



Full wwPDB EM Validation Report ⓘ

Jul 10, 2026 – 08:19 AM JST

PDB ID : 9XAJ / pdb_00009xaj
EMDB ID : EMD-66689
Title : Cryo-EM structure of the pre-40S ribosome (Enp1-Rrp12 Mut) from *Chaetomium thermophilum*, state Rrp12-A1*
Authors : Lau, B.; Li, Y.; Zhu, J.; Fischer, P.; Hong, X.; Yuan, R.; Beckmann, R.; Hurt, E.; Cheng, J.
Deposited on : 2025-10-22
Resolution : 3.10 Å (reported)
Based on initial model : 6G18

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.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

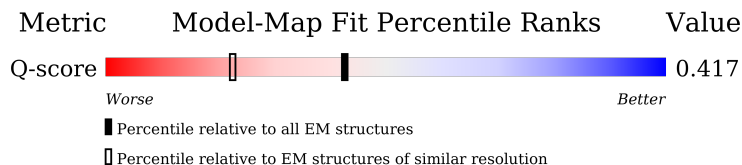
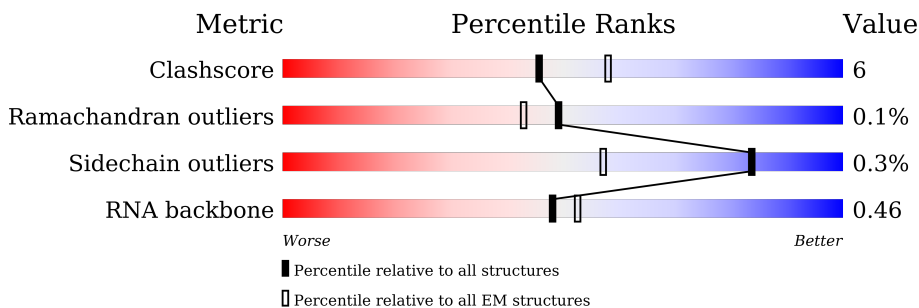
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	E	255	
2	H	264	
3	I	212	

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Mol	Chain	Length	Quality of chain
4	J	239	
5	K	203	
6	L	202	
7	M	190	
8	O	161	
9	P	144	
10	Q	151	
11	R	150	
12	S	153	
13	T	119	
14	V	156	
15	W	153	
16	Z	130	
17	a	145	
18	b	136	
19	c	99	
20	e	82	
21	f	68	
22	h	62	
23	i	154	
24	A	1797	
25	0	127	
26	1	282	
27	2	830	
28	3	259	

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Mol	Chain	Length	Quality of chain
29	4	480	48%8%44%
30	5	445	15%82%
31	6	519	7%92%
32	7	1235	81%70%11%19%
33	8	938	5%93%

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 81108 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 Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	E	213	Total	C	N	O	S	0	0
			1723	1096	319	303	5		

- Molecule 2 is a protein called 40S ribosomal protein S4.

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

- Molecule 3 is a protein called 40S ribosomal protein s5-like protein.

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

- Molecule 4 is a protein called 40S ribosomal protein S6.

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

- Molecule 5 is a protein called 40S ribosomal protein S7.

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

- Molecule 6 is a protein called 40S ribosomal protein S8.

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

- Molecule 7 is a protein called 40S ribosomal protein s9-like protein.

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

- Molecule 8 is a protein called 40S ribosomal protein S11-like protein.

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

- Molecule 9 is a protein called 40S ribosomal protein S12.

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

- Molecule 10 is a protein called 40S ribosomal protein S13-like protein.

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

- Molecule 11 is a protein called 40S ribosomal protein S14-like protein.

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

- Molecule 12 is a protein called 40S ribosomal protein s15-like protein.

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

- Molecule 13 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	T	117	Total	C	N	O	S	0	0
			909	588	162	158	1		

- Molecule 14 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	V	122	Total	C	N	O	S	0	0
			998	629	191	177	1		

- Molecule 15 is a protein called 40S ribosomal protein S19-like protein.

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

- Molecule 16 is a protein called 40S ribosomal protein S22-like protein.

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

- Molecule 17 is a protein called 40S ribosomal protein s23-like protein.

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

- Molecule 18 is a protein called Small ribosomal subunit protein eS24.

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

- Molecule 19 is a protein called 40S ribosomal protein S25.

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

- Molecule 20 is a protein called Ribosomal protein s27-like protein.

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

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

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

- Molecule 22 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	h	21	Total	C	N	O		0	0
			181	117	38	26			

- Molecule 23 is a protein called 40S ribosomal protein S27a-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	i	65	Total	C	N	O	S	0	0
			528	332	97	93	6		

- Molecule 24 is a RNA chain called pre-18S.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	A	1586	Total	C	N	O	P	0	0
			33827	15115	6032	11094	1586		

- Molecule 25 is a protein called Trm112.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	0	127	Total	C	N	O	S	0	0
			993	636	163	187	7		

- Molecule 26 is a protein called Methyltransferase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	1	267	Total	C	N	O	S	0	0
			2013	1260	355	388	10		

- Molecule 27 is a protein called Bms1-type G domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	2	699	Total	C	N	O	S	0	0
			5579	3506	997	1056	20		

- Molecule 28 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	3	184	Total	C	N	O	S	0	0
			1451	921	267	256	7		

- Molecule 29 is a protein called Bystin-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	4	270	Total	C	N	O	S	0	0
			2154	1401	377	366	10		

- Molecule 30 is a protein called Putative low-temperature viability protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	5	81	Total	C	N	O	S	0	0
			660	416	113	130	1		

- Molecule 31 is a protein called Serine/threonine-protein kinase RIO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	6	43	Total	C	N	O	S	0	0
			352	222	74	54	2		

- Molecule 32 is a protein called Ribosomal RNA-processing protein 12-like conserved domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	7	1004	Total	C	N	O	S	0	0
			7841	5009	1353	1441	38		

- Molecule 33 is a protein called Utp14.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	8	62	Total	C	N	O	S	0	0
			537	335	112	89	1		

- Molecule 34 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
34	Q	1	Total	Mg	0
			1	1	
34	a	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
34	A	1	Total	Mg	0
			1	1	

- Molecule 35 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
35	e	1	Total	Zn	0
			1	1	

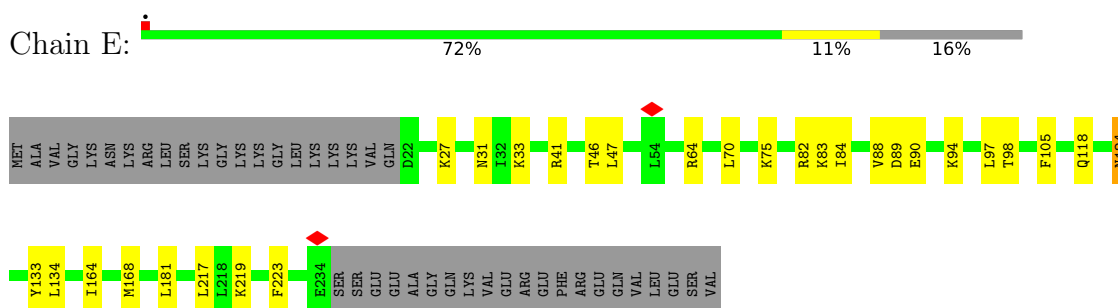
- Molecule 36 is water.

Mol	Chain	Residues	Atoms		AltConf
36	Q	1	Total	O	0
			1	1	
36	A	3	Total	O	0
			3	3	

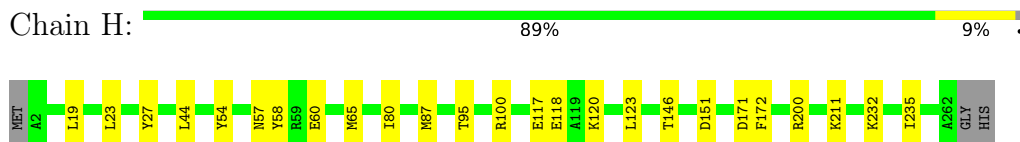
3 Residue-property plots

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.

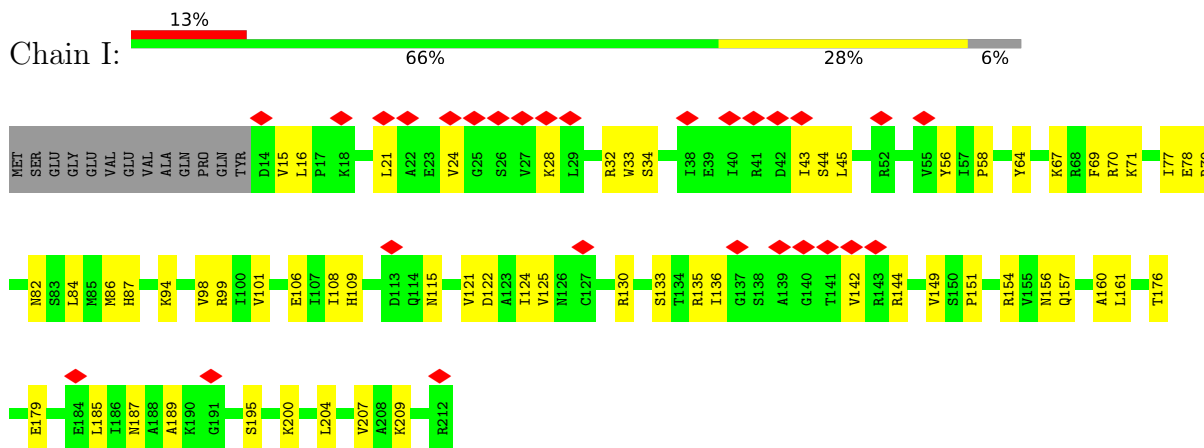
- Molecule 1: Small ribosomal subunit protein eS1



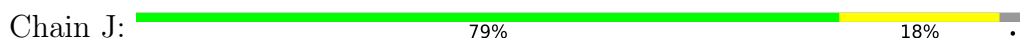
- Molecule 2: 40S ribosomal protein S4

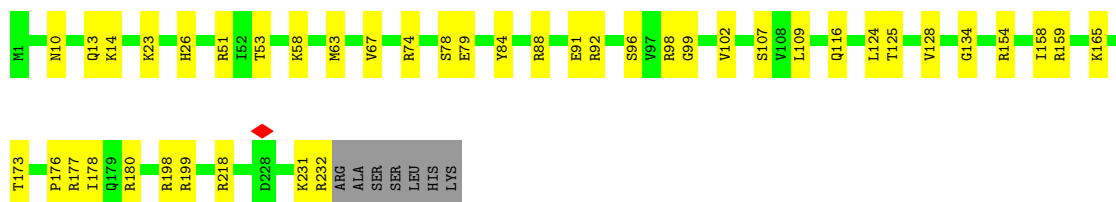


- Molecule 3: 40S ribosomal protein s5-like protein



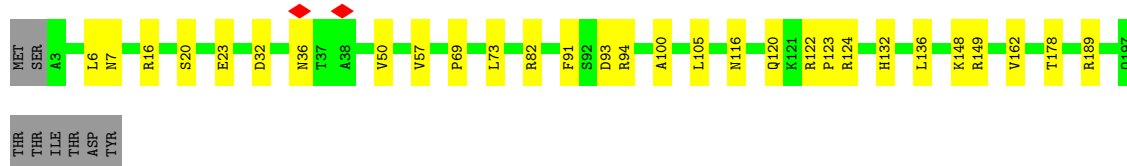
- Molecule 4: 40S ribosomal protein S6





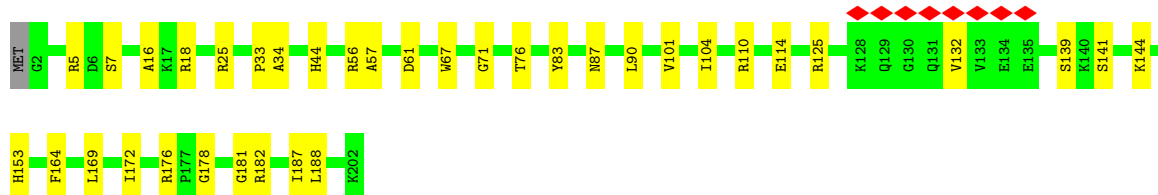
- Molecule 5: 40S ribosomal protein S7

Chain K: 82% 14% .



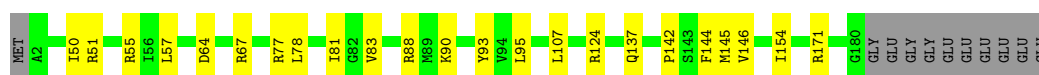
- Molecule 6: 40S ribosomal protein S8

Chain L: 82% 18%



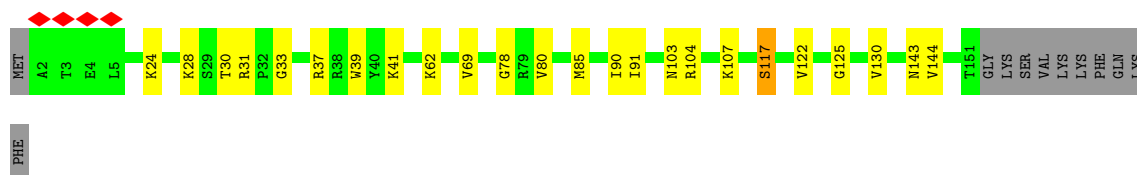
- Molecule 7: 40S ribosomal protein s9-like protein

Chain M: 82% 12% 6%



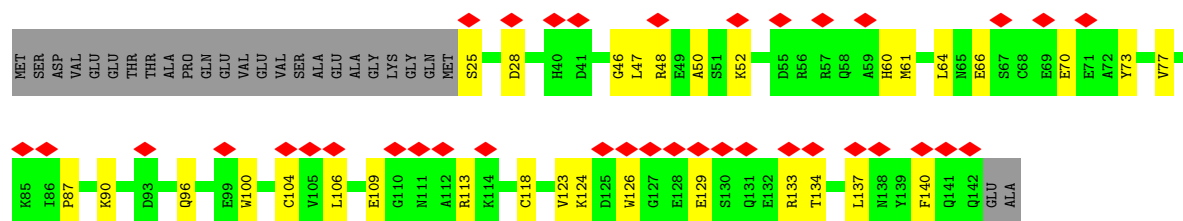
- Molecule 8: 40S ribosomal protein S11-like protein

Chain O: 78% 14% 7%

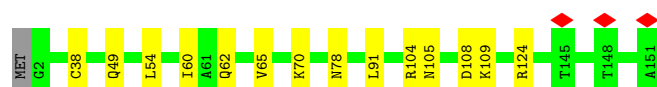
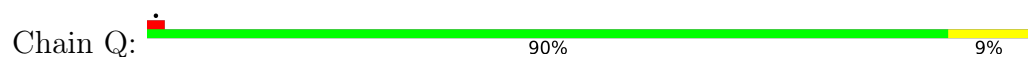


- Molecule 9: 40S ribosomal protein S12

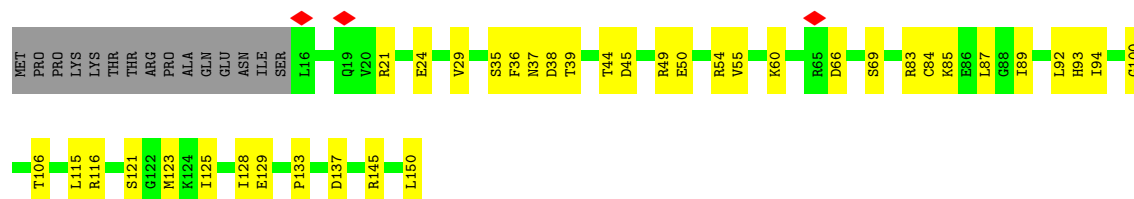
Chain P: 26% 60% 22% 18%



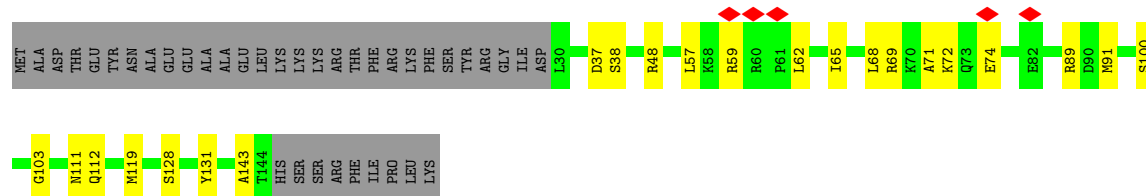
- Molecule 10: 40S ribosomal protein S13-like protein



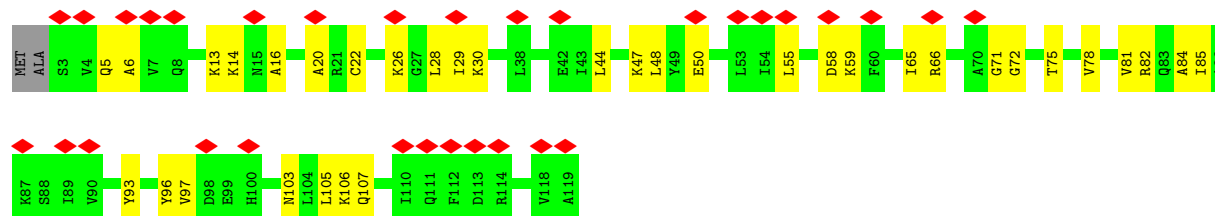
- Molecule 11: 40S ribosomal protein S14-like protein



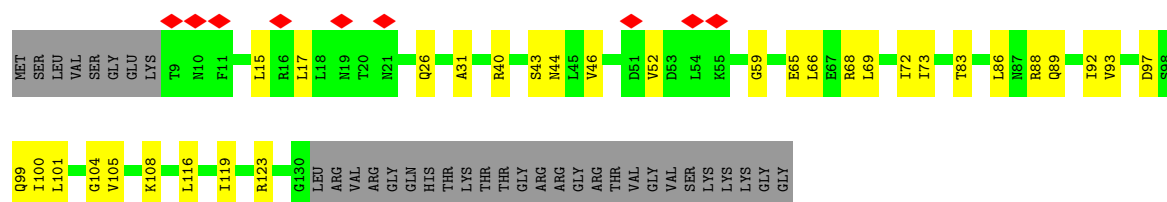
- Molecule 12: 40S ribosomal protein s15-like protein



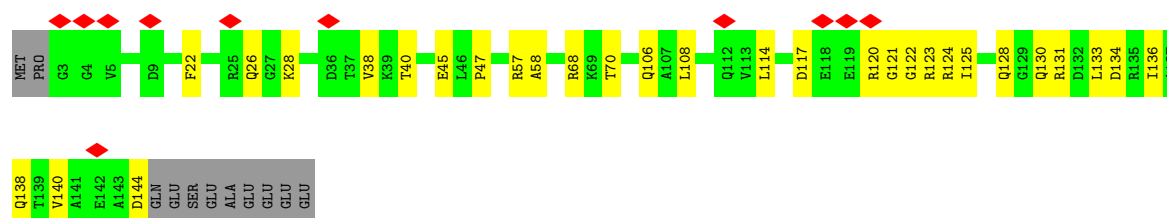
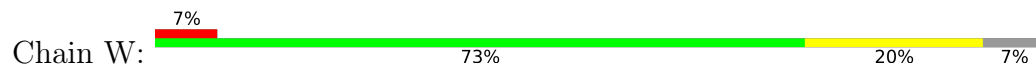
- Molecule 13: 40S ribosomal protein S16



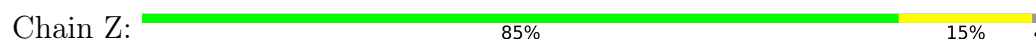
- Molecule 14: Putative ribosomal protein



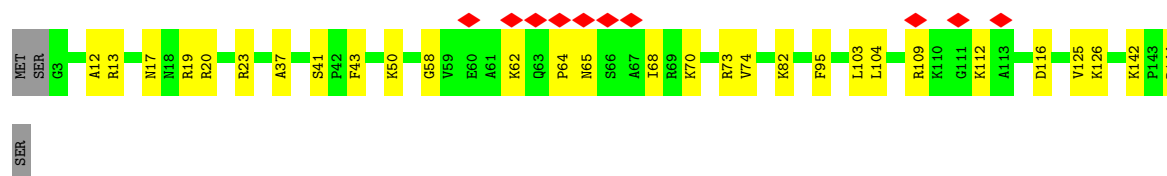
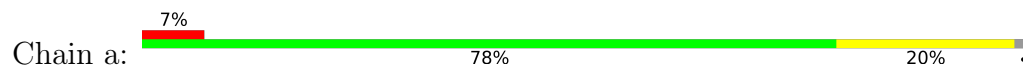
- Molecule 15: 40S ribosomal protein S19-like protein



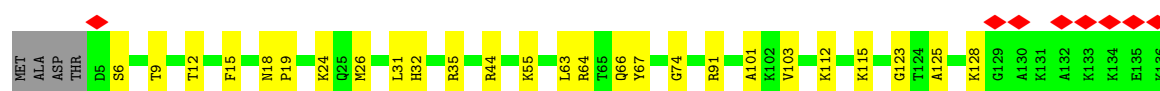
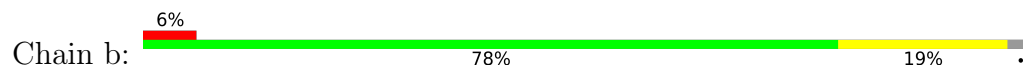
- Molecule 16: 40S ribosomal protein S22-like protein



- Molecule 17: 40S ribosomal protein s23-like protein



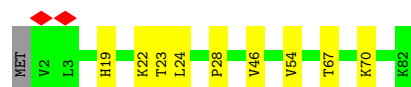
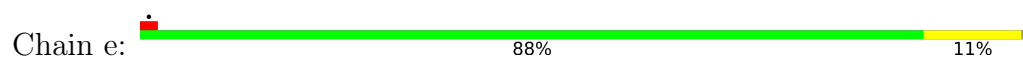
- Molecule 18: Small ribosomal subunit protein eS24



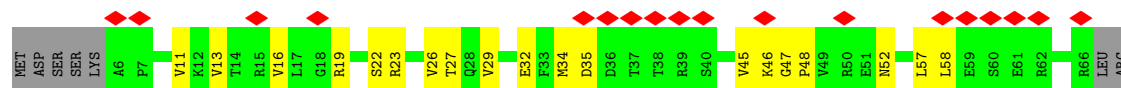
- Molecule 19: 40S ribosomal protein S25



- Molecule 20: Ribosomal protein s27-like protein



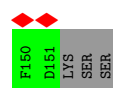
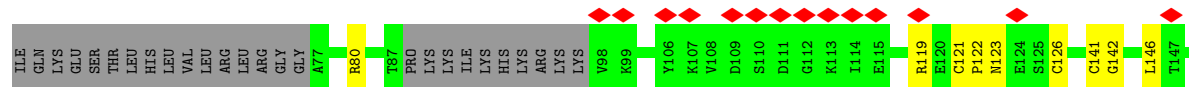
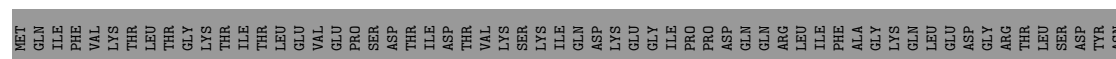
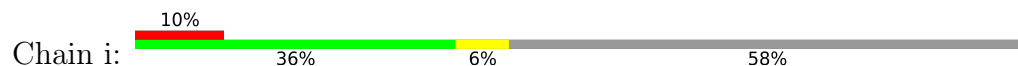
- Molecule 21: 40S ribosomal protein S28-like protein



- Molecule 22: 40S ribosomal protein S30



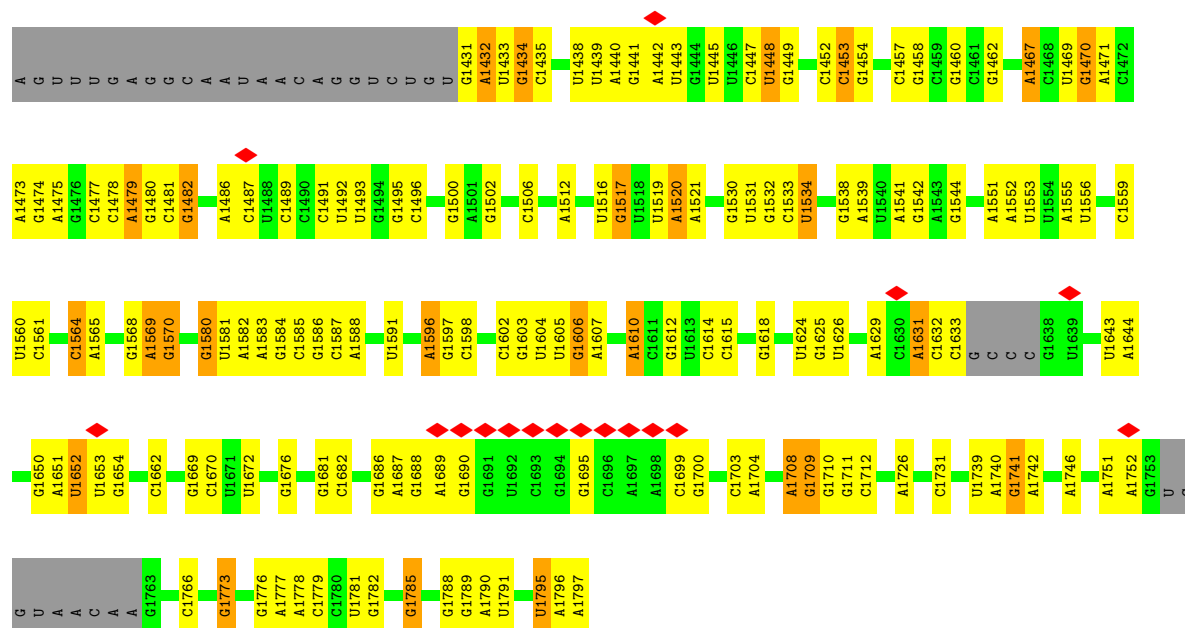
- Molecule 23: 40S ribosomal protein S27a-like protein



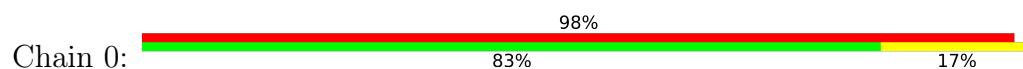
- Molecule 24: pre-18S



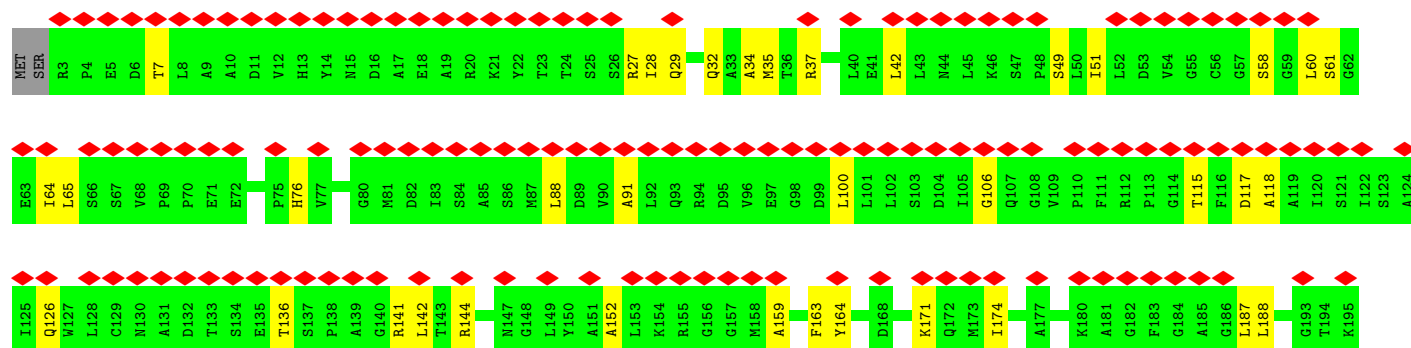
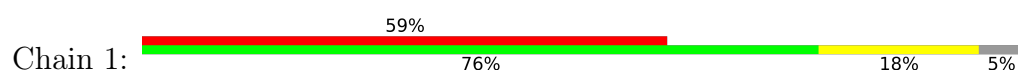


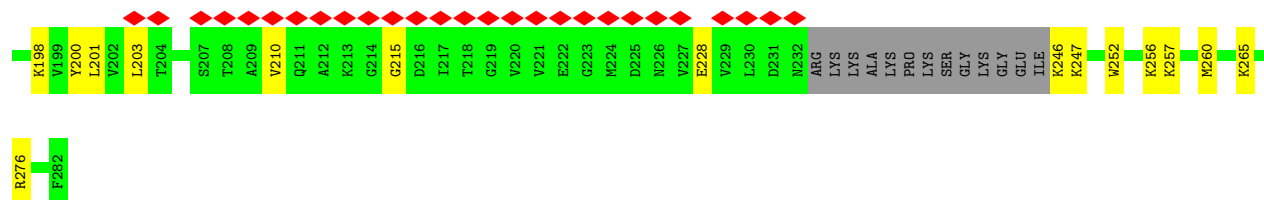


• Molecule 25: Trm112

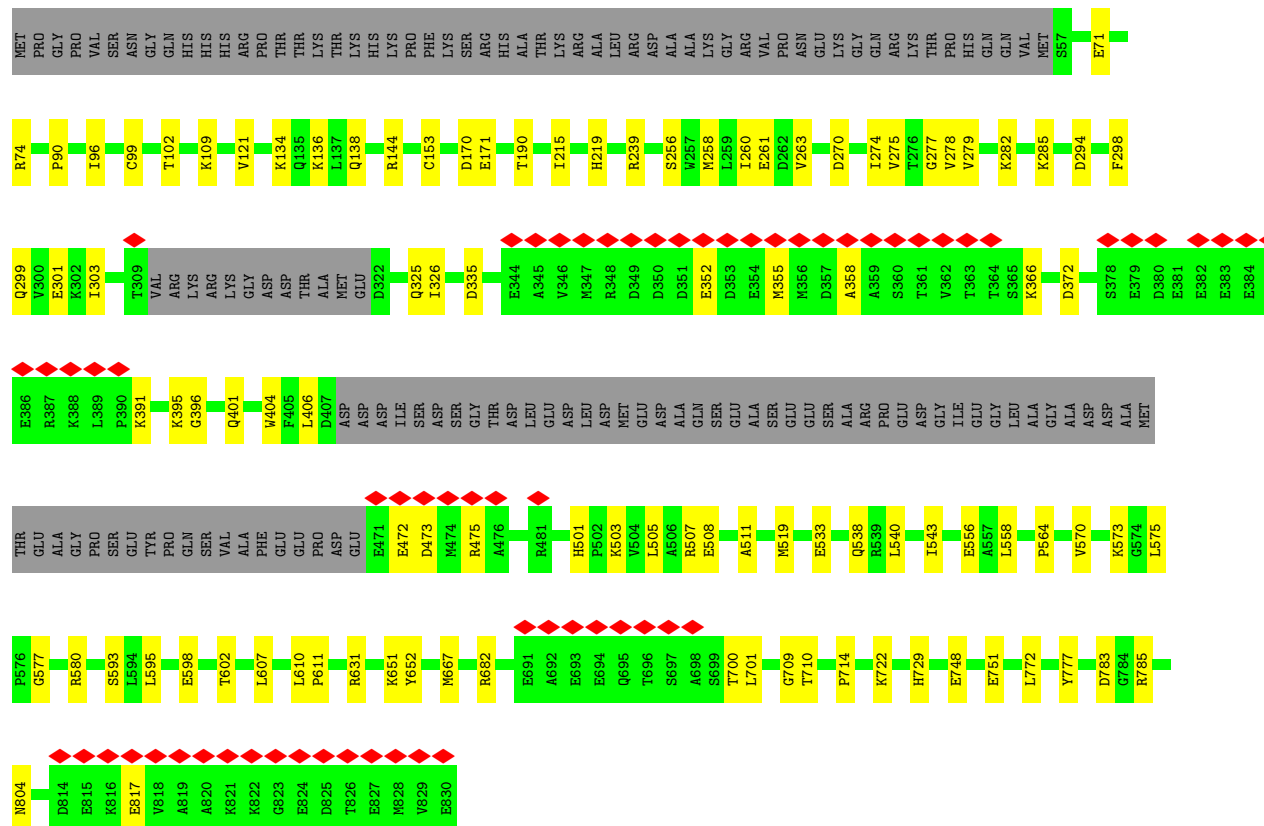


• Molecule 26: Methyltransferase-like protein

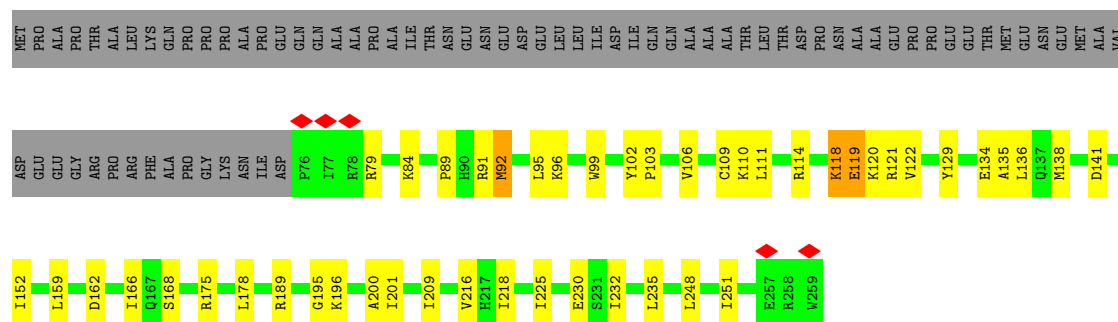




• Molecule 27: Bms1-type G domain-containing protein

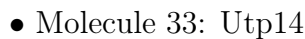


• Molecule 28: Pre-rRNA-processing protein PNO1



• Molecule 29: Bystin-like protein







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	211537	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE; Relion	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.485	Depositor
Minimum map value	-0.247	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.02	Depositor
Map size ($\text{\AA}$)	376.19998, 376.19998, 376.19998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.045, 1.045, 1.045	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	E	0.31	0/1752	0.57	0/2361
2	H	0.30	0/2112	0.53	1/2842 (0.0%)
3	I	0.21	0/1578	0.55	0/2130
4	J	0.33	0/1906	0.57	0/2547
5	K	0.23	0/1587	0.54	0/2140
6	L	0.28	0/1654	0.48	0/2213
7	M	0.27	0/1489	0.45	0/1993
8	O	0.52	1/1249 (0.1%)	0.71	0/1678
9	P	0.17	0/934	0.53	0/1255
10	Q	0.35	0/1205	0.54	0/1627
11	R	0.32	0/1014	0.65	0/1361
12	S	0.20	0/932	0.54	0/1248
13	T	0.19	0/922	0.56	0/1241
14	V	0.18	0/1012	0.50	0/1360
15	W	0.19	0/1137	0.55	0/1533
16	Z	0.39	0/1055	0.58	0/1416
17	a	0.28	0/1116	0.47	0/1489
18	b	0.27	0/1075	0.46	0/1431
19	c	0.19	0/550	0.53	0/736
20	e	0.30	0/623	0.64	0/843
21	f	0.22	0/487	0.64	0/653
22	h	0.61	0/184	0.98	0/242
23	i	0.19	0/535	0.54	0/710
24	A	0.28	0/37830	0.41	1/58939 (0.0%)
25	0	0.17	0/1013	0.48	0/1378
26	1	0.16	0/2043	0.46	0/2753
27	2	0.19	0/5694	0.43	0/7705
28	3	0.50	0/1475	0.79	2/1982 (0.1%)
29	4	0.19	0/2205	0.49	0/2990
30	5	0.22	0/670	0.66	0/896
31	6	0.20	0/356	0.43	0/462
32	7	0.18	0/7995	0.43	0/10857

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	8	0.82	0/544	1.33	4/717 (0.6%)
All	All	0.28	1/85933 (0.0%)	0.48	8/123728 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	O	117	SER	CA-CB	-5.69	1.44	1.53

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	A	1073	A	C4'-C3'-O3'	5.88	121.81	113.00
2	H	232	LYS	CA-CB-CG	5.77	125.64	114.10
33	8	404	LYS	N-CA-C	-5.71	105.57	112.54
28	3	118	LYS	CA-C-N	-5.38	111.62	122.55
28	3	118	LYS	C-N-CA	-5.38	111.62	122.55
33	8	444	ARG	N-CA-C	-5.32	106.47	113.12
33	8	412	ARG	CA-C-N	-5.02	113.16	120.29
33	8	412	ARG	C-N-CA	-5.02	113.16	120.29

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	1723	0	1804	17	0
2	H	2072	0	2155	21	0
3	I	1557	0	1608	37	0
4	J	1875	0	1983	31	0
5	K	1562	0	1641	20	0
6	L	1621	0	1645	26	0
7	M	1466	0	1582	17	0
8	O	1222	0	1289	13	0
9	P	923	0	946	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	Q	1182	0	1264	10	0
11	R	1002	0	1034	27	0
12	S	917	0	978	19	0
13	T	909	0	973	24	0
14	V	998	0	1042	22	0
15	W	1117	0	1133	21	0
16	Z	1037	0	1076	11	0
17	a	1099	0	1169	20	0
18	b	1061	0	1150	18	0
19	c	546	0	591	12	0
20	e	611	0	635	5	0
21	f	484	0	513	15	0
22	h	181	0	207	7	0
23	i	528	0	541	6	0
24	A	33827	0	17047	303	0
25	0	993	0	1018	13	0
26	1	2013	0	2043	35	0
27	2	5579	0	5570	65	0
28	3	1451	0	1524	48	0
29	4	2154	0	2242	26	0
30	5	660	0	648	12	0
31	6	352	0	402	7	0
32	7	7841	0	8114	82	0
33	8	537	0	573	12	0
34	A	1	0	0	0	0
34	Q	1	0	0	0	0
34	a	1	0	0	0	0
35	e	1	0	0	0	0
36	A	3	0	0	0	0
36	Q	1	0	0	0	0
All	All	81108	0	66140	896	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 6.

All (896) 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)
28:3:119:GLU:N	28:3:119:GLU:OE2	1.62	1.28
27:2:263:VAL:HA	27:2:274:ILE:O	1.34	1.23
28:3:119:GLU:HG3	28:3:121:ARG:HH11	1.07	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:198:ARG:HG2	24:A:175:G:H22	1.21	1.05
28:3:119:GLU:CD	28:3:119:GLU:H	1.67	1.02
24:A:1650:G:N2	24:A:1742:A:H62	1.59	0.99
24:A:443:A:N6	24:A:458:G:H21	1.61	0.98
28:3:119:GLU:HG2	28:3:121:ARG:CG	1.96	0.96
24:A:1272:A:H2	24:A:1431:G:H1	1.13	0.95
24:A:1269:U:H3	24:A:1435:C:N4	1.65	0.94
24:A:1650:G:H21	24:A:1742:A:H62	0.99	0.92
28:3:119:GLU:HG2	28:3:121:ARG:HG2	1.52	0.91
24:A:483:G:H1	24:A:498:U:H3	1.17	0.90
24:A:652:G:H1	24:A:673:U:H3	0.94	0.90
24:A:1584:G:H1	24:A:1604:U:H3	0.93	0.88
28:3:119:GLU:HG3	28:3:121:ARG:NH1	1.88	0.87
24:A:1650:G:H21	24:A:1742:A:N6	1.72	0.87
21:f:13:VAL:O	21:f:52:ASN:HA	1.76	0.86
4:J:198:ARG:HG2	24:A:175:G:N2	1.91	0.85
24:A:1272:A:C2	24:A:1431:G:N1	2.45	0.85
24:A:974:G:H1	24:A:1021:A:HO2'	1.23	0.84
24:A:709:G:H1	24:A:722:U:H3	1.21	0.84
24:A:820:U:H3	24:A:848:G:H1	1.24	0.83
28:3:119:GLU:CG	28:3:121:ARG:HH11	1.88	0.82
24:A:148:G:H22	24:A:160:G:H1	1.23	0.81
27:2:263:VAL:CA	27:2:274:ILE:O	2.25	0.80
30:5:395:GLU:O	30:5:399:ASN:HB2	1.80	0.80
24:A:702:A:H62	24:A:731:G:N2	1.79	0.79
24:A:1269:U:H3	24:A:1435:C:H42	1.21	0.79
24:A:893:G:H1	24:A:915:U:H3	1.32	0.77
9:P:106:LEU:H	9:P:113:ARG:HH22	1.34	0.76
27:2:256:SER:HB3	27:2:593:SER:HB3	1.70	0.73
28:3:92:MET:HE3	28:3:120:LYS:HG2	1.72	0.71
24:A:1269:U:N3	24:A:1435:C:N4	2.31	0.69
33:8:431:ILE:C	33:8:433:LYS:H	2.00	0.69
24:A:1651:A:N6	24:A:1741:G:H1	1.91	0.69
2:H:87:MET:HE2	2:H:123:LEU:HB2	1.73	0.69
24:A:1651:A:N6	24:A:1741:G:N1	2.40	0.69
13:T:29:ILE:HG23	13:T:65:ILE:HB	1.73	0.68
5:K:73:LEU:HD22	5:K:100:ALA:HB2	1.75	0.68
24:A:1272:A:H2	24:A:1431:G:N1	1.86	0.68
18:b:115:LYS:NZ	24:A:57:G:OP1	2.26	0.68
24:A:1200:A:C6	24:A:1551:A:C6	2.81	0.68
24:A:1516:U:H4'	24:A:1517:G:H3'	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:1200:A:N6	24:A:1551:A:N6	2.43	0.67
22:h:26:LYS:HA	24:A:502:A:C2	2.29	0.67
24:A:1269:U:C2	24:A:1434:G:O6	2.47	0.67
29:4:296:LEU:HG	29:4:331:ILE:HG21	1.76	0.66
28:3:201:ILE:HD13	28:3:248:LEU:HD11	1.76	0.66
4:J:13:GLN:HE22	24:A:148:G:H21	1.43	0.66
19:c:29:VAL:HG13	19:c:30:ILE:HD12	1.76	0.66
26:1:28:ILE:O	26:1:32:GLN:NE2	2.29	0.66
6:L:176:ARG:NH2	24:A:328:G:N7	2.43	0.65
15:W:120:ARG:NH1	15:W:121:GLY:O	2.29	0.65
3:I:108:ILE:HG21	3:I:185:LEU:HD11	1.79	0.65
24:A:1480:G:N2	24:A:1587:C:O2	2.29	0.65
27:2:303:ILE:HG12	27:2:570:VAL:HG22	1.79	0.65
32:7:335:LEU:O	32:7:343:ARG:NH2	2.28	0.65
12:S:128:SER:HA	27:2:401:GLN:HE22	1.60	0.65
24:A:702:A:N6	24:A:731:G:N2	2.45	0.65
7:M:88:ARG:HB3	7:M:93:TYR:HD2	1.61	0.64
25:0:101:LYS:HE3	25:0:110:GLU:HG2	1.77	0.64
28:3:84:LYS:HD2	28:3:121:ARG:HE	1.61	0.64
27:2:577:GLY:HA2	27:2:580:ARG:HD2	1.79	0.64
28:3:119:GLU:CG	28:3:121:ARG:HG2	2.28	0.64
4:J:23:LYS:O	4:J:26:HIS:ND1	2.31	0.64
13:T:44:LEU:HD21	13:T:78:VAL:HG21	1.80	0.63
24:A:443:A:N6	24:A:458:G:N2	2.42	0.63
24:A:1199:A:H62	24:A:1452:C:H3'	1.64	0.63
17:a:144:ARG:HH12	27:2:710:THR:HG22	1.64	0.63
3:I:130:ARG:HH12	21:f:58:LEU:HB3	1.63	0.63
32:7:440:VAL:HA	32:7:443:LYS:HZ2	1.62	0.63
32:7:699:LEU:HD13	32:7:703:SER:HB3	1.78	0.63
11:R:83:ARG:HH12	11:R:87:LEU:HB2	1.63	0.62
15:W:123:ARG:NH1	24:A:1495:G:OP1	2.32	0.62
10:Q:38:CYS:SG	10:Q:78:ASN:ND2	2.72	0.62
16:Z:2:VAL:N	24:A:1032:C:HO2'	1.97	0.62
24:A:1236:U:O2	24:A:1240:G:C2	2.52	0.62
27:2:505:LEU:HD12	27:2:507:ARG:HH12	1.63	0.62
27:2:772:LEU:O	27:2:777:TYR:HB2	2.00	0.62
7:M:77:ARG:NH2	24:A:761:A:OP1	2.33	0.62
24:A:1277:C:OP1	32:7:981:LYS:NZ	2.30	0.62
13:T:14:LYS:NZ	24:A:1606:G:N7	2.42	0.61
3:I:34:SER:O	3:I:115:ASN:ND2	2.32	0.61
14:V:88:ARG:HH21	14:V:108:LYS:HD2	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:141:SER:HA	6:L:144:LYS:HG3	1.82	0.61
26:1:126:GLN:HB3	26:1:163:PHE:HB2	1.82	0.61
18:b:123:GLY:O	18:b:128:LYS:NZ	2.29	0.61
32:7:401:GLY:HA2	32:7:443:LYS:HE3	1.81	0.61
24:A:1662:C:H42	24:A:1731:C:H42	1.47	0.60
24:A:487:U:H3	24:A:494:G:H1	1.49	0.60
24:A:1272:A:N1	24:A:1431:G:O6	2.33	0.60
25:0:57:ARG:HG2	25:0:68:LEU:HB2	1.83	0.60
26:1:65:LEU:HB3	26:1:76:HIS:HB2	1.83	0.60
9:P:61:MET:HA	9:P:87:PRO:HB2	1.82	0.60
9:P:70:GLU:HB3	9:P:73:TYR:HB3	1.83	0.60
11:R:100:GLY:HA3	11:R:133:PRO:HG2	1.84	0.60
24:A:184:G:C6	24:A:192:A:N6	2.69	0.60
24:A:1236:U:C2	24:A:1240:G:N1	2.70	0.60
24:A:574:G:H21	24:A:577:A:H5''	1.67	0.60
9:P:104:CYS:SG	9:P:113:ARG:NH2	2.75	0.60
13:T:103:ASN:O	13:T:107:GLN:NE2	2.35	0.60
13:T:30:LYS:HE3	13:T:66:ARG:HH12	1.67	0.59
24:A:1200:A:C5	24:A:1551:A:N1	2.69	0.59
24:A:866:G:H1	24:A:958:U:H3	1.50	0.59
25:0:31:GLU:HG3	25:0:99:GLU:HB2	1.82	0.59
24:A:378:C:O2'	24:A:754:A:N1	2.35	0.59
21:f:16:VAL:HG12	21:f:29:VAL:HG12	1.85	0.59
24:A:443:A:H61	24:A:458:G:H21	1.46	0.59
13:T:55:LEU:HD22	13:T:105:LEU:HD22	1.83	0.59
32:7:394:LEU:O	32:7:397:PHE:HB2	2.02	0.59
8:O:80:VAL:O	8:O:125:GLY:N	2.36	0.59
24:A:1269:U:O2	24:A:1434:G:O6	2.21	0.59
5:K:7:ASN:HA	5:K:16:ARG:HH12	1.67	0.58
24:A:1147:G:N2	24:A:1624:U:O2	2.35	0.58
28:3:92:MET:CE	28:3:120:LYS:HA	2.33	0.58
15:W:117:ASP:OD2	15:W:120:ARG:NH1	2.36	0.58
24:A:700:G:N2	24:A:732:A:C2	2.63	0.58
24:A:986:A:OP1	31:6:477:LYS:NZ	2.31	0.58
24:A:1198:G:O6	24:A:1591:U:O4	2.21	0.58
27:2:263:VAL:HG12	27:2:275:VAL:HG12	1.84	0.58
6:L:7:SER:O	6:L:18:ARG:NH1	2.36	0.58
10:Q:124:ARG:NH2	24:A:965:A:OP2	2.35	0.58
2:H:87:MET:HE1	2:H:235:ILE:HG21	1.86	0.58
7:M:51:ARG:NH1	7:M:95:LEU:O	2.37	0.58
18:b:91:ARG:HE	18:b:103:VAL:HG23	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:7:394:LEU:HD11	32:7:433:GLY:HA3	1.86	0.58
18:b:112:LYS:NZ	24:A:456:G:OP1	2.33	0.58
26:1:188:LEU:HB3	26:1:200:TYR:HB2	1.84	0.58
8:O:30:THR:O	8:O:37:ARG:NH2	2.37	0.58
9:P:109:GLU:OE1	30:5:345:THR:N	2.37	0.58
24:A:898:A:H3'	24:A:899:G:H21	1.69	0.58
32:7:605:LEU:HD22	32:7:645:ILE:HG21	1.85	0.58
3:I:187:ASN:HB3	3:I:195:SER:HB2	1.86	0.58
6:L:16:ALA:HB2	24:A:351:C:H5''	1.85	0.58
24:A:1493:U:O4	24:A:1506:C:N3	2.37	0.58
6:L:144:LYS:NZ	24:A:189:C:O2'	2.36	0.57
11:R:85:LYS:NZ	11:R:121:SER:O	2.33	0.57
24:A:1218:A:H2	24:A:1261:G:H22	1.52	0.57
1:E:64:ARG:HG2	11:R:49:ARG:HG3	1.84	0.57
1:E:83:LYS:NZ	11:R:129:GLU:OE1	2.34	0.57
1:E:124:ASN:C	1:E:124:ASN:HD22	2.12	0.57
12:S:89:ARG:NH2	12:S:128:SER:O	2.37	0.57
24:A:1467:A:H62	24:A:1534:U:H3	1.52	0.57
10:Q:109:LYS:NZ	24:A:974:G:OP1	2.34	0.57
11:R:92:LEU:HB2	11:R:125:ILE:HG22	1.85	0.57
14:V:86:LEU:HD22	14:V:99:GLN:HB2	1.86	0.57
7:M:107:LEU:HB2	7:M:144:PHE:HB3	1.85	0.57
5:K:69:PRO:O	5:K:73:LEU:N	2.36	0.57
24:A:1778:A:OP1	31:6:515:ASN:ND2	2.37	0.57
24:A:426:G:O2'	27:2:239:ARG:NH2	2.35	0.57
12:S:57:LEU:HD22	12:S:91:MET:HE1	1.87	0.56
18:b:125:ALA:HA	18:b:128:LYS:HE2	1.86	0.56
14:V:17:LEU:HD11	14:V:66:LEU:HD11	1.87	0.56
14:V:83:THR:OG1	14:V:97:ASP:OD2	2.23	0.56
24:A:317:U:H3'	24:A:318:C:H2'	1.87	0.56
27:2:144:ARG:HH22	27:2:170:ASP:HB2	1.70	0.56
6:L:5:ARG:NH1	24:A:333:G:O6	2.38	0.56
11:R:106:THR:HG21	28:3:168:SER:HB2	1.87	0.56
13:T:103:ASN:HA	13:T:106:LYS:HG2	1.86	0.56
24:A:1273:U:O2	24:A:1431:G:C6	2.59	0.56
32:7:49:LEU:HD22	32:7:69:LEU:HD13	1.88	0.56
3:I:122:ASP:HA	3:I:125:VAL:HG12	1.87	0.56
11:R:84:CYS:HB2	11:R:89:ILE:HB	1.88	0.56
24:A:1199:A:N6	24:A:1453:C:OP1	2.38	0.56
27:2:682:ARG:NH2	27:2:817:GLU:OE1	2.37	0.56
8:O:62:LYS:NZ	24:A:323:G:OP1	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:86:MET:HE3	3:I:87:HIS:H	1.71	0.56
32:7:404:PHE:HD2	32:7:443:LYS:HE2	1.71	0.56
6:L:169:LEU:HD22	6:L:187:ILE:HD13	1.88	0.56
24:A:1570:G:HO2'	26:1:27:ARG:HH12	1.54	0.56
29:4:225:PRO:HB3	29:4:261:VAL:HG11	1.87	0.55
24:A:563:C:H2'	24:A:564:A:H8	1.70	0.55
3:I:135:ARG:HH12	3:I:142:VAL:HA	1.72	0.55
17:a:65:ASN:ND2	17:a:116:ASP:OD2	2.40	0.55
4:J:199:ARG:NH2	24:A:282:G:OP1	2.38	0.55
21:f:26:VAL:HA	21:f:46:LYS:HA	1.89	0.55
24:A:1265:G:O6	24:A:1438:U:O4	2.23	0.55
32:7:161:ARG:HE	32:7:223:THR:HA	1.70	0.55
24:A:1168:A:H2'	24:A:1169:G:H8	1.72	0.55
32:7:501:MET:HE1	32:7:523:VAL:HG12	1.88	0.55
15:W:22:PHE:O	15:W:26:GLN:HB2	2.06	0.55
32:7:527:ILE:HA	32:7:530:ILE:HD12	1.88	0.55
6:L:139:SER:OG	24:A:186:C:N4	2.39	0.55
13:T:71:GLY:HA2	24:A:1479:A:H4'	1.89	0.55
12:S:103:GLY:HA2	12:S:111:ASN:O	2.07	0.55
24:A:1220:G:H22	24:A:1259:U:H3	1.55	0.55
28:3:118:LYS:HB3	28:3:119:GLU:OE2	2.07	0.55
28:3:138:MET:HG2	28:3:159:LEU:HD12	1.89	0.55
28:3:175:ARG:HD2	28:3:178:LEU:HD13	1.88	0.55
24:A:700:G:H21	24:A:732:A:H2	1.51	0.54
24:A:1457:C:H2'	24:A:1458:G:H8	1.71	0.54
28:3:189:ARG:NH1	28:3:235:LEU:O	2.36	0.54
29:4:275:ARG:O	29:4:279:HIS:ND1	2.37	0.54
32:7:794:SER:O	32:7:797:VAL:HB	2.07	0.54
2:H:151:ASP:OD2	4:J:218:ARG:NH1	2.40	0.54
4:J:116:GLN:HE22	4:J:125:THR:HB	1.72	0.54
24:A:707:A:N1	24:A:724:U:O2'	2.40	0.54
24:A:1480:G:N3	24:A:1602:C:O2'	2.34	0.54
24:A:1041:A:H5'	24:A:1041:A:C8	2.41	0.54
2:H:100:ARG:NH2	2:H:118:GLU:O	2.40	0.54
14:V:88:ARG:NH1	14:V:89:GLN:O	2.40	0.54
24:A:1500:G:N3	24:A:1559:C:O2'	2.39	0.54
27:2:519:MET:HE1	27:2:651:LYS:HB2	1.89	0.54
32:7:924:LEU:O	32:7:965:ARG:NH1	2.40	0.54
23:i:123:ASN:HB3	23:i:126:CYS:HB3	1.89	0.54
24:A:922:A:H2'	24:A:923:G:C8	2.43	0.54
26:1:34:ALA:HA	26:1:37:ARG:HH11	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:187:LEU:HB2	26:1:228:GLU:HB2	1.90	0.54
27:2:90:PRO:HD2	27:2:278:VAL:HG11	1.90	0.54
24:A:708:U:O2	24:A:723:G:O6	2.26	0.54
3:I:32:ARG:NH1	3:I:106:GLU:OE1	2.41	0.54
17:a:17:ASN:OD1	17:a:20:ARG:NH2	2.41	0.54
27:2:138:GLN:NE2	27:2:261:GLU:OE2	2.39	0.54
6:L:172:ILE:HG13	6:L:188:LEU:HD23	1.90	0.54
16:Z:55:ASN:C	16:Z:57:ARG:H	2.16	0.54
27:2:472:GLU:OE1	27:2:475:ARG:NH2	2.41	0.54
27:2:540:LEU:HD13	27:2:602:THR:HA	1.89	0.54
32:7:860:LEU:HD21	32:7:872:ILE:HG13	1.90	0.54
32:7:389:TYR:O	32:7:392:ALA:HB3	2.08	0.53
17:a:125:VAL:HG12	17:a:126:LYS:HG3	1.88	0.53
22:h:27:PRO:O	22:h:28:LYS:C	2.50	0.53
11:R:150:LEU:HD21	28:3:230:GLU:HG3	1.89	0.53
17:a:64:PRO:O	26:1:246:LYS:N	2.42	0.53
8:O:107:LYS:O	17:a:13:ARG:NH2	2.41	0.53
16:Z:83:LEU:O	16:Z:117:ARG:NH2	2.41	0.53
24:A:1259:U:H2'	24:A:1260:G:H8	1.72	0.53
25:0:46:ASN:ND2	26:1:117:ASP:OD2	2.41	0.53
3:I:45:LEU:HG	3:I:125:VAL:HG23	1.90	0.53
24:A:910:U:H5''	24:A:911:G:H3'	1.90	0.53
28:3:196:LYS:O	28:3:200:ALA:N	2.38	0.53
32:7:446:ARG:HB3	32:7:481:TYR:HB3	1.89	0.53
11:R:54:ARG:NH2	24:A:894:U:O2	2.42	0.53
17:a:74:VAL:HG11	17:a:104:LEU:HD11	1.90	0.53
24:A:1629:A:OP2	24:A:1631:A:N6	2.41	0.53
27:2:71:GLU:OE2	27:2:74:ARG:NH2	2.42	0.53
29:4:224:LEU:HD12	29:4:227:ILE:HD12	1.91	0.53
9:P:52:LYS:NZ	24:A:1251:U:OP2	2.42	0.53
19:c:67:LYS:HA	19:c:70:LYS:HG2	1.91	0.53
29:4:430:ARG:NH2	29:4:457:ARG:O	2.41	0.53
24:A:442:A:H1'	24:A:522:A:H5''	1.89	0.53
25:0:26:HIS:ND1	25:0:62:GLU:OE2	2.41	0.53
2:H:95:THR:HG22	18:b:19:PRO:HD2	1.91	0.52
16:Z:76:SER:HB2	24:A:1098:G:H5''	1.90	0.52
32:7:82:ARG:NH1	32:7:120:GLN:OE1	2.41	0.52
6:L:110:ARG:NH2	6:L:164:PHE:O	2.42	0.52
9:P:129:GLU:OE1	9:P:133:ARG:N	2.42	0.52
24:A:1651:A:N6	24:A:1741:G:C6	2.75	0.52
26:1:159:ALA:HB3	26:1:203:LEU:HB2	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:44:HIS:ND1	24:A:1672:U:OP1	2.40	0.52
12:S:112:GLN:NE2	27:2:395:LYS:O	2.42	0.52
14:V:26:GLN:HE21	14:V:31:ALA:HA	1.74	0.52
15:W:134:ASP:O	15:W:138:GLN:NE2	2.43	0.52
21:f:13:VAL:O	21:f:52:ASN:CA	2.55	0.52
24:A:702:A:N6	24:A:731:G:C2	2.77	0.52
24:A:1172:U:H2'	24:A:1173:G:H8	1.75	0.52
19:c:48:LEU:HD21	19:c:57:ARG:HH12	1.75	0.52
24:A:1570:G:O2'	26:1:27:ARG:NH1	2.36	0.52
31:6:514:ALA:HA	31:6:517:LYS:HB2	1.90	0.52
32:7:883:ARG:NH1	32:7:923:SER:OG	2.42	0.52
29:4:356:ARG:HG3	29:4:358:GLU:H	1.75	0.52
30:5:345:THR:OG1	30:5:346:GLU:OE1	2.27	0.52
1:E:134:LEU:HB3	1:E:219:LYS:HB3	1.92	0.52
7:M:146:VAL:HG11	7:M:154:ILE:HD11	1.91	0.52
11:R:116:ARG:NH2	28:3:141:ASP:OD2	2.41	0.52
27:2:299:GLN:NE2	27:2:335:ASP:O	2.42	0.52
32:7:888:LYS:NZ	32:7:892:THR:OG1	2.43	0.52
7:M:137:GLN:NE2	18:b:67:TYR:O	2.40	0.52
24:A:1168:A:H2'	24:A:1169:G:C8	2.44	0.52
3:I:133:SER:HB2	3:I:144:ARG:HB3	1.92	0.52
4:J:177:ARG:HG3	24:A:77:A:H2	1.75	0.52
7:M:57:LEU:HD22	7:M:67:ARG:HA	1.90	0.52
28:3:209:ILE:HD13	28:3:232:ILE:HD11	1.90	0.52
14:V:101:LEU:O	14:V:105:VAL:N	2.40	0.52
24:A:1581:U:H2'	24:A:1582:A:H8	1.74	0.52
28:3:109:CYS:HB3	28:3:135:ALA:HB1	1.92	0.51
28:3:111:LEU:HD11	28:3:136:LEU:HA	1.91	0.51
29:4:199:VAL:HG13	29:4:236:LEU:HD11	1.93	0.51
12:S:37:ASP:OD2	12:S:38:SER:N	2.42	0.51
14:V:123:ARG:NH2	24:A:1542:G:OP1	2.43	0.51
24:A:1480:G:H1	24:A:1587:C:H1'	1.73	0.51
27:2:215:ILE:O	27:2:219:HIS:N	2.34	0.51
27:2:285:LYS:NZ	27:2:556:GLU:O	2.40	0.51
24:A:1448:U:H2'	24:A:1449:G:H8	1.76	0.51
7:M:171:ARG:HE	24:A:508:A:H5'	1.73	0.51
30:5:401:GLN:HB3	30:5:412:LYS:HD3	1.91	0.51
25:0:2:LYS:HG2	25:0:96:GLN:HG2	1.92	0.51
11:R:66:ASP:HB2	11:R:69:SER:HB3	1.92	0.51
28:3:119:GLU:HG2	28:3:121:ARG:CD	2.41	0.51
29:4:324:ILE:HD11	29:4:366:LEU:HD21	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:e:19:HIS:HB3	20:e:22:LYS:HG3	1.93	0.51
32:7:939:ASN:O	32:7:942:VAL:HB	2.11	0.51
17:a:58:GLY:HA2	17:a:70:LYS:HA	1.93	0.51
26:1:32:GLN:HA	26:1:35:MET:HG2	1.93	0.51
7:M:50:ILE:HD13	7:M:78:LEU:HD21	1.93	0.51
8:O:85:MET:HE1	8:O:90:ILE:HG12	1.93	0.51
24:A:1482:G:H21	24:A:1588:A:H4'	1.75	0.51
32:7:454:LEU:HD12	32:7:489:HIS:HE1	1.76	0.51
20:e:67:THR:OG1	20:e:70:LYS:O	2.28	0.51
24:A:1055:A:N6	24:A:1058:U:OP1	2.44	0.51
24:A:1145:C:H2'	24:A:1147:G:C8	2.46	0.51
24:A:1709:G:H2'	24:A:1710:G:H8	1.76	0.51
28:3:151:ASP:OD1	28:3:152:ILE:N	2.43	0.51
6:L:182:ARG:NH1	24:A:255:C:O2	2.43	0.50
17:a:95:PHE:O	17:a:142:LYS:NZ	2.39	0.50
24:A:1145:C:N4	24:A:1147:G:O6	2.43	0.50
1:E:88:VAL:HA	1:E:98:THR:HA	1.94	0.50
13:T:78:VAL:HA	13:T:81:VAL:HG22	1.94	0.50
17:a:68:ILE:HD12	17:a:70:LYS:HE3	1.94	0.50
24:A:1146:G:H3'	24:A:1147:G:H4'	1.94	0.50
24:A:1462:G:O2'	24:A:1598:C:OP1	2.26	0.50
4:J:51:ARG:HD2	4:J:53:THR:HG22	1.94	0.50
6:L:57:ALA:HB2	6:L:181:GLY:HA2	1.94	0.50
24:A:1077:U:H2'	24:A:1078:A:H5''	1.93	0.50
3:I:149:VAL:O	3:I:154:ARG:NH1	2.45	0.50
4:J:198:ARG:CG	24:A:175:G:N2	2.70	0.50
15:W:128:GLN:HA	15:W:131:ARG:HG2	1.94	0.50
26:1:164:TYR:HE1	26:1:198:LYS:HG3	1.77	0.50
27:2:282:LYS:HE3	27:2:558:LEU:HD23	1.93	0.50
27:2:473:ASP:N	27:2:473:ASP:OD1	2.45	0.50
10:Q:104:ARG:NH2	10:Q:105:ASN:OD1	2.45	0.50
11:R:29:VAL:HG12	11:R:93:HIS:HB2	1.93	0.50
15:W:38:VAL:HG22	15:W:40:THR:H	1.77	0.50
24:A:798:U:H2'	24:A:799:G:C8	2.46	0.50
32:7:258:VAL:HA	32:7:261:ILE:HD12	1.94	0.50
24:A:29:U:H2'	24:A:30:G:H8	1.76	0.50
4:J:92:ARG:O	24:A:402:C:O2'	2.22	0.50
5:K:32:ASP:O	5:K:36:ASN:ND2	2.45	0.50
12:S:59:ARG:HG3	12:S:62:LEU:HD21	1.92	0.50
24:A:107:A:H2'	24:A:108:G:C8	2.46	0.50
24:A:552:A:N3	24:A:587:C:O2'	2.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:1272:A:N1	24:A:1431:G:C6	2.80	0.50
24:A:1448:U:H2'	24:A:1449:G:C8	2.45	0.50
6:L:33:PRO:HA	24:A:328:G:H5'	1.94	0.50
24:A:1200:A:C5	24:A:1551:A:C6	3.00	0.50
24:A:1480:G:H2'	24:A:1481:C:C6	2.47	0.50
24:A:1650:G:N2	24:A:1742:A:N6	2.41	0.50
26:1:163:PHE:HE1	26:1:201:LEU:HD23	1.77	0.50
33:8:431:ILE:C	33:8:433:LYS:N	2.63	0.50
3:I:67:LYS:HD3	3:I:69:PHE:H	1.76	0.49
7:M:51:ARG:HB3	7:M:55:ARG:HH21	1.77	0.49
27:2:543:ILE:HD12	27:2:714:PRO:HG2	1.94	0.49
32:7:85:PHE:HD1	32:7:116:LEU:HD13	1.77	0.49
12:S:68:LEU:HD11	12:S:100:SER:HB3	1.94	0.49
24:A:575:U:O4	27:2:785:ARG:NH1	2.45	0.49
32:7:121:ASP:OD1	32:7:121:ASP:N	2.43	0.49
11:R:37:ASN:ND2	24:A:900:G:OP2	2.45	0.49
11:R:94:ILE:HG21	11:R:115:LEU:HD13	1.95	0.49
19:c:32:ASP:OD1	19:c:32:ASP:N	2.44	0.49
2:H:65:MET:HG3	2:H:80:ILE:HG22	1.93	0.49
3:I:176:THR:OG1	3:I:179:GLU:OE1	2.31	0.49
15:W:57:ARG:NE	24:A:1475:A:OP1	2.41	0.49
24:A:17:C:O2'	24:A:1134:A:N1	2.44	0.49
24:A:1178:U:C2	24:A:1454:G:N1	2.80	0.49
24:A:1432:A:H2	24:A:1434:G:H8	1.61	0.49
32:7:815:LEU:HA	32:7:818:MET:HE2	1.94	0.49
14:V:68:ARG:O	14:V:72:ILE:HG12	2.13	0.49
19:c:43:VAL:O	19:c:92:ARG:NH1	2.45	0.49
23:i:80:ARG:HH21	27:2:729:HIS:CG	2.30	0.49
27:2:298:PHE:HE2	27:2:575:LEU:HD12	1.76	0.49
32:7:400:ILE:HG23	32:7:403:MET:HE2	1.95	0.49
1:E:90:GLU:HB3	1:E:97:LEU:HB2	1.95	0.49
4:J:67:VAL:HG23	4:J:99:GLY:HA2	1.94	0.49
24:A:1773:G:OP1	31:6:499:ARG:NH1	2.46	0.49
27:2:275:VAL:HG23	27:2:570:VAL:HB	1.94	0.49
21:f:45:VAL:HG12	21:f:47:GLY:H	1.78	0.49
28:3:96:LYS:HG2	33:8:829:TRP:CZ2	2.48	0.49
29:4:422:ARG:NH1	29:4:452:GLU:OE2	2.46	0.49
32:7:69:LEU:O	32:7:73:THR:OG1	2.28	0.49
5:K:91:PHE:HB3	5:K:94:ARG:HG3	1.95	0.49
24:A:1539:A:N6	24:A:1564:C:O2	2.45	0.49
24:A:1544:G:N1	24:A:1560:U:C4	2.81	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:4:230:TRP:HA	29:4:233:ILE:HD12	1.94	0.49
31:6:503:MET:HE3	31:6:508:LYS:HB2	1.93	0.49
1:E:31:ASN:ND2	1:E:94:LYS:O	2.43	0.48
5:K:6:LEU:O	5:K:16:ARG:NH1	2.46	0.48
27:2:783:ASP:N	27:2:783:ASP:OD1	2.46	0.48
28:3:103:PRO:HG3	33:8:827:PRO:HB2	1.94	0.48
24:A:588:A:H2'	24:A:589:A:C8	2.48	0.48
22:h:27:PRO:HD2	24:A:502:A:C4	2.47	0.48
27:2:109:LYS:HE3	27:2:121:VAL:HB	1.95	0.48
1:E:46:THR:OG1	11:R:45:ASP:OD2	2.29	0.48
13:T:50:GLU:HG3	13:T:82:ARG:HH21	1.78	0.48
14:V:15:LEU:HD11	14:V:59:GLY:HA2	1.96	0.48
18:b:91:ARG:NH2	18:b:101:ALA:O	2.47	0.48
27:2:595:LEU:HB2	27:2:598:GLU:HG3	1.94	0.48
2:H:27:TYR:O	24:A:444:U:O2'	2.31	0.48
3:I:151:PRO:HA	3:I:154:ARG:HB2	1.95	0.48
9:P:126:TRP:HB2	9:P:133:ARG:HH12	1.79	0.48
12:S:62:LEU:HA	12:S:65:ILE:HG22	1.95	0.48
14:V:65:GLU:HA	14:V:68:ARG:HG2	1.96	0.48
24:A:29:U:H2'	24:A:30:G:C8	2.49	0.48
26:1:115:THR:N	26:1:152:ALA:O	2.46	0.48
27:2:598:GLU:O	27:2:631:ARG:NH1	2.44	0.48
29:4:374:ARG:NH1	29:4:420:ARG:O	2.46	0.48
4:J:180:ARG:NH2	24:A:140:G:O6	2.47	0.48
10:Q:54:LEU:HD13	10:Q:60:ILE:HD11	1.96	0.48
24:A:158:U:H2'	24:A:159:A:H8	1.79	0.48
24:A:1585:C:H2'	24:A:1586:G:C8	2.49	0.48
4:J:102:VAL:HG13	4:J:109:LEU:HD21	1.95	0.48
11:R:21:ARG:NE	11:R:24:GLU:OE2	2.47	0.48
11:R:60:LYS:HA	11:R:60:LYS:HD3	1.63	0.48
24:A:485:G:O6	24:A:496:U:O4	2.32	0.48
9:P:137:LEU:HA	9:P:140:PHE:HD2	1.79	0.48
24:A:648:C:H2'	24:A:649:G:H8	1.78	0.48
24:A:1650:G:C2	24:A:1742:A:N6	2.81	0.48
24:A:1689:A:H2'	24:A:1690:G:H8	1.79	0.48
32:7:438:ASP:HB3	32:7:477:LEU:HD11	1.96	0.48
6:L:61:ASP:OD1	6:L:61:ASP:N	2.44	0.48
12:S:72:LYS:O	30:5:430:ARG:NH2	2.45	0.48
14:V:100:ILE:HD12	14:V:105:VAL:HA	1.96	0.48
15:W:106:GLN:NE2	24:A:1496:C:OP1	2.47	0.48
24:A:510:U:H2'	24:A:511:G:C8	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:561:G:N2	24:A:578:U:OP1	2.47	0.48
24:A:937:A:H2'	24:A:938:A:C8	2.48	0.48
26:1:171:LYS:HE2	26:1:187:LEU:HD22	1.95	0.48
4:J:165:LYS:HE3	24:A:70:C:H5'	1.96	0.47
13:T:58:ASP:OD1	13:T:58:ASP:N	2.47	0.47
32:7:422:ILE:HD13	32:7:440:VAL:HG11	1.95	0.47
17:a:19:ARG:O	17:a:23:ARG:HB2	2.15	0.47
8:O:78:GLY:HA3	8:O:91:ILE:HD12	1.96	0.47
14:V:40:ARG:NH2	15:W:45:GLU:OE2	2.47	0.47
17:a:109:ARG:HB3	17:a:112:LYS:HE2	1.96	0.47
26:1:49:SER:HB3	26:1:117:ASP:HB2	1.96	0.47
27:2:355:MET:O	27:2:358:ALA:HB3	2.13	0.47
27:2:610:LEU:HD12	27:2:611:PRO:HD2	1.96	0.47
32:7:387:ILE:O	32:7:390:GLN:HB2	2.14	0.47
12:S:119:MET:HG3	14:V:119:ILE:HD11	1.96	0.47
24:A:798:U:H2'	24:A:799:G:H8	1.79	0.47
24:A:1470:G:H2'	24:A:1471:A:C8	2.49	0.47
24:A:1652:U:O2	24:A:1741:G:N2	2.48	0.47
28:3:134:GLU:O	28:3:138:MET:HB2	2.15	0.47
32:7:892:THR:HG23	32:7:932:ARG:HH12	1.79	0.47
3:I:144:ARG:NH2	26:1:7:THR:O	2.46	0.47
13:T:26:LYS:HE3	13:T:28:LEU:HD23	1.96	0.47
15:W:26:GLN:HE22	15:W:28:LYS:HE3	1.79	0.47
21:f:11:VAL:HG21	21:f:57:LEU:HD12	1.95	0.47
22:h:38:LEU:HD23	22:h:42:ARG:HD3	1.97	0.47
23:i:119:ARG:NH1	23:i:121:CYS:SG	2.84	0.47
28:3:92:MET:HE2	28:3:120:LYS:HA	1.95	0.47
29:4:374:ARG:HD3	29:4:420:ARG:HD2	1.96	0.47
32:7:569:ARG:HH21	32:7:634:PRO:HB3	1.79	0.47
3:I:136:ILE:HD11	21:f:22:SER:H	1.80	0.47
16:Z:115:GLU:OE2	16:Z:119:LYS:NZ	2.45	0.47
24:A:1210:G:O6	24:A:1447:C:N4	2.48	0.47
24:A:1269:U:O2	24:A:1435:C:N3	2.47	0.47
32:7:704:PHE:HE2	32:7:739:VAL:HG13	1.79	0.47
9:P:134:THR:HA	9:P:137:LEU:HG	1.96	0.47
10:Q:70:LYS:NZ	24:A:961:A:N7	2.62	0.47
13:T:44:LEU:HD11	13:T:75:THR:HG22	1.95	0.47
31:6:495:LYS:HD2	31:6:499:ARG:HH21	1.80	0.47
6:L:34:ALA:HB2	6:L:56:ARG:HD3	1.96	0.47
9:P:47:LEU:HA	9:P:50:ALA:HB3	1.96	0.47
24:A:443:A:H61	24:A:458:G:N2	2.09	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:643:U:H2'	24:A:644:A:H8	1.79	0.47
27:2:260:ILE:HD12	27:2:275:VAL:HB	1.96	0.47
28:3:99:TRP:HA	28:3:102:TYR:CD1	2.50	0.47
29:4:197:LYS:HD2	30:5:397:LEU:HD11	1.95	0.47
29:4:230:TRP:HE1	29:4:264:ARG:HH21	1.63	0.47
11:R:92:LEU:HG	11:R:123:MET:HE2	1.97	0.47
24:A:607:G:O2'	24:A:610:G:O2'	2.26	0.47
33:8:408:LYS:HA	33:8:411:ILE:HD12	1.97	0.47
21:f:48:PRO:HG2	24:A:1610:A:H5'	1.95	0.47
24:A:552:A:H2'	24:A:553:A:C8	2.51	0.47
27:2:501:HIS:CE1	27:2:503:LYS:HG2	2.50	0.47
2:H:117:GLU:O	2:H:120:LYS:HG2	2.15	0.46
9:P:48:ARG:NH2	24:A:1250:U:OP2	2.49	0.46
18:b:9:THR:HG22	18:b:31:LEU:HB2	1.97	0.46
24:A:1178:U:O2	24:A:1454:G:C2	2.68	0.46
24:A:1795:U:H5''	33:8:423:ARG:HH22	1.79	0.46
28:3:99:TRP:CD1	33:8:826:LEU:HB3	2.50	0.46
29:4:289:PHE:HZ	29:4:330:ARG:HD3	1.80	0.46
3:I:209:LYS:HZ2	21:f:58:LEU:HD11	1.80	0.46
22:h:26:LYS:O	22:h:27:PRO:C	2.58	0.46
24:A:411:C:OP1	27:2:134:LYS:NZ	2.48	0.46
24:A:1703:C:H2'	24:A:1704:A:H8	1.81	0.46
32:7:613:ALA:O	32:7:617:LEU:HB2	2.16	0.46
16:Z:8:HIS:HB2	16:Z:74:VAL:HG11	1.97	0.46
17:a:62:LYS:NZ	24:A:1134:A:OP1	2.47	0.46
19:c:81:VAL:HB	19:c:89:ILE:HG13	1.96	0.46
24:A:485:G:H1	24:A:496:U:H3	1.61	0.46
24:A:1202:C:OP1	24:A:1204:C:O2'	2.32	0.46
4:J:58:LYS:HA	4:J:107:SER:HB3	1.98	0.46
19:c:35:THR:HA	19:c:38:LYS:HG2	1.97	0.46
23:i:141:CYS:SG	23:i:142:GLY:N	2.88	0.46
24:A:231:G:H2'	24:A:232:G:C8	2.50	0.46
24:A:483:G:N2	24:A:498:U:O2	2.33	0.46
27:2:366:LYS:HA	27:2:366:LYS:HD3	1.75	0.46
28:3:114:ARG:HB2	33:8:832:TRP:HA	1.97	0.46
32:7:358:VAL:HG21	32:7:406:ALA:HB1	1.97	0.46
32:7:535:CYS:HB3	32:7:574:LEU:HG	1.96	0.46
32:7:865:PRO:HB3	32:7:909:ILE:HD11	1.97	0.46
4:J:178:ILE:HG13	24:A:77:A:H1'	1.96	0.46
6:L:56:ARG:HH22	24:A:329:U:P	2.39	0.46
24:A:648:C:H2'	24:A:649:G:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:652:G:O6	24:A:673:U:O4	2.34	0.46
24:A:1198:G:O6	24:A:1591:U:C4	2.68	0.46
32:7:693:VAL:HG22	32:7:730:LEU:HD13	1.98	0.46
32:7:774:ILE:O	32:7:778:ILE:HG12	2.15	0.46
3:I:121:VAL:HA	3:I:124:ILE:HG12	1.98	0.46
18:b:63:LEU:HD23	18:b:74:GLY:HA3	1.97	0.46
33:8:826:LEU:O	33:8:827:PRO:C	2.59	0.46
4:J:176:PRO:HA	24:A:66:U:H5'	1.97	0.46
13:T:93:TYR:HA	13:T:97:VAL:HG12	1.98	0.46
24:A:1584:G:N2	24:A:1604:U:O2	2.35	0.46
24:A:1261:G:H2'	24:A:1262:G:H8	1.81	0.46
24:A:1651:A:N1	24:A:1741:G:N2	2.63	0.46
32:7:107:ARG:HD2	32:7:151:LYS:HB3	1.98	0.46
2:H:19:LEU:HD22	24:A:786:A:H2'	1.98	0.46
2:H:87:MET:HE1	2:H:235:ILE:HD13	1.97	0.46
3:I:64:TYR:HB3	3:I:71:LYS:HA	1.97	0.46
3:I:98:VAL:HA	3:I:101:VAL:HG12	1.98	0.46
4:J:14:LYS:HB3	4:J:124:LEU:HD12	1.97	0.46
4:J:198:ARG:NH2	24:A:281:G:OP1	2.49	0.46
7:M:64:ASP:HB3	7:M:67:ARG:HB3	1.98	0.46
13:T:65:ILE:HG21	13:T:85:ILE:HG22	1.98	0.46
18:b:64:ARG:NH1	24:A:527:C:O2	2.40	0.46
26:1:260:MET:HE2	26:1:265:LYS:HD2	1.98	0.46
28:3:91:ARG:HD2	28:3:91:ARG:HA	1.64	0.46
2:H:171:ASP:OD1	2:H:172:PHE:N	2.44	0.46
6:L:110:ARG:O	6:L:114:GLU:HG2	2.16	0.46
8:O:104:ARG:HG3	17:a:12:ALA:HB2	1.97	0.46
15:W:70:THR:HG23	15:W:122:GLY:HA3	1.97	0.46
24:A:425:A:N3	24:A:437:U:O2'	2.40	0.46
24:A:1473:A:H2'	24:A:1474:G:H8	1.81	0.46
25:0:1:MET:HG3	25:0:97:ILE:HB	1.98	0.46
26:1:106:GLY:O	26:1:144:ARG:NH2	2.47	0.46
27:2:96:ILE:HD11	27:2:153:CYS:SG	2.56	0.46
27:2:652:TYR:HB3	27:2:722:LYS:HA	1.98	0.46
14:V:101:LEU:HD12	14:V:104:GLY:H	1.80	0.45
24:A:1040:G:O2'	24:A:1041:A:H2'	2.16	0.45
24:A:1699:C:H2'	24:A:1700:G:H8	1.81	0.45
26:1:142:LEU:HD13	26:1:174:ILE:HG22	1.98	0.45
32:7:445:ILE:HG21	32:7:478:LEU:HD23	1.97	0.45
32:7:623:VAL:O	32:7:627:THR:OG1	2.25	0.45
5:K:57:VAL:HG21	5:K:178:THR:HA	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:S:59:ARG:HH22	30:5:411:GLY:HA3	1.80	0.45
24:A:979:U:OP1	31:6:499:ARG:NH2	2.49	0.45
32:7:252:GLU:HG2	32:7:256:MET:HE1	1.97	0.45
2:H:146:THR:HG21	24:A:122:G:H21	1.81	0.45
17:a:109:ARG:HE	17:a:112:LYS:HE2	1.81	0.45
19:c:38:LYS:O	19:c:42:ASP:HB2	2.16	0.45
23:i:121:CYS:HB2	23:i:123:ASN:HD21	1.80	0.45
24:A:1708:A:H2'	24:A:1709:G:C8	2.51	0.45
26:1:88:LEU:HD22	26:1:100:LEU:HD22	1.98	0.45
32:7:411:SER:HB3	32:7:448:MET:HE2	1.98	0.45
32:7:525:GLN:HG2	32:7:563:LEU:HD21	1.98	0.45
1:E:75:LYS:HE3	1:E:75:LYS:HB3	1.65	0.45
24:A:1078:A:H62	24:A:1088:A:H62	1.65	0.45
25:0:4:LEU:HD13	25:0:92:LEU:HD13	1.99	0.45
6:L:56:ARG:NH1	6:L:178:GLY:O	2.50	0.45
15:W:130:GLN:HA	15:W:133:LEU:HG	1.99	0.45
24:A:673:U:H2'	24:A:674:G:C8	2.51	0.45
24:A:1229:U:H2'	24:A:1230:G:C8	2.52	0.45
26:1:136:THR:HB	26:1:141:ARG:HD2	1.97	0.45
5:K:105:LEU:O	5:K:122:ARG:NH1	2.50	0.45
17:a:50:LYS:HG3	17:a:103:LEU:HD13	1.99	0.45
24:A:852:U:O4	24:A:853:A:N6	2.50	0.45
24:A:1541:A:H2'	24:A:1542:G:H8	1.82	0.45
24:A:1584:G:O6	24:A:1604:U:O4	2.35	0.45
25:0:101:LYS:HZ3	25:0:112:ALA:HB2	1.82	0.45
28:3:119:GLU:HG2	28:3:121:ARG:HG3	1.94	0.45
32:7:114:GLU:HA	32:7:163:ILE:HD11	1.99	0.45
3:I:78:GLU:OE2	3:I:82:ASN:ND2	2.49	0.45
12:S:69:ARG:NH2	30:5:426:LEU:HA	2.31	0.45
12:S:143:ALA:HB2	24:A:1175:G:H21	1.82	0.45
13:T:13:LYS:HG3	13:T:14:LYS:H	1.82	0.45
24:A:1520:A:H2'	24:A:1521:A:C8	2.52	0.45
24:A:1687:A:H2'	24:A:1688:G:C8	2.51	0.45
28:3:216:VAL:HG11	28:3:232:ILE:HD13	1.98	0.45
24:A:84:A:N3	24:A:145:A:O2'	2.47	0.45
6:L:25:ARG:HA	24:A:397:A:H5''	1.99	0.45
6:L:87:ASN:HB3	6:L:90:LEU:HG	1.98	0.45
8:O:41:LYS:NZ	8:O:69:VAL:O	2.44	0.45
24:A:565:G:H22	24:A:571:G:H1	1.62	0.45
27:2:90:PRO:HA	27:2:136:LYS:O	2.17	0.45
28:3:95:LEU:HD21	28:3:122:VAL:CG2	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:7:325:LEU:HD11	32:7:373:VAL:HG22	1.98	0.45
11:R:38:ASP:OD1	11:R:39:THR:N	2.49	0.45
12:S:71:ALA:HA	12:S:74:GLU:HG2	1.99	0.45
16:Z:55:ASN:C	16:Z:57:ARG:N	2.75	0.45
28:3:166:ILE:HA	28:3:218:ILE:O	2.16	0.45
32:7:720:ASP:HB3	32:7:723:ILE:HG22	1.98	0.45
32:7:802:GLU:O	32:7:808:ARG:NH1	2.41	0.45
3:I:84:LEU:HD23	3:I:84:LEU:HA	1.87	0.44
13:T:20:ALA:HB2	13:T:84:ALA:HB1	1.99	0.44
18:b:6:SER:O	18:b:35:ARG:NH1	2.49	0.44
24:A:1234:G:N1	24:A:1246:U:O4	2.50	0.44
25:0:2:LYS:HD3	25:0:93:MET:HA	1.99	0.44
26:1:51:ILE:HG12	26:1:118:ALA:HB3	2.00	0.44
27:2:109:LYS:HG3	27:2:121:VAL:HG21	1.99	0.44
28:3:218:ILE:HG22	28:3:225:ILE:HG12	1.98	0.44
29:4:283:LYS:HB2	29:4:283:LYS:HE2	1.82	0.44
32:7:234:LYS:HD2	32:7:235:LYS:HG2	1.99	0.44
21:f:19:ARG:HA	21:f:27:THR:HA	1.99	0.44
24:A:1001:A:C5	28:3:251:ILE:HD11	2.52	0.44
24:A:1161:G:H2'	24:A:1162:G:H8	1.83	0.44
24:A:1580:G:O2'	24:A:1606:G:O6	2.28	0.44
29:4:226:THR:O	30:5:386:ARG:NH1	2.50	0.44
18:b:12:THR:HB	18:b:26:MET:HG3	2.00	0.44
4:J:10:ASN:HD22	4:J:128:VAL:HG12	1.83	0.44
6:L:76:THR:HG21	6:L:104:ILE:HD12	2.00	0.44
15:W:117:ASP:CG	15:W:124:ARG:HH12	2.25	0.44
16:Z:87:GLU:HA	16:Z:90:VAL:HG22	1.99	0.44
21:f:23:ARG:HH21	24:A:1159:C:H4'	1.81	0.44
24:A:404:A:H2'	24:A:405:C:C6	2.52	0.44
24:A:692:C:H4'	24:A:693:U:H5''	1.99	0.44
28:3:99:TRP:HD1	33:8:826:LEU:HB3	1.82	0.44
30:5:406:LYS:HE2	30:5:406:LYS:HB3	1.87	0.44
1:E:70:LEU:HD13	1:E:84:ILE:HD12	1.99	0.44
3:I:58:PRO:HB3	3:I:77:ILE:HG22	2.00	0.44
4:J:88:ARG:HB3	4:J:91:GLU:HB2	1.99	0.44
24:A:1073:A:H4'	24:A:1074:C:OP2	2.17	0.44
32:7:459:LEU:HB3	32:7:461:LEU:HG	1.98	0.44
2:H:54:TYR:O	18:b:18:ASN:ND2	2.50	0.44
11:R:145:ARG:NH2	24:A:1785:G:N7	2.65	0.44
28:3:89:PRO:HA	28:3:92:MET:HB2	2.00	0.44
32:7:783:ASN:HA	32:7:786:LEU:HG	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:159:ARG:HH21	4:J:173:THR:HG23	1.81	0.44
15:W:58:ALA:HB1	15:W:108:LEU:HD12	2.00	0.44
23:i:122:PRO:HD2	23:i:146:LEU:HD13	2.00	0.44
24:A:844:G:H2'	24:A:845:A:H8	1.82	0.44
24:A:1001:A:C4	28:3:251:ILE:HD11	2.52	0.44
24:A:1643:U:H2'	24:A:1644:A:C8	2.52	0.44
24:A:1643:U:H2'	24:A:1644:A:H8	1.83	0.44
32:7:557:LEU:O	32:7:564:ARG:NE	2.49	0.44
3:I:21:LEU:HA	3:I:24:VAL:HG12	2.00	0.44
13:T:82:ARG:HA	13:T:85:ILE:HG12	2.00	0.44
21:f:32:GLU:HG3	21:f:34:MET:H	1.83	0.44
24:A:1084:A:H2'	24:A:1085:A:C8	2.51	0.44
27:2:391:LYS:NZ	27:2:406:LEU:O	2.47	0.44
2:H:65:MET:HE3	2:H:65:MET:HB3	1.74	0.44
5:K:20:SER:OG	5:K:23:GLU:OE1	2.28	0.44
9:P:61:MET:HE3	9:P:123:VAL:HB	2.00	0.44
15:W:144:ASP:N	15:W:144:ASP:OD1	2.51	0.44
27:2:607:LEU:O	27:2:709:GLY:HA3	2.18	0.44
2:H:211:LYS:HB3	2:H:211:LYS:HE3	1.85	0.43
5:K:93:ASP:OD2	5:K:94:ARG:NH2	2.51	0.43
5:K:120:GLN:HE22	24:A:814:G:H21	1.64	0.43
24:A:893:G:H2'	24:A:894:U:C6	2.52	0.43
24:A:1068:U:H2'	24:A:1069:C:C6	2.53	0.43
32:7:629:PRO:HA	32:7:632:ARG:HD2	1.99	0.43
3:I:33:TRP:HE1	3:I:109:HIS:CG	2.36	0.43
5:K:82:ARG:HD2	5:K:82:ARG:HA	1.88	0.43
9:P:60:HIS:HB2	9:P:124:LYS:HA	2.00	0.43
10:Q:62:GLN:HB2	10:Q:65:VAL:HG22	2.01	0.43
11:R:44:THR:OG1	11:R:45:ASP:N	2.51	0.43
15:W:68:ARG:CZ	24:A:1519:U:H3	2.31	0.43
24:A:824:U:O4	24:A:844:G:O6	2.37	0.43
24:A:945:C:H2'	24:A:946:G:H8	1.83	0.43
24:A:1161:G:H2'	24:A:1162:G:C8	2.53	0.43
24:A:1259:U:H2'	24:A:1260:G:C8	2.53	0.43
27:2:90:PRO:HB2	27:2:138:GLN:HB2	2.00	0.43
1:E:27:LYS:HB3	1:E:47:LEU:HD22	2.01	0.43
3:I:15:VAL:HG13	3:I:16:LEU:HG	2.01	0.43
12:S:131:TYR:O	27:2:404:TRP:NE1	2.36	0.43
17:a:37:ALA:O	17:a:41:SER:OG	2.27	0.43
24:A:31:C:O2'	24:A:544:U:OP1	2.36	0.43
24:A:1596:A:O2'	24:A:1598:C:N4	2.46	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:3:118:LYS:HD2	28:3:118:LYS:HA	1.86	0.43
1:E:89:ASP:HB3	1:E:223:PHE:HE1	1.84	0.43
3:I:99:ARG:HH12	19:c:86:LYS:HD2	1.83	0.43
17:a:116:ASP:OD1	17:a:116:ASP:N	2.44	0.43
24:A:1560:U:H2'	24:A:1561:C:C6	2.52	0.43
24:A:1686:G:H2'	24:A:1687:A:C8	2.54	0.43
27:2:270:ASP:OD1	27:2:270:ASP:N	2.49	0.43
6:L:67:TRP:O	6:L:71:GLY:N	2.50	0.43
10:Q:124:ARG:NH1	24:A:625:G:OP1	2.49	0.43
20:e:46:VAL:HG13	20:e:54:VAL:HG21	2.00	0.43
24:A:52:U:H2'	24:A:53:G:C8	2.53	0.43
24:A:557:U:O4	26:1:276:ARG:NH2	2.51	0.43
24:A:1207:C:H2'	24:A:1208:A:C8	2.54	0.43
20:e:23:THR:O	20:e:24:LEU:C	2.62	0.43
24:A:330:A:H2'	24:A:331:U:C6	2.54	0.43
24:A:696:U:H2'	24:A:697:G:H8	1.83	0.43
11:R:83:ARG:NH1	11:R:87:LEU:HB2	2.30	0.43
24:A:1183:U:O4	24:A:1205:A:N6	2.52	0.43
27:2:99:CYS:O	27:2:102:THR:OG1	2.37	0.43
27:2:258:MET:HG2	27:2:279:VAL:HA	1.99	0.43
32:7:396:THR:O	32:7:399:VAL:HB	2.19	0.43
9:P:96:GLN:OE1	9:P:100:TRP:NE1	2.51	0.43
13:T:59:LYS:HD3	13:T:105:LEU:HD11	2.00	0.43
24:A:589:A:O2'	24:A:593:C:OP1	2.37	0.43
24:A:1184:U:O4	24:A:1452:C:O2'	2.33	0.43
24:A:1452:C:H5'	24:A:1453:C:H5'	1.99	0.43
25:0:122:LEU:HD22	25:0:126:LEU:HD23	2.00	0.43
29:4:205:ILE:HA	29:4:208:ILE:HD12	1.99	0.43
32:7:142:LEU:HD23	32:7:220:LEU:HD11	2.01	0.43
2:H:58:TYR:OH	24:A:446:C:OP2	2.26	0.43
24:A:175:G:O2'	24:A:176:A:H5''	2.18	0.43
24:A:1581:U:H2'	24:A:1582:A:C8	2.53	0.43
25:0:44:LEU:HD21	25:0:93:MET:HE1	2.01	0.43
32:7:404:PHE:CD2	32:7:443:LYS:HE2	2.52	0.43
3:I:161:LEU:HD22	3:I:200:LYS:HD2	2.01	0.43
5:K:132:HIS:HB3	5:K:189:ARG:HH21	1.83	0.43
9:P:25:SER:OG	9:P:28:ASP:OD2	2.36	0.43
24:A:1467:A:N6	24:A:1534:U:H3	2.15	0.43
24:A:1739:U:H2'	24:A:1740:A:C8	2.54	0.43
12:S:112:GLN:HE21	27:2:396:GLY:HA3	1.84	0.42
24:A:1145:C:N3	24:A:1147:G:C6	2.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:1224:A:H5'	24:A:1225:G:H5'	2.00	0.42
24:A:1457:C:H2'	24:A:1458:G:C8	2.53	0.42
24:A:1473:A:H2'	24:A:1474:G:C8	2.54	0.42
27:2:325:GLN:NE2	27:2:326:ILE:O	2.49	0.42
32:7:127:MET:HE1	32:7:133:GLY:HA3	2.01	0.42
32:7:636:LEU:HA	32:7:639:ILE:HD12	2.00	0.42
32:7:636:LEU:O	32:7:639:ILE:HB	2.19	0.42
2:H:44:LEU:HD13	2:H:65:MET:HE1	2.00	0.42
24:A:990:A:O2'	24:A:1781:U:O2	2.37	0.42
27:2:352:GLU:O	27:2:355:MET:HB3	2.19	0.42
27:2:533:GLU:OE2	27:2:538:GLN:NE2	2.49	0.42
5:K:149:ARG:HE	16:Z:53:VAL:HG23	1.84	0.42
7:M:124:ARG:HD2	22:h:33:ARG:HD3	2.01	0.42
11:R:50:GLU:HA	24:A:893:G:H1'	2.00	0.42
26:1:29:GLN:HG2	26:1:60:LEU:HD13	2.00	0.42
32:7:778:ILE:HD13	32:7:781:ILE:HD12	1.99	0.42
14:V:92:ILE:HG13	14:V:93:VAL:H	1.84	0.42
14:V:116:LEU:HD21	14:V:123:ARG:HE	1.83	0.42
17:a:41:SER:OG	17:a:43:PHE:O	2.37	0.42
17:a:73:ARG:HH21	17:a:82:LYS:HB3	1.84	0.42
24:A:1583:A:H2'	24:A:1584:G:H8	1.84	0.42
26:1:247:LYS:H	26:1:252:TRP:CD1	2.38	0.42
32:7:475:LEU:HB3	32:7:479:ARG:HH12	1.84	0.42
6:L:153:HIS:HB3	8:O:24:LYS:HD3	2.02	0.42
13:T:5:GLN:HB2	13:T:96:TYR:CZ	2.55	0.42
26:1:42:LEU:HD21	26:1:188:LEU:HD22	2.02	0.42
32:7:795:GLU:HA	32:7:798:ILE:HD12	2.02	0.42
4:J:63:MET:HG2	4:J:98:ARG:HD2	2.02	0.42
5:K:136:LEU:HD23	5:K:148:LYS:HE2	2.01	0.42
9:P:66:GLU:HG2	9:P:90:LYS:HB3	2.01	0.42
24:A:276:G:N7	24:A:277:C:O2'	2.49	0.42
26:1:256:LYS:HA	26:1:256:LYS:HD2	1.84	0.42
19:c:69:LEU:HD21	19:c:90:TYR:HE2	1.85	0.42
24:A:639:G:H2'	24:A:640:G:H8	1.83	0.42
24:A:1153:C:H2'	24:A:1154:A:C8	2.55	0.42
24:A:1587:C:H2'	24:A:1588:A:H8	1.83	0.42
29:4:234:ILE:HD12	29:4:269:ILE:HD11	2.00	0.42
5:K:136:LEU:HD21	5:K:162:VAL:HG21	2.02	0.42
10:Q:108:ASP:OD1	24:A:876:G:O2'	2.28	0.42
20:e:28:PRO:HB3	24:A:957:U:OP1	2.19	0.42
24:A:697:G:H2'	24:A:698:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:1681:G:H2'	24:A:1682:C:C6	2.55	0.42
29:4:375:TYR:O	29:4:421:TYR:OH	2.34	0.42
29:4:428:ASP:N	29:4:428:ASP:OD1	2.52	0.42
3:I:67:LYS:HB3	3:I:70:ARG:HB2	2.02	0.42
4:J:154:ARG:HD2	24:A:77:A:C8	2.54	0.42
21:f:35:ASP:OD1	21:f:35:ASP:N	2.52	0.42
24:A:867:A:H61	24:A:956:U:H3	1.68	0.42
24:A:1178:U:C2	24:A:1454:G:C2	3.07	0.42
27:2:294:ASP:OD1	27:2:294:ASP:N	2.44	0.42
28:3:110:LYS:HE2	28:3:129:TYR:HB3	2.02	0.42
32:7:408:ARG:HG2	32:7:447:ALA:HA	2.01	0.42
3:I:157:GLN:HA	3:I:160:ALA:HB3	2.01	0.42
24:A:390:C:H2'	24:A:391:C:C6	2.55	0.42
24:A:814:G:H2'	24:A:815:A:H8	1.84	0.42
24:A:844:G:H2'	24:A:845:A:C8	2.55	0.42
24:A:1200:A:C6	24:A:1551:A:N6	2.88	0.42
24:A:1669:G:H2'	24:A:1670:C:H6	1.85	0.42
24:A:1709:G:H2'	24:A:1710:G:C8	2.54	0.42
29:4:230:TRP:CZ2	29:4:261:VAL:HG13	2.55	0.42
32:7:402:ALA:O	32:7:406:ALA:N	2.52	0.42
32:7:875:ILE:HG21	32:7:894:LEU:HD11	2.02	0.42
1:E:33:LYS:HE2	1:E:41:ARG:HG3	2.02	0.41
4:J:78:SER:OG	4:J:79:GLU:N	2.52	0.41
7:M:90:LYS:HB2	7:M:90:LYS:HE2	1.87	0.41
8:O:28:LYS:HD2	8:O:28:LYS:HA	1.80	0.41
8:O:31:ARG:NH1	24:A:209:G:OP2	2.52	0.41
11:R:94:ILE:HB	11:R:128:ILE:HG13	2.02	0.41
14:V:116:LEU:HD21	14:V:123:ARG:HG3	2.01	0.41
18:b:15:PHE:HZ	18:b:24:LYS:HD2	1.85	0.41
24:A:674:G:H2'	24:A:675:G:H8	1.86	0.41
24:A:727:C:N4	24:A:728:G:O6	2.53	0.41
26:1:28:ILE:HG23	26:1:32:GLN:HE22	1.84	0.41
27:2:301:GLU:HG3	27:2:573:LYS:HG2	2.02	0.41
5:K:124:ARG:HA	5:K:124:ARG:HD3	1.93	0.41
10:Q:91:LEU:HD23	10:Q:91:LEU:HA	1.90	0.41
24:A:824:U:H2'	24:A:825:C:C6	2.56	0.41
24:A:826:U:H2'	24:A:827:A:C8	2.56	0.41
24:A:966:U:H2'	24:A:967:C:O4'	2.20	0.41
24:A:1200:A:H62	24:A:1551:A:N6	2.14	0.41
29:4:386:VAL:HG11	29:4:429:GLN:HB3	2.02	0.41
32:7:113:LEU:HD13	32:7:137:VAL:HG13	2.00	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:A:549:G:OP2	26:1:257:LYS:NZ	2.51	0.41
24:A:1054:U:H2'	24:A:1055:A:C8	2.55	0.41
26:1:58:SER:HA	26:1:91:ALA:HB2	2.01	0.41
27:2:701:LEU:HD23	27:2:701:LEU:HA	1.92	0.41
29:4:373:LYS:HA	29:4:373:LYS:HD3	1.78	0.41
30:5:379:SER:N	30:5:382:GLN:OE1	2.53	0.41
4:J:84:TYR:OH	4:J:91:GLU:OE2	2.37	0.41
24:A:179:A:H2'	24:A:180:U:C6	2.56	0.41
24:A:622:C:H2'	24:A:623:U:C6	2.56	0.41
32:7:407:LEU:HB2	32:7:410:ARG:HB2	2.02	0.41
32:7:540:ASP:N	32:7:540:ASP:OD1	2.52	0.41
32:7:608:LEU:HA	32:7:612:PHE:HD2	1.84	0.41
32:7:933:LEU:HD22	32:7:937:ILE:HD11	2.02	0.41
4:J:74:ARG:HD2	4:J:96:SER:HB3	2.01	0.41
5:K:116:ASN:ND2	24:A:742:U:OP1	2.53	0.41
7:M:145:MET:HE3	7:M:145:MET:HB3	1.88	0.41
11:R:55:VAL:HG21	11:R:60:LYS:HE2	2.02	0.41
13:T:16:ALA:HB2	13:T:72:GLY:HA3	2.02	0.41
15:W:136:ILE:O	15:W:140:VAL:HG23	2.21	0.41
18:b:44:ARG:NH2	18:b:55:LYS:HE2	2.35	0.41
19:c:84:HIS:ND1	19:c:86:LYS:HG2	2.35	0.41
24:A:1687:A:H2'	24:A:1688:G:H8	1.85	0.41
27:2:190:THR:HG21	27:2:215:ILE:HG13	2.02	0.41
32:7:343:ARG:NH2	32:7:392:ALA:HB2	2.35	0.41
3:I:28:LYS:HE2	3:I:56:TYR:CZ	2.56	0.41
3:I:79:ARG:NH2	3:I:156:ASN:OD1	2.53	0.41
6:L:125:ARG:HE	6:L:132:VAL:HA	1.86	0.41
24:A:895:C:O2'	24:A:912:G:N2	2.54	0.41
27:2:508:GLU:HA	27:2:511:ALA:HB2	2.02	0.41
33:8:436:SER:O	33:8:440:ARG:HD2	2.20	0.41
1:E:94:LYS:HA	1:E:94:LYS:HD3	1.86	0.41
8:O:33:GLY:HA3	8:O:39:TRP:HD1	1.86	0.41
21:f:26:VAL:HG22	21:f:46:LYS:HB3	2.02	0.41
24:A:700:G:N2	24:A:731:G:O2'	2.47	0.41
24:A:1652:U:O2	24:A:1741:G:C2	2.74	0.41
27:2:261:GLU:OE1	27:2:277:GLY:HA2	2.21	0.41
27:2:279:VAL:HG12	27:2:564:PRO:HA	2.03	0.41
32:7:422:ILE:HG21	32:7:440:VAL:HG11	2.03	0.41
32:7:741:ARG:HG3	32:7:780:ILE:HG12	2.02	0.41
2:H:57:ASN:OD1	2:H:60:GLU:HG3	2.20	0.41
3:I:204:LEU:HA	3:I:207:VAL:HG12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:134:GLY:HA3	4:J:158:ILE:HD12	2.03	0.41
11:R:35:SER:OG	11:R:36:PHE:N	2.52	0.41
19:c:61:ASN:HB3	19:c:64:LEU:HD23	2.02	0.41
24:A:1227:A:H2	24:A:1252:G:H21	1.68	0.41
26:1:51:ILE:HA	26:1:118:ALA:O	2.21	0.41
26:1:61:SER:HA	26:1:64:ILE:HD12	2.03	0.41
28:3:84:LYS:HD2	28:3:121:ARG:NE	2.33	0.41
32:7:797:VAL:O	32:7:800:CYS:HB2	2.21	0.41
4:J:218:ARG:HA	4:J:218:ARG:HD3	1.95	0.41
7:M:137:GLN:OE1	18:b:66:GLN:NE2	2.41	0.41
14:V:44:ASN:HD22	15:W:47:PRO:HD2	1.86	0.41
14:V:46:VAL:HG21	14:V:73:ILE:HG12	2.03	0.41
24:A:694:U:H2'	24:A:695:C:C6	2.56	0.41
24:A:724:U:H3'	24:A:725:G:H5''	2.03	0.41
27:2:171:GLU:OE2	27:2:700:THR:OG1	2.31	0.41
27:2:667:MET:HB2	27:2:804:ASN:HA	2.02	0.41
5:K:122:ARG:HA	5:K:123:PRO:HD3	1.96	0.41
7:M:81:ILE:HG13	7:M:83:VAL:HG13	2.03	0.41
13:T:48:LEU:HD21	13:T:78:VAL:HB	2.03	0.41
14:V:43:SER:HA	14:V:46:VAL:HG12	2.01	0.41
18:b:32:HIS:HB2	18:b:35:ARG:HB2	2.01	0.41
22:h:31:LYS:HA	22:h:35:LYS:HB2	2.02	0.41
24:A:674:G:H2'	24:A:675:G:C8	2.56	0.41
24:A:700:G:N2	24:A:732:A:H2	2.12	0.41
24:A:1432:A:H2	24:A:1434:G:C8	2.39	0.41
32:7:397:PHE:HA	32:7:400:ILE:HD12	2.02	0.41
1:E:164:ILE:O	1:E:168:MET:HG3	2.22	0.40
3:I:43:ILE:HG13	3:I:44:SER:H	1.86	0.40
4:J:231:LYS:HD2	4:J:232:ARG:HG2	2.03	0.40
5:K:50:VAL:HG23	5:K:69:PRO:HD3	2.03	0.40
6:L:83:TYR:HB3	6:L:101:VAL:HB	2.03	0.40
7:M:142:PRO:HD2	24:A:471:A:H5''	2.03	0.40
8:O:130:VAL:HG12	8:O:144:VAL:HA	2.03	0.40
16:Z:25:VAL:O	16:Z:62:VAL:HA	2.21	0.40
24:A:90:G:OP1	24:A:394:A:N6	2.54	0.40
24:A:932:C:C6	33:8:429:LYS:HE3	2.56	0.40
25:0:90:THR:HA	25:0:94:GLU:HB2	2.02	0.40
28:3:162:ASP:N	28:3:162:ASP:OD1	2.54	0.40
1:E:133:TYR:CE2	1:E:181:LEU:HD22	2.57	0.40
3:I:136:ILE:HD12	3:I:136:ILE:HA	1.96	0.40
3:I:185:LEU:O	3:I:189:ALA:N	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:S:48:ARG:HA	12:S:48:ARG:HD3	1.83	0.40
12:S:65:ILE:HG13	12:S:69:ARG:HH21	1.86	0.40
16:Z:42:GLN:NE2	16:Z:48:GLY:O	2.48	0.40
24:A:597:U:H2'	24:A:598:A:C8	2.56	0.40
24:A:1114:U:H2'	24:A:1115:G:C8	2.56	0.40
26:1:210:VAL:HG13	26:1:215:GLY:HA2	2.03	0.40
28:3:79:ARG:HE	28:3:79:ARG:HB3	1.72	0.40
29:4:335:VAL:HG13	29:4:375:TYR:HB3	2.02	0.40
9:P:64:LEU:HD21	9:P:77:VAL:HG13	2.04	0.40
15:W:128:GLN:H	15:W:128:GLN:HG3	1.74	0.40
24:A:484:G:H2'	24:A:485:G:C8	2.56	0.40
24:A:563:C:H2'	24:A:564:A:C8	2.54	0.40
27:2:748:GLU:HA	27:2:751:GLU:HG2	2.03	0.40
1:E:82:ARG:HG2	1:E:105:PHE:CE1	2.57	0.40
2:H:23:LEU:HD23	2:H:23:LEU:HA	1.93	0.40
2:H:120:LYS:HE2	2:H:120:LYS:HB3	1.98	0.40
3:I:94:LYS:HE2	3:I:94:LYS:HB2	1.87	0.40
13:T:6:ALA:HA	13:T:22:CYS:O	2.22	0.40
13:T:47:LYS:HD2	13:T:47:LYS:HA	1.89	0.40
24:A:1568:G:H5'	24:A:1569:A:H5'	2.03	0.40
28:3:106:VAL:O	28:3:110:LYS:HA	2.21	0.40
29:4:201:VAL:HG13	30:5:396:PHE:CD2	2.57	0.40
32:7:280:ARG:HD2	32:7:280:ARG:HA	1.88	0.40
32:7:865:PRO:HA	32:7:868:ILE:HD12	2.04	0.40
2:H:200:ARG:HH21	24:A:737:G:H5'	1.87	0.40
9:P:46:GLY:N	9:P:118:CYS:SG	2.95	0.40
14:V:52:VAL:HG21	14:V:69:LEU:HD21	2.03	0.40
15:W:114:LEU:HB3	15:W:125:ILE:HD13	2.04	0.40
24:A:118:A:H1'	24:A:394:A:C5	2.56	0.40
24:A:1153:C:H2'	24:A:1154:A:H8	1.87	0.40
32:7:401:GLY:CA	32:7:443:LYS:HE3	2.49	0.40
32:7:732:PRO:HG3	32:7:773:ALA:HA	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

entries.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	211/255 (83%)	197 (93%)	14 (7%)	0	100	100
2	H	259/264 (98%)	250 (96%)	9 (4%)	0	100	100
3	I	197/212 (93%)	183 (93%)	14 (7%)	0	100	100
4	J	230/239 (96%)	223 (97%)	7 (3%)	0	100	100
5	K	193/203 (95%)	186 (96%)	7 (4%)	0	100	100
6	L	199/202 (98%)	188 (94%)	11 (6%)	0	100	100
7	M	177/190 (93%)	169 (96%)	8 (4%)	0	100	100
8	O	148/161 (92%)	139 (94%)	9 (6%)	0	100	100
9	P	116/144 (81%)	101 (87%)	15 (13%)	0	100	100
10	Q	148/151 (98%)	146 (99%)	2 (1%)	0	100	100
11	R	133/150 (89%)	119 (90%)	13 (10%)	1 (1%)	16	47
12	S	113/153 (74%)	105 (93%)	8 (7%)	0	100	100
13	T	115/119 (97%)	106 (92%)	9 (8%)	0	100	100
14	V	120/156 (77%)	112 (93%)	8 (7%)	0	100	100
15	W	140/153 (92%)	133 (95%)	7 (5%)	0	100	100
16	Z	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
17	a	140/145 (97%)	132 (94%)	8 (6%)	0	100	100
18	b	130/136 (96%)	125 (96%)	5 (4%)	0	100	100
19	c	67/99 (68%)	65 (97%)	2 (3%)	0	100	100
20	e	79/82 (96%)	74 (94%)	5 (6%)	0	100	100
21	f	59/68 (87%)	53 (90%)	6 (10%)	0	100	100
22	h	19/62 (31%)	15 (79%)	3 (16%)	1 (5%)	1	10
23	i	61/154 (40%)	55 (90%)	6 (10%)	0	100	100
25	0	125/127 (98%)	125 (100%)	0	0	100	100
26	1	263/282 (93%)	255 (97%)	8 (3%)	0	100	100
27	2	693/830 (84%)	673 (97%)	19 (3%)	1 (0%)	48	78
28	3	182/259 (70%)	172 (94%)	9 (5%)	1 (0%)	24	57
29	4	268/480 (56%)	258 (96%)	10 (4%)	0	100	100
30	5	77/445 (17%)	72 (94%)	5 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	6	41/519 (8%)	40 (98%)	1 (2%)	0	100	100
32	7	1002/1235 (81%)	988 (99%)	14 (1%)	0	100	100
33	8	58/938 (6%)	47 (81%)	9 (16%)	2 (3%)	3	16
All	All	5890/8743 (67%)	5627 (96%)	257 (4%)	6 (0%)	49	78

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	R	137	ASP
27	2	372	ASP
33	8	432	LYS
33	8	827	PRO
22	h	27	PRO
28	3	195	GLY

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	E	187/223 (84%)	184 (98%)	3 (2%)	55	75
2	H	219/221 (99%)	219 (100%)	0	100	100
3	I	167/178 (94%)	167 (100%)	0	100	100
4	J	198/204 (97%)	198 (100%)	0	100	100
5	K	169/177 (96%)	169 (100%)	0	100	100
6	L	163/164 (99%)	163 (100%)	0	100	100
7	M	154/162 (95%)	154 (100%)	0	100	100
8	O	133/143 (93%)	129 (97%)	4 (3%)	36	65
9	P	101/121 (84%)	101 (100%)	0	100	100
10	Q	129/130 (99%)	128 (99%)	1 (1%)	73	81
11	R	102/117 (87%)	102 (100%)	0	100	100
12	S	99/132 (75%)	99 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	T	95/96 (99%)	95 (100%)	0	100	100
14	V	108/135 (80%)	108 (100%)	0	100	100
15	W	114/124 (92%)	114 (100%)	0	100	100
16	Z	112/113 (99%)	110 (98%)	2 (2%)	51	73
17	a	113/116 (97%)	113 (100%)	0	100	100
18	b	112/115 (97%)	112 (100%)	0	100	100
19	c	60/80 (75%)	60 (100%)	0	100	100
20	e	70/71 (99%)	70 (100%)	0	100	100
21	f	54/61 (88%)	54 (100%)	0	100	100
22	h	19/52 (36%)	16 (84%)	3 (16%)	2	12
23	i	57/139 (41%)	57 (100%)	0	100	100
25	0	113/113 (100%)	113 (100%)	0	100	100
26	1	215/227 (95%)	215 (100%)	0	100	100
27	2	606/714 (85%)	606 (100%)	0	100	100
28	3	155/215 (72%)	153 (99%)	2 (1%)	61	77
29	4	229/411 (56%)	229 (100%)	0	100	100
30	5	70/373 (19%)	70 (100%)	0	100	100
31	6	36/447 (8%)	36 (100%)	0	100	100
32	7	864/1049 (82%)	864 (100%)	0	100	100
33	8	57/765 (8%)	56 (98%)	1 (2%)	51	73
All	All	5080/7388 (69%)	5064 (100%)	16 (0%)	84	87

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	118	GLN
1	E	124	ASN
1	E	217	LEU
8	O	103	ASN
8	O	117	SER
8	O	122	VAL
8	O	143	ASN
10	Q	49	GLN
16	Z	19	LYS
16	Z	28	ARG

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Mol	Chain	Res	Type
22	h	26	LYS
22	h	38	LEU
22	h	39	LEU
28	3	92	MET
28	3	119	GLU
33	8	826	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (43) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	118	GLN
1	E	124	ASN
2	H	201	HIS
3	I	31	ASN
3	I	91	ASN
4	J	81	HIS
5	K	120	GLN
5	K	132	HIS
6	L	52	ASN
6	L	163	GLN
8	O	22	ASN
8	O	97	HIS
8	O	132	GLN
9	P	65	ASN
12	S	112	GLN
13	T	15	ASN
13	T	77	GLN
13	T	107	GLN
14	V	10	ASN
14	V	44	ASN
15	W	26	GLN
15	W	93	HIS
15	W	106	GLN
16	Z	56	HIS
16	Z	64	GLN
17	a	10	ASN
17	a	94	ASN
18	b	116	ASN
23	i	139	GLN
25	0	67	GLN
26	1	32	GLN
27	2	92	ASN

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Mol	Chain	Res	Type
27	2	193	GLN
27	2	219	HIS
27	2	401	GLN
27	2	597	HIS
27	2	688	ASN
31	6	515	ASN
32	7	166	ASN
32	7	526	GLN
32	7	579	GLN
32	7	787	HIS
33	8	443	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
24	A	1576/1797 (87%)	378 (23%)	22 (1%)

All (378) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
24	A	2	A
24	A	3	C
24	A	4	C
24	A	5	U
24	A	6	G
24	A	14	C
24	A	25	C
24	A	26	A
24	A	27	U
24	A	34	G
24	A	42	G
24	A	45	U
24	A	47	A
24	A	57	G
24	A	66	U
24	A	68	A
24	A	69	G
24	A	70	C
24	A	72	A
24	A	73	U
24	A	74	U

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Mol	Chain	Res	Type
24	A	75	A
24	A	76	U
24	A	93	U
24	A	99	A
24	A	103	A
24	A	104	A
24	A	113	C
24	A	114	G
24	A	126	G
24	A	127	U
24	A	140	G
24	A	142	A
24	A	150	G
24	A	153	A
24	A	155	U
24	A	166	A
24	A	175	G
24	A	176	A
24	A	188	U
24	A	189	C
24	A	191	G
24	A	192	A
24	A	195	G
24	A	210	A
24	A	212	U
24	A	213	A
24	A	214	A
24	A	215	A
24	A	221	A
24	A	222	U
24	A	223	G
24	A	228	U
24	A	230	G
24	A	231	G
24	A	232	G
24	A	234	C
24	A	236	U
24	A	237	U
24	A	243	G
24	A	247	C
24	A	254	A
24	A	257	U

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Mol	Chain	Res	Type
24	A	258	C
24	A	262	A
24	A	264	U
24	A	268	A
24	A	269	C
24	A	270	G
24	A	274	U
24	A	275	U
24	A	277	C
24	A	296	A
24	A	301	U
24	A	311	C
24	A	313	A
24	A	317	U
24	A	319	G
24	A	321	C
24	A	326	G
24	A	332	U
24	A	334	G
24	A	335	C
24	A	348	C
24	A	349	A
24	A	357	A
24	A	358	C
24	A	377	C
24	A	387	G
24	A	396	A
24	A	397	A
24	A	398	A
24	A	399	C
24	A	401	G
24	A	414	A
24	A	415	G
24	A	420	G
24	A	421	C
24	A	422	A
24	A	423	G
24	A	431	G
24	A	436	U
24	A	441	C
24	A	442	A
24	A	451	A

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Mol	Chain	Res	Type
24	A	461	A
24	A	465	A
24	A	474	A
24	A	480	A
24	A	481	C
24	A	490	U
24	A	492	C
24	A	493	G
24	A	495	G
24	A	502	A
24	A	508	A
24	A	511	G
24	A	512	A
24	A	516	C
24	A	517	A
24	A	522	A
24	A	524	A
24	A	531	A
24	A	535	A
24	A	536	G
24	A	538	A
24	A	539	A
24	A	549	G
24	A	551	C
24	A	553	A
24	A	554	G
24	A	556	C
24	A	563	C
24	A	574	G
24	A	575	U
24	A	576	A
24	A	577	A
24	A	578	U
24	A	579	U
24	A	580	C
24	A	583	G
24	A	591	A
24	A	592	G
24	A	607	G
24	A	608	U
24	A	611	A
24	A	612	G

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Mol	Chain	Res	Type
24	A	616	A
24	A	617	A
24	A	618	A
24	A	619	A
24	A	620	A
24	A	621	G
24	A	636	U
24	A	641	C
24	A	647	C
24	A	677	U
24	A	678	G
24	A	679	G
24	A	680	G
24	A	683	G
24	A	686	C
24	A	691	C
24	A	692	C
24	A	693	U
24	A	705	G
24	A	709	G
24	A	710	C
24	A	724	U
24	A	725	G
24	A	726	U
24	A	727	C
24	A	728	G
24	A	729	G
24	A	730	G
24	A	731	G
24	A	732	A
24	A	738	G
24	A	742	U
24	A	753	C
24	A	754	A
24	A	764	G
24	A	765	C
24	A	773	A
24	A	774	G
24	A	777	C
24	A	779	A
24	A	780	U
24	A	781	G

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Mol	Chain	Res	Type
24	A	787	A
24	A	792	U
24	A	793	U
24	A	809	A
24	A	810	A
24	A	812	A
24	A	813	G
24	A	818	U
24	A	819	G
24	A	822	G
24	A	823	U
24	A	824	U
24	A	827	A
24	A	828	U
24	A	830	U
24	A	832	G
24	A	844	G
24	A	854	A
24	A	861	A
24	A	862	U
24	A	874	G
24	A	879	G
24	A	884	U
24	A	896	A
24	A	897	G
24	A	901	U
24	A	912	G
24	A	919	U
24	A	920	G
24	A	931	A
24	A	932	C
24	A	933	U
24	A	940	G
24	A	957	U
24	A	958	U
24	A	964	A
24	A	982	G
24	A	990	A
24	A	994	C
24	A	996	A
24	A	998	C
24	A	999	A

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Mol	Chain	Res	Type
24	A	1001	A
24	A	1019	C
24	A	1023	A
24	A	1024	A
24	A	1026	C
24	A	1030	G
24	A	1040	G
24	A	1041	A
24	A	1042	U
24	A	1054	U
24	A	1055	A
24	A	1056	U
24	A	1057	U
24	A	1059	U
24	A	1066	G
24	A	1073	A
24	A	1074	C
24	A	1078	A
24	A	1083	A
24	A	1089	A
24	A	1093	G
24	A	1094	U
24	A	1095	U
24	A	1097	G
24	A	1135	A
24	A	1140	A
24	A	1147	G
24	A	1148	A
24	A	1152	G
24	A	1155	C
24	A	1156	C
24	A	1157	A
24	A	1164	G
24	A	1182	U
24	A	1183	U
24	A	1198	G
24	A	1199	A
24	A	1200	A
24	A	1204	C
24	A	1209	G
24	A	1217	C
24	A	1222	U

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Mol	Chain	Res	Type
24	A	1224	A
24	A	1225	G
24	A	1226	G
24	A	1227	A
24	A	1228	U
24	A	1235	A
24	A	1236	U
24	A	1240	G
24	A	1241	A
24	A	1242	G
24	A	1243	C
24	A	1246	U
24	A	1248	U
24	A	1249	C
24	A	1253	A
24	A	1254	U
24	A	1255	U
24	A	1264	G
24	A	1266	U
24	A	1270	G
24	A	1271	C
24	A	1272	A
24	A	1432	A
24	A	1433	U
24	A	1434	G
24	A	1439	U
24	A	1440	A
24	A	1441	G
24	A	1442	A
24	A	1443	U
24	A	1445	U
24	A	1448	U
24	A	1453	C
24	A	1460	G
24	A	1467	A
24	A	1469	U
24	A	1470	G
24	A	1478	C
24	A	1479	A
24	A	1482	G
24	A	1486	A
24	A	1487	C

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Mol	Chain	Res	Type
24	A	1489	C
24	A	1491	C
24	A	1492	U
24	A	1502	G
24	A	1512	A
24	A	1517	G
24	A	1520	A
24	A	1530	G
24	A	1532	G
24	A	1533	C
24	A	1534	U
24	A	1538	G
24	A	1552	A
24	A	1553	U
24	A	1555	A
24	A	1556	U
24	A	1565	A
24	A	1569	A
24	A	1570	G
24	A	1580	G
24	A	1596	A
24	A	1597	G
24	A	1603	G
24	A	1605	U
24	A	1606	G
24	A	1607	A
24	A	1610	A
24	A	1612	G
24	A	1614	C
24	A	1615	C
24	A	1618	G
24	A	1625	G
24	A	1626	U
24	A	1631	A
24	A	1632	C
24	A	1633	C
24	A	1653	U
24	A	1654	G
24	A	1676	G
24	A	1695	G
24	A	1708	A
24	A	1709	G

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Mol	Chain	Res	Type
24	A	1711	G
24	A	1712	C
24	A	1726	A
24	A	1741	G
24	A	1746	A
24	A	1751	A
24	A	1752	A
24	A	1766	C
24	A	1773	G
24	A	1776	G
24	A	1777	A
24	A	1779	C
24	A	1782	G
24	A	1785	G
24	A	1788	G
24	A	1789	G
24	A	1790	A
24	A	1791	U
24	A	1795	U
24	A	1796	A
24	A	1797	A

All (22) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
24	A	126	G
24	A	211	U
24	A	231	G
24	A	233	G
24	A	269	C
24	A	414	A
24	A	522	A
24	A	552	A
24	A	611	A
24	A	678	G
24	A	792	U
24	A	1041	A
24	A	1073	A
24	A	1094	U
24	A	1224	A
24	A	1252	G
24	A	1477	C

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Mol	Chain	Res	Type
24	A	1531	U
24	A	1564	C
24	A	1569	A
24	A	1652	U
24	A	1795	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 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.

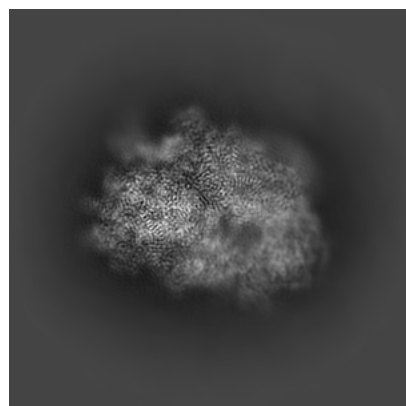
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-66689. These allow visual inspection of the internal detail of the map and identification of artifacts.

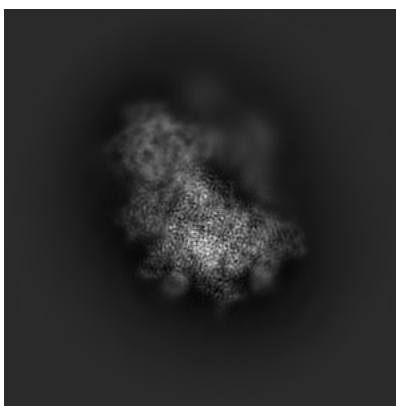
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

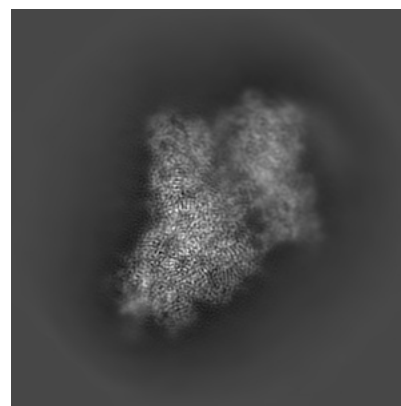
6.1.1 Primary map



X

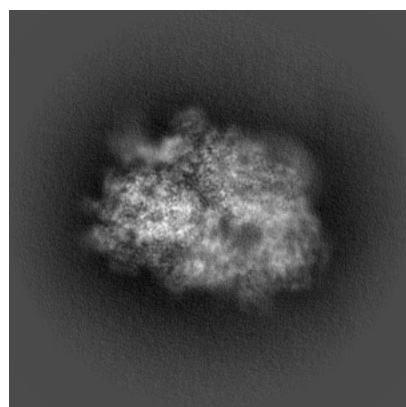


Y

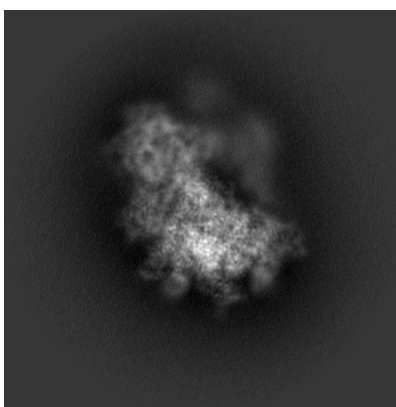


Z

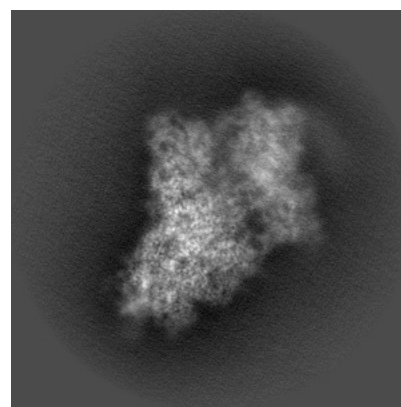
6.1.2 Raw map



X



Y

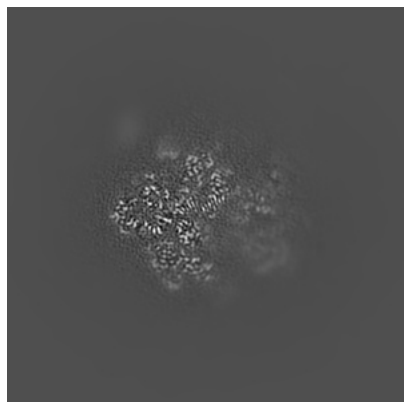


Z

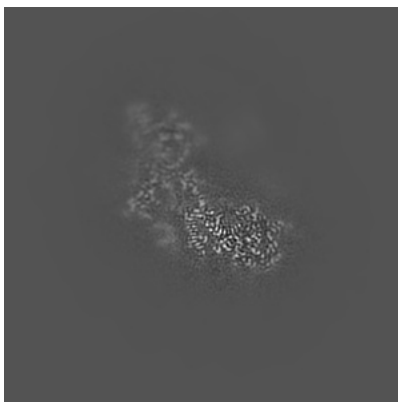
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

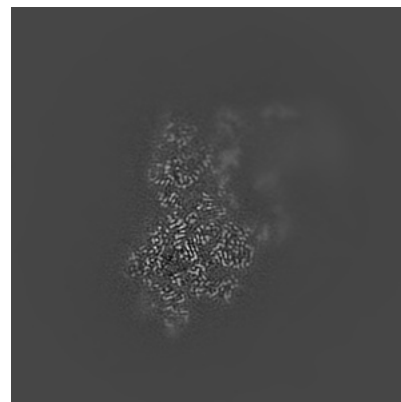
6.2.1 Primary map



X Index: 180

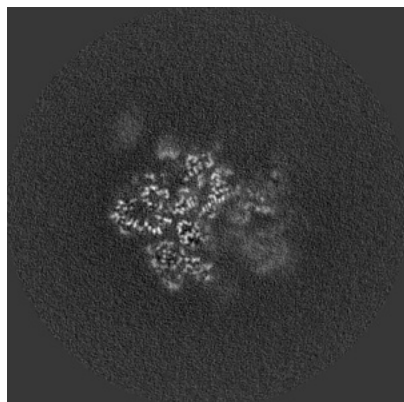


Y Index: 180

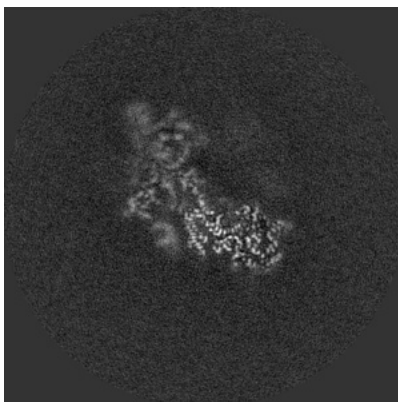


Z Index: 180

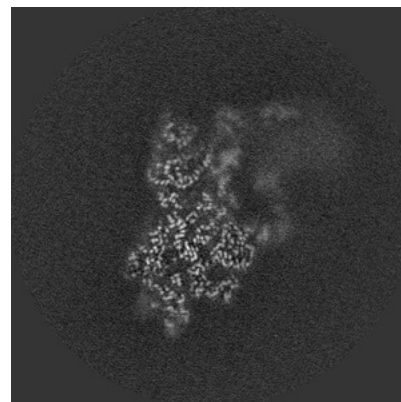
6.2.2 Raw map



X Index: 180



Y Index: 180

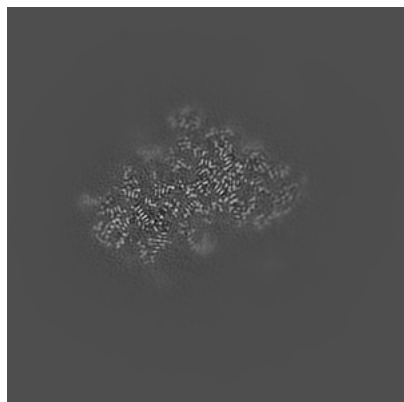


Z Index: 180

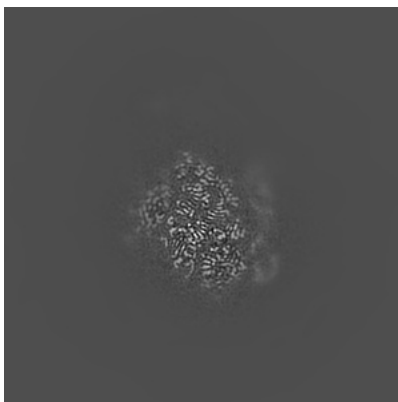
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

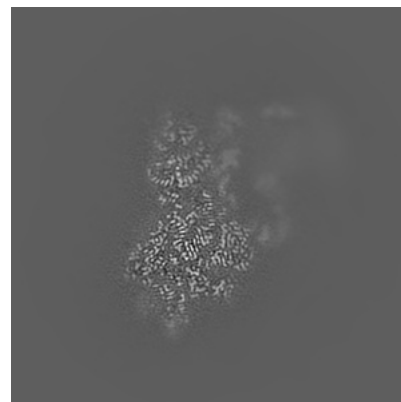
6.3.1 Primary map



X Index: 147

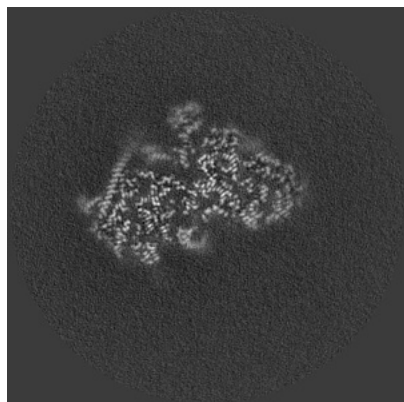


Y Index: 139

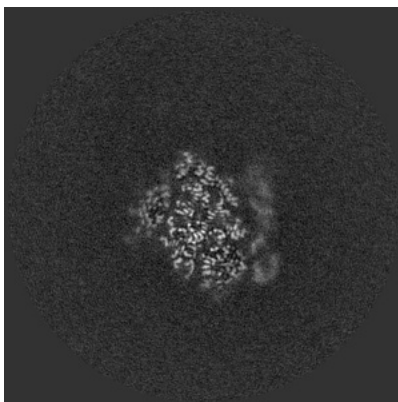


Z Index: 181

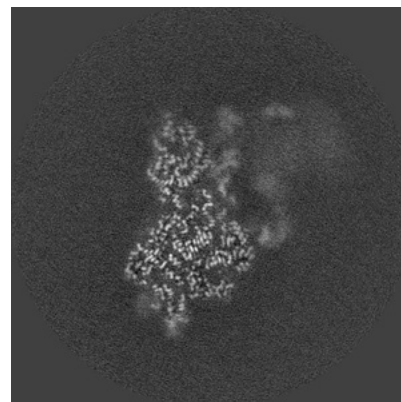
6.3.2 Raw map



X Index: 143



Y Index: 139

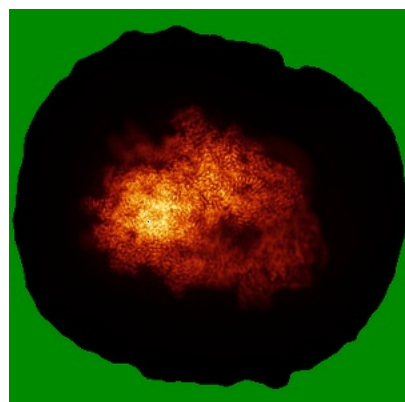


Z Index: 182

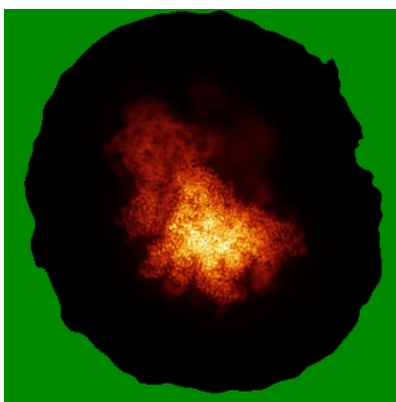
The images above show the largest variance slices of the map in three orthogonal directions.

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

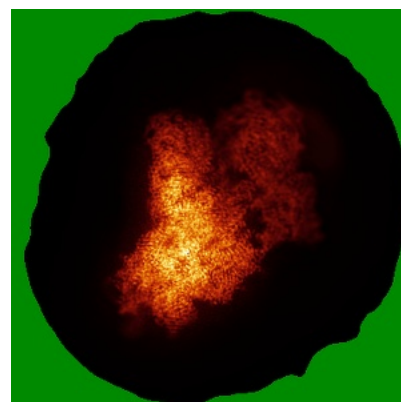
6.4.1 Primary map



X

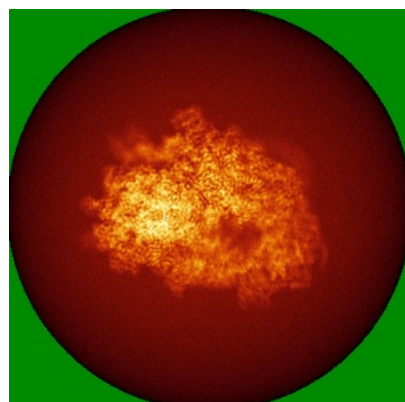


Y

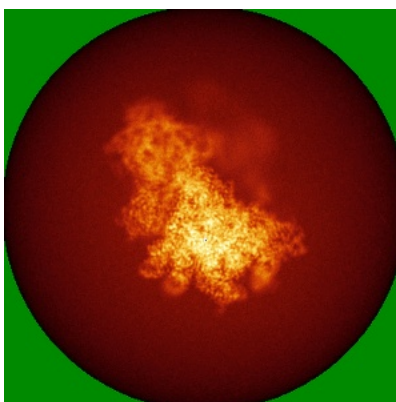


Z

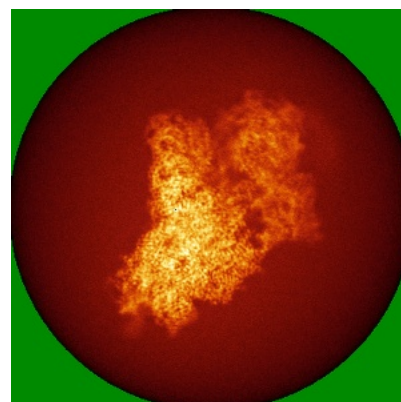
6.4.2 Raw map



X



Y

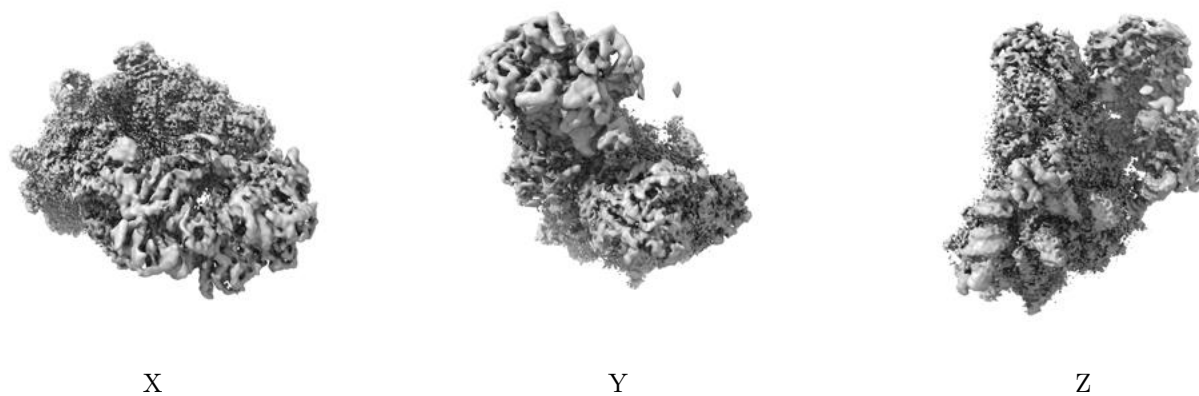


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

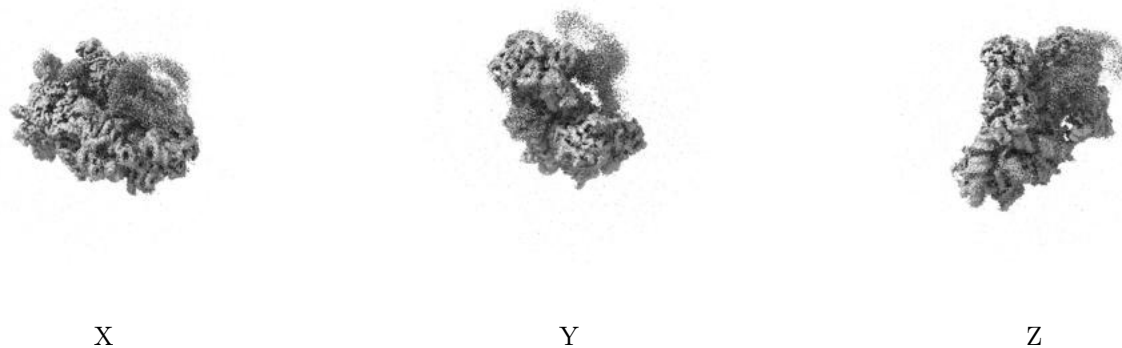
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. 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.

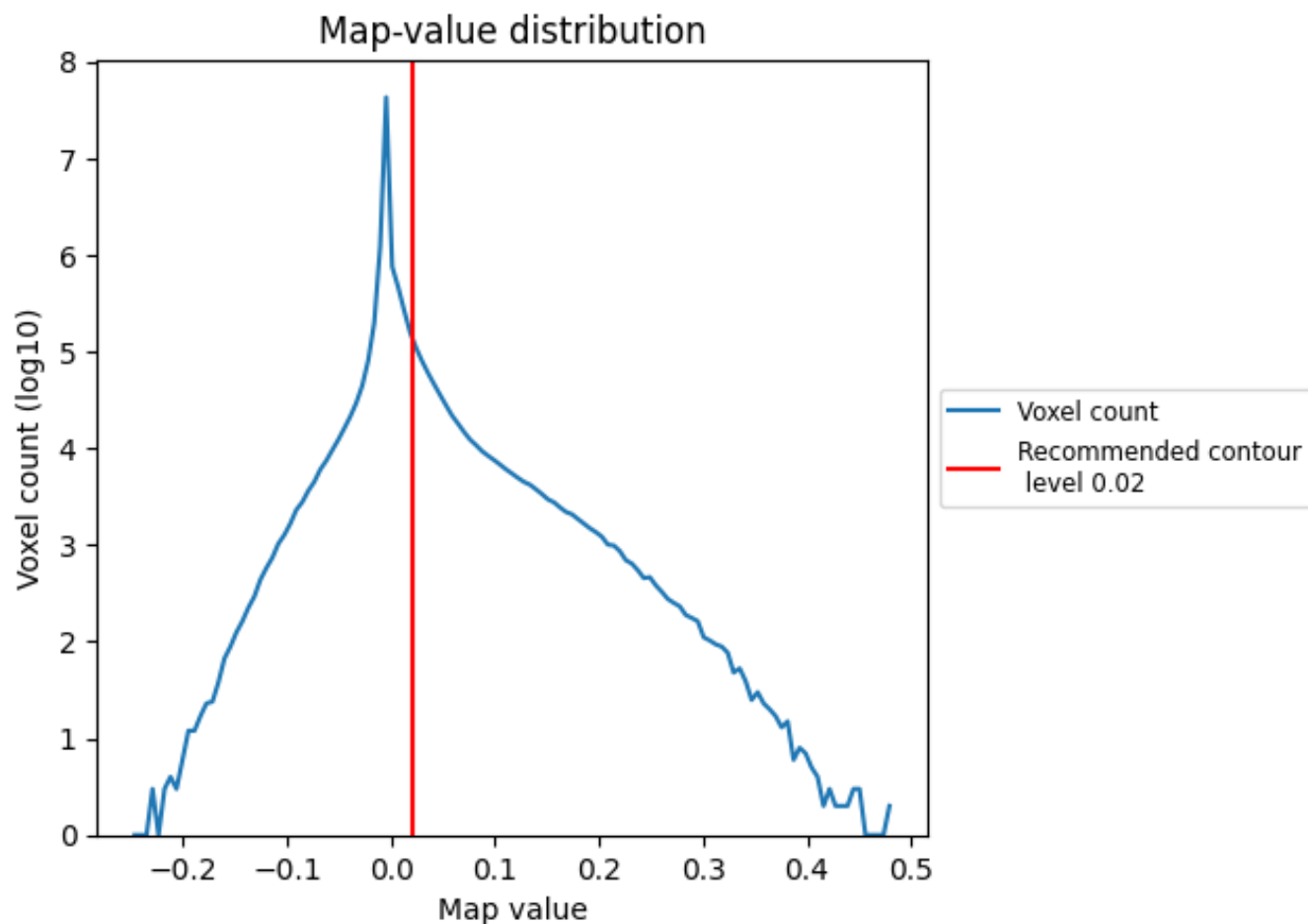
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

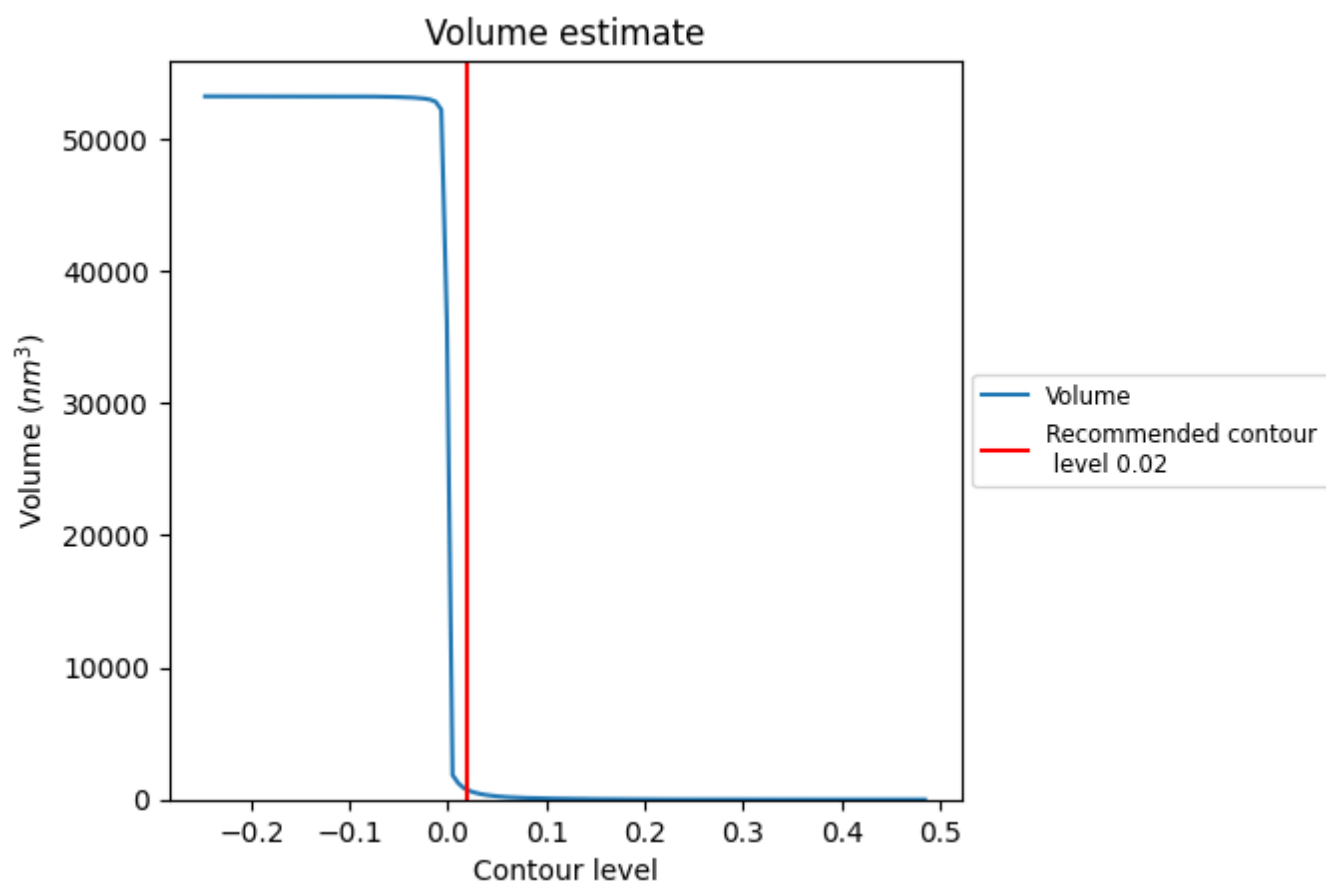
This section contains the results of statistical analysis of the map.

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.

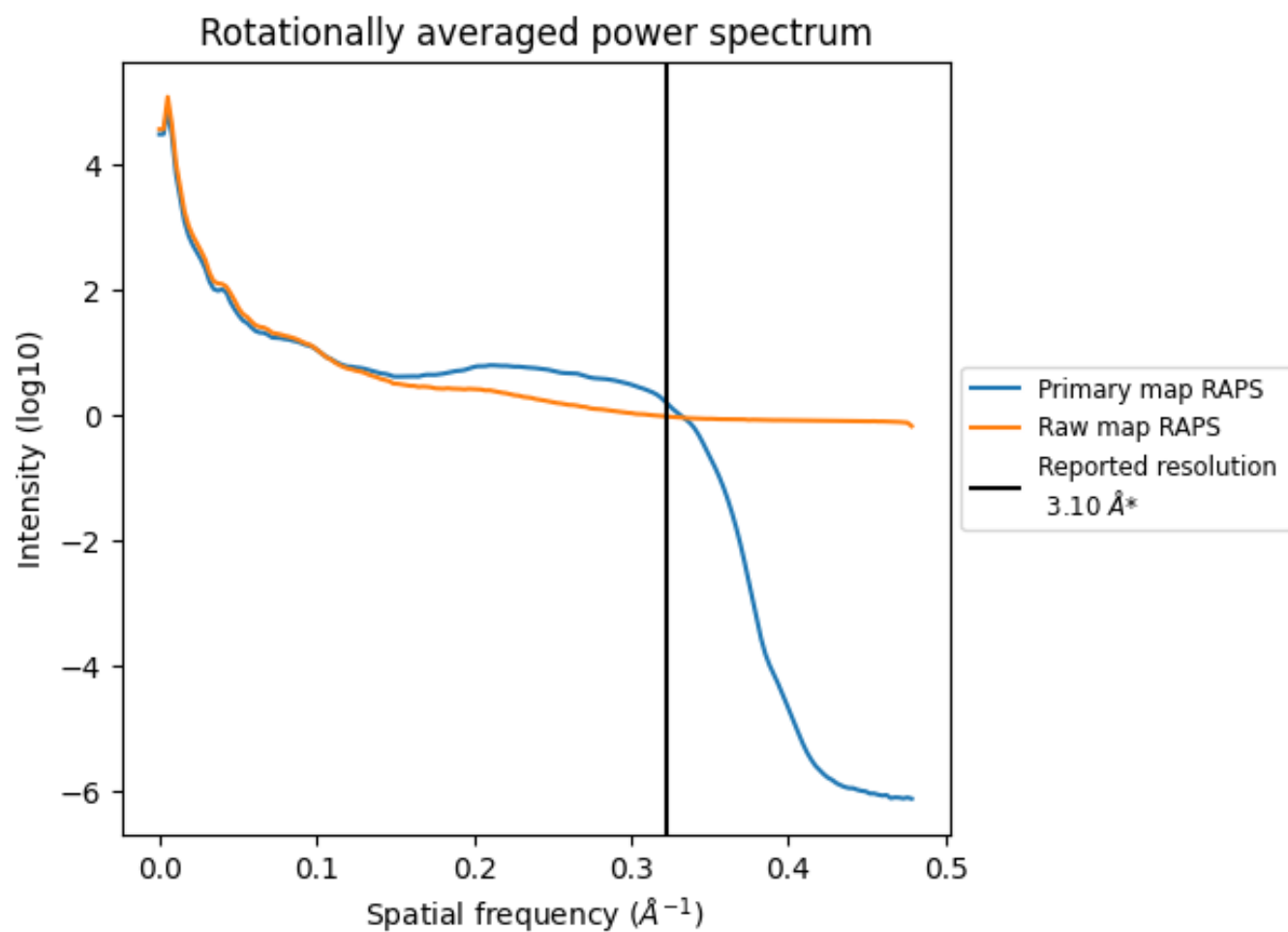
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 732 nm^3 ; this corresponds to an approximate mass of 661 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

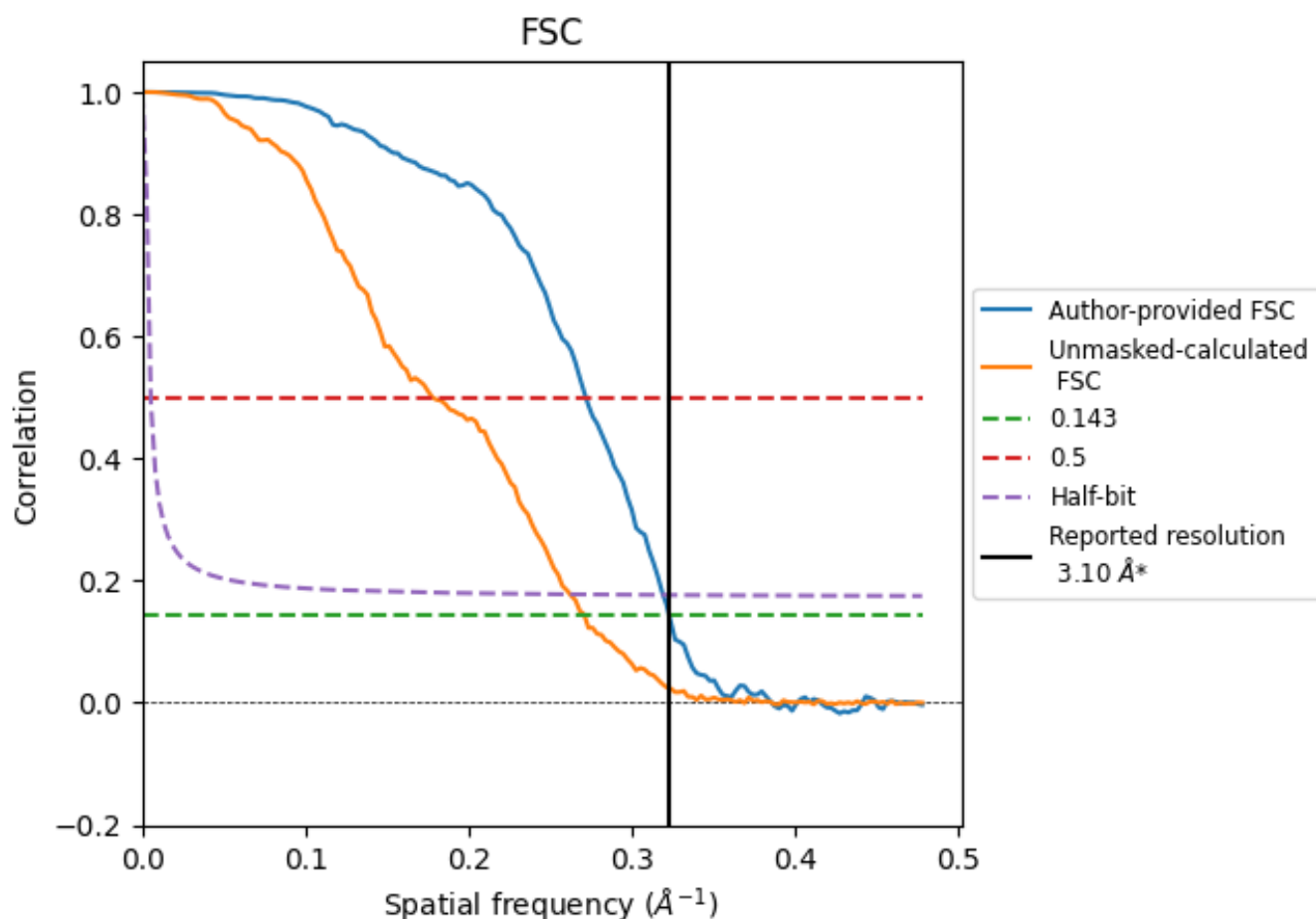


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

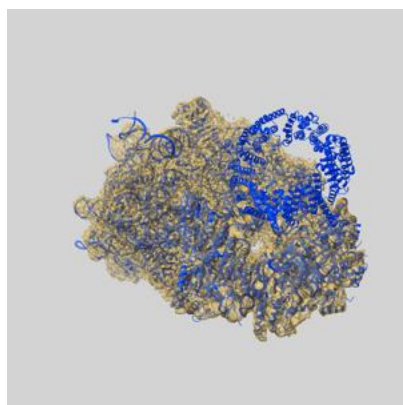
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.09	3.67	3.13
Unmasked-calculated*	3.69	5.62	3.81

*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 3.69 differs from the reported value 3.1 by more than 10 %

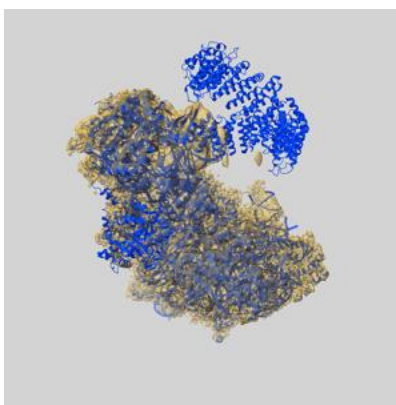
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-66689 and PDB model 9XAJ. Per-residue inclusion information can be found in section [3](#) on page [11](#).

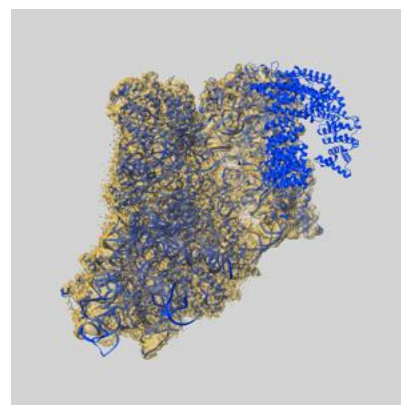
9.1 Map-model overlay [i](#)



X



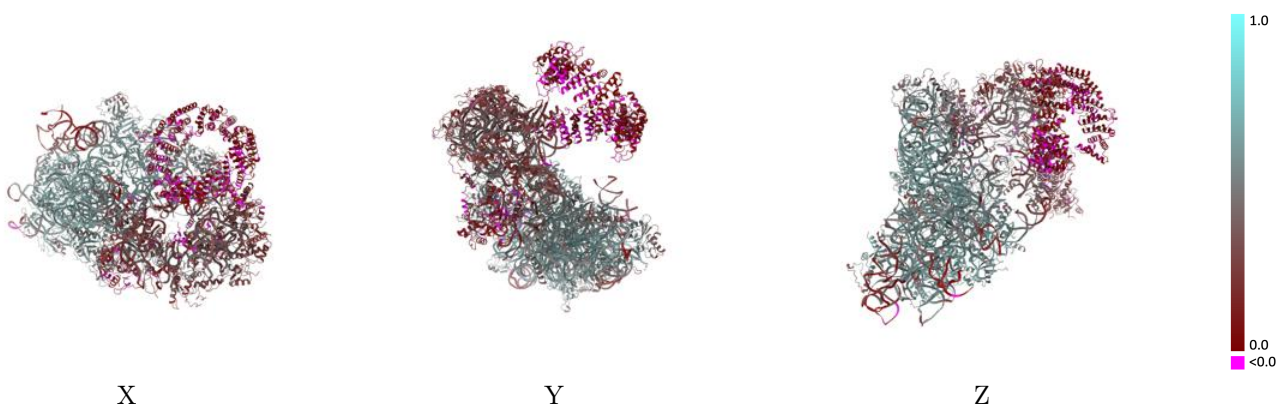
Y



Z

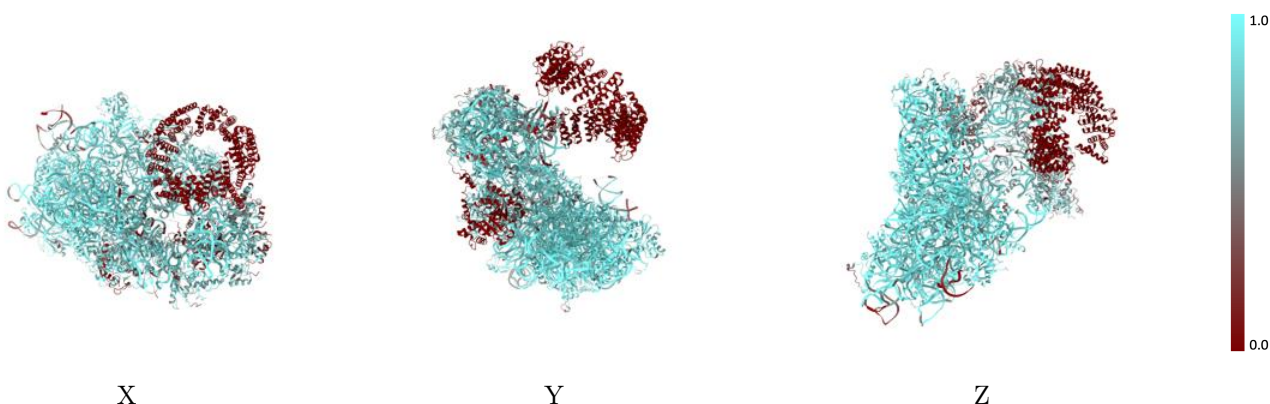
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



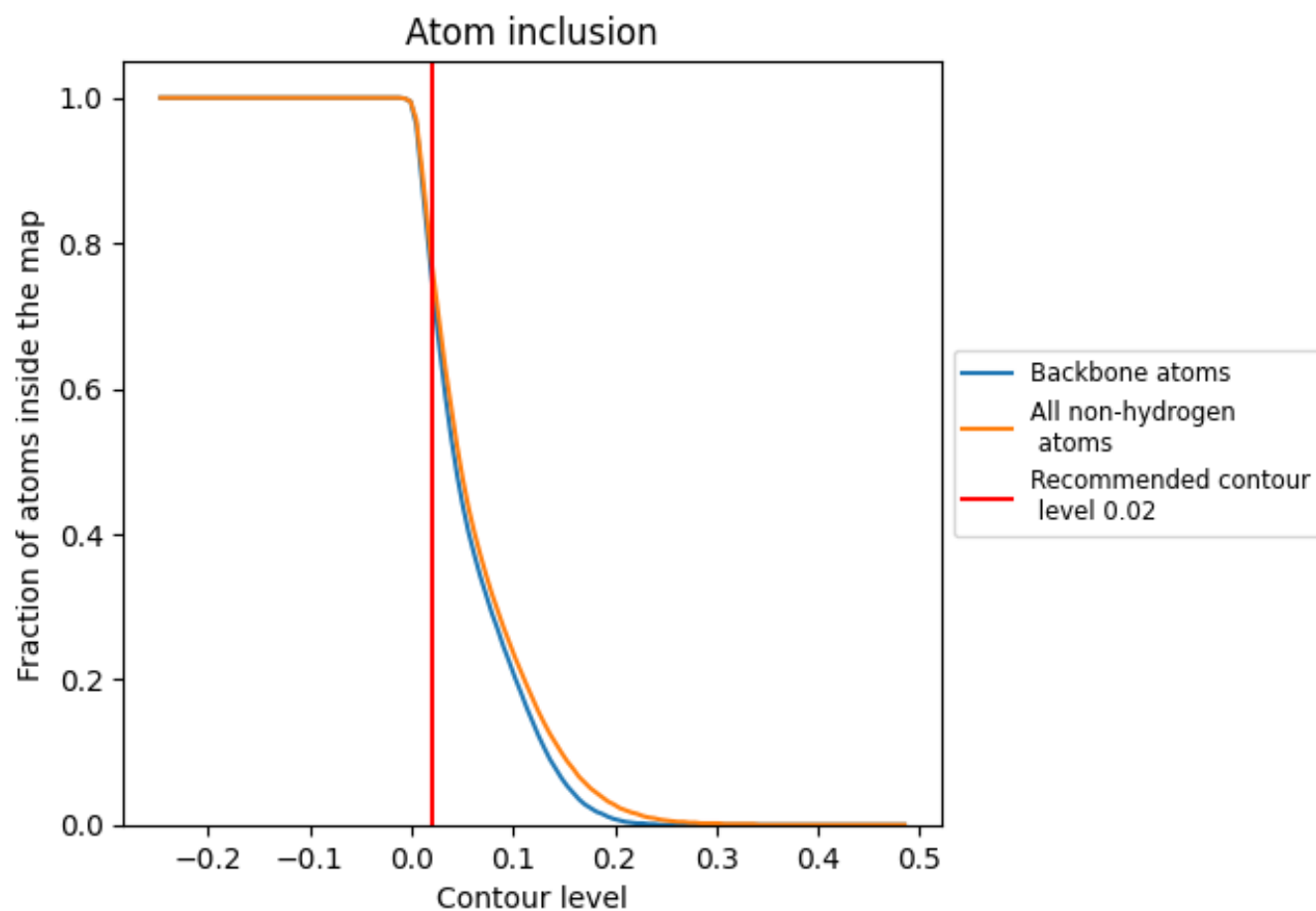
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 77% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7720	 0.4170
0	 0.0350	 0.1250
1	 0.3280	 0.2030
2	 0.8330	 0.4690
3	 0.8790	 0.4770
4	 0.7390	 0.3240
5	 0.6520	 0.2770
6	 0.7530	 0.4070
7	 0.0070	 0.0570
8	 0.7200	 0.3660
A	 0.9330	 0.4800
E	 0.9230	 0.5220
H	 0.9810	 0.6160
I	 0.6500	 0.2670
J	 0.9360	 0.5410
K	 0.9220	 0.4940
L	 0.9230	 0.5690
M	 0.9720	 0.5810
O	 0.9550	 0.6100
P	 0.5340	 0.1920
Q	 0.9590	 0.5810
R	 0.8820	 0.4880
S	 0.7830	 0.3750
T	 0.5840	 0.2630
V	 0.7450	 0.3350
W	 0.7300	 0.3190
Z	 0.9770	 0.6000
a	 0.8810	 0.5430
b	 0.9180	 0.5610
c	 0.4110	 0.2080
e	 0.9450	 0.5420
f	 0.5430	 0.2470
h	 0.9710	 0.5500
i	 0.6380	 0.2260

