



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:37 PM UTC

PDB ID : 4WYO / pdb_00004wyo
Title : Crystal structure of human-yeast chimera acetyl coA carboxylase CT domain bound to Compound 1
Authors : Vajdos, F.F.
Deposited on : 2014-11-17
Resolution : 2.89 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

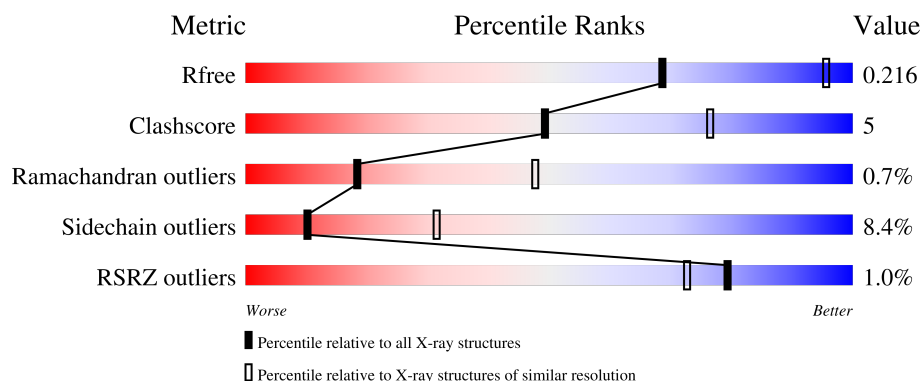
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.89 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	B	769	% 76% 17% • 5%
1	C	769	% 74% 18% •• 6%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12185 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 Acetyl-CoA carboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	733	Total	C	N	O	S	0	1	0
			5834	3710	1007	1100	17			
1	C	723	Total	C	N	O	S	0	0	0
			5744	3645	992	1089	18			

There are 40 discrepancies between the modelled and reference sequences:

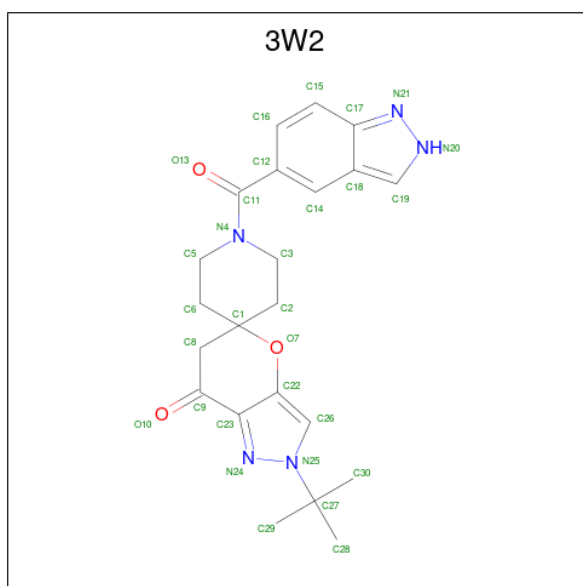
Chain	Residue	Modelled	Actual	Comment	Reference
B	1473	MET	-	initiating methionine	UNP Q00955
B	1474	ALA	-	expression tag	UNP Q00955
B	1475	SER	-	expression tag	UNP Q00955
B	1760	SER	PRO	engineered mutation	UNP Q00955
B	1762	LEU	ILE	engineered mutation	UNP Q00955
B	1765	VAL	MET	engineered mutation	UNP Q00955
B	1919	GLN	GLU	engineered mutation	UNP Q00955
B	1920	ALA	PRO	engineered mutation	UNP Q00955
B	1925	PHE	HIS	engineered mutation	UNP Q00955
B	2028	GLU	GLN	engineered mutation	UNP Q00955
B	2030	THR	MET	engineered mutation	UNP Q00955
B	2032	GLU	GLY	engineered mutation	UNP Q00955
B	2234	LEU	-	expression tag	UNP Q00955
B	2235	GLU	-	expression tag	UNP Q00955
B	2236	HIS	-	expression tag	UNP Q00955
B	2237	HIS	-	expression tag	UNP Q00955
B	2238	HIS	-	expression tag	UNP Q00955
B	2239	HIS	-	expression tag	UNP Q00955
B	2240	HIS	-	expression tag	UNP Q00955
B	2241	HIS	-	expression tag	UNP Q00955
C	1473	MET	-	initiating methionine	UNP Q00955
C	1474	ALA	-	expression tag	UNP Q00955
C	1475	SER	-	expression tag	UNP Q00955
C	1760	SER	PRO	engineered mutation	UNP Q00955
C	1762	LEU	ILE	engineered mutation	UNP Q00955

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1765	VAL	MET	engineered mutation	UNP Q00955
C	1919	GLN	GLU	engineered mutation	UNP Q00955
C	1920	ALA	PRO	engineered mutation	UNP Q00955
C	1925	PHE	HIS	engineered mutation	UNP Q00955
C	2028	GLU	GLN	engineered mutation	UNP Q00955
C	2030	THR	MET	engineered mutation	UNP Q00955
C	2032	GLU	GLY	engineered mutation	UNP Q00955
C	2234	LEU	-	expression tag	UNP Q00955
C	2235	GLU	-	expression tag	UNP Q00955
C	2236	HIS	-	expression tag	UNP Q00955
C	2237	HIS	-	expression tag	UNP Q00955
C	2238	HIS	-	expression tag	UNP Q00955
C	2239	HIS	-	expression tag	UNP Q00955
C	2240	HIS	-	expression tag	UNP Q00955
C	2241	HIS	-	expression tag	UNP Q00955

- Molecule 2 is 2'-tert-butyl-1-(2H-indazol-5-ylcarbonyl)-2'H-spiro[piperidine-4,5'-pyrano[3,2-c]pyrazol]-7'(6'H)-one (CCD ID: 3W2) (formula: C₂₂H₂₅N₅O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	O	0	0
			30	22	5	3		
2	C	1	Total	C	N	O	0	0
			30	22	5	3		

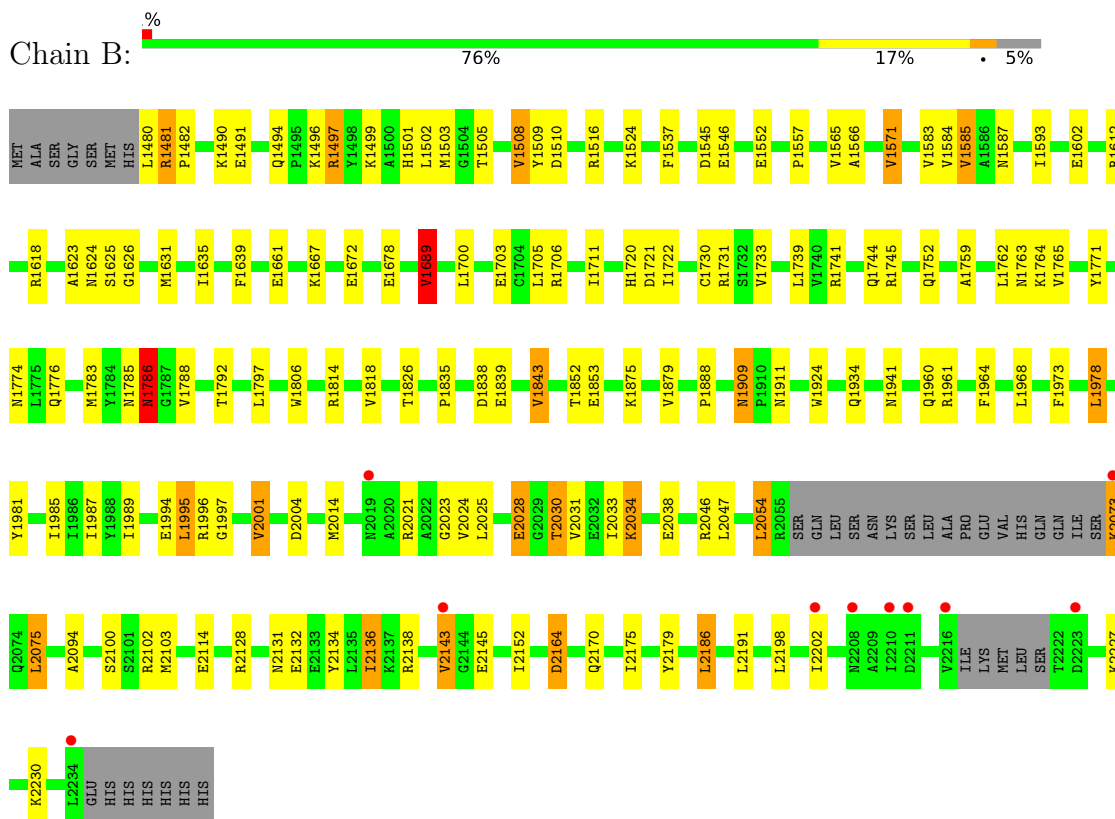
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	284	Total 284	O 284	0	0
3	C	263	Total 263	O 263	0	0

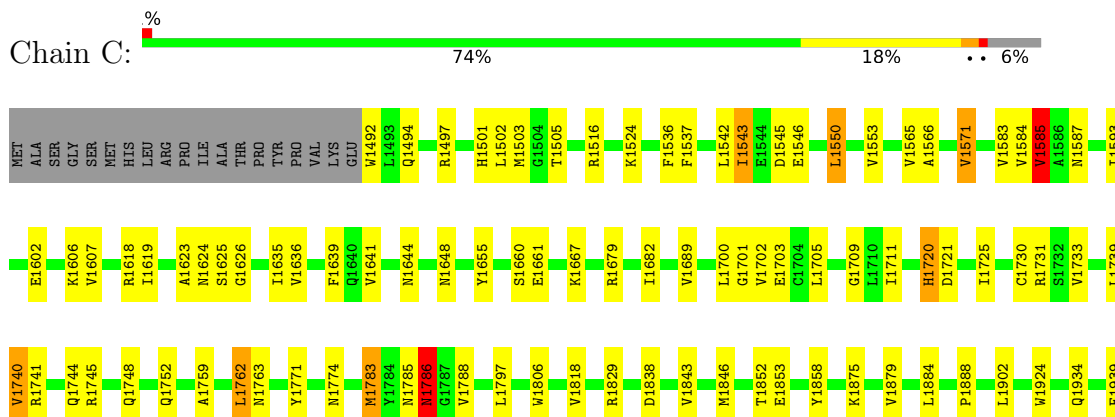
3 Residue-property plots

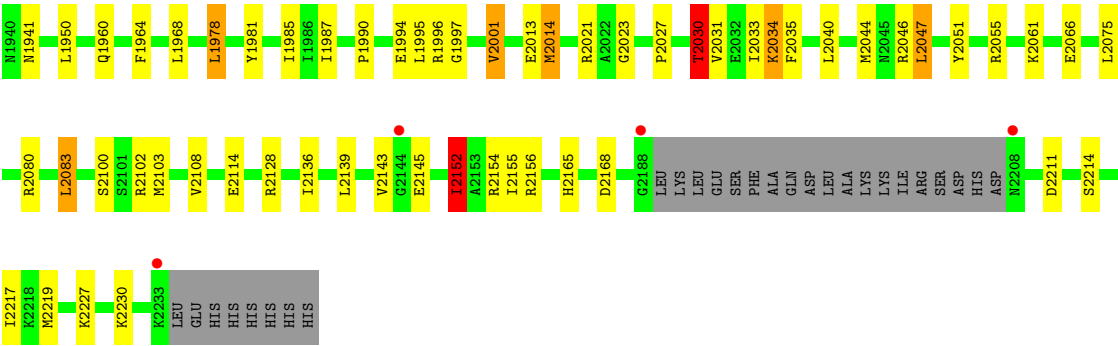
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Acetyl-CoA carboxylase



- Molecule 1: Acetyl-CoA carboxylase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	94.39Å 137.79Å 184.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.31 – 2.89 42.31 – 2.89	Depositor EDS
% Data completeness (in resolution range)	89.3 (42.31-2.89) 89.2 (42.31-2.89)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.91 (at 2.90Å)	Xtriage
Refinement program	BUSTER-TNT BUSTER 2.9.5	Depositor
R, R_{free}	0.154 , 0.207 0.160 , 0.216	Depositor DCC
R_{free} test set	2412 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	43.9	Xtriage
Anisotropy	0.291	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 64.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12185	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.13% of the height of the origin peak. No significant pseudotranslation is detected.*

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: 3W2

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	B	0.86	0/5958	1.38	29/8066 (0.4%)
1	C	0.86	2/5862 (0.0%)	1.37	32/7936 (0.4%)
All	All	0.86	2/11820 (0.0%)	1.37	61/16002 (0.4%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	1636	VAL	CA-CB	5.35	1.56	1.54
1	C	2014	MET	SD-CE	-5.17	1.66	1.79

All (61) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1785	ASN	CA-C-N	8.23	131.98	120.29
1	B	1785	ASN	C-N-CA	8.23	131.98	120.29
1	C	1785	ASN	CA-C-N	7.81	131.38	120.29
1	C	1785	ASN	C-N-CA	7.81	131.38	120.29
1	B	1786	ASN	CB-CA-C	-6.84	99.22	110.85
1	C	1740	VAL	N-CA-CB	6.78	118.48	110.55
1	C	1786	ASN	CB-CA-C	-6.63	99.57	110.85
1	B	1552	GLU	CB-CG-CD	6.55	123.73	112.60
1	C	1667	LYS	CA-C-N	6.39	129.13	120.38
1	C	1667	LYS	C-N-CA	6.39	129.13	120.38
1	B	2136	ILE	N-CA-C	-6.28	104.15	111.00
1	C	1545	ASP	CA-C-N	6.28	128.98	120.38
1	C	1545	ASP	C-N-CA	6.28	128.98	120.38
1	C	2031	VAL	CA-C-N	6.25	128.65	120.28
1	C	2031	VAL	C-N-CA	6.25	128.65	120.28
1	B	2034	LYS	N-CA-C	6.02	120.78	113.38
1	B	1973	PHE	CA-CB-CG	5.98	119.78	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1783	MET	N-CA-C	5.94	117.83	111.36
1	C	1788	VAL	N-CA-C	-5.92	104.96	110.53
1	B	2164	ASP	CA-CB-CG	5.91	118.51	112.60
1	B	1839	GLU	N-CA-C	5.82	118.89	109.40
1	C	1783	MET	N-CA-C	5.80	117.68	111.36
1	C	1585	VAL	N-CA-CB	5.74	117.88	110.99
1	B	1788	VAL	N-CA-C	-5.72	105.15	110.53
1	C	1702	VAL	N-CA-C	5.71	117.13	110.62
1	C	1635	ILE	CA-C-N	5.65	125.85	120.43
1	C	1635	ILE	C-N-CA	5.65	125.85	120.43
1	C	1786	ASN	CA-CB-CG	5.65	118.25	112.60
1	B	1585	VAL	N-CA-CB	5.60	117.71	110.99
1	C	2047	LEU	N-CA-C	5.52	120.02	113.12
1	C	1939	PHE	CA-CB-CG	5.49	119.29	113.80
1	C	2034	LYS	N-CA-C	5.47	120.83	113.72
1	C	2152	ILE	N-CA-CB	5.46	120.66	110.77
1	B	1545	ASP	CA-C-N	5.46	127.86	120.38
1	B	1545	ASP	C-N-CA	5.46	127.86	120.38
1	C	2051	TYR	CA-C-N	5.43	127.50	120.44
1	C	2051	TYR	C-N-CA	5.43	127.50	120.44
1	B	1667	LYS	CA-C-N	5.41	127.78	120.38
1	B	1667	LYS	C-N-CA	5.41	127.78	120.38
1	B	1635	ILE	CA-C-N	5.40	125.61	120.43
1	B	1635	ILE	C-N-CA	5.40	125.61	120.43
1	B	2031	VAL	CA-C-N	5.40	127.51	120.28
1	B	2031	VAL	C-N-CA	5.40	127.51	120.28
1	C	2080	ARG	CA-C-N	5.34	127.44	120.28
1	C	2080	ARG	C-N-CA	5.34	127.44	120.28
1	B	2030	THR	CB-CA-C	5.24	119.75	110.85
1	B	1960	GLN	N-CA-C	5.21	117.38	111.02
1	C	2030	THR	CB-CA-C	5.19	119.67	110.85
1	B	1909	ASN	CA-CB-CG	5.17	117.77	112.60
1	C	1545	ASP	CA-CB-CG	5.13	117.73	112.60
1	C	1644	ASN	N-CA-C	-5.12	105.78	111.36
1	C	1720	HIS	CA-C-N	5.11	129.25	120.71
1	C	1720	HIS	C-N-CA	5.11	129.25	120.71
1	B	1843	VAL	N-CA-CB	5.07	116.80	110.47
1	B	2073	LYS	CA-C-N	5.05	131.19	121.54
1	B	2073	LYS	C-N-CA	5.05	131.19	121.54
1	C	1660	SER	CA-C-N	5.02	126.96	120.44
1	C	1660	SER	C-N-CA	5.02	126.96	120.44
1	B	2094	ALA	CA-C-N	5.01	126.99	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	2094	ALA	C-N-CA	5.01	126.99	120.28
1	B	1689	VAL	N-CA-CB	5.00	116.25	110.49

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	B	5834	0	5756	74	0
1	C	5744	0	5663	67	0
2	B	30	0	25	1	0
2	C	30	0	25	1	0
3	B	284	0	0	6	0
3	C	263	0	0	4	0
All	All	12185	0	11469	124	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 5.

All (124) 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:B:1763:ASN:HD21	1:B:1771:TYR:H	1.22	0.82
1:C:1763:ASN:HD21	1:C:1771:TYR:H	1.24	0.82
1:B:2046:ARG:NH2	1:C:1639:PHE:O	2.20	0.73
1:B:1741:ARG:HH22	1:B:1934:GLN:HE22	1.36	0.73
1:B:1587:ASN:HD22	1:B:1623:ALA:H	1.40	0.70
1:B:1612:ARG:O	1:B:1814:ARG:NH2	2.27	0.68
1:C:1587:ASN:HD22	1:C:1623:ALA:H	1.42	0.67
1:B:1722:ILE:O	3:B:4317:HOH:O	2.13	0.66
1:C:2100:SER:HA	1:C:2103:MET:HE3	1.80	0.64
1:B:1745:ARG:NH2	3:B:4317:HOH:O	2.31	0.64
1:B:1730:CYS:HA	1:B:1752:GLN:NE2	2.13	0.64
1:C:1550:LEU:HD21	1:C:1607:VAL:HG22	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1494:GLN:HE21	1:B:1496:LYS:H	1.45	0.63
1:B:1639:PHE:O	1:C:2046:ARG:NH2	2.25	0.63
1:C:2044:MET:HE1	1:C:2083:LEU:HD13	1.81	0.62
1:C:1625:SER:HB3	1:C:1731:ARG:HH21	1.63	0.62
1:B:2136:ILE:HD11	1:B:2152:ILE:HG23	1.80	0.62
1:B:2054:LEU:HB3	1:B:2075:LEU:HG	1.81	0.61
1:C:1730:CYS:HA	1:C:1752:GLN:NE2	2.15	0.61
1:B:2131:ASN:HB3	1:B:2175:ILE:HG21	1.83	0.60
1:B:1624:ASN:HD22	1:B:1626:GLY:H	1.48	0.60
1:B:2033:ILE:HG22	1:B:2034:LYS:HG2	1.84	0.59
1:B:1625:SER:HB3	1:B:1731:ARG:HH21	1.65	0.59
1:C:1741:ARG:HH22	1:C:1934:GLN:HE22	1.51	0.59
1:C:1759:ALA:H	1:C:1774:ASN:ND2	2.01	0.59
1:C:1624:ASN:HD22	1:C:1626:GLY:H	1.51	0.58
1:B:1491:GLU:OE2	1:B:1501:HIS:HD2	1.86	0.58
1:C:1492:TRP:N	3:C:4210:HOH:O	2.35	0.58
1:C:2033:ILE:HG22	1:C:2034:LYS:HG2	1.85	0.58
1:B:1759:ALA:H	1:B:1774:ASN:ND2	2.02	0.58
1:B:1964:PHE:O	1:C:1786:ASN:ND2	2.36	0.58
1:C:1997:GLY:O	1:C:2001:VAL:HG12	2.04	0.58
1:B:1730:CYS:HA	1:B:1752:GLN:HE21	1.68	0.57
1:B:2100:SER:HA	1:B:2103:MET:HE3	1.86	0.57
1:C:2136:ILE:HD11	1:C:2152:ILE:HG23	1.87	0.56
1:C:1537:PHE:HD2	1:C:1571:VAL:HG13	1.71	0.55
1:B:1987:ILE:HB	1:B:2014:MET:HG3	1.87	0.55
1:B:2136:ILE:HD11	1:B:2152:ILE:CG2	2.35	0.55
1:C:1745:ARG:HG2	1:C:1806:TRP:CZ2	2.41	0.55
2:B:4000:3W2:H10	2:B:4000:3W2:C14	2.37	0.55
1:B:1537:PHE:HD2	1:B:1571:VAL:HG13	1.72	0.55
1:C:1542:LEU:HD13	1:C:1550:LEU:HD23	1.88	0.55
1:C:1730:CYS:HA	1:C:1752:GLN:HE21	1.72	0.55
1:B:1786:ASN:ND2	1:C:1964:PHE:O	2.40	0.54
1:B:1997:GLY:HA2	1:C:1705:LEU:HD22	1.89	0.54
1:B:1997:GLY:O	1:B:2001:VAL:HG12	2.08	0.54
1:B:1537:PHE:CD2	1:B:1571:VAL:HG13	2.43	0.54
1:B:1705:LEU:HD22	1:C:1997:GLY:HA2	1.88	0.54
1:C:1987:ILE:HB	1:C:2014:MET:HG3	1.90	0.54
1:B:1631:MET:HE1	1:C:2035:PHE:CD2	2.43	0.53
1:B:1745:ARG:HG2	1:B:1806:TRP:CZ2	2.44	0.53
1:C:1537:PHE:CD2	1:C:1571:VAL:HG13	2.43	0.53
1:B:2102:ARG:NH2	1:C:1703:GLU:OE1	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2013:GLU:HG2	3:C:4307:HOH:O	2.08	0.51
1:B:1678:GLU:HB3	1:B:1689:VAL:HG13	1.92	0.51
1:B:2164:ASP:H	1:B:2170:GLN:NE2	2.09	0.51
1:B:1741:ARG:HH22	1:B:1934:GLN:NE2	2.06	0.50
1:B:1765:VAL:HG21	2:C:4000:3W2:C3	2.42	0.50
1:C:1741:ARG:HH22	1:C:1934:GLN:NE2	2.10	0.49
1:B:1706:ARG:HD2	1:C:2108:VAL:HG12	1.95	0.49
1:B:1703:GLU:OE1	1:C:2102:ARG:NH2	2.47	0.48
1:C:1655:TYR:CE1	1:C:1689:VAL:HG22	2.49	0.48
1:C:1505:THR:HB	1:C:1730:CYS:HB2	1.95	0.48
1:B:1509:TYR:CB	1:B:1557:PRO:HB3	2.44	0.47
1:C:1543:ILE:HG12	1:C:1553:VAL:HG21	1.95	0.47
1:B:1997:GLY:HA2	1:C:1705:LEU:CD2	2.44	0.47
1:C:1711:ILE:HD12	1:C:1739:LEU:HD11	1.97	0.47
1:B:1481:ARG:HA	1:B:1482:PRO:HA	1.72	0.46
1:C:2156:ARG:HB3	1:C:2165:HIS:CE1	2.51	0.46
1:B:1505:THR:HB	1:B:1730:CYS:HB2	1.97	0.46
1:B:1624:ASN:ND2	1:B:1733:VAL:H	2.13	0.46
1:B:1711:ILE:HD12	1:B:1739:LEU:HD11	1.96	0.46
1:B:1703:GLU:CD	1:C:2102:ARG:HH22	2.24	0.46
1:B:2128:ARG:HE	1:B:2132:GLU:CD	2.24	0.46
1:B:2138:ARG:NH1	1:B:2186:LEU:HB3	2.31	0.46
1:B:1705:LEU:CD2	1:C:1997:GLY:HA2	2.46	0.45
1:B:1497:ARG:HD3	1:B:1510:ASP:OD2	2.15	0.45
1:C:1624:ASN:ND2	1:C:1733:VAL:H	2.15	0.45
1:C:1996:ARG:HA	1:C:2023:GLY:O	2.17	0.45
1:B:1909:ASN:HD21	1:B:1911:ASN:HB2	1.82	0.45
1:C:1994:GLU:HA	1:C:2021:ARG:O	2.16	0.45
1:C:1501:HIS:HE1	3:C:4335:HOH:O	2.00	0.45
1:C:2055:ARG:HG3	1:C:2075:LEU:HD11	1.99	0.45
1:B:1994:GLU:HA	1:B:2021:ARG:O	2.17	0.44
1:B:2102:ARG:HH22	1:C:1703:GLU:CD	2.24	0.44
1:C:1720:HIS:HA	1:C:1941:ASN:HD22	1.81	0.44
1:B:1566:ALA:HA	1:B:1584:VAL:O	2.17	0.44
1:C:2128:ARG:HD2	1:C:2168:ASP:OD1	2.18	0.44
1:C:1585:VAL:HG13	1:C:1607:VAL:HG11	2.00	0.44
1:C:1818:VAL:HB	1:C:1888:PRO:HG2	1.99	0.44
1:B:1961:ARG:HG3	3:C:4147:HOH:O	2.17	0.44
1:C:1566:ALA:HA	1:C:1584:VAL:O	2.18	0.44
1:B:2134:TYR:HE2	1:B:2179:TYR:CZ	2.36	0.43
1:C:1748:GLN:HE22	1:C:1783:MET:HB2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1995:LEU:HD12	1:B:1995:LEU:HA	1.94	0.43
1:B:1996:ARG:HA	1:B:2023:GLY:O	2.18	0.43
1:B:1835:PRO:HA	3:B:4230:HOH:O	2.19	0.43
1:B:2227:LYS:HA	1:B:2230:LYS:HE3	2.01	0.43
1:B:1678:GLU:O	1:B:1689:VAL:HG12	2.19	0.43
1:B:1720:HIS:HA	1:B:1941:ASN:HD22	1.83	0.42
1:B:1989:ILE:HG12	1:B:1995:LEU:HD22	2.01	0.42
1:B:2164:ASP:HB3	1:B:2170:GLN:NE2	2.34	0.42
1:B:1981:TYR:CG	1:B:1985:ILE:HD11	2.54	0.42
1:B:1508:VAL:HG22	3:B:4299:HOH:O	2.19	0.42
1:B:2024:VAL:HG23	1:C:1701:GLY:HA2	2.02	0.42
1:B:2073:LYS:NZ	3:B:4217:HOH:O	2.52	0.42
1:C:1981:TYR:CG	1:C:1985:ILE:HD11	2.55	0.42
1:B:1501:HIS:HE1	3:B:4104:HOH:O	2.03	0.42
1:C:2227:LYS:HA	1:C:2230:LYS:HE3	2.02	0.42
1:B:1818:VAL:HB	1:B:1888:PRO:HG2	2.01	0.42
1:C:1978:LEU:HD12	1:C:1978:LEU:HA	1.94	0.42
1:B:2004:ASP:HB3	1:C:1709:GLY:HA3	2.01	0.42
1:B:1776:GLN:O	1:C:1960:GLN:HG3	2.19	0.41
1:B:2047:LEU:HD23	1:C:1641:VAL:HG23	2.02	0.41
1:C:1537:PHE:HD2	1:C:1571:VAL:CG1	2.33	0.41
1:C:2027:PRO:HA	1:C:2030:THR:HG23	2.02	0.41
1:B:2028[B]:GLU:H	1:B:2028[B]:GLU:CD	2.29	0.41
1:C:1762:LEU:HD12	1:C:1762:LEU:HA	1.96	0.41
1:B:1978:LEU:HD12	1:B:1978:LEU:HA	1.94	0.40
1:C:1846:MET:HE1	1:C:1990:PRO:HB2	2.03	0.40
1:C:1655:TYR:CD1	1:C:1689:VAL:HG13	2.57	0.40
1:C:2139:LEU:HD21	1:C:2154:ARG:HD2	2.03	0.40
1:C:1829:ARG:CZ	1:C:1858:TYR:HB3	2.52	0.40
1:C:1619:ILE:HG13	1:C:1725:ILE:CG2	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	B	728/769 (95%)	695 (96%)	28 (4%)	5 (1%)	18	48
1	C	719/769 (94%)	689 (96%)	25 (4%)	5 (1%)	18	48
All	All	1447/1538 (94%)	1384 (96%)	53 (4%)	10 (1%)	18	48

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1744	GLN
1	B	1875	LYS
1	C	1744	GLN
1	C	1875	LYS
1	B	2143	VAL
1	C	2145	GLU
1	B	1481	ARG
1	C	2143	VAL
1	B	1593	ILE
1	C	1593	ILE

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	B	616/658 (94%)	565 (92%)	51 (8%)	10	32
1	C	610/658 (93%)	557 (91%)	53 (9%)	9	30
All	All	1226/1316 (93%)	1122 (92%)	104 (8%)	10	31

All (104) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1480	LEU
1	B	1490	LYS
1	B	1497	ARG

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Mol	Chain	Res	Type
1	B	1499	LYS
1	B	1502	LEU
1	B	1503	MET
1	B	1508	VAL
1	B	1516	ARG
1	B	1524	LYS
1	B	1546	GLU
1	B	1565	VAL
1	B	1571	VAL
1	B	1583	VAL
1	B	1585	VAL
1	B	1602	GLU
1	B	1618	ARG
1	B	1661	GLU
1	B	1672	GLU
1	B	1689	VAL
1	B	1700	LEU
1	B	1721	ASP
1	B	1762	LEU
1	B	1764	LYS
1	B	1786	ASN
1	B	1792	THR
1	B	1797	LEU
1	B	1826	THR
1	B	1838	ASP
1	B	1843	VAL
1	B	1852	THR
1	B	1853	GLU
1	B	1879	VAL
1	B	1924	TRP
1	B	1968	LEU
1	B	1978	LEU
1	B	1995	LEU
1	B	2001	VAL
1	B	2025	LEU
1	B	2028[A]	GLU
1	B	2028[B]	GLU
1	B	2030	THR
1	B	2038	GLU
1	B	2054	LEU
1	B	2075	LEU
1	B	2114	GLU

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Mol	Chain	Res	Type
1	B	2143	VAL
1	B	2145	GLU
1	B	2186	LEU
1	B	2191	LEU
1	B	2198	LEU
1	B	2202	ILE
1	C	1494	GLN
1	C	1497	ARG
1	C	1502	LEU
1	C	1503	MET
1	C	1516	ARG
1	C	1524	LYS
1	C	1536	PHE
1	C	1543	ILE
1	C	1546	GLU
1	C	1550	LEU
1	C	1565	VAL
1	C	1571	VAL
1	C	1583	VAL
1	C	1585	VAL
1	C	1602	GLU
1	C	1606	LYS
1	C	1618	ARG
1	C	1648	ASN
1	C	1661	GLU
1	C	1679	ARG
1	C	1682	ILE
1	C	1700	LEU
1	C	1721	ASP
1	C	1740	VAL
1	C	1762	LEU
1	C	1786	ASN
1	C	1797	LEU
1	C	1838	ASP
1	C	1843	VAL
1	C	1852	THR
1	C	1853	GLU
1	C	1879	VAL
1	C	1884	LEU
1	C	1902	LEU
1	C	1924	TRP
1	C	1950	LEU

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Mol	Chain	Res	Type
1	C	1968	LEU
1	C	1978	LEU
1	C	1995	LEU
1	C	2001	VAL
1	C	2030	THR
1	C	2040	LEU
1	C	2047	LEU
1	C	2061	LYS
1	C	2066	GLU
1	C	2083	LEU
1	C	2114	GLU
1	C	2152	ILE
1	C	2155	ILE
1	C	2211	ASP
1	C	2214	SER
1	C	2217	ILE
1	C	2219	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (47) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1494	GLN
1	B	1501	HIS
1	B	1587	ASN
1	B	1605	ASN
1	B	1624	ASN
1	B	1640	GLN
1	B	1648	ASN
1	B	1673	ASN
1	B	1683	ASN
1	B	1748	GLN
1	B	1752	GLN
1	B	1763	ASN
1	B	1774	ASN
1	B	1786	ASN
1	B	1815	ASN
1	B	1909	ASN
1	B	1919	GLN
1	B	1922	GLN
1	B	1934	GLN
1	B	1937	ASN
1	B	1941	ASN

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Mol	Chain	Res	Type
1	B	1983	GLN
1	B	2045	ASN
1	B	2165	HIS
1	B	2170	GLN
1	B	2178	ASN
1	C	1517	GLN
1	C	1587	ASN
1	C	1605	ASN
1	C	1624	ASN
1	C	1640	GLN
1	C	1673	ASN
1	C	1748	GLN
1	C	1752	GLN
1	C	1763	ASN
1	C	1774	ASN
1	C	1786	ASN
1	C	1815	ASN
1	C	1909	ASN
1	C	1911	ASN
1	C	1922	GLN
1	C	1934	GLN
1	C	1937	ASN
1	C	1941	ASN
1	C	2068	HIS
1	C	2070	GLN
1	C	2170	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

2 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	3W2	C	4000	-	31,34,34	2.06	8 (25%)	36,53,53	2.01	10 (27%)
2	3W2	B	4000	-	31,34,34	1.81	7 (22%)	36,53,53	2.30	12 (33%)

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	3W2	C	4000	-	-	0/14/40/40	0/5/5/5
2	3W2	B	4000	-	-	0/14/40/40	0/5/5/5

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	4000	3W2	N25-N24	-6.98	1.29	1.37
2	B	4000	3W2	N25-N24	-6.04	1.30	1.37
2	C	4000	3W2	C27-N25	-5.68	1.45	1.50
2	B	4000	3W2	C17-N21	3.18	1.37	1.33
2	B	4000	3W2	C27-N25	-3.17	1.47	1.50
2	C	4000	3W2	C17-N21	3.15	1.37	1.33
2	B	4000	3W2	C23-N24	-2.80	1.30	1.34
2	B	4000	3W2	C26-N25	2.60	1.37	1.35
2	C	4000	3W2	C8-C1	2.51	1.55	1.53
2	C	4000	3W2	C23-N24	-2.28	1.31	1.34
2	B	4000	3W2	N20-N21	2.23	1.40	1.36
2	C	4000	3W2	C26-N25	2.21	1.37	1.35
2	B	4000	3W2	C19-N20	-2.15	1.31	1.34
2	C	4000	3W2	C19-N20	-2.14	1.31	1.34
2	C	4000	3W2	N20-N21	2.09	1.40	1.36

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	4000	3W2	C6-C1-C8	-6.96	106.31	111.92
2	C	4000	3W2	C6-C1-C8	-6.38	106.78	111.92
2	B	4000	3W2	O7-C22-C26	6.02	132.51	124.55
2	C	4000	3W2	O7-C22-C26	5.19	131.41	124.55
2	B	4000	3W2	C2-C1-C8	-5.05	107.86	111.92
2	C	4000	3W2	C12-C14-C18	-3.70	118.92	121.92
2	B	4000	3W2	C23-N24-N25	3.57	109.47	104.36
2	B	4000	3W2	C12-C14-C18	-3.30	119.25	121.92
2	C	4000	3W2	C9-C23-N24	2.87	131.85	127.00
2	B	4000	3W2	C2-C1-C6	2.63	113.15	109.54
2	C	4000	3W2	C23-N24-N25	2.63	108.12	104.36
2	B	4000	3W2	O7-C1-C8	2.60	112.78	109.61
2	B	4000	3W2	C9-C23-N24	2.59	131.38	127.00
2	B	4000	3W2	C26-N25-N24	-2.42	110.60	112.65
2	C	4000	3W2	C2-C3-N4	-2.30	106.52	110.82
2	C	4000	3W2	C19-N20-N21	-2.19	109.24	112.59
2	C	4000	3W2	C12-C11-N4	2.19	121.39	118.66
2	C	4000	3W2	C8-C9-C23	-2.15	113.95	117.43
2	B	4000	3W2	C29-C27-N25	2.15	110.53	107.88
2	B	4000	3W2	C5-N4-C3	2.08	116.92	112.68
2	C	4000	3W2	O7-C1-C2	2.02	110.05	106.28
2	B	4000	3W2	C12-C11-N4	2.01	121.18	118.66

There are no chirality outliers.

There are no torsion outliers.

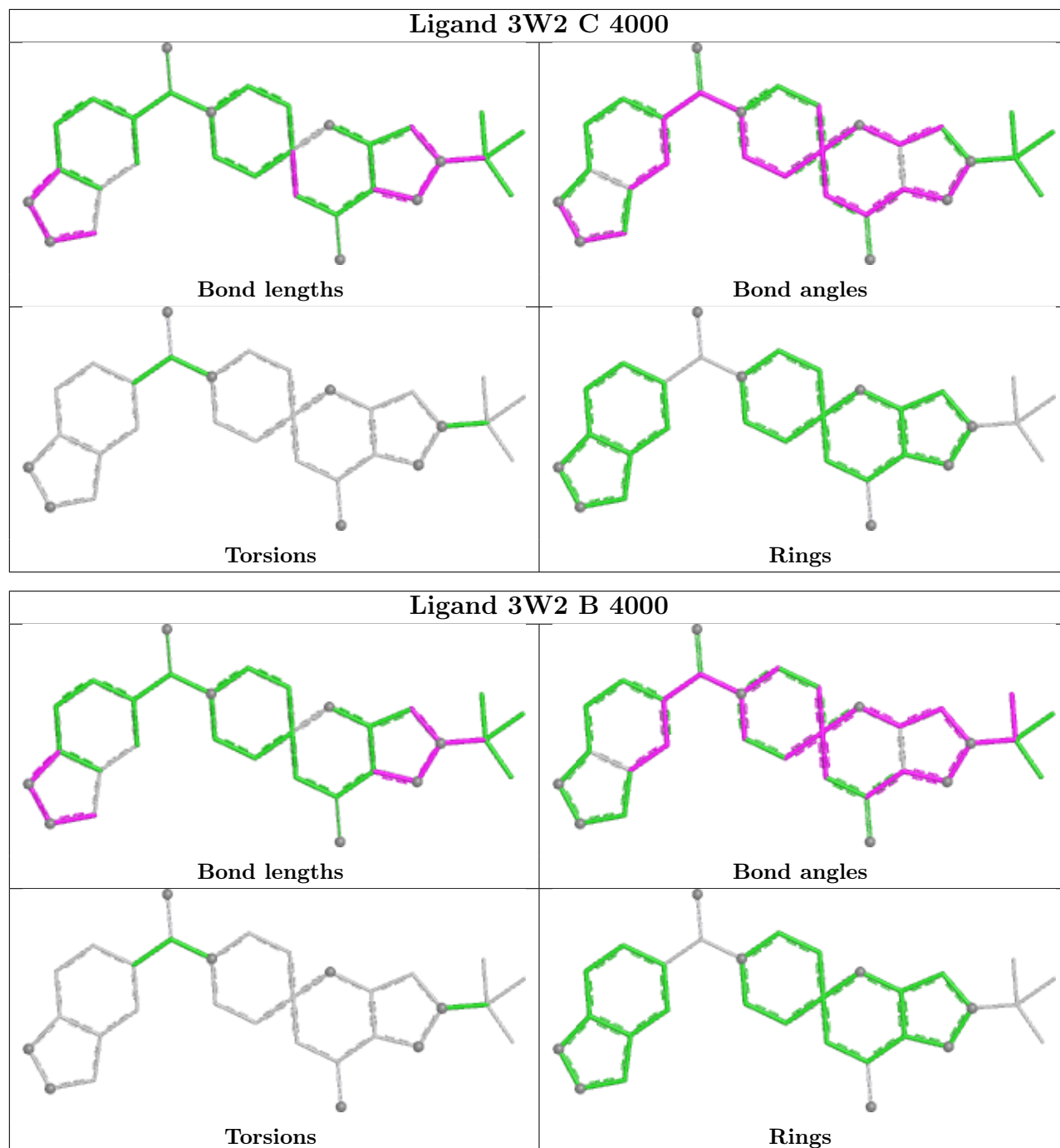
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	4000	3W2	1	0
2	B	4000	3W2	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 ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	B	733/769 (95%)	-0.51	10 (1%) 73 65	20, 42, 92, 118	1 (0%)
1	C	723/769 (94%)	-0.61	4 (0%) 85 81	18, 42, 77, 107	0
All	All	1456/1538 (94%)	-0.56	14 (0%) 79 73	18, 42, 85, 118	1 (0%)

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	2208	ASN	5.8
1	C	2188	GLY	4.6
1	B	2073	LYS	3.4
1	C	2144	GLY	3.1
1	B	2143	VAL	3.0
1	B	2216	VAL	2.8
1	B	2202	ILE	2.7
1	C	2233	LYS	2.6
1	B	2223	ASP	2.5
1	B	2210	ILE	2.3
1	B	2208	ASN	2.3
1	B	2211	ASP	2.3
1	B	2019	ASN	2.1
1	B	2234	LEU	2.1

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](#)

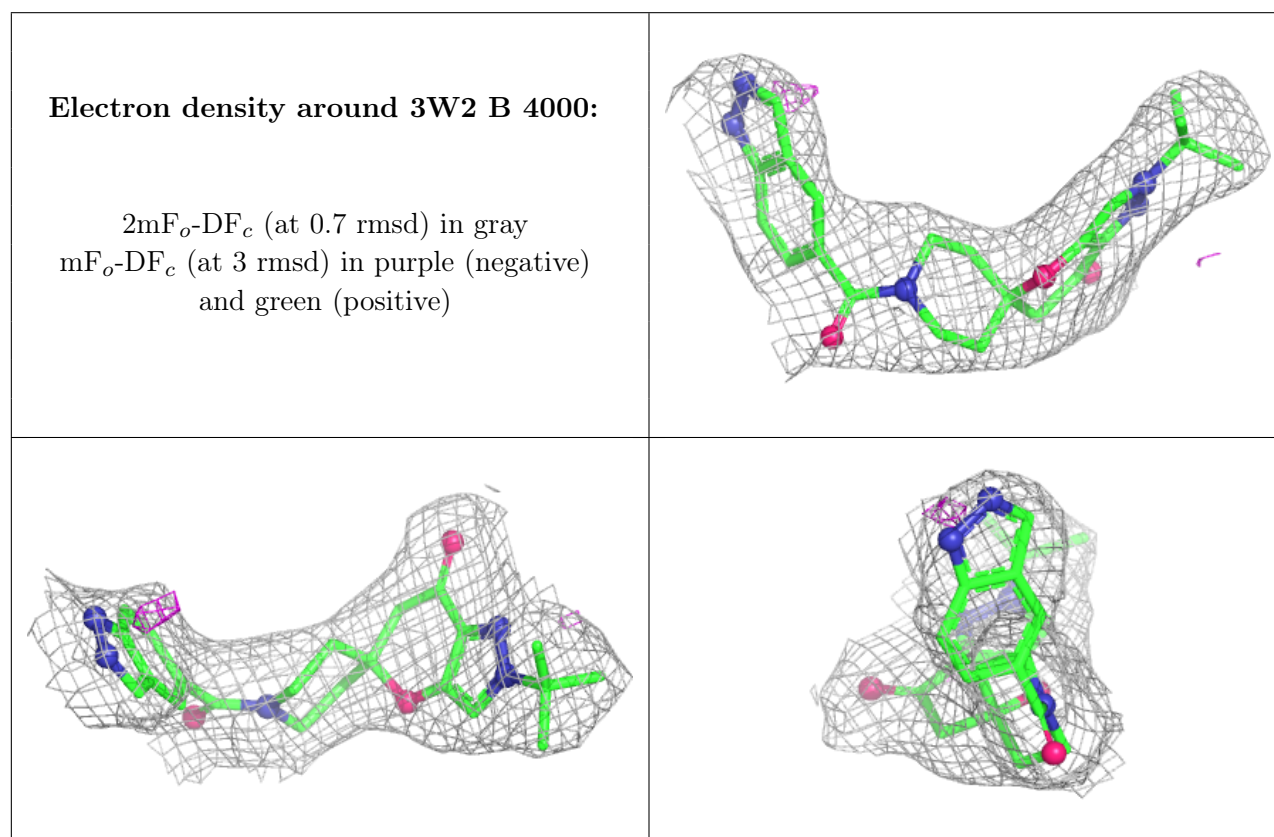
There are no oligosaccharides in this entry.

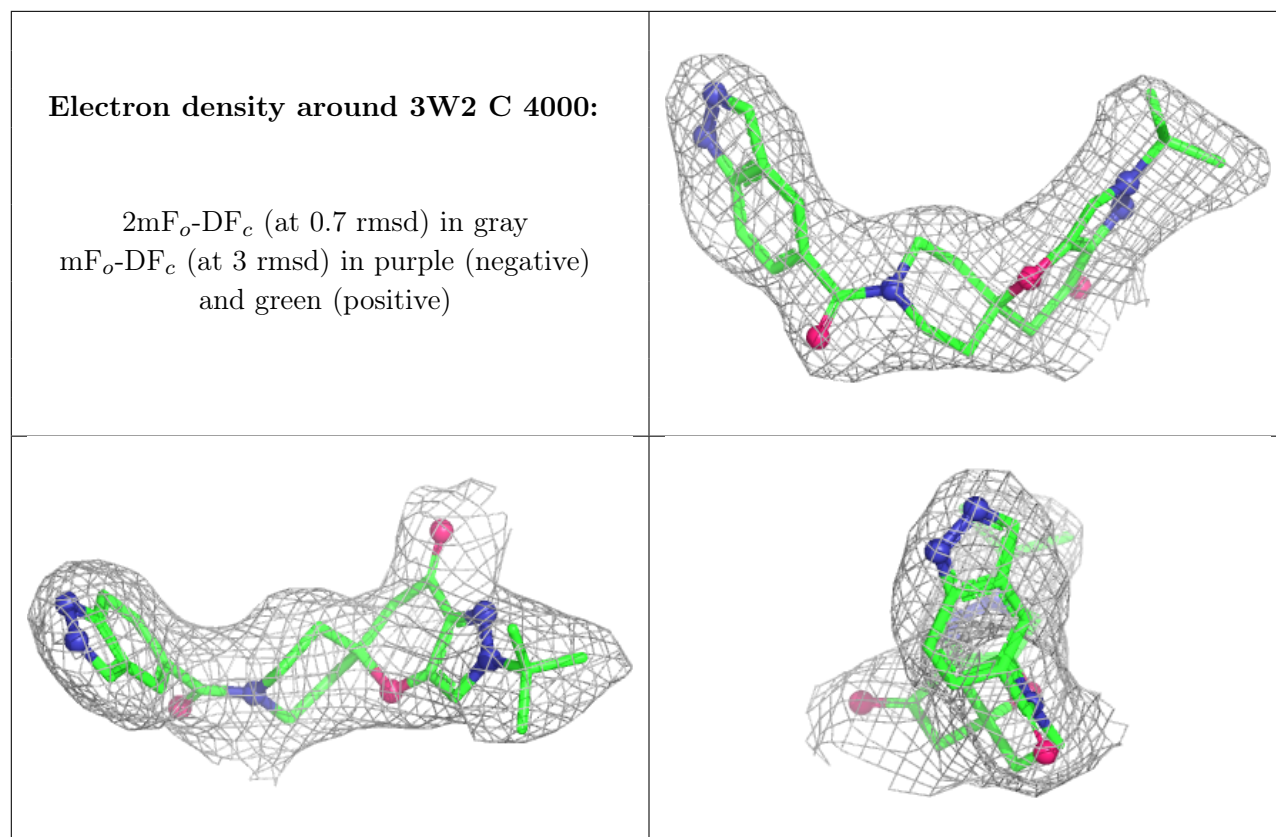
6.4 Ligands [i](#)

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	3W2	B	4000	30/30	0.97	0.07	33,38,45,45	0
2	3W2	C	4000	30/30	0.98	0.05	19,33,41,42	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.