



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 12:57 PM UTC

PDB ID : 1XL8 / pdb_00001xl8
Title : Crystal structure of mouse carnitine octanoyltransferase in complex with octanoylcarnitine
Authors : Jogl, G.; Hsiao, Y.S.; Tong, L.
Deposited on : 2004-09-30
Resolution : 2.20 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

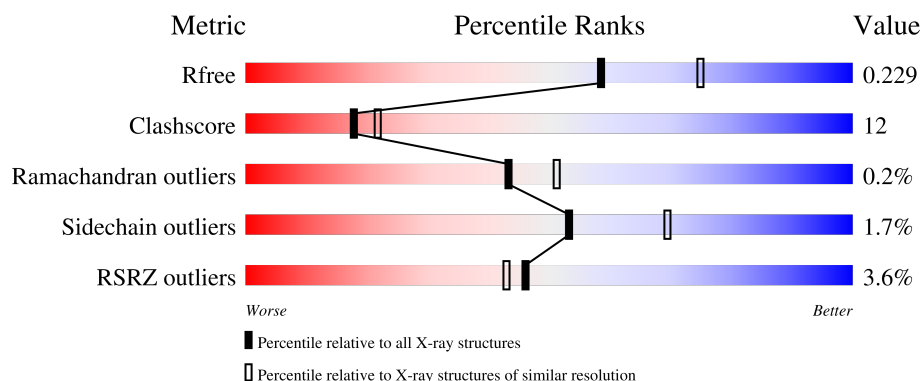
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	612	5% 68% 28% ..
1	B	612	2% 75% 22% ..

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10118 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 Peroxisomal carnitine O-octanoyltransferase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	591	Total	C	N	O	S	Se	0	0	0
			4776	3042	829	872	16	17			
1	B	600	Total	C	N	O	S	Se	0	2	0
			4857	3093	841	888	17	18			

There are 34 discrepancies between the modelled and reference sequences:

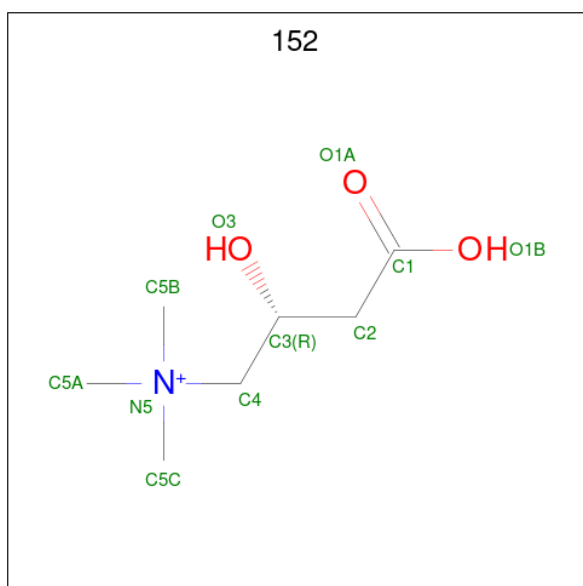
Chain	Residue	Modelled	Actual	Comment	Reference
A	127	MSE	MET	modified residue	UNP Q9DC50
A	128	MSE	MET	modified residue	UNP Q9DC50
A	156	MSE	MET	modified residue	UNP Q9DC50
A	161	MSE	MET	modified residue	UNP Q9DC50
A	177	MSE	MET	modified residue	UNP Q9DC50
A	296	MSE	MET	modified residue	UNP Q9DC50
A	333	MSE	MET	modified residue	UNP Q9DC50
A	335	MSE	MET	modified residue	UNP Q9DC50
A	443	MSE	MET	modified residue	UNP Q9DC50
A	469	MSE	MET	modified residue	UNP Q9DC50
A	483	MSE	MET	modified residue	UNP Q9DC50
A	493	MSE	MET	modified residue	UNP Q9DC50
A	494	MSE	MET	modified residue	UNP Q9DC50
A	558	MSE	MET	modified residue	UNP Q9DC50
A	595	MSE	MET	modified residue	UNP Q9DC50
A	603	MSE	MET	modified residue	UNP Q9DC50
A	607	MSE	MET	modified residue	UNP Q9DC50
B	127	MSE	MET	modified residue	UNP Q9DC50
B	128	MSE	MET	modified residue	UNP Q9DC50
B	156	MSE	MET	modified residue	UNP Q9DC50
B	161	MSE	MET	modified residue	UNP Q9DC50
B	177	MSE	MET	modified residue	UNP Q9DC50
B	296	MSE	MET	modified residue	UNP Q9DC50
B	333	MSE	MET	modified residue	UNP Q9DC50
B	335	MSE	MET	modified residue	UNP Q9DC50

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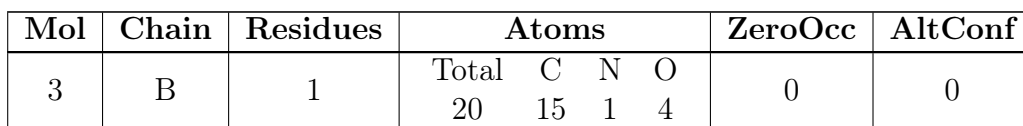
Chain	Residue	Modelled	Actual	Comment	Reference
B	443	MSE	MET	modified residue	UNP Q9DC50
B	469	MSE	MET	modified residue	UNP Q9DC50
B	483	MSE	MET	modified residue	UNP Q9DC50
B	493	MSE	MET	modified residue	UNP Q9DC50
B	494	MSE	MET	modified residue	UNP Q9DC50
B	558	MSE	MET	modified residue	UNP Q9DC50
B	595	MSE	MET	modified residue	UNP Q9DC50
B	603	MSE	MET	modified residue	UNP Q9DC50
B	607	MSE	MET	modified residue	UNP Q9DC50

- Molecule 2 is CARNITINE (CCD ID: 152) (formula: $C_7H_{16}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			11	7	1	3		

- Molecule 3 is OCTANOYLCARNITINE (CCD ID: OCB) (formula: $C_{15}H_{30}NO_4$).



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- The chemical structure of 2-methylpentane-2,4-diol (MPD) is shown. The molecule consists of a five-carbon chain. The second carbon (C2) is bonded to a methyl group (CM) and a hydroxyl group (OH, labeled O2). The fourth carbon (C4) is bonded to a hydroxyl group (OH, labeled O4) and a methyl group (C5). The third carbon (C3) is bonded to the second and fourth carbons. The labels C1, C2, C3, C4(S), and C5 are in green. The labels OH and O2 are in red. The label CM is in green. The label MPD is in black at the top.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total 8	C 6	O 2	0	0
4	B	1	Total 8	C 6	O 2	0	0
4	B	1	Total 8	C 6	O 2	0	0



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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			8	6	2		
4	B	1	Total	C	O	0	0
			8	6	2		

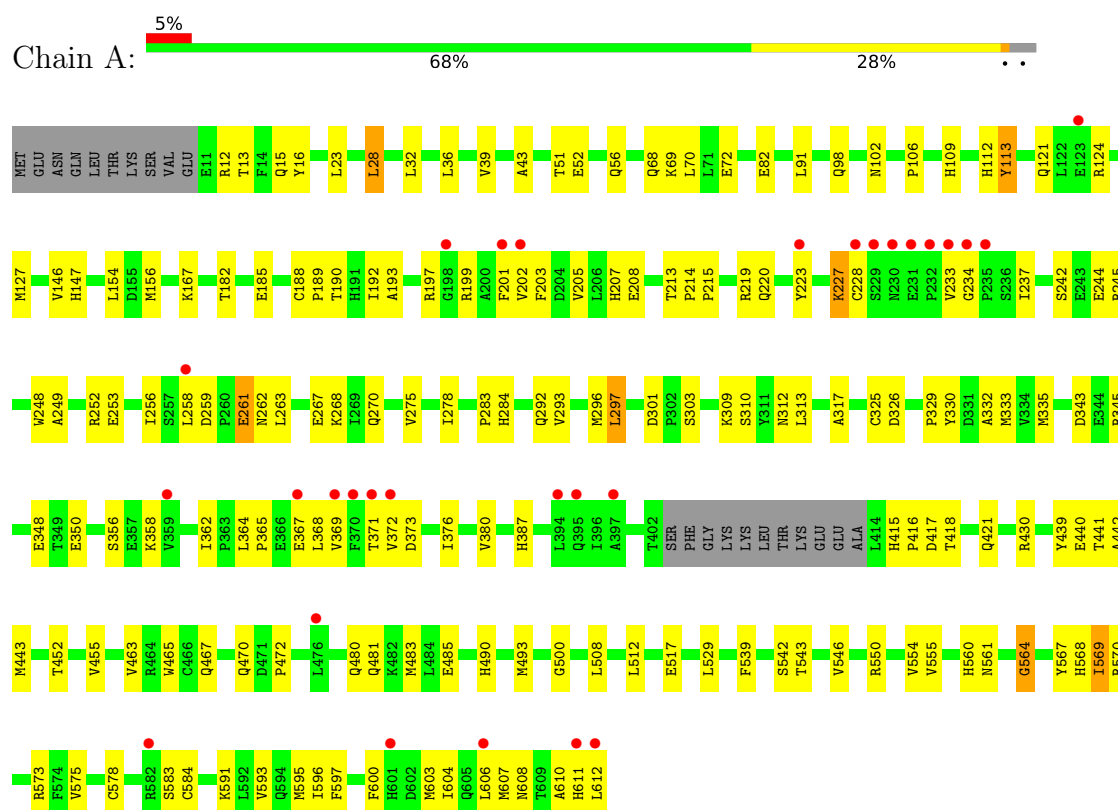
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	138	Total	O	0	0
			138	138		
5	B	276	Total	O	0	0
			276	276		

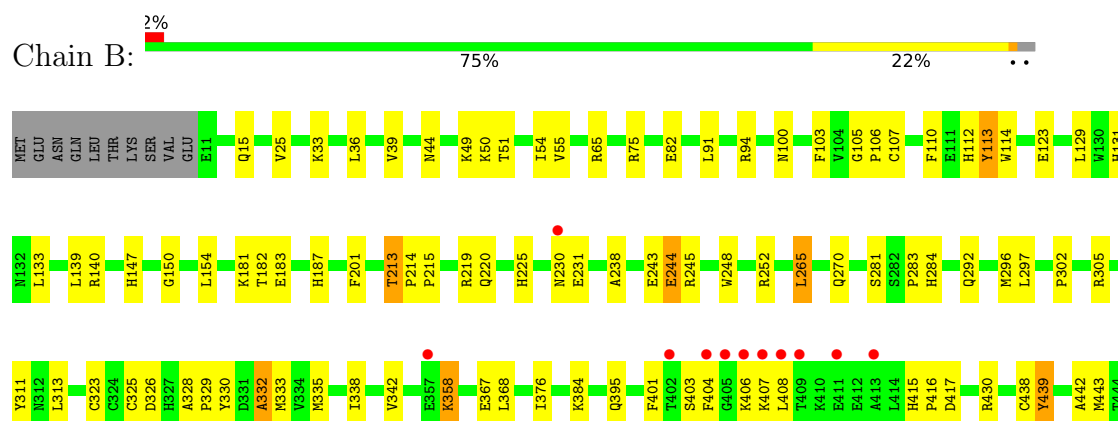
3 Residue-property plots

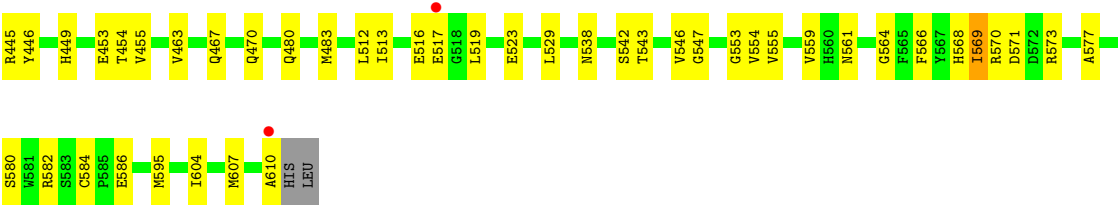
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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



• Molecule 1: Peroxisomal carnitine O-octanoyltransferase





4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	163.61Å 163.61Å 159.48Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.09 – 2.20 29.09 – 2.20	Depositor EDS
% Data completeness (in resolution range)	95.2 (29.09-2.20) 95.3 (29.09-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.23 (at 2.20Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.199 , 0.230 0.198 , 0.229	Depositor DCC
R_{free} test set	5806 reflections (7.20%)	wwPDB-VP
Wilson B-factor (Å ²)	27.7	Xtriage
Anisotropy	0.059	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 48.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.019 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10118	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.05% 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: MPD, 152, OCB

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	0.35	0/4884	0.85	11/6585 (0.2%)
1	B	0.41	0/4966	0.92	22/6694 (0.3%)
All	All	0.38	0/9850	0.88	33/13279 (0.2%)

There are no bond length outliers.

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	564	GLY	N-CA-C	-7.67	97.06	110.71
1	B	586	GLU	N-CA-C	7.04	118.60	111.07
1	B	244	GLU	N-CA-C	-6.84	100.32	110.23
1	B	245	ARG	N-CA-C	6.72	119.17	111.11
1	B	100	ASN	N-CA-C	6.69	121.27	113.18
1	B	543	THR	N-CA-C	6.60	118.97	109.14
1	A	332	ALA	N-CA-C	6.52	120.33	112.38
1	B	113	TYR	N-CA-C	6.39	120.34	112.54
1	A	244	GLU	N-CA-C	-6.03	101.48	110.23
1	B	91	LEU	N-CA-C	6.01	118.62	111.71
1	B	15	GLN	N-CA-C	5.98	118.59	111.71
1	B	243	GLU	N-CA-C	5.95	118.21	110.53
1	B	547	GLY	N-CA-C	5.92	119.28	111.52
1	B	332	ALA	N-CA-C	5.87	119.26	111.75
1	B	213	THR	N-CA-C	5.79	116.79	110.13
1	A	569	ILE	N-CA-C	5.70	116.09	108.11
1	B	446	TYR	N-CA-C	-5.67	105.24	111.82
1	A	113	TYR	N-CA-C	5.67	119.46	112.54
1	A	91	LEU	N-CA-C	5.67	118.23	111.71
1	A	452	THR	N-CA-C	5.66	117.58	109.14
1	B	569	ILE	N-CA-C	5.66	116.00	107.80
1	A	245	ARG	N-CA-C	5.62	118.13	111.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	150	GLY	N-CA-C	-5.62	99.86	113.18
1	B	25	VAL	N-CA-C	-5.42	101.55	107.73
1	B	333	MSE	N-CA-C	5.29	117.79	111.71
1	A	564	GLY	N-CA-C	-5.28	100.68	113.18
1	A	23	LEU	N-CA-C	-5.26	101.77	109.50
1	A	543	THR	N-CA-C	5.20	116.88	109.14
1	A	13	THR	N-CA-C	5.19	117.34	111.11
1	B	182	THR	N-CA-C	-5.11	103.94	110.53
1	B	438	CYS	N-CA-C	5.09	117.73	109.24
1	B	107	CYS	N-CA-C	-5.06	101.93	109.42
1	B	326	ASP	N-CA-C	-5.02	102.43	109.96

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	4776	0	4676	125	0
1	B	4857	0	4762	108	0
2	A	11	0	15	3	0
3	B	20	0	29	8	0
4	B	40	0	70	2	0
5	A	138	0	0	4	0
5	B	276	0	0	5	0
All	All	10118	0	9552	236	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 (236) 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:568:HIS:HE1	1:A:570:ARG:HE	1.15	0.91
1:A:219:ARG:HH21	1:A:220:GLN:HE22	1.20	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:568:HIS:HE1	1:B:570:ARG:HE	1.17	0.89
1:B:252:ARG:HH21	1:B:270:GLN:HE22	1.23	0.86
1:B:480:GLN:HG3	1:B:607:MSE:HE1	1.58	0.84
1:B:430:ARG:HE	1:B:470:GLN:HE22	1.25	0.83
1:A:604:ILE:HA	1:A:607:MSE:HE2	1.60	0.81
1:A:483:MSE:HE3	1:A:606:LEU:HD23	1.64	0.80
1:B:284:HIS:H	1:B:292:GLN:NE2	1.79	0.80
1:A:430:ARG:HE	1:A:470:GLN:NE2	1.80	0.79
1:A:345:ARG:HH21	1:A:348:GLU:CD	1.93	0.77
1:B:430:ARG:HE	1:B:470:GLN:NE2	1.83	0.77
1:A:430:ARG:HE	1:A:470:GLN:HE22	1.33	0.75
1:A:199:ARG:HH11	1:A:228:CYS:HB3	1.52	0.74
1:B:443:MSE:HE2	1:B:445:ARG:HD3	1.70	0.74
1:B:283:PRO:HA	1:B:292:GLN:HE21	1.53	0.73
1:A:199:ARG:NH1	1:A:228:CYS:HB3	2.05	0.72
1:B:65:ARG:HH22	1:B:519:LEU:HD11	1.55	0.72
1:B:154:LEU:HD13	1:B:443:MSE:HE1	1.71	0.72
1:A:416:PRO:HB2	1:A:569:ILE:HD13	1.72	0.70
1:A:600:PHE:O	1:A:604:ILE:HG12	1.92	0.70
1:B:404:PHE:CZ	1:B:604:ILE:HG13	2.27	0.69
1:B:416:PRO:HB2	1:B:569:ILE:HD13	1.73	0.69
1:B:325:CYS:SG	1:B:335[B]:MSE:HE3	2.34	0.68
1:B:219:ARG:HH21	1:B:220:GLN:HE22	1.42	0.67
1:B:284:HIS:H	1:B:292:GLN:HE21	1.43	0.67
1:A:292:GLN:HE21	1:A:296:MSE:HE1	1.59	0.67
1:A:112:HIS:CD2	1:A:113:TYR:H	2.14	0.65
1:A:542:SER:OG	2:A:613:152:H5C1	1.97	0.64
1:B:570:ARG:HD2	1:B:573:ARG:HH11	1.62	0.64
1:B:358:LYS:HB3	1:B:358:LYS:NZ	2.13	0.63
1:B:415:HIS:HD2	1:B:417:ASP:H	1.45	0.63
1:B:335[A]:MSE:SE	3:B:613:OCB:HAA3	2.48	0.62
1:A:154:LEU:HD13	1:A:443:MSE:HE1	1.81	0.62
1:B:395:GLN:HG2	1:B:582:ARG:HG3	1.80	0.62
1:B:65:ARG:NH2	1:B:519:LEU:HD11	2.14	0.62
1:A:603:MSE:O	1:A:607:MSE:HG3	1.99	0.62
1:A:219:ARG:NH2	1:A:220:GLN:HE22	1.93	0.62
1:A:421:GLN:NE2	1:A:440:GLU:HG3	2.15	0.61
1:B:395:GLN:HG2	1:B:582:ARG:CG	2.31	0.61
1:B:147:HIS:CD2	1:B:445:ARG:HH22	2.19	0.61
1:A:263:LEU:O	1:A:267:GLU:HG3	2.02	0.60
1:B:51:THR:OG1	1:B:529:LEU:HD12	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:568:HIS:CE1	1:A:570:ARG:HE	2.08	0.59
1:A:121:GLN:OE1	1:A:278:ILE:HG23	2.03	0.59
1:B:54:ILE:HG23	1:B:523:GLU:HG3	1.84	0.59
1:B:302:PRO:HG2	1:B:384:LYS:HG3	1.83	0.59
1:A:292:GLN:HG2	1:A:296:MSE:HE3	1.86	0.58
1:B:415:HIS:CD2	1:B:417:ASP:H	2.21	0.58
1:A:483:MSE:CE	1:A:606:LEU:HD23	2.33	0.57
1:B:311:TYR:CE1	1:B:335[B]:MSE:SE	3.08	0.57
1:A:259:ASP:HB3	1:A:262:ASN:ND2	2.20	0.57
1:A:292:GLN:HE21	1:A:296:MSE:CE	2.18	0.56
1:A:69:LYS:HE3	1:A:517:GLU:OE1	2.05	0.56
1:A:465:TRP:CZ2	1:A:483:MSE:HE2	2.40	0.56
1:A:604:ILE:HA	1:A:607:MSE:CE	2.34	0.56
1:A:442:ALA:HB2	1:A:455:VAL:HG23	1.88	0.55
1:B:358:LYS:HB3	1:B:358:LYS:HZ3	1.72	0.55
1:A:465:TRP:HZ2	1:A:483:MSE:HE2	1.71	0.55
1:A:608:ASN:O	1:A:611:HIS:HB2	2.07	0.55
1:B:33:LYS:NZ	5:B:775:HOH:O	2.40	0.55
1:A:109:HIS:HD2	1:A:343:ASP:OD1	1.90	0.55
1:B:407:LYS:CD	1:B:571:ASP:HB2	2.37	0.54
1:A:546:VAL:CG2	1:A:568:HIS:HB3	2.37	0.54
1:B:332:ALA:CB	3:B:613:OCB:HAD2	2.36	0.54
1:A:283:PRO:HA	1:A:292:GLN:HE21	1.72	0.54
2:A:613:152:O3	2:A:613:152:H5B3	2.08	0.54
3:B:613:OCB:OAK	3:B:613:OCB:HAJ3	2.06	0.54
1:A:36:LEU:HD21	1:A:52:GLU:HA	1.89	0.54
1:A:463:VAL:O	1:A:467:GLN:HG3	2.07	0.53
1:B:112:HIS:CD2	1:B:113:TYR:H	2.26	0.53
1:B:480:GLN:NE2	1:B:610:ALA:HB1	2.23	0.53
1:A:201:PHE:CE2	1:A:367:GLU:HB2	2.43	0.53
1:B:36:LEU:HD13	1:B:55:VAL:HG21	1.91	0.53
1:B:75:ARG:HG2	4:B:616:MPD:HM1	1.91	0.53
1:B:404:PHE:CE2	1:B:604:ILE:HG13	2.43	0.53
1:A:483:MSE:HE2	1:A:603:MSE:HG2	1.90	0.52
1:B:439:TYR:C	1:B:439:TYR:CD1	2.88	0.52
1:B:335[A]:MSE:CE	3:B:613:OCB:HAA3	2.39	0.52
1:B:554:VAL:CG1	1:B:577:ALA:HB1	2.40	0.52
1:A:546:VAL:HG22	1:A:567:TYR:O	2.09	0.52
1:A:52:GLU:O	1:A:56:GLN:HG3	2.10	0.52
1:A:591:LYS:O	1:A:595:MSE:HG2	2.10	0.52
1:B:512:LEU:O	1:B:516:GLU:HG3	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:242:SER:HB2	1:A:387:HIS:CD2	2.45	0.51
1:A:233:VAL:HG12	1:A:234:GLY:N	2.23	0.51
1:A:416:PRO:CB	1:A:569:ILE:HD13	2.41	0.51
1:A:51:THR:OG1	1:A:529:LEU:HD12	2.10	0.51
1:A:68:GLN:O	1:A:72:GLU:HG3	2.10	0.51
1:A:283:PRO:HA	1:A:292:GLN:NE2	2.25	0.51
1:B:480:GLN:HE22	1:B:610:ALA:HB1	1.76	0.51
1:B:404:PHE:CB	1:B:408:LEU:HD13	2.41	0.51
1:A:593:VAL:O	1:A:596:ILE:HG22	2.11	0.51
1:B:555:VAL:HG22	1:B:566:PHE:CZ	2.46	0.51
1:A:546:VAL:HG23	1:A:568:HIS:HB3	1.92	0.50
1:B:517:GLU:HB2	1:B:519:LEU:HG	1.93	0.50
1:B:36:LEU:O	1:B:39:VAL:HG22	2.10	0.50
1:A:43:ALA:HB2	1:A:529:LEU:HD21	1.94	0.50
1:A:560:HIS:HE1	1:A:583:SER:OG	1.93	0.50
1:A:439:TYR:CD1	1:A:439:TYR:C	2.90	0.49
1:A:252:ARG:O	1:A:256:ILE:HG13	2.12	0.49
1:B:442:ALA:HB2	1:B:455:VAL:HG23	1.94	0.49
1:A:12:ARG:O	1:A:15:GLN:HG2	2.12	0.49
1:B:546:VAL:O	1:B:546:VAL:HG12	2.13	0.49
1:A:219:ARG:NH2	1:A:362:ILE:O	2.38	0.49
1:B:554:VAL:CG1	1:B:577:ALA:CB	2.91	0.49
1:A:98:GLN:O	1:A:102:ASN:HB2	2.13	0.48
1:A:223:TYR:CD1	1:A:365:PRO:HD2	2.48	0.48
1:A:192:ILE:HD11	1:A:203:PHE:CZ	2.48	0.48
1:A:568:HIS:HE1	1:A:570:ARG:NE	1.97	0.47
1:B:463:VAL:O	1:B:467:GLN:HG3	2.13	0.47
1:B:607:MSE:HA	1:B:607:MSE:HE2	1.96	0.47
1:A:415:HIS:CD2	1:A:417:ASP:H	2.31	0.47
1:B:415:HIS:HD2	1:B:417:ASP:N	2.12	0.47
1:B:323[A]:CYS:HB2	1:B:335[A]:MSE:HE2	1.96	0.47
1:B:406:LYS:HG2	1:B:571:ASP:HA	1.95	0.47
1:B:407:LYS:HD2	1:B:571:ASP:HB2	1.97	0.47
1:A:124:ARG:HA	1:A:127:MSE:HE3	1.96	0.47
1:A:356:SER:OG	1:A:358:LYS:HG2	2.14	0.47
1:B:44:ASN:OD1	1:B:44:ASN:C	2.58	0.47
1:B:401:PHE:CE2	1:B:403:SER:HB2	2.49	0.47
1:B:483:MSE:HE2	1:B:607:MSE:HE3	1.97	0.47
1:A:249:ALA:O	1:A:253:GLU:HG3	2.13	0.47
1:B:110:PHE:HA	1:B:114:TRP:O	2.14	0.47
1:A:252:ARG:HH21	1:A:270:GLN:HE22	1.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:542:SER:OG	3:B:613:OCB:HAT1	2.14	0.46
1:A:293:VAL:O	1:A:297:LEU:HB2	2.16	0.46
1:A:36:LEU:O	1:A:39:VAL:HG22	2.15	0.46
1:A:275:VAL:HG23	1:A:309:LYS:HG2	1.98	0.46
1:A:214:PRO:HB2	1:A:215:PRO:HD3	1.96	0.46
1:A:197:ARG:O	1:A:199:ARG:HG3	2.15	0.46
1:B:265:LEU:HG	1:B:368:LEU:HB3	1.96	0.46
1:B:220:GLN:HE21	1:B:220:GLN:HA	1.80	0.46
1:A:480:GLN:NE2	1:A:610:ALA:HB3	2.30	0.46
1:A:182:THR:OG1	1:A:185:GLU:HG3	2.16	0.45
1:B:408:LEU:HD23	1:B:408:LEU:C	2.41	0.45
1:A:258:LEU:HD11	1:A:373:ASP:OD2	2.15	0.45
1:B:284:HIS:N	1:B:292:GLN:HE21	2.12	0.45
1:B:554:VAL:HG11	1:B:577:ALA:HB1	1.99	0.45
1:A:481:GLN:O	1:A:485:GLU:HG3	2.17	0.45
3:B:613:OCB:HAJ3	3:B:613:OCB:CAH	2.47	0.45
1:A:106:PRO:HB3	1:A:293:VAL:HG11	1.99	0.45
1:A:312:ASN:C	1:A:312:ASN:HD22	2.25	0.45
1:A:415:HIS:HD2	1:A:417:ASP:H	1.64	0.45
1:A:310:SER:O	1:A:325:CYS:HB3	2.16	0.45
1:B:129:LEU:O	1:B:133:LEU:HG	2.17	0.45
1:A:190:THR:O	1:A:205:VAL:HG22	2.17	0.44
1:A:470:GLN:O	1:A:472:PRO:HD3	2.17	0.44
1:A:490:HIS:HD2	5:A:687:HOH:O	2.01	0.44
1:A:199:ARG:NH2	1:A:367:GLU:OE1	2.39	0.44
1:B:36:LEU:HD21	4:B:615:MPD:HM2	1.99	0.44
1:B:123:GLU:HG3	5:B:802:HOH:O	2.16	0.44
1:B:513:ILE:O	1:B:517:GLU:HG2	2.18	0.44
1:B:453:GLU:HG3	1:B:454:THR:N	2.32	0.44
1:B:538:ASN:HA	1:B:559:VAL:HG11	1.98	0.44
1:B:570:ARG:CD	1:B:573:ARG:HH11	2.28	0.44
1:B:225:HIS:HE1	5:B:675:HOH:O	1.99	0.44
1:B:338:ILE:O	1:B:342:VAL:HG23	2.18	0.44
1:A:500:GLY:HA2	5:A:617:HOH:O	2.17	0.44
1:B:201:PHE:CE2	1:B:367:GLU:HB2	2.52	0.44
1:A:259:ASP:OD1	1:A:261:GLU:HB3	2.18	0.44
1:B:220:GLN:HA	1:B:220:GLN:NE2	2.33	0.44
1:B:181:LYS:HD2	1:B:187:HIS:O	2.17	0.43
1:B:395:GLN:HG3	1:B:580:SER:O	2.18	0.43
1:B:561:ASN:HA	1:B:584:CYS:SG	2.57	0.43
1:B:395:GLN:HG2	1:B:582:ARG:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:223:TYR:CZ	1:A:227:LYS:HD2	2.54	0.43
1:A:345:ARG:HA	1:A:345:ARG:NE	2.33	0.43
1:B:568:HIS:CE1	1:B:570:ARG:HE	2.10	0.43
1:B:404:PHE:HB3	1:B:408:LEU:HD13	2.00	0.43
1:A:16:TYR:HD2	1:A:146:VAL:HG11	1.82	0.43
1:A:147:HIS:H	1:A:156:MSE:SE	2.51	0.43
1:A:213:THR:OG1	1:A:215:PRO:HD2	2.18	0.43
1:B:252:ARG:HH21	1:B:270:GLN:NE2	2.04	0.43
1:A:568:HIS:CD2	1:A:575:VAL:HB	2.54	0.43
1:B:131:HIS:HD2	5:B:742:HOH:O	2.01	0.43
1:A:333:MSE:HG2	5:A:720:HOH:O	2.17	0.42
1:B:553:GLY:HA3	3:B:613:OCB:HAC2	2.01	0.42
1:A:441:THR:OG1	2:A:613:152:H3	2.19	0.42
1:B:50:LYS:NZ	1:B:54:ILE:HD11	2.34	0.42
1:A:284:HIS:H	1:A:292:GLN:NE2	2.17	0.42
1:A:508:LEU:O	1:A:512:LEU:HG	2.19	0.42
1:A:367:GLU:HG2	1:A:369:VAL:HG22	2.01	0.42
1:A:439:TYR:HB2	1:A:539:PHE:CG	2.54	0.42
1:A:440:GLU:HB3	1:A:455:VAL:HB	2.02	0.42
1:A:570:ARG:HB2	1:A:573:ARG:HG2	2.01	0.42
1:B:103:PHE:CE1	1:B:335[A]:MSE:HE3	2.54	0.42
1:A:188:CYS:O	1:A:189:PRO:C	2.62	0.42
1:A:207:HIS:CG	1:A:362:ILE:HG22	2.55	0.42
1:A:604:ILE:HD13	1:A:607:MSE:CE	2.50	0.42
1:B:401:PHE:CZ	1:B:403:SER:HB2	2.55	0.42
1:A:268:LYS:HD2	1:A:368:LEU:CD2	2.50	0.42
1:A:301:ASP:OD1	1:A:303:SER:OG	2.37	0.42
1:A:297:LEU:HD12	1:A:297:LEU:HA	1.92	0.42
1:B:213:THR:HB	1:B:214:PRO:HD2	2.02	0.42
1:B:406:LYS:C	1:B:408:LEU:H	2.28	0.42
1:A:121:GLN:NE2	1:A:317:ALA:HA	2.35	0.41
1:A:242:SER:HB2	1:A:387:HIS:HD2	1.84	0.41
1:A:326:ASP:O	1:A:329:PRO:HD2	2.20	0.41
1:A:418:THR:HG23	1:A:490:HIS:HB3	2.02	0.41
1:B:335[A]:MSE:SE	3:B:613:OCB:CAA	3.17	0.41
1:B:82:GLU:CD	1:B:449:HIS:HD1	2.27	0.41
1:B:94:ARG:O	1:B:244:GLU:HG2	2.20	0.41
1:B:140:ARG:O	1:B:183:GLU:HG3	2.20	0.41
1:B:595:MSE:HE3	5:B:778:HOH:O	2.19	0.41
1:A:113:TYR:CE2	1:A:350:GLU:HA	2.55	0.41
1:B:230:ASN:O	1:B:231:GLU:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:561:ASN:HA	1:A:584:CYS:SG	2.60	0.41
1:B:105:GLY:HA2	1:B:106:PRO:HD3	1.90	0.41
1:B:281:SER:HB2	1:B:296:MSE:HE1	2.02	0.41
1:B:328:ALA:HB3	1:B:329:PRO:HD3	2.02	0.41
1:B:407:LYS:HG3	1:B:571:ASP:HB2	2.03	0.41
1:B:439:TYR:C	1:B:439:TYR:HD1	2.27	0.41
1:A:376:ILE:O	1:A:380:VAL:HG23	2.21	0.41
1:A:564:GLY:O	1:A:578:CYS:HA	2.20	0.41
1:A:28:LEU:HD22	1:A:32:LEU:CD1	2.51	0.41
1:B:103:PHE:HA	1:B:555:VAL:HG12	2.03	0.41
1:A:554:VAL:HG22	1:A:555:VAL:H	1.85	0.41
1:B:213:THR:OG1	1:B:215:PRO:HD2	2.21	0.41
1:B:311:TYR:CD1	1:B:335[B]:MSE:HE1	2.55	0.41
1:A:193:ALA:HA	1:A:202:VAL:HG12	2.02	0.41
1:A:237:ILE:HD11	1:A:372:VAL:HG11	2.02	0.41
1:A:262:ASN:HD21	1:A:371:THR:HB	1.84	0.41
1:A:270:GLN:NE2	5:A:630:HOH:O	2.54	0.41
1:B:252:ARG:NH2	1:B:270:GLN:HE22	2.04	0.41
1:A:325:CYS:SG	1:A:335:MSE:HG3	2.60	0.41
1:B:238:ALA:HB1	1:B:305:ARG:O	2.21	0.41
1:A:207:HIS:O	1:A:208:GLU:HB2	2.21	0.40
1:A:554:VAL:HG22	1:A:555:VAL:N	2.36	0.40
1:A:596:ILE:HG23	1:A:597:PHE:HD2	1.86	0.40
1:A:219:ARG:NH2	1:A:364:LEU:HD23	2.37	0.40
1:A:490:HIS:HA	1:A:493:MSE:HE2	2.03	0.40
1:A:612:LEU:N	1:A:612:LEU:HD12	2.37	0.40
1:B:82:GLU:OE2	1:B:449:HIS:ND1	2.50	0.40
1:B:604:ILE:HD13	1:B:604:ILE:HA	1.99	0.40
1:A:167:LYS:HE3	1:A:326:ASP:OD2	2.21	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	A	587/612 (96%)	562 (96%)	23 (4%)	2 (0%)	36	42
1	B	600/612 (98%)	581 (97%)	19 (3%)	0	100	100
All	All	1187/1224 (97%)	1143 (96%)	42 (4%)	2 (0%)	43	51

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	550	ARG
1	A	82	GLU

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	522/524 (100%)	514 (98%)	8 (2%)	57	73
1	B	531/524 (101%)	521 (98%)	10 (2%)	50	66
All	All	1053/1048 (100%)	1035 (98%)	18 (2%)	53	69

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	LEU
1	A	70	LEU
1	A	227	LYS
1	A	248	TRP
1	A	261	GLU
1	A	297	LEU
1	A	313	LEU
1	A	330	TYR
1	B	49	LYS
1	B	139	LEU
1	B	248	TRP
1	B	265	LEU
1	B	297	LEU
1	B	313	LEU

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Mol	Chain	Res	Type
1	B	330	TYR
1	B	358	LYS
1	B	376	ILE
1	B	439	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (48) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	59	GLN
1	A	87	ASN
1	A	98	GLN
1	A	102	ASN
1	A	109	HIS
1	A	112	HIS
1	A	121	GLN
1	A	157	ASN
1	A	220	GLN
1	A	270	GLN
1	A	292	GLN
1	A	312	ASN
1	A	395	GLN
1	A	415	HIS
1	A	470	GLN
1	A	480	GLN
1	A	490	HIS
1	A	560	HIS
1	A	568	HIS
1	A	594	GLN
1	B	56	GLN
1	B	87	ASN
1	B	100	ASN
1	B	102	ASN
1	B	109	HIS
1	B	112	HIS
1	B	121	GLN
1	B	131	HIS
1	B	147	HIS
1	B	151	ASN
1	B	157	ASN
1	B	178	ASN
1	B	187	HIS
1	B	220	GLN

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Mol	Chain	Res	Type
1	B	225	HIS
1	B	270	GLN
1	B	292	GLN
1	B	337	ASN
1	B	395	GLN
1	B	415	HIS
1	B	470	GLN
1	B	480	GLN
1	B	481	GLN
1	B	490	HIS
1	B	499	HIS
1	B	568	HIS
1	B	594	GLN
1	B	601	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](#)

7 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
4	MPD	B	615	-	7,7,7	0.44	0	9,10,10	0.45	0
4	MPD	B	618	-	7,7,7	0.48	0	9,10,10	0.48	0
2	152	A	613	-	10,10,10	1.20	1 (10%)	13,14,14	1.06	1 (7%)
4	MPD	B	616	-	7,7,7	0.47	0	9,10,10	0.46	0
4	MPD	B	617	-	7,7,7	0.44	0	9,10,10	0.41	0
3	OCB	B	613	-	19,19,19	0.96	2 (10%)	24,24,24	1.09	1 (4%)
4	MPD	B	614	-	7,7,7	0.48	0	9,10,10	0.46	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
4	MPD	B	615	-	-	2/5/5/5	-
4	MPD	B	618	-	-	0/5/5/5	-
2	152	A	613	-	-	0/9/9/9	-
4	MPD	B	616	-	-	1/5/5/5	-
4	MPD	B	617	-	-	0/5/5/5	-
3	OCB	B	613	-	-	0/20/20/20	-
4	MPD	B	614	-	-	0/5/5/5	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	613	152	C4-N5	-2.32	1.47	1.52
3	B	613	OCB	CAO-NAN	-2.24	1.47	1.52
3	B	613	OCB	OAL-CAR	-2.15	1.23	1.30

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	613	OCB	OAK-CAH-CAG	3.19	118.39	111.48
2	A	613	152	C3-C4-N5	-3.10	111.00	116.70

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	616	MPD	C2-C3-C4-C5

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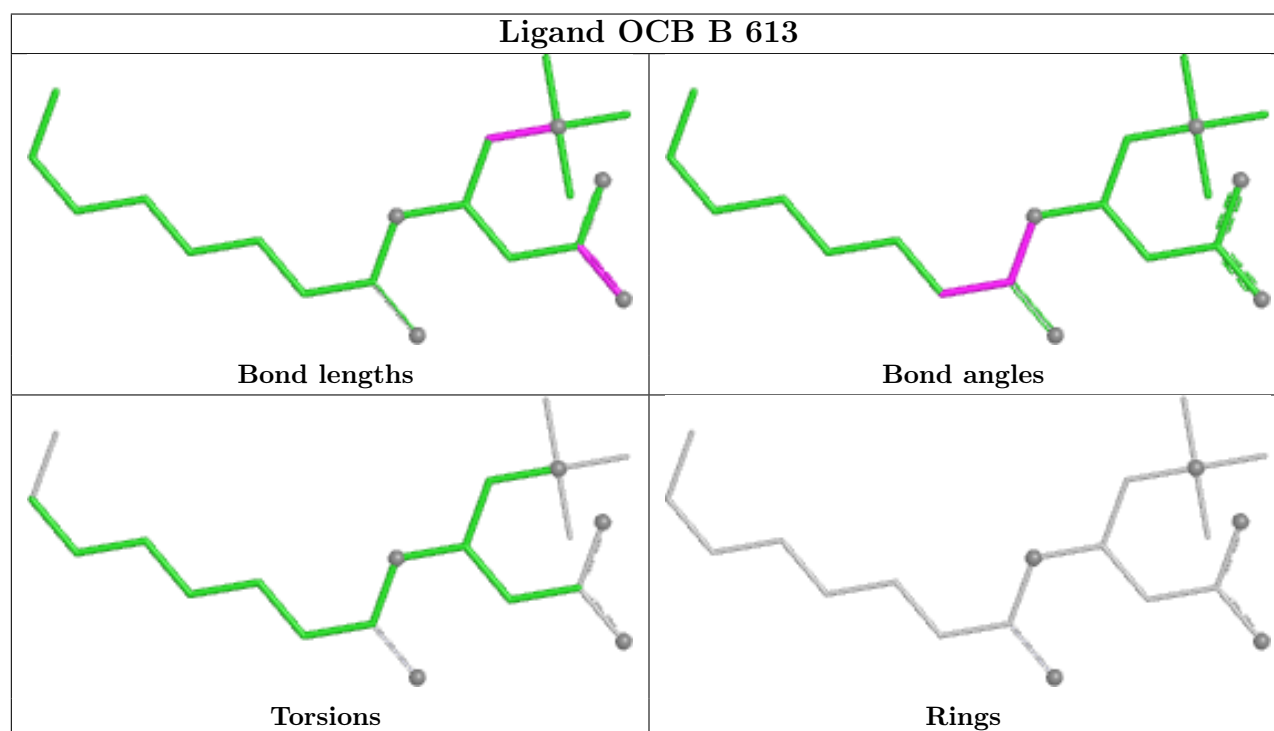
Mol	Chain	Res	Type	Atoms
4	B	615	MPD	C2-C3-C4-C5
4	B	615	MPD	C2-C3-C4-O4

There are no ring outliers.

4 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	615	MPD	1	0
2	A	613	152	3	0
4	B	616	MPD	1	0
3	B	613	OCB	8	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

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

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	574/612 (93%)	0.51	29 (5%)	33 30	23, 42, 64, 91	0
1	B	583/612 (95%)	-0.21	13 (2%)	62 59	12, 26, 48, 102	1 (0%)
All	All	1157/1224 (94%)	0.15	42 (3%)	46 43	12, 33, 63, 102	1 (0%)

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	408	LEU	4.7
1	A	234	GLY	4.6
1	A	612	LEU	4.3
1	B	404	PHE	4.1
1	A	232	PRO	3.9
1	A	233	VAL	3.9
1	B	407	LYS	3.7
1	B	409	THR	3.7
1	A	372	VAL	3.6
1	B	406	LYS	3.6
1	B	610	ALA	3.1
1	A	202	VAL	3.1
1	A	395	GLN	3.0
1	A	123	GLU	2.9
1	A	228	CYS	2.9
1	A	231	GLU	2.8
1	A	359	VAL	2.8
1	A	229	SER	2.8
1	B	230	ASN	2.7
1	A	606	LEU	2.7
1	A	230	ASN	2.7
1	A	201	PHE	2.7
1	A	371	THR	2.6
1	B	402	THR	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	357	GLU	2.5
1	B	405	GLY	2.5
1	A	258	LEU	2.5
1	A	611	HIS	2.5
1	A	369	VAL	2.4
1	A	601	HIS	2.4
1	A	370	PHE	2.4
1	A	235	PRO	2.3
1	A	223	TYR	2.3
1	A	476	LEU	2.2
1	A	198	GLY	2.2
1	B	413	ALA	2.1
1	A	582	ARG	2.1
1	B	411	GLU	2.1
1	A	394	LEU	2.1
1	A	367	GLU	2.0
1	B	517	GLU	2.0
1	A	397	ALA	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.

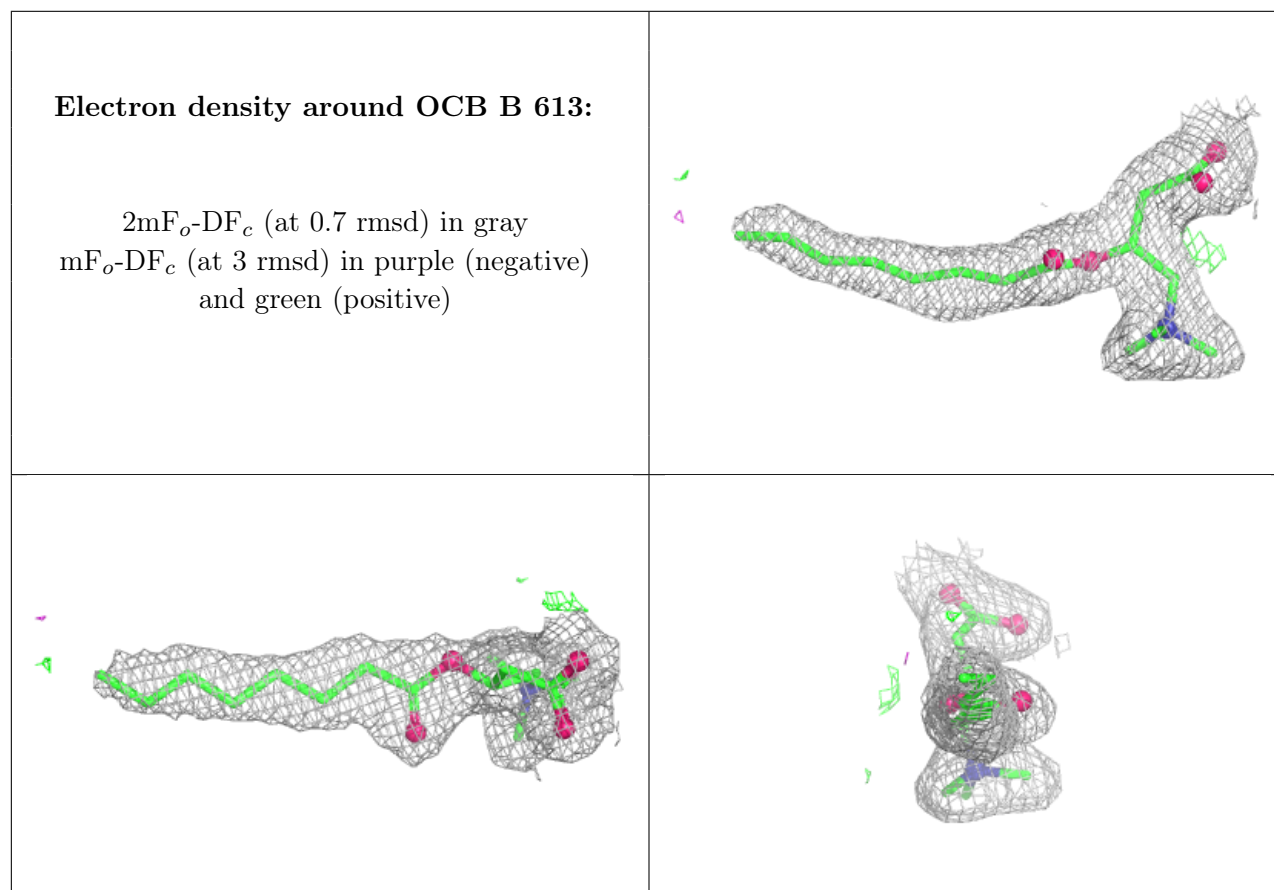
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	MPD	B	617	8/8	0.66	0.32	62,64,65,66	0
4	MPD	B	616	8/8	0.73	0.24	68,69,70,70	0
4	MPD	B	615	8/8	0.76	0.31	68,68,72,72	0
4	MPD	B	618	8/8	0.78	0.26	75,76,77,77	0
4	MPD	B	614	8/8	0.87	0.20	48,50,52,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	152	A	613	11/11	0.88	0.12	28,33,35,36	0
3	OCB	B	613	20/20	0.94	0.10	20,24,36,37	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 ⓘ

There are no such residues in this entry.