



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 07:06 PM UTC

PDB ID : 8ZIN / pdb_00008zin
Title : Terephthalate 1,2-cis-dihydrodioldehydrogenase/Decarboxylase in complex with 2,4-dihydroxybenzoate.
Authors : Kumar, K.A.; Pahwa, D.; Kumar, P.
Deposited on : 2024-05-14
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)
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

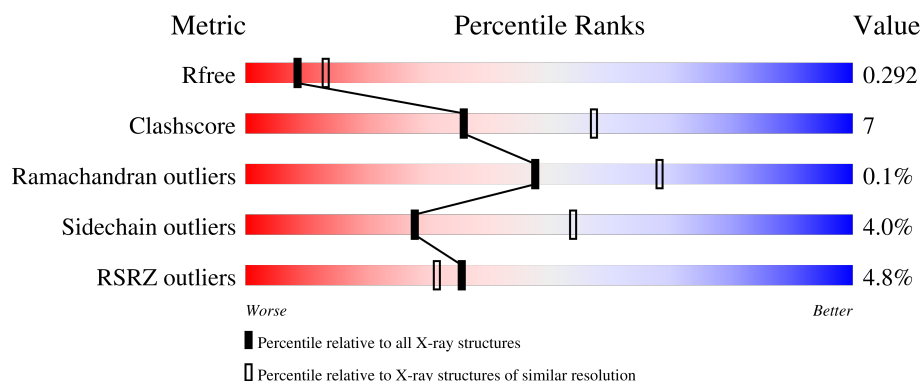
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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))
R_{free}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (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 $\leq 5\%$. 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	335	
1	B	335	
1	C	335	
1	D	335	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 9363 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 4-hydroxythreonine-4-phosphate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	313	Total	C	N	O	S	0	0	0
			2294	1440	411	431	12			
1	B	312	Total	C	N	O	S	0	0	0
			2286	1436	409	429	12			
1	C	313	Total	C	N	O	S	0	0	0
			2295	1440	411	431	13			
1	D	314	Total	C	N	O	S	0	0	0
			2302	1445	412	432	13			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP B7WRJ7
A	-18	GLY	-	expression tag	UNP B7WRJ7
A	-17	SER	-	expression tag	UNP B7WRJ7
A	-16	SER	-	expression tag	UNP B7WRJ7
A	-15	HIS	-	expression tag	UNP B7WRJ7
A	-14	HIS	-	expression tag	UNP B7WRJ7
A	-13	HIS	-	expression tag	UNP B7WRJ7
A	-12	HIS	-	expression tag	UNP B7WRJ7
A	-11	HIS	-	expression tag	UNP B7WRJ7
A	-10	HIS	-	expression tag	UNP B7WRJ7
A	-9	SER	-	expression tag	UNP B7WRJ7
A	-8	SER	-	expression tag	UNP B7WRJ7
A	-7	GLY	-	expression tag	UNP B7WRJ7
A	-6	LEU	-	expression tag	UNP B7WRJ7
A	-5	VAL	-	expression tag	UNP B7WRJ7
A	-4	PRO	-	expression tag	UNP B7WRJ7
A	-3	ARG	-	expression tag	UNP B7WRJ7
A	-2	GLY	-	expression tag	UNP B7WRJ7
A	-1	SER	-	expression tag	UNP B7WRJ7
A	0	HIS	-	expression tag	UNP B7WRJ7
B	-19	MET	-	initiating methionine	UNP B7WRJ7

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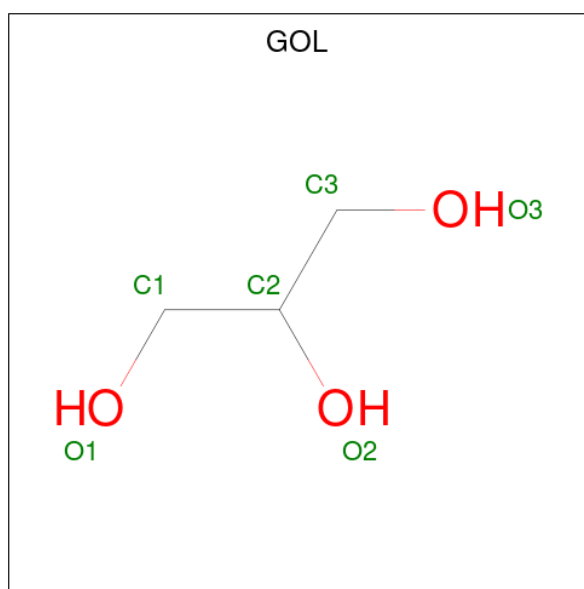
Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	expression tag	UNP B7WRJ7
B	-17	SER	-	expression tag	UNP B7WRJ7
B	-16	SER	-	expression tag	UNP B7WRJ7
B	-15	HIS	-	expression tag	UNP B7WRJ7
B	-14	HIS	-	expression tag	UNP B7WRJ7
B	-13	HIS	-	expression tag	UNP B7WRJ7
B	-12	HIS	-	expression tag	UNP B7WRJ7
B	-11	HIS	-	expression tag	UNP B7WRJ7
B	-10	HIS	-	expression tag	UNP B7WRJ7
B	-9	SER	-	expression tag	UNP B7WRJ7
B	-8	SER	-	expression tag	UNP B7WRJ7
B	-7	GLY	-	expression tag	UNP B7WRJ7
B	-6	LEU	-	expression tag	UNP B7WRJ7
B	-5	VAL	-	expression tag	UNP B7WRJ7
B	-4	PRO	-	expression tag	UNP B7WRJ7
B	-3	ARG	-	expression tag	UNP B7WRJ7
B	-2	GLY	-	expression tag	UNP B7WRJ7
B	-1	SER	-	expression tag	UNP B7WRJ7
B	0	HIS	-	expression tag	UNP B7WRJ7
C	-19	MET	-	initiating methionine	UNP B7WRJ7
C	-18	GLY	-	expression tag	UNP B7WRJ7
C	-17	SER	-	expression tag	UNP B7WRJ7
C	-16	SER	-	expression tag	UNP B7WRJ7
C	-15	HIS	-	expression tag	UNP B7WRJ7
C	-14	HIS	-	expression tag	UNP B7WRJ7
C	-13	HIS	-	expression tag	UNP B7WRJ7
C	-12	HIS	-	expression tag	UNP B7WRJ7
C	-11	HIS	-	expression tag	UNP B7WRJ7
C	-10	HIS	-	expression tag	UNP B7WRJ7
C	-9	SER	-	expression tag	UNP B7WRJ7
C	-8	SER	-	expression tag	UNP B7WRJ7
C	-7	GLY	-	expression tag	UNP B7WRJ7
C	-6	LEU	-	expression tag	UNP B7WRJ7
C	-5	VAL	-	expression tag	UNP B7WRJ7
C	-4	PRO	-	expression tag	UNP B7WRJ7
C	-3	ARG	-	expression tag	UNP B7WRJ7
C	-2	GLY	-	expression tag	UNP B7WRJ7
C	-1	SER	-	expression tag	UNP B7WRJ7
C	0	HIS	-	expression tag	UNP B7WRJ7
D	-19	MET	-	initiating methionine	UNP B7WRJ7
D	-18	GLY	-	expression tag	UNP B7WRJ7
D	-17	SER	-	expression tag	UNP B7WRJ7

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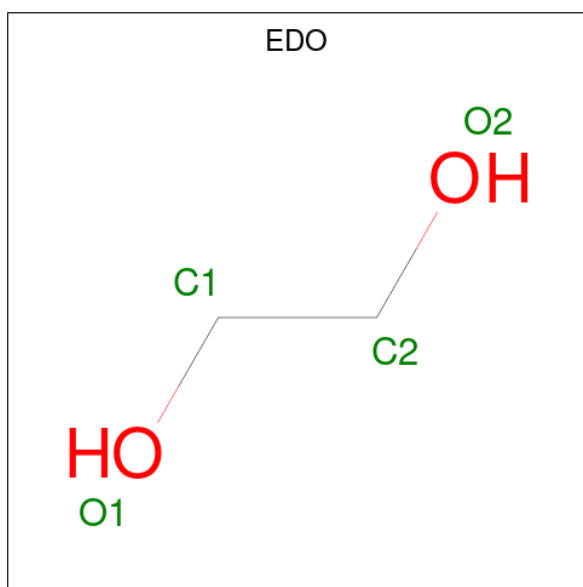
Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	expression tag	UNP B7WRJ7
D	-15	HIS	-	expression tag	UNP B7WRJ7
D	-14	HIS	-	expression tag	UNP B7WRJ7
D	-13	HIS	-	expression tag	UNP B7WRJ7
D	-12	HIS	-	expression tag	UNP B7WRJ7
D	-11	HIS	-	expression tag	UNP B7WRJ7
D	-10	HIS	-	expression tag	UNP B7WRJ7
D	-9	SER	-	expression tag	UNP B7WRJ7
D	-8	SER	-	expression tag	UNP B7WRJ7
D	-7	GLY	-	expression tag	UNP B7WRJ7
D	-6	LEU	-	expression tag	UNP B7WRJ7
D	-5	VAL	-	expression tag	UNP B7WRJ7
D	-4	PRO	-	expression tag	UNP B7WRJ7
D	-3	ARG	-	expression tag	UNP B7WRJ7
D	-2	GLY	-	expression tag	UNP B7WRJ7
D	-1	SER	-	expression tag	UNP B7WRJ7
D	0	HIS	-	expression tag	UNP B7WRJ7

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



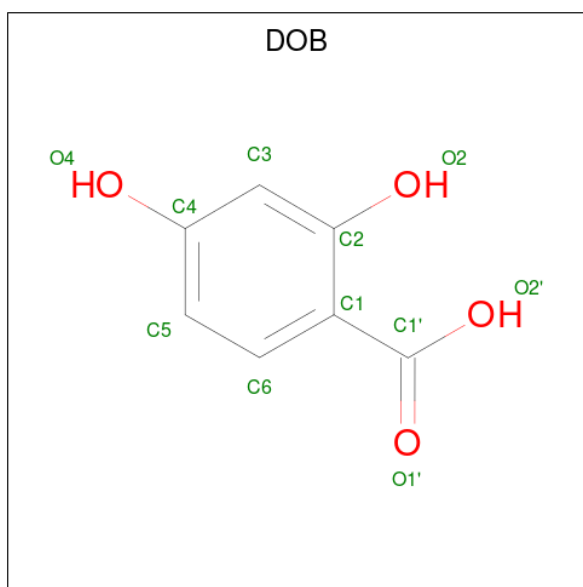
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is 2,4-DIHYDROXYBENZOIC ACID (CCD ID: DOB) (formula: $C_7H_6O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			11	7	4		
4	D	1	Total	C	O	0	0
			11	7	4		

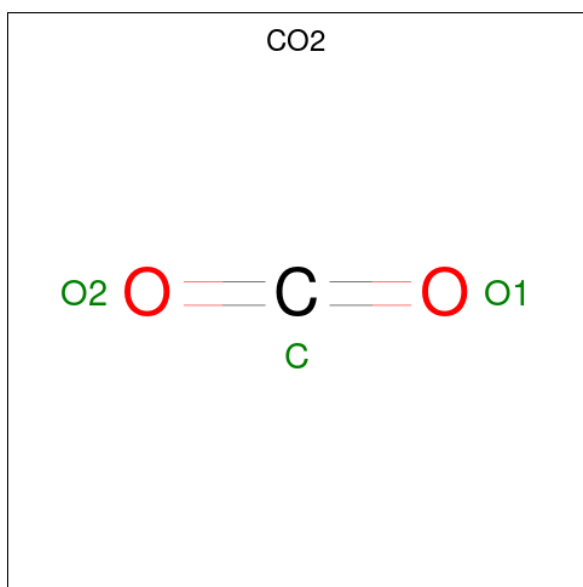
- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Zn	0	0
			1	1		
5	B	1	Total	Zn	0	0
			1	1		
5	C	1	Total	Zn	0	0
			1	1		
5	D	1	Total	Zn	0	0
			1	1		

- Molecule 6 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	C	1	Total	Cl	0	0
			1	1		

- Molecule 7 is CARBON DIOXIDE (CCD ID: CO2) (formula: CO₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	D	1	Total	C	O	0	0
			3	1	2		
7	D	1	Total	C	O	0	0
			3	1	2		

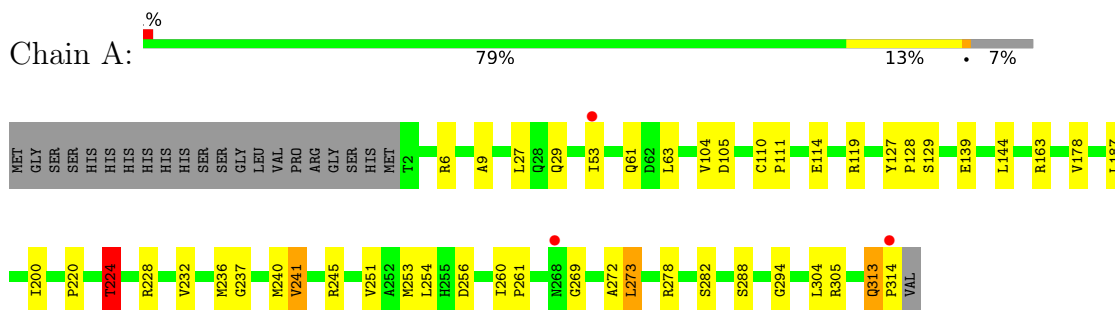
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	29	Total	O	0	0
			29	29		
8	B	25	Total	O	0	0
			25	25		
8	C	22	Total	O	0	0
			22	22		
8	D	47	Total	O	0	0
			47	47		

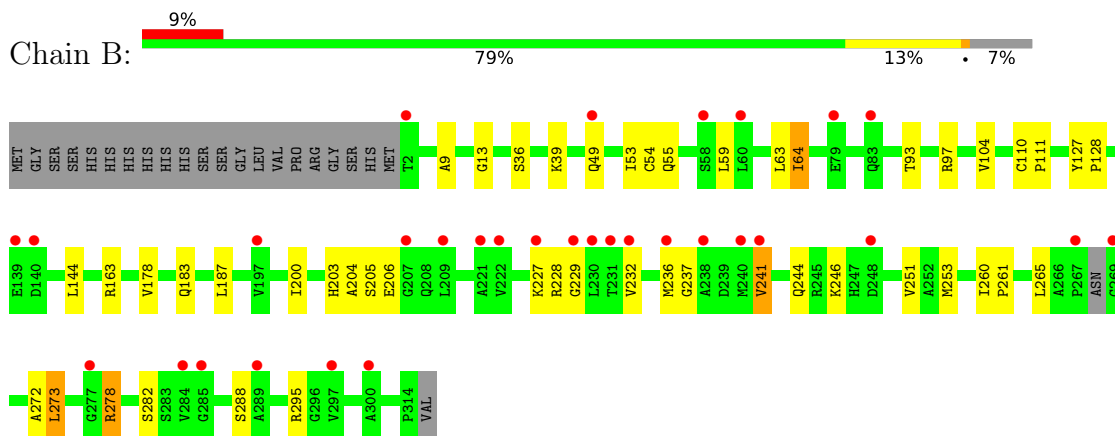
3 Residue-property plots [i](#)

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.

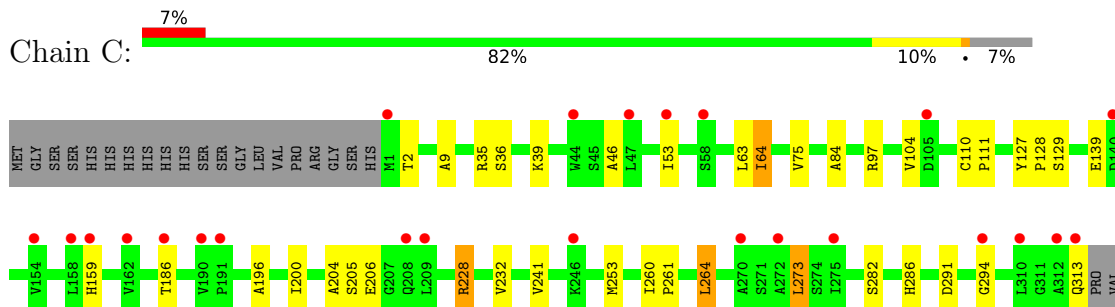
- Molecule 1: 4-hydroxythreonine-4-phosphate dehydrogenase



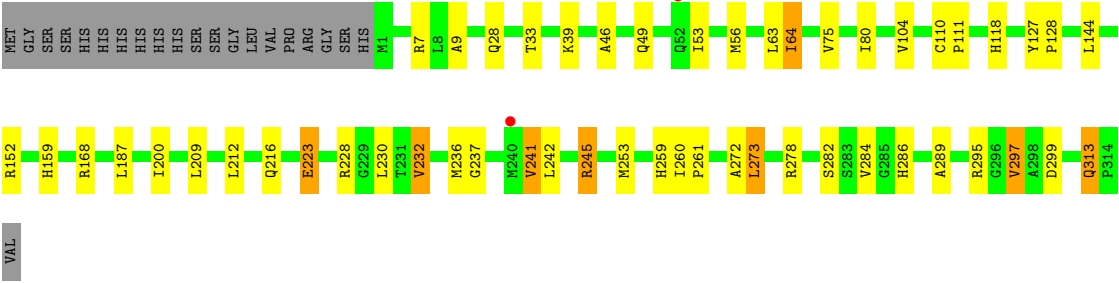
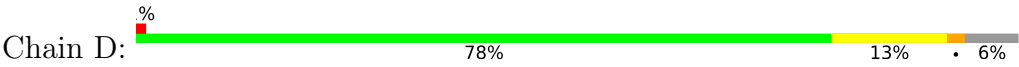
- Molecule 1: 4-hydroxythreonine-4-phosphate dehydrogenase



- Molecule 1: 4-hydroxythreonine-4-phosphate dehydrogenase



- Molecule 1: 4-hydroxythreonine-4-phosphate dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α , β , γ	86.30Å 93.63Å 165.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.93 – 2.50 24.93 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.5 (24.93-2.50) 99.5 (24.93-2.50)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.17 (at 2.50Å)	Xtriage
Refinement program	REFMAC 5.8.0415	Depositor
R, R_{free}	0.253 , 0.290 0.254 , 0.292	Depositor DCC
R_{free} test set	2351 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	29.8	Xtriage
Anisotropy	0.150	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 25.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	9363	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 30.53 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.2871e-03.*

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: CO2, ZN, DOB, EDO, CL, GOL

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	0.61	0/2331	1.08	1/3173 (0.0%)
1	B	0.56	0/2322	1.03	0/3159
1	C	0.54	0/2331	1.04	2/3171 (0.1%)
1	D	0.63	0/2339	1.14	3/3183 (0.1%)
All	All	0.59	0/9323	1.07	6/12686 (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	A	0	1
1	B	0	2
1	C	0	1
1	D	0	3
All	All	0	7

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	223	GLU	CB-CG-CD	6.16	123.06	112.60
1	C	186	THR	CA-CB-OG1	-5.86	100.81	109.60
1	A	224	THR	CB-CA-C	5.79	121.80	110.67
1	D	118	HIS	CA-CB-CG	-5.65	108.15	113.80
1	D	118	HIS	CB-CG-CD2	-5.48	124.07	131.20
1	C	2	THR	CB-CA-C	5.24	118.28	109.48

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	278	ARG	Sidechain
1	B	163	ARG	Sidechain
1	B	278	ARG	Sidechain
1	C	35	ARG	Sidechain
1	D	152	ARG	Sidechain
1	D	245	ARG	Sidechain
1	D	7	ARG	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	2294	0	2345	37	0
1	B	2286	0	2338	38	0
1	C	2295	0	2350	31	0
1	D	2302	0	2357	39	0
2	A	6	0	8	3	0
3	A	20	0	30	5	0
3	D	4	0	6	0	0
4	A	11	0	4	0	0
4	D	11	0	3	3	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
6	C	1	0	0	0	0
7	D	6	0	0	0	0
8	A	29	0	0	0	0
8	B	25	0	0	4	0
8	C	22	0	0	1	0
8	D	47	0	0	2	0
All	All	9363	0	9441	137	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 7.

All (137) 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:C:228:ARG:HH21	1:C:228:ARG:HG3	1.22	1.02
1:A:256:ASP:CG	3:A:407:EDO:H22	1.91	0.95
1:B:241:VAL:HG21	8:B:519:HOH:O	1.66	0.95
1:B:236:MET:HB2	8:B:519:HOH:O	1.65	0.94
1:D:259:HIS:NE2	4:D:401:DOB:O2	2.05	0.89
1:C:53:ILE:HD13	1:C:294:GLY:HA2	1.63	0.79
1:B:244:GLN:HB3	1:B:246:LYS:HE3	1.65	0.78
1:A:254:LEU:HD22	3:A:408:EDO:H22	1.66	0.78
1:D:236:MET:HB3	1:D:241:VAL:HG22	1.68	0.75
1:A:29:GLN:HG3	1:A:304:LEU:HD11	1.69	0.74
1:A:313:GLN:HB3	1:A:314:PRO:HD3	1.71	0.72
1:D:144:LEU:HD22	4:D:401:DOB:H3	1.73	0.70
1:D:273:LEU:HD22	1:D:282:SER:HB2	1.75	0.68
1:C:273:LEU:HD22	1:C:282:SER:HB2	1.76	0.67
1:C:228:ARG:HG3	1:C:228:ARG:NH2	2.01	0.67
1:D:242:LEU:O	1:D:245:ARG:HG2	1.95	0.67
1:A:273:LEU:HD22	1:A:282:SER:HB2	1.77	0.65
1:A:236:MET:HB3	1:A:241:VAL:HG22	1.77	0.65
1:A:119:ARG:CZ	1:B:229:GLY:O	2.45	0.64
1:B:273:LEU:HD22	1:B:282:SER:HB2	1.79	0.64
1:A:256:ASP:OD2	3:A:407:EDO:H22	1.96	0.64
1:C:36:SER:HA	1:C:64:ILE:HD13	1.80	0.64
1:B:64:ILE:HD12	1:B:64:ILE:N	2.14	0.62
1:D:49:GLN:HE21	1:D:53:ILE:CD1	2.12	0.62
1:A:256:ASP:H	3:A:407:EDO:HO1	1.49	0.61
1:C:313:GLN:HE21	1:C:313:GLN:HA	1.65	0.61
1:D:39:LYS:HG3	1:D:64:ILE:HG22	1.82	0.61
1:A:220:PRO:O	1:A:224:THR:HG22	2.01	0.60
1:B:236:MET:HB2	1:B:241:VAL:HG21	1.83	0.60
1:D:236:MET:CB	1:D:241:VAL:HG22	2.30	0.60
1:A:27:LEU:HD13	1:A:63:LEU:HD11	1.84	0.60
1:D:284:VAL:HG12	1:D:286:HIS:CD2	2.37	0.59
1:B:9:ALA:HB2	1:B:104:VAL:HG21	1.85	0.59
1:A:236:MET:CB	1:A:241:VAL:HG22	2.33	0.59
1:A:236:MET:SD	1:A:240:MET:HE1	2.42	0.58
1:C:286:HIS:ND1	1:D:297:VAL:HG11	2.18	0.58
1:B:265:LEU:HD11	1:C:264:LEU:HD11	1.86	0.58
1:D:46:ALA:HA	1:D:75:VAL:HG21	1.86	0.58
1:B:39:LYS:HG3	1:B:64:ILE:HG22	1.86	0.57
1:B:54:CYS:HB3	8:B:513:HOH:O	2.05	0.56
1:C:264:LEU:C	1:C:264:LEU:HD13	2.31	0.56
1:A:114:GLU:HB2	2:A:401:GOL:H31	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:110:CYS:HB3	1:B:111:PRO:CD	2.36	0.55
1:B:237:GLY:O	1:B:241:VAL:HG23	2.07	0.55
1:D:64:ILE:HD12	1:D:64:ILE:N	2.21	0.55
1:C:64:ILE:N	1:C:64:ILE:HD12	2.21	0.54
1:D:49:GLN:HE21	1:D:53:ILE:HD12	1.72	0.54
1:A:269:GLY:HA2	1:A:305:ARG:NH2	2.23	0.54
1:A:236:MET:HB2	1:A:241:VAL:CG2	2.38	0.53
1:B:203:HIS:CE1	1:C:159:HIS:CD2	2.97	0.53
1:B:203:HIS:CE1	1:C:159:HIS:NE2	2.76	0.53
1:D:236:MET:HB2	1:D:241:VAL:HG21	1.91	0.53
1:C:196:ALA:HB1	1:C:241:VAL:HG21	1.89	0.53
1:D:236:MET:CB	1:D:241:VAL:CG2	2.87	0.52
1:D:49:GLN:NE2	1:D:53:ILE:HD11	2.24	0.52
1:A:200:ILE:HG12	1:A:253:MET:HG3	1.92	0.52
1:A:236:MET:HB2	1:A:241:VAL:HG21	1.90	0.52
1:A:236:MET:HE3	1:A:241:VAL:HG11	1.92	0.52
1:A:236:MET:CB	1:A:241:VAL:CG2	2.88	0.52
1:D:236:MET:HB2	1:D:241:VAL:CG2	2.41	0.51
1:C:9:ALA:HB2	1:C:104:VAL:HG21	1.93	0.51
1:D:9:ALA:HB2	1:D:104:VAL:HG21	1.94	0.50
1:A:273:LEU:N	1:A:273:LEU:HD23	2.27	0.50
1:C:110:CYS:HB3	1:C:111:PRO:CD	2.42	0.49
1:D:110:CYS:HB3	1:D:111:PRO:CD	2.42	0.49
1:B:273:LEU:HD23	1:B:273:LEU:N	2.27	0.49
1:B:236:MET:HB3	1:B:241:VAL:CG2	2.42	0.49
1:C:286:HIS:CG	1:D:297:VAL:HG11	2.47	0.49
1:D:273:LEU:N	1:D:273:LEU:HD23	2.28	0.49
1:A:9:ALA:HB2	1:A:104:VAL:HG21	1.95	0.49
1:B:49:GLN:HE21	1:B:53:ILE:HD11	1.77	0.48
1:A:6:ARG:HD3	1:A:105:ASP:HB2	1.95	0.48
1:A:110:CYS:HB3	1:A:111:PRO:CD	2.43	0.48
1:B:144:LEU:HD11	1:B:272:ALA:HB1	1.95	0.48
1:C:228:ARG:HH21	1:C:228:ARG:CG	2.06	0.48
1:D:159:HIS:HE1	4:D:401:DOB:C3	2.26	0.48
1:B:236:MET:CB	1:B:241:VAL:CG2	2.91	0.48
1:B:295:ARG:CB	1:B:295:ARG:HH21	2.26	0.48
1:A:237:GLY:O	1:A:241:VAL:HG23	2.14	0.48
1:B:59:LEU:O	1:B:63:LEU:HG	2.13	0.48
1:D:49:GLN:HE21	1:D:53:ILE:HD11	1.78	0.48
1:C:200:ILE:HG12	1:C:253:MET:HG3	1.96	0.47
1:B:93:THR:O	1:B:97:ARG:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:46:ALA:HA	1:C:75:VAL:HG21	1.96	0.47
1:D:200:ILE:HG12	1:D:253:MET:HG3	1.96	0.46
1:A:127:TYR:N	1:A:128:PRO:CD	2.79	0.46
1:A:129:SER:HB3	1:A:139:GLU:OE2	2.15	0.46
1:C:273:LEU:HD23	1:C:273:LEU:N	2.30	0.46
1:D:278:ARG:HG2	8:D:524:HOH:O	2.15	0.46
1:C:36:SER:HA	1:C:64:ILE:CD1	2.44	0.46
1:A:53:ILE:HD13	1:A:294:GLY:HA2	1.98	0.45
1:A:236:MET:HE3	1:A:241:VAL:CG1	2.47	0.45
1:D:127:TYR:N	1:D:128:PRO:CD	2.80	0.45
1:D:168:ARG:HG3	1:D:168:ARG:HH11	1.81	0.45
1:B:200:ILE:HG12	1:B:253:MET:HG3	1.98	0.45
1:B:183:GLN:HE22	1:B:278:ARG:HA	1.81	0.45
1:D:230:LEU:HD23	1:D:232:VAL:HG22	1.99	0.45
1:B:260:ILE:N	1:B:261:PRO:HD2	2.32	0.44
1:A:260:ILE:N	1:A:261:PRO:HD2	2.32	0.44
1:C:264:LEU:HD13	1:C:264:LEU:O	2.18	0.44
1:D:237:GLY:O	1:D:241:VAL:HG23	2.18	0.44
1:B:64:ILE:N	1:B:64:ILE:CD1	2.81	0.44
1:B:127:TYR:N	1:B:128:PRO:CD	2.80	0.44
1:C:127:TYR:N	1:C:128:PRO:CD	2.80	0.44
1:B:36:SER:HA	1:B:64:ILE:HD13	2.01	0.43
1:C:204:ALA:O	1:C:205:SER:HB2	2.19	0.43
1:C:39:LYS:HG3	1:C:64:ILE:HG22	2.00	0.43
1:B:236:MET:HB3	1:B:241:VAL:HG22	2.00	0.43
1:A:114:GLU:H	2:A:401:GOL:C3	2.32	0.43
1:B:111:PRO:HB2	1:B:288:SER:HA	2.00	0.42
1:A:114:GLU:H	2:A:401:GOL:H31	1.83	0.42
1:C:264:LEU:C	1:C:264:LEU:CD1	2.92	0.42
1:B:236:MET:HB2	1:B:241:VAL:CG2	2.49	0.42
1:C:260:ILE:N	1:C:261:PRO:HD2	2.33	0.42
1:D:260:ILE:N	1:D:261:PRO:HD2	2.35	0.42
1:A:144:LEU:HD11	1:A:272:ALA:HB1	2.02	0.42
1:C:129:SER:OG	1:C:139:GLU:OE2	2.38	0.42
1:A:272:ALA:C	1:A:273:LEU:HD23	2.45	0.42
1:D:272:ALA:C	1:D:273:LEU:HD23	2.44	0.42
1:C:286:HIS:CE1	1:D:297:VAL:HG11	2.54	0.42
1:B:49:GLN:HE21	1:B:53:ILE:CD1	2.33	0.41
1:C:291:ASP:HB2	1:D:289:ALA:HA	2.02	0.41
1:D:212:LEU:O	1:D:216:GLN:HG3	2.20	0.41
1:A:178:VAL:HG22	1:A:251:VAL:HG21	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:13:GLY:HA2	8:B:515:HOH:O	2.20	0.41
1:B:110:CYS:HB3	1:B:111:PRO:HD2	2.01	0.41
1:D:313:GLN:HE21	1:D:313:GLN:HB2	1.59	0.41
1:C:84:ALA:HB3	8:C:511:HOH:O	2.20	0.41
1:A:254:LEU:CD2	3:A:408:EDO:H22	2.44	0.41
1:B:204:ALA:O	1:B:205:SER:HB2	2.21	0.40
1:A:111:PRO:HB2	1:A:288:SER:HA	2.04	0.40
1:B:272:ALA:C	1:B:273:LEU:HD23	2.47	0.40
1:D:80:ILE:HA	8:D:527:HOH:O	2.21	0.40
1:D:295:ARG:HH11	1:D:295:ARG:HG3	1.86	0.40
1:B:178:VAL:HG22	1:B:251:VAL:HG21	2.03	0.40
1:D:28:GLN:NE2	1:D:56:MET:HE2	2.37	0.40
1:D:49:GLN:NE2	1:D:53:ILE:CD1	2.81	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	311/335 (93%)	302 (97%)	8 (3%)	1 (0%)	36	55
1	B	308/335 (92%)	301 (98%)	7 (2%)	0	100	100
1	C	311/335 (93%)	304 (98%)	7 (2%)	0	100	100
1	D	312/335 (93%)	303 (97%)	9 (3%)	0	100	100
All	All	1242/1340 (93%)	1210 (97%)	31 (2%)	1 (0%)	48	68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	313	GLN

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	242/261 (93%)	233 (96%)	9 (4%)	30	57
1	B	241/261 (92%)	232 (96%)	9 (4%)	30	57
1	C	242/261 (93%)	234 (97%)	8 (3%)	33	61
1	D	243/261 (93%)	230 (95%)	13 (5%)	20	42
All	All	968/1044 (93%)	929 (96%)	39 (4%)	28	54

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

Mol	Chain	Res	Type
1	A	61	GLN
1	A	163	ARG
1	A	187	LEU
1	A	224	THR
1	A	228	ARG
1	A	232	VAL
1	A	241	VAL
1	A	245	ARG
1	A	273	LEU
1	B	55	GLN
1	B	64	ILE
1	B	187	LEU
1	B	206	GLU
1	B	227	LYS
1	B	228	ARG
1	B	232	VAL
1	B	241	VAL
1	B	273	LEU
1	C	63	LEU
1	C	64	ILE
1	C	97	ARG
1	C	206	GLU
1	C	228	ARG
1	C	232	VAL

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Mol	Chain	Res	Type
1	C	264	LEU
1	C	273	LEU
1	D	33	THR
1	D	63	LEU
1	D	64	ILE
1	D	187	LEU
1	D	209	LEU
1	D	223	GLU
1	D	228	ARG
1	D	232	VAL
1	D	241	VAL
1	D	273	LEU
1	D	297	VAL
1	D	299	ASP
1	D	313	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	73	GLN
1	A	76	GLN
1	A	118	HIS
1	A	313	GLN
1	B	28	GLN
1	B	49	GLN
1	B	73	GLN
1	B	76	GLN
1	B	118	HIS
1	B	183	GLN
1	B	247	HIS
1	B	286	HIS
1	C	244	GLN
1	C	286	HIS
1	C	313	GLN
1	D	49	GLN
1	D	76	GLN
1	D	201	ASN
1	D	203	HIS
1	D	313	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 16 ligands modelled in this entry, 5 are monoatomic - leaving 11 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	$\# Z > 2$
3	EDO	A	408	-	3,3,3	0.41	0	2,2,2	0.05	0
3	EDO	D	405	-	3,3,3	0.11	0	2,2,2	0.25	0
4	DOB	A	403	5	11,11,11	1.86	2 (18%)	15,15,15	1.52	3 (20%)
3	EDO	A	402	-	3,3,3	0.50	0	2,2,2	0.54	0
4	DOB	D	401	5	11,11,11	1.96	2 (18%)	15,15,15	1.09	1 (6%)
3	EDO	A	405	-	3,3,3	0.10	0	2,2,2	0.24	0
7	CO2	D	403	-	2,2,2	0.21	0	1,1,1	0.03	0
7	CO2	D	402	-	2,2,2	0.44	0	1,1,1	0.25	0
2	GOL	A	401	-	5,5,5	0.23	0	5,5,5	0.62	0
3	EDO	A	406	-	3,3,3	0.35	0	2,2,2	0.46	0
3	EDO	A	407	-	3,3,3	0.17	0	2,2,2	0.66	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
3	EDO	A	408	-	-	0/1/1/1	-
3	EDO	D	405	-	-	0/1/1/1	-
4	DOB	A	403	5	-	3/4/4/4	0/1/1/1
3	EDO	A	402	-	-	1/1/1/1	-
4	DOB	D	401	5	-	4/4/4/4	0/1/1/1
3	EDO	A	405	-	-	0/1/1/1	-
2	GOL	A	401	-	-	2/4/4/4	-
3	EDO	A	406	-	-	1/1/1/1	-
3	EDO	A	407	-	-	1/1/1/1	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	401	DOB	O2-C2	-5.44	1.25	1.36
4	A	403	DOB	C3-C2	4.85	1.45	1.38
4	A	403	DOB	O2-C2	-2.93	1.30	1.36
4	D	401	DOB	C3-C2	2.75	1.42	1.38

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	403	DOB	C3-C2-C1	-3.12	116.21	120.59
4	A	403	DOB	C2-C3-C4	2.53	122.01	119.67
4	D	401	DOB	O1'-C1'-C1	-2.09	116.97	121.97
4	A	403	DOB	C6-C1-C2	2.06	120.74	118.15

There are no chirality outliers.

All (12) torsion outliers are listed below:

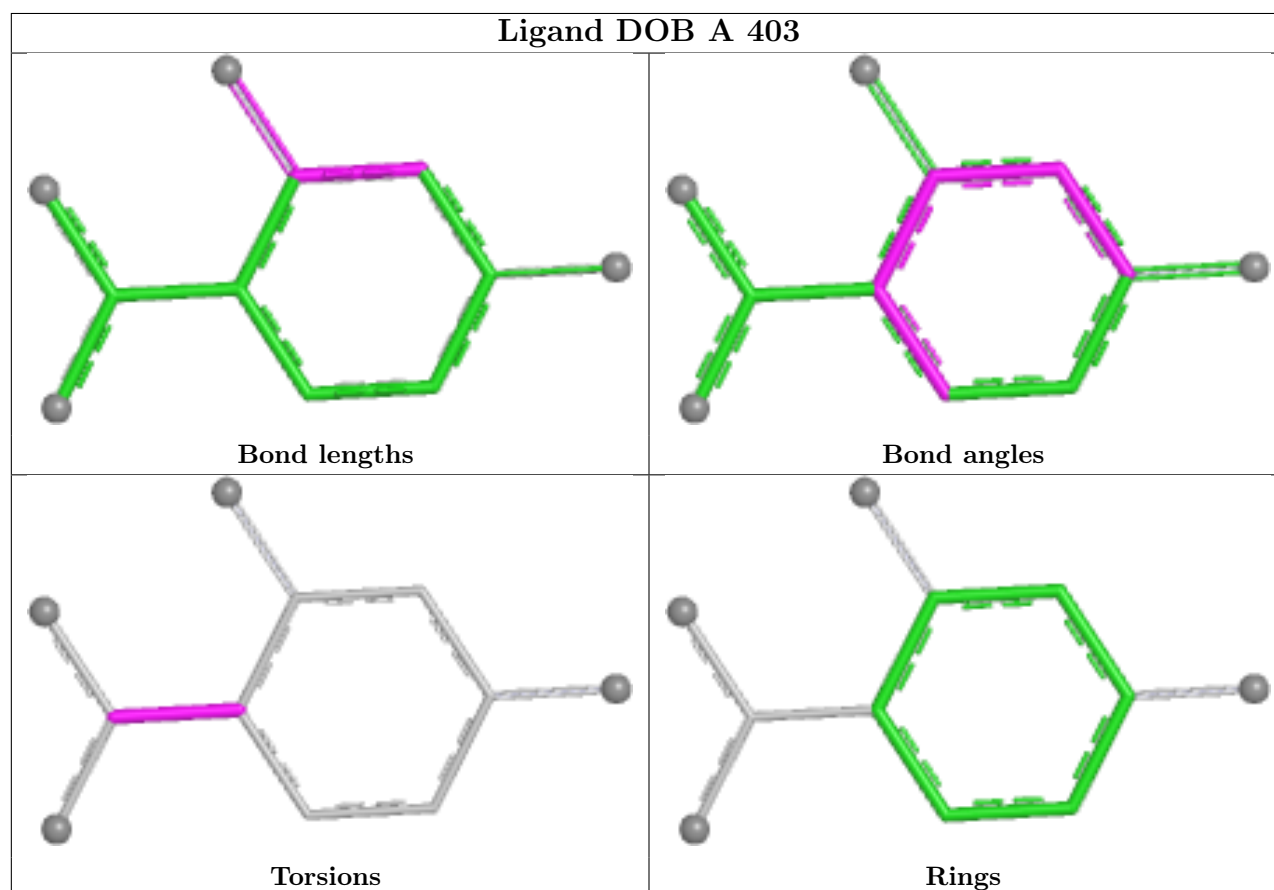
Mol	Chain	Res	Type	Atoms
4	A	403	DOB	C2-C1-C1'-O1'
4	A	403	DOB	C2-C1-C1'-O2'
4	D	401	DOB	C2-C1-C1'-O1'
4	D	401	DOB	C2-C1-C1'-O2'
2	A	401	GOL	O1-C1-C2-C3
2	A	401	GOL	O1-C1-C2-O2
3	A	407	EDO	O1-C1-C2-O2
3	A	402	EDO	O1-C1-C2-O2
3	A	406	EDO	O1-C1-C2-O2
4	D	401	DOB	C6-C1-C1'-O2'
4	D	401	DOB	C6-C1-C1'-O1'
4	A	403	DOB	C6-C1-C1'-O2'

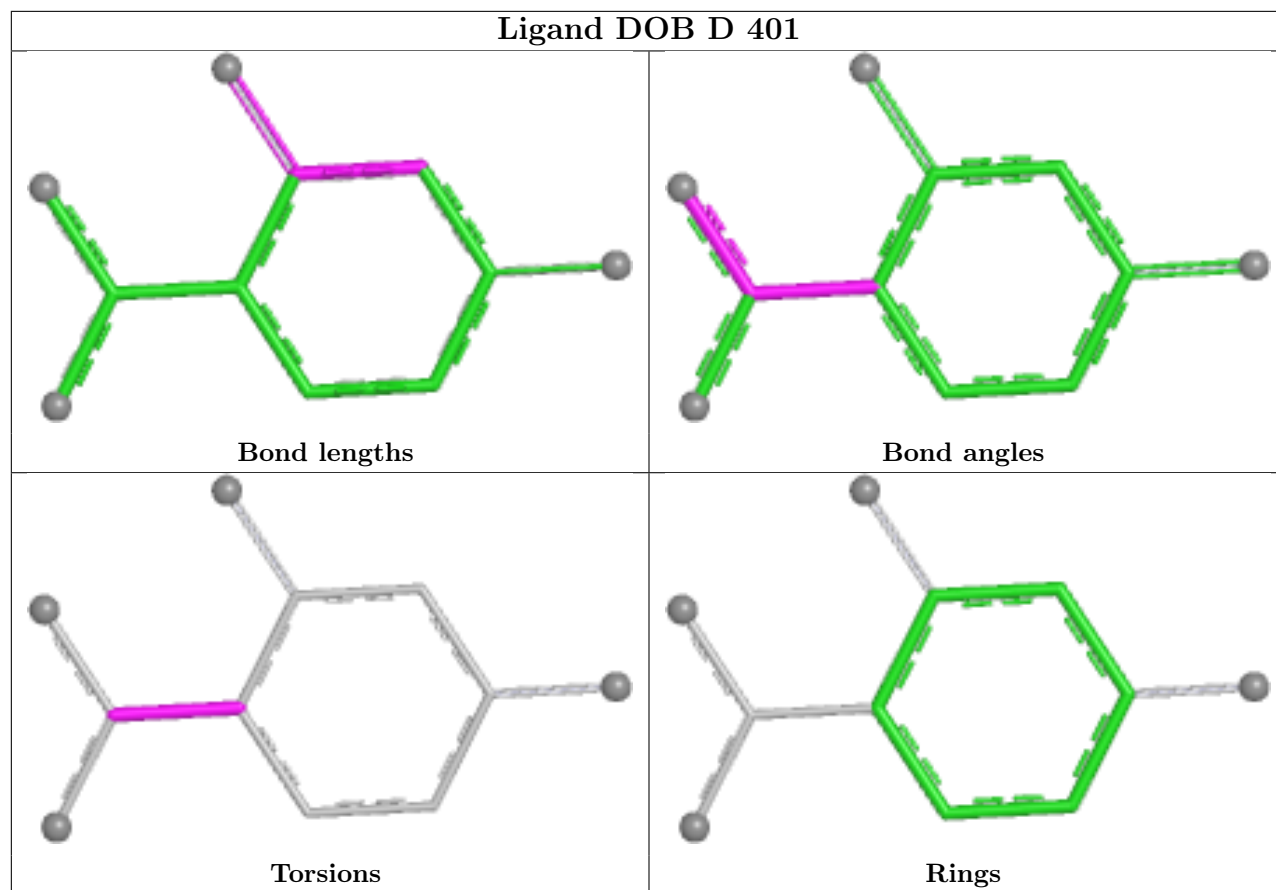
There are no ring outliers.

4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	408	EDO	2	0
4	D	401	DOB	3	0
2	A	401	GOL	3	0
3	A	407	EDO	3	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 ⓘ

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	313/335 (93%)	0.06	3 (0%) 79 76	10, 24, 43, 62	0
1	B	312/335 (93%)	1.02	31 (9%) 13 11	25, 47, 66, 81	0
1	C	313/335 (93%)	1.00	24 (7%) 19 17	26, 43, 63, 79	0
1	D	314/335 (93%)	0.02	2 (0%) 85 83	10, 23, 44, 58	0
All	All	1252/1340 (93%)	0.53	60 (4%) 35 31	10, 34, 61, 81	0

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	236	MET	4.4
1	C	47	LEU	4.4
1	B	285	GLY	4.1
1	B	238	ALA	3.3
1	C	1	MET	3.3
1	B	222	VAL	3.2
1	B	2	THR	3.2
1	B	229	GLY	3.1
1	B	83	GLN	3.1
1	B	269	GLY	3.0
1	B	240	MET	3.0
1	B	284	VAL	3.0
1	C	313	GLN	3.0
1	B	297	VAL	2.9
1	B	60	LEU	2.9
1	C	53	ILE	2.9
1	C	208	GLN	2.9
1	C	270	ALA	2.8
1	C	158	LEU	2.8
1	B	267	PRO	2.8
1	B	231	THR	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	294	GLY	2.7
1	C	275	ILE	2.7
1	A	314	PRO	2.7
1	C	190	VAL	2.7
1	B	289	ALA	2.6
1	B	197	VAL	2.5
1	B	232	VAL	2.5
1	C	312	ALA	2.5
1	B	277	GLY	2.5
1	B	79	GLU	2.4
1	B	230	LEU	2.4
1	C	159	HIS	2.4
1	B	139	GLU	2.4
1	C	310	LEU	2.4
1	C	154	VAL	2.4
1	B	58	SER	2.4
1	B	209	LEU	2.4
1	C	58	SER	2.3
1	D	52	GLN	2.3
1	C	140	ASP	2.3
1	B	227	LYS	2.3
1	B	49	GLN	2.2
1	C	44	TRP	2.2
1	C	272	ALA	2.2
1	B	207	GLY	2.2
1	A	53	ILE	2.2
1	A	268	ASN	2.1
1	C	105	ASP	2.1
1	C	191	PRO	2.1
1	B	221	ALA	2.1
1	C	186	THR	2.1
1	B	140	ASP	2.1
1	B	248	ASP	2.1
1	C	246	LYS	2.1
1	D	240	MET	2.1
1	C	162	VAL	2.0
1	B	300	ALA	2.0
1	B	241	VAL	2.0
1	C	209	LEU	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](#)

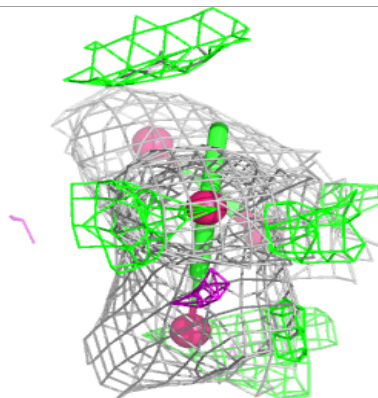
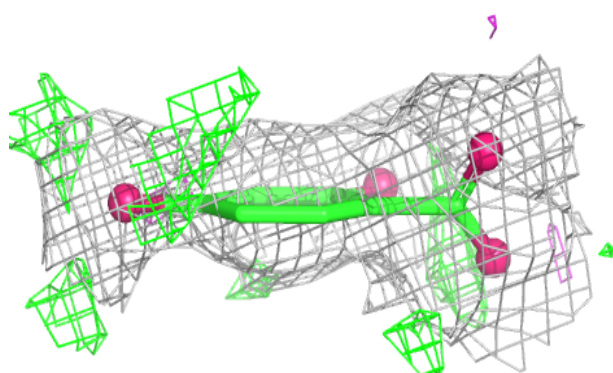
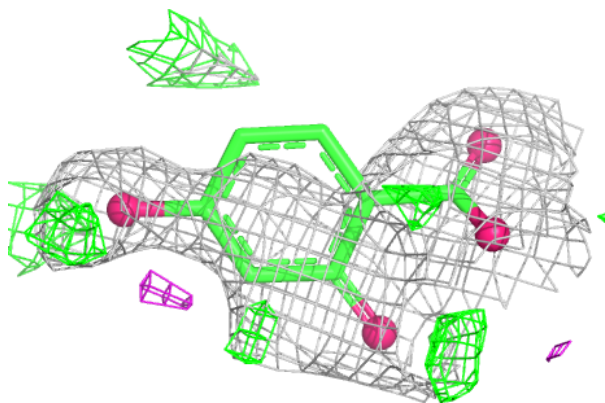
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
2	GOL	A	401	6/6	0.80	0.17	34,41,42,42	0
4	DOB	A	403	11/11	0.80	0.17	37,41,53,53	0
6	CL	C	402	1/1	0.82	0.20	76,76,76,76	0
7	CO2	D	403	3/3	0.82	0.13	40,40,42,43	0
3	EDO	A	402	4/4	0.83	0.13	31,34,34,36	0
3	EDO	D	405	4/4	0.85	0.16	42,43,43,46	0
3	EDO	A	406	4/4	0.86	0.15	33,34,36,38	0
4	DOB	D	401	11/11	0.88	0.12	33,38,41,41	0
3	EDO	A	405	4/4	0.91	0.09	23,24,24,25	0
3	EDO	A	408	4/4	0.92	0.12	6,6,6,6	4
5	ZN	A	404	1/1	0.94	0.05	22,22,22,22	0
7	CO2	D	402	3/3	0.95	0.06	22,22,22,22	0
5	ZN	D	404	1/1	0.95	0.04	25,25,25,25	0
3	EDO	A	407	4/4	0.97	0.09	12,13,13,14	4
5	ZN	B	401	1/1	0.97	0.04	43,43,43,43	0
5	ZN	C	401	1/1	0.98	0.04	39,39,39,39	0

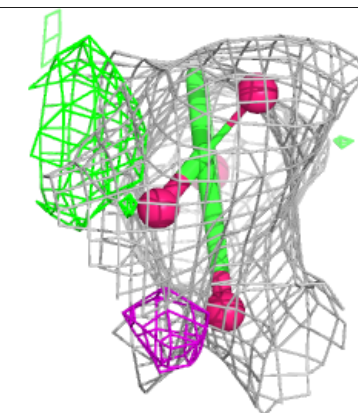
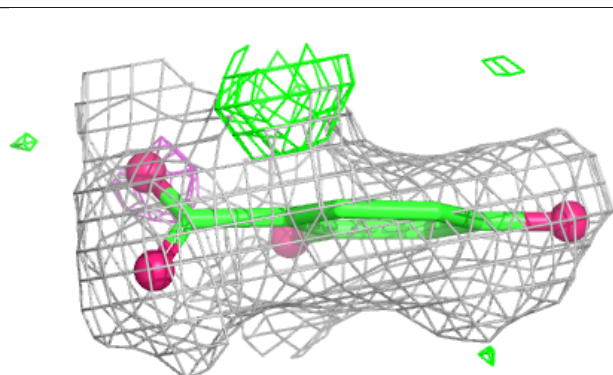
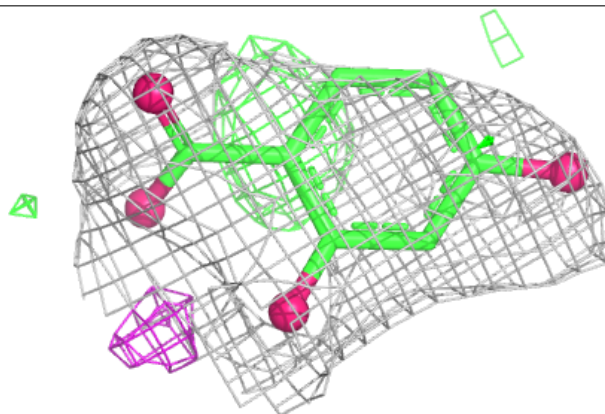
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around DOB A 403:

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

**Electron density around DOB D 401:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.