



Full wwPDB EM Validation Report ⓘ

Mar 12, 2026 – 09:29 AM UTC

PDB ID : 6O72 / pdb_00006o72
EMDB ID : EMD-0638
Title : Structure of the TRPM8 cold receptor by single particle electron cryo-microscopy, TC-I 2014-bound state
Authors : Diver, M.M.; Cheng, Y.; Julius, D.
Deposited on : 2019-03-07
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

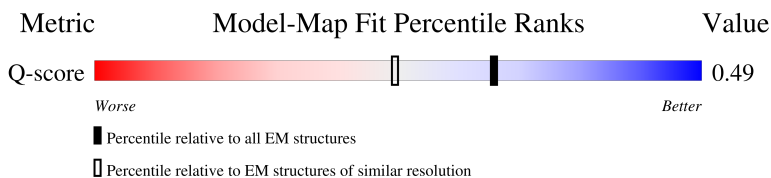
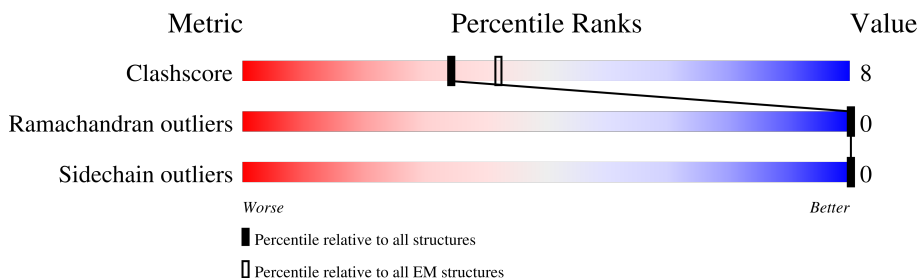
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.00 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	14081 (2.50 - 3.50)

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	1098	<p>6% (red), 64% (green), 14% (yellow), 22% (grey)</p>
1	B	1098	<p>6% (red), 64% (green), 14% (yellow), 22% (grey)</p>
1	C	1098	<p>6% (red), 64% (green), 14% (yellow), 22% (grey)</p>
1	D	1098	<p>6% (red), 63% (green), 14% (yellow), 22% (grey)</p>

2 Entry composition [i](#)

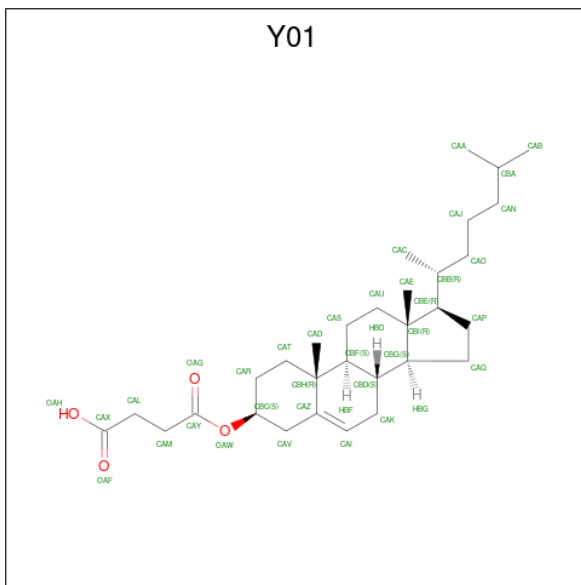
There are 6 unique types of molecules in this entry. The entry contains 28592 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Transient receptor potential cation channel subfamily M member 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	858	Total 7019	C 4591	N 1147	O 1244	S 37	0	0
1	B	858	Total 7019	C 4591	N 1147	O 1244	S 37	0	0
1	C	858	Total 7019	C 4591	N 1147	O 1244	S 37	0	0
1	D	858	Total 7019	C 4591	N 1147	O 1244	S 37	0	0

- Molecule 2 is CHOLESTEROL HEMISUCCINATE (CCD ID: Y01) (formula: C₃₁H₅₀O₄).



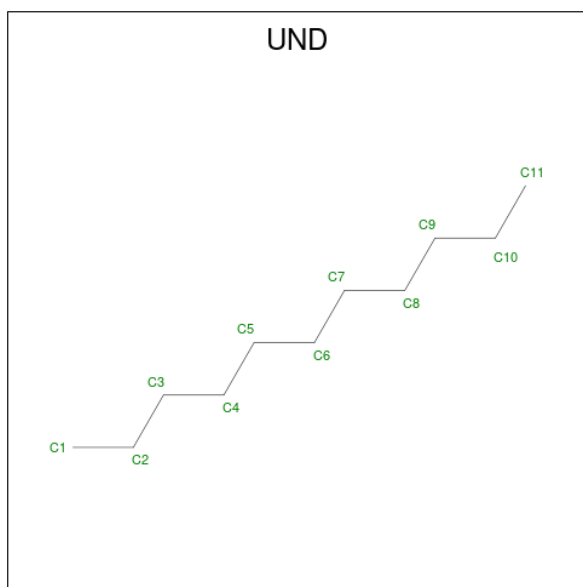
Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
2	A	1	Total 35	C 31	O 4	0
2	B	1	Total 35	C 31	O 4	0

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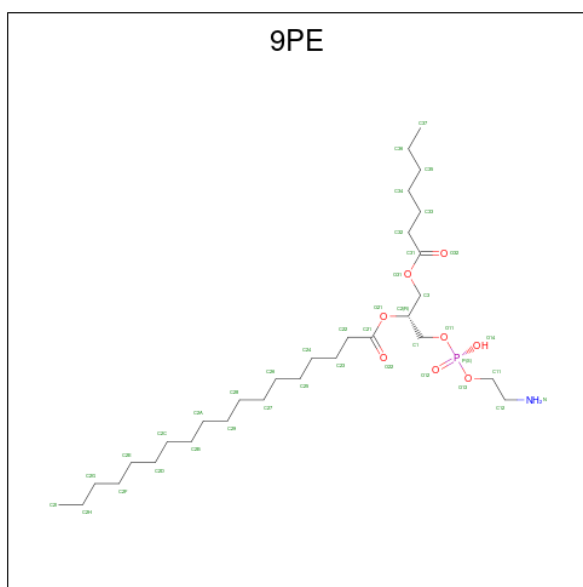
Mol	Chain	Residues	Atoms			AltConf
2	C	1	Total	C	O	0
			35	31	4	
2	D	1	Total	C	O	0
			35	31	4	

- Molecule 3 is UNDECANE (CCD ID: UND) (formula: C₁₁H₂₄).



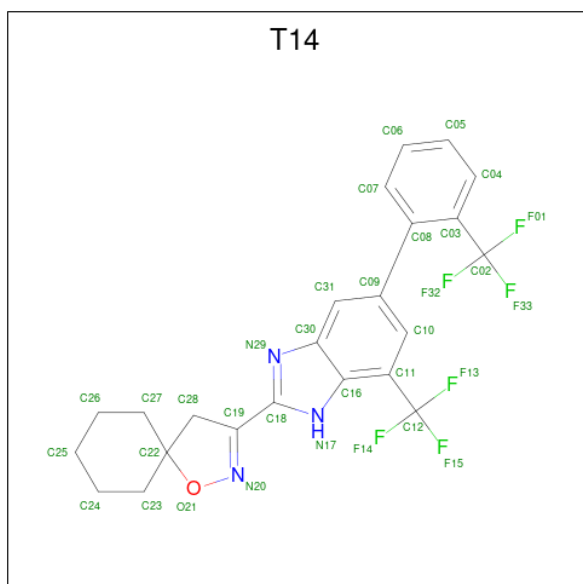
Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	C	0
			11	11	
3	A	1	Total	C	0
			11	11	
3	A	1	Total	C	0
			11	11	
3	B	1	Total	C	0
			11	11	
3	C	1	Total	C	0
			11	11	
3	C	1	Total	C	0
			11	11	
3	D	1	Total	C	0
			11	11	
3	D	1	Total	C	0
			11	11	

- Molecule 4 is (1R)-2-[[[(S)-(2-aminoethoxy)(hydroxy)phosphoryl]oxy]-1-[(heptanoyloxy)methyl]ethyl octadecanoate (CCD ID: 9PE) (formula: C₃₀H₆₀NO₈P).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
4	A	1	Total	C	N	O	P	0
			37	27	1	8	1	
4	B	1	Total	C	N	O	P	0
			37	27	1	8	1	
4	C	1	Total	C	N	O	P	0
			37	27	1	8	1	
4	D	1	Total	C	N	O	P	0
			37	27	1	8	1	

- Molecule 5 is 3-{7-(trifluoromethyl)-5-[2-(trifluoromethyl)phenyl]-1H-benzimidazol-2-yl}-1-oxa-2-azaspiro[4.5]dec-2-ene (CCD ID: T14) (formula: $C_{23}H_{19}F_6N_3O$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
5	A	1	Total	C	F	N	O	0
			33	23	6	3	1	
5	B	1	Total	C	F	N	O	0
			33	23	6	3	1	
5	C	1	Total	C	F	N	O	0
			33	23	6	3	1	
5	D	1	Total	C	F	N	O	0
			33	23	6	3	1	

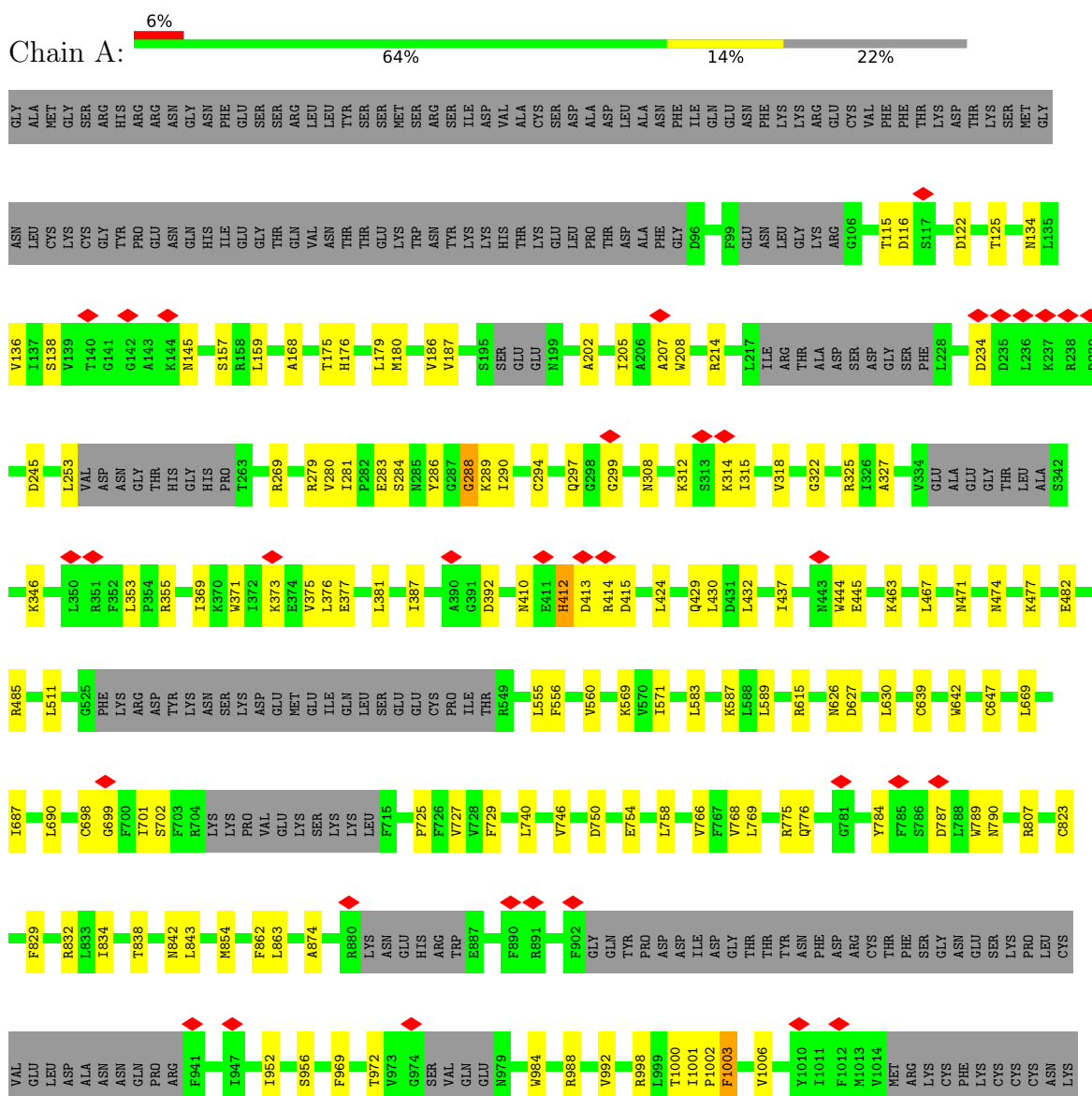
- Molecule 6 is SODIUM ION (CCD ID: NA) (formula: Na).

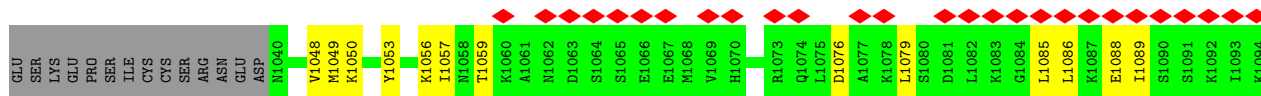
Mol	Chain	Residues	Atoms		AltConf
6	A	2	Total	Na	0
			2	2	
6	B	2	Total	Na	0
			2	2	
6	C	2	Total	Na	0
			2	2	
6	D	2	Total	Na	0
			2	2	

3 Residue-property plots [i](#)

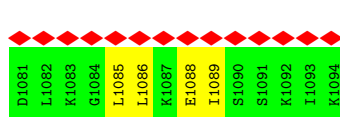
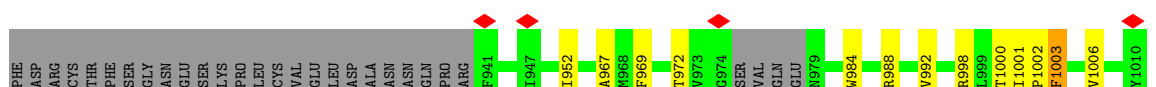
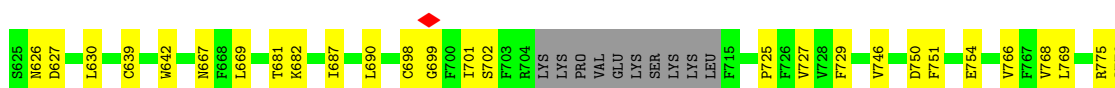
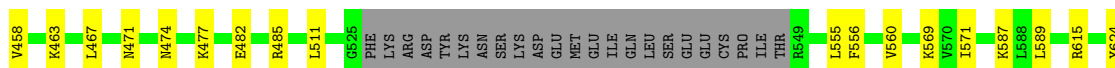
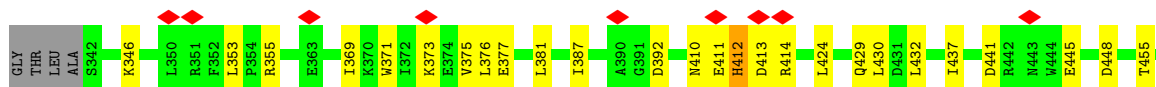
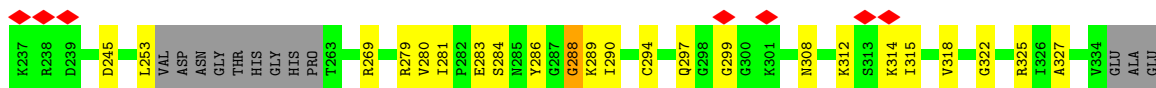
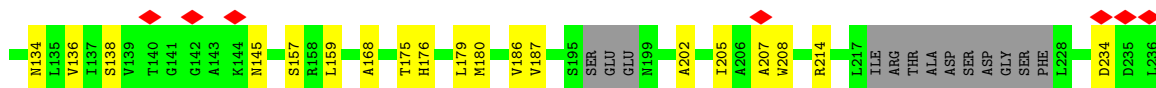
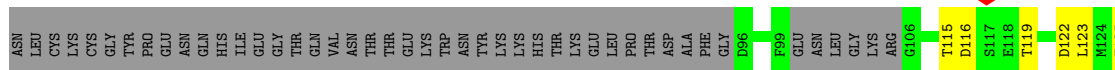
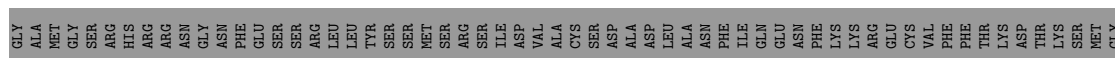
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: Transient receptor potential cation channel subfamily M member 8



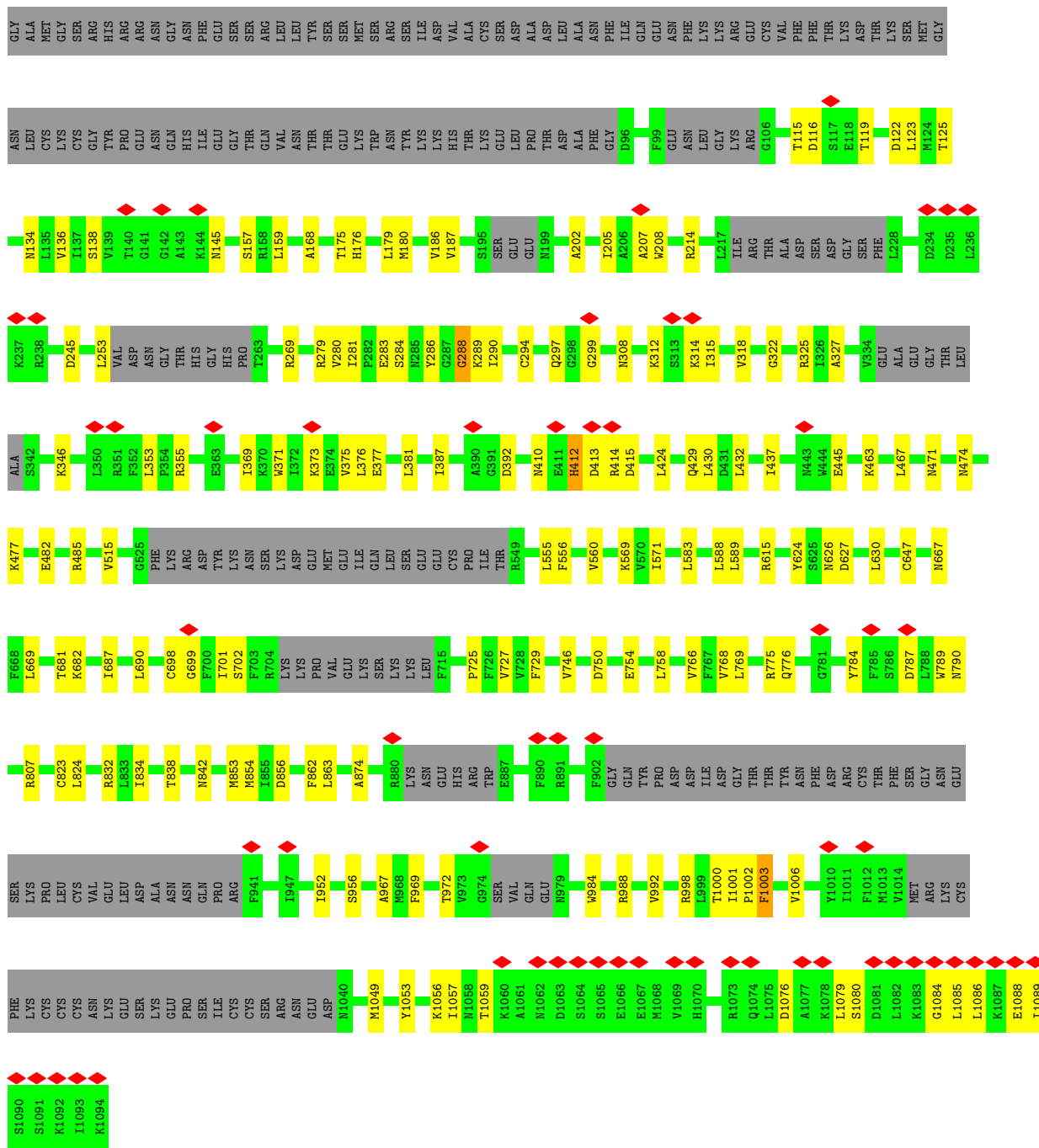


• Molecule 1: Transient receptor potential cation channel subfamily M member 8

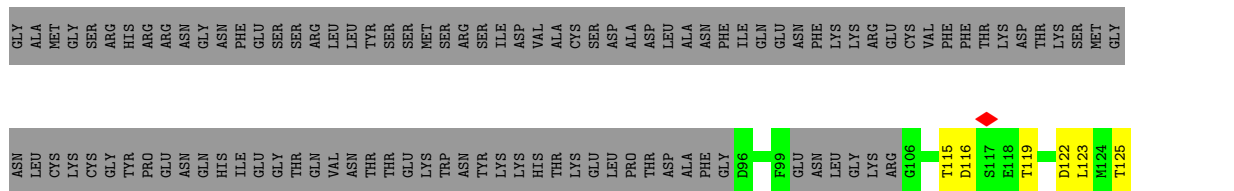


• Molecule 1: Transient receptor potential cation channel subfamily M member 8





• Molecule 1: Transient receptor potential cation channel subfamily M member 8



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	59569	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	70	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.225	Depositor
Minimum map value	-0.146	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.025	Depositor
Map size (Å)	338.88, 338.88, 338.88	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.059, 1.059, 1.059	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NA, T14, Y01, 9PE, UND

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	0.27	0/7178	0.64	8/9705 (0.1%)
1	B	0.27	0/7178	0.64	8/9705 (0.1%)
1	C	0.27	0/7178	0.64	8/9705 (0.1%)
1	D	0.27	0/7178	0.64	8/9705 (0.1%)
All	All	0.27	0/28712	0.64	32/38820 (0.1%)

There are no bond length outliers.

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1003	PHE	CA-C-N	-11.22	108.20	119.87
1	B	1003	PHE	C-N-CA	-11.22	108.20	119.87
1	A	1003	PHE	CA-C-N	-11.20	108.22	119.87
1	A	1003	PHE	C-N-CA	-11.20	108.22	119.87
1	C	1003	PHE	CA-C-N	-11.19	108.23	119.87
1	C	1003	PHE	C-N-CA	-11.19	108.23	119.87
1	D	1003	PHE	CA-C-N	-11.18	108.25	119.87
1	D	1003	PHE	C-N-CA	-11.18	108.25	119.87
1	B	412	HIS	N-CA-C	-10.56	99.93	112.92
1	C	412	HIS	N-CA-C	-10.56	99.93	112.92
1	A	412	HIS	N-CA-C	-10.55	99.94	112.92
1	D	412	HIS	N-CA-C	-10.54	99.95	112.92
1	D	288	GLY	N-CA-C	-8.09	95.97	110.86
1	A	288	GLY	N-CA-C	-8.08	96.00	110.86
1	C	288	GLY	N-CA-C	-8.07	96.01	110.86
1	B	288	GLY	N-CA-C	-8.07	96.02	110.86
1	C	392	ASP	CA-C-N	5.93	132.87	121.54
1	C	392	ASP	C-N-CA	5.93	132.87	121.54
1	D	392	ASP	CA-C-N	5.93	132.87	121.54
1	D	392	ASP	C-N-CA	5.93	132.87	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	392	ASP	CA-C-N	5.93	132.86	121.54
1	A	392	ASP	C-N-CA	5.93	132.86	121.54
1	B	392	ASP	CA-C-N	5.92	132.86	121.54
1	B	392	ASP	C-N-CA	5.92	132.86	121.54
1	A	207	ALA	CA-C-N	5.52	132.09	121.54
1	A	207	ALA	C-N-CA	5.52	132.09	121.54
1	C	207	ALA	CA-C-N	5.52	132.07	121.54
1	C	207	ALA	C-N-CA	5.52	132.07	121.54
1	B	207	ALA	CA-C-N	5.51	132.06	121.54
1	B	207	ALA	C-N-CA	5.51	132.06	121.54
1	D	207	ALA	CA-C-N	5.50	132.04	121.54
1	D	207	ALA	C-N-CA	5.50	132.04	121.54

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	7019	0	7057	111	0
1	B	7019	0	7057	113	0
1	C	7019	0	7057	110	0
1	D	7019	0	7057	113	0
2	A	35	0	48	13	0
2	B	35	0	48	11	0
2	C	35	0	48	14	0
2	D	35	0	48	13	0
3	A	33	0	72	0	0
3	B	11	0	24	0	0
3	C	22	0	48	0	0
3	D	22	0	48	0	0
4	A	37	0	50	10	0
4	B	37	0	50	10	0
4	C	37	0	50	10	0
4	D	37	0	50	10	0
5	A	33	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	33	0	0	1	0
5	C	33	0	0	1	0
5	D	33	0	0	1	0
6	A	2	0	0	0	0
6	B	2	0	0	0	0
6	C	2	0	0	0	0
6	D	2	0	0	0	0
All	All	28592	0	28812	465	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 8.

All (465) 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:C:315:ILE:CG2	1:C:381:LEU:HD11	1.57	1.35
1:B:315:ILE:CG2	1:B:381:LEU:HD11	1.57	1.34
1:D:315:ILE:CG2	1:D:381:LEU:HD11	1.57	1.33
1:A:315:ILE:CG2	1:A:381:LEU:HD11	1.57	1.31
1:A:315:ILE:HG23	1:A:381:LEU:CD1	1.66	1.26
1:B:315:ILE:HG23	1:B:381:LEU:CD1	1.66	1.26
1:D:315:ILE:HG23	1:D:381:LEU:CD1	1.66	1.25
1:C:315:ILE:HG23	1:C:381:LEU:CD1	1.66	1.25
2:A:1301:Y01:CAV	4:A:1303:9PE:H1A	1.84	1.07
2:C:1301:Y01:CAV	4:C:1303:9PE:H1A	1.84	1.07
2:D:1301:Y01:CAV	4:D:1303:9PE:H1A	1.84	1.06
2:B:1301:Y01:CAV	4:B:1303:9PE:H1A	1.84	1.06
1:B:768:VAL:HG23	1:B:1003:PHE:CZ	1.97	1.00
1:D:768:VAL:HG23	1:D:1003:PHE:CZ	1.97	1.00
1:C:768:VAL:HG23	1:C:1003:PHE:CZ	1.97	1.00
1:A:768:VAL:HG23	1:A:1003:PHE:CZ	1.97	1.00
1:C:315:ILE:HG23	1:C:381:LEU:HD11	0.95	0.94
2:B:1301:Y01:HAV1	4:B:1303:9PE:H1A	1.50	0.93
1:B:315:ILE:HG23	1:B:381:LEU:HD11	0.95	0.93
1:D:315:ILE:HG23	1:D:381:LEU:HD11	0.95	0.93
2:C:1301:Y01:HAV1	4:C:1303:9PE:H1A	1.50	0.93
2:D:1301:Y01:HAV1	4:D:1303:9PE:H1A	1.50	0.92
1:A:315:ILE:HG23	1:A:381:LEU:HD11	0.95	0.92
2:A:1301:Y01:HAV1	4:A:1303:9PE:H1A	1.50	0.91
1:D:701:ILE:HG22	1:D:702:SER:H	1.36	0.91
1:B:701:ILE:HG22	1:B:702:SER:H	1.36	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:701:ILE:HG22	1:C:702:SER:H	1.36	0.90
1:A:701:ILE:HG22	1:A:702:SER:H	1.36	0.89
1:A:315:ILE:HG22	1:A:315:ILE:O	1.75	0.87
1:D:315:ILE:O	1:D:315:ILE:HG22	1.75	0.87
1:C:315:ILE:HG22	1:C:315:ILE:O	1.75	0.86
1:B:315:ILE:O	1:B:315:ILE:HG22	1.75	0.85
2:B:1301:Y01:HAV2	4:B:1303:9PE:H1A	1.63	0.79
2:C:1301:Y01:HAV2	4:C:1303:9PE:H1A	1.63	0.78
2:D:1301:Y01:HAV2	4:D:1303:9PE:H1A	1.64	0.78
2:A:1301:Y01:HAV2	4:A:1303:9PE:H1A	1.63	0.77
1:A:862:PHE:HZ	4:B:1303:9PE:H29	1.47	0.77
1:D:315:ILE:CG2	1:D:381:LEU:CD1	2.44	0.77
1:C:862:PHE:HZ	4:D:1303:9PE:H29	1.50	0.76
1:B:862:PHE:HZ	4:C:1303:9PE:H29	1.49	0.75
1:B:701:ILE:HG22	1:B:702:SER:N	2.02	0.75
1:C:701:ILE:HG22	1:C:702:SER:N	2.02	0.74
1:D:286:TYR:O	1:D:288:GLY:O	2.06	0.74
1:A:286:TYR:O	1:A:288:GLY:O	2.06	0.74
1:A:701:ILE:HG22	1:A:702:SER:N	2.02	0.73
2:C:1301:Y01:HAV1	4:C:1303:9PE:C1	2.19	0.73
2:D:1301:Y01:HAV1	4:D:1303:9PE:C1	2.19	0.73
1:B:286:TYR:O	1:B:288:GLY:O	2.06	0.72
1:C:286:TYR:O	1:C:288:GLY:O	2.06	0.72
4:A:1303:9PE:H29	1:D:862:PHE:HZ	1.53	0.72
2:A:1301:Y01:HAV1	4:A:1303:9PE:C1	2.19	0.71
1:B:701:ILE:CG2	1:B:702:SER:H	2.03	0.71
1:C:701:ILE:CG2	1:C:702:SER:H	2.03	0.71
2:B:1301:Y01:HAV1	4:B:1303:9PE:C1	2.19	0.70
1:D:701:ILE:CG2	1:D:702:SER:H	2.03	0.70
1:A:701:ILE:CG2	1:A:702:SER:H	2.03	0.68
1:A:315:ILE:CG2	1:A:381:LEU:CD1	2.44	0.67
1:D:701:ILE:HG22	1:D:702:SER:N	2.02	0.66
4:D:1303:9PE:O32	4:D:1303:9PE:H34A	1.95	0.66
4:A:1303:9PE:O32	4:A:1303:9PE:H34A	1.95	0.66
1:C:862:PHE:CZ	4:D:1303:9PE:H29	2.30	0.66
4:C:1303:9PE:H34A	4:C:1303:9PE:O32	1.95	0.65
1:B:862:PHE:CZ	4:C:1303:9PE:H29	2.30	0.65
1:B:315:ILE:CG2	1:B:381:LEU:CD1	2.44	0.65
1:C:315:ILE:CG2	1:C:381:LEU:CD1	2.44	0.65
1:A:862:PHE:CZ	4:B:1303:9PE:H29	2.29	0.65
4:B:1303:9PE:O32	4:B:1303:9PE:H34A	1.95	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1303:9PE:H29	1:D:862:PHE:CZ	2.32	0.64
1:A:410:ASN:OD1	1:A:412:HIS:HB2	2.00	0.61
1:D:410:ASN:OD1	1:D:412:HIS:HB2	2.00	0.61
1:C:410:ASN:OD1	1:C:412:HIS:HB2	2.00	0.61
1:C:1001:ILE:HG23	1:C:1002:PRO:HD2	1.83	0.61
1:A:410:ASN:ND2	1:A:412:HIS:HD2	1.99	0.60
1:B:1001:ILE:HG23	1:B:1002:PRO:HD2	1.83	0.60
1:B:410:ASN:OD1	1:B:412:HIS:HB2	2.00	0.60
1:D:322:GLY:O	1:D:387:ILE:HD11	2.02	0.60
1:D:1001:ILE:HG23	1:D:1002:PRO:HD2	1.83	0.60
1:D:410:ASN:ND2	1:D:412:HIS:HD2	1.99	0.60
1:B:410:ASN:ND2	1:B:412:HIS:HD2	1.99	0.60
1:C:322:GLY:O	1:C:387:ILE:HD11	2.02	0.60
1:D:179:LEU:HD22	1:D:297:GLN:HE22	1.67	0.60
1:A:988:ARG:NH2	2:A:1301:Y01:OAF	2.33	0.60
1:C:179:LEU:HD22	1:C:297:GLN:HE22	1.67	0.59
1:A:322:GLY:O	1:A:387:ILE:HD11	2.02	0.59
1:A:626:ASN:ND2	1:A:1049:MET:SD	2.76	0.59
1:A:1001:ILE:HG23	1:A:1002:PRO:HD2	1.83	0.59
1:A:179:LEU:HD22	1:A:297:GLN:HE22	1.67	0.59
1:B:179:LEU:HD22	1:B:297:GLN:HE22	1.67	0.59
1:B:322:GLY:O	1:B:387:ILE:HD11	2.02	0.59
1:D:626:ASN:ND2	1:D:1049:MET:SD	2.76	0.59
1:C:410:ASN:ND2	1:C:412:HIS:HD2	1.99	0.59
1:D:208:TRP:HB2	1:D:253:LEU:HB3	1.85	0.59
1:C:988:ARG:NH2	2:C:1301:Y01:OAF	2.33	0.59
1:A:208:TRP:HB2	1:A:253:LEU:HB3	1.85	0.59
1:B:626:ASN:ND2	1:B:1049:MET:SD	2.76	0.59
1:C:626:ASN:ND2	1:C:1049:MET:SD	2.76	0.58
1:A:136:VAL:HG11	1:A:159:LEU:HD11	1.85	0.58
1:D:988:ARG:NH2	2:D:1301:Y01:OAF	2.33	0.58
1:C:208:TRP:HB2	1:C:253:LEU:HB3	1.85	0.58
1:B:988:ARG:NH2	2:B:1301:Y01:OAF	2.33	0.57
1:B:208:TRP:HB2	1:B:253:LEU:HB3	1.85	0.57
1:D:136:VAL:HG11	1:D:159:LEU:HD11	1.85	0.57
1:A:789:TRP:NE1	1:A:854:MET:SD	2.78	0.57
1:B:136:VAL:HG11	1:B:159:LEU:HD11	1.85	0.57
1:C:136:VAL:HG11	1:C:159:LEU:HD11	1.85	0.57
1:D:789:TRP:NE1	1:D:854:MET:SD	2.78	0.57
1:B:789:TRP:NE1	1:B:854:MET:SD	2.78	0.57
1:B:315:ILE:CG2	1:B:315:ILE:O	2.48	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:768:VAL:HG23	1:A:1003:PHE:HZ	1.67	0.56
1:D:729:PHE:HE2	2:D:1301:Y01:HAT2	1.71	0.56
1:A:729:PHE:HE2	2:A:1301:Y01:HAT2	1.71	0.56
1:C:789:TRP:NE1	1:C:854:MET:SD	2.78	0.56
1:B:729:PHE:HE2	2:B:1301:Y01:HAT2	1.71	0.55
1:A:556:PHE:O	1:A:560:VAL:HG23	2.07	0.55
1:B:556:PHE:O	1:B:560:VAL:HG23	2.07	0.55
1:C:729:PHE:HE2	2:C:1301:Y01:HAT2	1.71	0.55
1:D:556:PHE:O	1:D:560:VAL:HG23	2.06	0.55
1:A:746:VAL:HA	1:A:750:ASP:HB2	1.88	0.55
1:A:952:ILE:HG13	1:B:824:LEU:HD12	1.89	0.55
1:D:176:HIS:ND1	1:D:245:ASP:OD1	2.40	0.55
1:D:746:VAL:HA	1:D:750:ASP:HB2	1.88	0.55
1:C:315:ILE:CG2	1:C:315:ILE:O	2.48	0.55
1:C:746:VAL:HA	1:C:750:ASP:HB2	1.88	0.55
1:D:701:ILE:CG2	1:D:702:SER:N	2.67	0.55
1:D:138:SER:O	1:D:269:ARG:NH2	2.39	0.54
1:C:556:PHE:O	1:C:560:VAL:HG23	2.06	0.54
1:B:746:VAL:HA	1:B:750:ASP:HB2	1.88	0.54
2:C:1301:Y01:CAV	4:C:1303:9PE:C1	2.73	0.54
2:D:1301:Y01:CAV	4:D:1303:9PE:C1	2.73	0.54
1:B:138:SER:O	1:B:269:ARG:NH2	2.39	0.53
1:C:467:LEU:O	1:C:471:ASN:ND2	2.42	0.53
1:D:281:ILE:HG12	1:D:283:GLU:H	1.73	0.53
1:A:281:ILE:HG12	1:A:283:GLU:H	1.73	0.53
1:A:863:LEU:HD13	1:B:834:ILE:HG23	1.90	0.53
1:C:176:HIS:ND1	1:C:245:ASP:OD1	2.40	0.53
1:A:176:HIS:ND1	1:A:245:ASP:OD1	2.40	0.53
1:A:325:ARG:HB3	1:A:353:LEU:HB3	1.91	0.53
1:B:467:LEU:O	1:B:471:ASN:ND2	2.41	0.53
1:C:325:ARG:HB3	1:C:353:LEU:HB3	1.91	0.53
1:D:286:TYR:O	1:D:289:LYS:HB2	2.09	0.53
1:A:286:TYR:O	1:A:289:LYS:HB2	2.09	0.53
1:B:768:VAL:HG23	1:B:1003:PHE:HZ	1.67	0.53
1:B:325:ARG:HB3	1:B:353:LEU:HB3	1.91	0.53
1:C:138:SER:O	1:C:269:ARG:NH2	2.39	0.52
1:C:281:ILE:HG12	1:C:283:GLU:H	1.73	0.52
1:D:467:LEU:O	1:D:471:ASN:ND2	2.42	0.52
1:A:289:LYS:O	1:A:290:ILE:C	2.52	0.52
1:B:286:TYR:O	1:B:289:LYS:HB2	2.09	0.52
1:B:281:ILE:HG12	1:B:283:GLU:H	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:286:TYR:O	1:C:289:LYS:HB2	2.09	0.52
1:B:176:HIS:ND1	1:B:245:ASP:OD1	2.40	0.52
1:C:208:TRP:O	1:C:214:ARG:NH2	2.38	0.52
1:A:467:LEU:O	1:A:471:ASN:ND2	2.42	0.52
1:B:289:LYS:O	1:B:290:ILE:C	2.52	0.52
1:D:325:ARG:HB3	1:D:353:LEU:HB3	1.91	0.51
1:B:205:ILE:HG21	1:B:269:ARG:HB2	1.93	0.51
1:A:832:ARG:NH2	5:A:1305:T14:F14	2.33	0.51
1:A:138:SER:O	1:A:269:ARG:NH2	2.39	0.51
1:D:289:LYS:O	1:D:290:ILE:C	2.52	0.51
1:C:289:LYS:O	1:C:290:ILE:C	2.52	0.51
1:D:832:ARG:NH2	5:D:1305:T14:F14	2.33	0.51
1:B:832:ARG:NH2	5:B:1304:T14:F14	2.33	0.51
1:C:205:ILE:HG21	1:C:269:ARG:HB2	1.93	0.51
1:A:315:ILE:CG2	1:A:315:ILE:O	2.48	0.51
1:C:832:ARG:NH2	5:C:1305:T14:F14	2.33	0.51
1:A:823:CYS:HB3	1:D:874:ALA:HA	1.94	0.50
1:C:768:VAL:HG23	1:C:1003:PHE:HZ	1.67	0.50
1:D:115:THR:OG1	1:D:116:ASP:N	2.45	0.50
1:A:115:THR:OG1	1:A:116:ASP:N	2.45	0.50
1:A:560:VAL:HG13	1:A:589:LEU:HD11	1.93	0.50
1:C:560:VAL:HG13	1:C:589:LEU:HD11	1.93	0.50
1:A:175:THR:OG1	1:A:180:MET:SD	2.67	0.50
1:B:560:VAL:HG13	1:B:589:LEU:HD11	1.93	0.50
1:D:205:ILE:HG21	1:D:269:ARG:HB2	1.92	0.50
1:C:346:LYS:HD3	1:C:369:ILE:HD11	1.94	0.49
1:D:560:VAL:HG13	1:D:589:LEU:HD11	1.93	0.49
1:A:205:ILE:HG21	1:A:269:ARG:HB2	1.92	0.49
1:A:346:LYS:HD3	1:A:369:ILE:HD11	1.94	0.49
1:B:284:SER:HA	1:B:288:GLY:HA2	1.94	0.49
1:A:299:GLY:HA3	1:A:325:ARG:HB2	1.94	0.49
1:B:115:THR:OG1	1:B:116:ASP:N	2.45	0.49
1:B:874:ALA:HA	1:C:823:CYS:HB3	1.94	0.49
1:C:874:ALA:HA	1:D:823:CYS:HB3	1.93	0.49
1:D:315:ILE:CG2	1:D:315:ILE:O	2.48	0.49
1:D:775:ARG:HH22	1:D:998:ARG:HA	1.77	0.49
1:A:284:SER:HA	1:A:288:GLY:HA2	1.94	0.49
1:C:115:THR:OG1	1:C:116:ASP:N	2.45	0.49
1:C:284:SER:HA	1:C:288:GLY:HA2	1.94	0.49
1:C:775:ARG:HH22	1:C:998:ARG:HA	1.77	0.49
1:A:725:PRO:HG3	1:A:1000:THR:HG21	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:299:GLY:HA3	1:D:325:ARG:HB2	1.94	0.49
1:B:448:ASP:OD1	1:B:448:ASP:N	2.40	0.49
1:D:346:LYS:HD3	1:D:369:ILE:HD11	1.94	0.49
1:D:430:LEU:HD22	1:D:463:LYS:HB3	1.95	0.49
1:B:299:GLY:HA3	1:B:325:ARG:HB2	1.94	0.49
1:B:346:LYS:HD3	1:B:369:ILE:HD11	1.94	0.49
1:C:410:ASN:HD21	1:C:412:HIS:HD2	1.60	0.49
1:D:410:ASN:HD21	1:D:412:HIS:HD2	1.60	0.49
1:A:701:ILE:CG2	1:A:702:SER:N	2.67	0.49
1:B:122:ASP:HA	1:B:125:THR:HG22	1.95	0.49
1:B:430:LEU:HD22	1:B:463:LYS:HB3	1.95	0.49
1:C:122:ASP:HA	1:C:125:THR:HG22	1.95	0.48
1:D:725:PRO:HG3	1:D:1000:THR:HG21	1.95	0.48
1:B:775:ARG:HH22	1:B:998:ARG:HA	1.77	0.48
1:B:863:LEU:HD13	1:C:834:ILE:HG23	1.94	0.48
1:B:1076:ASP:HA	1:B:1079:LEU:HG	1.95	0.48
1:C:863:LEU:HD13	1:D:834:ILE:HG23	1.94	0.48
1:D:768:VAL:HG23	1:D:1003:PHE:HZ	1.67	0.48
1:D:1076:ASP:HA	1:D:1079:LEU:HG	1.95	0.48
1:A:410:ASN:HD21	1:A:412:HIS:HD2	1.60	0.48
1:A:775:ARG:HH22	1:A:998:ARG:HA	1.77	0.48
1:D:284:SER:HA	1:D:288:GLY:HA2	1.94	0.48
1:A:969:PHE:O	1:A:972:THR:OG1	2.31	0.48
1:A:444:TRP:O	1:D:145:ASN:ND2	2.47	0.48
1:B:725:PRO:HG3	1:B:1000:THR:HG21	1.95	0.48
1:A:122:ASP:HA	1:A:125:THR:HG22	1.95	0.48
1:B:281:ILE:HG23	1:B:284:SER:H	1.79	0.48
1:C:299:GLY:HA3	1:C:325:ARG:HB2	1.94	0.48
1:C:725:PRO:HG3	1:C:1000:THR:HG21	1.95	0.48
1:D:838:THR:O	1:D:842:ASN:ND2	2.36	0.48
1:A:1076:ASP:HA	1:A:1079:LEU:HG	1.95	0.47
1:B:838:THR:O	1:B:842:ASN:ND2	2.36	0.47
1:D:122:ASP:HA	1:D:125:THR:HG22	1.95	0.47
1:A:729:PHE:CE2	2:A:1301:Y01:HAT2	2.49	0.47
1:D:175:THR:OG1	1:D:180:MET:SD	2.67	0.47
1:D:729:PHE:CE2	2:D:1301:Y01:HAT2	2.49	0.47
1:B:410:ASN:HD21	1:B:412:HIS:HD2	1.60	0.47
1:C:175:THR:OG1	1:C:180:MET:SD	2.67	0.47
1:A:412:HIS:C	1:A:413:ASP:OD1	2.58	0.47
1:A:430:LEU:HD22	1:A:463:LYS:HB3	1.95	0.47
1:B:208:TRP:O	1:B:214:ARG:NH2	2.38	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:412:HIS:C	1:B:413:ASP:OD1	2.58	0.47
1:D:482:GLU:HA	1:D:485:ARG:HG2	1.96	0.47
1:A:145:ASN:HD21	1:B:445:GLU:HA	1.80	0.47
1:C:412:HIS:C	1:C:413:ASP:OD1	2.58	0.47
1:C:430:LEU:HD22	1:C:463:LYS:HB3	1.95	0.47
1:C:1076:ASP:HA	1:C:1079:LEU:HG	1.95	0.47
1:C:281:ILE:HG23	1:C:284:SER:H	1.79	0.47
1:D:412:HIS:C	1:D:413:ASP:OD1	2.58	0.47
1:D:1085:LEU:HD12	1:D:1088:GLU:HG3	1.97	0.47
1:B:729:PHE:CE2	2:B:1301:Y01:HAT2	2.49	0.47
1:C:355:ARG:NH2	1:D:414:ARG:O	2.46	0.47
1:D:375:VAL:HG23	1:D:376:LEU:HD12	1.97	0.47
1:A:375:VAL:HG23	1:A:376:LEU:HD12	1.97	0.47
1:A:482:GLU:HA	1:A:485:ARG:HG2	1.96	0.47
1:D:448:ASP:OD1	1:D:448:ASP:N	2.40	0.47
1:B:482:GLU:HA	1:B:485:ARG:HG2	1.96	0.46
1:A:208:TRP:O	1:A:214:ARG:NH2	2.38	0.46
1:A:1085:LEU:HD12	1:A:1088:GLU:HG3	1.97	0.46
1:B:1085:LEU:HD12	1:B:1088:GLU:HG3	1.97	0.46
1:C:482:GLU:HA	1:C:485:ARG:HG2	1.96	0.46
1:C:555:LEU:HG	1:C:571:ILE:HD13	1.98	0.46
1:A:874:ALA:HA	1:B:823:CYS:HB3	1.97	0.46
1:B:555:LEU:HG	1:B:571:ILE:HD13	1.98	0.46
1:C:729:PHE:CE2	2:C:1301:Y01:HAT2	2.49	0.46
1:D:281:ILE:HG23	1:D:284:SER:H	1.79	0.46
1:D:555:LEU:HG	1:D:571:ILE:HD13	1.98	0.46
1:A:308:ASN:HD21	1:A:371:TRP:HB3	1.81	0.46
1:B:969:PHE:O	1:B:972:THR:OG1	2.31	0.46
1:C:308:ASN:HD21	1:C:371:TRP:HB3	1.80	0.46
1:B:175:THR:OG1	1:B:180:MET:SD	2.67	0.46
1:A:555:LEU:HG	1:A:571:ILE:HD13	1.98	0.46
1:B:952:ILE:HG13	1:C:824:LEU:HD12	1.97	0.46
1:B:308:ASN:HD21	1:B:371:TRP:HB3	1.80	0.46
1:C:1085:LEU:HD12	1:C:1088:GLU:HG3	1.97	0.46
2:C:1301:Y01:HAC3	2:C:1301:Y01:HAJ1	1.77	0.46
1:A:281:ILE:HG23	1:A:284:SER:H	1.79	0.46
1:C:627:ASP:HB3	1:C:630:LEU:HB2	1.98	0.46
1:C:776:GLN:OE1	1:C:998:ARG:NH1	2.49	0.46
2:C:1301:Y01:HAO1	2:C:1301:Y01:HAP1	1.79	0.46
1:C:969:PHE:O	1:C:972:THR:OG1	2.32	0.46
1:B:375:VAL:HG23	1:B:376:LEU:HD12	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:208:TRP:O	1:D:214:ARG:NH2	2.38	0.45
1:D:627:ASP:HB3	1:D:630:LEU:HB2	1.98	0.45
1:D:776:GLN:OE1	1:D:998:ARG:NH1	2.49	0.45
2:A:1301:Y01:HAC3	2:A:1301:Y01:HAJ1	1.77	0.45
1:B:627:ASP:HB3	1:B:630:LEU:HB2	1.98	0.45
1:C:373:LYS:O	1:C:377:GLU:HG3	2.17	0.45
1:C:784:TYR:CZ	1:C:790:ASN:HB3	2.52	0.45
1:B:314:LYS:HG3	1:B:315:ILE:H	1.82	0.45
1:B:429:GLN:HE21	1:B:432:LEU:HD13	1.82	0.45
1:B:776:GLN:OE1	1:B:998:ARG:NH1	2.49	0.45
1:C:375:VAL:HG23	1:C:376:LEU:HD12	1.97	0.45
1:C:314:LYS:HG3	1:C:315:ILE:H	1.82	0.45
1:D:308:ASN:HD21	1:D:371:TRP:HB3	1.81	0.45
1:A:429:GLN:HE21	1:A:432:LEU:HD13	1.82	0.45
1:A:1056:LYS:HA	1:A:1059:THR:HG22	1.99	0.45
1:C:1086:LEU:HA	1:C:1089:ILE:HG12	1.98	0.45
1:D:314:LYS:HG3	1:D:315:ILE:H	1.82	0.45
1:D:429:GLN:HE21	1:D:432:LEU:HD13	1.82	0.45
1:B:784:TYR:CZ	1:B:790:ASN:HB3	2.52	0.45
1:B:1056:LYS:HA	1:B:1059:THR:HG22	1.99	0.45
1:B:1086:LEU:HA	1:B:1089:ILE:HG12	1.98	0.45
1:C:294:CYS:HB3	1:C:318:VAL:HG22	1.99	0.45
1:C:838:THR:O	1:C:842:ASN:ND2	2.36	0.45
1:A:627:ASP:HB3	1:A:630:LEU:HB2	1.98	0.45
1:D:698:CYS:SG	1:D:699:GLY:N	2.90	0.45
1:D:784:TYR:CZ	1:D:790:ASN:HB3	2.52	0.45
1:A:355:ARG:HB2	1:B:441:ASP:HB3	1.99	0.45
1:B:355:ARG:NH2	1:C:414:ARG:O	2.46	0.45
1:C:1056:LYS:HA	1:C:1059:THR:HG22	1.99	0.45
1:D:1056:LYS:HA	1:D:1059:THR:HG22	1.99	0.45
1:A:776:GLN:OE1	1:A:998:ARG:NH1	2.49	0.45
1:D:373:LYS:O	1:D:377:GLU:HG3	2.17	0.44
1:D:1003:PHE:HA	1:D:1006:VAL:HG23	1.99	0.44
1:A:314:LYS:HG3	1:A:315:ILE:H	1.82	0.44
1:B:698:CYS:SG	1:B:699:GLY:N	2.90	0.44
1:C:952:ILE:HG13	1:D:824:LEU:HD12	1.98	0.44
1:D:157:SER:HA	1:D:186:VAL:HG11	2.00	0.44
1:A:834:ILE:HG23	1:D:863:LEU:HD13	1.99	0.44
1:A:1086:LEU:HA	1:A:1089:ILE:HG12	1.98	0.44
1:B:279:ARG:NH1	1:B:280:VAL:O	2.50	0.44
1:C:698:CYS:SG	1:C:699:GLY:N	2.90	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1086:LEU:HA	1:D:1089:ILE:HG12	1.98	0.44
1:B:701:ILE:CG2	1:B:702:SER:N	2.68	0.44
1:C:429:GLN:HE21	1:C:432:LEU:HD13	1.82	0.44
1:A:784:TYR:CZ	1:A:790:ASN:HB3	2.52	0.44
1:B:115:THR:OG1	1:B:116:ASP:OD1	2.29	0.44
1:B:373:LYS:O	1:B:377:GLU:HG3	2.17	0.44
1:A:157:SER:HA	1:A:186:VAL:HG11	2.00	0.44
1:A:355:ARG:NH2	1:B:414:ARG:O	2.46	0.44
1:A:414:ARG:O	1:D:355:ARG:NH2	2.44	0.44
1:A:698:CYS:SG	1:A:699:GLY:N	2.90	0.44
2:A:1301:Y01:CAV	4:A:1303:9PE:C1	2.73	0.44
1:B:294:CYS:HB3	1:B:318:VAL:HG22	1.99	0.44
1:D:424:LEU:HD12	1:D:437:ILE:HD11	2.00	0.44
1:B:234:ASP:OD1	1:B:234:ASP:N	2.51	0.44
1:B:687:ILE:HD11	2:B:1301:Y01:HAK1	2.00	0.44
1:B:1003:PHE:HA	1:B:1006:VAL:HG23	1.99	0.44
1:D:294:CYS:HB3	1:D:318:VAL:HG22	1.99	0.44
2:D:1301:Y01:HAC3	2:D:1301:Y01:HAJ1	1.78	0.44
1:C:279:ARG:NH1	1:C:280:VAL:O	2.50	0.44
1:C:687:ILE:HD11	2:C:1301:Y01:HAK1	2.00	0.44
2:D:1301:Y01:CAE	4:D:1303:9PE:H25A	2.48	0.44
1:B:145:ASN:HD21	1:C:445:GLU:HA	1.83	0.44
1:C:424:LEU:HD12	1:C:437:ILE:HD11	2.00	0.44
2:C:1301:Y01:CAE	4:C:1303:9PE:H25A	2.48	0.44
1:D:766:VAL:HA	1:D:769:LEU:HB2	1.99	0.44
1:A:373:LYS:O	1:A:377:GLU:HG3	2.17	0.43
1:A:445:GLU:HA	1:D:145:ASN:HD21	1.83	0.43
1:B:424:LEU:HD12	1:B:437:ILE:HD11	2.00	0.43
1:B:1053:TYR:CZ	1:B:1057:ILE:HD11	2.53	0.43
1:C:157:SER:HA	1:C:186:VAL:HG11	2.00	0.43
1:C:1003:PHE:HA	1:C:1006:VAL:HG23	1.99	0.43
1:A:1053:TYR:CZ	1:A:1057:ILE:HD11	2.54	0.43
1:C:187:VAL:HG21	1:C:202:ALA:HB2	2.00	0.43
1:D:279:ARG:NH1	1:D:280:VAL:O	2.50	0.43
1:B:157:SER:HA	1:B:186:VAL:HG11	2.00	0.43
1:C:766:VAL:HA	1:C:769:LEU:HB2	1.99	0.43
1:C:952:ILE:O	1:C:956:SER:N	2.48	0.43
1:C:1053:TYR:CZ	1:C:1057:ILE:HD11	2.53	0.43
1:D:1050:LYS:HB3	1:D:1050:LYS:HE2	1.79	0.43
1:A:187:VAL:HG21	1:A:202:ALA:HB2	2.00	0.43
1:A:281:ILE:O	1:A:284:SER:OG	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1301:Y01:CAE	4:B:1303:9PE:H25A	2.48	0.43
1:A:279:ARG:NH1	1:A:280:VAL:O	2.50	0.43
1:A:424:LEU:HD12	1:A:437:ILE:HD11	2.00	0.43
1:A:766:VAL:HA	1:A:769:LEU:HB2	1.99	0.43
1:A:1003:PHE:HA	1:A:1006:VAL:HG23	1.99	0.43
2:A:1301:Y01:CAE	4:A:1303:9PE:H25A	2.48	0.43
1:B:187:VAL:HG21	1:B:202:ALA:HB2	2.00	0.43
1:A:234:ASP:N	1:A:234:ASP:OD1	2.51	0.43
1:A:297:GLN:HA	1:A:327:ALA:HB2	2.01	0.43
1:A:758:LEU:HD23	1:A:758:LEU:HA	1.91	0.43
1:D:1053:TYR:CZ	1:D:1057:ILE:HD11	2.54	0.43
1:A:294:CYS:HB3	1:A:318:VAL:HG22	1.99	0.43
1:B:119:THR:O	1:B:123:LEU:N	2.50	0.43
1:B:787:ASP:HB2	1:B:790:ASN:HB2	2.01	0.43
1:D:681:THR:OG1	1:D:682:LYS:N	2.51	0.43
1:A:569:LYS:HD3	1:A:615:ARG:HH21	1.83	0.43
1:C:115:THR:OG1	1:C:116:ASP:OD1	2.29	0.43
1:A:754:GLU:O	1:A:807:ARG:NH2	2.52	0.43
1:B:681:THR:OG1	1:B:682:LYS:N	2.52	0.43
1:D:297:GLN:HA	1:D:327:ALA:HB2	2.01	0.43
1:A:687:ILE:HD11	2:A:1301:Y01:HAK1	2.00	0.43
1:C:681:THR:OG1	1:C:682:LYS:N	2.52	0.43
1:D:281:ILE:O	1:D:284:SER:OG	2.34	0.43
1:D:569:LYS:HD3	1:D:615:ARG:HH21	1.83	0.43
1:D:624:TYR:OH	1:D:667:ASN:ND2	2.41	0.43
1:B:308:ASN:HB3	1:B:312:LYS:HE3	2.01	0.42
1:B:766:VAL:HA	1:B:769:LEU:HB2	1.99	0.42
1:C:758:LEU:HD23	1:C:758:LEU:HA	1.92	0.42
1:D:115:THR:OG1	1:D:116:ASP:OD1	2.29	0.42
1:D:308:ASN:HB3	1:D:312:LYS:HE3	2.01	0.42
1:A:952:ILE:O	1:A:956:SER:N	2.48	0.42
1:B:297:GLN:HA	1:B:327:ALA:HB2	2.01	0.42
1:B:639:CYS:SG	1:B:642:TRP:N	2.88	0.42
1:A:1050:LYS:HB3	1:A:1050:LYS:HE2	1.79	0.42
1:C:145:ASN:HD21	1:D:445:GLU:HA	1.84	0.42
1:D:187:VAL:HG21	1:D:202:ALA:HB2	2.00	0.42
1:D:687:ILE:HD11	2:D:1301:Y01:HAK1	2.00	0.42
1:B:984:TRP:NE1	1:B:988:ARG:HB2	2.35	0.42
2:B:1301:Y01:CAV	4:B:1303:9PE:C1	2.73	0.42
1:C:1080:SER:O	1:C:1084:GLY:N	2.52	0.42
1:B:754:GLU:O	1:B:807:ARG:NH2	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:754:GLU:O	1:D:807:ARG:NH2	2.52	0.42
1:B:569:LYS:HD3	1:B:615:ARG:HH21	1.83	0.42
1:C:754:GLU:O	1:C:807:ARG:NH2	2.52	0.42
1:C:984:TRP:NE1	1:C:988:ARG:HB2	2.35	0.42
2:A:1301:Y01:HAO1	2:A:1301:Y01:HAP1	1.79	0.42
1:C:787:ASP:HB2	1:C:790:ASN:HB2	2.01	0.42
1:D:787:ASP:HB2	1:D:790:ASN:HB2	2.01	0.42
1:A:984:TRP:NE1	1:A:988:ARG:HB2	2.35	0.42
1:A:787:ASP:HB2	1:A:790:ASN:HB2	2.01	0.42
1:B:624:TYR:OH	1:B:667:ASN:ND2	2.41	0.42
1:C:474:ASN:HB3	1:C:477:LYS:HB2	2.02	0.42
1:D:969:PHE:O	1:D:972:THR:OG1	2.32	0.42
2:A:1301:Y01:HAE2	4:A:1303:9PE:H25A	2.02	0.41
2:B:1301:Y01:HAE2	4:B:1303:9PE:H25A	2.02	0.41
1:C:297:GLN:HA	1:C:327:ALA:HB2	2.01	0.41
1:C:415:ASP:OD1	1:C:415:ASP:N	2.53	0.41
2:C:1301:Y01:HAE2	4:C:1303:9PE:H25A	2.02	0.41
1:D:1080:SER:O	1:D:1084:GLY:N	2.52	0.41
1:A:308:ASN:HB3	1:A:312:LYS:HE3	2.01	0.41
1:B:843:LEU:HD23	1:B:843:LEU:HA	1.89	0.41
1:C:119:THR:O	1:C:123:LEU:N	2.50	0.41
1:D:984:TRP:NE1	1:D:988:ARG:HB2	2.35	0.41
1:C:569:LYS:HD3	1:C:615:ARG:HH21	1.83	0.41
1:D:959:ILE:HD12	1:D:959:ILE:HA	1.97	0.41
1:C:308:ASN:HB3	1:C:312:LYS:HE3	2.01	0.41
1:D:583:LEU:HD12	1:D:647:CYS:HB3	2.03	0.41
1:B:134:ASN:HB3	1:B:168:ALA:HB2	2.03	0.41
1:B:474:ASN:HB3	1:B:477:LYS:HB2	2.03	0.41
1:C:134:ASN:HB3	1:C:168:ALA:HB2	2.03	0.41
1:C:281:ILE:O	1:C:284:SER:OG	2.34	0.41
1:C:583:LEU:HD12	1:C:647:CYS:HB3	2.03	0.41
1:D:952:ILE:O	1:D:956:SER:N	2.48	0.41
1:A:134:ASN:HB3	1:A:168:ALA:HB2	2.03	0.41
1:C:853:MET:HE3	1:C:853:MET:HB2	1.99	0.41
2:C:1301:Y01:HAE2	2:C:1301:Y01:HBB	1.91	0.41
1:A:415:ASP:OD1	1:A:415:ASP:N	2.53	0.41
1:D:690:LEU:HD21	1:D:727:VAL:HG13	2.03	0.41
1:A:690:LEU:HD21	1:A:727:VAL:HG13	2.03	0.41
1:B:511:LEU:HD13	1:B:587:LYS:HG2	2.03	0.41
1:C:669:LEU:HD21	1:C:992:VAL:HB	2.03	0.41
1:C:690:LEU:HD21	1:C:727:VAL:HG13	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:474:ASN:HB3	1:D:477:LYS:HB2	2.02	0.41
1:D:639:CYS:SG	1:D:642:TRP:N	2.88	0.41
1:A:583:LEU:HD12	1:A:647:CYS:HB3	2.03	0.41
1:B:281:ILE:O	1:B:284:SER:OG	2.34	0.41
1:B:690:LEU:HD21	1:B:727:VAL:HG13	2.03	0.41
1:B:750:ASP:HB3	1:B:751:PHE:H	1.76	0.40
1:C:624:TYR:OH	1:C:667:ASN:ND2	2.41	0.40
1:D:415:ASP:OD1	1:D:415:ASP:N	2.53	0.40
1:D:856:ASP:HB3	1:D:967:ALA:HA	2.04	0.40
1:A:639:CYS:SG	1:A:642:TRP:N	2.88	0.40
1:A:669:LEU:HD21	1:A:992:VAL:HB	2.03	0.40
1:A:1048:VAL:HG23	1:A:1049:MET:HE2	2.03	0.40
1:B:669:LEU:HD21	1:B:992:VAL:HB	2.03	0.40
1:C:515:VAL:HG11	1:C:588:LEU:HD11	2.03	0.40
1:D:119:THR:O	1:D:123:LEU:N	2.50	0.40
1:D:134:ASN:HB3	1:D:168:ALA:HB2	2.03	0.40
1:B:410:ASN:O	1:B:411:GLU:HB2	2.22	0.40
1:B:856:ASP:HB3	1:B:967:ALA:HA	2.03	0.40
1:D:511:LEU:HD13	1:D:587:LYS:HG2	2.03	0.40
2:D:1301:Y01:HAO1	2:D:1301:Y01:HAP1	1.79	0.40
1:A:740:LEU:HD21	1:A:829:PHE:HB3	2.04	0.40
1:A:838:THR:O	1:A:842:ASN:ND2	2.36	0.40
1:A:843:LEU:HA	1:A:843:LEU:HD23	1.89	0.40
1:C:856:ASP:HB3	1:C:967:ALA:HA	2.03	0.40
1:D:740:LEU:HD21	1:D:829:PHE:HB3	2.04	0.40
2:D:1301:Y01:HAE2	4:D:1303:9PE:H25A	2.02	0.40
1:A:474:ASN:HB3	1:A:477:LYS:HB2	2.02	0.40
1:A:511:LEU:HD13	1:A:587:LYS:HG2	2.03	0.40
1:B:455:THR:HA	1:B:458:VAL:HG22	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	834/1098 (76%)	772 (93%)	62 (7%)	0	100	100
1	B	834/1098 (76%)	773 (93%)	61 (7%)	0	100	100
1	C	834/1098 (76%)	771 (92%)	63 (8%)	0	100	100
1	D	834/1098 (76%)	772 (93%)	62 (7%)	0	100	100
All	All	3336/4392 (76%)	3088 (93%)	248 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	768/984 (78%)	768 (100%)	0	100	100
1	B	768/984 (78%)	768 (100%)	0	100	100
1	C	768/984 (78%)	768 (100%)	0	100	100
1	D	768/984 (78%)	768 (100%)	0	100	100
All	All	3072/3936 (78%)	3072 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	145	ASN
1	A	190	ASN
1	A	297	GLN
1	A	308	ASN
1	A	412	HIS
1	A	429	GLN
1	A	491	ASN
1	A	563	ASN
1	A	646	ASN
1	A	980	ASN

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Mol	Chain	Res	Type
1	A	987	GLN
1	B	145	ASN
1	B	190	ASN
1	B	297	GLN
1	B	308	ASN
1	B	412	HIS
1	B	429	GLN
1	B	491	ASN
1	B	563	ASN
1	B	646	ASN
1	B	980	ASN
1	B	987	GLN
1	C	145	ASN
1	C	190	ASN
1	C	297	GLN
1	C	308	ASN
1	C	412	HIS
1	C	429	GLN
1	C	491	ASN
1	C	646	ASN
1	C	979	ASN
1	C	987	GLN
1	D	190	ASN
1	D	297	GLN
1	D	308	ASN
1	D	412	HIS
1	D	429	GLN
1	D	491	ASN
1	D	646	ASN
1	D	980	ASN
1	D	987	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 28 ligands modelled in this entry, 8 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	UND	C	1302	-	10,10,10	0.28	0	9,9,9	0.84	0
2	Y01	A	1301	-	38,38,38	4.62	14 (36%)	57,57,57	2.22	20 (35%)
5	T14	D	1305	-	36,37,37	2.23	8 (22%)	47,58,58	2.60	9 (19%)
2	Y01	B	1301	-	38,38,38	4.62	14 (36%)	57,57,57	2.22	20 (35%)
4	9PE	D	1303	-	36,36,39	1.02	4 (11%)	39,41,44	0.97	2 (5%)
3	UND	A	1308	-	10,10,10	0.29	0	9,9,9	0.82	0
4	9PE	A	1303	-	36,36,39	1.02	4 (11%)	39,41,44	0.97	2 (5%)
3	UND	A	1304	-	10,10,10	0.29	0	9,9,9	0.82	0
5	T14	A	1305	-	36,37,37	2.23	8 (22%)	47,58,58	2.61	9 (19%)
4	9PE	C	1303	-	36,36,39	1.03	4 (11%)	39,41,44	0.96	2 (5%)
3	UND	C	1304	-	10,10,10	0.29	0	9,9,9	0.82	0
3	UND	D	1302	-	10,10,10	0.28	0	9,9,9	0.84	0
2	Y01	C	1301	-	38,38,38	4.62	14 (36%)	57,57,57	2.22	20 (35%)
3	UND	D	1304	-	10,10,10	0.29	0	9,9,9	0.82	0
4	9PE	B	1303	-	36,36,39	1.02	4 (11%)	39,41,44	0.97	2 (5%)
3	UND	B	1302	-	10,10,10	0.28	0	9,9,9	0.85	0
5	T14	B	1304	-	36,37,37	2.23	8 (22%)	47,58,58	2.61	9 (19%)
3	UND	A	1302	-	10,10,10	0.28	0	9,9,9	0.84	0
2	Y01	D	1301	-	38,38,38	4.62	14 (36%)	57,57,57	2.22	20 (35%)
5	T14	C	1305	-	36,37,37	2.24	8 (22%)	47,58,58	2.61	9 (19%)

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	UND	C	1302	-	-	0/8/8/8	-
2	Y01	A	1301	-	-	14/19/77/77	0/4/4/4
5	T14	D	1305	-	-	4/17/41/41	0/5/5/5
2	Y01	B	1301	-	-	14/19/77/77	0/4/4/4
4	9PE	D	1303	-	-	16/40/40/43	-
3	UND	A	1308	-	-	2/8/8/8	-
4	9PE	A	1303	-	-	16/40/40/43	-
3	UND	A	1304	-	-	2/8/8/8	-
5	T14	A	1305	-	-	4/17/41/41	0/5/5/5
4	9PE	C	1303	-	-	16/40/40/43	-
3	UND	C	1304	-	-	2/8/8/8	-
3	UND	D	1302	-	-	0/8/8/8	-
2	Y01	C	1301	-	-	14/19/77/77	0/4/4/4
3	UND	D	1304	-	-	2/8/8/8	-
4	9PE	B	1303	-	-	16/40/40/43	-
3	UND	B	1302	-	-	0/8/8/8	-
5	T14	B	1304	-	-	4/17/41/41	0/5/5/5
3	UND	A	1302	-	-	0/8/8/8	-
2	Y01	D	1301	-	-	14/19/77/77	0/4/4/4
5	T14	C	1305	-	-	4/17/41/41	0/5/5/5

All (104) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1301	Y01	CAI-CAZ	17.62	1.69	1.33
2	A	1301	Y01	CAI-CAZ	17.62	1.69	1.33
2	C	1301	Y01	CAI-CAZ	17.61	1.69	1.33
2	D	1301	Y01	CAI-CAZ	17.61	1.69	1.33
2	D	1301	Y01	CBH-CBF	10.02	1.72	1.56
2	C	1301	Y01	CBH-CBF	9.99	1.71	1.56
2	B	1301	Y01	CBB-CBE	-9.98	1.37	1.54
2	A	1301	Y01	CBH-CBF	9.98	1.71	1.56
2	D	1301	Y01	CBB-CBE	-9.97	1.37	1.54
2	A	1301	Y01	CBB-CBE	-9.96	1.37	1.54
2	C	1301	Y01	CBB-CBE	-9.94	1.37	1.54
2	B	1301	Y01	CBH-CBF	9.94	1.71	1.56
2	D	1301	Y01	CBI-CBE	8.16	1.70	1.55
2	B	1301	Y01	CBI-CBE	8.13	1.69	1.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1301	Y01	CBI-CBE	8.12	1.69	1.55
2	C	1301	Y01	CBI-CBE	8.12	1.69	1.55
5	C	1305	T14	C19-N20	8.04	1.45	1.29
5	B	1304	T14	C19-N20	8.03	1.45	1.29
5	A	1305	T14	C19-N20	8.02	1.45	1.29
5	D	1305	T14	C19-N20	8.00	1.44	1.29
2	C	1301	Y01	CAU-CBI	-7.57	1.41	1.54
2	D	1301	Y01	CAU-CBI	-7.52	1.41	1.54
2	B	1301	Y01	CAU-CBI	-7.52	1.41	1.54
2	A	1301	Y01	CAU-CBI	-7.51	1.41	1.54
2	B	1301	Y01	CAK-CBD	7.41	1.65	1.53
2	A	1301	Y01	CAK-CBD	7.41	1.65	1.53
2	C	1301	Y01	CAK-CBD	7.40	1.65	1.53
2	D	1301	Y01	CAK-CBD	7.40	1.65	1.53
2	C	1301	Y01	CAP-CBE	6.24	1.67	1.54
2	A	1301	Y01	CAP-CBE	6.23	1.67	1.54
2	D	1301	Y01	CAP-CBE	6.20	1.67	1.54
2	B	1301	Y01	CAP-CBE	6.20	1.67	1.54
5	B	1304	T14	C16-C30	-5.47	1.35	1.40
5	C	1305	T14	C16-C30	-5.47	1.35	1.40
5	A	1305	T14	C16-C30	-5.45	1.35	1.40
5	D	1305	T14	C16-C30	-5.38	1.35	1.40
2	C	1301	Y01	CAU-CAS	5.34	1.64	1.53
2	A	1301	Y01	CAU-CAS	5.29	1.64	1.53
2	B	1301	Y01	CAU-CAS	5.29	1.64	1.53
2	D	1301	Y01	CAU-CAS	5.28	1.63	1.53
5	D	1305	T14	C28-C19	-4.92	1.41	1.50
5	C	1305	T14	C28-C19	-4.91	1.41	1.50
5	A	1305	T14	C28-C19	-4.88	1.41	1.50
5	B	1304	T14	C28-C19	-4.87	1.41	1.50
5	C	1305	T14	O21-N20	4.24	1.49	1.42
5	D	1305	T14	O21-N20	4.24	1.49	1.42
5	B	1304	T14	O21-N20	4.24	1.49	1.42
5	A	1305	T14	O21-N20	4.24	1.49	1.42
2	D	1301	Y01	CAQ-CBG	3.01	1.60	1.54
2	A	1301	Y01	CAQ-CBG	3.00	1.60	1.54
2	C	1301	Y01	CAQ-CBG	2.99	1.60	1.54
2	B	1301	Y01	CAQ-CBG	2.99	1.60	1.54
5	D	1305	T14	C18-C19	2.98	1.52	1.47
5	A	1305	T14	C18-C19	2.97	1.52	1.47
5	C	1305	T14	C18-C19	2.96	1.52	1.47
5	B	1304	T14	C18-C19	2.91	1.52	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1301	Y01	CBD-CBF	-2.83	1.48	1.53
2	C	1301	Y01	CBD-CBF	-2.83	1.48	1.53
2	A	1301	Y01	CBD-CBF	-2.82	1.48	1.53
2	D	1301	Y01	CBD-CBF	-2.82	1.48	1.53
5	C	1305	T14	C28-C22	-2.73	1.49	1.53
4	C	1303	9PE	O21-C2	-2.72	1.40	1.46
5	D	1305	T14	C28-C22	-2.71	1.49	1.53
4	A	1303	9PE	O21-C2	-2.69	1.40	1.46
4	D	1303	9PE	O21-C2	-2.69	1.40	1.46
4	B	1303	9PE	O21-C2	-2.69	1.40	1.46
5	A	1305	T14	C28-C22	-2.67	1.49	1.53
5	B	1304	T14	C28-C22	-2.65	1.49	1.53
2	D	1301	Y01	CBH-CAZ	-2.62	1.47	1.52
2	A	1301	Y01	CBH-CAZ	-2.59	1.47	1.52
2	C	1301	Y01	CBH-CAZ	-2.59	1.47	1.52
2	B	1301	Y01	CBH-CAZ	-2.57	1.48	1.52
2	D	1301	Y01	CAC-CBB	2.55	1.59	1.53
2	C	1301	Y01	CAC-CBB	2.54	1.59	1.53
2	A	1301	Y01	CAC-CBB	2.52	1.59	1.53
2	B	1301	Y01	CAO-CBB	2.52	1.60	1.54
2	B	1301	Y01	CAC-CBB	2.52	1.59	1.53
2	A	1301	Y01	CAO-CBB	2.50	1.60	1.54
2	C	1301	Y01	CAO-CBB	2.50	1.60	1.54
2	D	1301	Y01	CAO-CBB	2.49	1.60	1.54
4	C	1303	9PE	O31-C31	2.44	1.40	1.33
4	A	1303	9PE	O31-C31	2.44	1.40	1.33
4	B	1303	9PE	O31-C31	2.43	1.40	1.33
4	D	1303	9PE	O31-C31	2.43	1.40	1.33
4	D	1303	9PE	O21-C21	2.15	1.40	1.34
4	A	1303	9PE	O31-C3	-2.15	1.40	1.45
4	B	1303	9PE	O31-C3	-2.15	1.40	1.45
4	C	1303	9PE	O31-C3	-2.14	1.40	1.45
4	D	1303	9PE	O31-C3	-2.14	1.40	1.45
4	A	1303	9PE	O21-C21	2.13	1.40	1.34
4	C	1303	9PE	O21-C21	2.12	1.40	1.34
4	B	1303	9PE	O21-C21	2.11	1.40	1.34
2	C	1301	Y01	OAW-CAY	2.08	1.40	1.34
2	A	1301	Y01	OAW-CAY	2.07	1.40	1.34
2	B	1301	Y01	OAW-CAY	2.06	1.40	1.34
5	B	1304	T14	C08-C09	2.05	1.53	1.49
2	D	1301	Y01	OAW-CAY	2.05	1.40	1.34
5	D	1305	T14	C08-C09	2.04	1.53	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	1305	T14	C08-C09	2.03	1.53	1.49
5	A	1305	T14	C08-C09	2.02	1.53	1.49
5	B	1304	T14	C30-N29	-2.02	1.35	1.39
5	C	1305	T14	C30-N29	-2.02	1.35	1.39
5	A	1305	T14	C30-N29	-2.01	1.35	1.39
5	D	1305	T14	C30-N29	-2.01	1.35	1.39

All (124) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	1304	T14	C27-C22-C28	-12.49	95.27	113.36
5	A	1305	T14	C27-C22-C28	-12.48	95.27	113.36
5	D	1305	T14	C27-C22-C28	-12.46	95.30	113.36
5	C	1305	T14	C27-C22-C28	-12.44	95.33	113.36
5	A	1305	T14	C28-C19-N20	-7.62	107.74	114.53
5	B	1304	T14	C28-C19-N20	-7.61	107.74	114.53
5	D	1305	T14	C28-C19-N20	-7.60	107.75	114.53
5	C	1305	T14	C28-C19-N20	-7.59	107.76	114.53
2	B	1301	Y01	CBH-CAZ-CAI	-6.90	112.85	122.93
2	A	1301	Y01	CBH-CAZ-CAI	-6.88	112.88	122.93
2	D	1301	Y01	CBH-CAZ-CAI	-6.87	112.89	122.93
2	C	1301	Y01	CBH-CAZ-CAI	-6.86	112.91	122.93
2	B	1301	Y01	CAK-CAI-CAZ	-5.35	115.99	125.02
2	D	1301	Y01	CAK-CAI-CAZ	-5.35	115.99	125.02
2	A	1301	Y01	CAK-CAI-CAZ	-5.35	115.99	125.02
2	C	1301	Y01	CAK-CAI-CAZ	-5.35	115.99	125.02
2	C	1301	Y01	CAV-CAZ-CAI	-4.96	113.84	120.57
2	D	1301	Y01	CAV-CAZ-CAI	-4.96	113.84	120.57
2	B	1301	Y01	CAV-CAZ-CAI	-4.96	113.84	120.57
2	A	1301	Y01	CAV-CAZ-CAI	-4.96	113.85	120.57
2	B	1301	Y01	CAU-CBI-CBE	4.10	122.64	116.60
2	D	1301	Y01	CAU-CBI-CBE	4.09	122.63	116.60
2	A	1301	Y01	CAU-CBI-CBE	4.08	122.61	116.60
2	C	1301	Y01	CAU-CBI-CBE	4.07	122.59	116.60
4	B	1303	9PE	O21-C21-C22	3.98	120.10	111.48
4	A	1303	9PE	O21-C21-C22	3.97	120.07	111.48
4	D	1303	9PE	O21-C21-C22	3.96	120.04	111.48
4	C	1303	9PE	O21-C21-C22	3.95	120.03	111.48
5	C	1305	T14	N17-C18-N29	-3.92	109.03	113.22
5	B	1304	T14	N17-C18-N29	-3.91	109.04	113.22
5	D	1305	T14	N17-C18-N29	-3.89	109.06	113.22
5	A	1305	T14	N17-C18-N29	-3.87	109.08	113.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1301	Y01	CAE-CBI-CAU	-3.43	105.55	110.61
2	B	1301	Y01	CAE-CBI-CAU	-3.42	105.57	110.61
2	C	1301	Y01	CAE-CBI-CAU	-3.41	105.58	110.61
2	A	1301	Y01	CAE-CBI-CAU	-3.41	105.58	110.61
5	B	1304	T14	C23-C22-C28	-3.31	108.56	113.36
2	B	1301	Y01	CAE-CBI-CBG	-3.29	105.70	111.68
2	A	1301	Y01	CAE-CBI-CBG	-3.28	105.72	111.68
2	D	1301	Y01	CAE-CBI-CBG	-3.28	105.73	111.68
5	A	1305	T14	C23-C22-C28	-3.28	108.61	113.36
2	C	1301	Y01	CAE-CBI-CBG	-3.28	105.73	111.68
5	C	1305	T14	C23-C22-C28	-3.27	108.62	113.36
5	D	1305	T14	C23-C22-C28	-3.24	108.67	113.36
5	C	1305	T14	C16-C30-N29	-3.19	107.73	109.91
5	B	1304	T14	C16-C30-N29	-3.17	107.74	109.91
5	D	1305	T14	C16-C30-N29	-3.16	107.75	109.91
2	D	1301	Y01	OAW-CAY-CAM	3.16	118.32	111.48
5	A	1305	T14	C16-C30-N29	-3.16	107.75	109.91
2	C	1301	Y01	OAW-CAY-CAM	3.16	118.31	111.48
2	A	1301	Y01	OAW-CAY-CAM	3.15	118.29	111.48
2	B	1301	Y01	OAW-CAY-CAM	3.14	118.28	111.48
2	D	1301	Y01	CAD-CBH-CBF	-3.08	108.20	111.66
2	C	1301	Y01	CAD-CBH-CBF	-3.05	108.23	111.66
2	A	1301	Y01	CAD-CBH-CBF	-3.04	108.24	111.66
5	C	1305	T14	C30-C16-N17	3.04	107.94	105.40
2	B	1301	Y01	CAD-CBH-CBF	-3.03	108.26	111.66
5	D	1305	T14	C30-C16-N17	3.02	107.91	105.40
5	B	1304	T14	C30-C16-N17	3.01	107.91	105.40
5	A	1305	T14	C30-C16-N17	3.01	107.91	105.40
5	B	1304	T14	C30-N29-C18	3.00	107.73	104.68
5	C	1305	T14	C30-N29-C18	2.99	107.71	104.68
5	D	1305	T14	C30-N29-C18	2.96	107.68	104.68
5	A	1305	T14	C30-N29-C18	2.95	107.68	104.68
2	D	1301	Y01	CAC-CBB-CBE	-2.80	108.68	112.88
2	C	1301	Y01	CAC-CBB-CBE	-2.80	108.69	112.88
2	A	1301	Y01	CAC-CBB-CBE	-2.80	108.69	112.88
2	B	1301	Y01	CAC-CBB-CBE	-2.78	108.72	112.88
2	C	1301	Y01	CAC-CBB-CAO	-2.71	106.14	110.34
2	B	1301	Y01	CAC-CBB-CAO	-2.70	106.16	110.34
2	A	1301	Y01	CAC-CBB-CAO	-2.69	106.18	110.34
2	D	1301	Y01	CAC-CBB-CAO	-2.69	106.18	110.34
2	C	1301	Y01	CAU-CBI-CBG	2.66	111.22	107.25
2	B	1301	Y01	CAU-CBI-CBG	2.66	111.22	107.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1301	Y01	CAU-CBI-CBG	2.66	111.22	107.25
2	B	1301	Y01	CAK-CBD-CBG	-2.64	107.20	110.93
2	C	1301	Y01	CAK-CBD-CBG	-2.63	107.20	110.93
2	A	1301	Y01	CAU-CBI-CBG	2.63	111.18	107.25
2	A	1301	Y01	CAK-CBD-CBG	-2.63	107.22	110.93
2	D	1301	Y01	CAK-CBD-CBG	-2.61	107.23	110.93
5	C	1305	T14	F01-C02-C03	-2.57	108.08	112.65
5	D	1305	T14	F01-C02-C03	-2.57	108.09	112.65
5	A	1305	T14	F01-C02-C03	-2.57	108.10	112.65
2	D	1301	Y01	CBG-CBI-CBE	2.55	103.03	100.10
5	B	1304	T14	F01-C02-C03	-2.54	108.14	112.65
2	A	1301	Y01	CBG-CBI-CBE	2.54	103.02	100.10
2	B	1301	Y01	CBG-CBI-CBE	2.53	103.01	100.10
4	D	1303	9PE	O31-C31-C32	2.53	119.55	111.83
2	C	1301	Y01	CBG-CBI-CBE	2.53	103.00	100.10
4	A	1303	9PE	O31-C31-C32	2.52	119.53	111.83
4	B	1303	9PE	O31-C31-C32	2.51	119.50	111.83
4	C	1303	9PE	O31-C31-C32	2.51	119.48	111.83
2	D	1301	Y01	CAS-CBF-CBD	-2.48	108.32	111.78
2	A	1301	Y01	CAS-CBF-CBD	-2.48	108.32	111.78
2	C	1301	Y01	CAS-CBF-CBD	-2.47	108.33	111.78
2	B	1301	Y01	CAS-CBF-CBD	-2.46	108.35	111.78
2	B	1301	Y01	CAS-CAU-CBI	2.45	116.88	112.74
2	A	1301	Y01	CAS-CAU-CBI	2.45	116.87	112.74
2	C	1301	Y01	CAS-CAU-CBI	2.44	116.85	112.74
2	D	1301	Y01	CAS-CAU-CBI	2.42	116.83	112.74
5	A	1305	T14	C09-C08-C03	-2.26	120.62	124.48
2	D	1301	Y01	CAE-CBI-CBE	-2.25	107.59	111.68
5	B	1304	T14	C09-C08-C03	-2.25	120.63	124.48
5	C	1305	T14	C09-C08-C03	-2.25	120.63	124.48
2	B	1301	Y01	CAE-CBI-CBE	-2.25	107.60	111.68
5	D	1305	T14	C09-C08-C03	-2.24	120.65	124.48
2	C	1301	Y01	CAE-CBI-CBE	-2.24	107.62	111.68
2	A	1301	Y01	CAE-CBI-CBE	-2.23	107.63	111.68
2	A	1301	Y01	CAR-CBC-CAV	-2.22	107.89	110.97
2	D	1301	Y01	CAR-CBC-CAV	-2.21	107.90	110.97
2	C	1301	Y01	CAR-CBC-CAV	-2.21	107.91	110.97
2	B	1301	Y01	CAR-CBC-CAV	-2.19	107.94	110.97
2	B	1301	Y01	CAV-CAZ-CBH	-2.16	113.65	116.42
2	C	1301	Y01	CAV-CAZ-CBH	-2.16	113.65	116.42
2	A	1301	Y01	CAV-CAZ-CBH	-2.16	113.66	116.42
2	B	1301	Y01	CBI-CBE-CBB	-2.15	116.17	119.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1301	Y01	CBF-CBD-CBG	2.15	111.89	109.09
2	B	1301	Y01	CBF-CBD-CBG	2.15	111.89	109.09
2	C	1301	Y01	CBF-CBD-CBG	2.15	111.89	109.09
2	D	1301	Y01	CAV-CAZ-CBH	-2.14	113.68	116.42
2	A	1301	Y01	CBI-CBE-CBB	-2.14	116.19	119.50
2	D	1301	Y01	CBI-CBE-CBB	-2.14	116.19	119.50
2	C	1301	Y01	CBI-CBE-CBB	-2.14	116.19	119.50
2	D	1301	Y01	CBF-CBD-CBG	2.13	111.87	109.09

There are no chirality outliers.

All (144) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1301	Y01	CAR-CBC-OAW-CAY
2	B	1301	Y01	CAR-CBC-OAW-CAY
2	C	1301	Y01	CAR-CBC-OAW-CAY
2	D	1301	Y01	CAR-CBC-OAW-CAY
4	A	1303	9PE	C31-C32-C33-C34
4	B	1303	9PE	C31-C32-C33-C34
4	C	1303	9PE	C31-C32-C33-C34
4	D	1303	9PE	C31-C32-C33-C34
2	A	1301	Y01	CAX-CAL-CAM-CAY
2	B	1301	Y01	CAX-CAL-CAM-CAY
2	C	1301	Y01	CAX-CAL-CAM-CAY
2	D	1301	Y01	CAX-CAL-CAM-CAY
2	A	1301	Y01	CAO-CAJ-CAN-CBA
2	B	1301	Y01	CAO-CAJ-CAN-CBA
2	C	1301	Y01	CAO-CAJ-CAN-CBA
2	D	1301	Y01	CAO-CAJ-CAN-CBA
2	A	1301	Y01	CAM-CAY-OAW-CBC
2	B	1301	Y01	CAM-CAY-OAW-CBC
2	C	1301	Y01	CAM-CAY-OAW-CBC
2	D	1301	Y01	CAM-CAY-OAW-CBC
2	A	1301	Y01	OAG-CAY-OAW-CBC
2	B	1301	Y01	OAG-CAY-OAW-CBC
2	C	1301	Y01	OAG-CAY-OAW-CBC
2	D	1301	Y01	OAG-CAY-OAW-CBC
4	A	1303	9PE	C29-C2A-C2B-C2C
4	B	1303	9PE	C29-C2A-C2B-C2C
4	C	1303	9PE	C29-C2A-C2B-C2C
4	D	1303	9PE	C29-C2A-C2B-C2C
2	A	1301	Y01	CAN-CAJ-CAO-CBB

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Mol	Chain	Res	Type	Atoms
2	B	1301	Y01	CAN-CAJ-CAO-CBB
2	C	1301	Y01	CAN-CAJ-CAO-CBB
2	D	1301	Y01	CAN-CAJ-CAO-CBB
4	A	1303	9PE	C27-C28-C29-C2A
4	B	1303	9PE	C27-C28-C29-C2A
4	D	1303	9PE	C27-C28-C29-C2A
4	C	1303	9PE	C27-C28-C29-C2A
2	A	1301	Y01	CAC-CBB-CBE-CBI
2	B	1301	Y01	CAC-CBB-CBE-CBI
2	C	1301	Y01	CAC-CBB-CBE-CBI
2	D	1301	Y01	CAC-CBB-CBE-CBI
4	A	1303	9PE	C22-C21-O21-C2
4	B	1303	9PE	C22-C21-O21-C2
4	C	1303	9PE	C22-C21-O21-C2
4	D	1303	9PE	C22-C21-O21-C2
2	A	1301	Y01	CAC-CBB-CBE-CAP
2	B	1301	Y01	CAC-CBB-CBE-CAP
2	C	1301	Y01	CAC-CBB-CBE-CAP
2	D	1301	Y01	CAC-CBB-CBE-CAP
3	A	1304	UND	C4-C5-C6-C7
3	A	1308	UND	C4-C5-C6-C7
3	C	1304	UND	C4-C5-C6-C7
3	D	1304	UND	C4-C5-C6-C7
4	A	1303	9PE	C1-C2-C3-O31
4	B	1303	9PE	C1-C2-C3-O31
4	C	1303	9PE	C1-C2-C3-O31
4	D	1303	9PE	C1-C2-C3-O31
4	A	1303	9PE	C22-C23-C24-C25
4	A	1303	9PE	C25-C26-C27-C28
4	B	1303	9PE	C22-C23-C24-C25
4	B	1303	9PE	C25-C26-C27-C28
4	D	1303	9PE	C22-C23-C24-C25
4	C	1303	9PE	C22-C23-C24-C25
4	C	1303	9PE	C25-C26-C27-C28
4	D	1303	9PE	C25-C26-C27-C28
3	A	1304	UND	C5-C6-C7-C8
3	A	1308	UND	C5-C6-C7-C8
3	D	1304	UND	C5-C6-C7-C8
3	C	1304	UND	C5-C6-C7-C8
4	A	1303	9PE	O22-C21-O21-C2
4	B	1303	9PE	O22-C21-O21-C2
4	C	1303	9PE	O22-C21-O21-C2

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Mol	Chain	Res	Type	Atoms
4	D	1303	9PE	O22-C21-O21-C2
2	A	1301	Y01	CAO-CBB-CBE-CBI
2	B	1301	Y01	CAO-CBB-CBE-CBI
2	C	1301	Y01	CAO-CBB-CBE-CBI
2	D	1301	Y01	CAO-CBB-CBE-CBI
4	A	1303	9PE	C26-C27-C28-C29
4	C	1303	9PE	C26-C27-C28-C29
4	D	1303	9PE	C26-C27-C28-C29
4	B	1303	9PE	C26-C27-C28-C29
4	A	1303	9PE	O21-C2-C3-O31
4	B	1303	9PE	O21-C2-C3-O31
4	C	1303	9PE	O21-C2-C3-O31
4	D	1303	9PE	O21-C2-C3-O31
2	A	1301	Y01	CAV-CBC-OAW-CAY
2	B	1301	Y01	CAV-CBC-OAW-CAY
2	D	1301	Y01	CAV-CBC-OAW-CAY
2	C	1301	Y01	CAV-CBC-OAW-CAY
4	C	1303	9PE	C28-C29-C2A-C2B
4	A	1303	9PE	C28-C29-C2A-C2B
4	B	1303	9PE	C28-C29-C2A-C2B
4	D	1303	9PE	C28-C29-C2A-C2B
2	A	1301	Y01	CAJ-CAN-CBA-CAB
2	B	1301	Y01	CAJ-CAN-CBA-CAB
2	C	1301	Y01	CAJ-CAN-CBA-CAB
2	D	1301	Y01	CAJ-CAN-CBA-CAB
2	B	1301	Y01	CAJ-CAN-CBA-CAA
2	C	1301	Y01	CAJ-CAN-CBA-CAA
2	D	1301	Y01	CAJ-CAN-CBA-CAA
2	A	1301	Y01	CAJ-CAN-CBA-CAA
2	A	1301	Y01	CAO-CBB-CBE-CAP
2	B	1301	Y01	CAO-CBB-CBE-CAP
2	C	1301	Y01	CAO-CBB-CBE-CAP
2	D	1301	Y01	CAO-CBB-CBE-CAP
5	C	1305	T14	C03-C08-C09-C31
5	D	1305	T14	C03-C08-C09-C31
5	A	1305	T14	C03-C08-C09-C31
5	B	1304	T14	C03-C08-C09-C31
5	A	1305	T14	C03-C08-C09-C10
5	B	1304	T14	C03-C08-C09-C10
5	C	1305	T14	C03-C08-C09-C10
5	D	1305	T14	C03-C08-C09-C10
5	B	1304	T14	C07-C08-C09-C31

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Mol	Chain	Res	Type	Atoms
5	C	1305	T14	C07-C08-C09-C31
5	D	1305	T14	C07-C08-C09-C31
5	A	1305	T14	C07-C08-C09-C31
5	A	1305	T14	C07-C08-C09-C10
5	B	1304	T14	C07-C08-C09-C10
5	C	1305	T14	C07-C08-C09-C10
5	D	1305	T14	C07-C08-C09-C10
4	A	1303	9PE	O21-C21-C22-C23
4	C	1303	9PE	O21-C21-C22-C23
4	D	1303	9PE	O21-C21-C22-C23
4	B	1303	9PE	O21-C21-C22-C23
4	C	1303	9PE	C32-C31-O31-C3
4	A	1303	9PE	C32-C31-O31-C3
4	B	1303	9PE	C32-C31-O31-C3
4	D	1303	9PE	C32-C31-O31-C3
4	B	1303	9PE	O32-C31-O31-C3
4	A	1303	9PE	O32-C31-O31-C3
4	C	1303	9PE	O32-C31-O31-C3
4	D	1303	9PE	O32-C31-O31-C3
4	A	1303	9PE	O22-C21-C22-C23
4	B	1303	9PE	O22-C21-C22-C23
4	C	1303	9PE	O22-C21-C22-C23
4	D	1303	9PE	O22-C21-C22-C23
4	B	1303	9PE	C2B-C2C-C2D-C2E
4	A	1303	9PE	C2B-C2C-C2D-C2E
4	C	1303	9PE	C2B-C2C-C2D-C2E
4	D	1303	9PE	C2B-C2C-C2D-C2E
2	A	1301	Y01	CAL-CAM-CAY-OAW
2	B	1301	Y01	CAL-CAM-CAY-OAW
2	C	1301	Y01	CAL-CAM-CAY-OAW
2	D	1301	Y01	CAL-CAM-CAY-OAW

There are no ring outliers.

12 monomers are involved in 67 short contacts:

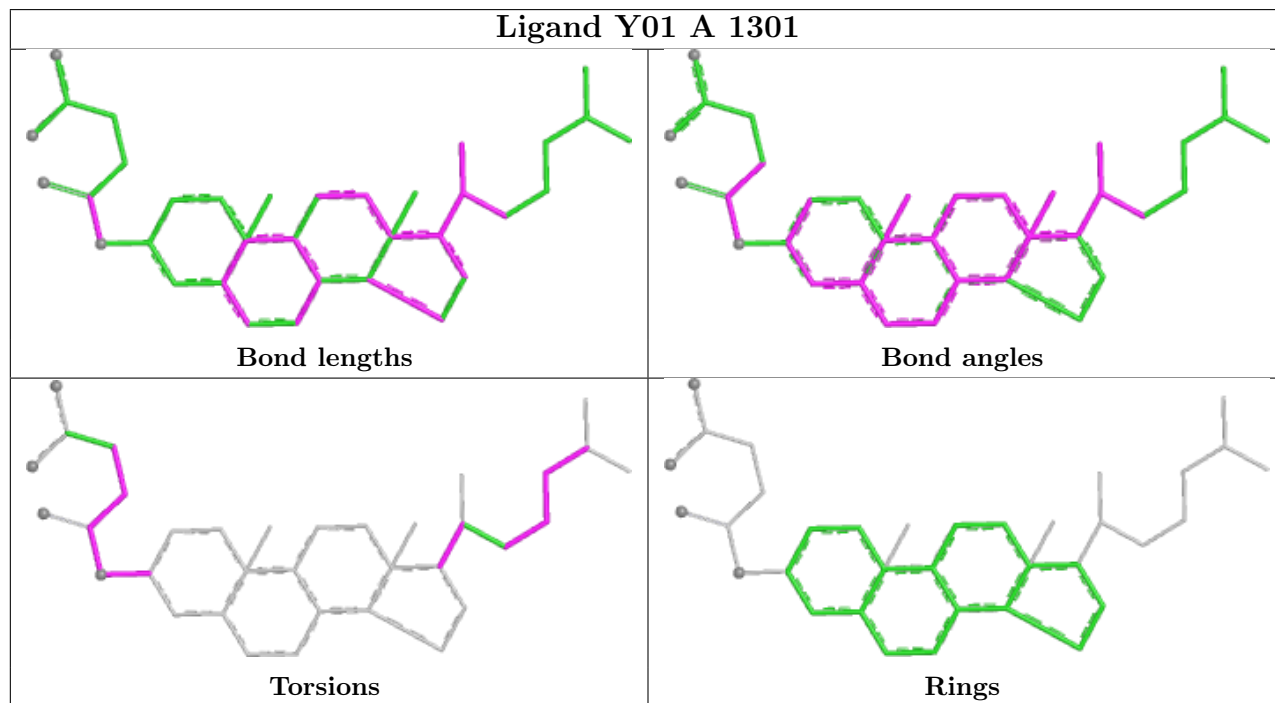
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1301	Y01	13	0
5	D	1305	T14	1	0
2	B	1301	Y01	11	0
4	D	1303	9PE	10	0
4	A	1303	9PE	10	0
5	A	1305	T14	1	0

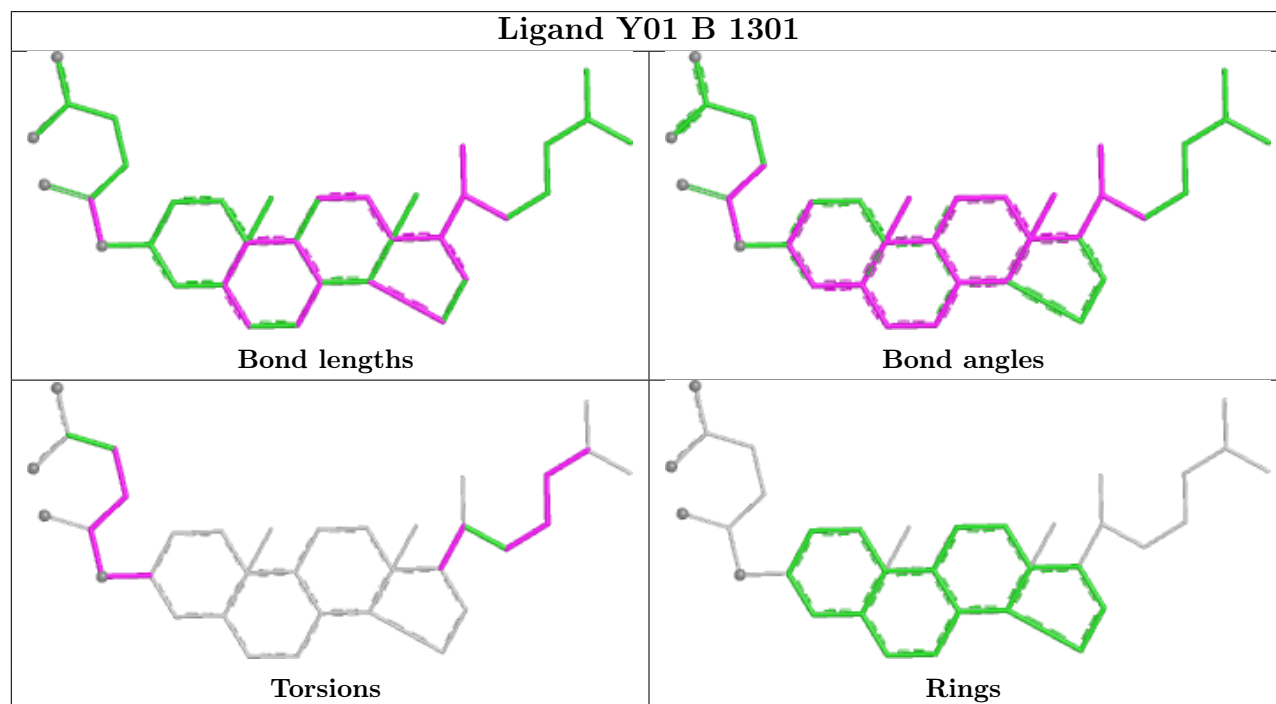
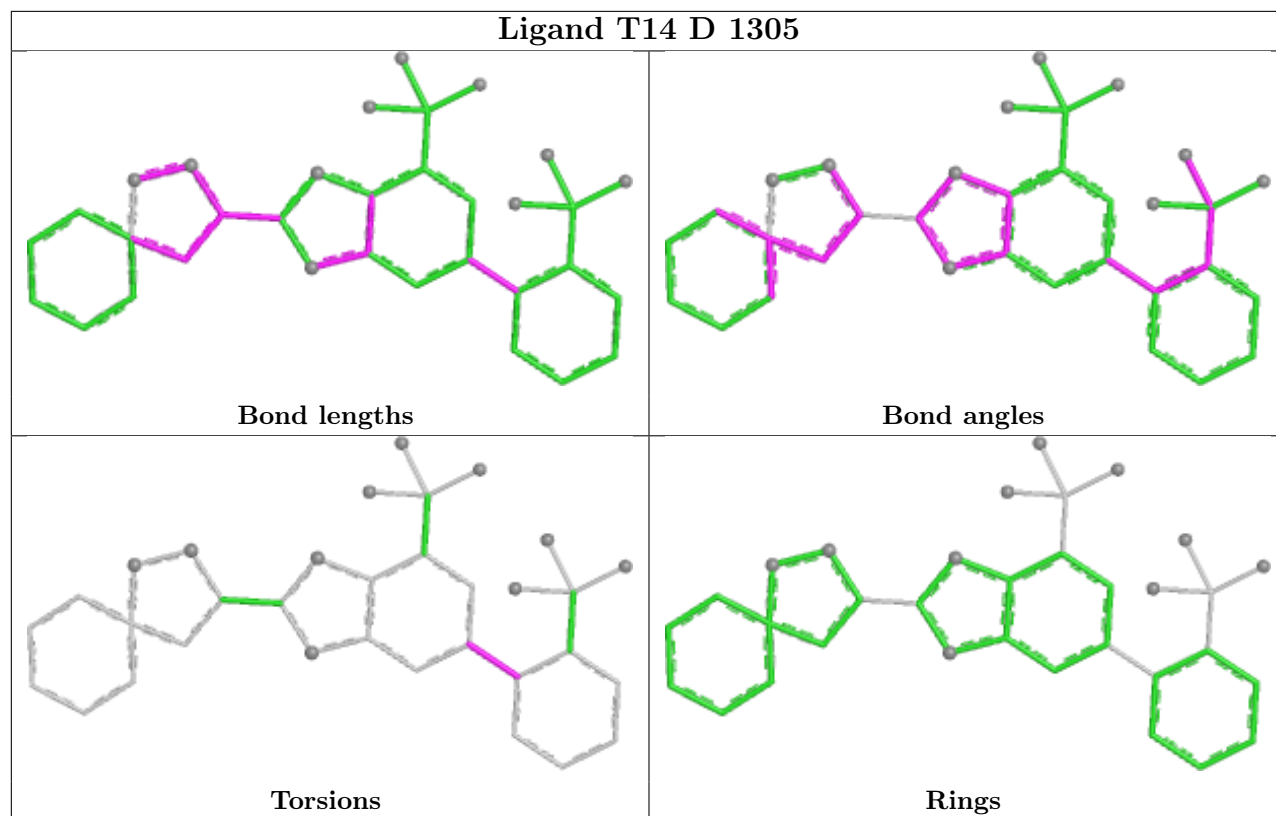
Continued on next page...

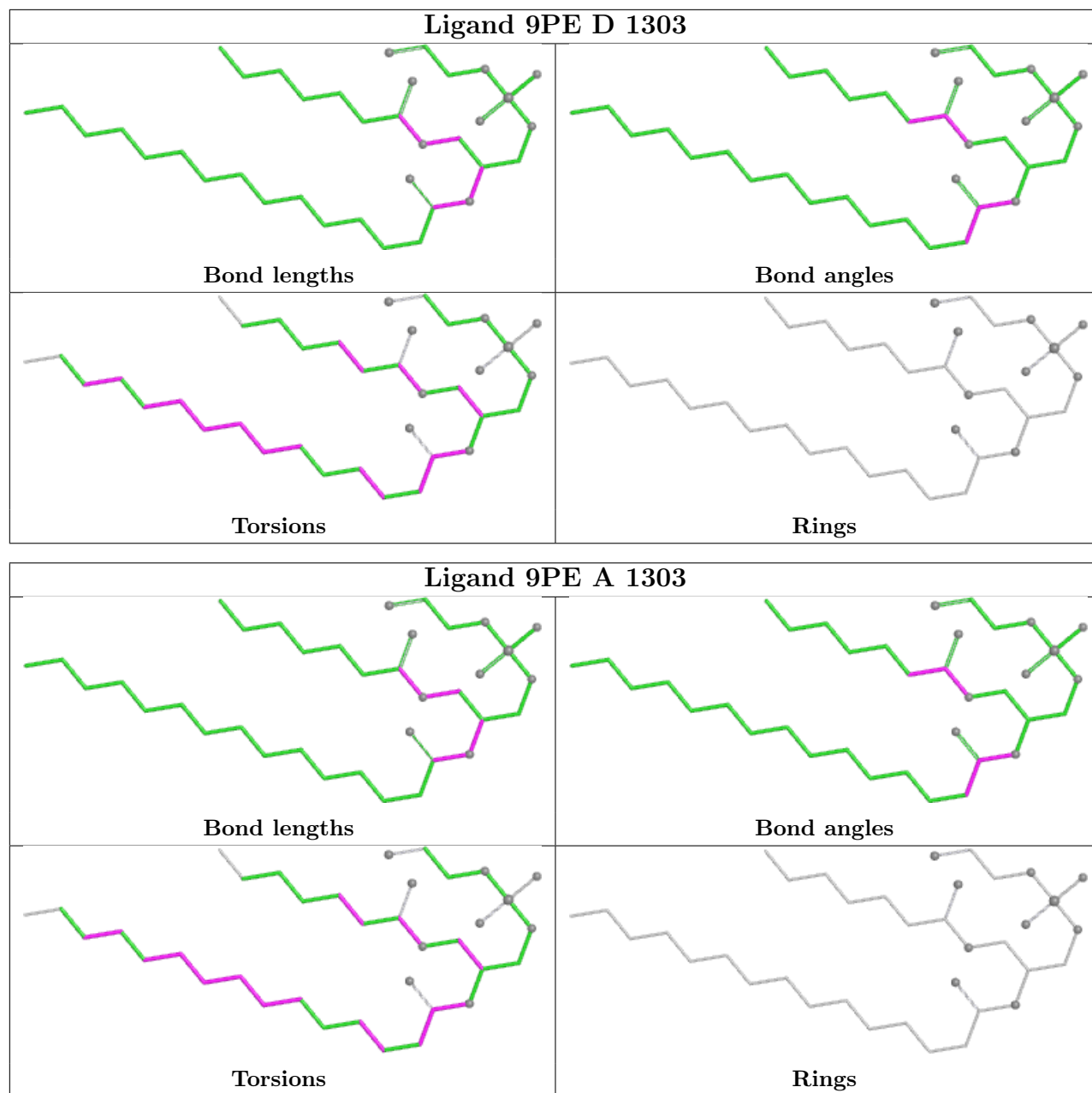
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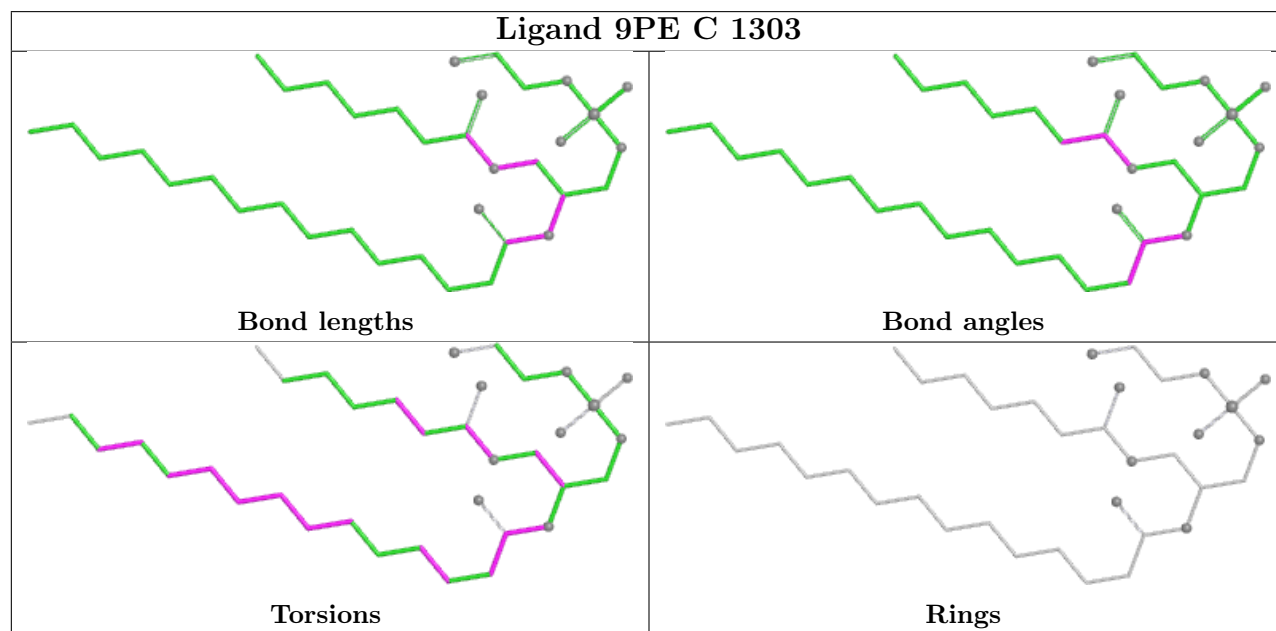
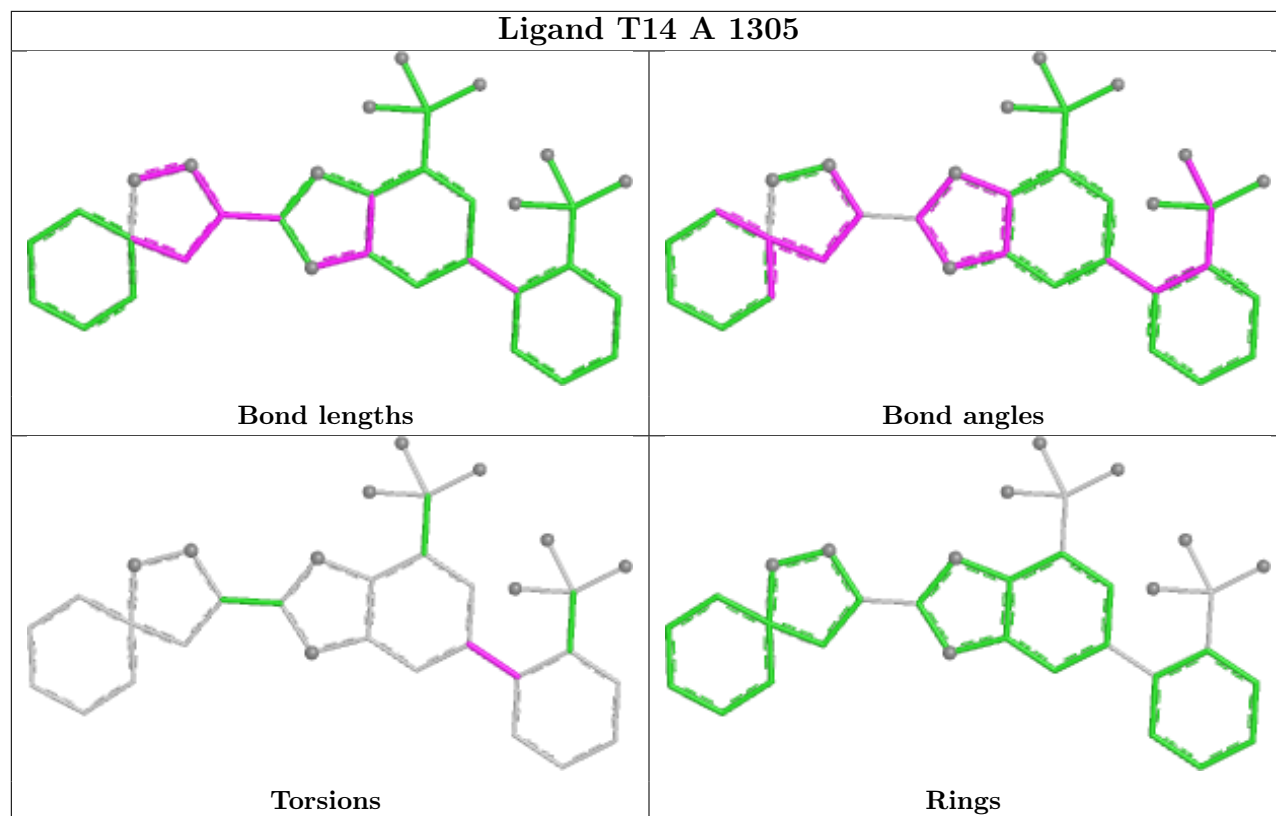
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	1303	9PE	10	0
2	C	1301	Y01	14	0
4	B	1303	9PE	10	0
5	B	1304	T14	1	0
2	D	1301	Y01	13	0
5	C	1305	T14	1	0

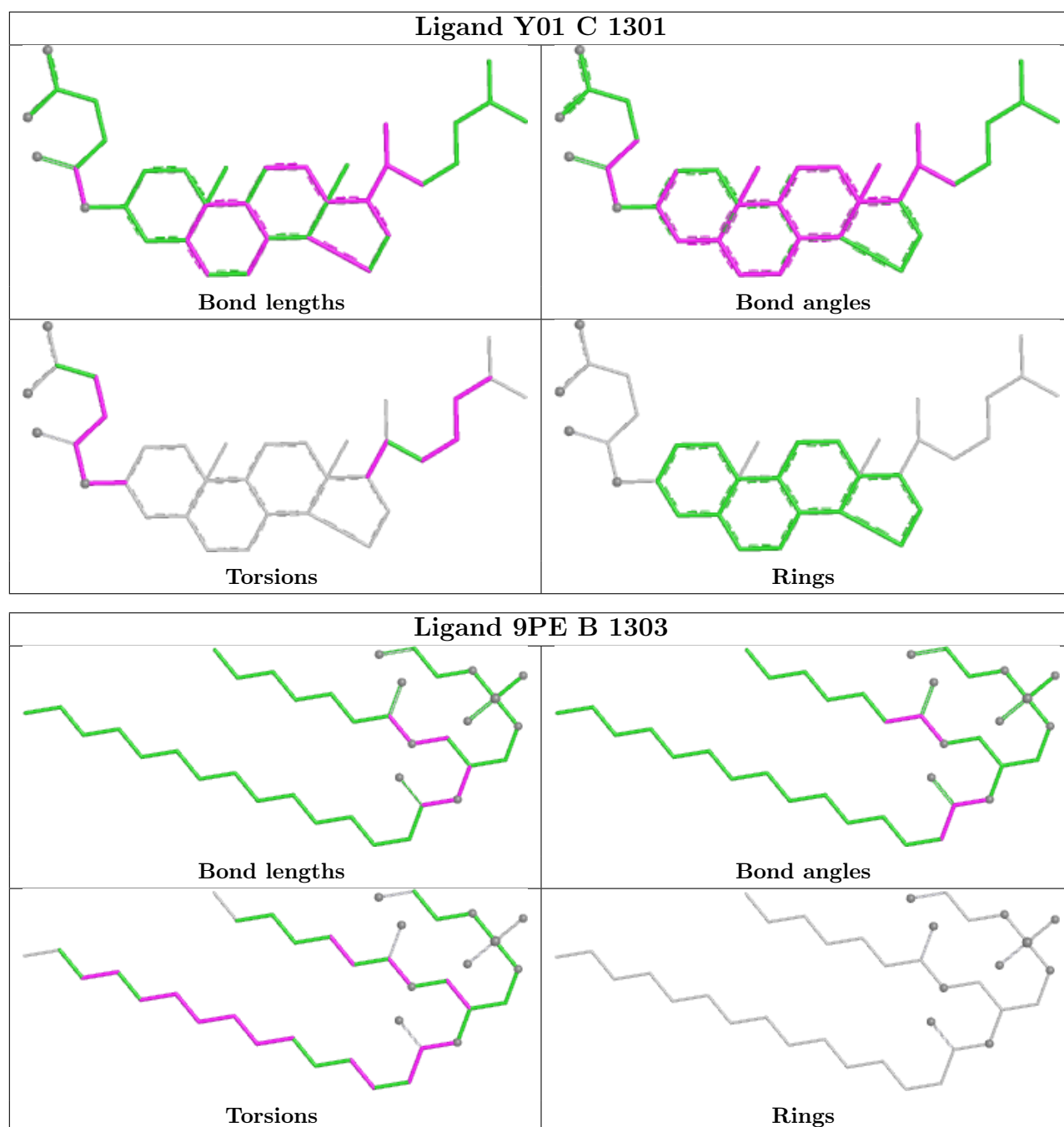
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

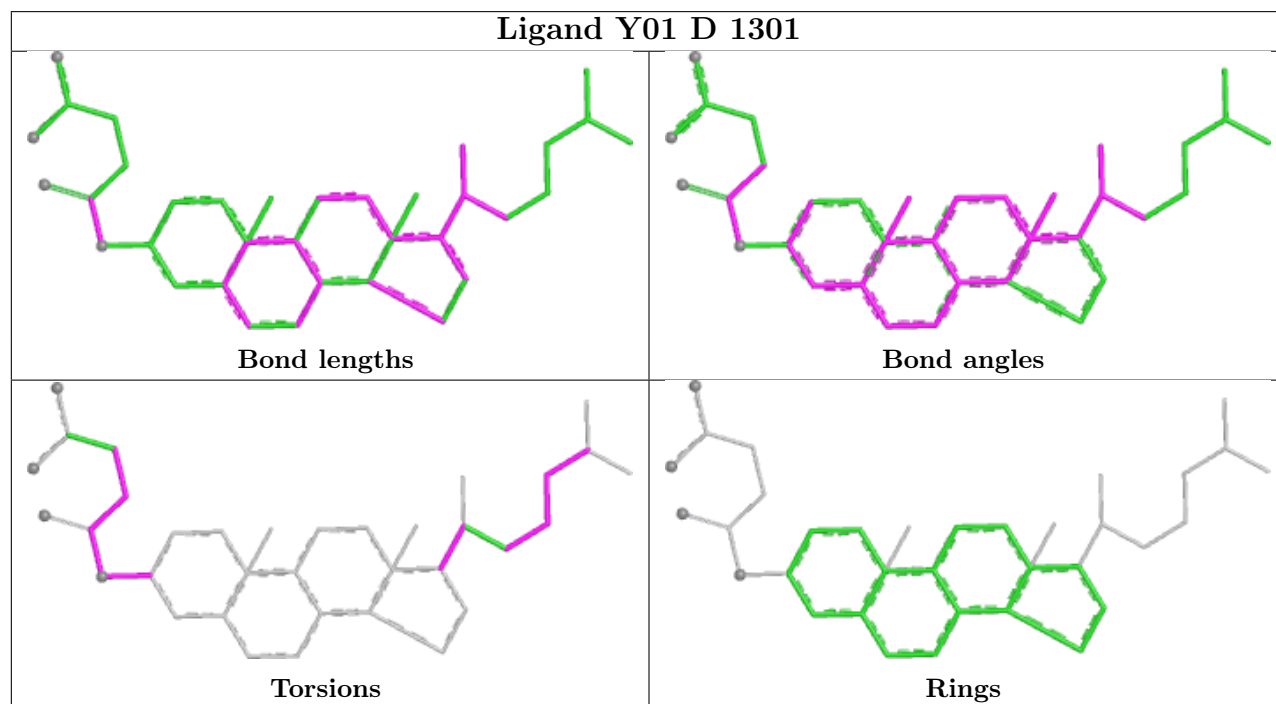
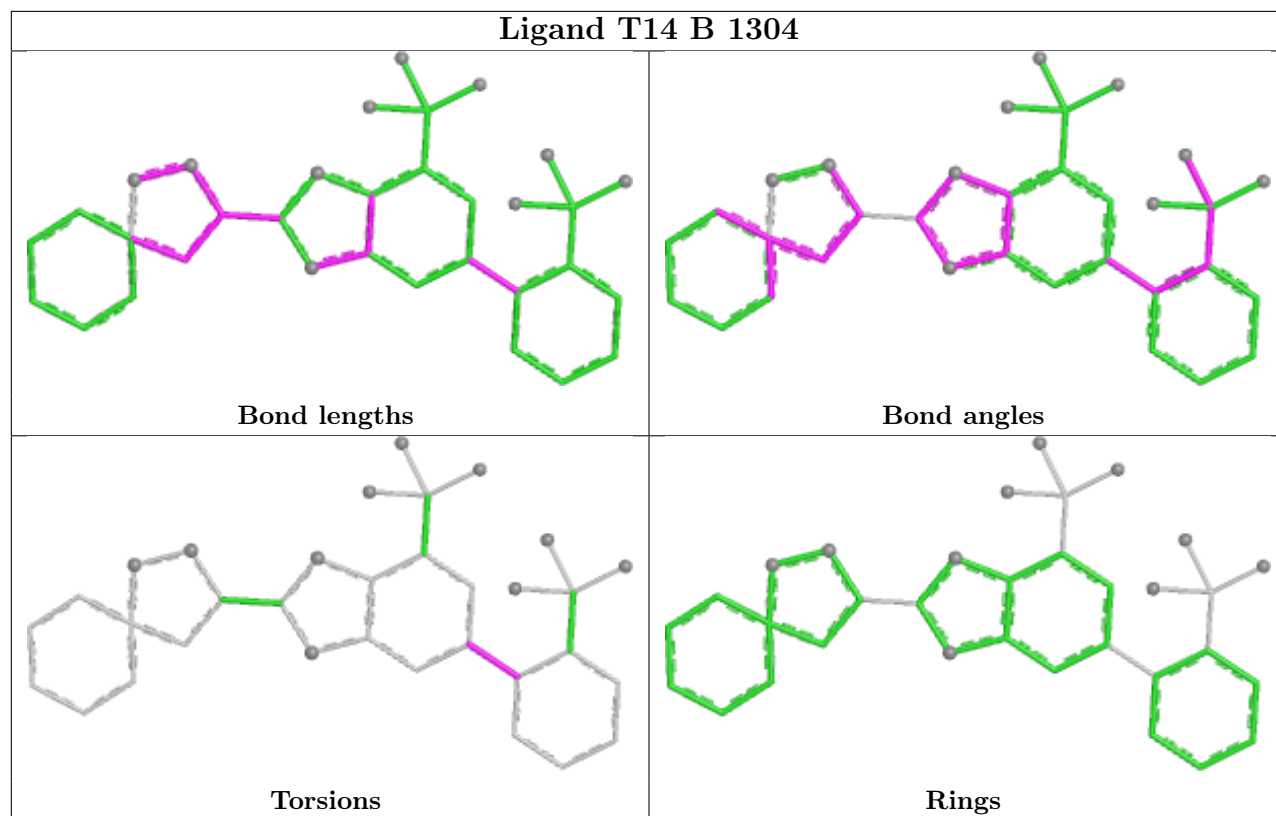


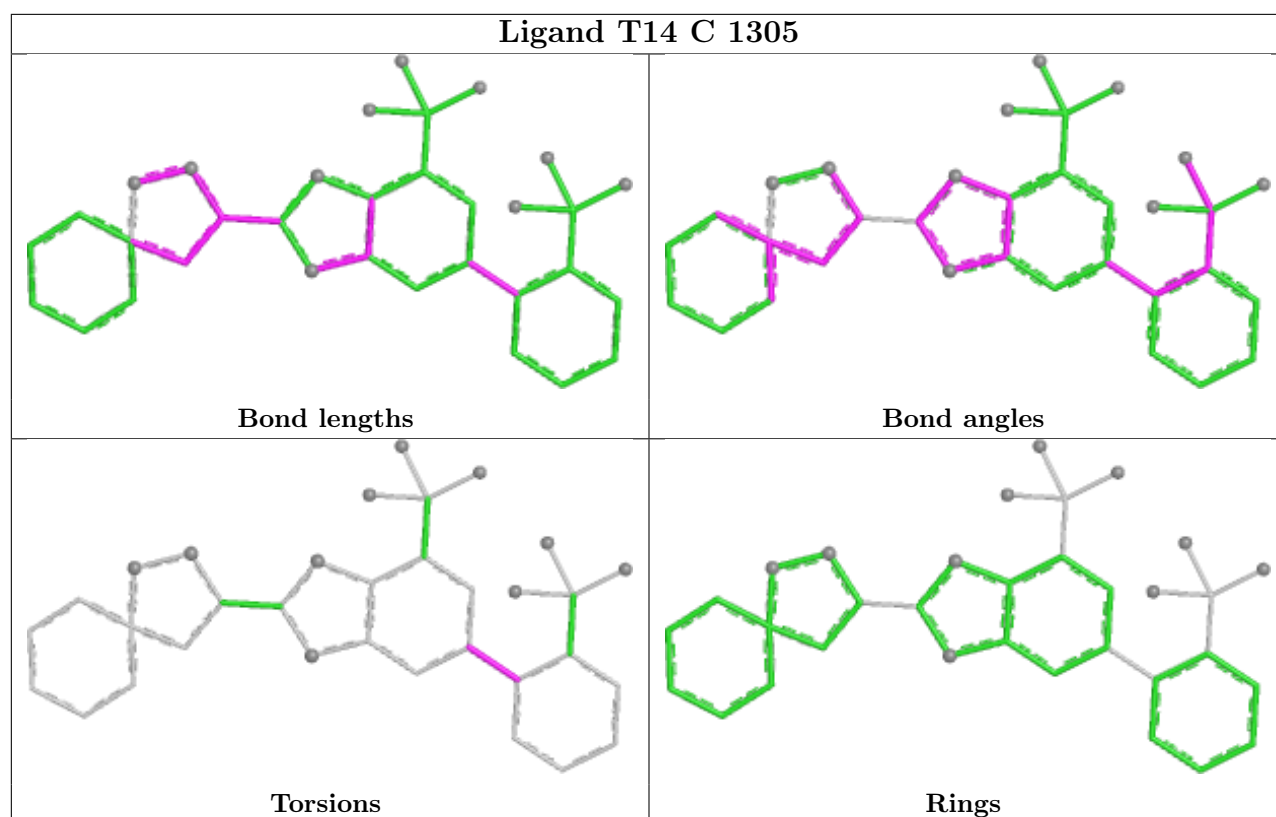












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

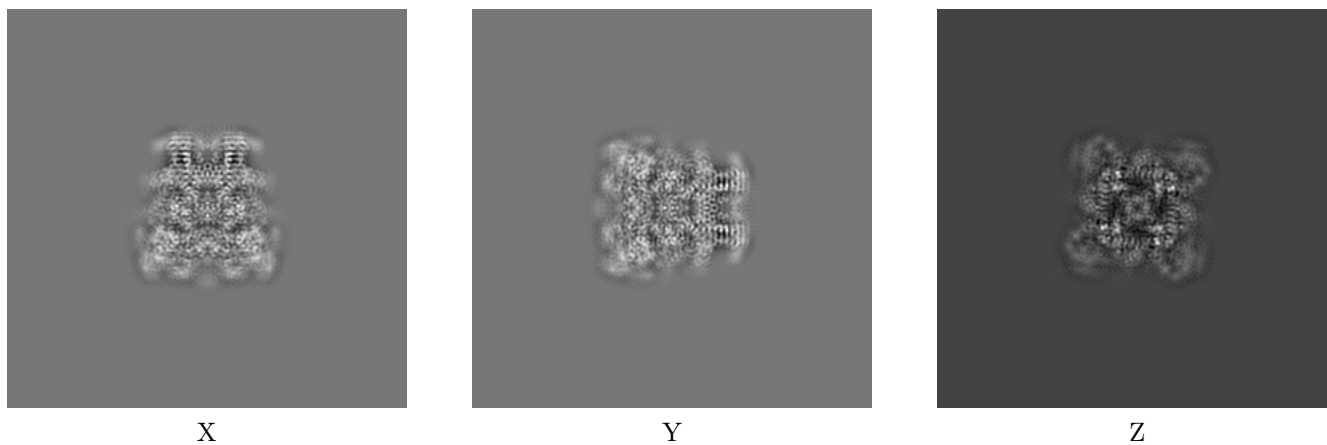
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0638. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

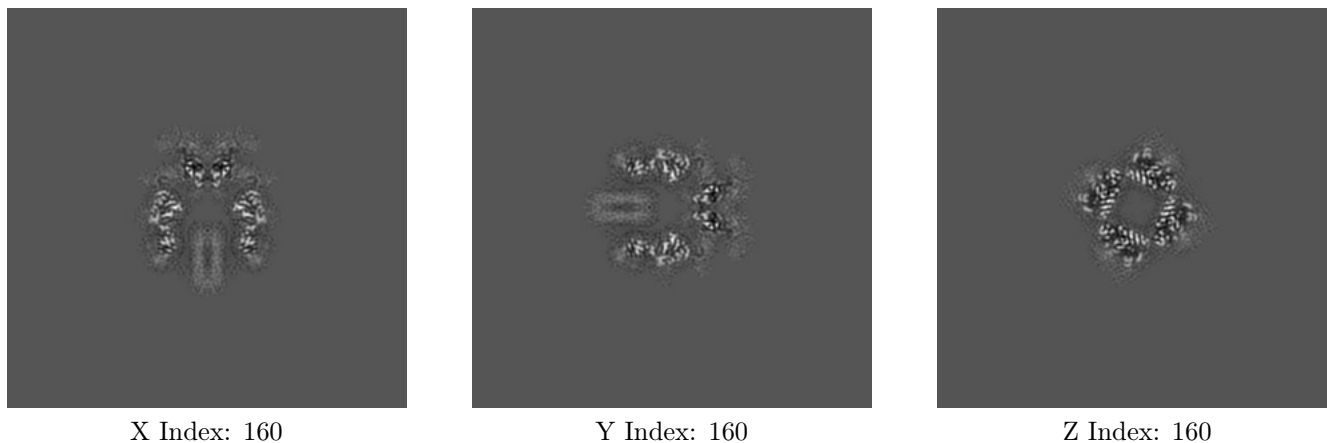
6.1.1 Primary map



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

6.2 Central slices [i](#)

6.2.1 Primary map



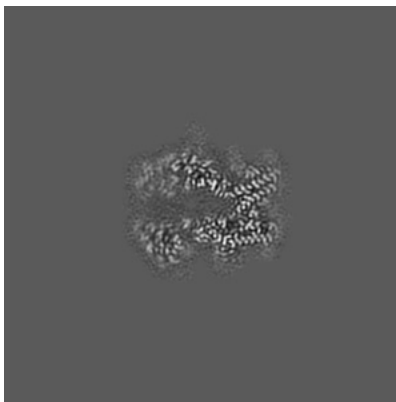
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

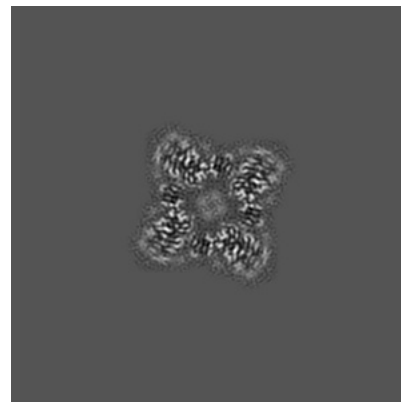
6.3.1 Primary map



X Index: 145



Y Index: 145

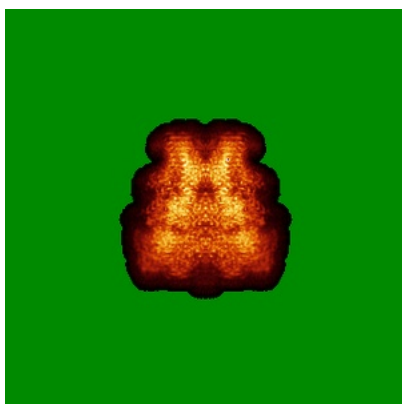


Z Index: 133

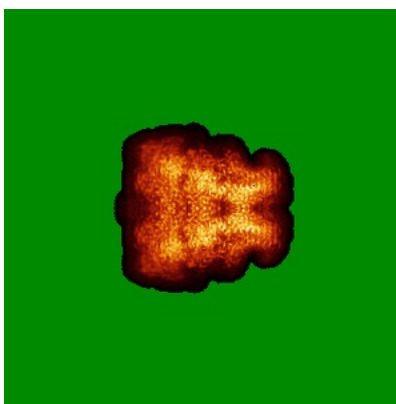
The images above show the largest variance slices of the map in three orthogonal directions.

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

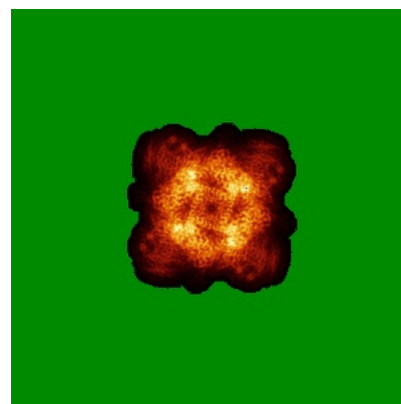
6.4.1 Primary map



X



Y

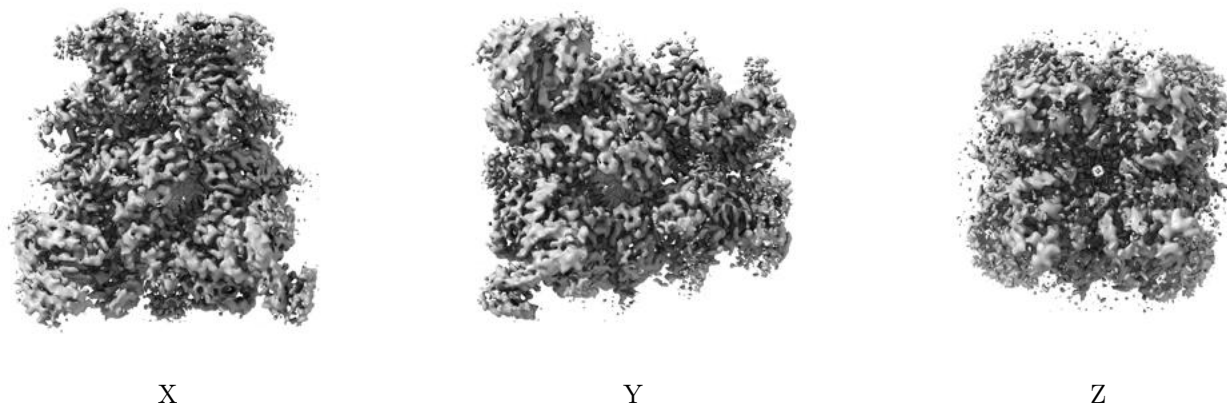


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

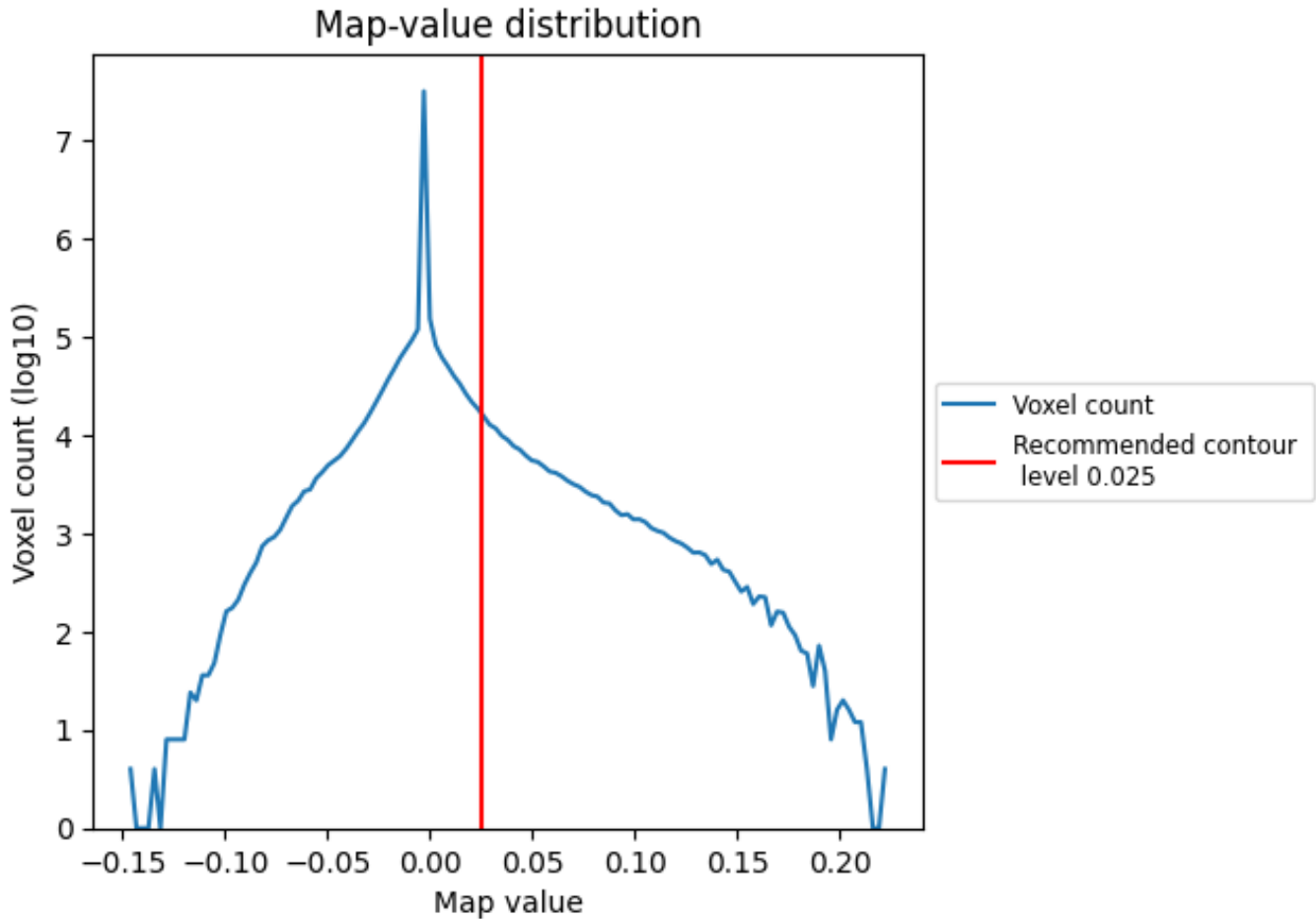
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

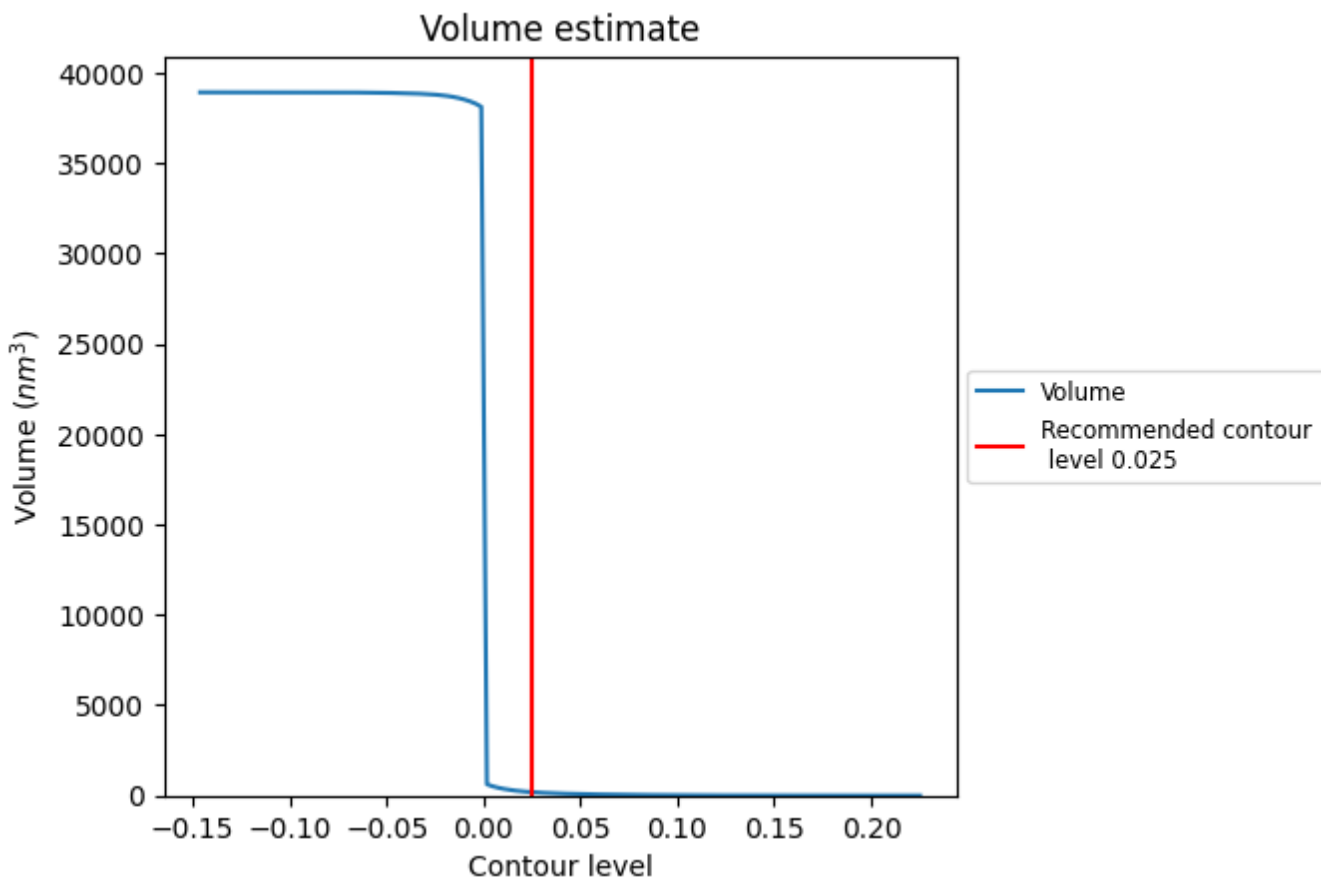
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

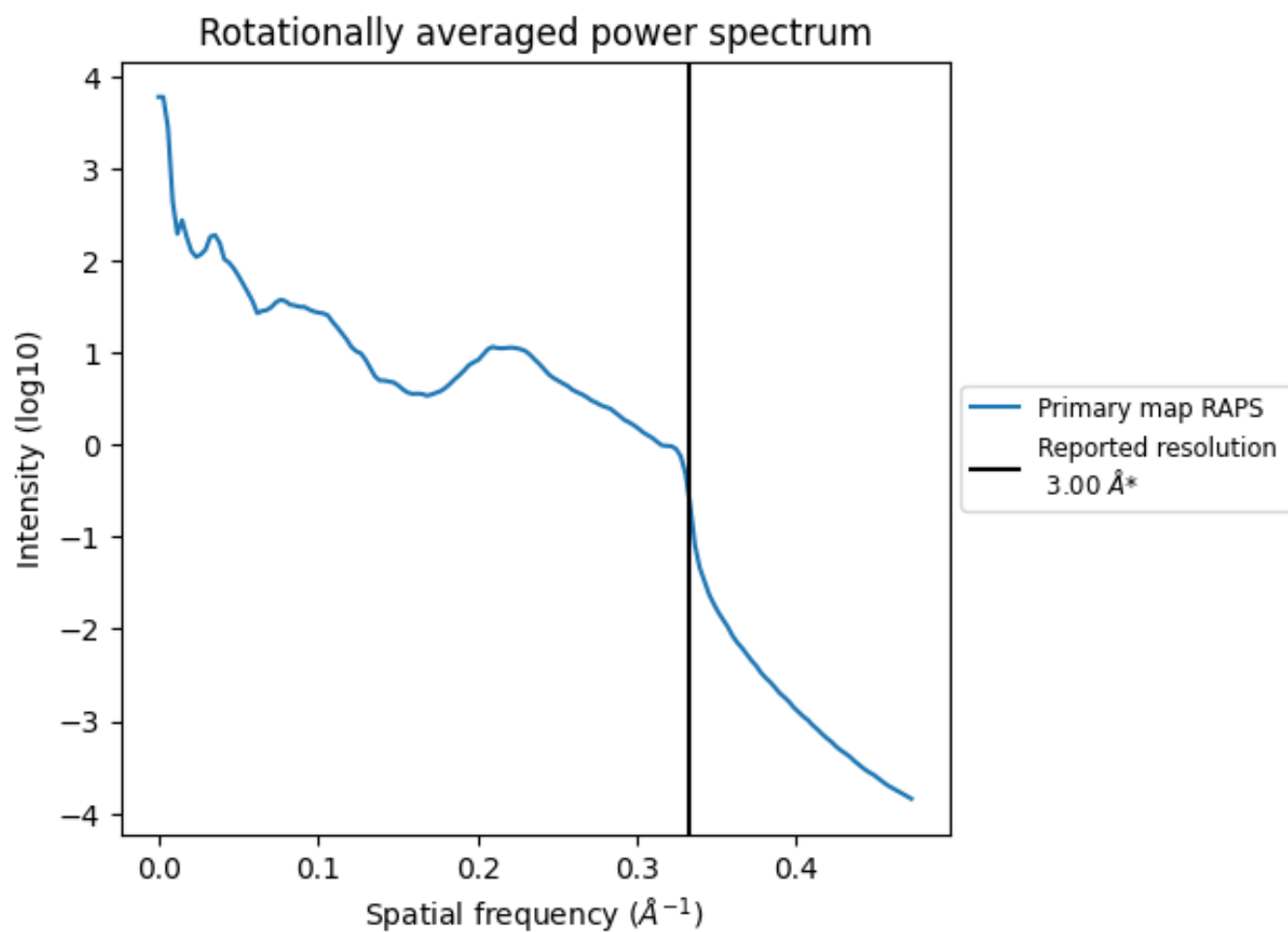
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 188 nm³; this corresponds to an approximate mass of 170 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 [i](#)

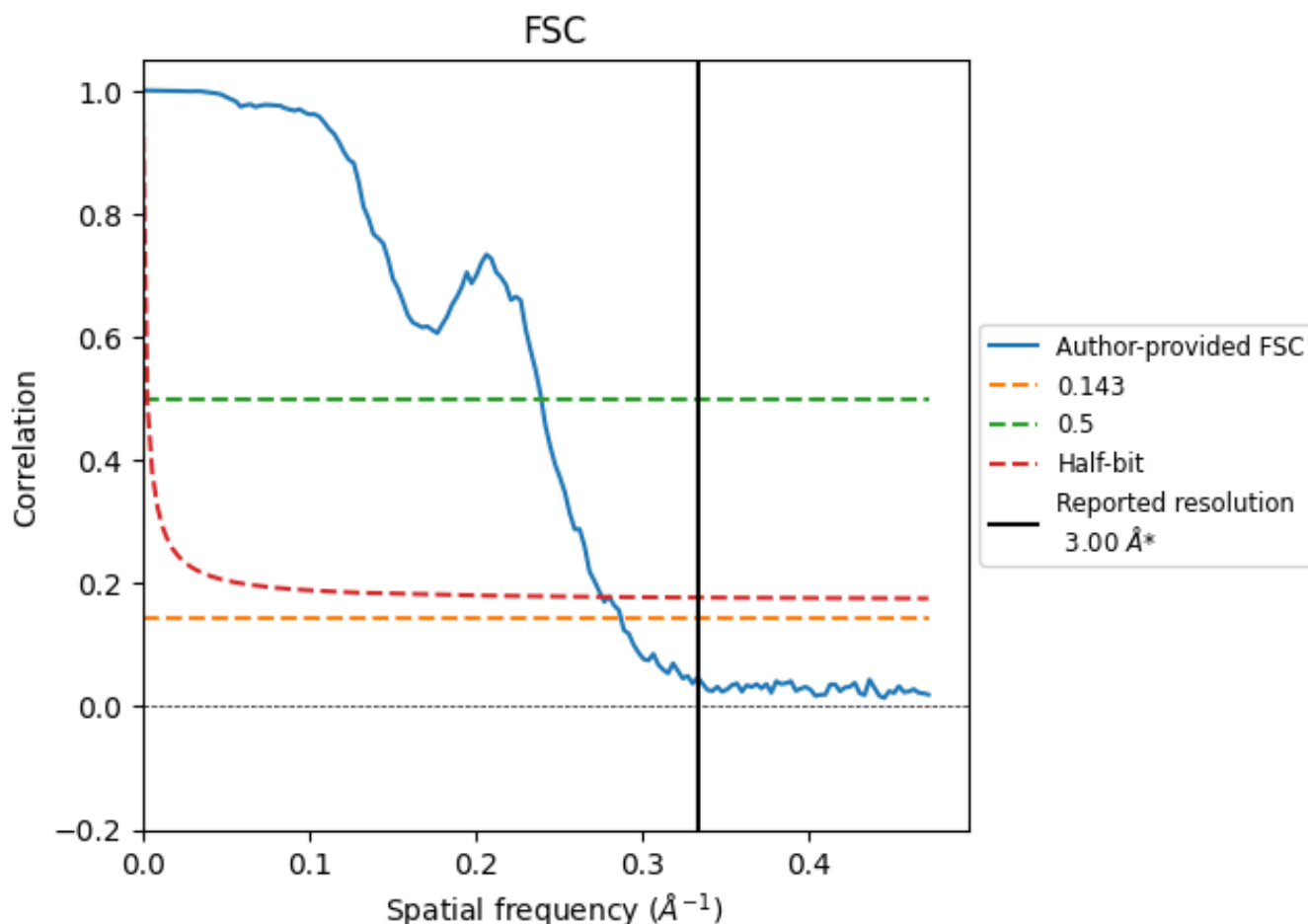


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.48	4.18	3.62
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.48 differs from the reported value 3.0 by more than 10 %

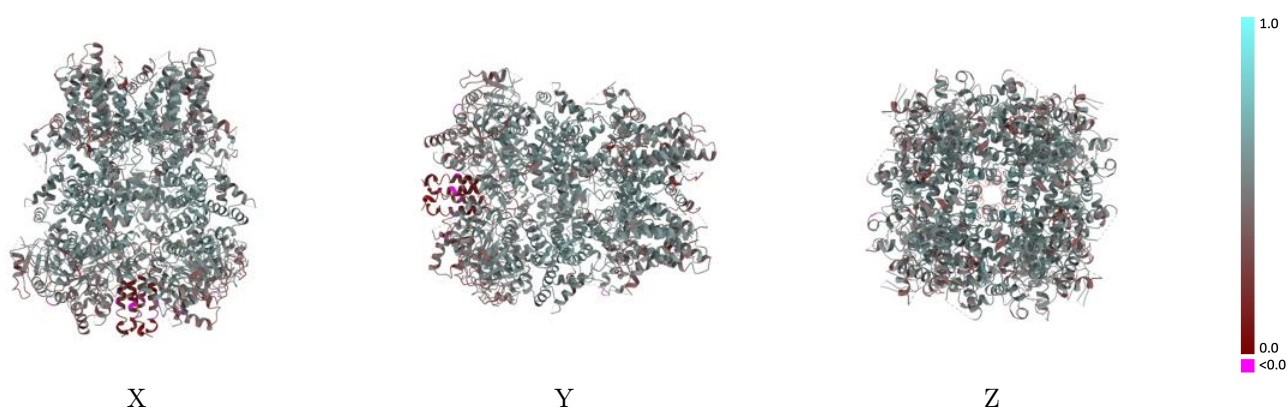
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0638 and PDB model 6O72. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)

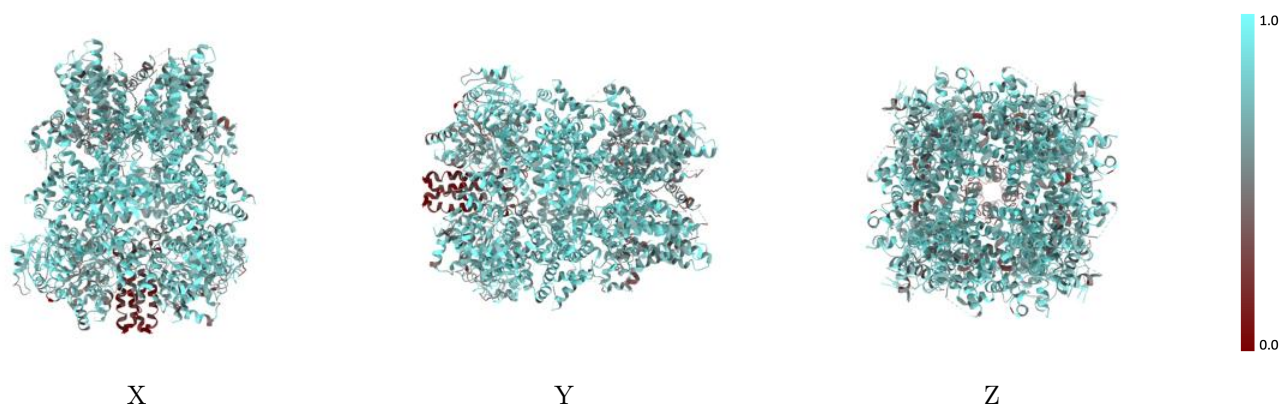
This section was not generated.

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



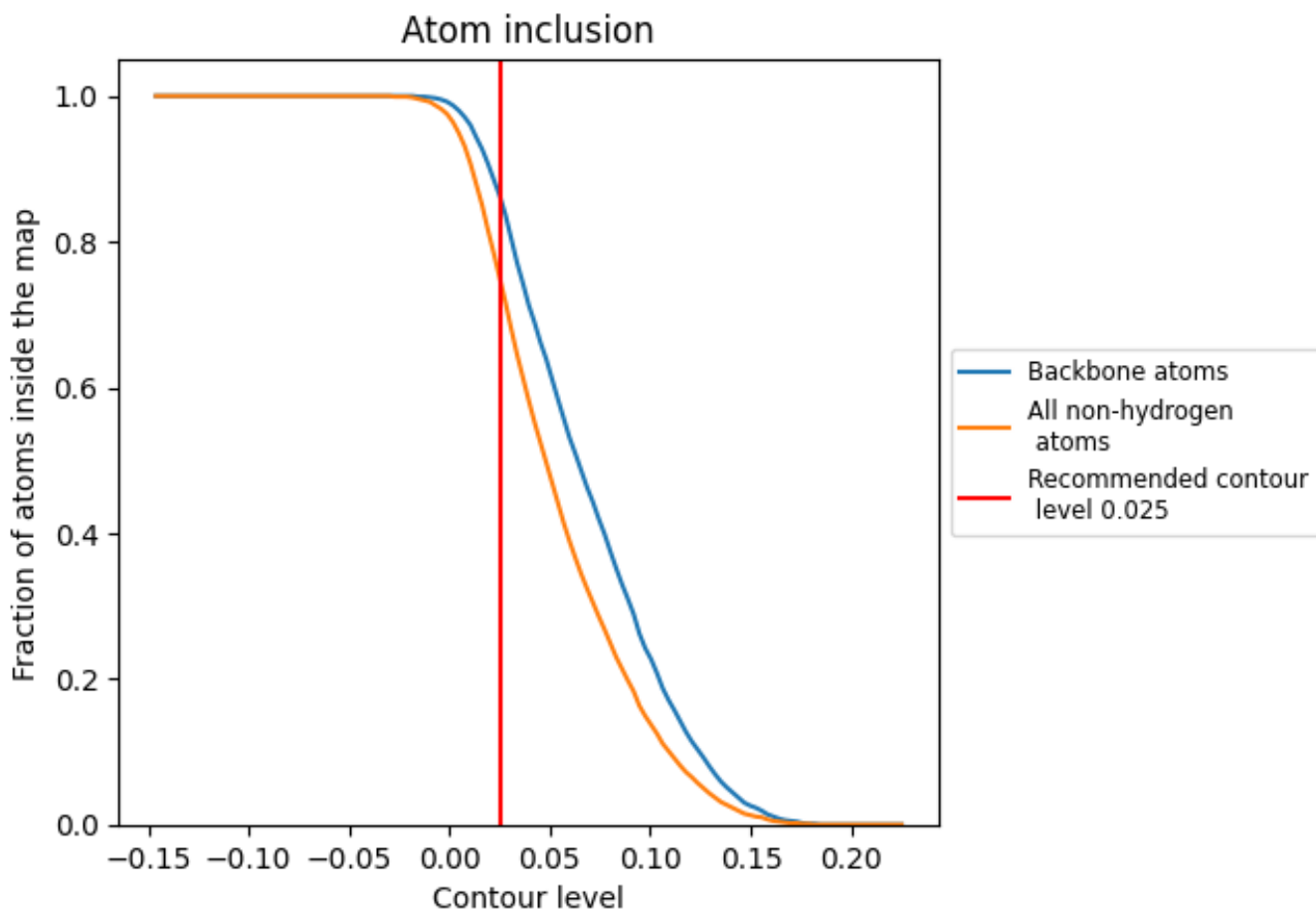
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.025).










9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 75% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7500	 0.4900
A	 0.7500	 0.4910
B	 0.7510	 0.4900
C	 0.7500	 0.4900
D	 0.7510	 0.4900

