



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 20, 2026 – 06:31 AM UTC

PDB ID : 7ZAZ / pdb_00007zaz
Title : macrocyclase OphP with ZPP
Authors : Song, H.; Naismith, J.H.
Deposited on : 2022-03-23
Resolution : 2.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

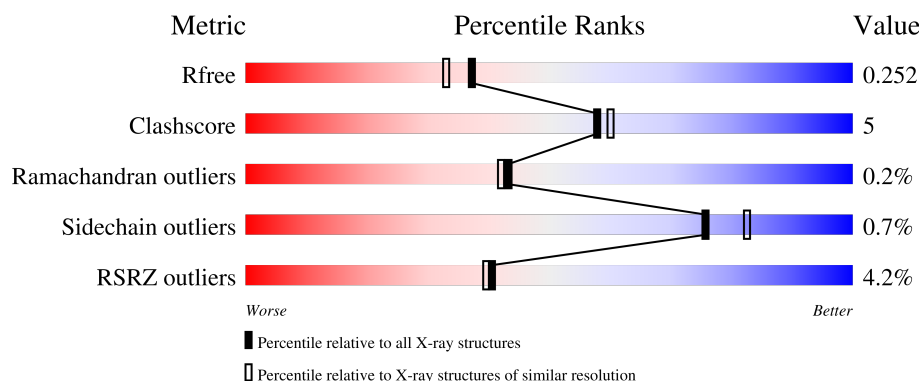
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	AAA	745	4% 89% 9% .
1	BBB	745	5% 85% 10% 5%
1	CCC	745	4% 83% 10% 7%
1	DDD	745	3% 86% 10% .

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
3	DMS	BBB	802	-	-	X	-

2 Entry composition [i](#)

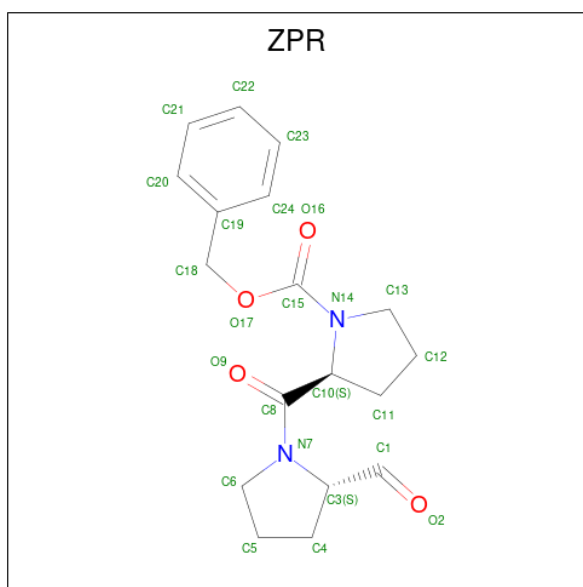
There are 9 unique types of molecules in this entry. The entry contains 24384 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Prolyl endopeptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	727	Total	C	N	O	S	0	2	0
			5834	3722	982	1104	26			
1	BBB	706	Total	C	N	O	S	0	1	0
			5663	3617	946	1073	27			
1	CCC	690	Total	C	N	O	S	0	0	0
			5549	3556	926	1041	26			
1	DDD	716	Total	C	N	O	S	0	2	0
			5753	3672	970	1085	26			

- Molecule 2 is N-BENZYLOXYCARBONYL-L-PROLYL-L-PROLINAL (CCD ID: ZPR) (formula: C₁₈H₂₂N₂O₄) (labeled as "Ligand of Interest" by depositor).



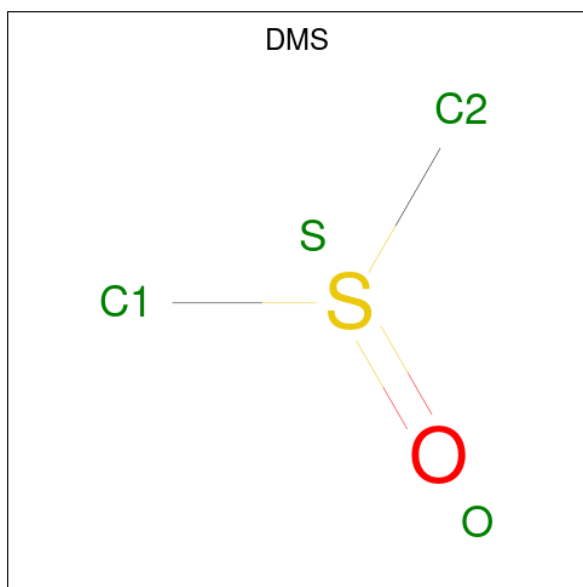
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	AAA	1	Total	C	N	O	0	0
			24	18	2	4		
2	BBB	1	Total	C	N	O	0	0
			24	18	2	4		

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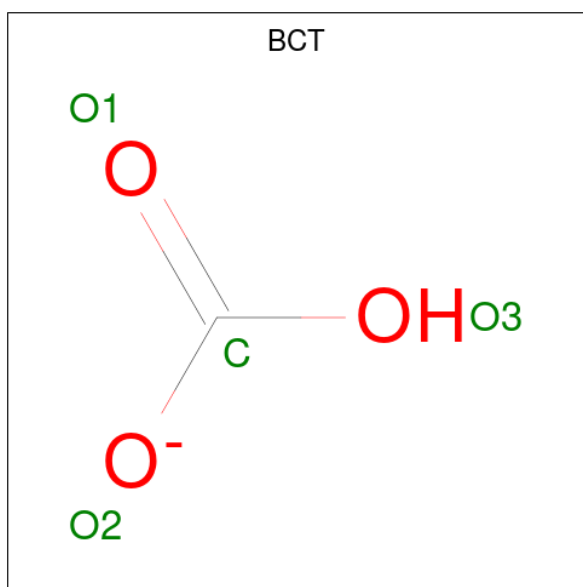
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	CCC	1	Total	C	N	O	0	0
			24	18	2	4		
2	DDD	1	Total	C	N	O	0	0
			24	18	2	4		

- Molecule 3 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C_2H_6OS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	AAA	1	Total	C	O	S	0	0
			4	2	1	1		
3	AAA	1	Total	C	O	S	0	0
			4	2	1	1		
3	BBB	1	Total	C	O	S	0	0
			4	2	1	1		
3	DDD	1	Total	C	O	S	0	0
			4	2	1	1		

- Molecule 4 is BICARBONATE ION (CCD ID: BCT) (formula: CHO_3).



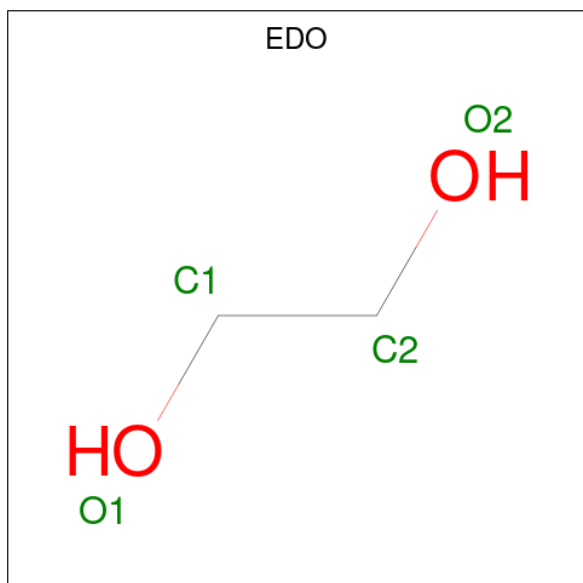
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	AAA	1	Total	C	O	0	0
			4	1	3		
4	AAA	1	Total	C	O	0	0
			4	1	3		
4	AAA	1	Total	C	O	0	0
			4	1	3		
4	AAA	1	Total	C	O	0	0
			4	1	3		
4	AAA	1	Total	C	O	0	0
			4	1	3		
4	AAA	1	Total	C	O	0	0
			4	1	3		
4	BBB	1	Total	C	O	0	0
			4	1	3		
4	BBB	1	Total	C	O	0	0
			4	1	3		
4	BBB	1	Total	C	O	0	0
			4	1	3		
4	BBB	1	Total	C	O	0	0
			4	1	3		
4	BBB	1	Total	C	O	0	0
			4	1	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	CCC	1	Total	C	O	0	0
			4	1	3		
4	CCC	1	Total	C	O	0	0
			4	1	3		
4	CCC	1	Total	C	O	0	0
			4	1	3		
4	CCC	1	Total	C	O	0	0
			4	1	3		
4	CCC	1	Total	C	O	0	0
			4	1	3		
4	DDD	1	Total	C	O	0	0
			4	1	3		
4	DDD	1	Total	C	O	0	0
			4	1	3		
4	DDD	1	Total	C	O	0	0
			4	1	3		
4	DDD	1	Total	C	O	0	0
			4	1	3		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



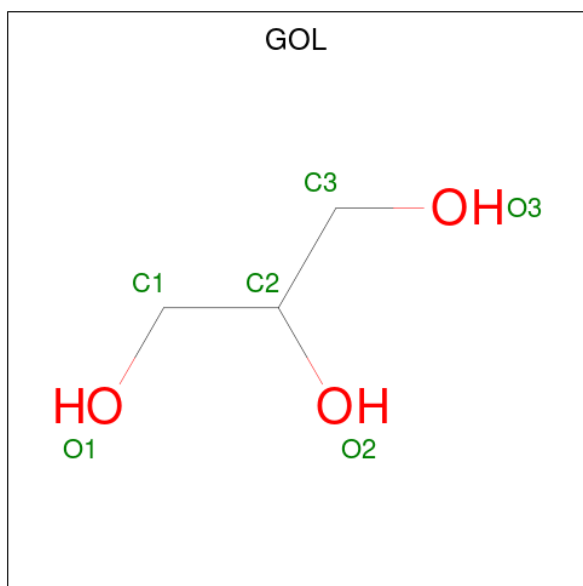
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	AAA	1	Total	C	O	0	0
			4	2	2		

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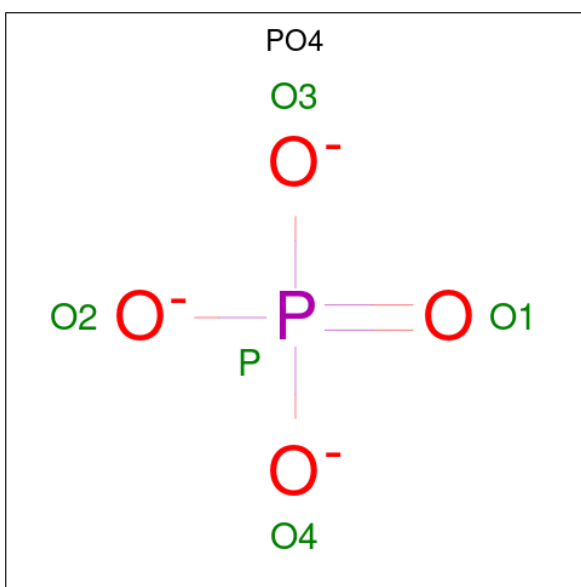
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	AAA	1	Total	C	O	0	0
			4	2	2		
5	AAA	1	Total	C	O	0	0
			4	2	2		
5	BBB	1	Total	C	O	0	0
			4	2	2		
5	CCC	1	Total	C	O	0	0
			4	2	2		
5	CCC	1	Total	C	O	0	0
			4	2	2		
5	DDD	1	Total	C	O	0	0
			4	2	2		
5	DDD	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	CCC	1	Total	C	O	0	0
			6	3	3		

- Molecule 7 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	DDD	1	Total	O	P	0	0
			5	4	1		
7	DDD	1	Total	O	P	0	0
			5	4	1		

- Molecule 8 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	DDD	1	Total	Na	0	0
			1	1		

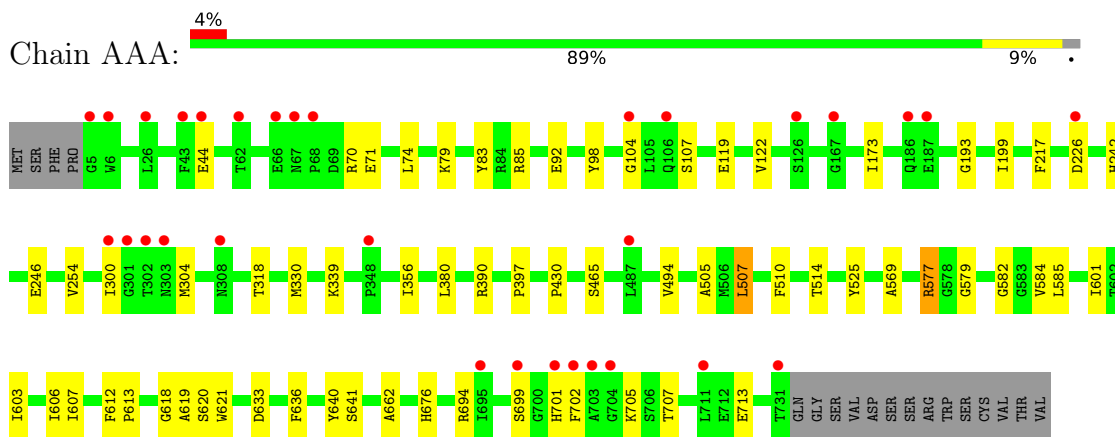
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	AAA	339	Total	O	0	0
			339	339		
9	BBB	288	Total	O	0	0
			288	288		
9	CCC	306	Total	O	0	0
			306	306		
9	DDD	395	Total	O	0	0
			395	395		

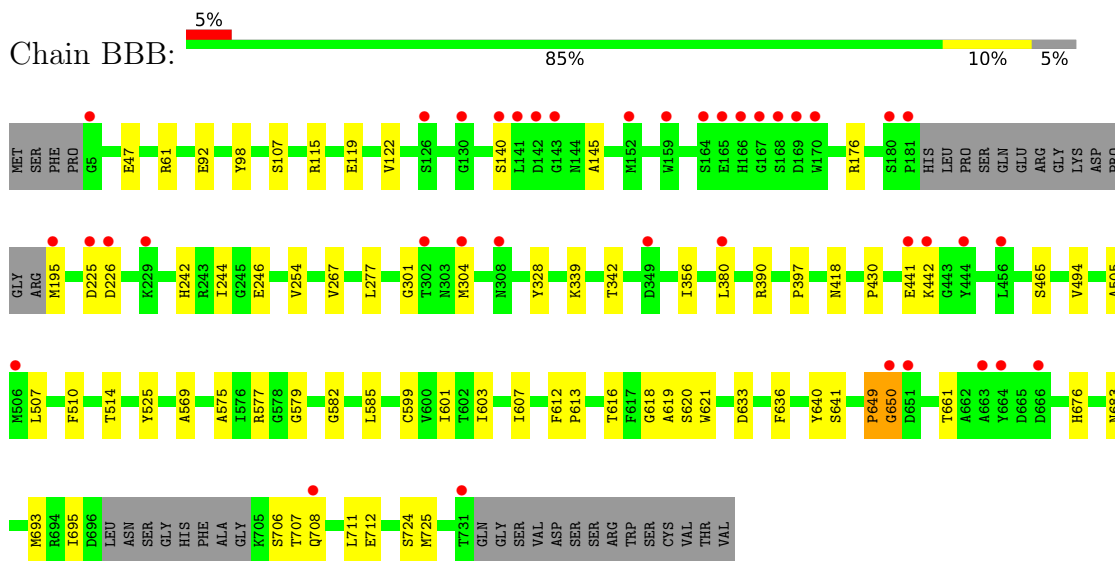
3 Residue-property plots [i](#)

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.

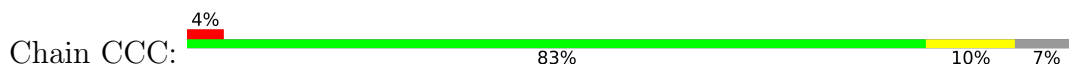
- Molecule 1: Prolyl endopeptidase

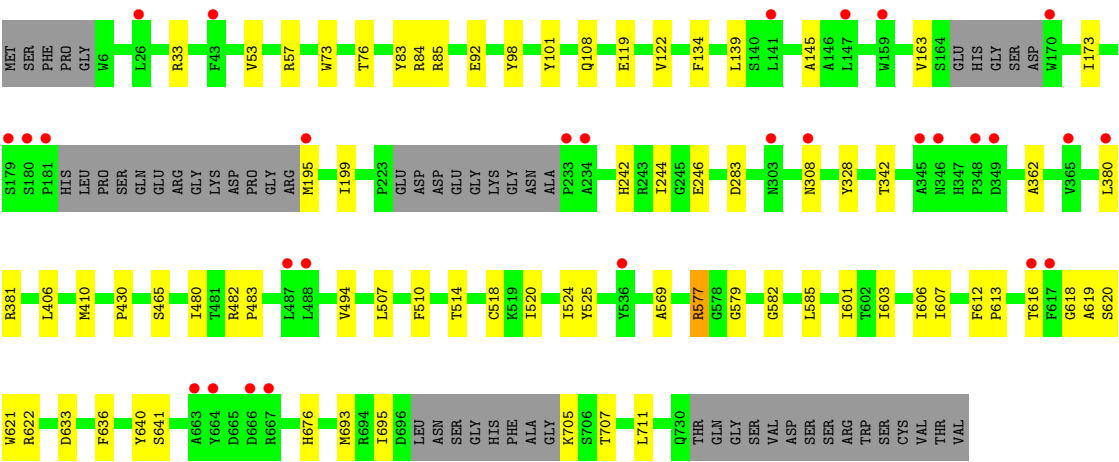


- Molecule 1: Prolyl endopeptidase

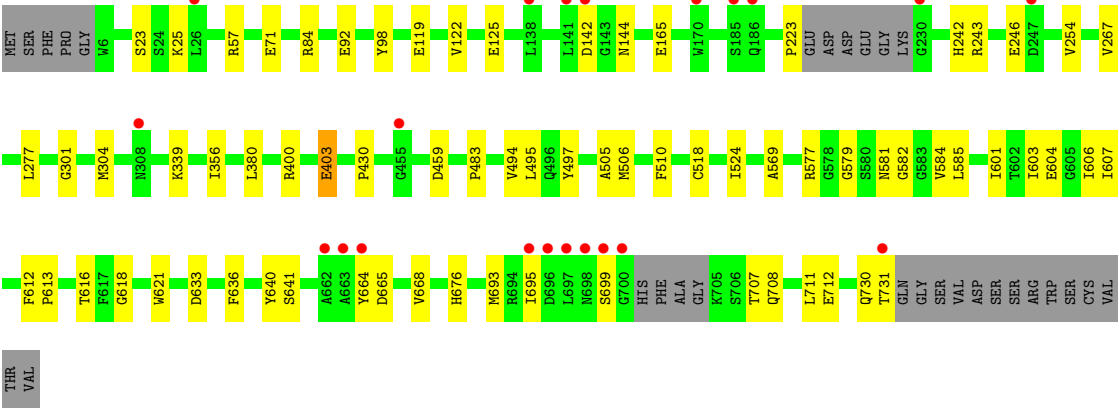


- Molecule 1: Prolyl endopeptidase





• Molecule 1: Prolyl endopeptidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	69.68Å 102.65Å 110.27Å 116.23° 101.09° 92.18°	Depositor
Resolution (Å)	67.80 – 2.00 67.80 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.5 (67.80-2.00) 97.6 (67.80-2.00)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.49 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.209 , 0.245 0.218 , 0.252	Depositor DCC
R_{free} test set	8559 reflections (4.76%)	wwPDB-VP
Wilson B-factor (Å ²)	26.0	Xtriage
Anisotropy	0.381	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 41.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.000 for -h,k,-k-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	24384	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 3.53% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, BCT, EDO, PO4, DMS, ZPR, NA

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	AAA	0.99	0/6004	1.25	0/8145
1	BBB	0.97	0/5826	1.26	1/7903 (0.0%)
1	CCC	0.97	0/5709	1.24	0/7741
1	DDD	0.98	0/5919	1.25	1/8029 (0.0%)
All	All	0.98	0/23458	1.25	2/31818 (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
1	CCC	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BBB	649	PRO	CB-CA-C	-7.93	99.84	112.21
1	DDD	403	GLU	CB-CA-C	-5.79	101.19	110.79

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	CCC	163	VAL	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	AAA	5834	0	5566	48	0
1	BBB	5663	0	5393	53	0
1	CCC	5549	0	5314	52	0
1	DDD	5753	0	5493	52	0
2	AAA	24	0	21	0	0
2	BBB	24	0	21	1	0
2	CCC	24	0	21	4	0
2	DDD	24	0	21	0	0
3	AAA	8	0	12	2	0
3	BBB	4	0	6	4	0
3	DDD	4	0	6	0	0
4	AAA	28	0	0	0	0
4	BBB	28	0	0	0	0
4	CCC	20	0	0	0	0
4	DDD	20	0	0	0	0
5	AAA	12	0	18	0	0
5	BBB	4	0	6	0	0
5	CCC	8	0	12	0	0
5	DDD	8	0	12	0	0
6	CCC	6	0	8	1	0
7	DDD	10	0	0	0	0
8	DDD	1	0	0	0	0
9	AAA	339	0	0	4	0
9	BBB	288	0	0	3	0
9	CCC	306	0	0	0	0
9	DDD	395	0	0	2	0
All	All	24384	0	21930	204	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.

The worst 5 of 204 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:CCC:693:MET:HE3	1:CCC:695:ILE:HD11	1.49	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AAA:584:VAL:CG2	1:AAA:606:ILE:HG23	1.99	0.93
1:BBB:619:ALA:HB3	3:BBB:802:DMS:H11	1.57	0.85
1:DDD:693:MET:HE3	1:DDD:695:ILE:HD11	1.57	0.84
1:DDD:581:ASN:O	1:DDD:584:VAL:HG12	1.79	0.83

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	AAA	727/745 (98%)	704 (97%)	22 (3%)	1 (0%)	48	46
1	BBB	701/745 (94%)	678 (97%)	20 (3%)	3 (0%)	30	27
1	CCC	680/745 (91%)	661 (97%)	18 (3%)	1 (0%)	48	46
1	DDD	712/745 (96%)	688 (97%)	23 (3%)	1 (0%)	48	46
All	All	2820/2980 (95%)	2731 (97%)	83 (3%)	6 (0%)	43	42

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	BBB	226	ASP
1	BBB	650	GLY
1	BBB	616	THR
1	CCC	616	THR
1	DDD	616	THR

5.3.2 Protein sidechains [i](#)

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	AAA	630/645 (98%)	626 (99%)	4 (1%)	78	85
1	BBB	612/645 (95%)	605 (99%)	7 (1%)	65	73
1	CCC	601/645 (93%)	598 (100%)	3 (0%)	81	87
1	DDD	622/645 (96%)	620 (100%)	2 (0%)	86	91
All	All	2465/2580 (96%)	2449 (99%)	16 (1%)	76	85

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	DDD	165	GLU
1	CCC	705	LYS
1	BBB	442	LYS
1	CCC	577	ARG
1	BBB	225	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 44 ligands modelled in this entry, 1 is monoatomic - leaving 43 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
5	EDO	AAA	813	-	3,3,3	0.04	0	2,2,2	0.06	0
3	DMS	AAA	802	-	3,3,3	0.21	0	3,3,3	0.08	0
3	DMS	BBB	802	-	3,3,3	0.21	0	3,3,3	0.31	0
4	BCT	BBB	804	-	3,3,3	0.97	0	2,3,3	1.68	1 (50%)
4	BCT	BBB	808	-	3,3,3	1.49	0	2,3,3	0.85	0
5	EDO	AAA	811	-	3,3,3	0.10	0	2,2,2	0.04	0
4	BCT	AAA	809	-	3,3,3	1.49	0	2,3,3	0.87	0
4	BCT	BBB	801	-	3,3,3	1.45	0	2,3,3	0.87	0
4	BCT	BBB	805	-	3,3,3	1.00	0	2,3,3	1.65	1 (50%)
2	ZPR	CCC	806	1	25,26,26	1.33	1 (4%)	31,35,35	1.90	4 (12%)
4	BCT	AAA	804	-	3,3,3	0.97	0	2,3,3	1.69	1 (50%)
2	ZPR	AAA	801	1	25,26,26	1.28	1 (4%)	31,35,35	1.71	3 (9%)
5	EDO	DDD	809	-	3,3,3	0.09	0	2,2,2	0.00	0
4	BCT	AAA	807	-	3,3,3	1.01	0	2,3,3	1.65	1 (50%)
7	PO4	DDD	808	-	4,4,4	0.76	0	6,6,6	0.49	0
5	EDO	CCC	809	-	3,3,3	0.03	0	2,2,2	0.10	0
4	BCT	CCC	803	-	3,3,3	1.39	0	2,3,3	0.98	0
4	BCT	AAA	806	-	3,3,3	1.02	0	2,3,3	1.60	1 (50%)
4	BCT	BBB	810	-	3,3,3	1.42	0	2,3,3	0.90	0
4	BCT	AAA	808	-	3,3,3	1.01	0	2,3,3	1.63	1 (50%)
4	BCT	CCC	804	-	3,3,3	1.05	0	2,3,3	1.58	1 (50%)
4	BCT	DDD	804	-	3,3,3	1.00	0	2,3,3	1.59	1 (50%)
4	BCT	DDD	806	-	3,3,3	1.49	0	2,3,3	0.83	0
7	PO4	DDD	805	-	4,4,4	0.65	0	6,6,6	0.49	0
5	EDO	DDD	810	-	3,3,3	0.10	0	2,2,2	0.03	0
5	EDO	CCC	808	-	3,3,3	0.09	0	2,2,2	0.09	0
6	GOL	CCC	807	-	5,5,5	0.09	0	5,5,5	0.30	0
2	ZPR	DDD	801	1	25,26,26	1.41	2 (8%)	31,35,35	1.93	4 (12%)
4	BCT	AAA	805	-	3,3,3	0.98	0	2,3,3	1.59	1 (50%)
5	EDO	AAA	812	-	3,3,3	0.11	0	2,2,2	0.16	0
4	BCT	DDD	811	-	3,3,3	0.99	0	2,3,3	1.68	1 (50%)
3	DMS	DDD	803	-	3,3,3	0.24	0	3,3,3	0.06	0
4	BCT	BBB	806	-	3,3,3	1.04	0	2,3,3	1.52	0
4	BCT	DDD	802	-	3,3,3	0.96	0	2,3,3	1.68	1 (50%)
3	DMS	AAA	803	-	3,3,3	0.22	0	3,3,3	0.16	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	BCT	CCC	802	-	3,3,3	1.04	0	2,3,3	1.71	1 (50%)
4	BCT	CCC	801	-	3,3,3	0.96	0	2,3,3	1.67	1 (50%)
4	BCT	CCC	805	-	3,3,3	1.42	0	2,3,3	0.91	0
2	ZPR	BBB	807	1	25,26,26	1.27	1 (4%)	31,35,35	1.93	4 (12%)
4	BCT	AAA	810	-	3,3,3	1.01	0	2,3,3	1.66	1 (50%)
4	BCT	DDD	807	-	3,3,3	0.97	0	2,3,3	1.72	1 (50%)
5	EDO	BBB	809	-	3,3,3	0.04	0	2,2,2	0.29	0
4	BCT	BBB	803	-	3,3,3	1.39	0	2,3,3	0.94	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
5	EDO	AAA	813	-	-	1/1/1/1	-
2	ZPR	DDD	801	1	-	5/17/39/39	0/3/3/3
5	EDO	AAA	812	-	-	0/1/1/1	-
2	ZPR	CCC	806	1	-	7/17/39/39	0/3/3/3
5	EDO	BBB	809	-	-	1/1/1/1	-
2	ZPR	BBB	807	1	-	6/17/39/39	0/3/3/3
2	ZPR	AAA	801	1	-	3/17/39/39	0/3/3/3
5	EDO	AAA	811	-	-	1/1/1/1	-
5	EDO	DDD	810	-	-	1/1/1/1	-
5	EDO	CCC	808	-	-	1/1/1/1	-
5	EDO	DDD	809	-	-	0/1/1/1	-
6	GOL	CCC	807	-	-	1/4/4/4	-
5	EDO	CCC	809	-	-	0/1/1/1	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	CCC	806	ZPR	O17-C15	5.98	1.46	1.34
2	DDD	801	ZPR	O17-C15	5.95	1.46	1.34
2	BBB	807	ZPR	O17-C15	5.62	1.45	1.34
2	AAA	801	ZPR	O17-C15	5.52	1.45	1.34
2	DDD	801	ZPR	C3-N7	-2.71	1.45	1.48

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	DDD	801	ZPR	O17-C15-N14	8.29	120.61	111.02
2	BBB	807	ZPR	O17-C15-N14	7.82	120.06	111.02
2	CCC	806	ZPR	O17-C15-N14	7.20	119.35	111.02
2	AAA	801	ZPR	O17-C15-N14	6.78	118.86	111.02
2	BBB	807	ZPR	O17-C15-O16	-4.67	116.64	124.76

There are no chirality outliers.

5 of 27 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	BBB	807	ZPR	N14-C15-O17-C18
2	BBB	807	ZPR	C10-C8-N7-C6
2	BBB	807	ZPR	C10-C8-N7-C3
2	BBB	807	ZPR	O9-C8-N7-C6
2	BBB	807	ZPR	O9-C8-N7-C3

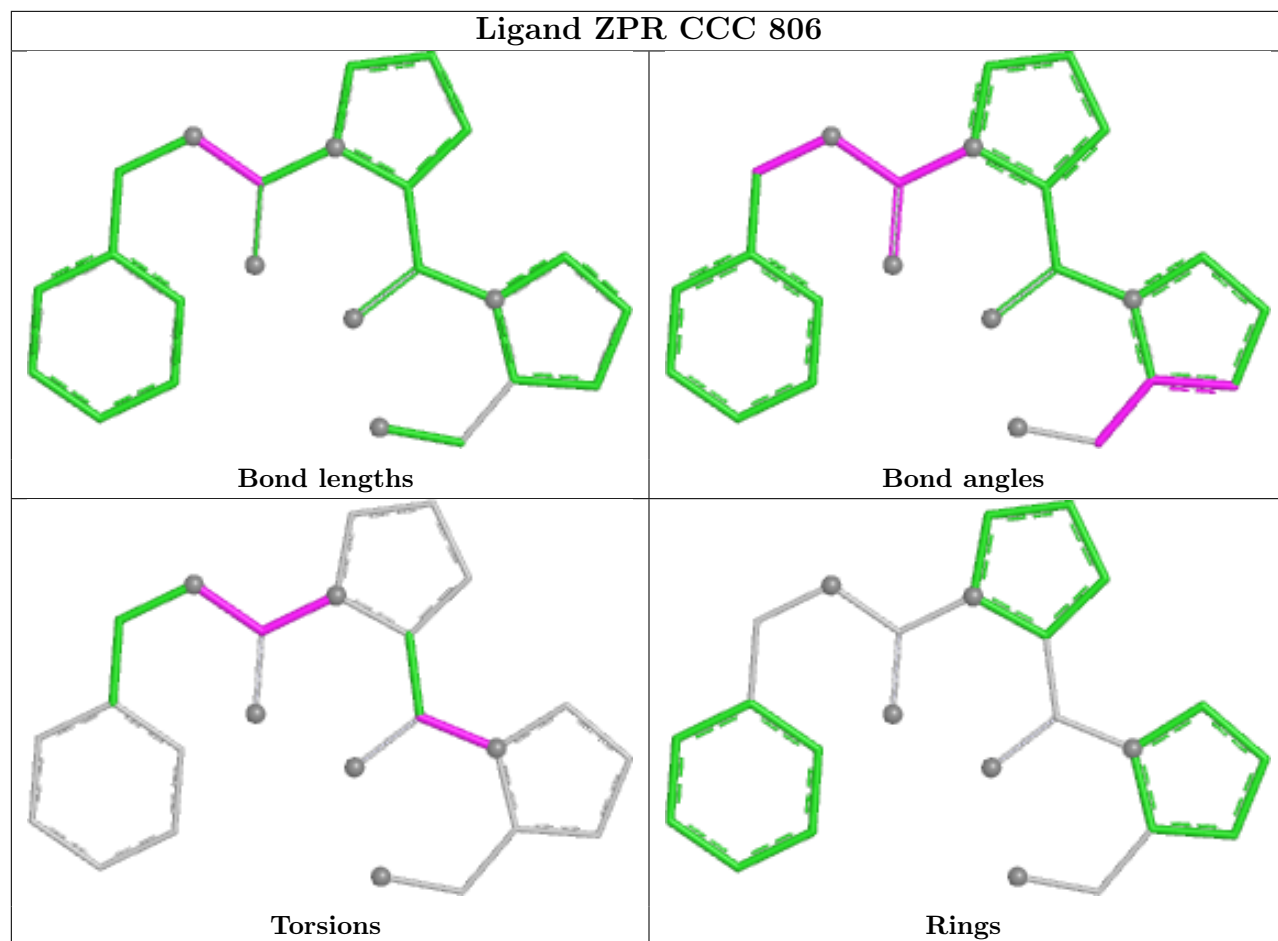
There are no ring outliers.

5 monomers are involved in 12 short contacts:

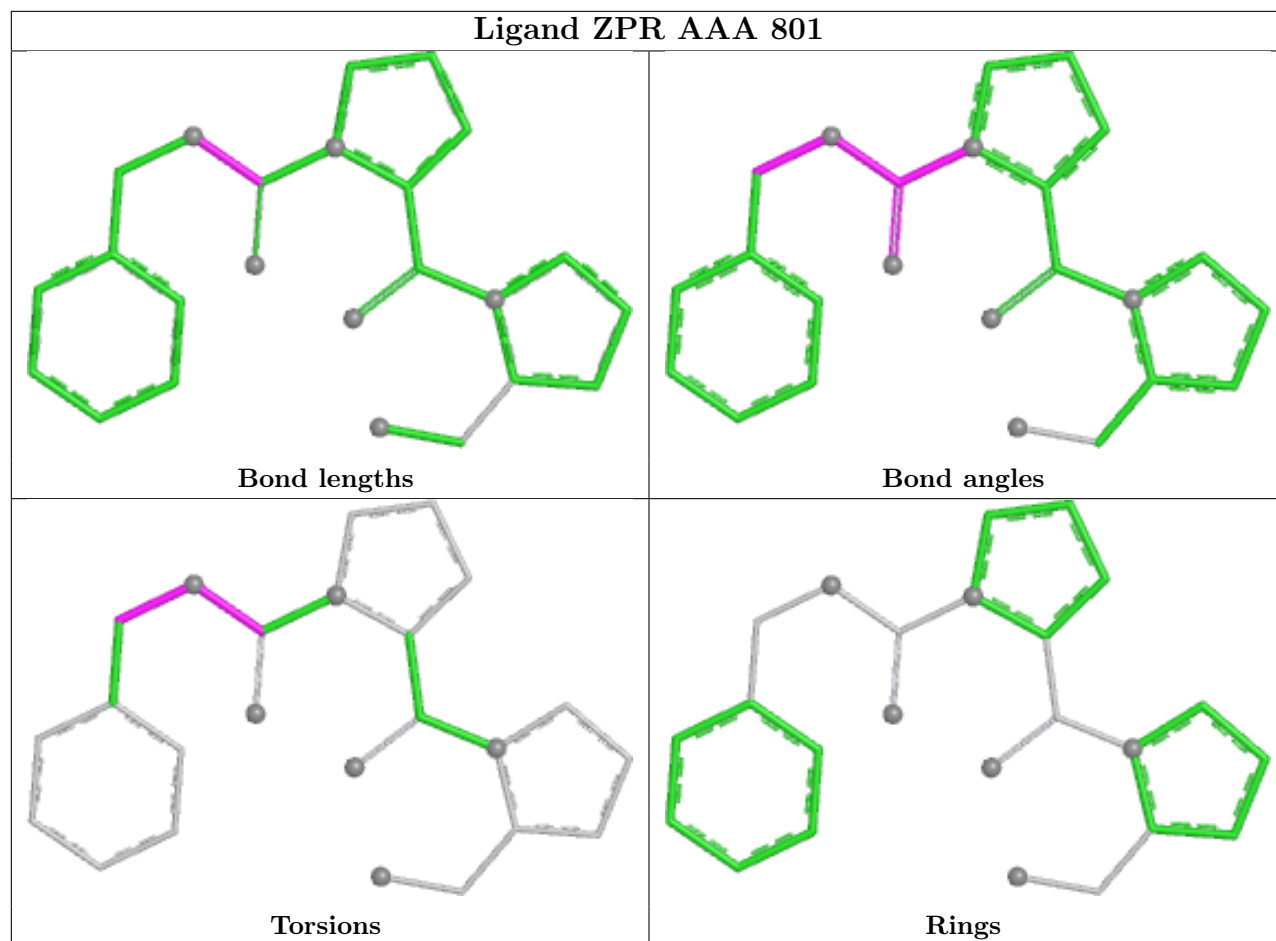
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	BBB	802	DMS	4	0
2	CCC	806	ZPR	4	0
6	CCC	807	GOL	1	0
3	AAA	803	DMS	2	0
2	BBB	807	ZPR	1	0

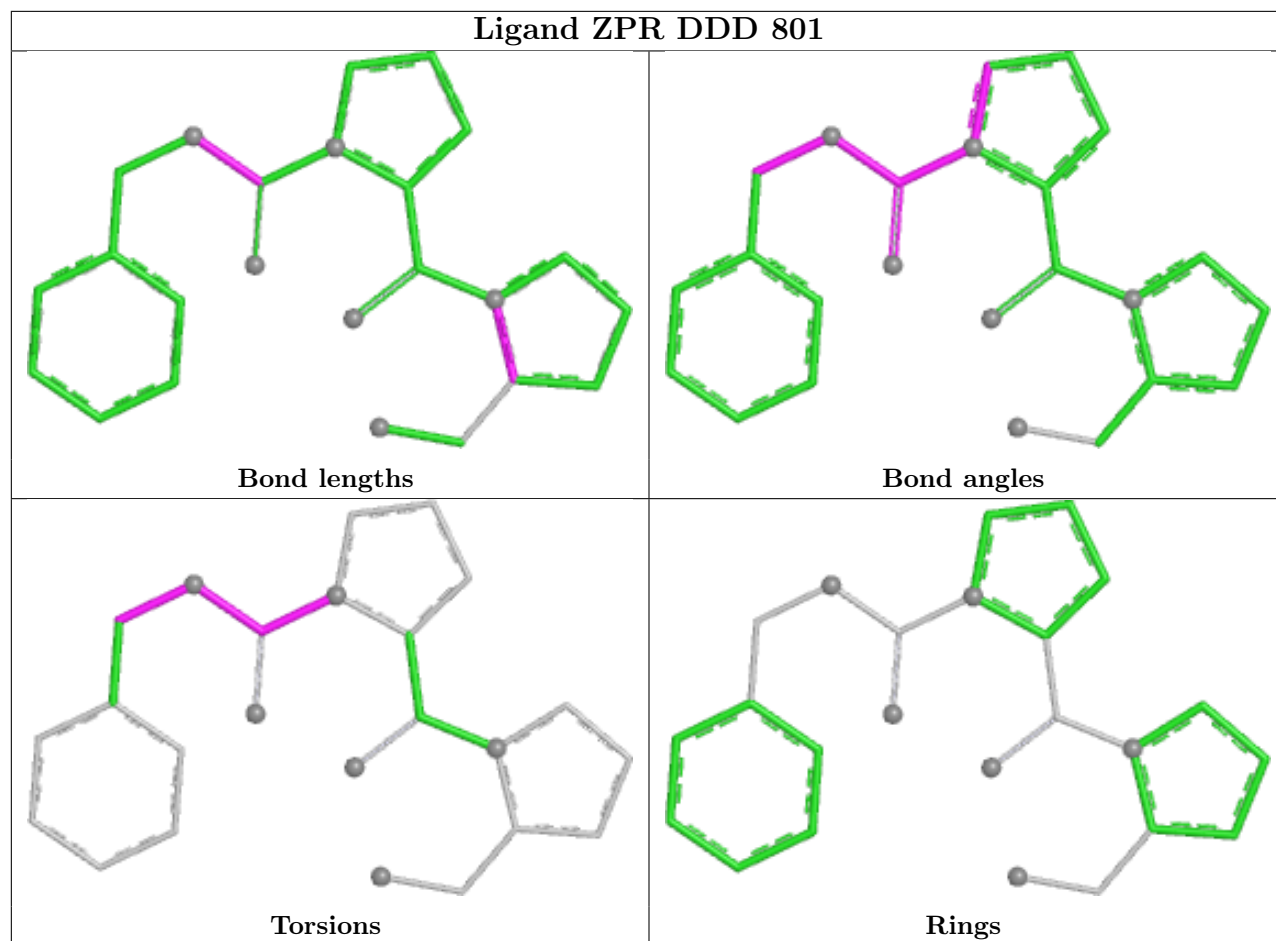
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

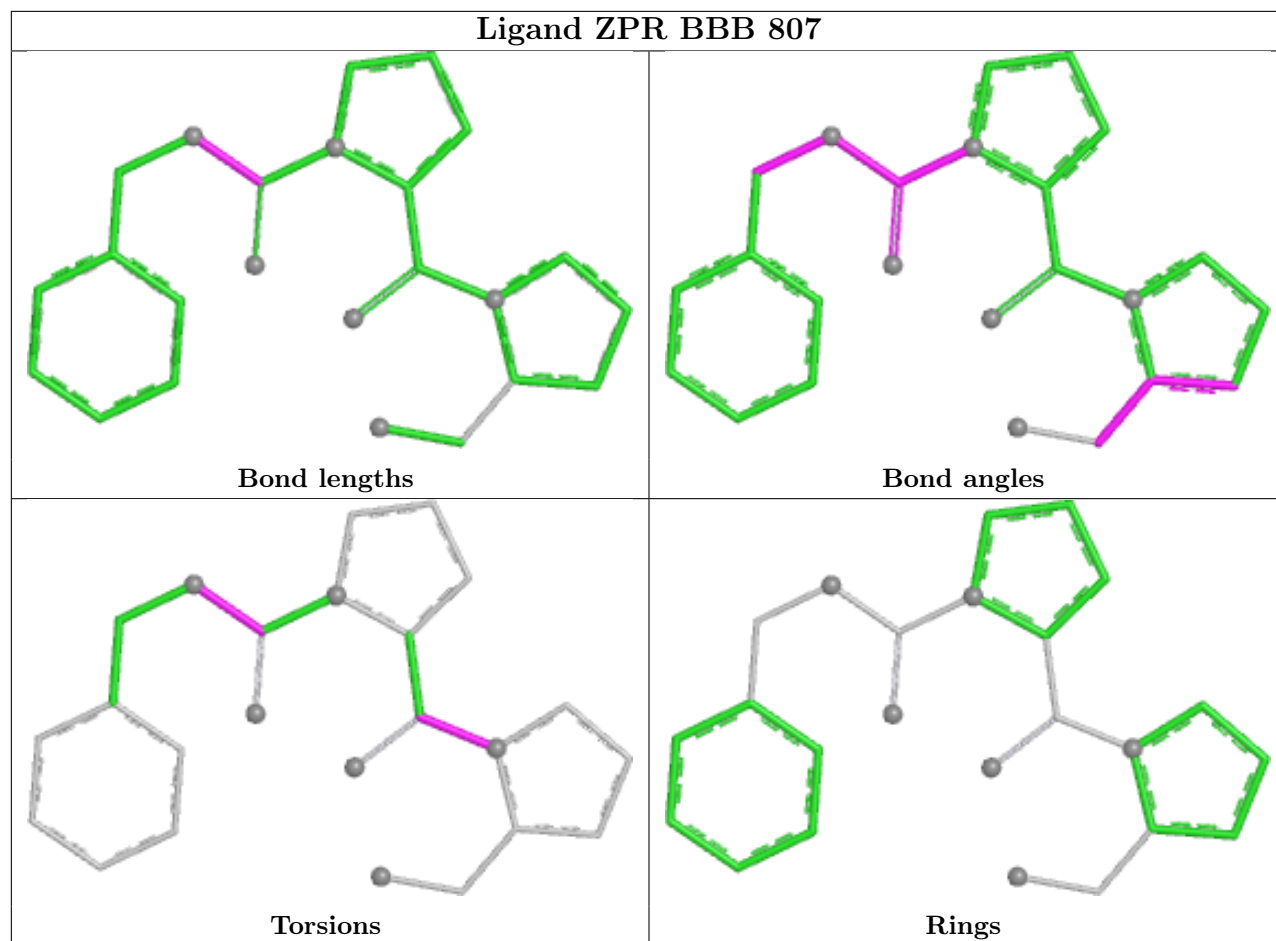
Ligand ZPR CCC 806



Ligand ZPR AAA 801







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	AAA	727/745 (97%)	0.39	31 (4%)	40	39	15, 33, 55, 91	2 (0%)
1	BBB	706/745 (94%)	0.52	39 (5%)	30	29	14, 36, 64, 111	1 (0%)
1	CCC	690/745 (92%)	0.48	29 (4%)	40	39	24, 35, 61, 94	0
1	DDD	716/745 (96%)	0.22	21 (2%)	53	52	13, 30, 49, 80	2 (0%)
All	All	2839/2980 (95%)	0.40	120 (4%)	40	39	13, 33, 58, 111	5 (0%)

The worst 5 of 120 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	CCC	233	PRO	6.0
1	AAA	702	PHE	4.7
1	BBB	664	TYR	4.7
1	BBB	181	PRO	4.6
1	CCC	617	PHE	4.4

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	ZPR	CCC	806	24/24	0.68	0.22	59,95,109,116	0
2	ZPR	BBB	807	24/24	0.74	0.22	47,92,100,102	0
4	BCT	AAA	806	4/4	0.75	0.17	52,53,55,60	0
5	EDO	DDD	810	4/4	0.75	0.17	47,49,52,53	0
5	EDO	DDD	809	4/4	0.77	0.17	47,48,49,52	0
7	PO4	DDD	808	5/5	0.79	0.15	47,53,55,56	0
5	EDO	CCC	808	4/4	0.80	0.16	40,42,44,46	0
5	EDO	AAA	813	4/4	0.80	0.16	46,47,47,49	0
4	BCT	BBB	804	4/4	0.81	0.14	51,54,60,62	0
8	NA	DDD	812	1/1	0.81	0.19	44,44,44,44	0
7	PO4	DDD	805	5/5	0.82	0.15	58,60,64,75	0
5	EDO	BBB	809	4/4	0.82	0.15	36,42,43,44	0
5	EDO	AAA	812	4/4	0.82	0.13	32,32,36,38	0
4	BCT	CCC	803	4/4	0.83	0.12	55,56,59,60	0
4	BCT	AAA	810	4/4	0.83	0.12	54,56,61,63	0
4	BCT	BBB	805	4/4	0.84	0.12	51,51,51,54	0
4	BCT	AAA	805	4/4	0.84	0.11	44,49,49,50	0
6	GOL	CCC	807	6/6	0.84	0.18	40,43,46,52	0
4	BCT	BBB	808	4/4	0.85	0.12	41,43,44,46	0
4	BCT	BBB	806	4/4	0.85	0.14	49,54,55,56	0
5	EDO	CCC	809	4/4	0.85	0.13	40,44,47,48	0
2	ZPR	DDD	801	24/24	0.86	0.14	31,45,78,84	0
4	BCT	BBB	801	4/4	0.86	0.11	41,45,45,48	0
4	BCT	AAA	807	4/4	0.86	0.12	42,45,51,57	0
4	BCT	DDD	811	4/4	0.86	0.12	57,58,60,61	0
4	BCT	AAA	809	4/4	0.86	0.12	44,49,50,55	0
4	BCT	CCC	805	4/4	0.87	0.10	50,55,55,62	0
4	BCT	DDD	806	4/4	0.87	0.11	42,45,45,46	0
5	EDO	AAA	811	4/4	0.88	0.14	43,44,45,47	0
4	BCT	CCC	804	4/4	0.88	0.09	39,40,45,45	0
4	BCT	BBB	810	4/4	0.88	0.11	41,42,42,45	0
2	ZPR	AAA	801	24/24	0.89	0.12	35,48,59,62	0
4	BCT	CCC	801	4/4	0.89	0.12	42,50,53,56	0
4	BCT	CCC	802	4/4	0.89	0.10	43,46,47,52	0
4	BCT	AAA	804	4/4	0.89	0.11	53,54,58,59	0
4	BCT	AAA	808	4/4	0.90	0.10	43,47,50,51	0
4	BCT	DDD	804	4/4	0.91	0.09	45,49,50,51	0
3	DMS	AAA	802	4/4	0.91	0.14	48,50,55,57	0
4	BCT	BBB	803	4/4	0.91	0.09	43,44,45,48	0
4	BCT	DDD	807	4/4	0.92	0.08	37,42,45,48	0
3	DMS	BBB	802	4/4	0.92	0.15	28,30,31,38	0
3	DMS	AAA	803	4/4	0.93	0.11	24,30,30,31	0
4	BCT	DDD	802	4/4	0.93	0.08	38,39,39,47	0

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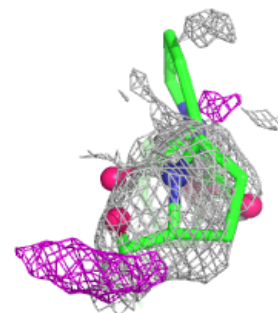
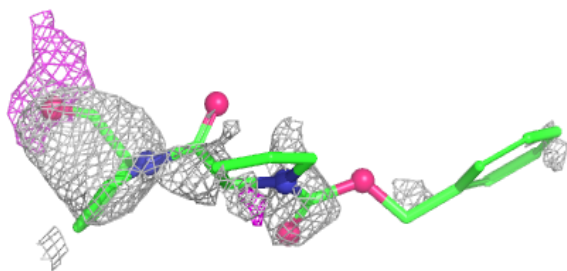
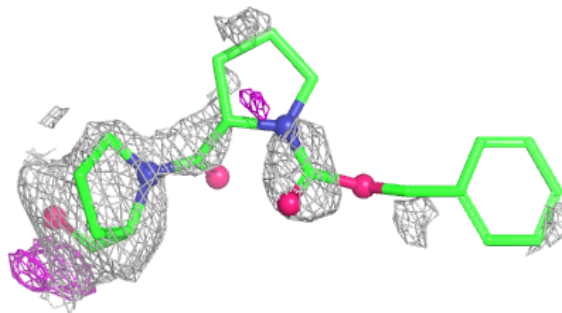
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	DMS	DDD	803	4/4	0.97	0.08	36,39,40,40	0

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

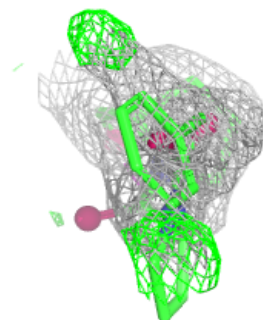
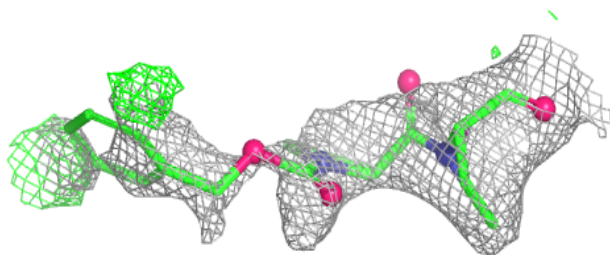
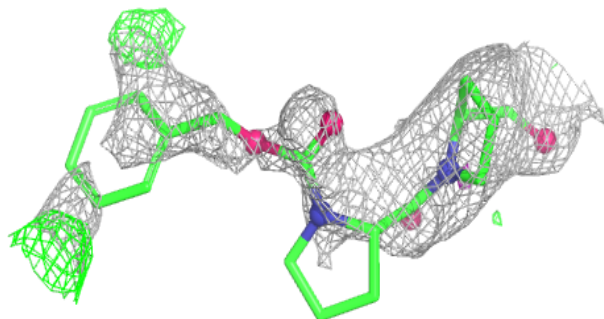
Electron density around ZPR CCC 806:

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

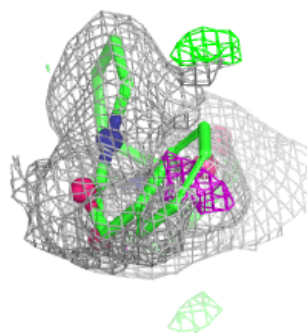
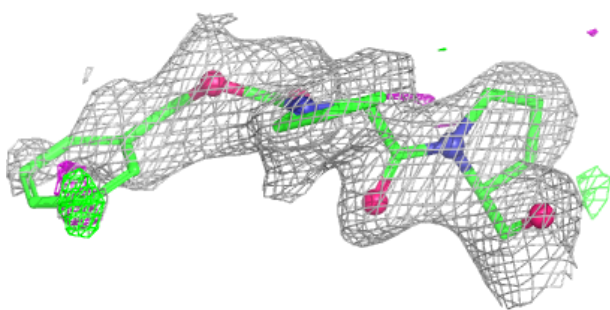
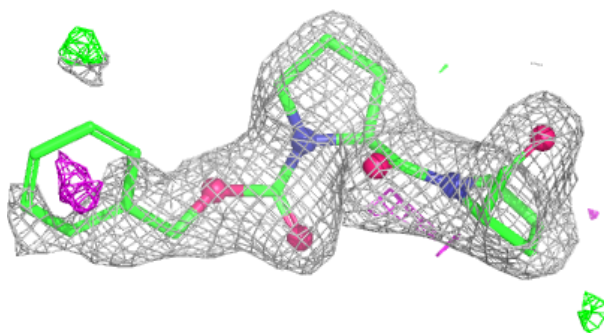


Electron density around ZPR BBB 807:

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

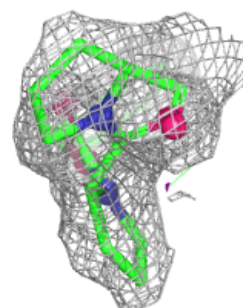
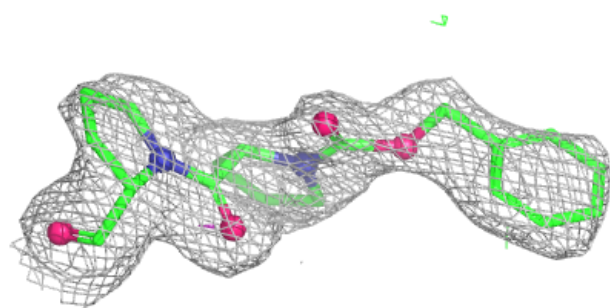
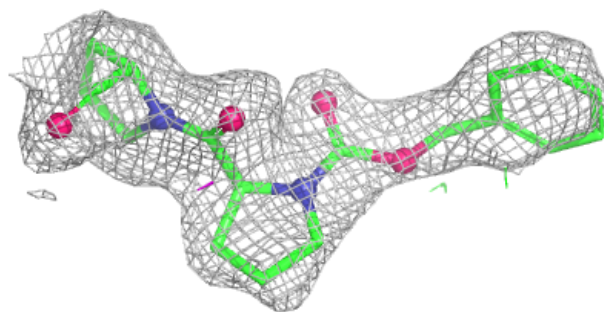
**Electron density around ZPR DDD 801:**

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



Electron density around ZPR AAA 801:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.