



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 06:20 AM UTC

PDB ID : 5JYG / pdb_00005jyg
EMDB ID : EMD-8180
Title : Cryo-EM structure of the MamK filament at 6.5 Å
Authors : Bergeron, J.R.C.; Hutto, R.; Kollman, J.M.
Deposited on : 2016-05-13
Resolution : 6.50 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

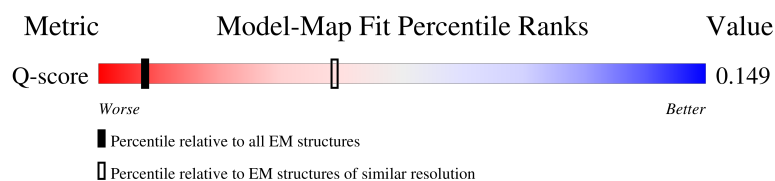
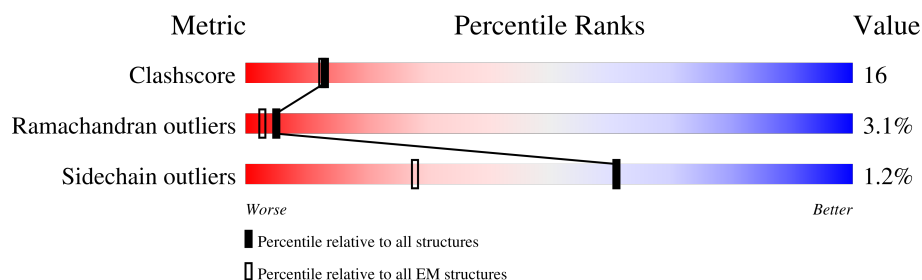
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 6.50 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	556 (6.00 - 7.00)

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	A	347	31% 79% 10% 5% 5%
1	B	347	29% 71% 16% 7% 5%
1	C	347	29% 76% 15% • 5%
1	D	347	31% 71% 18% 5% 5%

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Mol	Chain	Length	Quality of chain
1	E	347	
1	F	347	
1	G	347	
1	H	347	
1	I	347	
1	J	347	
1	K	347	
1	L	347	
1	M	347	
1	N	347	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 35462 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-like ATPase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	328	Total	C	N	O	S	0	0
			2505	1592	430	471	12		
1	B	328	Total	C	N	O	S	0	0
			2505	1592	430	471	12		
1	C	328	Total	C	N	O	S	0	0
			2505	1592	430	471	12		
1	D	328	Total	C	N	O	S	0	0
			2505	1592	430	471	12		
1	E	328	Total	C	N	O	S	0	0
			2505	1592	430	471	12		
1	F	328	Total	C	N	O	S	0	0
			2505	1592	430	471	12		
1	G	328	Total	C	N	O	S	0	0
			2505	1592	430	471	12		
1	H	328	Total	C	N	O	S	0	0
			2505	1592	430	471	12		
1	I	328	Total	C	N	O	S	0	0
			2505	1592	430	471	12		
1	J	328	Total	C	N	O	S	0	0
			2505	1592	430	471	12		
1	K	328	Total	C	N	O	S	0	0
			2505	1592	430	471	12		
1	L	328	Total	C	N	O	S	0	0
			2505	1592	430	471	12		
1	M	328	Total	C	N	O	S	0	0
			2505	1592	430	471	12		
1	N	328	Total	C	N	O	S	0	0
			2505	1592	430	471	12		

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

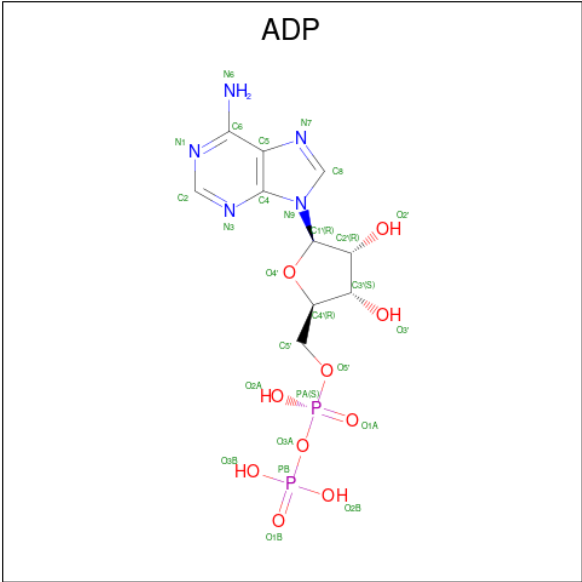
Mol	Chain	Residues	Atoms		AltConf
2	A	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
2	B	1	Total 1	Mg 1	0
2	C	1	Total 1	Mg 1	0
2	D	1	Total 1	Mg 1	0
2	E	1	Total 1	Mg 1	0
2	F	1	Total 1	Mg 1	0
2	G	1	Total 1	Mg 1	0
2	H	1	Total 1	Mg 1	0
2	I	1	Total 1	Mg 1	0
2	J	1	Total 1	Mg 1	0
2	K	1	Total 1	Mg 1	0
2	L	1	Total 1	Mg 1	0
2	M	1	Total 1	Mg 1	0
2	N	1	Total 1	Mg 1	0

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).

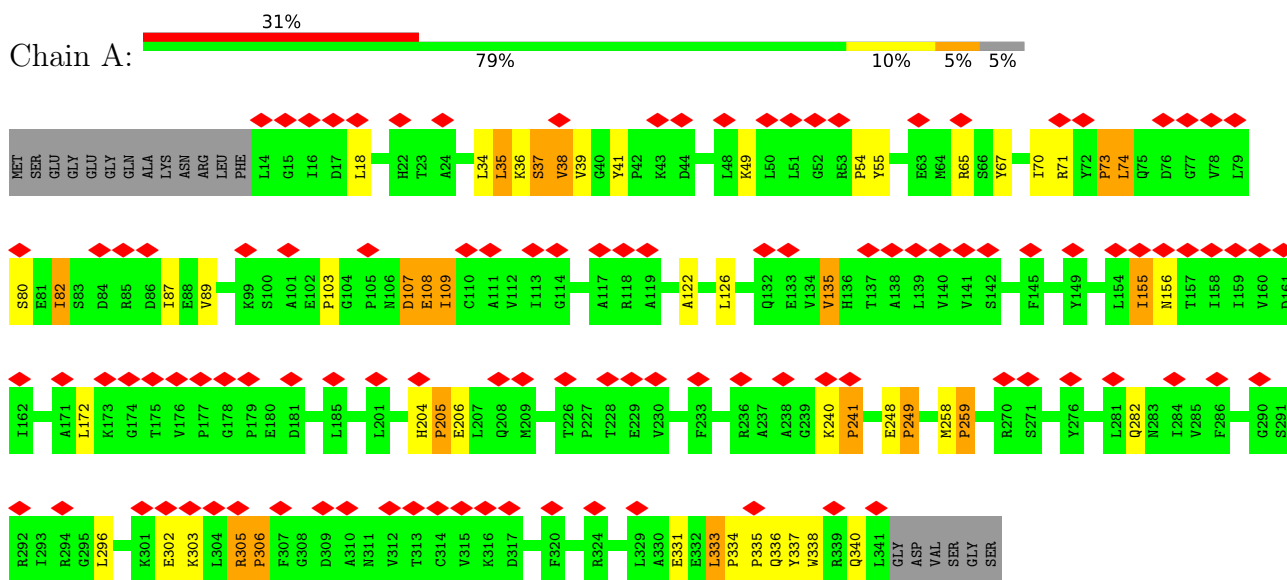


Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	B	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	C	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	D	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	E	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	F	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	G	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	H	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	I	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	J	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	K	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	L	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	M	1	Total	C	N	O	P	0
			27	10	5	10	2	
3	N	1	Total	C	N	O	P	0
			27	10	5	10	2	

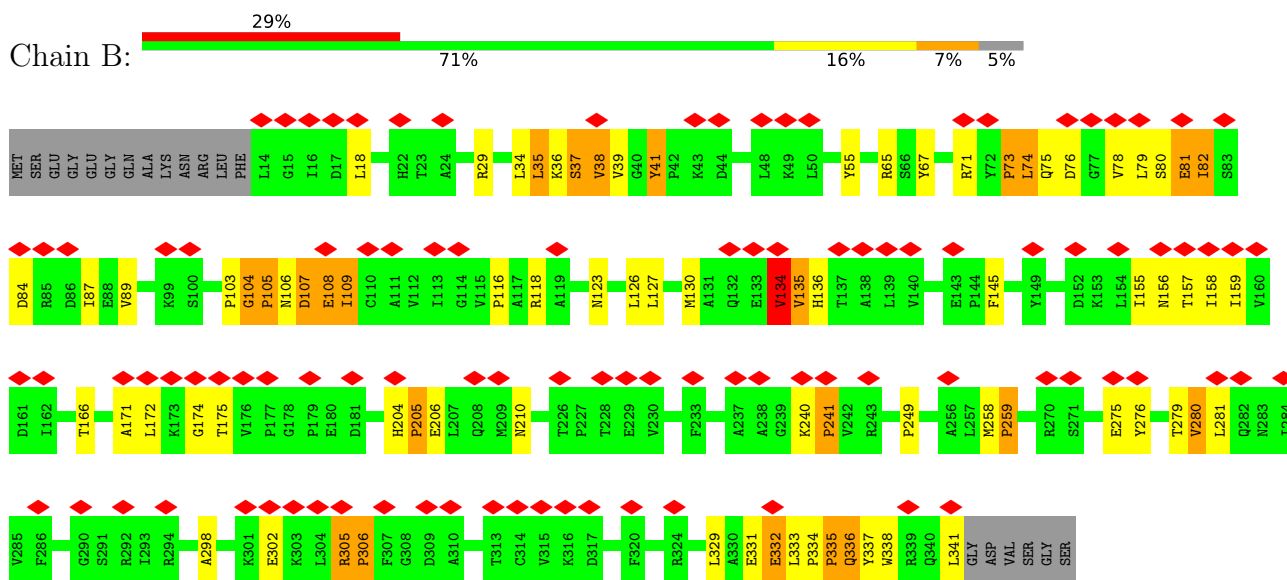
3 Residue-property plots

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-like ATPase

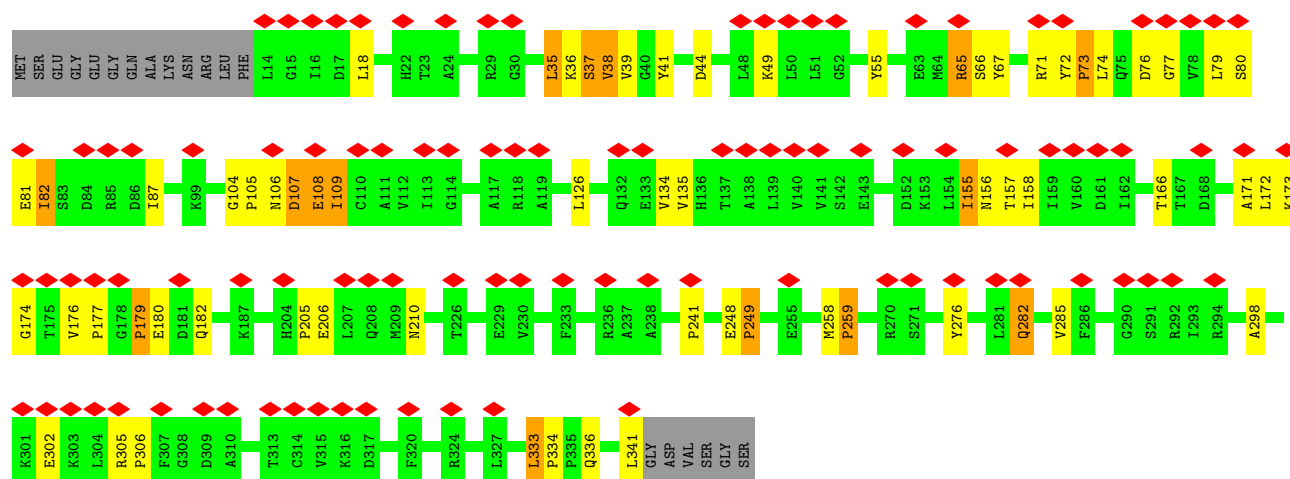


• Molecule 1: Actin-like ATPase



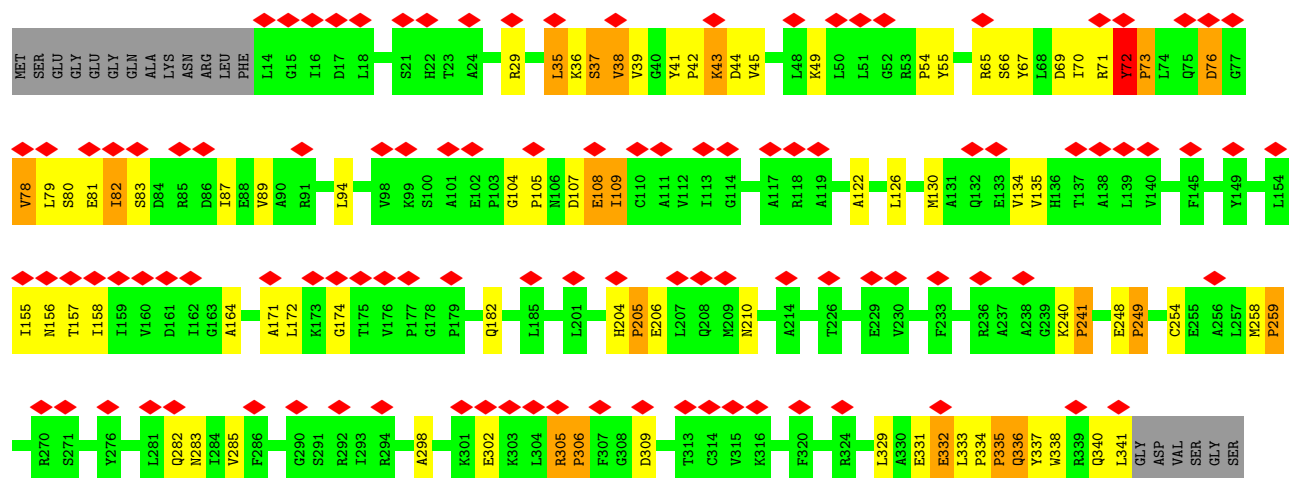
• Molecule 1: Actin-like ATPase

Chain C: 29% 76% 15% 5%



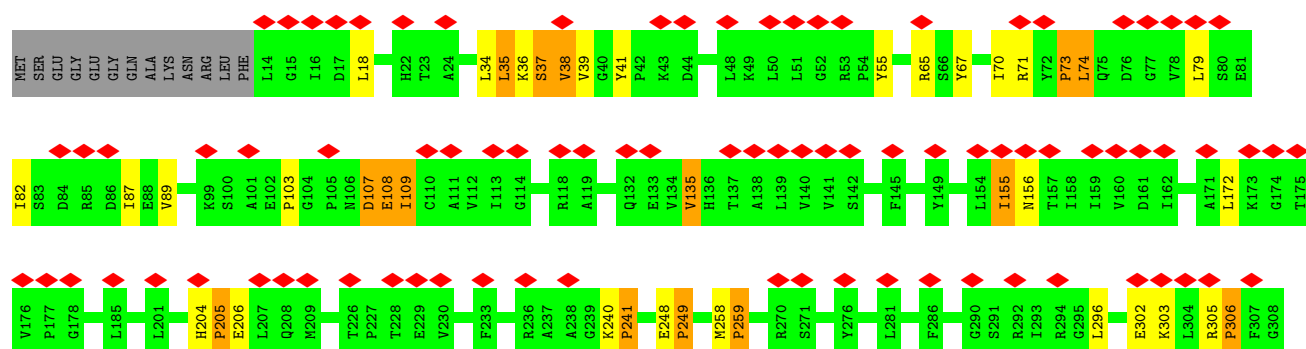
• Molecule 1: Actin-like ATPase

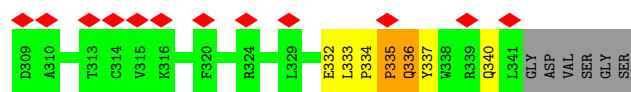
Chain D: 31% 71% 18% 5% 5%



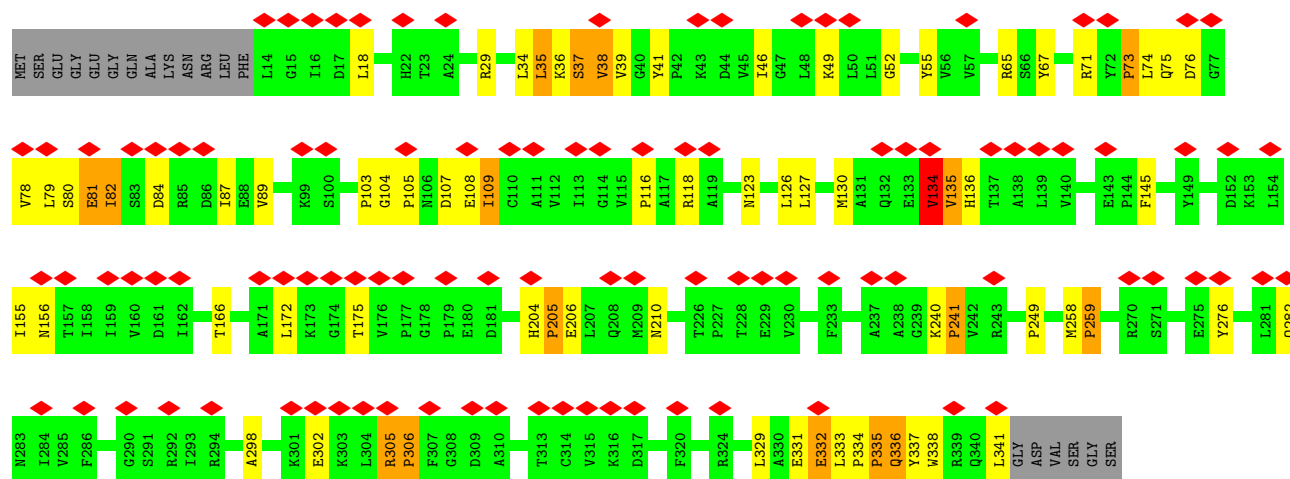
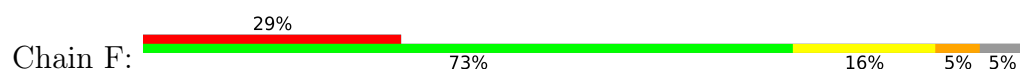
• Molecule 1: Actin-like ATPase

Chain E: 28% 81% 9% 5% 5%

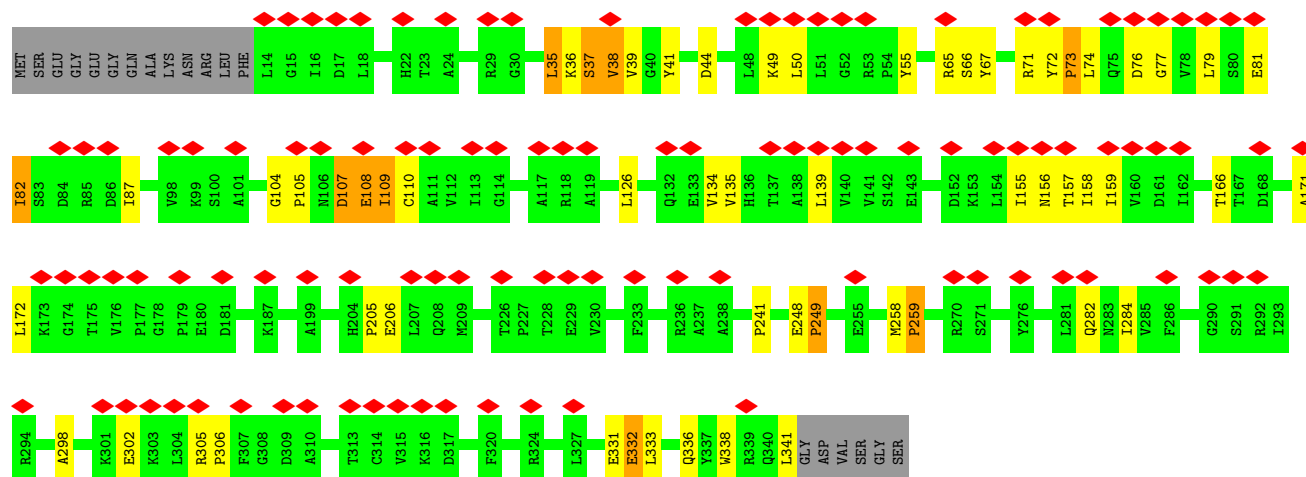
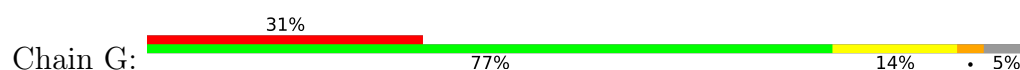




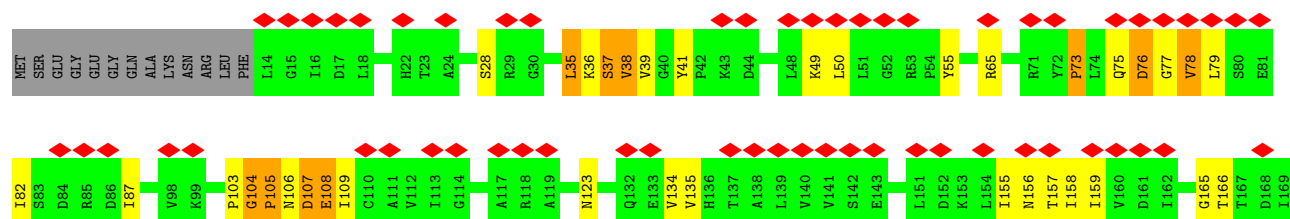
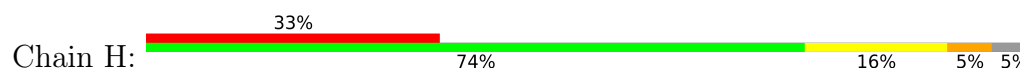
• Molecule 1: Actin-like ATPase

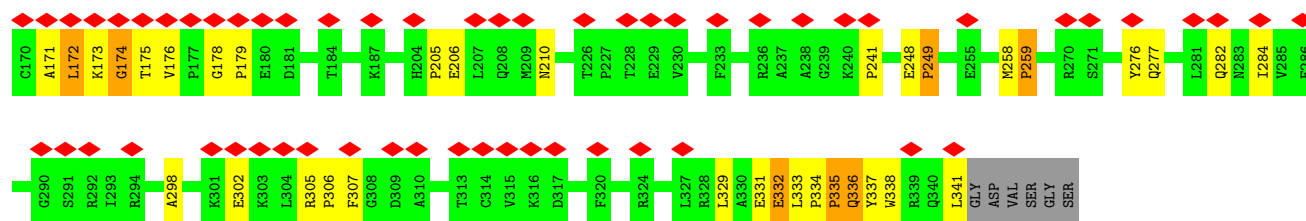


• Molecule 1: Actin-like ATPase

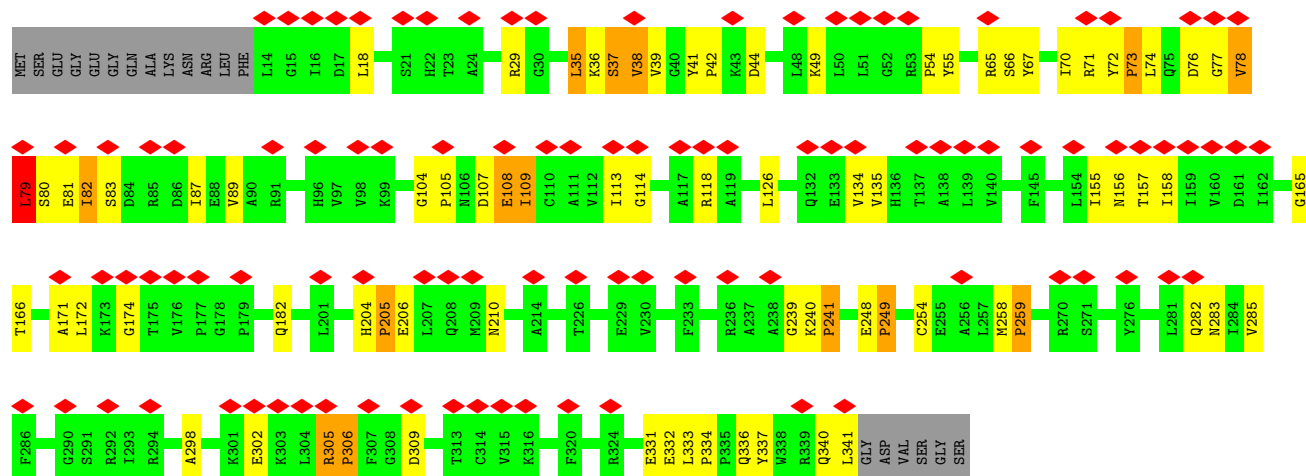


• Molecule 1: Actin-like ATPase

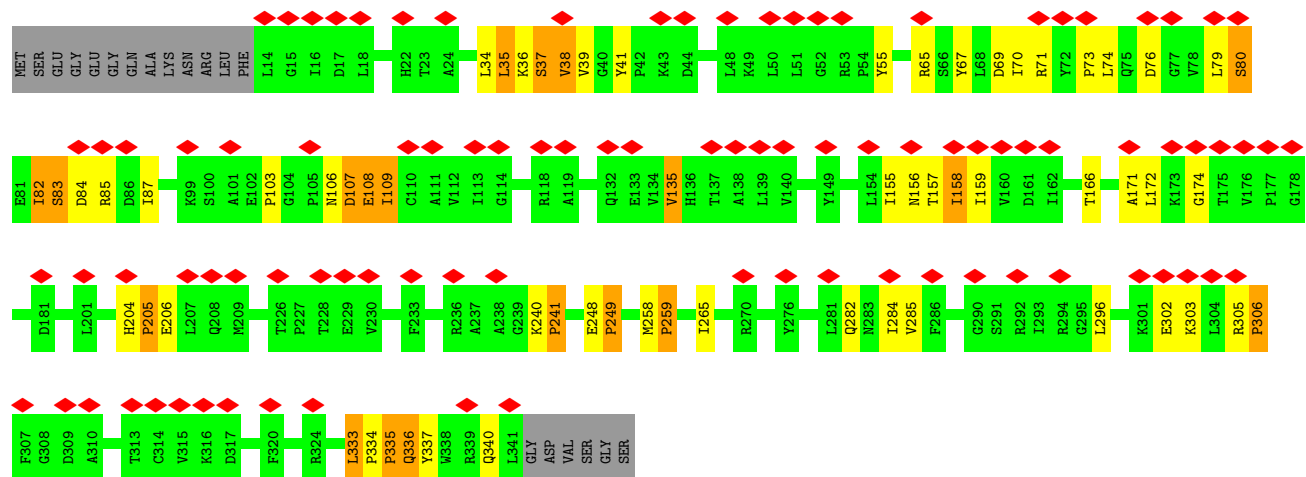
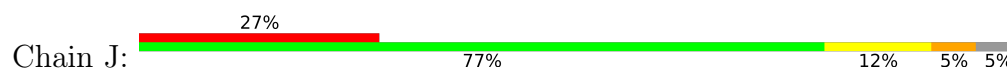




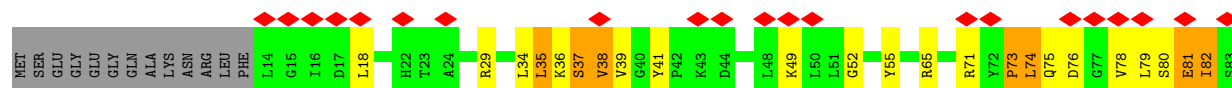
• Molecule 1: Actin-like ATPase

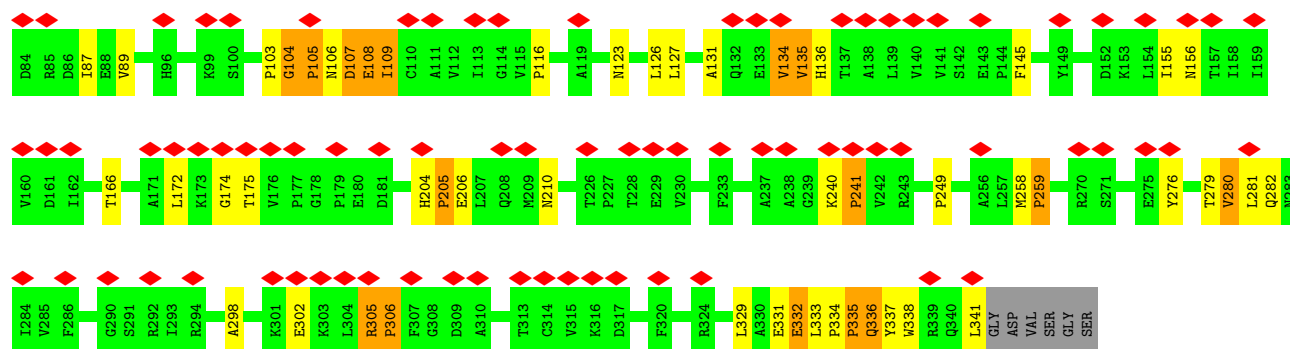


• Molecule 1: Actin-like ATPase

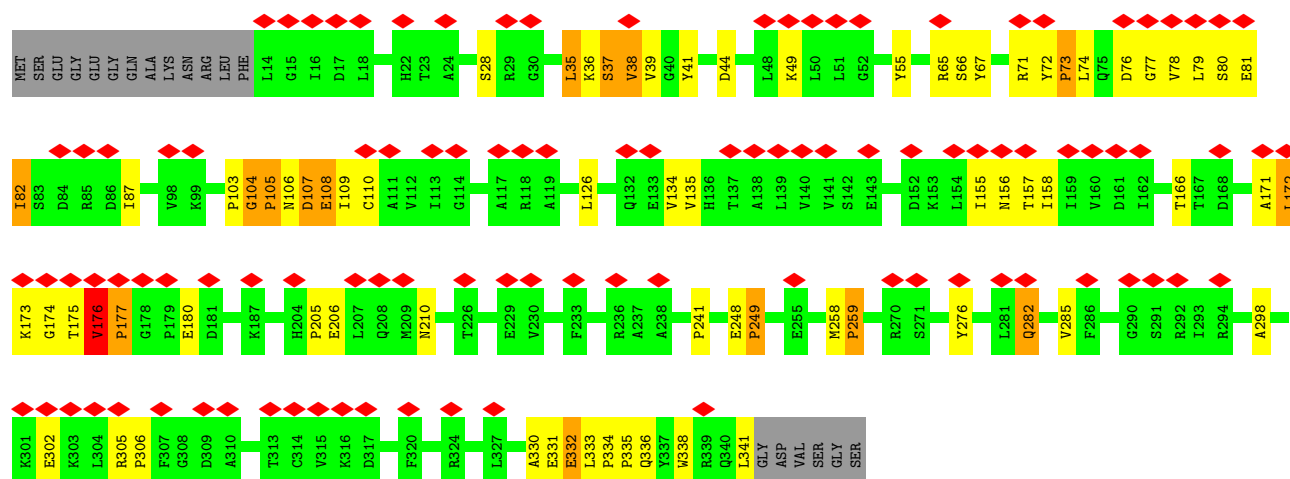


• Molecule 1: Actin-like ATPase

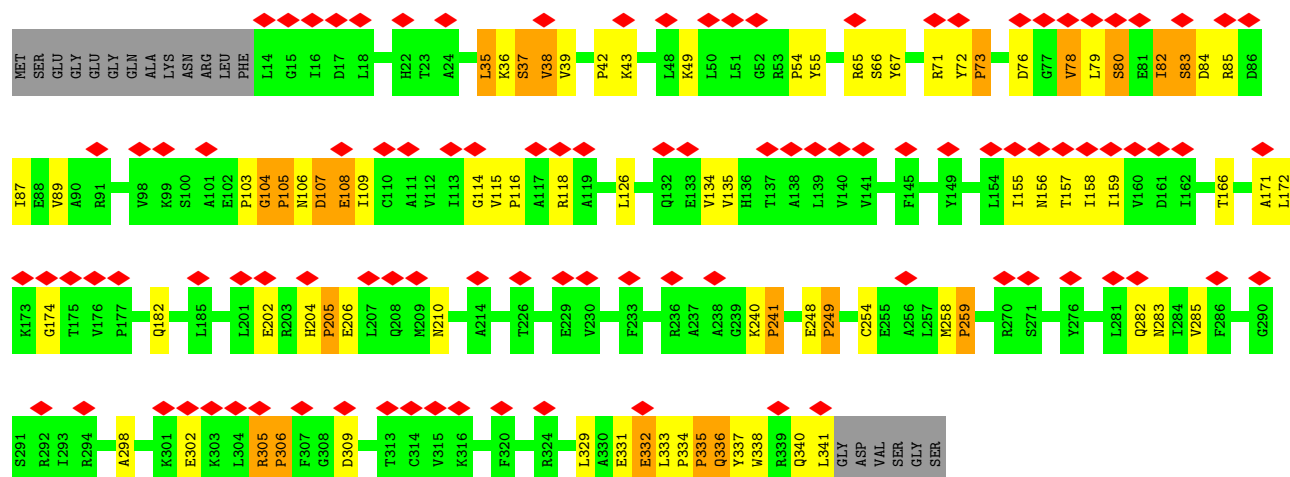
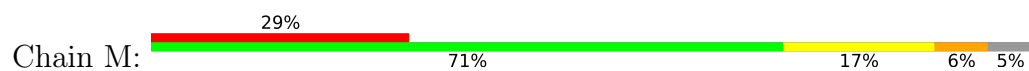




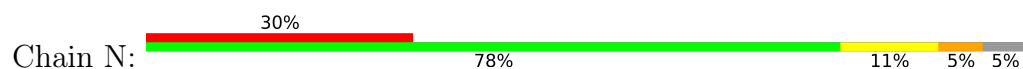
• Molecule 1: Actin-like ATPase

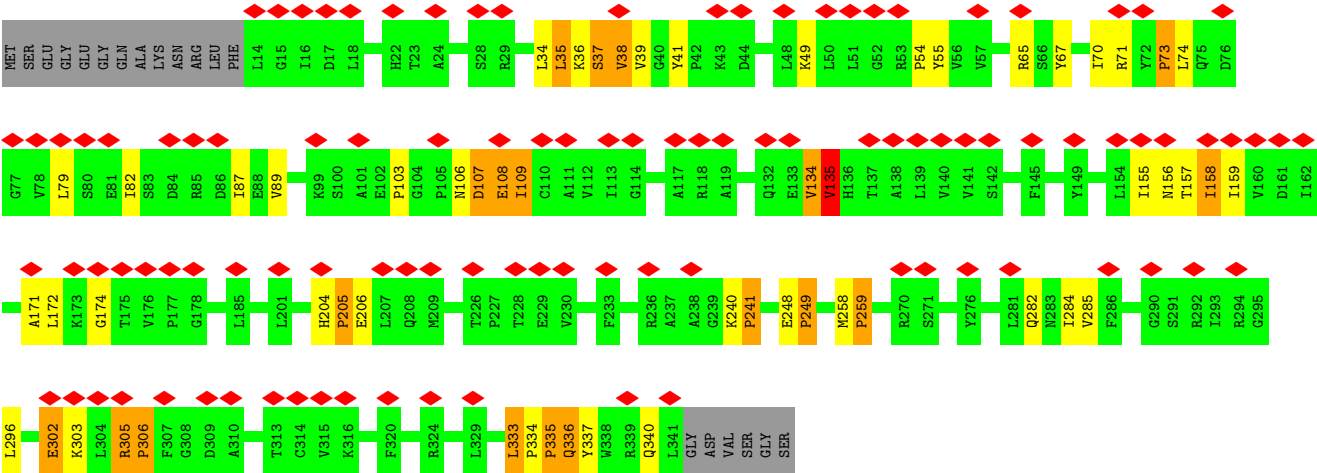


• Molecule 1: Actin-like ATPase



• Molecule 1: Actin-like ATPase





4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=24°, rise=53.8 Å, axial sym=C2	Depositor
Number of segments used	8129	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	11.791	Depositor
Minimum map value	-5.358	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.694	Depositor
Recommended contour level	5	Depositor
Map size (Å)	403.2, 403.2, 403.2	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.26, 1.26, 1.26	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.83	11/2550 (0.4%)	1.00	11/3462 (0.3%)
1	B	0.84	10/2550 (0.4%)	1.01	12/3462 (0.3%)
1	C	0.84	12/2550 (0.5%)	1.01	13/3462 (0.4%)
1	D	0.83	11/2550 (0.4%)	1.02	14/3462 (0.4%)
1	E	0.83	10/2550 (0.4%)	1.00	12/3462 (0.3%)
1	F	0.84	11/2550 (0.4%)	1.01	11/3462 (0.3%)
1	G	0.85	12/2550 (0.5%)	1.01	14/3462 (0.4%)
1	H	0.83	12/2550 (0.5%)	1.03	15/3462 (0.4%)
1	I	0.85	11/2550 (0.4%)	1.02	14/3462 (0.4%)
1	J	0.83	11/2550 (0.4%)	1.00	12/3462 (0.3%)
1	K	0.86	12/2550 (0.5%)	1.01	12/3462 (0.3%)
1	L	0.84	12/2550 (0.5%)	1.03	16/3462 (0.5%)
1	M	0.83	11/2550 (0.4%)	1.01	14/3462 (0.4%)
1	N	0.85	12/2550 (0.5%)	1.00	12/3462 (0.3%)
All	All	0.84	158/35700 (0.4%)	1.01	182/48468 (0.4%)

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	A	0	2
1	B	0	2
1	C	0	2
1	D	0	2
1	E	0	2
1	F	0	2
1	G	0	2
1	H	0	2
1	I	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	J	0	2
1	K	0	2
1	L	0	2
1	M	0	2
1	N	0	2
All	All	0	28

All (158) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	36	LYS	CA-C	8.92	1.63	1.52
1	K	36	LYS	CA-C	8.91	1.63	1.52
1	F	36	LYS	CA-C	8.88	1.63	1.52
1	A	36	LYS	CA-C	8.75	1.63	1.52
1	N	36	LYS	CA-C	8.72	1.63	1.52
1	J	36	LYS	CA-C	8.69	1.63	1.52
1	E	36	LYS	CA-C	8.68	1.63	1.52
1	I	36	LYS	CA-C	8.63	1.63	1.52
1	D	36	LYS	CA-C	8.59	1.63	1.52
1	M	36	LYS	CA-C	8.58	1.63	1.52
1	K	249	PRO	N-CD	8.58	1.59	1.47
1	B	249	PRO	N-CD	8.58	1.59	1.47
1	F	249	PRO	N-CD	8.56	1.59	1.47
1	C	205	PRO	N-CD	8.37	1.59	1.47
1	L	205	PRO	N-CD	8.36	1.59	1.47
1	D	205	PRO	N-CD	8.35	1.59	1.47
1	G	205	PRO	N-CD	8.34	1.59	1.47
1	H	205	PRO	N-CD	8.34	1.59	1.47
1	M	205	PRO	N-CD	8.30	1.59	1.47
1	I	205	PRO	N-CD	8.28	1.59	1.47
1	B	205	PRO	N-CD	8.25	1.59	1.47
1	F	205	PRO	N-CD	8.23	1.59	1.47
1	K	205	PRO	N-CD	8.23	1.59	1.47
1	F	37	SER	N-CA	8.21	1.55	1.46
1	B	37	SER	N-CA	8.16	1.55	1.46
1	K	37	SER	N-CA	8.16	1.55	1.46
1	L	36	LYS	CA-C	8.11	1.63	1.52
1	C	36	LYS	CA-C	8.11	1.63	1.52
1	G	36	LYS	CA-C	8.11	1.63	1.52
1	H	36	LYS	CA-C	8.03	1.63	1.52
1	I	37	SER	N-CA	8.02	1.55	1.46
1	M	37	SER	N-CA	8.02	1.55	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	N	205	PRO	N-CD	8.02	1.58	1.47
1	A	205	PRO	N-CD	7.97	1.58	1.47
1	J	205	PRO	N-CD	7.96	1.58	1.47
1	D	37	SER	N-CA	7.94	1.55	1.46
1	E	205	PRO	N-CD	7.93	1.58	1.47
1	K	134	VAL	CA-C	7.54	1.62	1.52
1	J	37	SER	N-CA	7.51	1.55	1.45
1	A	37	SER	N-CA	7.51	1.55	1.45
1	N	37	SER	N-CA	7.50	1.55	1.45
1	E	37	SER	N-CA	7.49	1.55	1.45
1	I	249	PRO	N-CD	7.41	1.58	1.47
1	M	249	PRO	N-CD	7.40	1.58	1.47
1	D	249	PRO	N-CD	7.37	1.58	1.47
1	N	249	PRO	N-CD	7.33	1.58	1.47
1	J	249	PRO	N-CD	7.31	1.57	1.47
1	C	249	PRO	N-CD	7.30	1.57	1.47
1	H	249	PRO	N-CD	7.28	1.57	1.47
1	A	249	PRO	N-CD	7.28	1.57	1.47
1	E	249	PRO	N-CD	7.27	1.57	1.47
1	G	249	PRO	N-CD	7.27	1.57	1.47
1	L	249	PRO	N-CD	7.24	1.57	1.47
1	A	37	SER	CA-C	7.24	1.62	1.53
1	M	37	SER	CA-C	7.21	1.62	1.53
1	J	37	SER	CA-C	7.20	1.62	1.53
1	D	37	SER	CA-C	7.19	1.62	1.53
1	I	37	SER	CA-C	7.18	1.62	1.53
1	N	37	SER	CA-C	7.17	1.62	1.53
1	E	37	SER	CA-C	7.15	1.62	1.53
1	B	37	SER	CA-C	7.08	1.62	1.53
1	K	37	SER	CA-C	7.06	1.62	1.53
1	F	37	SER	CA-C	7.01	1.62	1.53
1	H	37	SER	CA-C	6.97	1.62	1.53
1	C	37	SER	CA-C	6.95	1.62	1.53
1	L	37	SER	CA-C	6.95	1.62	1.53
1	B	206	GLU	C-N	6.94	1.42	1.33
1	G	37	SER	CA-C	6.90	1.62	1.53
1	F	206	GLU	C-N	6.89	1.42	1.33
1	K	206	GLU	C-N	6.89	1.42	1.33
1	G	37	SER	N-CA	6.88	1.55	1.45
1	C	37	SER	N-CA	6.86	1.55	1.45
1	D	206	GLU	C-N	6.86	1.42	1.33
1	I	206	GLU	C-N	6.85	1.42	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	37	SER	N-CA	6.85	1.55	1.45
1	M	206	GLU	C-N	6.82	1.42	1.33
1	L	37	SER	N-CA	6.81	1.55	1.45
1	H	206	GLU	C-N	6.78	1.42	1.33
1	N	134	VAL	CA-C	6.78	1.62	1.52
1	C	206	GLU	C-N	6.74	1.42	1.33
1	G	206	GLU	C-N	6.72	1.42	1.33
1	L	206	GLU	C-N	6.71	1.42	1.33
1	A	206	GLU	C-N	6.63	1.42	1.33
1	J	206	GLU	C-N	6.62	1.42	1.33
1	N	206	GLU	C-N	6.58	1.42	1.33
1	E	206	GLU	C-N	6.57	1.42	1.33
1	F	36	LYS	N-CA	6.50	1.53	1.45
1	M	134	VAL	CA-C	6.48	1.62	1.52
1	I	134	VAL	CA-C	6.46	1.62	1.52
1	K	36	LYS	N-CA	6.46	1.53	1.45
1	B	36	LYS	N-CA	6.45	1.53	1.45
1	D	134	VAL	CA-C	6.44	1.62	1.52
1	C	134	VAL	CA-C	6.42	1.62	1.52
1	L	134	VAL	CA-C	6.41	1.62	1.52
1	G	134	VAL	CA-C	6.40	1.62	1.52
1	H	134	VAL	CA-C	6.36	1.62	1.52
1	L	36	LYS	N-CA	6.25	1.53	1.45
1	G	36	LYS	N-CA	6.23	1.53	1.45
1	B	259	PRO	N-CD	6.21	1.56	1.47
1	K	259	PRO	N-CD	6.21	1.56	1.47
1	F	259	PRO	N-CD	6.20	1.56	1.47
1	A	259	PRO	N-CD	6.20	1.56	1.47
1	C	36	LYS	N-CA	6.19	1.53	1.45
1	H	36	LYS	N-CA	6.18	1.53	1.45
1	J	259	PRO	N-CD	6.17	1.56	1.47
1	E	259	PRO	N-CD	6.17	1.56	1.47
1	D	259	PRO	N-CD	6.16	1.56	1.47
1	G	259	PRO	N-CD	6.16	1.56	1.47
1	H	259	PRO	N-CD	6.15	1.56	1.47
1	C	259	PRO	N-CD	6.13	1.56	1.47
1	N	259	PRO	N-CD	6.13	1.56	1.47
1	I	259	PRO	N-CD	6.12	1.56	1.47
1	L	259	PRO	N-CD	6.11	1.56	1.47
1	M	259	PRO	N-CD	6.10	1.56	1.47
1	M	36	LYS	N-CA	6.05	1.53	1.45
1	I	36	LYS	N-CA	6.01	1.53	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	36	LYS	N-CA	6.00	1.53	1.45
1	E	36	LYS	N-CA	5.97	1.53	1.45
1	A	36	LYS	N-CA	5.96	1.53	1.45
1	J	36	LYS	N-CA	5.95	1.53	1.45
1	N	36	LYS	N-CA	5.90	1.53	1.45
1	G	241	PRO	N-CD	5.59	1.55	1.47
1	C	241	PRO	N-CD	5.59	1.55	1.47
1	H	241	PRO	N-CD	5.59	1.55	1.47
1	L	241	PRO	N-CD	5.58	1.55	1.47
1	D	306	PRO	N-CD	5.36	1.55	1.47
1	I	306	PRO	N-CD	5.30	1.55	1.47
1	M	306	PRO	N-CD	5.28	1.55	1.47
1	N	306	PRO	N-CD	5.20	1.55	1.47
1	J	306	PRO	N-CD	5.17	1.54	1.47
1	E	306	PRO	N-CD	5.16	1.54	1.47
1	K	306	PRO	N-CD	5.16	1.54	1.47
1	A	306	PRO	N-CD	5.15	1.54	1.47
1	F	306	PRO	N-CD	5.13	1.54	1.47
1	B	306	PRO	N-CD	5.13	1.54	1.47
1	N	34	LEU	C-N	-5.09	1.26	1.33
1	E	34	LEU	C-N	-5.09	1.26	1.33
1	L	282	GLN	C-N	5.09	1.40	1.33
1	G	282	GLN	C-N	5.08	1.40	1.33
1	A	282	GLN	C-N	5.07	1.40	1.33
1	A	34	LEU	C-N	-5.07	1.26	1.33
1	C	282	GLN	C-N	5.06	1.40	1.33
1	D	282	GLN	C-N	5.06	1.40	1.33
1	J	34	LEU	C-N	-5.06	1.26	1.33
1	L	306	PRO	N-CD	5.06	1.54	1.47
1	H	306	PRO	N-CD	5.06	1.54	1.47
1	I	282	GLN	C-N	5.06	1.40	1.33
1	M	282	GLN	C-N	5.04	1.40	1.33
1	K	34	LEU	C-N	-5.04	1.26	1.33
1	K	282	GLN	C-N	5.03	1.40	1.33
1	J	282	GLN	C-N	5.03	1.40	1.33
1	F	34	LEU	C-N	-5.03	1.26	1.33
1	H	282	GLN	C-N	5.03	1.40	1.33
1	C	306	PRO	N-CD	5.02	1.54	1.47
1	G	306	PRO	N-CD	5.02	1.54	1.47
1	B	34	LEU	C-N	-5.02	1.26	1.33
1	F	282	GLN	C-N	5.02	1.40	1.33
1	N	282	GLN	C-N	5.01	1.40	1.33

All (182) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	72	TYR	C-N-CD	-10.50	81.95	125.00
1	H	178	GLY	C-N-CD	-10.48	82.02	125.00
1	L	176	VAL	C-N-CD	-9.95	84.20	125.00
1	E	37	SER	N-CA-C	9.90	124.02	110.35
1	J	37	SER	N-CA-C	9.86	123.95	110.35
1	A	37	SER	N-CA-C	9.85	123.94	110.35
1	N	37	SER	N-CA-C	9.84	123.93	110.35
1	G	37	SER	N-CA-C	9.73	124.13	109.63
1	L	37	SER	N-CA-C	9.73	124.12	109.63
1	C	37	SER	N-CA-C	9.71	124.10	109.63
1	H	37	SER	N-CA-C	9.71	124.09	109.63
1	K	104	GLY	C-N-CD	-9.56	85.80	125.00
1	B	104	GLY	C-N-CD	-9.44	86.31	125.00
1	D	37	SER	N-CA-C	9.12	124.02	109.79
1	I	37	SER	N-CA-C	9.11	124.00	109.79
1	M	37	SER	N-CA-C	9.11	124.00	109.79
1	B	37	SER	N-CA-C	9.11	124.00	109.79
1	K	37	SER	N-CA-C	9.09	123.97	109.79
1	F	37	SER	N-CA-C	9.08	123.96	109.79
1	E	336	GLN	N-CA-C	-8.35	102.68	113.12
1	H	104	GLY	C-N-CD	-7.99	92.24	125.00
1	N	336	GLN	N-CA-C	-7.98	102.66	111.36
1	F	336	GLN	N-CA-C	-7.95	102.69	111.36
1	J	336	GLN	N-CA-C	-7.95	102.69	111.36
1	K	336	GLN	N-CA-C	-7.93	102.72	111.36
1	H	336	GLN	N-CA-C	-7.92	102.72	111.36
1	I	72	TYR	C-N-CD	-7.92	92.52	125.00
1	M	336	GLN	N-CA-C	-7.92	102.73	111.36
1	I	336	GLN	N-CA-C	-7.92	102.73	111.36
1	L	104	GLY	C-N-CD	-7.92	92.54	125.00
1	B	336	GLN	N-CA-C	-7.91	102.74	111.36
1	D	336	GLN	N-CA-C	-7.90	102.75	111.36
1	L	336	GLN	N-CA-C	-7.90	102.75	111.36
1	C	336	GLN	N-CA-C	-7.89	102.76	111.36
1	G	336	GLN	N-CA-C	-7.88	102.77	111.36
1	I	41	TYR	O-C-N	-7.68	116.48	121.85
1	D	41	TYR	O-C-N	-7.67	116.48	121.85
1	M	104	GLY	C-N-CD	-7.64	93.67	125.00
1	G	41	TYR	O-C-N	-7.57	116.55	121.85
1	C	41	TYR	O-C-N	-7.54	116.57	121.85
1	L	41	TYR	O-C-N	-7.53	116.58	121.85
1	H	41	TYR	O-C-N	-7.52	116.58	121.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	35	LEU	O-C-N	-7.26	114.93	123.06
1	H	35	LEU	O-C-N	-7.26	114.93	123.06
1	D	36	LYS	N-CA-C	7.25	120.91	109.81
1	L	35	LEU	O-C-N	-7.25	114.93	123.06
1	G	35	LEU	O-C-N	-7.25	114.94	123.06
1	M	36	LYS	N-CA-C	7.25	120.90	109.81
1	I	36	LYS	N-CA-C	7.24	120.89	109.81
1	A	36	LYS	N-CA-C	7.23	120.88	109.81
1	J	36	LYS	N-CA-C	7.23	120.88	109.81
1	N	36	LYS	N-CA-C	7.23	120.87	109.81
1	E	36	LYS	N-CA-C	7.22	120.86	109.81
1	I	35	LEU	O-C-N	-7.19	114.89	122.94
1	M	35	LEU	O-C-N	-7.19	114.89	122.94
1	D	35	LEU	O-C-N	-7.19	114.89	122.94
1	D	306	PRO	CA-N-CD	-7.01	102.19	112.00
1	I	306	PRO	CA-N-CD	-7.00	102.19	112.00
1	K	36	LYS	N-CA-C	6.99	120.90	109.85
1	B	36	LYS	N-CA-C	6.98	120.88	109.85
1	M	306	PRO	CA-N-CD	-6.98	102.23	112.00
1	F	36	LYS	N-CA-C	6.97	120.86	109.85
1	N	306	PRO	CA-N-CD	-6.96	102.26	112.00
1	J	306	PRO	CA-N-CD	-6.95	102.27	112.00
1	E	306	PRO	CA-N-CD	-6.95	102.27	112.00
1	F	306	PRO	CA-N-CD	-6.93	102.30	112.00
1	A	306	PRO	CA-N-CD	-6.93	102.30	112.00
1	K	306	PRO	CA-N-CD	-6.91	102.33	112.00
1	B	306	PRO	CA-N-CD	-6.89	102.36	112.00
1	L	241	PRO	CA-C-N	-6.85	114.21	123.12
1	L	241	PRO	C-N-CA	-6.85	114.21	123.12
1	G	241	PRO	CA-C-N	-6.85	114.22	123.12
1	G	241	PRO	C-N-CA	-6.85	114.22	123.12
1	G	306	PRO	CA-N-CD	-6.84	102.42	112.00
1	C	241	PRO	CA-C-N	-6.84	114.23	123.12
1	C	241	PRO	C-N-CA	-6.84	114.23	123.12
1	L	306	PRO	CA-N-CD	-6.83	102.44	112.00
1	C	306	PRO	CA-N-CD	-6.83	102.44	112.00
1	H	306	PRO	CA-N-CD	-6.82	102.45	112.00
1	H	241	PRO	CA-C-N	-6.81	114.27	123.12
1	H	241	PRO	C-N-CA	-6.81	114.27	123.12
1	J	41	TYR	O-C-N	-6.77	116.55	121.83
1	N	41	TYR	O-C-N	-6.77	116.55	121.83
1	A	41	TYR	O-C-N	-6.73	116.58	121.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	41	TYR	O-C-N	-6.71	116.59	121.83
1	G	72	TYR	C-N-CD	-6.69	97.56	125.00
1	H	36	LYS	N-CA-C	6.67	120.92	110.32
1	L	36	LYS	N-CA-C	6.65	120.90	110.32
1	C	36	LYS	N-CA-C	6.64	120.89	110.32
1	G	36	LYS	N-CA-C	6.63	120.86	110.32
1	D	65	ARG	N-CA-C	6.57	120.40	112.38
1	M	65	ARG	N-CA-C	6.57	120.40	112.38
1	I	65	ARG	N-CA-C	6.56	120.39	112.38
1	B	65	ARG	N-CA-C	6.55	120.37	112.38
1	L	65	ARG	N-CA-C	6.55	120.37	112.38
1	K	65	ARG	N-CA-C	6.55	120.37	112.38
1	F	65	ARG	N-CA-C	6.54	120.35	112.38
1	C	65	ARG	N-CA-C	6.53	120.35	112.38
1	H	65	ARG	N-CA-C	6.52	120.34	112.38
1	G	65	ARG	N-CA-C	6.50	120.31	112.38
1	A	65	ARG	N-CA-C	6.46	120.42	112.54
1	J	65	ARG	N-CA-C	6.41	120.36	112.54
1	N	65	ARG	N-CA-C	6.41	120.36	112.54
1	E	65	ARG	N-CA-C	6.40	120.34	112.54
1	L	109	ILE	N-CA-C	6.39	117.06	107.80
1	M	72	TYR	C-N-CD	-6.36	98.91	125.00
1	H	109	ILE	N-CA-C	6.36	117.02	107.80
1	M	109	ILE	N-CA-C	6.33	117.03	108.17
1	B	109	ILE	N-CA-C	6.19	117.03	107.99
1	K	109	ILE	N-CA-C	6.18	117.02	107.99
1	A	109	ILE	N-CA-C	6.16	116.99	107.99
1	E	109	ILE	N-CA-C	6.16	116.99	107.99
1	J	109	ILE	N-CA-C	6.16	116.99	107.99
1	N	109	ILE	N-CA-C	6.16	116.98	107.99
1	I	109	ILE	N-CA-C	6.16	117.02	108.89
1	D	109	ILE	N-CA-C	6.14	116.99	108.89
1	F	109	ILE	N-CA-C	5.97	116.99	108.93
1	I	241	PRO	CA-C-N	-5.90	114.21	122.71
1	I	241	PRO	C-N-CA	-5.90	114.21	122.71
1	D	241	PRO	CA-C-N	-5.90	114.22	122.71
1	D	241	PRO	C-N-CA	-5.90	114.22	122.71
1	M	241	PRO	CA-C-N	-5.88	114.25	122.71
1	M	241	PRO	C-N-CA	-5.88	114.25	122.71
1	C	72	TYR	C-N-CD	-5.87	100.94	125.00
1	L	72	TYR	C-N-CD	-5.83	101.11	125.00
1	G	109	ILE	N-CA-C	5.76	117.05	108.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	39	VAL	N-CA-C	-5.72	99.98	108.45
1	K	41	TYR	O-C-N	-5.71	116.51	121.71
1	B	41	TYR	O-C-N	-5.71	116.52	121.71
1	K	39	VAL	N-CA-C	-5.70	100.01	108.45
1	B	39	VAL	N-CA-C	-5.69	100.03	108.45
1	F	41	TYR	O-C-N	-5.67	116.55	121.71
1	N	39	VAL	N-CA-C	-5.67	99.96	108.12
1	G	39	VAL	N-CA-C	-5.67	99.96	108.12
1	L	39	VAL	N-CA-C	-5.66	99.97	108.12
1	H	39	VAL	N-CA-C	-5.66	99.97	108.12
1	C	39	VAL	N-CA-C	-5.65	99.99	108.12
1	A	39	VAL	N-CA-C	-5.65	99.99	108.12
1	J	39	VAL	N-CA-C	-5.63	100.02	108.12
1	E	39	VAL	N-CA-C	-5.62	100.02	108.12
1	I	39	VAL	N-CA-C	-5.58	100.03	108.17
1	D	39	VAL	N-CA-C	-5.57	100.03	108.17
1	M	39	VAL	N-CA-C	-5.57	100.03	108.17
1	J	35	LEU	O-C-N	-5.50	114.92	122.23
1	A	35	LEU	O-C-N	-5.49	114.93	122.23
1	E	35	LEU	O-C-N	-5.49	114.93	122.23
1	N	35	LEU	O-C-N	-5.49	114.93	122.23
1	B	35	LEU	O-C-N	-5.47	114.96	122.23
1	K	35	LEU	O-C-N	-5.44	115.00	122.23
1	F	35	LEU	O-C-N	-5.43	115.01	122.23
1	A	340	GLN	N-CA-C	5.22	116.97	111.28
1	E	340	GLN	N-CA-C	5.22	116.97	111.28
1	J	340	GLN	N-CA-C	5.18	116.93	111.28
1	N	340	GLN	N-CA-C	5.15	116.90	111.28
1	N	241	PRO	CA-C-N	-5.14	114.18	122.25
1	N	241	PRO	C-N-CA	-5.14	114.18	122.25
1	E	241	PRO	CA-C-N	-5.14	114.18	122.25
1	E	241	PRO	C-N-CA	-5.14	114.18	122.25
1	A	241	PRO	CA-C-N	-5.13	114.19	122.25
1	A	241	PRO	C-N-CA	-5.13	114.19	122.25
1	J	241	PRO	CA-C-N	-5.12	114.22	122.25
1	J	241	PRO	C-N-CA	-5.12	114.22	122.25
1	B	241	PRO	CA-C-N	-5.11	114.23	122.25
1	B	241	PRO	C-N-CA	-5.11	114.23	122.25
1	K	241	PRO	CA-C-N	-5.11	114.23	122.25
1	K	241	PRO	C-N-CA	-5.11	114.23	122.25
1	F	241	PRO	CA-C-N	-5.10	114.24	122.25
1	F	241	PRO	C-N-CA	-5.10	114.24	122.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	340	GLN	N-CA-C	5.08	116.90	111.36
1	D	254	CYS	N-CA-CB	-5.07	102.14	110.40
1	I	254	CYS	N-CA-CB	-5.07	102.14	110.40
1	M	254	CYS	N-CA-CB	-5.07	102.14	110.40
1	M	340	GLN	N-CA-C	5.06	116.88	111.36
1	I	340	GLN	N-CA-C	5.06	116.87	111.36
1	C	206	GLU	CA-C-N	-5.04	113.56	120.71
1	C	206	GLU	C-N-CA	-5.04	113.56	120.71
1	L	206	GLU	CA-C-N	-5.03	113.56	120.71
1	L	206	GLU	C-N-CA	-5.03	113.56	120.71
1	G	206	GLU	CA-C-N	-5.03	113.57	120.71
1	G	206	GLU	C-N-CA	-5.03	113.57	120.71
1	H	206	GLU	CA-C-N	-5.02	113.58	120.71
1	H	206	GLU	C-N-CA	-5.02	113.58	120.71

There are no chirality outliers.

All (28) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	305	ARG	Peptide
1	A	35	LEU	Mainchain
1	B	305	ARG	Peptide
1	B	35	LEU	Mainchain
1	C	305	ARG	Peptide
1	C	35	LEU	Mainchain
1	D	305	ARG	Peptide
1	D	35	LEU	Mainchain
1	E	305	ARG	Peptide
1	E	35	LEU	Mainchain
1	F	305	ARG	Peptide
1	F	35	LEU	Mainchain
1	G	305	ARG	Peptide
1	G	35	LEU	Mainchain
1	H	305	ARG	Peptide
1	H	35	LEU	Mainchain
1	I	305	ARG	Peptide
1	I	35	LEU	Mainchain
1	J	305	ARG	Peptide
1	J	35	LEU	Mainchain
1	K	305	ARG	Peptide
1	K	35	LEU	Mainchain
1	L	305	ARG	Peptide

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Mol	Chain	Res	Type	Group
1	L	35	LEU	Mainchain
1	M	305	ARG	Peptide
1	M	35	LEU	Mainchain
1	N	305	ARG	Peptide
1	N	35	LEU	Mainchain

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	2505	0	2553	39	0
1	B	2505	0	2551	120	0
1	C	2505	0	2553	91	0
1	D	2505	0	2552	104	0
1	E	2505	0	2553	46	0
1	F	2505	0	2552	93	0
1	G	2505	0	2553	65	0
1	H	2505	0	2553	94	0
1	I	2505	0	2553	107	0
1	J	2505	0	2553	77	0
1	K	2505	0	2553	97	0
1	L	2505	0	2553	125	0
1	M	2505	0	2552	141	0
1	N	2505	0	2553	64	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	1	0	0	0	0
2	L	1	0	0	0	0
2	M	1	0	0	0	0
2	N	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	27	0	12	0	0
3	B	27	0	12	0	0
3	C	27	0	12	0	0
3	D	27	0	12	0	0
3	E	27	0	12	0	0
3	F	27	0	12	0	0
3	G	27	0	12	0	0
3	H	27	0	12	0	0
3	I	27	0	12	2	0
3	J	27	0	12	0	0
3	K	27	0	12	0	0
3	L	27	0	12	0	0
3	M	27	0	12	0	0
3	N	27	0	12	0	0
All	All	35462	0	35905	1172	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 16.

All (1172) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:333:LEU:HD12	1:H:338:TRP:NE1	1.29	1.40
1:L:176:VAL:HG12	1:L:177:PRO:CD	1.50	1.40
1:L:176:VAL:CG1	1:L:177:PRO:HD2	1.51	1.40
1:L:155:ILE:CG2	1:M:67:TYR:OH	1.73	1.37
1:G:333:LEU:HD12	1:G:338:TRP:NE1	1.30	1.37
1:N:156:ASN:ND2	1:N:172:LEU:O	1.59	1.33
1:H:329:LEU:O	1:H:333:LEU:CD2	1.73	1.32
1:J:156:ASN:ND2	1:J:172:LEU:O	1.60	1.32
1:B:71:ARG:HD3	1:B:84:ASP:OD1	1.33	1.29
1:I:73:PRO:CG	1:I:89:VAL:HG11	1.63	1.28
1:J:107:ASP:O	1:J:109:ILE:HG12	1.34	1.28
1:K:134:VAL:O	1:K:135:VAL:HG12	1.31	1.27
1:L:155:ILE:CB	1:M:67:TYR:OH	1.81	1.27
1:E:107:ASP:O	1:E:109:ILE:HG12	1.35	1.27
1:H:276:TYR:OH	1:I:66:SER:HB3	1.24	1.26
1:L:110:CYS:SG	1:L:338:TRP:CZ3	2.27	1.26
1:C:176:VAL:HB	1:D:44:ASP:OD2	1.28	1.25
1:A:107:ASP:O	1:A:109:ILE:HG12	1.36	1.25
1:L:155:ILE:HG21	1:M:67:TYR:OH	1.20	1.25

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:107:ASP:O	1:N:109:ILE:HG12	1.33	1.25
1:H:333:LEU:CD1	1:H:338:TRP:HE1	1.49	1.24
1:M:82:ILE:O	1:M:84:ASP:N	1.70	1.22
1:C:156:ASN:ND2	1:C:172:LEU:O	1.72	1.22
1:B:175:THR:HG22	1:C:44:ASP:OD1	1.40	1.22
1:H:155:ILE:HB	1:I:67:TYR:OH	1.38	1.20
1:H:333:LEU:HB3	1:H:338:TRP:CZ2	1.78	1.19
1:M:80:SER:O	1:M:126:LEU:HD22	1.40	1.19
1:I:18:LEU:CD1	1:I:78:VAL:HA	1.73	1.19
1:L:333:LEU:HD12	1:L:333:LEU:O	1.41	1.19
1:L:276:TYR:OH	1:M:66:SER:HB2	1.39	1.19
1:D:43:LYS:HD2	1:D:69:ASP:HB2	1.23	1.18
1:G:110:CYS:SG	1:G:338:TRP:CZ3	2.37	1.17
1:C:177:PRO:HG3	1:C:180:GLU:OE1	1.45	1.17
1:F:333:LEU:HB3	1:F:338:TRP:NE1	1.59	1.17
1:H:76:ASP:HB3	1:H:165:GLY:HA2	1.17	1.17
1:M:82:ILE:HG23	1:M:89:VAL:HB	1.27	1.16
1:B:333:LEU:HB3	1:B:338:TRP:NE1	1.60	1.15
1:I:71:ARG:O	1:I:73:PRO:HD3	1.45	1.14
1:B:29:ARG:HH12	1:B:105:PRO:HG3	0.98	1.14
1:B:71:ARG:CD	1:B:84:ASP:OD1	1.96	1.14
1:D:73:PRO:HB3	1:D:89:VAL:HG11	1.30	1.14
1:H:174:GLY:HA2	1:I:44:ASP:OD2	1.45	1.13
1:B:130:MET:O	1:B:134:VAL:HG23	1.46	1.13
1:L:155:ILE:CG1	1:M:67:TYR:OH	1.96	1.13
1:L:173:LYS:HG2	1:L:180:GLU:CG	1.79	1.13
1:K:333:LEU:HB3	1:K:338:TRP:NE1	1.60	1.13
1:J:334:PRO:O	1:J:336:GLN:N	1.82	1.12
1:F:130:MET:O	1:F:134:VAL:HG23	1.45	1.12
1:J:74:LEU:HD23	1:J:79:LEU:CA	1.78	1.12
1:D:333:LEU:HB3	1:D:338:TRP:NE1	1.64	1.12
1:F:78:VAL:HB	1:F:116:PRO:HG3	1.16	1.12
1:L:155:ILE:HG12	1:M:67:TYR:OH	1.49	1.11
1:N:134:VAL:O	1:N:135:VAL:HG22	1.47	1.11
1:B:156:ASN:ND2	1:B:172:LEU:O	1.83	1.11
1:D:78:VAL:HG22	1:D:79:LEU:H	1.02	1.11
1:G:333:LEU:CD1	1:G:338:TRP:HE1	1.62	1.11
1:K:29:ARG:HH12	1:K:105:PRO:HG3	1.00	1.11
1:N:334:PRO:O	1:N:336:GLN:N	1.82	1.11
1:M:333:LEU:HB3	1:M:338:TRP:NE1	1.66	1.10
1:H:76:ASP:HB3	1:H:165:GLY:CA	1.80	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:173:LYS:HG2	1:H:174:GLY:H	1.07	1.10
1:C:177:PRO:HG2	1:C:180:GLU:HB2	1.17	1.09
1:B:29:ARG:NH1	1:B:105:PRO:HG3	1.67	1.09
1:L:173:LYS:HG3	1:L:174:GLY:H	0.97	1.09
1:C:276:TYR:OH	1:D:66:SER:HB2	1.53	1.08
1:I:78:VAL:CG1	1:I:113:ILE:HG22	1.81	1.08
1:K:78:VAL:HB	1:K:116:PRO:HG3	1.32	1.08
1:I:79:LEU:O	1:I:126:LEU:HD23	1.52	1.08
1:J:74:LEU:HD23	1:J:79:LEU:HA	1.15	1.08
1:H:329:LEU:O	1:H:333:LEU:HD23	1.41	1.07
1:K:104:GLY:N	1:K:105:PRO:CD	2.17	1.07
1:B:104:GLY:N	1:B:105:PRO:CD	2.17	1.07
1:M:78:VAL:HG12	1:M:79:LEU:N	1.65	1.07
1:B:78:VAL:HB	1:B:116:PRO:HG3	1.31	1.07
1:E:333:LEU:HG	1:E:337:TYR:CD1	1.89	1.06
1:M:79:LEU:O	1:M:126:LEU:HD23	1.54	1.06
1:H:79:LEU:CD1	1:H:123:ASN:OD1	2.03	1.06
1:G:156:ASN:ND2	1:G:172:LEU:O	1.88	1.05
1:F:175:THR:HG22	1:G:44:ASP:OD1	1.54	1.05
1:K:29:ARG:NH1	1:K:105:PRO:HG3	1.69	1.05
1:K:134:VAL:O	1:K:135:VAL:CG1	2.03	1.05
1:M:78:VAL:HG12	1:M:79:LEU:H	0.89	1.05
1:M:78:VAL:CG1	1:M:79:LEU:H	1.67	1.04
1:I:76:ASP:HB2	1:I:165:GLY:HA3	1.37	1.04
1:M:156:ASN:HD21	1:M:171:ALA:HB1	1.22	1.04
1:H:104:GLY:N	1:H:105:PRO:CD	2.21	1.03
1:H:329:LEU:O	1:H:333:LEU:HD21	1.53	1.02
1:B:79:LEU:HD11	1:B:127:LEU:HD21	1.41	1.02
1:I:78:VAL:CG1	1:I:113:ILE:CG2	2.36	1.02
1:B:104:GLY:N	1:B:105:PRO:HD2	1.73	1.02
1:B:71:ARG:HD3	1:B:84:ASP:CG	1.84	1.02
1:M:104:GLY:N	1:M:105:PRO:CD	2.22	1.02
1:I:78:VAL:HG11	1:I:113:ILE:HG22	1.38	1.01
1:L:104:GLY:N	1:L:105:PRO:CD	2.22	1.01
1:I:156:ASN:HD21	1:I:171:ALA:HB1	1.22	1.01
1:K:79:LEU:HD11	1:K:127:LEU:HD21	1.43	1.01
1:G:74:LEU:O	1:G:74:LEU:HD23	1.60	1.01
1:H:333:LEU:HB3	1:H:338:TRP:CE2	1.93	1.01
1:I:79:LEU:O	1:I:126:LEU:CD2	2.09	1.00
1:M:82:ILE:HG23	1:M:89:VAL:CB	1.91	1.00
1:H:104:GLY:N	1:H:105:PRO:HD2	1.76	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:171:ALA:O	1:H:172:LEU:O	1.78	1.00
1:M:79:LEU:HB3	1:M:126:LEU:HD21	1.43	1.00
1:K:104:GLY:N	1:K:105:PRO:HD2	1.74	1.00
1:C:74:LEU:CD2	1:C:79:LEU:HD12	1.92	1.00
1:H:276:TYR:OH	1:I:66:SER:CB	2.10	0.99
1:K:333:LEU:HB3	1:K:338:TRP:HE1	1.24	0.99
1:M:79:LEU:C	1:M:126:LEU:CD2	2.36	0.99
1:B:276:TYR:OH	1:C:66:SER:CB	2.10	0.99
1:D:156:ASN:HD21	1:D:171:ALA:HB1	1.27	0.99
1:K:175:THR:HG22	1:L:44:ASP:OD1	1.63	0.99
1:H:155:ILE:CB	1:I:67:TYR:OH	2.11	0.98
1:I:18:LEU:HD13	1:I:78:VAL:HA	1.38	0.98
1:H:79:LEU:HD13	1:H:123:ASN:OD1	1.62	0.98
1:I:73:PRO:HG3	1:I:89:VAL:CG1	1.91	0.98
1:L:104:GLY:N	1:L:105:PRO:HD2	1.77	0.98
1:L:155:ILE:HG21	1:M:67:TYR:HH	1.16	0.98
1:L:333:LEU:HD22	1:L:338:TRP:CZ2	1.98	0.98
1:G:333:LEU:CD1	1:G:338:TRP:NE1	2.23	0.97
1:M:104:GLY:N	1:M:105:PRO:HD2	1.77	0.97
1:L:110:CYS:HG	1:L:338:TRP:HZ3	0.99	0.97
1:H:174:GLY:O	1:I:44:ASP:OD1	1.81	0.97
1:C:176:VAL:CB	1:D:44:ASP:OD2	2.13	0.96
1:L:173:LYS:HG2	1:L:180:GLU:HG3	1.46	0.96
1:J:333:LEU:HG	1:J:337:TYR:CD1	1.99	0.96
1:B:333:LEU:HB3	1:B:338:TRP:HE1	1.24	0.96
1:I:73:PRO:HG3	1:I:89:VAL:HG11	0.98	0.96
1:C:177:PRO:CG	1:C:180:GLU:HB2	1.96	0.95
1:E:156:ASN:ND2	1:E:172:LEU:O	1.99	0.95
1:M:79:LEU:C	1:M:126:LEU:HD23	1.92	0.95
1:N:333:LEU:HG	1:N:337:TYR:CD1	1.99	0.95
1:A:156:ASN:ND2	1:A:172:LEU:O	2.00	0.95
1:G:74:LEU:HD21	1:G:77:GLY:HA2	1.47	0.95
1:B:71:ARG:CD	1:B:84:ASP:CG	2.39	0.94
1:M:157:THR:HG21	1:M:285:VAL:HG23	1.49	0.94
1:I:157:THR:HG21	1:I:285:VAL:HG23	1.49	0.94
1:M:333:LEU:HB3	1:M:338:TRP:CE2	2.02	0.94
1:B:276:TYR:OH	1:C:66:SER:HB2	1.67	0.94
1:L:176:VAL:CB	1:L:177:PRO:HD2	1.96	0.94
1:L:330:ALA:O	1:L:333:LEU:HD23	1.65	0.94
1:L:333:LEU:HD22	1:L:338:TRP:HZ2	1.30	0.94
1:C:18:LEU:HD21	1:C:74:LEU:HD11	1.46	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:78:VAL:HG22	1:D:79:LEU:N	1.82	0.94
1:L:173:LYS:HG3	1:L:174:GLY:N	1.80	0.94
1:J:82:ILE:O	1:J:84:ASP:N	2.00	0.93
1:L:176:VAL:CB	1:L:177:PRO:CD	2.43	0.93
1:H:333:LEU:CB	1:H:338:TRP:CZ2	2.50	0.93
1:I:18:LEU:CD1	1:I:78:VAL:HG12	1.97	0.93
1:L:333:LEU:HD13	1:L:338:TRP:CZ2	2.02	0.93
1:L:276:TYR:OH	1:M:66:SER:CB	2.17	0.93
1:K:175:THR:HG22	1:L:44:ASP:CG	1.94	0.92
1:I:78:VAL:HG11	1:I:113:ILE:CG2	1.97	0.92
1:D:157:THR:HG21	1:D:285:VAL:HG23	1.49	0.92
1:F:333:LEU:HB3	1:F:338:TRP:HE1	1.24	0.92
1:A:334:PRO:O	1:A:336:GLN:N	2.03	0.91
1:A:333:LEU:HG	1:A:337:TYR:CD1	2.05	0.91
1:E:333:LEU:HG	1:E:337:TYR:CE1	2.04	0.91
1:N:107:ASP:O	1:N:109:ILE:CG1	2.19	0.91
1:H:276:TYR:HH	1:I:66:SER:HB3	1.35	0.90
1:L:173:LYS:CG	1:L:174:GLY:H	1.80	0.90
1:D:333:LEU:HB3	1:D:338:TRP:CE2	2.07	0.90
1:D:73:PRO:CB	1:D:89:VAL:HG11	2.01	0.89
1:L:173:LYS:HG2	1:L:180:GLU:CB	2.01	0.89
1:L:176:VAL:CG1	1:L:177:PRO:CD	2.24	0.89
1:B:71:ARG:CZ	1:B:84:ASP:OD1	2.20	0.89
1:M:82:ILE:HG21	1:M:89:VAL:H	1.36	0.89
1:F:79:LEU:HD11	1:F:127:LEU:HD21	1.55	0.89
1:H:333:LEU:HD12	1:H:338:TRP:CD1	2.08	0.89
1:N:107:ASP:O	1:N:109:ILE:N	2.07	0.88
1:M:79:LEU:O	1:M:126:LEU:CD2	2.21	0.88
1:M:82:ILE:CG2	1:M:89:VAL:H	1.85	0.88
1:F:104:GLY:N	1:F:105:PRO:CD	2.36	0.88
1:I:18:LEU:HD11	1:I:78:VAL:HG12	1.51	0.88
1:L:176:VAL:HG12	1:L:177:PRO:HD2	0.88	0.88
1:M:329:LEU:O	1:M:333:LEU:CD2	2.22	0.88
1:J:107:ASP:O	1:J:109:ILE:N	2.07	0.88
1:E:107:ASP:O	1:E:109:ILE:N	2.08	0.87
1:J:70:ILE:HG22	1:J:70:ILE:O	1.70	0.87
1:H:173:LYS:HG2	1:H:174:GLY:N	1.89	0.87
1:M:79:LEU:HB3	1:M:126:LEU:CD2	2.05	0.87
1:B:29:ARG:HH12	1:B:105:PRO:CG	1.84	0.87
1:C:74:LEU:CD2	1:C:79:LEU:CD1	2.52	0.87
1:H:333:LEU:HD12	1:H:338:TRP:HE1	0.75	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:333:LEU:HD13	1:L:338:TRP:CH2	2.10	0.87
1:L:333:LEU:O	1:L:333:LEU:CD1	2.23	0.87
1:F:156:ASN:ND2	1:F:172:LEU:O	2.08	0.86
1:M:157:THR:CG2	1:M:285:VAL:HG23	2.06	0.86
1:J:107:ASP:O	1:J:109:ILE:CG1	2.21	0.86
1:N:71:ARG:O	1:N:73:PRO:HD3	1.75	0.86
1:D:79:LEU:HD21	1:D:130:MET:SD	2.15	0.86
1:F:78:VAL:HB	1:F:116:PRO:CG	2.02	0.86
1:B:175:THR:HG22	1:C:44:ASP:CG	2.01	0.85
1:C:177:PRO:HG2	1:C:180:GLU:CB	2.03	0.85
1:D:329:LEU:O	1:D:333:LEU:CD2	2.23	0.85
1:E:107:ASP:O	1:E:109:ILE:CG1	2.23	0.85
1:I:157:THR:CG2	1:I:285:VAL:HG23	2.06	0.85
1:J:74:LEU:CD2	1:J:79:LEU:CA	2.54	0.85
1:K:29:ARG:NH1	1:K:105:PRO:CG	2.39	0.85
1:I:78:VAL:HG12	1:I:113:ILE:CG2	2.04	0.85
1:B:71:ARG:NH1	1:B:84:ASP:OD1	2.10	0.85
1:F:104:GLY:N	1:F:105:PRO:HD2	1.91	0.85
1:L:155:ILE:HG21	1:M:67:TYR:CZ	2.11	0.85
1:A:107:ASP:O	1:A:109:ILE:N	2.08	0.85
1:B:71:ARG:NE	1:B:84:ASP:OD1	2.10	0.85
1:D:157:THR:CG2	1:D:285:VAL:HG23	2.06	0.85
1:K:29:ARG:HH12	1:K:105:PRO:CG	1.86	0.85
1:B:29:ARG:NH1	1:B:105:PRO:CG	2.38	0.85
1:L:173:LYS:HG2	1:L:180:GLU:HB3	1.59	0.85
1:E:71:ARG:O	1:E:73:PRO:HD3	1.77	0.84
1:F:333:LEU:CB	1:F:338:TRP:HE1	1.89	0.84
1:L:176:VAL:HG12	1:L:177:PRO:HD3	1.58	0.84
1:M:78:VAL:CG2	1:M:115:VAL:HA	2.07	0.84
1:B:329:LEU:O	1:B:333:LEU:CD2	2.25	0.84
1:K:329:LEU:O	1:K:333:LEU:CD2	2.25	0.84
1:H:28:SER:HB2	1:H:107:ASP:OD2	1.78	0.84
1:L:87:ILE:HG22	1:L:87:ILE:O	1.76	0.84
1:F:78:VAL:CB	1:F:116:PRO:HG3	2.06	0.84
1:C:74:LEU:HD22	1:C:79:LEU:HD12	1.59	0.84
1:I:18:LEU:HD12	1:I:78:VAL:CG1	2.06	0.84
1:C:155:ILE:HD11	1:C:172:LEU:HB2	1.60	0.84
1:F:49:LYS:O	1:F:52:GLY:O	1.96	0.84
1:G:87:ILE:O	1:G:87:ILE:HG22	1.76	0.84
1:I:104:GLY:N	1:I:105:PRO:HD2	1.93	0.84
1:D:104:GLY:N	1:D:105:PRO:HD2	1.93	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:79:LEU:CD1	1:K:127:LEU:HD21	2.06	0.83
1:G:104:GLY:N	1:G:105:PRO:HD2	1.93	0.83
1:K:49:LYS:O	1:K:52:GLY:O	1.96	0.83
1:B:79:LEU:CD1	1:B:127:LEU:HD21	2.07	0.83
1:B:71:ARG:CD	1:B:84:ASP:OD2	2.26	0.83
1:B:333:LEU:CB	1:B:338:TRP:HE1	1.91	0.83
1:K:333:LEU:CB	1:K:338:TRP:HE1	1.91	0.83
1:K:156:ASN:ND2	1:K:172:LEU:O	2.11	0.83
1:L:28:SER:HB2	1:L:107:ASP:OD2	1.78	0.83
1:H:87:ILE:HG22	1:H:87:ILE:O	1.76	0.83
1:B:71:ARG:HD2	1:B:84:ASP:OD2	1.79	0.83
1:C:87:ILE:HG22	1:C:87:ILE:O	1.76	0.83
1:J:71:ARG:O	1:J:73:PRO:HD3	1.79	0.83
1:I:104:GLY:N	1:I:105:PRO:CD	2.41	0.82
1:H:76:ASP:CB	1:H:165:GLY:HA2	2.04	0.82
1:J:157:THR:HG21	1:J:285:VAL:HG23	1.62	0.82
1:J:155:ILE:HG23	1:J:156:ASN:HB2	1.62	0.82
1:F:333:LEU:HB3	1:F:338:TRP:CE2	2.14	0.82
1:G:104:GLY:N	1:G:105:PRO:CD	2.43	0.82
1:M:79:LEU:CB	1:M:126:LEU:CD2	2.57	0.82
1:B:333:LEU:HB3	1:B:338:TRP:CE2	2.15	0.82
1:D:104:GLY:N	1:D:105:PRO:CD	2.41	0.81
1:H:333:LEU:CD1	1:H:338:TRP:NE1	2.19	0.81
1:A:107:ASP:O	1:A:109:ILE:CG1	2.25	0.81
1:C:18:LEU:CD2	1:C:74:LEU:HD11	2.10	0.81
1:J:69:ASP:OD1	1:J:71:ARG:HG3	1.80	0.81
1:N:155:ILE:HG23	1:N:156:ASN:HB2	1.63	0.81
1:D:334:PRO:O	1:D:336:GLN:N	2.15	0.80
1:F:329:LEU:O	1:F:333:LEU:CD2	2.28	0.80
1:J:156:ASN:OD1	1:J:172:LEU:N	2.15	0.80
1:B:155:ILE:HB	1:C:67:TYR:OH	1.82	0.80
1:F:175:THR:HG22	1:G:44:ASP:CG	2.06	0.80
1:H:28:SER:CB	1:H:107:ASP:OD2	2.30	0.80
1:L:28:SER:CB	1:L:107:ASP:OD2	2.30	0.80
1:K:333:LEU:HB3	1:K:338:TRP:CE2	2.16	0.79
1:M:329:LEU:O	1:M:333:LEU:HD23	1.79	0.79
1:M:82:ILE:C	1:M:84:ASP:H	1.89	0.79
1:I:76:ASP:CG	3:I:402:ADP:O2B	2.25	0.79
1:L:155:ILE:CG2	1:M:67:TYR:HH	1.74	0.79
1:N:134:VAL:O	1:N:135:VAL:CG2	2.30	0.78
1:F:107:ASP:O	1:F:109:ILE:N	2.13	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:42:PRO:HG2	1:M:49:LYS:HB2	1.65	0.78
1:M:333:LEU:CG	1:M:338:TRP:HE1	1.97	0.78
1:E:333:LEU:HG	1:E:337:TYR:CG	2.18	0.78
1:H:79:LEU:HD13	1:H:123:ASN:CG	2.08	0.78
1:B:78:VAL:HG23	1:B:116:PRO:HD2	1.66	0.78
1:E:87:ILE:HG22	1:E:87:ILE:O	1.84	0.78
1:N:73:PRO:HB3	1:N:89:VAL:HG11	1.64	0.78
1:N:156:ASN:OD1	1:N:172:LEU:N	2.16	0.78
1:E:73:PRO:HB3	1:E:89:VAL:HG11	1.65	0.78
1:M:87:ILE:HG22	1:M:87:ILE:O	1.84	0.77
1:I:18:LEU:CD1	1:I:78:VAL:CA	2.58	0.77
1:K:104:GLY:N	1:K:105:PRO:HD3	2.00	0.77
1:G:333:LEU:HD12	1:G:338:TRP:CD1	2.17	0.77
1:I:18:LEU:CD1	1:I:78:VAL:CG1	2.61	0.77
1:I:76:ASP:OD2	1:I:166:THR:N	2.14	0.77
1:D:71:ARG:O	1:D:72:TYR:O	2.01	0.77
1:K:134:VAL:C	1:K:135:VAL:HG12	2.09	0.77
1:B:104:GLY:N	1:B:105:PRO:HD3	2.00	0.77
1:H:155:ILE:CG2	1:I:67:TYR:OH	2.32	0.77
1:M:107:ASP:O	1:M:108:GLU:C	2.25	0.76
1:D:43:LYS:CD	1:D:69:ASP:HB2	2.12	0.76
1:D:333:LEU:HB3	1:D:338:TRP:HE1	1.46	0.76
1:M:333:LEU:HD12	1:M:338:TRP:CD1	2.20	0.76
1:M:333:LEU:HB3	1:M:338:TRP:HE1	1.49	0.76
1:M:333:LEU:CB	1:M:338:TRP:NE1	2.48	0.76
1:L:107:ASP:O	1:L:108:GLU:C	2.28	0.76
1:D:79:LEU:HD13	1:D:126:LEU:HB3	1.68	0.76
1:N:87:ILE:O	1:N:87:ILE:HG22	1.84	0.76
1:H:79:LEU:HD12	1:H:123:ASN:OD1	1.84	0.75
1:K:78:VAL:HG23	1:K:116:PRO:HD2	1.65	0.75
1:N:157:THR:HG21	1:N:285:VAL:HG23	1.68	0.75
1:J:74:LEU:CD2	1:J:79:LEU:HB2	2.15	0.75
1:A:334:PRO:C	1:A:336:GLN:H	1.93	0.75
1:A:87:ILE:HG22	1:A:87:ILE:O	1.84	0.75
1:F:79:LEU:CD1	1:F:127:LEU:HD21	2.16	0.75
1:B:78:VAL:CB	1:B:116:PRO:HG3	2.15	0.75
1:J:87:ILE:HG22	1:J:87:ILE:O	1.84	0.75
1:L:330:ALA:O	1:L:333:LEU:CD2	2.35	0.75
1:H:107:ASP:O	1:H:108:GLU:C	2.29	0.74
1:K:134:VAL:O	1:K:135:VAL:CB	2.35	0.74
1:G:333:LEU:HD12	1:G:338:TRP:HE1	0.93	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:334:PRO:O	1:M:336:GLN:N	2.20	0.74
1:L:155:ILE:HG12	1:M:67:TYR:HH	1.49	0.74
1:I:87:ILE:O	1:I:87:ILE:HG22	1.84	0.74
1:B:71:ARG:O	1:B:73:PRO:HD3	1.87	0.74
1:D:87:ILE:O	1:D:87:ILE:HG22	1.84	0.74
1:M:82:ILE:C	1:M:84:ASP:N	2.44	0.74
1:B:41:TYR:OH	1:B:71:ARG:NH2	2.20	0.74
1:H:76:ASP:CB	1:H:165:GLY:CA	2.65	0.74
1:K:71:ARG:O	1:K:73:PRO:HD3	1.88	0.74
1:C:276:TYR:OH	1:D:66:SER:CB	2.33	0.73
1:D:78:VAL:CG2	1:D:79:LEU:H	1.86	0.73
1:J:333:LEU:HG	1:J:337:TYR:CE1	2.22	0.73
1:D:156:ASN:ND2	1:D:171:ALA:HB1	2.01	0.73
1:H:173:LYS:CG	1:H:174:GLY:H	1.89	0.73
1:K:329:LEU:O	1:K:333:LEU:HD23	1.88	0.73
1:M:82:ILE:HD13	1:M:82:ILE:N	2.03	0.73
1:D:334:PRO:O	1:D:337:TYR:N	2.21	0.73
1:J:156:ASN:CG	1:J:172:LEU:O	2.31	0.73
1:D:155:ILE:HG23	1:D:156:ASN:HB2	1.70	0.73
1:M:73:PRO:HB3	1:M:89:VAL:HG11	1.71	0.73
1:F:78:VAL:HG23	1:F:116:PRO:HD2	1.69	0.73
1:L:155:ILE:HB	1:M:67:TYR:OH	1.87	0.73
1:N:156:ASN:CG	1:N:172:LEU:O	2.32	0.73
1:C:157:THR:OG1	1:C:282:GLN:HB3	1.89	0.72
1:K:131:ALA:HB1	1:K:136:HIS:O	1.88	0.72
1:B:279:THR:C	1:B:281:LEU:H	1.97	0.72
1:L:155:ILE:CG1	1:M:67:TYR:HH	2.02	0.72
1:M:334:PRO:O	1:M:337:TYR:N	2.21	0.72
1:F:329:LEU:O	1:F:333:LEU:HD23	1.88	0.72
1:M:157:THR:HG21	1:M:285:VAL:CG2	2.20	0.72
1:D:333:LEU:CB	1:D:338:TRP:NE1	2.49	0.72
1:B:279:THR:O	1:B:281:LEU:N	2.23	0.72
1:K:279:THR:C	1:K:281:LEU:H	1.97	0.72
1:N:333:LEU:HG	1:N:337:TYR:CE1	2.23	0.72
1:I:157:THR:HG21	1:I:285:VAL:CG2	2.20	0.72
1:J:74:LEU:CD2	1:J:79:LEU:CB	2.68	0.72
1:E:333:LEU:N	1:E:334:PRO:HD3	2.04	0.72
1:K:87:ILE:HG22	1:K:87:ILE:O	1.88	0.72
1:B:41:TYR:HE2	1:B:71:ARG:HE	1.35	0.72
1:B:329:LEU:O	1:B:333:LEU:HD23	1.89	0.72
1:F:87:ILE:HG22	1:F:87:ILE:O	1.88	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:107:ASP:O	1:H:108:GLU:O	2.08	0.71
1:M:333:LEU:HD12	1:M:338:TRP:NE1	2.05	0.71
1:B:87:ILE:O	1:B:87:ILE:HG22	1.88	0.71
1:G:110:CYS:HG	1:G:338:TRP:HZ3	1.25	0.71
1:L:175:THR:HG22	1:M:43:LYS:HE2	1.71	0.71
1:C:77:GLY:HA3	1:C:166:THR:HG23	1.72	0.71
1:D:156:ASN:CG	1:D:172:LEU:H	1.98	0.71
1:D:329:LEU:O	1:D:333:LEU:HD23	1.89	0.71
1:J:82:ILE:O	1:J:85:ARG:N	2.19	0.71
1:K:78:VAL:CB	1:K:116:PRO:HG3	2.15	0.71
1:K:175:THR:HG22	1:L:44:ASP:OD2	1.90	0.71
1:E:333:LEU:CG	1:E:337:TYR:CD1	2.70	0.71
1:M:107:ASP:O	1:M:108:GLU:O	2.08	0.71
1:D:79:LEU:HD11	1:D:130:MET:SD	2.30	0.71
1:F:276:TYR:OH	1:G:66:SER:CB	2.38	0.71
1:C:176:VAL:HB	1:D:44:ASP:CG	2.13	0.71
1:L:107:ASP:O	1:L:108:GLU:O	2.08	0.71
1:M:333:LEU:CB	1:M:338:TRP:HE1	2.03	0.71
1:F:107:ASP:O	1:F:109:ILE:HG12	1.91	0.71
1:N:134:VAL:C	1:N:135:VAL:HG13	2.14	0.71
1:D:333:LEU:CB	1:D:338:TRP:HE1	2.04	0.71
1:F:71:ARG:O	1:F:73:PRO:HD3	1.89	0.71
1:I:78:VAL:CG1	1:I:113:ILE:HG21	2.19	0.71
1:K:279:THR:O	1:K:281:LEU:N	2.22	0.71
1:L:157:THR:OG1	1:L:282:GLN:HB3	1.90	0.71
1:L:175:THR:CG2	1:M:43:LYS:HE2	2.21	0.71
1:L:77:GLY:HA3	1:L:166:THR:HG23	1.72	0.70
1:B:41:TYR:HE2	1:B:71:ARG:NE	1.89	0.70
1:D:157:THR:HG21	1:D:285:VAL:CG2	2.20	0.70
1:L:332:GLU:O	1:L:333:LEU:HG	1.91	0.70
1:B:334:PRO:O	1:B:337:TYR:N	2.24	0.70
1:I:76:ASP:CB	1:I:165:GLY:HA3	2.16	0.70
1:K:78:VAL:HB	1:K:116:PRO:CG	2.16	0.70
1:M:79:LEU:CB	1:M:126:LEU:HD21	2.18	0.70
1:K:175:THR:CG2	1:L:44:ASP:OD2	2.39	0.70
1:M:71:ARG:HG3	1:M:71:ARG:HH11	1.56	0.70
1:K:334:PRO:O	1:K:337:TYR:N	2.24	0.70
1:L:110:CYS:SG	1:L:338:TRP:HZ3	1.93	0.70
1:M:156:ASN:ND2	1:M:171:ALA:HB1	2.01	0.70
1:C:74:LEU:HD21	1:C:79:LEU:CD1	2.21	0.70
1:F:334:PRO:O	1:F:337:TYR:N	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:276:TYR:OH	1:G:66:SER:HB2	1.92	0.69
1:D:333:LEU:CG	1:D:338:TRP:HE1	2.05	0.69
1:H:104:GLY:H	1:H:105:PRO:CD	2.05	0.69
1:E:155:ILE:HD12	1:E:155:ILE:N	2.08	0.69
1:K:78:VAL:HG23	1:K:116:PRO:CD	2.23	0.69
1:M:78:VAL:HG21	1:M:115:VAL:HA	1.74	0.69
1:F:334:PRO:O	1:F:336:GLN:N	2.26	0.69
1:J:156:ASN:ND2	1:J:172:LEU:C	2.49	0.69
1:C:107:ASP:C	1:C:109:ILE:H	1.99	0.69
1:G:74:LEU:CD2	1:G:77:GLY:HA2	2.21	0.69
1:B:334:PRO:O	1:B:336:GLN:N	2.26	0.69
1:M:79:LEU:CB	1:M:126:LEU:HD23	2.21	0.69
1:M:82:ILE:HG23	1:M:89:VAL:CG2	2.22	0.69
1:A:155:ILE:N	1:A:155:ILE:HD12	2.08	0.68
1:B:78:VAL:HB	1:B:116:PRO:CG	2.15	0.68
1:G:110:CYS:SG	1:G:338:TRP:CH2	2.86	0.68
1:M:104:GLY:H	1:M:105:PRO:CD	2.05	0.68
1:G:77:GLY:HA3	1:G:166:THR:HG23	1.76	0.68
1:L:176:VAL:CG1	1:L:177:PRO:HD3	2.20	0.68
1:G:79:LEU:HB3	1:G:126:LEU:CD1	2.22	0.68
1:L:276:TYR:HH	1:M:66:SER:CB	2.05	0.68
1:F:109:ILE:CG2	1:F:136:HIS:CE1	2.77	0.68
1:F:333:LEU:CG	1:F:338:TRP:HE1	2.06	0.68
1:I:156:ASN:ND2	1:I:171:ALA:HB1	2.02	0.68
1:C:156:ASN:HD21	1:C:171:ALA:C	2.02	0.68
1:B:109:ILE:CG2	1:B:136:HIS:CE1	2.77	0.68
1:I:73:PRO:HG2	1:I:89:VAL:HG11	1.67	0.68
1:B:109:ILE:HG22	1:B:136:HIS:CE1	2.29	0.68
1:J:334:PRO:O	1:J:337:TYR:N	2.26	0.68
1:L:110:CYS:SG	1:L:338:TRP:CH2	2.84	0.68
1:L:173:LYS:CG	1:L:180:GLU:HG3	2.22	0.68
1:I:155:ILE:HG23	1:I:156:ASN:HB2	1.76	0.67
1:K:334:PRO:O	1:K:336:GLN:N	2.28	0.67
1:I:81:GLU:O	1:I:82:ILE:HB	1.91	0.67
1:M:155:ILE:HG23	1:M:156:ASN:HB2	1.75	0.67
1:K:103:PRO:C	1:K:105:PRO:HD2	2.20	0.67
1:C:156:ASN:HD21	1:C:172:LEU:N	1.93	0.67
1:A:73:PRO:HB3	1:A:89:VAL:HG11	1.76	0.67
1:I:18:LEU:HD12	1:I:78:VAL:HA	1.75	0.67
1:M:156:ASN:CG	1:M:172:LEU:H	2.02	0.67
1:B:103:PRO:C	1:B:105:PRO:HD2	2.19	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:77:GLY:HA3	1:G:166:THR:CG2	2.25	0.67
1:I:78:VAL:HG12	1:I:113:ILE:HG21	1.77	0.67
1:I:71:ARG:HG3	1:I:71:ARG:HH11	1.60	0.67
1:B:104:GLY:H	1:B:105:PRO:CD	2.08	0.67
1:C:108:GLU:O	1:C:108:GLU:HG2	1.95	0.67
1:M:71:ARG:HG3	1:M:71:ARG:NH1	2.09	0.67
1:L:331:GLU:HG2	1:L:332:GLU:HA	1.77	0.66
1:B:78:VAL:HG23	1:B:116:PRO:CD	2.24	0.66
1:F:109:ILE:HG22	1:F:136:HIS:CE1	2.29	0.66
1:H:104:GLY:H	1:H:105:PRO:HD2	1.60	0.66
1:N:157:THR:CG2	1:N:285:VAL:HG23	2.26	0.66
1:N:334:PRO:O	1:N:337:TYR:N	2.27	0.66
1:H:329:LEU:C	1:H:333:LEU:CD2	2.65	0.66
1:N:107:ASP:O	1:N:108:GLU:C	2.39	0.66
1:I:156:ASN:CG	1:I:172:LEU:H	2.03	0.66
1:C:156:ASN:ND2	1:C:172:LEU:C	2.54	0.66
1:M:82:ILE:HD13	1:M:82:ILE:H	1.58	0.66
1:J:334:PRO:O	1:J:335:PRO:C	2.39	0.66
1:J:157:THR:CG2	1:J:285:VAL:HG23	2.25	0.65
1:L:333:LEU:CD2	1:L:338:TRP:CZ2	2.79	0.65
1:J:74:LEU:HD21	1:J:79:LEU:HB2	1.77	0.65
1:K:104:GLY:H	1:K:105:PRO:CD	2.08	0.65
1:N:156:ASN:ND2	1:N:172:LEU:C	2.50	0.65
1:F:333:LEU:HD12	1:F:338:TRP:CD1	2.32	0.65
1:L:104:GLY:H	1:L:105:PRO:CD	2.06	0.65
1:L:106:ASN:O	1:L:108:GLU:N	2.27	0.65
1:B:333:LEU:CG	1:B:338:TRP:HE1	2.09	0.65
1:I:81:GLU:O	1:I:82:ILE:CB	2.44	0.65
1:K:18:LEU:HD21	1:K:74:LEU:HD11	1.77	0.65
1:B:18:LEU:HD21	1:B:74:LEU:HD11	1.79	0.65
1:J:74:LEU:HD23	1:J:79:LEU:CB	2.27	0.65
1:K:333:LEU:CG	1:K:338:TRP:HE1	2.09	0.65
1:N:334:PRO:O	1:N:335:PRO:C	2.39	0.65
1:G:331:GLU:HG2	1:G:332:GLU:HA	1.77	0.65
1:A:71:ARG:O	1:A:73:PRO:HD3	1.97	0.65
1:K:107:ASP:O	1:K:108:GLU:C	2.40	0.65
1:G:81:GLU:O	1:G:82:ILE:O	2.15	0.64
1:G:107:ASP:O	1:G:109:ILE:N	2.30	0.64
1:H:307:PHE:CE1	1:I:240:LYS:NZ	2.66	0.64
1:L:173:LYS:HE2	1:L:180:GLU:HG3	1.79	0.64
1:C:74:LEU:HD23	1:C:79:LEU:HA	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:334:PRO:C	1:N:336:GLN:N	2.55	0.64
1:M:73:PRO:CB	1:M:89:VAL:HG11	2.28	0.64
1:M:82:ILE:HG22	1:M:84:ASP:HB2	1.79	0.64
1:G:74:LEU:O	1:G:74:LEU:CD2	2.43	0.64
1:J:333:LEU:HG	1:J:337:TYR:CG	2.32	0.64
1:J:334:PRO:C	1:J:336:GLN:N	2.55	0.64
1:H:106:ASN:O	1:H:108:GLU:N	2.28	0.64
1:J:76:ASP:HB3	1:J:166:THR:HG23	1.80	0.64
1:B:75:GLN:O	1:B:78:VAL:HG12	1.99	0.63
1:B:79:LEU:CD1	1:B:127:LEU:CD2	2.76	0.63
1:J:333:LEU:CG	1:J:337:TYR:CD1	2.81	0.63
1:E:333:LEU:CG	1:E:337:TYR:CE1	2.80	0.63
1:K:79:LEU:CD1	1:K:127:LEU:CD2	2.76	0.63
1:D:329:LEU:O	1:D:333:LEU:HD21	1.99	0.63
1:M:82:ILE:HG21	1:M:89:VAL:N	2.11	0.63
1:N:333:LEU:HG	1:N:337:TYR:CG	2.33	0.63
1:I:107:ASP:O	1:I:109:ILE:N	2.32	0.63
1:J:82:ILE:C	1:J:84:ASP:N	2.56	0.63
1:L:77:GLY:HA3	1:L:166:THR:CG2	2.29	0.63
1:C:77:GLY:HA3	1:C:166:THR:CG2	2.29	0.62
1:J:82:ILE:C	1:J:84:ASP:H	2.06	0.62
1:L:333:LEU:CD1	1:L:338:TRP:CZ2	2.81	0.62
1:M:42:PRO:HG2	1:M:49:LYS:CB	2.27	0.62
1:M:78:VAL:HG21	1:M:115:VAL:HG12	1.81	0.62
1:D:107:ASP:O	1:D:109:ILE:N	2.32	0.62
1:E:332:GLU:O	1:E:333:LEU:C	2.40	0.62
1:I:71:ARG:HG3	1:I:71:ARG:NH1	2.13	0.62
1:N:333:LEU:CG	1:N:337:TYR:CD1	2.81	0.62
1:K:81:GLU:O	1:K:82:ILE:HB	1.99	0.62
1:B:79:LEU:HB3	1:B:126:LEU:HD23	1.82	0.62
1:B:106:ASN:C	1:B:108:GLU:H	2.07	0.62
1:C:174:GLY:HA3	1:D:66:SER:O	1.99	0.62
1:D:43:LYS:HD2	1:D:69:ASP:CB	2.14	0.62
1:D:45:VAL:HG12	1:D:45:VAL:O	2.00	0.62
1:N:334:PRO:C	1:N:336:GLN:H	2.08	0.62
1:J:107:ASP:O	1:J:108:GLU:C	2.41	0.62
1:H:331:GLU:HG2	1:H:332:GLU:HA	1.81	0.62
1:C:156:ASN:CG	1:C:172:LEU:O	2.43	0.62
1:B:81:GLU:O	1:B:82:ILE:HB	2.00	0.62
1:H:104:GLY:N	1:H:105:PRO:HD3	2.13	0.62
1:B:329:LEU:O	1:B:333:LEU:HD21	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:135:VAL:O	1:J:135:VAL:HG23	2.00	0.61
1:K:75:GLN:O	1:K:78:VAL:HG12	1.99	0.61
1:L:28:SER:OG	1:L:107:ASP:OD2	2.18	0.61
1:D:76:ASP:OD1	1:D:164:ALA:C	2.34	0.61
1:M:333:LEU:HD12	1:M:338:TRP:HE1	1.64	0.61
1:B:118:ARG:NH1	1:I:118:ARG:HH12	1.98	0.61
1:H:78:VAL:O	1:H:78:VAL:HG13	2.00	0.61
1:H:329:LEU:C	1:H:333:LEU:HD21	2.23	0.61
1:H:333:LEU:CG	1:H:338:TRP:HE1	2.11	0.61
1:A:333:LEU:N	1:A:334:PRO:HD3	2.14	0.61
1:D:49:LYS:O	1:D:54:PRO:CA	2.49	0.61
1:D:104:GLY:H	1:D:105:PRO:CD	2.13	0.61
1:F:81:GLU:O	1:F:82:ILE:HB	2.00	0.61
1:J:334:PRO:C	1:J:336:GLN:H	2.08	0.61
1:I:49:LYS:O	1:I:54:PRO:CA	2.49	0.61
1:M:49:LYS:O	1:M:54:PRO:CA	2.49	0.61
1:F:75:GLN:O	1:F:78:VAL:HG12	2.00	0.61
1:F:78:VAL:HG23	1:F:116:PRO:CD	2.31	0.61
1:E:155:ILE:HB	1:F:67:TYR:OH	2.01	0.60
1:G:108:GLU:O	1:G:108:GLU:HG2	2.01	0.60
1:G:110:CYS:SG	1:G:338:TRP:HZ3	2.12	0.60
1:A:155:ILE:HB	1:B:67:TYR:OH	2.02	0.60
1:C:174:GLY:HA2	1:D:67:TYR:CD1	2.35	0.60
1:M:333:LEU:CD1	1:M:338:TRP:HE1	2.14	0.60
1:E:135:VAL:HG23	1:E:135:VAL:O	2.00	0.60
1:K:106:ASN:C	1:K:108:GLU:H	2.09	0.60
1:E:107:ASP:O	1:E:108:GLU:C	2.43	0.60
1:F:155:ILE:CG1	1:G:67:TYR:OH	2.49	0.60
1:I:104:GLY:H	1:I:105:PRO:CD	2.13	0.60
1:A:135:VAL:HG23	1:A:135:VAL:O	2.00	0.60
1:M:78:VAL:HG23	1:M:115:VAL:HA	1.83	0.60
1:F:155:ILE:HG12	1:G:67:TYR:OH	2.01	0.60
1:M:73:PRO:HG3	1:M:89:VAL:HG11	1.84	0.60
1:C:155:ILE:HD11	1:C:172:LEU:CB	2.30	0.60
1:C:157:THR:O	1:C:157:THR:HG22	2.00	0.60
1:G:104:GLY:H	1:G:105:PRO:CD	2.13	0.60
1:L:74:LEU:HG	1:L:74:LEU:O	2.01	0.60
1:L:171:ALA:O	1:L:172:LEU:C	2.44	0.60
1:G:107:ASP:O	1:G:109:ILE:HG12	2.01	0.60
1:K:79:LEU:HB3	1:K:126:LEU:HD23	1.83	0.60
1:I:78:VAL:HG13	1:I:114:GLY:O	2.00	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:81:GLU:O	1:C:82:ILE:O	2.20	0.59
1:F:333:LEU:HD12	1:F:338:TRP:NE1	2.16	0.59
1:J:82:ILE:N	1:J:82:ILE:HD13	2.16	0.59
1:L:79:LEU:HB3	1:L:126:LEU:HD13	1.84	0.59
1:M:104:GLY:N	1:M:105:PRO:HD3	2.12	0.59
1:H:155:ILE:HG21	1:I:67:TYR:CE1	2.38	0.59
1:I:71:ARG:C	1:I:73:PRO:HD3	2.26	0.59
1:C:79:LEU:HB3	1:C:126:LEU:HD13	1.85	0.59
1:M:82:ILE:CG2	1:M:89:VAL:HB	2.18	0.59
1:B:155:ILE:HG12	1:C:67:TYR:OH	2.02	0.59
1:D:108:GLU:O	1:D:108:GLU:HG2	2.03	0.59
1:M:80:SER:O	1:M:126:LEU:CD2	2.33	0.59
1:F:78:VAL:HG22	1:F:123:ASN:ND2	2.18	0.59
1:H:76:ASP:HB3	1:H:165:GLY:HA3	1.79	0.59
1:H:171:ALA:O	1:H:172:LEU:C	2.46	0.59
1:B:333:LEU:HD12	1:B:338:TRP:CD1	2.38	0.59
1:D:333:LEU:HD12	1:D:338:TRP:CD1	2.37	0.59
1:E:332:GLU:C	1:E:334:PRO:HD3	2.27	0.59
1:A:107:ASP:O	1:A:108:GLU:C	2.45	0.59
1:N:135:VAL:HG23	1:N:135:VAL:O	2.02	0.59
1:F:104:GLY:H	1:F:105:PRO:CD	2.14	0.58
1:I:79:LEU:O	1:I:126:LEU:HD22	2.02	0.58
1:K:333:LEU:HD12	1:K:338:TRP:CD1	2.38	0.58
1:B:157:THR:O	1:B:159:ILE:HG13	2.03	0.58
1:H:329:LEU:C	1:H:333:LEU:HD23	2.23	0.58
1:K:81:GLU:O	1:K:82:ILE:CB	2.50	0.58
1:L:156:ASN:HD21	1:L:171:ALA:C	2.12	0.58
1:A:18:LEU:CD2	1:A:74:LEU:HD11	2.33	0.58
1:E:333:LEU:CD2	1:E:337:TYR:CE1	2.86	0.58
1:I:18:LEU:HD12	1:I:78:VAL:HG13	1.84	0.58
1:F:81:GLU:O	1:F:82:ILE:CB	2.52	0.58
1:B:155:ILE:CB	1:C:67:TYR:OH	2.52	0.58
1:D:71:ARG:HG3	1:D:71:ARG:HH11	1.68	0.58
1:C:176:VAL:HG12	1:C:176:VAL:O	2.02	0.58
1:B:73:PRO:HB3	1:B:89:VAL:HG11	1.85	0.58
1:G:87:ILE:O	1:G:87:ILE:CG2	2.49	0.58
1:L:333:LEU:CD1	1:L:338:TRP:CH2	2.86	0.58
1:I:18:LEU:HD12	1:I:78:VAL:CA	2.32	0.58
1:K:329:LEU:O	1:K:333:LEU:HD21	2.01	0.58
1:L:104:GLY:N	1:L:105:PRO:HD3	2.13	0.58
1:D:333:LEU:HD12	1:D:338:TRP:NE1	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:28:SER:OG	1:H:107:ASP:OD2	2.21	0.57
1:B:81:GLU:O	1:B:82:ILE:CB	2.52	0.57
1:D:182:GLN:N	1:D:182:GLN:OE1	2.38	0.57
1:L:81:GLU:O	1:L:82:ILE:O	2.21	0.57
1:F:333:LEU:HD12	1:F:338:TRP:HE1	1.70	0.57
1:I:107:ASP:O	1:I:109:ILE:HG12	2.04	0.57
1:M:82:ILE:O	1:M:85:ARG:N	2.35	0.57
1:C:104:GLY:N	1:C:105:PRO:HD2	2.20	0.57
1:L:173:LYS:CG	1:L:180:GLU:HB3	2.31	0.57
1:N:103:PRO:HA	1:N:107:ASP:OD2	2.04	0.57
1:K:73:PRO:HB3	1:K:89:VAL:HG11	1.87	0.57
1:M:182:GLN:N	1:M:182:GLN:OE1	2.38	0.57
1:M:329:LEU:O	1:M:333:LEU:HD21	2.04	0.57
1:C:107:ASP:HB3	1:C:109:ILE:HG12	1.85	0.57
1:H:76:ASP:CA	1:H:165:GLY:HA3	2.35	0.57
1:L:79:LEU:HB3	1:L:126:LEU:CD1	2.35	0.57
1:B:175:THR:CG2	1:C:44:ASP:CG	2.75	0.57
1:B:175:THR:CG2	1:C:44:ASP:OD2	2.52	0.57
1:K:135:VAL:O	1:K:135:VAL:HG13	2.04	0.57
1:D:107:ASP:O	1:D:109:ILE:HG12	2.05	0.56
1:I:182:GLN:N	1:I:182:GLN:OE1	2.38	0.56
1:K:333:LEU:HD12	1:K:338:TRP:NE1	2.20	0.56
1:B:155:ILE:CG1	1:C:67:TYR:OH	2.53	0.56
1:B:280:VAL:O	1:B:281:LEU:HD23	2.05	0.56
1:F:109:ILE:CG2	1:F:136:HIS:HE1	2.17	0.56
1:K:280:VAL:O	1:K:281:LEU:HD23	2.04	0.56
1:B:109:ILE:CG2	1:B:136:HIS:HE1	2.17	0.56
1:C:79:LEU:HB3	1:C:126:LEU:CD1	2.35	0.56
1:F:103:PRO:C	1:F:105:PRO:HD2	2.30	0.56
1:G:104:GLY:H	1:G:105:PRO:HD2	1.68	0.56
1:H:334:PRO:O	1:H:337:TYR:N	2.38	0.56
1:J:333:LEU:N	1:J:334:PRO:HD3	2.21	0.56
1:M:79:LEU:HB2	1:M:126:LEU:HD23	1.87	0.56
1:M:82:ILE:CG2	1:M:89:VAL:N	2.65	0.56
1:M:103:PRO:C	1:M:105:PRO:HD2	2.30	0.56
1:A:103:PRO:HA	1:A:107:ASP:OD2	2.06	0.56
1:B:333:LEU:HD12	1:B:338:TRP:NE1	2.20	0.56
1:C:107:ASP:O	1:C:109:ILE:N	2.38	0.56
1:D:71:ARG:O	1:D:72:TYR:C	2.47	0.56
1:G:156:ASN:HD21	1:G:172:LEU:N	2.03	0.56
1:D:334:PRO:O	1:D:335:PRO:C	2.48	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:75:GLN:HB3	1:H:78:VAL:HG12	1.87	0.56
1:J:103:PRO:HA	1:J:107:ASP:OD2	2.05	0.56
1:K:106:ASN:O	1:K:108:GLU:N	2.31	0.56
1:N:333:LEU:N	1:N:334:PRO:HD3	2.21	0.56
1:F:79:LEU:HB3	1:F:126:LEU:HD23	1.88	0.56
1:H:307:PHE:CZ	1:I:240:LYS:NZ	2.70	0.56
1:M:106:ASN:O	1:M:108:GLU:N	2.32	0.56
1:L:157:THR:O	1:L:157:THR:HG22	2.05	0.56
1:I:49:LYS:O	1:I:54:PRO:HA	2.06	0.56
1:L:74:LEU:HD12	1:L:78:VAL:N	2.20	0.56
1:L:155:ILE:HG12	1:M:67:TYR:CZ	2.38	0.56
1:B:106:ASN:O	1:B:108:GLU:N	2.38	0.56
1:C:157:THR:CG2	1:C:285:VAL:HG23	2.36	0.55
1:D:156:ASN:ND2	1:D:172:LEU:H	2.03	0.55
1:M:78:VAL:CG2	1:M:114:GLY:O	2.54	0.55
1:M:78:VAL:HG23	1:M:116:PRO:HD3	1.88	0.55
1:M:78:VAL:HG22	1:M:114:GLY:O	2.06	0.55
1:D:71:ARG:HG3	1:D:71:ARG:NH1	2.19	0.55
1:E:103:PRO:HA	1:E:107:ASP:OD2	2.06	0.55
1:L:156:ASN:HD21	1:L:172:LEU:N	2.03	0.55
1:H:175:THR:HG22	1:H:176:VAL:HG23	1.87	0.55
1:H:333:LEU:CB	1:H:338:TRP:CE2	2.82	0.55
1:B:41:TYR:CE2	1:B:71:ARG:NE	2.62	0.55
1:F:329:LEU:O	1:F:333:LEU:HD21	2.07	0.55
1:H:333:LEU:CB	1:H:338:TRP:HZ2	2.14	0.55
1:K:279:THR:C	1:K:281:LEU:N	2.64	0.55
1:G:79:LEU:HB3	1:G:126:LEU:HD13	1.88	0.55
1:D:80:SER:O	1:D:81:GLU:HG3	2.07	0.55
1:F:29:ARG:HD3	1:F:107:ASP:OD2	2.07	0.55
1:J:70:ILE:O	1:J:70:ILE:CG2	2.44	0.55
1:L:74:LEU:HD13	1:L:79:LEU:HD12	1.89	0.55
1:G:333:LEU:HD12	1:G:338:TRP:CE2	2.32	0.54
1:L:176:VAL:HB	1:L:177:PRO:HD2	1.89	0.54
1:L:104:GLY:H	1:L:105:PRO:HD2	1.61	0.54
1:D:156:ASN:HD21	1:D:171:ALA:CB	2.12	0.54
1:H:135:VAL:HG12	1:H:135:VAL:O	2.07	0.54
1:I:80:SER:O	1:I:81:GLU:HG3	2.08	0.54
1:K:333:LEU:HD12	1:K:338:TRP:HE1	1.72	0.54
1:D:49:LYS:O	1:D:54:PRO:HA	2.06	0.54
1:C:135:VAL:HG12	1:C:135:VAL:O	2.07	0.54
1:H:174:GLY:CA	1:I:44:ASP:OD2	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:103:PRO:C	1:L:105:PRO:HD2	2.33	0.54
1:D:135:VAL:HG12	1:D:135:VAL:O	2.08	0.54
1:J:82:ILE:HD13	1:J:82:ILE:H	1.71	0.54
1:J:156:ASN:HD21	1:J:171:ALA:C	2.16	0.54
1:F:135:VAL:HG12	1:F:135:VAL:O	2.07	0.54
1:G:135:VAL:HG12	1:G:135:VAL:O	2.07	0.54
1:E:303:LYS:HA	1:E:306:PRO:HB3	1.90	0.54
1:I:73:PRO:CG	1:I:89:VAL:CG1	2.59	0.54
1:M:49:LYS:O	1:M:54:PRO:HA	2.07	0.54
1:H:277:GLN:HE22	1:I:239:GLY:HA3	1.73	0.54
1:J:156:ASN:HD21	1:J:172:LEU:N	2.05	0.54
1:C:104:GLY:N	1:C:105:PRO:CD	2.71	0.54
1:H:171:ALA:C	1:H:172:LEU:O	2.44	0.54
1:L:135:VAL:HG12	1:L:135:VAL:O	2.07	0.54
1:B:107:ASP:O	1:B:108:GLU:C	2.51	0.53
1:I:135:VAL:HG12	1:I:135:VAL:O	2.07	0.53
1:M:334:PRO:O	1:M:335:PRO:C	2.50	0.53
1:M:76:ASP:HB3	1:M:166:THR:HG23	1.89	0.53
1:G:79:LEU:HB3	1:G:126:LEU:HD12	1.90	0.53
1:B:333:LEU:HD12	1:B:338:TRP:HE1	1.72	0.53
1:C:179:PRO:HA	1:C:182:GLN:HG2	1.90	0.53
1:F:333:LEU:CD1	1:F:338:TRP:HE1	2.21	0.53
1:M:333:LEU:HB3	1:M:338:TRP:CZ2	2.43	0.53
1:K:81:GLU:C	1:K:82:ILE:HG12	2.34	0.53
1:F:175:THR:CG2	1:G:44:ASP:OD2	2.57	0.53
1:I:76:ASP:OD1	3:I:402:ADP:O2B	2.25	0.53
1:C:107:ASP:C	1:C:109:ILE:N	2.66	0.53
1:A:303:LYS:HA	1:A:306:PRO:HB3	1.90	0.53
1:B:135:VAL:HG12	1:B:135:VAL:O	2.07	0.53
1:M:135:VAL:HG12	1:M:135:VAL:O	2.07	0.53
1:B:41:TYR:HE2	1:B:71:ARG:CD	2.22	0.53
1:H:103:PRO:C	1:H:105:PRO:HD2	2.32	0.53
1:K:104:GLY:H	1:K:105:PRO:HD3	1.69	0.53
1:K:107:ASP:HB2	1:K:109:ILE:HD11	1.91	0.53
1:D:81:GLU:O	1:D:82:ILE:HB	2.08	0.53
1:D:333:LEU:HD12	1:D:338:TRP:HE1	1.73	0.53
1:L:333:LEU:HD13	1:L:338:TRP:CE2	2.41	0.53
1:D:73:PRO:CB	1:D:89:VAL:CG1	2.83	0.52
1:E:333:LEU:HG	1:E:337:TYR:CZ	2.44	0.52
1:F:79:LEU:CD1	1:F:127:LEU:CD2	2.86	0.52
1:F:118:ARG:NH1	1:M:118:ARG:HH12	2.07	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:73:PRO:HB3	1:B:89:VAL:CG1	2.39	0.52
1:K:73:PRO:HB3	1:K:89:VAL:CG1	2.39	0.52
1:B:279:THR:C	1:B:281:LEU:N	2.63	0.52
1:I:76:ASP:HB2	1:I:165:GLY:CA	2.24	0.52
1:M:87:ILE:O	1:M:87:ILE:CG2	2.57	0.52
1:L:332:GLU:C	1:L:333:LEU:HG	2.35	0.52
1:I:81:GLU:C	1:I:82:ILE:HG12	2.34	0.52
1:L:155:ILE:HG23	1:L:156:ASN:HB2	1.91	0.52
1:B:175:THR:HG23	1:C:44:ASP:OD2	2.10	0.52
1:D:334:PRO:C	1:D:336:GLN:N	2.68	0.52
1:N:333:LEU:N	1:N:333:LEU:CD1	2.73	0.52
1:J:74:LEU:CD2	1:J:79:LEU:N	2.72	0.52
1:C:155:ILE:CD1	1:C:172:LEU:HB2	2.37	0.52
1:B:334:PRO:O	1:B:335:PRO:C	2.53	0.52
1:F:334:PRO:O	1:F:335:PRO:C	2.53	0.52
1:J:156:ASN:CG	1:J:172:LEU:N	2.67	0.52
1:C:71:ARG:O	1:C:73:PRO:HD3	2.10	0.52
1:D:155:ILE:HB	1:E:67:TYR:OH	2.10	0.52
1:L:87:ILE:O	1:L:87:ILE:CG2	2.49	0.52
1:M:155:ILE:HB	1:N:67:TYR:OH	2.10	0.52
1:I:155:ILE:HB	1:J:67:TYR:OH	2.10	0.51
1:J:303:LYS:HA	1:J:306:PRO:HB3	1.91	0.51
1:K:276:TYR:OH	1:L:66:SER:CB	2.58	0.51
1:L:71:ARG:O	1:L:73:PRO:HD3	2.10	0.51
1:E:87:ILE:O	1:E:87:ILE:CG2	2.57	0.51
1:N:303:LYS:HA	1:N:306:PRO:HB3	1.92	0.51
1:F:76:ASP:HB3	1:F:166:THR:CG2	2.40	0.51
1:F:155:ILE:HB	1:G:67:TYR:OH	2.10	0.51
1:J:157:THR:O	1:J:159:ILE:N	2.43	0.51
1:K:334:PRO:O	1:K:335:PRO:C	2.53	0.51
1:E:155:ILE:N	1:E:155:ILE:CD1	2.73	0.51
1:M:73:PRO:CG	1:M:89:VAL:HG11	2.40	0.51
1:B:333:LEU:CD1	1:B:338:TRP:HE1	2.24	0.51
1:I:108:GLU:O	1:I:108:GLU:HG2	2.09	0.51
1:K:155:ILE:HG22	1:K:276:TYR:CE1	2.45	0.51
1:N:73:PRO:O	1:N:79:LEU:HD23	2.11	0.51
1:J:333:LEU:HA	1:J:337:TYR:CB	2.40	0.51
1:A:122:ALA:O	1:A:126:LEU:HG	2.10	0.51
1:B:81:GLU:C	1:B:82:ILE:HG12	2.36	0.51
1:H:156:ASN:HD21	1:H:171:ALA:C	2.18	0.51
1:A:155:ILE:N	1:A:155:ILE:CD1	2.73	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:104:GLY:H	1:B:105:PRO:HD3	1.69	0.51
1:F:81:GLU:C	1:F:82:ILE:HG12	2.35	0.51
1:D:79:LEU:CD2	1:D:130:MET:SD	2.95	0.50
1:J:156:ASN:ND2	1:J:172:LEU:N	2.59	0.50
1:J:333:LEU:N	1:J:333:LEU:CD1	2.73	0.50
1:K:175:THR:HG23	1:L:44:ASP:OD2	2.10	0.50
1:L:173:LYS:CE	1:L:180:GLU:HG3	2.41	0.50
1:M:79:LEU:C	1:M:126:LEU:HD21	2.31	0.50
1:N:333:LEU:HA	1:N:337:TYR:CB	2.40	0.50
1:G:156:ASN:HD21	1:G:171:ALA:C	2.19	0.50
1:K:107:ASP:O	1:K:108:GLU:O	2.30	0.50
1:G:73:PRO:HB3	1:G:82:ILE:HD11	1.94	0.50
1:J:82:ILE:HG22	1:J:84:ASP:HB2	1.94	0.50
1:N:107:ASP:HB3	1:N:109:ILE:HD11	1.94	0.50
1:D:333:LEU:CD1	1:D:338:TRP:HE1	2.24	0.50
1:F:258:MET:N	1:F:259:PRO:CD	2.75	0.50
1:L:173:LYS:CG	1:L:180:GLU:CG	2.71	0.50
1:C:157:THR:HG21	1:C:285:VAL:HG23	1.94	0.50
1:D:122:ALA:O	1:D:126:LEU:HG	2.11	0.50
1:K:258:MET:N	1:K:259:PRO:CD	2.74	0.50
1:B:258:MET:N	1:B:259:PRO:CD	2.75	0.50
1:F:155:ILE:HG22	1:F:276:TYR:CE1	2.46	0.50
1:J:74:LEU:HD21	1:J:79:LEU:HD13	1.92	0.50
1:H:79:LEU:HG	1:H:79:LEU:O	2.12	0.49
1:J:296:LEU:HD23	1:J:296:LEU:C	2.37	0.49
1:N:158:ILE:O	1:N:284:ILE:HG23	2.12	0.49
1:E:296:LEU:HD23	1:E:296:LEU:C	2.37	0.49
1:E:334:PRO:C	1:E:336:GLN:H	2.20	0.49
1:H:87:ILE:O	1:H:87:ILE:CG2	2.49	0.49
1:M:82:ILE:O	1:M:84:ASP:CA	2.57	0.49
1:N:134:VAL:O	1:N:135:VAL:HG13	2.12	0.49
1:F:175:THR:CG2	1:G:44:ASP:CG	2.84	0.49
1:D:104:GLY:H	1:D:105:PRO:HD2	1.71	0.49
1:K:333:LEU:CD1	1:K:338:TRP:HE1	2.24	0.49
1:M:334:PRO:C	1:M:336:GLN:N	2.70	0.49
1:A:296:LEU:C	1:A:296:LEU:HD23	2.37	0.49
1:L:276:TYR:CZ	1:M:66:SER:HB2	2.42	0.49
1:M:73:PRO:HG3	1:M:89:VAL:CG1	2.43	0.49
1:H:76:ASP:CB	1:H:165:GLY:HA3	2.40	0.49
1:N:296:LEU:C	1:N:296:LEU:HD23	2.37	0.49
1:C:176:VAL:N	1:C:177:PRO:HD3	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:258:MET:N	1:I:259:PRO:CD	2.76	0.49
1:C:176:VAL:CG2	1:D:44:ASP:OD2	2.59	0.49
1:L:157:THR:CG2	1:L:285:VAL:HG23	2.43	0.49
1:E:107:ASP:HB3	1:E:109:ILE:HD11	1.94	0.49
1:D:71:ARG:C	1:D:72:TYR:O	2.56	0.48
1:C:87:ILE:O	1:C:87:ILE:CG2	2.49	0.48
1:C:155:ILE:HG13	1:C:156:ASN:CB	2.43	0.48
1:M:155:ILE:HA	1:M:156:ASN:HA	1.51	0.48
1:N:156:ASN:CG	1:N:172:LEU:N	2.71	0.48
1:I:78:VAL:HG11	1:I:113:ILE:HG21	1.87	0.48
1:J:107:ASP:HB3	1:J:109:ILE:HD11	1.94	0.48
1:N:156:ASN:HD21	1:N:171:ALA:C	2.22	0.48
1:N:87:ILE:O	1:N:87:ILE:CG2	2.57	0.48
1:C:157:THR:O	1:C:158:ILE:C	2.56	0.48
1:D:258:MET:N	1:D:259:PRO:CD	2.76	0.48
1:J:71:ARG:O	1:J:73:PRO:CD	2.57	0.48
1:M:258:MET:N	1:M:259:PRO:CD	2.76	0.48
1:A:107:ASP:HB3	1:A:109:ILE:HD11	1.94	0.48
1:I:81:GLU:O	1:I:82:ILE:HG12	2.13	0.48
1:L:176:VAL:HB	1:L:177:PRO:CD	2.37	0.48
1:C:105:PRO:O	1:C:106:ASN:C	2.56	0.48
1:C:179:PRO:HA	1:C:182:GLN:CD	2.39	0.48
1:D:331:GLU:HA	1:D:332:GLU:HA	1.60	0.48
1:N:155:ILE:HG12	1:N:174:GLY:HA2	1.96	0.48
1:N:156:ASN:HD21	1:N:172:LEU:N	2.11	0.48
1:I:87:ILE:O	1:I:87:ILE:CG2	2.57	0.48
1:J:155:ILE:HG12	1:J:174:GLY:HA2	1.96	0.48
1:K:78:VAL:CG2	1:K:116:PRO:CD	2.91	0.48
1:G:81:GLU:O	1:G:82:ILE:C	2.57	0.48
1:H:77:GLY:HA3	1:H:166:THR:HG23	1.94	0.48
1:H:334:PRO:O	1:H:336:GLN:N	2.47	0.48
1:L:175:THR:HG21	1:M:43:LYS:NZ	2.28	0.48
1:B:135:VAL:O	1:B:136:HIS:CG	2.67	0.47
1:B:156:ASN:HD21	1:B:172:LEU:N	2.12	0.47
1:D:94:LEU:HD21	1:D:130:MET:HE2	1.96	0.47
1:G:73:PRO:HB3	1:G:82:ILE:CD1	2.44	0.47
1:N:157:THR:O	1:N:159:ILE:N	2.47	0.47
1:B:76:ASP:HB3	1:B:166:THR:HG23	1.94	0.47
1:B:78:VAL:CG2	1:B:116:PRO:CD	2.92	0.47
1:B:106:ASN:C	1:B:108:GLU:N	2.72	0.47
1:G:71:ARG:O	1:G:73:PRO:HD3	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:74:LEU:HD22	1:J:79:LEU:N	2.29	0.47
1:K:155:ILE:CG1	1:L:67:TYR:OH	2.61	0.47
1:K:334:PRO:C	1:K:336:GLN:N	2.72	0.47
1:M:104:GLY:H	1:M:105:PRO:HD2	1.63	0.47
1:H:333:LEU:CG	1:H:338:TRP:NE1	2.74	0.47
1:I:155:ILE:HG12	1:I:174:GLY:HA2	1.97	0.47
1:J:204:HIS:N	1:J:205:PRO:CD	2.78	0.47
1:H:329:LEU:O	1:H:333:LEU:CG	2.53	0.47
1:A:334:PRO:O	1:A:337:TYR:N	2.47	0.47
1:E:204:HIS:N	1:E:205:PRO:CD	2.78	0.47
1:E:334:PRO:HB3	1:E:335:PRO:HD2	1.96	0.47
1:F:135:VAL:O	1:F:136:HIS:CG	2.67	0.47
1:F:331:GLU:HA	1:F:332:GLU:HA	1.59	0.47
1:L:173:LYS:HE2	1:L:180:GLU:CG	2.44	0.47
1:M:42:PRO:HG2	1:M:49:LYS:CG	2.44	0.47
1:A:204:HIS:N	1:A:205:PRO:CD	2.78	0.47
1:F:334:PRO:C	1:F:336:GLN:N	2.72	0.47
1:H:155:ILE:HA	1:H:156:ASN:HA	1.47	0.47
1:M:104:GLY:H	1:M:105:PRO:HD3	1.75	0.47
1:B:78:VAL:HG22	1:B:123:ASN:ND2	2.29	0.47
1:C:156:ASN:HD21	1:C:172:LEU:C	2.23	0.47
1:E:333:LEU:HA	1:E:337:TYR:CB	2.44	0.47
1:F:155:ILE:HA	1:F:156:ASN:HA	1.49	0.47
1:I:155:ILE:HA	1:I:156:ASN:HA	1.51	0.47
1:K:134:VAL:O	1:K:135:VAL:HB	2.12	0.47
1:L:333:LEU:HB2	1:L:338:TRP:CE2	2.49	0.47
1:N:157:THR:HG21	1:N:285:VAL:CG2	2.42	0.47
1:B:331:GLU:HA	1:B:332:GLU:HA	1.61	0.47
1:I:71:ARG:HH11	1:I:71:ARG:CG	2.27	0.47
1:K:106:ASN:C	1:K:108:GLU:N	2.72	0.47
1:N:204:HIS:N	1:N:205:PRO:CD	2.78	0.47
1:C:37:SER:O	1:C:38:VAL:HB	2.15	0.47
1:F:78:VAL:CG2	1:F:123:ASN:ND2	2.78	0.47
1:H:37:SER:O	1:H:38:VAL:HB	2.15	0.47
1:H:173:LYS:CG	1:H:174:GLY:N	2.59	0.47
1:K:331:GLU:HA	1:K:332:GLU:HA	1.61	0.47
1:B:334:PRO:C	1:B:336:GLN:N	2.72	0.46
1:G:37:SER:O	1:G:38:VAL:HB	2.15	0.46
1:G:76:ASP:O	1:G:166:THR:CG2	2.63	0.46
1:L:104:GLY:H	1:L:105:PRO:HD3	1.78	0.46
1:A:87:ILE:O	1:A:87:ILE:CG2	2.57	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:29:ARG:HH22	1:D:105:PRO:HD3	1.80	0.46
1:F:84:ASP:O	1:M:202:GLU:OE2	2.32	0.46
1:K:37:SER:O	1:K:38:VAL:HB	2.16	0.46
1:K:145:PHE:N	1:K:145:PHE:CD1	2.84	0.46
1:K:155:ILE:HG12	1:L:67:TYR:OH	2.16	0.46
1:L:110:CYS:HB2	1:L:338:TRP:CH2	2.51	0.46
1:L:175:THR:CG2	1:M:43:LYS:CE	2.92	0.46
1:A:258:MET:N	1:A:259:PRO:CD	2.79	0.46
1:F:37:SER:O	1:F:38:VAL:HB	2.16	0.46
1:J:87:ILE:O	1:J:87:ILE:CG2	2.57	0.46
1:K:155:ILE:HA	1:K:156:ASN:HA	1.48	0.46
1:C:74:LEU:HD21	1:C:79:LEU:HG	1.97	0.46
1:L:37:SER:O	1:L:38:VAL:HB	2.15	0.46
1:M:155:ILE:HG12	1:M:174:GLY:HA2	1.97	0.46
1:N:258:MET:N	1:N:259:PRO:CD	2.79	0.46
1:F:109:ILE:HB	1:F:136:HIS:HE1	1.81	0.46
1:I:29:ARG:HH22	1:I:105:PRO:HD3	1.81	0.46
1:J:82:ILE:O	1:J:83:SER:C	2.55	0.46
1:H:334:PRO:O	1:H:335:PRO:C	2.59	0.46
1:J:157:THR:HG21	1:J:285:VAL:CG2	2.39	0.46
1:K:78:VAL:HG22	1:K:123:ASN:ND2	2.30	0.46
1:M:71:ARG:HB3	1:M:83:SER:OG	2.16	0.46
1:C:74:LEU:CD2	1:C:79:LEU:CG	2.94	0.46
1:D:155:ILE:HA	1:D:156:ASN:HA	1.51	0.46
1:B:37:SER:O	1:B:38:VAL:HB	2.16	0.46
1:I:331:GLU:HA	1:I:332:GLU:HA	1.69	0.46
1:D:37:SER:O	1:D:38:VAL:HB	2.17	0.45
1:F:107:ASP:C	1:F:109:ILE:N	2.74	0.45
1:I:37:SER:O	1:I:38:VAL:HB	2.17	0.45
1:K:76:ASP:HB3	1:K:166:THR:HG23	1.98	0.45
1:B:78:VAL:CG2	1:B:116:PRO:CG	2.95	0.45
1:J:333:LEU:N	1:J:333:LEU:HD12	2.32	0.45
1:N:106:ASN:O	1:N:108:GLU:N	2.49	0.45
1:B:174:GLY:HA3	1:C:67:TYR:HE1	1.81	0.45
1:C:177:PRO:CG	1:C:180:GLU:CB	2.79	0.45
1:G:155:ILE:HA	1:G:156:ASN:HA	1.47	0.45
1:H:155:ILE:HG21	1:I:67:TYR:HE1	1.80	0.45
1:J:258:MET:N	1:J:259:PRO:CD	2.79	0.45
1:L:155:ILE:HD12	1:L:155:ILE:N	2.31	0.45
1:M:333:LEU:CD1	1:M:338:TRP:NE1	2.75	0.45
1:B:145:PHE:CD1	1:B:145:PHE:N	2.84	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:87:ILE:O	1:D:87:ILE:CG2	2.57	0.45
1:L:173:LYS:CD	1:L:180:GLU:HG3	2.46	0.45
1:N:156:ASN:ND2	1:N:172:LEU:N	2.65	0.45
1:D:155:ILE:HG12	1:D:174:GLY:HA2	1.98	0.45
1:F:175:THR:HG22	1:G:44:ASP:OD2	2.17	0.45
1:M:49:LYS:O	1:M:54:PRO:N	2.49	0.45
1:B:104:GLY:H	1:B:105:PRO:HD2	1.71	0.45
1:D:79:LEU:HB3	1:D:126:LEU:HD13	1.98	0.45
1:F:175:THR:HG23	1:G:44:ASP:OD2	2.17	0.45
1:E:258:MET:N	1:E:259:PRO:CD	2.79	0.45
1:E:73:PRO:O	1:E:79:LEU:HD23	2.17	0.45
1:I:49:LYS:O	1:I:54:PRO:N	2.50	0.45
1:K:78:VAL:CG2	1:K:116:PRO:CG	2.94	0.45
1:M:248:GLU:N	1:M:249:PRO:CD	2.80	0.45
1:D:42:PRO:HG2	1:D:49:LYS:HB2	1.99	0.45
1:F:145:PHE:N	1:F:145:PHE:CD1	2.84	0.45
1:L:80:SER:O	1:L:126:LEU:HD11	2.17	0.45
1:L:157:THR:HG21	1:L:285:VAL:HG23	1.98	0.45
1:H:258:MET:N	1:H:259:PRO:CD	2.80	0.44
1:M:298:ALA:O	1:M:302:GLU:HB2	2.17	0.44
1:N:157:THR:O	1:N:159:ILE:HG13	2.17	0.44
1:D:298:ALA:O	1:D:302:GLU:HB2	2.16	0.44
1:D:333:LEU:HB3	1:D:338:TRP:CZ2	2.52	0.44
1:I:204:HIS:N	1:I:205:PRO:CD	2.80	0.44
1:K:298:ALA:O	1:K:302:GLU:HB2	2.17	0.44
1:M:78:VAL:CG1	1:M:79:LEU:N	2.38	0.44
1:M:82:ILE:HG23	1:M:89:VAL:HG23	1.96	0.44
1:C:74:LEU:CD2	1:C:79:LEU:HG	2.48	0.44
1:D:49:LYS:O	1:D:54:PRO:N	2.50	0.44
1:D:204:HIS:N	1:D:205:PRO:CD	2.80	0.44
1:I:248:GLU:N	1:I:249:PRO:CD	2.80	0.44
1:J:258:MET:HB2	1:J:259:PRO:HD3	2.00	0.44
1:M:37:SER:O	1:M:38:VAL:HB	2.17	0.44
1:B:76:ASP:HB3	1:B:166:THR:CG2	2.48	0.44
1:B:107:ASP:O	1:B:108:GLU:O	2.35	0.44
1:D:248:GLU:N	1:D:249:PRO:CD	2.80	0.44
1:D:258:MET:HB2	1:D:259:PRO:HD3	1.99	0.44
1:I:42:PRO:HG2	1:I:49:LYS:HB2	1.99	0.44
1:I:71:ARG:HB3	1:I:83:SER:OG	2.18	0.44
1:I:258:MET:HB2	1:I:259:PRO:HD3	1.99	0.44
1:B:155:ILE:HA	1:B:156:ASN:HA	1.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:18:LEU:CD2	1:C:74:LEU:CD1	2.88	0.44
1:E:37:SER:O	1:E:38:VAL:HB	2.18	0.44
1:E:258:MET:HB2	1:E:259:PRO:HD3	2.00	0.44
1:C:80:SER:O	1:C:126:LEU:HD11	2.17	0.44
1:J:158:ILE:O	1:J:284:ILE:HG23	2.17	0.44
1:L:258:MET:N	1:L:259:PRO:CD	2.80	0.44
1:A:258:MET:HB2	1:A:259:PRO:HD3	2.00	0.44
1:G:258:MET:N	1:G:259:PRO:CD	2.80	0.44
1:I:333:LEU:CD1	1:I:337:TYR:CD1	3.01	0.44
1:M:82:ILE:O	1:M:83:SER:C	2.46	0.44
1:C:258:MET:N	1:C:259:PRO:CD	2.80	0.44
1:I:298:ALA:O	1:I:302:GLU:HB2	2.17	0.44
1:J:157:THR:O	1:J:159:ILE:HG13	2.18	0.44
1:M:204:HIS:N	1:M:205:PRO:CD	2.80	0.44
1:N:37:SER:O	1:N:38:VAL:HB	2.18	0.44
1:N:134:VAL:O	1:N:135:VAL:CB	2.66	0.44
1:N:333:LEU:N	1:N:333:LEU:HD12	2.32	0.44
1:N:333:LEU:CA	1:N:337:TYR:HB3	2.48	0.44
1:A:37:SER:O	1:A:38:VAL:HB	2.18	0.44
1:C:76:ASP:O	1:C:166:THR:CG2	2.66	0.44
1:C:155:ILE:HA	1:C:156:ASN:HA	1.50	0.44
1:E:334:PRO:O	1:E:336:GLN:N	2.51	0.44
1:L:334:PRO:HA	1:L:335:PRO:HD3	1.94	0.44
1:N:258:MET:HB2	1:N:259:PRO:HD3	2.00	0.44
1:A:80:SER:OG	1:A:82:ILE:HD13	2.18	0.43
1:E:155:ILE:HA	1:E:156:ASN:HA	1.49	0.43
1:E:334:PRO:C	1:E:336:GLN:N	2.74	0.43
1:L:258:MET:HB2	1:L:259:PRO:HD3	2.00	0.43
1:F:298:ALA:O	1:F:302:GLU:HB2	2.17	0.43
1:M:258:MET:HB2	1:M:259:PRO:HD3	1.99	0.43
1:D:240:LYS:N	1:D:241:PRO:CD	2.81	0.43
1:A:18:LEU:HD21	1:A:74:LEU:HD11	2.01	0.43
1:B:240:LYS:N	1:B:241:PRO:CD	2.82	0.43
1:B:298:ALA:O	1:B:302:GLU:HB2	2.17	0.43
1:H:104:GLY:H	1:H:105:PRO:HD3	1.77	0.43
1:M:331:GLU:HA	1:M:332:GLU:HA	1.60	0.43
1:B:109:ILE:HB	1:B:136:HIS:HE1	1.82	0.43
1:C:258:MET:HB2	1:C:259:PRO:HD3	2.00	0.43
1:H:331:GLU:CG	1:H:332:GLU:HA	2.48	0.43
1:I:240:LYS:N	1:I:241:PRO:CD	2.81	0.43
1:L:157:THR:HG1	1:L:282:GLN:HB3	1.79	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:79:LEU:CA	1:M:126:LEU:HD23	2.48	0.43
1:B:109:ILE:C	1:B:136:HIS:HD1	2.24	0.43
1:D:71:ARG:O	1:D:73:PRO:HD3	2.19	0.43
1:F:276:TYR:OH	1:G:66:SER:OG	2.35	0.43
1:H:276:TYR:CZ	1:I:66:SER:CB	3.00	0.43
1:K:135:VAL:O	1:K:135:VAL:HG22	2.18	0.43
1:K:155:ILE:CG2	1:K:276:TYR:CE1	3.01	0.43
1:K:258:MET:HB2	1:K:259:PRO:HD3	2.01	0.43
1:M:333:LEU:HG	1:M:338:TRP:HE1	1.81	0.43
1:E:240:LYS:N	1:E:241:PRO:CD	2.82	0.43
1:F:155:ILE:CG2	1:F:276:TYR:CE1	3.01	0.43
1:J:248:GLU:N	1:J:249:PRO:CD	2.82	0.43
1:J:333:LEU:CA	1:J:337:TYR:HB3	2.47	0.43
1:M:240:LYS:N	1:M:241:PRO:CD	2.81	0.43
1:N:240:LYS:N	1:N:241:PRO:CD	2.82	0.43
1:A:248:GLU:N	1:A:249:PRO:CD	2.82	0.43
1:E:248:GLU:N	1:E:249:PRO:CD	2.82	0.43
1:H:258:MET:HB2	1:H:259:PRO:HD3	2.00	0.43
1:H:341:LEU:O	1:H:341:LEU:HG	2.19	0.43
1:J:240:LYS:N	1:J:241:PRO:CD	2.82	0.43
1:D:79:LEU:CD1	1:D:126:LEU:HB3	2.42	0.43
1:G:341:LEU:O	1:G:341:LEU:HG	2.19	0.43
1:K:81:GLU:O	1:K:82:ILE:HG12	2.17	0.43
1:N:248:GLU:N	1:N:249:PRO:CD	2.82	0.43
1:A:240:LYS:N	1:A:241:PRO:CD	2.82	0.43
1:B:258:MET:HB2	1:B:259:PRO:HD3	2.01	0.43
1:B:305:ARG:N	1:B:306:PRO:HA	2.34	0.43
1:G:258:MET:HB2	1:G:259:PRO:HD3	2.00	0.43
1:H:77:GLY:HA3	1:H:166:THR:CG2	2.49	0.43
1:F:78:VAL:CB	1:F:116:PRO:CG	2.82	0.42
1:I:333:LEU:CD1	1:I:337:TYR:CE1	3.02	0.42
1:N:155:ILE:HA	1:N:156:ASN:HA	1.49	0.42
1:E:334:PRO:CB	1:E:335:PRO:CD	2.97	0.42
1:F:240:LYS:N	1:F:241:PRO:CD	2.82	0.42
1:G:110:CYS:HB2	1:G:338:TRP:CH2	2.53	0.42
1:I:18:LEU:HD13	1:I:77:GLY:O	2.19	0.42
1:J:37:SER:O	1:J:38:VAL:HB	2.18	0.42
1:L:341:LEU:HG	1:L:341:LEU:O	2.19	0.42
1:M:71:ARG:O	1:M:73:PRO:HD3	2.19	0.42
1:C:81:GLU:O	1:C:82:ILE:C	2.63	0.42
1:K:240:LYS:N	1:K:241:PRO:CD	2.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:341:LEU:O	1:B:341:LEU:HG	2.20	0.42
1:H:174:GLY:O	1:I:44:ASP:CG	2.57	0.42
1:J:106:ASN:O	1:J:108:GLU:N	2.52	0.42
1:B:156:ASN:HD21	1:B:171:ALA:C	2.27	0.42
1:C:179:PRO:HA	1:C:182:GLN:CG	2.49	0.42
1:D:71:ARG:HB3	1:D:83:SER:OG	2.20	0.42
1:I:305:ARG:N	1:I:306:PRO:HA	2.35	0.42
1:I:341:LEU:O	1:I:341:LEU:HG	2.20	0.42
1:K:109:ILE:CG2	1:K:136:HIS:CE1	3.02	0.42
1:K:204:HIS:N	1:K:205:PRO:CD	2.83	0.42
1:M:305:ARG:N	1:M:306:PRO:HA	2.35	0.42
1:F:76:ASP:HB3	1:F:166:THR:HG23	2.01	0.42
1:G:248:GLU:N	1:G:249:PRO:CD	2.83	0.42
1:H:248:GLU:N	1:H:249:PRO:CD	2.83	0.42
1:C:248:GLU:N	1:C:249:PRO:CD	2.83	0.42
1:D:29:ARG:HH22	1:D:105:PRO:CD	2.33	0.42
1:D:305:ARG:N	1:D:306:PRO:HA	2.35	0.42
1:F:78:VAL:CG2	1:F:116:PRO:CG	2.98	0.42
1:F:204:HIS:N	1:F:205:PRO:CD	2.83	0.42
1:G:157:THR:O	1:G:159:ILE:HG13	2.19	0.42
1:H:73:PRO:HB3	1:H:82:ILE:HD11	2.02	0.42
1:J:79:LEU:O	1:J:80:SER:O	2.38	0.42
1:K:109:ILE:HG22	1:K:136:HIS:CE1	2.54	0.42
1:L:157:THR:O	1:L:158:ILE:C	2.63	0.42
1:L:173:LYS:CB	1:L:180:GLU:HB3	2.49	0.42
1:A:333:LEU:HG	1:A:337:TYR:CE1	2.52	0.42
1:D:80:SER:C	1:D:81:GLU:HG3	2.45	0.42
1:F:18:LEU:CD2	1:F:74:LEU:HD21	2.49	0.42
1:F:109:ILE:O	1:F:136:HIS:ND1	2.33	0.42
1:F:258:MET:HB2	1:F:259:PRO:HD3	2.00	0.42
1:I:81:GLU:O	1:I:82:ILE:CG1	2.67	0.42
1:L:180:GLU:CD	1:L:180:GLU:C	2.86	0.42
1:L:333:LEU:CG	1:L:338:TRP:CZ2	3.03	0.42
1:M:156:ASN:ND2	1:M:172:LEU:H	2.17	0.42
1:A:333:LEU:HA	1:A:337:TYR:HB3	2.02	0.42
1:B:204:HIS:N	1:B:205:PRO:CD	2.83	0.42
1:E:18:LEU:CD2	1:E:74:LEU:HD11	2.49	0.42
1:E:333:LEU:N	1:E:334:PRO:CD	2.78	0.42
1:H:157:THR:O	1:H:159:ILE:HG13	2.19	0.42
1:I:29:ARG:HH22	1:I:105:PRO:CD	2.33	0.42
1:I:80:SER:C	1:I:81:GLU:HG3	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:210:ASN:OD1	1:M:210:ASN:C	2.63	0.42
1:D:210:ASN:OD1	1:D:210:ASN:C	2.63	0.42
1:F:81:GLU:O	1:F:82:ILE:HG12	2.20	0.42
1:F:109:ILE:HB	1:F:136:HIS:CE1	2.55	0.42
1:K:305:ARG:N	1:K:306:PRO:HA	2.34	0.42
1:B:107:ASP:HB2	1:B:109:ILE:HD11	2.01	0.41
1:C:210:ASN:C	1:C:210:ASN:OD1	2.63	0.41
1:F:305:ARG:N	1:F:306:PRO:HA	2.34	0.41
1:L:298:ALA:O	1:L:302:GLU:HB2	2.20	0.41
1:C:333:LEU:N	1:C:333:LEU:CD2	2.83	0.41
1:C:341:LEU:O	1:C:341:LEU:HG	2.19	0.41
1:F:333:LEU:HB3	1:F:338:TRP:CZ2	2.55	0.41
1:F:341:LEU:O	1:F:341:LEU:HG	2.19	0.41
1:G:77:GLY:HA3	1:G:166:THR:HG21	1.98	0.41
1:I:157:THR:HG23	1:I:283:ASN:O	2.20	0.41
1:L:73:PRO:HB3	1:L:82:ILE:HD11	2.02	0.41
1:L:248:GLU:N	1:L:249:PRO:CD	2.83	0.41
1:A:49:LYS:HB2	1:A:54:PRO:HA	2.02	0.41
1:D:334:PRO:C	1:D:336:GLN:H	2.27	0.41
1:E:334:PRO:O	1:E:337:TYR:N	2.53	0.41
1:F:104:GLY:H	1:F:105:PRO:HD3	1.83	0.41
1:H:156:ASN:HD21	1:H:172:LEU:N	2.17	0.41
1:K:76:ASP:HB3	1:K:166:THR:CG2	2.51	0.41
1:K:334:PRO:HA	1:K:335:PRO:HD3	1.91	0.41
1:L:76:ASP:O	1:L:166:THR:CG2	2.68	0.41
1:M:341:LEU:O	1:M:341:LEU:HG	2.20	0.41
1:N:134:VAL:C	1:N:135:VAL:CG1	2.84	0.41
1:B:41:TYR:OH	1:B:71:ARG:NE	2.54	0.41
1:I:78:VAL:HB	1:I:79:LEU:H	1.68	0.41
1:G:158:ILE:O	1:G:284:ILE:HG23	2.20	0.41
1:N:67:TYR:CD1	1:N:67:TYR:N	2.89	0.41
1:A:333:LEU:HB3	1:A:338:TRP:NE1	2.35	0.41
1:B:81:GLU:O	1:B:82:ILE:HG12	2.21	0.41
1:B:155:ILE:HG23	1:B:156:ASN:HB2	2.03	0.41
1:C:173:LYS:O	1:D:67:TYR:HE1	2.03	0.41
1:C:173:LYS:O	1:D:67:TYR:CE1	2.74	0.41
1:D:157:THR:HG23	1:D:283:ASN:O	2.20	0.41
1:D:341:LEU:O	1:D:341:LEU:HG	2.20	0.41
1:H:298:ALA:O	1:H:302:GLU:HB2	2.20	0.41
1:N:302:GLU:HB3	1:N:303:LYS:H	1.71	0.41
1:B:118:ARG:HH12	1:I:118:ARG:NH1	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:210:ASN:OD1	1:F:210:ASN:C	2.64	0.41
1:J:156:ASN:OD1	1:J:172:LEU:HB2	2.21	0.41
1:N:49:LYS:HB2	1:N:54:PRO:HA	2.03	0.41
1:B:87:ILE:O	1:B:87:ILE:CG2	2.61	0.41
1:K:341:LEU:O	1:K:341:LEU:HG	2.20	0.41
1:M:157:THR:HG23	1:M:283:ASN:O	2.21	0.41
1:A:334:PRO:C	1:A:336:GLN:N	2.58	0.41
1:B:109:ILE:HB	1:B:136:HIS:CE1	2.56	0.41
1:B:332:GLU:O	1:B:332:GLU:HG2	2.20	0.41
1:C:74:LEU:HD21	1:C:79:LEU:CG	2.50	0.41
1:D:29:ARG:NH2	1:D:105:PRO:CD	2.84	0.41
1:D:79:LEU:CD1	1:D:130:MET:SD	3.06	0.41
1:F:46:ILE:O	1:F:46:ILE:HG23	2.21	0.41
1:F:73:PRO:HB3	1:F:89:VAL:HG11	2.03	0.41
1:G:77:GLY:CA	1:G:166:THR:HG23	2.48	0.41
1:G:298:ALA:O	1:G:302:GLU:HB2	2.21	0.41
1:G:331:GLU:CG	1:G:332:GLU:HA	2.49	0.41
1:H:158:ILE:O	1:H:284:ILE:HG23	2.20	0.41
1:H:210:ASN:OD1	1:H:210:ASN:C	2.63	0.41
1:I:210:ASN:OD1	1:I:210:ASN:C	2.63	0.41
1:K:174:GLY:HA3	1:L:67:TYR:HE1	1.86	0.41
1:L:210:ASN:OD1	1:L:210:ASN:C	2.63	0.41
1:N:156:ASN:HD21	1:N:172:LEU:C	2.22	0.41
1:G:139:LEU:HD11	1:G:338:TRP:CE2	2.56	0.41
1:J:158:ILE:HD13	1:J:265:ILE:HG23	2.03	0.41
1:A:67:TYR:CD1	1:A:67:TYR:N	2.89	0.40
1:C:174:GLY:HA2	1:D:67:TYR:CE1	2.55	0.40
1:D:329:LEU:HA	1:D:333:LEU:HD21	2.03	0.40
1:F:334:PRO:HA	1:F:335:PRO:HD3	1.91	0.40
1:I:156:ASN:ND2	1:I:172:LEU:H	2.19	0.40
1:K:210:ASN:OD1	1:K:210:ASN:C	2.64	0.40
1:M:157:THR:O	1:M:159:ILE:HG13	2.21	0.40
1:B:275:GLU:HB3	1:C:65:ARG:NH2	2.36	0.40
1:C:176:VAL:N	1:C:177:PRO:CD	2.84	0.40
1:F:109:ILE:C	1:F:136:HIS:HD1	2.23	0.40
1:D:80:SER:O	1:D:81:GLU:CG	2.70	0.40
1:E:67:TYR:CD1	1:E:67:TYR:N	2.89	0.40
1:A:305:ARG:N	1:A:306:PRO:HA	2.37	0.40
1:B:210:ASN:OD1	1:B:210:ASN:C	2.64	0.40
1:C:298:ALA:O	1:C:302:GLU:HB2	2.21	0.40
1:K:276:TYR:OH	1:L:66:SER:HB2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:334:PRO:C	1:M:336:GLN:H	2.29	0.40
1:N:305:ARG:N	1:N:306:PRO:HA	2.37	0.40
1:H:76:ASP:C	1:H:165:GLY:HA3	2.47	0.40
1:J:67:TYR:CD1	1:J:67:TYR:N	2.89	0.40
1:M:71:ARG:HH11	1:M:71:ARG:CG	2.24	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	326/347 (94%)	287 (88%)	29 (9%)	10 (3%)	3	22
1	B	326/347 (94%)	285 (87%)	28 (9%)	13 (4%)	2	18
1	C	326/347 (94%)	282 (86%)	35 (11%)	9 (3%)	4	24
1	D	326/347 (94%)	281 (86%)	35 (11%)	10 (3%)	3	22
1	E	326/347 (94%)	287 (88%)	30 (9%)	9 (3%)	4	24
1	F	326/347 (94%)	288 (88%)	29 (9%)	9 (3%)	4	24
1	G	326/347 (94%)	289 (89%)	31 (10%)	6 (2%)	6	34
1	H	326/347 (94%)	279 (86%)	36 (11%)	11 (3%)	3	21
1	I	326/347 (94%)	285 (87%)	31 (10%)	10 (3%)	3	22
1	J	326/347 (94%)	287 (88%)	29 (9%)	10 (3%)	3	22
1	K	326/347 (94%)	287 (88%)	28 (9%)	11 (3%)	3	21
1	L	326/347 (94%)	282 (86%)	33 (10%)	11 (3%)	3	21
1	M	326/347 (94%)	283 (87%)	31 (10%)	12 (4%)	2	19
1	N	326/347 (94%)	289 (89%)	27 (8%)	10 (3%)	3	22
All	All	4564/4858 (94%)	3991 (87%)	432 (10%)	141 (3%)	5	22

All (141) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	55	TYR
1	A	108	GLU
1	B	55	TYR
1	B	105	PRO
1	B	134	VAL
1	B	280	VAL
1	C	55	TYR
1	C	73	PRO
1	D	55	TYR
1	D	72	TYR
1	D	73	PRO
1	D	108	GLU
1	D	335	PRO
1	E	55	TYR
1	E	108	GLU
1	F	55	TYR
1	F	73	PRO
1	F	108	GLU
1	F	134	VAL
1	G	55	TYR
1	G	73	PRO
1	G	82	ILE
1	G	108	GLU
1	H	55	TYR
1	H	105	PRO
1	H	108	GLU
1	H	172	LEU
1	H	179	PRO
1	I	73	PRO
1	I	82	ILE
1	I	108	GLU
1	J	55	TYR
1	J	80	SER
1	J	83	SER
1	J	107	ASP
1	J	108	GLU
1	J	158	ILE
1	J	335	PRO
1	K	55	TYR
1	K	105	PRO
1	K	135	VAL
1	K	280	VAL

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Mol	Chain	Res	Type
1	L	55	TYR
1	L	73	PRO
1	L	105	PRO
1	L	108	GLU
1	L	176	VAL
1	L	177	PRO
1	M	73	PRO
1	M	83	SER
1	M	105	PRO
1	M	108	GLU
1	M	335	PRO
1	N	55	TYR
1	N	107	ASP
1	N	108	GLU
1	N	158	ILE
1	N	335	PRO
1	A	38	VAL
1	A	107	ASP
1	B	38	VAL
1	B	82	ILE
1	B	107	ASP
1	B	158	ILE
1	B	335	PRO
1	C	38	VAL
1	C	82	ILE
1	C	108	GLU
1	D	38	VAL
1	D	309	ASP
1	E	38	VAL
1	E	107	ASP
1	F	38	VAL
1	F	82	ILE
1	F	335	PRO
1	G	38	VAL
1	H	38	VAL
1	H	107	ASP
1	I	38	VAL
1	I	55	TYR
1	I	79	LEU
1	I	309	ASP
1	J	38	VAL
1	K	38	VAL

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Mol	Chain	Res	Type
1	K	82	ILE
1	K	107	ASP
1	K	108	GLU
1	K	335	PRO
1	L	38	VAL
1	L	49	LYS
1	L	82	ILE
1	L	107	ASP
1	M	38	VAL
1	M	55	TYR
1	M	107	ASP
1	M	309	ASP
1	N	38	VAL
1	N	135	VAL
1	A	331	GLU
1	A	335	PRO
1	B	108	GLU
1	C	49	LYS
1	C	179	PRO
1	G	49	LYS
1	H	49	LYS
1	M	158	ILE
1	A	135	VAL
1	A	302	GLU
1	B	73	PRO
1	B	80	SER
1	C	334	PRO
1	D	78	VAL
1	D	158	ILE
1	E	135	VAL
1	E	302	GLU
1	F	80	SER
1	I	158	ILE
1	J	135	VAL
1	J	302	GLU
1	K	80	SER
1	M	80	SER
1	N	302	GLU
1	A	73	PRO
1	A	82	ILE
1	D	82	ILE
1	E	82	ILE

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Mol	Chain	Res	Type
1	H	335	PRO
1	I	78	VAL
1	I	334	PRO
1	K	73	PRO
1	L	172	LEU
1	N	82	ILE
1	B	135	VAL
1	E	73	PRO
1	F	135	VAL
1	H	174	GLY
1	N	73	PRO
1	E	335	PRO
1	H	73	PRO
1	M	78	VAL
1	C	109	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	271/285 (95%)	267 (98%)	4 (2%)	57	72
1	B	271/285 (95%)	267 (98%)	4 (2%)	57	72
1	C	271/285 (95%)	268 (99%)	3 (1%)	65	76
1	D	271/285 (95%)	267 (98%)	4 (2%)	57	72
1	E	271/285 (95%)	268 (99%)	3 (1%)	65	76
1	F	271/285 (95%)	268 (99%)	3 (1%)	65	76
1	G	271/285 (95%)	268 (99%)	3 (1%)	65	76
1	H	271/285 (95%)	267 (98%)	4 (2%)	57	72
1	I	271/285 (95%)	268 (99%)	3 (1%)	65	76
1	J	271/285 (95%)	269 (99%)	2 (1%)	76	81
1	K	271/285 (95%)	268 (99%)	3 (1%)	65	76
1	L	271/285 (95%)	269 (99%)	2 (1%)	76	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	M	271/285 (95%)	269 (99%)	2 (1%)	76	81
1	N	271/285 (95%)	267 (98%)	4 (2%)	57	72
All	All	3794/3990 (95%)	3750 (99%)	44 (1%)	61	75

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	70	ILE
1	A	74	LEU
1	A	155	ILE
1	A	333	LEU
1	B	74	LEU
1	B	81	GLU
1	B	134	VAL
1	B	332	GLU
1	C	107	ASP
1	C	155	ILE
1	C	333	LEU
1	D	43	LYS
1	D	70	ILE
1	D	76	ASP
1	D	332	GLU
1	E	70	ILE
1	E	74	LEU
1	E	155	ILE
1	F	81	GLU
1	F	134	VAL
1	F	332	GLU
1	G	50	LEU
1	G	107	ASP
1	G	332	GLU
1	H	50	LEU
1	H	76	ASP
1	H	78	VAL
1	H	332	GLU
1	I	70	ILE
1	I	74	LEU
1	I	79	LEU
1	J	82	ILE
1	J	333	LEU
1	K	74	LEU

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Mol	Chain	Res	Type
1	K	81	GLU
1	K	332	GLU
1	L	176	VAL
1	L	332	GLU
1	M	82	ILE
1	M	332	GLU
1	N	70	ILE
1	N	74	LEU
1	N	135	VAL
1	N	333	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	182	GLN
1	A	283	ASN
1	B	22	HIS
1	B	123	ASN
1	B	208	GLN
1	C	156	ASN
1	C	208	GLN
1	C	277	GLN
1	E	182	GLN
1	E	283	ASN
1	F	22	HIS
1	F	123	ASN
1	F	208	GLN
1	F	282	GLN
1	G	208	GLN
1	G	283	ASN
1	H	208	GLN
1	H	277	GLN
1	J	182	GLN
1	J	283	ASN
1	K	22	HIS
1	K	123	ASN
1	K	208	GLN
1	K	282	GLN
1	L	156	ASN
1	L	208	GLN
1	N	182	GLN
1	N	283	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 28 ligands modelled in this entry, 14 are monoatomic - leaving 14 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
3	ADP	N	402	-	28,29,29	1.45	5 (17%)	43,45,45	1.97	11 (25%)
3	ADP	E	402	-	28,29,29	1.44	4 (14%)	43,45,45	1.98	11 (25%)
3	ADP	H	402	-	28,29,29	1.46	5 (17%)	43,45,45	1.98	11 (25%)
3	ADP	C	402	-	28,29,29	1.46	5 (17%)	43,45,45	1.98	11 (25%)
3	ADP	D	402	-	28,29,29	1.48	5 (17%)	43,45,45	1.99	11 (25%)
3	ADP	L	402	-	28,29,29	1.46	5 (17%)	43,45,45	1.98	11 (25%)
3	ADP	I	402	-	28,29,29	1.47	5 (17%)	43,45,45	1.98	11 (25%)
3	ADP	J	402	-	28,29,29	1.45	5 (17%)	43,45,45	1.97	11 (25%)
3	ADP	G	402	-	28,29,29	1.45	5 (17%)	43,45,45	1.98	11 (25%)
3	ADP	A	402	-	28,29,29	1.45	5 (17%)	43,45,45	1.98	11 (25%)
3	ADP	B	402	-	28,29,29	1.46	5 (17%)	43,45,45	1.99	11 (25%)
3	ADP	K	402	-	28,29,29	1.47	5 (17%)	43,45,45	1.98	11 (25%)
3	ADP	F	402	-	28,29,29	1.47	5 (17%)	43,45,45	1.99	11 (25%)
3	ADP	M	402	-	28,29,29	1.46	5 (17%)	43,45,45	1.98	11 (25%)

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
3	ADP	N	402	-	-	5/16/32/32	0/3/3/3
3	ADP	E	402	-	-	5/16/32/32	0/3/3/3
3	ADP	H	402	-	-	0/16/32/32	0/3/3/3
3	ADP	C	402	-	-	0/16/32/32	0/3/3/3
3	ADP	D	402	-	-	3/16/32/32	0/3/3/3
3	ADP	L	402	-	-	0/16/32/32	0/3/3/3
3	ADP	I	402	-	-	3/16/32/32	0/3/3/3
3	ADP	J	402	-	-	5/16/32/32	0/3/3/3
3	ADP	G	402	-	-	0/16/32/32	0/3/3/3
3	ADP	A	402	-	-	5/16/32/32	0/3/3/3
3	ADP	B	402	-	-	3/16/32/32	0/3/3/3
3	ADP	K	402	-	-	3/16/32/32	0/3/3/3
3	ADP	F	402	-	-	3/16/32/32	0/3/3/3
3	ADP	M	402	-	-	3/16/32/32	0/3/3/3

All (69) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	402	ADP	PA-O3A	4.15	1.64	1.59
3	M	402	ADP	C5-C4	4.12	1.46	1.39
3	D	402	ADP	C5-C4	4.11	1.46	1.39
3	I	402	ADP	C5-C4	4.10	1.46	1.39
3	I	402	ADP	PA-O3A	4.09	1.63	1.59
3	A	402	ADP	C5-C4	4.09	1.46	1.39
3	F	402	ADP	C5-C4	4.08	1.46	1.39
3	C	402	ADP	C5-C4	4.06	1.46	1.39
3	K	402	ADP	C5-C4	4.06	1.46	1.39
3	L	402	ADP	C5-C4	4.06	1.46	1.39
3	H	402	ADP	C5-C4	4.05	1.46	1.39
3	J	402	ADP	C5-C4	4.04	1.46	1.39
3	F	402	ADP	PA-O3A	4.04	1.63	1.59
3	M	402	ADP	PA-O3A	4.03	1.63	1.59
3	E	402	ADP	C5-C4	4.03	1.46	1.39
3	G	402	ADP	C5-C4	4.02	1.46	1.39
3	B	402	ADP	C5-C4	4.02	1.46	1.39
3	N	402	ADP	C5-C4	4.01	1.46	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	K	402	ADP	PA-O3A	4.01	1.63	1.59
3	G	402	ADP	PA-O3A	3.99	1.63	1.59
3	B	402	ADP	PA-O3A	3.97	1.63	1.59
3	H	402	ADP	PA-O3A	3.97	1.63	1.59
3	C	402	ADP	PA-O3A	3.97	1.63	1.59
3	L	402	ADP	PA-O3A	3.96	1.63	1.59
3	N	402	ADP	PA-O3A	3.94	1.63	1.59
3	E	402	ADP	PA-O3A	3.91	1.63	1.59
3	J	402	ADP	PA-O3A	3.90	1.63	1.59
3	A	402	ADP	PA-O3A	3.86	1.63	1.59
3	H	402	ADP	C5-C6	2.79	1.48	1.41
3	N	402	ADP	C5-C6	2.79	1.48	1.41
3	B	402	ADP	C5-C6	2.78	1.48	1.41
3	C	402	ADP	C5-C6	2.77	1.48	1.41
3	J	402	ADP	C5-C6	2.77	1.48	1.41
3	I	402	ADP	C5-C6	2.77	1.48	1.41
3	K	402	ADP	C5-C6	2.77	1.48	1.41
3	F	402	ADP	C5-C6	2.77	1.48	1.41
3	L	402	ADP	C5-C6	2.77	1.48	1.41
3	G	402	ADP	C5-C6	2.77	1.48	1.41
3	E	402	ADP	C5-C6	2.77	1.48	1.41
3	M	402	ADP	C5-C6	2.76	1.48	1.41
3	D	402	ADP	C5-C6	2.76	1.48	1.41
3	A	402	ADP	C5-C6	2.75	1.48	1.41
3	K	402	ADP	C8-N7	2.29	1.36	1.31
3	H	402	ADP	C8-N7	2.29	1.36	1.31
3	B	402	ADP	C8-N7	2.28	1.36	1.31
3	L	402	ADP	C8-N7	2.28	1.36	1.31
3	F	402	ADP	C8-N7	2.27	1.36	1.31
3	G	402	ADP	C8-N7	2.27	1.36	1.31
3	A	402	ADP	C8-N7	2.26	1.36	1.31
3	C	402	ADP	C8-N7	2.26	1.36	1.31
3	J	402	ADP	C8-N7	2.24	1.36	1.31
3	N	402	ADP	C8-N7	2.24	1.36	1.31
3	D	402	ADP	C8-N7	2.24	1.36	1.31
3	I	402	ADP	C8-N7	2.22	1.36	1.31
3	E	402	ADP	C8-N7	2.19	1.35	1.31
3	M	402	ADP	C8-N7	2.19	1.35	1.31
3	F	402	ADP	C5-N7	-2.09	1.35	1.39
3	K	402	ADP	C5-N7	-2.05	1.35	1.39
3	B	402	ADP	C5-N7	-2.05	1.35	1.39
3	L	402	ADP	C5-N7	-2.05	1.35	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	402	ADP	C5-N7	-2.04	1.35	1.39
3	G	402	ADP	C5-N7	-2.04	1.35	1.39
3	A	402	ADP	C5-N7	-2.03	1.35	1.39
3	I	402	ADP	C5-N7	-2.03	1.35	1.39
3	J	402	ADP	C5-N7	-2.03	1.35	1.39
3	H	402	ADP	C5-N7	-2.03	1.35	1.39
3	D	402	ADP	C5-N7	-2.02	1.35	1.39
3	N	402	ADP	C5-N7	-2.01	1.35	1.39
3	M	402	ADP	C5-N7	-2.00	1.35	1.39

All (154) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	402	ADP	C5-C4-N3	-4.72	120.21	126.72
3	M	402	ADP	C5-C4-N3	-4.72	120.21	126.72
3	E	402	ADP	C5-C4-N3	-4.72	120.22	126.72
3	G	402	ADP	C5-C4-N3	-4.71	120.23	126.72
3	H	402	ADP	C5-C4-N3	-4.71	120.23	126.72
3	B	402	ADP	C5-C4-N3	-4.71	120.24	126.72
3	D	402	ADP	C5-C4-N3	-4.70	120.24	126.72
3	C	402	ADP	C5-C4-N3	-4.70	120.24	126.72
3	K	402	ADP	C5-C4-N3	-4.70	120.24	126.72
3	I	402	ADP	C5-C4-N3	-4.70	120.25	126.72
3	A	402	ADP	C5-C4-N3	-4.68	120.27	126.72
3	J	402	ADP	C5-C4-N3	-4.68	120.27	126.72
3	L	402	ADP	C5-C4-N3	-4.67	120.28	126.72
3	N	402	ADP	C5-C4-N3	-4.66	120.30	126.72
3	D	402	ADP	N3-C2-N1	-4.06	122.43	128.58
3	B	402	ADP	N3-C2-N1	-4.05	122.45	128.58
3	I	402	ADP	N3-C2-N1	-4.02	122.49	128.58
3	C	402	ADP	N3-C2-N1	-4.02	122.50	128.58
3	K	402	ADP	N3-C2-N1	-4.02	122.50	128.58
3	F	402	ADP	N3-C2-N1	-4.02	122.50	128.58
3	M	402	ADP	N3-C2-N1	-4.01	122.51	128.58
3	A	402	ADP	N3-C2-N1	-4.01	122.51	128.58
3	J	402	ADP	N3-C2-N1	-4.01	122.51	128.58
3	L	402	ADP	N3-C2-N1	-4.01	122.51	128.58
3	G	402	ADP	N3-C2-N1	-4.01	122.52	128.58
3	N	402	ADP	N3-C2-N1	-4.00	122.52	128.58
3	E	402	ADP	N3-C2-N1	-4.00	122.53	128.58
3	H	402	ADP	N3-C2-N1	-3.99	122.54	128.58
3	D	402	ADP	N3-C4-N9	3.90	133.80	127.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	M	402	ADP	N3-C4-N9	3.89	133.78	127.17
3	F	402	ADP	N3-C4-N9	3.88	133.76	127.17
3	H	402	ADP	N3-C4-N9	3.88	133.76	127.17
3	I	402	ADP	N3-C4-N9	3.88	133.76	127.17
3	B	402	ADP	N3-C4-N9	3.87	133.74	127.17
3	E	402	ADP	N3-C4-N9	3.86	133.73	127.17
3	C	402	ADP	N3-C4-N9	3.86	133.73	127.17
3	K	402	ADP	N3-C4-N9	3.86	133.73	127.17
3	L	402	ADP	N3-C4-N9	3.85	133.72	127.17
3	G	402	ADP	N3-C4-N9	3.85	133.71	127.17
3	A	402	ADP	N3-C4-N9	3.85	133.71	127.17
3	H	402	ADP	C4-N9-C8	3.84	109.78	105.74
3	J	402	ADP	N3-C4-N9	3.84	133.70	127.17
3	F	402	ADP	C4-N9-C8	3.84	109.77	105.74
3	N	402	ADP	N3-C4-N9	3.84	133.70	127.17
3	B	402	ADP	C4-N9-C8	3.84	109.77	105.74
3	D	402	ADP	C4-N9-C8	3.83	109.76	105.74
3	K	402	ADP	C4-N9-C8	3.83	109.76	105.74
3	L	402	ADP	C4-N9-C8	3.82	109.75	105.74
3	I	402	ADP	C4-N9-C8	3.81	109.73	105.74
3	M	402	ADP	C4-N9-C8	3.80	109.73	105.74
3	C	402	ADP	C4-N9-C8	3.80	109.73	105.74
3	N	402	ADP	C4-N9-C8	3.79	109.72	105.74
3	A	402	ADP	C4-N9-C8	3.78	109.71	105.74
3	J	402	ADP	C4-N9-C8	3.78	109.70	105.74
3	G	402	ADP	C4-N9-C8	3.77	109.70	105.74
3	E	402	ADP	C4-N9-C8	3.77	109.69	105.74
3	D	402	ADP	C2-N3-C4	3.70	120.87	111.83
3	B	402	ADP	C2-N3-C4	3.69	120.84	111.83
3	E	402	ADP	C2-N3-C4	3.68	120.83	111.83
3	I	402	ADP	C2-N3-C4	3.68	120.83	111.83
3	M	402	ADP	C4-C5-N7	-3.68	106.37	110.58
3	M	402	ADP	C2-N3-C4	3.68	120.82	111.83
3	F	402	ADP	C2-N3-C4	3.68	120.82	111.83
3	N	402	ADP	C2-N3-C4	3.68	120.81	111.83
3	K	402	ADP	C2-N3-C4	3.68	120.81	111.83
3	G	402	ADP	C2-N3-C4	3.67	120.81	111.83
3	J	402	ADP	C2-N3-C4	3.67	120.80	111.83
3	C	402	ADP	C2-N3-C4	3.67	120.80	111.83
3	A	402	ADP	C2-N3-C4	3.67	120.80	111.83
3	F	402	ADP	C4-C5-N7	-3.67	106.39	110.58
3	H	402	ADP	C2-N3-C4	3.67	120.78	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	402	ADP	C4-C5-N7	-3.66	106.40	110.58
3	K	402	ADP	C4-C5-N7	-3.66	106.40	110.58
3	C	402	ADP	C4-C5-N7	-3.65	106.40	110.58
3	I	402	ADP	C4-C5-N7	-3.65	106.40	110.58
3	L	402	ADP	C2-N3-C4	3.65	120.75	111.83
3	E	402	ADP	C4-C5-N7	-3.65	106.41	110.58
3	G	402	ADP	C4-C5-N7	-3.65	106.41	110.58
3	A	402	ADP	C4-C5-N7	-3.64	106.42	110.58
3	D	402	ADP	C4-C5-N7	-3.63	106.43	110.58
3	J	402	ADP	C4-C5-N7	-3.63	106.43	110.58
3	L	402	ADP	C4-C5-N7	-3.63	106.43	110.58
3	H	402	ADP	C4-C5-N7	-3.62	106.44	110.58
3	N	402	ADP	C4-C5-N7	-3.60	106.46	110.58
3	F	402	ADP	N9-C8-N7	-3.40	109.11	113.94
3	K	402	ADP	N9-C8-N7	-3.38	109.14	113.94
3	B	402	ADP	N9-C8-N7	-3.38	109.14	113.94
3	G	402	ADP	N9-C8-N7	-3.37	109.15	113.94
3	L	402	ADP	N9-C8-N7	-3.37	109.15	113.94
3	C	402	ADP	N9-C8-N7	-3.37	109.15	113.94
3	H	402	ADP	N9-C8-N7	-3.37	109.16	113.94
3	F	402	ADP	C5-N7-C8	3.35	108.72	103.45
3	D	402	ADP	N9-C8-N7	-3.35	109.19	113.94
3	C	402	ADP	C5-N7-C8	3.34	108.70	103.45
3	G	402	ADP	C5-N7-C8	3.34	108.70	103.45
3	I	402	ADP	N9-C8-N7	-3.34	109.20	113.94
3	N	402	ADP	N9-C8-N7	-3.34	109.20	113.94
3	I	402	ADP	C5-N7-C8	3.33	108.69	103.45
3	L	402	ADP	C5-N7-C8	3.33	108.69	103.45
3	J	402	ADP	N9-C8-N7	-3.33	109.21	113.94
3	K	402	ADP	C5-N7-C8	3.33	108.68	103.45
3	B	402	ADP	C5-N7-C8	3.33	108.68	103.45
3	A	402	ADP	N9-C8-N7	-3.33	109.21	113.94
3	D	402	ADP	C5-N7-C8	3.33	108.68	103.45
3	M	402	ADP	C5-N7-C8	3.33	108.68	103.45
3	E	402	ADP	N9-C8-N7	-3.32	109.23	113.94
3	M	402	ADP	N9-C8-N7	-3.32	109.23	113.94
3	A	402	ADP	C5-N7-C8	3.31	108.65	103.45
3	J	402	ADP	C5-N7-C8	3.31	108.65	103.45
3	H	402	ADP	C5-N7-C8	3.30	108.64	103.45
3	E	402	ADP	C5-N7-C8	3.30	108.64	103.45
3	N	402	ADP	C5-N7-C8	3.30	108.64	103.45
3	M	402	ADP	C6-C5-N7	2.94	137.77	132.09

Continued on next page...

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	402	ADP	C6-C5-N7	2.94	137.75	132.09
3	C	402	ADP	C6-C5-N7	2.93	137.75	132.09
3	I	402	ADP	C6-C5-N7	2.93	137.74	132.09
3	B	402	ADP	C6-C5-N7	2.93	137.73	132.09
3	K	402	ADP	C6-C5-N7	2.93	137.73	132.09
3	D	402	ADP	C6-C5-N7	2.92	137.73	132.09
3	G	402	ADP	C6-C5-N7	2.92	137.72	132.09
3	A	402	ADP	C6-C5-N7	2.92	137.72	132.09
3	L	402	ADP	C6-C5-N7	2.91	137.70	132.09
3	J	402	ADP	C6-C5-N7	2.91	137.70	132.09
3	N	402	ADP	C6-C5-N7	2.91	137.69	132.09
3	E	402	ADP	C6-C5-N7	2.90	137.69	132.09
3	H	402	ADP	C6-C5-N7	2.90	137.69	132.09
3	N	402	ADP	O4'-C1'-N9	2.68	113.23	108.09
3	H	402	ADP	O4'-C1'-N9	2.67	113.22	108.09
3	C	402	ADP	O4'-C1'-N9	2.66	113.21	108.09
3	G	402	ADP	O4'-C1'-N9	2.66	113.20	108.09
3	L	402	ADP	O4'-C1'-N9	2.66	113.20	108.09
3	K	402	ADP	O4'-C1'-N9	2.66	113.20	108.09
3	E	402	ADP	O4'-C1'-N9	2.66	113.19	108.09
3	J	402	ADP	O4'-C1'-N9	2.65	113.18	108.09
3	B	402	ADP	O4'-C1'-N9	2.65	113.18	108.09
3	D	402	ADP	O4'-C1'-N9	2.65	113.17	108.09
3	F	402	ADP	O4'-C1'-N9	2.65	113.17	108.09
3	A	402	ADP	O4'-C1'-N9	2.65	113.17	108.09
3	I	402	ADP	O4'-C1'-N9	2.64	113.16	108.09
3	M	402	ADP	O4'-C1'-N9	2.63	113.14	108.09
3	L	402	ADP	C2-N1-C6	2.43	122.72	118.73
3	C	402	ADP	C2-N1-C6	2.41	122.69	118.73
3	H	402	ADP	C2-N1-C6	2.40	122.67	118.73
3	B	402	ADP	C2-N1-C6	2.40	122.67	118.73
3	F	402	ADP	C2-N1-C6	2.39	122.65	118.73
3	I	402	ADP	C2-N1-C6	2.39	122.65	118.73
3	K	402	ADP	C2-N1-C6	2.39	122.65	118.73
3	M	402	ADP	C2-N1-C6	2.39	122.65	118.73
3	A	402	ADP	C2-N1-C6	2.38	122.64	118.73
3	D	402	ADP	C2-N1-C6	2.38	122.64	118.73
3	G	402	ADP	C2-N1-C6	2.38	122.64	118.73
3	J	402	ADP	C2-N1-C6	2.38	122.63	118.73
3	E	402	ADP	C2-N1-C6	2.36	122.61	118.73
3	N	402	ADP	C2-N1-C6	2.36	122.60	118.73

There are no chirality outliers.

All (38) torsion outliers are listed below:

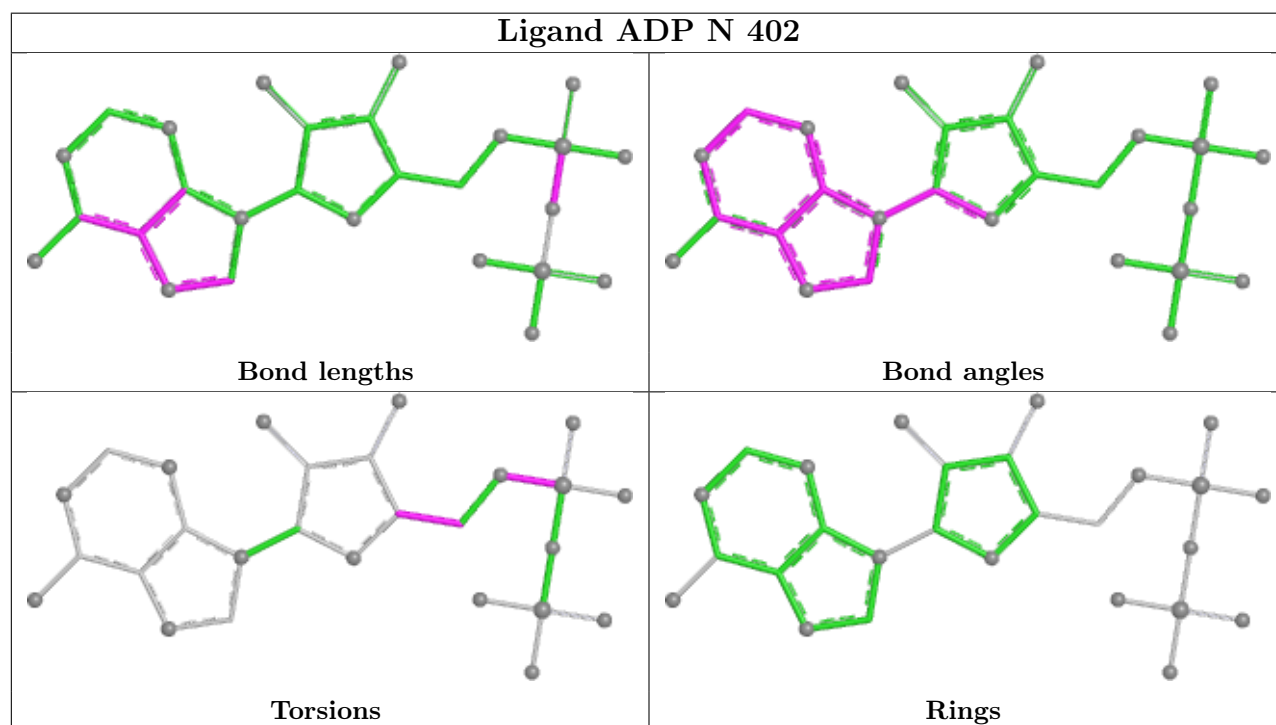
Mol	Chain	Res	Type	Atoms
3	A	402	ADP	C5'-O5'-PA-O1A
3	E	402	ADP	C5'-O5'-PA-O1A
3	J	402	ADP	C5'-O5'-PA-O1A
3	N	402	ADP	C5'-O5'-PA-O1A
3	A	402	ADP	C3'-C4'-C5'-O5'
3	E	402	ADP	C3'-C4'-C5'-O5'
3	J	402	ADP	C3'-C4'-C5'-O5'
3	N	402	ADP	C3'-C4'-C5'-O5'
3	A	402	ADP	O4'-C4'-C5'-O5'
3	B	402	ADP	C3'-C4'-C5'-O5'
3	E	402	ADP	O4'-C4'-C5'-O5'
3	F	402	ADP	C3'-C4'-C5'-O5'
3	J	402	ADP	O4'-C4'-C5'-O5'
3	K	402	ADP	C3'-C4'-C5'-O5'
3	N	402	ADP	O4'-C4'-C5'-O5'
3	B	402	ADP	PB-O3A-PA-O1A
3	F	402	ADP	PB-O3A-PA-O1A
3	K	402	ADP	PB-O3A-PA-O1A
3	D	402	ADP	C3'-C4'-C5'-O5'
3	I	402	ADP	C3'-C4'-C5'-O5'
3	M	402	ADP	C3'-C4'-C5'-O5'
3	D	402	ADP	PA-O3A-PB-O3B
3	I	402	ADP	PA-O3A-PB-O3B
3	M	402	ADP	PA-O3A-PB-O3B
3	A	402	ADP	C5'-O5'-PA-O2A
3	A	402	ADP	C5'-O5'-PA-O3A
3	E	402	ADP	C5'-O5'-PA-O2A
3	E	402	ADP	C5'-O5'-PA-O3A
3	J	402	ADP	C5'-O5'-PA-O2A
3	J	402	ADP	C5'-O5'-PA-O3A
3	N	402	ADP	C5'-O5'-PA-O2A
3	N	402	ADP	C5'-O5'-PA-O3A
3	B	402	ADP	PB-O3A-PA-O2A
3	F	402	ADP	PB-O3A-PA-O2A
3	K	402	ADP	PB-O3A-PA-O2A
3	D	402	ADP	PA-O3A-PB-O2B
3	I	402	ADP	PA-O3A-PB-O2B
3	M	402	ADP	PA-O3A-PB-O2B

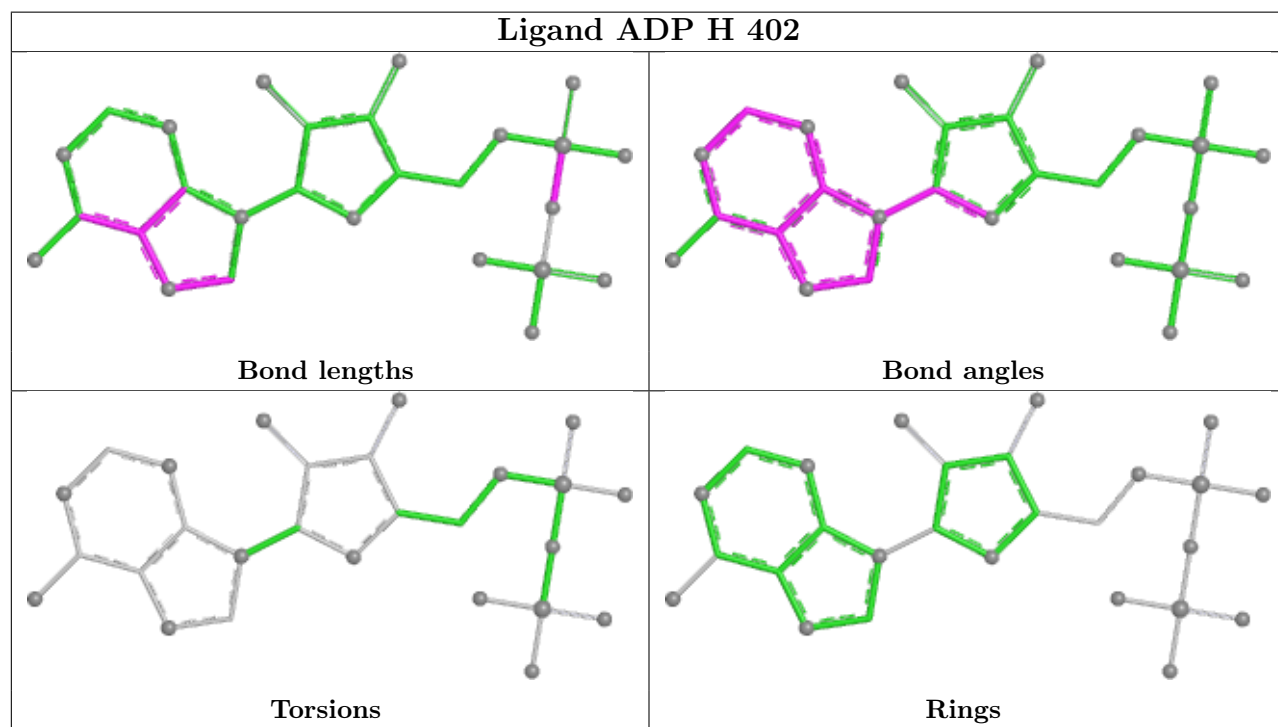
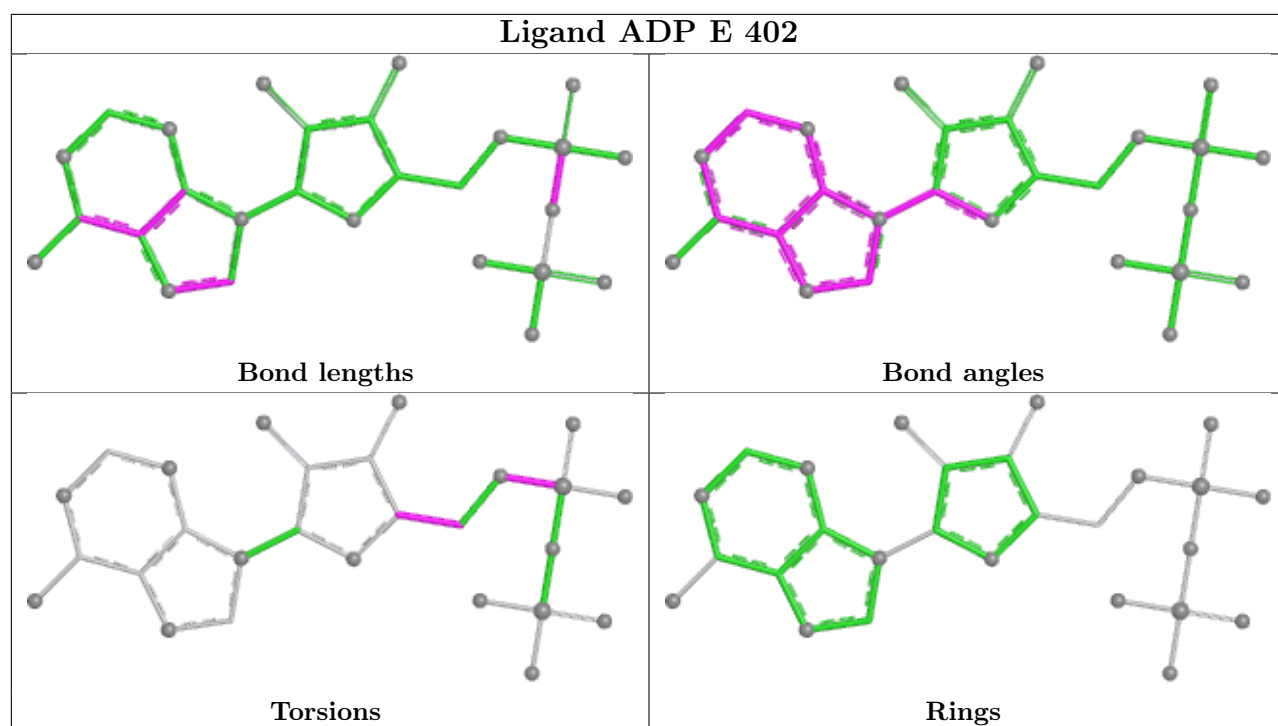
There are no ring outliers.

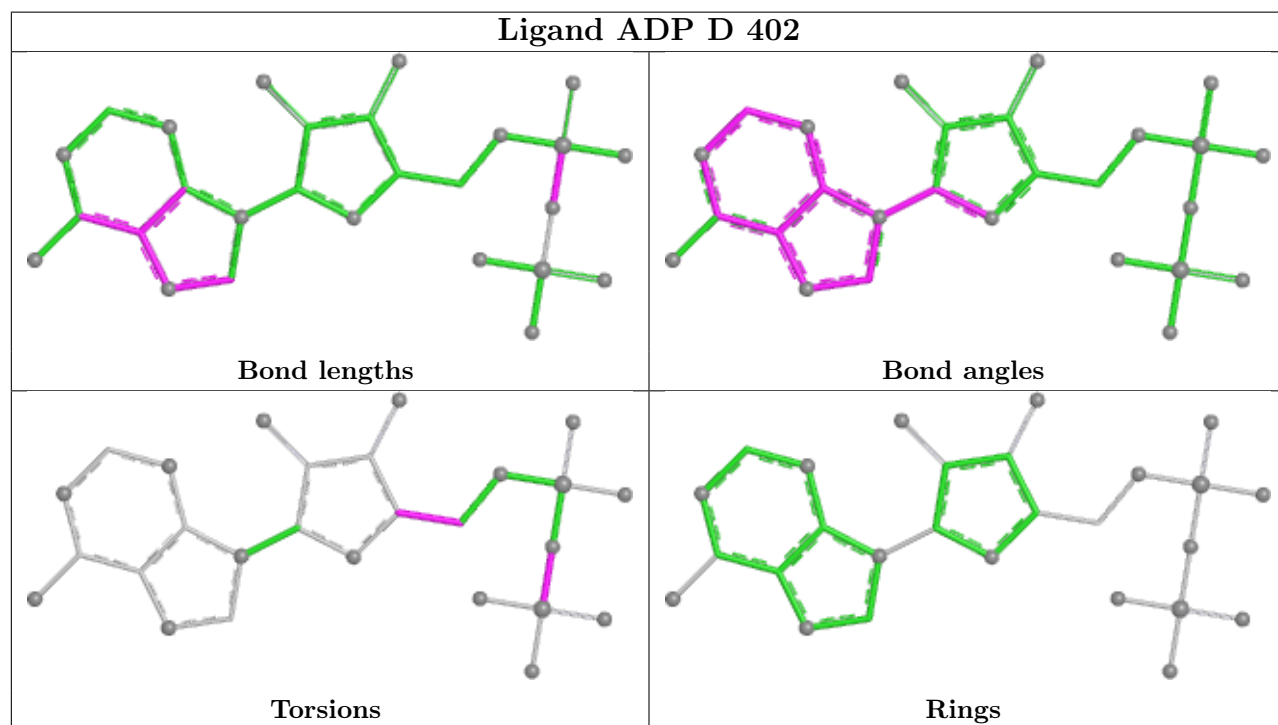
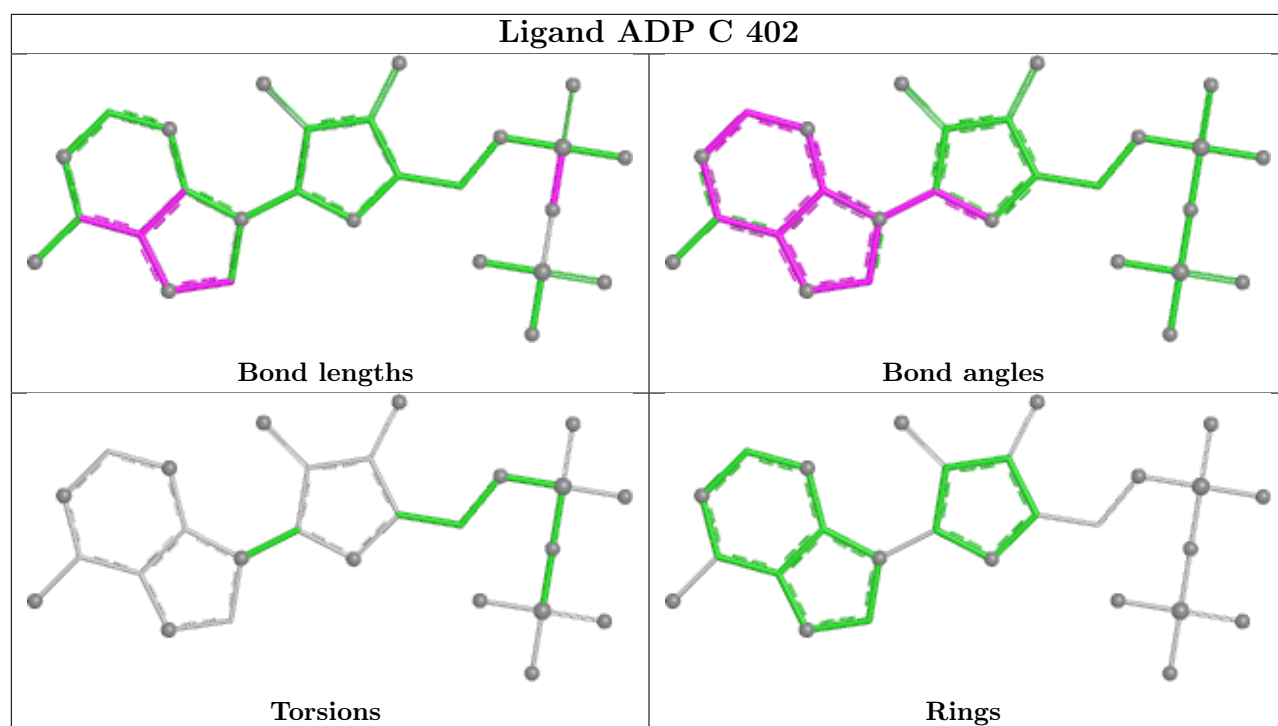
1 monomer is involved in 2 short contacts:

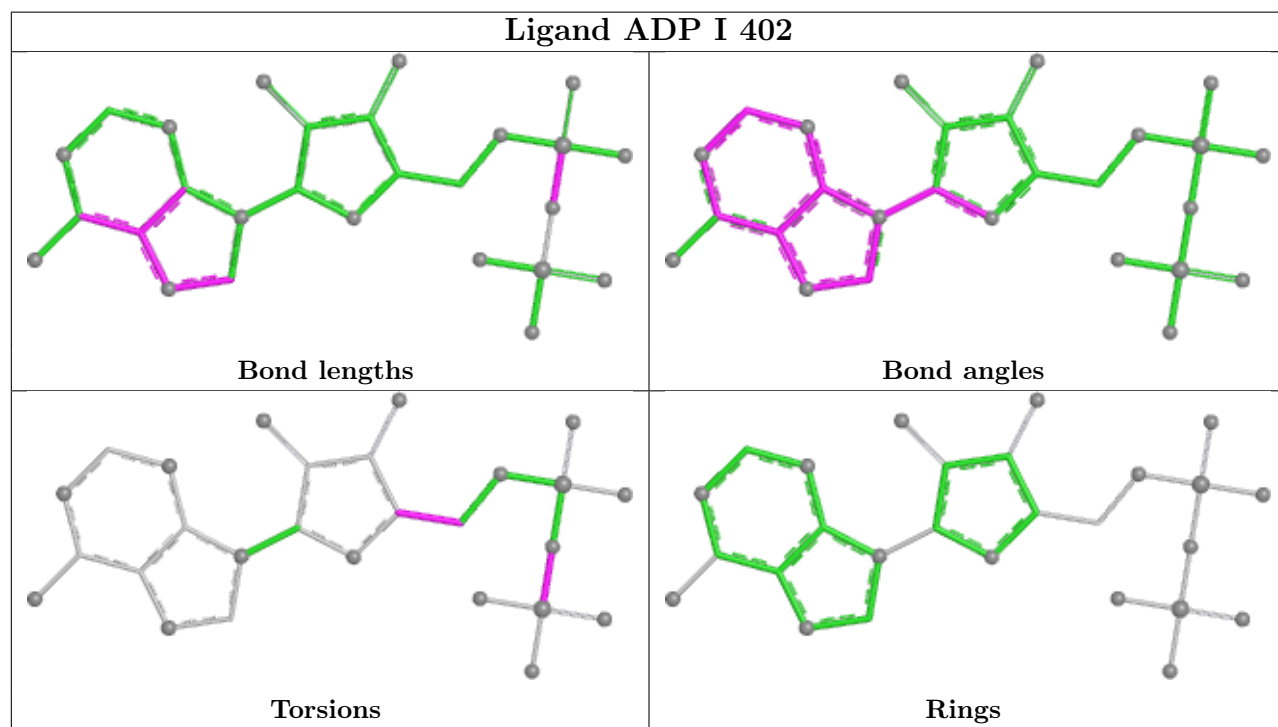
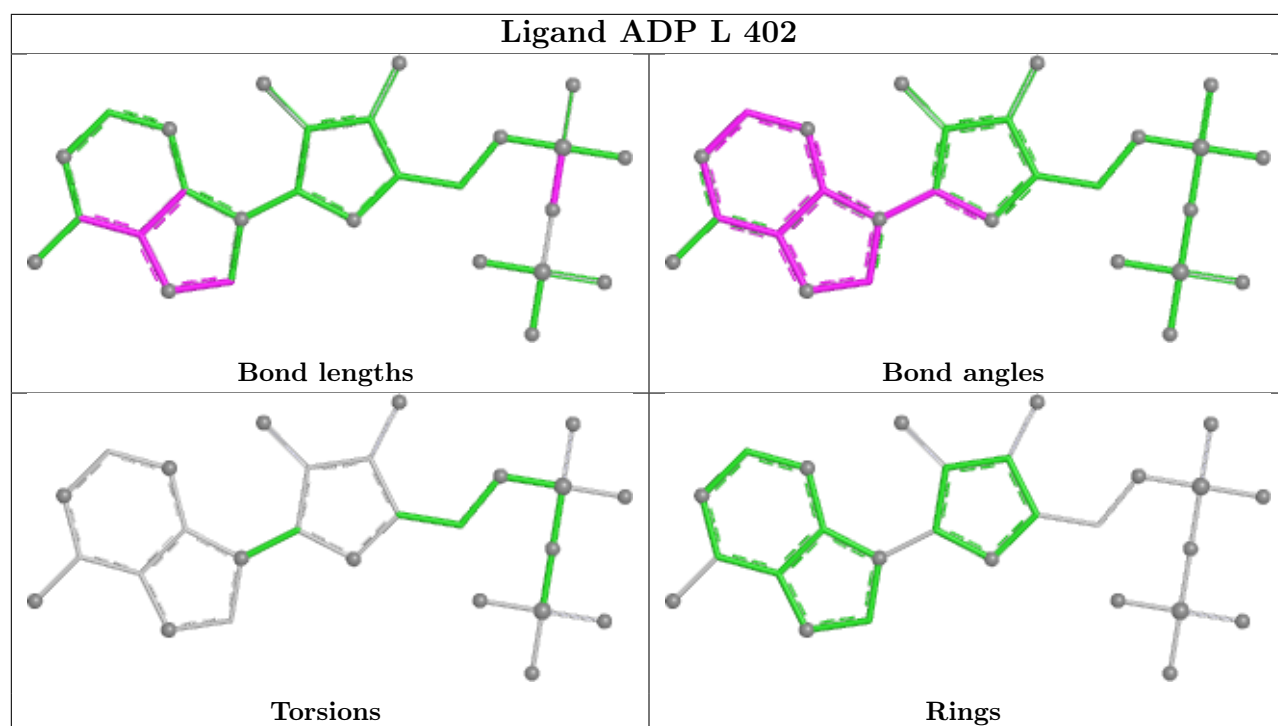
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	I	402	ADP	2	0

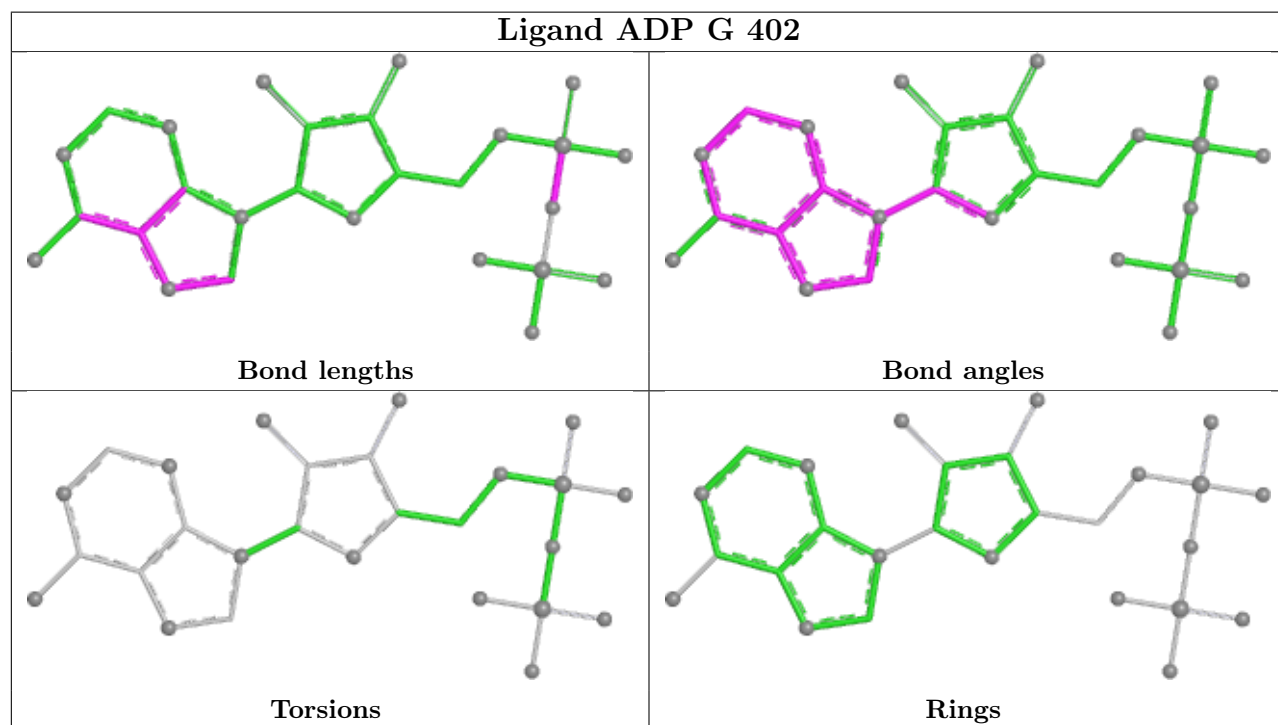
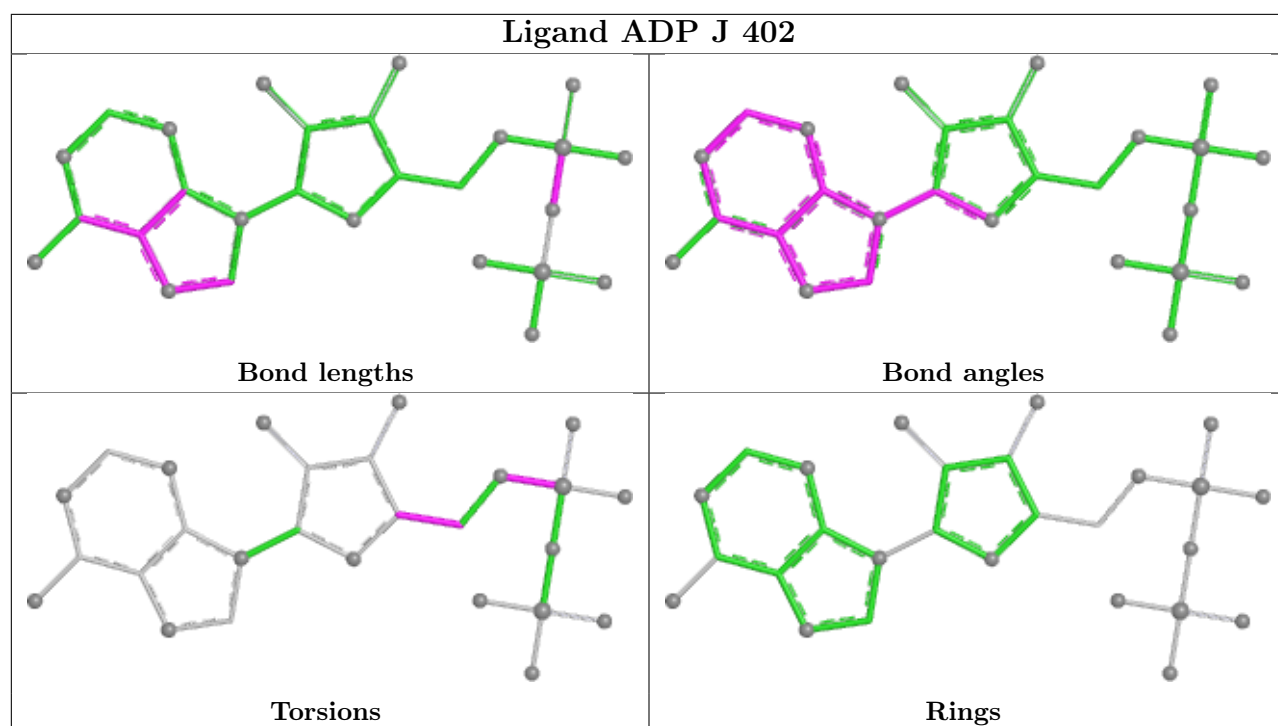
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

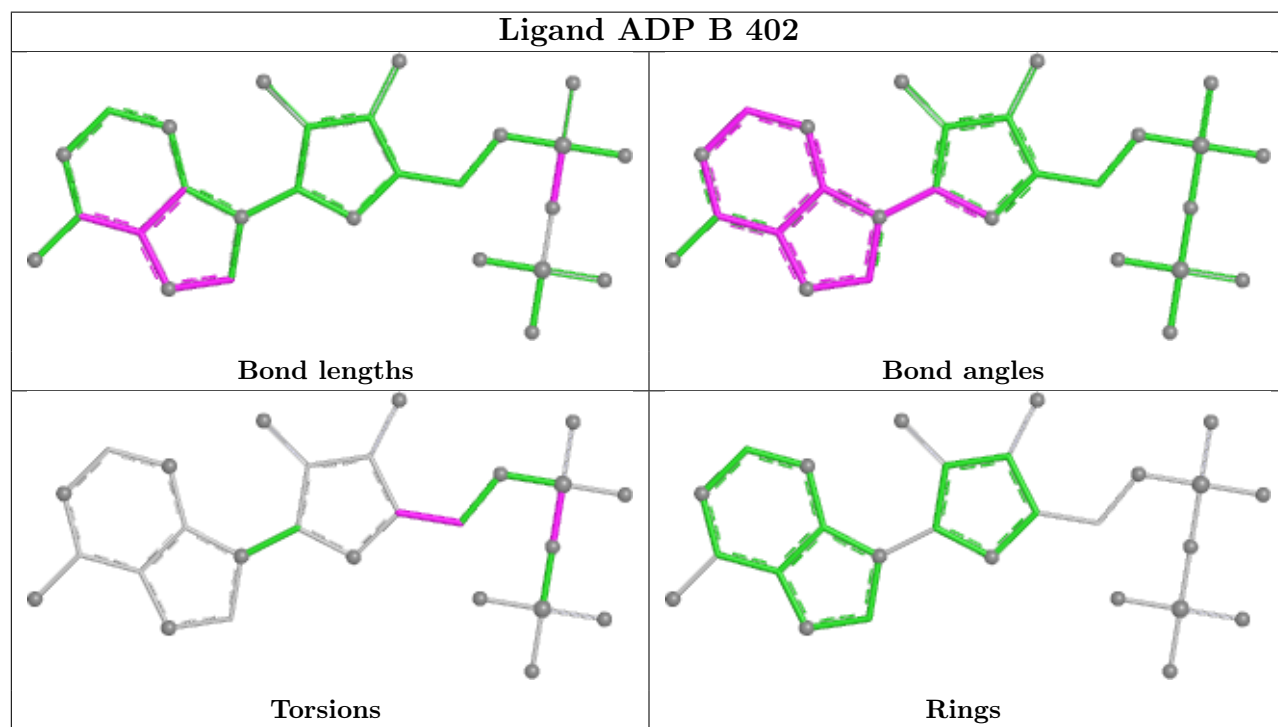
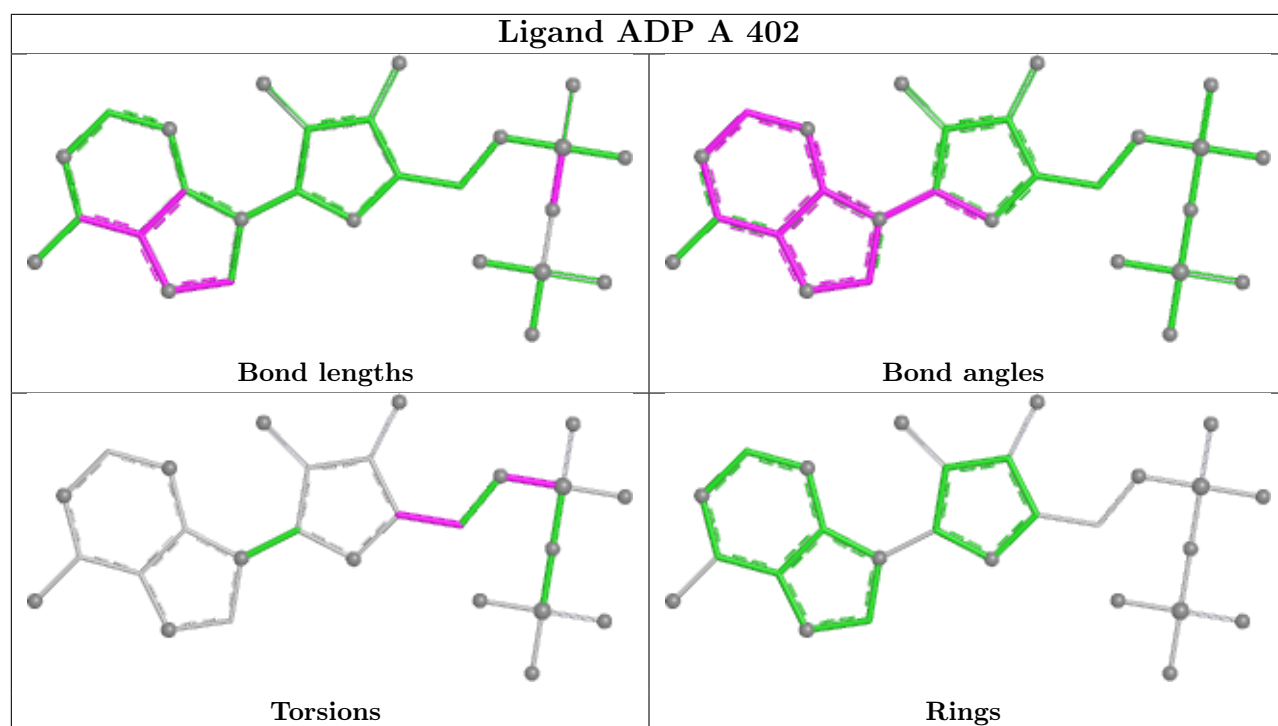


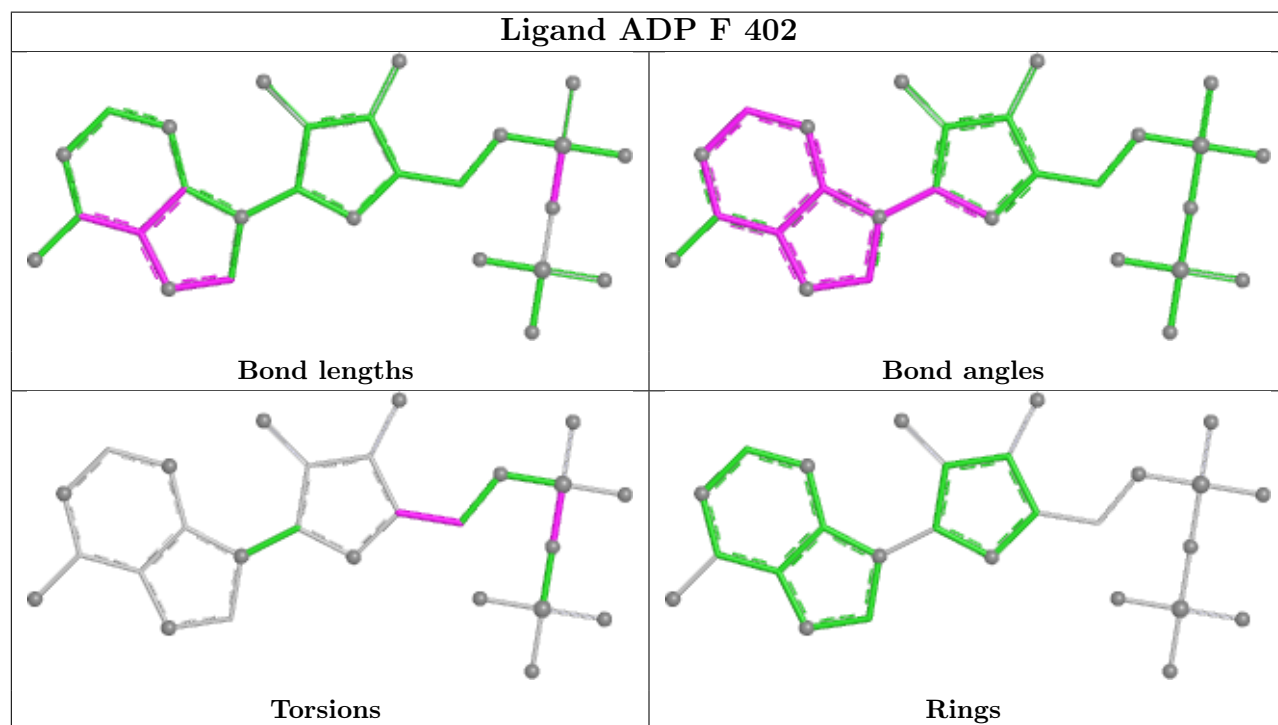
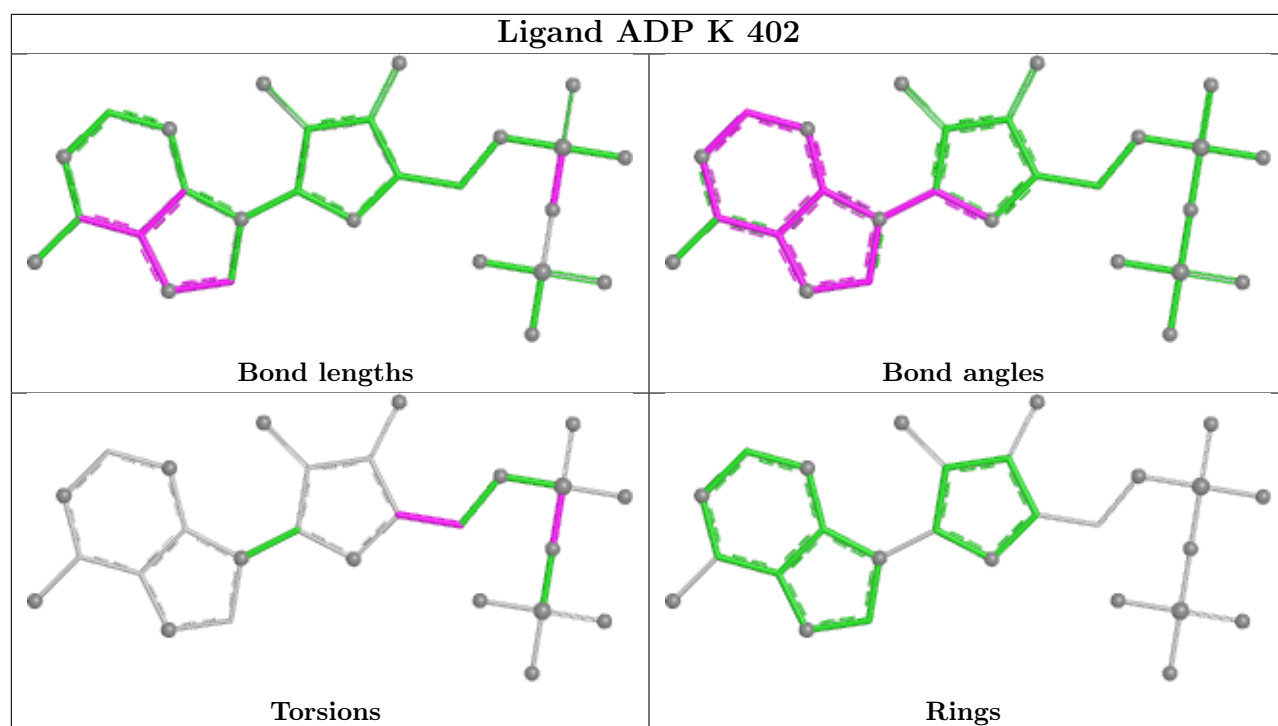


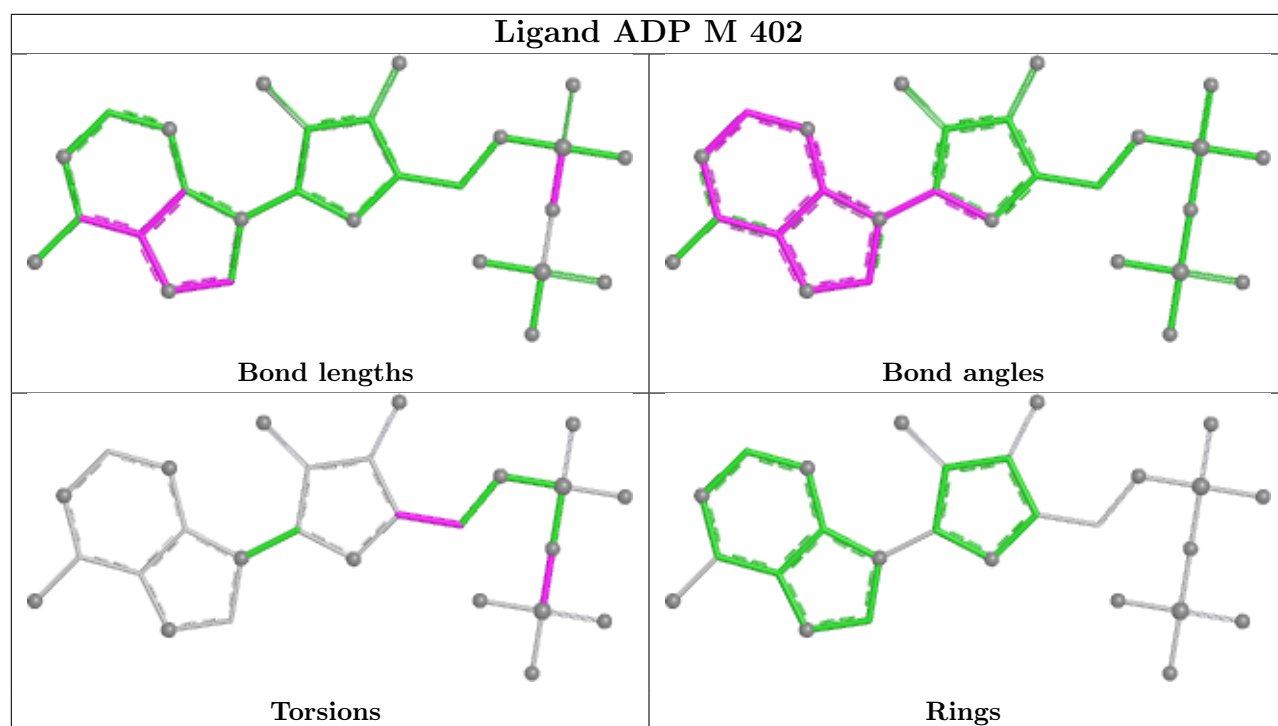












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

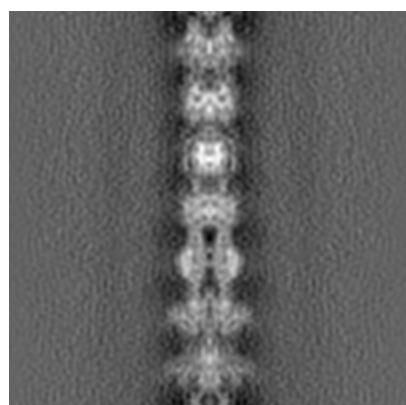
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8180. These allow visual inspection of the internal detail of the map and identification of artifacts.

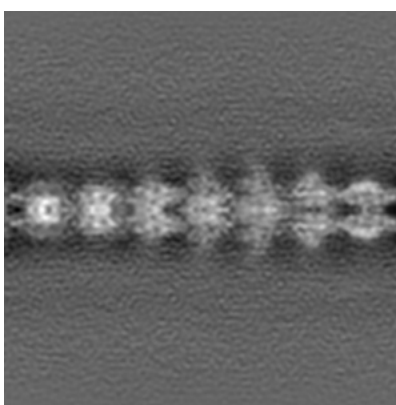
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

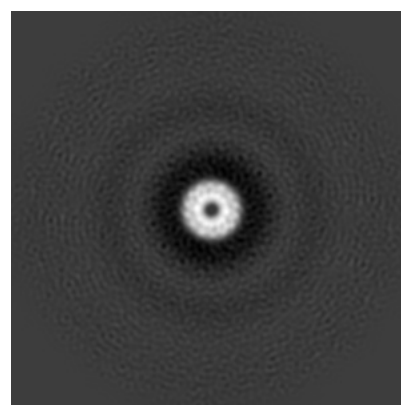
6.1.1 Primary map



X



Y

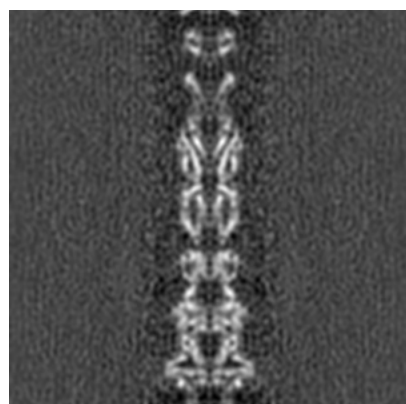


Z

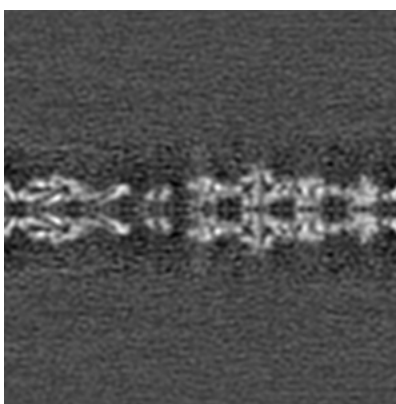
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

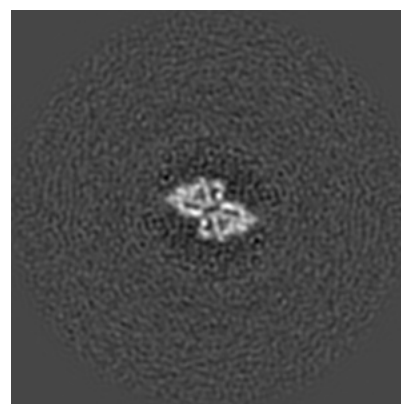
6.2.1 Primary map



X Index: 160



Y Index: 160

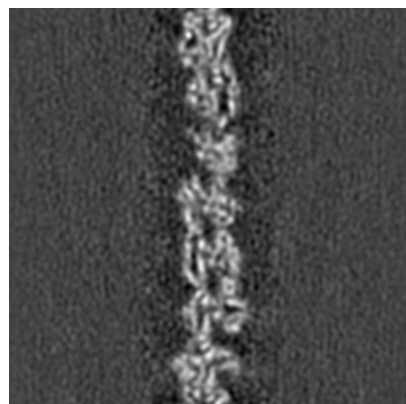


Z Index: 160

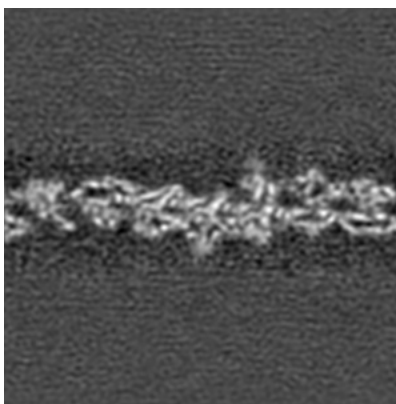
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

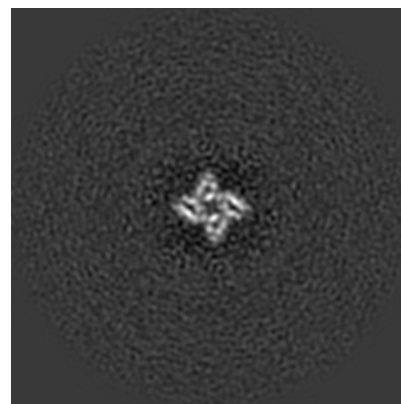
6.3.1 Primary map



X Index: 151



Y Index: 168

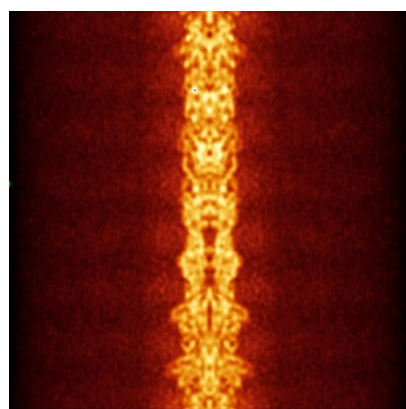


Z Index: 212

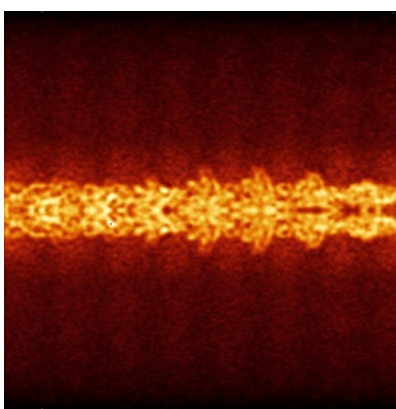
The images above show the largest variance slices of the map in three orthogonal directions.

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

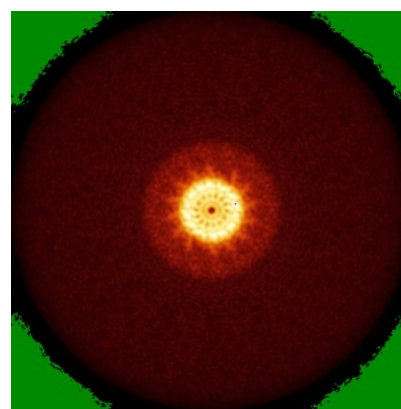
6.4.1 Primary map



X



Y

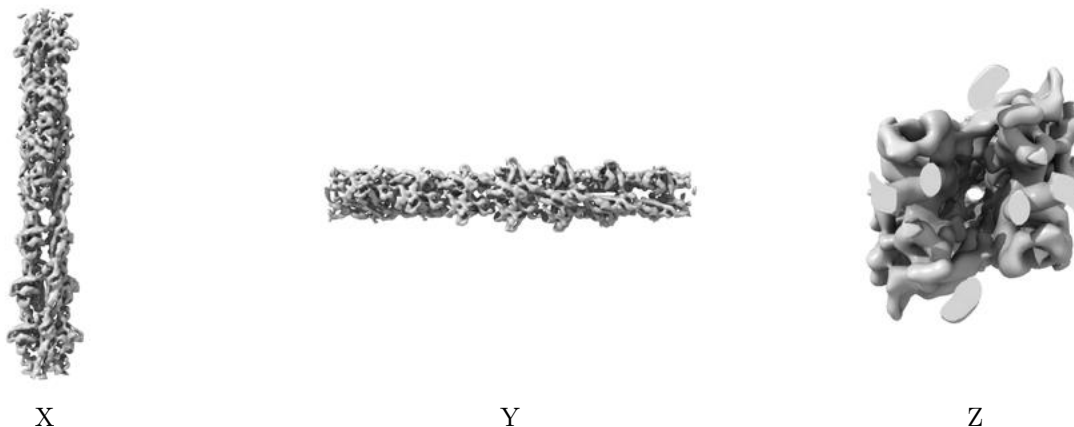


Z

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



The images above show the 3D surface view of the map at the recommended contour level 5.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

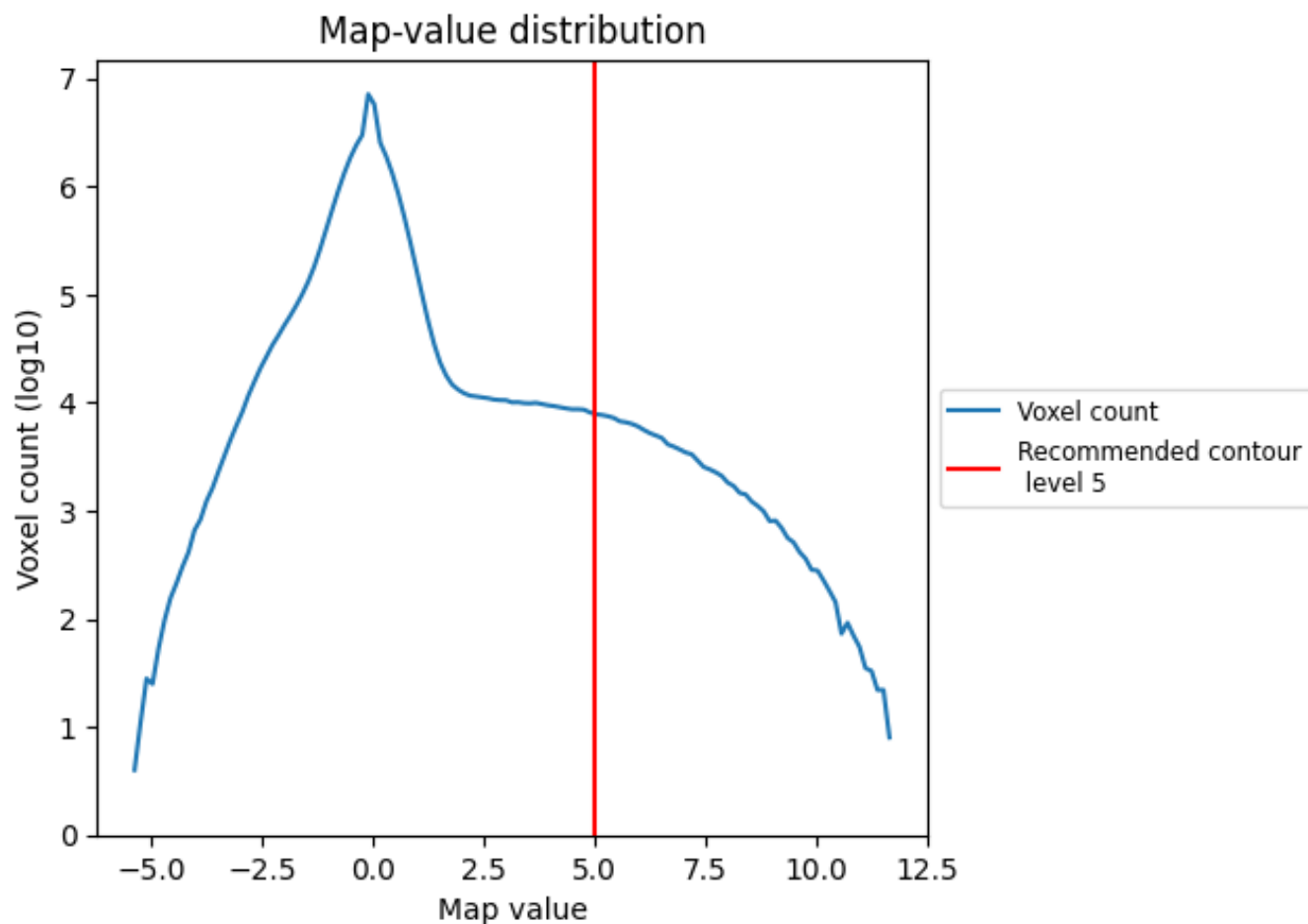
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

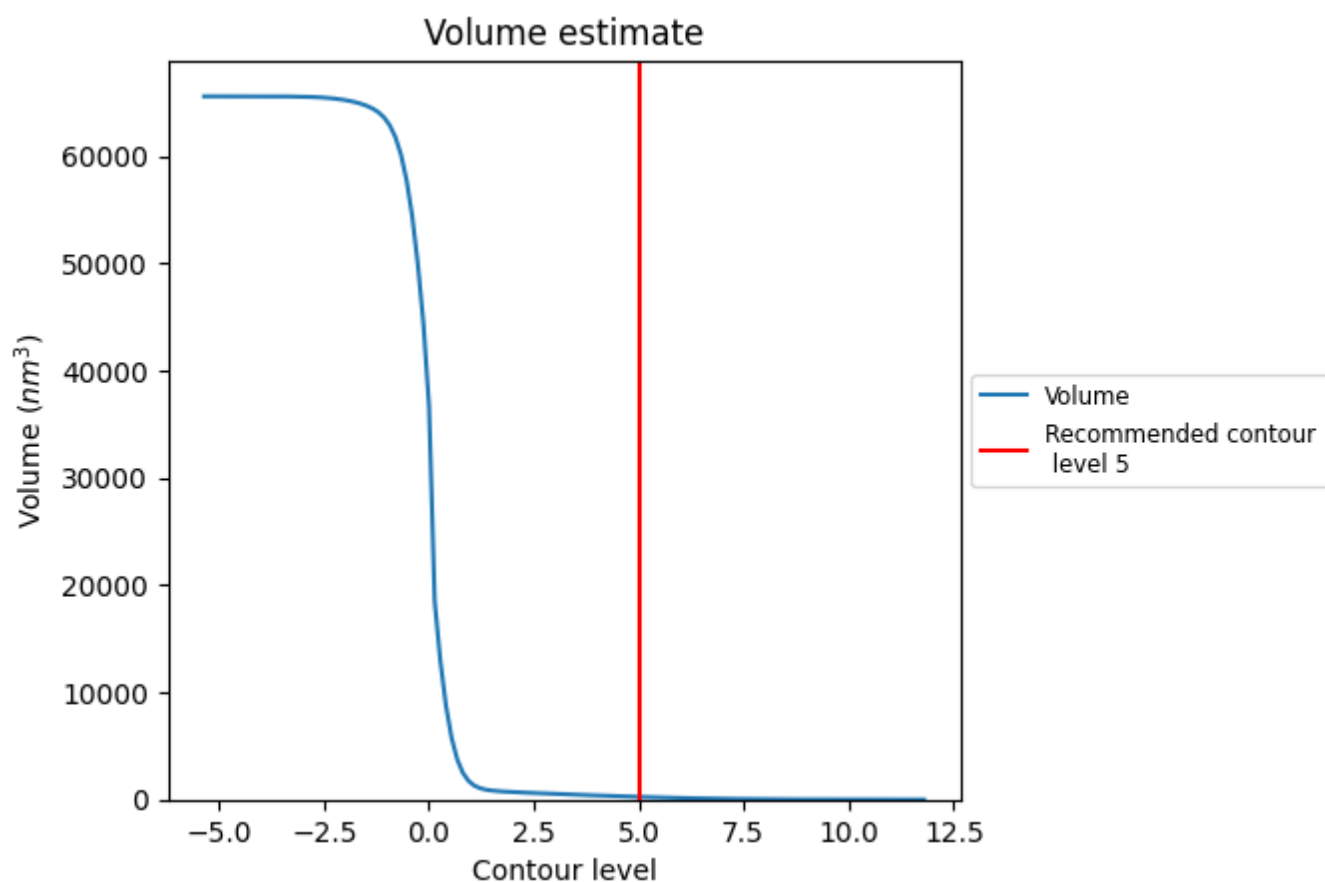
This section contains the results of statistical analysis of the map.

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.

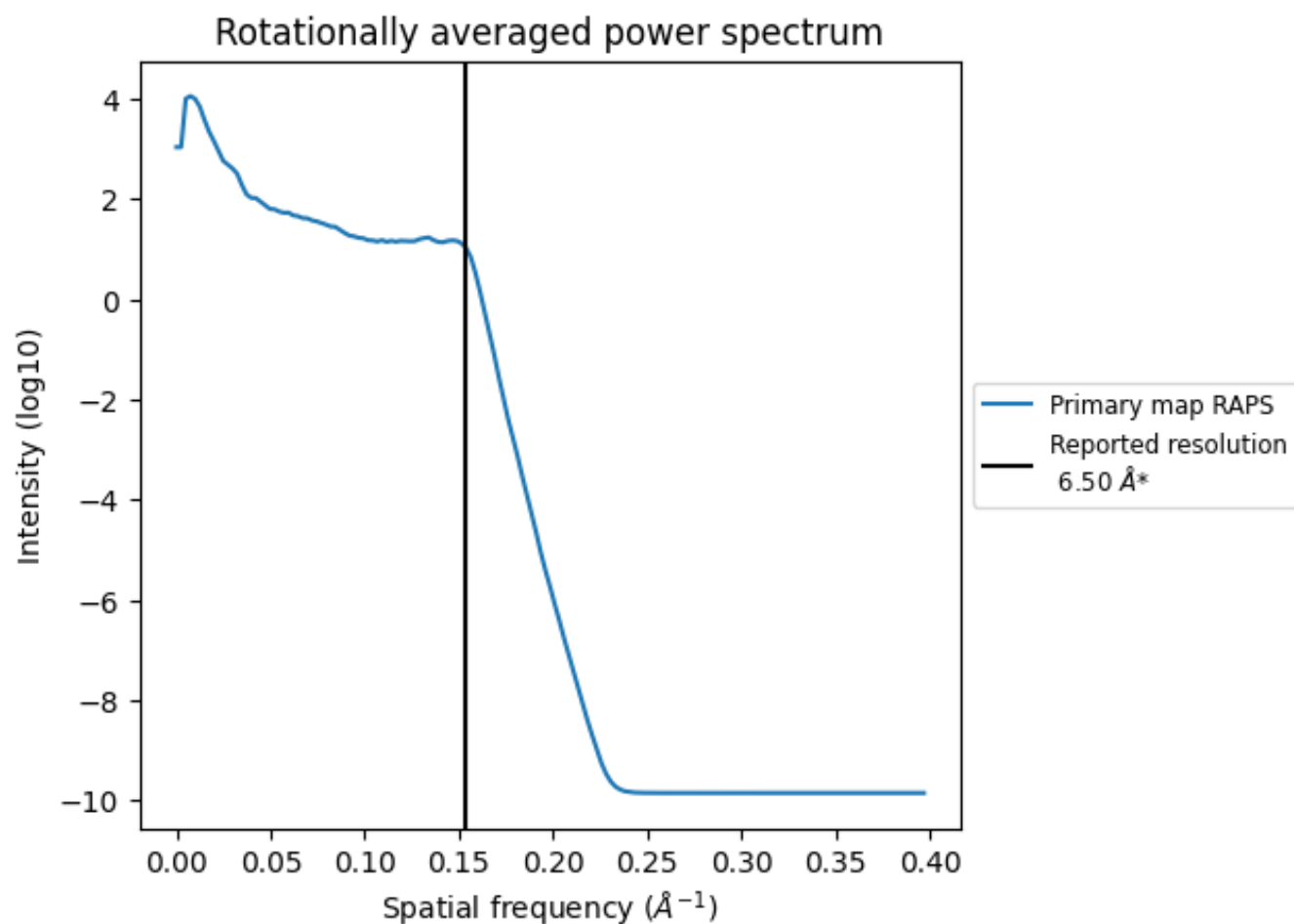
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 250 nm³; this corresponds to an approximate mass of 226 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 0.154 $\text{\AA}^{-1}$

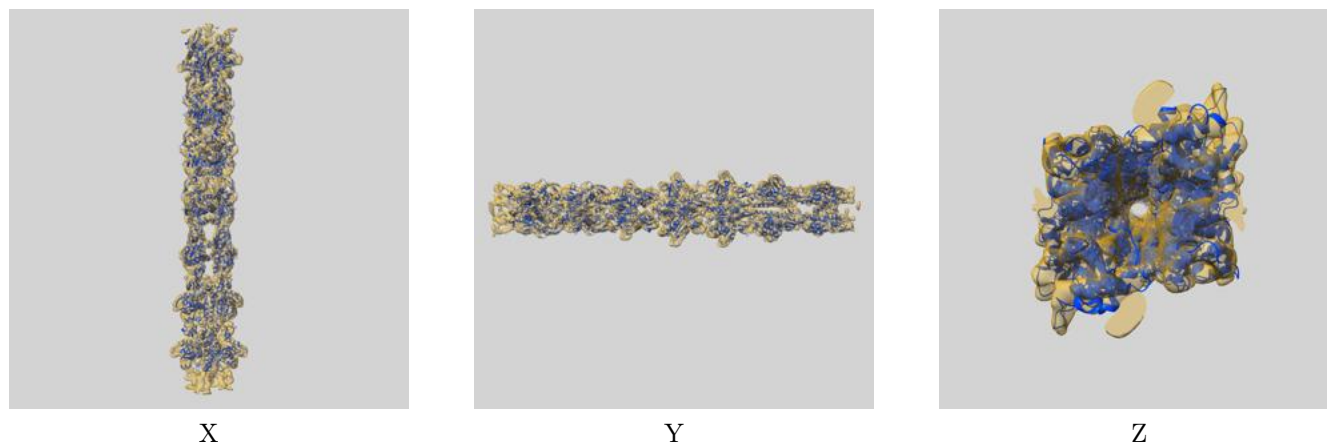
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

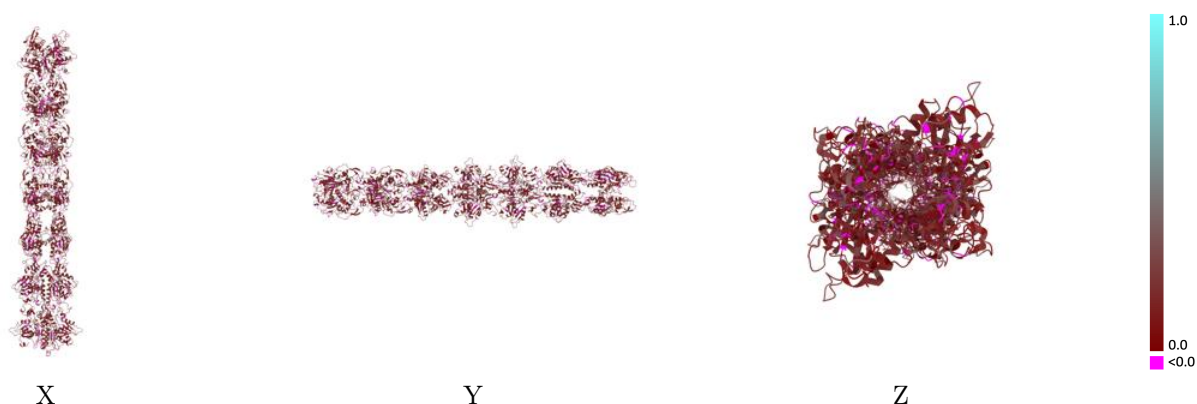
This section contains information regarding the fit between EMDB map EMD-8180 and PDB model 5JYG. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



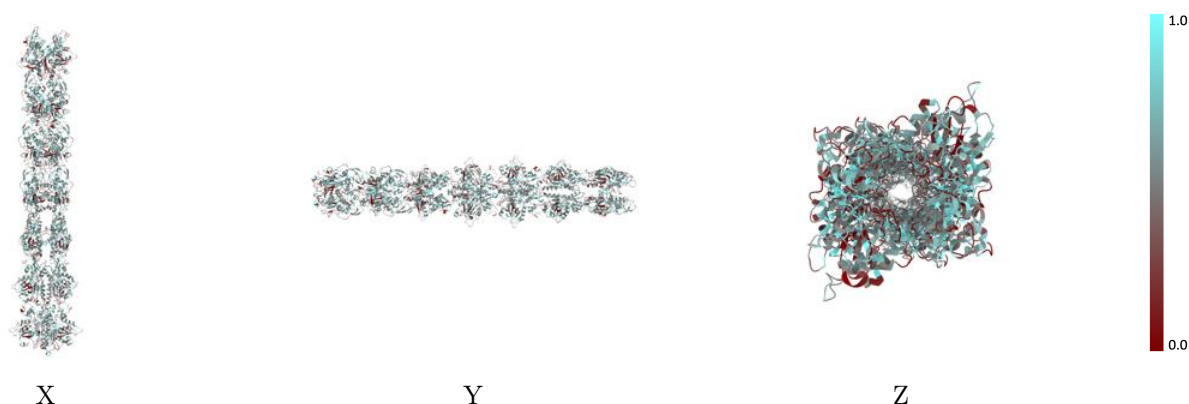
The images above show the 3D surface view of the map at the recommended contour level 5.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



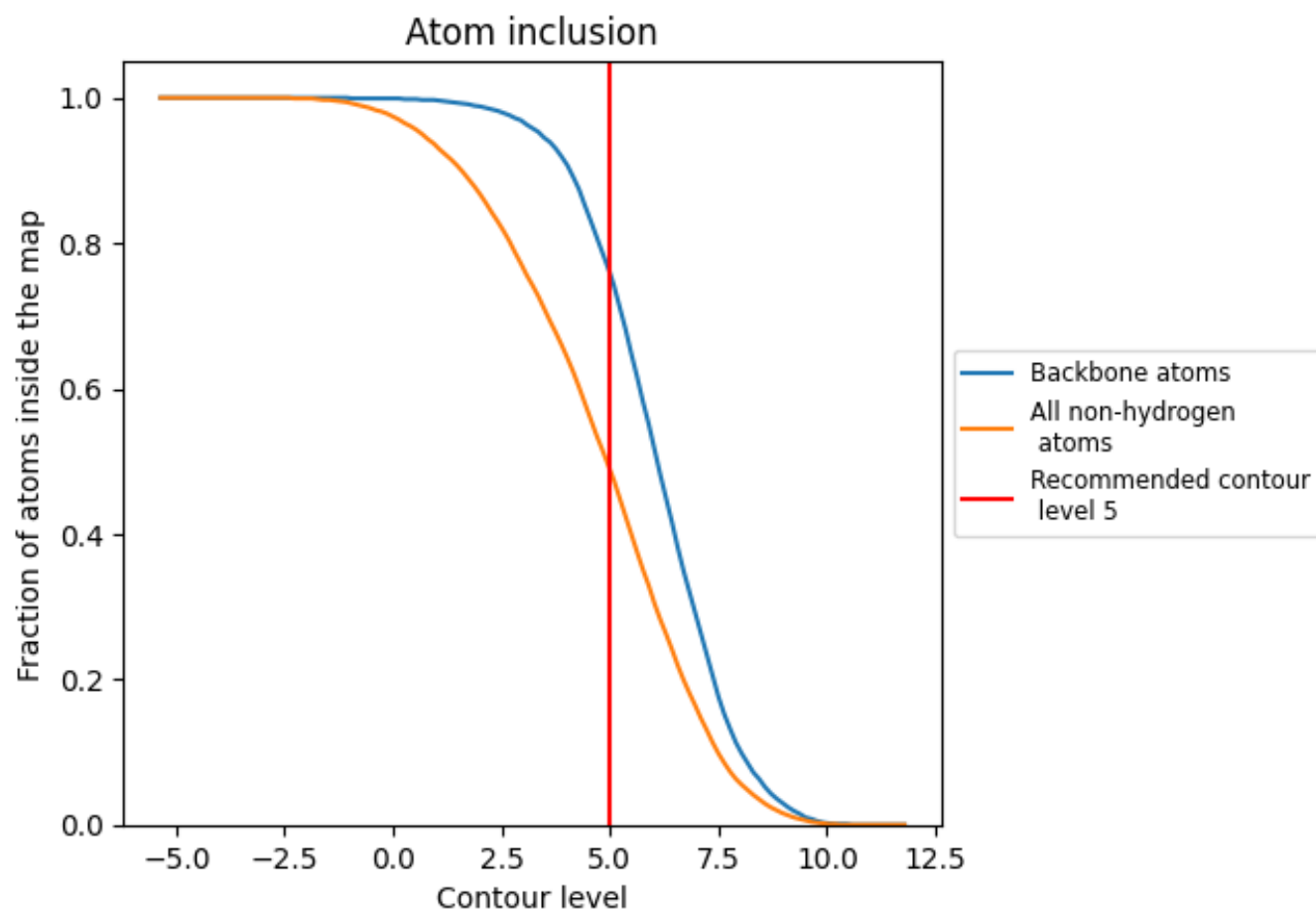
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 49% 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 (5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4880	0.1490
A	0.4780	0.1530
B	0.4880	0.1490
C	0.4900	0.1480
D	0.4930	0.1470
E	0.5040	0.1560
F	0.4920	0.1510
G	0.4720	0.1450
H	0.4640	0.1460
I	0.4910	0.1480
J	0.5000	0.1550
K	0.4910	0.1480
L	0.4890	0.1430
M	0.4950	0.1450
N	0.4880	0.1540

1.0

0.0

<0.0