



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 04:35 PM UTC

PDB ID : 6Z6P / pdb_00006z6p
EMDB ID : EMD-11102
Title : HDAC-PC-Nuc
Authors : Lee, J.-H.; Bollschweiler, D.; Schaefer, T.; Huber, R.
Deposited on : 2020-05-28
Resolution : 4.43 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

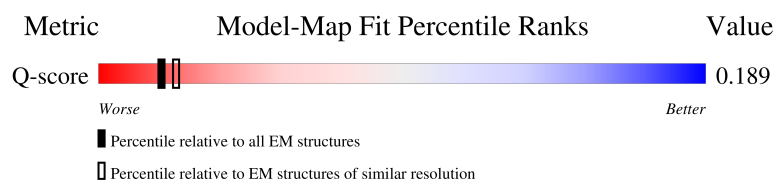
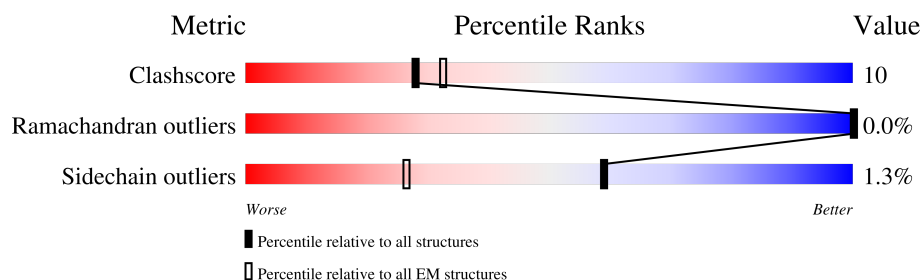
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.43 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	-
Q-score	-	25397	3083 (3.93 - 4.93)

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	K	661	
2	L	672	
3	M	543	
4	N	629	

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Mol	Chain	Length	Quality of chain
5	A	97	 66% 33% .
6	B	83	 65% 34% .
7	C	103	 73% 26% .
8	D	95	 66% 31% .
9	E	97	 79% 21%
10	F	78	 72% 28%
11	G	105	 76% 22% .
12	H	93	 66% 31% .
13	I	145	 82% 18%
14	J	145	 80% 20%

2 Entry composition [i](#)

There are 15 unique types of molecules in this entry. The entry contains 31115 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 Histone deacetylase HDA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	K	651	Total	C	N	O	S	0	0
			5178	3303	876	972	27		

- Molecule 2 is a protein called Histone deacetylase HDA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L	661	Total	C	N	O	S	0	0
			5245	3339	883	995	28		

- Molecule 3 is a protein called HDA1 complex subunit 3,HDA1 complex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	M	534	Total	C	N	O	S	0	0
			4376	2765	737	854	20		

- Molecule 4 is a protein called HDA1 complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	N	541	Total	C	N	O	S	0	0
			4416	2801	759	843	13		

- Molecule 5 is a protein called Histone H3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	97	Total	C	N	O	S	0	0
			802	506	155	138	3		

- Molecule 6 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	83	Total	C	N	O	S	0	0
			662	418	129	114	1		

- Molecule 7 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	C	103	Total	C	N	O	0	0
			795	501	155	139		

- Molecule 8 is a protein called Histone H2B.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	95	Total	C	N	O	S	0	0
			745	469	134	140	2		

- Molecule 9 is a protein called Histone H3.2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	97	Total	C	N	O	S	0	0
			801	504	155	139	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	102	ALA	GLY	conflict	UNP P84233

- Molecule 10 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	78	Total	C	N	O	S	0	0
			619	391	120	107	1		

- Molecule 11 is a protein called Histone H2A type 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	G	105	Total	C	N	O	0	0
			809	510	158	141		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	99	ARG	GLY	conflict	UNP P06897

- Molecule 12 is a protein called Histone H2B.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H	93	Total	C	N	O	S	0	0
			726	457	130	137	2		

- Molecule 13 is a DNA chain called DNA (145-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
13	I	145	Total	C	N	O	P	0	0
			2952	1404	537	867	144		

- Molecule 14 is a DNA chain called DNA (145-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J	145	Total	C	N	O	P	0	0
			2987	1416	558	869	144		

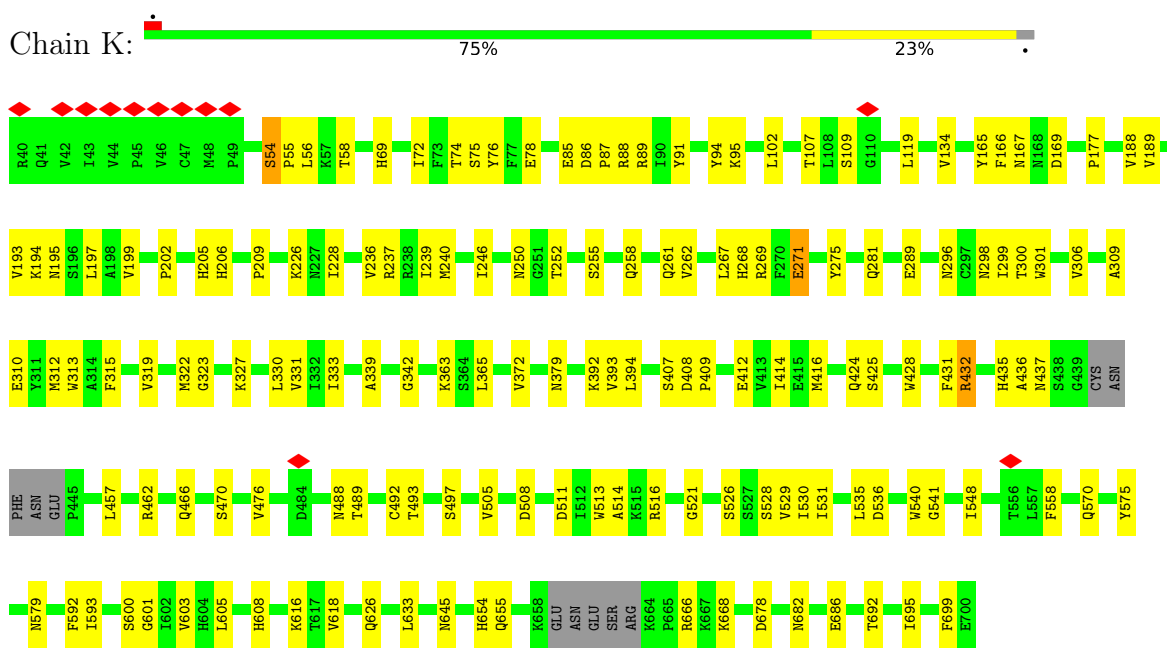
- Molecule 15 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
15	K	1	Total	Zn	0
			1	1	
15	L	1	Total	Zn	0
			1	1	

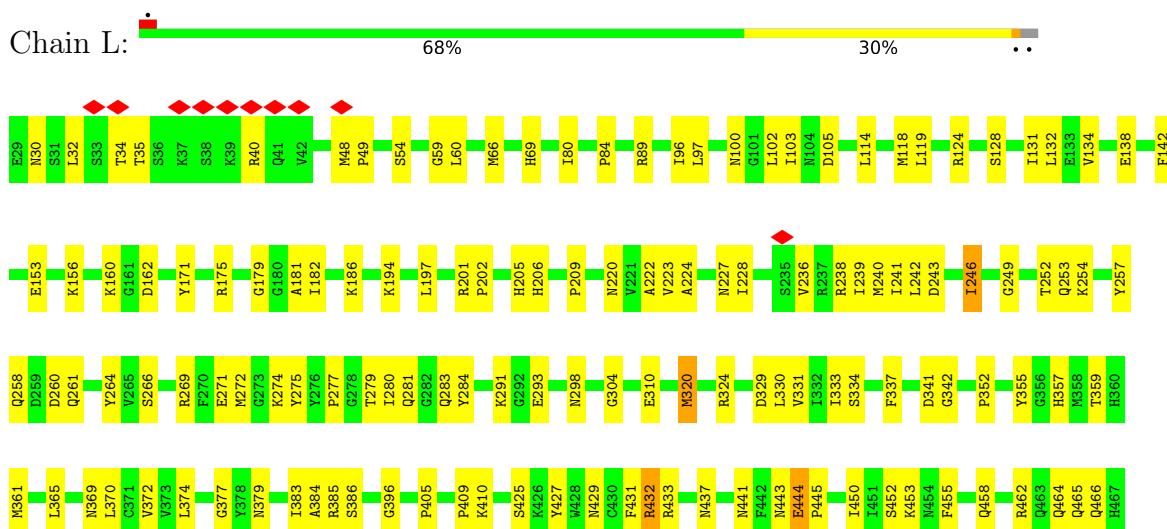
3 Residue-property plots

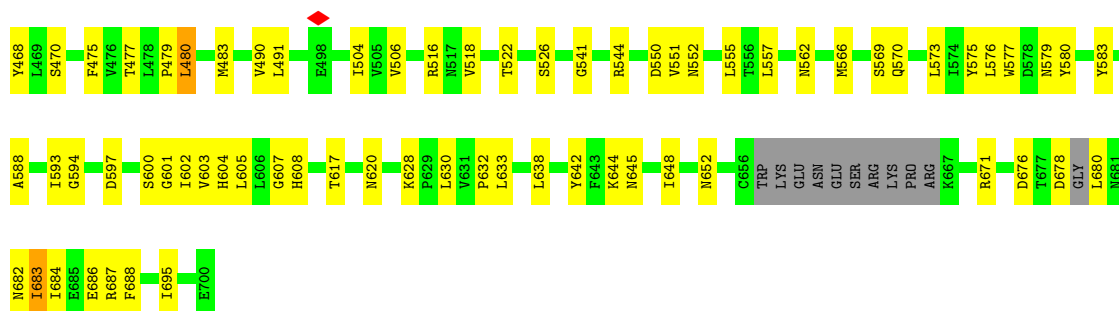
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: Histone deacetylase HDA1

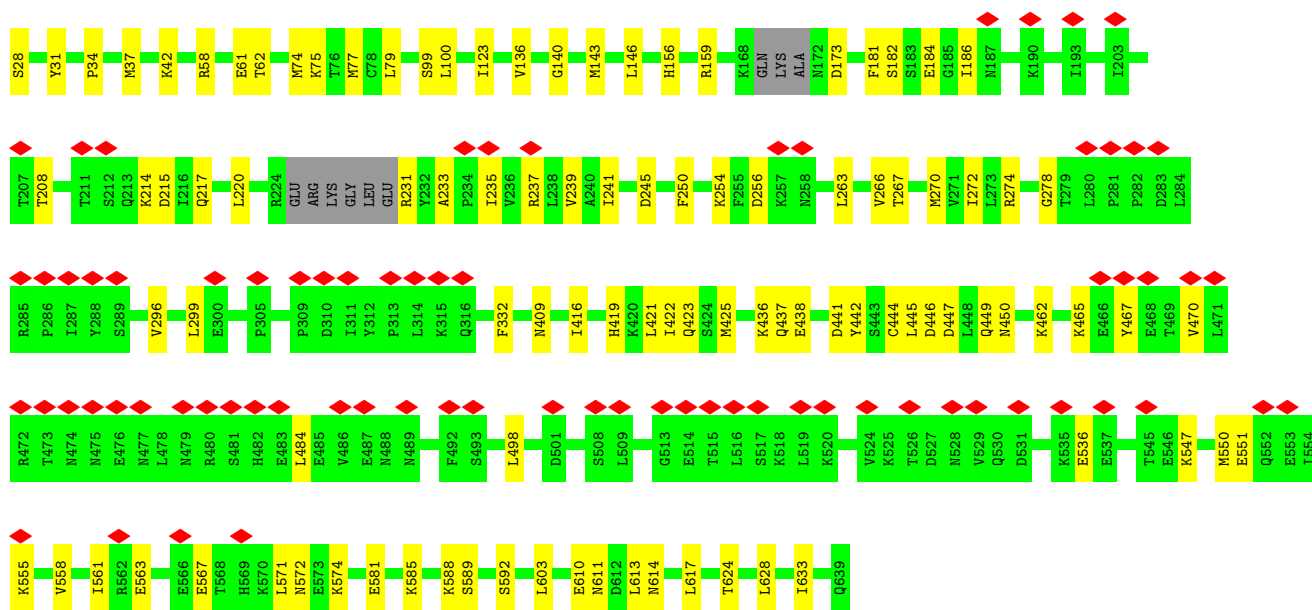
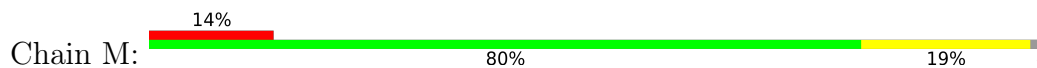


• Molecule 2: Histone deacetylase HDA1

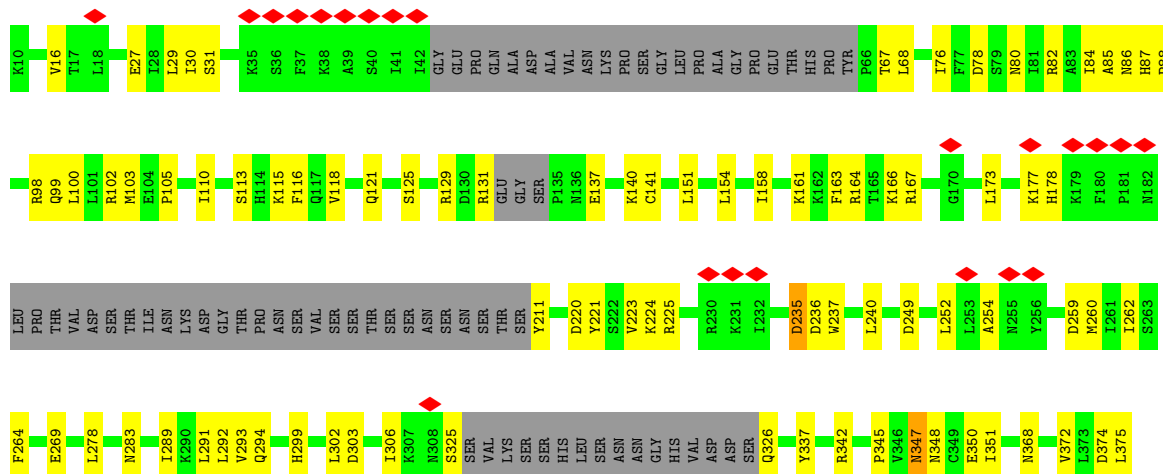


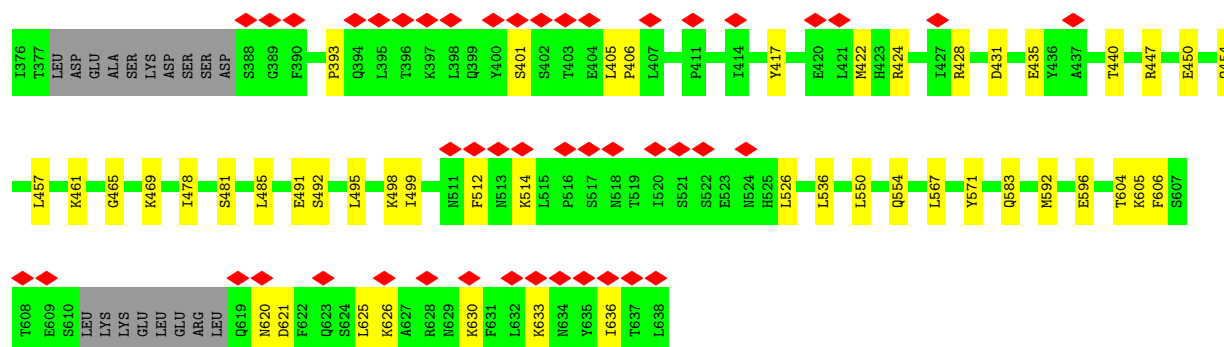


• Molecule 3: HDA1 complex subunit 3, HDA1 complex subunit 3



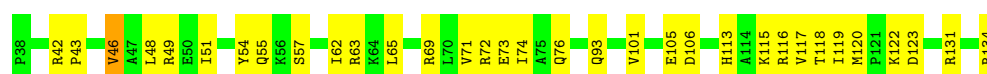
• Molecule 4: HDA1 complex subunit 2





• Molecule 5: Histone H3

Chain A: 66% 33% .



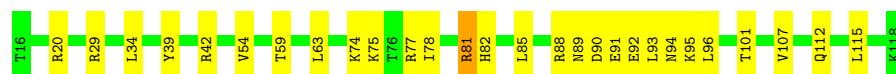
• Molecule 6: Histone H4

Chain B: 65% 34% .



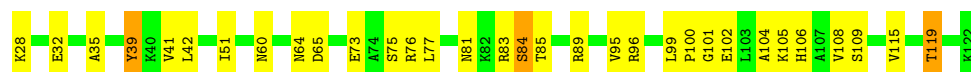
• Molecule 7: Histone H2A

Chain C: 73% 26% .



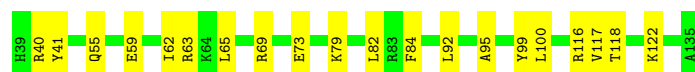
• Molecule 8: Histone H2B

Chain D: 66% 31% .



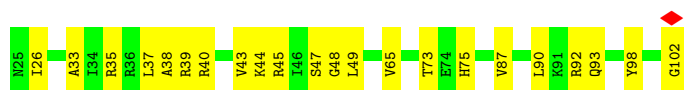
• Molecule 9: Histone H3.2

Chain E: 79% 21% .

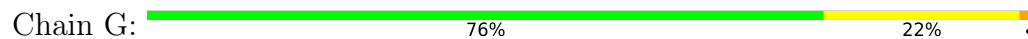


• Molecule 10: Histone H4

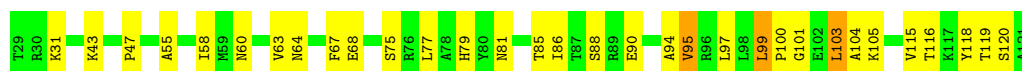
Chain F: 72% 28% .



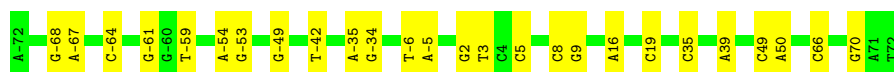
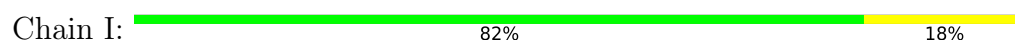
- Molecule 11: Histone H2A type 1



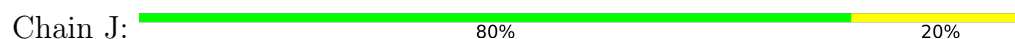
- Molecule 12: Histone H2B



- Molecule 13: DNA (145-MER)



- Molecule 14: DNA (145-MER)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	41279	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	77.2	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.271	Depositor
Minimum map value	-0.061	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.035	Depositor
Map size ($\text{\AA}$)	459.64798, 459.64798, 459.64798	wwPDB
Map dimensions	540, 540, 540	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.8512, 0.8512, 0.8512	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

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	K	0.41	0/5301	0.90	6/7189 (0.1%)
2	L	0.41	1/5366 (0.0%)	0.91	8/7277 (0.1%)
3	M	0.38	0/4449	0.83	1/5997 (0.0%)
4	N	0.38	0/4486	0.90	5/6037 (0.1%)
5	A	0.42	0/814	0.88	0/1092
6	B	0.42	0/669	0.99	2/894 (0.2%)
7	C	0.38	0/805	0.85	0/1088
8	D	0.44	0/756	0.93	0/1015
9	E	0.38	0/812	0.86	0/1088
10	F	0.44	0/626	0.99	2/837 (0.2%)
11	G	0.39	0/819	0.84	0/1106
12	H	0.42	0/737	0.98	0/993
13	I	0.60	0/3308	0.98	4/5099 (0.1%)
14	J	0.59	0/3354	1.01	9/5180 (0.2%)
All	All	0.44	1/32302 (0.0%)	0.92	37/44892 (0.1%)

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
1	K	0	3
2	L	0	5
3	M	0	3
4	N	0	7
6	B	0	2
7	C	0	1
8	D	0	1
10	F	0	1
All	All	0	23

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	320	MET	C-N	6.41	1.41	1.34

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	N	440	THR	CA-C-N	10.40	126.79	120.24
4	N	440	THR	C-N-CA	10.40	126.79	120.24
14	J	20	DG	O3'-P-O5'	-6.47	94.30	104.00
13	I	-53	DG	P-O3'-C3'	6.46	129.88	120.20
2	L	555	LEU	CA-C-N	6.25	133.49	121.54
2	L	555	LEU	C-N-CA	6.25	133.49	121.54
6	B	30	THR	CA-C-N	6.20	128.76	120.58
6	B	30	THR	C-N-CA	6.20	128.76	120.58
2	L	557	LEU	CA-C-N	6.18	133.35	121.54
2	L	557	LEU	C-N-CA	6.18	133.35	121.54
10	F	49	LEU	CA-C-N	6.13	133.01	121.97
10	F	49	LEU	C-N-CA	6.13	133.01	121.97
2	L	583	TYR	CA-C-N	5.88	138.02	120.69
2	L	583	TYR	C-N-CA	5.88	138.02	120.69
14	J	-21	DG	P-O3'-C3'	5.82	128.93	120.20
13	I	-35	DA	O4'-C1'-N9	-5.76	99.75	108.40
14	J	46	DG	OP1-P-O3'	5.74	125.23	108.00
3	M	272	ILE	CG1-CB-CG2	-5.60	93.91	110.70
1	K	654	HIS	CA-C-N	5.57	132.18	121.54
1	K	654	HIS	C-N-CA	5.57	132.18	121.54
14	J	20	DG	N9-C1'-C2'	5.55	121.82	113.50
4	N	269	GLU	CA-CB-CG	5.48	125.07	114.10
1	K	199	VAL	CG1-CB-CG2	-5.34	99.04	110.80
13	I	66	DC	P-O3'-C3'	5.33	128.20	120.20
13	I	-53	DG	OP2-P-O3'	5.33	123.98	108.00
14	J	-33	DG	P-O3'-C3'	5.32	128.18	120.20
2	L	432	ARG	CA-C-N	5.27	131.61	121.54
2	L	432	ARG	C-N-CA	5.27	131.61	121.54
4	N	269	GLU	CA-C-N	5.22	131.37	121.97
4	N	269	GLU	C-N-CA	5.22	131.37	121.97
14	J	50	DG	OP2-P-O3'	5.22	123.67	108.00
14	J	63	DG	P-O3'-C3'	5.20	128.00	120.20
14	J	54	DT	P-O3'-C3'	5.17	127.95	120.20
1	K	432	ARG	CA-C-N	5.13	131.34	121.54
1	K	432	ARG	C-N-CA	5.13	131.34	121.54
1	K	457	LEU	CA-CB-CG	5.07	134.05	116.30
14	J	21	DG	C2'-C3'-O3'	5.00	119.00	111.50

There are no chirality outliers.

All (23) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	B	50	ILE	Peptide
6	B	68	ASP	Peptide
7	C	74	LYS	Peptide
8	D	100	PRO	Peptide
10	F	45	ARG	Peptide
1	K	271	GLU	Peptide
1	K	408	ASP	Peptide
1	K	54	SER	Peptide
2	L	246	ILE	Peptide
2	L	445	PRO	Peptide
2	L	54	SER	Peptide
2	L	562	ASN	Peptide
2	L	588	ALA	Peptide
3	M	332	PHE	Peptide
3	M	442	TYR	Peptide
3	M	633	ILE	Peptide
4	N	306	ILE	Peptide
4	N	347	ASN	Peptide
4	N	372	VAL	Peptide
4	N	512	PHE	Peptide
4	N	514	LYS	Peptide
4	N	604	THR	Peptide
4	N	605	LYS	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	K	5178	0	5104	102	0
2	L	5245	0	5155	135	0
3	M	4376	0	4380	65	0
4	N	4416	0	4493	75	0
5	A	802	0	841	24	0
6	B	662	0	709	21	0
7	C	795	0	846	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	D	745	0	773	23	0
9	E	801	0	838	16	0
10	F	619	0	659	16	0
11	G	809	0	864	15	0
12	H	726	0	747	23	0
13	I	2952	0	1629	25	0
14	J	2987	0	1630	19	0
15	K	1	0	0	0	0
15	L	1	0	0	0	0
All	All	31115	0	28668	498	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 10.

All (498) 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)
13:I:3:DT:H3	14:J:-4:DG:H1	1.12	0.92
2:L:575:TYR:O	2:L:579:ASN:HB2	1.76	0.85
2:L:242:LEU:O	2:L:334:SER:HB3	1.76	0.84
3:M:28:SER:N	3:M:31:TYR:HH	1.76	0.82
2:L:156:LYS:O	2:L:160:LYS:HB2	1.81	0.81
2:L:600:SER:O	2:L:603:VAL:HB	1.88	0.74
4:N:140:LYS:HA	4:N:237:TRP:O	1.88	0.73
3:M:34:PRO:HA	3:M:239:VAL:O	1.90	0.71
5:A:72:ARG:O	5:A:76:GLN:HB2	1.91	0.71
2:L:684:ILE:O	2:L:688:PHE:HB2	1.91	0.70
2:L:128:SER:O	2:L:132:LEU:HB2	1.91	0.69
7:C:92:GLU:O	7:C:96:LEU:HB2	1.92	0.69
12:H:115:VAL:O	12:H:119:THR:HB	1.93	0.68
5:A:63:ARG:HH21	14:J:18:DG:H5'	1.59	0.68
1:K:268:HIS:O	1:K:300:THR:HA	1.93	0.68
1:K:575:TYR:O	1:K:579:ASN:HB2	1.93	0.67
4:N:76:ILE:O	4:N:80:ASN:HB2	1.94	0.67
1:K:309:ALA:O	1:K:313:TRP:HB3	1.98	0.64
2:L:638:LEU:O	2:L:642:TYR:HB3	1.98	0.64
2:L:678:ASP:HB2	2:L:682:ASN:HB2	1.80	0.63
7:C:91:GLU:O	7:C:95:LYS:HB2	1.98	0.63
3:M:143:MET:O	3:M:146:LEU:HB3	1.98	0.63
1:K:197:LEU:HA	1:K:372:VAL:O	1.99	0.63
1:K:682:ASN:O	1:K:686:GLU:HB3	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:435:HIS:O	1:K:516:ARG:NH2	2.34	0.60
1:K:592:PHE:HB2	1:K:618:VAL:HG23	1.83	0.60
12:H:63:VAL:O	12:H:67:PHE:HB2	2.01	0.60
7:C:59:THR:HG23	8:D:41:VAL:HG11	1.83	0.60
8:D:101:GLY:O	8:D:105:LYS:HB2	2.02	0.60
2:L:96:ILE:HG13	2:L:384:ALA:HB1	1.84	0.60
7:C:42:ARG:HG3	8:D:85:THR:HB	1.83	0.59
3:M:613:LEU:O	3:M:617:LEU:HB2	2.02	0.59
1:K:240:MET:O	1:K:331:VAL:HA	2.02	0.59
5:A:42:ARG:HG3	13:I:70:DG:H3'	1.85	0.58
2:L:608:HIS:HA	2:L:633:LEU:HB2	1.85	0.58
3:M:37:MET:HB2	3:M:42:LYS:HE3	1.85	0.58
5:A:54:TYR:HB3	6:B:40:ARG:HE	1.68	0.58
1:K:306:VAL:HB	1:K:310:GLU:HG2	1.84	0.58
4:N:351:ILE:HA	4:N:368:ASN:HD21	1.69	0.58
7:C:29:ARG:HH12	8:D:32:GLU:HB3	1.69	0.58
1:K:462:ARG:HE	1:K:489:THR:HA	1.68	0.58
1:K:188:VAL:HG11	1:K:330:LEU:HD13	1.86	0.57
1:K:570:GLN:HG3	1:K:601:GLY:HA2	1.85	0.57
4:N:299:HIS:O	4:N:303:ASP:HB2	2.04	0.57
2:L:238:ARG:HE	2:L:261:GLN:HA	1.69	0.57
4:N:447:ARG:HA	4:N:450:GLU:HB3	1.85	0.57
11:G:113:SER:HA	11:G:116:LEU:HD12	1.86	0.57
9:E:63:ARG:HH12	10:F:33:ALA:HB2	1.68	0.57
4:N:345:PRO:HD2	4:N:375:LEU:HD11	1.86	0.57
13:I:59:DT:H3	14:J:59:DA:H61	1.50	0.57
4:N:177:LYS:H	4:N:636:ILE:HD11	1.70	0.57
3:M:444:CYS:HB3	3:M:445:LEU:HD12	1.87	0.57
1:K:466:GLN:HE21	3:M:423:GLN:HG2	1.69	0.57
2:L:479:PRO:HG3	3:M:438:GLU:HA	1.87	0.57
1:K:228:ILE:HB	1:K:236:VAL:HG21	1.86	0.56
6:B:39:ARG:NH1	6:B:43:VAL:O	2.38	0.56
6:B:92:ARG:HH21	8:D:73:GLU:HG2	1.69	0.56
1:K:91:TYR:O	1:K:95:LYS:N	2.38	0.56
2:L:320:MET:HB3	2:L:324:ARG:HH12	1.70	0.56
4:N:118:VAL:HA	4:N:121:GLN:HB3	1.87	0.56
4:N:85:ALA:HB1	4:N:293:VAL:HG21	1.88	0.56
3:M:270:MET:O	3:M:274:ARG:HB2	2.05	0.56
1:K:246:ILE:HG12	1:K:269:ARG:HG3	1.87	0.56
1:K:327:LYS:HG2	2:L:405:PRO:HG2	1.88	0.56
7:C:78:ILE:HB	8:D:51:ILE:HG13	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:260:ASP:H	2:L:291:LYS:HZ3	1.54	0.55
2:L:310:GLU:HG3	2:L:409:PRO:HB3	1.87	0.55
1:K:535:LEU:HD22	2:L:450:ILE:HG23	1.88	0.55
2:L:491:LEU:HB2	2:L:550:ASP:HB3	1.89	0.55
5:A:62:ILE:O	5:A:93:GLN:NE2	2.39	0.55
2:L:223:VAL:O	2:L:227:ASN:ND2	2.39	0.55
6:B:68:ASP:O	6:B:71:THR:HB	2.07	0.55
3:M:624:THR:O	3:M:628:LEU:HB2	2.07	0.55
1:K:513:TRP:O	1:K:528:SER:HA	2.07	0.55
2:L:429:ASN:HA	2:L:432:ARG:HE	1.71	0.55
2:L:425:SER:O	2:L:432:ARG:NH1	2.40	0.55
3:M:77:MET:HE1	3:M:267:THR:HG23	1.89	0.55
11:G:67:GLY:O	11:G:71:ARG:HB2	2.05	0.55
1:K:107:THR:HB	2:L:40:ARG:HH21	1.72	0.54
7:C:54:VAL:HG21	8:D:95:VAL:HG21	1.89	0.54
2:L:579:ASN:ND2	3:M:446:ASP:OD1	2.40	0.54
2:L:236:VAL:HG13	2:L:329:ASP:HB2	1.89	0.54
5:A:116:ARG:NH1	5:A:118:THR:O	2.40	0.54
3:M:156:HIS:NE2	13:I:-49:DG:OP1	2.41	0.54
6:B:73:THR:HG21	6:B:81:VAL:HG22	1.88	0.54
2:L:202:PRO:O	2:L:220:ASN:ND2	2.40	0.54
2:L:462:ARG:NH2	2:L:550:ASP:O	2.39	0.54
1:K:363:LYS:NZ	1:K:393:VAL:O	2.36	0.54
2:L:333:ILE:HB	2:L:372:VAL:HA	1.90	0.54
3:M:99:SER:OG	3:M:100:LEU:N	2.40	0.54
8:D:35:ALA:O	8:D:39:TYR:HB2	2.07	0.54
4:N:431:ASP:O	4:N:435:GLU:HB2	2.08	0.54
3:M:220:LEU:HG	3:M:233:ALA:HB3	1.90	0.53
11:G:27:VAL:O	11:G:31:HIS:HB2	2.07	0.53
1:K:323:GLY:HA3	1:K:365:LEU:HD21	1.91	0.53
1:K:432:ARG:HA	1:K:437:ASN:HB2	1.91	0.53
4:N:158:ILE:HG23	4:N:161:LYS:HD2	1.91	0.53
2:L:59:GLY:HA2	2:L:119:LEU:O	2.08	0.53
13:I:64:DC:O2	14:J:64:DG:N2	2.42	0.53
13:I:3:DT:O4	14:J:-4:DG:O6	2.27	0.53
2:L:284:TYR:HA	2:L:298:ASN:HB2	1.91	0.53
2:L:620:ASN:HB3	2:L:648:ILE:HG12	1.91	0.53
4:N:131:ARG:NH2	4:N:137:GLU:O	2.42	0.53
8:D:60:ASN:O	8:D:64:ASN:ND2	2.41	0.53
1:K:541:GLY:HA3	1:K:548:ILE:HD11	1.91	0.53
2:L:186:LYS:NZ	2:L:227:ASN:OD1	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:462:ARG:HH21	2:L:490:VAL:HA	1.72	0.53
4:N:262:ILE:HA	4:N:289:ILE:O	2.09	0.53
11:G:92:GLU:HB3	12:H:103:LEU:HD22	1.90	0.53
2:L:678:ASP:OD2	2:L:680:LEU:N	2.42	0.53
3:M:250:PHE:O	3:M:254:LYS:NZ	2.42	0.53
4:N:102:ARG:O	4:N:626:LYS:NZ	2.42	0.53
13:I:16:DA:N6	14:J:-17:DT:O4	2.42	0.53
1:K:425:SER:O	1:K:432:ARG:NH1	2.42	0.53
4:N:166:LYS:HE3	4:N:178:HIS:HB2	1.91	0.52
4:N:592:MET:O	4:N:596:GLU:HB2	2.09	0.52
3:M:611:ASN:HA	3:M:614:ASN:HB2	1.91	0.52
10:F:39:ARG:NH1	10:F:43:VAL:O	2.43	0.52
1:K:102:LEU:HD21	1:K:392:LYS:HE2	1.90	0.52
2:L:644:LYS:O	2:L:671:ARG:NH2	2.42	0.52
4:N:27:GLU:HB3	4:N:393:PRO:HB2	1.92	0.52
8:D:77:LEU:O	8:D:81:ASN:ND2	2.42	0.52
2:L:441:ASN:OD1	2:L:443:ASN:ND2	2.43	0.52
4:N:499:ILE:HG21	4:N:526:LEU:HD13	1.91	0.52
1:K:424:GLN:O	1:K:428:TRP:N	2.43	0.52
2:L:153:GLU:HA	2:L:156:LYS:HB2	1.92	0.52
3:M:74:MET:HE2	3:M:267:THR:HG21	1.92	0.52
1:K:255:SER:O	1:K:258:GLN:NE2	2.43	0.52
2:L:138:GLU:O	2:L:142:PHE:HB2	2.10	0.52
4:N:325:SER:OG	4:N:326:GLN:N	2.44	0.51
4:N:350:GLU:O	4:N:368:ASN:ND2	2.44	0.51
8:D:83:ARG:HH21	13:I:-34:DG:H3'	1.73	0.51
13:I:35:DC:O2	14:J:-35:DG:N2	2.43	0.51
2:L:441:ASN:ND2	2:L:444:GLU:OE2	2.43	0.51
2:L:258:GLN:O	2:L:291:LYS:NZ	2.43	0.51
3:M:231:ARG:NH2	3:M:233:ALA:O	2.44	0.51
5:A:106:ASP:OD2	5:A:131:ARG:NH2	2.43	0.51
1:K:342:GLY:O	1:K:379:ASN:ND2	2.44	0.51
2:L:80:ILE:HD13	4:N:469:LYS:HD3	1.93	0.51
1:K:412:GLU:O	1:K:416:MET:HB2	2.11	0.51
1:K:530:ILE:HB	2:L:455:PHE:HB2	1.93	0.51
3:M:215:ASP:OD1	3:M:215:ASP:N	2.40	0.51
4:N:454:GLN:NE2	4:N:571:TYR:OH	2.43	0.51
3:M:173:ASP:N	3:M:173:ASP:OD1	2.44	0.51
3:M:555:LYS:HA	3:M:558:VAL:HG12	1.92	0.51
4:N:151:LEU:HD12	4:N:154:LEU:HD12	1.93	0.51
1:K:237:ARG:O	1:K:261:GLN:NE2	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:683:ILE:O	2:L:687:ARG:HB2	2.11	0.51
4:N:211:TYR:N	4:N:220:ASP:OD1	2.44	0.51
2:L:131:ILE:HG13	2:L:223:VAL:HG11	1.92	0.51
2:L:480:LEU:HB2	2:L:483:MET:HB3	1.93	0.51
4:N:294:GLN:HB2	4:N:347:ASN:HD22	1.76	0.51
2:L:342:GLY:O	2:L:379:ASN:ND2	2.44	0.50
2:L:458:GLN:NE2	2:L:552:ASN:OD1	2.44	0.50
8:D:32:GLU:HA	14:J:49:DC:H5"	1.92	0.50
10:F:47:SER:OG	10:F:48:GLY:N	2.42	0.50
2:L:506:VAL:HA	2:L:551:VAL:HG23	1.93	0.50
7:C:39:TYR:HD1	8:D:75:SER:HB2	1.77	0.50
1:K:309:ALA:HA	1:K:312:MET:HB2	1.92	0.50
2:L:171:TYR:O	2:L:175:ARG:NE	2.43	0.50
2:L:603:VAL:HG21	2:L:628:LYS:HB2	1.94	0.50
3:M:140:GLY:O	3:M:143:MET:HB2	2.11	0.50
3:M:563:GLU:O	3:M:567:GLU:HB2	2.12	0.50
9:E:41:TYR:HB2	13:I:9:DG:H5"	1.94	0.50
12:H:43:LYS:HD2	12:H:47:PRO:HA	1.92	0.50
1:K:633:LEU:HD22	12:H:119:THR:HG22	1.94	0.50
2:L:490:VAL:HG23	2:L:551:VAL:HA	1.93	0.50
4:N:31:SER:OG	4:N:424:ARG:NH1	2.44	0.50
12:H:60:ASN:O	12:H:64:ASN:ND2	2.45	0.50
1:K:169:ASP:OD2	3:M:58:ARG:NH1	2.45	0.50
1:K:333:ILE:HB	1:K:372:VAL:HA	1.94	0.50
2:L:333:ILE:HD11	2:L:370:LEU:HB3	1.94	0.50
2:L:576:LEU:HA	2:L:580:TYR:HD2	1.76	0.50
2:L:222:ALA:HB2	2:L:252:THR:HG23	1.94	0.50
2:L:630:LEU:HG	2:L:632:PRO:HD3	1.93	0.50
4:N:78:ASP:OD2	4:N:82:ARG:NH1	2.45	0.50
1:K:267:LEU:HA	1:K:299:ILE:O	2.12	0.49
1:K:678:ASP:OD2	2:L:433:ARG:NH1	2.44	0.49
4:N:67:THR:OG1	4:N:68:LEU:N	2.45	0.49
4:N:294:GLN:NE2	4:N:348:ASN:OD1	2.45	0.49
5:A:57:SER:OG	6:B:40:ARG:NH2	2.45	0.49
1:K:513:TRP:HA	2:L:522:THR:HA	1.94	0.49
2:L:462:ARG:O	2:L:466:GLN:HB2	2.11	0.49
4:N:30:ILE:HD13	4:N:342:ARG:HH11	1.77	0.49
2:L:304:GLY:O	2:L:410:LYS:NZ	2.45	0.49
11:G:21:ALA:HB2	12:H:118:TYR:HB2	1.93	0.49
4:N:29:LEU:HD13	4:N:80:ASN:HB3	1.94	0.49
12:H:77:LEU:O	12:H:81:ASN:ND2	2.40	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:84:PRO:O	2:L:89:ARG:NH1	2.46	0.49
1:K:195:ASN:ND2	1:K:394:LEU:O	2.41	0.49
4:N:129:ARG:NH2	4:N:236:ASP:OD1	2.44	0.49
6:B:69:ALA:O	6:B:72:TYR:HB2	2.13	0.49
7:C:81:ARG:NH2	7:C:107:VAL:O	2.44	0.49
2:L:205:HIS:HB2	2:L:249:GLY:HA2	1.94	0.48
2:L:124:ARG:HG2	4:N:583:GLN:HE22	1.78	0.48
9:E:84:PHE:N	14:J:-23:DT:OP1	2.44	0.48
1:K:88:ARG:NH1	1:K:91:TYR:OH	2.47	0.48
4:N:254:ALA:HA	4:N:278:LEU:HD13	1.94	0.48
4:N:630:LYS:HG2	4:N:633:LYS:HB2	1.94	0.48
5:A:120:MET:SD	5:A:122:LYS:NZ	2.80	0.48
1:K:497:SER:OG	3:M:409:ASN:ND2	2.47	0.48
1:K:85:GLU:OE2	1:K:89:ARG:NH1	2.46	0.48
11:G:65:LEU:HD23	11:G:68:ASN:HD22	1.77	0.48
12:H:116:THR:O	12:H:120:SER:CB	2.61	0.48
1:K:119:LEU:HD12	1:K:193:VAL:HG12	1.96	0.48
1:K:505:VAL:HA	1:K:593:ILE:O	2.13	0.48
4:N:457:LEU:HB3	4:N:461:LYS:HE3	1.94	0.48
6:B:64:ASN:O	6:B:93:GLN:NE2	2.46	0.48
9:E:69:ARG:O	9:E:73:GLU:HB2	2.13	0.48
12:H:94:ALA:HA	12:H:97:LEU:HD12	1.95	0.48
1:K:493:THR:OG1	1:K:548:ILE:N	2.46	0.48
6:B:35:ARG:NH2	6:B:51:TYR:OH	2.46	0.48
2:L:464:GLN:O	2:L:468:TYR:HB2	2.14	0.48
4:N:292:LEU:HD11	4:N:299:HIS:HA	1.96	0.48
13:I:50:DA:N6	14:J:-51:DG:O6	2.47	0.48
2:L:96:ILE:O	2:L:100:ASN:ND2	2.46	0.47
4:N:167:ARG:HA	4:N:240:LEU:HB2	1.96	0.47
2:L:337:PHE:HD2	2:L:383:ILE:HG13	1.79	0.47
4:N:567:LEU:O	4:N:571:TYR:HB2	2.13	0.47
5:A:73:GLU:OE1	6:B:25:ASN:ND2	2.46	0.47
5:A:134:ARG:HB2	7:C:95:LYS:HG3	1.94	0.47
6:B:58:LEU:O	6:B:61:PHE:HB3	2.13	0.47
7:C:112:GLN:H	7:C:115:LEU:HD12	1.79	0.47
2:L:283:GLN:O	2:L:298:ASN:ND2	2.48	0.47
4:N:88:PRO:HD2	4:N:113:SER:HB2	1.97	0.47
1:K:322:MET:HE3	1:K:431:PHE:HE2	1.80	0.47
1:K:414:ILE:HG22	2:L:518:VAL:HG13	1.95	0.47
4:N:422:MET:HG3	4:N:606:PHE:HB2	1.95	0.47
12:H:75:SER:O	12:H:79:HIS:ND1	2.42	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:540:TRP:NE1	1:K:692:THR:OG1	2.47	0.47
4:N:221:TYR:HA	4:N:224:LYS:HE2	1.96	0.47
7:C:85:LEU:O	7:C:89:ASN:ND2	2.48	0.47
11:G:81:ARG:NH2	11:G:107:VAL:O	2.44	0.47
12:H:85:THR:OG1	12:H:86:ILE:N	2.48	0.47
2:L:330:LEU:HD12	2:L:369:ASN:HB3	1.95	0.47
2:L:477:THR:HA	2:L:491:LEU:HA	1.97	0.47
4:N:428:ARG:NH1	4:N:431:ASP:OD2	2.48	0.47
9:E:116:ARG:NH1	9:E:118:THR:O	2.48	0.47
2:L:341:ASP:O	2:L:385:ARG:NH2	2.42	0.47
3:M:296:VAL:HG22	3:M:299:LEU:HD12	1.97	0.47
4:N:99:GLN:OE1	4:N:102:ARG:NH2	2.48	0.47
12:H:116:THR:O	12:H:120:SER:HB3	2.15	0.47
2:L:272:MET:O	2:L:274:LYS:NZ	2.44	0.47
2:L:240:MET:O	2:L:331:VAL:HA	2.15	0.47
2:L:470:SER:HA	2:L:475:PHE:H	1.79	0.47
2:L:516:ARG:HG2	2:L:518:VAL:HB	1.97	0.47
4:N:80:ASN:ND2	4:N:417:TYR:OH	2.48	0.47
1:K:69:HIS:HE1	1:K:166:PHE:HA	1.79	0.46
2:L:352:PRO:HB3	2:L:386:SER:HA	1.97	0.46
3:M:437:GLN:O	3:M:441:ASP:HB3	2.14	0.46
3:M:547:LYS:HA	3:M:547:LYS:HD3	1.78	0.46
4:N:86:ASN:OD1	4:N:115:LYS:NZ	2.47	0.46
2:L:66:MET:O	2:L:201:ARG:NH1	2.48	0.46
2:L:444:GLU:HB3	2:L:452:SER:HA	1.97	0.46
1:K:616:LYS:O	1:K:645:ASN:ND2	2.48	0.46
2:L:464:GLN:O	2:L:468:TYR:CB	2.63	0.46
1:K:462:ARG:NH2	1:K:489:THR:O	2.41	0.46
3:M:498:LEU:HD22	3:M:536:GLU:HG2	1.96	0.46
13:I:19:DC:H42	14:J:-19:DG:H1	1.62	0.46
2:L:504:ILE:O	2:L:593:ILE:N	2.42	0.46
4:N:105:PRO:HA	4:N:625:LEU:HD22	1.97	0.46
1:K:72:ILE:HD11	1:K:167:ASN:HA	1.97	0.46
1:K:91:TYR:HA	1:K:94:TYR:HB3	1.98	0.46
1:K:281:GLN:O	1:K:298:ASN:ND2	2.49	0.46
1:K:412:GLU:O	1:K:416:MET:CB	2.64	0.46
2:L:570:GLN:HA	2:L:573:LEU:HD12	1.98	0.46
9:E:62:ILE:HD11	10:F:37:LEU:HD11	1.98	0.46
1:K:315:PHE:O	1:K:319:VAL:HB	2.16	0.46
4:N:98:ARG:HG2	4:N:173:LEU:HD22	1.98	0.46
9:E:79:LYS:HB3	9:E:82:LEU:HD11	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:466:GLN:O	1:K:470:SER:CB	2.63	0.46
1:K:600:SER:HA	1:K:603:VAL:HB	1.98	0.46
2:L:541:GLY:HA2	2:L:544:ARG:HG2	1.98	0.46
2:L:597:ASP:OD1	2:L:597:ASP:N	2.49	0.46
2:L:604:HIS:O	2:L:608:HIS:ND1	2.47	0.46
5:A:69:ARG:NH2	14:J:17:DA:OP1	2.49	0.46
12:H:116:THR:O	12:H:120:SER:OG	2.34	0.46
2:L:206:HIS:HE1	2:L:277:PRO:HD3	1.81	0.46
3:M:270:MET:O	3:M:274:ARG:CB	2.64	0.46
9:E:95:ALA:O	9:E:99:TYR:HB3	2.16	0.46
10:F:87:VAL:HA	10:F:90:LEU:HD12	1.98	0.46
2:L:253:GLN:HE22	2:L:281:GLN:HE21	1.64	0.45
3:M:581:GLU:OE1	3:M:585:LYS:NZ	2.49	0.45
10:F:87:VAL:HG11	10:F:102:GLY:HA2	1.97	0.45
1:K:516:ARG:NH1	1:K:521:GLY:O	2.50	0.45
2:L:357:HIS:HD1	2:L:361:MET:HE3	1.81	0.45
4:N:164:ARG:HG3	4:N:235:ASP:HB2	1.98	0.45
7:C:88:ARG:NH1	7:C:94:ASN:OD1	2.42	0.45
1:K:666:ARG:HD2	1:K:668:LYS:HG2	1.98	0.45
2:L:69:HIS:O	2:L:201:ARG:NH2	2.40	0.45
11:G:17:ARG:HH21	11:G:28:GLY:HA2	1.81	0.45
14:J:18:DG:H1'	14:J:19:DC:H5'	1.98	0.45
1:K:205:HIS:HA	1:K:252:THR:HG23	1.98	0.45
1:K:626:GLN:HG3	1:K:655:GLN:HE22	1.81	0.45
3:M:436:LYS:HG3	3:M:603:LEU:HD13	1.97	0.45
3:M:467:TYR:OH	3:M:572:ASN:ND2	2.50	0.45
3:M:610:GLU:O	3:M:614:ASN:ND2	2.44	0.45
4:N:84:ILE:HG23	4:N:88:PRO:HB3	1.98	0.45
5:A:48:LEU:HD23	5:A:51:ILE:HD12	1.97	0.45
2:L:97:LEU:HB3	2:L:102:LEU:HD12	1.98	0.45
2:L:103:ILE:HG22	2:L:105:ASP:H	1.81	0.45
2:L:279:THR:OG1	2:L:280:ILE:N	2.50	0.45
4:N:491:GLU:O	4:N:495:LEU:HB2	2.17	0.45
2:L:128:SER:HA	2:L:131:ILE:HG22	1.98	0.45
1:K:682:ASN:O	1:K:686:GLU:CB	2.64	0.45
2:L:425:SER:HB2	2:L:432:ARG:HB3	1.98	0.45
2:L:506:VAL:HB	2:L:594:GLY:HA2	1.98	0.45
3:M:263:LEU:HA	3:M:266:VAL:HG12	1.98	0.45
4:N:292:LEU:HD13	4:N:302:LEU:HD22	1.99	0.45
2:L:444:GLU:HG2	2:L:453:LYS:HG2	1.97	0.45
1:K:258:GLN:HA	1:K:289:GLU:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:425:SER:OG	1:K:437:ASN:ND2	2.41	0.45
2:L:607:GLY:O	2:L:633:LEU:N	2.50	0.45
3:M:449:GLN:NE2	3:M:589:SER:OG	2.50	0.45
8:D:115:VAL:O	8:D:119:THR:OG1	2.33	0.45
1:K:267:LEU:HD23	1:K:301:TRP:HZ2	1.83	0.44
1:K:476:VAL:HG21	3:M:416:ILE:HG12	1.99	0.44
1:K:511:ASP:HB2	1:K:531:ILE:HB	1.98	0.44
3:M:467:TYR:HA	3:M:470:VAL:HG12	1.98	0.44
3:M:610:GLU:OE2	3:M:614:ASN:ND2	2.49	0.44
4:N:100:LEU:HA	4:N:103:MET:HB2	1.99	0.44
4:N:431:ASP:O	4:N:435:GLU:CB	2.64	0.44
2:L:601:GLY:O	2:L:604:HIS:HB3	2.17	0.44
3:M:182:SER:H	3:M:186:ILE:HG23	1.81	0.44
3:M:571:LEU:HD12	3:M:574:LYS:HD3	1.98	0.44
1:K:431:PHE:O	1:K:437:ASN:ND2	2.51	0.44
1:K:514:ALA:HA	1:K:528:SER:HA	1.99	0.44
3:M:484:LEU:HD11	3:M:551:GLU:HA	1.99	0.44
1:K:608:HIS:HD2	12:H:120:SER:HB2	1.82	0.44
2:L:197:LEU:HA	2:L:372:VAL:HB	2.00	0.44
2:L:254:LYS:HA	2:L:257:TYR:HB2	1.99	0.44
6:B:29:ILE:O	6:B:55:ARG:NE	2.48	0.44
9:E:40:ARG:NH2	13:I:8:DC:O2	2.51	0.44
11:G:54:VAL:HG21	12:H:95:VAL:HG21	1.99	0.44
2:L:465:GLN:HA	2:L:468:TYR:HB3	2.00	0.44
6:B:75:HIS:O	8:D:89:ARG:NH2	2.49	0.44
7:C:90:ASP:HB3	7:C:93:LEU:HB2	1.98	0.44
9:E:40:ARG:NH2	13:I:9:DG:N3	2.65	0.44
9:E:59:GLU:O	10:F:40:ARG:NH1	2.42	0.44
10:F:35:ARG:NH2	13:I:8:DC:OP2	2.50	0.44
1:K:102:LEU:HD11	1:K:392:LYS:HG2	2.00	0.44
1:K:271:GLU:HB2	1:K:275:TYR:HB3	2.00	0.44
8:D:102:GLU:O	8:D:106:HIS:ND1	2.50	0.44
13:I:5:DC:H6	13:I:5:DC:H2'	1.68	0.44
14:J:39:DA:H1'	14:J:40:DC:H5'	2.00	0.44
13:I:-68:DG:H2''	13:I:-67:DA:H5''	1.99	0.44
1:K:189:VAL:HG11	1:K:236:VAL:HG22	2.00	0.44
2:L:114:LEU:HD11	2:L:118:MET:H	1.83	0.44
4:N:626:LYS:HD3	4:N:626:LYS:HA	1.85	0.44
3:M:558:VAL:HA	3:M:561:ILE:HG12	1.99	0.43
4:N:283:ASN:OD1	4:N:283:ASN:N	2.50	0.43
5:A:71:VAL:HA	5:A:74:ILE:HD12	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:E:92:LEU:HD21	10:F:65:VAL:HG11	2.01	0.43
10:F:75:HIS:NE2	12:H:90:GLU:OE2	2.50	0.43
2:L:617:THR:HA	2:L:645:ASN:HB3	2.00	0.43
3:M:159:ARG:HE	3:M:159:ARG:HB3	1.61	0.43
4:N:16:VAL:HB	4:N:293:VAL:HA	2.00	0.43
7:C:29:ARG:NH1	8:D:32:GLU:OE1	2.52	0.43
14:J:-27:DC:H4'	14:J:-26:DC:H5'	2.01	0.43
2:L:320:MET:HE3	2:L:365:LEU:HD13	1.99	0.43
2:L:441:ASN:HD21	2:L:443:ASN:HB2	1.84	0.43
4:N:492:SER:HB3	4:N:536:LEU:HD21	2.00	0.43
5:A:46:VAL:HG13	5:A:49:ARG:HD3	2.01	0.43
1:K:75:SER:OG	1:K:76:TYR:N	2.52	0.43
1:K:466:GLN:OE1	1:K:488:ASN:ND2	2.52	0.43
3:M:42:LYS:HE2	3:M:278:GLY:HA3	2.01	0.43
5:A:55:GLN:NE2	6:B:40:ARG:O	2.44	0.43
5:A:118:THR:HA	6:B:45:ARG:HB3	1.99	0.43
6:B:55:ARG:O	6:B:58:LEU:HB3	2.17	0.43
8:D:96:ARG:HE	8:D:108:VAL:HG21	1.83	0.43
13:I:-6:DT:H2''	13:I:-5:DA:C8	2.54	0.43
1:K:134:VAL:HG12	1:K:209:PRO:HG3	2.00	0.43
3:M:421:LEU:O	3:M:425:MET:HB2	2.19	0.43
4:N:221:TYR:O	4:N:225:ARG:N	2.40	0.43
4:N:620:ASN:HA	4:N:621:ASP:HA	1.80	0.43
1:K:239:ILE:O	1:K:262:VAL:HA	2.18	0.43
1:K:526:SER:HA	2:L:458:GLN:HB2	2.00	0.43
2:L:355:TYR:O	2:L:359:THR:OG1	2.33	0.43
3:M:421:LEU:O	3:M:425:MET:CB	2.67	0.43
4:N:141:CYS:HA	4:N:260:MET:O	2.18	0.43
7:C:34:LEU:HA	7:C:39:TYR:HE2	1.83	0.43
8:D:65:ASP:OD2	10:F:98:TYR:OH	2.33	0.43
12:H:100:PRO:HD2	12:H:103:LEU:HD23	2.01	0.43
2:L:462:ARG:O	2:L:466:GLN:CB	2.66	0.42
2:L:566:MET:O	2:L:569:SER:OG	2.36	0.42
6:B:92:ARG:HH21	8:D:76:ARG:HH12	1.67	0.42
7:C:82:HIS:HA	7:C:85:LEU:HD12	2.01	0.42
13:I:-61:DG:N1	14:J:61:DC:O2	2.52	0.42
1:K:536:ASP:OD1	1:K:536:ASP:N	2.52	0.42
2:L:35:THR:OG1	3:M:61:GLU:OE2	2.37	0.42
8:D:99:LEU:HB2	8:D:104:ALA:HB2	2.01	0.42
1:K:513:TRP:HB3	1:K:529:VAL:HG22	2.01	0.42
2:L:32:LEU:HA	3:M:62:THR:HG23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:550:MET:HE2	3:M:550:MET:HB3	1.83	0.42
10:F:92:ARG:HG3	10:F:93:GLN:HG2	2.00	0.42
1:K:296:ASN:O	1:K:424:GLN:NE2	2.43	0.42
4:N:465:GLY:O	4:N:469:LYS:HB2	2.19	0.42
7:C:115:LEU:O	10:F:44:LYS:NZ	2.44	0.42
2:L:617:THR:HG21	2:L:695:ILE:HG12	2.01	0.42
3:M:136:VAL:HG12	3:M:181:PHE:HB2	2.02	0.42
11:G:42:ARG:HG2	13:I:39:DA:H5"	2.00	0.42
14:J:-6:DG:H2"	14:J:-5:DG:C8	2.55	0.42
3:M:34:PRO:HB3	3:M:241:ILE:HB	2.00	0.42
3:M:75:LYS:O	3:M:79:LEU:HB2	2.20	0.42
4:N:264:PHE:HD2	4:N:291:LEU:HD12	1.84	0.42
12:H:101:GLY:O	12:H:105:LYS:HB2	2.18	0.42
1:K:309:ALA:HB3	1:K:407:SER:HB3	2.02	0.42
1:K:605:LEU:HD12	1:K:605:LEU:HA	1.87	0.42
2:L:239:ILE:HG12	2:L:330:LEU:HB3	2.01	0.42
2:L:241:ILE:HB	2:L:264:TYR:HD1	1.84	0.42
4:N:163:PHE:HD1	4:N:236:ASP:HB2	1.85	0.42
5:A:101:VAL:HG11	6:B:40:ARG:HG2	2.02	0.42
1:K:436:ALA:HB1	1:K:521:GLY:H	1.84	0.42
2:L:480:LEU:H	2:L:480:LEU:HG	1.41	0.42
4:N:110:ILE:HG22	4:N:116:PHE:HB3	2.01	0.42
5:A:49:ARG:NH2	14:J:-66:DG:O4'	2.51	0.42
5:A:119:ILE:O	6:B:47:SER:OG	2.30	0.42
7:C:20:ARG:NH2	13:I:-42:DT:OP1	2.48	0.42
1:K:177:PRO:HG2	1:K:202:PRO:HD2	2.01	0.42
1:K:409:PRO:O	2:L:433:ARG:NH2	2.53	0.42
3:M:462:LYS:HA	3:M:465:LYS:HG2	2.01	0.42
4:N:140:LYS:HB2	4:N:259:ASP:H	1.84	0.42
4:N:401:SER:OG	4:N:435:GLU:OE1	2.38	0.42
1:K:85:GLU:OE1	1:K:165:TYR:OH	2.33	0.42
1:K:109:SER:OG	2:L:40:ARG:NH2	2.53	0.42
4:N:481:SER:O	4:N:485:LEU:HB2	2.20	0.42
6:B:57:VAL:O	6:B:61:PHE:N	2.53	0.42
1:K:86:ASP:HA	1:K:87:PRO:HD3	1.93	0.41
1:K:476:VAL:O	1:K:492:CYS:N	2.44	0.41
2:L:377:GLY:HA3	2:L:383:ILE:HD12	2.02	0.41
3:M:256:ASP:OD1	3:M:256:ASP:N	2.53	0.41
3:M:419:HIS:HA	3:M:422:ILE:HG22	2.02	0.41
10:F:38:ALA:HB1	10:F:43:VAL:HB	2.01	0.41
12:H:31:LYS:H	13:I:49:DC:H5"	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:246:ILE:HA	1:K:268:HIS:HA	2.01	0.41
2:L:60:LEU:HG	2:L:197:LEU:HD21	2.02	0.41
3:M:181:PHE:HB3	3:M:186:ILE:HD13	2.02	0.41
3:M:214:LYS:HA	3:M:217:GLN:HB3	2.03	0.41
5:A:42:ARG:H	13:I:70:DG:H5"	1.84	0.41
1:K:58:THR:OG1	1:K:194:LYS:NZ	2.50	0.41
3:M:235:ILE:HG13	3:M:237:ARG:HH11	1.85	0.41
3:M:588:LYS:O	3:M:592:SER:HB3	2.19	0.41
9:E:59:GLU:H	10:F:40:ARG:HH22	1.68	0.41
11:G:27:VAL:O	11:G:31:HIS:CB	2.68	0.41
1:K:55:PRO:HD2	1:K:56:LEU:HG	2.01	0.41
2:L:246:ILE:HG12	2:L:269:ARG:HG3	2.02	0.41
2:L:506:VAL:HG21	2:L:602:ILE:HD11	2.03	0.41
1:K:206:HIS:ND1	1:K:250:ASN:OD1	2.52	0.41
1:K:246:ILE:HB	1:K:339:ALA:HB2	2.02	0.41
2:L:179:GLY:HA2	2:L:182:ILE:HD12	2.03	0.41
2:L:181:ALA:HB1	2:L:224:ALA:HB2	2.02	0.41
2:L:682:ASN:O	2:L:686:GLU:HB2	2.20	0.41
4:N:249:ASP:HB3	4:N:252:LEU:HD13	2.02	0.41
7:C:92:GLU:O	7:C:96:LEU:CB	2.65	0.41
11:G:69:ALA:O	11:G:73:ASN:ND2	2.52	0.41
12:H:55:ALA:HA	12:H:58:ILE:HD12	2.01	0.41
2:L:243:ASP:HB3	2:L:266:SER:HA	2.03	0.41
2:L:293:GLU:OE1	2:L:427:TYR:OH	2.38	0.41
2:L:431:PHE:O	2:L:437:ASN:ND2	2.47	0.41
11:G:34:LEU:HB3	11:G:43:VAL:HG21	2.02	0.41
6:B:98:TYR:HD2	12:H:58:ILE:HG23	1.85	0.41
1:K:74:THR:OG1	1:K:78:GLU:OE2	2.35	0.41
1:K:695:ILE:O	1:K:699:PHE:N	2.46	0.41
2:L:48:MET:HE3	2:L:49:PRO:HD2	2.03	0.41
2:L:194:LYS:HE3	2:L:194:LYS:HB2	1.91	0.41
3:M:184:GLU:OE2	3:M:208:THR:OG1	2.38	0.41
4:N:337:TYR:OH	4:N:374:ASP:OD1	2.35	0.41
4:N:405:LEU:HA	4:N:406:PRO:HD3	1.94	0.41
4:N:478:ILE:HA	4:N:481:SER:HB3	2.03	0.41
4:N:550:LEU:O	4:N:554:GLN:HB2	2.20	0.41
9:E:55:GLN:NE2	10:F:40:ARG:O	2.39	0.41
1:K:508:ASP:OD1	1:K:508:ASP:N	2.54	0.41
3:M:123:ILE:HD13	3:M:123:ILE:HA	1.98	0.41
3:M:447:ASP:HA	3:M:450:ASN:HB3	2.02	0.41
4:N:121:GLN:O	4:N:125:SER:OG	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:113:HIS:HE1	9:E:122:LYS:HG3	1.86	0.41
7:C:75:LYS:HB2	7:C:82:HIS:HE1	1.85	0.41
2:L:134:VAL:HG22	2:L:209:PRO:HG3	2.03	0.40
3:M:245:ASP:OD1	3:M:245:ASP:N	2.53	0.40
5:A:120:MET:N	5:A:123:ASP:OD2	2.45	0.40
7:C:63:LEU:HD22	8:D:42:LEU:HD13	2.01	0.40
7:C:77:ARG:HD2	13:I:-54:DA:H4'	2.04	0.40
9:E:100:LEU:HD23	9:E:100:LEU:HA	1.94	0.40
1:K:54:SER:OG	2:L:396:GLY:O	2.35	0.40
2:L:374:LEU:HD11	2:L:383:ILE:HD11	2.04	0.40
11:G:79:ILE:HA	11:G:80:PRO:HD3	1.88	0.40
11:G:93:LEU:HD22	11:G:97:LEU:HG	2.04	0.40
2:L:102:LEU:HB2	2:L:103:ILE:HD12	2.03	0.40
5:A:42:ARG:HA	5:A:43:PRO:HD3	1.94	0.40
2:L:162:ASP:OD1	2:L:162:ASP:N	2.48	0.40
2:L:271:GLU:HB2	2:L:275:TYR:H	1.86	0.40
2:L:577:TRP:HB2	2:L:605:LEU:HD21	2.03	0.40
2:L:652:ASN:ND2	2:L:676:ASP:O	2.52	0.40
7:C:42:ARG:N	8:D:84:SER:O	2.47	0.40
1:K:558:PHE:H	2:L:526:SER:HB2	1.86	0.40
4:N:495:LEU:HA	4:N:498:LYS:HD2	2.03	0.40
12:H:99:LEU:HB2	12:H:104:ALA:HB2	2.03	0.40
13:I:2:DG:O6	14:J:-3:DA:N6	2.54	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	K	645/661 (98%)	585 (91%)	60 (9%)	0	100	100
2	L	655/672 (98%)	590 (90%)	65 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	M	526/543 (97%)	499 (95%)	27 (5%)	0	100	100
4	N	527/629 (84%)	485 (92%)	41 (8%)	1 (0%)	43	77
5	A	95/97 (98%)	92 (97%)	3 (3%)	0	100	100
6	B	81/83 (98%)	75 (93%)	6 (7%)	0	100	100
7	C	101/103 (98%)	96 (95%)	5 (5%)	0	100	100
8	D	93/95 (98%)	87 (94%)	6 (6%)	0	100	100
9	E	95/97 (98%)	92 (97%)	3 (3%)	0	100	100
10	F	76/78 (97%)	73 (96%)	3 (4%)	0	100	100
11	G	103/105 (98%)	98 (95%)	5 (5%)	0	100	100
12	H	91/93 (98%)	84 (92%)	7 (8%)	0	100	100
All	All	3088/3256 (95%)	2856 (92%)	231 (8%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	N	87	HIS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K	575/585 (98%)	574 (100%)	1 (0%)	87	85
2	L	586/596 (98%)	580 (99%)	6 (1%)	68	76
3	M	504/511 (99%)	504 (100%)	0	100	100
4	N	504/582 (87%)	502 (100%)	2 (0%)	84	82
5	A	85/85 (100%)	80 (94%)	5 (6%)	18	40
6	B	68/68 (100%)	65 (96%)	3 (4%)	25	47
7	C	82/82 (100%)	80 (98%)	2 (2%)	43	63
8	D	81/81 (100%)	76 (94%)	5 (6%)	16	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	E	84/84 (100%)	82 (98%)	2 (2%)	43	63
10	F	63/63 (100%)	61 (97%)	2 (3%)	34	55
11	G	83/83 (100%)	80 (96%)	3 (4%)	31	52
12	H	79/79 (100%)	74 (94%)	5 (6%)	16	38
All	All	2794/2899 (96%)	2758 (99%)	36 (1%)	59	72

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	226	LYS
2	L	30	ASN
2	L	34	THR
2	L	228	ILE
2	L	444	GLU
2	L	480	LEU
2	L	683	ILE
4	N	223	VAL
4	N	235	ASP
5	A	46	VAL
5	A	65	LEU
5	A	105	GLU
5	A	115	LYS
5	A	117	VAL
6	B	21	VAL
6	B	80	THR
6	B	95	ARG
7	C	81	ARG
7	C	101	THR
8	D	28	LYS
8	D	39	TYR
8	D	84	SER
8	D	109	SER
8	D	119	THR
9	E	65	LEU
9	E	117	VAL
10	F	26	ILE
10	F	73	THR
11	G	34	LEU
11	G	72	ASP
11	G	81	ARG
12	H	68	GLU

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Mol	Chain	Res	Type
12	H	88	SER
12	H	95	VAL
12	H	99	LEU
12	H	103	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (66) such sidechains are listed below:

Mol	Chain	Res	Type
1	K	41	GLN
1	K	100	ASN
1	K	317	GLN
1	K	349	HIS
1	K	465	GLN
1	K	488	ASN
1	K	495	ASN
1	K	517	ASN
1	K	552	ASN
1	K	579	ASN
1	K	608	HIS
1	K	620	ASN
1	K	655	GLN
2	L	168	ASN
2	L	231	ASN
2	L	253	GLN
2	L	441	ASN
2	L	443	ASN
2	L	454	ASN
2	L	458	GLN
2	L	467	HIS
2	L	620	ASN
2	L	681	ASN
3	M	47	GLN
3	M	94	HIS
3	M	112	ASN
3	M	242	ASN
3	M	258	ASN
3	M	265	ASN
3	M	316	GLN
3	M	409	ASN
3	M	435	GLN
3	M	449	GLN
3	M	452	HIS

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Mol	Chain	Res	Type
3	M	488	ASN
3	M	572	ASN
3	M	575	GLN
3	M	576	ASN
4	N	80	ASN
4	N	121	GLN
4	N	294	GLN
4	N	340	GLN
4	N	347	ASN
4	N	348	ASN
4	N	368	ASN
4	N	454	GLN
4	N	472	GLN
4	N	479	ASN
4	N	497	ASN
4	N	500	ASN
4	N	505	ASN
4	N	524	ASN
4	N	543	ASN
4	N	554	GLN
4	N	583	GLN
4	N	620	ASN
5	A	108	ASN
7	C	31	HIS
8	D	79	HIS
8	D	92	GLN
10	F	27	GLN
11	G	31	HIS
11	G	68	ASN
11	G	84	GLN
12	H	44	GLN
12	H	64	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	M	1
4	N	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	M	334:LYS	C	404:ASN	N	81.01
1	N	308:ASN	C	325:SER	N	26.70

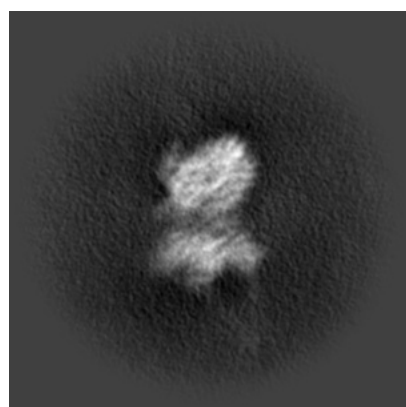
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11102. These allow visual inspection of the internal detail of the map and identification of artifacts.

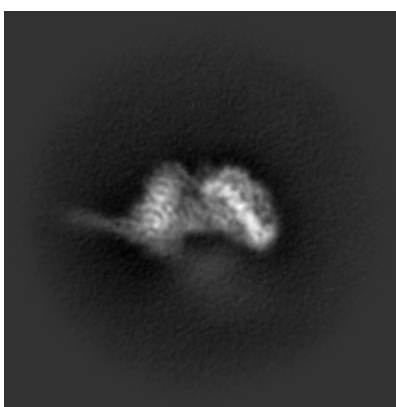
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

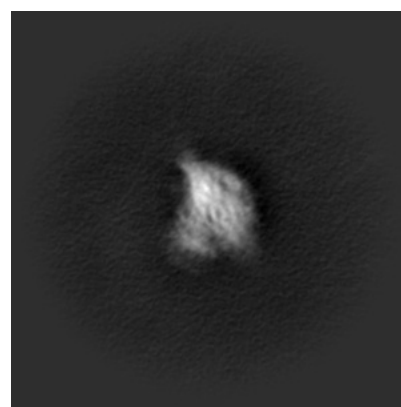
6.1.1 Primary map



X



Y

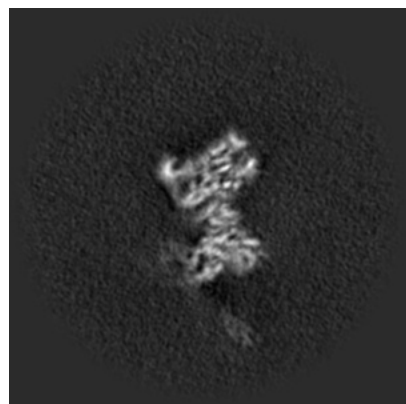


Z

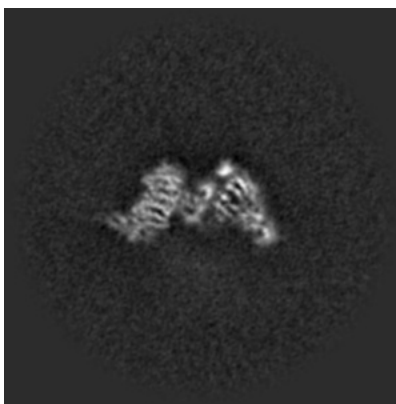
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

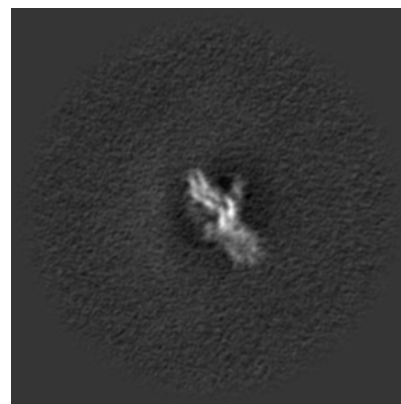
6.2.1 Primary map



X Index: 270



Y Index: 270

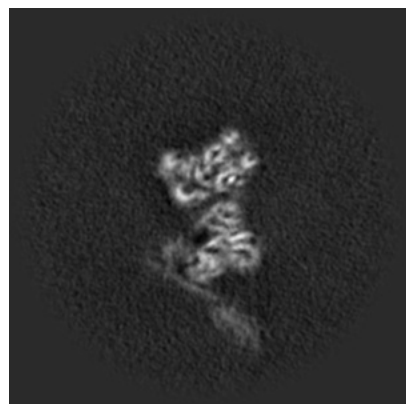


Z Index: 270

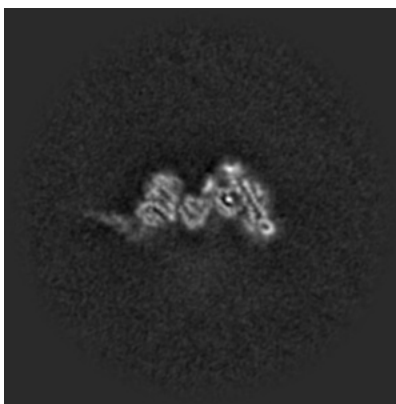
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

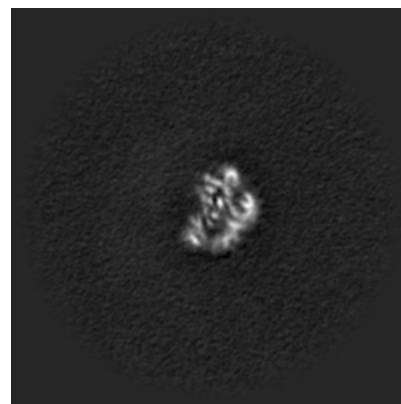
6.3.1 Primary map



X Index: 261



Y Index: 280

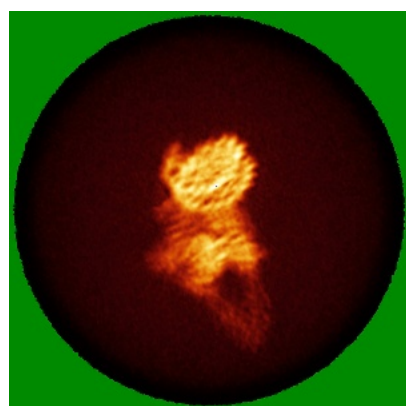


Z Index: 301

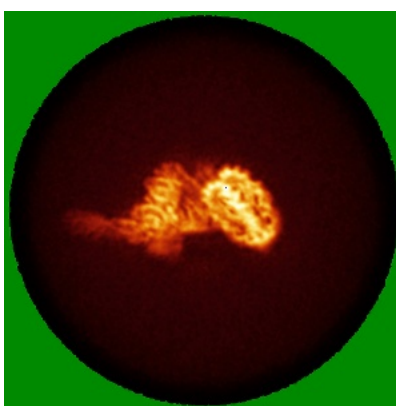
The images above show the largest variance slices of the map in three orthogonal directions.

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

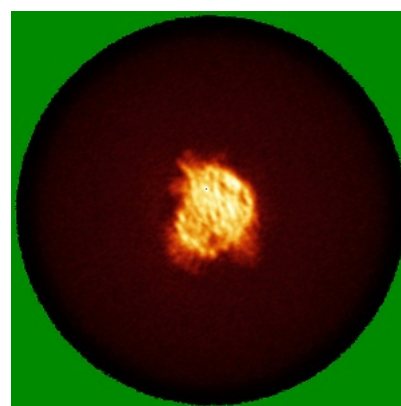
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

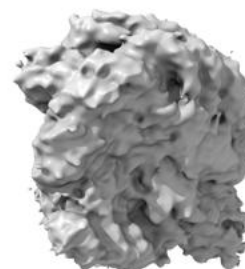
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

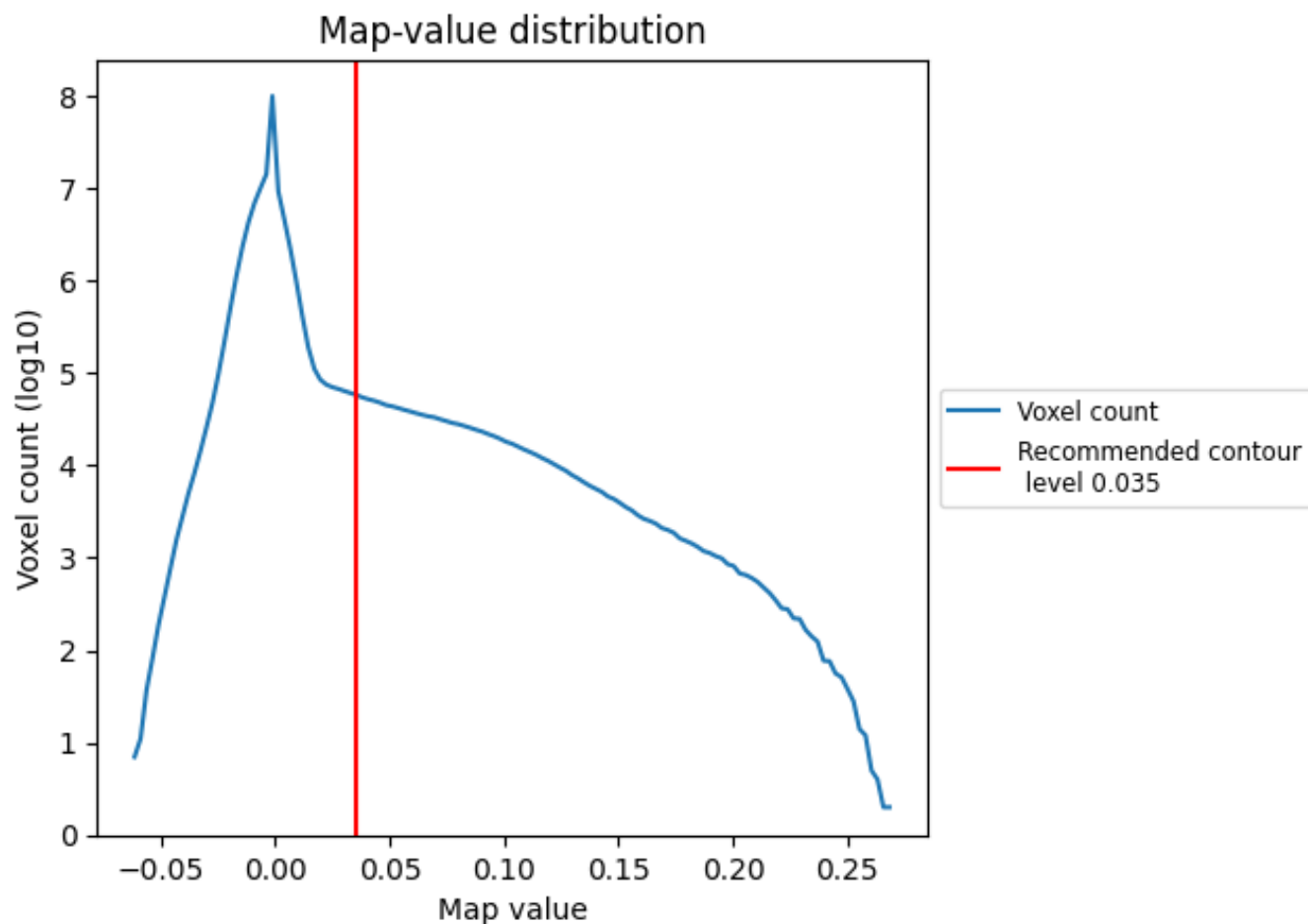
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

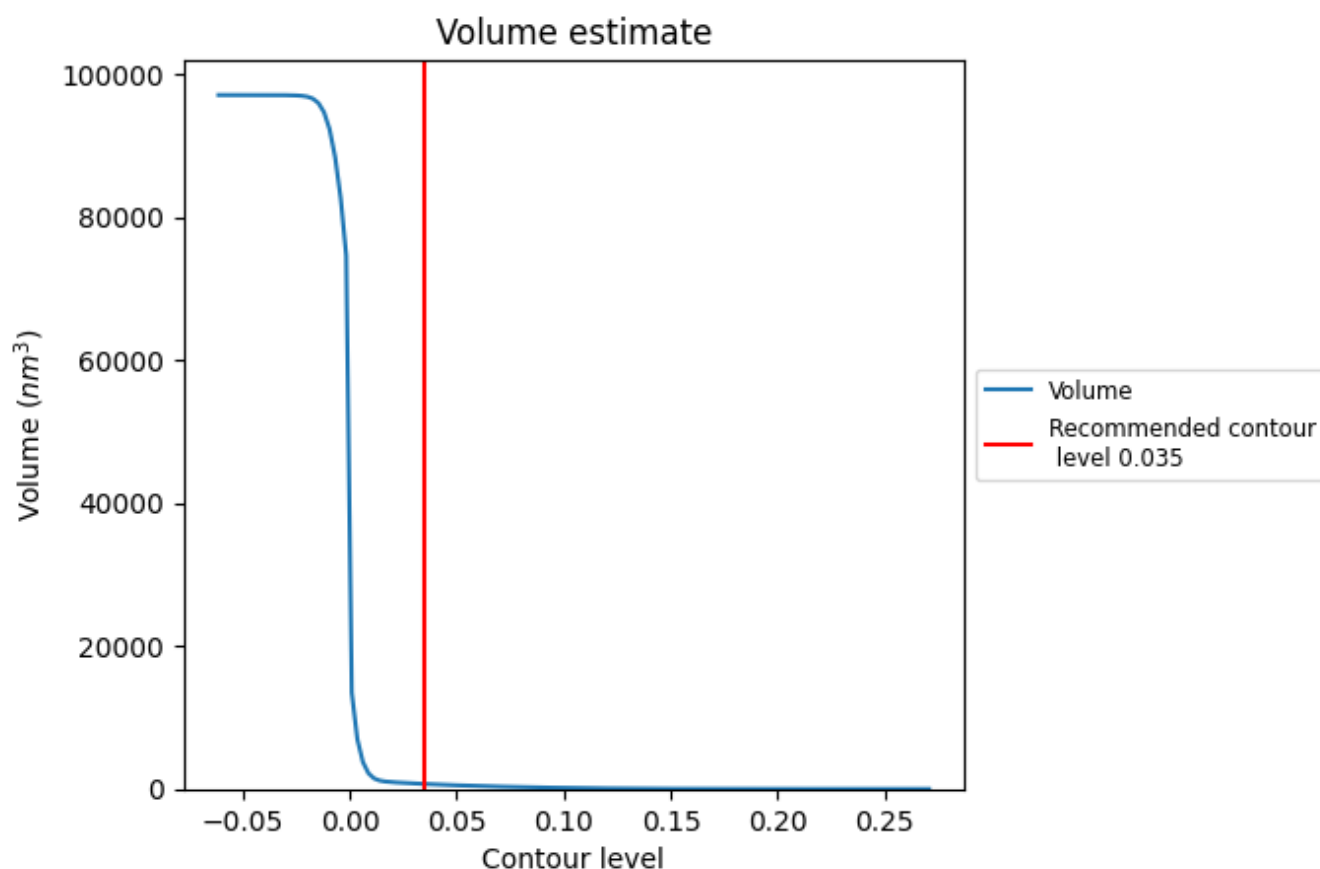
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

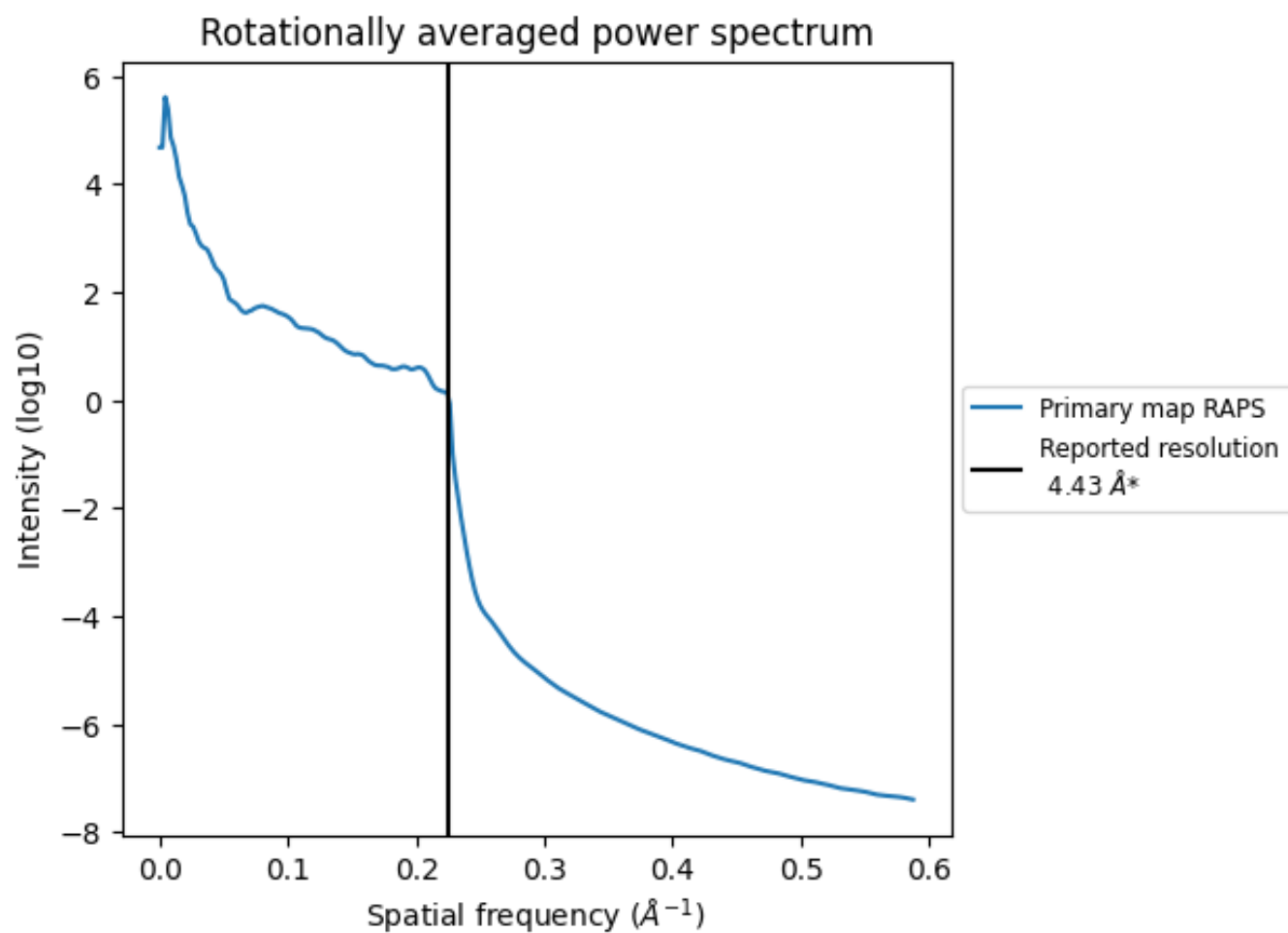
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 699 nm^3 ; this corresponds to an approximate mass of 632 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 0.226 Å⁻¹

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-11102 and PDB model 6Z6P. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)

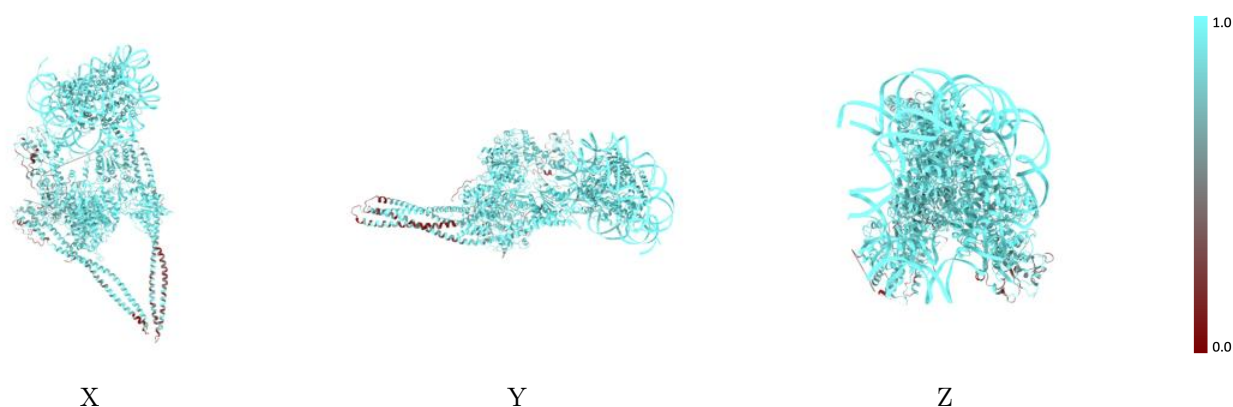
This section was not generated.

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



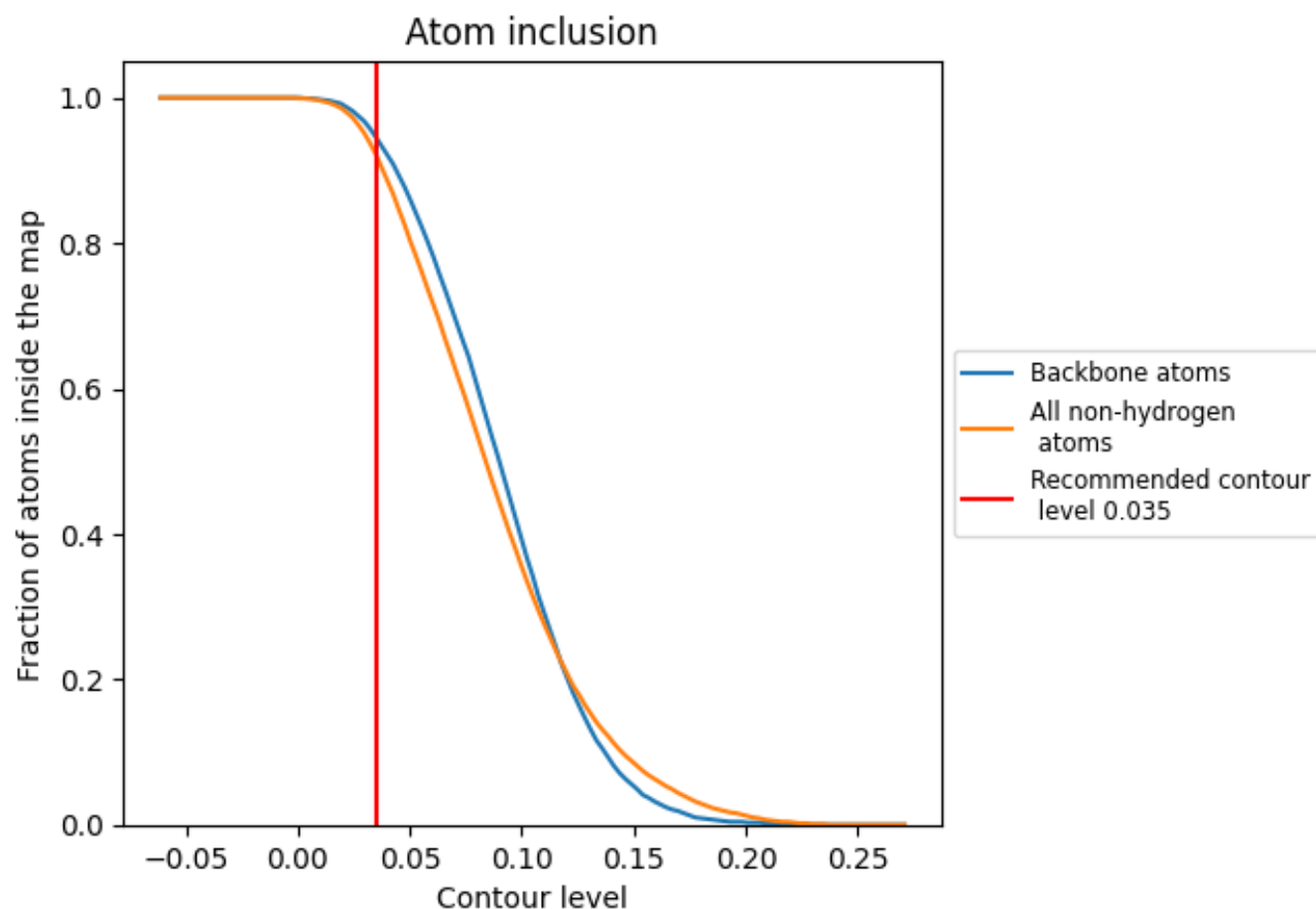
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.035).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 92% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9210	 0.1890
A	 0.9920	 0.2030
B	 0.9860	 0.2190
C	 0.9860	 0.2120
D	 0.9840	 0.2110
E	 0.9650	 0.1990
F	 0.9450	 0.1960
G	 0.9780	 0.2200
H	 0.9690	 0.2090
I	 1.0000	 0.2250
J	 1.0000	 0.2280
K	 0.9540	 0.1840
L	 0.9470	 0.1900
M	 0.7810	 0.1500
N	 0.8100	 0.1530

