



Full wwPDB EM Validation Report ⓘ

Mar 26, 2026 – 02:16 PM UTC

PDB ID : 8OO0 / pdb_00008oo0
EMDB ID : EMD-17004
Title : Chaetomium thermophilum Methionine Aminopeptidase 2 autoproteolysis product at the 80S ribosome
Authors : Klein, M.A.; Wild, K.; Kisonaite, M.; Sinning, I.
Deposited on : 2023-04-04
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

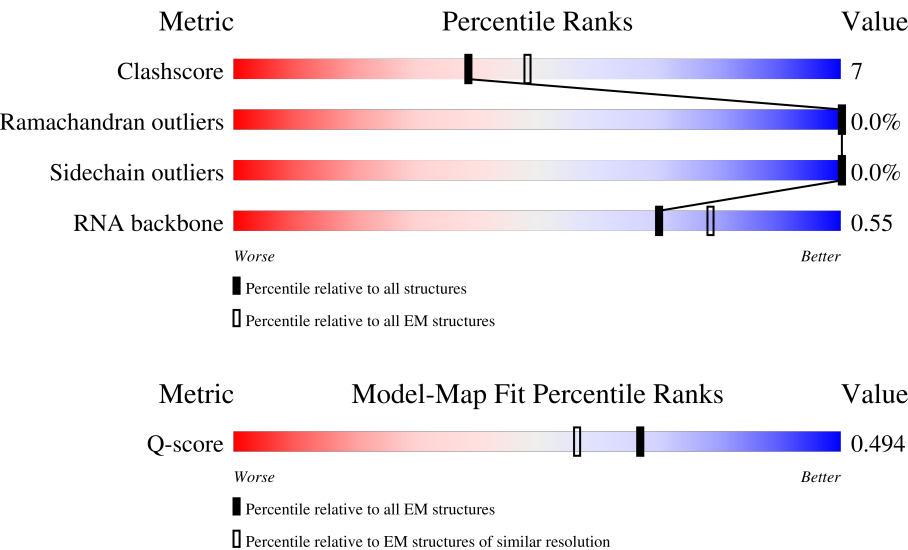
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.10 Å.

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



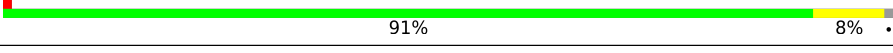
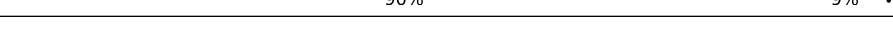
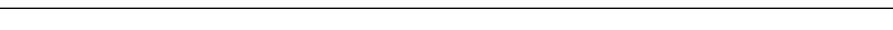
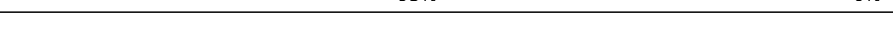
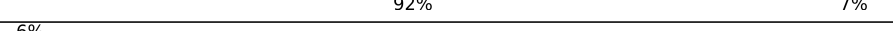
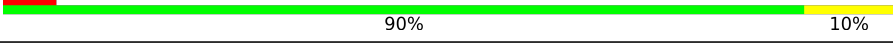
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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

Mol	Chain	Length	Quality of chain
1	1	3337	71%21%.
2	2	1796	64%27%7%.
3	3	120	80%18%..

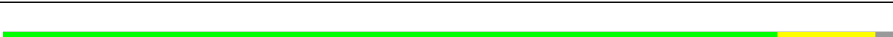
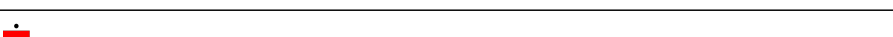
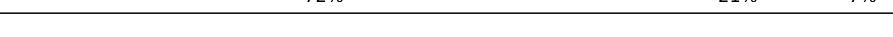
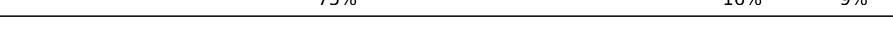
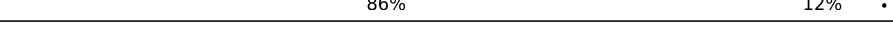
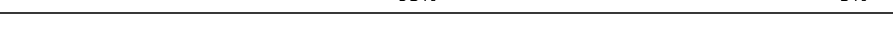
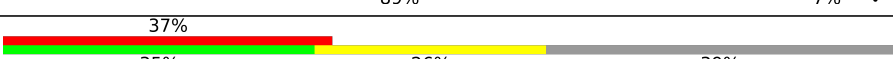
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Mol	Chain	Length	Quality of chain
4	4	156	
5	A	316	
6	B	302	
7	C	614	
8	LA	254	
9	LB	388	
10	LC	365	
11	LD	304	
12	LE	200	
13	LF	249	
14	LG	262	
15	LH	192	
16	LI	219	
17	LJ	173	
18	LK	165	
19	LL	213	
20	LM	142	
21	LN	203	
22	LO	204	
23	LP	186	
24	LQ	213	
25	LR	192	
26	LS	174	
27	LT	160	
28	LU	127	

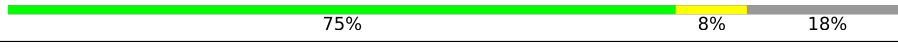
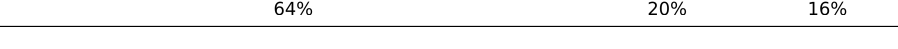
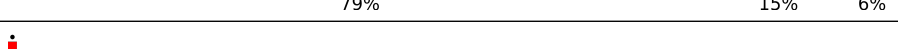
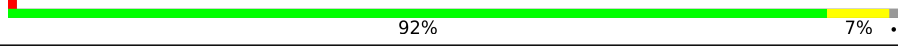
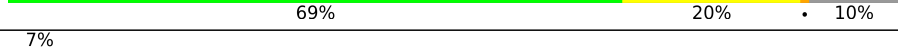
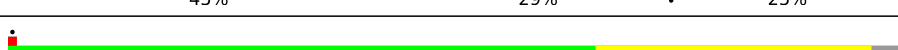
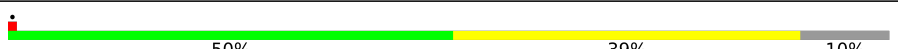
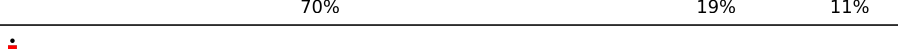
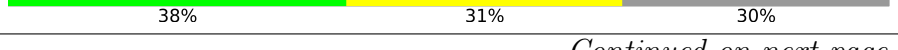
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Mol	Chain	Length	Quality of chain
29	LV	139	
30	LW	161	
31	LX	156	
32	LY	138	
33	LZ	135	
34	La	149	
35	Lb	65	
36	Lc	108	
37	Ld	120	
38	Le	131	
39	Lf	109	
40	Lg	119	
41	Lh	126	
42	Li	110	
43	Lj	95	
44	Lk	80	
45	Ll	51	
46	Lm	128	
47	Ln	25	
47	Lr	25	
48	Lo	106	
49	Lp	92	
50	Lq	147	
51	Ls	312	
52	SA	285	

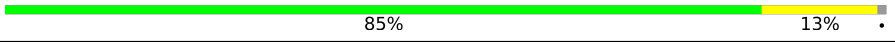
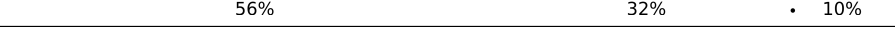
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Mol	Chain	Length	Quality of chain
53	SB	255	
54	SC	263	
55	SD	254	
56	SE	264	
57	SF	212	
58	SG	239	
59	SH	203	
60	SI	202	
61	SJ	190	
62	SK	159	
63	SL	161	
64	SM	144	
65	SN	151	
66	SO	150	
67	SP	153	
68	SQ	143	
69	SR	143	
70	SS	156	
71	ST	153	
72	SU	116	
73	SV	98	
74	SW	130	
75	SX	145	
76	SY	136	
77	SZ	99	

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Mol	Chain	Length	Quality of chain
78	Sa	119	
79	Sb	82	
80	Sc	68	
81	Sd	56	
82	Se	61	
83	Sf	154	
84	D	371	

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 208770 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 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	3191	Total	C	N	O	P	0	0
			68242	30465	12334	22252	3191		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	2578	OMG	N	conflict	GB 7OLC_1

- Molecule 2 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1765	Total	C	N	O	P	0	0
			37645	16822	6706	12352	1765		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	1	U	N	conflict	GB 7OLC_2
2	1188	B8N	N	conflict	GB 7OLC_2

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	119	Total	C	N	O	P	0	0
			2535	1132	453	831	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	1	A	N	conflict	GB 7OLC_3

- Molecule 4 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	156	Total	C	N	O	P	0	0
			3319	1484	589	1090	156		

- Molecule 5 is a protein called Putative guanine nucleotide-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	312	Total	C	N	O	S	0	0
			2438	1534	424	468	12		

- Molecule 6 is a protein called Hyaluronan/mRNA-binding protein domain-containing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	B	32	Total	C	N	O	0	0
			244	145	49	50		

- Molecule 7 is a protein called Ribosome-associated molecular chaperone SSB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	78	Total	C	N	O	S	0	0
			619	388	106	123	2		

- Molecule 8 is a protein called 60S ribosomal protein L2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LA	252	Total	C	N	O	S	0	0
			1925	1203	385	334	3		

- Molecule 9 is a protein called 60S ribosomal protein L3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LB	387	Total	C	N	O	S	0	0
			3088	1964	576	535	13		

- Molecule 10 is a protein called 60S ribosomal protein L4-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LC	363	Total	C	N	O	S	0	0
			2758	1741	527	481	9		

- Molecule 11 is a protein called 60S ribosomal protein l5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LD	300	Total	C	N	O	S	0	0
			2440	1545	431	461	3		

- Molecule 12 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LE	194	Total	C	N	O	S	0	0
			1518	974	274	267	3		

- Molecule 13 is a protein called 60S ribosomal protein l7-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LF	247	Total	C	N	O	S	0	0
			2017	1294	376	344	3		

- Molecule 14 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LG	235	Total	C	N	O	S	0	0
			1900	1218	351	326	5		

- Molecule 15 is a protein called 60S ribosomal protein l9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LH	191	Total	C	N	O	S	0	0
			1505	955	269	275	6		

- Molecule 16 is a protein called 60S ribosomal protein L10-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LI	217	Total	C	N	O	S	0	0
			1760	1109	343	299	9		

- Molecule 17 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LJ	167	Total	C	N	O	S	0	0
			1367	854	268	239	6		

- Molecule 18 is a protein called 60S ribosomal protein L12-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	LK	155	Total	C	N	O		
			762	452	155	155	0	0

- Molecule 19 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LL	209	Total	C	N	O	S		
			1666	1037	340	287	2	0	0

- Molecule 20 is a protein called 60S ribosomal protein L14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LM	141	Total	C	N	O	S		
			1125	714	216	194	1	0	0

- Molecule 21 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LN	202	Total	C	N	O	S		
			1703	1062	360	277	4	0	0

- Molecule 22 is a protein called 60S ribosomal protein L16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LO	203	Total	C	N	O	S		
			1613	1036	305	267	5	0	0

- Molecule 23 is a protein called 60S ribosomal protein l17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LP	186	Total	C	N	O	S		
			1472	912	295	262	3	0	0

- Molecule 24 is a protein called Ribosomal protein L18-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LQ	183	Total	C	N	O	S		
			1481	935	306	238	2	0	0

- Molecule 25 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LR	184	Total	C	N	O	S	0	0
			1506	928	324	249	5		

- Molecule 26 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LS	173	Total	C	N	O	S	0	0
			1425	917	266	238	4		

- Molecule 27 is a protein called 60S ribosomal protein l21-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LT	158	Total	C	N	O	S	0	0
			1266	803	246	215	2		

- Molecule 28 is a protein called 60S ribosomal protein L22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LU	101	Total	C	N	O	S	0	0
			819	532	142	144	1		

- Molecule 29 is a protein called 60S ribosomal protein l23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LV	135	Total	C	N	O	S	0	0
			994	633	185	169	7		

- Molecule 30 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LW	133	Total	C	N	O	S	0	0
			1075	667	221	185	2		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LW	5	GLU	ASP	conflict	UNP G2Q623
LW	7	THR	SER	conflict	UNP G2Q623
LW	102	ASN	SER	conflict	UNP G2Q623
LW	117	ALA	GLN	conflict	UNP G2Q623
LW	139	PRO	ALA	conflict	UNP G2Q623
LW	140	GLN	ALA	conflict	UNP G2Q623

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Chain	Residue	Modelled	Actual	Comment	Reference
LW	154	VAL	ILE	conflict	UNP G2Q623
LW	157	ALA	GLN	conflict	UNP G2Q623

- Molecule 31 is a protein called 60S ribosomal protein L25-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	LX	121	Total	C	N	O	0	0
			965	620	175	170		

- Molecule 32 is a protein called 60S ribosomal protein L26-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LY	134	Total	C	N	O	S	0	0
			1065	664	215	184	2		

- Molecule 33 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LZ	135	Total	C	N	O	S	0	0
			1111	713	207	187	4		

- Molecule 34 is a protein called Ribosomal protein L18e/L15P domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	La	148	Total	C	N	O	S	0	0
			1180	745	239	194	2		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
La	70	ARG	ALA	conflict	UNP G2QB77
La	72	SER	THR	conflict	UNP G2QB77
La	84	SER	ALA	conflict	UNP G2QB77
La	85	ASP	GLU	conflict	UNP G2QB77
La	86	VAL	THR	conflict	UNP G2QB77
La	94	GLN	ALA	conflict	UNP G2QB77
La	96	LYS	THR	conflict	UNP G2QB77
La	120	GLU	GLN	conflict	UNP G2QB77
La	123	VAL	PHE	conflict	UNP G2QB77
La	139	LYS	THR	conflict	UNP G2QB77

- Molecule 35 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	Lb	62	Total	C	N	O	0	0
			508	310	112	86		

- Molecule 36 is a protein called 60S ribosomal protein l30-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lc	97	Total	C	N	O	S	0	0
			722	458	125	134	5		

- Molecule 37 is a protein called Putative 60S ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ld	112	Total	C	N	O	S	0	0
			911	575	178	157	1		

- Molecule 38 is a protein called 60S ribosomal protein L32-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Le	124	Total	C	N	O	S	0	0
			1001	629	205	161	6		

- Molecule 39 is a protein called 60S ribosomal protein l33-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lf	107	Total	C	N	O	S	0	0
			853	540	170	142	1		

- Molecule 40 is a protein called Ribosomal protein l34-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lg	112	Total	C	N	O	S	0	0
			891	554	181	152	4		

- Molecule 41 is a protein called dolichyl-diphosphooligosaccharide--protein glycotransferase.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	Lh	122	Total	C	N	O	0	0
			1003	637	198	168		

- Molecule 42 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Li	102	Total	C	N	O	S	0	0
			836	515	184	136	1		

- Molecule 43 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lj	86	Total	C	N	O	S	0	0
			684	418	152	109	5		

- Molecule 44 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lk	76	Total	C	N	O	S	0	0
			632	400	121	109	2		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lk	5	VAL	ILE	conflict	UNP G2Q8J4
Lk	6	SER	GLY	conflict	UNP G2Q8J4
Lk	53	ASP	GLU	conflict	UNP G2Q8J4
Lk	78	LYS	SER	conflict	UNP G2Q8J4

- Molecule 45 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	Ll	50	Total	C	N	O	0	0
			435	275	97	63		

- Molecule 46 is a protein called Ubiquitin-like domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lm	52	Total	C	N	O	S	0	0
			418	261	86	65	6		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lm	24	GLU	ASP	conflict	UNP A0A2A9PNA8
Lm	28	ALA	SER	conflict	UNP A0A2A9PNA8

- Molecule 47 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Ln	24	Total	C	N	O	S	0	0
			224	136	61	26	1		
47	Lr	24	Total	C	N	O	S	0	0
			224	136	61	26	1		

- Molecule 48 is a protein called 60S ribosomal protein L44-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Lo	104	Total	C	N	O	S	0	0
			822	520	161	136	5		

- Molecule 49 is a protein called 60S ribosomal protein L43-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Lp	91	Total	C	N	O	S	0	0
			697	430	138	123	6		

- Molecule 50 is a protein called Putative 60S ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Lq	141	Total	C	N	O	S	0	0
			1083	678	215	190			

- Molecule 51 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Ls	189	Total	C	N	O	S	0	0
			1449	927	250	265	7		

- Molecule 52 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SA	208	Total	C	N	O	S	0	0
			1641	1051	289	295	6		

- Molecule 53 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SB	232	Total	C	N	O	S	0	0
			1871	1190	351	325	5		

- Molecule 54 is a protein called 40S ribosomal protein S2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SC	216	Total	C	N	O	S	0	0
			1672	1074	294	301	3		

- Molecule 55 is a protein called 40S ribosomal protein S3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SD	214	Total	C	N	O	S	0	0
			1688	1068	307	305	8		

- Molecule 56 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SE	261	Total	C	N	O	S	0	0
			2072	1314	389	362	7		

- Molecule 57 is a protein called 40S ribosomal protein s5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SF	199	Total	C	N	O	S	0	0
			1557	971	294	285	7		

- Molecule 58 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SG	232	Total	C	N	O	S	0	0
			1875	1171	376	323	5		

- Molecule 59 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SH	195	Total	C	N	O		0	0
			1562	983	300	279			

- Molecule 60 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SI	201	Total	C	N	O	S	0	0
			1621	1009	330	281	1		

- Molecule 61 is a protein called 40S ribosomal protein s9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SJ	179	Total	C	N	O	S	0	0
			1466	933	290	241	2		

- Molecule 62 is a protein called 40S ribosomal protein s10-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SK	89	Total	C	N	O	S	0	0
			742	487	124	129	2		

- Molecule 63 is a protein called 40S ribosomal protein S11-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SL	150	Total	C	N	O	S	0	0
			1222	780	236	201	5		

- Molecule 64 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SM	118	Total	C	N	O	S	0	0
			923	577	167	171	8		

- Molecule 65 is a protein called 40S ribosomal protein S13-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SN	150	Total	C	N	O	S	0	0
			1182	756	220	205	1		

- Molecule 66 is a protein called 40S ribosomal protein S14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SO	135	Total	C	N	O	S	0	0
			1002	614	199	184	5		

- Molecule 67 is a protein called 40S ribosomal protein s15-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SP	115	Total	C	N	O	S	0	0
			917	583	172	159	3		

- Molecule 68 is a protein called 40S ribosomal protein S16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SQ	138	Total	C	N	O	S	0	0
			1081	693	202	184	2		

- Molecule 69 is a protein called 40S ribosomal protein S17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SR	128	Total	C	N	O	S	0	0
			1045	657	190	195	3		

- Molecule 70 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SS	137	Total	C	N	O	S	0	0
			1118	699	222	196	1		

- Molecule 71 is a protein called 40S ribosomal protein S19-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	ST	142	Total	C	N	O	S	0	0
			1117	694	221	201	1		

- Molecule 72 is a protein called 40S ribosomal protein S20-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SU	103	Total	C	N	O	S	0	0
			819	517	150	148	4		

- Molecule 73 is a protein called 40S ribosomal protein S21-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SV	86	Total	C	N	O	S	0	0
			664	408	124	128	4		

- Molecule 74 is a protein called 40S ribosomal protein S22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SW	129	Total	C	N	O	S	0	0
			1037	659	195	178	5		

- Molecule 75 is a protein called 40S ribosomal protein s23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SX	142	Total	C	N	O	S	0	0
			1099	694	215	188	2		

- Molecule 76 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SY	132	Total	C	N	O	S	0	0
			1061	668	209	182	2		

- Molecule 77 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SZ	69	Total	C	N	O	S	0	0
			546	345	101	98	2		

- Molecule 78 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sa	104	Total	C	N	O	S	0	0
			839	518	177	137	7		

- Molecule 79 is a protein called Ribosomal protein s27-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sb	81	Total	C	N	O	S	0	0
			611	386	111	107	7		

- Molecule 80 is a protein called 40S ribosomal protein S28-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sc	61	Total	C	N	O	S	0	0
			484	298	97	88	1		

- Molecule 81 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Sd	52	Total	C	N	O	S	0	0
			419	261	84	70	4		

- Molecule 82 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
82	Se	44	Total	C	N	O	0	0
			353	222	74	57		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Se	4	ALA	-	insertion	UNP Q2H4C5

- Molecule 83 is a protein called 40S ribosomal protein S27a-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Sf	73	Total	C	N	O	S	0	0
			604	382	115	101	6		

- Molecule 84 is a protein called Methionine aminopeptidase 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	D	371	Total	C	N	O	S	0	0
			2911	1832	513	559	7		

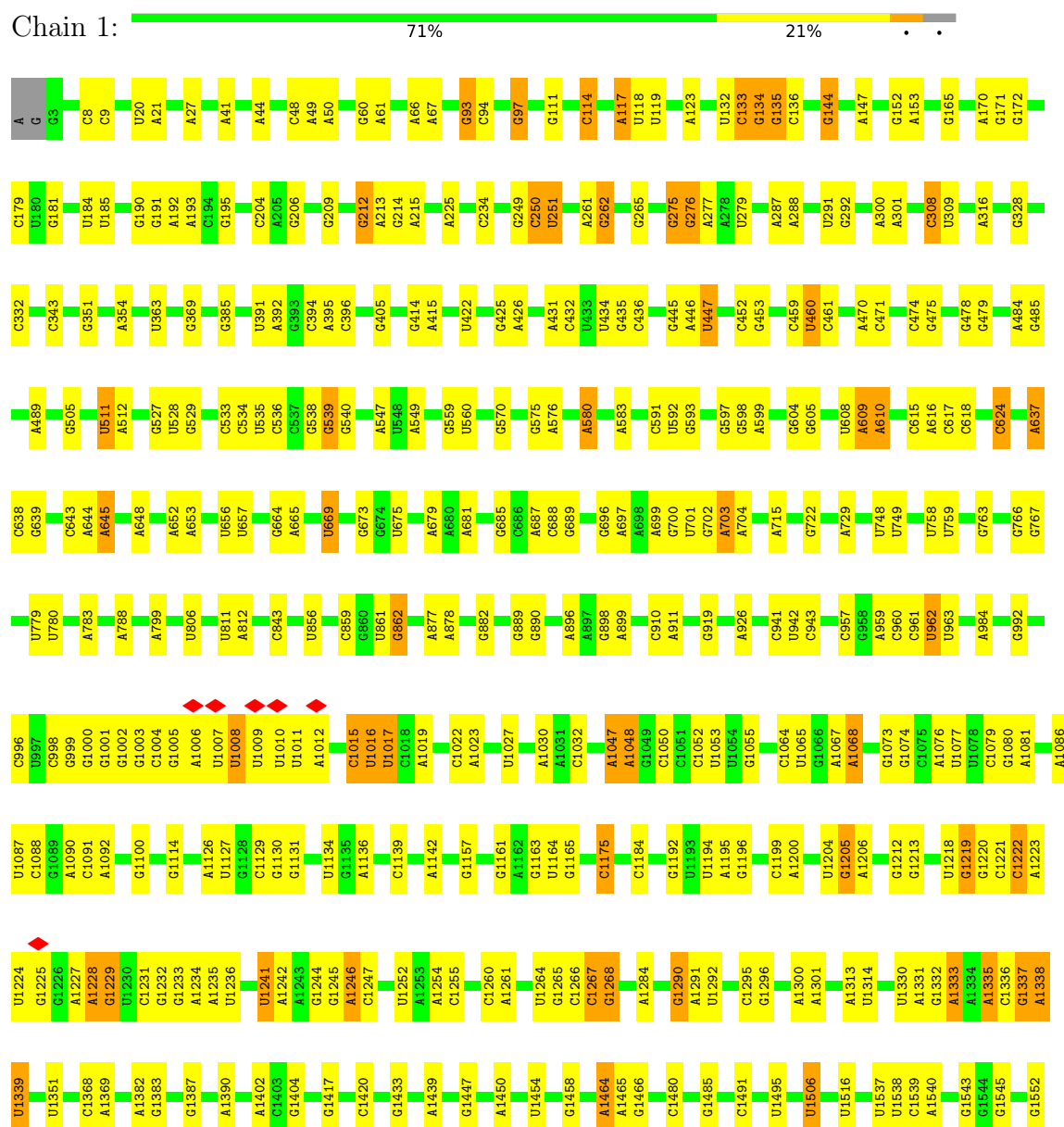
- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn).

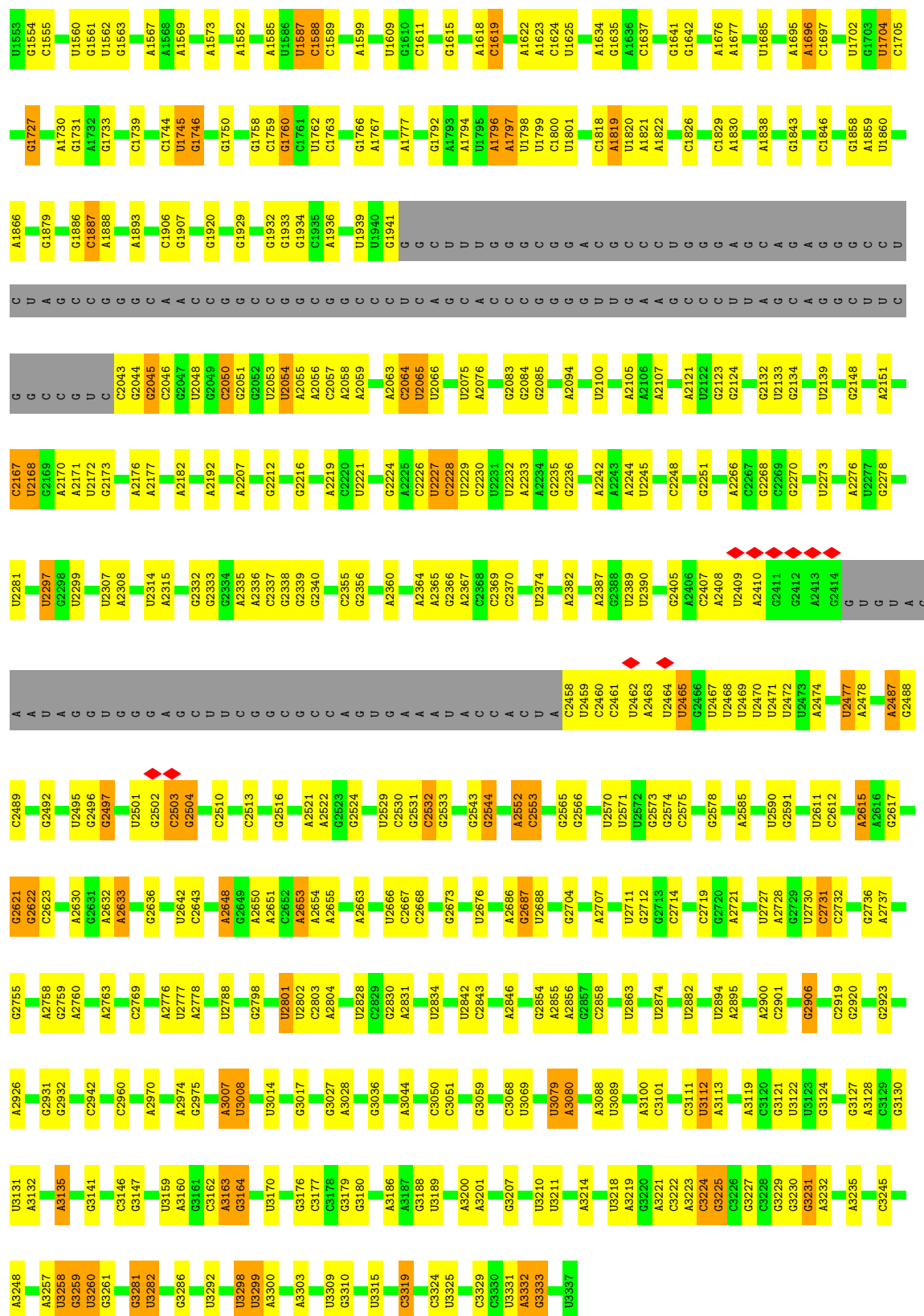
Mol	Chain	Residues	Atoms		AltConf
85	Lg	1	Total	Zn	0
			1	1	
85	Lj	1	Total	Zn	0
			1	1	
85	Lm	1	Total	Zn	0
			1	1	
85	Lo	1	Total	Zn	0
			1	1	
85	Lp	1	Total	Zn	0
			1	1	
85	Sa	1	Total	Zn	0
			1	1	
85	Sb	1	Total	Zn	0
			1	1	
85	Sd	1	Total	Zn	0
			1	1	

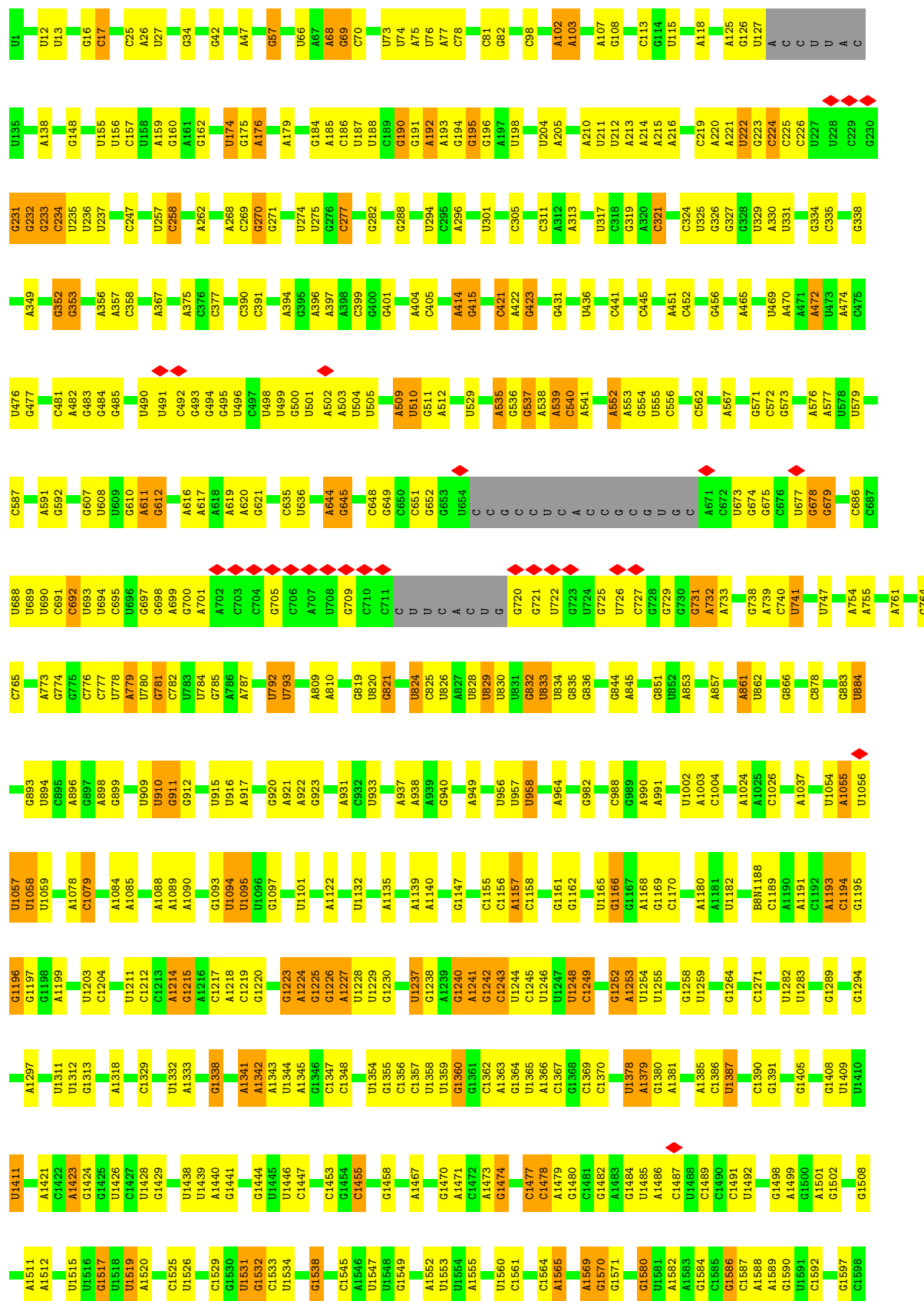
3 Residue-property plots

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

• Molecule 1: 28S rRNA

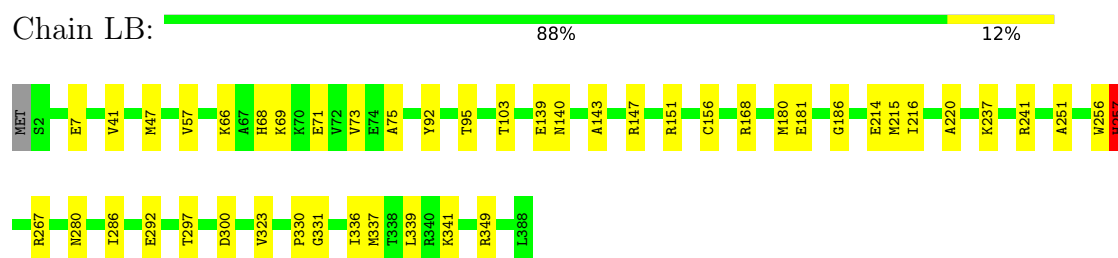




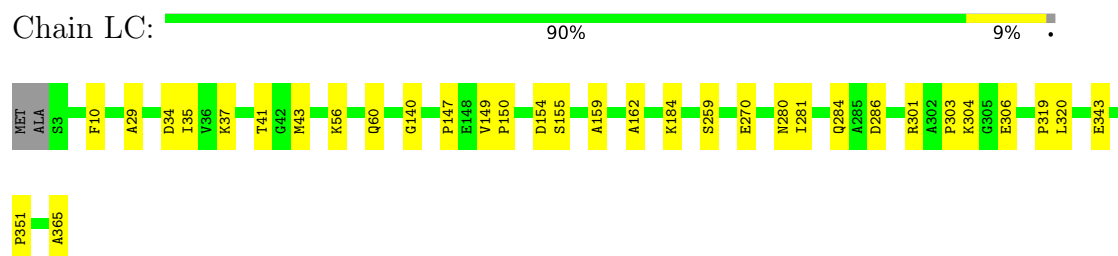




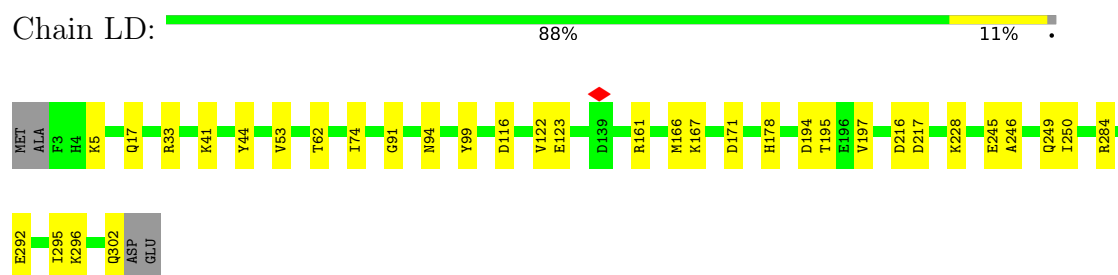
- Molecule 9: 60S ribosomal protein L3-like protein



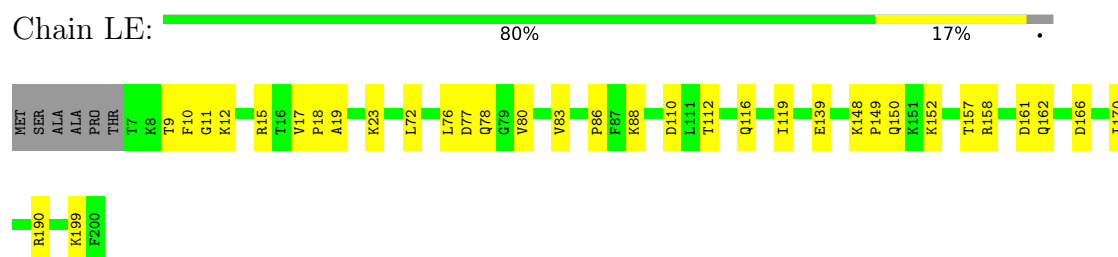
- Molecule 10: 60S ribosomal protein L4-like protein



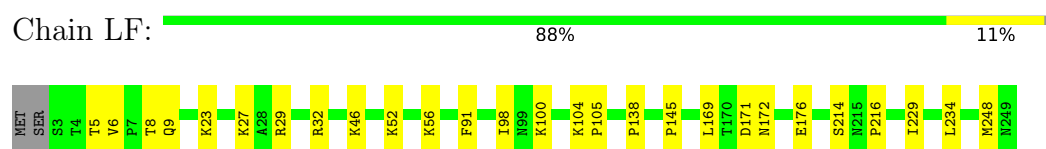
- Molecule 11: 60S ribosomal protein l5-like protein



- Molecule 12: 60S ribosomal protein L6

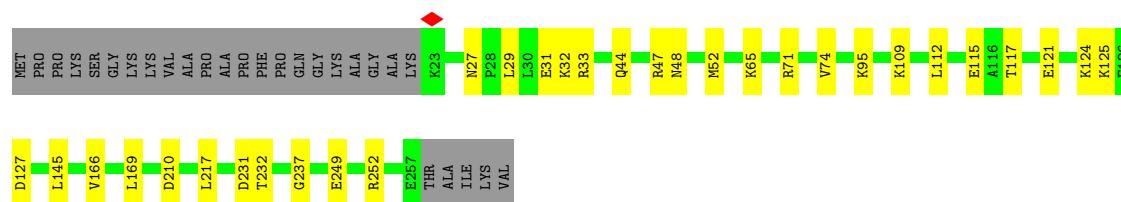


- Molecule 13: 60S ribosomal protein l7-like protein



- Molecule 14: 60S ribosomal protein L8

Chain LG:  78% 12% 10%



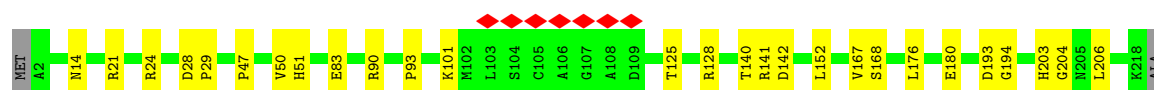
- Molecule 15: 60S ribosomal protein l9-like protein

Chain LH:  86% 13% .



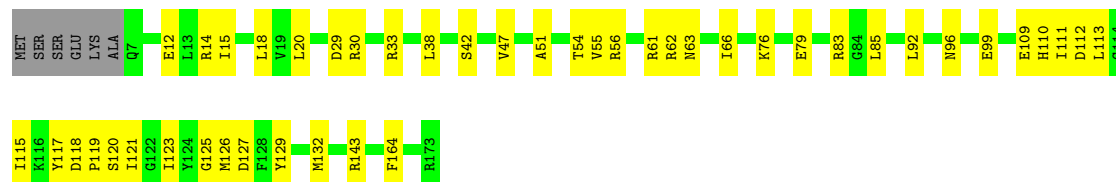
- Molecule 16: 60S ribosomal protein L10-like protein

Chain LI:  87% 12% .

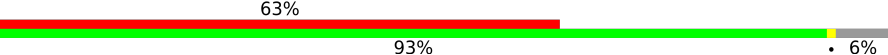


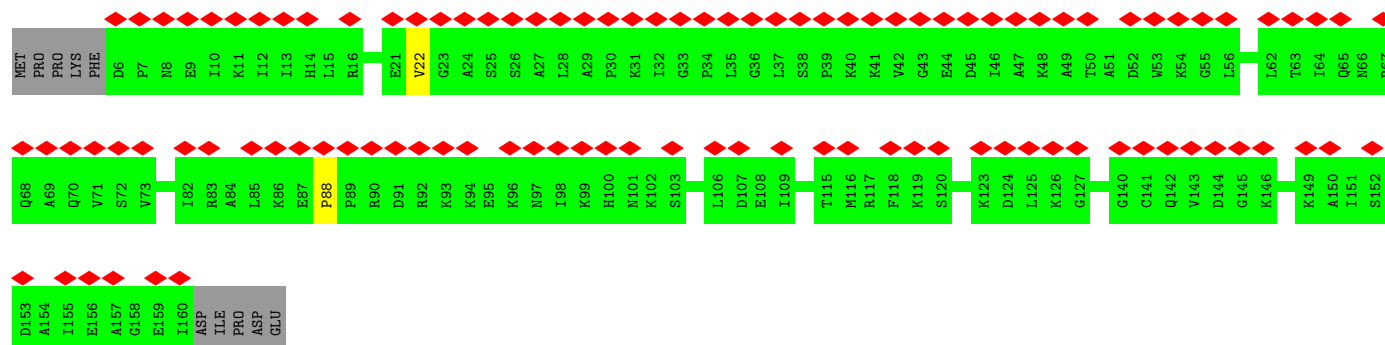
- Molecule 17: Putative ribosomal protein

Chain LJ:  71% 26% .



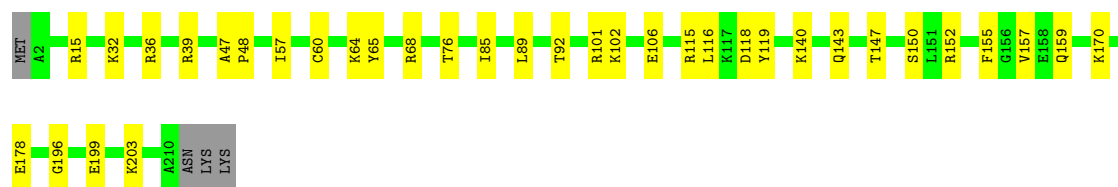
- Molecule 18: 60S ribosomal protein L12-like protein

Chain LK:  63% 93% 6% .



- Molecule 19: 60S ribosomal protein L13

Chain LL:  82% 16%



- Molecule 20: 60S ribosomal protein L14-like protein

Chain LM:  83% 16%

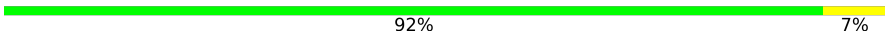


- Molecule 21: Ribosomal protein L15

Chain LN:  83% 16%



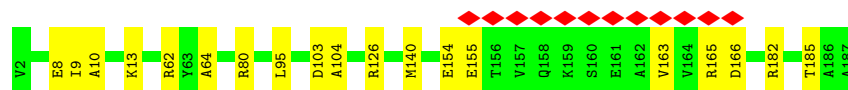
- Molecule 22: 60S ribosomal protein L16-like protein

Chain LO:  92% 7%



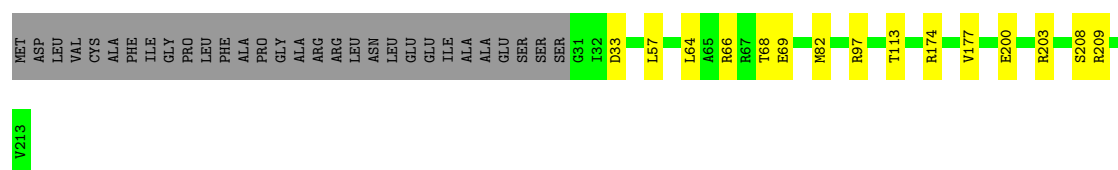
- Molecule 23: 60S ribosomal protein L17-like protein

Chain LP:  6% 90% 10%



- Molecule 24: Ribosomal protein L18-like protein

Chain LQ:  79% 7% 14%



- Molecule 25: Ribosomal protein L19

Chain LR:  85% 11%



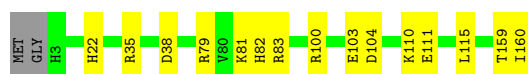
- Molecule 26: 60S ribosomal protein L20

Chain LS: 86% 14% .



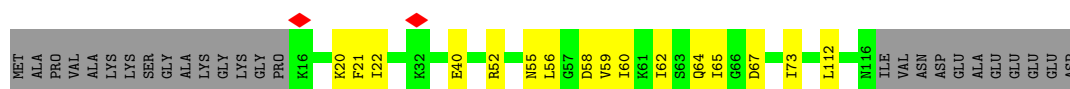
- Molecule 27: 60S ribosomal protein l21-like protein

Chain LT: 89% 9% .



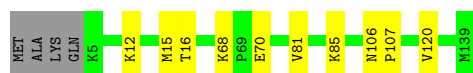
- Molecule 28: 60S ribosomal protein L22-like protein

Chain LU: 67% 13% 20%



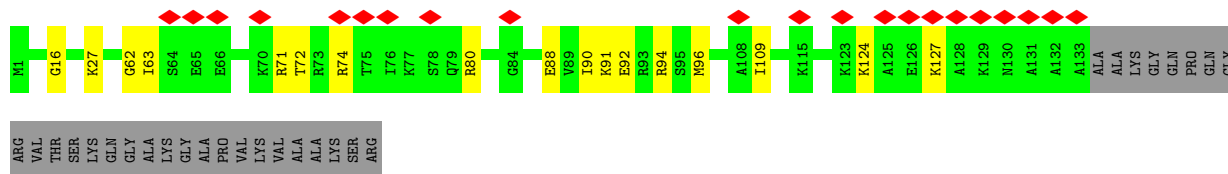
- Molecule 29: 60S ribosomal protein l23-like protein

Chain LV: 90% 7% .



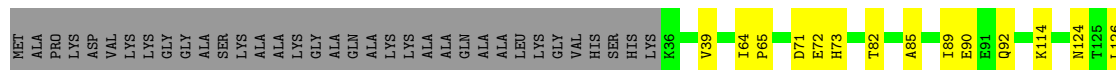
- Molecule 30: 60S ribosomal protein L24

Chain LW: 13% 72% 11% 17%



- Molecule 31: 60S ribosomal protein L25-like protein

Chain LX: 62% 15% 22%





- Molecule 32: 60S ribosomal protein L26-like protein

Chain LY: 79% 17%



- Molecule 33: 60S ribosomal protein L27

Chain LZ: 79% 21%



- Molecule 34: Ribosomal protein L18e/L15P domain-containing protein

Chain La: 86% 13%



- Molecule 35: 60S ribosomal protein L29

Chain Lb: 77% 18% 5%



- Molecule 36: 60S ribosomal protein l30-like protein

Chain Lc: 74% 16% 10%



- Molecule 37: Putative 60S ribosomal protein

Chain Ld: 79% 14% 7%

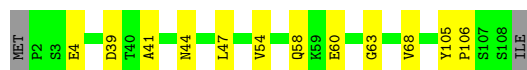
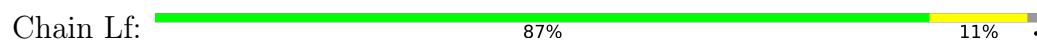


- Molecule 38: 60S ribosomal protein L32-like protein

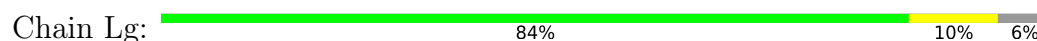
Chain Le: 87% 8% 5%



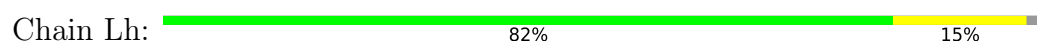
- Molecule 39: 60S ribosomal protein l33-like protein



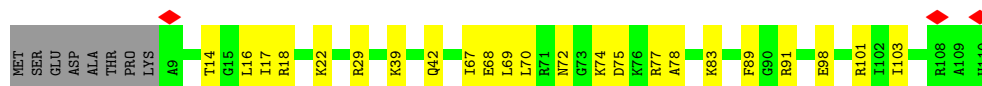
- Molecule 40: Ribosomal protein l34-like protein



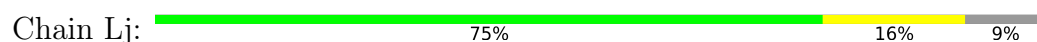
- Molecule 41: dolichyl-diphosphooligosaccharide--protein glycotransferase



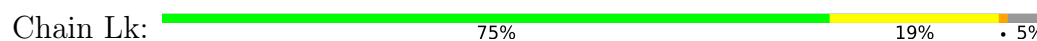
- Molecule 42: 60S ribosomal protein L36



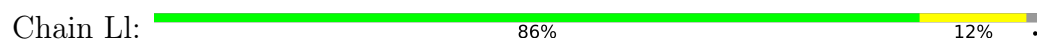
- Molecule 43: Ribosomal protein L37



- Molecule 44: 60S ribosomal protein L38



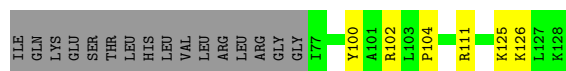
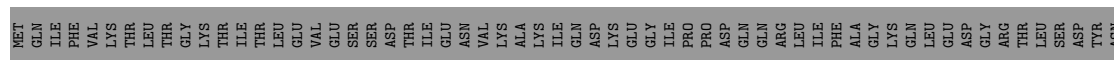
- Molecule 45: 60S ribosomal protein L39





- Molecule 46: Ubiquitin-like domain-containing protein

Chain Lm: 36% 5% 59%



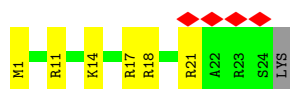
- Molecule 47: 60S ribosomal protein L41-A

Chain Ln: 88% 8% .



- Molecule 47: 60S ribosomal protein L41-A

Chain Lr: 16% 72% 24% .



- Molecule 48: 60S ribosomal protein L44-like protein

Chain Lo: 87% 10% ..



- Molecule 49: 60S ribosomal protein L43-like protein

Chain Lp: 93% 5% .

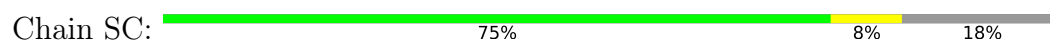


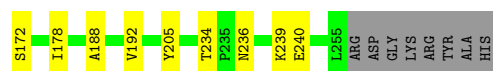
- Molecule 50: Putative 60S ribosomal protein

Chain Lq: 89% 7% .

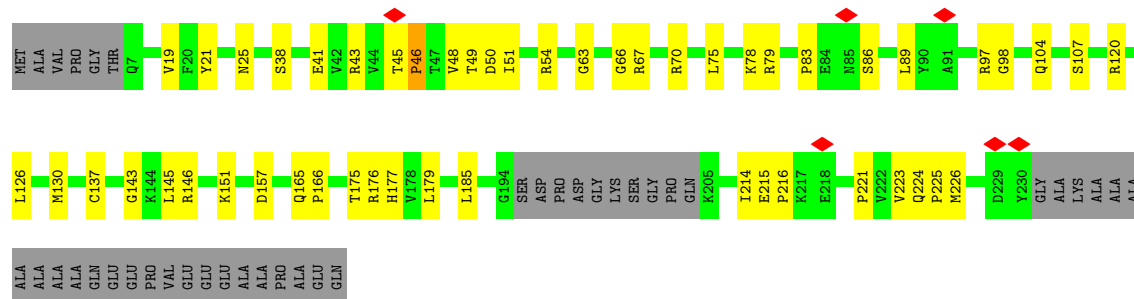


Chain Ls:

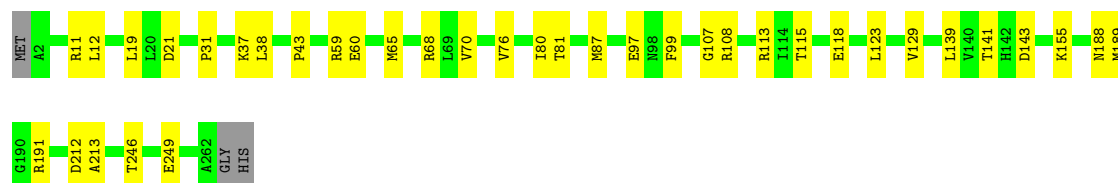
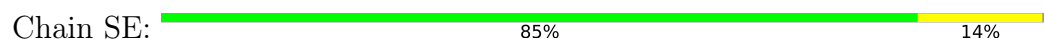




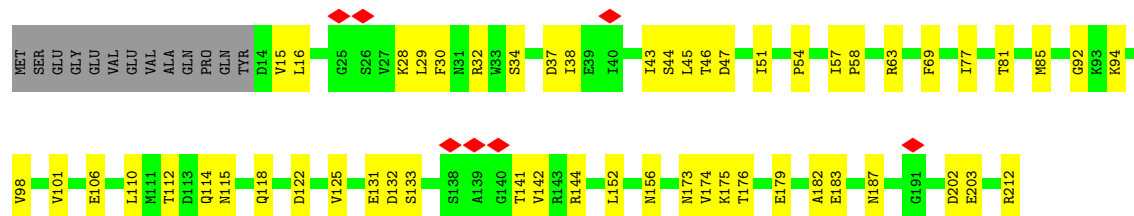
- Molecule 55: 40S ribosomal protein S3-like protein



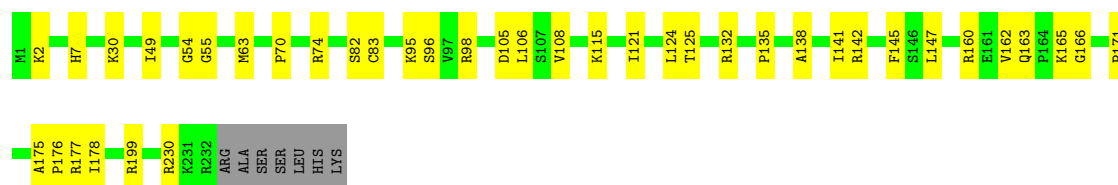
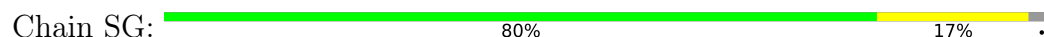
- Molecule 56: 40S ribosomal protein S4



- Molecule 57: 40S ribosomal protein s5-like protein

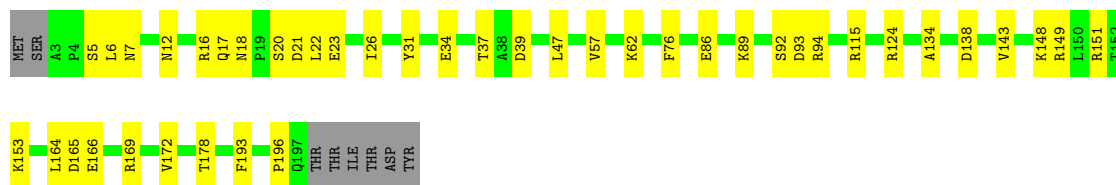


- Molecule 58: 40S ribosomal protein S6



- Molecule 59: 40S ribosomal protein S7

Chain SH:  75% 21% .



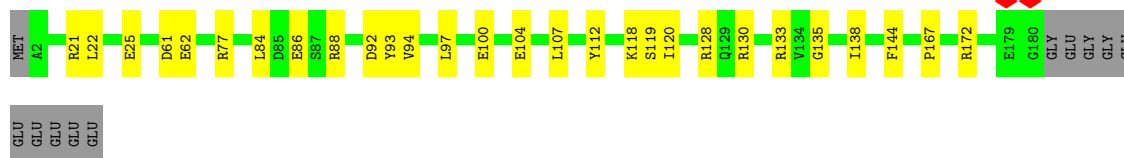
- Molecule 60: 40S ribosomal protein S8

Chain SI:  79% 21%



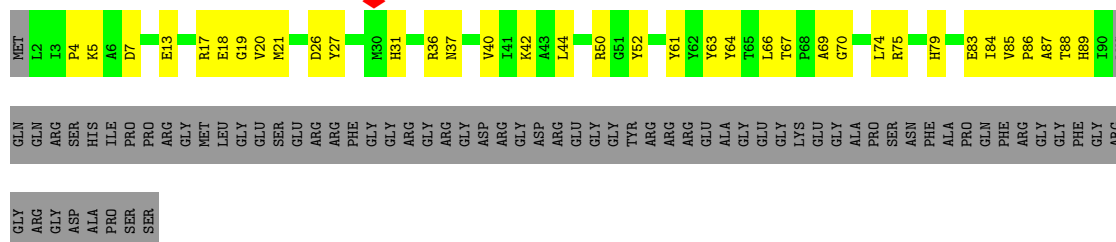
- Molecule 61: 40S ribosomal protein s9-like protein

Chain SJ:  79% 15% 6%



- Molecule 62: 40S ribosomal protein s10-like protein

Chain SK:  33% 23% 44%

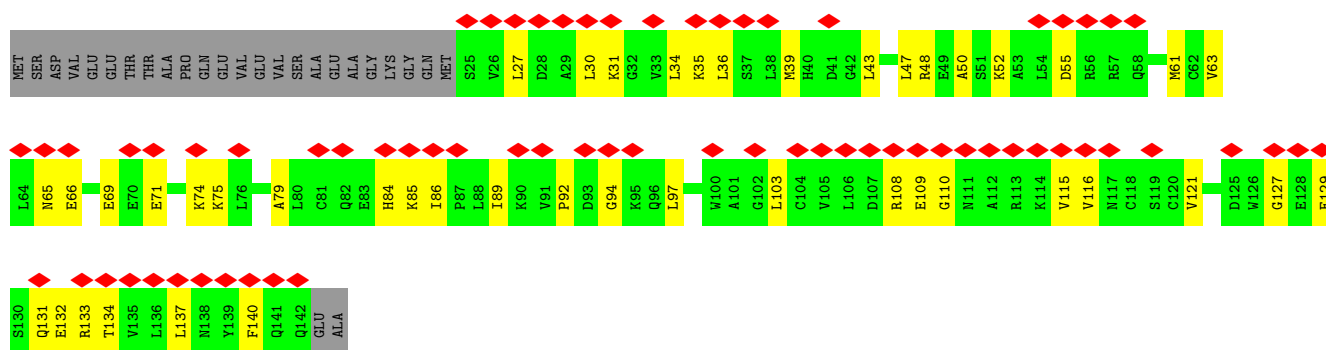


- Molecule 63: 40S ribosomal protein S11-like protein

Chain SL:  80% 13% 7%



- Molecule 64: 40S ribosomal protein S12



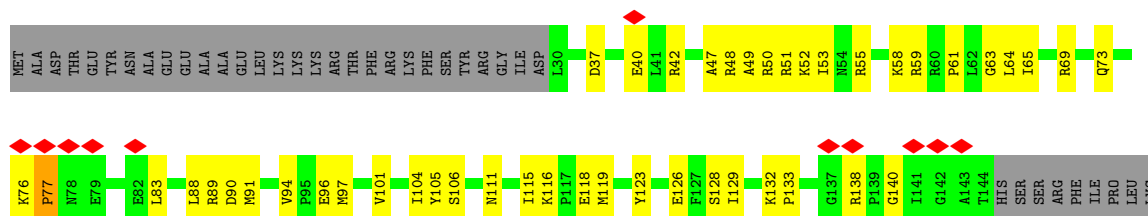
- Molecule 65: 40S ribosomal protein S13-like protein



- Molecule 66: 40S ribosomal protein S14-like protein



- Molecule 67: 40S ribosomal protein s15-like protein

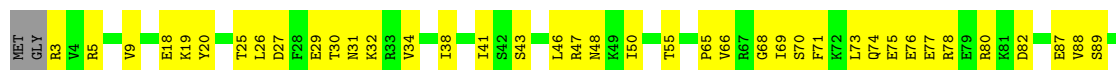


- Molecule 68: 40S ribosomal protein S16-like protein

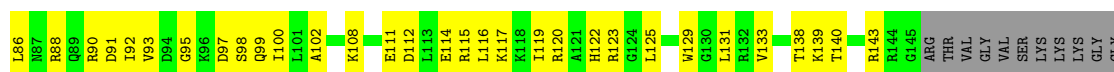




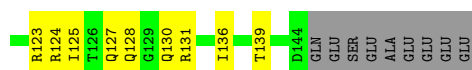
- Molecule 69: 40S ribosomal protein S17-like protein



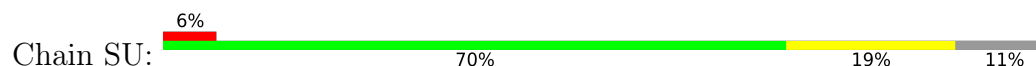
- Molecule 70: Putative ribosomal protein



- Molecule 71: 40S ribosomal protein S19-like protein



- Molecule 72: 40S ribosomal protein S20-like protein



- Molecule 73: 40S ribosomal protein S21-like protein





- Molecule 74: 40S ribosomal protein S22-like protein

Chain SW: 84% 15%



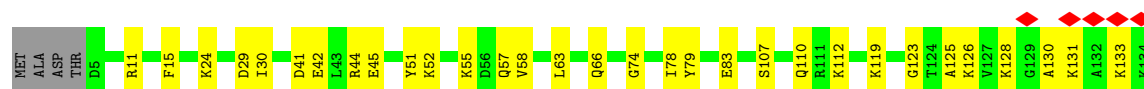
- Molecule 75: 40S ribosomal protein s23-like protein

Chain SX: 79% 19%



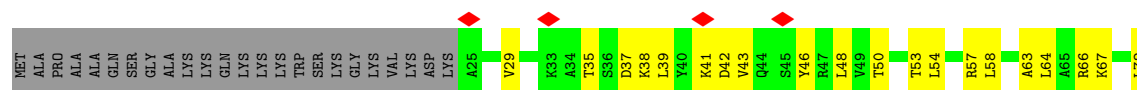
- Molecule 76: 40S ribosomal protein S24

Chain SY: 5% 74% 23%



- Molecule 77: 40S ribosomal protein S25

Chain SZ: 38% 31% 30%



- Molecule 78: 40S ribosomal protein S26

Chain Sa: 74% 13% 13%



- Molecule 79: Ribosomal protein s27-like protein

Chain Sb: 85% 13%



- Molecule 80: 40S ribosomal protein S28-like protein

Chain Sc: 56% 32% 10%



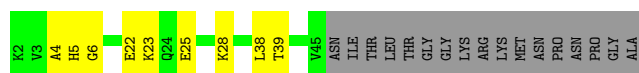
- Molecule 81: 40S ribosomal protein S29

Chain Sd: 61% 32% 7%



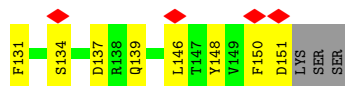
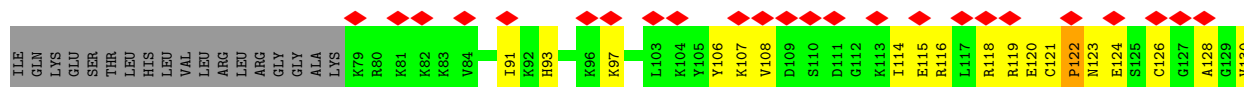
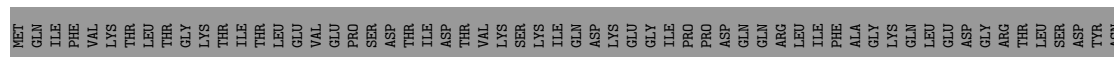
- Molecule 82: 40S ribosomal protein S30

Chain Se: 57% 15% 28%



- Molecule 83: 40S ribosomal protein S27a-like protein

Chain Sf: 18% 30% 17% 53%



- Molecule 84: Methionine aminopeptidase 2

Chain D: 88% 12%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	119160	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 ($e^-/\text{\AA}^2$)	54.8	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	2100	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	1.870	Depositor
Minimum map value	-0.608	Depositor
Average map value	-0.003	Depositor
Map value standard deviation	0.062	Depositor
Recommended contour level	0.22	Depositor
Map size (Å)	666.0, 666.0, 666.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.11, 1.11, 1.11	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: B8N, ZN, SAC, OMG

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	1	0.15	0/76339	0.32	0/119028
2	2	0.14	0/42072	0.32	0/65562
3	3	0.14	0/2833	0.31	0/4413
4	4	0.14	0/3710	0.30	0/5778
5	A	0.11	0/2495	0.33	0/3390
6	B	0.12	0/243	0.40	0/316
7	C	0.27	0/622	0.74	2/827 (0.2%)
8	LA	0.14	0/1964	0.32	0/2641
9	LB	0.12	0/3156	0.32	0/4238
10	LC	0.12	0/2815	0.27	0/3795
11	LD	0.12	0/2487	0.31	0/3341
12	LE	0.12	0/1547	0.31	0/2081
13	LF	0.12	0/2055	0.28	0/2758
14	LG	0.11	0/1929	0.29	0/2579
15	LH	0.12	0/1525	0.32	0/2050
16	LI	0.11	0/1797	0.27	0/2413
17	LJ	0.45	1/1389 (0.1%)	0.35	0/1856
18	LK	0.08	0/761	0.31	0/1056
19	LL	0.12	0/1695	0.30	0/2276
20	LM	0.11	0/1144	0.28	0/1539
21	LN	0.13	0/1740	0.28	0/2332
22	LO	0.12	0/1638	0.29	0/2197
23	LP	0.13	0/1495	0.32	0/2014
24	LQ	0.13	0/1507	0.30	0/2017
25	LR	0.12	0/1525	0.24	0/2028
26	LS	0.12	0/1460	0.29	0/1965
27	LT	0.12	0/1292	0.31	0/1738
28	LU	0.13	0/832	0.37	0/1112
29	LV	0.13	0/1012	0.33	0/1361
30	LW	0.11	0/1088	0.32	0/1443
31	LX	0.13	0/981	0.32	0/1324
32	LY	0.13	0/1079	0.36	0/1443

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LZ	0.11	0/1134	0.28	0/1519
34	La	0.14	0/1212	0.32	0/1627
35	Lb	0.13	0/518	0.40	0/684
36	Lc	0.14	0/731	0.31	0/983
37	Ld	0.13	0/925	0.29	0/1238
38	Le	0.13	0/1019	0.27	0/1358
39	Lf	0.13	0/874	0.28	0/1176
40	Lg	0.14	0/904	0.32	0/1210
41	Lh	0.11	0/1014	0.27	0/1349
42	Li	0.12	0/844	0.31	0/1115
43	Lj	0.13	0/697	0.31	0/922
44	Lk	0.16	0/640	0.39	1/850 (0.1%)
45	Ll	0.12	0/445	0.28	0/593
46	Lm	0.11	0/424	0.29	0/561
47	Ln	0.13	0/225	0.24	0/289
47	Lr	0.08	0/225	0.25	0/289
48	Lo	0.17	0/835	0.51	1/1105 (0.1%)
49	Lp	0.12	0/705	0.30	0/940
50	Lq	0.12	0/1101	0.27	0/1482
51	Ls	0.21	1/1477 (0.1%)	0.38	0/1995
52	SA	0.12	0/1683	0.32	0/2299
53	SB	0.12	0/1900	0.33	0/2551
54	SC	0.11	0/1703	0.28	0/2303
55	SD	2.44	2/1712 (0.1%)	0.99	3/2299 (0.1%)
56	SE	0.11	0/2112	0.29	0/2842
57	SF	0.11	0/1578	0.34	0/2130
58	SG	0.10	0/1906	0.26	0/2547
59	SH	0.11	0/1587	0.31	0/2140
60	SI	0.12	0/1654	0.30	0/2213
61	SJ	0.12	0/1489	0.29	0/1993
62	SK	0.12	0/764	0.38	0/1038
63	SL	0.12	0/1249	0.27	0/1678
64	SM	0.12	0/934	0.37	0/1255
65	SN	0.12	0/1205	0.28	0/1627
66	SO	0.14	0/1014	0.42	2/1361 (0.1%)
67	SP	0.61	1/932 (0.1%)	0.63	2/1248 (0.2%)
68	SQ	0.12	0/1098	0.39	0/1472
69	SR	0.15	0/1060	0.41	0/1424
70	SS	0.13	0/1133	0.39	0/1520
71	ST	0.13	0/1137	0.37	0/1533
72	SU	0.10	0/828	0.33	0/1112
73	SV	0.13	0/671	0.36	0/900
74	SW	0.14	0/1055	0.41	0/1416

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	SX	0.21	0/1116	0.37	0/1489
76	SY	0.16	0/1075	0.42	0/1431
77	SZ	0.16	0/550	0.55	0/736
78	Sa	0.12	0/852	0.30	0/1136
79	Sb	0.13	0/623	0.39	0/843
80	Sc	5.21	1/487 (0.2%)	1.92	2/653 (0.3%)
81	Sd	0.14	0/427	0.41	0/570
82	Se	0.13	0/357	0.42	0/470
83	Sf	2.01	1/614 (0.2%)	0.89	2/813 (0.2%)
84	D	0.18	0/2972	0.39	0/4023
All	All	0.37	7/223653 (0.0%)	0.35	15/327261 (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
9	LB	0	1
84	D	0	1
All	All	0	2

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
80	Sc	7	PRO	N-CD	115.01	3.08	1.47
55	SD	221	PRO	N-CD	99.63	2.87	1.47
83	Sf	122	PRO	N-CD	49.79	2.17	1.47
67	SP	77	PRO	N-CD	17.86	1.72	1.47
55	SD	46	PRO	N-CD	16.64	1.71	1.47
17	LJ	119	PRO	N-CD	-16.38	1.24	1.47
51	Ls	23	PRO	N-CD	-6.59	1.38	1.47

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
80	Sc	7	PRO	N-CD-CG	-36.22	48.87	103.20
55	SD	221	PRO	CA-N-CD	-29.90	70.14	112.00
55	SD	221	PRO	N-CD-CG	-29.47	58.99	103.20
80	Sc	7	PRO	CA-N-CD	-29.44	70.78	112.00
83	Sf	122	PRO	N-CD-CG	-20.97	71.74	103.20
55	SD	46	PRO	CA-N-CD	-14.67	91.46	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
67	SP	77	PRO	CA-N-CD	-13.72	92.79	112.00
83	Sf	122	PRO	CA-N-CD	-11.30	96.18	112.00
67	SP	133	PRO	CA-N-CD	-7.37	101.68	112.00
66	SO	63	ALA	CA-C-N	5.92	132.86	121.54
66	SO	63	ALA	C-N-CA	5.92	132.86	121.54
48	Lo	90	HIS	CB-CA-C	-5.87	100.68	110.19
44	Lk	64	PRO	CA-N-CD	-5.44	104.38	112.00
7	C	583	MET	CA-CB-CG	5.39	124.87	114.10
7	C	583	MET	N-CA-CB	5.26	118.43	110.28

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
84	D	384	ARG	Sidechain
9	LB	257	HIS	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	68242	0	34377	411	0
2	2	37645	0	18955	360	0
3	3	2535	0	1284	11	0
4	4	3319	0	1678	15	0
5	A	2438	0	2385	85	0
6	B	244	0	233	32	0
7	C	619	0	654	41	0
8	LA	1925	0	1999	19	0
9	LB	3088	0	3206	40	0
10	LC	2758	0	2883	35	0
11	LD	2440	0	2431	40	0
12	LE	1518	0	1619	44	0
13	LF	2017	0	2130	25	0
14	LG	1900	0	2066	30	0
15	LH	1505	0	1581	28	0
16	LI	1760	0	1798	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	LJ	1367	0	1405	47	0
18	LK	762	0	362	0	0
19	LL	1666	0	1756	27	0
20	LM	1125	0	1198	27	0
21	LN	1703	0	1767	29	0
22	LO	1613	0	1706	13	0
23	LP	1472	0	1518	22	0
24	LQ	1481	0	1596	20	0
25	LR	1506	0	1603	22	0
26	LS	1425	0	1484	22	0
27	LT	1266	0	1328	13	0
28	LU	819	0	864	17	0
29	LV	994	0	1055	10	0
30	LW	1075	0	1146	17	0
31	LX	965	0	1049	29	0
32	LY	1065	0	1156	24	0
33	LZ	1111	0	1181	26	0
34	La	1180	0	1203	28	0
35	Lb	508	0	526	13	0
36	Lc	722	0	766	13	0
37	Ld	911	0	965	15	0
38	Le	1001	0	1070	9	0
39	Lf	853	0	880	8	0
40	Lg	891	0	958	18	0
41	Lh	1003	0	1116	18	0
42	Li	836	0	915	30	0
43	Lj	684	0	712	13	0
44	Lk	632	0	693	19	0
45	Ll	435	0	473	6	0
46	Lm	418	0	459	5	0
47	Ln	224	0	271	2	0
47	Lr	224	0	271	7	0
48	Lo	822	0	891	23	0
49	Lp	697	0	737	4	0
50	Lq	1083	0	1140	27	0
51	Ls	1449	0	1488	120	0
52	SA	1641	0	1650	22	0
53	SB	1871	0	1989	49	0
54	SC	1672	0	1777	16	0
55	SD	1688	0	1750	54	0
56	SE	2072	0	2155	28	0
57	SF	1557	0	1608	49	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	SG	1875	0	1983	35	0
59	SH	1562	0	1641	30	0
60	SI	1621	0	1645	28	0
61	SJ	1466	0	1582	34	0
62	SK	742	0	738	44	0
63	SL	1222	0	1289	20	0
64	SM	923	0	944	44	0
65	SN	1182	0	1264	10	0
66	SO	1002	0	1034	56	0
67	SP	917	0	978	59	0
68	SQ	1081	0	1151	49	0
69	SR	1045	0	1083	60	0
70	SS	1118	0	1172	57	0
71	ST	1117	0	1133	40	0
72	SU	819	0	895	25	0
73	SV	664	0	662	27	0
74	SW	1037	0	1076	23	0
75	SX	1099	0	1169	26	0
76	SY	1061	0	1150	22	0
77	SZ	546	0	591	36	0
78	Sa	839	0	891	16	0
79	Sb	611	0	633	12	0
80	Sc	484	0	513	25	0
81	Sd	419	0	418	23	0
82	Se	353	0	399	10	0
83	Sf	604	0	640	41	0
84	D	2911	0	2865	46	0
85	Lg	1	0	0	0	0
85	Lj	1	0	0	0	0
85	Lm	1	0	0	0	0
85	Lo	1	0	0	0	0
85	Lp	1	0	0	0	0
85	Sa	1	0	0	0	0
85	Sb	1	0	0	0	0
85	Sd	1	0	0	0	0
All	All	208770	0	157455	2657	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 (2657) 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)
11:LD:166:MET:CE	11:LD:178:HIS:CG	1.91	1.54
83:Sf:122:PRO:HD2	83:Sf:146:LEU:CD1	1.16	1.53
83:Sf:122:PRO:CD	83:Sf:146:LEU:HD13	1.07	1.52
1:1:1589:C:C5'	31:LX:92:GLN:NE2	1.70	1.52
7:C:608:THR:HA	7:C:611:MET:CE	1.43	1.46
61:SJ:112:TYR:HE2	61:SJ:119:SER:C	1.27	1.39
7:C:608:THR:CA	7:C:611:MET:HE2	1.48	1.38
1:1:1242:A:C6	51:Ls:53:MET:SD	2.17	1.38
1:1:1589:C:H5'	31:LX:92:GLN:NE2	1.10	1.35
51:Ls:126:THR:HB	51:Ls:128:MET:CE	1.57	1.34
55:SD:46:PRO:N	55:SD:46:PRO:CD	1.71	1.33
67:SP:77:PRO:CD	67:SP:77:PRO:N	1.72	1.31
53:SB:4:GLY:H	66:SO:62:LYS:NZ	1.29	1.30
66:SO:120:ARG:HD3	78:Sa:52:ASP:OD1	1.22	1.29
11:LD:166:MET:HE1	11:LD:178:HIS:CG	1.58	1.28
10:LC:301:ARG:HD3	24:LQ:69:GLU:OE1	1.22	1.28
50:Lq:139:ARG:HB3	50:Lq:140:ARG:NH2	1.44	1.27
6:B:89:ARG:CZ	6:B:90:ARG:HB3	1.64	1.26
1:1:703:A:OP1	34:La:133:GLU:HG3	1.25	1.26
48:Lo:91:PHE:CZ	48:Lo:93:LEU:HD21	1.70	1.25
14:LG:65:LYS:HE2	21:LN:29:GLU:OE2	1.36	1.24
61:SJ:112:TYR:CE2	61:SJ:119:SER:C	2.15	1.23
2:2:1525:C:H5'	68:SQ:42:GLU:CD	1.62	1.22
12:LE:162:GLN:O	12:LE:166:ASP:OD2	1.58	1.22
25:LR:39:GLN:OE1	25:LR:42:ARG:NH1	1.71	1.21
67:SP:69:ARG:O	67:SP:73:GLN:HG2	1.40	1.21
6:B:89:ARG:HE	6:B:90:ARG:N	1.38	1.20
1:1:2801:U:O2	84:D:121:MET:HE3	1.38	1.20
66:SO:149:ARG:O	66:SO:150:LEU:HD12	1.39	1.20
51:Ls:126:THR:CB	51:Ls:128:MET:HE1	1.70	1.20
6:B:89:ARG:NE	6:B:90:ARG:HB3	1.55	1.19
50:Lq:139:ARG:CB	50:Lq:140:ARG:HH22	1.54	1.19
67:SP:88:LEU:HD13	67:SP:91:MET:CE	1.73	1.17
6:B:89:ARG:NE	6:B:90:ARG:CB	2.07	1.17
83:Sf:122:PRO:CD	83:Sf:146:LEU:CD1	1.83	1.17
84:D:164:VAL:HG21	84:D:183:MET:SD	1.84	1.17
62:SK:13:GLU:OE2	62:SK:17:ARG:HD2	1.43	1.16
34:La:92:SER:HB2	34:La:94:GLN:HE22	1.06	1.15
61:SJ:112:TYR:OH	61:SJ:119:SER:HA	1.46	1.15
67:SP:88:LEU:HD13	67:SP:91:MET:HE3	1.16	1.15
11:LD:166:MET:CE	11:LD:178:HIS:ND1	2.09	1.14
34:La:97:ASP:OD2	34:La:98:THR:HG23	1.45	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:SC:116:ASP:OD1	54:SC:116:ASP:O	1.64	1.13
1:1:703:A:OP1	34:La:133:GLU:CG	1.96	1.12
2:2:1525:C:C5'	68:SQ:42:GLU:OE1	1.98	1.12
72:SU:81:MET:HE3	81:Sd:52:PHE:CE1	1.84	1.12
1:1:2408:A:O3'	42:Li:72:ASN:ND2	1.81	1.12
12:LE:12:LYS:HZ3	12:LE:15:ARG:HG3	1.10	1.12
50:Lq:139:ARG:C	50:Lq:140:ARG:NH2	2.08	1.11
51:Ls:64:LYS:HA	51:Ls:67:MET:HE1	1.33	1.11
11:LD:166:MET:HE3	11:LD:178:HIS:ND1	1.64	1.11
67:SP:97:MET:SD	67:SP:97:MET:O	2.09	1.11
6:B:89:ARG:HE	6:B:90:ARG:CB	1.62	1.10
12:LE:12:LYS:NZ	12:LE:15:ARG:HG3	1.66	1.10
51:Ls:19:LEU:HA	51:Ls:88:PHE:CZ	1.86	1.10
82:Se:4:ALA:O	82:Se:5:HIS:CD2	2.04	1.10
14:LG:124:LYS:O	14:LG:127:ASP:OD2	1.69	1.10
1:1:2408:A:C3'	42:Li:72:ASN:HD21	1.64	1.10
2:2:1525:C:H5''	68:SQ:42:GLU:OE1	1.51	1.09
72:SU:81:MET:CE	81:Sd:52:PHE:CE1	2.33	1.09
1:1:1589:C:H5''	31:LX:92:GLN:NE2	1.68	1.09
7:C:598:LYS:HD2	48:Lo:89:LYS:HB2	1.27	1.08
51:Ls:126:THR:HB	51:Ls:128:MET:HE1	1.11	1.08
53:SB:4:GLY:N	66:SO:62:LYS:NZ	2.01	1.08
1:1:3027:G:H5'	25:LR:57:MET:HE1	1.35	1.08
11:LD:166:MET:HE3	11:LD:178:HIS:CG	1.77	1.08
56:SE:65:MET:HE3	56:SE:65:MET:HA	1.08	1.07
10:LC:154:ASP:O	10:LC:154:ASP:OD2	1.73	1.07
14:LG:65:LYS:CE	21:LN:29:GLU:OE2	2.02	1.07
12:LE:157:THR:O	12:LE:161:ASP:OD2	1.73	1.06
55:SD:225:PRO:C	55:SD:226:MET:SD	2.38	1.06
2:2:1525:C:C5'	68:SQ:42:GLU:CD	2.28	1.06
1:1:3027:G:H5'	25:LR:57:MET:CE	1.86	1.06
53:SB:4:GLY:N	66:SO:62:LYS:HZ1	1.50	1.06
17:LJ:15:ILE:HA	17:LJ:132:MET:HE1	1.37	1.05
55:SD:223:VAL:HG13	55:SD:226:MET:HE1	1.38	1.05
11:LD:166:MET:CE	11:LD:178:HIS:CB	2.34	1.04
61:SJ:112:TYR:CE2	61:SJ:120:ILE:N	2.25	1.04
15:LH:179:GLN:OE1	15:LH:180:LYS:N	1.91	1.04
6:B:89:ARG:HE	6:B:90:ARG:CA	1.70	1.03
11:LD:166:MET:HE1	11:LD:178:HIS:CB	1.86	1.03
71:ST:105:MET:HE2	71:ST:123:ARG:HH11	1.15	1.03
55:SD:225:PRO:O	55:SD:226:MET:HE3	1.58	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:Lq:139:ARG:HB2	50:Lq:140:ARG:HH12	1.20	1.03
58:SG:55:GLY:N	58:SG:63:MET:HE2	1.74	1.03
12:LE:12:LYS:HE2	12:LE:12:LYS:HA	1.34	1.03
10:LC:301:ARG:CD	24:LQ:69:GLU:OE1	2.07	1.02
74:SW:111:MET:HE2	74:SW:115:GLU:OE1	1.60	1.01
6:B:93:PHE:CD2	6:B:94:ARG:N	2.28	1.01
8:LA:142:ASP:C	8:LA:143:GLU:OE1	2.04	1.01
36:Lc:76:THR:N	36:Lc:79:GLU:OE2	1.94	1.00
62:SK:13:GLU:OE2	62:SK:17:ARG:CD	2.09	1.00
51:Ls:126:THR:C	51:Ls:128:MET:HE1	1.85	1.00
67:SP:69:ARG:CA	67:SP:73:GLN:HE21	1.75	1.00
1:1:1589:C:H5'	31:LX:92:GLN:CD	1.87	1.00
34:La:92:SER:CB	34:La:94:GLN:HE22	1.75	1.00
67:SP:69:ARG:HA	67:SP:73:GLN:HE21	1.26	1.00
83:Sf:122:PRO:CD	83:Sf:122:PRO:N	2.17	0.99
30:LW:92:GLU:OE2	30:LW:96:MET:HE2	1.60	0.99
29:LV:12:LYS:NZ	29:LV:15:MET:HE3	1.77	0.99
74:SW:51:GLU:OE2	79:Sb:8:LEU:HG	1.62	0.99
6:B:89:ARG:NE	6:B:90:ARG:N	2.10	0.99
56:SE:65:MET:HE3	56:SE:65:MET:CA	1.91	0.99
59:SH:134:ALA:O	59:SH:138:ASP:OD1	1.81	0.99
2:2:477:G:P	61:SJ:118:LYS:NZ	2.36	0.98
51:Ls:79:PHE:O	51:Ls:79:PHE:CD1	2.17	0.98
56:SE:65:MET:HA	56:SE:65:MET:CE	1.93	0.98
66:SO:120:ARG:CD	78:Sa:52:ASP:OD1	2.11	0.98
2:2:1004:C:O2'	66:SO:150:LEU:CD1	2.11	0.98
83:Sf:122:PRO:HD2	83:Sf:146:LEU:HD11	1.01	0.97
34:La:94:GLN:N	34:La:94:GLN:OE1	1.97	0.97
1:1:2630:A:O2'	17:LJ:99:GLU:OE1	1.81	0.97
50:Lq:139:ARG:CB	50:Lq:140:ARG:HH12	1.78	0.96
55:SD:223:VAL:HG13	55:SD:226:MET:CE	1.94	0.96
17:LJ:132:MET:HA	17:LJ:132:MET:HE2	1.47	0.95
61:SJ:86:GLU:N	61:SJ:86:GLU:OE2	1.97	0.95
6:B:89:ARG:NH2	6:B:90:ARG:HB3	1.80	0.95
2:2:1004:C:O2'	66:SO:150:LEU:HD11	1.64	0.95
73:SV:49:GLU:OE1	73:SV:49:GLU:N	1.99	0.95
51:Ls:128:MET:H	51:Ls:128:MET:HE2	1.28	0.95
6:B:93:PHE:HE2	6:B:94:ARG:HE	1.08	0.95
67:SP:69:ARG:O	67:SP:73:GLN:CG	2.13	0.95
1:1:729:A:H1'	35:Lb:27:GLN:NE2	1.81	0.95
50:Lq:139:ARG:HB3	50:Lq:140:ARG:HH22	0.79	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:SR:27:ASP:OD1	69:SR:30:THR:N	2.00	0.94
1:1:729:A:C1'	35:Lb:27:GLN:HE22	1.79	0.94
51:Ls:126:THR:CA	51:Ls:128:MET:HE1	1.97	0.94
33:LZ:82:THR:O	36:Lc:65:MET:HE1	1.67	0.94
55:SD:46:PRO:HD2	55:SD:46:PRO:O	1.66	0.94
67:SP:69:ARG:HA	67:SP:73:GLN:NE2	1.83	0.94
34:La:92:SER:HB2	34:La:94:GLN:NE2	1.81	0.94
73:SV:41:GLU:OE1	73:SV:41:GLU:N	2.01	0.94
26:LS:130:GLU:OE1	26:LS:130:GLU:N	2.01	0.94
50:Lq:139:ARG:C	50:Lq:140:ARG:CZ	2.41	0.93
50:Lq:139:ARG:CB	50:Lq:140:ARG:NH2	2.22	0.93
1:1:1242:A:N6	51:Ls:53:MET:SD	2.40	0.93
23:LP:8:GLU:OE1	23:LP:8:GLU:O	1.84	0.93
2:2:709:G:H1	2:2:722:U:H3	1.05	0.93
36:Lc:79:GLU:OE1	36:Lc:79:GLU:N	2.01	0.93
84:D:85:ILE:CG1	84:D:134:GLU:OE2	2.17	0.93
53:SB:4:GLY:H	66:SO:62:LYS:HZ1	0.95	0.93
28:LU:56:LEU:HD12	28:LU:60:ILE:HD13	1.51	0.93
30:LW:92:GLU:OE2	30:LW:96:MET:CE	2.17	0.92
51:Ls:126:THR:CB	51:Ls:128:MET:CE	2.37	0.92
50:Lq:139:ARG:HB3	50:Lq:140:ARG:CZ	2.00	0.92
70:SS:81:ILE:HG22	70:SS:82:PRO:HD2	1.51	0.91
69:SR:68:GLY:C	69:SR:69:ILE:HD13	1.96	0.91
52:SA:37:GLN:C	52:SA:37:GLN:OE1	2.13	0.91
51:Ls:15:LEU:CD1	51:Ls:61:ARG:NH1	2.34	0.91
84:D:85:ILE:HG12	84:D:134:GLU:OE2	1.70	0.91
1:1:2630:A:H4'	17:LJ:99:GLU:OE1	1.70	0.91
33:LZ:87:GLU:N	33:LZ:87:GLU:OE2	2.04	0.90
53:SB:224:ASP:O	53:SB:224:ASP:OD2	1.87	0.90
6:B:89:ARG:NE	6:B:89:ARG:C	2.29	0.90
51:Ls:126:THR:HB	51:Ls:128:MET:HE3	1.54	0.90
67:SP:88:LEU:CD1	67:SP:91:MET:HE3	2.01	0.90
55:SD:225:PRO:O	55:SD:226:MET:CE	2.19	0.90
70:SS:9:THR:HG23	70:SS:9:THR:O	1.70	0.89
1:1:1242:A:C5	51:Ls:53:MET:SD	2.65	0.89
31:LX:90:GLU:OE1	31:LX:90:GLU:N	2.05	0.89
1:1:2801:U:O2	84:D:121:MET:CE	2.19	0.89
2:2:477:G:P	61:SJ:118:LYS:HZ1	1.92	0.89
53:SB:4:GLY:H	66:SO:62:LYS:HZ3	1.19	0.89
68:SQ:29:ILE:CD1	68:SQ:65:ILE:HD12	2.02	0.89
64:SM:131:GLN:C	64:SM:131:GLN:OE1	2.16	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:Lg:110:SER:C	40:Lg:111:GLN:NE2	2.30	0.88
23:LP:8:GLU:OE1	23:LP:8:GLU:C	2.15	0.88
71:ST:105:MET:HE2	71:ST:123:ARG:NH1	1.87	0.88
67:SP:88:LEU:CD1	67:SP:91:MET:CE	2.50	0.88
41:Lh:15:LYS:HD2	41:Lh:19:GLU:OE2	1.74	0.88
66:SO:93:HIS:C	66:SO:94:ILE:HD13	1.99	0.88
55:SD:226:MET:SD	55:SD:226:MET:N	2.47	0.88
12:LE:12:LYS:HE2	12:LE:12:LYS:CA	2.00	0.88
64:SM:108:ARG:CD	64:SM:110:GLY:H	1.65	0.88
48:Lo:91:PHE:CZ	48:Lo:93:LEU:CD2	2.57	0.87
7:C:561:PRO:HD3	17:LJ:56:ARG:HG3	1.57	0.87
1:1:1090:A:OP2	35:Lb:22:LYS:NZ	2.06	0.87
15:LH:54:LYS:HD2	20:LM:3:GLU:CG	2.05	0.87
19:LL:178:GLU:OE2	19:LL:178:GLU:N	2.08	0.87
1:1:1941:G:N2	1:1:2043:C:O2	2.07	0.87
72:SU:15:LYS:O	72:SU:17:HIS:CE1	2.28	0.87
12:LE:12:LYS:HZ3	12:LE:15:ARG:CG	1.87	0.86
33:LZ:102:GLU:OE2	33:LZ:105:GLN:HG3	1.74	0.86
51:Ls:19:LEU:HD23	51:Ls:61:ARG:NH1	1.89	0.86
2:2:1055:A:OP1	53:SB:199:LYS:NZ	2.08	0.86
29:LV:12:LYS:HZ3	29:LV:15:MET:HE3	1.38	0.85
1:1:2630:A:C4'	17:LJ:99:GLU:OE1	2.24	0.85
58:SG:54:GLY:HA2	58:SG:63:MET:HE3	1.58	0.85
69:SR:104:ILE:HD12	69:SR:105:ASP:H	1.42	0.85
64:SM:131:GLN:OE1	64:SM:132:GLU:N	2.09	0.85
1:1:1739:C:O2	1:1:1746:G:N2	2.09	0.85
59:SH:7:ASN:O	59:SH:7:ASN:OD1	1.95	0.85
6:B:89:ARG:HE	6:B:89:ARG:C	1.82	0.85
51:Ls:15:LEU:CD1	51:Ls:61:ARG:HH11	1.90	0.85
53:SB:3:VAL:HA	66:SO:62:LYS:NZ	1.91	0.85
67:SP:69:ARG:O	67:SP:73:GLN:NE2	2.09	0.85
50:Lq:139:ARG:O	50:Lq:140:ARG:NH2	2.09	0.84
58:SG:55:GLY:N	58:SG:63:MET:CE	2.40	0.84
1:1:703:A:P	34:La:133:GLU:OE1	2.35	0.84
1:1:1739:C:N3	1:1:1746:G:N1	2.25	0.84
34:La:97:ASP:OD2	34:La:98:THR:CG2	2.25	0.84
24:LQ:64:LEU:O	24:LQ:68:THR:OG1	1.95	0.84
83:Sf:115:GLU:C	83:Sf:115:GLU:OE2	2.21	0.84
50:Lq:139:ARG:CB	50:Lq:140:ARG:NH1	2.40	0.84
1:1:2630:A:HO2'	17:LJ:99:GLU:CD	1.86	0.84
52:SA:157:GLU:OE1	52:SA:157:GLU:N	2.09	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:SO:116:ARG:HH12	80:Sc:63:GLU:CD	1.84	0.84
67:SP:138:ARG:HD2	67:SP:138:ARG:O	1.78	0.84
11:LD:166:MET:HE1	11:LD:178:HIS:CD2	2.12	0.83
76:SY:107:SER:OG	76:SY:110:GLN:OE1	1.96	0.83
51:Ls:19:LEU:HA	51:Ls:88:PHE:HZ	1.35	0.83
51:Ls:92:ASP:OD2	51:Ls:94:LYS:N	2.11	0.83
67:SP:69:ARG:C	67:SP:73:GLN:HE21	1.85	0.83
51:Ls:64:LYS:CA	51:Ls:67:MET:HE1	2.07	0.83
5:A:49:GLU:C	5:A:49:GLU:OE1	2.20	0.83
69:SR:27:ASP:OD1	69:SR:30:THR:HG23	1.78	0.83
20:LM:86:GLU:OE2	20:LM:86:GLU:C	2.22	0.83
77:SZ:79:ARG:NH1	77:SZ:92:ARG:O	2.11	0.83
6:B:89:ARG:C	6:B:89:ARG:CD	2.50	0.82
83:Sf:122:PRO:HD3	83:Sf:146:LEU:HD13	0.84	0.82
1:1:703:A:OP1	34:La:133:GLU:CD	2.22	0.82
11:LD:166:MET:HE3	11:LD:178:HIS:CB	2.04	0.82
40:Lg:110:SER:CB	40:Lg:111:GLN:NE2	2.43	0.82
52:SA:37:GLN:OE1	52:SA:37:GLN:O	1.96	0.82
54:SC:114:ASP:OD2	54:SC:116:ASP:N	2.11	0.82
1:1:703:A:OP1	34:La:133:GLU:OE1	1.96	0.82
6:B:135:GLU:O	6:B:136:GLN:HG3	1.80	0.82
53:SB:3:VAL:HA	66:SO:62:LYS:HZ1	1.45	0.82
51:Ls:15:LEU:HD13	51:Ls:61:ARG:NH1	1.93	0.82
58:SG:54:GLY:C	58:SG:63:MET:CE	2.52	0.82
1:1:1000:G:H1	1:1:1017:U:H3	1.26	0.82
11:LD:166:MET:CE	11:LD:178:HIS:CD2	2.63	0.82
2:2:648:C:O2	2:2:678:G:N2	2.11	0.81
62:SK:13:GLU:CD	62:SK:17:ARG:CD	2.53	0.81
74:SW:111:MET:HE1	74:SW:119:LYS:CE	2.10	0.81
60:SI:87:ASN:HB3	60:SI:90:LEU:HD23	1.63	0.81
70:SS:81:ILE:CG2	70:SS:82:PRO:HD2	2.10	0.81
1:1:2651:A:H5"	7:C:568:LYS:HE3	1.63	0.81
62:SK:13:GLU:O	62:SK:17:ARG:HG2	1.81	0.81
50:Lq:139:ARG:HB2	50:Lq:140:ARG:NH1	1.95	0.81
51:Ls:104:ARG:HD2	51:Ls:184:GLY:HA3	1.63	0.80
15:LH:54:LYS:HB3	20:LM:3:GLU:OE1	1.81	0.80
21:LN:124:ASP:OD1	21:LN:125:SER:N	2.13	0.80
10:LC:270:GLU:O	10:LC:270:GLU:CD	2.25	0.80
76:SY:57:GLN:NE2	76:SY:79:TYR:O	2.13	0.80
1:1:1934:G:N1	1:1:2050:C:N3	2.27	0.80
68:SQ:3:SER:OG	68:SQ:4:VAL:N	2.13	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LE:139:GLU:HG2	12:LE:152:LYS:HE2	1.62	0.80
1:1:2408:A:C3'	42:Li:72:ASN:ND2	2.40	0.80
12:LE:12:LYS:HA	12:LE:12:LYS:CE	2.03	0.80
14:LG:65:LYS:NZ	21:LN:29:GLU:OE2	2.14	0.80
53:SB:59:ASP:OD1	53:SB:60:ALA:N	2.15	0.80
2:2:862:U:H5''	74:SW:28:ARG:HH22	1.47	0.80
75:SX:141:GLU:OE1	75:SX:141:GLU:N	2.15	0.79
1:1:729:A:C1'	35:Lb:27:GLN:NE2	2.41	0.79
51:Ls:104:ARG:HD2	51:Ls:184:GLY:CA	2.12	0.79
10:LC:270:GLU:O	10:LC:270:GLU:OE2	2.01	0.79
29:LV:70:GLU:OE2	29:LV:70:GLU:N	2.12	0.79
34:La:94:GLN:HA	34:La:96:LYS:NZ	1.97	0.79
41:Lh:37:GLN:O	41:Lh:37:GLN:CD	2.24	0.79
1:1:2408:A:H4'	42:Li:72:ASN:ND2	1.98	0.79
68:SQ:28:LEU:HD21	68:SQ:30:LYS:HE2	1.63	0.79
7:C:595:GLU:O	48:Lo:90:HIS:HE1	1.66	0.79
42:Li:98:GLU:OE2	42:Li:101:ARG:NH1	2.15	0.79
51:Ls:15:LEU:HD13	51:Ls:61:ARG:HH11	1.46	0.79
1:1:1634:A:O3'	40:Lg:41:THR:HG21	1.83	0.79
23:LP:8:GLU:OE1	23:LP:9:ILE:HD13	1.81	0.79
84:D:122:GLN:O	84:D:126:LEU:CD1	2.31	0.79
50:Lq:140:ARG:HA	50:Lq:140:ARG:NE	1.96	0.79
69:SR:107:GLU:HA	69:SR:110:ASP:OD2	1.83	0.79
1:1:702:G:O3'	34:La:133:GLU:OE1	2.01	0.79
51:Ls:126:THR:C	51:Ls:128:MET:CE	2.56	0.78
74:SW:111:MET:HE1	74:SW:119:LYS:HE3	1.64	0.78
41:Lh:37:GLN:O	41:Lh:37:GLN:OE1	2.01	0.78
62:SK:13:GLU:CD	62:SK:17:ARG:HH11	1.92	0.78
1:1:957:C:H5''	24:LQ:82:MET:HE2	1.64	0.78
12:LE:12:LYS:HZ3	12:LE:15:ARG:HA	1.48	0.78
15:LH:179:GLN:NE2	15:LH:180:LYS:O	2.16	0.78
53:SB:121:ILE:HG22	53:SB:168:MET:HE1	1.65	0.78
77:SZ:38:LYS:HA	77:SZ:41:LYS:NZ	1.97	0.78
51:Ls:25:ILE:HG12	51:Ls:88:PHE:CE1	2.18	0.78
83:Sf:107:LYS:HD2	83:Sf:115:GLU:OE1	1.84	0.78
51:Ls:128:MET:HE2	51:Ls:128:MET:N	1.99	0.78
42:Li:70:LEU:HD13	42:Li:78:ALA:HB1	1.66	0.78
1:1:2621:G:H2'	1:1:2622:G:C8	2.18	0.77
68:SQ:29:ILE:HD11	68:SQ:65:ILE:HD12	1.66	0.77
78:Sa:61:GLU:OE1	78:Sa:61:GLU:O	2.02	0.77
70:SS:9:THR:O	70:SS:9:THR:CG2	2.31	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:LX:114:LYS:HB2	31:LX:114:LYS:HZ3	1.49	0.77
58:SG:55:GLY:CA	58:SG:63:MET:HE2	2.14	0.77
15:LH:179:GLN:CD	15:LH:180:LYS:N	2.43	0.77
12:LE:149:PRO:C	12:LE:150:GLN:OE1	2.28	0.77
57:SF:132:ASP:OD1	57:SF:133:SER:N	2.18	0.77
1:1:1204:U:H5''	51:Ls:58:MET:CE	2.15	0.76
13:LF:29:ARG:HD3	13:LF:32:ARG:HH11	1.50	0.76
1:1:681:A:H5''	10:LC:43:MET:HE3	1.68	0.76
1:1:2900:A:N7	9:LB:257:HIS:NE2	2.32	0.76
2:2:1525:C:C5'	68:SQ:42:GLU:OE2	2.32	0.76
17:LJ:15:ILE:HA	17:LJ:132:MET:CE	2.13	0.76
66:SO:19:GLN:C	66:SO:19:GLN:OE1	2.29	0.76
2:2:78:C:H5'	58:SG:175:ALA:HB3	1.68	0.76
11:LD:166:MET:HE1	11:LD:178:HIS:HB2	1.67	0.76
53:SB:3:VAL:CA	66:SO:62:LYS:HZ1	1.98	0.76
1:1:1337:G:N2	1:1:1339:U:O2'	2.19	0.76
33:LZ:82:THR:C	36:Lc:65:MET:HE1	2.11	0.76
73:SV:41:GLU:H	73:SV:41:GLU:CD	1.91	0.76
20:LM:86:GLU:OE2	20:LM:87:ALA:N	2.18	0.76
62:SK:31:HIS:CE1	62:SK:37:ASN:H	2.04	0.76
1:1:2408:A:C4'	42:Li:72:ASN:HD21	1.99	0.76
83:Sf:146:LEU:HB3	83:Sf:148:TYR:CE2	2.20	0.76
2:2:1525:C:H5'	68:SQ:42:GLU:OE2	1.86	0.75
2:2:222:U:O2	2:2:832:G:O6	2.03	0.75
50:Lq:140:ARG:CZ	50:Lq:140:ARG:N	2.49	0.75
62:SK:13:GLU:CD	62:SK:17:ARG:HD2	2.11	0.75
69:SR:68:GLY:O	69:SR:69:ILE:HD13	1.87	0.75
73:SV:22:ARG:NH1	73:SV:58:PHE:CD2	2.55	0.75
1:1:2477:U:OP1	14:LG:71:ARG:NH1	2.19	0.75
10:LC:34:ASP:OD2	10:LC:35:ILE:N	2.19	0.75
28:LU:52:ARG:HH12	28:LU:55:ASN:HB2	1.51	0.75
2:2:1264:G:H1	2:2:1438:U:H3	1.32	0.75
11:LD:166:MET:HE2	11:LD:178:HIS:ND1	1.98	0.75
68:SQ:128:LYS:O	68:SQ:129:PHE:HD2	1.70	0.75
41:Lh:63:ILE:O	41:Lh:67:GLN:HG3	1.87	0.75
74:SW:32:LYS:HB2	74:SW:32:LYS:HZ3	1.50	0.75
6:B:89:ARG:O	6:B:89:ARG:HD2	1.86	0.75
12:LE:77:ASP:OD1	12:LE:78:GLN:N	2.20	0.75
50:Lq:139:ARG:CA	50:Lq:140:ARG:NH2	2.50	0.75
3:3:108:C:OP1	11:LD:284:ARG:NH1	2.19	0.74
67:SP:88:LEU:HB2	67:SP:91:MET:HE1	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:LC:149:VAL:HG13	10:LC:150:PRO:HD3	1.69	0.74
51:Ls:57:THR:HB	51:Ls:60:ARG:HB2	1.68	0.74
66:SO:19:GLN:C	66:SO:19:GLN:CD	2.53	0.74
2:2:648:C:N3	2:2:678:G:N1	2.29	0.74
53:SB:59:ASP:OD1	53:SB:59:ASP:C	2.29	0.74
44:Lk:30:LYS:O	44:Lk:32:GLN:NE2	2.20	0.74
68:SQ:29:ILE:CD1	68:SQ:65:ILE:CD1	2.65	0.74
66:SO:61:VAL:HG11	66:SO:66:ASP:HB2	1.70	0.74
1:1:673:G:OP1	19:LL:39:ARG:NH2	2.20	0.74
17:LJ:20:LEU:HD13	17:LJ:126:MET:HE1	1.68	0.74
51:Ls:141:ILE:HG22	51:Ls:143:THR:HG23	1.68	0.74
11:LD:166:MET:HE2	11:LD:178:HIS:CG	2.16	0.74
23:LP:8:GLU:OE2	23:LP:9:ILE:HD11	1.86	0.74
33:LZ:98:ASP:OD2	33:LZ:98:ASP:C	2.30	0.74
51:Ls:106:LYS:NZ	51:Ls:179:SER:O	2.21	0.74
34:La:97:ASP:OD2	34:La:97:ASP:C	2.31	0.73
54:SC:114:ASP:OD2	54:SC:114:ASP:C	2.31	0.73
84:D:241:PRO:HB2	84:D:279:VAL:HG12	1.68	0.73
1:1:1204:U:C5'	51:Ls:58:MET:CE	2.66	0.73
2:2:219:C:O2	2:2:835:G:N2	2.14	0.73
29:LV:106:ASN:OD1	29:LV:107:PRO:HD2	1.88	0.73
2:2:1525:C:H4'	68:SQ:42:GLU:OE2	1.89	0.73
8:LA:143:GLU:OE1	8:LA:143:GLU:N	2.22	0.73
57:SF:45:LEU:HG	57:SF:125:VAL:HG23	1.69	0.73
17:LJ:20:LEU:HD13	17:LJ:126:MET:CE	2.18	0.73
29:LV:12:LYS:HZ1	29:LV:15:MET:HE3	1.53	0.73
73:SV:7:GLU:N	73:SV:7:GLU:OE2	2.19	0.73
1:1:114:C:OP1	21:LN:147:ARG:NE	2.16	0.73
28:LU:56:LEU:CD1	28:LU:60:ILE:HD13	2.19	0.73
74:SW:51:GLU:OE2	79:Sb:8:LEU:CG	2.35	0.73
77:SZ:57:ARG:NH1	77:SZ:58:LEU:HD13	2.04	0.73
80:Sc:15:ARG:HH22	80:Sc:30:ARG:HD2	1.54	0.73
52:SA:165:THR:HG21	52:SA:176:ILE:HG13	1.71	0.73
61:SJ:112:TYR:CE2	61:SJ:119:SER:CA	2.72	0.73
67:SP:89:ARG:NH2	67:SP:105:TYR:O	2.22	0.73
2:2:1217:C:O3'	62:SK:50:ARG:NH1	2.21	0.73
17:LJ:111:ILE:HG12	17:LJ:117:TYR:HB2	1.70	0.73
23:LP:8:GLU:OE2	23:LP:9:ILE:CD1	2.36	0.73
51:Ls:19:LEU:CA	51:Ls:88:PHE:CZ	2.71	0.73
62:SK:13:GLU:CD	62:SK:17:ARG:HD3	2.14	0.72
1:1:1589:C:C5'	31:LX:92:GLN:CD	2.56	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1941:G:N1	1:1:2043:C:N3	2.29	0.72
12:LE:10:PHE:HE2	12:LE:12:LYS:HE3	1.54	0.72
26:LS:136:LYS:O	26:LS:141:LYS:NZ	2.22	0.72
4:4:55:U:H3	4:4:62:A:H2	1.36	0.72
26:LS:130:GLU:H	26:LS:130:GLU:CD	1.96	0.72
2:2:78:C:H1'	58:SG:177:ARG:HG3	1.71	0.72
2:2:691:C:H4'	2:2:692:C:H5'	1.70	0.72
11:LD:166:MET:HE3	11:LD:178:HIS:HB3	1.71	0.72
33:LZ:87:GLU:O	33:LZ:88:LEU:HD23	1.90	0.72
40:Lg:110:SER:HB2	40:Lg:111:GLN:HE21	1.54	0.72
66:SO:116:ARG:NH1	80:Sc:63:GLU:OE1	2.23	0.72
16:LI:14:ASN:O	16:LI:128:ARG:NH2	2.22	0.72
55:SD:223:VAL:CG1	55:SD:226:MET:CE	2.68	0.72
10:LC:284:GLN:HE22	10:LC:286:ASP:HB3	1.53	0.72
62:SK:37:ASN:HA	62:SK:40:VAL:HG12	1.72	0.72
1:1:2524:G:OP2	33:LZ:54:ARG:NH1	2.23	0.71
20:LM:86:GLU:CD	20:LM:87:ALA:N	2.48	0.71
53:SB:3:VAL:C	66:SO:62:LYS:HZ1	1.98	0.71
56:SE:65:MET:HE1	56:SE:70:VAL:HG12	1.72	0.71
64:SM:108:ARG:CD	64:SM:110:GLY:N	2.42	0.71
83:Sf:137:ASP:OD2	83:Sf:151:ASP:OD1	2.08	0.71
70:SS:26:GLN:HE22	70:SS:31:ALA:HA	1.53	0.71
12:LE:19:ALA:HB3	12:LE:23:LYS:HG2	1.71	0.71
23:LP:103:ASP:OD1	23:LP:104:ALA:N	2.24	0.71
56:SE:107:GLY:HA2	56:SE:189:MET:HG2	1.72	0.71
69:SR:104:ILE:CD1	69:SR:105:ASP:H	2.02	0.71
61:SJ:112:TYR:HE2	61:SJ:119:SER:CA	2.04	0.71
66:SO:30:ALA:HB2	66:SO:92:LEU:HD23	1.73	0.71
84:D:183:MET:HA	84:D:183:MET:HE3	1.70	0.71
4:4:95:G:OP2	43:Lj:72:ARG:NH1	2.22	0.71
57:SF:133:SER:HB2	57:SF:144:ARG:HB3	1.71	0.71
1:1:2487:A:O4'	14:LG:52:MET:HE3	1.90	0.71
2:2:1525:C:H5'	68:SQ:42:GLU:OE1	1.72	0.71
51:Ls:15:LEU:HD12	51:Ls:61:ARG:NH1	2.03	0.71
61:SJ:21:ARG:HG2	61:SJ:25:GLU:OE2	1.91	0.71
70:SS:60:GLU:OE1	70:SS:60:GLU:HA	1.90	0.71
83:Sf:115:GLU:OE2	83:Sf:116:ARG:O	2.09	0.71
1:1:1242:A:N1	51:Ls:53:MET:SD	2.64	0.71
2:2:1363:A:O3'	71:ST:8:ARG:NH1	2.24	0.71
11:LD:166:MET:HE2	11:LD:178:HIS:CE1	2.26	0.71
1:1:1205:G:N7	51:Ls:58:MET:HE3	2.06	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LE:10:PHE:HD2	12:LE:11:GLY:O	1.72	0.70
42:Li:68:GLU:OE1	42:Li:69:LEU:N	2.24	0.70
55:SD:67:ARG:NH1	62:SK:87:ALA:O	2.24	0.70
66:SO:116:ARG:NH1	80:Sc:63:GLU:CD	2.49	0.70
62:SK:13:GLU:OE1	62:SK:17:ARG:HD3	1.90	0.70
31:LX:71:ASP:C	31:LX:71:ASP:OD2	2.33	0.70
2:2:476:U:O3'	61:SJ:118:LYS:NZ	2.22	0.70
1:1:3135:A:OP2	22:LO:173:LYS:NZ	2.24	0.70
5:A:199:THR:HG21	5:A:240:VAL:HA	1.72	0.70
7:C:571:GLN:O	7:C:575:ILE:HG13	1.90	0.70
54:SC:116:ASP:OD1	54:SC:116:ASP:C	2.34	0.70
2:2:824:U:H3	2:2:844:G:H1	1.40	0.70
12:LE:10:PHE:CD2	12:LE:11:GLY:O	2.44	0.70
50:Lq:139:ARG:CB	50:Lq:140:ARG:CZ	2.66	0.70
75:SX:56:LYS:HD3	75:SX:93:LEU:HD22	1.72	0.70
55:SD:45:THR:OG1	55:SD:48:VAL:O	2.08	0.70
5:A:4:GLN:NE2	5:A:313:MET:HG2	2.06	0.70
2:2:103:A:OP2	2:2:305:C:N4	2.24	0.69
23:LP:64:ALA:O	23:LP:80:ARG:NH1	2.25	0.69
55:SD:225:PRO:C	55:SD:226:MET:CE	2.65	0.69
59:SH:37:THR:OG1	59:SH:39:ASP:OD1	2.10	0.69
17:LJ:20:LEU:HD11	17:LJ:38:LEU:HD11	1.75	0.69
17:LJ:132:MET:HA	17:LJ:132:MET:CE	2.19	0.69
21:LN:68:ARG:NH1	21:LN:124:ASP:O	2.25	0.69
37:Ld:9:ARG:O	37:Ld:13:ALA:N	2.24	0.69
83:Sf:146:LEU:HB3	83:Sf:148:TYR:HE2	1.56	0.69
1:1:675:U:OP2	19:LL:36:ARG:NH2	2.25	0.69
5:A:210:GLY:HA3	5:A:236:ILE:HD11	1.73	0.69
1:1:1157:G:N2	22:LO:89:MET:HE2	2.08	0.69
5:A:33:SER:OG	5:A:43:TRP:NE1	2.25	0.69
57:SF:112:THR:HB	57:SF:114:GLN:OE1	1.92	0.69
68:SQ:29:ILE:HD11	68:SQ:65:ILE:CD1	2.22	0.69
72:SU:81:MET:HE3	81:Sd:52:PHE:HE1	1.53	0.69
1:1:3124:G:OP1	39:Lf:58:GLN:HG2	1.92	0.69
6:B:93:PHE:HE2	6:B:94:ARG:NE	1.87	0.69
76:SY:126:LYS:H	76:SY:126:LYS:HD2	1.58	0.69
21:LN:145:ASP:OD1	21:LN:147:ARG:N	2.24	0.69
64:SM:108:ARG:HD3	64:SM:110:GLY:H	1.57	0.69
67:SP:69:ARG:O	67:SP:73:GLN:CD	2.36	0.69
55:SD:216:PRO:HG3	69:SR:20:TYR:HE2	1.58	0.69
51:Ls:159:VAL:HG11	51:Ls:165:VAL:HG22	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:Sf:122:PRO:HD3	83:Sf:146:LEU:CD1	1.81	0.68
1:1:1934:G:N2	1:1:2050:C:O2	2.15	0.68
12:LE:150:GLN:OE1	12:LE:150:GLN:N	2.26	0.68
70:SS:45:LEU:HD21	70:SS:81:ILE:CG2	2.23	0.68
72:SU:65:ARG:NH2	72:SU:70:GLY:HA2	2.08	0.68
6:B:89:ARG:C	6:B:89:ARG:HD2	2.18	0.68
50:Lq:139:ARG:HB3	50:Lq:140:ARG:NH1	2.06	0.68
50:Lq:140:ARG:HG2	50:Lq:140:ARG:HH11	1.57	0.68
67:SP:73:GLN:CD	67:SP:73:GLN:N	2.48	0.68
1:1:3027:G:H5'	25:LR:57:MET:HE2	1.73	0.68
26:LS:96:GLU:OE2	26:LS:102:ALA:N	2.27	0.68
76:SY:44:ARG:HD2	76:SY:58:VAL:HG23	1.75	0.68
8:LA:2:GLY:HA2	8:LA:207:VAL:HG23	1.76	0.68
8:LA:122:ASP:C	8:LA:122:ASP:OD1	2.36	0.68
50:Lq:139:ARG:CA	50:Lq:140:ARG:HH22	2.06	0.68
58:SG:54:GLY:C	58:SG:63:MET:HE2	2.17	0.68
7:C:561:PRO:HB3	17:LJ:55:VAL:HA	1.74	0.68
1:1:1157:G:H21	22:LO:89:MET:HE2	1.58	0.68
1:1:2856:A:H5''	46:Lm:125:LYS:HG3	1.76	0.68
55:SD:46:PRO:CD	55:SD:46:PRO:O	2.40	0.68
10:LC:154:ASP:OD2	10:LC:154:ASP:C	2.36	0.68
52:SA:157:GLU:N	52:SA:157:GLU:CD	2.52	0.67
63:SL:123:GLU:OE1	63:SL:123:GLU:N	2.27	0.67
28:LU:65:ILE:HG13	28:LU:67:ASP:OD1	1.93	0.67
51:Ls:37:GLN:HE22	51:Ls:105:ILE:HD12	1.60	0.67
55:SD:216:PRO:HG3	69:SR:20:TYR:CE2	2.29	0.67
64:SM:66:GLU:OE1	64:SM:92:PRO:HB3	1.94	0.67
1:1:1727:G:H21	44:Lk:2:PRO:HG2	1.60	0.67
2:2:148:G:H22	2:2:160:G:H1	1.42	0.67
2:2:607:G:O2'	2:2:610:G:O2'	2.12	0.67
2:2:1689:A:H2'	2:2:1690:G:H8	1.59	0.67
51:Ls:116:PRO:HD2	51:Ls:180:PRO:HB2	1.77	0.67
83:Sf:120:GLU:OE2	83:Sf:130:VAL:O	2.11	0.67
84:D:259:ILE:HG22	84:D:260:ASP:OD2	1.93	0.67
1:1:1204:U:C5'	51:Ls:58:MET:HE1	2.24	0.67
67:SP:51:ARG:HH21	67:SP:55:ARG:HH21	1.43	0.67
77:SZ:57:ARG:HD3	77:SZ:57:ARG:H	1.59	0.67
21:LN:145:ASP:OD1	21:LN:145:ASP:C	2.37	0.67
28:LU:58:ASP:CG	28:LU:58:ASP:O	2.38	0.67
40:Lg:110:SER:HB2	40:Lg:111:GLN:NE2	2.06	0.67
70:SS:48:LYS:NZ	71:ST:36:ASP:OD2	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2630:A:O2'	17:LJ:99:GLU:CD	2.33	0.67
66:SO:149:ARG:C	66:SO:150:LEU:HD12	2.17	0.67
7:C:595:GLU:OE1	48:Lo:92:GLU:OE1	2.12	0.67
7:C:598:LYS:HB3	48:Lo:90:HIS:CE1	2.29	0.67
61:SJ:112:TYR:CZ	61:SJ:119:SER:HA	2.30	0.67
62:SK:86:PRO:HA	62:SK:89:HIS:HB3	1.75	0.67
82:Se:5:HIS:HD2	82:Se:6:GLY:H	1.43	0.67
83:Sf:91:ILE:O	83:Sf:91:ILE:HG13	1.93	0.67
2:2:1605:U:O2'	57:SF:92:GLY:O	2.12	0.66
57:SF:133:SER:OG	57:SF:144:ARG:NH1	2.27	0.66
6:B:89:ARG:NE	6:B:90:ARG:HB2	2.07	0.66
73:SV:47:GLN:OE1	73:SV:48:GLY:N	2.28	0.66
6:B:93:PHE:HD2	6:B:94:ARG:N	1.92	0.66
58:SG:54:GLY:CA	58:SG:63:MET:HE3	2.25	0.66
78:Sa:61:GLU:OE1	78:Sa:61:GLU:C	2.39	0.66
35:Lb:57:PHE:O	35:Lb:57:PHE:CD1	2.48	0.66
50:Lq:31:ASP:HB3	50:Lq:34:ASN:HB2	1.77	0.66
2:2:834:U:H2'	2:2:835:G:H8	1.61	0.66
51:Ls:67:MET:SD	51:Ls:69:ASP:OD1	2.54	0.66
67:SP:88:LEU:HB2	67:SP:91:MET:CE	2.26	0.66
1:1:1204:U:C5'	51:Ls:58:MET:HE2	2.25	0.66
15:LH:54:LYS:HD2	20:LM:3:GLU:HG2	1.78	0.66
68:SQ:128:LYS:O	68:SQ:129:PHE:CD2	2.49	0.66
72:SU:81:MET:CE	81:Sd:52:PHE:CD1	2.79	0.66
15:LH:14:GLU:OE2	20:LM:2:ALA:N	2.28	0.66
73:SV:46:ILE:HG22	73:SV:49:GLU:CD	2.20	0.66
29:LV:68:LYS:HB3	29:LV:70:GLU:OE2	1.96	0.66
1:1:2408:A:C4'	42:Li:72:ASN:ND2	2.57	0.66
12:LE:12:LYS:NZ	12:LE:15:ARG:HA	2.11	0.66
13:LF:29:ARG:HH11	13:LF:29:ARG:HG3	1.61	0.66
40:Lg:110:SER:HB3	40:Lg:111:GLN:HE22	1.60	0.66
54:SC:178:ILE:HB	54:SC:205:TYR:HB2	1.77	0.66
1:1:1196:G:OP1	26:LS:137:ARG:NH1	2.28	0.66
51:Ls:25:ILE:HG12	51:Ls:88:PHE:HE1	1.59	0.66
53:SB:67:GLU:OE1	53:SB:67:GLU:N	2.29	0.66
81:Sd:10:ARG:HE	81:Sd:11:PRO:HD2	1.60	0.66
1:1:275:G:O2'	1:1:276:G:OP2	2.11	0.65
5:A:193:GLY:N	5:A:213:ASP:OD1	2.28	0.65
20:LM:12:ARG:HB3	20:LM:18:ARG:HH12	1.61	0.65
1:1:2408:A:O2'	42:Li:72:ASN:ND2	2.29	0.65
1:1:3329:C:OP2	37:Ld:9:ARG:NH2	2.26	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:LR:181:ARG:NH2	25:LR:182:ASN:HB2	2.12	0.65
42:Li:70:LEU:HD13	42:Li:78:ALA:CB	2.26	0.65
71:ST:19:TYR:HD1	71:ST:136:ILE:HD13	1.61	0.65
1:1:2487:A:C4'	14:LG:52:MET:HE3	2.27	0.65
13:LF:216:PRO:HD3	13:LF:248:MET:HE3	1.78	0.65
66:SO:19:GLN:OE1	66:SO:19:GLN:O	2.14	0.65
1:1:729:A:H1'	35:Lb:27:GLN:HE22	1.47	0.65
34:La:93:GLY:C	34:La:94:GLN:OE1	2.39	0.65
66:SO:62:LYS:HA	66:SO:62:LYS:HE3	1.78	0.65
1:1:2654:A:H5''	7:C:609:LYS:CD	2.26	0.65
7:C:607:VAL:O	7:C:611:MET:HG3	1.97	0.65
51:Ls:104:ARG:HD2	51:Ls:183:TYR:C	2.21	0.65
2:2:1517:G:O2'	2:2:1519:U:OP2	2.14	0.65
1:1:2801:U:C2	84:D:121:MET:HE3	2.28	0.65
5:A:311:GLY:O	5:A:313:MET:SD	2.55	0.65
9:LB:215:MET:CE	9:LB:280:ASN:HA	2.26	0.65
23:LP:10:ALA:H	23:LP:13:LYS:HE2	1.61	0.65
67:SP:76:LYS:C	67:SP:77:PRO:CD	2.64	0.65
70:SS:23:ASP:OD1	70:SS:24:GLY:N	2.29	0.65
76:SY:123:GLY:O	76:SY:128:LYS:NZ	2.27	0.65
67:SP:94:VAL:HG23	67:SP:96:GLU:HG3	1.77	0.65
76:SY:29:ASP:C	76:SY:30:ILE:HD12	2.22	0.65
1:1:144:G:H3'	21:LN:49:ARG:HH22	1.61	0.65
1:1:2405:G:H1	1:1:2468:U:H3	1.45	0.65
2:2:1561:C:OP1	70:SS:41:ARG:NH1	2.30	0.65
64:SM:36:LEU:HD22	64:SM:129:GLU:HB3	1.77	0.65
16:LI:28:ASP:OD2	16:LI:29:PRO:HD2	1.97	0.64
28:LU:52:ARG:NH1	28:LU:55:ASN:HB2	2.11	0.64
5:A:107:ASP:OD2	5:A:125:ARG:NH1	2.30	0.64
12:LE:148:LYS:O	12:LE:150:GLN:OE1	2.15	0.64
2:2:1004:C:C2'	66:SO:150:LEU:HD11	2.26	0.64
12:LE:157:THR:O	12:LE:161:ASP:CG	2.41	0.64
73:SV:69:LEU:HD12	73:SV:69:LEU:O	1.98	0.64
74:SW:32:LYS:HB2	74:SW:32:LYS:NZ	2.11	0.64
2:2:1294:G:N2	2:2:1297:A:OP2	2.26	0.64
2:2:1686:G:N2	2:2:1708:A:N7	2.44	0.64
51:Ls:79:PHE:CD1	51:Ls:79:PHE:C	2.73	0.64
75:SX:37:ALA:O	75:SX:41:SER:OG	2.16	0.64
1:1:2224:G:O2'	1:1:2226:C:N4	2.30	0.64
5:A:54:TYR:OH	68:SQ:103:ASN:OD1	2.15	0.64
19:LL:118:ASP:C	19:LL:118:ASP:OD2	2.40	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:LW:92:GLU:CD	30:LW:96:MET:HE2	2.22	0.64
34:La:94:GLN:HA	34:La:96:LYS:HZ2	1.63	0.64
1:1:1796:A:H2'	1:1:1797:A:C8	2.33	0.64
1:1:1887:C:O2	9:LB:241:ARG:NH2	2.30	0.64
30:LW:124:LYS:HA	30:LW:127:LYS:HE2	1.79	0.64
36:Lc:43:LYS:NZ	36:Lc:96:LEU:O	2.29	0.64
63:SL:127:MET:HB2	63:SL:148:LEU:HD12	1.79	0.64
1:1:1727:G:N2	44:Lk:2:PRO:HG2	2.13	0.64
2:2:1354:U:H2'	2:2:1355:G:C8	2.33	0.64
30:LW:94:ARG:HG2	58:SG:145:PHE:HA	1.80	0.64
58:SG:74:ARG:HD2	58:SG:96:SER:HB3	1.78	0.64
64:SM:108:ARG:HG2	64:SM:109:GLU:N	2.13	0.64
64:SM:108:ARG:HG2	64:SM:109:GLU:OE1	1.98	0.64
66:SO:79:ASP:C	66:SO:79:ASP:OD2	2.40	0.64
1:1:1939:U:H3	1:1:2046:C:H42	1.45	0.64
2:2:893:G:H1	2:2:915:U:H3	1.46	0.64
9:LB:47:MET:HE2	9:LB:336:ILE:HD11	1.79	0.64
48:Lo:91:PHE:CE2	48:Lo:93:LEU:HD21	2.32	0.64
61:SJ:112:TYR:HE2	61:SJ:119:SER:O	1.78	0.64
2:2:648:C:H2'	2:2:649:G:H8	1.63	0.64
59:SH:164:LEU:HD11	59:SH:193:PHE:HD2	1.63	0.64
11:LD:166:MET:HE3	11:LD:178:HIS:HD1	1.59	0.64
42:Li:68:GLU:C	42:Li:68:GLU:CD	2.65	0.64
62:SK:85:VAL:HG22	62:SK:87:ALA:H	1.62	0.64
2:2:1538:G:N2	2:2:1565:A:OP2	2.31	0.63
53:SB:67:GLU:N	53:SB:67:GLU:CD	2.56	0.63
64:SM:48:ARG:H	64:SM:48:ARG:HD2	1.64	0.63
70:SS:114:GLU:HA	70:SS:117:LYS:HB3	1.80	0.63
2:2:159:A:H2'	2:2:160:G:C8	2.34	0.63
70:SS:120:ARG:HG2	70:SS:125:LEU:HD11	1.81	0.63
78:Sa:51:ARG:HH21	80:Sc:39:ARG:HA	1.62	0.63
2:2:747:U:OP1	74:SW:82:ARG:NH1	2.32	0.63
17:LJ:132:MET:HE2	17:LJ:132:MET:CA	2.27	0.63
62:SK:44:LEU:HD12	62:SK:44:LEU:N	2.13	0.63
74:SW:54:ASP:OD1	74:SW:54:ASP:O	2.17	0.63
84:D:122:GLN:O	84:D:126:LEU:HD13	1.97	0.63
1:1:291:U:OP2	42:Li:42:GLN:NE2	2.31	0.63
1:1:2719:C:N3	48:Lo:63:LYS:NZ	2.46	0.63
20:LM:42:ASP:C	20:LM:42:ASP:OD2	2.42	0.63
1:1:2630:A:C2'	17:LJ:99:GLU:OE1	2.47	0.63
2:2:1484:G:H3'	2:2:1511:A:H61	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:Ls:104:ARG:CD	51:Ls:184:GLY:HA3	2.29	0.63
56:SE:65:MET:CA	56:SE:65:MET:CE	2.66	0.63
57:SF:81:THR:HG22	57:SF:101:VAL:HG21	1.81	0.63
76:SY:30:ILE:HD12	76:SY:30:ILE:N	2.14	0.63
51:Ls:19:LEU:CA	51:Ls:88:PHE:HZ	2.09	0.63
64:SM:47:LEU:HA	64:SM:50:ALA:HB3	1.80	0.63
69:SR:76:GLU:OE1	69:SR:76:GLU:HA	1.98	0.63
2:2:701:A:N6	2:2:731:G:H1'	2.13	0.63
11:LD:53:VAL:HG12	11:LD:62:THR:HG22	1.80	0.63
15:LH:54:LYS:HD2	20:LM:3:GLU:HG3	1.81	0.63
47:Lr:17:ARG:O	47:Lr:21:ARG:HG2	1.99	0.63
1:1:1252:U:N3	1:1:1255:C:OP2	2.26	0.63
2:2:701:A:H62	2:2:731:G:H1'	1.64	0.63
53:SB:224:ASP:OD2	53:SB:224:ASP:C	2.42	0.63
1:1:2854:G:O2'	46:Lm:100:TYR:O	2.17	0.62
2:2:833:U:H2'	2:2:834:U:C6	2.33	0.62
8:LA:96:LEU:HD23	49:Lp:83:LEU:HD21	1.81	0.62
37:Ld:105:ASN:O	37:Ld:105:ASN:OD1	2.15	0.62
46:Lm:126:LYS:N	46:Lm:126:LYS:HD2	2.14	0.62
60:SI:157:ASP:C	60:SI:157:ASP:OD2	2.41	0.62
1:1:1733:G:OP1	44:Lk:77:ARG:NH2	2.32	0.62
29:LV:81:VAL:HB	29:LV:120:VAL:HG23	1.81	0.62
59:SH:7:ASN:HA	59:SH:16:ARG:HH12	1.64	0.62
84:D:122:GLN:O	84:D:126:LEU:HD12	1.99	0.62
1:1:766:G:N2	24:LQ:97:ARG:HE	1.98	0.62
2:2:1223:G:O2'	2:2:1253:A:N6	2.24	0.62
2:2:1474:G:OP1	71:ST:44:LYS:NZ	2.27	0.62
17:LJ:15:ILE:CA	17:LJ:132:MET:HE1	2.22	0.62
50:Lq:140:ARG:NE	50:Lq:140:ARG:CA	2.61	0.62
70:SS:139:LYS:HG3	70:SS:140:THR:HG23	1.81	0.62
1:1:209:G:OP1	32:LY:11:ARG:NH1	2.32	0.62
1:1:1204:U:H5''	51:Ls:58:MET:HE1	1.80	0.62
15:LH:101:ASP:C	15:LH:101:ASP:OD1	2.43	0.62
1:1:2461:C:H2'	1:1:2462:U:C6	2.33	0.62
2:2:282:G:OP1	58:SG:199:ARG:NH2	2.33	0.62
2:2:537:G:N2	2:2:539:A:N7	2.47	0.62
4:4:8:C:H2'	4:4:9:A:H8	1.65	0.62
41:Lh:19:GLU:O	41:Lh:23:ILE:HG22	1.99	0.62
2:2:157:C:O2'	58:SG:95:LYS:NZ	2.33	0.62
2:2:956:U:OP2	79:Sb:20:LYS:NZ	2.30	0.62
2:2:1199:A:H1'	2:2:1204:C:H42	1.63	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:LV:70:GLU:H	29:LV:70:GLU:CD	2.06	0.62
57:SF:85:MET:CE	57:SF:92:GLY:H	2.12	0.62
1:1:729:A:O2'	35:Lb:27:GLN:NE2	2.33	0.62
1:1:1229:G:N2	1:1:1247:C:O2'	2.33	0.62
7:C:575:ILE:HG12	7:C:606:LEU:HG	1.81	0.62
14:LG:74:VAL:HB	14:LG:237:GLY:HA3	1.80	0.62
49:Lp:33:GLN:OE1	49:Lp:49:ARG:NH1	2.33	0.62
59:SH:23:GLU:HA	59:SH:26:ILE:CG1	2.29	0.62
67:SP:96:GLU:OE2	67:SP:97:MET:HB3	1.99	0.62
7:C:573:ASP:HA	7:C:576:GLU:HG2	1.82	0.62
67:SP:91:MET:N	67:SP:91:MET:SD	2.73	0.62
70:SS:64:GLU:HA	70:SS:67:GLU:OE2	2.00	0.62
1:1:206:G:OP2	32:LY:1:MET:N	2.32	0.62
2:2:162:G:O2'	30:LW:80:ARG:NH2	2.32	0.62
2:2:477:G:O5'	61:SJ:118:LYS:NZ	2.32	0.62
8:LA:142:ASP:C	8:LA:143:GLU:CD	2.68	0.62
34:La:149:ALA:HB2	42:Li:16:LEU:HA	1.82	0.62
83:Sf:115:GLU:OE2	83:Sf:115:GLU:O	2.18	0.62
64:SM:108:ARG:HD3	64:SM:110:GLY:N	2.14	0.62
23:LP:8:GLU:OE2	23:LP:9:ILE:HG12	2.00	0.61
76:SY:41:ASP:OD1	76:SY:42:GLU:N	2.32	0.61
2:2:324:C:O2'	63:SL:10:GLU:OE1	2.10	0.61
2:2:1363:A:O2'	71:ST:8:ARG:NH1	2.33	0.61
2:2:1687:A:H2'	2:2:1688:G:C8	2.35	0.61
15:LH:12:VAL:HG11	20:LM:4:ILE:HD11	1.81	0.61
69:SR:66:VAL:HG13	69:SR:69:ILE:HG12	1.82	0.61
75:SX:107:PHE:HE1	75:SX:123:LYS:HB3	1.66	0.61
2:2:1215:G:N2	2:2:1440:A:OP2	2.33	0.61
2:2:1355:G:H4'	71:ST:131:ARG:HB3	1.82	0.61
9:LB:139:GLU:HG2	9:LB:140:ASN:OD1	2.01	0.61
10:LC:365:ALA:HB3	26:LS:28:ARG:HD2	1.81	0.61
56:SE:65:MET:HE1	56:SE:70:VAL:CG1	2.29	0.61
75:SX:63:GLN:HA	75:SX:63:GLN:OE1	1.99	0.61
4:4:82:U:OP1	4:4:85:G:N2	2.32	0.61
5:A:147:HIS:HD2	5:A:151:VAL:HG12	1.65	0.61
70:SS:48:LYS:HZ3	71:ST:36:ASP:CG	2.08	0.61
55:SD:46:PRO:CD	55:SD:46:PRO:C	2.69	0.61
64:SM:127:GLY:O	64:SM:133:ARG:NH2	2.34	0.61
1:1:97:G:H4'	19:LL:15:ARG:HH12	1.64	0.61
1:1:2461:C:H2'	1:1:2462:U:H6	1.66	0.61
8:LA:142:ASP:O	8:LA:143:GLU:CD	2.43	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:SA:87:ARG:NH2	69:SR:82:ASP:O	2.34	0.61
2:2:1199:A:N6	2:2:1453:C:OP1	2.34	0.61
2:2:1329:C:O2'	55:SD:165:GLN:NE2	2.32	0.61
10:LC:34:ASP:OD2	10:LC:34:ASP:C	2.43	0.61
5:A:36:ARG:HA	5:A:65:ILE:HG13	1.82	0.61
13:LF:29:ARG:HG3	13:LF:29:ARG:NH1	2.16	0.61
84:D:392:GLU:HG2	84:D:393:LYS:HG2	1.83	0.61
2:2:1354:U:O3'	71:ST:127:GLN:NE2	2.22	0.61
2:2:539:A:N1	82:Se:28:LYS:NZ	2.38	0.61
83:Sf:121:CYS:HB3	83:Sf:122:PRO:CD	2.31	0.61
1:1:1695:A:H4'	1:1:1696:A:H5'	1.82	0.60
2:2:700:G:N2	2:2:731:G:O2'	2.31	0.60
2:2:1703:C:H2'	2:2:1704:A:H8	1.66	0.60
11:LD:91:GLY:O	11:LD:94:ASN:ND2	2.34	0.60
42:Li:74:LYS:H	42:Li:74:LYS:HD2	1.65	0.60
51:Ls:104:ARG:HD2	51:Ls:184:GLY:N	2.16	0.60
57:SF:37:ASP:CG	57:SF:37:ASP:O	2.44	0.60
74:SW:54:ASP:OD1	74:SW:54:ASP:C	2.44	0.60
1:1:1739:C:N4	1:1:1746:G:O6	2.31	0.60
1:1:2100:U:OP2	1:1:2105:A:N6	2.34	0.60
72:SU:81:MET:HE1	81:Sd:52:PHE:CZ	2.35	0.60
72:SU:81:MET:HE1	81:Sd:52:PHE:CE1	2.35	0.60
1:1:117:A:OP2	21:LN:2:GLY:N	2.34	0.60
2:2:1710:G:H2'	2:2:1711:G:C8	2.37	0.60
5:A:313:MET:SD	5:A:313:MET:N	2.73	0.60
38:Le:35:LYS:HE3	38:Le:53:MET:HE1	1.83	0.60
63:SL:123:GLU:OE2	63:SL:126:ASP:OD2	2.18	0.60
72:SU:49:VAL:HG23	72:SU:90:LEU:HD21	1.83	0.60
2:2:224:C:H2'	2:2:225:C:C6	2.37	0.60
4:4:23:U:OP1	32:LY:15:ARG:NH1	2.34	0.60
5:A:49:GLU:C	5:A:49:GLU:CD	2.69	0.60
12:LE:17:VAL:O	13:LF:5:THR:HG23	2.01	0.60
40:Lg:110:SER:CB	40:Lg:111:GLN:HE22	2.14	0.60
45:Ll:27:ILE:HG23	45:Ll:30:ARG:HH21	1.65	0.60
59:SH:23:GLU:HA	59:SH:26:ILE:HG12	1.83	0.60
68:SQ:129:PHE:HA	68:SQ:135:ARG:HH22	1.66	0.60
1:1:1641:G:H2'	1:1:1642:G:C8	2.36	0.60
1:1:3207:G:OP2	12:LE:88:LYS:NZ	2.33	0.60
2:2:1132:U:OP2	75:SX:121:ARG:NH2	2.34	0.60
14:LG:217:LEU:O	14:LG:217:LEU:HD23	2.01	0.60
58:SG:55:GLY:HA3	58:SG:63:MET:HE2	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:806:U:H5''	8:LA:21:ARG:HD3	1.83	0.60
30:LW:62:GLY:O	30:LW:63:ILE:HD13	2.02	0.60
1:1:1221:C:H3'	1:1:1222:C:H5''	1.82	0.60
10:LC:270:GLU:CD	10:LC:270:GLU:C	2.70	0.60
59:SH:20:SER:N	59:SH:23:GLU:OE2	2.34	0.60
67:SP:88:LEU:HD13	67:SP:91:MET:HE2	1.75	0.60
1:1:1295:C:O2	22:LO:89:MET:HE3	2.02	0.60
51:Ls:79:PHE:O	51:Ls:79:PHE:HD1	1.81	0.60
65:SN:47:PRO:HG2	65:SN:86:GLU:OE2	2.00	0.60
72:SU:81:MET:CE	81:Sd:52:PHE:CZ	2.84	0.60
2:2:834:U:H2'	2:2:835:G:C8	2.37	0.60
60:SI:110:ARG:NH2	60:SI:122:GLY:O	2.35	0.60
2:2:1587:C:H2'	2:2:1588:A:H8	1.67	0.59
25:LR:15:LEU:HD13	25:LR:52:LYS:HB2	1.81	0.59
83:Sf:137:ASP:CG	83:Sf:151:ASP:OD1	2.44	0.59
1:1:2974:A:H2'	1:1:2975:G:H8	1.67	0.59
2:2:57:G:OP2	76:SY:119:LYS:NZ	2.34	0.59
9:LB:331:GLY:HA3	9:LB:337:MET:HE1	1.83	0.59
42:Li:14:THR:HG23	42:Li:16:LEU:H	1.66	0.59
55:SD:224:GLN:O	55:SD:226:MET:SD	2.60	0.59
60:SI:36:THR:HG21	60:SI:177:PRO:HB2	1.83	0.59
70:SS:28:VAL:O	70:SS:32:LEU:HD23	2.03	0.59
2:2:1214:A:O4'	62:SK:42:LYS:NZ	2.33	0.59
60:SI:141:SER:HA	60:SI:144:LYS:HE2	1.83	0.59
2:2:1765:U:OP1	6:B:98:LYS:NZ	2.34	0.59
5:A:170:TRP:HA	5:A:194:TYR:HB2	1.84	0.59
42:Li:70:LEU:CD1	42:Li:78:ALA:CB	2.79	0.59
44:Lk:30:LYS:C	44:Lk:32:GLN:NE2	2.60	0.59
57:SF:85:MET:HE1	57:SF:92:GLY:H	1.66	0.59
1:1:1447:G:N2	1:1:1450:A:OP2	2.35	0.59
19:LL:118:ASP:OD2	19:LL:119:TYR:N	2.36	0.59
51:Ls:38:MET:HE2	51:Ls:38:MET:N	2.18	0.59
79:Sb:8:LEU:HD22	79:Sb:8:LEU:N	2.17	0.59
1:1:1244:G:OP2	1:1:1244:G:N2	2.35	0.59
5:A:32:LEU:HD12	5:A:71:ILE:HG12	1.84	0.59
6:B:129:GLU:HA	6:B:132:LEU:HD13	1.84	0.59
8:LA:142:ASP:CB	8:LA:143:GLU:OE1	2.51	0.59
52:SA:58:GLU:OE1	52:SA:58:GLU:N	2.32	0.59
57:SF:37:ASP:O	57:SF:37:ASP:OD2	2.21	0.59
1:1:1175:C:N4	1:1:1284:A:O2'	2.36	0.59
27:LT:81:LYS:O	27:LT:82:HIS:ND1	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:LZ:32:THR:OG1	33:LZ:34:SER:O	2.19	0.59
77:SZ:54:LEU:HA	77:SZ:57:ARG:NH1	2.18	0.59
5:A:23:THR:HG21	5:A:292:SER:HA	1.82	0.59
8:LA:142:ASP:HB2	8:LA:143:GLU:OE1	2.02	0.59
11:LD:166:MET:CE	11:LD:178:HIS:CE1	2.83	0.59
34:La:93:GLY:N	34:La:94:GLN:OE1	2.36	0.59
56:SE:246:THR:OG1	56:SE:249:GLU:OE1	2.21	0.59
63:SL:107:LYS:O	75:SX:13:ARG:NH2	2.36	0.59
67:SP:138:ARG:NH1	67:SP:140:GLY:HA2	2.17	0.59
47:Lr:17:ARG:HA	47:Lr:17:ARG:NE	2.18	0.59
62:SK:26:ASP:O	62:SK:37:ASN:ND2	2.35	0.59
1:1:2064:C:H2'	1:1:2065:U:C6	2.38	0.59
2:2:1354:U:H2'	2:2:1355:G:H8	1.67	0.59
13:LF:214:SER:O	13:LF:248:MET:HG2	2.02	0.59
69:SR:25:THR:OG1	69:SR:26:LEU:N	2.36	0.59
1:1:2176:A:H2'	1:1:2177:A:C8	2.38	0.58
2:2:204:U:H2'	2:2:205:A:H8	1.68	0.58
7:C:598:LYS:CD	48:Lo:89:LYS:HB2	2.17	0.58
82:Se:5:HIS:HD2	82:Se:6:GLY:N	1.99	0.58
16:LI:93:PRO:HB2	16:LI:125:THR:HG22	1.86	0.58
51:Ls:33:VAL:HG11	51:Ls:38:MET:HE1	1.85	0.58
55:SD:75:LEU:HD22	62:SK:63:TYR:HD1	1.68	0.58
59:SH:6:LEU:O	59:SH:16:ARG:NH2	2.34	0.58
2:2:503:A:H2'	2:2:504:U:C6	2.37	0.58
2:2:1525:C:C4'	68:SQ:42:GLU:OE2	2.51	0.58
5:A:29:ASN:HA	5:A:45:LEU:HB2	1.84	0.58
5:A:49:GLU:CD	5:A:50:THR:N	2.61	0.58
5:A:64:HIS:CD2	5:A:65:ILE:HG22	2.39	0.58
28:LU:112:LEU:N	28:LU:112:LEU:HD12	2.17	0.58
61:SJ:100:GLU:H	61:SJ:100:GLU:CD	2.10	0.58
71:ST:105:MET:CE	71:ST:123:ARG:HH11	2.03	0.58
1:1:1619:C:OP2	40:Lg:75:ARG:NH2	2.36	0.58
1:1:1067:A:H4'	11:LD:44:TYR:CE2	2.38	0.58
1:1:3160:A:OP2	20:LM:125:LYS:NZ	2.35	0.58
1:1:3260:U:O4	9:LB:168:ARG:NH2	2.37	0.58
8:LA:117:GLU:HG2	8:LA:124:GLY:H	1.67	0.58
14:LG:31:GLU:OE2	14:LG:33:ARG:NH1	2.37	0.58
70:SS:45:LEU:HD21	70:SS:81:ILE:HG23	1.83	0.58
1:1:1204:U:H5''	51:Ls:58:MET:HE2	1.85	0.58
1:1:1220:G:O6	1:1:1235:A:N6	2.36	0.58
2:2:648:C:H2'	2:2:649:G:C8	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:LP:8:GLU:CD	23:LP:9:ILE:CD1	2.77	0.58
51:Ls:80:VAL:O	51:Ls:81:LYS:HE2	2.04	0.58
54:SC:116:ASP:O	54:SC:116:ASP:CG	2.43	0.58
69:SR:41:ILE:HG21	69:SR:47:ARG:HB2	1.86	0.58
82:Se:5:HIS:CD2	82:Se:6:GLY:H	2.22	0.58
7:C:608:THR:CA	7:C:611:MET:CE	2.35	0.58
70:SS:97:ASP:OD1	70:SS:98:SER:N	2.36	0.58
78:Sa:100:ARG:O	78:Sa:102:ARG:NH1	2.37	0.58
1:1:190:G:N1	1:1:193:A:OP2	2.36	0.58
1:1:1219:G:N1	1:1:1227:A:OP1	2.28	0.58
1:1:2960:C:O2'	9:LB:181:GLU:OE2	2.16	0.58
74:SW:111:MET:HE1	74:SW:119:LYS:HE2	1.86	0.58
1:1:405:G:OP1	23:LP:62:ARG:NH1	2.36	0.58
1:1:2487:A:O4'	14:LG:52:MET:CE	2.52	0.58
2:2:477:G:OP1	61:SJ:118:LYS:NZ	2.32	0.58
2:2:483:G:H2'	2:2:484:G:C8	2.39	0.58
60:SI:82:VAL:HG22	60:SI:200:LEU:HD11	1.86	0.58
64:SM:131:GLN:C	64:SM:131:GLN:CD	2.71	0.58
69:SR:92:ASP:OD2	69:SR:95:GLN:NE2	2.37	0.58
77:SZ:63:ALA:O	77:SZ:67:LYS:HG2	2.03	0.58
1:1:2654:A:H5''	7:C:609:LYS:HD3	1.84	0.58
2:2:331:U:O4	60:SI:5:ARG:NH2	2.36	0.58
2:2:1455:C:OP2	70:SS:138:THR:OG1	2.22	0.58
2:2:1708:A:OP1	2:2:1708:A:H4'	2.04	0.58
11:LD:216:ASP:OD1	11:LD:217:ASP:N	2.37	0.58
23:LP:8:GLU:OE2	23:LP:9:ILE:CG1	2.52	0.58
2:2:1477:C:O2'	2:2:1478:C:O5'	2.22	0.57
2:2:1520:A:N3	2:2:1586:G:O2'	2.36	0.57
19:LL:178:GLU:H	19:LL:178:GLU:CD	2.05	0.57
55:SD:21:TYR:O	55:SD:25:ASN:ND2	2.37	0.57
55:SD:145:LEU:HD12	55:SD:151:LYS:HG3	1.86	0.57
9:LB:215:MET:HE1	9:LB:280:ASN:CA	2.33	0.57
12:LE:12:LYS:HZ3	12:LE:15:ARG:CA	2.16	0.57
79:Sb:15:GLU:OE1	79:Sb:15:GLU:HA	2.01	0.57
5:A:30:MET:HE2	5:A:30:MET:HA	1.86	0.57
7:C:540:ARG:NE	7:C:591:SER:O	2.35	0.57
67:SP:90:ASP:OD1	67:SP:91:MET:SD	2.63	0.57
70:SS:82:PRO:HG2	70:SS:85:PHE:HB2	1.86	0.57
1:1:287:A:OP2	21:LN:15:GLN:NE2	2.37	0.57
1:1:1599:A:OP1	47:Lr:11:ARG:NE	2.34	0.57
1:1:1929:G:OP1	25:LR:104:ARG:NH1	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1789:G:O6	78:Sa:34:LYS:NZ	2.36	0.57
6:B:89:ARG:NH2	6:B:90:ARG:O	2.30	0.57
13:LF:171:ASP:OD1	13:LF:172:ASN:N	2.36	0.57
44:Lk:29:PRO:O	44:Lk:32:GLN:OE1	2.22	0.57
69:SR:77:GLU:HG2	69:SR:80:ARG:HH12	1.68	0.57
2:2:1054:U:H2'	2:2:1055:A:C8	2.39	0.57
6:B:89:ARG:HH21	6:B:90:ARG:C	2.12	0.57
68:SQ:32:ASN:OD1	68:SQ:68:ARG:NH1	2.34	0.57
72:SU:55:MET:HB2	72:SU:85:LYS:HB2	1.85	0.57
2:2:1226:G:N7	64:SM:48:ARG:HD3	2.19	0.57
10:LC:301:ARG:NH1	24:LQ:69:GLU:OE2	2.38	0.57
69:SR:89:SER:HB3	69:SR:92:ASP:HB2	1.85	0.57
1:1:1204:U:H5'	51:Ls:58:MET:HE2	1.85	0.57
1:1:2623:C:OP2	17:LJ:143:ARG:NH1	2.37	0.57
2:2:1189:C:O2'	68:SQ:137:ARG:NH2	2.38	0.57
36:Lc:51:THR:HG23	36:Lc:56:LYS:HE2	1.87	0.57
63:SL:123:GLU:CD	63:SL:126:ASP:OD2	2.47	0.57
64:SM:69:GLU:N	64:SM:69:GLU:CD	2.63	0.57
2:2:1699:C:H2'	2:2:1700:G:C8	2.40	0.57
5:A:20:SER:OG	5:A:67:SER:O	2.20	0.57
5:A:81:ALA:HB1	5:A:108:VAL:HG23	1.87	0.57
15:LH:101:ASP:OD1	15:LH:101:ASP:O	2.22	0.57
44:Lk:67:GLN:CD	44:Lk:67:GLN:N	2.62	0.57
51:Ls:121:VAL:HG23	51:Ls:158:LEU:HD11	1.86	0.57
73:SV:25:LYS:HG3	73:SV:28:ASP:HB2	1.87	0.57
1:1:351:G:N2	1:1:354:A:OP2	2.33	0.57
5:A:195:ILE:HA	5:A:211:GLY:HA3	1.86	0.57
9:LB:330:PRO:O	9:LB:337:MET:HE1	2.04	0.57
44:Lk:29:PRO:O	44:Lk:32:GLN:NE2	2.37	0.57
51:Ls:57:THR:HA	51:Ls:60:ARG:HE	1.70	0.57
2:2:1547:U:O4	67:SP:48:ARG:NH1	2.38	0.57
2:2:1582:A:OP1	68:SQ:132:ARG:N	2.37	0.57
3:3:107:C:OP2	16:LI:203:HIS:NE2	2.25	0.57
32:LY:112:LYS:HA	32:LY:115:GLU:OE2	2.05	0.57
33:LZ:87:GLU:N	33:LZ:87:GLU:CD	2.63	0.57
68:SQ:129:PHE:HB3	68:SQ:134:ALA:HA	1.87	0.57
70:SS:81:ILE:HG22	70:SS:82:PRO:CD	2.31	0.57
80:Sc:45:VAL:HG21	80:Sc:49:VAL:HG21	1.87	0.57
2:2:321:C:OP1	63:SL:138:LYS:NZ	2.35	0.56
2:2:1689:A:H2'	2:2:1690:G:C8	2.40	0.56
10:LC:155:SER:HG	10:LC:259:SER:HG	1.52	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Lc:79:GLU:HA	36:Lc:82:THR:HG22	1.86	0.56
57:SF:176:THR:CB	77:SZ:87:MET:HE2	2.35	0.56
62:SK:44:LEU:HD12	62:SK:44:LEU:H	1.69	0.56
66:SO:38:ASP:OD1	66:SO:39:THR:N	2.38	0.56
67:SP:64:LEU:HD13	67:SP:88:LEU:HD11	1.87	0.56
1:1:446:A:HO2'	1:1:447:U:H6	1.53	0.56
5:A:236:ILE:HG22	5:A:252:THR:HG22	1.87	0.56
17:LJ:42:SER:O	17:LJ:76:LYS:NZ	2.33	0.56
17:LJ:51:ALA:HB2	17:LJ:66:ILE:HD13	1.86	0.56
41:Lh:37:GLN:CD	41:Lh:37:GLN:C	2.72	0.56
51:Ls:37:GLN:HB2	51:Ls:38:MET:CE	2.35	0.56
59:SH:169:ARG:NH2	59:SH:196:PRO:O	2.39	0.56
73:SV:80:LYS:O	73:SV:82:VAL:HG23	2.05	0.56
77:SZ:37:ASP:C	77:SZ:41:LYS:HZ2	2.13	0.56
84:D:126:LEU:HD12	84:D:126:LEU:H	1.70	0.56
2:2:1004:C:C2'	66:SO:150:LEU:CD1	2.83	0.56
57:SF:28:LYS:NZ	57:SF:54:PRO:HB2	2.19	0.56
59:SH:7:ASN:O	59:SH:7:ASN:CG	2.47	0.56
1:1:1506:U:O2'	31:LX:124:ASN:ND2	2.38	0.56
2:2:231:G:H2'	2:2:232:G:C8	2.40	0.56
6:B:89:ARG:NH2	6:B:90:ARG:CB	2.62	0.56
64:SM:65:ASN:O	64:SM:74:LYS:NZ	2.37	0.56
73:SV:47:GLN:O	73:SV:49:GLU:OE1	2.24	0.56
2:2:824:U:H2'	2:2:825:C:C6	2.40	0.56
4:4:97:A:OP1	41:Lh:68:ARG:NH2	2.39	0.56
28:LU:56:LEU:HD21	28:LU:62:ILE:HD11	1.87	0.56
32:LY:63:LYS:HB3	32:LY:64:ASP:OD2	2.06	0.56
43:Lj:64:MET:HE3	43:Lj:67:LEU:HD23	1.87	0.56
83:Sf:115:GLU:C	83:Sf:115:GLU:CD	2.74	0.56
1:1:1704:U:H1'	1:1:1705:C:C6	2.40	0.56
2:2:327:G:OP2	60:SI:176:ARG:NH1	2.39	0.56
1:1:643:C:H2'	1:1:644:A:H8	1.69	0.56
22:LO:77:ALA:HB3	22:LO:80:ARG:HG2	1.88	0.56
51:Ls:48:GLN:NE2	51:Ls:90:ASN:OD1	2.35	0.56
73:SV:58:PHE:CD1	73:SV:58:PHE:C	2.83	0.56
78:Sa:61:GLU:O	78:Sa:61:GLU:CD	2.49	0.56
1:1:1196:G:H4'	26:LS:90:MET:SD	2.45	0.56
2:2:1708:A:N1	30:LW:74:ARG:NH2	2.54	0.56
5:A:28:PRO:O	5:A:47:ARG:NH2	2.39	0.56
5:A:161:GLN:NE2	5:A:162:ASN:HB3	2.21	0.56
13:LF:91:PHE:HB2	13:LF:145:PRO:HG3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:LS:130:GLU:HG2	26:LS:131:LYS:HG2	1.88	0.56
39:Lf:60:GLU:OE2	39:Lf:63:GLY:HA2	2.06	0.56
51:Ls:15:LEU:HD12	51:Ls:61:ARG:HH11	1.66	0.56
2:2:673:U:H2'	2:2:674:G:C8	2.41	0.56
2:2:835:G:H2'	2:2:836:G:H8	1.71	0.56
2:2:1195:G:OP1	2:2:1196:G:O2'	2.22	0.56
2:2:1390:C:H2'	2:2:1391:G:H8	1.70	0.56
2:2:1498:G:N2	2:2:1501:A:OP2	2.39	0.56
14:LG:166:VAL:HA	14:LG:169:LEU:HD23	1.87	0.56
16:LI:50:VAL:HG12	16:LI:167:VAL:HG22	1.86	0.56
36:Lc:102:ASP:OD2	36:Lc:102:ASP:N	2.39	0.56
83:Sf:115:GLU:O	83:Sf:115:GLU:CD	2.49	0.56
11:LD:295:ILE:HG13	16:LI:206:LEU:HD21	1.87	0.55
52:SA:193:ASN:HB3	52:SA:196:THR:HG22	1.88	0.55
1:1:2463:A:O2'	1:1:2465:U:O4'	2.24	0.55
1:1:3068:C:O2'	15:LH:194:SER:OG	2.21	0.55
2:2:235:U:OP2	2:2:832:G:O2'	2.23	0.55
2:2:483:G:H1	2:2:498:U:H3	1.54	0.55
2:2:644:A:H2'	2:2:645:G:C8	2.41	0.55
40:Lg:46:GLY:N	40:Lg:80:SER:O	2.39	0.55
51:Ls:98:GLU:HA	51:Ls:101:LEU:HD23	1.88	0.55
63:SL:104:ARG:HG3	75:SX:12:ALA:HB2	1.88	0.55
69:SR:20:TYR:CD1	69:SR:38:ILE:HD12	2.41	0.55
69:SR:104:ILE:CG1	69:SR:105:ASP:N	2.70	0.55
1:1:308:C:OP1	19:LL:102:LYS:NZ	2.39	0.55
9:LB:297:THR:HG23	9:LB:300:ASP:H	1.71	0.55
12:LE:11:GLY:O	12:LE:12:LYS:HE2	2.07	0.55
12:LE:86:PRO:HB3	12:LE:170:ILE:HD11	1.89	0.55
23:LP:8:GLU:OE1	23:LP:9:ILE:CD1	2.52	0.55
29:LV:12:LYS:HZ3	29:LV:15:MET:CE	2.15	0.55
44:Lk:32:GLN:CD	44:Lk:32:GLN:N	2.63	0.55
51:Ls:18:LEU:HB3	51:Ls:88:PHE:CE2	2.41	0.55
57:SF:69:PHE:CE1	80:Sc:50:ARG:HD3	2.41	0.55
2:2:1473:A:H5'	71:ST:46:LEU:HD21	1.88	0.55
70:SS:38:VAL:HG23	70:SS:42:TYR:HB3	1.88	0.55
83:Sf:137:ASP:OD1	83:Sf:151:ASP:OD1	2.23	0.55
2:2:893:G:H2'	2:2:894:U:C6	2.41	0.55
15:LH:144:ALA:O	15:LH:145:GLU:HG3	2.06	0.55
73:SV:80:LYS:C	73:SV:81:ASN:OD1	2.49	0.55
2:2:195:G:H2'	2:2:196:G:H8	1.72	0.55
82:Se:4:ALA:O	82:Se:5:HIS:CG	2.57	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:D:431:ARG:NH1	84:D:436:GLU:OE1	2.40	0.55
1:1:2387:A:OP1	21:LN:90:ASN:ND2	2.39	0.55
1:1:2906:G:C2	9:LB:251:ALA:HB1	2.42	0.55
2:2:66:U:C5	58:SG:176:PRO:HB3	2.41	0.55
2:2:833:U:H2'	2:2:834:U:H6	1.71	0.55
2:2:1223:G:HO2'	2:2:1253:A:H61	1.54	0.55
62:SK:40:VAL:HG22	62:SK:44:LEU:HD11	1.89	0.55
69:SR:104:ILE:HG13	69:SR:105:ASP:N	2.22	0.55
72:SU:81:MET:HE2	81:Sd:52:PHE:CD1	2.40	0.55
78:Sa:23:CYS:HB3	78:Sa:28:ARG:H	1.72	0.55
83:Sf:134:SER:HA	83:Sf:139:GLN:HG3	1.88	0.55
84:D:398:LEU:O	84:D:398:LEU:HD23	2.07	0.55
1:1:2730:U:O2'	1:1:2731:C:O4'	2.25	0.55
12:LE:10:PHE:HE2	12:LE:12:LYS:CE	2.18	0.55
41:Lh:15:LYS:HD2	41:Lh:19:GLU:CD	2.31	0.55
70:SS:45:LEU:HD21	70:SS:81:ILE:HG21	1.88	0.55
73:SV:47:GLN:OE1	73:SV:47:GLN:HA	2.06	0.55
77:SZ:42:ASP:OD2	77:SZ:46:TYR:HE1	1.90	0.55
1:1:1464:A:O2'	1:1:1838:A:H1'	2.07	0.55
1:1:1796:A:H2'	1:1:1797:A:H8	1.71	0.55
2:2:1341:A:H2'	2:2:1342:A:C8	2.40	0.55
5:A:31:LEU:HB3	5:A:43:TRP:HB2	1.88	0.55
12:LE:157:THR:C	12:LE:161:ASP:OD2	2.49	0.55
17:LJ:79:GLU:OE2	17:LJ:83:ARG:NH1	2.40	0.55
19:LL:115:ARG:NH2	19:LL:155:PHE:O	2.30	0.55
56:SE:99:PHE:HE1	56:SE:113:ARG:HD3	1.72	0.55
71:ST:23:LEU:HD13	71:ST:29:LEU:HD11	1.88	0.55
1:1:261:A:OP1	21:LN:50:ARG:NH1	2.40	0.55
1:1:1387:G:N2	1:1:1390:A:OP2	2.38	0.55
1:1:1634:A:O3'	40:Lg:41:THR:CG2	2.54	0.55
1:1:2612:C:H5''	7:C:598:LYS:HE3	1.88	0.55
2:2:125:A:H62	2:2:288:G:H21	1.55	0.55
26:LS:31:ALA:HB1	26:LS:36:VAL:HG23	1.88	0.55
51:Ls:126:THR:O	51:Ls:128:MET:SD	2.65	0.55
53:SB:190:PRO:HG2	53:SB:192:VAL:HG23	1.89	0.55
56:SE:188:ASN:HB3	56:SE:191:ARG:HD3	1.89	0.55
70:SS:25:LYS:HE3	77:SZ:29:VAL:HG23	1.88	0.55
1:1:1016:U:H2'	1:1:1017:U:C6	2.42	0.54
1:1:1139:C:OP2	13:LF:100:LYS:NZ	2.40	0.54
1:1:1589:C:P	31:LX:92:GLN:NE2	2.80	0.54
7:C:559:SER:HB2	17:LJ:61:ARG:NH1	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:LB:143:ALA:O	9:LB:147:ARG:HG2	2.06	0.54
15:LH:54:LYS:CE	20:LM:3:GLU:OE1	2.56	0.54
26:LS:82:ASP:HB2	26:LS:120:SER:HB2	1.89	0.54
27:LT:83:ARG:HG2	27:LT:83:ARG:HH11	1.71	0.54
39:Lf:105:TYR:HB2	39:Lf:106:PRO:HD3	1.89	0.54
52:SA:95:HIS:ND1	52:SA:205:TYR:OH	2.32	0.54
66:SO:92:LEU:CD1	66:SO:123:MET:SD	2.95	0.54
1:1:669:U:O2'	1:1:685:G:O6	2.26	0.54
2:2:694:U:H2'	2:2:695:C:C6	2.42	0.54
5:A:4:GLN:NE2	5:A:313:MET:CG	2.70	0.54
23:LP:8:GLU:C	23:LP:8:GLU:CD	2.74	0.54
30:LW:92:GLU:OE2	30:LW:96:MET:HE1	2.06	0.54
33:LZ:59:ALA:O	33:LZ:62:GLU:HG3	2.08	0.54
51:Ls:64:LYS:C	51:Ls:67:MET:HE1	2.32	0.54
60:SI:105:ASP:C	60:SI:105:ASP:OD2	2.49	0.54
76:SY:125:ALA:HA	76:SY:128:LYS:HE2	1.88	0.54
1:1:1333:A:H2'	1:1:1335:A:H5''	1.89	0.54
1:1:2355:C:O2'	9:LB:267:ARG:NH2	2.38	0.54
44:Lk:64:PRO:HD2	44:Lk:65:ASN:OD1	2.07	0.54
53:SB:146:ARG:HD3	53:SB:147:PRO:HD2	1.89	0.54
56:SE:141:THR:OG1	56:SE:143:ASP:OD1	2.25	0.54
61:SJ:94:VAL:HA	61:SJ:97:LEU:HD13	1.90	0.54
71:ST:11:ASP:HB3	71:ST:14:LYS:HG2	1.90	0.54
79:Sb:35:VAL:HG11	79:Sb:63:LEU:HD12	1.88	0.54
1:1:2268:G:OP2	1:1:2268:G:N2	2.37	0.54
1:1:2654:A:H5''	7:C:609:LYS:HD2	1.89	0.54
2:2:674:G:H2'	2:2:675:G:H8	1.73	0.54
51:Ls:15:LEU:HB2	51:Ls:61:ARG:NH1	2.22	0.54
51:Ls:98:GLU:OE2	51:Ls:101:LEU:HG	2.08	0.54
56:SE:80:ILE:HG13	56:SE:81:THR:HG23	1.90	0.54
64:SM:65:ASN:HD21	64:SM:94:GLY:HA3	1.71	0.54
71:ST:136:ILE:O	71:ST:139:THR:OG1	2.22	0.54
76:SY:83:GLU:OE1	76:SY:83:GLU:N	2.39	0.54
84:D:183:MET:HA	84:D:183:MET:CE	2.30	0.54
1:1:2666:U:H2'	1:1:2667:C:C6	2.42	0.54
2:2:1359:U:H4'	2:2:1360:G:C2	2.42	0.54
2:2:1479:A:H4'	68:SQ:72:GLY:H	1.73	0.54
7:C:584:ALA:HB1	48:Lo:96:ASP:OD1	2.07	0.54
10:LC:149:VAL:CG1	10:LC:150:PRO:HD3	2.35	0.54
51:Ls:151:GLU:OE2	51:Ls:153:THR:HA	2.07	0.54
76:SY:45:GLU:OE2	76:SY:55:LYS:HD2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:D:262:ARG:NH1	84:D:320:LYS:HE2	2.22	0.54
1:1:1615:G:N2	1:1:1618:A:OP2	2.38	0.54
1:1:1759:C:N4	25:LR:88:ARG:O	2.40	0.54
31:LX:82:THR:H	31:LX:85:ALA:HB3	1.72	0.54
45:LI:51:LEU:N	45:LI:51:LEU:HD12	2.23	0.54
50:Lq:140:ARG:NH1	50:Lq:140:ARG:HG2	2.23	0.54
47:Lr:17:ARG:HA	47:Lr:17:ARG:HE	1.72	0.54
55:SD:98:GLY:HA2	55:SD:104:GLN:NE2	2.23	0.54
2:2:552:A:N3	2:2:587:C:O2'	2.38	0.54
16:LI:47:PRO:HG2	16:LI:142:ASP:OD1	2.07	0.54
28:LU:21:PHE:O	28:LU:22:ILE:HD13	2.06	0.54
37:Ld:9:ARG:HB3	37:Ld:13:ALA:HB2	1.90	0.54
51:Ls:62:ALA:O	51:Ls:65:THR:OG1	2.24	0.54
51:Ls:133:THR:HG21	51:Ls:145:ILE:HD11	1.88	0.54
61:SJ:61:ASP:OD1	61:SJ:62:GLU:N	2.41	0.54
66:SO:93:HIS:O	66:SO:94:ILE:HD13	2.06	0.54
68:SQ:38:LEU:HD11	71:ST:11:ASP:HA	1.88	0.54
73:SV:47:GLN:C	73:SV:49:GLU:OE1	2.51	0.54
84:D:208:LEU:HD23	84:D:235:TRP:HH2	1.72	0.54
1:1:2532:C:C2	33:LZ:56:MET:HE2	2.43	0.54
51:Ls:19:LEU:CD2	51:Ls:61:ARG:NH1	2.68	0.54
67:SP:73:GLN:CD	67:SP:73:GLN:H	2.12	0.54
67:SP:104:ILE:N	67:SP:111:ASN:O	2.35	0.54
71:ST:66:TYR:C	71:ST:66:TYR:CD2	2.85	0.54
75:SX:63:GLN:OE1	75:SX:63:GLN:CA	2.54	0.54
1:1:859:C:HO2'	1:1:862:G:HO2'	1.51	0.54
1:1:1204:U:H4'	51:Ls:58:MET:HE1	1.90	0.54
2:2:277:C:H5''	30:LW:109:ILE:HD11	1.89	0.54
2:2:844:G:H2'	2:2:845:A:H8	1.73	0.54
14:LG:124:LYS:C	14:LG:127:ASP:OD2	2.48	0.54
32:LY:50:ARG:HG2	32:LY:51:LYS:H	1.73	0.54
33:LZ:51:LYS:O	33:LZ:64:ARG:NH1	2.41	0.54
51:Ls:18:LEU:HB3	51:Ls:88:PHE:CD2	2.43	0.54
51:Ls:57:THR:HA	51:Ls:60:ARG:HH21	1.73	0.54
62:SK:40:VAL:CG2	62:SK:44:LEU:HD11	2.37	0.54
68:SQ:89:ILE:HD11	68:SQ:93:TYR:OH	2.08	0.54
5:A:43:TRP:HA	5:A:55:PRO:HA	1.90	0.54
34:La:82:VAL:HG13	34:La:87:ARG:HB2	1.89	0.54
2:2:1470:G:H2'	2:2:1471:A:H8	1.71	0.53
5:A:175:LYS:HB3	5:A:184:LEU:HD13	1.89	0.53
73:SV:4:ASP:OD1	73:SV:4:ASP:N	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:Sd:30:LEU:HD21	81:Sd:37:ASN:HA	1.89	0.53
1:1:20:U:H2'	1:1:21:A:C8	2.44	0.53
1:1:1196:G:H5''	26:LS:137:ARG:HH12	1.73	0.53
1:1:2460:C:H2'	1:1:2461:C:C6	2.43	0.53
1:1:3007:A:C6	9:LB:75:ALA:HB2	2.43	0.53
2:2:878:C:OP1	65:SN:107:LYS:NZ	2.42	0.53
2:2:1364:G:O3'	71:ST:69:LYS:NZ	2.34	0.53
2:2:1686:G:H2'	2:2:1687:A:H8	1.73	0.53
21:LN:159:ARG:HB2	21:LN:164:LEU:HB2	1.91	0.53
21:LN:183:THR:HG22	21:LN:187:ARG:HB2	1.89	0.53
26:LS:12:ARG:NH2	26:LS:57:GLU:OE2	2.42	0.53
32:LY:53:ASP:OD2	32:LY:53:ASP:N	2.41	0.53
32:LY:111:ASP:N	32:LY:111:ASP:OD1	2.40	0.53
74:SW:111:MET:SD	74:SW:116:ALA:HB2	2.47	0.53
84:D:74:PRO:HD2	84:D:76:GLN:OE1	2.09	0.53
2:2:1589:A:H2'	2:2:1590:G:H8	1.73	0.53
4:4:75:G:OP2	32:LY:73:TYR:OH	2.27	0.53
17:LJ:15:ILE:HG12	17:LJ:132:MET:HE1	1.89	0.53
69:SR:88:VAL:HG23	69:SR:95:GLN:NE2	2.23	0.53
69:SR:102:LEU:H	69:SR:102:LEU:HD23	1.73	0.53
1:1:535:U:H2'	1:1:536:C:H5''	1.90	0.53
1:1:1205:G:C8	51:Ls:58:MET:HE3	2.43	0.53
1:1:2229:U:H2'	1:1:2230:C:C6	2.44	0.53
28:LU:52:ARG:HH11	28:LU:52:ARG:HB2	1.74	0.53
53:SB:4:GLY:N	66:SO:62:LYS:HZ3	1.86	0.53
64:SM:108:ARG:HD3	64:SM:108:ARG:C	2.33	0.53
2:2:1675:G:H21	2:2:1718:A:H62	1.56	0.53
21:LN:99:ARG:NH2	21:LN:118:SER:O	2.41	0.53
31:LX:71:ASP:OD2	31:LX:72:GLU:N	2.41	0.53
53:SB:144:LYS:HB2	53:SB:208:GLN:HB3	1.90	0.53
55:SD:83:PRO:O	55:SD:86:SER:OG	2.22	0.53
55:SD:165:GLN:N	55:SD:166:PRO:HD2	2.23	0.53
55:SD:175:THR:O	55:SD:176:ARG:NH1	2.37	0.53
60:SI:176:ARG:HE	60:SI:179:GLN:HG3	1.74	0.53
2:2:257:U:H3'	2:2:258:C:H5'	1.89	0.53
5:A:64:HIS:HD2	5:A:83:TRP:HB2	1.74	0.53
6:B:93:PHE:CD2	6:B:93:PHE:C	2.87	0.53
23:LP:154:GLU:HG2	23:LP:155:GLU:H	1.74	0.53
53:SB:189:ILE:HG13	53:SB:190:PRO:HD3	1.90	0.53
59:SH:5:SER:HA	59:SH:31:TYR:HD2	1.74	0.53
1:1:575:G:H2'	1:1:576:A:H8	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2632:A:O2'	17:LJ:127:ASP:OD1	2.24	0.53
2:2:1122:A:OP1	47:Ln:18:ARG:NH1	2.42	0.53
24:LQ:203:ARG:O	34:La:51:GLY:HA2	2.09	0.53
58:SG:49:ILE:HG12	58:SG:115:LYS:HB3	1.91	0.53
70:SS:92:ILE:HG12	70:SS:93:VAL:H	1.73	0.53
1:1:3298:U:O2'	1:1:3299:U:OP1	2.23	0.53
2:2:1078:A:N3	2:2:1079:C:N4	2.57	0.53
2:2:1385:A:H5''	69:SR:48:ASN:HD21	1.73	0.53
2:2:1781:U:OP1	66:SO:149:ARG:NH2	2.41	0.53
64:SM:134:THR:HA	64:SM:137:LEU:CD2	2.38	0.53
67:SP:138:ARG:HD2	67:SP:138:ARG:C	2.33	0.53
2:2:1529:C:OP2	77:SZ:66:ARG:NH2	2.34	0.53
5:A:165:ILE:HG13	5:A:177:TRP:HB2	1.90	0.53
52:SA:30:LYS:NZ	52:SA:47:GLY:O	2.38	0.53
52:SA:37:GLN:O	52:SA:37:GLN:CD	2.52	0.53
58:SG:135:PRO:HG2	58:SG:141:ILE:HD13	1.91	0.53
65:SN:92:ILE:HD13	65:SN:122:ILE:HD13	1.91	0.53
75:SX:63:GLN:OE1	75:SX:63:GLN:O	2.27	0.53
1:1:309:U:O2'	42:Li:39:LYS:NZ	2.41	0.53
2:2:1526:U:O5'	77:SZ:85:SER:OG	2.27	0.53
9:LB:215:MET:HE1	9:LB:280:ASN:C	2.34	0.53
20:LM:86:GLU:C	20:LM:86:GLU:CD	2.77	0.53
52:SA:37:GLN:C	52:SA:37:GLN:CD	2.77	0.53
53:SB:3:VAL:CA	66:SO:62:LYS:NZ	2.64	0.53
63:SL:31:ARG:O	63:SL:37:ARG:NH1	2.42	0.53
2:2:1588:A:H2'	2:2:1589:A:H8	1.75	0.52
19:LL:47:ALA:HB3	19:LL:48:PRO:HD3	1.91	0.52
58:SG:2:LYS:HB2	58:SG:108:VAL:HG22	1.91	0.52
1:1:2919:C:H2'	1:1:2920:G:C8	2.44	0.52
2:2:204:U:H2'	2:2:205:A:C8	2.44	0.52
2:2:732:A:H3'	2:2:733:A:H8	1.73	0.52
11:LD:245:GLU:OE1	11:LD:249:GLN:NE2	2.42	0.52
13:LF:8:THR:HG22	13:LF:9:GLN:H	1.74	0.52
14:LG:44:GLN:OE1	14:LG:47:ARG:NH2	2.41	0.52
55:SD:67:ARG:HD2	62:SK:88:THR:HG22	1.91	0.52
58:SG:105:ASP:OD1	58:SG:106:LEU:HD12	2.09	0.52
70:SS:26:GLN:HE22	70:SS:31:ALA:CA	2.20	0.52
71:ST:125:ILE:HD12	71:ST:130:GLN:HB3	1.92	0.52
75:SX:69:ARG:HG3	75:SX:117:ILE:HG12	1.90	0.52
80:Sc:32:GLU:HA	80:Sc:32:GLU:OE2	2.08	0.52
2:2:674:G:H2'	2:2:675:G:C8	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:LB:214:GLU:OE2	9:LB:341:LYS:NZ	2.41	0.52
39:Lf:44:ASN:HA	39:Lf:47:LEU:HD23	1.89	0.52
51:Ls:189:GLN:OE1	51:Ls:193:GLN:N	2.42	0.52
56:SE:87:MET:CE	56:SE:123:LEU:HG	2.39	0.52
57:SF:43:ILE:HG13	57:SF:44:SER:H	1.75	0.52
64:SM:108:ARG:HG2	64:SM:109:GLU:CD	2.35	0.52
68:SQ:3:SER:HG	68:SQ:4:VAL:H	1.55	0.52
1:1:2532:C:O2	33:LZ:56:MET:HE2	2.08	0.52
1:1:3008:U:O2'	30:LW:16:GLY:O	2.27	0.52
1:1:3332:A:O2'	1:1:3333:G:OP1	2.24	0.52
2:2:1248:U:HO2'	2:2:1249:C:H6	1.56	0.52
5:A:66:VAL:HA	5:A:82:SER:HA	1.91	0.52
5:A:79:LEU:HD23	5:A:113:PHE:HZ	1.74	0.52
55:SD:49:THR:N	55:SD:86:SER:O	2.31	0.52
61:SJ:112:TYR:CE2	61:SJ:120:ILE:CA	2.92	0.52
69:SR:27:ASP:OD1	69:SR:30:THR:CG2	2.53	0.52
70:SS:45:LEU:CD2	70:SS:81:ILE:HG21	2.40	0.52
1:1:2227:U:H2'	1:1:2228:C:H6	1.74	0.52
2:2:270:G:H2'	2:2:271:G:H8	1.75	0.52
2:2:1217:C:H2'	2:2:1218:A:C8	2.45	0.52
28:LU:40:GLU:OE1	28:LU:64:GLN:NE2	2.42	0.52
33:LZ:75:ASN:OD1	33:LZ:76:TYR:N	2.43	0.52
68:SQ:128:LYS:C	68:SQ:129:PHE:CD2	2.87	0.52
69:SR:104:ILE:HD12	69:SR:105:ASP:N	2.18	0.52
77:SZ:38:LYS:HA	77:SZ:41:LYS:HZ3	1.73	0.52
1:1:3179:G:H2'	1:1:3180:G:H8	1.74	0.52
2:2:469:U:H2'	2:2:470:A:H8	1.75	0.52
5:A:79:LEU:HD23	5:A:113:PHE:CZ	2.44	0.52
45:Ll:21:ARG:NH1	45:Ll:22:PRO:O	2.42	0.52
57:SF:115:ASN:HB3	57:SF:118:GLN:HG2	1.91	0.52
63:SL:137:SER:OG	63:SL:138:LYS:N	2.43	0.52
84:D:208:LEU:HD23	84:D:235:TRP:CH2	2.44	0.52
1:1:1264:U:H2'	1:1:1265:G:H8	1.73	0.52
4:4:8:C:H2'	4:4:9:A:C8	2.45	0.52
9:LB:41:VAL:HG12	9:LB:186:GLY:HA3	1.91	0.52
17:LJ:12:GLU:OE2	17:LJ:14:ARG:NH2	2.36	0.52
51:Ls:65:THR:HG22	51:Ls:74:GLU:N	2.25	0.52
54:SC:74:TYR:C	54:SC:74:TYR:CD2	2.88	0.52
68:SQ:73:GLY:O	68:SQ:77:GLN:HG3	2.09	0.52
79:Sb:59:CYS:SG	79:Sb:61:ASN:ND2	2.82	0.52
1:1:2919:C:H2'	1:1:2920:G:H8	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:825:C:H2'	2:2:826:U:C6	2.45	0.52
2:2:1157:A:H2'	2:2:1158:C:C6	2.45	0.52
3:3:39:C:C6	17:LJ:47:VAL:HG11	2.45	0.52
17:LJ:109:GLU:HG3	17:LJ:112:ASP:HB3	1.91	0.52
59:SH:5:SER:HA	59:SH:31:TYR:CD2	2.44	0.52
63:SL:91:ILE:HD11	63:SL:112:LEU:HD23	1.92	0.52
1:1:97:G:H4'	19:LL:15:ARG:NH1	2.25	0.52
2:2:1790:A:OP2	78:Sa:4:LYS:NZ	2.34	0.52
24:LQ:33:ASP:O	24:LQ:33:ASP:OD2	2.27	0.52
26:LS:73:LYS:NZ	26:LS:97:THR:O	2.42	0.52
31:LX:144:ASP:OD2	31:LX:147:ASP:OD1	2.27	0.52
55:SD:97:ARG:O	55:SD:104:GLN:NE2	2.38	0.52
57:SF:131:GLU:OE1	57:SF:212:ARG:NH2	2.37	0.52
82:Se:5:HIS:CD2	82:Se:6:GLY:N	2.77	0.52
84:D:85:ILE:CD1	84:D:134:GLU:OE2	2.58	0.52
1:1:1439:A:N7	37:Ld:34:LYS:NZ	2.49	0.52
1:1:3179:G:H2'	1:1:3180:G:C8	2.45	0.52
2:2:118:A:H1'	2:2:394:A:C5	2.45	0.52
2:2:1707:C:H3'	2:2:1708:A:H5''	1.92	0.52
5:A:118:ARG:HH12	5:A:133:ASN:HB2	1.75	0.52
7:C:598:LYS:HD3	48:Lo:90:HIS:CG	2.44	0.52
12:LE:12:LYS:CA	12:LE:12:LYS:CE	2.75	0.52
43:Lj:64:MET:HE2	43:Lj:67:LEU:HB3	1.91	0.52
57:SF:110:LEU:HD11	77:SZ:48:LEU:HB2	1.91	0.52
57:SF:183:GLU:OE2	57:SF:187:ASN:ND2	2.43	0.52
1:1:1227:A:H5''	1:1:1254:A:H4'	1.91	0.51
2:2:1428:U:H4'	2:2:1429:G:H5''	1.93	0.51
2:2:1485:U:OP2	2:2:1511:A:N6	2.44	0.51
37:Ld:54:THR:HG23	37:Ld:56:ASP:H	1.75	0.51
53:SB:137:LEU:HG	53:SB:215:VAL:HG22	1.93	0.51
2:2:219:C:N3	2:2:835:G:N1	2.40	0.51
2:2:1362:C:O3'	68:SQ:30:LYS:NZ	2.39	0.51
21:LN:35:VAL:HG12	21:LN:36:ILE:HG13	1.92	0.51
37:Ld:94:LYS:HB3	37:Ld:95:GLU:OE1	2.11	0.51
62:SK:27:TYR:HA	62:SK:37:ASN:HD21	1.75	0.51
72:SU:79:TYR:HB3	81:Sd:52:PHE:HB3	1.91	0.51
1:1:687:A:H4'	19:LL:68:ARG:HH12	1.74	0.51
1:1:1225:G:OP1	1:1:1225:G:N2	2.33	0.51
1:1:2064:C:O2'	1:1:2065:U:OP1	2.27	0.51
1:1:2227:U:H2'	1:1:2228:C:C6	2.45	0.51
1:1:2460:C:H2'	1:1:2461:C:H6	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:853:A:OP1	59:SH:12:ASN:ND2	2.44	0.51
2:2:1705:C:H2'	2:2:1706:U:C6	2.46	0.51
35:Lb:57:PHE:CD1	35:Lb:57:PHE:C	2.88	0.51
41:Lh:15:LYS:CD	41:Lh:19:GLU:OE2	2.54	0.51
51:Ls:92:ASP:OD2	51:Ls:93:LEU:N	2.43	0.51
55:SD:146:ARG:HG3	55:SD:146:ARG:O	2.10	0.51
70:SS:56:LYS:HD3	70:SS:60:GLU:CG	2.40	0.51
73:SV:40:ASP:HB2	73:SV:41:GLU:OE1	2.11	0.51
1:1:656:U:H2'	1:1:657:U:C6	2.46	0.51
1:1:664:G:O6	24:LQ:113:THR:HG21	2.10	0.51
2:2:483:G:H2'	2:2:484:G:H8	1.75	0.51
2:2:678:G:O2'	2:2:679:G:OP1	2.26	0.51
2:2:720:G:H1'	2:2:721:G:C8	2.46	0.51
12:LE:76:LEU:HB2	12:LE:80:VAL:HG23	1.91	0.51
59:SH:17:GLN:OE1	59:SH:18:ASN:ND2	2.44	0.51
60:SI:59:ARG:O	60:SI:60:LEU:HD23	2.11	0.51
1:1:1052:C:H2'	1:1:1053:U:H6	1.75	0.51
1:1:1368:C:O3'	50:Lq:30:ARG:NH1	2.44	0.51
2:2:499:U:H2'	2:2:500:G:C8	2.46	0.51
2:2:1217:C:H2'	2:2:1218:A:H8	1.75	0.51
2:2:1616:C:O2'	2:2:1617:U:OP1	2.28	0.51
5:A:35:SER:OG	5:A:36:ARG:N	2.44	0.51
20:LM:130:GLU:HG2	22:LO:191:VAL:HG21	1.93	0.51
32:LY:50:ARG:HG2	32:LY:51:LYS:N	2.25	0.51
61:SJ:88:ARG:HB3	61:SJ:93:TYR:CD2	2.46	0.51
68:SQ:10:PHE:CE2	68:SQ:12:LYS:HE3	2.45	0.51
1:1:2704:G:N2	1:1:2707:A:OP2	2.42	0.51
2:2:485:G:N2	2:2:496:U:O2	2.36	0.51
2:2:835:G:H2'	2:2:836:G:C8	2.46	0.51
2:2:1355:G:H2'	2:2:1356:C:C6	2.45	0.51
46:Lm:104:PRO:HD3	46:Lm:111:ARG:HH21	1.75	0.51
63:SL:29:SER:O	63:SL:37:ARG:NH1	2.44	0.51
67:SP:94:VAL:CG2	67:SP:96:GLU:HG3	2.40	0.51
84:D:183:MET:HE3	84:D:219:GLY:O	2.11	0.51
1:1:2621:G:H2'	1:1:2622:G:H8	1.74	0.51
2:2:611:A:OP2	75:SX:5:LYS:NZ	2.44	0.51
12:LE:12:LYS:NZ	12:LE:15:ARG:CG	2.54	0.51
13:LF:29:ARG:HD3	13:LF:32:ARG:NH1	2.23	0.51
20:LM:72:LEU:HD12	20:LM:73:PRO:HD2	1.92	0.51
56:SE:68:ARG:HB3	56:SE:76:VAL:HG21	1.92	0.51
71:ST:105:MET:O	71:ST:109:GLU:HG2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:697:G:H2'	2:2:698:G:H8	1.76	0.51
13:LF:23:LYS:O	13:LF:27:LYS:HG2	2.11	0.51
70:SS:90:ARG:O	70:SS:90:ARG:HD3	2.11	0.51
76:SY:63:LEU:HD23	76:SY:74:GLY:HA3	1.92	0.51
2:2:222:U:C2	2:2:832:G:O6	2.64	0.51
2:2:829:U:O3'	58:SG:230:ARG:NH2	2.44	0.51
5:A:236:ILE:HD12	5:A:239:LEU:HD11	1.91	0.51
20:LM:104:LEU:HG	20:LM:108:ARG:HH12	1.75	0.51
51:Ls:27:VAL:HG21	51:Ls:79:PHE:CE2	2.46	0.51
55:SD:66:GLY:O	55:SD:70:ARG:NH1	2.43	0.51
57:SF:37:ASP:OD2	57:SF:37:ASP:C	2.53	0.51
62:SK:84:ILE:HD12	62:SK:85:VAL:H	1.76	0.51
1:1:811:U:H3	1:1:877:A:N6	2.09	0.51
2:2:66:U:H5	58:SG:176:PRO:HB3	1.74	0.51
34:La:112:LEU:HD22	34:La:125:VAL:HG11	1.93	0.51
53:SB:9:LEU:HG	53:SB:12:GLY:HA2	1.92	0.51
69:SR:104:ILE:HG22	69:SR:122:VAL:HB	1.91	0.51
70:SS:91:ASP:OD1	70:SS:92:ILE:N	2.44	0.51
84:D:130:ARG:O	84:D:134:GLU:HG2	2.11	0.51
2:2:329:U:P	60:SI:56:ARG:HH22	2.34	0.50
2:2:607:G:H2'	2:2:611:A:C8	2.46	0.50
2:2:898:A:H3'	2:2:899:G:H21	1.76	0.50
2:2:1203:U:H4'	81:Sd:27:GLN:HE21	1.76	0.50
10:LC:159:ALA:HB3	10:LC:162:ALA:HB2	1.93	0.50
27:LT:79:ARG:HG2	27:LT:79:ARG:HH11	1.75	0.50
54:SC:172:SER:O	54:SC:172:SER:OG	2.28	0.50
57:SF:29:LEU:HD12	57:SF:30:PHE:O	2.11	0.50
64:SM:108:ARG:HG2	64:SM:109:GLU:H	1.76	0.50
1:1:2552:A:H4'	1:1:2553:C:O5'	2.11	0.50
1:1:3186:A:H4'	9:LB:95:THR:HG22	1.93	0.50
2:2:741:U:O2	59:SH:115:ARG:NH1	2.44	0.50
5:A:191:HIS:CE1	5:A:195:ILE:HG21	2.46	0.50
5:A:292:SER:OG	5:A:294:ASP:OD1	2.28	0.50
11:LD:99:TYR:OH	11:LD:171:ASP:OD2	2.27	0.50
14:LG:249:GLU:OE1	14:LG:252:ARG:NH2	2.38	0.50
19:LL:140:LYS:HA	19:LL:143:GLN:HG3	1.92	0.50
41:Lh:45:LYS:H	41:Lh:45:LYS:HD2	1.75	0.50
57:SF:179:GLU:HA	57:SF:182:ALA:HB3	1.93	0.50
62:SK:79:HIS:CD2	64:SM:39:MET:HB2	2.46	0.50
73:SV:2:GLU:N	73:SV:10:ASP:OD1	2.37	0.50
73:SV:22:ARG:NH1	73:SV:58:PHE:CE2	2.79	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:SW:51:GLU:OE2	79:Sb:8:LEU:CD1	2.60	0.50
81:Sd:47:ALA:O	81:Sd:50:ILE:HG22	2.11	0.50
83:Sf:122:PRO:HG2	83:Sf:146:LEU:HD22	1.92	0.50
2:2:68:A:H5''	58:SG:162:VAL:HG21	1.93	0.50
9:LB:220:ALA:HB2	9:LB:337:MET:SD	2.51	0.50
32:LY:53:ASP:HB3	32:LY:109:HIS:H	1.76	0.50
60:SI:36:THR:OG1	60:SI:96:LEU:O	2.29	0.50
71:ST:114:LEU:HB2	71:ST:124:ARG:O	2.11	0.50
48:Lo:25:VAL:HG22	48:Lo:72:LEU:HD22	1.94	0.50
51:Ls:51:VAL:HG12	51:Ls:87:VAL:HG22	1.92	0.50
54:SC:155:ASN:ND2	73:SV:3:ASN:O	2.45	0.50
58:SG:54:GLY:C	58:SG:63:MET:HE3	2.32	0.50
58:SG:121:ILE:H	58:SG:125:THR:HG22	1.75	0.50
66:SO:19:GLN:CD	66:SO:20:VAL:N	2.70	0.50
67:SP:90:ASP:OD1	67:SP:90:ASP:N	2.45	0.50
70:SS:62:THR:OG1	70:SS:65:GLU:OE1	2.30	0.50
70:SS:116:LEU:HA	70:SS:119:ILE:HG22	1.93	0.50
76:SY:130:ALA:O	76:SY:133:LYS:NZ	2.41	0.50
1:1:511:U:C4	10:LC:351:PRO:HB3	2.47	0.50
1:1:1027:U:OP1	16:LI:90:ARG:NH2	2.39	0.50
1:1:2053:U:H4'	1:1:2054:U:H5''	1.94	0.50
1:1:2653:A:H5'	7:C:574:LYS:NZ	2.26	0.50
2:2:857:A:C6	65:SN:73:ARG:HD3	2.47	0.50
2:2:1242:G:H21	83:Sf:93:HIS:CD2	2.30	0.50
2:2:1429:G:N2	81:Sd:45:GLU:OE2	2.40	0.50
12:LE:12:LYS:HZ3	12:LE:15:ARG:CB	2.24	0.50
21:LN:11:SER:O	21:LN:14:LYS:NZ	2.39	0.50
77:SZ:38:LYS:HA	77:SZ:41:LYS:HZ2	1.72	0.50
2:2:225:C:H2'	2:2:226:C:C6	2.47	0.50
2:2:1227:A:OP1	83:Sf:97:LYS:NZ	2.43	0.50
5:A:57:ARG:HH22	5:A:94:THR:HA	1.76	0.50
5:A:291:TRP:CE2	5:A:298:LEU:HD13	2.47	0.50
11:LD:122:VAL:O	11:LD:123:GLU:HG2	2.11	0.50
12:LE:158:ARG:HA	12:LE:161:ASP:OD2	2.12	0.50
24:LQ:33:ASP:OD2	24:LQ:33:ASP:C	2.55	0.50
31:LX:89:ILE:HB	31:LX:90:GLU:OE1	2.11	0.50
38:Le:124:LYS:C	38:Le:124:LYS:HZ2	2.19	0.50
50:Lq:35:LEU:O	50:Lq:36:THR:OG1	2.25	0.50
55:SD:43:ARG:HD3	72:SU:106:ALA:HB2	1.94	0.50
63:SL:7:VAL:HG13	63:SL:8:GLN:HG2	1.94	0.50
64:SM:108:ARG:CG	64:SM:109:GLU:N	2.72	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:SU:31:LEU:HD21	72:SU:86:ARG:HB2	1.94	0.50
77:SZ:39:LEU:O	77:SZ:43:VAL:HG22	2.11	0.50
83:Sf:122:PRO:CD	83:Sf:146:LEU:CG	2.81	0.50
1:1:615:C:H2'	1:1:616:A:C8	2.47	0.50
1:1:1818:C:H5''	1:1:1819:A:H5'	1.94	0.50
1:1:3281:G:O2'	1:1:3282:U:OP1	2.28	0.50
2:2:1703:C:H2'	2:2:1704:A:C8	2.46	0.50
59:SH:92:SER:OG	59:SH:93:ASP:N	2.45	0.50
70:SS:120:ARG:O	70:SS:120:ARG:HD2	2.12	0.50
1:1:328:G:OP2	32:LY:13:LYS:NZ	2.34	0.50
1:1:643:C:H2'	1:1:644:A:C8	2.46	0.50
2:2:535:A:H5'	2:2:540:C:C5	2.47	0.50
2:2:651:C:H2'	2:2:652:G:C8	2.47	0.50
2:2:1693:C:H2'	2:2:1694:G:C8	2.47	0.50
2:2:1708:A:H2'	2:2:1709:G:H8	1.77	0.50
9:LB:57:VAL:HG22	9:LB:73:VAL:HG22	1.94	0.50
57:SF:85:MET:HG3	57:SF:85:MET:O	2.11	0.50
66:SO:94:ILE:HD13	66:SO:94:ILE:N	2.20	0.50
71:ST:45:GLU:N	71:ST:45:GLU:OE1	2.45	0.50
2:2:324:C:H2'	2:2:325:U:C6	2.47	0.50
23:LP:8:GLU:CD	23:LP:9:ILE:HG12	2.37	0.50
42:Li:17:ILE:HA	42:Li:22:LYS:HB2	1.93	0.50
61:SJ:100:GLU:O	61:SJ:104:GLU:HG2	2.12	0.50
64:SM:103:LEU:O	64:SM:115:VAL:HG11	2.12	0.50
80:Sc:7:PRO:O	80:Sc:9:LYS:HD2	2.11	0.50
1:1:644:A:H2'	1:1:645:A:C8	2.47	0.49
1:1:2176:A:H2'	1:1:2177:A:H8	1.75	0.49
2:2:191:G:O2'	2:2:192:A:H8	1.95	0.49
2:2:1492:U:H4'	2:2:1515:U:O2'	2.12	0.49
30:LW:88:GLU:HA	30:LW:91:LYS:NZ	2.27	0.49
33:LZ:25:ILE:CD1	33:LZ:91:LEU:HD12	2.42	0.49
80:Sc:9:LYS:HE2	80:Sc:60:SER:OG	2.12	0.49
2:2:148:G:N2	2:2:160:G:H1	2.10	0.49
2:2:421:C:O2'	2:2:423:G:OP1	2.25	0.49
3:3:76:G:N2	3:3:101:A:OP2	2.38	0.49
5:A:166:VAL:HG12	5:A:176:VAL:HG22	1.94	0.49
12:LE:23:LYS:HD2	13:LF:6:VAL:HG21	1.94	0.49
31:LX:92:GLN:HG3	31:LX:92:GLN:O	2.13	0.49
41:Lh:47:ASN:OD1	41:Lh:47:ASN:O	2.30	0.49
54:SC:117:GLY:HA2	54:SC:147:VAL:HG22	1.93	0.49
58:SG:70:PRO:HA	58:SG:98:ARG:HH12	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1843:G:N1	1:1:1846:C:OP2	2.45	0.49
2:2:916:U:H2'	2:2:917:A:C8	2.47	0.49
13:LF:29:ARG:O	13:LF:32:ARG:HG2	2.12	0.49
23:LP:165:ARG:NH2	23:LP:166:ASP:OD2	2.45	0.49
33:LZ:29:ASP:HB2	33:LZ:30:GLN:NE2	2.28	0.49
43:Lj:25:ARG:HH11	45:Ll:51:LEU:HD11	1.76	0.49
56:SE:129:VAL:HG12	56:SE:139:LEU:HB3	1.95	0.49
72:SU:22:THR:HB	72:SU:111:GLU:HG2	1.94	0.49
77:SZ:29:VAL:O	77:SZ:64:LEU:HD22	2.12	0.49
1:1:1893:A:N3	1:1:2083:G:H2'	2.27	0.49
2:2:301:U:OP1	63:SL:141:ARG:NH1	2.46	0.49
5:A:44:ASN:ND2	5:A:56:LYS:HB3	2.28	0.49
26:LS:130:GLU:N	26:LS:130:GLU:CD	2.65	0.49
51:Ls:129:GLU:CD	51:Ls:130:PRO:HD2	2.38	0.49
60:SI:172:ILE:HG13	60:SI:188:LEU:HD23	1.94	0.49
70:SS:88:ARG:HD3	70:SS:100:ILE:HD11	1.94	0.49
74:SW:15:ASN:HD21	74:SW:71:LYS:HG3	1.76	0.49
80:Sc:26:VAL:HG11	80:Sc:44:ASN:HD21	1.78	0.49
82:Se:22:GLU:HG3	82:Se:23:LYS:N	2.26	0.49
83:Sf:123:ASN:HB3	83:Sf:126:CYS:C	2.38	0.49
1:1:701:U:OP1	42:Li:18:ARG:NH2	2.46	0.49
1:1:1758:G:O2'	1:1:1760:G:OP2	2.30	0.49
2:2:922:A:H2'	2:2:923:G:C8	2.47	0.49
2:2:1332:U:H2'	2:2:1333:A:H8	1.78	0.49
2:2:1569:A:H4'	2:2:1570:G:OP2	2.12	0.49
8:LA:113:VAL:HG12	8:LA:166:ILE:HD13	1.95	0.49
10:LC:365:ALA:HB2	26:LS:26:ARG:HH12	1.77	0.49
17:LJ:29:ASP:OD2	17:LJ:30:ARG:N	2.45	0.49
51:Ls:26:PHE:HA	51:Ls:190:VAL:HG21	1.95	0.49
51:Ls:27:VAL:HG22	51:Ls:190:VAL:HB	1.94	0.49
55:SD:215:GLU:OE2	69:SR:19:LYS:NZ	2.44	0.49
1:1:1792:G:O6	33:LZ:63:LYS:NZ	2.43	0.49
1:1:1920:G:H21	1:1:3303:A:H8	1.60	0.49
1:1:2266:A:OP1	47:Ln:23:ARG:NH1	2.37	0.49
1:1:2574:G:H2'	1:1:2575:C:H6	1.77	0.49
50:Lq:54:ILE:HG12	50:Lq:63:VAL:HG22	1.94	0.49
74:SW:115:GLU:OE1	74:SW:119:LYS:NZ	2.38	0.49
2:2:352:G:H2'	2:2:353:G:H8	1.77	0.49
10:LC:301:ARG:NH1	24:LQ:69:GLU:OE1	2.46	0.49
27:LT:104:ASP:OD2	27:LT:104:ASP:C	2.56	0.49
43:Lj:64:MET:CE	43:Lj:67:LEU:HD23	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:ST:99:SER:HB3	71:ST:103:LYS:HZ3	1.78	0.49
71:ST:112:GLN:HB3	71:ST:128:GLN:HE22	1.78	0.49
2:2:179:A:H61	2:2:198:U:H3	1.59	0.49
7:C:582:ALA:HA	7:C:599:LYS:NZ	2.28	0.49
23:LP:154:GLU:OE1	23:LP:154:GLU:N	2.45	0.49
34:La:82:VAL:O	34:La:87:ARG:NH1	2.45	0.49
58:SG:142:ARG:HG3	58:SG:147:LEU:HB2	1.95	0.49
64:SM:131:GLN:OE1	64:SM:132:GLU:CA	2.60	0.49
1:1:445:G:N2	1:1:474:C:O2	2.46	0.49
1:1:2405:G:N2	1:1:2468:U:O2	2.30	0.49
2:2:1699:C:H2'	2:2:1700:G:H8	1.77	0.49
15:LH:186:SER:HB2	15:LH:226:ILE:HD11	1.95	0.49
25:LR:181:ARG:HH22	25:LR:182:ASN:HB2	1.76	0.49
31:LX:148:ILE:HA	31:LX:151:THR:HG22	1.94	0.49
53:SB:198:GLU:CA	53:SB:198:GLU:OE2	2.60	0.49
70:SS:90:ARG:HA	70:SS:95:GLY:HA3	1.94	0.49
5:A:147:HIS:CD2	5:A:151:VAL:HG12	2.46	0.49
11:LD:166:MET:CE	11:LD:178:HIS:HB3	2.29	0.49
53:SB:83:LYS:NZ	66:SO:129:GLU:OE2	2.46	0.49
71:ST:112:GLN:HB3	71:ST:128:GLN:NE2	2.28	0.49
84:D:262:ARG:HH12	84:D:320:LYS:HE2	1.76	0.49
1:1:2167:C:H2'	1:1:2168:U:C6	2.47	0.48
1:1:2487:A:H4'	14:LG:52:MET:HE3	1.93	0.48
1:1:3231:G:H2'	1:1:3232:A:C8	2.48	0.48
2:2:233:G:O2'	2:2:234:C:OP1	2.26	0.48
2:2:1380:G:P	72:SU:86:ARG:HH22	2.35	0.48
2:2:1712:C:O2'	2:2:1713:C:H5''	2.12	0.48
6:B:89:ARG:HH21	6:B:90:ARG:HB3	1.74	0.48
37:Ld:91:GLU:CD	37:Ld:91:GLU:H	2.21	0.48
39:Lf:54:VAL:HG12	39:Lf:68:VAL:HG22	1.95	0.48
45:Ll:36:ARG:HG2	45:Ll:36:ARG:HH11	1.77	0.48
55:SD:45:THR:C	55:SD:46:PRO:CD	2.70	0.48
55:SD:75:LEU:HG	62:SK:20:VAL:HB	1.95	0.48
57:SF:28:LYS:HZ3	57:SF:54:PRO:HB2	1.77	0.48
83:Sf:108:VAL:HG23	83:Sf:114:ILE:HG12	1.95	0.48
84:D:85:ILE:HG13	84:D:134:GLU:OE2	2.10	0.48
2:2:1411:U:OP2	69:SR:3:ARG:NH2	2.45	0.48
2:2:1531:U:H4'	2:2:1532:G:O5'	2.14	0.48
3:3:12:U:OP2	3:3:68:C:O2'	2.31	0.48
51:Ls:37:GLN:HB2	51:Ls:38:MET:HE2	1.95	0.48
57:SF:57:ILE:HG13	57:SF:58:PRO:HD2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:SQ:10:PHE:HE2	68:SQ:12:LYS:HE3	1.77	0.48
1:1:2314:U:H2'	1:1:2315:A:H8	1.78	0.48
2:2:1470:G:H2'	2:2:1471:A:C8	2.47	0.48
5:A:42:ILE:HG23	5:A:56:LYS:HG2	1.95	0.48
5:A:49:GLU:OE1	5:A:49:GLU:O	2.32	0.48
5:A:79:LEU:HD12	5:A:87:LEU:HD21	1.94	0.48
5:A:212:LYS:HD3	5:A:235:GLU:HG3	1.95	0.48
13:LF:8:THR:HG22	13:LF:9:GLN:N	2.28	0.48
21:LN:119:TYR:OH	21:LN:131:GLU:OE1	2.30	0.48
31:LX:126:LEU:HD21	31:LX:134:LYS:HE3	1.95	0.48
37:Ld:37:ALA:H	37:Ld:72:ILE:HG23	1.78	0.48
56:SE:97:GLU:N	56:SE:97:GLU:OE1	2.46	0.48
58:SG:138:ALA:HA	58:SG:178:ILE:HD11	1.96	0.48
68:SQ:50:GLU:O	68:SQ:54:ILE:HG12	2.12	0.48
73:SV:47:GLN:OE1	73:SV:47:GLN:CA	2.62	0.48
2:2:414:A:H4'	2:2:415:G:O5'	2.13	0.48
2:2:535:A:H5'	2:2:540:C:H5	1.78	0.48
2:2:784:U:H2'	2:2:785:G:C8	2.48	0.48
2:2:1258:G:H2'	2:2:1259:U:C6	2.48	0.48
55:SD:63:GLY:N	55:SD:67:ARG:O	2.34	0.48
55:SD:126:LEU:O	55:SD:130:MET:HE2	2.13	0.48
64:SM:131:GLN:OE1	64:SM:132:GLU:CD	2.56	0.48
67:SP:115:ILE:HD12	67:SP:119:MET:HE3	1.95	0.48
73:SV:58:PHE:CD1	73:SV:58:PHE:O	2.66	0.48
77:SZ:38:LYS:O	77:SZ:42:ASP:HB3	2.13	0.48
1:1:811:U:H3	1:1:877:A:H61	1.60	0.48
1:1:1005:G:N1	1:1:1009:U:O4	2.46	0.48
1:1:1745:U:H4'	1:1:1745:U:OP1	2.13	0.48
3:3:64:A:H8	16:LI:204:GLY:O	1.96	0.48
16:LI:168:SER:OG	27:LT:160:ILE:O	2.28	0.48
25:LR:31:GLU:N	25:LR:31:GLU:OE1	2.44	0.48
78:Sa:44:MET:HG3	78:Sa:65:PRO:HG2	1.95	0.48
81:Sd:10:ARG:NE	81:Sd:11:PRO:HD2	2.28	0.48
1:1:2651:A:OP1	7:C:568:LYS:HD3	2.14	0.48
1:1:3079:U:H1'	1:1:3080:A:H5''	1.95	0.48
2:2:635:C:N3	59:SH:124:ARG:NH2	2.61	0.48
2:2:1669:G:H2'	2:2:1670:C:C6	2.47	0.48
5:A:161:GLN:NE2	5:A:162:ASN:CB	2.77	0.48
7:C:551:ILE:O	7:C:555:GLU:HG2	2.14	0.48
12:LE:110:ASP:OD1	12:LE:112:THR:HG23	2.14	0.48
24:LQ:200:GLU:OE1	24:LQ:200:GLU:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:LZ:85:THR:HB	33:LZ:87:GLU:OE1	2.14	0.48
53:SB:32:ILE:HD11	53:SB:46:THR:OG1	2.13	0.48
62:SK:21:MET:HE3	62:SK:21:MET:HA	1.96	0.48
1:1:2621:G:O2'	1:1:2622:G:OP1	2.29	0.48
2:2:1219:C:H2'	2:2:1220:G:C8	2.49	0.48
5:A:109:LEU:N	5:A:123:GLY:O	2.41	0.48
32:LY:54:GLU:HB2	32:LY:107:LYS:HB3	1.95	0.48
43:Lj:25:ARG:HH11	45:Ll:51:LEU:CD1	2.26	0.48
55:SD:78:LYS:HE3	62:SK:18:GLU:HG2	1.94	0.48
56:SE:87:MET:HE2	56:SE:123:LEU:CD1	2.43	0.48
57:SF:32:ARG:NH1	57:SF:106:GLU:OE2	2.47	0.48
59:SH:165:ASP:OD1	59:SH:166:GLU:N	2.47	0.48
77:SZ:50:THR:HG22	77:SZ:53:THR:HG23	1.96	0.48
84:D:369:LEU:O	84:D:373:LYS:HG2	2.13	0.48
1:1:3332:A:H2'	1:1:3333:G:H8	1.77	0.48
15:LH:68:ARG:NH1	15:LH:188:ASN:OD1	2.47	0.48
17:LJ:112:ASP:OD1	17:LJ:113:LEU:N	2.45	0.48
31:LX:90:GLU:H	31:LX:90:GLU:CD	2.20	0.48
51:Ls:33:VAL:HG12	51:Ls:38:MET:HE3	1.95	0.48
52:SA:183:GLU:OE2	52:SA:183:GLU:HA	2.13	0.48
62:SK:18:GLU:HG3	62:SK:20:VAL:HG22	1.96	0.48
1:1:2923:G:N2	1:1:2926:A:OP2	2.37	0.48
10:LC:56:LYS:HG3	10:LC:60:GLN:HE21	1.78	0.48
17:LJ:18:LEU:HD12	17:LJ:129:TYR:O	2.13	0.48
23:LP:103:ASP:OD1	23:LP:103:ASP:C	2.57	0.48
27:LT:35:ARG:O	27:LT:38:ASP:CG	2.57	0.48
60:SI:183:ALA:C	60:SI:184:ASP:OD1	2.57	0.48
61:SJ:133:ARG:NH1	61:SJ:135:GLY:O	2.46	0.48
68:SQ:101:SER:C	68:SQ:105:LEU:HD23	2.39	0.48
80:Sc:11:VAL:HG12	80:Sc:33:PHE:HA	1.96	0.48
1:1:2064:C:H2'	1:1:2065:U:H6	1.77	0.48
1:1:2468:U:H2'	1:1:2469:U:C6	2.49	0.48
7:C:598:LYS:HB2	48:Lo:89:LYS:HB3	1.96	0.48
10:LC:306:GLU:OE2	13:LF:29:ARG:NE	2.47	0.48
28:LU:52:ARG:NH1	28:LU:52:ARG:HB2	2.29	0.48
55:SD:130:MET:HE3	55:SD:157:ASP:OD2	2.14	0.48
69:SR:32:LYS:HD2	69:SR:47:ARG:NH2	2.29	0.48
73:SV:46:ILE:HG22	73:SV:49:GLU:OE1	2.14	0.48
77:SZ:57:ARG:HG2	77:SZ:58:LEU:HD12	1.95	0.48
77:SZ:78:ILE:HD12	77:SZ:90:TYR:CG	2.49	0.48
1:1:1266:C:H2'	1:1:1267:C:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1744:C:H3'	1:1:1745:U:H5''	1.95	0.47
1:1:2730:U:OP2	1:1:2731:C:N4	2.45	0.47
2:2:911:G:C6	53:SB:13:LYS:HD3	2.49	0.47
5:A:242:SER:OG	5:A:245:ARG:O	2.30	0.47
31:LX:114:LYS:HB2	31:LX:114:LYS:NZ	2.18	0.47
44:Lk:67:GLN:N	44:Lk:67:GLN:NE2	2.62	0.47
47:Lr:1:MET:HE3	47:Lr:1:MET:HB3	1.81	0.47
55:SD:38:SER:O	55:SD:54:ARG:HB2	2.14	0.47
61:SJ:112:TYR:CD2	61:SJ:120:ILE:HA	2.49	0.47
65:SN:87:ASP:OD2	65:SN:88:LEU:N	2.47	0.47
70:SS:88:ARG:HB3	70:SS:98:SER:HB2	1.95	0.47
71:ST:23:LEU:HA	71:ST:26:GLN:OE1	2.13	0.47
74:SW:82:ARG:HB2	74:SW:85:GLU:HG2	1.95	0.47
84:D:151:LYS:N	84:D:151:LYS:HD2	2.29	0.47
84:D:187:VAL:O	84:D:199:ASN:ND2	2.40	0.47
2:2:66:U:O2	58:SG:160:ARG:HD3	2.15	0.47
2:2:851:G:OP1	25:LR:176:ARG:NH1	2.45	0.47
2:2:1004:C:O2'	66:SO:150:LEU:HD13	2.09	0.47
2:2:1166:G:N1	2:2:1571:G:OP2	2.47	0.47
2:2:1229:U:H2'	2:2:1230:G:C8	2.49	0.47
2:2:1426:U:H1'	72:SU:69:CYS:SG	2.54	0.47
2:2:1763:G:OP1	2:2:1766:C:H4'	2.13	0.47
10:LC:154:ASP:O	10:LC:154:ASP:CG	2.48	0.47
40:Lg:110:SER:CB	40:Lg:111:GLN:HE21	2.15	0.47
53:SB:13:LYS:H	53:SB:13:LYS:HD2	1.78	0.47
57:SF:38:ILE:HG13	57:SF:51:ILE:HD12	1.95	0.47
72:SU:65:ARG:HH22	72:SU:70:GLY:HA2	1.78	0.47
81:Sd:49:ASP:OD1	81:Sd:50:ILE:N	2.47	0.47
84:D:372:ILE:HG13	84:D:373:LYS:N	2.29	0.47
1:1:1330:U:OP2	24:LQ:66:ARG:NH1	2.40	0.47
1:1:1939:U:H3	1:1:2046:C:N4	2.11	0.47
1:1:2332:G:H2'	1:1:2333:G:C8	2.50	0.47
2:2:1584:G:N1	2:2:1605:U:N3	2.62	0.47
7:C:598:LYS:HG2	48:Lo:90:HIS:NE2	2.29	0.47
12:LE:10:PHE:CD2	12:LE:10:PHE:C	2.90	0.47
20:LM:7:GLU:HA	20:LM:7:GLU:OE2	2.14	0.47
20:LM:104:LEU:HG	20:LM:108:ARG:NH1	2.30	0.47
48:Lo:91:PHE:HZ	48:Lo:93:LEU:HD21	1.60	0.47
57:SF:141:THR:HG22	57:SF:142:VAL:H	1.80	0.47
2:2:909:U:O2	53:SB:7:LYS:NZ	2.46	0.47
51:Ls:128:MET:CE	51:Ls:128:MET:N	2.74	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:SB:82:ARG:HD3	53:SB:105:PHE:HE1	1.79	0.47
71:ST:77:ARG:NH1	71:ST:95:ASP:OD2	2.47	0.47
1:1:1006:A:N3	1:1:1008:U:H5''	2.30	0.47
1:1:1338:A:H4'	1:1:1339:U:O5'	2.15	0.47
1:1:2900:A:OP2	9:LB:257:HIS:HD2	1.97	0.47
2:2:1369:C:H4'	2:2:1370:C:H5''	1.96	0.47
7:C:608:THR:CB	7:C:611:MET:CE	2.93	0.47
26:LS:42:TRP:CD1	26:LS:53:LYS:HD2	2.49	0.47
57:SF:46:THR:HG22	57:SF:47:ASP:N	2.29	0.47
64:SM:34:LEU:HB2	64:SM:43:LEU:HD12	1.95	0.47
65:SN:104:ARG:HH11	65:SN:104:ARG:HG3	1.79	0.47
66:SO:130:ASP:C	66:SO:130:ASP:OD2	2.56	0.47
67:SP:58:LYS:C	67:SP:61:PRO:HD2	2.40	0.47
1:1:1073:G:H2'	1:1:1074:G:H8	1.79	0.47
2:2:148:G:N2	2:2:160:G:H22	2.13	0.47
14:LG:231:ASP:OD2	14:LG:232:THR:N	2.48	0.47
19:LL:32:LYS:O	19:LL:36:ARG:HG3	2.15	0.47
32:LY:30:MET:HB3	32:LY:100:PRO:HG2	1.95	0.47
36:Lc:23:SER:OG	36:Lc:99:GLY:HA3	2.15	0.47
41:Lh:24:LEU:HD11	41:Lh:28:LYS:HE3	1.96	0.47
53:SB:35:PRO:HG3	53:SB:99:ASN:HA	1.97	0.47
57:SF:176:THR:HB	77:SZ:87:MET:HE2	1.97	0.47
74:SW:28:ARG:HB3	74:SW:29:PRO:HD3	1.95	0.47
1:1:779:U:H2'	1:1:780:U:C6	2.49	0.47
1:1:1267:C:O2'	1:1:1268:G:OP1	2.24	0.47
1:1:2409:U:H2'	1:1:2410:A:H8	1.79	0.47
2:2:195:G:H2'	2:2:196:G:C8	2.49	0.47
2:2:390:C:H2'	2:2:391:C:C6	2.49	0.47
2:2:784:U:H2'	2:2:785:G:H8	1.78	0.47
2:2:866:G:H1	2:2:958:U:H3	1.62	0.47
2:2:1168:A:H2'	2:2:1169:G:H8	1.79	0.47
2:2:1219:C:H2'	2:2:1220:G:H8	1.80	0.47
2:2:1224:A:O2'	2:2:1225:G:OP2	2.32	0.47
2:2:1338:G:H22	2:2:1381:A:H2	1.63	0.47
4:4:47:C:O2'	4:4:62:A:OP2	2.33	0.47
7:C:554:VAL:HG23	7:C:607:VAL:HG21	1.96	0.47
11:LD:116:ASP:OD1	11:LD:116:ASP:N	2.47	0.47
19:LL:85:ILE:HD12	19:LL:116:LEU:HD21	1.96	0.47
24:LQ:174:ARG:HB3	24:LQ:177:VAL:HG23	1.95	0.47
28:LU:58:ASP:O	28:LU:58:ASP:OD1	2.32	0.47
39:Lf:39:ASP:OD2	39:Lf:41:ALA:HB3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:Li:68:GLU:OE1	42:Li:68:GLU:C	2.57	0.47
47:Lr:14:LYS:HE2	47:Lr:18:ARG:NH2	2.30	0.47
57:SF:46:THR:HG22	57:SF:47:ASP:H	1.80	0.47
62:SK:13:GLU:CD	62:SK:17:ARG:NH1	2.69	0.47
67:SP:37:ASP:OD1	67:SP:40:GLU:HB2	2.15	0.47
69:SR:104:ILE:HD11	69:SR:108:THR:CB	2.44	0.47
70:SS:48:LYS:NZ	71:ST:36:ASP:CG	2.70	0.47
84:D:398:LEU:HD23	84:D:398:LEU:C	2.40	0.47
1:1:171:G:H2'	1:1:172:G:H8	1.80	0.47
1:1:1480:C:O2'	1:1:1582:A:N3	2.43	0.47
30:LW:71:ARG:NH2	30:LW:72:THR:HA	2.30	0.47
36:Lc:97:ASP:OD2	36:Lc:98:ALA:N	2.48	0.47
44:Lk:16:ARG:O	44:Lk:16:ARG:HG3	2.15	0.47
70:SS:56:LYS:HD3	70:SS:60:GLU:HG3	1.97	0.47
71:ST:118:GLU:HG3	71:ST:118:GLU:O	2.14	0.47
74:SW:52:GLU:N	74:SW:52:GLU:OE2	2.48	0.47
1:1:615:C:H2'	1:1:616:A:H8	1.80	0.47
2:2:778:U:O2'	2:2:779:A:O4'	2.32	0.47
2:2:921:A:H2'	2:2:922:A:C8	2.50	0.47
5:A:286:CYS:HB2	5:A:302:TYR:CE1	2.50	0.47
15:LH:59:SER:O	15:LH:59:SER:OG	2.33	0.47
25:LR:105:LEU:HD23	25:LR:138:LEU:HD23	1.97	0.47
56:SE:11:ARG:O	56:SE:12:LEU:HB2	2.15	0.47
57:SF:57:ILE:HG22	68:SQ:47:LYS:HD3	1.97	0.47
67:SP:129:ILE:HA	70:SS:122:HIS:CE1	2.50	0.47
78:Sa:71:LEU:HD23	78:Sa:71:LEU:N	2.29	0.47
80:Sc:14:THR:HG23	80:Sc:32:GLU:HG2	1.97	0.47
84:D:164:VAL:CG2	84:D:183:MET:SD	2.78	0.47
2:2:231:G:H2'	2:2:232:G:H8	1.80	0.47
2:2:352:G:HO2'	2:2:353:G:P	2.37	0.47
2:2:792:U:H1'	2:2:793:U:OP2	2.15	0.47
11:LD:194:ASP:O	11:LD:195:THR:OG1	2.26	0.47
19:LL:147:THR:HA	41:Lh:124:LYS:HA	1.97	0.47
48:Lo:91:PHE:CE1	48:Lo:93:LEU:CD2	2.98	0.47
47:Lr:14:LYS:HE2	47:Lr:18:ARG:HH21	1.80	0.47
61:SJ:112:TYR:OH	61:SJ:119:SER:CA	2.38	0.47
66:SO:90:THR:C	66:SO:123:MET:SD	2.98	0.47
1:1:2058:A:H2'	1:1:2059:A:C8	2.50	0.46
1:1:2727:U:H2'	1:1:2728:A:H8	1.79	0.46
1:1:3224:C:H2'	1:1:3225:G:C8	2.50	0.46
5:A:134:THR:HG23	5:A:135:LEU:HD22	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:274:PHE:CE2	5:A:284:PRO:HD2	2.50	0.46
7:C:603:LEU:O	7:C:607:VAL:HG12	2.15	0.46
15:LH:140:VAL:HG13	15:LH:140:VAL:O	2.15	0.46
62:SK:19:GLY:HA2	62:SK:66:LEU:HD12	1.97	0.46
66:SO:64:ASP:C	66:SO:64:ASP:OD2	2.58	0.46
67:SP:42:ARG:HB3	67:SP:53:ILE:HD11	1.96	0.46
67:SP:123:TYR:HB2	67:SP:126:GLU:OE1	2.15	0.46
71:ST:108:LEU:O	71:ST:108:LEU:HD23	2.15	0.46
1:1:48:C:OP2	1:1:49:A:O2'	2.28	0.46
2:2:644:A:H2'	2:2:645:G:H8	1.79	0.46
2:2:781:G:H2'	2:2:782:C:H6	1.80	0.46
9:LB:68:HIS:CD2	9:LB:69:LYS:HG3	2.50	0.46
28:LU:60:ILE:HA	28:LU:73:ILE:O	2.15	0.46
32:LY:54:GLU:HA	32:LY:54:GLU:OE2	2.15	0.46
33:LZ:114:LYS:O	33:LZ:118:GLU:HG3	2.15	0.46
38:Le:124:LYS:NZ	38:Le:125:ALA:HA	2.29	0.46
44:Lk:29:PRO:O	44:Lk:32:GLN:CD	2.58	0.46
69:SR:74:GLN:O	69:SR:78:ARG:HG3	2.14	0.46
72:SU:39:ILE:HG13	72:SU:49:VAL:HG21	1.96	0.46
84:D:85:ILE:HG12	84:D:134:GLU:CD	2.39	0.46
2:2:12:U:H2'	2:2:13:U:C6	2.50	0.46
2:2:1584:G:C6	2:2:1605:U:N3	2.83	0.46
8:LA:250:GLN:OE1	8:LA:250:GLN:N	2.41	0.46
52:SA:151:ASP:OD1	52:SA:152:THR:N	2.42	0.46
53:SB:108:ASP:N	53:SB:108:ASP:OD1	2.48	0.46
56:SE:212:ASP:OD1	56:SE:213:ALA:N	2.42	0.46
57:SF:29:LEU:HD22	57:SF:34:SER:HB3	1.96	0.46
59:SH:31:TYR:HD1	59:SH:34:GLU:HB3	1.80	0.46
64:SM:36:LEU:O	64:SM:39:MET:HG2	2.15	0.46
66:SO:26:VAL:HG13	66:SO:89:ILE:HA	1.96	0.46
69:SR:92:ASP:O	69:SR:96:ASN:OD1	2.33	0.46
1:1:696:G:N2	1:1:699:A:OP2	2.44	0.46
1:1:3027:G:C2	1:1:3028:A:C8	3.04	0.46
2:2:188:U:O2'	2:2:190:G:O6	2.25	0.46
2:2:1237:U:N3	2:2:1240:G:OP2	2.27	0.46
2:2:1458:G:OP2	70:SS:143:ARG:NH1	2.49	0.46
65:SN:3:ARG:HB2	65:SN:6:SER:HB3	1.98	0.46
67:SP:116:LYS:HB3	67:SP:118:GLU:OE1	2.15	0.46
71:ST:105:MET:CE	71:ST:123:ARG:HD3	2.46	0.46
73:SV:2:GLU:HG3	73:SV:10:ASP:OD1	2.16	0.46
1:1:2469:U:H2'	1:1:2470:U:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2676:U:H4'	48:Lo:13:LYS:HD2	1.98	0.46
2:2:499:U:H2'	2:2:500:G:H8	1.80	0.46
2:2:539:A:O2'	2:2:540:C:H3'	2.15	0.46
2:2:1708:A:H2'	2:2:1709:G:C8	2.50	0.46
13:LF:98:ILE:HD12	24:LQ:33:ASP:HB2	1.98	0.46
16:LI:176:LEU:HD22	16:LI:180:GLU:HG2	1.97	0.46
26:LS:137:ARG:C	26:LS:141:LYS:HZ3	2.22	0.46
67:SP:49:ALA:O	67:SP:53:ILE:HG12	2.16	0.46
69:SR:71:PHE:CZ	69:SR:74:GLN:HG3	2.51	0.46
78:Sa:44:MET:HG2	78:Sa:65:PRO:O	2.15	0.46
84:D:126:LEU:HD12	84:D:126:LEU:N	2.29	0.46
1:1:2630:A:C1'	17:LJ:99:GLU:OE1	2.64	0.46
2:2:1193:A:H4'	2:2:1194:C:O5'	2.16	0.46
2:2:1385:A:H5''	69:SR:48:ASN:ND2	2.31	0.46
9:LB:286:ILE:HG12	9:LB:323:VAL:HG12	1.98	0.46
12:LE:12:LYS:HZ2	12:LE:15:ARG:HG3	1.70	0.46
28:LU:59:VAL:HB	28:LU:60:ILE:HD12	1.98	0.46
43:Lj:51:GLU:HA	43:Lj:51:GLU:OE2	2.16	0.46
48:Lo:96:ASP:C	48:Lo:96:ASP:OD2	2.59	0.46
55:SD:130:MET:HE1	55:SD:137:CYS:SG	2.55	0.46
58:SG:165:LYS:HG3	58:SG:166:GLY:H	1.81	0.46
69:SR:104:ILE:HD11	69:SR:108:THR:OG1	2.16	0.46
2:2:174:U:O2'	2:2:176:A:OP2	2.34	0.46
2:2:573:G:O6	75:SX:65:ASN:ND2	2.38	0.46
2:2:844:G:H2'	2:2:845:A:C8	2.50	0.46
2:2:1362:C:H2'	2:2:1363:A:C8	2.50	0.46
2:2:1584:G:O6	2:2:1605:U:O4	2.33	0.46
7:C:543:ALA:HB1	7:C:596:LEU:HB2	1.96	0.46
9:LB:215:MET:HE2	9:LB:280:ASN:OD1	2.16	0.46
13:LF:169:LEU:HD12	13:LF:169:LEU:O	2.16	0.46
14:LG:117:THR:O	14:LG:121:GLU:HG2	2.15	0.46
17:LJ:54:THR:HG23	17:LJ:61:ARG:HA	1.98	0.46
21:LN:17:ASP:OD1	21:LN:18:VAL:N	2.49	0.46
35:Lb:58:LYS:HB2	35:Lb:59:GLU:OE1	2.16	0.46
39:Lf:4:GLU:OE1	39:Lf:4:GLU:N	2.47	0.46
53:SB:198:GLU:OE2	53:SB:198:GLU:HA	2.16	0.46
68:SQ:36:LEU:HD13	68:SQ:49:TYR:HE1	1.81	0.46
70:SS:108:LYS:HA	70:SS:111:GLU:OE2	2.15	0.46
1:1:2667:C:H2'	1:1:2668:C:H6	1.80	0.46
1:1:3111:C:N4	1:1:3113:A:H1'	2.30	0.46
1:1:3163:A:H5''	1:1:3164:G:C5	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:218:LEU:HD21	5:A:228:TYR:CE2	2.51	0.46
7:C:598:LYS:HG2	48:Lo:90:HIS:CE1	2.51	0.46
20:LM:86:GLU:OE2	20:LM:87:ALA:CA	2.64	0.46
55:SD:179:LEU:HD23	55:SD:179:LEU:H	1.80	0.46
57:SF:16:LEU:HD11	68:SQ:52:ILE:HG21	1.97	0.46
69:SR:71:PHE:HE2	69:SR:73:LEU:HB3	1.81	0.46
1:1:609:A:H4'	1:1:610:A:O5'	2.16	0.46
1:1:1766:G:H2'	1:1:1767:A:C8	2.51	0.46
1:1:2227:U:O2'	1:1:2228:C:OP1	2.29	0.46
1:1:2495:U:H2'	1:1:2496:G:H8	1.81	0.46
1:1:2974:A:H2'	1:1:2975:G:C8	2.49	0.46
2:2:294:U:H5''	56:SE:37:LYS:HD2	1.98	0.46
5:A:24:SER:O	5:A:293:ALA:HB2	2.16	0.46
10:LC:140:GLY:O	10:LC:184:LYS:NZ	2.49	0.46
15:LH:142:LYS:HD3	15:LH:142:LYS:HA	1.83	0.46
51:Ls:64:LYS:O	51:Ls:67:MET:SD	2.74	0.46
53:SB:3:VAL:HA	66:SO:62:LYS:HZ2	1.74	0.46
57:SF:63:ARG:NH1	68:SQ:122:ARG:HE	2.14	0.46
76:SY:24:LYS:HB2	76:SY:78:ILE:HB	1.98	0.46
1:1:2167:C:O2'	1:1:2168:U:OP1	2.33	0.46
1:1:2307:U:H2'	1:1:2308:A:H8	1.81	0.46
2:2:1094:U:H4'	2:2:1095:U:O5'	2.16	0.46
19:LL:76:THR:HG22	19:LL:101:ARG:HB3	1.98	0.46
39:Lf:60:GLU:OE2	39:Lf:63:GLY:CA	2.64	0.46
51:Ls:176:LEU:HB3	51:Ls:178:ILE:HG22	1.98	0.46
54:SC:156:LEU:HD12	61:SJ:92:ASP:OD2	2.16	0.46
78:Sa:101:VAL:HG12	78:Sa:104:ASN:H	1.80	0.46
1:1:1702:U:O4'	25:LR:96:MET:HG3	2.16	0.45
7:C:547:LEU:HD11	7:C:599:LYS:HD2	1.97	0.45
44:Lk:5:VAL:HG11	44:Lk:11:PHE:HB2	1.98	0.45
57:SF:69:PHE:CZ	80:Sc:50:ARG:HD3	2.50	0.45
57:SF:122:ASP:HA	57:SF:125:VAL:HG12	1.97	0.45
69:SR:106:GLN:O	69:SR:110:ASP:OD2	2.34	0.45
77:SZ:74:GLU:HG2	77:SZ:75:LYS:HD3	1.97	0.45
1:1:1001:G:H2'	1:1:1002:G:C8	2.51	0.45
1:1:1907:G:C8	49:Lp:16:THR:HG22	2.50	0.45
1:1:2245:U:OP1	1:1:2932:G:O2'	2.27	0.45
2:2:1491:C:H42	2:2:1508:G:H1	1.63	0.45
5:A:5:LEU:HB3	5:A:310:TRP:HB3	1.98	0.45
5:A:49:GLU:OE1	5:A:50:THR:N	2.50	0.45
51:Ls:45:LEU:HD11	51:Ls:99:LYS:HD3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:Ls:189:GLN:NE2	51:Ls:193:GLN:O	2.48	0.45
52:SA:16:ASP:OD1	52:SA:182:ARG:NH2	2.48	0.45
55:SD:79:ARG:HD3	62:SK:61:TYR:CD2	2.50	0.45
66:SO:94:ILE:HG21	66:SO:115:LEU:HD13	1.97	0.45
1:1:446:A:O2'	1:1:447:U:C6	2.68	0.45
1:1:1091:C:H2'	1:1:1092:A:H8	1.82	0.45
1:1:1204:U:C4'	51:Ls:58:MET:HE1	2.45	0.45
2:2:820:U:H2'	2:2:821:G:H5''	1.98	0.45
5:A:294:ASP:OD2	5:A:296:GLN:NE2	2.50	0.45
51:Ls:94:LYS:HD2	51:Ls:97:ARG:HH21	1.82	0.45
59:SH:47:LEU:HB3	59:SH:76:PHE:CE2	2.52	0.45
66:SO:92:LEU:HD13	66:SO:123:MET:SD	2.57	0.45
73:SV:41:GLU:N	73:SV:41:GLU:CD	2.61	0.45
77:SZ:42:ASP:OD2	77:SZ:46:TYR:CE1	2.69	0.45
1:1:1052:C:H2'	1:1:1053:U:C6	2.51	0.45
1:1:1589:C:OP1	31:LX:92:GLN:NE2	2.50	0.45
1:1:2407:C:H2'	1:1:2408:A:H8	1.81	0.45
1:1:2496:G:O2'	1:1:2497:G:H5'	2.17	0.45
1:1:3068:C:H2'	1:1:3069:U:C6	2.52	0.45
2:2:824:U:H2'	2:2:825:C:H6	1.80	0.45
2:2:1161:G:H2'	2:2:1162:G:H8	1.82	0.45
2:2:1271:C:O2	2:2:1423:A:O2'	2.25	0.45
3:3:3:A:H2'	3:3:4:U:C6	2.51	0.45
10:LC:37:LYS:O	10:LC:41:THR:HG23	2.17	0.45
21:LN:30:TYR:C	21:LN:32:GLN:H	2.25	0.45
44:Lk:30:LYS:C	44:Lk:32:GLN:HE22	2.23	0.45
66:SO:63:ALA:C	66:SO:65:ARG:H	2.25	0.45
78:Sa:33:ASP:OD2	78:Sa:33:ASP:C	2.59	0.45
84:D:85:ILE:HD11	84:D:134:GLU:OE2	2.16	0.45
1:1:1047:A:H4'	1:1:1048:A:O5'	2.16	0.45
1:1:2407:C:H2'	1:1:2408:A:C8	2.50	0.45
2:2:107:A:H2'	2:2:108:G:C8	2.52	0.45
2:2:1180:A:OP1	67:SP:132:LYS:NZ	2.49	0.45
2:2:1245:C:H2'	2:2:1246:U:H6	1.82	0.45
25:LR:180:LYS:HB2	25:LR:180:LYS:HE2	1.73	0.45
30:LW:88:GLU:HA	30:LW:91:LYS:HZ3	1.80	0.45
31:LX:142:ASP:OD1	31:LX:143:VAL:N	2.50	0.45
33:LZ:102:GLU:N	33:LZ:102:GLU:OE1	2.50	0.45
67:SP:47:ALA:HA	67:SP:50:ARG:HE	1.82	0.45
81:Sd:21:CYS:HB3	81:Sd:26:HIS:H	1.82	0.45
81:Sd:26:HIS:NE2	81:Sd:28:ALA:HB3	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:D:363:SER:HA	84:D:366:LYS:HD2	1.97	0.45
1:1:446:A:H1'	1:1:447:U:H5'	1.98	0.45
2:2:219:C:H2'	2:2:220:A:C8	2.52	0.45
2:2:1199:A:H1'	2:2:1204:C:N4	2.30	0.45
2:2:1592:C:OP1	81:Sd:19:ARG:NH2	2.29	0.45
5:A:121:VAL:HG13	5:A:156:PHE:CZ	2.52	0.45
5:A:172:LYS:HD2	5:A:191:HIS:O	2.17	0.45
34:La:5:PHE:CD1	34:La:5:PHE:O	2.69	0.45
57:SF:141:THR:HG22	57:SF:142:VAL:N	2.32	0.45
63:SL:10:GLU:HG3	63:SL:11:ARG:H	1.80	0.45
64:SM:61:MET:SD	64:SM:89:ILE:HD13	2.56	0.45
73:SV:46:ILE:CG2	73:SV:49:GLU:CD	2.89	0.45
83:Sf:124:GLU:H	83:Sf:124:GLU:CD	2.24	0.45
1:1:2182:A:P	42:Li:77:ARG:HH21	2.39	0.45
2:2:777:C:H2'	2:2:778:U:H2'	1.99	0.45
2:2:1203:U:OP2	2:2:1204:C:O2'	2.29	0.45
2:2:1379:A:O3'	72:SU:86:ARG:NH2	2.27	0.45
2:2:1599:U:H2'	2:2:1600:U:C6	2.52	0.45
4:4:95:G:O2'	43:Lj:81:GLY:O	2.27	0.45
16:LI:83:GLU:N	16:LI:83:GLU:OE1	2.50	0.45
17:LJ:126:MET:HE2	17:LJ:126:MET:HB3	1.74	0.45
34:La:75:ILE:HG22	34:La:115:LYS:H	1.82	0.45
35:Lb:33:LYS:HE3	35:Lb:33:LYS:HB3	1.77	0.45
55:SD:225:PRO:CA	55:SD:226:MET:SD	3.02	0.45
56:SE:19:LEU:HD11	56:SE:108:ARG:HD2	1.97	0.45
64:SM:86:ILE:O	64:SM:86:ILE:HG22	2.17	0.45
69:SR:31:ASN:HD22	69:SR:55:THR:HB	1.82	0.45
80:Sc:35:ASP:OD1	80:Sc:36:ASP:N	2.50	0.45
1:1:192:A:N3	1:1:212:G:O2'	2.49	0.45
1:1:250:C:O2'	1:1:251:U:OP1	2.29	0.45
1:1:445:G:N2	1:1:474:C:C2	2.85	0.45
1:1:1067:A:H2'	1:1:1068:A:C8	2.52	0.45
1:1:2409:U:H2'	1:1:2410:A:C8	2.52	0.45
2:2:937:A:H2'	2:2:938:A:C8	2.52	0.45
2:2:1531:U:O2'	2:2:1532:G:OP2	2.29	0.45
2:2:1599:U:H2'	2:2:1600:U:H6	1.82	0.45
2:2:1700:G:H2'	2:2:1701:A:H8	1.81	0.45
12:LE:10:PHE:CE2	12:LE:12:LYS:HE3	2.43	0.45
20:LM:112:LEU:HD22	20:LM:116:ASP:OD2	2.17	0.45
32:LY:51:LYS:HD2	32:LY:70:THR:O	2.16	0.45
33:LZ:8:ARG:HD3	33:LZ:8:ARG:HA	1.71	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:Lb:55:LYS:HD2	35:Lb:56:GLU:OE2	2.16	0.45
51:Ls:39:HIS:O	51:Ls:43:LYS:HG3	2.17	0.45
66:SO:91:ALA:C	66:SO:92:LEU:HD12	2.42	0.45
1:1:604:G:H2'	1:1:605:G:C8	2.52	0.45
1:1:617:C:H2'	1:1:618:C:C6	2.52	0.45
5:A:91:GLU:OE1	5:A:93:SER:OG	2.24	0.45
15:LH:98:SER:OG	15:LH:99:ARG:N	2.50	0.45
38:Le:124:LYS:HZ3	38:Le:125:ALA:CA	2.30	0.45
42:Li:83:LYS:HD2	42:Li:89:PHE:HD1	1.82	0.45
53:SB:154:THR:OG1	53:SB:205:TYR:OH	2.35	0.45
57:SF:110:LEU:HD11	77:SZ:48:LEU:HD12	1.98	0.45
59:SH:57:VAL:HG21	59:SH:178:THR:HA	1.99	0.45
60:SI:201:HIS:ND1	60:SI:201:HIS:O	2.49	0.45
61:SJ:167:PRO:O	61:SJ:172:ARG:NH1	2.50	0.45
69:SR:98:GLU:OE1	69:SR:99:THR:HG23	2.17	0.45
1:1:701:U:P	42:Li:18:ARG:HH22	2.39	0.45
1:1:996:C:H42	1:1:1019:A:H61	1.64	0.45
1:1:1022:C:H2'	1:1:1023:A:C8	2.52	0.45
1:1:1260:C:C2	1:1:1261:A:C8	3.05	0.45
2:2:572:C:N4	75:SX:65:ASN:HD21	2.15	0.45
2:2:1365:U:H2'	2:2:1366:A:C8	2.52	0.45
7:C:598:LYS:HB2	48:Lo:89:LYS:CB	2.46	0.45
51:Ls:19:LEU:HD23	51:Ls:61:ARG:CZ	2.46	0.45
57:SF:152:LEU:O	57:SF:156:ASN:ND2	2.49	0.45
60:SI:26:ALA:O	60:SI:29:LEU:HD23	2.17	0.45
60:SI:57:ALA:HB2	60:SI:181:GLY:HA2	1.99	0.45
64:SM:84:HIS:ND1	64:SM:85:LYS:HG2	2.32	0.45
66:SO:21:ARG:HG2	66:SO:21:ARG:HH11	1.82	0.45
70:SS:112:ASP:OD2	70:SS:115:ARG:NH2	2.50	0.45
1:1:1129:C:H2'	1:1:1130:G:H8	1.82	0.44
1:1:1932:G:C6	1:1:2058:A:C6	3.05	0.44
1:1:2123:G:H2'	1:1:2124:G:H8	1.81	0.44
2:2:1588:A:H2'	2:2:1589:A:C8	2.52	0.44
51:Ls:65:THR:HG21	51:Ls:74:GLU:HA	1.99	0.44
51:Ls:94:LYS:CD	51:Ls:97:ARG:HH21	2.30	0.44
51:Ls:97:ARG:O	51:Ls:98:GLU:OE1	2.35	0.44
52:SA:38:PRO:O	52:SA:55:LYS:NZ	2.37	0.44
75:SX:73:ARG:HD2	75:SX:84:THR:HG22	1.98	0.44
83:Sf:122:PRO:CD	83:Sf:146:LEU:CD2	2.95	0.44
1:1:624:C:O2	1:1:2340:G:O2'	2.31	0.44
1:1:3027:G:C5'	25:LR:57:MET:CE	2.78	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3176:G:H2'	1:1:3177:C:C6	2.53	0.44
2:2:193:A:H2'	2:2:194:G:H5'	1.99	0.44
2:2:1211:U:H2'	2:2:1212:C:C6	2.52	0.44
5:A:127:LYS:HG2	5:A:149:GLU:HA	1.99	0.44
6:B:89:ARG:HH21	6:B:90:ARG:CB	2.30	0.44
10:LC:284:GLN:NE2	10:LC:286:ASP:HB3	2.27	0.44
11:LD:246:ALA:O	11:LD:250:ILE:HG12	2.16	0.44
13:LF:56:LYS:HB3	13:LF:56:LYS:HE2	1.79	0.44
26:LS:27:MET:HE2	26:LS:27:MET:HB3	1.88	0.44
44:Lk:51:ASP:HB3	44:Lk:54:LYS:HE2	1.99	0.44
52:SA:192:TYR:O	52:SA:192:TYR:CG	2.70	0.44
56:SE:31:PRO:HG2	56:SE:38:LEU:HG	1.98	0.44
67:SP:106:SER:HB2	67:SP:129:ILE:O	2.17	0.44
69:SR:104:ILE:CG1	69:SR:105:ASP:H	2.30	0.44
70:SS:28:VAL:O	70:SS:32:LEU:CD2	2.65	0.44
77:SZ:35:THR:HA	77:SZ:38:LYS:HD3	1.99	0.44
80:Sc:52:ASN:OD1	80:Sc:52:ASN:O	2.35	0.44
83:Sf:119:ARG:HH21	83:Sf:150:PHE:HZ	1.63	0.44
1:1:478:G:H2'	1:1:479:G:H8	1.80	0.44
1:1:2686:A:OP2	1:1:2687:G:N2	2.45	0.44
2:2:270:G:H2'	2:2:271:G:C8	2.51	0.44
30:LW:27:LYS:HA	30:LW:27:LYS:HD2	1.67	0.44
69:SR:98:GLU:CD	69:SR:99:THR:HG23	2.42	0.44
77:SZ:72:LEU:O	77:SZ:72:LEU:HD23	2.16	0.44
79:Sb:8:LEU:N	79:Sb:8:LEU:CD2	2.80	0.44
1:1:688:C:H2'	1:1:689:G:H8	1.81	0.44
1:1:1762:U:H2'	1:1:1763:C:C6	2.53	0.44
1:1:2469:U:H2'	1:1:2470:U:H6	1.82	0.44
1:1:3159:U:H1'	12:LE:190:ARG:NH1	2.33	0.44
2:2:1245:C:C2	2:2:1246:U:C5	3.06	0.44
2:2:1341:A:H4'	2:2:1342:A:OP1	2.17	0.44
2:2:1446:U:H2'	2:2:1447:C:C6	2.53	0.44
5:A:165:ILE:CG1	5:A:177:TRP:HB2	2.47	0.44
10:LC:301:ARG:NH1	24:LQ:69:GLU:CD	2.76	0.44
12:LE:9:THR:O	12:LE:18:PRO:HD2	2.18	0.44
41:Lh:22:LYS:O	41:Lh:26:GLU:OE1	2.35	0.44
51:Ls:37:GLN:NE2	51:Ls:105:ILE:HD12	2.31	0.44
51:Ls:74:GLU:HA	51:Ls:77:LEU:HG	1.99	0.44
60:SI:139:SER:O	60:SI:140:LYS:HE2	2.16	0.44
60:SI:155:LYS:HG3	60:SI:156:VAL:N	2.32	0.44
62:SK:5:LYS:HA	62:SK:5:LYS:HE3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:SO:42:HIS:ND1	66:SO:54:ARG:HD3	2.33	0.44
67:SP:59:ARG:O	67:SP:63:GLY:N	2.50	0.44
71:ST:53:TRP:HA	71:ST:56:ILE:HG22	1.99	0.44
79:Sb:15:GLU:OE1	79:Sb:18:LYS:HD2	2.18	0.44
1:1:1233:G:H2'	1:1:1234:A:C8	2.53	0.44
9:LB:297:THR:HG22	9:LB:300:ASP:HB3	1.99	0.44
11:LD:292:GLU:O	11:LD:296:LYS:HG2	2.17	0.44
17:LJ:83:ARG:HE	17:LJ:113:LEU:HD12	1.82	0.44
60:SI:128:LYS:O	60:SI:129:GLN:HG3	2.17	0.44
64:SM:137:LEU:HA	64:SM:140:PHE:HB3	2.00	0.44
67:SP:76:LYS:HD2	67:SP:77:PRO:O	2.18	0.44
67:SP:90:ASP:C	67:SP:91:MET:SD	3.01	0.44
69:SR:71:PHE:CE2	69:SR:73:LEU:HB3	2.53	0.44
70:SS:20:THR:CG2	70:SS:35:ILE:HG22	2.47	0.44
71:ST:128:GLN:HA	71:ST:131:ARG:HG2	2.00	0.44
72:SU:90:LEU:HD23	72:SU:90:LEU:HA	1.83	0.44
77:SZ:72:LEU:HA	77:SZ:75:LYS:HG2	2.00	0.44
1:1:528:U:C2	1:1:529:G:C8	3.06	0.44
2:2:81:C:H2'	2:2:82:G:O4'	2.18	0.44
2:2:472:A:OP1	61:SJ:128:ARG:HG3	2.18	0.44
2:2:776:C:H2'	2:2:777:C:C5	2.53	0.44
2:2:1347:C:H2'	2:2:1348:C:C6	2.52	0.44
15:LH:146:THR:HG23	15:LH:148:CYS:SG	2.57	0.44
57:SF:77:ILE:H	57:SF:77:ILE:HD12	1.81	0.44
1:1:250:C:HO2'	1:1:251:U:P	2.40	0.44
2:2:572:C:H41	75:SX:65:ASN:HD21	1.65	0.44
5:A:101:PHE:CE1	5:A:136:GLY:HA2	2.53	0.44
13:LF:104:LYS:HB3	13:LF:105:PRO:HD3	2.00	0.44
19:LL:89:LEU:O	19:LL:92:THR:HG22	2.18	0.44
25:LR:15:LEU:HD21	25:LR:45:VAL:HG21	2.00	0.44
33:LZ:105:GLN:HA	33:LZ:108:GLU:HG3	2.00	0.44
34:La:88:GLU:O	34:La:92:SER:OG	2.21	0.44
37:Ld:60:ASP:OD1	37:Ld:100:TYR:OH	2.30	0.44
55:SD:223:VAL:CG1	55:SD:226:MET:HE2	2.47	0.44
58:SG:82:SER:OG	58:SG:83:CYS:N	2.50	0.44
58:SG:132:ARG:HD2	58:SG:132:ARG:HA	1.86	0.44
69:SR:65:PRO:HB3	69:SR:74:GLN:NE2	2.32	0.44
71:ST:105:MET:HE1	71:ST:123:ARG:HD3	1.98	0.44
2:2:69:G:H2'	2:2:70:C:C6	2.52	0.44
6:B:134:ASP:O	55:SD:120:ARG:NH2	2.51	0.44
13:LF:52:LYS:HB2	13:LF:52:LYS:HE2	1.75	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:Li:75:ASP:C	42:Li:75:ASP:OD2	2.61	0.44
43:Lj:29:ASN:O	43:Lj:32:LYS:NZ	2.32	0.44
51:Ls:53:MET:SD	51:Ls:53:MET:C	3.01	0.44
51:Ls:104:ARG:HD2	51:Ls:183:TYR:O	2.18	0.44
53:SB:126:THR:HG22	53:SB:136:ARG:HE	1.83	0.44
55:SD:19:VAL:HG11	81:Sd:22:ARG:HH12	1.83	0.44
64:SM:66:GLU:HB3	64:SM:92:PRO:HA	2.00	0.44
64:SM:79:ALA:HB1	83:Sf:114:ILE:HD11	1.99	0.44
69:SR:46:LEU:O	69:SR:50:ILE:HG12	2.17	0.44
75:SX:53:VAL:HG12	75:SX:100:ASP:H	1.83	0.44
75:SX:126:LYS:HG2	75:SX:131:GLY:HA2	2.00	0.44
77:SZ:37:ASP:O	77:SZ:41:LYS:HG2	2.18	0.44
84:D:257:ALA:HB1	84:D:321:MET:HE1	2.00	0.44
1:1:2467:U:H2'	1:1:2468:U:H6	1.83	0.44
1:1:2615:A:C8	1:1:2617:G:C8	3.06	0.44
1:1:2621:G:HO2'	1:1:2622:G:P	2.40	0.44
1:1:2855:A:OP1	46:Lm:102:ARG:NE	2.38	0.44
1:1:3298:U:H2'	1:1:3299:U:C6	2.53	0.44
2:2:1364:G:P	71:ST:8:ARG:HH12	2.40	0.44
8:LA:3:ARG:HG2	8:LA:207:VAL:HG22	2.00	0.44
20:LM:11:TRP:CZ2	26:LS:153:PRO:HB3	2.53	0.44
31:LX:64:ILE:HG13	31:LX:65:PRO:HD2	1.99	0.44
33:LZ:25:ILE:HD11	33:LZ:91:LEU:CD1	2.48	0.44
50:Lq:140:ARG:CZ	50:Lq:140:ARG:CA	2.94	0.44
57:SF:175:LYS:HG2	57:SF:179:GLU:OE2	2.18	0.44
64:SM:133:ARG:O	64:SM:137:LEU:HD23	2.17	0.44
65:SN:47:PRO:CG	65:SN:86:GLU:OE2	2.64	0.44
70:SS:30:TYR:O	70:SS:33:THR:OG1	2.28	0.44
80:Sc:11:VAL:O	80:Sc:54:ILE:HD12	2.18	0.44
80:Sc:43:ARG:HH11	80:Sc:44:ASN:H	1.66	0.44
1:1:135:G:H2'	1:1:136:C:C6	2.53	0.43
2:2:1161:G:O2'	2:2:1608:U:O2	2.36	0.43
5:A:178:ASP:HB3	5:A:181:SER:OG	2.17	0.43
5:A:235:GLU:O	5:A:253:ALA:N	2.51	0.43
9:LB:66:LYS:HE2	9:LB:66:LYS:HB2	1.88	0.43
9:LB:237:LYS:HB2	9:LB:237:LYS:HE2	1.69	0.43
38:Le:68:MET:HB2	38:Le:69:PRO:HD2	1.99	0.43
62:SK:52:TYR:CD1	62:SK:70:GLY:HA2	2.53	0.43
1:1:1223:A:H61	1:1:1228:A:P	2.40	0.43
5:A:51:GLN:CG	5:A:52:TYR:N	2.81	0.43
8:LA:207:VAL:HG13	8:LA:208:ASP:OD1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:LY:10:SER:OG	32:LY:13:LYS:HB2	2.17	0.43
40:Lg:110:SER:O	40:Lg:111:GLN:NE2	2.51	0.43
52:SA:142:VAL:HG23	52:SA:144:ILE:CD1	2.48	0.43
53:SB:199:LYS:HD3	53:SB:199:LYS:HA	1.87	0.43
54:SC:234:THR:OG1	54:SC:236:ASN:OD1	2.24	0.43
55:SD:214:ILE:O	69:SR:20:TYR:OH	2.36	0.43
56:SE:31:PRO:HB3	56:SE:43:PRO:HG3	2.00	0.43
56:SE:115:THR:HG23	56:SE:118:GLU:H	1.83	0.43
1:1:1050:C:O3'	27:LT:110:LYS:NZ	2.45	0.43
1:1:1232:G:H2'	1:1:1233:G:H8	1.83	0.43
2:2:1586:G:H2'	2:2:1587:C:H6	1.83	0.43
3:3:46:C:OP1	11:LD:161:ARG:HG3	2.17	0.43
7:C:611:MET:HE3	7:C:611:MET:HB2	1.85	0.43
9:LB:151:ARG:HE	9:LB:151:ARG:HB2	1.65	0.43
13:LF:46:LYS:NZ	13:LF:176:GLU:OE1	2.40	0.43
17:LJ:115:ILE:O	17:LJ:115:ILE:HG22	2.18	0.43
30:LW:90:ILE:HG13	30:LW:91:LYS:N	2.33	0.43
30:LW:90:ILE:HB	30:LW:94:ARG:HH12	1.83	0.43
32:LY:60:GLY:O	32:LY:63:LYS:HG3	2.18	0.43
54:SC:239:LYS:HD3	54:SC:240:GLU:O	2.19	0.43
60:SI:36:THR:HG22	60:SI:57:ALA:O	2.18	0.43
62:SK:75:ARG:NH1	62:SK:83:GLU:O	2.42	0.43
69:SR:88:VAL:CG2	69:SR:95:GLN:CD	2.92	0.43
69:SR:103:ASP:O	69:SR:103:ASP:OD2	2.37	0.43
1:1:1004:C:H2'	1:1:1005:G:C8	2.53	0.43
1:1:1744:C:OP2	25:LR:43:LYS:NZ	2.49	0.43
1:1:3299:U:H2'	1:1:3300:A:H8	1.83	0.43
2:2:1139:A:H5''	78:Sa:2:VAL:CG1	2.49	0.43
60:SI:105:ASP:OD2	60:SI:107:ALA:N	2.33	0.43
60:SI:117:TYR:OH	60:SI:153:HIS:ND1	2.35	0.43
61:SJ:84:LEU:HD12	61:SJ:97:LEU:HD11	2.00	0.43
67:SP:116:LYS:HE2	67:SP:119:MET:HE2	2.00	0.43
69:SR:69:ILE:HD13	69:SR:69:ILE:N	2.22	0.43
70:SS:36:LYS:HB3	70:SS:102:ALA:HA	2.00	0.43
84:D:259:ILE:H	84:D:259:ILE:HD12	1.83	0.43
1:1:171:G:H2'	1:1:172:G:C8	2.54	0.43
1:1:1387:G:O6	38:Le:17:ARG:NH1	2.51	0.43
1:1:2471:U:H2'	1:1:2472:U:C6	2.53	0.43
6:B:94:ARG:HG3	6:B:95:GLY:H	1.82	0.43
60:SI:137:LYS:HD2	60:SI:143:GLU:OE2	2.18	0.43
63:SL:140:VAL:C	63:SL:141:ARG:HD2	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:SR:31:ASN:HA	69:SR:34:VAL:HG22	2.00	0.43
69:SR:101:MET:SD	69:SR:123:ASN:HB2	2.58	0.43
70:SS:123:ARG:HG3	70:SS:133:VAL:HG21	2.00	0.43
76:SY:66:GLN:HE21	76:SY:66:GLN:HB3	1.71	0.43
80:Sc:49:VAL:C	80:Sc:50:ARG:HD2	2.42	0.43
83:Sf:121:CYS:HB3	83:Sf:122:PRO:HD3	2.00	0.43
84:D:249:ALA:HB2	84:D:274:MET:HB2	2.00	0.43
1:1:191:G:H21	1:1:212:G:H21	1.64	0.43
1:1:652:A:H2'	1:1:653:A:C8	2.54	0.43
2:2:1560:U:H2'	2:2:1561:C:C6	2.54	0.43
4:4:71:A:OP2	32:LY:50:ARG:NH1	2.51	0.43
5:A:248:LEU:O	5:A:259:PHE:N	2.46	0.43
15:LH:68:ARG:HB2	15:LH:119:VAL:O	2.19	0.43
53:SB:107:THR:HG21	66:SO:130:ASP:O	2.19	0.43
59:SH:148:LYS:C	59:SH:149:ARG:HD2	2.44	0.43
62:SK:44:LEU:H	62:SK:44:LEU:CD1	2.30	0.43
74:SW:80:ASN:OD1	74:SW:124:LYS:NZ	2.48	0.43
83:Sf:137:ASP:OD2	83:Sf:151:ASP:HA	2.18	0.43
1:1:265:G:H1'	42:Li:91:ARG:HH12	1.82	0.43
1:1:474:C:H2'	1:1:475:G:H8	1.84	0.43
1:1:2307:U:H2'	1:1:2308:A:C8	2.54	0.43
3:3:5:A:H2	11:LD:74:ILE:HD11	1.83	0.43
3:3:36:C:H2'	3:3:37:G:C8	2.54	0.43
5:A:110:SER:HB3	5:A:154:VAL:HG22	2.01	0.43
27:LT:100:ARG:O	27:LT:103:GLU:HG3	2.19	0.43
37:Ld:83:ILE:HG12	37:Ld:101:VAL:HG12	2.01	0.43
51:Ls:92:ASP:O	51:Ls:95:GLU:HG3	2.18	0.43
53:SB:222:LYS:HE2	53:SB:222:LYS:HB3	1.84	0.43
55:SD:224:GLN:HB3	55:SD:225:PRO:HD3	2.01	0.43
67:SP:51:ARG:NH2	67:SP:55:ARG:HH21	2.12	0.43
67:SP:52:LYS:NZ	67:SP:91:MET:HA	2.34	0.43
68:SQ:41:PRO:HG2	68:SQ:44:LEU:HD12	1.99	0.43
72:SU:60:LEU:HD12	81:Sd:34:TYR:CZ	2.54	0.43
75:SX:140:LYS:C	75:SX:141:GLU:OE1	2.62	0.43
83:Sf:122:PRO:HD2	83:Sf:146:LEU:CG	2.23	0.43
83:Sf:137:ASP:CG	83:Sf:151:ASP:HA	2.44	0.43
1:1:452:C:H2'	1:1:453:G:H8	1.84	0.43
1:1:2458:C:H2'	1:1:2459:U:C6	2.54	0.43
2:2:781:G:H2'	2:2:782:C:C6	2.53	0.43
2:2:1243:C:H2'	2:2:1244:U:C6	2.54	0.43
9:LB:292:GLU:OE1	9:LB:292:GLU:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LF:229:ILE:HG12	26:LS:36:VAL:HG12	1.99	0.43
14:LG:95:LYS:HE2	14:LG:95:LYS:HB2	1.83	0.43
17:LJ:118:ASP:OD2	17:LJ:120:SER:OG	2.30	0.43
22:LO:99:ALA:HA	22:LO:102:GLU:OE1	2.18	0.43
33:LZ:89:GLU:H	33:LZ:89:GLU:CD	2.26	0.43
40:Lg:21:THR:HB	40:Lg:33:VAL:HG13	2.00	0.43
51:Ls:13:ASP:OD1	51:Ls:14:LYS:N	2.52	0.43
59:SH:86:GLU:HA	59:SH:89:LYS:NZ	2.33	0.43
60:SI:140:LYS:O	60:SI:144:LYS:NZ	2.33	0.43
61:SJ:107:LEU:HB2	61:SJ:144:PHE:HB3	2.01	0.43
62:SK:31:HIS:CE1	62:SK:36:ARG:HH11	2.36	0.43
63:SL:104:ARG:HB2	75:SX:9:LEU:O	2.19	0.43
70:SS:64:GLU:O	70:SS:67:GLU:HG2	2.19	0.43
82:Se:25:GLU:OE1	82:Se:25:GLU:N	2.51	0.43
1:1:474:C:H2'	1:1:475:G:C8	2.54	0.43
1:1:1454:U:OP1	25:LR:5:ARG:NH1	2.52	0.43
1:1:2633:A:N6	17:LJ:125:GLY:O	2.51	0.43
1:1:2842:U:H2'	1:1:2843:C:C6	2.54	0.43
2:2:862:U:O2	79:Sb:21:LEU:HB3	2.19	0.43
2:2:1169:G:H2'	2:2:1170:C:C6	2.54	0.43
12:LE:72:LEU:HA	12:LE:83:VAL:HG12	1.99	0.43
15:LH:54:LYS:CD	20:LM:3:GLU:OE1	2.67	0.43
19:LL:64:LYS:HD2	34:La:69:TRP:CD1	2.54	0.43
31:LX:151:THR:HG23	31:LX:152:LYS:HE3	2.00	0.43
41:Lh:19:GLU:O	41:Lh:19:GLU:HG2	2.14	0.43
69:SR:101:MET:HG2	69:SR:121:PRO:C	2.44	0.43
76:SY:11:ARG:O	76:SY:29:ASP:OD2	2.37	0.43
1:1:638:C:H2'	1:1:639:G:C8	2.54	0.43
1:1:1126:A:H5'	1:1:1351:U:H1'	2.01	0.43
1:1:1676:A:H2'	1:1:1677:A:C8	2.53	0.43
1:1:1879:G:O2'	1:1:2297:U:O4	2.24	0.43
2:2:861:A:O2'	2:2:862:U:H5'	2.19	0.43
2:2:910:U:H5'	53:SB:11:LYS:O	2.19	0.43
2:2:1693:C:H2'	2:2:1694:G:H8	1.84	0.43
15:LH:53:LEU:HD23	15:LH:53:LEU:H	1.84	0.43
17:LJ:33:ARG:NH1	17:LJ:121:ILE:O	2.51	0.43
19:LL:150:SER:C	19:LL:152:ARG:H	2.27	0.43
19:LL:203:LYS:HE3	19:LL:203:LYS:HB3	1.87	0.43
51:Ls:15:LEU:C	51:Ls:61:ARG:HH12	2.27	0.43
56:SE:59:ARG:HE	56:SE:60:GLU:HG3	1.84	0.43
56:SE:65:MET:CE	56:SE:70:VAL:HG12	2.45	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:Sf:118:ARG:HH21	83:Sf:131:PHE:HB3	1.83	0.43
1:1:1016:U:H2'	1:1:1017:U:C5	2.54	0.42
2:2:529:U:OP1	61:SJ:130:ARG:NH2	2.52	0.42
2:2:673:U:H2'	2:2:674:G:H8	1.80	0.42
10:LC:10:PHE:CZ	10:LC:147:PRO:HB2	2.54	0.42
59:SH:172:VAL:HG23	59:SH:172:VAL:O	2.19	0.42
62:SK:21:MET:HB3	62:SK:64:TYR:CD1	2.54	0.42
68:SQ:49:TYR:O	68:SQ:53:LEU:HD12	2.19	0.42
68:SQ:97:VAL:HG22	68:SQ:98:ASP:H	1.84	0.42
74:SW:111:MET:CE	74:SW:115:GLU:OE1	2.49	0.42
79:Sb:67:THR:OG1	79:Sb:68:GLY:N	2.51	0.42
1:1:2050:C:H2'	1:1:2051:G:H8	1.84	0.42
2:2:500:G:H2'	2:2:501:U:C6	2.54	0.42
2:2:1289:G:H21	52:SA:114:ILE:HD11	1.84	0.42
7:C:569:ARG:HA	17:LJ:62:ARG:HH12	1.85	0.42
8:LA:178:PRO:HD2	49:Lp:26:VAL:HG22	2.00	0.42
19:LL:196:GLY:O	19:LL:199:GLU:HG3	2.19	0.42
20:LM:103:GLN:O	20:LM:107:GLU:HG3	2.19	0.42
64:SM:52:LYS:HE3	83:Sf:128:ALA:O	2.19	0.42
68:SQ:101:SER:O	68:SQ:105:LEU:HD23	2.19	0.42
84:D:215:LYS:HD3	84:D:215:LYS:N	2.34	0.42
2:2:102:A:H4'	2:2:103:A:O5'	2.19	0.42
2:2:194:G:N3	2:2:195:G:C8	2.88	0.42
2:2:1161:G:H2'	2:2:1162:G:C8	2.54	0.42
2:2:1405:G:N2	2:2:1408:G:OP2	2.49	0.42
2:2:1477:C:H4'	2:2:1478:C:OP1	2.19	0.42
4:4:9:A:H2'	4:4:10:A:H8	1.84	0.42
6:B:139:GLU:OE1	6:B:139:GLU:N	2.52	0.42
7:C:605:ARG:O	7:C:608:THR:HG22	2.19	0.42
9:LB:180:MET:HE2	9:LB:181:GLU:O	2.18	0.42
26:LS:137:ARG:HD3	26:LS:137:ARG:HA	1.68	0.42
43:Lj:84:LYS:HG3	43:Lj:85:GLY:N	2.34	0.42
44:Lk:51:ASP:CG	44:Lk:52:SER:N	2.76	0.42
44:Lk:54:LYS:HA	44:Lk:57:LYS:HE2	2.00	0.42
51:Ls:97:ARG:C	51:Ls:98:GLU:OE1	2.62	0.42
59:SH:6:LEU:C	59:SH:16:ARG:HH22	2.23	0.42
59:SH:151:ARG:HH21	59:SH:153:LYS:HD3	1.82	0.42
67:SP:138:ARG:HH11	67:SP:140:GLY:HA2	1.79	0.42
77:SZ:37:ASP:C	77:SZ:41:LYS:NZ	2.76	0.42
77:SZ:84:HIS:H	77:SZ:88:LYS:HZ1	1.67	0.42
84:D:140:ARG:NE	84:D:443:ASP:OD2	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1199:C:H2'	1:1:1200:A:H8	1.84	0.42
1:1:1796:A:HO2'	1:1:1797:A:P	2.43	0.42
1:1:2044:G:O2'	1:1:2045:G:N7	2.52	0.42
1:1:2503:C:H1'	1:1:2504:G:OP2	2.18	0.42
1:1:3221:A:O2'	1:1:3222:C:H6	2.02	0.42
2:2:1054:U:O2	2:2:1055:A:N6	2.52	0.42
2:2:1366:A:H2'	2:2:1367:C:H6	1.84	0.42
11:LD:17:GLN:NE2	27:LT:22:HIS:O	2.49	0.42
12:LE:12:LYS:CD	12:LE:15:ARG:HG3	2.49	0.42
14:LG:65:LYS:HZ3	21:LN:29:GLU:CD	2.27	0.42
21:LN:127:TYR:HB3	21:LN:129:TYR:HE1	1.83	0.42
22:LO:145:HIS:HB3	22:LO:146:GLU:OE1	2.19	0.42
37:Ld:9:ARG:O	37:Ld:12:ILE:N	2.50	0.42
55:SD:51:ILE:HB	55:SD:89:LEU:HD23	2.01	0.42
70:SS:20:THR:HG21	70:SS:35:ILE:HG22	2.01	0.42
83:Sf:146:LEU:HB3	83:Sf:148:TYR:CD2	2.54	0.42
1:1:249:G:H2'	1:1:250:C:H6	1.83	0.42
1:1:2050:C:H2'	1:1:2051:G:C8	2.54	0.42
1:1:2148:G:OP1	8:LA:202:VAL:HG23	2.19	0.42
1:1:2544:G:H2'	1:1:2544:G:N3	2.35	0.42
2:2:1473:A:H2'	2:2:1474:G:C8	2.55	0.42
2:2:1736:G:H2'	2:2:1737:U:C6	2.53	0.42
5:A:244:ASN:HD21	5:A:245:ARG:NH1	2.17	0.42
57:SF:15:VAL:HG22	68:SQ:36:LEU:HD21	2.02	0.42
58:SG:30:LYS:HD3	58:SG:30:LYS:HA	1.80	0.42
68:SQ:13:LYS:HA	68:SQ:13:LYS:HD2	1.84	0.42
1:1:1212:G:H4'	51:Ls:32:ASN:ND2	2.34	0.42
1:1:3224:C:H2'	1:1:3225:G:H8	1.84	0.42
2:2:404:A:H2'	2:2:405:C:C6	2.55	0.42
2:2:1712:C:HO2'	2:2:1713:C:H6	1.66	0.42
3:3:7:G:OP1	11:LD:33:ARG:NH1	2.53	0.42
5:A:185:GLN:HG2	5:A:186:THR:N	2.34	0.42
16:LI:101:LYS:HD2	16:LI:101:LYS:HA	1.90	0.42
19:LL:60:CYS:HB2	19:LL:65:TYR:O	2.20	0.42
31:LX:82:THR:O	31:LX:85:ALA:N	2.52	0.42
52:SA:12:PRO:O	52:SA:13:THR:OG1	2.31	0.42
55:SD:126:LEU:HD21	55:SD:157:ASP:OD2	2.19	0.42
75:SX:63:GLN:HB3	75:SX:64:PRO:HD3	2.02	0.42
1:1:911:A:O2'	43:Lj:49:TRP:O	2.36	0.42
1:1:1194:U:H2'	1:1:1195:A:C8	2.55	0.42
1:1:1222:C:H2'	1:1:1223:A:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:509:A:O2'	2:2:510:U:OP1	2.36	0.42
2:2:1711:G:H2'	2:2:1712:C:H5'	2.02	0.42
5:A:17:TRP:CE2	5:A:303:THR:HB	2.55	0.42
9:LB:349:ARG:O	9:LB:349:ARG:HG2	2.20	0.42
21:LN:68:ARG:HA	21:LN:98:LEU:HD21	2.02	0.42
51:Ls:27:VAL:HG11	51:Ls:79:PHE:HE2	1.85	0.42
51:Ls:33:VAL:CG1	51:Ls:38:MET:CE	2.97	0.42
62:SK:17:ARG:HG2	62:SK:17:ARG:H	1.58	0.42
70:SS:86:LEU:HD12	70:SS:97:ASP:CG	2.44	0.42
72:SU:93:PRO:HD2	72:SU:96:ILE:HG21	2.02	0.42
75:SX:53:VAL:HG13	75:SX:99:ASN:H	1.85	0.42
75:SX:69:ARG:HD3	75:SX:69:ARG:HA	1.75	0.42
76:SY:55:LYS:O	76:SY:58:VAL:HG22	2.19	0.42
2:2:883:G:H2'	2:2:884:U:C6	2.54	0.42
2:2:920:G:H2'	2:2:921:A:C8	2.54	0.42
2:2:1224:A:H5''	64:SM:116:VAL:HG21	2.00	0.42
2:2:1640:C:H2'	2:2:1641:G:H8	1.83	0.42
12:LE:148:LYS:C	12:LE:150:GLN:OE1	2.63	0.42
13:LF:29:ARG:HB3	13:LF:32:ARG:HD3	2.02	0.42
43:Lj:31:LYS:HB3	43:Lj:33:VAL:HG22	2.01	0.42
53:SB:129:THR:OG1	53:SB:131:ASP:O	2.29	0.42
70:SS:129:TRP:HB3	70:SS:131:LEU:HD13	2.02	0.42
1:1:3315:U:H2'	1:1:3319:C:H41	1.85	0.42
2:2:832:G:O2'	2:2:833:U:OP1	2.37	0.42
2:2:1785:G:OP2	66:SO:145:ARG:NH2	2.53	0.42
4:4:79:A:H2'	4:4:80:A:C8	2.55	0.42
10:LC:280:ASN:OD1	10:LC:281:ILE:N	2.53	0.42
13:LF:138:PRO:HA	13:LF:234:LEU:HD13	2.01	0.42
17:LJ:113:LEU:O	17:LJ:115:ILE:HD12	2.20	0.42
20:LM:83:LYS:O	20:LM:86:GLU:OE1	2.37	0.42
53:SB:3:VAL:HG21	66:SO:64:ASP:HB3	2.02	0.42
69:SR:87:GLU:OE1	69:SR:87:GLU:O	2.37	0.42
80:Sc:50:ARG:N	80:Sc:53:ASP:OD2	2.32	0.42
1:1:8:C:H2'	1:1:9:C:C6	2.55	0.42
1:1:505:G:O2'	10:LC:343:GLU:OE1	2.31	0.42
1:1:1236:U:O2	1:1:1246:A:H5''	2.20	0.42
1:1:2064:C:HO2'	1:1:2065:U:P	2.42	0.42
2:2:481:C:H2'	2:2:482:A:C8	2.55	0.42
2:2:1549:G:N1	2:2:1552:A:OP2	2.53	0.42
5:A:91:GLU:OE2	5:A:95:GLY:N	2.53	0.42
15:LH:54:LYS:HE2	20:LM:3:GLU:OE1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LI:51:HIS:CD2	16:LI:168:SER:HB2	2.55	0.42
36:Lc:22:LYS:HB3	36:Lc:22:LYS:HE3	1.74	0.42
41:Lh:30:GLU:HA	41:Lh:33:GLN:HB3	2.02	0.42
42:Li:67:ILE:HG13	42:Li:103:ILE:HD11	2.02	0.42
44:Lk:75:ASN:OD1	44:Lk:75:ASN:N	2.53	0.42
48:Lo:92:GLU:N	48:Lo:92:GLU:OE2	2.53	0.42
62:SK:67:THR:HG22	62:SK:69:ALA:H	1.84	0.42
63:SL:30:THR:C	63:SL:37:ARG:HH12	2.28	0.42
66:SO:61:VAL:HG12	66:SO:63:ALA:H	1.85	0.42
67:SP:83:LEU:HA	67:SP:101:VAL:HG23	2.02	0.42
75:SX:48:HIS:HB3	75:SX:103:LEU:HD11	2.01	0.42
80:Sc:38:THR:CG2	80:Sc:39:ARG:N	2.83	0.42
83:Sf:106:TYR:HB3	83:Sf:116:ARG:HH21	1.85	0.42
1:1:300:A:H2'	1:1:301:A:H8	1.85	0.41
2:2:222:U:O2	2:2:832:G:C6	2.73	0.41
2:2:1084:A:H2'	2:2:1085:A:C8	2.55	0.41
10:LC:303:PRO:O	10:LC:304:LYS:HG2	2.20	0.41
15:LH:131:TYR:HA	15:LH:216:ASP:OD1	2.20	0.41
16:LI:140:THR:OG1	16:LI:141:ARG:N	2.52	0.41
19:LL:159:GLN:O	19:LL:159:GLN:HG3	2.20	0.41
37:Ld:105:ASN:OD1	37:Ld:105:ASN:C	2.63	0.41
55:SD:41:GLU:OE2	55:SD:43:ARG:HG2	2.19	0.41
57:SF:202:ASP:OD1	57:SF:203:GLU:N	2.53	0.41
60:SI:27:PHE:HD2	60:SI:28:GLU:HG3	1.84	0.41
61:SJ:21:ARG:CG	61:SJ:25:GLU:OE2	2.66	0.41
62:SK:13:GLU:OE2	62:SK:17:ARG:NH1	2.53	0.41
62:SK:13:GLU:O	62:SK:17:ARG:CG	2.60	0.41
63:SL:80:VAL:HG22	63:SL:126:ASP:H	1.84	0.41
75:SX:141:GLU:N	75:SX:141:GLU:CD	2.78	0.41
76:SY:15:PHE:CZ	76:SY:24:LYS:HD3	2.55	0.41
77:SZ:83:GLY:HA2	77:SZ:88:LYS:HZ3	1.85	0.41
1:1:292:G:C6	42:Li:39:LYS:HB3	2.56	0.41
1:1:2496:G:H2'	1:1:2497:G:C8	2.55	0.41
2:2:832:G:C5	2:2:833:U:C5	3.08	0.41
9:LB:215:MET:HE1	9:LB:280:ASN:HA	1.95	0.41
9:LB:256:TRP:CD1	9:LB:256:TRP:C	2.99	0.41
11:LD:5:LYS:HE3	11:LD:5:LYS:HB3	1.86	0.41
17:LJ:92:LEU:HD12	17:LJ:96:ASN:HD22	1.84	0.41
22:LO:144:SER:OG	22:LO:149:TRP:CE3	2.73	0.41
23:LP:182:ARG:HA	23:LP:185:THR:HG22	2.03	0.41
40:Lg:52:LEU:HA	40:Lg:53:PRO:HD3	1.94	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:SB:121:ILE:CG2	53:SB:168:MET:HE1	2.41	0.41
57:SF:44:SER:HA	80:Sc:54:ILE:HG21	2.02	0.41
57:SF:85:MET:HE1	57:SF:92:GLY:N	2.31	0.41
59:SH:21:ASP:OD1	59:SH:22:LEU:N	2.53	0.41
64:SM:31:LYS:O	64:SM:35:LYS:HG2	2.19	0.41
67:SP:106:SER:HB3	67:SP:128:SER:OG	2.20	0.41
68:SQ:13:LYS:HG3	68:SQ:14:LYS:H	1.84	0.41
70:SS:15:LEU:HB2	70:SS:22:VAL:HG22	2.02	0.41
70:SS:32:LEU:HD22	70:SS:32:LEU:N	2.35	0.41
80:Sc:15:ARG:HH12	80:Sc:30:ARG:HD3	1.85	0.41
80:Sc:38:THR:HG23	80:Sc:39:ARG:N	2.35	0.41
84:D:126:LEU:CD1	84:D:126:LEU:H	2.33	0.41
1:1:962:U:H2'	1:1:963:U:C6	2.55	0.41
1:1:1213:G:O2'	51:Ls:35:SER:HB3	2.20	0.41
1:1:2648:A:H2'	1:1:2648:A:N3	2.36	0.41
2:2:1245:C:H2'	2:2:1246:U:C6	2.55	0.41
5:A:301:GLY:O	5:A:302:TYR:CD1	2.73	0.41
10:LC:29:ALA:O	50:Lq:3:ASN:ND2	2.51	0.41
20:LM:34:ILE:HG22	20:LM:35:ASP:OD1	2.19	0.41
21:LN:14:LYS:HA	21:LN:19:VAL:HG11	2.02	0.41
51:Ls:19:LEU:HD23	51:Ls:61:ARG:HH12	1.79	0.41
51:Ls:160:GLU:HG2	51:Ls:163:ALA:HB2	2.02	0.41
57:SF:44:SER:HA	80:Sc:54:ILE:CG2	2.50	0.41
66:SO:62:LYS:HE3	66:SO:62:LYS:CA	2.44	0.41
68:SQ:30:LYS:HD2	68:SQ:33:GLY:O	2.21	0.41
69:SR:27:ASP:OD1	69:SR:30:THR:CB	2.68	0.41
69:SR:104:ILE:CG1	69:SR:108:THR:HB	2.51	0.41
82:Se:38:LEU:HD12	82:Se:39:THR:N	2.34	0.41
1:1:580:A:N6	1:1:598:G:H1'	2.35	0.41
1:1:1001:G:H2'	1:1:1002:G:H8	1.85	0.41
1:1:1290:G:H5'	22:LO:61:LYS:HE3	2.02	0.41
1:1:2590:U:H2'	1:1:2591:G:H8	1.85	0.41
1:1:3163:A:H4'	1:1:3164:G:O5'	2.20	0.41
2:2:1603:G:H2'	2:2:1604:U:H6	1.86	0.41
10:LC:301:ARG:CZ	24:LQ:69:GLU:OE1	2.68	0.41
14:LG:31:GLU:HG2	33:LZ:127:ARG:HH12	1.84	0.41
14:LG:48:ASN:OD1	31:LX:39:VAL:HG13	2.20	0.41
17:LJ:85:LEU:HD11	17:LJ:164:PHE:HE1	1.85	0.41
19:LL:57:ILE:HD12	19:LL:157:VAL:HG12	2.03	0.41
21:LN:145:ASP:OD1	21:LN:146:PRO:N	2.53	0.41
22:LO:139:THR:HG22	22:LO:141:GLY:H	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:Lg:79:GLY:O	40:Lg:80:SER:OG	2.28	0.41
51:Ls:25:ILE:CG1	51:Ls:88:PHE:HE1	2.29	0.41
56:SE:155:LYS:HD3	56:SE:155:LYS:HA	1.77	0.41
63:SL:137:SER:HB3	63:SL:140:VAL:HB	2.01	0.41
65:SN:104:ARG:HG3	65:SN:104:ARG:NH1	2.35	0.41
72:SU:37:GLU:OE1	72:SU:41:ARG:NH2	2.51	0.41
84:D:157:SER:OG	84:D:384:ARG:NH2	2.54	0.41
1:1:1300:A:O2'	1:1:1301:A:H3'	2.21	0.41
2:2:98:C:OP2	2:2:375:A:O2'	2.30	0.41
2:2:1101:U:OP1	75:SX:14:LYS:NZ	2.54	0.41
2:2:1196:G:C4	81:Sd:40:ARG:HD3	2.56	0.41
2:2:1258:G:H2'	2:2:1259:U:H6	1.84	0.41
2:2:1479:A:H2'	2:2:1480:G:C8	2.56	0.41
5:A:246:TYR:HE2	5:A:261:LEU:HD22	1.84	0.41
7:C:582:ALA:HA	7:C:599:LYS:HZ2	1.84	0.41
8:LA:134:VAL:HG12	8:LA:151:PRO:HD3	2.02	0.41
9:LB:71:GLU:OE1	9:LB:71:GLU:N	2.49	0.41
9:LB:92:TYR:N	9:LB:156:CYS:SG	2.93	0.41
9:LB:103:THR:HG21	9:LB:151:ARG:HD2	2.03	0.41
11:LD:194:ASP:OD2	11:LD:197:VAL:HG23	2.21	0.41
12:LE:116:GLN:HA	12:LE:119:ILE:HD12	2.02	0.41
16:LI:152:LEU:HD23	16:LI:152:LEU:HA	1.92	0.41
21:LN:173:GLY:HA3	21:LN:183:THR:OG1	2.20	0.41
23:LP:126:ARG:CZ	23:LP:140:MET:HE1	2.50	0.41
31:LX:139:LEU:HD12	31:LX:145:ALA:HB2	2.02	0.41
32:LY:73:TYR:CD2	32:LY:76:LYS:HB2	2.55	0.41
33:LZ:25:ILE:HD11	33:LZ:91:LEU:HD12	2.01	0.41
34:La:7:LYS:HA	34:La:7:LYS:HD3	1.85	0.41
42:Li:75:ASP:OD2	42:Li:75:ASP:O	2.38	0.41
51:Ls:37:GLN:C	51:Ls:38:MET:HE2	2.45	0.41
51:Ls:126:THR:O	51:Ls:128:MET:HE1	2.16	0.41
62:SK:4:PRO:HG2	62:SK:7:ASP:OD2	2.21	0.41
69:SR:29:GLU:OE1	69:SR:29:GLU:HA	2.20	0.41
73:SV:58:PHE:CE1	73:SV:62:MET:HE2	2.55	0.41
1:1:193:A:O2'	1:1:195:G:N7	2.46	0.41
1:1:2389:U:H2'	1:1:2390:U:C6	2.55	0.41
2:2:16:G:H2'	2:2:17:C:C6	2.55	0.41
2:2:1386:C:H2'	2:2:1387:U:H4'	2.02	0.41
4:4:79:A:H2'	4:4:80:A:H8	1.85	0.41
6:B:89:ARG:HH21	6:B:90:ARG:CA	2.33	0.41
8:LA:181:LYS:HB2	8:LA:184:ARG:HG3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LG:210:ASP:OD1	14:LG:210:ASP:N	2.50	0.41
29:LV:16:THR:HG21	29:LV:85:LYS:HE3	2.03	0.41
38:Le:124:LYS:NZ	38:Le:125:ALA:CA	2.84	0.41
51:Ls:56:ASN:O	51:Ls:60:ARG:NH2	2.48	0.41
51:Ls:92:ASP:OD2	51:Ls:92:ASP:C	2.63	0.41
61:SJ:22:LEU:HD23	61:SJ:22:LEU:HA	1.91	0.41
67:SP:64:LEU:HD23	67:SP:64:LEU:H	1.86	0.41
69:SR:5:ARG:HB3	69:SR:9:VAL:HG21	2.03	0.41
69:SR:70:SER:HB3	69:SR:75:GLU:OE2	2.21	0.41
74:SW:10:ALA:HB1	74:SW:27:ILE:HD13	2.02	0.41
1:1:8:C:H2'	1:1:9:C:H6	1.86	0.41
1:1:300:A:H2'	1:1:301:A:C8	2.56	0.41
1:1:435:G:H2'	1:1:436:C:C6	2.55	0.41
1:1:533:C:H2'	1:1:534:C:C6	2.56	0.41
1:1:575:G:H2'	1:1:576:A:C8	2.53	0.41
1:1:1241:U:H3	1:1:1244:G:H22	1.68	0.41
1:1:1573:A:OP1	40:Lg:61:ARG:NH1	2.53	0.41
1:1:1635:G:P	40:Lg:41:THR:HG21	2.61	0.41
2:2:738:G:H2'	2:2:739:A:C8	2.56	0.41
2:2:1004:C:H2'	66:SO:150:LEU:HD11	2.01	0.41
2:2:1545:C:H5''	67:SP:50:ARG:HH22	1.85	0.41
5:A:240:VAL:HG12	5:A:289:LEU:HD23	2.01	0.41
14:LG:217:LEU:HD23	14:LG:217:LEU:C	2.45	0.41
16:LI:193:ASP:OD1	16:LI:194:GLY:N	2.43	0.41
23:LP:95:LEU:HD23	23:LP:95:LEU:HA	1.89	0.41
24:LQ:208:SER:OG	24:LQ:209:ARG:NH1	2.54	0.41
27:LT:79:ARG:HG2	27:LT:79:ARG:NH1	2.34	0.41
37:Ld:14:ASP:OD2	37:Ld:14:ASP:N	2.54	0.41
43:Lj:39:TYR:CD1	43:Lj:40:PRO:HA	2.56	0.41
51:Ls:21:GLU:HG3	51:Ls:22:TYR:CD1	2.56	0.41
53:SB:26:ARG:NH1	53:SB:49:ASN:OD1	2.52	0.41
68:SQ:20:ALA:HB2	68:SQ:67:ILE:HG12	2.03	0.41
71:ST:116:LYS:HE2	71:ST:123:ARG:HH21	1.85	0.41
1:1:446:A:O2'	1:1:447:U:H6	2.03	0.41
1:1:1587:U:O2'	1:1:1588:C:P	2.78	0.41
2:2:698:G:H2'	2:2:699:A:C8	2.55	0.41
2:2:1709:G:H2'	2:2:1710:G:C8	2.54	0.41
14:LG:109:LYS:HD3	14:LG:109:LYS:HA	1.72	0.41
17:LJ:110:HIS:HE1	17:LJ:123:ILE:HA	1.85	0.41
28:LU:20:LYS:HE3	28:LU:20:LYS:HB2	1.69	0.41
36:Lc:60:GLU:OE1	36:Lc:60:GLU:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:SB:94:LYS:HD3	53:SB:94:LYS:HA	1.78	0.41
57:SF:173:ASN:OD1	57:SF:174:VAL:N	2.53	0.41
70:SS:76:PRO:HG3	70:SS:99:GLN:HB3	2.02	0.41
71:ST:86:ARG:NH2	71:ST:89:ARG:HD3	2.35	0.41
77:SZ:50:THR:O	77:SZ:53:THR:OG1	2.35	0.41
1:1:425:G:H2'	1:1:426:A:C8	2.55	0.41
1:1:452:C:H2'	1:1:453:G:C8	2.56	0.41
1:1:2056:A:O2'	1:1:2057:C:OP2	2.32	0.41
1:1:2369:C:H2'	1:1:2370:C:C6	2.55	0.41
2:2:330:A:N7	60:SI:49:ARG:NH1	2.69	0.41
2:2:732:A:H2'	2:2:733:A:O4'	2.21	0.41
2:2:761:A:OP1	61:SJ:77:ARG:NH2	2.54	0.41
2:2:1057:U:H3'	2:2:1058:U:C5	2.56	0.41
5:A:107:ASP:OD1	5:A:107:ASP:N	2.52	0.41
6:B:93:PHE:CG	6:B:94:ARG:N	2.81	0.41
7:C:607:VAL:HG22	7:C:611:MET:SD	2.61	0.41
11:LD:41:LYS:HD3	11:LD:41:LYS:HA	1.87	0.41
11:LD:99:TYR:HE2	11:LD:167:LYS:HG3	1.86	0.41
14:LG:115:GLU:OE1	14:LG:125:LYS:HG3	2.21	0.41
19:LL:106:GLU:HG3	42:Li:29:ARG:HD2	2.03	0.41
24:LQ:57:LEU:HD12	24:LQ:57:LEU:HA	1.91	0.41
25:LR:30:SER:OG	25:LR:31:GLU:OE1	2.33	0.41
27:LT:115:LEU:HD23	27:LT:115:LEU:C	2.45	0.41
27:LT:159:THR:HG23	27:LT:160:ILE:N	2.35	0.41
31:LX:72:GLU:HG2	31:LX:73:HIS:N	2.34	0.41
31:LX:114:LYS:HZ3	31:LX:114:LYS:CB	2.23	0.41
31:LX:152:LYS:HA	31:LX:152:LYS:HD3	1.81	0.41
32:LY:2:LYS:HE3	32:LY:7:VAL:O	2.21	0.41
32:LY:51:LYS:HA	32:LY:69:VAL:HG23	2.02	0.41
34:La:59:ARG:NH2	48:Lo:38:GLN:OE1	2.52	0.41
51:Ls:62:ALA:HA	51:Ls:65:THR:OG1	2.21	0.41
51:Ls:63:LEU:HA	51:Ls:66:PHE:CD2	2.56	0.41
52:SA:73:PRO:HB2	52:SA:97:GLY:HA3	2.02	0.41
56:SE:21:ASP:OD1	56:SE:21:ASP:N	2.54	0.41
57:SF:94:LYS:O	57:SF:98:VAL:HG23	2.20	0.41
58:SG:7:HIS:HB2	58:SG:124:LEU:HD21	2.03	0.41
59:SH:143:VAL:HG21	59:SH:164:LEU:HD23	2.03	0.41
61:SJ:133:ARG:HB3	61:SJ:138:ILE:HD13	2.03	0.41
64:SM:63:VAL:HB	64:SM:121:VAL:HG23	2.03	0.41
77:SZ:38:LYS:CA	77:SZ:41:LYS:NZ	2.77	0.41
84:D:415:ASP:OD1	84:D:416:GLU:N	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:93:G:OP2	1:1:94:C:H5''	2.20	0.41
1:1:882:G:H1'	1:1:1569:A:N6	2.36	0.41
1:1:910:C:H2'	1:1:911:A:C8	2.56	0.41
1:1:1003:G:C6	1:1:1015:C:C4	3.08	0.41
1:1:1212:G:H4'	51:Ls:32:ASN:CG	2.46	0.41
1:1:1796:A:O2'	1:1:1797:A:P	2.79	0.41
1:1:3112:U:O2'	1:1:3113:A:N7	2.44	0.41
2:2:481:C:H2'	2:2:482:A:H8	1.86	0.41
2:2:1485:U:H6	2:2:1485:U:H2'	1.72	0.41
2:2:1694:G:H2'	2:2:1695:G:C8	2.56	0.41
5:A:201:SER:OG	5:A:203:ASP:OD1	2.35	0.41
11:LD:228:LYS:HD3	11:LD:228:LYS:HA	1.91	0.41
14:LG:27:ASN:OD1	14:LG:29:LEU:HD23	2.21	0.41
14:LG:145:LEU:HD23	14:LG:145:LEU:HA	1.94	0.41
19:LL:170:LYS:HB2	19:LL:170:LYS:HE3	1.81	0.41
26:LS:13:HIS:HD2	26:LS:51:VAL:HG22	1.86	0.41
32:LY:53:ASP:HB3	32:LY:109:HIS:N	2.36	0.41
32:LY:63:LYS:CB	32:LY:64:ASP:OD2	2.69	0.41
53:SB:29:TRP:CE2	53:SB:47:LEU:HD13	2.56	0.41
53:SB:135:LEU:HA	53:SB:217:LEU:HA	2.03	0.41
58:SG:54:GLY:HA2	58:SG:63:MET:CE	2.41	0.41
59:SH:62:LYS:HE2	59:SH:94:ARG:CZ	2.51	0.41
64:SM:71:GLU:O	64:SM:75:LYS:HG3	2.21	0.41
70:SS:60:GLU:CG	70:SS:60:GLU:O	2.69	0.41
76:SY:51:TYR:O	76:SY:52:LYS:HE2	2.21	0.41
1:1:147:A:P	21:LN:147:ARG:HH22	2.44	0.40
1:1:2065:U:H2'	1:1:2066:U:C6	2.56	0.40
1:1:2522:A:N3	14:LG:32:LYS:HB2	2.36	0.40
1:1:3258:U:H1'	1:1:3259:G:OP2	2.22	0.40
2:2:1226:G:N3	2:2:1252:G:N2	2.69	0.40
5:A:120:ILE:HG13	5:A:132:TRP:HB2	2.03	0.40
9:LB:216:ILE:HD12	9:LB:339:LEU:HD22	2.03	0.40
10:LC:301:ARG:NE	24:LQ:69:GLU:OE1	2.50	0.40
14:LG:112:LEU:HD23	14:LG:112:LEU:HA	1.91	0.40
15:LH:179:GLN:CD	15:LH:179:GLN:C	2.90	0.40
16:LI:21:ARG:O	16:LI:24:ARG:NH1	2.54	0.40
25:LR:51:ILE:HG22	25:LR:52:LYS:N	2.37	0.40
28:LU:112:LEU:HD12	28:LU:112:LEU:H	1.83	0.40
58:SG:163:GLN:HB3	58:SG:171:PRO:HB3	2.02	0.40
64:SM:55:ASP:CG	83:Sf:128:ALA:HB1	2.46	0.40
64:SM:94:GLY:HA2	64:SM:97:LEU:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:SZ:35:THR:HA	77:SZ:38:LYS:CD	2.51	0.40
84:D:259:ILE:HG22	84:D:260:ASP:CG	2.46	0.40
1:1:262:G:H5'	21:LN:14:LYS:HE2	2.02	0.40
1:1:1091:C:H2'	1:1:1092:A:C8	2.57	0.40
5:A:192:THR:OG1	5:A:213:ASP:OD1	2.23	0.40
9:LB:180:MET:HE3	9:LB:180:MET:HB2	1.94	0.40
22:LO:187:ALA:O	22:LO:191:VAL:HG22	2.21	0.40
35:Lb:5:LYS:HE3	35:Lb:8:SER:HB2	2.04	0.40
40:Lg:110:SER:C	40:Lg:111:GLN:CD	2.88	0.40
55:SD:43:ARG:HB2	55:SD:50:ASP:OD1	2.21	0.40
55:SD:143:GLY:HA3	55:SD:185:LEU:HD13	2.03	0.40
67:SP:97:MET:SD	67:SP:97:MET:C	2.98	0.40
69:SR:43:SER:HB3	69:SR:46:LEU:HD23	2.04	0.40
70:SS:14:ILE:C	70:SS:15:LEU:HD12	2.46	0.40
74:SW:76:SER:OG	74:SW:77:PRO:HD3	2.21	0.40
1:1:637:A:H2'	1:1:638:C:C6	2.56	0.40
1:1:1223:A:N6	1:1:1228:A:OP1	2.54	0.40
2:2:494:G:H2'	2:2:495:G:H8	1.85	0.40
2:2:1580:G:C8	68:SQ:122:ARG:HD3	2.56	0.40
4:4:9:A:H2'	4:4:10:A:C8	2.56	0.40
5:A:286:CYS:HB2	5:A:302:TYR:HE1	1.86	0.40
25:LR:10:LEU:HD23	25:LR:10:LEU:HA	1.93	0.40
54:SC:53:VAL:HG22	54:SC:58:ILE:HD11	2.03	0.40
54:SC:161:SER:OG	54:SC:162:LEU:N	2.54	0.40
62:SK:70:GLY:O	62:SK:74:LEU:HD12	2.22	0.40
65:SN:86:GLU:H	65:SN:86:GLU:HG2	1.63	0.40
66:SO:90:THR:O	66:SO:123:MET:SD	2.79	0.40
69:SR:18:GLU:OE1	69:SR:19:LYS:HG3	2.21	0.40
77:SZ:57:ARG:HD3	77:SZ:57:ARG:N	2.31	0.40
1:1:2570:U:H2'	1:1:2571:U:C6	2.56	0.40
1:1:2874:U:C5	9:LB:7:GLU:HG3	2.56	0.40
2:2:612:G:O4'	2:2:612:G:OP1	2.38	0.40
2:2:1378:U:O2'	2:2:1379:A:OP1	2.36	0.40
5:A:20:SER:OG	5:A:68:ASP:HA	2.21	0.40
10:LC:319:PRO:O	10:LC:320:LEU:HB2	2.20	0.40
17:LJ:63:ASN:HB2	48:Lo:103:ALA:HB3	2.02	0.40
17:LJ:110:HIS:CE1	17:LJ:123:ILE:HA	2.57	0.40
25:LR:181:ARG:HH12	25:LR:182:ASN:HA	1.87	0.40
27:LT:111:GLU:C	27:LT:111:GLU:CD	2.89	0.40
36:Lc:19:LEU:HD23	36:Lc:101:SER:HB3	2.02	0.40
37:Ld:72:ILE:H	37:Ld:72:ILE:HD12	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:Le:19:MET:HE3	38:Le:20:ARG:O	2.21	0.40
41:Lh:49:ILE:HG13	41:Lh:50:HIS:N	2.36	0.40
54:SC:188:ALA:HB1	54:SC:192:VAL:HG23	2.03	0.40
55:SD:104:GLN:HA	55:SD:107:SER:OG	2.22	0.40
71:ST:119:GLU:OE2	71:ST:120:ARG:NE	2.51	0.40
71:ST:128:GLN:H	71:ST:128:GLN:HG3	1.69	0.40
84:D:131:GLN:O	84:D:134:GLU:HG3	2.22	0.40
1:1:133:C:H5''	1:1:134:G:C4	2.56	0.40
1:1:459:C:H4'	1:1:460:U:O4'	2.21	0.40
1:1:539:G:H2'	1:1:540:G:H8	1.87	0.40
1:1:604:G:H2'	1:1:605:G:H8	1.85	0.40
1:1:1157:G:N2	22:LO:89:MET:CE	2.82	0.40
1:1:2642:U:H2'	1:1:2643:C:C6	2.57	0.40
2:2:456:G:OP1	76:SY:112:LYS:NZ	2.52	0.40
2:2:1241:A:O2'	81:Sd:4:GLU:OE1	2.38	0.40
2:2:1343:A:OP2	2:2:1345:A:N6	2.53	0.40
5:A:236:ILE:HA	5:A:252:THR:HA	2.03	0.40
12:LE:199:LYS:HB2	12:LE:199:LYS:HE2	1.96	0.40
15:LH:77:HIS:CD2	15:LH:77:HIS:H	2.38	0.40
17:LJ:20:LEU:HD13	17:LJ:126:MET:HE3	1.97	0.40
35:Lb:61:LYS:HE2	35:Lb:63:GLU:OE1	2.21	0.40
38:Le:114:LYS:HB2	38:Le:114:LYS:HE3	1.83	0.40
41:Lh:60:LEU:HD23	41:Lh:60:LEU:HA	1.89	0.40
51:Ls:48:GLN:NE2	51:Ls:90:ASN:H	2.20	0.40
52:SA:20:LEU:HD23	52:SA:20:LEU:HA	1.91	0.40
64:SM:27:LEU:HA	64:SM:30:LEU:HD22	2.03	0.40
67:SP:65:ILE:O	67:SP:69:ARG:HG2	2.22	0.40
67:SP:119:MET:HB3	70:SS:119:ILE:HD11	2.02	0.40
68:SQ:29:ILE:CD1	68:SQ:65:ILE:HD13	2.47	0.40
69:SR:101:MET:HE3	69:SR:101:MET:HB3	1.73	0.40
71:ST:11:ASP:OD1	71:ST:12:ALA:N	2.55	0.40
76:SY:131:LYS:HB2	76:SY:131:LYS:HE2	1.87	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	
5	A	310/316 (98%)	294 (95%)	16 (5%)	0	100	100
6	B	28/302 (9%)	19 (68%)	9 (32%)	0	100	100
7	C	76/614 (12%)	76 (100%)	0	0	100	100
8	LA	250/254 (98%)	236 (94%)	14 (6%)	0	100	100
9	LB	385/388 (99%)	367 (95%)	17 (4%)	1 (0%)	36	67
10	LC	361/365 (99%)	345 (96%)	16 (4%)	0	100	100
11	LD	298/304 (98%)	291 (98%)	7 (2%)	0	100	100
12	LE	192/200 (96%)	176 (92%)	16 (8%)	0	100	100
13	LF	245/249 (98%)	237 (97%)	8 (3%)	0	100	100
14	LG	233/262 (89%)	228 (98%)	5 (2%)	0	100	100
15	LH	189/192 (98%)	183 (97%)	6 (3%)	0	100	100
16	LI	215/219 (98%)	202 (94%)	13 (6%)	0	100	100
17	LJ	165/173 (95%)	159 (96%)	6 (4%)	0	100	100
18	LK	153/165 (93%)	134 (88%)	17 (11%)	2 (1%)	9	35
19	LL	207/213 (97%)	201 (97%)	6 (3%)	0	100	100
20	LM	139/142 (98%)	136 (98%)	3 (2%)	0	100	100
21	LN	200/203 (98%)	191 (96%)	9 (4%)	0	100	100
22	LO	201/204 (98%)	195 (97%)	6 (3%)	0	100	100
23	LP	184/186 (99%)	175 (95%)	8 (4%)	1 (0%)	24	57
24	LQ	181/213 (85%)	174 (96%)	7 (4%)	0	100	100
25	LR	182/192 (95%)	178 (98%)	4 (2%)	0	100	100
26	LS	171/174 (98%)	166 (97%)	5 (3%)	0	100	100
27	LT	156/160 (98%)	150 (96%)	6 (4%)	0	100	100
28	LU	99/127 (78%)	95 (96%)	4 (4%)	0	100	100
29	LV	133/139 (96%)	131 (98%)	2 (2%)	0	100	100
30	LW	131/161 (81%)	126 (96%)	5 (4%)	0	100	100
31	LX	119/156 (76%)	112 (94%)	7 (6%)	0	100	100
32	LY	132/138 (96%)	128 (97%)	4 (3%)	0	100	100
33	LZ	133/135 (98%)	132 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	La	146/149 (98%)	137 (94%)	9 (6%)	0	100	100
35	Lb	60/65 (92%)	58 (97%)	2 (3%)	0	100	100
36	Lc	95/108 (88%)	95 (100%)	0	0	100	100
37	Ld	110/120 (92%)	107 (97%)	3 (3%)	0	100	100
38	Le	122/131 (93%)	119 (98%)	3 (2%)	0	100	100
39	Lf	105/109 (96%)	99 (94%)	6 (6%)	0	100	100
40	Lg	110/119 (92%)	104 (94%)	6 (6%)	0	100	100
41	Lh	120/126 (95%)	118 (98%)	2 (2%)	0	100	100
42	Li	100/110 (91%)	94 (94%)	6 (6%)	0	100	100
43	Lj	84/95 (88%)	80 (95%)	4 (5%)	0	100	100
44	Lk	74/80 (92%)	72 (97%)	2 (3%)	0	100	100
45	Ll	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
46	Lm	50/128 (39%)	50 (100%)	0	0	100	100
47	Ln	22/25 (88%)	22 (100%)	0	0	100	100
47	Lr	22/25 (88%)	22 (100%)	0	0	100	100
48	Lo	102/106 (96%)	98 (96%)	4 (4%)	0	100	100
49	Lp	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
50	Lq	139/147 (95%)	133 (96%)	6 (4%)	0	100	100
51	Ls	187/312 (60%)	184 (98%)	3 (2%)	0	100	100
52	SA	206/285 (72%)	193 (94%)	13 (6%)	0	100	100
53	SB	230/255 (90%)	216 (94%)	14 (6%)	0	100	100
54	SC	214/263 (81%)	206 (96%)	8 (4%)	0	100	100
55	SD	210/254 (83%)	199 (95%)	11 (5%)	0	100	100
56	SE	259/264 (98%)	248 (96%)	11 (4%)	0	100	100
57	SF	197/212 (93%)	182 (92%)	15 (8%)	0	100	100
58	SG	230/239 (96%)	221 (96%)	9 (4%)	0	100	100
59	SH	193/203 (95%)	185 (96%)	8 (4%)	0	100	100
60	SI	199/202 (98%)	192 (96%)	7 (4%)	0	100	100
61	SJ	177/190 (93%)	171 (97%)	6 (3%)	0	100	100
62	SK	87/159 (55%)	87 (100%)	0	0	100	100
63	SL	148/161 (92%)	146 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
64	SM	116/144 (81%)	104 (90%)	12 (10%)	0	100	100
65	SN	148/151 (98%)	144 (97%)	4 (3%)	0	100	100
66	SO	133/150 (89%)	127 (96%)	6 (4%)	0	100	100
67	SP	113/153 (74%)	108 (96%)	5 (4%)	0	100	100
68	SQ	136/143 (95%)	130 (96%)	6 (4%)	0	100	100
69	SR	126/143 (88%)	123 (98%)	3 (2%)	0	100	100
70	SS	135/156 (86%)	123 (91%)	12 (9%)	0	100	100
71	ST	140/153 (92%)	135 (96%)	5 (4%)	0	100	100
72	SU	101/116 (87%)	94 (93%)	7 (7%)	0	100	100
73	SV	84/98 (86%)	82 (98%)	2 (2%)	0	100	100
74	SW	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
75	SX	140/145 (97%)	131 (94%)	9 (6%)	0	100	100
76	SY	130/136 (96%)	128 (98%)	2 (2%)	0	100	100
77	SZ	67/99 (68%)	66 (98%)	1 (2%)	0	100	100
78	Sa	102/119 (86%)	99 (97%)	3 (3%)	0	100	100
79	Sb	79/82 (96%)	75 (95%)	4 (5%)	0	100	100
80	Sc	59/68 (87%)	54 (92%)	5 (8%)	0	100	100
81	Sd	50/56 (89%)	48 (96%)	2 (4%)	0	100	100
82	Se	42/61 (69%)	39 (93%)	3 (7%)	0	100	100
83	Sf	71/154 (46%)	62 (87%)	9 (13%)	0	100	100
84	D	369/371 (100%)	365 (99%)	4 (1%)	0	100	100
All	All	12071/14159 (85%)	11564 (96%)	503 (4%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
18	LK	88	PRO
18	LK	22	VAL
23	LP	163	VAL
9	LB	257	HIS

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	
5	A	271/274 (99%)	271 (100%)	0	100	100
6	B	21/224 (9%)	21 (100%)	0	100	100
7	C	68/511 (13%)	68 (100%)	0	100	100
8	LA	196/198 (99%)	196 (100%)	0	100	100
9	LB	327/328 (100%)	327 (100%)	0	100	100
10	LC	284/285 (100%)	284 (100%)	0	100	100
11	LD	250/253 (99%)	249 (100%)	1 (0%)	84	86
12	LE	162/166 (98%)	162 (100%)	0	100	100
13	LF	213/215 (99%)	213 (100%)	0	100	100
14	LG	203/222 (91%)	203 (100%)	0	100	100
15	LH	168/169 (99%)	168 (100%)	0	100	100
16	LI	182/183 (100%)	182 (100%)	0	100	100
17	LJ	145/150 (97%)	145 (100%)	0	100	100
19	LL	172/176 (98%)	172 (100%)	0	100	100
20	LM	116/117 (99%)	116 (100%)	0	100	100
21	LN	179/180 (99%)	179 (100%)	0	100	100
22	LO	161/162 (99%)	161 (100%)	0	100	100
23	LP	151/151 (100%)	151 (100%)	0	100	100
24	LQ	155/178 (87%)	155 (100%)	0	100	100
25	LR	153/160 (96%)	153 (100%)	0	100	100
26	LS	153/154 (99%)	153 (100%)	0	100	100
27	LT	134/135 (99%)	134 (100%)	0	100	100
28	LU	89/108 (82%)	89 (100%)	0	100	100
29	LV	99/102 (97%)	99 (100%)	0	100	100
30	LW	107/125 (86%)	107 (100%)	0	100	100
31	LX	108/129 (84%)	108 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	LY	117/119 (98%)	116 (99%)	1 (1%)	70	80
33	LZ	121/121 (100%)	121 (100%)	0	100	100
34	La	121/122 (99%)	121 (100%)	0	100	100
35	Lb	53/55 (96%)	53 (100%)	0	100	100
36	Lc	78/88 (89%)	78 (100%)	0	100	100
37	Ld	97/105 (92%)	97 (100%)	0	100	100
38	Le	107/114 (94%)	107 (100%)	0	100	100
39	Lf	88/90 (98%)	88 (100%)	0	100	100
40	Lg	97/102 (95%)	97 (100%)	0	100	100
41	Lh	109/112 (97%)	109 (100%)	0	100	100
42	Li	86/93 (92%)	86 (100%)	0	100	100
43	Lj	70/78 (90%)	70 (100%)	0	100	100
44	Lk	73/77 (95%)	73 (100%)	0	100	100
45	Ll	45/46 (98%)	45 (100%)	0	100	100
46	Lm	47/115 (41%)	47 (100%)	0	100	100
47	Ln	22/23 (96%)	22 (100%)	0	100	100
47	Lr	22/23 (96%)	22 (100%)	0	100	100
48	Lo	88/90 (98%)	88 (100%)	0	100	100
49	Lp	73/74 (99%)	73 (100%)	0	100	100
50	Lq	109/112 (97%)	109 (100%)	0	100	100
51	Ls	155/255 (61%)	154 (99%)	1 (1%)	78	83
52	SA	178/225 (79%)	178 (100%)	0	100	100
53	SB	203/223 (91%)	203 (100%)	0	100	100
54	SC	181/206 (88%)	181 (100%)	0	100	100
55	SD	182/206 (88%)	181 (100%)	1 (0%)	81	85
56	SE	219/221 (99%)	219 (100%)	0	100	100
57	SF	167/178 (94%)	167 (100%)	0	100	100
58	SG	198/204 (97%)	198 (100%)	0	100	100
59	SH	169/177 (96%)	169 (100%)	0	100	100
60	SI	163/164 (99%)	163 (100%)	0	100	100
61	SJ	154/162 (95%)	154 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
62	SK	77/126 (61%)	77 (100%)	0	100	100
63	SL	133/143 (93%)	133 (100%)	0	100	100
64	SM	101/121 (84%)	101 (100%)	0	100	100
65	SN	129/130 (99%)	129 (100%)	0	100	100
66	SO	102/117 (87%)	102 (100%)	0	100	100
67	SP	99/132 (75%)	99 (100%)	0	100	100
68	SQ	111/115 (96%)	110 (99%)	1 (1%)	70	80
69	SR	119/131 (91%)	119 (100%)	0	100	100
70	SS	120/135 (89%)	120 (100%)	0	100	100
71	ST	114/124 (92%)	114 (100%)	0	100	100
72	SU	93/103 (90%)	93 (100%)	0	100	100
73	SV	69/80 (86%)	69 (100%)	0	100	100
74	SW	112/113 (99%)	112 (100%)	0	100	100
75	SX	113/116 (97%)	113 (100%)	0	100	100
76	SY	112/115 (97%)	112 (100%)	0	100	100
77	SZ	60/80 (75%)	60 (100%)	0	100	100
78	Sa	91/103 (88%)	91 (100%)	0	100	100
79	Sb	70/71 (99%)	70 (100%)	0	100	100
80	Sc	54/61 (88%)	54 (100%)	0	100	100
81	Sd	43/46 (94%)	43 (100%)	0	100	100
82	Se	37/50 (74%)	37 (100%)	0	100	100
83	Sf	66/139 (48%)	66 (100%)	0	100	100
84	D	315/315 (100%)	315 (100%)	0	100	100
All	All	10199/11701 (87%)	10194 (100%)	5 (0%)	100	100

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	LD	302	GLN
32	LY	115	GLU
51	Ls	177	ASN
55	SD	177	HIS
68	SQ	83	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (90) such sidechains are listed below:

Mol	Chain	Res	Type
5	A	64	HIS
5	A	117	ASN
5	A	119	GLN
8	LA	8	GLN
9	LB	260	HIS
10	LC	60	GLN
10	LC	141	HIS
10	LC	203	HIS
10	LC	284	GLN
13	LF	82	HIS
13	LF	178	ASN
13	LF	206	ASN
14	LG	246	GLN
16	LI	14	ASN
16	LI	73	ASN
17	LJ	63	ASN
17	LJ	96	ASN
20	LM	5	ASN
21	LN	91	GLN
23	LP	97	ASN
23	LP	116	HIS
24	LQ	179	HIS
25	LR	7	GLN
25	LR	91	GLN
25	LR	118	HIS
26	LS	62	ASN
26	LS	74	ASN
27	LT	22	HIS
27	LT	54	HIS
28	LU	24	ASN
29	LV	76	HIS
29	LV	100	ASN
32	LY	109	HIS
33	LZ	30	GLN
33	LZ	126	ASN
35	Lb	27	GLN
37	Ld	25	HIS
37	Ld	64	ASN
37	Ld	105	ASN
38	Le	21	HIS
39	Lf	26	HIS

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Mol	Chain	Res	Type
39	Lf	58	GLN
40	Lg	111	GLN
41	Lh	64	ASN
42	Li	72	ASN
44	Lk	32	GLN
44	Lk	41	GLN
44	Lk	67	GLN
45	Ll	4	HIS
48	Lo	90	HIS
51	Ls	32	ASN
52	SA	19	GLN
52	SA	49	ASN
53	SB	21	GLN
53	SB	74	GLN
55	SD	25	ASN
55	SD	85	ASN
55	SD	162	HIS
55	SD	224	GLN
55	SD	228	GLN
56	SE	9	GLN
57	SF	90	ASN
58	SG	13	GLN
58	SG	119	GLN
59	SH	12	ASN
59	SH	18	ASN
60	SI	44	HIS
60	SI	53	HIS
61	SJ	121	HIS
61	SJ	137	GLN
62	SK	31	HIS
65	SN	62	GLN
65	SN	78	ASN
67	SP	46	HIS
67	SP	73	GLN
68	SQ	83	GLN
69	SR	48	ASN
70	SS	26	GLN
70	SS	136	GLN
71	ST	130	GLN
72	SU	29	GLN
74	SW	15	ASN
75	SX	65	ASN

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Mol	Chain	Res	Type
79	Sb	61	ASN
79	Sb	65	GLN
82	Se	5	HIS
83	Sf	136	GLN
84	D	201	ASN
84	D	399	ASN
84	D	400	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3188/3337 (95%)	477 (14%)	39 (1%)
2	2	1761/1796 (98%)	316 (17%)	34 (1%)
3	3	118/120 (98%)	9 (7%)	1 (0%)
4	4	155/156 (99%)	20 (12%)	0
All	All	5222/5409 (96%)	822 (15%)	74 (1%)

All (822) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	27	A
1	1	41	A
1	1	44	A
1	1	50	A
1	1	60	G
1	1	61	A
1	1	66	A
1	1	67	A
1	1	93	G
1	1	97	G
1	1	111	G
1	1	114	C
1	1	117	A
1	1	118	U
1	1	119	U
1	1	123	A
1	1	132	U
1	1	133	C
1	1	134	G
1	1	135	G
1	1	144	G

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Mol	Chain	Res	Type
1	1	152	G
1	1	153	A
1	1	165	G
1	1	170	A
1	1	179	C
1	1	181	G
1	1	184	U
1	1	185	U
1	1	204	C
1	1	212	G
1	1	213	A
1	1	214	G
1	1	215	A
1	1	225	A
1	1	234	C
1	1	251	U
1	1	262	G
1	1	276	G
1	1	277	A
1	1	279	U
1	1	288	A
1	1	308	C
1	1	316	A
1	1	332	C
1	1	343	C
1	1	363	U
1	1	369	G
1	1	385	G
1	1	391	U
1	1	392	A
1	1	394	C
1	1	395	A
1	1	396	C
1	1	414	G
1	1	415	A
1	1	422	U
1	1	432	C
1	1	434	U
1	1	447	U
1	1	460	U
1	1	461	C
1	1	470	A

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Mol	Chain	Res	Type
1	1	471	C
1	1	485	G
1	1	489	A
1	1	511	U
1	1	512	A
1	1	527	G
1	1	538	G
1	1	539	G
1	1	547	A
1	1	549	A
1	1	559	G
1	1	560	U
1	1	570	G
1	1	580	A
1	1	583	A
1	1	591	C
1	1	592	U
1	1	593	G
1	1	597	G
1	1	599	A
1	1	608	U
1	1	609	A
1	1	610	A
1	1	624	C
1	1	637	A
1	1	645	A
1	1	648	A
1	1	665	A
1	1	669	U
1	1	679	A
1	1	697	A
1	1	700	G
1	1	703	A
1	1	704	A
1	1	715	A
1	1	722	G
1	1	748	U
1	1	749	U
1	1	758	U
1	1	759	U
1	1	763	G
1	1	767	G

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Mol	Chain	Res	Type
1	1	783	A
1	1	788	A
1	1	799	A
1	1	812	A
1	1	843	C
1	1	856	U
1	1	861	U
1	1	862	G
1	1	878	A
1	1	889	G
1	1	890	G
1	1	896	A
1	1	898	G
1	1	899	A
1	1	919	G
1	1	926	A
1	1	941	C
1	1	942	U
1	1	943	C
1	1	959	A
1	1	960	C
1	1	961	C
1	1	962	U
1	1	984	A
1	1	992	G
1	1	998	C
1	1	999	G
1	1	1007	U
1	1	1008	U
1	1	1010	U
1	1	1011	U
1	1	1012	A
1	1	1015	C
1	1	1017	U
1	1	1030	A
1	1	1032	C
1	1	1047	A
1	1	1048	A
1	1	1055	G
1	1	1064	C
1	1	1065	U
1	1	1068	A

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Mol	Chain	Res	Type
1	1	1076	A
1	1	1077	U
1	1	1079	C
1	1	1080	G
1	1	1081	A
1	1	1086	A
1	1	1087	U
1	1	1088	C
1	1	1100	G
1	1	1114	G
1	1	1127	U
1	1	1131	G
1	1	1134	U
1	1	1136	A
1	1	1142	A
1	1	1161	G
1	1	1163	G
1	1	1164	U
1	1	1165	G
1	1	1175	C
1	1	1184	C
1	1	1192	G
1	1	1205	G
1	1	1206	A
1	1	1218	U
1	1	1219	G
1	1	1222	C
1	1	1224	U
1	1	1228	A
1	1	1229	G
1	1	1231	C
1	1	1241	U
1	1	1245	G
1	1	1246	A
1	1	1268	G
1	1	1290	G
1	1	1291	A
1	1	1292	U
1	1	1296	G
1	1	1313	A
1	1	1314	U
1	1	1331	A

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Mol	Chain	Res	Type
1	1	1332	G
1	1	1333	A
1	1	1335	A
1	1	1336	C
1	1	1337	G
1	1	1339	U
1	1	1369	A
1	1	1382	A
1	1	1383	G
1	1	1402	A
1	1	1404	G
1	1	1417	G
1	1	1420	C
1	1	1433	G
1	1	1458	G
1	1	1464	A
1	1	1465	A
1	1	1466	G
1	1	1485	G
1	1	1491	C
1	1	1495	U
1	1	1506	U
1	1	1516	U
1	1	1537	U
1	1	1538	U
1	1	1539	C
1	1	1540	A
1	1	1543	G
1	1	1545	G
1	1	1552	G
1	1	1554	G
1	1	1555	C
1	1	1560	U
1	1	1561	G
1	1	1562	U
1	1	1563	G
1	1	1567	A
1	1	1585	A
1	1	1587	U
1	1	1588	C
1	1	1609	U
1	1	1611	C

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Mol	Chain	Res	Type
1	1	1619	C
1	1	1622	A
1	1	1623	A
1	1	1624	C
1	1	1625	U
1	1	1637	C
1	1	1685	U
1	1	1696	A
1	1	1697	C
1	1	1704	U
1	1	1727	G
1	1	1730	A
1	1	1731	G
1	1	1745	U
1	1	1746	G
1	1	1750	G
1	1	1760	G
1	1	1777	A
1	1	1794	A
1	1	1796	A
1	1	1797	A
1	1	1798	U
1	1	1799	U
1	1	1800	C
1	1	1801	U
1	1	1819	A
1	1	1820	U
1	1	1821	A
1	1	1822	A
1	1	1826	C
1	1	1829	C
1	1	1830	A
1	1	1858	G
1	1	1859	A
1	1	1860	U
1	1	1866	A
1	1	1886	G
1	1	1887	C
1	1	1888	A
1	1	1906	C
1	1	1933	G
1	1	1936	A

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Mol	Chain	Res	Type
1	1	2045	G
1	1	2048	U
1	1	2050	C
1	1	2054	U
1	1	2055	A
1	1	2063	A
1	1	2065	U
1	1	2076	A
1	1	2084	G
1	1	2085	G
1	1	2094	A
1	1	2107	A
1	1	2121	A
1	1	2132	G
1	1	2133	U
1	1	2134	G
1	1	2139	U
1	1	2151	A
1	1	2168	U
1	1	2170	A
1	1	2171	A
1	1	2172	U
1	1	2173	G
1	1	2192	A
1	1	2207	A
1	1	2212	G
1	1	2216	G
1	1	2219	A
1	1	2221	U
1	1	2228	C
1	1	2233	A
1	1	2235	G
1	1	2236	G
1	1	2242	A
1	1	2244	A
1	1	2248	C
1	1	2251	G
1	1	2270	G
1	1	2273	U
1	1	2276	A
1	1	2278	G
1	1	2281	U

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Mol	Chain	Res	Type
1	1	2297	U
1	1	2299	U
1	1	2335	A
1	1	2336	A
1	1	2337	C
1	1	2338	G
1	1	2339	G
1	1	2356	G
1	1	2360	A
1	1	2364	A
1	1	2365	A
1	1	2366	G
1	1	2367	A
1	1	2374	U
1	1	2382	A
1	1	2464	U
1	1	2465	U
1	1	2474	A
1	1	2477	U
1	1	2478	A
1	1	2487	A
1	1	2488	G
1	1	2489	C
1	1	2492	G
1	1	2497	G
1	1	2501	U
1	1	2502	G
1	1	2503	C
1	1	2504	G
1	1	2510	C
1	1	2513	C
1	1	2516	G
1	1	2521	A
1	1	2529	U
1	1	2530	C
1	1	2531	G
1	1	2532	C
1	1	2533	G
1	1	2543	G
1	1	2544	G
1	1	2552	A
1	1	2553	C

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Mol	Chain	Res	Type
1	1	2565	G
1	1	2566	G
1	1	2573	G
1	1	2578	OMG
1	1	2585	A
1	1	2611	U
1	1	2615	A
1	1	2622	G
1	1	2633	A
1	1	2636	G
1	1	2648	A
1	1	2650	A
1	1	2653	A
1	1	2655	A
1	1	2663	A
1	1	2673	G
1	1	2687	G
1	1	2688	U
1	1	2711	U
1	1	2712	G
1	1	2714	C
1	1	2721	A
1	1	2731	C
1	1	2732	C
1	1	2736	G
1	1	2737	A
1	1	2755	G
1	1	2758	A
1	1	2759	G
1	1	2760	A
1	1	2763	A
1	1	2769	C
1	1	2776	A
1	1	2777	U
1	1	2778	A
1	1	2788	U
1	1	2798	G
1	1	2801	U
1	1	2802	U
1	1	2803	C
1	1	2804	A
1	1	2828	U

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Mol	Chain	Res	Type
1	1	2830	G
1	1	2831	A
1	1	2834	U
1	1	2846	A
1	1	2858	C
1	1	2863	U
1	1	2882	U
1	1	2894	U
1	1	2895	A
1	1	2901	C
1	1	2906	G
1	1	2931	G
1	1	2942	C
1	1	2970	A
1	1	3007	A
1	1	3008	U
1	1	3014	U
1	1	3017	G
1	1	3036	G
1	1	3044	A
1	1	3050	C
1	1	3051	C
1	1	3059	G
1	1	3080	A
1	1	3088	A
1	1	3089	U
1	1	3100	A
1	1	3101	C
1	1	3112	U
1	1	3119	A
1	1	3122	U
1	1	3127	G
1	1	3128	A
1	1	3130	G
1	1	3131	U
1	1	3132	A
1	1	3135	A
1	1	3141	G
1	1	3146	C
1	1	3147	G
1	1	3162	C
1	1	3163	A

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Mol	Chain	Res	Type
1	1	3164	G
1	1	3170	U
1	1	3188	G
1	1	3189	U
1	1	3200	A
1	1	3201	A
1	1	3211	U
1	1	3214	A
1	1	3218	U
1	1	3219	A
1	1	3223	A
1	1	3225	G
1	1	3227	G
1	1	3229	G
1	1	3230	G
1	1	3231	G
1	1	3235	A
1	1	3245	C
1	1	3248	A
1	1	3257	A
1	1	3258	U
1	1	3259	G
1	1	3260	U
1	1	3261	G
1	1	3282	U
1	1	3286	G
1	1	3292	U
1	1	3299	U
1	1	3309	U
1	1	3310	G
1	1	3319	C
1	1	3324	C
1	1	3325	U
1	1	3331	U
1	1	3332	A
1	1	3333	G
2	2	17	C
2	2	25	C
2	2	26	A
2	2	27	U
2	2	34	G
2	2	42	G

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Mol	Chain	Res	Type
2	2	47	A
2	2	57	G
2	2	68	A
2	2	69	G
2	2	73	U
2	2	74	U
2	2	75	A
2	2	76	U
2	2	77	A
2	2	103	A
2	2	113	C
2	2	115	U
2	2	126	G
2	2	127	U
2	2	138	A
2	2	155	U
2	2	156	U
2	2	174	U
2	2	175	G
2	2	176	A
2	2	184	G
2	2	185	A
2	2	186	C
2	2	187	U
2	2	190	G
2	2	192	A
2	2	195	G
2	2	210	A
2	2	212	U
2	2	213	A
2	2	214	A
2	2	215	A
2	2	216	A
2	2	221	A
2	2	222	U
2	2	223	G
2	2	224	C
2	2	231	G
2	2	232	G
2	2	234	C
2	2	236	U
2	2	237	U

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Mol	Chain	Res	Type
2	2	247	C
2	2	258	C
2	2	262	A
2	2	268	A
2	2	269	C
2	2	270	G
2	2	274	U
2	2	275	U
2	2	277	C
2	2	296	A
2	2	311	C
2	2	313	A
2	2	317	U
2	2	319	G
2	2	321	C
2	2	326	G
2	2	334	G
2	2	335	C
2	2	338	G
2	2	349	A
2	2	353	G
2	2	356	A
2	2	357	A
2	2	358	C
2	2	367	A
2	2	377	C
2	2	396	A
2	2	397	A
2	2	399	C
2	2	401	G
2	2	414	A
2	2	415	G
2	2	421	C
2	2	422	A
2	2	423	G
2	2	431	G
2	2	436	U
2	2	441	C
2	2	445	C
2	2	451	A
2	2	452	C
2	2	465	A

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Mol	Chain	Res	Type
2	2	472	A
2	2	474	A
2	2	490	U
2	2	491	U
2	2	492	C
2	2	493	G
2	2	502	A
2	2	505	U
2	2	510	U
2	2	511	G
2	2	512	A
2	2	535	A
2	2	536	G
2	2	537	G
2	2	538	A
2	2	539	A
2	2	540	C
2	2	541	A
2	2	552	A
2	2	553	A
2	2	554	G
2	2	555	U
2	2	556	C
2	2	562	C
2	2	567	A
2	2	571	G
2	2	576	A
2	2	577	A
2	2	579	U
2	2	591	A
2	2	592	G
2	2	608	U
2	2	611	A
2	2	612	G
2	2	616	A
2	2	617	A
2	2	619	A
2	2	620	A
2	2	621	G
2	2	636	U
2	2	645	G
2	2	677	U

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Mol	Chain	Res	Type
2	2	679	G
2	2	686	C
2	2	688	U
2	2	689	U
2	2	690	U
2	2	692	C
2	2	693	U
2	2	705	G
2	2	725	G
2	2	726	U
2	2	727	C
2	2	729	G
2	2	731	G
2	2	732	A
2	2	741	U
2	2	754	A
2	2	755	A
2	2	764	G
2	2	765	C
2	2	773	A
2	2	774	G
2	2	779	A
2	2	780	U
2	2	781	G
2	2	787	A
2	2	792	U
2	2	793	U
2	2	809	A
2	2	810	A
2	2	819	G
2	2	821	G
2	2	824	U
2	2	828	U
2	2	829	U
2	2	830	U
2	2	832	G
2	2	833	U
2	2	861	A
2	2	884	U
2	2	896	A
2	2	910	U
2	2	911	G

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Mol	Chain	Res	Type
2	2	912	G
2	2	931	A
2	2	933	U
2	2	940	G
2	2	949	A
2	2	957	U
2	2	958	U
2	2	964	A
2	2	982	G
2	2	988	C
2	2	990	A
2	2	991	A
2	2	1002	U
2	2	1003	A
2	2	1024	A
2	2	1026	C
2	2	1037	A
2	2	1055	A
2	2	1056	U
2	2	1057	U
2	2	1058	U
2	2	1059	U
2	2	1079	C
2	2	1088	A
2	2	1089	A
2	2	1090	A
2	2	1093	G
2	2	1094	U
2	2	1095	U
2	2	1097	G
2	2	1135	A
2	2	1140	A
2	2	1147	G
2	2	1155	C
2	2	1156	C
2	2	1157	A
2	2	1166	G
2	2	1182	U
2	2	1191	A
2	2	1193	A
2	2	1194	C
2	2	1196	G

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Mol	Chain	Res	Type
2	2	1197	G
2	2	1214	A
2	2	1215	G
2	2	1223	G
2	2	1224	A
2	2	1225	G
2	2	1226	G
2	2	1227	A
2	2	1228	U
2	2	1237	U
2	2	1238	G
2	2	1240	G
2	2	1241	A
2	2	1242	G
2	2	1243	C
2	2	1248	U
2	2	1249	C
2	2	1252	G
2	2	1253	A
2	2	1254	U
2	2	1255	U
2	2	1282	U
2	2	1283	U
2	2	1311	U
2	2	1312	U
2	2	1313	G
2	2	1318	A
2	2	1338	G
2	2	1341	A
2	2	1342	A
2	2	1344	U
2	2	1357	C
2	2	1358	U
2	2	1360	G
2	2	1379	A
2	2	1387	U
2	2	1409	U
2	2	1411	U
2	2	1421	A
2	2	1423	A
2	2	1424	G
2	2	1439	U

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Mol	Chain	Res	Type
2	2	1441	G
2	2	1444	G
2	2	1455	C
2	2	1467	A
2	2	1474	G
2	2	1478	C
2	2	1482	G
2	2	1486	A
2	2	1487	C
2	2	1489	C
2	2	1499	A
2	2	1502	G
2	2	1512	A
2	2	1517	G
2	2	1519	U
2	2	1532	G
2	2	1533	C
2	2	1534	U
2	2	1538	G
2	2	1553	U
2	2	1555	A
2	2	1564	C
2	2	1565	A
2	2	1570	G
2	2	1580	G
2	2	1586	G
2	2	1597	G
2	2	1612	G
2	2	1615	C
2	2	1617	U
2	2	1627	A
2	2	1631	A
2	2	1653	U
2	2	1654	G
2	2	1684	C
2	2	1699	C
2	2	1708	A
2	2	1711	G
2	2	1712	C
2	2	1713	C
2	2	1726	A
2	2	1752	A

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Mol	Chain	Res	Type
2	2	1753	G
2	2	1756	G
2	2	1762	A
2	2	1763	G
2	2	1765	U
2	2	1766	C
2	2	1776	G
2	2	1778	A
2	2	1779	C
2	2	1788	G
2	2	1789	G
2	2	1790	A
2	2	1791	U
2	2	1792	C
2	2	1795	U
2	2	1796	U
3	3	7	G
3	3	54	U
3	3	55	A
3	3	65	G
3	3	73	U
3	3	90	G
3	3	92	C
3	3	101	A
3	3	111	G
4	4	23	U
4	4	34	U
4	4	35	C
4	4	48	A
4	4	59	A
4	4	62	A
4	4	63	G
4	4	79	A
4	4	81	U
4	4	82	U
4	4	83	C
4	4	87	G
4	4	88	A
4	4	95	G
4	4	104	A
4	4	106	C
4	4	111	A

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Mol	Chain	Res	Type
4	4	113	U
4	4	125	U
4	4	138	A

All (74) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	133	C
1	1	250	C
1	1	275	G
1	1	431	A
1	1	484	A
1	1	609	A
1	1	703	A
1	1	898	G
1	1	960	C
1	1	1016	U
1	1	1047	A
1	1	1064	C
1	1	1267	C
1	1	1290	G
1	1	1338	A
1	1	1587	U
1	1	1796	A
1	1	2064	C
1	1	2075	U
1	1	2167	C
1	1	2172	U
1	1	2227	U
1	1	2232	U
1	1	2503	C
1	1	2532	C
1	1	2552	A
1	1	2621	G
1	1	2731	C
1	1	2801	U
1	1	3079	U
1	1	3121	G
1	1	3163	A
1	1	3210	U
1	1	3224	C
1	1	3230	G

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Mol	Chain	Res	Type
1	1	3258	U
1	1	3281	G
1	1	3298	U
1	1	3332	A
2	2	102	A
2	2	184	G
2	2	211	U
2	2	231	G
2	2	233	G
2	2	269	C
2	2	352	G
2	2	414	A
2	2	509	A
2	2	539	A
2	2	552	A
2	2	555	U
2	2	644	A
2	2	678	G
2	2	726	U
2	2	740	C
2	2	754	A
2	2	792	U
2	2	832	G
2	2	1094	U
2	2	1165	U
2	2	1193	A
2	2	1224	A
2	2	1241	A
2	2	1252	G
2	2	1282	U
2	2	1341	A
2	2	1378	U
2	2	1477	C
2	2	1531	U
2	2	1564	C
2	2	1569	A
2	2	1616	C
2	2	1653	U
3	3	72	G

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

3 non-standard protein/DNA/RNA residues are modelled in this entry.

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
2	B8N	2	1188	2	25,29,30	2.56	5 (20%)	28,42,45	1.37	4 (14%)
22	SAC	LO	2	22	7,8,9	1.04	0	7,9,11	1.03	0
1	OMG	1	2578	1	23,26,27	0.47	0	32,38,41	0.47	0

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
2	B8N	2	1188	2	-	1/16/34/35	0/2/2/2
22	SAC	LO	2	22	-	3/7/8/10	-
1	OMG	1	2578	1	-	2/9/27/28	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1188	B8N	O4-C4	9.57	1.42	1.23
2	2	1188	B8N	C2-N3	-3.76	1.32	1.38
2	2	1188	B8N	C4-N3	-3.70	1.33	1.40
2	2	1188	B8N	C4-C5	-3.39	1.39	1.47
2	2	1188	B8N	C6-C5	3.18	1.39	1.35

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1188	B8N	N3-C2-N1	3.49	120.98	116.72
2	2	1188	B8N	C4-N3-C2	-3.19	121.69	125.62
2	2	1188	B8N	C1'-C5-C4	2.65	121.63	117.61
2	2	1188	B8N	O4'-C1'-C2'	2.29	108.31	105.15

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
22	LO	2	SAC	O-C-CA-CB
22	LO	2	SAC	N-CA-CB-OG
22	LO	2	SAC	C-CA-CB-OG
1	1	2578	OMG	O4'-C4'-C5'-O5'
2	2	1188	B8N	C31-C32-C33-C34
1	1	2578	OMG	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

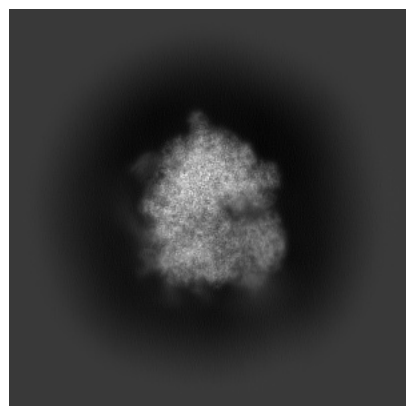
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17004. These allow visual inspection of the internal detail of the map and identification of artifacts.

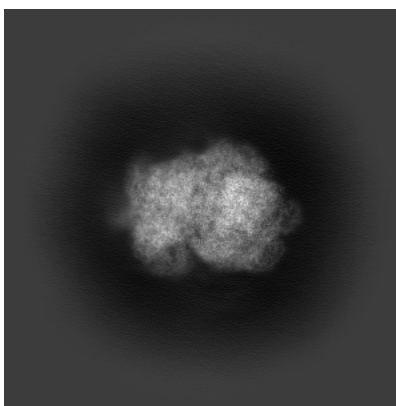
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

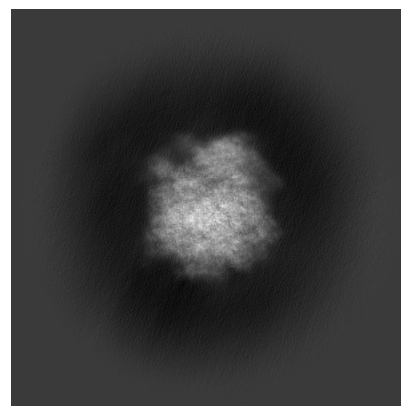
6.1.1 Primary map



X

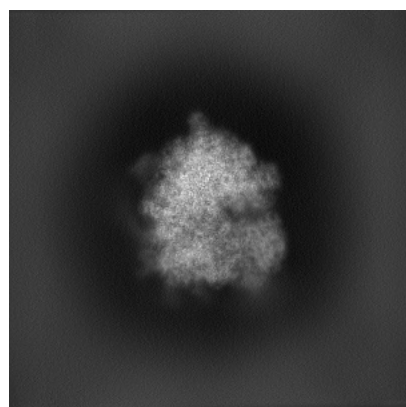


Y

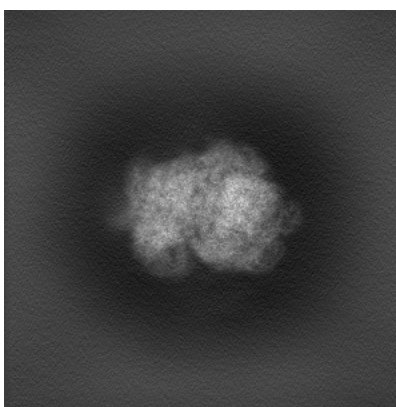


Z

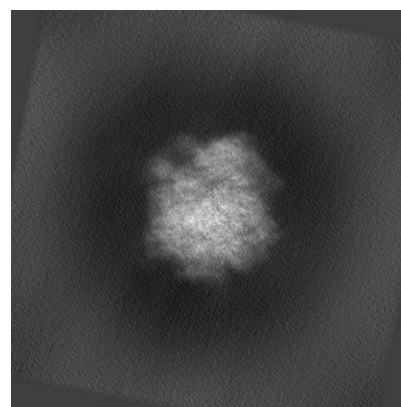
6.1.2 Raw map



X



Y

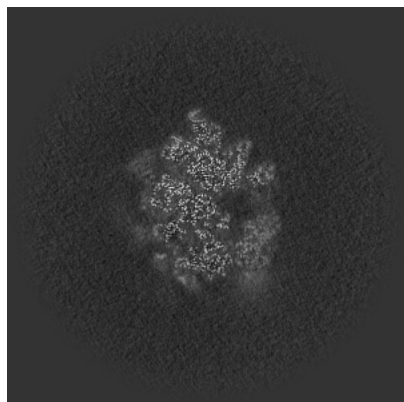


Z

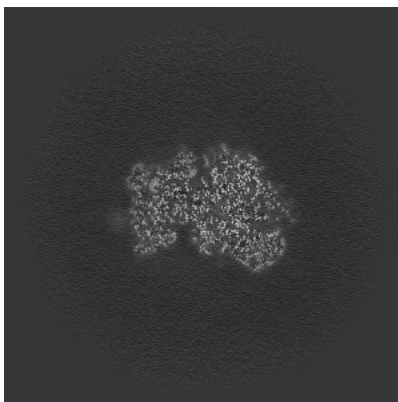
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

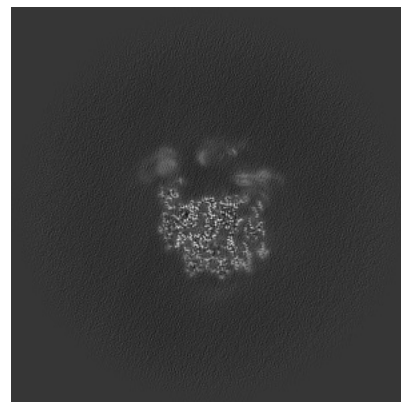
6.2.1 Primary map



X Index: 300

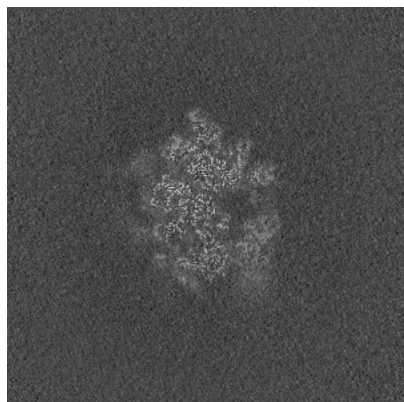


Y Index: 300

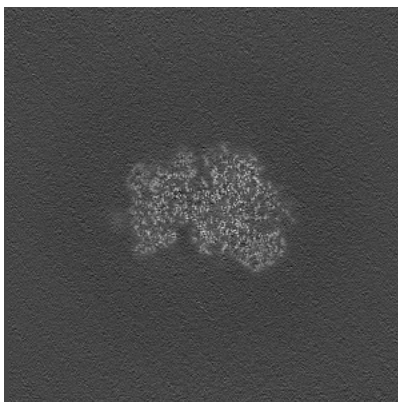


Z Index: 300

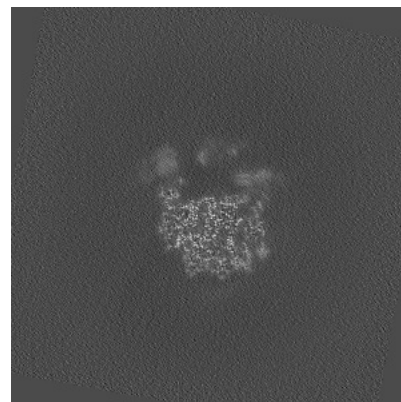
6.2.2 Raw map



X Index: 300



Y Index: 300

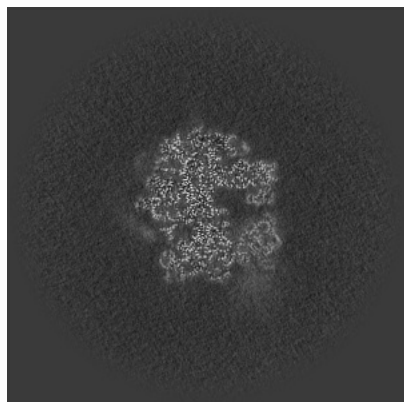


Z Index: 300

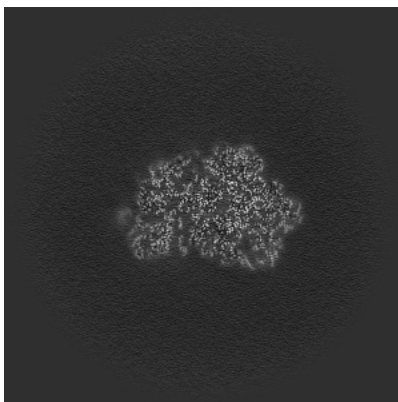
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

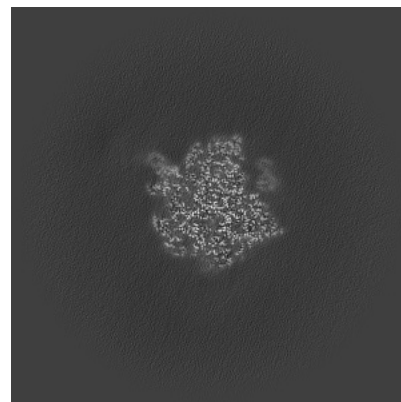
6.3.1 Primary map



X Index: 317

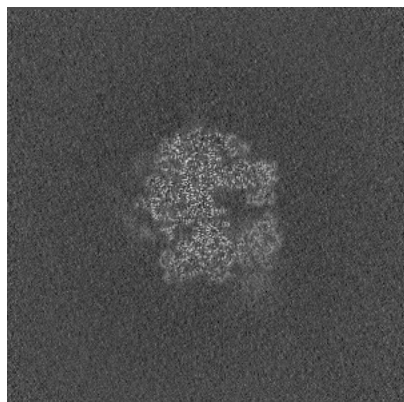


Y Index: 286

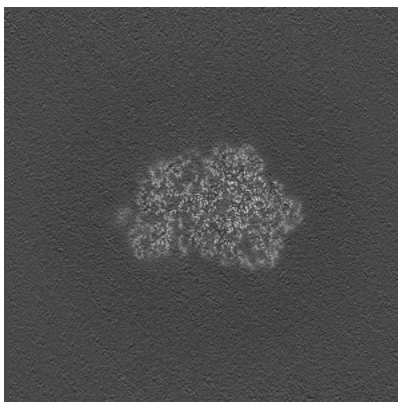


Z Index: 337

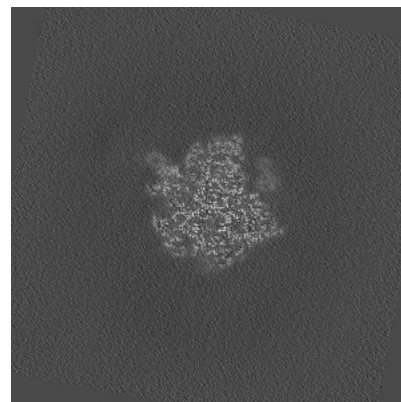
6.3.2 Raw map



X Index: 317



Y Index: 286

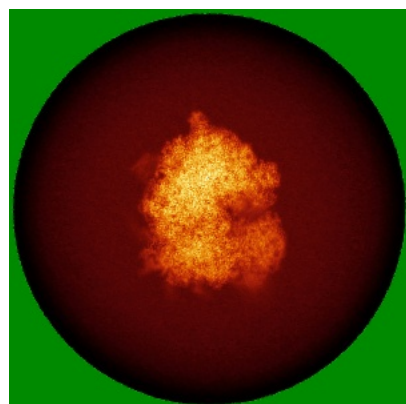


Z Index: 337

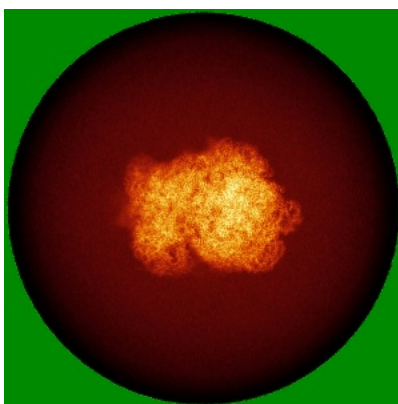
The images above show the largest variance slices of the map in three orthogonal directions.

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

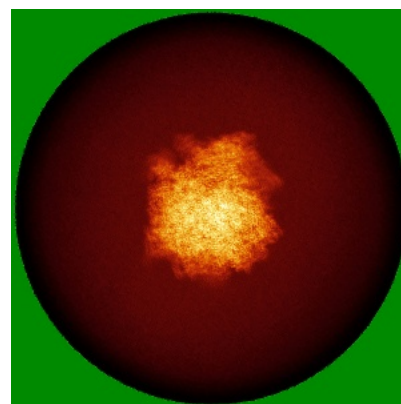
6.4.1 Primary map



X

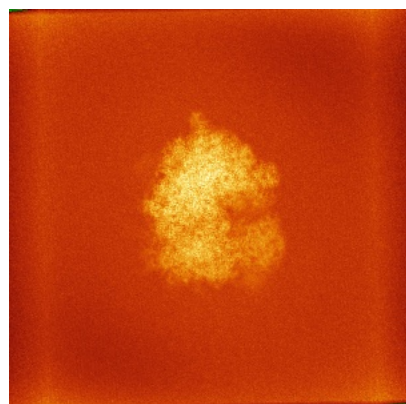


Y

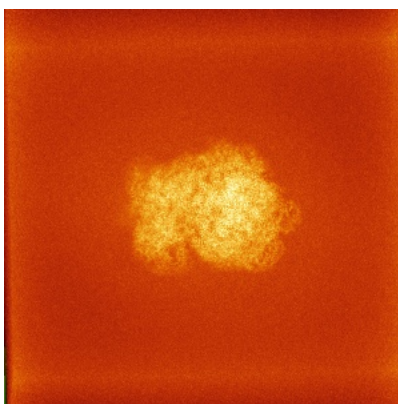


Z

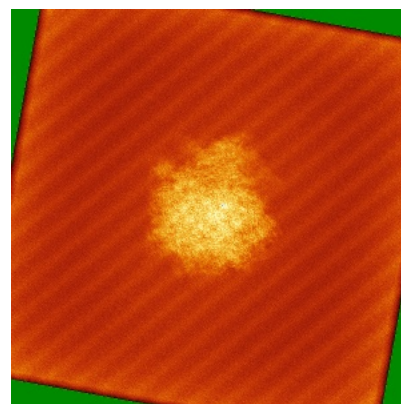
6.4.2 Raw map



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](#)

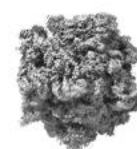
6.5.1 Primary map



X



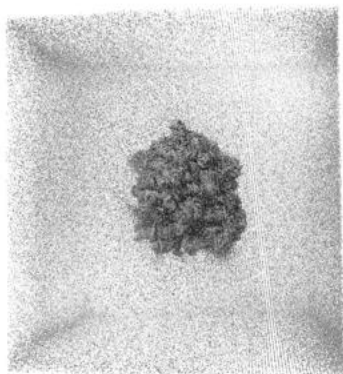
Y



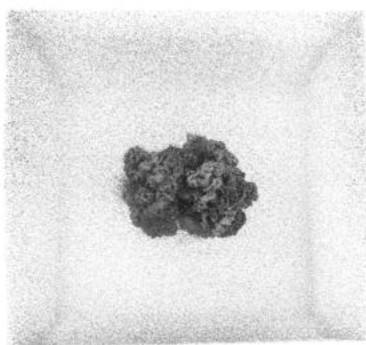
Z

The images above show the 3D surface view of the map at the recommended contour level 0.22. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

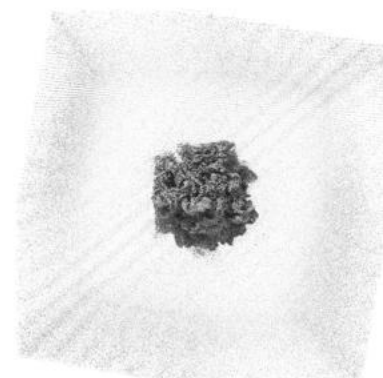
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

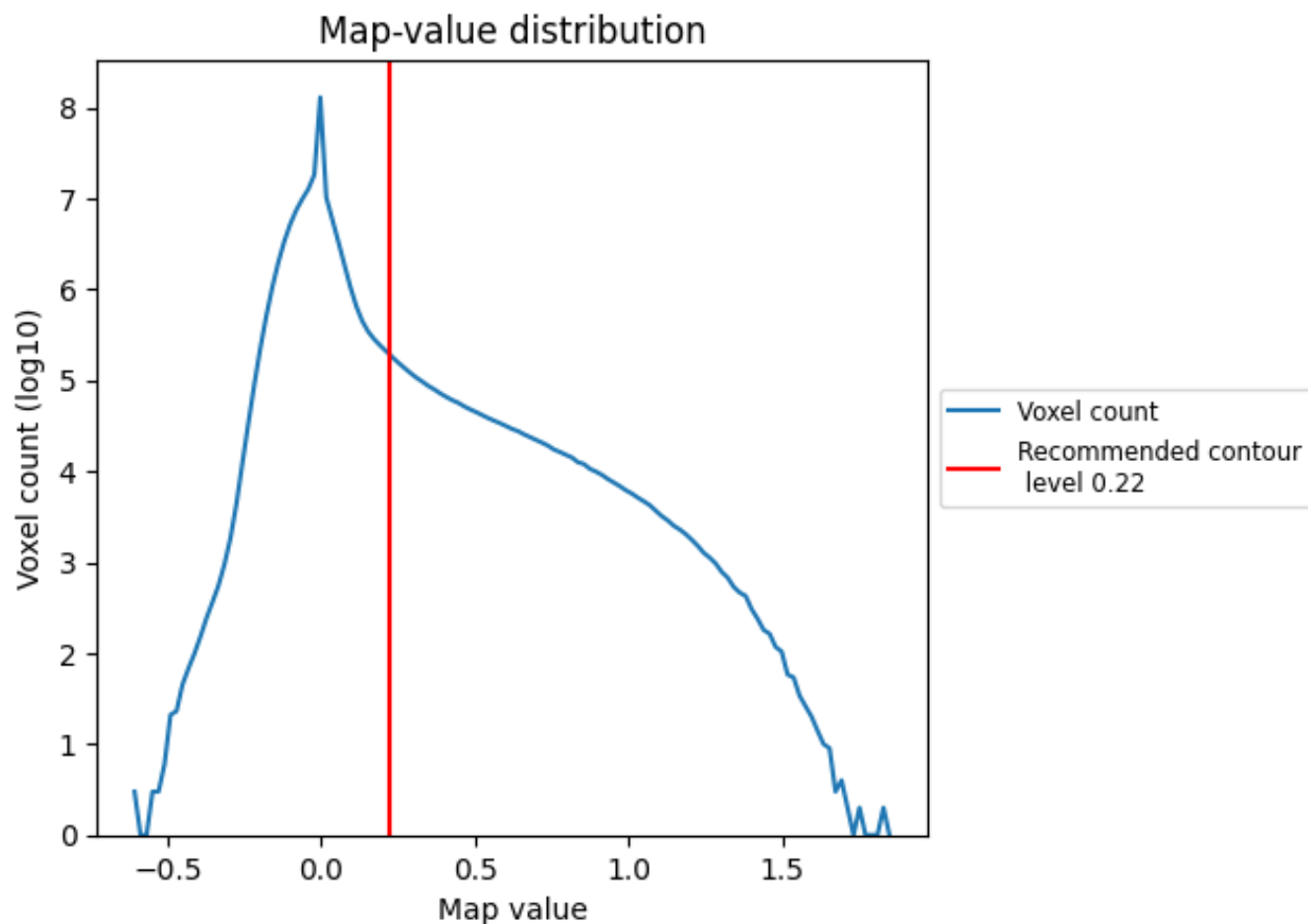
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

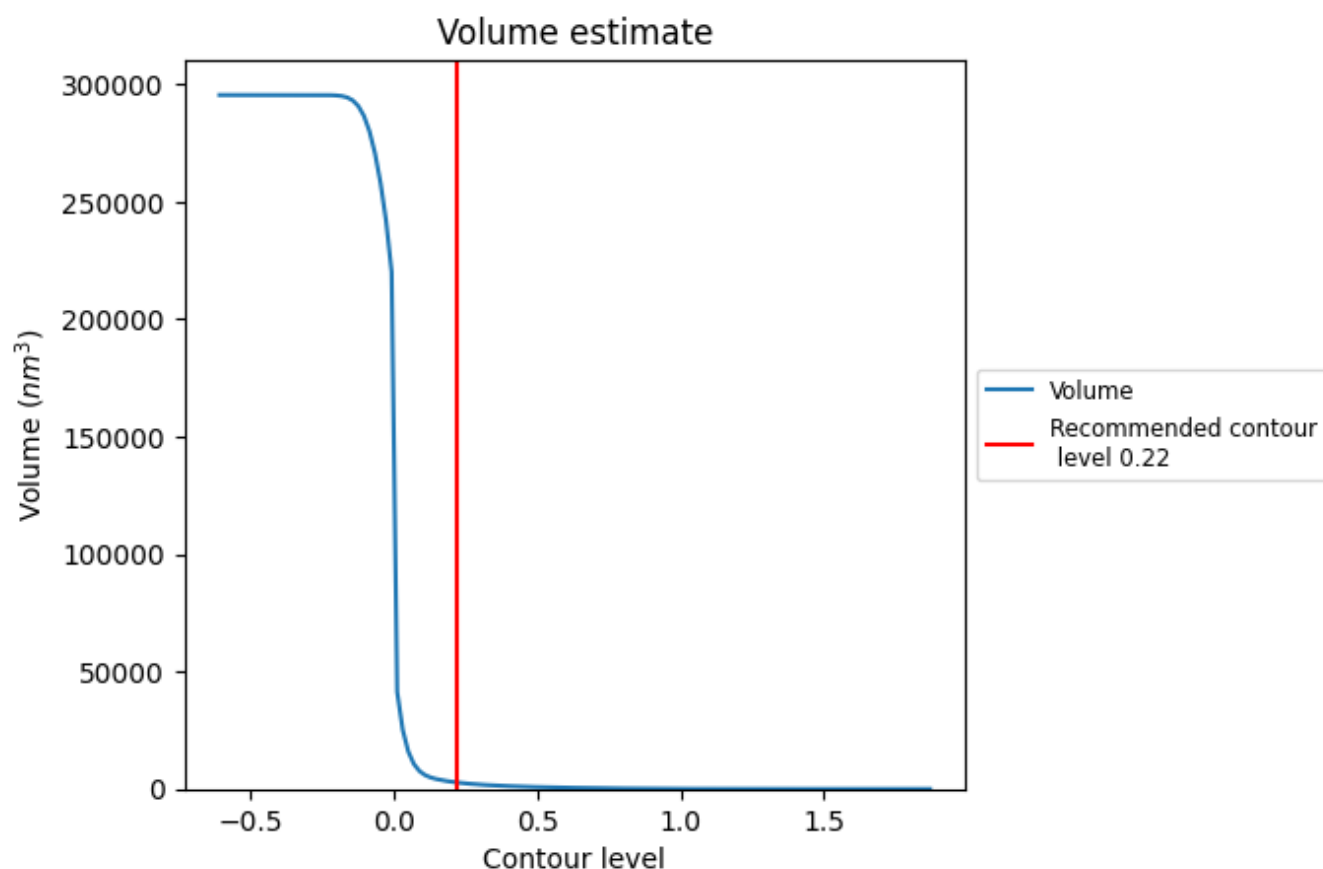
This section contains the results of statistical analysis of the map.

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.

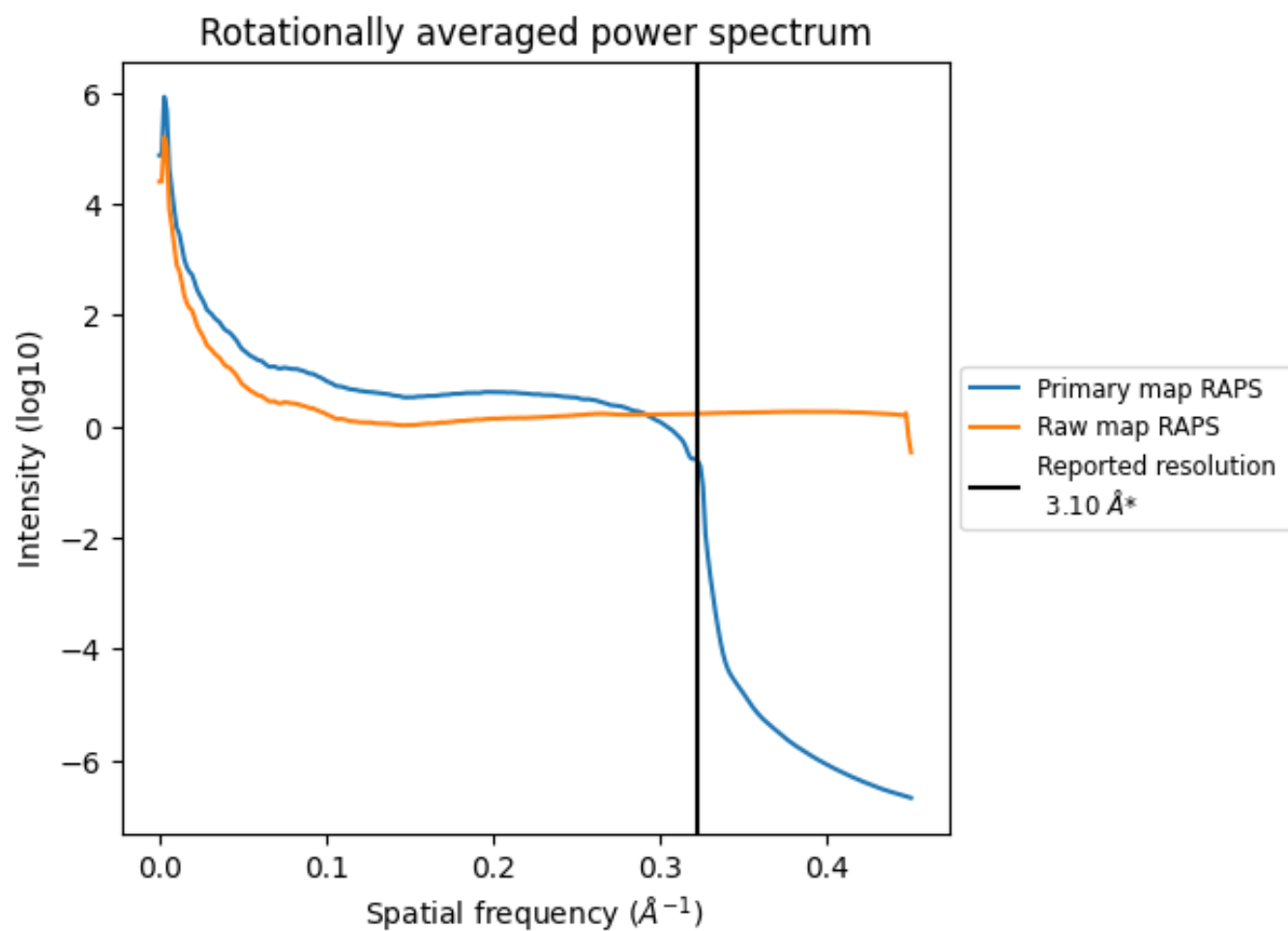
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2763 nm^3 ; this corresponds to an approximate mass of 2496 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 ⓘ

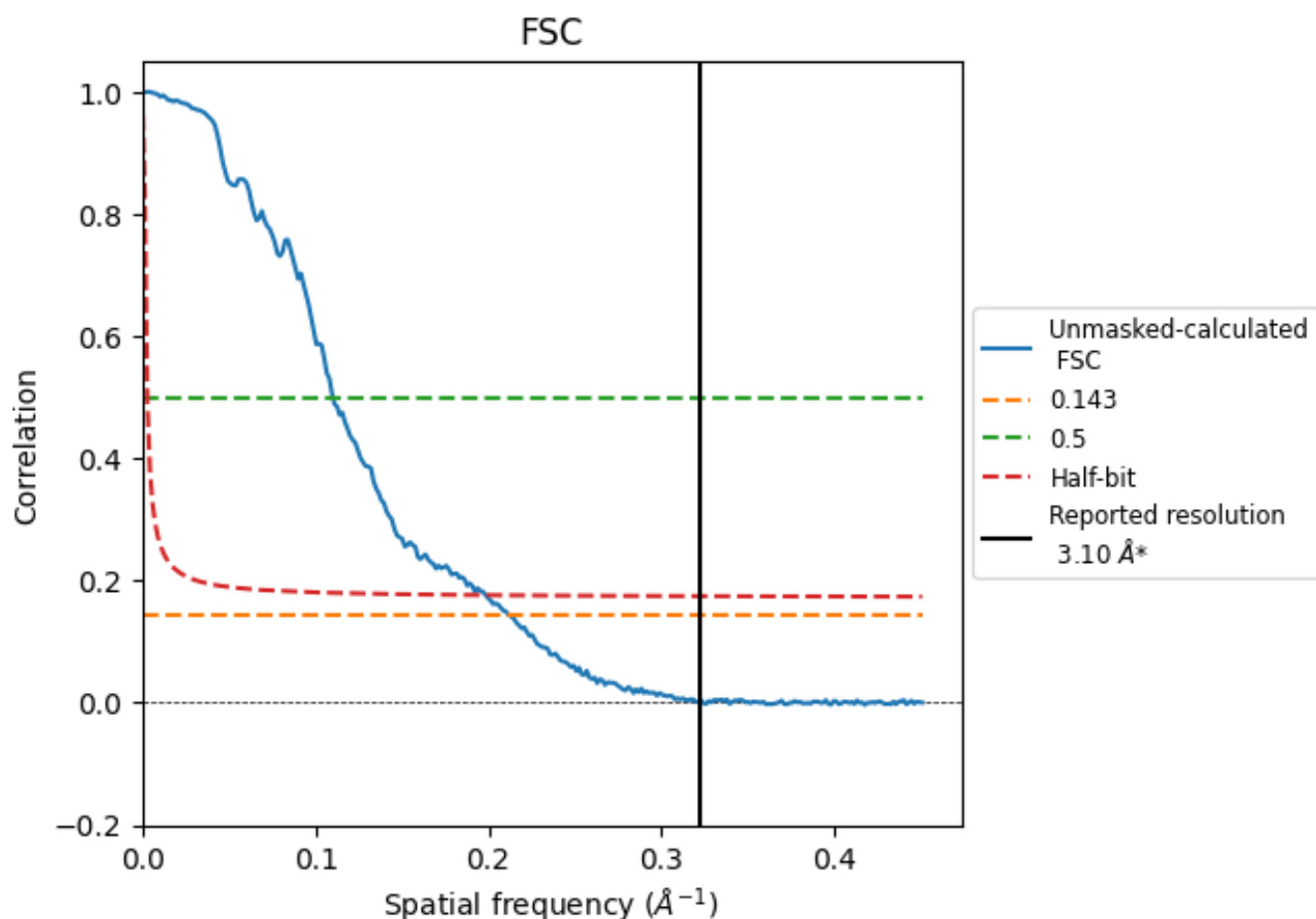


*Reported resolution corresponds to spatial frequency of 0.323 $\text{\AA}^{-1}$

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 $0.323 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

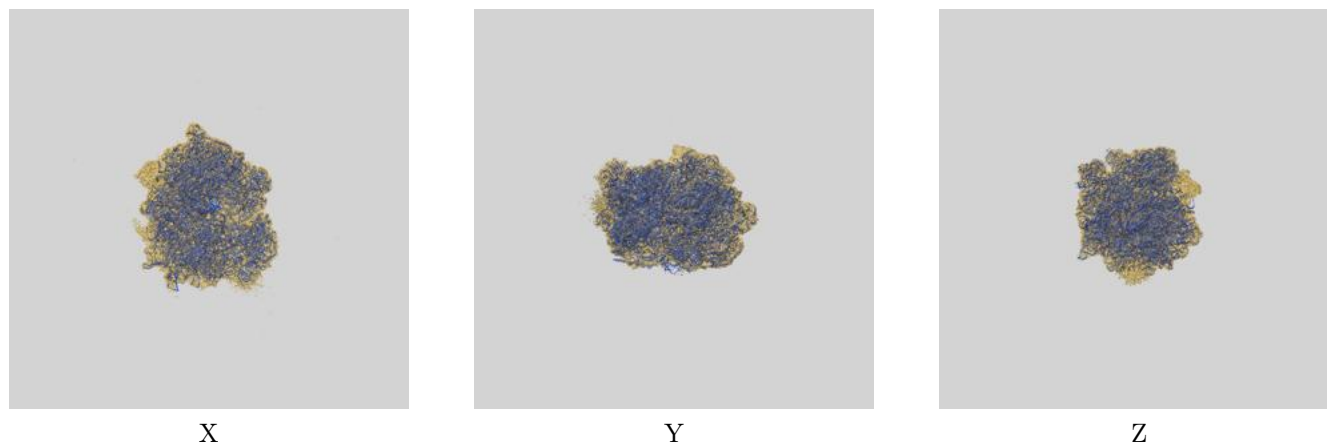
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.72	9.08	5.04

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.72 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

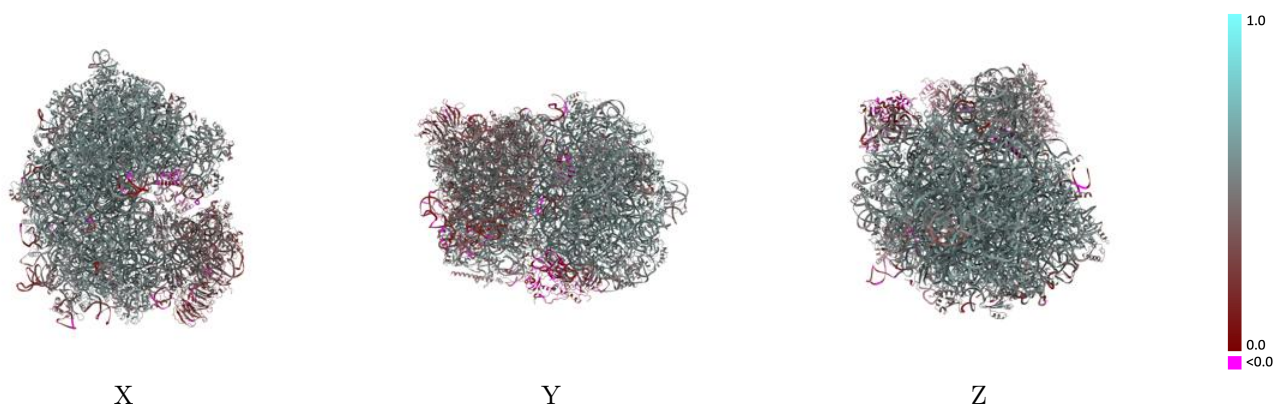
This section contains information regarding the fit between EMDB map EMD-17004 and PDB model 8000. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



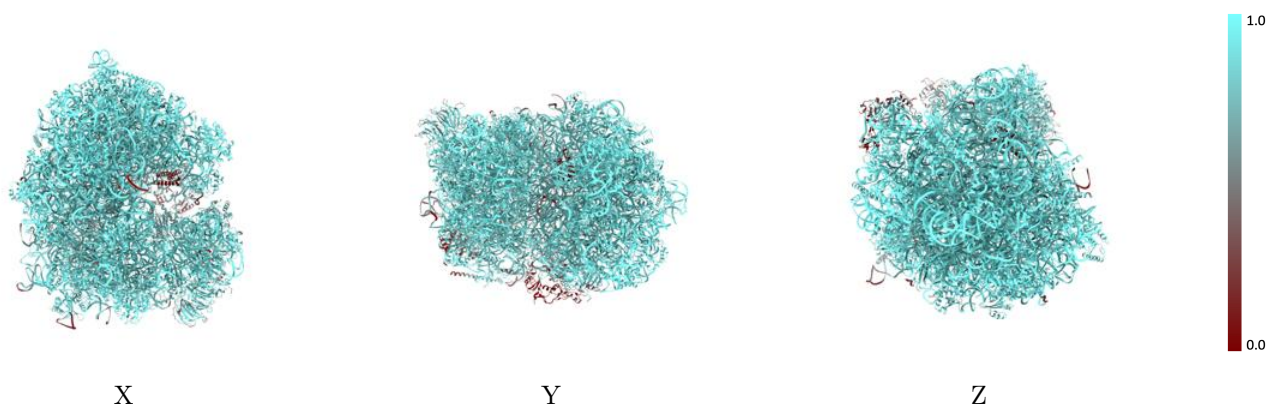
The images above show the 3D surface view of the map at the recommended contour level 0.22 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



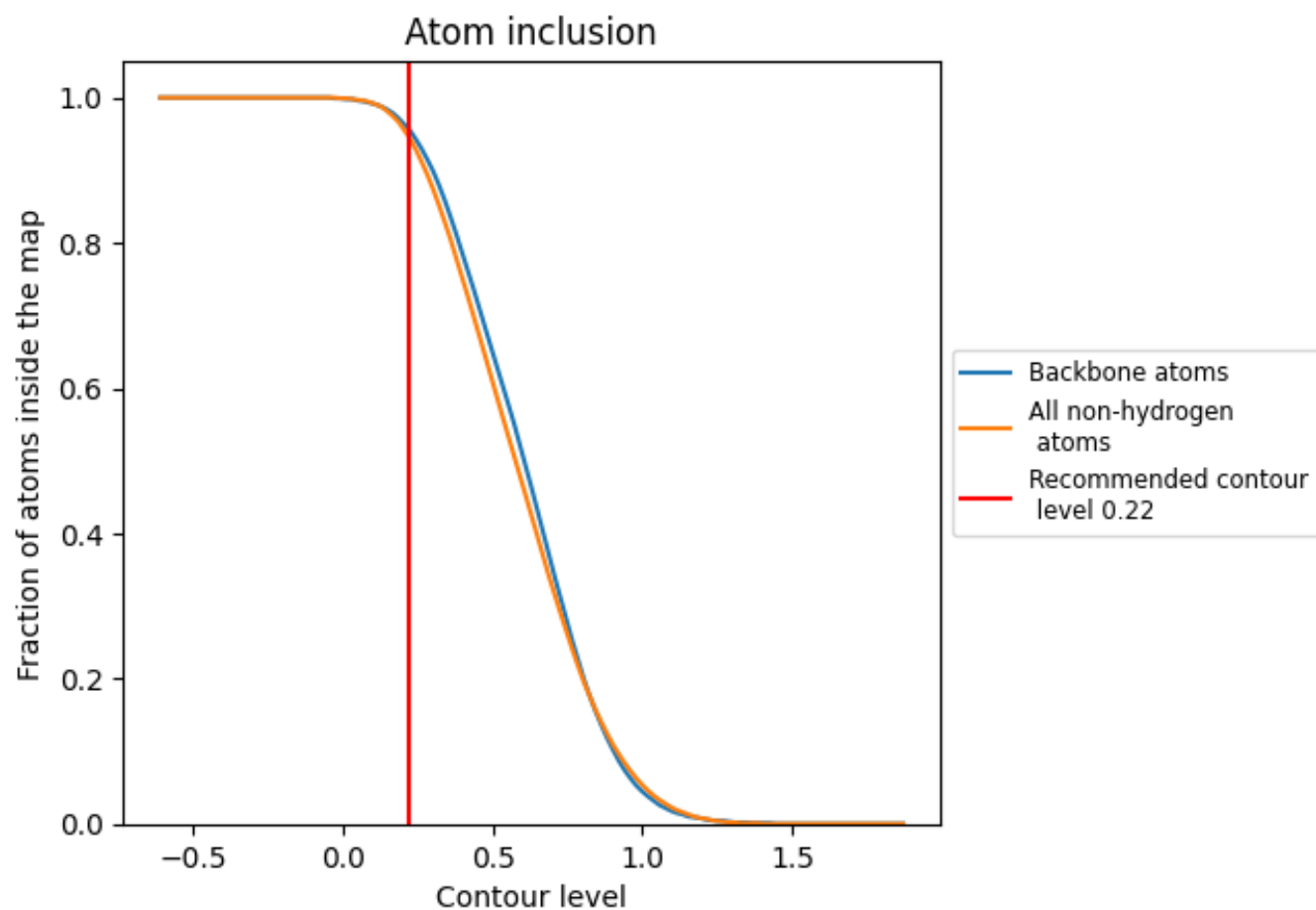
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.22).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 95% 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 (0.22) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9470	 0.4940
1	 0.9860	 0.5310
2	 0.9600	 0.4630
3	 0.9990	 0.5300
4	 0.9900	 0.5360
A	 0.7890	 0.2830
B	 0.5680	 0.2140
C	 0.0880	 0.0170
D	 0.8550	 0.4440
LA	 0.9800	 0.5690
LB	 0.9770	 0.5490
LC	 0.9790	 0.5530
LD	 0.9440	 0.4910
LE	 0.9620	 0.4950
LF	 0.9760	 0.5440
LG	 0.9490	 0.5090
LH	 0.9440	 0.5080
LI	 0.9450	 0.5300
LJ	 0.9210	 0.4610
LK	 0.3400	 0.1100
LL	 0.9710	 0.5420
LM	 0.9730	 0.5170
LN	 0.9970	 0.5710
LO	 0.9870	 0.5440
LP	 0.9240	 0.5150
LQ	 0.9940	 0.5680
LR	 0.9640	 0.5410
LS	 0.9870	 0.5480
LT	 0.9770	 0.5440
LU	 0.9140	 0.4490
LV	 0.9830	 0.5620
LW	 0.7770	 0.4090
LX	 0.9590	 0.5210
LY	 0.9810	 0.5360
LZ	 0.9800	 0.5310



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Chain	Atom inclusion	Q-score
La	 0.9880	 0.5700
Lb	 0.9640	 0.5040
Lc	 0.9760	 0.5310
Ld	 0.9310	 0.5200
Le	 0.9930	 0.5660
Lf	 0.9980	 0.5630
Lg	 0.9810	 0.5510
Lh	 0.9580	 0.5150
Li	 0.9520	 0.5050
Lj	 0.9950	 0.5790
Lk	 0.9120	 0.4860
Ll	 0.9980	 0.5520
Lm	 0.9730	 0.5390
Ln	 0.9900	 0.5740
Lo	 0.9620	 0.5300
Lp	 0.9540	 0.5470
Lq	 0.9860	 0.5460
Lr	 0.8280	 0.4600
Ls	 0.3360	 0.1420
SA	 0.9600	 0.4990
SB	 0.9110	 0.4900
SC	 0.9570	 0.5220
SD	 0.8430	 0.3590
SE	 0.9650	 0.5170
SF	 0.8470	 0.3920
SG	 0.9360	 0.4620
SH	 0.9230	 0.4690
SI	 0.9350	 0.5110
SJ	 0.9620	 0.5120
SK	 0.9290	 0.3020
SL	 0.9760	 0.5450
SM	 0.3590	 0.1780
SN	 0.9640	 0.5380
SO	 0.9570	 0.5130
SP	 0.7780	 0.2790
SQ	 0.9050	 0.3790
SR	 0.8740	 0.3980
SS	 0.8570	 0.3640
ST	 0.8990	 0.3730
SU	 0.8630	 0.3800
SV	 0.9520	 0.5190
SW	 0.9810	 0.5450

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Chain	Atom inclusion	Q-score
SX	 0.9630	 0.5360
SY	 0.9040	 0.4810
SZ	 0.8290	 0.3560
Sa	 0.9440	 0.5150
Sb	 0.9640	 0.5100
Sc	 0.8900	 0.4380
Sd	 0.9730	 0.4040
Se	 0.9210	 0.4950
Sf	 0.5140	 0.1400