



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:52 PM UTC

PDB ID : 456C / pdb_0000456c
Title : CRYSTAL STRUCTURE OF COLLAGENASE-3 (MMP-13) COMPLEXED
TO A DIPHENYL-ETHER SULPHONE BASED HYDROXAMIC ACID
Authors : Lovejoy, B.; Welch, A.; Carr, S.; Luong, C.; Broka, C.; Hendricks, R.T.; Campbell, J.; Walker, K.; Martin, R.; Van Wart, H.; Browner, M.F.
Deposited on : 1998-08-06
Resolution : 2.40 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
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

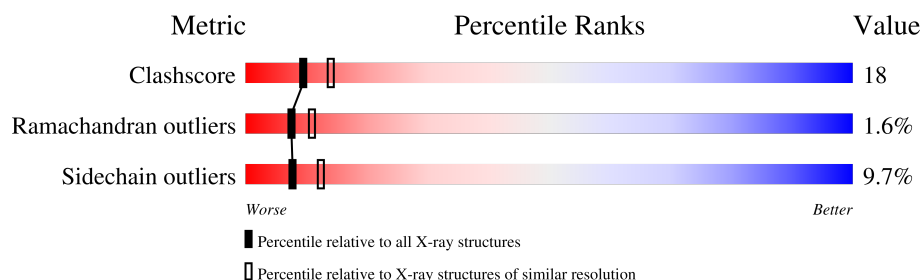
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)

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	168	
1	B	168	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3426 atoms, of which 738 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 MMP-13.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	160	Total	C	H	N	O	S	0	0	0
			1512	819	247	204	237	5			
1	B	159	Total	C	H	N	O	S	0	0	0
			1503	815	245	203	235	5			

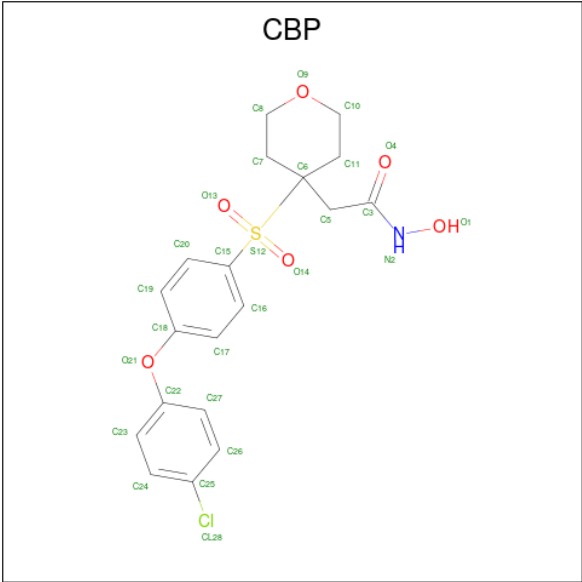
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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	1	Total	Ca	0	0
			1	1		
3	B	1	Total	Ca	0	0
			1	1		

- Molecule 4 is 2-{4-[4-(4-CHLORO-PHENOXY)-BENZENESULFONYL]-TETRAHYDRO-PYRAN-4-YL}-N-HYDROXY-ACETAMIDE (CCD ID: CBP) (formula: C₁₉H₂₀ClNO₆S).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
4	A	1	Total	C	Cl	H	N	O	S	0	0
			48	19	1	20	1	6	1		
4	B	1	Total	C	Cl	H	N	O	S	0	0
			48	19	1	20	1	6	1		

- Molecule 5 is water.

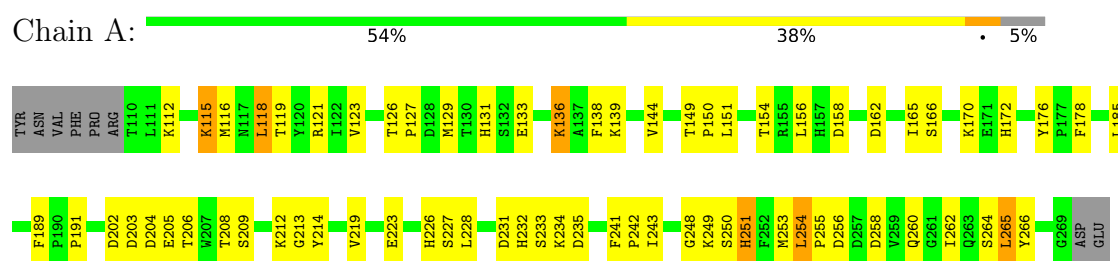
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	52	Total	H	O	0	0
			156	104	52		
5	B	51	Total	H	O	0	0
			153	102	51		

3 Residue-property plots

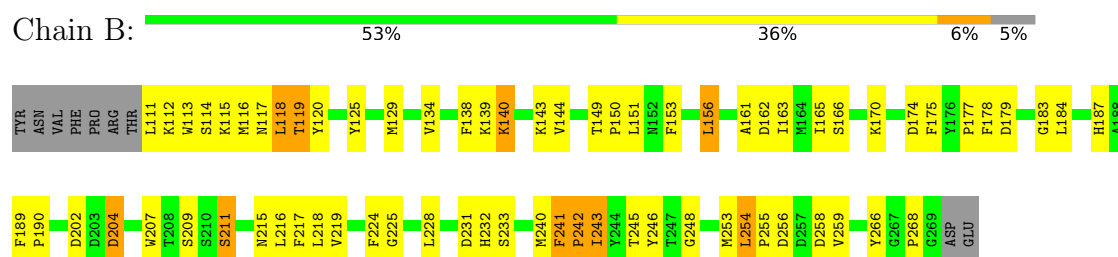
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: MMP-13



• Molecule 1: MMP-13



4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	134.00Å 35.62Å 94.88Å 90.00° 131.19° 90.00°	Depositor
Resolution (Å)	7.00 – 2.40	Depositor
% Data completeness (in resolution range)	90.7 (7.00-2.40)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.216 , 0.338	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3426	wwPDB-VP
Average B, all atoms (Å ²)	10.0	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: CBP, ZN, CA

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	0.57	0/1310	1.05	7/1780 (0.4%)
1	B	0.56	0/1303	1.10	9/1770 (0.5%)
All	All	0.56	0/2613	1.08	16/3550 (0.5%)

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	241	PHE	CA-C-N	7.35	128.00	119.47
1	A	241	PHE	C-N-CA	7.35	128.00	119.47
1	B	225	GLY	N-CA-C	-6.60	104.84	112.50
1	B	174	ASP	N-CA-C	-6.16	98.95	109.24
1	A	264	SER	N-CA-C	-6.13	105.06	112.54
1	B	211	SER	N-CA-C	5.87	121.35	113.72
1	A	204	ASP	N-CA-C	-5.72	105.49	112.88
1	B	241	PHE	CA-C-N	5.65	126.91	119.84
1	B	241	PHE	C-N-CA	5.65	126.91	119.84
1	A	251	HIS	N-CA-C	-5.38	103.86	110.65
1	A	123	VAL	N-CA-C	5.29	115.43	110.30
1	B	114	SER	N-CA-C	-5.25	105.23	111.69
1	B	204	ASP	N-CA-C	-5.24	106.74	113.02
1	A	209	SER	N-CA-C	-5.21	105.79	113.61
1	B	125	TYR	N-CA-C	5.18	117.54	109.52
1	B	170	LYS	CB-CA-C	-5.05	110.74	116.54

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1265	247	1183	33	0
1	B	1258	245	1176	55	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	28	20	19	1	0
4	B	28	20	20	1	0
5	A	52	104	0	2	0
5	B	51	102	0	7	0
All	All	2688	738	2398	88	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 18.

All (88) 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:136:LYS:HA	1:A:139:LYS:HD2	1.43	0.98
1:B:116:MET:HE1	1:B:266:TYR:HD1	1.47	0.78
1:B:211:SER:HB3	1:B:246:TYR:CE1	2.21	0.75
1:B:119:THR:HG22	1:B:162:ASP:H	1.53	0.73
1:B:240:MET:HB2	5:B:292:HOH:O	1.88	0.72
1:A:139:LYS:HG3	5:A:21:HOH:O	1.92	0.70
1:A:116:MET:SD	1:A:150:PRO:HG2	2.32	0.68
1:B:140:LYS:O	1:B:140:LYS:HE3	1.94	0.67
1:A:119:THR:HB	1:A:156:LEU:HD13	1.76	0.66
1:B:120:TYR:HB3	1:B:163:ILE:HG23	1.78	0.65
1:A:170:LYS:HA	1:A:178:PHE:O	1.99	0.63
1:A:208:THR:HG21	1:A:212:LYS:O	1.99	0.63
1:B:113:TRP:CD1	1:B:266:TYR:HH	2.17	0.61
1:A:144:VAL:CG1	1:A:254:LEU:HG	2.31	0.60
1:B:256:ASP:HA	1:B:259:VAL:HG22	1.82	0.60
1:A:149:THR:HB	1:A:150:PRO:HD2	1.85	0.58
1:B:118:LEU:CD2	1:B:151:LEU:HD12	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:120:TYR:CB	1:B:163:ILE:HG23	2.34	0.57
1:A:206:THR:HG23	1:A:213:GLY:HA3	1.87	0.57
1:A:265:LEU:HB3	1:A:266:TYR:CD2	2.41	0.56
1:B:232:HIS:CE1	1:B:242:PRO:HB3	2.40	0.56
1:A:112:LYS:HA	1:A:191:PRO:HG2	1.87	0.56
1:B:140:LYS:HD2	5:B:322:HOH:O	2.06	0.56
1:B:253:MET:HE1	1:B:255:PRO:HG3	1.88	0.55
1:A:131:HIS:HB2	5:A:86:HOH:O	2.08	0.53
1:A:121:ARG:HD2	1:A:158:ASP:HA	1.90	0.53
1:B:246:TYR:CE1	1:B:248:GLY:HA2	2.42	0.53
1:B:254:LEU:HB2	5:B:296:HOH:O	2.07	0.53
1:B:151:LEU:HD21	1:B:266:TYR:CG	2.43	0.53
1:B:149:THR:HB	1:B:150:PRO:CD	2.38	0.53
1:B:246:TYR:CZ	1:B:248:GLY:HA2	2.44	0.53
1:A:256:ASP:O	1:A:260:GLN:HG2	2.09	0.53
1:A:219:VAL:O	1:A:223:GLU:HG2	2.09	0.52
1:B:144:VAL:HA	5:B:286:HOH:O	2.09	0.52
1:A:115:LYS:HE3	1:A:118:LEU:HD12	1.91	0.52
1:B:254:LEU:HD22	1:B:258:ASP:HB2	1.90	0.52
1:A:189:PHE:O	1:A:227:SER:HA	2.11	0.51
1:B:113:TRP:HD1	1:B:266:TYR:HH	1.57	0.51
1:A:232:HIS:HB3	1:A:242:PRO:HG3	1.94	0.50
1:A:233:SER:OG	1:A:235:ASP:HB3	2.12	0.50
1:A:129:MET:HB3	1:A:133:GLU:HB2	1.94	0.50
1:B:115:LYS:HD3	1:B:117:ASN:O	2.11	0.50
1:A:255:PRO:HB2	1:A:258:ASP:OD2	2.12	0.49
1:B:202:ASP:OD1	1:B:204:ASP:HB2	2.12	0.49
1:B:215:ASN:O	1:B:219:VAL:HG23	2.14	0.47
1:B:256:ASP:O	1:B:259:VAL:HG22	2.14	0.47
1:B:143:LYS:HE3	5:B:322:HOH:O	2.15	0.47
1:B:175:PHE:C	1:B:177:PRO:HD3	2.39	0.47
1:B:175:PHE:O	1:B:177:PRO:HD3	2.14	0.47
1:A:202:ASP:HB3	1:A:205:GLU:HG2	1.97	0.47
1:B:134:VAL:HG13	1:B:216:LEU:HD21	1.97	0.46
1:A:172:HIS:HE1	1:A:176:TYR:O	1.98	0.46
1:B:129:MET:HE3	1:B:209:SER:OG	2.16	0.46
1:B:207:TRP:HZ3	1:B:219:VAL:HG21	1.81	0.45
1:B:118:LEU:HD21	1:B:151:LEU:HD12	1.97	0.45
1:B:140:LYS:HG3	1:B:217:PHE:CE1	2.51	0.45
1:B:116:MET:HE1	1:B:266:TYR:CD1	2.38	0.45
1:A:206:THR:HG23	1:A:213:GLY:CA	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:262:ILE:O	1:A:265:LEU:HB2	2.17	0.45
1:B:119:THR:CG2	1:B:156:LEU:HD22	2.46	0.45
1:B:241:PHE:HD2	1:B:243:ILE:HG22	1.81	0.44
1:B:115:LYS:HD2	1:B:118:LEU:HD12	1.99	0.44
1:B:232:HIS:NE2	4:B:1:CBP:O4	2.48	0.44
1:A:129:MET:HB3	1:A:133:GLU:CB	2.48	0.43
1:B:118:LEU:HD22	1:B:151:LEU:HD12	2.00	0.43
1:B:118:LEU:HD23	1:B:153:PHE:CE1	2.54	0.43
1:A:138:PHE:CE2	1:A:165:ILE:HG21	2.55	0.42
1:B:179:ASP:OD2	1:B:183:GLY:HA3	2.19	0.42
1:B:119:THR:CG2	1:B:161:ALA:HA	2.50	0.42
1:B:178:PHE:HA	1:B:184:LEU:HD23	2.02	0.42
1:A:144:VAL:HG13	1:A:254:LEU:HG	2.01	0.42
1:B:232:HIS:NE2	1:B:242:PRO:HB3	2.35	0.42
1:B:149:THR:CB	1:B:151:LEU:HD23	2.50	0.42
1:B:165:ILE:HG22	5:B:297:HOH:O	2.19	0.42
1:B:187:HIS:O	1:B:187:HIS:HD2	2.02	0.42
1:B:233:SER:HB2	5:B:292:HOH:O	2.20	0.42
1:B:255:PRO:HB2	1:B:258:ASP:OD2	2.19	0.41
1:A:219:VAL:HG13	4:A:1:CBP:H171	2.02	0.41
1:A:223:GLU:O	1:A:226:HIS:HB2	2.19	0.41
1:A:185:LEU:HD22	1:A:214:TYR:CE2	2.56	0.41
1:B:112:LYS:HE2	1:B:112:LYS:HB3	1.93	0.41
1:B:224:PHE:O	1:B:228:LEU:HG	2.20	0.41
1:B:134:VAL:HG12	1:B:138:PHE:CE2	2.56	0.41
1:B:189:PHE:HA	1:B:190:PRO:HD3	1.91	0.41
1:A:118:LEU:HA	1:A:162:ASP:OD2	2.21	0.40
1:B:218:LEU:HD12	1:B:246:TYR:HD2	1.86	0.40
1:A:126:THR:HA	1:A:127:PRO:HD3	1.89	0.40
1:B:241:PHE:CD2	1:B:243:ILE:HG22	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	158/168 (94%)	139 (88%)	16 (10%)	3 (2%)	6	8
1	B	157/168 (94%)	142 (90%)	13 (8%)	2 (1%)	9	14
All	All	315/336 (94%)	281 (89%)	29 (9%)	5 (2%)	7	11

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	248	GLY
1	B	268	PRO
1	A	249	LYS
1	A	250	SER
1	B	242	PRO

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	135/143 (94%)	120 (89%)	15 (11%)	6	9
1	B	134/143 (94%)	123 (92%)	11 (8%)	10	18
All	All	269/286 (94%)	243 (90%)	26 (10%)	8	12

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

Mol	Chain	Res	Type
1	A	115	LYS
1	A	118	LEU
1	A	136	LYS
1	A	151	LEU
1	A	154	THR
1	A	166	SER
1	A	203	ASP
1	A	228	LEU

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Mol	Chain	Res	Type
1	A	231	ASP
1	A	234	LYS
1	A	243	ILE
1	A	251	HIS
1	A	253	MET
1	A	254	LEU
1	A	265	LEU
1	B	111	LEU
1	B	118	LEU
1	B	119	THR
1	B	139	LYS
1	B	140	LYS
1	B	156	LEU
1	B	166	SER
1	B	231	ASP
1	B	243	ILE
1	B	245	THR
1	B	254	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	152	ASN
1	A	194	ASN
1	A	263	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 8 ligands modelled in this entry, 6 are monoatomic - leaving 2 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	CBP	B	1	2	28,30,30	0.73	0	37,43,43	1.83	8 (21%)
4	CBP	A	1	2	28,30,30	0.97	2 (7%)	37,43,43	1.62	8 (21%)

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	CBP	B	1	2	-	0/25/36/36	0/3/3/3
4	CBP	A	1	2	-	0/25/36/36	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1	CBP	C5-C3	2.71	1.54	1.51
4	A	1	CBP	C11-C6	2.51	1.57	1.54

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1	CBP	O14-S12-C15	-5.31	101.73	108.35
4	B	1	CBP	C6-S12-C15	4.99	117.05	106.10
4	A	1	CBP	O4-C3-N2	-3.88	118.50	123.27
4	A	1	CBP	O14-S12-C15	-3.36	104.16	108.35
4	A	1	CBP	O1-N2-C3	-3.06	115.27	119.79
4	A	1	CBP	O9-C8-C7	-3.02	108.49	111.50
4	B	1	CBP	O9-C10-C11	-2.80	108.71	111.50
4	B	1	CBP	C10-O9-C8	2.55	118.13	109.88
4	B	1	CBP	O1-N2-C3	-2.54	116.03	119.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1	CBP	O4-C3-C5	2.49	125.28	122.12
4	A	1	CBP	C16-C15-S12	2.33	121.34	119.36
4	A	1	CBP	C11-C6-C7	-2.32	108.25	109.70
4	B	1	CBP	C11-C6-C7	-2.26	108.30	109.70
4	B	1	CBP	C11-C6-C5	-2.16	107.17	110.42
4	A	1	CBP	C6-S12-C15	2.11	110.74	106.10
4	A	1	CBP	C7-C6-C5	2.01	113.45	110.42

There are no chirality outliers.

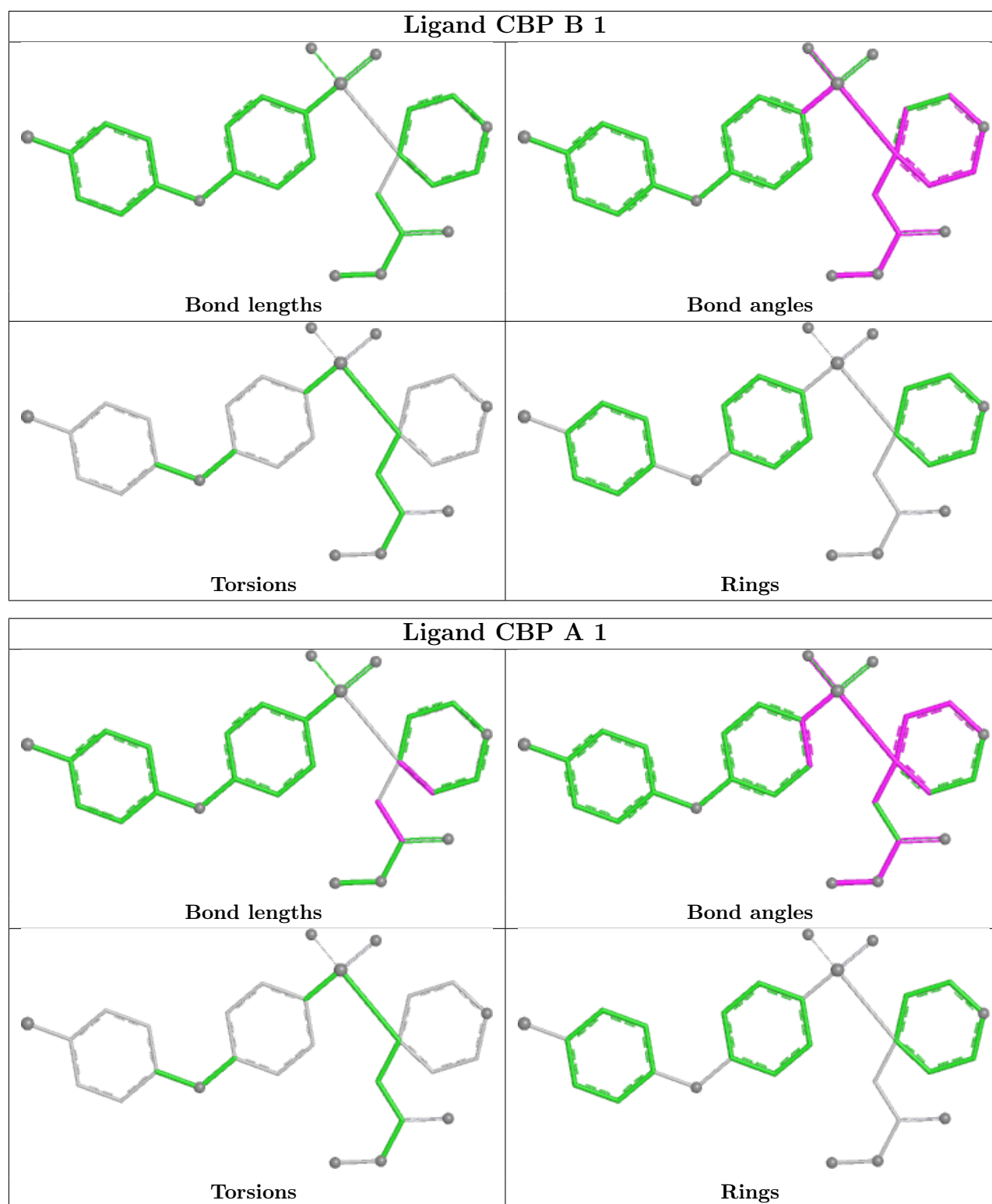
There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1	CBP	1	0
4	A	1	CBP	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 ⓘ

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.