



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:30 PM UTC

PDB ID : 1BIW / pdb_00001biw
Title : DESIGN AND SYNTHESIS OF CONFORMATIONALLY-CONSTRAINED
MMP INHIBITORS
Authors : Natchus, M.G.; Cheng, M.; Wahl, C.T.; Pikul, S.; Almstead, N.G.; Bradley,
R.S.; Taiwo, Y.O.; Mieling, G.E.; Dunaway, C.M.; Snider, C.E.; McIver, J.M.;
Barnett, B.L.; McPhail, S.J.; Anastasio, M.B.; De, B.
Deposited on : 1998-06-19
Resolution : 2.50 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)
Xtrriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

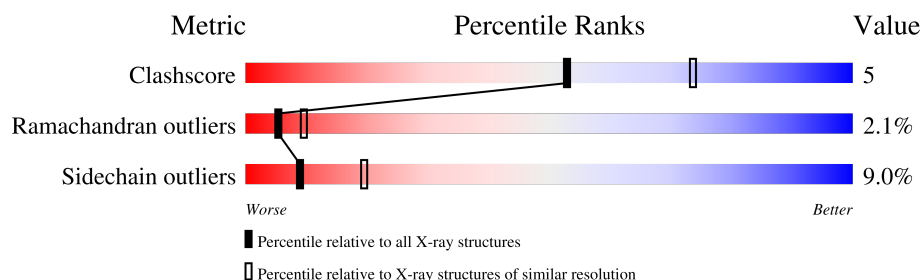
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)

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	173	
1	B	173	

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	S80	B	401	X	-	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 2813 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 PROTEIN (STROMELYSIN-1 COMPLEX).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	169	Total	C	N	O	S	0	0	0
			1346	865	224	255	2			
1	B	173	Total	C	N	O	S	0	0	0
			1376	882	228	264	2			

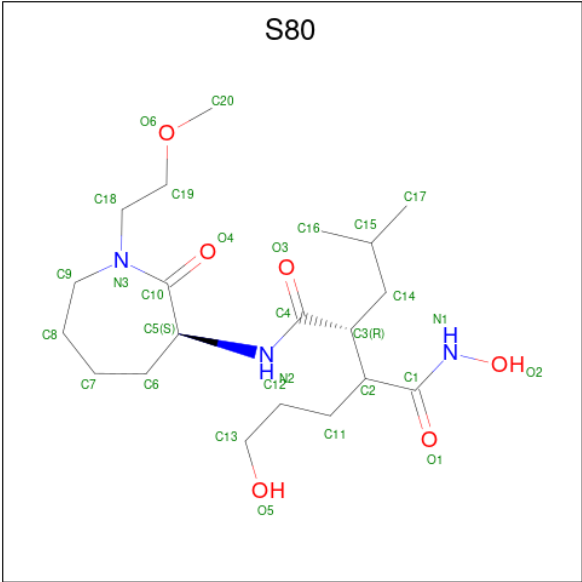
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Zn	0	0
			2	2		
2	B	2	Total	Zn	0	0
			2	2		

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	Ca	0	0
			3	3		
3	B	3	Total	Ca	0	0
			3	3		

- Molecule 4 is N1-HYDROXY-2-(3-HYDROXY-PROPYL)-3-ISOBUTYL-N4-[1-(2-METHOXY-ETHYL)-2-OXO-AZEPAN-3-YL]-SUCCINAMIDE (CCD ID: S80) (formula: C₂₀H₃₇N₃O₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			29	20	3	6		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	23	Total	O	0	0
			23	23		
5	B	29	Total	O	0	0
			29	29		

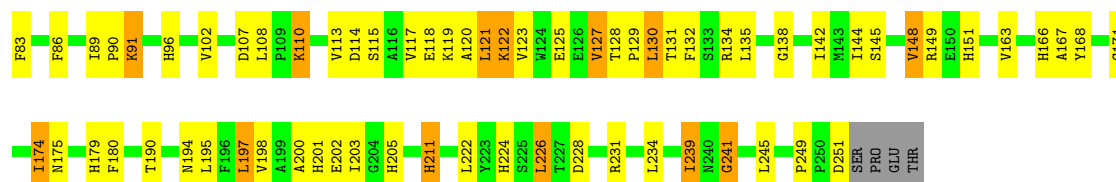
3 Residue-property plots

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.

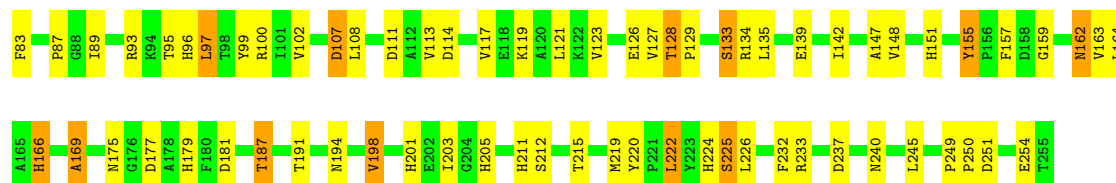
• Molecule 1: PROTEIN (STROMEALYSIN-1 COMPLEX)

Chain A: 



• Molecule 1: PROTEIN (STROMEALYSIN-1 COMPLEX)

Chain B: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	38.06Å 77.28Å 106.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.50	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-2.50)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	0.10	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.247 , 0.275	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2813	wwPDB-VP
Average B, all atoms (Å ²)	12.0	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: ZN, CA, S80

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	1.47	13/1390 (0.9%)	2.15	54/1899 (2.8%)
1	B	1.27	10/1421 (0.7%)	2.09	48/1941 (2.5%)
All	All	1.37	23/2811 (0.8%)	2.12	102/3840 (2.7%)

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	3
1	B	0	1
All	All	0	4

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	211	HIS	CE1-NE2	23.47	1.56	1.32
1	A	211	HIS	ND1-CE1	15.76	1.48	1.32
1	A	201	HIS	CE1-NE2	8.74	1.41	1.32
1	A	151	HIS	CE1-NE2	7.65	1.40	1.32
1	B	201	HIS	CE1-NE2	7.24	1.39	1.32
1	B	166	HIS	CE1-NE2	6.95	1.39	1.32
1	A	127	VAL	CA-CB	-6.64	1.47	1.54
1	B	179	HIS	ND1-CE1	6.45	1.39	1.32
1	B	254	GLU	CB-CG	6.39	1.71	1.52
1	A	205	HIS	CE1-NE2	6.16	1.38	1.32
1	B	211	HIS	CE1-NE2	6.12	1.38	1.32
1	B	151	HIS	CE1-NE2	6.09	1.38	1.32
1	A	166	HIS	CE1-NE2	6.01	1.38	1.32
1	B	205	HIS	CE1-NE2	5.61	1.38	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	96	HIS	ND1-CE1	5.51	1.38	1.32
1	A	166	HIS	CG-CD2	5.38	1.41	1.35
1	B	128	THR	C-N	5.38	1.38	1.33
1	A	205	HIS	CG-ND1	-5.36	1.32	1.38
1	B	254	GLU	CA-CB	-5.28	1.45	1.53
1	A	211	HIS	CG-ND1	-5.20	1.32	1.38
1	B	166	HIS	CG-CD2	5.19	1.41	1.35
1	A	224	HIS	ND1-CE1	5.15	1.37	1.32
1	A	179	HIS	CG-CD2	5.01	1.41	1.35

All (102) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	117	VAL	N-CA-C	12.90	122.80	110.42
1	A	113	VAL	N-CA-C	12.49	122.41	110.30
1	A	127	VAL	N-CA-CB	-10.07	99.07	112.16
1	B	127	VAL	N-CA-CB	-9.87	99.29	112.22
1	A	117	VAL	N-CA-C	9.75	120.37	110.23
1	B	198	VAL	N-CA-C	9.73	119.77	110.42
1	A	102	VAL	N-CA-C	9.59	123.08	111.09
1	B	148	VAL	CA-CB-CG1	9.08	125.84	110.40
1	A	198	VAL	N-CA-C	8.94	119.75	110.72
1	A	148	VAL	CA-CB-CG1	8.71	125.21	110.40
1	B	113	VAL	N-CA-C	8.51	118.59	110.42
1	B	123	VAL	CA-CB-CG1	8.47	124.80	110.40
1	A	123	VAL	CA-CB-CG1	8.17	124.29	110.40
1	B	117	VAL	CA-CB-CG1	8.09	124.15	110.40
1	B	191	THR	N-CA-C	7.91	120.66	111.02
1	A	102	VAL	CA-CB-CG1	7.81	123.68	110.40
1	A	251	ASP	N-CA-CB	7.68	123.56	110.50
1	A	117	VAL	CA-CB-CG1	7.62	123.35	110.40
1	A	127	VAL	N-CA-C	7.58	119.40	112.43
1	A	211	HIS	ND1-CE1-NE2	-7.56	100.84	108.40
1	B	232	PHE	CA-CB-CG	-7.54	106.26	113.80
1	B	198	VAL	CA-CB-CG1	7.53	123.20	110.40
1	B	254	GLU	N-CA-CB	-7.46	98.86	110.57
1	B	102	VAL	N-CA-C	7.38	120.28	111.05
1	A	113	VAL	CA-CB-CG1	7.24	122.70	110.40
1	B	163	VAL	CA-CB-CG2	7.17	122.59	110.40
1	A	127	VAL	CA-CB-CG2	7.14	122.54	110.40
1	B	163	VAL	CA-CB-CG1	7.12	122.51	110.40
1	A	91	LYS	N-CA-C	7.08	120.18	109.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	148	VAL	N-CA-C	7.06	118.05	108.17
1	A	119	LYS	N-CA-C	7.03	118.94	111.28
1	B	127	VAL	CA-CB-CG2	6.97	122.25	110.40
1	A	198	VAL	CA-CB-CG2	6.94	122.20	110.40
1	B	113	VAL	CA-CB-CG1	6.87	122.08	110.40
1	B	123	VAL	N-CA-C	6.85	120.62	111.17
1	A	163	VAL	CA-CB-CG1	6.83	122.01	110.40
1	B	102	VAL	CA-CB-CG1	6.81	121.97	110.40
1	A	205	HIS	N-CA-C	6.73	118.27	111.07
1	B	107	ASP	N-CA-C	6.63	118.16	111.07
1	B	102	VAL	CA-CB-CG2	6.58	121.59	110.40
1	A	226	LEU	N-CA-C	6.53	119.89	108.52
1	A	163	VAL	CA-CB-CG2	6.50	121.44	110.40
1	A	138	GLY	CA-C-N	-6.40	113.66	122.30
1	A	138	GLY	C-N-CA	-6.40	113.66	122.30
1	A	249	PRO	O-C-N	6.37	124.24	121.31
1	A	200	ALA	N-CA-C	6.33	117.84	111.07
1	A	167	ALA	N-CA-C	6.23	118.64	109.24
1	B	111	ASP	N-CA-C	6.16	118.50	111.11
1	A	202	GLU	N-CA-C	6.15	117.65	111.07
1	A	107	ASP	N-CA-C	6.12	119.59	111.75
1	A	110	LYS	N-CA-C	6.10	117.93	111.28
1	B	181	ASP	N-CA-C	6.09	117.92	109.15
1	A	115	SER	N-CA-C	6.09	118.71	111.71
1	A	251	ASP	CA-CB-CG	6.05	118.65	112.60
1	A	198	VAL	CA-CB-CG1	6.01	120.62	110.40
1	B	187	THR	N-CA-CB	-5.96	100.52	111.37
1	A	117	VAL	CA-CB-CG2	5.91	120.44	110.40
1	B	127	VAL	CA-CB-CG1	5.88	120.40	110.40
1	A	228	ASP	N-CA-C	5.85	118.70	109.39
1	B	240	ASN	N-CA-C	5.83	118.38	111.33
1	B	97	LEU	CB-CG-CD1	5.78	128.03	110.70
1	A	211	HIS	CE1-NE2-CD2	-5.76	103.24	109.00
1	B	97	LEU	CA-C-N	-5.75	113.61	122.87
1	B	97	LEU	C-N-CA	-5.75	113.61	122.87
1	A	123	VAL	CA-CB-CG2	5.74	120.16	110.40
1	B	142	ILE	N-CA-C	5.74	115.60	106.88
1	A	120	ALA	N-CA-C	5.73	117.52	111.28
1	A	241	GLY	N-CA-C	5.70	120.70	113.24
1	A	113	VAL	CA-CB-CG2	5.63	119.98	110.40
1	B	126	GLU	CA-C-N	-5.63	113.67	122.56
1	B	126	GLU	C-N-CA	-5.63	113.67	122.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	113	VAL	CA-CB-CG2	5.60	119.91	110.40
1	A	123	VAL	N-CA-C	5.58	118.88	111.17
1	A	89	ILE	N-CA-C	5.56	120.90	108.88
1	B	166	HIS	CE1-NE2-CD2	-5.56	103.44	109.00
1	A	142	ILE	N-CA-C	5.49	115.22	106.88
1	A	145	SER	N-CA-C	5.47	117.50	109.24
1	A	148	VAL	CA-CB-CG2	5.45	119.67	110.40
1	B	95	THR	N-CA-C	5.45	119.93	113.28
1	B	177	ASP	N-CA-C	5.43	118.55	110.52
1	B	205	HIS	N-CA-C	5.43	117.05	111.03
1	B	219	MET	N-CA-C	5.42	119.75	113.20
1	B	212	SER	N-CA-C	5.36	117.60	110.53
1	A	163	VAL	N-CA-C	5.35	120.47	109.34
1	A	127	VAL	CA-CB-CG1	5.34	119.48	110.40
1	A	96	HIS	CA-CB-CG	-5.33	108.47	113.80
1	A	123	VAL	CB-CA-C	-5.32	104.28	112.05
1	A	239	ILE	N-CA-C	5.30	115.51	110.42
1	A	234	LEU	CA-C-N	-5.28	111.36	120.97
1	A	234	LEU	C-N-CA	-5.28	111.36	120.97
1	B	127	VAL	N-CA-C	5.19	117.17	111.77
1	A	190	THR	N-CA-C	5.19	118.63	112.72
1	B	198	VAL	CA-CB-CG2	5.17	119.19	110.40
1	B	224	HIS	N-CA-C	5.17	118.13	110.48
1	B	123	VAL	CA-CB-CG2	5.13	119.12	110.40
1	B	135	LEU	CA-C-N	-5.12	113.05	121.92
1	B	135	LEU	C-N-CA	-5.12	113.05	121.92
1	B	99	TYR	N-CA-C	5.09	117.75	109.24
1	B	215	THR	N-CA-C	5.08	117.48	111.33
1	A	245	LEU	N-CA-C	5.08	117.60	111.40
1	B	164	LEU	CB-CG-CD2	5.08	125.92	110.70
1	A	132	PHE	CA-CB-CG	-5.06	108.74	113.80

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	168	TYR	Sidechain
1	A	211	HIS	Sidechain
1	A	231	ARG	Sidechain
1	B	155	TYR	Sidechain

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	1346	0	1270	12	0
1	B	1376	0	1295	16	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
4	B	29	0	33	1	0
5	A	23	0	0	0	0
5	B	29	0	0	1	0
All	All	2813	0	2598	27	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 (27) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:121:LEU:HD23	1:B:203:ILE:HD13	1.80	0.64
1:B:128:THR:HB	1:B:129:PRO:HD2	1.82	0.62
1:A:121:LEU:HD13	1:A:203:ILE:HD13	1.85	0.59
1:A:128:THR:HB	1:A:129:PRO:HD2	1.92	0.50
1:B:220:TYR:HE2	1:B:222:LEU:HD22	1.75	0.49
1:B:147:ALA:HB3	1:B:157:PHE:HE1	1.77	0.49
1:B:155:TYR:O	1:B:166:HIS:HE1	1.95	0.48
1:B:96:HIS:CE1	1:B:133:SER:HB2	2.47	0.48
1:B:225:SER:HA	5:B:829:HOH:O	2.13	0.48
1:A:144:ILE:HG23	1:A:180:PHE:HE1	1.80	0.47
1:A:110:LYS:NZ	1:B:108:LEU:O	2.46	0.46
1:B:114:ASP:CG	1:B:134:ARG:HH12	2.23	0.46
1:A:114:ASP:CG	1:A:134:ARG:HH22	2.25	0.45
1:B:89:ILE:O	1:B:89:ILE:HG22	2.17	0.45
1:A:127:VAL:HG11	1:A:239:ILE:HG12	1.99	0.44
1:A:118:GLU:O	1:A:122:LYS:HB2	2.17	0.44
1:B:162:ASN:O	4:B:401:S80:H91	2.17	0.44
1:A:194:ASN:HD22	1:A:197:LEU:HB2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:147:ALA:HB3	1:B:157:PHE:CE1	2.53	0.43
1:A:171:GLY:C	1:A:175:ASN:HB2	2.44	0.43
1:B:194:ASN:O	1:B:198:VAL:HG23	2.19	0.42
1:B:249:PRO:HA	1:B:250:PRO:HD3	1.89	0.42
1:B:83:PHE:N	1:B:237:ASP:OD1	2.52	0.42
1:A:83:PHE:CE1	1:A:241:GLY:HA2	2.55	0.41
1:A:125:GLU:HG3	1:A:130:LEU:O	2.21	0.41
1:A:86:PHE:HB2	1:A:90:PRO:HD2	2.02	0.41
1:B:169:ALA:O	1:B:175:ASN:HB3	2.20	0.41

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	A	167/173 (96%)	147 (88%)	18 (11%)	2 (1%)	10	20
1	B	171/173 (99%)	152 (89%)	14 (8%)	5 (3%)	3	5
All	All	338/346 (98%)	299 (88%)	32 (10%)	7 (2%)	5	9

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	159	GLY
1	B	225	SER
1	B	87	PRO
1	B	162	ASN
1	A	149	ARG
1	A	174	ILE
1	B	169	ALA

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	143/147 (97%)	130 (91%)	13 (9%)	9	19
1	B	147/147 (100%)	134 (91%)	13 (9%)	9	20
All	All	290/294 (99%)	264 (91%)	26 (9%)	9	19

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	91	LYS
1	A	108	LEU
1	A	121	LEU
1	A	122	LYS
1	A	130	LEU
1	A	131	THR
1	A	135	LEU
1	A	148	VAL
1	A	174	ILE
1	A	195	LEU
1	A	197	LEU
1	A	222	LEU
1	A	226	LEU
1	B	93	ARG
1	B	97	LEU
1	B	100	ARG
1	B	107	ASP
1	B	119	LYS
1	B	133	SER
1	B	139	GLU
1	B	187	THR
1	B	222	LEU
1	B	226	LEU
1	B	233	ARG
1	B	245	LEU
1	B	251	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	96	HIS
1	A	194	ASN
1	B	96	HIS
1	B	214	ASN
1	B	236	GLN
1	B	240	ASN

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 11 ligands modelled in this entry, 10 are monoatomic - leaving 1 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	S80	B	401	2	28,29,29	1.51	3 (10%)	31,37,37	3.54	19 (61%)

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	S80	B	401	2	1/1/8/10	7/30/45/45	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	401	S80	C14-C3	-5.13	1.47	1.54
4	B	401	S80	C6-C5	-3.11	1.48	1.53
4	B	401	S80	C3-C4	-2.47	1.47	1.51

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	401	S80	C3-C14-C15	9.40	130.91	115.82
4	B	401	S80	O3-C4-C3	-7.38	112.83	121.67
4	B	401	S80	C2-C1-N1	6.55	124.05	115.99
4	B	401	S80	C6-C5-C10	6.01	119.32	111.65
4	B	401	S80	C3-C4-N2	5.47	122.64	116.01
4	B	401	S80	O1-C1-C2	-4.41	116.39	121.67
4	B	401	S80	C6-C5-N2	4.02	117.12	109.76
4	B	401	S80	C12-C11-C2	-3.83	107.52	114.28
4	B	401	S80	C7-C6-C5	3.80	121.63	114.23
4	B	401	S80	C2-C3-C4	3.45	115.50	109.56
4	B	401	S80	C17-C15-C14	3.21	122.63	111.08
4	B	401	S80	C18-N3-C9	-2.82	113.78	117.55
4	B	401	S80	C16-C15-C14	2.58	120.36	111.08
4	B	401	S80	C9-N3-C10	2.50	125.34	122.42
4	B	401	S80	C14-C3-C4	2.50	118.72	110.98
4	B	401	S80	C3-C2-C1	2.49	113.84	109.56
4	B	401	S80	C5-N2-C4	2.33	126.66	121.65
4	B	401	S80	C10-C5-N2	2.19	113.34	108.73
4	B	401	S80	O4-C10-C5	-2.00	117.08	121.04

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	B	401	S80	C2

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	401	S80	O1-C1-C2-C11
4	B	401	S80	N1-C1-C2-C11

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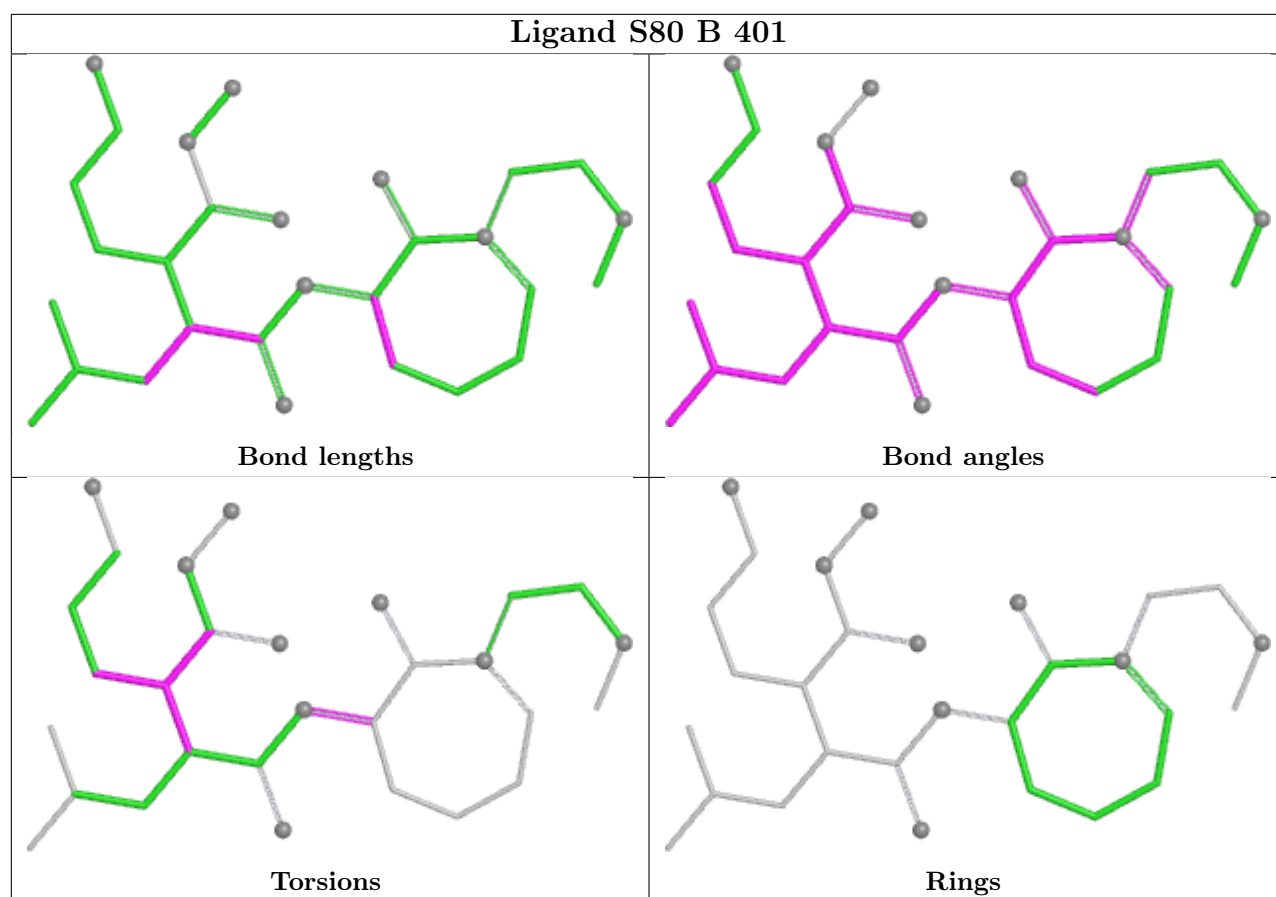
Mol	Chain	Res	Type	Atoms
4	B	401	S80	C12-C11-C2-C3
4	B	401	S80	C11-C2-C3-C4
4	B	401	S80	C1-C2-C3-C14
4	B	401	S80	C11-C2-C3-C14
4	B	401	S80	C6-C5-N2-C4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	401	S80	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [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.