



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 04:46 AM UTC

PDB ID : 2Y6I / pdb_00002y6i
Title : Crystal Structure of Collagenase G from Clostridium histolyticum in complex with Isoamylphosphonyl-Gly-Pro-Ala at 3.25 Angstrom Resolution
Authors : Eckhard, U.; Brandstetter, H.
Deposited on : 2011-01-21
Resolution : 3.25 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
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

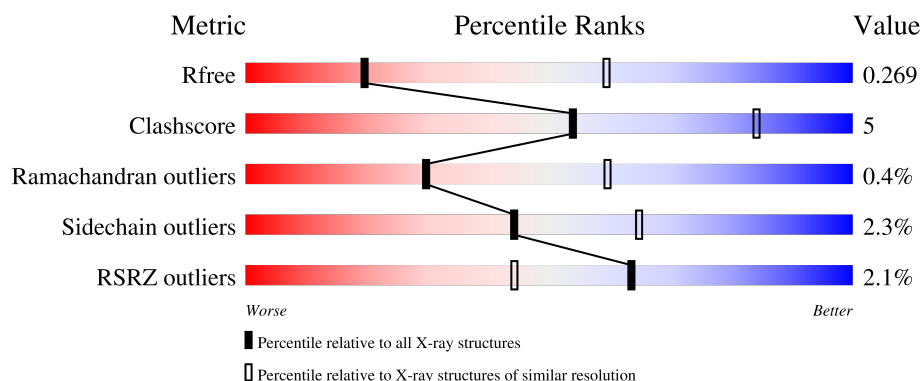
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

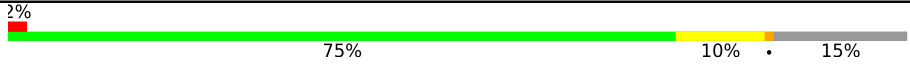
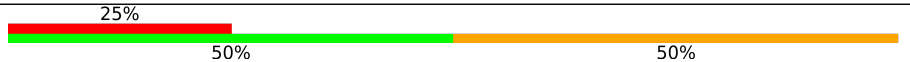
The reported resolution of this entry is 3.25 Å.

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	1605 (3.30-3.22)
Clashscore	190562	1660 (3.30-3.22)
Ramachandran outliers	187476	1630 (3.30-3.22)
Sidechain outliers	187428	1629 (3.30-3.22)
RSRZ outliers	180081	1605 (3.30-3.22)

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	785	
2	B	4	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 5378 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 COLLAGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	671	5241	3359	837	1032	13	0	0	0

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	96	MET	-	expression tag	UNP Q9X721
A	97	GLY	-	expression tag	UNP Q9X721
A	98	SER	-	expression tag	UNP Q9X721
A	99	SER	-	expression tag	UNP Q9X721
A	100	HIS	-	expression tag	UNP Q9X721
A	101	HIS	-	expression tag	UNP Q9X721
A	102	HIS	-	expression tag	UNP Q9X721
A	103	HIS	-	expression tag	UNP Q9X721
A	104	HIS	-	expression tag	UNP Q9X721
A	105	HIS	-	expression tag	UNP Q9X721
A	106	SER	-	expression tag	UNP Q9X721
A	107	SER	-	expression tag	UNP Q9X721
A	108	GLY	-	expression tag	UNP Q9X721
A	109	GLU	-	expression tag	UNP Q9X721
A	110	ASN	-	expression tag	UNP Q9X721
A	111	LEU	-	expression tag	UNP Q9X721
A	112	TYR	-	expression tag	UNP Q9X721
A	113	PHE	-	expression tag	UNP Q9X721
A	114	GLN	-	expression tag	UNP Q9X721
A	115	GLY	-	expression tag	UNP Q9X721
A	116	GLY	-	expression tag	UNP Q9X721
A	117	THR	-	expression tag	UNP Q9X721
A	118	MET	-	expression tag	UNP Q9X721
A	575	LEU	SER	SEE REMARK 999	UNP Q9X721
A	665	VAL	ALA	SEE REMARK 999	UNP Q9X721
A	790	GLY	ALA	SEE REMARK 999	UNP Q9X721

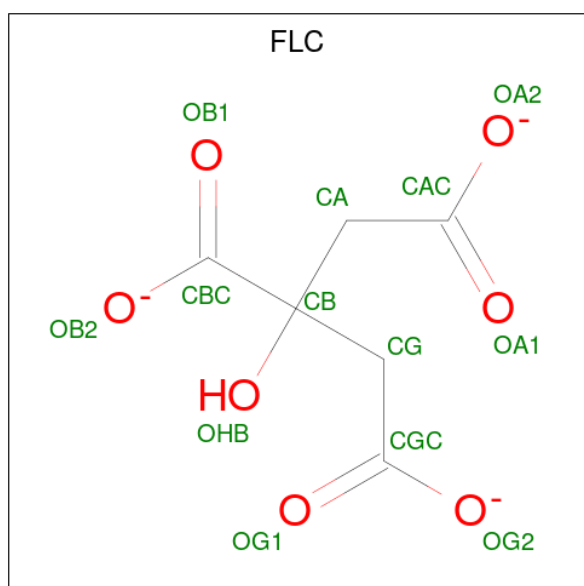
- Molecule 2 is a protein called ISOAMYLPHOSPHONYL-GLY-PRO-ALA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	4	Total	C	N	O	P	0	0	0
			25	15	3	6	1			

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		

- Molecule 4 is CITRATE ANION (CCD ID: FLC) (formula: C₆H₅O₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			13	6	7		

- Molecule 5 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: C₄H₁₂NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			8	4	1	3		
5	A	1	Total	C	N	O	0	0
			8	4	1	3		
5	A	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 6 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



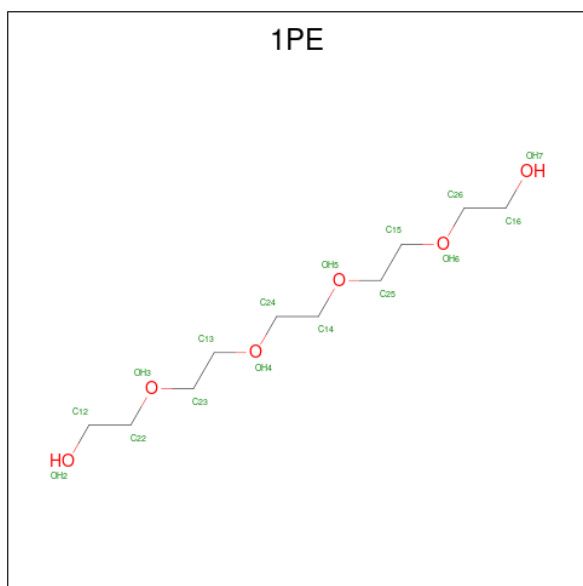
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			7	4	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			7	4	3		

- Molecule 7 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: $C_{10}H_{22}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			16	10	6		

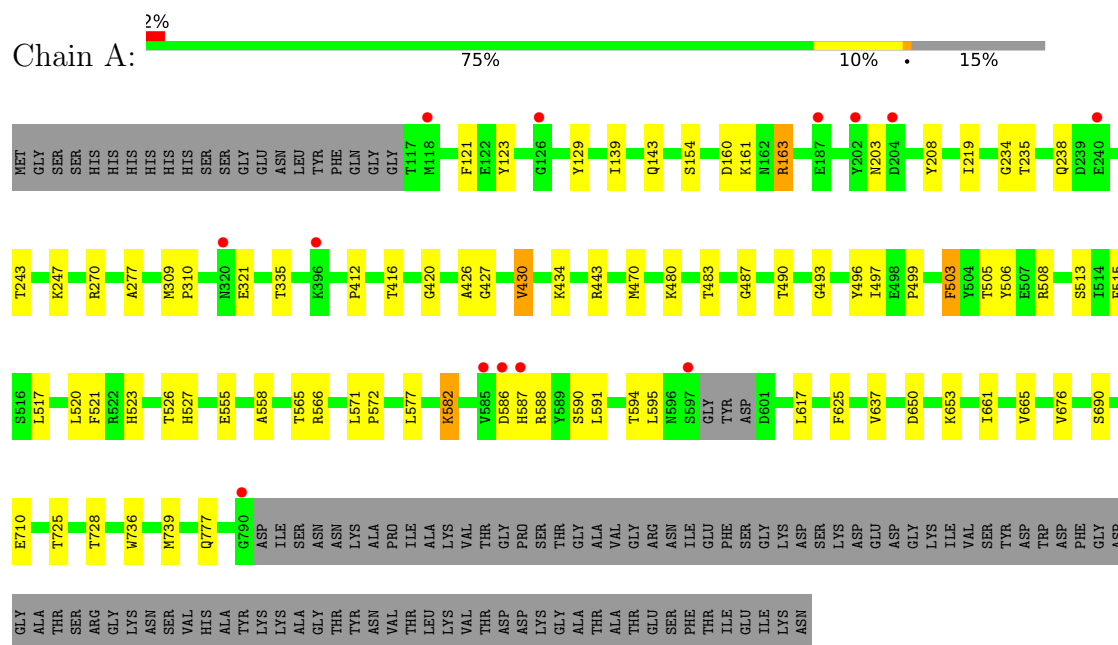
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	44	Total	O	0	0
			44	44		

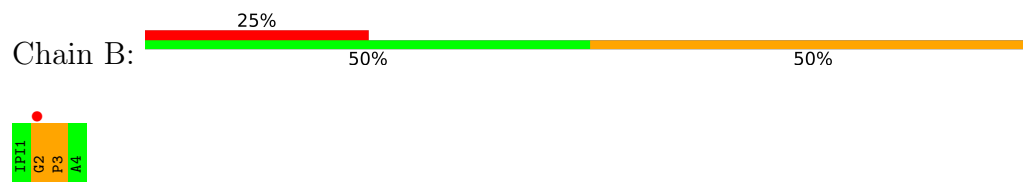
3 Residue-property plots [i](#)

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

• Molecule 1: COLLAGENASE



• Molecule 2: ISOAMYLPHOSPHONYL-GLY-PRO-ALA



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	58.12Å 108.84Å 181.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	93.28 – 3.25 93.28 – 3.25	Depositor EDS
% Data completeness (in resolution range)	99.1 (93.28-3.25) 99.1 (93.28-3.25)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.18 (at 3.25Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.216 , 0.266 0.220 , 0.269	Depositor DCC
R_{free} test set	958 reflections (5.15%)	wwPDB-VP
Wilson B-factor (Å ²)	73.3	Xtriage
Anisotropy	0.134	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 81.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5378	wwPDB-VP
Average B, all atoms (Å ²)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.61% 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: 1PE, IPI, ZN, TRS, FLC, PEG

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	0.42	1/5365 (0.0%)	0.81	1/7293 (0.0%)
2	B	1.34	0/17	1.46	0/21
All	All	0.43	1/5382 (0.0%)	0.81	1/7314 (0.0%)

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
2	B	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	219	ILE	CA-CB	5.81	1.57	1.54

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	203	ASN	N-CA-C	5.07	117.16	108.90

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	2	GLY	Peptide
2	B	3	PRO	Peptide

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	5241	0	4785	50	0
2	B	25	0	26	1	0
3	A	1	0	0	0	0
4	A	13	0	5	3	0
5	A	24	0	36	2	0
6	A	14	0	20	0	0
7	A	16	0	22	0	0
8	A	44	0	0	1	0
All	All	5378	0	4894	50	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 (50) 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:480:LYS:HA	1:A:490:THR:HG21	1.47	0.95
1:A:508:ARG:HD2	1:A:515:PHE:O	1.87	0.74
1:A:508:ARG:HD3	1:A:513:SER:HB3	1.69	0.73
1:A:586:ASP:O	1:A:588:ARG:N	2.23	0.70
1:A:736:TRP:HZ3	4:A:1793:FLC:HG2	1.56	0.69
1:A:470:MET:HG2	1:A:503:PHE:CE2	2.30	0.67
1:A:426:ALA:HB1	1:A:430:VAL:HG11	1.78	0.66
1:A:520:LEU:HD11	2:B:2:GLY:O	1.96	0.65
1:A:527:HIS:CD2	8:A:2042:HOH:O	2.52	0.63
1:A:565:THR:HG21	1:A:571:LEU:HD12	1.83	0.61
1:A:725:THR:HB	1:A:777:GLN:HE21	1.67	0.59
1:A:483:THR:HB	1:A:490:THR:OG1	2.02	0.58
1:A:277:ALA:HB3	1:A:335:THR:HG22	1.89	0.55
1:A:243:THR:O	1:A:247:LYS:HG3	2.06	0.55
1:A:555:GLU:HA	1:A:555:GLU:OE1	2.07	0.55
1:A:139:ILE:HB	1:A:143:GLN:OE1	2.08	0.53
1:A:434:LYS:HD2	1:A:517:LEU:HD23	1.89	0.53
1:A:736:TRP:CZ3	4:A:1793:FLC:HG2	2.40	0.51
1:A:617:LEU:HB3	1:A:625:PHE:HB2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:572:PRO:HB2	1:A:577:LEU:HD11	1.95	0.49
1:A:591:LEU:O	1:A:595:LEU:HG	2.14	0.48
1:A:426:ALA:HB1	1:A:430:VAL:CG1	2.42	0.47
1:A:496:TYR:HD1	1:A:503:PHE:HB3	1.79	0.47
1:A:508:ARG:CD	1:A:515:PHE:O	2.62	0.47
1:A:235:THR:HG23	1:A:238:GLN:H	1.80	0.47
1:A:736:TRP:HZ3	4:A:1793:FLC:CG	2.26	0.47
1:A:270:ARG:NH1	1:A:321:GLU:OE2	2.49	0.46
1:A:129:TYR:HE1	1:A:163:ARG:HH11	1.64	0.45
1:A:566:ARG:H	5:A:1795:TRS:H32	1.81	0.45
1:A:582:LYS:HD2	1:A:582:LYS:C	2.41	0.45
1:A:309:MET:HA	1:A:310:PRO:HD3	1.86	0.44
1:A:161:LYS:HG2	1:A:208:TYR:CE2	2.53	0.44
1:A:661:ILE:O	1:A:665:VAL:HG23	2.18	0.44
1:A:123:TYR:C	1:A:123:TYR:CD1	2.96	0.43
1:A:427:GLY:O	1:A:430:VAL:HG12	2.19	0.43
1:A:505:THR:OG1	1:A:506:TYR:N	2.52	0.43
1:A:497:ILE:HG22	1:A:499:PRO:HD2	2.01	0.42
1:A:416:THR:HG23	1:A:420:GLY:HA2	2.00	0.42
1:A:503:PHE:HZ	1:A:521:PHE:CD1	2.38	0.42
1:A:565:THR:HB	5:A:1795:TRS:H31	2.01	0.42
1:A:443:ARG:HD3	1:A:443:ARG:HA	1.80	0.42
1:A:526:THR:HG21	1:A:558:ALA:HA	2.01	0.41
1:A:483:THR:O	1:A:487:GLY:HA2	2.21	0.41
1:A:523:HIS:CD2	1:A:523:HIS:C	2.98	0.41
1:A:412:PRO:HD2	1:A:427:GLY:HA2	2.01	0.41
1:A:160:ASP:HB3	1:A:163:ARG:HB2	2.03	0.41
1:A:493:GLY:C	1:A:520:LEU:HD21	2.45	0.41
1:A:650:ASP:HB3	1:A:653:LYS:HB2	2.02	0.41
1:A:480:LYS:O	1:A:483:THR:HG22	2.21	0.41
1:A:121:PHE:CE1	1:A:154:SER:HA	2.56	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	667/785 (85%)	639 (96%)	26 (4%)	2 (0%)	36	66
2	B	1/4 (25%)	0	0	1 (100%)	0	0
All	All	668/789 (85%)	639 (96%)	26 (4%)	3 (0%)	30	59

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	3	PRO
1	A	234	GLY
1	A	587	HIS

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	517/672 (77%)	505 (98%)	12 (2%)	44	65
2	B	1/1 (100%)	1 (100%)	0	100	100
All	All	518/673 (77%)	506 (98%)	12 (2%)	44	65

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	163	ARG
1	A	430	VAL
1	A	503	PHE
1	A	582	LYS
1	A	590	SER
1	A	594	THR
1	A	637	VAL
1	A	676	VAL
1	A	690	SER
1	A	710	GLU

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Mol	Chain	Res	Type
1	A	728	THR
1	A	739	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	165	GLN
1	A	287	ASN
1	A	355	ASN
1	A	409	HIS
1	A	486	ASN
1	A	492	ASN
1	A	587	HIS
1	A	596	ASN
1	A	777	GLN

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](#)

Of 8 ligands modelled in this entry, 1 is monoatomic - leaving 7 for Mogul analysis.

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	FLC	A	1793	-	12,12,12	1.37	1 (8%)	17,17,17	1.03	0
5	TRS	A	1795	-	7,7,7	0.39	0	9,9,9	0.77	0
6	PEG	A	1798	-	6,6,6	0.44	0	5,5,5	0.33	0
6	PEG	A	1797	-	6,6,6	0.47	0	5,5,5	0.29	0
7	1PE	A	1799	-	15,15,15	0.50	0	14,14,14	0.23	0
5	TRS	A	1794	-	7,7,7	0.35	0	9,9,9	0.59	0
5	TRS	A	1796	-	7,7,7	0.40	0	9,9,9	0.58	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	FLC	A	1793	-	-	9/16/16/16	-
5	TRS	A	1795	-	-	6/9/9/9	-
6	PEG	A	1798	-	-	2/4/4/4	-
6	PEG	A	1797	-	-	4/4/4/4	-
7	1PE	A	1799	-	-	9/13/13/13	-
5	TRS	A	1794	-	-	3/9/9/9	-
5	TRS	A	1796	-	-	5/9/9/9	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1793	FLC	CB-CBC	-3.20	1.50	1.53

There are no bond angle outliers.

There are no chirality outliers.

All (38) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1793	FLC	CAC-CA-CB-CBC
4	A	1793	FLC	CAC-CA-CB-OHB
4	A	1793	FLC	CA-CB-CBC-OB1
4	A	1793	FLC	CA-CB-CBC-OB2
4	A	1793	FLC	OHB-CB-CBC-OB1
4	A	1793	FLC	OHB-CB-CBC-OB2
5	A	1795	TRS	C2-C-C1-O1

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Mol	Chain	Res	Type	Atoms
5	A	1795	TRS	C3-C-C1-O1
5	A	1795	TRS	N-C-C1-O1
5	A	1795	TRS	C1-C-C3-O3
5	A	1795	TRS	C2-C-C3-O3
7	A	1799	1PE	OH5-C14-C24-OH4
4	A	1793	FLC	CAC-CA-CB-CG
7	A	1799	1PE	OH4-C13-C23-OH3
7	A	1799	1PE	OH6-C15-C25-OH5
6	A	1797	PEG	O1-C1-C2-O2
6	A	1797	PEG	O2-C3-C4-O4
7	A	1799	1PE	OH7-C16-C26-OH6
5	A	1794	TRS	C3-C-C1-O1
7	A	1799	1PE	C15-C25-OH5-C14
7	A	1799	1PE	C23-C13-OH4-C24
4	A	1793	FLC	CBC-CB-CG-CGC
6	A	1797	PEG	C1-C2-O2-C3
7	A	1799	1PE	C14-C24-OH4-C13
7	A	1799	1PE	OH2-C12-C22-OH3
5	A	1794	TRS	C2-C-C1-O1
5	A	1796	TRS	C3-C-C1-O1
5	A	1796	TRS	C3-C-C2-O2
6	A	1798	PEG	O1-C1-C2-O2
4	A	1793	FLC	CA-CB-CG-CGC
6	A	1798	PEG	O2-C3-C4-O4
5	A	1794	TRS	N-C-C1-O1
5	A	1795	TRS	N-C-C3-O3
6	A	1797	PEG	C4-C3-O2-C2
5	A	1796	TRS	C2-C-C1-O1
5	A	1796	TRS	C1-C-C2-O2
5	A	1796	TRS	N-C-C2-O2
7	A	1799	1PE	C16-C26-OH6-C15

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1793	FLC	3	0
5	A	1795	TRS	2	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 [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	A	671/785 (85%)	0.09	13 (1%) 66 48	40, 73, 113, 181	0
2	B	3/4 (75%)	1.90	1 (33%) 1 1	84, 84, 89, 91	0
All	All	674/789 (85%)	0.10	14 (2%) 63 44	40, 74, 113, 181	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	240	GLU	3.9
1	A	597	SER	3.8
1	A	202	TYR	3.2
1	A	586	ASP	3.2
1	A	587	HIS	3.1
1	A	204	ASP	2.7
2	B	2	GLY	2.6
1	A	187	GLU	2.5
1	A	790	GLY	2.3
1	A	320	ASN	2.3
1	A	118	MET	2.2
1	A	396	LYS	2.1
1	A	126	GLY	2.1
1	A	585	VAL	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	PEG	A	1798	7/7	0.61	0.18	98,98,98,99	0
5	TRS	A	1795	8/8	0.73	0.15	80,81,81,81	0
5	TRS	A	1794	8/8	0.77	0.15	79,80,80,81	0
5	TRS	A	1796	8/8	0.85	0.15	79,79,79,79	0
4	FLC	A	1793	13/13	0.87	0.15	59,60,62,62	0
7	1PE	A	1799	16/16	0.88	0.14	79,80,81,81	0
6	PEG	A	1797	7/7	0.90	0.19	92,92,92,93	0
3	ZN	A	1791	1/1	0.99	0.09	55,55,55,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.