



## Full wwPDB EM Validation Report ⓘ

May 22, 2025 – 06:21 PM EDT

PDB ID : 9MO4 / pdb\_00009mo4  
EMDB ID : EMD-48447  
Title : Structure of native murine cardiac thin filament at pCa=5.8 in Ca<sup>2+</sup>-free state (lower strand)  
Authors : Risi, C.M.; Galkin, V.E.  
Deposited on : 2024-12-25  
Resolution : 5.30 Å (reported)  
Based on initial models : 7KO4, 8UYD, 8DD0, 7UTL

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.dev118  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0rc1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1

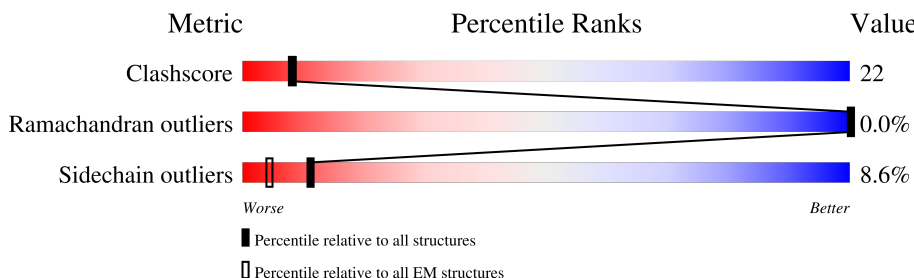
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 5.30 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.




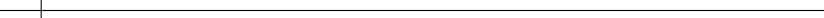



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\geq 3$ , 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	A	377	
1	B	377	
1	C	377	
1	D	377	
1	E	377	
1	F	377	
2	G	161	
3	H	211	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	I	291	
4	J	291	
5	K	284	
5	L	284	
5	M	284	
5	N	284	

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 25967 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 Actin, alpha cardiac muscle 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	371	Total	C	N	O	S	0	0
			2898	1836	489	553	20		
1	B	371	Total	C	N	O	S	0	0
			2898	1836	489	553	20		
1	C	371	Total	C	N	O	S	0	0
			2898	1836	489	553	20		
1	D	371	Total	C	N	O	S	0	0
			2898	1836	489	553	20		
1	E	371	Total	C	N	O	S	0	0
			2898	1836	489	553	20		
1	F	371	Total	C	N	O	S	0	0
			2898	1836	489	553	20		

- Molecule 2 is a protein called Troponin C, slow skeletal and cardiac muscles.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	160	Total	C	N	O	S	0	0
			1273	787	195	278	13		

- Molecule 3 is a protein called Troponin I, cardiac muscle.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	170	Total	C	N	O	S	0	0
			1389	855	266	261	7		

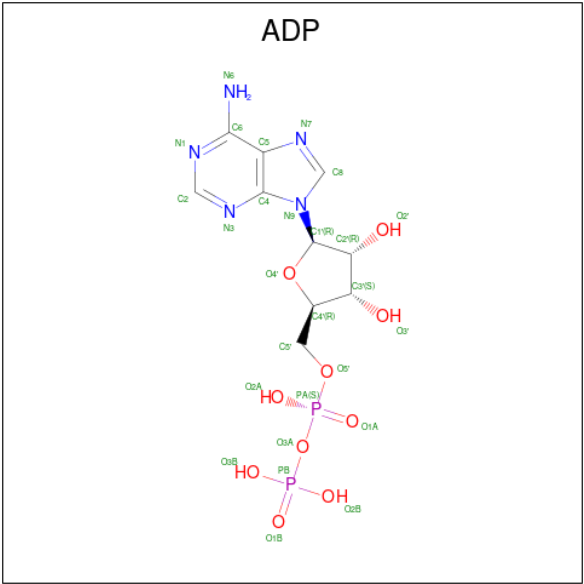
- Molecule 4 is a protein called Isoform A2 of Troponin T, cardiac muscle.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	I	74	Total	C	N	O	0	0
			639	396	125	118		
4	J	77	Total	C	N	O	0	0
			670	405	136	129		

- Molecule 5 is a protein called Tropomyosin alpha-1 chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	K	221	Total	C	N	O	S	0	0
			1783	1091	302	386	4		
5	L	221	Total	C	N	O	S	0	0
			1783	1091	302	386	4		
5	M	55	Total	C	N	O	S	0	0
			437	266	77	91	3		
5	N	55	Total	C	N	O	S	0	0
			437	266	77	91	3		

- Molecule 6 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					AltConf
6	A	1	Total	C	N	O	P	0
			27	10	5	10	2	
6	B	1	Total	C	N	O	P	0
			27	10	5	10	2	
6	C	1	Total	C	N	O	P	0
			27	10	5	10	2	
6	D	1	Total	C	N	O	P	0
			27	10	5	10	2	
6	E	1	Total	C	N	O	P	0
			27	10	5	10	2	
6	F	1	Total	C	N	O	P	0
			27	10	5	10	2	

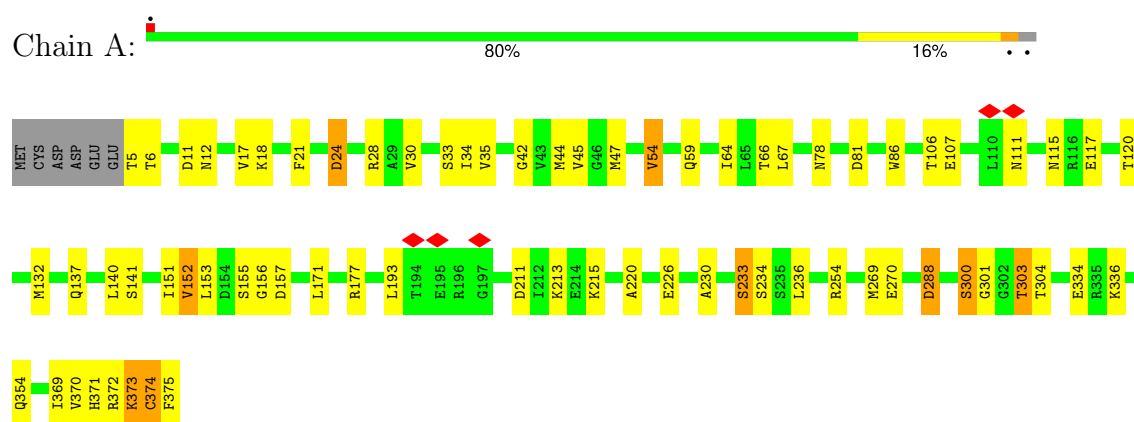
- Molecule 7 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
7	A	1	Total 1	Mg 1	0
7	B	1	Total 1	Mg 1	0
7	C	1	Total 1	Mg 1	0
7	D	1	Total 1	Mg 1	0
7	E	1	Total 1	Mg 1	0
7	F	1	Total 1	Mg 1	0

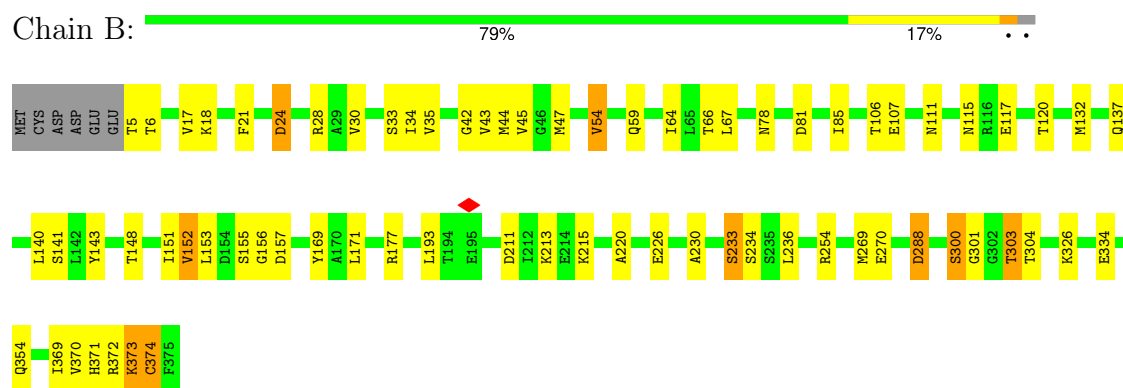
### 3 Residue-property plots

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.

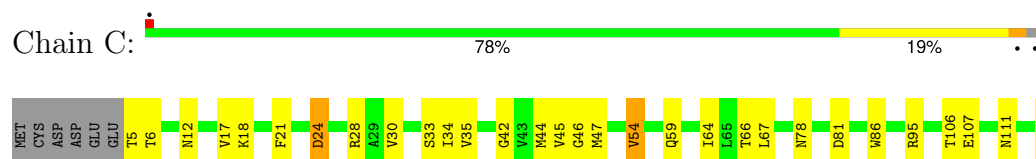
- Molecule 1: Actin, alpha cardiac muscle 1

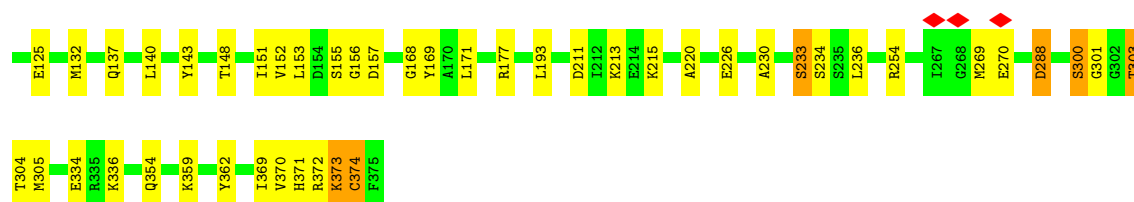


- Molecule 1: Actin, alpha cardiac muscle 1

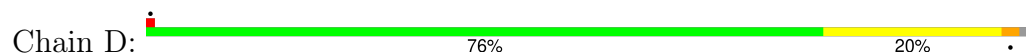


- Molecule 1: Actin, alpha cardiac muscle 1

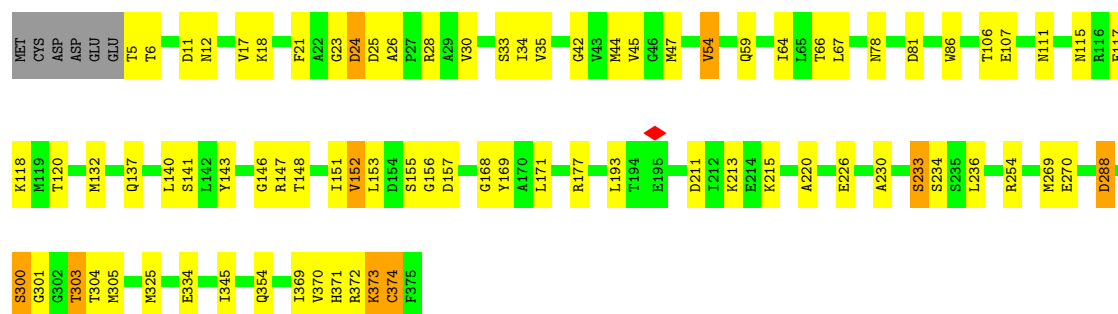




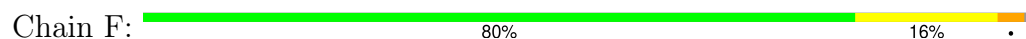
- Molecule 1: Actin, alpha cardiac muscle 1



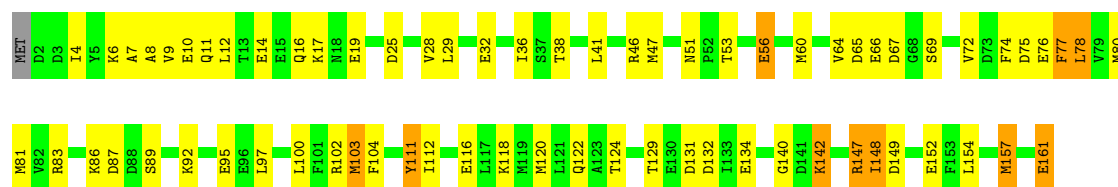
- Molecule 1: Actin, alpha cardiac muscle 1

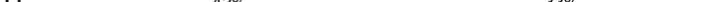


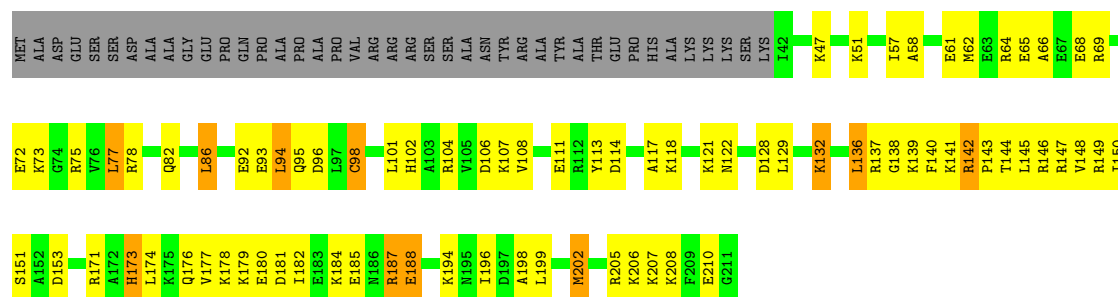
- Molecule 1: Actin, alpha cardiac muscle 1



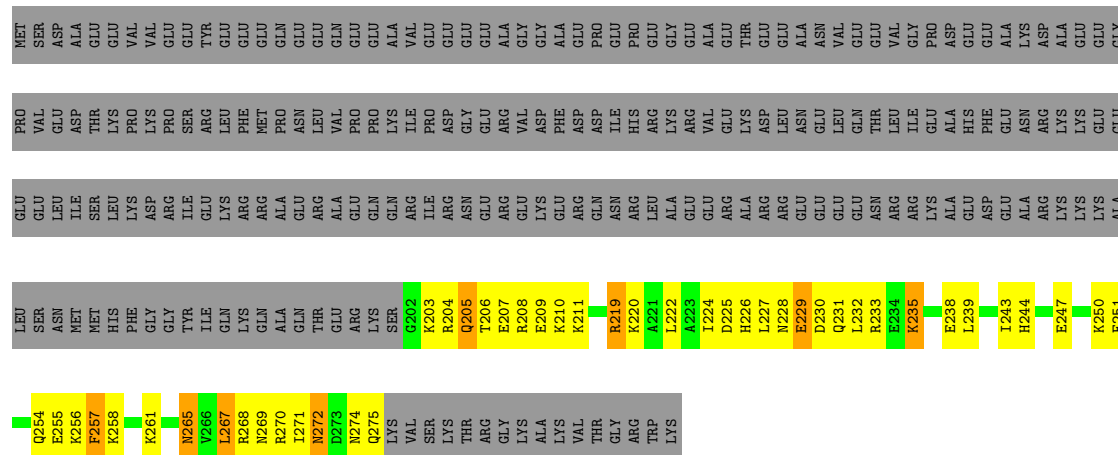
- Molecule 2: Troponin C, slow skeletal and cardiac muscles



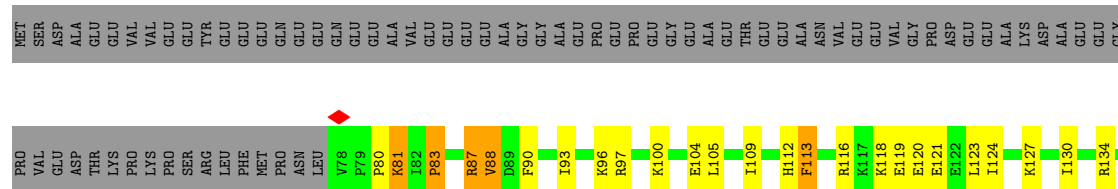
Chain H:  42% 33% 5% 19%

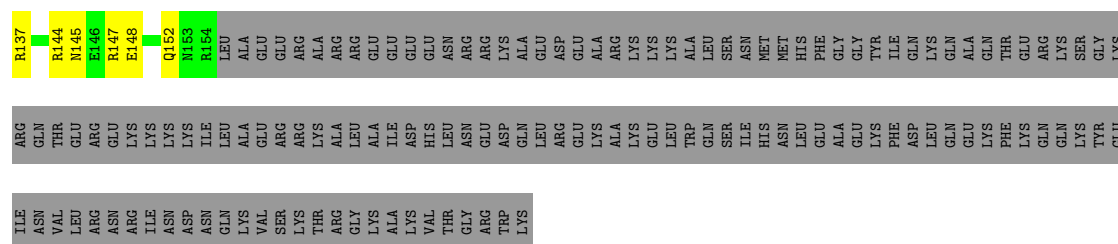


Chain I:  10% 13% 75%



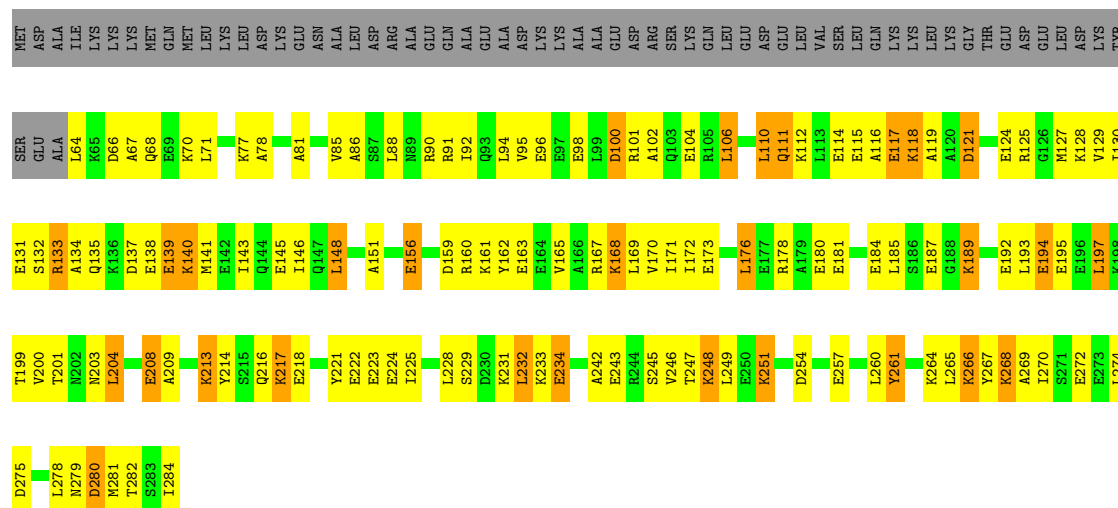
Chain J:  16% 9% 74%





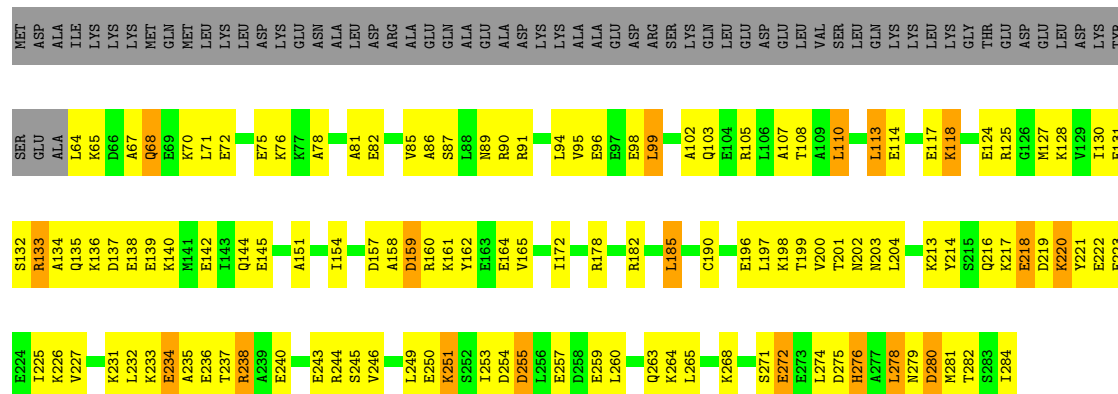
• Molecule 5: Tropomyosin alpha-1 chain

Chain K: 31% 37% 10% 22%



• Molecule 5: Tropomyosin alpha-1 chain

Chain L: 34% 38% 6% 22%



• Molecule 5: Tropomyosin alpha-1 chain

Chain M: 13% 6% 81%



[illegible]

- Molecule 5: Tropomyosin alpha-1 chain



GLU	ASP	GLU	LEU	TYR	ALA	GLN	ASP	LEU	ASP	LYS	H1
ASP	GLU	LEU	THR	THR	VAL	ASN	GLU	THR	GLU	ALA	
LEU	TYR	THR	THR	MET	GLU	ASP	LYS	ASP	ASP	THR	I4
ALA	ASN	GLN	ASN	ILE	GLU	THR	ASP	ALA	GLU	ALA	K6
LYS	LEU	LEU	LEU	GLN	GLN	GLN	GLN	ASP	ALA	ALA	K7
LEU	LEU	LYS	LYS	GLU	ILE	ILE	GLU	VAL	VAL	VAL	K8
TYR	TYR	LEU	LEU	GLN	ILE	ILE	GLN	SER	SER	ALA	Q9
LYS	LYS	GLU	GLU	LEU	LYS	LYS	LEU	LEU	LEU	ALA	L11
ALA	ALA	ALA	ALA	LYS	LYS	LYS	LYS	ASN	ASN	ASN	K12
ILE	ILE	SER	GLN	GLU	ALA	GLU	GLU	ARG	ARG	ARG	L19
GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	ILE	ILE	ILE	R21
GLU	GLU	LYS	LYS	ILE	ILE	ILE	GLN	GLN	LEU	LEU	A22
LEU	LEU	TYR	TYR	ILE	ILE	ILE	ALA	VAL	VAL	VAL	E26
ASP	ASP	SER	SER	ALA	GLU	GLU	GLU	GLU	GLU	GLU	K29
HIS	ALA	LEU	LYS	ASP	ASP	ASP	ASP	GLU	GLU	GLU	
ALA	ASN	ASN	ASP	ASP	ASP	ASP	ASP	LEU	LEU	LEU	D34
ASP	ASP	LYS	LYS	ARG	ARG	ARG	ARG	ASP	ASP	ASP	R35
MET	MET	THR	THR	LYS	LYS	LYS	LYS	ARG	ARG	ARG	S36
THR	THR	GLU	GLU	TYR	TYR	TYR	TYR	ALA	ALA	ALA	K37
SER	SER	GLU	GLU	GLU	GLU	GLU	GLU	GLN	GLN	GLN	D38
ILE	ILE	ILE	ILE	VAL	VAL	VAL	VAL	ARG	ARG	ARG	L39
		LYS	LYS	ALA	ALA	ALA	ALA	LEU	LEU	LEU	E40
		VAL	VAL	ARG	ARG	ARG	ARG	ALA	ALA	ALA	D41
		LEU	LEU	LYS	LYS	LYS	LYS	THR	THR	THR	L46
		SER	SER	LEU	LEU	LEU	LEU	ALA	ALA	ALA	Q47
		ASP	ASP	VAL	VAL	VAL	VAL	LEU	LEU	LEU	K48
		LYS	LYS	ILE	ILE	ILE	ILE	GLN	GLN	GLN	
		LYS	LYS	GLU	GLU	GLU	GLU	LEU	LEU	LEU	K51
		ALA	ALA	SER	SER	SER	SER	GLU	GLU	GLU	S52
		ALA	ALA	ASP	ASP	ASP	ASP	GLU	GLU	GLU	T53
		GLU	GLU	LEU	LEU	LEU	LEU	ALA	ALA	ALA	E54
		THR	THR	GLU	GLU	GLU	GLU	LEU	LEU	LEU	D55
		ALA	ALA	THR	THR	THR	THR	GLU	GLU	GLU	GLU
		ARG	ARG	GLU	GLU	GLU	GLU	LEU	LEU	LEU	LEU
		ALA	ALA	GLU	GLU	GLU	GLU	ASP	ASP	ASP	ASP
		SER	SER	VAL	VAL	VAL	VAL	GLY	GLY	GLY	GLY
		THR	THR	LYS	LYS	LYS	LYS	VAL	VAL	VAL	VAL
		GLU	GLU	LYS	LYS	LYS	LYS	ILE	ILE	ILE	ILE
		LYS	LYS	ALA	ALA	ALA	ALA	GLU	GLU	GLU	GLU
		LEU	LEU	GLU	GLU	GLU	GLU	SER	SER	SER	SER
		ILE	ILE	ILE	ILE	ILE	ILE	ARG	ARG	ARG	ARG
		ASP	ASP	GLU	GLU	GLU	GLU	GLN	GLN	GLN	GLN
		LEU	LEU	ASP	ASP	ASP	ASP	LYS	LYS	LYS	LYS

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	62156	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	34	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	9.533	Depositor
Minimum map value	-2.619	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.275	Depositor
Recommended contour level	0.515	Depositor
Map size (Å)	439.344, 439.344, 439.344	wwPDB
Map dimensions	324, 324, 324	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.356, 1.356, 1.356	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: ADP, 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	A	0.38	0/2961	0.45	0/4011
1	B	0.38	0/2961	0.45	0/4011
1	C	0.38	0/2961	0.46	0/4011
1	D	0.38	0/2961	0.46	0/4011
1	E	0.38	0/2961	0.46	0/4011
1	F	0.38	0/2961	0.45	0/4011
2	G	0.12	0/1286	0.32	0/1718
3	H	0.16	0/1399	0.32	0/1858
4	I	0.15	0/645	0.32	0/855
4	J	0.38	1/676 (0.1%)	0.68	2/898 (0.2%)
5	K	0.25	0/1790	0.40	0/2388
5	L	0.26	0/1790	0.41	0/2388
5	M	0.21	0/436	0.36	0/574
5	N	0.21	0/436	0.36	0/574
All	All	0.34	1/26224 (0.0%)	0.44	2/35319 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	J	83	PRO	N-CD	5.49	1.55	1.47

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	J	87	ARG	CA-C-N	8.56	137.11	121.70
4	J	87	ARG	C-N-CA	8.56	137.11	121.70

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	A	2898	0	2871	62	0
1	B	2898	0	2871	78	0
1	C	2898	0	2871	112	0
1	D	2898	0	2871	121	0
1	E	2898	0	2871	98	0
1	F	2898	0	2871	63	0
2	G	1273	0	1199	61	0
3	H	1389	0	1446	170	0
4	I	639	0	657	71	0
4	J	670	0	673	100	0
5	K	1783	0	1779	237	0
5	L	1783	0	1779	247	0
5	M	437	0	458	56	0
5	N	437	0	458	59	0
6	A	27	0	12	2	0
6	B	27	0	12	2	0
6	C	27	0	12	2	0
6	D	27	0	12	2	0
6	E	27	0	12	2	0
6	F	27	0	12	2	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
7	E	1	0	0	0	0
7	F	1	0	0	0	0
All	All	25967	0	25747	1115	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 22.

All (1115) 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)
5:K:281:MET:CG	5:M:7:LYS:CE	1.78	1.56

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:47:MET:HA	3:H:139:LYS:CE	1.34	1.55
5:K:281:MET:CB	5:M:7:LYS:HE3	1.36	1.52
5:L:284:ILE:HG21	5:N:7:LYS:CE	1.41	1.49
4:J:124:ILE:CD1	5:L:268:LYS:CD	1.93	1.44
4:J:124:ILE:CD1	5:L:268:LYS:HD3	0.98	1.44
5:L:280:ASP:HB3	5:M:5:LYS:NZ	1.23	1.42
1:E:23:GLY:O	3:H:184:LYS:CB	1.69	1.41
1:C:125:GLU:CG	4:I:204:ARG:HH11	1.30	1.40
5:K:284:ILE:HG13	5:N:8:MET:CE	1.51	1.39
1:C:125:GLU:CA	4:I:204:ARG:HD2	1.50	1.39
5:L:284:ILE:CG2	5:N:7:LYS:HE2	1.51	1.39
5:K:281:MET:CG	5:M:7:LYS:HE3	0.91	1.39
4:J:109:ILE:HD11	5:L:281:MET:CE	1.53	1.36
4:J:116:ARG:NE	5:L:275:ASP:OD2	1.57	1.34
4:J:112:HIS:NE2	5:L:278:LEU:HD22	1.41	1.34
2:G:46:ARG:HG3	5:K:160:ARG:NH2	1.37	1.34
1:C:125:GLU:HA	4:I:204:ARG:CD	1.59	1.32
1:D:348:SER:HB2	3:H:146:ARG:NH1	1.43	1.30
1:D:24:ASP:CG	3:H:150:ILE:HG21	1.55	1.29
1:D:348:SER:CB	3:H:146:ARG:NH1	1.96	1.29
4:J:109:ILE:CG1	5:L:281:MET:HE1	1.63	1.29
5:N:6:LYS:CG	5:N:10:MET:HE1	1.62	1.28
1:D:348:SER:CB	3:H:146:ARG:HH12	1.47	1.28
4:J:112:HIS:NE2	5:L:278:LEU:CD2	1.97	1.28
2:G:46:ARG:CG	5:K:160:ARG:NH2	1.95	1.27
5:K:278:LEU:HA	5:K:281:MET:CE	1.65	1.26
1:E:23:GLY:C	3:H:184:LYS:HB3	1.61	1.25
4:J:112:HIS:CD2	5:L:278:LEU:HD22	1.71	1.25
5:L:280:ASP:CB	5:M:5:LYS:NZ	2.00	1.23
5:K:281:MET:CB	5:M:7:LYS:CE	2.03	1.23
3:H:199:LEU:HB2	5:K:98:GLU:OE2	1.34	1.22
5:L:284:ILE:HD13	5:N:7:LYS:CG	1.69	1.21
4:J:124:ILE:HD12	5:L:268:LYS:CD	1.59	1.20
5:L:284:ILE:HD13	5:N:7:LYS:CD	1.72	1.18
5:K:281:MET:HB3	5:M:7:LYS:CE	1.70	1.18
5:L:196:GLU:O	5:L:199:THR:HG22	1.43	1.18
4:J:109:ILE:CD1	5:L:281:MET:HE1	1.73	1.18
1:C:125:GLU:HG2	4:I:204:ARG:NH1	1.57	1.17
5:K:281:MET:HB3	5:M:7:LYS:NZ	1.58	1.17
1:D:24:ASP:HB3	3:H:150:ILE:HG22	1.25	1.16
4:J:109:ILE:CD1	5:L:281:MET:CE	2.22	1.16

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:47:MET:HE2	1:C:148:THR:OG1	1.46	1.16
5:L:284:ILE:CD1	5:N:7:LYS:CD	2.24	1.15
4:J:96:LYS:HD2	4:J:96:LYS:O	1.46	1.15
1:D:24:ASP:CG	3:H:150:ILE:CG2	2.19	1.14
4:J:120:GLU:OE1	5:L:268:LYS:HA	1.41	1.14
3:H:199:LEU:HD13	5:K:98:GLU:OE2	1.47	1.14
1:C:47:MET:HA	3:H:139:LYS:HE2	1.27	1.13
1:E:23:GLY:O	3:H:184:LYS:HB3	0.99	1.13
1:D:28:ARG:HH12	3:H:151:SER:CB	1.60	1.13
4:J:137:ARG:NH2	5:L:254:ASP:OD1	1.79	1.13
4:J:130:ILE:CG2	5:L:257:GLU:OE2	1.96	1.13
4:J:109:ILE:HG13	5:L:281:MET:HE1	1.23	1.12
5:L:284:ILE:HD12	5:N:7:LYS:HD3	1.30	1.12
5:K:281:MET:HG2	5:M:7:LYS:CE	1.76	1.12
1:D:24:ASP:OD1	3:H:150:ILE:HG21	1.46	1.11
1:C:47:MET:CA	3:H:139:LYS:CE	2.28	1.11
1:E:345:ILE:CG2	3:H:177:VAL:CG1	2.29	1.10
4:J:124:ILE:CG1	5:L:268:LYS:HD3	1.80	1.10
5:L:284:ILE:HD13	5:N:7:LYS:HG2	1.22	1.09
5:L:280:ASP:CB	5:M:5:LYS:HZ3	1.61	1.09
1:C:46:GLY:O	3:H:139:LYS:NZ	1.86	1.08
1:D:28:ARG:HH12	3:H:151:SER:HB3	1.16	1.08
5:K:278:LEU:CA	5:K:281:MET:HE2	1.82	1.08
1:B:326:LYS:NZ	5:K:257:GLU:HG2	1.68	1.08
1:C:125:GLU:CG	4:I:204:ARG:NH1	2.14	1.07
5:K:281:MET:HG3	5:M:7:LYS:CE	1.58	1.07
5:L:284:ILE:CD1	5:N:7:LYS:HD3	1.83	1.07
1:A:47:MET:HE2	1:B:148:THR:OG1	1.54	1.06
1:C:47:MET:HE2	1:D:148:THR:OG1	1.55	1.06
3:H:199:LEU:CB	5:K:98:GLU:OE2	2.04	1.05
5:N:6:LYS:HG3	5:N:10:MET:HE1	1.06	1.05
1:E:345:ILE:HG21	3:H:177:VAL:HG12	1.38	1.04
1:C:95:ARG:CD	4:I:268:ARG:HD3	1.86	1.04
1:E:345:ILE:CG2	3:H:177:VAL:HG12	1.84	1.04
4:J:109:ILE:HD11	5:L:281:MET:HE3	1.37	1.03
5:M:21:ARG:HD2	5:N:26:GLU:OE2	1.56	1.03
5:L:280:ASP:CG	5:M:5:LYS:HZ1	1.65	1.03
1:C:47:MET:HA	3:H:139:LYS:HE3	1.10	1.03
1:D:47:MET:HE2	1:E:148:THR:OG1	1.59	1.03
1:E:345:ILE:HG23	3:H:177:VAL:CG1	1.88	1.02
4:J:124:ILE:HD12	5:L:268:LYS:CE	1.86	1.02

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:284:ILE:CG1	5:N:8:MET:CE	2.36	1.02
1:D:23:GLY:HA2	3:H:146:ARG:CD	1.89	1.02
1:D:23:GLY:HA2	3:H:146:ARG:HD3	1.42	1.01
5:L:279:ASN:O	5:L:282:THR:OG1	1.78	1.01
1:D:24:ASP:HA	3:H:147:ARG:O	1.59	1.01
1:C:95:ARG:HD3	4:I:268:ARG:CD	1.91	1.01
5:K:284:ILE:HG13	5:N:8:MET:HE1	1.02	1.01
1:A:373:LYS:HD2	1:A:373:LYS:N	1.76	1.00
1:C:373:LYS:HD2	1:C:373:LYS:N	1.76	0.99
5:L:284:ILE:CD1	5:N:7:LYS:HG2	1.92	0.99
1:B:373:LYS:N	1:B:373:LYS:HD2	1.76	0.99
1:F:373:LYS:HD2	1:F:373:LYS:N	1.76	0.99
3:H:199:LEU:CD1	5:K:98:GLU:OE2	2.11	0.99
1:C:125:GLU:HG2	4:I:204:ARG:HH11	0.82	0.99
1:E:148:THR:HG22	3:H:171:ARG:NH1	1.79	0.98
4:J:124:ILE:HD12	5:L:268:LYS:HD3	0.99	0.98
1:E:373:LYS:HD2	1:E:373:LYS:N	1.76	0.98
1:C:95:ARG:HD3	4:I:268:ARG:HD3	0.98	0.98
5:L:284:ILE:CD1	5:N:7:LYS:CG	2.42	0.98
4:J:124:ILE:HD11	5:L:268:LYS:HD3	1.01	0.97
1:D:23:GLY:HA2	3:H:146:ARG:NE	1.79	0.97
5:N:6:LYS:HG3	5:N:10:MET:CE	1.92	0.97
1:D:24:ASP:CB	3:H:150:ILE:HG22	1.93	0.97
1:E:47:MET:HE2	1:F:148:THR:OG1	1.64	0.97
5:K:284:ILE:CG1	5:N:8:MET:HE1	1.93	0.97
1:B:42:GLY:HA2	1:C:169:TYR:HA	1.46	0.97
5:K:278:LEU:CA	5:K:281:MET:CE	2.39	0.97
1:A:373:LYS:H	1:A:373:LYS:NZ	1.63	0.96
1:C:47:MET:SD	3:H:139:LYS:HE3	2.04	0.96
1:D:373:LYS:HD2	1:D:373:LYS:N	1.76	0.96
1:B:373:LYS:N	1:B:373:LYS:HZ3	1.62	0.96
1:A:373:LYS:N	1:A:373:LYS:HZ3	1.62	0.96
1:D:24:ASP:CB	3:H:150:ILE:CG2	2.44	0.96
1:D:373:LYS:N	1:D:373:LYS:HZ3	1.62	0.96
5:L:280:ASP:CB	5:M:5:LYS:HZ1	1.71	0.96
1:B:373:LYS:H	1:B:373:LYS:NZ	1.63	0.95
1:D:373:LYS:H	1:D:373:LYS:NZ	1.63	0.95
1:E:373:LYS:N	1:E:373:LYS:HZ3	1.63	0.95
1:E:373:LYS:H	1:E:373:LYS:NZ	1.63	0.95
5:L:284:ILE:HD13	5:N:7:LYS:CE	1.96	0.95
1:C:373:LYS:H	1:C:373:LYS:NZ	1.63	0.95

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:105:LEU:HD21	5:L:284:ILE:HD12	1.49	0.94
1:C:373:LYS:N	1:C:373:LYS:HZ2	1.63	0.94
4:J:127:LYS:HZ3	5:L:264:LYS:HE2	1.30	0.94
1:C:125:GLU:HG3	4:I:204:ARG:HH11	1.30	0.94
1:D:349:LEU:CD2	3:H:142:ARG:HD2	1.98	0.94
1:F:373:LYS:N	1:F:373:LYS:HZ3	1.63	0.94
1:D:42:GLY:HA2	1:E:169:TYR:HA	1.49	0.94
1:F:373:LYS:H	1:F:373:LYS:NZ	1.63	0.94
5:K:278:LEU:N	5:K:281:MET:HE1	1.77	0.93
5:K:278:LEU:HA	5:K:281:MET:HE2	0.93	0.92
5:K:135:GLN:OE1	5:L:133:ARG:NH2	2.03	0.92
5:K:281:MET:HG3	5:M:7:LYS:HE3	0.94	0.91
1:B:326:LYS:HB2	5:K:261:TYR:HE2	1.36	0.91
4:J:112:HIS:NE2	5:L:278:LEU:HD23	1.83	0.90
1:D:23:GLY:HA2	3:H:146:ARG:CZ	2.01	0.90
1:E:345:ILE:HG23	3:H:177:VAL:HG13	1.53	0.90
2:G:46:ARG:CG	5:K:160:ARG:HH21	1.82	0.90
4:J:81:LYS:HA	4:J:81:LYS:NZ	1.87	0.89
5:L:217:LYS:O	5:L:220:LYS:NZ	2.05	0.89
1:D:24:ASP:HB3	3:H:150:ILE:CG2	2.03	0.89
5:N:6:LYS:HG2	5:N:10:MET:HE1	1.55	0.88
2:G:46:ARG:HG2	5:K:160:ARG:NH2	1.85	0.88
3:H:146:ARG:HG3	3:H:147:ARG:N	1.86	0.88
1:C:42:GLY:HA2	1:D:169:TYR:HA	1.54	0.88
4:J:127:LYS:HE2	5:L:264:LYS:HD2	1.55	0.88
2:G:74:PHE:O	2:G:78:LEU:HB2	1.73	0.88
4:J:120:GLU:OE1	5:L:268:LYS:CA	2.21	0.88
4:J:130:ILE:HG22	5:L:257:GLU:OE2	1.73	0.88
1:A:42:GLY:HA2	1:B:169:TYR:HA	1.53	0.87
1:D:348:SER:OG	3:H:146:ARG:NH1	2.06	0.87
2:G:46:ARG:HG3	5:K:160:ARG:CZ	2.04	0.87
5:K:216:GLN:OE1	5:K:217:LYS:NZ	2.07	0.87
5:K:284:ILE:CD1	5:N:8:MET:HE2	2.04	0.87
5:K:101:ARG:O	5:K:104:GLU:HG3	1.75	0.87
5:L:284:ILE:CB	5:N:7:LYS:HE2	2.05	0.86
1:D:28:ARG:NH1	3:H:151:SER:CB	2.38	0.86
5:L:124:GLU:OE1	5:L:125:ARG:NE	2.09	0.86
4:J:127:LYS:NZ	5:L:264:LYS:HE2	1.91	0.85
5:L:139:GLU:O	5:L:142:GLU:HG2	1.77	0.85
1:C:47:MET:CA	3:H:139:LYS:HE2	1.96	0.85
5:L:284:ILE:HG21	5:N:7:LYS:HE3	1.57	0.84

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:104:GLU:OE2	5:N:6:LYS:NZ	2.09	0.83
1:C:373:LYS:H	1:C:373:LYS:HZ2	0.84	0.83
5:L:280:ASP:CG	5:M:5:LYS:NZ	2.31	0.83
5:L:220:LYS:HZ2	5:L:220:LYS:HB3	1.42	0.83
5:L:275:ASP:O	5:L:279:ASN:ND2	2.11	0.82
1:E:23:GLY:O	3:H:184:LYS:HB2	1.80	0.82
5:L:284:ILE:CD1	5:N:7:LYS:HE2	2.09	0.82
1:C:125:GLU:HG2	4:I:204:ARG:HD3	1.59	0.82
1:F:373:LYS:HZ3	1:F:373:LYS:H	0.83	0.82
3:H:199:LEU:CG	5:K:98:GLU:OE2	2.28	0.82
1:E:148:THR:CG2	3:H:171:ARG:HH12	1.93	0.82
4:J:124:ILE:HD11	5:L:268:LYS:CD	1.77	0.82
1:D:23:GLY:CA	3:H:146:ARG:HD3	2.09	0.81
5:K:281:MET:CB	5:M:7:LYS:NZ	2.34	0.81
1:A:373:LYS:H	1:A:373:LYS:HZ3	0.84	0.81
5:K:199:THR:O	5:K:203:ASN:ND2	2.14	0.81
5:K:232:LEU:HD23	5:K:233:LYS:HD2	1.63	0.81
1:B:326:LYS:HB2	5:K:261:TYR:CE2	2.14	0.81
5:L:284:ILE:HD13	5:N:7:LYS:HE2	1.59	0.81
4:J:109:ILE:HD11	5:L:281:MET:SD	2.20	0.81
1:C:47:MET:SD	3:H:139:LYS:CE	2.69	0.81
2:G:46:ARG:HG3	5:K:160:ARG:HH22	1.46	0.81
1:D:373:LYS:HZ3	1:D:373:LYS:H	0.82	0.80
3:H:146:ARG:HG3	3:H:147:ARG:H	1.44	0.80
5:K:141:MET:CE	5:L:140:LYS:HB3	2.12	0.80
5:L:284:ILE:CD1	5:N:7:LYS:CE	2.57	0.80
5:K:231:LYS:NZ	5:K:234:GLU:OE2	2.13	0.80
4:J:109:ILE:CG1	5:L:281:MET:CE	2.52	0.79
4:J:116:ARG:CD	5:L:275:ASP:OD2	2.29	0.79
5:K:141:MET:HE2	5:L:140:LYS:HB3	1.64	0.79
1:D:348:SER:HB2	3:H:146:ARG:HH11	1.45	0.79
4:J:116:ARG:CZ	5:L:275:ASP:OD2	2.30	0.79
1:E:373:LYS:H	1:E:373:LYS:HZ3	0.82	0.79
1:B:373:LYS:HZ3	1:B:373:LYS:H	0.82	0.78
5:L:86:ALA:O	5:L:90:ARG:HD3	1.84	0.78
5:L:91:ARG:HE	5:L:94:LEU:HD21	1.49	0.78
3:H:199:LEU:HD13	5:K:98:GLU:CD	2.08	0.78
5:K:281:MET:CG	5:M:7:LYS:HE2	2.08	0.78
1:E:23:GLY:C	3:H:184:LYS:CB	2.37	0.78
5:K:232:LEU:CD2	5:K:233:LYS:HD2	2.14	0.78
1:D:28:ARG:NH1	3:H:151:SER:HB3	1.98	0.77

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:113:PHE:CE1	5:L:278:LEU:HD11	2.19	0.77
5:L:198:LYS:O	5:L:202:ASN:ND2	2.17	0.77
5:K:243:GLU:OE2	5:L:238:ARG:NH1	2.17	0.77
1:C:47:MET:CE	1:D:148:THR:OG1	2.33	0.77
1:D:348:SER:HB2	3:H:146:ARG:HH12	1.06	0.77
5:K:284:ILE:CG1	5:N:8:MET:HE2	2.14	0.77
4:J:130:ILE:HG21	5:L:257:GLU:OE2	1.82	0.77
5:K:247:THR:OG1	5:K:248:LYS:NZ	2.18	0.77
1:C:359:LYS:NZ	4:I:204:ARG:HH21	1.83	0.76
1:E:42:GLY:HA2	1:F:169:TYR:HA	1.68	0.76
4:J:96:LYS:HD2	4:J:96:LYS:C	2.10	0.76
1:D:23:GLY:CA	3:H:146:ARG:NE	2.48	0.76
1:B:326:LYS:HZ1	5:K:257:GLU:HG2	1.50	0.76
5:K:278:LEU:N	5:K:281:MET:CE	2.49	0.76
4:J:96:LYS:O	4:J:96:LYS:CD	2.32	0.76
5:K:170:VAL:O	5:K:173:GLU:HG3	1.86	0.76
5:K:194:GLU:OE1	5:K:195:GLU:N	2.18	0.76
1:B:47:MET:CE	1:C:148:THR:OG1	2.30	0.76
1:E:148:THR:HG22	3:H:171:ARG:HH12	1.46	0.76
1:C:125:GLU:HG2	4:I:204:ARG:CD	2.16	0.76
1:C:125:GLU:HG3	4:I:204:ARG:NH1	1.93	0.76
1:C:47:MET:CA	3:H:139:LYS:HE3	2.01	0.75
5:K:189:LYS:HA	5:K:189:LYS:HZ3	1.52	0.75
1:B:326:LYS:CE	5:K:257:GLU:HG2	2.15	0.75
1:C:373:LYS:N	1:C:373:LYS:CD	2.50	0.75
1:D:23:GLY:O	3:H:147:ARG:HB2	1.87	0.75
1:F:211:ASP:OD1	1:F:215:LYS:HE2	1.87	0.75
4:J:118:LYS:HD2	4:J:118:LYS:C	2.11	0.75
1:A:211:ASP:OD1	1:A:215:LYS:HE2	1.87	0.75
5:K:268:LYS:O	5:K:272:GLU:HG2	1.87	0.75
1:B:211:ASP:OD1	1:B:215:LYS:HE2	1.87	0.74
1:F:349:LEU:CD1	3:H:210:GLU:HG2	2.16	0.74
1:B:373:LYS:N	1:B:373:LYS:CD	2.50	0.74
1:E:345:ILE:HG21	3:H:177:VAL:CG1	2.07	0.74
1:C:211:ASP:OD1	1:C:215:LYS:HE2	1.87	0.74
5:K:281:MET:HG3	5:M:7:LYS:HE2	1.68	0.74
1:D:25:ASP:HB3	3:H:148:VAL:HA	1.68	0.74
1:F:373:LYS:N	1:F:373:LYS:CD	2.50	0.74
5:L:259:GLU:O	5:L:263:GLN:HG2	1.87	0.74
5:L:280:ASP:OD2	5:M:5:LYS:HE2	1.87	0.74
1:D:373:LYS:N	1:D:373:LYS:CD	2.50	0.74

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:211:ASP:OD1	1:E:215:LYS:HE2	1.87	0.74
5:L:196:GLU:O	5:L:199:THR:CG2	2.29	0.74
1:B:326:LYS:HZ2	5:K:257:GLU:HG2	1.51	0.73
1:D:211:ASP:OD1	1:D:215:LYS:HE2	1.87	0.73
1:E:148:THR:CG2	3:H:171:ARG:NH1	2.50	0.73
1:A:373:LYS:O	4:J:80:PRO:HB3	1.89	0.73
2:G:46:ARG:HG2	5:K:160:ARG:HH21	1.43	0.73
5:L:222:GLU:O	5:L:226:LYS:HG3	1.87	0.73
5:K:242:ALA:O	5:K:246:VAL:HG23	1.89	0.73
1:A:373:LYS:N	1:A:373:LYS:CD	2.50	0.73
1:D:349:LEU:HD21	3:H:142:ARG:CD	2.19	0.73
1:E:373:LYS:N	1:E:373:LYS:CD	2.50	0.73
2:G:7:ALA:O	2:G:11:GLN:HB3	1.88	0.73
5:L:284:ILE:CG2	5:N:7:LYS:CE	2.32	0.73
5:K:78:ALA:HA	5:L:78:ALA:HB2	1.71	0.72
1:D:349:LEU:CD2	3:H:142:ARG:CD	2.68	0.72
1:F:107:GLU:OE2	1:F:115:ASN:ND2	2.23	0.72
4:J:119:GLU:CD	4:J:123:LEU:HD11	2.15	0.72
4:J:124:ILE:HD11	5:L:268:LYS:CG	2.18	0.72
1:D:25:ASP:CG	3:H:149:ARG:H	1.97	0.72
5:K:178:ARG:O	5:K:181:GLU:HG3	1.89	0.72
1:A:107:GLU:OE2	1:A:115:ASN:ND2	2.23	0.72
1:B:107:GLU:OE2	1:B:115:ASN:ND2	2.23	0.72
1:C:107:GLU:OE2	1:C:115:ASN:ND2	2.23	0.72
4:J:109:ILE:CD1	5:L:281:MET:SD	2.78	0.72
5:K:151:ALA:HB1	5:L:151:ALA:CB	2.20	0.72
1:E:107:GLU:OE2	1:E:115:ASN:ND2	2.23	0.72
5:L:284:ILE:HG21	5:N:7:LYS:HE2	0.75	0.72
1:D:107:GLU:OE2	1:D:115:ASN:ND2	2.23	0.71
5:L:81:ALA:O	5:L:85:VAL:HG23	1.91	0.71
4:J:119:GLU:OE2	4:J:123:LEU:HD11	1.90	0.71
1:D:23:GLY:CA	3:H:146:ARG:CZ	2.69	0.71
1:C:288:ASP:OD1	1:C:288:ASP:N	2.24	0.71
1:D:349:LEU:HD23	3:H:142:ARG:HD2	1.73	0.71
2:G:112:ILE:HG23	2:G:116:GLU:HB2	1.72	0.71
5:K:284:ILE:HD12	5:N:8:MET:HE2	1.70	0.71
5:L:91:ARG:O	5:L:95:VAL:HG23	1.91	0.71
1:B:288:ASP:N	1:B:288:ASP:OD1	2.24	0.70
5:K:163:GLU:O	5:K:167:ARG:HG2	1.91	0.70
1:D:348:SER:CB	3:H:146:ARG:HH11	2.00	0.70
2:G:60:MET:O	2:G:64:VAL:N	2.22	0.70

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:288:ASP:OD1	1:F:288:ASP:N	2.24	0.70
4:J:124:ILE:HG13	5:L:268:LYS:CD	2.21	0.70
5:K:140:LYS:HE3	5:K:140:LYS:HA	1.72	0.70
1:C:47:MET:HA	3:H:139:LYS:NZ	2.05	0.70
3:H:72:GLU:HB3	3:H:75:ARG:HH21	1.56	0.70
1:D:23:GLY:CA	3:H:146:ARG:CD	2.68	0.70
1:A:288:ASP:OD1	1:A:288:ASP:N	2.24	0.70
2:G:102:ARG:NH2	3:H:62:MET:SD	2.65	0.69
5:K:278:LEU:CA	5:K:281:MET:HE1	2.17	0.69
5:K:281:MET:HB3	5:M:7:LYS:HZ2	1.57	0.69
1:D:349:LEU:HD21	3:H:142:ARG:HD3	1.74	0.69
5:K:140:LYS:HA	5:K:140:LYS:CE	2.21	0.69
5:K:151:ALA:HB1	5:L:151:ALA:HB1	1.73	0.69
1:E:288:ASP:OD1	1:E:288:ASP:N	2.24	0.69
2:G:14:GLU:HA	2:G:17:LYS:HB2	1.74	0.69
5:K:221:TYR:HB3	5:L:221:TYR:CD1	2.28	0.69
5:K:115:GLU:O	5:K:118:LYS:HG3	1.93	0.69
2:G:41:LEU:HD11	2:G:81:MET:HB2	1.75	0.68
3:H:98:CYS:O	3:H:102:HIS:ND1	2.25	0.68
4:J:81:LYS:HA	4:J:81:LYS:HZ2	1.58	0.68
5:K:189:LYS:HA	5:K:189:LYS:NZ	2.08	0.68
2:G:111:TYR:HB3	2:G:148:ILE:H	1.58	0.68
4:J:127:LYS:HZ3	5:L:264:LYS:CE	2.04	0.68
1:D:288:ASP:N	1:D:288:ASP:OD1	2.24	0.68
4:J:124:ILE:CG1	5:L:268:LYS:CD	2.53	0.68
4:J:127:LYS:HE3	5:L:260:LEU:HD22	1.76	0.68
5:K:138:GLU:OE2	5:L:133:ARG:NH2	2.26	0.67
5:K:281:MET:CA	5:M:7:LYS:HD3	2.24	0.67
5:M:35:ARG:NH2	5:N:40:GLU:OE1	2.27	0.67
1:A:47:MET:CE	1:B:148:THR:OG1	2.40	0.67
5:K:281:MET:HB3	5:M:7:LYS:HZ1	1.54	0.67
5:K:218:GLU:HB2	5:L:217:LYS:HE3	1.76	0.67
5:L:240:GLU:O	5:L:244:ARG:HG2	1.93	0.67
5:L:130:ILE:HD12	5:L:133:ARG:HD2	1.75	0.67
1:A:373:LYS:CD	1:A:374:CYS:H	2.08	0.67
1:F:349:LEU:HD13	3:H:210:GLU:HG2	1.76	0.67
5:K:131:GLU:O	5:K:135:GLN:NE2	2.27	0.67
5:K:281:MET:CG	5:M:7:LYS:NZ	2.58	0.67
1:E:300:SER:OG	1:E:301:GLY:N	2.28	0.67
1:F:373:LYS:CD	1:F:374:CYS:H	2.08	0.67
5:K:281:MET:CA	5:M:7:LYS:HE3	2.22	0.67

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:373:LYS:CD	1:C:374:CYS:H	2.08	0.67
5:K:118:LYS:HZ2	5:K:118:LYS:C	2.03	0.67
1:E:373:LYS:CD	1:E:374:CYS:H	2.08	0.66
1:B:373:LYS:CD	1:B:374:CYS:H	2.08	0.66
1:C:362:TYR:HE2	4:I:204:ARG:HH12	1.42	0.66
1:D:373:LYS:CD	1:D:374:CYS:H	2.08	0.66
4:I:235:LYS:NZ	4:I:238:GLU:OE1	2.27	0.66
5:K:275:ASP:O	5:K:279:ASN:ND2	2.27	0.66
4:J:81:LYS:HA	4:J:81:LYS:HZ3	1.60	0.66
1:B:326:LYS:NZ	5:K:257:GLU:CG	2.55	0.66
1:D:300:SER:OG	1:D:301:GLY:N	2.28	0.66
1:A:300:SER:OG	1:A:301:GLY:N	2.28	0.65
1:D:28:ARG:NH1	3:H:151:SER:HB2	2.09	0.65
5:K:242:ALA:O	5:K:245:SER:OG	2.13	0.65
1:F:300:SER:OG	1:F:301:GLY:N	2.28	0.65
2:G:131:ASP:OD2	3:H:47:LYS:NZ	2.28	0.65
1:B:45:VAL:HG12	1:C:143:TYR:OH	1.97	0.65
5:K:117:GLU:N	5:K:117:GLU:OE1	2.30	0.65
5:K:281:MET:HA	5:M:7:LYS:CD	2.27	0.65
5:L:199:THR:HG23	5:L:200:VAL:N	2.11	0.65
5:L:220:LYS:NZ	5:L:220:LYS:HB3	2.08	0.64
2:G:124:THR:HB	3:H:57:ILE:HG21	1.80	0.64
5:K:197:LEU:HD22	5:K:201:THR:HG23	1.79	0.64
1:E:25:ASP:OD1	1:E:26:ALA:N	2.30	0.64
5:L:233:LYS:HD3	5:L:234:GLU:N	2.12	0.64
1:C:125:GLU:CB	4:I:204:ARG:HD2	2.26	0.64
4:J:127:LYS:NZ	5:L:264:LYS:CE	2.59	0.64
5:K:279:ASN:O	5:K:282:THR:OG1	2.11	0.64
5:L:159:ASP:OD1	5:L:160:ARG:N	2.31	0.64
1:D:25:ASP:OD1	1:D:26:ALA:N	2.31	0.64
5:L:284:ILE:HD12	5:N:7:LYS:CD	2.04	0.64
1:C:125:GLU:CG	4:I:204:ARG:HD3	2.28	0.64
5:K:281:MET:CB	5:M:7:LYS:CD	2.74	0.64
2:G:60:MET:SD	2:G:83:ARG:NH2	2.71	0.63
3:H:137:ARG:HH21	3:H:140:PHE:HD2	1.43	0.63
1:A:373:LYS:HD2	1:A:373:LYS:H	1.63	0.63
1:B:300:SER:OG	1:B:301:GLY:N	2.28	0.63
1:C:300:SER:OG	1:C:301:GLY:N	2.28	0.63
1:E:47:MET:CE	1:F:148:THR:OG1	2.45	0.63
4:J:124:ILE:HG13	5:L:268:LYS:HD2	1.79	0.63
1:C:213:LYS:NZ	6:C:401:ADP:O2'	2.27	0.63

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:233:LYS:HE3	5:L:237:THR:HG21	1.81	0.63
5:K:111:GLN:HA	5:K:114:GLU:OE2	1.99	0.63
5:K:169:LEU:HD12	5:K:172:ILE:HD11	1.81	0.63
2:G:118:LYS:NZ	2:G:122:GLN:OE1	2.27	0.63
4:I:247:GLU:HA	4:I:250:LYS:HD3	1.81	0.63
5:K:88:LEU:HD21	5:L:89:ASN:OD1	1.98	0.63
5:K:134:ALA:HB2	5:L:134:ALA:HB2	1.79	0.63
5:K:180:GLU:O	5:K:184:GLU:HG2	1.98	0.63
4:J:127:LYS:CE	5:L:264:LYS:HD2	2.28	0.62
4:I:265:ASN:OD1	4:I:268:ARG:NH2	2.30	0.62
5:K:218:GLU:OE1	5:L:217:LYS:HE2	2.00	0.62
5:K:278:LEU:O	5:K:282:THR:HG23	2.00	0.62
5:M:21:ARG:CD	5:N:26:GLU:OE2	2.40	0.62
5:K:132:SER:CB	5:K:133:ARG:HH21	2.13	0.62
1:B:213:LYS:NZ	6:B:401:ADP:O2'	2.27	0.62
3:H:196:ILE:CD1	5:L:103:GLN:HG2	2.30	0.62
5:K:222:GLU:CD	5:L:221:TYR:HH	2.05	0.62
5:K:281:MET:CB	5:M:7:LYS:HZ1	2.10	0.62
5:M:26:GLU:OE2	5:N:21:ARG:NH2	2.33	0.62
1:B:326:LYS:CB	5:K:261:TYR:HE2	2.12	0.62
5:K:284:ILE:CD1	5:N:8:MET:CE	2.74	0.61
5:L:217:LYS:HG2	5:L:221:TYR:CE2	2.34	0.61
4:I:269:ASN:O	4:I:272:ASN:ND2	2.31	0.61
3:H:66:ALA:HA	3:H:69:ARG:HD3	1.82	0.61
2:G:65:ASP:OD2	2:G:69:SER:N	2.33	0.61
4:J:90:PHE:O	4:J:90:PHE:CD1	2.53	0.61
5:K:156:GLU:OE1	5:K:156:GLU:N	2.34	0.61
5:L:278:LEU:C	5:L:278:LEU:HD12	2.26	0.61
5:K:141:MET:SD	5:L:140:LYS:HB3	2.41	0.61
1:F:233:SER:OG	1:F:234:SER:N	2.33	0.61
2:G:6:LYS:NZ	2:G:10:GLU:OE2	2.33	0.61
5:L:217:LYS:NZ	5:L:221:TYR:OH	2.33	0.61
5:M:24:GLN:OE1	5:N:29:LYS:NZ	2.34	0.61
5:L:280:ASP:HB3	5:M:5:LYS:HZ3	0.66	0.60
2:G:72:VAL:HB	2:G:77:PHE:HB3	1.82	0.60
5:K:265:LEU:HA	5:K:268:LYS:HG2	1.83	0.60
5:L:72:GLU:O	5:L:75:GLU:HG3	2.01	0.60
1:B:373:LYS:HD2	1:B:374:CYS:H	1.67	0.60
4:J:118:LYS:HD2	4:J:118:LYS:O	2.00	0.60
1:D:233:SER:OG	1:D:234:SER:N	2.33	0.60
1:D:23:GLY:O	3:H:147:ARG:CB	2.49	0.60

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:233:SER:OG	1:C:234:SER:N	2.33	0.60
1:A:373:LYS:HD2	1:A:374:CYS:H	1.66	0.60
4:J:137:ARG:HD2	4:J:137:ARG:C	2.26	0.60
1:A:157:ASP:HB2	6:A:401:ADP:H4'	1.84	0.59
1:D:45:VAL:HG12	1:E:143:TYR:OH	2.01	0.59
5:K:66:ASP:OD1	5:K:67:ALA:N	2.34	0.59
1:C:45:VAL:HG12	1:D:143:TYR:OH	2.02	0.59
1:E:233:SER:OG	1:E:234:SER:N	2.33	0.59
5:L:135:GLN:HG3	5:L:136:LYS:HD2	1.83	0.59
1:A:45:VAL:HG12	1:B:143:TYR:OH	2.02	0.59
1:E:157:ASP:HB2	6:E:401:ADP:H4'	1.84	0.59
1:E:373:LYS:HD2	1:E:374:CYS:H	1.66	0.59
1:C:125:GLU:CA	4:I:204:ARG:CD	2.43	0.59
1:D:157:ASP:HB2	6:D:401:ADP:H4'	1.84	0.59
4:J:127:LYS:HE3	5:L:260:LEU:CD2	2.32	0.59
2:G:103:MET:HE1	3:H:61:GLU:HB3	1.83	0.59
3:H:86:LEU:HB2	4:I:233:ARG:HD3	1.83	0.59
5:K:281:MET:CA	5:M:7:LYS:CD	2.81	0.59
5:L:222:GLU:HA	5:L:225:ILE:HD12	1.83	0.59
1:A:213:LYS:NZ	6:A:401:ADP:O2'	2.27	0.59
1:C:373:LYS:HD2	1:C:374:CYS:H	1.67	0.59
1:F:220:ALA:HB1	1:F:226:GLU:HG3	1.85	0.59
1:B:233:SER:OG	1:B:234:SER:N	2.33	0.59
1:D:117:GLU:OE2	1:D:371:HIS:NE2	2.35	0.59
1:D:373:LYS:HD2	1:D:374:CYS:H	1.67	0.59
5:K:251:LYS:NZ	5:K:254:ASP:OD2	2.36	0.59
1:E:220:ALA:HB1	1:E:226:GLU:HG3	1.85	0.58
1:F:157:ASP:HB2	6:F:401:ADP:H4'	1.84	0.58
5:K:187:GLU:OE2	5:L:182:ARG:NH1	2.35	0.58
1:B:157:ASP:HB2	6:B:401:ADP:H4'	1.84	0.58
1:C:300:SER:O	1:C:304:THR:OG1	2.20	0.58
4:J:124:ILE:HG12	5:L:265:LEU:HD12	1.85	0.58
5:L:117:GLU:OE1	5:L:118:LYS:NZ	2.26	0.58
1:C:157:ASP:HB2	6:C:401:ADP:H4'	1.84	0.58
1:C:220:ALA:HB1	1:C:226:GLU:HG3	1.85	0.58
5:L:204:LEU:HD23	5:L:204:LEU:O	2.04	0.58
5:K:200:VAL:HG23	5:L:200:VAL:HG11	1.84	0.58
5:K:281:MET:HG2	5:M:7:LYS:NZ	2.18	0.58
5:L:281:MET:O	5:L:284:ILE:N	2.30	0.58
1:E:213:LYS:NZ	6:E:401:ADP:O2'	2.27	0.58
5:L:280:ASP:CG	5:M:5:LYS:CE	2.77	0.58

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:300:SER:O	1:D:304:THR:OG1	2.20	0.58
5:K:257:GLU:HA	5:K:260:LEU:CD2	2.34	0.58
5:K:267:TYR:HD2	5:K:267:TYR:O	1.86	0.58
1:B:117:GLU:OE2	1:B:371:HIS:NE2	2.36	0.58
1:C:117:GLU:OE2	1:C:371:HIS:NE2	2.36	0.58
1:D:213:LYS:NZ	6:D:401:ADP:O2'	2.27	0.58
1:B:373:LYS:H	1:B:373:LYS:CD	2.15	0.57
1:C:373:LYS:H	1:C:373:LYS:CD	2.15	0.57
1:D:47:MET:CE	1:E:148:THR:OG1	2.45	0.57
3:H:205:ARG:NH2	3:H:206:LYS:O	2.37	0.57
1:D:373:LYS:H	1:D:373:LYS:CD	2.15	0.57
1:A:220:ALA:HB1	1:A:226:GLU:HG3	1.85	0.57
5:K:111:GLN:NE2	5:K:112:LYS:HD2	2.18	0.57
5:L:132:SER:O	5:L:136:LYS:HD3	2.05	0.57
5:L:233:LYS:HD3	5:L:233:LYS:C	2.30	0.57
5:M:32:ALA:O	5:M:36:SER:OG	2.23	0.57
1:A:233:SER:OG	1:A:234:SER:N	2.34	0.57
1:A:373:LYS:H	1:A:373:LYS:CD	2.15	0.57
1:B:220:ALA:HB1	1:B:226:GLU:HG3	1.85	0.57
1:C:359:LYS:HZ1	4:I:204:ARG:HH21	1.51	0.57
1:D:220:ALA:HB1	1:D:226:GLU:HG3	1.85	0.57
4:J:120:GLU:OE1	5:L:268:LYS:CB	2.52	0.57
5:K:249:LEU:CD1	5:L:246:VAL:HG23	2.35	0.57
5:K:281:MET:HA	5:M:7:LYS:HD3	1.84	0.57
5:L:246:VAL:O	5:L:250:GLU:HG2	2.03	0.57
1:E:373:LYS:H	1:E:373:LYS:CD	2.15	0.57
2:G:148:ILE:HG13	2:G:152:GLU:HB2	1.86	0.57
1:F:213:LYS:NZ	6:F:401:ADP:O2'	2.27	0.57
1:F:373:LYS:HD2	1:F:374:CYS:H	1.67	0.57
5:K:102:ALA:HB1	5:L:102:ALA:HB1	1.87	0.57
5:K:213:LYS:HA	5:K:213:LYS:HZ3	1.70	0.57
3:H:205:ARG:HH21	3:H:206:LYS:HG3	1.70	0.56
4:J:87:ARG:HB3	4:J:88:VAL:HG22	1.87	0.56
4:I:270:ARG:O	4:I:274:ASN:ND2	2.38	0.56
1:A:111:ASN:OD1	1:A:177:ARG:NH1	2.38	0.56
1:B:111:ASN:OD1	1:B:177:ARG:NH1	2.38	0.56
1:C:372:ARG:HB3	1:C:373:LYS:NZ	2.20	0.56
1:D:111:ASN:OD1	1:D:177:ARG:NH1	2.38	0.56
1:D:372:ARG:HB3	1:D:373:LYS:NZ	2.20	0.56
2:G:129:THR:OG1	2:G:132:ASP:OD1	2.24	0.56
4:I:205:GLN:HA	4:I:208:ARG:HB3	1.87	0.56

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:130:ILE:HG22	5:L:257:GLU:CD	2.30	0.56
5:K:281:MET:HB3	5:M:7:LYS:CD	2.33	0.56
1:C:125:GLU:CB	4:I:204:ARG:CD	2.82	0.56
1:E:111:ASN:OD1	1:E:177:ARG:NH1	2.38	0.56
1:F:373:LYS:H	1:F:373:LYS:CD	2.15	0.56
2:G:149:ASP:N	2:G:152:GLU:OE1	2.38	0.56
5:N:34:ASP:HA	5:N:37:LYS:HE2	1.88	0.56
1:A:372:ARG:HB3	1:A:373:LYS:NZ	2.20	0.56
1:E:372:ARG:HB3	1:E:373:LYS:NZ	2.20	0.56
1:F:111:ASN:OD1	1:F:177:ARG:NH1	2.38	0.56
5:L:197:LEU:O	5:L:201:THR:HG23	2.06	0.56
1:B:372:ARG:HB3	1:B:373:LYS:NZ	2.20	0.56
1:C:111:ASN:OD1	1:C:177:ARG:NH1	2.38	0.56
5:K:141:MET:HE1	5:L:144:GLN:CD	2.31	0.56
5:K:284:ILE:HD12	5:N:12:LYS:HD2	1.88	0.56
1:B:5:THR:OG1	1:B:6:THR:N	2.39	0.56
1:C:125:GLU:HG2	4:I:204:ARG:CZ	2.32	0.56
1:F:117:GLU:OE2	1:F:371:HIS:NE2	2.36	0.56
5:K:162:TYR:OH	5:L:161:LYS:HD2	2.05	0.56
1:E:5:THR:OG1	1:E:6:THR:N	2.39	0.56
2:G:89:SER:HB3	2:G:161:GLU:HB3	1.88	0.56
5:K:197:LEU:C	5:K:197:LEU:HD13	2.31	0.56
1:A:156:GLY:O	1:A:303:THR:OG1	2.24	0.55
1:C:5:THR:OG1	1:C:6:THR:N	2.39	0.55
1:C:47:MET:C	3:H:139:LYS:HE2	2.31	0.55
1:E:117:GLU:OE2	1:E:371:HIS:NE2	2.35	0.55
1:A:5:THR:OG1	1:A:6:THR:N	2.39	0.55
5:K:208:GLU:OE1	5:K:209:ALA:N	2.39	0.55
1:B:326:LYS:HE3	5:K:257:GLU:HG2	1.87	0.55
1:C:125:GLU:HA	4:I:204:ARG:HD2	0.66	0.55
1:F:372:ARG:HB3	1:F:373:LYS:NZ	2.20	0.55
2:G:19:GLU:N	2:G:19:GLU:OE1	2.38	0.55
3:H:199:LEU:HD21	5:K:91:ARG:HH21	1.71	0.55
5:K:251:LYS:NZ	5:K:251:LYS:HA	2.22	0.55
1:F:156:GLY:O	1:F:303:THR:OG1	2.24	0.55
4:I:206:THR:O	4:I:210:LYS:NZ	2.40	0.55
5:K:115:GLU:O	5:K:118:LYS:HE3	2.06	0.55
5:K:192:GLU:HA	5:K:192:GLU:OE1	2.07	0.55
1:A:21:PHE:HD2	1:A:28:ARG:HH21	1.55	0.55
4:J:116:ARG:HD2	5:L:272:GLU:OE1	2.06	0.55
5:L:91:ARG:HE	5:L:94:LEU:CD2	2.19	0.55

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:156:GLY:O	1:E:303:THR:OG1	2.24	0.54
3:H:138:GLY:HA2	3:H:142:ARG:HB2	1.89	0.54
4:I:207:GLU:OE1	4:I:207:GLU:N	2.33	0.54
5:K:185:LEU:O	5:K:189:LYS:HG2	2.07	0.54
4:I:219:ARG:NH1	4:I:220:LYS:O	2.40	0.54
1:C:156:GLY:O	1:C:303:THR:OG1	2.24	0.54
5:L:185:LEU:C	5:L:185:LEU:HD13	2.33	0.54
1:B:21:PHE:HD2	1:B:28:ARG:HH21	1.55	0.54
3:H:122:ASN:ND2	4:I:257:PHE:O	2.40	0.54
5:K:92:ILE:O	5:K:96:GLU:HG3	2.06	0.54
5:K:224:GLU:HA	5:K:224:GLU:OE1	2.06	0.54
5:K:232:LEU:HD23	5:K:233:LYS:N	2.22	0.54
5:L:232:LEU:HD12	5:L:233:LYS:N	2.22	0.54
1:E:23:GLY:HA3	3:H:184:LYS:HG2	1.88	0.54
1:F:373:LYS:HD2	1:F:373:LYS:H	1.63	0.54
5:K:267:TYR:HA	5:K:270:ILE:HG22	1.89	0.54
5:L:213:LYS:HA	5:L:216:GLN:HG2	1.89	0.54
5:M:21:ARG:HE	5:N:22:ALA:HB1	1.73	0.54
4:J:120:GLU:HB3	5:L:268:LYS:HG3	1.88	0.54
5:K:213:LYS:HA	5:K:213:LYS:NZ	2.22	0.54
5:L:274:LEU:HD13	5:L:274:LEU:C	2.32	0.54
1:A:117:GLU:OE2	1:A:371:HIS:NE2	2.36	0.54
2:G:72:VAL:HG11	2:G:76:GLU:HB3	1.90	0.54
3:H:94:LEU:HD11	4:I:233:ARG:HG3	1.89	0.54
3:H:142:ARG:NH2	3:H:145:LEU:O	2.31	0.54
4:J:124:ILE:HD12	5:L:268:LYS:NZ	2.23	0.54
5:K:140:LYS:HA	5:K:140:LYS:HZ1	1.73	0.54
5:K:278:LEU:HD23	5:K:281:MET:HE1	1.90	0.54
5:L:64:LEU:HB2	5:L:67:ALA:HB3	1.90	0.54
5:L:113:LEU:HD23	5:L:114:GLU:N	2.23	0.54
1:D:21:PHE:HD2	1:D:28:ARG:HH21	1.55	0.53
1:F:21:PHE:HD2	1:F:28:ARG:HH21	1.55	0.53
5:K:223:GLU:OE1	5:K:224:GLU:N	2.41	0.53
1:C:46:GLY:C	3:H:139:LYS:HZ1	1.99	0.53
1:C:125:GLU:CG	4:I:204:ARG:CD	2.86	0.53
1:C:21:PHE:HD2	1:C:28:ARG:HH21	1.55	0.53
1:A:300:SER:O	1:A:304:THR:OG1	2.20	0.53
1:D:5:THR:OG1	1:D:6:THR:N	2.39	0.53
1:D:156:GLY:O	1:D:303:THR:OG1	2.24	0.53
3:H:95:GLN:HG2	4:I:224:ILE:HD12	1.90	0.53
5:K:165:VAL:HG11	5:L:165:VAL:HG21	1.91	0.53

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:M:22:ALA:HB2	5:N:22:ALA:HA	1.90	0.53
1:E:21:PHE:HD2	1:E:28:ARG:HH21	1.55	0.53
4:J:80:PRO:O	4:J:81:LYS:NZ	2.29	0.53
5:K:112:LYS:NZ	5:K:115:GLU:OE2	2.28	0.53
5:K:143:ILE:O	5:K:146:ILE:HG13	2.09	0.53
5:K:162:TYR:CE2	5:L:161:LYS:HE3	2.43	0.53
5:K:140:LYS:HA	5:K:140:LYS:NZ	2.24	0.53
1:C:47:MET:SD	3:H:139:LYS:CD	2.97	0.53
1:E:23:GLY:CA	3:H:184:LYS:CB	2.86	0.53
2:G:149:ASP:HB2	4:I:270:ARG:HH21	1.74	0.53
1:B:326:LYS:HZ2	5:K:257:GLU:CG	2.17	0.53
1:C:359:LYS:HZ3	4:I:204:ARG:HH21	1.52	0.53
1:F:5:THR:OG1	1:F:6:THR:N	2.39	0.53
3:H:146:ARG:HE	3:H:147:ARG:H	1.56	0.53
1:C:372:ARG:HB3	1:C:373:LYS:CE	2.40	0.52
2:G:12:LEU:O	2:G:17:LYS:NZ	2.42	0.52
5:K:275:ASP:HA	5:K:278:LEU:HG	1.91	0.52
4:J:120:GLU:HB3	5:L:268:LYS:HE2	1.90	0.52
1:C:95:ARG:CD	4:I:268:ARG:CD	2.70	0.52
1:E:23:GLY:O	3:H:181:ASP:O	2.27	0.52
5:L:284:ILE:CG1	5:N:7:LYS:HE2	2.39	0.52
1:B:156:GLY:O	1:B:303:THR:OG1	2.24	0.52
5:L:99:LEU:C	5:L:99:LEU:HD12	2.35	0.52
1:A:372:ARG:HB3	1:A:373:LYS:CE	2.40	0.52
1:D:23:GLY:HA2	3:H:146:ARG:NH1	2.24	0.52
1:D:23:GLY:C	3:H:146:ARG:CD	2.83	0.52
4:J:120:GLU:OE1	5:L:268:LYS:HG3	2.10	0.52
4:J:120:GLU:O	5:L:268:LYS:HD2	2.09	0.52
5:L:199:THR:CG2	5:L:200:VAL:N	2.72	0.52
1:B:372:ARG:HB3	1:B:373:LYS:CE	2.40	0.52
4:J:104:GLU:OE2	5:N:6:LYS:CE	2.57	0.52
1:B:326:LYS:HD2	5:K:261:TYR:CE2	2.45	0.52
1:D:244:ASP:C	1:E:325:MET:HE3	2.35	0.52
2:G:89:SER:O	2:G:92:LYS:NZ	2.40	0.52
3:H:198:ALA:CB	5:L:103:GLN:HE22	2.22	0.52
4:J:127:LYS:HG3	5:L:264:LYS:HD2	1.91	0.52
2:G:41:LEU:HG	2:G:77:PHE:CE2	2.44	0.52
5:K:71:LEU:HD21	5:L:67:ALA:HB1	1.91	0.52
1:E:372:ARG:HB3	1:E:373:LYS:CE	2.40	0.51
3:H:108:VAL:HB	4:I:243:ILE:HD11	1.90	0.51
4:I:271:ILE:HA	4:I:274:ASN:HD22	1.75	0.51

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:118:LYS:HZ2	5:K:119:ALA:N	2.08	0.51
5:K:216:GLN:O	5:K:216:GLN:NE2	2.44	0.51
5:L:245:SER:O	5:L:249:LEU:HG	2.10	0.51
1:F:372:ARG:HB3	1:F:373:LYS:CE	2.40	0.51
1:D:372:ARG:HB3	1:D:373:LYS:CE	2.40	0.51
1:F:17:VAL:HG23	1:F:33:SER:HB3	1.93	0.51
5:K:260:LEU:C	5:K:260:LEU:HD12	2.35	0.51
2:G:28:VAL:HA	2:G:32:GLU:HG3	1.93	0.51
3:H:129:LEU:HD12	4:I:267:LEU:HB3	1.92	0.51
4:J:123:LEU:HD22	5:L:264:LYS:CE	2.40	0.51
5:K:229:SER:O	5:K:233:LYS:HG2	2.11	0.51
3:H:114:ASP:O	3:H:118:LYS:HG3	2.11	0.51
3:H:146:ARG:CG	3:H:147:ARG:N	2.65	0.51
5:L:275:ASP:OD1	5:L:279:ASN:ND2	2.42	0.51
5:K:106:LEU:HD12	5:K:106:LEU:C	2.36	0.51
5:K:112:LYS:HA	5:K:115:GLU:OE1	2.10	0.51
3:H:179:LYS:O	3:H:182:ILE:HG12	2.11	0.51
4:J:123:LEU:HD22	5:L:264:LYS:HE3	1.92	0.51
1:C:373:LYS:H	1:C:373:LYS:CE	2.24	0.51
1:E:345:ILE:HD11	3:H:178:LYS:HA	1.92	0.51
4:J:119:GLU:O	4:J:123:LEU:HG	2.11	0.51
5:L:130:ILE:CD1	5:L:133:ARG:HD2	2.41	0.51
1:A:354:GLN:N	1:A:354:GLN:OE1	2.44	0.51
3:H:171:ARG:HD3	3:H:174:LEU:HD12	1.93	0.51
1:A:17:VAL:HG23	1:A:33:SER:HB3	1.93	0.50
1:A:35:VAL:HG13	1:A:54:VAL:HG12	1.93	0.50
2:G:87:ASP:OD1	2:G:87:ASP:N	2.43	0.50
5:L:278:LEU:HD12	5:L:278:LEU:O	2.11	0.50
1:D:35:VAL:HG13	1:D:54:VAL:HG12	1.94	0.50
1:F:354:GLN:N	1:F:354:GLN:OE1	2.44	0.50
3:H:104:ARG:HA	3:H:107:LYS:HG2	1.92	0.50
5:K:249:LEU:HD13	5:L:246:VAL:HG23	1.93	0.50
5:K:257:GLU:O	5:K:260:LEU:HG	2.10	0.50
1:D:373:LYS:H	1:D:373:LYS:CE	2.25	0.50
5:K:213:LYS:HA	5:K:213:LYS:CE	2.42	0.50
1:B:354:GLN:N	1:B:354:GLN:OE1	2.44	0.50
1:B:373:LYS:H	1:B:373:LYS:CE	2.24	0.50
1:D:17:VAL:HG23	1:D:33:SER:HB3	1.93	0.50
1:B:35:VAL:HG13	1:B:54:VAL:HG12	1.94	0.50
1:C:17:VAL:HG23	1:C:33:SER:HB3	1.92	0.50
1:D:373:LYS:CG	1:D:374:CYS:N	2.75	0.50

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:373:LYS:H	1:E:373:LYS:CE	2.24	0.50
1:F:35:VAL:HG13	1:F:54:VAL:HG12	1.94	0.50
1:B:17:VAL:HG23	1:B:33:SER:HB3	1.93	0.50
1:E:35:VAL:HG13	1:E:54:VAL:HG12	1.94	0.50
5:L:260:LEU:HD23	5:L:260:LEU:C	2.36	0.50
1:C:373:LYS:CG	1:C:374:CYS:N	2.75	0.50
1:D:23:GLY:C	3:H:146:ARG:HD3	2.37	0.50
1:E:17:VAL:HG23	1:E:33:SER:HB3	1.93	0.50
4:I:227:LEU:HB2	4:I:232:LEU:HD21	1.94	0.50
5:L:223:GLU:O	5:L:227:VAL:HG23	2.11	0.50
1:B:47:MET:CE	1:C:148:THR:CB	2.89	0.50
1:D:25:ASP:HB3	3:H:148:VAL:CA	2.40	0.50
4:J:119:GLU:HG3	4:J:123:LEU:HD12	1.93	0.50
1:A:44:MET:HB3	1:A:47:MET:CG	2.42	0.50
1:C:35:VAL:HG13	1:C:54:VAL:HG12	1.94	0.50
3:H:111:GLU:OE1	4:I:250:LYS:HD2	2.11	0.50
3:H:141:LYS:O	3:H:144:THR:OG1	2.25	0.50
5:K:162:TYR:OH	5:L:161:LYS:HB3	2.12	0.50
5:L:196:GLU:C	5:L:199:THR:HG22	2.32	0.50
1:C:44:MET:HB3	1:C:47:MET:CG	2.42	0.49
1:C:354:GLN:N	1:C:354:GLN:OE1	2.44	0.49
1:A:373:LYS:CG	1:A:374:CYS:N	2.75	0.49
5:K:64:LEU:O	5:K:68:GLN:N	2.36	0.49
5:L:281:MET:HG2	5:L:284:ILE:HG12	1.94	0.49
1:B:373:LYS:CG	1:B:374:CYS:N	2.75	0.49
1:C:47:MET:SD	3:H:139:LYS:HD2	2.51	0.49
5:L:128:LYS:HA	5:L:131:GLU:HG2	1.94	0.49
1:A:230:ALA:HB2	1:A:236:LEU:HD12	1.95	0.49
1:E:345:ILE:CD1	3:H:178:LYS:HA	2.42	0.49
1:E:373:LYS:HD2	1:E:373:LYS:H	1.64	0.49
3:H:94:LEU:HD21	4:I:233:ARG:HB2	1.93	0.49
1:B:373:LYS:HG2	1:B:374:CYS:N	2.28	0.49
1:E:44:MET:HB3	1:E:47:MET:CG	2.42	0.49
1:E:230:ALA:HB2	1:E:236:LEU:HD12	1.94	0.49
5:L:105:ARG:HA	5:L:108:THR:HG22	1.94	0.49
5:L:281:MET:O	5:L:284:ILE:HG12	2.12	0.49
1:F:373:LYS:H	1:F:373:LYS:CE	2.24	0.49
2:G:142:LYS:HG3	2:G:147:ARG:HH22	1.77	0.49
1:B:230:ALA:HB2	1:B:236:LEU:HD12	1.95	0.49
1:C:155:SER:HB3	1:C:304:THR:HG23	1.95	0.49
1:E:373:LYS:CG	1:E:374:CYS:N	2.75	0.49

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:91:ARG:HH21	5:L:94:LEU:CD2	2.25	0.49
1:C:230:ALA:HB2	1:C:236:LEU:HD12	1.95	0.49
1:D:155:SER:HB3	1:D:304:THR:HG23	1.95	0.49
1:D:230:ALA:HB2	1:D:236:LEU:HD12	1.95	0.49
5:K:281:MET:O	5:M:7:LYS:HD3	2.13	0.49
1:D:44:MET:HB3	1:D:47:MET:CG	2.43	0.49
1:F:373:LYS:HG2	1:F:374:CYS:N	2.28	0.49
4:J:134:ARG:HD3	5:L:257:GLU:OE1	2.13	0.49
5:K:132:SER:OG	5:K:133:ARG:NH2	2.45	0.49
1:A:373:LYS:H	1:A:373:LYS:CE	2.25	0.49
1:B:44:MET:HB3	1:B:47:MET:CG	2.42	0.49
1:F:373:LYS:CG	1:F:374:CYS:N	2.75	0.49
5:K:110:LEU:HG	5:K:111:GLN:N	2.27	0.49
1:A:373:LYS:HG2	1:A:374:CYS:N	2.28	0.48
1:D:354:GLN:N	1:D:354:GLN:OE1	2.44	0.48
1:B:155:SER:HB3	1:B:304:THR:HG23	1.95	0.48
1:F:230:ALA:HB2	1:F:236:LEU:HD12	1.95	0.48
1:F:349:LEU:CD2	3:H:210:GLU:HG2	2.43	0.48
2:G:11:GLN:NE2	2:G:87:ASP:OD2	2.45	0.48
5:K:284:ILE:HG21	5:N:12:LYS:HE2	1.94	0.48
1:E:354:GLN:OE1	1:E:354:GLN:N	2.44	0.48
1:F:300:SER:O	1:F:304:THR:OG1	2.20	0.48
5:L:274:LEU:HD13	5:L:274:LEU:O	2.13	0.48
5:K:92:ILE:HA	5:K:95:VAL:HG22	1.94	0.48
1:A:24:ASP:OD1	1:A:24:ASP:N	2.47	0.48
1:C:47:MET:CE	3:H:139:LYS:HD2	2.43	0.48
1:E:45:VAL:HG12	1:F:143:TYR:OH	2.13	0.48
1:E:155:SER:HB3	1:E:304:THR:HG23	1.95	0.48
1:F:155:SER:HB3	1:F:304:THR:HG23	1.95	0.48
4:J:127:LYS:HE2	5:L:264:LYS:CD	2.37	0.48
5:K:132:SER:HB2	5:K:133:ARG:HH21	1.77	0.48
5:K:204:LEU:HD11	5:L:203:ASN:HB2	1.96	0.48
1:C:373:LYS:HG2	1:C:374:CYS:N	2.28	0.48
5:K:127:MET:O	5:K:131:GLU:HG2	2.14	0.48
5:K:257:GLU:HA	5:K:260:LEU:HD23	1.95	0.48
1:E:147:ARG:C	3:H:174:LEU:HD13	2.39	0.48
5:K:137:ASP:OD2	5:L:138:GLU:N	2.46	0.48
5:L:243:GLU:O	5:L:246:VAL:HG12	2.13	0.48
5:L:263:GLN:HA	5:L:263:GLN:OE1	2.14	0.48
1:F:44:MET:HB3	1:F:47:MET:CG	2.43	0.48
4:J:112:HIS:CE1	5:L:274:LEU:CD1	2.96	0.48

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:373:LYS:HG2	1:D:374:CYS:N	2.28	0.48
1:E:373:LYS:HG2	1:E:374:CYS:N	2.28	0.48
2:G:66:GLU:CD	2:G:66:GLU:H	2.22	0.48
4:J:105:LEU:HD21	5:L:284:ILE:CD1	2.34	0.48
5:K:197:LEU:O	5:K:201:THR:HG23	2.14	0.48
5:K:232:LEU:HD23	5:K:232:LEU:C	2.39	0.48
2:G:4:ILE:O	2:G:8:ALA:N	2.36	0.48
3:H:136:LEU:HD21	4:I:271:ILE:HD13	1.96	0.48
1:E:148:THR:HB	3:H:174:LEU:HD11	1.96	0.47
1:E:300:SER:O	1:E:304:THR:OG1	2.20	0.47
3:H:92:GLU:CD	3:H:92:GLU:H	2.21	0.47
1:B:24:ASP:OD1	1:B:24:ASP:N	2.47	0.47
5:K:165:VAL:HG23	5:K:168:LYS:NZ	2.29	0.47
1:A:155:SER:HB3	1:A:304:THR:HG23	1.95	0.47
1:B:43:VAL:N	1:C:168:GLY:O	2.45	0.47
5:L:233:LYS:O	5:L:236:GLU:HG3	2.13	0.47
1:B:300:SER:O	1:B:304:THR:OG1	2.20	0.47
3:H:47:LYS:O	3:H:51:LYS:HG2	2.14	0.47
4:J:123:LEU:HB3	5:L:264:LYS:HD3	1.96	0.47
5:L:68:GLN:O	5:L:71:LEU:HG	2.15	0.47
5:L:220:LYS:C	5:L:220:LYS:HD2	2.39	0.47
4:I:206:THR:O	4:I:210:LYS:HG2	2.14	0.47
5:K:214:TYR:OH	5:L:218:GLU:N	2.47	0.47
5:L:87:SER:O	5:L:91:ARG:HG2	2.15	0.47
1:E:23:GLY:HA3	3:H:184:LYS:CB	2.45	0.47
5:K:86:ALA:O	5:K:90:ARG:NH1	2.48	0.47
5:K:141:MET:HE1	5:L:144:GLN:NE2	2.30	0.47
5:L:78:ALA:O	5:L:82:GLU:HG2	2.14	0.47
1:E:345:ILE:HG23	3:H:177:VAL:HG12	1.64	0.47
3:H:173:HIS:ND1	3:H:176:GLN:OE1	2.41	0.47
3:H:202:MET:HB2	5:K:94:LEU:CD2	2.45	0.47
5:K:193:LEU:HD12	5:L:190:CYS:SG	2.55	0.47
5:L:260:LEU:HD23	5:L:260:LEU:O	2.14	0.47
5:M:35:ARG:HH12	5:N:36:SER:HB3	1.80	0.47
1:B:44:MET:HB2	1:B:47:MET:HG3	1.97	0.47
3:H:94:LEU:HD21	4:I:233:ARG:HE	1.80	0.47
5:L:105:ARG:HB3	5:L:105:ARG:CZ	2.44	0.47
1:D:44:MET:HB2	1:D:47:MET:HG3	1.97	0.47
5:L:217:LYS:HZ1	5:L:221:TYR:HH	1.55	0.47
1:F:44:MET:HB2	1:F:47:MET:HG3	1.97	0.47
2:G:41:LEU:HG	2:G:77:PHE:HE2	1.81	0.47

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:132:SER:OG	5:K:133:ARG:NE	2.45	0.47
5:K:267:TYR:C	5:K:267:TYR:CD2	2.93	0.47
5:K:280:ASP:OD1	5:N:8:MET:HE1	2.15	0.47
5:M:5:LYS:O	5:M:9:GLN:HG2	2.15	0.47
1:A:44:MET:HB2	1:A:47:MET:HG3	1.97	0.46
1:B:33:SER:O	1:B:33:SER:OG	2.33	0.46
1:E:44:MET:HB2	1:E:47:MET:HG3	1.97	0.46
5:K:280:ASP:OD1	5:N:8:MET:SD	2.73	0.46
1:C:44:MET:HB2	1:C:47:MET:HG3	1.97	0.46
1:D:34:ILE:HD11	1:D:59:GLN:HG2	1.97	0.46
1:F:24:ASP:OD1	1:F:24:ASP:N	2.47	0.46
5:N:35:ARG:HE	5:N:39:LEU:HD11	1.79	0.46
1:C:34:ILE:HD11	1:C:59:GLN:HG2	1.97	0.46
1:C:120:THR:OG1	1:C:132:MET:SD	2.67	0.46
1:F:12:ASN:OD1	1:F:86:TRP:NE1	2.42	0.46
3:H:82:GLN:CD	3:H:82:GLN:H	2.23	0.46
5:K:268:LYS:HG3	5:K:269:ALA:N	2.30	0.46
2:G:67:ASP:OD1	2:G:67:ASP:N	2.49	0.46
5:L:251:LYS:NZ	5:L:255:ASP:HB3	2.31	0.46
1:D:24:ASP:OD1	1:D:24:ASP:N	2.47	0.46
1:E:148:THR:HG22	3:H:171:ARG:CZ	2.41	0.46
2:G:80:MET:HA	2:G:83:ARG:HE	1.81	0.46
5:K:221:TYR:HB3	5:L:221:TYR:CE1	2.50	0.46
1:C:24:ASP:OD1	1:C:24:ASP:N	2.47	0.46
1:B:120:THR:OG1	1:B:132:MET:SD	2.67	0.46
1:D:34:ILE:HD12	1:D:67:LEU:HD13	1.98	0.46
1:D:120:THR:OG1	1:D:132:MET:SD	2.67	0.46
1:E:34:ILE:HD11	1:E:59:GLN:HG2	1.98	0.46
3:H:65:GLU:CD	3:H:69:ARG:HD2	2.40	0.46
5:K:274:LEU:O	5:K:278:LEU:HG	2.15	0.46
1:B:34:ILE:HD11	1:B:59:GLN:HG2	1.97	0.46
4:J:109:ILE:HD12	5:L:281:MET:SD	2.54	0.46
4:J:127:LYS:CE	5:L:260:LEU:CD2	2.93	0.46
5:K:213:LYS:HA	5:K:213:LYS:HE2	1.98	0.46
1:C:78:ASN:ND2	1:C:81:ASP:OD2	2.49	0.46
1:C:359:LYS:HZ3	4:I:204:ARG:NH2	2.13	0.46
1:D:78:ASN:ND2	1:D:81:ASP:OD2	2.49	0.46
2:G:157:MET:HB3	3:H:51:LYS:HB3	1.98	0.46
3:H:146:ARG:CG	3:H:147:ARG:H	2.20	0.46
1:E:24:ASP:OD1	1:E:24:ASP:N	2.47	0.46
1:F:34:ILE:HD11	1:F:59:GLN:HG2	1.97	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:115:GLU:HG2	5:K:116:ALA:N	2.31	0.46
2:G:95:GLU:H	2:G:95:GLU:CD	2.24	0.45
5:K:284:ILE:HG21	5:N:12:LYS:CE	2.46	0.45
5:L:219:ASP:O	5:L:222:GLU:HG3	2.15	0.45
1:A:78:ASN:ND2	1:A:81:ASP:OD2	2.49	0.45
2:G:56:GLU:OE1	2:G:83:ARG:NH1	2.48	0.45
5:K:111:GLN:HE22	5:K:112:LYS:HD2	1.80	0.45
5:L:220:LYS:HZ2	5:L:220:LYS:CB	2.22	0.45
5:L:280:ASP:CG	5:M:5:LYS:HE2	2.40	0.45
1:F:349:LEU:HD11	3:H:210:GLU:HG2	1.97	0.45
4:J:127:LYS:CE	5:L:260:LEU:HD22	2.44	0.45
5:L:91:ARG:HH21	5:L:94:LEU:HD23	1.81	0.45
1:A:33:SER:O	1:A:33:SER:OG	2.33	0.45
1:A:34:ILE:HD12	1:A:67:LEU:HD13	1.98	0.45
1:F:349:LEU:CD2	3:H:210:GLU:CG	2.94	0.45
1:F:373:LYS:NZ	1:F:373:LYS:HB3	2.31	0.45
5:L:145:GLU:OE1	5:L:145:GLU:HA	2.16	0.45
1:A:34:ILE:HD11	1:A:59:GLN:HG2	1.97	0.45
1:B:34:ILE:HD12	1:B:67:LEU:HD13	1.98	0.45
1:D:373:LYS:NZ	1:D:373:LYS:HB3	2.31	0.45
1:E:373:LYS:HD2	1:E:374:CYS:N	2.31	0.45
1:E:373:LYS:NZ	1:E:373:LYS:HB3	2.31	0.45
1:F:78:ASN:ND2	1:F:81:ASP:OD2	2.49	0.45
3:H:102:HIS:CE1	4:I:222:LEU:HD13	2.51	0.45
4:J:90:PHE:O	4:J:90:PHE:CG	2.69	0.45
5:N:35:ARG:NE	5:N:39:LEU:HD11	2.31	0.45
1:B:373:LYS:NZ	1:B:373:LYS:HB3	2.31	0.45
1:C:373:LYS:NZ	1:C:373:LYS:HB3	2.31	0.45
1:E:23:GLY:HA3	3:H:184:LYS:CG	2.47	0.45
1:F:373:LYS:HD2	1:F:374:CYS:N	2.32	0.45
2:G:53:THR:HB	2:G:56:GLU:HG2	1.96	0.45
4:I:229:GLU:OE1	4:I:230:ASP:N	2.50	0.45
5:K:214:TYR:CD2	5:L:214:TYR:CG	3.04	0.45
5:L:234:GLU:OE1	5:L:235:ALA:N	2.50	0.45
5:L:280:ASP:OD2	5:M:5:LYS:CE	2.61	0.45
5:M:54:GLU:HG3	5:N:53:THR:HG21	1.98	0.45
1:C:34:ILE:HD12	1:C:67:LEU:HD13	1.99	0.45
1:F:34:ILE:HD12	1:F:67:LEU:HD13	1.98	0.45
4:J:120:GLU:OE1	5:L:271:SER:HB3	2.15	0.45
5:K:100:ASP:N	5:K:100:ASP:OD1	2.50	0.45
5:L:85:VAL:O	5:L:89:ASN:ND2	2.50	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:88:LEU:HD21	5:L:89:ASN:CG	2.41	0.45
5:L:157:ASP:OD1	5:L:158:ALA:N	2.50	0.45
5:L:196:GLU:O	5:L:200:VAL:HG23	2.16	0.45
1:A:373:LYS:NZ	1:A:373:LYS:HB3	2.31	0.45
1:B:78:ASN:ND2	1:B:81:ASP:OD2	2.49	0.45
1:E:44:MET:CB	1:E:47:MET:HG3	2.47	0.45
1:E:78:ASN:ND2	1:E:81:ASP:OD2	2.49	0.45
1:D:373:LYS:HD2	1:D:374:CYS:N	2.32	0.45
1:F:44:MET:CB	1:F:47:MET:HG3	2.47	0.45
3:H:102:HIS:NE2	4:I:222:LEU:HD13	2.32	0.45
5:K:106:LEU:HD12	5:K:106:LEU:O	2.16	0.45
1:C:373:LYS:HD2	1:C:374:CYS:N	2.32	0.44
1:F:120:THR:OG1	1:F:132:MET:SD	2.67	0.44
3:H:185:GLU:OE2	3:H:187:ARG:HG3	2.16	0.44
4:J:100:LYS:O	4:J:104:GLU:HB3	2.17	0.44
5:K:148:LEU:HD12	5:K:148:LEU:C	2.42	0.44
5:K:281:MET:C	5:M:7:LYS:HD3	2.42	0.44
1:A:373:LYS:HD3	1:A:374:CYS:SG	2.58	0.44
1:D:373:LYS:HD2	1:D:373:LYS:H	1.63	0.44
1:E:34:ILE:HD12	1:E:67:LEU:HD13	1.98	0.44
1:E:305:MET:HE3	1:E:305:MET:HB3	1.93	0.44
2:G:140:GLY:HA2	2:G:152:GLU:HB3	1.99	0.44
4:I:205:GLN:O	4:I:209:GLU:N	2.39	0.44
4:I:268:ARG:NH2	4:I:269:ASN:HB2	2.32	0.44
1:A:47:MET:CE	1:B:148:THR:CB	2.96	0.44
1:E:146:GLY:O	3:H:174:LEU:HB3	2.17	0.44
1:E:373:LYS:HD3	1:E:374:CYS:SG	2.58	0.44
1:F:373:LYS:HD3	1:F:374:CYS:SG	2.58	0.44
5:K:128:LYS:HD2	5:K:128:LYS:N	2.31	0.44
5:L:140:LYS:O	5:L:144:GLN:HG2	2.18	0.44
1:A:12:ASN:OD1	1:A:86:TRP:NE1	2.42	0.44
1:B:47:MET:HE1	1:C:148:THR:HB	1.99	0.44
1:B:373:LYS:HD3	1:B:374:CYS:SG	2.58	0.44
2:G:104:PHE:HB2	2:G:112:ILE:HG12	2.00	0.44
1:C:373:LYS:HD3	1:C:374:CYS:SG	2.58	0.44
1:E:12:ASN:OD1	1:E:86:TRP:NE1	2.42	0.44
3:H:98:CYS:SG	4:I:224:ILE:HD13	2.58	0.44
5:K:111:GLN:OE1	5:K:112:LYS:HG2	2.17	0.44
5:K:112:LYS:HB3	5:L:113:LEU:HD12	1.98	0.44
5:L:217:LYS:HE3	5:L:221:TYR:CE2	2.53	0.44
1:A:120:THR:OG1	1:A:132:MET:SD	2.67	0.44

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:43:VAL:N	1:E:168:GLY:O	2.47	0.44
1:D:373:LYS:HD3	1:D:374:CYS:SG	2.58	0.44
5:K:260:LEU:HD12	5:K:261:TYR:N	2.32	0.44
4:J:120:GLU:HG3	5:L:271:SER:OG	2.18	0.44
1:D:24:ASP:OD1	3:H:147:ARG:NH2	2.48	0.44
1:D:24:ASP:CB	3:H:150:ILE:HG21	2.21	0.44
2:G:28:VAL:HG13	2:G:32:GLU:HG3	2.00	0.44
4:I:224:ILE:HA	4:I:232:LEU:HD22	1.99	0.44
5:K:111:GLN:CD	5:K:112:LYS:HD2	2.43	0.44
5:K:129:VAL:O	5:K:133:ARG:HD2	2.18	0.44
5:K:161:LYS:HB3	5:L:162:TYR:CE1	2.53	0.44
5:L:204:LEU:HD23	5:L:204:LEU:C	2.42	0.44
5:N:48:LYS:HE2	5:N:48:LYS:HB3	1.85	0.44
1:E:120:THR:OG1	1:E:132:MET:SD	2.67	0.44
2:G:74:PHE:HA	2:G:77:PHE:HE1	1.83	0.44
2:G:97:LEU:HD13	2:G:154:LEU:HA	1.99	0.44
3:H:128:ASP:O	3:H:132:LYS:HG2	2.17	0.44
3:H:149:ARG:HB3	3:H:153:ASP:CG	2.42	0.44
1:A:44:MET:CB	1:A:47:MET:HG3	2.48	0.43
1:A:373:LYS:HD2	1:A:374:CYS:N	2.31	0.43
1:B:44:MET:CB	1:B:47:MET:HG3	2.48	0.43
1:D:47:MET:HE2	1:E:148:THR:CB	2.46	0.43
5:K:121:ASP:O	5:K:124:GLU:HG2	2.18	0.43
5:L:164:GLU:HA	5:L:164:GLU:OE1	2.17	0.43
1:D:33:SER:O	1:D:33:SER:OG	2.33	0.43
1:D:44:MET:CB	1:D:47:MET:HG3	2.48	0.43
4:I:228:ASN:HB3	4:I:231:GLN:CD	2.43	0.43
4:J:124:ILE:HD12	5:L:268:LYS:HE3	1.91	0.43
1:B:373:LYS:CD	1:B:374:CYS:N	2.80	0.43
1:C:33:SER:O	1:C:33:SER:OG	2.33	0.43
1:D:18:LYS:HG2	1:D:30:VAL:HG22	2.01	0.43
1:D:23:GLY:O	3:H:147:ARG:N	2.51	0.43
1:A:18:LYS:HG2	1:A:30:VAL:HG22	2.01	0.43
4:J:137:ARG:HD2	4:J:137:ARG:O	2.18	0.43
1:C:44:MET:CB	1:C:47:MET:HG3	2.48	0.43
1:D:23:GLY:O	3:H:146:ARG:HG3	2.19	0.43
3:H:104:ARG:HA	3:H:107:LYS:HE3	2.00	0.43
4:I:251:PHE:HA	4:I:254:GLN:NE2	2.33	0.43
1:B:18:LYS:HG2	1:B:30:VAL:HG22	2.01	0.43
1:B:373:LYS:HD2	1:B:374:CYS:N	2.31	0.43
4:J:104:GLU:OE2	5:N:6:LYS:HE3	2.18	0.43

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:124:ILE:HD11	5:L:268:LYS:CB	2.48	0.43
5:K:204:LEU:HD11	5:L:203:ASN:CB	2.49	0.43
5:L:154:ILE:HA	5:L:157:ASP:OD2	2.18	0.43
3:H:68:GLU:O	3:H:72:GLU:HG2	2.18	0.43
2:G:132:ASP:O	2:G:134:GLU:N	2.49	0.43
5:K:124:GLU:HG3	5:K:125:ARG:N	2.30	0.43
5:L:107:ALA:O	5:L:110:LEU:HG	2.19	0.43
5:N:10:MET:SD	5:N:10:MET:N	2.92	0.43
3:H:77:LEU:HB3	4:I:244:HIS:CE1	2.54	0.43
4:I:203:LYS:HE3	4:I:203:LYS:HB3	1.91	0.43
4:I:251:PHE:O	4:I:255:GLU:HG2	2.19	0.43
4:J:137:ARG:HH21	5:L:254:ASP:CG	2.08	0.43
5:L:238:ARG:NH1	5:L:238:ARG:HB2	2.34	0.43
5:M:3:ALA:HB1	5:M:7:LYS:HZ1	1.84	0.43
5:M:35:ARG:NH1	5:N:36:SER:HB3	2.34	0.43
5:K:279:ASN:C	5:K:282:THR:HG1	2.19	0.43
3:H:185:GLU:OE2	3:H:188:GLU:N	2.52	0.42
4:J:144:ARG:HD3	4:J:147:ARG:HD3	1.99	0.42
5:K:145:GLU:HA	5:K:148:LEU:HD23	1.99	0.42
5:L:96:GLU:HA	5:L:99:LEU:HD23	2.01	0.42
5:L:281:MET:HE2	5:L:284:ILE:HG13	2.00	0.42
5:M:51:LYS:HB3	5:M:51:LYS:HE3	1.77	0.42
1:C:47:MET:CA	3:H:139:LYS:NZ	2.73	0.42
1:D:12:ASN:OD1	1:D:86:TRP:NE1	2.42	0.42
2:G:6:LYS:HA	2:G:9:VAL:HG12	2.01	0.42
3:H:199:LEU:HD21	5:K:91:ARG:NH2	2.34	0.42
3:H:208:LYS:HE3	3:H:208:LYS:HB3	1.90	0.42
5:K:171:ILE:N	5:K:171:ILE:HD13	2.33	0.42
1:B:193:LEU:HD23	1:B:193:LEU:HA	1.82	0.42
1:C:193:LEU:HD23	1:C:193:LEU:HA	1.83	0.42
3:H:51:LYS:HA	3:H:51:LYS:HD3	1.84	0.42
4:J:105:LEU:CD2	5:L:284:ILE:HD12	2.34	0.42
5:K:267:TYR:O	5:K:270:ILE:HG22	2.19	0.42
5:L:82:GLU:O	5:L:85:VAL:HB	2.19	0.42
2:G:8:ALA:O	2:G:12:LEU:HG	2.19	0.42
3:H:122:ASN:HD21	4:I:261:LYS:N	2.18	0.42
5:K:111:GLN:NE2	5:K:115:GLU:OE1	2.52	0.42
5:K:167:ARG:O	5:K:171:ILE:HG12	2.20	0.42
5:K:214:TYR:HH	5:L:218:GLU:N	2.18	0.42
1:A:11:ASP:OD1	1:A:106:THR:OG1	2.36	0.42
1:A:193:LEU:HD23	1:A:193:LEU:HA	1.83	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:142:LEU:HD12	1:D:142:LEU:HA	1.84	0.42
1:D:336:LYS:HB3	1:D:336:LYS:HE2	1.81	0.42
1:E:18:LYS:HG2	1:E:30:VAL:HG22	2.01	0.42
5:K:284:ILE:O	5:N:8:MET:HE3	2.19	0.42
1:A:369:ILE:HD12	1:A:372:ARG:HD3	2.01	0.42
1:D:305:MET:HE3	1:D:305:MET:HB3	1.93	0.42
3:H:117:ALA:O	3:H:121:LYS:HG2	2.20	0.42
4:I:258:LYS:HB3	4:I:258:LYS:HE2	1.84	0.42
5:L:178:ARG:CZ	5:L:178:ARG:HB3	2.50	0.42
1:A:336:LYS:HE2	1:A:336:LYS:HB3	1.81	0.42
3:H:142:ARG:N	3:H:143:PRO:HD2	2.35	0.42
5:M:36:SER:OG	5:N:36:SER:OG	2.17	0.42
1:C:47:MET:O	3:H:139:LYS:HE2	2.19	0.42
1:C:125:GLU:CB	4:I:204:ARG:HD3	2.50	0.42
1:C:336:LYS:HE2	1:C:336:LYS:HB3	1.81	0.42
1:F:18:LYS:HG2	1:F:30:VAL:HG22	2.01	0.42
3:H:202:MET:HB2	5:K:94:LEU:HD21	2.01	0.42
5:K:134:ALA:HB1	5:L:133:ARG:HD3	2.02	0.42
1:A:354:GLN:HE21	4:J:83:PRO:CG	2.32	0.42
1:C:18:LYS:HG2	1:C:30:VAL:HG22	2.01	0.42
1:E:345:ILE:CG2	3:H:177:VAL:HG11	2.42	0.42
1:F:106:THR:HB	1:F:137:GLN:HG2	2.02	0.42
2:G:76:GLU:O	2:G:80:MET:HG2	2.19	0.42
4:J:118:LYS:C	4:J:118:LYS:CD	2.86	0.42
1:B:44:MET:CG	1:C:168:GLY:HA2	2.50	0.42
4:J:93:ILE:O	4:J:97:ARG:HB3	2.19	0.42
5:L:251:LYS:HZ3	5:L:255:ASP:HB3	1.85	0.42
1:E:369:ILE:HD12	1:E:372:ARG:HD3	2.01	0.41
3:H:207:LYS:HA	3:H:207:LYS:HD2	1.84	0.41
4:J:121:GLU:OE1	4:J:121:GLU:N	2.53	0.41
5:K:139:GLU:HG2	5:K:140:LYS:N	2.35	0.41
1:C:47:MET:C	3:H:139:LYS:CE	2.91	0.41
1:C:369:ILE:HD12	1:C:372:ARG:HD3	2.01	0.41
1:C:373:LYS:CD	1:C:374:CYS:N	2.80	0.41
1:F:369:ILE:HD12	1:F:372:ARG:HD3	2.01	0.41
2:G:100:LEU:HD22	3:H:58:ALA:HB1	2.02	0.41
1:D:42:GLY:HA2	1:E:168:GLY:O	2.19	0.41
1:D:369:ILE:HD12	1:D:372:ARG:HD3	2.01	0.41
1:E:33:SER:O	1:E:33:SER:OG	2.32	0.41
1:E:106:THR:HB	1:E:137:GLN:HG2	2.02	0.41
1:E:141:SER:OG	1:E:152:VAL:HG21	2.20	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:147:ARG:HE	2:G:147:ARG:C	2.26	0.41
5:K:111:GLN:O	5:K:114:GLU:HG2	2.21	0.41
5:K:137:ASP:OD2	5:L:137:ASP:C	2.64	0.41
5:L:250:GLU:HA	5:L:253:ILE:HD12	2.02	0.41
1:A:106:THR:HB	1:A:137:GLN:HG2	2.02	0.41
1:A:375:PHE:HB2	4:J:80:PRO:HG3	2.02	0.41
1:D:106:THR:HB	1:D:137:GLN:HG2	2.02	0.41
1:E:11:ASP:OD1	1:E:106:THR:OG1	2.36	0.41
1:F:141:SER:OG	1:F:152:VAL:HG21	2.21	0.41
2:G:89:SER:N	2:G:161:GLU:OE1	2.53	0.41
5:K:71:LEU:HD23	5:L:71:LEU:HB3	2.01	0.41
5:K:117:GLU:OE1	5:K:117:GLU:CA	2.69	0.41
5:K:278:LEU:HD23	5:K:281:MET:CE	2.51	0.41
5:M:20:ASP:OD1	5:M:21:ARG:N	2.54	0.41
1:B:369:ILE:HD12	1:B:372:ARG:HD3	2.01	0.41
1:D:11:ASP:OD1	1:D:106:THR:OG1	2.36	0.41
1:E:118:LYS:HE3	1:E:118:LYS:HB3	1.83	0.41
2:G:46:ARG:CG	5:K:160:ARG:HH22	2.05	0.41
4:I:209:GLU:HB3	4:I:210:LYS:HZ2	1.85	0.41
4:I:211:LYS:HE3	4:I:211:LYS:HB3	1.90	0.41
5:K:162:TYR:CE2	5:L:161:LYS:HB2	2.54	0.41
5:K:176:LEU:HD13	5:K:176:LEU:O	2.21	0.41
5:K:266:LYS:HZ3	5:K:266:LYS:C	2.28	0.41
5:L:64:LEU:O	5:L:68:GLN:N	2.47	0.41
5:L:68:GLN:HA	5:L:71:LEU:HD23	2.02	0.41
5:L:251:LYS:NZ	5:L:255:ASP:OD2	2.52	0.41
1:A:47:MET:HE2	1:B:148:THR:CB	2.46	0.41
1:B:47:MET:HE1	1:C:148:THR:CB	2.51	0.41
1:B:141:SER:OG	1:B:152:VAL:HG21	2.21	0.41
1:D:25:ASP:HB3	3:H:148:VAL:HG12	2.02	0.41
3:H:113:TYR:OH	4:I:210:LYS:HB2	2.19	0.41
5:K:92:ILE:HD11	5:L:91:ARG:CB	2.50	0.41
5:K:274:LEU:CD1	5:K:278:LEU:HD21	2.50	0.41
5:K:278:LEU:N	5:K:278:LEU:HD23	2.36	0.41
5:L:234:GLU:CD	5:L:234:GLU:C	2.88	0.41
5:L:276:HIS:HA	5:L:279:ASN:HD22	1.86	0.41
1:C:106:THR:HB	1:C:137:GLN:HG2	2.02	0.41
1:F:334:GLU:OE2	5:K:90:ARG:NH2	2.53	0.41
5:K:81:ALA:O	5:K:85:VAL:HG12	2.21	0.41
1:F:85:ILE:HD13	1:F:85:ILE:HA	1.95	0.41
5:M:50:LEU:HD22	5:N:46:LEU:HD11	2.02	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:141:SER:OG	1:A:152:VAL:HG21	2.21	0.41
1:C:373:LYS:HD2	1:C:373:LYS:H	1.63	0.41
1:D:28:ARG:CZ	3:H:151:SER:HB2	2.51	0.41
1:D:141:SER:OG	1:D:152:VAL:HG21	2.21	0.41
1:D:193:LEU:HD23	1:D:193:LEU:HA	1.82	0.41
1:E:372:ARG:HE	1:E:373:LYS:HE2	1.86	0.41
1:F:373:LYS:CD	1:F:374:CYS:N	2.80	0.41
2:G:112:ILE:HG13	2:G:116:GLU:OE1	2.20	0.41
4:I:224:ILE:HG13	4:I:225:ASP:H	1.85	0.41
4:I:255:GLU:HA	4:I:258:LYS:HE2	2.03	0.41
4:J:87:ARG:HA	4:J:87:ARG:HD3	1.64	0.41
5:K:127:MET:O	5:K:130:ILE:HG22	2.21	0.41
5:K:214:TYR:CZ	5:L:214:TYR:O	2.74	0.41
5:K:217:LYS:HE3	5:K:217:LYS:HA	2.03	0.41
5:K:234:GLU:C	5:K:234:GLU:CD	2.88	0.41
5:K:281:MET:HG2	5:M:7:LYS:HE2	1.81	0.41
5:L:91:ARG:NE	5:L:91:ARG:HA	2.36	0.41
5:L:127:MET:O	5:L:130:ILE:HG22	2.21	0.41
5:N:35:ARG:O	5:N:39:LEU:HG	2.21	0.41
1:B:85:ILE:HD13	1:B:85:ILE:HA	1.96	0.41
1:B:372:ARG:HE	1:B:373:LYS:HE2	1.87	0.41
1:D:47:MET:CE	1:E:148:THR:CB	2.98	0.41
1:D:118:LYS:HE3	1:D:118:LYS:HB3	1.83	0.41
3:H:142:ARG:NH2	3:H:145:LEU:HB2	2.36	0.41
5:K:197:LEU:HD22	5:K:201:THR:CG2	2.48	0.41
5:M:36:SER:O	5:M:40:GLU:HG3	2.20	0.41
1:D:373:LYS:CD	1:D:374:CYS:N	2.80	0.40
1:E:373:LYS:CD	1:E:374:CYS:N	2.80	0.40
3:H:73:LYS:HB3	3:H:73:LYS:HE2	1.78	0.40
3:H:75:ARG:HG3	3:H:78:ARG:NH2	2.37	0.40
5:K:162:TYR:CE2	5:L:161:LYS:CB	3.04	0.40
1:C:305:MET:HE3	1:C:305:MET:HB3	1.93	0.40
5:K:162:TYR:HE2	5:L:161:LYS:CB	2.35	0.40
5:K:267:TYR:HD2	5:K:267:TYR:C	2.30	0.40
1:E:193:LEU:HD23	1:E:193:LEU:HA	1.82	0.40
1:F:372:ARG:HE	1:F:373:LYS:HE2	1.86	0.40
2:G:103:MET:SD	3:H:62:MET:HG2	2.61	0.40
4:I:272:ASN:HA	4:I:275:GLN:NE2	2.36	0.40
5:L:124:GLU:C	5:L:124:GLU:CD	2.90	0.40
1:D:124:PHE:HD1	1:D:124:PHE:HA	1.77	0.40
1:D:372:ARG:HE	1:D:373:LYS:HE2	1.86	0.40

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:118:LYS:HE3	1:F:118:LYS:HB3	1.83	0.40
5:K:88:LEU:HD22	5:L:85:VAL:HA	2.04	0.40
1:B:106:THR:HB	1:B:137:GLN:HG2	2.02	0.40
1:C:12:ASN:OD1	1:C:86:TRP:NE1	2.42	0.40
1:C:372:ARG:HE	1:C:373:LYS:HE2	1.86	0.40
1:D:132:MET:HE2	1:D:132:MET:HB2	2.02	0.40
4:I:235:LYS:O	4:I:239:LEU:HG	2.22	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	A	369/377 (98%)	352 (95%)	17 (5%)	0	100	100
1	B	369/377 (98%)	352 (95%)	17 (5%)	0	100	100
1	C	369/377 (98%)	353 (96%)	16 (4%)	0	100	100
1	D	369/377 (98%)	353 (96%)	16 (4%)	0	100	100
1	E	369/377 (98%)	351 (95%)	18 (5%)	0	100	100
1	F	369/377 (98%)	351 (95%)	18 (5%)	0	100	100
2	G	158/161 (98%)	143 (90%)	14 (9%)	1 (1%)	22	60
3	H	168/211 (80%)	165 (98%)	3 (2%)	0	100	100
4	I	72/291 (25%)	70 (97%)	2 (3%)	0	100	100
4	J	75/291 (26%)	71 (95%)	4 (5%)	0	100	100
5	K	219/284 (77%)	219 (100%)	0	0	100	100
5	L	219/284 (77%)	217 (99%)	2 (1%)	0	100	100
5	M	53/284 (19%)	52 (98%)	1 (2%)	0	100	100
5	N	53/284 (19%)	52 (98%)	1 (2%)	0	100	100

*Continued on next page...*

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	3231/4352 (74%)	3101 (96%)	129 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	G	36	ILE

### 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	A	314/320 (98%)	294 (94%)	20 (6%)	14	36
1	B	314/320 (98%)	294 (94%)	20 (6%)	14	36
1	C	314/320 (98%)	294 (94%)	20 (6%)	14	36
1	D	314/320 (98%)	294 (94%)	20 (6%)	14	36
1	E	314/320 (98%)	294 (94%)	20 (6%)	14	36
1	F	314/320 (98%)	294 (94%)	20 (6%)	14	36
2	G	141/142 (99%)	122 (86%)	19 (14%)	3	14
3	H	148/179 (83%)	130 (88%)	18 (12%)	4	15
4	I	68/257 (26%)	58 (85%)	10 (15%)	2	12
4	J	73/257 (28%)	67 (92%)	6 (8%)	9	28
5	K	191/245 (78%)	156 (82%)	35 (18%)	1	8
5	L	191/245 (78%)	167 (87%)	24 (13%)	3	15
5	M	47/245 (19%)	43 (92%)	4 (8%)	8	27
5	N	47/245 (19%)	44 (94%)	3 (6%)	14	36
All	All	2790/3735 (75%)	2551 (91%)	239 (9%)	11	27

All (239) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	ASP

Continued on next page...

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	54	VAL
1	A	64	ILE
1	A	66	THR
1	A	140	LEU
1	A	151	ILE
1	A	152	VAL
1	A	153	LEU
1	A	171	LEU
1	A	233	SER
1	A	254	ARG
1	A	269	MET
1	A	270	GLU
1	A	288	ASP
1	A	300	SER
1	A	303	THR
1	A	334	GLU
1	A	370	VAL
1	A	373	LYS
1	A	374	CYS
1	B	24	ASP
1	B	54	VAL
1	B	64	ILE
1	B	66	THR
1	B	140	LEU
1	B	151	ILE
1	B	152	VAL
1	B	153	LEU
1	B	171	LEU
1	B	233	SER
1	B	254	ARG
1	B	269	MET
1	B	270	GLU
1	B	288	ASP
1	B	300	SER
1	B	303	THR
1	B	334	GLU
1	B	370	VAL
1	B	373	LYS
1	B	374	CYS
1	C	24	ASP
1	C	54	VAL
1	C	64	ILE

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	C	66	THR
1	C	140	LEU
1	C	151	ILE
1	C	152	VAL
1	C	153	LEU
1	C	171	LEU
1	C	233	SER
1	C	254	ARG
1	C	269	MET
1	C	270	GLU
1	C	288	ASP
1	C	300	SER
1	C	303	THR
1	C	334	GLU
1	C	370	VAL
1	C	373	LYS
1	C	374	CYS
1	D	24	ASP
1	D	54	VAL
1	D	64	ILE
1	D	66	THR
1	D	140	LEU
1	D	151	ILE
1	D	152	VAL
1	D	153	LEU
1	D	171	LEU
1	D	233	SER
1	D	254	ARG
1	D	269	MET
1	D	270	GLU
1	D	288	ASP
1	D	300	SER
1	D	303	THR
1	D	334	GLU
1	D	370	VAL
1	D	373	LYS
1	D	374	CYS
1	E	24	ASP
1	E	54	VAL
1	E	64	ILE
1	E	66	THR
1	E	140	LEU

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	E	151	ILE
1	E	152	VAL
1	E	153	LEU
1	E	171	LEU
1	E	233	SER
1	E	254	ARG
1	E	269	MET
1	E	270	GLU
1	E	288	ASP
1	E	300	SER
1	E	303	THR
1	E	334	GLU
1	E	370	VAL
1	E	373	LYS
1	E	374	CYS
1	F	24	ASP
1	F	54	VAL
1	F	64	ILE
1	F	66	THR
1	F	140	LEU
1	F	151	ILE
1	F	152	VAL
1	F	153	LEU
1	F	171	LEU
1	F	233	SER
1	F	254	ARG
1	F	269	MET
1	F	270	GLU
1	F	288	ASP
1	F	300	SER
1	F	303	THR
1	F	334	GLU
1	F	370	VAL
1	F	373	LYS
1	F	374	CYS
2	G	16	GLN
2	G	25	ASP
2	G	29	LEU
2	G	38	THR
2	G	47	MET
2	G	51	ASN
2	G	56	GLU

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
2	G	75	ASP
2	G	77	PHE
2	G	78	LEU
2	G	86	LYS
2	G	103	MET
2	G	111	TYR
2	G	120	MET
2	G	142	LYS
2	G	147	ARG
2	G	148	ILE
2	G	157	MET
2	G	161	GLU
3	H	64	ARG
3	H	77	LEU
3	H	86	LEU
3	H	93	GLU
3	H	94	LEU
3	H	96	ASP
3	H	98	CYS
3	H	101	LEU
3	H	106	ASP
3	H	132	LYS
3	H	136	LEU
3	H	142	ARG
3	H	173	HIS
3	H	180	GLU
3	H	187	ARG
3	H	188	GLU
3	H	194	LYS
3	H	202	MET
4	I	205	GLN
4	I	219	ARG
4	I	226	HIS
4	I	229	GLU
4	I	235	LYS
4	I	256	LYS
4	I	257	PHE
4	I	265	ASN
4	I	267	LEU
4	I	272	ASN
4	J	81	LYS
4	J	88	VAL

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
4	J	113	PHE
4	J	145	ASN
4	J	148	GLU
4	J	152	GLN
5	K	70	LYS
5	K	77	LYS
5	K	100	ASP
5	K	106	LEU
5	K	110	LEU
5	K	111	GLN
5	K	117	GLU
5	K	118	LYS
5	K	121	ASP
5	K	133	ARG
5	K	139	GLU
5	K	140	LYS
5	K	148	LEU
5	K	156	GLU
5	K	159	ASP
5	K	168	LYS
5	K	176	LEU
5	K	189	LYS
5	K	194	GLU
5	K	197	LEU
5	K	204	LEU
5	K	208	GLU
5	K	213	LYS
5	K	217	LYS
5	K	225	ILE
5	K	228	LEU
5	K	232	LEU
5	K	234	GLU
5	K	248	LYS
5	K	251	LYS
5	K	261	TYR
5	K	264	LYS
5	K	266	LYS
5	K	268	LYS
5	K	280	ASP
5	L	65	LYS
5	L	68	GLN
5	L	70	LYS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
5	L	76	LYS
5	L	98	GLU
5	L	99	LEU
5	L	110	LEU
5	L	113	LEU
5	L	118	LYS
5	L	133	ARG
5	L	159	ASP
5	L	172	ILE
5	L	185	LEU
5	L	218	GLU
5	L	220	LYS
5	L	231	LYS
5	L	234	GLU
5	L	238	ARG
5	L	251	LYS
5	L	255	ASP
5	L	272	GLU
5	L	276	HIS
5	L	278	LEU
5	L	280	ASP
5	M	4	ILE
5	M	7	LYS
5	M	13	LEU
5	M	36	SER
5	N	4	ILE
5	N	19	LEU
5	N	41	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	115	ASN
1	B	115	ASN
1	C	59	GLN
1	C	115	ASN
1	D	115	ASN
1	E	115	ASN
1	F	115	ASN
2	G	16	GLN
2	G	58	GLN
3	H	56	GLN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
3	H	95	GLN
3	H	122	ASN
4	I	244	HIS
4	I	269	ASN
4	J	140	GLN
4	J	145	ASN
4	J	152	GLN
4	J	153	ASN
5	K	89	ASN
5	K	93	GLN
5	K	153	HIS
5	L	89	ASN
5	L	103	GLN
5	L	135	GLN
5	L	144	GLN
5	L	202	ASN
5	L	279	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 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 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	ADP	F	401	7	24,29,29	0.86	0	29,45,45	1.17	2 (6%)
6	ADP	E	401	7	24,29,29	0.82	0	29,45,45	1.16	2 (6%)
6	ADP	C	401	7	24,29,29	0.82	0	29,45,45	1.17	2 (6%)
6	ADP	A	401	7	24,29,29	0.84	0	29,45,45	1.18	2 (6%)
6	ADP	B	401	7	24,29,29	0.84	0	29,45,45	1.16	2 (6%)
6	ADP	D	401	7	24,29,29	0.87	0	29,45,45	1.19	2 (6%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	ADP	F	401	7	-	3/12/32/32	0/3/3/3
6	ADP	E	401	7	-	3/12/32/32	0/3/3/3
6	ADP	C	401	7	-	3/12/32/32	0/3/3/3
6	ADP	A	401	7	-	3/12/32/32	0/3/3/3
6	ADP	B	401	7	-	3/12/32/32	0/3/3/3
6	ADP	D	401	7	-	3/12/32/32	0/3/3/3

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	401	ADP	N3-C2-N1	-3.19	124.34	128.67
6	A	401	ADP	N3-C2-N1	-3.13	124.42	128.67
6	F	401	ADP	N3-C2-N1	-3.11	124.45	128.67
6	C	401	ADP	N3-C2-N1	-3.09	124.47	128.67
6	B	401	ADP	N3-C2-N1	-3.05	124.53	128.67
6	E	401	ADP	N3-C2-N1	-2.99	124.61	128.67
6	A	401	ADP	C4-C5-N7	-2.44	106.76	109.34
6	C	401	ADP	C4-C5-N7	-2.42	106.78	109.34
6	D	401	ADP	C4-C5-N7	-2.37	106.83	109.34
6	E	401	ADP	C4-C5-N7	-2.30	106.91	109.34
6	F	401	ADP	C4-C5-N7	-2.30	106.91	109.34
6	B	401	ADP	C4-C5-N7	-2.29	106.92	109.34

There are no chirality outliers.

All (18) torsion outliers are listed below:

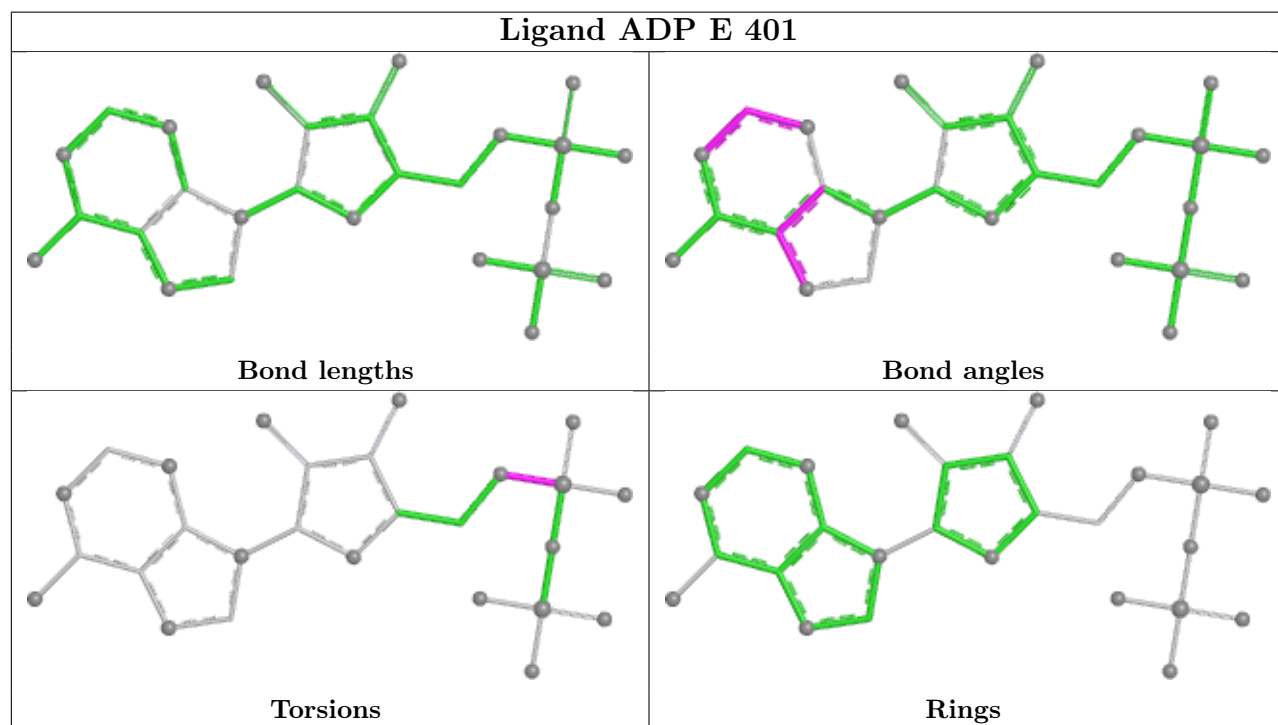
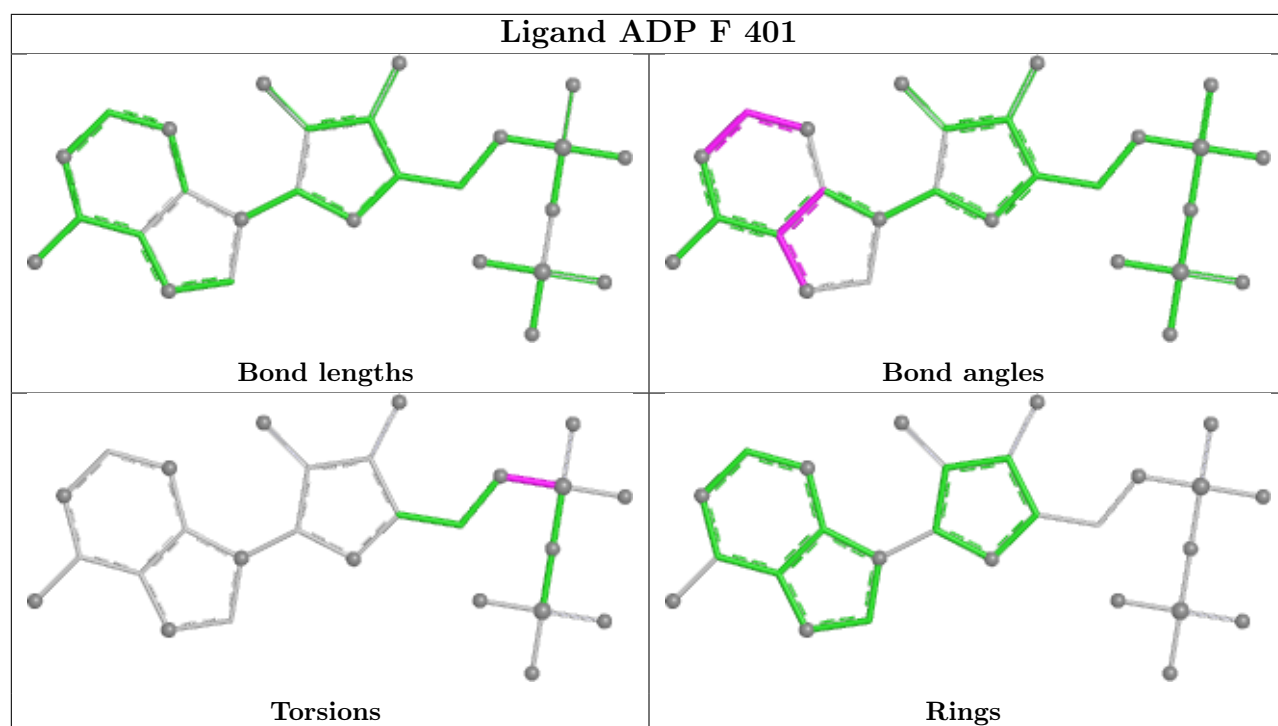
Mol	Chain	Res	Type	Atoms
6	A	401	ADP	C5'-O5'-PA-O1A
6	A	401	ADP	C5'-O5'-PA-O2A
6	A	401	ADP	C5'-O5'-PA-O3A
6	B	401	ADP	C5'-O5'-PA-O1A
6	B	401	ADP	C5'-O5'-PA-O2A
6	B	401	ADP	C5'-O5'-PA-O3A
6	C	401	ADP	C5'-O5'-PA-O1A
6	C	401	ADP	C5'-O5'-PA-O2A
6	C	401	ADP	C5'-O5'-PA-O3A
6	D	401	ADP	C5'-O5'-PA-O1A
6	D	401	ADP	C5'-O5'-PA-O2A
6	D	401	ADP	C5'-O5'-PA-O3A
6	E	401	ADP	C5'-O5'-PA-O1A
6	E	401	ADP	C5'-O5'-PA-O2A
6	E	401	ADP	C5'-O5'-PA-O3A
6	F	401	ADP	C5'-O5'-PA-O1A
6	F	401	ADP	C5'-O5'-PA-O2A
6	F	401	ADP	C5'-O5'-PA-O3A

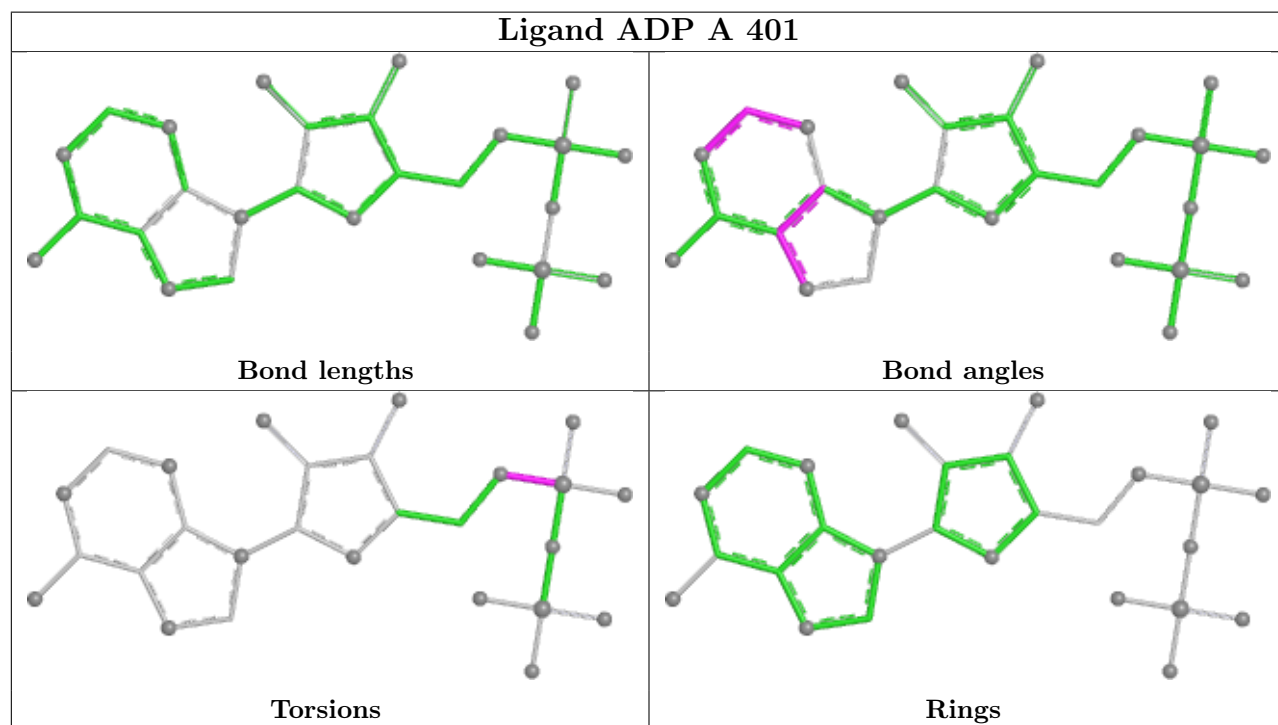
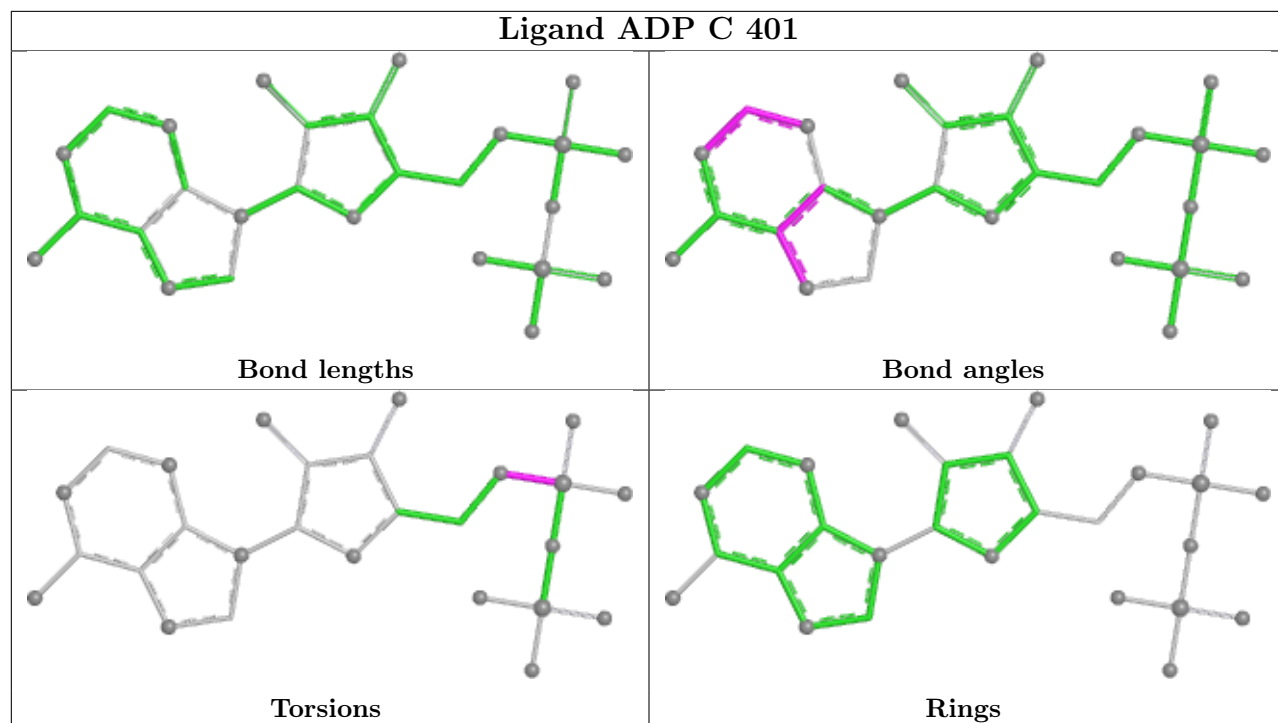
There are no ring outliers.

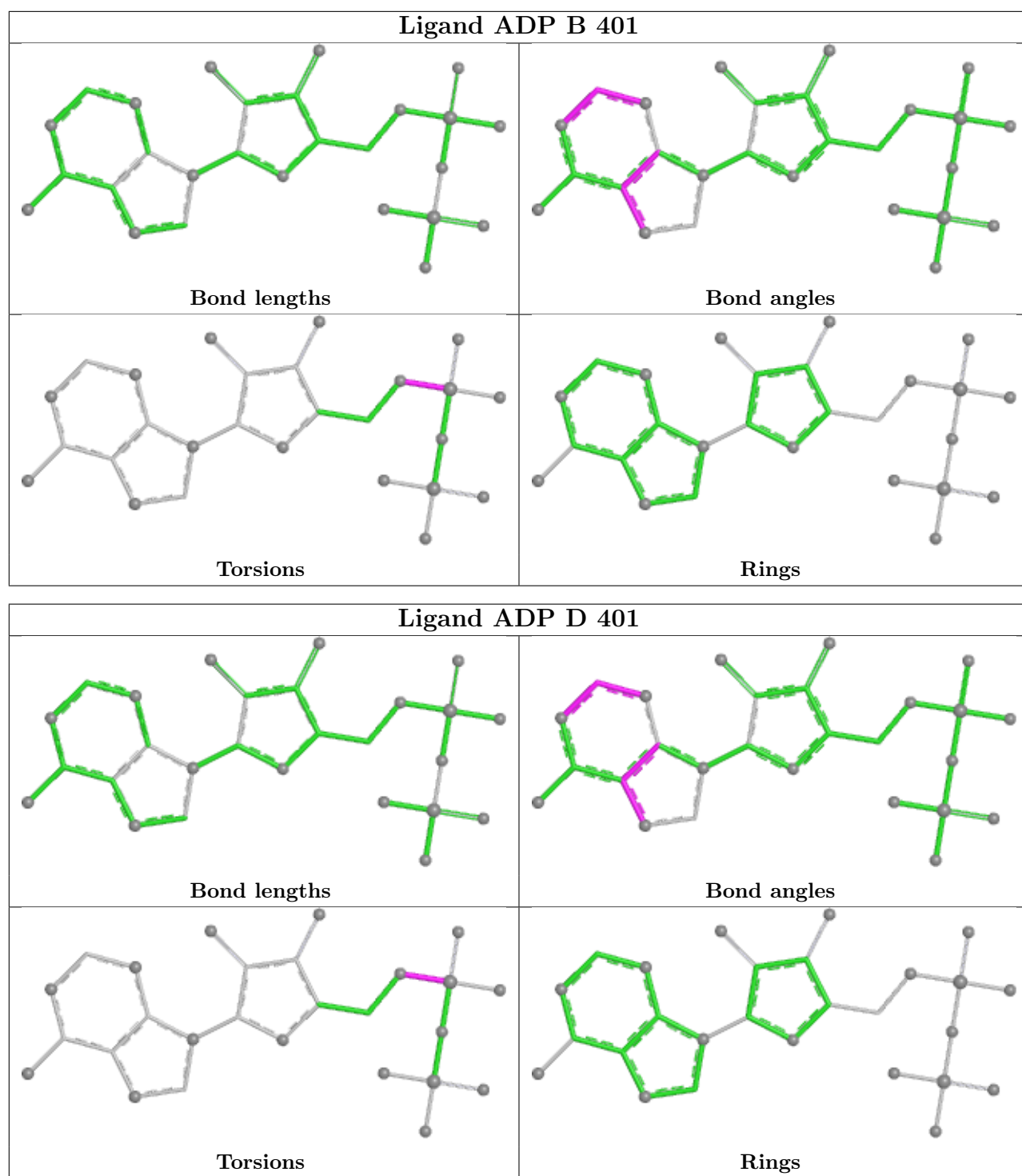
6 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	F	401	ADP	2	0
6	E	401	ADP	2	0
6	C	401	ADP	2	0
6	A	401	ADP	2	0
6	B	401	ADP	2	0
6	D	401	ADP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-48447. These allow visual inspection of the internal detail of the map and identification of artifacts.

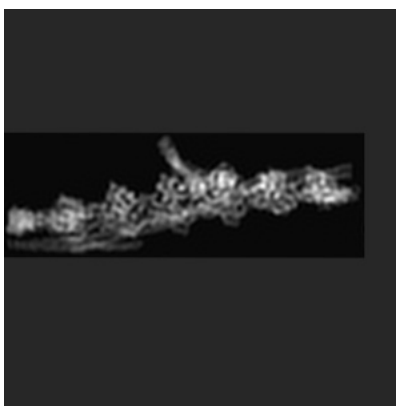
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

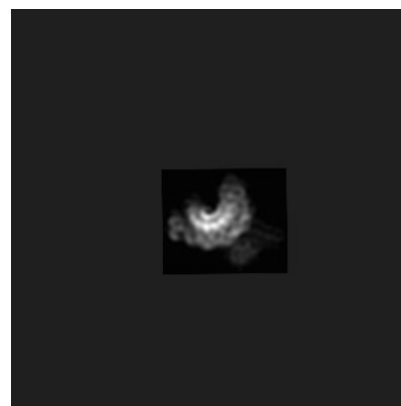
#### 6.1.1 Primary map



X

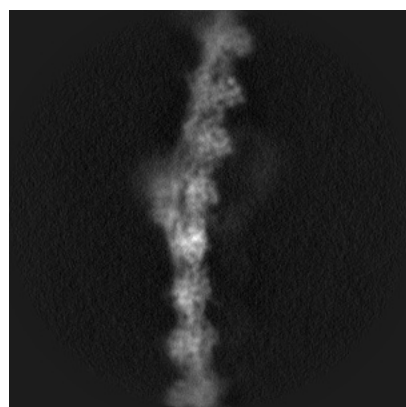


Y

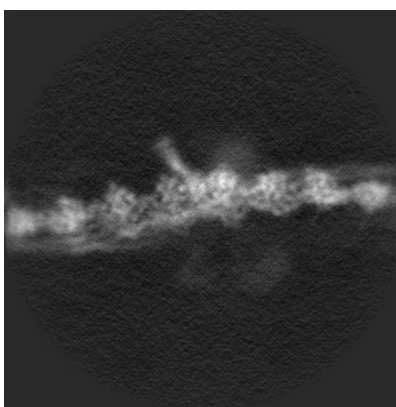


Z

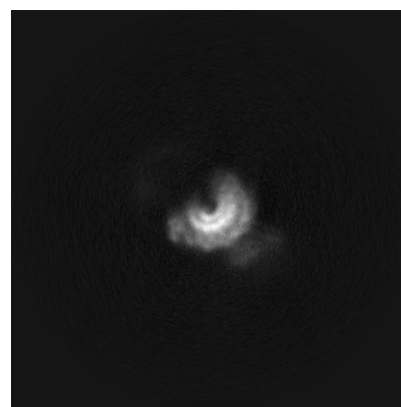
#### 6.1.2 Raw map



X



Y



Z

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

## 6.2 Central slices [i](#)

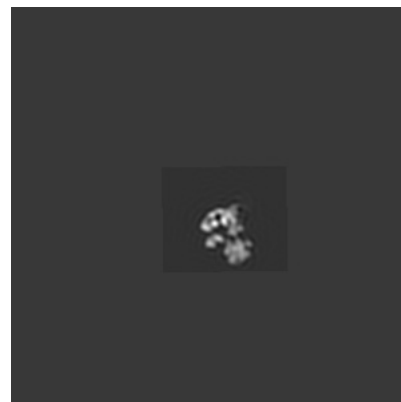
### 6.2.1 Primary map



X Index: 162

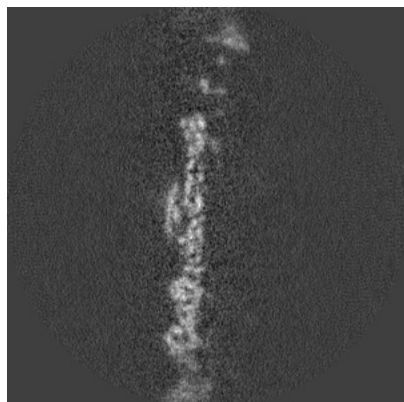


Y Index: 162

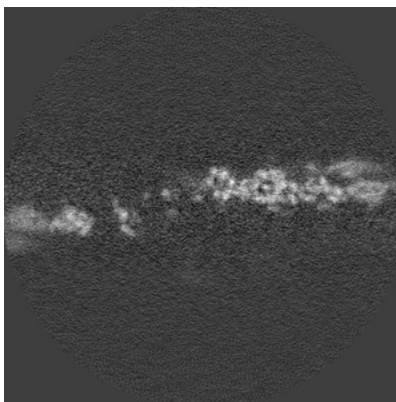


Z Index: 162

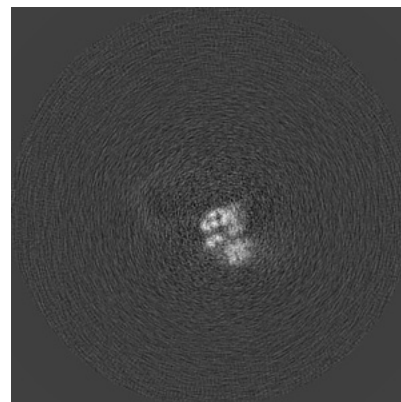
### 6.2.2 Raw map



X Index: 162



Y Index: 162



Z Index: 162

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

## 6.3 Largest variance slices [i](#)

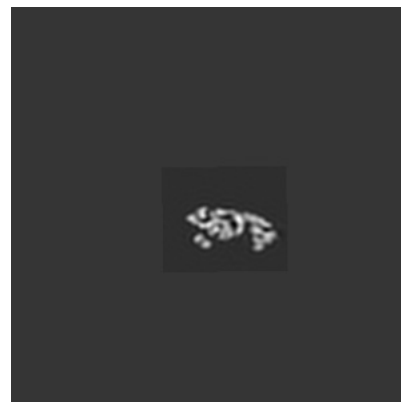
### 6.3.1 Primary map



X Index: 172

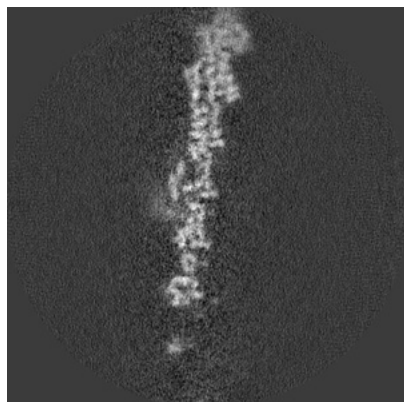


Y Index: 149

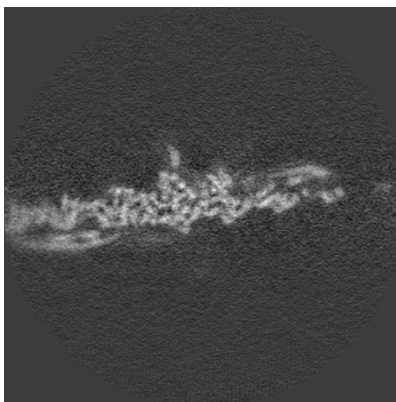


Z Index: 137

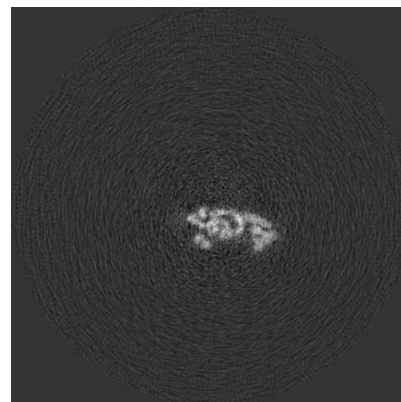
### 6.3.2 Raw map



X Index: 172



Y Index: 149

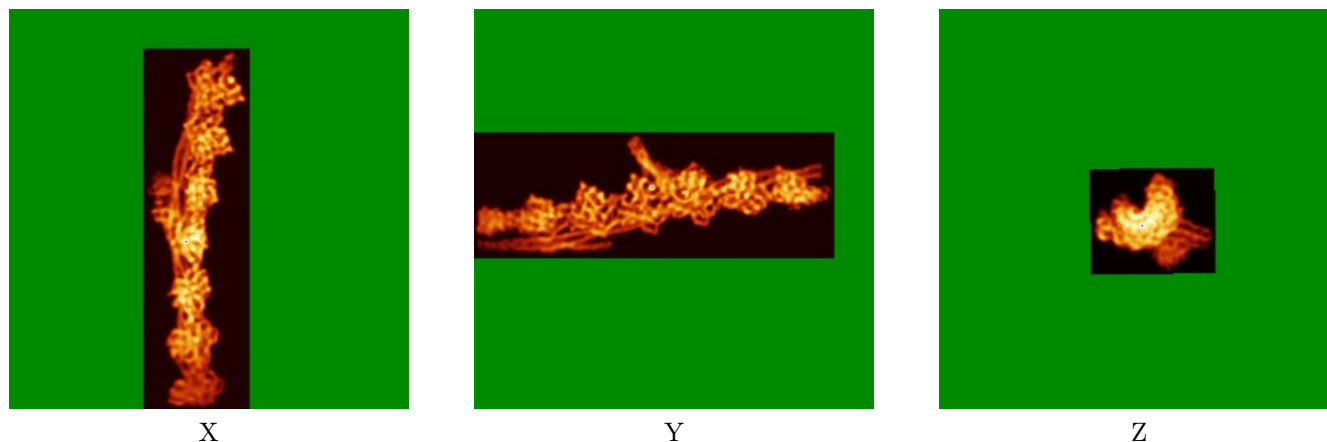


Z Index: 137

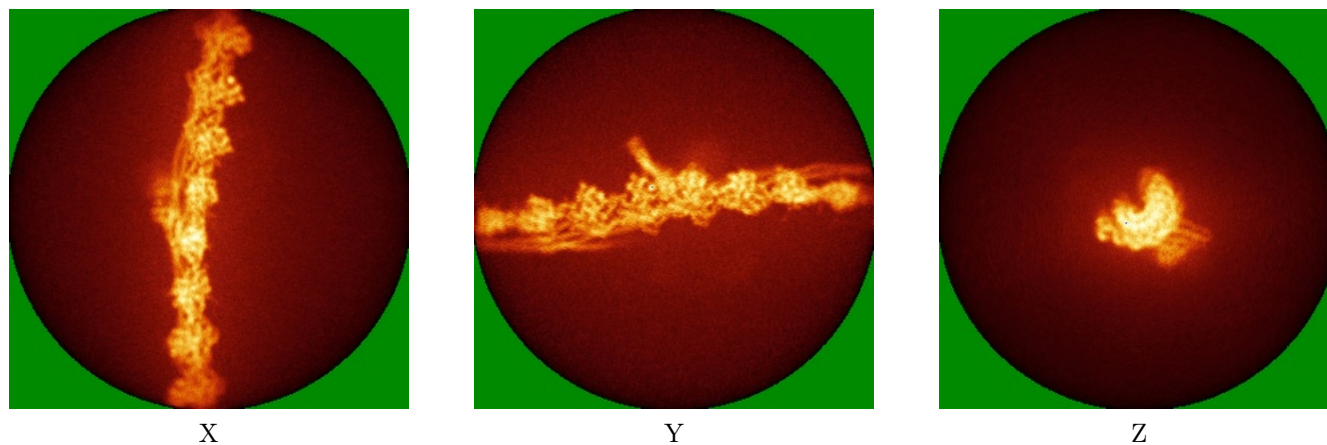
The images above show the largest variance slices of the map in three orthogonal directions.

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

### 6.4.1 Primary map



### 6.4.2 Raw map



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.

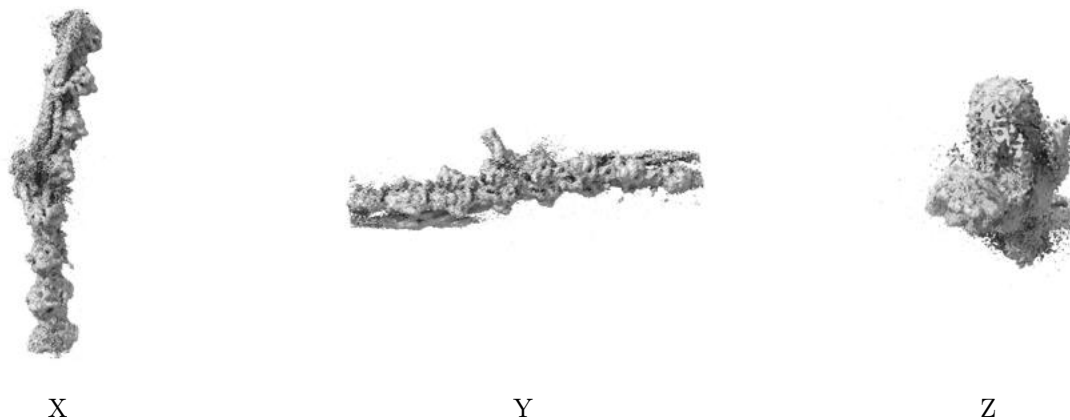
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.515. 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.

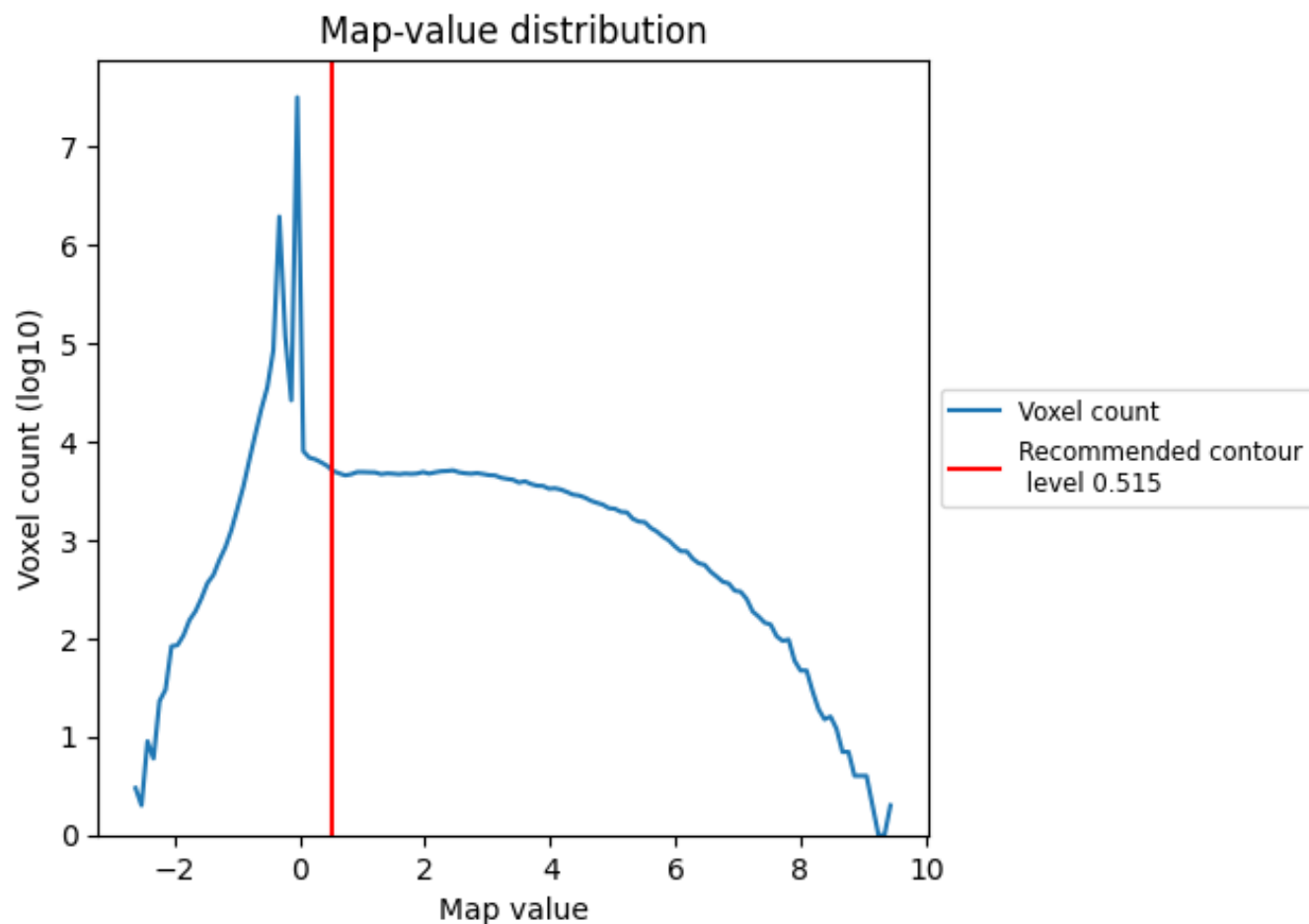
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

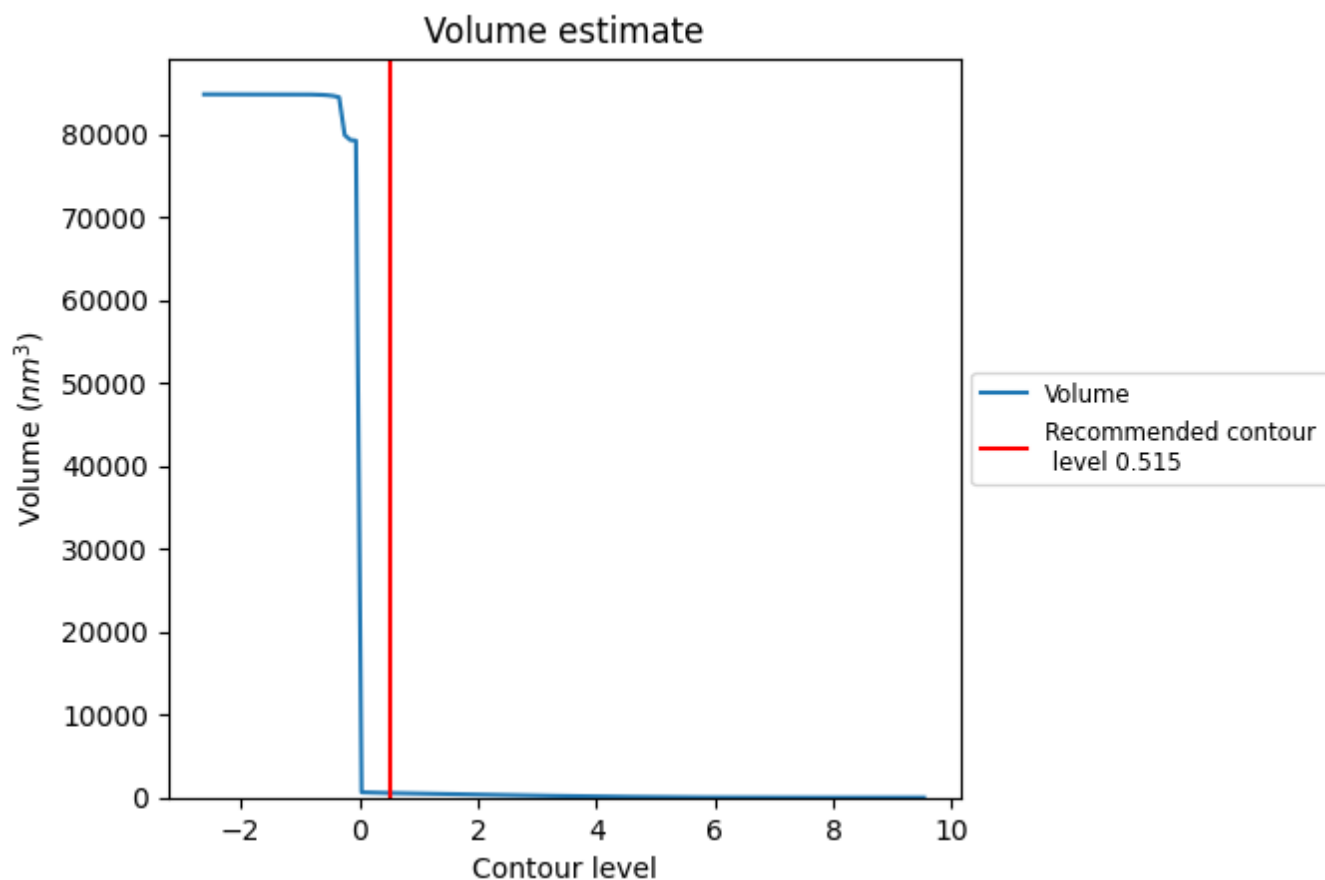
This section contains the results of statistical analysis of the map.

### 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.

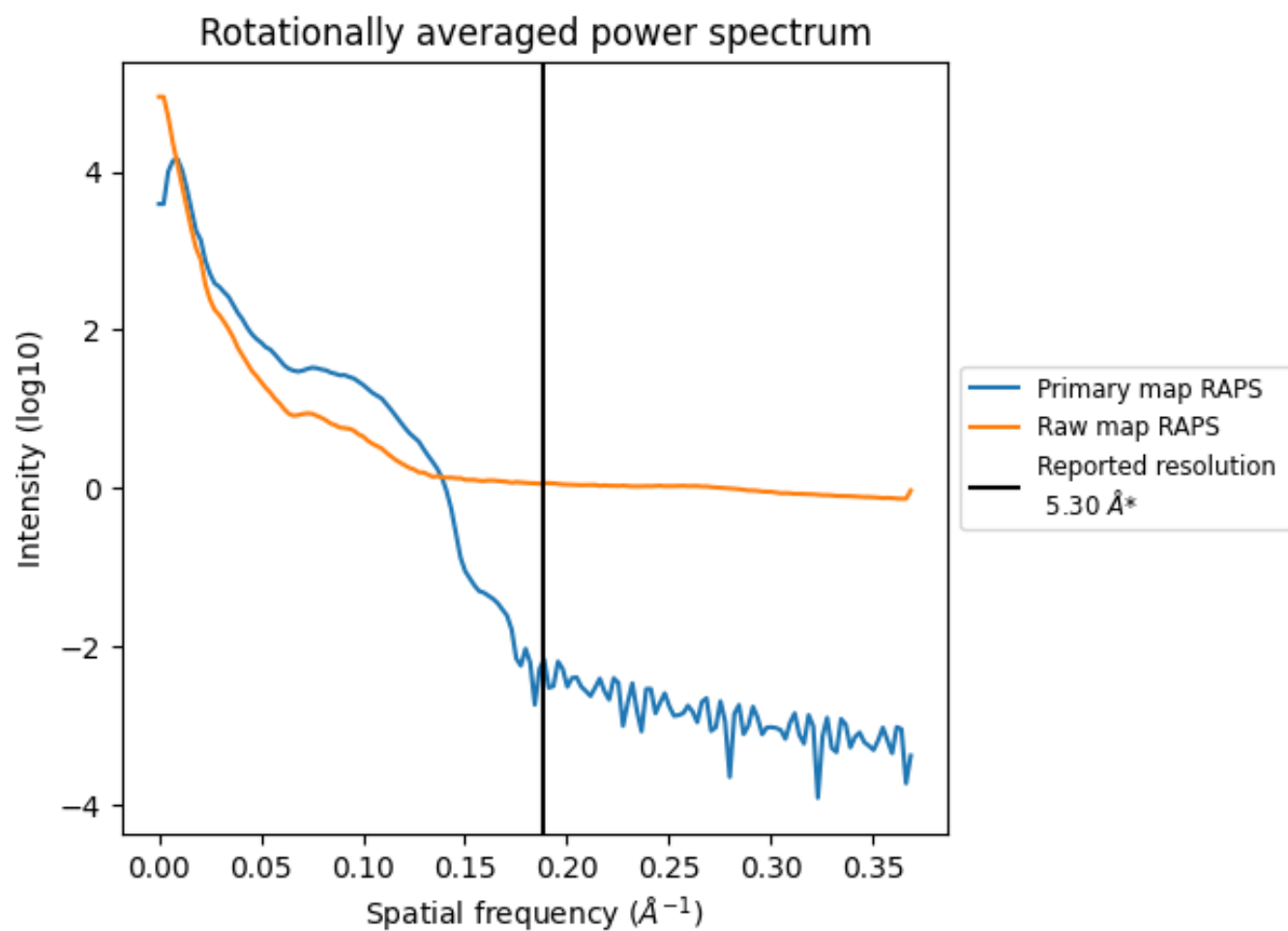
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 548 nm<sup>3</sup>; this corresponds to an approximate mass of 495 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 ⓘ

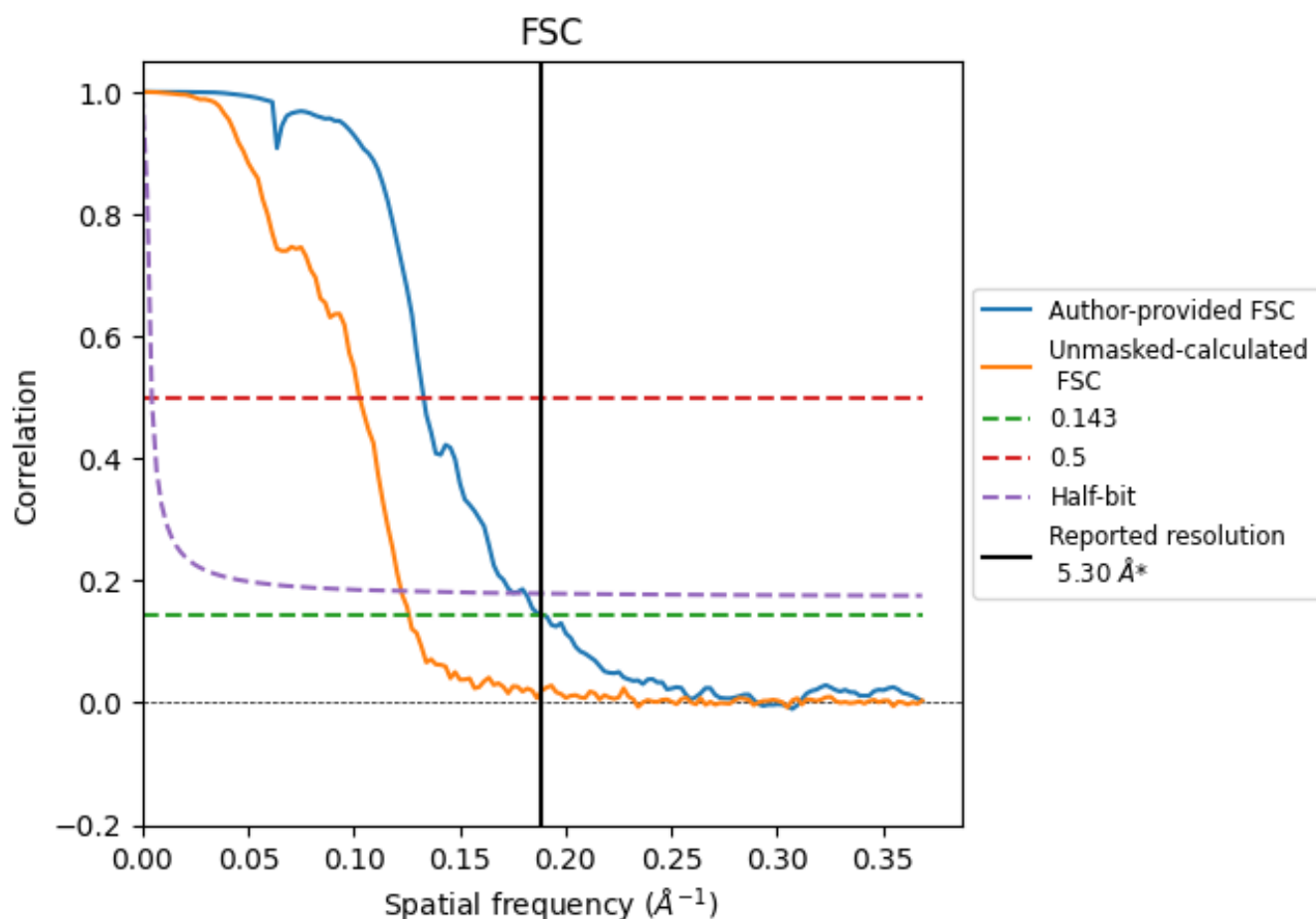


\*Reported resolution corresponds to spatial frequency of 0.189 Å<sup>-1</sup>

## 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 0.189  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

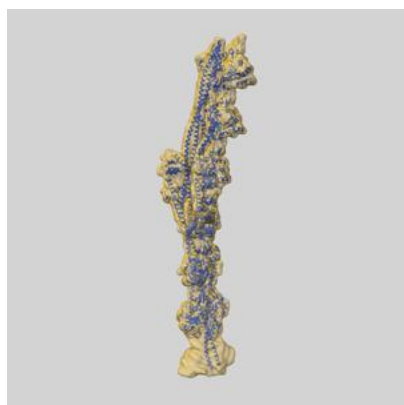
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.30	-	-
Author-provided FSC curve	5.28	7.52	5.52
Unmasked-calculated*	7.93	9.74	8.16

\*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 7.93 differs from the reported value 5.3 by more than 10 %

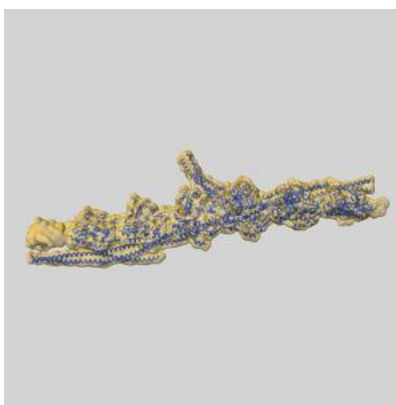
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-48447 and PDB model 9MO4. Per-residue inclusion information can be found in section [3](#) on page [7](#).

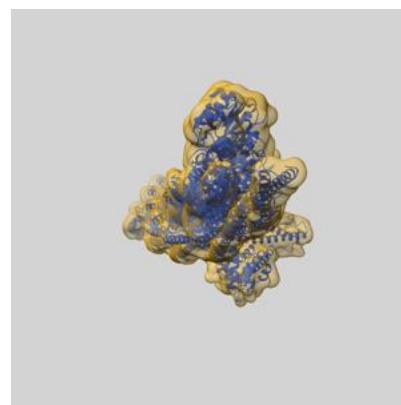
### 9.1 Map-model overlay [i](#)



X



Y



Z

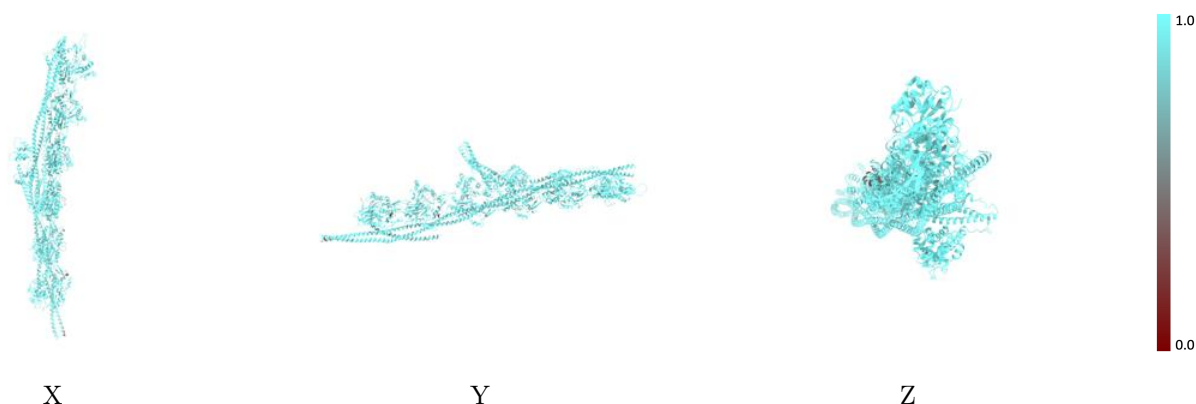
The images above show the 3D surface view of the map at the recommended contour level 0.515 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



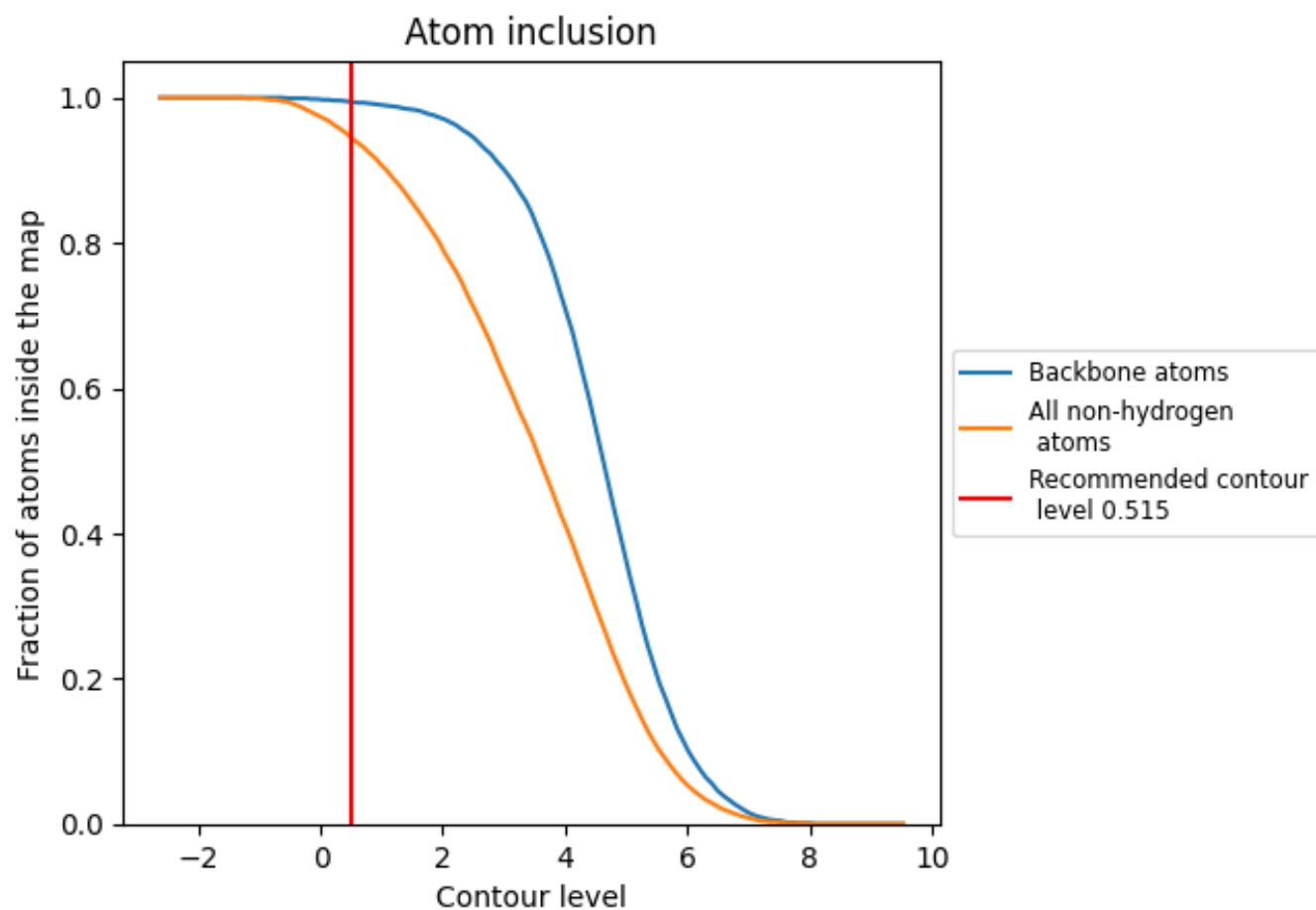
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.515).































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.515) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9440	 0.1790
A	 0.9490	 0.1660
B	 0.9390	 0.1700
C	 0.9320	 0.1660
D	 0.9330	 0.1640
E	 0.9340	 0.1670
F	 0.9540	 0.1690
G	 0.9800	 0.2320
H	 0.9600	 0.2220
I	 0.9740	 0.2100
J	 0.9160	 0.1670
K	 0.9540	 0.2000
L	 0.9500	 0.2010
M	 0.9420	 0.1930
N	 0.8910	 0.1720

