95	0.48
33:AG:138:ASP:OD1	33:AG:138:ASP:N	2.44	0.48
34:B1:730:LEU:HD22	34:B1:754:VAL:HG22	1.94	0.48
35:B2:916:HIS:NE2	36:B3:774:GLU:OE2	2.43	0.48
41:5C:116:ILE:HG13	41:5C:125:LEU:HD11	1.96	0.48
53:RE:793:PRO:HG2	53:RE:799:LEU:HA	1.95	0.48
22:3B:100:ARG:HA	22:3B:104:ASP:HB3	1.96	0.48
26:3G:62:GLU:HA	26:3G:65:LEU:HD23	1.96	0.48
30:A9:477:LYS:HA	30:A9:480:LYS:HB3	1.95	0.48
33:AG:431:SER:OG	33:AG:432:ARG:N	2.47	0.48
35:B2:49:VAL:HG22	35:B2:63:LEU:HB3	1.95	0.48
35:B2:367:ILE:HD13	35:B2:379:PRO:HB3	1.94	0.48
38:BE:323:VAL:HB	38:BE:343:LEU:HD22	1.95	0.48
53:RE:779:PHE:HB3	53:RE:851:LYS:HG3	1.94	0.48
53:RE:1225:ALA:HB1	54:RF:160:TYR:HE2	1.79	0.48
3:SA:88:U:H2'	3:SA:89:G:H8	1.79	0.48
5:SF:140:VAL:HG12	5:SF:146:THR:HG22	1.96	0.48
10:SK:38:ASN:N	10:SK:38:ASN:OD1	2.43	0.48
13:SO:49:GLN:HA	13:SO:52:VAL:HG12	1.96	0.48
21:Sd:11:LYS:HB2	21:Sd:33:LEU:HD21	1.96	0.48
24:3E:430:ASP:HA	38:BE:125:GLY:HA2	1.95	0.48
27:A4:453:LEU:HD12	27:A4:460:LEU:HD12	1.95	0.48
27:A4:658:ASP:HB3	27:A4:661:VAL:HG22	1.95	0.48
28:A5:251:GLY:O	28:A5:288:LYS:NZ	2.45	0.48
29:A8:315:SER:N	29:A8:320:LEU:O	2.45	0.48
31:AE:109:TRP:CH2	31:AE:118:THR:HG21	2.49	0.48
33:AG:240:PRO:O	33:AG:243:SER:OG	2.30	0.48
33:AG:720:ILE:HG23	33:AG:745:ILE:HG22	1.96	0.48
47:5I:344:HIS:NE2	47:5I:418:HIS:O	2.47	0.48
53:RE:257:SER:OG	53:RE:590:SER:O	2.27	0.48
55:RG:36:LYS:HB3	55:RG:172:PRO:HA	1.95	0.48
57:RJ:830:ARG:NH2	57:RJ:831:ARG:O	2.47	0.48
3:SA:1227:A:N1	3:SA:1255:G:O2'	2.45	0.48
15:SR:113:ASP:N	15:SR:113:ASP:OD1	2.46	0.48
16:ST:3:LEU:HD22	32:AF:254:ALA:HB2	1.96	0.48
29:A8:268:GLU:HA	29:A8:284:LEU:HA	1.96	0.48
32:AF:133:HIS:CD2	32:AF:136:ASP:H	2.32	0.48
36:B3:151:LYS:H	36:B3:164:ALA:HB3	1.78	0.48
38:BE:120:HIS:HB2	38:BE:131:SER:HB3	1.96	0.48
43:5E:447:LYS:HA	43:5E:450:VAL:HG12	1.95	0.48
53:RE:720:SER:OG	53:RE:721:VAL:N	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:RJ:252:LEU:HD11	57:RJ:790:ARG:HH22	1.79	0.48
1:3A:94:A:H2'	1:3A:95:A:C8	2.49	0.47
2:5A:548:A:N6	2:5A:590:G:O6	2.46	0.47
3:SA:573:C:OP2	42:5D:13:HIS:NE2	2.45	0.47
3:SA:1041:G:H2'	3:SA:1042:G:C8	2.49	0.47
4:SC:61:LEU:HD23	4:SC:64:ARG:HD2	1.96	0.47
14:SP:22:SER:OG	14:SP:23:PHE:O	2.24	0.47
16:ST:120:ARG:NH2	43:5E:341:LEU:O	2.43	0.47
32:AF:276:SER:O	32:AF:276:SER:OG	2.29	0.47
32:AF:504:ILE:HA	32:AF:507:MET:HG2	1.96	0.47
33:AG:524:ASP:OD1	33:AG:524:ASP:N	2.37	0.47
33:AG:869:MET:SD	33:AG:869:MET:N	2.87	0.47
35:B2:440:PRO:HG3	35:B2:485:GLY:HA3	1.96	0.47
41:5C:183:GLU:HB3	49:5K:16:THR:HG22	1.95	0.47
46:5H:603:THR:O	46:5H:603:THR:OG1	2.32	0.47
47:5I:1:MET:HE3	47:5I:1:MET:HB2	1.77	0.47
50:RA:298:LYS:HE3	50:RA:300:TRP:CD1	2.48	0.47
53:RE:151:SER:HA	53:RE:154:LYS:HB2	1.95	0.47
57:RJ:781:GLU:OE2	57:RJ:784:LYS:NZ	2.33	0.47
63:RQ:322:ASN:N	63:RQ:322:ASN:OD1	2.47	0.47
3:SA:1163:A:N3	3:SA:1613:U:O2'	2.42	0.47
3:SA:1672:G:H2'	3:SA:1673:G:H8	1.78	0.47
3:SA:1751:C:H5''	35:B2:142:ASP:HA	1.96	0.47
8:SI:143:LEU:HD21	47:5I:221:ASN:HB3	1.96	0.47
22:3B:239:CYS:SG	22:3B:240:VAL:N	2.86	0.47
22:3C:242:ALA:HB3	22:3C:269:ILE:HA	1.96	0.47
27:A4:298:ALA:HB2	27:A4:304:ILE:HG12	1.96	0.47
27:A4:579:ARG:NH1	27:A4:659:PHE:O	2.47	0.47
28:A5:369:PHE:N	28:A5:524:SER:OG	2.45	0.47
29:A8:679:ILE:HB	30:A9:483:LYS:HD3	1.96	0.47
32:AF:52:PRO:HB2	32:AF:309:PRO:HD2	1.96	0.47
33:AG:360:MET:HE3	33:AG:360:MET:HB2	1.75	0.47
36:B3:97:ARG:NH1	36:B3:134:GLY:H	2.12	0.47
37:B8:406:ASP:HB3	37:B8:458:ILE:HG22	1.96	0.47
54:RF:144:TYR:HA	54:RF:147:LEU:HG	1.97	0.47
55:RG:98:THR:OG1	55:RG:242:CYS:SG	2.72	0.47
56:RI:33:ASP:OD1	56:RI:33:ASP:N	2.44	0.47
56:RI:50:ARG:HE	56:RI:52:ASN:HD21	1.62	0.47
57:RJ:831:ARG:NH2	57:RJ:835:HIS:O	2.47	0.47
3:SA:1134:C:H1'	35:B2:610:SER:HB2	1.94	0.47
3:SA:1540:G:H2'	3:SA:1541:G:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:SF:175:PHE:HA	5:SF:227:VAL:HG21	1.97	0.47
16:ST:15:LEU:N	16:ST:22:VAL:O	2.47	0.47
30:A9:474:HIS:HA	30:A9:477:LYS:HZ2	1.79	0.47
31:AE:12:ALA:HB2	41:5C:142:GLY:HA3	1.97	0.47
34:B1:348:THR:HG23	34:B1:362:THR:HG23	1.96	0.47
34:B1:373:ASP:OD2	34:B1:376:SER:OG	2.28	0.47
35:B2:144:ASN:OD1	35:B2:160:ARG:NH1	2.35	0.47
35:B2:400:SER:HB3	35:B2:404:LYS:HB2	1.95	0.47
38:BE:938:THR:OG1	38:BE:939:ALA:N	2.48	0.47
41:5C:312:VAL:HG21	41:5C:353:PRO:HG2	1.94	0.47
50:RA:300:TRP:HB3	50:RA:307:ALA:HA	1.96	0.47
53:RE:248:LEU:HD13	53:RE:252:LEU:HD12	1.95	0.47
2:5A:104:A:OP2	32:AF:411:LYS:NZ	2.47	0.47
3:SA:511:A:H5'	10:SK:173:ALA:HB2	1.95	0.47
4:SC:158:SER:HA	4:SC:161:ILE:HB	1.96	0.47
8:SI:24:PHE:HE1	8:SI:77:LEU:HD13	1.80	0.47
12:SN:33:ARG:HH12	60:RN:272:ILE:HA	1.78	0.47
24:3E:206:ALA:HB2	24:3E:262:ILE:HD11	1.96	0.47
27:A4:33:VAL:HA	27:A4:752:LEU:O	2.14	0.47
28:A5:120:ILE:HB	28:A5:151:LEU:HD23	1.96	0.47
29:A8:608:GLN:NE2	29:A8:651:GLU:OE2	2.47	0.47
34:B1:472:HIS:NE2	34:B1:490:SER:OG	2.40	0.47
35:B2:861:ILE:O	35:B2:865:HIS:HB2	2.13	0.47
36:B3:548:LEU:HD23	36:B3:560:TRP:HB2	1.97	0.47
38:BE:121:LEU:HA	38:BE:129:CYS:O	2.14	0.47
60:RN:515:HIS:HB3	60:RN:518:ILE:HG22	1.97	0.47
60:RN:603:ASP:OD1	60:RN:603:ASP:N	2.46	0.47
65:RT:256:PRO:HA	65:RT:259:VAL:HG12	1.97	0.47
27:A4:164:THR:HG22	27:A4:185:ARG:HG2	1.96	0.47
34:B1:430:ARG:NE	43:5E:460:PRO:O	2.48	0.47
39:B6:82:SER:OG	39:B6:83:LEU:N	2.42	0.47
47:5I:283:ASP:OD1	47:5I:283:ASP:N	2.46	0.47
50:RA:66:ARG:HH22	50:RA:106:ILE:HG13	1.78	0.47
5:SF:93:ASP:OD1	5:SF:93:ASP:N	2.47	0.47
22:3C:258:HIS:HD1	22:3C:320:TYR:HH	1.58	0.47
28:A5:492:THR:O	32:AF:497:LYS:NZ	2.43	0.47
28:A5:543:LEU:HD22	32:AF:491:VAL:HG21	1.97	0.47
33:AG:334:LEU:HD22	33:AG:379:LEU:HD23	1.96	0.47
33:AG:528:ILE:HG12	33:AG:548:ILE:HG22	1.96	0.47
33:AG:614:ALA:HB3	33:AG:623:PHE:HB2	1.96	0.47
34:B1:275:LEU:HB2	34:B1:289:LEU:HD22	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5D:64:TYR:H	42:5D:67:MET:HE3	1.79	0.47
53:RE:567:THR:HB	53:RE:583:ILE:HD13	1.96	0.47
53:RE:870:ALA:O	53:RE:875:LYS:NZ	2.48	0.47
53:RE:1102:LEU:HG	53:RE:1231:VAL:HG22	1.97	0.47
53:RE:1221:HIS:NE2	54:RF:21:PRO:O	2.33	0.47
55:RG:176:ARG:O	55:RG:220:TYR:OH	2.29	0.47
57:RJ:853:ARG:HE	57:RJ:853:ARG:HB2	1.55	0.47
59:RM:26:PHE:HA	59:RM:199:LEU:O	2.15	0.47
1:3A:84:U:OP2	24:3E:361:ARG:NH2	2.47	0.47
1:3A:94:A:H2'	1:3A:95:A:H8	1.79	0.47
13:SO:64:ARG:HH21	13:SO:70:LYS:HE3	1.80	0.47
20:Sc:80:ARG:HD3	54:RF:211:GLY:HA3	1.97	0.47
22:3B:102:LYS:O	48:5J:136:TYR:OH	2.28	0.47
22:3B:219:PRO:O	23:3D:159:SER:OG	2.28	0.47
24:3E:125:PRO:HB3	24:3E:136:LEU:HD22	1.96	0.47
24:3E:373:TYR:HD1	26:3G:62:GLU:HB2	1.79	0.47
27:A4:82:ARG:NH1	27:A4:686:ASN:O	2.47	0.47
27:A4:573:VAL:HG22	27:A4:584:VAL:HG12	1.96	0.47
28:A5:103:ASN:ND2	28:A5:127:TYR:OH	2.48	0.47
28:A5:238:SER:OG	28:A5:239:GLY:N	2.48	0.47
32:AF:431:LEU:O	32:AF:470:TYR:OH	2.27	0.47
33:AG:47:PRO:HB3	33:AG:88:ILE:HD13	1.96	0.47
33:AG:610:SER:OG	33:AG:659:ILE:O	2.32	0.47
33:AG:714:ASP:OD1	33:AG:715:GLU:N	2.48	0.47
34:B1:598:ASN:OD1	34:B1:598:ASN:N	2.39	0.47
35:B2:197:ILE:O	36:B3:671:ASN:ND2	2.40	0.47
36:B3:22:VAL:HG23	36:B3:305:VAL:HG21	1.95	0.47
36:B3:265:ALA:HA	36:B3:290:ILE:HG13	1.95	0.47
38:BE:359:ALA:O	38:BE:421:ASN:ND2	2.47	0.47
39:B6:413:TYR:O	39:B6:417:ASN:CB	2.62	0.47
40:5B:181:LEU:HD11	42:5D:136:PHE:HB3	1.97	0.47
41:5C:488:PRO:O	41:5C:527:ARG:NE	2.45	0.47
48:5J:155:ASP:OD1	48:5J:155:ASP:N	2.46	0.47
50:RA:80:GLN:OE1	50:RA:82:HIS:NE2	2.44	0.47
50:RA:258:ARG:HA	59:RM:511:SER:HA	1.96	0.47
53:RE:639:SER:OG	53:RE:641:GLU:OE1	2.31	0.47
53:RE:682:VAL:O	53:RE:686:LEU:HB2	2.14	0.47
55:RG:177:LYS:HD2	55:RG:222:ASP:H	1.79	0.47
57:RJ:1148:GLU:OE2	57:RJ:1152:ARG:NH1	2.47	0.47
59:RM:614:ILE:O	59:RM:618:ILE:CB	2.63	0.47
60:RN:5:GLN:HE22	60:RN:57:PRO:HD3	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3A:327:G:OP1	42:5D:222:ARG:NH2	2.48	0.47
4:SC:33:LYS:O	4:SC:98:THR:OG1	2.32	0.47
5:SF:159:THR:HB	5:SF:173:ILE:O	2.14	0.47
31:AE:692:ILE:HA	31:AE:695:TYR:HB2	1.97	0.47
33:AG:370:GLN:NE2	33:AG:384:SER:OG	2.43	0.47
34:B1:288:ASP:HB2	34:B1:295:ILE:HD11	1.97	0.47
34:B1:476:VAL:HA	34:B1:492:SER:HB3	1.96	0.47
36:B3:8:LYS:HG2	36:B3:645:LYS:HB2	1.95	0.47
53:RE:161:PRO:HG2	53:RE:229:SER:HB2	1.96	0.47
55:RG:113:TYR:HD2	55:RG:167:ILE:HD11	1.79	0.47
3:SA:575:C:O2	57:RJ:1052:SER:OG	2.30	0.47
18:SY:52:ILE:HG12	57:RJ:56:VAL:HG12	1.96	0.47
22:3C:159:LEU:HD12	22:3C:162:LEU:HD12	1.97	0.47
25:3F:164:GLN:HE21	25:3F:527:VAL:HA	1.80	0.47
25:3F:398:CYS:O	25:3F:419:ASN:ND2	2.48	0.47
26:3H:39:GLU:HA	26:3H:42:LYS:HE3	1.97	0.47
27:A4:213:TRP:HA	27:A4:225:LEU:HA	1.97	0.47
31:AE:656:ASN:HA	31:AE:659:LEU:HB2	1.96	0.47
32:AF:75:LYS:HD2	32:AF:111:TYR:HA	1.97	0.47
38:BE:28:ARG:NH2	38:BE:383:ASP:OD2	2.41	0.47
38:BE:529:TYR:HA	38:BE:536:LEU:HA	1.96	0.47
3:SA:1169:G:N1	3:SA:1575:G:OP2	2.45	0.47
4:SC:40:ASN:OD1	4:SC:40:ASN:N	2.45	0.47
7:SH:63:MET:HE3	7:SH:106:LEU:HD11	1.97	0.47
26:3H:111:LYS:HD2	26:3H:111:LYS:HA	1.71	0.47
27:A4:284:LEU:HD21	40:5B:206:LEU:HD21	1.97	0.47
28:A5:156:ALA:O	28:A5:159:SER:OG	2.33	0.47
28:A5:478:VAL:HA	28:A5:481:LEU:HD12	1.96	0.47
33:AG:741:SER:O	33:AG:758:THR:HA	2.14	0.47
35:B2:17:ILE:HG13	35:B2:360:ASN:HB2	1.97	0.47
38:BE:309:ILE:HG22	38:BE:323:VAL:HG23	1.97	0.47
45:5G:144:GLU:HA	45:5G:149:PRO:HA	1.96	0.47
46:5H:576:LEU:HD11	46:5H:580:ARG:HD3	1.97	0.47
49:5K:87:MET:HE2	49:5K:87:MET:HB3	1.84	0.47
53:RE:657:ARG:HB3	53:RE:663:ILE:HD13	1.97	0.47
55:RG:232:LEU:HD13	55:RG:236:VAL:HG12	1.96	0.47
57:RJ:133:LYS:NZ	57:RJ:850:GLY:O	2.40	0.47
57:RJ:186:SER:OG	57:RJ:189:ARG:NH2	2.47	0.47
62:RP:1880:ILE:O	62:RP:1884:ARG:CB	2.63	0.47
1:3A:30:A:N6	47:5I:342:ILE:O	2.42	0.46
18:SY:50:LYS:HB3	18:SY:77:ILE:HD12	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3D:50:LEU:HD22	23:3D:139:PHE:HA	1.97	0.46
27:A4:207:ASP:O	27:A4:233:LYS:NZ	2.45	0.46
32:AF:262:GLU:OE2	32:AF:269:GLN:NE2	2.48	0.46
33:AG:704:ASN:OD1	33:AG:704:ASN:N	2.47	0.46
34:B1:389:SER:HB3	34:B1:407:LEU:HD12	1.97	0.46
35:B2:393:ASP:OD1	35:B2:393:ASP:N	2.35	0.46
36:B3:28:ASN:OD1	36:B3:28:ASN:N	2.42	0.46
38:BE:114:THR:OG1	38:BE:115:ASP:N	2.46	0.46
41:5C:489:ASP:OD1	41:5C:489:ASP:N	2.41	0.46
44:5F:63:LEU:HB3	66:RV:204:GLY:HA2	1.97	0.46
53:RE:1099:VAL:HB	53:RE:1235:GLU:HB2	1.96	0.46
58:RK:117:LEU:HA	58:RK:166:VAL:O	2.15	0.46
59:RL:375:HIS:O	59:RL:377:VAL:N	2.48	0.46
60:RN:600:LEU:HD22	60:RN:633:VAL:HG22	1.97	0.46
4:SC:154:SER:O	4:SC:154:SER:OG	2.30	0.46
7:SH:31:ARG:HB3	7:SH:101:ILE:HG13	1.97	0.46
9:SJ:190:ALA:HA	9:SJ:193:LEU:HB2	1.96	0.46
22:3C:224:ALA:O	22:3C:256:ASN:ND2	2.39	0.46
29:A8:674:GLU:O	29:A8:678:LEU:HB2	2.15	0.46
33:AG:46:ILE:HD13	33:AG:385:ILE:HG21	1.97	0.46
34:B1:25:ASP:O	34:B1:27:LYS:N	2.45	0.46
35:B2:128:GLN:HE22	35:B2:171:CYS:H	1.64	0.46
35:B2:281:ILE:HG13	35:B2:338:ILE:HD13	1.97	0.46
36:B3:308:ASP:OD1	36:B3:308:ASP:N	2.48	0.46
50:RA:277:ILE:HG22	50:RA:291:THR:HA	1.97	0.46
53:RE:911:PRO:HB2	53:RE:954:LEU:HD13	1.96	0.46
55:RG:143:GLN:HE21	55:RG:147:LYS:HB3	1.79	0.46
61:RO:257:PHE:O	61:RO:261:TRP:HB2	2.14	0.46
64:RS:280:ASN:ND2	64:RS:320:GLY:O	2.48	0.46
2:5A:516:U:O2'	2:5A:518:A:N7	2.40	0.46
4:SC:64:ARG:HE	14:SP:36:LYS:HD3	1.80	0.46
7:SH:63:MET:HE1	7:SH:102:VAL:HA	1.97	0.46
27:A4:150:ASN:ND2	27:A4:198:ASP:OD2	2.48	0.46
27:A4:575:ILE:HG22	27:A4:582:VAL:HG12	1.98	0.46
27:A4:652:THR:O	27:A4:652:THR:OG1	2.33	0.46
31:AE:109:TRP:HH2	31:AE:118:THR:HG21	1.79	0.46
35:B2:840:MET:HE2	35:B2:840:MET:HB3	1.76	0.46
37:B8:521:LEU:HD12	37:B8:530:LEU:HD11	1.96	0.46
41:5C:510:ASP:N	41:5C:510:ASP:OD1	2.47	0.46
53:RE:145:SER:OG	53:RE:146:LEU:N	2.48	0.46
53:RE:1108:LEU:O	53:RE:1112:CYS:HB2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:RJ:1042:MET:HE2	57:RJ:1042:MET:HB3	1.80	0.46
2:5A:7:A:N6	33:AG:579:ASN:OD1	2.46	0.46
2:5A:102:A:OP1	32:AF:454:ARG:NH1	2.48	0.46
4:SC:86:LEU:HB3	4:SC:98:THR:HB	1.98	0.46
23:3D:194:ARG:HG3	24:3E:169:LEU:HD21	1.97	0.46
26:3G:61:ILE:HG23	26:3G:65:LEU:HD22	1.98	0.46
27:A4:274:GLN:HE22	27:A4:319:ARG:HA	1.79	0.46
29:A8:443:CYS:HA	33:AG:728:LEU:HD22	1.97	0.46
30:A9:434:PHE:O	30:A9:438:SER:HB3	2.16	0.46
37:B8:351:THR:O	37:B8:351:THR:OG1	2.31	0.46
41:5C:538:ILE:HB	41:5C:542:HIS:CE1	2.51	0.46
47:5I:341:GLU:OE1	47:5I:417:ARG:NH1	2.49	0.46
53:RE:1137:ASN:O	53:RE:1140:SER:OG	2.34	0.46
56:RI:224:THR:HA	56:RI:235:ILE:HB	1.97	0.46
58:RK:244:THR:HG23	58:RK:259:GLU:HB3	1.97	0.46
60:RN:422:LEU:HA	60:RN:425:PHE:CE2	2.51	0.46
3:SA:524:U:N3	3:SA:527:A:OP2	2.40	0.46
3:SA:1542:G:O6	3:SA:1568:C:N4	2.48	0.46
6:SG:79:ASN:OD1	6:SG:83:ARG:NH1	2.49	0.46
7:SH:3:LEU:O	7:SH:15:THR:HA	2.14	0.46
9:SJ:11:ARG:HH12	9:SJ:17:LYS:HD3	1.81	0.46
12:SN:59:LEU:HD12	12:SN:87:PRO:HG2	1.97	0.46
12:SN:92:ALA:HB3	12:SN:97:LEU:HD12	1.97	0.46
25:3F:565:SER:O	25:3F:565:SER:OG	2.34	0.46
27:A4:441:VAL:HG12	27:A4:450:VAL:HG22	1.97	0.46
32:AF:109:ASP:OD1	32:AF:115:THR:OG1	2.33	0.46
33:AG:27:SER:OG	33:AG:171:TYR:OH	2.34	0.46
37:B8:414:ILE:HD11	37:B8:420:ARG:HH11	1.80	0.46
38:BE:356:ILE:HG22	38:BE:633:LYS:HG3	1.97	0.46
38:BE:442:THR:OG1	38:BE:453:TRP:O	2.32	0.46
41:5C:343:ASP:O	41:5C:351:SER:OG	2.31	0.46
41:5C:493:LYS:O	41:5C:498:ARG:NH1	2.46	0.46
41:5C:495:SER:O	41:5C:495:SER:OG	2.33	0.46
45:5G:138:ASP:HA	45:5G:155:SER:O	2.16	0.46
53:RE:481:THR:HG23	53:RE:484:SER:H	1.80	0.46
66:RV:326:ILE:O	66:RV:330:SER:OG	2.29	0.46
3:SA:421:A:O2'	3:SA:422:G:O4'	2.33	0.46
6:SG:73:THR:OG1	6:SG:91:GLU:OE1	2.33	0.46
16:ST:27:LYS:HA	16:ST:57:ARG:HA	1.98	0.46
23:3D:281:LEU:HD23	24:3E:261:GLN:HE21	1.81	0.46
33:AG:27:SER:HG	33:AG:171:TYR:HH	1.61	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B1:459:SER:HB2	34:B1:466:LEU:HD12	1.96	0.46
34:B1:665:GLN:NE2	44:5F:145:ASP:OD1	2.49	0.46
36:B3:168:THR:HA	36:B3:192:ALA:HA	1.97	0.46
38:BE:173:LEU:HB3	38:BE:214:PRO:HB3	1.97	0.46
44:5F:115:MET:HB2	44:5F:115:MET:HE3	1.59	0.46
46:5H:496:GLN:HA	46:5H:499:GLN:HG2	1.96	0.46
47:5I:45:LEU:HD13	47:5I:410:ILE:HG22	1.97	0.46
48:5J:114:ARG:NH1	48:5J:145:GLU:O	2.48	0.46
53:RE:495:THR:HA	53:RE:498:MET:HG2	1.98	0.46
55:RH:39:LYS:NZ	55:RH:197:ASP:O	2.40	0.46
55:RH:177:LYS:HG2	55:RH:203:CYS:HB3	1.97	0.46
56:RI:117:GLN:O	56:RI:121:ASP:HB2	2.16	0.46
60:RN:590:ASN:N	60:RN:590:ASN:OD1	2.48	0.46
2:5A:404:G:H1	2:5A:451:G:HO2'	1.62	0.46
3:SA:532:U:O2'	19:SZ:33:ALA:O	2.27	0.46
3:SA:1227:A:H2'	12:SN:118:ALA:HA	1.97	0.46
7:SH:68:LEU:HG	7:SH:69:LEU:HB2	1.98	0.46
17:SX:5:SER:OG	17:SX:6:VAL:N	2.48	0.46
22:3B:155:ILE:HD11	22:3B:162:LEU:HD21	1.98	0.46
25:3F:160:ILE:H	25:3F:523:LYS:HG2	1.81	0.46
31:AE:667:LYS:HB3	31:AE:667:LYS:HE2	1.65	0.46
33:AG:124:LYS:HA	33:AG:124:LYS:HD2	1.76	0.46
35:B2:393:ASP:HB3	35:B2:677:HIS:HD2	1.81	0.46
35:B2:500:TRP:HB3	35:B2:522:LEU:HD12	1.98	0.46
36:B3:269:LEU:HD23	36:B3:279:LYS:HB2	1.98	0.46
36:B3:691:PRO:HB3	36:B3:742:ARG:NE	2.31	0.46
38:BE:51:VAL:HG21	38:BE:90:VAL:HG11	1.96	0.46
46:5H:438:ASP:OD1	46:5H:438:ASP:N	2.47	0.46
47:5I:122:ARG:HB2	47:5I:192:SER:HB3	1.97	0.46
47:5I:210:LYS:HD3	47:5I:210:LYS:HA	1.63	0.46
49:5K:155:THR:OG1	49:5K:156:ASN:N	2.48	0.46
53:RE:758:SER:HA	53:RE:761:ARG:HG2	1.97	0.46
53:RE:822:ARG:HE	53:RE:1136:LEU:HD21	1.79	0.46
2:5A:528:G:H2'	2:5A:529:A:H8	1.81	0.46
23:3D:126:ASP:HA	23:3D:129:ARG:HG2	1.98	0.46
23:3D:160:ARG:NH2	24:3E:243:MET:O	2.48	0.46
31:AE:405:GLU:HA	31:AE:408:ILE:HG12	1.97	0.46
34:B1:317:LEU:O	34:B1:329:VAL:HA	2.16	0.46
35:B2:54:ILE:HG12	35:B2:364:TYR:HB2	1.98	0.46
35:B2:181:SER:OG	35:B2:182:LYS:N	2.49	0.46
35:B2:235:ASN:ND2	35:B2:240:GLY:O	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:B8:338:LYS:NZ	37:B8:340:GLU:OE1	2.46	0.46
38:BE:591:PHE:HA	38:BE:601:VAL:O	2.16	0.46
39:B6:285:TYR:HD1	39:B6:308:THR:HG22	1.81	0.46
53:RE:358:SER:O	53:RE:358:SER:OG	2.34	0.46
53:RE:400:LEU:HB3	53:RE:412:LEU:HD22	1.98	0.46
53:RE:437:ASP:N	53:RE:437:ASP:OD1	2.48	0.46
53:RE:753:ILE:HD11	53:RE:852:PHE:HE1	1.81	0.46
53:RE:944:ASP:OD1	53:RE:944:ASP:N	2.49	0.46
56:RI:10:SER:OG	56:RI:11:GLY:N	2.48	0.46
56:RI:77:LYS:HD2	56:RI:130:ARG:HE	1.80	0.46
59:RL:44:MET:HE3	59:RL:44:MET:HB3	1.82	0.46
59:RL:137:ARG:HD3	59:RL:137:ARG:HA	1.75	0.46
66:RV:212:GLU:OE2	66:RV:285:ARG:NH1	2.46	0.46
3:SA:35:U:H3	3:SA:473:A:H61	1.62	0.46
3:SA:438:A:N6	57:RJ:204:LEU:O	2.48	0.46
5:SF:110:ALA:HB1	25:3F:112:LEU:HD21	1.98	0.46
8:SI:131:PHE:O	8:SI:133:THR:N	2.45	0.46
22:3C:258:HIS:ND1	22:3C:320:TYR:OH	2.42	0.46
26:3H:45:ASN:HA	26:3H:74:LYS:HE2	1.98	0.46
27:A4:57:ILE:HD13	27:A4:340:GLN:HG2	1.97	0.46
33:AG:156:THR:OG1	33:AG:169:GLN:NE2	2.37	0.46
33:AG:387:GLY:O	33:AG:458:GLN:NE2	2.40	0.46
33:AG:478:ASN:N	33:AG:478:ASN:OD1	2.49	0.46
34:B1:451:ASP:OD1	34:B1:451:ASP:N	2.47	0.46
34:B1:711:LEU:HA	38:BE:596:GLU:HB2	1.97	0.46
36:B3:128:VAL:HB	36:B3:138:HIS:HB2	1.98	0.46
36:B3:661:LEU:HA	36:B3:664:GLU:HG2	1.97	0.46
41:5C:125:LEU:HD23	41:5C:137:MET:HE2	1.97	0.46
53:RE:498:MET:HE1	53:RE:947:PRO:HB3	1.98	0.46
56:RI:105:ASN:HA	56:RI:108:ARG:HB3	1.98	0.46
56:RI:211:GLU:O	56:RI:215:ASN:ND2	2.48	0.46
60:RN:485:TYR:HD1	60:RN:493:LEU:HD11	1.81	0.46
3:SA:1151:A:H2'	3:SA:1152:A:H8	1.81	0.46
19:SZ:82:ALA:O	19:SZ:86:GLU:HB2	2.16	0.46
22:3B:107:VAL:HG13	22:3B:141:TYR:HB3	1.98	0.46
23:3D:382:LYS:HD2	23:3D:404:LEU:HD22	1.97	0.46
25:3F:197:THR:HG21	25:3F:210:LYS:HE2	1.97	0.46
27:A4:610:VAL:N	31:AE:629:GLU:OE1	2.49	0.46
28:A5:245:ALA:HB2	28:A5:296:ILE:HD12	1.98	0.46
35:B2:223:ASP:OD1	35:B2:223:ASP:N	2.49	0.46
66:RV:148:ASN:OD1	66:RV:148:ASN:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5A:512:A:H2'	2:5A:513:G:H8	1.82	0.45
2:5A:528:G:H2'	2:5A:529:A:C8	2.50	0.45
3:SA:313:U:H4'	3:SA:314:C:H5''	1.97	0.45
3:SA:418:G:H8	7:SH:59:GLN:HE21	1.64	0.45
3:SA:578:U:OP1	57:RJ:1039:ARG:NH1	2.40	0.45
9:SJ:32:GLN:O	9:SJ:56:ARG:NH1	2.49	0.45
24:3E:284:ALA:O	24:3E:288:THR:OG1	2.28	0.45
25:3F:331:LEU:HD23	25:3F:331:LEU:HA	1.81	0.45
25:3F:500:LYS:HG2	25:3F:511:LEU:HG	1.98	0.45
27:A4:232:ASP:H	27:A4:263:LYS:HE3	1.81	0.45
27:A4:389:ARG:NH2	27:A4:405:GLY:O	2.47	0.45
27:A4:775:VAL:HB	32:AF:429:VAL:HG22	1.96	0.45
32:AF:87:ALA:HA	32:AF:97:CYS:O	2.15	0.45
34:B1:11:LEU:HD11	34:B1:374:ILE:HA	1.98	0.45
35:B2:198:GLU:OE2	35:B2:200:HIS:NE2	2.40	0.45
35:B2:262:ILE:O	35:B2:270:SER:HA	2.15	0.45
36:B3:227:MET:HB3	36:B3:228:LYS:HE2	1.98	0.45
38:BE:390:SER:HB3	38:BE:449:ARG:HG3	1.98	0.45
45:5G:87:ARG:O	45:5G:136:THR:OG1	2.35	0.45
48:5J:80:ASN:OD1	48:5J:80:ASN:N	2.49	0.45
48:5J:174:LEU:HG	48:5J:178:MET:HE2	1.96	0.45
48:5J:196:GLU:HA	48:5J:199:THR:HG22	1.97	0.45
52:RC:180:LEU:HA	52:RC:180:LEU:HD23	1.81	0.45
53:RE:1196:PHE:HB3	53:RE:1212:VAL:HG21	1.98	0.45
56:RI:192:ASN:OD1	56:RI:192:ASN:N	2.49	0.45
61:RO:467:ALA:HA	61:RO:470:MET:HG3	1.98	0.45
64:RS:394:PHE:HE2	64:RS:439:PHE:HB2	1.81	0.45
3:SA:580:A:OP1	57:RJ:1046:THR:OG1	2.32	0.45
3:SA:1736:G:H2'	3:SA:1737:G:C8	2.51	0.45
5:SF:111:VAL:H	25:3F:112:LEU:HD11	1.82	0.45
18:SY:138:GLU:OE2	57:RJ:830:ARG:NH1	2.42	0.45
24:3E:209:ILE:HD11	24:3E:259:ALA:HB2	1.96	0.45
27:A4:476:LYS:NZ	27:A4:531:ILE:O	2.39	0.45
31:AE:605:TYR:HD1	31:AE:609:VAL:HG12	1.82	0.45
32:AF:279:GLY:O	32:AF:297:LYS:HA	2.16	0.45
33:AG:588:ASP:OD1	33:AG:588:ASP:N	2.44	0.45
34:B1:250:ILE:HD11	34:B1:253:LYS:HG2	1.97	0.45
34:B1:335:GLU:O	38:BE:745:LYS:NZ	2.39	0.45
37:B8:511:LEU:HD13	37:B8:544:VAL:HG11	1.98	0.45
38:BE:464:LYS:HD3	38:BE:464:LYS:HA	1.79	0.45
38:BE:631:ASN:O	38:BE:643:THR:HA	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5D:128:LYS:HA	42:5D:128:LYS:HD3	1.74	0.45
56:RI:67:PRO:HG2	56:RI:181:ARG:HG2	1.99	0.45
59:RL:59:TYR:O	59:RL:108:TYR:N	2.47	0.45
64:RS:383:PRO:O	64:RS:386:THR:OG1	2.29	0.45
67:X1:191:UNK:O	67:X1:195:UNK:N	2.49	0.45
8:SI:129:LEU:HD11	8:SI:172:VAL:HG23	1.98	0.45
9:SJ:97:THR:OG1	9:SJ:98:LYS:N	2.49	0.45
13:SO:37:ILE:HG12	13:SO:54:LEU:HD11	1.98	0.45
27:A4:545:ARG:HG3	27:A4:549:VAL:HB	1.99	0.45
27:A4:636:ILE:HG23	27:A4:648:PHE:HD2	1.81	0.45
31:AE:408:ILE:HG22	31:AE:415:VAL:HG11	1.98	0.45
31:AE:555:GLU:HB2	31:AE:556:LYS:HD3	1.97	0.45
32:AF:252:ASN:HB3	61:RO:333:GLU:HG2	1.99	0.45
33:AG:113:ASN:OD1	33:AG:140:LYS:NZ	2.50	0.45
36:B3:90:LEU:O	36:B3:92:THR:N	2.49	0.45
37:B8:251:ILE:HG13	37:B8:584:GLY:HA2	1.98	0.45
53:RE:691:SER:OG	53:RE:692:LYS:N	2.49	0.45
56:RI:85:GLU:OE1	56:RI:89:LYS:NZ	2.49	0.45
57:RJ:613:PRO:HD3	58:RK:292:ASN:HB3	1.98	0.45
59:RM:657:LEU:O	59:RM:661:PHE:CB	2.65	0.45
61:RO:142:PHE:H	61:RO:244:PRO:HG3	1.80	0.45
64:RS:344:LYS:HE3	64:RS:345:VAL:HB	1.99	0.45
2:5A:490:G:H1'	2:5A:495:G:H5'	1.99	0.45
3:SA:895:G:H22	3:SA:917:U:H3	1.65	0.45
3:SA:1493:A:OP1	42:5D:25:TYR:OH	2.30	0.45
19:SZ:44:LEU:HA	19:SZ:47:VAL:HG12	1.98	0.45
31:AE:664:PRO:HA	31:AE:667:LYS:HE2	1.98	0.45
34:B1:274:LEU:HD11	34:B1:286:LEU:HD13	1.98	0.45
34:B1:777:ARG:HH12	34:B1:781:PHE:HB2	1.81	0.45
35:B2:800:THR:HG23	35:B2:803:GLN:H	1.81	0.45
36:B3:460:ASP:OD1	36:B3:460:ASP:N	2.46	0.45
45:5G:9:ARG:HD2	45:5G:9:ARG:HA	1.70	0.45
52:RC:128:ILE:HB	52:RC:191:MET:HG3	1.97	0.45
55:RH:35:ASP:O	55:RH:40:ARG:NH2	2.50	0.45
57:RJ:366:MET:HE1	57:RJ:371:VAL:HG22	1.98	0.45
57:RJ:951:MET:SD	57:RJ:987:TYR:OH	2.67	0.45
57:RJ:1078:PRO:HD2	57:RJ:1081:SER:HB2	1.96	0.45
61:RO:227:LYS:HG3	61:RO:236:LEU:HD21	1.98	0.45
2:5A:308:A:O2'	38:BE:45:GLY:O	2.34	0.45
12:SN:62:LEU:HD11	12:SN:71:ILE:HD13	1.99	0.45
15:SR:91:ALA:HB2	44:5F:180:PHE:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:ST:116:LEU:HD21	43:5E:341:LEU:HD13	1.98	0.45
22:3B:210:MET:HE2	22:3B:210:MET:HB3	1.84	0.45
24:3E:419:VAL:HG21	38:BE:323:VAL:HG21	1.99	0.45
28:A5:342:ASP:OD2	33:AG:382:LYS:NZ	2.48	0.45
28:A5:452:LEU:HA	28:A5:455:THR:HG22	1.98	0.45
32:AF:135:GLN:NE2	32:AF:178:PRO:O	2.50	0.45
34:B1:190:HIS:CD2	34:B1:210:SER:HB3	2.51	0.45
34:B1:546:ASP:O	34:B1:548:LYS:N	2.48	0.45
34:B1:839:THR:HG22	38:BE:882:GLU:HG3	1.97	0.45
41:5C:244:ASN:OD1	41:5C:244:ASN:N	2.48	0.45
43:5E:368:MET:HE3	43:5E:368:MET:HB3	1.84	0.45
50:RA:195:LEU:O	50:RA:206:PHE:HA	2.17	0.45
53:RE:440:LEU:HG	53:RE:457:TYR:HA	1.98	0.45
53:RE:1102:LEU:HA	53:RE:1231:VAL:HA	1.98	0.45
59:RL:746:TYR:O	59:RL:765:VAL:HA	2.17	0.45
60:RN:682:ARG:O	60:RN:686:ASN:ND2	2.42	0.45
2:5A:142:U:O2'	2:5A:144:C:N4	2.42	0.45
3:SA:162:A:H3'	3:SA:163:G:H21	1.82	0.45
3:SA:370:A:N3	3:SA:370:A:C2'	2.79	0.45
8:SI:82:GLU:O	8:SI:86:GLN:HA	2.16	0.45
23:3D:4:ILE:HG23	23:3D:20:VAL:HG21	1.97	0.45
27:A4:302:ARG:NH2	27:A4:330:GLY:O	2.49	0.45
32:AF:14:PRO:HD3	33:AG:548:ILE:HD11	1.99	0.45
34:B1:450:LEU:HA	34:B1:475:PRO:HB3	1.99	0.45
35:B2:127:LEU:HD12	35:B2:136:LEU:HD11	1.96	0.45
36:B3:440:VAL:HB	36:B3:454:LEU:HD11	1.96	0.45
44:5F:135:HIS:HB3	44:5F:160:TRP:CD1	2.52	0.45
50:RA:123:ILE:O	50:RA:134:THR:HA	2.16	0.45
54:RF:46:ASN:HB2	54:RF:49:GLU:HB2	1.98	0.45
54:RF:103:LEU:HD12	54:RF:103:LEU:HA	1.84	0.45
57:RJ:629:ASP:OD1	57:RJ:629:ASP:N	2.47	0.45
58:RK:172:SER:O	58:RK:172:SER:OG	2.35	0.45
58:RK:263:ASP:OD1	58:RK:263:ASP:N	2.49	0.45
13:SO:27:LYS:HA	13:SO:27:LYS:HD3	1.85	0.45
22:3C:230:TYR:OH	22:3C:256:ASN:OD1	2.31	0.45
26:3H:12:ALA:HB1	26:3H:16:LEU:HB3	1.98	0.45
27:A4:287:THR:OG1	27:A4:288:THR:N	2.50	0.45
28:A5:49:ASN:OD1	28:A5:49:ASN:N	2.50	0.45
34:B1:350:SER:OG	34:B1:351:LEU:N	2.50	0.45
35:B2:217:LEU:HB3	35:B2:229:TRP:HB2	1.98	0.45
35:B2:492:SER:OG	35:B2:493:ALA:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:B2:831:LYS:HE2	35:B2:831:LYS:HB3	1.79	0.45
36:B3:645:LYS:HA	36:B3:645:LYS:HD2	1.86	0.45
38:BE:528:PHE:HZ	38:BE:570:ILE:HD11	1.82	0.45
38:BE:584:HIS:NE2	38:BE:602:SER:OG	2.36	0.45
45:5G:173:ARG:HD2	45:5G:182:GLN:HE21	1.82	0.45
50:RA:254:ILE:HG22	50:RA:264:ILE:H	1.80	0.45
52:RC:212:ARG:HH11	52:RC:215:LEU:HD22	1.82	0.45
52:RC:281:LEU:HG	52:RC:284:GLN:HE21	1.82	0.45
58:RK:155:LYS:HG3	58:RK:164:GLY:HA2	1.97	0.45
59:RM:728:GLY:N	59:RM:765:VAL:O	2.46	0.45
64:RS:284:LEU:HD12	64:RS:321:PHE:HB2	1.99	0.45
3:SA:398:G:OP1	9:SJ:50:GLY:N	2.49	0.45
3:SA:413:U:O4	3:SA:421:A:N6	2.49	0.45
3:SA:448:C:OP1	5:SF:49:ARG:NH1	2.38	0.45
3:SA:527:A:H2'	3:SA:528:U:H6	1.82	0.45
3:SA:1787:C:H4'	36:B3:133:ASN:HB2	1.99	0.45
24:3E:214:ILE:HD11	24:3E:252:LEU:HD22	1.99	0.45
25:3F:452:SER:OG	25:3F:453:GLY:N	2.49	0.45
28:A5:240:GLN:NE2	28:A5:242:ASP:OD2	2.48	0.45
31:AE:130:LYS:HD3	31:AE:130:LYS:HA	1.83	0.45
32:AF:33:ALA:HA	32:AF:329:ILE:O	2.17	0.45
33:AG:317:TRP:HZ3	33:AG:361:THR:HG21	1.82	0.45
34:B1:748:GLU:OE2	34:B1:777:ARG:NH2	2.37	0.45
34:B1:814:LYS:HE3	34:B1:814:LYS:HB2	1.70	0.45
36:B3:16:TYR:O	36:B3:336:ASN:ND2	2.50	0.45
39:B6:17:ASP:OD2	39:B6:84:SER:OG	2.28	0.45
47:5I:241:ASP:OD1	47:5I:243:SER:OG	2.30	0.45
47:5I:378:LYS:HB2	47:5I:381:GLU:HB2	1.99	0.45
50:RA:212:ARG:HH12	52:RC:310:ALA:H	1.63	0.45
56:RI:128:ASP:HB3	56:RI:131:VAL:HG22	1.99	0.45
57:RJ:72:VAL:HG22	57:RJ:137:LEU:HB3	1.98	0.45
58:RK:110:SER:OG	58:RK:112:LYS:O	2.30	0.45
58:RK:326:LEU:HD13	58:RK:326:LEU:HA	1.83	0.45
60:RN:636:LEU:HD23	60:RN:637:LEU:HD22	1.98	0.45
2:5A:20:C:H2'	2:5A:21:A:C8	2.52	0.45
2:5A:467:A:N1	2:5A:468:A:N6	2.65	0.45
2:5A:545:G:O2'	39:B6:79:LYS:NZ	2.47	0.45
7:SH:33:GLY:O	7:SH:51:LYS:NZ	2.50	0.45
10:SK:82:ARG:NH1	51:RB:323:GLU:OE2	2.48	0.45
14:SP:20:TYR:HB3	14:SP:27:PHE:HB2	1.98	0.45
22:3B:248:ASP:OD1	22:3B:248:ASP:N	2.39	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3D:142:LEU:HD21	39:B6:139:LEU:HD22	1.99	0.45
25:3F:304:ILE:HD11	25:3F:325:VAL:HG11	1.99	0.45
28:A5:364:THR:OG1	28:A5:365:SER:N	2.50	0.45
31:AE:109:TRP:HA	31:AE:114:THR:HG21	1.99	0.45
35:B2:760:ILE:HG13	35:B2:831:LYS:HB2	1.99	0.45
36:B3:438:THR:OG1	36:B3:497:LEU:N	2.49	0.45
36:B3:673:MET:HE2	36:B3:693:ARG:HG2	1.99	0.45
38:BE:221:ILE:HG22	38:BE:233:PHE:HB3	1.99	0.45
41:5C:443:THR:OG1	41:5C:445:ASP:O	2.35	0.45
50:RA:62:ILE:HG22	50:RA:332:ALA:HB2	1.98	0.45
50:RA:162:LEU:HD23	50:RA:176:PHE:HD2	1.82	0.45
50:RA:297:ALA:HB3	50:RA:311:MET:HB2	1.99	0.45
52:RC:134:ASN:OD1	52:RC:134:ASN:N	2.37	0.45
53:RE:542:SER:OG	53:RE:543:LEU:N	2.49	0.45
53:RE:578:ILE:HG21	53:RE:617:LEU:HD22	1.99	0.45
56:RI:35:ASP:N	56:RI:35:ASP:OD1	2.50	0.45
56:RI:59:LEU:H	56:RI:186:ASN:HD22	1.64	0.45
56:RI:83:TYR:O	56:RI:87:LEU:HB2	2.17	0.45
57:RJ:839:LEU:H	57:RJ:875:THR:HG22	1.82	0.45
62:RP:879:PRO:O	62:RP:882:ASN:C	2.60	0.45
64:RS:243:GLN:HA	64:RS:246:ILE:HG22	1.99	0.45
3:SA:898:A:N1	3:SA:911:U:O2'	2.43	0.45
5:SF:75:LYS:HD2	5:SF:77:ARG:HH21	1.82	0.45
18:SY:47:SER:OG	18:SY:48:HIS:ND1	2.50	0.45
23:3D:69:ILE:HD13	23:3D:69:ILE:HA	1.84	0.45
25:3F:344:ARG:HA	25:3F:402:ILE:HG12	1.99	0.45
25:3F:350:LYS:O	25:3F:354:GLU:N	2.50	0.45
31:AE:262:VAL:HG21	33:AG:892:MET:HE1	1.97	0.45
47:5I:73:ILE:HG12	47:5I:85:THR:HG22	1.99	0.45
50:RA:171:ARG:NH2	67:X1:466:UNK:O	2.50	0.45
53:RE:741:ILE:HA	53:RE:744:MET:HE3	1.99	0.45
53:RE:773:TYR:HD2	53:RE:1139:LEU:HG	1.82	0.45
53:RE:931:ASP:OD1	53:RE:931:ASP:N	2.49	0.45
55:RG:39:LYS:HA	55:RG:200:GLU:O	2.17	0.45
57:RJ:105:ILE:HG23	57:RJ:356:ALA:HB2	1.98	0.45
61:RO:452:ASP:OD2	61:RO:455:LEU:N	2.47	0.45
62:RP:2242:PRO:O	62:RP:2246:VAL:CB	2.65	0.45
64:RS:215:THR:O	64:RS:219:SER:OG	2.29	0.45
64:RS:322:LEU:HA	64:RS:325:LEU:HD23	1.99	0.45
3:SA:1137:A:C6	35:B2:573:LYS:HD3	2.51	0.44
17:SX:67:GLY:O	49:5K:114:ARG:NH1	2.44	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:3B:198:GLU:OE2	22:3B:199:PHE:N	2.48	0.44
22:3B:269:ILE:O	22:3B:315:ILE:HA	2.18	0.44
23:3D:171:ASP:N	23:3D:171:ASP:OD1	2.38	0.44
24:3E:121:LYS:HA	24:3E:124:LEU:HG	1.99	0.44
33:AG:80:GLN:NE2	33:AG:83:GLU:O	2.37	0.44
34:B1:524:ARG:HG3	34:B1:585:TYR:CE2	2.52	0.44
38:BE:738:ASP:OD1	38:BE:738:ASP:N	2.49	0.44
38:BE:880:LEU:HA	38:BE:883:THR:HG22	1.99	0.44
41:5C:188:LYS:HB2	41:5C:188:LYS:HE3	1.77	0.44
41:5C:263:MET:HB3	41:5C:263:MET:HE3	1.81	0.44
47:5I:145:VAL:HB	47:5I:176:PHE:HB2	1.99	0.44
50:RA:268:GLN:HG3	50:RA:271:GLY:H	1.81	0.44
51:RB:266:ILE:HG22	51:RB:274:ILE:HG23	1.99	0.44
64:RS:271:THR:OG1	64:RS:274:GLU:OE1	2.36	0.44
3:SA:29:U:H2'	3:SA:30:G:C8	2.51	0.44
3:SA:30:G:H4'	18:SY:131:SER:HB3	1.99	0.44
3:SA:929:A:OP2	3:SA:931:C:N4	2.49	0.44
5:SF:45:ILE:HB	5:SF:80:THR:HB	1.99	0.44
5:SF:101:LEU:HB3	5:SF:111:VAL:HG12	1.98	0.44
22:3C:245:ALA:HA	22:3C:249:GLN:HE22	1.81	0.44
23:3D:296:MET:HG3	23:3D:304:SER:HB3	1.99	0.44
27:A4:214:SER:OG	27:A4:214:SER:O	2.32	0.44
29:A8:539:ASN:ND2	29:A8:560:ASN:O	2.42	0.44
33:AG:90:LYS:HG2	33:AG:144:VAL:HB	1.99	0.44
34:B1:777:ARG:HA	34:B1:777:ARG:HD2	1.81	0.44
34:B1:847:ARG:O	34:B1:851:SER:HB3	2.17	0.44
36:B3:271:ASP:OD2	36:B3:276:SER:OG	2.34	0.44
36:B3:343:MET:HB3	36:B3:343:MET:HE2	1.75	0.44
38:BE:432:THR:HG21	38:BE:443:TRP:HE1	1.82	0.44
38:BE:579:ARG:NH2	38:BE:615:PRO:O	2.49	0.44
45:5G:220:ARG:HD3	45:5G:235:GLN:HE21	1.82	0.44
53:RE:1095:ASP:N	53:RE:1095:ASP:OD1	2.50	0.44
62:RP:465:PHE:HA	62:RP:468:ALA:HB3	1.99	0.44
6:SG:92:ARG:HH22	6:SG:169:ASN:ND2	2.16	0.44
11:SM:125:VAL:HG12	11:SM:139:VAL:HA	1.98	0.44
17:SX:114:GLU:O	17:SX:118:ARG:HB2	2.17	0.44
23:3D:267:ASP:OD1	23:3D:267:ASP:N	2.49	0.44
24:3E:386:ILE:HD13	24:3E:386:ILE:HA	1.82	0.44
25:3F:185:LEU:H	25:3F:202:THR:HB	1.83	0.44
27:A4:532:ASN:N	27:A4:544:SER:O	2.46	0.44
31:AE:316:PRO:HD2	31:AE:319:ILE:HB	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:AE:595:THR:HG21	31:AE:616:PRO:HA	1.99	0.44
31:AE:598:TYR:O	31:AE:615:ASN:ND2	2.50	0.44
33:AG:283:VAL:HG12	33:AG:290:ILE:HG22	1.99	0.44
37:B8:465:THR:OG1	37:B8:466:THR:N	2.49	0.44
38:BE:50:ILE:HD13	38:BE:311:VAL:HG11	2.00	0.44
51:RB:226:ASP:OD1	51:RB:226:ASP:N	2.46	0.44
52:RC:304:ILE:HD12	52:RC:304:ILE:HA	1.87	0.44
55:RH:16:GLN:HG3	55:RH:17:LYS:HD3	1.98	0.44
56:RI:23:GLN:OE1	56:RI:27:ASN:ND2	2.39	0.44
64:RS:277:LYS:HA	64:RS:277:LYS:HD3	1.77	0.44
3:SA:1052:U:H4'	47:5I:449:LYS:HE2	1.99	0.44
3:SA:1160:A:H2'	3:SA:1161:C:H6	1.82	0.44
3:SA:1197:C:OP1	55:RG:136:ARG:NH1	2.50	0.44
3:SA:1731:A:H3'	3:SA:1732:A:H8	1.83	0.44
4:SC:55:LYS:HD2	4:SC:60:ALA:HB2	2.00	0.44
15:SR:47:LYS:HA	15:SR:47:LYS:HD2	1.78	0.44
22:3B:241:PHE:HE1	22:3B:243:ASP:HB2	1.82	0.44
22:3C:101:GLY:N	22:3C:104:ASP:OD1	2.44	0.44
22:3C:103:GLU:HG2	22:3C:105:LEU:HD22	1.99	0.44
22:3C:144:TRP:HH2	22:3C:151:LEU:HD23	1.82	0.44
26:3G:49:SER:OG	26:3G:101:SER:OG	2.28	0.44
27:A4:69:ILE:O	27:A4:76:ILE:HA	2.18	0.44
27:A4:433:LEU:HD13	27:A4:440:LEU:HB2	1.99	0.44
33:AG:339:GLY:HA3	33:AG:358:LEU:HB3	1.99	0.44
37:B8:129:ASP:OD2	38:BE:194:ARG:NH2	2.50	0.44
37:B8:545:HIS:O	37:B8:549:CYS:N	2.51	0.44
41:5C:289:MET:HE2	41:5C:303:ILE:HD11	1.99	0.44
47:5I:123:PHE:HA	47:5I:207:ASN:HD21	1.81	0.44
50:RA:123:ILE:HD13	50:RA:135:THR:HG23	1.98	0.44
53:RE:395:ILE:HD11	53:RE:476:ILE:HG21	1.99	0.44
56:RI:189:TYR:OH	56:RI:231:GLN:O	2.34	0.44
58:RK:196:TYR:HA	58:RK:228:ASP:O	2.18	0.44
62:RP:452:ASN:O	62:RP:456:GLU:N	2.43	0.44
64:RS:392:TYR:HA	64:RS:395:MET:HG2	1.98	0.44
1:3A:2:U:H3	3:SA:1123:C:N4	2.15	0.44
2:5A:281:G:N3	37:B8:558:SER:OG	2.51	0.44
2:5A:354:G:O6	41:5C:485:ASP:N	2.51	0.44
2:5A:411:A:H2'	2:5A:412:A:C8	2.52	0.44
2:5A:550:C:H2'	2:5A:551:A:C8	2.53	0.44
9:SJ:83:TYR:HB3	9:SJ:101:ILE:HD11	1.98	0.44
11:SM:117:VAL:HG13	11:SM:121:ASP:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:SM:123:VAL:HG22	11:SM:142:VAL:HG12	1.99	0.44
32:AF:127:THR:HA	32:AF:144:SER:HA	1.99	0.44
34:B1:223:ARG:HB3	34:B1:249:ARG:HH21	1.81	0.44
37:B8:137:ILE:HG22	37:B8:138:LEU:HD23	1.99	0.44
39:B6:297:ASP:OD1	39:B6:297:ASP:N	2.35	0.44
41:5C:311:SER:O	41:5C:311:SER:OG	2.30	0.44
44:5F:61:LEU:HG	44:5F:75:GLU:HG2	1.98	0.44
52:RC:121:MET:HE2	52:RC:121:MET:HB2	1.91	0.44
54:RF:202:VAL:HG12	54:RF:216:VAL:HG21	2.00	0.44
56:RI:20:LEU:HD13	56:RI:244:VAL:HG12	1.99	0.44
56:RI:216:ILE:O	56:RI:220:ILE:HG12	2.18	0.44
59:RL:122:CYS:HB3	59:RL:148:VAL:HG23	1.98	0.44
59:RM:27:VAL:HA	59:RM:150:ILE:O	2.18	0.44
2:5A:264:C:H2'	2:5A:265:A:H8	1.82	0.44
8:SI:89:HIS:CE1	8:SI:91:ILE:HD11	2.52	0.44
16:ST:41:ARG:HG2	16:ST:85:PHE:HE1	1.83	0.44
16:ST:69:ILE:O	16:ST:73:MET:HG2	2.18	0.44
23:3D:48:ILE:HD13	23:3D:48:ILE:HA	1.89	0.44
25:3F:465:GLN:HG2	26:3H:6:PRO:HG3	1.98	0.44
26:3H:16:LEU:HD13	26:3H:120:LYS:HE2	1.98	0.44
28:A5:364:THR:HA	32:AF:14:PRO:HB3	1.99	0.44
33:AG:507:MET:HE2	33:AG:507:MET:HB3	1.89	0.44
34:B1:720:ASP:OD1	34:B1:720:ASP:N	2.38	0.44
53:RE:1207:VAL:HB	54:RF:3:ILE:HD11	2.00	0.44
54:RF:160:TYR:HE1	54:RF:163:PRO:HD2	1.83	0.44
55:RG:233:SER:OG	55:RG:234:ALA:N	2.51	0.44
59:RL:130:LEU:HD23	59:RL:130:LEU:HA	1.90	0.44
61:RO:407:ARG:NH2	61:RO:488:PHE:O	2.51	0.44
2:5A:69:U:O4	2:5A:70:A:N6	2.51	0.44
3:SA:422:G:H1'	3:SA:423:G:H5'	1.99	0.44
3:SA:931:C:H5''	4:SC:116:LYS:HB3	1.98	0.44
14:SP:64:ALA:HB3	14:SP:104:ALA:HB3	2.00	0.44
17:SX:83:ILE:HG13	17:SX:122:SER:HB3	1.98	0.44
25:3F:348:LEU:O	25:3F:356:ARG:HA	2.18	0.44
31:AE:95:ASP:HB2	31:AE:131:ASN:HD21	1.83	0.44
31:AE:556:LYS:HE2	31:AE:556:LYS:HB2	1.84	0.44
34:B1:6:LYS:HA	34:B1:6:LYS:HD3	1.80	0.44
34:B1:201:HIS:CE1	38:BE:766:LYS:HB2	2.52	0.44
35:B2:334:SER:OG	35:B2:335:LEU:N	2.49	0.44
37:B8:513:GLN:H	37:B8:513:GLN:HG2	1.60	0.44
43:5E:486:ASN:OD1	43:5E:486:ASN:N	2.45	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:5H:550:LEU:HD23	46:5H:550:LEU:HA	1.85	0.44
47:5I:85:THR:HG21	47:5I:372:VAL:HG21	1.99	0.44
53:RE:1038:GLN:NE2	53:RE:1056:ILE:O	2.44	0.44
56:RI:241:SER:OG	56:RI:242:ILE:N	2.50	0.44
1:3A:115:G:O2'	1:3A:257:A:N3	2.43	0.44
3:SA:413:U:H2'	3:SA:414:C:H6	1.82	0.44
3:SA:642:G:H1'	8:SI:116:ARG:HD2	1.99	0.44
3:SA:861:U:O2'	17:SX:56:HIS:O	2.36	0.44
21:Sd:35:ASP:OD1	21:Sd:35:ASP:N	2.47	0.44
23:3D:12:PRO:HG2	23:3D:151:GLN:HG3	1.99	0.44
26:3G:20:ILE:HD13	26:3G:79:VAL:HG11	1.99	0.44
26:3H:121:ILE:HA	26:3H:124:LEU:HB3	2.00	0.44
27:A4:157:SER:OG	27:A4:195:TRP:NE1	2.50	0.44
28:A5:277:LYS:NZ	28:A5:322:ILE:O	2.50	0.44
29:A8:631:SER:HA	29:A8:634:LEU:HD12	2.00	0.44
33:AG:531:PHE:HD2	33:AG:545:THR:HG23	1.82	0.44
34:B1:713:ASP:N	34:B1:713:ASP:OD1	2.47	0.44
36:B3:9:GLY:HA2	36:B3:643:PHE:O	2.17	0.44
36:B3:111:ASP:OD1	36:B3:111:ASP:N	2.48	0.44
37:B8:280:LYS:HD3	37:B8:280:LYS:HA	1.83	0.44
39:B6:125:SER:HB3	39:B6:128:LYS:HD3	1.99	0.44
50:RA:69:GLN:HG3	50:RA:86:PHE:HB2	1.99	0.44
53:RE:711:PRO:HB2	53:RE:713:LEU:HG	2.00	0.44
63:RQ:284:ARG:HE	63:RQ:284:ARG:HB3	1.59	0.44
2:5A:386:A:H4'	41:5C:224:LEU:HD23	1.98	0.44
3:SA:-5:G:OP1	63:RQ:306:ARG:NH1	2.45	0.44
3:SA:99:C:H2'	3:SA:100:A:C8	2.52	0.44
3:SA:1060:U:H3	3:SA:1061:A:H62	1.65	0.44
3:SA:1511:U:H2'	3:SA:1512:G:C8	2.53	0.44
6:SG:174:LEU:HD23	6:SG:174:LEU:HA	1.89	0.44
21:Sd:27:GLN:HG2	21:Sd:43:ASN:HB3	2.00	0.44
24:3E:170:LEU:HG	24:3E:272:LEU:HD22	1.99	0.44
26:3H:120:LYS:O	26:3H:123:THR:OG1	2.35	0.44
28:A5:503:LYS:HE2	32:AF:504:ILE:HD11	2.00	0.44
31:AE:671:LEU:O	31:AE:675:ASN:HB3	2.17	0.44
32:AF:75:LYS:HD3	32:AF:113:PRO:HD3	1.99	0.44
33:AG:498:LEU:HA	33:AG:508:ILE:O	2.18	0.44
35:B2:291:GLU:HA	35:B2:294:ARG:HG2	2.00	0.44
36:B3:260:THR:HG22	36:B3:269:LEU:HD13	2.00	0.44
37:B8:426:VAL:HG21	37:B8:455:ILE:HG21	1.98	0.44
38:BE:489:MET:HE3	38:BE:489:MET:HB3	1.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:5C:84:PHE:HA	41:5C:369:MET:HA	2.00	0.44
47:5I:456:GLU:HA	47:5I:459:LYS:HE2	2.00	0.44
53:RE:200:GLY:HA2	53:RE:289:ARG:HB2	1.99	0.44
54:RF:52:CYS:HA	54:RF:127:LYS:HA	2.00	0.44
62:RP:998:THR:O	62:RP:1002:ASN:CB	2.65	0.44
3:SA:115:G:H5'	11:SM:129:ARG:HG3	2.00	0.43
5:SF:131:LEU:HD11	5:SF:135:GLY:HA2	2.00	0.43
5:SF:180:LEU:N	5:SF:229:GLY:O	2.47	0.43
6:SG:125:THR:O	6:SG:125:THR:OG1	2.34	0.43
23:3D:194:ARG:HA	23:3D:194:ARG:HD3	1.81	0.43
25:3F:421:ASN:HA	25:3F:436:GLU:O	2.18	0.43
28:A5:210:ARG:NH1	38:BE:563:ASP:OD2	2.51	0.43
29:A8:638:LEU:HD21	29:A8:658:LEU:HD21	2.00	0.43
31:AE:306:LEU:O	31:AE:346:LYS:NZ	2.41	0.43
32:AF:259:ASP:N	32:AF:259:ASP:OD1	2.49	0.43
33:AG:210:HIS:NE2	33:AG:226:SER:OG	2.51	0.43
33:AG:347:LEU:HD22	33:AG:355:SER:HB3	2.00	0.43
34:B1:493:TRP:HA	34:B1:517:ASP:HB2	1.99	0.43
34:B1:495:LYS:HD3	34:B1:516:SER:HA	1.99	0.43
35:B2:288:LYS:HD2	35:B2:288:LYS:HA	1.84	0.43
38:BE:523:ASP:OD1	38:BE:523:ASP:N	2.50	0.43
38:BE:854:SER:O	38:BE:854:SER:OG	2.33	0.43
42:5D:123:LYS:HE3	42:5D:123:LYS:HB3	1.85	0.43
45:5G:9:ARG:HH21	45:5G:159:HIS:CD2	2.36	0.43
47:5I:449:LYS:HD3	47:5I:449:LYS:HA	1.80	0.43
57:RJ:1080:LYS:HA	57:RJ:1080:LYS:HD2	1.73	0.43
58:RK:190:SER:OG	58:RK:222:GLU:O	2.32	0.43
60:RN:600:LEU:O	60:RN:675:TYR:OH	2.35	0.43
3:SA:58:U:O2'	3:SA:456:A:O2'	2.29	0.43
7:SH:102:VAL:HG21	7:SH:109:LEU:HD21	2.00	0.43
10:SK:151:ASP:N	10:SK:151:ASP:OD1	2.51	0.43
26:3G:105:ASN:HB3	26:3G:108:SER:HB3	2.00	0.43
33:AG:90:LYS:HB3	33:AG:110:PHE:HB2	2.00	0.43
33:AG:544:LYS:HA	33:AG:544:LYS:HD3	1.76	0.43
35:B2:397:ILE:HA	35:B2:406:LEU:O	2.17	0.43
36:B3:359:SER:OG	36:B3:361:SER:O	2.35	0.43
37:B8:22:LEU:HG	39:B6:66:LEU:HB2	1.99	0.43
38:BE:482:GLY:HA2	38:BE:505:VAL:HG23	1.98	0.43
45:5G:183:SER:HB3	45:5G:220:ARG:HG3	2.00	0.43
49:5K:72:ILE:HD11	49:5K:98:ILE:HD11	1.99	0.43
1:3A:198:U:H3	1:3A:200:C:H5	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:423:G:O2'	3:SA:425:A:OP1	2.35	0.43
24:3E:355:ASN:OD1	24:3E:355:ASN:N	2.50	0.43
27:A4:52:SER:HA	27:A4:104:TRP:CG	2.53	0.43
33:AG:223:LYS:HE2	33:AG:241:LEU:HD21	2.00	0.43
33:AG:584:PHE:HD2	33:AG:597:LYS:HB2	1.82	0.43
35:B2:281:ILE:HB	35:B2:332:ILE:HG23	2.00	0.43
35:B2:914:LEU:HD13	65:RT:258:LYS:HB2	1.99	0.43
36:B3:387:HIS:HE1	36:B3:405:THR:HG23	1.84	0.43
38:BE:370:SER:OG	38:BE:372:ASP:OD1	2.26	0.43
39:B6:169:GLN:HG2	63:RQ:338:LEU:HD22	1.99	0.43
55:RG:51:GLU:OE2	55:RG:82:ARG:NH1	2.51	0.43
60:RN:623:ASP:O	60:RN:627:HIS:CB	2.64	0.43
60:RN:752:MET:HE3	60:RN:752:MET:HB2	1.83	0.43
2:5A:6:A:N6	2:5A:8:A:N3	2.65	0.43
3:SA:147:A:N7	3:SA:168:A:N6	2.66	0.43
3:SA:1755:A:N6	43:5E:506:GLU:O	2.50	0.43
5:SF:19:LEU:HB2	5:SF:51:ARG:NH2	2.33	0.43
8:SI:28:GLU:OE1	8:SI:39:ARG:NH2	2.51	0.43
17:SX:71:LYS:HE2	17:SX:71:LYS:HB2	1.81	0.43
23:3D:199:TYR:OH	23:3D:268:MET:SD	2.71	0.43
27:A4:313:LYS:NZ	33:AG:269:GLN:OE1	2.41	0.43
27:A4:442:VAL:O	27:A4:448:THR:OG1	2.26	0.43
31:AE:717:GLU:HA	31:AE:720:LEU:HB2	2.01	0.43
32:AF:82:ASP:HB3	32:AF:101:ALA:HB3	2.01	0.43
33:AG:31:ASN:OD1	33:AG:31:ASN:N	2.46	0.43
33:AG:677:THR:OG1	33:AG:678:LEU:N	2.51	0.43
36:B3:294:LEU:HB2	36:B3:303:PHE:HB2	2.01	0.43
36:B3:792:HIS:HD2	36:B3:795:ARG:HH12	1.66	0.43
39:B6:15:MET:SD	39:B6:33:MET:HE2	2.59	0.43
47:5I:92:ILE:HG22	47:5I:113:VAL:HG11	2.00	0.43
47:5I:238:THR:O	47:5I:238:THR:OG1	2.35	0.43
47:5I:339:SER:OG	47:5I:340:ARG:N	2.51	0.43
47:5I:411:LYS:O	47:5I:415:ARG:HB2	2.18	0.43
53:RE:780:GLN:O	53:RE:851:LYS:N	2.40	0.43
55:RH:177:LYS:HB3	55:RH:205:PHE:HE1	1.83	0.43
57:RJ:138:VAL:HB	57:RJ:167:VAL:HG22	1.99	0.43
57:RJ:265:ILE:HD13	57:RJ:265:ILE:HA	1.91	0.43
57:RJ:303:LYS:HE2	57:RJ:787:SER:HB3	1.99	0.43
59:RL:56:LEU:HD12	59:RL:104:ARG:HB3	2.00	0.43
60:RN:482:GLN:HE21	61:RO:507:LEU:HD12	1.83	0.43
61:RO:462:SER:OG	61:RO:463:LEU:N	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:RP:378:HIS:O	62:RP:382:PHE:CB	2.66	0.43
66:RV:203:ILE:HG22	66:RV:204:GLY:H	1.83	0.43
3:SA:576:G:OP2	57:RJ:873:LYS:NZ	2.33	0.43
3:SA:1518:C:N4	56:RI:137:GLU:O	2.50	0.43
4:SC:174:LYS:HE3	4:SC:174:LYS:HB3	1.93	0.43
8:SI:123:ASP:OD2	8:SI:138:LYS:NZ	2.42	0.43
13:SO:43:LYS:HE3	13:SO:43:LYS:HB2	1.88	0.43
18:SY:47:SER:OG	18:SY:48:HIS:N	2.50	0.43
22:3B:122:ARG:HG2	22:3B:142:ARG:HG3	1.99	0.43
22:3B:123:ILE:HG12	48:5J:152:ILE:HG12	2.00	0.43
27:A4:394:TRP:HB3	27:A4:399:VAL:HG12	1.99	0.43
28:A5:90:VAL:HG23	28:A5:91:LEU:HD22	1.99	0.43
28:A5:503:LYS:HE2	28:A5:503:LYS:HB3	1.79	0.43
31:AE:764:ASN:O	31:AE:768:LYS:CB	2.65	0.43
32:AF:255:VAL:HA	32:AF:276:SER:HA	2.01	0.43
32:AF:256:THR:HG21	32:AF:303:LEU:HD12	2.00	0.43
33:AG:656:ASP:OD1	33:AG:656:ASP:N	2.48	0.43
35:B2:414:LEU:HD22	35:B2:428:PHE:CD2	2.53	0.43
35:B2:565:PHE:HE1	35:B2:568:SER:HB3	1.83	0.43
36:B3:469:PRO:HB2	36:B3:475:MET:HG3	1.99	0.43
37:B8:137:ILE:HD13	37:B8:137:ILE:HA	1.80	0.43
37:B8:264:LEU:HD11	37:B8:272:LEU:HD12	2.01	0.43
41:5C:491:LYS:HD3	41:5C:491:LYS:HA	1.75	0.43
41:5C:540:GLU:O	41:5C:542:HIS:ND1	2.42	0.43
47:5I:272:MET:HE3	47:5I:272:MET:HB3	1.88	0.43
50:RA:290:VAL:HG22	50:RA:299:ILE:HB	2.00	0.43
52:RC:158:LEU:HD21	66:RV:166:SER:HB2	2.00	0.43
53:RE:110:LEU:HD21	53:RE:368:LEU:HD23	1.99	0.43
53:RE:840:LEU:HD23	53:RE:852:PHE:HB2	2.00	0.43
55:RG:99:LEU:HD13	55:RG:130:ILE:HD13	1.99	0.43
55:RG:180:LEU:HD13	55:RG:180:LEU:HA	1.89	0.43
56:RI:91:GLU:H	56:RI:94:SER:HB2	1.84	0.43
58:RK:118:PHE:O	58:RK:165:GLU:HA	2.18	0.43
59:RL:44:MET:HE2	59:RL:121:MET:HE2	2.00	0.43
61:RO:214:LYS:HA	61:RO:268:GLN:HE21	1.84	0.43
64:RS:266:PHE:O	64:RS:270:LEU:HB2	2.18	0.43
65:RT:96:SER:HA	65:RT:139:LEU:O	2.19	0.43
3:SA:1210:C:H2'	3:SA:1211:A:C8	2.54	0.43
9:SJ:100:ALA:O	9:SJ:168:CYS:HA	2.18	0.43
9:SJ:101:ILE:HA	9:SJ:167:ALA:O	2.19	0.43
11:SM:57:LYS:O	11:SM:138:ASN:ND2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:SN:59:LEU:O	12:SN:122:VAL:HA	2.18	0.43
25:3F:145:ALA:HB2	25:3F:568:ILE:HD13	1.99	0.43
27:A4:744:VAL:HG12	27:A4:754:ILE:HG23	2.00	0.43
30:A9:504:GLU:HA	30:A9:507:ARG:HG2	2.00	0.43
33:AG:404:SER:OG	33:AG:405:ALA:N	2.51	0.43
36:B3:534:ARG:O	36:B3:552:SER:OG	2.34	0.43
38:BE:20:ASN:ND2	38:BE:21:SER:O	2.51	0.43
38:BE:21:SER:HB2	38:BE:623:ILE:HG12	2.00	0.43
41:5C:69:GLU:OE2	47:5I:13:TYR:OH	2.25	0.43
42:5D:70:ARG:HD3	42:5D:78:LEU:HD11	2.00	0.43
47:5I:369:ASP:OD1	47:5I:369:ASP:N	2.48	0.43
47:5I:450:ASP:OD1	47:5I:450:ASP:N	2.49	0.43
55:RH:129:ARG:HA	55:RH:129:ARG:HD2	1.79	0.43
56:RI:115:LEU:HA	56:RI:115:LEU:HD23	1.84	0.43
2:5A:20:C:H2'	2:5A:21:A:H8	1.84	0.43
3:SA:29:U:H2'	3:SA:30:G:H8	1.83	0.43
3:SA:900:A:OP1	14:SP:43:THR:OG1	2.30	0.43
3:SA:1234:A:H1'	3:SA:1235:C:H5	1.84	0.43
24:3E:248:THR:OG1	24:3E:251:ASP:OD2	2.37	0.43
24:3E:302:HIS:CD2	24:3E:320:LEU:HG	2.54	0.43
27:A4:382:VAL:HG22	27:A4:393:SER:HB2	2.00	0.43
32:AF:439:LEU:HD23	32:AF:439:LEU:HA	1.88	0.43
33:AG:390:PRO:HB2	33:AG:438:THR:HG21	1.99	0.43
34:B1:273:ARG:NH2	34:B1:288:ASP:OD1	2.51	0.43
36:B3:290:ILE:HD13	36:B3:304:LEU:HD22	2.00	0.43
38:BE:360:ASP:N	38:BE:360:ASP:OD1	2.49	0.43
38:BE:564:ASP:OD1	38:BE:564:ASP:N	2.48	0.43
47:5I:191:ASN:O	47:5I:193:THR:OG1	2.36	0.43
48:5J:213:ARG:HH21	57:RJ:997:MET:HB3	1.84	0.43
53:RE:465:PRO:HB2	53:RE:477:LEU:HB3	2.00	0.43
53:RE:834:ASN:OD1	53:RE:834:ASN:N	2.51	0.43
57:RJ:59:VAL:HG13	57:RJ:758:ILE:HD11	2.00	0.43
61:RO:205:ASP:O	61:RO:209:GLN:N	2.40	0.43
64:RS:359:LEU:HA	64:RS:362:LEU:HD12	2.00	0.43
65:RT:107:THR:O	65:RT:111:ASN:ND2	2.52	0.43
2:5A:64:U:H4'	33:AG:166:ASN:HA	2.01	0.43
2:5A:375:C:H5''	63:RQ:834:LYS:HG3	2.01	0.43
2:5A:547:C:H2'	2:5A:548:A:C8	2.54	0.43
23:3D:31:LEU:HD21	47:5I:59:VAL:HG13	2.01	0.43
25:3F:156:ASN:HD21	25:3F:546:GLU:HB2	1.83	0.43
26:3G:33:LEU:HD11	26:3G:35:LYS:HE3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A4:166:VAL:HG22	27:A4:182:ILE:HG12	2.00	0.43
27:A4:612:THR:O	27:A4:615:SER:OG	2.31	0.43
28:A5:492:THR:OG1	28:A5:533:ARG:NH1	2.52	0.43
30:A9:450:ASN:O	30:A9:454:LEU:CB	2.67	0.43
34:B1:418:ARG:HH22	43:5E:491:ALA:HA	1.84	0.43
35:B2:140:SER:OG	35:B2:142:ASP:OD1	2.36	0.43
36:B3:567:VAL:HG23	36:B3:568:MET:HG2	1.99	0.43
45:5G:88:ILE:HG12	45:5G:138:ASP:HB2	1.99	0.43
45:5G:156:HIS:HB3	45:5G:161:PRO:HD2	2.00	0.43
50:RA:237:ARG:NE	50:RA:239:ASP:OD2	2.49	0.43
53:RE:197:GLN:NE2	53:RE:371:GLN:OE1	2.52	0.43
61:RO:384:ALA:HA	61:RO:387:THR:HG22	2.00	0.43
64:RS:369:THR:HG21	64:RS:417:TRP:CD1	2.53	0.43
1:3A:2:U:H3	3:SA:1123:C:H42	1.66	0.43
2:5A:296:C:O2'	38:BE:68:LEU:O	2.24	0.43
3:SA:243:G:H2'	3:SA:244:A:H8	1.84	0.43
5:SF:207:LEU:HD13	5:SF:220:THR:H	1.82	0.43
25:3F:123:GLU:HA	25:3F:125:VAL:HG23	2.01	0.43
25:3F:417:SER:HB2	25:3F:421:ASN:HB2	1.99	0.43
25:3F:467:LYS:HB3	25:3F:467:LYS:HE2	1.84	0.43
25:3F:552:TRP:NE1	26:3H:93:VAL:O	2.47	0.43
27:A4:183:LEU:HD22	27:A4:223:GLY:HA2	2.00	0.43
31:AE:795:LEU:HA	31:AE:796:PRO:HD3	1.89	0.43
33:AG:319:LYS:HD2	33:AG:339:GLY:N	2.34	0.43
36:B3:534:ARG:HH11	36:B3:535:GLY:H	1.67	0.43
37:B8:581:ASN:OD1	37:B8:581:ASN:N	2.49	0.43
38:BE:118:VAL:HA	38:BE:132:THR:HA	2.00	0.43
39:B6:57:ILE:HG23	39:B6:92:ILE:HG23	2.00	0.43
54:RF:53:LEU:HD12	54:RF:128:PHE:HE1	1.84	0.43
57:RJ:1158:LYS:HB2	57:RJ:1158:LYS:HE3	1.75	0.43
59:RM:739:ASN:O	59:RM:743:VAL:CB	2.67	0.43
61:RO:189:ALA:HA	61:RO:192:GLN:HE21	1.84	0.43
3:SA:90:C:H2'	3:SA:91:G:H8	1.83	0.43
3:SA:325:G:H2'	3:SA:326:G:C8	2.54	0.43
3:SA:1194:A:N6	55:RG:129:ARG:O	2.37	0.43
16:ST:52:VAL:HG11	16:ST:69:ILE:HD11	2.01	0.43
22:3B:134:VAL:HA	22:3B:135:PRO:HD3	1.85	0.43
27:A4:340:GLN:HG3	27:A4:345:ASP:HB3	2.01	0.43
27:A4:487:VAL:HA	27:A4:496:PHE:O	2.18	0.43
27:A4:642:ASN:HD21	27:A4:659:PHE:HE1	1.67	0.43
28:A5:308:ASN:HB2	28:A5:311:MET:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:AE:8:LEU:HD23	31:AE:8:LEU:HA	1.83	0.43
31:AE:16:ALA:O	31:AE:24:ARG:NH2	2.52	0.43
31:AE:366:ILE:HA	31:AE:369:LEU:HG	2.01	0.43
33:AG:41:GLN:H	33:AG:41:GLN:HG2	1.61	0.43
35:B2:275:GLN:HE22	35:B2:340:SER:HA	1.83	0.43
35:B2:398:ASP:HB2	35:B2:406:LEU:HB3	2.00	0.43
36:B3:245:SER:O	36:B3:245:SER:OG	2.29	0.43
50:RA:247:THR:OG1	50:RA:248:SER:N	2.51	0.43
52:RC:281:LEU:HA	52:RC:284:GLN:HG3	2.01	0.43
53:RE:527:TYR:O	53:RE:614:ARG:HA	2.19	0.43
59:RL:73:ARG:HH21	59:RL:99:SER:HA	1.84	0.43
60:RN:702:LEU:HG	61:RO:485:ALA:HB2	2.01	0.43
2:5A:446:U:H5'	57:RJ:1118:THR:HB	2.01	0.42
3:SA:123:G:H21	5:SF:146:THR:HG21	1.84	0.42
3:SA:1768:G:H1'	3:SA:1769:U:H5	1.83	0.42
7:SH:14:LYS:HE2	7:SH:14:LYS:HB3	1.85	0.42
8:SI:155:ASP:OD1	8:SI:155:ASP:N	2.52	0.42
15:SR:97:VAL:HG12	15:SR:98:ASP:H	1.84	0.42
23:3D:183:GLN:HE21	24:3E:183:ARG:HH22	1.67	0.42
23:3D:307:ILE:HD13	23:3D:379:LEU:HD11	2.00	0.42
27:A4:438:GLN:HE21	27:A4:452:HIS:CE1	2.37	0.42
32:AF:256:THR:N	32:AF:275:SER:O	2.52	0.42
32:AF:450:ILE:HD12	32:AF:450:ILE:HA	1.91	0.42
33:AG:227:VAL:O	33:AG:236:ASN:HA	2.19	0.42
33:AG:634:ASP:OD1	33:AG:638:PHE:N	2.52	0.42
34:B1:443:GLU:HG2	34:B1:444:VAL:HG23	2.01	0.42
34:B1:779:LEU:HD23	34:B1:779:LEU:HA	1.86	0.42
36:B3:160:ILE:HG23	36:B3:227:MET:HE1	2.01	0.42
36:B3:250:LYS:HD3	36:B3:250:LYS:HA	1.89	0.42
37:B8:321:MET:HE1	37:B8:375:VAL:HG21	1.99	0.42
38:BE:743:ARG:HD3	43:5E:474:ILE:O	2.19	0.42
39:B6:63:VAL:HG13	39:B6:88:ILE:HD11	2.00	0.42
39:B6:187:LYS:O	39:B6:191:ASN:ND2	2.31	0.42
44:5F:66:PRO:HG3	66:RV:207:ARG:NH1	2.33	0.42
53:RE:529:VAL:HB	53:RE:613:VAL:HB	2.01	0.42
53:RE:563:ALA:HB1	53:RE:583:ILE:HD12	2.01	0.42
53:RE:1109:LYS:HD2	53:RE:1170:GLY:HA3	2.01	0.42
55:RG:173:THR:OG1	55:RG:174:LYS:N	2.52	0.42
58:RK:206:ASN:HA	58:RK:209:ILE:HG12	2.01	0.42
58:RK:245:LEU:HB3	58:RK:279:LEU:HD22	2.00	0.42
60:RN:640:MET:HE2	60:RN:680:LYS:HE3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3A:8:U:H2'	1:3A:9:A:C8	2.54	0.42
2:5A:207:G:H2'	2:5A:208:A:C8	2.53	0.42
3:SA:32:U:O2'	3:SA:594:A:N1	2.50	0.42
5:SF:31:PRO:HA	5:SF:81:THR:HB	2.00	0.42
22:3B:151:LEU:HD13	22:3B:241:PHE:HE2	1.84	0.42
22:3B:198:GLU:O	22:3B:221:ILE:HA	2.18	0.42
31:AE:40:ALA:HB1	31:AE:123:ARG:HH12	1.84	0.42
31:AE:328:ASP:O	31:AE:331:SER:OG	2.32	0.42
31:AE:540:LYS:HE3	31:AE:540:LYS:HB2	1.80	0.42
32:AF:319:VAL:HG13	32:AF:329:ILE:HG12	2.01	0.42
32:AF:332:LYS:HE3	32:AF:332:LYS:HB2	1.85	0.42
32:AF:435:ASP:N	32:AF:435:ASP:OD1	2.52	0.42
33:AG:29:THR:OG1	33:AG:30:GLY:N	2.52	0.42
33:AG:39:GLN:HG2	33:AG:40:ASP:H	1.84	0.42
33:AG:174:TYR:HB3	33:AG:187:VAL:HB	2.01	0.42
34:B1:821:MET:HB3	34:B1:821:MET:HE3	1.82	0.42
35:B2:183:ASP:OD1	35:B2:183:ASP:N	2.40	0.42
36:B3:356:ALA:HB2	36:B3:394:LEU:HD23	2.01	0.42
36:B3:441:GLY:H	36:B3:497:LEU:HD22	1.83	0.42
36:B3:778:MET:HE2	36:B3:778:MET:HB2	1.77	0.42
54:RF:224:ASN:OD1	54:RF:228:LYS:NZ	2.50	0.42
3:SA:460:A:H3'	3:SA:461:G:H8	1.84	0.42
4:SC:181:LEU:HA	4:SC:181:LEU:HD23	1.86	0.42
22:3C:205:ARG:HE	24:3E:152:LEU:HG	1.83	0.42
24:3E:373:TYR:HA	26:3G:62:GLU:HB3	2.01	0.42
27:A4:616:LYS:HG3	31:AE:627:LEU:HD21	2.01	0.42
34:B1:300:MET:HE2	34:B1:300:MET:HB3	1.71	0.42
36:B3:343:MET:O	36:B3:344:ARG:NH1	2.41	0.42
38:BE:332:SER:OG	38:BE:333:GLY:N	2.51	0.42
38:BE:847:LEU:HD13	65:RT:269:ARG:HB2	2.01	0.42
41:5C:197:ASP:HB2	41:5C:238:MET:HE3	2.02	0.42
41:5C:230:THR:HG22	41:5C:232:ALA:H	1.84	0.42
48:5J:119:ARG:NH1	57:RJ:1106:GLU:OE1	2.53	0.42
48:5J:207:LYS:HB3	48:5J:207:LYS:HE2	1.68	0.42
53:RE:209:MET:HB2	53:RE:299:PRO:HD3	2.01	0.42
56:RI:74:LEU:HB3	56:RI:100:ILE:HG12	2.01	0.42
57:RJ:1025:GLU:OE1	57:RJ:1025:GLU:N	2.52	0.42
60:RN:640:MET:HE2	60:RN:640:MET:HB3	1.76	0.42
2:5A:130:G:H2'	2:5A:131:C:C6	2.54	0.42
2:5A:426:G:C2	2:5A:428:A:H5''	2.54	0.42
3:SA:1151:A:H2'	3:SA:1152:A:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:3E:256:ASN:HD22	24:3E:256:ASN:HA	1.70	0.42
24:3E:326:LEU:HD12	24:3E:336:THR:HB	2.00	0.42
25:3F:242:VAL:HG23	25:3F:253:THR:HB	2.01	0.42
28:A5:364:THR:OG1	28:A5:368:ASN:OD1	2.32	0.42
28:A5:441:LEU:HD11	28:A5:480:LEU:HD13	2.01	0.42
30:A9:435:LEU:HD13	30:A9:478:ASN:HD21	1.84	0.42
32:AF:134:THR:OG1	32:AF:135:GLN:OE1	2.37	0.42
32:AF:147:ARG:HG2	32:AF:170:TYR:H	1.83	0.42
33:AG:440:VAL:HG11	33:AG:449:LEU:HD12	2.02	0.42
36:B3:174:VAL:HG11	36:B3:225:PHE:CZ	2.55	0.42
36:B3:581:CYS:HB3	36:B3:591:ILE:HG22	2.00	0.42
42:5D:145:GLU:OE1	42:5D:147:THR:N	2.53	0.42
43:5E:330:VAL:HG21	57:RJ:932:LEU:HD12	2.01	0.42
48:5J:119:ARG:HD3	57:RJ:1113:ILE:HG13	2.01	0.42
57:RJ:552:LEU:HD21	57:RJ:566:ARG:HH11	1.85	0.42
59:RL:280:ALA:HA	59:RL:464:GLN:HA	2.01	0.42
2:5A:190:U:H3	2:5A:207:G:H1	1.67	0.42
3:SA:1736:G:H2'	3:SA:1737:G:H8	1.84	0.42
5:SF:18:TRP:NE1	5:SF:41:SER:O	2.51	0.42
17:SX:32:LYS:HE3	17:SX:32:LYS:HB2	1.78	0.42
17:SX:111:MET:HE3	17:SX:111:MET:HB2	1.83	0.42
19:SZ:72:PHE:HZ	51:RB:290:GLU:HG3	1.85	0.42
22:3C:103:GLU:HA	42:5D:194:LYS:HE3	2.01	0.42
23:3D:169:LYS:HA	23:3D:299:VAL:HG22	2.02	0.42
24:3E:183:ARG:HA	24:3E:186:GLU:HG2	2.01	0.42
25:3F:289:ARG:HG3	25:3F:292:SER:HB2	2.01	0.42
26:3G:5:ASN:HA	26:3G:6:PRO:HD3	1.88	0.42
28:A5:336:ASN:OD1	28:A5:336:ASN:N	2.53	0.42
34:B1:205:LYS:HG2	34:B1:219:GLU:HG2	2.00	0.42
35:B2:840:MET:HE2	35:B2:846:LEU:HD13	2.02	0.42
36:B3:171:MET:HE3	36:B3:171:MET:HB2	1.88	0.42
36:B3:362:LEU:HD22	36:B3:391:LEU:HD21	2.00	0.42
42:5D:218:MET:HB2	42:5D:218:MET:HE3	1.77	0.42
47:5I:226:LYS:HD2	47:5I:226:LYS:HA	1.88	0.42
49:5K:171:PRO:HA	49:5K:184:LYS:HB2	2.01	0.42
51:RB:312:GLU:HG3	51:RB:316:ARG:HH12	1.85	0.42
53:RE:361:GLU:HG3	53:RE:418:SER:HB3	2.00	0.42
53:RE:416:PHE:CD1	53:RE:420:GLN:HB2	2.55	0.42
53:RE:597:ARG:H	53:RE:597:ARG:HG2	1.48	0.42
53:RE:1100:VAL:HB	53:RE:1182:ILE:HB	2.01	0.42
54:RF:15:VAL:HG12	54:RF:17:PRO:HD3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:RN:804:LYS:HA	60:RN:804:LYS:HD3	1.81	0.42
64:RS:305:ARG:HA	64:RS:305:ARG:HD3	1.91	0.42
2:5A:255:U:H5'	56:RI:166:GLN:HA	2.00	0.42
3:SA:397:A:OP2	9:SJ:47:ARG:NH2	2.52	0.42
3:SA:400:A:H61	9:SJ:29:LEU:HA	1.85	0.42
3:SA:625:C:H2'	3:SA:626:U:C6	2.54	0.42
7:SH:32:ILE:HD13	7:SH:65:GLN:HA	2.02	0.42
20:Sc:78:SER:HB3	54:RF:212:PHE:HB3	2.01	0.42
22:3B:259:MET:HE3	22:3B:259:MET:HB3	1.72	0.42
25:3F:253:THR:HG22	25:3F:263:TRP:HE1	1.84	0.42
26:3H:16:LEU:HD21	26:3H:121:ILE:HG22	2.02	0.42
27:A4:249:ARG:HB2	27:A4:292:ASN:HD22	1.84	0.42
29:A8:566:LEU:HD23	29:A8:586:ILE:HB	2.02	0.42
31:AE:685:SER:O	31:AE:685:SER:OG	2.33	0.42
32:AF:62:ARG:HA	32:AF:77:PHE:O	2.19	0.42
32:AF:188:SER:OG	32:AF:194:ARG:NH2	2.44	0.42
33:AG:172:ARG:HD3	33:AG:174:TYR:CZ	2.54	0.42
33:AG:445:ILE:HG12	33:AG:504:GLY:HA3	2.01	0.42
34:B1:650:ASN:HD22	34:B1:650:ASN:HA	1.69	0.42
36:B3:599:ILE:HG22	36:B3:611:LYS:HB3	2.02	0.42
38:BE:235:MET:HE3	38:BE:235:MET:HB3	1.78	0.42
38:BE:847:LEU:HG	65:RT:242:MET:HE3	2.01	0.42
41:5C:63:THR:O	41:5C:66:LEU:N	2.50	0.42
45:5G:286:LYS:HG2	60:RN:771:ASN:ND2	2.35	0.42
53:RE:807:LEU:HD23	53:RE:807:LEU:HA	1.88	0.42
55:RG:167:ILE:HG21	55:RG:205:PHE:HZ	1.85	0.42
60:RN:669:SER:HA	60:RN:672:THR:HG22	2.00	0.42
63:RQ:865:ILE:HG22	63:RQ:878:LEU:HD13	2.02	0.42
64:RS:267:VAL:HG11	64:RS:312:TYR:HB3	2.01	0.42
1:3A:27:U:H4'	1:3A:28:A:C8	2.55	0.42
2:5A:21:A:H2'	2:5A:22:A:C8	2.55	0.42
3:SA:966:A:OP2	13:SO:124:ARG:NH1	2.52	0.42
3:SA:1226:A:H5''	12:SN:116:VAL:HG13	2.01	0.42
6:SG:99:MET:HE3	6:SG:99:MET:HB2	1.66	0.42
18:SY:78:LYS:O	57:RJ:749:THR:OG1	2.35	0.42
22:3C:294:ARG:HE	40:5B:181:LEU:HD23	1.84	0.42
24:3E:113:THR:HA	24:3E:116:ILE:HG12	2.02	0.42
24:3E:191:HIS:CD2	24:3E:247:ILE:HG12	2.55	0.42
25:3F:363:ASP:OD1	25:3F:363:ASP:N	2.45	0.42
25:3F:398:CYS:SG	26:3H:18:GLN:HG2	2.59	0.42
28:A5:150:LYS:HA	28:A5:150:LYS:HD3	1.91	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:A5:344:ASP:OD1	28:A5:344:ASP:N	2.53	0.42
33:AG:877:ASP:OD1	33:AG:877:ASP:N	2.53	0.42
34:B1:210:SER:OG	34:B1:212:ASP:OD1	2.37	0.42
35:B2:756:LEU:HD23	35:B2:756:LEU:HA	1.91	0.42
35:B2:822:MET:HE3	35:B2:859:PHE:HZ	1.84	0.42
36:B3:133:ASN:OD1	36:B3:133:ASN:N	2.53	0.42
36:B3:264:ASP:HB3	36:B3:266:ILE:HG12	2.00	0.42
36:B3:311:LEU:N	36:B3:334:ALA:O	2.45	0.42
36:B3:625:THR:HA	36:B3:633:VAL:HG22	2.02	0.42
36:B3:771:LYS:HE2	36:B3:771:LYS:HB3	1.80	0.42
37:B8:386:ILE:HD13	37:B8:437:LEU:HD13	2.02	0.42
39:B6:45:SER:OG	39:B6:46:ARG:O	2.37	0.42
40:5B:186:ASP:HA	40:5B:189:THR:HG22	2.00	0.42
47:5I:280:ALA:HB2	47:5I:311:VAL:HB	2.02	0.42
48:5J:172:THR:HB	48:5J:175:GLU:HG2	2.01	0.42
49:5K:79:LYS:NZ	66:RV:308:ILE:O	2.35	0.42
51:RB:265:ASP:OD1	51:RB:265:ASP:N	2.41	0.42
3:SA:260:U:OP2	9:SJ:41:LYS:NZ	2.34	0.42
3:SA:496:G:OP2	57:RJ:1135:ARG:NH2	2.36	0.42
3:SA:871:G:H2'	3:SA:872:G:C8	2.54	0.42
3:SA:1690:G:H21	3:SA:1712:A:H62	1.68	0.42
15:SR:68:ARG:HE	15:SR:68:ARG:HB3	1.70	0.42
16:ST:24:GLY:HA2	16:ST:58:ALA:HB3	2.02	0.42
20:Sc:33:LEU:HD12	20:Sc:79:PHE:HB2	2.00	0.42
22:3C:114:GLY:N	22:3C:140:GLU:OE1	2.52	0.42
24:3E:315:SER:O	24:3E:319:ILE:HG12	2.20	0.42
26:3H:10:PRO:HD2	26:3H:80:PHE:HD2	1.85	0.42
27:A4:534:LEU:HB3	27:A4:543:ILE:HG22	2.01	0.42
31:AE:219:ASN:HD21	33:AG:872:PHE:C	2.28	0.42
32:AF:123:SER:HB2	32:AF:150:ARG:HH12	1.85	0.42
34:B1:356:ASP:O	34:B1:358:SER:N	2.50	0.42
35:B2:7:ARG:O	35:B2:687:THR:N	2.50	0.42
35:B2:264:ASN:ND2	35:B2:265:SER:O	2.53	0.42
35:B2:537:VAL:HG12	35:B2:548:ILE:HG22	2.01	0.42
37:B8:477:LYS:HA	37:B8:477:LYS:HD3	1.80	0.42
38:BE:517:MET:HE3	38:BE:517:MET:HB2	1.80	0.42
41:5C:137:MET:HA	41:5C:144:LEU:HA	2.01	0.42
41:5C:138:ASP:OD1	41:5C:140:ARG:NH2	2.53	0.42
53:RE:152:PHE:O	53:RE:156:LYS:NZ	2.45	0.42
53:RE:217:LYS:O	53:RE:223:ARG:NH1	2.53	0.42
53:RE:345:TYR:HB3	53:RE:391:PHE:HZ	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:RE:746:LEU:HD21	53:RE:810:ILE:HG12	2.01	0.42
55:RH:39:LYS:NZ	55:RH:200:GLU:O	2.39	0.42
57:RJ:101:ILE:HB	57:RJ:105:ILE:HD11	2.02	0.42
61:RO:472:HIS:CD2	61:RO:474:HIS:H	2.38	0.42
2:5A:21:A:H2'	2:5A:22:A:H8	1.85	0.42
3:SA:629:U:H5''	52:RC:258:ARG:HG3	2.01	0.42
5:SF:20:LEU:HA	5:SF:20:LEU:HD23	1.81	0.42
6:SG:188:LYS:HE3	6:SG:193:THR:HG22	2.01	0.42
8:SI:125:ILE:O	8:SI:129:LEU:HB2	2.20	0.42
19:SZ:28:LEU:HD13	25:3F:315:LEU:HD12	2.01	0.42
25:3F:488:ILE:HB	25:3F:524:ILE:HG21	2.01	0.42
32:AF:413:LEU:HD23	32:AF:413:LEU:HA	1.91	0.42
32:AF:492:ARG:HA	32:AF:492:ARG:HD3	1.79	0.42
34:B1:296:GLN:HG2	38:BE:750:PRO:HB2	2.02	0.42
34:B1:446:CYS:HA	34:B1:456:HIS:O	2.20	0.42
36:B3:122:THR:HA	36:B3:146:THR:HG23	2.01	0.42
36:B3:333:ILE:HG13	36:B3:381:VAL:HG13	2.01	0.42
41:5C:475:ASN:O	41:5C:479:THR:OG1	2.23	0.42
41:5C:504:LYS:HD3	41:5C:504:LYS:HA	1.77	0.42
50:RA:216:SER:HB2	50:RA:218:LEU:HD13	2.01	0.42
53:RE:902:ILE:HD13	53:RE:902:ILE:HA	1.74	0.42
53:RE:933:LEU:HD13	53:RE:1041:VAL:HG11	2.01	0.42
54:RF:41:ARG:HD3	54:RF:138:TRP:CG	2.55	0.42
5:SF:87:MET:HE2	5:SF:87:MET:HB3	1.81	0.42
13:SO:58:HIS:O	13:SO:60:VAL:N	2.47	0.42
19:SZ:20:ARG:HE	19:SZ:20:ARG:HB3	1.66	0.42
25:3F:251:VAL:HG12	25:3F:263:TRP:HB2	2.02	0.42
28:A5:342:ASP:HA	33:AG:60:ARG:HD2	2.02	0.42
29:A8:672:ASN:HB2	30:A9:486:LEU:HD22	2.01	0.42
32:AF:436:GLU:OE1	32:AF:477:SER:OG	2.33	0.42
36:B3:24:THR:HG21	36:B3:69:LEU:HD12	2.02	0.42
36:B3:32:LEU:HA	36:B3:41:ASN:HA	2.01	0.42
50:RA:273:ASP:HB2	50:RA:294:LYS:HE3	2.01	0.42
53:RE:557:THR:OG1	53:RE:558:LEU:N	2.52	0.42
53:RE:858:ARG:HD2	53:RE:861:ILE:HD11	2.02	0.42
57:RJ:794:GLU:OE1	57:RJ:794:GLU:N	2.51	0.42
57:RJ:1108:LYS:HE2	57:RJ:1108:LYS:HB3	1.84	0.42
64:RS:267:VAL:HG21	64:RS:310:SER:HA	2.02	0.42
64:RS:322:LEU:HD21	64:RS:359:LEU:HD11	2.01	0.42
2:5A:84:G:C6	27:A4:774:LEU:HB2	2.55	0.41
3:SA:1663:G:O6	3:SA:1738:U:O4	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:SO:76:LYS:HE2	13:SO:76:LYS:HB3	1.96	0.41
16:ST:80:LYS:HB3	16:ST:80:LYS:HE2	1.88	0.41
22:3C:269:ILE:HG21	22:3C:293:LEU:HD11	2.01	0.41
24:3E:149:ARG:HA	24:3E:149:ARG:HD2	1.86	0.41
25:3F:495:SER:HA	25:3F:514:LEU:O	2.20	0.41
28:A5:22:VAL:HG22	28:A5:27:GLN:HG2	2.02	0.41
31:AE:549:LYS:HD3	31:AE:549:LYS:HA	1.85	0.41
33:AG:20:PRO:HA	33:AG:48:PHE:HA	2.02	0.41
33:AG:319:LYS:HD2	33:AG:339:GLY:H	1.85	0.41
35:B2:817:LEU:HD11	35:B2:856:ASN:HD21	1.85	0.41
37:B8:565:VAL:HG13	37:B8:579:VAL:HG13	2.01	0.41
39:B6:309:LEU:HD12	39:B6:309:LEU:HA	1.83	0.41
46:5H:437:ASP:OD1	46:5H:437:ASP:N	2.53	0.41
49:5K:77:GLN:HG3	66:RV:307:LYS:HB3	2.01	0.41
49:5K:135:THR:O	49:5K:135:THR:OG1	2.29	0.41
50:RA:17:SER:OG	50:RA:338:MET:O	2.31	0.41
57:RJ:191:LYS:HE2	57:RJ:191:LYS:HB3	1.89	0.41
58:RK:134:LYS:HE3	58:RK:134:LYS:HB2	1.89	0.41
59:RM:281:LEU:HA	59:RM:409:ALA:HB3	2.02	0.41
3:SA:608:U:O2'	3:SA:609:U:O4'	2.37	0.41
3:SA:629:U:H2'	3:SA:630:A:H8	1.86	0.41
3:SA:1777:G:H5''	36:B3:139:SER:HB2	2.01	0.41
9:SJ:65:PHE:HA	9:SJ:181:GLY:O	2.20	0.41
15:SR:64:ASP:N	15:SR:64:ASP:OD1	2.53	0.41
25:3F:290:LYS:HA	25:3F:290:LYS:HD3	1.83	0.41
25:3F:397:PHE:HZ	25:3F:472:PRO:HD3	1.85	0.41
28:A5:185:PRO:O	28:A5:215:TYR:OH	2.31	0.41
28:A5:490:ARG:HD3	28:A5:490:ARG:HA	1.83	0.41
31:AE:124:ARG:NH1	31:AE:124:ARG:O	2.53	0.41
31:AE:491:TYR:CZ	31:AE:528:ARG:HG3	2.56	0.41
34:B1:526:ASP:HB3	34:B1:815:TYR:CZ	2.55	0.41
34:B1:636:THR:OG1	34:B1:639:GLY:O	2.38	0.41
37:B8:266:GLY:HA3	37:B8:295:ILE:HD11	2.02	0.41
38:BE:148:LYS:HD3	38:BE:148:LYS:HA	1.87	0.41
38:BE:217:VAL:HG23	38:BE:220:ILE:HB	2.01	0.41
38:BE:611:THR:HB	38:BE:621:ASP:HB3	2.01	0.41
38:BE:632:VAL:HG22	38:BE:643:THR:HG22	2.01	0.41
39:B6:176:PRO:O	39:B6:284:HIS:ND1	2.47	0.41
42:5D:235:ASP:OD1	42:5D:239:LYS:N	2.53	0.41
44:5F:38:ILE:HD11	44:5F:107:CYS:SG	2.60	0.41
50:RA:94:ASP:OD1	50:RA:94:ASP:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:RA:266:LYS:HE3	50:RA:305:GLY:HA3	2.02	0.41
53:RE:1165:SER:OG	53:RE:1166:ARG:N	2.53	0.41
55:RH:155:SER:O	55:RH:155:SER:OG	2.30	0.41
56:RI:222:PHE:HE1	56:RI:228:LYS:HG2	1.84	0.41
57:RJ:358:MET:HE2	57:RJ:804:PHE:HZ	1.85	0.41
57:RJ:774:PRO:HA	57:RJ:777:ARG:HG2	2.02	0.41
61:RO:196:GLN:HG3	61:RO:253:PHE:HE1	1.84	0.41
64:RS:214:TYR:HB3	64:RS:249:THR:HG22	2.02	0.41
1:3A:305:G:H2'	1:3A:306:G:H8	1.85	0.41
2:5A:427:A:H2'	2:5A:428:A:H4'	2.02	0.41
2:5A:508:C:H2'	2:5A:509:A:H8	1.85	0.41
3:SA:1140:G:H2'	3:SA:1141:G:H8	1.85	0.41
3:SA:1202:A:N6	3:SA:1203:A:N1	2.68	0.41
11:SM:109:VAL:HG22	11:SM:137:PHE:HB2	2.02	0.41
15:SR:94:GLN:HB2	15:SR:102:LYS:HE2	2.00	0.41
17:SX:28:ARG:HB3	17:SX:60:LYS:HG2	2.03	0.41
17:SX:44:HIS:HE2	17:SX:112:ASP:CG	2.26	0.41
20:Sc:50:ALA:O	20:Sc:52:THR:N	2.53	0.41
22:3B:144:TRP:CD1	22:3B:152:ALA:HB2	2.55	0.41
22:3B:168:LYS:HA	22:3B:168:LYS:HD2	1.87	0.41
23:3D:27:ILE:H	23:3D:27:ILE:HG13	1.71	0.41
25:3F:199:TYR:HA	25:3F:209:LYS:O	2.19	0.41
25:3F:252:VAL:HG21	25:3F:295:LEU:HD22	2.02	0.41
28:A5:64:LYS:HE2	28:A5:64:LYS:HB2	1.83	0.41
28:A5:225:VAL:O	28:A5:272:SER:HA	2.20	0.41
31:AE:526:LEU:HD13	31:AE:543:SER:HA	2.02	0.41
33:AG:155:THR:O	33:AG:171:TYR:HA	2.20	0.41
33:AG:304:SER:OG	33:AG:344:CYS:O	2.31	0.41
34:B1:176:ASP:OD1	34:B1:176:ASP:N	2.41	0.41
34:B1:385:GLU:HB2	34:B1:414:TRP:HH2	1.85	0.41
36:B3:137:THR:HG23	36:B3:138:HIS:ND1	2.34	0.41
37:B8:440:ASN:O	37:B8:442:HIS:N	2.53	0.41
38:BE:356:ILE:HD13	38:BE:356:ILE:HA	1.93	0.41
41:5C:497:LEU:HD22	41:5C:516:VAL:HG13	2.02	0.41
43:5E:369:ILE:HD13	45:5G:236:HIS:CD2	2.55	0.41
47:5I:66:HIS:O	49:5K:121:ARG:NH2	2.54	0.41
50:RA:139:LYS:HA	50:RA:139:LYS:HD3	1.76	0.41
50:RA:189:ASN:HD21	50:RA:240:GLY:HA2	1.84	0.41
55:RG:215:ASN:HB2	55:RG:218:ASP:HB2	2.02	0.41
55:RH:77:LEU:HD12	55:RH:82:ARG:HB2	2.02	0.41
56:RI:8:ILE:HG12	56:RI:255:TYR:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:RK:117:LEU:HB3	58:RK:167:HIS:CD2	2.55	0.41
3:SA:115:G:O2'	3:SA:116:U:O4'	2.38	0.41
3:SA:328:A:H2'	3:SA:329:G:C8	2.54	0.41
3:SA:1642:G:OP2	43:5E:530:ARG:NH2	2.53	0.41
8:SI:153:LEU:HD23	8:SI:186:PRO:HG3	2.02	0.41
24:3E:176:GLU:HA	24:3E:179:THR:HG22	2.01	0.41
24:3E:281:LYS:HB3	24:3E:281:LYS:HE2	1.73	0.41
25:3F:308:SER:O	25:3F:312:PHE:N	2.54	0.41
27:A4:35:ARG:HH12	27:A4:738:TYR:HA	1.86	0.41
27:A4:470:LEU:HD21	27:A4:498:VAL:HG21	2.02	0.41
31:AE:109:TRP:HB2	31:AE:142:TYR:CZ	2.55	0.41
31:AE:364:ASN:N	31:AE:399:GLN:OE1	2.50	0.41
34:B1:269:HIS:HB2	34:B1:310:VAL:HG11	2.02	0.41
36:B3:40:ILE:HG23	36:B3:52:ILE:HG12	2.03	0.41
36:B3:409:ASP:OD1	36:B3:409:ASP:N	2.53	0.41
38:BE:132:THR:OG1	38:BE:134:ASP:OD1	2.34	0.41
40:5B:194:LYS:HD2	40:5B:199:ILE:HG13	2.02	0.41
41:5C:444:LEU:HD12	41:5C:444:LEU:HA	1.92	0.41
45:5G:128:VAL:HG13	45:5G:157:PHE:HE1	1.86	0.41
50:RA:232:THR:OG1	50:RA:274:ILE:O	2.33	0.41
52:RC:106:ARG:HA	52:RC:106:ARG:HD2	1.79	0.41
53:RE:385:LEU:HD11	53:RE:522:LYS:HE2	2.03	0.41
58:RK:143:LYS:NZ	58:RK:252:LYS:O	2.42	0.41
2:5A:2:U:OP2	33:AG:427:LYS:NZ	2.54	0.41
3:SA:279:G:H1'	3:SA:281:G:H8	1.85	0.41
3:SA:299:A:H2'	3:SA:300:A:H8	1.86	0.41
3:SA:959:U:H5''	13:SO:14:SER:HB2	2.02	0.41
3:SA:1108:G:O2'	3:SA:1109:G:N7	2.50	0.41
24:3E:88:ILE:HA	24:3E:106:ASN:O	2.21	0.41
25:3F:293:ASP:OD2	25:3F:310:ASN:N	2.54	0.41
27:A4:481:ILE:HD11	27:A4:487:VAL:HB	2.02	0.41
28:A5:162:GLN:HA	28:A5:173:ILE:O	2.20	0.41
31:AE:136:LEU:HD21	31:AE:155:ILE:HG12	2.02	0.41
31:AE:200:ILE:HD11	31:AE:245:LEU:HD23	2.02	0.41
31:AE:336:LEU:HD22	31:AE:373:ILE:HG21	2.02	0.41
32:AF:116:ILE:HD11	32:AF:119:SER:HB3	2.01	0.41
32:AF:303:LEU:HD12	32:AF:303:LEU:HA	1.91	0.41
35:B2:26:ILE:HA	35:B2:27:PRO:HD3	1.92	0.41
41:5C:108:LEU:N	41:5C:396:THR:O	2.42	0.41
50:RA:160:ASN:HA	50:RA:178:LEU:HB2	2.00	0.41
53:RE:221:ASN:ND2	53:RE:316:ARG:HH21	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:RE:525:LEU:HD23	53:RE:525:LEU:HA	1.91	0.41
64:RS:243:GLN:HG3	64:RS:277:LYS:HB3	2.02	0.41
3:SA:127:G:H5'	3:SA:204:G:H1'	2.03	0.41
3:SA:683:C:H2'	3:SA:684:A:C8	2.56	0.41
3:SA:688:G:H2'	3:SA:689:G:C8	2.55	0.41
3:SA:956:C:OP1	3:SA:1072:C:O2'	2.36	0.41
4:SC:82:ARG:HD3	4:SC:105:PHE:HE1	1.85	0.41
12:SN:65:SER:O	12:SN:65:SER:OG	2.34	0.41
23:3D:115:TYR:OH	63:RQ:331:GLN:NE2	2.51	0.41
23:3D:161:ALA:HB2	39:B6:293:TYR:HE1	1.86	0.41
27:A4:106:ASN:OD1	27:A4:106:ASN:N	2.54	0.41
27:A4:113:ARG:HD3	27:A4:174:PRO:HA	2.03	0.41
28:A5:262:SER:O	28:A5:262:SER:OG	2.35	0.41
29:A8:635:PHE:HZ	29:A8:665:GLN:HG3	1.86	0.41
29:A8:668:ILE:HA	29:A8:671:ARG:HG3	2.01	0.41
35:B2:100:ASP:OD1	35:B2:100:ASP:N	2.47	0.41
35:B2:281:ILE:HD11	35:B2:355:LEU:HD13	2.01	0.41
35:B2:292:ILE:HG23	35:B2:324:PHE:HE2	1.85	0.41
36:B3:505:ILE:HD12	36:B3:517:ILE:HD11	2.02	0.41
37:B8:208:LEU:HD12	37:B8:208:LEU:HA	1.90	0.41
43:5E:314:LEU:HA	43:5E:317:GLU:HB3	2.03	0.41
43:5E:470:GLU:HG3	43:5E:490:LEU:HB2	2.03	0.41
44:5F:108:ARG:O	44:5F:117:ARG:NH1	2.51	0.41
44:5F:138:VAL:HG12	44:5F:158:VAL:HG22	2.01	0.41
50:RA:125:PHE:O	50:RA:132:HIS:N	2.48	0.41
50:RA:343:ILE:HG22	50:RA:345:SER:H	1.86	0.41
54:RF:267:LYS:HD2	54:RF:267:LYS:HA	1.91	0.41
55:RH:197:ASP:OD1	55:RH:197:ASP:N	2.48	0.41
56:RI:20:LEU:HD12	56:RI:252:LEU:HD23	2.02	0.41
56:RI:38:ILE:HG22	56:RI:244:VAL:HG22	2.03	0.41
57:RJ:174:LEU:HD11	57:RJ:206:TYR:HB3	2.02	0.41
59:RL:104:ARG:HG3	59:RL:106:VAL:HG13	2.01	0.41
60:RN:649:THR:O	60:RN:652:LYS:NZ	2.54	0.41
61:RO:44:GLU:O	61:RO:48:THR:CB	2.69	0.41
61:RO:436:LYS:HA	61:RO:439:LYS:HG2	2.03	0.41
64:RS:457:ARG:HH22	64:RS:461:LEU:HD12	1.85	0.41
1:3A:59:G:OP1	34:B1:573:ASN:ND2	2.48	0.41
2:5A:357:G:C6	2:5A:369:G:C6	3.08	0.41
8:SI:140:VAL:HG13	17:SX:52:TYR:HB3	2.03	0.41
10:SK:86:LEU:HD12	10:SK:86:LEU:HA	1.87	0.41
14:SP:70:LYS:HE2	14:SP:70:LYS:HB2	1.78	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:3C:302:GLU:OE2	42:5D:133:HIS:NE2	2.43	0.41
25:3F:537:PHE:O	25:3F:567:VAL:HA	2.21	0.41
28:A5:219:SER:OG	28:A5:220:GLY:N	2.54	0.41
29:A8:563:LEU:HD13	29:A8:586:ILE:HD11	2.02	0.41
32:AF:195:LEU:HD11	32:AF:207:TYR:CZ	2.56	0.41
33:AG:358:LEU:HD11	33:AG:372:LEU:HD13	2.02	0.41
41:5C:23:ARG:O	63:RQ:862:ARG:NH2	2.39	0.41
46:5H:435:LYS:HB3	46:5H:435:LYS:HE2	1.78	0.41
50:RA:276:LYS:HG3	50:RA:320:ILE:H	1.86	0.41
53:RE:365:LEU:HD12	53:RE:365:LEU:HA	1.87	0.41
53:RE:528:ASP:OD1	53:RE:614:ARG:NH1	2.53	0.41
53:RE:1203:ASN:CG	54:RF:57:ASN:HD21	2.29	0.41
54:RF:216:VAL:HG23	54:RF:226:ILE:HD11	2.03	0.41
60:RN:784:ILE:HA	60:RN:787:THR:HG22	2.01	0.41
61:RO:314:VAL:HG12	61:RO:318:LEU:HD13	2.02	0.41
1:3A:36:C:H5'	47:5I:393:LYS:HD2	2.01	0.41
3:SA:1134:C:O2	35:B2:598:LYS:NZ	2.40	0.41
3:SA:1209:C:N3	3:SA:1210:C:N4	2.68	0.41
6:SG:125:THR:HB	6:SG:127:GLN:HE21	1.86	0.41
11:SM:38:ALA:HB2	11:SM:60:PHE:HA	2.03	0.41
22:3B:179:THR:OG1	22:3B:180:SER:N	2.54	0.41
24:3E:175:LYS:HE2	24:3E:175:LYS:HB3	1.86	0.41
25:3F:476:THR:HG22	25:3F:491:SER:HA	2.02	0.41
29:A8:605:LEU:O	29:A8:609:ASN:ND2	2.54	0.41
29:A8:703:LEU:HA	29:A8:704:PRO:HD3	1.95	0.41
30:A9:444:ASN:HD22	30:A9:447:ASN:HB2	1.85	0.41
31:AE:91:ILE:HD13	31:AE:91:ILE:HA	1.95	0.41
31:AE:124:ARG:HA	31:AE:124:ARG:HD2	1.92	0.41
31:AE:280:GLU:O	31:AE:284:SER:OG	2.35	0.41
33:AG:692:PHE:HE2	33:AG:750:LEU:HB3	1.85	0.41
35:B2:478:SER:HB3	35:B2:537:VAL:HG22	2.03	0.41
36:B3:679:THR:HG21	36:B3:723:GLU:HG3	2.03	0.41
38:BE:440:ALA:HB3	38:BE:455:PHE:HB2	2.01	0.41
43:5E:312:GLU:OE2	43:5E:316:ASN:ND2	2.54	0.41
47:5I:299:ASN:ND2	47:5I:334:THR:O	2.54	0.41
50:RA:280:LEU:HD12	50:RA:288:LYS:HB2	2.02	0.41
53:RE:946:ALA:HA	53:RE:947:PRO:HA	1.91	0.41
55:RG:227:LEU:HA	55:RG:227:LEU:HD23	1.72	0.41
57:RJ:254:HIS:ND1	57:RJ:256:GLU:OE2	2.53	0.41
57:RJ:831:ARG:HD3	57:RJ:838:ILE:HD12	2.03	0.41
61:RO:326:LEU:HD12	61:RO:326:LEU:HA	1.92	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:RP:786:PRO:HA	62:RP:789:ALA:HB3	2.01	0.41
64:RS:421:PHE:HA	64:RS:424:PHE:HB3	2.03	0.41
66:RV:230:LYS:HE3	66:RV:230:LYS:HB3	1.89	0.41
2:5A:96:C:O2	2:5A:155:A:O2'	2.36	0.41
3:SA:454:U:H3	19:SZ:84:LYS:HE2	1.86	0.41
3:SA:1071:U:H2'	3:SA:1072:C:C6	2.56	0.41
3:SA:1207:C:H5''	3:SA:1208:A:C8	2.56	0.41
4:SC:32:ILE:HA	4:SC:96:LEU:HB2	2.02	0.41
5:SF:58:GLY:HA2	5:SF:61:VAL:HG12	2.03	0.41
5:SF:104:ASP:HA	25:3F:107:PHE:HE1	1.85	0.41
6:SG:108:LEU:HD21	15:SR:44:LEU:HD11	2.03	0.41
6:SG:114:ILE:HA	6:SG:117:THR:HG22	2.03	0.41
9:SJ:103:GLN:HA	9:SJ:165:LEU:O	2.21	0.41
9:SJ:187:GLU:O	9:SJ:191:PHE:HB2	2.21	0.41
17:SX:75:ILE:HG12	17:SX:127:GLY:HA2	2.03	0.41
24:3E:72:LEU:O	24:3E:76:LEU:CB	2.69	0.41
25:3F:457:GLU:N	25:3F:460:ARG:HH21	2.19	0.41
26:3H:50:GLU:OE2	26:3H:111:LYS:NZ	2.54	0.41
27:A4:274:GLN:HE22	27:A4:320:TRP:H	1.68	0.41
27:A4:392:VAL:HG13	27:A4:401:ILE:HD13	2.02	0.41
27:A4:442:VAL:HG22	27:A4:451:PHE:HE2	1.86	0.41
27:A4:497:ILE:HD11	27:A4:511:VAL:HG23	2.03	0.41
29:A8:120:LEU:HA	29:A8:132:ILE:HA	2.03	0.41
29:A8:314:LEU:HA	29:A8:321:ILE:HA	2.02	0.41
31:AE:549:LYS:HA	31:AE:552:ASN:HB2	2.03	0.41
32:AF:149:THR:HG22	32:AF:171:VAL:HG11	2.02	0.41
32:AF:315:ASN:HB3	32:AF:317:HIS:HE1	1.84	0.41
33:AG:140:LYS:HA	33:AG:140:LYS:HD3	1.90	0.41
33:AG:225:ILE:HD12	33:AG:244:ILE:HD12	2.03	0.41
33:AG:765:TRP:O	33:AG:776:PHE:HA	2.21	0.41
34:B1:851:SER:O	34:B1:851:SER:OG	2.35	0.41
35:B2:80:ALA:HB1	35:B2:98:TYR:HB3	2.03	0.41
35:B2:392:THR:OG1	35:B2:411:ASN:OD1	2.32	0.41
35:B2:652:LYS:HE3	35:B2:652:LYS:HB2	1.84	0.41
35:B2:746:LEU:HB3	35:B2:750:GLU:HG3	2.02	0.41
36:B3:286:GLU:HB2	36:B3:288:LEU:HD23	2.02	0.41
36:B3:389:ASP:O	36:B3:407:SER:OG	2.36	0.41
37:B8:264:LEU:HD11	37:B8:272:LEU:HB2	2.01	0.41
37:B8:472:GLN:NE2	37:B8:474:SER:OG	2.54	0.41
37:B8:516:THR:HG21	37:B8:537:VAL:HG13	2.02	0.41
38:BE:571:ASP:OD1	38:BE:571:ASP:N	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:BE:724:SER:O	38:BE:728:ARG:NH2	2.54	0.41
39:B6:91:ARG:HH21	39:B6:91:ARG:HD2	1.75	0.41
42:5D:29:GLU:O	57:RJ:970:SER:OG	2.38	0.41
42:5D:137:VAL:HB	42:5D:142:LYS:HB2	2.03	0.41
42:5D:166:LEU:HD23	42:5D:166:LEU:HA	1.86	0.41
47:5I:51:GLU:OE1	47:5I:401:LYS:NZ	2.39	0.41
47:5I:66:HIS:ND1	47:5I:87:SER:HB3	2.36	0.41
47:5I:196:THR:HG22	47:5I:204:TRP:HE1	1.86	0.41
51:RB:288:SER:O	51:RB:292:ASP:HB2	2.21	0.41
53:RE:209:MET:HB3	53:RE:213:LEU:HD21	2.02	0.41
53:RE:1103:ARG:HD3	53:RE:1103:ARG:HA	1.91	0.41
57:RJ:290:ILE:HD12	57:RJ:296:PHE:HD2	1.86	0.41
57:RJ:1121:LYS:HE2	57:RJ:1121:LYS:HB2	1.87	0.41
58:RK:47:ASP:OD1	58:RK:47:ASP:N	2.53	0.41
60:RN:547:VAL:HA	60:RN:550:VAL:HG12	2.03	0.41
61:RO:391:PRO:O	61:RO:395:ILE:HG12	2.21	0.41
64:RS:294:SER:O	64:RS:294:SER:OG	2.38	0.41
64:RS:444:VAL:HG13	64:RS:452:ILE:HB	2.02	0.41
1:3A:204:U:H3'	1:3A:205:G:H5''	2.03	0.41
2:5A:354:G:N1	41:5C:485:ASP:O	2.54	0.41
2:5A:542:U:H2'	2:5A:543:C:C6	2.55	0.41
3:SA:332:U:OP2	9:SJ:175:GLN:NE2	2.54	0.41
4:SC:171:ILE:HD11	4:SC:196:GLU:HB3	2.02	0.41
5:SF:189:LEU:HD23	51:RB:228:PHE:CD1	2.57	0.41
18:SY:133:LEU:HD23	18:SY:133:LEU:HA	1.80	0.41
26:3G:54:MET:HE1	26:3G:68:PRO:HG3	2.03	0.41
27:A4:649:TRP:CH2	27:A4:743:PHE:HA	2.56	0.41
28:A5:212:LEU:HB2	28:A5:226:LEU:HB2	2.03	0.41
31:AE:189:LEU:HD12	31:AE:189:LEU:HA	1.89	0.41
31:AE:639:ARG:HH12	31:AE:643:PRO:HD3	1.85	0.41
32:AF:431:LEU:HD23	32:AF:431:LEU:HA	1.89	0.41
32:AF:434:ARG:HB3	32:AF:439:LEU:HG	2.03	0.41
33:AG:45:ILE:HG21	33:AG:107:ILE:HD13	2.03	0.41
34:B1:852:THR:HG22	36:B3:765:MET:HA	2.02	0.41
35:B2:365:TYR:HA	35:B2:381:LYS:HA	2.02	0.41
35:B2:565:PHE:CE1	35:B2:568:SER:HB3	2.56	0.41
35:B2:892:LYS:HA	35:B2:895:GLU:HG2	2.03	0.41
36:B3:296:ILE:HD13	36:B3:296:ILE:HA	1.94	0.41
36:B3:407:SER:OG	36:B3:408:LYS:N	2.54	0.41
37:B8:298:CYS:HA	37:B8:313:PHE:O	2.21	0.41
39:B6:265:LEU:HD23	39:B6:265:LEU:HA	1.96	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:5E:538:LYS:HE2	43:5E:538:LYS:HB2	1.91	0.41
45:5G:60:GLN:OE1	66:RV:207:ARG:NH1	2.54	0.41
46:5H:563:VAL:HA	46:5H:566:ARG:HB3	2.02	0.41
47:5I:40:GLU:HB2	47:5I:400:LEU:HD11	2.03	0.41
49:5K:170:ILE:O	49:5K:184:LYS:NZ	2.44	0.41
53:RE:366:GLY:HA3	53:RE:393:PHE:CE2	2.56	0.41
53:RE:405:GLY:HA3	53:RE:409:ASN:HB2	2.02	0.41
56:RI:80:SER:HB3	56:RI:102:SER:HB3	2.03	0.41
58:RK:319:ASP:H	58:RK:322:PHE:HB3	1.86	0.41
65:RT:120:LEU:HD11	65:RT:159:ILE:HD11	2.01	0.41
9:SJ:81:VAL:HG12	9:SJ:102:VAL:HG22	2.04	0.40
16:ST:116:LEU:HA	16:ST:116:LEU:HD12	1.80	0.40
23:3D:264:SER:OG	23:3D:265:GLU:N	2.47	0.40
24:3E:153:LYS:HD3	24:3E:153:LYS:HA	1.93	0.40
27:A4:112:LEU:HD13	27:A4:524:LYS:HG3	2.03	0.40
27:A4:742:LEU:HA	27:A4:742:LEU:HD12	1.88	0.40
29:A8:637:LEU:HD12	29:A8:637:LEU:HA	1.92	0.40
31:AE:646:ASN:HB2	31:AE:650:PHE:HE1	1.86	0.40
32:AF:43:THR:O	32:AF:304:SER:OG	2.32	0.40
32:AF:162:LEU:HD12	32:AF:162:LEU:HA	1.88	0.40
35:B2:134:THR:O	35:B2:149:ASP:HA	2.21	0.40
35:B2:414:LEU:HD22	35:B2:428:PHE:HD2	1.86	0.40
37:B8:226:LYS:HD2	37:B8:226:LYS:HA	1.71	0.40
37:B8:545:HIS:HB2	37:B8:552:PHE:CZ	2.55	0.40
42:5D:102:GLN:HG3	57:RJ:1098:ARG:HH11	1.87	0.40
45:5G:53:GLN:HB3	66:RV:215:LEU:HD13	2.03	0.40
47:5I:82:LYS:HA	47:5I:95:TRP:O	2.21	0.40
53:RE:111:LEU:HA	53:RE:114:VAL:HG22	2.02	0.40
53:RE:702:LYS:HE3	53:RE:702:LYS:HB3	1.82	0.40
53:RE:1200:LEU:HD12	53:RE:1202:CYS:H	1.86	0.40
54:RF:44:SER:H	54:RF:50:SER:HA	1.86	0.40
55:RH:122:ILE:HG21	55:RH:144:LEU:HD21	2.02	0.40
57:RJ:44:GLN:O	57:RJ:48:ASP:HB2	2.21	0.40
57:RJ:844:PRO:HG3	57:RJ:1032:LEU:HG	2.03	0.40
59:RL:55:VAL:O	59:RL:103:ILE:HA	2.20	0.40
59:RM:249:SER:O	59:RM:253:LEU:CB	2.68	0.40
63:RQ:832:ASN:HD22	63:RQ:834:LYS:HD2	1.86	0.40
65:RT:220:THR:HG21	65:RT:243:ALA:HB2	2.03	0.40
2:5A:90:G:O2'	2:5A:91:U:O4'	2.28	0.40
2:5A:480:C:N3	39:B6:46:ARG:NH2	2.56	0.40
3:SA:19:A:N3	57:RJ:1156:LYS:HD2	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:115:G:N7	11:SM:67:ARG:NH2	2.62	0.40
3:SA:129:U:O2'	62:RP:903:THR:O	2.38	0.40
13:SO:129:TYR:HB3	13:SO:135:LEU:HD22	2.04	0.40
15:SR:19:VAL:O	15:SR:67:VAL:HA	2.21	0.40
22:3B:234:ILE:HD13	22:3B:234:ILE:HG21	1.87	0.40
22:3B:297:ARG:NH2	22:3B:322:ARG:O	2.54	0.40
27:A4:89:MET:HE3	27:A4:89:MET:HB2	1.91	0.40
27:A4:120:SER:OG	27:A4:121:THR:N	2.45	0.40
27:A4:389:ARG:HB3	27:A4:404:MET:HB2	2.02	0.40
28:A5:202:PHE:O	28:A5:214:VAL:HA	2.20	0.40
28:A5:513:LEU:H	28:A5:513:LEU:HG	1.77	0.40
28:A5:513:LEU:HA	28:A5:516:ILE:HD12	2.02	0.40
35:B2:91:THR:HG23	35:B2:93:LEU:HD13	2.02	0.40
36:B3:99:MET:HE3	36:B3:99:MET:HB2	1.85	0.40
38:BE:456:ASP:OD1	38:BE:457:THR:N	2.53	0.40
39:B6:41:HIS:O	39:B6:45:SER:HB3	2.22	0.40
41:5C:199:LEU:HD12	41:5C:204:LEU:HD12	2.02	0.40
41:5C:351:SER:OG	41:5C:351:SER:O	2.39	0.40
47:5I:281:ASN:OD1	47:5I:281:ASN:N	2.53	0.40
50:RA:319:ASP:OD1	50:RA:319:ASP:N	2.54	0.40
54:RF:127:LYS:HE3	54:RF:127:LYS:HB2	1.90	0.40
54:RF:226:ILE:O	54:RF:230:ILE:HG12	2.21	0.40
57:RJ:128:MET:HE3	57:RJ:128:MET:HB2	1.91	0.40
58:RK:104:LEU:O	58:RK:300:TYR:OH	2.38	0.40
58:RK:287:ALA:HB2	58:RK:314:ASN:HB3	2.03	0.40
59:RL:29:VAL:HG12	59:RL:152:LEU:HB2	2.02	0.40
63:RQ:895:LYS:HE2	63:RQ:895:LYS:HB3	1.89	0.40
2:5A:170:U:P	40:5B:204:ARG:HH21	2.45	0.40
2:5A:224:G:H1	40:5B:204:ARG:HH22	1.69	0.40
3:SA:224:C:H2'	3:SA:225:A:C8	2.56	0.40
3:SA:679:U:H2'	3:SA:680:U:C6	2.56	0.40
5:SF:22:LYS:H	5:SF:22:LYS:HG2	1.68	0.40
14:SP:128:LYS:HE3	14:SP:128:LYS:HB3	1.85	0.40
16:ST:41:ARG:HE	16:ST:84:TRP:HH2	1.69	0.40
25:3F:396:PHE:HB2	25:3F:437:ARG:NH2	2.36	0.40
27:A4:388:GLN:HB2	27:A4:390:LEU:HD22	2.02	0.40
29:A8:533:PRO:HG2	33:AG:656:ASP:HA	2.03	0.40
32:AF:95:LEU:HD12	32:AF:107:VAL:HG21	2.03	0.40
32:AF:375:HIS:CD2	37:B8:339:ILE:HD11	2.57	0.40
33:AG:71:ASN:OD1	33:AG:71:ASN:N	2.54	0.40
33:AG:508:ILE:HD12	33:AG:531:PHE:HD1	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:B3:468:ILE:HA	36:B3:469:PRO:HD3	1.79	0.40
36:B3:680:ASN:HA	36:B3:683:LEU:HG	2.02	0.40
41:5C:122:GLY:O	41:5C:139:TRP:NE1	2.38	0.40
41:5C:369:MET:HB3	41:5C:369:MET:HE2	1.78	0.40
45:5G:54:LYS:HB3	45:5G:54:LYS:HE2	1.80	0.40
47:5I:14:VAL:HA	47:5I:15:PRO:HD3	1.90	0.40
53:RE:1057:PRO:HB2	53:RE:1059:PRO:HD2	2.03	0.40
57:RJ:940:LYS:HE2	57:RJ:940:LYS:HB2	1.73	0.40
59:RM:747:LEU:HA	59:RM:764:ASN:O	2.21	0.40
2:5A:190:U:O4	2:5A:207:G:O6	2.40	0.40
8:SI:156:SER:HA	8:SI:159:VAL:HG13	2.04	0.40
9:SJ:195:ARG:NH2	11:SM:11:ARG:O	2.55	0.40
22:3B:326:LYS:H	22:3B:326:LYS:HG3	1.67	0.40
22:3C:145:ASN:HB3	22:3C:148:ARG:HB3	2.04	0.40
25:3F:399:GLU:OE2	25:3F:417:SER:HB3	2.21	0.40
26:3G:65:LEU:HA	26:3G:68:PRO:HD2	2.03	0.40
28:A5:25:ASP:OD1	28:A5:56:SER:OG	2.35	0.40
28:A5:191:VAL:HA	28:A5:206:ALA:HA	2.03	0.40
28:A5:488:ILE:HG13	28:A5:529:THR:HG21	2.02	0.40
28:A5:544:ASP:HB3	32:AF:491:VAL:HG11	2.04	0.40
33:AG:334:LEU:HD12	33:AG:334:LEU:HA	1.84	0.40
33:AG:878:ASN:OD1	33:AG:878:ASN:N	2.54	0.40
36:B3:678:TRP:CE3	36:B3:697:VAL:HG23	2.56	0.40
36:B3:686:MET:HE3	36:B3:686:MET:HB3	1.91	0.40
36:B3:698:LEU:HD23	36:B3:698:LEU:HA	1.86	0.40
38:BE:343:LEU:HD12	38:BE:343:LEU:HA	1.97	0.40
43:5E:490:LEU:HD23	43:5E:490:LEU:HA	1.94	0.40
45:5G:38:GLN:O	45:5G:40:LYS:N	2.53	0.40
47:5I:59:VAL:HG21	47:5I:362:TYR:HE2	1.87	0.40
47:5I:179:GLU:OE2	47:5I:179:GLU:N	2.55	0.40
53:RE:195:ILE:HD11	53:RE:364:VAL:HG23	2.04	0.40
53:RE:481:THR:OG1	53:RE:482:VAL:N	2.55	0.40
53:RE:841:ASN:ND2	53:RE:851:LYS:HG2	2.36	0.40
57:RJ:195:TRP:NE1	57:RJ:202:ALA:O	2.48	0.40
2:5A:486:U:H4'	2:5A:487:A:H5''	2.03	0.40
2:5A:489:G:N2	2:5A:495:G:O3'	2.54	0.40
3:SA:67:A:H2'	3:SA:69:G:H8	1.86	0.40
3:SA:253:A:OP2	5:SF:135:GLY:N	2.46	0.40
3:SA:1255:G:H21	3:SA:1256:A:N6	2.19	0.40
3:SA:1512:G:O6	56:RI:145:HIS:NE2	2.50	0.40
4:SC:58:SER:O	4:SC:62:LYS:NZ	2.39	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:SR:98:ASP:OD1	15:SR:101:SER:OG	2.27	0.40
17:SX:10:ALA:HB1	17:SX:27:LEU:HD13	2.04	0.40
22:3C:148:ARG:HD3	22:3C:179:THR:HB	2.02	0.40
23:3D:101:SER:O	23:3D:101:SER:OG	2.36	0.40
24:3E:262:ILE:HA	24:3E:265:PHE:HB2	2.04	0.40
27:A4:135:ARG:HA	27:A4:135:ARG:HD2	1.87	0.40
28:A5:53:LEU:HD11	28:A5:60:VAL:HG23	2.03	0.40
34:B1:262:LYS:HE2	34:B1:262:LYS:HB3	1.82	0.40
35:B2:84:TYR:HD2	35:B2:127:LEU:HD23	1.86	0.40
35:B2:105:VAL:HB	35:B2:115:LEU:HB2	2.03	0.40
35:B2:338:ILE:HG12	35:B2:355:LEU:HD11	2.03	0.40
35:B2:522:LEU:HD13	35:B2:522:LEU:HA	1.95	0.40
36:B3:189:HIS:NE2	36:B3:217:ASP:OD1	2.53	0.40
36:B3:430:TYR:HD2	36:B3:454:LEU:HD23	1.86	0.40
36:B3:443:PRO:HA	36:B3:499:VAL:HG11	2.03	0.40
36:B3:536:LEU:HD13	36:B3:550:THR:HG21	2.03	0.40
37:B8:231:LYS:HD3	37:B8:550:SER:HB2	2.04	0.40
38:BE:525:ILE:HG22	38:BE:541:LYS:HD3	2.03	0.40
38:BE:925:LEU:HD12	38:BE:925:LEU:HA	1.93	0.40
39:B6:28:GLU:H	39:B6:28:GLU:HG2	1.76	0.40
41:5C:434:LEU:HD12	41:5C:434:LEU:HA	1.93	0.40
42:5D:211:LEU:HA	42:5D:214:VAL:HG12	2.03	0.40
43:5E:369:ILE:HG12	45:5G:223:THR:HG21	2.03	0.40
44:5F:78:LEU:HD12	44:5F:78:LEU:HA	1.87	0.40
45:5G:238:TYR:HB3	45:5G:247:ILE:HD13	2.02	0.40
47:5I:75:LYS:NZ	47:5I:356:TYR:O	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	SC	217/255 (85%)	186 (86%)	30 (14%)	1 (0%)	24	54
5	SF	227/261 (87%)	192 (85%)	35 (15%)	0	100	100
6	SG	211/225 (94%)	197 (93%)	14 (7%)	0	100	100
7	SH	108/236 (46%)	98 (91%)	9 (8%)	1 (1%)	14	42
8	SI	161/190 (85%)	139 (86%)	22 (14%)	0	100	100
9	SJ	162/200 (81%)	141 (87%)	21 (13%)	0	100	100
10	SK	169/197 (86%)	163 (96%)	6 (4%)	0	100	100
11	SM	119/156 (76%)	99 (83%)	20 (17%)	0	100	100
12	SN	117/143 (82%)	96 (82%)	21 (18%)	0	100	100
13	SO	132/151 (87%)	125 (95%)	7 (5%)	0	100	100
14	SP	116/137 (85%)	102 (88%)	14 (12%)	0	100	100
15	SR	123/143 (86%)	113 (92%)	10 (8%)	0	100	100
16	ST	109/146 (75%)	100 (92%)	9 (8%)	0	100	100
17	SX	125/130 (96%)	115 (92%)	10 (8%)	0	100	100
18	SY	101/145 (70%)	91 (90%)	10 (10%)	0	100	100
19	SZ	100/135 (74%)	86 (86%)	14 (14%)	0	100	100
20	Sc	78/82 (95%)	68 (87%)	10 (13%)	0	100	100
21	Sd	61/67 (91%)	55 (90%)	6 (10%)	0	100	100
22	3B	236/327 (72%)	222 (94%)	14 (6%)	0	100	100
22	3C	221/327 (68%)	203 (92%)	18 (8%)	0	100	100
23	3D	359/504 (71%)	344 (96%)	15 (4%)	0	100	100
24	3E	427/511 (84%)	394 (92%)	33 (8%)	0	100	100
25	3F	428/573 (75%)	384 (90%)	43 (10%)	1 (0%)	43	71
26	3G	119/126 (94%)	109 (92%)	9 (8%)	1 (1%)	16	44
26	3H	119/126 (94%)	110 (92%)	9 (8%)	0	100	100
27	A4	648/776 (84%)	576 (89%)	72 (11%)	0	100	100
28	A5	504/643 (78%)	460 (91%)	44 (9%)	0	100	100
29	A8	534/713 (75%)	407 (76%)	124 (23%)	3 (1%)	21	50
30	A9	126/575 (22%)	119 (94%)	7 (6%)	0	100	100
31	AE	773/1769 (44%)	710 (92%)	63 (8%)	0	100	100
32	AF	489/513 (95%)	437 (89%)	51 (10%)	1 (0%)	43	71
33	AG	812/896 (91%)	730 (90%)	82 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	B1	830/923 (90%)	752 (91%)	76 (9%)	2 (0%)	43	71
35	B2	839/943 (89%)	750 (89%)	88 (10%)	1 (0%)	48	78
36	B3	733/817 (90%)	599 (82%)	132 (18%)	2 (0%)	36	65
37	B8	469/594 (79%)	423 (90%)	46 (10%)	0	100	100
38	BE	857/939 (91%)	792 (92%)	65 (8%)	0	100	100
39	B6	368/440 (84%)	337 (92%)	31 (8%)	0	100	100
40	5B	58/214 (27%)	55 (95%)	3 (5%)	0	100	100
41	5C	531/554 (96%)	472 (89%)	58 (11%)	1 (0%)	43	71
42	5D	231/250 (92%)	204 (88%)	27 (12%)	0	100	100
43	5E	200/593 (34%)	187 (94%)	11 (6%)	2 (1%)	12	40
44	5F	180/183 (98%)	169 (94%)	11 (6%)	0	100	100
45	5G	278/290 (96%)	249 (90%)	29 (10%)	0	100	100
46	5H	132/610 (22%)	121 (92%)	11 (8%)	0	100	100
47	5I	457/489 (94%)	420 (92%)	37 (8%)	0	100	100
48	5J	138/217 (64%)	129 (94%)	9 (6%)	0	100	100
49	5K	171/189 (90%)	160 (94%)	11 (6%)	0	100	100
50	RA	332/707 (47%)	287 (86%)	45 (14%)	0	100	100
51	RB	132/357 (37%)	116 (88%)	16 (12%)	0	100	100
52	RC	276/316 (87%)	260 (94%)	16 (6%)	0	100	100
53	RE	1067/1237 (86%)	984 (92%)	83 (8%)	0	100	100
54	RF	233/297 (78%)	214 (92%)	19 (8%)	0	100	100
55	RG	212/252 (84%)	186 (88%)	26 (12%)	0	100	100
55	RH	226/252 (90%)	212 (94%)	14 (6%)	0	100	100
56	RI	250/274 (91%)	228 (91%)	22 (9%)	0	100	100
57	RJ	784/1183 (66%)	723 (92%)	61 (8%)	0	100	100
58	RK	358/367 (98%)	335 (94%)	23 (6%)	0	100	100
59	RL	781/1056 (74%)	670 (86%)	109 (14%)	2 (0%)	36	65
59	RM	737/1056 (70%)	640 (87%)	93 (13%)	4 (0%)	24	54
60	RN	573/810 (71%)	524 (91%)	48 (8%)	1 (0%)	43	71
61	RO	523/552 (95%)	457 (87%)	66 (13%)	0	100	100
62	RP	1992/2493 (80%)	1801 (90%)	189 (10%)	2 (0%)	48	78

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	RQ	220/899 (24%)	197 (90%)	23 (10%)	0	100	100
64	RS	247/483 (51%)	223 (90%)	23 (9%)	1 (0%)	30	59
65	RT	165/326 (51%)	151 (92%)	14 (8%)	0	100	100
66	RV	184/346 (53%)	168 (91%)	16 (9%)	0	100	100
All	All	23995/32886 (73%)	21566 (90%)	2403 (10%)	26 (0%)	49	78

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
43	5E	454	VAL
59	RL	744	PRO
59	RM	744	PRO
62	RP	119	PRO
29	A8	309	PRO
36	B3	91	LYS
59	RM	905	PRO
62	RP	1993	PRO
34	B1	670	LEU
43	5E	460	PRO
59	RM	904	LEU
60	RN	285	PRO
25	3F	552	TRP
29	A8	308	PHE
34	B1	442	GLY
35	B2	132	THR
41	5C	492	GLY
36	B3	71	PRO
59	RL	743	VAL
59	RM	743	VAL
32	AF	49	PRO
64	RS	414	PRO
4	SC	221	PRO
7	SH	70	PRO
26	3G	10	PRO
29	A8	267	ILE

5.3.2 Protein sidechains ⓘ

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	SC	195/224 (87%)	192 (98%)	3 (2%)	57	69
5	SF	196/222 (88%)	191 (97%)	5 (3%)	40	61
6	SG	180/191 (94%)	179 (99%)	1 (1%)	78	80
7	SH	95/201 (47%)	95 (100%)	0	100	100
8	SI	146/170 (86%)	143 (98%)	3 (2%)	47	64
9	SJ	136/161 (84%)	135 (99%)	1 (1%)	76	78
10	SK	147/166 (89%)	145 (99%)	2 (1%)	59	70
11	SM	110/137 (80%)	110 (100%)	0	100	100
12	SN	88/119 (74%)	88 (100%)	0	100	100
13	SO	117/128 (91%)	114 (97%)	3 (3%)	40	61
14	SP	90/105 (86%)	88 (98%)	2 (2%)	45	63
15	SR	105/119 (88%)	103 (98%)	2 (2%)	50	66
16	ST	101/129 (78%)	101 (100%)	0	100	100
17	SX	108/111 (97%)	106 (98%)	2 (2%)	50	66
18	SY	85/120 (71%)	83 (98%)	2 (2%)	43	62
19	SZ	85/113 (75%)	83 (98%)	2 (2%)	43	62
20	Sc	69/71 (97%)	69 (100%)	0	100	100
21	Sd	56/60 (93%)	54 (96%)	2 (4%)	31	56
22	3B	201/240 (84%)	200 (100%)	1 (0%)	81	81
22	3C	190/240 (79%)	189 (100%)	1 (0%)	81	81
23	3D	296/435 (68%)	293 (99%)	3 (1%)	68	75
24	3E	262/433 (60%)	259 (99%)	3 (1%)	65	74
25	3F	378/503 (75%)	374 (99%)	4 (1%)	65	74
26	3G	100/104 (96%)	100 (100%)	0	100	100
26	3H	100/104 (96%)	99 (99%)	1 (1%)	68	75
27	A4	591/713 (83%)	583 (99%)	8 (1%)	59	70
28	A5	433/574 (75%)	428 (99%)	5 (1%)	63	72
29	A8	174/657 (26%)	173 (99%)	1 (1%)	78	80
30	A9	89/533 (17%)	89 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	AE	708/1633 (43%)	704 (99%)	4 (1%)	78	80
32	AF	437/454 (96%)	429 (98%)	8 (2%)	51	67
33	AG	750/826 (91%)	738 (98%)	12 (2%)	55	68
34	B1	730/812 (90%)	715 (98%)	15 (2%)	47	64
35	B2	736/832 (88%)	721 (98%)	15 (2%)	48	65
36	B3	665/719 (92%)	656 (99%)	9 (1%)	59	70
37	B8	421/529 (80%)	419 (100%)	2 (0%)	81	81
38	BE	757/819 (92%)	744 (98%)	13 (2%)	53	67
39	B6	251/414 (61%)	250 (100%)	1 (0%)	84	83
40	5B	57/196 (29%)	56 (98%)	1 (2%)	51	67
41	5C	465/480 (97%)	454 (98%)	11 (2%)	43	62
42	5D	221/234 (94%)	219 (99%)	2 (1%)	70	76
43	5E	185/535 (35%)	182 (98%)	3 (2%)	55	68
44	5F	171/172 (99%)	171 (100%)	0	100	100
45	5G	251/258 (97%)	247 (98%)	4 (2%)	55	68
46	5H	107/538 (20%)	105 (98%)	2 (2%)	50	66
47	5I	416/443 (94%)	404 (97%)	12 (3%)	37	60
48	5J	133/200 (66%)	132 (99%)	1 (1%)	73	77
49	5K	157/169 (93%)	155 (99%)	2 (1%)	61	71
50	RA	303/636 (48%)	301 (99%)	2 (1%)	76	78
51	RB	117/315 (37%)	117 (100%)	0	100	100
52	RC	231/289 (80%)	230 (100%)	1 (0%)	84	83
53	RE	984/1125 (88%)	977 (99%)	7 (1%)	76	78
54	RF	221/274 (81%)	217 (98%)	4 (2%)	51	67
55	RG	195/222 (88%)	194 (100%)	1 (0%)	81	81
55	RH	206/222 (93%)	201 (98%)	5 (2%)	43	62
56	RI	235/256 (92%)	233 (99%)	2 (1%)	70	76
57	RJ	683/1039 (66%)	679 (99%)	4 (1%)	78	80
58	RK	307/312 (98%)	305 (99%)	2 (1%)	76	78
59	RL	164/934 (18%)	162 (99%)	2 (1%)	63	72
60	RN	406/732 (56%)	404 (100%)	2 (0%)	81	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
61	RO	329/506 (65%)	324 (98%)	5 (2%)	57	69
63	RQ	148/808 (18%)	145 (98%)	3 (2%)	48	65
64	RS	225/424 (53%)	222 (99%)	3 (1%)	61	71
65	RT	148/282 (52%)	146 (99%)	2 (1%)	59	70
66	RV	141/304 (46%)	138 (98%)	3 (2%)	47	64
All	All	17584/26026 (68%)	17362 (99%)	222 (1%)	59	71

All (222) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	SC	91	VAL
4	SC	176	VAL
4	SC	225	VAL
5	SF	19	LEU
5	SF	181	VAL
5	SF	183	VAL
5	SF	196	VAL
5	SF	208	VAL
6	SG	123	VAL
8	SI	140	VAL
8	SI	159	VAL
8	SI	189	THR
9	SJ	43	ILE
10	SK	74	ASN
10	SK	136	VAL
13	SO	58	HIS
13	SO	71	ILE
13	SO	87	ASP
14	SP	42	VAL
14	SP	86	THR
15	SR	69	VAL
15	SR	75	VAL
17	SX	66	ASN
17	SX	83	ILE
18	SY	120	VAL
18	SY	125	VAL
19	SZ	5	VAL
19	SZ	81	GLU
21	Sd	7	VAL
21	Sd	66	LEU

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Mol	Chain	Res	Type
22	3B	107	VAL
22	3C	197	VAL
23	3D	10	GLU
23	3D	48	ILE
23	3D	399	VAL
24	3E	198	ILE
24	3E	265	PHE
24	3E	371	LEU
25	3F	190	VAL
25	3F	223	THR
25	3F	293	ASP
25	3F	475	ILE
26	3H	81	VAL
27	A4	33	VAL
27	A4	75	ASN
27	A4	130	THR
27	A4	190	VAL
27	A4	282	ASP
27	A4	585	ILE
27	A4	648	PHE
27	A4	775	VAL
28	A5	77	ILE
28	A5	95	VAL
28	A5	139	HIS
28	A5	235	LEU
28	A5	310	THR
29	A8	563	LEU
31	AE	85	VAL
31	AE	147	VAL
31	AE	366	ILE
31	AE	485	THR
32	AF	20	THR
32	AF	148	VAL
32	AF	149	THR
32	AF	218	VAL
32	AF	236	VAL
32	AF	255	VAL
32	AF	261	VAL
32	AF	511	LEU
33	AG	88	ILE
33	AG	109	VAL
33	AG	131	HIS

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Mol	Chain	Res	Type
33	AG	155	THR
33	AG	259	VAL
33	AG	271	LEU
33	AG	283	VAL
33	AG	391	VAL
33	AG	567	VAL
33	AG	606	HIS
33	AG	698	VAL
33	AG	744	ILE
34	B1	76	ASP
34	B1	167	ASP
34	B1	215	VAL
34	B1	250	ILE
34	B1	351	LEU
34	B1	393	VAL
34	B1	519	LEU
34	B1	526	ASP
34	B1	530	VAL
34	B1	559	ILE
34	B1	603	LEU
34	B1	657	ILE
34	B1	661	LEU
34	B1	698	THR
34	B1	711	LEU
35	B2	159	LEU
35	B2	212	VAL
35	B2	270	SER
35	B2	331	THR
35	B2	343	TRP
35	B2	392	THR
35	B2	434	LEU
35	B2	447	LEU
35	B2	481	LEU
35	B2	496	THR
35	B2	555	VAL
35	B2	576	VAL
35	B2	579	ILE
35	B2	663	LEU
35	B2	938	VAL
36	B3	12	LEU
36	B3	22	VAL
36	B3	24	THR

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Mol	Chain	Res	Type
36	B3	130	ASP
36	B3	168	THR
36	B3	220	ILE
36	B3	482	VAL
36	B3	520	LEU
36	B3	539	VAL
37	B8	544	VAL
37	B8	546	LEU
38	BE	51	VAL
38	BE	173	LEU
38	BE	207	ASP
38	BE	209	ILE
38	BE	286	VAL
38	BE	309	ILE
38	BE	312	THR
38	BE	419	ILE
38	BE	470	GLN
38	BE	494	LEU
38	BE	570	ILE
38	BE	713	LEU
38	BE	813	PHE
39	B6	297	ASP
40	5B	211	LEU
41	5C	63	THR
41	5C	121	ASN
41	5C	153	THR
41	5C	230	THR
41	5C	253	ASN
41	5C	268	VAL
41	5C	291	THR
41	5C	296	ARG
41	5C	347	LEU
41	5C	392	VAL
41	5C	505	THR
42	5D	91	LEU
42	5D	159	VAL
43	5E	297	LEU
43	5E	330	VAL
43	5E	340	LEU
45	5G	176	ILE
45	5G	219	GLU
45	5G	222	ILE

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Mol	Chain	Res	Type
45	5G	223	THR
46	5H	540	ILE
46	5H	579	VAL
47	5I	14	VAL
47	5I	62	LEU
47	5I	91	VAL
47	5I	113	VAL
47	5I	119	THR
47	5I	124	HIS
47	5I	201	ILE
47	5I	214	ASP
47	5I	232	THR
47	5I	261	THR
47	5I	351	VAL
47	5I	410	ILE
48	5J	55	ILE
49	5K	17	LEU
49	5K	41	THR
50	RA	155	VAL
50	RA	192	ASN
52	RC	81	THR
53	RE	232	LEU
53	RE	337	LEU
53	RE	477	LEU
53	RE	595	THR
53	RE	862	LEU
53	RE	976	ILE
53	RE	1114	ILE
54	RF	53	LEU
54	RF	176	ASP
54	RF	207	VAL
54	RF	231	LEU
55	RG	97	LEU
55	RH	30	VAL
55	RH	31	LEU
55	RH	116	THR
55	RH	167	ILE
55	RH	168	THR
56	RI	17	LEU
56	RI	70	LEU
57	RJ	271	ILE
57	RJ	913	ILE

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Mol	Chain	Res	Type
57	RJ	1060	VAL
57	RJ	1069	VAL
58	RK	166	VAL
58	RK	219	LEU
59	RL	10	ILE
59	RL	134	LEU
60	RN	445	VAL
60	RN	685	LEU
61	RO	203	LEU
61	RO	397	THR
61	RO	456	THR
61	RO	493	TYR
61	RO	507	LEU
63	RQ	319	THR
63	RQ	830	ILE
63	RQ	861	LEU
64	RS	225	THR
64	RS	258	VAL
64	RS	311	LEU
65	RT	139	LEU
65	RT	182	ILE
66	RV	164	LEU
66	RV	202	VAL
66	RV	315	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (400) such sidechains are listed below:

Mol	Chain	Res	Type
4	SC	16	GLN
4	SC	101	HIS
4	SC	118	GLN
4	SC	157	GLN
4	SC	183	GLN
4	SC	199	ASN
5	SF	96	ASN
5	SF	153	ASN
5	SF	188	ASN
5	SF	224	ASN
6	SG	63	GLN
6	SG	66	GLN
6	SG	86	GLN
6	SG	104	ASN

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Mol	Chain	Res	Type
6	SG	127	GLN
6	SG	131	GLN
6	SG	169	ASN
6	SG	186	ASN
7	SH	59	GLN
8	SI	180	GLN
9	SJ	64	ASN
9	SJ	103	GLN
10	SK	112	GLN
11	SM	18	HIS
11	SM	81	HIS
11	SM	92	HIS
11	SM	98	ASN
11	SM	106	ASN
11	SM	138	ASN
12	SN	38	HIS
12	SN	142	GLN
13	SO	36	GLN
13	SO	49	GLN
13	SO	58	HIS
13	SO	123	HIS
14	SP	24	ASN
15	SR	74	HIS
16	ST	21	ASN
16	ST	99	HIS
17	SX	12	ASN
17	SX	16	ASN
17	SX	80	ASN
18	SY	63	GLN
19	SZ	15	ASN
19	SZ	29	HIS
19	SZ	77	ASN
20	Sc	19	HIS
22	3C	145	ASN
22	3C	201	HIS
22	3C	274	ASN
23	3D	134	HIS
23	3D	172	ASN
23	3D	183	GLN
23	3D	302	ASN
23	3D	381	ASN
24	3E	178	ASN

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Mol	Chain	Res	Type
24	3E	191	HIS
24	3E	254	ASN
24	3E	256	ASN
24	3E	286	ASN
24	3E	334	HIS
24	3E	400	GLN
25	3F	226	HIS
25	3F	485	ASN
25	3F	525	GLN
26	3G	25	GLN
26	3G	38	ASN
26	3H	5	ASN
26	3H	18	GLN
26	3H	45	ASN
26	3H	66	HIS
27	A4	83	ASN
27	A4	273	ASN
27	A4	274	GLN
27	A4	292	ASN
27	A4	317	ASN
27	A4	452	HIS
27	A4	454	GLN
27	A4	467	ASN
27	A4	483	ASN
27	A4	529	ASN
27	A4	539	ASN
27	A4	621	ASN
27	A4	632	ASN
27	A4	642	ASN
27	A4	731	HIS
27	A4	771	GLN
28	A5	103	ASN
28	A5	133	GLN
28	A5	302	ASN
28	A5	308	ASN
28	A5	316	ASN
28	A5	324	ASN
28	A5	495	GLN
29	A8	553	GLN
29	A8	609	ASN
30	A9	443	GLN
30	A9	444	ASN

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Mol	Chain	Res	Type
30	A9	474	HIS
30	A9	478	ASN
31	AE	7	GLN
31	AE	51	ASN
31	AE	96	ASN
31	AE	141	ASN
31	AE	166	ASN
31	AE	202	HIS
31	AE	219	ASN
31	AE	293	HIS
31	AE	309	GLN
31	AE	477	ASN
31	AE	480	ASN
31	AE	552	ASN
31	AE	559	ASN
31	AE	709	ASN
31	AE	773	GLN
31	AE	774	ASN
31	AE	781	ASN
32	AF	24	GLN
32	AF	44	HIS
32	AF	48	ASN
32	AF	51	HIS
32	AF	64	GLN
32	AF	72	GLN
32	AF	133	HIS
32	AF	161	GLN
32	AF	217	ASN
32	AF	250	ASN
32	AF	289	ASN
32	AF	317	HIS
32	AF	391	ASN
32	AF	403	ASN
32	AF	502	GLN
33	AG	165	HIS
33	AG	169	GLN
33	AG	190	GLN
33	AG	325	GLN
33	AG	350	GLN
33	AG	393	ASN
33	AG	398	HIS
33	AG	401	GLN

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Mol	Chain	Res	Type
33	AG	424	GLN
33	AG	489	ASN
33	AG	535	ASN
33	AG	571	GLN
33	AG	660	GLN
33	AG	706	HIS
33	AG	727	GLN
33	AG	759	HIS
33	AG	760	HIS
34	B1	44	ASN
34	B1	91	HIS
34	B1	92	HIS
34	B1	142	HIS
34	B1	190	HIS
34	B1	201	HIS
34	B1	302	GLN
34	B1	303	ASN
34	B1	349	ASN
34	B1	386	HIS
34	B1	432	GLN
34	B1	434	ASN
34	B1	456	HIS
34	B1	461	GLN
34	B1	650	ASN
34	B1	795	ASN
34	B1	837	ASN
34	B1	842	ASN
35	B2	128	GLN
35	B2	195	GLN
35	B2	264	ASN
35	B2	276	ASN
35	B2	383	HIS
35	B2	524	HIS
35	B2	614	HIS
35	B2	657	GLN
35	B2	677	HIS
35	B2	770	ASN
35	B2	798	ASN
35	B2	816	GLN
35	B2	856	ASN
35	B2	865	HIS
36	B3	143	HIS

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Mol	Chain	Res	Type
36	B3	184	HIS
36	B3	301	GLN
36	B3	309	GLN
36	B3	315	ASN
36	B3	478	GLN
36	B3	502	ASN
36	B3	616	HIS
36	B3	667	GLN
36	B3	747	ASN
36	B3	749	ASN
36	B3	767	HIS
36	B3	790	GLN
36	B3	792	HIS
36	B3	802	GLN
37	B8	41	ASN
37	B8	159	HIS
37	B8	162	ASN
37	B8	282	ASN
37	B8	283	HIS
37	B8	308	ASN
37	B8	352	GLN
37	B8	357	ASN
37	B8	472	GLN
37	B8	478	GLN
37	B8	479	ASN
37	B8	492	ASN
37	B8	520	ASN
37	B8	528	GLN
38	BE	20	ASN
38	BE	59	GLN
38	BE	67	HIS
38	BE	135	ASN
38	BE	163	GLN
38	BE	203	ASN
38	BE	305	ASN
38	BE	447	ASN
38	BE	481	ASN
38	BE	501	HIS
38	BE	627	ASN
38	BE	649	ASN
38	BE	708	ASN
38	BE	732	ASN

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Mol	Chain	Res	Type
38	BE	903	GLN
39	B6	64	ASN
39	B6	90	GLN
39	B6	115	ASN
40	5B	179	GLN
40	5B	207	ASN
41	5C	101	ASN
41	5C	133	HIS
41	5C	143	GLN
41	5C	164	GLN
41	5C	170	GLN
41	5C	195	HIS
41	5C	202	HIS
41	5C	308	GLN
41	5C	410	ASN
41	5C	468	GLN
41	5C	474	ASN
41	5C	480	ASN
41	5C	494	ASN
41	5C	507	ASN
41	5C	517	GLN
41	5C	531	HIS
42	5D	45	GLN
42	5D	144	ASN
42	5D	153	ASN
43	5E	526	ASN
44	5F	39	GLN
44	5F	59	ASN
44	5F	99	ASN
44	5F	116	HIS
44	5F	135	HIS
44	5F	144	ASN
45	5G	18	GLN
45	5G	26	GLN
45	5G	126	ASN
45	5G	143	HIS
45	5G	156	HIS
45	5G	159	HIS
45	5G	182	GLN
45	5G	208	HIS
46	5H	515	ASN
47	5I	46	ASN

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Mol	Chain	Res	Type
47	5I	76	ASN
47	5I	202	HIS
47	5I	207	ASN
47	5I	260	GLN
47	5I	276	ASN
47	5I	284	HIS
47	5I	336	HIS
47	5I	371	ASN
47	5I	392	ASN
47	5I	406	HIS
48	5J	53	GLN
48	5J	126	HIS
48	5J	139	GLN
48	5J	184	ASN
48	5J	192	ASN
48	5J	195	GLN
49	5K	43	ASN
49	5K	57	GLN
50	RA	101	ASN
50	RA	118	GLN
50	RA	166	ASN
50	RA	238	ASN
50	RA	333	ASN
51	RB	269	HIS
51	RB	301	ASN
51	RB	314	ASN
52	RC	68	ASN
52	RC	112	GLN
52	RC	151	ASN
52	RC	199	HIS
52	RC	255	GLN
52	RC	284	GLN
53	RE	197	GLN
53	RE	221	ASN
53	RE	293	ASN
53	RE	311	ASN
53	RE	313	ASN
53	RE	342	HIS
53	RE	371	GLN
53	RE	402	ASN
53	RE	414	HIS
53	RE	420	GLN

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Mol	Chain	Res	Type
53	RE	500	ASN
53	RE	520	ASN
53	RE	568	ASN
53	RE	607	HIS
53	RE	634	HIS
53	RE	698	ASN
53	RE	729	ASN
53	RE	834	ASN
53	RE	841	ASN
53	RE	901	ASN
53	RE	923	HIS
53	RE	1023	ASN
53	RE	1045	ASN
53	RE	1159	ASN
53	RE	1180	ASN
54	RF	23	HIS
54	RF	90	ASN
54	RF	146	ASN
54	RF	268	GLN
55	RG	105	ASN
55	RG	125	ASN
55	RG	143	GLN
55	RG	215	ASN
55	RH	69	ASN
56	RI	37	HIS
56	RI	41	ASN
56	RI	52	ASN
56	RI	133	HIS
56	RI	186	ASN
56	RI	192	ASN
56	RI	215	ASN
56	RI	221	ASN
57	RJ	55	HIS
57	RJ	126	ASN
57	RJ	162	HIS
57	RJ	239	ASN
57	RJ	261	GLN
57	RJ	289	HIS
57	RJ	761	GLN
57	RJ	776	GLN
57	RJ	1043	ASN
57	RJ	1074	GLN

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Mol	Chain	Res	Type
57	RJ	1151	GLN
58	RK	16	ASN
58	RK	88	HIS
58	RK	167	HIS
58	RK	317	GLN
58	RK	334	ASN
59	RL	16	ASN
59	RL	19	GLN
59	RL	75	ASN
60	RN	107	ASN
60	RN	432	HIS
60	RN	444	ASN
60	RN	452	GLN
60	RN	482	GLN
60	RN	527	GLN
60	RN	569	GLN
60	RN	617	HIS
60	RN	738	ASN
60	RN	771	ASN
60	RN	797	ASN
61	RO	228	HIS
61	RO	256	ASN
61	RO	260	ASN
61	RO	268	GLN
61	RO	273	GLN
61	RO	290	HIS
61	RO	304	ASN
61	RO	309	ASN
61	RO	346	ASN
61	RO	370	HIS
63	RQ	279	GLN
63	RQ	321	HIS
63	RQ	331	GLN
63	RQ	832	ASN
63	RQ	839	ASN
64	RS	276	GLN
64	RS	302	HIS
64	RS	385	GLN
65	RT	111	ASN
65	RT	127	GLN
65	RT	218	ASN
65	RT	232	HIS

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Mol	Chain	Res	Type
66	RV	151	ASN
66	RV	156	GLN
66	RV	163	HIS
66	RV	222	ASN
66	RV	224	HIS
66	RV	225	GLN
66	RV	237	HIS
66	RV	271	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	169/333 (50%)	46 (27%)	2 (1%)
2	5A	516/700 (73%)	146 (28%)	10 (1%)
3	SA	1290/1807 (71%)	461 (35%)	16 (1%)
All	All	1975/2840 (69%)	653 (33%)	28 (1%)

All (653) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3A	2	U
1	3A	5	A
1	3A	14	A
1	3A	15	U
1	3A	24	U
1	3A	25	U
1	3A	28	A
1	3A	30	A
1	3A	33	A
1	3A	35	U
1	3A	56	A
1	3A	60	A
1	3A	61	G
1	3A	82	G
1	3A	87	G
1	3A	88	U
1	3A	89	C
1	3A	90	C
1	3A	91	C
1	3A	102	U
1	3A	104	C

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Mol	Chain	Res	Type
1	3A	111	G
1	3A	114	A
1	3A	115	G
1	3A	198	U
1	3A	199	G
1	3A	200	C
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	265	C
1	3A	266	C
1	3A	305	G
1	3A	309	G
1	3A	310	G
1	3A	313	A
1	3A	314	C
1	3A	322	A
1	3A	324	U
1	3A	325	C
1	3A	329	C
2	5A	5	G
2	5A	6	A
2	5A	7	A
2	5A	8	A
2	5A	13	U
2	5A	62	C
2	5A	63	G
2	5A	64	U
2	5A	70	A
2	5A	82	A
2	5A	83	U
2	5A	85	G
2	5A	86	C
2	5A	87	C
2	5A	103	G
2	5A	104	A
2	5A	109	C

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Mol	Chain	Res	Type
2	5A	110	G
2	5A	114	G
2	5A	124	A
2	5A	125	G
2	5A	126	A
2	5A	127	U
2	5A	128	C
2	5A	129	U
2	5A	130	G
2	5A	140	U
2	5A	142	U
2	5A	144	C
2	5A	148	G
2	5A	150	G
2	5A	151	U
2	5A	156	U
2	5A	161	A
2	5A	163	G
2	5A	169	A
2	5A	170	U
2	5A	171	G
2	5A	172	C
2	5A	173	G
2	5A	174	U
2	5A	177	U
2	5A	185	A
2	5A	190	U
2	5A	200	A
2	5A	201	U
2	5A	211	G
2	5A	219	U
2	5A	220	U
2	5A	223	C
2	5A	224	G
2	5A	225	U
2	5A	226	U
2	5A	227	U
2	5A	235	A
2	5A	240	C
2	5A	256	U
2	5A	259	G
2	5A	260	A

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Mol	Chain	Res	Type
2	5A	261	U
2	5A	266	U
2	5A	267	U
2	5A	268	G
2	5A	271	G
2	5A	279	A
2	5A	280	A
2	5A	281	G
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	316	U
2	5A	324	U
2	5A	325	U
2	5A	326	C
2	5A	327	A
2	5A	328	A
2	5A	337	G
2	5A	339	A
2	5A	353	A
2	5A	354	G
2	5A	359	U
2	5A	360	C
2	5A	363	A
2	5A	364	A
2	5A	365	G
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	393	C
2	5A	395	C
2	5A	407	A

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Mol	Chain	Res	Type
2	5A	419	A
2	5A	427	A
2	5A	428	A
2	5A	429	A
2	5A	430	C
2	5A	431	A
2	5A	432	C
2	5A	433	C
2	5A	440	U
2	5A	443	G
2	5A	461	A
2	5A	462	G
2	5A	464	G
2	5A	468	A
2	5A	469	C
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	489	G
2	5A	490	G
2	5A	491	U
2	5A	493	A
2	5A	517	A
2	5A	519	A
2	5A	525	U
2	5A	526	U
2	5A	533	G
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	547	C
2	5A	549	G
2	5A	555	A
2	5A	585	C
2	5A	586	A

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Mol	Chain	Res	Type
2	5A	587	G
2	5A	589	U
2	5A	590	G
3	SA	-5	G
3	SA	-4	A
3	SA	-1	G
3	SA	0	U
3	SA	1	U
3	SA	6	G
3	SA	10	G
3	SA	17	C
3	SA	18	C
3	SA	21	U
3	SA	24	U
3	SA	25	C
3	SA	26	A
3	SA	36	C
3	SA	37	U
3	SA	51	A
3	SA	53	G
3	SA	54	C
3	SA	55	A
3	SA	56	U
3	SA	57	G
3	SA	59	C
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	77	U
3	SA	80	A
3	SA	81	G
3	SA	85	A
3	SA	89	G
3	SA	92	A
3	SA	93	A

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Mol	Chain	Res	Type
3	SA	96	G
3	SA	97	C
3	SA	100	A
3	SA	102	U
3	SA	104	A
3	SA	105	A
3	SA	114	C
3	SA	115	G
3	SA	126	A
3	SA	127	G
3	SA	128	U
3	SA	129	U
3	SA	130	C
3	SA	131	C
3	SA	141	U
3	SA	145	A
3	SA	146	U
3	SA	153	G
3	SA	159	U
3	SA	160	C
3	SA	163	G
3	SA	168	A
3	SA	170	U
3	SA	174	U
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	203	U
3	SA	211	U
3	SA	214	G
3	SA	228	G

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Mol	Chain	Res	Type
3	SA	231	U
3	SA	233	C
3	SA	234	G
3	SA	236	A
3	SA	237	C
3	SA	238	U
3	SA	239	C
3	SA	241	U
3	SA	242	U
3	SA	246	G
3	SA	254	A
3	SA	255	U
3	SA	256	A
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	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	288	A
3	SA	290	G
3	SA	311	U
3	SA	313	U
3	SA	315	A
3	SA	316	A
3	SA	319	U
3	SA	320	U
3	SA	321	C
3	SA	322	G
3	SA	333	A
3	SA	334	G
3	SA	337	G
3	SA	339	C
3	SA	350	U

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Mol	Chain	Res	Type
3	SA	351	C
3	SA	352	A
3	SA	356	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	376	C
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	404	G
3	SA	405	C
3	SA	407	A
3	SA	410	A
3	SA	411	C
3	SA	416	A
3	SA	418	G
3	SA	420	A
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	428	A
3	SA	431	C
3	SA	436	A

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Mol	Chain	Res	Type
3	SA	437	A
3	SA	439	U
3	SA	440	U
3	SA	441	A
3	SA	444	C
3	SA	445	A
3	SA	452	A
3	SA	454	U
3	SA	455	C
3	SA	456	A
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	485	A
3	SA	486	G
3	SA	487	G
3	SA	493	U
3	SA	496	G
3	SA	501	U
3	SA	502	U
3	SA	505	A
3	SA	506	A
3	SA	507	U
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	551	G
3	SA	557	G
3	SA	563	U
3	SA	564	G
3	SA	570	A
3	SA	572	C
3	SA	575	C

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Mol	Chain	Res	Type
3	SA	579	A
3	SA	580	A
3	SA	583	C
3	SA	584	C
3	SA	585	A
3	SA	586	G
3	SA	587	C
3	SA	594	A
3	SA	595	G
3	SA	603	U
3	SA	604	A
3	SA	606	A
3	SA	608	U
3	SA	609	U
3	SA	610	G
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	649	U
3	SA	652	G
3	SA	654	C
3	SA	656	G
3	SA	657	U
3	SA	658	C
3	SA	659	C
3	SA	677	G
3	SA	678	A
3	SA	680	U
3	SA	682	C
3	SA	687	G
3	SA	689	G
3	SA	691	C
3	SA	692	C
3	SA	859	A
3	SA	860	U

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Mol	Chain	Res	Type
3	SA	861	U
3	SA	863	A
3	SA	864	U
3	SA	865	A
3	SA	876	G
3	SA	894	U
3	SA	901	G
3	SA	906	A
3	SA	913	G
3	SA	914	G
3	SA	932	U
3	SA	933	A
3	SA	935	U
3	SA	940	A
3	SA	945	U
3	SA	951	A
3	SA	960	U
3	SA	966	A
3	SA	969	C
3	SA	970	A
3	SA	1021	C
3	SA	1022	C
3	SA	1023	A
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	1036	A
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	1058	U
3	SA	1059	U
3	SA	1060	U
3	SA	1062	A
3	SA	1063	U
3	SA	1064	G

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Mol	Chain	Res	Type
3	SA	1075	C
3	SA	1076	A
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	1118	G
3	SA	1119	G
3	SA	1122	G
3	SA	1125	A
3	SA	1127	G
3	SA	1128	C
3	SA	1131	A
3	SA	1132	A
3	SA	1145	U
3	SA	1146	G
3	SA	1147	A
3	SA	1158	C
3	SA	1164	G
3	SA	1191	U
3	SA	1192	C
3	SA	1193	A
3	SA	1196	A
3	SA	1197	C
3	SA	1198	G
3	SA	1199	G
3	SA	1200	G
3	SA	1201	G
3	SA	1202	A
3	SA	1205	C
3	SA	1207	C
3	SA	1208	A
3	SA	1210	C
3	SA	1213	G
3	SA	1217	A

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Mol	Chain	Res	Type
3	SA	1218	G
3	SA	1219	A
3	SA	1226	A
3	SA	1227	A
3	SA	1228	G
3	SA	1229	G
3	SA	1232	U
3	SA	1235	C
3	SA	1236	A
3	SA	1253	U
3	SA	1255	G
3	SA	1258	U
3	SA	1259	U
3	SA	1266	U
3	SA	1268	G
3	SA	1271	G
3	SA	1272	U
3	SA	1273	G
3	SA	1274	C
3	SA	1275	A
3	SA	1436	A
3	SA	1437	U
3	SA	1440	C
3	SA	1443	U
3	SA	1450	U
3	SA	1457	C
3	SA	1461	C
3	SA	1469	A
3	SA	1472	C
3	SA	1473	U
3	SA	1474	G
3	SA	1475	A
3	SA	1477	G
3	SA	1485	C
3	SA	1488	G
3	SA	1489	U
3	SA	1492	A
3	SA	1493	A
3	SA	1496	U
3	SA	1498	G
3	SA	1506	G
3	SA	1517	U

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Mol	Chain	Res	Type
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	1531	G
3	SA	1535	U
3	SA	1536	G
3	SA	1539	G
3	SA	1541	G
3	SA	1543	A
3	SA	1544	U
3	SA	1567	U
3	SA	1568	C
3	SA	1569	A
3	SA	1570	A
3	SA	1573	A
3	SA	1584	G
3	SA	1590	G
3	SA	1594	G
3	SA	1595	U
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	1629	G
3	SA	1630	U
3	SA	1631	A
3	SA	1639	C
3	SA	1651	A
3	SA	1658	G
3	SA	1659	A
3	SA	1664	C
3	SA	1670	G
3	SA	1671	A
3	SA	1672	G
3	SA	1677	C
3	SA	1678	A
3	SA	1679	G

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Mol	Chain	Res	Type
3	SA	1680	G
3	SA	1681	A
3	SA	1682	U
3	SA	1683	C
3	SA	1684	U
3	SA	1685	G
3	SA	1690	G
3	SA	1695	G
3	SA	1700	C
3	SA	1702	A
3	SA	1707	A
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	1724	U
3	SA	1725	U
3	SA	1727	G
3	SA	1731	A
3	SA	1732	A
3	SA	1736	G
3	SA	1737	G
3	SA	1742	U
3	SA	1743	U
3	SA	1745	G
3	SA	1747	G
3	SA	1749	A
3	SA	1751	C
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	1765	A
3	SA	1766	A
3	SA	1768	G
3	SA	1772	C
3	SA	1779	U
3	SA	1780	G

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Mol	Chain	Res	Type
3	SA	1781	A
3	SA	1782	A

All (28) RNA pucker outliers are listed below:

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

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

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
69	GTP	RJ	1201	70	33,34,34	0.89	0	50,54,54	1.62	9 (18%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
69	GTP	RJ	1201	70	-	2/22/38/38	0/3/3/3

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
69	RJ	1201	GTP	C5-C4-N3	-4.86	120.66	128.39
69	RJ	1201	GTP	C2-N3-C4	4.49	120.03	112.30
69	RJ	1201	GTP	C2-N1-C6	-3.12	119.46	125.11
69	RJ	1201	GTP	N9-C4-N3	2.94	131.83	125.95
69	RJ	1201	GTP	N9-C8-N7	-2.85	108.12	113.40
69	RJ	1201	GTP	O4'-C1'-N9	2.84	114.79	108.36
69	RJ	1201	GTP	C5-C6-N1	2.64	119.98	113.25
69	RJ	1201	GTP	C8-N7-C5	2.59	108.88	104.26
69	RJ	1201	GTP	O6-C6-C5	-2.34	120.36	126.53

There are no chirality outliers.

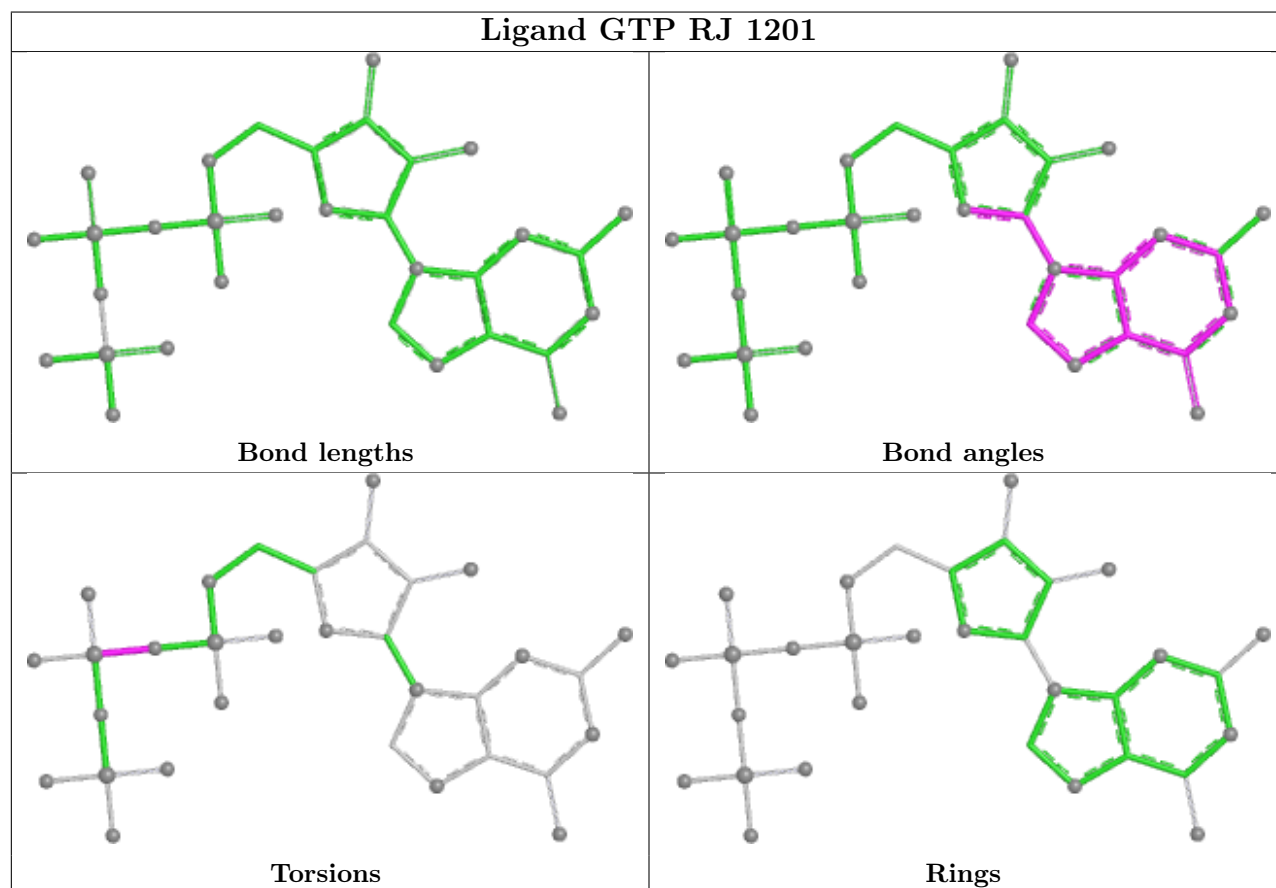
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
69	RJ	1201	GTP	PA-O3A-PB-O2B
69	RJ	1201	GTP	PA-O3A-PB-O1B

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

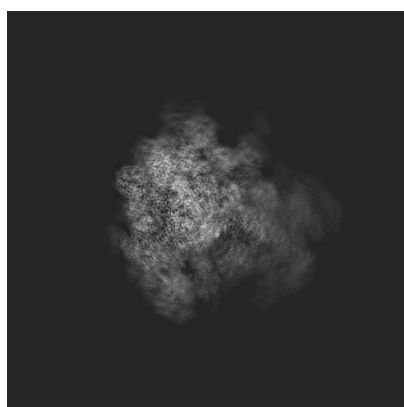
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9964. These allow visual inspection of the internal detail of the map and identification of artifacts.

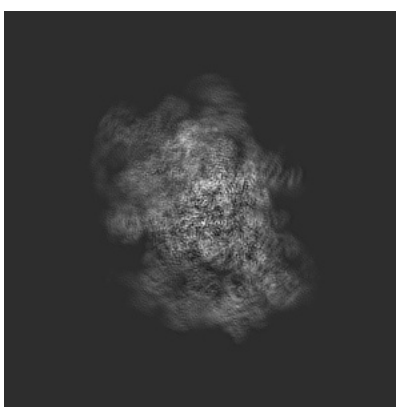
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

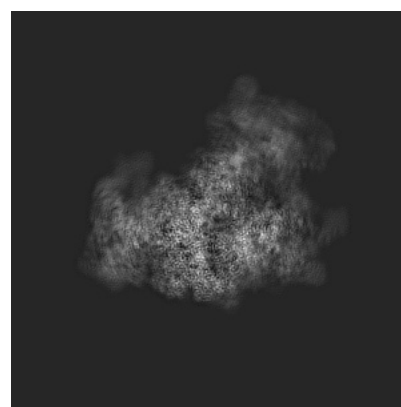
6.1.1 Primary map



X



Y

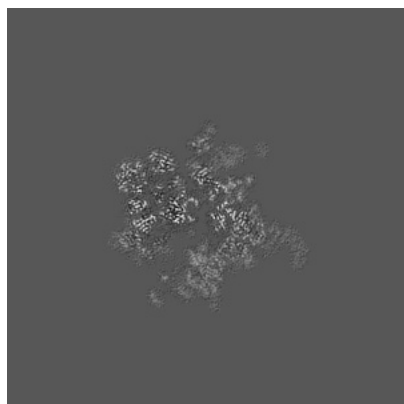


Z

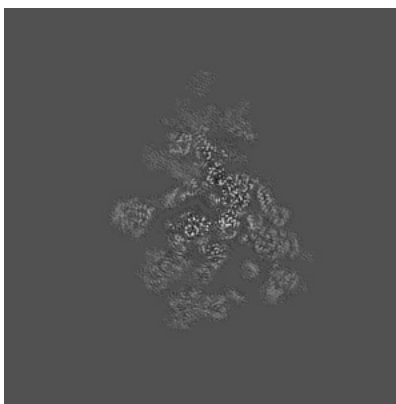
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

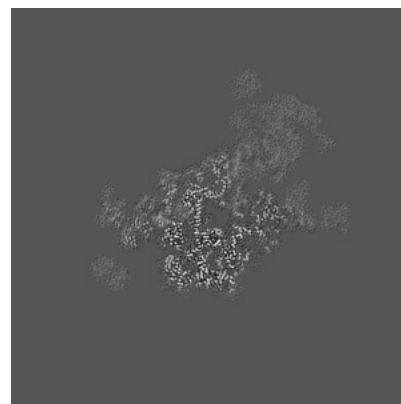
6.2.1 Primary map



X Index: 256



Y Index: 256

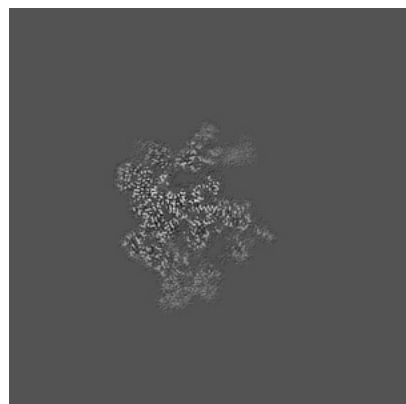


Z Index: 256

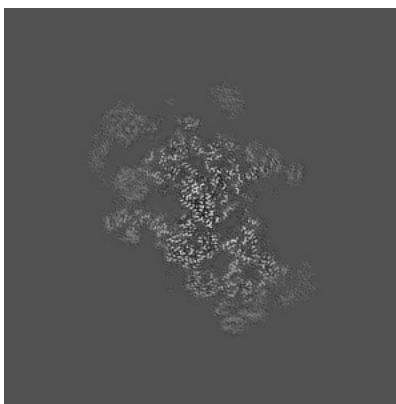
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

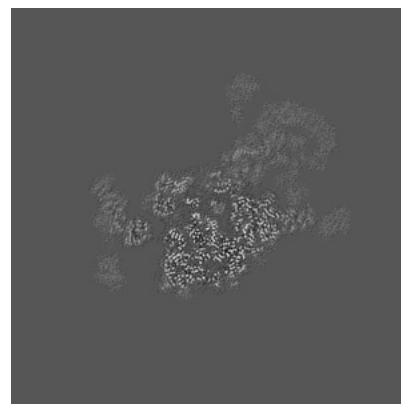
6.3.1 Primary map



X Index: 240



Y Index: 216

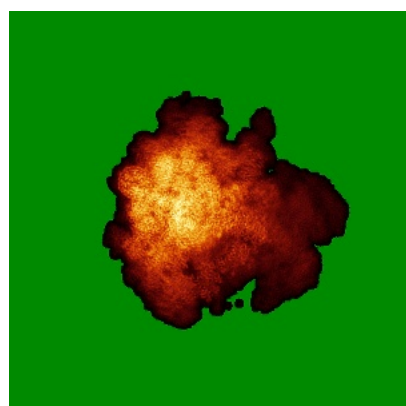


Z Index: 267

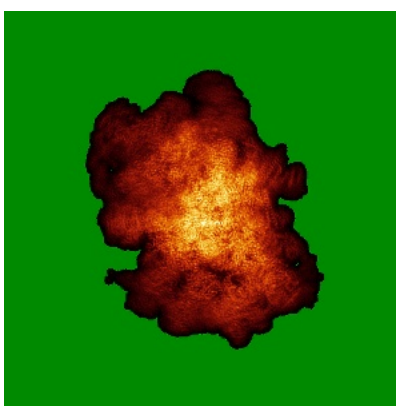
The images above show the largest variance slices of the map in three orthogonal directions.

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

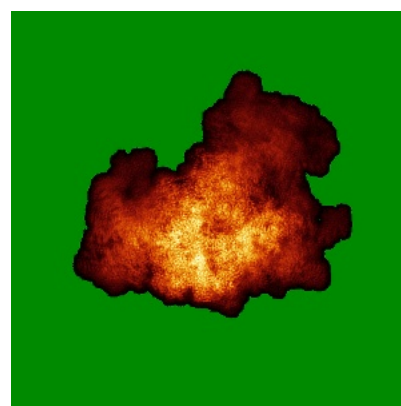
6.4.1 Primary map



X



Y

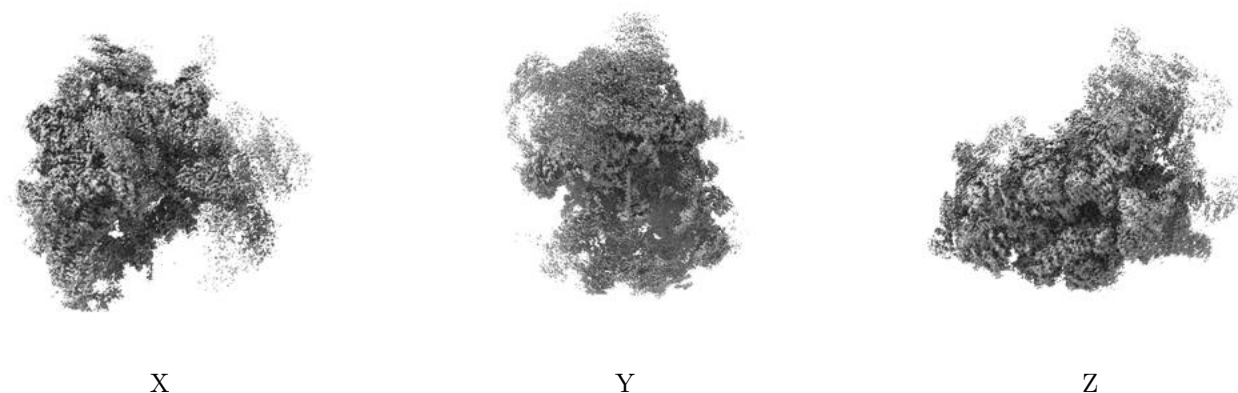


Z

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

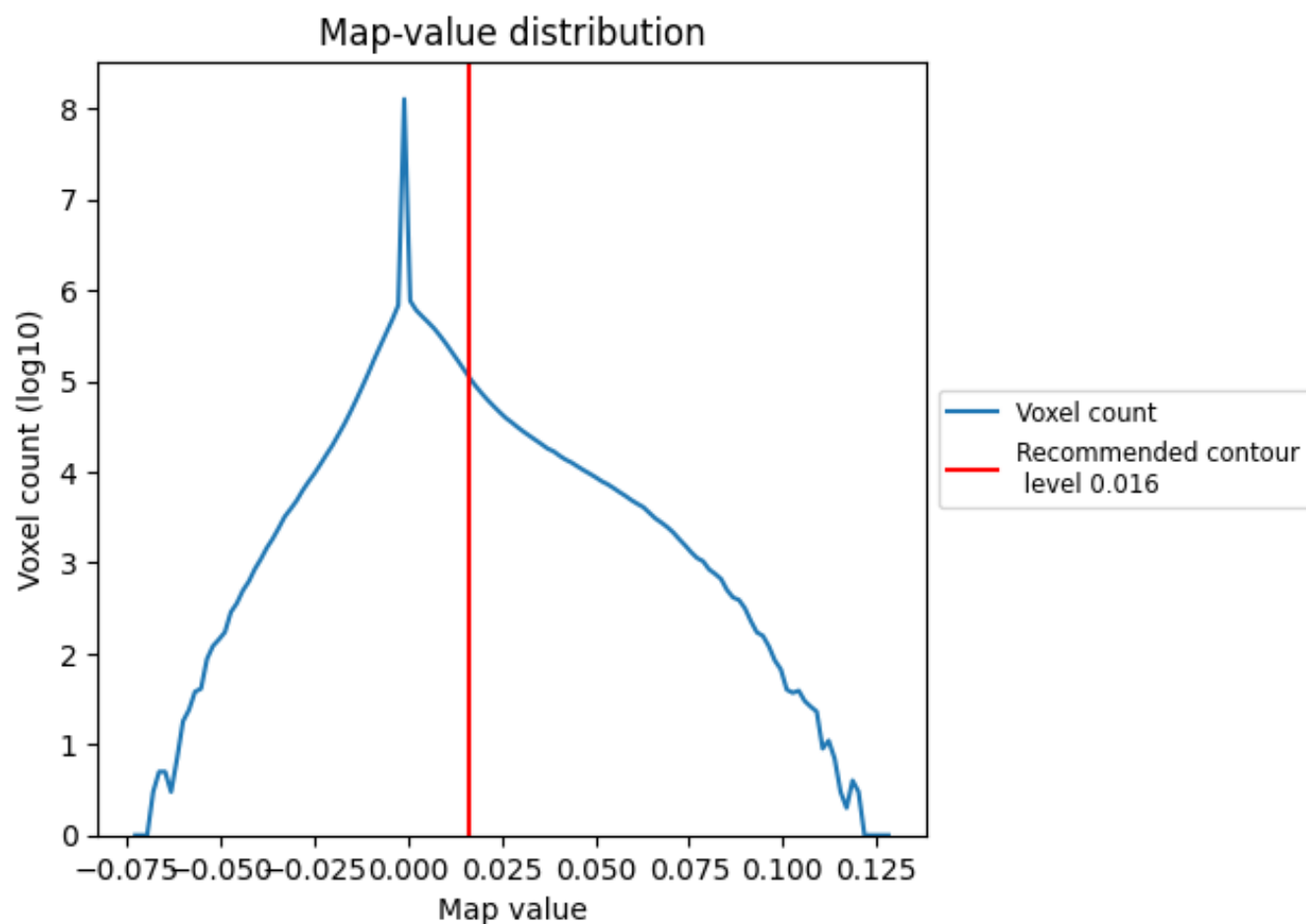
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

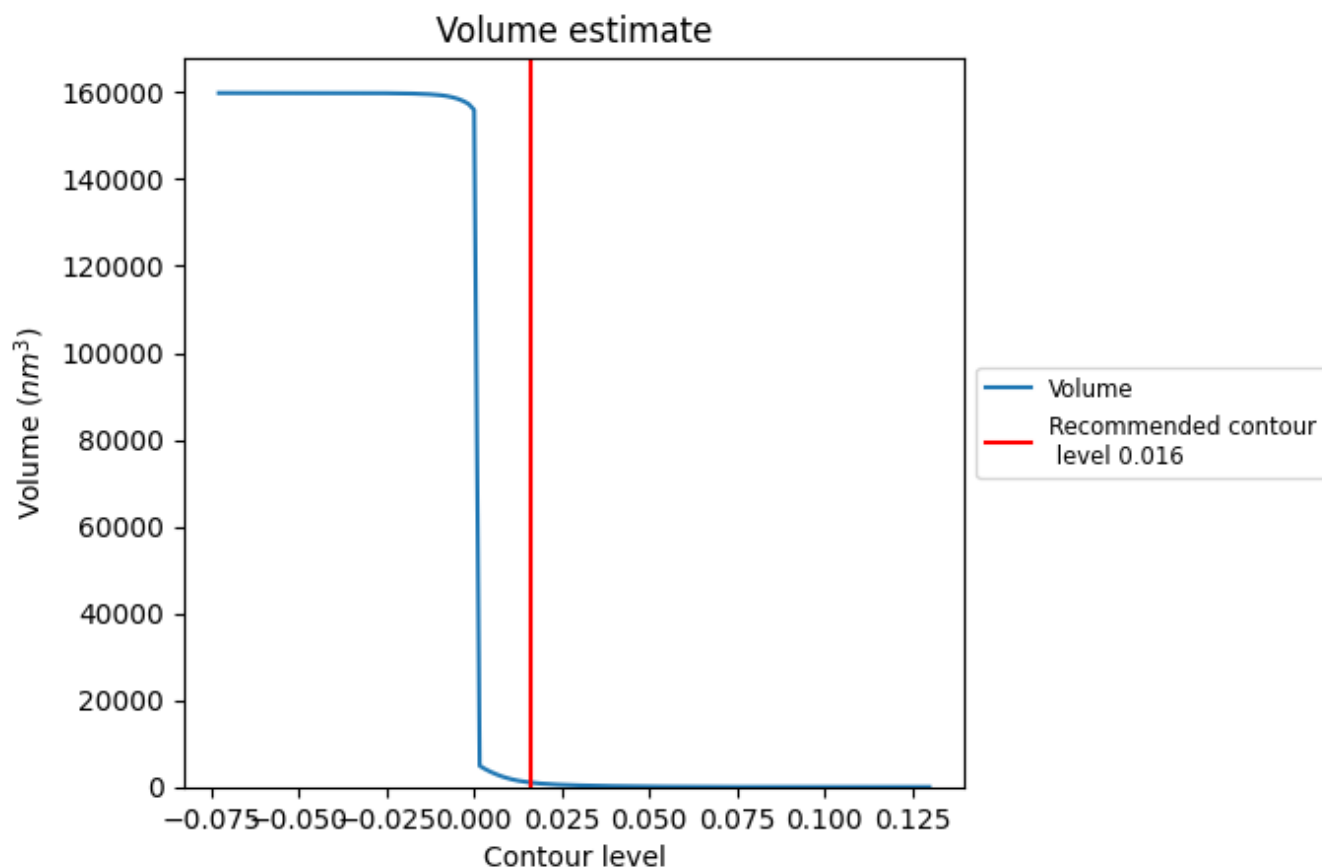
This section contains the results of statistical analysis of the map.

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.

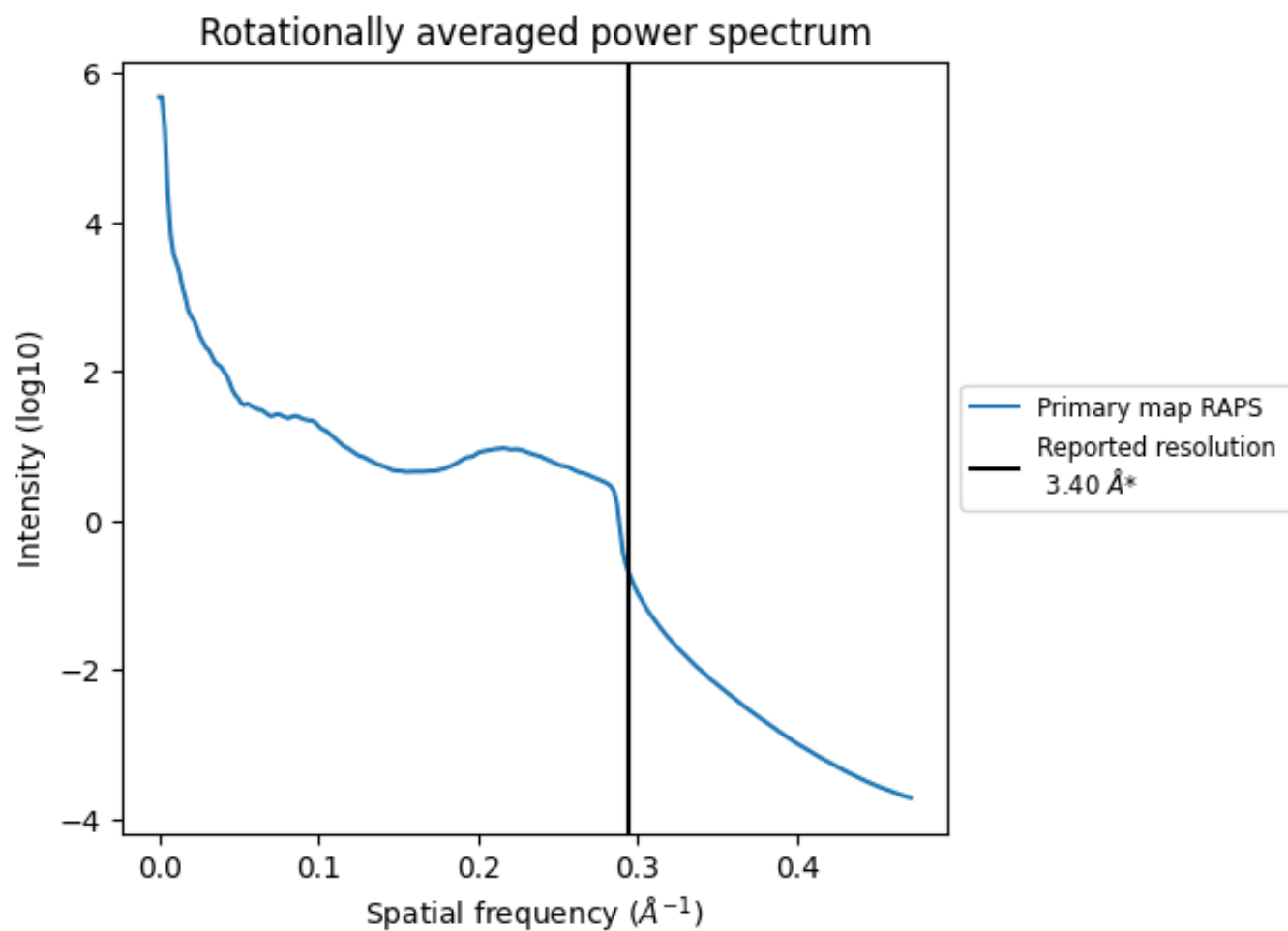
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1022 nm^3 ; this corresponds to an approximate mass of 923 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 ⓘ

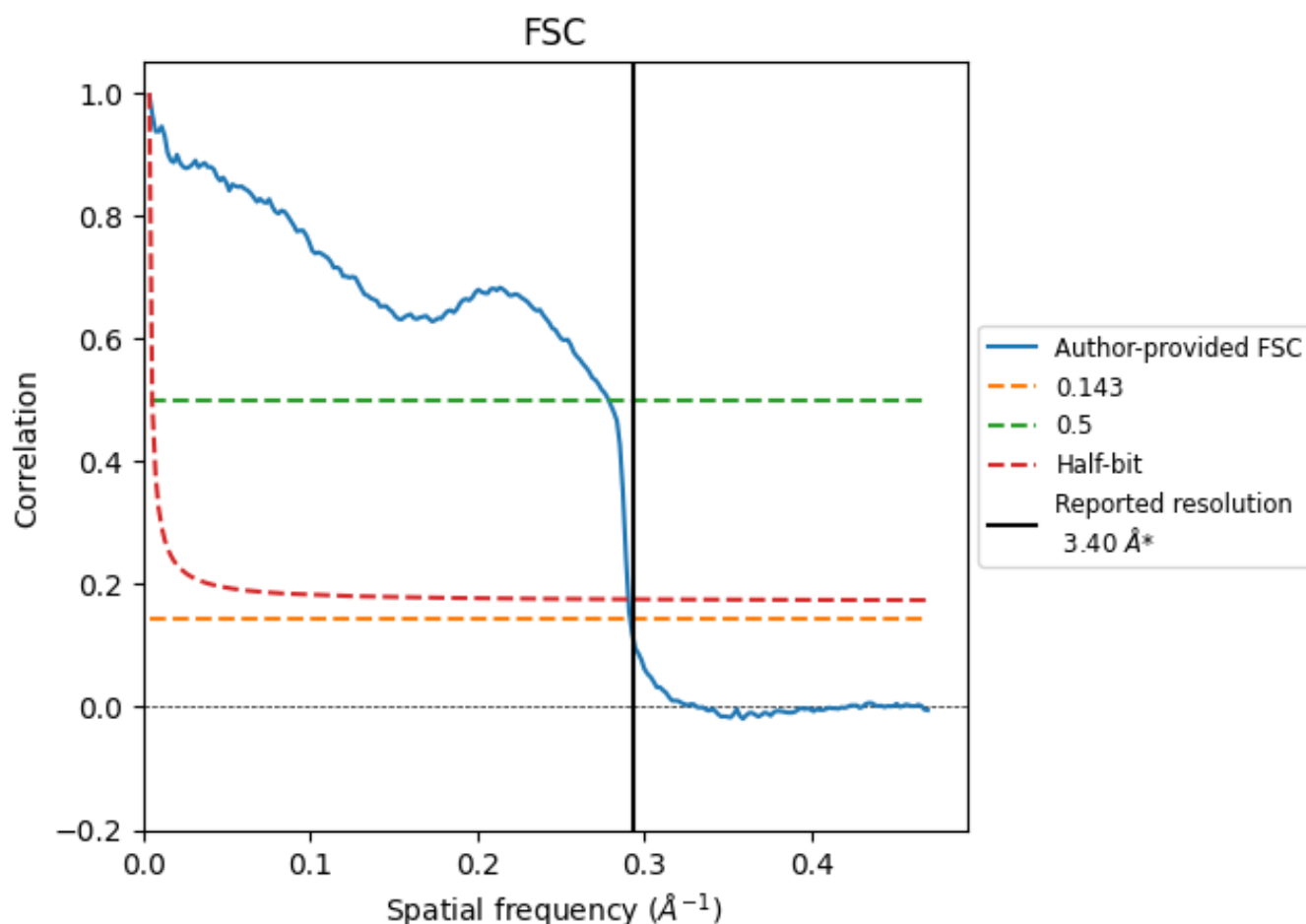


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

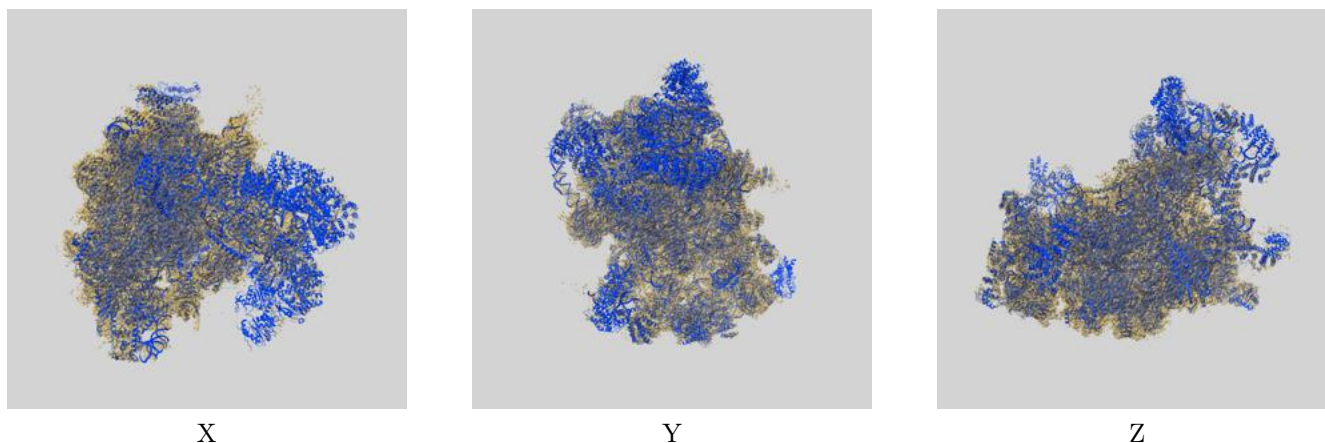
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.43	3.59	3.44
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

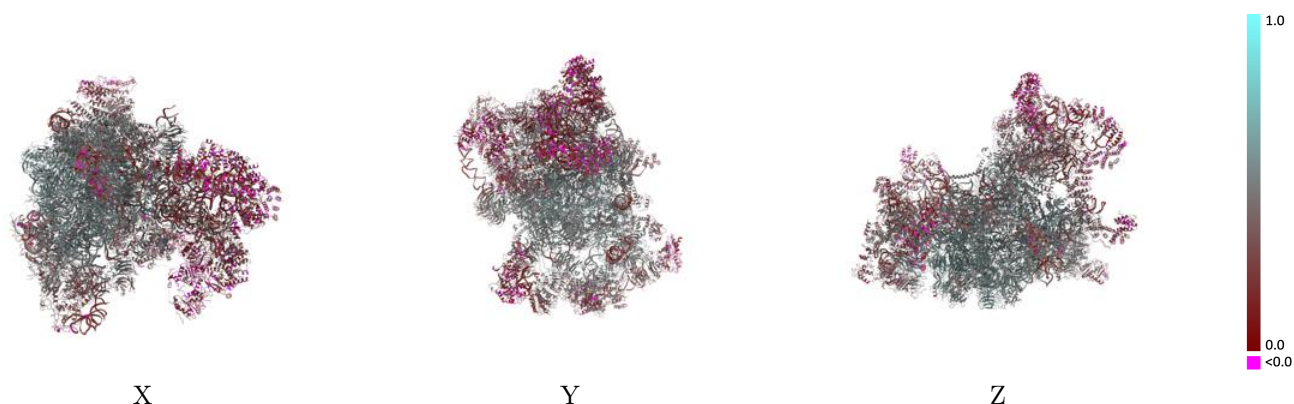
This section contains information regarding the fit between EMDB map EMD-9964 and PDB model 6KE6. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



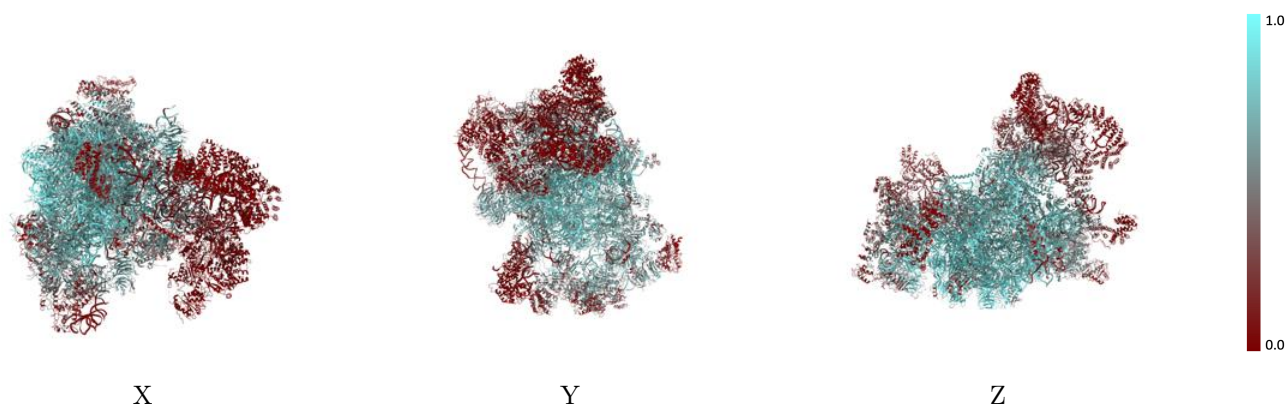
The images above show the 3D surface view of the map at the recommended contour level 0.016 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



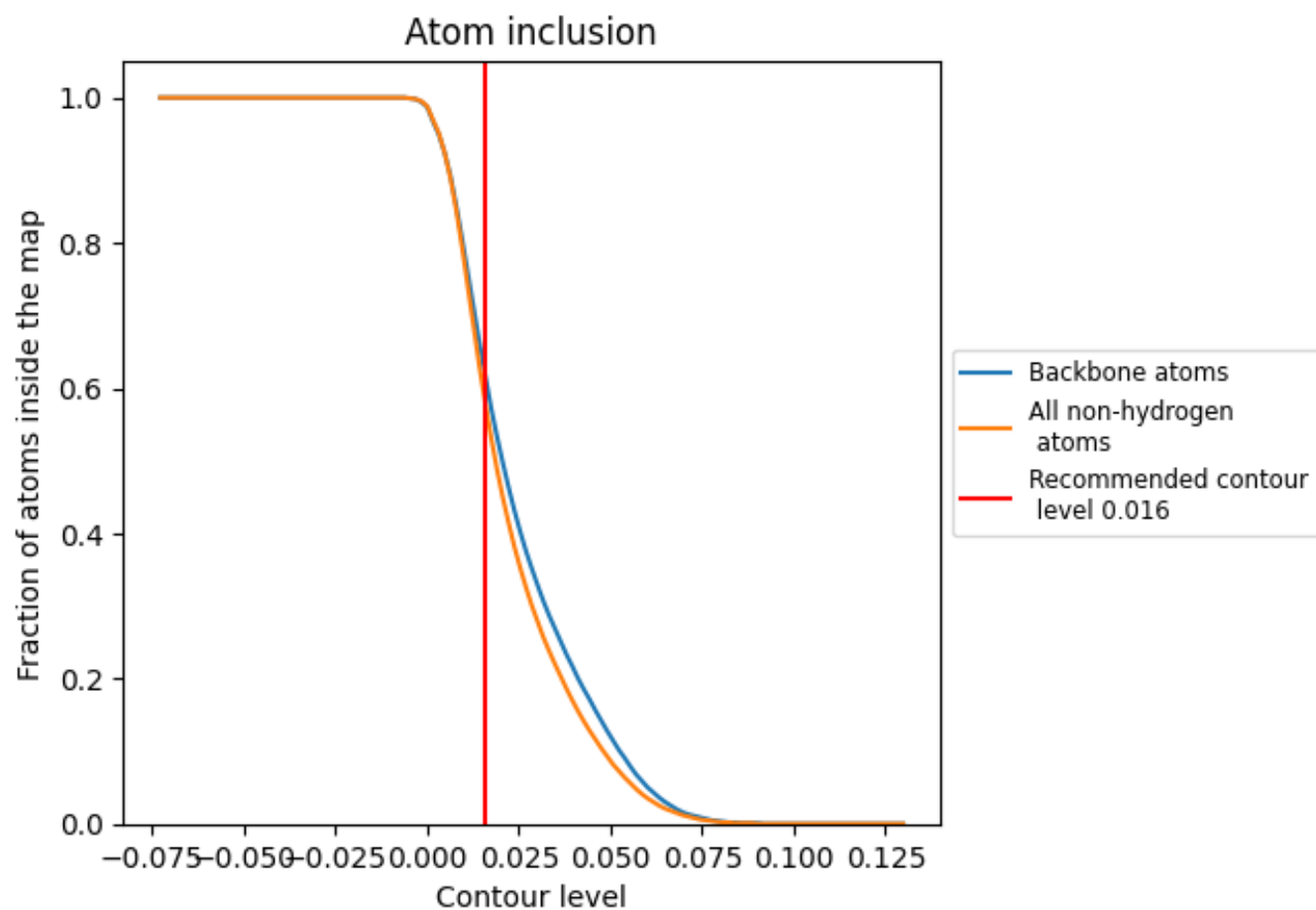
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.016).

9.4 Atom inclusion ⓘ



At the recommended contour level, 61% of all backbone atoms, 57% 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 (0.016) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5740	 0.4270
3A	 0.8270	 0.4550
3B	 0.8620	 0.5570
3C	 0.5800	 0.4410
3D	 0.7370	 0.4890
3E	 0.6830	 0.4590
3F	 0.6610	 0.4530
3G	 0.8340	 0.5450
3H	 0.7580	 0.5110
5A	 0.7640	 0.4290
5B	 0.4040	 0.3970
5C	 0.8460	 0.5510
5D	 0.7550	 0.5110
5E	 0.7530	 0.5240
5F	 0.8870	 0.5690
5G	 0.8110	 0.5500
5H	 0.7230	 0.5000
5I	 0.8630	 0.5500
5J	 0.6630	 0.4970
5K	 0.8570	 0.5580
A4	 0.6830	 0.4510
A5	 0.7530	 0.4910
A8	 0.2280	 0.3060
A9	 0.3970	 0.3630
AE	 0.3780	 0.3480
AF	 0.7590	 0.5060
AG	 0.6910	 0.4690
B1	 0.8810	 0.5590
B2	 0.6660	 0.4520
B3	 0.5920	 0.4230
B6	 0.6690	 0.4400
B8	 0.8480	 0.5430
BE	 0.8700	 0.5550
RA	 0.0960	 0.2760
RB	 0.4640	 0.4280



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Chain	Atom inclusion	Q-score
RC	 0.6170	 0.4820
RE	 0.3870	 0.4000
RF	 0.2960	 0.3630
RG	 0.3630	 0.3870
RH	 0.5720	 0.4780
RI	 0.7660	 0.4930
RJ	 0.7420	 0.5030
RK	 0.6830	 0.4860
RL	 0.1200	 0.3130
RM	 0.0190	 0.1970
RN	 0.3310	 0.3780
RO	 0.4480	 0.3860
RP	 0.0910	 0.2260
RQ	 0.5790	 0.4680
RS	 0.0370	 0.2090
RT	 0.6790	 0.4800
RV	 0.7190	 0.5180
SA	 0.5130	 0.3620
SC	 0.7480	 0.5170
SF	 0.2900	 0.3660
SG	 0.8170	 0.5350
SH	 0.0940	 0.3450
SI	 0.5210	 0.4250
SJ	 0.1430	 0.2790
SK	 0.8060	 0.5300
SM	 0.1530	 0.2840
SN	 0.0050	 0.1060
SO	 0.7580	 0.5080
SP	 0.7590	 0.5120
SR	 0.8490	 0.5530
ST	 0.3320	 0.4150
SX	 0.7840	 0.5300
SY	 0.7750	 0.5270
SZ	 0.4900	 0.4280
Sc	 0.7680	 0.5200
Sd	 0.8410	 0.5500
X1	 0.3290	 0.3770