



Full wwPDB EM Validation Report ⓘ

Jan 1, 2023 – 12:17 AM JST

PDB ID : 7XJ1
EMDB ID : EMD-33216
Title : Structure of human TRPV3_G573S in complex with Trpvicin in C2 symmetry
Authors : Fan, J.; Yue, Z.; Jiang, D.; Lei, X.
Deposited on : 2022-04-14
Resolution : 2.93 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:

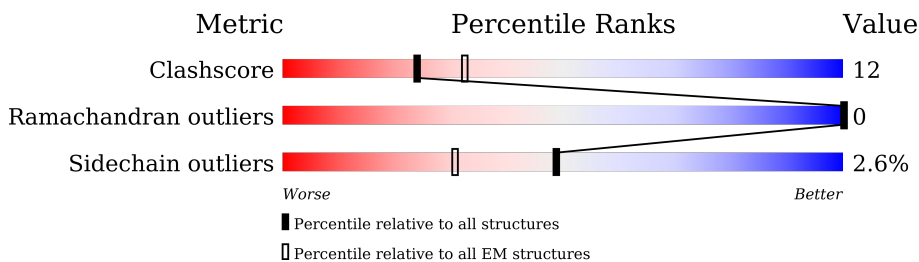
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

1 Overall quality at a glance

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

The reported resolution of this entry is 2.93 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	1061	44% 14% 42%
1	B	1061	43% 14% 43%
1	C	1061	42% 16% 42%
1	D	1061	43% 14% 43%

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
3	EQK	B	1603	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 18910 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 Fusion protein of Transient receptor potential cation channel subfamily V member 3 and 3C-GFP.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	B	606	4593	3023	766	776	28	0	0
1	C	616	4647	3055	773	792	27	0	0
1	A	616	4641	3052	771	791	27	0	0
1	D	606	4570	3008	759	775	28	0	0

There are 24 discrepancies between the modelled and reference sequences:

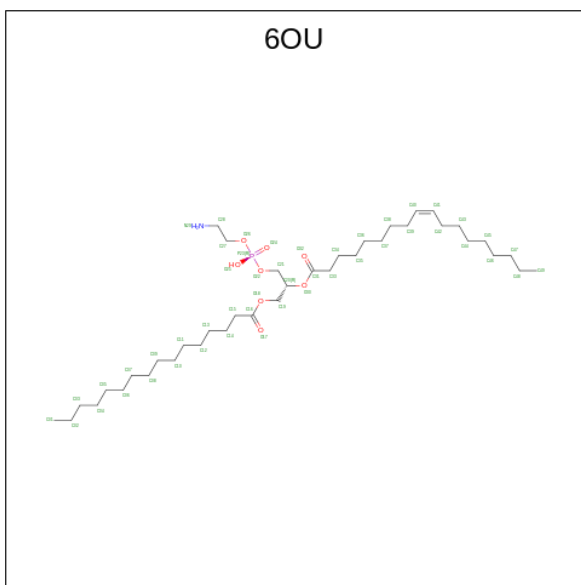
Chain	Residue	Modelled	Actual	Comment	Reference
B	25	ILE	VAL	conflict	UNP B2KYM6
B	117	ARG	GLY	conflict	UNP B2KYM6
B	246	LYS	ARG	conflict	UNP B2KYM6
B	247	GLY	GLU	conflict	UNP B2KYM6
B	573	SER	GLY	conflict	UNP B2KYM6
B	772	ASN	ASP	conflict	UNP B2KYM6
C	25	ILE	VAL	conflict	UNP B2KYM6
C	117	ARG	GLY	conflict	UNP B2KYM6
C	246	LYS	ARG	conflict	UNP B2KYM6
C	247	GLY	GLU	conflict	UNP B2KYM6
C	573	SER	GLY	conflict	UNP B2KYM6
C	772	ASN	ASP	conflict	UNP B2KYM6
A	25	ILE	VAL	conflict	UNP B2KYM6
A	117	ARG	GLY	conflict	UNP B2KYM6
A	246	LYS	ARG	conflict	UNP B2KYM6
A	247	GLY	GLU	conflict	UNP B2KYM6
A	573	SER	GLY	conflict	UNP B2KYM6
A	772	ASN	ASP	conflict	UNP B2KYM6
D	25	ILE	VAL	conflict	UNP B2KYM6
D	117	ARG	GLY	conflict	UNP B2KYM6
D	246	LYS	ARG	conflict	UNP B2KYM6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	247	GLY	GLU	conflict	UNP B2KYM6
D	573	SER	GLY	conflict	UNP B2KYM6
D	772	ASN	ASP	conflict	UNP B2KYM6

- Molecule 2 is [(2 {R})-1-[2-azanylethoxy(oxidanyl)phosphoryl]oxy-3-hexadecanoyloxy-prop an-2-yl] ({Z})-octadec-9-enoate (three-letter code: 6OU) (formula: C₃₉H₇₆NO₈P).



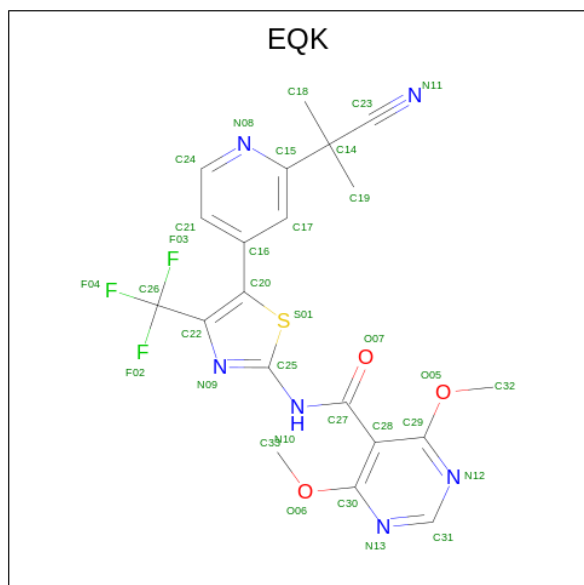
Mol	Chain	Residues	Atoms	AltConf
2	B	1	Total C 38 38	0
2	B	1	Total C 38 38	0
2	B	1	Total C 38 38	0
2	C	1	Total C 40 40	0
2	C	1	Total C 40 40	0
2	C	1	Total C 40 40	0
2	A	1	Total C 25 25	0
2	A	1	Total C 25 25	0
2	D	1	Total C 26 26	0

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Mol	Chain	Residues	Atoms	AltConf
2	D	1	Total C 26 26	0

- Molecule 3 is N-[5-[2-(2-cyanopropan-2-yl)pyridin-4-yl]-4-(trifluoromethyl)-1,3-thiazol-2-yl]-4,6-dimethoxy-pyrimidine-5-carboxamide (three-letter code: EQK) (formula: C₂₀H₁₇F₃N₆O₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf	
			Total	C	F	N	O		S
3	B	1	Total 66	C 40	F 6	N 12	O 6	S 2	0
3	B	1	Total 66	C 40	F 6	N 12	O 6	S 2	0
3	C	1	Total 99	C 60	F 9	N 18	O 9	S 3	0
3	C	1	Total 99	C 60	F 9	N 18	O 9	S 3	0
3	C	1	Total 99	C 60	F 9	N 18	O 9	S 3	0
3	A	1	Total 99	C 60	F 9	N 18	O 9	S 3	0
3	A	1	Total 99	C 60	F 9	N 18	O 9	S 3	0
3	A	1	Total 99	C 60	F 9	N 18	O 9	S 3	0
3	D	1	Total 66	C 40	F 6	N 12	O 6	S 2	0

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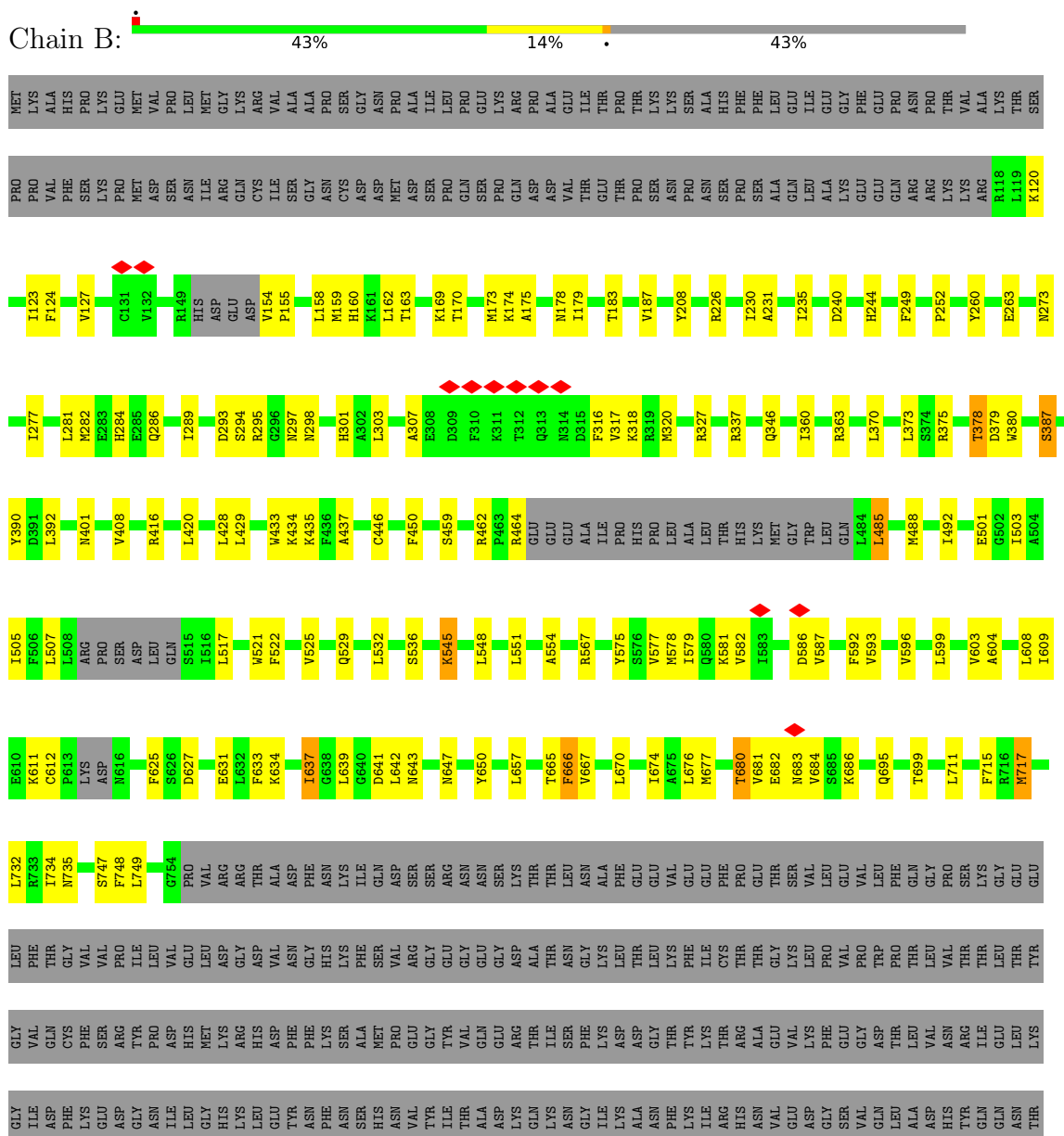
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Mol	Chain	Residues	Atoms					AltConf	
			Total	C	F	N	O		S
3	D	1	66	40	6	12	6	2	0

3 Residue-property plots

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

- Molecule 1: Fusion protein of Transient receptor potential cation channel subfamily V member 3 and 3C-GFP



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	152978	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	5.415	Depositor
Minimum map value	-2.931	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.103	Depositor
Recommended contour level	0.43	Depositor
Map size (\AA)	332.8, 332.8, 332.8	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.04, 1.04, 1.04	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: 6OU, EQK

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	0.29	0/4741	0.44	0/6455
1	B	0.29	0/4691	0.44	0/6381
1	C	0.30	0/4747	0.44	0/6462
1	D	0.29	0/4668	0.45	0/6354
All	All	0.29	0/18847	0.44	0/25652

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [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	4641	0	4479	125	0
1	B	4593	0	4468	110	0
1	C	4647	0	4491	128	0
1	D	4570	0	4412	115	0
2	A	25	0	0	0	0
2	B	38	0	0	0	0
2	C	40	0	0	0	0
2	D	26	0	0	0	0
3	A	99	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	66	0	0	13	0
3	C	99	0	0	9	0
3	D	66	0	0	2	0
All	All	18910	0	17850	442	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 12.

All (442) 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:A:674:ILE:CD1	1:D:677:MET:HG3	1.58	1.30
3:C:1106:EQK:C19	1:D:670:LEU:HD13	1.64	1.25
1:A:674:ILE:HD11	1:D:677:MET:CG	1.65	1.25
1:B:639:LEU:CD2	1:C:643:ASN:HD21	1.64	1.09
1:A:674:ILE:HD11	1:D:677:MET:HG3	1.16	1.08
1:B:639:LEU:HD22	1:C:643:ASN:ND2	1.69	1.07
1:A:432:LYS:HG3	1:A:717:MET:HE1	1.36	1.07
1:A:621:SER:HB2	1:A:631:GLU:OE2	1.57	1.04
1:A:674:ILE:HD11	1:D:677:MET:SD	1.99	1.02
1:B:639:LEU:HD22	1:C:643:ASN:HD21	0.87	1.01
1:A:710:TRP:HZ3	1:A:714:ARG:HH11	1.15	0.94
1:C:710:TRP:HZ3	1:C:714:ARG:HH11	1.16	0.89
1:C:574:MET:HA	1:C:688:SER:OG	1.75	0.87
1:B:639:LEU:CD2	1:C:643:ASN:ND2	2.29	0.87
1:A:505:ILE:HA	1:A:508:LEU:CD1	2.06	0.86
1:A:674:ILE:CD1	1:D:677:MET:CG	2.37	0.85
1:C:416:ARG:HH12	1:C:698:ARG:NH2	1.73	0.84
1:C:416:ARG:HH12	1:C:698:ARG:HH21	1.24	0.84
1:C:397:THR:HG22	1:C:397:THR:O	1.80	0.82
1:D:163:THR:HG22	1:D:170:THR:HG22	1.63	0.81
1:B:670:LEU:HD12	3:B:1603:EQK:C18	2.11	0.81
3:B:1603:EQK:F02	1:A:590:PHE:HE2	1.52	0.81
3:B:1603:EQK:N11	3:A:1801:EQK:C33	2.43	0.80
1:D:318:LYS:NZ	1:D:355:GLU:CB	2.46	0.78
1:D:264:THR:HG22	1:D:267:ALA:H	1.49	0.77
1:D:127:VAL:CG1	1:D:175:ALA:HB2	2.16	0.76
1:D:310:PHE:CD1	1:D:311:LYS:N	2.54	0.75
3:B:1603:EQK:F02	1:A:590:PHE:CE2	2.30	0.75
1:A:674:ILE:HD13	1:D:677:MET:HG3	1.66	0.74
1:D:567:ARG:NH2	1:D:695:GLN:OE1	2.21	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:620:SER:HB3	1:A:647:ASN:HB3	1.70	0.73
1:D:363:ARG:NH1	1:D:373:LEU:O	2.21	0.73
1:A:431:MET:HB2	1:A:717:MET:SD	2.29	0.73
1:A:504:ALA:O	1:A:508:LEU:HG	1.88	0.73
1:A:363:ARG:NH1	1:A:373:LEU:O	2.22	0.73
1:B:363:ARG:NH1	1:B:373:LEU:O	2.22	0.72
1:B:158:LEU:O	1:B:162:LEU:HG	1.88	0.72
1:B:674:ILE:HA	1:B:677:MET:HG2	1.72	0.72
1:B:665:THR:OG1	3:B:1602:EQK:C31	2.38	0.71
1:D:174:LYS:O	1:D:178:ASN:ND2	2.22	0.71
1:D:567:ARG:HE	1:D:576:SER:HB2	1.53	0.71
1:C:363:ARG:NH1	1:C:373:LEU:O	2.22	0.71
1:D:665:THR:OG1	3:D:1103:EQK:C31	2.39	0.71
1:D:433:TRP:HA	1:D:437:ALA:HB3	1.74	0.70
1:B:433:TRP:HA	1:B:437:ALA:HB3	1.74	0.69
1:B:127:VAL:CG2	1:B:175:ALA:HB2	2.22	0.69
1:C:573:SER:OG	1:C:692:TRP:HB2	1.92	0.69
1:B:174:LYS:O	1:B:178:ASN:ND2	2.25	0.69
1:B:666:PHE:HB3	3:B:1603:EQK:C21	2.23	0.68
1:D:522:PHE:HA	1:D:525:VAL:HG22	1.74	0.68
1:C:567:ARG:HH21	1:C:580:GLN:HE22	1.41	0.68
1:B:642:LEU:HD12	1:B:642:LEU:O	1.94	0.68
1:A:432:LYS:HG3	1:A:717:MET:CE	2.18	0.68
1:D:488:MET:HG2	1:D:492:ILE:CD1	2.24	0.67
1:D:456:THR:HA	1:D:555:MET:SD	2.35	0.67
1:B:666:PHE:CB	3:B:1603:EQK:C21	2.72	0.66
1:C:464:ARG:HD2	1:D:611:LYS:HE3	1.77	0.66
1:C:710:TRP:HZ3	1:C:714:ARG:NH1	1.93	0.66
1:B:163:THR:HG22	1:B:170:THR:HG22	1.78	0.66
1:D:484:LEU:O	1:D:484:LEU:HD12	1.96	0.65
1:B:642:LEU:CD1	1:A:630:LEU:HD11	2.26	0.65
1:A:599:LEU:HD22	1:A:625:PHE:HZ	1.62	0.65
1:C:634:LYS:HA	1:C:637:ILE:HG12	1.79	0.65
3:C:1105:EQK:O06	3:C:1105:EQK:N10	2.29	0.64
1:A:621:SER:CB	1:A:631:GLU:OE2	2.40	0.64
1:C:575:TYR:HE2	1:D:593:VAL:HG21	1.63	0.64
1:A:634:LYS:HA	1:A:637:ILE:HG12	1.77	0.64
1:B:611:LYS:HE3	1:A:464:ARG:HD2	1.78	0.64
1:B:681:VAL:HG21	1:C:678:GLY:HA3	1.79	0.64
1:A:567:ARG:HH21	1:A:580:GLN:HE22	1.45	0.64
1:C:464:ARG:NH2	1:D:609:ILE:O	2.29	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:673:LEU:CD1	1:D:670:LEU:HD11	2.28	0.63
1:B:501:GLU:O	1:B:505:ILE:HG13	1.98	0.63
1:B:642:LEU:HD11	1:A:630:LEU:HD11	1.81	0.62
1:B:127:VAL:HG22	1:B:175:ALA:HB2	1.81	0.62
3:C:1106:EQK:C23	1:D:670:LEU:CD1	2.77	0.62
1:B:609:ILE:O	1:A:464:ARG:NH2	2.30	0.62
1:A:609:ILE:O	1:D:464:ARG:NH2	2.31	0.62
1:D:307:ALA:HB2	1:D:317:VAL:HG11	1.80	0.62
1:D:681:VAL:HA	1:D:684:VAL:HG12	1.82	0.62
1:C:205:ASN:HD21	1:C:240:ASP:H	1.46	0.61
1:A:599:LEU:CD2	1:A:625:PHE:HZ	2.14	0.61
1:C:379:ASP:HB2	1:C:749:LEU:H	1.66	0.61
1:D:252:PRO:HD2	1:D:260:TYR:HB2	1.83	0.61
1:A:590:PHE:HB2	1:A:672:MET:HG3	1.81	0.61
1:B:633:PHE:CZ	1:B:637:ILE:HD12	2.36	0.61
3:B:1603:EQK:C33	1:A:636:THR:O	2.48	0.61
1:C:205:ASN:ND2	1:C:240:ASP:H	1.99	0.60
1:A:505:ILE:HA	1:A:508:LEU:HD12	1.82	0.60
1:A:621:SER:HB2	1:A:631:GLU:CD	2.20	0.60
1:B:252:PRO:HD2	1:B:260:TYR:HB2	1.83	0.60
1:A:622:TYR:CD2	1:A:631:GLU:OE1	2.55	0.60
1:C:456:THR:HG23	1:D:603:VAL:HG11	1.83	0.60
1:A:432:LYS:CG	1:A:717:MET:HE1	2.22	0.60
1:A:379:ASP:HB2	1:A:749:LEU:H	1.67	0.60
1:D:297:ASN:HB3	1:D:301:HIS:HB2	1.84	0.59
1:C:563:LEU:HD12	1:C:576:SER:HB3	1.83	0.59
1:A:710:TRP:HZ3	1:A:714:ARG:NH1	1.94	0.59
1:C:205:ASN:HD21	1:C:239:ALA:HA	1.67	0.59
1:B:603:VAL:HG11	1:A:456:THR:HG23	1.83	0.59
1:D:318:LYS:HZ3	1:D:355:GLU:CB	2.13	0.59
1:C:673:LEU:HD13	1:D:670:LEU:HD11	1.85	0.59
1:B:297:ASN:HB3	1:B:301:HIS:HB2	1.85	0.59
1:A:433:TRP:HA	1:A:437:ALA:HB3	1.84	0.59
1:C:687:GLU:OE2	1:C:690:ARG:NH2	2.36	0.58
1:D:301:HIS:O	1:D:305:THR:HG23	2.03	0.58
1:C:433:TRP:HA	1:C:437:ALA:HB3	1.85	0.58
1:C:590:PHE:HB2	1:C:672:MET:HG3	1.84	0.58
1:B:681:VAL:HA	1:B:684:VAL:HG12	1.86	0.58
1:A:590:PHE:CE1	1:A:669:LEU:HD23	2.39	0.58
1:D:529:GLN:NE2	1:D:554:ALA:O	2.33	0.58
1:B:567:ARG:NH2	1:B:695:GLN:OE1	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:673:LEU:HD13	1:D:670:LEU:CD1	2.34	0.57
1:A:462:ARG:HD3	1:A:548:LEU:HD13	1.86	0.57
1:A:678:GLY:HA3	1:D:681:VAL:HG21	1.84	0.57
1:C:545:LYS:O	1:D:650:TYR:OH	2.22	0.57
1:A:710:TRP:O	1:A:714:ARG:HG3	2.05	0.57
1:C:304:VAL:HG22	1:C:356:ILE:HG21	1.86	0.57
1:C:462:ARG:HD3	1:C:548:LEU:HD13	1.87	0.57
1:B:169:LYS:HG3	1:B:173:MET:HB2	1.86	0.57
1:D:380:TRP:CG	1:D:387:SER:HB3	2.40	0.56
1:C:710:TRP:O	1:C:714:ARG:HG3	2.04	0.56
1:A:682:GLU:O	1:A:685:SER:OG	2.20	0.56
1:D:501:GLU:O	1:D:505:ILE:HG13	2.04	0.56
1:B:464:ARG:NH2	1:C:609:ILE:O	2.34	0.56
1:B:593:VAL:HG21	1:A:575:TYR:HE2	1.69	0.56
1:C:569:PHE:O	1:C:573:SER:HB2	2.05	0.56
1:D:379:ASP:HA	1:D:749:LEU:H	1.70	0.56
1:C:235:ILE:HD13	1:C:281:LEU:HD23	1.88	0.56
1:D:633:PHE:CZ	1:D:637:ILE:HD12	2.41	0.56
1:B:680:THR:O	1:B:683:ASN:N	2.39	0.55
1:A:235:ILE:HD13	1:A:281:LEU:HD23	1.88	0.55
1:D:231:ALA:O	1:D:235:ILE:HG13	2.07	0.55
1:B:522:PHE:HA	1:B:525:VAL:HG22	1.87	0.55
1:C:610:GLU:HG3	1:C:649:LYS:HD3	1.88	0.55
1:C:682:GLU:O	1:C:685:SER:OG	2.25	0.55
1:C:381:ALA:HB3	1:C:745:HIS:CG	2.42	0.55
1:B:582:VAL:HG11	1:B:676:LEU:HD12	1.89	0.55
3:C:1105:EQK:C31	3:C:1106:EQK:N11	2.69	0.55
1:B:282:MET:CE	1:B:327:ARG:HG3	2.37	0.55
1:B:536:SER:OG	1:B:551:LEU:HB2	2.06	0.55
1:C:742:TRP:HZ2	1:D:273:ASN:HD22	1.53	0.55
1:A:304:VAL:HG22	1:A:356:ILE:HG21	1.87	0.55
1:B:650:TYR:OH	1:A:545:LYS:O	2.25	0.54
1:C:491:LEU:HD22	1:C:537:VAL:HG11	1.88	0.54
1:D:123:ILE:O	1:D:127:VAL:HG23	2.07	0.54
1:B:187:VAL:HG21	1:B:230:ILE:HG23	1.89	0.54
1:D:303:LEU:HD22	1:D:317:VAL:HG13	1.90	0.54
1:B:379:ASP:HA	1:B:749:LEU:H	1.72	0.54
1:B:380:TRP:CG	1:B:387:SER:HB3	2.42	0.54
1:B:529:GLN:NE2	1:B:554:ALA:O	2.34	0.54
1:C:392:LEU:HD22	1:C:428:LEU:HD11	1.89	0.54
1:C:665:THR:O	1:C:669:LEU:HG	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:745:HIS:NE2	1:C:747:SER:O	2.41	0.54
1:A:665:THR:O	1:A:669:LEU:HG	2.08	0.54
1:D:682:GLU:O	1:D:686:LYS:HG2	2.08	0.54
1:B:231:ALA:O	1:B:235:ILE:HG13	2.07	0.54
1:A:176:LEU:HD21	1:A:230:ILE:HG21	1.90	0.54
1:A:379:ASP:HA	1:A:748:PHE:HA	1.90	0.54
1:A:745:HIS:NE2	1:A:747:SER:O	2.41	0.54
1:D:318:LYS:HZ1	1:D:355:GLU:CB	2.19	0.54
1:C:416:ARG:NH1	1:C:698:ARG:HH21	2.01	0.53
1:C:176:LEU:HD21	1:C:230:ILE:HG21	1.90	0.53
3:C:1106:EQK:C23	1:D:670:LEU:HD13	2.37	0.53
1:A:605:LEU:HD12	1:A:632:LEU:HD21	1.90	0.53
1:B:408:VAL:O	1:B:416:ARG:NH1	2.39	0.53
1:A:381:ALA:HB3	1:A:745:HIS:CG	2.43	0.53
1:A:127:VAL:HG21	1:A:190:LEU:HD11	1.88	0.53
1:B:159:MET:HA	1:B:162:LEU:HB2	1.90	0.53
1:C:127:VAL:HG21	1:C:190:LEU:HD11	1.89	0.53
1:B:735:ASN:ND2	1:C:256:HIS:O	2.41	0.53
1:A:392:LEU:HD22	1:A:428:LEU:HD11	1.91	0.53
1:C:605:LEU:HD12	1:C:632:LEU:HD21	1.91	0.53
1:D:282:MET:HG2	1:D:289:ILE:HD12	1.90	0.52
1:B:124:PHE:HA	1:B:127:VAL:HG12	1.91	0.52
1:A:172:LEU:HD11	1:A:187:VAL:HG23	1.92	0.52
1:B:282:MET:HE3	1:B:327:ARG:HG3	1.90	0.52
1:A:622:TYR:CE2	1:A:631:GLU:OE1	2.63	0.52
1:D:521:TRP:CD1	1:D:579:ILE:HD11	2.45	0.52
1:A:307:ALA:HB2	1:A:317:VAL:HG11	1.92	0.52
1:C:364:GLU:OE1	1:C:378:THR:N	2.37	0.52
1:A:381:ALA:HB3	1:A:745:HIS:CD2	2.45	0.52
1:C:381:ALA:HB3	1:C:745:HIS:CD2	2.44	0.52
1:A:568:GLY:O	1:A:696:ARG:NH2	2.43	0.52
1:B:120:LYS:NZ	1:B:160:HIS:O	2.43	0.52
1:C:379:ASP:HA	1:C:748:PHE:HA	1.91	0.52
1:D:408:VAL:O	1:D:416:ARG:NH1	2.40	0.52
3:B:1603:EQK:C19	1:A:587:VAL:HG22	2.39	0.52
1:C:519:ASP:OD2	1:C:698:ARG:HD2	2.09	0.52
1:A:505:ILE:HA	1:A:508:LEU:CG	2.39	0.51
1:A:505:ILE:HA	1:A:508:LEU:HD11	1.90	0.51
1:B:682:GLU:O	1:B:686:LYS:HG2	2.10	0.51
1:C:392:LEU:HD11	1:C:732:LEU:HB2	1.93	0.51
1:B:282:MET:HG2	1:B:289:ILE:HD12	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:172:LEU:HD11	1:C:187:VAL:HG23	1.93	0.51
1:A:187:VAL:HG11	1:A:230:ILE:HG23	1.92	0.51
1:D:401:ASN:OD1	1:D:401:ASN:N	2.44	0.51
1:B:488:MET:O	1:B:492:ILE:HD12	2.11	0.51
1:C:187:VAL:HG11	1:C:230:ILE:HG23	1.92	0.51
1:C:669:LEU:HB3	3:C:1105:EQK:N12	2.25	0.51
1:D:695:GLN:O	1:D:699:THR:HG22	2.10	0.51
1:B:545:LYS:O	1:C:650:TYR:OH	2.27	0.51
1:A:298:ASN:OD1	1:A:301:HIS:HD2	1.93	0.51
1:B:273:ASN:HD22	1:A:742:TRP:HZ2	1.58	0.51
1:B:316:PHE:O	1:B:320:MET:HG2	2.10	0.51
1:C:568:GLY:O	1:C:696:ARG:NH1	2.39	0.51
1:A:392:LEU:HD11	1:A:732:LEU:HB2	1.92	0.51
1:A:365:ILE:H	1:A:374:SER:HG	1.57	0.51
1:A:598:LEU:HG	1:A:629:VAL:HG13	1.92	0.51
1:A:687:GLU:OE2	1:A:690:ARG:NH2	2.43	0.51
1:C:298:ASN:OD1	1:C:301:HIS:HD2	1.94	0.50
1:D:619:CYS:HB2	1:D:647:ASN:HB2	1.93	0.50
1:B:307:ALA:HB2	1:B:317:VAL:HG11	1.93	0.50
1:A:332:GLU:O	1:A:336:THR:OG1	2.28	0.50
1:A:522:PHE:HA	1:A:525:VAL:HG22	1.93	0.50
1:C:307:ALA:HB2	1:C:317:VAL:HG11	1.93	0.50
1:C:590:PHE:CE1	1:C:669:LEU:HD23	2.46	0.50
1:C:684:VAL:HA	1:C:687:GLU:HB3	1.93	0.50
1:A:231:ALA:O	1:A:235:ILE:HG13	2.11	0.50
1:D:392:LEU:HD11	1:D:732:LEU:HB2	1.94	0.50
1:D:488:MET:HG2	1:D:492:ILE:HD12	1.94	0.50
1:C:401:ASN:OD1	1:C:401:ASN:N	2.45	0.50
1:B:123:ILE:O	1:B:127:VAL:HG12	2.12	0.50
1:B:695:GLN:O	1:B:699:THR:HG22	2.12	0.50
1:A:505:ILE:HA	1:A:508:LEU:HG	1.94	0.50
1:A:680:THR:O	1:A:684:VAL:HG22	2.12	0.50
1:D:710:TRP:O	1:D:714:ARG:HG3	2.12	0.50
1:C:231:ALA:O	1:C:235:ILE:HG13	2.12	0.49
1:C:416:ARG:NH1	1:C:698:ARG:NH2	2.51	0.49
1:D:680:THR:O	1:D:683:ASN:N	2.45	0.49
1:B:666:PHE:HB2	3:B:1603:EQK:C21	2.42	0.49
1:C:316:PHE:O	1:C:320:MET:HG2	2.12	0.49
1:C:454:THR:O	1:C:458:VAL:HG13	2.12	0.49
1:A:316:PHE:O	1:A:320:MET:HG2	2.12	0.49
1:A:401:ASN:OD1	1:A:401:ASN:N	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:454:THR:O	1:A:458:VAL:HG13	2.13	0.49
3:A:1801:EQK:N10	3:A:1801:EQK:O05	2.45	0.49
1:D:608:LEU:HD11	1:D:657:LEU:HD12	1.94	0.49
1:A:581:LYS:HD2	1:A:585:HIS:CD2	2.48	0.49
1:C:205:ASN:ND2	1:C:240:ASP:OD1	2.45	0.49
3:C:1106:EQK:C32	1:D:666:PHE:HZ	2.25	0.49
1:B:293:ASP:OD1	1:B:295:ARG:N	2.45	0.49
1:C:673:LEU:CD1	1:D:670:LEU:CD1	2.89	0.49
1:A:264:THR:HG22	1:A:266:LEU:H	1.78	0.49
1:D:612:CYS:HB2	1:D:647:ASN:HD21	1.77	0.49
1:C:397:THR:O	1:C:397:THR:CG2	2.53	0.49
1:C:264:THR:HG22	1:C:266:LEU:H	1.77	0.48
1:D:187:VAL:HG21	1:D:230:ILE:HG23	1.93	0.48
1:C:385:VAL:HG13	1:C:737:VAL:HG22	1.94	0.48
1:C:567:ARG:NH2	1:C:580:GLN:HE22	2.08	0.48
1:D:310:PHE:CG	1:D:311:LYS:N	2.81	0.48
1:B:485:LEU:H	1:B:485:LEU:HD22	1.78	0.48
1:C:332:GLU:O	1:C:336:THR:OG1	2.30	0.48
1:A:650:TYR:OH	1:D:545:LYS:O	2.31	0.48
1:C:598:LEU:HG	1:C:629:VAL:HG13	1.96	0.48
3:C:1105:EQK:N13	3:C:1106:EQK:N11	2.62	0.48
1:D:158:LEU:O	1:D:162:LEU:HB2	2.13	0.48
1:B:273:ASN:ND2	1:A:742:TRP:HZ2	2.12	0.48
1:C:155:PRO:HB2	1:C:199:ILE:HD13	1.96	0.48
1:A:563:LEU:HD12	1:A:576:SER:HB3	1.96	0.48
1:B:401:ASN:N	1:B:401:ASN:OD1	2.47	0.48
1:B:608:LEU:HD11	1:B:657:LEU:HD12	1.95	0.48
1:C:365:ILE:H	1:C:374:SER:HG	1.59	0.48
1:A:278:VAL:HG21	1:A:320:MET:HE1	1.96	0.48
1:B:318:LYS:HE3	1:B:318:LYS:HB2	1.61	0.47
1:C:591:LEU:O	1:C:595:ILE:HG12	2.14	0.47
1:C:641:ASP:OD1	1:C:641:ASP:N	2.45	0.47
1:B:633:PHE:CZ	1:B:637:ILE:CD1	2.97	0.47
1:B:666:PHE:O	1:B:670:LEU:HG	2.14	0.47
1:C:573:SER:O	1:C:577:VAL:HG23	2.14	0.47
1:D:298:ASN:H	1:D:301:HIS:CD2	2.32	0.47
1:B:667:VAL:HG23	3:B:1603:EQK:C24	2.44	0.47
1:C:742:TRP:HZ2	1:D:273:ASN:ND2	2.12	0.47
1:C:522:PHE:HA	1:C:525:VAL:HG22	1.96	0.47
1:C:741:GLU:O	1:D:313:GLN:NE2	2.48	0.47
1:A:641:ASP:OD1	1:A:641:ASP:N	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:298:ASN:H	1:B:301:HIS:CD2	2.32	0.47
1:B:277:ILE:HG22	1:B:281:LEU:HD23	1.96	0.47
1:C:708:PRO:HD2	1:C:711:LEU:HD12	1.96	0.47
1:A:351:MET:O	1:A:353:LYS:N	2.44	0.47
1:A:603:VAL:HG11	1:D:456:THR:HG23	1.97	0.47
1:D:277:ILE:HG22	1:D:281:LEU:HD23	1.97	0.47
1:D:493:TRP:O	1:D:497:ILE:HG13	2.15	0.47
1:A:428:LEU:HD23	1:A:717:MET:SD	2.55	0.47
1:B:378:THR:O	1:B:748:PHE:HA	2.15	0.46
1:C:593:VAL:HG13	1:C:668:LEU:HD21	1.97	0.46
1:D:293:ASP:OD1	1:D:295:ARG:N	2.45	0.46
1:D:378:THR:O	1:D:748:PHE:HA	2.14	0.46
1:B:420:LEU:HD22	1:B:429:LEU:HD11	1.97	0.46
1:B:717:MET:HE2	1:B:717:MET:H	1.80	0.46
1:B:392:LEU:HD11	1:B:732:LEU:HB2	1.98	0.46
1:C:240:ASP:OD1	1:C:240:ASP:N	2.49	0.46
1:C:668:LEU:O	1:C:672:MET:HG2	2.15	0.46
1:A:668:LEU:O	1:A:672:MET:HG2	2.16	0.46
1:A:593:VAL:HG13	1:A:668:LEU:HD21	1.97	0.46
1:A:628:ALA:O	1:A:632:LEU:HG	2.16	0.46
1:D:642:LEU:HD23	1:D:658:LEU:HD23	1.97	0.46
1:A:591:LEU:O	1:A:595:ILE:HG12	2.15	0.46
1:D:316:PHE:O	1:D:320:MET:HG2	2.16	0.46
1:A:708:PRO:HD2	1:A:711:LEU:HD12	1.98	0.45
1:A:380:TRP:CG	1:A:387:SER:HB3	2.51	0.45
1:A:486:GLY:O	1:A:490:VAL:HG13	2.16	0.45
1:A:567:ARG:NH2	1:A:580:GLN:HE22	2.10	0.45
1:C:159:MET:HE1	1:C:203:PHE:HA	1.99	0.45
1:C:278:VAL:HG21	1:C:320:MET:HE1	1.98	0.45
1:D:420:LEU:HD22	1:D:429:LEU:HD11	1.99	0.45
1:A:573:SER:O	1:A:577:VAL:HG23	2.17	0.45
1:C:321:TYR:OH	1:C:334:GLU:OE2	2.26	0.45
1:C:680:THR:O	1:C:684:VAL:HG22	2.16	0.45
1:C:673:LEU:HD12	1:D:670:LEU:HD11	1.98	0.45
1:C:581:LYS:HD2	1:C:585:HIS:CD2	2.52	0.44
1:A:669:LEU:HB3	3:A:1801:EQK:N13	2.32	0.44
1:C:380:TRP:CG	1:C:387:SER:HB3	2.53	0.44
1:D:633:PHE:CZ	1:D:637:ILE:CD1	3.00	0.44
1:C:351:MET:O	1:C:353:LYS:N	2.44	0.44
1:C:716:ARG:HA	1:C:716:ARG:HD3	1.42	0.44
1:A:622:TYR:HE2	1:A:644:ILE:HG12	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:434:LYS:HE2	1:D:434:LYS:HB3	1.77	0.44
1:B:612:CYS:HB2	1:B:647:ASN:HD21	1.83	0.44
1:C:329:GLY:HA2	1:C:373:LEU:HD11	2.00	0.44
1:A:720:LEU:HD13	1:A:730:LEU:HD22	1.99	0.44
1:B:503:ILE:O	1:B:507:LEU:HG	2.18	0.44
1:C:387:SER:HB2	1:C:735:ASN:ND2	2.33	0.44
1:B:592:PHE:O	1:B:596:VAL:HG23	2.18	0.44
1:C:410:ASN:HD21	1:C:413:ILE:HD13	1.82	0.44
1:A:371:ARG:HG3	1:A:371:ARG:HH11	1.83	0.44
1:B:360:ILE:O	1:B:375:ARG:HD3	2.18	0.44
1:C:299:ILE:HG12	1:C:324:ILE:HG21	2.00	0.44
1:C:486:GLY:O	1:C:490:VAL:HG13	2.17	0.44
3:D:1103:EQK:O06	3:D:1103:EQK:N10	2.50	0.44
1:C:133:GLU:O	1:C:136:VAL:HG12	2.18	0.44
1:B:169:LYS:HD3	1:B:208:TYR:OH	2.18	0.43
1:B:578:MET:O	1:B:582:VAL:HG22	2.17	0.43
1:C:572:MET:O	1:C:576:SER:OG	2.28	0.43
1:C:682:GLU:OE1	1:C:682:GLU:N	2.51	0.43
1:D:390:TYR:CE1	1:D:734:ILE:HD12	2.53	0.43
1:B:634:LYS:HB3	1:B:634:LYS:HE2	1.87	0.43
1:D:459:SER:HA	1:D:551:LEU:HD21	2.01	0.43
1:A:299:ILE:HG12	1:A:324:ILE:HG21	1.99	0.43
1:A:329:GLY:HA2	1:A:373:LEU:HD11	2.00	0.43
1:B:380:TRP:HB3	1:B:387:SER:H	1.82	0.43
1:B:428:LEU:HD23	1:B:428:LEU:HA	1.82	0.43
1:C:389:LEU:HD22	1:C:731:CYS:HB3	2.01	0.43
1:D:362:SER:O	1:D:362:SER:OG	2.33	0.43
1:B:586:ASP:OD1	1:B:587:VAL:N	2.52	0.43
1:B:179:ILE:HD12	1:B:183:THR:HG21	2.00	0.43
1:C:371:ARG:HG3	1:C:371:ARG:HH11	1.84	0.43
1:C:508:LEU:HD21	1:C:513:LEU:HD21	2.01	0.43
1:A:154:VAL:HB	1:A:155:PRO:HD3	2.01	0.43
1:D:451:TYR:HE1	1:D:490:VAL:HG13	1.84	0.43
1:D:284:HIS:CD2	1:D:286:GLN:H	2.36	0.43
1:B:284:HIS:CD2	1:B:286:GLN:H	2.37	0.42
1:B:532:LEU:HB3	1:B:554:ALA:HB2	2.01	0.42
1:C:349:ALA:HB2	1:C:403:VAL:HG13	2.01	0.42
1:A:410:ASN:HD21	1:A:413:ILE:HD13	1.84	0.42
1:A:622:TYR:CG	1:A:631:GLU:OE1	2.71	0.42
1:A:369:ARG:HG3	1:A:370:LEU:HG	2.01	0.42
1:D:360:ILE:O	1:D:375:ARG:HD3	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:380:TRP:HB3	1:D:387:SER:H	1.83	0.42
1:B:154:VAL:HB	1:B:155:PRO:HD3	2.00	0.42
1:B:575:TYR:O	1:B:579:ILE:HG13	2.19	0.42
1:B:577:VAL:O	1:B:581:LYS:HG3	2.19	0.42
1:A:169:LYS:HG3	1:A:173:MET:HB2	2.00	0.42
1:A:312:THR:O	1:D:739:TRP:HB2	2.19	0.42
1:D:328:SER:O	1:D:328:SER:OG	2.23	0.42
1:B:303:LEU:HD22	1:B:317:VAL:HG13	2.01	0.42
1:D:154:VAL:HB	1:D:155:PRO:HD3	2.02	0.42
1:D:431:MET:HE2	1:D:717:MET:HB3	2.01	0.42
1:B:459:SER:HA	1:B:551:LEU:HD21	2.02	0.42
1:B:517:LEU:O	1:B:521:TRP:HB2	2.20	0.42
1:A:513:LEU:HB3	1:A:521:TRP:CZ2	2.54	0.42
1:A:622:TYR:CD2	1:A:622:TYR:N	2.87	0.42
1:A:716:ARG:HD3	1:A:716:ARG:HA	1.75	0.42
1:D:455:LEU:HD13	1:D:490:VAL:HG11	2.00	0.42
1:B:604:ALA:O	1:B:608:LEU:HG	2.20	0.42
1:D:604:ALA:O	1:D:608:LEU:HG	2.20	0.42
1:B:599:LEU:HD22	1:B:625:PHE:HZ	1.83	0.42
1:C:387:SER:HA	1:C:735:ASN:HA	2.01	0.42
1:C:720:LEU:HD13	1:C:730:LEU:HD22	1.99	0.42
1:A:389:LEU:HD22	1:A:731:CYS:HB3	2.02	0.42
1:D:451:TYR:CE1	1:D:490:VAL:HG13	2.55	0.42
1:B:179:ILE:HB	1:A:746:VAL:HB	2.02	0.42
3:B:1602:EQK:O06	3:B:1602:EQK:N10	2.52	0.42
1:A:376:LYS:HD2	1:A:390:TYR:CZ	2.55	0.42
1:D:446:CYS:SG	1:D:450:PHE:CE2	3.12	0.42
1:C:612:CYS:HB3	1:C:619:CYS:SG	2.59	0.42
1:A:427:THR:O	1:A:431:MET:HG2	2.19	0.42
1:A:711:LEU:HD22	1:A:715:PHE:CE2	2.55	0.42
1:D:179:ILE:HD12	1:D:183:THR:HG21	2.01	0.42
1:D:244:HIS:HA	1:D:263:GLU:O	2.20	0.42
1:C:361:LEU:HD23	1:C:361:LEU:HA	1.88	0.41
1:C:711:LEU:HD22	1:C:715:PHE:CE2	2.54	0.41
1:A:364:GLU:OE1	1:A:378:THR:N	2.36	0.41
1:D:462:ARG:HD3	1:D:548:LEU:HD13	2.02	0.41
1:A:432:LYS:CG	1:A:717:MET:CE	2.92	0.41
1:D:532:LEU:HB3	1:D:554:ALA:HB2	2.03	0.41
1:B:677:MET:HB2	1:C:674:ILE:HD11	2.02	0.41
1:B:390:TYR:CE1	1:B:734:ILE:HD12	2.55	0.41
1:C:376:LYS:HD2	1:C:390:TYR:CZ	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:620:SER:OG	1:C:647:ASN:HB3	2.19	0.41
1:A:133:GLU:O	1:A:136:VAL:HG12	2.20	0.41
1:D:428:LEU:HD23	1:D:428:LEU:HA	1.82	0.41
1:B:226:ARG:NH2	1:B:273:ASN:O	2.54	0.41
1:B:244:HIS:HA	1:B:263:GLU:O	2.20	0.41
1:B:337:ARG:NH1	1:B:346:GLN:HE22	2.18	0.41
1:B:446:CYS:SG	1:B:450:PHE:CE2	3.13	0.41
1:B:637:ILE:O	1:B:637:ILE:CG2	2.69	0.41
3:B:1603:EQK:O07	3:B:1603:EQK:S01	2.79	0.41
1:C:172:LEU:HD12	1:C:172:LEU:HA	1.93	0.41
1:C:380:TRP:HH2	1:D:249:PHE:CE1	2.38	0.41
1:D:592:PHE:O	1:D:596:VAL:HG23	2.19	0.41
1:B:462:ARG:HD3	1:B:548:LEU:HD13	2.03	0.41
1:B:711:LEU:HD12	1:B:711:LEU:HA	1.82	0.41
1:C:169:LYS:HG3	1:C:173:MET:HB2	2.01	0.41
1:A:349:ALA:HB2	1:A:403:VAL:HG13	2.02	0.41
1:A:682:GLU:N	1:A:682:GLU:OE1	2.54	0.41
1:D:627:ASP:O	1:D:631:GLU:HG2	2.21	0.41
1:D:637:ILE:O	1:D:637:ILE:CG2	2.69	0.41
1:C:303:LEU:HD11	1:C:324:ILE:HD12	2.01	0.41
1:C:516:ILE:HG12	1:C:584:LEU:HD13	2.03	0.41
1:C:617:LYS:O	1:C:619:CYS:N	2.53	0.41
1:C:630:LEU:O	1:C:634:LYS:HG2	2.21	0.41
1:D:397:THR:HG22	1:D:405:GLU:HG3	2.02	0.41
1:D:635:LEU:HD12	1:D:635:LEU:HA	1.89	0.41
1:B:370:LEU:HB3	1:B:373:LEU:HD12	2.02	0.41
1:C:562:MET:O	1:C:566:THR:HG23	2.21	0.41
1:D:364:GLU:HG3	1:D:376:LYS:O	2.21	0.40
1:B:434:LYS:HB3	1:B:434:LYS:HE2	1.74	0.40
1:B:627:ASP:O	1:B:631:GLU:HG2	2.21	0.40
1:C:682:GLU:HG2	1:C:683:ASN:OD1	2.21	0.40
1:D:419:MET:HB3	1:D:419:MET:HE2	1.89	0.40
1:C:504:ALA:O	1:C:508:LEU:HB2	2.21	0.40
1:A:562:MET:O	1:A:566:THR:HG23	2.21	0.40
1:D:376:LYS:HA	1:D:389:LEU:O	2.21	0.40
1:A:159:MET:HE1	1:A:203:PHE:HA	2.03	0.40
1:D:169:LYS:HG3	1:D:173:MET:HB2	2.03	0.40
1:D:484:LEU:O	1:D:484:LEU:CD1	2.66	0.40
1:D:484:LEU:HD12	1:D:484:LEU:C	2.42	0.40
1:B:249:PHE:CE1	1:A:380:TRP:HH2	2.40	0.40
1:B:435:LYS:NZ	1:B:715:PHE:O	2.42	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:1106:EQK:C26	3:C:1106:EQK:C21	3.00	0.40
1:A:720:LEU:HD12	1:A:720:LEU:HA	1.87	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	608/1061 (57%)	567 (93%)	41 (7%)	0	100	100
1	B	596/1061 (56%)	556 (93%)	40 (7%)	0	100	100
1	C	608/1061 (57%)	563 (93%)	45 (7%)	0	100	100
1	D	596/1061 (56%)	559 (94%)	37 (6%)	0	100	100
All	All	2408/4244 (57%)	2245 (93%)	163 (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	443/934 (47%)	433 (98%)	10 (2%)	50	78
1	B	442/934 (47%)	429 (97%)	13 (3%)	42	73
1	C	444/934 (48%)	434 (98%)	10 (2%)	50	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	435/934 (47%)	422 (97%)	13 (3%)	41	72
All	All	1764/3736 (47%)	1718 (97%)	46 (3%)	49	75

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	240	ASP
1	B	294	SER
1	B	378	THR
1	B	387	SER
1	B	485	LEU
1	B	545	LYS
1	B	637	ILE
1	B	641	ASP
1	B	643	ASN
1	B	666	PHE
1	B	680	THR
1	B	717	MET
1	B	747	SER
1	C	127	VAL
1	C	136	VAL
1	C	157	PHE
1	C	158	LEU
1	C	213	TYR
1	C	220	ASN
1	C	328	SER
1	C	444	SER
1	C	571	SER
1	C	747	SER
1	A	127	VAL
1	A	136	VAL
1	A	156	ASP
1	A	159	MET
1	A	328	SER
1	A	397	THR
1	A	444	SER
1	A	586	ASP
1	A	739	TRP
1	A	742	TRP
1	D	162	LEU
1	D	264	THR
1	D	327	ARG

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Mol	Chain	Res	Type
1	D	328	SER
1	D	387	SER
1	D	402	SER
1	D	410	ASN
1	D	536	SER
1	D	588	LEU
1	D	637	ILE
1	D	641	ASP
1	D	666	PHE
1	D	747	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	273	ASN
1	B	284	HIS
1	B	301	HIS
1	B	346	GLN
1	B	647	ASN
1	B	671	ASN
1	C	197	ASN
1	C	205	ASN
1	C	301	HIS
1	C	430	HIS
1	C	483	GLN
1	C	580	GLN
1	C	585	HIS
1	C	643	ASN
1	A	180	ASN
1	A	197	ASN
1	A	301	HIS
1	A	430	HIS
1	A	570	GLN
1	A	580	GLN
1	A	585	HIS
1	A	647	ASN
1	D	160	HIS
1	D	273	ASN
1	D	284	HIS
1	D	301	HIS
1	D	346	GLN
1	D	580	GLN

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Mol	Chain	Res	Type
1	D	647	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

20 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$
3	EQK	C	1105	-	29,35,35	4.59	19 (65%)	33,52,52	2.28	12 (36%)
2	6OU	A	1804	-	11,11,48	0.30	0	10,10,53	0.79	0
3	EQK	D	1101	-	29,35,35	4.67	19 (65%)	33,52,52	2.18	12 (36%)
2	6OU	D	1102	-	13,13,48	0.30	0	12,12,53	0.78	0
2	6OU	C	1104	-	11,11,48	0.31	0	9,10,53	0.85	0
3	EQK	C	1101	-	29,35,35	4.76	19 (65%)	33,52,52	2.12	11 (33%)
3	EQK	C	1106	-	29,35,35	4.37	19 (65%)	33,52,52	1.98	9 (27%)
2	6OU	D	1104	-	11,11,48	0.30	0	10,10,53	0.78	0
3	EQK	A	1801	-	29,35,35	4.70	19 (65%)	33,52,52	2.25	13 (39%)
2	6OU	B	1601	-	13,13,48	0.30	0	12,12,53	0.79	0
2	6OU	C	1102	-	13,13,48	0.28	0	12,12,53	0.84	0
2	6OU	C	1103	-	13,13,48	0.32	0	12,12,53	0.72	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EQK	B	1603	-	29,35,35	4.87	19 (65%)	33,52,52	2.30	13 (39%)
3	EQK	A	1805	-	29,35,35	4.74	20 (68%)	33,52,52	2.10	10 (30%)
3	EQK	D	1103	-	29,35,35	4.54	19 (65%)	33,52,52	2.19	12 (36%)
2	6OU	B	1604	-	11,11,48	0.30	0	10,10,53	0.75	0
3	EQK	A	1802	-	29,35,35	4.57	19 (65%)	33,52,52	2.09	12 (36%)
2	6OU	A	1803	-	12,12,48	0.30	0	11,11,53	0.77	0
3	EQK	B	1602	-	29,35,35	4.54	19 (65%)	33,52,52	2.25	14 (42%)
2	6OU	B	1605	-	11,11,48	0.31	0	10,10,53	0.73	0

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	EQK	C	1105	-	-	9/26/31/31	0/3/3/3
2	6OU	A	1804	-	-	5/9/9/52	-
3	EQK	D	1101	-	-	9/26/31/31	0/3/3/3
2	6OU	D	1102	-	-	2/11/11/52	-
2	6OU	C	1104	-	-	4/9/9/52	-
3	EQK	C	1101	-	-	6/26/31/31	0/3/3/3
3	EQK	C	1106	-	-	4/26/31/31	0/3/3/3
2	6OU	D	1104	-	-	2/9/9/52	-
3	EQK	A	1801	-	-	8/26/31/31	0/3/3/3
2	6OU	B	1601	-	-	6/11/11/52	-
2	6OU	C	1102	-	-	4/11/11/52	-
2	6OU	C	1103	-	-	4/11/11/52	-
3	EQK	B	1603	-	-	9/26/31/31	0/3/3/3
3	EQK	A	1805	-	-	6/26/31/31	0/3/3/3
3	EQK	D	1103	-	-	13/26/31/31	0/3/3/3
2	6OU	B	1604	-	-	4/9/9/52	-
3	EQK	A	1802	-	-	4/26/31/31	0/3/3/3
2	6OU	A	1803	-	-	4/10/10/52	-
3	EQK	B	1602	-	-	13/26/31/31	0/3/3/3
2	6OU	B	1605	-	-	2/9/9/52	-

All (191) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1603	EQK	C31-N12	8.46	1.49	1.33
3	B	1603	EQK	C31-N13	8.36	1.49	1.33
3	C	1105	EQK	C31-N12	8.34	1.49	1.33
3	A	1801	EQK	C31-N13	8.33	1.49	1.33
3	D	1103	EQK	C31-N12	8.31	1.49	1.33
3	B	1602	EQK	C31-N12	8.25	1.49	1.33
3	C	1101	EQK	C31-N12	8.22	1.49	1.33
3	A	1805	EQK	C31-N12	8.20	1.49	1.33
3	D	1101	EQK	C31-N12	8.10	1.49	1.33
3	A	1802	EQK	C31-N13	8.09	1.49	1.33
3	C	1106	EQK	C31-N13	8.08	1.48	1.33
3	C	1106	EQK	C31-N12	8.08	1.48	1.33
3	C	1101	EQK	C31-N13	8.07	1.48	1.33
3	A	1805	EQK	C31-N13	8.06	1.48	1.33
3	A	1802	EQK	C31-N12	8.05	1.48	1.33
3	B	1602	EQK	C31-N13	8.03	1.48	1.33
3	D	1103	EQK	C31-N13	8.01	1.48	1.33
3	A	1801	EQK	C31-N12	7.99	1.48	1.33
3	D	1101	EQK	C31-N13	7.98	1.48	1.33
3	C	1105	EQK	C31-N13	7.96	1.48	1.33
3	A	1805	EQK	C17-C15	7.73	1.53	1.39
3	A	1801	EQK	C17-C15	7.72	1.53	1.39
3	B	1603	EQK	C17-C15	7.58	1.53	1.39
3	D	1101	EQK	C17-C15	7.57	1.53	1.39
3	C	1106	EQK	C17-C15	7.45	1.52	1.39
3	C	1101	EQK	C17-C15	7.34	1.52	1.39
3	C	1101	EQK	C21-C24	7.30	1.53	1.38
3	A	1802	EQK	C17-C15	7.25	1.52	1.39
3	B	1603	EQK	C21-C24	7.20	1.53	1.38
3	B	1602	EQK	C17-C15	7.19	1.52	1.39
3	A	1805	EQK	C21-C24	7.07	1.52	1.38
3	D	1101	EQK	C21-C24	7.05	1.52	1.38
3	D	1103	EQK	C21-C24	7.04	1.52	1.38
3	B	1603	EQK	C30-N13	7.04	1.45	1.32
3	C	1105	EQK	C21-C24	7.02	1.52	1.38
3	C	1105	EQK	C17-C15	7.01	1.52	1.39
3	D	1103	EQK	C17-C15	7.00	1.52	1.39
3	B	1603	EQK	C29-N12	6.98	1.45	1.32
3	D	1101	EQK	C15-N08	6.91	1.49	1.34
3	C	1101	EQK	C24-N08	6.90	1.49	1.34
3	A	1805	EQK	C15-N08	6.89	1.49	1.34
3	A	1801	EQK	C21-C24	6.88	1.52	1.38
3	A	1802	EQK	C21-C24	6.88	1.52	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1603	EQK	C15-N08	6.86	1.49	1.34
3	B	1603	EQK	C24-N08	6.86	1.49	1.34
3	B	1602	EQK	C21-C24	6.84	1.52	1.38
3	D	1101	EQK	C24-N08	6.83	1.49	1.34
3	C	1105	EQK	C15-N08	6.83	1.49	1.34
3	C	1105	EQK	C24-N08	6.80	1.48	1.34
3	A	1801	EQK	C15-N08	6.79	1.48	1.34
3	C	1101	EQK	C15-N08	6.79	1.48	1.34
3	A	1801	EQK	C24-N08	6.78	1.48	1.34
3	A	1801	EQK	C30-N13	6.75	1.45	1.32
3	A	1805	EQK	C29-N12	6.72	1.45	1.32
3	C	1101	EQK	C29-N12	6.68	1.45	1.32
3	B	1602	EQK	C29-N12	6.63	1.44	1.32
3	A	1802	EQK	C24-N08	6.63	1.48	1.34
3	B	1602	EQK	C15-N08	6.63	1.48	1.34
3	D	1103	EQK	C29-N12	6.62	1.44	1.32
3	A	1802	EQK	C30-N13	6.61	1.44	1.32
3	C	1105	EQK	C30-N13	6.61	1.44	1.32
3	A	1805	EQK	C30-N13	6.60	1.44	1.32
3	A	1801	EQK	C29-N12	6.59	1.44	1.32
3	D	1101	EQK	C29-N12	6.59	1.44	1.32
3	D	1103	EQK	C30-N13	6.58	1.44	1.32
3	C	1105	EQK	C29-N12	6.58	1.44	1.32
3	B	1602	EQK	C30-N13	6.57	1.44	1.32
3	C	1101	EQK	C30-N13	6.57	1.44	1.32
3	D	1101	EQK	C30-N13	6.53	1.44	1.32
3	B	1602	EQK	C24-N08	6.53	1.48	1.34
3	C	1106	EQK	C21-C24	6.52	1.51	1.38
3	A	1802	EQK	C15-N08	6.52	1.48	1.34
3	A	1805	EQK	C24-N08	6.51	1.48	1.34
3	D	1103	EQK	C24-N08	6.50	1.48	1.34
3	D	1103	EQK	C15-N08	6.44	1.48	1.34
3	A	1802	EQK	C29-N12	6.42	1.44	1.32
3	C	1106	EQK	C30-N13	6.35	1.44	1.32
3	C	1106	EQK	C15-N08	6.30	1.47	1.34
3	C	1106	EQK	C29-N12	6.29	1.44	1.32
3	C	1106	EQK	C24-N08	6.22	1.47	1.34
3	B	1603	EQK	C28-C29	5.85	1.49	1.41
3	B	1603	EQK	C28-C30	5.84	1.49	1.41
3	A	1801	EQK	C28-C29	5.77	1.49	1.41
3	D	1101	EQK	C17-C16	5.76	1.49	1.39
3	B	1603	EQK	C17-C16	5.74	1.49	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1101	EQK	C28-C30	5.66	1.48	1.41
3	C	1101	EQK	C17-C16	5.62	1.49	1.39
3	A	1805	EQK	C28-C29	5.59	1.48	1.41
3	A	1805	EQK	C28-C30	5.57	1.48	1.41
3	C	1101	EQK	C28-C29	5.56	1.48	1.41
3	C	1105	EQK	C28-C30	5.55	1.48	1.41
3	C	1101	EQK	C16-C20	5.54	1.53	1.48
3	A	1801	EQK	C28-C30	5.53	1.48	1.41
3	A	1802	EQK	C17-C16	5.50	1.49	1.39
3	D	1101	EQK	C28-C30	5.48	1.48	1.41
3	A	1805	EQK	C16-C20	5.48	1.53	1.48
3	A	1801	EQK	C17-C16	5.44	1.49	1.39
3	A	1802	EQK	C28-C29	5.37	1.48	1.41
3	B	1602	EQK	C28-C30	5.35	1.48	1.41
3	D	1103	EQK	C28-C30	5.32	1.48	1.41
3	C	1105	EQK	C17-C16	5.29	1.48	1.39
3	A	1805	EQK	C17-C16	5.26	1.48	1.39
3	B	1602	EQK	C28-C29	5.22	1.48	1.41
3	D	1101	EQK	C28-C29	5.22	1.48	1.41
3	B	1603	EQK	C25-N10	5.19	1.45	1.36
3	D	1101	EQK	C16-C20	5.17	1.53	1.48
3	D	1103	EQK	C28-C29	5.17	1.48	1.41
3	B	1603	EQK	C16-C20	5.11	1.53	1.48
3	A	1802	EQK	C28-C30	5.08	1.48	1.41
3	C	1105	EQK	C28-C29	5.05	1.48	1.41
3	A	1805	EQK	C25-N10	5.04	1.45	1.36
3	C	1106	EQK	C17-C16	5.04	1.48	1.39
3	C	1101	EQK	C25-N10	5.03	1.45	1.36
3	D	1103	EQK	C17-C16	4.89	1.48	1.39
3	B	1603	EQK	C21-C16	4.84	1.49	1.39
3	C	1101	EQK	C21-C16	4.83	1.49	1.39
3	C	1105	EQK	C21-C16	4.82	1.49	1.39
3	A	1801	EQK	C21-C16	4.80	1.49	1.39
3	B	1602	EQK	C17-C16	4.78	1.48	1.39
3	C	1106	EQK	C28-C29	4.75	1.47	1.41
3	A	1805	EQK	C21-C16	4.71	1.49	1.39
3	D	1101	EQK	C21-C16	4.71	1.49	1.39
3	A	1801	EQK	C25-N10	4.69	1.44	1.36
3	D	1101	EQK	C25-N10	4.67	1.44	1.36
3	D	1103	EQK	C25-N10	4.61	1.44	1.36
3	B	1602	EQK	C25-N10	4.58	1.44	1.36
3	A	1802	EQK	C21-C16	4.57	1.49	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1802	EQK	C16-C20	4.54	1.52	1.48
3	D	1103	EQK	C21-C16	4.52	1.49	1.39
3	C	1106	EQK	C21-C16	4.51	1.48	1.39
3	B	1602	EQK	C21-C16	4.48	1.48	1.39
3	C	1106	EQK	C28-C30	4.48	1.47	1.41
3	A	1802	EQK	C25-N10	4.43	1.44	1.36
3	A	1801	EQK	C16-C20	4.36	1.52	1.48
3	C	1105	EQK	C16-C20	4.30	1.52	1.48
3	C	1105	EQK	C25-N10	4.19	1.44	1.36
3	B	1603	EQK	C22-N09	4.18	1.57	1.36
3	C	1106	EQK	C16-C20	4.07	1.52	1.48
3	A	1805	EQK	C22-N09	4.01	1.56	1.36
3	B	1602	EQK	C22-N09	4.00	1.56	1.36
3	D	1103	EQK	C16-C20	4.00	1.52	1.48
3	A	1801	EQK	C22-N09	3.96	1.56	1.36
3	D	1103	EQK	C22-N09	3.96	1.56	1.36
3	C	1101	EQK	C22-N09	3.96	1.56	1.36
3	D	1101	EQK	C22-N09	3.92	1.56	1.36
3	B	1602	EQK	C16-C20	3.90	1.52	1.48
3	C	1105	EQK	C22-N09	3.88	1.55	1.36
3	A	1802	EQK	C22-N09	3.88	1.55	1.36
3	B	1603	EQK	C27-N10	3.67	1.45	1.35
3	C	1106	EQK	C22-N09	3.65	1.54	1.36
3	C	1101	EQK	C27-N10	3.53	1.45	1.35
3	A	1805	EQK	C27-N10	3.48	1.45	1.35
3	A	1801	EQK	C27-N10	3.38	1.44	1.35
3	B	1602	EQK	C27-N10	3.30	1.44	1.35
3	B	1603	EQK	O06-C30	3.29	1.40	1.35
3	D	1103	EQK	C27-N10	3.28	1.44	1.35
3	B	1603	EQK	O05-C29	3.26	1.40	1.35
3	C	1106	EQK	O06-C30	3.25	1.40	1.35
3	A	1801	EQK	O05-C29	3.24	1.40	1.35
3	C	1105	EQK	C27-N10	3.22	1.44	1.35
3	C	1105	EQK	O06-C30	3.17	1.40	1.35
3	C	1106	EQK	O07-C27	-3.15	1.16	1.23
3	D	1101	EQK	C27-N10	3.14	1.44	1.35
3	C	1106	EQK	C25-N10	3.12	1.42	1.36
3	A	1801	EQK	O06-C30	3.09	1.40	1.35
3	A	1802	EQK	C27-N10	3.08	1.43	1.35
3	C	1101	EQK	O05-C29	3.02	1.39	1.35
3	A	1805	EQK	O05-C29	3.02	1.39	1.35
3	C	1101	EQK	O06-C30	3.00	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	1103	EQK	O05-C29	2.99	1.39	1.35
3	A	1802	EQK	O05-C29	2.96	1.39	1.35
3	B	1602	EQK	O06-C30	2.94	1.39	1.35
3	D	1103	EQK	O06-C30	2.94	1.39	1.35
3	A	1805	EQK	O06-C30	2.93	1.39	1.35
3	B	1602	EQK	O05-C29	2.93	1.39	1.35
3	D	1101	EQK	O06-C30	2.92	1.39	1.35
3	D	1101	EQK	O05-C29	2.90	1.39	1.35
3	A	1802	EQK	O06-C30	2.90	1.39	1.35
3	C	1105	EQK	O05-C29	2.88	1.39	1.35
3	C	1106	EQK	O05-C29	2.71	1.39	1.35
3	A	1801	EQK	O07-C27	-2.55	1.18	1.23
3	A	1802	EQK	O07-C27	-2.50	1.18	1.23
3	D	1101	EQK	O07-C27	-2.49	1.18	1.23
3	A	1805	EQK	O07-C27	-2.41	1.18	1.23
3	B	1602	EQK	O07-C27	-2.38	1.18	1.23
3	C	1106	EQK	C27-N10	2.38	1.42	1.35
3	C	1101	EQK	O07-C27	-2.38	1.18	1.23
3	D	1103	EQK	O07-C27	-2.31	1.18	1.23
3	C	1105	EQK	O07-C27	-2.22	1.18	1.23
3	B	1603	EQK	O07-C27	-2.19	1.18	1.23
3	A	1805	EQK	C19-C14	-2.00	1.51	1.54

All (118) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1101	EQK	N13-C31-N12	-5.90	119.37	128.60
3	A	1805	EQK	N13-C31-N12	-5.79	119.54	128.60
3	C	1101	EQK	N13-C31-N12	-5.78	119.56	128.60
3	A	1802	EQK	N13-C31-N12	-5.76	119.59	128.60
3	B	1603	EQK	N13-C31-N12	-5.72	119.65	128.60
3	A	1801	EQK	N13-C31-N12	-5.70	119.69	128.60
3	C	1105	EQK	N13-C31-N12	-5.51	119.97	128.60
3	C	1106	EQK	N13-C31-N12	-5.45	120.07	128.60
3	D	1103	EQK	N13-C31-N12	-5.32	120.28	128.60
3	B	1602	EQK	N13-C31-N12	-5.31	120.29	128.60
3	B	1603	EQK	C26-C22-N09	5.14	125.83	119.69
3	C	1105	EQK	C32-O05-C29	-4.88	112.37	117.21
3	A	1801	EQK	C26-C22-N09	4.55	125.12	119.69
3	D	1103	EQK	C26-C22-N09	4.45	125.00	119.69
3	B	1602	EQK	C26-C22-N09	4.44	124.99	119.69
3	D	1101	EQK	C32-O05-C29	-4.36	112.89	117.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1105	EQK	C26-C22-N09	4.31	124.84	119.69
3	A	1801	EQK	C21-C24-N08	-4.06	118.92	123.96
3	A	1802	EQK	C33-O06-C30	-4.06	113.19	117.21
3	B	1602	EQK	C33-O06-C30	-4.04	113.21	117.21
3	C	1106	EQK	C21-C24-N08	-4.03	118.96	123.96
3	B	1602	EQK	C32-O05-C29	-3.93	113.31	117.21
3	C	1101	EQK	C33-O06-C30	-3.91	113.34	117.21
3	A	1805	EQK	C32-O05-C29	-3.91	113.34	117.21
3	D	1103	EQK	C33-O06-C30	-3.86	113.39	117.21
3	A	1805	EQK	C33-O06-C30	-3.82	113.42	117.21
3	C	1101	EQK	C32-O05-C29	-3.81	113.43	117.21
3	D	1101	EQK	C33-O06-C30	-3.78	113.47	117.21
3	C	1106	EQK	C32-O05-C29	-3.77	113.47	117.21
3	D	1103	EQK	C32-O05-C29	-3.77	113.48	117.21
3	A	1801	EQK	C33-O06-C30	-3.71	113.54	117.21
3	A	1802	EQK	C21-C24-N08	-3.63	119.45	123.96
3	C	1105	EQK	C14-C15-N08	3.61	121.23	115.22
3	A	1801	EQK	C32-O05-C29	-3.55	113.69	117.21
3	B	1602	EQK	C18-C14-C15	-3.46	105.05	111.79
3	B	1603	EQK	C26-C22-C20	-3.42	126.04	129.29
3	C	1105	EQK	C21-C24-N08	-3.42	119.71	123.96
3	C	1106	EQK	C26-C22-N09	3.42	123.77	119.69
3	D	1101	EQK	C21-C24-N08	-3.41	119.72	123.96
3	B	1603	EQK	C33-O06-C30	-3.39	113.86	117.21
3	B	1603	EQK	C32-O05-C29	-3.38	113.86	117.21
3	A	1802	EQK	C32-O05-C29	-3.36	113.89	117.21
3	B	1602	EQK	C21-C24-N08	-3.34	119.80	123.96
3	B	1602	EQK	C14-C15-N08	3.32	120.75	115.22
3	B	1603	EQK	C21-C24-N08	-3.24	119.94	123.96
3	A	1802	EQK	C26-C22-N09	3.23	123.55	119.69
3	C	1101	EQK	C26-C22-N09	3.23	123.55	119.69
3	C	1101	EQK	C21-C24-N08	-3.21	119.97	123.96
3	D	1103	EQK	C14-C15-N08	3.17	120.50	115.22
3	D	1103	EQK	C21-C24-N08	-3.14	120.05	123.96
3	A	1805	EQK	C26-C22-N09	3.10	123.40	119.69
3	C	1101	EQK	C14-C15-N08	3.10	120.38	115.22
3	D	1103	EQK	C18-C14-C15	-3.05	105.85	111.79
3	A	1801	EQK	C31-N13-C30	3.04	120.97	115.88
3	C	1105	EQK	C33-O06-C30	-3.03	114.20	117.21
3	A	1805	EQK	C14-C15-N08	2.98	120.18	115.22
3	D	1101	EQK	C26-C22-N09	2.94	123.20	119.69
3	C	1105	EQK	C31-N12-C29	2.92	120.77	115.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1801	EQK	C26-C22-C20	-2.87	126.56	129.29
3	B	1603	EQK	C14-C15-N08	2.84	119.94	115.22
3	C	1105	EQK	C26-C22-C20	-2.81	126.62	129.29
3	A	1802	EQK	C31-N13-C30	2.77	120.51	115.88
3	B	1602	EQK	C17-C15-C14	-2.75	117.43	123.31
3	D	1101	EQK	C14-C15-N08	2.74	119.78	115.22
3	D	1101	EQK	C31-N12-C29	2.73	120.45	115.88
3	A	1805	EQK	C21-C24-N08	-2.69	120.62	123.96
3	A	1805	EQK	C31-N12-C29	2.65	120.31	115.88
3	C	1106	EQK	C31-N13-C30	2.64	120.31	115.88
3	C	1101	EQK	C31-N12-C29	2.63	120.29	115.88
3	D	1103	EQK	C31-N12-C29	2.60	120.24	115.88
3	B	1602	EQK	C31-N12-C29	2.59	120.22	115.88
3	A	1801	EQK	C24-N08-C15	2.59	121.03	117.49
3	D	1101	EQK	C31-N13-C30	2.58	120.20	115.88
3	B	1603	EQK	C28-C27-N10	2.58	119.75	114.91
3	D	1103	EQK	C18-C14-C23	2.57	111.37	107.25
3	B	1603	EQK	C31-N12-C29	2.57	120.18	115.88
3	B	1603	EQK	C31-N13-C30	2.54	120.14	115.88
3	C	1106	EQK	O07-C27-C28	2.54	124.77	120.95
3	D	1101	EQK	C17-C15-N08	-2.52	119.21	123.31
3	A	1805	EQK	C31-N13-C30	2.52	120.10	115.88
3	C	1101	EQK	C31-N13-C30	2.52	120.10	115.88
3	A	1805	EQK	C17-C15-N08	-2.50	119.24	123.31
3	B	1603	EQK	C25-N10-C27	-2.47	120.52	126.64
3	D	1103	EQK	C17-C15-C14	-2.47	118.04	123.31
3	A	1801	EQK	C14-C15-N08	2.47	119.32	115.22
3	A	1801	EQK	F03-C26-C22	-2.44	108.50	112.32
3	A	1802	EQK	C31-N12-C29	2.42	119.93	115.88
3	A	1802	EQK	C14-C15-N08	2.41	119.22	115.22
3	B	1602	EQK	C19-C14-C23	2.37	111.05	107.25
3	D	1101	EQK	C24-N08-C15	2.33	120.68	117.49
3	C	1105	EQK	F02-C26-C22	-2.32	108.69	112.32
3	A	1802	EQK	F03-C26-C22	-2.32	108.69	112.32
3	A	1805	EQK	F04-C26-C22	-2.32	108.70	112.32
3	C	1101	EQK	C17-C15-N08	-2.31	119.55	123.31
3	A	1802	EQK	C18-C14-C23	2.30	110.93	107.25
3	D	1101	EQK	C15-C14-C23	2.25	111.83	108.51
3	B	1602	EQK	F04-C26-C22	-2.24	108.82	112.32
3	C	1106	EQK	C31-N12-C29	2.23	119.61	115.88
3	C	1106	EQK	F02-C26-C22	-2.22	108.84	112.32
3	A	1802	EQK	F04-C26-C22	-2.22	108.84	112.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1101	EQK	F02-C26-C22	-2.22	108.85	112.32
3	A	1801	EQK	C31-N12-C29	2.20	119.57	115.88
3	C	1106	EQK	C24-N08-C15	2.20	120.50	117.49
3	C	1105	EQK	C24-N08-C15	2.19	120.49	117.49
3	D	1103	EQK	F03-C26-C22	-2.16	108.94	112.32
3	B	1602	EQK	C18-C14-C23	2.14	110.68	107.25
3	B	1602	EQK	C26-C22-C20	-2.12	127.27	129.29
3	C	1105	EQK	C17-C15-N08	-2.10	119.90	123.31
3	C	1105	EQK	C17-C15-C14	-2.08	118.87	123.31
3	B	1603	EQK	C24-N08-C15	2.08	120.33	117.49
3	D	1101	EQK	F04-C26-C22	-2.08	109.07	112.32
3	B	1603	EQK	C17-C15-N08	-2.07	119.95	123.31
3	A	1801	EQK	C19-C14-C23	2.06	110.54	107.25
3	B	1602	EQK	C31-N13-C30	2.05	119.32	115.88
3	D	1103	EQK	C31-N13-C30	2.04	119.30	115.88
3	A	1801	EQK	F04-C26-C22	-2.04	109.14	112.32
3	A	1802	EQK	C24-N08-C15	2.02	120.26	117.49
3	C	1101	EQK	C24-N08-C15	2.01	120.24	117.49

There are no chirality outliers.

All (118) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	1104	6OU	C38-C39-C40-C41
3	B	1602	EQK	C23-C14-C15-N08
3	B	1602	EQK	C17-C16-C20-S01
3	B	1602	EQK	C21-C16-C20-S01
3	B	1602	EQK	O07-C27-C28-C30
3	B	1603	EQK	N09-C22-C26-F04
3	B	1603	EQK	C28-C29-O05-C32
3	B	1603	EQK	C28-C30-O06-C33
3	B	1603	EQK	N13-C30-O06-C33
3	C	1101	EQK	C23-C14-C15-C17
3	C	1101	EQK	C23-C14-C15-N08
3	C	1105	EQK	C23-C14-C15-N08
3	C	1105	EQK	C28-C29-O05-C32
3	C	1105	EQK	C28-C30-O06-C33
3	C	1106	EQK	N12-C29-O05-C32
3	C	1106	EQK	C28-C29-O05-C32
3	C	1106	EQK	C28-C30-O06-C33
3	C	1106	EQK	N13-C30-O06-C33
3	A	1801	EQK	N10-C27-C28-C29

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Mol	Chain	Res	Type	Atoms
3	A	1801	EQK	O07-C27-C28-C29
3	A	1801	EQK	N12-C29-O05-C32
3	A	1801	EQK	C28-C29-O05-C32
3	A	1805	EQK	C23-C14-C15-C17
3	A	1805	EQK	C23-C14-C15-N08
3	D	1101	EQK	C23-C14-C15-C17
3	D	1101	EQK	C23-C14-C15-N08
3	D	1101	EQK	N10-C27-C28-C30
3	D	1101	EQK	O07-C27-C28-C30
3	D	1103	EQK	C23-C14-C15-N08
3	D	1103	EQK	C17-C16-C20-S01
3	D	1103	EQK	C21-C16-C20-S01
3	D	1103	EQK	N10-C27-C28-C30
3	D	1103	EQK	O07-C27-C28-C30
3	B	1603	EQK	N12-C29-O05-C32
3	C	1105	EQK	N12-C29-O05-C32
3	C	1105	EQK	N13-C30-O06-C33
2	C	1102	6OU	C45-C46-C47-C48
2	B	1601	6OU	C43-C44-C45-C46
2	C	1103	6OU	C45-C46-C47-C48
2	B	1601	6OU	C44-C45-C46-C47
2	D	1102	6OU	C44-C45-C46-C47
2	A	1803	6OU	C41-C42-C43-C44
3	B	1603	EQK	N09-C22-C26-F03
3	A	1802	EQK	O07-C27-C28-C29
3	B	1602	EQK	N10-C27-C28-C30
3	A	1802	EQK	N10-C27-C28-C29
2	B	1604	6OU	C43-C44-C45-C46
2	C	1103	6OU	C40-C41-C42-C43
2	B	1601	6OU	C42-C43-C44-C45
2	C	1103	6OU	C46-C47-C48-C49
2	C	1104	6OU	C46-C47-C48-C49
3	B	1602	EQK	C19-C14-C15-N08
3	A	1801	EQK	C19-C14-C15-N08
3	D	1103	EQK	C19-C14-C15-N08
3	D	1101	EQK	N09-C22-C26-F02
2	A	1803	6OU	C44-C45-C46-C47
2	C	1104	6OU	C45-C46-C47-C48
2	B	1604	6OU	C42-C43-C44-C45
2	C	1104	6OU	C40-C41-C42-C43
2	B	1601	6OU	C45-C46-C47-C48
2	B	1605	6OU	C37-C38-C39-C40

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Mol	Chain	Res	Type	Atoms
2	A	1804	6OU	C42-C43-C44-C45
3	B	1603	EQK	N09-C22-C26-F02
3	D	1101	EQK	N09-C22-C26-F03
3	D	1101	EQK	N09-C22-C26-F04
3	C	1105	EQK	C18-C14-C15-C17
3	A	1801	EQK	C18-C14-C15-C17
3	A	1805	EQK	C18-C14-C15-C17
3	B	1603	EQK	C17-C16-C20-S01
3	B	1603	EQK	C21-C16-C20-S01
3	C	1105	EQK	C17-C16-C20-S01
3	A	1801	EQK	C17-C16-C20-S01
3	A	1801	EQK	C21-C16-C20-S01
3	A	1802	EQK	C17-C16-C20-S01
3	A	1802	EQK	C21-C16-C20-S01
2	A	1803	6OU	C40-C41-C42-C43
3	C	1101	EQK	N12-C29-O05-C32
3	A	1805	EQK	N12-C29-O05-C32
2	C	1102	6OU	C40-C41-C42-C43
2	C	1102	6OU	C41-C42-C43-C44
3	B	1602	EQK	C18-C14-C15-N08
3	D	1103	EQK	C18-C14-C15-N08
2	A	1804	6OU	C43-C44-C45-C46
3	B	1602	EQK	N09-C22-C26-F02
3	B	1602	EQK	N09-C22-C26-F03
3	D	1103	EQK	N09-C22-C26-F02
3	D	1103	EQK	N09-C22-C26-F04
2	C	1103	6OU	C38-C39-C40-C41
2	D	1104	6OU	C43-C44-C45-C46
3	C	1101	EQK	C28-C29-O05-C32
3	A	1805	EQK	C28-C29-O05-C32
2	B	1601	6OU	C41-C42-C43-C44
3	B	1602	EQK	C19-C14-C15-C17
3	C	1101	EQK	C18-C14-C15-C17
3	D	1101	EQK	C19-C14-C15-C17
3	D	1103	EQK	C19-C14-C15-C17
2	A	1804	6OU	C40-C41-C42-C43
3	B	1602	EQK	N09-C22-C26-F04
3	D	1103	EQK	N09-C22-C26-F03
3	B	1602	EQK	C17-C16-C20-C22
2	B	1601	6OU	C38-C39-C40-C41
2	B	1604	6OU	C38-C39-C40-C41
2	B	1604	6OU	C40-C41-C42-C43

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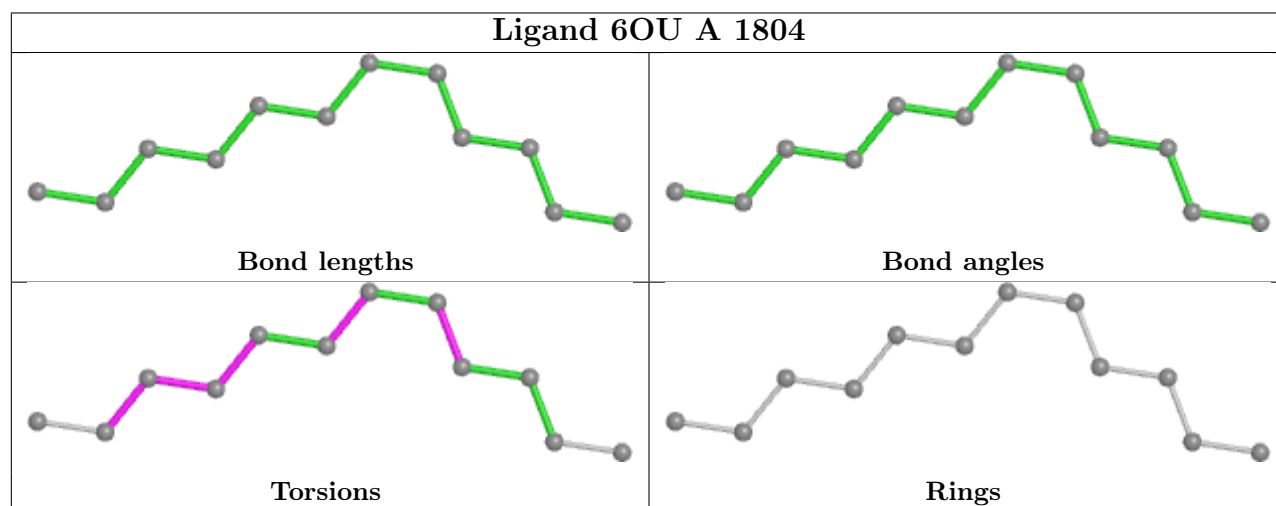
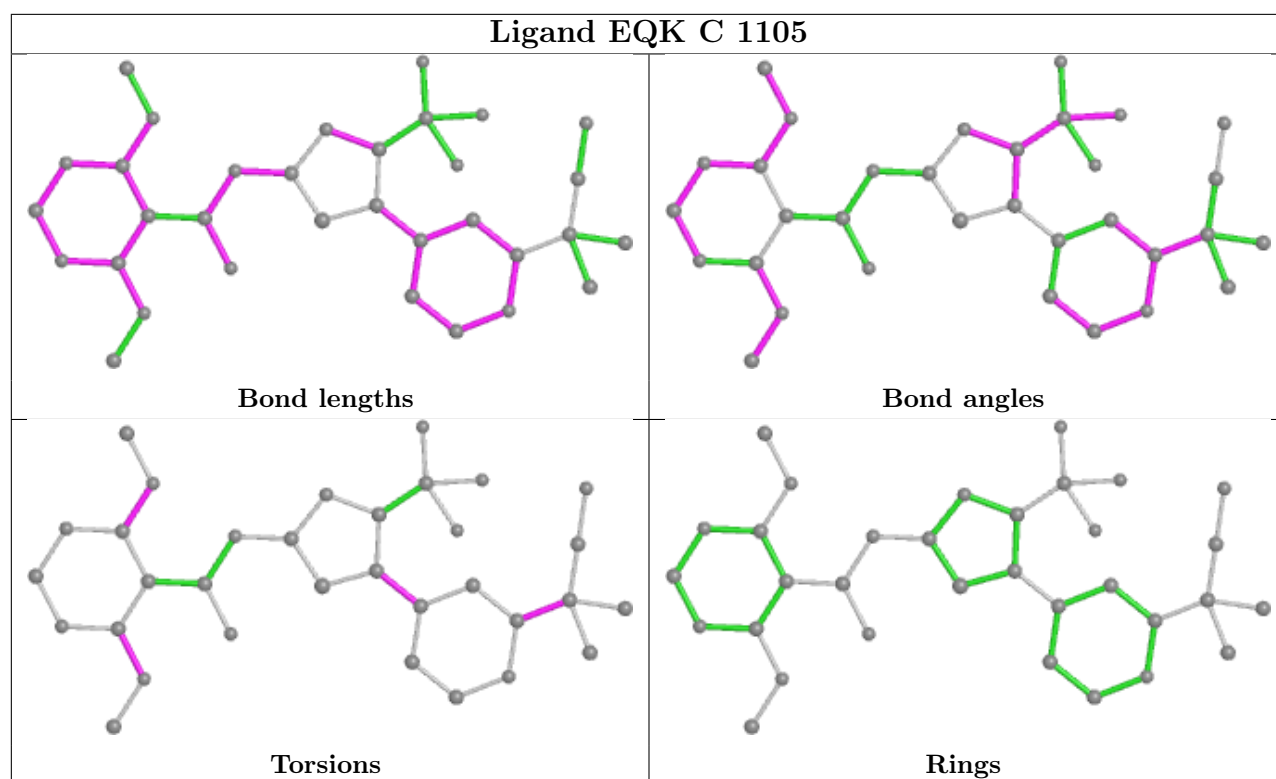
Mol	Chain	Res	Type	Atoms
2	B	1605	6OU	C38-C39-C40-C41
2	A	1804	6OU	C38-C39-C40-C41
2	A	1804	6OU	C44-C45-C46-C47
2	A	1803	6OU	C38-C39-C40-C41
2	D	1102	6OU	C45-C46-C47-C48
2	D	1104	6OU	C42-C43-C44-C45
2	C	1102	6OU	C38-C39-C40-C41
3	D	1103	EQK	C17-C16-C20-C22
3	B	1602	EQK	C21-C16-C20-C22
3	C	1105	EQK	C18-C14-C15-N08
3	C	1105	EQK	C19-C14-C15-N08
3	D	1103	EQK	C21-C16-C20-C22
3	C	1101	EQK	C19-C14-C15-C17
3	A	1805	EQK	C19-C14-C15-C17
3	D	1101	EQK	C18-C14-C15-C17

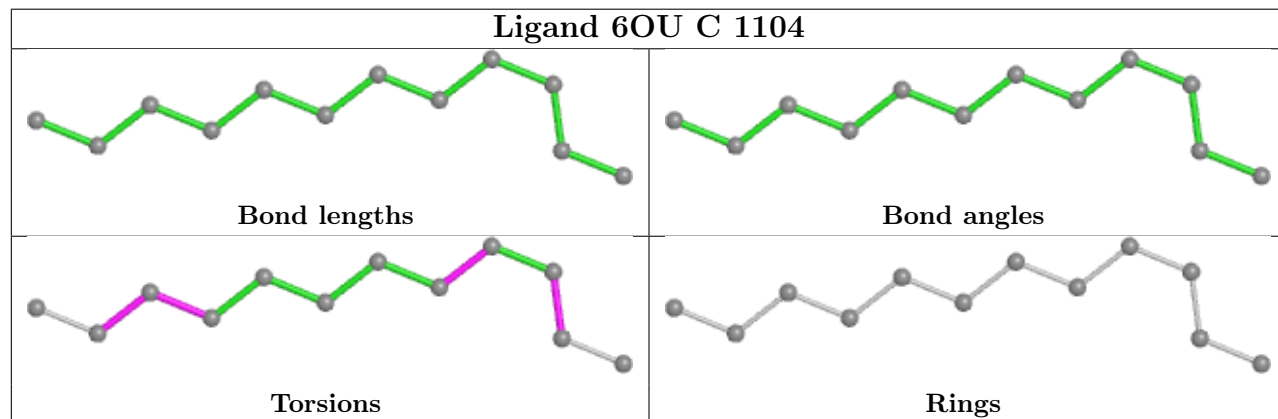
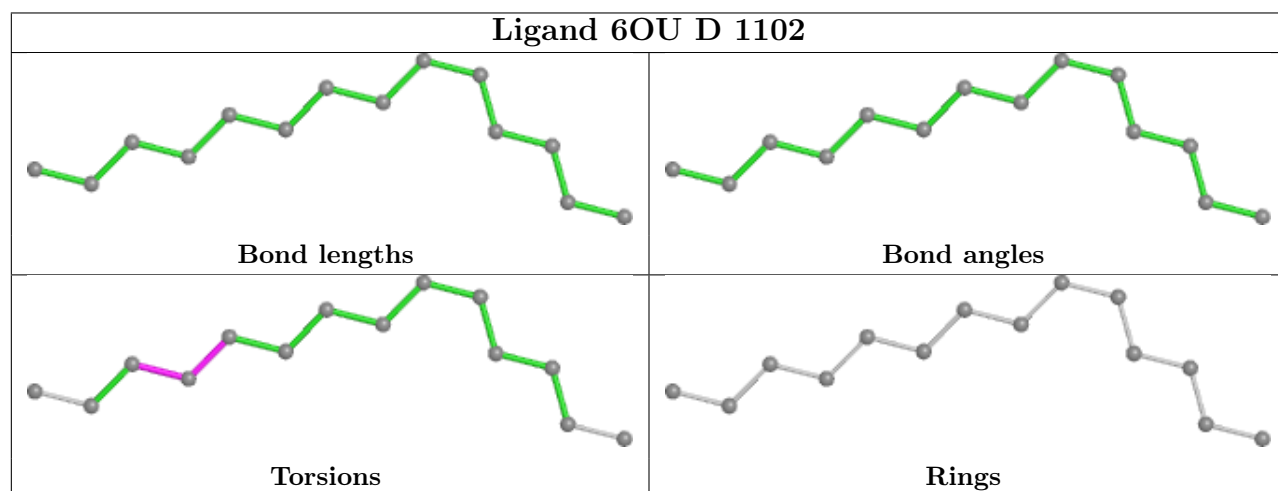
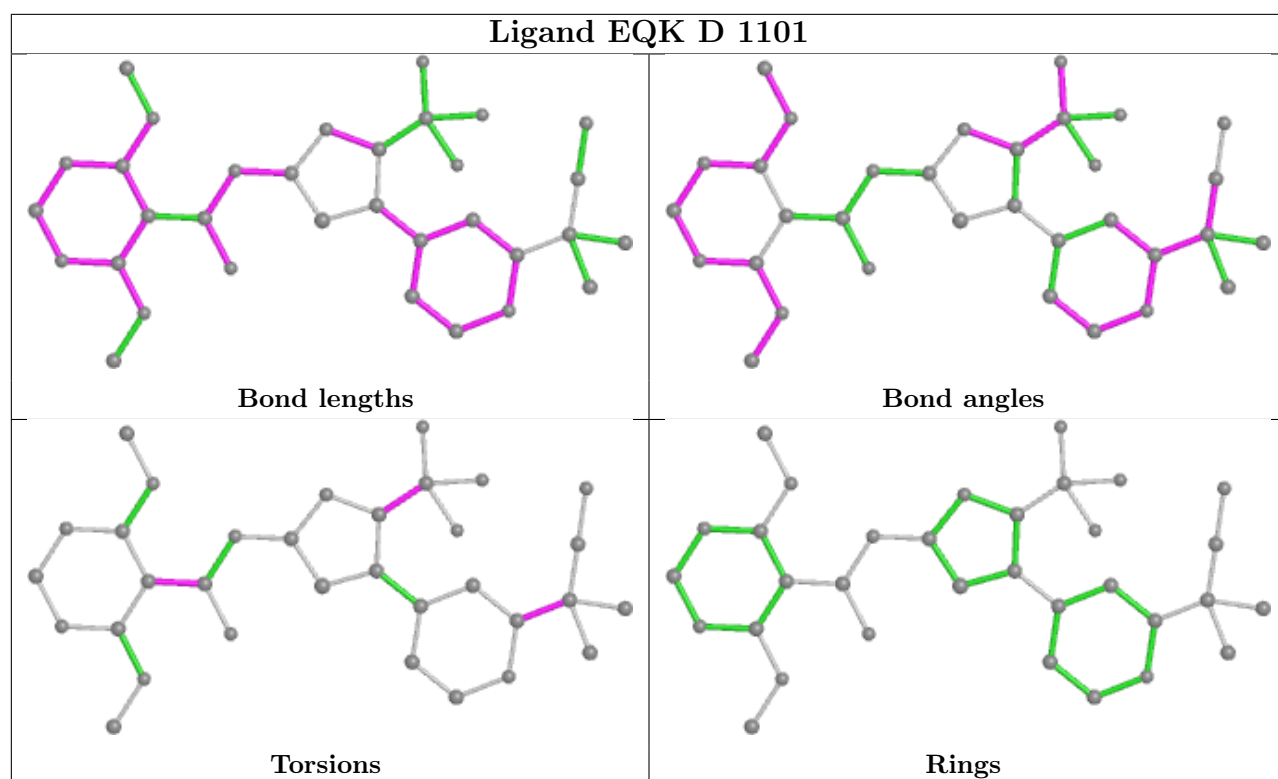
There are no ring outliers.

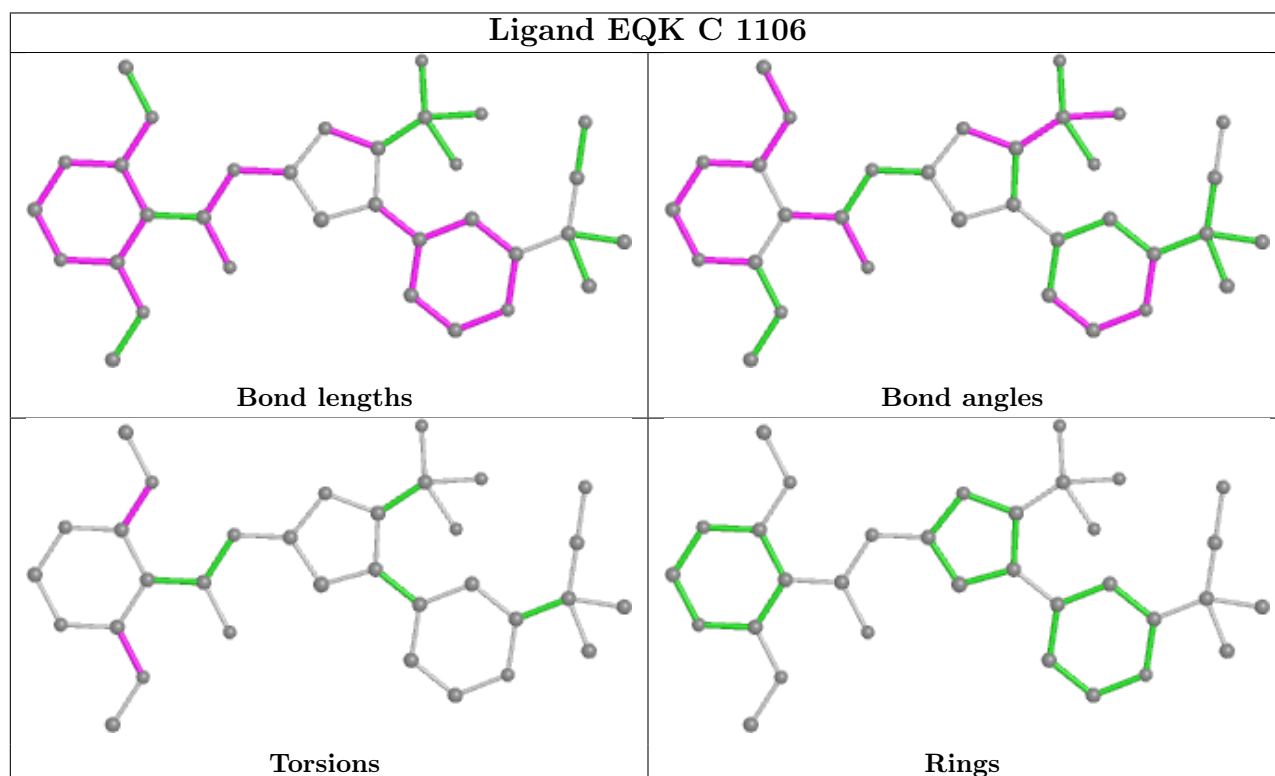
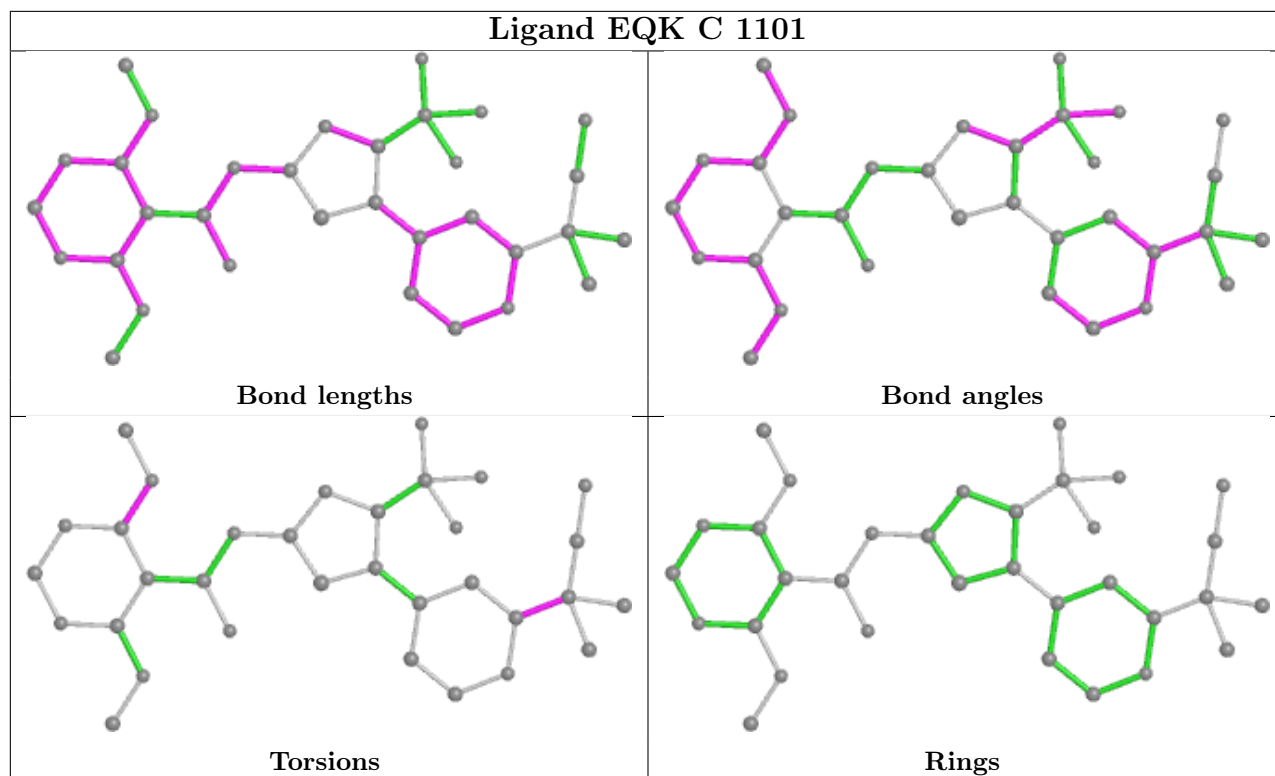
6 monomers are involved in 26 short contacts:

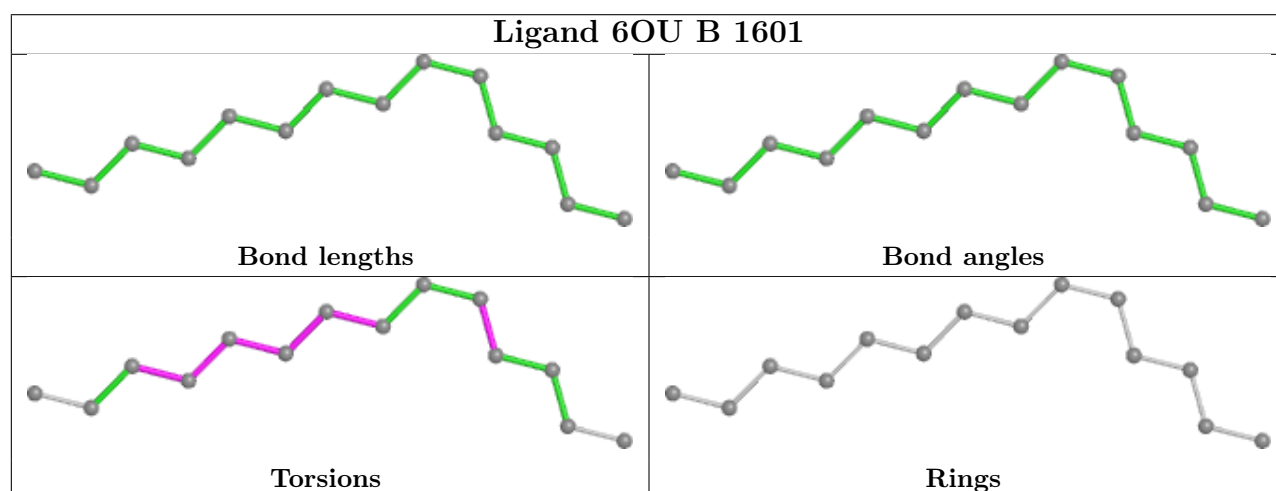
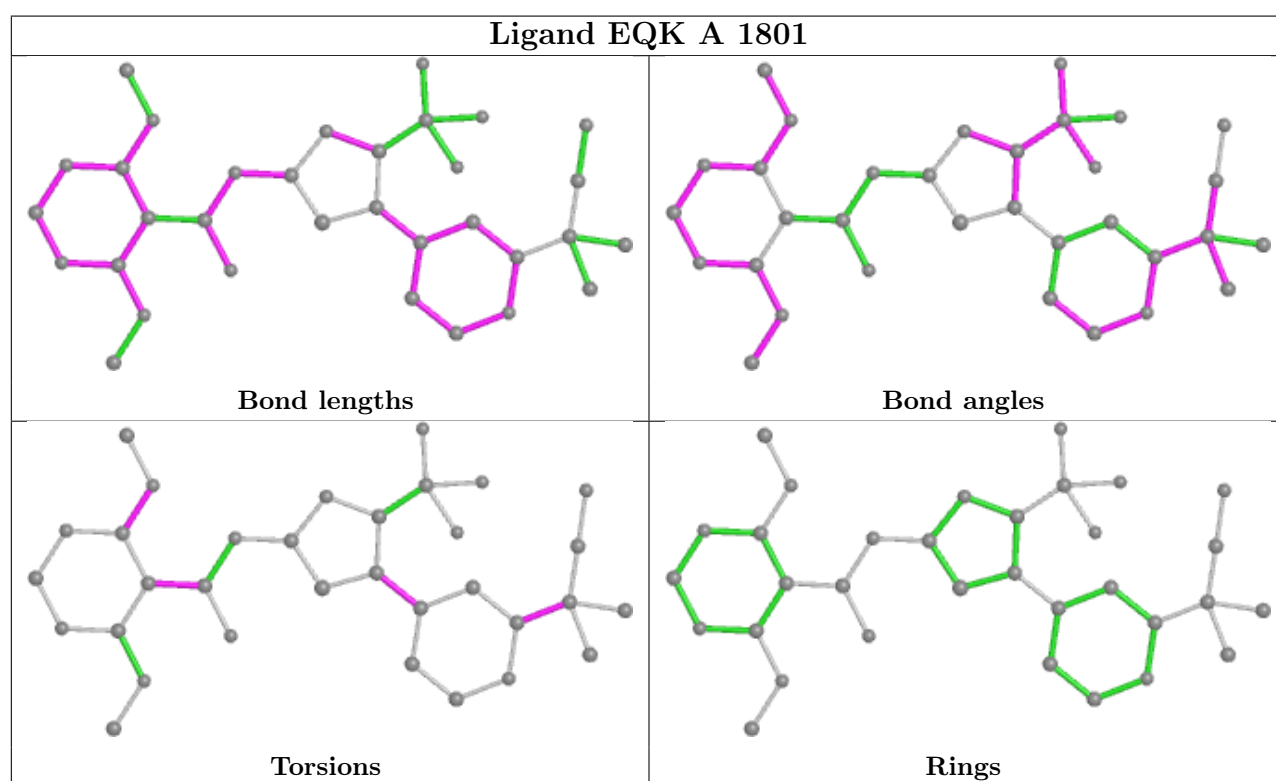
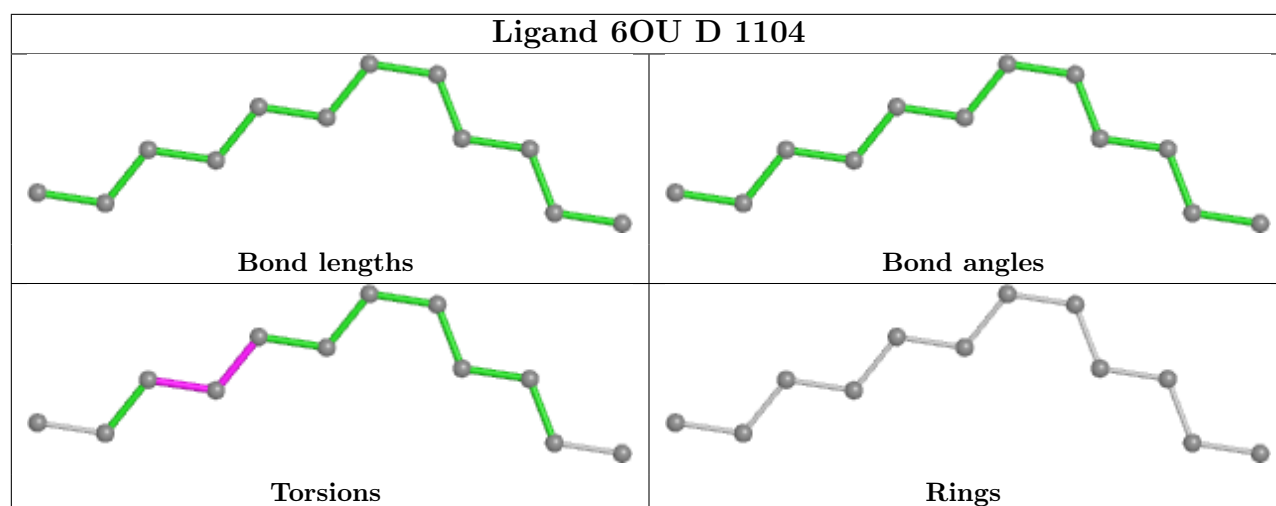
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1105	EQK	4	0
3	C	1106	EQK	7	0
3	A	1801	EQK	3	0
3	B	1603	EQK	11	0
3	D	1103	EQK	2	0
3	B	1602	EQK	2	0

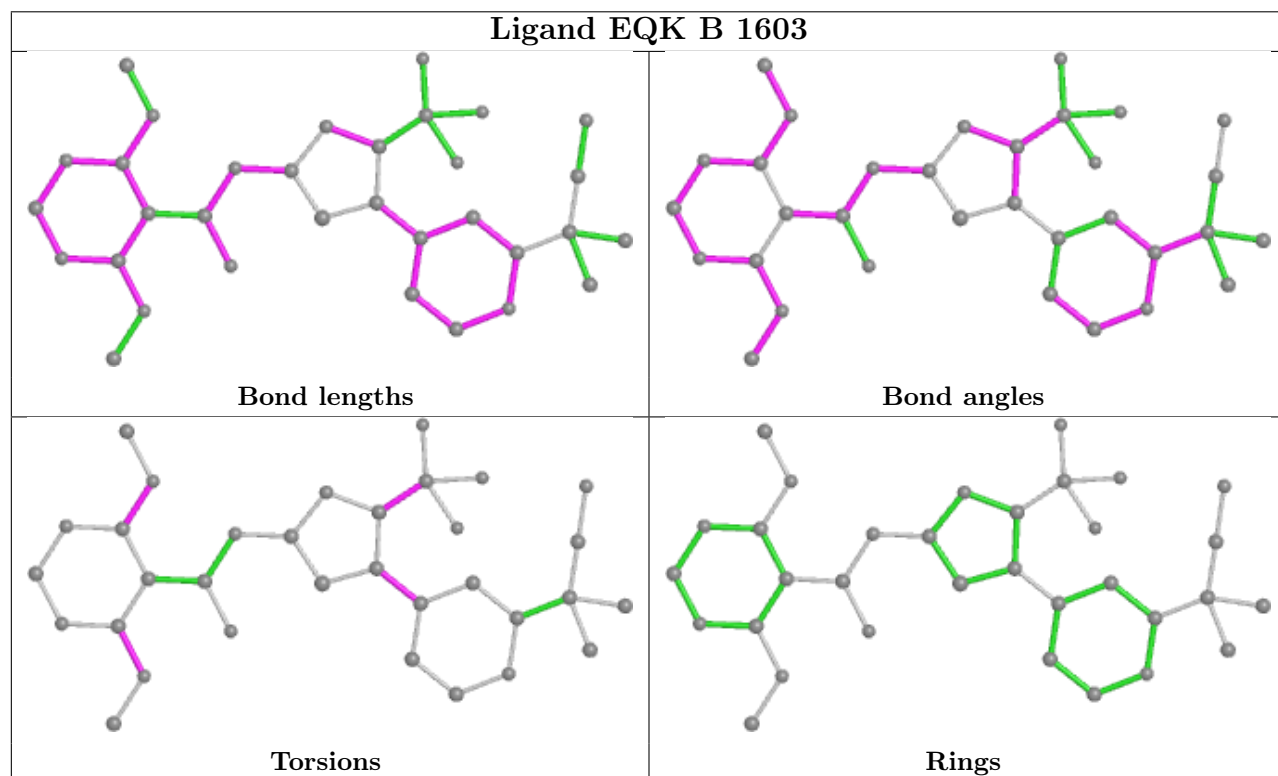
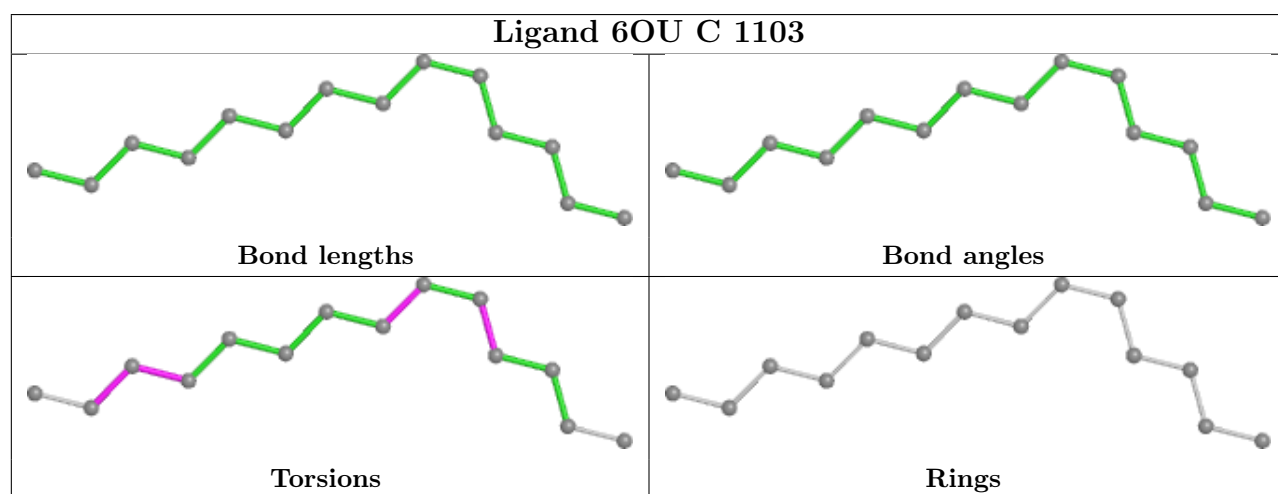
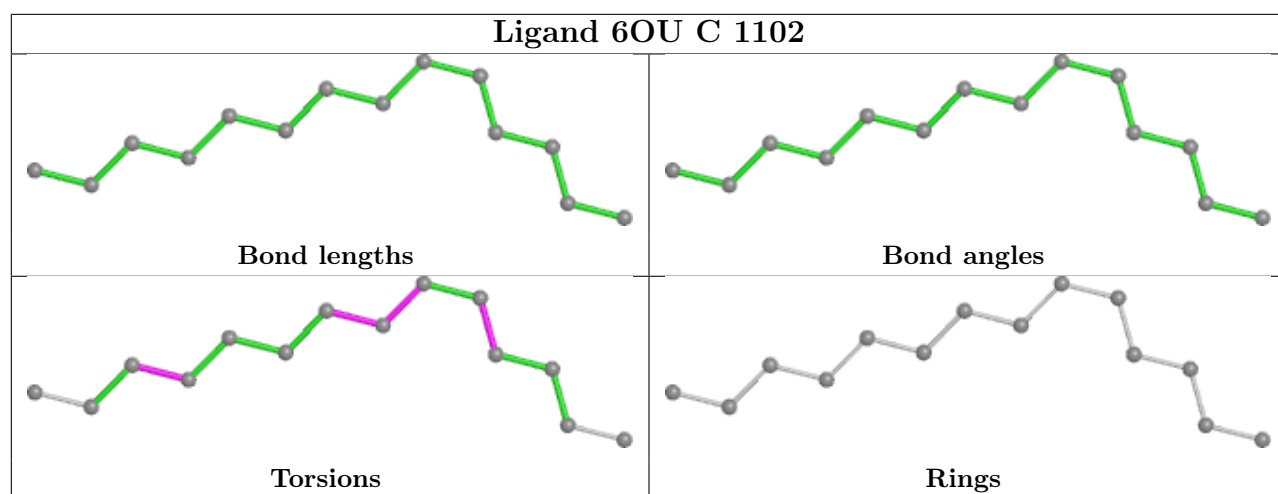
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

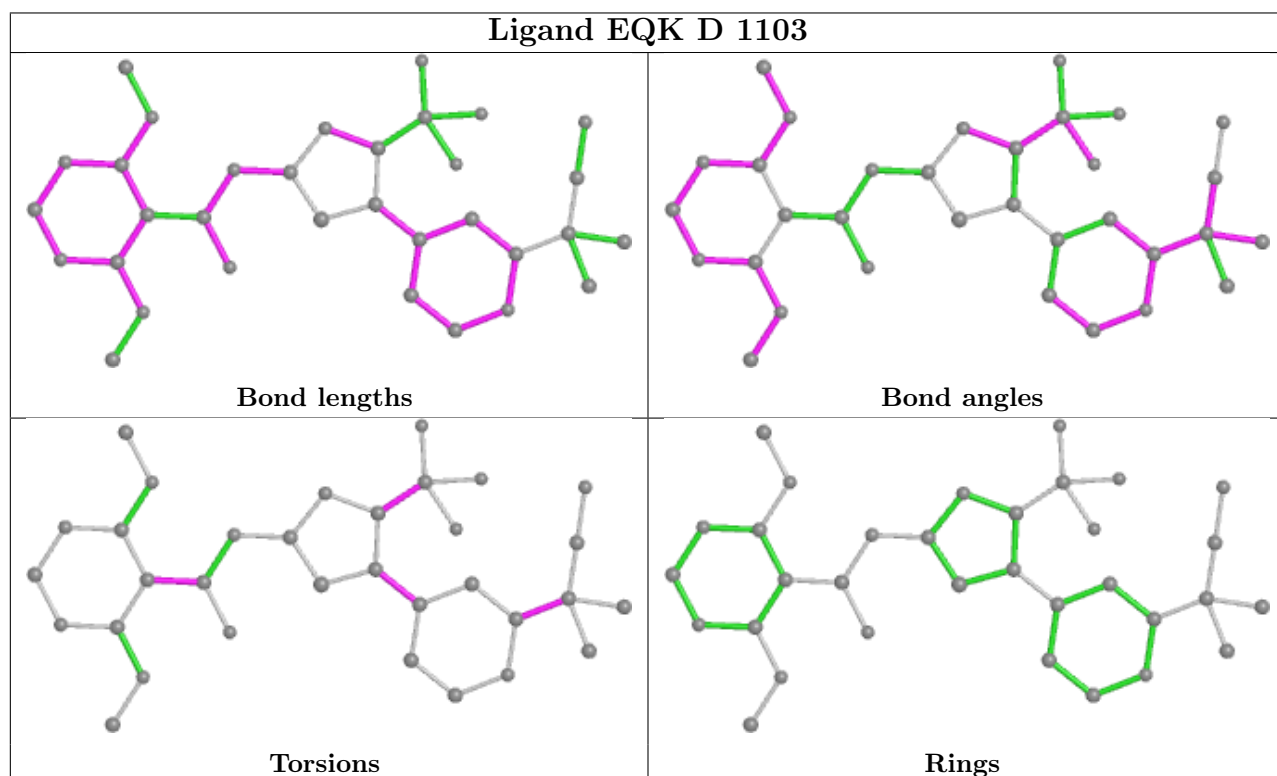
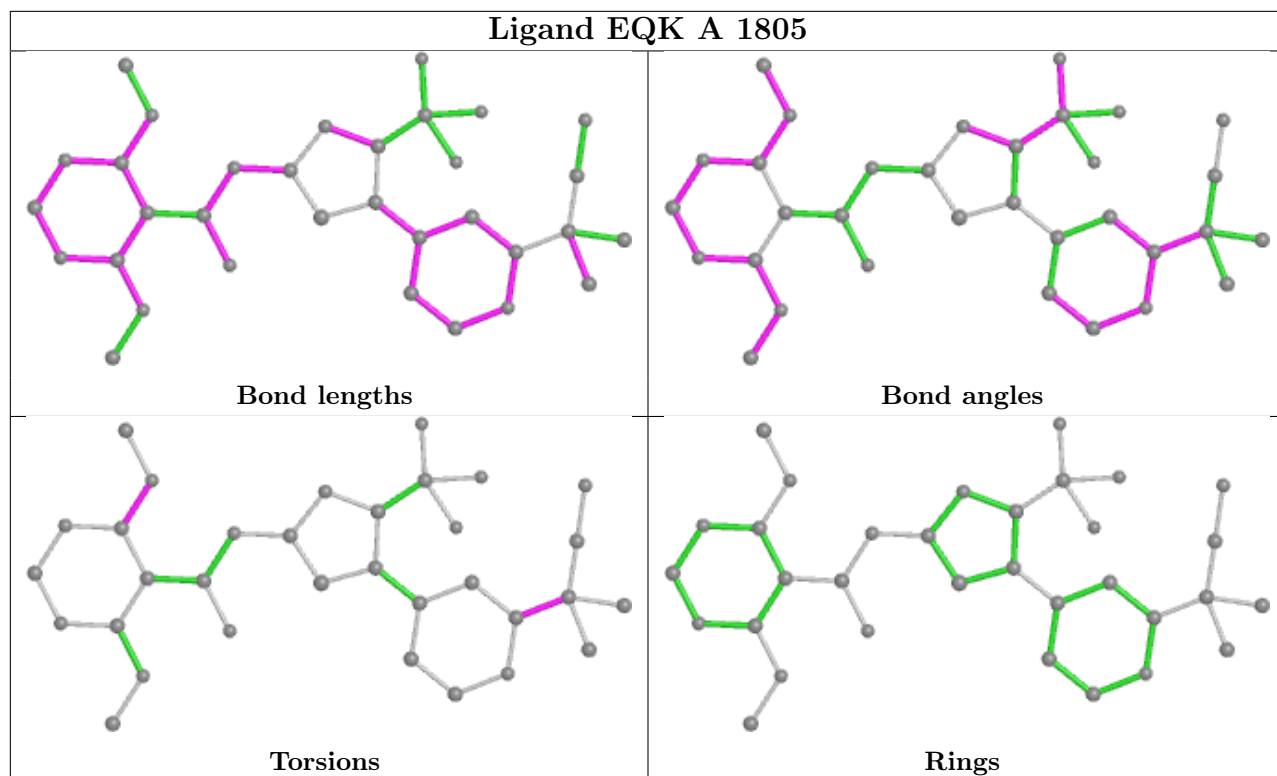


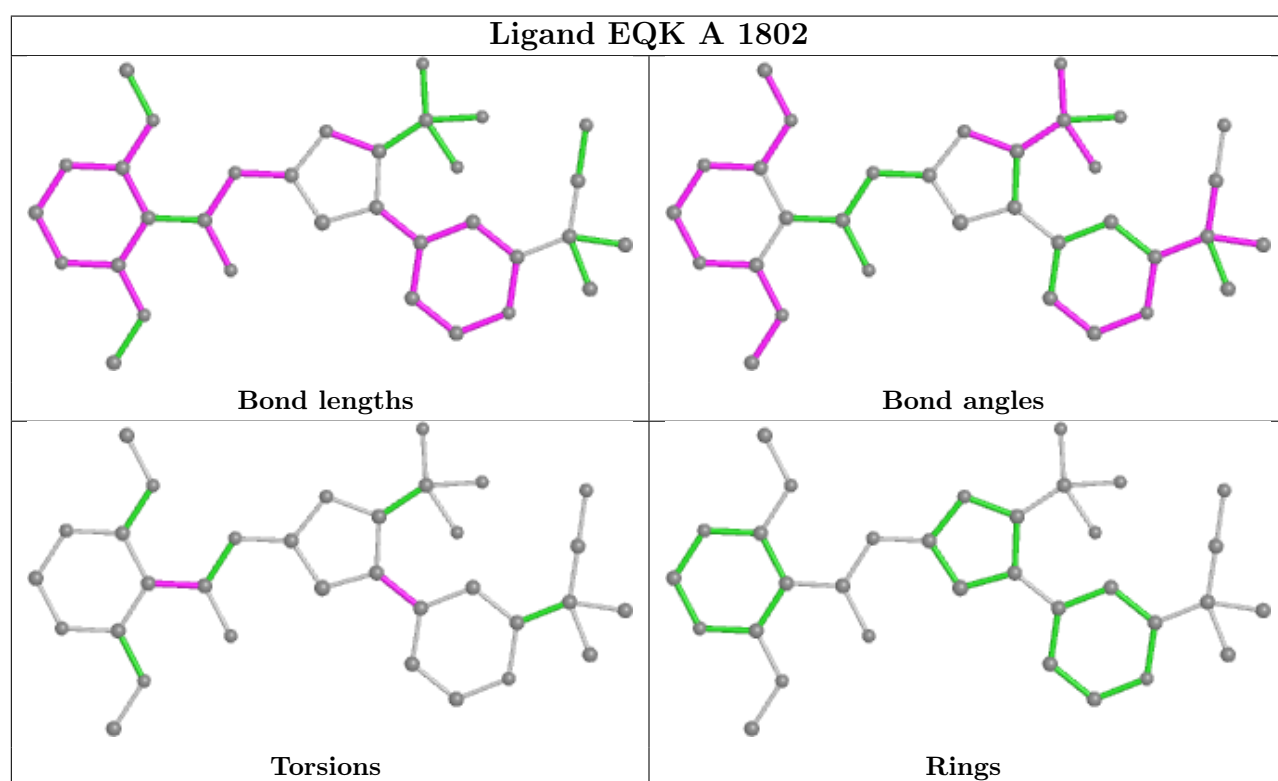
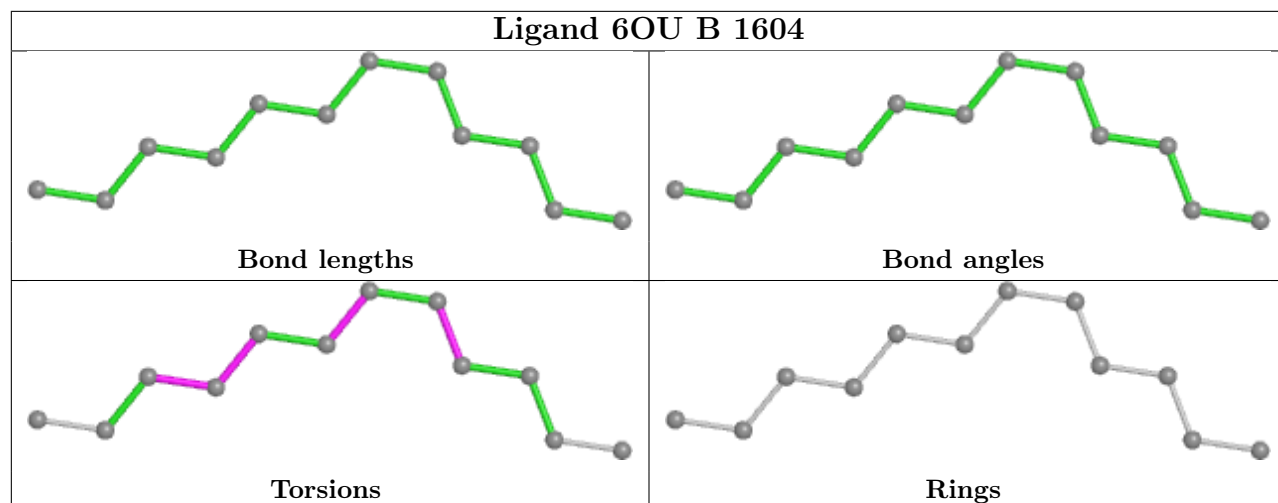


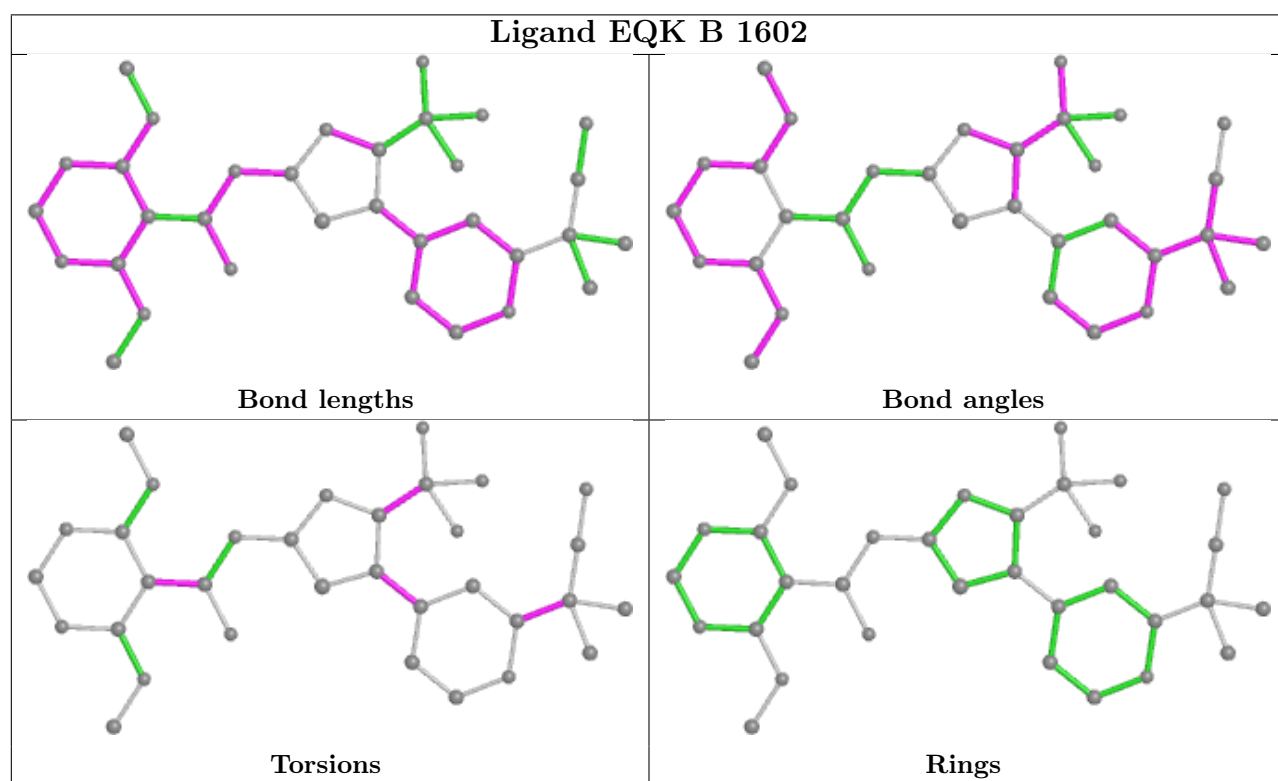
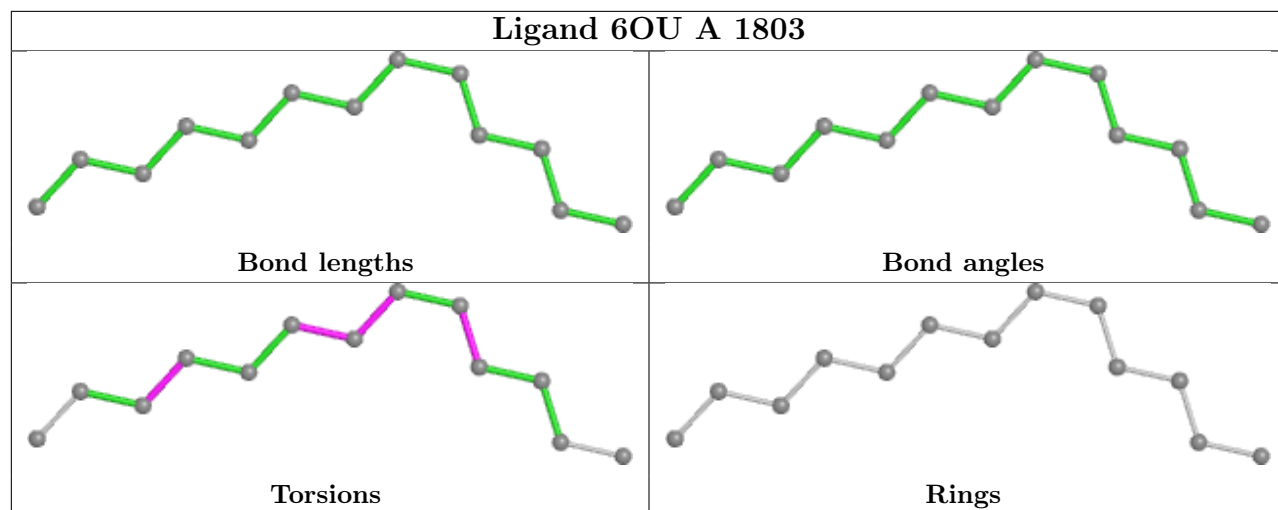


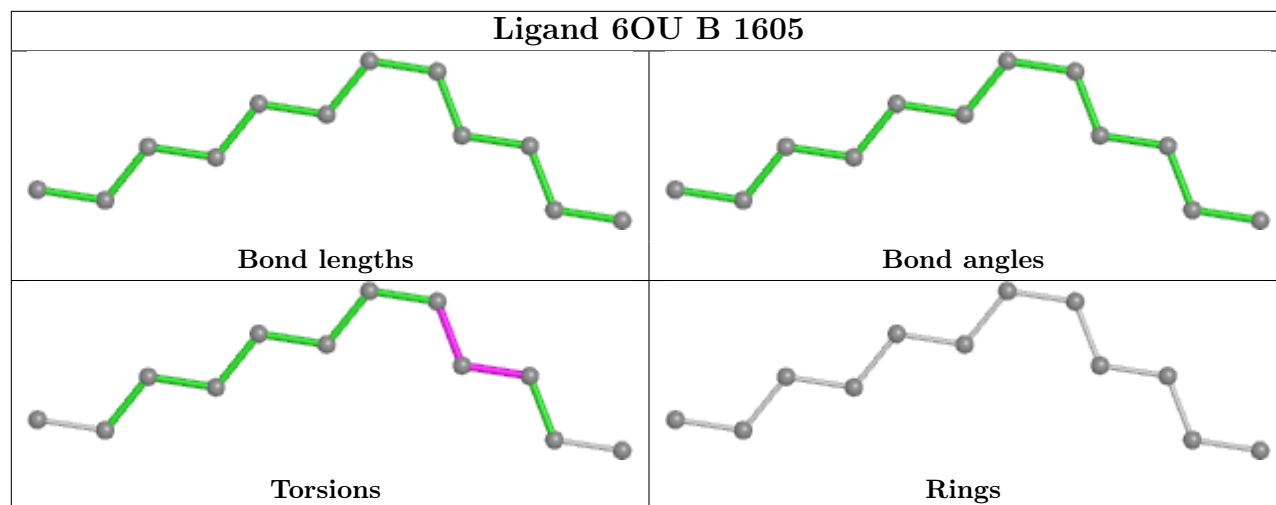












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

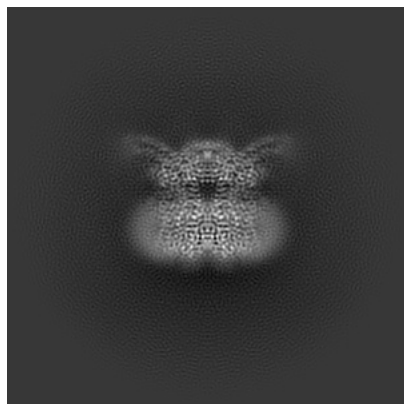
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33216. These allow visual inspection of the internal detail of the map and identification of artifacts.

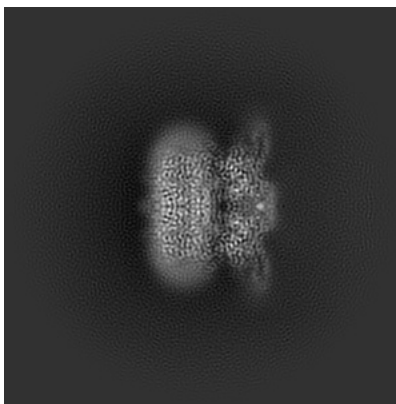
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

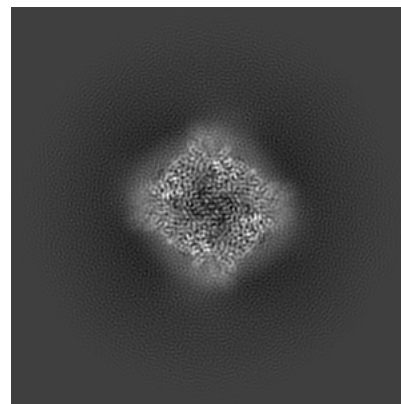
6.1.1 Primary map



X

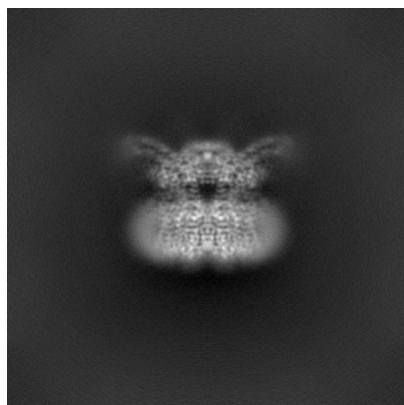


Y

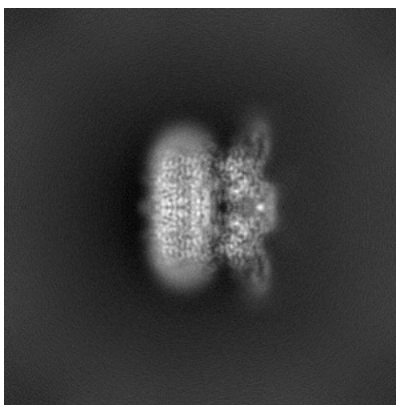


Z

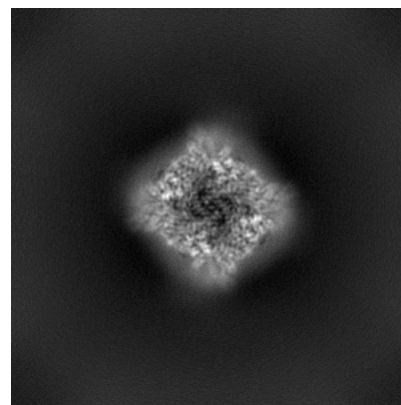
6.1.2 Raw map



X



Y

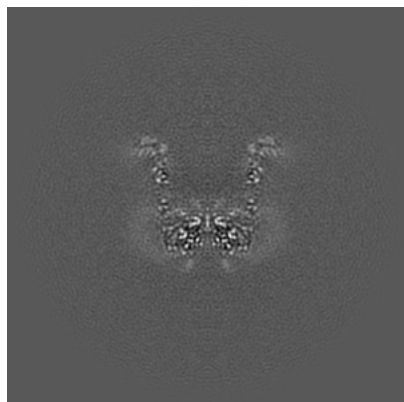


Z

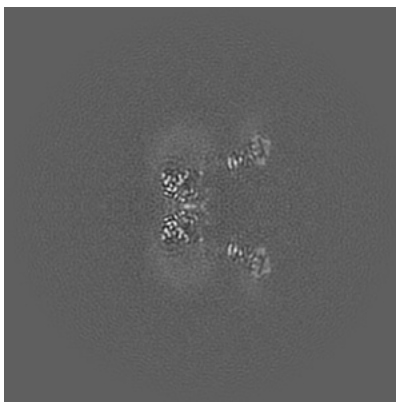
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

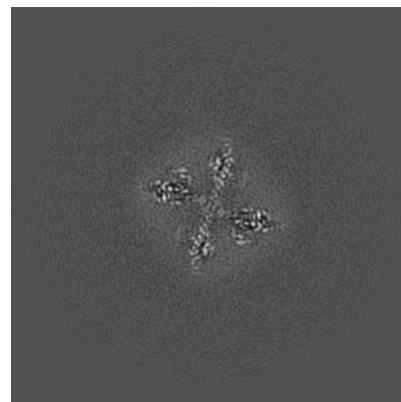
6.2.1 Primary map



X Index: 160

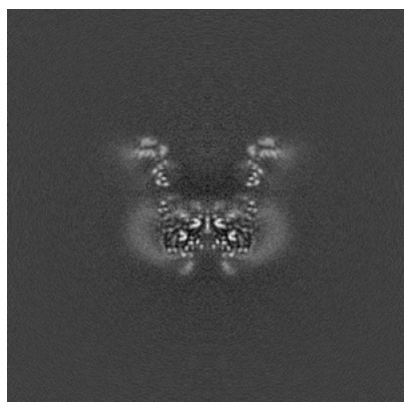


Y Index: 160

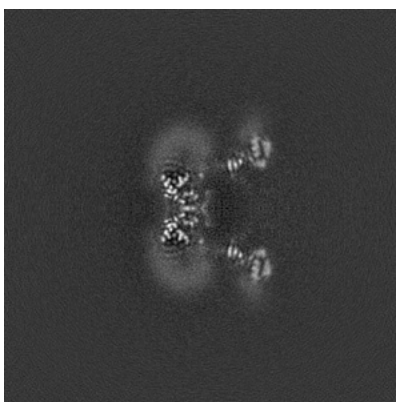


Z Index: 160

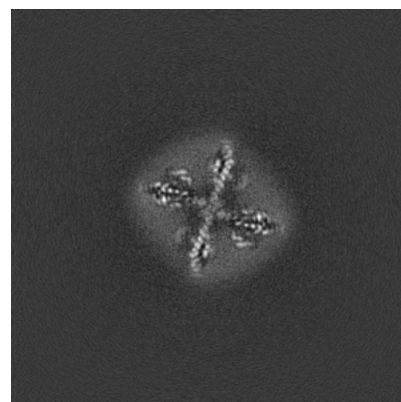
6.2.2 Raw map



X Index: 160



Y Index: 160

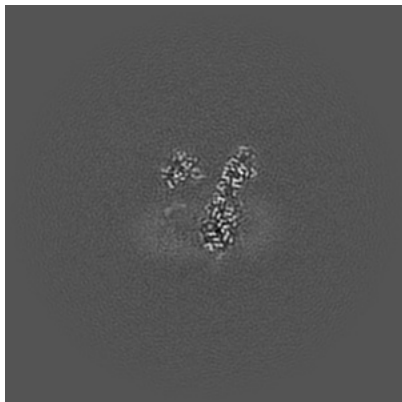


Z Index: 160

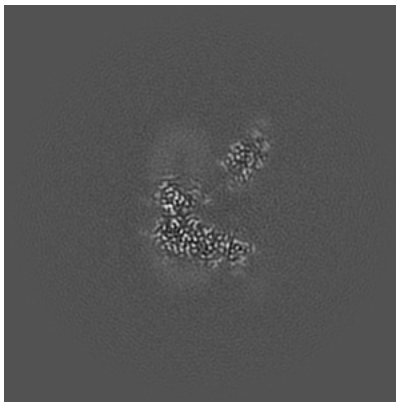
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

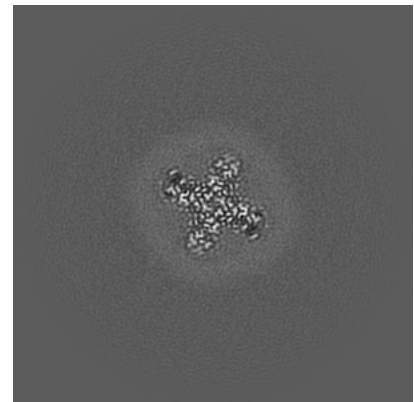
6.3.1 Primary map



X Index: 134

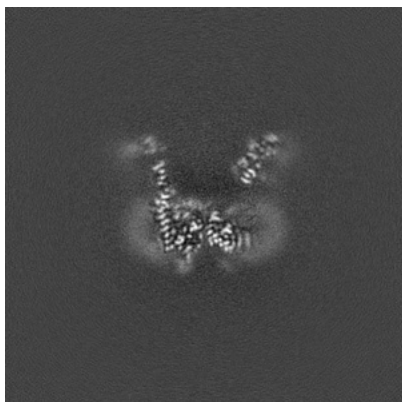


Y Index: 172

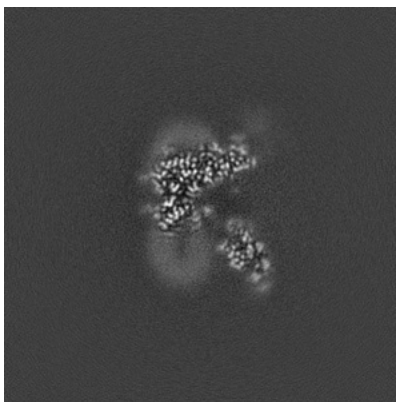


Z Index: 136

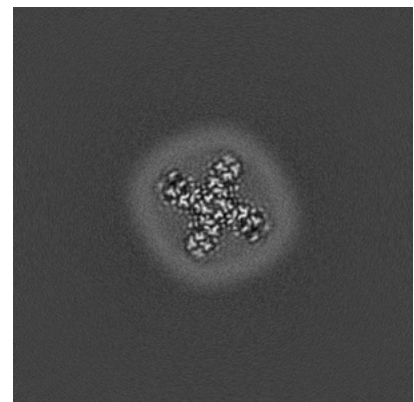
6.3.2 Raw map



X Index: 157



Y Index: 148

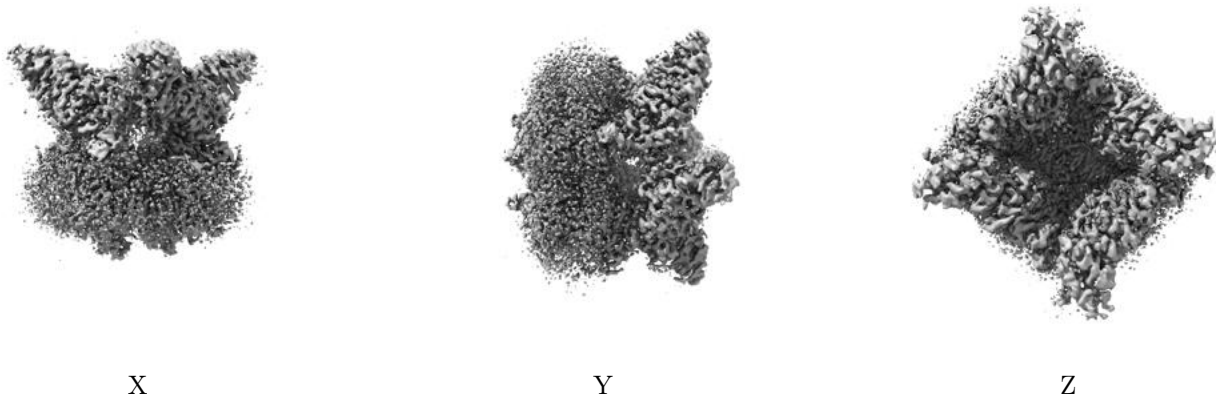


Z Index: 136

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

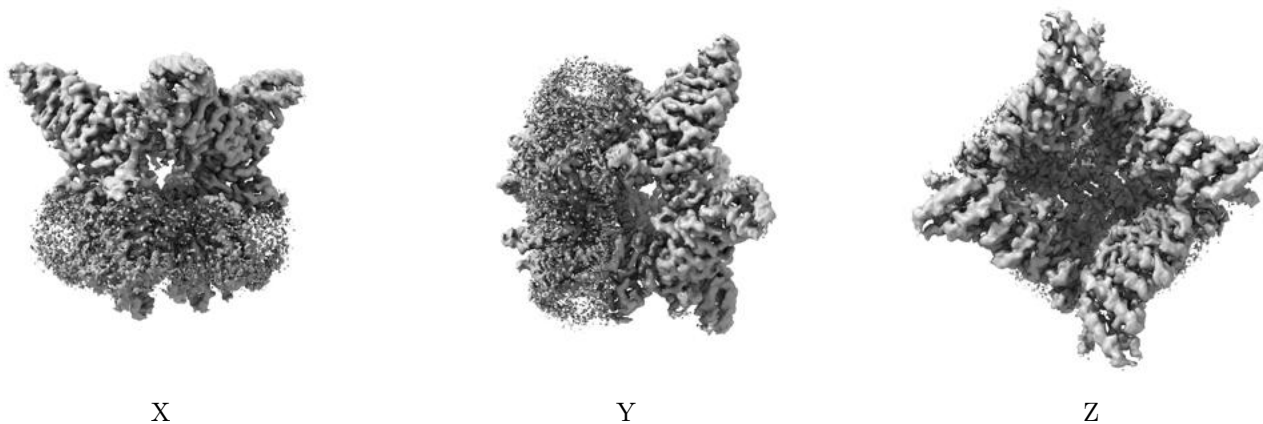
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.43. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map



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

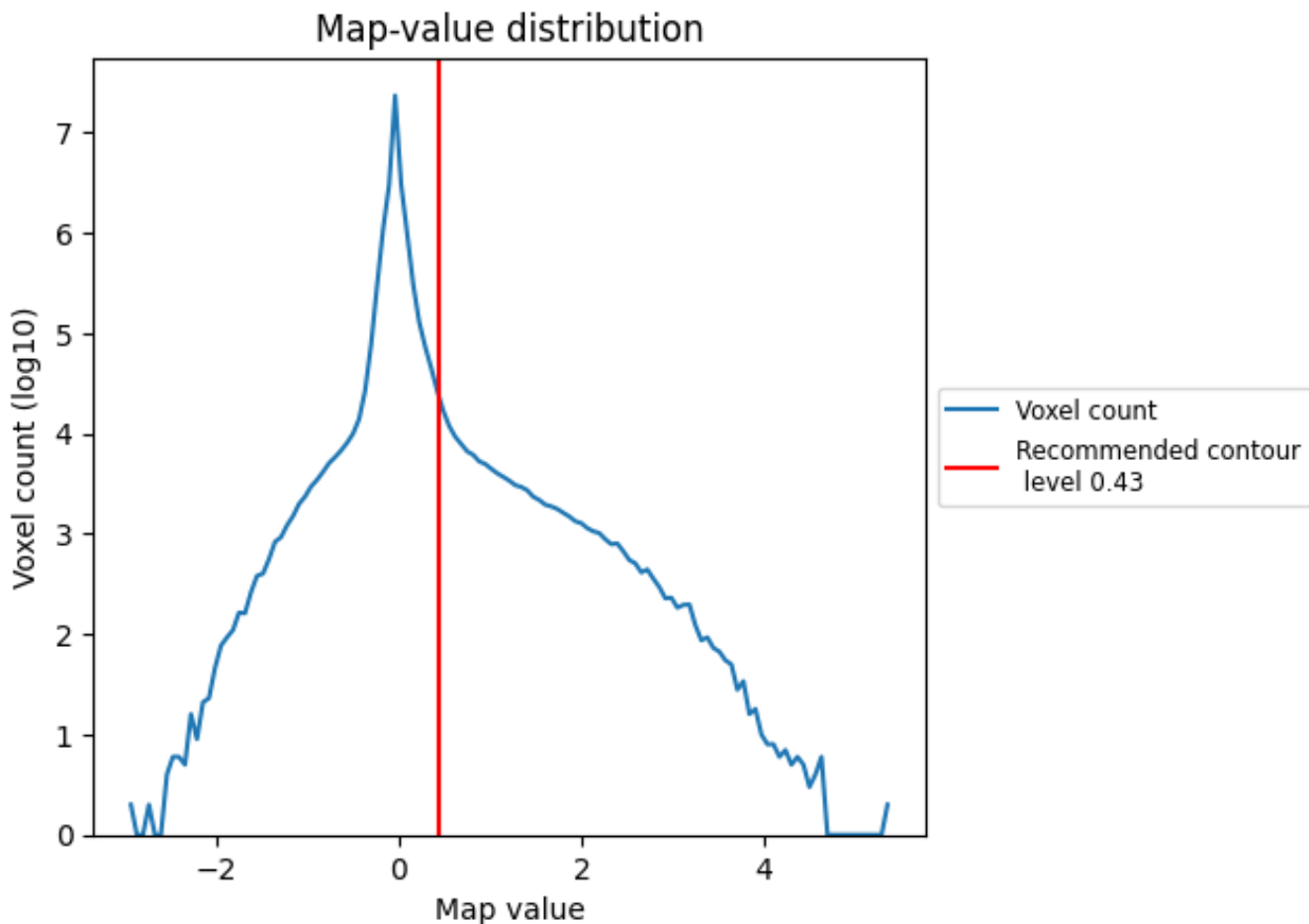
6.5 Mask visualisation [i](#)

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

7 Map analysis [i](#)

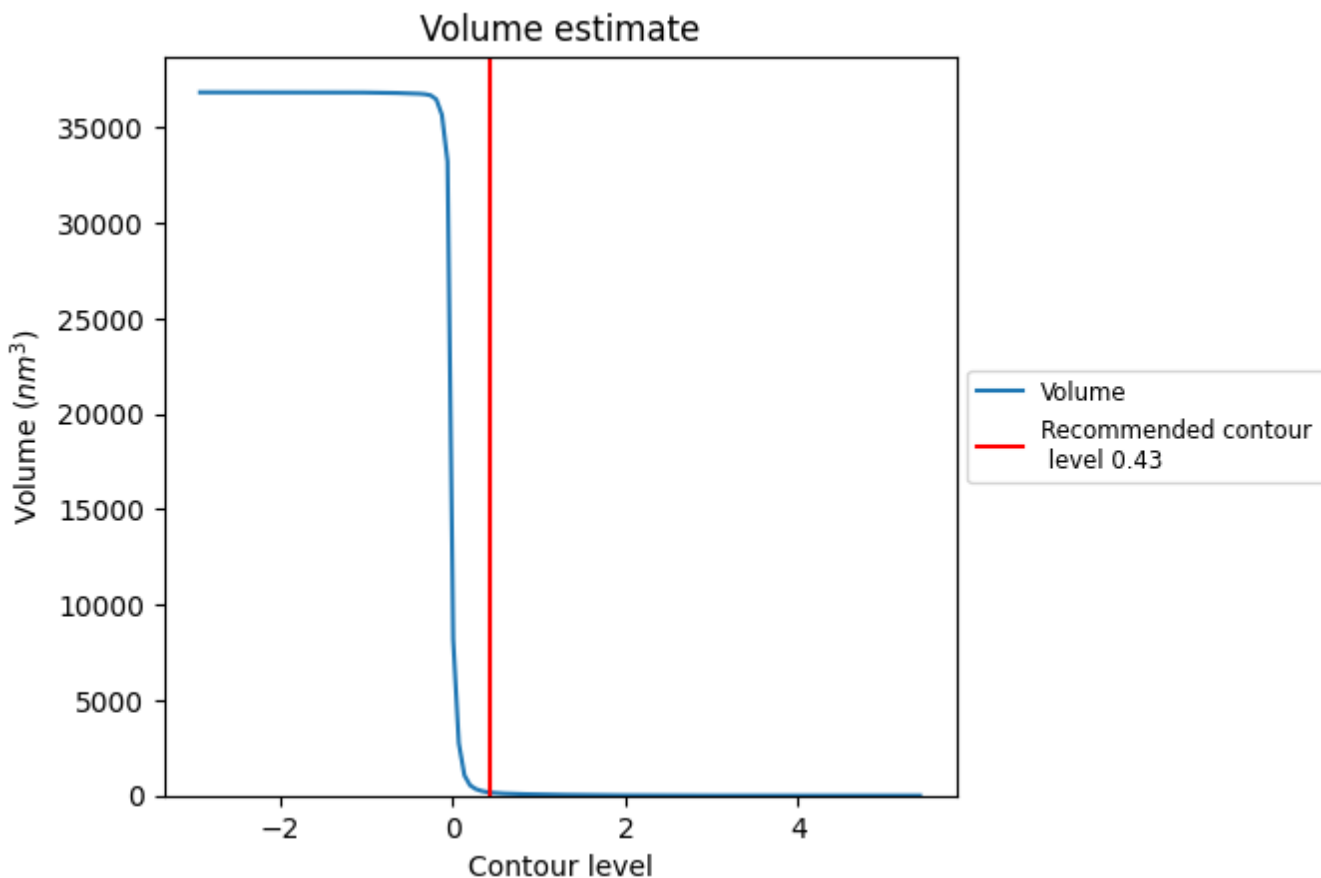
This section contains the results of statistical analysis of the map.

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.

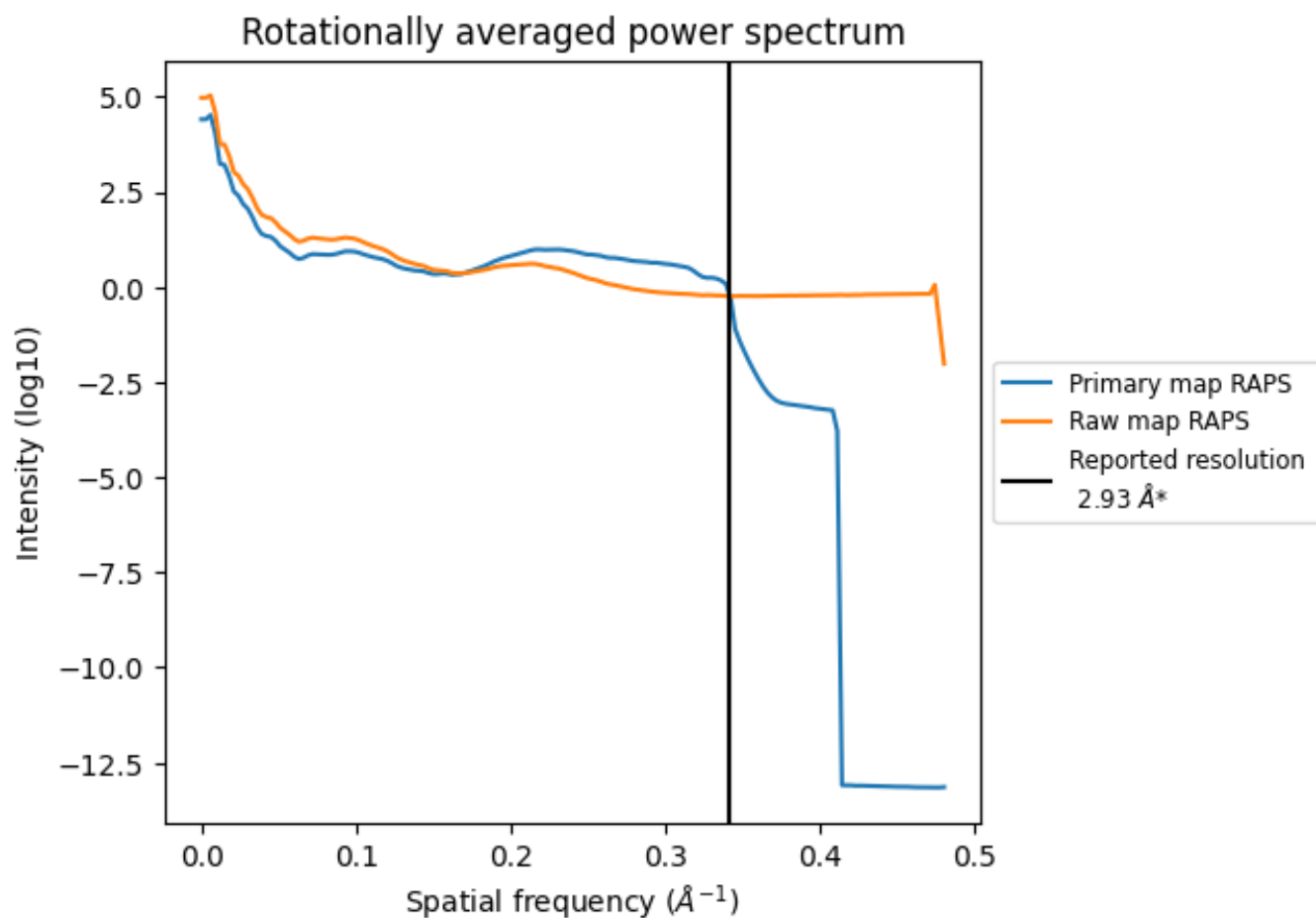
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 162 nm^3 ; this corresponds to an approximate mass of 147 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](#)

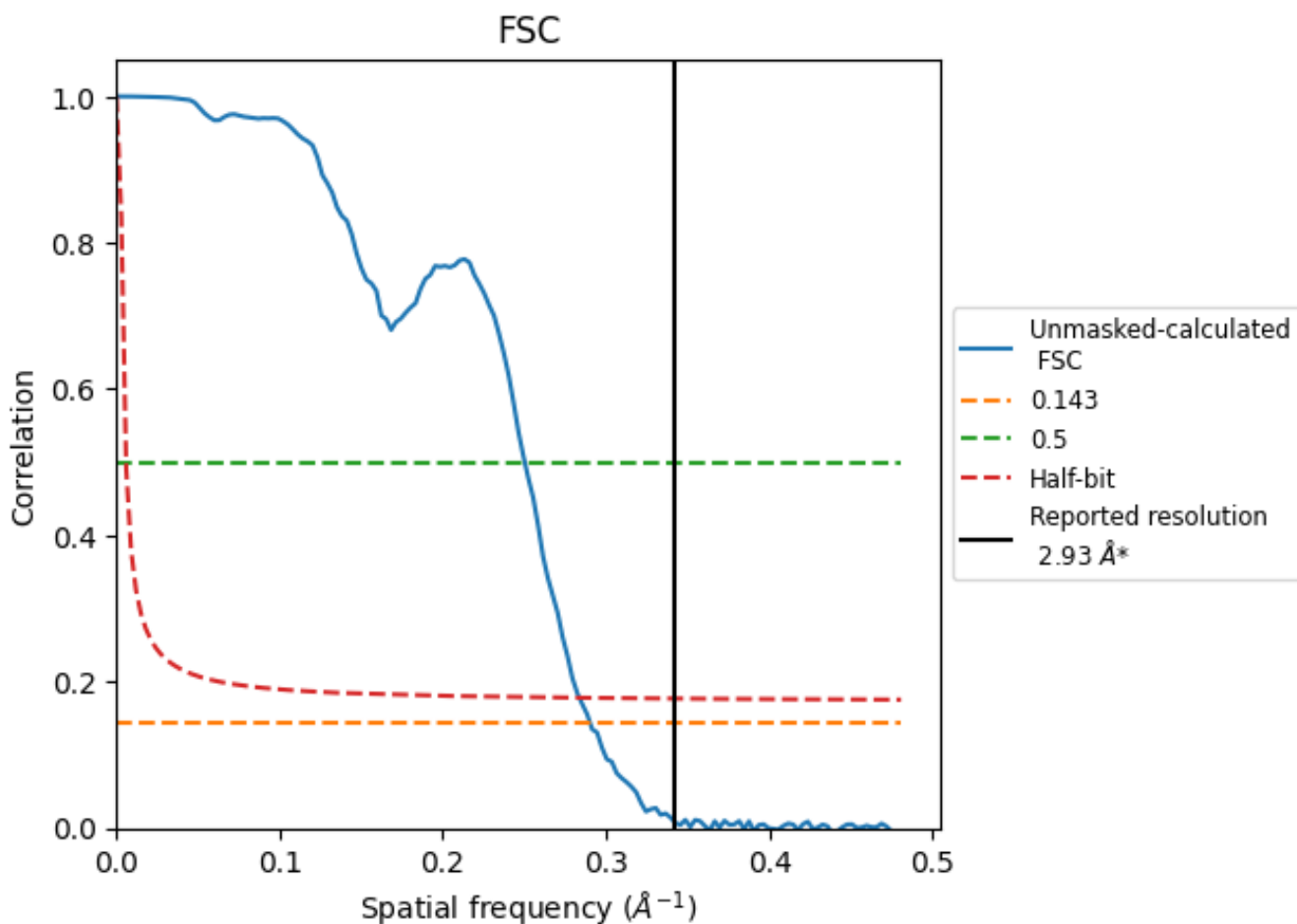


*Reported resolution corresponds to spatial frequency of 0.341 Å⁻¹

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 0.341 Å⁻¹

8.2 Resolution estimates [i](#)

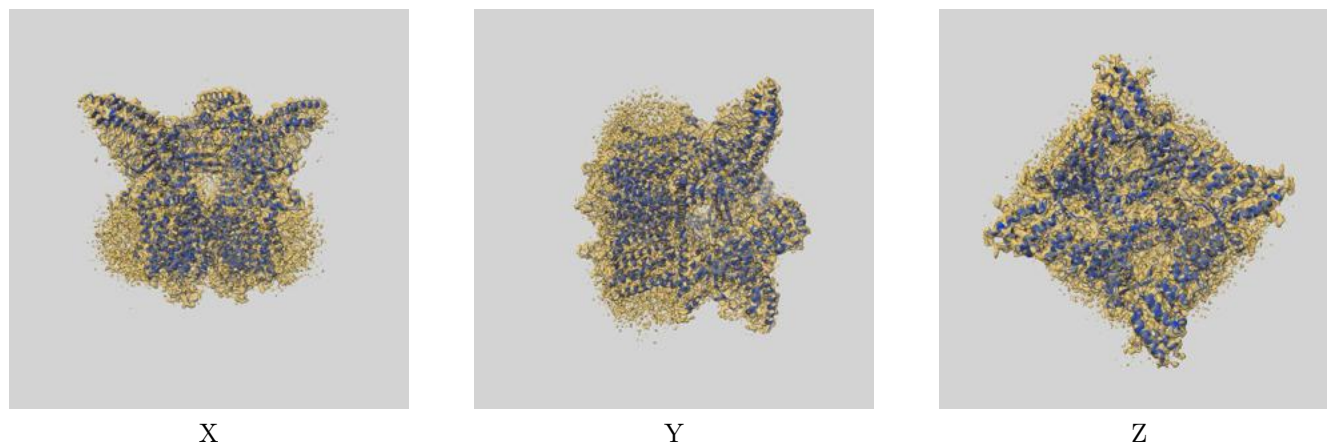
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.93	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.45	4.00	3.53

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.45 differs from the reported value 2.93 by more than 10 %

9 Map-model fit [i](#)

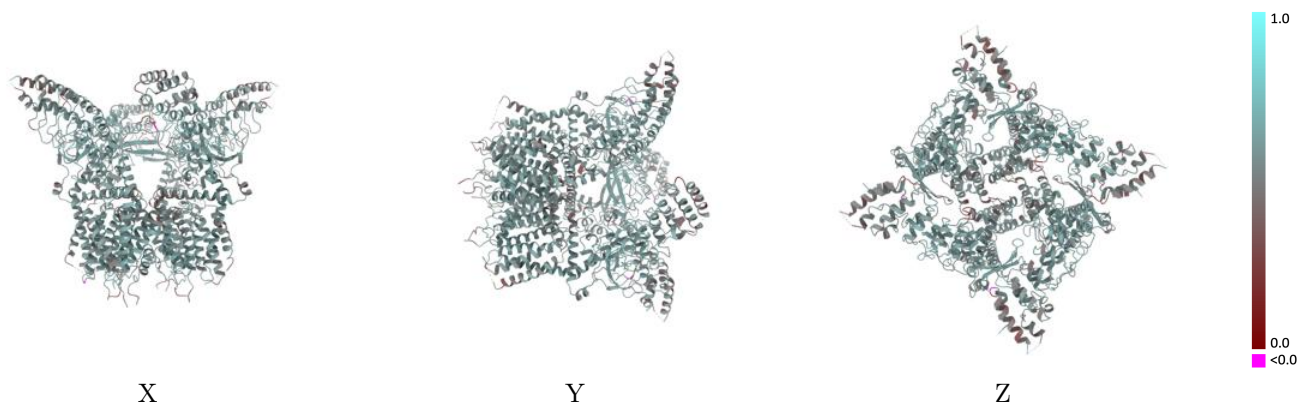
This section contains information regarding the fit between EMDB map EMD-33216 and PDB model 7XJ1. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



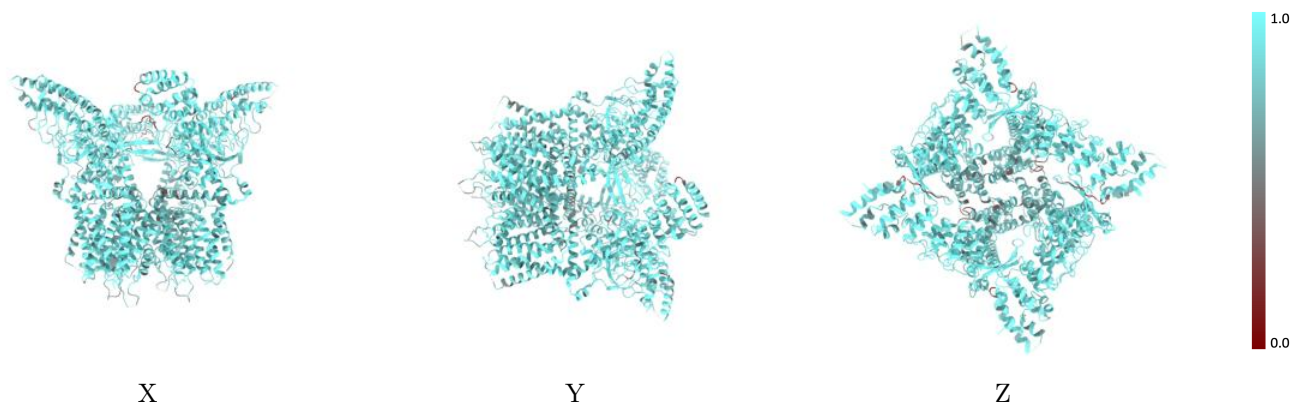
The images above show the 3D surface view of the map at the recommended contour level 0.43 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



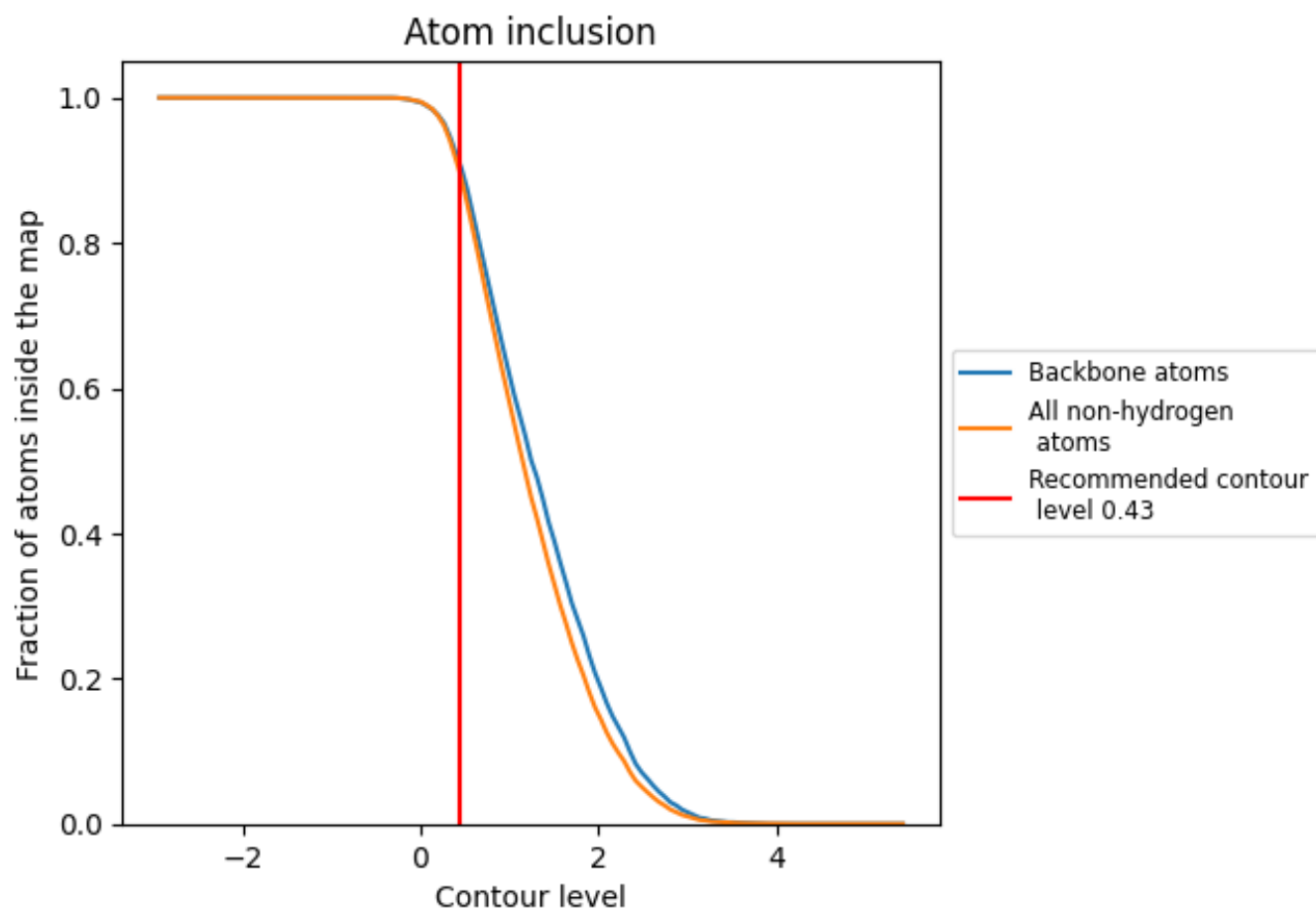
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.43).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.43) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9018	 0.5630
A	 0.9027	 0.5650
B	 0.9016	 0.5630
C	 0.9025	 0.5640
D	 0.9003	 0.5620

