



Full wwPDB EM Validation Report ⓘ

Mar 7, 2026 – 02:35 AM UTC

PDB ID : 8W23 / pdb_00008w23
EMDB ID : EMD-43738
Title : Cryo-EM structure of human tankyrase 2 SAM-PARP filament bound to compound, TDI-2804 (consensus map).
Authors : Malone, B.F.; Zimmerman, J.L.; Dow, L.E.; Hite, R.K.
Deposited on : 2024-02-19
Resolution : 2.28 Å(reported)
Based on initial model : 8ALY

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

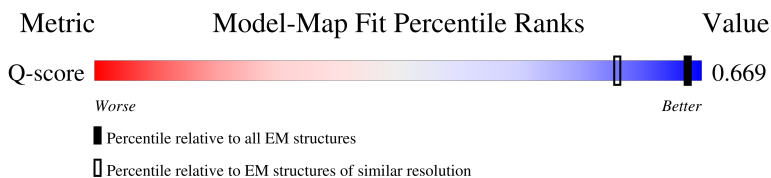
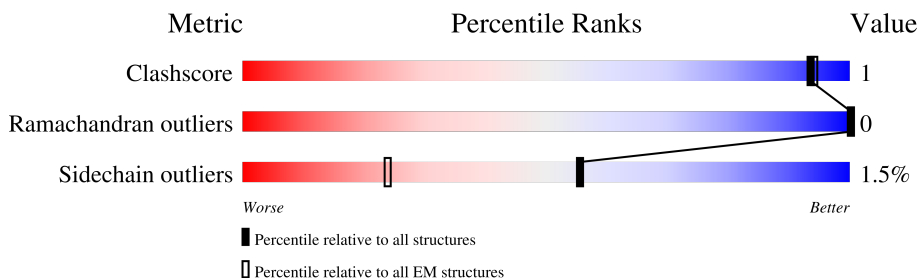
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.28 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.



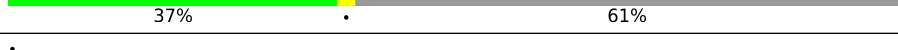
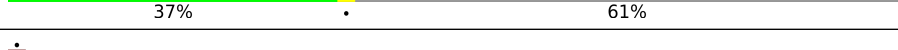
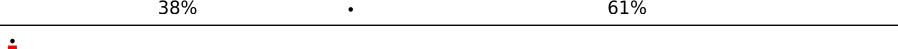
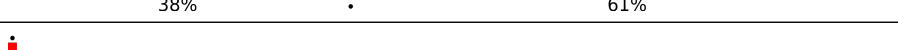
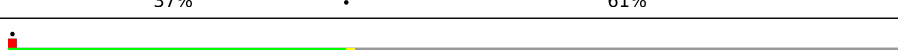
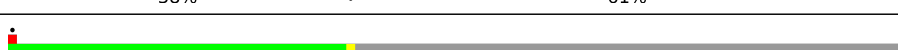
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	3643 (1.78 - 2.78)

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	729	
1	B	729	
1	C	729	
1	D	729	

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Mol	Chain	Length	Quality of chain
1	E	729	
1	F	729	
1	G	729	
1	H	729	
1	I	729	
1	K	729	
1	L	729	
1	M	729	
1	N	729	
1	O	729	
1	P	729	
1	Q	729	
1	R	729	
1	S	729	
1	T	729	
1	U	729	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 45580 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 Maltose/maltodextrin-binding periplasmic protein,Poly [ADP-ribose] polymerase tankyrase-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	284	Total	C	N	O	S	0	0
			2240	1420	408	399	13		
1	B	284	Total	C	N	O	S	0	0
			2240	1420	408	399	13		
1	C	284	Total	C	N	O	S	0	0
			2240	1420	408	399	13		
1	D	284	Total	C	N	O	S	0	0
			2240	1420	408	399	13		
1	E	284	Total	C	N	O	S	0	0
			2240	1420	408	399	13		
1	F	284	Total	C	N	O	S	0	0
			2240	1420	408	399	13		
1	G	284	Total	C	N	O	S	0	0
			2240	1420	408	399	13		
1	H	284	Total	C	N	O	S	0	0
			2240	1420	408	399	13		
1	I	284	Total	C	N	O	S	0	0
			2240	1420	408	399	13		
1	K	284	Total	C	N	O	S	0	0
			2240	1420	408	399	13		
1	L	284	Total	C	N	O	S	0	0
			2240	1420	408	399	13		
1	M	284	Total	C	N	O	S	0	0
			2240	1420	408	399	13		
1	N	284	Total	C	N	O	S	0	0
			2240	1420	408	399	13		
1	O	284	Total	C	N	O	S	0	0
			2240	1420	408	399	13		
1	P	284	Total	C	N	O	S	0	0
			2240	1420	408	399	13		
1	Q	284	Total	C	N	O	S	0	0
			2240	1420	408	399	13		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	284	Total	C	N	O	S	0	0
			2240	1420	408	399	13		
1	S	284	Total	C	N	O	S	0	0
			2240	1420	408	399	13		
1	T	284	Total	C	N	O	S	0	0
			2240	1420	408	399	13		
1	U	284	Total	C	N	O	S	0	0
			2240	1420	408	399	13		

There are 940 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	438	MET	-	initiating methionine	UNP P0AEY0
A	439	SER	-	expression tag	UNP P0AEY0
A	440	ALA	-	expression tag	UNP P0AEY0
A	441	TRP	-	expression tag	UNP P0AEY0
A	442	SER	-	expression tag	UNP P0AEY0
A	443	HIS	-	expression tag	UNP P0AEY0
A	444	PRO	-	expression tag	UNP P0AEY0
A	445	GLN	-	expression tag	UNP P0AEY0
A	446	PHE	-	expression tag	UNP P0AEY0
A	447	GLU	-	expression tag	UNP P0AEY0
A	448	LYS	-	expression tag	UNP P0AEY0
A	449	GLY	-	expression tag	UNP P0AEY0
A	450	GLY	-	expression tag	UNP P0AEY0
A	451	GLY	-	expression tag	UNP P0AEY0
A	452	SER	-	expression tag	UNP P0AEY0
A	453	GLY	-	expression tag	UNP P0AEY0
A	454	GLY	-	expression tag	UNP P0AEY0
A	455	GLY	-	expression tag	UNP P0AEY0
A	456	SER	-	expression tag	UNP P0AEY0
A	457	GLY	-	expression tag	UNP P0AEY0
A	458	GLY	-	expression tag	UNP P0AEY0
A	459	SER	-	expression tag	UNP P0AEY0
A	460	ALA	-	expression tag	UNP P0AEY0
A	461	TRP	-	expression tag	UNP P0AEY0
A	462	SER	-	expression tag	UNP P0AEY0
A	463	HIS	-	expression tag	UNP P0AEY0
A	464	PRO	-	expression tag	UNP P0AEY0
A	465	GLN	-	expression tag	UNP P0AEY0
A	466	PHE	-	expression tag	UNP P0AEY0
A	467	GLU	-	expression tag	UNP P0AEY0
A	468	LYS	-	expression tag	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
A	469	THR	-	expression tag	UNP P0AEY0
A	470	GLY	-	expression tag	UNP P0AEY0
A	471	SER	-	expression tag	UNP P0AEY0
A	472	MET	-	expression tag	UNP P0AEY0
A	473	GLY	-	expression tag	UNP P0AEY0
A	839	GLU	-	linker	UNP P0AEY0
A	840	LEU	-	linker	UNP P0AEY0
A	841	GLU	-	linker	UNP P0AEY0
A	842	LEU	-	linker	UNP P0AEY0
A	843	GLU	-	linker	UNP P0AEY0
A	844	VAL	-	linker	UNP P0AEY0
A	845	LEU	-	linker	UNP P0AEY0
A	846	PHE	-	linker	UNP P0AEY0
A	847	GLN	-	linker	UNP P0AEY0
A	848	GLY	-	linker	UNP P0AEY0
A	849	PRO	-	linker	UNP P0AEY0
B	438	MET	-	initiating methionine	UNP P0AEY0
B	439	SER	-	expression tag	UNP P0AEY0
B	440	ALA	-	expression tag	UNP P0AEY0
B	441	TRP	-	expression tag	UNP P0AEY0
B	442	SER	-	expression tag	UNP P0AEY0
B	443	HIS	-	expression tag	UNP P0AEY0
B	444	PRO	-	expression tag	UNP P0AEY0
B	445	GLN	-	expression tag	UNP P0AEY0
B	446	PHE	-	expression tag	UNP P0AEY0
B	447	GLU	-	expression tag	UNP P0AEY0
B	448	LYS	-	expression tag	UNP P0AEY0
B	449	GLY	-	expression tag	UNP P0AEY0
B	450	GLY	-	expression tag	UNP P0AEY0
B	451	GLY	-	expression tag	UNP P0AEY0
B	452	SER	-	expression tag	UNP P0AEY0
B	453	GLY	-	expression tag	UNP P0AEY0
B	454	GLY	-	expression tag	UNP P0AEY0
B	455	GLY	-	expression tag	UNP P0AEY0
B	456	SER	-	expression tag	UNP P0AEY0
B	457	GLY	-	expression tag	UNP P0AEY0
B	458	GLY	-	expression tag	UNP P0AEY0
B	459	SER	-	expression tag	UNP P0AEY0
B	460	ALA	-	expression tag	UNP P0AEY0
B	461	TRP	-	expression tag	UNP P0AEY0
B	462	SER	-	expression tag	UNP P0AEY0
B	463	HIS	-	expression tag	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	464	PRO	-	expression tag	UNP P0AEY0
B	465	GLN	-	expression tag	UNP P0AEY0
B	466	PHE	-	expression tag	UNP P0AEY0
B	467	GLU	-	expression tag	UNP P0AEY0
B	468	LYS	-	expression tag	UNP P0AEY0
B	469	THR	-	expression tag	UNP P0AEY0
B	470	GLY	-	expression tag	UNP P0AEY0
B	471	SER	-	expression tag	UNP P0AEY0
B	472	MET	-	expression tag	UNP P0AEY0
B	473	GLY	-	expression tag	UNP P0AEY0
B	839	GLU	-	linker	UNP P0AEY0
B	840	LEU	-	linker	UNP P0AEY0
B	841	GLU	-	linker	UNP P0AEY0
B	842	LEU	-	linker	UNP P0AEY0
B	843	GLU	-	linker	UNP P0AEY0
B	844	VAL	-	linker	UNP P0AEY0
B	845	LEU	-	linker	UNP P0AEY0
B	846	PHE	-	linker	UNP P0AEY0
B	847	GLN	-	linker	UNP P0AEY0
B	848	GLY	-	linker	UNP P0AEY0
B	849	PRO	-	linker	UNP P0AEY0
C	438	MET	-	initiating methionine	UNP P0AEY0
C	439	SER	-	expression tag	UNP P0AEY0
C	440	ALA	-	expression tag	UNP P0AEY0
C	441	TRP	-	expression tag	UNP P0AEY0
C	442	SER	-	expression tag	UNP P0AEY0
C	443	HIS	-	expression tag	UNP P0AEY0
C	444	PRO	-	expression tag	UNP P0AEY0
C	445	GLN	-	expression tag	UNP P0AEY0
C	446	PHE	-	expression tag	UNP P0AEY0
C	447	GLU	-	expression tag	UNP P0AEY0
C	448	LYS	-	expression tag	UNP P0AEY0
C	449	GLY	-	expression tag	UNP P0AEY0
C	450	GLY	-	expression tag	UNP P0AEY0
C	451	GLY	-	expression tag	UNP P0AEY0
C	452	SER	-	expression tag	UNP P0AEY0
C	453	GLY	-	expression tag	UNP P0AEY0
C	454	GLY	-	expression tag	UNP P0AEY0
C	455	GLY	-	expression tag	UNP P0AEY0
C	456	SER	-	expression tag	UNP P0AEY0
C	457	GLY	-	expression tag	UNP P0AEY0
C	458	GLY	-	expression tag	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
C	459	SER	-	expression tag	UNP P0AEY0
C	460	ALA	-	expression tag	UNP P0AEY0
C	461	TRP	-	expression tag	UNP P0AEY0
C	462	SER	-	expression tag	UNP P0AEY0
C	463	HIS	-	expression tag	UNP P0AEY0
C	464	PRO	-	expression tag	UNP P0AEY0
C	465	GLN	-	expression tag	UNP P0AEY0
C	466	PHE	-	expression tag	UNP P0AEY0
C	467	GLU	-	expression tag	UNP P0AEY0
C	468	LYS	-	expression tag	UNP P0AEY0
C	469	THR	-	expression tag	UNP P0AEY0
C	470	GLY	-	expression tag	UNP P0AEY0
C	471	SER	-	expression tag	UNP P0AEY0
C	472	MET	-	expression tag	UNP P0AEY0
C	473	GLY	-	expression tag	UNP P0AEY0
C	839	GLU	-	linker	UNP P0AEY0
C	840	LEU	-	linker	UNP P0AEY0
C	841	GLU	-	linker	UNP P0AEY0
C	842	LEU	-	linker	UNP P0AEY0
C	843	GLU	-	linker	UNP P0AEY0
C	844	VAL	-	linker	UNP P0AEY0
C	845	LEU	-	linker	UNP P0AEY0
C	846	PHE	-	linker	UNP P0AEY0
C	847	GLN	-	linker	UNP P0AEY0
C	848	GLY	-	linker	UNP P0AEY0
C	849	PRO	-	linker	UNP P0AEY0
D	438	MET	-	initiating methionine	UNP P0AEY0
D	439	SER	-	expression tag	UNP P0AEY0
D	440	ALA	-	expression tag	UNP P0AEY0
D	441	TRP	-	expression tag	UNP P0AEY0
D	442	SER	-	expression tag	UNP P0AEY0
D	443	HIS	-	expression tag	UNP P0AEY0
D	444	PRO	-	expression tag	UNP P0AEY0
D	445	GLN	-	expression tag	UNP P0AEY0
D	446	PHE	-	expression tag	UNP P0AEY0
D	447	GLU	-	expression tag	UNP P0AEY0
D	448	LYS	-	expression tag	UNP P0AEY0
D	449	GLY	-	expression tag	UNP P0AEY0
D	450	GLY	-	expression tag	UNP P0AEY0
D	451	GLY	-	expression tag	UNP P0AEY0
D	452	SER	-	expression tag	UNP P0AEY0
D	453	GLY	-	expression tag	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
D	454	GLY	-	expression tag	UNP P0AEY0
D	455	GLY	-	expression tag	UNP P0AEY0
D	456	SER	-	expression tag	UNP P0AEY0
D	457	GLY	-	expression tag	UNP P0AEY0
D	458	GLY	-	expression tag	UNP P0AEY0
D	459	SER	-	expression tag	UNP P0AEY0
D	460	ALA	-	expression tag	UNP P0AEY0
D	461	TRP	-	expression tag	UNP P0AEY0
D	462	SER	-	expression tag	UNP P0AEY0
D	463	HIS	-	expression tag	UNP P0AEY0
D	464	PRO	-	expression tag	UNP P0AEY0
D	465	GLN	-	expression tag	UNP P0AEY0
D	466	PHE	-	expression tag	UNP P0AEY0
D	467	GLU	-	expression tag	UNP P0AEY0
D	468	LYS	-	expression tag	UNP P0AEY0
D	469	THR	-	expression tag	UNP P0AEY0
D	470	GLY	-	expression tag	UNP P0AEY0
D	471	SER	-	expression tag	UNP P0AEY0
D	472	MET	-	expression tag	UNP P0AEY0
D	473	GLY	-	expression tag	UNP P0AEY0
D	839	GLU	-	linker	UNP P0AEY0
D	840	LEU	-	linker	UNP P0AEY0
D	841	GLU	-	linker	UNP P0AEY0
D	842	LEU	-	linker	UNP P0AEY0
D	843	GLU	-	linker	UNP P0AEY0
D	844	VAL	-	linker	UNP P0AEY0
D	845	LEU	-	linker	UNP P0AEY0
D	846	PHE	-	linker	UNP P0AEY0
D	847	GLN	-	linker	UNP P0AEY0
D	848	GLY	-	linker	UNP P0AEY0
D	849	PRO	-	linker	UNP P0AEY0
E	438	MET	-	initiating methionine	UNP P0AEY0
E	439	SER	-	expression tag	UNP P0AEY0
E	440	ALA	-	expression tag	UNP P0AEY0
E	441	TRP	-	expression tag	UNP P0AEY0
E	442	SER	-	expression tag	UNP P0AEY0
E	443	HIS	-	expression tag	UNP P0AEY0
E	444	PRO	-	expression tag	UNP P0AEY0
E	445	GLN	-	expression tag	UNP P0AEY0
E	446	PHE	-	expression tag	UNP P0AEY0
E	447	GLU	-	expression tag	UNP P0AEY0
E	448	LYS	-	expression tag	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
E	449	GLY	-	expression tag	UNP P0AEY0
E	450	GLY	-	expression tag	UNP P0AEY0
E	451	GLY	-	expression tag	UNP P0AEY0
E	452	SER	-	expression tag	UNP P0AEY0
E	453	GLY	-	expression tag	UNP P0AEY0
E	454	GLY	-	expression tag	UNP P0AEY0
E	455	GLY	-	expression tag	UNP P0AEY0
E	456	SER	-	expression tag	UNP P0AEY0
E	457	GLY	-	expression tag	UNP P0AEY0
E	458	GLY	-	expression tag	UNP P0AEY0
E	459	SER	-	expression tag	UNP P0AEY0
E	460	ALA	-	expression tag	UNP P0AEY0
E	461	TRP	-	expression tag	UNP P0AEY0
E	462	SER	-	expression tag	UNP P0AEY0
E	463	HIS	-	expression tag	UNP P0AEY0
E	464	PRO	-	expression tag	UNP P0AEY0
E	465	GLN	-	expression tag	UNP P0AEY0
E	466	PHE	-	expression tag	UNP P0AEY0
E	467	GLU	-	expression tag	UNP P0AEY0
E	468	LYS	-	expression tag	UNP P0AEY0
E	469	THR	-	expression tag	UNP P0AEY0
E	470	GLY	-	expression tag	UNP P0AEY0
E	471	SER	-	expression tag	UNP P0AEY0
E	472	MET	-	expression tag	UNP P0AEY0
E	473	GLY	-	expression tag	UNP P0AEY0
E	839	GLU	-	linker	UNP P0AEY0
E	840	LEU	-	linker	UNP P0AEY0
E	841	GLU	-	linker	UNP P0AEY0
E	842	LEU	-	linker	UNP P0AEY0
E	843	GLU	-	linker	UNP P0AEY0
E	844	VAL	-	linker	UNP P0AEY0
E	845	LEU	-	linker	UNP P0AEY0
E	846	PHE	-	linker	UNP P0AEY0
E	847	GLN	-	linker	UNP P0AEY0
E	848	GLY	-	linker	UNP P0AEY0
E	849	PRO	-	linker	UNP P0AEY0
F	438	MET	-	initiating methionine	UNP P0AEY0
F	439	SER	-	expression tag	UNP P0AEY0
F	440	ALA	-	expression tag	UNP P0AEY0
F	441	TRP	-	expression tag	UNP P0AEY0
F	442	SER	-	expression tag	UNP P0AEY0
F	443	HIS	-	expression tag	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
F	444	PRO	-	expression tag	UNP P0AEY0
F	445	GLN	-	expression tag	UNP P0AEY0
F	446	PHE	-	expression tag	UNP P0AEY0
F	447	GLU	-	expression tag	UNP P0AEY0
F	448	LYS	-	expression tag	UNP P0AEY0
F	449	GLY	-	expression tag	UNP P0AEY0
F	450	GLY	-	expression tag	UNP P0AEY0
F	451	GLY	-	expression tag	UNP P0AEY0
F	452	SER	-	expression tag	UNP P0AEY0
F	453	GLY	-	expression tag	UNP P0AEY0
F	454	GLY	-	expression tag	UNP P0AEY0
F	455	GLY	-	expression tag	UNP P0AEY0
F	456	SER	-	expression tag	UNP P0AEY0
F	457	GLY	-	expression tag	UNP P0AEY0
F	458	GLY	-	expression tag	UNP P0AEY0
F	459	SER	-	expression tag	UNP P0AEY0
F	460	ALA	-	expression tag	UNP P0AEY0
F	461	TRP	-	expression tag	UNP P0AEY0
F	462	SER	-	expression tag	UNP P0AEY0
F	463	HIS	-	expression tag	UNP P0AEY0
F	464	PRO	-	expression tag	UNP P0AEY0
F	465	GLN	-	expression tag	UNP P0AEY0
F	466	PHE	-	expression tag	UNP P0AEY0
F	467	GLU	-	expression tag	UNP P0AEY0
F	468	LYS	-	expression tag	UNP P0AEY0
F	469	THR	-	expression tag	UNP P0AEY0
F	470	GLY	-	expression tag	UNP P0AEY0
F	471	SER	-	expression tag	UNP P0AEY0
F	472	MET	-	expression tag	UNP P0AEY0
F	473	GLY	-	expression tag	UNP P0AEY0
F	839	GLU	-	linker	UNP P0AEY0
F	840	LEU	-	linker	UNP P0AEY0
F	841	GLU	-	linker	UNP P0AEY0
F	842	LEU	-	linker	UNP P0AEY0
F	843	GLU	-	linker	UNP P0AEY0
F	844	VAL	-	linker	UNP P0AEY0
F	845	LEU	-	linker	UNP P0AEY0
F	846	PHE	-	linker	UNP P0AEY0
F	847	GLN	-	linker	UNP P0AEY0
F	848	GLY	-	linker	UNP P0AEY0
F	849	PRO	-	linker	UNP P0AEY0
G	438	MET	-	initiating methionine	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
G	439	SER	-	expression tag	UNP P0AEY0
G	440	ALA	-	expression tag	UNP P0AEY0
G	441	TRP	-	expression tag	UNP P0AEY0
G	442	SER	-	expression tag	UNP P0AEY0
G	443	HIS	-	expression tag	UNP P0AEY0
G	444	PRO	-	expression tag	UNP P0AEY0
G	445	GLN	-	expression tag	UNP P0AEY0
G	446	PHE	-	expression tag	UNP P0AEY0
G	447	GLU	-	expression tag	UNP P0AEY0
G	448	LYS	-	expression tag	UNP P0AEY0
G	449	GLY	-	expression tag	UNP P0AEY0
G	450	GLY	-	expression tag	UNP P0AEY0
G	451	GLY	-	expression tag	UNP P0AEY0
G	452	SER	-	expression tag	UNP P0AEY0
G	453	GLY	-	expression tag	UNP P0AEY0
G	454	GLY	-	expression tag	UNP P0AEY0
G	455	GLY	-	expression tag	UNP P0AEY0
G	456	SER	-	expression tag	UNP P0AEY0
G	457	GLY	-	expression tag	UNP P0AEY0
G	458	GLY	-	expression tag	UNP P0AEY0
G	459	SER	-	expression tag	UNP P0AEY0
G	460	ALA	-	expression tag	UNP P0AEY0
G	461	TRP	-	expression tag	UNP P0AEY0
G	462	SER	-	expression tag	UNP P0AEY0
G	463	HIS	-	expression tag	UNP P0AEY0
G	464	PRO	-	expression tag	UNP P0AEY0
G	465	GLN	-	expression tag	UNP P0AEY0
G	466	PHE	-	expression tag	UNP P0AEY0
G	467	GLU	-	expression tag	UNP P0AEY0
G	468	LYS	-	expression tag	UNP P0AEY0
G	469	THR	-	expression tag	UNP P0AEY0
G	470	GLY	-	expression tag	UNP P0AEY0
G	471	SER	-	expression tag	UNP P0AEY0
G	472	MET	-	expression tag	UNP P0AEY0
G	473	GLY	-	expression tag	UNP P0AEY0
G	839	GLU	-	linker	UNP P0AEY0
G	840	LEU	-	linker	UNP P0AEY0
G	841	GLU	-	linker	UNP P0AEY0
G	842	LEU	-	linker	UNP P0AEY0
G	843	GLU	-	linker	UNP P0AEY0
G	844	VAL	-	linker	UNP P0AEY0
G	845	LEU	-	linker	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
G	846	PHE	-	linker	UNP P0AEY0
G	847	GLN	-	linker	UNP P0AEY0
G	848	GLY	-	linker	UNP P0AEY0
G	849	PRO	-	linker	UNP P0AEY0
H	438	MET	-	initiating methionine	UNP P0AEY0
H	439	SER	-	expression tag	UNP P0AEY0
H	440	ALA	-	expression tag	UNP P0AEY0
H	441	TRP	-	expression tag	UNP P0AEY0
H	442	SER	-	expression tag	UNP P0AEY0
H	443	HIS	-	expression tag	UNP P0AEY0
H	444	PRO	-	expression tag	UNP P0AEY0
H	445	GLN	-	expression tag	UNP P0AEY0
H	446	PHE	-	expression tag	UNP P0AEY0
H	447	GLU	-	expression tag	UNP P0AEY0
H	448	LYS	-	expression tag	UNP P0AEY0
H	449	GLY	-	expression tag	UNP P0AEY0
H	450	GLY	-	expression tag	UNP P0AEY0
H	451	GLY	-	expression tag	UNP P0AEY0
H	452	SER	-	expression tag	UNP P0AEY0
H	453	GLY	-	expression tag	UNP P0AEY0
H	454	GLY	-	expression tag	UNP P0AEY0
H	455	GLY	-	expression tag	UNP P0AEY0
H	456	SER	-	expression tag	UNP P0AEY0
H	457	GLY	-	expression tag	UNP P0AEY0
H	458	GLY	-	expression tag	UNP P0AEY0
H	459	SER	-	expression tag	UNP P0AEY0
H	460	ALA	-	expression tag	UNP P0AEY0
H	461	TRP	-	expression tag	UNP P0AEY0
H	462	SER	-	expression tag	UNP P0AEY0
H	463	HIS	-	expression tag	UNP P0AEY0
H	464	PRO	-	expression tag	UNP P0AEY0
H	465	GLN	-	expression tag	UNP P0AEY0
H	466	PHE	-	expression tag	UNP P0AEY0
H	467	GLU	-	expression tag	UNP P0AEY0
H	468	LYS	-	expression tag	UNP P0AEY0
H	469	THR	-	expression tag	UNP P0AEY0
H	470	GLY	-	expression tag	UNP P0AEY0
H	471	SER	-	expression tag	UNP P0AEY0
H	472	MET	-	expression tag	UNP P0AEY0
H	473	GLY	-	expression tag	UNP P0AEY0
H	839	GLU	-	linker	UNP P0AEY0
H	840	LEU	-	linker	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
H	841	GLU	-	linker	UNP P0AEY0
H	842	LEU	-	linker	UNP P0AEY0
H	843	GLU	-	linker	UNP P0AEY0
H	844	VAL	-	linker	UNP P0AEY0
H	845	LEU	-	linker	UNP P0AEY0
H	846	PHE	-	linker	UNP P0AEY0
H	847	GLN	-	linker	UNP P0AEY0
H	848	GLY	-	linker	UNP P0AEY0
H	849	PRO	-	linker	UNP P0AEY0
I	438	MET	-	initiating methionine	UNP P0AEY0
I	439	SER	-	expression tag	UNP P0AEY0
I	440	ALA	-	expression tag	UNP P0AEY0
I	441	TRP	-	expression tag	UNP P0AEY0
I	442	SER	-	expression tag	UNP P0AEY0
I	443	HIS	-	expression tag	UNP P0AEY0
I	444	PRO	-	expression tag	UNP P0AEY0
I	445	GLN	-	expression tag	UNP P0AEY0
I	446	PHE	-	expression tag	UNP P0AEY0
I	447	GLU	-	expression tag	UNP P0AEY0
I	448	LYS	-	expression tag	UNP P0AEY0
I	449	GLY	-	expression tag	UNP P0AEY0
I	450	GLY	-	expression tag	UNP P0AEY0
I	451	GLY	-	expression tag	UNP P0AEY0
I	452	SER	-	expression tag	UNP P0AEY0
I	453	GLY	-	expression tag	UNP P0AEY0
I	454	GLY	-	expression tag	UNP P0AEY0
I	455	GLY	-	expression tag	UNP P0AEY0
I	456	SER	-	expression tag	UNP P0AEY0
I	457	GLY	-	expression tag	UNP P0AEY0
I	458	GLY	-	expression tag	UNP P0AEY0
I	459	SER	-	expression tag	UNP P0AEY0
I	460	ALA	-	expression tag	UNP P0AEY0
I	461	TRP	-	expression tag	UNP P0AEY0
I	462	SER	-	expression tag	UNP P0AEY0
I	463	HIS	-	expression tag	UNP P0AEY0
I	464	PRO	-	expression tag	UNP P0AEY0
I	465	GLN	-	expression tag	UNP P0AEY0
I	466	PHE	-	expression tag	UNP P0AEY0
I	467	GLU	-	expression tag	UNP P0AEY0
I	468	LYS	-	expression tag	UNP P0AEY0
I	469	THR	-	expression tag	UNP P0AEY0
I	470	GLY	-	expression tag	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
I	471	SER	-	expression tag	UNP P0AEY0
I	472	MET	-	expression tag	UNP P0AEY0
I	473	GLY	-	expression tag	UNP P0AEY0
I	839	GLU	-	linker	UNP P0AEY0
I	840	LEU	-	linker	UNP P0AEY0
I	841	GLU	-	linker	UNP P0AEY0
I	842	LEU	-	linker	UNP P0AEY0
I	843	GLU	-	linker	UNP P0AEY0
I	844	VAL	-	linker	UNP P0AEY0
I	845	LEU	-	linker	UNP P0AEY0
I	846	PHE	-	linker	UNP P0AEY0
I	847	GLN	-	linker	UNP P0AEY0
I	848	GLY	-	linker	UNP P0AEY0
I	849	PRO	-	linker	UNP P0AEY0
K	438	MET	-	initiating methionine	UNP P0AEY0
K	439	SER	-	expression tag	UNP P0AEY0
K	440	ALA	-	expression tag	UNP P0AEY0
K	441	TRP	-	expression tag	UNP P0AEY0
K	442	SER	-	expression tag	UNP P0AEY0
K	443	HIS	-	expression tag	UNP P0AEY0
K	444	PRO	-	expression tag	UNP P0AEY0
K	445	GLN	-	expression tag	UNP P0AEY0
K	446	PHE	-	expression tag	UNP P0AEY0
K	447	GLU	-	expression tag	UNP P0AEY0
K	448	LYS	-	expression tag	UNP P0AEY0
K	449	GLY	-	expression tag	UNP P0AEY0
K	450	GLY	-	expression tag	UNP P0AEY0
K	451	GLY	-	expression tag	UNP P0AEY0
K	452	SER	-	expression tag	UNP P0AEY0
K	453	GLY	-	expression tag	UNP P0AEY0
K	454	GLY	-	expression tag	UNP P0AEY0
K	455	GLY	-	expression tag	UNP P0AEY0
K	456	SER	-	expression tag	UNP P0AEY0
K	457	GLY	-	expression tag	UNP P0AEY0
K	458	GLY	-	expression tag	UNP P0AEY0
K	459	SER	-	expression tag	UNP P0AEY0
K	460	ALA	-	expression tag	UNP P0AEY0
K	461	TRP	-	expression tag	UNP P0AEY0
K	462	SER	-	expression tag	UNP P0AEY0
K	463	HIS	-	expression tag	UNP P0AEY0
K	464	PRO	-	expression tag	UNP P0AEY0
K	465	GLN	-	expression tag	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
K	466	PHE	-	expression tag	UNP P0AEY0
K	467	GLU	-	expression tag	UNP P0AEY0
K	468	LYS	-	expression tag	UNP P0AEY0
K	469	THR	-	expression tag	UNP P0AEY0
K	470	GLY	-	expression tag	UNP P0AEY0
K	471	SER	-	expression tag	UNP P0AEY0
K	472	MET	-	expression tag	UNP P0AEY0
K	473	GLY	-	expression tag	UNP P0AEY0
K	839	GLU	-	linker	UNP P0AEY0
K	840	LEU	-	linker	UNP P0AEY0
K	841	GLU	-	linker	UNP P0AEY0
K	842	LEU	-	linker	UNP P0AEY0
K	843	GLU	-	linker	UNP P0AEY0
K	844	VAL	-	linker	UNP P0AEY0
K	845	LEU	-	linker	UNP P0AEY0
K	846	PHE	-	linker	UNP P0AEY0
K	847	GLN	-	linker	UNP P0AEY0
K	848	GLY	-	linker	UNP P0AEY0
K	849	PRO	-	linker	UNP P0AEY0
L	438	MET	-	initiating methionine	UNP P0AEY0
L	439	SER	-	expression tag	UNP P0AEY0
L	440	ALA	-	expression tag	UNP P0AEY0
L	441	TRP	-	expression tag	UNP P0AEY0
L	442	SER	-	expression tag	UNP P0AEY0
L	443	HIS	-	expression tag	UNP P0AEY0
L	444	PRO	-	expression tag	UNP P0AEY0
L	445	GLN	-	expression tag	UNP P0AEY0
L	446	PHE	-	expression tag	UNP P0AEY0
L	447	GLU	-	expression tag	UNP P0AEY0
L	448	LYS	-	expression tag	UNP P0AEY0
L	449	GLY	-	expression tag	UNP P0AEY0
L	450	GLY	-	expression tag	UNP P0AEY0
L	451	GLY	-	expression tag	UNP P0AEY0
L	452	SER	-	expression tag	UNP P0AEY0
L	453	GLY	-	expression tag	UNP P0AEY0
L	454	GLY	-	expression tag	UNP P0AEY0
L	455	GLY	-	expression tag	UNP P0AEY0
L	456	SER	-	expression tag	UNP P0AEY0
L	457	GLY	-	expression tag	UNP P0AEY0
L	458	GLY	-	expression tag	UNP P0AEY0
L	459	SER	-	expression tag	UNP P0AEY0
L	460	ALA	-	expression tag	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
L	461	TRP	-	expression tag	UNP P0AEY0
L	462	SER	-	expression tag	UNP P0AEY0
L	463	HIS	-	expression tag	UNP P0AEY0
L	464	PRO	-	expression tag	UNP P0AEY0
L	465	GLN	-	expression tag	UNP P0AEY0
L	466	PHE	-	expression tag	UNP P0AEY0
L	467	GLU	-	expression tag	UNP P0AEY0
L	468	LYS	-	expression tag	UNP P0AEY0
L	469	THR	-	expression tag	UNP P0AEY0
L	470	GLY	-	expression tag	UNP P0AEY0
L	471	SER	-	expression tag	UNP P0AEY0
L	472	MET	-	expression tag	UNP P0AEY0
L	473	GLY	-	expression tag	UNP P0AEY0
L	839	GLU	-	linker	UNP P0AEY0
L	840	LEU	-	linker	UNP P0AEY0
L	841	GLU	-	linker	UNP P0AEY0
L	842	LEU	-	linker	UNP P0AEY0
L	843	GLU	-	linker	UNP P0AEY0
L	844	VAL	-	linker	UNP P0AEY0
L	845	LEU	-	linker	UNP P0AEY0
L	846	PHE	-	linker	UNP P0AEY0
L	847	GLN	-	linker	UNP P0AEY0
L	848	GLY	-	linker	UNP P0AEY0
L	849	PRO	-	linker	UNP P0AEY0
M	438	MET	-	initiating methionine	UNP P0AEY0
M	439	SER	-	expression tag	UNP P0AEY0
M	440	ALA	-	expression tag	UNP P0AEY0
M	441	TRP	-	expression tag	UNP P0AEY0
M	442	SER	-	expression tag	UNP P0AEY0
M	443	HIS	-	expression tag	UNP P0AEY0
M	444	PRO	-	expression tag	UNP P0AEY0
M	445	GLN	-	expression tag	UNP P0AEY0
M	446	PHE	-	expression tag	UNP P0AEY0
M	447	GLU	-	expression tag	UNP P0AEY0
M	448	LYS	-	expression tag	UNP P0AEY0
M	449	GLY	-	expression tag	UNP P0AEY0
M	450	GLY	-	expression tag	UNP P0AEY0
M	451	GLY	-	expression tag	UNP P0AEY0
M	452	SER	-	expression tag	UNP P0AEY0
M	453	GLY	-	expression tag	UNP P0AEY0
M	454	GLY	-	expression tag	UNP P0AEY0
M	455	GLY	-	expression tag	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
M	456	SER	-	expression tag	UNP P0AEY0
M	457	GLY	-	expression tag	UNP P0AEY0
M	458	GLY	-	expression tag	UNP P0AEY0
M	459	SER	-	expression tag	UNP P0AEY0
M	460	ALA	-	expression tag	UNP P0AEY0
M	461	TRP	-	expression tag	UNP P0AEY0
M	462	SER	-	expression tag	UNP P0AEY0
M	463	HIS	-	expression tag	UNP P0AEY0
M	464	PRO	-	expression tag	UNP P0AEY0
M	465	GLN	-	expression tag	UNP P0AEY0
M	466	PHE	-	expression tag	UNP P0AEY0
M	467	GLU	-	expression tag	UNP P0AEY0
M	468	LYS	-	expression tag	UNP P0AEY0
M	469	THR	-	expression tag	UNP P0AEY0
M	470	GLY	-	expression tag	UNP P0AEY0
M	471	SER	-	expression tag	UNP P0AEY0
M	472	MET	-	expression tag	UNP P0AEY0
M	473	GLY	-	expression tag	UNP P0AEY0
M	839	GLU	-	linker	UNP P0AEY0
M	840	LEU	-	linker	UNP P0AEY0
M	841	GLU	-	linker	UNP P0AEY0
M	842	LEU	-	linker	UNP P0AEY0
M	843	GLU	-	linker	UNP P0AEY0
M	844	VAL	-	linker	UNP P0AEY0
M	845	LEU	-	linker	UNP P0AEY0
M	846	PHE	-	linker	UNP P0AEY0
M	847	GLN	-	linker	UNP P0AEY0
M	848	GLY	-	linker	UNP P0AEY0
M	849	PRO	-	linker	UNP P0AEY0
N	438	MET	-	initiating methionine	UNP P0AEY0
N	439	SER	-	expression tag	UNP P0AEY0
N	440	ALA	-	expression tag	UNP P0AEY0
N	441	TRP	-	expression tag	UNP P0AEY0
N	442	SER	-	expression tag	UNP P0AEY0
N	443	HIS	-	expression tag	UNP P0AEY0
N	444	PRO	-	expression tag	UNP P0AEY0
N	445	GLN	-	expression tag	UNP P0AEY0
N	446	PHE	-	expression tag	UNP P0AEY0
N	447	GLU	-	expression tag	UNP P0AEY0
N	448	LYS	-	expression tag	UNP P0AEY0
N	449	GLY	-	expression tag	UNP P0AEY0
N	450	GLY	-	expression tag	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
N	451	GLY	-	expression tag	UNP P0AEY0
N	452	SER	-	expression tag	UNP P0AEY0
N	453	GLY	-	expression tag	UNP P0AEY0
N	454	GLY	-	expression tag	UNP P0AEY0
N	455	GLY	-	expression tag	UNP P0AEY0
N	456	SER	-	expression tag	UNP P0AEY0
N	457	GLY	-	expression tag	UNP P0AEY0
N	458	GLY	-	expression tag	UNP P0AEY0
N	459	SER	-	expression tag	UNP P0AEY0
N	460	ALA	-	expression tag	UNP P0AEY0
N	461	TRP	-	expression tag	UNP P0AEY0
N	462	SER	-	expression tag	UNP P0AEY0
N	463	HIS	-	expression tag	UNP P0AEY0
N	464	PRO	-	expression tag	UNP P0AEY0
N	465	GLN	-	expression tag	UNP P0AEY0
N	466	PHE	-	expression tag	UNP P0AEY0
N	467	GLU	-	expression tag	UNP P0AEY0
N	468	LYS	-	expression tag	UNP P0AEY0
N	469	THR	-	expression tag	UNP P0AEY0
N	470	GLY	-	expression tag	UNP P0AEY0
N	471	SER	-	expression tag	UNP P0AEY0
N	472	MET	-	expression tag	UNP P0AEY0
N	473	GLY	-	expression tag	UNP P0AEY0
N	839	GLU	-	linker	UNP P0AEY0
N	840	LEU	-	linker	UNP P0AEY0
N	841	GLU	-	linker	UNP P0AEY0
N	842	LEU	-	linker	UNP P0AEY0
N	843	GLU	-	linker	UNP P0AEY0
N	844	VAL	-	linker	UNP P0AEY0
N	845	LEU	-	linker	UNP P0AEY0
N	846	PHE	-	linker	UNP P0AEY0
N	847	GLN	-	linker	UNP P0AEY0
N	848	GLY	-	linker	UNP P0AEY0
N	849	PRO	-	linker	UNP P0AEY0
O	438	MET	-	initiating methionine	UNP P0AEY0
O	439	SER	-	expression tag	UNP P0AEY0
O	440	ALA	-	expression tag	UNP P0AEY0
O	441	TRP	-	expression tag	UNP P0AEY0
O	442	SER	-	expression tag	UNP P0AEY0
O	443	HIS	-	expression tag	UNP P0AEY0
O	444	PRO	-	expression tag	UNP P0AEY0
O	445	GLN	-	expression tag	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
O	446	PHE	-	expression tag	UNP P0AEY0
O	447	GLU	-	expression tag	UNP P0AEY0
O	448	LYS	-	expression tag	UNP P0AEY0
O	449	GLY	-	expression tag	UNP P0AEY0
O	450	GLY	-	expression tag	UNP P0AEY0
O	451	GLY	-	expression tag	UNP P0AEY0
O	452	SER	-	expression tag	UNP P0AEY0
O	453	GLY	-	expression tag	UNP P0AEY0
O	454	GLY	-	expression tag	UNP P0AEY0
O	455	GLY	-	expression tag	UNP P0AEY0
O	456	SER	-	expression tag	UNP P0AEY0
O	457	GLY	-	expression tag	UNP P0AEY0
O	458	GLY	-	expression tag	UNP P0AEY0
O	459	SER	-	expression tag	UNP P0AEY0
O	460	ALA	-	expression tag	UNP P0AEY0
O	461	TRP	-	expression tag	UNP P0AEY0
O	462	SER	-	expression tag	UNP P0AEY0
O	463	HIS	-	expression tag	UNP P0AEY0
O	464	PRO	-	expression tag	UNP P0AEY0
O	465	GLN	-	expression tag	UNP P0AEY0
O	466	PHE	-	expression tag	UNP P0AEY0
O	467	GLU	-	expression tag	UNP P0AEY0
O	468	LYS	-	expression tag	UNP P0AEY0
O	469	THR	-	expression tag	UNP P0AEY0
O	470	GLY	-	expression tag	UNP P0AEY0
O	471	SER	-	expression tag	UNP P0AEY0
O	472	MET	-	expression tag	UNP P0AEY0
O	473	GLY	-	expression tag	UNP P0AEY0
O	839	GLU	-	linker	UNP P0AEY0
O	840	LEU	-	linker	UNP P0AEY0
O	841	GLU	-	linker	UNP P0AEY0
O	842	LEU	-	linker	UNP P0AEY0
O	843	GLU	-	linker	UNP P0AEY0
O	844	VAL	-	linker	UNP P0AEY0
O	845	LEU	-	linker	UNP P0AEY0
O	846	PHE	-	linker	UNP P0AEY0
O	847	GLN	-	linker	UNP P0AEY0
O	848	GLY	-	linker	UNP P0AEY0
O	849	PRO	-	linker	UNP P0AEY0
P	438	MET	-	initiating methionine	UNP P0AEY0
P	439	SER	-	expression tag	UNP P0AEY0
P	440	ALA	-	expression tag	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
P	441	TRP	-	expression tag	UNP P0AEY0
P	442	SER	-	expression tag	UNP P0AEY0
P	443	HIS	-	expression tag	UNP P0AEY0
P	444	PRO	-	expression tag	UNP P0AEY0
P	445	GLN	-	expression tag	UNP P0AEY0
P	446	PHE	-	expression tag	UNP P0AEY0
P	447	GLU	-	expression tag	UNP P0AEY0
P	448	LYS	-	expression tag	UNP P0AEY0
P	449	GLY	-	expression tag	UNP P0AEY0
P	450	GLY	-	expression tag	UNP P0AEY0
P	451	GLY	-	expression tag	UNP P0AEY0
P	452	SER	-	expression tag	UNP P0AEY0
P	453	GLY	-	expression tag	UNP P0AEY0
P	454	GLY	-	expression tag	UNP P0AEY0
P	455	GLY	-	expression tag	UNP P0AEY0
P	456	SER	-	expression tag	UNP P0AEY0
P	457	GLY	-	expression tag	UNP P0AEY0
P	458	GLY	-	expression tag	UNP P0AEY0
P	459	SER	-	expression tag	UNP P0AEY0
P	460	ALA	-	expression tag	UNP P0AEY0
P	461	TRP	-	expression tag	UNP P0AEY0
P	462	SER	-	expression tag	UNP P0AEY0
P	463	HIS	-	expression tag	UNP P0AEY0
P	464	PRO	-	expression tag	UNP P0AEY0
P	465	GLN	-	expression tag	UNP P0AEY0
P	466	PHE	-	expression tag	UNP P0AEY0
P	467	GLU	-	expression tag	UNP P0AEY0
P	468	LYS	-	expression tag	UNP P0AEY0
P	469	THR	-	expression tag	UNP P0AEY0
P	470	GLY	-	expression tag	UNP P0AEY0
P	471	SER	-	expression tag	UNP P0AEY0
P	472	MET	-	expression tag	UNP P0AEY0
P	473	GLY	-	expression tag	UNP P0AEY0
P	839	GLU	-	linker	UNP P0AEY0
P	840	LEU	-	linker	UNP P0AEY0
P	841	GLU	-	linker	UNP P0AEY0
P	842	LEU	-	linker	UNP P0AEY0
P	843	GLU	-	linker	UNP P0AEY0
P	844	VAL	-	linker	UNP P0AEY0
P	845	LEU	-	linker	UNP P0AEY0
P	846	PHE	-	linker	UNP P0AEY0
P	847	GLN	-	linker	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
P	848	GLY	-	linker	UNP P0AEY0
P	849	PRO	-	linker	UNP P0AEY0
Q	438	MET	-	initiating methionine	UNP P0AEY0
Q	439	SER	-	expression tag	UNP P0AEY0
Q	440	ALA	-	expression tag	UNP P0AEY0
Q	441	TRP	-	expression tag	UNP P0AEY0
Q	442	SER	-	expression tag	UNP P0AEY0
Q	443	HIS	-	expression tag	UNP P0AEY0
Q	444	PRO	-	expression tag	UNP P0AEY0
Q	445	GLN	-	expression tag	UNP P0AEY0
Q	446	PHE	-	expression tag	UNP P0AEY0
Q	447	GLU	-	expression tag	UNP P0AEY0
Q	448	LYS	-	expression tag	UNP P0AEY0
Q	449	GLY	-	expression tag	UNP P0AEY0
Q	450	GLY	-	expression tag	UNP P0AEY0
Q	451	GLY	-	expression tag	UNP P0AEY0
Q	452	SER	-	expression tag	UNP P0AEY0
Q	453	GLY	-	expression tag	UNP P0AEY0
Q	454	GLY	-	expression tag	UNP P0AEY0
Q	455	GLY	-	expression tag	UNP P0AEY0
Q	456	SER	-	expression tag	UNP P0AEY0
Q	457	GLY	-	expression tag	UNP P0AEY0
Q	458	GLY	-	expression tag	UNP P0AEY0
Q	459	SER	-	expression tag	UNP P0AEY0
Q	460	ALA	-	expression tag	UNP P0AEY0
Q	461	TRP	-	expression tag	UNP P0AEY0
Q	462	SER	-	expression tag	UNP P0AEY0
Q	463	HIS	-	expression tag	UNP P0AEY0
Q	464	PRO	-	expression tag	UNP P0AEY0
Q	465	GLN	-	expression tag	UNP P0AEY0
Q	466	PHE	-	expression tag	UNP P0AEY0
Q	467	GLU	-	expression tag	UNP P0AEY0
Q	468	LYS	-	expression tag	UNP P0AEY0
Q	469	THR	-	expression tag	UNP P0AEY0
Q	470	GLY	-	expression tag	UNP P0AEY0
Q	471	SER	-	expression tag	UNP P0AEY0
Q	472	MET	-	expression tag	UNP P0AEY0
Q	473	GLY	-	expression tag	UNP P0AEY0
Q	839	GLU	-	linker	UNP P0AEY0
Q	840	LEU	-	linker	UNP P0AEY0
Q	841	GLU	-	linker	UNP P0AEY0
Q	842	LEU	-	linker	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	843	GLU	-	linker	UNP P0AEY0
Q	844	VAL	-	linker	UNP P0AEY0
Q	845	LEU	-	linker	UNP P0AEY0
Q	846	PHE	-	linker	UNP P0AEY0
Q	847	GLN	-	linker	UNP P0AEY0
Q	848	GLY	-	linker	UNP P0AEY0
Q	849	PRO	-	linker	UNP P0AEY0
R	438	MET	-	initiating methionine	UNP P0AEY0
R	439	SER	-	expression tag	UNP P0AEY0
R	440	ALA	-	expression tag	UNP P0AEY0
R	441	TRP	-	expression tag	UNP P0AEY0
R	442	SER	-	expression tag	UNP P0AEY0
R	443	HIS	-	expression tag	UNP P0AEY0
R	444	PRO	-	expression tag	UNP P0AEY0
R	445	GLN	-	expression tag	UNP P0AEY0
R	446	PHE	-	expression tag	UNP P0AEY0
R	447	GLU	-	expression tag	UNP P0AEY0
R	448	LYS	-	expression tag	UNP P0AEY0
R	449	GLY	-	expression tag	UNP P0AEY0
R	450	GLY	-	expression tag	UNP P0AEY0
R	451	GLY	-	expression tag	UNP P0AEY0
R	452	SER	-	expression tag	UNP P0AEY0
R	453	GLY	-	expression tag	UNP P0AEY0
R	454	GLY	-	expression tag	UNP P0AEY0
R	455	GLY	-	expression tag	UNP P0AEY0
R	456	SER	-	expression tag	UNP P0AEY0
R	457	GLY	-	expression tag	UNP P0AEY0
R	458	GLY	-	expression tag	UNP P0AEY0
R	459	SER	-	expression tag	UNP P0AEY0
R	460	ALA	-	expression tag	UNP P0AEY0
R	461	TRP	-	expression tag	UNP P0AEY0
R	462	SER	-	expression tag	UNP P0AEY0
R	463	HIS	-	expression tag	UNP P0AEY0
R	464	PRO	-	expression tag	UNP P0AEY0
R	465	GLN	-	expression tag	UNP P0AEY0
R	466	PHE	-	expression tag	UNP P0AEY0
R	467	GLU	-	expression tag	UNP P0AEY0
R	468	LYS	-	expression tag	UNP P0AEY0
R	469	THR	-	expression tag	UNP P0AEY0
R	470	GLY	-	expression tag	UNP P0AEY0
R	471	SER	-	expression tag	UNP P0AEY0
R	472	MET	-	expression tag	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
R	473	GLY	-	expression tag	UNP P0AEY0
R	839	GLU	-	linker	UNP P0AEY0
R	840	LEU	-	linker	UNP P0AEY0
R	841	GLU	-	linker	UNP P0AEY0
R	842	LEU	-	linker	UNP P0AEY0
R	843	GLU	-	linker	UNP P0AEY0
R	844	VAL	-	linker	UNP P0AEY0
R	845	LEU	-	linker	UNP P0AEY0
R	846	PHE	-	linker	UNP P0AEY0
R	847	GLN	-	linker	UNP P0AEY0
R	848	GLY	-	linker	UNP P0AEY0
R	849	PRO	-	linker	UNP P0AEY0
S	438	MET	-	initiating methionine	UNP P0AEY0
S	439	SER	-	expression tag	UNP P0AEY0
S	440	ALA	-	expression tag	UNP P0AEY0
S	441	TRP	-	expression tag	UNP P0AEY0
S	442	SER	-	expression tag	UNP P0AEY0
S	443	HIS	-	expression tag	UNP P0AEY0
S	444	PRO	-	expression tag	UNP P0AEY0
S	445	GLN	-	expression tag	UNP P0AEY0
S	446	PHE	-	expression tag	UNP P0AEY0
S	447	GLU	-	expression tag	UNP P0AEY0
S	448	LYS	-	expression tag	UNP P0AEY0
S	449	GLY	-	expression tag	UNP P0AEY0
S	450	GLY	-	expression tag	UNP P0AEY0
S	451	GLY	-	expression tag	UNP P0AEY0
S	452	SER	-	expression tag	UNP P0AEY0
S	453	GLY	-	expression tag	UNP P0AEY0
S	454	GLY	-	expression tag	UNP P0AEY0
S	455	GLY	-	expression tag	UNP P0AEY0
S	456	SER	-	expression tag	UNP P0AEY0
S	457	GLY	-	expression tag	UNP P0AEY0
S	458	GLY	-	expression tag	UNP P0AEY0
S	459	SER	-	expression tag	UNP P0AEY0
S	460	ALA	-	expression tag	UNP P0AEY0
S	461	TRP	-	expression tag	UNP P0AEY0
S	462	SER	-	expression tag	UNP P0AEY0
S	463	HIS	-	expression tag	UNP P0AEY0
S	464	PRO	-	expression tag	UNP P0AEY0
S	465	GLN	-	expression tag	UNP P0AEY0
S	466	PHE	-	expression tag	UNP P0AEY0
S	467	GLU	-	expression tag	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
S	468	LYS	-	expression tag	UNP P0AEY0
S	469	THR	-	expression tag	UNP P0AEY0
S	470	GLY	-	expression tag	UNP P0AEY0
S	471	SER	-	expression tag	UNP P0AEY0
S	472	MET	-	expression tag	UNP P0AEY0
S	473	GLY	-	expression tag	UNP P0AEY0
S	839	GLU	-	linker	UNP P0AEY0
S	840	LEU	-	linker	UNP P0AEY0
S	841	GLU	-	linker	UNP P0AEY0
S	842	LEU	-	linker	UNP P0AEY0
S	843	GLU	-	linker	UNP P0AEY0
S	844	VAL	-	linker	UNP P0AEY0
S	845	LEU	-	linker	UNP P0AEY0
S	846	PHE	-	linker	UNP P0AEY0
S	847	GLN	-	linker	UNP P0AEY0
S	848	GLY	-	linker	UNP P0AEY0
S	849	PRO	-	linker	UNP P0AEY0
T	438	MET	-	initiating methionine	UNP P0AEY0
T	439	SER	-	expression tag	UNP P0AEY0
T	440	ALA	-	expression tag	UNP P0AEY0
T	441	TRP	-	expression tag	UNP P0AEY0
T	442	SER	-	expression tag	UNP P0AEY0
T	443	HIS	-	expression tag	UNP P0AEY0
T	444	PRO	-	expression tag	UNP P0AEY0
T	445	GLN	-	expression tag	UNP P0AEY0
T	446	PHE	-	expression tag	UNP P0AEY0
T	447	GLU	-	expression tag	UNP P0AEY0
T	448	LYS	-	expression tag	UNP P0AEY0
T	449	GLY	-	expression tag	UNP P0AEY0
T	450	GLY	-	expression tag	UNP P0AEY0
T	451	GLY	-	expression tag	UNP P0AEY0
T	452	SER	-	expression tag	UNP P0AEY0
T	453	GLY	-	expression tag	UNP P0AEY0
T	454	GLY	-	expression tag	UNP P0AEY0
T	455	GLY	-	expression tag	UNP P0AEY0
T	456	SER	-	expression tag	UNP P0AEY0
T	457	GLY	-	expression tag	UNP P0AEY0
T	458	GLY	-	expression tag	UNP P0AEY0
T	459	SER	-	expression tag	UNP P0AEY0
T	460	ALA	-	expression tag	UNP P0AEY0
T	461	TRP	-	expression tag	UNP P0AEY0
T	462	SER	-	expression tag	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
T	463	HIS	-	expression tag	UNP P0AEY0
T	464	PRO	-	expression tag	UNP P0AEY0
T	465	GLN	-	expression tag	UNP P0AEY0
T	466	PHE	-	expression tag	UNP P0AEY0
T	467	GLU	-	expression tag	UNP P0AEY0
T	468	LYS	-	expression tag	UNP P0AEY0
T	469	THR	-	expression tag	UNP P0AEY0
T	470	GLY	-	expression tag	UNP P0AEY0
T	471	SER	-	expression tag	UNP P0AEY0
T	472	MET	-	expression tag	UNP P0AEY0
T	473	GLY	-	expression tag	UNP P0AEY0
T	839	GLU	-	linker	UNP P0AEY0
T	840	LEU	-	linker	UNP P0AEY0
T	841	GLU	-	linker	UNP P0AEY0
T	842	LEU	-	linker	UNP P0AEY0
T	843	GLU	-	linker	UNP P0AEY0
T	844	VAL	-	linker	UNP P0AEY0
T	845	LEU	-	linker	UNP P0AEY0
T	846	PHE	-	linker	UNP P0AEY0
T	847	GLN	-	linker	UNP P0AEY0
T	848	GLY	-	linker	UNP P0AEY0
T	849	PRO	-	linker	UNP P0AEY0
U	438	MET	-	initiating methionine	UNP P0AEY0
U	439	SER	-	expression tag	UNP P0AEY0
U	440	ALA	-	expression tag	UNP P0AEY0
U	441	TRP	-	expression tag	UNP P0AEY0
U	442	SER	-	expression tag	UNP P0AEY0
U	443	HIS	-	expression tag	UNP P0AEY0
U	444	PRO	-	expression tag	UNP P0AEY0
U	445	GLN	-	expression tag	UNP P0AEY0
U	446	PHE	-	expression tag	UNP P0AEY0
U	447	GLU	-	expression tag	UNP P0AEY0
U	448	LYS	-	expression tag	UNP P0AEY0
U	449	GLY	-	expression tag	UNP P0AEY0
U	450	GLY	-	expression tag	UNP P0AEY0
U	451	GLY	-	expression tag	UNP P0AEY0
U	452	SER	-	expression tag	UNP P0AEY0
U	453	GLY	-	expression tag	UNP P0AEY0
U	454	GLY	-	expression tag	UNP P0AEY0
U	455	GLY	-	expression tag	UNP P0AEY0
U	456	SER	-	expression tag	UNP P0AEY0
U	457	GLY	-	expression tag	UNP P0AEY0

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Chain	Residue	Modelled	Actual	Comment	Reference
U	458	GLY	-	expression tag	UNP P0AEY0
U	459	SER	-	expression tag	UNP P0AEY0
U	460	ALA	-	expression tag	UNP P0AEY0
U	461	TRP	-	expression tag	UNP P0AEY0
U	462	SER	-	expression tag	UNP P0AEY0
U	463	HIS	-	expression tag	UNP P0AEY0
U	464	PRO	-	expression tag	UNP P0AEY0
U	465	GLN	-	expression tag	UNP P0AEY0
U	466	PHE	-	expression tag	UNP P0AEY0
U	467	GLU	-	expression tag	UNP P0AEY0
U	468	LYS	-	expression tag	UNP P0AEY0
U	469	THR	-	expression tag	UNP P0AEY0
U	470	GLY	-	expression tag	UNP P0AEY0
U	471	SER	-	expression tag	UNP P0AEY0
U	472	MET	-	expression tag	UNP P0AEY0
U	473	GLY	-	expression tag	UNP P0AEY0
U	839	GLU	-	linker	UNP P0AEY0
U	840	LEU	-	linker	UNP P0AEY0
U	841	GLU	-	linker	UNP P0AEY0
U	842	LEU	-	linker	UNP P0AEY0
U	843	GLU	-	linker	UNP P0AEY0
U	844	VAL	-	linker	UNP P0AEY0
U	845	LEU	-	linker	UNP P0AEY0
U	846	PHE	-	linker	UNP P0AEY0
U	847	GLN	-	linker	UNP P0AEY0
U	848	GLY	-	linker	UNP P0AEY0
U	849	PRO	-	linker	UNP P0AEY0

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

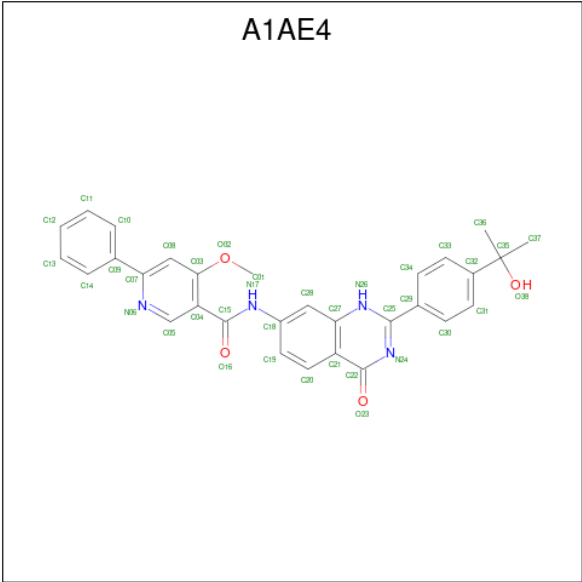
Mol	Chain	Residues	Atoms	AltConf
2	A	1	Total Zn 1 1	0
2	B	1	Total Zn 1 1	0
2	C	1	Total Zn 1 1	0
2	D	1	Total Zn 1 1	0
2	E	1	Total Zn 1 1	0
2	F	1	Total Zn 1 1	0

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Mol	Chain	Residues	Atoms		AltConf
2	G	1	Total 1	Zn 1	0
2	H	1	Total 1	Zn 1	0
2	I	1	Total 1	Zn 1	0
2	K	1	Total 1	Zn 1	0
2	L	1	Total 1	Zn 1	0
2	M	1	Total 1	Zn 1	0
2	N	1	Total 1	Zn 1	0
2	O	1	Total 1	Zn 1	0
2	P	1	Total 1	Zn 1	0
2	Q	1	Total 1	Zn 1	0
2	R	1	Total 1	Zn 1	0
2	S	1	Total 1	Zn 1	0
2	T	1	Total 1	Zn 1	0
2	U	1	Total 1	Zn 1	0

- Molecule 3 is N-{2-[4-(2-hydroxypropan-2-yl)phenyl]-4-oxo-1,4-dihydroquinazolin-7-yl}-4-methoxy-6-phenylpyridine-3-carboxamide (CCD ID: A1AE4) (formula: C₃₀H₂₆N₄O₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	N	O	0
			38	30	4	4	
3	B	1	Total	C	N	O	0
			38	30	4	4	
3	C	1	Total	C	N	O	0
			38	30	4	4	
3	D	1	Total	C	N	O	0
			38	30	4	4	
3	E	1	Total	C	N	O	0
			38	30	4	4	
3	F	1	Total	C	N	O	0
			38	30	4	4	
3	G	1	Total	C	N	O	0
			38	30	4	4	
3	H	1	Total	C	N	O	0
			38	30	4	4	
3	I	1	Total	C	N	O	0
			38	30	4	4	
3	K	1	Total	C	N	O	0
			38	30	4	4	
3	L	1	Total	C	N	O	0
			38	30	4	4	
3	M	1	Total	C	N	O	0
			38	30	4	4	
3	N	1	Total	C	N	O	0
			38	30	4	4	
3	O	1	Total	C	N	O	0
			38	30	4	4	

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Mol	Chain	Residues	Atoms				AltConf
3	P	1	Total 38	C 30	N 4	O 4	0
3	Q	1	Total 38	C 30	N 4	O 4	0
3	R	1	Total 38	C 30	N 4	O 4	0
3	S	1	Total 38	C 30	N 4	O 4	0
3	T	1	Total 38	C 30	N 4	O 4	0
3	U	1	Total 38	C 30	N 4	O 4	0

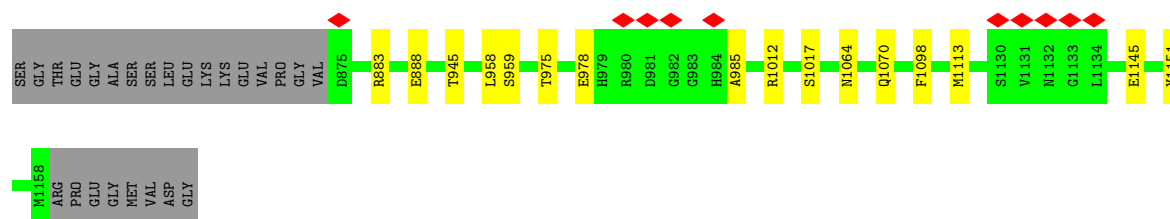
● Molecule 1: Maltose/maltodextrin-binding periplasmic protein, Poly [ADP-ribose] polymerase tankyrase-2

[illegible]

● Molecule 1: Maltose/maltodextrin-binding periplasmic protein, Poly [ADP-ribose] polymerase tankyrase-2

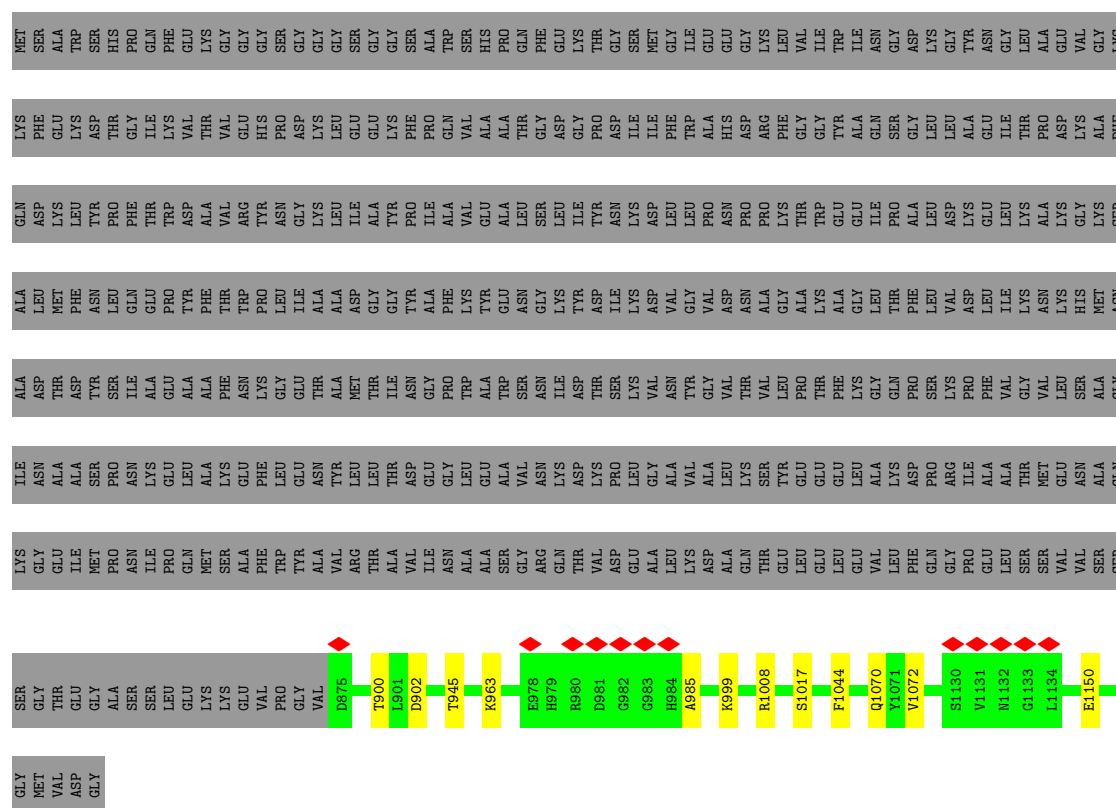


LYS	TLE	ALA	ALA	GLN	LYS	MET
GLY	ASN	ASP	LEU	ASP	PHE	SER
GLU	ALA	THR	MET	LYS	GLU	ALA
ILE	ALA	ASP	PHE	LEU	LYS	TRP
MET	SER	TYP	ASN	TYR	ASP	TRP
PRO	PRO	SER	LEU	PRO	THR	HIS
ASN	ASN	ILE	GLN	PHE	ILE	PRO
ILE	LYS	ALA	GLU	THR	GLY	GLN
PRO	GLU	GLU	PRO	TYR	LYS	PHE
GLN	LEU	ALA	TYR	ASP	VAL	GLU
MET	ALA	PHE	PHE	ALA	THR	LYS
SER	LYS	ASN	THR	VAL	VAL	GLY
ALA	GLU	ASN	TRP	ARG	GLU	GLY
PHE	PHE	LYS	PRO	TYR	HIS	GLY
TRP	LEU	GLY	LEU	ASN	PRO	SER
TYR	GLU	ILE	ILE	GLY	ASP	GLY
ALA	ASN	THR	ALA	LYS	LYS	GLY
VAL	TYR	ALA	ALA	LEU	LEU	GLY
ARG	LEU	MET	ASP	ILE	GLU	SER
ALA	LEU	THR	GLY	ALA	VAL	TRP
ALA	GLU	ALA	TYR	VAL	GLN	HIS
SER	ALA	TRP	GLU	ALA	ALA	PRO
GLY	VAL	SER	ASN	LEU	THR	GLN
ARG	ASN	ASN	GLY	SER	GLY	PHE
GLN	LYS	ILE	LYS	LEU	ASP	GLU
THR	ASP	ASP	TYR	ILE	GLY	LYS
VAL	LYS	THR	ASP	TYR	PRO	THR
ALA	PRO	SER	ILE	ASN	ASP	GLY
ALA	LEU	VAL	LYS	LYS	ILE	SER
ALA	GLY	VAL	ASP	ASP	ILE	MET
LEU	ALA	ASN	VAL	LEU	GLY	GLY
LYS	VAL	ASN	GLY	LEU	THR	ILE
LEU	VAL	GLY	VAL	PRO	PHE	ALA
ASP	ALA	GLY	VAL	ASN	ALA	GLU
ALA	LEU	VAL	ASP	PRO	HIS	GLU
GLN	LYS	THR	ASN	PRO	ARG	LYS
THR	SER	VAL	VAL	PRO	ASP	LYS
GLU	TYR	LEU	GLY	LYS	PHE	LEU
LEU	GLU	PRO	ALA	THR	GLY	VAL
GLU	GLU	THR	LYS	TRP	GLY	VAL
LEU	GLU	PHE	ALA	GLU	TYR	TRP
GLU	LEU	LYS	GLY	GLU	ALA	ILE
VAL	ALA	GLY	LEU	ILE	GLN	ASN
LEU	LYS	GLN	THR	PRO	SER	GLY
PHE	ASP	PRO	PHE	ALA	GLY	ASP
GLY	PRO	SER	LEU	ASP	LEU	LYS
GLY	ARG	LYS	VAL	LEU	LEU	GLY
PRO	ILE	PRO	ASP	LYS	ALA	TYR
LEU	ALA	PHE	LEU	GLU	GLU	ASN
GLU	ALA	VAL	ILE	LEU	ILE	GLY
SER	THR	GLY	LYS	LEU	THR	LEU
SER	MET	VAL	ASN	ALA	PRO	ALA
VAL	GLU	VAL	LYS	LYS	ASP	GLU
VAL	ASN	SER	HIS	GLY	LYS	VAL
SER	ALA	ALA	MET	LYS	ALA	GLY



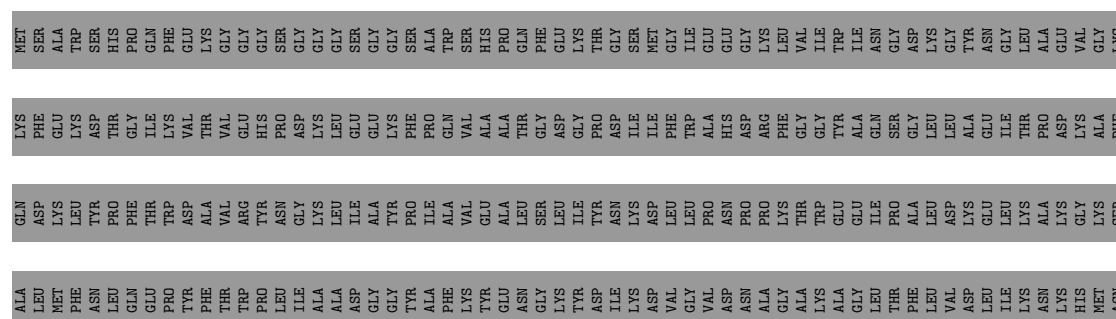
- Molecule 1: Maltose/maltodextrin-binding periplasmic protein, Poly [ADP-ribose] polymerase tankyrase-2

Chain F: 37% 61%

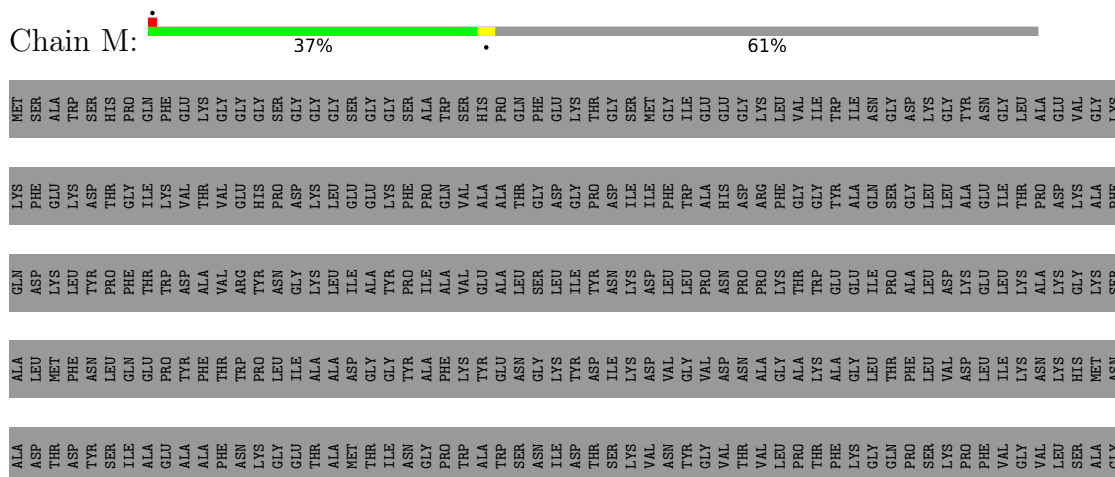


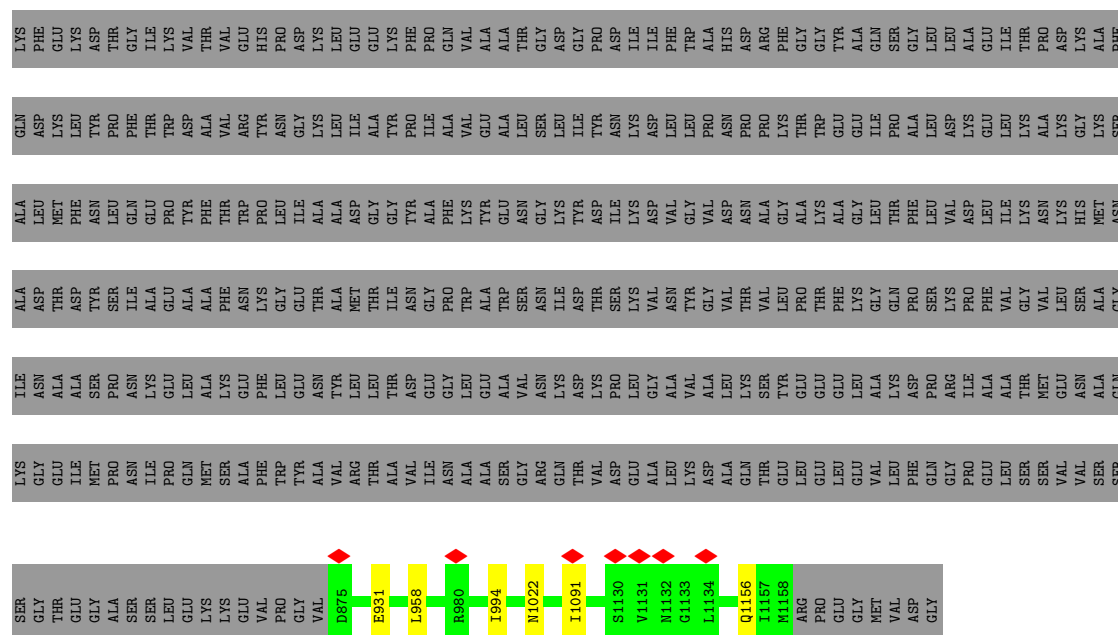
- Molecule 1: Maltose/maltodextrin-binding periplasmic protein, Poly [ADP-ribose] polymerase tankyrase-2

Chain G: 37% 61%



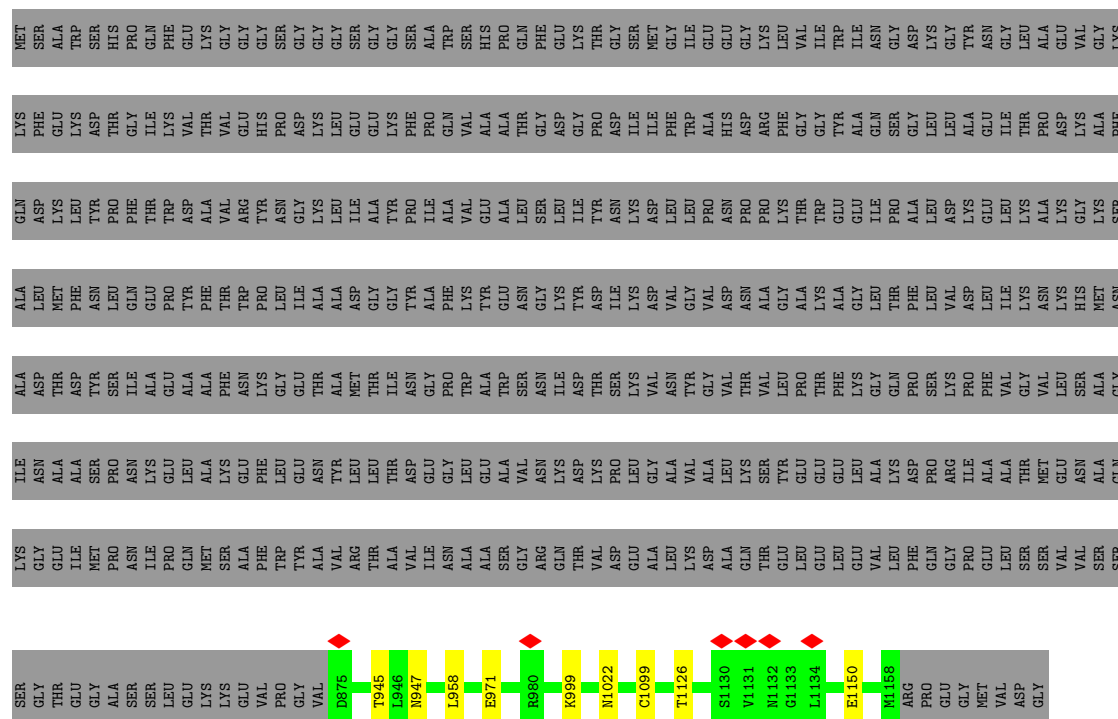






- Molecule 1: Maltose/maltodextrin-binding periplasmic protein, Poly [ADP-ribose] polymerase tankyrase-2

Chain R: 38% 61%



- Molecule 1: Maltose/maltodextrin-binding periplasmic protein, Poly [ADP-ribose] polymerase tankyrase-2

Chain S: 37% 61%

- Molecule 1: Maltose/maltodextrin-binding periplasmic protein, Poly [ADP-ribose] polymerase tankyrase-2

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1310954	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	55.7	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	29000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.933	Depositor
Minimum map value	-1.370	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.037	Depositor
Recommended contour level	0.22	Depositor
Map size ($\text{\AA}$)	422.912, 422.912, 422.912	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.826, 0.826, 0.826	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, A1AE4

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	0.15	0/2293	0.27	0/3087
1	B	0.17	0/2293	0.28	0/3087
1	C	0.19	0/2293	0.30	0/3087
1	D	0.21	0/2293	0.31	0/3087
1	E	0.22	0/2293	0.32	0/3087
1	F	0.22	0/2293	0.32	0/3087
1	G	0.21	0/2293	0.34	0/3087
1	H	0.21	0/2293	0.32	0/3087
1	I	0.19	0/2293	0.30	0/3087
1	K	0.17	0/2293	0.30	0/3087
1	L	0.19	0/2293	0.31	0/3087
1	M	0.21	0/2293	0.31	0/3087
1	N	0.21	0/2293	0.32	0/3087
1	O	0.22	0/2293	0.33	0/3087
1	P	0.22	0/2293	0.32	0/3087
1	Q	0.21	0/2293	0.31	0/3087
1	R	0.19	0/2293	0.29	0/3087
1	S	0.17	0/2293	0.28	0/3087
1	T	0.15	0/2293	0.27	0/3087
1	U	0.14	0/2293	0.26	0/3087
All	All	0.19	0/45860	0.30	0/61740

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2240	0	2165	8	0
1	B	2240	0	2165	6	0
1	C	2240	0	2165	11	0
1	D	2240	0	2165	7	0
1	E	2240	0	2165	8	0
1	F	2240	0	2165	5	0
1	G	2240	0	2165	5	0
1	H	2240	0	2165	6	0
1	I	2240	0	2165	8	0
1	K	2240	0	2165	12	0
1	L	2240	0	2165	7	0
1	M	2240	0	2165	3	0
1	N	2240	0	2165	5	0
1	O	2240	0	2165	4	0
1	P	2240	0	2165	6	0
1	Q	2240	0	2165	3	0
1	R	2240	0	2165	4	0
1	S	2240	0	2165	8	0
1	T	2240	0	2165	7	0
1	U	2240	0	2165	8	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	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
2	O	1	0	0	0	0
2	P	1	0	0	0	0
2	Q	1	0	0	0	0
2	R	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	S	1	0	0	0	0
2	T	1	0	0	0	0
2	U	1	0	0	0	0
3	A	38	0	0	0	0
3	B	38	0	0	0	0
3	C	38	0	0	0	0
3	D	38	0	0	0	0
3	E	38	0	0	0	0
3	F	38	0	0	0	0
3	G	38	0	0	0	0
3	H	38	0	0	0	0
3	I	38	0	0	0	0
3	K	38	0	0	0	0
3	L	38	0	0	0	0
3	M	38	0	0	1	0
3	N	38	0	0	0	0
3	O	38	0	0	0	0
3	P	38	0	0	0	0
3	Q	38	0	0	0	0
3	R	38	0	0	0	0
3	S	38	0	0	0	0
3	T	38	0	0	0	0
3	U	38	0	0	0	0
All	All	45580	0	43300	111	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 1.

All (111) 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:K:999:LYS:NZ	1:L:940:LEU:O	2.04	0.91
1:Q:1091:ILE:O	1:Q:1156:GLN:NE2	2.07	0.86
1:A:900:THR:OG1	1:A:902:ASP:OD1	1.99	0.78
1:C:900:THR:OG1	1:C:902:ASP:OD1	2.03	0.76
1:F:900:THR:OG1	1:F:902:ASP:OD1	2.04	0.75
1:B:900:THR:OG1	1:B:902:ASP:OD1	2.01	0.75
1:B:1109:GLN:NE2	1:B:1111:SER:O	2.27	0.67
1:F:985:ALA:HB3	1:F:1070:GLN:HG2	1.78	0.66
1:G:900:THR:OG1	1:G:902:ASP:OD1	2.04	0.66
1:K:900:THR:OG1	1:K:902:ASP:OD1	2.05	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:900:THR:OG1	1:O:902:ASP:OD1	2.12	0.62
1:K:1081:CYS:SG	1:K:1084:HIS:HB2	2.39	0.62
1:I:1106:SER:HG	1:I:1124:SER:HG	1.46	0.60
1:N:1108:LEU:HD22	1:N:1126:THR:HG23	1.82	0.59
1:A:1100:ARG:NH2	1:T:1022:ASN:O	2.34	0.59
1:N:900:THR:OG1	1:N:902:ASP:OD1	2.18	0.59
1:B:1100:ARG:NH2	1:S:1022:ASN:O	2.36	0.58
1:K:1081:CYS:SG	1:K:1084:HIS:CD2	2.97	0.57
1:F:999:LYS:NZ	1:F:1150:GLU:OE2	2.39	0.55
1:C:999:LYS:NZ	1:D:940:LEU:O	2.36	0.55
1:G:896:ARG:NH2	1:K:892:ASP:OD1	2.39	0.55
1:H:900:THR:OG1	1:H:902:ASP:OD1	2.09	0.53
1:D:900:THR:OG1	1:D:902:ASP:OD1	2.26	0.53
1:T:975:THR:O	1:T:1064:ASN:ND2	2.38	0.53
1:E:985:ALA:HB3	1:E:1070:GLN:HG2	1.90	0.53
1:M:1138:GLU:OE2	3:M:1202:A1AE4:N17	2.43	0.52
1:U:1143:ARG:NH1	1:U:1145:GLU:OE2	2.42	0.52
1:P:1108:LEU:HD22	1:P:1126:THR:HG23	1.91	0.51
1:U:1069:ASN:HA	1:U:1072:VAL:HG23	1.94	0.50
1:A:958:LEU:HD22	1:B:945:THR:HG23	1.93	0.50
1:K:1081:CYS:SG	1:K:1084:HIS:HD2	2.34	0.50
1:N:999:LYS:NZ	1:N:1150:GLU:OE2	2.45	0.50
1:A:972:MET:HE2	1:A:1153:ILE:HG21	1.95	0.49
1:A:945:THR:HG22	1:U:964:GLU:OE1	2.13	0.49
1:C:1014:LYS:NZ	1:C:1014:LYS:HB3	2.28	0.49
1:P:999:LYS:NZ	1:P:1150:GLU:OE2	2.45	0.49
1:S:1026:GLU:OE2	1:S:1100:ARG:NH1	2.45	0.48
1:S:977:ARG:NH1	1:S:978:GLU:O	2.47	0.48
1:H:985:ALA:HB3	1:H:1070:GLN:HG2	1.96	0.47
1:U:1021:HIS:ND1	1:U:1021:HIS:O	2.48	0.47
1:T:1026:GLU:OE1	1:T:1100:ARG:NH1	2.47	0.47
1:I:900:THR:OG1	1:I:902:ASP:OD1	2.31	0.47
1:F:1008:ARG:NH2	1:F:1044:PHE:O	2.46	0.47
1:S:900:THR:OG1	1:S:902:ASP:OD1	2.26	0.47
1:U:1039:ILE:O	1:U:1043:GLY:N	2.41	0.47
1:I:1088:SER:O	1:I:1088:SER:OG	2.33	0.46
1:T:1078:GLY:O	1:T:1087:ARG:NH1	2.48	0.46
1:C:1081:CYS:SG	1:C:1084:HIS:HB2	2.55	0.46
1:N:1108:LEU:HD22	1:N:1126:THR:CG2	2.46	0.46
1:H:971:GLU:HG2	1:H:1098:PHE:CZ	2.51	0.45
1:U:900:THR:OG1	1:U:902:ASP:OD1	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:985:ALA:HB3	1:G:1070:GLN:HG2	1.98	0.45
1:U:891:MET:HE3	1:U:894:PHE:HB2	1.98	0.45
1:L:972:MET:SD	1:L:1153:ILE:HG21	2.57	0.45
1:U:1102:THR:O	1:U:1146:GLN:NE2	2.48	0.45
1:P:900:THR:OG1	1:P:902:ASP:OD1	2.10	0.44
1:P:975:THR:HB	1:P:1064:ASN:HA	1.99	0.44
1:G:878:ILE:HD11	1:G:904:LEU:HD22	1.99	0.44
1:H:953:THR:OG1	1:H:1002:ASN:ND2	2.49	0.44
1:S:958:LEU:CD2	1:T:945:THR:HG23	2.48	0.44
1:K:1021:HIS:O	1:K:1021:HIS:ND1	2.50	0.44
1:C:1100:ARG:NH2	1:R:1022:ASN:O	2.46	0.43
1:L:1098:PHE:HB3	1:L:1151:TYR:HB2	2.00	0.43
1:B:958:LEU:HD22	1:C:945:THR:HG23	1.99	0.43
1:R:999:LYS:NZ	1:R:1150:GLU:OE2	2.50	0.43
1:E:975:THR:HB	1:E:1064:ASN:HA	2.01	0.43
1:L:1000:VAL:HG21	1:L:1040:ILE:HD12	2.01	0.43
1:P:988:ILE:O	1:P:1090:TYR:OH	2.23	0.43
1:O:1098:PHE:HB3	1:O:1151:TYR:HB2	2.01	0.43
1:I:1022:ASN:OD1	1:M:941:ASN:ND2	2.48	0.42
1:K:1091:ILE:O	1:K:1156:GLN:NE2	2.52	0.42
1:B:1098:PHE:HB3	1:B:1151:TYR:HB2	2.02	0.42
1:P:977:ARG:NH1	1:P:978:GLU:O	2.53	0.42
1:D:975:THR:HB	1:D:1064:ASN:HA	2.01	0.42
1:E:958:LEU:CD2	1:F:945:THR:HG23	2.49	0.42
1:E:1113:MET:HE3	1:E:1113:MET:HB2	1.95	0.42
1:L:975:THR:HB	1:L:1064:ASN:HA	2.01	0.42
1:A:953:THR:OG1	1:A:1002:ASN:ND2	2.43	0.42
1:I:971:GLU:HG2	1:I:1098:PHE:CZ	2.54	0.42
1:G:1125:VAL:HG22	1:G:1140:VAL:HG12	2.01	0.42
1:R:958:LEU:CD2	1:S:945:THR:HG23	2.50	0.42
1:T:988:ILE:O	1:T:988:ILE:HG13	2.20	0.42
1:C:1098:PHE:HB3	1:C:1151:TYR:HB2	2.02	0.42
1:L:900:THR:OG1	1:L:902:ASP:OD1	2.29	0.42
1:Q:958:LEU:CD2	1:R:945:THR:HG23	2.50	0.41
1:C:958:LEU:HD22	1:D:945:THR:HG23	2.02	0.41
1:H:958:LEU:HD22	1:I:945:THR:HG23	2.02	0.41
1:S:1098:PHE:HB3	1:S:1151:TYR:HB2	2.02	0.41
1:N:958:LEU:HD22	1:O:945:THR:HG23	2.02	0.41
1:A:1069:ASN:HA	1:A:1072:VAL:HG23	2.03	0.41
1:L:1125:VAL:HB	1:L:1140:VAL:HG13	2.02	0.41
1:E:1098:PHE:HB3	1:E:1151:TYR:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:941:ASN:HB3	1:C:944:LEU:HD12	2.02	0.41
1:H:1098:PHE:HB3	1:H:1151:TYR:HB2	2.03	0.41
1:K:965:PHE:C	1:K:965:PHE:CD1	2.99	0.41
1:O:888:GLU:CD	1:O:888:GLU:H	2.29	0.41
1:E:1012:ARG:HG2	1:E:1145:GLU:HG2	2.03	0.40
1:A:1021:HIS:O	1:A:1021:HIS:ND1	2.53	0.40
1:D:958:LEU:HD22	1:E:945:THR:HG23	2.03	0.40
1:D:1100:ARG:NH2	1:Q:1022:ASN:O	2.48	0.40
1:K:953:THR:OG1	1:K:1002:ASN:ND2	2.43	0.40
1:E:883:ARG:HA	1:E:888:GLU:HG3	2.04	0.40
1:I:1106:SER:OG	1:I:1124:SER:OG	2.18	0.40
1:S:958:LEU:HD22	1:T:945:THR:HG23	2.03	0.40
1:C:1037:ASN:HA	1:C:1040:ILE:HG12	2.04	0.40
1:C:971:GLU:HG2	1:C:1098:PHE:CZ	2.56	0.40
1:D:888:GLU:H	1:D:888:GLU:CD	2.30	0.40
1:I:1098:PHE:HB3	1:I:1151:TYR:HB2	2.04	0.40
1:K:1098:PHE:HB3	1:K:1151:TYR:HB2	2.03	0.40
1:K:1106:SER:OG	1:K:1124:SER:OG	2.29	0.40
1:M:1098:PHE:HB3	1:M:1151:TYR:HB2	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	282/729 (39%)	279 (99%)	3 (1%)	0	100	100
1	B	282/729 (39%)	278 (99%)	4 (1%)	0	100	100
1	C	282/729 (39%)	278 (99%)	4 (1%)	0	100	100
1	D	282/729 (39%)	278 (99%)	4 (1%)	0	100	100
1	E	282/729 (39%)	279 (99%)	3 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	282/729 (39%)	278 (99%)	4 (1%)	0	100	100
1	G	282/729 (39%)	276 (98%)	6 (2%)	0	100	100
1	H	282/729 (39%)	279 (99%)	3 (1%)	0	100	100
1	I	282/729 (39%)	277 (98%)	5 (2%)	0	100	100
1	K	282/729 (39%)	278 (99%)	4 (1%)	0	100	100
1	L	282/729 (39%)	277 (98%)	5 (2%)	0	100	100
1	M	282/729 (39%)	280 (99%)	2 (1%)	0	100	100
1	N	282/729 (39%)	279 (99%)	3 (1%)	0	100	100
1	O	282/729 (39%)	276 (98%)	6 (2%)	0	100	100
1	P	282/729 (39%)	280 (99%)	2 (1%)	0	100	100
1	Q	282/729 (39%)	278 (99%)	4 (1%)	0	100	100
1	R	282/729 (39%)	279 (99%)	3 (1%)	0	100	100
1	S	282/729 (39%)	280 (99%)	2 (1%)	0	100	100
1	T	282/729 (39%)	281 (100%)	1 (0%)	0	100	100
1	U	282/729 (39%)	279 (99%)	3 (1%)	0	100	100
All	All	5640/14580 (39%)	5569 (99%)	71 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	230/596 (39%)	228 (99%)	2 (1%)	70	82
1	B	230/596 (39%)	227 (99%)	3 (1%)	61	76
1	C	230/596 (39%)	227 (99%)	3 (1%)	61	76
1	D	230/596 (39%)	226 (98%)	4 (2%)	53	70
1	E	230/596 (39%)	227 (99%)	3 (1%)	61	76
1	F	230/596 (39%)	227 (99%)	3 (1%)	61	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	230/596 (39%)	223 (97%)	7 (3%)	36	51
1	H	230/596 (39%)	228 (99%)	2 (1%)	70	82
1	I	230/596 (39%)	225 (98%)	5 (2%)	45	62
1	K	230/596 (39%)	223 (97%)	7 (3%)	36	51
1	L	230/596 (39%)	227 (99%)	3 (1%)	61	76
1	M	230/596 (39%)	223 (97%)	7 (3%)	36	51
1	N	230/596 (39%)	226 (98%)	4 (2%)	53	70
1	O	230/596 (39%)	227 (99%)	3 (1%)	61	76
1	P	230/596 (39%)	227 (99%)	3 (1%)	61	76
1	Q	230/596 (39%)	228 (99%)	2 (1%)	70	82
1	R	230/596 (39%)	226 (98%)	4 (2%)	53	70
1	S	230/596 (39%)	228 (99%)	2 (1%)	70	82
1	T	230/596 (39%)	229 (100%)	1 (0%)	84	91
1	U	230/596 (39%)	228 (99%)	2 (1%)	70	82
All	All	4600/11920 (39%)	4530 (98%)	70 (2%)	55	72

All (70) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	928	LYS
1	A	975	THR
1	B	949	SER
1	B	963	LYS
1	B	1007	GLU
1	C	1036	VAL
1	C	1084	HIS
1	C	1126	THR
1	D	875	ASP
1	D	1036	VAL
1	D	1105	LYS
1	D	1106	SER
1	E	959	SER
1	E	978	GLU
1	E	1017	SER
1	F	963	LYS
1	F	1017	SER
1	F	1072	VAL

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Mol	Chain	Res	Type
1	G	877	SER
1	G	1004	LYS
1	G	1065	SER
1	G	1102	THR
1	G	1106	SER
1	G	1125	VAL
1	G	1126	THR
1	H	947	ASN
1	H	1065	SER
1	I	928	LYS
1	I	963	LYS
1	I	1036	VAL
1	I	1065	SER
1	I	1106	SER
1	K	877	SER
1	K	928	LYS
1	K	949	SER
1	K	995	LEU
1	K	1111	SER
1	K	1126	THR
1	K	1146	GLN
1	L	1017	SER
1	L	1029	LEU
1	L	1108	LEU
1	M	977	ARG
1	M	995	LEU
1	M	1017	SER
1	M	1040	ILE
1	M	1106	SER
1	M	1108	LEU
1	M	1157	ILE
1	N	877	SER
1	N	991	ARG
1	N	1010	THR
1	N	1126	THR
1	O	959	SER
1	O	1072	VAL
1	O	1108	LEU
1	P	991	ARG
1	P	1106	SER
1	P	1126	THR
1	Q	931	GLU

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Mol	Chain	Res	Type
1	Q	994	ILE
1	R	947	ASN
1	R	971	GLU
1	R	1099	CYS
1	R	1126	THR
1	S	1099	CYS
1	S	1126	THR
1	T	949	SER
1	U	949	SER
1	U	954	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (94) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1002	ASN
1	A	1070	GLN
1	B	880	GLN
1	B	993	ASN
1	B	1002	ASN
1	C	918	ASN
1	C	922	HIS
1	C	993	ASN
1	C	1070	GLN
1	D	880	GLN
1	D	984	HIS
1	D	1011	HIS
1	D	1041	HIS
1	E	880	GLN
1	E	918	ASN
1	E	922	HIS
1	E	966	GLN
1	E	1011	HIS
1	E	1037	ASN
1	F	898	GLN
1	F	924	HIS
1	F	941	ASN
1	F	984	HIS
1	F	1011	HIS
1	F	1022	ASN
1	G	922	HIS
1	G	924	HIS
1	G	1002	ASN

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Mol	Chain	Res	Type
1	G	1022	ASN
1	G	1109	GLN
1	G	1122	HIS
1	H	880	GLN
1	H	922	HIS
1	H	924	HIS
1	H	947	ASN
1	H	990	ASN
1	H	1002	ASN
1	H	1011	HIS
1	H	1022	ASN
1	H	1122	HIS
1	I	880	GLN
1	I	1011	HIS
1	K	922	HIS
1	K	937	GLN
1	K	1002	ASN
1	K	1037	ASN
1	K	1070	GLN
1	K	1084	HIS
1	K	1117	HIS
1	L	880	GLN
1	L	924	HIS
1	L	993	ASN
1	L	1109	GLN
1	M	880	GLN
1	M	1011	HIS
1	M	1070	GLN
1	N	880	GLN
1	N	922	HIS
1	N	937	GLN
1	N	941	ASN
1	N	1070	GLN
1	O	880	GLN
1	O	937	GLN
1	O	1095	GLN
1	P	880	GLN
1	P	937	GLN
1	P	947	ASN
1	P	966	GLN
1	P	1022	ASN
1	P	1122	HIS

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Mol	Chain	Res	Type
1	Q	924	HIS
1	Q	937	GLN
1	Q	1002	ASN
1	Q	1011	HIS
1	R	880	GLN
1	R	924	HIS
1	R	941	ASN
1	S	880	GLN
1	S	1002	ASN
1	S	1011	HIS
1	S	1022	ASN
1	S	1095	GLN
1	S	1122	HIS
1	T	922	HIS
1	T	924	HIS
1	T	937	GLN
1	T	1011	HIS
1	T	1095	GLN
1	U	922	HIS
1	U	990	ASN
1	U	993	ASN
1	U	1002	ASN
1	U	1070	GLN
1	U	1117	HIS

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 40 ligands modelled in this entry, 20 are monoatomic - leaving 20 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	A1AE4	U	1202	-	42,42,42	2.26	14 (33%)	58,61,61	1.26	7 (12%)
3	A1AE4	B	1202	-	42,42,42	2.24	14 (33%)	58,61,61	1.30	7 (12%)
3	A1AE4	A	1202	-	42,42,42	2.26	14 (33%)	58,61,61	1.26	6 (10%)
3	A1AE4	L	1202	-	42,42,42	2.25	14 (33%)	58,61,61	1.25	7 (12%)
3	A1AE4	M	1202	-	42,42,42	2.24	14 (33%)	58,61,61	1.24	7 (12%)
3	A1AE4	K	1202	-	42,42,42	2.27	14 (33%)	58,61,61	1.23	7 (12%)
3	A1AE4	T	1202	-	42,42,42	2.26	13 (30%)	58,61,61	1.25	7 (12%)
3	A1AE4	N	1202	-	42,42,42	2.22	15 (35%)	58,61,61	1.27	8 (13%)
3	A1AE4	C	1202	-	42,42,42	2.24	14 (33%)	58,61,61	1.30	7 (12%)
3	A1AE4	I	1202	-	42,42,42	2.24	15 (35%)	58,61,61	1.26	7 (12%)
3	A1AE4	D	1202	-	42,42,42	2.26	15 (35%)	58,61,61	1.24	7 (12%)
3	A1AE4	R	1202	-	42,42,42	2.23	15 (35%)	58,61,61	1.28	7 (12%)
3	A1AE4	S	1202	-	42,42,42	2.24	14 (33%)	58,61,61	1.24	7 (12%)
3	A1AE4	E	1202	-	42,42,42	2.22	15 (35%)	58,61,61	1.30	7 (12%)
3	A1AE4	H	1202	-	42,42,42	2.23	15 (35%)	58,61,61	1.31	8 (13%)
3	A1AE4	G	1202	-	42,42,42	2.22	15 (35%)	58,61,61	1.37	9 (15%)
3	A1AE4	Q	1202	-	42,42,42	2.22	15 (35%)	58,61,61	1.34	8 (13%)
3	A1AE4	P	1202	-	42,42,42	2.20	15 (35%)	58,61,61	1.29	7 (12%)
3	A1AE4	O	1202	-	42,42,42	2.20	15 (35%)	58,61,61	1.29	8 (13%)
3	A1AE4	F	1202	-	42,42,42	2.22	15 (35%)	58,61,61	1.37	8 (13%)

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	A1AE4	U	1202	-	-	8/24/24/24	0/5/5/5
3	A1AE4	B	1202	-	-	9/24/24/24	0/5/5/5
3	A1AE4	A	1202	-	-	8/24/24/24	0/5/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	A1AE4	L	1202	-	-	5/24/24/24	0/5/5/5
3	A1AE4	M	1202	-	-	5/24/24/24	0/5/5/5
3	A1AE4	K	1202	-	-	6/24/24/24	0/5/5/5
3	A1AE4	T	1202	-	-	7/24/24/24	0/5/5/5
3	A1AE4	N	1202	-	-	4/24/24/24	0/5/5/5
3	A1AE4	C	1202	-	-	8/24/24/24	0/5/5/5
3	A1AE4	I	1202	-	-	4/24/24/24	0/5/5/5
3	A1AE4	D	1202	-	-	5/24/24/24	0/5/5/5
3	A1AE4	R	1202	-	-	5/24/24/24	0/5/5/5
3	A1AE4	S	1202	-	-	5/24/24/24	0/5/5/5
3	A1AE4	E	1202	-	-	6/24/24/24	0/5/5/5
3	A1AE4	H	1202	-	-	6/24/24/24	0/5/5/5
3	A1AE4	G	1202	-	-	6/24/24/24	0/5/5/5
3	A1AE4	Q	1202	-	-	6/24/24/24	0/5/5/5
3	A1AE4	P	1202	-	-	4/24/24/24	0/5/5/5
3	A1AE4	O	1202	-	-	5/24/24/24	0/5/5/5
3	A1AE4	F	1202	-	-	5/24/24/24	0/5/5/5

All (290) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	U	1202	A1AE4	O23-C22	9.96	1.40	1.23
3	K	1202	A1AE4	O23-C22	9.94	1.40	1.23
3	T	1202	A1AE4	O23-C22	9.93	1.40	1.23
3	A	1202	A1AE4	O23-C22	9.93	1.40	1.23
3	C	1202	A1AE4	O23-C22	9.75	1.39	1.23
3	S	1202	A1AE4	O23-C22	9.72	1.39	1.23
3	B	1202	A1AE4	O23-C22	9.71	1.39	1.23
3	R	1202	A1AE4	O23-C22	9.70	1.39	1.23
3	L	1202	A1AE4	O23-C22	9.69	1.39	1.23
3	M	1202	A1AE4	O23-C22	9.67	1.39	1.23
3	Q	1202	A1AE4	O23-C22	9.65	1.39	1.23
3	D	1202	A1AE4	O23-C22	9.64	1.39	1.23
3	I	1202	A1AE4	O23-C22	9.61	1.39	1.23
3	H	1202	A1AE4	O23-C22	9.61	1.39	1.23
3	F	1202	A1AE4	O23-C22	9.60	1.39	1.23
3	N	1202	A1AE4	O23-C22	9.60	1.39	1.23
3	G	1202	A1AE4	O23-C22	9.56	1.39	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	1202	A1AE4	O23-C22	9.52	1.39	1.23
3	P	1202	A1AE4	O23-C22	9.50	1.39	1.23
3	O	1202	A1AE4	O23-C22	9.47	1.39	1.23
3	U	1202	A1AE4	C15-N17	3.84	1.46	1.35
3	H	1202	A1AE4	C15-N17	3.81	1.46	1.35
3	B	1202	A1AE4	C15-N17	3.78	1.46	1.35
3	I	1202	A1AE4	C15-N17	3.77	1.46	1.35
3	A	1202	A1AE4	C15-N17	3.77	1.46	1.35
3	K	1202	A1AE4	C15-N17	3.73	1.46	1.35
3	D	1202	A1AE4	C15-N17	3.72	1.46	1.35
3	L	1202	A1AE4	C15-N17	3.72	1.46	1.35
3	G	1202	A1AE4	C15-N17	3.71	1.46	1.35
3	S	1202	A1AE4	C15-N17	3.71	1.46	1.35
3	T	1202	A1AE4	C15-N17	3.67	1.46	1.35
3	P	1202	A1AE4	C15-N17	3.67	1.46	1.35
3	M	1202	A1AE4	C15-N17	3.66	1.46	1.35
3	E	1202	A1AE4	C15-N17	3.66	1.46	1.35
3	C	1202	A1AE4	C15-N17	3.65	1.46	1.35
3	R	1202	A1AE4	C15-N17	3.65	1.46	1.35
3	Q	1202	A1AE4	C15-N17	3.64	1.46	1.35
3	N	1202	A1AE4	C15-N17	3.62	1.46	1.35
3	F	1202	A1AE4	C15-N17	3.61	1.46	1.35
3	O	1202	A1AE4	C15-N17	3.59	1.46	1.35
3	T	1202	A1AE4	C29-C25	3.44	1.53	1.47
3	K	1202	A1AE4	C29-C25	3.36	1.53	1.47
3	L	1202	A1AE4	C29-C25	3.33	1.53	1.47
3	A	1202	A1AE4	C29-C25	3.32	1.53	1.47
3	S	1202	A1AE4	C29-C25	3.32	1.53	1.47
3	U	1202	A1AE4	C29-C25	3.31	1.53	1.47
3	I	1202	A1AE4	C29-C25	3.29	1.53	1.47
3	H	1202	A1AE4	C29-C25	3.28	1.53	1.47
3	B	1202	A1AE4	C29-C25	3.28	1.53	1.47
3	E	1202	A1AE4	C29-C25	3.25	1.53	1.47
3	D	1202	A1AE4	C09-C07	3.22	1.53	1.49
3	C	1202	A1AE4	C29-C25	3.21	1.53	1.47
3	G	1202	A1AE4	C22-N24	-3.19	1.32	1.38
3	D	1202	A1AE4	C29-C25	3.18	1.53	1.47
3	O	1202	A1AE4	C22-N24	-3.15	1.32	1.38
3	H	1202	A1AE4	C09-C07	3.13	1.53	1.49
3	Q	1202	A1AE4	C29-C25	3.13	1.53	1.47
3	U	1202	A1AE4	C09-C07	3.12	1.53	1.49
3	F	1202	A1AE4	O38-C35	-3.12	1.40	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1202	A1AE4	C09-C07	3.11	1.53	1.49
3	I	1202	A1AE4	O38-C35	-3.11	1.40	1.44
3	F	1202	A1AE4	C29-C25	3.10	1.53	1.47
3	N	1202	A1AE4	C29-C25	3.10	1.53	1.47
3	E	1202	A1AE4	O38-C35	-3.10	1.40	1.44
3	P	1202	A1AE4	C09-C07	3.09	1.53	1.49
3	R	1202	A1AE4	C09-C07	3.09	1.53	1.49
3	R	1202	A1AE4	C29-C25	3.09	1.53	1.47
3	E	1202	A1AE4	C09-C07	3.08	1.53	1.49
3	T	1202	A1AE4	C09-C07	3.08	1.53	1.49
3	M	1202	A1AE4	C29-C25	3.08	1.53	1.47
3	I	1202	A1AE4	C09-C07	3.08	1.53	1.49
3	M	1202	A1AE4	O38-C35	-3.07	1.40	1.44
3	K	1202	A1AE4	C09-C07	3.07	1.53	1.49
3	L	1202	A1AE4	C09-C07	3.07	1.53	1.49
3	O	1202	A1AE4	C09-C07	3.07	1.53	1.49
3	E	1202	A1AE4	C22-N24	-3.07	1.32	1.38
3	G	1202	A1AE4	C29-C25	3.07	1.53	1.47
3	N	1202	A1AE4	O38-C35	-3.07	1.40	1.44
3	D	1202	A1AE4	O38-C35	-3.07	1.40	1.44
3	G	1202	A1AE4	C09-C07	3.07	1.53	1.49
3	Q	1202	A1AE4	C09-C07	3.07	1.53	1.49
3	B	1202	A1AE4	C09-C07	3.06	1.53	1.49
3	M	1202	A1AE4	C09-C07	3.06	1.53	1.49
3	L	1202	A1AE4	O38-C35	-3.03	1.40	1.44
3	G	1202	A1AE4	O38-C35	-3.03	1.40	1.44
3	K	1202	A1AE4	O38-C35	-3.02	1.40	1.44
3	O	1202	A1AE4	C29-C25	3.02	1.53	1.47
3	P	1202	A1AE4	O38-C35	-3.02	1.40	1.44
3	F	1202	A1AE4	C22-N24	-3.02	1.32	1.38
3	S	1202	A1AE4	O38-C35	-3.02	1.40	1.44
3	C	1202	A1AE4	O38-C35	-3.01	1.40	1.44
3	N	1202	A1AE4	C09-C07	3.01	1.53	1.49
3	Q	1202	A1AE4	C22-N24	-3.01	1.32	1.38
3	T	1202	A1AE4	O38-C35	-3.01	1.40	1.44
3	O	1202	A1AE4	O38-C35	-3.00	1.40	1.44
3	D	1202	A1AE4	C22-N24	-3.00	1.32	1.38
3	P	1202	A1AE4	C29-C25	3.00	1.52	1.47
3	H	1202	A1AE4	O38-C35	-3.00	1.40	1.44
3	R	1202	A1AE4	C22-N24	-3.00	1.32	1.38
3	R	1202	A1AE4	O38-C35	-2.99	1.40	1.44
3	L	1202	A1AE4	C22-N24	-2.98	1.32	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1202	A1AE4	C09-C07	2.98	1.53	1.49
3	Q	1202	A1AE4	O38-C35	-2.97	1.40	1.44
3	E	1202	A1AE4	C21-C22	-2.96	1.43	1.48
3	P	1202	A1AE4	C22-N24	-2.95	1.32	1.38
3	S	1202	A1AE4	C09-C07	2.94	1.53	1.49
3	F	1202	A1AE4	C09-C07	2.94	1.53	1.49
3	N	1202	A1AE4	C22-N24	-2.93	1.32	1.38
3	B	1202	A1AE4	O38-C35	-2.92	1.40	1.44
3	L	1202	A1AE4	C21-C27	-2.92	1.36	1.41
3	H	1202	A1AE4	C22-N24	-2.92	1.32	1.38
3	B	1202	A1AE4	C22-N24	-2.91	1.32	1.38
3	C	1202	A1AE4	C22-N24	-2.91	1.32	1.38
3	A	1202	A1AE4	O38-C35	-2.91	1.40	1.44
3	U	1202	A1AE4	O38-C35	-2.90	1.40	1.44
3	M	1202	A1AE4	C22-N24	-2.90	1.32	1.38
3	S	1202	A1AE4	C21-C27	-2.89	1.36	1.41
3	C	1202	A1AE4	C21-C27	-2.87	1.36	1.41
3	D	1202	A1AE4	C21-C27	-2.87	1.36	1.41
3	B	1202	A1AE4	C21-C27	-2.86	1.36	1.41
3	S	1202	A1AE4	C22-N24	-2.86	1.33	1.38
3	T	1202	A1AE4	C21-C27	-2.85	1.36	1.41
3	E	1202	A1AE4	C21-C27	-2.84	1.36	1.41
3	M	1202	A1AE4	C21-C27	-2.84	1.36	1.41
3	I	1202	A1AE4	C22-N24	-2.82	1.33	1.38
3	U	1202	A1AE4	C28-C27	2.81	1.44	1.39
3	P	1202	A1AE4	C21-C22	-2.81	1.43	1.48
3	G	1202	A1AE4	C21-C22	-2.81	1.43	1.48
3	L	1202	A1AE4	C21-C22	-2.81	1.43	1.48
3	D	1202	A1AE4	C21-C22	-2.79	1.43	1.48
3	I	1202	A1AE4	C21-C27	-2.79	1.36	1.41
3	K	1202	A1AE4	C21-C27	-2.79	1.36	1.41
3	I	1202	A1AE4	C21-C22	-2.79	1.43	1.48
3	A	1202	A1AE4	C22-N24	-2.78	1.33	1.38
3	S	1202	A1AE4	C21-C22	-2.78	1.43	1.48
3	U	1202	A1AE4	C21-C27	-2.78	1.36	1.41
3	A	1202	A1AE4	C21-C27	-2.78	1.36	1.41
3	F	1202	A1AE4	C21-C27	-2.76	1.36	1.41
3	C	1202	A1AE4	C21-C22	-2.76	1.43	1.48
3	P	1202	A1AE4	C25-N26	-2.76	1.32	1.36
3	P	1202	A1AE4	C21-C27	-2.76	1.36	1.41
3	Q	1202	A1AE4	C21-C22	-2.75	1.43	1.48
3	T	1202	A1AE4	C22-N24	-2.75	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	U	1202	A1AE4	C22-N24	-2.75	1.33	1.38
3	H	1202	A1AE4	C21-C27	-2.75	1.36	1.41
3	H	1202	A1AE4	C21-C22	-2.74	1.43	1.48
3	K	1202	A1AE4	C22-N24	-2.74	1.33	1.38
3	N	1202	A1AE4	C21-C22	-2.73	1.43	1.48
3	K	1202	A1AE4	C28-C27	2.73	1.43	1.39
3	Q	1202	A1AE4	C21-C27	-2.72	1.36	1.41
3	O	1202	A1AE4	C21-C22	-2.72	1.43	1.48
3	B	1202	A1AE4	C21-C22	-2.71	1.43	1.48
3	M	1202	A1AE4	C21-C22	-2.71	1.43	1.48
3	A	1202	A1AE4	C28-C27	2.71	1.43	1.39
3	U	1202	A1AE4	C18-N17	2.70	1.47	1.41
3	H	1202	A1AE4	C18-N17	2.70	1.47	1.41
3	K	1202	A1AE4	C21-C22	-2.69	1.43	1.48
3	F	1202	A1AE4	C25-N26	-2.69	1.32	1.36
3	R	1202	A1AE4	C21-C27	-2.69	1.36	1.41
3	B	1202	A1AE4	C18-N17	2.69	1.47	1.41
3	N	1202	A1AE4	C25-N26	-2.69	1.32	1.36
3	N	1202	A1AE4	C21-C27	-2.68	1.36	1.41
3	F	1202	A1AE4	C21-C22	-2.68	1.43	1.48
3	R	1202	A1AE4	C21-C22	-2.68	1.43	1.48
3	T	1202	A1AE4	C21-C22	-2.68	1.43	1.48
3	O	1202	A1AE4	C25-N26	-2.66	1.32	1.36
3	T	1202	A1AE4	C28-C27	2.66	1.43	1.39
3	I	1202	A1AE4	C18-N17	2.65	1.47	1.41
3	O	1202	A1AE4	C21-C27	-2.63	1.37	1.41
3	D	1202	A1AE4	C25-N26	-2.63	1.32	1.36
3	G	1202	A1AE4	C25-N26	-2.63	1.32	1.36
3	A	1202	A1AE4	C18-N17	2.62	1.47	1.41
3	E	1202	A1AE4	C25-N26	-2.62	1.32	1.36
3	S	1202	A1AE4	C18-N17	2.62	1.46	1.41
3	Q	1202	A1AE4	C25-N26	-2.62	1.32	1.36
3	A	1202	A1AE4	C21-C22	-2.62	1.43	1.48
3	T	1202	A1AE4	C18-N17	2.61	1.46	1.41
3	M	1202	A1AE4	C18-N17	2.60	1.46	1.41
3	H	1202	A1AE4	C25-N26	-2.60	1.32	1.36
3	D	1202	A1AE4	C18-N17	2.60	1.46	1.41
3	K	1202	A1AE4	C18-N17	2.60	1.46	1.41
3	D	1202	A1AE4	C28-C27	2.59	1.43	1.39
3	R	1202	A1AE4	C25-N26	-2.57	1.32	1.36
3	C	1202	A1AE4	C25-N26	-2.57	1.32	1.36
3	S	1202	A1AE4	C25-N26	-2.57	1.32	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	U	1202	A1AE4	C21-C22	-2.56	1.43	1.48
3	B	1202	A1AE4	C28-C27	2.56	1.43	1.39
3	L	1202	A1AE4	C18-N17	2.55	1.46	1.41
3	I	1202	A1AE4	C25-N26	-2.55	1.32	1.36
3	M	1202	A1AE4	C28-C27	2.54	1.43	1.39
3	M	1202	A1AE4	C25-N26	-2.54	1.32	1.36
3	R	1202	A1AE4	C18-N17	2.53	1.46	1.41
3	G	1202	A1AE4	C21-C27	-2.51	1.37	1.41
3	C	1202	A1AE4	C18-N17	2.51	1.46	1.41
3	R	1202	A1AE4	C28-C27	2.50	1.43	1.39
3	B	1202	A1AE4	C25-N26	-2.48	1.32	1.36
3	Q	1202	A1AE4	C18-N17	2.48	1.46	1.41
3	L	1202	A1AE4	C25-N26	-2.47	1.32	1.36
3	G	1202	A1AE4	C18-N17	2.47	1.46	1.41
3	O	1202	A1AE4	C18-N17	2.47	1.46	1.41
3	N	1202	A1AE4	C28-C27	2.46	1.43	1.39
3	K	1202	A1AE4	C25-N26	-2.45	1.32	1.36
3	P	1202	A1AE4	C18-N17	2.45	1.46	1.41
3	S	1202	A1AE4	C28-C27	2.43	1.43	1.39
3	C	1202	A1AE4	C28-C27	2.43	1.43	1.39
3	L	1202	A1AE4	C28-C27	2.42	1.43	1.39
3	I	1202	A1AE4	C28-C27	2.41	1.43	1.39
3	O	1202	A1AE4	C28-C27	2.40	1.43	1.39
3	N	1202	A1AE4	C18-N17	2.39	1.46	1.41
3	C	1202	A1AE4	O02-C03	2.38	1.41	1.37
3	T	1202	A1AE4	C25-N26	-2.38	1.32	1.36
3	I	1202	A1AE4	O02-C03	2.37	1.41	1.37
3	A	1202	A1AE4	C25-N26	-2.36	1.32	1.36
3	U	1202	A1AE4	O02-C03	2.34	1.41	1.37
3	B	1202	A1AE4	O02-C03	2.34	1.41	1.37
3	Q	1202	A1AE4	C28-C27	2.34	1.43	1.39
3	D	1202	A1AE4	O02-C03	2.34	1.41	1.37
3	F	1202	A1AE4	O02-C03	2.32	1.40	1.37
3	E	1202	A1AE4	C18-N17	2.32	1.46	1.41
3	T	1202	A1AE4	O02-C03	2.32	1.40	1.37
3	K	1202	A1AE4	O02-C03	2.31	1.40	1.37
3	L	1202	A1AE4	O02-C03	2.30	1.40	1.37
3	S	1202	A1AE4	O02-C03	2.30	1.40	1.37
3	A	1202	A1AE4	O02-C03	2.30	1.40	1.37
3	O	1202	A1AE4	O02-C03	2.30	1.40	1.37
3	H	1202	A1AE4	O02-C03	2.30	1.40	1.37
3	A	1202	A1AE4	C20-C21	2.30	1.43	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	1202	A1AE4	C20-C21	2.29	1.43	1.39
3	U	1202	A1AE4	C25-N26	-2.29	1.33	1.36
3	G	1202	A1AE4	O02-C03	2.28	1.40	1.37
3	L	1202	A1AE4	C20-C21	2.28	1.43	1.39
3	R	1202	A1AE4	O02-C03	2.27	1.40	1.37
3	G	1202	A1AE4	C28-C27	2.26	1.43	1.39
3	S	1202	A1AE4	C20-C21	2.26	1.43	1.39
3	H	1202	A1AE4	C28-C27	2.26	1.43	1.39
3	F	1202	A1AE4	C18-N17	2.26	1.46	1.41
3	N	1202	A1AE4	O02-C03	2.25	1.40	1.37
3	M	1202	A1AE4	O02-C03	2.25	1.40	1.37
3	Q	1202	A1AE4	C20-C21	2.24	1.43	1.39
3	K	1202	A1AE4	C20-C21	2.23	1.43	1.39
3	T	1202	A1AE4	C20-C21	2.21	1.43	1.39
3	H	1202	A1AE4	C20-C21	2.20	1.43	1.39
3	F	1202	A1AE4	C28-C27	2.20	1.43	1.39
3	P	1202	A1AE4	O02-C03	2.20	1.40	1.37
3	N	1202	A1AE4	C20-C21	2.19	1.43	1.39
3	Q	1202	A1AE4	O02-C03	2.19	1.40	1.37
3	R	1202	A1AE4	C20-C21	2.19	1.43	1.39
3	U	1202	A1AE4	C04-C15	2.19	1.54	1.50
3	G	1202	A1AE4	C20-C21	2.18	1.43	1.39
3	D	1202	A1AE4	C20-C21	2.17	1.43	1.39
3	P	1202	A1AE4	C28-C27	2.17	1.43	1.39
3	E	1202	A1AE4	O02-C03	2.17	1.40	1.37
3	I	1202	A1AE4	C20-C21	2.17	1.43	1.39
3	C	1202	A1AE4	C20-C21	2.17	1.43	1.39
3	B	1202	A1AE4	C20-C21	2.16	1.43	1.39
3	M	1202	A1AE4	C20-C21	2.15	1.43	1.39
3	O	1202	A1AE4	C20-C21	2.15	1.43	1.39
3	K	1202	A1AE4	C04-C15	2.14	1.54	1.50
3	U	1202	A1AE4	C20-C21	2.14	1.43	1.39
3	L	1202	A1AE4	C35-C32	2.14	1.54	1.53
3	H	1202	A1AE4	C04-C15	2.12	1.54	1.50
3	F	1202	A1AE4	C35-C32	2.12	1.54	1.53
3	M	1202	A1AE4	C04-C15	2.11	1.54	1.50
3	P	1202	A1AE4	O16-C15	-2.11	1.18	1.23
3	A	1202	A1AE4	C04-C15	2.11	1.54	1.50
3	Q	1202	A1AE4	O16-C15	-2.11	1.18	1.23
3	O	1202	A1AE4	O16-C15	-2.10	1.18	1.23
3	E	1202	A1AE4	C28-C27	2.09	1.42	1.39
3	I	1202	A1AE4	C04-C15	2.09	1.54	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	1202	A1AE4	C35-C32	2.09	1.54	1.53
3	D	1202	A1AE4	C04-C15	2.09	1.54	1.50
3	R	1202	A1AE4	C04-C15	2.09	1.54	1.50
3	F	1202	A1AE4	O16-C15	-2.08	1.18	1.23
3	H	1202	A1AE4	O16-C15	-2.08	1.18	1.23
3	G	1202	A1AE4	O16-C15	-2.07	1.18	1.23
3	C	1202	A1AE4	C04-C15	2.07	1.54	1.50
3	S	1202	A1AE4	O16-C15	-2.07	1.18	1.23
3	N	1202	A1AE4	C04-C15	2.07	1.54	1.50
3	I	1202	A1AE4	O16-C15	-2.07	1.18	1.23
3	B	1202	A1AE4	C04-C15	2.06	1.54	1.50
3	G	1202	A1AE4	C04-C15	2.05	1.54	1.50
3	E	1202	A1AE4	O16-C15	-2.05	1.18	1.23
3	P	1202	A1AE4	C20-C21	2.05	1.43	1.39
3	D	1202	A1AE4	O16-C15	-2.03	1.18	1.23
3	R	1202	A1AE4	O16-C15	-2.02	1.18	1.23
3	O	1202	A1AE4	C04-C15	2.02	1.54	1.50
3	Q	1202	A1AE4	C04-C15	2.01	1.54	1.50
3	E	1202	A1AE4	C20-C21	2.01	1.43	1.39
3	P	1202	A1AE4	C04-C15	2.01	1.54	1.50
3	N	1202	A1AE4	O16-C15	-2.00	1.18	1.23

All (146) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	1202	A1AE4	C03-C04-C15	-4.73	117.71	126.24
3	F	1202	A1AE4	C03-C04-C15	-4.68	117.79	126.24
3	E	1202	A1AE4	C03-C04-C15	-4.59	117.95	126.24
3	H	1202	A1AE4	C03-C04-C15	-4.39	118.31	126.24
3	Q	1202	A1AE4	C03-C04-C15	-4.35	118.40	126.24
3	N	1202	A1AE4	C03-C04-C15	-4.34	118.42	126.24
3	R	1202	A1AE4	C03-C04-C15	-4.31	118.47	126.24
3	O	1202	A1AE4	C03-C04-C15	-4.24	118.59	126.24
3	P	1202	A1AE4	C03-C04-C15	-4.23	118.61	126.24
3	C	1202	A1AE4	C03-C04-C15	-4.20	118.67	126.24
3	D	1202	A1AE4	C03-C04-C15	-4.14	118.77	126.24
3	I	1202	A1AE4	C03-C04-C15	-4.12	118.80	126.24
3	M	1202	A1AE4	C03-C04-C15	-4.09	118.85	126.24
3	L	1202	A1AE4	C03-C04-C15	-4.07	118.89	126.24
3	T	1202	A1AE4	C03-C04-C15	-3.95	119.12	126.24
3	K	1202	A1AE4	C03-C04-C15	-3.94	119.14	126.24
3	U	1202	A1AE4	C03-C04-C15	-3.91	119.20	126.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1202	A1AE4	C03-C04-C15	-3.85	119.30	126.24
3	S	1202	A1AE4	C03-C04-C15	-3.78	119.42	126.24
3	A	1202	A1AE4	C03-C04-C15	-3.64	119.67	126.24
3	B	1202	A1AE4	O02-C03-C04	3.04	120.98	116.55
3	F	1202	A1AE4	C05-C04-C03	2.96	119.88	117.16
3	C	1202	A1AE4	O02-C03-C04	2.96	120.85	116.55
3	T	1202	A1AE4	O02-C03-C04	2.89	120.76	116.55
3	U	1202	A1AE4	O02-C03-C04	2.88	120.75	116.55
3	A	1202	A1AE4	O02-C03-C04	2.87	120.72	116.55
3	Q	1202	A1AE4	O02-C03-C04	2.86	120.71	116.55
3	F	1202	A1AE4	O02-C03-C04	2.85	120.69	116.55
3	E	1202	A1AE4	C05-C04-C03	2.82	119.75	117.16
3	M	1202	A1AE4	O02-C03-C04	2.81	120.64	116.55
3	N	1202	A1AE4	O02-C03-C04	2.81	120.64	116.55
3	O	1202	A1AE4	O02-C03-C04	2.81	120.63	116.55
3	P	1202	A1AE4	C05-C04-C03	2.79	119.72	117.16
3	F	1202	A1AE4	C27-C21-C22	-2.79	117.10	120.11
3	G	1202	A1AE4	C08-C07-C09	-2.79	118.04	121.82
3	O	1202	A1AE4	C05-C04-C03	2.78	119.70	117.16
3	S	1202	A1AE4	O02-C03-C04	2.75	120.55	116.55
3	L	1202	A1AE4	O02-C03-C04	2.72	120.51	116.55
3	K	1202	A1AE4	O02-C03-C04	2.71	120.50	116.55
3	R	1202	A1AE4	O02-C03-C04	2.66	120.41	116.55
3	H	1202	A1AE4	C27-C21-C22	-2.65	117.25	120.11
3	L	1202	A1AE4	C05-C04-C03	2.65	119.59	117.16
3	R	1202	A1AE4	C08-C07-C09	-2.62	118.27	121.82
3	E	1202	A1AE4	C27-C21-C22	-2.62	117.28	120.11
3	G	1202	A1AE4	C27-C21-C22	-2.62	117.28	120.11
3	D	1202	A1AE4	O02-C03-C04	2.61	120.35	116.55
3	Q	1202	A1AE4	C05-C04-C03	2.61	119.55	117.16
3	I	1202	A1AE4	O02-C03-C04	2.61	120.34	116.55
3	Q	1202	A1AE4	C08-C07-C09	-2.60	118.29	121.82
3	G	1202	A1AE4	O02-C03-C04	2.58	120.30	116.55
3	S	1202	A1AE4	C05-C04-C03	2.57	119.52	117.16
3	L	1202	A1AE4	C27-C21-C22	-2.55	117.35	120.11
3	P	1202	A1AE4	O02-C03-C04	2.55	120.26	116.55
3	I	1202	A1AE4	C27-C21-C22	-2.55	117.36	120.11
3	M	1202	A1AE4	C05-N06-C07	2.55	121.25	117.93
3	H	1202	A1AE4	O02-C03-C04	2.54	120.25	116.55
3	G	1202	A1AE4	C05-C04-C03	2.52	119.47	117.16
3	D	1202	A1AE4	C05-N06-C07	2.52	121.21	117.93
3	E	1202	A1AE4	C04-C05-N06	-2.52	120.78	124.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	1202	A1AE4	C04-C05-N06	-2.52	120.78	124.32
3	N	1202	A1AE4	C05-C04-C03	2.51	119.46	117.16
3	C	1202	A1AE4	C27-C21-C22	-2.51	117.40	120.11
3	P	1202	A1AE4	C04-C05-N06	-2.50	120.80	124.32
3	T	1202	A1AE4	C05-C04-C03	2.48	119.43	117.16
3	I	1202	A1AE4	C05-C04-C03	2.48	119.43	117.16
3	N	1202	A1AE4	C05-N06-C07	2.48	121.15	117.93
3	P	1202	A1AE4	C05-N06-C07	2.47	121.15	117.93
3	A	1202	A1AE4	C05-N06-C07	2.47	121.14	117.93
3	H	1202	A1AE4	C08-C07-C09	-2.46	118.48	121.82
3	H	1202	A1AE4	C05-C04-C03	2.46	119.42	117.16
3	N	1202	A1AE4	C27-C21-C22	-2.46	117.45	120.11
3	C	1202	A1AE4	C05-C04-C03	2.46	119.41	117.16
3	A	1202	A1AE4	C27-C21-C22	-2.46	117.45	120.11
3	U	1202	A1AE4	C08-C07-C09	-2.45	118.49	121.82
3	L	1202	A1AE4	C05-N06-C07	2.45	121.12	117.93
3	B	1202	A1AE4	C27-C21-C22	-2.44	117.47	120.11
3	F	1202	A1AE4	C08-C07-C09	-2.44	118.51	121.82
3	Q	1202	A1AE4	C04-C05-N06	-2.44	120.88	124.32
3	K	1202	A1AE4	C05-N06-C07	2.44	121.11	117.93
3	G	1202	A1AE4	C04-C05-N06	-2.44	120.88	124.32
3	C	1202	A1AE4	C05-N06-C07	2.44	121.10	117.93
3	R	1202	A1AE4	C05-C04-C03	2.44	119.39	117.16
3	Q	1202	A1AE4	C27-C21-C22	-2.44	117.48	120.11
3	E	1202	A1AE4	C05-N06-C07	2.43	121.10	117.93
3	N	1202	A1AE4	C04-C05-N06	-2.43	120.90	124.32
3	P	1202	A1AE4	C27-C21-C22	-2.43	117.49	120.11
3	T	1202	A1AE4	C08-C07-C09	-2.43	118.53	121.82
3	S	1202	A1AE4	C27-C21-C22	-2.42	117.49	120.11
3	O	1202	A1AE4	C04-C05-N06	-2.42	120.91	124.32
3	D	1202	A1AE4	C05-C04-C03	2.42	119.38	117.16
3	H	1202	A1AE4	C05-N06-C07	2.42	121.07	117.93
3	K	1202	A1AE4	C05-C04-C03	2.41	119.36	117.16
3	L	1202	A1AE4	C04-C05-N06	-2.40	120.94	124.32
3	O	1202	A1AE4	C27-C21-C22	-2.40	117.52	120.11
3	R	1202	A1AE4	C27-C21-C22	-2.39	117.53	120.11
3	B	1202	A1AE4	C05-C04-C03	2.39	119.35	117.16
3	B	1202	A1AE4	C05-N06-C07	2.39	121.04	117.93
3	M	1202	A1AE4	C05-C04-C03	2.38	119.34	117.16
3	O	1202	A1AE4	C05-N06-C07	2.38	121.03	117.93
3	U	1202	A1AE4	C05-N06-C07	2.38	121.02	117.93
3	C	1202	A1AE4	C08-C07-C09	-2.38	118.60	121.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1202	A1AE4	C04-C05-N06	-2.37	120.98	124.32
3	K	1202	A1AE4	C04-C05-N06	-2.37	120.99	124.32
3	Q	1202	A1AE4	C05-N06-C07	2.36	121.01	117.93
3	G	1202	A1AE4	C05-N06-C07	2.36	121.00	117.93
3	M	1202	A1AE4	C04-C05-N06	-2.36	121.00	124.32
3	D	1202	A1AE4	C04-C05-N06	-2.35	121.01	124.32
3	H	1202	A1AE4	C04-C05-N06	-2.35	121.01	124.32
3	A	1202	A1AE4	C05-C04-C03	2.35	119.31	117.16
3	I	1202	A1AE4	C05-N06-C07	2.34	120.97	117.93
3	B	1202	A1AE4	C04-C05-N06	-2.34	121.03	124.32
3	A	1202	A1AE4	C04-C05-N06	-2.34	121.03	124.32
3	E	1202	A1AE4	O02-C03-C04	2.33	119.93	116.55
3	R	1202	A1AE4	C04-C05-N06	-2.32	121.06	124.32
3	B	1202	A1AE4	C08-C07-C09	-2.31	118.69	121.82
3	F	1202	A1AE4	C05-N06-C07	2.31	120.93	117.93
3	T	1202	A1AE4	C27-C21-C22	-2.30	117.62	120.11
3	R	1202	A1AE4	C05-N06-C07	2.29	120.92	117.93
3	N	1202	A1AE4	C08-C07-C09	-2.29	118.71	121.82
3	K	1202	A1AE4	C27-C21-C22	-2.29	117.63	120.11
3	I	1202	A1AE4	C08-C07-C09	-2.29	118.71	121.82
3	M	1202	A1AE4	C27-C21-C22	-2.28	117.64	120.11
3	T	1202	A1AE4	C05-N06-C07	2.28	120.90	117.93
3	U	1202	A1AE4	C04-C05-N06	-2.28	121.11	124.32
3	I	1202	A1AE4	C04-C05-N06	-2.28	121.12	124.32
3	S	1202	A1AE4	C05-N06-C07	2.27	120.89	117.93
3	S	1202	A1AE4	C04-C05-N06	-2.27	121.13	124.32
3	D	1202	A1AE4	C27-C21-C22	-2.26	117.67	120.11
3	G	1202	A1AE4	C33-C32-C35	-2.26	118.19	121.33
3	T	1202	A1AE4	C04-C05-N06	-2.26	121.14	124.32
3	U	1202	A1AE4	C05-C04-C03	2.26	119.23	117.16
3	M	1202	A1AE4	C08-C07-C09	-2.19	118.84	121.82
3	Q	1202	A1AE4	C37-C35-C36	-2.17	107.88	110.53
3	O	1202	A1AE4	C08-C07-C09	-2.15	118.91	121.82
3	S	1202	A1AE4	C08-C07-C09	-2.13	118.92	121.82
3	U	1202	A1AE4	C27-C21-C22	-2.13	117.81	120.11
3	E	1202	A1AE4	C08-C07-C09	-2.12	118.94	121.82
3	G	1202	A1AE4	C09-C07-N06	2.11	120.79	116.87
3	D	1202	A1AE4	C08-C07-C09	-2.09	118.98	121.82
3	L	1202	A1AE4	C08-C07-C09	-2.08	119.00	121.82
3	K	1202	A1AE4	C08-C07-C09	-2.06	119.03	121.82
3	H	1202	A1AE4	C33-C32-C35	-2.05	118.48	121.33
3	F	1202	A1AE4	C08-C03-C04	-2.03	117.58	121.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	N	1202	A1AE4	C37-C35-C36	-2.03	108.05	110.53
3	P	1202	A1AE4	C37-C35-C36	-2.02	108.06	110.53
3	O	1202	A1AE4	C08-C03-C04	-2.01	117.61	121.39

There are no chirality outliers.

All (117) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1202	A1AE4	C31-C32-C35-O38
3	A	1202	A1AE4	C33-C32-C35-O38
3	B	1202	A1AE4	C31-C32-C35-O38
3	B	1202	A1AE4	C33-C32-C35-O38
3	C	1202	A1AE4	C31-C32-C35-O38
3	C	1202	A1AE4	C33-C32-C35-O38
3	D	1202	A1AE4	C31-C32-C35-O38
3	D	1202	A1AE4	C33-C32-C35-O38
3	E	1202	A1AE4	C31-C32-C35-O38
3	E	1202	A1AE4	C33-C32-C35-O38
3	F	1202	A1AE4	C31-C32-C35-O38
3	F	1202	A1AE4	C33-C32-C35-O38
3	G	1202	A1AE4	C31-C32-C35-O38
3	H	1202	A1AE4	C31-C32-C35-O38
3	H	1202	A1AE4	C33-C32-C35-O38
3	I	1202	A1AE4	C31-C32-C35-O38
3	I	1202	A1AE4	C33-C32-C35-O38
3	K	1202	A1AE4	C31-C32-C35-O38
3	K	1202	A1AE4	C33-C32-C35-O38
3	L	1202	A1AE4	C31-C32-C35-O38
3	L	1202	A1AE4	C33-C32-C35-O38
3	M	1202	A1AE4	C31-C32-C35-O38
3	M	1202	A1AE4	C33-C32-C35-O38
3	N	1202	A1AE4	C31-C32-C35-O38
3	N	1202	A1AE4	C33-C32-C35-O38
3	O	1202	A1AE4	C31-C32-C35-O38
3	O	1202	A1AE4	C33-C32-C35-O38
3	P	1202	A1AE4	C31-C32-C35-O38
3	P	1202	A1AE4	C33-C32-C35-O38
3	Q	1202	A1AE4	C31-C32-C35-O38
3	Q	1202	A1AE4	C33-C32-C35-O38
3	R	1202	A1AE4	C31-C32-C35-O38
3	R	1202	A1AE4	C33-C32-C35-O38
3	S	1202	A1AE4	C31-C32-C35-O38

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Mol	Chain	Res	Type	Atoms
3	S	1202	A1AE4	C33-C32-C35-O38
3	T	1202	A1AE4	C31-C32-C35-O38
3	T	1202	A1AE4	C33-C32-C35-O38
3	U	1202	A1AE4	C31-C32-C35-O38
3	U	1202	A1AE4	C33-C32-C35-O38
3	K	1202	A1AE4	C05-C04-C15-N17
3	C	1202	A1AE4	C31-C32-C35-C36
3	G	1202	A1AE4	C31-C32-C35-C37
3	G	1202	A1AE4	C33-C32-C35-O38
3	A	1202	A1AE4	C05-C04-C15-N17
3	H	1202	A1AE4	C03-C04-C15-O16
3	U	1202	A1AE4	C05-C04-C15-N17
3	A	1202	A1AE4	C31-C32-C35-C36
3	G	1202	A1AE4	C03-C04-C15-O16
3	P	1202	A1AE4	C03-C04-C15-O16
3	B	1202	A1AE4	C08-C03-O02-C01
3	E	1202	A1AE4	C03-C04-C15-O16
3	F	1202	A1AE4	C03-C04-C15-O16
3	I	1202	A1AE4	C03-C04-C15-O16
3	D	1202	A1AE4	C03-C04-C15-O16
3	T	1202	A1AE4	C05-C04-C15-N17
3	M	1202	A1AE4	C03-C04-C15-O16
3	N	1202	A1AE4	C03-C04-C15-O16
3	Q	1202	A1AE4	C03-C04-C15-O16
3	G	1202	A1AE4	C03-C04-C15-N17
3	H	1202	A1AE4	C03-C04-C15-N17
3	P	1202	A1AE4	C03-C04-C15-N17
3	A	1202	A1AE4	C05-C04-C15-O16
3	K	1202	A1AE4	C05-C04-C15-O16
3	S	1202	A1AE4	C03-C04-C15-O16
3	E	1202	A1AE4	C03-C04-C15-N17
3	I	1202	A1AE4	C03-C04-C15-N17
3	B	1202	A1AE4	C03-C04-C15-O16
3	D	1202	A1AE4	C03-C04-C15-N17
3	C	1202	A1AE4	C03-C04-C15-O16
3	O	1202	A1AE4	C03-C04-C15-O16
3	F	1202	A1AE4	C03-C04-C15-N17
3	M	1202	A1AE4	C03-C04-C15-N17
3	D	1202	A1AE4	C31-C32-C35-C36
3	E	1202	A1AE4	C31-C32-C35-C37
3	E	1202	A1AE4	C33-C32-C35-C37
3	F	1202	A1AE4	C31-C32-C35-C37

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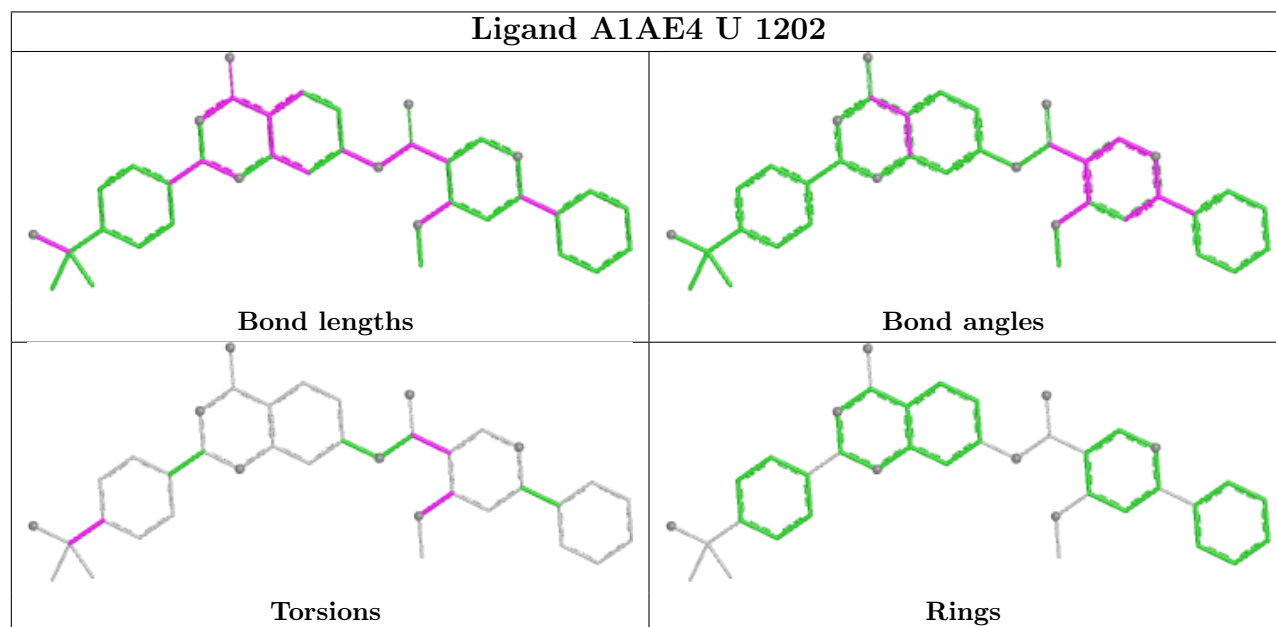
Mol	Chain	Res	Type	Atoms
3	G	1202	A1AE4	C33-C32-C35-C37
3	H	1202	A1AE4	C31-C32-C35-C37
3	Q	1202	A1AE4	C31-C32-C35-C37
3	R	1202	A1AE4	C05-C04-C15-N17
3	U	1202	A1AE4	C31-C32-C35-C36
3	N	1202	A1AE4	C03-C04-C15-N17
3	Q	1202	A1AE4	C03-C04-C15-N17
3	L	1202	A1AE4	C03-C04-C15-O16
3	R	1202	A1AE4	C03-C04-C15-O16
3	A	1202	A1AE4	C08-C03-O02-C01
3	B	1202	A1AE4	C04-C03-O02-C01
3	U	1202	A1AE4	C05-C04-C15-O16
3	S	1202	A1AE4	C03-C04-C15-N17
3	L	1202	A1AE4	C05-C04-C15-N17
3	C	1202	A1AE4	C03-C04-C15-N17
3	O	1202	A1AE4	C03-C04-C15-N17
3	B	1202	A1AE4	C03-C04-C15-N17
3	L	1202	A1AE4	C03-C04-C15-N17
3	K	1202	A1AE4	C08-C03-O02-C01
3	U	1202	A1AE4	C08-C03-O02-C01
3	T	1202	A1AE4	C03-C04-C15-O16
3	A	1202	A1AE4	C33-C32-C35-C36
3	B	1202	A1AE4	C31-C32-C35-C36
3	B	1202	A1AE4	C33-C32-C35-C36
3	K	1202	A1AE4	C31-C32-C35-C37
3	Q	1202	A1AE4	C33-C32-C35-C37
3	S	1202	A1AE4	C33-C32-C35-C36
3	R	1202	A1AE4	C03-C04-C15-N17
3	C	1202	A1AE4	C05-C04-C15-N17
3	O	1202	A1AE4	C05-C04-C15-N17
3	A	1202	A1AE4	C04-C03-O02-C01
3	C	1202	A1AE4	C08-C03-O02-C01
3	T	1202	A1AE4	C05-C04-C15-O16
3	B	1202	A1AE4	C05-C04-C15-N17
3	U	1202	A1AE4	C04-C03-O02-C01
3	T	1202	A1AE4	C03-C04-C15-N17
3	C	1202	A1AE4	C33-C32-C35-C36
3	H	1202	A1AE4	C33-C32-C35-C37
3	M	1202	A1AE4	C33-C32-C35-C36
3	T	1202	A1AE4	C33-C32-C35-C36
3	U	1202	A1AE4	C33-C32-C35-C36

There are no ring outliers.

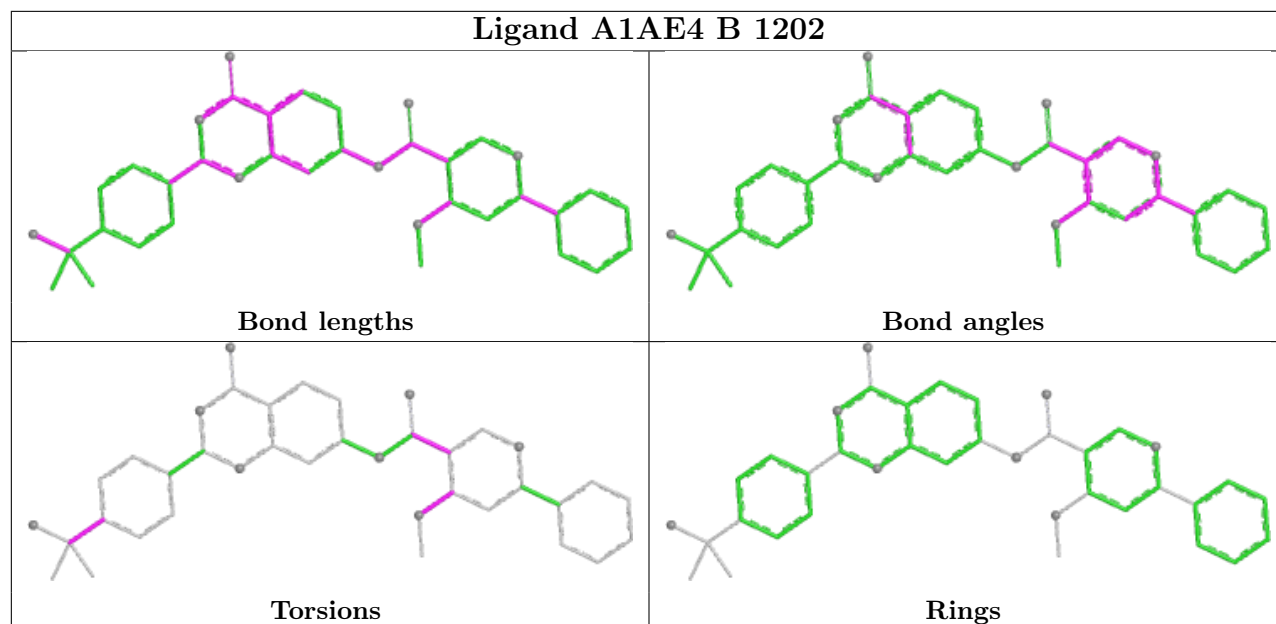
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	M	1202	A1AE4	1	0

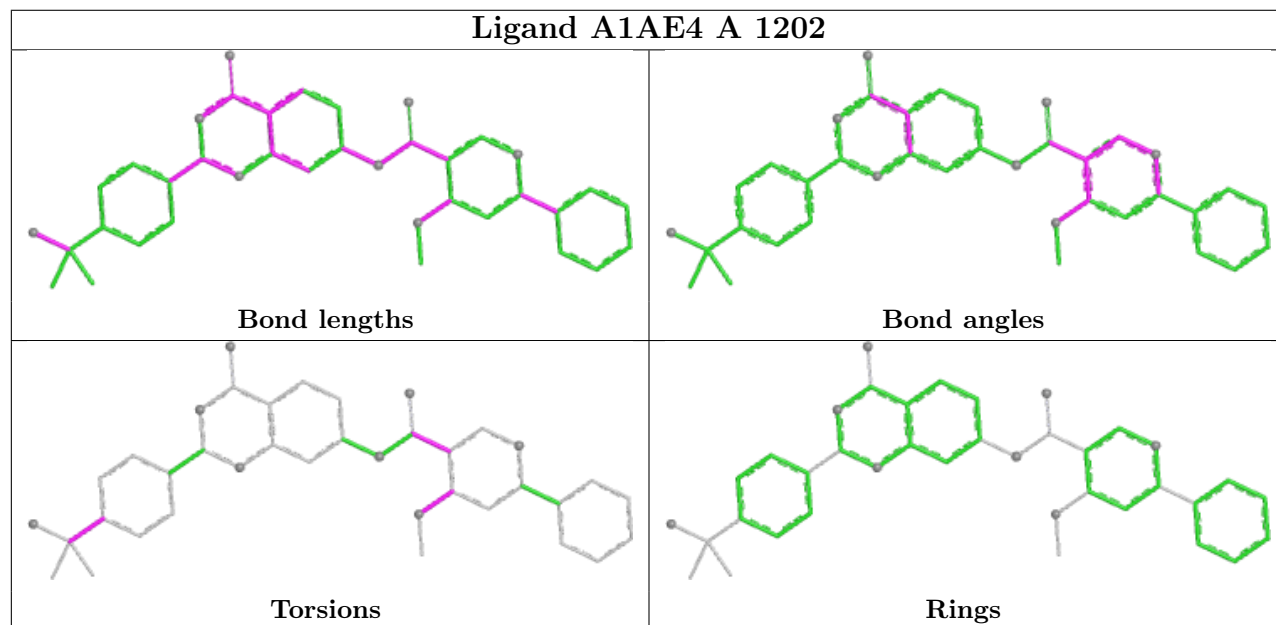
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



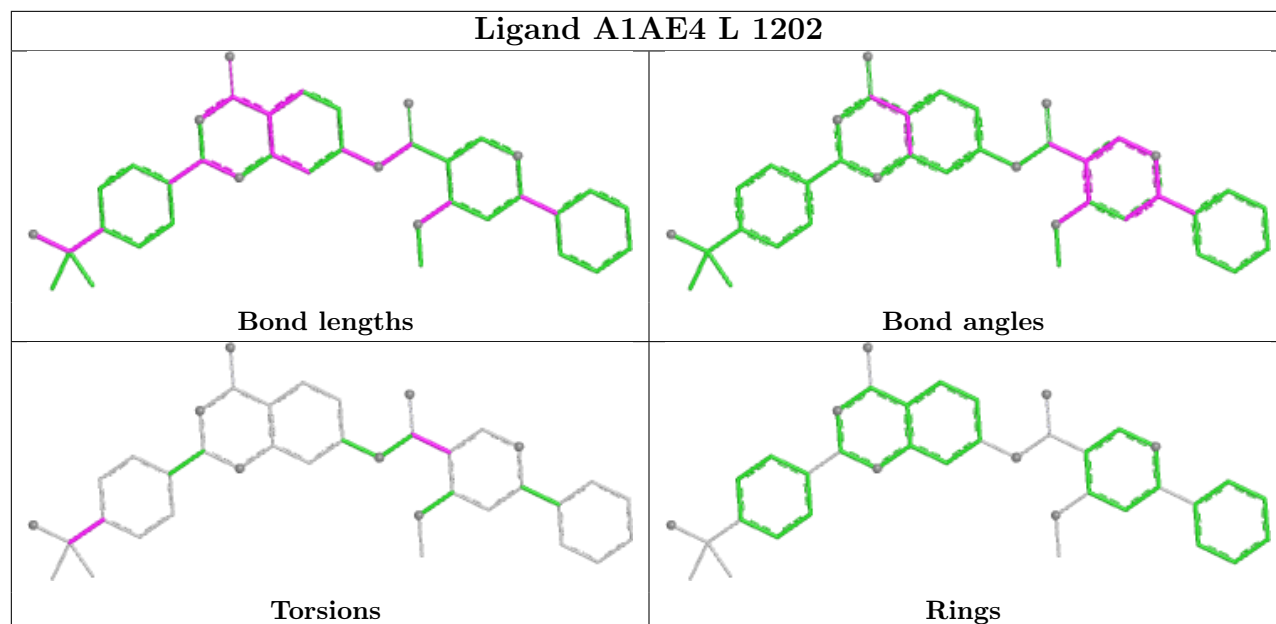
Ligand A1AE4 B 1202



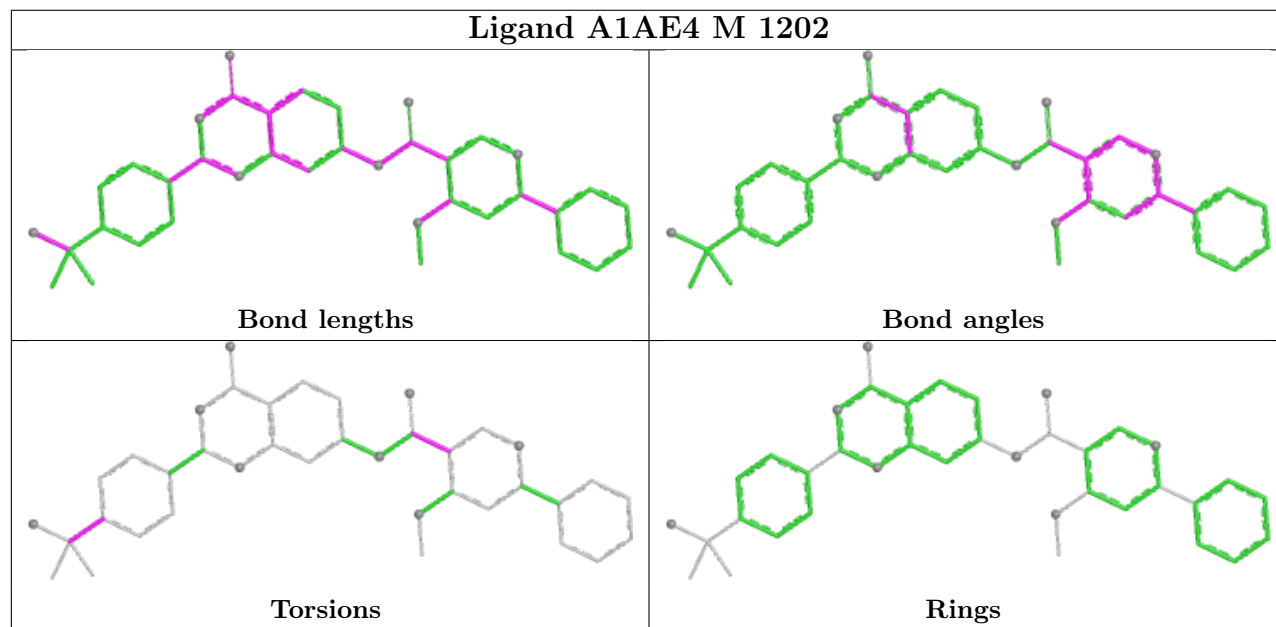
Ligand A1AE4 A 1202



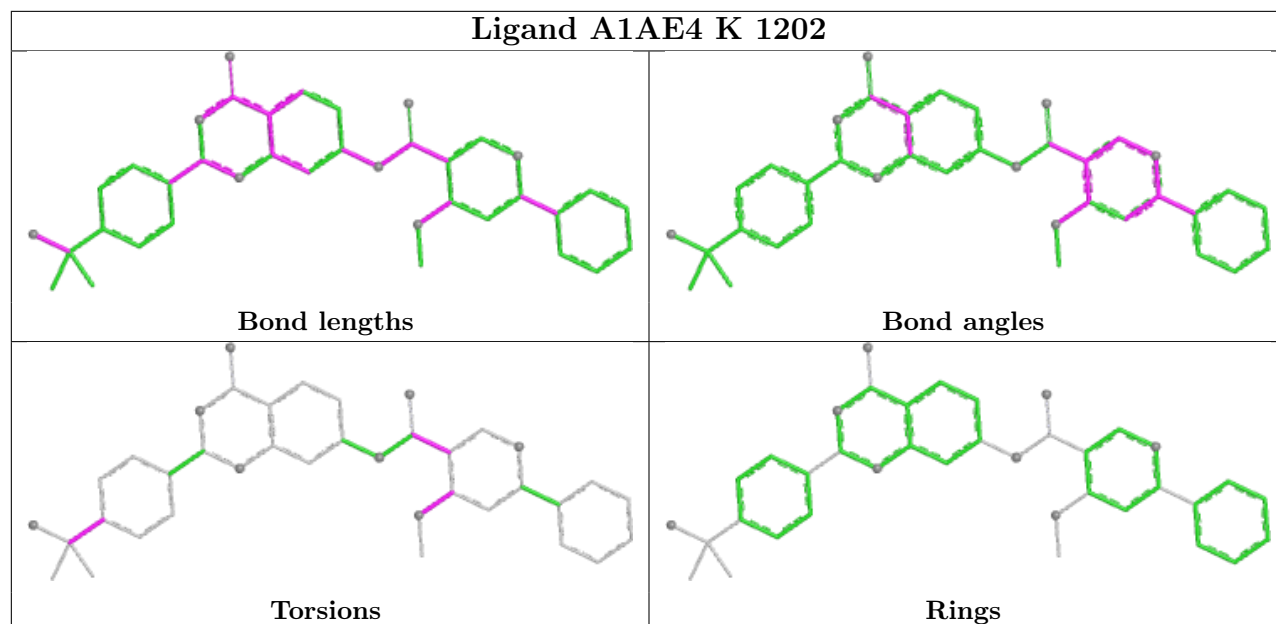
Ligand A1AE4 L 1202



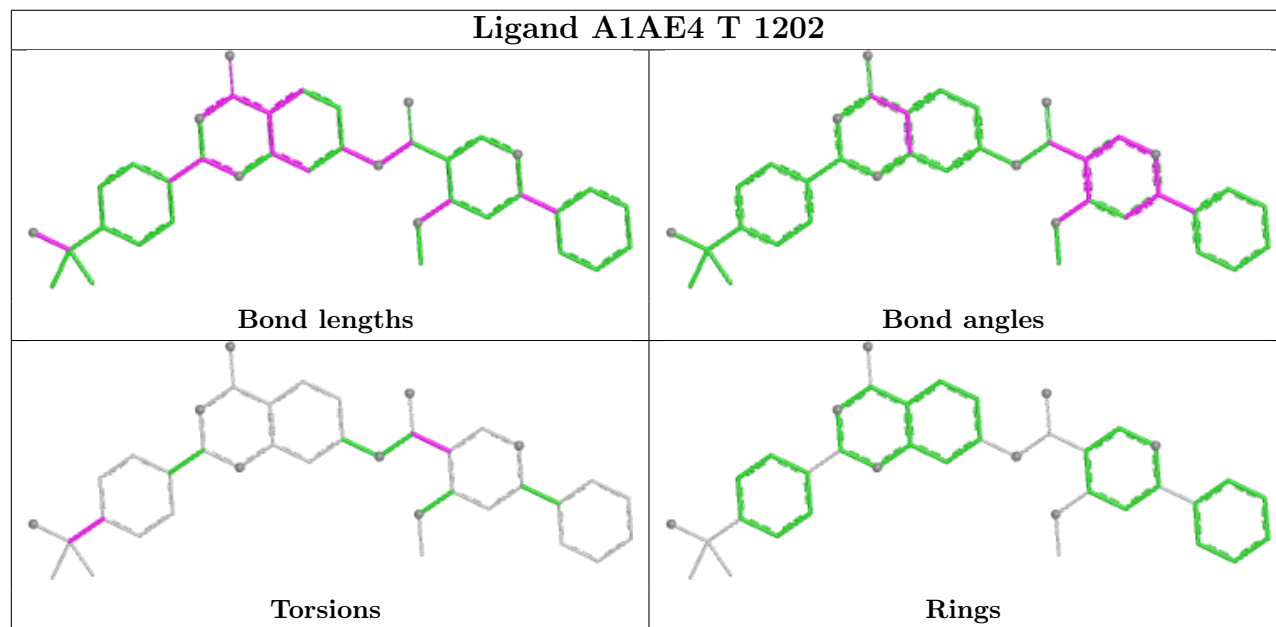
Ligand A1AE4 M 1202



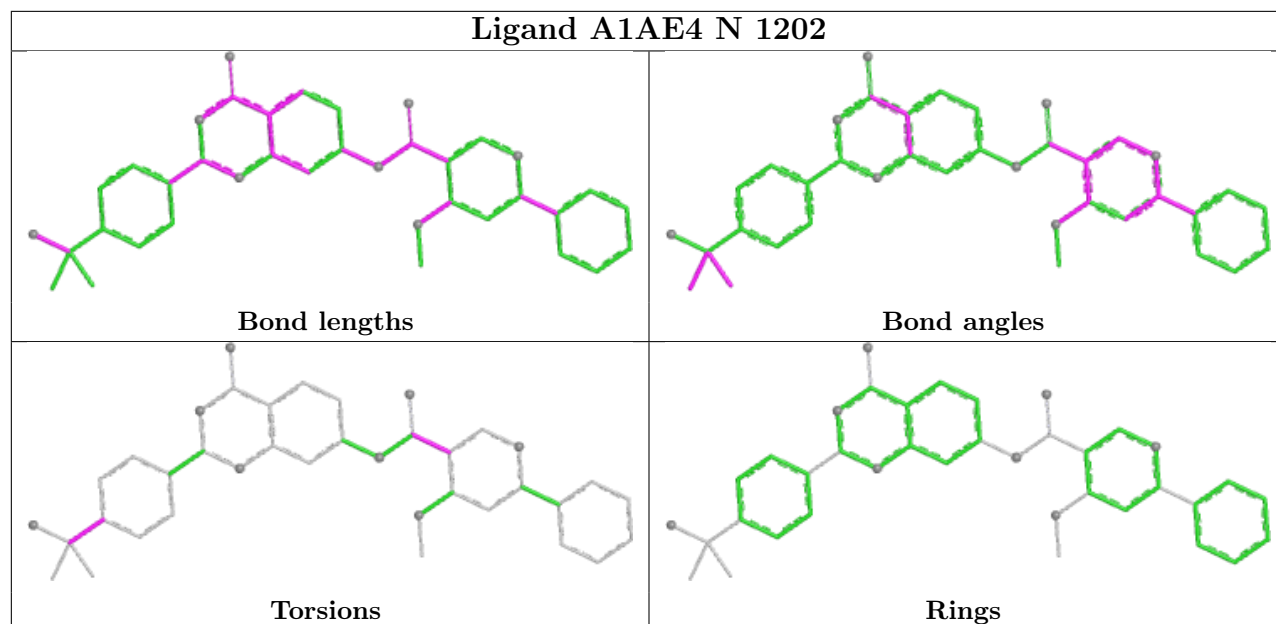
Ligand A1AE4 K 1202



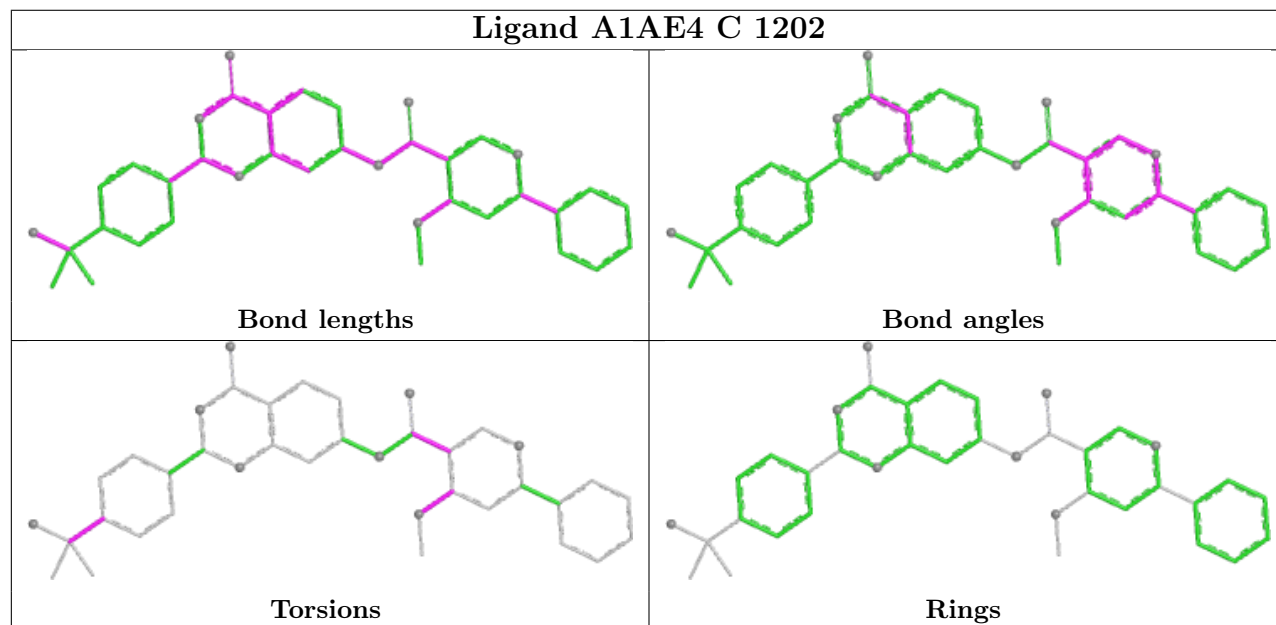
Ligand A1AE4 T 1202



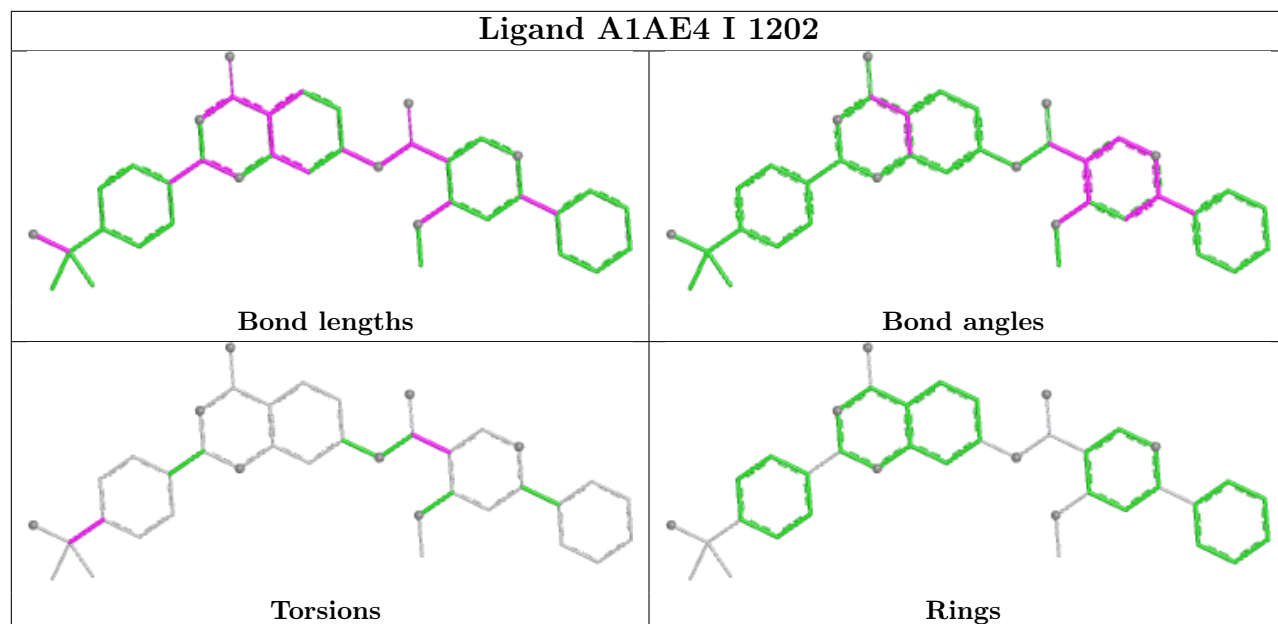
Ligand A1AE4 N 1202



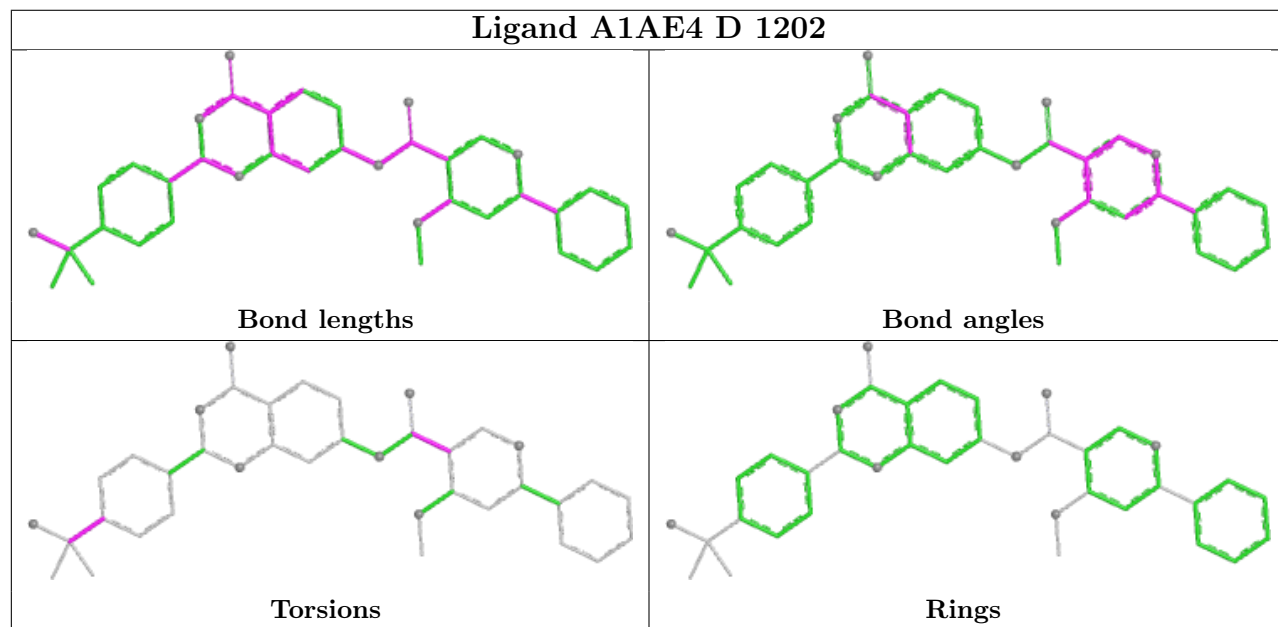
Ligand A1AE4 C 1202



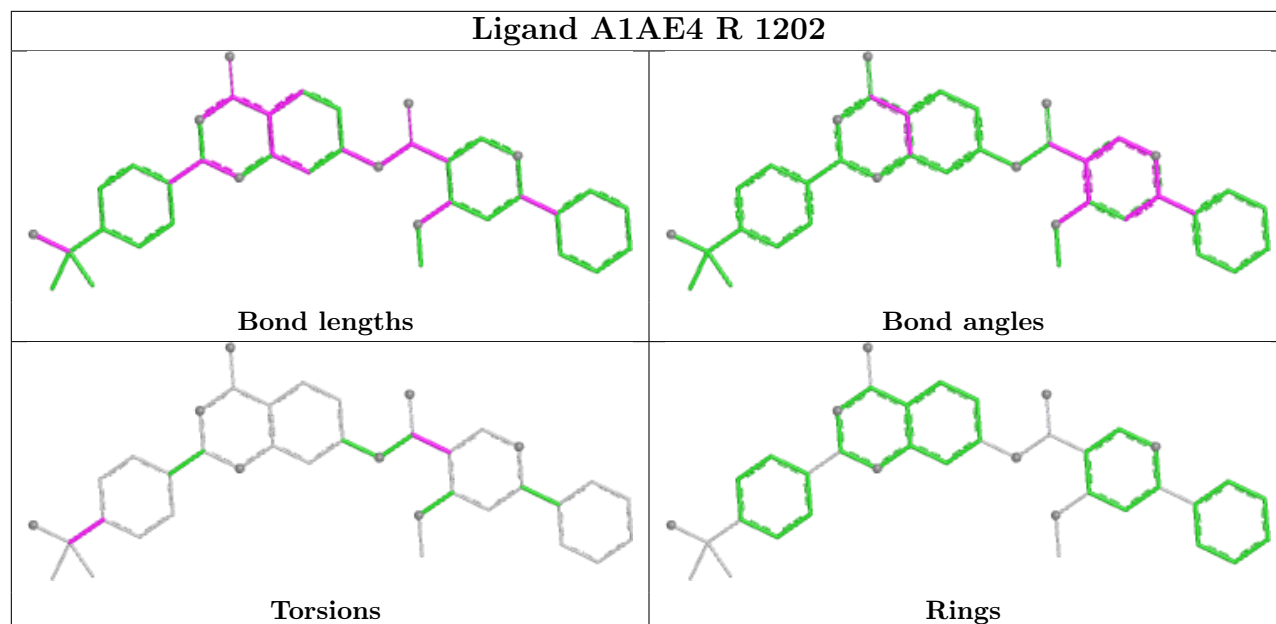
Ligand A1AE4 I 1202



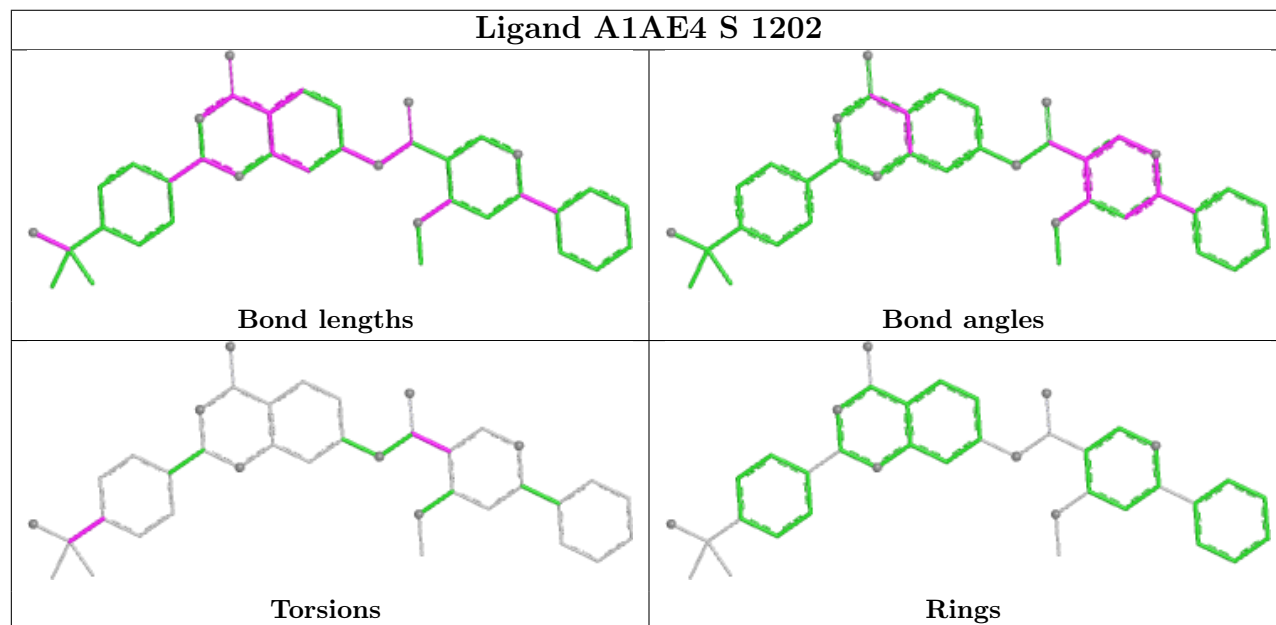
Ligand A1AE4 D 1202



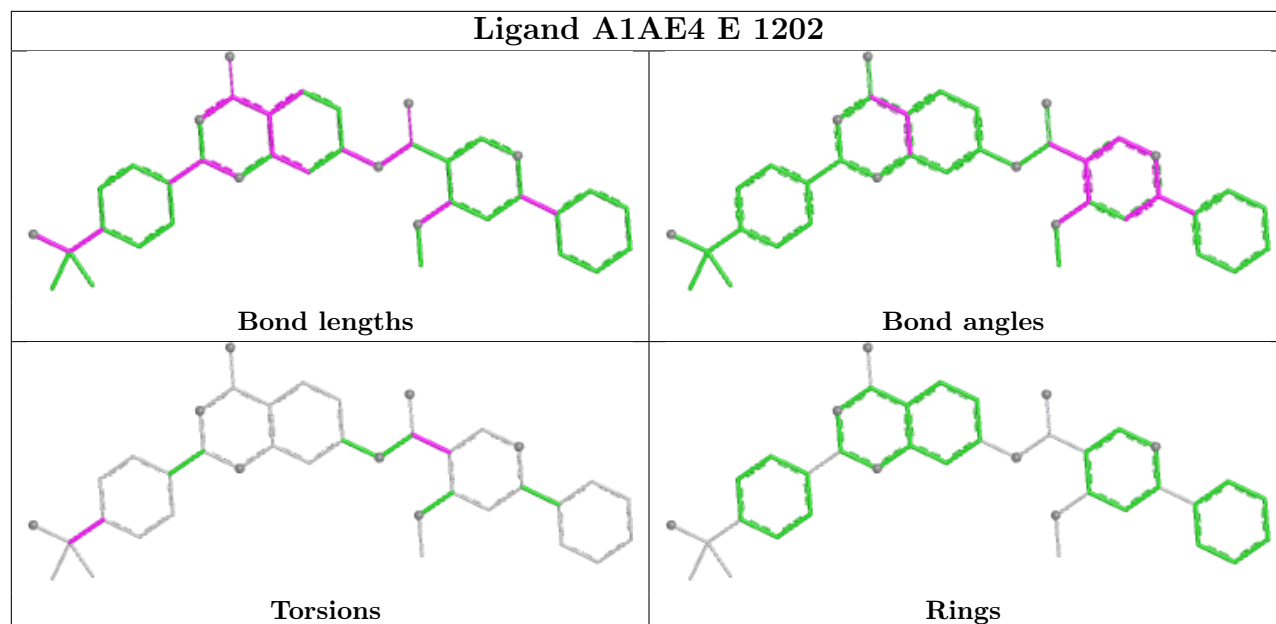
Ligand A1AE4 R 1202



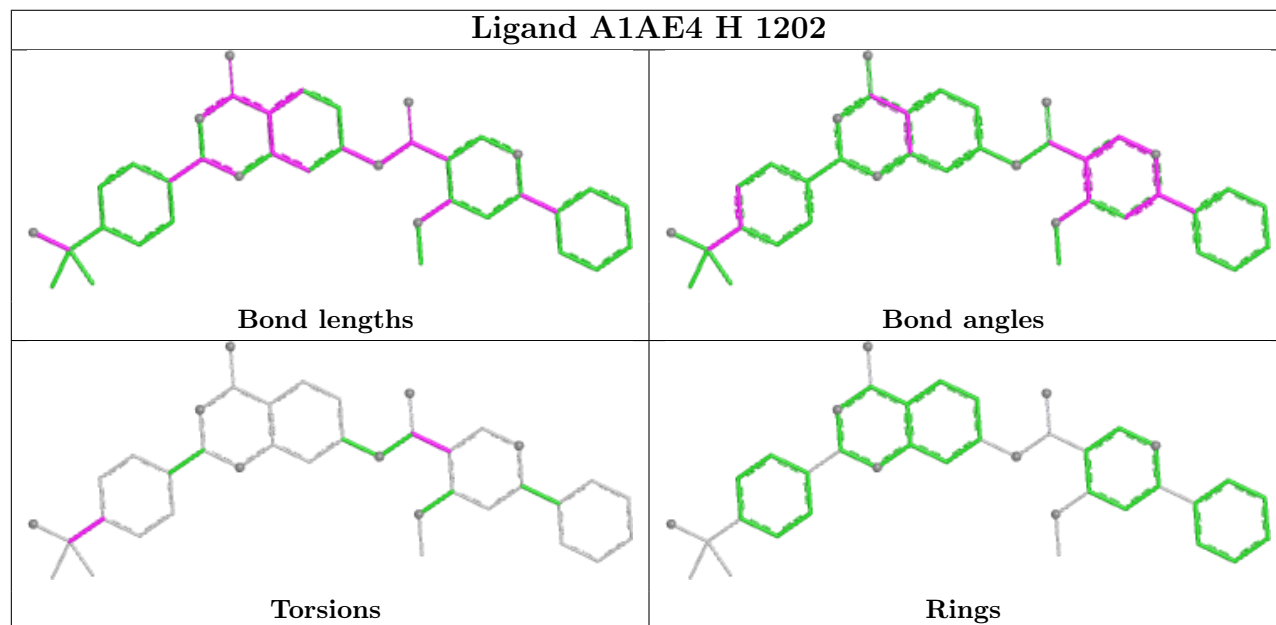
Ligand A1AE4 S 1202



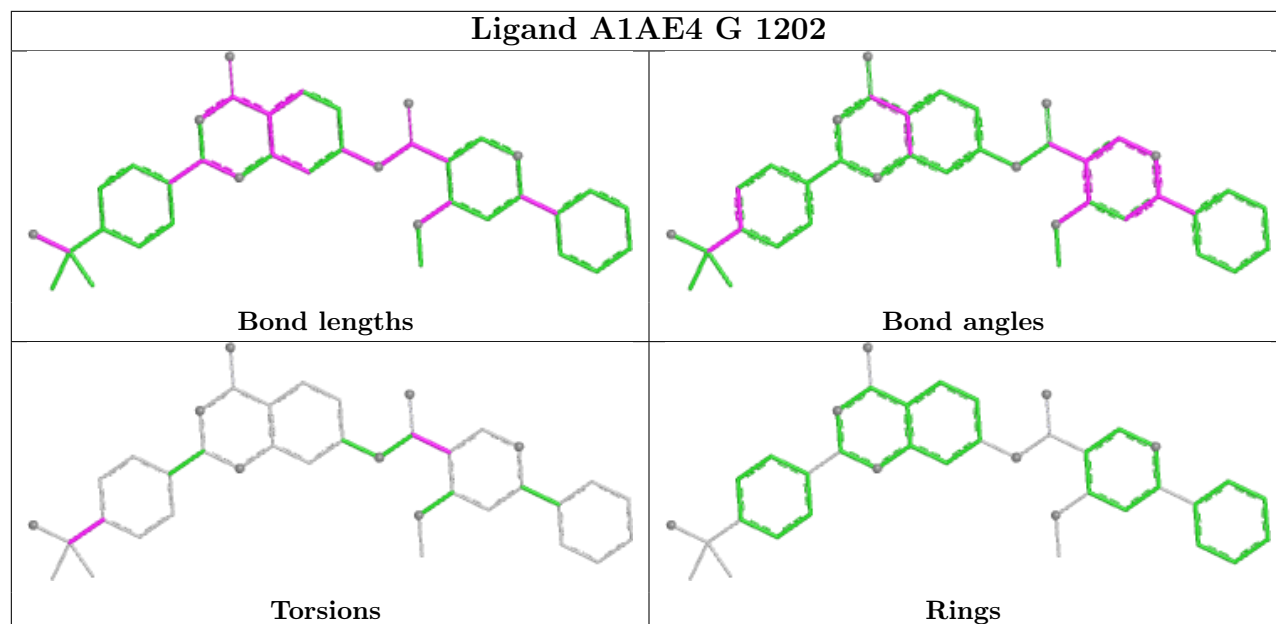
Ligand A1AE4 E 1202



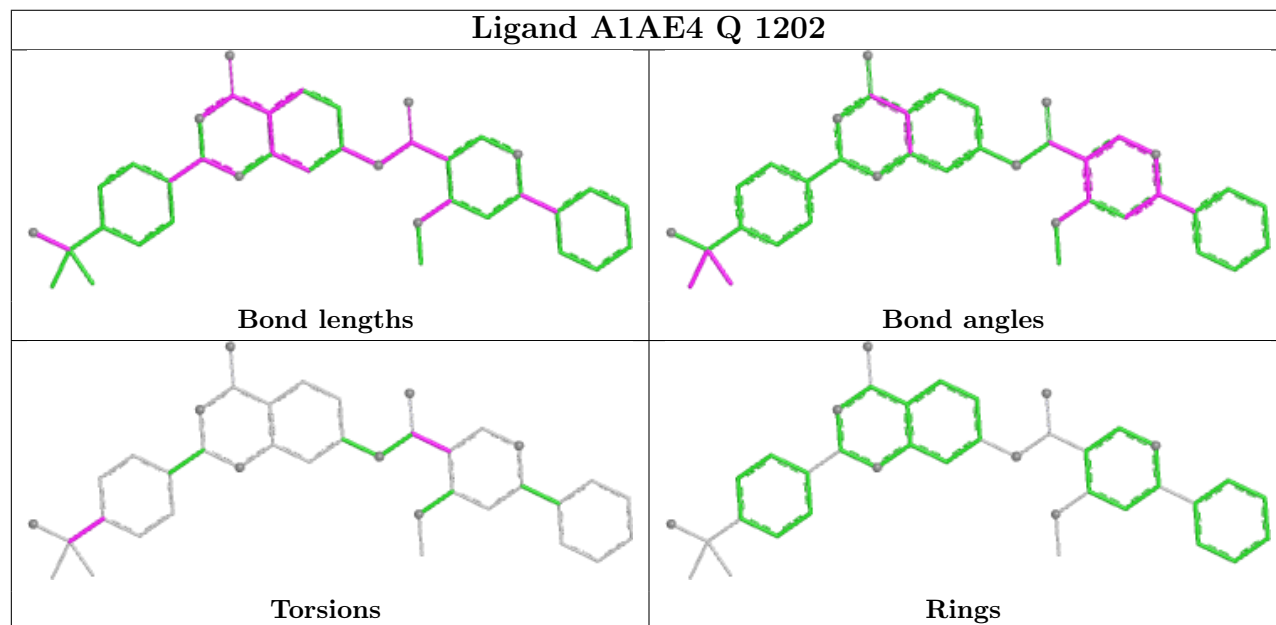
Ligand A1AE4 H 1202



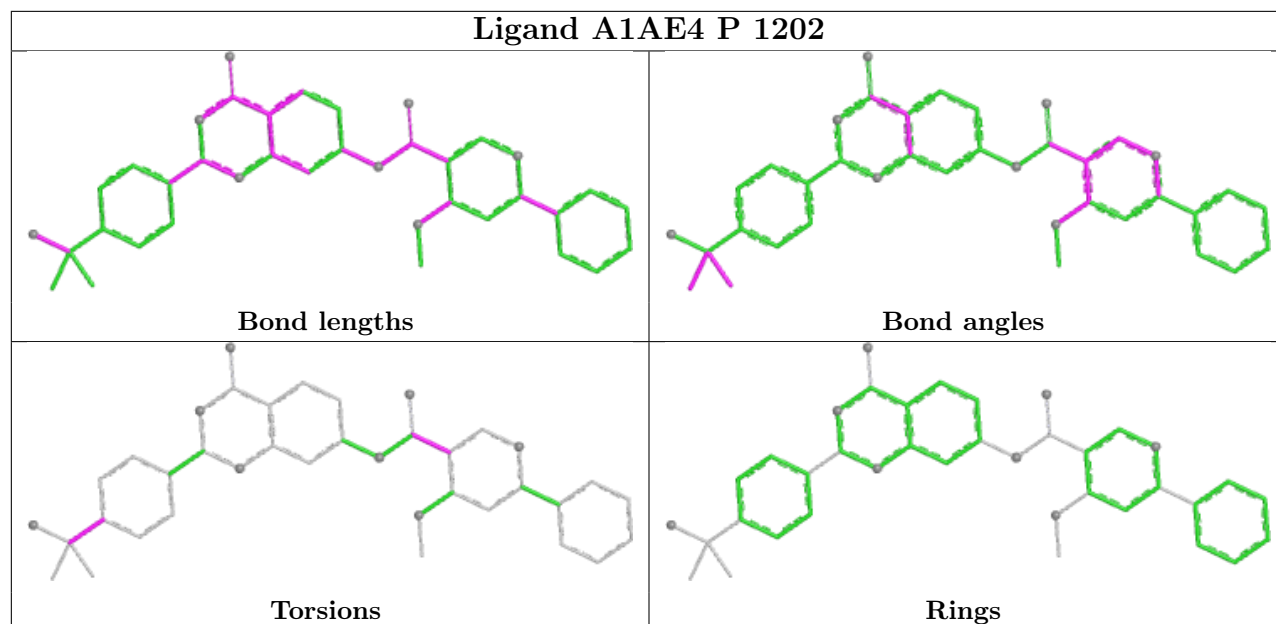
Ligand A1AE4 G 1202



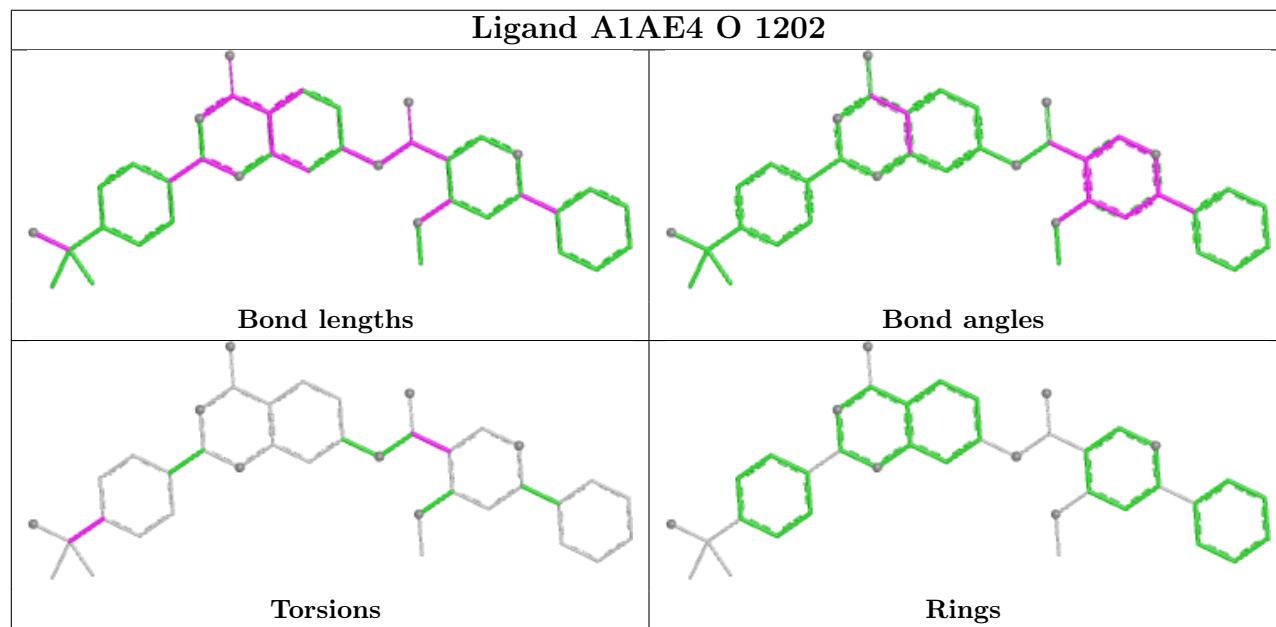
Ligand A1AE4 Q 1202

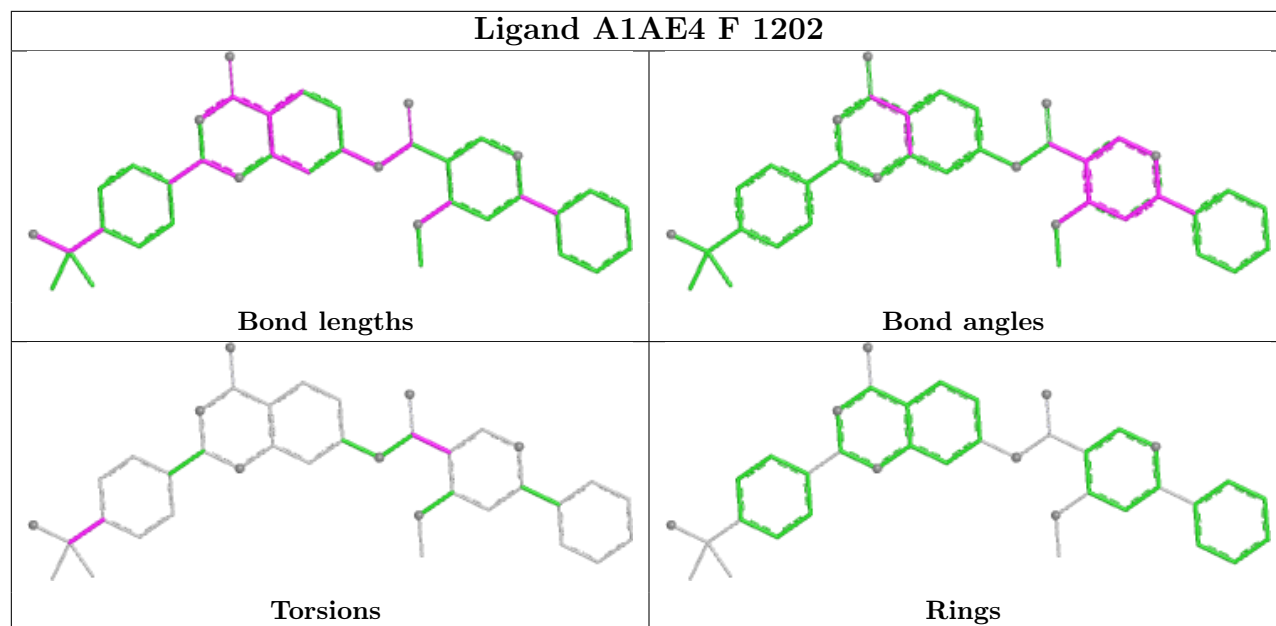


Ligand A1AE4 P 1202



Ligand A1AE4 O 1202





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.

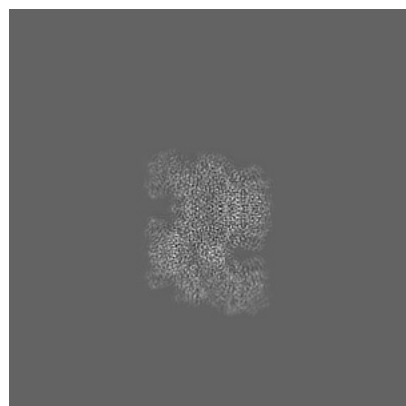
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43738. These allow visual inspection of the internal detail of the map and identification of artifacts.

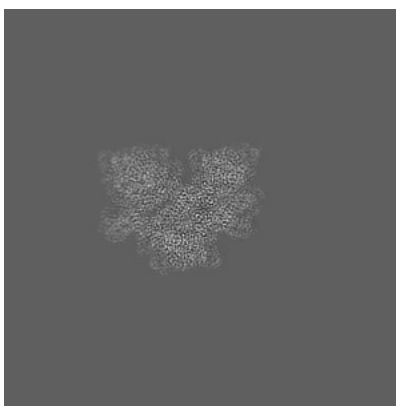
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

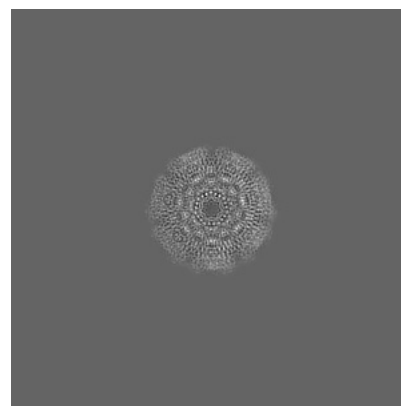
6.1.1 Primary map



X

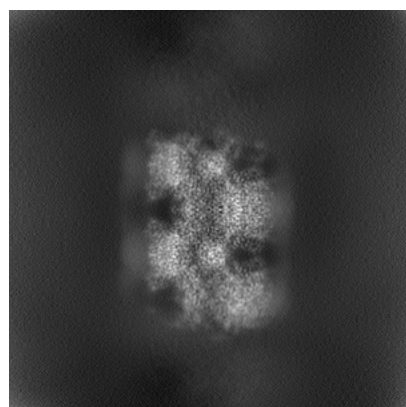


Y

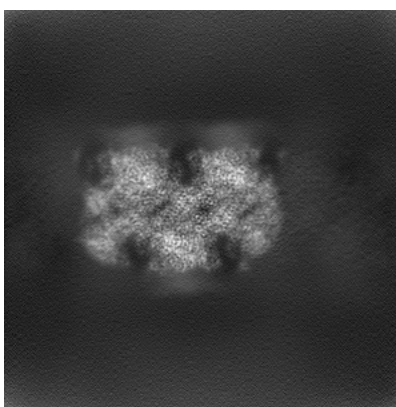


Z

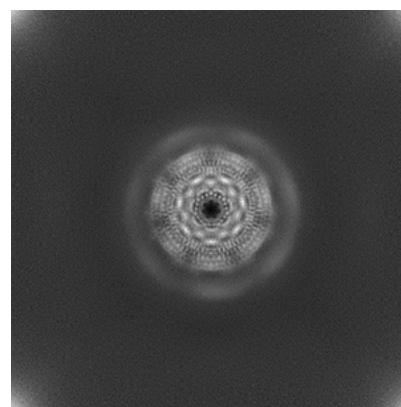
6.1.2 Raw map



X



Y



Z

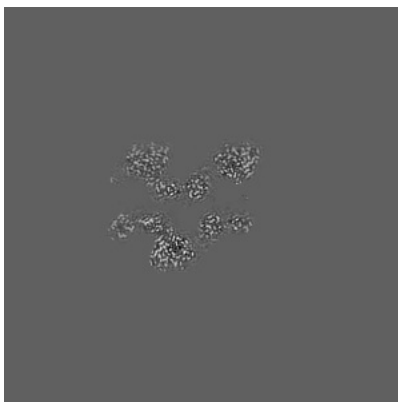
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

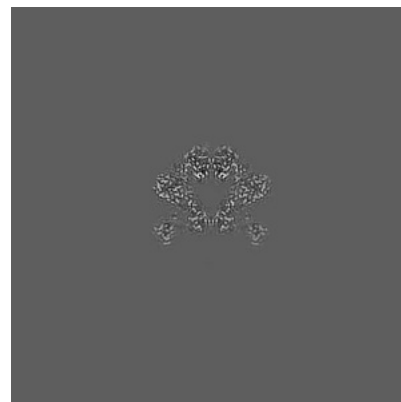
6.2.1 Primary map



X Index: 256

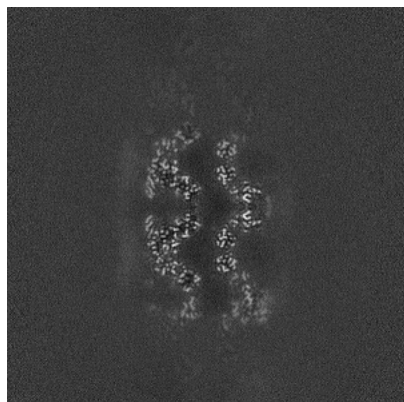


Y Index: 256

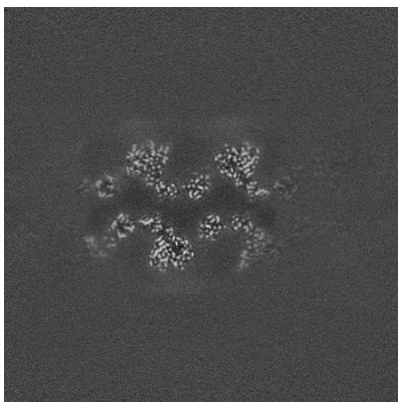


Z Index: 256

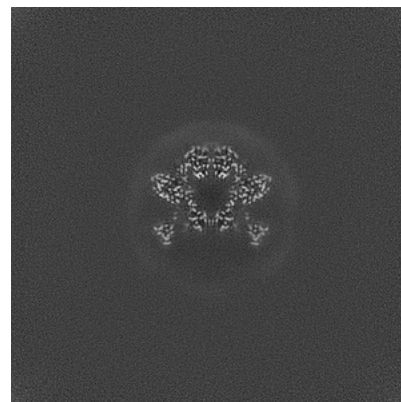
6.2.2 Raw map



X Index: 256



Y Index: 256



Z Index: 256

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

6.3 Largest variance slices [i](#)

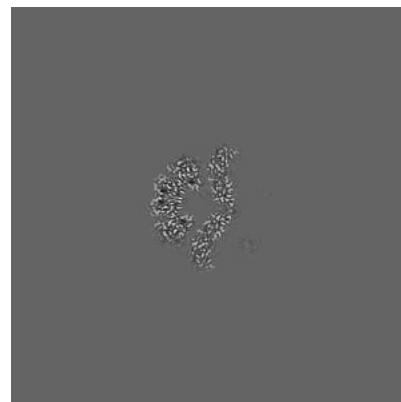
6.3.1 Primary map



X Index: 239

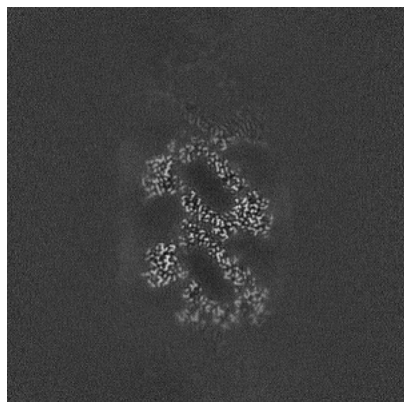


Y Index: 280

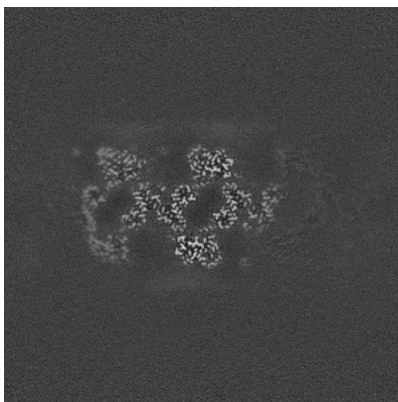


Z Index: 231

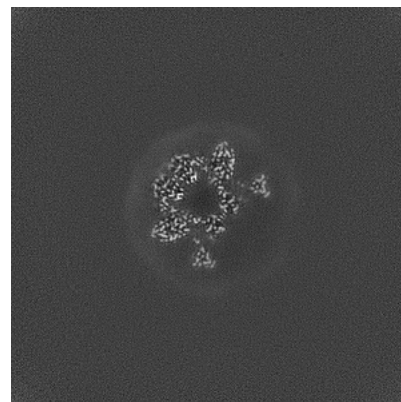
6.3.2 Raw map



X Index: 272



Y Index: 280

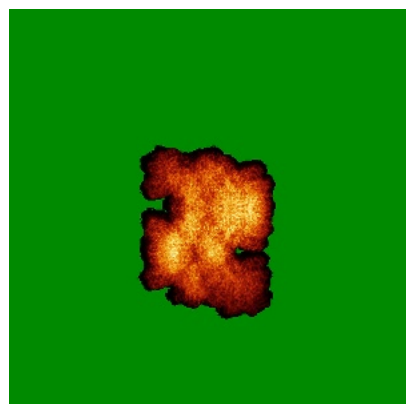


Z Index: 239

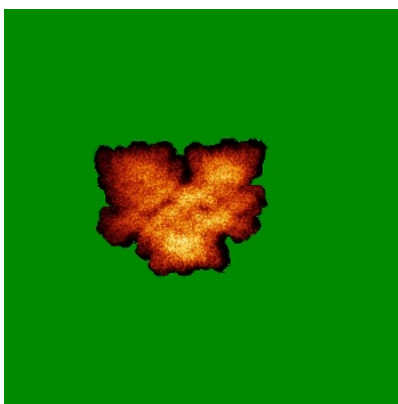
The images above show the largest variance slices of the map in three orthogonal directions.

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

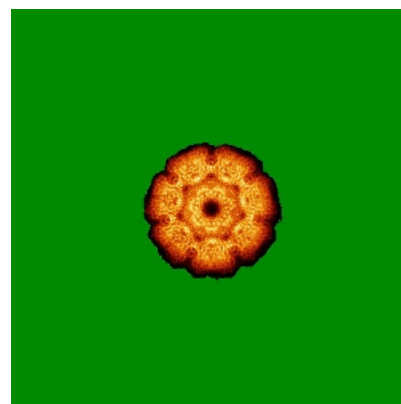
6.4.1 Primary map



X

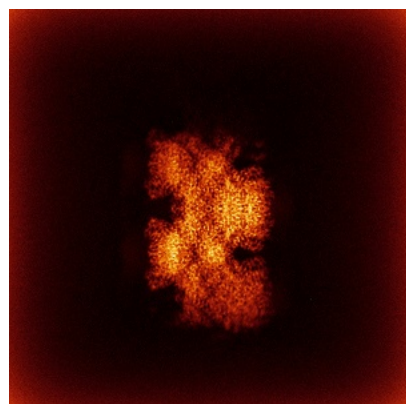


Y

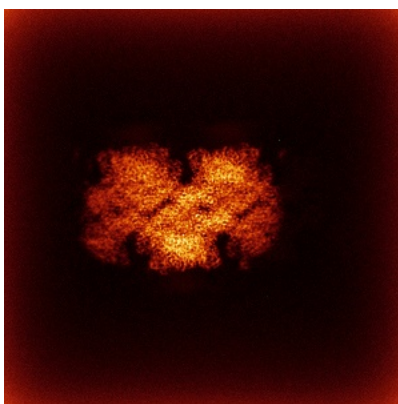


Z

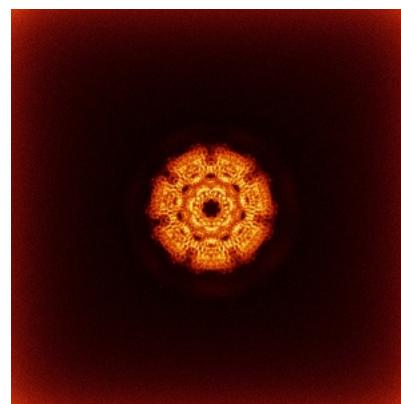
6.4.2 Raw map



X



Y

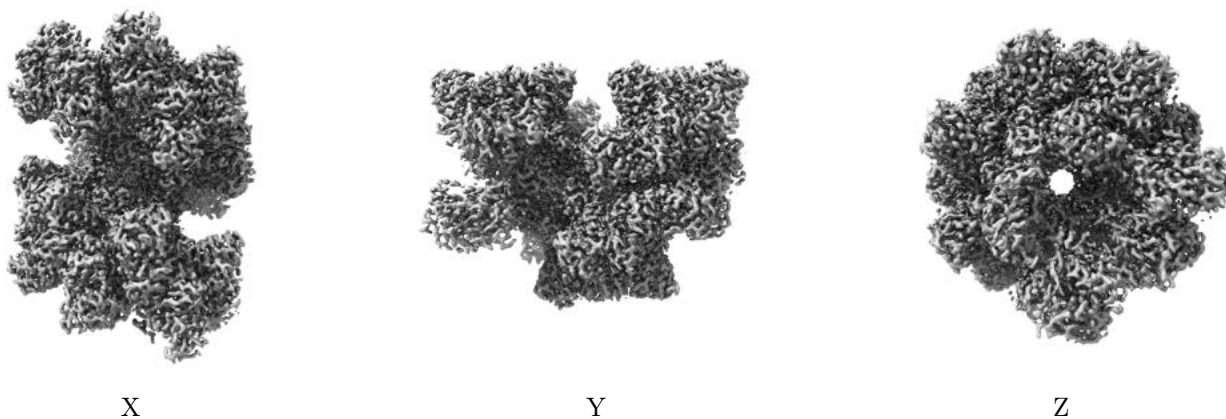


Z

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

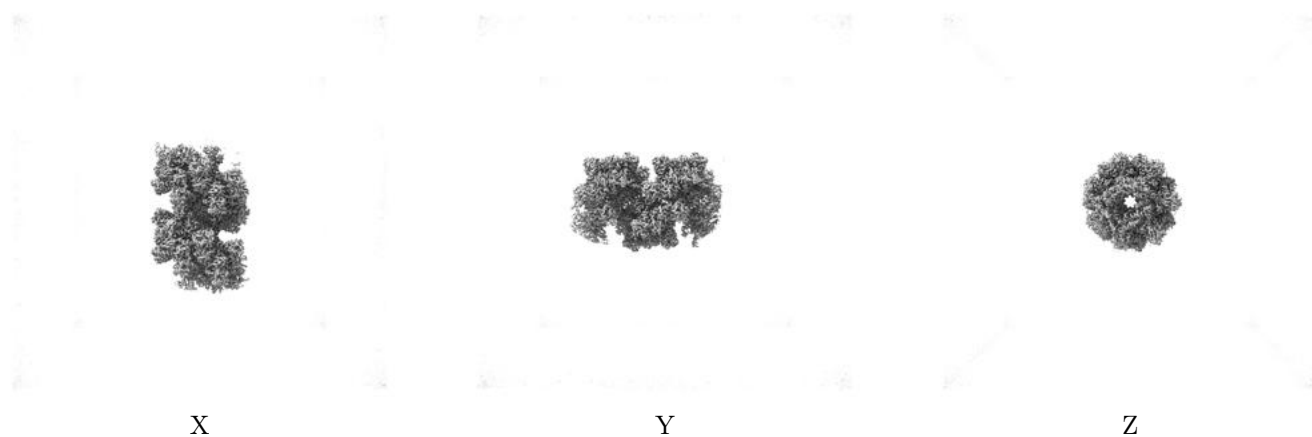
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.22. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

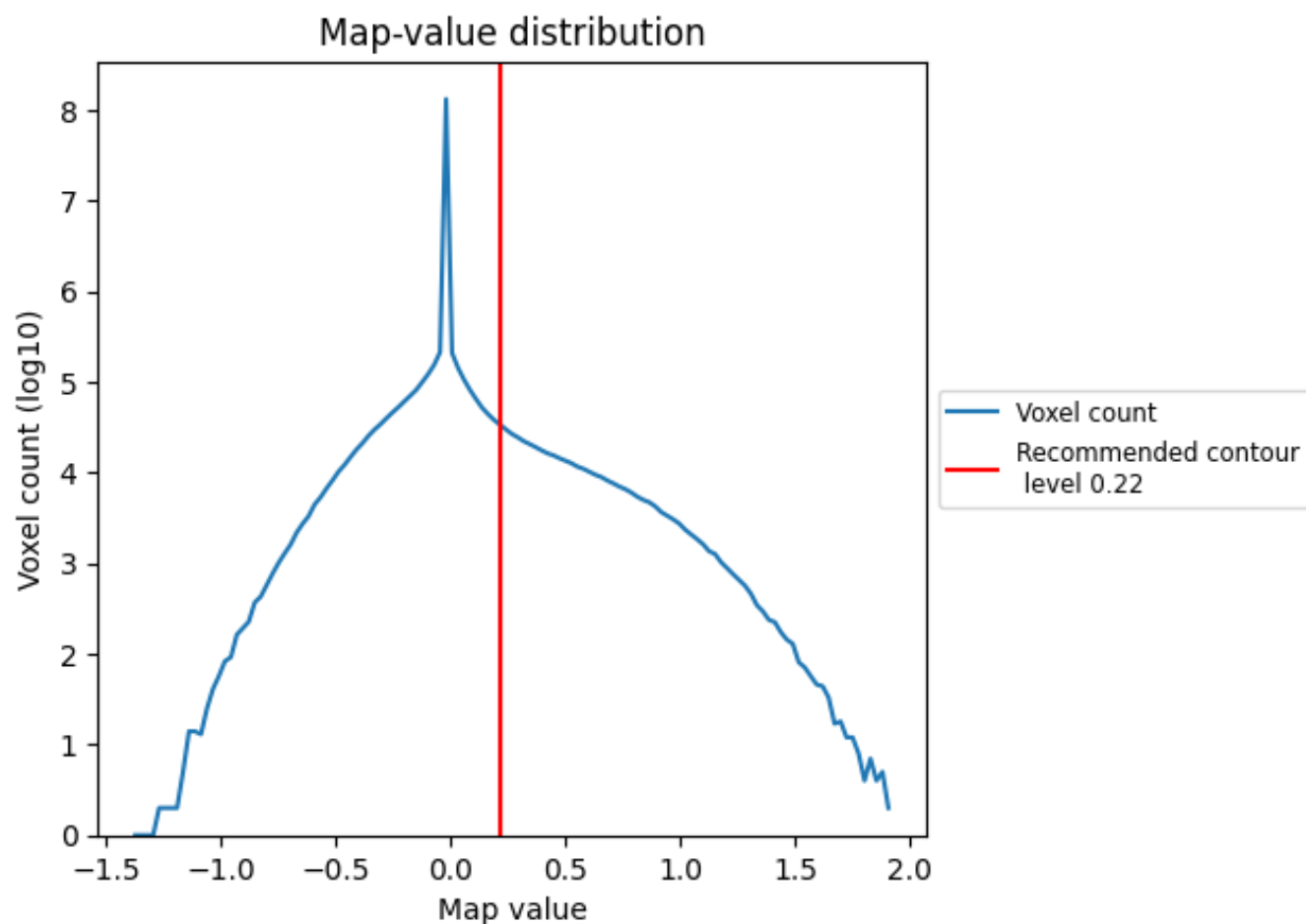
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

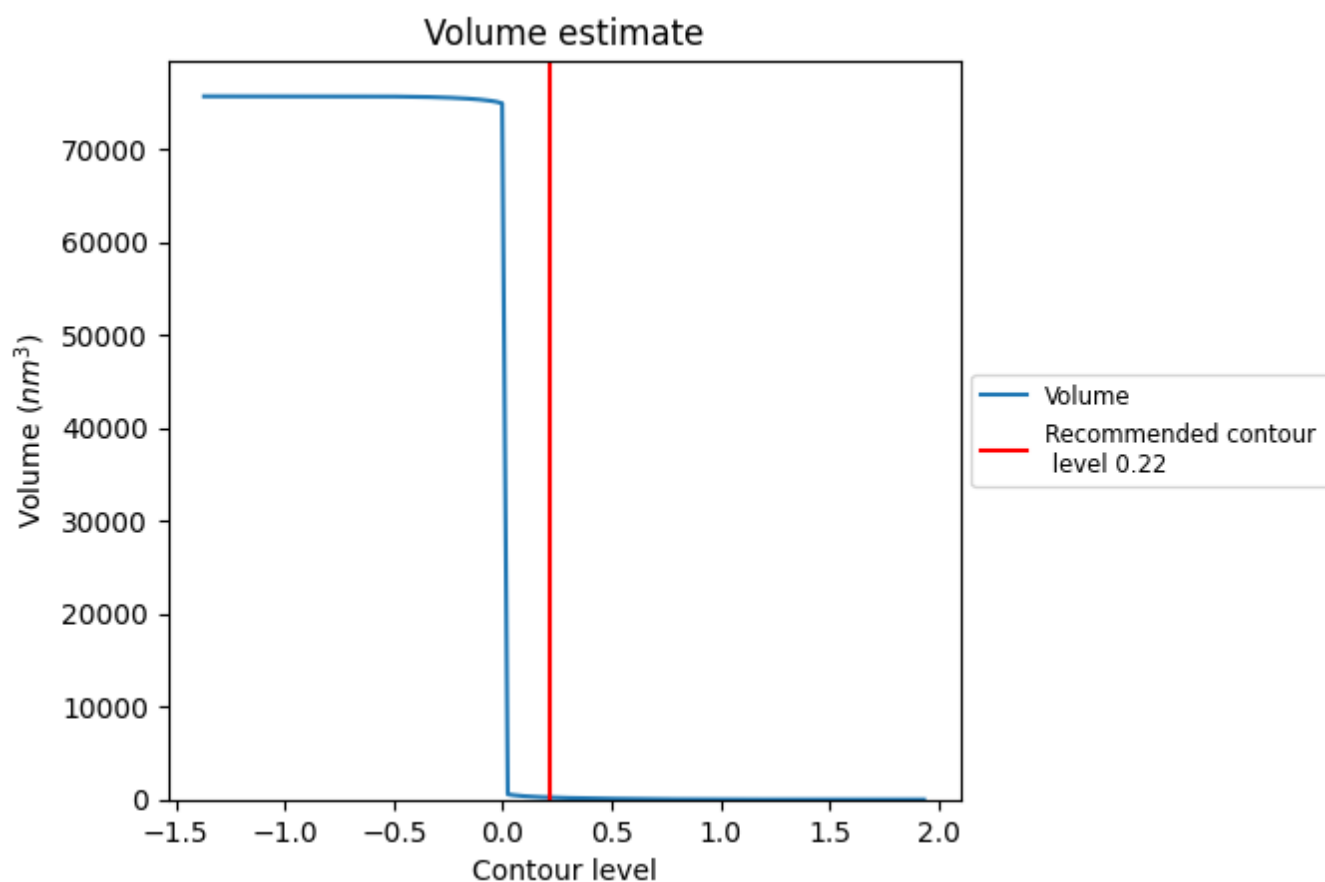
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

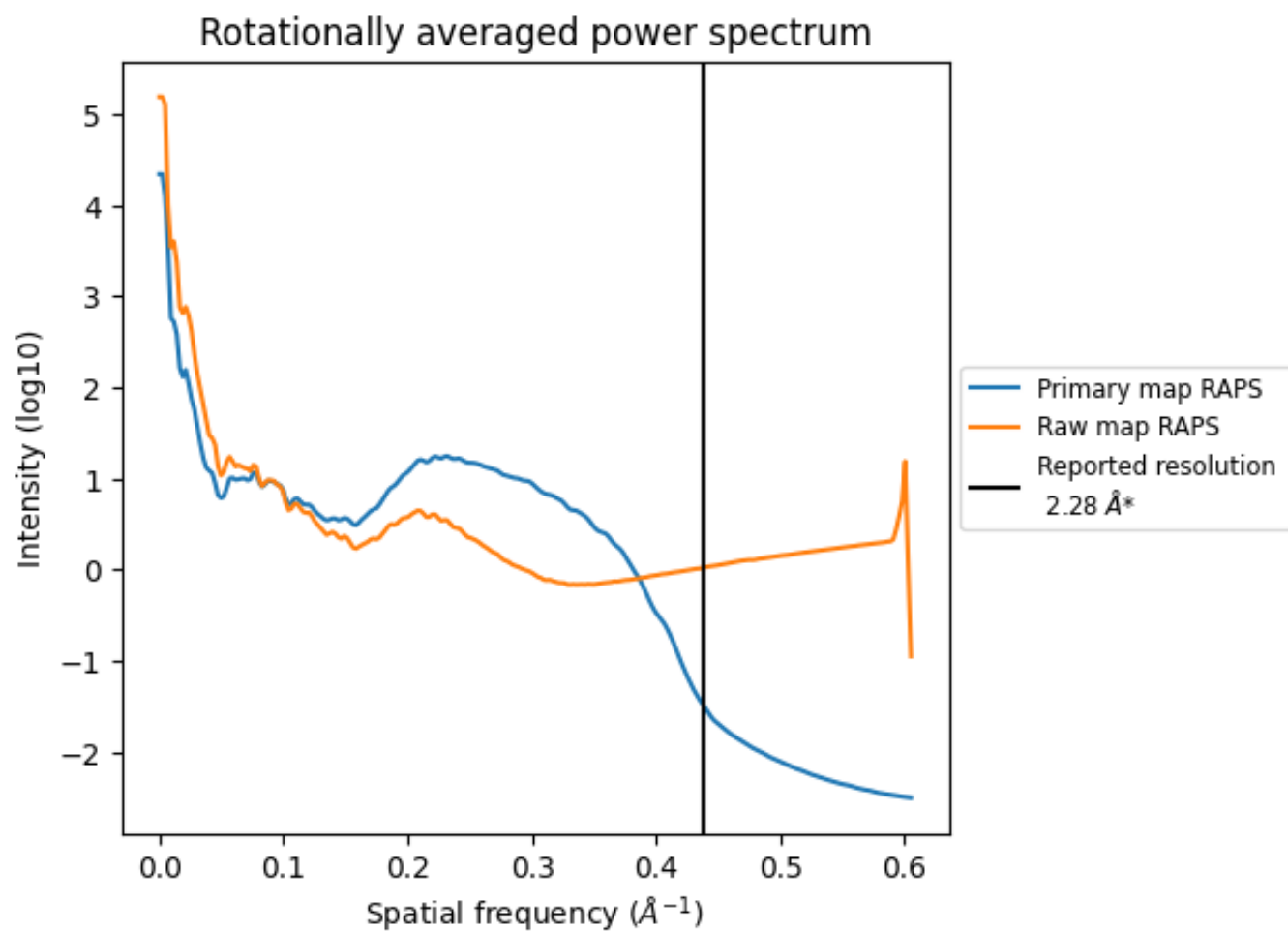
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 224 nm^3 ; this corresponds to an approximate mass of 203 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 ⓘ

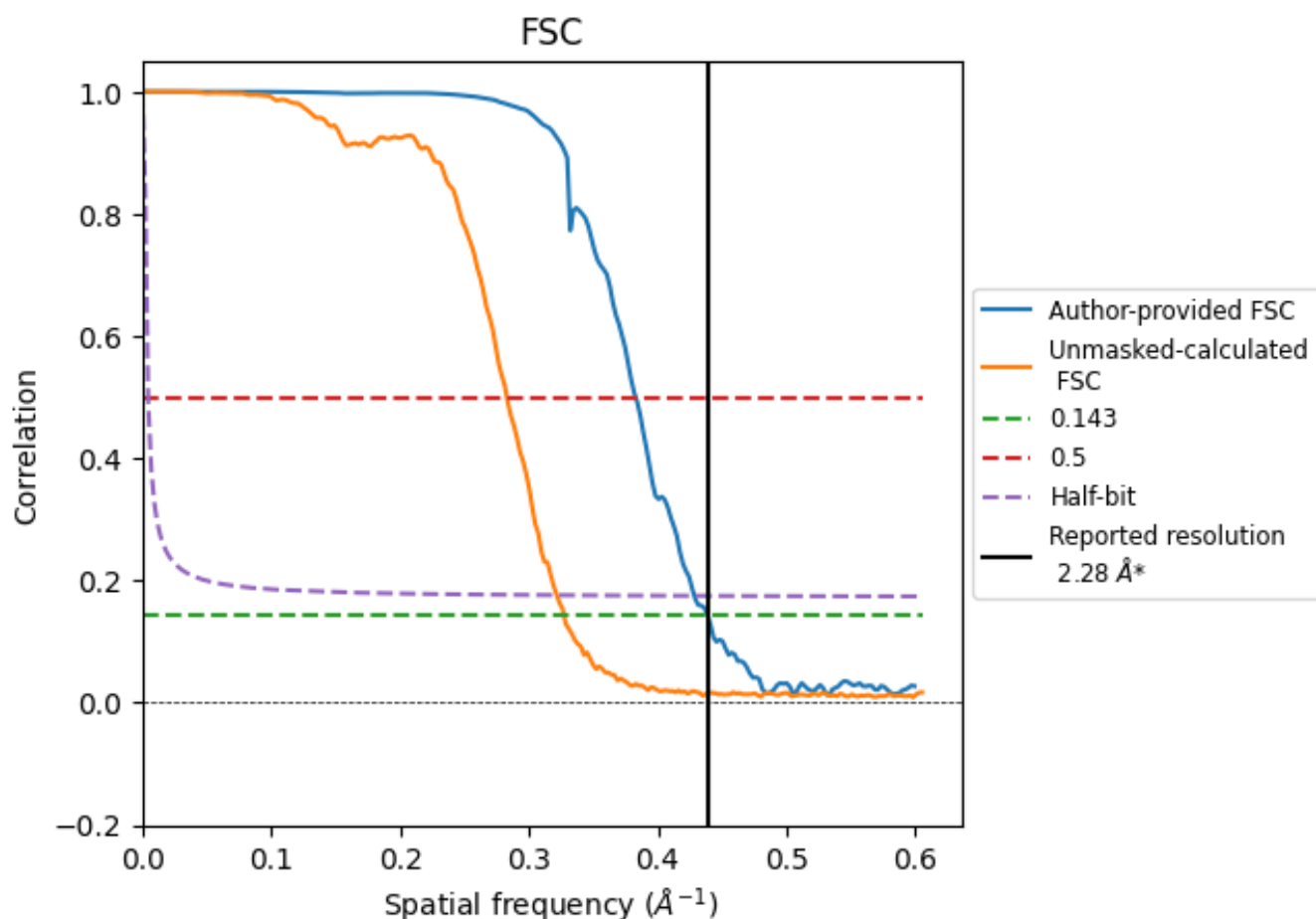


*Reported resolution corresponds to spatial frequency of 0.439 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.439 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

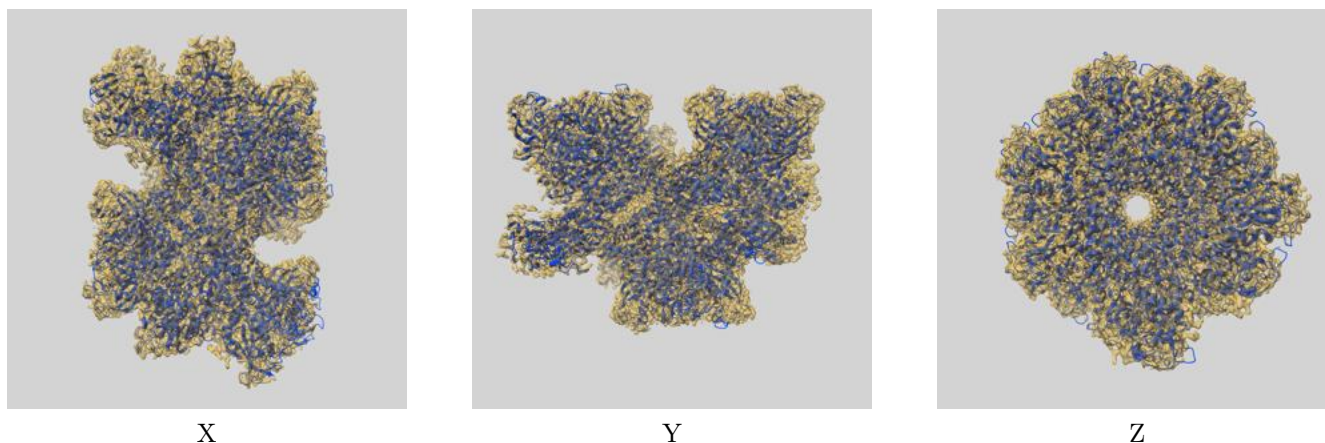
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.28	-	-
Author-provided FSC curve	2.28	2.61	2.33
Unmasked-calculated*	3.06	3.53	3.11

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.06 differs from the reported value 2.28 by more than 10 %

9 Map-model fit [i](#)

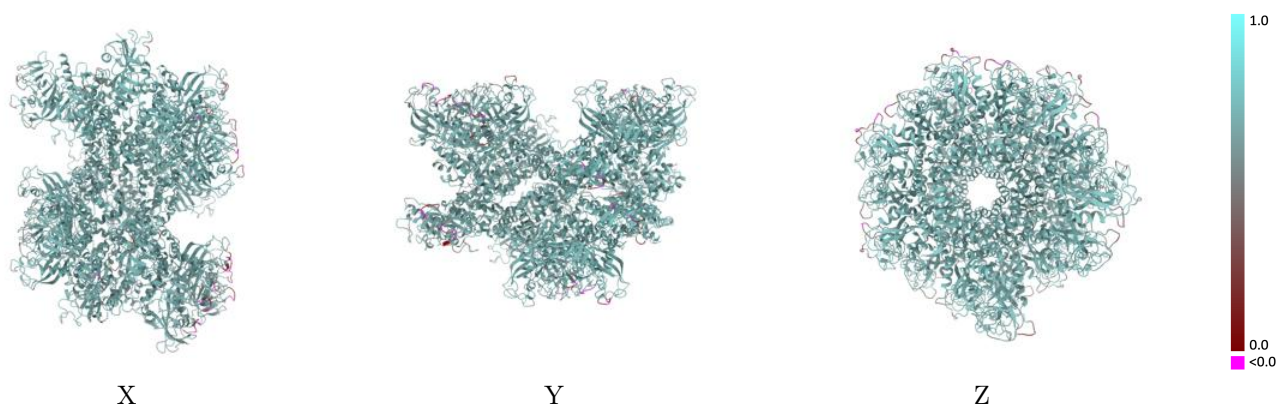
This section contains information regarding the fit between EMDB map EMD-43738 and PDB model 8W23. Per-residue inclusion information can be found in section 3 on page 31.

9.1 Map-model overlay [i](#)



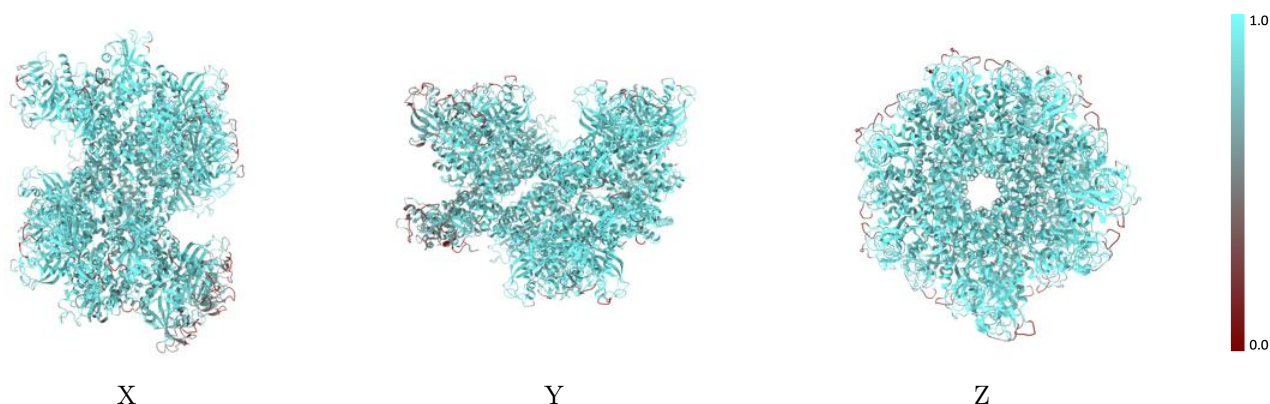
The images above show the 3D surface view of the map at the recommended contour level 0.22 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



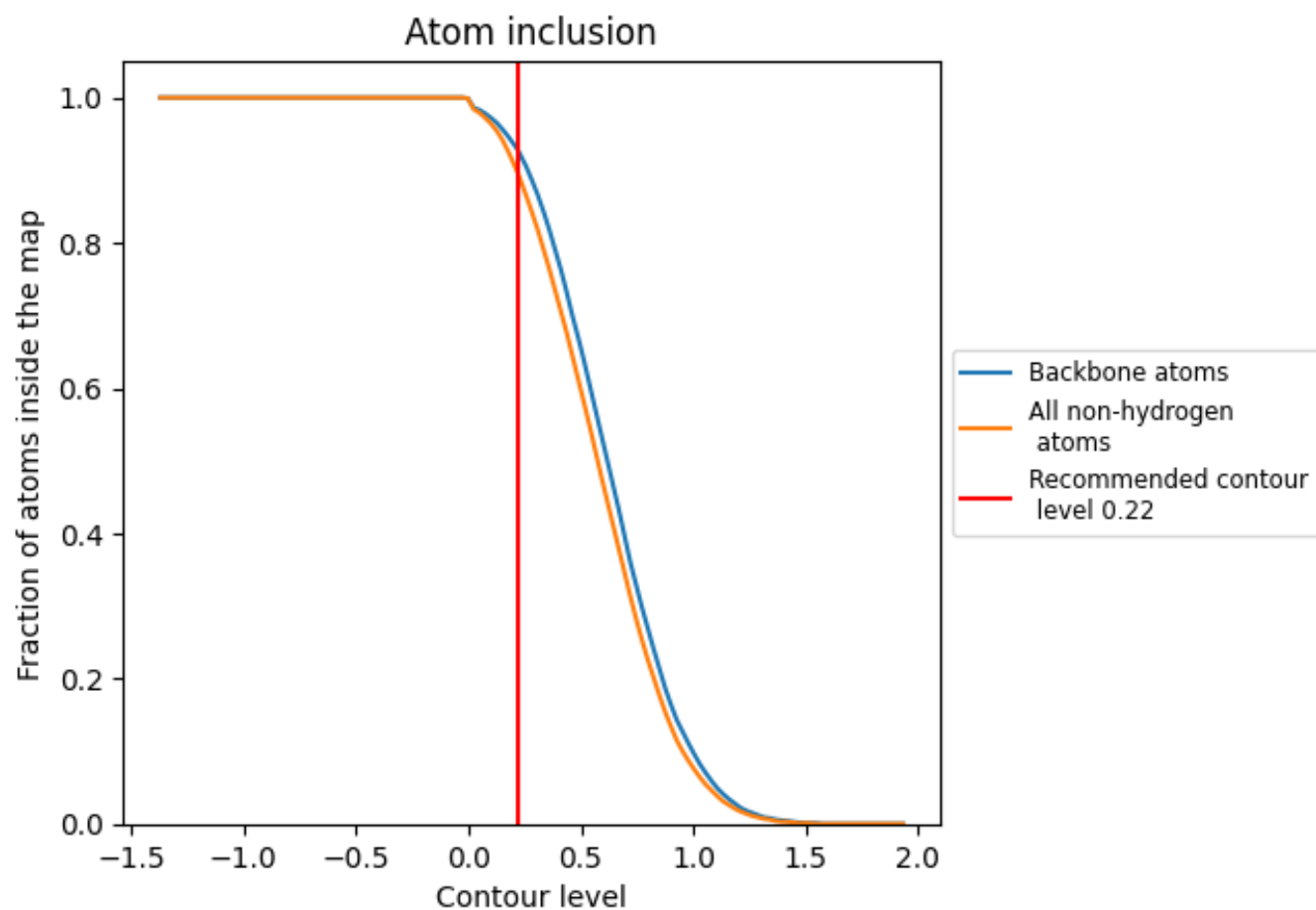
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.22).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.22) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8960	 0.6690
A	 0.8110	 0.6340
B	 0.8820	 0.6640
C	 0.9200	 0.6820
D	 0.9390	 0.6900
E	 0.9380	 0.6850
F	 0.9300	 0.6790
G	 0.9280	 0.6780
H	 0.9210	 0.6780
I	 0.9150	 0.6730
K	 0.8800	 0.6580
L	 0.9210	 0.6810
M	 0.9390	 0.6860
N	 0.9370	 0.6830
O	 0.9420	 0.6850
P	 0.9510	 0.6900
Q	 0.9340	 0.6830
R	 0.9210	 0.6780
S	 0.8760	 0.6570
T	 0.7700	 0.6260
U	 0.6720	 0.6030

