



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:21 AM UTC

PDB ID : 6OHS / pdb_00006ohs
Title : Structure of compound 3 (ML299) bound human Phospholipase D2 catalytic domain
Authors : Metrick, C.M.; Chodaparambil, J.V.
Deposited on : 2019-04-06
Resolution : 3.20 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

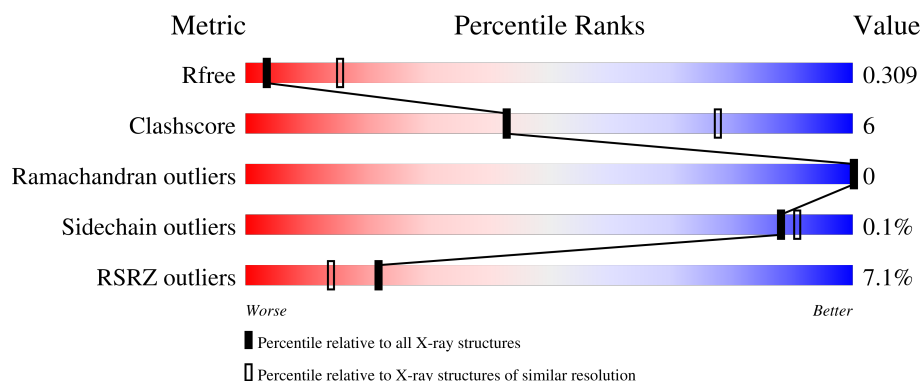
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	640	8% 78% 13% 9%
1	B	640	4% 79% 12% 9%
1	C	640	7% 77% 15% 9%
1	D	640	6% 73% 18% 9%

2 Entry composition [i](#)

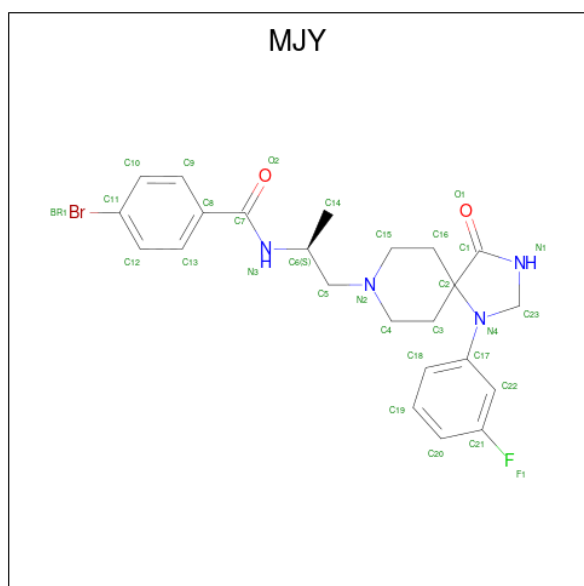
There are 2 unique types of molecules in this entry. The entry contains 18932 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Phospholipase D2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	584	Total	C	N	O	S	0	0	0
			4702	3015	825	846	16			
1	B	584	Total	C	N	O	S	0	0	0
			4702	3015	825	846	16			
1	C	584	Total	C	N	O	S	0	0	0
			4702	3015	825	846	16			
1	D	584	Total	C	N	O	S	0	0	0
			4702	3015	825	846	16			

- Molecule 2 is 4-bromo-N-{(2S)-1-[1-(3-fluorophenyl)-4-oxo-1,3,8-triazaspiro[4.5]decan-8-yl]propan-2-yl}benzamide (CCD ID: MJY) (formula: C₂₃H₂₆BrFN₄O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	Br	C	F	N	O	0	0
			31	1	23	1	4	2		

Continued on next page...

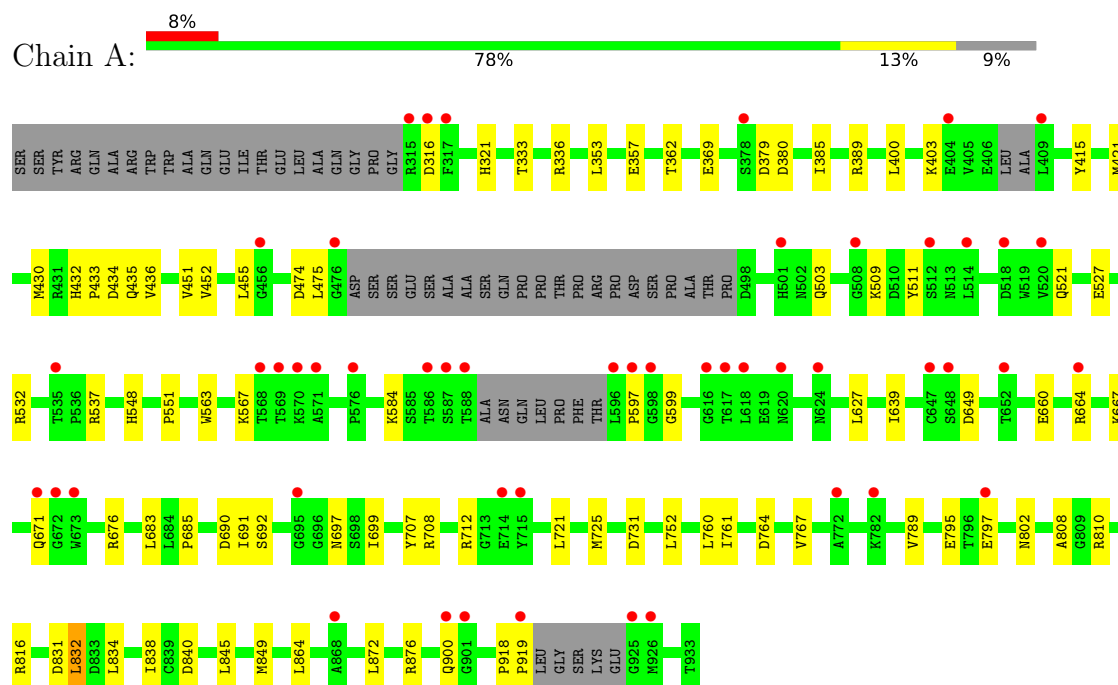
Continued from previous page...

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	B	1	Total	Br	C	F	N	O	0	0
			31	1	23	1	4	2		
2	C	1	Total	Br	C	F	N	O	0	0
			31	1	23	1	4	2		
2	D	1	Total	Br	C	F	N	O	0	0
			31	1	23	1	4	2		

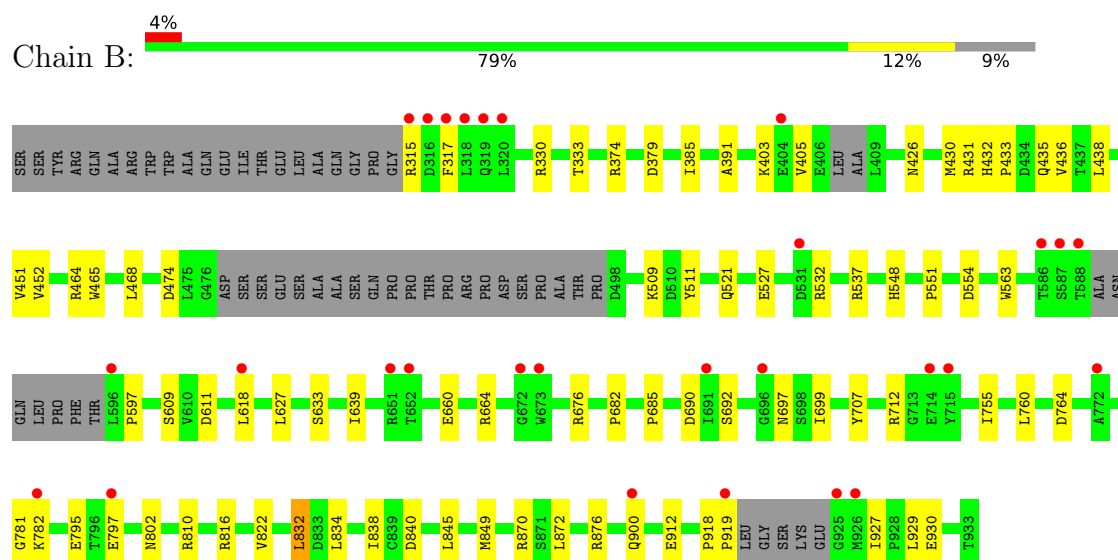
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

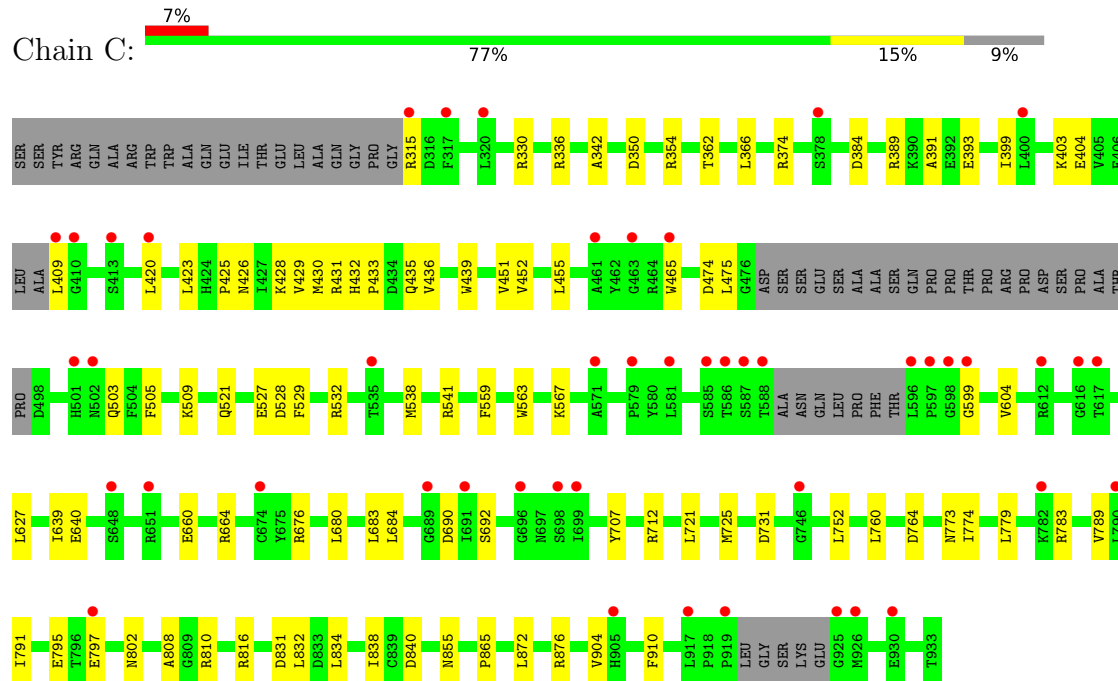
• Molecule 1: Phospholipase D2



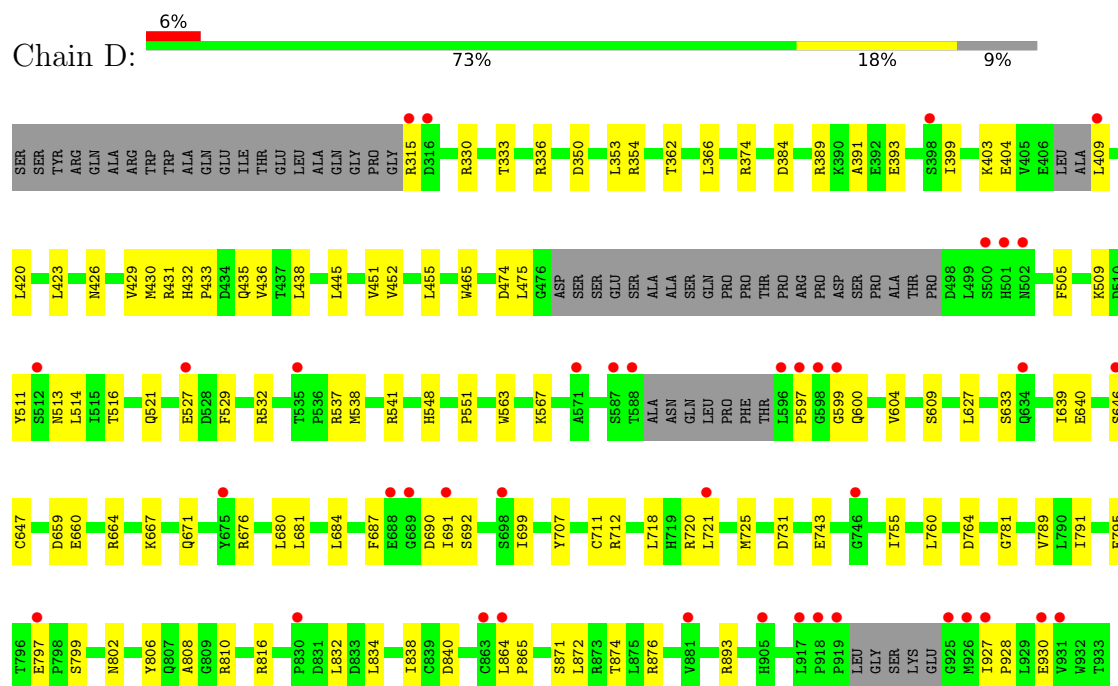
• Molecule 1: Phospholipase D2



● Molecule 1: Phospholipase D2



● Molecule 1: Phospholipase D2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	89.06Å 132.32Å 114.61Å 90.00° 100.01° 90.00°	Depositor
Resolution (Å)	48.17 – 3.20 48.17 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.5 (48.17-3.20) 99.5 (48.17-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.18 (at 3.19Å)	Xtriage
Refinement program	PHENIX (1.14_3260: ???)	Depositor
R, R_{free}	0.278 , 0.319 0.272 , 0.309	Depositor DCC
R_{free} test set	2147 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	56.9	Xtriage
Anisotropy	0.503	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 58.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	18932	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 52.44 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.8634e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0.14	0/4823	0.45	0/6553
1	B	0.15	0/4823	0.45	0/6553
1	C	0.14	0/4823	0.45	0/6553
1	D	0.13	0/4823	0.45	0/6553
All	All	0.14	0/19292	0.45	0/26212

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4702	0	4634	57	0
1	B	4702	0	4634	51	0
1	C	4702	0	4634	64	1
1	D	4702	0	4634	72	1
2	A	31	0	0	0	0
2	B	31	0	0	1	0
2	C	31	0	0	1	0
2	D	31	0	0	1	0
All	All	18932	0	18536	231	1

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 6.

All (231) 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:503:GLN:HG2	1:C:831:ASP:HB3	1.65	0.79
1:C:712:ARG:NH2	1:C:910:PHE:O	2.18	0.77
1:D:797:GLU:HG2	1:D:810:ARG:HG2	1.67	0.77
1:B:509:LYS:NZ	1:B:521:GLN:O	2.17	0.76
1:A:797:GLU:HG2	1:A:810:ARG:HG2	1.68	0.73
1:D:816:ARG:NH2	1:D:834:LEU:O	2.19	0.73
1:B:438:LEU:HD21	1:D:438:LEU:HD21	1.72	0.72
1:A:831:ASP:HB3	1:C:503:GLN:HG2	1.71	0.71
1:B:927:ILE:HD13	1:D:927:ILE:HD13	1.73	0.71
1:A:509:LYS:NZ	1:A:521:GLN:O	2.24	0.70
1:B:464:ARG:NH2	2:B:1001:MJY:O2	2.24	0.70
1:C:816:ARG:NH2	1:C:834:LEU:O	2.21	0.69
1:B:816:ARG:NH2	1:B:834:LEU:O	2.23	0.68
1:C:627:LEU:HD22	1:C:660:GLU:HG3	1.76	0.67
1:C:795:GLU:OE1	1:C:810:ARG:NH1	2.28	0.66
1:B:797:GLU:HG2	1:B:810:ARG:HG2	1.75	0.66
1:C:797:GLU:HG2	1:C:810:ARG:HG2	1.77	0.66
1:B:618:LEU:HD13	1:B:782:LYS:HE3	1.77	0.65
1:D:509:LYS:NZ	1:D:521:GLN:O	2.30	0.65
1:B:795:GLU:OE1	1:B:810:ARG:NH1	2.31	0.63
1:A:872:LEU:O	1:A:876:ARG:HD3	1.98	0.63
1:D:627:LEU:HD22	1:D:660:GLU:HG3	1.80	0.63
1:B:832:LEU:HD23	1:B:834:LEU:HD21	1.79	0.63
1:A:357:GLU:OE2	1:A:584:LYS:NZ	2.24	0.63
1:C:872:LEU:O	1:C:876:ARG:HD3	1.98	0.62
1:A:816:ARG:NH2	1:A:834:LEU:O	2.31	0.62
1:B:872:LEU:O	1:B:876:ARG:HD3	2.00	0.61
1:C:676:ARG:NH1	1:C:731:ASP:O	2.30	0.61
1:C:773:ASN:ND2	2:C:1001:MJY:O1	2.34	0.61
1:B:845:LEU:HD21	1:B:849:MET:HE3	1.82	0.61
1:D:350:ASP:HB3	1:D:354:ARG:HH21	1.64	0.60
1:B:697:ASN:HB2	1:B:918:PRO:HB3	1.81	0.60
1:D:707:TYR:HB3	1:D:712:ARG:HD2	1.82	0.60
1:C:604:VAL:HG22	1:C:791:ILE:HG12	1.84	0.60
1:C:684:LEU:HG	1:C:865:PRO:HD3	1.82	0.60
1:B:405:VAL:HG11	1:D:928:PRO:HB3	1.84	0.60
1:D:676:ARG:NH2	1:D:840:ASP:OD1	2.35	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:627:LEU:HD22	1:B:660:GLU:HG3	1.84	0.59
1:A:795:GLU:OE1	1:A:810:ARG:NH1	2.35	0.59
1:A:503:GLN:CG	1:C:831:ASP:HB3	2.32	0.59
1:B:685:PRO:HD2	1:B:699:ILE:HG23	1.84	0.59
1:D:832:LEU:HD23	1:D:834:LEU:HD21	1.84	0.58
1:C:374:ARG:NH1	1:C:505:PHE:O	2.36	0.58
1:C:676:ARG:NH2	1:C:840:ASP:OD1	2.37	0.58
1:C:832:LEU:HD23	1:C:834:LEU:HD21	1.86	0.57
1:A:548:HIS:NE2	1:A:597:PRO:HD2	2.19	0.57
1:A:676:ARG:NH2	1:A:840:ASP:OD1	2.37	0.57
1:C:797:GLU:N	1:C:808:ALA:O	2.33	0.57
1:D:474:ASP:O	1:D:532:ARG:HD3	2.05	0.56
1:A:802:ASN:HB2	1:A:838:ILE:HD11	1.88	0.56
1:C:455:LEU:HD11	1:C:789:VAL:HG13	1.87	0.56
1:D:455:LEU:HD11	1:D:789:VAL:HG13	1.88	0.56
1:D:509:LYS:HE2	1:D:529:PHE:HB3	1.87	0.55
1:B:391:ALA:HB1	1:B:426:ASN:HB2	1.89	0.55
1:B:403:LYS:HB2	1:B:431:ARG:HB3	1.89	0.55
1:C:509:LYS:NZ	1:C:521:GLN:O	2.40	0.54
1:B:315:ARG:N	1:B:330:ARG:HH12	2.04	0.54
1:B:676:ARG:NH2	1:B:840:ASP:OD1	2.37	0.54
1:C:430:MET:HE2	1:C:563:TRP:CD2	2.42	0.54
1:A:627:LEU:HD22	1:A:660:GLU:HG3	1.89	0.53
1:A:832:LEU:HD23	1:A:834:LEU:HD21	1.90	0.53
1:B:436:VAL:HG21	1:D:930:GLU:HG3	1.90	0.53
1:A:333:THR:HG21	1:A:551:PRO:HG2	1.91	0.53
1:A:831:ASP:HB3	1:C:503:GLN:CG	2.38	0.53
1:D:333:THR:HG21	1:D:551:PRO:HG2	1.91	0.52
1:D:676:ARG:NH1	1:D:731:ASP:O	2.42	0.52
1:A:380:ASP:OD1	1:A:389:ARG:NH2	2.40	0.52
1:B:430:MET:HE2	1:B:563:TRP:CD2	2.45	0.52
1:C:474:ASP:O	1:C:532:ARG:HD3	2.10	0.52
1:C:391:ALA:HB1	1:C:426:ASN:HB2	1.91	0.52
1:D:511:TYR:CE2	1:D:537:ARG:HG3	2.45	0.52
1:B:930:GLU:HG3	1:D:436:VAL:HG21	1.92	0.52
1:D:451:VAL:HG23	1:D:452:VAL:HG23	1.92	0.52
1:D:667:LYS:O	1:D:671:GLN:HG2	2.11	0.51
1:C:336:ARG:HB2	1:C:599:GLY:HA2	1.92	0.51
1:B:451:VAL:HG23	1:B:452:VAL:HG23	1.93	0.51
1:C:403:LYS:HB2	1:C:431:ARG:HB3	1.92	0.51
1:A:509:LYS:HE3	1:A:527:GLU:O	2.11	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:548:HIS:NE2	1:D:597:PRO:HD2	2.25	0.51
1:C:475:LEU:HD23	1:C:532:ARG:HG2	1.93	0.51
1:D:639:ILE:HG12	1:D:760:LEU:HD12	1.92	0.51
1:D:795:GLU:OE1	1:D:810:ARG:NH1	2.44	0.51
1:A:685:PRO:HD2	1:A:699:ILE:HG23	1.93	0.50
1:C:639:ILE:HG12	1:C:760:LEU:HD12	1.92	0.50
1:D:430:MET:HE2	1:D:563:TRP:CD2	2.47	0.50
1:D:797:GLU:N	1:D:808:ALA:O	2.38	0.50
1:B:432:HIS:CG	1:B:433:PRO:HA	2.47	0.50
1:D:403:LYS:HB2	1:D:431:ARG:HB3	1.93	0.50
1:A:831:ASP:HB3	1:C:503:GLN:HE21	1.77	0.49
1:B:317:PHE:HZ	1:B:554:ASP:OD1	1.95	0.49
1:D:432:HIS:CG	1:D:433:PRO:HA	2.47	0.49
1:D:475:LEU:HD23	1:D:532:ARG:HG2	1.93	0.49
1:A:451:VAL:HG23	1:A:452:VAL:HG23	1.94	0.49
1:B:435:GLN:HG3	1:B:436:VAL:N	2.28	0.49
1:B:802:ASN:HB2	1:B:838:ILE:HD11	1.93	0.49
1:C:432:HIS:CG	1:C:433:PRO:HA	2.47	0.49
1:B:849:MET:SD	1:B:900:GLN:HG3	2.53	0.49
1:B:764:ASP:OD1	1:B:816:ARG:HD3	2.12	0.49
1:D:690:ASP:OD1	1:D:692:SER:OG	2.30	0.49
1:B:379:ASP:HB3	1:B:385:ILE:HG13	1.95	0.48
1:C:451:VAL:HG23	1:C:452:VAL:HG23	1.94	0.48
1:A:639:ILE:HG12	1:A:760:LEU:HD12	1.95	0.48
1:C:690:ASP:OD1	1:C:692:SER:OG	2.30	0.48
1:C:509:LYS:HE2	1:C:529:PHE:HB3	1.95	0.48
1:A:690:ASP:OD1	1:A:692:SER:OG	2.31	0.48
1:A:676:ARG:NH1	1:A:731:ASP:O	2.43	0.48
1:A:567:LYS:HB3	1:A:567:LYS:HE3	1.71	0.47
1:B:690:ASP:OD1	1:B:692:SER:OG	2.32	0.47
1:D:567:LYS:HB3	1:D:567:LYS:HE3	1.61	0.47
1:D:633:SER:O	1:D:664:ARG:NH2	2.43	0.47
1:C:802:ASN:HB2	1:C:838:ILE:HD11	1.97	0.47
1:D:399:ILE:HB	1:D:429:VAL:HG22	1.97	0.47
1:A:764:ASP:HB3	1:A:808:ALA:HB1	1.97	0.47
1:A:707:TYR:HB3	1:A:712:ARG:HD2	1.97	0.47
1:B:333:THR:HG21	1:B:551:PRO:HG2	1.96	0.47
1:C:509:LYS:HE3	1:C:527:GLU:O	2.15	0.47
1:D:384:ASP:HB2	1:D:423:LEU:HD11	1.97	0.46
1:D:687:PHE:HB2	1:D:699:ILE:HD11	1.96	0.46
1:B:430:MET:HE1	1:B:563:TRP:O	2.16	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:659:ASP:HA	1:D:720:ARG:HH22	1.80	0.46
1:A:432:HIS:CG	1:A:433:PRO:HA	2.51	0.46
1:D:743:GLU:CD	1:D:893:ARG:HE	2.23	0.46
1:B:870:ARG:NE	1:B:912:GLU:OE2	2.49	0.46
1:C:640:GLU:HG3	1:C:680:LEU:HB3	1.97	0.46
1:B:633:SER:O	1:B:664:ARG:NH2	2.49	0.45
1:D:315:ARG:N	1:D:330:ARG:HH12	2.14	0.45
1:B:374:ARG:HG3	1:B:465:TRP:CE2	2.52	0.45
1:D:538:MET:HE2	1:D:538:MET:HB3	1.89	0.45
1:D:684:LEU:HG	1:D:865:PRO:HD3	1.98	0.45
1:A:683:LEU:HB2	1:A:752:LEU:HD22	1.99	0.45
1:A:379:ASP:HB3	1:A:385:ILE:HG13	1.99	0.45
1:A:761:ILE:HG12	1:A:767:VAL:HG22	1.99	0.45
1:B:511:TYR:CE2	1:B:537:ARG:HG3	2.52	0.45
1:B:609:SER:HB3	1:B:781:GLY:HA2	1.98	0.45
1:A:435:GLN:HG3	1:A:436:VAL:N	2.31	0.45
1:B:474:ASP:O	1:B:532:ARG:HD3	2.17	0.45
1:C:764:ASP:OD1	1:C:816:ARG:HD3	2.18	0.44
1:D:513:ASN:HB3	1:D:516:THR:HB	2.00	0.44
1:D:799:SER:N	1:D:806:TYR:O	2.47	0.44
1:D:391:ALA:HB1	1:D:426:ASN:HB2	1.99	0.44
1:D:366:LEU:HD22	1:D:420:LEU:HD11	1.99	0.44
1:A:697:ASN:HB2	1:A:918:PRO:HB3	2.00	0.44
1:B:509:LYS:HE3	1:B:527:GLU:O	2.18	0.44
1:C:567:LYS:HB3	1:C:567:LYS:HE3	1.64	0.44
1:D:336:ARG:HB2	1:D:599:GLY:HA2	1.99	0.44
1:D:802:ASN:HB2	1:D:838:ILE:HD11	1.99	0.44
1:A:362:THR:HG22	1:A:400:LEU:HB2	2.00	0.44
1:C:404:GLU:HB2	1:C:409:LEU:HD12	1.99	0.44
1:B:432:HIS:CD2	1:B:433:PRO:HA	2.53	0.44
1:D:435:GLN:HG3	1:D:436:VAL:N	2.33	0.44
1:A:845:LEU:HD21	1:A:849:MET:HE3	2.00	0.44
1:A:849:MET:SD	1:A:900:GLN:HG3	2.57	0.43
1:B:468:LEU:HD22	1:B:822:VAL:HG21	2.00	0.43
1:C:362:THR:HG23	1:C:559:PHE:HD2	1.83	0.43
1:C:430:MET:HE1	1:C:563:TRP:O	2.18	0.43
1:D:711:CYS:HB3	1:D:718:LEU:HD12	2.00	0.43
1:C:541:ARG:HE	1:C:640:GLU:CD	2.25	0.43
1:D:430:MET:HE1	1:D:563:TRP:O	2.19	0.43
1:C:374:ARG:HG3	1:C:465:TRP:CE2	2.53	0.43
1:D:404:GLU:HB2	1:D:409:LEU:HD12	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:795:GLU:HB3	1:A:810:ARG:NH1	2.34	0.43
1:B:918:PRO:HA	1:B:919:PRO:HD3	1.89	0.43
1:A:503:GLN:HE21	1:C:831:ASP:HB3	1.84	0.43
1:A:511:TYR:CE2	1:A:537:ARG:HG3	2.54	0.43
1:B:611:ASP:OD1	1:B:782:LYS:HD3	2.19	0.43
1:C:366:LEU:HD22	1:C:420:LEU:HD11	2.00	0.43
1:C:384:ASP:HB2	1:C:423:LEU:HD11	2.01	0.43
1:A:403:LYS:NZ	1:A:434:ASP:OD1	2.34	0.43
1:A:430:MET:HE2	1:A:563:TRP:CD2	2.54	0.43
1:C:435:GLN:HG3	1:C:436:VAL:N	2.34	0.43
1:A:369:GLU:OE2	1:A:415:TYR:OH	2.22	0.42
1:A:664:ARG:HD2	1:A:664:ARG:HA	1.82	0.42
1:C:425:PRO:O	1:C:428:LYS:HE3	2.18	0.42
1:D:721:LEU:O	1:D:725:MET:HG2	2.18	0.42
1:C:683:LEU:HD11	1:C:904:VAL:HG21	2.01	0.42
1:D:691:ILE:HG23	1:D:864:LEU:HD12	2.01	0.42
1:D:764:ASP:OD1	1:D:816:ARG:HD3	2.18	0.42
1:D:871:SER:OG	1:D:874:THR:HG22	2.20	0.42
1:A:831:ASP:HB3	1:C:503:GLN:NE2	2.34	0.42
1:A:764:ASP:OD1	1:A:816:ARG:HD3	2.19	0.42
1:C:342:ALA:HA	1:C:465:TRP:NE1	2.34	0.42
1:D:609:SER:HB3	1:D:781:GLY:HA2	2.00	0.42
1:B:707:TYR:HB3	1:B:712:ARG:HD2	2.01	0.42
1:D:600:GLN:NE2	1:D:795:GLU:OE1	2.50	0.42
1:A:336:ARG:HB2	1:A:599:GLY:HA2	2.02	0.42
1:A:421:MET:HE2	1:A:421:MET:HB3	1.96	0.42
1:B:927:ILE:HD13	1:D:927:ILE:CD1	2.45	0.42
1:C:350:ASP:HB3	1:C:354:ARG:HH21	1.85	0.42
1:D:353:LEU:HD12	1:D:353:LEU:HA	1.89	0.42
1:D:374:ARG:NH1	1:D:505:PHE:O	2.50	0.42
1:A:353:LEU:HD12	1:A:353:LEU:HA	1.86	0.42
1:C:315:ARG:N	1:C:330:ARG:HH12	2.18	0.42
1:C:399:ILE:HB	1:C:429:VAL:HG22	2.02	0.42
1:A:455:LEU:HD11	1:A:789:VAL:HG13	2.01	0.41
1:A:721:LEU:O	1:A:725:MET:HG2	2.19	0.41
1:A:918:PRO:HA	1:A:919:PRO:HD3	1.91	0.41
1:C:538:MET:HE2	1:C:538:MET:HB3	1.96	0.41
1:D:604:VAL:HG22	1:D:791:ILE:HG12	2.01	0.41
1:D:640:GLU:HG3	1:D:680:LEU:HB3	2.02	0.41
1:A:691:ILE:HG23	1:A:864:LEU:HD12	2.02	0.41
1:B:682:PRO:HD3	1:B:755:ILE:HB	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:667:LYS:O	1:A:671:GLN:HG2	2.20	0.41
1:B:639:ILE:HG12	1:B:760:LEU:HD12	2.02	0.41
1:C:683:LEU:HB2	1:C:752:LEU:HD22	2.00	0.41
1:C:707:TYR:HB3	1:C:712:ARG:HD2	2.03	0.41
1:B:548:HIS:NE2	1:B:597:PRO:HD2	2.35	0.41
1:D:389:ARG:O	1:D:393:GLU:HG3	2.19	0.41
1:D:681:LEU:C	1:D:755:ILE:HD12	2.46	0.41
1:C:541:ARG:NE	1:C:640:GLU:OE2	2.50	0.41
1:C:774:ILE:HA	1:C:779:LEU:HD11	2.03	0.41
1:D:646:SER:OG	1:D:647:CYS:N	2.52	0.41
1:D:795:GLU:HB3	1:D:810:ARG:NH1	2.35	0.41
1:A:649:ASP:HB3	1:A:708:ARG:HH21	1.86	0.41
1:D:374:ARG:HG3	1:D:465:TRP:CE2	2.56	0.41
1:D:509:LYS:HE3	1:D:527:GLU:O	2.21	0.41
1:D:362:THR:OG1	1:D:445:LEU:HB3	2.20	0.41
1:A:475:LEU:HD23	1:A:532:ARG:HG2	2.03	0.40
1:B:929:LEU:HD23	1:B:929:LEU:HA	1.90	0.40
1:C:389:ARG:O	1:C:393:GLU:HG3	2.20	0.40
1:C:721:LEU:O	1:C:725:MET:HG2	2.20	0.40
1:D:541:ARG:HE	1:D:640:GLU:CD	2.29	0.40
1:D:872:LEU:O	1:D:876:ARG:HD3	2.21	0.40
1:A:474:ASP:O	1:A:532:ARG:HD3	2.20	0.40
1:B:685:PRO:HB2	1:B:699:ILE:HD13	2.03	0.40
1:C:664:ARG:HD2	1:C:664:ARG:HA	1.79	0.40
1:D:514:LEU:HD21	2:D:1001:MJY:C14	2.50	0.40
1:A:316:ASP:O	1:A:321:HIS:NE2	2.54	0.40
1:C:527:GLU:HG2	1:C:528:ASP:O	2.21	0.40
1:C:439:TRP:CE2	1:C:783:ARG:HG2	2.57	0.40
1:C:683:LEU:O	1:C:865:PRO:HG3	2.22	0.40
1:D:664:ARG:HD2	1:D:664:ARG:HA	1.83	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:855:ASN:ND2	1:D:671:GLN:O[1_554]	2.02	0.18

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	574/640 (90%)	551 (96%)	23 (4%)	0	100	100
1	B	574/640 (90%)	553 (96%)	21 (4%)	0	100	100
1	C	574/640 (90%)	553 (96%)	21 (4%)	0	100	100
1	D	574/640 (90%)	552 (96%)	22 (4%)	0	100	100
All	All	2296/2560 (90%)	2209 (96%)	87 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	504/554 (91%)	503 (100%)	1 (0%)	87	89
1	B	504/554 (91%)	503 (100%)	1 (0%)	87	89
1	C	504/554 (91%)	504 (100%)	0	100	100
1	D	504/554 (91%)	504 (100%)	0	100	100
All	All	2016/2216 (91%)	2014 (100%)	2 (0%)	88	91

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	832	LEU
1	B	832	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	340	ASN
1	A	503	GLN
1	A	521	GLN
1	A	642	GLN
1	A	818	HIS
1	A	902	HIS
1	B	323	HIS
1	B	340	ASN
1	B	818	HIS
1	B	902	HIS
1	C	321	HIS
1	C	340	ASN
1	C	377	HIS
1	C	635	HIS
1	C	642	GLN
1	D	521	GLN
1	D	635	HIS
1	D	818	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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	MJY	D	1001	-	34,34,34	0.86	1 (2%)	48,49,49	1.01	3 (6%)
2	MJY	A	1001	-	34,34,34	0.68	1 (2%)	48,49,49	1.40	6 (12%)
2	MJY	C	1001	-	34,34,34	0.77	1 (2%)	48,49,49	1.51	7 (14%)
2	MJY	B	1001	-	34,34,34	0.90	1 (2%)	48,49,49	0.95	3 (6%)

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	MJY	D	1001	-	-	2/16/45/45	0/4/4/4
2	MJY	A	1001	-	-	4/16/45/45	0/4/4/4
2	MJY	C	1001	-	-	5/16/45/45	0/4/4/4
2	MJY	B	1001	-	-	2/16/45/45	0/4/4/4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1001	MJY	C23-N1	4.67	1.48	1.44
2	D	1001	MJY	C23-N1	4.45	1.48	1.44
2	C	1001	MJY	C23-N1	4.10	1.47	1.44
2	A	1001	MJY	C23-N1	3.39	1.47	1.44

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1001	MJY	C16-C2-N4	7.35	118.09	112.87
2	A	1001	MJY	C16-C2-N4	4.45	116.03	112.87
2	A	1001	MJY	C3-C2-N4	3.78	115.56	112.87
2	A	1001	MJY	C4-C3-C2	3.66	116.16	113.05
2	D	1001	MJY	C23-N4-C17	3.49	122.00	117.94
2	D	1001	MJY	C16-C2-N4	-3.34	110.49	112.87
2	B	1001	MJY	C23-N4-C17	3.23	121.70	117.94
2	A	1001	MJY	C15-C16-C2	3.13	115.71	113.05
2	A	1001	MJY	C3-C2-C1	-2.86	106.05	109.91

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1001	MJY	C3-C2-N4	2.79	114.85	112.87
2	A	1001	MJY	C16-C2-C1	-2.70	106.27	109.91
2	C	1001	MJY	C1-C2-N4	-2.69	99.65	100.98
2	B	1001	MJY	C15-C16-C2	-2.64	110.81	113.05
2	B	1001	MJY	C1-C2-N4	2.62	102.27	100.98
2	D	1001	MJY	C1-C2-N4	2.61	102.27	100.98
2	C	1001	MJY	C16-C2-C1	-2.36	106.72	109.91
2	C	1001	MJY	C3-C2-C1	-2.27	106.84	109.91
2	C	1001	MJY	C23-N4-C17	2.22	120.52	117.94
2	C	1001	MJY	N1-C23-N4	-2.00	101.90	102.92

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1001	MJY	N2-C5-C6-C14
2	A	1001	MJY	N2-C5-C6-N3
2	A	1001	MJY	C8-C7-N3-C6
2	B	1001	MJY	C6-C5-N2-C15
2	C	1001	MJY	N2-C5-C6-N3
2	C	1001	MJY	C18-C17-N4-C23
2	C	1001	MJY	C22-C17-N4-C23
2	C	1001	MJY	C8-C7-N3-C6
2	D	1001	MJY	C6-C5-N2-C15
2	C	1001	MJY	O2-C7-N3-C6
2	A	1001	MJY	O2-C7-N3-C6
2	B	1001	MJY	N2-C5-C6-C14
2	D	1001	MJY	C5-C6-N3-C7

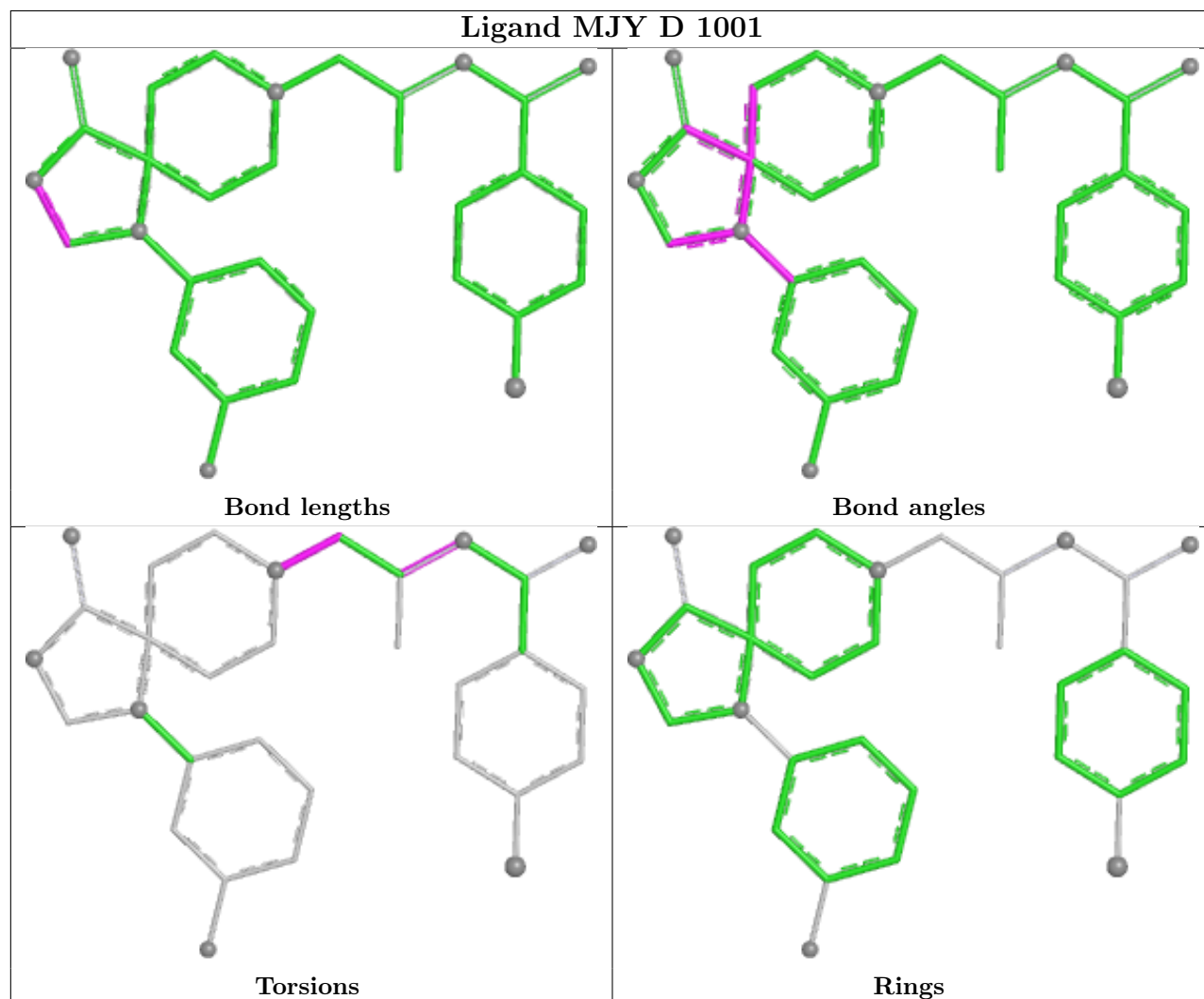
There are no ring outliers.

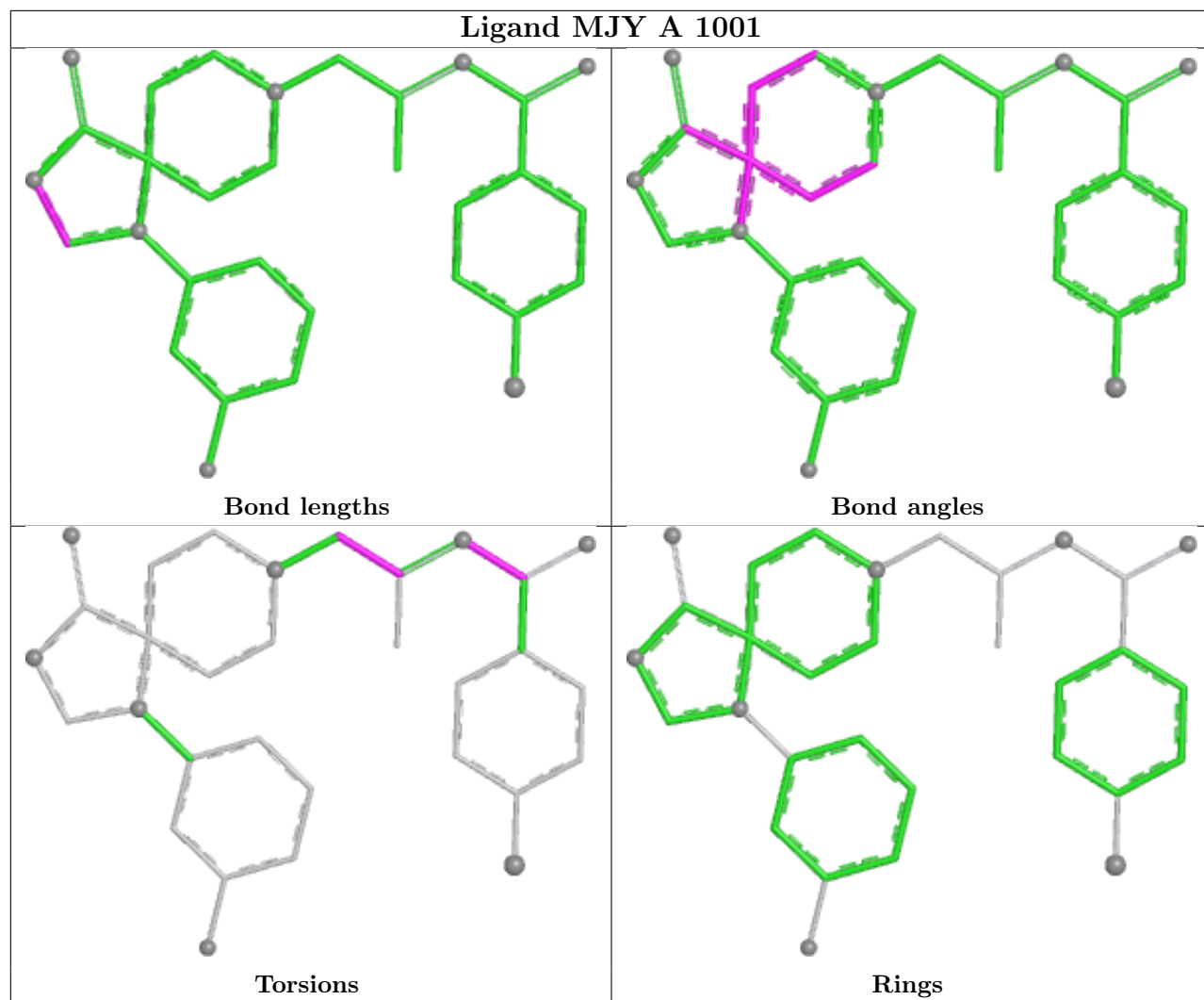
3 monomers are involved in 3 short contacts:

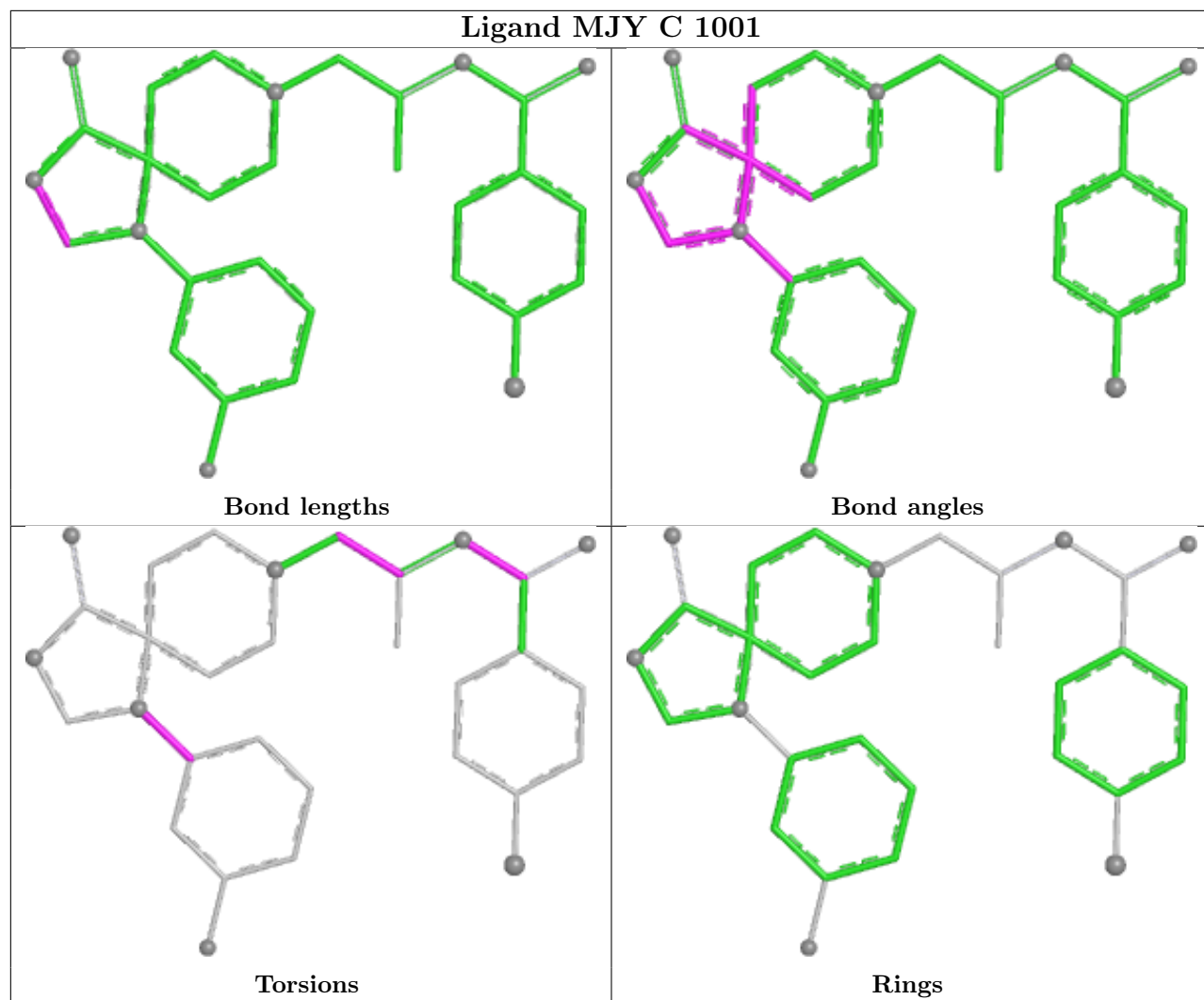
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1001	MJY	1	0
2	C	1001	MJY	1	0
2	B	1001	MJY	1	0

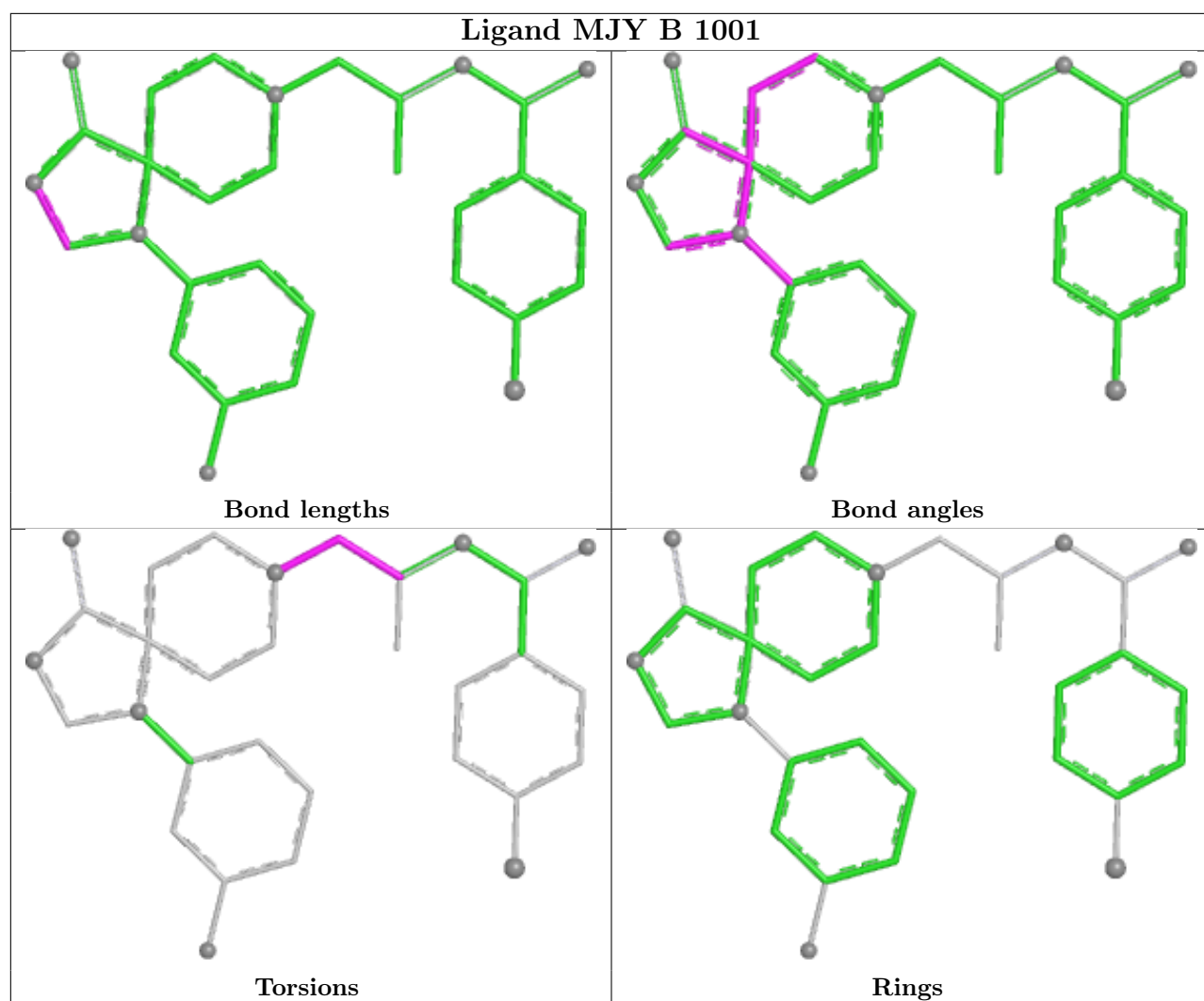
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	A	584/640 (91%)	0.69	50 (8%)	16	11	28, 54, 105, 178	0
1	B	584/640 (91%)	0.37	28 (4%)	35	22	15, 43, 93, 172	0
1	C	584/640 (91%)	0.83	47 (8%)	18	12	37, 77, 123, 197	0
1	D	584/640 (91%)	0.66	40 (6%)	23	15	34, 69, 115, 180	0
All	All	2336/2560 (91%)	0.64	165 (7%)	22	14	15, 62, 114, 197	0

All (165) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	925	GLY	6.6
1	C	926	MET	5.3
1	C	925	GLY	4.7
1	A	597	PRO	4.6
1	A	315	ARG	4.6
1	A	616	GLY	4.5
1	C	598	GLY	4.4
1	B	926	MET	4.2
1	D	691	ILE	3.9
1	A	514	LEU	3.9
1	D	598	GLY	3.9
1	A	518	ASP	3.8
1	C	616	GLY	3.8
1	D	597	PRO	3.8
1	B	588	THR	3.8
1	C	597	PRO	3.8
1	A	618	LEU	3.7
1	D	689	GLY	3.7
1	A	587	SER	3.6
1	A	316	ASP	3.6
1	D	500	SER	3.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	746	GLY	3.5
1	A	596	LEU	3.5
1	B	531	ASP	3.5
1	B	925	GLY	3.5
1	A	617	THR	3.5
1	D	599	GLY	3.5
1	C	689	GLY	3.4
1	B	797	GLU	3.4
1	A	900	GLN	3.4
1	B	316	ASP	3.3
1	C	691	ILE	3.3
1	A	317	PHE	3.3
1	A	569	THR	3.2
1	A	926	MET	3.2
1	C	599	GLY	3.2
1	D	926	MET	3.2
1	A	673	TRP	3.2
1	B	315	ARG	3.2
1	B	587	SER	3.2
1	A	797	GLU	3.1
1	A	588	THR	3.1
1	A	652	THR	3.1
1	B	673	TRP	3.1
1	D	315	ARG	3.1
1	B	900	GLN	3.1
1	C	501	HIS	3.0
1	A	671	GLN	3.0
1	A	919	PRO	3.0
1	C	588	THR	3.0
1	A	404	GLU	3.0
1	D	501	HIS	3.0
1	B	919	PRO	2.9
1	C	571	ALA	2.9
1	A	476	GLY	2.9
1	C	463	GLY	2.9
1	B	714	GLU	2.9
1	C	919	PRO	2.9
1	A	647	CYS	2.9
1	C	587	SER	2.9
1	D	830	PRO	2.9
1	C	409	LEU	2.9
1	D	596	LEU	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	698	SER	2.8
1	D	930	GLU	2.8
1	C	648	SER	2.8
1	D	919	PRO	2.8
1	A	576	PRO	2.8
1	B	320	LEU	2.8
1	A	598	GLY	2.8
1	C	696	GLY	2.8
1	B	715	TYR	2.8
1	A	501	HIS	2.8
1	B	319	GLN	2.7
1	D	588	THR	2.7
1	B	596	LEU	2.7
1	D	927	ILE	2.7
1	A	715	TYR	2.7
1	C	420	LEU	2.7
1	C	930	GLU	2.7
1	A	535	THR	2.7
1	C	461	ALA	2.7
1	D	634	GLN	2.6
1	D	502	ASN	2.6
1	C	782	LYS	2.6
1	A	901	GLY	2.6
1	D	797	GLU	2.6
1	A	409	LEU	2.6
1	C	596	LEU	2.6
1	C	410	GLY	2.5
1	B	317	PHE	2.5
1	C	674	CYS	2.5
1	D	512	SER	2.5
1	D	698	SER	2.5
1	C	315	ARG	2.5
1	B	696	GLY	2.5
1	C	797	GLU	2.5
1	A	586	THR	2.5
1	B	404	GLU	2.4
1	B	651	ARG	2.4
1	A	782	LYS	2.4
1	A	520	VAL	2.4
1	B	772	ALA	2.4
1	C	585	SER	2.4
1	C	617	THR	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	456	GLY	2.4
1	C	746	GLY	2.3
1	C	502	ASN	2.3
1	D	587	SER	2.3
1	D	918	PRO	2.3
1	C	651	ARG	2.3
1	C	586	THR	2.3
1	C	378	SER	2.3
1	D	688	GLU	2.3
1	A	925	GLY	2.3
1	D	864	LEU	2.2
1	A	624	ASN	2.2
1	B	691	ILE	2.2
1	B	672	GLY	2.2
1	C	579	PRO	2.2
1	D	721	LEU	2.2
1	A	378	SER	2.2
1	A	620	ASN	2.2
1	B	618	LEU	2.2
1	C	612	ARG	2.2
1	D	905	HIS	2.2
1	C	413	SER	2.2
1	A	512	SER	2.2
1	A	868	ALA	2.2
1	B	586	THR	2.1
1	D	931	VAL	2.1
1	A	570	LYS	2.1
1	A	568	THR	2.1
1	C	917	LEU	2.1
1	A	571	ALA	2.1
1	A	648	SER	2.1
1	D	881	VAL	2.1
1	B	652	THR	2.1
1	C	699	ILE	2.1
1	D	409	LEU	2.1
1	C	905	HIS	2.1
1	D	316	ASP	2.1
1	D	675	TYR	2.1
1	A	695	GLY	2.1
1	A	714	GLU	2.1
1	D	646	SER	2.1
1	B	318	LEU	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	581	LEU	2.1
1	A	664	ARG	2.0
1	C	535	THR	2.0
1	D	535	THR	2.0
1	D	571	ALA	2.0
1	A	672	GLY	2.0
1	C	317	PHE	2.0
1	D	398	SER	2.0
1	C	465	TRP	2.0
1	A	772	ALA	2.0
1	A	508	GLY	2.0
1	B	782	LYS	2.0
1	D	863	CYS	2.0
1	D	527	GLU	2.0
1	C	320	LEU	2.0
1	C	400	LEU	2.0
1	C	790	LEU	2.0
1	D	917	LEU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

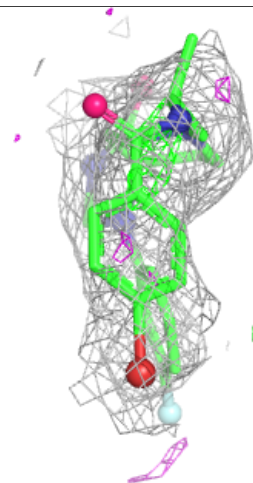
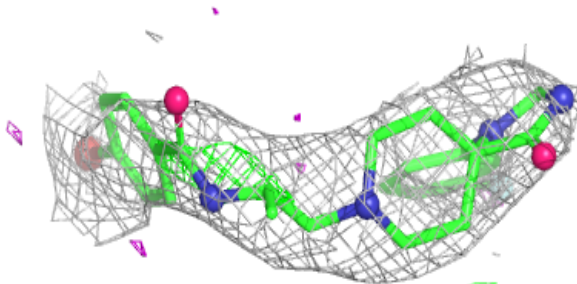
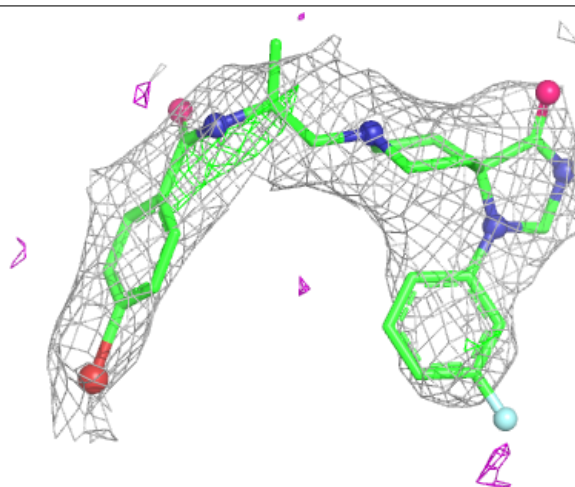
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MJY	C	1001	31/31	0.81	0.27	85,93,236,291	0
2	MJY	D	1001	31/31	0.81	0.29	71,77,244,300	0
2	MJY	A	1001	31/31	0.82	0.28	59,79,195,242	0
2	MJY	B	1001	31/31	0.88	0.31	64,99,213,269	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

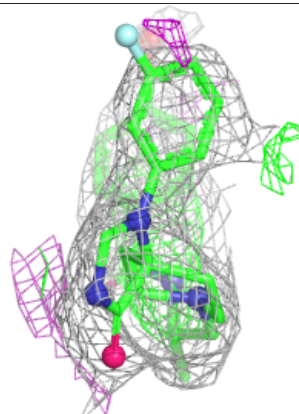
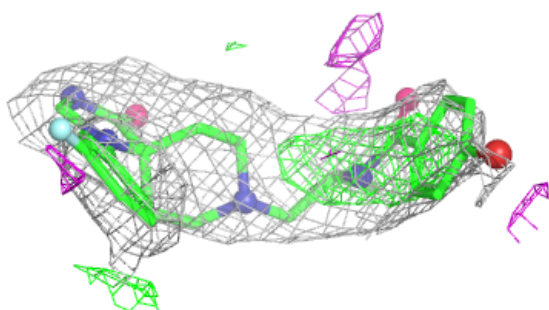
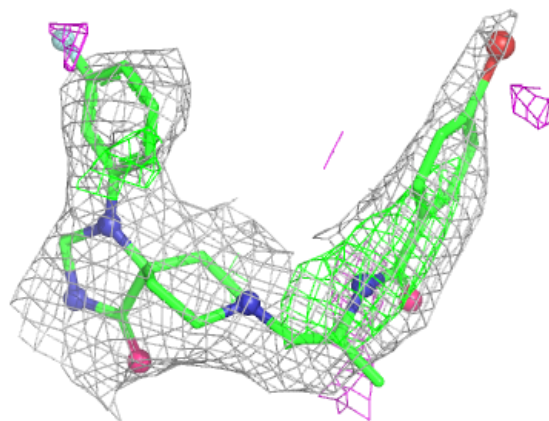
Electron density around MJY C 1001:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



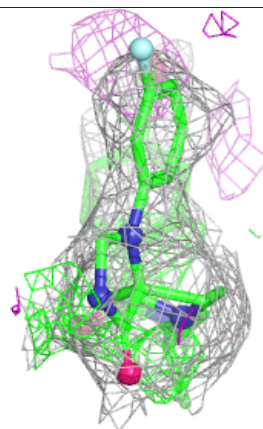
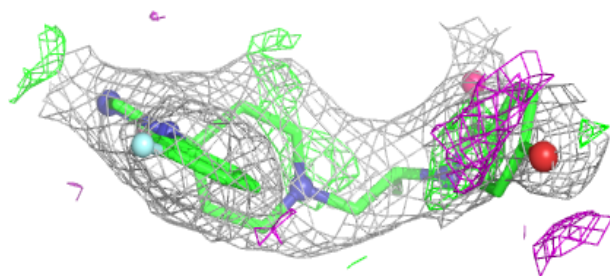
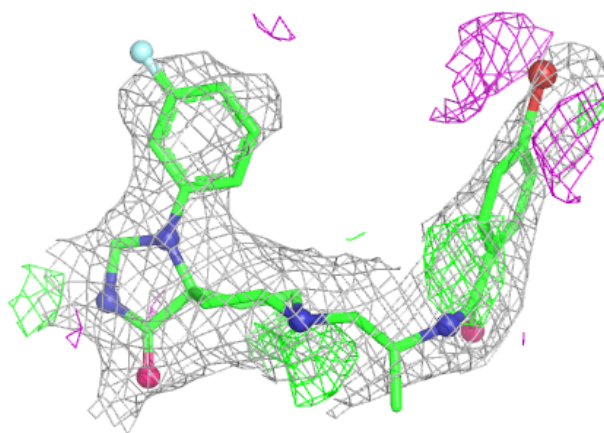
Electron density around MJY D 1001:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



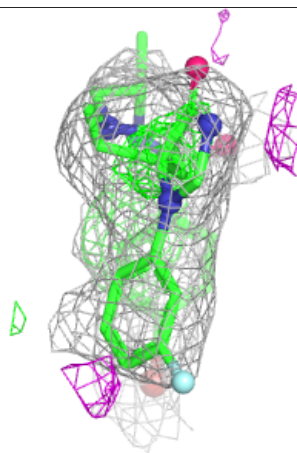
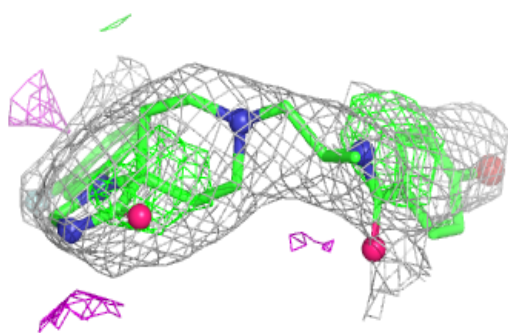
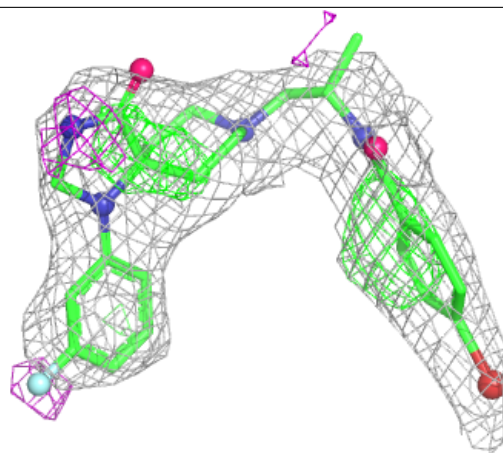
Electron density around MJY A 1001:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around MJY B 1001:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers ⓘ

There are no such residues in this entry.