



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:22 AM UTC

PDB ID : 1YVX / pdb_00001yvX
Title : Hepatitis C Virus RNA Polymerase Genotype 2a In Complex With Non- Nucleoside Analogue Inhibitor
Authors : Biswal, B.K.; Cherney, M.M.; Wang, M.; Chan, L.; Yannopoulos, C.G.; Bilimoria, D.; Nicolas, O.; Bedard, J.; James, M.N.G.
Deposited on : 2005-02-16
Resolution : 2.00 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

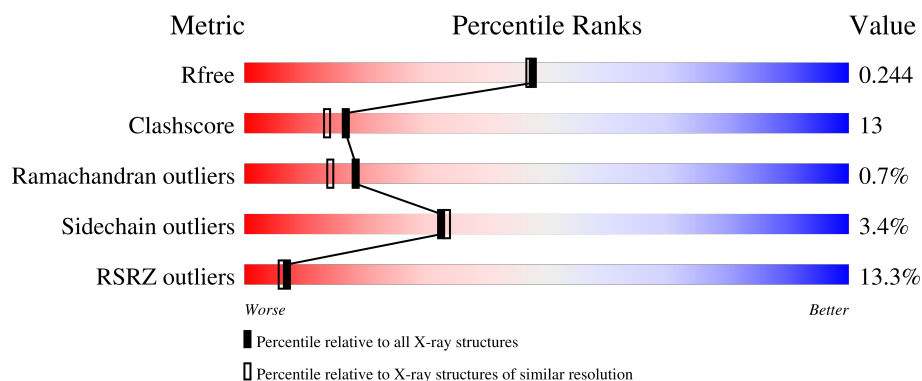
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	570	13% 71% 22% • •

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4819 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.

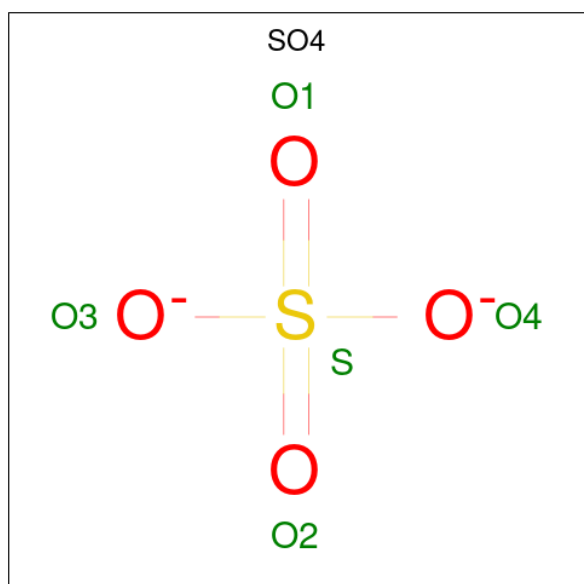
- Molecule 1 is a protein called RNA dependent RNA polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	548	4276	2704	751	793	28	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

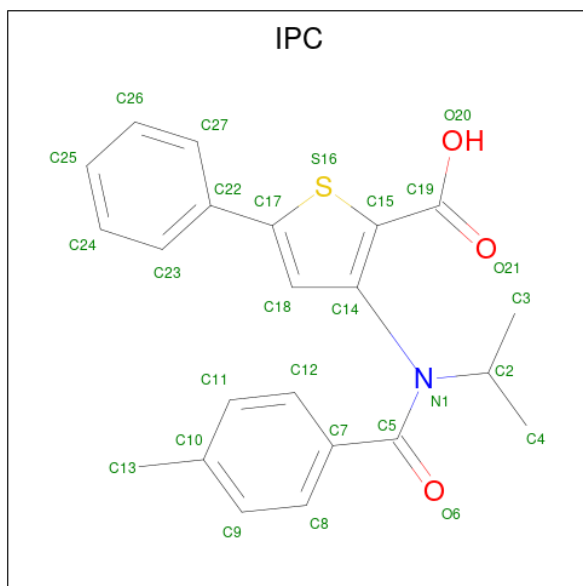
Chain	Residue	Modelled	Actual	Comment	Reference
A	25	PRO	SER	SEE REMARK 999	UNP P26660
A	150	THR	ALA	SEE REMARK 999	UNP P26660
A	156	ALA	PRO	SEE REMARK 999	UNP P26660
A	212	LYS	ARG	SEE REMARK 999	UNP P26660
A	309	VAL	ILE	SEE REMARK 999	UNP P26660
A	391	PRO	SER	SEE REMARK 999	UNP P26660

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



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

- Molecule 3 is 3-[ISOPROPYL(4-METHYLBENZOYL)AMINO]-5-PHENYLTHIOPHENE-2-CARBOXYLIC ACID (CCD ID: IPC) (formula: C₂₂H₂₁NO₃S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O S 27 22 1 3 1	0	0

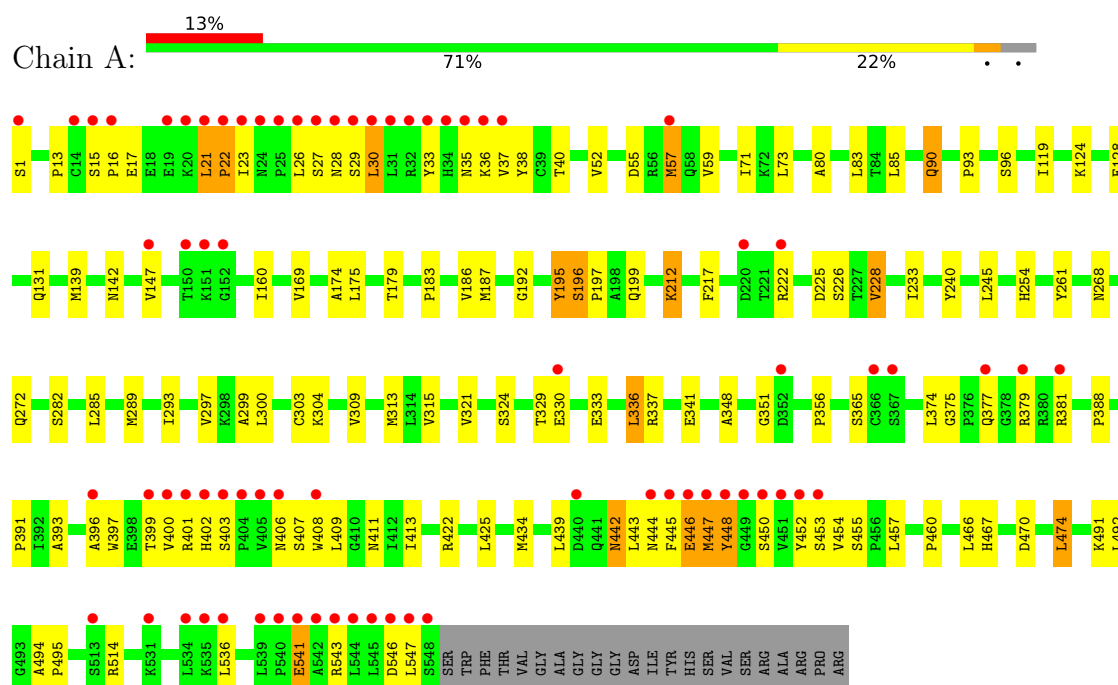
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	471	Total 471	O 471	0	0

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: RNA dependent RNA polymerase



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	61.11Å 214.82Å 124.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.69 – 2.00 38.69 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.3 (38.69-2.00) 99.3 (38.69-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.80 (at 2.00Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.209 , 0.244 0.208 , 0.244	Depositor DCC
R_{free} test set	2802 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	25.4	Xtriage
Anisotropy	0.614	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 46.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4819	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.78% 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, IPC

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	0.38	0/4371	0.90	13/5934 (0.2%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	447	MET	N-CA-C	-9.34	95.89	110.36
1	A	448	TYR	N-CA-C	6.83	118.52	111.14
1	A	348	ALA	CA-C-N	6.25	124.23	119.66
1	A	348	ALA	C-N-CA	6.25	124.23	119.66
1	A	195	TYR	N-CA-C	6.01	119.27	109.59
1	A	196	SER	N-CA-C	-6.01	101.30	110.07
1	A	192	GLY	N-CA-C	5.81	121.16	113.37
1	A	446	GLU	N-CA-C	5.50	117.72	107.99
1	A	27	SER	N-CA-C	-5.25	106.06	113.20
1	A	174	ALA	N-CA-C	5.11	117.97	111.69
1	A	407	SER	N-CA-C	-5.04	107.67	113.88
1	A	351	GLY	N-CA-C	-5.04	101.24	113.18
1	A	425	LEU	N-CA-C	5.02	116.44	111.07

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	4276	0	4317	111	0
2	A	45	0	0	0	0
3	A	27	0	20	1	0
4	A	471	0	0	13	0
All	All	4819	0	4337	111	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 13.

All (111) 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:377:GLN:HE22	1:A:381:ARG:NH1	1.66	0.93
1:A:57:MET:HE1	1:A:59:VAL:HG12	1.55	0.89
1:A:21:LEU:HG	1:A:22:PRO:HD2	1.58	0.86
1:A:268:ASN:HD21	1:A:272:GLN:HE21	1.21	0.85
1:A:160:ILE:HD12	1:A:282:SER:OG	1.78	0.84
1:A:71:ILE:CD1	1:A:297:VAL:HG22	2.15	0.76
1:A:21:LEU:HD11	1:A:400:VAL:HB	1.71	0.73
1:A:299:ALA:HB1	1:A:313:MET:HE1	1.71	0.72
1:A:71:ILE:HD12	1:A:297:VAL:HG22	1.71	0.71
1:A:131:GLN:NE2	4:A:954:HOH:O	2.25	0.70
1:A:21:LEU:HG	1:A:22:PRO:CD	2.20	0.69
1:A:439:LEU:HB3	1:A:457:LEU:HD11	1.74	0.69
1:A:379:ARG:NH2	1:A:381:ARG:NH2	2.41	0.69
1:A:57:MET:HE1	1:A:59:VAL:CG1	2.24	0.68
1:A:57:MET:CE	1:A:59:VAL:HG12	2.23	0.67
1:A:446:GLU:HG2	1:A:447:MET:O	1.95	0.67
1:A:293:ILE:O	1:A:297:VAL:HG23	1.96	0.65
1:A:196:SER:H	1:A:199:GLN:HE21	1.45	0.65
1:A:377:GLN:NE2	1:A:381:ARG:NH1	2.43	0.63
1:A:187:MET:HE1	1:A:315:VAL:HB	1.79	0.63
1:A:409:LEU:HB3	1:A:445:PHE:HB3	1.79	0.63
1:A:21:LEU:HD23	1:A:35:ASN:HD21	1.62	0.62
1:A:196:SER:H	1:A:199:GLN:NE2	1.99	0.61
1:A:93:PRO:HG2	1:A:96:SER:HB3	1.82	0.61
1:A:454:VAL:HG23	4:A:866:HOH:O	2.01	0.60
1:A:212:LYS:N	1:A:212:LYS:HD2	2.17	0.59
1:A:514:ARG:HH21	1:A:514:ARG:HG3	1.66	0.59
1:A:470:ASP:O	1:A:474:LEU:HD13	2.02	0.59
1:A:321:VAL:HG21	1:A:365:SER:HB2	1.86	0.57
1:A:26:LEU:C	1:A:28:ASN:H	2.12	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:ILE:O	1:A:400:VAL:HG21	2.05	0.56
1:A:36:LYS:HB3	1:A:147:VAL:HG22	1.87	0.56
1:A:222:ARG:HD2	4:A:752:HOH:O	2.05	0.56
1:A:26:LEU:HD13	1:A:396:ALA:HB2	1.88	0.56
1:A:454:VAL:HG22	1:A:455:SER:N	2.20	0.55
1:A:124:LYS:O	1:A:128:GLU:HG3	2.06	0.55
1:A:547:LEU:HD12	1:A:547:LEU:N	2.22	0.54
1:A:197:PRO:HG2	4:A:829:HOH:O	2.06	0.54
1:A:377:GLN:CD	1:A:379:ARG:HG2	2.32	0.54
1:A:409:LEU:HB3	1:A:445:PHE:CB	2.38	0.54
1:A:1:SER:HB2	1:A:55:ASP:OD2	2.08	0.53
1:A:15:SER:HB2	1:A:16:PRO:HD2	1.92	0.52
1:A:217:PHE:CD2	1:A:336:LEU:HD11	2.44	0.52
1:A:381:ARG:NH2	1:A:470:ASP:OD2	2.42	0.52
1:A:21:LEU:HD21	1:A:23:ILE:O	2.08	0.52
1:A:29:SER:O	1:A:30:LEU:C	2.52	0.52
1:A:90:GLN:HG2	4:A:1007:HOH:O	2.09	0.52
1:A:401:ARG:O	1:A:403:SER:N	2.42	0.52
1:A:442:ASN:ND2	1:A:455:SER:HB2	2.23	0.52
1:A:413:ILE:O	1:A:467:HIS:HE1	1.93	0.52
1:A:183:PRO:HG2	4:A:619:HOH:O	2.10	0.51
1:A:304:LYS:NZ	4:A:712:HOH:O	2.44	0.51
1:A:460:PRO:HG2	4:A:667:HOH:O	2.10	0.51
1:A:377:GLN:HE22	1:A:381:ARG:CZ	2.23	0.50
1:A:26:LEU:C	1:A:26:LEU:HD23	2.36	0.50
1:A:268:ASN:HD21	1:A:272:GLN:NE2	1.99	0.50
1:A:422:ARG:NH1	1:A:474:LEU:O	2.44	0.50
1:A:541:GLU:C	1:A:543:ARG:H	2.20	0.49
1:A:80:ALA:HB3	1:A:245:LEU:CD2	2.42	0.49
1:A:175:LEU:O	1:A:179:THR:HG23	2.12	0.48
1:A:444:ASN:ND2	1:A:453:SER:HB2	2.28	0.48
1:A:240:TYR:CZ	1:A:289:MET:HE3	2.49	0.48
1:A:337:ARG:HD3	4:A:759:HOH:O	2.14	0.48
1:A:299:ALA:CB	1:A:313:MET:HE1	2.40	0.47
1:A:57:MET:O	1:A:57:MET:HE3	2.14	0.47
1:A:186:VAL:HG23	1:A:187:MET:HG3	1.96	0.47
1:A:337:ARG:O	1:A:341:GLU:HG3	2.13	0.47
1:A:422:ARG:HD2	4:A:588:HOH:O	2.14	0.47
1:A:254:HIS:HE1	4:A:939:HOH:O	1.98	0.47
1:A:454:VAL:CG2	1:A:455:SER:N	2.78	0.47
1:A:59:VAL:HG13	1:A:59:VAL:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:85:LEU:C	1:A:85:LEU:HD23	2.40	0.47
1:A:309:VAL:O	1:A:324:SER:HB2	2.15	0.47
1:A:406:ASN:HB3	1:A:408:TRP:CD1	2.50	0.47
1:A:381:ARG:CZ	1:A:470:ASP:OD1	2.63	0.46
1:A:422:ARG:CD	4:A:588:HOH:O	2.63	0.46
1:A:26:LEU:C	1:A:28:ASN:N	2.74	0.46
1:A:52:VAL:HB	1:A:226:SER:OG	2.15	0.46
1:A:514:ARG:HG3	1:A:514:ARG:NH2	2.30	0.45
1:A:240:TYR:CE2	1:A:289:MET:HE3	2.51	0.45
1:A:329:THR:O	1:A:333:GLU:HG3	2.17	0.45
1:A:36:LYS:HB3	1:A:147:VAL:CG2	2.46	0.45
1:A:422:ARG:NH1	3:A:580:IPC:H9	2.31	0.45
1:A:233:ILE:HD13	1:A:261:TYR:O	2.16	0.44
1:A:303:CYS:SG	1:A:313:MET:HE3	2.57	0.44
1:A:13:PRO:HB3	1:A:17:GLU:OE2	2.18	0.44
1:A:40:THR:O	1:A:142:ASN:HA	2.17	0.44
1:A:391:PRO:HB3	1:A:411:ASN:ND2	2.33	0.43
1:A:119:ILE:HD13	1:A:169:VAL:HG11	2.01	0.43
1:A:422:ARG:HD3	4:A:591:HOH:O	2.19	0.43
1:A:397:TRP:C	1:A:399:THR:H	2.27	0.42
1:A:448:TYR:N	1:A:448:TYR:CD1	2.85	0.42
1:A:434:MET:HG2	1:A:439:LEU:HD11	2.01	0.42
1:A:375:GLY:HA3	1:A:381:ARG:HE	1.84	0.42
1:A:450:SER:HB2	1:A:452:TYR:CZ	2.53	0.42
1:A:139:MET:HB2	1:A:160:ILE:CG2	2.49	0.42
1:A:388:PRO:HA	1:A:391:PRO:HG2	2.00	0.42
1:A:299:ALA:HB1	1:A:313:MET:CE	2.44	0.42
1:A:33:TYR:CD1	1:A:33:TYR:C	2.97	0.42
1:A:336:LEU:HD22	1:A:356:PRO:HD3	2.01	0.42
1:A:546:ASP:OD1	1:A:547:LEU:N	2.52	0.42
1:A:443:LEU:O	1:A:453:SER:HA	2.21	0.41
1:A:225:ASP:O	1:A:228:VAL:HG13	2.20	0.41
1:A:393:ALA:HB2	1:A:492:LEU:HD21	2.02	0.41
1:A:494:ALA:HB1	1:A:495:PRO:HD2	2.01	0.41
1:A:36:LYS:HD2	1:A:491:LYS:O	2.21	0.41
1:A:195:TYR:HA	1:A:199:GLN:HE21	1.87	0.40
1:A:196:SER:HB2	1:A:197:PRO:HD2	2.01	0.40
1:A:37:VAL:HG12	1:A:38:TYR:N	2.35	0.40
1:A:377:GLN:HE22	1:A:381:ARG:HH11	1.61	0.40
1:A:541:GLU:C	1:A:543:ARG:N	2.80	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	546/570 (96%)	524 (96%)	18 (3%)	4 (1%)	18	14

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	402	HIS
1	A	22	PRO
1	A	30	LEU
1	A	536	LEU

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	467/483 (97%)	451 (97%)	16 (3%)	32	33

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	LEU
1	A	57	MET
1	A	73	LEU
1	A	83	LEU
1	A	90	GLN
1	A	212	LYS
1	A	228	VAL

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Mol	Chain	Res	Type
1	A	285	LEU
1	A	300	LEU
1	A	330	GLU
1	A	336	LEU
1	A	374	LEU
1	A	442	ASN
1	A	466	LEU
1	A	474	LEU
1	A	541	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	ASN
1	A	58	GLN
1	A	95	HIS
1	A	131	GLN
1	A	180	GLN
1	A	184	GLN
1	A	199	GLN
1	A	272	GLN
1	A	327	GLN
1	A	335	ASN
1	A	377	GLN
1	A	402	HIS
1	A	411	ASN
1	A	414	GLN
1	A	428	HIS
1	A	436	GLN
1	A	441	GLN
1	A	442	ASN
1	A	444	ASN
1	A	467	HIS
1	A	475	HIS
1	A	480	HIS

5.3.3 RNA ⓘ

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](#)

10 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	574	-	4,4,4	0.35	0	6,6,6	0.07	0
2	SO4	A	572	-	4,4,4	0.37	0	6,6,6	0.07	0
2	SO4	A	577	-	4,4,4	0.36	0	6,6,6	0.09	0
2	SO4	A	571	-	4,4,4	0.35	0	6,6,6	0.10	0
2	SO4	A	573	-	4,4,4	0.35	0	6,6,6	0.08	0
2	SO4	A	576	-	4,4,4	0.37	0	6,6,6	0.08	0
3	IPC	A	580	-	28,29,29	5.37	15 (53%)	36,41,41	3.29	14 (38%)
2	SO4	A	579	-	4,4,4	0.38	0	6,6,6	0.08	0
2	SO4	A	578	-	4,4,4	0.36	0	6,6,6	0.08	0
2	SO4	A	575	-	4,4,4	0.36	0	6,6,6	0.07	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	IPC	A	580	-	-	0/23/24/24	0/3/3/3

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	580	IPC	C2-N1	12.42	1.66	1.48
3	A	580	IPC	C7-C5	11.02	1.68	1.50
3	A	580	IPC	C9-C8	10.89	1.56	1.38
3	A	580	IPC	C14-C15	9.81	1.52	1.39
3	A	580	IPC	C27-C22	9.62	1.54	1.39
3	A	580	IPC	C8-C7	6.71	1.49	1.39
3	A	580	IPC	C9-C10	6.52	1.54	1.38
3	A	580	IPC	C23-C22	5.86	1.48	1.39
3	A	580	IPC	O6-C5	5.01	1.32	1.22
3	A	580	IPC	C24-C23	3.69	1.45	1.38
3	A	580	IPC	C15-S16	-3.36	1.67	1.74
3	A	580	IPC	C26-C25	3.30	1.45	1.38
3	A	580	IPC	C25-C24	3.28	1.45	1.38
3	A	580	IPC	C4-C2	3.27	1.60	1.52
3	A	580	IPC	C5-N1	2.22	1.44	1.39

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	580	IPC	C9-C8-C7	-10.63	109.45	120.80
3	A	580	IPC	C18-C14-C15	-7.33	104.88	113.58
3	A	580	IPC	C14-C18-C17	6.39	116.97	111.57
3	A	580	IPC	C12-C7-C8	5.75	125.88	118.57
3	A	580	IPC	O6-C5-C7	-5.11	110.15	120.29
3	A	580	IPC	C7-C5-N1	5.00	125.91	118.14
3	A	580	IPC	C14-C15-S16	4.71	114.69	111.16
3	A	580	IPC	C3-C2-N1	3.96	117.24	111.69
3	A	580	IPC	C4-C2-N1	3.78	116.99	111.69
3	A	580	IPC	O20-C19-O21	-3.09	116.55	123.90
3	A	580	IPC	O20-C19-C15	2.95	124.55	115.22
3	A	580	IPC	C4-C2-C3	-2.18	106.54	112.46
3	A	580	IPC	O6-C5-N1	2.14	123.93	120.73
3	A	580	IPC	C11-C12-C7	2.05	122.99	120.80

There are no chirality outliers.

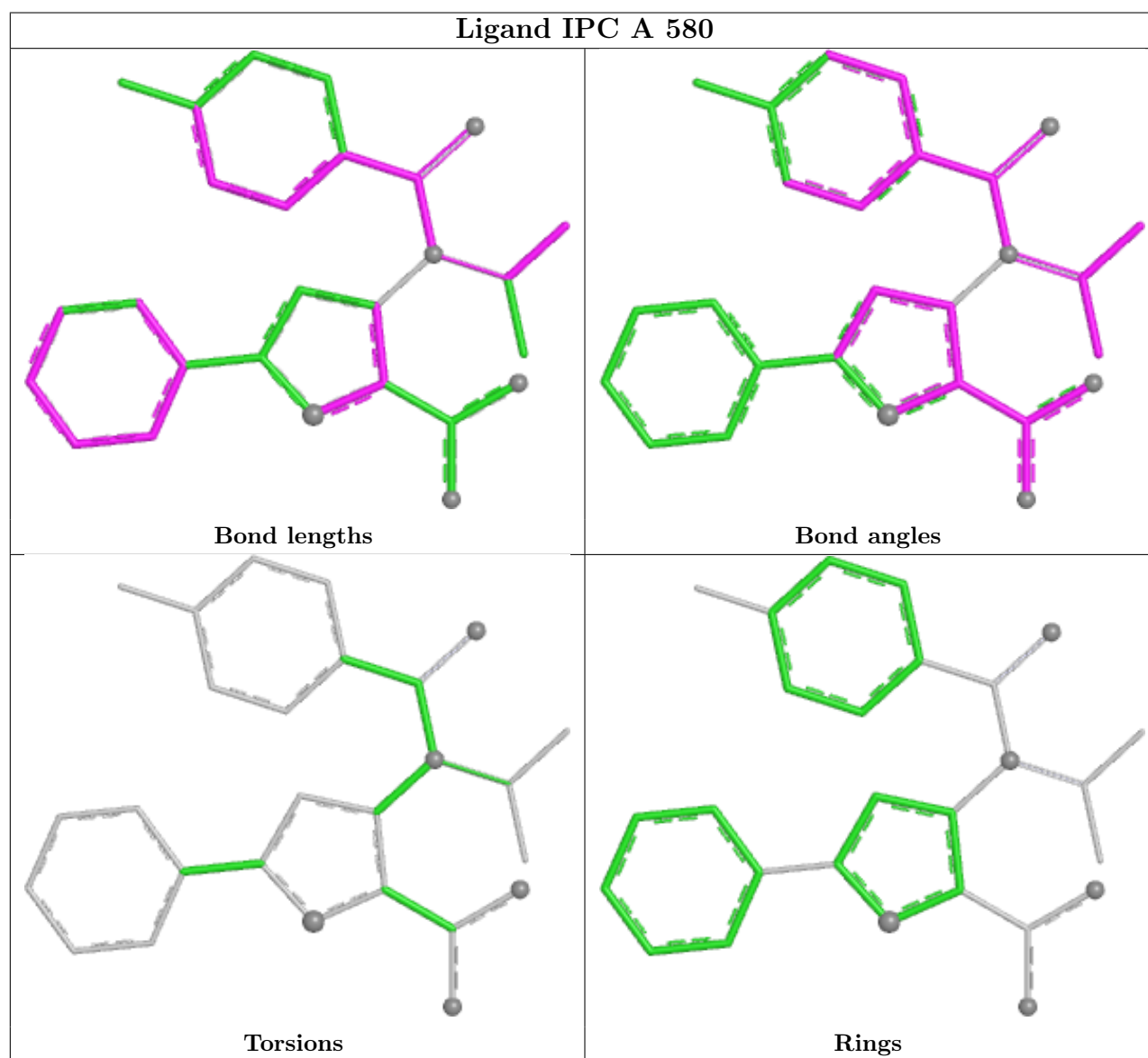
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	580	IPC	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

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	548/570 (96%)	0.59	73 (13%) 7 6	17, 27, 82, 112	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	25	PRO	10.0
1	A	26	LEU	9.9
1	A	448	TYR	9.7
1	A	30	LEU	9.2
1	A	23	ILE	8.2
1	A	547	LEU	7.7
1	A	28	ASN	7.5
1	A	27	SER	7.2
1	A	24	ASN	6.8
1	A	31	LEU	6.6
1	A	545	LEU	6.5
1	A	21	LEU	6.3
1	A	541	GLU	6.2
1	A	29	SER	6.1
1	A	540	PRO	6.0
1	A	548	SER	5.9
1	A	451	VAL	5.9
1	A	544	LEU	5.8
1	A	35	ASN	5.5
1	A	402	HIS	5.5
1	A	33	TYR	5.1
1	A	400	VAL	5.0
1	A	447	MET	4.8
1	A	542	ALA	4.7
1	A	546	ASP	4.5
1	A	452	TYR	4.3
1	A	37	VAL	4.2

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Mol	Chain	Res	Type	RSRZ
1	A	32	ARG	4.1
1	A	449	GLY	4.1
1	A	404	PRO	3.8
1	A	22	PRO	3.7
1	A	450	SER	3.7
1	A	401	ARG	3.7
1	A	445	PHE	3.6
1	A	539	LEU	3.5
1	A	534	LEU	3.3
1	A	405	VAL	3.2
1	A	381	ARG	3.2
1	A	446	GLU	3.2
1	A	399	THR	3.1
1	A	36	LYS	3.0
1	A	536	LEU	3.0
1	A	366	CYS	3.0
1	A	19	GLU	2.9
1	A	34	HIS	2.9
1	A	352	ASP	2.9
1	A	1	SER	2.9
1	A	406	ASN	2.9
1	A	16	PRO	2.8
1	A	367	SER	2.8
1	A	513	SER	2.7
1	A	151	LYS	2.7
1	A	150	THR	2.7
1	A	396	ALA	2.6
1	A	14	CYS	2.6
1	A	403	SER	2.6
1	A	147	VAL	2.5
1	A	57	MET	2.5
1	A	535	LYS	2.5
1	A	330	GLU	2.4
1	A	377	GLN	2.4
1	A	15	SER	2.4
1	A	20	LYS	2.4
1	A	453	SER	2.4
1	A	440	ASP	2.4
1	A	543	ARG	2.4
1	A	379	ARG	2.4
1	A	531	LYS	2.3
1	A	222	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	444	ASN	2.1
1	A	408	TRP	2.1
1	A	220	ASP	2.0
1	A	152	GLY	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](#)

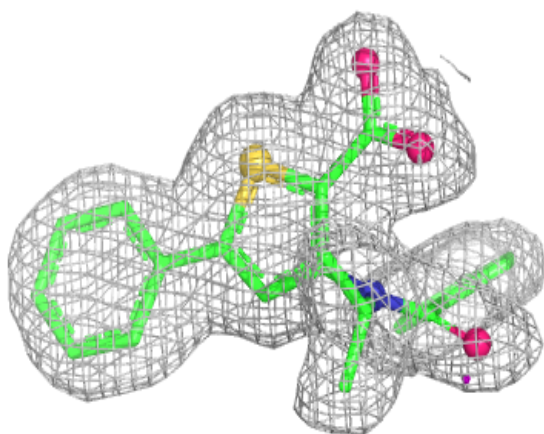
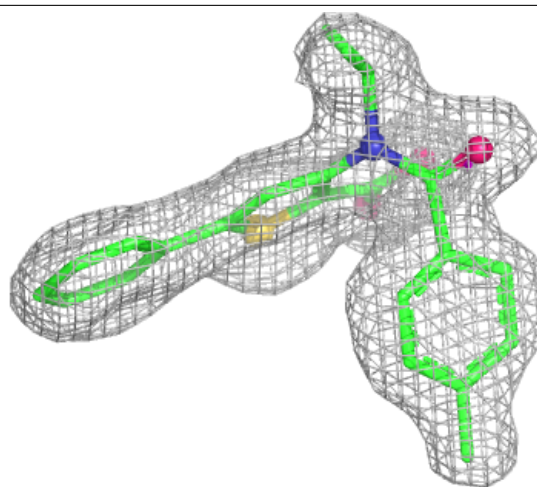
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	SO4	A	578	5/5	0.66	0.14	124,125,125,125	0
2	SO4	A	573	5/5	0.70	0.19	119,120,120,120	0
2	SO4	A	576	5/5	0.71	0.23	119,119,119,119	0
2	SO4	A	572	5/5	0.77	0.19	93,94,94,94	0
2	SO4	A	571	5/5	0.77	0.21	88,89,89,89	0
2	SO4	A	579	5/5	0.82	0.18	103,103,103,103	0
2	SO4	A	577	5/5	0.83	0.22	130,130,130,130	0
2	SO4	A	574	5/5	0.84	0.13	65,66,67,67	0
2	SO4	A	575	5/5	0.89	0.19	88,88,89,89	0
3	IPC	A	580	27/27	0.95	0.08	22,25,28,29	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 IPC A 580:

$2mF_o-DF_c$ (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.