



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:35 PM UTC

PDB ID : 3GCH / pdb_00003gch
Title : CHEMISTRY OF CAGED ENZYMES. BINDING OF PHOTOREVERSIBLE CINNAMATES TO CHYMOTRYPSIN
Authors : Stoddard, B.L.; Ringe, D.; Petsko, G.A.
Deposited on : 1989-09-25
Resolution : 1.90 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

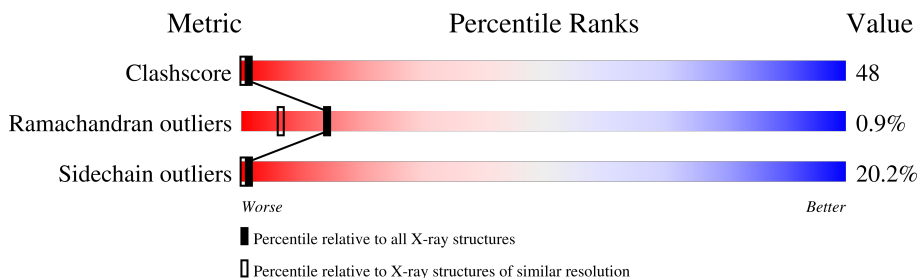
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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))
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)

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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	13	23% 15% 38% 8% 15%
2	B	131	19% 43% 31% 8%
3	C	97	20% 43% 29% 6%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	OAC	C	246	X	X	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 1824 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 GAMMA-CHYMOTRYPSIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	11	Total	C	N	O	S	0	0	1
			69	45	12	11	1			

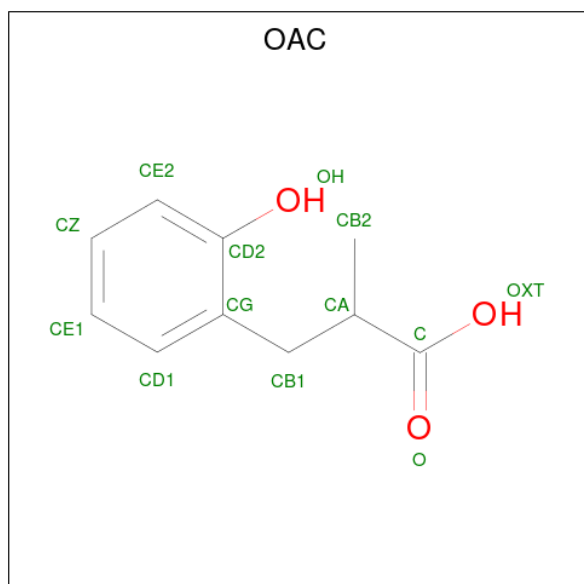
- Molecule 2 is a protein called GAMMA-CHYMOTRYPSIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	131	Total	C	N	O	S	0	0	0
			979	618	162	195	4			

- Molecule 3 is a protein called GAMMA-CHYMOTRYPSIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	95	Total	C	N	O	S	0	0	0
			688	429	120	132	7			

- Molecule 4 is TRANS-O-HYDROXY-ALPHA-METHYL CINNAMATE (CCD ID: OAC) (formula: C₁₀H₁₂O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			12	10	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	4	Total	O	0	0
			4	4		
5	B	52	Total	O	0	0
			52	52		
5	C	20	Total	O	0	0
			20	20		

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. 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. 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.

Note EDS was not executed.

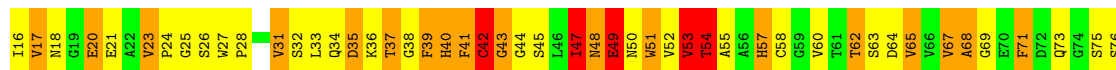
• Molecule 1: GAMMA-CHYMOTRYPSIN

Chain A: 



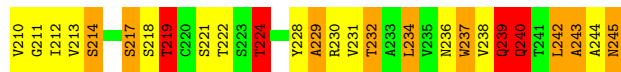
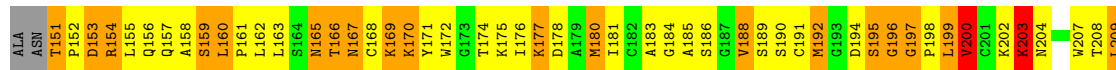
• Molecule 2: GAMMA-CHYMOTRYPSIN

Chain B: 



• Molecule 3: GAMMA-CHYMOTRYPSIN

Chain C: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α , β , γ	69.70 Å 69.70 Å 97.50 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.90	Depositor
% Data completeness (in resolution range)	(Not available) (50.00-1.90)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.203 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1824	wwPDB-VP
Average B, all atoms (Å ²)	9.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	1.31	0/70	3.08	17/97 (17.5%)
2	B	1.46	6/999 (0.6%)	3.07	132/1361 (9.7%)
3	C	1.54	5/701 (0.7%)	3.07	80/955 (8.4%)
All	All	1.49	11/1770 (0.6%)	3.07	229/2413 (9.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	B	0	1
3	C	0	1
All	All	0	3

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	184	GLY	N-CA	-8.44	1.37	1.45
3	C	160	LEU	N-CA	7.36	1.53	1.46
2	B	43	GLY	N-CA	6.49	1.50	1.44
2	B	18	ASN	C-N	-6.10	1.27	1.33
2	B	45	SER	N-CA	5.74	1.53	1.46
3	C	198	PRO	N-CD	5.70	1.55	1.47
2	B	53	VAL	C-N	-5.49	1.26	1.33
3	C	211	GLY	N-CA	5.45	1.51	1.45
2	B	137	VAL	C-O	5.24	1.29	1.24
2	B	38	GLY	N-CA	5.20	1.52	1.45
3	C	183	ALA	C-N	-5.18	1.26	1.32

All (229) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	183	ALA	CA-C-N	22.38	140.89	121.86
3	C	183	ALA	C-N-CA	22.38	140.89	121.86
3	C	204	ASN	CA-CB-CG	20.28	132.88	112.60
2	B	101	ASN	CA-C-N	14.78	143.92	122.05
2	B	101	ASN	C-N-CA	14.78	143.92	122.05
2	B	146	TYR	CA-C-O	11.79	140.84	120.80
3	C	153	ASP	CA-CB-CG	11.57	124.17	112.60
2	B	36	LYS	CA-CB-CG	10.52	135.15	114.10
2	B	80	ILE	CB-CA-C	-10.48	100.07	111.59
2	B	126	ALA	N-CA-C	-10.30	99.86	111.71
3	C	240	GLN	CA-C-O	-9.95	109.19	120.24
2	B	18	ASN	CA-C-N	9.93	134.79	122.77
2	B	18	ASN	C-N-CA	9.93	134.79	122.77
2	B	23	VAL	CA-C-N	9.90	132.21	119.84
2	B	23	VAL	C-N-CA	9.90	132.21	119.84
2	B	129	ASP	CA-CB-CG	9.89	122.49	112.60
2	B	49	GLU	CB-CG-CD	9.71	129.11	112.60
2	B	43	GLY	CA-C-O	-9.45	107.72	122.27
3	C	198	PRO	N-CA-C	9.38	125.47	111.03
2	B	125	SER	CA-C-O	-9.34	110.73	121.47
2	B	146	TYR	CA-CB-CG	-9.23	97.28	113.90
2	B	78	GLU	CB-CG-CD	9.10	128.06	112.60
3	C	197	GLY	CA-C-N	9.08	129.63	119.83
3	C	197	GLY	C-N-CA	9.08	129.63	119.83
3	C	151	THR	CA-CB-OG1	-9.04	96.03	109.60
3	C	218	SER	CA-C-O	9.02	130.47	119.38
2	B	53	VAL	CB-CA-C	-8.88	97.49	110.63
2	B	117	THR	CA-C-O	-8.85	108.73	119.18
1	A	7	GLN	CB-CA-C	8.76	123.52	109.51
2	B	107	LYS	CB-CA-C	8.61	124.14	110.19
3	C	184	GLY	N-CA-C	8.54	121.95	111.45
2	B	126	ALA	O-C-N	8.52	132.19	122.22
3	C	198	PRO	CA-C-O	8.47	130.29	121.23
3	C	224	THR	CB-CA-C	8.47	121.71	109.26
2	B	60	VAL	CA-CB-CG2	8.40	124.68	110.40
2	B	65	VAL	CB-CA-C	8.31	123.00	110.62
2	B	138	THR	CA-CB-OG1	-8.30	97.14	109.60
2	B	101	ASN	O-C-N	-8.26	113.33	122.67
3	C	196	GLY	N-CA-C	-8.23	103.56	114.25
2	B	35	ASP	CA-C-O	-8.21	112.29	121.89
2	B	95	ASN	OD1-CG-ND2	8.17	130.77	122.60
3	C	218	SER	CA-C-N	8.15	135.12	122.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	218	SER	C-N-CA	8.15	135.12	122.49
3	C	245	ASN	CA-C-O	-8.09	107.04	120.80
2	B	62	THR	CB-CA-C	8.07	124.73	110.37
3	C	244	ALA	N-CA-C	8.04	119.68	111.07
3	C	242	LEU	O-C-N	8.00	130.73	122.09
2	B	135	THR	CA-C-O	7.93	129.57	120.60
3	C	218	SER	CA-CB-OG	7.86	126.82	111.10
2	B	67	VAL	CB-CA-C	7.80	120.95	110.42
1	A	9	VAL	CA-C-O	-7.79	111.56	120.67
3	C	239	GLN	CA-C-O	7.70	128.94	120.63
2	B	141	TRP	CA-C-N	7.61	131.41	121.13
2	B	141	TRP	C-N-CA	7.61	131.41	121.13
2	B	47	ILE	N-CA-C	-7.58	105.17	113.43
3	C	162	LEU	CA-C-O	-7.56	113.31	121.56
3	C	184	GLY	CA-C-O	7.55	127.29	120.64
2	B	114	PHE	N-CA-CB	7.52	121.42	110.06
3	C	232	THR	N-CA-CB	-7.49	98.69	110.22
2	B	87	LYS	O-C-N	-7.47	114.24	123.36
2	B	138	THR	CA-C-N	7.46	134.30	122.36
2	B	138	THR	C-N-CA	7.46	134.30	122.36
2	B	31	VAL	O-C-N	7.29	130.77	122.97
3	C	198	PRO	CB-CA-C	-7.28	102.47	111.64
2	B	100	ASN	CA-C-O	-7.27	112.33	120.54
2	B	42	CYS	CA-C-O	-7.25	113.47	121.23
2	B	39	PHE	CA-CB-CG	7.24	121.04	113.80
3	C	166	THR	CA-CB-OG1	-7.24	98.73	109.60
1	A	7	GLN	OE1-CD-NE2	-7.24	115.36	122.60
3	C	219	THR	O-C-N	7.24	131.00	122.24
2	B	38	GLY	N-CA-C	-7.23	104.85	115.63
2	B	81	GLN	CG-CD-NE2	7.23	127.25	116.40
3	C	174	THR	CB-CA-C	7.20	123.27	110.81
3	C	160	LEU	CB-CA-C	7.19	119.70	109.92
2	B	53	VAL	CA-C-N	7.16	134.14	122.39
2	B	53	VAL	C-N-CA	7.16	134.14	122.39
3	C	190	SER	N-CA-C	-7.16	101.61	110.41
2	B	81	GLN	CA-C-O	-7.09	112.88	120.46
2	B	104	THR	N-CA-CB	7.05	123.76	111.00
3	C	160	LEU	N-CA-CB	-7.03	101.00	110.77
3	C	151	THR	N-CA-CB	-7.00	99.59	111.50
2	B	57	HIS	CA-C-N	-7.00	110.31	120.82
2	B	57	HIS	C-N-CA	-7.00	110.31	120.82
2	B	47	ILE	CA-C-O	7.00	125.61	118.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	130	PHE	CA-C-N	6.91	132.86	121.39
2	B	130	PHE	C-N-CA	6.91	132.86	121.39
3	C	218	SER	O-C-N	-6.89	113.19	122.43
3	C	234	LEU	N-CA-CB	-6.89	101.88	110.98
3	C	236	ASN	CB-CA-C	6.87	121.67	110.88
3	C	219	THR	N-CA-CB	-6.86	100.25	110.61
3	C	199	LEU	N-CA-CB	6.79	121.90	110.69
2	B	51	TRP	CA-C-O	-6.75	111.10	120.21
2	B	144	THR	N-CA-CB	6.75	120.59	110.53
2	B	68	ALA	CA-C-O	6.73	128.99	121.11
2	B	134	THR	CA-C-N	6.71	131.98	121.99
2	B	134	THR	C-N-CA	6.71	131.98	121.99
3	C	185	ALA	N-CA-C	-6.68	102.73	111.74
3	C	192	MET	O-C-N	6.66	131.05	123.06
3	C	236	ASN	CA-C-N	6.65	129.19	120.28
3	C	236	ASN	C-N-CA	6.65	129.19	120.28
2	B	104	THR	O-C-N	6.65	131.38	123.27
2	B	71	PHE	N-CA-CB	6.58	121.61	110.49
2	B	131	ALA	CA-C-N	6.55	130.17	120.87
2	B	131	ALA	C-N-CA	6.55	130.17	120.87
3	C	200	VAL	N-CA-C	6.54	119.10	108.97
2	B	77	SER	CA-C-O	6.53	127.33	119.43
2	B	95	ASN	CA-C-O	6.49	131.69	120.85
2	B	27	TRP	O-C-N	6.49	126.48	121.23
2	B	90	LYS	CA-C-O	-6.48	113.30	120.69
2	B	88	VAL	N-CA-CB	-6.44	103.70	110.72
2	B	110	THR	CA-C-N	6.43	129.85	120.71
2	B	110	THR	C-N-CA	6.43	129.85	120.71
2	B	114	PHE	CA-C-O	6.43	128.38	121.05
2	B	117	THR	O-C-N	6.39	129.74	122.20
2	B	41	PHE	CA-CB-CG	-6.38	107.42	113.80
3	C	214	SER	CA-C-O	-6.36	111.72	119.61
3	C	170	LYS	CA-C-N	6.33	132.22	122.42
3	C	170	LYS	C-N-CA	6.33	132.22	122.42
3	C	245	ASN	CA-CB-CG	-6.32	106.28	112.60
3	C	207	TRP	CB-CA-C	6.28	120.08	109.84
2	B	21	GLU	CA-C-O	-6.28	114.13	121.16
2	B	54	THR	CA-CB-OG1	-6.27	100.20	109.60
2	B	104	THR	CA-C-N	-6.24	112.03	122.64
2	B	104	THR	C-N-CA	-6.24	112.03	122.64
2	B	68	ALA	CB-CA-C	6.24	122.42	109.38
3	C	221	SER	CA-C-N	6.20	132.52	120.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	221	SER	C-N-CA	6.20	132.52	120.99
2	B	103	ILE	CB-CA-C	6.20	120.08	110.28
1	A	9	VAL	CB-CA-C	-6.17	101.42	110.62
2	B	31	VAL	N-CA-CB	6.17	122.83	112.47
2	B	52	VAL	CA-C-O	-6.16	114.71	121.92
2	B	109	SER	O-C-N	6.15	129.83	122.27
2	B	81	GLN	N-CA-C	6.13	118.83	107.99
3	C	232	THR	OG1-CB-CG2	6.10	121.50	109.30
2	B	31	VAL	CB-CA-C	6.09	119.67	110.90
2	B	67	VAL	CA-C-O	6.08	126.41	120.27
3	C	167	ASN	N-CA-C	-6.08	105.12	112.54
3	C	242	LEU	CA-C-O	-6.05	114.47	120.70
2	B	78	GLU	CA-C-N	6.04	133.08	121.54
2	B	78	GLU	C-N-CA	6.04	133.08	121.54
2	B	131	ALA	N-CA-C	6.02	119.39	110.48
1	A	7	GLN	CG-CD-OE1	6.02	132.83	120.80
2	B	49	GLU	N-CA-C	6.00	120.22	113.02
2	B	65	VAL	CA-C-O	5.99	127.67	120.67
2	B	138	THR	CA-C-O	-5.95	114.39	121.11
2	B	91	ASN	CA-C-O	-5.94	114.66	121.19
3	C	229	ALA	N-CA-C	-5.84	102.81	110.53
1	A	6	ILE	CB-CG1-CD1	5.82	126.01	113.80
3	C	237	TRP	CA-C-N	5.82	127.89	120.56
3	C	237	TRP	C-N-CA	5.82	127.89	120.56
2	B	44	GLY	CA-C-O	-5.81	114.81	121.49
3	C	157	GLN	OE1-CD-NE2	5.81	128.41	122.60
3	C	195	SER	N-CA-C	5.78	118.21	110.35
2	B	38	GLY	CA-C-O	5.78	124.73	118.95
2	B	121	VAL	CA-CB-CG1	5.76	120.19	110.40
2	B	42	CYS	CA-C-N	-5.75	116.48	122.69
2	B	42	CYS	C-N-CA	-5.75	116.48	122.69
1	A	6	ILE	CB-CA-C	-5.72	103.23	111.19
3	C	155	LEU	N-CA-C	5.71	118.64	110.24
2	B	125	SER	O-C-N	5.71	129.41	122.96
3	C	158	ALA	O-C-N	5.66	130.03	123.41
3	C	243	ALA	CA-C-N	5.65	127.79	120.44
3	C	243	ALA	C-N-CA	5.65	127.79	120.44
2	B	114	PHE	CA-CB-CG	5.64	119.44	113.80
1	A	8	PRO	CA-C-O	-5.63	115.13	121.43
2	B	144	THR	N-CA-C	-5.63	106.46	113.38
2	B	51	TRP	N-CA-CB	-5.59	101.44	110.71
2	B	17	VAL	CA-C-O	-5.58	114.16	120.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	18	ASN	N-CA-C	5.58	122.68	110.80
2	B	88	VAL	CA-CB-CG2	-5.56	100.94	110.40
2	B	35	ASP	O-C-N	5.56	129.18	122.68
3	C	203	LYS	CA-C-O	5.51	127.91	120.47
3	C	160	LEU	CA-C-O	-5.51	114.42	119.76
3	C	239	GLN	CB-CG-CD	5.50	121.96	112.60
2	B	93	LYS	CA-CB-CG	5.47	125.05	114.10
2	B	135	THR	CA-CB-OG1	-5.47	101.40	109.60
2	B	115	SER	O-C-N	5.45	129.49	122.68
2	B	101	ASN	OD1-CG-ND2	-5.43	117.17	122.60
2	B	69	GLY	N-CA-C	-5.42	107.63	115.27
3	C	236	ASN	CA-CB-CG	5.41	118.01	112.60
2	B	36	LYS	CA-C-N	5.40	127.95	120.29
2	B	36	LYS	C-N-CA	5.40	127.95	120.29
2	B	102	ASP	CA-C-O	5.40	129.59	122.63
1	A	7	GLN	CB-CG-CD	5.37	121.73	112.60
2	B	57	HIS	N-CA-C	-5.36	105.61	111.82
2	B	20	GLU	CB-CA-C	-5.35	98.81	109.79
3	C	177	LYS	CA-C-O	-5.35	115.37	121.68
2	B	49	GLU	CA-CB-CG	5.34	124.78	114.10
1	A	4	PRO	CA-C-O	-5.33	114.64	122.31
3	C	188	VAL	CA-C-O	-5.32	115.47	121.75
3	C	239	GLN	OE1-CD-NE2	-5.32	117.28	122.60
2	B	100	ASN	CA-CB-CG	-5.31	107.29	112.60
2	B	40	HIS	ND1-CE1-NE2	5.29	113.69	108.40
2	B	129	ASP	CB-CA-C	5.27	118.87	109.38
2	B	20	GLU	O-C-N	5.26	129.99	123.15
2	B	145	ARG	CD-NE-CZ	-5.26	117.04	124.40
3	C	203	LYS	CA-C-N	5.25	129.82	122.36
3	C	203	LYS	C-N-CA	5.25	129.82	122.36
3	C	180	MET	CB-CG-SD	-5.25	96.95	112.70
2	B	121	VAL	O-C-N	5.24	128.65	122.36
2	B	87	LYS	N-CA-C	5.23	117.94	108.69
2	B	88	VAL	CB-CA-C	5.23	117.39	110.91
2	B	106	LEU	CA-C-O	5.23	126.01	120.36
3	C	239	GLN	CA-C-N	5.22	129.51	120.58
3	C	239	GLN	C-N-CA	5.22	129.51	120.58
1	A	3	VAL	CA-CB-CG1	5.22	119.27	110.40
1	A	8	PRO	N-CA-CB	5.21	107.70	103.32
2	B	133	GLY	N-CA-C	-5.20	108.15	115.32
1	A	5	ALA	CA-C-O	5.17	125.64	119.60
2	B	85	ILE	CA-CB-CG1	-5.16	101.62	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	83	LEU	N-CA-C	5.15	118.01	109.46
1	A	7	GLN	CA-C-N	5.14	125.13	119.89
1	A	7	GLN	C-N-CA	5.14	125.13	119.89
3	C	169	LYS	CA-C-O	5.13	125.70	119.49
1	A	3	VAL	CA-C-N	5.13	125.86	120.11
1	A	3	VAL	C-N-CA	5.13	125.86	120.11
3	C	204	ASN	OD1-CG-ND2	-5.13	117.47	122.60
2	B	95	ASN	CB-CG-ND2	-5.12	108.72	116.40
2	B	78	GLU	N-CA-CB	-5.12	101.93	110.37
2	B	112	ALA	CA-C-N	5.11	129.57	122.77
2	B	112	ALA	C-N-CA	5.11	129.57	122.77
3	C	166	THR	N-CA-C	5.10	116.53	111.07
2	B	21	GLU	CG-CD-OE2	-5.08	106.72	118.40
2	B	110	THR	CA-CB-OG1	-5.08	101.98	109.60
2	B	81	GLN	CB-CG-CD	-5.04	104.04	112.60
3	C	188	VAL	CA-CB-CG2	5.02	118.94	110.40
3	C	154	ARG	NE-CZ-NH1	5.02	126.52	121.50
3	C	156	GLN	CA-CB-CG	-5.02	104.06	114.10
3	C	165	ASN	CA-CB-CG	5.01	117.61	112.60

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	10	LEU	Mainchain
2	B	145	ARG	Sidechain
3	C	200	VAL	Mainchain

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	69	0	76	9	0
2	B	979	0	951	113	1
3	C	688	0	686	79	3
4	C	12	0	10	3	0
5	A	4	0	0	1	3

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	52	0	0	12	4
5	C	20	0	0	7	1
All	All	1824	0	1723	166	7

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 48.

All (166) 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)
2:B:143:LEU:CD1	3:C:192:MET:HE2	1.74	1.17
2:B:31:VAL:HG12	2:B:68:ALA:HB2	1.30	1.07
3:C:172:TRP:HB2	3:C:176:ILE:HD11	1.36	1.02
2:B:90:LYS:HA	2:B:104:THR:HG22	1.38	1.01
2:B:58:CYS:HB2	5:B:271:HOH:O	1.61	1.01
3:C:230:ARG:NE	5:C:316:HOH:O	1.93	1.00
1:A:5:ALA:CB	2:B:116:GLN:HG3	1.93	0.98
3:C:239:GLN:HE21	3:C:239:GLN:HA	1.25	0.97
4:C:246:OAC:HB23	5:C:247:HOH:O	1.64	0.96
2:B:48:ASN:C	2:B:48:ASN:HD22	1.72	0.94
2:B:55:ALA:O	5:B:271:HOH:O	1.87	0.93
1:A:5:ALA:HB3	2:B:116:GLN:HG3	1.52	0.90
2:B:48:ASN:O	5:B:272:HOH:O	1.92	0.88
2:B:143:LEU:HD12	3:C:192:MET:HE2	1.57	0.86
3:C:239:GLN:HA	3:C:239:GLN:NE2	1.91	0.83
2:B:143:LEU:HD12	3:C:192:MET:HB2	1.62	0.82
2:B:131:ALA:O	2:B:134:THR:OG1	1.99	0.81
3:C:172:TRP:HB2	3:C:176:ILE:CD1	2.12	0.80
3:C:172:TRP:CB	3:C:176:ILE:HD11	2.11	0.80
2:B:35:ASP:OD2	2:B:37:THR:HB	1.82	0.80
2:B:143:LEU:CD1	3:C:192:MET:HB2	2.13	0.79
3:C:217:SER:OG	3:C:219:THR:HG23	1.84	0.78
2:B:25:GLY:HA3	2:B:117:THR:HG22	1.66	0.76
3:C:165:ASN:N	5:C:311:HOH:O	2.08	0.76
1:A:5:ALA:N	5:A:296:HOH:O	2.17	0.76
2:B:28:PRO:HG2	2:B:119:SER:OG	1.87	0.75
2:B:31:VAL:CG1	2:B:68:ALA:HB2	2.14	0.74
2:B:90:LYS:CA	2:B:104:THR:HG22	2.17	0.74
2:B:90:LYS:HA	2:B:104:THR:CG2	2.14	0.73
2:B:34:GLN:HA	2:B:39:PHE:O	1.89	0.73
2:B:143:LEU:HD13	3:C:192:MET:HE2	1.69	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:47:ILE:O	2:B:48:ASN:HB3	1.91	0.70
2:B:80:ILE:HG13	2:B:80:ILE:O	1.89	0.70
2:B:125:SER:HB2	2:B:128:ASP:H	1.56	0.70
3:C:217:SER:O	4:C:246:OAC:HZ	1.91	0.70
2:B:71:PHE:O	3:C:154:ARG:HA	1.92	0.69
2:B:122:CYS:O	3:C:209:LEU:N	2.24	0.69
2:B:57:HIS:O	2:B:58:CYS:C	2.34	0.68
2:B:54:THR:OG1	2:B:55:ALA:N	2.24	0.67
3:C:212:ILE:HB	3:C:229:ALA:HB3	1.77	0.67
2:B:104:THR:HG21	5:B:287:HOH:O	1.96	0.66
3:C:209:LEU:HD13	3:C:231:VAL:HG21	1.76	0.66
2:B:95:ASN:O	2:B:99:ILE:N	2.27	0.66
2:B:73:GLN:HG3	3:C:153:ASP:O	1.96	0.66
2:B:49:GLU:C	5:B:272:HOH:O	2.39	0.65
2:B:146:TYR:CE1	3:C:192:MET:HE1	2.33	0.64
2:B:144:THR:CG2	3:C:152:PRO:HG3	2.28	0.63
2:B:23:VAL:O	2:B:26:SER:OG	2.10	0.63
3:C:230:ARG:CZ	5:C:316:HOH:O	2.38	0.63
2:B:80:ILE:HD11	2:B:82:LYS:HE2	1.81	0.62
3:C:177:LYS:HG2	3:C:180:MET:HE3	1.82	0.62
2:B:50:ASN:N	5:B:272:HOH:O	2.33	0.61
2:B:48:ASN:C	2:B:48:ASN:ND2	2.51	0.61
2:B:16:ILE:HA	3:C:189:SER:O	2.01	0.61
2:B:62:THR:HG22	2:B:88:VAL:CG2	2.31	0.60
2:B:47:ILE:CG2	2:B:123:LEU:HD21	2.31	0.60
3:C:167:ASN:O	3:C:170:LYS:HB2	2.02	0.60
2:B:68:ALA:HB1	5:B:263:HOH:O	2.01	0.59
3:C:230:ARG:NH1	5:C:316:HOH:O	2.36	0.58
1:A:5:ALA:HB1	2:B:116:GLN:HG3	1.83	0.57
2:B:49:GLU:OE2	2:B:49:GLU:N	2.27	0.56
2:B:103:ILE:HG21	3:C:234:LEU:HD13	1.86	0.56
2:B:53:VAL:HG13	2:B:105:LEU:CD2	2.36	0.55
4:C:246:OAC:CB2	5:C:247:HOH:O	2.39	0.55
3:C:191:CYS:O	3:C:194:ASP:HB2	2.05	0.55
2:B:117:THR:O	5:B:278:HOH:O	2.18	0.55
2:B:47:ILE:HG21	2:B:123:LEU:HD21	1.89	0.55
2:B:103:ILE:CG2	3:C:234:LEU:HD13	2.37	0.54
3:C:172:TRP:O	3:C:175:LYS:HG3	2.06	0.54
2:B:80:ILE:CD1	2:B:82:LYS:HE2	2.37	0.54
3:C:167:ASN:HA	3:C:170:LYS:HD2	1.89	0.54
2:B:130:PHE:CE2	3:C:203:LYS:HD3	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:197:GLY:C	5:C:267:HOH:O	2.50	0.53
2:B:55:ALA:H	3:C:196:GLY:HA2	1.74	0.53
2:B:40:HIS:C	2:B:40:HIS:CD2	2.86	0.53
2:B:143:LEU:HD11	3:C:192:MET:HE2	1.79	0.53
3:C:217:SER:OG	3:C:219:THR:CG2	2.56	0.52
2:B:33:LEU:HD12	2:B:42:CYS:HB3	1.91	0.52
2:B:142:GLY:O	2:B:143:LEU:C	2.52	0.52
2:B:48:ASN:ND2	2:B:50:ASN:H	2.08	0.52
2:B:62:THR:CG2	2:B:88:VAL:CG2	2.88	0.51
2:B:114:PHE:CD1	2:B:118:VAL:HG12	2.45	0.51
2:B:103:ILE:HG13	3:C:212:ILE:HD13	1.91	0.51
2:B:90:LYS:HG3	2:B:104:THR:CG2	2.41	0.50
3:C:181:ILE:O	3:C:181:ILE:HG23	2.11	0.50
2:B:144:THR:HG23	3:C:152:PRO:HG3	1.93	0.50
3:C:165:ASN:O	3:C:168:CYS:HB3	2.12	0.49
2:B:39:PHE:CE2	2:B:41:PHE:HB3	2.47	0.49
2:B:125:SER:CB	2:B:128:ASP:H	2.24	0.49
3:C:242:LEU:O	3:C:243:ALA:C	2.56	0.48
2:B:130:PHE:CD2	3:C:210:VAL:HG21	2.48	0.48
2:B:84:LYS:HG2	5:B:277:HOH:O	2.14	0.48
2:B:125:SER:HB2	2:B:128:ASP:N	2.26	0.47
2:B:146:TYR:CD1	2:B:146:TYR:C	2.84	0.47
2:B:125:SER:C	2:B:127:SER:N	2.63	0.47
3:C:238:VAL:O	3:C:242:LEU:HD12	2.14	0.47
2:B:128:ASP:HB3	2:B:130:PHE:CE1	2.49	0.47
2:B:55:ALA:N	3:C:196:GLY:HA2	2.29	0.47
3:C:172:TRP:CB	3:C:176:ILE:CD1	2.82	0.47
2:B:17:VAL:N	3:C:189:SER:O	2.46	0.47
2:B:51:TRP:HH2	2:B:89:PHE:CD1	2.33	0.47
2:B:62:THR:CG2	2:B:88:VAL:HG23	2.46	0.46
2:B:137:VAL:O	3:C:200:VAL:HG22	2.16	0.46
3:C:219:THR:O	3:C:219:THR:OG1	2.30	0.46
3:C:197:GLY:O	3:C:213:VAL:HG23	2.16	0.46
2:B:47:ILE:HG22	2:B:123:LEU:HD21	1.98	0.46
3:C:172:TRP:CZ2	3:C:224:THR:HG22	2.51	0.46
2:B:32:SER:HB2	2:B:141:TRP:CZ3	2.50	0.45
2:B:35:ASP:C	2:B:37:THR:N	2.72	0.45
3:C:186:SER:OG	3:C:188:VAL:HG22	2.16	0.45
2:B:34:GLN:HG2	2:B:40:HIS:HA	1.98	0.45
1:A:8:PRO:HA	2:B:26:SER:HB2	1.99	0.45
3:C:161:PRO:CD	3:C:186:SER:HB3	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:9:VAL:HG12	1:A:10:LEU:N	2.28	0.44
2:B:23:VAL:HA	2:B:24:PRO:HD3	1.80	0.44
2:B:100:ASN:HD22	2:B:100:ASN:HA	1.43	0.44
2:B:35:ASP:C	2:B:37:THR:H	2.25	0.44
3:C:238:VAL:O	3:C:242:LEU:CD1	2.66	0.44
2:B:49:GLU:HA	5:B:272:HOH:O	2.16	0.43
2:B:51:TRP:CZ3	2:B:105:LEU:HB3	2.54	0.43
1:A:6:ILE:HG21	5:B:261:HOH:O	2.19	0.43
2:B:146:TYR:HD1	2:B:146:TYR:HA	1.66	0.43
3:C:167:ASN:OD1	3:C:170:LYS:HD3	2.19	0.43
2:B:146:TYR:CE1	3:C:192:MET:CE	3.01	0.43
2:B:51:TRP:HA	2:B:106:LEU:O	2.19	0.43
3:C:165:ASN:ND2	3:C:230:ARG:HH11	2.17	0.43
2:B:146:TYR:HE1	3:C:192:MET:CE	2.32	0.43
3:C:245:ASN:ND2	3:C:245:ASN:N	2.66	0.43
2:B:88:VAL:HG23	2:B:88:VAL:H	1.51	0.43
2:B:144:THR:HG23	3:C:152:PRO:CG	2.49	0.43
2:B:125:SER:O	2:B:126:ALA:C	2.61	0.43
3:C:165:ASN:ND2	3:C:230:ARG:NH1	2.67	0.43
3:C:195:SER:C	3:C:197:GLY:H	2.27	0.43
2:B:49:GLU:CA	5:B:272:HOH:O	2.67	0.42
1:A:3:VAL:CG2	1:A:3:VAL:O	2.67	0.42
2:B:51:TRP:CH2	2:B:89:PHE:CD1	3.07	0.42
2:B:41:PHE:CD1	2:B:41:PHE:C	2.97	0.42
2:B:87:LYS:HE2	2:B:87:LYS:HB3	1.75	0.42
2:B:16:ILE:N	3:C:194:ASP:OD1	2.52	0.42
3:C:165:ASN:O	3:C:169:LYS:N	2.52	0.42
3:C:228:TYR:CD1	3:C:228:TYR:N	2.88	0.42
2:B:51:TRP:CH2	2:B:107:LYS:HB2	2.55	0.42
3:C:165:ASN:HD21	3:C:230:ARG:NH1	2.17	0.42
2:B:67:VAL:HG22	2:B:82:LYS:HG2	2.01	0.42
3:C:167:ASN:HA	3:C:170:LYS:CD	2.49	0.41
3:C:209:LEU:HD23	3:C:209:LEU:HA	1.83	0.41
2:B:43:GLY:N	3:C:195:SER:O	2.36	0.41
2:B:28:PRO:HB2	2:B:119:SER:N	2.35	0.41
2:B:103:ILE:HD13	3:C:237:TRP:HZ3	1.85	0.41
3:C:165:ASN:HD21	3:C:230:ARG:HH11	1.67	0.41
2:B:53:VAL:HG13	2:B:105:LEU:HD23	2.03	0.41
2:B:86:ALA:HB2	2:B:109:SER:HA	2.03	0.41
2:B:43:GLY:O	3:C:196:GLY:HA3	2.21	0.41
2:B:54:THR:HA	3:C:196:GLY:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:100:ASN:ND2	3:C:180:MET:HG3	2.34	0.41
2:B:103:ILE:HG13	3:C:212:ILE:CD1	2.50	0.41
3:C:168:CYS:O	3:C:171:TYR:HB2	2.20	0.41
3:C:172:TRP:CZ2	3:C:224:THR:CG2	3.04	0.41
3:C:212:ILE:O	3:C:213:VAL:C	2.64	0.41
3:C:159:SER:O	3:C:160:LEU:HB3	2.21	0.41
2:B:116:GLN:HE21	2:B:116:GLN:HB2	1.40	0.40
3:C:154:ARG:H	3:C:154:ARG:HG2	1.43	0.40
2:B:25:GLY:CA	2:B:117:THR:HG22	2.44	0.40
2:B:35:ASP:O	2:B:37:THR:N	2.54	0.40
2:B:64:ASP:O	2:B:85:ILE:HD12	2.20	0.40
1:A:6:ILE:HD11	2:B:116:GLN:HG2	2.03	0.40

All (7) 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)
3:C:240:GLN:NE2	5:A:251:HOH:O[5_646]	0.51	1.69
5:B:273:HOH:O	5:B:273:HOH:O[2_675]	0.78	1.42
3:C:240:GLN:CD	5:A:251:HOH:O[5_646]	1.29	0.91
5:B:274:HOH:O	5:B:286:HOH:O[2_675]	1.64	0.56
2:B:82:LYS:NZ	5:B:302:HOH:O[6_476]	1.75	0.45
5:B:276:HOH:O	5:C:322:HOH:O[6_476]	1.86	0.34
3:C:240:GLN:CG	5:A:251:HOH:O[5_646]	2.07	0.13

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	9/13 (69%)	7 (78%)	2 (22%)	0	100	100
2	B	129/131 (98%)	116 (90%)	11 (8%)	2 (2%)	7	2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	93/97 (96%)	87 (94%)	6 (6%)	0	100	100
All	All	231/241 (96%)	210 (91%)	19 (8%)	2 (1%)	14	6

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	79	LYS
2	B	99	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	A	8/10 (80%)	7 (88%)	1 (12%)	4	1
2	B	109/109 (100%)	89 (82%)	20 (18%)	2	0
3	C	76/77 (99%)	58 (76%)	18 (24%)	1	0
All	All	193/196 (98%)	154 (80%)	39 (20%)	1	0

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	VAL
2	B	20	GLU
2	B	37	THR
2	B	42	CYS
2	B	47	ILE
2	B	48	ASN
2	B	49	GLU
2	B	53	VAL
2	B	54	THR
2	B	63	SER
2	B	65	VAL
2	B	75	SER
2	B	76	SER

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Mol	Chain	Res	Type
2	B	90	LYS
2	B	99	ILE
2	B	103	ILE
2	B	104	THR
2	B	106	LEU
2	B	110	THR
2	B	124	PRO
2	B	127	SER
3	C	151	THR
3	C	159	SER
3	C	163	LEU
3	C	166	THR
3	C	178	ASP
3	C	199	LEU
3	C	202	LYS
3	C	203	LYS
3	C	208	THR
3	C	209	LEU
3	C	214	SER
3	C	217	SER
3	C	219	THR
3	C	222	THR
3	C	224	THR
3	C	232	THR
3	C	239	GLN
3	C	240	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	48	ASN
2	B	100	ASN
2	B	116	GLN
3	C	165	ASN
3	C	239	GLN

5.3.3 RNA ⓘ

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](#)

1 ligand is 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	OAC	C	246	-	11,12,13	3.71	6 (54%)	14,15,17	7.98	9 (64%)

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	OAC	C	246	-	1/1/1/2	4/6/6/8	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	246	OAC	CE2-CD2	8.00	1.53	1.39
4	C	246	OAC	CZ-CE2	5.51	1.48	1.38
4	C	246	OAC	OH-CD2	4.14	1.44	1.36
4	C	246	OAC	O-C	4.11	1.35	1.20
4	C	246	OAC	CB1-CG	3.19	1.56	1.51
4	C	246	OAC	CE1-CD1	-2.26	1.35	1.38

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	246	OAC	CB2-CA-CB1	25.30	138.91	109.83
4	C	246	OAC	CG-CB1-CA	12.55	131.87	113.83
4	C	246	OAC	OH-CD2-CG	3.85	128.51	118.79
4	C	246	OAC	CB1-CG-CD2	-3.82	116.71	121.05
4	C	246	OAC	CE2-CD2-CG	-3.82	116.07	120.43
4	C	246	OAC	O-C-CA	3.65	133.46	125.33
4	C	246	OAC	CB1-CA-C	3.48	117.79	110.81
4	C	246	OAC	CD1-CG-CD2	3.46	121.93	118.16
4	C	246	OAC	CZ-CE2-CD2	-2.40	117.08	120.05

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	C	246	OAC	CA

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	246	OAC	O-C-CA-CB1
4	C	246	OAC	CB2-CA-CB1-CG
4	C	246	OAC	CA-CB1-CG-CD2
4	C	246	OAC	CA-CB1-CG-CD1

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	246	OAC	3	0

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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.