



Full wwPDB EM Validation Report ⓘ

Nov 3, 2025 – 04:25 pm GMT

PDB ID : 9I78 / pdb_00009i78
EMDB ID : EMD-52656
Title : Cryo-EM structure of Chaetomium thermophilum ribosome-bound SND3 translocon
Authors : Yang, T.J.; McDowell, M.A.
Deposited on : 2025-01-31
Resolution : 2.20 Å (reported)
Based on initial models : ., 7OLC

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:

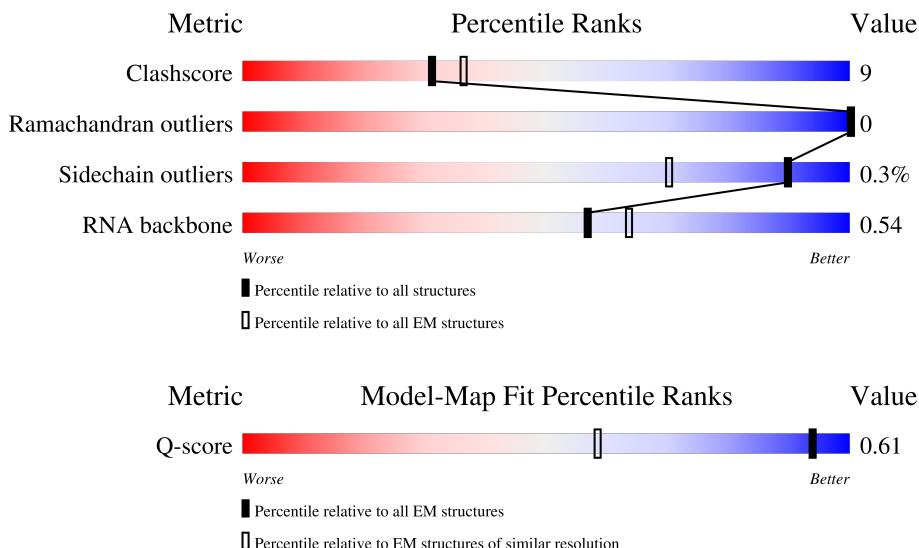
EMDB validation analysis : 0.0.1.dev129
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.46

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 2.20 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	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	3184 (1.71 - 2.70)

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	1	476	
2	2	124	
3	3	70	



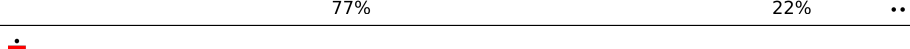
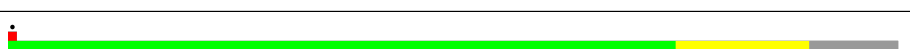



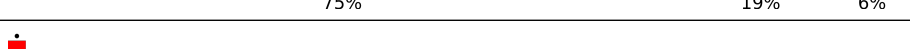
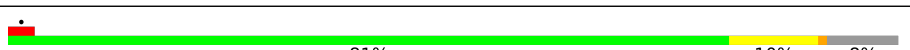


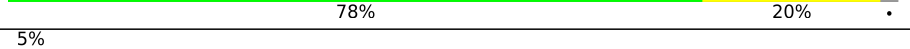

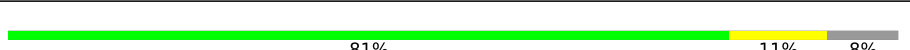


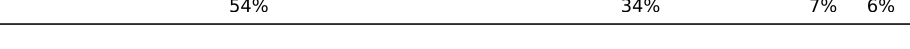





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Mol	Chain	Length	Quality of chain
4	4	455	
5	6	224	
6	7	278	
7	LA	254	
8	LB	392	
9	LC	365	
10	LD	304	
11	LE	200	
12	LF	249	
13	LG	262	
14	LH	192	
15	LI	219	
16	LJ	173	
17	LL	213	
18	LM	142	
19	LN	203	
20	LO	204	
21	LP	187	
22	LQ	213	
23	LR	192	
24	LS	174	
25	LT	160	
26	LU	127	
27	LV	139	
28	LX	156	

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Mol	Chain	Length	Quality of chain
29	LY	138	
30	LZ	135	
31	La	149	
32	Lb	65	
33	Lc	108	
34	Ld	120	
35	Le	131	
36	Lf	109	
37	Lg	119	
38	Lh	126	
39	Li	110	
40	Lj	95	
41	Lk	81	
42	Ll	51	
43	Lm	128	
44	Ln	25	
45	Lo	106	
46	Lp	92	
47	Lq	147	
48	L1	3337	
49	L2	156	
50	L3	120	

2 Entry composition

There are 51 unique types of molecules in this entry. The entry contains 133840 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 Translocon Sec61/SecY plug domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	462	Total	C	N	O	S	0	0
			3579	2338	577	640	24		

- Molecule 2 is a protein called SEC61 beta subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	98	Total	C	N	O	S	0	0
			717	451	137	128	1		

- Molecule 3 is a protein called SEC61 gamma subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	65	Total	C	N	O	S	0	0
			524	343	91	89	1		

- Molecule 4 is a protein called CCDC47.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	371	Total	C	N	O	S	0	0
			2990	1907	523	554	6		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	53	ASP	-	insertion	UNP G0S5M5
4	54	TYR	-	insertion	UNP G0S5M5
4	55	LYS	-	insertion	UNP G0S5M5
4	56	ASP	-	insertion	UNP G0S5M5
4	57	ASP	-	insertion	UNP G0S5M5
4	58	ASP	-	insertion	UNP G0S5M5
4	59	ASP	-	insertion	UNP G0S5M5
4	60	LYS	-	insertion	UNP G0S5M5

- Molecule 5 is a protein called Putative inorganic phosphate transporter protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	6	188	Total	C	N	O	S	0	0
			1443	934	239	259	11		

There are 33 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
6	192	GLY	-	expression tag	UNP G0RYQ7
6	193	SER	-	expression tag	UNP G0RYQ7
6	194	GLY	-	expression tag	UNP G0RYQ7
6	195	SER	-	expression tag	UNP G0RYQ7
6	196	ALA	-	expression tag	UNP G0RYQ7
6	197	TRP	-	expression tag	UNP G0RYQ7
6	198	SER	-	expression tag	UNP G0RYQ7
6	199	HIS	-	expression tag	UNP G0RYQ7
6	200	PRO	-	expression tag	UNP G0RYQ7
6	201	GLN	-	expression tag	UNP G0RYQ7
6	202	PHE	-	expression tag	UNP G0RYQ7
6	203	GLU	-	expression tag	UNP G0RYQ7
6	204	LYS	-	expression tag	UNP G0RYQ7
6	205	GLY	-	expression tag	UNP G0RYQ7
6	206	GLY	-	expression tag	UNP G0RYQ7
6	207	GLY	-	expression tag	UNP G0RYQ7
6	208	SER	-	expression tag	UNP G0RYQ7
6	209	GLY	-	expression tag	UNP G0RYQ7
6	210	GLY	-	expression tag	UNP G0RYQ7
6	211	GLY	-	expression tag	UNP G0RYQ7
6	212	SER	-	expression tag	UNP G0RYQ7
6	213	GLY	-	expression tag	UNP G0RYQ7
6	214	GLY	-	expression tag	UNP G0RYQ7
6	215	SER	-	expression tag	UNP G0RYQ7
6	216	ALA	-	expression tag	UNP G0RYQ7
6	217	TRP	-	expression tag	UNP G0RYQ7
6	218	SER	-	expression tag	UNP G0RYQ7
6	219	HIS	-	expression tag	UNP G0RYQ7
6	220	PRO	-	expression tag	UNP G0RYQ7
6	221	GLN	-	expression tag	UNP G0RYQ7
6	222	PHE	-	expression tag	UNP G0RYQ7
6	223	GLU	-	expression tag	UNP G0RYQ7
6	224	LYS	-	expression tag	UNP G0RYQ7

- Molecule 6 is a protein called Translocon-associated protein subunit alpha.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	7	30	Total	C	N	O	0	0
			267	190	35	42		

- Molecule 7 is a protein called 60S ribosomal protein L2-like protein.

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

- Molecule 8 is a protein called 60S ribosomal protein L3-like protein.

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

- Molecule 9 is a protein called 60S ribosomal protein L4-like protein.

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

- Molecule 10 is a protein called 60S ribosomal protein l5-like protein.

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

- Molecule 11 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LE	180	Total	C	N	O	S	0	0
			1416	909	255	249	3		

- Molecule 12 is a protein called 60S ribosomal protein l7-like protein.

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

- Molecule 13 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LG	234	Total	C	N	O	S	0	0
			1891	1212	349	325	5		

- Molecule 14 is a protein called 60S ribosomal protein l9-like protein.

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

There are 37 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	PHE	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	PHE	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	ASN	deletion	UNP G0S0E5
LH	?	-	ASP	deletion	UNP G0S0E5
LH	?	-	TYR	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	PHE	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	GLU	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	SER	deletion	UNP G0S0E5
LH	?	-	SER	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	ILE	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5

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Chain	Residue	Modelled	Actual	Comment	Reference
LH	?	-	GLU	deletion	UNP G0S0E5
LH	?	-	LEU	deletion	UNP G0S0E5
LH	?	-	ASP	deletion	UNP G0S0E5
LH	?	-	ILE	deletion	UNP G0S0E5
LH	?	-	ASN	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5

- Molecule 15 is a protein called 60S ribosomal protein L10-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LI	208	Total	C	N	O	S	0	0
			1699	1073	331	287	8		

- Molecule 16 is a protein called Putative ribosomal protein.

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

- Molecule 17 is a protein called 60S ribosomal protein L13.

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

- Molecule 18 is a protein called 60S ribosomal protein L14-like protein.

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

- Molecule 19 is a protein called Ribosomal protein L15.

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

- Molecule 20 is a protein called 60S ribosomal protein L16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LO	204	Total	C	N	O	S	0	0
			1613	1036	305	267	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LO	2	ACE	-	acetylation	UNP G0SH61

- Molecule 21 is a protein called 60S ribosomal protein l17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LP	170	Total	C	N	O	S	0	0
			1349	835	272	239	3		

- Molecule 22 is a protein called Ribosomal protein L18-like protein.

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

- Molecule 23 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LR	179	Total	C	N	O	S	0	0
			1466	903	315	243	5		

- Molecule 24 is a protein called 60S ribosomal protein L20.

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

- Molecule 25 is a protein called 60S ribosomal protein l21-like protein.

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

- Molecule 26 is a protein called 60S ribosomal protein L22-like protein.

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

- Molecule 27 is a protein called 60S ribosomal protein l23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LV	132	Total	C	N	O	S	0	0
			970	619	178	166	7		

- Molecule 28 is a protein called 60S ribosomal protein L25-like protein.

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

- Molecule 29 is a protein called 60S ribosomal protein L26-like protein.

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

- Molecule 30 is a protein called 60S ribosomal protein L27.

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

- Molecule 31 is a protein called 60S ribosomal protein L28-like protein.

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

- Molecule 32 is a protein called 60S ribosomal protein L29.

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

- Molecule 33 is a protein called 60S ribosomal protein l30-like protein.

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

- Molecule 34 is a protein called Putative 60S ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ld	109	Total	C	N	O	S	0	0
			885	561	171	152	1		

- Molecule 35 is a protein called 60S ribosomal protein L32-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Le	123	Total	C	N	O	S	0	0
			994	624	204	160	6		

- Molecule 36 is a protein called 60S ribosomal protein l33-like protein.

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

- Molecule 37 is a protein called Ribosomal protein l34-like protein.

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

- Molecule 38 is a protein called Dolichyl-diphosphooligosaccharide--protein glycotransferase.

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

- Molecule 39 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Li	101	Total	C	N	O	S	0	0
			826	509	181	135	1		

- Molecule 40 is a protein called Ribosomal protein L37.

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

- Molecule 41 is a protein called 60S ribosomal protein L38-like protein.

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

- Molecule 42 is a protein called Ribosomal protein eL39.

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

- Molecule 43 is a protein called Putative ribosomal protein.

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

- Molecule 44 is a protein called 60S ribosomal protein L41-A.

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

- Molecule 45 is a protein called 60S ribosomal protein L44-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lo	98	Total	C	N	O	S	0	0
			784	495	154	130	5		

- Molecule 46 is a protein called 60S ribosomal protein L43-like protein.

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

- Molecule 47 is a protein called Putative 60S ribosomal protein.

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

- Molecule 48 is a RNA chain called 26S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	L1	3146	Total	C	N	O	P	0	0
			67284	30038	12169	21931	3146		

- Molecule 49 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	L2	149	Total	C	N	O	P	0	0
			3173	1419	567	1038	149		

- Molecule 50 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	L3	119	Total	C	N	O	P	0	0
			2535	1132	453	831	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L3	1	A	N	conflict	GB 7OLC_3

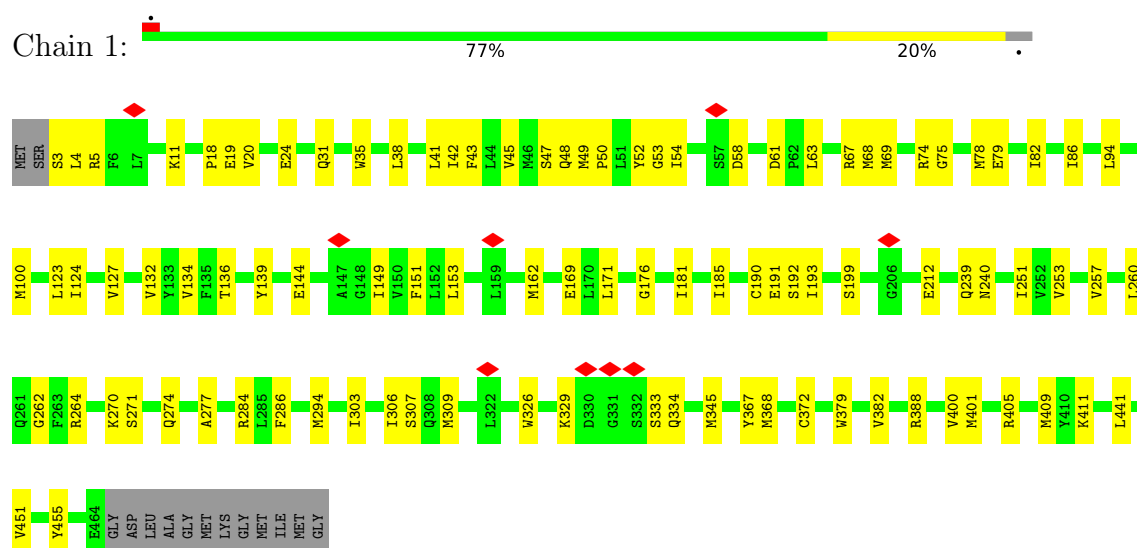
- Molecule 51 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
51	LC	2	Total	Mg	0
			2	2	
51	LN	1	Total	Mg	0
			1	1	
51	LQ	1	Total	Mg	0
			1	1	
51	Lb	2	Total	Mg	0
			2	2	
51	L1	359	Total	Mg	0
			359	359	
51	L2	14	Total	Mg	0
			14	14	

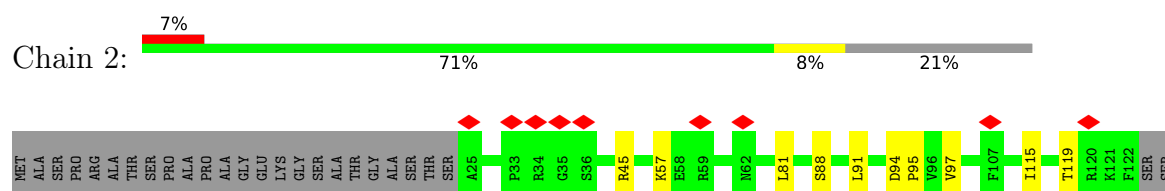
3 Residue-property plots

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

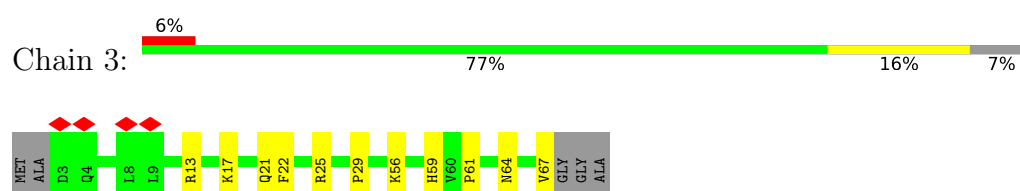
- Molecule 1: Translocon Sec61/SecY plug domain-containing protein



- Molecule 2: SEC61 beta subunit



- Molecule 3: SEC61 gamma subunit




- Molecule 4: CCDC47

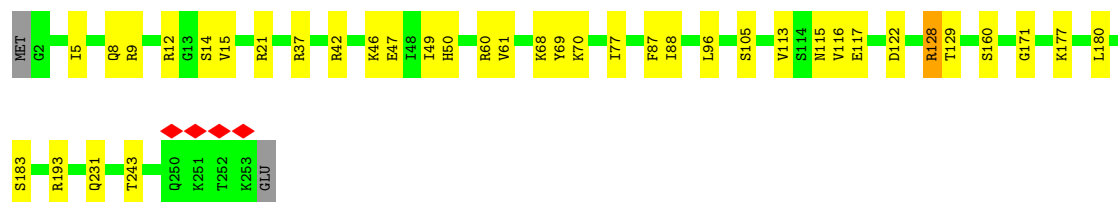





GLY
ASN
THR
SER
GLY
ALA
GLY
GLY
LYS
GLU
TYR
ASP
GLU
SER
TRP
ILE
PRO
ALA
HIS
HIS
ILE
ASN
ARG
PRO
VAL
ALA
ARG
LYS
VAL
LYS
GLY
GLY
SER
LYS
SER
LYS

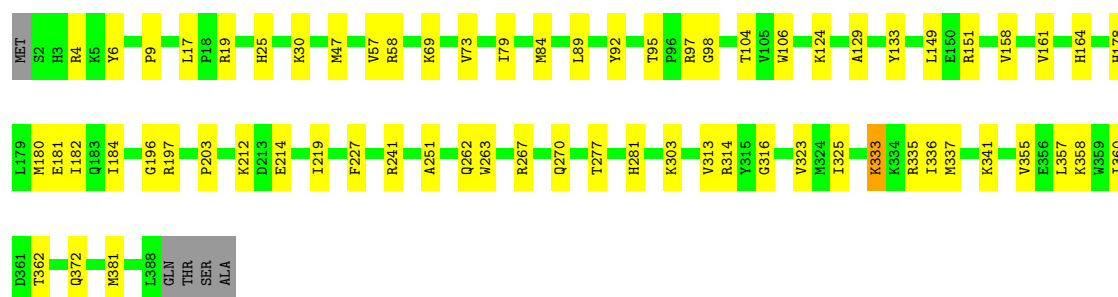
- Molecule 7: 60S ribosomal protein L2-like protein

Chain LA:  84% 15%



- Molecule 8: 60S ribosomal protein L3-like protein

Chain LB:  82% 17%




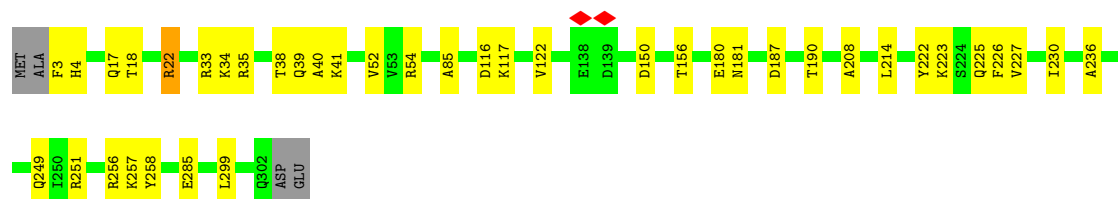
- Molecule 9: 60S ribosomal protein L4-like protein

Chain LC:  89% 10%

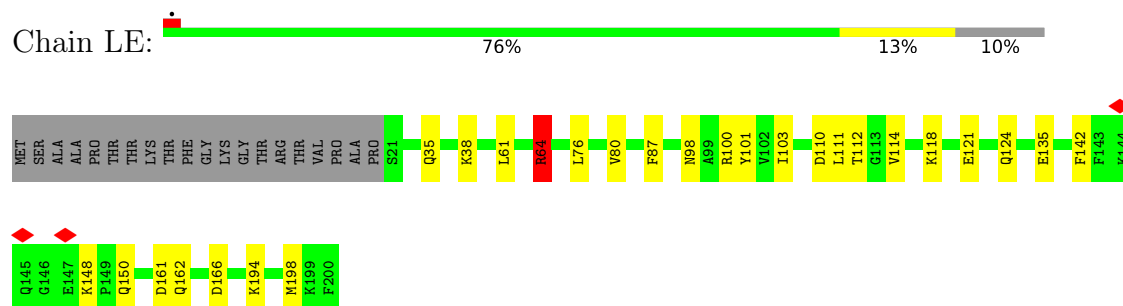


- Molecule 10: 60S ribosomal protein l5-like protein

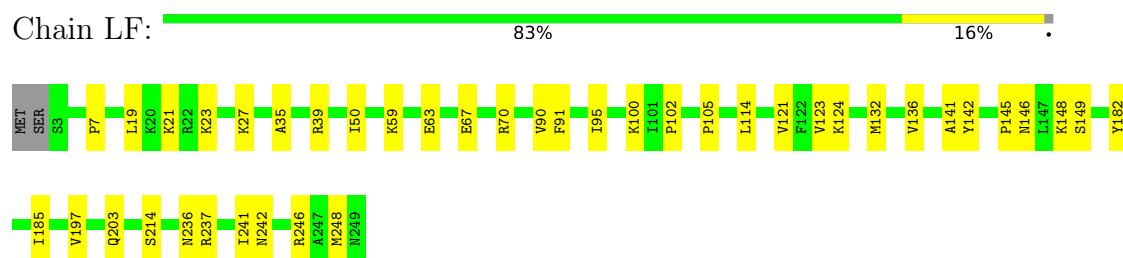
Chain LD:  85% 13%



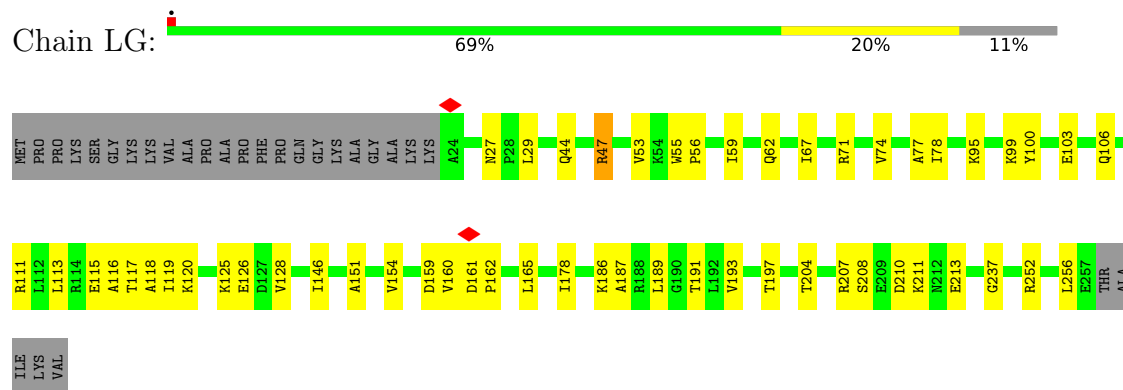
- Molecule 11: 60S ribosomal protein L6



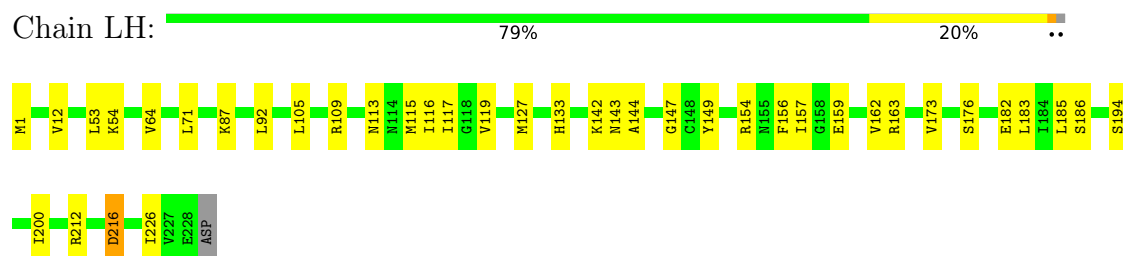
- Molecule 12: 60S ribosomal protein l7-like protein



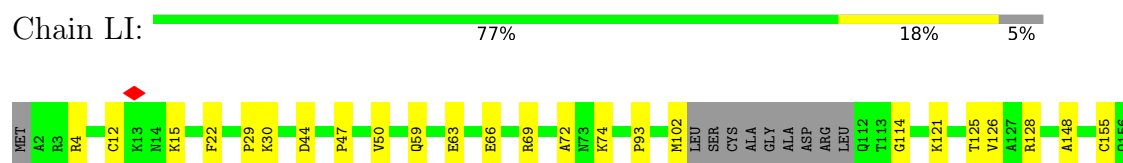
- Molecule 13: 60S ribosomal protein L8



- Molecule 14: 60S ribosomal protein l9-like protein

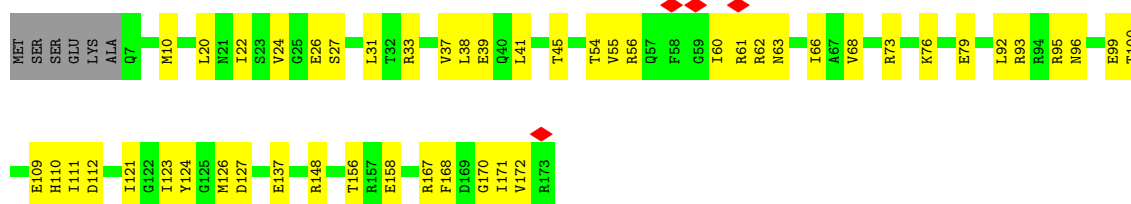


- Molecule 15: 60S ribosomal protein L10-like protein

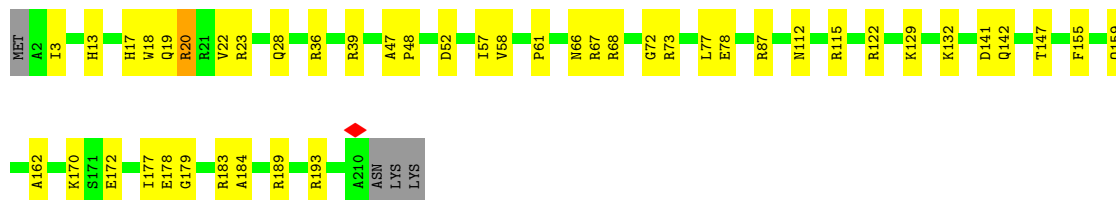
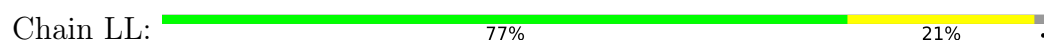




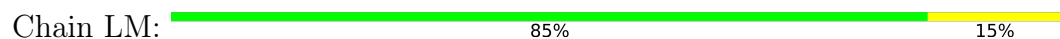
- Molecule 16: Putative ribosomal protein



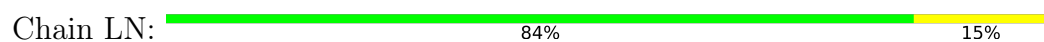
- Molecule 17: 60S ribosomal protein L13



- Molecule 18: 60S ribosomal protein L14-like protein



- Molecule 19: Ribosomal protein L15

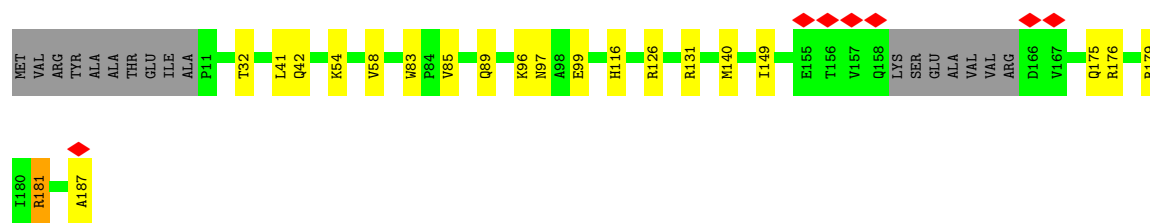


- Molecule 20: 60S ribosomal protein L16-like protein



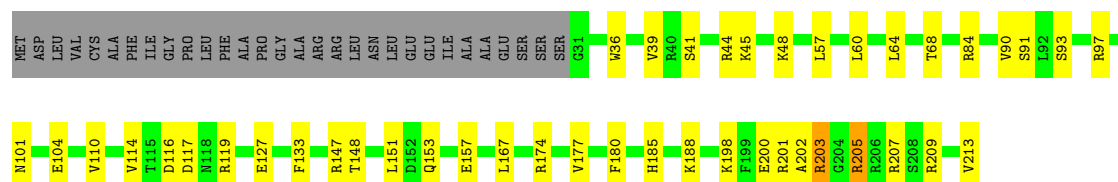
- Molecule 21: 60S ribosomal protein l17-like protein





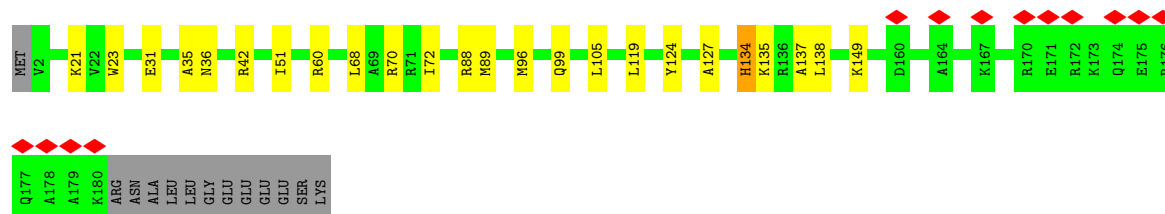
- Molecule 22: Ribosomal protein L18-like protein

Chain LQ: 65% 20% 14%



- Molecule 23: Ribosomal protein L19

Chain LR: 7% 81% 12% 7%



- Molecule 24: 60S ribosomal protein L20

Chain LS: 89% 11%



- Molecule 25: 60S ribosomal protein L21-like protein

Chain LT: 85% 13%



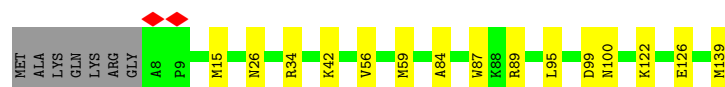
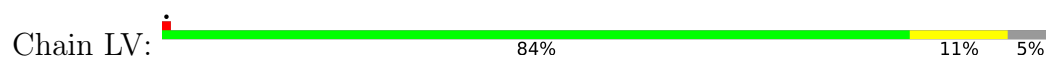
- Molecule 26: 60S ribosomal protein L22-like protein

Chain LU: 46% 33% 20%

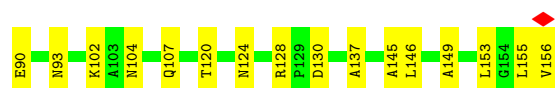
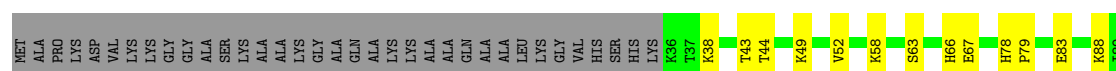




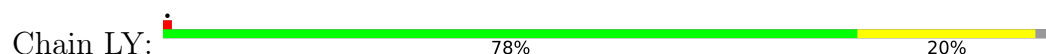
- Molecule 27: 60S ribosomal protein l23-like protein



- Molecule 28: 60S ribosomal protein L25-like protein



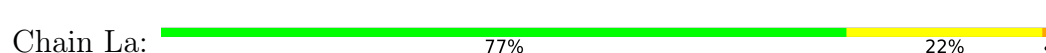
- Molecule 29: 60S ribosomal protein L26-like protein



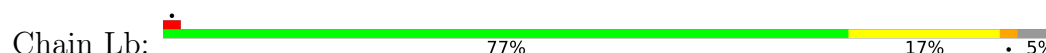
- Molecule 30: 60S ribosomal protein L27

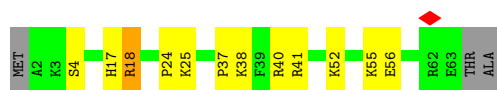


- Molecule 31: 60S ribosomal protein L28-like protein

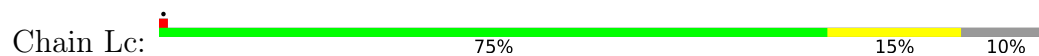


- Molecule 32: 60S ribosomal protein L29

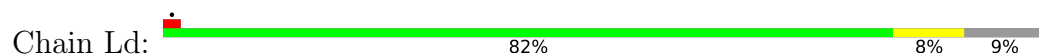




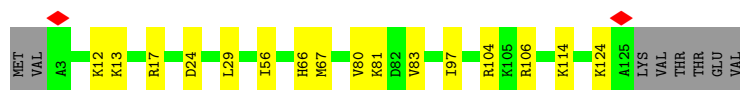
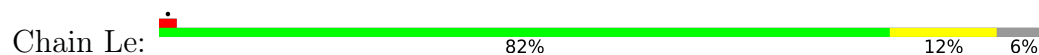
- Molecule 33: 60S ribosomal protein l30-like protein



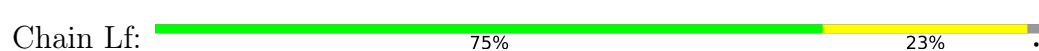
- Molecule 34: Putative 60S ribosomal protein



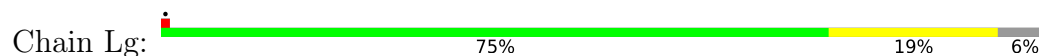
- Molecule 35: 60S ribosomal protein L32-like protein



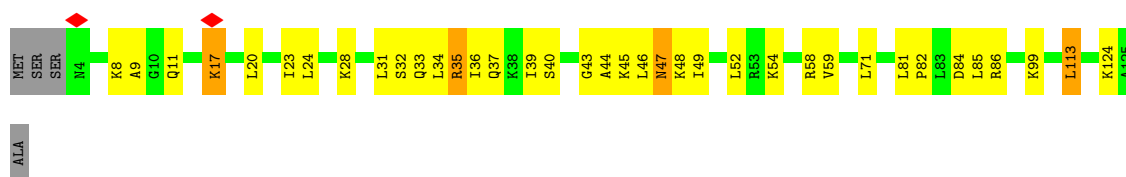
- Molecule 36: 60S ribosomal protein l33-like protein




- Molecule 37: Ribosomal protein l34-like protein



- Molecule 38: Dolichyl-diphosphooligosaccharide--protein glycotransferase




- Molecule 39: 60S ribosomal protein L36

Chain Li:  81% 10% 8%



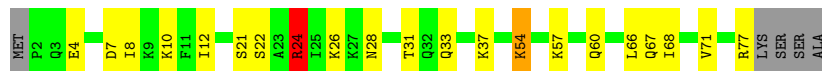
- Molecule 40: Ribosomal protein L37

Chain Lj:  75% 15% 9%




- Molecule 41: 60S ribosomal protein L38-like protein

Chain Lk:  68% 23% 6%




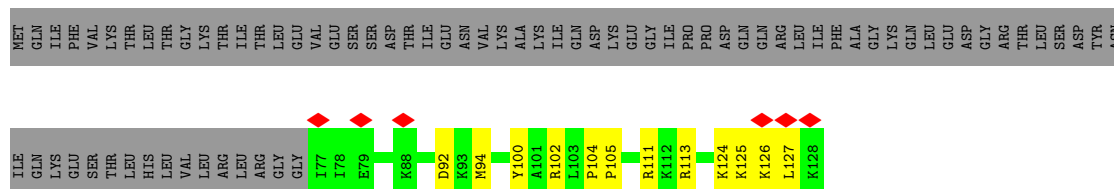
- Molecule 42: Ribosomal protein eL39

Chain Ll:  78% 20% 2%




- Molecule 43: Putative ribosomal protein

Chain Lm:  5% 31% 9% 55%




- Molecule 44: 60S ribosomal protein L41-A

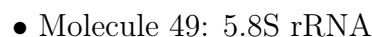
Chain Ln:  80% 16% 4%

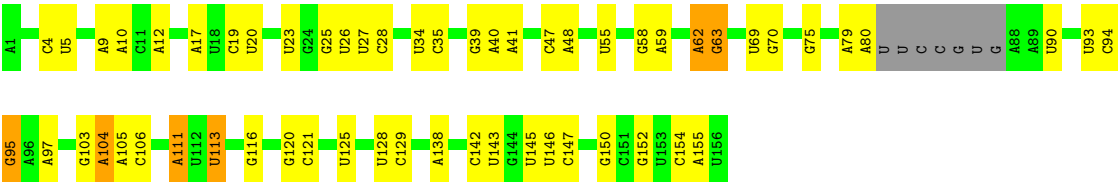


- Molecule 45: 60S ribosomal protein L44-like protein

Chain Lo:  81% 11% 8%







• Molecule 50: 5S rRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	119533	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	40.187	Depositor
Minimum map value	-12.158	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3	Depositor
Map size (Å)	535.68, 535.68, 535.68	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04625, 1.04625, 1.04625	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.23	1/3659 (0.0%)	0.44	0/4965
2	2	0.13	0/730	0.33	0/990
3	3	0.26	0/533	0.55	0/718
4	4	0.15	0/3047	0.35	0/4104
5	6	0.38	1/1470 (0.1%)	0.54	0/1982
6	7	0.11	0/279	0.40	0/381
7	LA	0.17	0/1964	0.34	0/2641
8	LB	0.17	0/3156	0.34	0/4238
9	LC	0.17	0/2815	0.36	2/3795 (0.1%)
10	LD	0.18	0/2487	0.34	0/3341
11	LE	0.19	0/1442	0.41	1/1938 (0.1%)
12	LF	0.21	0/2055	0.35	0/2758
13	LG	0.24	0/1920	0.43	0/2568
14	LH	0.20	0/1525	0.39	0/2050
15	LI	0.20	0/1735	0.39	0/2328
16	LJ	0.21	0/1389	0.42	0/1856
17	LL	0.24	0/1695	0.43	0/2276
18	LM	0.13	0/1144	0.26	0/1539
19	LN	0.22	0/1740	0.34	0/2332
20	LO	0.21	0/1645	0.32	0/2207
21	LP	0.17	0/1370	0.34	0/1842
22	LQ	0.26	0/1507	0.45	1/2017 (0.0%)
23	LR	0.20	0/1485	0.35	0/1974
24	LS	0.17	0/1460	0.35	0/1965
25	LT	0.27	0/1292	0.45	1/1738 (0.1%)
26	LU	0.32	1/832 (0.1%)	0.55	2/1112 (0.2%)
27	LV	0.14	0/988	0.32	0/1331
28	LX	0.15	0/981	0.31	0/1324
29	LY	0.41	1/1079 (0.1%)	0.62	1/1443 (0.1%)
30	LZ	0.31	0/1134	0.48	0/1519
31	La	0.33	0/1212	0.47	0/1627
32	Lb	0.51	2/518 (0.4%)	0.54	0/684

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Lc	0.14	0/731	0.28	0/983
34	Ld	0.26	0/899	0.36	0/1204
35	Le	0.14	0/1012	0.29	0/1348
36	Lf	0.20	0/874	0.34	0/1176
37	Lg	0.24	0/904	0.39	0/1210
38	Lh	0.53	0/1014	0.70	1/1349 (0.1%)
39	Li	0.26	0/833	0.41	0/1100
40	Lj	0.29	0/697	0.38	0/922
41	Lk	0.24	0/640	0.41	0/850
42	Ll	0.15	0/445	0.29	0/593
43	Lm	0.23	0/424	0.34	0/561
44	Ln	0.11	0/225	0.28	0/289
45	Lo	0.14	0/797	0.29	0/1054
46	Lp	0.22	0/705	0.40	0/940
47	Lq	0.15	0/1101	0.35	0/1482
48	L1	0.18	0/75268	0.31	0/117356
49	L2	0.17	0/3547	0.27	0/5522
50	L3	0.15	0/2833	0.24	0/4413
All	All	0.20	6/143237 (0.0%)	0.34	9/209935 (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
5	6	0	1
7	LA	0	1
9	LC	0	1
10	LD	0	2
11	LE	0	1
13	LG	0	1
14	LH	0	1
16	LJ	0	1
17	LL	0	1
19	LN	0	1
21	LP	0	1
22	LQ	0	3
25	LT	0	3
26	LU	0	1
29	LY	0	1
30	LZ	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
31	La	0	2
32	Lb	0	1
37	Lg	0	1
38	Lh	0	1
39	Li	0	1
41	Lk	0	1
43	Lm	0	1
46	Lp	0	1
All	All	0	30

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	6	174	LYS	C-N	8.09	1.44	1.33
32	Lb	24	PRO	C-N	-7.01	1.24	1.33
32	Lb	17	HIS	C-N	-5.65	1.26	1.33
29	LY	73	TYR	C-N	-5.57	1.26	1.33
26	LU	81	ARG	C-N	5.50	1.41	1.33
1	1	151	PHE	C-N	5.45	1.40	1.33

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	LC	201	ARG	N-CA-CB	-6.93	100.30	110.49
26	LU	81	ARG	CA-C-N	-6.33	111.70	120.38
26	LU	81	ARG	C-N-CA	-6.33	111.70	120.38
38	Lh	47	ASN	N-CA-C	-6.24	105.79	113.41
9	LC	121	PHE	CA-CB-CG	6.07	119.87	113.80
25	LT	81	LYS	CB-CA-C	-5.88	109.23	117.23
29	LY	109	HIS	CB-CA-C	-5.81	100.76	110.29
22	LQ	119	ARG	CB-CA-C	5.36	121.52	110.31
11	LE	64	ARG	CB-CA-C	-5.15	102.09	110.85

There are no chirality outliers.

All (30) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	6	153	ARG	Sidechain
7	LA	128	ARG	Sidechain
9	LC	201	ARG	Sidechain
10	LD	22	ARG	Sidechain

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Mol	Chain	Res	Type	Group
10	LD	35	ARG	Sidechain
11	LE	64	ARG	Sidechain
13	LG	47	ARG	Sidechain
14	LH	109	ARG	Sidechain
16	LJ	93	ARG	Sidechain
17	LL	20	ARG	Sidechain
19	LN	172	ARG	Sidechain
21	LP	181	ARG	Sidechain
22	LQ	201	ARG	Sidechain
22	LQ	203	ARG	Sidechain
22	LQ	205	ARG	Sidechain
25	LT	107	ARG	Sidechain
25	LT	130	ARG	Sidechain
25	LT	79	ARG	Sidechain
26	LU	81	ARG	Sidechain
29	LY	114	ARG	Sidechain
30	LZ	8	ARG	Sidechain
31	La	136	ARG	Sidechain
31	La	59	ARG	Sidechain
32	Lb	18	ARG	Sidechain
37	Lg	81	ARG	Sidechain
38	Lh	35	ARG	Sidechain
39	Li	45	ARG	Sidechain
41	Lk	24	ARG	Sidechain
43	Lm	111	ARG	Sidechain
46	Lp	36	ARG	Sidechain

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	1	3579	0	3685	108	0
2	2	717	0	757	9	0
3	3	524	0	549	17	0
4	4	2990	0	3052	78	0
5	6	1443	0	1520	55	0
6	7	267	0	255	0	0
7	LA	1925	0	1999	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	LB	3088	0	3206	46	0
9	LC	2758	0	2883	31	0
10	LD	2440	0	2431	37	0
11	LE	1416	0	1509	26	0
12	LF	2017	0	2130	50	0
13	LG	1891	0	2053	49	0
14	LH	1505	0	1581	40	0
15	LI	1699	0	1735	40	0
16	LJ	1367	0	1405	75	0
17	LL	1666	0	1756	59	0
18	LM	1125	0	1198	14	0
19	LN	1703	0	1767	28	0
20	LO	1613	0	1706	22	0
21	LP	1349	0	1388	24	0
22	LQ	1481	0	1596	37	0
23	LR	1466	0	1557	39	0
24	LS	1425	0	1484	24	0
25	LT	1266	0	1328	28	0
26	LU	819	0	864	32	0
27	LV	970	0	1026	13	0
28	LX	965	0	1050	34	0
29	LY	1065	0	1156	34	0
30	LZ	1111	0	1181	30	0
31	La	1180	0	1203	37	0
32	Lb	508	0	526	12	0
33	Lc	722	0	766	14	0
34	Ld	885	0	939	15	0
35	Le	994	0	1061	13	0
36	Lf	853	0	880	21	0
37	Lg	891	0	962	20	0
38	Lh	1003	0	1116	50	0
39	Li	826	0	908	16	0
40	Lj	684	0	716	20	0
41	Lk	632	0	693	16	0
42	Ll	435	0	473	9	0
43	Lm	418	0	463	9	0
44	Ln	224	0	271	2	0
45	Lo	784	0	849	9	0
46	Lp	697	0	741	29	0
47	Lq	1083	0	1140	26	0
48	L1	67284	0	33893	861	0
49	L2	3173	0	1605	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	L3	2535	0	1284	28	0
51	L1	359	0	0	0	0
51	L2	14	0	0	0	0
51	LC	2	0	0	0	0
51	LN	1	0	0	0	0
51	LQ	1	0	0	0	0
51	Lb	2	0	0	0	0
All	All	133840	0	100296	1982	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (1982) 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)
1:1:52:TYR:CE2	1:1:149:ILE:HD11	1.27	1.65
1:1:52:TYR:HE2	1:1:149:ILE:CD1	1.09	1.63
16:LJ:27:SER:HA	16:LJ:31:LEU:CD1	1.34	1.58
3:3:25:ARG:CZ	28:LX:156:VAL:HG21	1.44	1.46
1:1:132:VAL:HG13	1:1:309:MET:CE	1.52	1.40
15:LI:72:ALA:HB2	15:LI:155:CYS:SG	1.60	1.40
5:6:156:LYS:NZ	5:6:169:SER:HB2	1.34	1.39
16:LJ:27:SER:CA	16:LJ:31:LEU:HD12	1.56	1.34
1:1:43:PHE:CE1	1:1:78:MET:HE2	1.62	1.32
23:LR:119:LEU:HD13	23:LR:149:LYS:NZ	1.44	1.30
13:LG:146:ILE:HD11	13:LG:154:VAL:CG2	1.62	1.29
25:LT:129:LYS:HG3	48:L1:1081:A:O5'	1.22	1.29
1:1:345:MET:HE3	1:1:367:TYR:CE1	1.69	1.28
1:1:52:TYR:CE2	1:1:149:ILE:CD1	1.98	1.26
4:4:256:LYS:CE	5:6:84:THR:OG1	1.83	1.26
13:LG:146:ILE:CD1	13:LG:154:VAL:HG21	1.66	1.23
38:Lh:45:LYS:HD2	38:Lh:48:LYS:CD	1.69	1.22
1:1:132:VAL:CG1	1:1:309:MET:HE2	1.68	1.22
12:LF:19:LEU:CD1	12:LF:23:LYS:HE3	1.70	1.21
28:LX:90:GLU:OE2	28:LX:146:LEU:HD11	1.05	1.20
38:Lh:45:LYS:CD	38:Lh:48:LYS:HD3	1.72	1.20
1:1:52:TYR:CD2	1:1:149:ILE:HD11	1.77	1.19
16:LJ:10:MET:HE1	50:L3:52:G:N2	1.56	1.19
17:LL:189:ARG:CD	39:Li:18:ARG:HH21	1.56	1.19
3:3:25:ARG:NH1	28:LX:156:VAL:HG21	1.58	1.18
29:LY:2:LYS:NZ	48:L1:329:A:OP1	1.75	1.18

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:LL:189:ARG:HD2	39:Li:18:ARG:NH2	1.59	1.17
28:LX:90:GLU:OE2	28:LX:146:LEU:CD1	1.93	1.16
15:LI:72:ALA:CB	15:LI:155:CYS:SG	2.33	1.15
4:4:256:LYS:HE3	5:6:84:THR:OG1	0.97	1.14
1:1:68:MET:HE3	1:1:192:SER:HB3	1.31	1.12
17:LL:17:HIS:CD2	17:LL:20:ARG:HH21	1.67	1.12
16:LJ:10:MET:CE	50:L3:52:G:H21	1.63	1.12
14:LH:12:VAL:HG13	14:LH:53:LEU:HD11	1.29	1.11
17:LL:17:HIS:CD2	17:LL:20:ARG:NH2	2.18	1.11
11:LE:64:ARG:HH11	21:LP:181:ARG:NH1	1.49	1.11
14:LH:154:ARG:HG2	14:LH:162:VAL:HG22	1.26	1.10
25:LT:129:LYS:CG	48:L1:1081:A:O5'	1.97	1.10
1:1:52:TYR:HE2	1:1:149:ILE:HD13	1.14	1.10
46:Lp:49:ARG:NH2	46:Lp:52:VAL:HA	1.67	1.09
1:1:75:GLY:HA2	1:1:139:TYR:OH	1.50	1.09
1:1:123:LEU:HD21	1:1:162:MET:CE	1.82	1.09
13:LG:146:ILE:HG23	13:LG:178:ILE:HD12	1.34	1.08
16:LJ:10:MET:HE1	50:L3:52:G:H21	0.95	1.08
1:1:75:GLY:N	1:1:139:TYR:OH	1.87	1.07
1:1:123:LEU:HD21	1:1:162:MET:HE1	1.12	1.07
12:LF:19:LEU:HD11	12:LF:23:LYS:CE	1.84	1.07
1:1:75:GLY:CA	1:1:139:TYR:OH	2.01	1.07
5:6:156:LYS:NZ	5:6:169:SER:CB	2.18	1.07
1:1:345:MET:HE3	1:1:367:TYR:CZ	1.89	1.06
3:3:25:ARG:CZ	28:LX:156:VAL:CG2	2.33	1.06
5:6:156:LYS:HD2	5:6:169:SER:CB	1.85	1.06
16:LJ:27:SER:CA	16:LJ:31:LEU:CD1	2.25	1.06
17:LL:3:ILE:HD12	31:La:44:ASN:OD1	1.56	1.06
1:1:136:THR:HG23	1:1:309:MET:HE1	1.37	1.06
12:LF:95:ILE:HD11	12:LF:141:ALA:HB3	1.37	1.05
17:LL:189:ARG:HD2	39:Li:18:ARG:HH21	0.94	1.05
33:Lc:25:LYS:NZ	33:Lc:96:LEU:HD12	1.71	1.05
5:6:156:LYS:CE	5:6:169:SER:HB2	1.86	1.05
1:1:368:MET:HE2	1:1:372:CYS:SG	1.96	1.05
24:LS:90:MET:CE	24:LS:92:LYS:HD2	1.87	1.05
16:LJ:26:GLU:O	16:LJ:31:LEU:CG	2.04	1.05
46:Lp:36:ARG:HD3	46:Lp:45:ASN:O	1.57	1.04
1:1:43:PHE:CD1	1:1:78:MET:HE2	1.93	1.04
3:3:25:ARG:NH1	28:LX:156:VAL:CG2	2.20	1.03
47:Lq:22:LYS:HG3	47:Lq:27:THR:CG2	1.88	1.03
5:6:156:LYS:HZ2	5:6:169:SER:CB	1.69	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:LT:114:GLU:OE2	25:LT:117:LYS:HE2	1.59	1.02
22:LQ:44:ARG:NH2	22:LQ:48:LYS:HD2	1.73	1.02
12:LF:95:ILE:HD11	12:LF:141:ALA:CB	1.88	1.02
17:LL:17:HIS:CG	17:LL:20:ARG:HH21	1.77	1.01
4:4:257:LYS:CE	4:4:310:GLU:OE2	2.09	1.00
15:LI:72:ALA:CA	15:LI:155:CYS:SG	2.50	1.00
23:LR:119:LEU:CD1	23:LR:149:LYS:HZ2	1.74	1.00
47:Lq:22:LYS:HG3	47:Lq:27:THR:HG22	1.42	1.00
14:LH:12:VAL:CG1	14:LH:53:LEU:HD11	1.91	1.00
48:L1:1198:A:H2	48:L1:1272:G:N1	1.60	0.99
48:L1:1198:A:C2	48:L1:1272:G:N1	2.30	0.99
13:LG:62:GLN:HE22	49:L2:150:G:H21	1.04	0.99
23:LR:119:LEU:CD1	23:LR:149:LYS:NZ	2.25	0.98
1:1:136:THR:CG2	1:1:309:MET:HE1	1.95	0.97
1:1:136:THR:HG21	1:1:309:MET:SD	2.04	0.97
16:LJ:26:GLU:O	16:LJ:31:LEU:CD1	2.13	0.97
12:LF:95:ILE:CD1	12:LF:141:ALA:HB2	1.94	0.97
29:LY:55:VAL:HB	29:LY:103:VAL:HG21	1.47	0.97
13:LG:146:ILE:HD11	13:LG:154:VAL:HG21	0.98	0.97
1:1:132:VAL:CG1	1:1:309:MET:CE	2.36	0.96
5:6:156:LYS:HZ3	5:6:169:SER:HB2	1.28	0.96
25:LT:129:LYS:HD3	48:L1:1081:A:H5'	1.47	0.96
1:1:75:GLY:HA2	1:1:139:TYR:CZ	2.00	0.96
16:LJ:26:GLU:O	16:LJ:31:LEU:HD11	1.66	0.96
16:LJ:26:GLU:O	16:LJ:31:LEU:HG	1.65	0.95
29:LY:55:VAL:HB	29:LY:103:VAL:CG2	1.97	0.95
1:1:123:LEU:CD2	1:1:162:MET:HE1	1.95	0.94
1:1:345:MET:CE	1:1:367:TYR:CZ	2.49	0.94
5:6:156:LYS:CD	5:6:169:SER:HB2	1.97	0.94
16:LJ:26:GLU:C	16:LJ:31:LEU:HD11	1.93	0.94
33:Lc:25:LYS:HZ2	33:Lc:96:LEU:HD12	1.30	0.94
23:LR:96:MET:HE1	48:L1:1643:C:C5'	1.97	0.94
12:LF:95:ILE:CD1	12:LF:141:ALA:CB	2.46	0.94
4:4:256:LYS:HE3	5:6:84:THR:HG1	1.16	0.93
12:LF:19:LEU:HD11	12:LF:23:LYS:HE3	0.97	0.93
1:1:43:PHE:HE1	1:1:78:MET:HE2	1.14	0.93
16:LJ:24:VAL:HB	16:LJ:31:LEU:CD2	1.98	0.93
5:6:156:LYS:HZ2	5:6:169:SER:HB2	1.22	0.92
23:LR:119:LEU:HD13	23:LR:149:LYS:HZ1	1.23	0.91
37:Lg:30:GLN:HE21	37:Lg:32:ARG:HH21	1.13	0.91
29:LY:2:LYS:HZ2	29:LY:9:SER:H	1.19	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:LS:90:MET:HE2	24:LS:92:LYS:HD2	1.51	0.90
23:LR:119:LEU:HD13	23:LR:149:LYS:HZ2	1.21	0.90
5:6:156:LYS:CD	5:6:169:SER:CB	2.50	0.89
17:LL:3:ILE:HD11	31:La:45:LEU:CD1	2.03	0.89
47:Lq:7:ASP:OD1	47:Lq:41:ARG:NH1	2.04	0.89
16:LJ:20:LEU:CD1	16:LJ:38:LEU:HD21	2.03	0.89
10:LD:223:LYS:O	10:LD:227:VAL:CG2	2.21	0.89
38:Lh:33:GLN:O	38:Lh:36:ILE:HG22	1.72	0.89
24:LS:90:MET:HE2	24:LS:92:LYS:CD	2.03	0.88
29:LY:51:LYS:HE3	29:LY:70:THR:O	1.74	0.88
4:4:257:LYS:HE3	4:4:310:GLU:OE2	1.74	0.87
15:LI:72:ALA:N	15:LI:155:CYS:SG	2.47	0.87
14:LH:92:LEU:HD13	14:LH:105:LEU:CD1	2.05	0.87
29:LY:2:LYS:NZ	29:LY:9:SER:OG	2.07	0.87
12:LF:148:LYS:CG	12:LF:246:ARG:NH2	2.38	0.86
12:LF:148:LYS:CG	12:LF:246:ARG:HH21	1.87	0.86
24:LS:90:MET:HE2	24:LS:92:LYS:CG	2.05	0.86
17:LL:3:ILE:CD1	31:La:45:LEU:CD1	2.54	0.86
17:LL:179:GLY:O	17:LL:183:ARG:HD3	1.76	0.86
4:4:208:ARG:NH1	4:4:257:LYS:NZ	2.24	0.86
5:6:156:LYS:HD2	5:6:169:SER:HB3	1.54	0.86
19:LN:2:GLY:N	39:Li:45:ARG:HH22	1.73	0.86
24:LS:90:MET:HE1	24:LS:92:LYS:HD2	1.57	0.85
31:La:76:ASP:HB3	31:La:116:GLY:HA3	1.58	0.85
16:LJ:24:VAL:HB	16:LJ:31:LEU:HD23	1.59	0.85
10:LD:223:LYS:O	10:LD:227:VAL:HG23	1.76	0.85
12:LF:148:LYS:HB3	12:LF:246:ARG:NH2	1.92	0.85
23:LR:119:LEU:CD2	23:LR:149:LYS:HZ2	1.90	0.85
29:LY:2:LYS:NZ	29:LY:9:SER:H	1.73	0.85
14:LH:92:LEU:CD1	14:LH:105:LEU:CD1	2.55	0.85
46:Lp:49:ARG:HH21	46:Lp:52:VAL:HA	1.36	0.84
16:LJ:111:ILE:HG21	16:LJ:123:ILE:CD1	2.08	0.84
23:LR:119:LEU:HD22	23:LR:149:LYS:HZ2	1.43	0.84
25:LT:129:LYS:HG2	48:L1:1081:A:H4'	1.60	0.83
14:LH:92:LEU:CD1	14:LH:105:LEU:HD11	2.08	0.83
4:4:254:CYS:HB3	4:4:257:LYS:HE2	1.60	0.83
19:LN:126:THR:HG23	19:LN:127:TYR:CD2	2.14	0.83
21:LP:181:ARG:HD3	48:L1:3211:U:O4	1.78	0.83
9:LC:287:LEU:HB3	47:Lq:7:ASP:OD2	1.77	0.83
14:LH:154:ARG:HG2	14:LH:162:VAL:CG2	2.08	0.83
16:LJ:20:LEU:CD1	16:LJ:38:LEU:CD2	2.56	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LE:64:ARG:NH1	21:LP:181:ARG:NH1	2.26	0.82
15:LI:59:GLN:HB3	15:LI:126:VAL:HG11	1.59	0.82
4:4:375:ARG:O	4:4:379:VAL:HG23	1.78	0.82
27:LV:87:TRP:CZ2	27:LV:95:LEU:HD11	2.14	0.82
48:L1:1135:G:H1	48:L1:1183:A:H61	1.27	0.82
4:4:257:LYS:NZ	4:4:310:GLU:OE2	2.12	0.82
1:1:284:ARG:HH12	1:1:455:TYR:HE2	1.25	0.82
25:LT:129:LYS:CG	48:L1:1081:A:C5'	2.57	0.82
11:LE:64:ARG:NH1	21:LP:181:ARG:HH11	1.78	0.81
23:LR:119:LEU:CG	23:LR:149:LYS:HZ2	1.93	0.81
47:Lq:22:LYS:CG	47:Lq:27:THR:HG22	2.10	0.81
38:Lh:33:GLN:HA	38:Lh:36:ILE:HG22	1.62	0.81
11:LE:64:ARG:HH11	21:LP:181:ARG:HH11	1.25	0.81
48:L1:821:C:H5	48:L1:836:G:H1	1.24	0.81
5:6:149:GLY:O	5:6:152:LYS:HG3	1.80	0.81
4:4:208:ARG:HH12	4:4:257:LYS:NZ	1.78	0.80
28:LX:79:PRO:HD2	38:Lh:39:ILE:HD11	1.63	0.80
12:LF:148:LYS:CB	12:LF:246:ARG:NH2	2.45	0.80
48:L1:1785:C:H2'	48:L1:1786:G:H8	1.47	0.80
29:LY:2:LYS:HZ2	29:LY:9:SER:N	1.79	0.80
12:LF:148:LYS:HG2	12:LF:246:ARG:NH2	1.96	0.79
48:L1:3289:G:H22	48:L1:3298:U:H3	1.29	0.79
5:6:111:MET:HE3	5:6:112:HIS:HB2	1.64	0.79
16:LJ:27:SER:HA	16:LJ:31:LEU:HD11	1.59	0.79
1:1:43:PHE:CE1	1:1:78:MET:CE	2.57	0.79
1:1:68:MET:HE3	1:1:192:SER:CB	2.11	0.78
26:LU:38:ALA:HA	26:LU:41:LYS:HE2	1.65	0.78
1:1:75:GLY:HA2	1:1:139:TYR:CE1	2.18	0.78
48:L1:1627:A:H2	48:L1:1788:G:H21	1.28	0.78
8:LB:95:THR:HG22	8:LB:97:ARG:H	1.49	0.78
12:LF:95:ILE:HD12	12:LF:141:ALA:HB2	1.64	0.78
49:L2:55:U:H3	49:L2:62:A:H2	1.30	0.78
46:Lp:36:ARG:HD2	46:Lp:45:ASN:ND2	1.99	0.77
16:LJ:24:VAL:CB	16:LJ:31:LEU:HD23	2.15	0.77
28:LX:90:GLU:CD	28:LX:146:LEU:HD11	2.08	0.77
13:LG:186:LYS:HG2	13:LG:197:THR:HB	1.67	0.77
4:4:198:PHE:HA	5:6:99:LYS:HE2	1.67	0.76
4:4:256:LYS:HE3	5:6:84:THR:CB	2.15	0.76
48:L1:990:U:O2'	48:L1:991:A:OP1	2.03	0.76
38:Lh:45:LYS:HD2	38:Lh:48:LYS:HD3	0.83	0.76
47:Lq:9:ILE:HG22	47:Lq:47:VAL:HG12	1.67	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:Lh:33:GLN:HA	38:Lh:36:ILE:CG2	2.15	0.76
25:LT:129:LYS:HD3	48:L1:1081:A:C5'	2.16	0.75
25:LT:129:LYS:HG3	48:L1:1081:A:C5'	2.16	0.75
16:LJ:20:LEU:HD11	16:LJ:38:LEU:CD2	2.16	0.75
7:LA:183:SER:HB3	48:L1:842:G:H8	1.50	0.75
12:LF:148:LYS:HB3	12:LF:246:ARG:HH21	1.49	0.75
17:LL:3:ILE:CD1	31:La:45:LEU:HD12	2.17	0.75
48:L1:2621:G:H2'	48:L1:2622:G:H8	1.51	0.75
48:L1:2701:C:H5	48:L1:2710:G:H1	1.34	0.75
26:LU:100:LEU:HD23	26:LU:112:LEU:HD23	1.69	0.74
29:LY:1:MET:HE3	29:LY:2:LYS:HG2	1.69	0.74
4:4:256:LYS:CE	5:6:84:THR:CB	2.65	0.74
15:LI:203:HIS:NE2	50:L3:107:C:OP2	2.19	0.74
21:LP:181:ARG:CD	48:L1:3211:U:O4	2.35	0.74
48:L1:1198:A:N1	48:L1:1272:G:O6	2.20	0.74
14:LH:92:LEU:HD13	14:LH:105:LEU:HD12	1.68	0.74
24:LS:90:MET:HE2	24:LS:92:LYS:HG3	1.67	0.74
48:L1:2172:U:H2'	48:L1:2173:G:H8	1.52	0.74
12:LF:148:LYS:CB	12:LF:246:ARG:HH21	1.98	0.74
1:1:136:THR:CG2	1:1:309:MET:CE	2.64	0.74
5:6:156:LYS:CE	5:6:169:SER:CB	2.63	0.74
48:L1:2981:U:H3	48:L1:2990:A:H2	1.35	0.74
38:Lh:33:GLN:O	38:Lh:36:ILE:CG2	2.36	0.74
23:LR:134:HIS:HD2	23:LR:137:ALA:H	1.34	0.73
38:Lh:36:ILE:O	38:Lh:39:ILE:HG12	1.88	0.73
24:LS:162:LYS:HG3	36:Lf:38:ASP:HB3	1.69	0.73
40:Lj:82:VAL:HG13	40:Lj:83:PRO:HD2	1.70	0.73
37:Lg:30:GLN:NE2	37:Lg:32:ARG:HH21	1.86	0.73
14:LH:159:GLU:OE2	14:LH:163:ARG:NH2	2.22	0.73
15:LI:30:LYS:HG3	15:LI:63:GLU:HG3	1.69	0.73
29:LY:56:GLN:O	29:LY:103:VAL:HG23	1.88	0.73
1:1:43:PHE:HE1	1:1:78:MET:CE	1.97	0.73
5:6:147:ALA:CB	5:6:153:ARG:HH11	2.02	0.73
11:LE:64:ARG:HD3	21:LP:181:ARG:NH1	2.04	0.73
17:LL:115:ARG:NH2	17:LL:155:PHE:O	2.20	0.73
26:LU:59:VAL:HG23	26:LU:75:HIS:HB2	1.71	0.73
48:L1:1641:G:H2'	48:L1:1642:G:C8	2.23	0.73
23:LR:70:ARG:NH2	48:L1:1843:G:OP1	2.20	0.73
35:Le:17:ARG:NH1	48:L1:1387:G:O6	2.22	0.73
1:1:132:VAL:CG1	1:1:309:MET:SD	2.77	0.72
13:LG:146:ILE:HD11	13:LG:154:VAL:HG22	1.66	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:LR:96:MET:HE1	48:L1:1643:C:H4'	1.71	0.72
1:1:264:ARG:HB3	1:1:284:ARG:HD3	1.69	0.72
48:L1:1198:A:H2	48:L1:1272:G:H1	0.81	0.72
17:LL:39:ARG:NH2	48:L1:673:G:OP1	2.14	0.72
9:LC:185:VAL:HG11	9:LC:231:GLY:HA3	1.70	0.72
21:LP:131:ARG:NH2	48:L1:2319:A:N3	2.36	0.72
12:LF:148:LYS:CD	12:LF:246:ARG:HH21	2.03	0.72
34:Ld:83:ILE:HG23	34:Ld:101:VAL:HG12	1.71	0.72
26:LU:101:ARG:NH2	48:L1:1737:G:OP1	2.21	0.72
12:LF:149:SER:N	12:LF:246:ARG:HH22	1.88	0.72
17:LL:3:ILE:CD1	31:La:44:ASN:OD1	2.37	0.72
48:L1:643:C:H2'	48:L1:644:A:H8	1.55	0.72
1:1:75:GLY:H	1:1:139:TYR:HH	1.36	0.72
7:LA:77:ILE:HD11	7:LA:128:ARG:HE	1.52	0.72
1:1:68:MET:CE	1:1:192:SER:HB3	2.14	0.72
7:LA:117:GLU:HB3	7:LA:122:ASP:OD1	1.90	0.71
24:LS:90:MET:CE	24:LS:92:LYS:CD	2.64	0.71
1:1:405:ARG:NH1	28:LX:83:GLU:OE1	2.23	0.71
15:LI:198:GLN:HE22	48:L1:1023:A:H8	1.38	0.71
48:L1:1135:G:N2	48:L1:1183:A:N1	2.38	0.71
15:LI:59:GLN:HB3	15:LI:126:VAL:CG1	2.19	0.71
48:L1:758:U:O4	48:L1:2696:C:N3	2.23	0.71
16:LJ:20:LEU:HD13	16:LJ:38:LEU:HD21	1.71	0.71
16:LJ:148:ARG:NH2	48:L1:2646:G:OP2	2.24	0.71
17:LL:77:LEU:HD13	48:L1:153:A:OP1	1.91	0.71
23:LR:119:LEU:HD22	23:LR:149:LYS:NZ	2.06	0.71
27:LV:87:TRP:CH2	27:LV:95:LEU:HD11	2.25	0.71
14:LH:12:VAL:CG1	14:LH:53:LEU:CD1	2.69	0.70
21:LP:176:ARG:NH2	48:L1:606:C:OP1	2.23	0.70
34:Ld:83:ILE:HG12	34:Ld:101:VAL:HG12	1.72	0.70
5:6:137:MET:HA	5:6:140:ILE:HG12	1.74	0.70
12:LF:148:LYS:HD3	12:LF:246:ARG:HH21	1.56	0.70
48:L1:1135:G:H1	48:L1:1183:A:N6	1.89	0.70
48:L1:2075:U:H4'	48:L1:2076:A:H5'	1.73	0.70
7:LA:70:LYS:NZ	48:L1:1560:U:O4	2.24	0.70
1:1:284:ARG:NH1	1:1:455:TYR:HE2	1.89	0.70
36:Lf:59:LYS:HD2	48:L1:426:A:P	2.31	0.70
48:L1:1611:C:H5	48:L1:1791:G:H1	1.38	0.70
10:LD:223:LYS:O	10:LD:227:VAL:HG22	1.91	0.70
16:LJ:111:ILE:HG21	16:LJ:123:ILE:HD11	1.74	0.70
23:LR:119:LEU:HB2	23:LR:149:LYS:NZ	2.06	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:Ld:83:ILE:HG23	34:Ld:101:VAL:CG1	2.22	0.70
45:Lo:41:ARG:NH1	48:L1:277:A:OP2	2.25	0.70
25:LT:114:GLU:OE2	25:LT:117:LYS:CE	2.38	0.69
13:LG:146:ILE:HD13	13:LG:154:VAL:HG21	1.73	0.69
17:LL:3:ILE:HD11	31:La:45:LEU:HD13	1.73	0.69
14:LH:92:LEU:HD12	14:LH:92:LEU:O	1.93	0.69
1:1:43:PHE:CD1	1:1:78:MET:CE	2.71	0.69
1:1:132:VAL:HG13	1:1:309:MET:HE2	0.75	0.69
13:LG:53:VAL:HG12	28:LX:43:THR:HA	1.75	0.69
16:LJ:111:ILE:CG2	16:LJ:123:ILE:CD1	2.69	0.69
28:LX:78:HIS:HB2	38:Lh:39:ILE:HD13	1.73	0.69
28:LX:79:PRO:CD	38:Lh:36:ILE:HG13	2.22	0.69
29:LY:37:GLU:N	29:LY:37:GLU:OE2	2.23	0.69
38:Lh:31:LEU:CD1	38:Lh:49:ILE:HG23	2.23	0.69
26:LU:22:ILE:HB	26:LU:109:VAL:HG12	1.75	0.69
29:LY:55:VAL:CB	29:LY:103:VAL:HG21	2.22	0.69
12:LF:91:PHE:HB2	12:LF:145:PRO:HG3	1.75	0.69
48:L1:652:A:H2'	48:L1:653:A:C8	2.27	0.69
38:Lh:31:LEU:HD11	38:Lh:49:ILE:HG23	1.74	0.68
48:L1:2700:C:O2'	48:L1:2701:C:O2	2.11	0.68
17:LL:178:GLU:OE1	17:LL:178:GLU:N	2.24	0.68
48:L1:960:C:H42	48:L1:1087:U:H3	1.42	0.68
19:LN:182:LYS:NZ	48:L1:274:G:N7	2.41	0.68
48:L1:1229:G:N2	48:L1:1247:C:O2'	2.25	0.68
15:LI:12:CYS:SG	15:LI:59:GLN:HG3	2.34	0.68
45:Lo:3:ASN:HD21	45:Lo:95:GLY:H	1.39	0.68
13:LG:62:GLN:NE2	49:L2:150:G:H21	1.87	0.68
47:Lq:22:LYS:HG3	47:Lq:27:THR:HG21	1.71	0.68
23:LR:96:MET:HE1	48:L1:1643:C:H5''	1.73	0.68
28:LX:79:PRO:HD3	38:Lh:36:ILE:HG13	1.75	0.68
16:LJ:20:LEU:HD11	16:LJ:38:LEU:HD22	1.74	0.67
17:LL:3:ILE:HD11	31:La:45:LEU:HD12	1.75	0.67
4:4:254:CYS:HB3	4:4:257:LYS:CE	2.23	0.67
22:LQ:202:ALA:HB2	31:La:56:VAL:HG23	1.76	0.67
14:LH:92:LEU:HD12	14:LH:105:LEU:HD11	1.75	0.67
48:L1:960:C:N4	48:L1:1087:U:H3	1.92	0.67
10:LD:257:LYS:HE2	10:LD:257:LYS:HA	1.77	0.67
12:LF:7:PRO:HG2	47:Lq:88:ARG:HB3	1.76	0.67
48:L1:2621:G:H2'	48:L1:2622:G:C8	2.29	0.67
13:LG:165:LEU:HA	19:LN:7:LEU:HD11	1.77	0.67
45:Lo:98:LYS:HE3	48:L1:2615:A:H4'	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:L1:2856:A:OP2	48:L1:2858:C:N4	2.28	0.66
26:LU:29:ALA:O	26:LU:32:LYS:NZ	2.29	0.66
47:Lq:44:ALA:O	47:Lq:47:VAL:HG22	1.94	0.66
25:LT:129:LYS:CD	48:L1:1081:A:H5'	2.23	0.66
10:LD:214:LEU:HB3	10:LD:222:TYR:HB2	1.76	0.66
22:LQ:202:ALA:O	31:La:51:GLY:HA2	1.96	0.66
1:1:345:MET:CE	1:1:367:TYR:CE1	2.62	0.66
48:L1:2984:G:N2	48:L1:2987:A:OP2	2.28	0.66
15:LI:59:GLN:HE21	15:LI:128:ARG:HE	1.42	0.66
19:LN:36:ILE:HG12	19:LN:64:VAL:HG23	1.78	0.66
30:LZ:32:THR:OG1	30:LZ:34:SER:O	2.11	0.66
48:L1:2919:C:H2'	48:L1:2920:G:C8	2.30	0.66
16:LJ:55:VAL:HB	16:LJ:60:ILE:HB	1.78	0.66
17:LL:189:ARG:HD3	39:Li:18:ARG:HH21	1.57	0.66
4:4:254:CYS:CB	4:4:257:LYS:HE2	2.25	0.66
29:LY:3:VAL:HG22	48:L1:223:A:H5''	1.78	0.66
14:LH:92:LEU:HD13	14:LH:105:LEU:HD11	1.73	0.65
48:L1:1199:C:H2'	48:L1:1200:A:H8	1.61	0.65
38:Lh:33:GLN:CA	38:Lh:36:ILE:HG22	2.25	0.65
1:1:368:MET:CE	1:1:372:CYS:SG	2.80	0.65
29:LY:55:VAL:HB	29:LY:103:VAL:HG22	1.79	0.65
30:LZ:102:GLU:HB2	30:LZ:105:GLN:HG3	1.79	0.65
23:LR:119:LEU:CG	23:LR:149:LYS:NZ	2.57	0.65
26:LU:111:GLU:OE1	26:LU:111:GLU:N	2.29	0.65
9:LC:47:LYS:NZ	48:L1:679:A:OP1	2.29	0.65
22:LQ:203:ARG:HA	22:LQ:209:ARG:O	1.97	0.65
48:L1:2224:G:O2'	48:L1:2226:C:N4	2.29	0.65
12:LF:35:ALA:O	12:LF:39:ARG:HG3	1.97	0.65
48:L1:643:C:H2'	48:L1:644:A:C8	2.32	0.65
11:LE:150:GLN:OE1	11:LE:150:GLN:N	2.29	0.65
13:LG:53:VAL:CG2	13:LG:55:TRP:CE2	2.80	0.65
13:LG:106:GLN:N	13:LG:106:GLN:OE1	2.25	0.65
19:LN:64:VAL:HG11	19:LN:102:ALA:HB1	1.79	0.65
13:LG:71:ARG:HG3	48:L1:2477:U:H5'	1.79	0.64
48:L1:813:G:O2'	48:L1:1844:A:N3	2.30	0.64
7:LA:69:TYR:OH	48:L1:2518:G:OP1	2.14	0.64
17:LL:189:ARG:CD	39:Li:18:ARG:NH2	2.37	0.64
48:L1:2801:U:OP1	48:L1:2857:G:N2	2.30	0.64
40:Lj:82:VAL:CG1	40:Lj:86:ALA:HB3	2.27	0.64
48:L1:2919:C:H2'	48:L1:2920:G:H8	1.61	0.64
26:LU:43:LEU:HD12	26:LU:47:ILE:HD11	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LJ:73:ARG:NH1	50:L3:40:C:O2	2.30	0.64
38:Lh:32:SER:HA	38:Lh:35:ARG:NH2	2.12	0.64
38:Lh:33:GLN:C	38:Lh:36:ILE:HG22	2.23	0.64
40:Lj:82:VAL:HG11	40:Lj:86:ALA:HB3	1.80	0.64
48:L1:3229:G:O2'	48:L1:3230:G:O5'	2.15	0.64
48:L1:2221:U:H2'	48:L1:2222:A:H8	1.63	0.64
16:LJ:111:ILE:HD13	16:LJ:123:ILE:HD11	1.79	0.64
35:Le:66:HIS:HB3	47:Lq:25:THR:HG22	1.80	0.64
48:L1:2799:C:N4	48:L1:2804:A:O2'	2.28	0.64
15:LI:93:PRO:HB2	15:LI:125:THR:HG23	1.79	0.64
16:LJ:61:ARG:HE	16:LJ:62:ARG:HB3	1.63	0.64
37:Lg:102:VAL:HA	37:Lg:105:VAL:HG12	1.80	0.64
48:L1:1623:A:O2'	48:L1:1624:C:O5'	2.14	0.64
48:L1:2477:U:OP2	48:L1:2545:G:N2	2.31	0.64
5:6:140:ILE:HG22	5:6:151:LEU:HD13	1.80	0.63
31:La:36:GLY:HA2	31:La:39:HIS:HD2	1.63	0.63
32:Lb:40:ARG:HB3	32:Lb:40:ARG:HH11	1.62	0.63
4:4:256:LYS:HE2	5:6:84:THR:CB	2.27	0.63
23:LR:96:MET:HE1	48:L1:1643:C:C4'	2.27	0.63
4:4:256:LYS:HE2	5:6:84:THR:HB	1.80	0.63
31:La:94:GLN:N	31:La:94:GLN:OE1	2.31	0.63
36:Lf:61:VAL:HG12	36:Lf:62:ARG:HG3	1.79	0.63
4:4:163:THR:HG22	4:4:176:VAL:HB	1.80	0.63
5:6:86:VAL:CG2	5:6:153:ARG:HH21	2.10	0.63
17:LL:68:ARG:NH2	48:L1:104:G:O3'	2.31	0.63
17:LL:193:ARG:HH12	48:L1:2734:U:P	2.22	0.63
48:L1:565:C:H2'	48:L1:566:C:C6	2.33	0.63
16:LJ:95:ARG:NH2	48:L1:2633:A:OP2	2.32	0.63
48:L1:1200:A:O2'	48:L1:1201:U:OP1	2.16	0.63
3:3:25:ARG:NH2	28:LX:156:VAL:HG21	2.08	0.63
13:LG:74:VAL:HB	13:LG:237:GLY:HA3	1.80	0.63
16:LJ:26:GLU:O	16:LJ:31:LEU:CD2	2.46	0.63
28:LX:104:ASN:H	28:LX:107:GLN:HE21	1.47	0.63
8:LB:129:ALA:O	48:L1:3107:G:O2'	2.13	0.63
15:LI:12:CYS:SG	15:LI:59:GLN:CG	2.87	0.63
25:LT:129:LYS:CD	48:L1:1081:A:C5'	2.76	0.63
28:LX:52:VAL:HG13	48:L1:14:A:O2'	1.99	0.63
48:L1:882:G:H1'	48:L1:1569:A:N6	2.14	0.63
1:1:136:THR:HG21	1:1:309:MET:CE	2.28	0.62
7:LA:183:SER:HB3	48:L1:842:G:C8	2.33	0.62
1:1:368:MET:HA	1:1:368:MET:HE3	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:LL:13:HIS:HE1	48:L1:99:G:N7	1.97	0.62
19:LN:125:SER:HB2	48:L1:2396:U:H1'	1.81	0.62
36:Lf:22:ARG:NH1	48:L1:1132:G:OP1	2.33	0.62
23:LR:89:MET:HB2	48:L1:2065:U:H4'	1.80	0.62
48:L1:702:G:HO2'	48:L1:735:C:HO2'	1.46	0.62
48:L1:2172:U:H2'	48:L1:2173:G:C8	2.32	0.62
1:1:345:MET:HE2	1:1:367:TYR:CZ	2.34	0.62
43:Lm:113:ARG:NH2	48:L1:1174:U:O2'	2.33	0.62
48:L1:637:A:OP2	48:L1:2827:U:O2'	2.17	0.62
13:LG:189:LEU:O	13:LG:193:VAL:HG22	2.00	0.62
14:LH:71:LEU:HD12	14:LH:119:VAL:HG23	1.82	0.62
17:LL:57:ILE:H	17:LL:112:ASN:HD21	1.46	0.62
14:LH:53:LEU:C	14:LH:53:LEU:HD12	2.24	0.62
48:L1:856:U:OP2	48:L1:1887:C:O2'	2.14	0.62
48:L1:1476:G:N2	48:L1:1476:G:OP2	2.32	0.62
9:LC:365:ALA:HB3	24:LS:28:ARG:HD2	1.81	0.62
30:LZ:49:PRO:HD3	30:LZ:67:ILE:HG12	1.82	0.62
2:2:57:LYS:NZ	23:LR:31:GLU:OE2	2.32	0.62
14:LH:87:LYS:HD3	14:LH:87:LYS:N	2.14	0.62
17:LL:3:ILE:HD13	31:La:45:LEU:CD1	2.29	0.61
48:L1:2100:U:OP2	48:L1:2105:A:N6	2.32	0.61
48:L1:3204:C:H2'	48:L1:3205:G:H8	1.62	0.61
4:4:310:GLU:HG2	4:4:337:LYS:HD3	1.81	0.61
7:LA:5:ILE:HG12	7:LA:8:GLN:HE21	1.64	0.61
9:LC:36:VAL:HG21	9:LC:251:LEU:HD21	1.82	0.61
13:LG:151:ALA:HA	13:LG:204:THR:HG22	1.81	0.61
46:Lp:8:VAL:HG23	48:L1:1907:G:OP1	2.00	0.61
48:L1:997:U:O3'	48:L1:998:C:H4'	2.01	0.61
10:LD:52:VAL:HG22	10:LD:150:ASP:HB3	1.82	0.61
22:LQ:104:GLU:OE1	22:LQ:104:GLU:N	2.27	0.61
48:L1:1758:G:O2'	48:L1:1760:G:OP2	2.16	0.61
22:LQ:97:ARG:HD2	48:L1:766:G:C2	2.36	0.61
17:LL:179:GLY:HA3	17:LL:183:ARG:NH1	2.15	0.61
19:LN:90:ASN:ND2	48:L1:2387:A:OP1	2.33	0.61
48:L1:448:C:N4	48:L1:468:G:O2'	2.34	0.61
3:3:25:ARG:NH2	28:LX:156:VAL:CG2	2.63	0.61
19:LN:49:ARG:NH2	48:L1:145:U:OP1	2.34	0.61
30:LZ:89:GLU:H	30:LZ:89:GLU:CD	2.08	0.61
1:1:52:TYR:CG	1:1:53:GLY:N	2.69	0.61
4:4:317:GLN:O	4:4:333:ARG:NH2	2.34	0.61
48:L1:652:A:H2'	48:L1:653:A:H8	1.64	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:LC:39:VAL:HG12	9:LC:242:LEU:CD2	2.30	0.61
29:LY:2:LYS:HZ3	29:LY:9:SER:CB	2.13	0.61
48:L1:133:C:H5''	48:L1:134:G:C4	2.36	0.61
48:L1:961:C:N4	48:L1:963:U:O2'	2.34	0.61
27:LV:87:TRP:CH2	27:LV:95:LEU:CD1	2.84	0.61
48:L1:468:G:OP1	48:L1:469:C:N4	2.34	0.61
48:L1:1627:A:OP2	48:L1:1788:G:N2	2.33	0.61
1:1:100:MET:N	1:1:100:MET:SD	2.73	0.60
8:LB:212:LYS:NZ	8:LB:355:VAL:O	2.34	0.60
9:LC:133:ALA:HB2	9:LC:149:VAL:HG21	1.83	0.60
16:LJ:27:SER:N	16:LJ:31:LEU:HD11	2.15	0.60
8:LB:124:LYS:NZ	48:L1:3238:U:O4	2.33	0.60
12:LF:100:LYS:NZ	48:L1:1139:C:OP2	2.34	0.60
15:LI:189:ARG:HG3	15:LI:200:LEU:HB3	1.83	0.60
48:L1:1464:A:O2'	48:L1:1838:A:H1'	2.00	0.60
1:1:52:TYR:CE2	1:1:149:ILE:HD13	2.01	0.60
4:4:174:LEU:HB2	4:4:213:LEU:HD23	1.81	0.60
26:LU:94:MET:HA	26:LU:94:MET:HE3	1.82	0.60
38:Lh:81:LEU:HD12	38:Lh:86:ARG:HG3	1.84	0.60
48:L1:656:U:H2'	48:L1:657:U:C6	2.35	0.60
1:1:68:MET:CE	1:1:192:SER:CB	2.76	0.60
1:1:270:LYS:NZ	1:1:271:SER:O	2.34	0.60
7:LA:37:ARG:NH1	48:L1:2489:C:OP1	2.24	0.60
15:LI:72:ALA:HA	15:LI:155:CYS:SG	2.40	0.60
29:LY:86:ARG:NH2	48:L1:386:U:O3'	2.34	0.60
24:LS:92:LYS:NZ	48:L1:1194:U:O3'	2.34	0.60
1:1:345:MET:CE	1:1:367:TYR:OH	2.50	0.60
20:LO:76:ARG:HG3	20:LO:147:VAL:HG23	1.83	0.60
48:L1:2656:A:H2'	48:L1:2657:G:C8	2.37	0.60
17:LL:142:GLN:OE1	17:LL:142:GLN:N	2.34	0.60
48:L1:565:C:H2'	48:L1:566:C:H6	1.66	0.60
48:L1:827:G:H21	48:L1:830:A:H2	1.50	0.60
8:LB:270:GLN:NE2	48:L1:3247:G:OP1	2.35	0.60
35:Le:80:VAL:HA	35:Le:83:VAL:HG12	1.83	0.60
48:L1:1766:G:H2'	48:L1:1767:A:C8	2.37	0.60
48:L1:2092:U:H2'	48:L1:2093:G:C8	2.37	0.60
5:6:81:LEU:HD22	5:6:181:GLU:HA	1.84	0.60
28:LX:149:ALA:HA	28:LX:153:LEU:HB2	1.83	0.60
50:L3:23:A:N3	50:L3:119:U:O2'	2.34	0.60
1:1:54:ILE:HG23	1:1:139:TYR:HD1	1.67	0.59
10:LD:52:VAL:HG13	10:LD:54:ARG:NH1	2.16	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LJ:24:VAL:HB	16:LJ:31:LEU:HD21	1.82	0.59
22:LQ:44:ARG:NH2	22:LQ:48:LYS:CD	2.60	0.59
31:La:125:VAL:HB	31:La:145:VAL:HG12	1.83	0.59
48:L1:2227:U:H2'	48:L1:2228:C:H6	1.67	0.59
28:LX:44:THR:HG21	48:L1:1560:U:H5'	1.84	0.59
37:Lg:16:THR:HG21	48:L1:1569:A:H1'	1.83	0.59
37:Lg:24:ILE:HD13	37:Lg:34:LEU:HD22	1.84	0.59
48:L1:410:A:H2'	48:L1:411:A:C8	2.38	0.59
48:L1:2974:A:H2'	48:L1:2975:G:H8	1.67	0.59
48:L1:3000:U:OP2	48:L1:3050:C:N4	2.35	0.59
43:Lm:100:TYR:O	48:L1:2854:G:O2'	2.19	0.59
11:LE:110:ASP:OD1	11:LE:112:THR:HG23	2.02	0.59
19:LN:183:THR:HG22	19:LN:187:ARG:HB2	1.85	0.59
12:LF:7:PRO:HB3	47:Lq:92:LYS:HD2	1.83	0.59
47:Lq:11:GLU:OE1	47:Lq:14:ARG:NH2	2.36	0.59
20:LO:91:PRO:HD3	48:L1:1159:C:H4'	1.84	0.59
29:LY:56:GLN:C	29:LY:103:VAL:HG23	2.27	0.59
7:LA:77:ILE:CD1	7:LA:128:ARG:HE	2.15	0.59
18:LM:78:THR:HB	48:L1:516:G:H5''	1.85	0.59
48:L1:1299:C:H5'	48:L1:1300:A:H5''	1.85	0.59
48:L1:1779:A:H2'	48:L1:1780:A:C8	2.38	0.59
1:1:400:VAL:HA	1:1:409:MET:HE1	1.85	0.59
5:6:42:ASN:O	5:6:45:ILE:HG13	2.03	0.59
7:LA:21:ARG:HD3	48:L1:806:U:H5''	1.84	0.59
34:Ld:54:THR:HG21	34:Ld:99:SER:HB3	1.84	0.59
38:Lh:45:LYS:C	38:Lh:47:ASN:H	2.09	0.59
8:LB:241:ARG:NH2	48:L1:1887:C:O2	2.34	0.58
9:LC:286:ASP:HB3	9:LC:289:ARG:HB2	1.84	0.58
22:LQ:41:SER:OG	22:LQ:45:LYS:HE2	2.03	0.58
41:Lk:24:ARG:HD2	41:Lk:37:LYS:HB2	1.84	0.58
46:Lp:58:LYS:O	46:Lp:61:LYS:NZ	2.26	0.58
48:L1:3221:A:HO2'	48:L1:3222:C:H6	1.49	0.58
14:LH:113:ASN:O	14:LH:117:ILE:HG22	2.03	0.58
48:L1:131:U:HO2'	48:L1:134:G:H1	1.49	0.58
48:L1:1615:G:N2	48:L1:1618:A:OP2	2.31	0.58
48:L1:1920:G:H21	48:L1:3303:A:H8	1.51	0.58
19:LN:64:VAL:CG1	19:LN:102:ALA:HB1	2.32	0.58
22:LQ:91:SER:OG	48:L1:767:G:OP2	2.20	0.58
26:LU:21:PHE:HB2	26:LU:72:ILE:HB	1.83	0.58
40:Lj:82:VAL:CG1	40:Lj:83:PRO:HD2	2.33	0.58
8:LB:227:PHE:O	48:L1:1866:A:O2'	2.20	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LJ:24:VAL:CB	16:LJ:31:LEU:CD2	2.74	0.58
37:Lg:77:TYR:N	48:L1:1786:G:OP1	2.25	0.58
48:L1:1517:A:H2'	48:L1:1518:A:C8	2.38	0.58
48:L1:1818:C:H5''	48:L1:1819:A:H5'	1.84	0.58
9:LC:211:ILE:HB	9:LC:234:THR:HG22	1.84	0.58
20:LO:5:GLU:H	20:LO:32:GLN:HE22	1.50	0.58
20:LO:170:TYR:OH	48:L1:3144:U:OP1	2.17	0.58
30:LZ:64:ARG:NH2	48:L1:1789:A:OP2	2.37	0.58
34:Ld:50:LYS:HE2	48:L1:3263:G:O2'	2.03	0.58
48:L1:1198:A:N1	48:L1:1272:G:C6	2.71	0.58
19:LN:68:ARG:NH2	48:L1:285:U:OP2	2.36	0.58
38:Lh:84:ASP:OD1	38:Lh:84:ASP:N	2.33	0.58
48:L1:1449:G:N2	48:L1:1493:G:H5''	2.19	0.58
48:L1:1549:C:N4	48:L1:1552:G:OP2	2.37	0.58
48:L1:3288:A:H2'	48:L1:3289:G:C8	2.39	0.58
50:L3:27:U:H2'	50:L3:28:C:C6	2.39	0.58
4:4:250:VAL:HG21	4:4:283:MET:HE3	1.86	0.58
8:LB:267:ARG:NH2	48:L1:2355:C:O2'	2.24	0.58
9:LC:294:THR:HB	48:L1:1332:G:N2	2.19	0.58
15:LI:29:PRO:HB3	15:LI:125:THR:HG21	1.84	0.58
15:LI:157:TYR:OH	48:L1:1189:G:OP1	2.19	0.58
17:LL:189:ARG:HB2	39:Li:18:ARG:HE	1.67	0.58
30:LZ:4:LEU:HD21	30:LZ:81:PRO:HB3	1.86	0.58
46:Lp:7:LYS:NZ	48:L1:1906:C:OP2	2.33	0.58
1:1:379:TRP:HH2	2:2:81:LEU:HD23	1.69	0.58
8:LB:357:LEU:HD23	8:LB:360:ILE:HD11	1.85	0.58
14:LH:173:VAL:HG22	14:LH:185:LEU:HG	1.86	0.58
25:LT:129:LYS:CG	48:L1:1081:A:H4'	2.34	0.58
40:Lj:82:VAL:CG1	40:Lj:86:ALA:CB	2.82	0.58
46:Lp:4:ARG:NH1	48:L1:820:G:O6	2.33	0.58
21:LP:42:GLN:H	21:LP:42:GLN:CD	2.11	0.58
22:LQ:101:ASN:HD21	48:L1:707:U:H3	1.49	0.58
22:LQ:180:PHE:O	22:LQ:188:LYS:NZ	2.33	0.58
29:LY:2:LYS:NZ	29:LY:9:SER:N	2.45	0.58
48:L1:1454:U:H2'	48:L1:1455:G:H8	1.69	0.58
26:LU:67:ASP:OD1	26:LU:67:ASP:N	2.37	0.58
41:Lk:31:THR:HG22	41:Lk:33:GLN:HB2	1.84	0.58
4:4:198:PHE:HA	5:6:99:LYS:CE	2.33	0.57
9:LC:39:VAL:HG12	9:LC:242:LEU:HD23	1.84	0.57
11:LE:135:GLU:OE2	48:L1:3210:U:N3	2.37	0.57
27:LV:95:LEU:C	27:LV:95:LEU:HD12	2.29	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:61:ASP:O	1:1:334:GLN:NE2	2.30	0.57
16:LJ:111:ILE:HD13	16:LJ:123:ILE:CD1	2.34	0.57
24:LS:90:MET:CE	24:LS:92:LYS:CG	2.80	0.57
36:Lf:18:TYR:OH	36:Lf:91:LEU:O	2.22	0.57
48:L1:282:U:H2'	48:L1:283:G:H8	1.68	0.57
48:L1:967:U:H2'	48:L1:968:U:H6	1.68	0.57
48:L1:1192:G:H22	48:L1:1280:C:H1'	1.68	0.57
1:1:94:LEU:HD23	1:1:382:VAL:HG21	1.85	0.57
28:LX:63:SER:HB2	38:Lh:71:LEU:HD13	1.86	0.57
48:L1:3181:C:O2'	48:L1:3182:C:OP1	2.20	0.57
13:LG:100:TYR:OH	13:LG:210:ASP:OD1	2.20	0.57
22:LQ:153:GLN:O	22:LQ:157:GLU:HG3	2.04	0.57
26:LU:19:LYS:NZ	26:LU:76:ASN:O	2.38	0.57
35:Le:97:ILE:HG21	35:Le:106:ARG:HG2	1.87	0.57
1:1:262:GLY:HA3	3:3:29:PRO:HG3	1.87	0.57
4:4:208:ARG:HH12	4:4:257:LYS:HZ3	1.50	0.57
7:LA:14:SER:OG	7:LA:15:VAL:N	2.31	0.57
26:LU:97:ARG:NH1	48:L1:1662:U:O4	2.38	0.57
29:LY:1:MET:N	48:L1:206:G:OP2	2.36	0.57
48:L1:300:A:H2'	48:L1:301:A:C8	2.39	0.57
48:L1:1638:G:H2'	48:L1:1639:A:C8	2.40	0.57
10:LD:85:ALA:HB2	10:LD:258:TYR:HB2	1.86	0.57
17:LL:47:ALA:HB3	17:LL:48:PRO:HD3	1.86	0.57
37:Lg:93:ALA:O	37:Lg:97:GLU:HG2	2.04	0.57
13:LG:56:PRO:HG2	13:LG:59:ILE:HD12	1.87	0.57
23:LR:119:LEU:HD13	23:LR:149:LYS:CE	2.32	0.57
38:Lh:8:LYS:HD2	38:Lh:11:GLN:HE22	1.69	0.57
48:L1:2925:G:H2'	48:L1:2926:A:C8	2.39	0.57
12:LF:95:ILE:HD12	12:LF:141:ALA:CB	2.28	0.57
34:Ld:28:LEU:HD11	34:Ld:40:ALA:HB2	1.87	0.57
48:L1:1843:G:N1	48:L1:1846:C:OP2	2.27	0.57
11:LE:64:ARG:HD3	21:LP:181:ARG:HH12	1.69	0.57
49:L2:103:G:OP2	49:L2:105:A:O2'	2.23	0.57
46:Lp:20:ALA:O	46:Lp:24:LYS:HG3	2.05	0.57
48:L1:400:A:C2	49:L2:17:A:H1'	2.40	0.57
4:4:187:LEU:H	4:4:187:LEU:HD12	1.69	0.56
15:LI:4:ARG:NH1	48:L1:1111:U:OP1	2.30	0.56
23:LR:96:MET:HE1	48:L1:1643:C:H5'	1.83	0.56
23:LR:99:GLN:NE2	23:LR:127:ALA:O	2.37	0.56
30:LZ:5:LYS:HA	30:LZ:27:PRO:HG3	1.87	0.56
48:L1:1186:A:H2'	48:L1:1187:A:H8	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:L1:1709:A:H3'	48:L1:1710:G:H5'	1.87	0.56
48:L1:1480:C:H2'	48:L1:1481:A:H8	1.68	0.56
9:LC:105:LYS:NZ	48:L1:782:G:O6	2.33	0.56
10:LD:3:PHE:N	48:L1:1020:U:O2	2.39	0.56
12:LF:242:ASN:O	12:LF:246:ARG:HG2	2.05	0.56
18:LM:59:LEU:O	24:LS:155:ARG:NH1	2.39	0.56
23:LR:119:LEU:CB	23:LR:149:LYS:NZ	2.69	0.56
26:LU:62:ILE:HG22	26:LU:72:ILE:HD12	1.88	0.56
28:LX:90:GLU:OE2	28:LX:146:LEU:CG	2.53	0.56
31:La:13:GLY:HA2	48:L1:925:U:H3'	1.86	0.56
34:Ld:32:THR:HG23	48:L1:2308:A:H5''	1.88	0.56
48:L1:1066:G:H2'	48:L1:1067:A:C8	2.40	0.56
1:1:58:ASP:O	1:1:333:SER:OG	2.16	0.56
37:Lg:92:ARG:O	37:Lg:96:ILE:HG12	2.05	0.56
48:L1:575:G:H2'	48:L1:576:A:H8	1.70	0.56
48:L1:95:G:H2'	48:L1:96:A:C8	2.40	0.56
48:L1:1202:C:H4'	48:L1:1203:U:H6	1.70	0.56
48:L1:1627:A:H62	48:L1:2520:U:H3	1.54	0.56
48:L1:2635:A:H5'	48:L1:2636:G:C8	2.40	0.56
48:L1:3121:G:O2'	48:L1:3122:U:O5'	2.22	0.56
24:LS:73:LYS:NZ	24:LS:97:THR:O	2.39	0.56
48:L1:604:G:H2'	48:L1:605:G:C8	2.40	0.56
48:L1:1816:C:O2'	48:L1:1822:A:N1	2.36	0.56
48:L1:3297:G:H2'	48:L1:3298:U:C6	2.41	0.56
1:1:4:LEU:HD23	1:1:4:LEU:H	1.71	0.56
15:LI:15:LYS:NZ	48:L1:2594:A:OP2	2.37	0.56
48:L1:1464:A:O2'	48:L1:1838:A:N3	2.27	0.56
2:2:94:ASP:HB2	2:2:97:VAL:HG23	1.88	0.56
12:LF:19:LEU:CD1	12:LF:23:LYS:CE	2.59	0.56
25:LT:110:LYS:O	25:LT:114:GLU:HG2	2.06	0.56
34:Ld:83:ILE:HG12	34:Ld:101:VAL:CG1	2.35	0.56
37:Lg:21:THR:HB	37:Lg:33:VAL:HG13	1.87	0.56
48:L1:831:C:O2'	48:L1:832:U:H5''	2.05	0.56
48:L1:1387:G:N2	48:L1:1390:A:OP2	2.34	0.56
49:L2:79:A:H2'	49:L2:80:A:C8	2.41	0.56
4:4:325:LEU:HA	4:4:328:THR:HG22	1.87	0.56
10:LD:225:GLN:NE2	50:L3:30:G:H21	2.04	0.56
12:LF:124:LYS:HE2	25:LT:134:MET:HE1	1.88	0.56
20:LO:116:LYS:HA	48:L1:3134:A:C4	2.40	0.56
30:LZ:51:LYS:O	30:LZ:64:ARG:NH1	2.39	0.56
48:L1:706:G:OP2	48:L1:706:G:N2	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:L1:2148:G:O2'	48:L1:2277:U:OP2	2.24	0.56
39:Li:40:GLY:HA3	48:L1:292:G:C8	2.40	0.56
23:LR:105:LEU:HD22	23:LR:135:LYS:HG3	1.87	0.55
40:Lj:63:ARG:NH1	49:L2:58:G:O6	2.39	0.55
41:Lk:8:ILE:O	41:Lk:12:ILE:HG22	2.07	0.55
9:LC:192:ARG:HG2	9:LC:194:GLY:H	1.72	0.55
13:LG:125:LYS:O	13:LG:126:GLU:HG3	2.05	0.55
16:LJ:26:GLU:C	16:LJ:31:LEU:CD1	2.67	0.55
16:LJ:167:ARG:HD3	16:LJ:168:PHE:HE1	1.70	0.55
22:LQ:44:ARG:HG3	48:L1:956:U:H5'	1.86	0.55
31:La:34:MET:HE1	31:La:45:LEU:HD11	1.88	0.55
48:L1:1779:A:H2'	48:L1:1780:A:H8	1.70	0.55
5:6:45:ILE:HD11	5:6:101:GLN:NE2	2.21	0.55
48:L1:21:A:H2'	48:L1:22:G:C8	2.41	0.55
11:LE:61:LEU:HD11	11:LE:103:ILE:HG13	1.88	0.55
16:LJ:24:VAL:HG12	16:LJ:26:GLU:H	1.72	0.55
20:LO:173:LYS:NZ	48:L1:3135:A:OP2	2.28	0.55
43:Lm:94:MET:HG2	43:Lm:105:PRO:HA	1.89	0.55
26:LU:24:ASN:HB3	26:LU:111:GLU:HB3	1.87	0.55
48:L1:2330:A:H2'	48:L1:2331:A:C8	2.41	0.55
10:LD:33:ARG:NH1	50:L3:7:G:OP1	2.40	0.55
29:LY:86:ARG:NH1	29:LY:87:GLU:O	2.40	0.55
34:Ld:50:LYS:NZ	48:L1:3263:G:H4'	2.21	0.55
10:LD:22:ARG:HD3	50:L3:7:G:H5''	1.88	0.55
48:L1:133:C:H4'	48:L1:134:G:O5'	2.07	0.55
16:LJ:27:SER:HA	16:LJ:31:LEU:HD12	0.61	0.55
48:L1:1576:C:H2'	48:L1:1577:C:C6	2.42	0.55
4:4:198:PHE:HD1	5:6:99:LYS:HE2	1.72	0.55
5:6:86:VAL:HG21	5:6:153:ARG:HH21	1.70	0.55
13:LG:53:VAL:HG23	13:LG:55:TRP:CE2	2.41	0.55
21:LP:32:THR:HG23	21:LP:58:VAL:HG21	1.88	0.55
38:Lh:81:LEU:HD12	38:Lh:82:PRO:O	2.07	0.55
43:Lm:125:LYS:HD3	48:L1:2856:A:H5''	1.89	0.55
1:1:144:GLU:N	1:1:144:GLU:OE2	2.38	0.55
12:LF:59:LYS:NZ	12:LF:63:GLU:OE2	2.35	0.55
13:LG:113:LEU:O	13:LG:117:THR:HG23	2.06	0.55
16:LJ:20:LEU:CD1	16:LJ:38:LEU:HD22	2.34	0.55
47:Lq:64:ILE:HG22	47:Lq:80:THR:HG23	1.89	0.55
48:L1:2332:G:H2'	48:L1:2333:G:C8	2.42	0.55
14:LH:115:MET:O	14:LH:119:VAL:HG23	2.06	0.54
18:LM:121:MET:HG3	48:L1:3159:U:C4	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:LY:2:LYS:NZ	29:LY:9:SER:CB	2.70	0.54
29:LY:103:VAL:HG22	29:LY:104:VAL:N	2.21	0.54
32:Lb:4:SER:HB2	48:L1:1100:G:OP1	2.07	0.54
1:1:82:ILE:HD11	1:1:185:ILE:HG13	1.89	0.54
23:LR:96:MET:CE	48:L1:1643:C:H4'	2.37	0.54
40:Lj:55:ARG:NH2	48:L1:346:G:O6	2.37	0.54
16:LJ:111:ILE:CG2	16:LJ:123:ILE:HD13	2.36	0.54
18:LM:4:ILE:C	18:LM:5:ASN:HD22	2.15	0.54
42:Ll:13:LEU:HD22	48:L1:1476:G:H2'	1.89	0.54
48:L1:351:G:N2	48:L1:354:A:OP2	2.32	0.54
48:L1:2320:A:H2'	48:L1:2321:A:C8	2.43	0.54
48:L1:2984:G:H21	48:L1:2987:A:H2	1.54	0.54
13:LG:146:ILE:HG12	13:LG:151:ALA:HB3	1.89	0.54
30:LZ:41:LEU:HD22	30:LZ:73:VAL:HG22	1.88	0.54
38:Lh:81:LEU:HD13	38:Lh:85:LEU:HB2	1.89	0.54
43:Lm:92:ASP:OD1	43:Lm:126:LYS:NZ	2.35	0.54
48:L1:1016:U:H2'	48:L1:1017:U:C6	2.43	0.54
48:L1:2841:U:H2'	48:L1:2842:U:C6	2.43	0.54
1:1:61:ASP:OD1	1:1:67:ARG:NH2	2.32	0.54
7:LA:113:VAL:HG23	7:LA:116:VAL:CG2	2.38	0.54
8:LB:151:ARG:NH1	48:L1:3188:G:O6	2.35	0.54
9:LC:199:ARG:NH1	48:L1:333:C:OP2	2.32	0.54
10:LD:225:GLN:HE21	50:L3:30:G:H21	1.56	0.54
17:LL:179:GLY:CA	17:LL:183:ARG:NH1	2.70	0.54
17:LL:193:ARG:NH1	48:L1:2734:U:OP1	2.36	0.54
22:LQ:93:SER:HB2	48:L1:766:G:H8	1.72	0.54
38:Lh:45:LYS:C	38:Lh:47:ASN:N	2.63	0.54
48:L1:9:C:H2'	48:L1:10:U:C6	2.43	0.54
48:L1:1195:A:H61	48:L1:1275:C:H42	1.54	0.54
48:L1:1595:C:H2'	48:L1:1596:U:C6	2.43	0.54
8:LB:313:VAL:O	8:LB:333:LYS:HE2	2.07	0.54
12:LF:50:ILE:HD11	12:LF:185:ILE:HG13	1.89	0.54
32:Lb:52:LYS:O	32:Lb:56:GLU:HG2	2.08	0.54
48:L1:644:A:H2'	48:L1:645:A:C8	2.42	0.54
48:L1:1534:C:H2'	48:L1:1535:G:O4'	2.08	0.54
8:LB:149:LEU:HD13	8:LB:197:ARG:HD2	1.88	0.54
10:LD:52:VAL:HA	10:LD:150:ASP:HB3	1.89	0.54
28:LX:66:HIS:ND1	28:LX:67:GLU:O	2.38	0.54
48:L1:604:G:H2'	48:L1:605:G:H8	1.73	0.54
48:L1:1795:U:O2	48:L1:1796:A:N6	2.41	0.54
48:L1:2683:U:O2'	48:L1:2684:U:OP1	2.25	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:LI:177:ARG:HB2	15:LI:180:GLU:HG2	1.89	0.54
19:LN:158:HIS:HB3	19:LN:161:CYS:HB2	1.89	0.54
48:L1:1460:A:OP1	48:L1:3033:G:O2'	2.23	0.54
48:L1:2195:A:H2'	48:L1:2196:A:C8	2.42	0.54
49:L2:26:U:H2'	49:L2:27:U:C6	2.43	0.54
10:LD:257:LYS:NZ	50:L3:118:G:OP1	2.41	0.54
15:LI:121:LYS:HD3	15:LI:121:LYS:N	2.22	0.54
16:LJ:26:GLU:O	16:LJ:31:LEU:HD21	2.07	0.54
17:LL:159:GLN:O	17:LL:159:GLN:HG3	2.08	0.54
22:LQ:93:SER:HB2	48:L1:766:G:C8	2.43	0.54
26:LU:80:GLY:HA2	26:LU:83:LEU:HD12	1.90	0.54
38:Lh:81:LEU:CD1	38:Lh:86:ARG:HG3	2.38	0.54
40:Lj:52:LYS:NZ	48:L1:357:G:OP2	2.30	0.54
48:L1:1195:A:H2'	48:L1:1196:G:C8	2.43	0.54
48:L1:1196:G:H22	48:L1:1274:A:H2	1.54	0.54
48:L1:1778:A:H2'	48:L1:1779:A:C8	2.42	0.54
48:L1:2656:A:H2'	48:L1:2657:G:H8	1.72	0.54
48:L1:2795:C:H5	48:L1:2811:C:H42	1.54	0.54
48:L1:2956:U:H2'	48:L1:2957:C:C6	2.43	0.54
4:4:116:GLU:HG3	4:4:357:LEU:HD13	1.90	0.54
10:LD:52:VAL:HG22	10:LD:150:ASP:CB	2.38	0.54
26:LU:28:PRO:HB2	26:LU:34:PHE:HB2	1.90	0.54
40:Lj:72:ARG:NH1	49:L2:95:G:OP2	2.40	0.54
48:L1:2369:C:H2'	48:L1:2370:C:C6	2.43	0.54
1:1:18:PRO:HA	2:2:91:LEU:HB2	1.90	0.53
9:LC:132:VAL:HG12	9:LC:134:PRO:HD2	1.90	0.53
16:LJ:110:HIS:N	16:LJ:124:TYR:O	2.41	0.53
23:LR:119:LEU:HB2	23:LR:149:LYS:HZ3	1.72	0.53
43:Lm:124:LYS:NZ	48:L1:2856:A:OP2	2.42	0.53
13:LG:208:SER:HA	13:LG:211:LYS:HG3	1.90	0.53
17:LL:78:GLU:OE1	39:Li:29:ARG:NH2	2.39	0.53
26:LU:40:GLU:HG2	26:LU:62:ILE:HD12	1.89	0.53
48:L1:2570:U:H2'	48:L1:2571:U:C6	2.43	0.53
12:LF:19:LEU:HD13	12:LF:23:LYS:HE3	1.81	0.53
25:LT:126:VAL:O	48:L1:1078:U:N3	2.40	0.53
31:La:35:ALA:HB1	48:L1:41:A:H5''	1.90	0.53
41:Lk:4:GLU:OE1	48:L1:1726:C:O2'	2.26	0.53
48:L1:250:C:O2'	48:L1:251:U:OP1	2.26	0.53
7:LA:193:ARG:NH1	48:L1:2137:G:OP2	2.41	0.53
13:LG:27:ASN:OD1	13:LG:27:ASN:N	2.38	0.53
16:LJ:56:ARG:NH1	16:LJ:56:ARG:O	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:LL:61:PRO:O	48:L1:73:C:H1'	2.08	0.53
33:Lc:25:LYS:NZ	33:Lc:96:LEU:CD1	2.59	0.53
48:L1:393:G:H4'	48:L1:394:C:H5''	1.89	0.53
48:L1:3228:C:N4	48:L1:3229:G:O6	2.41	0.53
14:LH:127:MET:HE1	14:LH:200:ILE:HB	1.89	0.53
28:LX:79:PRO:HD2	38:Lh:39:ILE:CD1	2.36	0.53
13:LG:29:LEU:HG	30:LZ:52:ILE:HD11	1.91	0.53
48:L1:1067:A:H2'	48:L1:1068:A:C8	2.44	0.53
4:4:208:ARG:NH1	4:4:257:LYS:HZ2	2.06	0.53
13:LG:118:ALA:HB2	13:LG:128:VAL:HG21	1.91	0.53
17:LL:179:GLY:CA	17:LL:183:ARG:HH11	2.22	0.53
23:LR:35:ALA:O	23:LR:36:ASN:ND2	2.41	0.53
30:LZ:83:ARG:HA	33:Lc:65:MET:HE1	1.89	0.53
42:L1:10:LYS:NZ	48:L1:1813:G:OP1	2.42	0.53
48:L1:2666:U:H2'	48:L1:2667:C:C6	2.43	0.53
7:LA:47:GLU:CG	7:LA:60:ARG:HD2	2.38	0.53
8:LB:362:THR:H	8:LB:372:GLN:HE22	1.55	0.53
48:L1:2058:A:H2'	48:L1:2059:A:C8	2.44	0.53
48:L1:576:A:H2'	48:L1:577:C:C6	2.43	0.53
5:6:189:LYS:HG3	5:6:189:LYS:O	2.09	0.53
8:LB:79:ILE:HD12	8:LB:337:MET:HG3	1.89	0.53
28:LX:128:ARG:HB2	28:LX:130:ASP:OD1	2.10	0.53
31:La:35:ALA:HB2	48:L1:40:A:H5''	1.91	0.53
48:L1:119:U:O2	48:L1:122:A:H5''	2.09	0.53
17:LL:189:ARG:HD2	39:Li:18:ARG:CZ	2.34	0.52
22:LQ:97:ARG:NH1	48:L1:766:G:H22	2.06	0.52
26:LU:38:ALA:HA	26:LU:41:LYS:HG2	1.90	0.52
47:Lq:9:ILE:CG2	47:Lq:47:VAL:HG12	2.37	0.52
48:L1:399:G:OP1	48:L1:1398:U:O2'	2.21	0.52
48:L1:741:U:H2'	48:L1:742:G:H5'	1.91	0.52
16:LJ:41:LEU:HD23	16:LJ:126:MET:HE1	1.91	0.52
17:LL:87:ARG:NH2	48:L1:153:A:OP1	2.42	0.52
43:Lm:104:PRO:HG2	48:L1:3077:U:H4'	1.91	0.52
47:Lq:136:ALA:HA	47:Lq:139:ARG:NH1	2.24	0.52
48:L1:1337:G:N2	48:L1:1339:U:O2'	2.30	0.52
48:L1:1676:A:H2'	48:L1:1677:A:C8	2.43	0.52
48:L1:2320:A:H2'	48:L1:2321:A:H8	1.75	0.52
30:LZ:57:SER:HB3	48:L1:2531:G:H5''	1.90	0.52
37:Lg:16:THR:C	37:Lg:18:SER:H	2.15	0.52
48:L1:1215:C:H3'	48:L1:1216:G:C8	2.44	0.52
48:L1:2974:A:H2'	48:L1:2975:G:C8	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LB:281:HIS:HB3	8:LB:325:ILE:HG23	1.90	0.52
20:LO:13:LYS:NZ	48:L1:3138:A:OP2	2.42	0.52
27:LV:26:ASN:ND2	27:LV:99:ASP:OD2	2.37	0.52
36:Lf:59:LYS:O	36:Lf:67:ARG:NH2	2.42	0.52
46:Lp:38:THR:HA	46:Lp:45:ASN:HA	1.91	0.52
48:L1:1224:U:O2'	48:L1:1226:G:OP2	2.18	0.52
48:L1:2100:U:H5	48:L1:2105:A:N7	2.07	0.52
48:L1:2391:U:H2'	48:L1:2392:G:H8	1.73	0.52
49:L2:9:A:H2'	49:L2:10:A:C8	2.45	0.52
17:LL:177:ILE:HG21	17:LL:184:ALA:HB2	1.92	0.52
24:LS:90:MET:HE3	48:L1:1195:A:H4'	1.90	0.52
46:Lp:7:LYS:HE2	48:L1:1906:C:H2'	1.90	0.52
5:6:156:LYS:HD2	5:6:169:SER:CA	2.37	0.52
48:L1:669:U:O2'	48:L1:685:G:O6	2.27	0.52
48:L1:1186:A:H2'	48:L1:1187:A:C8	2.44	0.52
1:1:68:MET:CE	1:1:192:SER:OG	2.58	0.52
10:LD:18:THR:HG23	50:L3:11:A:C8	2.45	0.52
13:LG:187:ALA:O	13:LG:191:THR:HG22	2.10	0.52
15:LI:102:MET:HE3	15:LI:102:MET:HA	1.91	0.52
21:LP:54:LYS:HA	21:LP:83:TRP:CD1	2.45	0.52
45:Lo:19:LYS:HG3	48:L1:2701:C:OP1	2.09	0.52
48:L1:2971:U:H2'	48:L1:2972:U:C6	2.44	0.52
5:6:45:ILE:HD11	5:6:101:GLN:CD	2.35	0.52
8:LB:58:ARG:HA	8:LB:358:LYS:HG3	1.92	0.52
14:LH:71:LEU:HD12	14:LH:119:VAL:CG2	2.39	0.52
16:LJ:55:VAL:N	16:LJ:60:ILE:O	2.42	0.52
46:Lp:86:LEU:HD12	46:Lp:89:ILE:HD11	1.91	0.52
48:L1:650:U:H2'	48:L1:651:C:C6	2.45	0.52
10:LD:18:THR:CG2	50:L3:11:A:C8	2.93	0.52
15:LI:74:LYS:NZ	48:L1:2797:A:O2'	2.43	0.52
48:L1:8:C:O2'	48:L1:9:C:H6	1.93	0.52
48:L1:976:G:N2	48:L1:977:U:O4	2.41	0.52
50:L3:4:U:H2'	50:L3:5:A:H8	1.74	0.52
9:LC:29:ALA:O	47:Lq:3:ASN:ND2	2.43	0.52
23:LR:42:ARG:HH22	48:L1:1581:U:P	2.33	0.52
23:LR:119:LEU:CD1	23:LR:149:LYS:HZ1	2.04	0.52
48:L1:1216:G:N1	48:L1:1217:G:O6	2.43	0.52
3:3:61:PRO:HA	3:3:64:ASN:ND2	2.25	0.51
4:4:386:ARG:HA	4:4:389:GLN:HE21	1.76	0.51
9:LC:39:VAL:CG1	9:LC:242:LEU:CD2	2.88	0.51
30:LZ:69:PRO:HG3	30:LZ:114:LYS:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:Lc:20:VAL:HG22	33:Lc:101:SER:OG	2.10	0.51
36:Lf:23:ARG:NH2	48:L1:1132:G:OP2	2.38	0.51
48:L1:1673:C:O2'	48:L1:1752:U:O2'	2.25	0.51
4:4:310:GLU:HG3	4:4:311:TYR:CD2	2.45	0.51
11:LE:98:ASN:HB3	11:LE:101:TYR:HD1	1.74	0.51
37:Lg:98:GLU:O	37:Lg:102:VAL:HG13	2.10	0.51
48:L1:639:G:O2'	48:L1:1418:A:OP1	2.29	0.51
48:L1:1064:C:O2'	48:L1:1065:U:OP2	2.26	0.51
12:LF:149:SER:HA	12:LF:246:ARG:HH12	1.75	0.51
17:LL:52:ASP:OD1	17:LL:52:ASP:N	2.41	0.51
21:LP:181:ARG:HD2	48:L1:3211:U:O4	2.10	0.51
37:Lg:7:THR:HG22	48:L1:1469:G:H21	1.75	0.51
1:1:49:MET:SD	1:1:50:PRO:HD2	2.51	0.51
4:4:116:GLU:OE1	4:4:168:ARG:NH1	2.32	0.51
4:4:259:ARG:NH1	4:4:265:LEU:O	2.43	0.51
11:LE:110:ASP:OD1	11:LE:111:LEU:N	2.44	0.51
31:La:36:GLY:HA3	31:La:40:HIS:CE1	2.46	0.51
34:Ld:50:LYS:HZ1	48:L1:3263:G:H4'	1.76	0.51
35:Le:81:LYS:NZ	48:L1:1369:A:OP2	2.29	0.51
48:L1:1893:A:N3	48:L1:2083:G:H2'	2.25	0.51
48:L1:2058:A:H2'	48:L1:2059:A:H8	1.74	0.51
48:L1:2964:A:H2'	48:L1:2965:U:O4'	2.10	0.51
50:L3:83:G:H2'	50:L3:84:G:C8	2.45	0.51
17:LL:147:THR:HA	38:Lh:124:LYS:HA	1.92	0.51
34:Ld:50:LYS:NZ	48:L1:3263:G:O2'	2.41	0.51
37:Lg:16:THR:O	37:Lg:17:THR:HG22	2.11	0.51
42:Ll:36:ARG:NH2	48:L1:394:C:O2'	2.43	0.51
48:L1:410:A:H2'	48:L1:411:A:H8	1.76	0.51
48:L1:869:G:H2'	48:L1:870:A:C8	2.45	0.51
11:LE:118:LYS:NZ	11:LE:161:ASP:OD1	2.41	0.51
14:LH:159:GLU:HB2	48:L1:2992:C:C2	2.46	0.51
30:LZ:89:GLU:OE2	30:LZ:89:GLU:N	2.36	0.51
48:L1:637:A:H2'	48:L1:638:C:C6	2.46	0.51
48:L1:3182:C:O2'	48:L1:3183:U:H5''	2.11	0.51
30:LZ:3:PHE:HE2	30:LZ:81:PRO:HG3	1.76	0.51
4:4:103:LYS:HA	4:4:106:ILE:HG22	1.93	0.51
12:LF:146:ASN:H	12:LF:242:ASN:HD21	1.59	0.51
12:LF:148:LYS:HD3	12:LF:246:ARG:HE	1.76	0.51
16:LJ:96:ASN:HD22	16:LJ:96:ASN:N	2.09	0.51
17:LL:18:TRP:NE1	48:L1:781:G:O2'	2.42	0.51
21:LP:175:GLN:O	21:LP:179:ARG:HG2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:Lg:22:ARG:NH2	48:L1:1677:A:OP1	2.44	0.51
38:Lh:20:LEU:HA	38:Lh:23:ILE:HD12	1.93	0.51
48:L1:1159:C:H2'	48:L1:1160:G:N2	2.26	0.51
48:L1:2525:U:H2'	48:L1:2526:C:C6	2.46	0.51
2:2:115:ILE:O	2:2:119:THR:HG23	2.10	0.51
4:4:259:ARG:NH2	5:6:181:GLU:O	2.43	0.51
38:Lh:54:LYS:NZ	49:L2:62:A:OP1	2.44	0.51
40:Lj:8:PHE:HA	40:Lj:11:ARG:HD3	1.92	0.51
48:L1:651:C:H2'	48:L1:652:A:H8	1.75	0.51
13:LG:78:ILE:HD11	19:LN:18:VAL:HG13	1.93	0.51
16:LJ:62:ARG:NH1	16:LJ:62:ARG:HB2	2.25	0.51
16:LJ:92:LEU:O	16:LJ:172:VAL:HA	2.11	0.51
22:LQ:203:ARG:H	22:LQ:209:ARG:HB2	1.76	0.51
48:L1:967:U:H2'	48:L1:968:U:C6	2.46	0.51
48:L1:2390:U:H2'	48:L1:2391:U:C6	2.46	0.51
48:L1:2495:U:H2'	48:L1:2496:G:C8	2.46	0.51
5:6:93:GLN:HA	5:6:96:ILE:HG22	1.93	0.50
17:LL:17:HIS:CD2	17:LL:20:ARG:HH22	2.17	0.50
17:LL:58:VAL:HG11	17:LL:72:GLY:HA3	1.93	0.50
8:LB:214:GLU:OE2	8:LB:341:LYS:NZ	2.41	0.50
13:LG:103:GLU:OE2	13:LG:111:ARG:NH1	2.43	0.50
32:Lb:40:ARG:HB3	32:Lb:40:ARG:NH1	2.26	0.50
46:Lp:2:SER:HB2	48:L1:835:G:H1	1.77	0.50
46:Lp:7:LYS:HE3	48:L1:1906:C:P	2.50	0.50
48:L1:8:C:HO2'	48:L1:9:C:H6	1.58	0.50
48:L1:1029:A:H2'	48:L1:1032:C:C5	2.46	0.50
48:L1:2246:G:O2'	48:L1:2248:C:N4	2.44	0.50
9:LC:49:GLN:NE2	48:L1:329:A:O2'	2.44	0.50
30:LZ:71:ILE:HG21	30:LZ:95:ILE:HG21	1.92	0.50
38:Lh:31:LEU:HB2	38:Lh:52:LEU:HB3	1.93	0.50
46:Lp:36:ARG:CD	46:Lp:45:ASN:O	2.45	0.50
47:Lq:62:LYS:HE3	47:Lq:80:THR:HG21	1.92	0.50
48:L1:1222:C:H2'	48:L1:1223:A:O4'	2.12	0.50
3:3:13:ARG:O	3:3:17:LYS:HG3	2.12	0.50
4:4:247:TRP:HE1	4:4:290:THR:HA	1.74	0.50
8:LB:161:VAL:HG13	8:LB:184:ILE:HD11	1.94	0.50
12:LF:149:SER:CA	12:LF:246:ARG:HH12	2.25	0.50
48:L1:1638:G:H2'	48:L1:1639:A:H8	1.76	0.50
49:L2:69:U:H2'	49:L2:70:G:O4'	2.12	0.50
1:1:193:ILE:HG13	1:1:441:LEU:HB2	1.92	0.50
9:LC:56:LYS:NZ	40:Lj:51:GLU:OE1	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LJ:156:THR:HG22	16:LJ:158:GLU:H	1.76	0.50
23:LR:105:LEU:HD23	23:LR:138:LEU:HD23	1.93	0.50
37:Lg:34:LEU:HD21	48:L1:1677:A:H5'	1.94	0.50
48:L1:575:G:H2'	48:L1:576:A:C8	2.47	0.50
48:L1:889:G:H4'	48:L1:890:G:H5'	1.94	0.50
48:L1:2074:G:O2'	48:L1:2075:U:H5'	2.11	0.50
25:LT:17:ARG:HG3	48:L1:2659:G:H5''	1.93	0.50
43:Lm:102:ARG:HE	48:L1:2855:A:P	2.35	0.50
48:L1:1444:A:H2'	48:L1:1445:A:H8	1.76	0.50
48:L1:2307:U:H2'	48:L1:2308:A:C8	2.47	0.50
48:L1:2369:C:H2'	48:L1:2370:C:H6	1.77	0.50
48:L1:2842:U:H2'	48:L1:2843:C:C6	2.47	0.50
1:1:31:GLN:O	1:1:35:TRP:HD1	1.95	0.50
5:6:48:ILE:HD12	5:6:49:SER:N	2.26	0.50
15:LI:179:GLU:CD	15:LI:179:GLU:H	2.20	0.50
31:La:126:ARG:HB3	31:La:148:VAL:HG11	1.94	0.50
36:Lf:34:ILE:HG23	36:Lf:102:ILE:HD13	1.93	0.50
47:Lq:92:LYS:NZ	48:L1:462:A:OP1	2.44	0.50
48:L1:1047:A:H4'	48:L1:1048:A:O5'	2.12	0.50
48:L1:3005:U:O2'	48:L1:3006:A:H5'	2.11	0.50
48:L1:3119:A:H61	48:L1:3226:C:H42	1.58	0.50
4:4:310:GLU:HB3	4:4:337:LYS:O	2.11	0.50
7:LA:12:ARG:NH2	48:L1:887:U:O2'	2.44	0.50
27:LV:34:ARG:HH11	27:LV:34:ARG:HG3	1.76	0.50
31:La:76:ASP:OD1	31:La:77:LYS:N	2.45	0.50
38:Lh:17:LYS:HA	38:Lh:20:LEU:HD12	1.94	0.50
38:Lh:43:GLY:C	38:Lh:45:LYS:N	2.69	0.50
48:L1:1215:C:H3'	48:L1:1216:G:H8	1.76	0.50
48:L1:1330:U:H2'	48:L1:1338:A:H61	1.77	0.50
48:L1:1752:U:H5''	48:L1:1753:C:H5'	1.94	0.50
48:L1:2123:G:H2'	48:L1:2124:G:H8	1.76	0.50
48:L1:2227:U:H2'	48:L1:2228:C:C6	2.45	0.50
4:4:171:VAL:HG22	4:4:360:PRO:HG2	1.94	0.50
7:LA:105:SER:HB3	7:LA:160:SER:HB3	1.93	0.50
8:LB:180:MET:HE2	8:LB:182:ILE:HG12	1.93	0.50
12:LF:149:SER:OG	12:LF:246:ARG:NH1	2.43	0.50
19:LN:36:ILE:CG1	19:LN:64:VAL:HG23	2.41	0.50
29:LY:55:VAL:CG2	29:LY:103:VAL:HG21	2.41	0.50
46:Lp:11:SER:HB3	46:Lp:27:LYS:HB2	1.93	0.50
48:L1:115:A:N1	48:L1:259:C:O2'	2.40	0.50
48:L1:1577:C:H2'	48:L1:1578:G:C8	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:L1:2370:C:H2'	48:L1:2371:U:H6	1.77	0.50
21:LP:41:LEU:HD21	21:LP:99:GLU:CG	2.42	0.49
25:LT:107:ARG:HH22	25:LT:108:ARG:HG3	1.76	0.49
48:L1:927:C:H2'	48:L1:928:C:C6	2.46	0.49
48:L1:2270:G:O2'	48:L1:2273:U:OP2	2.29	0.49
48:L1:2774:G:N2	48:L1:2777:U:O2	2.38	0.49
17:LL:28:GLN:NE2	48:L1:672:G:OP2	2.40	0.49
30:LZ:21:LYS:HE3	30:LZ:131:THR:O	2.12	0.49
48:L1:804:G:H2'	48:L1:805:C:H6	1.77	0.49
48:L1:1197:U:H2'	48:L1:1198:A:C8	2.46	0.49
48:L1:2258:A:N3	48:L1:2888:C:O2'	2.36	0.49
1:1:134:VAL:HG12	1:1:153:LEU:HD23	1.94	0.49
19:LN:14:LYS:HE2	48:L1:262:G:H5''	1.95	0.49
48:L1:1140:G:O2'	48:L1:1152:A:N3	2.37	0.49
48:L1:2185:A:H2'	48:L1:2186:A:C8	2.48	0.49
48:L1:2236:G:O2'	48:L1:2274:G:O6	2.26	0.49
48:L1:2391:U:H2'	48:L1:2392:G:C8	2.47	0.49
48:L1:2840:C:H2'	48:L1:2841:U:C6	2.47	0.49
48:L1:2860:G:O2'	48:L1:2982:A:N1	2.45	0.49
48:L1:3288:A:O2'	48:L1:3289:G:OP1	2.28	0.49
12:LF:142:TYR:CZ	12:LF:236:ASN:HB2	2.48	0.49
16:LJ:27:SER:CA	16:LJ:31:LEU:HD11	2.20	0.49
33:Lc:46:LEU:HD22	33:Lc:71:HIS:HB3	1.93	0.49
48:L1:2795:C:H5	48:L1:2811:C:N4	2.10	0.49
4:4:251:HIS:NE2	4:4:253:GLU:HG2	2.28	0.49
4:4:258:ALA:O	4:4:262:ARG:HB2	2.12	0.49
7:LA:117:GLU:CB	7:LA:122:ASP:OD1	2.59	0.49
15:LI:63:GLU:HB3	48:L1:2812:G:H5''	1.95	0.49
36:Lf:105:TYR:HB2	36:Lf:106:PRO:HD3	1.94	0.49
44:Ln:17:ARG:HA	44:Ln:20:VAL:HG12	1.94	0.49
48:L1:804:G:H2'	48:L1:805:C:C6	2.47	0.49
48:L1:1091:C:H2'	48:L1:1092:A:H8	1.77	0.49
48:L1:2186:A:H2'	48:L1:2187:A:C8	2.47	0.49
48:L1:2721:A:H2'	48:L1:2722:U:H6	1.77	0.49
4:4:178:ILE:HG23	4:4:209:VAL:HG22	1.93	0.49
7:LA:129:THR:HG21	48:L1:2143:G:H5'	1.93	0.49
8:LB:30:LYS:NZ	48:L1:3097:A:OP2	2.31	0.49
12:LF:95:ILE:CD1	12:LF:141:ALA:HB3	2.20	0.49
25:LT:116:LYS:HG3	25:LT:128:LEU:HD11	1.93	0.49
40:Lj:82:VAL:HG12	40:Lj:86:ALA:CB	2.43	0.49
8:LB:84:MET:O	8:LB:203:PRO:HA	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:LI:44:ASP:OD1	15:LI:181:TYR:OH	2.30	0.49
28:LX:102:LYS:HG2	49:L2:113:U:O4	2.12	0.49
39:Li:77:ARG:HH11	39:Li:77:ARG:HG3	1.76	0.49
46:Lp:7:LYS:CE	48:L1:1906:C:OP2	2.61	0.49
48:L1:1004:C:H2'	48:L1:1005:G:H8	1.77	0.49
48:L1:1323:C:H2'	48:L1:1324:U:C6	2.47	0.49
48:L1:2057:C:H2'	48:L1:2058:A:C8	2.47	0.49
48:L1:2195:A:H2'	48:L1:2196:A:H8	1.78	0.49
48:L1:2642:U:H2'	48:L1:2643:C:C6	2.48	0.49
4:4:178:ILE:HG12	4:4:209:VAL:HG13	1.93	0.49
5:6:45:ILE:HA	5:6:48:ILE:HG13	1.95	0.49
23:LR:42:ARG:NH2	48:L1:1581:U:OP2	2.45	0.49
27:LV:84:ALA:H	27:LV:100:ASN:ND2	2.10	0.49
29:LY:111:ASP:O	29:LY:112:LYS:C	2.56	0.49
48:L1:758:U:O2'	48:L1:759:U:H5'	2.12	0.49
48:L1:1480:C:H2'	48:L1:1481:A:C8	2.46	0.49
48:L1:2560:A:H2'	48:L1:2561:G:H8	1.78	0.49
48:L1:3042:C:H2'	48:L1:3043:G:O4'	2.12	0.49
8:LB:251:ALA:HB3	48:L1:2839:U:H1'	1.95	0.49
8:LB:262:GLN:HG2	20:LO:65:TYR:HA	1.95	0.49
12:LF:114:LEU:HD21	12:LF:121:VAL:HG22	1.95	0.49
22:LQ:207:ARG:NH1	48:L1:2749:A:OP1	2.46	0.49
41:Lk:77:ARG:NH2	48:L1:1733:G:OP1	2.45	0.49
48:L1:1066:G:H2'	48:L1:1067:A:H8	1.77	0.49
48:L1:2064:C:H2'	48:L1:2065:U:C6	2.47	0.49
48:L1:2574:G:H2'	48:L1:2575:C:H6	1.78	0.49
48:L1:2920:G:H2'	48:L1:2921:U:C6	2.47	0.49
4:4:372:GLU:N	4:4:372:GLU:OE2	2.45	0.49
11:LE:194:LYS:O	11:LE:198:MET:HG3	2.13	0.49
19:LN:68:ARG:NH1	19:LN:124:ASP:O	2.40	0.49
19:LN:178:HIS:ND1	48:L1:70:C:OP1	2.30	0.49
48:L1:20:U:H2'	48:L1:21:A:C8	2.47	0.49
48:L1:168:C:H3'	48:L1:169:G:H8	1.78	0.49
48:L1:391:U:N3	49:L2:12:A:OP1	2.31	0.49
48:L1:423:G:H2'	48:L1:424:U:C6	2.48	0.49
48:L1:425:G:H2'	48:L1:426:A:C8	2.48	0.49
50:L3:4:U:H2'	50:L3:5:A:C8	2.48	0.49
10:LD:187:ASP:HB3	10:LD:190:THR:HG22	1.95	0.48
34:Ld:50:LYS:CE	48:L1:3263:G:O2'	2.60	0.48
41:Lk:22:SER:HB3	41:Lk:67:GLN:HE21	1.78	0.48
48:L1:293:G:H2'	48:L1:294:G:H8	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:L1:1089:G:H2'	48:L1:1090:A:C8	2.48	0.48
1:1:199:SER:HB3	1:1:212:GLU:OE1	2.13	0.48
38:Lh:39:ILE:HG13	38:Lh:40:SER:N	2.28	0.48
48:L1:2376:A:H2'	48:L1:2377:G:H8	1.77	0.48
48:L1:3174:C:H5	48:L1:3198:G:H22	1.60	0.48
8:LB:263:TRP:CD1	8:LB:263:TRP:H	2.32	0.48
9:LC:59:HIS:CE1	9:LC:99:ARG:HH11	2.31	0.48
10:LD:226:PHE:O	10:LD:230:ILE:HG12	2.14	0.48
15:LI:66:GLU:OE1	15:LI:69:ARG:NH2	2.46	0.48
16:LJ:24:VAL:CG1	16:LJ:31:LEU:CD2	2.92	0.48
18:LM:113:THR:H	18:LM:116:ASP:HB2	1.78	0.48
20:LO:87:ARG:HG3	20:LO:101:LEU:HD11	1.95	0.48
41:Lk:26:LYS:HE2	48:L1:1731:G:H5'	1.95	0.48
47:Lq:100:LYS:HZ3	48:L1:461:C:H5''	1.76	0.48
48:L1:536:C:H4'	48:L1:537:C:H2'	1.96	0.48
48:L1:1762:U:H2'	48:L1:1763:C:C6	2.48	0.48
1:1:35:TRP:CZ3	2:2:95:PRO:HB2	2.49	0.48
4:4:87:PHE:CE1	4:4:187:LEU:HD11	2.48	0.48
20:LO:62:MET:HE3	20:LO:71:GLY:HA3	1.94	0.48
24:LS:96:GLU:HG3	24:LS:102:ALA:HA	1.96	0.48
25:LT:129:LYS:HG2	48:L1:1081:A:O5'	2.04	0.48
38:Lh:24:LEU:HB2	38:Lh:59:VAL:HG11	1.95	0.48
48:L1:2392:G:H2'	48:L1:2393:A:H8	1.78	0.48
48:L1:2760:A:O2'	48:L1:2761:A:H2'	2.13	0.48
16:LJ:38:LEU:HD12	16:LJ:68:VAL:HG13	1.95	0.48
22:LQ:57:LEU:HD21	22:LQ:151:LEU:HB2	1.95	0.48
25:LT:39:ILE:HG22	25:LT:99:SER:HB3	1.95	0.48
25:LT:43:LYS:HD3	48:L1:974:A:H5''	1.96	0.48
30:LZ:71:ILE:HD11	30:LZ:113:VAL:HG21	1.95	0.48
33:Lc:20:VAL:CG2	33:Lc:101:SER:OG	2.62	0.48
37:Lg:99:GLN:OE1	37:Lg:99:GLN:HA	2.14	0.48
39:Li:81:PHE:O	39:Li:85:LYS:HG2	2.13	0.48
41:Lk:54:LYS:HA	41:Lk:57:LYS:HG2	1.95	0.48
48:L1:657:U:H2'	48:L1:658:U:C6	2.48	0.48
48:L1:1200:A:H2'	48:L1:1201:U:C6	2.49	0.48
48:L1:2842:U:H2'	48:L1:2843:C:H6	1.78	0.48
48:L1:3169:U:H2'	48:L1:3170:U:O4'	2.13	0.48
36:Lf:4:GLU:HB2	48:L1:3159:U:H5''	1.96	0.48
48:L1:833:C:H2'	48:L1:834:U:C6	2.48	0.48
48:L1:975:G:N3	48:L1:2596:A:H2'	2.28	0.48
48:L1:1215:C:H5'	48:L1:1216:G:OP2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:L1:2176:A:H2'	48:L1:2177:A:C8	2.48	0.48
48:L1:2560:A:H2'	48:L1:2561:G:C8	2.48	0.48
13:LG:116:ALA:O	13:LG:120:LYS:HG3	2.13	0.48
22:LQ:198:LYS:NZ	48:L1:90:A:N7	2.61	0.48
36:Lf:59:LYS:HD2	48:L1:426:A:OP2	2.14	0.48
48:L1:1402:A:OP1	49:L2:20:U:O2'	2.31	0.48
48:L1:3124:G:O2'	48:L1:3125:U:H5'	2.13	0.48
4:4:385:ILE:O	4:4:389:GLN:HG3	2.13	0.48
48:L1:37:C:H4'	48:L1:790:A:C2	2.49	0.48
48:L1:3079:U:H1'	48:L1:3080:A:H5''	1.96	0.48
50:L3:89:U:H2'	50:L3:90:G:O4'	2.13	0.48
8:LB:251:ALA:HB1	48:L1:2906:G:C2	2.48	0.48
14:LH:186:SER:HB2	14:LH:226:ILE:HD11	1.94	0.48
21:LP:85:VAL:O	21:LP:89:GLN:HG3	2.13	0.48
21:LP:116:HIS:HB3	21:LP:149:ILE:HB	1.95	0.48
40:Lj:82:VAL:HG11	40:Lj:86:ALA:CB	2.44	0.48
48:L1:519:C:HO2'	48:L1:520:A:P	2.35	0.48
48:L1:748:U:H4'	48:L1:749:U:O4'	2.14	0.48
15:LI:50:VAL:HG21	15:LI:148:ALA:HB1	1.95	0.48
17:LL:3:ILE:HD13	31:La:45:LEU:HD11	1.95	0.48
17:LL:162:ALA:O	31:La:106:SER:OG	2.30	0.48
33:Lc:77:ASN:N	33:Lc:77:ASN:OD1	2.47	0.48
40:Lj:32:LYS:NZ	49:L2:111:A:C8	2.81	0.48
47:Lq:10:TRP:O	47:Lq:14:ARG:HB2	2.13	0.48
48:L1:231:A:H2'	48:L1:232:A:O4'	2.13	0.48
48:L1:1177:G:H2'	48:L1:1178:A:C8	2.49	0.48
48:L1:2577:G:O2'	48:L1:2824:U:OP1	2.21	0.48
9:LC:324:GLN:HE21	48:L1:588:G:H21	1.62	0.47
13:LG:252:ARG:O	13:LG:256:LEU:HG	2.14	0.47
29:LY:120:ARG:NH2	49:L2:70:G:OP1	2.44	0.47
48:L1:519:C:O2'	48:L1:520:A:OP1	2.28	0.47
48:L1:580:A:H8	48:L1:581:G:C8	2.31	0.47
48:L1:585:C:O2'	48:L1:586:G:H5'	2.13	0.47
48:L1:779:U:H2'	48:L1:780:U:C6	2.48	0.47
48:L1:2379:U:H2'	48:L1:2380:U:C6	2.49	0.47
16:LJ:24:VAL:CG1	16:LJ:31:LEU:HD23	2.43	0.47
45:Lo:25:VAL:HG22	45:Lo:72:LEU:HD22	1.95	0.47
46:Lp:7:LYS:HE3	48:L1:1906:C:OP2	2.14	0.47
48:L1:48:C:OP2	48:L1:49:A:O2'	2.22	0.47
48:L1:1875:A:O2'	48:L1:3011:G:H4'	2.14	0.47
48:L1:2725:U:H2'	48:L1:2726:U:C6	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:L2:19:C:H2'	49:L2:20:U:C6	2.50	0.47
49:L2:128:U:OP1	49:L2:129:C:N4	2.33	0.47
9:LC:102:ALA:HA	48:L1:782:G:H22	1.79	0.47
20:LO:132:GLN:HE21	48:L1:1299:C:H1'	1.79	0.47
48:L1:171:G:H2'	48:L1:172:G:H8	1.80	0.47
48:L1:626:C:N4	48:L1:627:G:O6	2.48	0.47
48:L1:1584:U:H2'	48:L1:1585:A:O4'	2.13	0.47
48:L1:2470:U:H2'	48:L1:2471:U:C6	2.48	0.47
1:1:19:GLU:OE1	2:2:88:SER:N	2.47	0.47
7:LA:46:LYS:HD2	7:LA:46:LYS:HA	1.65	0.47
25:LT:114:GLU:HA	25:LT:117:LYS:HG2	1.97	0.47
30:LZ:28:VAL:HG12	30:LZ:30:GLN:O	2.14	0.47
31:La:8:THR:HG21	48:L1:650:U:OP1	2.15	0.47
48:L1:2056:A:H2'	48:L1:2057:C:C6	2.48	0.47
19:LN:147:ARG:HE	48:L1:114:C:P	2.37	0.47
26:LU:84:LYS:HE2	26:LU:88:LYS:HE3	1.96	0.47
40:Lj:81:GLY:O	49:L2:95:G:O2'	2.26	0.47
48:L1:307:U:H2'	48:L1:308:C:C6	2.50	0.47
48:L1:2149:U:H2'	48:L1:2150:G:O4'	2.14	0.47
48:L1:2682:U:H2'	48:L1:2683:U:C6	2.50	0.47
48:L1:3238:U:H2'	48:L1:3239:C:H6	1.79	0.47
4:4:391:ALA:HA	4:4:394:GLU:HG3	1.97	0.47
16:LJ:100:THR:HG21	48:L1:2643:C:O2'	2.13	0.47
26:LU:43:LEU:HB2	26:LU:62:ILE:HD13	1.97	0.47
35:Le:104:ARG:HD2	48:L1:1374:C:C2	2.49	0.47
41:Lk:21:SER:O	41:Lk:67:GLN:NE2	2.48	0.47
48:L1:1454:U:H2'	48:L1:1455:G:C8	2.49	0.47
48:L1:1796:A:O2'	48:L1:1797:A:O5'	2.31	0.47
12:LF:90:VAL:HG23	12:LF:123:VAL:HB	1.96	0.47
12:LF:132:MET:O	12:LF:136:VAL:HG22	2.15	0.47
13:LG:77:ALA:HB3	19:LN:18:VAL:HG21	1.97	0.47
14:LH:212:ARG:HE	43:Lm:127:LEU:HB2	1.80	0.47
18:LM:93:LYS:O	18:LM:97:THR:HG23	2.15	0.47
32:Lb:55:LYS:NZ	32:Lb:56:GLU:OE2	2.48	0.47
35:Le:80:VAL:O	35:Le:83:VAL:HG12	2.15	0.47
38:Lh:24:LEU:HG	38:Lh:28:LYS:HD2	1.96	0.47
48:L1:498:U:H2'	48:L1:499:C:C6	2.50	0.47
48:L1:1089:G:H2'	48:L1:1090:A:H8	1.80	0.47
48:L1:1198:A:H2	48:L1:1272:G:C2	2.30	0.47
48:L1:1577:C:H2'	48:L1:1578:G:H8	1.78	0.47
48:L1:2339:G:H2'	48:L1:2340:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:L1:2509:A:H5''	48:L1:2510:C:OP1	2.14	0.47
48:L1:3118:C:O2'	48:L1:3119:A:H8	1.98	0.47
1:1:329:LYS:HE2	1:1:329:LYS:HA	1.97	0.47
3:3:25:ARG:NH1	28:LX:156:VAL:HG23	2.24	0.47
13:LG:207:ARG:O	13:LG:211:LYS:HG3	2.14	0.47
36:Lf:16:LEU:HD11	36:Lf:33:LYS:HB2	1.97	0.47
47:Lq:22:LYS:HA	47:Lq:27:THR:HG22	1.97	0.47
48:L1:289:A:H2'	48:L1:290:A:C8	2.50	0.47
48:L1:414:G:O6	48:L1:2346:C:O2'	2.22	0.47
48:L1:995:A:H61	48:L1:1020:U:H3	1.63	0.47
48:L1:2393:A:H2'	48:L1:2394:C:C6	2.48	0.47
49:L2:142:C:H2'	49:L2:143:U:C6	2.49	0.47
1:1:74:ARG:HA	1:1:79:GLU:CD	2.40	0.47
8:LB:9:PRO:HG3	48:L1:2873:G:H5'	1.96	0.47
26:LU:38:ALA:O	26:LU:41:LYS:HG2	2.14	0.47
32:Lb:25:LYS:HE3	48:L1:1090:A:OP1	2.15	0.47
48:L1:698:A:H2'	48:L1:699:A:C8	2.50	0.47
48:L1:802:A:H2'	48:L1:803:U:C6	2.50	0.47
48:L1:1016:U:O2'	48:L1:1017:U:OP1	2.30	0.47
48:L1:1508:G:H5'	48:L1:1810:G:OP2	2.15	0.47
48:L1:2904:G:O2'	48:L1:2907:C:OP2	2.32	0.47
50:L3:72:G:O2'	50:L3:73:U:OP1	2.28	0.47
1:1:45:VAL:O	1:1:49:MET:HB2	2.15	0.47
2:2:45:ARG:HH11	2:2:45:ARG:HG2	1.78	0.47
8:LB:362:THR:H	8:LB:372:GLN:NE2	2.13	0.47
14:LH:53:LEU:HD12	14:LH:53:LEU:O	2.15	0.47
25:LT:43:LYS:HD2	25:LT:58:HIS:CE1	2.50	0.47
34:Ld:83:ILE:CG1	34:Ld:101:VAL:HG12	2.42	0.47
48:L1:9:C:H2'	48:L1:10:U:H6	1.77	0.47
48:L1:30:C:H4'	48:L1:63:A:H4'	1.97	0.47
48:L1:651:C:H2'	48:L1:652:A:C8	2.49	0.47
48:L1:1004:C:H2'	48:L1:1005:G:C8	2.50	0.47
48:L1:3229:G:C4	48:L1:3230:G:C8	3.03	0.47
49:L2:146:U:H2'	49:L2:147:C:C6	2.50	0.47
1:1:190:CYS:O	1:1:193:ILE:HG22	2.15	0.46
4:4:86:VAL:O	4:4:90:LEU:HG	2.14	0.46
8:LB:92:TYR:HB2	8:LB:158:VAL:HB	1.96	0.46
48:L1:511:U:H4'	48:L1:512:A:O5'	2.15	0.46
48:L1:564:A:HO2'	48:L1:565:C:H6	1.60	0.46
48:L1:1186:A:N3	48:L1:2814:C:O2'	2.43	0.46
48:L1:3171:C:H1'	48:L1:3201:A:N6	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:82:ILE:O	1:1:86:ILE:HD12	2.14	0.46
13:LG:161:ASP:HB3	13:LG:162:PRO:HD3	1.97	0.46
14:LH:143:ASN:OD1	14:LH:144:ALA:N	2.48	0.46
28:LX:149:ALA:HB1	28:LX:155:LEU:HB2	1.97	0.46
29:LY:90:THR:HG22	48:L1:371:A:H4'	1.98	0.46
36:Lf:90:PRO:O	48:L1:422:U:O2'	2.31	0.46
48:L1:159:U:H2'	48:L1:160:G:C8	2.50	0.46
48:L1:1769:G:H2'	48:L1:1770:U:H6	1.80	0.46
1:1:388:ARG:HD3	1:1:388:ARG:HA	1.73	0.46
14:LH:64:VAL:HG12	14:LH:119:VAL:HG21	1.96	0.46
18:LM:27:LEU:HD11	18:LM:94:TRP:CG	2.50	0.46
18:LM:44:PRO:HG3	18:LM:81:VAL:HG12	1.96	0.46
48:L1:171:G:H2'	48:L1:172:G:C8	2.51	0.46
48:L1:2470:U:H2'	48:L1:2471:U:H6	1.80	0.46
1:1:69:MET:HB2	1:1:69:MET:HE3	1.58	0.46
1:1:368:MET:HE2	1:1:372:CYS:HG	1.75	0.46
12:LF:182:TYR:CZ	12:LF:203:GLN:HG2	2.50	0.46
23:LR:60:ARG:NH1	48:L1:1652:C:OP1	2.49	0.46
26:LU:40:GLU:OE1	26:LU:64:GLN:NE2	2.31	0.46
33:Lc:65:MET:HE2	33:Lc:65:MET:HA	1.98	0.46
48:L1:6:G:C2	48:L1:7:A:C8	3.04	0.46
48:L1:341:C:O2	48:L1:345:A:O2'	2.34	0.46
48:L1:997:U:H1'	48:L1:998:C:H1'	1.98	0.46
48:L1:1346:A:H2'	48:L1:1347:G:H8	1.81	0.46
48:L1:1785:C:H2'	48:L1:1786:G:C8	2.37	0.46
48:L1:2081:C:H2'	48:L1:2082:A:O4'	2.14	0.46
5:6:93:GLN:O	5:6:96:ILE:HG22	2.16	0.46
29:LY:31:SER:HA	29:LY:48:PRO:HA	1.97	0.46
35:Le:124:LYS:HB3	35:Le:124:LYS:HE2	1.60	0.46
41:Lk:28:ASN:HD22	41:Lk:33:GLN:HB3	1.79	0.46
48:L1:170:A:H3'	48:L1:171:G:H8	1.80	0.46
48:L1:404:U:H2'	48:L1:405:G:H8	1.80	0.46
48:L1:1444:A:H2'	48:L1:1445:A:C8	2.49	0.46
48:L1:1625:U:H2'	48:L1:1626:G:O4'	2.16	0.46
48:L1:2057:C:H2'	48:L1:2058:A:H8	1.79	0.46
48:L1:2245:U:OP1	48:L1:2932:G:O2'	2.25	0.46
5:6:147:ALA:HA	5:6:151:LEU:HB3	1.96	0.46
21:LP:96:LYS:HD2	21:LP:96:LYS:HA	1.54	0.46
23:LR:88:ARG:O	48:L1:1759:C:N4	2.48	0.46
24:LS:141:LYS:HA	24:LS:144:VAL:HG22	1.98	0.46
36:Lf:74:THR:HG22	48:L1:576:A:H4'	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:L1:489:A:O2'	48:L1:3214:A:N1	2.42	0.46
48:L1:684:C:H2'	48:L1:685:G:C8	2.51	0.46
48:L1:1522:A:N7	48:L1:1536:U:O2	2.49	0.46
48:L1:2327:G:H22	48:L1:2359:G:H1'	1.80	0.46
1:1:123:LEU:CD2	1:1:162:MET:CE	2.71	0.46
10:LD:39:GLN:HE21	10:LD:40:ALA:H	1.64	0.46
10:LD:122:VAL:O	10:LD:251:ARG:NH2	2.49	0.46
10:LD:299:LEU:HD23	10:LD:299:LEU:HA	1.79	0.46
11:LE:121:GLU:HA	11:LE:124:GLN:HG2	1.97	0.46
26:LU:60:ILE:HA	26:LU:73:ILE:O	2.15	0.46
27:LV:15:MET:HE1	27:LV:56:VAL:HB	1.98	0.46
36:Lf:73:ILE:HD12	36:Lf:83:VAL:HG21	1.98	0.46
40:Lj:82:VAL:HG12	40:Lj:86:ALA:HB3	1.98	0.46
41:Lk:66:LEU:CD1	41:Lk:68:ILE:HD11	2.46	0.46
48:L1:705:C:OP1	48:L1:733:A:O2'	2.34	0.46
48:L1:2392:G:H2'	48:L1:2393:A:C8	2.51	0.46
48:L1:2402:A:H2'	48:L1:2403:A:C8	2.51	0.46
48:L1:3131:U:O2'	48:L1:3132:A:OP1	2.32	0.46
8:LB:104:THR:HG22	48:L1:3105:A:O2'	2.16	0.46
22:LQ:174:ARG:HB3	22:LQ:177:VAL:HG23	1.96	0.46
48:L1:425:G:H2'	48:L1:426:A:H8	1.81	0.46
48:L1:449:A:N6	48:L1:468:G:H1'	2.31	0.46
48:L1:1063:A:C2	48:L1:1065:U:H5''	2.50	0.46
48:L1:1091:C:H2'	48:L1:1092:A:C8	2.51	0.46
48:L1:2168:U:O2'	48:L1:2170:A:N6	2.48	0.46
48:L1:3137:A:H2'	48:L1:3138:A:H8	1.81	0.46
48:L1:3174:C:H5	48:L1:3198:G:H1	1.64	0.46
48:L1:3230:G:H2'	48:L1:3231:G:H8	1.81	0.46
48:L1:3243:U:H2'	48:L1:3244:G:C8	2.51	0.46
1:1:253:VAL:O	1:1:257:VAL:HG12	2.16	0.46
5:6:56:VAL:O	5:6:87:HIS:NE2	2.48	0.46
15:LI:210:MET:HE2	15:LI:210:MET:HB3	1.75	0.46
16:LJ:99:GLU:OE1	48:L1:2630:A:O2'	2.27	0.46
17:LL:23:ARG:HG2	17:LL:23:ARG:HH11	1.80	0.46
26:LU:38:ALA:CA	26:LU:41:LYS:HE2	2.41	0.46
31:La:58:MET:HE2	48:L1:2746:G:O2'	2.15	0.46
32:Lb:18:ARG:HD2	32:Lb:18:ARG:HA	1.67	0.46
41:Lk:66:LEU:HD12	41:Lk:66:LEU:O	2.15	0.46
42:Ll:30:ARG:HH21	42:Ll:33:ASN:HD22	1.63	0.46
48:L1:780:U:H2'	48:L1:781:G:O4'	2.16	0.46
1:1:48:GLN:O	3:3:59:HIS:NE2	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LB:4:ARG:HD3	8:LB:6:TYR:O	2.15	0.46
8:LB:17:LEU:O	8:LB:19:ARG:N	2.49	0.46
24:LS:40:ARG:HA	24:LS:40:ARG:HD2	1.78	0.46
29:LY:2:LYS:CE	29:LY:9:SER:OG	2.63	0.46
32:Lb:38:LYS:HG3	32:Lb:41:ARG:HH21	1.81	0.46
41:Lk:26:LYS:HD3	41:Lk:71:VAL:HG11	1.97	0.46
48:L1:833:C:H2'	48:L1:834:U:H6	1.80	0.46
48:L1:929:G:H2'	48:L1:930:C:C6	2.51	0.46
48:L1:996:C:H5'	48:L1:997:U:C5	2.51	0.46
48:L1:2370:C:H2'	48:L1:2371:U:C6	2.51	0.46
48:L1:2495:U:H2'	48:L1:2496:G:H8	1.79	0.46
48:L1:2655:A:H2'	48:L1:2656:A:C8	2.51	0.46
1:1:345:MET:HE2	1:1:367:TYR:OH	2.15	0.45
10:LD:117:LYS:HA	10:LD:117:LYS:HD3	1.57	0.45
32:Lb:25:LYS:HE3	48:L1:1089:G:H4'	1.98	0.45
38:Lh:17:LYS:HE2	38:Lh:17:LYS:HB2	1.55	0.45
48:L1:378:A:H2'	48:L1:379:A:C8	2.51	0.45
48:L1:882:G:H1'	48:L1:1569:A:H61	1.81	0.45
48:L1:1323:C:H2'	48:L1:1324:U:H6	1.82	0.45
48:L1:1346:A:H2'	48:L1:1347:G:C8	2.51	0.45
48:L1:2769:C:OP2	48:L1:2914:U:O2'	2.34	0.45
48:L1:3071:A:H2'	48:L1:3072:A:O4'	2.16	0.45
4:4:212:THR:HA	4:4:334:VAL:O	2.15	0.45
15:LI:180:GLU:HA	15:LI:183:GLU:HG2	1.98	0.45
27:LV:89:ARG:HH12	27:LV:139:MET:HG3	1.81	0.45
28:LX:88:LYS:HE2	28:LX:88:LYS:HB3	1.79	0.45
29:LY:47:ILE:HG12	29:LY:48:PRO:HD2	1.99	0.45
45:Lo:28:TYR:HB3	45:Lo:69:VAL:HB	1.98	0.45
48:L1:3:G:H2'	48:L1:4:U:C6	2.52	0.45
48:L1:564:A:C4	48:L1:565:C:C5	3.04	0.45
48:L1:663:C:O2'	48:L1:667:U:OP1	2.34	0.45
48:L1:937:U:H2'	48:L1:938:U:C6	2.50	0.45
4:4:246:VAL:HG23	4:4:381:ARG:HH22	1.81	0.45
5:6:173:ASP:OD1	5:6:175:LYS:N	2.49	0.45
9:LC:133:ALA:HB2	9:LC:149:VAL:CG2	2.46	0.45
14:LH:176:SER:HB3	14:LH:182:GLU:HB3	1.99	0.45
15:LI:12:CYS:SG	15:LI:128:ARG:HG2	2.56	0.45
17:LL:73:ARG:NH2	48:L1:111:G:OP2	2.46	0.45
30:LZ:22:VAL:HG12	30:LZ:44:GLY:HA3	1.97	0.45
33:Lc:55:ARG:NH1	48:L1:1709:A:O4'	2.37	0.45
38:Lh:82:PRO:HB2	38:Lh:84:ASP:OD1	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:Lp:44:LYS:NZ	48:L1:1707:G:OP1	2.39	0.45
48:L1:2382:A:H2'	48:L1:2383:C:C6	2.51	0.45
12:LF:102:PRO:HB2	12:LF:105:PRO:HD2	1.98	0.45
14:LH:92:LEU:HD12	14:LH:92:LEU:C	2.40	0.45
18:LM:122:ARG:NH1	48:L1:3202:U:OP1	2.49	0.45
23:LR:96:MET:HE2	48:L1:1702:U:C6	2.52	0.45
23:LR:134:HIS:CD2	23:LR:137:ALA:H	2.25	0.45
26:LU:104:ALA:HB2	26:LU:110:TYR:CD1	2.51	0.45
35:Le:114:LYS:HD2	35:Le:114:LYS:HA	1.80	0.45
48:L1:662:G:H2'	48:L1:663:C:C6	2.51	0.45
48:L1:1511:G:O2'	48:L1:1568:A:N3	2.45	0.45
48:L1:2227:U:O2'	48:L1:2228:C:OP1	2.31	0.45
48:L1:2336:A:N3	48:L1:2783:G:O2'	2.31	0.45
48:L1:2389:U:H2'	48:L1:2390:U:C6	2.52	0.45
14:LH:53:LEU:HD21	14:LH:116:ILE:HG23	1.97	0.45
48:L1:359:A:H2'	48:L1:360:A:O4'	2.16	0.45
48:L1:1515:C:H2'	48:L1:1516:U:C6	2.51	0.45
48:L1:2771:C:H2'	48:L1:2772:A:C8	2.51	0.45
4:4:354:GLU:O	4:4:358:ARG:HG3	2.17	0.45
7:LA:68:LYS:HG2	7:LA:69:TYR:N	2.32	0.45
7:LA:96:LEU:HD23	46:Lp:87:ARG:HB2	1.99	0.45
19:LN:140:LYS:HD3	48:L1:128:G:P	2.57	0.45
25:LT:129:LYS:CG	48:L1:1081:A:C4'	2.94	0.45
48:L1:769:G:H2'	48:L1:770:C:C6	2.51	0.45
48:L1:3116:C:H2'	48:L1:3117:G:C8	2.52	0.45
49:L2:63:G:OP1	49:L2:90:U:H5'	2.17	0.45
1:1:307:SER:OG	1:1:326:TRP:NE1	2.49	0.45
12:LF:149:SER:CB	12:LF:246:ARG:HH12	2.28	0.45
16:LJ:109:GLU:HG3	16:LJ:111:ILE:HG12	1.99	0.45
48:L1:1361:U:H2'	48:L1:1362:G:H8	1.81	0.45
48:L1:1892:U:N3	48:L1:2085:G:OP2	2.48	0.45
48:L1:3237:A:H2'	48:L1:3238:U:C6	2.52	0.45
12:LF:124:LYS:HG3	12:LF:197:VAL:HG11	1.99	0.45
16:LJ:76:LYS:O	16:LJ:79:GLU:HG3	2.17	0.45
40:Lj:76:ASN:ND2	49:L2:95:G:OP1	2.38	0.45
48:L1:1244:G:H4'	48:L1:1261:A:N1	2.31	0.45
48:L1:3163:A:H5''	48:L1:3164:G:C5	2.52	0.45
48:L1:3231:G:H2'	48:L1:3232:A:C8	2.51	0.45
1:1:54:ILE:HA	1:1:139:TYR:HB3	1.97	0.45
1:1:405:ARG:HH11	1:1:405:ARG:HG3	1.81	0.45
4:4:254:CYS:SG	4:4:310:GLU:OE2	2.75	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LJ:10:MET:HE2	50:L3:52:G:H21	1.71	0.45
16:LJ:33:ARG:HD2	16:LJ:121:ILE:HA	1.99	0.45
19:LN:2:GLY:N	39:Li:45:ARG:NH2	2.54	0.45
22:LQ:133:PHE:CE1	22:LQ:148:THR:HG23	2.52	0.45
24:LS:134:ASP:OD1	24:LS:134:ASP:N	2.37	0.45
35:Le:24:ASP:OD2	48:L1:417:G:O2'	2.32	0.45
38:Lh:44:ALA:C	38:Lh:46:LEU:N	2.75	0.45
46:Lp:8:VAL:HG11	46:Lp:12:GLY:HA2	1.98	0.45
48:L1:115:A:H2'	48:L1:116:A:O4'	2.17	0.45
48:L1:838:G:O2'	48:L1:839:G:OP1	2.26	0.45
48:L1:2166:U:H2'	48:L1:2167:C:C6	2.52	0.45
48:L1:2185:A:H4'	48:L1:2186:A:OP1	2.17	0.45
48:L1:2578:OMG:H1'	48:L1:2578:OMG:HM23	1.76	0.45
48:L1:3203:U:H2'	48:L1:3204:C:O4'	2.16	0.45
48:L1:3288:A:H2'	48:L1:3289:G:H8	1.82	0.45
49:L2:4:C:H2'	49:L2:5:U:C6	2.52	0.45
49:L2:145:U:H2'	49:L2:146:U:C6	2.52	0.45
3:3:22:PHE:C	3:3:22:PHE:CD1	2.94	0.45
4:4:117:PHE:HZ	4:4:171:VAL:HG11	1.81	0.45
10:LD:116:ASP:OD1	10:LD:116:ASP:N	2.47	0.45
13:LG:252:ARG:HG2	13:LG:252:ARG:HH11	1.82	0.45
19:LN:44:ARG:NH1	48:L1:262:G:OP2	2.39	0.45
24:LS:92:LYS:HE2	24:LS:109:ASP:OD2	2.16	0.45
24:LS:131:LYS:HB3	24:LS:133:GLU:OE2	2.17	0.45
30:LZ:45:ILE:HG23	30:LZ:67:ILE:HG23	1.99	0.45
35:Le:29:LEU:HD11	48:L1:1416:A:C6	2.52	0.45
36:Lf:49:LYS:HD2	36:Lf:104:LEU:HA	1.99	0.45
48:L1:638:C:H2'	48:L1:639:G:C8	2.52	0.45
48:L1:981:G:H2'	48:L1:982:C:C6	2.52	0.45
48:L1:1225:G:H21	48:L1:1225:G:P	2.40	0.45
48:L1:1259:U:H2'	48:L1:1260:C:C6	2.52	0.45
48:L1:3174:C:H41	48:L1:3198:G:H1	1.63	0.45
1:1:82:ILE:HD12	1:1:181:ILE:HA	1.99	0.44
7:LA:61:VAL:HG11	7:LA:88:ILE:HD11	1.98	0.44
9:LC:151:LEU:HD23	9:LC:256:VAL:HG22	1.99	0.44
22:LQ:97:ARG:HD2	48:L1:766:G:N2	2.32	0.44
30:LZ:102:GLU:HA	30:LZ:102:GLU:OE2	2.15	0.44
32:Lb:38:LYS:HG3	32:Lb:41:ARG:NH2	2.32	0.44
36:Lf:55:TYR:CZ	36:Lf:67:ARG:HB2	2.52	0.44
48:L1:714:G:N1	48:L1:725:C:OP2	2.42	0.44
48:L1:969:U:H2'	48:L1:970:U:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LB:381:MET:HE3	8:LB:381:MET:HB3	1.77	0.44
10:LD:156:THR:HG21	48:L1:2705:A:N1	2.32	0.44
12:LF:67:GLU:HA	12:LF:70:ARG:HG2	1.99	0.44
15:LI:22:PHE:CZ	48:L1:1031:A:H2'	2.52	0.44
18:LM:103:GLN:HA	18:LM:106:GLN:HE21	1.82	0.44
48:L1:479:G:H2'	48:L1:480:G:H8	1.82	0.44
48:L1:585:C:H2'	48:L1:597:G:O6	2.18	0.44
48:L1:722:G:HO2'	48:L1:723:C:H6	1.64	0.44
48:L1:1138:C:O2'	48:L1:1180:A:N1	2.44	0.44
48:L1:1797:A:O2'	48:L1:1798:U:O5'	2.35	0.44
48:L1:2544:G:N3	48:L1:2544:G:H2'	2.32	0.44
48:L1:3266:A:H2'	48:L1:3267:G:H8	1.82	0.44
1:1:124:ILE:O	1:1:127:VAL:HG12	2.17	0.44
4:4:209:VAL:O	4:4:337:LYS:HA	2.18	0.44
10:LD:156:THR:HG21	48:L1:2705:A:C6	2.53	0.44
11:LE:142:PHE:HB3	11:LE:150:GLN:HE22	1.81	0.44
12:LF:237:ARG:HD2	12:LF:241:ILE:HA	1.99	0.44
15:LI:47:PRO:HB3	15:LI:171:TRP:CZ2	2.52	0.44
20:LO:35:VAL:HG22	20:LO:105:LYS:HB2	1.99	0.44
22:LQ:116:ASP:OD1	22:LQ:117:ASP:N	2.50	0.44
27:LV:89:ARG:CZ	27:LV:95:LEU:HD21	2.47	0.44
30:LZ:114:LYS:NZ	48:L1:1610:G:OP2	2.50	0.44
47:Lq:8:LEU:O	47:Lq:12:VAL:HG13	2.17	0.44
48:L1:452:C:H2'	48:L1:453:G:H8	1.81	0.44
48:L1:835:G:H2'	48:L1:836:G:O4'	2.18	0.44
48:L1:882:G:H2'	48:L1:883:A:C8	2.52	0.44
48:L1:1322:C:H2'	48:L1:1323:C:C6	2.52	0.44
48:L1:1697:C:H2'	48:L1:1698:A:C8	2.52	0.44
48:L1:1769:G:H2'	48:L1:1770:U:C6	2.53	0.44
48:L1:2059:A:H2'	48:L1:2060:C:C6	2.52	0.44
48:L1:2111:U:H2'	48:L1:2112:A:C8	2.53	0.44
49:L2:47:C:O2'	49:L2:62:A:OP2	2.36	0.44
50:L3:111:G:H2'	50:L3:112:U:C6	2.52	0.44
7:LA:42:ARG:HD3	7:LA:87:PHE:CD1	2.53	0.44
8:LB:181:GLU:OE2	48:L1:2960:C:O2'	2.23	0.44
12:LF:214:SER:O	12:LF:248:MET:HE3	2.18	0.44
23:LR:23:TRP:CE3	23:LR:51:ILE:HD12	2.51	0.44
31:La:26:ARG:HD2	48:L1:920:C:C5	2.52	0.44
37:Lg:103:LYS:HE3	37:Lg:103:LYS:HB2	1.57	0.44
42:Ll:25:GLN:HA	42:Ll:25:GLN:OE1	2.18	0.44
48:L1:442:G:H2'	48:L1:443:C:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:L1:2985:A:H8	48:L1:2985:A:OP1	2.00	0.44
48:L1:3047:C:H2'	48:L1:3048:U:O4'	2.18	0.44
49:L2:63:G:H22	49:L2:97:A:H2	1.64	0.44
1:1:38:LEU:O	1:1:42:ILE:HD12	2.18	0.44
4:4:242:TYR:CE2	4:4:363:LEU:HB3	2.53	0.44
11:LE:162:GLN:NE2	11:LE:166:ASP:OD2	2.36	0.44
20:LO:159:GLU:OE2	48:L1:3186:A:N6	2.50	0.44
25:LT:123:GLY:HA2	48:L1:1077:U:O4	2.16	0.44
28:LX:93:ASN:ND2	28:LX:145:ALA:H	2.15	0.44
48:L1:27:A:N3	48:L1:321:C:O2'	2.43	0.44
48:L1:462:A:H2'	48:L1:463:C:C6	2.53	0.44
48:L1:833:C:HO2'	48:L1:834:U:P	2.40	0.44
48:L1:1595:C:H2'	48:L1:1596:U:H6	1.82	0.44
48:L1:1744:C:H3'	48:L1:1745:U:H5''	1.98	0.44
4:4:106:ILE:HG21	4:4:150:ASP:HA	1.98	0.44
9:LC:236:PRO:HG2	9:LC:239:ALA:HB3	1.98	0.44
9:LC:273:LYS:HB2	9:LC:273:LYS:HE2	1.74	0.44
11:LE:76:LEU:HB2	11:LE:80:VAL:HB	1.99	0.44
11:LE:111:LEU:HD22	11:LE:114:VAL:HG21	1.99	0.44
13:LG:44:GLN:OE1	13:LG:47:ARG:NH2	2.46	0.44
13:LG:71:ARG:NH1	48:L1:2477:U:OP1	2.46	0.44
16:LJ:63:ASN:HD22	16:LJ:63:ASN:HA	1.61	0.44
31:La:15:VAL:O	31:La:16:SER:OG	2.35	0.44
48:L1:854:U:H2'	48:L1:855:C:C6	2.53	0.44
48:L1:1136:A:O2'	48:L1:1137:A:H5'	2.17	0.44
48:L1:1345:G:H2'	48:L1:1346:A:C8	2.53	0.44
49:L2:27:U:H2'	49:L2:28:C:C6	2.52	0.44
1:1:257:VAL:HG13	1:1:451:VAL:HG11	2.00	0.44
5:6:46:LEU:CD2	5:6:101:GLN:HE22	2.31	0.44
5:6:175:LYS:HB2	29:LY:61:ALA:O	2.17	0.44
14:LH:142:LYS:HG3	14:LH:149:TYR:CE1	2.53	0.44
24:LS:171:SER:HB2	24:LS:173:PHE:CD2	2.52	0.44
42:L1:49:LEU:HG	48:L1:1476:G:OP1	2.18	0.44
48:L1:411:A:H2'	48:L1:412:G:C8	2.53	0.44
48:L1:498:U:H2'	48:L1:499:C:H6	1.82	0.44
48:L1:1670:C:H2'	48:L1:1671:U:C6	2.52	0.44
48:L1:1895:A:H2'	48:L1:1896:U:C6	2.53	0.44
48:L1:2307:U:H2'	48:L1:2308:A:H8	1.81	0.44
48:L1:2508:A:H2'	48:L1:2509:A:C8	2.53	0.44
7:LA:47:GLU:HG3	7:LA:60:ARG:HD2	1.99	0.44
10:LD:34:LYS:O	10:LD:38:THR:OG1	2.28	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LF:21:LYS:HD3	48:L1:1334:A:H2'	1.99	0.44
16:LJ:170:GLY:C	16:LJ:171:ILE:HD13	2.43	0.44
20:LO:112:PRO:N	20:LO:113:PRO:HD2	2.33	0.44
27:LV:122:LYS:O	27:LV:126:GLU:HG3	2.18	0.44
46:Lp:14:TYR:OH	46:Lp:30:GLU:OE2	2.35	0.44
47:Lq:7:ASP:OD1	47:Lq:41:ARG:CZ	2.62	0.44
48:L1:415:A:C2	48:L1:2326:A:H4'	2.53	0.44
48:L1:543:U:H2'	48:L1:544:G:O4'	2.18	0.44
48:L1:735:C:H2'	48:L1:736:G:H8	1.83	0.44
48:L1:1534:C:HO2'	48:L1:2133:U:HO2'	1.65	0.44
48:L1:2352:C:H2'	48:L1:2353:A:C8	2.53	0.44
48:L1:2376:A:H2'	48:L1:2377:G:C8	2.53	0.44
50:L3:29:G:O6	50:L3:49:A:N6	2.51	0.44
8:LB:25:HIS:CE1	8:LB:335:ARG:HE	2.35	0.44
14:LH:1:MET:HG3	24:LS:139:TYR:HB3	2.00	0.44
15:LI:208:GLU:OE2	15:LI:212:ARG:NH2	2.51	0.44
29:LY:2:LYS:HD3	29:LY:9:SER:HB3	2.00	0.44
29:LY:46:SER:OG	48:L1:219:C:OP1	2.36	0.44
38:Lh:33:GLN:O	38:Lh:34:LEU:C	2.61	0.44
48:L1:459:C:H4'	48:L1:460:U:O4'	2.17	0.44
5:6:29:ASN:O	5:6:33:MET:HG2	2.17	0.43
19:LN:8:GLU:HG3	19:LN:50:ARG:NH2	2.33	0.43
36:Lf:59:LYS:CD	48:L1:426:A:OP2	2.66	0.43
45:Lo:82:GLN:NE2	48:L1:2727:U:O2'	2.51	0.43
48:L1:467:U:H2'	48:L1:468:G:O4'	2.18	0.43
48:L1:2182:A:H2'	48:L1:2183:A:C8	2.53	0.43
48:L1:2471:U:H2'	48:L1:2472:U:H6	1.83	0.43
48:L1:2574:G:H2'	48:L1:2575:C:C6	2.53	0.43
48:L1:2870:A:H4'	48:L1:2871:G:C8	2.53	0.43
3:3:64:ASN:HA	3:3:67:VAL:HG22	2.00	0.43
4:4:397:ALA:HA	4:4:400:ARG:HG2	1.98	0.43
9:LC:287:LEU:HD11	22:LQ:60:LEU:HB2	1.99	0.43
26:LU:110:TYR:OH	48:L1:1657:A:OP2	2.33	0.43
27:LV:42:LYS:HG3	27:LV:59:MET:HB3	1.99	0.43
35:Le:12:LYS:O	35:Le:13:LYS:HB2	2.17	0.43
48:L1:39:U:H2'	48:L1:40:A:O4'	2.18	0.43
48:L1:1195:A:H2'	48:L1:1196:G:H8	1.80	0.43
48:L1:1200:A:N1	48:L1:1270:A:H2	2.16	0.43
48:L1:1626:G:O2'	48:L1:1789:A:N6	2.51	0.43
48:L1:1836:C:H2'	48:L1:1837:C:H6	1.84	0.43
48:L1:1879:G:O2'	48:L1:2297:U:O4	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:L1:2143:G:H2'	48:L1:2144:C:C6	2.53	0.43
48:L1:3204:C:H2'	48:L1:3205:G:C8	2.48	0.43
49:L2:9:A:H2'	49:L2:10:A:H8	1.83	0.43
1:1:35:TRP:CH2	2:2:95:PRO:HB2	2.54	0.43
4:4:251:HIS:CE1	4:4:253:GLU:HG2	2.53	0.43
5:6:101:GLN:HE21	5:6:105:ILE:HD11	1.84	0.43
16:LJ:38:LEU:HD23	16:LJ:38:LEU:HA	1.83	0.43
21:LP:83:TRP:O	48:L1:2315:A:H5''	2.17	0.43
31:La:55:LYS:HE2	48:L1:94:C:C2	2.53	0.43
41:Lk:7:ASP:OD1	41:Lk:10:LYS:HB2	2.19	0.43
48:L1:28:C:O2'	48:L1:320:A:N3	2.45	0.43
48:L1:424:U:H2'	48:L1:425:G:C8	2.53	0.43
48:L1:927:C:H2'	48:L1:928:C:H6	1.83	0.43
48:L1:942:U:H4'	48:L1:945:G:C2	2.53	0.43
48:L1:1261:A:OP2	48:L1:1262:C:N4	2.49	0.43
48:L1:1271:U:H2'	48:L1:1272:G:H8	1.83	0.43
49:L2:120:G:H2'	49:L2:121:C:H6	1.82	0.43
11:LE:100:ARG:HG3	48:L1:491:C:H5''	2.01	0.43
22:LQ:185:HIS:H	22:LQ:213:VAL:CG1	2.32	0.43
24:LS:90:MET:HB2	48:L1:1195:A:H4'	2.01	0.43
31:La:114:GLY:O	31:La:137:LYS:NZ	2.41	0.43
38:Lh:36:ILE:HG23	38:Lh:37:GLN:N	2.33	0.43
38:Lh:81:LEU:HD12	38:Lh:81:LEU:C	2.43	0.43
48:L1:118:U:O2'	48:L1:120:U:OP2	2.29	0.43
48:L1:1111:U:H2'	48:L1:1112:A:O4'	2.18	0.43
48:L1:1140:G:H2'	48:L1:1141:A:O4'	2.19	0.43
48:L1:2619:G:OP1	48:L1:2709:U:O2'	2.37	0.43
48:L1:2620:G:H2'	48:L1:2621:G:C8	2.52	0.43
48:L1:2885:A:H2'	48:L1:2886:C:C6	2.54	0.43
48:L1:3184:C:H2'	48:L1:3188:G:H21	1.82	0.43
3:3:56:LYS:HB2	3:3:56:LYS:HE3	1.84	0.43
4:4:348:SER:O	4:4:351:PRO:HD2	2.18	0.43
10:LD:17:GLN:HE22	25:LT:22:HIS:H	1.65	0.43
17:LL:129:LYS:HE3	17:LL:132:LYS:HD2	2.01	0.43
20:LO:63:THR:HG22	20:LO:66:ASN:H	1.83	0.43
47:Lq:96:SER:HA	47:Lq:100:LYS:HG2	2.00	0.43
48:L1:586:G:N2	48:L1:597:G:OP1	2.48	0.43
48:L1:2636:G:H2'	48:L1:2636:G:N3	2.33	0.43
48:L1:3121:G:H4'	48:L1:3122:U:OP1	2.18	0.43
4:4:254:CYS:HG	4:4:310:GLU:CD	2.26	0.43
5:6:85:THR:HG23	5:6:88:ALA:H	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:LD:41:LYS:HB2	25:LT:68:THR:O	2.19	0.43
11:LE:38:LYS:HA	11:LE:38:LYS:HD3	1.66	0.43
22:LQ:36:TRP:HB3	22:LQ:39:VAL:HG21	2.01	0.43
22:LQ:64:LEU:O	22:LQ:68:THR:OG1	2.23	0.43
22:LQ:127:GLU:HG3	22:LQ:147:ARG:HB3	2.00	0.43
34:Ld:108:ASN:HA	34:Ld:109:PRO:HD3	1.84	0.43
39:Li:42:GLN:HG2	48:L1:290:A:O2'	2.18	0.43
48:L1:138:C:H2'	48:L1:139:G:O4'	2.19	0.43
48:L1:405:G:H2'	48:L1:406:U:C6	2.53	0.43
48:L1:1668:U:H2'	48:L1:1669:U:C6	2.54	0.43
15:LI:170:ASN:HA	15:LI:177:ARG:HA	2.01	0.43
18:LM:42:ASP:HB3	18:LM:54:ARG:HA	2.01	0.43
20:LO:66:ASN:ND2	48:L1:2947:C:OP1	2.34	0.43
26:LU:89:LYS:NZ	48:L1:1666:U:O4	2.36	0.43
33:Lc:37:LEU:HD13	33:Lc:62:TYR:HB3	1.99	0.43
35:Le:56:ILE:HD12	35:Le:56:ILE:HA	1.91	0.43
48:L1:374:U:H2'	48:L1:375:U:C6	2.54	0.43
48:L1:444:G:H2'	48:L1:445:G:C8	2.53	0.43
48:L1:955:G:H2'	48:L1:956:U:O4'	2.19	0.43
48:L1:1522:A:N7	48:L1:1536:U:C2	2.87	0.43
48:L1:2618:G:H4'	48:L1:2710:G:O2'	2.19	0.43
48:L1:3052:A:H2'	48:L1:3053:U:C6	2.54	0.43
19:LN:46:ASP:OD1	19:LN:46:ASP:N	2.51	0.43
20:LO:76:ARG:NH2	48:L1:3092:A:OP1	2.51	0.43
30:LZ:91:LEU:HD22	30:LZ:113:VAL:HG22	2.00	0.43
37:Lg:15:ASN:O	48:L1:809:G:H5''	2.18	0.43
48:L1:225:A:H2'	48:L1:226:G:O4'	2.17	0.43
48:L1:282:U:H2'	48:L1:283:G:C8	2.52	0.43
48:L1:497:U:H2'	48:L1:498:U:O4'	2.19	0.43
48:L1:1173:A:H2'	48:L1:1173:A:N3	2.34	0.43
48:L1:1207:C:C2	48:L1:1208:A:C8	3.06	0.43
48:L1:2194:C:O2'	48:L1:2195:A:O5'	2.25	0.43
48:L1:2909:G:OP2	48:L1:2909:G:N2	2.44	0.43
48:L1:3030:C:H2'	48:L1:3031:G:O4'	2.18	0.43
4:4:282:VAL:HG11	4:4:290:THR:HG23	2.01	0.43
13:LG:116:ALA:O	13:LG:119:ILE:HD12	2.19	0.43
16:LJ:137:GLU:O	16:LJ:137:GLU:HG3	2.19	0.43
19:LN:16:SER:O	19:LN:20:ARG:HB2	2.19	0.43
40:Lj:84:LYS:HE2	40:Lj:84:LYS:HB2	1.60	0.43
46:Lp:49:ARG:HB2	46:Lp:55:TRP:CZ3	2.53	0.43
48:L1:1229:G:N2	48:L1:1247:C:HO2'	2.15	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:52:TYR:CD2	1:1:53:GLY:N	2.87	0.43
4:4:208:ARG:NH1	4:4:257:LYS:HZ1	2.14	0.43
16:LJ:22:ILE:HG13	16:LJ:38:LEU:HD11	2.00	0.43
37:Lg:16:THR:O	37:Lg:18:SER:N	2.52	0.43
48:L1:2275:A:OP1	48:L1:2277:U:H5	2.02	0.43
48:L1:2799:C:H2'	48:L1:2800:G:O4'	2.19	0.43
48:L1:3230:G:H2'	48:L1:3231:G:C8	2.53	0.43
48:L1:3266:A:H2'	48:L1:3267:G:C8	2.54	0.43
49:L2:40:A:H2'	49:L2:41:A:C8	2.54	0.43
1:1:24:GLU:OE2	4:4:406:LYS:HE2	2.19	0.42
7:LA:115:ASN:OD1	7:LA:128:ARG:CD	2.66	0.42
8:LB:219:ILE:HG12	8:LB:277:THR:HG23	2.01	0.42
14:LH:194:SER:OG	48:L1:3068:C:O2'	2.36	0.42
22:LQ:203:ARG:H	22:LQ:209:ARG:CB	2.32	0.42
38:Lh:9:ALA:HB2	38:Lh:58:ARG:HD2	2.00	0.42
44:Ln:2:ARG:HD3	44:Ln:5:TRP:NE1	2.34	0.42
48:L1:301:A:H1'	48:L1:2185:A:N3	2.34	0.42
48:L1:1561:G:H1'	48:L1:1562:U:H2'	2.01	0.42
48:L1:2115:A:H2'	48:L1:2116:U:H6	1.84	0.42
5:6:189:LYS:O	5:6:190:GLU:C	2.62	0.42
10:LD:208:ALA:HB2	10:LD:239:LEU:HD12	2.00	0.42
34:Ld:83:ILE:CG2	34:Ld:101:VAL:HG12	2.42	0.42
48:L1:532:U:H2'	48:L1:533:C:C6	2.53	0.42
48:L1:644:A:H2'	48:L1:645:A:H8	1.81	0.42
48:L1:1738:A:H2'	48:L1:1739:C:C6	2.54	0.42
48:L1:2489:C:H2'	48:L1:2490:G:H8	1.83	0.42
4:4:264:ASP:N	4:4:264:ASP:OD1	2.52	0.42
13:LG:29:LEU:HD23	13:LG:29:LEU:H	1.84	0.42
22:LQ:110:VAL:HG22	22:LQ:167:LEU:HB2	2.01	0.42
23:LR:21:LYS:NZ	48:L1:1854:G:OP2	2.35	0.42
38:Lh:113:LEU:HD12	38:Lh:113:LEU:HA	1.82	0.42
41:Lk:7:ASP:OD1	41:Lk:10:LYS:HD2	2.20	0.42
42:Ll:15:LYS:O	42:Ll:19:GLN:HG3	2.18	0.42
48:L1:828:A:H4'	48:L1:829:A:OP1	2.19	0.42
48:L1:1199:C:H2'	48:L1:1200:A:C8	2.49	0.42
50:L3:69:G:H2'	50:L3:70:G:H8	1.84	0.42
1:1:43:PHE:HD1	1:1:78:MET:CE	2.26	0.42
11:LE:35:GLN:O	48:L1:582:G:O2'	2.35	0.42
28:LX:120:THR:HG21	28:LX:137:ALA:HB1	2.01	0.42
48:L1:447:U:H1'	48:L1:448:C:H5'	2.00	0.42
48:L1:617:C:H2'	48:L1:618:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:L1:703:A:N1	48:L1:763:G:O2'	2.50	0.42
48:L1:1376:A:N6	48:L1:1400:G:H1'	2.34	0.42
48:L1:3221:A:O2'	48:L1:3222:C:H6	2.01	0.42
48:L1:3237:A:H2'	48:L1:3238:U:H6	1.85	0.42
8:LB:79:ILE:HB	8:LB:323:VAL:HG22	2.00	0.42
13:LG:159:ASP:OD1	13:LG:159:ASP:N	2.52	0.42
26:LU:81:ARG:O	26:LU:82:TYR:C	2.58	0.42
28:LX:58:LYS:HE2	28:LX:58:LYS:HB3	1.67	0.42
31:La:96:LYS:HB2	31:La:96:LYS:HE2	1.77	0.42
42:Ll:9:ILE:O	42:Ll:13:LEU:HG	2.19	0.42
48:L1:317:A:H2'	48:L1:318:A:C8	2.54	0.42
48:L1:1373:A:N6	48:L1:1401:A:O2'	2.52	0.42
48:L1:1740:A:H2	48:L1:1745:U:C4	2.37	0.42
48:L1:2771:C:H2'	48:L1:2772:A:H8	1.85	0.42
48:L1:2991:A:H2'	48:L1:2992:C:H6	1.84	0.42
48:L1:3108:A:H2'	48:L1:3109:U:O4'	2.20	0.42
8:LB:95:THR:HB	8:LB:98:GLY:O	2.20	0.42
8:LB:316:GLY:HA2	48:L1:3320:C:H4'	2.00	0.42
16:LJ:33:ARG:O	16:LJ:37:VAL:HG12	2.19	0.42
16:LJ:54:THR:HA	16:LJ:61:ARG:HA	2.01	0.42
17:LL:141:ASP:HB2	17:LL:142:GLN:OE1	2.20	0.42
27:LV:139:MET:HE3	27:LV:139:MET:HB3	1.76	0.42
38:Lh:36:ILE:O	38:Lh:39:ILE:CG1	2.63	0.42
42:Ll:30:ARG:HG2	49:L2:75:G:C8	2.55	0.42
47:Lq:7:ASP:OD1	47:Lq:41:ARG:NH2	2.52	0.42
48:L1:816:U:H2'	48:L1:817:G:O4'	2.20	0.42
48:L1:1333:A:O2'	48:L1:1335:A:OP1	2.38	0.42
48:L1:1875:A:HO2'	48:L1:3011:G:H4'	1.84	0.42
48:L1:2704:G:N7	48:L1:2706:A:H5''	2.35	0.42
50:L3:69:G:H2'	50:L3:70:G:C8	2.55	0.42
8:LB:57:VAL:HG22	8:LB:73:VAL:HG22	2.02	0.42
13:LG:78:ILE:CD1	19:LN:18:VAL:HG13	2.49	0.42
14:LH:142:LYS:HE3	14:LH:147:GLY:HA2	2.01	0.42
16:LJ:20:LEU:HA	16:LJ:127:ASP:O	2.20	0.42
20:LO:52:LYS:HB3	20:LO:52:LYS:HE3	1.95	0.42
22:LQ:188:LYS:HA	22:LQ:188:LYS:HD2	1.84	0.42
48:L1:179:C:H2'	48:L1:180:U:C6	2.55	0.42
48:L1:390:A:H4'	48:L1:391:U:H3'	2.00	0.42
48:L1:855:C:H5''	48:L1:856:U:O5'	2.20	0.42
48:L1:1334:A:H5''	48:L1:1335:A:H2	1.84	0.42
48:L1:2064:C:HO2'	48:L1:2065:U:P	2.41	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:L1:3191:G:H2'	48:L1:3192:C:C2	2.54	0.42
1:1:20:VAL:HG22	1:1:169:GLU:HG2	2.02	0.42
4:4:254:CYS:SG	4:4:310:GLU:CD	3.03	0.42
13:LG:160:VAL:O	13:LG:161:ASP:C	2.63	0.42
14:LH:183:LEU:HD12	14:LH:183:LEU:HA	1.88	0.42
16:LJ:112:ASP:OD1	16:LJ:112:ASP:N	2.52	0.42
21:LP:41:LEU:HD21	21:LP:99:GLU:HG3	2.01	0.42
46:Lp:16:THR:HG22	48:L1:1907:G:C8	2.55	0.42
48:L1:165:G:C6	48:L1:242:G:C5	3.08	0.42
48:L1:300:A:H2'	48:L1:301:A:H8	1.81	0.42
48:L1:1804:C:C2	48:L1:1805:G:C8	3.08	0.42
48:L1:2882:U:H2'	48:L1:2883:U:C6	2.55	0.42
48:L1:2948:U:H2'	48:L1:2949:G:O4'	2.20	0.42
50:L3:90:G:H2'	50:L3:91:A:C8	2.55	0.42
4:4:328:THR:HG23	4:4:328:THR:O	2.20	0.42
4:4:358:ARG:HG3	4:4:358:ARG:HH11	1.84	0.42
9:LC:59:HIS:NE2	9:LC:99:ARG:HD3	2.35	0.42
17:LL:122:ARG:O	38:Lh:124:LYS:HG2	2.20	0.42
19:LN:99:ARG:O	19:LN:103:GLU:HG3	2.19	0.42
22:LQ:84:ARG:NH1	48:L1:662:G:O6	2.49	0.42
40:Lj:3:LYS:HB3	48:L1:2101:A:C4	2.54	0.42
48:L1:404:U:H2'	48:L1:405:G:C8	2.55	0.42
48:L1:484:A:O2'	48:L1:485:G:OP1	2.32	0.42
48:L1:1576:C:H2'	48:L1:1577:C:H6	1.82	0.42
48:L1:1674:U:O2'	48:L1:1675:U:H5'	2.20	0.42
48:L1:1737:G:H2'	48:L1:1738:A:C8	2.55	0.42
48:L1:2228:C:H2'	48:L1:2229:U:C6	2.55	0.42
4:4:269:TYR:HA	5:6:181:GLU:HG2	2.02	0.42
5:6:140:ILE:HG13	5:6:141:HIS:N	2.34	0.42
8:LB:164:HIS:HA	8:LB:178:HIS:O	2.20	0.42
9:LC:56:LYS:NZ	40:Lj:51:GLU:CD	2.78	0.42
10:LD:285:GLU:CD	10:LD:285:GLU:H	2.27	0.42
14:LH:133:HIS:CG	48:L1:2982:A:H5'	2.55	0.42
22:LQ:205:ARG:NH2	48:L1:762:A:N7	2.67	0.42
48:L1:1062:A:H2'	48:L1:1063:A:O4'	2.20	0.42
50:L3:50:U:C2	50:L3:51:A:C8	3.08	0.42
7:LA:9:ARG:HD2	48:L1:893:C:OP2	2.20	0.41
7:LA:243:THR:HB	48:L1:2207:A:H5''	2.01	0.41
13:LG:115:GLU:O	13:LG:119:ILE:HG13	2.20	0.41
17:LL:112:ASN:HD22	17:LL:112:ASN:HA	1.65	0.41
17:LL:170:LYS:C	17:LL:172:GLU:H	2.27	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:LP:126:ARG:HA	21:LP:140:MET:SD	2.60	0.41
26:LU:99:TRP:HD1	26:LU:116:ASN:HB3	1.85	0.41
32:Lb:37:PRO:O	32:Lb:41:ARG:HG3	2.20	0.41
38:Lh:33:GLN:HA	38:Lh:36:ILE:HG21	1.99	0.41
38:Lh:45:LYS:O	38:Lh:48:LYS:N	2.53	0.41
48:L1:306:U:H2'	48:L1:307:U:C6	2.54	0.41
48:L1:1660:G:H2'	48:L1:1661:U:H6	1.84	0.41
4:4:111:ALA:HB3	4:4:112:PRO:HD3	2.02	0.41
7:LA:171:GLY:O	46:Lp:68:ALA:HB2	2.20	0.41
9:LC:10:PHE:CZ	9:LC:147:PRO:HB2	2.56	0.41
10:LD:34:LYS:HE3	25:LT:30:TYR:CE1	2.55	0.41
10:LD:208:ALA:HB1	10:LD:236:ALA:HB1	2.02	0.41
16:LJ:95:ARG:NE	48:L1:2632:A:OP1	2.41	0.41
16:LJ:99:GLU:OE1	16:LJ:99:GLU:N	2.53	0.41
48:L1:1660:G:H2'	48:L1:1661:U:C6	2.55	0.41
48:L1:1737:G:H2'	48:L1:1738:A:H8	1.84	0.41
48:L1:3289:G:H2'	48:L1:3290:C:C6	2.55	0.41
4:4:389:GLN:HG3	4:4:389:GLN:H	1.70	0.41
4:4:415:GLU:HA	4:4:418:GLN:HE21	1.85	0.41
7:LA:177:LYS:HB3	46:Lp:29:GLN:HG3	2.01	0.41
8:LB:106:TRP:HB2	8:LB:133:TYR:CE1	2.55	0.41
30:LZ:64:ARG:HH22	48:L1:1789:A:P	2.43	0.41
30:LZ:71:ILE:HG23	30:LZ:95:ILE:HD13	2.00	0.41
31:La:26:ARG:NH1	48:L1:920:C:OP2	2.54	0.41
48:L1:168:C:H2'	48:L1:169:G:O4'	2.20	0.41
48:L1:203:A:H4'	48:L1:205:A:N7	2.35	0.41
48:L1:250:C:HO2'	48:L1:251:U:P	2.43	0.41
48:L1:286:C:H2'	48:L1:287:A:O4'	2.20	0.41
48:L1:293:G:H2'	48:L1:294:G:C8	2.54	0.41
48:L1:619:A:H2'	48:L1:620:G:C8	2.55	0.41
48:L1:934:A:H4'	48:L1:950:G:N2	2.34	0.41
48:L1:1239:G:H2'	48:L1:1239:G:N3	2.35	0.41
48:L1:1486:A:C4	48:L1:1487:A:C8	3.08	0.41
48:L1:2889:A:H2'	48:L1:2890:C:C6	2.56	0.41
48:L1:3240:C:C2	48:L1:3241:U:C5	3.08	0.41
1:1:47:SER:HA	1:1:78:MET:CG	2.50	0.41
4:4:354:GLU:HA	4:4:357:LEU:HD12	2.01	0.41
15:LI:12:CYS:SG	15:LI:128:ARG:CD	3.08	0.41
20:LO:159:GLU:HA	20:LO:162:ARG:HG2	2.01	0.41
22:LQ:202:ALA:HB2	31:La:56:VAL:CG2	2.47	0.41
30:LZ:17:TYR:CE1	30:LZ:46:GLU:HG3	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Lf:59:LYS:HD2	48:L1:426:A:OP1	2.19	0.41
45:Lo:63:LYS:NZ	48:L1:2719:C:N3	2.68	0.41
48:L1:64:A:N3	48:L1:79:U:O2'	2.43	0.41
48:L1:102:G:H2'	48:L1:103:C:O4'	2.20	0.41
48:L1:235:C:H2'	48:L1:236:A:O4'	2.20	0.41
48:L1:950:G:H2'	48:L1:951:C:C6	2.55	0.41
48:L1:1481:A:H2'	48:L1:1482:U:C6	2.55	0.41
48:L1:1802:C:H2'	48:L1:1803:A:H8	1.84	0.41
48:L1:1921:C:H2'	48:L1:1922:U:C6	2.56	0.41
48:L1:2281:U:H2'	48:L1:2282:U:O4'	2.20	0.41
48:L1:3232:A:H2'	48:L1:3233:U:C6	2.55	0.41
1:1:63:LEU:O	1:1:67:ARG:HG3	2.21	0.41
4:4:298:LEU:HD23	4:4:355:TYR:CD1	2.55	0.41
7:LA:50:HIS:HE1	48:L1:1775:U:OP2	2.03	0.41
7:LA:231:GLN:HG2	48:L1:2127:A:OP2	2.20	0.41
17:LL:142:GLN:H	17:LL:142:GLN:CD	2.28	0.41
17:LL:189:ARG:HE	48:L1:700:G:H5'	1.85	0.41
21:LP:97:ASN:ND2	48:L1:381:G:O2'	2.53	0.41
23:LR:68:LEU:O	23:LR:72:ILE:HG12	2.20	0.41
45:Lo:72:LEU:HD11	45:Lo:83:LEU:HD12	2.02	0.41
48:L1:66:A:H1'	48:L1:78:A:H1'	2.02	0.41
48:L1:696:G:N2	48:L1:699:A:OP2	2.50	0.41
48:L1:1889:A:H2'	48:L1:1890:A:C8	2.54	0.41
48:L1:2080:A:O2'	48:L1:3038:G:O2'	2.32	0.41
48:L1:2324:A:H2'	48:L1:2325:C:H6	1.85	0.41
48:L1:3236:A:H2'	48:L1:3237:A:C8	2.56	0.41
49:L2:39:G:H1'	49:L2:104:A:N6	2.36	0.41
1:1:401:MET:HB3	1:1:401:MET:HE3	1.82	0.41
5:6:159:GLY:HA3	5:6:163:GLY:HA3	2.02	0.41
7:LA:180:LEU:HD22	46:Lp:26:VAL:HG21	2.03	0.41
14:LH:1:MET:HE3	24:LS:139:TYR:HA	2.03	0.41
15:LI:50:VAL:HG12	15:LI:167:VAL:HG22	2.01	0.41
20:LO:135:ARG:HG3	48:L1:1299:C:OP1	2.20	0.41
33:Lc:45:ILE:HG12	33:Lc:70:VAL:HG22	2.03	0.41
38:Lh:44:ALA:C	38:Lh:46:LEU:H	2.28	0.41
48:L1:540:G:H2'	48:L1:541:A:H8	1.85	0.41
48:L1:1052:C:H2'	48:L1:1053:U:C6	2.56	0.41
48:L1:1300:A:O2'	48:L1:1301:A:H3'	2.21	0.41
48:L1:1426:G:H2'	48:L1:1427:G:C8	2.55	0.41
48:L1:2483:A:H2'	48:L1:2484:U:C6	2.55	0.41
48:L1:3275:U:H4'	48:L1:3276:A:H5'	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:251:ILE:HD13	1:1:251:ILE:HA	1.89	0.41
1:1:274:GLN:NE2	1:1:277:ALA:HB2	2.34	0.41
11:LE:118:LYS:HA	11:LE:121:GLU:HG2	2.02	0.41
12:LF:27:LYS:HD2	12:LF:27:LYS:O	2.20	0.41
14:LH:216:ASP:N	14:LH:216:ASP:OD1	2.53	0.41
26:LU:44:ASN:OD1	26:LU:62:ILE:HD11	2.21	0.41
28:LX:38:LYS:H	28:LX:38:LYS:HG2	1.71	0.41
29:LY:15:ARG:NH1	49:L2:23:U:OP1	2.53	0.41
47:Lq:136:ALA:HA	47:Lq:139:ARG:HH11	1.84	0.41
48:L1:256:C:H2'	48:L1:257:G:O4'	2.21	0.41
48:L1:1628:A:H3'	48:L1:1629:C:H6	1.85	0.41
48:L1:1764:U:H2'	48:L1:1765:C:C6	2.55	0.41
48:L1:3307:G:H2'	48:L1:3308:C:C6	2.55	0.41
1:1:239:GLN:O	1:1:240:ASN:ND2	2.54	0.41
3:3:25:ARG:HH12	28:LX:156:VAL:CG2	2.26	0.41
4:4:310:GLU:HG2	4:4:337:LYS:CD	2.48	0.41
12:LF:145:PRO:HA	12:LF:242:ASN:HD21	1.86	0.41
14:LH:156:PHE:O	14:LH:157:ILE:HG12	2.20	0.41
22:LQ:90:VAL:O	22:LQ:114:VAL:HA	2.21	0.41
31:La:85:ASP:N	31:La:85:ASP:OD1	2.53	0.41
32:Lb:55:LYS:NZ	32:Lb:55:LYS:HB3	2.35	0.41
48:L1:1262:C:H2'	48:L1:1263:C:C6	2.55	0.41
48:L1:1596:U:H2'	48:L1:1597:G:C8	2.56	0.41
48:L1:3273:U:H2'	48:L1:3274:G:O4'	2.21	0.41
1:1:41:LEU:HD23	1:1:41:LEU:HA	1.87	0.41
1:1:171:LEU:HD22	1:1:176:GLY:HA3	2.03	0.41
1:1:294:MET:HB3	1:1:294:MET:HE3	1.79	0.41
4:4:118:ALA:HB3	4:4:167:GLY:HA3	2.02	0.41
4:4:242:TYR:CE1	4:4:332:LYS:HD3	2.56	0.41
5:6:142:LEU:HD12	5:6:142:LEU:HA	1.91	0.41
8:LB:69:LYS:HZ2	8:LB:69:LYS:HG2	1.82	0.41
8:LB:303:LYS:NZ	8:LB:303:LYS:HB3	2.36	0.41
11:LE:87:PHE:CZ	48:L1:3208:U:H2'	2.55	0.41
13:LG:67:ILE:O	13:LG:71:ARG:HG2	2.20	0.41
13:LG:99:LYS:NZ	13:LG:213:GLU:OE1	2.50	0.41
14:LH:54:LYS:HB2	18:LM:3:GLU:HG2	2.02	0.41
16:LJ:168:PHE:N	16:LJ:168:PHE:CD1	2.88	0.41
17:LL:66:ASN:OD1	48:L1:73:C:O2'	2.38	0.41
31:La:34:MET:HB3	31:La:34:MET:HE3	1.83	0.41
31:La:75:ILE:HG12	31:La:114:GLY:HA2	2.03	0.41
46:Lp:8:VAL:HG12	46:Lp:12:GLY:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:L1:363:U:H4'	48:L1:397:G:H5'	2.03	0.41
48:L1:364:G:H4'	48:L1:389:A:N1	2.36	0.41
48:L1:657:U:H2'	48:L1:658:U:H6	1.85	0.41
48:L1:686:C:H2'	48:L1:687:A:O4'	2.21	0.41
48:L1:853:U:H2'	48:L1:854:U:C6	2.56	0.41
48:L1:2092:U:H2'	48:L1:2093:G:H8	1.85	0.41
48:L1:2245:U:O2	48:L1:2273:U:H4'	2.20	0.41
48:L1:2246:G:O2'	48:L1:2247:C:P	2.79	0.41
48:L1:2648:A:H2'	48:L1:2648:A:N3	2.35	0.41
48:L1:2686:A:OP2	48:L1:2687:G:N2	2.53	0.41
49:L2:93:U:H2'	49:L2:94:C:O4'	2.20	0.41
1:1:3:SER:O	1:1:5:ARG:NH1	2.54	0.41
4:4:106:ILE:HD12	4:4:106:ILE:HA	1.96	0.41
4:4:305:ALA:HB2	4:4:352:ILE:HG12	2.02	0.41
7:LA:47:GLU:CD	7:LA:60:ARG:HD2	2.46	0.41
10:LD:249:GLN:OE1	10:LD:256:ARG:NH1	2.29	0.41
11:LE:148:LYS:NZ	21:LP:187:ALA:O	2.51	0.41
18:LM:58:PRO:HG2	18:LM:61:ARG:HG3	2.02	0.41
20:LO:194:LYS:HE2	20:LO:194:LYS:HB2	1.94	0.41
22:LQ:147:ARG:HH22	22:LQ:157:GLU:CD	2.28	0.41
23:LR:124:TYR:OH	48:L1:1701:U:OP2	2.37	0.41
30:LZ:5:LYS:O	30:LZ:8:ARG:HB3	2.21	0.41
39:Li:14:THR:HG23	39:Li:21:ASN:HB2	2.02	0.41
48:L1:65:G:H22	48:L1:316:A:H2	1.69	0.41
48:L1:264:C:H2'	48:L1:265:G:O4'	2.21	0.41
48:L1:1442:U:H2'	48:L1:1443:C:C6	2.56	0.41
48:L1:1546:G:H2'	48:L1:1547:C:H6	1.86	0.41
48:L1:1738:A:H2'	48:L1:1739:C:H6	1.86	0.41
48:L1:2217:U:H2'	48:L1:2224:G:N2	2.36	0.41
48:L1:2659:G:H2'	48:L1:2660:U:C6	2.56	0.41
1:1:411:LYS:HB3	1:1:411:LYS:HE3	1.80	0.40
7:LA:115:ASN:OD1	7:LA:128:ARG:HD2	2.21	0.40
8:LB:47:MET:HB3	8:LB:336:ILE:HD11	2.03	0.40
8:LB:314:ARG:CZ	48:L1:3318:G:H21	2.34	0.40
9:LC:324:GLN:NE2	48:L1:589:C:H1'	2.36	0.40
10:LD:4:HIS:ND1	10:LD:4:HIS:N	2.68	0.40
15:LI:208:GLU:OE2	15:LI:212:ARG:NE	2.54	0.40
16:LJ:39:GLU:HG2	16:LJ:45:THR:HA	2.02	0.40
31:La:118:LEU:HD12	31:La:118:LEU:HA	1.97	0.40
48:L1:140:C:H2'	48:L1:141:G:O4'	2.21	0.40
48:L1:1309:A:H2'	48:L1:1310:C:O4'	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:L1:2064:C:H2'	48:L1:2065:U:H6	1.85	0.40
48:L1:2069:A:H2'	48:L1:2070:A:C8	2.56	0.40
48:L1:2538:G:OP2	48:L1:2539:A:O2'	2.35	0.40
48:L1:3163:A:H4'	48:L1:3164:G:O5'	2.20	0.40
50:L3:60:A:H2'	50:L3:61:C:C6	2.57	0.40
1:1:260:LEU:HB3	1:1:286:PHE:CZ	2.56	0.40
3:3:17:LYS:O	3:3:21:GLN:HG3	2.22	0.40
5:6:130:LYS:HD2	5:6:130:LYS:HA	1.65	0.40
8:LB:89:LEU:HD21	8:LB:196:GLY:HA3	2.03	0.40
11:LE:100:ARG:HD3	11:LE:100:ARG:HA	1.95	0.40
13:LG:116:ALA:HA	13:LG:119:ILE:HD11	2.02	0.40
18:LM:5:ASN:HD22	18:LM:5:ASN:N	2.18	0.40
30:LZ:6:THR:O	30:LZ:7:SER:HB2	2.22	0.40
33:Lc:21:ILE:CD1	33:Lc:84:CYS:HA	2.51	0.40
36:Lf:2:PRO:HD3	48:L1:3199:U:H4'	2.03	0.40
38:Lh:99:LYS:C	38:Lh:99:LYS:HD3	2.46	0.40
48:L1:68:A:N1	48:L1:293:G:O2'	2.50	0.40
48:L1:564:A:O2'	48:L1:565:C:H6	2.05	0.40
48:L1:2188:U:H2'	48:L1:2189:U:C6	2.56	0.40
48:L1:2352:C:H2'	48:L1:2353:A:H8	1.86	0.40
48:L1:2521:A:O2'	48:L1:2522:A:O5'	2.37	0.40
48:L1:2553:C:H2'	48:L1:2554:A:O4'	2.21	0.40
48:L1:2568:A:H2'	48:L1:2569:G:C8	2.55	0.40
48:L1:3115:C:C2	48:L1:3231:G:C2	3.10	0.40
3:3:61:PRO:HA	3:3:64:ASN:HD22	1.87	0.40
4:4:76:SER:O	4:4:79:ILE:HG13	2.21	0.40
5:6:40:ALA:O	5:6:44:ILE:HG12	2.21	0.40
5:6:189:LYS:HG3	5:6:191:GLU:HG2	2.04	0.40
15:LI:114:GLY:HA2	48:L1:2823:A:H5''	2.03	0.40
16:LJ:111:ILE:HG23	16:LJ:123:ILE:CD1	2.49	0.40
16:LJ:168:PHE:N	16:LJ:168:PHE:HD1	2.20	0.40
17:LL:36:ARG:NH1	48:L1:675:U:OP2	2.32	0.40
33:Lc:64:MET:HE3	33:Lc:64:MET:HB3	1.86	0.40
37:Lg:102:VAL:HA	37:Lg:105:VAL:CG1	2.49	0.40
48:L1:124:A:C6	48:L1:146:A:C5	3.10	0.40
48:L1:169:G:H1'	48:L1:238:G:N2	2.36	0.40
48:L1:855:C:H3'	48:L1:856:U:H4'	2.03	0.40
48:L1:2268:G:OP2	48:L1:2268:G:N2	2.37	0.40
48:L1:2570:U:H2'	48:L1:2571:U:H6	1.86	0.40
48:L1:2956:U:H2'	48:L1:2957:C:H6	1.86	0.40
1:1:303:ILE:O	1:1:306:ILE:HG22	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:LD:181:ASN:ND2	10:LD:181:ASN:H	2.19	0.40
13:LG:95:LYS:HB2	13:LG:95:LYS:HE2	1.88	0.40
15:LI:12:CYS:SG	15:LI:59:GLN:HG2	2.61	0.40
16:LJ:60:ILE:HD13	16:LJ:66:ILE:HG21	2.03	0.40
28:LX:124:ASN:ND2	48:L1:1506:U:O2'	2.48	0.40
39:Li:39:LYS:HZ2	48:L1:309:U:HO2'	1.61	0.40
41:Lk:57:LYS:O	41:Lk:60:GLN:HG3	2.21	0.40
46:Lp:85:ARG:O	46:Lp:89:ILE:HG23	2.21	0.40
48:L1:514:A:N6	48:L1:562:A:N7	2.69	0.40
48:L1:1129:C:H4'	48:L1:1314:U:C4	2.56	0.40
48:L1:2498:A:O2'	48:L1:2499:C:H6	2.03	0.40
48:L1:2969:A:N1	48:L1:3001:C:O2'	2.48	0.40
48:L1:3278:G:H2'	48:L1:3279:C:C6	2.56	0.40
7:LA:49:ILE:HD13	7:LA:60:ARG:HE	1.87	0.40
13:LG:186:LYS:CG	13:LG:197:THR:HB	2.45	0.40
17:LL:19:GLN:HA	17:LL:22:VAL:HG23	2.03	0.40
17:LL:67:ARG:HD2	31:La:105:LEU:O	2.22	0.40
20:LO:116:LYS:HA	48:L1:3134:A:N9	2.35	0.40
26:LU:20:LYS:HG3	26:LU:71:GLU:OE2	2.22	0.40
29:LY:100:PRO:O	29:LY:103:VAL:HG12	2.21	0.40
30:LZ:17:TYR:HE1	30:LZ:46:GLU:HG3	1.86	0.40
36:Lf:18:TYR:OH	36:Lf:93:ALA:HB2	2.21	0.40
48:L1:81:G:H2'	48:L1:82:C:H6	1.85	0.40
48:L1:146:A:C4	48:L1:147:A:C8	3.10	0.40
48:L1:338:G:O2'	49:L2:25:G:N3	2.55	0.40
48:L1:615:C:H2'	48:L1:616:A:C8	2.57	0.40
48:L1:2643:C:H2'	48:L1:2644:C:C6	2.57	0.40
48:L1:3247:G:O2'	48:L1:3249:C:OP2	2.35	0.40
50:L3:72:G:HO2'	50:L3:73:U:P	2.44	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	460/476 (97%)	444 (96%)	16 (4%)	0	100	100
2	2	96/124 (77%)	95 (99%)	1 (1%)	0	100	100
3	3	63/70 (90%)	63 (100%)	0	0	100	100
4	4	369/455 (81%)	366 (99%)	3 (1%)	0	100	100
5	6	186/224 (83%)	180 (97%)	6 (3%)	0	100	100
6	7	28/278 (10%)	27 (96%)	1 (4%)	0	100	100
7	LA	250/254 (98%)	246 (98%)	4 (2%)	0	100	100
8	LB	385/392 (98%)	377 (98%)	8 (2%)	0	100	100
9	LC	361/365 (99%)	355 (98%)	6 (2%)	0	100	100
10	LD	298/304 (98%)	293 (98%)	5 (2%)	0	100	100
11	LE	178/200 (89%)	172 (97%)	6 (3%)	0	100	100
12	LF	245/249 (98%)	239 (98%)	6 (2%)	0	100	100
13	LG	232/262 (88%)	223 (96%)	9 (4%)	0	100	100
14	LH	189/192 (98%)	185 (98%)	4 (2%)	0	100	100
15	LI	204/219 (93%)	201 (98%)	3 (2%)	0	100	100
16	LJ	165/173 (95%)	161 (98%)	4 (2%)	0	100	100
17	LL	207/213 (97%)	199 (96%)	8 (4%)	0	100	100
18	LM	139/142 (98%)	135 (97%)	4 (3%)	0	100	100
19	LN	200/203 (98%)	193 (96%)	7 (4%)	0	100	100
20	LO	202/204 (99%)	199 (98%)	3 (2%)	0	100	100
21	LP	166/187 (89%)	164 (99%)	2 (1%)	0	100	100
22	LQ	181/213 (85%)	171 (94%)	10 (6%)	0	100	100
23	LR	177/192 (92%)	174 (98%)	3 (2%)	0	100	100
24	LS	171/174 (98%)	168 (98%)	3 (2%)	0	100	100
25	LT	156/160 (98%)	155 (99%)	1 (1%)	0	100	100
26	LU	99/127 (78%)	97 (98%)	2 (2%)	0	100	100
27	LV	130/139 (94%)	129 (99%)	1 (1%)	0	100	100
28	LX	119/156 (76%)	115 (97%)	4 (3%)	0	100	100
29	LY	132/138 (96%)	128 (97%)	4 (3%)	0	100	100
30	LZ	133/135 (98%)	128 (96%)	5 (4%)	0	100	100
31	La	146/149 (98%)	135 (92%)	11 (8%)	0	100	100
32	Lb	60/65 (92%)	59 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	Lc	95/108 (88%)	93 (98%)	2 (2%)	0	100	100
34	Ld	107/120 (89%)	102 (95%)	5 (5%)	0	100	100
35	Le	121/131 (92%)	117 (97%)	4 (3%)	0	100	100
36	Lf	105/109 (96%)	102 (97%)	3 (3%)	0	100	100
37	Lg	110/119 (92%)	105 (96%)	5 (4%)	0	100	100
38	Lh	120/126 (95%)	110 (92%)	10 (8%)	0	100	100
39	Li	99/110 (90%)	96 (97%)	3 (3%)	0	100	100
40	Lj	84/95 (88%)	80 (95%)	4 (5%)	0	100	100
41	Lk	74/81 (91%)	72 (97%)	2 (3%)	0	100	100
42	Ll	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
43	Lm	50/128 (39%)	49 (98%)	1 (2%)	0	100	100
44	Ln	22/25 (88%)	22 (100%)	0	0	100	100
45	Lo	96/106 (91%)	95 (99%)	1 (1%)	0	100	100
46	Lp	89/92 (97%)	87 (98%)	2 (2%)	0	100	100
47	Lq	139/147 (95%)	133 (96%)	6 (4%)	0	100	100
All	All	7486/8382 (89%)	7286 (97%)	200 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	1	391/400 (98%)	389 (100%)	2 (0%)	86	93
2	2	76/93 (82%)	76 (100%)	0	100	100
3	3	57/58 (98%)	57 (100%)	0	100	100
4	4	319/390 (82%)	318 (100%)	1 (0%)	91	96
5	6	158/181 (87%)	156 (99%)	2 (1%)	65	78
6	7	27/222 (12%)	27 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	LA	196/198 (99%)	196 (100%)	0	100	100
8	LB	327/331 (99%)	326 (100%)	1 (0%)	91	96
9	LC	284/285 (100%)	284 (100%)	0	100	100
10	LD	250/253 (99%)	249 (100%)	1 (0%)	89	95
11	LE	151/166 (91%)	150 (99%)	1 (1%)	81	90
12	LF	213/215 (99%)	213 (100%)	0	100	100
13	LG	202/222 (91%)	202 (100%)	0	100	100
14	LH	168/169 (99%)	167 (99%)	1 (1%)	84	91
15	LI	176/183 (96%)	176 (100%)	0	100	100
16	LJ	145/150 (97%)	145 (100%)	0	100	100
17	LL	172/176 (98%)	172 (100%)	0	100	100
18	LM	116/117 (99%)	116 (100%)	0	100	100
19	LN	179/180 (99%)	179 (100%)	0	100	100
20	LO	162/162 (100%)	162 (100%)	0	100	100
21	LP	139/152 (91%)	139 (100%)	0	100	100
22	LQ	155/178 (87%)	154 (99%)	1 (1%)	84	91
23	LR	149/160 (93%)	148 (99%)	1 (1%)	81	90
24	LS	153/154 (99%)	153 (100%)	0	100	100
25	LT	134/135 (99%)	134 (100%)	0	100	100
26	LU	89/108 (82%)	89 (100%)	0	100	100
27	LV	97/102 (95%)	97 (100%)	0	100	100
28	LX	108/129 (84%)	107 (99%)	1 (1%)	75	86
29	LY	117/119 (98%)	117 (100%)	0	100	100
30	LZ	121/121 (100%)	121 (100%)	0	100	100
31	La	121/122 (99%)	120 (99%)	1 (1%)	79	88
32	Lb	53/55 (96%)	53 (100%)	0	100	100
33	Lc	78/88 (89%)	78 (100%)	0	100	100
34	Ld	94/105 (90%)	94 (100%)	0	100	100
35	Le	106/114 (93%)	105 (99%)	1 (1%)	75	86
36	Lf	88/90 (98%)	88 (100%)	0	100	100
37	Lg	97/102 (95%)	97 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	Lh	109/112 (97%)	107 (98%)	2 (2%)	54	69
39	Li	85/93 (91%)	84 (99%)	1 (1%)	67	80
40	Lj	70/78 (90%)	69 (99%)	1 (1%)	62	77
41	Lk	73/77 (95%)	71 (97%)	2 (3%)	40	53
42	Ll	45/46 (98%)	45 (100%)	0	100	100
43	Lm	47/115 (41%)	47 (100%)	0	100	100
44	Ln	22/23 (96%)	22 (100%)	0	100	100
45	Lo	85/90 (94%)	85 (100%)	0	100	100
46	Lp	73/74 (99%)	73 (100%)	0	100	100
47	Lq	109/112 (97%)	109 (100%)	0	100	100
All	All	6386/7005 (91%)	6366 (100%)	20 (0%)	90	96

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	11	LYS
1	1	191	GLU
4	4	76	SER
5	6	157	GLN
5	6	190	GLU
8	LB	333	LYS
10	LD	180	GLU
11	LE	64	ARG
14	LH	216	ASP
22	LQ	200	GLU
23	LR	134	HIS
28	LX	49	LYS
31	La	59	ARG
35	Le	67	MET
38	Lh	17	LYS
38	Lh	113	LEU
39	Li	55	GLU
40	Lj	84	LYS
41	Lk	24	ARG
41	Lk	54	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (134) such sidechains are listed below:

Mol	Chain	Res	Type
1	1	73	ASN
1	1	188	ASN
1	1	240	ASN
1	1	308	GLN
1	1	360	HIS
2	2	63	GLN
3	3	64	ASN
4	4	389	GLN
4	4	414	GLN
4	4	418	GLN
5	6	29	ASN
5	6	42	ASN
5	6	101	GLN
5	6	157	GLN
7	LA	7	ASN
7	LA	8	GLN
7	LA	50	HIS
7	LA	132	ASN
7	LA	187	HIS
7	LA	194	ASN
7	LA	205	ASN
7	LA	215	ASN
7	LA	216	HIS
8	LB	185	ASN
8	LB	257	HIS
8	LB	372	GLN
9	LC	49	GLN
9	LC	60	GLN
9	LC	228	ASN
9	LC	244	GLN
9	LC	250	HIS
9	LC	324	GLN
10	LD	17	GLN
10	LD	39	GLN
10	LD	57	ASN
10	LD	81	HIS
10	LD	89	ASN
10	LD	181	ASN
10	LD	225	GLN
11	LE	25	GLN
11	LE	124	GLN
12	LF	9	GLN
12	LF	64	GLN

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Mol	Chain	Res	Type
12	LF	119	ASN
12	LF	163	ASN
12	LF	206	ASN
12	LF	217	ASN
12	LF	242	ASN
13	LG	62	GLN
13	LG	246	GLN
14	LH	72	GLN
14	LH	133	HIS
14	LH	225	ASN
15	LI	59	GLN
15	LI	73	ASN
15	LI	156	GLN
16	LJ	16	GLN
16	LJ	63	ASN
16	LJ	96	ASN
17	LL	13	HIS
17	LL	17	HIS
17	LL	112	ASN
17	LL	159	GLN
18	LM	5	ASN
18	LM	36	HIS
18	LM	106	GLN
18	LM	110	GLN
19	LN	86	ASN
19	LN	95	GLN
19	LN	175	ASN
19	LN	194	HIS
20	LO	32	GLN
20	LO	43	ASN
20	LO	132	GLN
21	LP	97	ASN
21	LP	118	GLN
21	LP	120	ASN
21	LP	125	GLN
21	LP	137	ASN
21	LP	142	ASN
21	LP	175	GLN
22	LQ	43	HIS
22	LQ	86	ASN
22	LQ	101	ASN
22	LQ	103	ASN

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Mol	Chain	Res	Type
22	LQ	163	ASN
22	LQ	185	HIS
23	LR	3	ASN
23	LR	34	ASN
23	LR	58	HIS
23	LR	134	HIS
23	LR	141	HIS
23	LR	174	GLN
24	LS	62	ASN
25	LT	66	ASN
25	LT	112	ASN
27	LV	76	HIS
27	LV	100	ASN
28	LX	73	HIS
28	LX	78	HIS
28	LX	93	ASN
28	LX	107	GLN
29	LY	56	GLN
29	LY	92	GLN
29	LY	116	ASN
30	LZ	26	GLN
30	LZ	105	GLN
31	La	39	HIS
31	La	60	HIS
31	La	66	ASN
32	Lb	43	HIS
32	Lb	45	HIS
34	Ld	62	GLN
34	Ld	102	GLN
35	Le	21	HIS
35	Le	66	HIS
36	Lf	79	ASN
37	Lg	30	GLN
38	Lh	11	GLN
39	Li	24	HIS
40	Lj	12	HIS
40	Lj	13	ASN
41	Lk	3	GLN
41	Lk	28	ASN
42	Ll	17	GLN
42	Ll	33	ASN
43	Lm	117	HIS

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Mol	Chain	Res	Type
45	Lo	3	ASN
45	Lo	27	GLN
45	Lo	82	GLN
46	Lp	29	GLN
46	Lp	33	GLN
46	Lp	34	HIS
46	Lp	45	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
48	L1	3142/3337 (94%)	532 (16%)	54 (1%)
49	L2	147/156 (94%)	17 (11%)	0
50	L3	118/120 (98%)	8 (6%)	1 (0%)
All	All	3407/3613 (94%)	557 (16%)	55 (1%)

All (557) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
48	L1	7	A
48	L1	9	C
48	L1	15	U
48	L1	16	C
48	L1	27	A
48	L1	41	A
48	L1	44	A
48	L1	50	A
48	L1	60	G
48	L1	61	A
48	L1	66	A
48	L1	67	A
48	L1	93	G
48	L1	97	G
48	L1	110	A
48	L1	111	G
48	L1	112	C
48	L1	117	A
48	L1	118	U
48	L1	123	A
48	L1	132	U
48	L1	133	C

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Mol	Chain	Res	Type
48	L1	134	G
48	L1	135	G
48	L1	152	G
48	L1	153	A
48	L1	156	G
48	L1	157	G
48	L1	158	A
48	L1	170	A
48	L1	174	U
48	L1	181	G
48	L1	184	U
48	L1	185	U
48	L1	212	G
48	L1	213	A
48	L1	214	G
48	L1	215	A
48	L1	225	A
48	L1	232	A
48	L1	234	C
48	L1	251	U
48	L1	262	G
48	L1	277	A
48	L1	279	U
48	L1	288	A
48	L1	298	U
48	L1	316	A
48	L1	322	C
48	L1	330	G
48	L1	332	C
48	L1	343	C
48	L1	369	G
48	L1	391	U
48	L1	392	A
48	L1	394	C
48	L1	395	A
48	L1	396	C
48	L1	414	G
48	L1	415	A
48	L1	422	U
48	L1	430	G
48	L1	431	A
48	L1	434	U

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Mol	Chain	Res	Type
48	L1	437	G
48	L1	448	C
48	L1	449	A
48	L1	460	U
48	L1	461	C
48	L1	471	C
48	L1	472	U
48	L1	485	G
48	L1	512	A
48	L1	514	A
48	L1	515	G
48	L1	516	G
48	L1	519	C
48	L1	520	A
48	L1	527	G
48	L1	536	C
48	L1	537	C
48	L1	538	G
48	L1	539	G
48	L1	545	U
48	L1	547	A
48	L1	549	A
48	L1	556	G
48	L1	558	U
48	L1	559	G
48	L1	561	A
48	L1	564	A
48	L1	565	C
48	L1	566	C
48	L1	583	A
48	L1	586	G
48	L1	587	C
48	L1	588	G
48	L1	589	C
48	L1	591	C
48	L1	592	U
48	L1	593	G
48	L1	597	G
48	L1	599	A
48	L1	608	U
48	L1	609	A
48	L1	610	A

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Mol	Chain	Res	Type
48	L1	613	G
48	L1	624	C
48	L1	625	C
48	L1	637	A
48	L1	648	A
48	L1	659	U
48	L1	665	A
48	L1	669	U
48	L1	700	G
48	L1	703	A
48	L1	713	A
48	L1	719	U
48	L1	720	C
48	L1	722	G
48	L1	723	C
48	L1	724	G
48	L1	740	C
48	L1	741	U
48	L1	742	G
48	L1	749	U
48	L1	751	G
48	L1	756	G
48	L1	757	A
48	L1	758	U
48	L1	759	U
48	L1	763	G
48	L1	767	G
48	L1	768	A
48	L1	781	G
48	L1	788	A
48	L1	799	A
48	L1	812	A
48	L1	826	G
48	L1	828	A
48	L1	829	A
48	L1	830	A
48	L1	831	C
48	L1	832	U
48	L1	834	U
48	L1	839	G
48	L1	840	A
48	L1	843	C

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Mol	Chain	Res	Type
48	L1	856	U
48	L1	861	U
48	L1	878	A
48	L1	889	G
48	L1	896	A
48	L1	898	G
48	L1	899	A
48	L1	903	A
48	L1	905	C
48	L1	906	G
48	L1	919	G
48	L1	926	A
48	L1	935	G
48	L1	941	C
48	L1	942	U
48	L1	962	U
48	L1	964	C
48	L1	984	A
48	L1	991	A
48	L1	992	G
48	L1	996	C
48	L1	997	U
48	L1	998	C
48	L1	1010	U
48	L1	1011	U
48	L1	1012	A
48	L1	1017	U
48	L1	1023	A
48	L1	1024	U
48	L1	1030	A
48	L1	1032	C
48	L1	1047	A
48	L1	1048	A
48	L1	1055	G
48	L1	1062	A
48	L1	1063	A
48	L1	1064	C
48	L1	1065	U
48	L1	1066	G
48	L1	1076	A
48	L1	1077	U
48	L1	1080	G

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Mol	Chain	Res	Type
48	L1	1081	A
48	L1	1086	A
48	L1	1087	U
48	L1	1088	C
48	L1	1090	A
48	L1	1100	G
48	L1	1107	U
48	L1	1114	G
48	L1	1127	U
48	L1	1142	A
48	L1	1143	C
48	L1	1163	G
48	L1	1164	U
48	L1	1165	G
48	L1	1175	C
48	L1	1180	A
48	L1	1184	C
48	L1	1187	A
48	L1	1189	G
48	L1	1191	C
48	L1	1192	G
48	L1	1193	U
48	L1	1201	U
48	L1	1203	U
48	L1	1204	U
48	L1	1214	A
48	L1	1216	G
48	L1	1219	G
48	L1	1220	G
48	L1	1222	C
48	L1	1225	G
48	L1	1228	A
48	L1	1229	G
48	L1	1233	G
48	L1	1240	C
48	L1	1241	U
48	L1	1242	A
48	L1	1243	A
48	L1	1246	A
48	L1	1253	A
48	L1	1254	A
48	L1	1255	C

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Mol	Chain	Res	Type
48	L1	1268	G
48	L1	1290	G
48	L1	1291	A
48	L1	1292	U
48	L1	1313	A
48	L1	1331	A
48	L1	1332	G
48	L1	1333	A
48	L1	1334	A
48	L1	1335	A
48	L1	1336	C
48	L1	1337	G
48	L1	1339	U
48	L1	1370	G
48	L1	1382	A
48	L1	1383	G
48	L1	1402	A
48	L1	1417	G
48	L1	1420	C
48	L1	1429	A
48	L1	1464	A
48	L1	1465	A
48	L1	1466	G
48	L1	1477	U
48	L1	1485	G
48	L1	1491	C
48	L1	1522	A
48	L1	1536	U
48	L1	1539	C
48	L1	1540	A
48	L1	1543	G
48	L1	1545	G
48	L1	1552	G
48	L1	1554	G
48	L1	1555	C
48	L1	1561	G
48	L1	1562	U
48	L1	1563	G
48	L1	1567	A
48	L1	1569	A
48	L1	1576	C
48	L1	1600	U

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Mol	Chain	Res	Type
48	L1	1609	U
48	L1	1610	G
48	L1	1611	C
48	L1	1623	A
48	L1	1624	C
48	L1	1625	U
48	L1	1637	C
48	L1	1685	U
48	L1	1697	C
48	L1	1704	U
48	L1	1709	A
48	L1	1710	G
48	L1	1721	A
48	L1	1730	A
48	L1	1731	G
48	L1	1739	C
48	L1	1743	U
48	L1	1745	U
48	L1	1746	G
48	L1	1750	G
48	L1	1760	G
48	L1	1777	A
48	L1	1781	U
48	L1	1786	G
48	L1	1788	G
48	L1	1790	G
48	L1	1793	A
48	L1	1794	A
48	L1	1797	A
48	L1	1798	U
48	L1	1799	U
48	L1	1820	U
48	L1	1821	A
48	L1	1822	A
48	L1	1826	C
48	L1	1830	A
48	L1	1838	A
48	L1	1846	C
48	L1	1858	G
48	L1	1859	A
48	L1	1860	U
48	L1	1866	A

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Mol	Chain	Res	Type
48	L1	1886	G
48	L1	1905	U
48	L1	1914	G
48	L1	1933	G
48	L1	2063	A
48	L1	2065	U
48	L1	2075	U
48	L1	2076	A
48	L1	2084	G
48	L1	2085	G
48	L1	2094	A
48	L1	2103	U
48	L1	2107	A
48	L1	2121	A
48	L1	2132	G
48	L1	2151	A
48	L1	2170	A
48	L1	2171	A
48	L1	2172	U
48	L1	2173	G
48	L1	2185	A
48	L1	2186	A
48	L1	2192	A
48	L1	2195	A
48	L1	2207	A
48	L1	2212	G
48	L1	2219	A
48	L1	2228	C
48	L1	2235	G
48	L1	2236	G
48	L1	2242	A
48	L1	2244	A
48	L1	2246	G
48	L1	2247	C
48	L1	2248	C
48	L1	2270	G
48	L1	2273	U
48	L1	2276	A
48	L1	2278	G
48	L1	2297	U
48	L1	2298	G
48	L1	2299	U

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Mol	Chain	Res	Type
48	L1	2336	A
48	L1	2337	C
48	L1	2338	G
48	L1	2356	G
48	L1	2357	G
48	L1	2360	A
48	L1	2364	A
48	L1	2365	A
48	L1	2366	G
48	L1	2367	A
48	L1	2374	U
48	L1	2398	G
48	L1	2404	A
48	L1	2474	A
48	L1	2477	U
48	L1	2478	A
48	L1	2487	A
48	L1	2488	G
48	L1	2489	C
48	L1	2492	G
48	L1	2494	C
48	L1	2497	G
48	L1	2499	C
48	L1	2501	U
48	L1	2502	G
48	L1	2504	G
48	L1	2506	C
48	L1	2510	C
48	L1	2512	U
48	L1	2513	C
48	L1	2521	A
48	L1	2522	A
48	L1	2526	C
48	L1	2529	U
48	L1	2536	C
48	L1	2544	G
48	L1	2552	A
48	L1	2565	G
48	L1	2566	G
48	L1	2573	G
48	L1	2578	OMG
48	L1	2585	A

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Mol	Chain	Res	Type
48	L1	2607	G
48	L1	2611	U
48	L1	2615	A
48	L1	2622	G
48	L1	2625	C
48	L1	2631	G
48	L1	2633	A
48	L1	2635	A
48	L1	2636	G
48	L1	2640	U
48	L1	2648	A
48	L1	2650	A
48	L1	2653	A
48	L1	2673	G
48	L1	2679	G
48	L1	2684	U
48	L1	2687	G
48	L1	2688	U
48	L1	2694	U
48	L1	2695	A
48	L1	2698	A
48	L1	2705	A
48	L1	2706	A
48	L1	2707	A
48	L1	2712	G
48	L1	2714	C
48	L1	2721	A
48	L1	2726	U
48	L1	2727	U
48	L1	2732	C
48	L1	2736	G
48	L1	2737	A
48	L1	2755	G
48	L1	2758	A
48	L1	2759	G
48	L1	2760	A
48	L1	2762	A
48	L1	2769	C
48	L1	2776	A
48	L1	2777	U
48	L1	2804	A
48	L1	2815	G

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Mol	Chain	Res	Type
48	L1	2830	G
48	L1	2831	A
48	L1	2846	A
48	L1	2882	U
48	L1	2894	U
48	L1	2895	A
48	L1	2901	C
48	L1	2906	G
48	L1	2910	G
48	L1	2914	U
48	L1	2942	C
48	L1	2949	G
48	L1	2970	A
48	L1	2982	A
48	L1	2988	G
48	L1	3014	U
48	L1	3017	G
48	L1	3036	G
48	L1	3044	A
48	L1	3050	C
48	L1	3051	C
48	L1	3059	G
48	L1	3062	U
48	L1	3067	G
48	L1	3073	C
48	L1	3075	C
48	L1	3080	A
48	L1	3088	A
48	L1	3089	U
48	L1	3100	A
48	L1	3101	C
48	L1	3119	A
48	L1	3122	U
48	L1	3123	U
48	L1	3127	G
48	L1	3128	A
48	L1	3131	U
48	L1	3132	A
48	L1	3134	A
48	L1	3135	A
48	L1	3141	G
48	L1	3146	C

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Mol	Chain	Res	Type
48	L1	3148	G
48	L1	3162	C
48	L1	3163	A
48	L1	3164	G
48	L1	3171	C
48	L1	3172	C
48	L1	3174	C
48	L1	3176	G
48	L1	3178	C
48	L1	3180	G
48	L1	3182	C
48	L1	3183	U
48	L1	3184	C
48	L1	3185	G
48	L1	3188	G
48	L1	3190	G
48	L1	3192	C
48	L1	3193	C
48	L1	3200	A
48	L1	3204	C
48	L1	3211	U
48	L1	3218	U
48	L1	3219	A
48	L1	3222	C
48	L1	3223	A
48	L1	3225	G
48	L1	3230	G
48	L1	3231	G
48	L1	3245	C
48	L1	3248	A
48	L1	3254	U
48	L1	3257	A
48	L1	3258	U
48	L1	3259	G
48	L1	3260	U
48	L1	3261	G
48	L1	3282	U
48	L1	3283	A
48	L1	3286	G
48	L1	3289	G
48	L1	3292	U
48	L1	3294	G

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Mol	Chain	Res	Type
48	L1	3310	G
48	L1	3319	C
48	L1	3323	C
48	L1	3325	U
48	L1	3331	U
48	L1	3332	A
49	L2	34	U
49	L2	35	C
49	L2	48	A
49	L2	59	A
49	L2	62	A
49	L2	63	G
49	L2	95	G
49	L2	104	A
49	L2	106	C
49	L2	111	A
49	L2	113	U
49	L2	116	G
49	L2	125	U
49	L2	138	A
49	L2	152	G
49	L2	154	C
49	L2	155	A
50	L3	7	G
50	L3	54	U
50	L3	55	A
50	L3	65	G
50	L3	73	U
50	L3	92	C
50	L3	101	A
50	L3	111	G

All (55) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
48	L1	133	C
48	L1	250	C
48	L1	447	U
48	L1	484	A
48	L1	511	U
48	L1	519	C
48	L1	557	G

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Mol	Chain	Res	Type
48	L1	565	C
48	L1	612	G
48	L1	757	A
48	L1	828	A
48	L1	833	C
48	L1	838	G
48	L1	855	C
48	L1	898	G
48	L1	990	U
48	L1	1016	U
48	L1	1022	C
48	L1	1047	A
48	L1	1062	A
48	L1	1089	G
48	L1	1192	G
48	L1	1200	A
48	L1	1267	C
48	L1	1290	G
48	L1	1338	A
48	L1	1623	A
48	L1	1785	C
48	L1	1793	A
48	L1	1796	A
48	L1	2064	C
48	L1	2075	U
48	L1	2172	U
48	L1	2185	A
48	L1	2194	C
48	L1	2227	U
48	L1	2246	G
48	L1	2503	C
48	L1	2509	A
48	L1	2621	G
48	L1	2624	U
48	L1	2683	U
48	L1	2725	U
48	L1	3079	U
48	L1	3121	G
48	L1	3163	A
48	L1	3181	C
48	L1	3191	G
48	L1	3224	C

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Mol	Chain	Res	Type
48	L1	3230	G
48	L1	3258	U
48	L1	3281	G
48	L1	3282	U
48	L1	3288	A
50	L3	72	G

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
48	OMG	L1	2578	48	18,26,27	1.17	2 (11%)	19,38,41	0.81	1 (5%)

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
48	OMG	L1	2578	48	-	3/5/27/28	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	L1	2578	OMG	C8-N7	-2.88	1.30	1.35
48	L1	2578	OMG	C5-C6	-2.43	1.42	1.47

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	L1	2578	OMG	O6-C6-C5	2.33	128.92	124.37

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
48	L1	2578	OMG	O4'-C4'-C5'-O5'
48	L1	2578	OMG	C3'-C4'-C5'-O5'
48	L1	2578	OMG	C1'-C2'-O2'-CM2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
48	L1	2578	OMG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 379 ligands modelled in this entry, 379 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

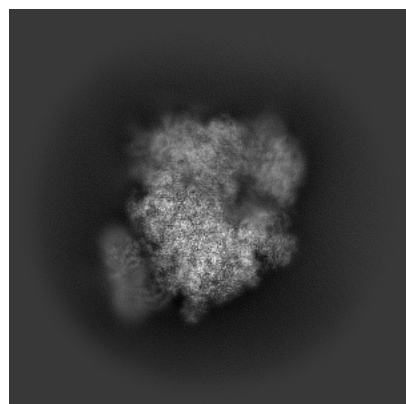
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-52656. These allow visual inspection of the internal detail of the map and identification of artifacts.

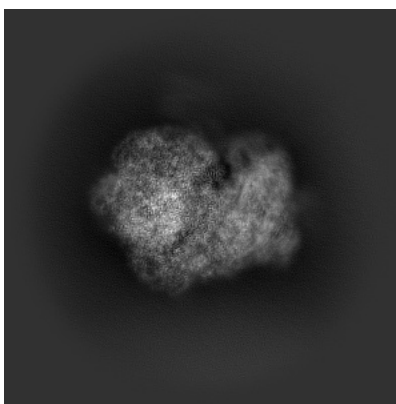
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

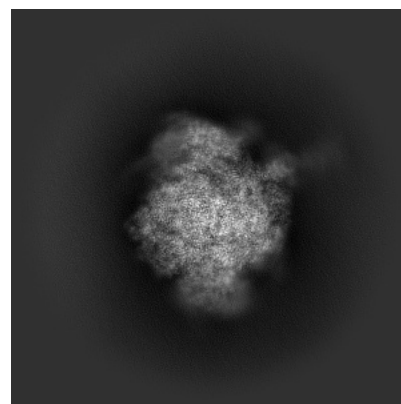
6.1.1 Primary map



X

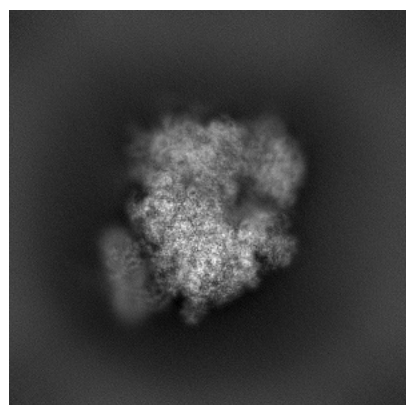


Y

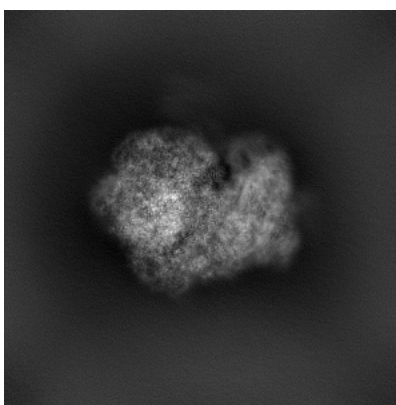


Z

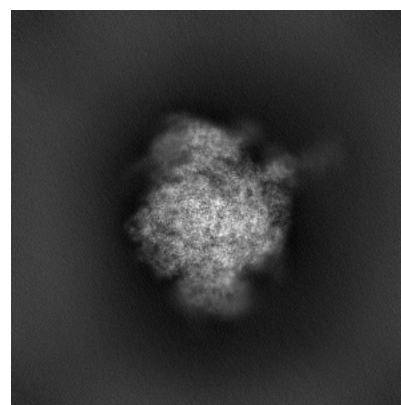
6.1.2 Raw map



X



Y

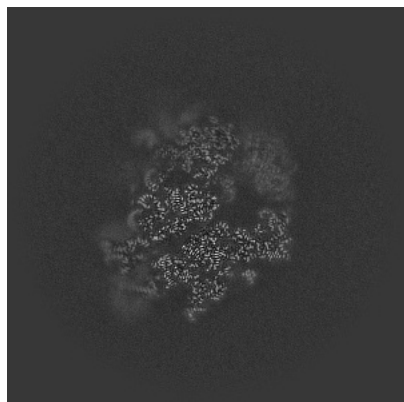


Z

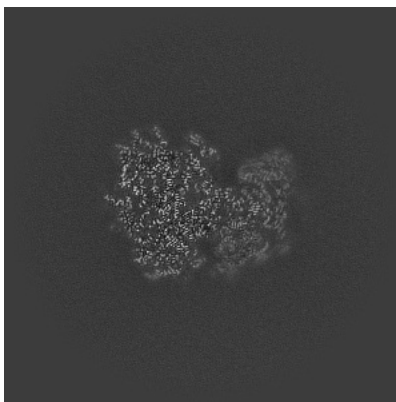
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

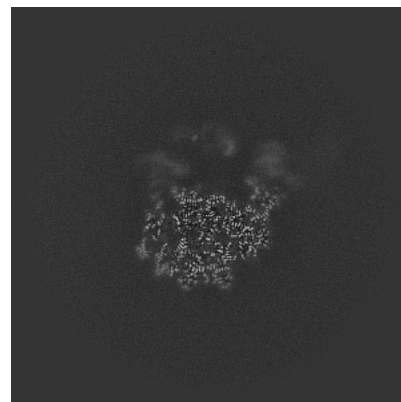
6.2.1 Primary map



X Index: 256

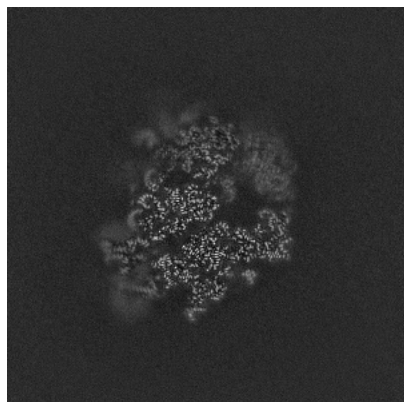


Y Index: 256

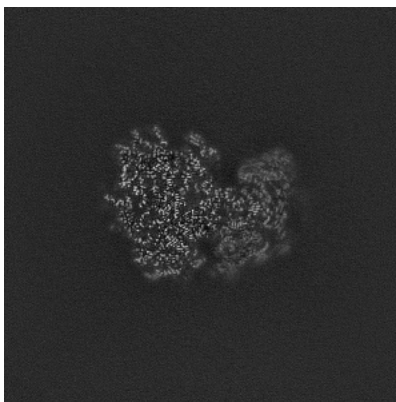


Z Index: 256

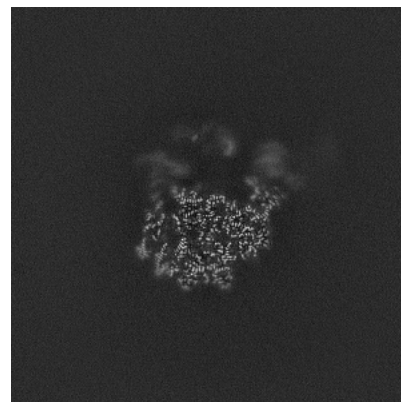
6.2.2 Raw map



X Index: 256



Y Index: 256

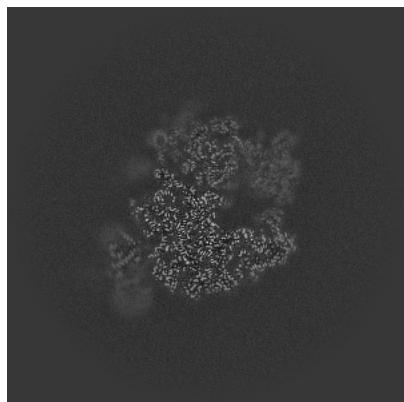


Z Index: 256

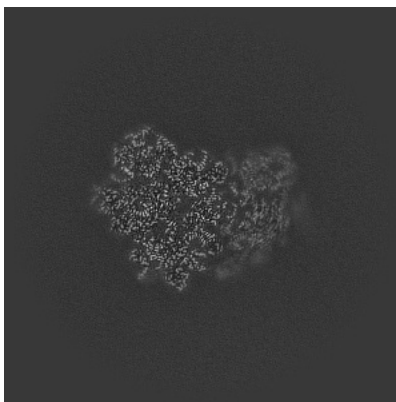
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

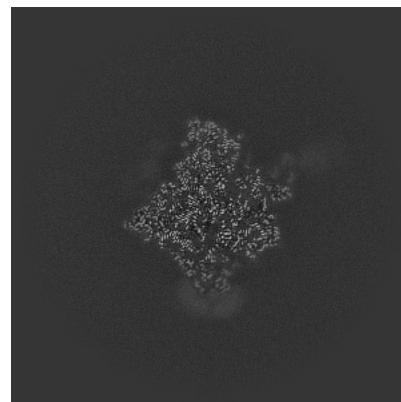
6.3.1 Primary map



X Index: 239

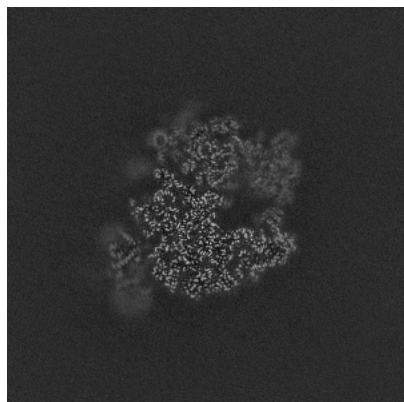


Y Index: 242

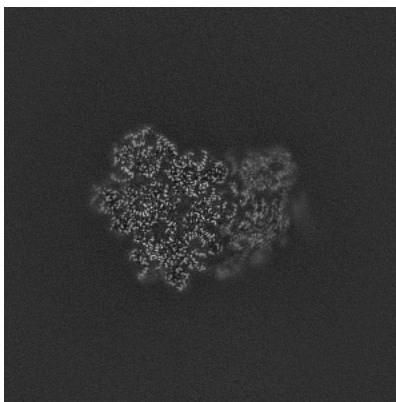


Z Index: 214

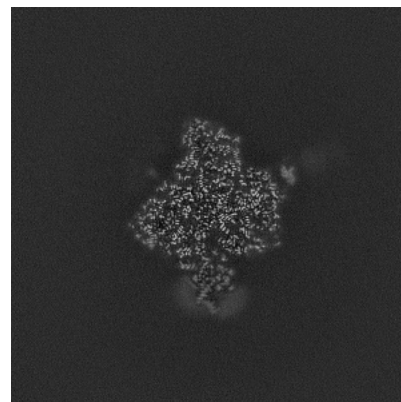
6.3.2 Raw map



X Index: 239



Y Index: 242

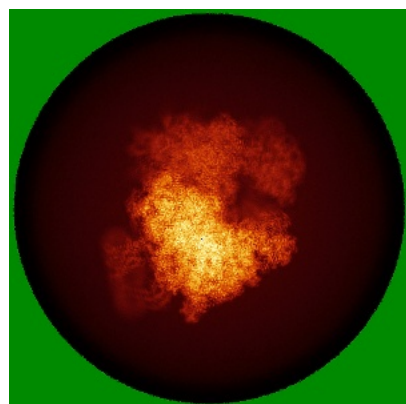


Z Index: 207

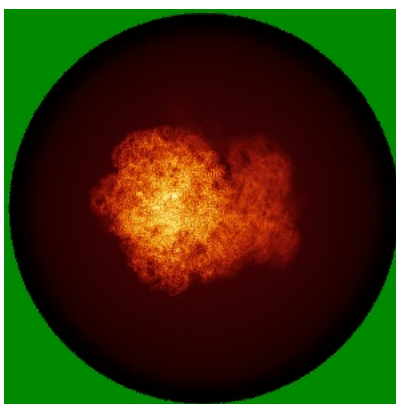
The images above show the largest variance slices of the map in three orthogonal directions.

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

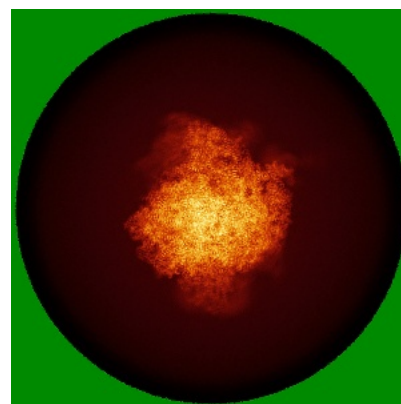
6.4.1 Primary map



X

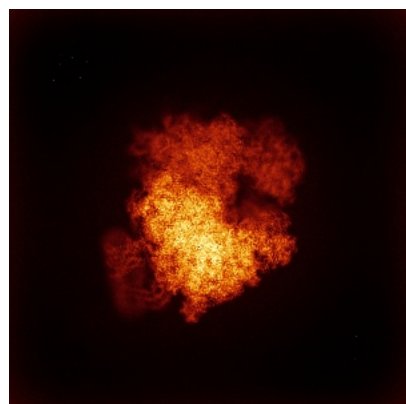


Y

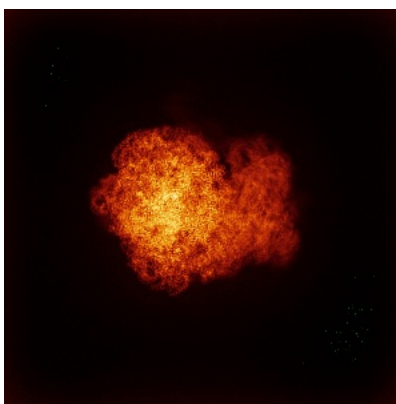


Z

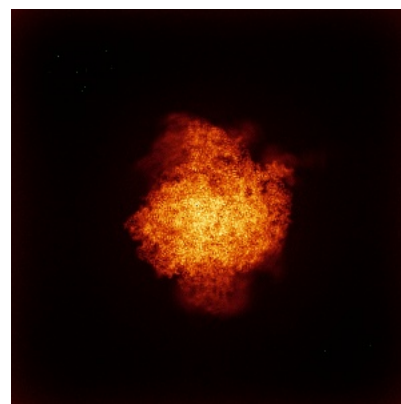
6.4.2 Raw map



X



Y

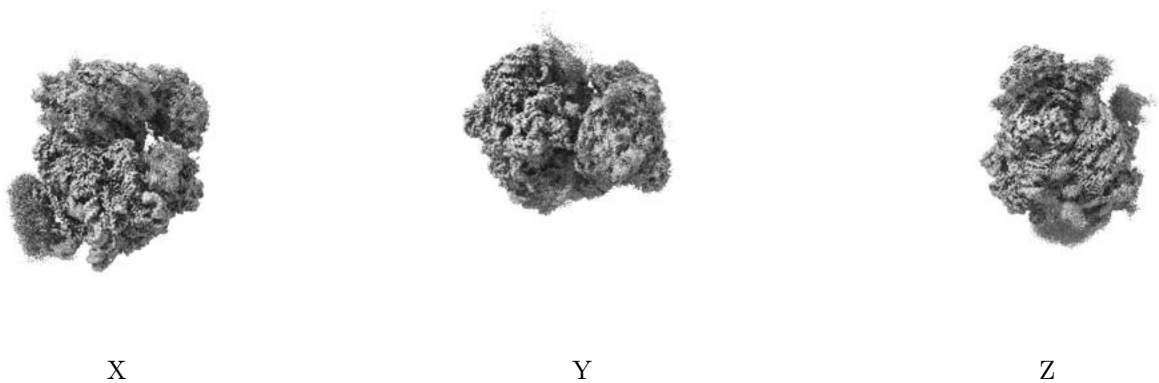


Z

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.

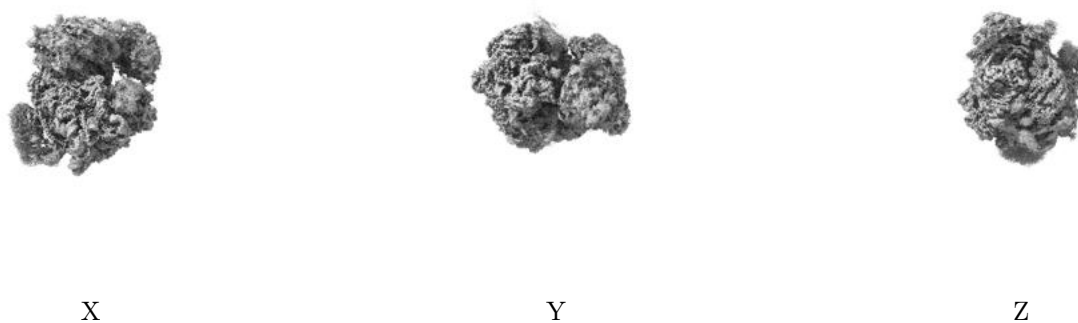
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.0. 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.

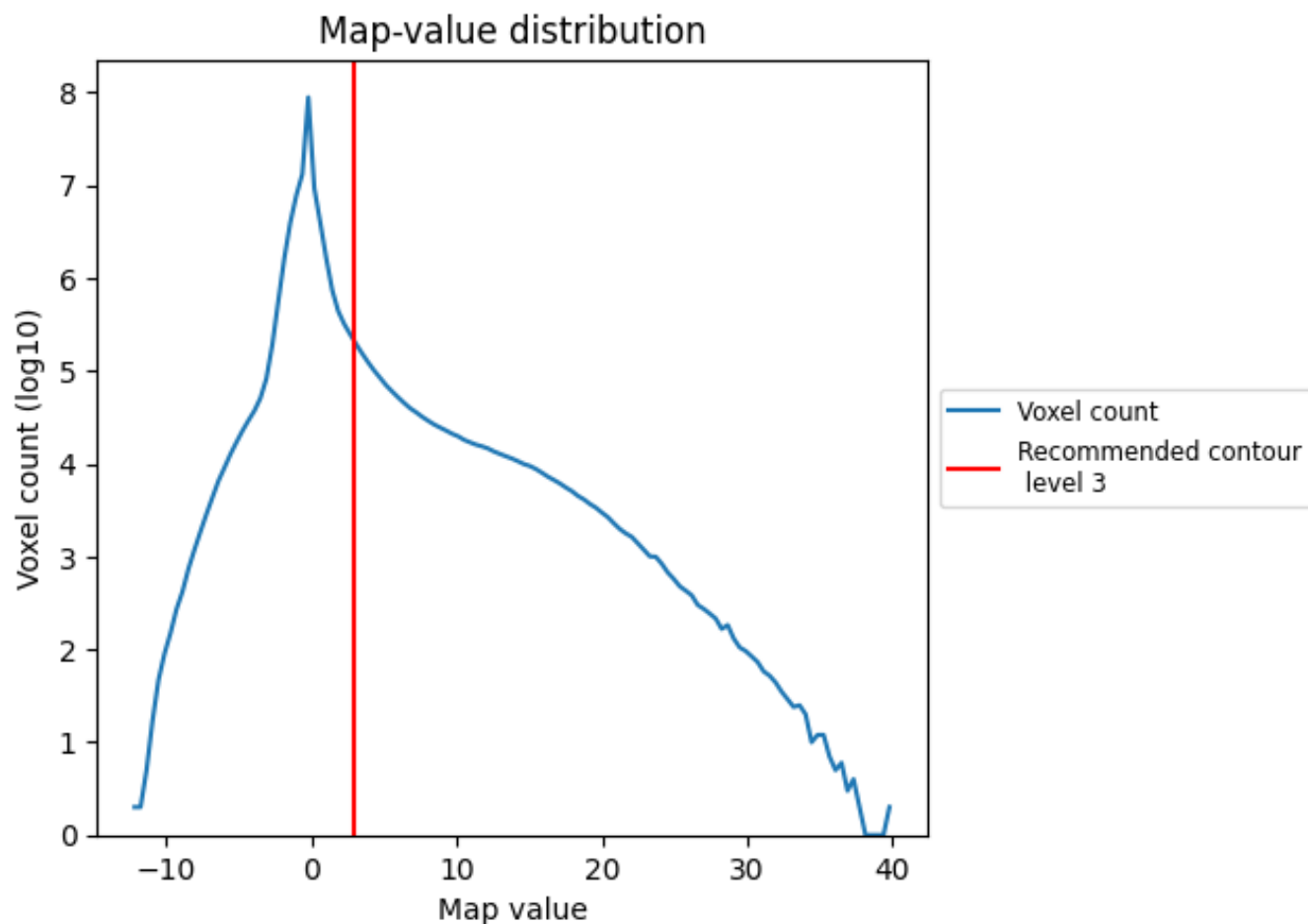
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

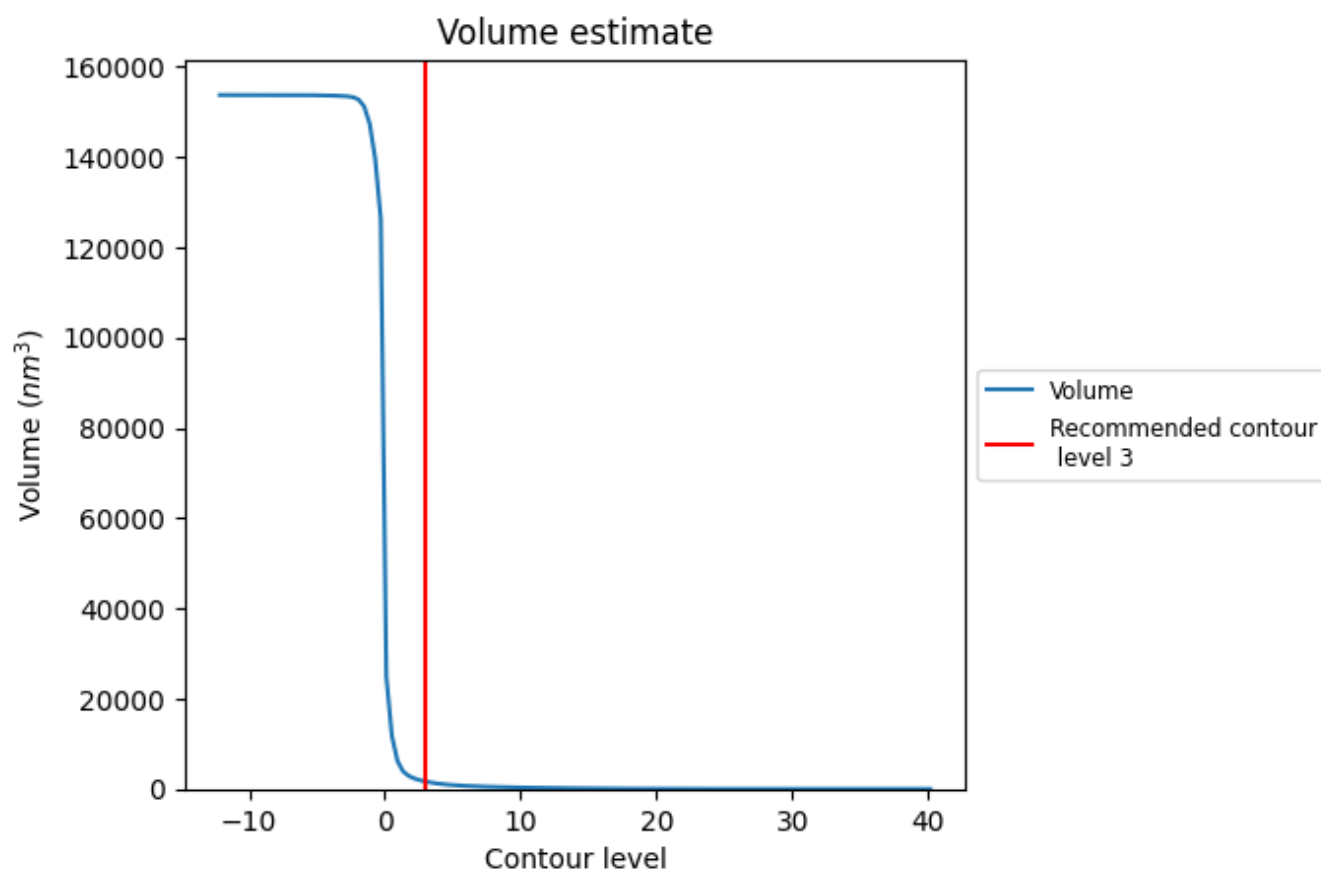
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

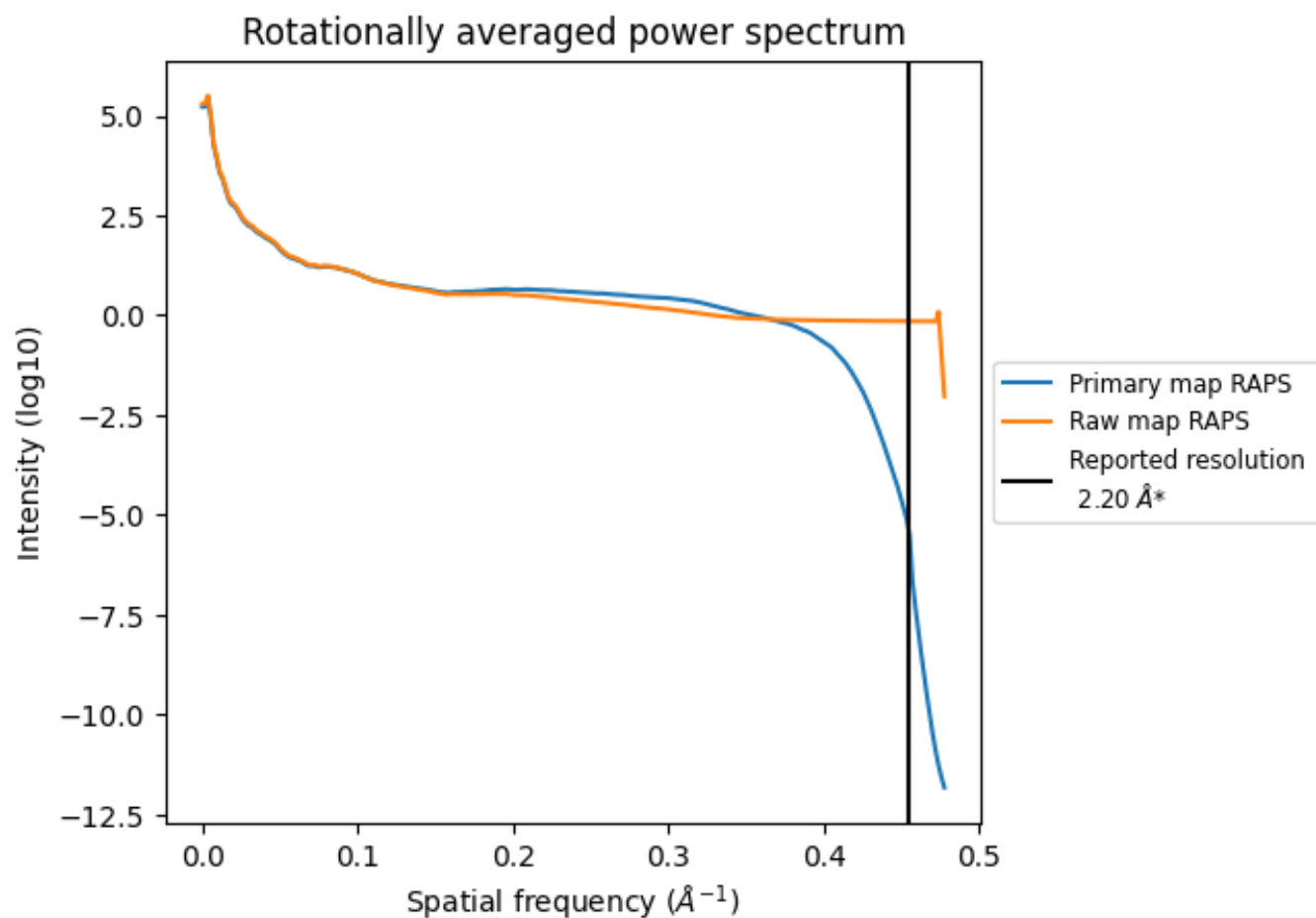
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1640 nm^3 ; this corresponds to an approximate mass of 1481 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 ⓘ

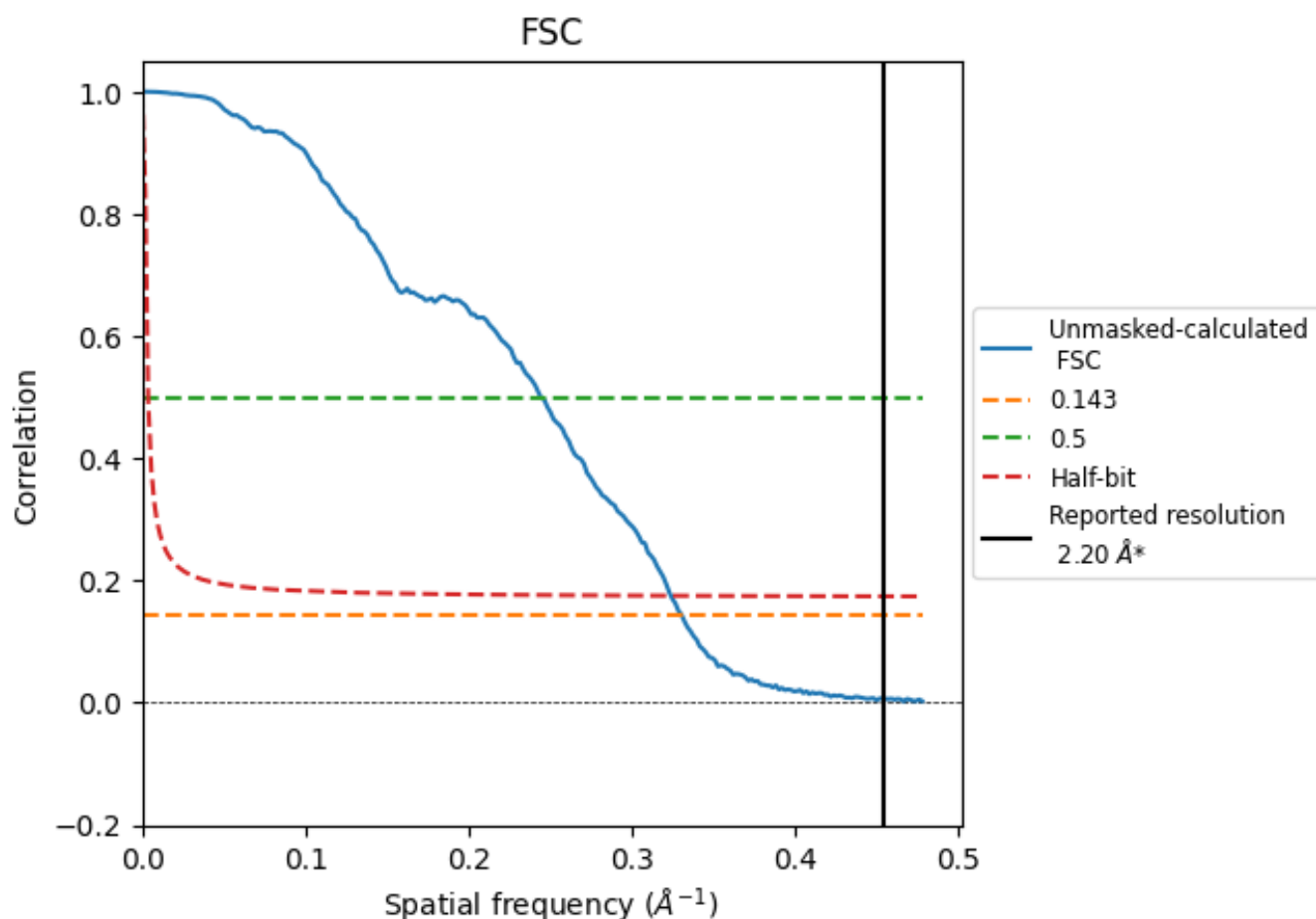


*Reported resolution corresponds to spatial frequency of 0.455 \AA^{-1}

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 0.455 \AA^{-1}

8.2 Resolution estimates [i](#)

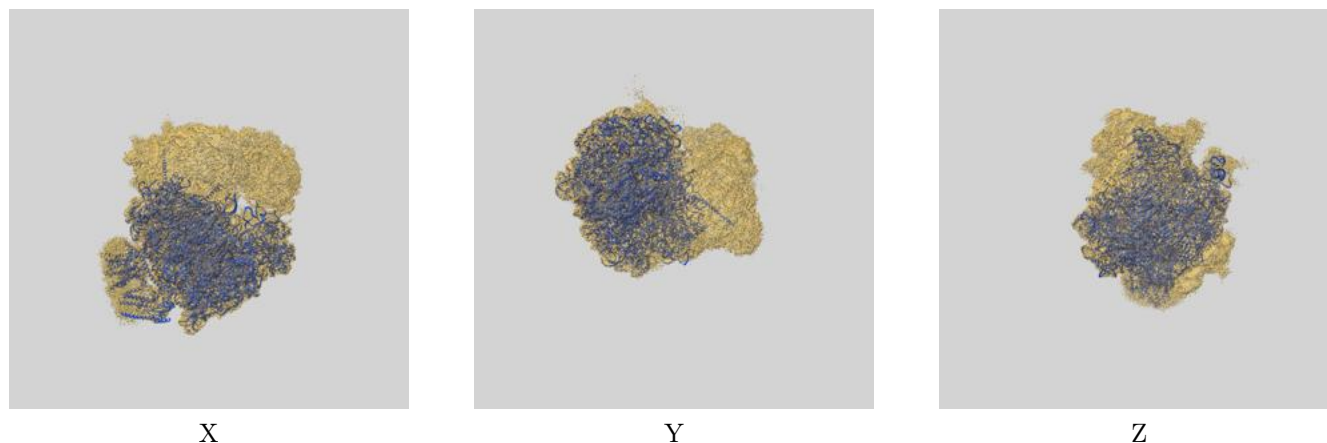
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.02	4.09	3.09

*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 3.02 differs from the reported value 2.2 by more than 10 %

9 Map-model fit [i](#)

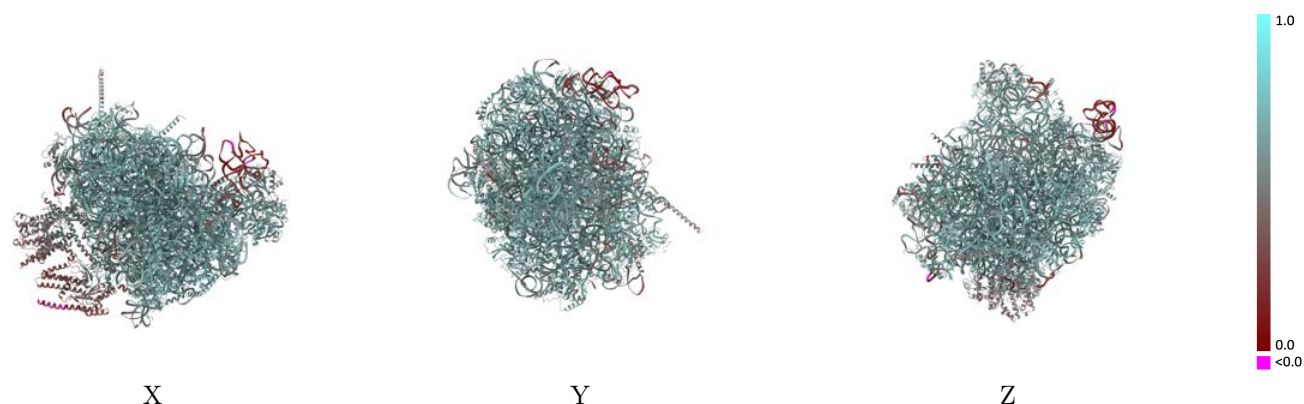
This section contains information regarding the fit between EMDB map EMD-52656 and PDB model 9I78. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



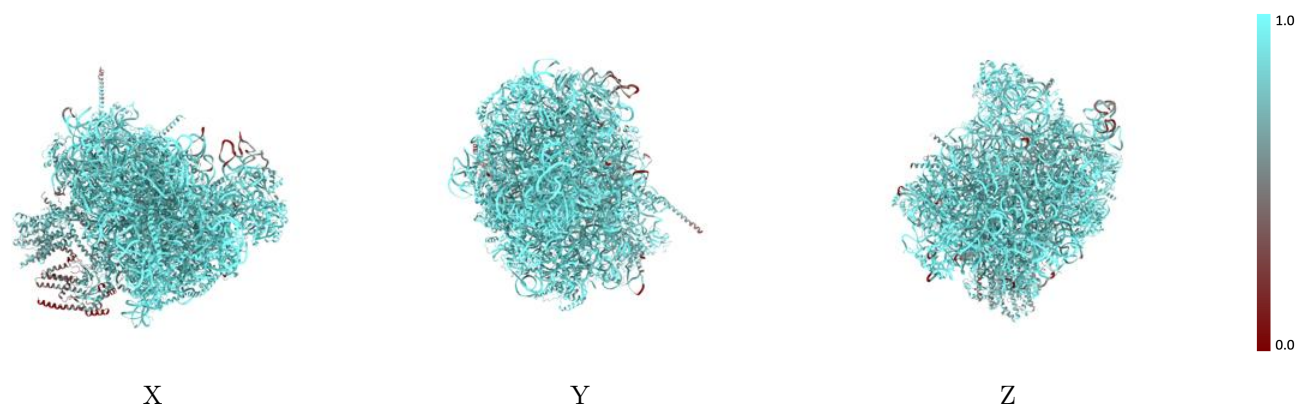
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



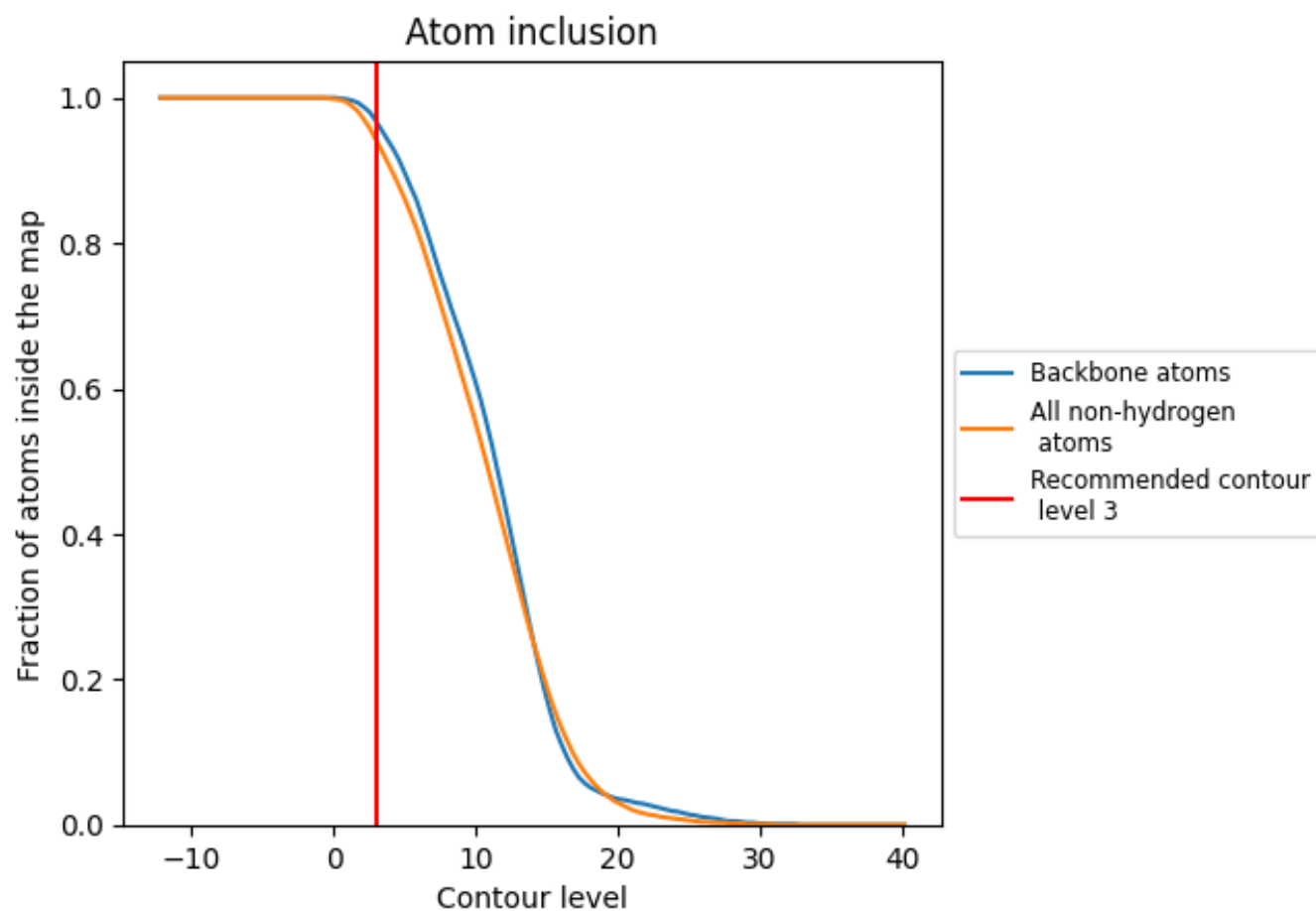
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 94% 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 (3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9420	 0.6100
1	 0.7860	 0.4600
2	 0.7410	 0.4670
3	 0.6970	 0.4120
4	 0.5890	 0.3930
6	 0.5020	 0.3130
7	 0.3170	 0.2490
L1	 0.9710	 0.6170
L2	 0.9900	 0.6380
L3	 0.9990	 0.6330
LA	 0.9570	 0.6630
LB	 0.9780	 0.6610
LC	 0.9740	 0.6620
LD	 0.9420	 0.6120
LE	 0.9400	 0.6140
LF	 0.9700	 0.6540
LG	 0.9310	 0.6120
LH	 0.9370	 0.6070
LI	 0.9600	 0.6340
LJ	 0.8780	 0.5330
LL	 0.9560	 0.6390
LM	 0.9700	 0.6430
LN	 0.9930	 0.6790
LO	 0.9780	 0.6620
LP	 0.9330	 0.6440
LQ	 0.9850	 0.6670
LR	 0.8920	 0.6100
LS	 0.9780	 0.6550
LT	 0.9610	 0.6440
LU	 0.8880	 0.5510
LV	 0.9620	 0.6610
LX	 0.9410	 0.6390
LY	 0.9470	 0.6420
LZ	 0.9580	 0.6230
La	 0.9760	 0.6600



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Chain	Atom inclusion	Q-score
Lb	 0.9410	 0.5950
Lc	 0.9450	 0.6180
Ld	 0.9280	 0.6340
Le	 0.9770	 0.6720
Lf	 0.9900	 0.6720
Lg	 0.9410	 0.6310
Lh	 0.8960	 0.5840
Li	 0.9110	 0.5920
Lj	 0.9830	 0.6690
Lk	 0.8750	 0.5730
Ll	 0.9590	 0.6510
Lm	 0.7010	 0.5500
Ln	 0.7980	 0.5700
Lo	 0.9620	 0.6570
Lp	 0.9120	 0.6200
Lq	 0.9640	 0.6470