



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 01:41 AM UTC

PDB ID : 5ALS / pdb_00005als
Title : ligand complex structure of soluble epoxide hydrolase
Authors : Oster, L.; Tapani, S.; Xue, Y.; Kack, H.
Deposited on : 2015-03-08
Resolution : 2.57 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

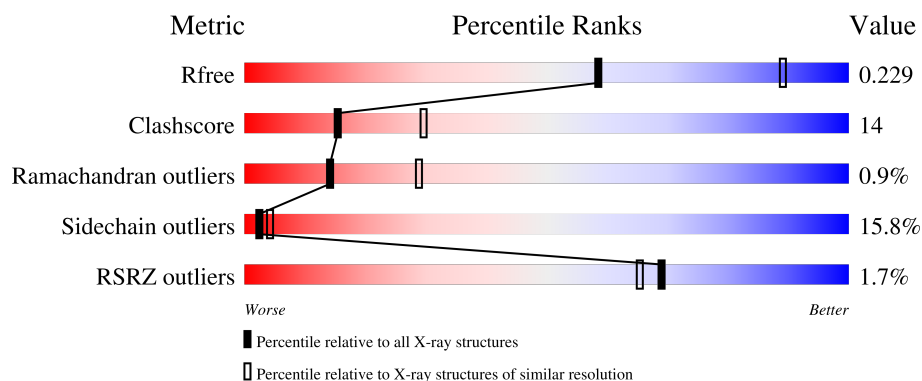
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.57 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	4770 (2.60-2.56)
Clashscore	190562	5124 (2.60-2.56)
Ramachandran outliers	187476	5046 (2.60-2.56)
Sidechain outliers	187428	5046 (2.60-2.56)
RSRZ outliers	180081	4770 (2.60-2.56)

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	549	

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	5DQ	A	1551	-	X	-	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4574 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 BIFUNCTIONAL EPOXIDE HYDROLASE 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	542	4295	2752	723	783	37	0	1	1

There is a discrepancy between the modelled and reference sequences:

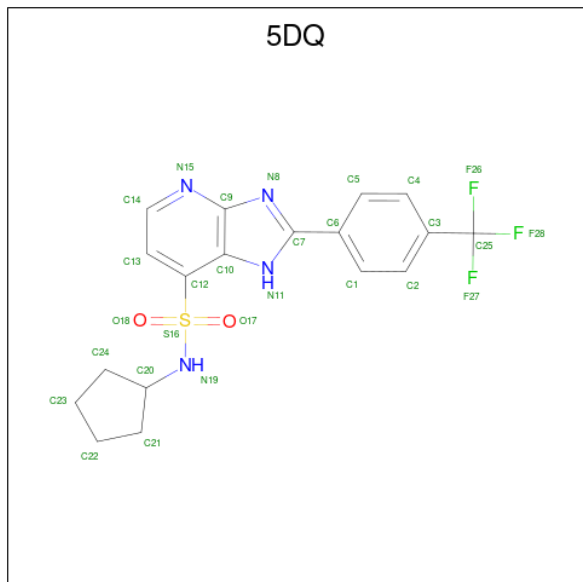
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP P34913

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0
2	A	1	5	4	1	0	0
2	A	1	5	4	1	0	0

- Molecule 3 is N-CYCLOPENTYL-2-[4-(TRIFLUOROMETHYL)PHENYL]-3H-IMIDAZO[4,5-B]PYRIDINE-7-SULFONAMIDE (CCD ID: 5DQ) (formula: $C_{18}H_{17}F_3N_4O_2S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	F	N	O		
3	A	1	28	18	3	4	2	0	0

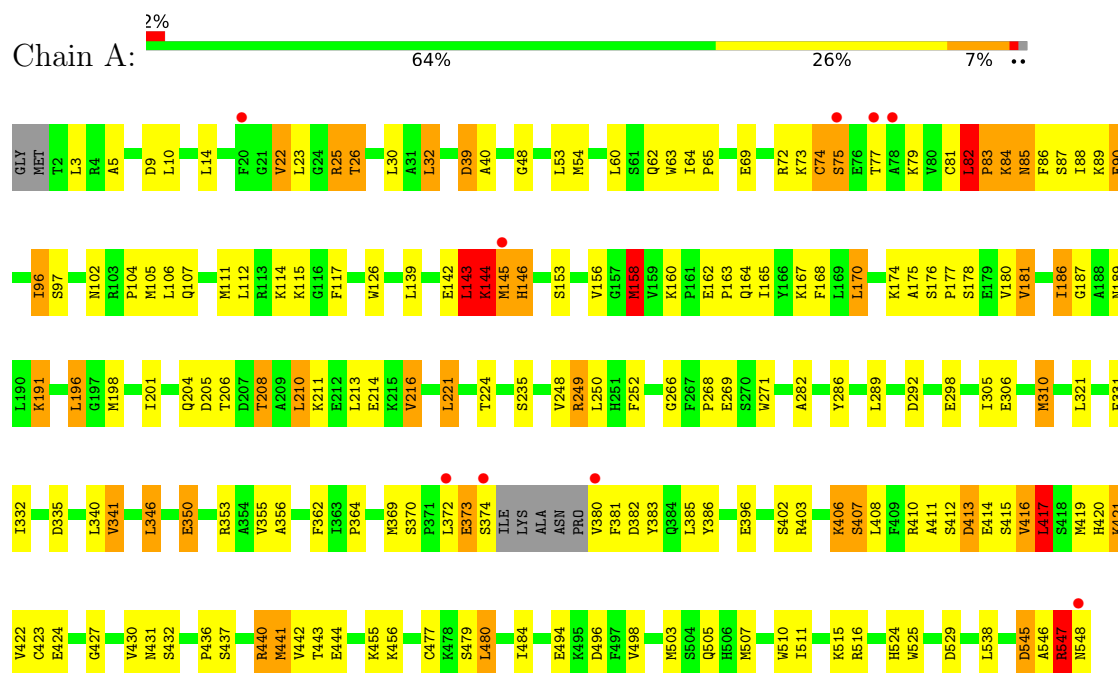
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	236	Total	O	0	0
			236	236		

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 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: BIFUNCTIONAL EPOXIDE HYDROLASE 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	93.72Å 93.72Å 244.92Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	81.17 – 2.57 81.17 – 2.57	Depositor EDS
% Data completeness (in resolution range)	99.4 (81.17-2.57) 99.4 (81.17-2.57)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.94 (at 2.58Å)	Xtriage
Refinement program	BUSTER 2.11.1	Depositor
R, R_{free}	0.203 , 0.214 0.207 , 0.229	Depositor DCC
R_{free} test set	1071 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	51.0	Xtriage
Anisotropy	0.268	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 43.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4574	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.57% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, 5DQ

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	0.89	7/4398 (0.2%)	1.45	40/5957 (0.7%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	441	MET	SD-CE	-13.32	1.46	1.79
1	A	158	MET	SD-CE	-8.80	1.57	1.79
1	A	419	MET	SD-CE	-8.24	1.58	1.79
1	A	547	ARG	C-N	-6.64	1.24	1.33
1	A	143	LEU	CA-C	-6.16	1.45	1.52
1	A	144	LYS	CA-C	-5.69	1.45	1.52
1	A	310	MET	SD-CE	-5.55	1.65	1.79

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	144	LYS	CA-C-O	-9.13	107.45	120.51
1	A	416	VAL	N-CA-C	8.87	119.67	110.36
1	A	269	GLU	N-CA-C	7.49	119.85	109.29
1	A	144	LYS	CB-CA-C	7.13	124.61	110.42
1	A	505	GLN	N-CA-C	7.09	120.83	111.75
1	A	292	ASP	N-CA-C	-6.81	95.94	107.99
1	A	146	HIS	N-CA-C	6.76	121.41	113.23
1	A	381	PHE	CA-C-N	6.62	129.14	120.28
1	A	381	PHE	C-N-CA	6.62	129.14	120.28
1	A	196	LEU	N-CA-C	-6.57	105.17	113.72
1	A	271	TRP	N-CA-C	-6.43	104.36	111.82
1	A	144	LYS	CA-CB-CG	-6.42	101.27	114.10
1	A	415	SER	CA-C-N	6.36	128.80	120.60
1	A	415	SER	C-N-CA	6.36	128.80	120.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	545	ASP	N-CA-C	6.12	121.81	113.97
1	A	83	PRO	CA-C-N	6.12	128.47	120.28
1	A	83	PRO	C-N-CA	6.12	128.47	120.28
1	A	411	ALA	CA-C-N	5.96	128.59	120.54
1	A	411	ALA	C-N-CA	5.96	128.59	120.54
1	A	144	LYS	N-CA-CB	5.92	120.49	110.49
1	A	432	SER	N-CA-C	5.76	117.88	110.39
1	A	23	LEU	CA-C-N	5.68	126.24	119.94
1	A	23	LEU	C-N-CA	5.68	126.24	119.94
1	A	516	ARG	CA-C-N	5.61	126.78	121.46
1	A	516	ARG	C-N-CA	5.61	126.78	121.46
1	A	40	ALA	CA-C-N	5.43	127.56	120.28
1	A	40	ALA	C-N-CA	5.43	127.56	120.28
1	A	160	LYS	N-CA-C	-5.39	103.27	110.07
1	A	248	VAL	N-CA-CB	5.38	118.99	112.10
1	A	525	TRP	CA-C-N	5.33	127.74	120.54
1	A	525	TRP	C-N-CA	5.33	127.74	120.54
1	A	9	ASP	N-CA-C	-5.24	103.47	110.55
1	A	176	SER	N-CA-C	-5.21	103.47	109.93
1	A	443	THR	N-CA-C	-5.15	102.84	110.46
1	A	204	GLN	N-CA-C	-5.11	103.72	111.34
1	A	82	LEU	N-CA-C	5.11	116.00	110.13
1	A	48	GLY	CA-C-N	5.01	126.99	120.28
1	A	48	GLY	C-N-CA	5.01	126.99	120.28
1	A	305	ILE	CA-C-N	5.01	127.69	120.38
1	A	305	ILE	C-N-CA	5.01	127.69	120.38

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	4295	0	4294	117	0
2	A	15	0	0	0	0
3	A	28	0	16	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	236	0	0	1	0
All	All	4574	0	4310	117	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 14.

All (117) 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:413:ASP:OD1	1:A:440:ARG:NH1	1.66	1.27
1:A:144:LYS:O	1:A:146:HIS:N	1.80	1.12
1:A:22:VAL:O	1:A:26:THR:HG22	1.56	1.04
1:A:84:LYS:HD2	1:A:84:LYS:H	1.19	1.03
1:A:515:LYS:NZ	1:A:545:ASP:OD1	1.91	1.02
1:A:205:ASP:OD2	1:A:208:THR:OG1	1.80	0.99
1:A:39:ASP:OD1	1:A:74:CYS:SG	2.22	0.98
1:A:170:LEU:HD23	1:A:175:ALA:O	1.66	0.95
1:A:26:THR:O	1:A:30:LEU:HD23	1.66	0.94
1:A:341:VAL:HG13	1:A:355:VAL:HG23	1.49	0.92
1:A:85:ASN:H	1:A:85:ASN:HD22	1.15	0.91
1:A:331:PHE:HB3	1:A:341:VAL:HG22	1.54	0.88
1:A:87:SER:HB3	1:A:90:GLU:HB2	1.57	0.86
1:A:111:MET:HE2	1:A:115:LYS:HE2	1.56	0.85
1:A:420:HIS:C	1:A:421:LYS:HG3	2.02	0.83
1:A:413:ASP:OD1	1:A:440:ARG:CZ	2.27	0.82
1:A:84:LYS:H	1:A:84:LYS:CD	1.93	0.81
1:A:310:MET:HE1	1:A:340:LEU:HA	1.67	0.76
1:A:205:ASP:CG	1:A:208:THR:OG1	2.29	0.75
1:A:416:VAL:O	1:A:417:LEU:HB3	1.85	0.74
1:A:515:LYS:NZ	1:A:545:ASP:CG	2.46	0.72
1:A:413:ASP:CG	1:A:440:ARG:HH12	1.92	0.71
1:A:546:ALA:O	1:A:548:ASN:N	2.23	0.71
1:A:84:LYS:HD2	1:A:84:LYS:N	2.01	0.71
1:A:266:GLY:HA3	1:A:335:ASP:HB3	1.74	0.70
1:A:85:ASN:H	1:A:85:ASN:ND2	1.82	0.68
1:A:112:LEU:O	1:A:117:PHE:HB2	1.94	0.68
1:A:180:VAL:HG11	1:A:198:MET:HE3	1.75	0.67
1:A:413:ASP:OD1	1:A:440:ARG:NH2	2.28	0.67
1:A:310:MET:CE	1:A:340:LEU:HA	2.24	0.67
1:A:410:ARG:NH2	1:A:437:SER:OG	2.30	0.65
1:A:144:LYS:C	1:A:146:HIS:N	2.35	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:206:THR:HG22	1:A:210:LEU:HD22	1.79	0.65
1:A:5:ALA:HB3	1:A:180:VAL:HG22	1.80	0.63
1:A:383:TYR:CE1	3:A:1551:5DQ:H1	2.35	0.61
1:A:515:LYS:HZ1	1:A:545:ASP:CG	2.09	0.61
1:A:142:GLU:HA	1:A:145[A]:MET:HE3	1.82	0.61
1:A:158:MET:HE1	1:A:168:PHE:HB2	1.82	0.60
1:A:214:GLU:HG3	1:A:221:LEU:HB2	1.84	0.59
1:A:72:ARG:O	1:A:75:SER:OG	2.18	0.59
1:A:503:MET:HE1	3:A:1551:5DQ:H231	1.85	0.57
1:A:341:VAL:CG1	1:A:355:VAL:HG23	2.31	0.56
1:A:420:HIS:O	1:A:421:LYS:HG3	2.05	0.56
1:A:170:LEU:CD2	1:A:175:ALA:O	2.49	0.55
1:A:158:MET:HE3	1:A:165:ILE:HA	1.89	0.54
1:A:32:LEU:HD21	1:A:82:LEU:HD11	1.89	0.54
1:A:382:ASP:OD2	1:A:423:CYS:HB2	2.08	0.54
1:A:69:GLU:OE1	1:A:73:LYS:HE2	2.07	0.54
1:A:477:CYS:HA	1:A:480:LEU:HD22	1.88	0.54
1:A:3:LEU:HD11	1:A:216:VAL:HG13	1.90	0.54
1:A:427:GLY:HA3	1:A:430:VAL:HG23	1.89	0.54
1:A:380:VAL:O	1:A:380:VAL:HG23	2.08	0.53
1:A:3:LEU:HD13	1:A:181:VAL:HG22	1.90	0.53
1:A:54:MET:HE1	1:A:126:TRP:HE3	1.73	0.53
1:A:249:ARG:NH1	1:A:298:GLU:O	2.42	0.53
1:A:380:VAL:HG23	1:A:382:ASP:HB2	1.91	0.52
1:A:310:MET:HE1	1:A:340:LEU:CA	2.39	0.52
1:A:370:SER:O	1:A:373:GLU:HB2	2.10	0.52
1:A:362:PHE:HB3	1:A:507:MET:HE3	1.92	0.51
1:A:3:LEU:HD13	1:A:181:VAL:CG2	2.41	0.51
1:A:156:VAL:HG23	1:A:158:MET:HG3	1.93	0.50
1:A:180:VAL:HG11	1:A:198:MET:CE	2.40	0.50
1:A:413:ASP:CG	1:A:440:ARG:HH22	2.20	0.50
1:A:63:TRP:CE3	1:A:64:ILE:HD13	2.47	0.50
1:A:96:ILE:CD1	1:A:126:TRP:HZ2	2.24	0.50
1:A:64:ILE:HD12	1:A:88:ILE:HG22	1.93	0.50
1:A:180:VAL:CG1	1:A:198:MET:HE3	2.42	0.50
1:A:177:PRO:HB3	1:A:198:MET:HG3	1.92	0.50
1:A:83:PRO:HD2	1:A:86:PHE:HB2	1.92	0.50
1:A:346:LEU:HG	1:A:479:SER:HB2	1.95	0.49
1:A:62:GLN:O	1:A:65:PRO:HD2	2.12	0.49
1:A:72:ARG:HA	1:A:75:SER:OG	2.12	0.49
1:A:102:ASN:ND2	1:A:104:PRO:HD2	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:484:ILE:HB	1:A:511:ILE:HG12	1.94	0.48
1:A:186:ILE:HG22	1:A:189:ASN:H	1.79	0.48
1:A:403:ARG:O	1:A:407:SER:OG	2.22	0.48
1:A:406:LYS:NZ	1:A:444:GLU:OE1	2.48	0.47
1:A:153:SER:HB2	1:A:158:MET:O	2.15	0.47
1:A:25:ARG:HA	1:A:25:ARG:HD2	1.72	0.47
1:A:187:GLY:O	1:A:191:LYS:HG2	2.14	0.47
1:A:406:LYS:HB2	1:A:436:PRO:HG2	1.95	0.47
1:A:85:ASN:HD22	1:A:85:ASN:N	1.97	0.46
1:A:112:LEU:C	1:A:117:PHE:HB2	2.39	0.46
1:A:441:MET:HE2	1:A:529:ASP:HA	1.98	0.46
1:A:53:LEU:HD23	1:A:54:MET:HE2	1.97	0.45
1:A:143:LEU:C	1:A:144:LYS:O	2.58	0.45
1:A:380:VAL:CG2	1:A:421:LYS:H	2.30	0.45
1:A:496:ASP:OD2	1:A:524:HIS:HD2	2.00	0.45
1:A:420:HIS:C	1:A:421:LYS:CG	2.82	0.45
1:A:180:VAL:CG1	1:A:198:MET:CE	2.95	0.45
1:A:402:SER:O	1:A:406:LYS:HG3	2.16	0.44
1:A:252:PHE:CE2	1:A:289:LEU:HD23	2.52	0.44
1:A:410:ARG:HE	1:A:414:GLU:HB3	1.83	0.43
1:A:105:MET:HE2	1:A:206:THR:HG23	2.00	0.43
1:A:112:LEU:HD11	1:A:213:LEU:HD21	2.01	0.43
1:A:143:LEU:O	1:A:144:LYS:O	2.37	0.43
1:A:441:MET:CE	1:A:529:ASP:HA	2.49	0.43
1:A:332:ILE:HG12	1:A:356:ALA:HB3	2.00	0.42
1:A:32:LEU:HD21	1:A:82:LEU:CD1	2.49	0.42
1:A:162:GLU:O	1:A:165:ILE:HG22	2.19	0.42
1:A:350:GLU:H	1:A:350:GLU:HG3	1.40	0.42
1:A:524:HIS:HE1	4:A:2003:HOH:O	2.03	0.42
1:A:310:MET:HE1	1:A:340:LEU:CB	2.49	0.42
1:A:282:ALA:HA	1:A:286:TYR:O	2.19	0.42
1:A:144:LYS:HE3	1:A:145[B]:MET:HE1	2.01	0.42
1:A:441:MET:HE2	1:A:529:ASP:CA	2.50	0.42
1:A:382:ASP:OD2	1:A:423:CYS:N	2.27	0.41
1:A:364:PRO:HG2	1:A:510:TRP:NE1	2.35	0.41
1:A:386:TYR:OH	1:A:396:GLU:OE1	2.31	0.41
1:A:346:LEU:HD21	1:A:362:PHE:CE1	2.56	0.41
1:A:162:GLU:HA	1:A:163:PRO:HD3	1.97	0.41
1:A:252:PHE:CD2	1:A:289:LEU:HD23	2.55	0.41
1:A:210:LEU:HD12	1:A:210:LEU:HA	1.95	0.41
1:A:380:VAL:C	1:A:382:ASP:N	2.79	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:10:LEU:HA	1:A:14:LEU:HB2	2.03	0.40

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	539/549 (98%)	518 (96%)	15 (3%)	6 (1%)	11	24

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	144	LYS
1	A	145[A]	MET
1	A	145[B]	MET
1	A	547	ARG
1	A	417	LEU
1	A	268	PRO

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	A	469/474 (99%)	395 (84%)	74 (16%)	2	4

All (74) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	VAL
1	A	25	ARG
1	A	26	THR
1	A	32	LEU
1	A	39	ASP
1	A	60	LEU
1	A	74	CYS
1	A	75	SER
1	A	77	THR
1	A	79	LYS
1	A	81	CYS
1	A	82	LEU
1	A	84	LYS
1	A	85	ASN
1	A	89	LYS
1	A	90	GLU
1	A	96	ILE
1	A	97	SER
1	A	106	LEU
1	A	107	GLN
1	A	114	LYS
1	A	139	LEU
1	A	143	LEU
1	A	144	LYS
1	A	158	MET
1	A	164	GLN
1	A	167	LYS
1	A	170	LEU
1	A	174	LYS
1	A	178	SER
1	A	181	VAL
1	A	186	ILE
1	A	191	LYS
1	A	196	LEU
1	A	201	ILE
1	A	208	THR
1	A	210	LEU
1	A	211	LYS
1	A	216	VAL
1	A	221	LEU
1	A	224	THR
1	A	235	SER

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Mol	Chain	Res	Type
1	A	249	ARG
1	A	250	LEU
1	A	306	GLU
1	A	321	LEU
1	A	341	VAL
1	A	346	LEU
1	A	350	GLU
1	A	353	ARG
1	A	369	MET
1	A	372	LEU
1	A	373	GLU
1	A	374	SER
1	A	385	LEU
1	A	406	LYS
1	A	407	SER
1	A	408	LEU
1	A	412	SER
1	A	413	ASP
1	A	417	LEU
1	A	421	LYS
1	A	422	VAL
1	A	424	GLU
1	A	431	ASN
1	A	440	ARG
1	A	442	VAL
1	A	455	LYS
1	A	456	LYS
1	A	480	LEU
1	A	494	GLU
1	A	498	VAL
1	A	538	LEU
1	A	547	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	85	ASN
1	A	146	HIS
1	A	155	GLN
1	A	164	GLN
1	A	384	GLN
1	A	448	GLN

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Mol	Chain	Res	Type
1	A	505	GLN
1	A	524	HIS

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 ⓘ

4 ligands are modelled in this entry.

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	$\# Z > 2$
2	SO4	A	1550	-	4,4,4	0.38	0	6,6,6	0.07	0
2	SO4	A	1548	-	4,4,4	0.30	0	6,6,6	0.16	0
3	5DQ	A	1551	-	31,31,31	4.17	17 (54%)	45,47,47	4.06	27 (60%)
2	SO4	A	1549	-	4,4,4	0.30	0	6,6,6	0.31	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	5DQ	A	1551	-	-	2/21/28/28	0/4/4/4

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1551	5DQ	C13-C12	11.96	1.53	1.39
3	A	1551	5DQ	C7-N11	-8.51	1.19	1.36
3	A	1551	5DQ	C10-C12	6.75	1.54	1.40
3	A	1551	5DQ	C4-C3	6.46	1.50	1.39
3	A	1551	5DQ	C2-C3	5.89	1.49	1.39
3	A	1551	5DQ	C12-S16	5.42	1.85	1.77
3	A	1551	5DQ	C9-N8	-5.26	1.29	1.38
3	A	1551	5DQ	C1-C6	4.67	1.46	1.39
3	A	1551	5DQ	S16-N19	4.56	1.69	1.61
3	A	1551	5DQ	C6-C7	-4.36	1.39	1.47
3	A	1551	5DQ	C13-C14	4.07	1.46	1.38
3	A	1551	5DQ	C20-N19	3.84	1.53	1.47
3	A	1551	5DQ	C5-C6	3.11	1.44	1.39
3	A	1551	5DQ	O18-S16	-2.80	1.40	1.43
3	A	1551	5DQ	C9-N15	2.79	1.41	1.35
3	A	1551	5DQ	C23-C24	-2.44	1.42	1.51
3	A	1551	5DQ	C7-N8	-2.30	1.28	1.33

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1551	5DQ	C10-C9-N8	-15.54	97.10	110.40
3	A	1551	5DQ	C12-S16-N19	-9.84	93.24	108.28
3	A	1551	5DQ	C10-C9-N15	7.60	130.81	124.21
3	A	1551	5DQ	C2-C1-C6	7.02	128.29	120.80
3	A	1551	5DQ	C12-C10-N11	6.15	137.58	130.94
3	A	1551	5DQ	C1-C2-C3	-5.35	113.78	121.17
3	A	1551	5DQ	C6-C7-N8	4.70	132.36	124.20
3	A	1551	5DQ	C24-C20-C21	4.67	112.14	103.38
3	A	1551	5DQ	F26-C25-C3	4.36	122.23	112.90
3	A	1551	5DQ	O18-S16-O17	4.08	124.48	119.52
3	A	1551	5DQ	N11-C7-N8	-3.93	105.74	112.44
3	A	1551	5DQ	C20-N19-S16	3.40	128.16	122.18
3	A	1551	5DQ	C5-C4-C3	-3.03	116.99	121.17
3	A	1551	5DQ	C1-C6-C7	2.98	126.12	120.83
3	A	1551	5DQ	C9-C10-N11	2.88	107.42	105.28
3	A	1551	5DQ	C4-C3-C2	2.87	122.32	118.03
3	A	1551	5DQ	C13-C12-C10	-2.81	116.48	120.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1551	5DQ	O18-S16-N19	-2.67	102.04	106.88
3	A	1551	5DQ	O17-S16-N19	2.66	111.71	106.88
3	A	1551	5DQ	F28-C25-F26	-2.58	96.46	105.77
3	A	1551	5DQ	C5-C6-C1	-2.56	115.31	118.57
3	A	1551	5DQ	F27-C25-F26	2.47	114.67	105.77
3	A	1551	5DQ	N15-C9-N8	2.38	132.08	124.94
3	A	1551	5DQ	C4-C5-C6	2.33	123.29	120.80
3	A	1551	5DQ	O17-S16-C12	2.16	111.24	107.68
3	A	1551	5DQ	C23-C22-C21	2.02	112.71	105.97
3	A	1551	5DQ	C22-C21-C20	-2.01	98.15	104.38

There are no chirality outliers.

All (2) torsion outliers are listed below:

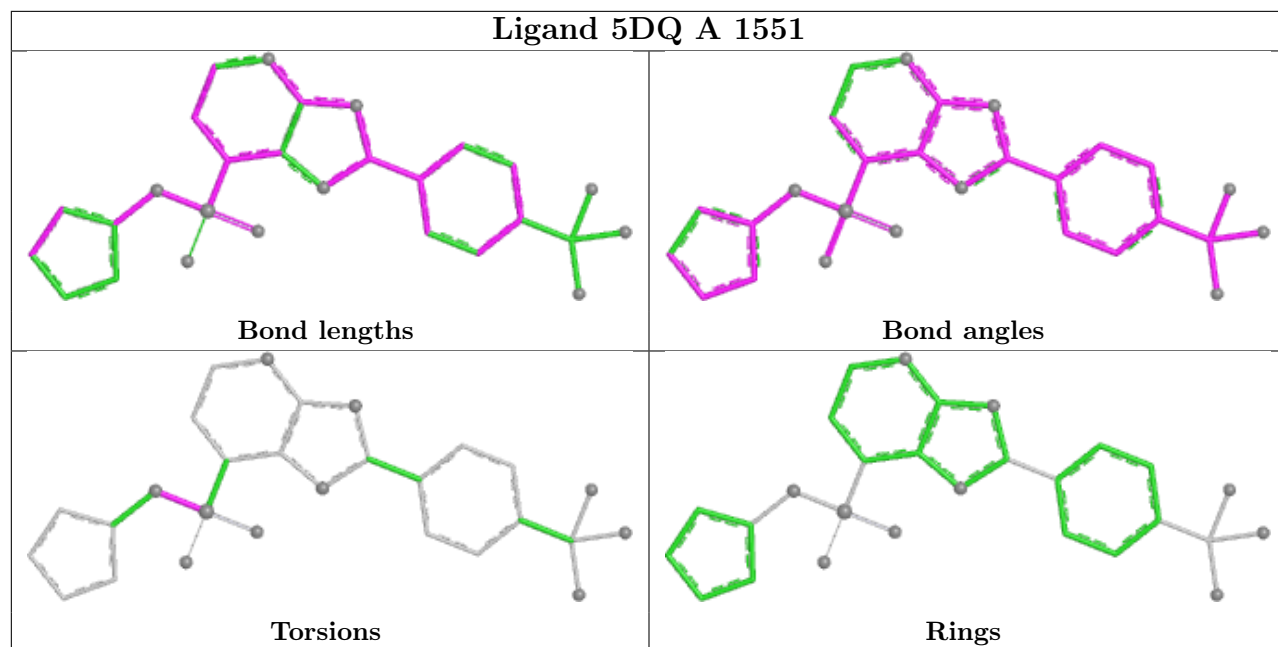
Mol	Chain	Res	Type	Atoms
3	A	1551	5DQ	C20-N19-S16-C12
3	A	1551	5DQ	C20-N19-S16-O18

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1551	5DQ	2	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	542/549 (98%)	0.08	9 (1%) 69 65	25, 53, 86, 126	1 (0%)

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	548	ASN	6.0
1	A	374	SER	4.0
1	A	380	VAL	3.6
1	A	78	ALA	3.0
1	A	20	PHE	2.6
1	A	77	THR	2.5
1	A	75	SER	2.3
1	A	372	LEU	2.2
1	A	145[A]	MET	2.2

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](#)

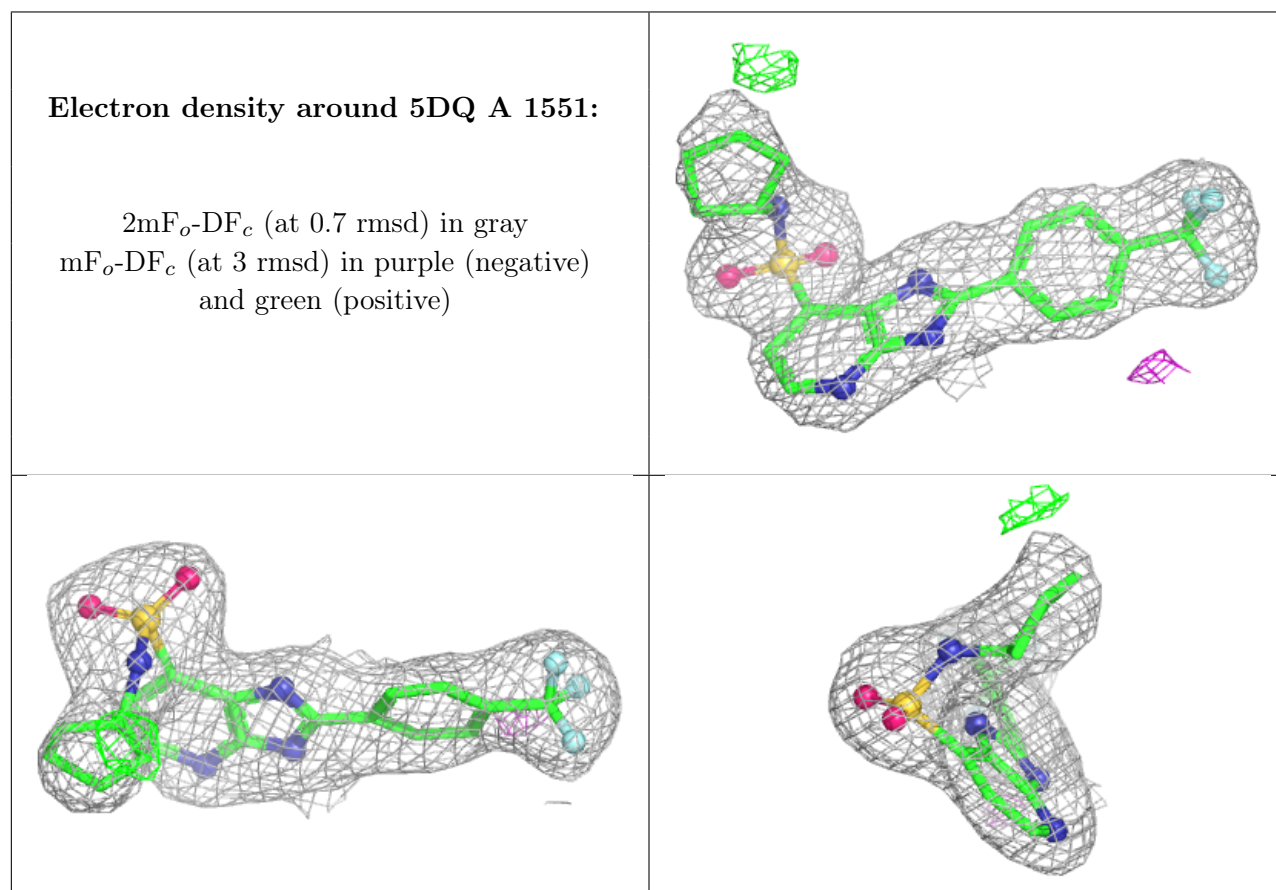
There are no oligosaccharides in this entry.

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	SO4	A	1550	5/5	0.80	0.15	104,108,109,109	0
2	SO4	A	1548	5/5	0.84	0.11	92,97,98,98	0
2	SO4	A	1549	5/5	0.86	0.12	111,115,115,116	0
3	5DQ	A	1551	28/28	0.94	0.08	50,52,65,66	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.



6.5 Other polymers ⓘ

There are no such residues in this entry.