



Full wwPDB EM Validation Report ⓘ

Mar 19, 2024 – 05:14 PM JST

PDB ID : 5ZX5
EMDB ID : EMD-6975
Title : 3.3 angstrom structure of mouse TRPM7 with EDTA
Authors : Zhang, J.; Li, Z.; Duan, J.; Li, J.; Hulse, R.E.; Santa-Cruz, A.; Abiria, S.A.; Krapivinsky, G.; Clapham, D.E.
Deposited on : 2018-05-18
Resolution : 3.28 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.dev70
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

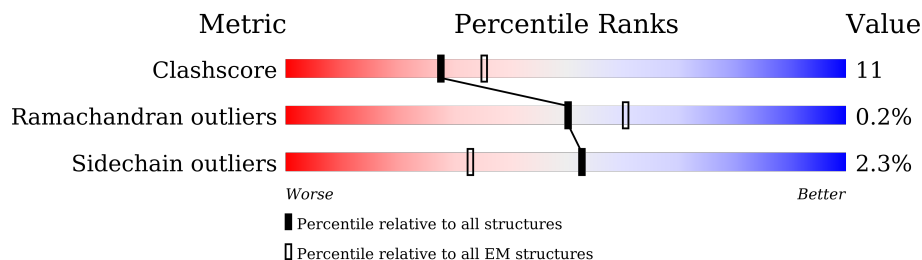
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.28 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	1229	
1	B	1229	
1	C	1229	
1	D	1229	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	Y01	A	1305	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	Y01	D	1303	-	-	X	-

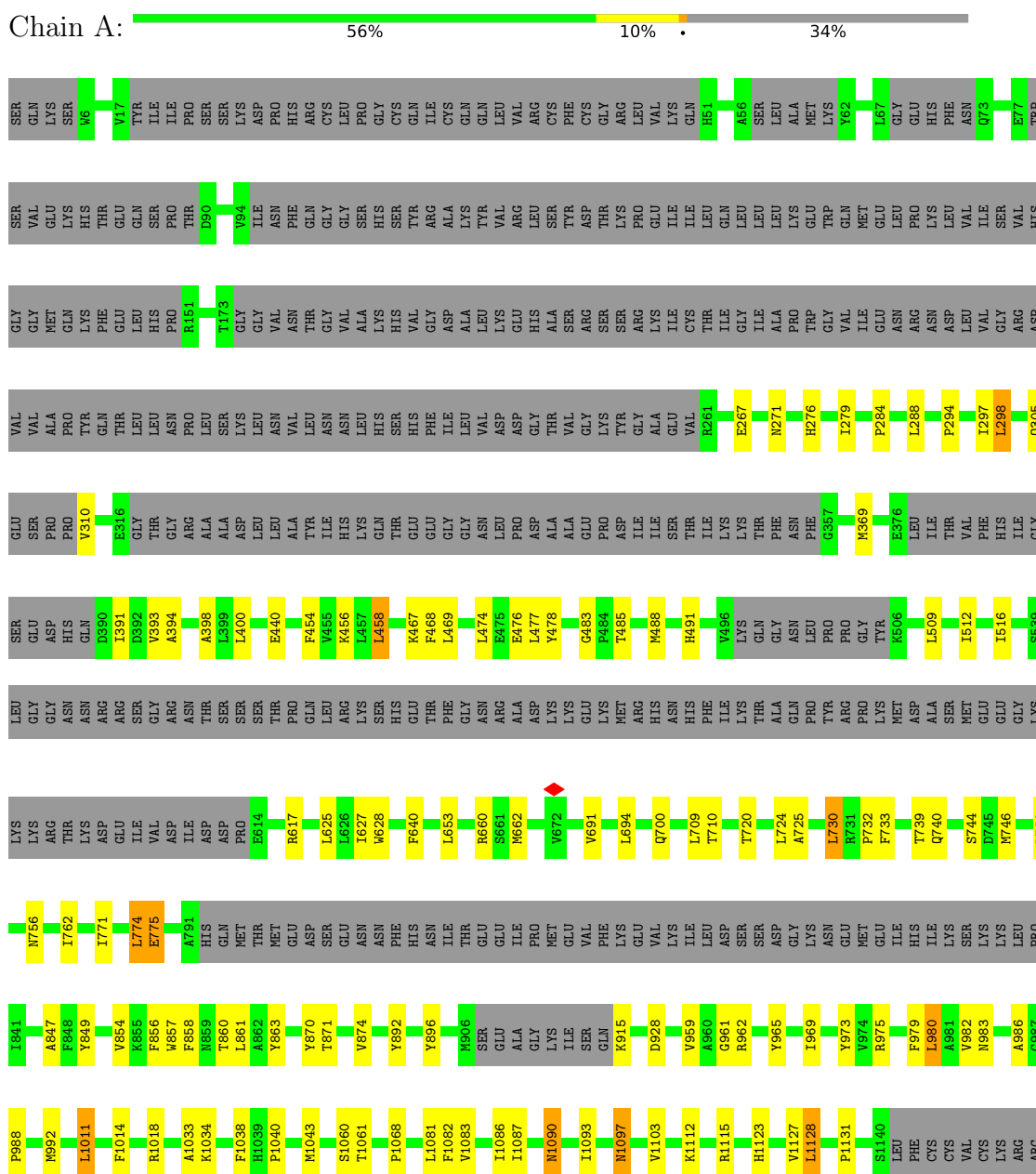
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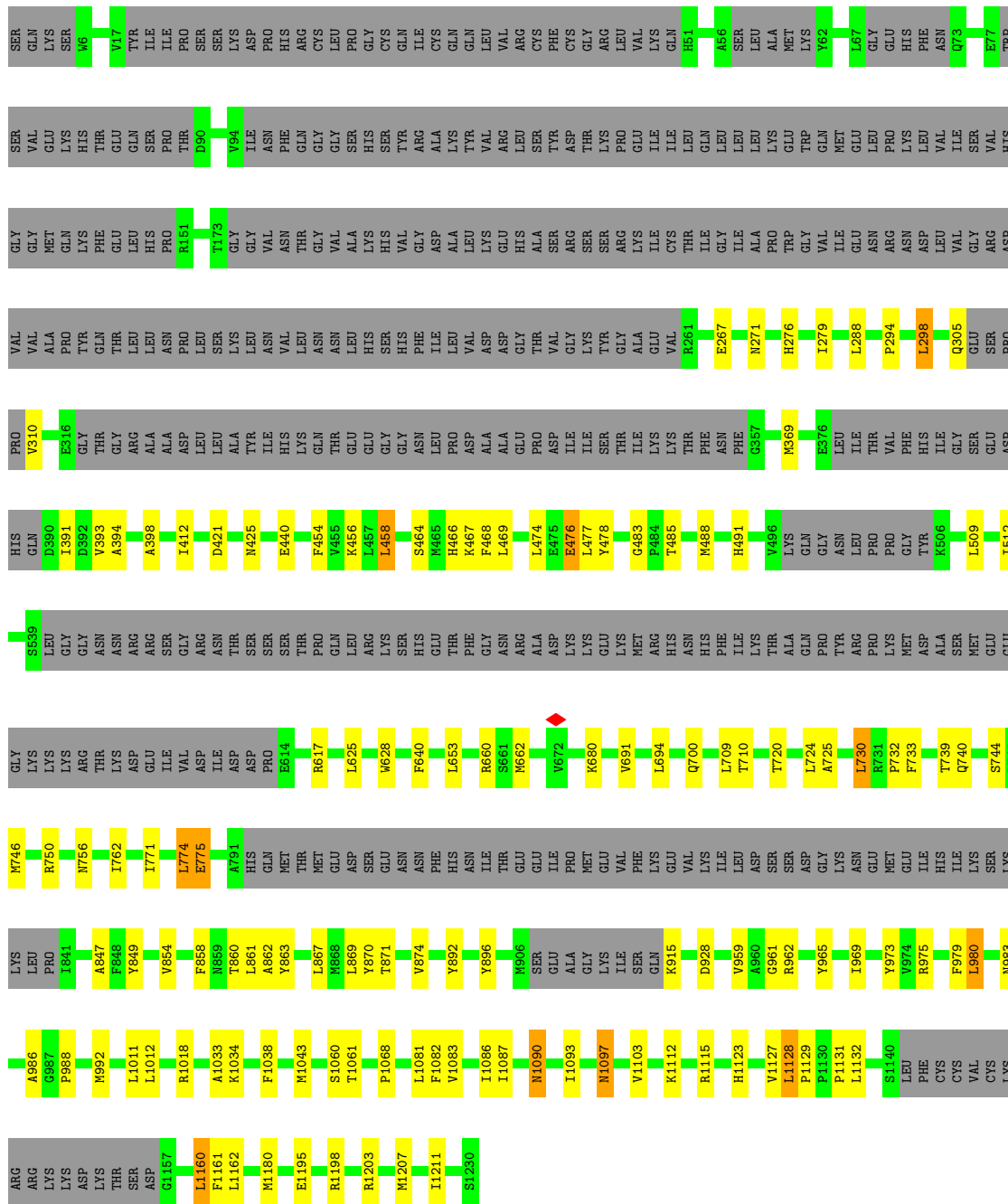
Mol	Chain	Residues	Atoms			AltConf
2	A	1	Total	C	O	0
			35	31	4	
2	A	1	Total	C	O	0
			35	31	4	
2	A	1	Total	C	O	0
			35	31	4	
2	B	1	Total	C	O	0
			35	31	4	
2	B	1	Total	C	O	0
			35	31	4	
2	C	1	Total	C	O	0
			35	31	4	
2	C	1	Total	C	O	0
			35	31	4	
2	D	1	Total	C	O	0
			35	31	4	
2	D	1	Total	C	O	0
			35	31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

3 Residue-property plots

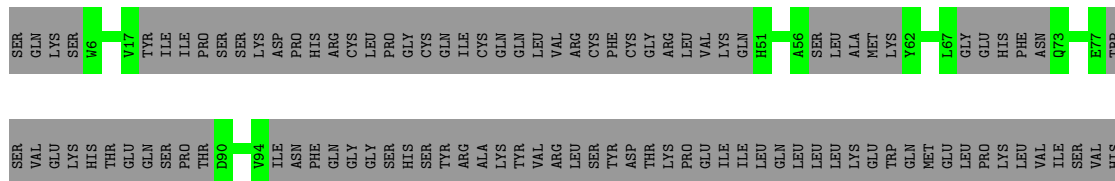
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: Transient receptor potential cation channel subfamily M member 7





● Molecule 1: Transient receptor potential cation channel subfamily M member 7



G1157	V1010	A847	I771	IIE	SER	HIS	PRO	VAL	GLY	VAL	VAL	GLY	GLY
L1011	L1012	F848	L774	ASP	GLY	GLN	D390	ALA	GLY	ALA	ALA	ALA	GLY
S1013	F1014	Y849	E775	IIE	ASN	I391	ILE	PRO	MET	PRO	ALA	GLN	GLY
F1014	R1018	V854	Y776	ASP	THR	D392	THR	GLN	PHE	THR	TYR	GLN	PHE
R1018	A1033	K855	P786	PRO	SER	V393	GLY	THR	GLY	THR	GLY	THR	GLY
A1033	K1034	F856	A791	E614	SER	A394	ARG	LEU	ARG	LEU	LEU	LEU	HIS
K1034	F1038	H857	HIS	R617	THR	A398	THR	ALA	ALA	ALA	ALA	LEU	HIS
F1038	M1043	F858	GLN	L625	PRO	E440	GLN	ASP	PRO	PRO	PRO	ASN	R151
M1043	P1068	L861	THR	W628	GLN	F454	LEU	LEU	LEU	LEU	LEU	LEU	T173
P1068	L1081	M868	MET	F640	ASN	V455	ARG	LEU	LEU	LEU	LEU	LEU	GLY
L1081	F1082	L889	GLU	L653	THR	K456	THR	ALA	ALA	ALA	ALA	LEU	GLY
F1082	V1083	T871	ASP	R660	GLY	L457	GLY	ALA	ALA	ALA	ALA	LEU	GLY
V1083	I1086	V874	SER	M662	ASN	L458	GLU	ALA	ALA	ALA	ALA	LEU	GLY
I1086	I1087	Y892	ASN	V672	THR	K467	THR	ALA	ALA	ALA	ALA	LEU	GLY
I1087	M1090	Y896	ILE	V691	THR	F468	GLY	ALA	ALA	ALA	ALA	LEU	GLY
M1090	I1093	S861	THR	L694	GLY	L469	ASN	ALA	ALA	ALA	ALA	LEU	GLY
I1093	M1097	M662	GLU	Q700	GLY	L474	ASN	ALA	ALA	ALA	ALA	LEU	GLY
M1097	V1103	V672	GLU	L709	THR	E475	ASN	ALA	ALA	ALA	ALA	LEU	GLY
V1103	K1112	V691	VAL	T710	ASN	L477	LEU	ALA	ALA	ALA	ALA	LEU	GLY
K1112	R1115	V691	PHE	T717	HIS	Y478	LEU	ALA	ALA	ALA	ALA	LEU	GLY
R1115	H1123	D928	LYS	S717	ASN	G483	LEU	ALA	ALA	ALA	ALA	LEU	GLY
H1123	V1127	V959	VAL	T720	THR	P484	LEU	ALA	ALA	ALA	ALA	LEU	GLY
V1127	L1128	A880	VAL	L724	ALA	T485	LEU	ALA	ALA	ALA	ALA	LEU	GLY
L1128	P1131	G961	VAL	A725	GLN	M488	LEU	ALA	ALA	ALA	ALA	LEU	GLY
P1131	S1140	R962	VAL	L730	THR	M488	LEU	ALA	ALA	ALA	ALA	LEU	GLY
S1140	LEU	Y965	VAL	R731	THR	H491	LEU	ALA	ALA	ALA	ALA	LEU	GLY
LEU	PHE	I969	VAL	F733	THR	V496	LEU	ALA	ALA	ALA	ALA	LEU	GLY
PHE	CYS	Y973	VAL	T739	ALA	LYS	LEU	ALA	ALA	ALA	ALA	LEU	GLY
CYS	CYS	V974	VAL	Q740	ASP	GLN	LEU	ALA	ALA	ALA	ALA	LEU	GLY
CYS	VAL	R975	VAL	R730	THR	ASN	LEU	ALA	ALA	ALA	ALA	LEU	GLY
VAL	CYS	L980	VAL	R731	THR	ASN	LEU	ALA	ALA	ALA	ALA	LEU	GLY
CYS	LYS	A981	VAL	F733	THR	ASN	LEU	ALA	ALA	ALA	ALA	LEU	GLY
LYS	ARG	V982	VAL	T739	ALA	ASN	LEU	ALA	ALA	ALA	ALA	LEU	GLY
ARG	ARG	R983	VAL	Q740	ASP	ASN	LEU	ALA	ALA	ALA	ALA	LEU	GLY
ARG	LYS	N983	VAL	S744	THR	ASN	LEU	ALA	ALA	ALA	ALA	LEU	GLY
LYS	LYS	P988	VAL	D746	THR	ASN	LEU	ALA	ALA	ALA	ALA	LEU	GLY
LYS	LYS	N982	VAL	W747	THR	ASN	LEU	ALA	ALA	ALA	ALA	LEU	GLY
LYS	ASP	P988	VAL	M746	THR	ASN	LEU	ALA	ALA	ALA	ALA	LEU	GLY
ASP	LYS	N992	VAL	W747	THR	ASN	LEU	ALA	ALA	ALA	ALA	LEU	GLY
LYS	THR	A1008	VAL	R750	THR	ASN	LEU	ALA	ALA	ALA	ALA	LEU	GLY
THR	THR	L1009	VAL	M756	THR	ASN	LEU	ALA	ALA	ALA	ALA	LEU	GLY
THR	ASP	L1009	VAL	I762	THR	ASN	LEU	ALA	ALA	ALA	ALA	LEU	GLY
ASP	ASP		VAL	I762	THR	ASN	LEU	ALA	ALA	ALA	ALA	LEU	GLY

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	1039775	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	56	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 BASE (4k x 4k)	Depositor
Maximum map value	0.377	Depositor
Minimum map value	-0.206	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.013	Depositor
Map size (Å)	314.88, 314.88, 314.88	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.23, 1.23, 1.23	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: Y01

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	0.68	0/6390	0.71	1/8683 (0.0%)
1	B	0.69	0/6390	0.71	2/8683 (0.0%)
1	C	0.68	0/6390	0.71	2/8683 (0.0%)
1	D	0.68	0/6390	0.70	2/8683 (0.0%)
All	All	0.68	0/25560	0.71	7/34732 (0.0%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	476	GLU	N-CA-C	-5.47	96.24	111.00
1	D	476	GLU	N-CA-C	-5.46	96.27	111.00
1	C	476	GLU	N-CA-C	-5.45	96.30	111.00
1	B	298	LEU	CA-CB-CG	-5.37	102.94	115.30
1	C	298	LEU	CA-CB-CG	-5.37	102.94	115.30
1	D	298	LEU	CA-CB-CG	-5.37	102.94	115.30
1	A	298	LEU	N-CA-C	5.31	125.33	111.00

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	6255	0	6057	142	0
1	B	6255	0	6057	132	0
1	C	6255	0	6057	116	0
1	D	6255	0	6057	125	0
2	A	175	0	245	57	0
2	B	70	0	98	17	0
2	C	70	0	98	13	0
2	D	105	0	147	32	0
All	All	25440	0	24816	536	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 11.

All (536) 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:D:982:VAL:HG23	2:D:1303:Y01:CAB	1.59	1.32
1:B:982:VAL:HG23	2:B:1302:Y01:CAA	1.75	1.16
2:C:1301:Y01:HAA3	2:C:1302:Y01:HAR2	1.16	1.13
2:C:1301:Y01:HAA3	2:C:1302:Y01:CAR	1.82	1.10
1:D:982:VAL:HG23	2:D:1303:Y01:HAB1	1.31	1.08
1:A:298:LEU:HD12	1:A:400:LEU:HD11	1.32	1.08
1:A:298:LEU:CD1	1:A:400:LEU:HD11	1.85	1.06
1:A:982:VAL:CG2	2:A:1305:Y01:HAB2	1.83	1.06
2:A:1305:Y01:HAE2	2:A:1305:Y01:HAO2	1.38	1.05
1:B:982:VAL:HG23	2:B:1302:Y01:HAA2	1.42	1.01
2:D:1302:Y01:HAA3	2:D:1303:Y01:CAR	1.89	1.01
1:D:856:PHE:HE2	2:D:1303:Y01:HAC3	1.29	0.97
1:D:856:PHE:CE2	2:D:1303:Y01:HAC3	2.02	0.95
1:D:982:VAL:CG2	2:D:1303:Y01:CAB	2.45	0.94
1:A:982:VAL:CG2	2:A:1305:Y01:CAB	2.46	0.93
1:C:694:LEU:CD1	1:C:709:LEU:HD21	1.99	0.92
1:B:694:LEU:CD1	1:B:709:LEU:HD21	1.99	0.92
1:A:694:LEU:CD1	1:A:709:LEU:HD21	1.99	0.92
2:A:1305:Y01:HAN2	2:A:1305:Y01:HAC3	1.50	0.92
2:C:1302:Y01:HAE2	2:C:1302:Y01:HAC1	1.54	0.90
1:B:982:VAL:HG23	2:B:1302:Y01:HAA1	1.52	0.89
2:A:1305:Y01:HAI	1:D:1009:LEU:HD11	1.55	0.88
2:D:1302:Y01:HAA3	2:D:1303:Y01:HAR1	1.55	0.88
2:A:1305:Y01:HAC3	2:A:1305:Y01:HAB1	1.55	0.88
1:A:298:LEU:CD1	1:A:400:LEU:CD1	2.52	0.86
2:C:1301:Y01:CAA	2:C:1302:Y01:HAR2	2.04	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1302:Y01:HAC1	2:B:1302:Y01:HAU2	1.58	0.85
1:D:775:GLU:O	1:D:776:TYR:CD1	2.29	0.85
1:B:775:GLU:O	1:B:776:TYR:CD1	2.29	0.85
2:A:1305:Y01:HAE3	2:A:1305:Y01:HAC2	1.58	0.85
1:A:874:VAL:HG11	1:A:969:ILE:HD11	1.60	0.83
1:B:874:VAL:HG11	1:B:969:ILE:HD11	1.61	0.83
1:B:1034:LYS:O	1:B:1038:PHE:HB2	1.79	0.83
1:D:1034:LYS:O	1:D:1038:PHE:HB2	1.79	0.83
1:D:874:VAL:HG11	1:D:969:ILE:HD11	1.60	0.82
1:C:1034:LYS:O	1:C:1038:PHE:HB2	1.79	0.82
2:A:1305:Y01:HAB1	2:A:1305:Y01:CAC	2.10	0.82
1:A:1034:LYS:O	1:A:1038:PHE:HB2	1.79	0.82
1:B:1160:LEU:HD22	1:B:1161:PHE:N	1.94	0.82
1:A:1160:LEU:HD22	1:A:1161:PHE:N	1.94	0.82
1:C:1160:LEU:HD22	1:C:1161:PHE:N	1.94	0.82
2:A:1304:Y01:HAA3	2:A:1305:Y01:HBC	1.62	0.81
1:A:982:VAL:HG23	2:A:1305:Y01:HAB2	1.62	0.81
1:D:1160:LEU:HD22	1:D:1161:PHE:N	1.94	0.81
1:C:874:VAL:HG11	1:C:969:ILE:HD11	1.60	0.81
1:B:454:PHE:O	1:B:458:LEU:HB2	1.83	0.79
1:D:454:PHE:O	1:D:458:LEU:HB2	1.83	0.79
1:A:454:PHE:O	1:A:458:LEU:HB2	1.83	0.79
1:A:477:LEU:HD23	1:A:477:LEU:O	1.83	0.79
1:A:298:LEU:HD12	1:A:400:LEU:CD1	2.14	0.78
1:D:980:LEU:HD22	1:D:980:LEU:O	1.84	0.78
2:A:1305:Y01:HAC3	2:A:1305:Y01:CAN	2.13	0.78
1:D:694:LEU:CD1	1:D:709:LEU:HD21	2.14	0.78
1:C:454:PHE:O	1:C:458:LEU:HB2	1.83	0.77
1:D:849:TYR:HB3	1:D:1127:VAL:HG11	1.67	0.77
1:B:982:VAL:CG2	2:B:1302:Y01:HAA1	2.15	0.77
1:A:849:TYR:HB3	1:A:1127:VAL:HG11	1.67	0.77
1:A:857:TRP:CH2	2:A:1305:Y01:HAO1	2.21	0.76
1:A:857:TRP:HH2	2:A:1305:Y01:HAO1	1.50	0.76
2:A:1305:Y01:HAC2	2:A:1305:Y01:CAE	2.15	0.76
1:A:694:LEU:HD11	1:A:709:LEU:HD21	1.69	0.75
1:A:982:VAL:HG21	2:A:1305:Y01:HAB2	1.67	0.75
2:A:1303:Y01:HAA3	2:B:1302:Y01:HAV1	1.69	0.75
1:B:694:LEU:HD11	1:B:709:LEU:HD21	1.68	0.74
1:D:477:LEU:HD23	1:D:477:LEU:O	1.88	0.74
1:C:1207:MET:HG2	1:D:1207:MET:HE3	1.69	0.74
1:C:709:LEU:HD13	1:C:739:THR:HG22	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:477:LEU:O	1:C:477:LEU:HD23	1.88	0.74
1:A:1014:PHE:HB2	2:A:1301:Y01:CAB	2.18	0.73
1:A:774:LEU:H	1:A:774:LEU:HD23	1.54	0.73
1:C:694:LEU:HD11	1:C:709:LEU:HD21	1.68	0.72
1:D:747:TRP:HE1	2:D:1303:Y01:HAA3	1.53	0.72
1:B:477:LEU:HD23	1:B:477:LEU:O	1.88	0.72
1:B:709:LEU:HD13	1:B:739:THR:HG22	1.69	0.72
1:B:1207:MET:HG2	1:C:1207:MET:HE3	1.71	0.72
1:A:709:LEU:HD13	1:A:739:THR:HG22	1.69	0.72
2:A:1305:Y01:HAN2	2:A:1305:Y01:CAC	2.19	0.72
1:D:982:VAL:HG23	2:D:1303:Y01:HAB3	1.69	0.72
1:D:694:LEU:HD11	1:D:709:LEU:HD21	1.72	0.71
1:A:476:GLU:O	1:A:477:LEU:HB3	1.89	0.71
2:D:1302:Y01:HAA3	2:D:1303:Y01:OAW	1.91	0.71
1:C:774:LEU:HD23	1:C:774:LEU:H	1.54	0.71
1:D:774:LEU:CG	1:D:775:GLU:H	2.04	0.70
1:A:1160:LEU:HD22	1:A:1161:PHE:H	1.53	0.70
1:B:774:LEU:CG	1:B:775:GLU:H	2.04	0.70
1:C:1127:VAL:O	1:C:1128:LEU:HD22	1.92	0.69
2:A:1305:Y01:HAE2	2:A:1305:Y01:CAO	2.15	0.69
1:B:774:LEU:HG	1:B:775:GLU:H	1.58	0.69
1:D:474:LEU:O	1:D:478:TYR:HB2	1.92	0.69
2:A:1305:Y01:CAB	2:A:1305:Y01:HAC3	2.22	0.69
1:B:1127:VAL:O	1:B:1128:LEU:HD13	1.92	0.69
1:A:474:LEU:O	1:A:478:TYR:HB2	1.92	0.69
1:D:774:LEU:HG	1:D:775:GLU:H	1.57	0.69
1:B:474:LEU:O	1:B:478:TYR:HB2	1.92	0.69
1:B:1011:LEU:HD23	1:B:1011:LEU:O	1.93	0.69
1:C:1011:LEU:HD23	1:C:1011:LEU:O	1.93	0.69
1:C:474:LEU:O	1:C:478:TYR:HB2	1.92	0.69
1:D:982:VAL:CG2	2:D:1303:Y01:HAB3	2.23	0.69
1:B:1127:VAL:O	1:B:1128:LEU:HD22	1.92	0.69
1:C:1127:VAL:O	1:C:1128:LEU:HD13	1.92	0.69
1:A:982:VAL:HG22	2:A:1305:Y01:HAB1	1.76	0.68
2:A:1301:Y01:HAU2	2:A:1301:Y01:HAC1	1.74	0.68
1:C:1160:LEU:HD22	1:C:1161:PHE:H	1.59	0.68
1:D:1011:LEU:O	1:D:1011:LEU:HD23	1.93	0.68
1:D:1160:LEU:HD22	1:D:1161:PHE:H	1.59	0.67
1:C:710:THR:HA	1:C:720:THR:HG23	1.77	0.67
1:B:710:THR:HA	1:B:720:THR:HG23	1.77	0.67
1:A:857:TRP:CZ2	2:A:1305:Y01:HAJ1	2.30	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1303:Y01:HAA3	2:B:1302:Y01:CAV	2.24	0.66
1:B:1160:LEU:HD22	1:B:1161:PHE:H	1.59	0.66
2:C:1301:Y01:CAA	2:C:1302:Y01:CAR	2.70	0.66
1:A:710:THR:HA	1:A:720:THR:HG23	1.77	0.65
1:B:980:LEU:HA	2:B:1302:Y01:CAE	2.27	0.65
1:D:982:VAL:HG23	2:D:1303:Y01:HAB2	1.68	0.65
1:A:1207:MET:CE	1:D:1211:ILE:HD12	2.27	0.64
1:B:988:PRO:O	1:B:992:MET:HB2	1.97	0.64
1:A:988:PRO:O	1:A:992:MET:HB2	1.97	0.64
1:C:988:PRO:O	1:C:992:MET:HB2	1.97	0.64
1:A:1207:MET:HG2	1:B:1207:MET:HE3	1.80	0.64
2:D:1302:Y01:CAA	2:D:1303:Y01:HAR1	2.26	0.64
1:D:988:PRO:O	1:D:992:MET:HB2	1.97	0.63
1:A:983:ASN:HB3	2:A:1305:Y01:HBA	1.80	0.63
1:B:896:TYR:OH	1:B:975:ARG:NH1	2.32	0.63
1:C:896:TYR:OH	1:C:975:ARG:NH1	2.32	0.63
1:A:1033:ALA:HB2	2:A:1303:Y01:HAK1	1.81	0.62
1:D:896:TYR:OH	1:D:975:ARG:NH1	2.32	0.62
1:D:710:THR:HA	1:D:720:THR:HG23	1.81	0.62
1:A:979:PHE:HB3	2:A:1305:Y01:CAP	2.29	0.62
1:A:730:LEU:HD12	1:A:733:PHE:HB2	1.82	0.62
1:A:896:TYR:OH	1:A:975:ARG:NH1	2.32	0.62
1:A:857:TRP:CZ2	2:A:1305:Y01:CAJ	2.83	0.62
1:B:771:ILE:O	1:B:774:LEU:HD22	2.00	0.62
1:D:730:LEU:HD12	1:D:733:PHE:HB2	1.82	0.62
1:A:961:GLY:O	1:A:965:TYR:HB2	2.00	0.61
1:B:774:LEU:HD23	1:B:774:LEU:H	1.65	0.61
1:D:961:GLY:O	1:D:965:TYR:HB2	2.00	0.61
1:C:961:GLY:O	1:C:965:TYR:HB2	2.00	0.61
1:A:1093:ILE:O	1:A:1097:ASN:HB2	2.01	0.61
1:A:982:VAL:HG22	2:A:1305:Y01:CAB	2.26	0.61
1:D:1093:ILE:O	1:D:1097:ASN:HB2	2.01	0.61
1:B:1093:ILE:O	1:B:1097:ASN:HB2	2.01	0.61
1:C:730:LEU:HD12	1:C:733:PHE:HB2	1.82	0.61
1:B:961:GLY:O	1:B:965:TYR:HB2	2.00	0.61
1:D:771:ILE:O	1:D:774:LEU:HD22	2.00	0.60
1:D:774:LEU:HD23	1:D:774:LEU:H	1.65	0.60
1:C:1093:ILE:O	1:C:1097:ASN:HB2	2.01	0.60
1:B:730:LEU:HD12	1:B:733:PHE:HB2	1.82	0.60
2:D:1302:Y01:HAA3	2:D:1303:Y01:CBC	2.32	0.60
1:D:1195:GLU:OE2	1:D:1198:ARG:NH1	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1195:GLU:OE2	1:A:1198:ARG:NH1	2.35	0.59
1:A:1207:MET:HE3	1:D:1207:MET:HG2	1.85	0.59
1:B:980:LEU:CD2	1:B:986:ALA:CB	2.81	0.59
1:A:980:LEU:CD2	1:A:986:ALA:CB	2.81	0.59
1:C:980:LEU:CD2	1:C:986:ALA:CB	2.81	0.59
1:C:1195:GLU:OE2	1:C:1198:ARG:NH1	2.35	0.59
1:C:771:ILE:O	1:C:774:LEU:HD22	2.03	0.59
1:B:1034:LYS:O	1:B:1038:PHE:CB	2.51	0.58
1:B:863:TYR:CD2	1:B:979:PHE:HE2	2.21	0.58
1:B:1195:GLU:OE2	1:B:1198:ARG:NH1	2.35	0.58
1:D:1127:VAL:O	1:D:1128:LEU:HD13	2.03	0.58
1:D:1083:VAL:HA	1:D:1087:ILE:HD12	1.85	0.58
1:C:863:TYR:CD2	1:C:979:PHE:HE2	2.21	0.58
1:D:1034:LYS:O	1:D:1038:PHE:CB	2.51	0.58
1:A:709:LEU:CD1	1:A:739:THR:HG22	2.34	0.58
1:A:863:TYR:CD2	1:A:979:PHE:HE2	2.21	0.58
1:A:1207:MET:HE3	1:D:1211:ILE:HD12	1.84	0.58
1:A:771:ILE:O	1:A:774:LEU:HD22	2.03	0.58
1:A:1083:VAL:HA	1:A:1087:ILE:HD12	1.85	0.58
1:B:1008:ALA:HB1	2:C:1302:Y01:HAL2	1.85	0.57
1:D:744:SER:OG	1:D:1115:ARG:NH2	2.37	0.57
2:D:1302:Y01:HAB2	2:D:1303:Y01:HAR2	1.86	0.57
1:B:980:LEU:HA	2:B:1302:Y01:HAE3	1.85	0.57
1:A:1011:LEU:O	1:A:1011:LEU:HD23	2.03	0.57
1:A:1127:VAL:O	1:A:1128:LEU:HD13	2.04	0.57
1:B:744:SER:OG	1:B:1115:ARG:NH2	2.37	0.57
1:C:744:SER:OG	1:C:1115:ARG:NH2	2.37	0.57
1:D:488:MET:HA	1:D:491:HIS:HD2	1.70	0.57
1:D:709:LEU:HD13	1:D:739:THR:HG22	1.85	0.57
1:A:488:MET:HA	1:A:491:HIS:HD2	1.70	0.57
1:C:488:MET:HA	1:C:491:HIS:HD2	1.70	0.57
1:A:979:PHE:HB3	2:A:1305:Y01:HAP2	1.86	0.57
1:A:509:LEU:HA	1:A:512:ILE:HD12	1.87	0.57
1:B:509:LEU:HA	1:B:512:ILE:HD12	1.87	0.57
1:C:1083:VAL:HA	1:C:1087:ILE:HD12	1.85	0.57
1:A:271:ASN:HD22	1:A:297:ILE:CD1	2.18	0.56
1:C:509:LEU:HA	1:C:512:ILE:HD12	1.87	0.56
1:C:980:LEU:HD21	1:C:986:ALA:CB	2.35	0.56
1:A:982:VAL:HG23	2:A:1305:Y01:CAB	2.28	0.56
1:B:1083:VAL:HA	1:B:1087:ILE:HD12	1.85	0.56
1:D:509:LEU:HA	1:D:512:ILE:HD12	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1304:Y01:CAA	2:A:1305:Y01:HBC	2.33	0.56
1:B:980:LEU:HD21	1:B:986:ALA:CB	2.35	0.56
1:C:980:LEU:HD23	1:C:980:LEU:O	2.06	0.56
1:C:1211:ILE:CD1	1:D:1207:MET:HE2	2.35	0.56
1:D:476:GLU:O	1:D:477:LEU:HB3	2.05	0.56
1:A:744:SER:OG	1:A:1115:ARG:NH2	2.37	0.56
1:A:980:LEU:HD23	1:A:980:LEU:O	2.06	0.56
1:C:476:GLU:O	1:C:477:LEU:HB3	2.05	0.56
1:C:874:VAL:HG21	1:C:969:ILE:HD11	1.87	0.56
1:A:980:LEU:HD21	1:A:986:ALA:CB	2.35	0.56
1:B:709:LEU:CD1	1:B:739:THR:HG22	2.34	0.56
1:A:467:LYS:HA	1:A:617:ARG:HE	1.71	0.56
1:D:874:VAL:HG21	1:D:969:ILE:HD11	1.87	0.56
2:C:1302:Y01:HAN1	2:C:1302:Y01:HAP1	1.87	0.56
1:B:874:VAL:HG21	1:B:969:ILE:HD11	1.87	0.56
1:B:980:LEU:O	1:B:980:LEU:HD23	2.06	0.56
1:A:874:VAL:HG21	1:A:969:ILE:HD11	1.87	0.55
1:A:1207:MET:HE2	1:D:1211:ILE:CD1	2.36	0.55
1:B:267:GLU:O	1:B:271:ASN:HB2	2.06	0.55
1:B:488:MET:HA	1:B:491:HIS:HD2	1.70	0.55
1:C:1127:VAL:C	1:C:1128:LEU:HD22	2.26	0.55
1:D:982:VAL:CG2	2:D:1303:Y01:HAB1	2.21	0.55
1:B:467:LYS:HA	1:B:617:ARG:HE	1.71	0.55
1:D:774:LEU:CD2	1:D:775:GLU:H	2.20	0.55
1:A:476:GLU:O	1:A:477:LEU:CB	2.53	0.55
1:A:477:LEU:HD21	1:A:628:TRP:CE2	2.41	0.55
1:B:1127:VAL:C	1:B:1128:LEU:HD22	2.26	0.55
1:A:271:ASN:ND2	1:A:297:ILE:HD13	2.22	0.55
1:C:267:GLU:O	1:C:271:ASN:HB2	2.06	0.55
1:C:1034:LYS:O	1:C:1038:PHE:CB	2.51	0.55
1:A:1034:LYS:O	1:A:1038:PHE:CB	2.51	0.55
1:B:476:GLU:O	1:B:477:LEU:HB3	2.05	0.55
1:B:774:LEU:CD2	1:B:775:GLU:H	2.20	0.55
1:C:709:LEU:CD1	1:C:739:THR:HG22	2.34	0.55
1:A:267:GLU:O	1:A:271:ASN:HB2	2.06	0.54
1:C:467:LYS:HA	1:C:617:ARG:HE	1.71	0.54
1:D:267:GLU:O	1:D:271:ASN:HB2	2.06	0.54
1:A:774:LEU:H	1:A:774:LEU:CD2	2.21	0.54
1:C:762:ILE:HG23	1:C:861:LEU:HD11	1.90	0.54
1:C:849:TYR:HB3	1:C:1127:VAL:HG11	1.90	0.54
1:D:467:LYS:HA	1:D:617:ARG:HE	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:762:ILE:HG23	1:D:861:LEU:HD11	1.90	0.54
1:B:762:ILE:HG23	1:B:861:LEU:HD11	1.90	0.54
1:B:849:TYR:HB3	1:B:1127:VAL:HG11	1.90	0.53
1:B:1211:ILE:CD1	1:C:1207:MET:HE2	2.37	0.53
1:B:1014:PHE:HB2	2:B:1301:Y01:HAA1	1.90	0.53
1:C:862:ALA:HB3	1:C:1129:PRO:HB3	1.91	0.53
1:A:284:PRO:HG2	1:A:298:LEU:HB2	1.90	0.53
1:A:857:TRP:CH2	2:A:1305:Y01:CAO	2.89	0.53
1:A:1127:VAL:O	1:A:1128:LEU:HD22	2.09	0.53
1:A:762:ILE:HG23	1:A:861:LEU:HD11	1.90	0.53
1:B:862:ALA:HB3	1:B:1129:PRO:HB3	1.91	0.53
1:C:394:ALA:O	1:C:398:ALA:CB	2.57	0.53
1:A:394:ALA:O	1:A:398:ALA:CB	2.57	0.53
1:D:1127:VAL:O	1:D:1128:LEU:HD22	2.09	0.53
1:D:394:ALA:O	1:D:398:ALA:HB3	2.09	0.53
1:A:394:ALA:O	1:A:398:ALA:HB3	2.09	0.52
2:A:1305:Y01:CAB	2:A:1305:Y01:CAC	2.85	0.52
1:B:394:ALA:O	1:B:398:ALA:CB	2.57	0.52
1:D:394:ALA:O	1:D:398:ALA:CB	2.57	0.52
1:B:394:ALA:O	1:B:398:ALA:HB3	2.09	0.52
1:A:750:ARG:HG2	1:A:847:ALA:HB1	1.92	0.52
2:A:1301:Y01:HAR1	1:B:923:TYR:CB	2.39	0.52
2:A:1305:Y01:HAL2	1:D:1008:ALA:HB1	1.91	0.52
1:D:509:LEU:HD23	1:D:512:ILE:HD12	1.92	0.52
1:A:440:GLU:HG3	1:A:468:PHE:HD1	1.75	0.52
1:B:750:ARG:HG2	1:B:847:ALA:HB1	1.92	0.52
1:D:440:GLU:HG3	1:D:468:PHE:HD1	1.75	0.52
1:B:1082:PHE:O	1:B:1086:ILE:HB	2.10	0.52
1:C:440:GLU:HG3	1:C:468:PHE:HD1	1.75	0.52
1:B:440:GLU:HG3	1:B:468:PHE:HD1	1.75	0.51
1:B:1207:MET:HG2	1:C:1207:MET:CE	2.39	0.51
2:C:1301:Y01:HAA3	2:C:1302:Y01:HAR1	1.85	0.51
1:D:774:LEU:H	1:D:774:LEU:CD2	2.23	0.51
1:A:477:LEU:CD2	1:A:628:TRP:CE2	2.93	0.51
1:A:509:LEU:HD23	1:A:512:ILE:HD12	1.92	0.51
2:C:1302:Y01:HAR1	2:C:1302:Y01:OAG	2.10	0.51
1:B:1211:ILE:HD12	1:C:1207:MET:CE	2.41	0.51
1:C:1082:PHE:O	1:C:1086:ILE:HB	2.10	0.51
1:D:750:ARG:HG2	1:D:847:ALA:HB1	1.92	0.51
1:C:774:LEU:N	1:C:774:LEU:CD2	2.73	0.51
1:A:1207:MET:CE	1:D:1211:ILE:CD1	2.88	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:391:ILE:HG22	1:D:393:VAL:H	1.76	0.51
1:A:774:LEU:CD2	1:A:774:LEU:N	2.73	0.51
1:C:394:ALA:O	1:C:398:ALA:HB3	2.09	0.51
1:C:774:LEU:H	1:C:774:LEU:CD2	2.21	0.51
1:C:1211:ILE:HD12	1:D:1207:MET:CE	2.41	0.51
1:A:1207:MET:CE	1:D:1207:MET:HG2	2.41	0.51
1:A:1211:ILE:HD12	1:B:1207:MET:CE	2.41	0.51
1:C:750:ARG:HG2	1:C:847:ALA:HB1	1.92	0.51
2:D:1303:Y01:CAB	2:D:1303:Y01:HAO2	2.41	0.51
1:A:1014:PHE:HB2	2:A:1301:Y01:HAB1	1.91	0.51
1:C:509:LEU:HD23	1:C:512:ILE:HD12	1.92	0.51
2:A:1305:Y01:HAR1	2:A:1305:Y01:OAG	2.11	0.51
1:A:1082:PHE:O	1:A:1086:ILE:HB	2.10	0.50
1:B:509:LEU:HD23	1:B:512:ILE:HD12	1.92	0.50
1:B:774:LEU:H	1:B:774:LEU:CD2	2.23	0.50
1:D:774:LEU:HD23	1:D:775:GLU:H	1.77	0.50
1:A:488:MET:HE1	1:A:662:MET:HB3	1.93	0.50
2:A:1301:Y01:HAU2	2:A:1301:Y01:CAC	2.40	0.50
1:C:1129:PRO:HB2	1:C:1131:PRO:HD2	1.93	0.50
1:C:1211:ILE:HD12	1:D:1207:MET:HE2	1.92	0.50
1:D:1082:PHE:O	1:D:1086:ILE:HB	2.10	0.50
1:B:391:ILE:HG22	1:B:393:VAL:H	1.76	0.50
1:A:774:LEU:HD23	1:A:774:LEU:N	2.23	0.50
1:B:276:HIS:HB2	1:B:279:ILE:HB	1.94	0.50
1:B:1129:PRO:HB2	1:B:1131:PRO:HD2	1.93	0.50
1:A:391:ILE:HG22	1:A:393:VAL:H	1.76	0.50
1:A:474:LEU:HB3	1:A:509:LEU:HD21	1.93	0.50
1:B:474:LEU:HB3	1:B:509:LEU:HD21	1.93	0.50
1:C:391:ILE:HG22	1:C:393:VAL:H	1.76	0.50
1:C:474:LEU:HB3	1:C:509:LEU:HD21	1.93	0.50
1:D:474:LEU:HB3	1:D:509:LEU:HD21	1.93	0.50
1:D:774:LEU:CG	1:D:775:GLU:N	2.73	0.50
1:A:305:GLN:HA	1:A:310:VAL:HG21	1.94	0.50
1:D:1043:MET:HB3	1:D:1081:LEU:HD21	1.94	0.50
1:B:982:VAL:CG2	2:B:1302:Y01:CAA	2.65	0.50
1:A:1207:MET:HG2	1:B:1207:MET:CE	2.42	0.49
1:B:1043:MET:HB3	1:B:1081:LEU:HD21	1.94	0.49
1:C:276:HIS:HB2	1:C:279:ILE:HB	1.94	0.49
1:C:1043:MET:HB3	1:C:1081:LEU:HD21	1.94	0.49
1:C:1207:MET:HG2	1:D:1207:MET:CE	2.39	0.49
1:A:857:TRP:CH2	2:A:1305:Y01:CAJ	2.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1043:MET:HB3	1:A:1081:LEU:HD21	1.94	0.49
2:A:1305:Y01:CAC	2:A:1305:Y01:CAE	2.85	0.49
1:A:276:HIS:HB2	1:A:279:ILE:HB	1.94	0.49
1:B:1129:PRO:C	1:B:1131:PRO:HD2	2.33	0.49
1:A:271:ASN:HD22	1:A:297:ILE:HD13	1.77	0.49
1:D:305:GLN:HA	1:D:310:VAL:HG21	1.94	0.49
1:B:305:GLN:HA	1:B:310:VAL:HG21	1.94	0.49
1:D:276:HIS:HB2	1:D:279:ILE:HB	1.94	0.49
1:B:774:LEU:HD23	1:B:775:GLU:H	1.76	0.49
1:C:928:ASP:OD2	1:C:975:ARG:NH1	2.46	0.49
1:D:488:MET:HE1	1:D:662:MET:HB3	1.95	0.48
1:A:298:LEU:HD13	1:A:400:LEU:CD1	2.40	0.48
1:A:856:PHE:HE2	2:A:1305:Y01:HAB3	1.78	0.48
1:B:980:LEU:CD2	1:B:986:ALA:HB1	2.43	0.48
1:C:288:LEU:O	1:C:294:PRO:HD2	2.13	0.48
1:D:288:LEU:O	1:D:294:PRO:HD2	2.13	0.48
1:B:488:MET:HE1	1:B:662:MET:HB3	1.95	0.48
1:B:928:ASP:OD2	1:B:975:ARG:NH1	2.46	0.48
1:B:774:LEU:HD23	1:B:775:GLU:N	2.29	0.48
1:C:305:GLN:HA	1:C:310:VAL:HG21	1.94	0.48
1:D:709:LEU:CD1	1:D:739:THR:HG22	2.43	0.48
2:B:1302:Y01:HAC1	2:B:1302:Y01:CAU	2.35	0.48
1:A:928:ASP:OD2	1:A:975:ARG:NH1	2.46	0.48
2:A:1301:Y01:HAV1	1:B:994:GLY:HA3	1.96	0.48
1:A:477:LEU:HD23	1:A:477:LEU:C	2.34	0.48
1:B:1033:ALA:HB2	2:C:1301:Y01:HAK1	1.95	0.47
1:C:1129:PRO:C	1:C:1131:PRO:HD2	2.33	0.47
1:A:288:LEU:O	1:A:294:PRO:HD2	2.13	0.47
1:C:488:MET:HE1	1:C:662:MET:HB3	1.96	0.47
1:A:980:LEU:CD2	1:A:986:ALA:HB1	2.43	0.47
2:A:1305:Y01:CAE	2:A:1305:Y01:CAO	2.85	0.47
1:C:980:LEU:CD2	1:C:986:ALA:HB1	2.43	0.47
1:D:928:ASP:OD2	1:D:975:ARG:NH1	2.46	0.47
2:D:1302:Y01:CAA	2:D:1303:Y01:CAR	2.79	0.47
2:A:1305:Y01:HAO2	2:A:1305:Y01:CAE	2.26	0.47
2:A:1305:Y01:HAC3	2:A:1305:Y01:CBA	2.45	0.47
1:B:774:LEU:CG	1:B:775:GLU:N	2.73	0.47
1:B:1211:ILE:HD12	1:C:1207:MET:HE2	1.95	0.47
2:D:1302:Y01:CAA	2:D:1303:Y01:OAW	2.63	0.47
1:C:980:LEU:CD2	1:C:986:ALA:HB3	2.45	0.47
1:D:1011:LEU:HD23	1:D:1011:LEU:C	2.35	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:288:LEU:O	1:B:294:PRO:HD2	2.13	0.47
1:B:980:LEU:CD2	1:B:986:ALA:HB3	2.45	0.46
1:D:856:PHE:CZ	2:D:1303:Y01:HAC3	2.49	0.46
1:C:1011:LEU:HD23	1:C:1011:LEU:C	2.35	0.46
1:A:863:TYR:CG	1:A:979:PHE:HE2	2.33	0.46
1:B:653:LEU:HD13	1:B:725:ALA:HB2	1.97	0.46
1:D:477:LEU:O	1:D:628:TRP:NE1	2.49	0.46
1:D:856:PHE:CZ	2:D:1303:Y01:CAC	2.98	0.46
1:C:477:LEU:O	1:C:628:TRP:NE1	2.49	0.46
1:C:863:TYR:CG	1:C:979:PHE:HE2	2.33	0.46
1:D:774:LEU:HD23	1:D:775:GLU:N	2.29	0.46
1:A:740:GLN:NE2	1:A:1112:LYS:O	2.49	0.46
1:B:774:LEU:CD2	1:B:774:LEU:N	2.79	0.46
1:B:863:TYR:CG	1:B:979:PHE:HE2	2.33	0.46
1:D:740:GLN:NE2	1:D:1112:LYS:O	2.49	0.46
1:A:653:LEU:HD13	1:A:725:ALA:HB2	1.97	0.46
1:C:740:GLN:NE2	1:C:1112:LYS:O	2.49	0.46
2:D:1303:Y01:HAB3	2:D:1303:Y01:HAO2	1.98	0.46
1:A:477:LEU:HD21	1:A:628:TRP:CD2	2.50	0.46
1:B:477:LEU:O	1:B:628:TRP:NE1	2.49	0.46
1:D:983:ASN:HB3	2:D:1303:Y01:HAN2	1.98	0.46
1:B:740:GLN:NE2	1:B:1112:LYS:O	2.49	0.45
1:B:854:VAL:O	1:B:858:PHE:HB2	2.16	0.45
1:B:860:THR:HG22	1:B:979:PHE:CD1	2.52	0.45
1:B:1090:ASN:HD21	1:C:1093:ILE:HA	1.81	0.45
2:B:1302:Y01:HAC3	2:B:1302:Y01:HAJ1	1.79	0.45
2:A:1305:Y01:HAB3	2:A:1305:Y01:HBB	1.98	0.45
1:C:860:THR:HG22	1:C:979:PHE:CD1	2.51	0.45
1:B:1060:SER:OG	1:B:1061:THR:O	2.34	0.45
1:D:774:LEU:CD2	1:D:774:LEU:N	2.79	0.45
1:A:298:LEU:CD1	1:A:400:LEU:HD12	2.45	0.45
1:A:980:LEU:CD2	1:A:986:ALA:HB3	2.45	0.45
2:A:1304:Y01:HAK1	1:D:1033:ALA:HB2	1.98	0.45
1:A:1090:ASN:HD21	1:B:1093:ILE:HA	1.81	0.45
1:C:1090:ASN:HD21	1:D:1093:ILE:HA	1.81	0.45
2:D:1302:Y01:HAA3	2:D:1303:Y01:HAR2	1.86	0.45
2:D:1303:Y01:HAU2	2:D:1303:Y01:HAC1	1.99	0.45
1:B:983:ASN:ND2	2:B:1302:Y01:HAC3	2.31	0.45
2:A:1302:Y01:HAB1	1:D:1014:PHE:HB2	1.98	0.45
1:B:1011:LEU:HD23	1:B:1011:LEU:C	2.35	0.45
1:C:653:LEU:HD13	1:C:725:ALA:HB2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1207:MET:SD	1:B:1207:MET:HE1	2.57	0.45
2:A:1305:Y01:CAI	1:D:1009:LEU:HD11	2.37	0.45
1:C:1011:LEU:C	1:C:1011:LEU:CD2	2.86	0.45
1:A:474:LEU:HA	1:A:474:LEU:HD23	1.71	0.45
1:D:653:LEU:HD13	1:D:725:ALA:HB2	1.97	0.45
1:D:710:THR:HG21	1:D:786:PRO:HG3	1.98	0.45
1:A:774:LEU:HG	1:A:775:GLU:H	1.83	0.44
1:A:854:VAL:O	1:A:858:PHE:HB2	2.16	0.44
1:A:860:THR:HG22	1:A:979:PHE:CD1	2.51	0.44
1:A:1060:SER:OG	1:A:1061:THR:O	2.34	0.44
1:B:1011:LEU:C	1:B:1011:LEU:CD2	2.86	0.44
1:C:854:VAL:O	1:C:858:PHE:HB2	2.16	0.44
1:A:1093:ILE:HA	1:D:1090:ASN:HD21	1.81	0.44
1:D:856:PHE:CE2	2:D:1303:Y01:CAC	2.87	0.44
1:A:1207:MET:HE1	1:D:1207:MET:CE	2.48	0.44
1:A:1011:LEU:C	1:A:1011:LEU:CD2	2.85	0.44
1:A:1033:ALA:HB2	2:A:1303:Y01:CAK	2.46	0.44
1:C:1129:PRO:HD2	1:C:1132:LEU:HD12	1.99	0.44
1:A:700:GLN:HE22	1:A:1180:MET:HG3	1.83	0.44
1:B:1129:PRO:HD2	1:B:1132:LEU:HD12	1.99	0.44
1:C:774:LEU:HG	1:C:775:GLU:H	1.83	0.44
1:C:1203:ARG:O	1:C:1207:MET:HB2	2.18	0.44
1:D:980:LEU:HD23	2:D:1303:Y01:HBG	1.99	0.44
1:B:1203:ARG:O	1:B:1207:MET:HB2	2.17	0.44
1:D:1011:LEU:C	1:D:1011:LEU:CD2	2.86	0.44
1:D:1203:ARG:O	1:D:1207:MET:HB2	2.18	0.44
1:B:746:MET:HB3	1:B:1123:HIS:HE1	1.83	0.44
1:B:870:TYR:O	1:B:874:VAL:HG23	2.17	0.44
1:A:1211:ILE:HD12	1:B:1207:MET:HE3	1.99	0.43
1:C:700:GLN:HE22	1:C:1180:MET:HG3	1.83	0.43
1:D:746:MET:HB3	1:D:1123:HIS:HE1	1.83	0.43
1:D:854:VAL:O	1:D:858:PHE:HB2	2.16	0.43
1:A:746:MET:HB3	1:A:1123:HIS:HE1	1.83	0.43
1:B:691:VAL:HG21	1:B:732:PRO:HB2	2.00	0.43
2:C:1302:Y01:CAC	2:C:1302:Y01:HAU2	2.48	0.43
1:B:1207:MET:CE	1:C:1207:MET:HE1	2.49	0.43
1:C:858:PHE:CE2	1:C:1129:PRO:HD3	2.53	0.43
1:D:298:LEU:HD23	1:D:298:LEU:HA	1.80	0.43
2:D:1303:Y01:OAG	2:D:1303:Y01:HAV2	2.17	0.43
1:A:870:TYR:O	1:A:874:VAL:HG23	2.18	0.43
1:B:858:PHE:CE2	1:B:1129:PRO:HD3	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:680:LYS:HE3	1:C:680:LYS:HB2	1.86	0.43
1:C:870:TYR:O	1:C:874:VAL:HG23	2.18	0.43
2:B:1301:Y01:HAJ1	2:B:1301:Y01:HAC3	1.77	0.43
1:C:1207:MET:CE	1:D:1207:MET:HE1	2.49	0.43
1:D:691:VAL:HG21	1:D:732:PRO:HB2	2.00	0.43
1:D:870:TYR:O	1:D:874:VAL:HG23	2.18	0.43
1:C:1033:ALA:HB2	2:D:1302:Y01:HAK1	2.00	0.43
1:A:469:LEU:HD11	1:A:625:LEU:HG	2.01	0.43
1:A:871:THR:HG21	1:A:973:TYR:OH	2.19	0.43
1:B:469:LEU:HD11	1:B:625:LEU:HG	2.01	0.43
1:C:871:THR:HG21	1:C:973:TYR:OH	2.19	0.43
1:D:700:GLN:HE22	1:D:1180:MET:HG3	1.83	0.43
1:D:871:THR:HG21	1:D:973:TYR:OH	2.19	0.43
1:B:871:THR:HG21	1:B:973:TYR:OH	2.19	0.43
1:C:691:VAL:HG21	1:C:732:PRO:HB2	2.00	0.43
1:D:774:LEU:HD23	1:D:774:LEU:N	2.34	0.42
1:A:477:LEU:HD23	1:A:628:TRP:NE1	2.34	0.42
2:A:1301:Y01:HAC1	2:A:1301:Y01:HAE2	2.01	0.42
1:B:892:TYR:CE2	1:B:1131:PRO:HD3	2.55	0.42
1:C:469:LEU:HD11	1:C:625:LEU:HG	2.01	0.42
1:D:868:MET:HG2	2:D:1302:Y01:HAE2	2.00	0.42
2:A:1303:Y01:HAB2	2:B:1302:Y01:HAV2	2.00	0.42
1:B:774:LEU:HG	1:B:775:GLU:N	2.30	0.42
1:C:746:MET:HB3	1:C:1123:HIS:HE1	1.83	0.42
1:D:469:LEU:HD11	1:D:625:LEU:HG	2.01	0.42
1:D:992:MET:HG3	1:D:1103:VAL:HG12	2.02	0.42
1:A:691:VAL:HG21	1:A:732:PRO:HB2	2.00	0.42
1:B:474:LEU:HD23	1:B:474:LEU:HA	1.71	0.42
1:A:892:TYR:CE2	1:A:1131:PRO:HD3	2.55	0.42
1:A:959:VAL:HG11	1:D:1068:PRO:HB2	2.02	0.42
1:B:700:GLN:HE22	1:B:1180:MET:HG3	1.83	0.42
1:D:774:LEU:HG	1:D:775:GLU:N	2.30	0.42
1:B:717:SER:O	1:B:717:SER:OG	2.30	0.42
1:A:1068:PRO:HB2	1:B:959:VAL:HG11	2.02	0.42
1:B:288:LEU:HB3	1:B:294:PRO:HG2	2.02	0.42
1:C:474:LEU:HA	1:C:474:LEU:HD23	1.71	0.42
1:C:983:ASN:HB3	2:C:1302:Y01:HAN2	2.02	0.42
1:A:1207:MET:CE	1:B:1207:MET:HE1	2.49	0.42
1:B:1160:LEU:HD13	1:B:1162:LEU:HG	2.02	0.42
1:D:474:LEU:HD23	1:D:474:LEU:HA	1.71	0.42
2:A:1303:Y01:HAD2	2:A:1303:Y01:HAS2	1.81	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1305:Y01:HAJ1	2:A:1305:Y01:HAB3	1.82	0.42
1:B:288:LEU:O	1:B:294:PRO:CD	2.68	0.42
1:B:980:LEU:CD2	1:B:980:LEU:C	2.89	0.42
1:C:288:LEU:O	1:C:294:PRO:CD	2.68	0.42
1:D:288:LEU:HB3	1:D:294:PRO:HG2	2.02	0.41
2:A:1305:Y01:CAM	1:D:1012:LEU:HD11	2.51	0.41
1:B:980:LEU:HA	2:B:1302:Y01:HAE2	2.02	0.41
1:C:892:TYR:CE2	1:C:1131:PRO:HD3	2.55	0.41
1:C:1012:LEU:HD11	2:D:1303:Y01:HAM1	2.01	0.41
1:D:483:GLY:O	1:D:485:THR:HG23	2.20	0.41
1:D:892:TYR:CE2	1:D:1131:PRO:HD3	2.55	0.41
1:A:288:LEU:O	1:A:294:PRO:CD	2.68	0.41
1:C:1160:LEU:HD13	1:C:1162:LEU:HG	2.02	0.41
1:A:980:LEU:CD2	1:A:980:LEU:C	2.89	0.41
1:C:483:GLY:O	1:C:485:THR:HG23	2.20	0.41
1:A:288:LEU:HB3	1:A:294:PRO:HG2	2.02	0.41
1:A:483:GLY:O	1:A:485:THR:HG23	2.20	0.41
1:A:1211:ILE:CD1	1:B:1207:MET:HE2	2.50	0.41
1:B:992:MET:HG3	1:B:1103:VAL:HG12	2.02	0.41
1:A:992:MET:HG3	1:A:1103:VAL:HG12	2.02	0.41
1:B:1068:PRO:HB2	1:C:959:VAL:HG11	2.02	0.41
1:C:869:LEU:HD23	1:C:869:LEU:HA	1.90	0.41
2:D:1301:Y01:HAD2	2:D:1301:Y01:HAS2	1.84	0.41
1:C:774:LEU:CG	1:C:775:GLU:H	2.34	0.41
1:A:892:TYR:CD2	1:A:1131:PRO:HD3	2.56	0.41
1:D:717:SER:O	1:D:717:SER:OG	2.30	0.41
1:A:694:LEU:HD12	1:A:709:LEU:HD21	1.97	0.41
1:A:774:LEU:CG	1:A:775:GLU:H	2.34	0.41
1:C:1068:PRO:HB2	1:D:959:VAL:HG11	2.02	0.41
1:D:288:LEU:O	1:D:294:PRO:CD	2.68	0.41
1:A:456:LYS:HG2	1:A:640:PHE:CE1	2.56	0.41
1:B:869:LEU:HD23	1:B:869:LEU:HA	1.90	0.41
1:C:456:LYS:HG2	1:C:640:PHE:CE1	2.56	0.41
1:D:1160:LEU:HD13	1:D:1162:LEU:HG	2.02	0.41
1:A:730:LEU:HD22	1:A:730:LEU:HA	1.91	0.40
1:B:456:LYS:HG2	1:B:640:PHE:CE1	2.56	0.40
1:B:730:LEU:HD22	1:B:730:LEU:HA	1.91	0.40
1:C:288:LEU:HB3	1:C:294:PRO:HG2	2.02	0.40
1:C:298:LEU:HD23	1:C:298:LEU:HA	1.80	0.40
1:C:867:LEU:HA	1:C:867:LEU:HD23	1.89	0.40
1:C:980:LEU:CD2	1:C:980:LEU:C	2.89	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:892:TYR:CD2	1:D:1131:PRO:HD3	2.56	0.40
1:C:892:TYR:CD2	1:C:1131:PRO:HD3	2.56	0.40
1:C:992:MET:HG3	1:C:1103:VAL:HG12	2.02	0.40
1:B:421:ASP:O	1:B:425:ASN:ND2	2.55	0.40
1:B:483:GLY:O	1:B:485:THR:HG23	2.20	0.40
1:B:892:TYR:CD2	1:B:1131:PRO:HD3	2.56	0.40
1:A:298:LEU:HD13	1:A:400:LEU:HD12	2.03	0.40
1:A:516:ILE:CD1	1:A:627:ILE:HG21	2.51	0.40
1:A:1160:LEU:HD13	1:A:1162:LEU:HG	2.03	0.40
2:A:1305:Y01:HAM1	1:D:1012:LEU:HD11	2.04	0.40
1:B:874:VAL:CG1	1:B:969:ILE:HD11	2.41	0.40
1:C:421:ASP:O	1:C:425:ASN:ND2	2.55	0.40
1:A:1011:LEU:HD21	1:A:1040:PRO:HG2	2.02	0.40
1:C:412:ILE:HG21	1:C:412:ILE:HD13	1.90	0.40
1:C:464:SER:OG	1:C:466:HIS:O	2.34	0.40
1:C:1060:SER:OG	1:C:1061:THR:O	2.34	0.40
2:C:1302:Y01:HAE2	2:C:1302:Y01:CAC	2.30	0.40
1:D:456:LYS:HG2	1:D:640:PHE:CE1	2.56	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	784/1229 (64%)	750 (96%)	32 (4%)	2 (0%)	41	72
1	B	784/1229 (64%)	751 (96%)	32 (4%)	1 (0%)	51	82
1	C	784/1229 (64%)	750 (96%)	32 (4%)	2 (0%)	41	72
1	D	784/1229 (64%)	753 (96%)	30 (4%)	1 (0%)	51	82
All	All	3136/4916 (64%)	3004 (96%)	126 (4%)	6 (0%)	50	77

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	369	MET
1	B	369	MET
1	C	369	MET
1	D	369	MET
1	A	775	GLU
1	C	775	GLU

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	625/1094 (57%)	610 (98%)	15 (2%)	49 73
1	B	625/1094 (57%)	611 (98%)	14 (2%)	52 74
1	C	625/1094 (57%)	611 (98%)	14 (2%)	52 74
1	D	625/1094 (57%)	610 (98%)	15 (2%)	49 73
All	All	2500/4376 (57%)	2442 (98%)	58 (2%)	53 73

All (58) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	458	LEU
1	A	660	ARG
1	A	724	LEU
1	A	730	LEU
1	A	756	ASN
1	A	774	LEU
1	A	915	LYS
1	A	962	ARG
1	A	980	LEU
1	A	1011	LEU
1	A	1018	ARG
1	A	1090	ASN
1	A	1097	ASN
1	A	1128	LEU
1	A	1160	LEU
1	B	458	LEU

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Mol	Chain	Res	Type
1	B	660	ARG
1	B	724	LEU
1	B	730	LEU
1	B	756	ASN
1	B	774	LEU
1	B	915	LYS
1	B	962	ARG
1	B	980	LEU
1	B	1018	ARG
1	B	1090	ASN
1	B	1097	ASN
1	B	1128	LEU
1	B	1160	LEU
1	C	458	LEU
1	C	660	ARG
1	C	724	LEU
1	C	730	LEU
1	C	756	ASN
1	C	774	LEU
1	C	915	LYS
1	C	962	ARG
1	C	980	LEU
1	C	1018	ARG
1	C	1090	ASN
1	C	1097	ASN
1	C	1128	LEU
1	C	1160	LEU
1	D	458	LEU
1	D	660	ARG
1	D	710	THR
1	D	724	LEU
1	D	730	LEU
1	D	756	ASN
1	D	774	LEU
1	D	915	LYS
1	D	962	ARG
1	D	980	LEU
1	D	1018	ARG
1	D	1090	ASN
1	D	1097	ASN
1	D	1128	LEU
1	D	1160	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	271	ASN
1	A	276	HIS
1	A	432	GLN
1	A	491	HIS
1	A	756	ASN
1	A	789	GLN
1	A	885	GLN
1	A	1090	ASN
1	A	1123	HIS
1	A	1137	HIS
1	B	276	HIS
1	B	425	ASN
1	B	432	GLN
1	B	491	HIS
1	B	756	ASN
1	B	789	GLN
1	B	885	GLN
1	B	1090	ASN
1	B	1123	HIS
1	B	1137	HIS
1	C	276	HIS
1	C	425	ASN
1	C	432	GLN
1	C	491	HIS
1	C	756	ASN
1	C	789	GLN
1	C	885	GLN
1	C	1090	ASN
1	C	1123	HIS
1	C	1137	HIS
1	D	276	HIS
1	D	425	ASN
1	D	432	GLN
1	D	491	HIS
1	D	756	ASN
1	D	789	GLN
1	D	885	GLN
1	D	1090	ASN
1	D	1123	HIS
1	D	1137	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

12 ligands are modelled in this entry.

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
2	Y01	A	1302	-	38,38,38	1.70	4 (10%)	57,57,57	1.80	13 (22%)
2	Y01	A	1303	-	38,38,38	2.08	7 (18%)	57,57,57	2.42	19 (33%)
2	Y01	C	1301	-	38,38,38	2.19	6 (15%)	57,57,57	2.53	20 (35%)
2	Y01	D	1301	-	38,38,38	1.76	6 (15%)	57,57,57	1.76	12 (21%)
2	Y01	C	1302	-	38,38,38	1.89	6 (15%)	57,57,57	1.50	6 (10%)
2	Y01	B	1301	-	38,38,38	1.76	4 (10%)	57,57,57	1.63	10 (17%)
2	Y01	D	1302	-	38,38,38	2.20	6 (15%)	57,57,57	2.57	20 (35%)
2	Y01	D	1303	-	38,38,38	1.74	6 (15%)	57,57,57	1.65	13 (22%)
2	Y01	A	1304	-	38,38,38	2.27	7 (18%)	57,57,57	2.60	18 (31%)
2	Y01	A	1305	-	38,38,38	1.84	6 (15%)	57,57,57	1.55	8 (14%)
2	Y01	A	1301	-	38,38,38	1.78	5 (13%)	57,57,57	1.57	8 (14%)
2	Y01	B	1302	-	38,38,38	1.84	8 (21%)	57,57,57	2.04	16 (28%)

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
2	Y01	A	1302	-	-	6/19/77/77	0/4/4/4
2	Y01	A	1303	-	-	10/19/77/77	0/4/4/4
2	Y01	C	1301	-	-	10/19/77/77	0/4/4/4
2	Y01	D	1301	-	-	4/19/77/77	0/4/4/4
2	Y01	C	1302	-	-	10/19/77/77	0/4/4/4
2	Y01	B	1301	-	-	3/19/77/77	0/4/4/4
2	Y01	D	1302	-	-	12/19/77/77	0/4/4/4
2	Y01	D	1303	-	-	5/19/77/77	0/4/4/4
2	Y01	A	1304	-	-	10/19/77/77	0/4/4/4
2	Y01	A	1305	-	-	9/19/77/77	0/4/4/4
2	Y01	A	1301	-	-	5/19/77/77	0/4/4/4
2	Y01	B	1302	-	-	10/19/77/77	0/4/4/4

All (71) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1303	Y01	CBH-CAZ	-6.17	1.40	1.52
2	A	1304	Y01	CBH-CAZ	-6.13	1.40	1.52
2	D	1302	Y01	CAK-CAI	-6.09	1.37	1.50
2	A	1304	Y01	CAK-CAI	-6.03	1.37	1.50
2	C	1301	Y01	CBH-CAZ	-6.00	1.41	1.52
2	A	1304	Y01	CAV-CAZ	-5.97	1.38	1.51
2	D	1302	Y01	CBH-CAZ	-5.95	1.41	1.52
2	C	1302	Y01	CAV-CAZ	-5.92	1.38	1.51
2	C	1301	Y01	CAK-CAI	-5.90	1.37	1.50
2	D	1302	Y01	CAV-CAZ	-5.83	1.39	1.51
2	C	1301	Y01	CAV-CAZ	-5.74	1.39	1.51
2	A	1303	Y01	CAV-CAZ	-5.67	1.39	1.51
2	A	1303	Y01	CAK-CAI	-5.55	1.38	1.50
2	A	1305	Y01	CBH-CAZ	-5.53	1.41	1.52
2	C	1302	Y01	CBH-CAZ	-5.52	1.41	1.52
2	B	1302	Y01	CBH-CAZ	-5.51	1.41	1.52
2	A	1301	Y01	CAV-CAZ	-5.51	1.39	1.51
2	A	1305	Y01	CAV-CAZ	-5.43	1.39	1.51
2	D	1303	Y01	CAV-CAZ	-5.43	1.39	1.51
2	A	1301	Y01	CBH-CAZ	-5.41	1.42	1.52
2	B	1301	Y01	CBH-CAZ	-5.33	1.42	1.52
2	B	1301	Y01	CAV-CAZ	-5.28	1.40	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1301	Y01	CAK-CAI	-5.27	1.38	1.50
2	D	1301	Y01	CBH-CAZ	-5.24	1.42	1.52
2	A	1302	Y01	CBH-CAZ	-5.18	1.42	1.52
2	D	1301	Y01	CAV-CAZ	-5.17	1.40	1.51
2	D	1301	Y01	CAK-CAI	-5.12	1.39	1.50
2	D	1303	Y01	CBH-CAZ	-5.11	1.42	1.52
2	A	1304	Y01	CAK-CBD	-5.04	1.44	1.53
2	B	1302	Y01	CAV-CAZ	-5.01	1.40	1.51
2	D	1302	Y01	CAK-CBD	-4.86	1.44	1.53
2	A	1302	Y01	CAK-CAI	-4.71	1.40	1.50
2	C	1301	Y01	CAK-CBD	-4.67	1.45	1.53
2	A	1302	Y01	CAV-CAZ	-4.65	1.41	1.51
2	A	1304	Y01	CBI-CBG	-4.60	1.46	1.55
2	C	1302	Y01	CAK-CAI	-4.56	1.40	1.50
2	D	1302	Y01	CBI-CBG	-4.47	1.46	1.55
2	D	1303	Y01	CAK-CAI	-4.43	1.40	1.50
2	A	1301	Y01	CAK-CAI	-4.43	1.40	1.50
2	C	1301	Y01	CBI-CBG	-4.41	1.46	1.55
2	A	1305	Y01	CAK-CAI	-4.22	1.41	1.50
2	B	1302	Y01	CAK-CAI	-4.08	1.41	1.50
2	A	1303	Y01	CBI-CBG	-4.04	1.47	1.55
2	A	1305	Y01	CAI-CAZ	3.36	1.40	1.33
2	A	1303	Y01	CAK-CBD	-3.34	1.47	1.53
2	C	1302	Y01	CAI-CAZ	3.31	1.40	1.33
2	B	1302	Y01	CAI-CAZ	3.25	1.40	1.33
2	D	1303	Y01	CAI-CAZ	3.21	1.40	1.33
2	A	1301	Y01	CAI-CAZ	3.10	1.39	1.33
2	A	1302	Y01	CAI-CAZ	2.94	1.39	1.33
2	A	1305	Y01	CAQ-CBG	-2.89	1.48	1.54
2	D	1301	Y01	CAI-CAZ	2.82	1.39	1.33
2	B	1301	Y01	CAI-CAZ	2.67	1.38	1.33
2	C	1302	Y01	CBD-CBG	-2.67	1.48	1.53
2	A	1303	Y01	CAI-CAZ	2.66	1.38	1.33
2	C	1302	Y01	CBI-CBG	-2.56	1.50	1.55
2	B	1302	Y01	CBI-CBG	-2.55	1.50	1.55
2	B	1302	Y01	CBI-CBE	-2.54	1.50	1.55
2	C	1301	Y01	CAI-CAZ	2.44	1.38	1.33
2	D	1303	Y01	CBI-CBG	-2.40	1.50	1.55
2	D	1302	Y01	CAI-CAZ	2.35	1.38	1.33
2	A	1301	Y01	CBI-CBG	-2.33	1.50	1.55
2	A	1305	Y01	CBI-CBG	-2.27	1.50	1.55
2	D	1303	Y01	CBD-CBG	-2.26	1.49	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1304	Y01	CAI-CAZ	2.25	1.37	1.33
2	B	1302	Y01	CBD-CBG	-2.12	1.49	1.53
2	D	1301	Y01	OAW-CBC	-2.09	1.41	1.46
2	D	1301	Y01	CAQ-CBG	-2.08	1.50	1.54
2	A	1303	Y01	CBI-CBE	-2.04	1.51	1.55
2	B	1302	Y01	CAT-CBH	-2.03	1.50	1.54
2	A	1304	Y01	CBD-CBG	-2.01	1.49	1.53

All (163) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1304	Y01	CBG-CBI-CBE	-9.30	89.06	100.07
2	A	1303	Y01	CAC-CBB-CBE	-8.67	99.65	112.92
2	C	1301	Y01	CAC-CBB-CBE	-8.20	100.36	112.92
2	D	1302	Y01	CAC-CBB-CBE	-8.06	100.58	112.92
2	C	1301	Y01	CBG-CBI-CBE	-7.81	90.83	100.07
2	A	1304	Y01	CAC-CBB-CBE	-7.60	101.29	112.92
2	D	1302	Y01	CBG-CBI-CBE	-7.45	91.25	100.07
2	A	1303	Y01	CBG-CBI-CBE	-7.42	91.28	100.07
2	D	1302	Y01	CAV-CAZ-CBH	5.84	124.17	116.42
2	A	1304	Y01	CAK-CBD-CBG	-5.11	103.50	110.91
2	B	1302	Y01	CBI-CBE-CBB	-5.11	111.49	119.49
2	C	1301	Y01	CAV-CAZ-CBH	5.09	123.18	116.42
2	A	1304	Y01	CAV-CAZ-CBH	5.00	123.07	116.42
2	D	1302	Y01	CAV-CAZ-CAI	-4.94	113.49	120.61
2	D	1302	Y01	CAK-CBD-CBG	-4.86	103.87	110.91
2	B	1302	Y01	CAV-CAZ-CBH	4.84	122.86	116.42
2	A	1303	Y01	CAV-CAZ-CBH	4.66	122.61	116.42
2	B	1301	Y01	CAV-CAZ-CBH	4.65	122.60	116.42
2	C	1301	Y01	CAK-CBD-CBG	-4.61	104.22	110.91
2	D	1303	Y01	CAQ-CBG-CBD	-4.59	111.52	119.08
2	C	1302	Y01	CAQ-CBG-CBD	-4.53	111.62	119.08
2	D	1301	Y01	CAV-CAZ-CBH	4.51	122.41	116.42
2	A	1304	Y01	CAK-CBD-CBF	-4.51	104.25	109.71
2	A	1301	Y01	CBI-CBE-CBB	-4.38	112.62	119.49
2	A	1303	Y01	CBH-CBF-CBD	-4.34	106.22	112.73
2	A	1302	Y01	CAV-CAZ-CBH	4.34	122.18	116.42
2	C	1301	Y01	CBH-CBF-CBD	-4.24	106.38	112.73
2	C	1301	Y01	CAV-CAZ-CAI	-4.21	114.54	120.61
2	A	1304	Y01	CAV-CAZ-CAI	-4.09	114.71	120.61
2	D	1302	Y01	CBH-CBF-CBD	-4.09	106.60	112.73
2	A	1302	Y01	CBH-CBF-CBD	-4.05	106.66	112.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1304	Y01	CBH-CBF-CBD	-4.01	106.72	112.73
2	D	1303	Y01	CBI-CBE-CBB	-4.00	113.22	119.49
2	B	1301	Y01	CAQ-CBG-CBD	-3.97	112.54	119.08
2	D	1301	Y01	CAQ-CBG-CBD	-3.95	112.58	119.08
2	B	1302	Y01	CAQ-CBG-CBD	-3.94	112.58	119.08
2	A	1302	Y01	CAQ-CBG-CBD	-3.93	112.61	119.08
2	A	1305	Y01	CBI-CBG-CBD	-3.90	108.60	114.38
2	C	1302	Y01	CBI-CBG-CBD	-3.88	108.63	114.38
2	A	1303	Y01	CAV-CAZ-CAI	-3.88	115.02	120.61
2	C	1302	Y01	CBI-CBE-CBB	-3.82	113.50	119.49
2	A	1301	Y01	CAQ-CBG-CBD	-3.77	112.87	119.08
2	A	1302	Y01	CAP-CBE-CBB	-3.77	106.32	112.15
2	A	1305	Y01	CAQ-CBG-CBD	-3.75	112.90	119.08
2	B	1302	Y01	CBI-CBG-CBD	-3.74	108.84	114.38
2	B	1301	Y01	CAV-CAZ-CAI	-3.73	115.24	120.61
2	A	1303	Y01	CBI-CBG-CBD	-3.71	108.89	114.38
2	D	1301	Y01	CAP-CBE-CBB	-3.67	106.46	112.15
2	B	1302	Y01	CBC-CAV-CAZ	3.66	117.20	111.52
2	C	1301	Y01	CBI-CBG-CBD	-3.58	109.08	114.38
2	D	1302	Y01	CBI-CBG-CBD	-3.53	109.16	114.38
2	A	1303	Y01	CAK-CBD-CBG	-3.52	105.81	110.91
2	A	1304	Y01	CAJ-CAO-CBB	-3.51	104.94	115.03
2	D	1301	Y01	CBH-CBF-CBD	-3.51	107.47	112.73
2	A	1305	Y01	CAP-CAQ-CBG	-3.49	98.21	105.13
2	A	1302	Y01	CAD-CBH-CBF	-3.47	107.54	111.68
2	C	1301	Y01	CAK-CBD-CBF	-3.47	105.51	109.71
2	D	1301	Y01	CBG-CBI-CBE	-3.47	95.97	100.07
2	D	1302	Y01	CAD-CBH-CBF	-3.47	107.55	111.68
2	A	1305	Y01	CBF-CBH-CAZ	3.46	115.08	109.65
2	A	1302	Y01	CBG-CBI-CBE	-3.46	95.98	100.07
2	A	1304	Y01	CAE-CBI-CBE	3.44	118.12	111.71
2	A	1303	Y01	CAO-CBB-CBE	3.39	117.30	110.28
2	D	1301	Y01	CAV-CAZ-CAI	-3.38	115.73	120.61
2	B	1302	Y01	CAD-CBH-CBF	-3.38	107.65	111.68
2	B	1302	Y01	CBC-OAW-CAY	-3.37	109.48	117.79
2	C	1301	Y01	CAJ-CAO-CBB	-3.36	105.36	115.03
2	A	1304	Y01	CBI-CBG-CBD	-3.35	109.42	114.38
2	D	1302	Y01	CAJ-CAO-CBB	-3.32	105.49	115.03
2	C	1301	Y01	CAD-CBH-CBF	-3.32	107.73	111.68
2	C	1301	Y01	CAO-CBB-CBE	3.31	117.12	110.28
2	A	1304	Y01	CAD-CBH-CBF	-3.30	107.75	111.68
2	C	1302	Y01	CAP-CBE-CBB	-3.29	107.05	112.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1302	Y01	CBH-CBF-CBD	-3.29	107.80	112.73
2	D	1303	Y01	CBI-CBG-CBD	-3.25	109.56	114.38
2	B	1302	Y01	CBF-CBH-CAZ	3.25	114.75	109.65
2	D	1302	Y01	CAO-CBB-CBE	3.25	117.00	110.28
2	B	1302	Y01	CAV-CAZ-CAI	-3.21	115.98	120.61
2	D	1302	Y01	CAK-CBD-CBF	-3.18	105.86	109.71
2	D	1301	Y01	CAC-CBB-CAO	-3.16	105.41	110.36
2	B	1302	Y01	CAC-CBB-CBE	-3.13	108.14	112.92
2	A	1303	Y01	CAD-CBH-CBF	-3.11	107.98	111.68
2	A	1301	Y01	CBF-CBH-CAZ	3.09	114.50	109.65
2	A	1304	Y01	CAQ-CAP-CBE	-3.08	99.02	105.13
2	A	1301	Y01	CBI-CBG-CBD	-3.07	109.83	114.38
2	C	1301	Y01	CAQ-CBG-CBD	-3.04	114.07	119.08
2	A	1304	Y01	CAO-CBB-CBE	3.02	116.52	110.28
2	A	1303	Y01	CAJ-CAO-CBB	-3.01	106.39	115.03
2	A	1302	Y01	CAC-CBB-CAO	-3.01	105.65	110.36
2	C	1301	Y01	CAC-CBB-CAO	-3.00	105.65	110.36
2	D	1302	Y01	CAQ-CBG-CBD	-2.97	114.18	119.08
2	A	1304	Y01	CAQ-CBG-CBD	-2.97	114.18	119.08
2	A	1305	Y01	CBC-OAW-CAY	-2.97	110.49	117.79
2	D	1302	Y01	CBC-CAV-CAZ	2.97	116.12	111.52
2	D	1303	Y01	CAD-CBH-CBF	-2.96	108.15	111.68
2	D	1302	Y01	CBC-OAW-CAY	-2.95	110.53	117.79
2	C	1302	Y01	CBF-CBH-CAZ	2.93	114.25	109.65
2	B	1301	Y01	CBH-CBF-CBD	-2.91	108.36	112.73
2	D	1302	Y01	CAC-CBB-CAO	-2.90	105.82	110.36
2	B	1302	Y01	CAS-CAU-CBI	-2.89	107.83	112.78
2	A	1301	Y01	CAS-CAU-CBI	-2.86	107.88	112.78
2	A	1303	Y01	CAQ-CBG-CBD	-2.86	114.37	119.08
2	A	1305	Y01	CBI-CBE-CBB	-2.83	115.05	119.49
2	B	1301	Y01	CBG-CBI-CBE	-2.80	96.75	100.07
2	D	1301	Y01	CAD-CBH-CBF	-2.80	108.34	111.68
2	A	1303	Y01	CBC-CAV-CAZ	2.75	115.80	111.52
2	C	1301	Y01	CBC-OAW-CAY	-2.75	111.02	117.79
2	A	1302	Y01	CAV-CAZ-CAI	-2.74	116.66	120.61
2	A	1302	Y01	CAC-CBB-CBE	2.70	117.06	112.92
2	A	1305	Y01	CAQ-CBG-CBI	-2.69	100.61	103.84
2	A	1304	Y01	CAK-CAI-CAZ	-2.68	120.12	125.06
2	B	1301	Y01	CAP-CBE-CBB	-2.66	108.02	112.15
2	B	1302	Y01	CAR-CBC-CAV	2.66	114.95	110.99
2	A	1303	Y01	CBC-OAW-CAY	-2.65	111.28	117.79
2	D	1303	Y01	CAC-CBB-CBE	-2.64	108.89	112.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1302	Y01	CAS-CBF-CBD	-2.64	107.96	111.75
2	C	1301	Y01	CBC-CAV-CAZ	2.63	115.61	111.52
2	A	1303	Y01	CAQ-CAP-CBE	-2.63	99.92	105.13
2	C	1301	Y01	CAQ-CAP-CBE	-2.62	99.94	105.13
2	D	1303	Y01	CBF-CBH-CAZ	2.60	113.73	109.65
2	D	1303	Y01	CAP-CBE-CBB	-2.59	108.13	112.15
2	A	1304	Y01	CBC-OAW-CAY	-2.58	111.44	117.79
2	A	1301	Y01	CAC-CBB-CBE	-2.56	109.00	112.92
2	C	1302	Y01	CAC-CBB-CBE	-2.51	109.07	112.92
2	C	1301	Y01	CAS-CBF-CBD	-2.51	108.14	111.75
2	A	1304	Y01	CBC-CAV-CAZ	2.50	115.41	111.52
2	D	1302	Y01	CAQ-CAP-CBE	-2.49	100.19	105.13
2	B	1301	Y01	CAD-CBH-CBF	-2.46	108.75	111.68
2	D	1301	Y01	CAM-CAL-CAX	-2.45	108.33	113.60
2	B	1301	Y01	CAM-CAL-CAX	-2.45	108.33	113.60
2	A	1303	Y01	CAS-CBF-CBD	-2.44	108.24	111.75
2	C	1301	Y01	CAE-CBI-CBE	2.43	116.25	111.71
2	A	1303	Y01	CAE-CBI-CBE	2.40	116.19	111.71
2	D	1303	Y01	CAS-CAU-CBI	-2.37	108.71	112.78
2	B	1301	Y01	CAK-CBD-CBG	-2.33	107.54	110.91
2	A	1302	Y01	CAK-CBD-CBF	-2.32	106.90	109.71
2	D	1303	Y01	CAT-CAR-CBC	-2.32	106.37	110.33
2	A	1301	Y01	CAP-CBE-CBB	-2.30	108.58	112.15
2	A	1302	Y01	CAP-CBE-CBI	-2.29	101.08	103.84
2	A	1302	Y01	CAS-CBF-CBH	-2.27	110.08	113.08
2	D	1302	Y01	CBI-CBE-CBB	-2.27	115.93	119.49
2	A	1305	Y01	CAJ-CAO-CBB	-2.26	108.53	115.03
2	D	1303	Y01	CAV-CAZ-CBH	2.25	119.41	116.42
2	C	1301	Y01	CBI-CBE-CBB	-2.25	115.96	119.49
2	B	1302	Y01	CBD-CAK-CAI	2.23	115.94	112.73
2	D	1302	Y01	CAE-CBI-CBE	2.22	115.86	111.71
2	A	1301	Y01	CAV-CAZ-CBH	2.20	119.34	116.42
2	A	1304	Y01	CAS-CBF-CBD	-2.19	108.60	111.75
2	D	1303	Y01	CAP-CAQ-CBG	-2.19	100.80	105.13
2	A	1303	Y01	CAC-CBB-CAO	-2.19	106.93	110.36
2	A	1303	Y01	CAK-CBD-CBF	-2.18	107.07	109.71
2	D	1303	Y01	CBH-CBF-CBD	-2.17	109.48	112.73
2	D	1301	Y01	CAP-CBE-CBI	-2.17	101.23	103.84
2	C	1301	Y01	CAK-CAI-CAZ	-2.15	121.09	125.06
2	D	1303	Y01	CAR-CBC-CAV	-2.15	107.78	110.99
2	D	1302	Y01	CAK-CAI-CAZ	-2.13	121.13	125.06
2	D	1301	Y01	CAC-CBB-CBE	2.12	116.17	112.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1303	Y01	CBI-CBE-CBB	-2.12	116.17	119.49
2	A	1302	Y01	CAR-CAT-CBH	-2.08	108.23	112.74
2	D	1301	Y01	CAS-CBF-CBH	-2.06	110.36	113.08
2	B	1302	Y01	CBF-CBD-CBG	-2.05	106.34	109.09
2	B	1301	Y01	CAP-CAQ-CBG	-2.04	101.08	105.13
2	B	1302	Y01	OAW-CAY-CAM	2.02	115.85	111.50

There are no chirality outliers.

All (94) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1301	Y01	CAX-CAL-CAM-CAY
2	D	1303	Y01	CAV-CBC-OAW-CAY
2	A	1305	Y01	CAO-CBB-CBE-CAP
2	A	1305	Y01	CAO-CBB-CBE-CBI
2	B	1302	Y01	CAM-CAY-OAW-CBC
2	B	1302	Y01	OAG-CAY-OAW-CBC
2	C	1302	Y01	CAJ-CAO-CBB-CBE
2	C	1302	Y01	CAJ-CAO-CBB-CAC
2	D	1302	Y01	CAO-CBB-CBE-CAP
2	A	1303	Y01	CAO-CBB-CBE-CBI
2	A	1304	Y01	CAO-CBB-CBE-CBI
2	C	1301	Y01	CAO-CBB-CBE-CBI
2	D	1302	Y01	CAO-CBB-CBE-CBI
2	D	1302	Y01	CAJ-CAO-CBB-CAC
2	A	1305	Y01	CAO-CAJ-CAN-CBA
2	A	1303	Y01	CAC-CBB-CBE-CAP
2	C	1301	Y01	CAC-CBB-CBE-CAP
2	D	1302	Y01	CAC-CBB-CBE-CAP
2	D	1301	Y01	CAX-CAL-CAM-CAY
2	D	1302	Y01	CAX-CAL-CAM-CAY
2	A	1303	Y01	CAC-CBB-CBE-CBI
2	C	1301	Y01	CAC-CBB-CBE-CBI
2	D	1302	Y01	CAC-CBB-CBE-CBI
2	C	1301	Y01	CAO-CBB-CBE-CAP
2	A	1304	Y01	CAJ-CAO-CBB-CAC
2	C	1301	Y01	CAJ-CAO-CBB-CAC
2	A	1304	Y01	CAC-CBB-CBE-CAP
2	A	1305	Y01	CAC-CBB-CBE-CAP
2	A	1304	Y01	CAC-CBB-CBE-CBI
2	A	1301	Y01	CAX-CAL-CAM-CAY
2	A	1302	Y01	CAX-CAL-CAM-CAY

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Mol	Chain	Res	Type	Atoms
2	A	1305	Y01	CAX-CAL-CAM-CAY
2	C	1301	Y01	CAX-CAL-CAM-CAY
2	A	1303	Y01	CAN-CAJ-CAO-CBB
2	C	1301	Y01	CAN-CAJ-CAO-CBB
2	D	1302	Y01	CAN-CAJ-CAO-CBB
2	A	1304	Y01	CAN-CAJ-CAO-CBB
2	A	1303	Y01	CAO-CBB-CBE-CAP
2	A	1301	Y01	CAJ-CAN-CBA-CAB
2	C	1302	Y01	CAO-CBB-CBE-CAP
2	B	1301	Y01	CAN-CAJ-CAO-CBB
2	B	1302	Y01	CAO-CAJ-CAN-CBA
2	A	1301	Y01	CAJ-CAN-CBA-CAA
2	A	1303	Y01	CAJ-CAO-CBB-CAC
2	A	1303	Y01	CAX-CAL-CAM-CAY
2	A	1304	Y01	CAX-CAL-CAM-CAY
2	D	1303	Y01	CAJ-CAO-CBB-CAC
2	A	1305	Y01	CAM-CAY-OAW-CBC
2	A	1305	Y01	OAG-CAY-OAW-CBC
2	B	1302	Y01	CAJ-CAO-CBB-CAC
2	C	1301	Y01	CAJ-CAN-CBA-CAA
2	A	1302	Y01	CAN-CAJ-CAO-CBB
2	A	1303	Y01	CAJ-CAN-CBA-CAA
2	A	1304	Y01	CAJ-CAN-CBA-CAA
2	B	1302	Y01	CAX-CAL-CAM-CAY
2	D	1302	Y01	CAM-CAY-OAW-CBC
2	D	1302	Y01	CAJ-CAN-CBA-CAA
2	A	1302	Y01	CAM-CAY-OAW-CBC
2	A	1304	Y01	CAO-CAJ-CAN-CBA
2	D	1302	Y01	CAO-CAJ-CAN-CBA
2	A	1302	Y01	OAG-CAY-OAW-CBC
2	D	1301	Y01	CAN-CAJ-CAO-CBB
2	C	1301	Y01	CAO-CAJ-CAN-CBA
2	D	1303	Y01	CAO-CAJ-CAN-CBA
2	A	1303	Y01	CAO-CAJ-CAN-CBA
2	A	1303	Y01	CAJ-CAN-CBA-CAB
2	C	1301	Y01	CAJ-CAN-CBA-CAB
2	D	1302	Y01	CAJ-CAN-CBA-CAB
2	D	1302	Y01	OAG-CAY-OAW-CBC
2	A	1304	Y01	CAJ-CAN-CBA-CAB
2	C	1302	Y01	CAN-CAJ-CAO-CBB
2	D	1303	Y01	CAJ-CAO-CBB-CBE
2	A	1304	Y01	CAO-CBB-CBE-CAP

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Mol	Chain	Res	Type	Atoms
2	C	1302	Y01	CAV-CBC-OAW-CAY
2	B	1302	Y01	CAJ-CAN-CBA-CAA
2	D	1303	Y01	CAR-CBC-OAW-CAY
2	A	1302	Y01	CAJ-CAN-CBA-CAA
2	C	1302	Y01	CAR-CBC-OAW-CAY
2	C	1302	Y01	OAG-CAY-OAW-CBC
2	B	1302	Y01	CAM-CAL-CAX-OAF
2	A	1301	Y01	CAL-CAM-CAY-OAW
2	A	1305	Y01	CAM-CAL-CAX-OAF
2	B	1302	Y01	CAM-CAL-CAX-OAH
2	A	1305	Y01	CAM-CAL-CAX-OAH
2	D	1301	Y01	CAL-CAM-CAY-OAW
2	B	1302	Y01	CAN-CAJ-CAO-CBB
2	B	1301	Y01	CAL-CAM-CAY-OAW
2	C	1302	Y01	CAM-CAY-OAW-CBC
2	D	1301	Y01	CAM-CAL-CAX-OAH
2	A	1301	Y01	OAG-CAY-OAW-CBC
2	C	1302	Y01	CAL-CAM-CAY-OAW
2	C	1302	Y01	CAL-CAM-CAY-OAG
2	A	1302	Y01	CAM-CAL-CAX-OAF
2	B	1302	Y01	CAJ-CAN-CBA-CAB

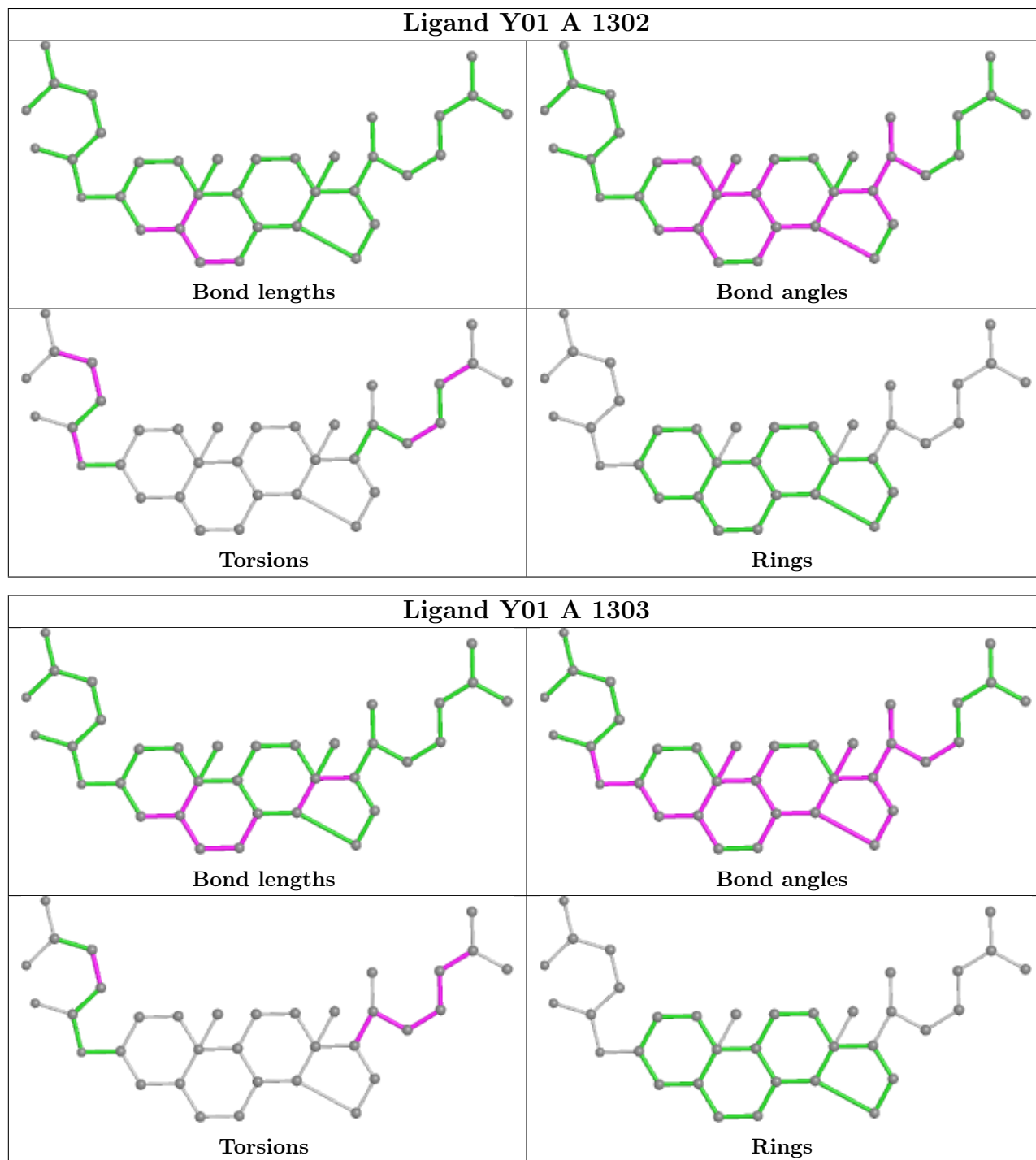
There are no ring outliers.

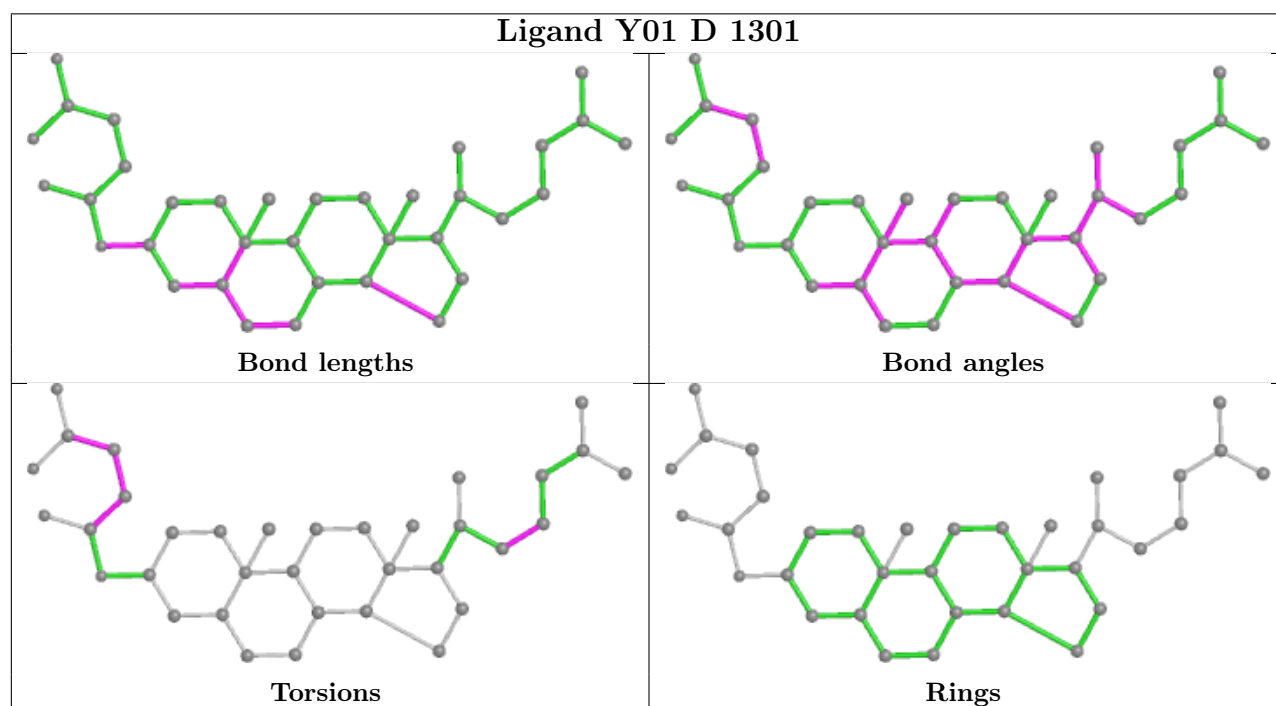
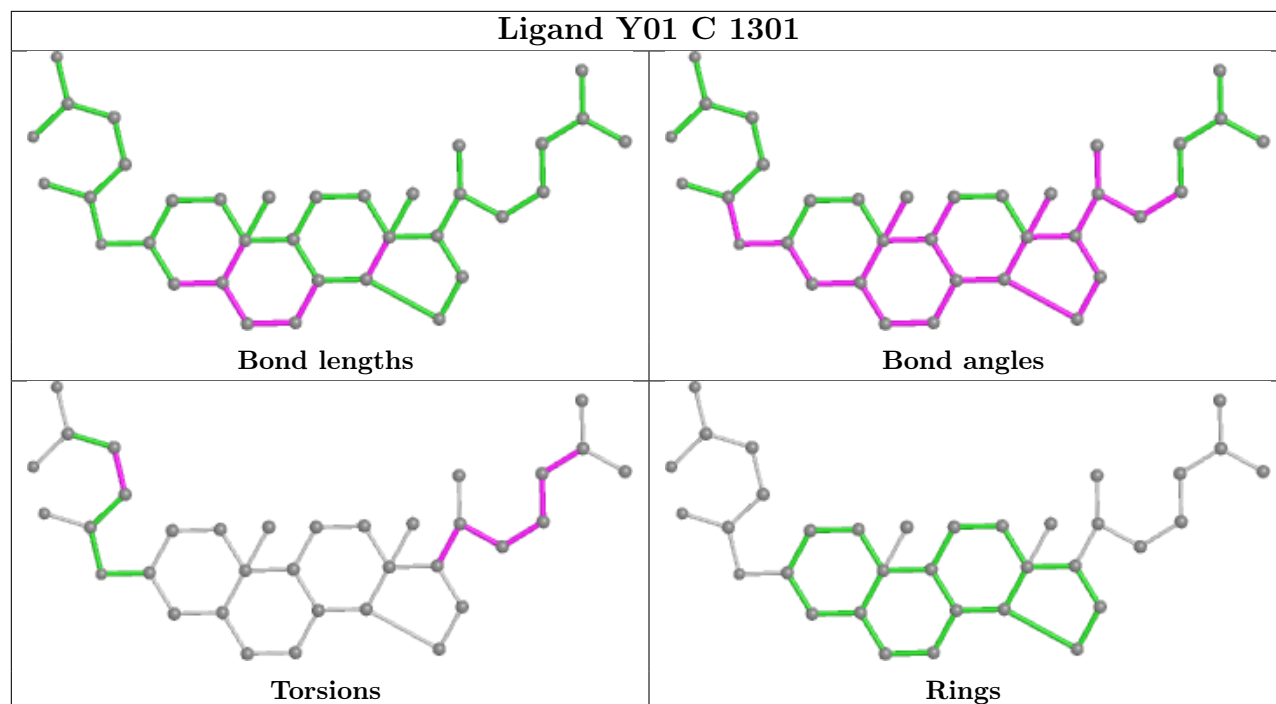
12 monomers are involved in 116 short contacts:

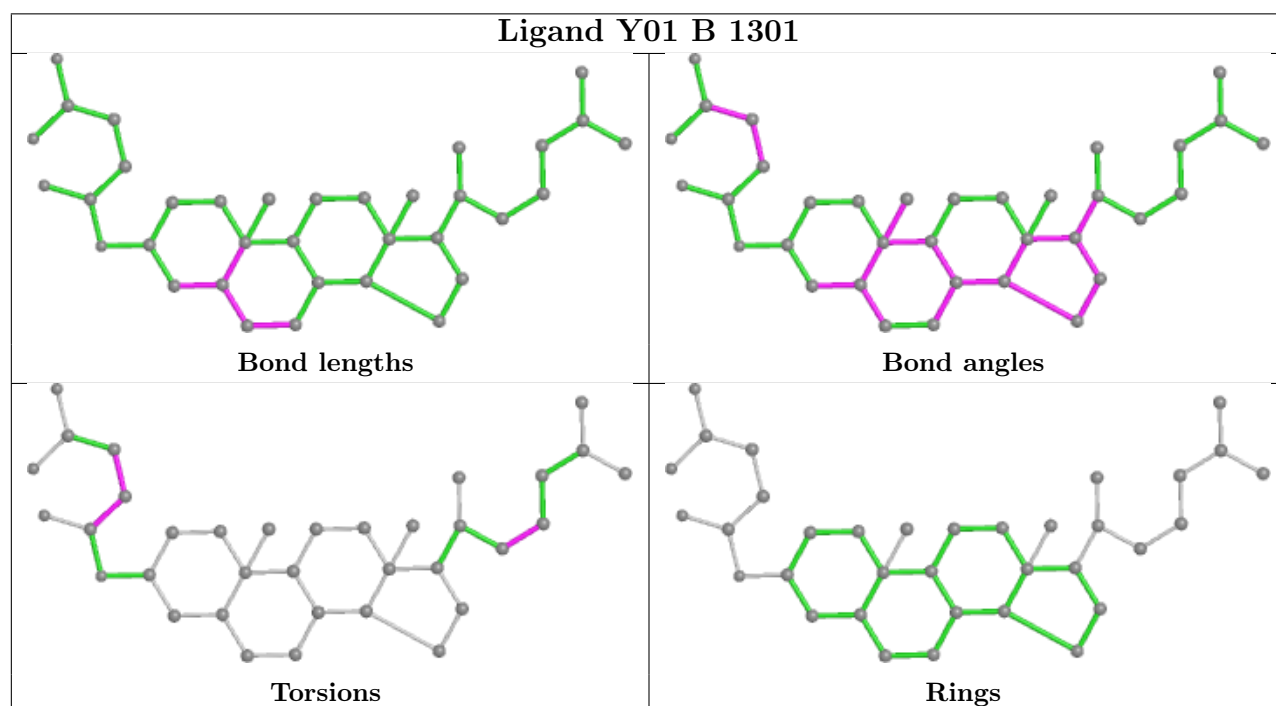
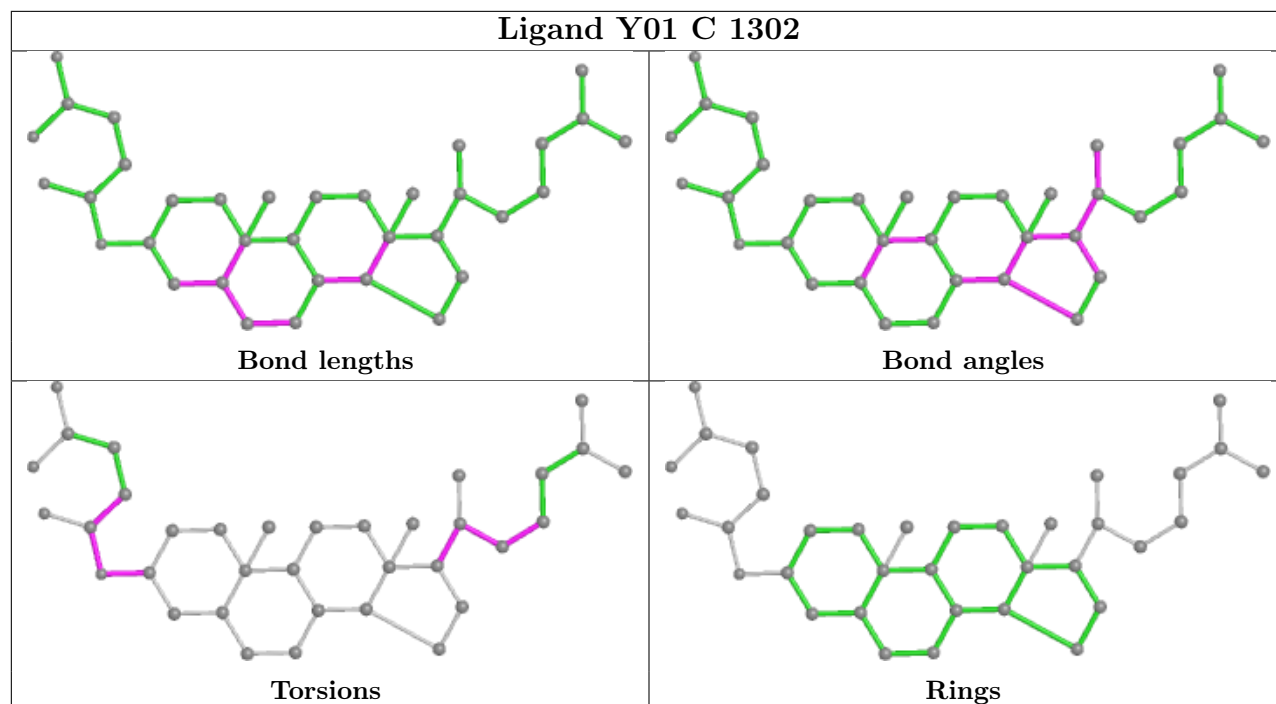
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1302	Y01	1	0
2	A	1303	Y01	6	0
2	C	1301	Y01	6	0
2	D	1301	Y01	1	0
2	C	1302	Y01	12	0
2	B	1301	Y01	2	0
2	D	1302	Y01	11	0
2	D	1303	Y01	29	0
2	A	1304	Y01	3	0
2	A	1305	Y01	42	0
2	A	1301	Y01	7	0
2	B	1302	Y01	15	0

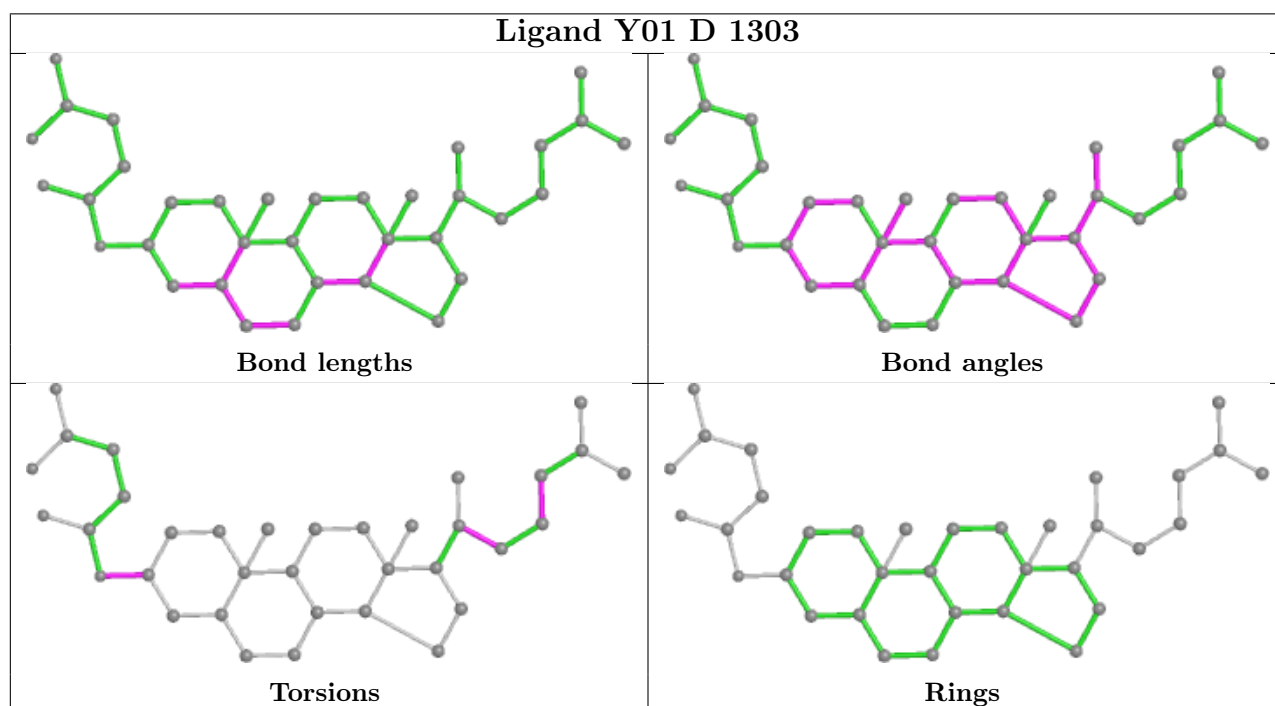
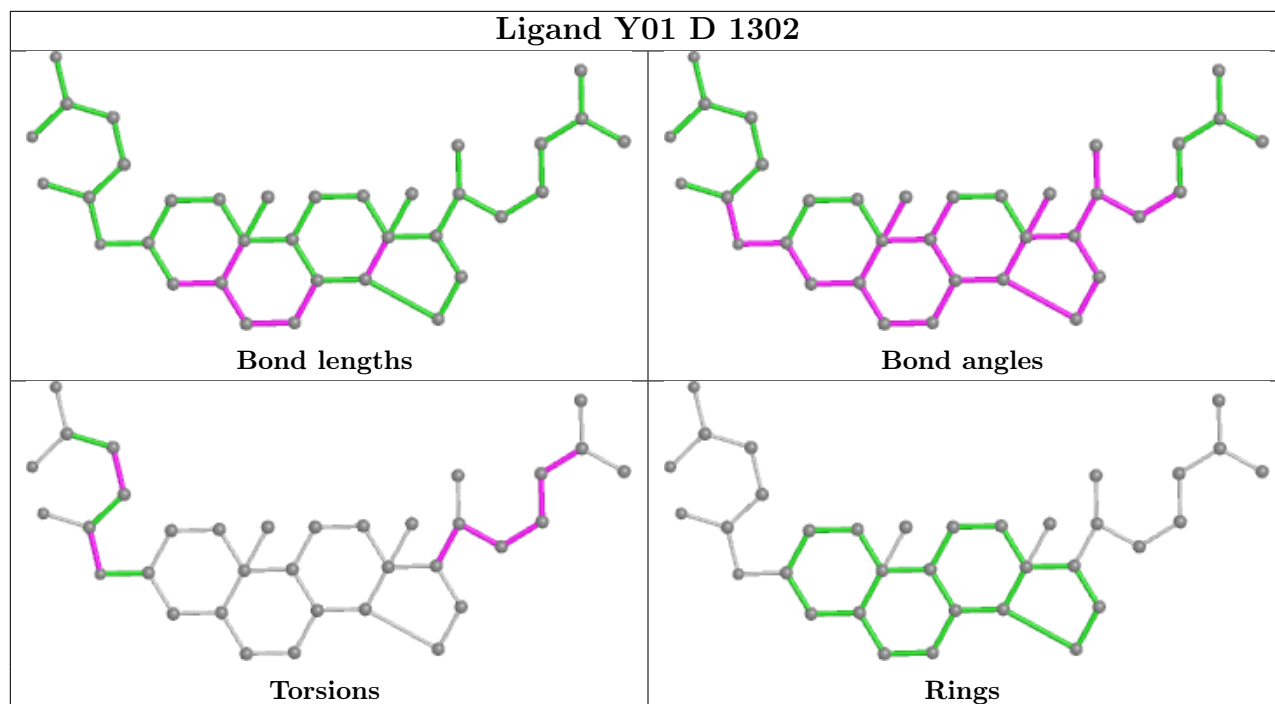
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

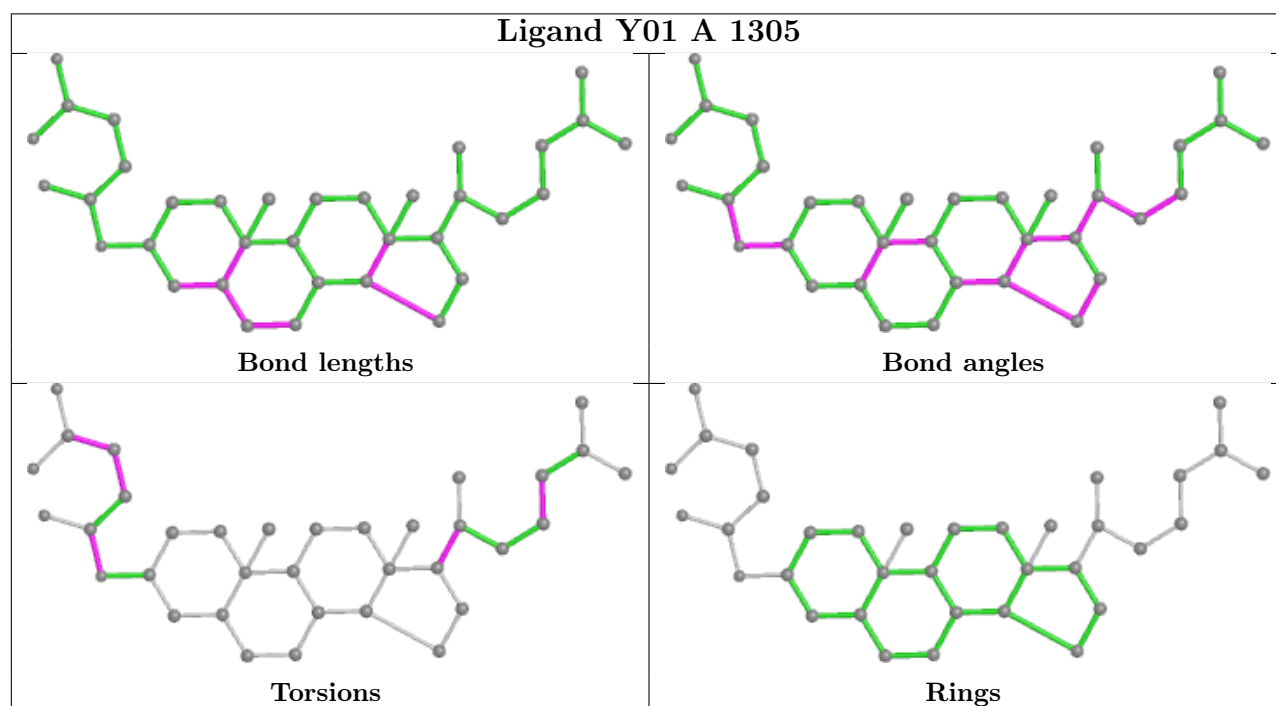
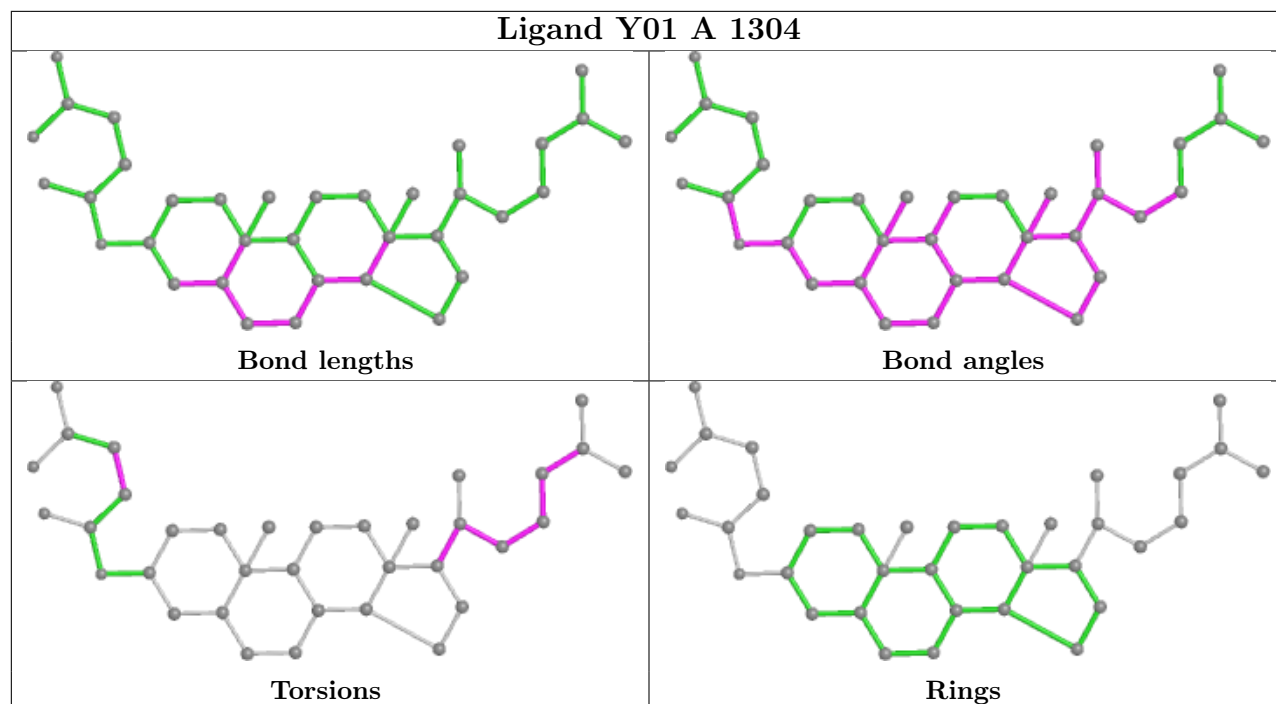
also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted 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.

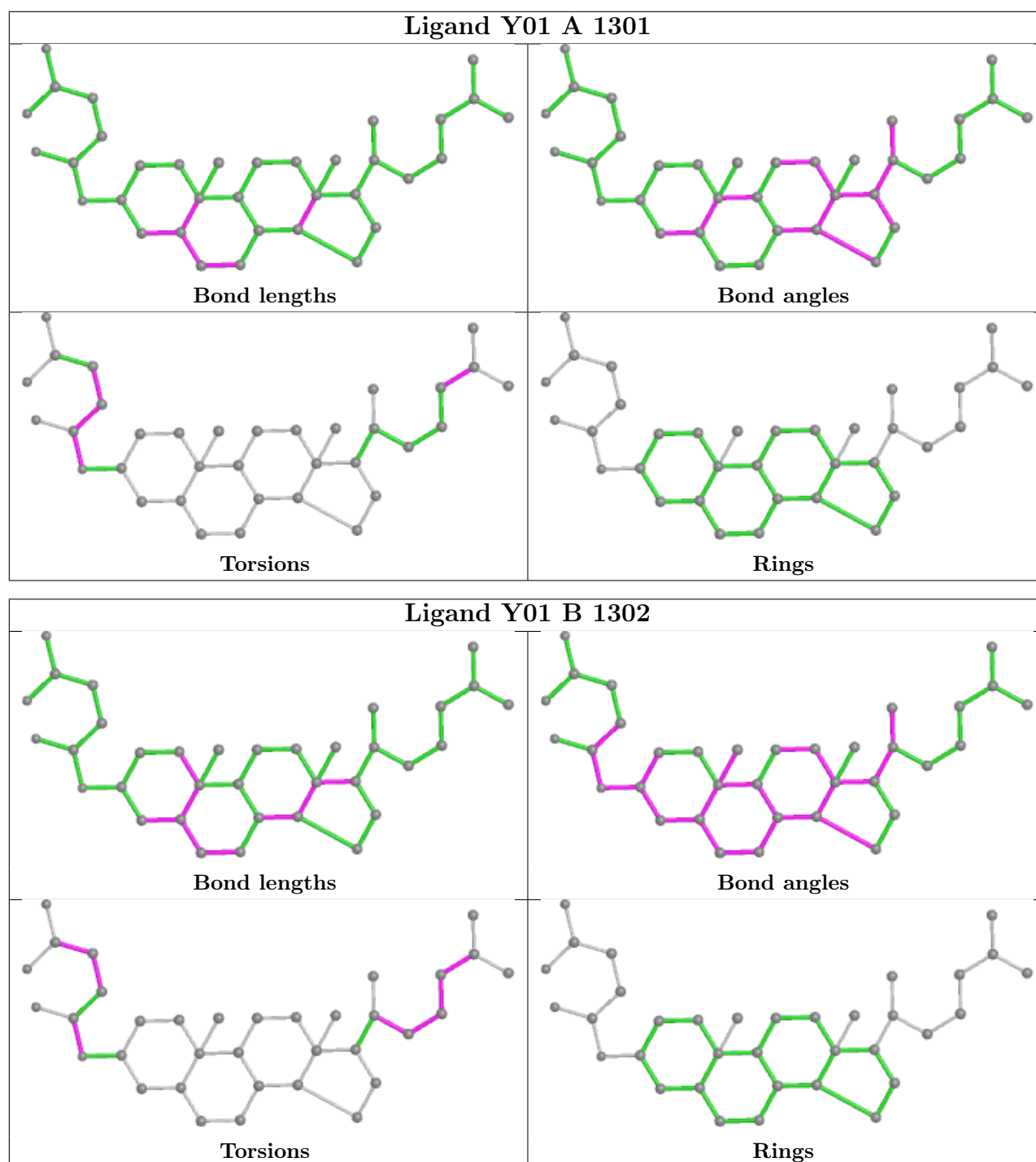












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

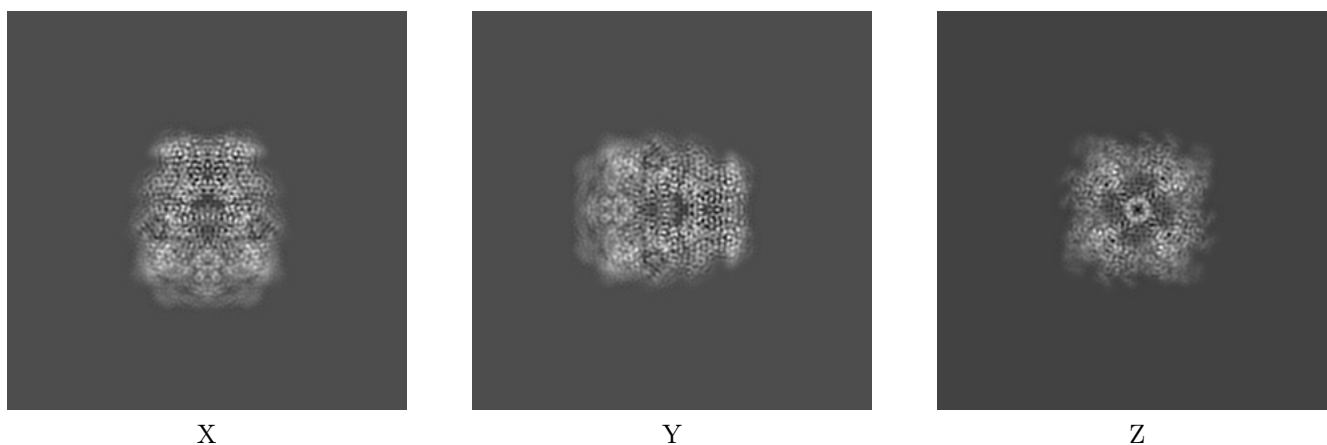
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6975. 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](#)

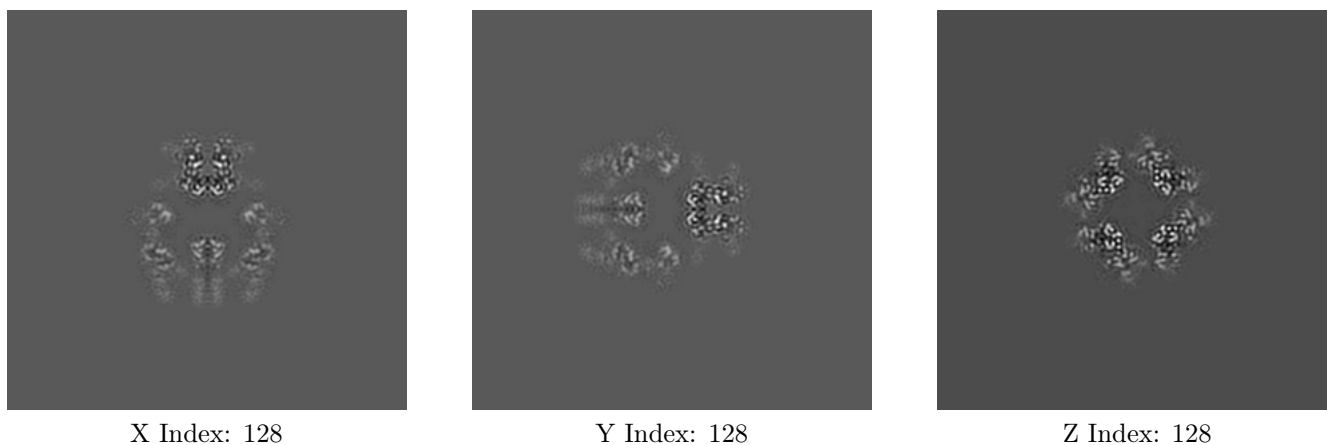
6.1.1 Primary map



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

6.2 Central slices [i](#)

6.2.1 Primary map



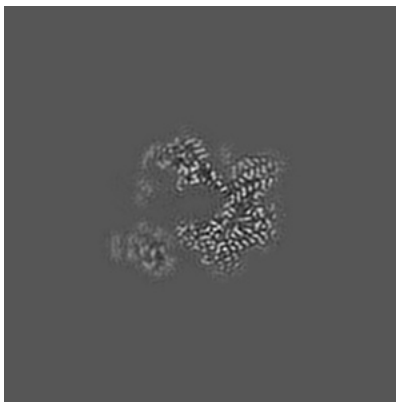
The images above show central slices of the map in three orthogonal directions.

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

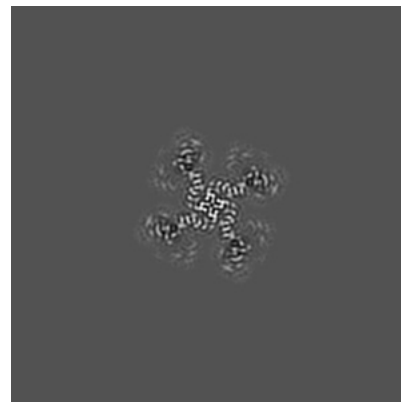
6.3.1 Primary map



X Index: 142



Y Index: 114

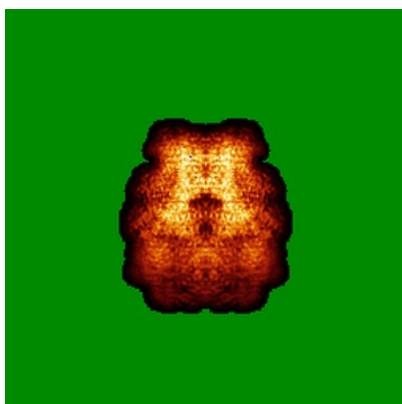


Z Index: 142

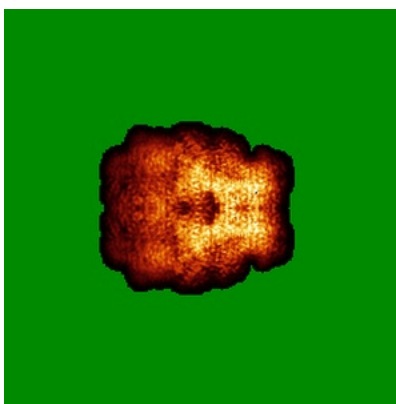
The images above show the largest variance slices of the map in three orthogonal directions.

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

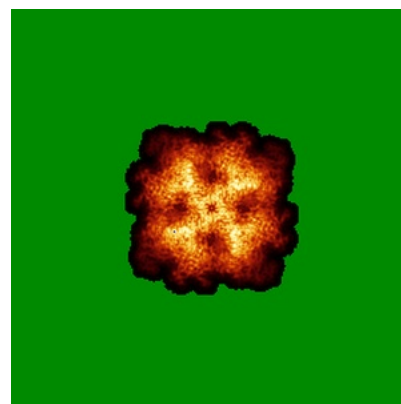
6.4.1 Primary map



X



Y

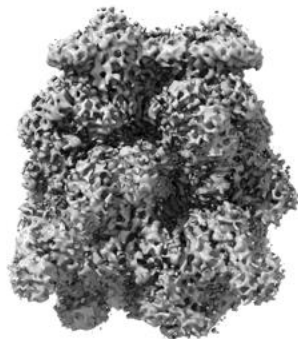


Z

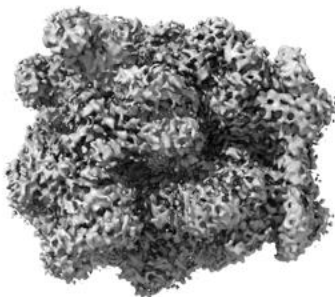
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

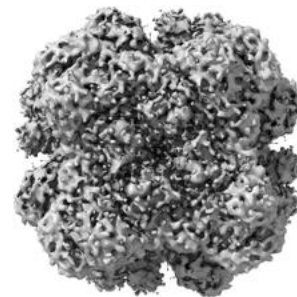
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.013. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

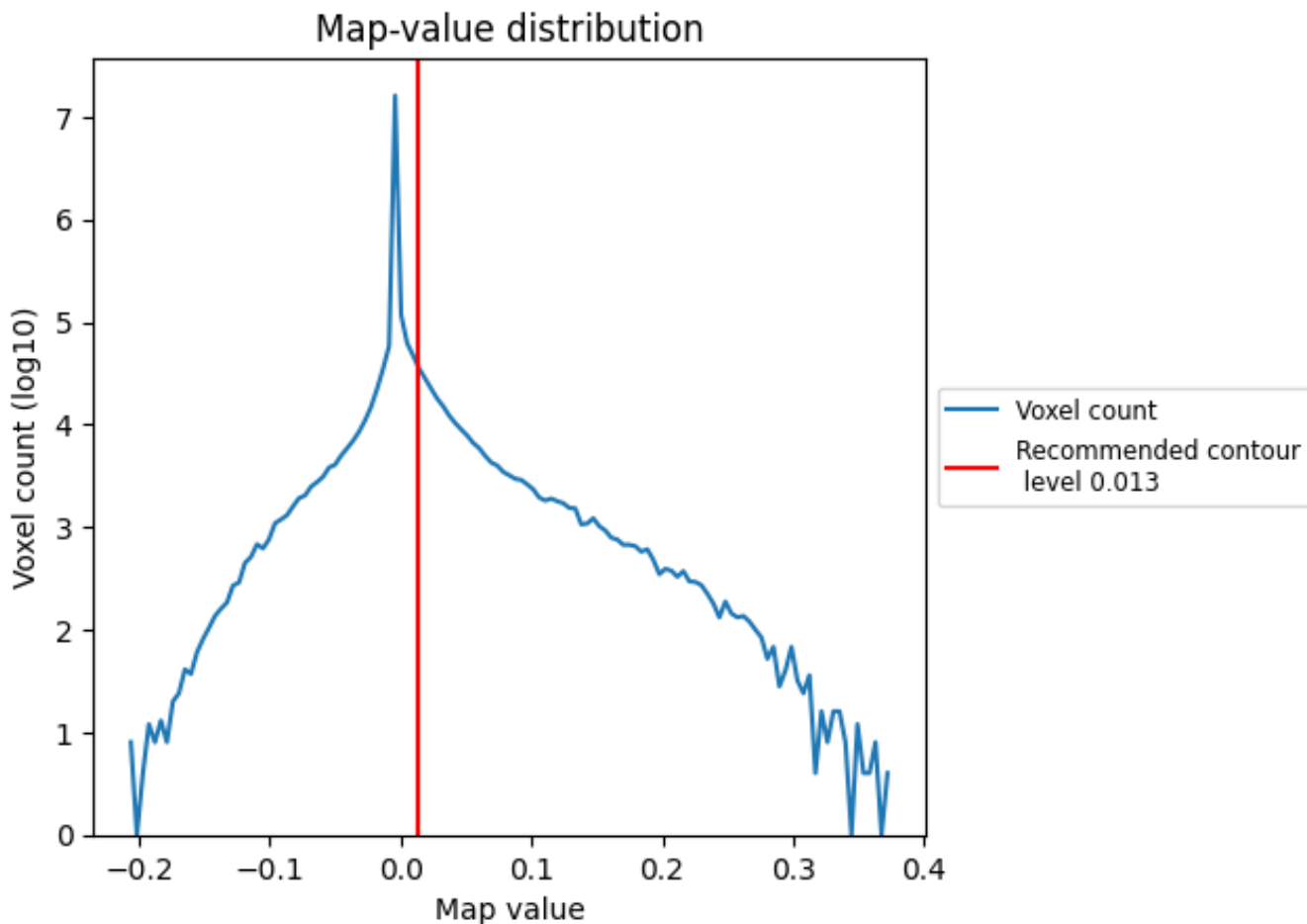
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

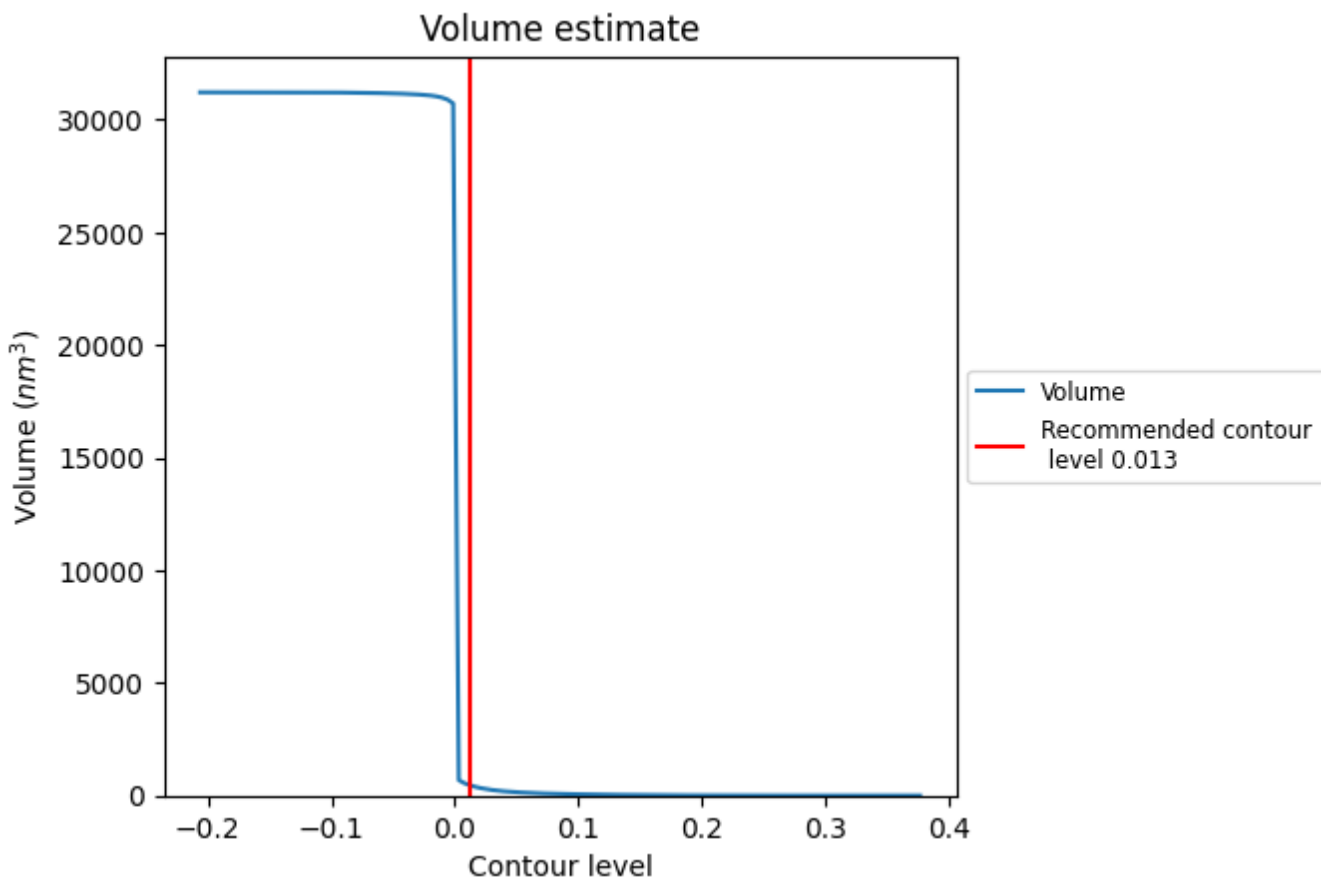
This section contains the results of statistical analysis of the map.

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.

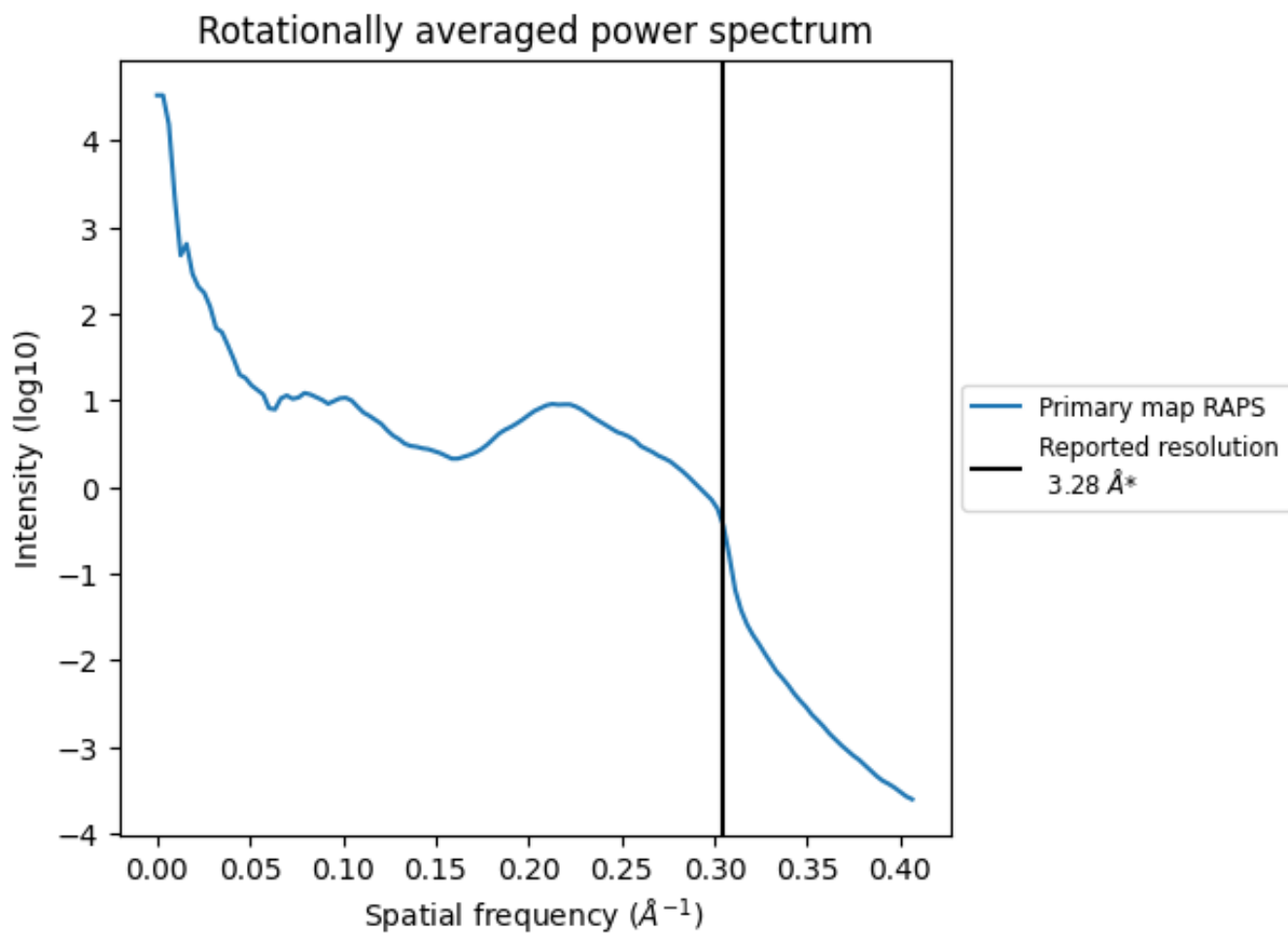
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 445 nm³; this corresponds to an approximate mass of 402 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](#)

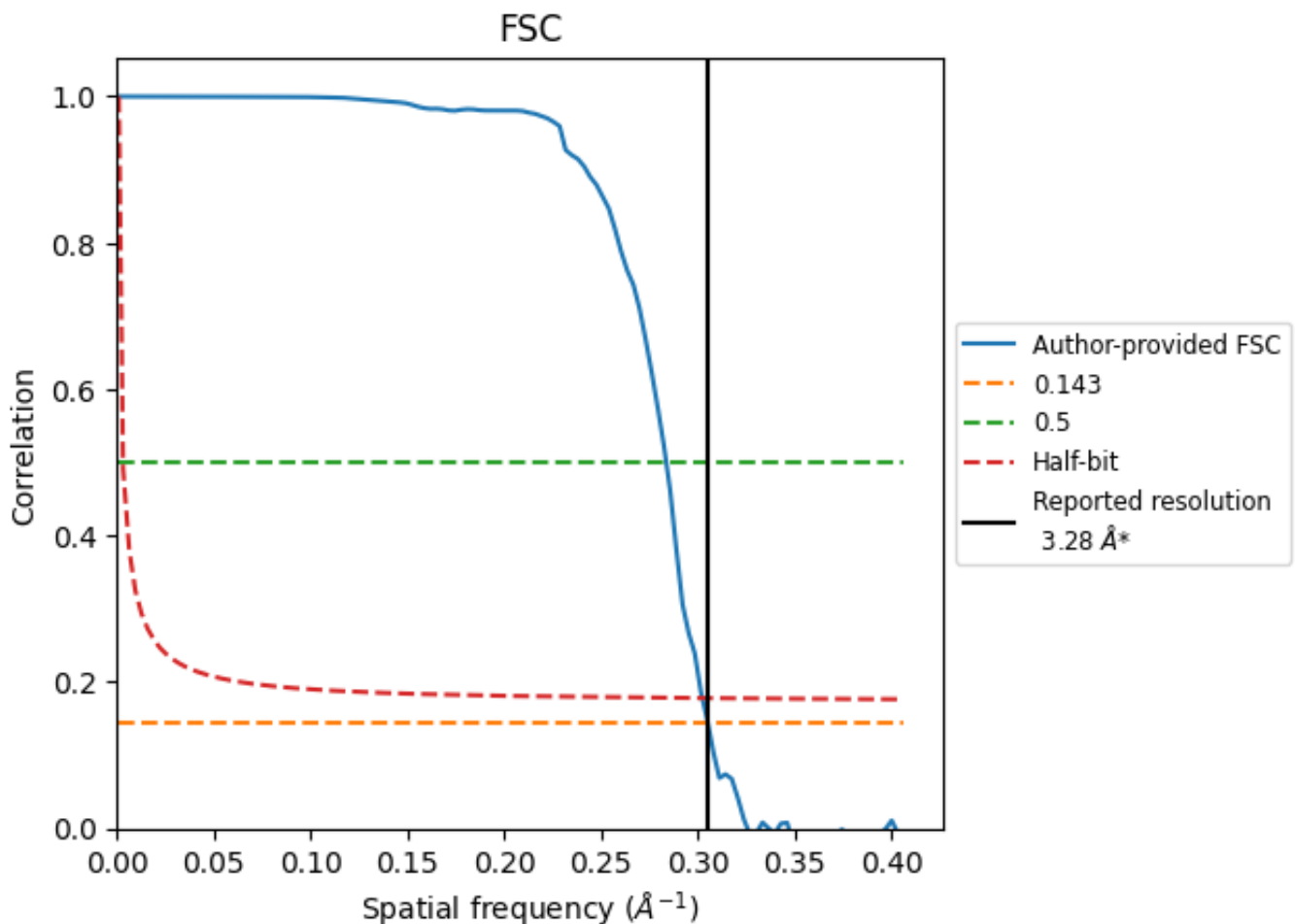


*Reported resolution corresponds to spatial frequency of 0.305 Å⁻¹

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 0.305 Å⁻¹

8.2 Resolution estimates [i](#)

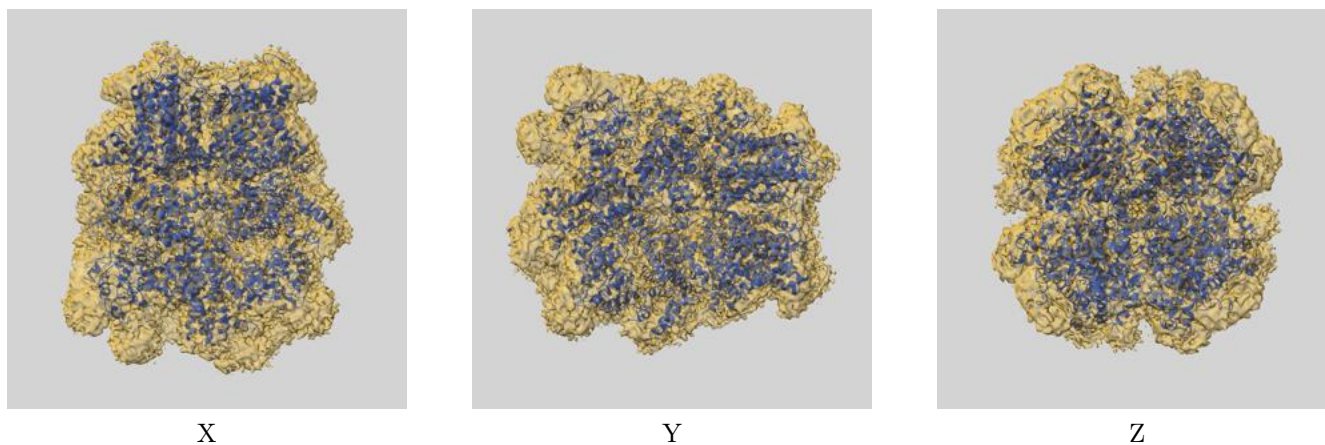
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.28	-	-
Author-provided FSC curve	3.28	3.52	3.31
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

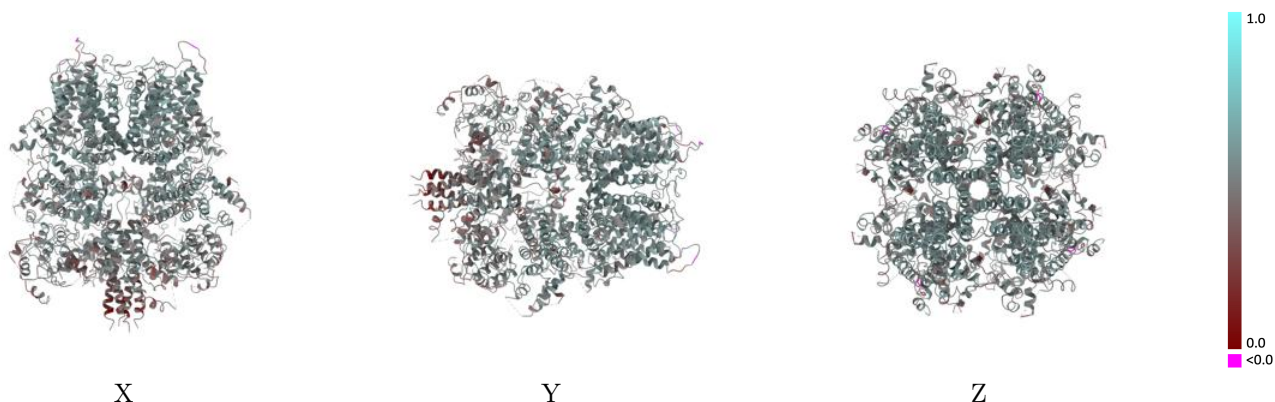
This section contains information regarding the fit between EMDB map EMD-6975 and PDB model 5ZX5. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



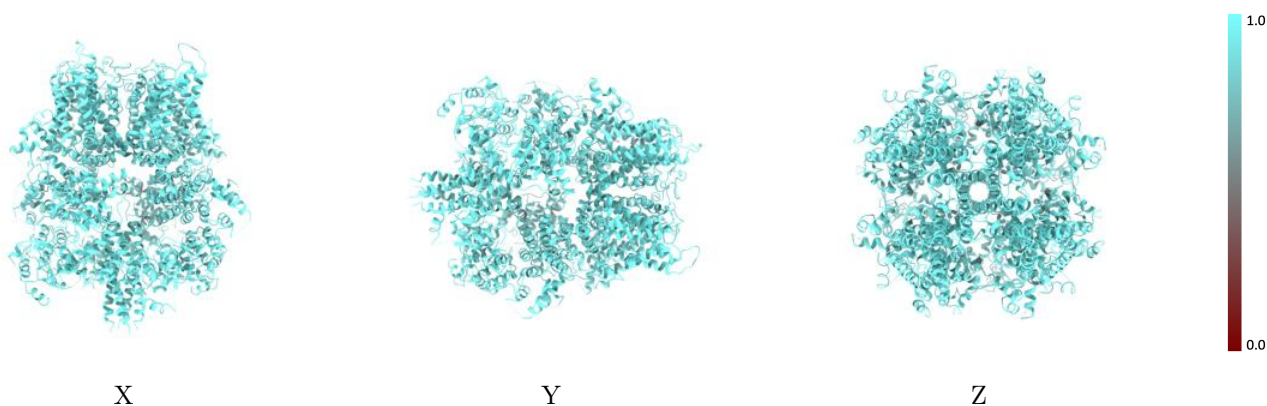
The images above show the 3D surface view of the map at the recommended contour level 0.013 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



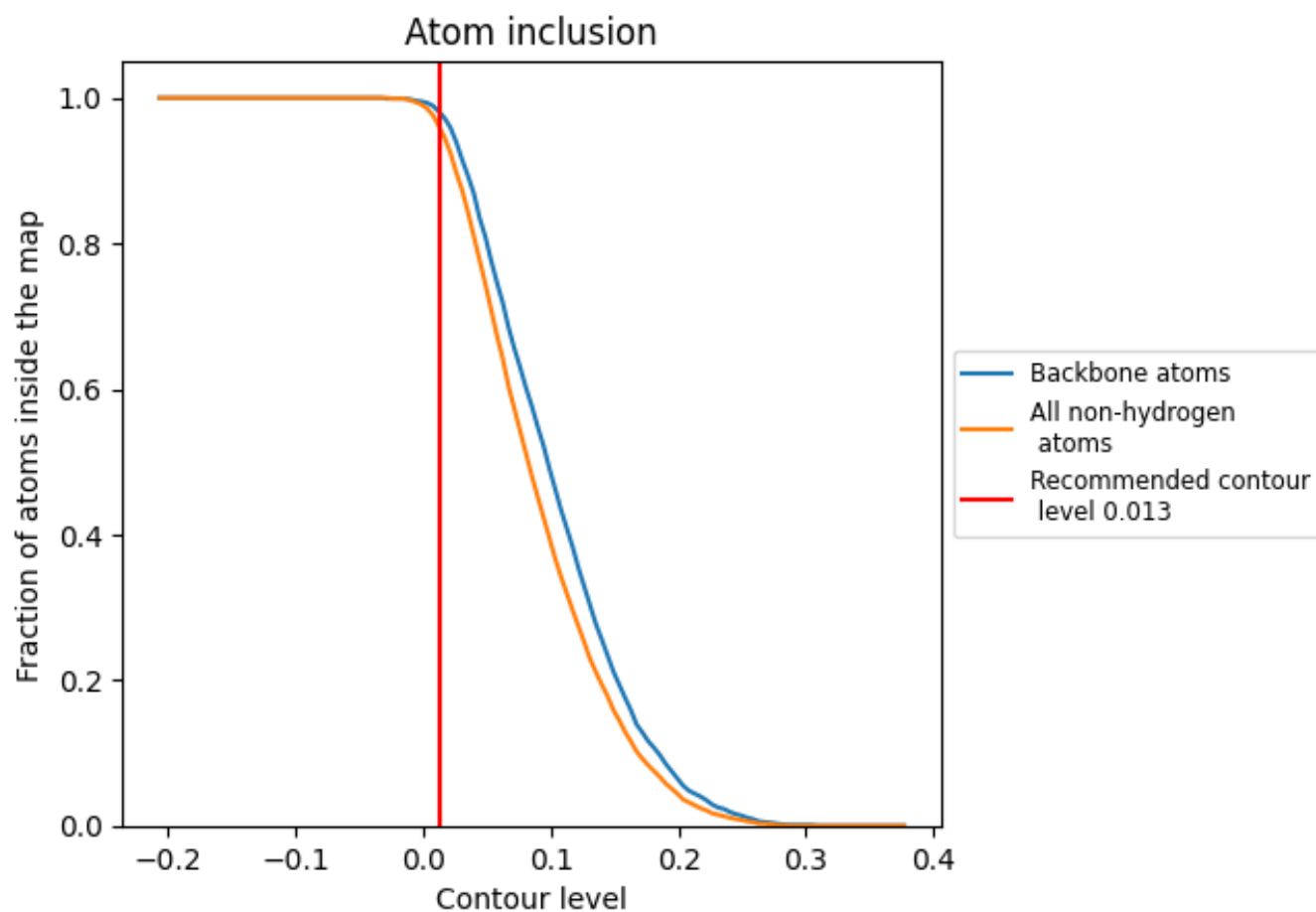
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.013).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 96% 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 (0.013) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9590	 0.5110
A	 0.9590	 0.5110
B	 0.9600	 0.5110
C	 0.9590	 0.5110
D	 0.9590	 0.5110

