



Full wwPDB EM Validation Report ⓘ

Jun 21, 2026 – 04:42 am BST

PDB ID : 7NSH / pdb_00007nsh
EMDB ID : EMD-12567
Title : 39S mammalian mitochondrial large ribosomal subunit with mtRRF (post)
and mtEFG2
Authors : Kummer, E.; Schubert, K.; Ban, N.
Deposited on : 2021-03-07
Resolution : 3.20 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 : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

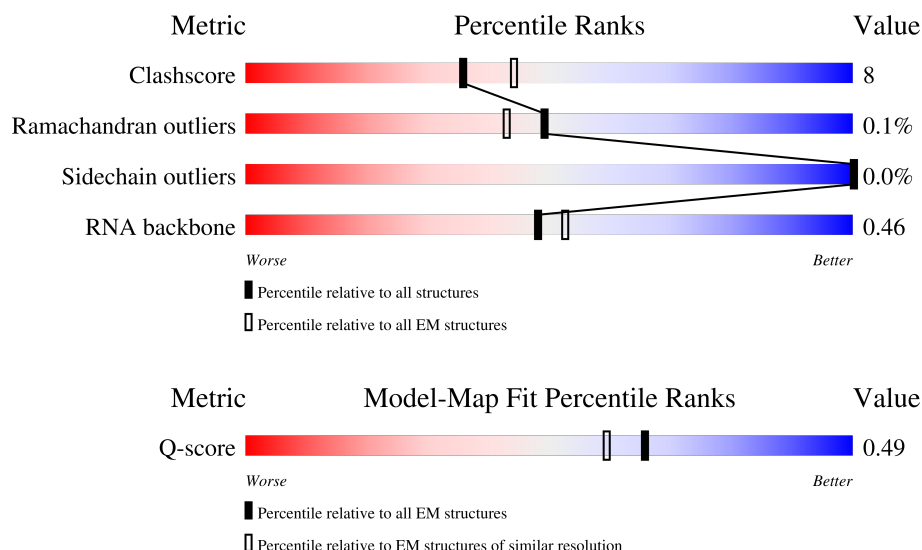
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	B0	148	
2	BY	216	
3	Ba	423	

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Mol	Chain	Length	Quality of chain
4	B8	188	
5	Bb	380	
6	Bc	334	
7	Bd	206	
8	Be	135	
9	Bf	142	
10	Bg	159	
11	Bh	332	
12	Bi	306	
13	Bj	279	
14	Bk	269	
15	Bl	166	
16	Bm	198	
17	Bn	128	
18	Bo	124	
19	Bp	112	
20	Bq	138	
21	Bt	102	
22	Bu	205	
23	Bv	222	
24	Bw	433	
25	Bx	196	
26	CL	198	
26	DL	198	
26	EL	198	

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Mol	Chain	Length	Quality of chain
26	FL	198	
26	GL	198	
26	HL	198	
26	LL	198	
27	B1	256	
28	B9	100	
29	BA	1571	
30	B2	252	
31	B3	161	
32	B4	126	
33	B5	188	
34	B6	65	
35	B7	95	
36	BB	73	
37	BC	755	
38	BD	306	
39	BG	257	
40	BQ	251	
41	BE	399	
42	BF	294	
43	BI	268	
44	BJ	262	
45	BK	192	
46	BN	178	
47	BO	145	

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Mol	Chain	Length	Quality of chain
48	BP	296	76% 21%
49	BR	169	69% 22% 9%
50	BS	180	52% 28% 21%
51	BT	292	62% 14% 24%
52	BU	149	5% 70% 23% 6%
53	BV	209	56% 18% 26%
54	BW	210	65% 14% 21%
55	BX	150	13% 87% 13%

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 112448 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 protein called Mitochondrial ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B0	110	Total	C	N	O	S	0	0
			857	553	156	145	3		

- Molecule 2 is a protein called uL24m.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	BY	206	Total	C	N	O	S	0	0
			1678	1056	308	309	5		

- Molecule 3 is a protein called Mitochondrial ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Ba	393	Total	C	N	O	S	0	0
			3173	2040	556	565	12		

- Molecule 4 is a protein called Mitochondrial ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B8	95	Total	C	N	O	S	0	0
			833	539	163	129	2		

- Molecule 5 is a protein called Mitochondrial ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Bb	354	Total	C	N	O	S	0	0
			2952	1876	542	525	9		

- Molecule 6 is a protein called Mitochondrial ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Bc	295	Total	C	N	O	S	0	0
			2408	1541	410	441	16		

- Molecule 7 is a protein called Mitochondrial ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Bd	140	Total	C	N	O	S	0	0
			1177	742	213	221	1		

- Molecule 8 is a protein called Mitochondrial ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Be	122	Total	C	N	O	S	0	0
			972	628	168	173	3		

- Molecule 9 is a protein called mL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Bf	108	Total	C	N	O	S	0	0
			827	519	154	150	4		

- Molecule 10 is a protein called Mitochondrial ribosomal protein L43.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Bg	148	Total	C	N	O	S	0	0
			1167	727	225	212	3		

- Molecule 11 is a protein called mL44.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Bh	289	Total	C	N	O	S	0	0
			2319	1486	399	426	8		

- Molecule 12 is a protein called Mitochondrial ribosomal protein L45.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Bi	260	Total	C	N	O	S	0	0
			2138	1370	379	379	10		

- Molecule 13 is a protein called Mitochondrial ribosomal protein L46.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Bj	217	Total	C	N	O	S	0	0
			1775	1137	311	321	6		

- Molecule 14 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Bk	155	Total	C	N	O	S	0	0
			1246	796	214	231	5		

- Molecule 15 is a protein called Mrpl34.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Bl	133	Total	C	N	O	S	0	0
			1097	709	192	194	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Bl	59	ARG	LYS	conflict	UNP A0A0R4J8D6

- Molecule 16 is a protein called Mitochondrial ribosomal protein L50.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Bm	109	Total	C	N	O	S	0	0
			893	568	160	162	3		

- Molecule 17 is a protein called Mitochondrial ribosomal protein L51.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Bn	97	Total	C	N	O	S	0	0
			837	539	166	128	4		

- Molecule 18 is a protein called mL52.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Bo	97	Total	C	N	O	S	0	0
			772	481	148	141	2		

- Molecule 19 is a protein called mL53.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Bp	97	Total	C	N	O	S	0	0
			742	459	143	134	6		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Bp	12	ALA	SER	conflict	UNP A0A341D604

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Chain	Residue	Modelled	Actual	Comment	Reference
Bp	107	SER	GLY	conflict	UNP A0A341D604

- Molecule 20 is a protein called mL54.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Bq	80	Total	C	N	O	S	0	0
			672	431	123	116	2		

- Molecule 21 is a protein called Mitochondrial ribosomal protein L57.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Bt	94	Total	C	N	O	S	0	0
			780	485	168	126	1		

- Molecule 22 is a protein called mL62 (ICT1).

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Bu	151	Total	C	N	O	S	0	0
			1198	738	233	222	5		

- Molecule 23 is a protein called mL64.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Bv	135	Total	C	N	O	S	0	0
			1131	692	223	211	5		

- Molecule 24 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Bw	387	Total	C	N	O	S	0	0
			3126	2011	548	555	12		

- Molecule 25 is a protein called Mitochondrial ribosomal protein S18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Bx	162	Total	C	N	O	S	0	0
			1325	845	249	224	7		

- Molecule 26 is a protein called Mitochondrial ribosomal protein L12.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	CL	45	Total	C	N	O	0	0
			317	203	52	62		
26	DL	27	Total	C	N	O	0	0
			213	137	33	43		
26	EL	28	Total	C	N	O	0	0
			222	143	35	44		
26	FL	27	Total	C	N	O	0	0
			213	137	33	43		
26	GL	27	Total	C	N	O	0	0
			213	137	33	43		
26	HL	26	Total	C	N	O	0	0
			205	131	32	42		
26	LL	70	Total	C	N	O	0	0
			537	346	93	98		

- Molecule 27 is a protein called Mitochondrial ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	B1	244	Total	C	N	O	S	0	0
			2036	1315	363	353	5		

- Molecule 28 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	B9	38	Total	C	N	O	S	0	0
			335	214	70	47	4		

- Molecule 29 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BA	1544	Total	C	N	O	P	0	0
			32844	14750	5972	10578	1544		

- Molecule 30 is a protein called Mitochondrial ribosomal protein L47.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	B2	179	Total	C	N	O	S	0	0
			1548	992	290	260	6		

- Molecule 31 is a protein called uL30m.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	B3	118	Total	C	N	O	S	0	0
			968	622	178	165	3		

- Molecule 32 is a protein called bL31m.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B4	62	Total	C	N	O	S	0	0
			474	296	94	81	3		

- Molecule 33 is a protein called bL32m.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	B5	110	Total	C	N	O	S	0	0
			902	553	181	162	6		

- Molecule 34 is a protein called bL33m.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	B6	52	Total	C	N	O	S	0	0
			425	274	78	71	2		

- Molecule 35 is a protein called Mitochondrial ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	B7	46	Total	C	N	O	S	0	0
			387	239	89	58	1		

- Molecule 36 is a RNA chain called CP tRNAPhe.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BB	67	Total	C	N	O	P	0	0
			1427	640	261	459	67		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BB	71	C	-	insertion	GB 76262549

- Molecule 37 is a protein called Ribosome-releasing factor 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BC	700	Total	C	N	O	S	0	0
			5434	3428	936	1045	25		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BC	25	MET	-	initiating methionine	UNP Q969S9
BC	26	HIS	-	expression tag	UNP Q969S9
BC	27	HIS	-	expression tag	UNP Q969S9
BC	28	HIS	-	expression tag	UNP Q969S9
BC	29	HIS	-	expression tag	UNP Q969S9
BC	30	HIS	-	expression tag	UNP Q969S9
BC	31	HIS	-	expression tag	UNP Q969S9
BC	32	GLU	-	expression tag	UNP Q969S9
BC	33	ASN	-	expression tag	UNP Q969S9
BC	34	LEU	-	expression tag	UNP Q969S9
BC	35	TYR	-	expression tag	UNP Q969S9
BC	36	PHE	-	expression tag	UNP Q969S9
BC	37	GLN	-	expression tag	UNP Q969S9
BC	38	SER	-	expression tag	UNP Q969S9
BC	39	GLY	-	expression tag	UNP Q969S9
BC	40	GLY	-	expression tag	UNP Q969S9
BC	41	SER	-	expression tag	UNP Q969S9
BC	42	GLY	-	expression tag	UNP Q969S9
BC	43	SER	-	expression tag	UNP Q969S9
BC	44	GLY	-	expression tag	UNP Q969S9

- Molecule 38 is a protein called uL2m.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BD	240	Total	C	N	O	S	0	0
			1860	1160	371	319	10		

- Molecule 39 is a protein called Ribosome-recycling factor, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BG	196	Total	C	N	O	S	0	0
			1520	940	273	299	8		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BG	6	MET	-	initiating methionine	UNP Q96E11

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Chain	Residue	Modelled	Actual	Comment	Reference
BG	7	HIS	-	expression tag	UNP Q96E11
BG	8	HIS	-	expression tag	UNP Q96E11
BG	9	HIS	-	expression tag	UNP Q96E11
BG	10	HIS	-	expression tag	UNP Q96E11
BG	11	HIS	-	expression tag	UNP Q96E11
BG	12	HIS	-	expression tag	UNP Q96E11
BG	13	GLU	-	expression tag	UNP Q96E11
BG	14	ASN	-	expression tag	UNP Q96E11
BG	15	LEU	-	expression tag	UNP Q96E11
BG	16	TYR	-	expression tag	UNP Q96E11
BG	17	PHE	-	expression tag	UNP Q96E11
BG	18	GLN	-	expression tag	UNP Q96E11
BG	19	SER	-	expression tag	UNP Q96E11
BG	20	GLY	-	expression tag	UNP Q96E11
BG	21	GLY	-	expression tag	UNP Q96E11
BG	22	SER	-	expression tag	UNP Q96E11
BG	23	GLY	-	expression tag	UNP Q96E11
BG	24	SER	-	expression tag	UNP Q96E11
BG	25	GLY	-	expression tag	UNP Q96E11

- Molecule 40 is a protein called uL16m.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BQ	222	Total	C	N	O	S	0	0
			1803	1156	331	306	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BQ	237	HIS	TYR	conflict	UNP F1RI89

- Molecule 41 is a protein called ICT1.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BE	307	Total	C	N	O	S	0	0
			2420	1554	426	430	10		

- Molecule 42 is a protein called Mitochondrial ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BF	250	Total	C	N	O	S	0	0
			2011	1294	367	344	6		

- Molecule 43 is a protein called Mitochondrial ribosomal protein L9.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	BI	98	Total	C	N	O	0	0
			805	509	155	141		

- Molecule 44 is a protein called Mitochondrial ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BJ	212	Total	C	N	O	S	0	0
			1705	1100	306	290	9		

- Molecule 45 is a protein called Mitochondrial ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BK	176	Total	C	N	O	S	0	0
			1339	851	243	243	2		

- Molecule 46 is a protein called uL13m.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BN	177	Total	C	N	O	S	0	0
			1444	926	258	253	7		

- Molecule 47 is a protein called uL14m.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BO	115	Total	C	N	O	S	0	0
			896	562	176	154	4		

- Molecule 48 is a protein called uL15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BP	288	Total	C	N	O	S	0	0
			2312	1473	430	403	6		

- Molecule 49 is a protein called bL17m.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BR	153	Total	C	N	O	S	0	0
			1240	777	236	222	5		

- Molecule 50 is a protein called Mitochondrial ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BS	143	Total	C	N	O	S	0	0
			1168	733	227	204	4		

- Molecule 51 is a protein called Mitochondrial ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BT	223	Total	C	N	O	S	0	0
			1851	1184	322	336	9		

- Molecule 52 is a protein called Mitochondrial ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BU	140	Total	C	N	O	S	0	0
			1159	732	239	185	3		

- Molecule 53 is a protein called Mitochondrial ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BV	155	Total	C	N	O	S	0	0
			1231	789	219	219	4		

- Molecule 54 is a protein called uL22m.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BW	166	Total	C	N	O	S	0	0
			1374	876	258	234	6		

- Molecule 55 is a protein called uL23m.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BX	149	Total	C	N	O	S	0	0
			1181	752	227	200	2		

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	B0	1	Total	Mg	0
			1	1	
56	Bb	1	Total	Mg	0
			1	1	
56	Be	1	Total	Mg	0
			1	1	

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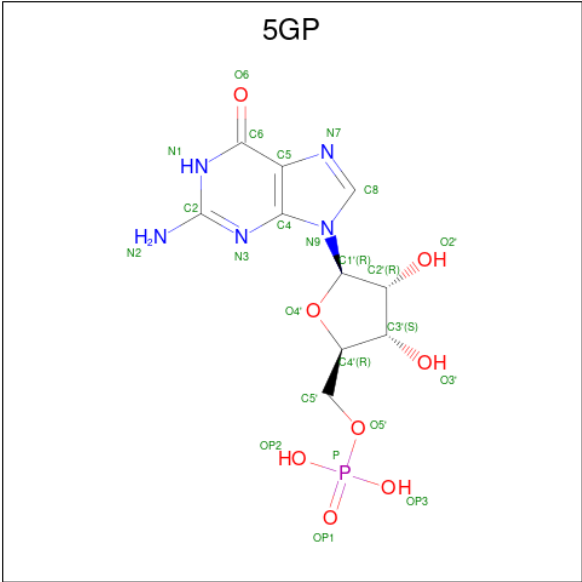
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Mol	Chain	Residues	Atoms		AltConf
56	Bl	1	Total 1	Mg 1	0
56	Bt	1	Total 1	Mg 1	0
56	BA	205	Total 205	Mg 205	0
56	B3	1	Total 1	Mg 1	0
56	BC	1	Total 1	Mg 1	0
56	BD	3	Total 3	Mg 3	0
56	BQ	1	Total 1	Mg 1	0
56	BE	1	Total 1	Mg 1	0
56	BJ	1	Total 1	Mg 1	0
56	BP	2	Total 2	Mg 2	0
56	BR	1	Total 1	Mg 1	0

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

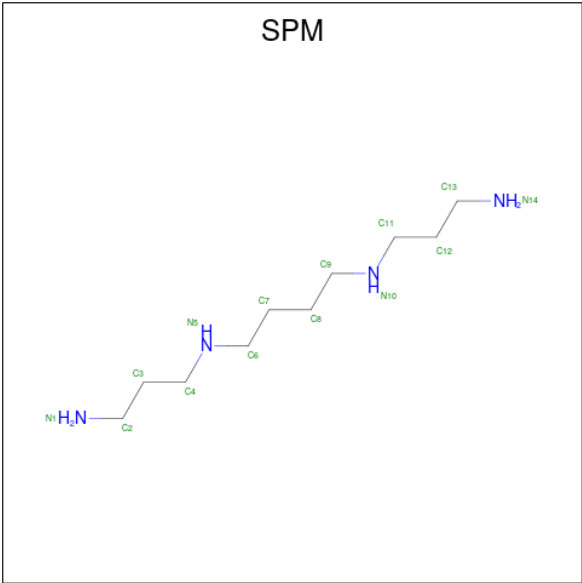
Mol	Chain	Residues	Atoms		AltConf
57	Bx	1	Total 1	Zn 1	0
57	B9	1	Total 1	Zn 1	0
57	B5	1	Total 1	Zn 1	0

- Molecule 58 is GUANOSINE-5'-MONOPHOSPHATE (CCD ID: 5GP) (formula: C₁₀H₁₄N₅O₈P).



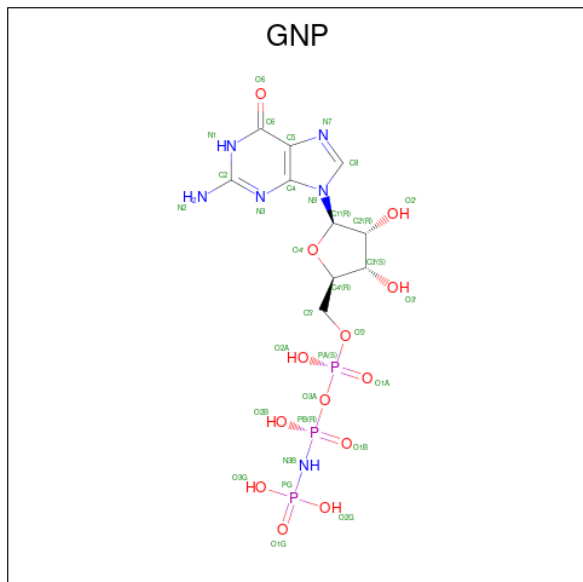
Mol	Chain	Residues	Atoms					AltConf
58	BA	1	Total	C	N	O	P	0
			24	10	5	8	1	
58	BA	1	Total	C	N	O	P	0
			24	10	5	8	1	

- Molecule 59 is SPERMINE (CCD ID: SPM) (formula: C₁₀H₂₆N₄).



Mol	Chain	Residues	Atoms			AltConf
59	BA	1	Total	C	N	0
			14	10	4	
59	BA	1	Total	C	N	0
			14	10	4	

- Molecule 60 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
60	BC	1	Total	C	N	O	P	0
			32	10	6	13	3	

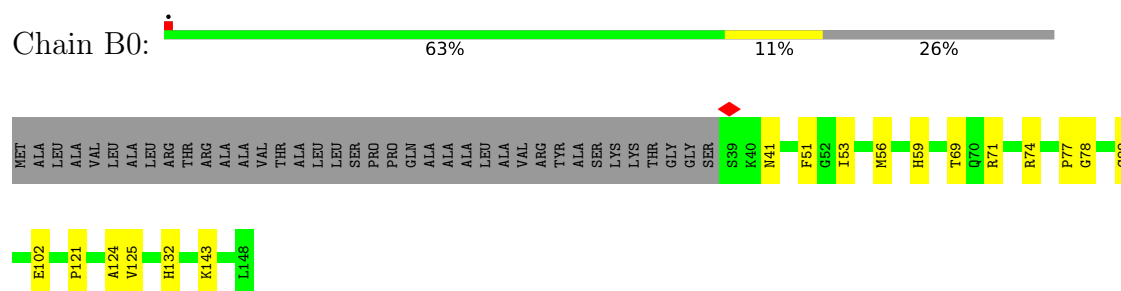
- Molecule 61 is water.

Mol	Chain	Residues	Atoms		AltConf
61	BC	2	Total	O	0
			2	2	

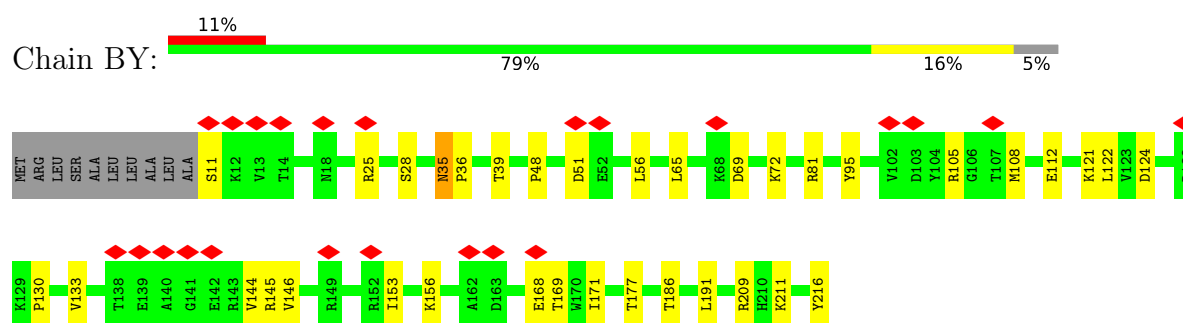
3 Residue-property plots [i](#)

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

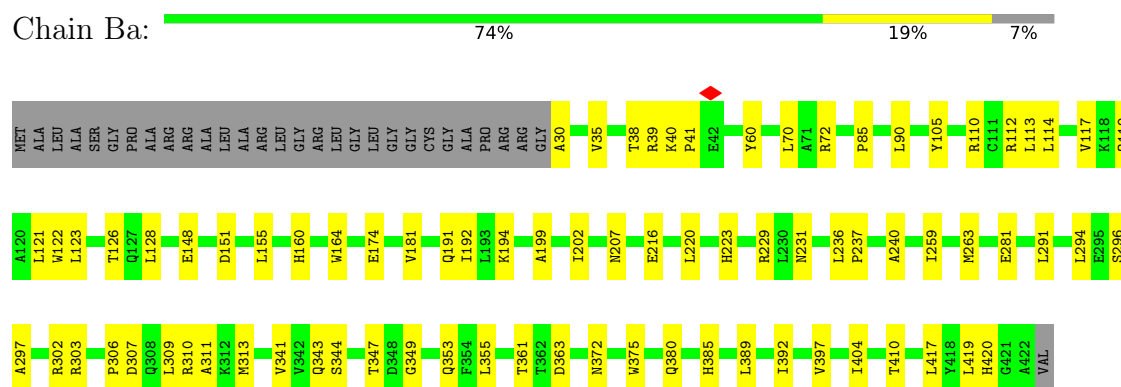
- Molecule 1: Mitochondrial ribosomal protein L27



- Molecule 2: uL24m



- Molecule 3: Mitochondrial ribosomal protein L37



- Molecule 4: Mitochondrial ribosomal protein L35

Response	Percentage
Used	39%
Not used	12%
Don't know	49%



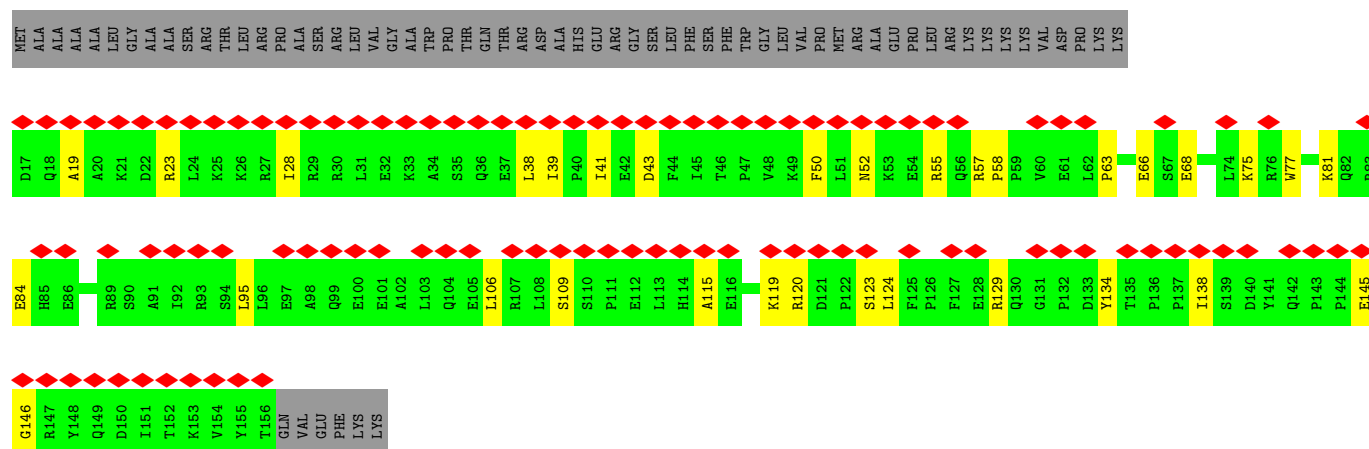
Frequency	Percentage
Daily	68%
Weekly	25%
Monthly	7%



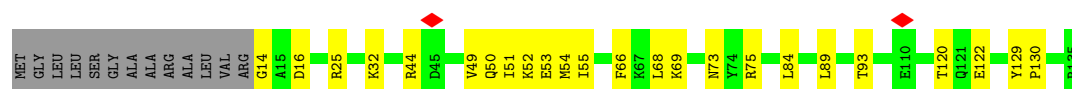
Frequency	Percentage
Daily	63%
Weekly	25%
Monthly	12%



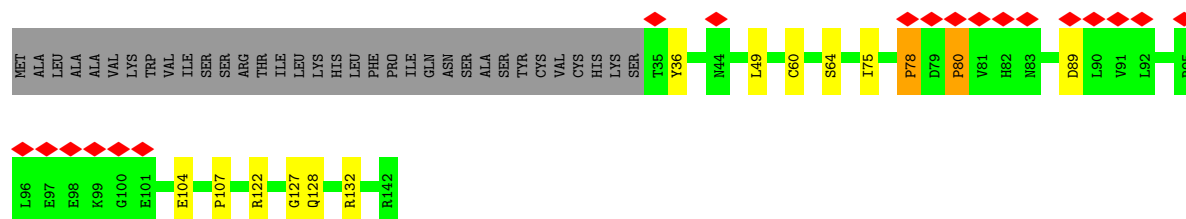
Government	Percentage
Current government	50%
Previous government	52%
Next government	16%
Next government	32%



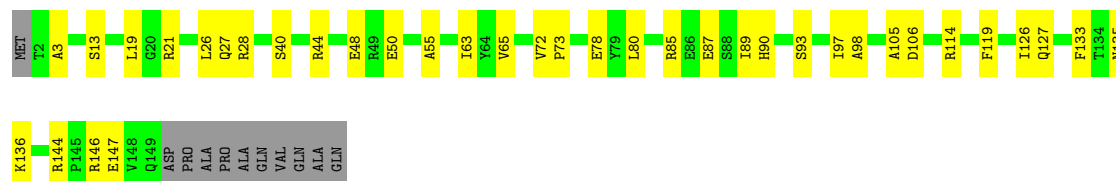
• Molecule 8: Mitochondrial ribosomal protein L41



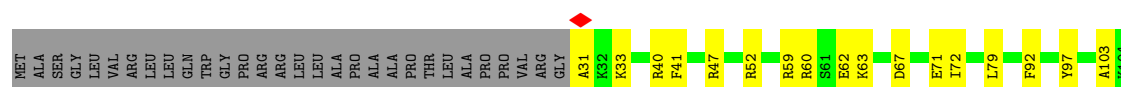
• Molecule 9: mL42



• Molecule 10: Mitochondrial ribosomal protein L43

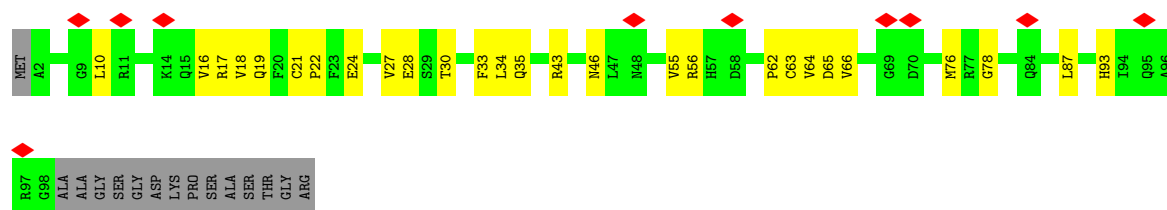


• Molecule 11: mL44

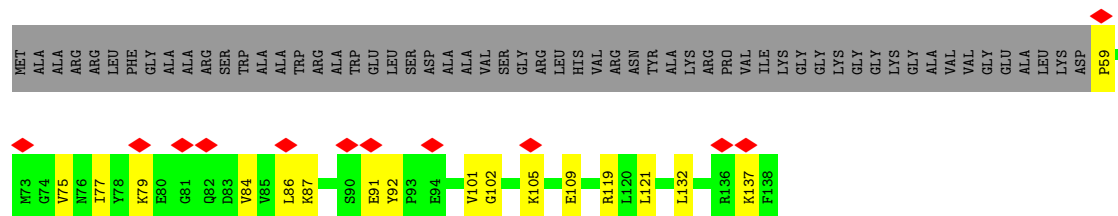




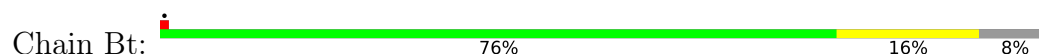
• Molecule 19: mL53



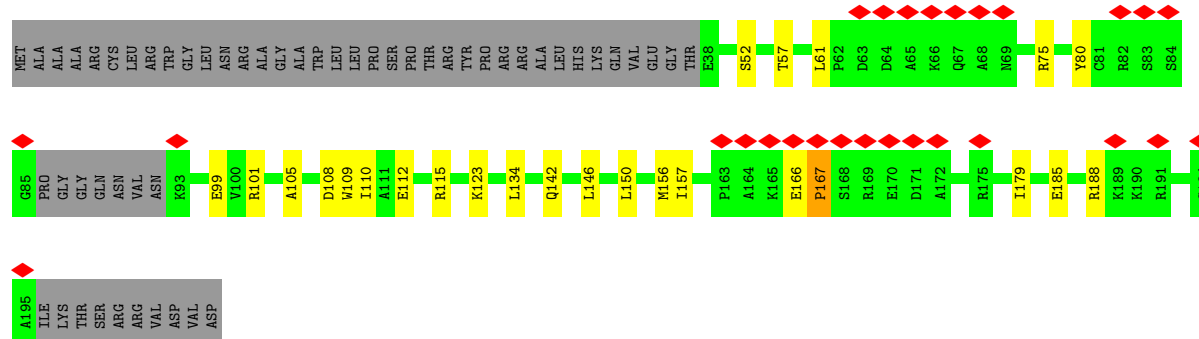
• Molecule 20: mL54



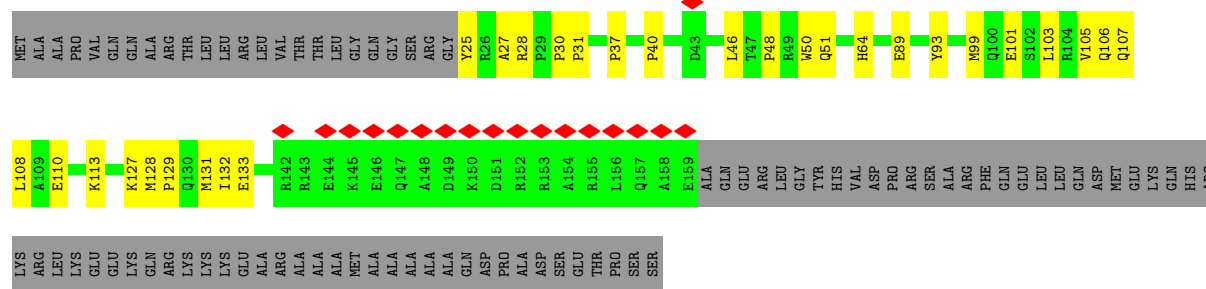
• Molecule 21: Mitochondrial ribosomal protein L57



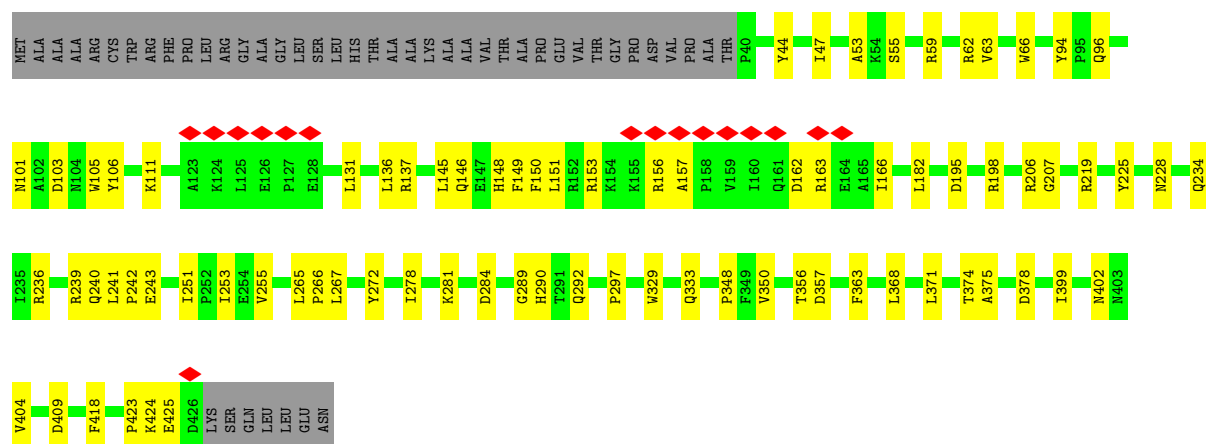
• Molecule 22: mL62 (ICT1)



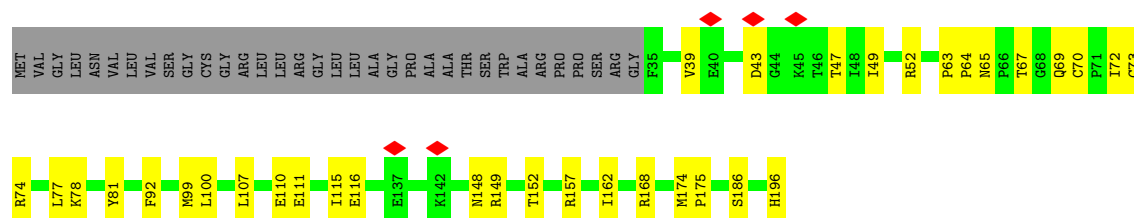
• Molecule 23: mL64



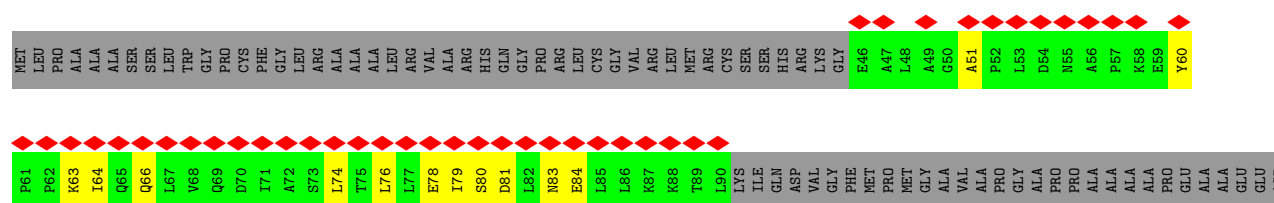
- Molecule 24: 39S ribosomal protein S30, mitochondrial

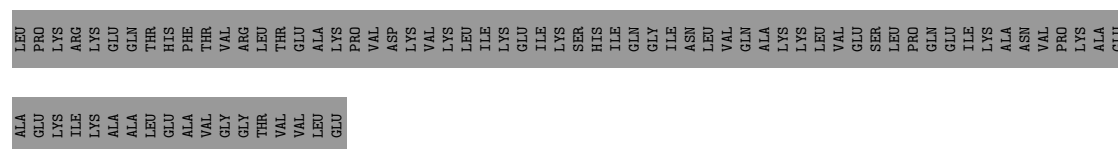


- Molecule 25: Mitochondrial ribosomal protein S18A

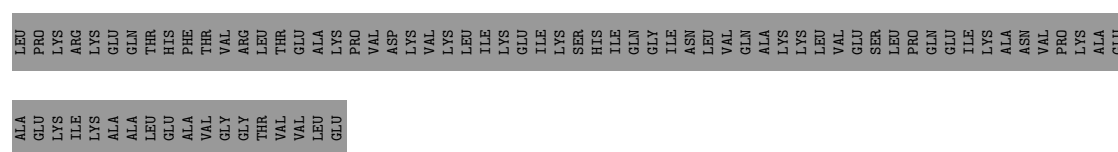
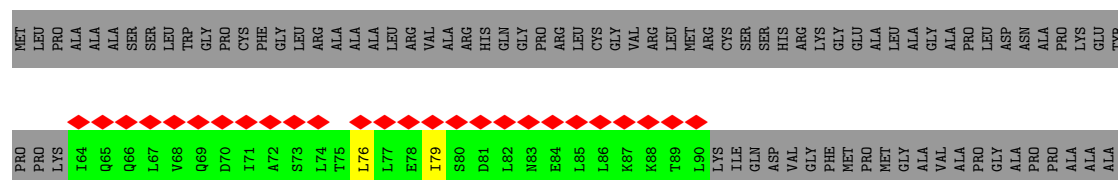


- Molecule 26: Mitochondrial ribosomal protein L12

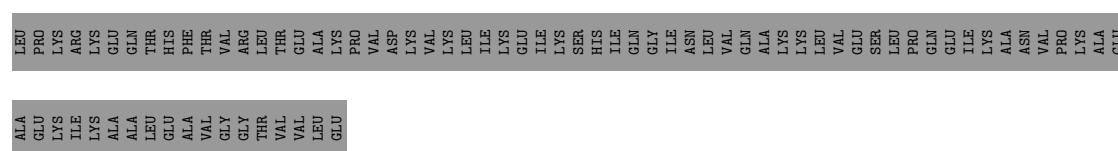
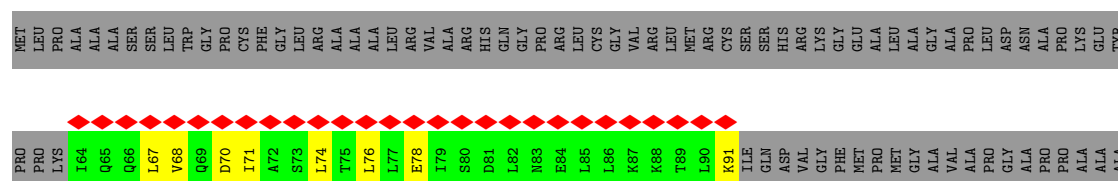




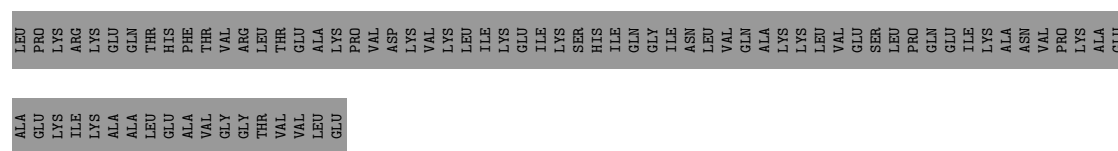
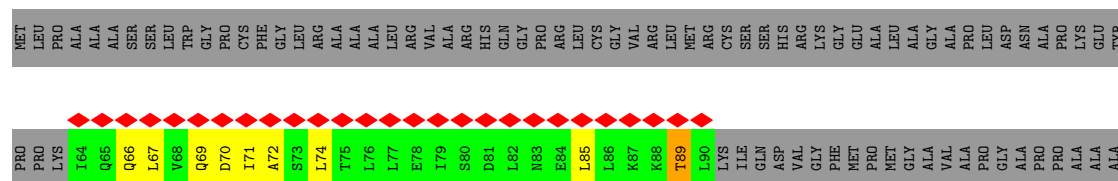
- Molecule 26: Mitochondrial ribosomal protein L12



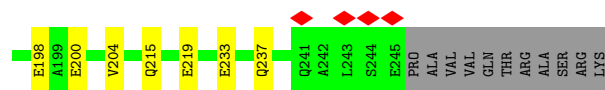
- Molecule 26: Mitochondrial ribosomal protein L12



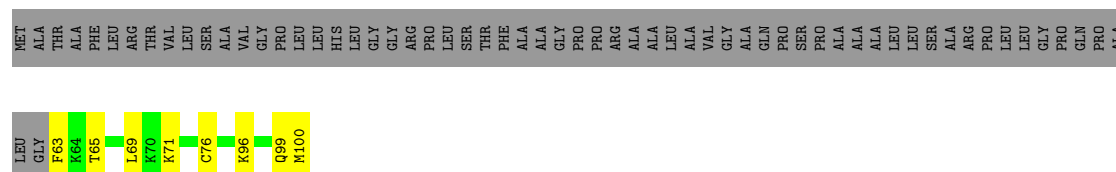
- Molecule 26: Mitochondrial ribosomal protein L12



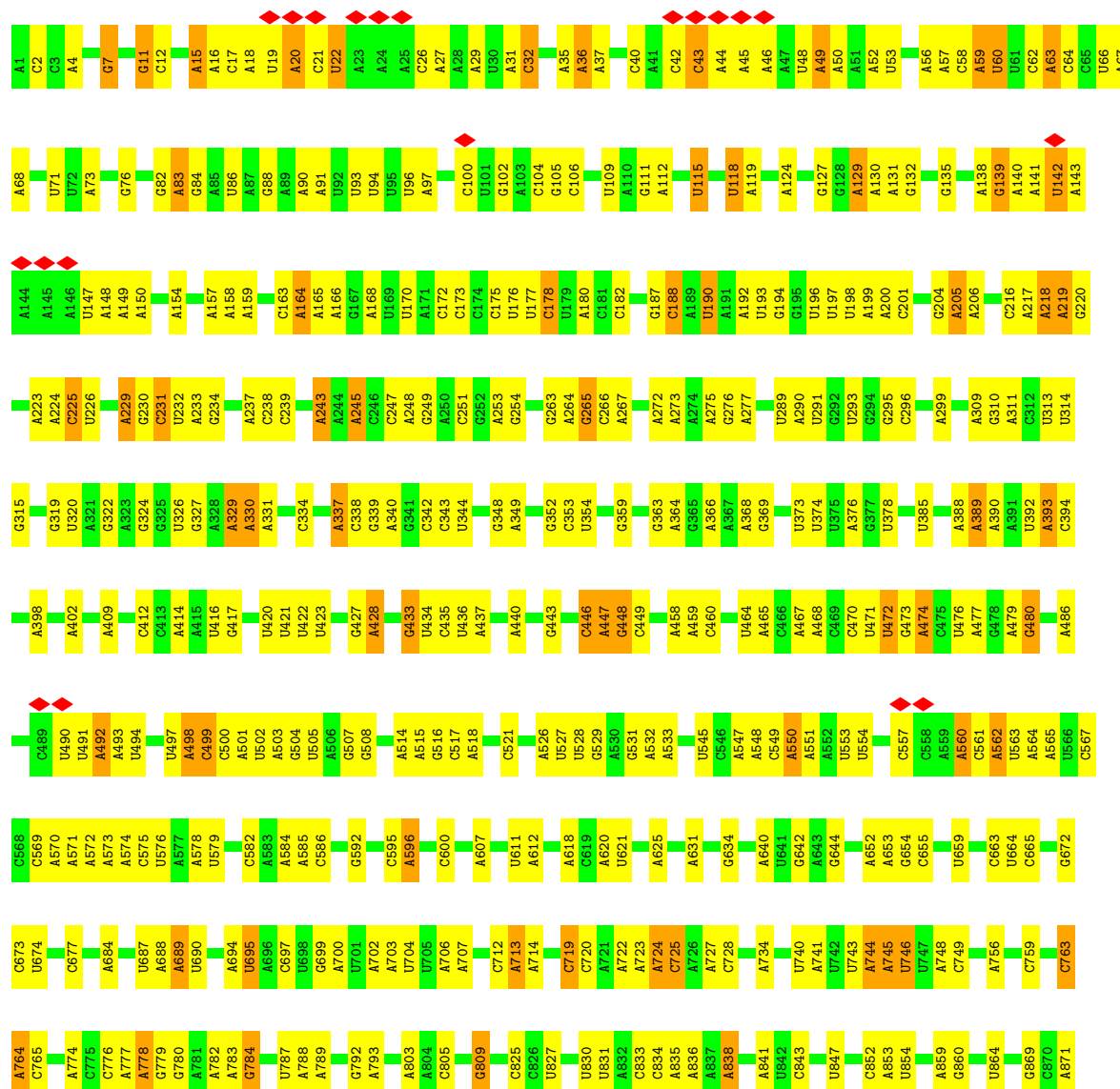
- Molecule 26: Mitochondrial ribosomal protein L12



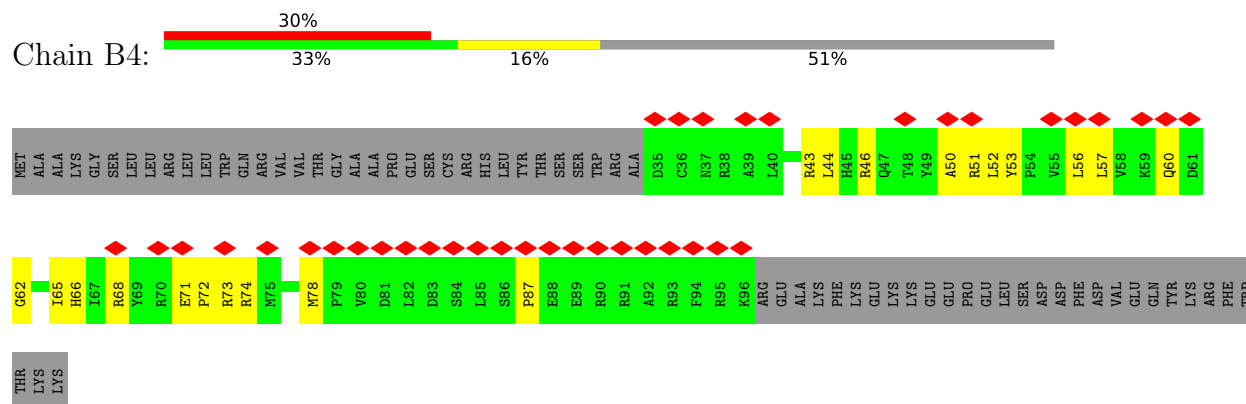
• Molecule 28: Ribosomal protein



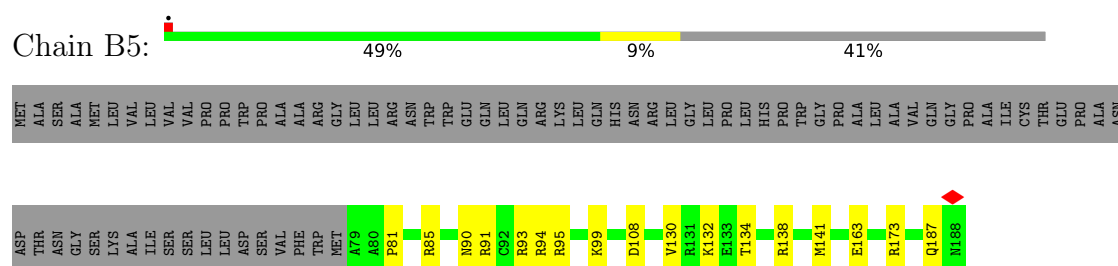
• Molecule 29: 16S rRNA



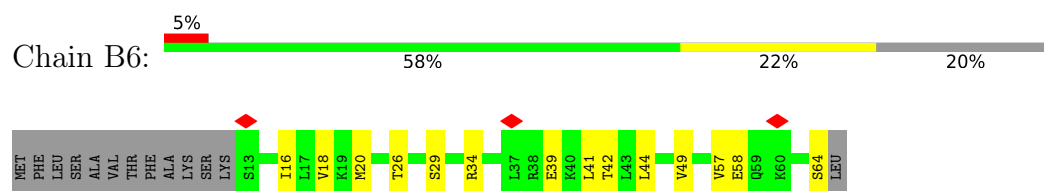
- Molecule 32: bL31m



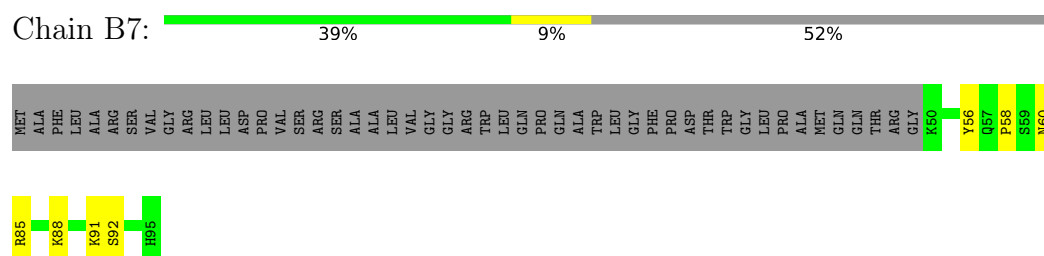
- Molecule 33: bL32m



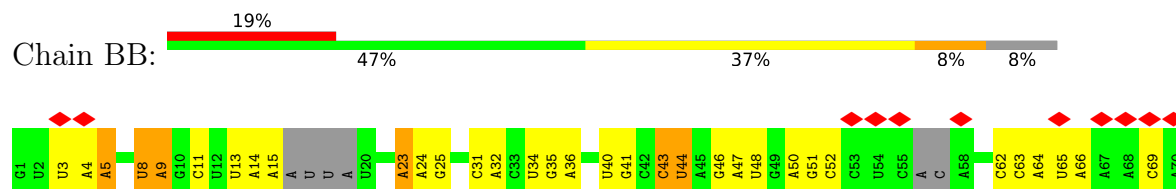
- Molecule 34: bL33m



- Molecule 35: Mitochondrial ribosomal protein L34

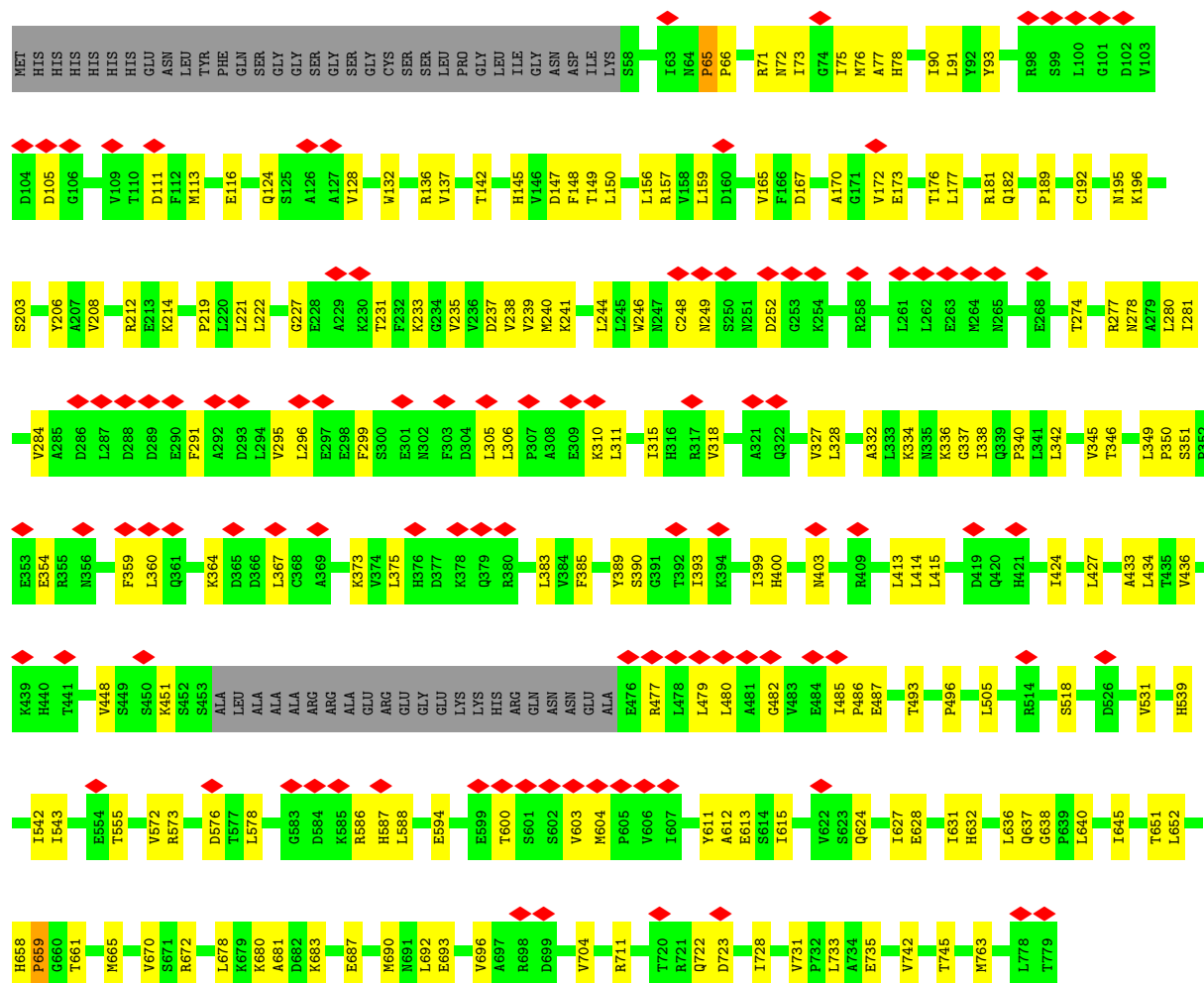


- Molecule 36: CP tRNA^{Phe}

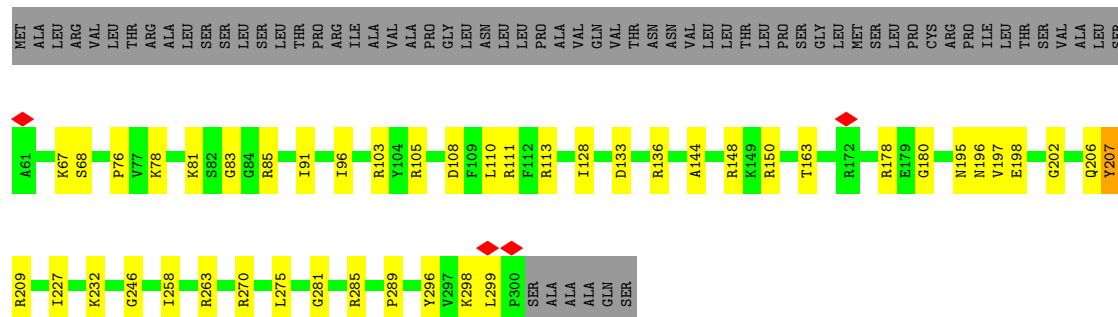




• Molecule 37: Ribosome-releasing factor 2, mitochondrial



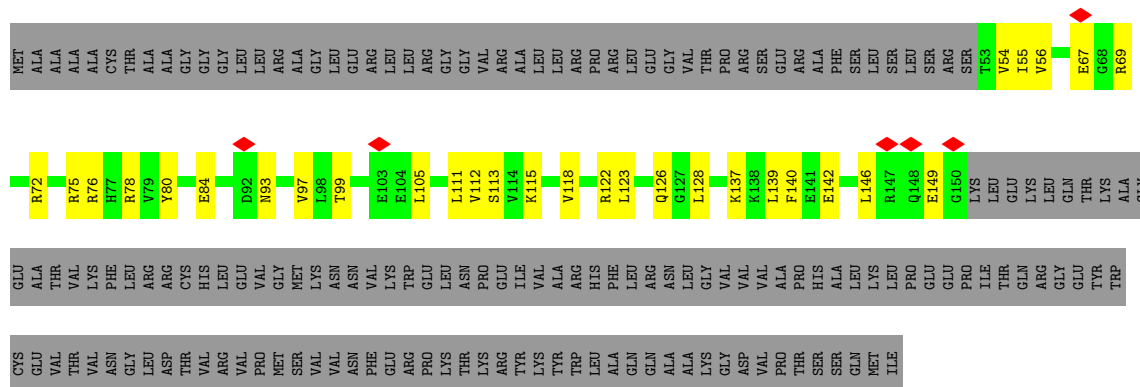
• Molecule 38: uL2m



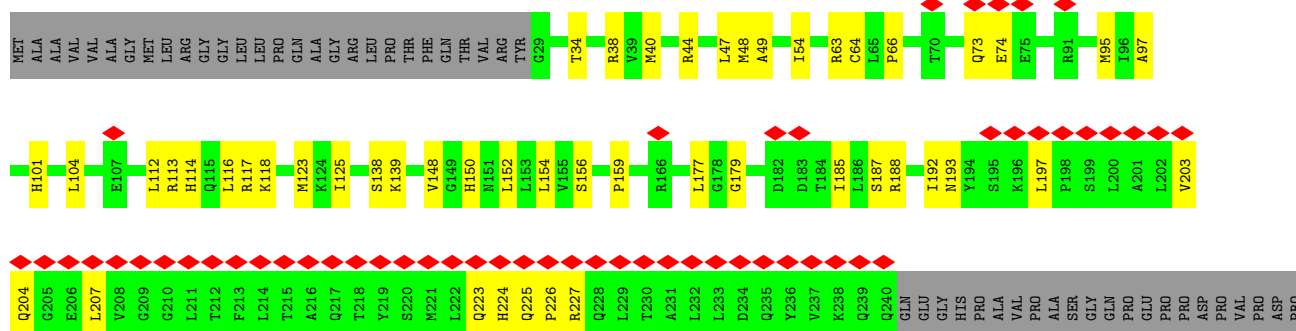
- Chain BF: 68% 17% 15%
- | Residue | Category |
|---------|----------|
| MET | Chain BF |
| LEU | Chain BF |
| GLN | Chain BF |
| LEU | Chain BF |
| VAL | Chain BF |
| ARG | Chain BF |
| ALA | Chain BF |
| GLY | Chain BF |
| ALA | Chain BF |
| K107 | Chain BF |
| R108 | Chain BF |
| THR | Chain BF |
| TRP | Chain BF |
| PHE | Chain BF |
| ARG | Chain BF |
| PRO | Chain BF |
| SER | Chain BF |
| GLY | Chain BF |
| CYS | Chain BF |
| ARG | Chain BF |
| GLY | Chain BF |
| LEU | Chain BF |
| ASN | Chain BF |
| THR | Chain BF |
| LEU | Chain BF |
| ALA | Chain BF |
| GLU | Chain BF |
| GLU | Chain BF |
| ALA | Chain BF |
| VAL | Chain BF |
| GLN | Chain BF |
| GLN | Chain BF |
| ALA | Chain BF |
| GLU | Chain BF |
| LYS | Chain BF |
| PRO | Chain BF |
| GLU | Chain BF |
| SER | Chain BF |
| VAL | Chain BF |
| Q201 | Chain BF |
| Y202 | Chain BF |
| E205 | Chain BF |
| R208 | Chain BF |
| Y209 | Chain BF |
| R210 | Chain BF |
| R211 | Chain BF |
| W212 | Chain BF |
| L218 | Chain BF |
| V219 | Chain BF |
| D220 | Chain BF |
| L221 | Chain BF |
| P227 | Chain BF |
| V230 | Chain BF |
| L237 | Chain BF |
| D94 | Other |
| V99 | Other |
| W102 | Other |
| Q103 | Other |
| F106 | Other |
| K107 | Other |
| R108 | Other |
| K113 | Other |
| A118 | Other |
| G123 | Other |
| K131 | Other |
| I141 | Other |
| R142 | Other |
| R147 | Other |
| G157 | Other |
| Y161 | Other |
| V171 | Other |
| Q172 | Other |
| G173 | Other |
| Q184 | Other |
| E193 | Other |
| L194 | Other |
| L195 | Other |
| Q201 | Other |
| Y202 | Other |
| E205 | Other |
| R208 | Other |
| Y209 | Other |
| R210 | Other |
| R211 | Other |
| W212 | Other |
| L218 | Other |
| V219 | Other |
| D220 | Other |
| L221 | Other |
| P227 | Other |
| V230 | Other |
| L237 | Other |
| P45 | Other |
| P46 | Other |
| I66 | Other |
| E67 | Other |
| S68 | Other |
| L69 | Other |
| Y72 | Other |
| T80 | Other |
| H83 | Other |
| P84 | Other |
| D85 | Other |



• Molecule 43: Mitochondrial ribosomal protein L9

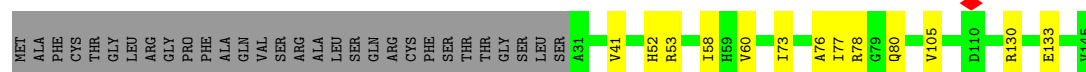


• Molecule 44: Mitochondrial ribosomal protein L10

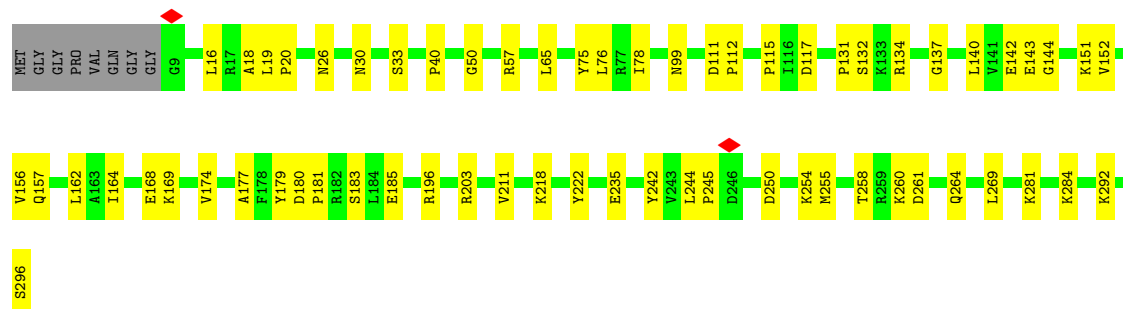
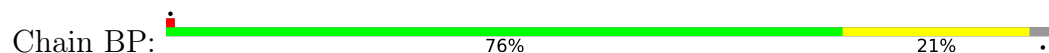




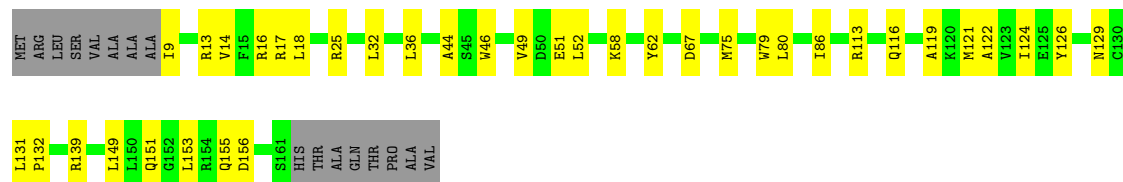
- Molecule 47: uL14m



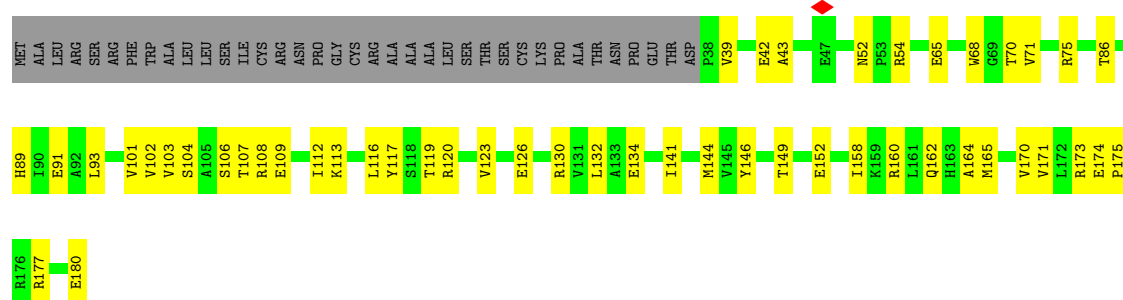
- Molecule 48: uL15m



- Molecule 49: bL17m

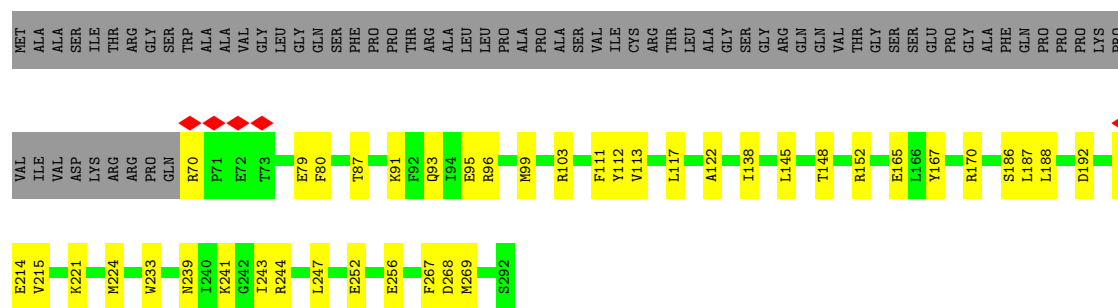


- Molecule 50: Mitochondrial ribosomal protein L18



- Molecule 51: Mitochondrial ribosomal protein L19

Chain BT: 



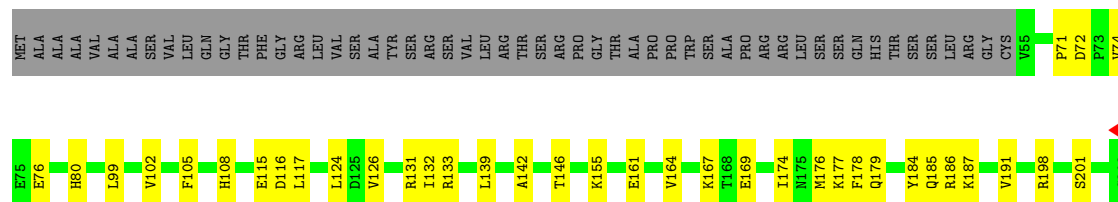
- Molecule 52: Mitochondrial ribosomal protein L20

Chain BU: 



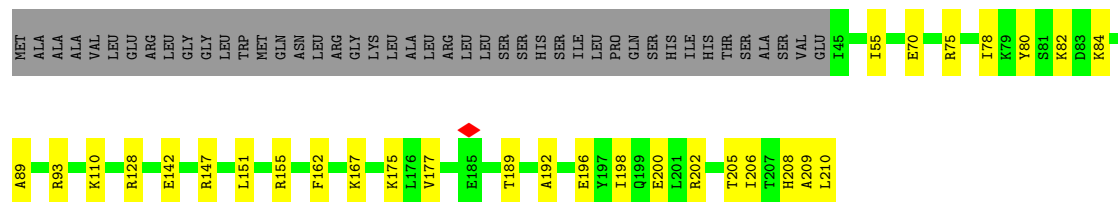
- Molecule 53: Mitochondrial ribosomal protein L21

Chain BV: 



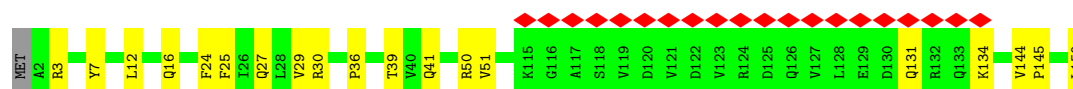
- Molecule 54: uL22m

Chain BW: 



- Molecule 55: uL23m

Chain BX: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	224731	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.284	Depositor
Minimum map value	-0.144	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.028	Depositor
Map size (Å)	521.76, 521.76, 521.76	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.087, 1.087, 1.087	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SPM, MG, ZN, 5GP, GNP

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	B0	0.12	0/880	0.27	0/1189
2	BY	0.11	0/1719	0.32	0/2329
3	Ba	0.12	0/3267	0.31	0/4455
4	B8	0.12	0/853	0.31	0/1136
5	Bb	0.13	0/3047	0.34	0/4139
6	Bc	0.12	0/2464	0.32	0/3330
7	Bd	0.12	0/1203	0.30	0/1622
8	Be	0.11	0/1000	0.28	0/1345
9	Bf	0.13	0/851	0.48	2/1159 (0.2%)
10	Bg	0.13	0/1191	0.33	0/1614
11	Bh	0.12	0/2372	0.29	0/3211
12	Bi	0.11	0/2199	0.32	0/2980
13	Bj	0.12	0/1811	0.39	2/2436 (0.1%)
14	Bk	0.10	0/1270	0.30	0/1714
15	Bl	0.12	0/1135	0.30	0/1549
16	Bm	0.09	0/917	0.25	0/1248
17	Bn	0.14	0/860	0.34	0/1150
18	Bo	0.10	0/787	0.26	0/1056
19	Bp	0.10	0/752	0.34	0/1013
20	Bq	0.11	0/692	0.36	1/936 (0.1%)
21	Bt	0.13	0/798	0.34	0/1073
22	Bu	0.11	0/1214	0.40	1/1630 (0.1%)
23	Bv	0.11	0/1157	0.28	0/1560
24	Bw	0.13	0/3206	0.32	0/4354
25	Bx	0.14	0/1364	0.34	0/1849
26	CL	0.08	0/319	0.25	0/435
26	DL	0.08	0/212	0.23	0/286
26	EL	0.09	0/221	0.28	0/297
26	FL	0.43	1/212 (0.5%)	0.28	0/286
26	GL	0.07	0/212	0.22	0/286
26	HL	0.08	0/204	0.26	0/275
26	LL	0.13	0/542	0.35	0/729

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
27	B1	0.11	0/2093	0.27	0/2835
28	B9	0.13	0/342	0.33	0/450
29	BA	0.12	0/36784	0.25	0/57270
30	B2	0.12	0/1586	0.30	0/2123
31	B3	0.13	0/993	0.32	0/1341
32	B4	0.14	0/481	0.49	1/653 (0.2%)
33	B5	0.13	0/917	0.32	0/1227
34	B6	0.10	0/430	0.29	0/570
35	B7	0.12	0/395	0.31	0/524
36	BB	0.07	0/1595	0.18	0/2475
37	BC	0.15	1/5523 (0.0%)	0.42	3/7495 (0.0%)
38	BD	0.16	0/1898	0.36	1/2555 (0.0%)
39	BG	0.12	0/1529	0.34	0/2058
40	BQ	0.14	0/1850	0.35	0/2491
41	BE	0.12	0/2493	0.31	0/3387
42	BF	0.13	0/2069	0.34	0/2816
43	BI	0.12	0/819	0.32	0/1101
44	BJ	0.12	0/1742	0.34	0/2358
45	BK	0.12	0/1359	0.33	0/1828
46	BN	0.12	0/1487	0.29	0/2017
47	BO	0.12	0/912	0.29	0/1231
48	BP	0.13	0/2368	0.31	0/3198
49	BR	0.13	0/1262	0.33	0/1700
50	BS	0.13	0/1197	0.38	0/1624
51	BT	0.13	0/1894	0.32	0/2555
52	BU	0.13	0/1179	0.32	0/1578
53	BV	0.13	0/1256	0.33	0/1706
54	BW	0.13	0/1407	0.31	0/1891
55	BX	0.14	0/1211	0.32	0/1646
All	All	0.12	2/118002 (0.0%)	0.30	11/167374 (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
17	Bn	0	1
26	FL	1	0
38	BD	0	1
All	All	1	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	FL	89	THR	CB-OG1	5.59	1.52	1.43
37	BC	659	PRO	CG-CD	-5.51	1.32	1.50

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	BC	659	PRO	N-CD-CG	-8.85	89.93	103.20
37	BC	65	PRO	N-CA-CB	8.19	111.02	103.08
9	Bf	80	PRO	N-CA-CB	7.60	111.23	103.25
22	Bu	167	PRO	N-CA-CB	7.53	111.15	103.25
9	Bf	78	PRO	N-CA-CB	7.51	111.14	103.25
20	Bq	59	PRO	N-CA-CB	6.78	110.46	103.00
37	BC	66	PRO	N-CA-CB	6.76	110.35	103.25
38	BD	289	PRO	N-CD-CG	-6.31	93.73	103.20
32	B4	87	PRO	N-CA-CB	6.18	110.13	103.33
13	Bj	83	LEU	CA-C-N	5.56	134.32	121.87
13	Bj	83	LEU	C-N-CA	5.56	134.32	121.87

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
26	FL	89	THR	CB

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
38	BD	207	TYR	Peptide
17	Bn	65	ASN	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B0	857	0	878	14	0
2	BY	1678	0	1683	28	0
3	Ba	3173	0	3153	55	0
4	B8	833	0	883	22	0
5	Bb	2952	0	2840	70	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	Bc	2408	0	2415	57	0
7	Bd	1177	0	1182	31	0
8	Be	972	0	971	19	0
9	Bf	827	0	736	10	0
10	Bg	1167	0	1173	28	0
11	Bh	2319	0	2332	41	0
12	Bi	2138	0	2139	52	0
13	Bj	1775	0	1797	55	0
14	Bk	1246	0	1251	30	0
15	Bl	1097	0	1080	13	0
16	Bm	893	0	878	8	0
17	Bn	837	0	860	14	0
18	Bo	772	0	773	11	0
19	Bp	742	0	749	19	0
20	Bq	672	0	647	18	0
21	Bt	780	0	792	18	0
22	Bu	1198	0	1192	15	0
23	Bv	1131	0	1093	21	0
24	Bw	3126	0	3153	49	0
25	Bx	1325	0	1354	30	0
26	CL	317	0	309	9	0
26	DL	213	0	234	3	0
26	EL	222	0	247	8	0
26	FL	213	0	234	7	0
26	GL	213	0	234	4	0
26	HL	205	0	223	6	0
26	LL	537	0	591	16	0
27	B1	2036	0	2058	24	0
28	B9	335	0	359	6	0
29	BA	32844	0	16617	370	0
30	B2	1548	0	1583	24	0
31	B3	968	0	1018	21	0
32	B4	474	0	454	16	0
33	B5	902	0	916	21	0
34	B6	425	0	471	9	0
35	B7	387	0	413	9	0
36	BB	1427	0	726	18	0
37	BC	5434	0	5482	131	0
38	BD	1860	0	1923	31	0
39	BG	1520	0	1603	39	0
40	BQ	1803	0	1841	18	0
41	BE	2420	0	2418	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	BF	2011	0	2049	42	0
43	BI	805	0	845	19	0
44	BJ	1705	0	1804	40	0
45	BK	1339	0	1407	27	0
46	BN	1444	0	1437	18	0
47	BO	896	0	946	7	0
48	BP	2312	0	2373	49	0
49	BR	1240	0	1260	31	0
50	BS	1168	0	1159	36	0
51	BT	1851	0	1867	27	0
52	BU	1159	0	1228	30	0
53	BV	1231	0	1278	30	0
54	BW	1374	0	1405	22	0
55	BX	1181	0	1139	18	0
56	B0	1	0	0	0	0
56	B3	1	0	0	0	0
56	BA	205	0	0	0	0
56	BC	1	0	0	0	0
56	BD	3	0	0	0	0
56	BE	1	0	0	0	0
56	BJ	1	0	0	0	0
56	BP	2	0	0	0	0
56	BQ	1	0	0	0	0
56	BR	1	0	0	0	0
56	Bb	1	0	0	0	0
56	Be	1	0	0	0	0
56	Bl	1	0	0	0	0
56	Bt	1	0	0	0	0
57	B5	1	0	0	0	0
57	B9	1	0	0	0	0
57	Bx	1	0	0	0	0
58	BA	48	0	24	0	0
59	BA	28	0	52	1	0
60	BC	32	0	13	0	0
61	BC	2	0	0	0	0
All	All	112448	0	96244	1604	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 8.

All (1604) 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)
44:BJ:63:ARG:HH11	44:BJ:64:CYS:HB3	1.40	0.86
26:FL:85:LEU:O	26:FL:89:THR:HG23	1.77	0.85
3:Ba:126:THR:HG22	3:Ba:372:ASN:HB2	1.59	0.84
6:Bc:315:ARG:NH1	49:BR:156:ASP:OD2	2.10	0.83
17:Bn:55:GLY:O	42:BF:249:ASN:ND2	2.13	0.81
10:Bg:127:GLN:HE21	52:BU:111:LYS:HB2	1.46	0.80
19:Bp:55:VAL:HB	44:BJ:188:ARG:HD2	1.64	0.79
3:Ba:41:PRO:HG2	29:BA:42:C:H41	1.45	0.79
6:Bc:156:LYS:HG3	9:Bf:89:ASP:H	1.46	0.79
37:BC:383:LEU:HB3	37:BC:434:LEU:HD11	1.64	0.79
37:BC:248:CYS:HB3	37:BC:252:ASP:HA	1.65	0.78
37:BC:373:LYS:HB3	37:BC:385:PHE:HB2	1.65	0.78
42:BF:205:GLU:OE1	42:BF:208:ARG:NH2	2.17	0.78
29:BA:112:A:N6	29:BA:115:U:OP2	2.18	0.77
37:BC:711:ARG:HH22	37:BC:742:VAL:HG21	1.50	0.76
29:BA:392:U:H2'	29:BA:393:A:H8	1.50	0.76
28:B9:63:PHE:N	29:BA:1349:G:HO2'	1.84	0.75
10:Bg:19:LEU:HD11	53:BV:115:GLU:HG2	1.68	0.75
29:BA:1331:G:H1	29:BA:1403:U:H3	1.32	0.74
37:BC:306:LEU:HD11	37:BC:310:LYS:H	1.53	0.74
2:BY:112:GLU:OE2	12:Bi:74:ARG:NH1	2.21	0.74
28:B9:69:LEU:HD11	28:B9:99:GLN:HB2	1.70	0.74
38:BD:133:ASP:OD2	38:BD:136:ARG:NH1	2.20	0.74
5:Bb:53:SER:OG	5:Bb:55:ASP:OD1	2.05	0.73
26:LL:134:LEU:HG	26:LL:168:LEU:HD21	1.70	0.73
6:Bc:175:ALA:HB2	6:Bc:316:SER:HB2	1.70	0.73
29:BA:672:G:H4'	35:B7:58:PRO:HB2	1.71	0.73
12:Bi:176:ILE:HD13	55:BX:145:PRO:HG3	1.70	0.72
14:Bk:201:ARG:HD3	14:Bk:204:LEU:HD13	1.71	0.72
6:Bc:76:PHE:HB3	6:Bc:78:MET:HE2	1.72	0.71
29:BA:831:U:OP2	29:BA:836:A:N6	2.20	0.71
1:B0:125:VAL:HG21	5:Bb:64:GLU:HG3	1.73	0.71
7:Bd:106:LEU:HB2	13:Bj:212:HIS:HE1	1.55	0.71
38:BD:113:ARG:O	38:BD:148:ARG:NH2	2.24	0.71
10:Bg:72:VAL:HG23	10:Bg:90:HIS:HB2	1.73	0.71
9:Bf:122:ARG:NH2	54:BW:200:GLU:OE1	2.24	0.71
29:BA:1569:A:N1	41:BE:69:ASN:ND2	2.38	0.71
10:Bg:133:PHE:HZ	11:Bh:261:SER:HB2	1.57	0.70
12:Bi:157:HIS:O	12:Bi:161:HIS:ND1	2.23	0.70
40:BQ:226:ILE:HG12	44:BJ:47:LEU:HD22	1.74	0.70
25:Bx:92:PHE:HZ	25:Bx:115:ILE:HD13	1.55	0.70
38:BD:76:PRO:HB2	38:BD:103:ARG:HE	1.57	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:BV:174:ILE:HD12	53:BV:187:LYS:HZ1	1.57	0.70
39:BG:77:ALA:HA	39:BG:80:GLU:HG3	1.72	0.70
32:B4:57:LEU:HD23	32:B4:65:ILE:HD11	1.74	0.69
37:BC:573:ARG:HD3	37:BC:594:GLU:HB3	1.73	0.69
2:BY:177:THR:HG22	8:Be:69:LYS:H	1.58	0.69
12:Bi:267:PRO:HG2	12:Bi:270:ALA:HB2	1.72	0.69
37:BC:90:ILE:HG23	37:BC:342:LEU:HD11	1.74	0.69
29:BA:148:A:H4'	29:BA:149:A:H5''	1.74	0.69
29:BA:1081:U:O4	29:BA:1135:C:N3	2.26	0.69
32:B4:60:GLN:NE2	32:B4:78:MET:SD	2.65	0.69
37:BC:227:GLY:HA3	37:BC:231:THR:HG23	1.75	0.69
37:BC:493:THR:HG22	37:BC:531:VAL:HG12	1.74	0.69
49:BR:58:LYS:NZ	51:BT:269:MET:O	2.26	0.69
50:BS:102:VAL:HG12	50:BS:103:VAL:HG23	1.74	0.69
51:BT:70:ARG:NH2	51:BT:214:GLU:OE2	2.26	0.69
54:BW:142:GLU:HB2	54:BW:175:LYS:HB3	1.75	0.69
1:B0:71:ARG:NH1	29:BA:1162:G:OP1	2.26	0.69
52:BU:14:VAL:HB	52:BU:17:ARG:HH21	1.58	0.69
3:Ba:236:LEU:HD12	3:Ba:237:PRO:HD2	1.75	0.69
29:BA:471:U:OP1	31:B3:73:LYS:NZ	2.25	0.69
29:BA:975:G:O2'	29:BA:977:G:OP2	2.10	0.69
19:Bp:30:THR:HG21	19:Bp:62:PRO:HB2	1.74	0.68
39:BG:159:ILE:HD11	39:BG:178:ILE:HD12	1.75	0.68
29:BA:508:G:H4'	45:BK:151:LEU:HD23	1.75	0.68
29:BA:869:G:O2'	29:BA:966:U:OP2	2.11	0.68
37:BC:73:ILE:HG21	37:BC:349:LEU:HD13	1.75	0.68
29:BA:877:U:H5''	29:BA:878:G:H5'	1.75	0.68
37:BC:696:VAL:HG11	37:BC:704:VAL:HG21	1.76	0.68
21:Bt:9:ARG:NH2	29:BA:564:A:OP1	2.26	0.68
29:BA:993:U:OP2	41:BE:238:ARG:NH2	2.27	0.68
46:BN:27:PRO:HG2	46:BN:30:LYS:HB2	1.76	0.68
43:BI:111:LEU:HD21	43:BI:137:LYS:HD3	1.75	0.67
39:BG:104:ASN:O	39:BG:108:ASN:ND2	2.23	0.67
49:BR:25:ARG:NH1	49:BR:51:GLU:OE1	2.27	0.67
41:BE:202:GLN:NE2	41:BE:301:ASP:OD1	2.27	0.67
44:BJ:95:MET:HB2	44:BJ:159:PRO:HB3	1.74	0.67
7:Bd:109:SER:OG	13:Bj:230:LYS:NZ	2.24	0.67
3:Ba:160:HIS:HA	3:Ba:164:TRP:HB2	1.77	0.67
12:Bi:90:PRO:HB2	12:Bi:269:TRP:HH2	1.58	0.67
24:Bw:146:GLN:HA	24:Bw:150:PHE:HB2	1.76	0.67
6:Bc:186:LEU:HG	6:Bc:189:TRP:HE1	1.60	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BA:472:U:H5''	31:B3:74:SER:HB3	1.76	0.67
27:B1:44:ARG:NH2	43:BI:84:GLU:OE1	2.27	0.66
38:BD:258:ILE:HG23	38:BD:263:ARG:HB3	1.77	0.66
18:Bo:23:ALA:O	18:Bo:28:ARG:NH2	2.28	0.66
37:BC:296:LEU:HD21	26:LL:142:LYS:HG3	1.76	0.66
21:Bt:78:GLN:NE2	29:BA:420:U:O4	2.28	0.66
26:HL:74:LEU:HD22	26:HL:78:GLU:HG2	1.76	0.66
37:BC:687:GLU:HB3	37:BC:763:MET:HE3	1.78	0.66
48:BP:137:GLY:HA3	48:BP:157:GLN:HG3	1.78	0.66
2:BY:69:ASP:HB2	2:BY:72:LYS:HD2	1.78	0.66
19:Bp:43:ARG:HH11	44:BJ:104:LEU:HD22	1.60	0.66
29:BA:175:C:H5''	46:BN:115:ASN:HB2	1.77	0.65
39:BG:92:MET:HB3	39:BG:245:THR:HG21	1.77	0.65
10:Bg:73:PRO:HB2	10:Bg:89:ILE:HG13	1.77	0.65
29:BA:135:G:N1	29:BA:138:A:OP2	2.28	0.65
29:BA:1014:A:OP1	52:BU:34:ARG:NH2	2.30	0.65
10:Bg:135:ASN:ND2	52:BU:78:GLU:OE1	2.24	0.65
29:BA:446:C:H2'	29:BA:447:A:C8	2.31	0.65
39:BG:84:ASN:HB3	39:BG:87:GLU:HB2	1.77	0.65
37:BC:332:ALA:HA	37:BC:338:ILE:HD11	1.78	0.65
6:Bc:147:MET:HE3	6:Bc:178:TYR:HB2	1.79	0.65
37:BC:239:VAL:HG23	37:BC:311:LEU:HD23	1.77	0.65
37:BC:75:ILE:O	37:BC:142:THR:OG1	2.15	0.65
52:BU:54:THR:HG21	53:BV:176:MET:H	1.61	0.65
49:BR:126:TYR:O	49:BR:129:ASN:ND2	2.28	0.65
7:Bd:129:ARG:HB3	14:Bk:184:LEU:HB3	1.78	0.65
29:BA:83:A:OP2	29:BA:1235:C:O2'	2.13	0.65
25:Bx:175:PRO:HD3	29:BA:492:A:H62	1.61	0.65
32:B4:43:ARG:NH1	32:B4:44:LEU:O	2.29	0.65
53:BV:102:VAL:HB	53:BV:139:LEU:HB3	1.78	0.65
13:Bj:147:THR:OG1	13:Bj:252:HIS:O	2.15	0.64
50:BS:144:MET:HE2	50:BS:170:VAL:HG11	1.80	0.64
12:Bi:111:ARG:O	12:Bi:115:ASN:ND2	2.30	0.64
17:Bn:77:PRO:HG2	17:Bn:80:LEU:HB2	1.80	0.64
11:Bh:97:TYR:HB2	11:Bh:181:SER:HA	1.79	0.64
39:BG:111:THR:HG21	39:BG:169:LEU:HD21	1.77	0.64
5:Bb:279:ILE:HD11	5:Bb:310:ALA:HB3	1.78	0.64
26:DL:76:LEU:HG	44:BJ:197:LEU:HD23	1.78	0.64
21:Bt:32:LYS:HE2	44:BJ:49:ALA:HB1	1.79	0.64
31:B3:142:ASN:ND2	31:B3:144:GLU:OE1	2.30	0.64
6:Bc:244:ASN:ND2	6:Bc:248:ILE:O	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:BJ:113:ARG:HH21	44:BJ:117:ARG:HH12	1.44	0.64
34:B6:16:ILE:HD12	34:B6:64:SER:HA	1.80	0.64
13:Bj:255:VAL:HB	13:Bj:259:GLU:HB2	1.80	0.63
3:Ba:309:LEU:O	3:Ba:313:MET:HG3	1.99	0.63
18:Bo:78:VAL:HG21	31:B3:134:MET:HE1	1.79	0.63
2:BY:146:VAL:HG22	2:BY:153:ILE:HG22	1.79	0.63
43:BI:67:GLU:OE1	43:BI:69:ARG:NH1	2.31	0.63
53:BV:71:PRO:HB2	53:BV:76:GLU:HG2	1.80	0.63
1:B0:88:CYS:SG	29:BA:1207:C:O2'	2.56	0.63
33:B5:163:GLU:OE2	33:B5:187:GLN:NE2	2.25	0.63
40:BQ:163:MET:HE1	40:BQ:175:PHE:HZ	1.61	0.63
5:Bb:120:GLU:OE2	7:Bd:75:LYS:NZ	2.32	0.63
32:B4:43:ARG:NH2	36:BB:32:A:OP1	2.24	0.63
7:Bd:106:LEU:HB2	13:Bj:212:HIS:CE1	2.33	0.63
10:Bg:28:ARG:HG2	10:Bg:78:GLU:HB2	1.79	0.63
29:BA:743:U:H3'	29:BA:744:A:H5''	1.81	0.63
22:Bu:52:SER:HB2	22:Bu:57:THR:HG21	1.80	0.63
24:Bw:368:LEU:HD21	24:Bw:371:LEU:HD13	1.81	0.62
25:Bx:81:TYR:OH	25:Bx:111:GLU:OE2	2.11	0.62
37:BC:637:GLN:NE2	39:BG:105:LYS:O	2.32	0.62
42:BF:66:ILE:HD11	42:BF:80:THR:HB	1.82	0.62
45:BK:43:GLY:HA3	45:BK:76:ARG:HD2	1.81	0.62
13:Bj:152:LYS:HB2	13:Bj:157:LEU:HD11	1.79	0.62
22:Bu:105:ALA:O	22:Bu:115:ARG:NH1	2.31	0.62
19:Bp:21:CYS:HB2	19:Bp:24:GLU:HG2	1.82	0.62
37:BC:612:ALA:HB3	37:BC:651:THR:HG22	1.80	0.62
2:BY:112:GLU:N	2:BY:112:GLU:OE1	2.32	0.62
12:Bi:235:GLN:NE2	12:Bi:237:ASP:OD1	2.31	0.62
37:BC:113:MET:HE1	37:BC:124:GLN:HG3	1.81	0.62
4:B8:113:ARG:NH2	29:BA:84:G:OP2	2.33	0.62
33:B5:90:ASN:OD1	33:B5:93:ARG:NH2	2.33	0.62
43:BI:115:LYS:HG3	43:BI:118:VAL:HG22	1.81	0.62
3:Ba:174:GLU:HA	3:Ba:296:SER:HB2	1.81	0.62
20:Bq:86:LEU:HD13	45:BK:115:LYS:HZ3	1.65	0.62
29:BA:154:A:OP2	33:B5:91:ARG:NH1	2.33	0.62
29:BA:229:A:H4'	29:BA:230:G:H5'	1.81	0.62
42:BF:83:HIS:HD2	42:BF:85:ASP:HB2	1.64	0.62
29:BA:62:C:OP1	43:BI:76:ARG:NH1	2.33	0.62
29:BA:1306:C:N3	40:BQ:182:LYS:NZ	2.44	0.62
37:BC:295:VAL:HG22	37:BC:305:LEU:HD21	1.81	0.62
37:BC:624:GLN:O	37:BC:628:GLU:HG2	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Bw:145:LEU:HD22	24:Bw:402:ASN:HA	1.82	0.61
29:BA:129:A:OP1	42:BF:142:ARG:NH2	2.33	0.61
37:BC:612:ALA:O	37:BC:651:THR:HA	1.99	0.61
3:Ba:310:ARG:HD2	3:Ba:353:GLN:HG2	1.81	0.61
11:Bh:41:PHE:HE2	17:Bn:36:VAL:HG12	1.65	0.61
29:BA:198:U:H2'	29:BA:199:A:H8	1.65	0.61
29:BA:234:G:N2	48:BP:33:SER:O	2.32	0.61
33:B5:134:THR:HG23	49:BR:131:LEU:HD22	1.82	0.61
18:Bo:80:LEU:HD22	31:B3:101:LYS:HE3	1.82	0.61
29:BA:433:G:H22	29:BA:458:A:H2	1.46	0.61
29:BA:788:A:O2'	49:BR:17:ARG:NH2	2.28	0.61
14:Bk:48:TYR:HB3	14:Bk:51:LYS:HG2	1.81	0.61
21:Bt:51:ARG:NH2	31:B3:59:ASP:O	2.33	0.61
48:BP:142:GLU:HG3	48:BP:162:LEU:HD23	1.82	0.61
6:Bc:99:LYS:NZ	33:B5:108:ASP:OD1	2.34	0.61
25:Bx:157:ARG:NH1	29:BA:1526:U:O2'	2.33	0.61
28:B9:69:LEU:H	29:BA:560:A:H62	1.48	0.61
42:BF:201:GLN:O	42:BF:205:GLU:HG2	2.00	0.61
54:BW:151:LEU:HB2	54:BW:167:LYS:HB2	1.83	0.61
39:BG:129:ALA:HB3	39:BG:132:GLN:HG3	1.83	0.61
29:BA:565:A:N6	29:BA:1314:U:OP1	2.32	0.61
29:BA:1569:A:H5'	41:BE:62:LYS:HE2	1.83	0.61
39:BG:74:ILE:HG13	39:BG:75:ASN:H	1.66	0.61
13:Bj:85:SER:HB3	32:B4:51:ARG:HB3	1.82	0.61
29:BA:1404:G:OP2	29:BA:1404:G:N2	2.25	0.61
39:BG:155:THR:O	39:BG:159:ILE:HG12	2.01	0.61
11:Bh:52:ARG:NH1	29:BA:148:A:OP1	2.34	0.61
14:Bk:90:VAL:HG12	14:Bk:160:SER:HA	1.83	0.61
37:BC:147:ASP:HB3	37:BC:539:HIS:HB2	1.82	0.61
4:B8:175:ASP:HB3	4:B8:178:GLN:HB2	1.83	0.61
15:Bl:41:SER:OG	48:BP:284:LYS:NZ	2.26	0.61
37:BC:351:SER:HB2	37:BC:354:GLU:HG3	1.81	0.61
37:BC:587:HIS:HB2	37:BC:661:THR:HG22	1.82	0.61
19:Bp:28:GLU:HG2	44:BJ:148:VAL:HG11	1.83	0.60
24:Bw:278:ILE:HD11	24:Bw:333:GLN:HG2	1.83	0.60
18:Bo:74:ALA:HB2	31:B3:137:THR:HG21	1.83	0.60
29:BA:178:C:O2	52:BU:52:LYS:NZ	2.33	0.60
37:BC:299:PHE:HB2	37:BC:305:LEU:HG	1.83	0.60
47:BO:77:ILE:HG22	47:BO:78:ARG:HG3	1.82	0.60
29:BA:655:C:OP1	33:B5:138:ARG:NH1	2.30	0.60
31:B3:123:LYS:HB2	31:B3:144:GLU:HG3	1.81	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Bw:59:ARG:NH1	29:BA:778:A:OP1	2.35	0.60
8:Be:120:THR:HG22	8:Be:122:GLU:H	1.66	0.60
12:Bi:219:ARG:HE	12:Bi:239:PRO:HB2	1.67	0.60
19:Bp:18:VAL:HG12	19:Bp:64:VAL:HG12	1.83	0.60
22:Bu:134:LEU:HD21	22:Bu:156:MET:HE1	1.83	0.60
26:CL:74:LEU:HD22	26:CL:78:GLU:HG3	1.83	0.60
30:B2:175:PHE:O	30:B2:214:ARG:NH2	2.29	0.60
29:BA:672:G:H21	29:BA:759:C:H5'	1.67	0.60
26:LL:163:LYS:HA	26:LL:166:GLU:HG2	1.83	0.60
16:Bm:92:LEU:HD23	16:Bm:98:LYS:HG3	1.84	0.60
30:B2:185:GLN:NE2	55:BX:7:TYR:O	2.31	0.60
20:Bq:101:VAL:HG11	45:BK:114:LEU:HD11	1.84	0.59
12:Bi:165:THR:HG23	12:Bi:167:ASN:H	1.67	0.59
29:BA:677:C:OP1	29:BA:695:U:O2'	2.20	0.59
5:Bb:130:ILE:HB	50:BS:130:ARG:HH21	1.66	0.59
6:Bc:129:ASP:OD1	6:Bc:130:ASP:N	2.34	0.59
14:Bk:127:MET:SD	14:Bk:128:PRO:HD2	2.42	0.59
23:Bv:40:PRO:HG3	23:Bv:51:GLN:HB3	1.83	0.59
27:B1:96:LYS:O	29:BA:60:U:O2'	2.20	0.59
14:Bk:127:MET:HB3	14:Bk:154:GLU:HB3	1.82	0.59
37:BC:177:LEU:HD21	37:BC:181:ARG:HH22	1.67	0.59
39:BG:146:VAL:HB	39:BG:178:ILE:HB	1.84	0.59
4:B8:146:GLU:OE1	5:Bb:364:ARG:NH1	2.28	0.59
7:Bd:146:GLY:HA2	14:Bk:144:MET:HE1	1.83	0.59
11:Bh:59:ARG:NH1	11:Bh:181:SER:O	2.34	0.59
43:BI:105:LEU:HD12	43:BI:112:VAL:HG21	1.85	0.59
15:Bl:40:GLU:HG2	48:BP:281:LYS:HD2	1.85	0.59
29:BA:150:A:N3	29:BA:198:U:O2'	2.29	0.59
52:BU:85:ALA:O	52:BU:89:ASN:ND2	2.35	0.59
22:Bu:99:GLU:OE2	22:Bu:101:ARG:NH1	2.36	0.59
26:HL:70:ASP:O	26:HL:74:LEU:HG	2.02	0.59
39:BG:67:GLN:NE2	39:BG:69:GLN:O	2.29	0.59
39:BG:223:LYS:HD3	39:BG:231:ILE:HG21	1.83	0.59
29:BA:569:C:N4	29:BA:1020:C:O2	2.36	0.59
5:Bb:159:ARG:O	5:Bb:163:HIS:ND1	2.35	0.59
5:Bb:238:THR:HG21	5:Bb:281:PHE:HZ	1.66	0.59
29:BA:53:U:O4	29:BA:62:C:N3	2.36	0.59
29:BA:243:A:N3	29:BA:1266:U:O2'	2.34	0.59
49:BR:18:LEU:HB2	49:BR:25:ARG:HG3	1.85	0.59
5:Bb:304:TYR:O	5:Bb:308:GLN:HB2	2.03	0.59
48:BP:261:ASP:HB3	48:BP:264:GLN:HB2	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:Bb:217:LEU:HD13	5:Bb:236:LEU:HD13	1.85	0.58
7:Bd:77:TRP:CG	13:Bj:70:MET:HE2	2.38	0.58
12:Bi:211:GLN:HA	12:Bi:248:PHE:O	2.03	0.58
20:Bq:92:TYR:HE2	45:BK:115:LYS:HG3	1.68	0.58
37:BC:413:LEU:HD11	37:BC:433:ALA:HB1	1.85	0.58
10:Bg:13:SER:OG	53:BV:198:ARG:NH2	2.36	0.58
15:Bl:110:ILE:HD11	15:Bl:157:LEU:HD13	1.84	0.58
31:B3:104:PRO:HA	31:B3:107:ASN:HB2	1.84	0.58
40:BQ:211:ASN:HB3	44:BJ:54:ILE:HD12	1.86	0.58
44:BJ:73:GLN:NE2	44:BJ:74:GLU:O	2.36	0.58
53:BV:99:LEU:HD23	53:BV:142:ALA:HB2	1.85	0.58
3:Ba:72:ARG:HH12	29:BA:43:C:H1'	1.69	0.58
4:B8:110:VAL:O	4:B8:114:PHE:HB2	2.03	0.58
27:B1:26:ARG:NH2	27:B1:33:GLU:OE2	2.33	0.58
53:BV:126:VAL:HG11	53:BV:132:ILE:HD11	1.85	0.58
3:Ba:113:LEU:HD23	3:Ba:119:GLN:HB3	1.86	0.58
12:Bi:177:ARG:NH2	29:BA:142:U:O4	2.33	0.58
37:BC:627:ILE:O	37:BC:631:ILE:HG12	2.03	0.58
44:BJ:204:GLN:HA	44:BJ:207:LEU:HD12	1.85	0.58
45:BK:56:LYS:HD2	45:BK:82:ILE:HD12	1.85	0.58
29:BA:220:G:N3	29:BA:231:C:O2'	2.36	0.58
29:BA:789:A:O2'	41:BE:215:PHE:O	2.20	0.58
29:BA:1569:A:N6	41:BE:152:VAL:O	2.37	0.58
39:BG:188:GLU:O	39:BG:192:MET:HG3	2.03	0.58
51:BT:252:GLU:O	51:BT:256:GLU:HG3	2.04	0.58
4:B8:183:ARG:NH2	5:Bb:356:ARG:O	2.36	0.58
12:Bi:126:ARG:HH21	12:Bi:133:LYS:HA	1.69	0.58
29:BA:29:A:N3	29:BA:35:A:O2'	2.32	0.58
38:BD:108:ASP:OD1	38:BD:150:ARG:NH1	2.36	0.58
46:BN:114:LYS:HA	46:BN:118:ARG:HH11	1.69	0.58
10:Bg:48:GLU:OE2	21:Bt:101:TRP:NE1	2.25	0.58
24:Bw:53:ALA:O	24:Bw:62:ARG:NH2	2.36	0.58
24:Bw:195:ASP:HB3	24:Bw:198:ARG:HG3	1.85	0.58
29:BA:1262:A:H61	29:BA:1408:U:H5'	1.68	0.58
29:BA:1269:G:N2	29:BA:1272:U:O2	2.35	0.58
38:BD:197:VAL:HG11	38:BD:227:ILE:HD13	1.86	0.58
40:BQ:234:ASP:OD2	44:BJ:44:ARG:NH1	2.35	0.58
29:BA:1131:U:H2'	29:BA:1132:G:H8	1.68	0.58
37:BC:248:CYS:SG	37:BC:249:ASN:N	2.76	0.58
37:BC:274:THR:O	37:BC:278:ASN:ND2	2.37	0.58
42:BF:212:TRP:O	42:BF:258:THR:OG1	2.21	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:BK:114:LEU:HD13	45:BK:157:LYS:HA	1.86	0.58
50:BS:86:THR:O	50:BS:120:ARG:NH1	2.36	0.57
23:Bv:132:ILE:HD12	34:B6:44:LEU:HD21	1.86	0.57
17:Bn:79:TRP:HH2	29:BA:15:A:H5'	1.68	0.57
23:Bv:25:TYR:N	42:BF:237:LEU:O	2.36	0.57
44:BJ:113:ARG:HD3	44:BJ:123:MET:HE2	1.86	0.57
5:Bb:128:ALA:HB3	50:BS:123:VAL:HG21	1.85	0.57
21:Bt:15:ARG:HB2	21:Bt:18:ILE:HG12	1.85	0.57
24:Bw:399:ILE:HG22	24:Bw:404:VAL:HA	1.87	0.57
26:CL:51:ALA:HB2	44:BJ:185:ILE:HG22	1.87	0.57
26:GL:86:LEU:HD12	26:GL:90:LEU:HD13	1.87	0.57
41:BE:210:THR:OG1	41:BE:262:GLY:O	2.16	0.57
49:BR:32:LEU:HB3	49:BR:52:LEU:HD22	1.84	0.57
24:Bw:63:VAL:HA	24:Bw:66:TRP:CD1	2.39	0.57
38:BD:198:GLU:OE1	38:BD:202:GLY:N	2.37	0.57
48:BP:151:LYS:NZ	48:BP:250:ASP:OD2	2.34	0.57
2:BY:51:ASP:OD1	2:BY:81:ARG:NH1	2.30	0.57
5:Bb:220:ASN:HB3	5:Bb:232:TYR:HB2	1.85	0.57
12:Bi:218:THR:HG23	12:Bi:220:GLN:NE2	2.19	0.57
26:GL:71:ILE:HD11	26:HL:86:LEU:HD21	1.87	0.57
26:LL:148:GLU:HG3	26:LL:191:VAL:HG21	1.86	0.57
1:B0:102:GLU:OE2	1:B0:132:HIS:NE2	2.34	0.57
20:Bq:75:VAL:HG21	20:Bq:84:VAL:HG12	1.87	0.57
20:Bq:102:GLY:O	45:BK:149:ARG:NH2	2.37	0.57
29:BA:1158:C:O2'	29:BA:1251:C:OP2	2.22	0.57
50:BS:132:LEU:HD23	50:BS:165:MET:HE1	1.86	0.57
3:Ba:123:LEU:HD22	3:Ba:220:LEU:HD11	1.86	0.57
6:Bc:109:PRO:HB2	6:Bc:264:PRO:HG3	1.87	0.57
24:Bw:228:ASN:OD1	24:Bw:272:TYR:OH	2.19	0.57
29:BA:909:U:OP2	39:BG:118:LYS:NZ	2.34	0.57
31:B3:72:ILE:HD11	31:B3:118:ARG:HB2	1.86	0.57
38:BD:195:ASN:ND2	38:BD:246:GLY:O	2.33	0.57
54:BW:82:LYS:HD3	54:BW:147:ARG:HB3	1.85	0.57
53:BV:105:PHE:HZ	53:BV:124:LEU:HD21	1.69	0.57
2:BY:144:VAL:HG12	2:BY:156:LYS:HE3	1.85	0.57
5:Bb:106:ARG:NH1	36:BB:23:A:OP2	2.34	0.57
8:Be:44:ARG:HH12	24:Bw:157:ALA:HB3	1.70	0.57
27:B1:177:HIS:O	27:B1:184:ARG:NH2	2.37	0.57
29:BA:296:C:OP2	59:BA:3208:SPM:N1	2.38	0.57
37:BC:173:GLU:O	37:BC:176:THR:N	2.38	0.57
44:BJ:97:ALA:HB3	44:BJ:154:LEU:HB2	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:BN:25:MET:O	46:BN:149:ARG:NH1	2.37	0.57
6:Bc:61:LYS:HD2	6:Bc:77:VAL:HG12	1.86	0.56
37:BC:578:LEU:HD21	37:BC:665:MET:HE3	1.87	0.56
13:Bj:137:LEU:HD12	13:Bj:140:ALA:HB3	1.87	0.56
29:BA:354:U:O2'	29:BA:1055:A:N1	2.34	0.56
37:BC:189:PRO:HG2	37:BC:350:PRO:HG3	1.88	0.56
12:Bi:207:ASN:HB2	12:Bi:251:HIS:HE1	1.70	0.56
29:BA:52:A:O2'	29:BA:245:A:N1	2.33	0.56
29:BA:1005:G:H5''	54:BW:110:LYS:HB2	1.87	0.56
39:BG:136:ILE:HG12	39:BG:146:VAL:HG22	1.86	0.56
51:BT:138:ILE:HD11	51:BT:152:ARG:HB2	1.86	0.56
21:Bt:92:LEU:HB3	48:BP:19:LEU:HD11	1.88	0.56
29:BA:550:A:N6	29:BA:551:A:N1	2.53	0.56
45:BK:86:THR:HG22	45:BK:88:SER:H	1.70	0.56
29:BA:1331:G:O6	29:BA:1403:U:O4	2.23	0.56
29:BA:885:G:N2	38:BD:281:GLY:O	2.36	0.56
41:BE:50:ASP:O	49:BR:139:ARG:NH1	2.38	0.56
11:Bh:184:PHE:O	11:Bh:186:VAL:HG23	2.06	0.56
30:B2:120:GLU:OE1	55:BX:30:ARG:NH1	2.38	0.56
37:BC:627:ILE:HD13	37:BC:670:VAL:HG21	1.87	0.56
26:LL:134:LEU:HD21	26:LL:145:LEU:HD21	1.86	0.56
51:BT:96:ARG:HA	51:BT:99:MET:HG2	1.88	0.56
22:Bu:75:ARG:NH2	22:Bu:108:ASP:OD1	2.29	0.56
25:Bx:69:GLN:HB2	44:BJ:64:CYS:HB2	1.88	0.56
29:BA:170:U:O2	54:BW:205:THR:OG1	2.19	0.56
50:BS:174:GLU:HG3	50:BS:175:PRO:HD2	1.88	0.56
6:Bc:163:LEU:HB3	6:Bc:178:TYR:HE2	1.71	0.56
7:Bd:52:ASN:HA	7:Bd:55:ARG:HH12	1.70	0.56
14:Bk:90:VAL:HG23	14:Bk:189:HIS:HB3	1.88	0.56
40:BQ:98:HIS:CD2	40:BQ:100:GLY:H	2.23	0.56
29:BA:421:U:H2'	29:BA:422:U:C6	2.42	0.55
29:BA:1026:A:O2'	29:BA:1277:G:N2	2.39	0.55
38:BD:128:ILE:HD11	38:BD:144:ALA:HB2	1.87	0.55
41:BE:206:VAL:HG11	41:BE:289:VAL:HG13	1.86	0.55
42:BF:103:GLN:HE22	42:BF:249:ASN:HB2	1.71	0.55
46:BN:173:PRO:HG2	46:BN:176:TYR:HB2	1.87	0.55
6:Bc:145:MET:HE2	6:Bc:254:PHE:HD1	1.71	0.55
29:BA:165:A:H2'	29:BA:166:A:C8	2.42	0.55
29:BA:193:U:H2'	29:BA:194:G:C8	2.42	0.55
29:BA:699:G:H2'	29:BA:700:A:C8	2.42	0.55
10:Bg:127:GLN:NE2	52:BU:111:LYS:HB2	2.19	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:Bh:245:LEU:HB3	11:Bh:250:ILE:HB	1.86	0.55
15:Bl:111:ARG:NH2	29:BA:216:C:OP2	2.40	0.55
17:Bn:66:PHE:HD2	42:BF:286:PHE:HB2	1.72	0.55
23:Bv:103:LEU:O	23:Bv:107:GLN:HG2	2.07	0.55
25:Bx:152:THR:HA	46:BN:69:GLY:HA2	1.88	0.55
13:Bj:58:LEU:HD12	13:Bj:153:LEU:HD22	1.88	0.55
21:Bt:16:GLN:OE1	29:BA:465:A:N6	2.38	0.55
25:Bx:72:ILE:HG23	25:Bx:77:LEU:HB2	1.87	0.55
26:EL:68:VAL:HA	26:EL:71:ILE:HG12	1.89	0.55
3:Ba:40:LYS:HD3	3:Ba:41:PRO:HD2	1.89	0.55
6:Bc:192:THR:OG1	6:Bc:195:ASN:OD1	2.24	0.55
11:Bh:59:ARG:HB2	11:Bh:62:GLU:HG2	1.88	0.55
24:Bw:234:GLN:HG2	24:Bw:292:GLN:HG2	1.87	0.55
54:BW:128:ARG:HG3	54:BW:128:ARG:HH11	1.72	0.55
4:B8:94:VAL:HG21	48:BP:65:LEU:HD12	1.88	0.55
9:Bf:60:CYS:SG	53:BV:146:THR:HB	2.47	0.55
13:Bj:64:THR:HB	13:Bj:67:GLN:HG3	1.89	0.55
17:Bn:57:TYR:OH	23:Bv:28:ARG:O	2.25	0.55
20:Bq:119:ARG:NE	29:BA:529:G:OP1	2.39	0.55
26:FL:66:GLN:HA	26:FL:69:GLN:HG2	1.89	0.55
4:B8:125:ARG:HD3	4:B8:147:PHE:CE2	2.42	0.55
5:Bb:233:VAL:HG13	5:Bb:298:PHE:HB2	1.88	0.55
29:BA:73:A:O2'	29:BA:224:A:O2'	2.23	0.55
6:Bc:52:GLN:HG3	6:Bc:216:LEU:HD11	1.89	0.55
7:Bd:43:ASP:O	32:B4:46:ARG:NH1	2.39	0.55
29:BA:392:U:H2'	29:BA:393:A:C8	2.38	0.55
29:BA:960:U:O4	39:BG:210:LYS:NZ	2.39	0.55
37:BC:167:ASP:HB2	37:BC:170:ALA:HB2	1.89	0.55
30:B2:87:TRP:HB3	30:B2:92:LEU:HD21	1.88	0.55
41:BE:116:LYS:NZ	51:BT:165:GLU:OE2	2.39	0.55
43:BI:146:LEU:HA	43:BI:149:GLU:HG2	1.89	0.55
6:Bc:223:ALA:HA	6:Bc:226:ILE:HG22	1.89	0.54
7:Bd:57:ARG:HD2	7:Bd:58:PRO:HD2	1.88	0.54
8:Be:66:PHE:CZ	8:Be:68:LEU:HD12	2.42	0.54
13:Bj:151:ARG:NH1	13:Bj:254:TRP:O	2.39	0.54
36:BB:65:U:H2'	36:BB:66:A:C8	2.41	0.54
37:BC:291:PHE:HE1	37:BC:310:LYS:HG3	1.73	0.54
5:Bb:175:VAL:HG22	5:Bb:204:VAL:HG12	1.89	0.54
6:Bc:104:LEU:HG	6:Bc:125:LEU:HD11	1.90	0.54
13:Bj:159:LEU:HD11	13:Bj:252:HIS:HD2	1.73	0.54
29:BA:443:G:H5''	40:BQ:134:LYS:HD3	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:B7:85:ARG:NH1	35:B7:92:SER:O	2.40	0.54
45:BK:66:LEU:HD13	45:BK:82:ILE:HG23	1.89	0.54
8:Be:50:GLN:HG2	8:Be:55:ILE:HD11	1.89	0.54
10:Bg:126:ILE:O	10:Bg:127:GLN:HG2	2.08	0.54
13:Bj:266:PRO:HG2	13:Bj:269:LEU:HB2	1.88	0.54
41:BE:163:GLU:O	41:BE:167:GLU:HG3	2.07	0.54
53:BV:116:ASP:OD1	53:BV:117:LEU:N	2.39	0.54
54:BW:75:ARG:HB3	54:BW:78:ILE:HD11	1.89	0.54
27:B1:133:ASP:O	27:B1:137:GLN:HG3	2.05	0.54
26:GL:85:LEU:HD23	26:HL:68:VAL:HG21	1.89	0.54
6:Bc:191:PRO:HG2	6:Bc:280:VAL:HG21	1.89	0.54
43:BI:56:VAL:HB	43:BI:80:TYR:HB3	1.90	0.54
37:BC:149:THR:OG1	37:BC:182:GLN:NE2	2.34	0.54
5:Bb:273:PHE:HB3	5:Bb:311:MET:HB3	1.88	0.54
29:BA:787:U:OP1	49:BR:16:ARG:NH1	2.40	0.54
43:BI:72:ARG:NH1	43:BI:72:ARG:HB3	2.23	0.54
3:Ba:114:LEU:HD23	3:Ba:259:ILE:HD13	1.90	0.54
3:Ba:240:ALA:HB2	3:Ba:375:TRP:HH2	1.73	0.54
6:Bc:273:PHE:HB2	6:Bc:300:VAL:HG22	1.89	0.54
20:Bq:86:LEU:HD22	45:BK:115:LYS:HD2	1.90	0.54
42:BF:94:ASP:OD2	48:BP:30:ASN:ND2	2.41	0.54
46:BN:17:VAL:O	46:BN:55:ASP:HB3	2.08	0.54
5:Bb:240:ILE:HD12	5:Bb:245:VAL:HA	1.89	0.54
8:Be:53:GLU:HA	55:BX:16:GLN:HG2	1.89	0.54
10:Bg:21:ARG:NH1	11:Bh:79:LEU:O	2.41	0.54
24:Bw:239:ARG:HH22	24:Bw:425:GLU:HA	1.72	0.54
25:Bx:92:PHE:CZ	25:Bx:107:LEU:HD11	2.43	0.54
29:BA:1328:G:N2	29:BA:1329:U:O4	2.40	0.54
36:BB:9:A:H8	36:BB:11:C:H41	1.55	0.54
48:BP:132:SER:O	48:BP:134:ARG:NH1	2.40	0.54
15:Bl:42:VAL:HG22	48:BP:281:LYS:HG2	1.90	0.54
25:Bx:148:ASN:O	46:BN:72:TRP:NE1	2.39	0.54
29:BA:198:U:H2'	29:BA:199:A:C8	2.43	0.54
29:BA:470:C:OP2	31:B3:77:ARG:NH1	2.39	0.54
37:BC:413:LEU:HD12	37:BC:414:LEU:H	1.73	0.54
18:Bo:77:VAL:HG22	31:B3:99:VAL:HG21	1.88	0.53
37:BC:403:ASN:HA	37:BC:477:ARG:HH22	1.73	0.53
7:Bd:129:ARG:HH22	13:Bj:56:PRO:HG3	1.73	0.53
25:Bx:149:ARG:HD3	25:Bx:152:THR:HG21	1.90	0.53
53:BV:76:GLU:OE1	53:BV:80:HIS:NE2	2.41	0.53
4:B8:168:ARG:NE	29:BA:226:U:OP1	2.31	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Bg:85:ARG:NH1	10:Bg:87:GLU:OE1	2.40	0.53
18:Bo:45:GLU:OE2	18:Bo:70:ARG:NH2	2.33	0.53
29:BA:199:A:H2'	29:BA:200:A:H8	1.73	0.53
29:BA:706:A:OP1	55:BX:50:ARG:NH2	2.39	0.53
29:BA:1009:A:H2'	29:BA:1010:A:C8	2.44	0.53
28:B9:65:THR:HG22	28:B9:100:MET:HB3	1.90	0.53
29:BA:118:U:OP1	35:B7:91:LYS:N	2.38	0.53
29:BA:199:A:H2'	29:BA:200:A:C8	2.43	0.53
29:BA:486:A:H61	29:BA:582:C:H42	1.56	0.53
29:BA:776:C:O2'	29:BA:778:A:N7	2.41	0.53
45:BK:124:LYS:NZ	45:BK:127:ASP:OD2	2.41	0.53
3:Ba:35:VAL:HG21	38:BD:67:LYS:HB2	1.90	0.53
12:Bi:180:THR:HB	12:Bi:225:TYR:HB2	1.89	0.53
48:BP:164:ILE:HG12	48:BP:174:VAL:HG11	1.91	0.53
44:BJ:138:SER:OG	44:BJ:139:LYS:N	2.41	0.53
19:Bp:19:GLN:OE1	19:Bp:56:ARG:NH2	2.42	0.53
29:BA:22:U:O4	30:B2:172:ARG:NH1	2.42	0.53
29:BA:157:A:OP2	33:B5:95:ARG:NH1	2.42	0.53
24:Bw:242:PRO:HD3	24:Bw:423:PRO:HA	1.91	0.53
29:BA:124:A:N3	29:BA:251:C:O2'	2.37	0.53
42:BF:66:ILE:HD13	42:BF:263:LEU:HD11	1.91	0.53
1:B0:121:PRO:HA	5:Bb:50:LYS:HG2	1.90	0.53
5:Bb:267:ARG:HD3	50:BS:52:ASN:HD22	1.73	0.53
6:Bc:172:ILE:O	6:Bc:315:ARG:NH2	2.41	0.53
13:Bj:86:ASP:O	13:Bj:90:ARG:HG2	2.09	0.53
13:Bj:170:ILE:HB	13:Bj:172:MET:HE3	1.91	0.53
29:BA:230:G:H2'	29:BA:231:C:C6	2.43	0.53
29:BA:1506:A:H2'	29:BA:1507:G:C8	2.44	0.53
5:Bb:103:LEU:O	5:Bb:107:LYS:HG3	2.07	0.53
14:Bk:97:ALA:HB2	14:Bk:182:VAL:HG12	1.91	0.53
29:BA:1323:U:H5'	29:BA:1324:C:OP2	2.09	0.53
37:BC:77:ALA:HB2	37:BC:165:VAL:HB	1.90	0.53
50:BS:123:VAL:HA	50:BS:126:GLU:HG2	1.91	0.53
13:Bj:47:LEU:HD13	13:Bj:178:TRP:CE2	2.44	0.52
17:Bn:62:ILE:HA	17:Bn:66:PHE:HE1	1.74	0.52
27:B1:105:TRP:HB3	43:BI:54:VAL:HG21	1.91	0.52
27:B1:177:HIS:HB3	27:B1:180:ASP:HB2	1.90	0.52
29:BA:745:A:H3'	29:BA:746:U:H5''	1.90	0.52
29:BA:1191:A:N1	29:BA:1213:A:N6	2.57	0.52
31:B3:68:ILE:HD11	31:B3:122:LEU:HD13	1.91	0.52
50:BS:152:GLU:HG2	50:BS:158:ILE:HD12	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Bc:78:MET:HB3	6:Bc:83:SER:OG	2.09	0.52
24:Bw:151:LEU:HD23	24:Bw:153:ARG:HH21	1.75	0.52
11:Bh:33:LYS:NZ	29:BA:106:C:OP1	2.43	0.52
12:Bi:251:HIS:CD2	12:Bi:254:ASP:HB2	2.44	0.52
37:BC:383:LEU:HD13	37:BC:434:LEU:HD21	1.92	0.52
39:BG:112:SER:O	39:BG:115:SER:OG	2.23	0.52
41:BE:50:ASP:HB3	49:BR:139:ARG:HH12	1.75	0.52
41:BE:218:VAL:HG23	41:BE:222:TRP:HD1	1.73	0.52
6:Bc:296:LEU:HD11	49:BR:149:LEU:HD21	1.92	0.52
29:BA:1390:G:H2'	29:BA:1391:U:C6	2.44	0.52
29:BA:1528:A:H2'	29:BA:1529:A:H8	1.74	0.52
37:BC:241:LYS:HE3	37:BC:277:ARG:HH11	1.75	0.52
3:Ba:164:TRP:HA	24:Bw:281:LYS:HG3	1.91	0.52
29:BA:1234:U:O2'	48:BP:76:LEU:O	2.27	0.52
29:BA:1210:A:H5''	50:BS:180:GLU:HB3	1.90	0.52
37:BC:658:HIS:O	37:BC:661:THR:HG23	2.09	0.52
44:BJ:95:MET:HB3	44:BJ:156:SER:HB2	1.91	0.52
3:Ba:181:VAL:HG21	3:Ba:294:LEU:HD22	1.90	0.52
14:Bk:147:ASP:OD1	32:B4:73:ARG:NH1	2.39	0.52
17:Bn:96:ARG:HH11	17:Bn:96:ARG:HG2	1.75	0.52
23:Bv:27:ALA:HB2	42:BF:243:VAL:HG12	1.92	0.52
29:BA:1452:C:H2'	29:BA:1453:U:C6	2.45	0.52
31:B3:75:THR:HB	31:B3:83:LYS:HG2	1.91	0.52
45:BK:112:VAL:HG23	45:BK:153:ILE:HG21	1.92	0.52
47:BO:58:ILE:HD11	47:BO:76:ALA:HB2	1.90	0.52
7:Bd:28:ILE:HG13	14:Bk:207:LEU:HD23	1.92	0.52
12:Bi:240:ARG:HH21	55:BX:150:LEU:HD22	1.75	0.52
24:Bw:111:LYS:HA	24:Bw:255:VAL:HG11	1.92	0.52
29:BA:1452:C:H2'	29:BA:1453:U:H6	1.75	0.52
37:BC:415:LEU:HD12	37:BC:424:ILE:HG13	1.91	0.52
39:BG:169:LEU:HD13	39:BG:180:VAL:HG11	1.91	0.52
41:BE:96:ARG:HH21	41:BE:197:HIS:CE1	2.28	0.52
48:BP:181:PRO:O	48:BP:185:GLU:HG3	2.10	0.52
19:Bp:10:LEU:O	19:Bp:46:ASN:ND2	2.43	0.52
26:EL:76:LEU:HD21	26:HL:79:ILE:HG21	1.92	0.52
29:BA:416:U:H2'	29:BA:417:G:C8	2.45	0.52
29:BA:881:C:H4'	29:BA:882:A:H5'	1.91	0.52
6:Bc:164:VAL:HG13	6:Bc:232:TYR:HB3	1.92	0.52
8:Be:32:LYS:HG3	29:BA:36:A:C4	2.45	0.52
20:Bq:137:LYS:H	20:Bq:137:LYS:HD2	1.75	0.52
29:BA:904:C:H2'	29:BA:905:G:H8	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BC:485:ILE:HG22	37:BC:487:GLU:H	1.75	0.52
38:BD:111:ARG:NH2	38:BD:180:GLY:O	2.39	0.52
38:BD:207:TYR:OH	38:BD:296:TYR:OH	2.20	0.52
41:BE:244:SER:HB2	41:BE:251:VAL:HG12	1.91	0.52
41:BE:248:VAL:HG12	41:BE:250:ARG:HG2	1.90	0.52
42:BF:113:LYS:HD2	42:BF:157:GLY:HA2	1.90	0.52
1:B0:59:HIS:NE2	29:BA:412:C:O2'	2.38	0.51
6:Bc:103:ALA:O	6:Bc:110:TRP:N	2.42	0.51
9:Bf:127:GLY:N	29:BA:159:A:OP2	2.34	0.51
13:Bj:178:TRP:CD1	13:Bj:187:THR:HG21	2.45	0.51
20:Bq:132:LEU:HD21	40:BQ:168:GLU:HB3	1.92	0.51
25:Bx:162:ILE:HD11	25:Bx:174:MET:HE2	1.93	0.51
29:BA:1066:A:H2'	29:BA:1067:G:H8	1.75	0.51
29:BA:1218:U:H5'	50:BS:173:ARG:HE	1.75	0.51
42:BF:123:GLY:HA3	42:BF:142:ARG:HG2	1.92	0.51
45:BK:157:LYS:HG3	45:BK:158:ASP:H	1.75	0.51
5:Bb:364:ARG:HD2	29:BA:1194:U:H5''	1.92	0.51
10:Bg:93:SER:O	10:Bg:97:ILE:HG12	2.10	0.51
29:BA:165:A:H2'	29:BA:166:A:H8	1.75	0.51
29:BA:734:A:OP2	38:BD:105:ARG:NH2	2.33	0.51
29:BA:1531:C:H3'	29:BA:1532:U:H5''	1.92	0.51
3:Ba:347:THR:HG22	3:Ba:349:GLY:H	1.75	0.51
29:BA:127:G:OP2	35:B7:88:LYS:NZ	2.36	0.51
29:BA:1050:C:N4	29:BA:1323:U:H1'	2.25	0.51
50:BS:107:THR:HB	50:BS:119:THR:HB	1.92	0.51
11:Bh:47:ARG:HH11	11:Bh:47:ARG:HG2	1.74	0.51
13:Bj:48:LEU:HD11	13:Bj:175:GLN:HG2	1.91	0.51
17:Bn:126:LYS:NZ	48:BP:50:GLY:O	2.37	0.51
29:BA:888:A:O2'	29:BA:891:A:N6	2.30	0.51
31:B3:78:ARG:O	31:B3:83:LYS:NZ	2.43	0.51
42:BF:102:TRP:O	42:BF:106:PHE:HD1	1.93	0.51
54:BW:206:ILE:HG22	54:BW:209:ALA:HB2	1.91	0.51
5:Bb:50:LYS:O	5:Bb:52:ARG:NH1	2.42	0.51
12:Bi:245:TYR:HB2	12:Bi:265:ILE:HB	1.93	0.51
29:BA:158:A:N3	29:BA:1039:A:O2'	2.31	0.51
29:BA:784:G:O6	29:BA:1004:A:N6	2.43	0.51
42:BF:184:GLN:NE2	48:BP:20:PRO:O	2.44	0.51
3:Ba:113:LEU:HD22	3:Ba:311:ALA:HB1	1.92	0.51
14:Bk:95:LEU:O	14:Bk:154:GLU:HA	2.11	0.51
36:BB:50:A:H2'	36:BB:51:G:H8	1.76	0.51
6:Bc:78:MET:HE1	6:Bc:91:HIS:CD2	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Bc:209:LYS:HE3	6:Bc:211:LEU:HD11	1.93	0.51
13:Bj:57:PRO:HD3	13:Bj:156:ASN:HB3	1.92	0.51
25:Bx:92:PHE:CZ	25:Bx:115:ILE:HG21	2.45	0.51
29:BA:90:A:H2'	29:BA:91:A:H8	1.76	0.51
29:BA:653:A:H2'	29:BA:654:G:O4'	2.11	0.51
37:BC:71:ARG:HB2	37:BC:137:VAL:HG12	1.93	0.51
52:BU:50:PHE:O	52:BU:54:THR:HG23	2.11	0.51
5:Bb:221:LEU:HB2	5:Bb:267:ARG:HG3	1.92	0.51
12:Bi:227:ARG:NH2	54:BW:55:ILE:O	2.44	0.51
14:Bk:201:ARG:HB3	14:Bk:204:LEU:HB3	1.93	0.51
29:BA:1344:C:O2'	29:BA:1387:A:N3	2.40	0.51
36:BB:40:U:H2'	36:BB:41:G:H8	1.75	0.51
37:BC:658:HIS:CE1	37:BC:659:PRO:HG2	2.45	0.51
51:BT:221:LYS:HB3	51:BT:244:ARG:HG3	1.92	0.51
5:Bb:109:ALA:HA	5:Bb:112:GLU:HG2	1.93	0.51
5:Bb:138:GLU:O	5:Bb:142:THR:HG22	2.11	0.51
27:B1:101:VAL:HG13	29:BA:1076:A:O2'	2.10	0.51
29:BA:248:A:H2'	29:BA:249:G:C8	2.46	0.51
37:BC:208:VAL:HG11	37:BC:221:LEU:HD11	1.93	0.51
37:BC:291:PHE:HD1	37:BC:310:LYS:HZ3	1.59	0.51
37:BC:345:VAL:HG13	37:BC:349:LEU:HD12	1.93	0.51
40:BQ:172:VAL:HA	40:BQ:175:PHE:CE2	2.46	0.51
3:Ba:361:THR:OG1	3:Ba:363:ASP:OD1	2.29	0.51
12:Bi:94:ASP:HA	12:Bi:97:ILE:HG22	1.92	0.51
29:BA:1059:C:H2'	29:BA:1060:C:H6	1.76	0.51
5:Bb:275:GLN:HB3	5:Bb:311:MET:HG2	1.93	0.50
12:Bi:166:GLU:OE1	12:Bi:260:ARG:NH2	2.42	0.50
37:BC:172:VAL:O	37:BC:176:THR:OG1	2.29	0.50
45:BK:20:ILE:HD11	45:BK:42:ARG:HG3	1.93	0.50
45:BK:71:PHE:HB2	45:BK:79:GLU:HG2	1.91	0.50
54:BW:189:THR:HG23	54:BW:192:ALA:H	1.74	0.50
1:B0:74:ARG:HG3	29:BA:402:A:C4	2.46	0.50
21:Bt:23:ARG:NH2	25:Bx:168:ARG:HD2	2.26	0.50
24:Bw:265:LEU:HD23	24:Bw:267:LEU:HG	1.93	0.50
29:BA:130:A:H2'	29:BA:131:A:O4'	2.11	0.50
29:BA:205:A:O2'	29:BA:206:A:N7	2.44	0.50
29:BA:644:G:N2	29:BA:1008:A:OP2	2.33	0.50
29:BA:1059:C:H2'	29:BA:1060:C:C6	2.46	0.50
37:BC:587:HIS:NE2	37:BC:665:MET:HE2	2.27	0.50
3:Ba:297:ALA:HB3	3:Ba:303:ARG:HG3	1.92	0.50
5:Bb:126:GLN:HB3	50:BS:160:ARG:HH22	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Bd:115:ALA:O	7:Bd:119:LYS:NZ	2.45	0.50
29:BA:187:G:H1'	29:BA:467:A:N6	2.26	0.50
29:BA:480:G:OP2	53:BV:108:HIS:ND1	2.44	0.50
33:B5:141:MET:HB2	33:B5:173:ARG:HH12	1.75	0.50
37:BC:306:LEU:HD21	37:BC:310:LYS:HB3	1.93	0.50
42:BF:69:LEU:O	42:BF:202:TYR:OH	2.29	0.50
43:BI:99:THR:HG22	43:BI:140:PHE:HZ	1.76	0.50
5:Bb:157:LEU:HD11	5:Bb:318:PHE:CG	2.46	0.50
24:Bw:55:SER:HB2	29:BA:659:U:H5''	1.93	0.50
29:BA:505:U:C2	29:BA:507:G:H5'	2.47	0.50
34:B6:16:ILE:N	34:B6:34:ARG:O	2.43	0.50
37:BC:72:ASN:HB3	37:BC:159:LEU:HD22	1.91	0.50
37:BC:93:TYR:HE2	37:BC:338:ILE:HB	1.76	0.50
44:BJ:101:HIS:HB3	44:BJ:150:HIS:HB3	1.92	0.50
19:Bp:76:MET:HG2	25:Bx:49:ILE:HG12	1.92	0.50
24:Bw:289:GLY:HA3	24:Bw:329:TRP:CZ2	2.47	0.50
25:Bx:196:HIS:HB2	29:BA:573:A:N6	2.26	0.50
29:BA:702:A:OP1	30:B2:119:GLN:NE2	2.42	0.50
29:BA:1527:U:O2	29:BA:1527:U:H2'	2.12	0.50
42:BF:68:SER:O	42:BF:210:ARG:NH2	2.40	0.50
20:Bq:105:LYS:HE3	20:Bq:109:GLU:HG2	1.94	0.50
29:BA:1026:A:N3	29:BA:1278:C:O2'	2.37	0.50
37:BC:604:MET:HE2	37:BC:604:MET:HA	1.94	0.50
39:BG:159:ILE:HG23	39:BG:171:PRO:HG2	1.94	0.50
42:BF:221:LEU:HD22	42:BF:264:PRO:HB2	1.94	0.50
52:BU:90:LEU:HD11	52:BU:116:LEU:HD22	1.94	0.50
2:BY:124:ASP:OD1	2:BY:124:ASP:N	2.44	0.50
31:B3:38:ARG:HH11	31:B3:38:ARG:HG3	1.76	0.50
34:B6:20:MET:O	34:B6:29:SER:HA	2.11	0.50
44:BJ:101:HIS:HB2	44:BJ:152:LEU:HG	1.94	0.50
48:BP:203:ARG:NH1	48:BP:264:GLN:O	2.45	0.50
52:BU:73:THR:HG22	52:BU:83:TYR:HB2	1.93	0.50
42:BF:193:LEU:HD11	42:BF:218:LEU:HD23	1.93	0.50
2:BY:105:ARG:HG3	12:Bi:174:TRP:CZ3	2.47	0.50
5:Bb:99:ARG:HH12	36:BB:15:A:H4'	1.76	0.50
21:Bt:99:ARG:NH2	48:BP:18:ALA:O	2.45	0.50
29:BA:115:U:H2'	29:BA:131:A:H61	1.77	0.50
29:BA:197:U:H2'	29:BA:198:U:C6	2.46	0.50
29:BA:1000:A:H2'	29:BA:1001:A:C8	2.47	0.50
36:BB:43:C:H2'	36:BB:44:U:H5'	1.94	0.50
41:BE:334:ASP:HB3	41:BE:337:VAL:HG23	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:BU:137:GLU:HG2	52:BU:138:PRO:HD3	1.94	0.50
20:Bq:92:TYR:CE2	45:BK:115:LYS:HG3	2.47	0.49
23:Bv:46:LEU:HD11	27:B1:6:VAL:HG22	1.94	0.49
24:Bw:94:TYR:O	24:Bw:106:TYR:OH	2.29	0.49
29:BA:225:C:OP1	48:BP:132:SER:OG	2.17	0.49
32:B4:71:GLU:O	32:B4:73:ARG:N	2.44	0.49
37:BC:281:ILE:HD13	37:BC:305:LEU:HD13	1.94	0.49
5:Bb:124:ARG:NH1	7:Bd:68:GLU:OE2	2.45	0.49
7:Bd:145:GLU:HG2	14:Bk:137:LEU:HD13	1.93	0.49
13:Bj:61:LYS:HE2	13:Bj:155:ARG:HG2	1.94	0.49
13:Bj:83:LEU:O	13:Bj:84:TYR:CD1	2.66	0.49
24:Bw:240:GLN:NE2	24:Bw:348:PRO:O	2.45	0.49
37:BC:640:LEU:HD22	37:BC:683:LYS:HG3	1.93	0.49
40:BQ:89:ILE:HD11	40:BQ:176:LEU:HD22	1.93	0.49
41:BE:105:GLY:HA3	51:BT:91:LYS:HD2	1.94	0.49
52:BU:122:ARG:O	52:BU:126:GLU:HG3	2.12	0.49
16:Bm:70:ARG:NH1	16:Bm:108:ASP:OD1	2.44	0.49
29:BA:908:A:H61	29:BA:911:C:H3'	1.77	0.49
29:BA:1448:A:H2'	29:BA:1449:U:C6	2.47	0.49
37:BC:588:LEU:HB3	37:BC:658:HIS:HB2	1.93	0.49
37:BC:658:HIS:ND1	37:BC:659:PRO:HG2	2.27	0.49
42:BF:106:PHE:CE2	42:BF:107:LYS:HG3	2.47	0.49
48:BP:164:ILE:O	48:BP:168:GLU:HG2	2.12	0.49
50:BS:91:GLU:HG3	50:BS:106:SER:HB3	1.94	0.49
52:BU:112:THR:HG23	53:BV:146:THR:HG21	1.95	0.49
2:BY:25:ARG:O	2:BY:28:SER:OG	2.24	0.49
9:Bf:128:GLN:O	9:Bf:132:ARG:HG3	2.12	0.49
29:BA:434:U:H2'	29:BA:435:C:C6	2.46	0.49
49:BR:36:LEU:HD13	49:BR:124:ILE:HG23	1.95	0.49
3:Ba:191:GLN:OE1	3:Ba:194:LYS:HE2	2.13	0.49
5:Bb:240:ILE:HD13	5:Bb:248:GLY:HA3	1.94	0.49
11:Bh:278:ARG:HG3	11:Bh:278:ARG:HH11	1.77	0.49
13:Bj:146:ARG:NH2	13:Bj:259:GLU:OE1	2.46	0.49
17:Bn:66:PHE:CD2	42:BF:286:PHE:HB2	2.48	0.49
22:Bu:112:GLU:OE1	22:Bu:115:ARG:NH2	2.32	0.49
27:B1:19:GLY:O	27:B1:22:SER:OG	2.29	0.49
29:BA:353:C:O2	29:BA:1267:A:O2'	2.30	0.49
37:BC:367:LEU:HD21	37:BC:393:ILE:HG13	1.94	0.49
41:BE:96:ARG:NH2	41:BE:197:HIS:O	2.45	0.49
52:BU:71:ARG:NH1	54:BW:208:HIS:O	2.45	0.49
4:B8:126:LYS:HG2	4:B8:144:LEU:HD23	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:Bb:226:LEU:HD11	50:BS:43:ALA:HB1	1.95	0.49
23:Bv:89:GLU:HA	23:Bv:93:TYR:HD2	1.77	0.49
29:BA:421:U:H2'	29:BA:422:U:H6	1.77	0.49
29:BA:436:U:H2'	29:BA:437:A:H8	1.77	0.49
29:BA:789:A:N6	29:BA:1000:A:O2'	2.46	0.49
34:B6:34:ARG:NH1	34:B6:39:GLU:O	2.46	0.49
26:LL:135:THR:C	26:LL:168:LEU:HD23	2.38	0.49
46:BN:13:THR:HG21	54:BW:206:ILE:HD11	1.94	0.49
21:Bt:82:PHE:CG	21:Bt:83:PRO:HD2	2.48	0.49
29:BA:642:G:OP1	33:B5:93:ARG:NH2	2.46	0.49
39:BG:75:ASN:C	39:BG:77:ALA:H	2.21	0.49
44:BJ:40:MET:HE1	44:BJ:48:MET:HE2	1.94	0.49
51:BT:239:ASN:OD1	51:BT:241:LYS:NZ	2.46	0.49
6:Bc:100:SER:HB2	6:Bc:124:PHE:HB3	1.94	0.49
29:BA:220:G:H1'	29:BA:231:C:H1'	1.94	0.49
45:BK:140:VAL:O	45:BK:144:ILE:HG12	2.12	0.49
48:BP:169:LYS:HG3	48:BP:242:TYR:CG	2.47	0.49
1:B0:53:ILE:HG21	1:B0:56:MET:HE2	1.94	0.49
8:Be:129:TYR:HB3	8:Be:130:PRO:HD3	1.94	0.49
10:Bg:65:VAL:HB	16:Bm:155:ILE:HG23	1.95	0.49
24:Bw:356:THR:HG22	24:Bw:357:ASP:O	2.12	0.49
37:BC:105:ASP:OD1	37:BC:105:ASP:N	2.46	0.49
37:BC:145:HIS:HB2	37:BC:148:PHE:CD2	2.48	0.49
37:BC:638:GLY:HA2	37:BC:645:ILE:HD11	1.95	0.49
5:Bb:257:PRO:HB3	5:Bb:268:PHE:CZ	2.48	0.49
10:Bg:3:ALA:HB1	10:Bg:114:ARG:NH1	2.28	0.49
10:Bg:106:ASP:HB3	53:BV:167:LYS:HB2	1.95	0.49
29:BA:164:A:H4'	29:BA:165:A:C8	2.48	0.49
29:BA:1182:G:H4'	29:BA:1230:U:O2'	2.13	0.49
6:Bc:141:ARG:NH1	6:Bc:262:GLU:O	2.46	0.48
20:Bq:132:LEU:HD13	40:BQ:170:LYS:HD3	1.95	0.48
27:B1:95:ASP:O	27:B1:98:SER:OG	2.28	0.48
29:BA:689:A:OP2	29:BA:764:A:O2'	2.29	0.48
38:BD:298:LYS:NZ	38:BD:299:LEU:O	2.45	0.48
53:BV:178:PHE:HD1	53:BV:185:GLN:HG2	1.78	0.48
37:BC:222:LEU:HB2	37:BC:328:LEU:HD23	1.95	0.48
4:B8:142:ARG:O	4:B8:146:GLU:HG3	2.13	0.48
8:Be:73:ASN:OD1	8:Be:75:ARG:HG2	2.13	0.48
9:Bf:36:TYR:OH	52:BU:125:GLU:OE1	2.32	0.48
12:Bi:218:THR:HG23	12:Bi:220:GLN:HE21	1.78	0.48
38:BD:83:GLY:O	38:BD:85:ARG:HD2	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:BG:143:LEU:HD11	39:BG:179:ARG:HG2	1.95	0.48
42:BF:123:GLY:HA2	42:BF:141:ILE:HG12	1.94	0.48
29:BA:723:A:H3'	29:BA:724:A:H5''	1.95	0.48
29:BA:952:A:H2'	29:BA:953:G:H8	1.79	0.48
50:BS:112:ILE:O	50:BS:116:LEU:HB3	2.14	0.48
4:B8:125:ARG:NH1	4:B8:145:ARG:O	2.46	0.48
7:Bd:63:PRO:HG2	7:Bd:66:GLU:OE2	2.12	0.48
29:BA:1089:G:N1	29:BA:1125:U:O4	2.46	0.48
42:BF:69:LEU:HD21	42:BF:212:TRP:HH2	1.77	0.48
48:BP:292:LYS:O	48:BP:296:SER:HB3	2.13	0.48
3:Ba:38:THR:HB	38:BD:68:SER:HB3	1.94	0.48
6:Bc:85:PRO:HG2	6:Bc:112:MET:HA	1.95	0.48
11:Bh:59:ARG:HH22	11:Bh:182:ALA:HA	1.79	0.48
11:Bh:240:LEU:HB3	11:Bh:301:LEU:HD11	1.96	0.48
23:Bv:46:LEU:HD13	29:BA:20:A:H62	1.79	0.48
29:BA:299:A:OP2	29:BA:833:C:N4	2.47	0.48
39:BG:88:VAL:O	39:BG:92:MET:HG3	2.13	0.48
26:LL:164:LEU:HD12	26:LL:170:GLN:HG2	1.95	0.48
26:LL:188:LEU:HB3	26:LL:195:VAL:HG21	1.95	0.48
45:BK:39:LEU:HD11	45:BK:70:ILE:HG21	1.96	0.48
12:Bi:238:VAL:HG22	12:Bi:240:ARG:HG2	1.96	0.48
17:Bn:95:LYS:NZ	29:BA:64:C:O3'	2.47	0.48
25:Bx:43:ASP:OD1	25:Bx:43:ASP:N	2.46	0.48
25:Bx:70:CYS:O	25:Bx:74:ARG:HG2	2.14	0.48
26:CL:76:LEU:HA	26:CL:79:ILE:HD12	1.96	0.48
37:BC:364:LYS:HA	37:BC:390:SER:HB2	1.95	0.48
37:BC:477:ARG:HH21	37:BC:479:LEU:HD13	1.79	0.48
19:Bp:22:PRO:HB3	44:BJ:177:LEU:HD22	1.96	0.48
26:CL:63:LYS:O	26:CL:66:GLN:HG3	2.14	0.48
26:CL:76:LEU:HD23	26:FL:72:ALA:HA	1.95	0.48
29:BA:803:A:O2'	29:BA:809:G:N7	2.39	0.48
29:BA:1345:A:H2	29:BA:1366:A:N6	2.12	0.48
30:B2:111:ARG:HD3	55:BX:25:PHE:CD1	2.49	0.48
2:BY:211:LYS:NZ	55:BX:12:LEU:O	2.47	0.48
5:Bb:308:GLN:O	18:Bo:113:LYS:NZ	2.47	0.48
6:Bc:285:THR:OG1	6:Bc:288:SER:O	2.27	0.48
29:BA:1345:A:H2	29:BA:1366:A:H61	1.61	0.48
29:BA:1426:G:H2'	29:BA:1427:G:H8	1.77	0.48
29:BA:1463:A:N6	37:BC:745:THR:OG1	2.45	0.48
37:BC:711:ARG:NH2	37:BC:742:VAL:HG21	2.24	0.48
51:BT:268:ASP:O	51:BT:269:MET:HG2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:BU:69:ILE:O	52:BU:73:THR:HG23	2.13	0.48
4:B8:105:LYS:NZ	29:BA:88:G:N7	2.58	0.48
4:B8:113:ARG:HD3	48:BP:78:ILE:O	2.13	0.48
5:Bb:362:PRO:HB2	5:Bb:364:ARG:HG2	1.96	0.48
23:Bv:127:LYS:O	23:Bv:131:MET:HG3	2.13	0.48
24:Bw:149:PHE:CD2	24:Bw:402:ASN:HB3	2.49	0.48
37:BC:237:ASP:OD2	37:BC:238:VAL:N	2.46	0.48
51:BT:244:ARG:HE	51:BT:247:LEU:HD11	1.79	0.48
13:Bj:48:LEU:HD21	13:Bj:175:GLN:OE1	2.14	0.47
26:GL:75:THR:HG23	26:GL:78:GLU:H	1.79	0.47
29:BA:1011:U:O2	33:B5:81:PRO:HG2	2.13	0.47
29:BA:1060:C:H2'	29:BA:1061:U:H6	1.79	0.47
33:B5:94:ARG:HA	33:B5:99:LYS:HD2	1.96	0.47
37:BC:172:VAL:HB	37:BC:214:LYS:HD2	1.95	0.47
37:BC:246:TRP:HB3	37:BC:252:ASP:HB3	1.96	0.47
38:BD:163:THR:O	38:BD:178:ARG:NH2	2.47	0.47
40:BQ:204:GLU:HA	40:BQ:207:ARG:HG2	1.96	0.47
53:BV:179:GLN:HB2	53:BV:184:TYR:HB3	1.95	0.47
5:Bb:199:ALA:HA	5:Bb:256:PRO:HB3	1.95	0.47
5:Bb:262:GLY:HA3	5:Bb:342:PHE:HB2	1.95	0.47
7:Bd:41:ILE:HG22	7:Bd:43:ASP:H	1.79	0.47
20:Bq:77:ILE:HG22	45:BK:60:ILE:HD12	1.95	0.47
27:B1:46:HIS:NE2	27:B1:62:VAL:HG13	2.29	0.47
29:BA:988:U:H4'	41:BE:230:THR:HG22	1.95	0.47
29:BA:1315:U:H2'	29:BA:1316:U:C6	2.49	0.47
37:BC:640:LEU:HD13	37:BC:683:LYS:HD2	1.95	0.47
48:BP:180:ASP:OD1	48:BP:183:SER:OG	2.31	0.47
24:Bw:251:ILE:HG22	24:Bw:253:ILE:H	1.79	0.47
26:CL:80:SER:HA	26:CL:83:ASN:HD21	1.80	0.47
29:BA:922:A:H2'	29:BA:923:A:C8	2.50	0.47
29:BA:1570:C:H5''	29:BA:1571:A:H2'	1.97	0.47
46:BN:36:SER:O	46:BN:40:GLN:HG3	2.14	0.47
53:BV:126:VAL:HG21	53:BV:164:VAL:HG21	1.96	0.47
5:Bb:90:ILE:O	5:Bb:90:ILE:HG13	2.15	0.47
14:Bk:94:HIS:CD2	14:Bk:187:ARG:HH21	2.32	0.47
19:Bp:27:VAL:HG12	19:Bp:62:PRO:HG3	1.97	0.47
23:Bv:48:PRO:HB2	23:Bv:50:TRP:CD1	2.49	0.47
27:B1:100:ARG:HH12	43:BI:75:ARG:CZ	2.28	0.47
37:BC:195:ASN:OD1	37:BC:196:LYS:N	2.36	0.47
49:BR:113:ARG:HH21	49:BR:119:ALA:HB2	1.79	0.47
51:BT:103:ARG:NE	51:BT:167:TYR:OH	2.41	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Bc:281:HIS:HB3	6:Bc:319:MET:HE1	1.96	0.47
10:Bg:136:LYS:O	11:Bh:259:ARG:NH2	2.46	0.47
16:Bm:64:PRO:HD2	16:Bm:67:LEU:HD13	1.97	0.47
29:BA:50:A:N3	29:BA:247:C:O2'	2.40	0.47
3:Ba:151:ASP:O	3:Ba:155:LEU:HD23	2.15	0.47
6:Bc:253:ARG:HD2	6:Bc:258:ILE:HG12	1.96	0.47
11:Bh:105:ARG:HB2	11:Bh:112:LYS:HD3	1.97	0.47
14:Bk:125:TYR:OH	14:Bk:197:ARG:NH1	2.48	0.47
22:Bu:110:ILE:HG21	22:Bu:157:ILE:HD12	1.97	0.47
24:Bw:96:GLN:OE1	24:Bw:297:PRO:HD3	2.15	0.47
29:BA:291:U:H4'	29:BA:793:A:H4'	1.96	0.47
30:B2:193:ASN:HB3	30:B2:196:TYR:HB3	1.96	0.47
2:BY:168:GLU:HG3	2:BY:169:THR:HG23	1.96	0.47
3:Ba:30:ALA:HB2	38:BD:110:LEU:HD22	1.96	0.47
3:Ba:344:SER:HB2	3:Ba:355:LEU:HB3	1.96	0.47
6:Bc:70:THR:HG1	6:Bc:96:TYR:HH	1.38	0.47
10:Bg:119:PHE:HE2	54:BW:210:LEU:HB3	1.79	0.47
20:Bq:87:LYS:HB3	20:Bq:91:GLU:HB2	1.96	0.47
21:Bt:23:ARG:NH1	29:BA:464:U:OP1	2.47	0.47
29:BA:289:U:H2'	29:BA:290:A:C8	2.50	0.47
37:BC:632:HIS:O	37:BC:636:LEU:HG	2.15	0.47
38:BD:85:ARG:NH1	38:BD:91:ILE:HG12	2.29	0.47
38:BD:195:ASN:OD1	38:BD:196:ASN:ND2	2.36	0.47
41:BE:221:ARG:HG3	41:BE:261:LEU:HB2	1.96	0.47
41:BE:308:LYS:HE2	41:BE:308:LYS:HA	1.95	0.47
6:Bc:220:ALA:O	6:Bc:224:LEU:HD23	2.14	0.47
7:Bd:120:ARG:HE	7:Bd:124:LEU:HD23	1.78	0.47
10:Bg:26:LEU:HD22	10:Bg:105:ALA:HA	1.96	0.47
13:Bj:159:LEU:HD11	13:Bj:252:HIS:CD2	2.50	0.47
29:BA:52:A:O2'	29:BA:349:A:N3	2.47	0.47
50:BS:177:ARG:HD3	50:BS:180:GLU:HA	1.97	0.47
9:Bf:104:GLU:HB2	9:Bf:107:PRO:HD2	1.95	0.47
13:Bj:54:GLN:C	13:Bj:238:LEU:HD23	2.40	0.47
15:Bl:91:MET:HE3	29:BA:219:A:H5''	1.96	0.47
29:BA:49:A:H2'	29:BA:50:A:C8	2.50	0.47
37:BC:334:LYS:HB3	37:BC:336:LYS:HZ2	1.80	0.47
42:BF:195:LEU:HG	42:BF:202:TYR:HE2	1.79	0.47
44:BJ:224:HIS:HA	44:BJ:227:ARG:HB2	1.97	0.47
54:BW:192:ALA:O	54:BW:196:GLU:HG3	2.14	0.47
3:Ba:192:ILE:HD11	3:Ba:199:ALA:HB2	1.97	0.47
6:Bc:163:LEU:HD23	6:Bc:180:VAL:HG23	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:Bh:72:ILE:HD13	11:Bh:178:LEU:HD23	1.97	0.47
25:Bx:99:MET:HG3	25:Bx:116:GLU:HG3	1.96	0.47
37:BC:71:ARG:NH1	37:BC:351:SER:OG	2.48	0.47
37:BC:413:LEU:HD12	37:BC:414:LEU:N	2.30	0.47
37:BC:611:TYR:CE1	37:BC:631:ILE:HD12	2.50	0.47
7:Bd:50:PHE:HE2	32:B4:50:ALA:HB2	1.79	0.46
24:Bw:163:ARG:HA	24:Bw:166:ILE:HG22	1.97	0.46
24:Bw:374:THR:O	24:Bw:378:ASP:HB2	2.16	0.46
29:BA:744:A:H4'	29:BA:744:A:OP1	2.15	0.46
37:BC:680:LYS:O	37:BC:680:LYS:HG3	2.14	0.46
47:BO:60:VAL:HG13	47:BO:73:ILE:HG22	1.96	0.46
47:BO:130:ARG:NH2	47:BO:133:GLU:OE2	2.37	0.46
49:BR:49:VAL:HG13	49:BR:124:ILE:HB	1.97	0.46
6:Bc:51:ARG:HD2	6:Bc:51:ARG:C	2.41	0.46
10:Bg:144:ARG:HB2	10:Bg:147:GLU:HB2	1.98	0.46
24:Bw:241:LEU:HD21	24:Bw:290:HIS:HD2	1.79	0.46
29:BA:188:C:O2'	29:BA:190:U:OP2	2.25	0.46
29:BA:293:U:O2'	29:BA:1434:U:O2'	2.29	0.46
29:BA:1267:A:OP2	42:BF:131:LYS:HE2	2.15	0.46
37:BC:572:VAL:HG11	37:BC:681:ALA:HA	1.98	0.46
37:BC:722:GLN:NE2	37:BC:723:ASP:OD2	2.39	0.46
2:BY:216:TYR:HE1	30:B2:193:ASN:HD22	1.64	0.46
5:Bb:154:TYR:HE2	50:BS:54:ARG:HD2	1.80	0.46
19:Bp:33:PHE:HD1	19:Bp:87:LEU:HD22	1.79	0.46
29:BA:504:G:H2'	29:BA:505:U:C5	2.49	0.46
29:BA:827:U:O4	29:BA:841:A:H2	1.98	0.46
31:B3:73:LYS:HE2	31:B3:73:LYS:HB3	1.82	0.46
32:B4:53:TYR:CG	32:B4:72:PRO:HB3	2.50	0.46
39:BG:201:THR:HG22	39:BG:205:LYS:HE2	1.98	0.46
6:Bc:44:LEU:HB2	6:Bc:226:ILE:HD13	1.97	0.46
9:Bf:49:LEU:HD23	9:Bf:60:CYS:HB3	1.98	0.46
11:Bh:67:ASP:O	11:Bh:71:GLU:HG2	2.15	0.46
12:Bi:290:TRP:HB3	33:B5:132:LYS:HD2	1.97	0.46
13:Bj:190:ARG:O	13:Bj:194:THR:HG22	2.15	0.46
40:BQ:101:HIS:CE1	40:BQ:184:PRO:HG3	2.50	0.46
27:B1:166:LEU:HD12	27:B1:204:VAL:HG21	1.98	0.46
28:B9:71:LYS:NZ	28:B9:76:CYS:O	2.47	0.46
29:BA:838:A:H1'	29:BA:933:A:N6	2.30	0.46
37:BC:337:GLY:HA2	37:BC:340:PRO:HG2	1.97	0.46
42:BF:227:PRO:HG2	42:BF:230:VAL:HG12	1.97	0.46
49:BR:79:TRP:NE1	51:BT:267:PHE:O	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Bw:156:ARG:NH1	24:Bw:162:ASP:OD1	2.48	0.46
27:B1:44:ARG:HG3	43:BI:55:ILE:HG21	1.97	0.46
29:BA:740:U:H2'	29:BA:741:A:H8	1.80	0.46
29:BA:749:C:C2	55:BX:51:VAL:HG12	2.51	0.46
37:BC:600:THR:HB	37:BC:603:VAL:HB	1.98	0.46
50:BS:65:GLU:OE2	50:BS:75:ARG:NH1	2.49	0.46
6:Bc:141:ARG:HH22	6:Bc:264:PRO:HD2	1.81	0.46
7:Bd:138:ILE:H	32:B4:62:GLY:HA3	1.81	0.46
11:Bh:228:LEU:HB2	11:Bh:307:PHE:CD1	2.51	0.46
23:Bv:128:MET:O	23:Bv:132:ILE:HG12	2.16	0.46
29:BA:607:A:O2'	52:BU:16:ASP:OD2	2.33	0.46
26:LL:165:VAL:O	26:LL:168:LEU:HD13	2.14	0.46
43:BI:93:ASN:ND2	43:BI:113:SER:OG	2.48	0.46
51:BT:87:THR:HG21	51:BT:91:LYS:HD3	1.98	0.46
13:Bj:53:LEU:HD23	13:Bj:238:LEU:HD21	1.97	0.46
13:Bj:160:LEU:HD23	13:Bj:255:VAL:HG21	1.97	0.46
23:Bv:28:ARG:NH1	29:BA:100:C:O2	2.49	0.46
26:CL:60:TYR:HB3	26:CL:64:ILE:HD11	1.97	0.46
29:BA:642:G:H5''	33:B5:85:ARG:HH21	1.81	0.46
29:BA:880:C:O2'	29:BA:922:A:H1'	2.16	0.46
29:BA:1020:C:H2'	29:BA:1021:C:C6	2.50	0.46
29:BA:1230:U:H5'	29:BA:1231:U:H5'	1.96	0.46
29:BA:1450:U:H2'	29:BA:1451:U:H6	1.81	0.46
37:BC:692:LEU:HD22	37:BC:731:VAL:HG11	1.98	0.46
15:Bl:106:GLN:HB3	15:Bl:152:TYR:CE1	2.51	0.46
17:Bn:96:ARG:HG2	17:Bn:96:ARG:NH1	2.31	0.46
29:BA:52:A:H4'	29:BA:245:A:H2	1.81	0.46
29:BA:498:A:H5''	29:BA:499:C:H5	1.81	0.46
29:BA:1450:U:H2'	29:BA:1451:U:C6	2.50	0.46
31:B3:42:PRO:HG2	31:B3:45:VAL:HG23	1.97	0.46
37:BC:296:LEU:HD22	26:LL:146:ILE:HG13	1.97	0.46
51:BT:148:THR:HG22	51:BT:165:GLU:HG2	1.98	0.46
51:BT:192:ASP:OD2	51:BT:233:TRP:NE1	2.32	0.46
2:BY:65:LEU:HD11	2:BY:121:LYS:HE3	1.97	0.46
4:B8:157:LEU:O	4:B8:161:MET:HG3	2.16	0.46
11:Bh:138:THR:O	11:Bh:142:GLU:HG3	2.16	0.46
12:Bi:250:LYS:HD3	12:Bi:259:TRP:CE2	2.50	0.46
13:Bj:159:LEU:HB2	13:Bj:254:TRP:CZ3	2.51	0.46
29:BA:175:C:H2'	29:BA:176:U:C6	2.51	0.46
29:BA:329:A:C5	38:BD:275:LEU:HB2	2.51	0.46
29:BA:644:G:OP2	33:B5:93:ARG:NH1	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BA:673:C:H42	29:BA:756:A:H61	1.62	0.46
41:BE:252:TRP:HB3	46:BN:84:PRO:HD3	1.98	0.46
5:Bb:194:THR:HG22	5:Bb:196:THR:H	1.81	0.45
6:Bc:315:ARG:HG3	6:Bc:315:ARG:HH11	1.81	0.45
7:Bd:129:ARG:HH21	14:Bk:175:HIS:HD2	1.63	0.45
8:Be:16:ASP:OD2	8:Be:25:ARG:NH2	2.49	0.45
10:Bg:27:GLN:HB2	10:Bg:80:LEU:HD12	1.98	0.45
26:HL:66:GLN:O	26:HL:69:GLN:HG3	2.16	0.45
29:BA:528:U:C4	44:BJ:125:ILE:HD13	2.51	0.45
30:B2:87:TRP:HB3	30:B2:92:LEU:CD2	2.46	0.45
42:BF:99:VAL:HG21	42:BF:173:GLY:HA3	1.96	0.45
50:BS:68:TRP:HB3	50:BS:71:VAL:HG22	1.98	0.45
3:Ba:117:VAL:O	3:Ba:121:LEU:HG	2.15	0.45
13:Bj:159:LEU:HD13	13:Bj:254:TRP:CE2	2.52	0.45
22:Bu:185:GLU:HA	22:Bu:188:ARG:HB3	1.99	0.45
37:BC:78:HIS:HB2	37:BC:176:THR:HG23	1.97	0.45
51:BT:122:ALA:O	51:BT:170:ARG:NH1	2.49	0.45
53:BV:161:GLU:OE1	53:BV:201:SER:OG	2.31	0.45
54:BW:198:ILE:O	54:BW:202:ARG:HG3	2.16	0.45
55:BX:3:ARG:HB3	55:BX:24:PHE:HE1	1.81	0.45
12:Bi:173:VAL:HA	12:Bi:176:ILE:HG22	1.99	0.45
29:BA:477:A:OP1	52:BU:57:ARG:NH1	2.48	0.45
29:BA:1143:U:H2'	29:BA:1144:U:C6	2.52	0.45
36:BB:43:C:C2'	36:BB:44:U:H5'	2.47	0.45
40:BQ:109:ILE:O	40:BQ:113:MET:HB3	2.16	0.45
54:BW:70:GLU:HG2	54:BW:177:VAL:HG22	1.97	0.45
14:Bk:195:LYS:HA	14:Bk:195:LYS:HD3	1.82	0.45
22:Bu:80:TYR:CE1	22:Bu:142:GLN:HB2	2.51	0.45
27:B1:150:LYS:HA	27:B1:159:MET:HE3	1.97	0.45
29:BA:942:U:H2'	29:BA:943:C:C6	2.51	0.45
29:BA:978:G:H4'	29:BA:1429:C:H4'	1.98	0.45
29:BA:1292:A:N6	29:BA:1304:G:O2'	2.47	0.45
29:BA:1302:U:OP1	29:BA:1360:U:O2'	2.26	0.45
41:BE:100:ILE:HG22	41:BE:296:LEU:HD12	1.98	0.45
42:BF:83:HIS:CD2	42:BF:85:ASP:HB2	2.46	0.45
49:BR:46:TRP:CD1	49:BR:122:ALA:HB2	2.51	0.45
37:BC:157:ARG:HE	37:BC:482:GLY:HA2	1.81	0.45
37:BC:291:PHE:CE1	37:BC:310:LYS:HG3	2.49	0.45
44:BJ:63:ARG:HD3	44:BJ:63:ARG:C	2.42	0.45
49:BR:62:TYR:CZ	49:BR:75:MET:HE3	2.52	0.45
51:BT:80:PHE:CZ	51:BT:99:MET:HE2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Bd:123:SER:O	13:Bj:203:LYS:NZ	2.49	0.45
20:Bq:121:LEU:HD11	40:BQ:35:PRO:HA	1.97	0.45
26:CL:80:SER:HA	26:CL:83:ASN:ND2	2.32	0.45
29:BA:276:G:O2'	29:BA:310:G:H4'	2.16	0.45
29:BA:1026:A:C6	29:BA:1321:C:H1'	2.52	0.45
36:BB:40:U:H2'	36:BB:41:G:C8	2.50	0.45
37:BC:136:ARG:HH21	37:BC:415:LEU:HD13	1.80	0.45
37:BC:173:GLU:O	37:BC:176:THR:OG1	2.32	0.45
48:BP:264:GLN:NE2	48:BP:269:LEU:O	2.47	0.45
52:BU:24:VAL:HG11	52:BU:43:VAL:HG12	1.98	0.45
5:Bb:377:TYR:H	48:BP:143:GLU:HG3	1.82	0.45
7:Bd:19:ALA:O	7:Bd:23:ARG:HG2	2.17	0.45
7:Bd:81:LYS:HA	7:Bd:84:GLU:HG2	1.99	0.45
11:Bh:59:ARG:HG2	11:Bh:184:PHE:HB2	1.99	0.45
27:B1:171:ARG:HG3	27:B1:198:GLU:OE2	2.17	0.45
26:DL:79:ILE:HB	44:BJ:207:LEU:HD11	1.99	0.45
29:BA:567:C:O2'	29:BA:1020:C:O2'	2.31	0.45
29:BA:1476:A:H2'	29:BA:1477:A:C8	2.51	0.45
34:B6:26:THR:HG21	34:B6:49:VAL:HB	1.99	0.45
39:BG:190:ARG:NH1	39:BG:260:LEU:O	2.48	0.45
52:BU:87:ILE:O	52:BU:91:ILE:HG12	2.17	0.45
55:BX:131:GLN:HA	55:BX:134:LYS:HE3	1.99	0.45
12:Bi:90:PRO:HB2	12:Bi:269:TRP:CH2	2.45	0.45
13:Bj:184:LEU:HD12	13:Bj:185:ARG:N	2.32	0.45
19:Bp:16:VAL:HG22	19:Bp:66:VAL:HG13	1.98	0.45
24:Bw:131:LEU:HD13	24:Bw:136:LEU:HD12	1.98	0.45
24:Bw:363:PHE:HB3	24:Bw:418:PHE:CE2	2.51	0.45
26:EL:70:ASP:HB3	26:FL:67:LEU:HD21	1.99	0.45
29:BA:76:G:O2'	29:BA:88:G:O6	2.34	0.45
42:BF:83:HIS:CG	42:BF:274:LEU:HD11	2.52	0.45
49:BR:113:ARG:HE	49:BR:119:ALA:HB3	1.82	0.45
53:BV:116:ASP:O	53:BV:198:ARG:HA	2.17	0.45
6:Bc:262:GLU:N	6:Bc:262:GLU:OE1	2.50	0.45
6:Bc:313:LEU:O	6:Bc:317:ARG:HG2	2.17	0.45
29:BA:388:A:H2'	29:BA:389:A:C8	2.52	0.45
36:BB:4:A:H3'	36:BB:5:A:H5''	1.99	0.45
37:BC:375:LEU:HB3	37:BC:383:LEU:HB2	1.99	0.45
37:BC:690:MET:HE1	37:BC:733:LEU:HB2	1.98	0.45
37:BC:711:ARG:HD3	37:BC:735:GLU:O	2.17	0.45
43:BI:139:LEU:O	43:BI:142:GLU:HG2	2.16	0.45
44:BJ:114:HIS:O	44:BJ:118:LYS:HG2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:BP:115:PRO:HD3	48:BP:255:MET:HG2	1.98	0.45
8:Be:84:LEU:HD21	8:Be:89:LEU:HB2	1.99	0.45
12:Bi:179:LYS:HG2	12:Bi:232:MET:HE1	1.98	0.45
19:Bp:63:CYS:SG	19:Bp:64:VAL:N	2.89	0.45
22:Bu:146:LEU:HD23	22:Bu:150:LEU:HG	1.99	0.45
25:Bx:70:CYS:HB3	25:Bx:73:CYS:HB2	1.99	0.45
29:BA:690:U:O2	49:BR:116:GLN:NE2	2.50	0.45
29:BA:1242:U:H2'	29:BA:1243:U:O4'	2.17	0.45
29:BA:1543:U:C2	29:BA:1544:A:C8	3.05	0.45
36:BB:24:A:H2'	36:BB:25:G:C8	2.52	0.45
39:BG:237:GLN:O	39:BG:241:MET:HG3	2.17	0.45
41:BE:133:THR:HB	41:BE:144:ALA:HB3	1.98	0.45
44:BJ:187:SER:OG	44:BJ:188:ARG:N	2.50	0.45
46:BN:62:THR:HG21	46:BN:101:VAL:HA	1.99	0.45
3:Ba:90:LEU:HD21	29:BA:714:A:H2	1.81	0.44
3:Ba:112:ARG:HG3	29:BA:719:C:O2'	2.17	0.44
29:BA:253:A:N1	29:BA:334:C:H1'	2.32	0.44
37:BC:505:LEU:HD13	37:BC:555:THR:HG21	1.99	0.44
46:BN:40:GLN:NE2	46:BN:113:PRO:HD3	2.32	0.44
4:B8:179:LYS:O	5:Bb:370:ARG:NH1	2.50	0.44
24:Bw:136:LEU:HD11	24:Bw:182:LEU:HD21	1.99	0.44
29:BA:388:A:H2'	29:BA:389:A:H8	1.82	0.44
29:BA:763:C:OP2	29:BA:765:C:N4	2.37	0.44
29:BA:792:G:H4'	41:BE:235:LYS:HB3	1.99	0.44
29:BA:1380:A:H2'	29:BA:1381:A:C8	2.53	0.44
33:B5:130:VAL:HG13	49:BR:132:PRO:HB2	1.98	0.44
26:LL:177:PRO:HG2	26:LL:180:GLU:HB2	1.98	0.44
46:BN:114:LYS:HA	46:BN:118:ARG:NH1	2.31	0.44
48:BP:140:LEU:HG	48:BP:156:VAL:HG11	1.99	0.44
11:Bh:103:ALA:O	11:Bh:106:GLN:HG3	2.17	0.44
15:Bl:138:THR:HG22	15:Bl:149:VAL:HG22	2.00	0.44
15:Bl:154:ASP:N	15:Bl:154:ASP:OD1	2.49	0.44
29:BA:196:U:O2'	29:BA:1014:A:OP1	2.31	0.44
29:BA:266:C:H5''	29:BA:267:A:H5'	1.98	0.44
29:BA:1131:U:H2'	29:BA:1132:G:C8	2.50	0.44
51:BT:79:GLU:OE2	51:BT:103:ARG:NH2	2.46	0.44
51:BT:224:MET:HE2	51:BT:243:ILE:HD13	1.99	0.44
3:Ba:216:GLU:O	3:Ba:216:GLU:HG2	2.17	0.44
5:Bb:216:LEU:HD21	5:Bb:270:PHE:HD2	1.82	0.44
11:Bh:156:LEU:HD22	11:Bh:231:MET:SD	2.57	0.44
12:Bi:47:GLN:HG2	12:Bi:48:PRO:HD2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:Bi:84:ILE:HG13	12:Bi:262:HIS:HD2	1.82	0.44
13:Bj:162:ARG:HH22	13:Bj:171:TRP:HA	1.82	0.44
14:Bk:162:LEU:HG	14:Bk:167:ALA:HB2	1.99	0.44
19:Bp:17:ARG:HG3	19:Bp:65:ASP:HB2	1.99	0.44
29:BA:15:A:N6	29:BA:102:G:O6	2.50	0.44
29:BA:703:A:OP1	55:BX:41:GLN:NE2	2.37	0.44
36:BB:50:A:H2'	36:BB:51:G:C8	2.52	0.44
39:BG:82:ILE:HD13	39:BG:226:VAL:HG21	2.00	0.44
41:BE:199:ARG:HA	41:BE:199:ARG:HD3	1.72	0.44
42:BF:108:ARG:HD3	42:BF:161:TYR:CD1	2.53	0.44
50:BS:70:THR:HG23	50:BS:71:VAL:HG13	1.99	0.44
4:B8:188:VAL:HG12	15:Bl:104:ASN:HB3	2.00	0.44
5:Bb:58:ARG:O	5:Bb:62:GLU:HG3	2.17	0.44
11:Bh:124:GLU:O	11:Bh:127:GLU:HG2	2.18	0.44
12:Bi:47:GLN:HB2	54:BW:162:PHE:CZ	2.53	0.44
12:Bi:251:HIS:HD2	12:Bi:254:ASP:HB2	1.82	0.44
13:Bj:265:LYS:HG3	13:Bj:266:PRO:HD3	1.98	0.44
29:BA:93:U:H5'	48:BP:196:ARG:HD3	1.98	0.44
29:BA:789:A:OP2	49:BR:9:ILE:N	2.50	0.44
29:BA:1336:A:H2'	29:BA:1337:G:C8	2.53	0.44
30:B2:174:ILE:HD11	35:B7:73:LEU:HG	2.00	0.44
37:BC:192:CYS:HB2	37:BC:327:VAL:HG22	1.98	0.44
37:BC:212:ARG:HE	37:BC:219:PRO:HD2	1.82	0.44
39:BG:113:PRO:HB3	39:BG:136:ILE:HG22	2.00	0.44
53:BV:174:ILE:HD12	53:BV:187:LYS:NZ	2.31	0.44
4:B8:147:PHE:O	5:Bb:362:PRO:HA	2.18	0.44
8:Be:52:LYS:HA	8:Be:55:ILE:HD12	1.99	0.44
11:Bh:40:ARG:HB3	52:BU:19:TRP:CZ2	2.53	0.44
11:Bh:60:ARG:HA	11:Bh:63:LYS:HG3	1.98	0.44
22:Bu:179:ILE:HD13	50:BS:171:VAL:HG11	2.00	0.44
25:Bx:78:LYS:NZ	25:Bx:110:GLU:OE2	2.42	0.44
26:FL:74:LEU:HD23	26:FL:74:LEU:HA	1.85	0.44
37:BC:91:LEU:HD21	37:BC:128:VAL:HG21	2.00	0.44
38:BD:81:LYS:HE2	38:BD:81:LYS:HB3	1.74	0.44
42:BF:72:TYR:HE2	42:BF:202:TYR:CE1	2.34	0.44
1:B0:143:LYS:HE2	1:B0:143:LYS:HB3	1.81	0.44
3:Ba:117:VAL:HG23	3:Ba:307:ASP:OD2	2.18	0.44
3:Ba:385:HIS:O	3:Ba:404:ILE:N	2.40	0.44
4:B8:94:VAL:N	29:BA:86:U:OP1	2.50	0.44
6:Bc:315:ARG:HB2	49:BR:153:LEU:HD13	1.99	0.44
26:DL:76:LEU:HD11	44:BJ:203:VAL:HG11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BA:1308:A:H5'	40:BQ:184:PRO:HA	1.98	0.44
33:B5:132:LYS:HB3	33:B5:132:LYS:HE3	1.61	0.44
37:BC:586:ARG:HG3	37:BC:586:ARG:HH11	1.83	0.44
50:BS:149:THR:OG1	50:BS:152:GLU:HB2	2.18	0.44
55:BX:3:ARG:HB3	55:BX:24:PHE:CE1	2.53	0.44
3:Ba:60:TYR:HB3	3:Ba:70:LEU:HD12	1.99	0.44
13:Bj:44:PRO:HG2	13:Bj:227:LEU:HA	2.00	0.44
14:Bk:132:MET:HE3	14:Bk:132:MET:HB3	1.85	0.44
36:BB:62:C:H2'	36:BB:63:C:C6	2.53	0.44
37:BC:359:PHE:CE2	37:BC:480:LEU:HD22	2.52	0.44
37:BC:615:ILE:O	37:BC:615:ILE:HG13	2.17	0.44
43:BI:97:VAL:HG22	43:BI:111:LEU:HG	1.98	0.44
53:BV:72:ASP:OD2	53:BV:74:VAL:HG22	2.18	0.44
5:Bb:195:PRO:HG3	5:Bb:321:CYS:SG	2.58	0.44
8:Be:54:MET:HE2	8:Be:54:MET:HB3	1.87	0.44
11:Bh:160:LEU:HD23	11:Bh:160:LEU:HA	1.82	0.44
11:Bh:261:SER:OG	46:BN:17:VAL:HA	2.17	0.44
16:Bm:99:PHE:CE2	42:BF:46:PRO:HB3	2.53	0.44
22:Bu:61:LEU:HD23	22:Bu:61:LEU:HA	1.83	0.44
23:Bv:37:PRO:HG3	23:Bv:64:HIS:CG	2.53	0.44
23:Bv:99:MET:HE3	48:BP:211:VAL:HG21	2.00	0.44
29:BA:2:C:O2'	54:BW:147:ARG:O	2.20	0.44
29:BA:16:A:H2'	29:BA:17:C:C6	2.53	0.44
29:BA:264:A:H2'	29:BA:265:G:H8	1.82	0.44
29:BA:289:U:H2'	29:BA:290:A:H8	1.82	0.44
29:BA:330:A:H8	29:BA:830:U:O2'	2.01	0.44
29:BA:1006:U:H2'	29:BA:1007:G:O4'	2.18	0.44
29:BA:1569:A:H62	41:BE:153:SER:HA	1.83	0.44
2:BY:35:ASN:O	2:BY:35:ASN:ND2	2.48	0.43
3:Ba:35:VAL:O	3:Ba:39:ARG:HG3	2.18	0.43
5:Bb:55:ASP:O	5:Bb:59:ARG:HG3	2.17	0.43
5:Bb:204:VAL:HG23	5:Bb:245:VAL:HG21	2.00	0.43
8:Be:51:ILE:HB	8:Be:54:MET:HG3	1.99	0.43
10:Bg:133:PHE:CZ	11:Bh:261:SER:HB2	2.45	0.43
25:Bx:92:PHE:CZ	25:Bx:115:ILE:HD13	2.45	0.43
26:EL:71:ILE:HG22	26:FL:67:LEU:HD13	2.00	0.43
29:BA:803:A:N3	29:BA:805:C:N4	2.65	0.43
33:B5:138:ARG:HA	33:B5:141:MET:HG2	2.00	0.43
37:BC:235:VAL:HG12	37:BC:244:LEU:HB2	2.00	0.43
41:BE:76:LYS:HG3	41:BE:170:LEU:HD21	1.99	0.43
44:BJ:97:ALA:HA	44:BJ:179:GLY:HA3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:BP:218:LYS:NZ	48:BP:235:GLU:OE1	2.39	0.43
53:BV:174:ILE:HG23	53:BV:187:LYS:HZ3	1.83	0.43
2:BY:48:PRO:HG3	30:B2:236:LEU:HD13	1.99	0.43
2:BY:171:ILE:O	30:B2:82:LYS:NZ	2.42	0.43
14:Bk:172:GLU:CD	14:Bk:175:HIS:HE1	2.26	0.43
24:Bw:63:VAL:HA	24:Bw:66:TRP:HD1	1.83	0.43
29:BA:1046:A:OP1	41:BE:239:ARG:HD3	2.18	0.43
37:BC:351:SER:N	37:BC:354:GLU:OE2	2.43	0.43
37:BC:496:PRO:HG2	39:BG:186:THR:HG22	1.99	0.43
3:Ba:343:GLN:HE22	3:Ba:420:HIS:HB3	1.83	0.43
5:Bb:196:THR:OG1	5:Bb:324:ASP:OD2	2.24	0.43
6:Bc:289:LEU:H	6:Bc:289:LEU:HD23	1.84	0.43
13:Bj:184:LEU:HD13	13:Bj:234:PHE:CE2	2.53	0.43
23:Bv:106:GLN:O	23:Bv:110:GLU:HG2	2.19	0.43
24:Bw:236:ARG:NH1	24:Bw:284:ASP:OD2	2.49	0.43
29:BA:176:U:H2'	29:BA:177:U:C6	2.53	0.43
29:BA:1338:G:H2'	29:BA:1339:A:H8	1.83	0.43
37:BC:334:LYS:HA	37:BC:334:LYS:HD3	1.75	0.43
46:BN:117:HIS:O	46:BN:121:MET:HG2	2.18	0.43
48:BP:16:LEU:HD23	48:BP:19:LEU:HD12	2.01	0.43
48:BP:177:ALA:HA	48:BP:222:TYR:CD1	2.53	0.43
2:BY:121:LYS:HD2	2:BY:130:PRO:HB2	2.00	0.43
2:BY:122:LEU:HD21	2:BY:145:ARG:HH21	1.83	0.43
3:Ba:85:PRO:HB3	29:BA:744:A:OP2	2.19	0.43
6:Bc:37:LEU:HA	6:Bc:40:MET:HG2	2.01	0.43
6:Bc:127:PHE:HB3	6:Bc:302:LEU:HD11	2.01	0.43
13:Bj:191:THR:O	13:Bj:195:LEU:HB2	2.18	0.43
19:Bp:93:HIS:CE1	25:Bx:47:THR:HG21	2.53	0.43
24:Bw:44:TYR:OH	49:BR:67:ASP:OD2	2.21	0.43
29:BA:232:U:H2'	29:BA:233:A:H8	1.83	0.43
37:BC:157:ARG:HD3	37:BC:157:ARG:C	2.43	0.43
37:BC:241:LYS:HG3	37:BC:277:ARG:NH1	2.33	0.43
2:BY:108:MET:HE3	12:Bi:170:PRO:HG3	2.00	0.43
2:BY:191:LEU:HD21	8:Be:93:THR:HG21	2.00	0.43
7:Bd:66:GLU:OE2	7:Bd:66:GLU:N	2.49	0.43
8:Be:89:LEU:O	8:Be:93:THR:HG22	2.19	0.43
13:Bj:260:LEU:HA	13:Bj:264:LEU:HD23	2.01	0.43
24:Bw:219:ARG:HH12	29:BA:779:G:H5''	1.83	0.43
25:Bx:65:ASN:O	25:Bx:74:ARG:HB2	2.19	0.43
25:Bx:92:PHE:HB2	25:Bx:100:LEU:HD12	2.01	0.43
29:BA:787:U:H2'	29:BA:788:A:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BC:78:HIS:CG	37:BC:173:GLU:HB3	2.53	0.43
39:BG:117:ASP:CG	39:BG:131:ASN:HD22	2.27	0.43
39:BG:171:PRO:HB3	39:BG:180:VAL:HG22	2.01	0.43
49:BR:151:GLN:O	49:BR:155:GLN:HG3	2.19	0.43
1:B0:41:ASN:HD21	29:BA:1177:U:H3'	1.82	0.43
5:Bb:113:LEU:HD22	50:BS:117:TYR:HB2	2.01	0.43
12:Bi:244:GLU:N	12:Bi:244:GLU:OE2	2.52	0.43
22:Bu:109:TRP:CD1	22:Bu:110:ILE:HG23	2.54	0.43
27:B1:233:GLU:O	27:B1:237:GLN:HG2	2.19	0.43
29:BA:71:U:H3	29:BA:94:U:H3	1.65	0.43
29:BA:428:A:N3	29:BA:600:C:O2'	2.48	0.43
29:BA:620:A:H2'	29:BA:621:U:C6	2.53	0.43
29:BA:1000:A:H2'	29:BA:1001:A:H8	1.84	0.43
29:BA:1046:A:OP2	29:BA:1046:A:H8	2.02	0.43
29:BA:1351:U:H2'	29:BA:1353:C:O5'	2.19	0.43
36:BB:31:C:H2'	36:BB:32:A:H8	1.83	0.43
26:LL:176:VAL:HG13	26:LL:181:ALA:HB2	2.00	0.43
41:BE:111:THR:HG23	41:BE:336:ASN:HB3	1.99	0.43
41:BE:177:LYS:HD3	41:BE:177:LYS:HA	1.78	0.43
3:Ba:229:ARG:HG3	3:Ba:291:LEU:HD23	2.00	0.43
13:Bj:205:LEU:HB3	14:Bk:168:GLU:HG3	2.00	0.43
29:BA:476:U:H2'	29:BA:477:A:H8	1.84	0.43
29:BA:942:U:H2'	29:BA:943:C:H6	1.83	0.43
29:BA:1060:C:H2'	29:BA:1061:U:C6	2.54	0.43
29:BA:1569:A:H2	41:BE:66:SER:HA	1.84	0.43
5:Bb:259:PRO:O	5:Bb:327:VAL:HG11	2.17	0.43
10:Bg:28:ARG:HH12	11:Bh:71:GLU:CD	2.27	0.43
25:Bx:39:VAL:HG11	25:Bx:52:ARG:HH12	1.83	0.43
29:BA:197:U:H2'	29:BA:198:U:H6	1.83	0.43
37:BC:693:GLU:HG2	37:BC:728:ILE:HG13	2.00	0.43
49:BR:113:ARG:HG2	49:BR:121:MET:HE2	2.01	0.43
52:BU:73:THR:HG22	52:BU:83:TYR:CB	2.49	0.43
2:BY:95:TYR:HB3	2:BY:108:MET:SD	2.58	0.43
3:Ba:281:GLU:OE1	3:Ba:281:GLU:N	2.49	0.43
5:Bb:92:LEU:HB2	5:Bb:170:ARG:HG3	2.01	0.43
6:Bc:137:LYS:O	6:Bc:141:ARG:NE	2.51	0.43
6:Bc:239:GLU:O	6:Bc:242:SER:OG	2.37	0.43
10:Bg:40:SER:O	10:Bg:44:ARG:HG3	2.19	0.43
12:Bi:288:LYS:HA	12:Bi:288:LYS:HD3	1.70	0.43
19:Bp:18:VAL:HG21	19:Bp:34:LEU:HD13	2.00	0.43
22:Bu:123:LYS:HE3	22:Bu:123:LYS:HB2	1.80	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Bx:186:SER:HA	29:BA:575:C:H5	1.83	0.43
29:BA:204:G:H2'	48:BP:40:PRO:HG3	2.01	0.43
29:BA:327:G:OP1	38:BD:270:ARG:NH1	2.48	0.43
29:BA:474:A:O2'	29:BA:596:A:O4'	2.36	0.43
29:BA:572:A:H2'	29:BA:573:A:C8	2.54	0.43
29:BA:713:A:H2'	29:BA:714:A:H8	1.83	0.43
29:BA:1519:U:OP2	29:BA:1520:U:O2'	2.29	0.43
37:BC:415:LEU:HD11	37:BC:427:LEU:HD21	2.00	0.43
48:BP:179:TYR:CE2	48:BP:203:ARG:HD2	2.54	0.43
48:BP:180:ASP:OD1	48:BP:180:ASP:N	2.50	0.43
50:BS:109:GLU:O	50:BS:113:LYS:HB2	2.19	0.43
3:Ba:122:TRP:HE3	3:Ba:123:LEU:HD23	1.84	0.43
11:Bh:92:PHE:HE1	11:Bh:175:VAL:HG13	1.83	0.43
11:Bh:148:LEU:HD12	11:Bh:149:PRO:HD2	1.99	0.43
14:Bk:96:ILE:HB	14:Bk:183:LYS:HB2	2.00	0.43
19:Bp:62:PRO:HG2	19:Bp:78:GLY:O	2.19	0.43
26:EL:67:LEU:O	26:EL:71:ILE:HG23	2.19	0.43
29:BA:42:C:OP1	30:B2:194:LYS:HD2	2.19	0.43
29:BA:611:U:H2'	29:BA:612:A:H8	1.84	0.43
37:BC:613:GLU:HG3	37:BC:652:LEU:HB2	2.01	0.43
51:BT:70:ARG:NH2	51:BT:212:ASN:O	2.42	0.43
3:Ba:119:GLN:NE2	3:Ba:263:MET:O	2.41	0.42
6:Bc:169:VAL:HG12	6:Bc:322:GLU:HB2	2.00	0.42
10:Bg:55:ALA:HB2	10:Bg:63:ILE:HD12	2.01	0.42
12:Bi:72:LEU:HD23	29:BA:139:G:C6	2.54	0.42
12:Bi:88:TYR:CZ	12:Bi:195:VAL:HG11	2.54	0.42
13:Bj:48:LEU:HD12	13:Bj:176:SER:O	2.18	0.42
18:Bo:107:LYS:HA	18:Bo:107:LYS:HD2	1.87	0.42
27:B1:27:HIS:CE1	27:B1:200:GLU:HG2	2.54	0.42
26:EL:74:LEU:HB3	26:EL:78:GLU:HB2	2.01	0.42
29:BA:948:A:O2'	29:BA:1382:C:O2	2.35	0.42
29:BA:1072:A:H2'	29:BA:1073:A:C8	2.53	0.42
30:B2:119:GLN:HG2	55:BX:29:VAL:HG12	2.00	0.42
33:B5:138:ARG:HA	33:B5:141:MET:SD	2.59	0.42
34:B6:42:THR:HG23	34:B6:57:VAL:HG12	2.00	0.42
37:BC:399:ILE:HG13	37:BC:448:VAL:O	2.19	0.42
37:BC:576:ASP:OD2	37:BC:672:ARG:NH1	2.52	0.42
41:BE:219:MET:SD	41:BE:238:ARG:HG2	2.58	0.42
43:BI:126:GLN:HB2	43:BI:128:LEU:HD13	2.01	0.42
3:Ba:380:GLN:HB3	3:Ba:410:THR:HG22	2.01	0.42
3:Ba:389:LEU:H	29:BA:725:C:H5	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:Bb:217:LEU:HD21	5:Bb:298:PHE:CE2	2.54	0.42
7:Bd:38:LEU:HD23	7:Bd:38:LEU:H	1.84	0.42
7:Bd:134:TYR:CG	32:B4:66:HIS:HE1	2.36	0.42
8:Be:14:GLY:HA2	35:B7:56:TYR:CE2	2.54	0.42
12:Bi:88:TYR:HB2	12:Bi:196:GLN:HE21	1.84	0.42
13:Bj:137:LEU:HD23	13:Bj:137:LEU:H	1.83	0.42
16:Bm:54:PRO:HD2	42:BF:72:TYR:HD1	1.84	0.42
29:BA:1199:A:H2'	29:BA:1200:A:O4'	2.19	0.42
29:BA:1226:C:OP1	29:BA:1227:U:N3	2.45	0.42
29:BA:1344:C:H2'	29:BA:1345:A:C8	2.54	0.42
29:BA:1448:A:H2'	29:BA:1449:U:H6	1.84	0.42
37:BC:203:SER:HB3	37:BC:206:TYR:HB3	2.01	0.42
37:BC:315:ILE:HA	37:BC:318:VAL:HG22	2.01	0.42
38:BD:83:GLY:HA2	38:BD:96:ILE:HG22	2.01	0.42
39:BG:248:GLU:OE2	39:BG:251:ARG:NH2	2.45	0.42
2:BY:36:PRO:O	2:BY:39:THR:HG22	2.20	0.42
6:Bc:118:LYS:HE2	6:Bc:118:LYS:HB3	1.89	0.42
6:Bc:182:LEU:HD23	6:Bc:291:ARG:HG3	2.02	0.42
6:Bc:324:LYS:HD3	6:Bc:324:LYS:HA	1.91	0.42
7:Bd:95:LEU:HB3	14:Bk:169:ILE:HD12	2.00	0.42
29:BA:11:G:O6	30:B2:231:LYS:NZ	2.40	0.42
29:BA:319:G:H2'	29:BA:320:U:C6	2.55	0.42
29:BA:788:A:HO2'	49:BR:17:ARG:HH21	1.62	0.42
29:BA:838:A:H1'	29:BA:933:A:H61	1.83	0.42
29:BA:995:C:OP1	49:BR:13:ARG:NH2	2.50	0.42
29:BA:1008:A:H1'	54:BW:155:ARG:HD3	2.00	0.42
29:BA:1270:G:H2'	29:BA:1323:U:H5''	2.01	0.42
34:B6:18:VAL:HB	34:B6:58:GLU:HG3	1.99	0.42
38:BD:232:LYS:HD3	38:BD:232:LYS:HA	1.81	0.42
5:Bb:270:PHE:HB2	5:Bb:317:ALA:HB3	2.02	0.42
11:Bh:301:LEU:HD23	11:Bh:301:LEU:HA	1.91	0.42
12:Bi:207:ASN:HA	12:Bi:253:VAL:HG21	2.00	0.42
13:Bj:101:LYS:HD2	13:Bj:101:LYS:HA	1.83	0.42
24:Bw:148:HIS:HA	24:Bw:166:ILE:HD11	2.00	0.42
26:EL:74:LEU:HD13	26:EL:78:GLU:HB3	2.01	0.42
29:BA:363:G:H2'	29:BA:364:A:C8	2.55	0.42
29:BA:891:A:H3'	29:BA:892:G:H8	1.84	0.42
29:BA:1418:G:N2	29:BA:1421:A:OP2	2.40	0.42
37:BC:383:LEU:HD22	37:BC:436:VAL:HG22	2.00	0.42
44:BJ:38:ARG:O	44:BJ:38:ARG:HD3	2.19	0.42
3:Ba:148:GLU:H	3:Ba:148:GLU:HG2	1.63	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:Bb:238:THR:HG21	5:Bb:281:PHE:CZ	2.52	0.42
22:Bu:61:LEU:HD21	48:BP:244:LEU:HD23	2.02	0.42
24:Bw:101:ASN:O	24:Bw:105:TRP:HD1	2.03	0.42
24:Bw:207:GLY:HA2	24:Bw:375:ALA:HB2	2.02	0.42
29:BA:314:U:H2'	29:BA:315:G:H8	1.84	0.42
35:B7:74:ARG:HA	35:B7:74:ARG:HD3	1.76	0.42
37:BC:239:VAL:HG13	37:BC:240:MET:HG3	2.00	0.42
26:LL:184:ILE:HG13	26:LL:185:LYS:N	2.35	0.42
41:BE:82:ASP:OD1	41:BE:82:ASP:N	2.50	0.42
3:Ba:392:ILE:HG13	3:Ba:397:VAL:HG22	2.01	0.42
5:Bb:45:LEU:O	5:Bb:50:LYS:NZ	2.51	0.42
13:Bj:194:THR:HG23	13:Bj:195:LEU:HD22	2.02	0.42
24:Bw:47:ILE:HG22	24:Bw:47:ILE:O	2.19	0.42
27:B1:215:GLN:NE2	27:B1:219:GLU:OE2	2.35	0.42
29:BA:1497:G:H1'	29:BA:1498:C:H2'	2.02	0.42
30:B2:137:VAL:O	30:B2:141:MET:HG3	2.19	0.42
30:B2:194:LYS:HE2	30:B2:198:ARG:HH12	1.84	0.42
43:BI:122:ARG:HE	43:BI:123:LEU:HD12	1.85	0.42
47:BO:41:VAL:HG22	47:BO:105:VAL:O	2.19	0.42
3:Ba:202:ILE:HG22	3:Ba:231:ASN:HB2	2.02	0.42
3:Ba:306:PRO:O	3:Ba:310:ARG:NE	2.50	0.42
5:Bb:40:ILE:HD11	14:Bk:62:LEU:HD22	2.02	0.42
6:Bc:178:TYR:OH	6:Bc:259:ASP:OD2	2.35	0.42
29:BA:12:C:O2	29:BA:111:G:O2'	2.36	0.42
29:BA:1050:C:O5'	29:BA:1051:G:H5''	2.19	0.42
29:BA:1454:C:H2'	29:BA:1455:C:C6	2.54	0.42
50:BS:146:TYR:HD2	50:BS:162:GLN:HE21	1.68	0.42
4:B8:109:ALA:O	4:B8:113:ARG:HG2	2.19	0.42
6:Bc:227:PHE:CE1	6:Bc:233:LYS:HG2	2.55	0.42
6:Bc:273:PHE:CD2	6:Bc:274:GLN:HG3	2.55	0.42
8:Be:25:ARG:O	35:B7:60:ASN:ND2	2.53	0.42
10:Bg:146:ARG:HA	10:Bg:146:ARG:HD3	1.73	0.42
13:Bj:128:PHE:HB2	32:B4:74:ARG:HB2	2.01	0.42
13:Bj:151:ARG:HH12	13:Bj:255:VAL:HG12	1.83	0.42
14:Bk:155:ARG:HA	14:Bk:155:ARG:HD3	1.86	0.42
21:Bt:66:ARG:NH2	29:BA:417:G:OP2	2.52	0.42
29:BA:129:A:H2'	29:BA:130:A:C8	2.55	0.42
29:BA:435:C:H2'	29:BA:436:U:H6	1.83	0.42
32:B4:56:LEU:HD12	32:B4:56:LEU:HA	1.87	0.42
36:BB:63:C:H2'	36:BB:64:A:H8	1.85	0.42
44:BJ:188:ARG:NH1	44:BJ:192:ILE:HD11	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:BP:131:PRO:HG2	48:BP:185:GLU:HG2	2.02	0.42
50:BS:39:VAL:HB	50:BS:42:GLU:HB2	2.02	0.42
53:BV:131:ARG:HH12	53:BV:161:GLU:HG2	1.84	0.42
2:BY:209:ARG:HA	2:BY:209:ARG:HD3	1.88	0.42
4:B8:113:ARG:HD2	48:BP:75:TYR:O	2.20	0.42
7:Bd:134:TYR:CD1	32:B4:66:HIS:HE1	2.37	0.42
11:Bh:239:GLY:O	11:Bh:242:VAL:HG12	2.20	0.42
24:Bw:103:ASP:OD1	24:Bw:103:ASP:N	2.51	0.42
29:BA:843:C:N4	29:BA:871:A:O2'	2.53	0.42
29:BA:1236:C:H2'	29:BA:1237:A:H8	1.84	0.42
32:B4:52:LEU:HB3	32:B4:68:ARG:HB3	2.01	0.42
42:BF:83:HIS:HB2	42:BF:270:GLU:OE2	2.20	0.42
51:BT:93:GLN:HG2	51:BT:96:ARG:HH21	1.85	0.42
1:B0:51:PHE:HA	1:B0:69:THR:HG23	2.01	0.42
14:Bk:207:LEU:HA	14:Bk:210:LYS:HG2	2.02	0.42
29:BA:571:A:N3	46:BN:111:MET:HG2	2.35	0.42
29:BA:927:A:H2'	29:BA:928:G:O4'	2.20	0.42
37:BC:233:LYS:HB3	37:BC:233:LYS:HE2	1.79	0.42
53:BV:177:LYS:HG3	53:BV:186:ARG:NH1	2.35	0.42
7:Bd:39:ILE:HG12	14:Bk:199:LYS:HD3	2.02	0.41
8:Be:49:VAL:HG21	29:BA:746:U:H3	1.84	0.41
12:Bi:245:TYR:HE1	12:Bi:267:PRO:HD3	1.84	0.41
12:Bi:290:TRP:HA	33:B5:132:LYS:NZ	2.34	0.41
24:Bw:206:ARG:HB3	24:Bw:225:TYR:HE1	1.84	0.41
24:Bw:242:PRO:HB3	24:Bw:424:LYS:HG2	2.02	0.41
29:BA:343:C:H2'	29:BA:344:U:C6	2.54	0.41
29:BA:435:C:H2'	29:BA:436:U:C6	2.55	0.41
29:BA:562:A:N3	29:BA:562:A:H3'	2.35	0.41
29:BA:582:C:OP1	52:BU:99:ARG:NH2	2.32	0.41
29:BA:895:U:OP1	38:BD:285:ARG:NH1	2.53	0.41
29:BA:1493:A:C6	49:BR:14:VAL:HG21	2.54	0.41
37:BC:76:MET:SD	37:BC:156:LEU:HD11	2.60	0.41
37:BC:400:HIS:CD2	37:BC:451:LYS:HD3	2.55	0.41
37:BC:542:ILE:HG13	37:BC:543:ILE:N	2.35	0.41
38:BD:206:GLN:HA	38:BD:209:ARG:HH21	1.85	0.41
48:BP:99:ASN:HB2	48:BP:144:GLY:HA3	2.01	0.41
48:BP:254:LYS:HB3	48:BP:254:LYS:HE3	1.77	0.41
49:BR:80:LEU:HD12	49:BR:86:ILE:HG12	2.02	0.41
50:BS:93:LEU:HD23	50:BS:101:VAL:HG22	2.02	0.41
52:BU:101:VAL:HG11	53:BV:102:VAL:HG11	2.02	0.41
3:Ba:110:ARG:NH2	3:Ba:302:ARG:O	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:Bb:187:VAL:HG13	5:Bb:319:PHE:HB3	2.02	0.41
15:Bl:111:ARG:HD2	29:BA:217:A:H62	1.85	0.41
21:Bt:23:ARG:HH21	25:Bx:168:ARG:HD2	1.85	0.41
25:Bx:196:HIS:HB2	29:BA:573:A:C6	2.55	0.41
29:BA:230:G:H2'	29:BA:231:C:H6	1.83	0.41
29:BA:232:U:C2	29:BA:233:A:C8	3.08	0.41
29:BA:326:U:OP1	38:BD:91:ILE:HG13	2.21	0.41
29:BA:364:A:O2'	29:BA:385:U:OP1	2.38	0.41
29:BA:1370:U:H2'	29:BA:1371:C:C6	2.55	0.41
36:BB:35:G:H2'	36:BB:36:A:H8	1.85	0.41
40:BQ:53:VAL:HG21	40:BQ:102:PHE:HB3	2.02	0.41
41:BE:94:SER:HA	41:BE:182:THR:HG21	2.02	0.41
44:BJ:34:THR:OG1	44:BJ:38:ARG:HB2	2.20	0.41
51:BT:112:TYR:CE1	51:BT:215:VAL:HG21	2.54	0.41
51:BT:186:SER:HB2	51:BT:188:LEU:HD23	2.01	0.41
2:BY:186:THR:HG23	30:B2:96:SER:H	1.85	0.41
3:Ba:105:TYR:HB2	3:Ba:220:LEU:HD23	2.00	0.41
3:Ba:207:ASN:HB3	24:Bw:151:LEU:HD11	2.01	0.41
3:Ba:236:LEU:HB3	3:Ba:341:VAL:HG13	2.03	0.41
5:Bb:176:ALA:HB1	5:Bb:184:LEU:HG	2.03	0.41
12:Bi:108:ARG:HA	12:Bi:108:ARG:HD3	1.89	0.41
13:Bj:198:ASN:HD22	13:Bj:243:PHE:HA	1.84	0.41
21:Bt:15:ARG:HG3	29:BA:448:G:C2	2.56	0.41
26:CL:81:ASP:HA	26:CL:84:GLU:HG2	2.02	0.41
27:B1:40:PRO:HG3	27:B1:45:PRO:HG3	2.03	0.41
29:BA:663:C:H2'	29:BA:664:U:O4'	2.20	0.41
31:B3:82:GLU:OE2	31:B3:115:HIS:NE2	2.47	0.41
34:B6:34:ARG:HG3	34:B6:41:LEU:HD22	2.02	0.41
37:BC:306:LEU:HD11	37:BC:310:LYS:N	2.27	0.41
40:BQ:98:HIS:HD2	40:BQ:100:GLY:H	1.69	0.41
26:LL:142:LYS:NZ	26:LL:165:VAL:HG12	2.35	0.41
47:BO:77:ILE:O	47:BO:80:GLN:HG2	2.20	0.41
53:BV:133:ARG:NH2	53:BV:155:LYS:O	2.53	0.41
1:B0:77:PRO:HG2	50:BS:68:TRP:O	2.20	0.41
1:B0:124:ALA:HB1	14:Bk:62:LEU:HD13	2.01	0.41
5:Bb:226:LEU:HD21	50:BS:43:ALA:HB3	2.03	0.41
6:Bc:145:MET:HE2	6:Bc:254:PHE:CD1	2.52	0.41
9:Bf:75:ILE:HG23	11:Bh:289:VAL:HG11	2.02	0.41
12:Bi:233:TYR:CD1	55:BX:144:VAL:HG11	2.56	0.41
12:Bi:290:TRP:HB3	33:B5:132:LYS:CD	2.50	0.41
13:Bj:74:LEU:HA	13:Bj:77:ILE:HG12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Bm:117:ARG:O	16:Bm:121:MET:HG2	2.21	0.41
29:BA:1552:C:H5'	29:BA:1553:A:OP1	2.20	0.41
30:B2:198:ARG:HD2	35:B7:74:ARG:HH21	1.86	0.41
12:Bi:288:LYS:HG3	12:Bi:290:TRP:CZ2	2.56	0.41
17:Bn:32:PHE:CD2	29:BA:199:A:H5''	2.56	0.41
29:BA:585:A:H5''	52:BU:58:ARG:NH1	2.35	0.41
29:BA:713:A:H2'	29:BA:714:A:C8	2.55	0.41
29:BA:1451:U:H2'	29:BA:1452:C:C6	2.55	0.41
29:BA:1451:U:H2'	29:BA:1452:C:H6	1.85	0.41
39:BG:130:LEU:HD23	39:BG:130:LEU:HA	1.91	0.41
46:BN:90:VAL:HG22	46:BN:94:GLN:HB2	2.03	0.41
50:BS:102:VAL:HG11	50:BS:141:ILE:HD11	2.02	0.41
53:BV:169:GLU:HB3	53:BV:191:VAL:HG12	2.03	0.41
3:Ba:281:GLU:H	3:Ba:281:GLU:CD	2.28	0.41
11:Bh:31:ALA:HA	29:BA:7:G:OP1	2.21	0.41
12:Bi:219:ARG:NE	12:Bi:239:PRO:HB2	2.32	0.41
19:Bp:35:GLN:HE22	44:BJ:150:HIS:CG	2.39	0.41
24:Bw:137:ARG:NH1	24:Bw:409:ASP:OD2	2.54	0.41
24:Bw:243:GLU:HA	24:Bw:350:VAL:HG21	2.03	0.41
25:Bx:63:PRO:HA	25:Bx:64:PRO:HD3	1.96	0.41
29:BA:17:C:H2'	29:BA:18:A:O4'	2.21	0.41
29:BA:32:C:O2'	29:BA:36:A:N6	2.53	0.41
29:BA:342:C:H2'	29:BA:343:C:C6	2.55	0.41
29:BA:521:C:O2'	45:BK:104:THR:O	2.35	0.41
29:BA:882:A:C8	29:BA:922:A:C4	3.08	0.41
44:BJ:223:GLN:O	44:BJ:226:PRO:HD2	2.20	0.41
50:BS:89:HIS:CG	50:BS:108:ARG:HG2	2.55	0.41
50:BS:130:ARG:HG2	50:BS:164:ALA:HB1	2.03	0.41
54:BW:89:ALA:O	54:BW:93:ARG:HG3	2.20	0.41
55:BX:36:PRO:HG2	55:BX:39:THR:OG1	2.21	0.41
4:B8:108:LYS:HA	4:B8:108:LYS:HD3	1.90	0.41
5:Bb:252:CYS:SG	5:Bb:286:ARG:HG3	2.60	0.41
12:Bi:43:PRO:HG3	29:BA:337:A:C6	2.56	0.41
12:Bi:67:ILE:O	12:Bi:71:ARG:HB2	2.21	0.41
13:Bj:60:THR:HG21	14:Bk:180:GLU:CD	2.46	0.41
15:Bl:128:LEU:HB2	15:Bl:136:PRO:HG3	2.02	0.41
18:Bo:98:LYS:O	18:Bo:101:GLU:HG3	2.21	0.41
20:Bq:75:VAL:HG11	45:BK:119:GLU:HB3	2.01	0.41
28:B9:96:LYS:NZ	29:BA:1513:U:OP1	2.38	0.41
29:BA:164:A:H3'	52:BU:35:LYS:NZ	2.36	0.41
29:BA:1222:A:H2'	29:BA:1223:U:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:BJ:112:LEU:O	44:BJ:116:LEU:HD23	2.20	0.41
44:BJ:193:ASN:O	44:BJ:197:LEU:HD13	2.20	0.41
53:BV:179:GLN:HG3	53:BV:184:TYR:HD2	1.85	0.41
2:BY:56:LEU:HD23	2:BY:56:LEU:HA	1.94	0.41
5:Bb:150:ARG:NH2	50:BS:104:SER:OG	2.37	0.41
21:Bt:98:THR:OG1	48:BP:26:ASN:ND2	2.54	0.41
29:BA:1017:U:O2'	29:BA:1440:U:H5'	2.20	0.41
29:BA:1124:C:H2'	29:BA:1125:U:C6	2.56	0.41
36:BB:8:U:O2	36:BB:14:A:N6	2.54	0.41
37:BC:150:LEU:HD22	37:BC:518:SER:HB3	2.03	0.41
39:BG:117:ASP:OD1	39:BG:136:ILE:HD12	2.21	0.41
41:BE:69:ASN:HD21	41:BE:154:HIS:HE1	1.69	0.41
2:BY:11:SER:N	30:B2:135:GLU:OE1	2.54	0.41
3:Ba:121:LEU:HD11	3:Ba:128:LEU:HB2	2.03	0.41
3:Ba:223:HIS:NE2	29:BA:741:A:OP1	2.38	0.41
3:Ba:417:LEU:HD23	3:Ba:417:LEU:HA	1.92	0.41
6:Bc:233:LYS:HA	6:Bc:233:LYS:HD3	1.80	0.41
10:Bg:50:GLU:OE2	10:Bg:98:ALA:HB2	2.21	0.41
11:Bh:166:VAL:HG11	11:Bh:192:ARG:HG3	2.02	0.41
11:Bh:188:PRO:N	11:Bh:189:PRO:HD2	2.36	0.41
12:Bi:203:MET:HE3	12:Bi:203:MET:O	2.20	0.41
18:Bo:84:MET:HE3	31:B3:103:ILE:HG23	2.02	0.41
21:Bt:14:GLY:H	29:BA:1279:G:H5''	1.85	0.41
23:Bv:30:PRO:HA	23:Bv:31:PRO:HD3	1.96	0.41
23:Bv:101:GLU:O	23:Bv:105:VAL:HG23	2.20	0.41
23:Bv:113:LYS:HB3	23:Bv:113:LYS:HE2	1.93	0.41
24:Bw:265:LEU:N	24:Bw:266:PRO:HA	2.36	0.41
26:FL:70:ASP:OD1	26:FL:71:ILE:HG23	2.20	0.41
29:BA:63:A:H2'	29:BA:63:A:N3	2.36	0.41
29:BA:187:G:H2'	29:BA:1025:A:N7	2.35	0.41
29:BA:348:G:C8	42:BF:118:ALA:HB2	2.55	0.41
29:BA:526:A:H4'	45:BK:139:SER:HB3	2.03	0.41
29:BA:652:A:H2'	29:BA:653:A:C8	2.56	0.41
30:B2:75:ASN:HA	30:B2:78:GLU:HG2	2.03	0.41
37:BC:645:ILE:HD13	37:BC:678:LEU:HD13	2.02	0.41
45:BK:51:LYS:O	45:BK:55:GLU:HG2	2.21	0.41
45:BK:76:ARG:HA	45:BK:76:ARG:HD3	1.89	0.41
45:BK:110:GLY:HA2	45:BK:167:PHE:HE2	1.86	0.41
51:BT:113:VAL:HG12	51:BT:187:LEU:HD13	2.03	0.41
53:BV:176:MET:HA	53:BV:186:ARG:O	2.21	0.41
4:B8:183:ARG:HD2	5:Bb:354:GLN:NE2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Bm:123:ARG:HH22	16:Bm:125:ARG:HE	1.68	0.41
25:Bx:67:THR:OG1	44:BJ:66:PRO:HG3	2.21	0.41
27:B1:85:TRP:CD1	27:B1:106:LYS:HG2	2.56	0.41
29:BA:130:A:OP1	42:BF:147:ARG:NH2	2.54	0.41
29:BA:1301:A:H1'	29:BA:1351:U:O2'	2.21	0.41
39:BG:219:LEU:HD11	39:BG:234:ILE:HG22	2.02	0.41
41:BE:197:HIS:CD2	41:BE:318:THR:HA	2.56	0.41
48:BP:111:ASP:OD1	48:BP:111:ASP:N	2.43	0.41
5:Bb:27:ARG:N	29:BA:1168:A:N1	2.69	0.40
5:Bb:234:HIS:O	5:Bb:254:TYR:HA	2.21	0.40
12:Bi:137:PHE:N	12:Bi:138:PRO:HD2	2.36	0.40
13:Bj:257:LYS:NZ	13:Bj:277:LEU:O	2.54	0.40
20:Bq:79:LYS:HD2	20:Bq:79:LYS:HA	1.88	0.40
29:BA:378:U:H5''	48:BP:57:ARG:HH21	1.86	0.40
29:BA:446:C:O2'	29:BA:447:A:O5'	2.31	0.40
30:B2:115:LEU:HB3	55:BX:27:GLN:HG2	2.02	0.40
33:B5:90:ASN:O	33:B5:94:ARG:HG2	2.22	0.40
37:BC:132:TRP:CD1	37:BC:346:THR:HG21	2.56	0.40
37:BC:280:LEU:O	37:BC:284:VAL:HG22	2.21	0.40
37:BC:477:ARG:HE	37:BC:479:LEU:HB2	1.86	0.40
42:BF:220:ASP:O	42:BF:245:ALA:N	2.55	0.40
47:BO:52:HIS:CD2	47:BO:53:ARG:HG3	2.55	0.40
49:BR:44:ALA:HB3	49:BR:49:VAL:HG23	2.03	0.40
51:BT:95:GLU:OE2	51:BT:145:LEU:N	2.45	0.40
52:BU:90:LEU:HG	52:BU:95:VAL:HB	2.03	0.40
3:Ba:191:GLN:HG2	3:Ba:419:LEU:HD21	2.03	0.40
5:Bb:214:TRP:CZ3	5:Bb:274:LYS:HB2	2.56	0.40
11:Bh:187:PRO:HA	11:Bh:188:PRO:HD3	1.92	0.40
13:Bj:48:LEU:HG	13:Bj:231:VAL:HG23	2.03	0.40
13:Bj:53:LEU:CD2	13:Bj:238:LEU:HD21	2.51	0.40
23:Bv:108:LEU:HD12	23:Bv:108:LEU:HA	1.97	0.40
23:Bv:129:PRO:O	23:Bv:133:GLU:HG2	2.21	0.40
29:BA:1195:A:N6	29:BA:1208:A:O2'	2.54	0.40
39:BG:119:ILE:HG22	39:BG:161:ALA:HB1	2.03	0.40
39:BG:155:THR:HG23	39:BG:178:ILE:HD11	2.04	0.40
41:BE:233:GLN:H	41:BE:233:GLN:HG2	1.72	0.40
48:BP:112:PRO:HB3	48:BP:152:VAL:HG12	2.03	0.40
51:BT:111:PHE:CD2	51:BT:117:LEU:HD11	2.56	0.40
2:BY:133:VAL:HG11	2:BY:145:ARG:HD2	2.03	0.40
5:Bb:132:LEU:HD13	50:BS:134:GLU:OE2	2.21	0.40
6:Bc:307:THR:HG21	41:BE:154:HIS:HB3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Bd:77:TRP:CD1	13:Bj:70:MET:HE2	2.56	0.40
11:Bh:60:ARG:NH1	11:Bh:63:LYS:HB2	2.36	0.40
12:Bi:240:ARG:HH21	55:BX:150:LEU:CD2	2.34	0.40
13:Bj:161:VAL:HG12	13:Bj:252:HIS:HB3	2.03	0.40
15:Bl:60:PRO:HA	15:Bl:61:PRO:HD3	1.95	0.40
17:Bn:105:ASP:OD1	30:B2:220:ARG:NH2	2.54	0.40
18:Bo:75:ARG:HE	31:B3:134:MET:HG3	1.86	0.40
27:B1:50:PHE:HE1	27:B1:61:ARG:HG3	1.85	0.40
26:EL:91:LYS:HB2	26:EL:91:LYS:HE3	1.71	0.40
29:BA:58:C:H2'	29:BA:59:A:H5''	2.04	0.40
29:BA:218:A:H4'	29:BA:219:A:H5'	2.04	0.40
29:BA:447:A:H8	29:BA:447:A:OP2	2.04	0.40
29:BA:529:G:H1'	29:BA:549:C:H1'	2.03	0.40
29:BA:607:A:N3	52:BU:20:ARG:NH2	2.69	0.40
29:BA:687:U:O2'	29:BA:688:A:H5'	2.21	0.40
29:BA:1224:C:H2'	29:BA:1225:A:C8	2.57	0.40
29:BA:1278:C:H2'	29:BA:1279:G:H8	1.86	0.40
29:BA:1569:A:C2	41:BE:65:VAL:HG12	2.57	0.40
38:BD:298:LYS:HA	38:BD:298:LYS:HD2	1.77	0.40
42:BF:99:VAL:O	42:BF:103:GLN:HG3	2.21	0.40
42:BF:171:VAL:HG13	42:BF:273:LEU:HD22	2.03	0.40
42:BF:274:LEU:HD23	42:BF:274:LEU:HA	1.94	0.40
44:BJ:225:GLN:HB2	44:BJ:226:PRO:HD3	2.03	0.40
48:BP:244:LEU:HD12	48:BP:245:PRO:HD2	2.02	0.40
54:BW:80:TYR:OH	54:BW:84:LYS:HB3	2.21	0.40
5:Bb:139:TRP:O	5:Bb:144:GLY:N	2.54	0.40
9:Bf:64:SER:HB2	52:BU:111:LYS:NZ	2.36	0.40
20:Bq:77:ILE:O	45:BK:61:LYS:HG3	2.22	0.40
21:Bt:15:ARG:HG3	29:BA:448:G:N1	2.37	0.40
27:B1:87:LEU:O	43:BI:78:ARG:NH1	2.54	0.40
29:BA:1453:U:H2'	29:BA:1454:C:H6	1.87	0.40
37:BC:111:ASP:HA	37:BC:116:GLU:OE1	2.21	0.40
37:BC:150:LEU:HD13	37:BC:486:PRO:HD3	2.04	0.40
37:BC:360:LEU:HD21	37:BC:389:TYR:HB3	2.03	0.40
38:BD:78:LYS:HB2	38:BD:78:LYS:HE3	1.79	0.40
26:LL:141:ASP:CG	26:LL:192:GLY:HA3	2.46	0.40
48:BP:117:ASP:OD2	48:BP:260:LYS:NZ	2.39	0.40
48:BP:255:MET:O	48:BP:258:THR:HG22	2.22	0.40
1:B0:78:GLY:HA3	1:B0:132:HIS:ND1	2.36	0.40
5:Bb:241:PRO:O	5:Bb:244:ARG:HG2	2.22	0.40
11:Bh:195:PHE:O	11:Bh:199:ILE:HG12	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Bw:163:ARG:HA	24:Bw:163:ARG:HD3	1.89	0.40
39:BG:79:VAL:HG11	39:BG:83:ILE:HG22	2.03	0.40
39:BG:256:LYS:HE2	39:BG:260:LEU:HG	2.02	0.40
26:LL:188:LEU:HD23	26:LL:195:VAL:HG22	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	
1	B0	108/148 (73%)	106 (98%)	2 (2%)	0	100	100
2	BY	204/216 (94%)	199 (98%)	5 (2%)	0	100	100
3	Ba	391/423 (92%)	371 (95%)	20 (5%)	0	100	100
4	B8	93/188 (50%)	91 (98%)	2 (2%)	0	100	100
5	Bb	352/380 (93%)	334 (95%)	18 (5%)	0	100	100
6	Bc	293/334 (88%)	278 (95%)	15 (5%)	0	100	100
7	Bd	138/206 (67%)	131 (95%)	7 (5%)	0	100	100
8	Be	120/135 (89%)	114 (95%)	6 (5%)	0	100	100
9	Bf	106/142 (75%)	100 (94%)	4 (4%)	2 (2%)	6	33
10	Bg	146/159 (92%)	136 (93%)	10 (7%)	0	100	100
11	Bh	287/332 (86%)	272 (95%)	15 (5%)	0	100	100
12	Bi	258/306 (84%)	245 (95%)	13 (5%)	0	100	100
13	Bj	211/279 (76%)	203 (96%)	8 (4%)	0	100	100
14	Bk	151/269 (56%)	146 (97%)	5 (3%)	0	100	100
15	Bl	131/166 (79%)	128 (98%)	3 (2%)	0	100	100
16	Bm	107/198 (54%)	103 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	Bn	95/128 (74%)	92 (97%)	3 (3%)	0	100	100
18	Bo	95/124 (77%)	93 (98%)	2 (2%)	0	100	100
19	Bp	95/112 (85%)	88 (93%)	7 (7%)	0	100	100
20	Bq	78/138 (56%)	72 (92%)	6 (8%)	0	100	100
21	Bt	92/102 (90%)	88 (96%)	4 (4%)	0	100	100
22	Bu	147/205 (72%)	141 (96%)	4 (3%)	2 (1%)	9	39
23	Bv	133/222 (60%)	133 (100%)	0	0	100	100
24	Bw	385/433 (89%)	367 (95%)	18 (5%)	0	100	100
25	Bx	160/196 (82%)	153 (96%)	7 (4%)	0	100	100
26	CL	43/198 (22%)	40 (93%)	3 (7%)	0	100	100
26	DL	25/198 (13%)	25 (100%)	0	0	100	100
26	EL	26/198 (13%)	26 (100%)	0	0	100	100
26	FL	25/198 (13%)	25 (100%)	0	0	100	100
26	GL	25/198 (13%)	25 (100%)	0	0	100	100
26	HL	24/198 (12%)	24 (100%)	0	0	100	100
26	LL	68/198 (34%)	67 (98%)	1 (2%)	0	100	100
27	B1	242/256 (94%)	240 (99%)	2 (1%)	0	100	100
28	B9	36/100 (36%)	36 (100%)	0	0	100	100
30	B2	177/252 (70%)	174 (98%)	3 (2%)	0	100	100
31	B3	116/161 (72%)	114 (98%)	2 (2%)	0	100	100
32	B4	60/126 (48%)	52 (87%)	8 (13%)	0	100	100
33	B5	108/188 (57%)	108 (100%)	0	0	100	100
34	B6	50/65 (77%)	49 (98%)	1 (2%)	0	100	100
35	B7	44/95 (46%)	43 (98%)	1 (2%)	0	100	100
37	BC	696/755 (92%)	637 (92%)	58 (8%)	1 (0%)	48	79
38	BD	238/306 (78%)	226 (95%)	12 (5%)	0	100	100
39	BG	194/257 (76%)	178 (92%)	14 (7%)	2 (1%)	12	45
40	BQ	220/251 (88%)	215 (98%)	5 (2%)	0	100	100
41	BE	305/399 (76%)	289 (95%)	16 (5%)	0	100	100
42	BF	248/294 (84%)	241 (97%)	7 (3%)	0	100	100
43	BI	96/268 (36%)	94 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	BJ	210/262 (80%)	199 (95%)	11 (5%)	0	100	100
45	BK	174/192 (91%)	164 (94%)	10 (6%)	0	100	100
46	BN	175/178 (98%)	171 (98%)	4 (2%)	0	100	100
47	BO	113/145 (78%)	111 (98%)	2 (2%)	0	100	100
48	BP	286/296 (97%)	275 (96%)	11 (4%)	0	100	100
49	BR	151/169 (89%)	143 (95%)	8 (5%)	0	100	100
50	BS	141/180 (78%)	133 (94%)	8 (6%)	0	100	100
51	BT	221/292 (76%)	218 (99%)	3 (1%)	0	100	100
52	BU	138/149 (93%)	137 (99%)	1 (1%)	0	100	100
53	BV	153/209 (73%)	147 (96%)	6 (4%)	0	100	100
54	BW	164/210 (78%)	158 (96%)	6 (4%)	0	100	100
55	BX	147/150 (98%)	143 (97%)	4 (3%)	0	100	100
All	All	9515/13132 (72%)	9111 (96%)	397 (4%)	7 (0%)	49	79

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	Bf	80	PRO
22	Bu	167	PRO
9	Bf	78	PRO
37	BC	65	PRO
22	Bu	166	GLU
39	BG	74	ILE
39	BG	183	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B0	90/115 (78%)	90 (100%)	0	100	100
2	BY	185/192 (96%)	184 (100%)	1 (0%)	81	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	Ba	348/365 (95%)	348 (100%)	0	100	100
4	B8	87/162 (54%)	87 (100%)	0	100	100
5	Bb	310/328 (94%)	310 (100%)	0	100	100
6	Bc	271/299 (91%)	271 (100%)	0	100	100
7	Bd	129/181 (71%)	129 (100%)	0	100	100
8	Be	100/108 (93%)	100 (100%)	0	100	100
9	Bf	80/133 (60%)	80 (100%)	0	100	100
10	Bg	128/136 (94%)	128 (100%)	0	100	100
11	Bh	251/284 (88%)	251 (100%)	0	100	100
12	Bi	236/275 (86%)	236 (100%)	0	100	100
13	Bj	190/242 (78%)	190 (100%)	0	100	100
14	Bk	135/226 (60%)	135 (100%)	0	100	100
15	Bl	122/147 (83%)	122 (100%)	0	100	100
16	Bm	103/178 (58%)	103 (100%)	0	100	100
17	Bn	88/113 (78%)	88 (100%)	0	100	100
18	Bo	77/97 (79%)	77 (100%)	0	100	100
19	Bp	79/88 (90%)	79 (100%)	0	100	100
20	Bq	70/114 (61%)	70 (100%)	0	100	100
21	Bt	75/82 (92%)	75 (100%)	0	100	100
22	Bu	126/177 (71%)	126 (100%)	0	100	100
23	Bv	115/183 (63%)	115 (100%)	0	100	100
24	Bw	340/373 (91%)	340 (100%)	0	100	100
25	Bx	149/173 (86%)	149 (100%)	0	100	100
26	CL	30/157 (19%)	30 (100%)	0	100	100
26	DL	26/157 (17%)	26 (100%)	0	100	100
26	EL	27/157 (17%)	27 (100%)	0	100	100
26	FL	26/157 (17%)	26 (100%)	0	100	100
26	GL	26/157 (17%)	26 (100%)	0	100	100
26	HL	25/157 (16%)	25 (100%)	0	100	100
26	LL	59/157 (38%)	59 (100%)	0	100	100
27	B1	219/229 (96%)	219 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	B9	36/77 (47%)	36 (100%)	0	100	100
30	B2	164/228 (72%)	164 (100%)	0	100	100
31	B3	110/150 (73%)	109 (99%)	1 (1%)	70	81
32	B4	45/114 (40%)	45 (100%)	0	100	100
33	B5	99/163 (61%)	99 (100%)	0	100	100
34	B6	49/60 (82%)	49 (100%)	0	100	100
35	B7	41/78 (53%)	41 (100%)	0	100	100
37	BC	600/651 (92%)	600 (100%)	0	100	100
38	BD	193/248 (78%)	193 (100%)	0	100	100
39	BG	175/224 (78%)	175 (100%)	0	100	100
40	BQ	190/210 (90%)	190 (100%)	0	100	100
41	BE	263/320 (82%)	263 (100%)	0	100	100
42	BF	217/251 (86%)	217 (100%)	0	100	100
43	BI	88/228 (39%)	88 (100%)	0	100	100
44	BJ	192/230 (84%)	192 (100%)	0	100	100
45	BK	138/151 (91%)	138 (100%)	0	100	100
46	BN	156/157 (99%)	156 (100%)	0	100	100
47	BO	99/123 (80%)	99 (100%)	0	100	100
48	BP	245/249 (98%)	245 (100%)	0	100	100
49	BR	132/143 (92%)	132 (100%)	0	100	100
50	BS	123/153 (80%)	123 (100%)	0	100	100
51	BT	205/258 (80%)	205 (100%)	0	100	100
52	BU	118/127 (93%)	118 (100%)	0	100	100
53	BV	136/178 (76%)	136 (100%)	0	100	100
54	BW	144/180 (80%)	144 (100%)	0	100	100
55	BX	116/134 (87%)	116 (100%)	0	100	100
All	All	8396/11184 (75%)	8394 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	BY	35	ASN
31	B3	142	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (87) such sidechains are listed below:

Mol	Chain	Res	Type
1	B0	41	ASN
2	BY	118	ASN
3	Ba	214	ASN
3	Ba	221	GLN
3	Ba	251	HIS
3	Ba	343	GLN
3	Ba	407	GLN
5	Bb	239	ASN
5	Bb	249	GLN
5	Bb	295	GLN
5	Bb	354	GLN
5	Bb	359	HIS
6	Bc	42	ASN
6	Bc	284	GLN
9	Bf	102	HIS
10	Bg	127	GLN
11	Bh	42	GLN
11	Bh	94	ASN
11	Bh	222	GLN
12	Bi	59	HIS
12	Bi	69	HIS
12	Bi	119	GLN
12	Bi	157	HIS
12	Bi	235	GLN
12	Bi	251	HIS
13	Bj	156	ASN
13	Bj	212	HIS
13	Bj	252	HIS
14	Bk	116	HIS
14	Bk	136	GLN
14	Bk	158	GLN
15	Bl	92	HIS
16	Bm	88	GLN
17	Bn	65	ASN
17	Bn	120	HIS
19	Bp	35	GLN
20	Bq	100	ASN
21	Bt	10	ASN
23	Bv	130	GLN
24	Bw	60	GLN
24	Bw	290	HIS

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Mol	Chain	Res	Type
24	Bw	421	ASN
25	Bx	123	HIS
27	B1	93	ASN
27	B1	175	GLN
26	HL	83	ASN
30	B2	90	GLN
31	B3	47	GLN
31	B3	53	HIS
31	B3	98	GLN
32	B4	47	GLN
32	B4	60	GLN
32	B4	66	HIS
33	B5	118	GLN
37	BC	265	ASN
37	BC	302	ASN
37	BC	632	HIS
37	BC	637	GLN
37	BC	653	HIS
37	BC	710	GLN
37	BC	724	ASN
38	BD	90	GLN
39	BG	73	ASN
39	BG	214	ASN
40	BQ	68	ASN
40	BQ	98	HIS
40	BQ	210	GLN
41	BE	154	HIS
41	BE	156	HIS
42	BF	83	HIS
42	BF	103	GLN
42	BF	153	HIS
42	BF	228	GLN
42	BF	251	HIS
43	BI	93	ASN
44	BJ	141	GLN
46	BN	40	GLN
46	BN	89	GLN
47	BO	89	HIS
47	BO	113	ASN
48	BP	91	HIS
48	BP	94	GLN
49	BR	116	GLN

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Mol	Chain	Res	Type
50	BS	52	ASN
50	BS	96	HIS
55	BX	98	GLN
55	BX	103	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
29	BA	1542/1571 (98%)	373 (24%)	1 (0%)
36	BB	64/73 (87%)	14 (21%)	0
All	All	1606/1644 (97%)	387 (24%)	1 (0%)

All (387) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
29	BA	4	A
29	BA	7	G
29	BA	11	G
29	BA	15	A
29	BA	19	U
29	BA	20	A
29	BA	21	C
29	BA	22	U
29	BA	26	C
29	BA	27	A
29	BA	31	A
29	BA	32	C
29	BA	36	A
29	BA	37	A
29	BA	40	C
29	BA	43	C
29	BA	44	A
29	BA	45	A
29	BA	46	A
29	BA	49	A
29	BA	56	A
29	BA	57	A
29	BA	59	A
29	BA	60	U
29	BA	63	A
29	BA	66	U

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Mol	Chain	Res	Type
29	BA	67	A
29	BA	68	A
29	BA	82	G
29	BA	83	A
29	BA	96	U
29	BA	97	A
29	BA	104	C
29	BA	105	G
29	BA	109	U
29	BA	115	U
29	BA	118	U
29	BA	119	A
29	BA	129	A
29	BA	132	G
29	BA	139	G
29	BA	140	A
29	BA	141	A
29	BA	142	U
29	BA	143	A
29	BA	147	U
29	BA	163	C
29	BA	164	A
29	BA	168	A
29	BA	172	C
29	BA	173	C
29	BA	178	C
29	BA	180	A
29	BA	182	C
29	BA	188	C
29	BA	190	U
29	BA	192	A
29	BA	201	C
29	BA	205	A
29	BA	218	A
29	BA	219	A
29	BA	223	A
29	BA	225	C
29	BA	229	A
29	BA	231	C
29	BA	237	A
29	BA	238	C
29	BA	239	C

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Mol	Chain	Res	Type
29	BA	243	A
29	BA	245	A
29	BA	254	G
29	BA	263	G
29	BA	265	G
29	BA	272	A
29	BA	273	A
29	BA	275	A
29	BA	277	A
29	BA	295	G
29	BA	309	A
29	BA	311	A
29	BA	313	U
29	BA	322	G
29	BA	324	G
29	BA	329	A
29	BA	330	A
29	BA	331	A
29	BA	337	A
29	BA	338	C
29	BA	339	G
29	BA	340	A
29	BA	352	G
29	BA	359	G
29	BA	366	A
29	BA	368	A
29	BA	369	G
29	BA	373	U
29	BA	374	U
29	BA	376	A
29	BA	389	A
29	BA	390	A
29	BA	393	A
29	BA	394	C
29	BA	398	A
29	BA	409	A
29	BA	414	A
29	BA	423	U
29	BA	427	G
29	BA	428	A
29	BA	433	G
29	BA	440	A

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Mol	Chain	Res	Type
29	BA	446	C
29	BA	447	A
29	BA	448	G
29	BA	449	C
29	BA	459	A
29	BA	460	C
29	BA	468	A
29	BA	472	U
29	BA	473	G
29	BA	474	A
29	BA	479	A
29	BA	480	G
29	BA	490	U
29	BA	491	U
29	BA	492	A
29	BA	493	A
29	BA	494	U
29	BA	497	U
29	BA	498	A
29	BA	499	C
29	BA	500	C
29	BA	501	A
29	BA	502	U
29	BA	503	A
29	BA	514	A
29	BA	515	A
29	BA	516	G
29	BA	517	C
29	BA	518	A
29	BA	527	U
29	BA	531	G
29	BA	532	A
29	BA	533	A
29	BA	545	U
29	BA	547	A
29	BA	548	A
29	BA	550	A
29	BA	553	U
29	BA	554	U
29	BA	557	C
29	BA	560	A
29	BA	561	C

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Mol	Chain	Res	Type
29	BA	562	A
29	BA	563	U
29	BA	570	A
29	BA	574	A
29	BA	576	U
29	BA	578	A
29	BA	579	U
29	BA	584	A
29	BA	586	C
29	BA	592	G
29	BA	595	C
29	BA	596	A
29	BA	618	A
29	BA	625	A
29	BA	631	A
29	BA	634	G
29	BA	640	A
29	BA	665	C
29	BA	674	U
29	BA	684	A
29	BA	689	A
29	BA	694	A
29	BA	695	U
29	BA	697	C
29	BA	704	U
29	BA	707	A
29	BA	712	C
29	BA	713	A
29	BA	719	C
29	BA	720	C
29	BA	722	A
29	BA	724	A
29	BA	725	C
29	BA	727	A
29	BA	728	C
29	BA	744	A
29	BA	745	A
29	BA	746	U
29	BA	748	A
29	BA	763	C
29	BA	764	A
29	BA	774	A

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Mol	Chain	Res	Type
29	BA	777	A
29	BA	778	A
29	BA	780	G
29	BA	782	A
29	BA	783	A
29	BA	784	G
29	BA	809	G
29	BA	825	C
29	BA	834	C
29	BA	835	A
29	BA	838	A
29	BA	847	U
29	BA	852	C
29	BA	853	A
29	BA	854	U
29	BA	859	A
29	BA	860	G
29	BA	864	U
29	BA	872	A
29	BA	883	G
29	BA	889	C
29	BA	892	G
29	BA	894	U
29	BA	897	A
29	BA	899	G
29	BA	902	C
29	BA	913	G
29	BA	914	A
29	BA	922	A
29	BA	923	A
29	BA	924	G
29	BA	925	G
29	BA	931	U
29	BA	932	A
29	BA	935	C
29	BA	948	A
29	BA	958	U
29	BA	959	G
29	BA	960	U
29	BA	961	A
29	BA	964	A
29	BA	965	A

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Mol	Chain	Res	Type
29	BA	967	G
29	BA	970	C
29	BA	977	G
29	BA	983	U
29	BA	986	U
29	BA	992	U
29	BA	1008	A
29	BA	1015	C
29	BA	1016	C
29	BA	1018	U
29	BA	1026	A
29	BA	1027	G
29	BA	1028	A
29	BA	1035	A
29	BA	1038	A
29	BA	1041	A
29	BA	1045	U
29	BA	1050	C
29	BA	1055	A
29	BA	1056	G
29	BA	1057	A
29	BA	1063	U
29	BA	1064	G
29	BA	1071	U
29	BA	1072	A
29	BA	1074	U
29	BA	1075	U
29	BA	1081	U
29	BA	1089	G
29	BA	1091	U
29	BA	1092	A
29	BA	1093	A
29	BA	1127	A
29	BA	1129	C
29	BA	1140	A
29	BA	1146	G
29	BA	1167	C
29	BA	1168	A
29	BA	1169	A
29	BA	1180	G
29	BA	1183	U
29	BA	1188	U

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Mol	Chain	Res	Type
29	BA	1194	U
29	BA	1195	A
29	BA	1204	A
29	BA	1206	U
29	BA	1207	C
29	BA	1217	A
29	BA	1218	U
29	BA	1219	A
29	BA	1220	A
29	BA	1221	C
29	BA	1222	A
29	BA	1226	C
29	BA	1231	U
29	BA	1233	A
29	BA	1234	U
29	BA	1237	A
29	BA	1238	A
29	BA	1239	A
29	BA	1241	U
29	BA	1246	A
29	BA	1247	U
29	BA	1248	C
29	BA	1249	A
29	BA	1253	G
29	BA	1254	A
29	BA	1258	A
29	BA	1264	C
29	BA	1271	A
29	BA	1287	G
29	BA	1288	U
29	BA	1291	U
29	BA	1294	A
29	BA	1298	C
29	BA	1299	C
29	BA	1303	C
29	BA	1314	U
29	BA	1323	U
29	BA	1325	G
29	BA	1326	A
29	BA	1328	G
29	BA	1336	A
29	BA	1341	A

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Mol	Chain	Res	Type
29	BA	1342	C
29	BA	1348	U
29	BA	1352	G
29	BA	1358	G
29	BA	1385	U
29	BA	1386	U
29	BA	1387	A
29	BA	1388	A
29	BA	1389	A
29	BA	1390	G
29	BA	1396	C
29	BA	1407	U
29	BA	1408	U
29	BA	1409	C
29	BA	1420	A
29	BA	1425	A
29	BA	1426	G
29	BA	1433	U
29	BA	1436	U
29	BA	1438	U
29	BA	1445	U
29	BA	1448	A
29	BA	1455	C
29	BA	1457	A
29	BA	1465	A
29	BA	1468	A
29	BA	1474	G
29	BA	1493	A
29	BA	1494	A
29	BA	1498	C
29	BA	1504	A
29	BA	1505	G
29	BA	1509	U
29	BA	1514	A
29	BA	1521	U
29	BA	1522	A
29	BA	1526	U
29	BA	1527	U
29	BA	1528	A
29	BA	1529	A
29	BA	1531	C
29	BA	1532	U

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Mol	Chain	Res	Type
29	BA	1533	A
29	BA	1536	U
29	BA	1548	A
29	BA	1549	A
29	BA	1551	C
29	BA	1552	C
29	BA	1553	A
29	BA	1554	G
29	BA	1558	U
29	BA	1559	A
29	BA	1571	A
36	BB	3	U
36	BB	5	A
36	BB	8	U
36	BB	9	A
36	BB	13	U
36	BB	23	A
36	BB	34	U
36	BB	43	C
36	BB	44	U
36	BB	46	G
36	BB	47	A
36	BB	48	U
36	BB	52	C
36	BB	69	C

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
29	BA	48	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 229 ligands modelled in this entry, 224 are monoatomic - leaving 5 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
58	5GP	BA	3207	56	26,26,26	0.99	2 (7%)	40,40,40	1.69	8 (20%)
60	GNP	BC	1000	56	33,34,34	1.29	5 (15%)	46,54,54	0.71	1 (2%)
59	SPM	BA	3208	-	13,13,13	0.31	0	12,12,12	0.79	0
59	SPM	BA	3209	-	13,13,13	0.34	0	12,12,12	0.75	0
58	5GP	BA	3206	-	26,26,26	0.98	2 (7%)	40,40,40	1.75	7 (17%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	5GP	BA	3207	56	-	0/10/26/26	0/3/3/3
60	GNP	BC	1000	56	-	2/18/38/38	0/3/3/3
59	SPM	BA	3208	-	-	2/11/11/11	-
59	SPM	BA	3209	-	-	2/11/11/11	-
58	5GP	BA	3206	-	-	1/10/26/26	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	BC	1000	GNP	PB-O3A	4.37	1.64	1.59
60	BC	1000	GNP	PB-O1B	3.06	1.51	1.46
60	BC	1000	GNP	PG-N3B	3.00	1.71	1.63
60	BC	1000	GNP	PG-O1G	2.70	1.50	1.46
58	BA	3206	5GP	C6-N1	-2.56	1.34	1.38
58	BA	3207	5GP	C6-N1	-2.55	1.34	1.38
60	BC	1000	GNP	PB-O2B	-2.23	1.50	1.56
58	BA	3206	5GP	C5-N7	-2.06	1.35	1.39
58	BA	3207	5GP	C5-N7	-2.04	1.35	1.39

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	BA	3206	5GP	C5-C4-N3	-5.96	118.79	128.46
58	BA	3207	5GP	C5-C4-N3	-5.67	119.26	128.46
58	BA	3206	5GP	C2-N3-C4	4.59	120.48	112.30
58	BA	3207	5GP	C2-N3-C4	4.35	120.05	112.30
58	BA	3206	5GP	N9-C4-N3	3.86	133.69	125.94
58	BA	3207	5GP	N9-C4-N3	3.61	133.20	125.94
60	BC	1000	GNP	PB-O3A-PA	-2.69	123.15	132.62
58	BA	3206	5GP	C5-C6-N1	2.53	119.62	113.19
58	BA	3207	5GP	C5-C6-N1	2.47	119.47	113.19
58	BA	3206	5GP	O6-C6-C5	-2.43	120.15	126.60
58	BA	3207	5GP	O6-C6-C5	-2.43	120.15	126.60
58	BA	3206	5GP	C2-N1-C6	-2.36	120.79	125.10
58	BA	3207	5GP	C2-N1-C6	-2.31	120.89	125.10
58	BA	3207	5GP	N9-C8-N7	-2.27	109.11	113.39
58	BA	3206	5GP	N9-C8-N7	-2.21	109.24	113.39
58	BA	3207	5GP	C4-C5-N7	-2.01	107.54	110.72

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
60	BC	1000	GNP	PG-N3B-PB-O1B
60	BC	1000	GNP	PG-N3B-PB-O3A
59	BA	3208	SPM	C7-C8-C9-N10
59	BA	3209	SPM	C7-C8-C9-N10
59	BA	3208	SPM	C7-C6-N5-C4
59	BA	3209	SPM	C7-C6-N5-C4
58	BA	3206	5GP	O4'-C4'-C5'-O5'

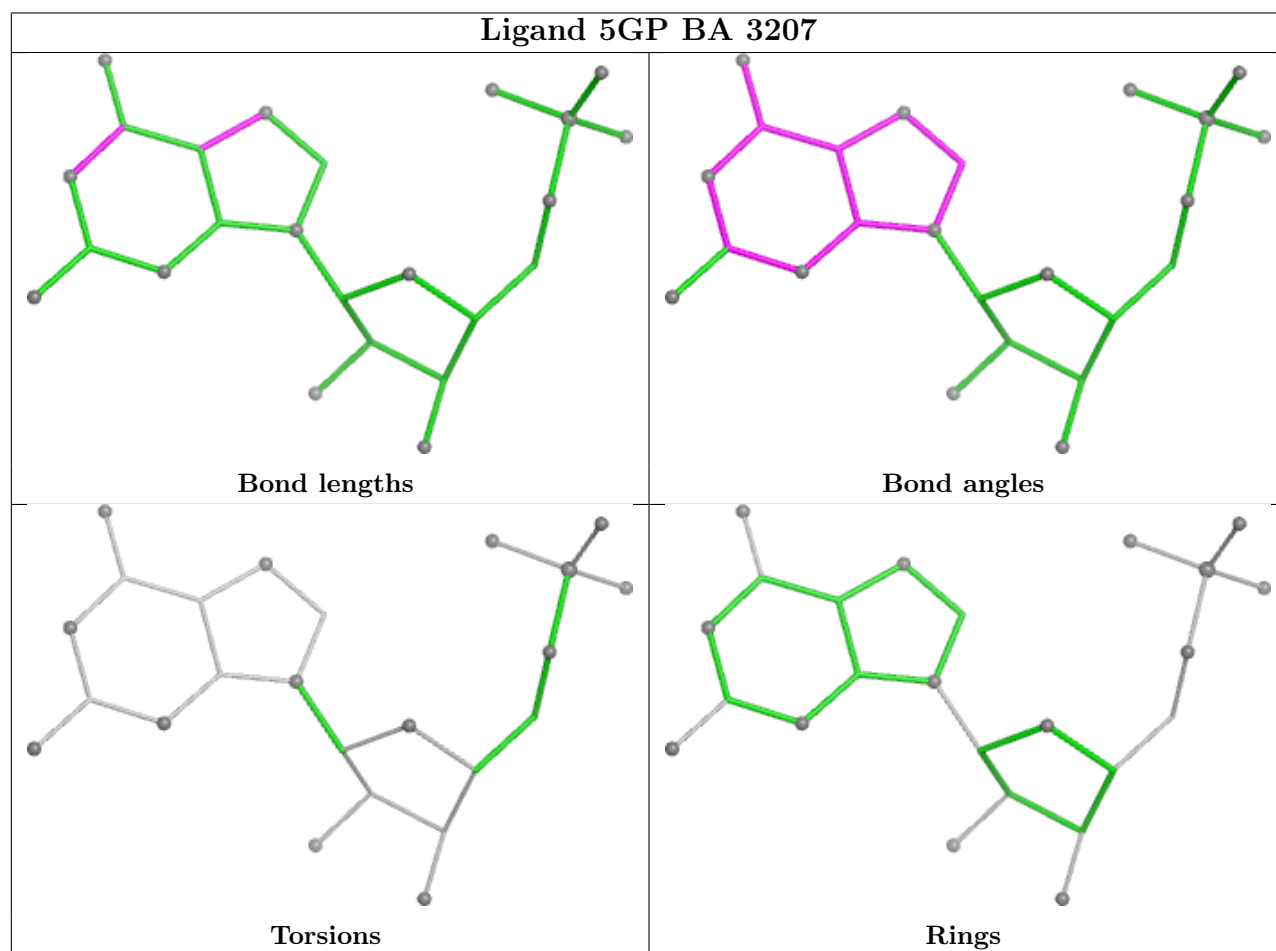
There are no ring outliers.

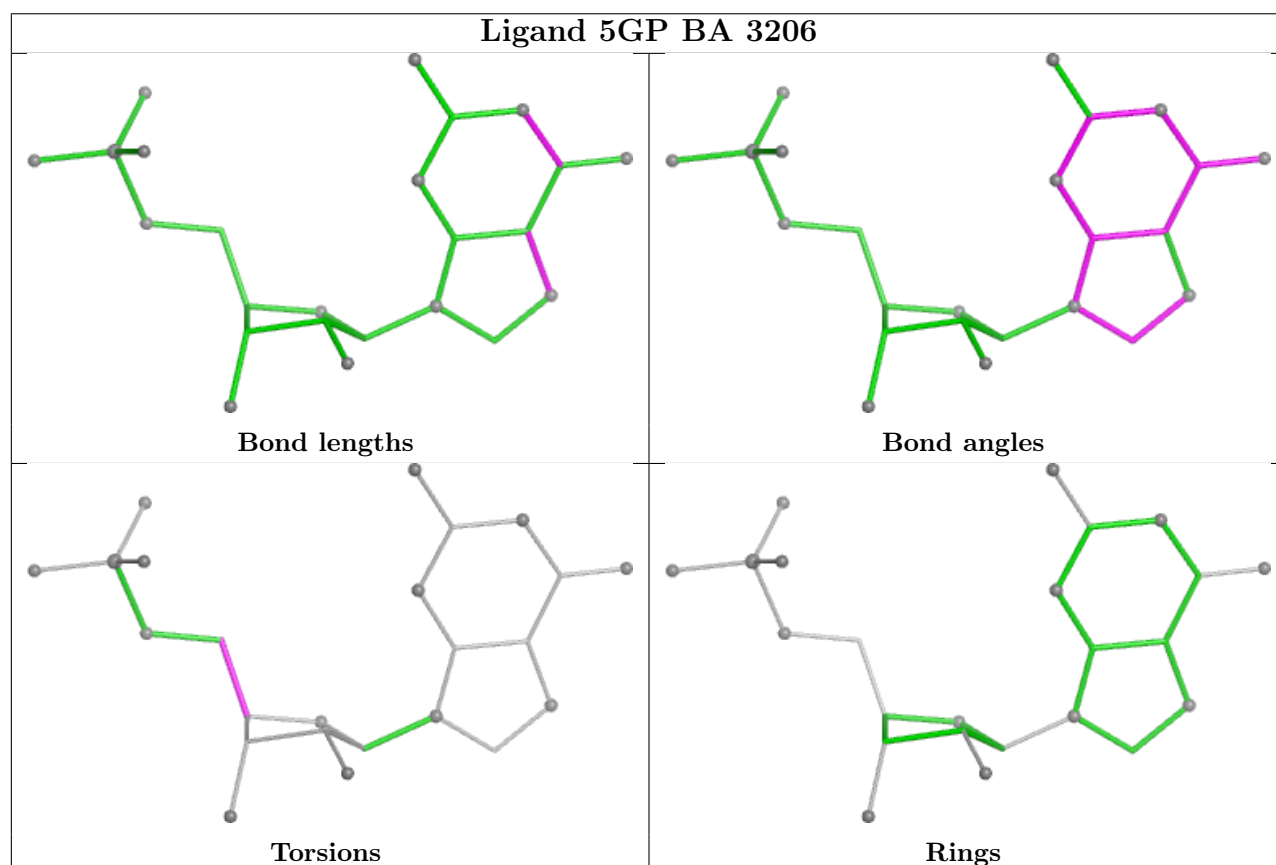
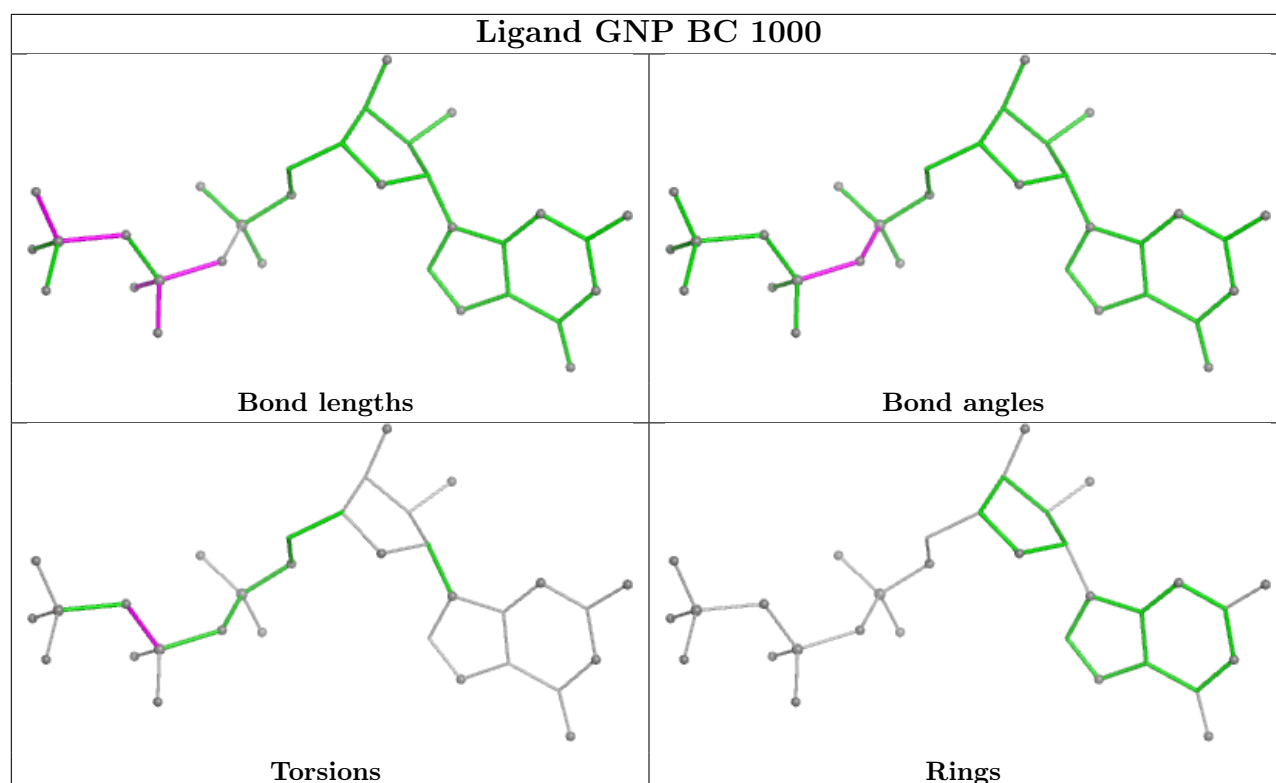
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	BA	3208	SPM	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

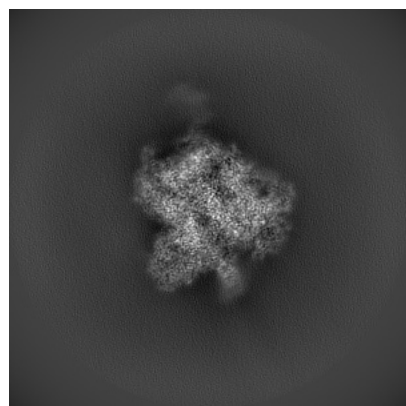
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12567. These allow visual inspection of the internal detail of the map and identification of artifacts.

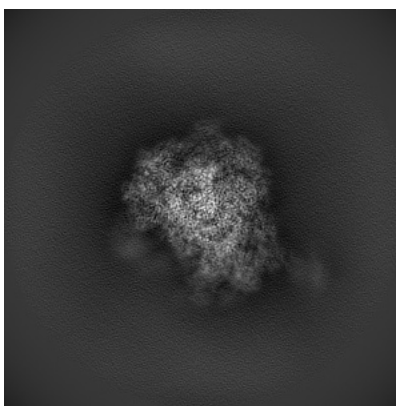
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

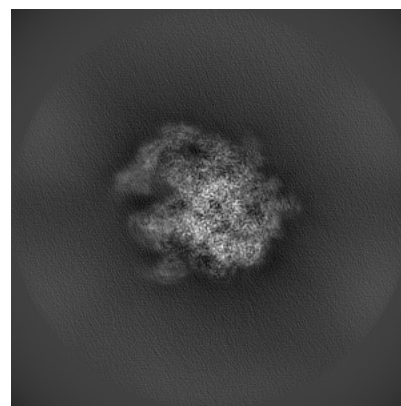
6.1.1 Primary map



X

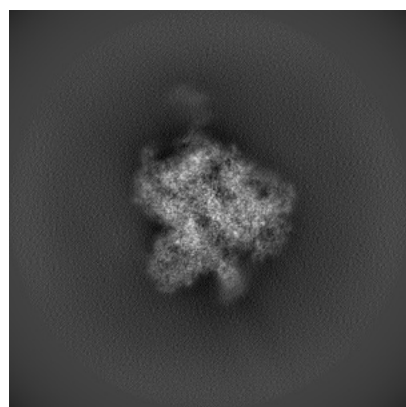


Y

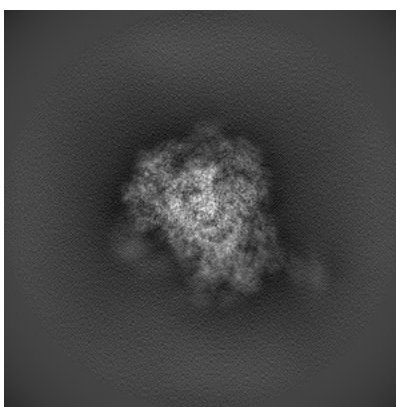


Z

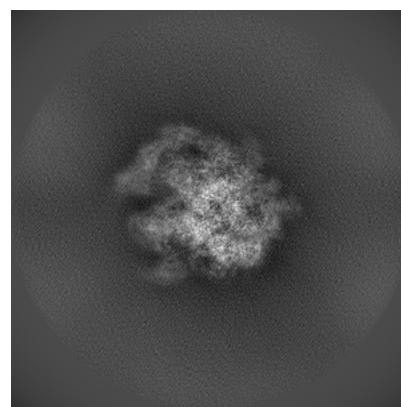
6.1.2 Raw map



X



Y

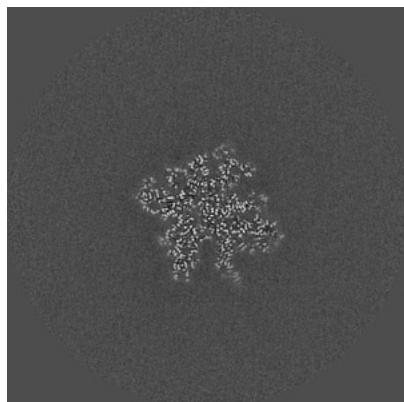


Z

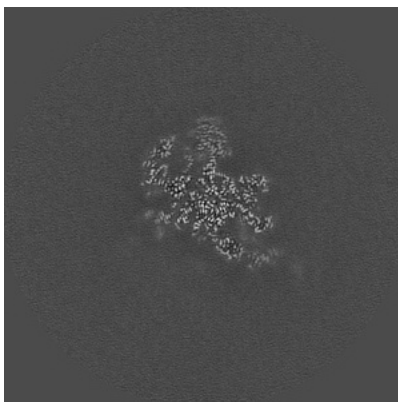
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

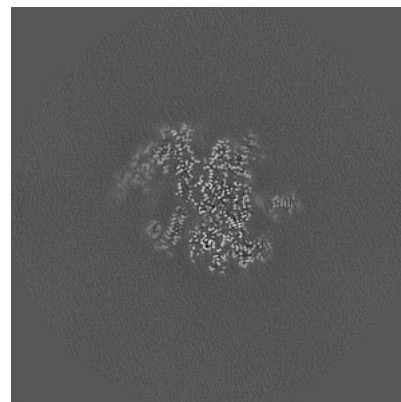
6.2.1 Primary map



X Index: 240

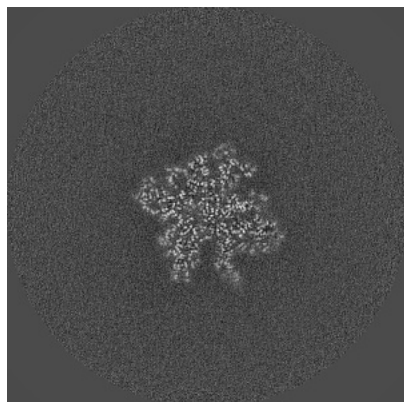


Y Index: 240

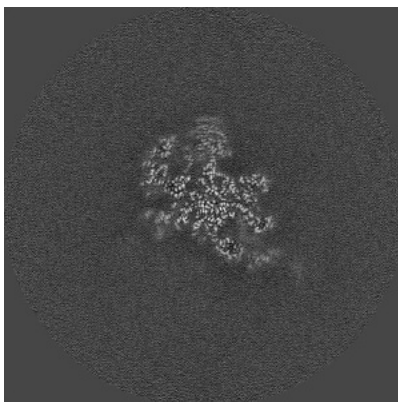


Z Index: 240

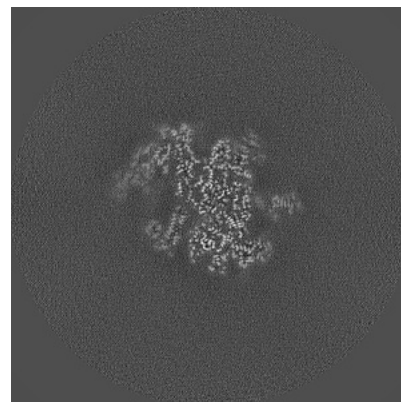
6.2.2 Raw map



X Index: 240



Y Index: 240

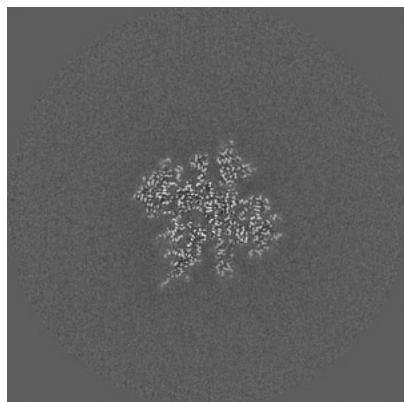


Z Index: 240

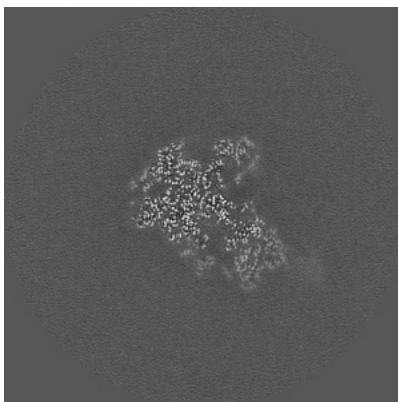
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

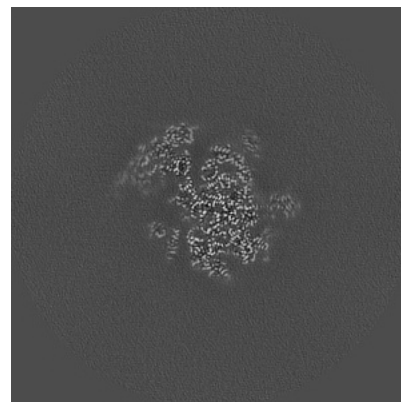
6.3.1 Primary map



X Index: 246

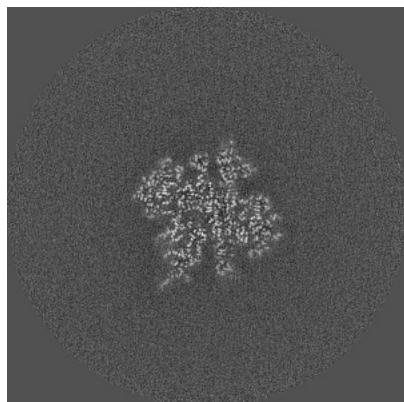


Y Index: 219

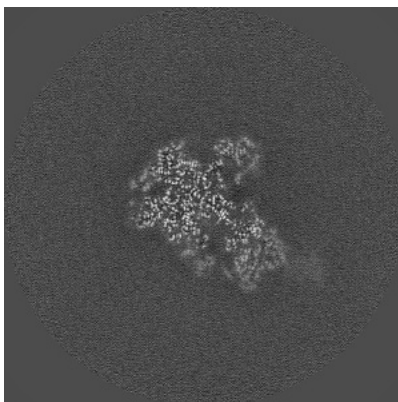


Z Index: 247

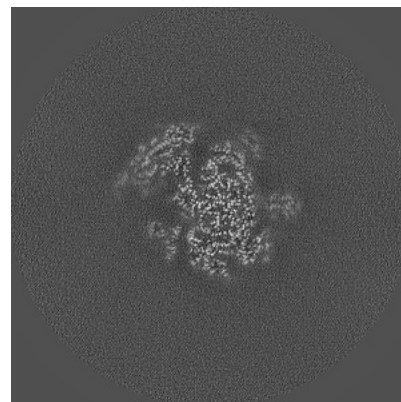
6.3.2 Raw map



X Index: 246



Y Index: 219

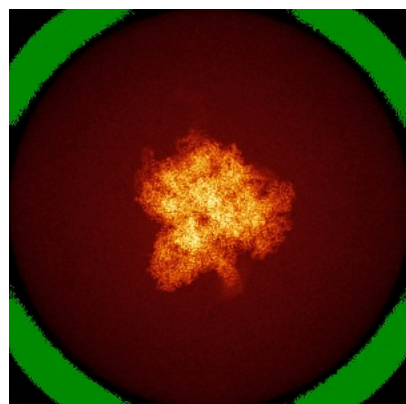


Z Index: 246

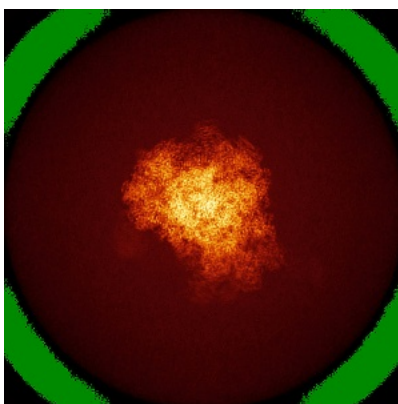
The images above show the largest variance slices of the map in three orthogonal directions.

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

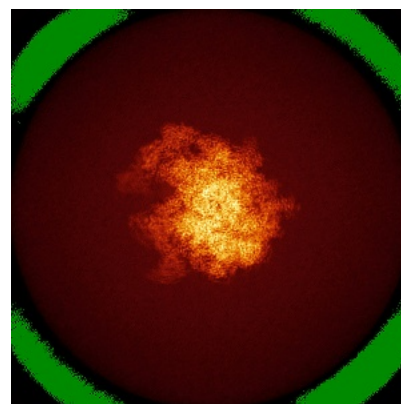
6.4.1 Primary map



X

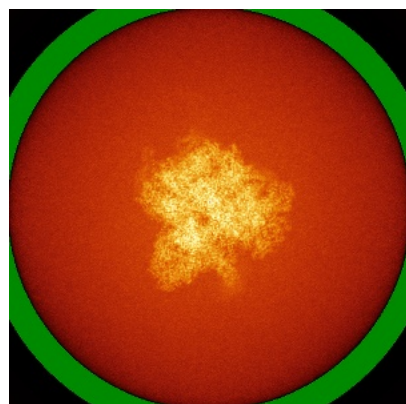


Y

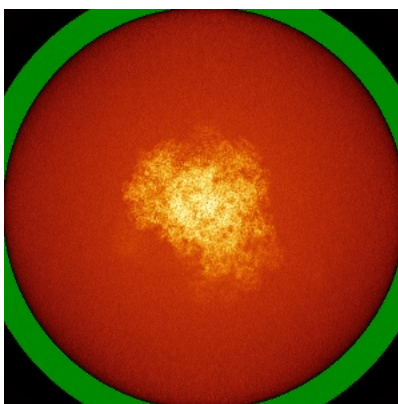


Z

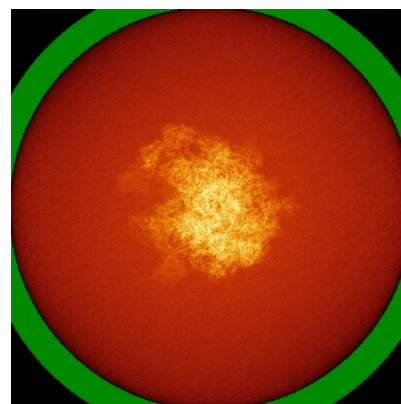
6.4.2 Raw map



X



Y

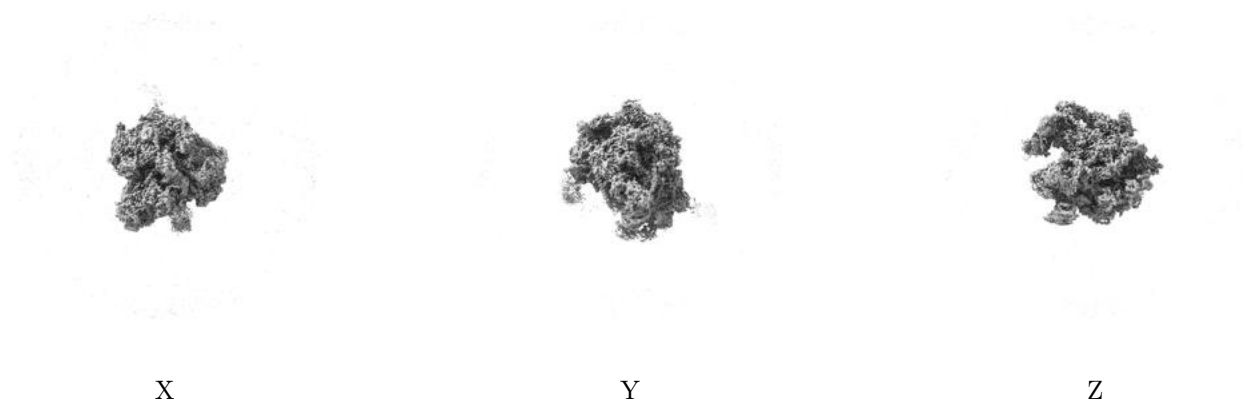


Z

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.

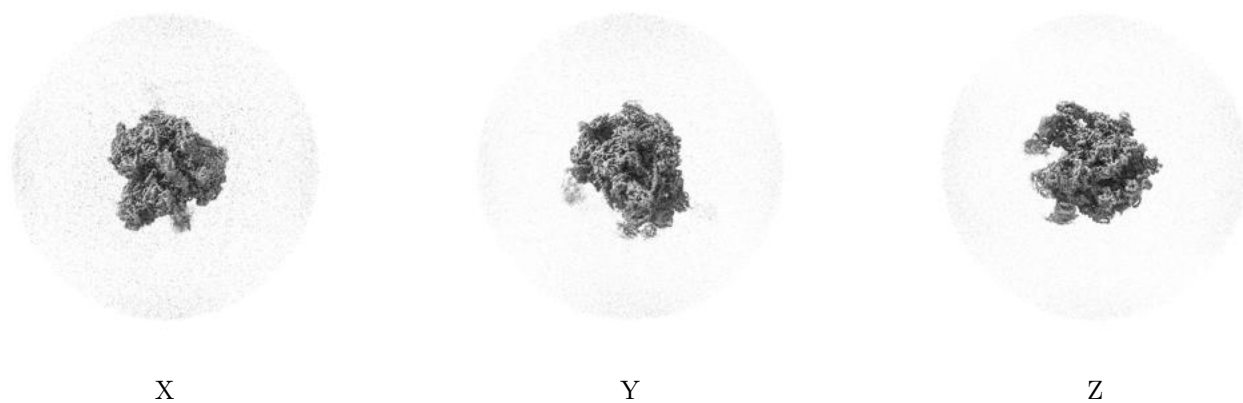
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.028. 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



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.

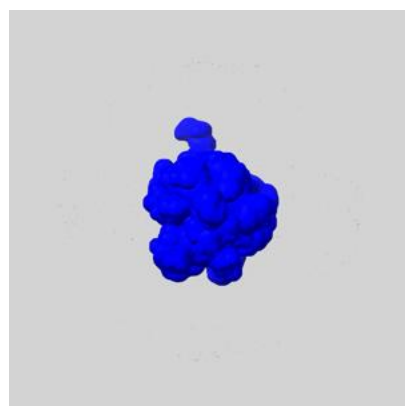
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

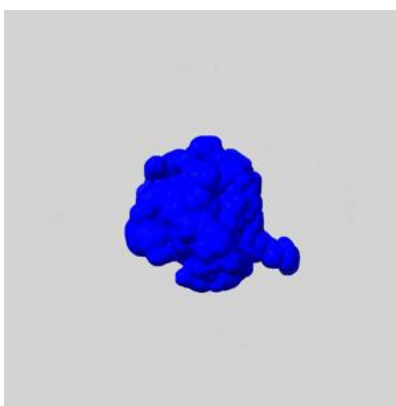
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

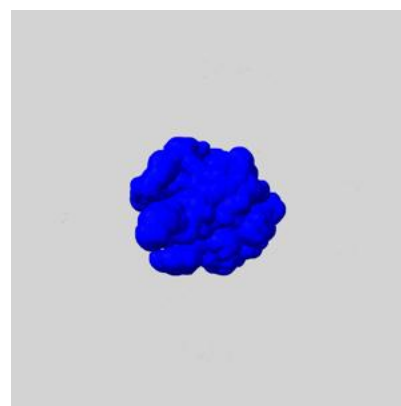
6.6.1 emd_12567_msk_1.map [i](#)



X



Y

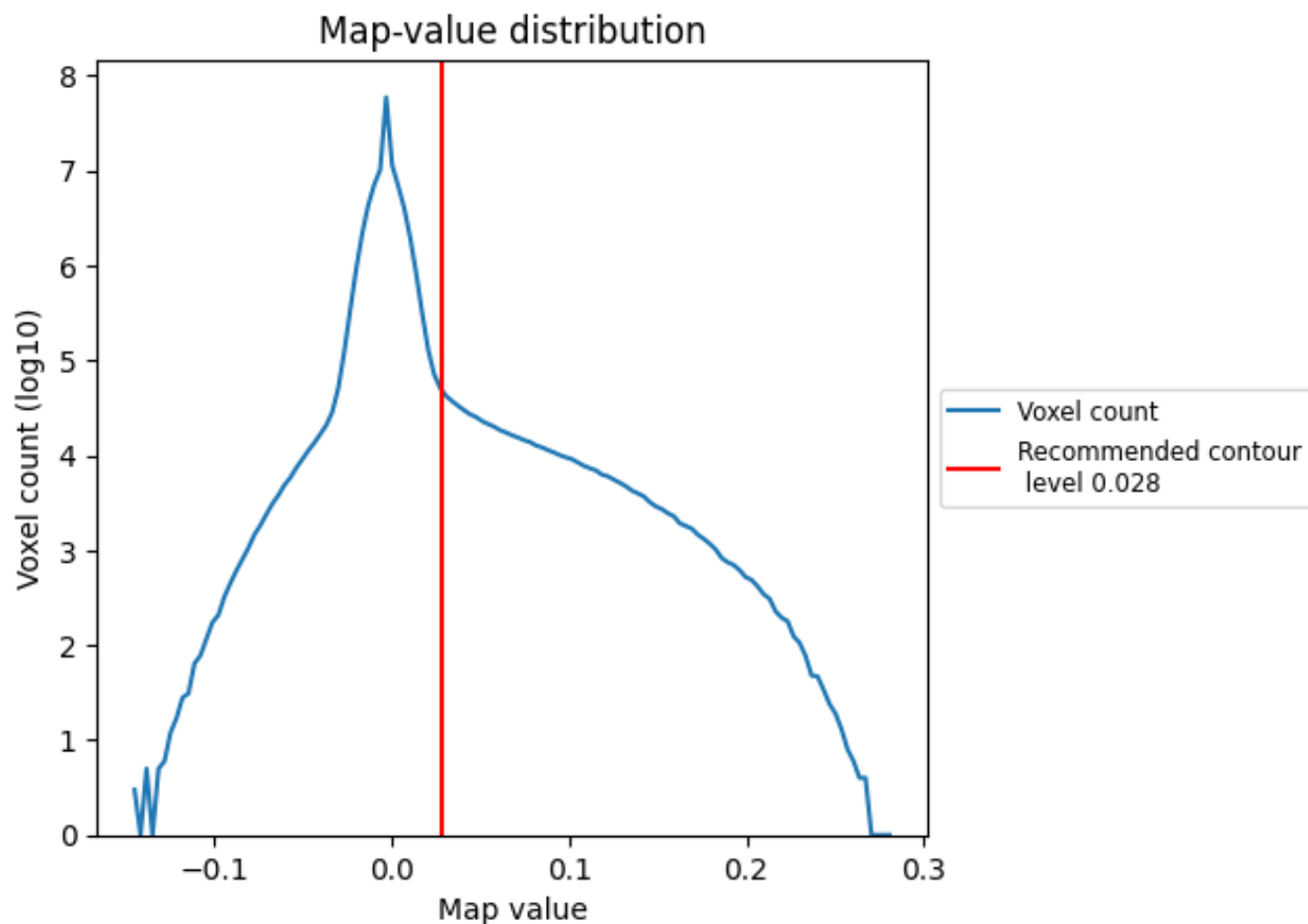


Z

7 Map analysis [i](#)

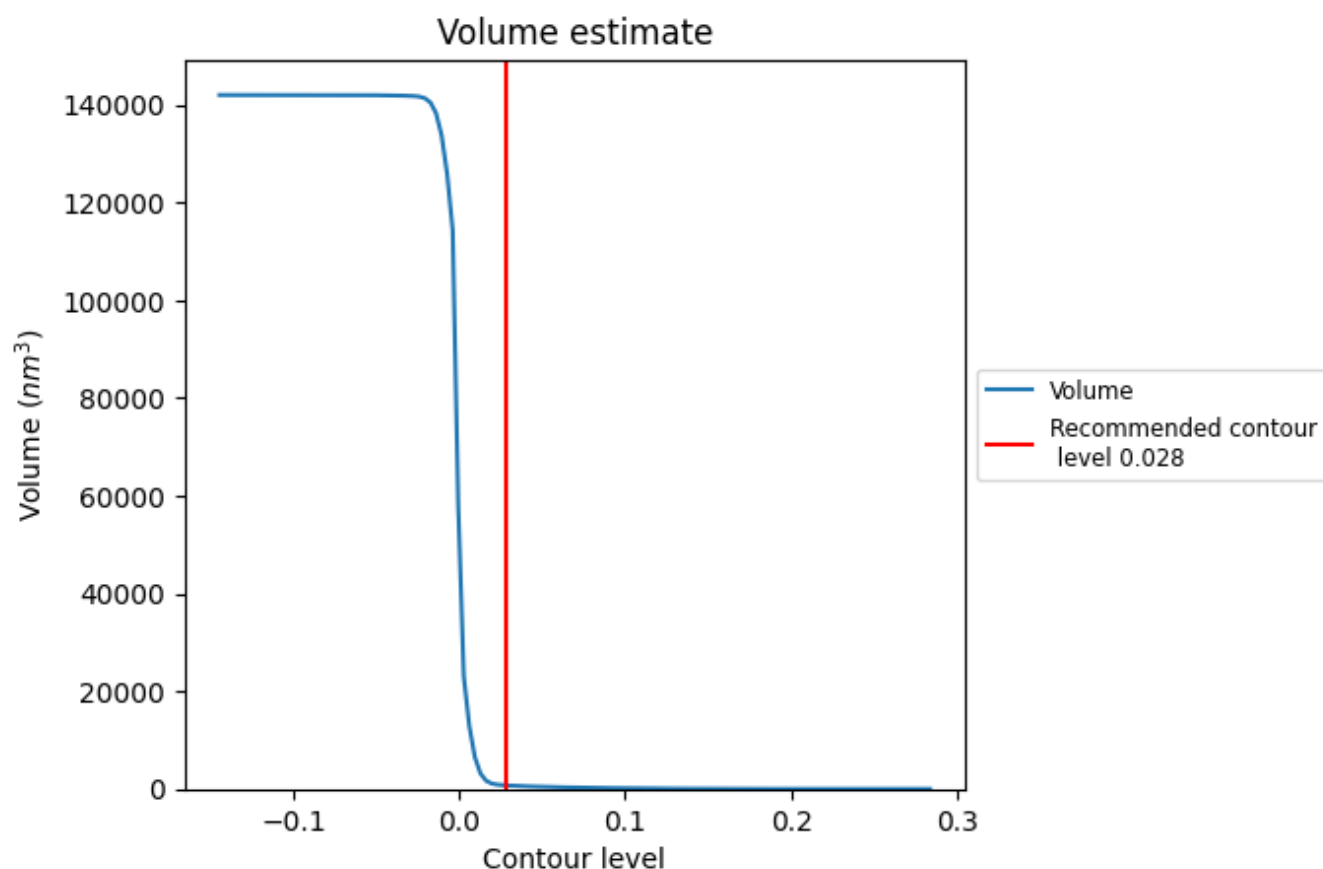
This section contains the results of statistical analysis of the map.

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.

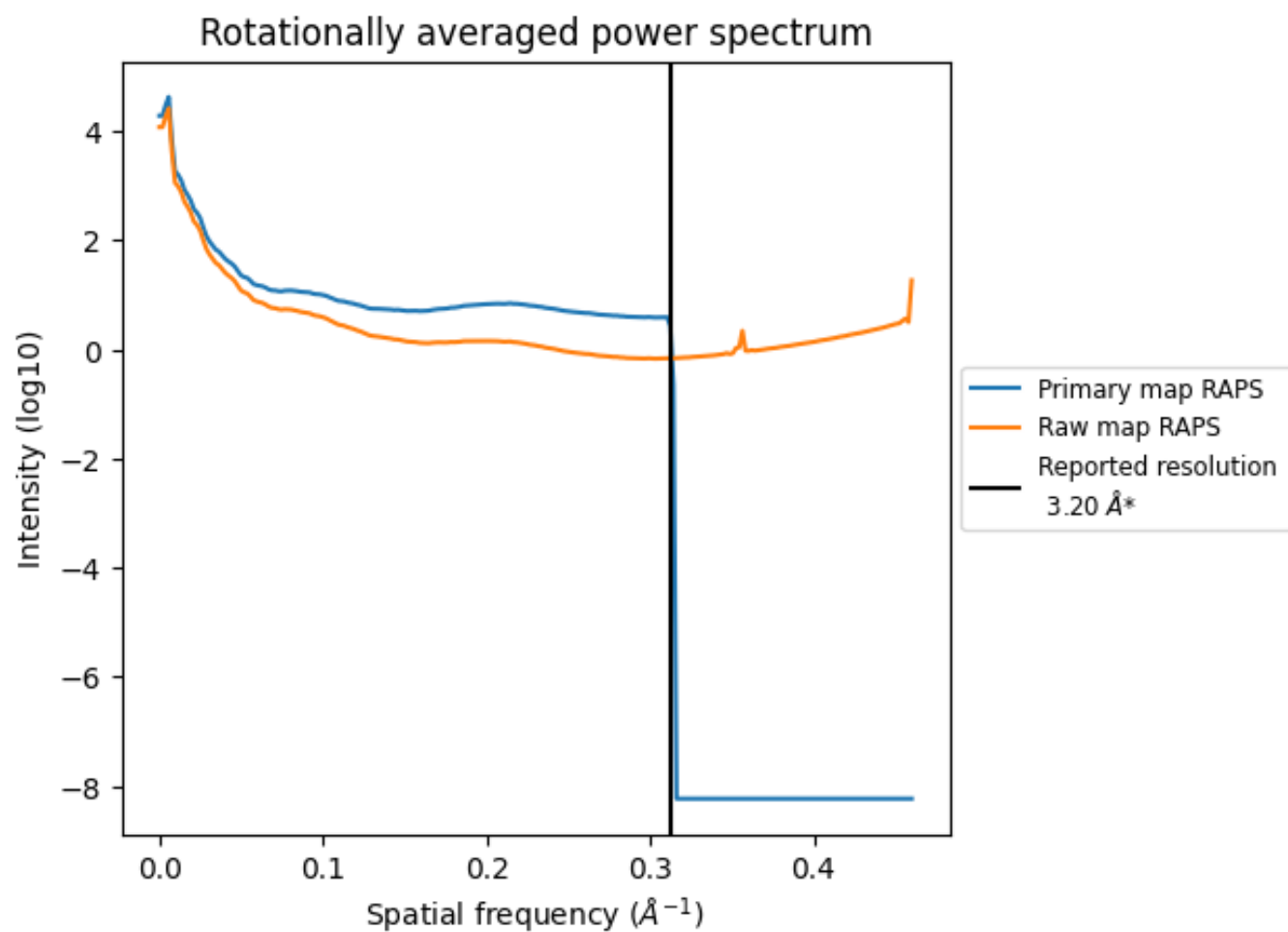
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 742 nm^3 ; this corresponds to an approximate mass of 670 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

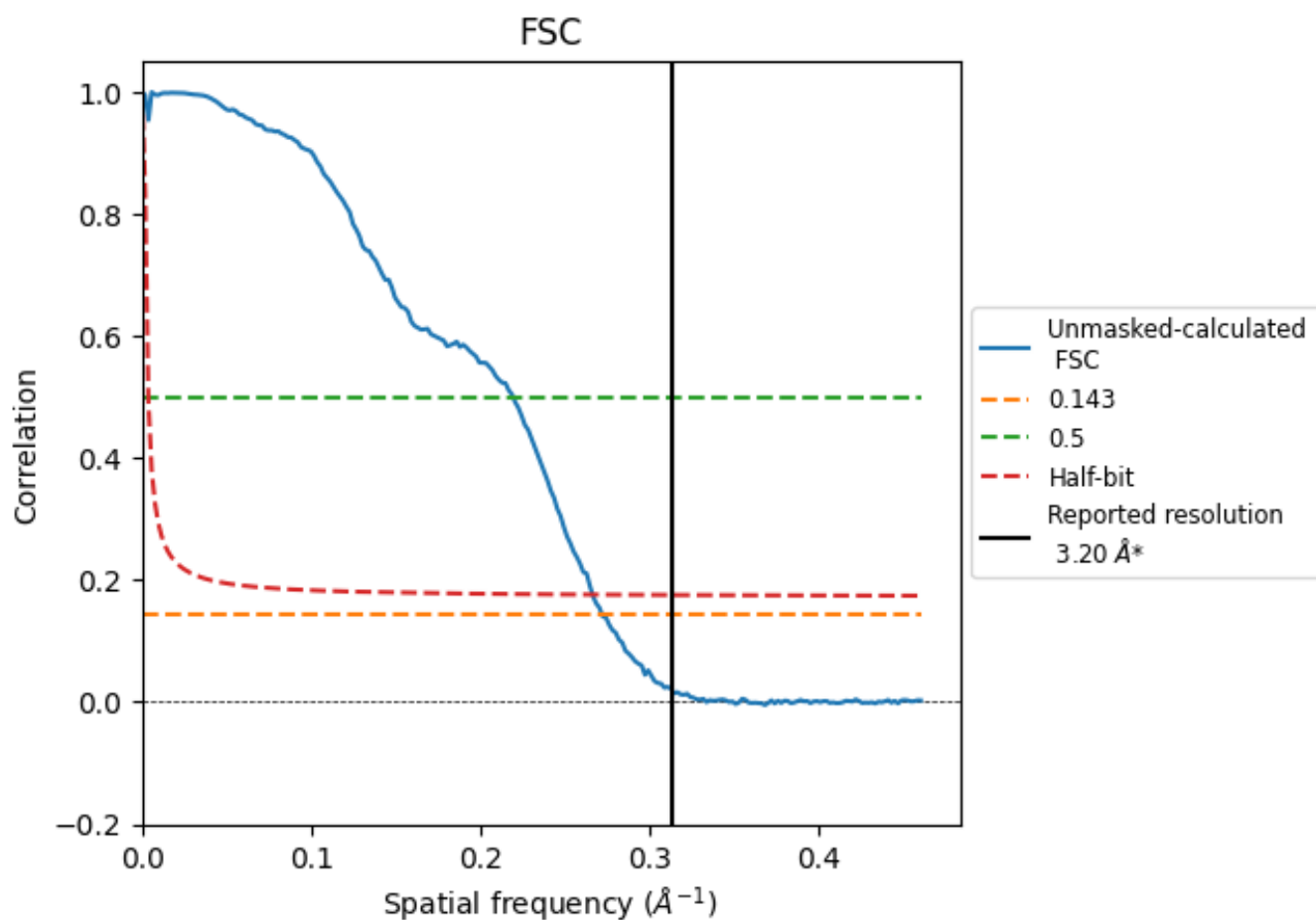


*Reported resolution corresponds to spatial frequency of 0.312 $\text{\AA}^{-1}$

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 $0.312 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

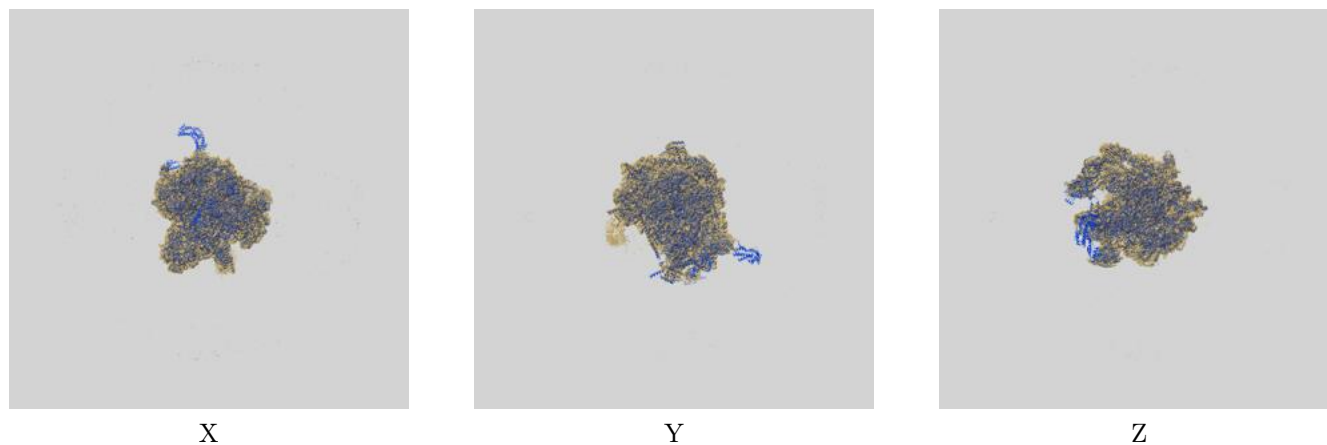
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.68	4.56	3.76

*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 3.68 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

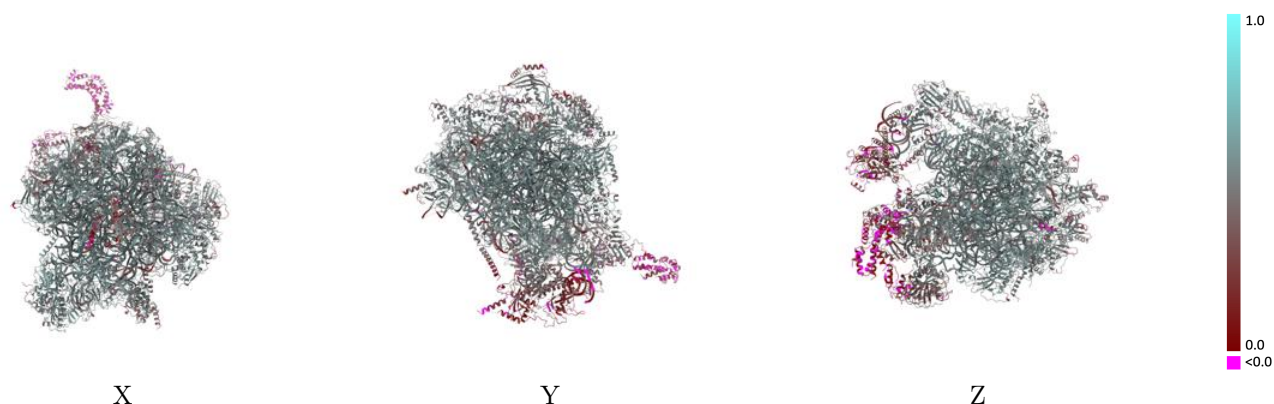
This section contains information regarding the fit between EMDB map EMD-12567 and PDB model 7NSH. Per-residue inclusion information can be found in section 3 on page 19.

9.1 Map-model overlay [i](#)



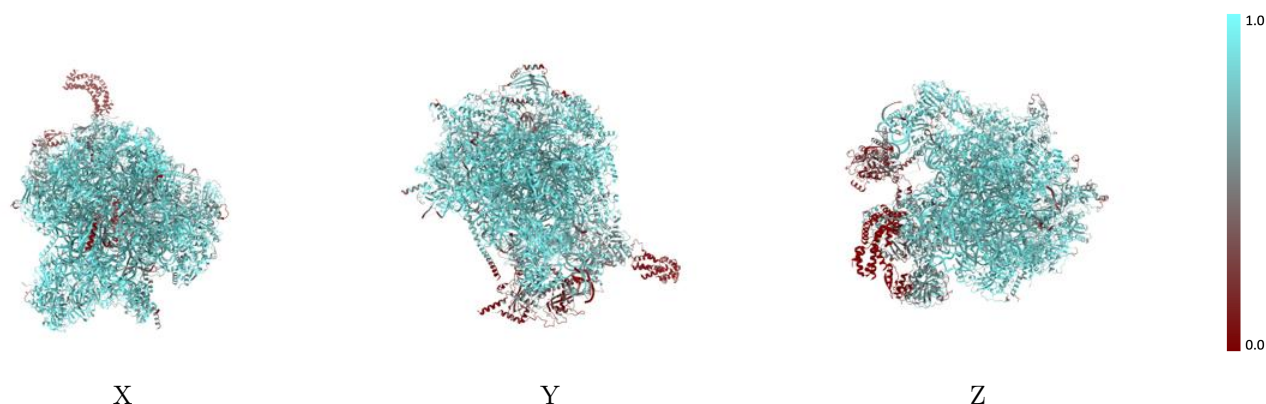
The images above show the 3D surface view of the map at the recommended contour level 0.028 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



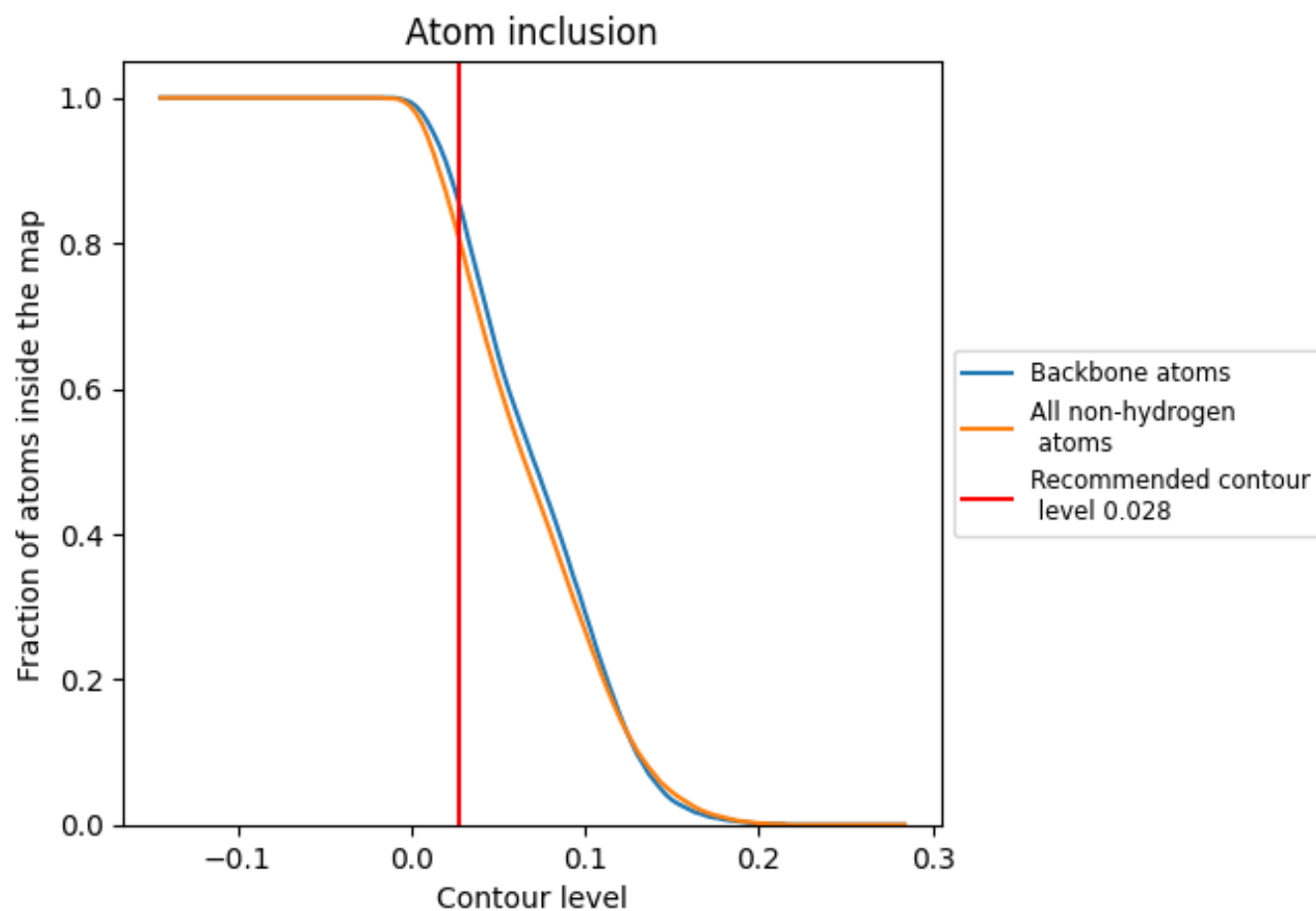
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.028).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 80% 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 (0.028) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8020	 0.4900
B0	 0.9130	 0.5640
B1	 0.8250	 0.5160
B2	 0.8650	 0.5270
B3	 0.8630	 0.5440
B4	 0.3600	 0.2400
B5	 0.8620	 0.5290
B6	 0.7690	 0.4910
B7	 0.9270	 0.5790
B8	 0.9010	 0.5690
B9	 0.9280	 0.5790
BA	 0.9290	 0.5330
BB	 0.6760	 0.2790
BC	 0.6050	 0.4180
BD	 0.8980	 0.5540
BE	 0.8930	 0.5450
BF	 0.8850	 0.5470
BG	 0.6690	 0.4700
BI	 0.7790	 0.4800
BJ	 0.5610	 0.3680
BK	 0.5480	 0.3740
BN	 0.9000	 0.5560
BO	 0.9000	 0.5560
BP	 0.8890	 0.5430
BQ	 0.8740	 0.5390
BR	 0.8930	 0.5440
BS	 0.8690	 0.5200
BT	 0.8660	 0.5260
BU	 0.8730	 0.5390
BV	 0.8730	 0.5380
BW	 0.8850	 0.5500
BX	 0.8310	 0.5150
BY	 0.7050	 0.4750
Ba	 0.8820	 0.5320
Bb	 0.8460	 0.4930



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Bc	 0.8090	 0.4770
Bd	 0.2540	 0.2300
Be	 0.8400	 0.4990
Bf	 0.7910	 0.4800
Bg	 0.8990	 0.5490
Bh	 0.8470	 0.5030
Bi	 0.6120	 0.4210
Bj	 0.2090	 0.1820
Bk	 0.3780	 0.3010
Bl	 0.8820	 0.5320
Bm	 0.5500	 0.4460
Bn	 0.8820	 0.5480
Bo	 0.8390	 0.5200
Bp	 0.6630	 0.4130
Bq	 0.6580	 0.4240
Bt	 0.8780	 0.5540
Bu	 0.6960	 0.4440
Bv	 0.7300	 0.4450
Bw	 0.8610	 0.5240
Bx	 0.8550	 0.5120
CL	 0.0440	 0.1680
DL	 0.0280	 0.0720
EL	 0.0000	 0.0540
FL	 0.0000	 0.0730
GL	 0.0000	 0.0210
HL	 0.0000	 0.0750
LL	 0.0000	 0.0820