Full wwPDB X-ray Structure Validation Report (i)

Feb 21, 2024 – 01:29 PM EST

PDB ID	:	4OK3
Title	:	Crystal Structure of Hepatitis C Virus NS3 Helicase Inhibitor Co-complex with Compound 7 [[1-(3-chlorobenzyl)-1H-indol-3-yl]acetic acid]
Authors	:	Padyana, A.K.
Deposited on	:	2014-01-21
Resolution	:	2.30 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 (i) 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 (i)) were used in the production of this report:

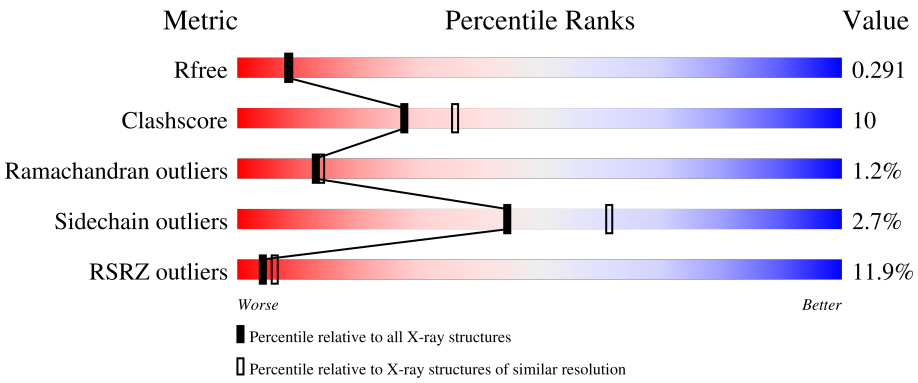
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 <=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	464	13% 71% 19% • 8%
1	B	464	8% 74% 14% • 9%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 6495 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 Serine protease NS3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	426	3203	2026	542	612	23	0	1	0
1	B	420	3165	2008	531	604	22	0	1	0

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	167	MET	-	expression tag	UNP K4KA16
A	168	GLY	-	expression tag	UNP K4KA16
A	169	SER	-	expression tag	UNP K4KA16
A	170	SER	-	expression tag	UNP K4KA16
A	171	HIS	-	expression tag	UNP K4KA16
A	172	HIS	-	expression tag	UNP K4KA16
A	173	HIS	-	expression tag	UNP K4KA16
A	174	HIS	-	expression tag	UNP K4KA16
A	175	HIS	-	expression tag	UNP K4KA16
A	176	HIS	-	expression tag	UNP K4KA16
A	177	SER	-	expression tag	UNP K4KA16
A	178	SER	-	expression tag	UNP K4KA16
A	179	GLY	-	expression tag	UNP K4KA16
A	403	ASN	SER	conflict	UNP K4KA16
A	505	MET	THR	conflict	UNP K4KA16
B	167	MET	-	expression tag	UNP K4KA16
B	168	GLY	-	expression tag	UNP K4KA16
B	169	SER	-	expression tag	UNP K4KA16
B	170	SER	-	expression tag	UNP K4KA16
B	171	HIS	-	expression tag	UNP K4KA16
B	172	HIS	-	expression tag	UNP K4KA16
B	173	HIS	-	expression tag	UNP K4KA16
B	174	HIS	-	expression tag	UNP K4KA16
B	175	HIS	-	expression tag	UNP K4KA16
B	176	HIS	-	expression tag	UNP K4KA16

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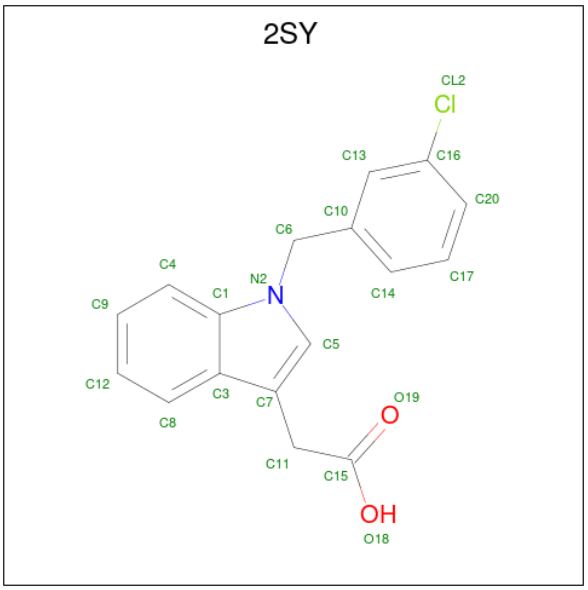
Chain	Residue	Modelled	Actual	Comment	Reference
B	177	SER	-	expression tag	UNP K4KA16
B	178	SER	-	expression tag	UNP K4KA16
B	179	GLY	-	expression tag	UNP K4KA16
B	403	ASN	SER	conflict	UNP K4KA16
B	505	MET	THR	conflict	UNP K4KA16

- Molecule 2 is [1-(3-chlorobenzyl)-1H-indol-3-yl]acetic acid (three-letter code: 2SY) (formula: $C_{17}H_{14}ClNO_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Cl	N	O		
2	A	1	21	17	1	1	2	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
3	A	2	2	2	0	0

- Molecule 4 is water.

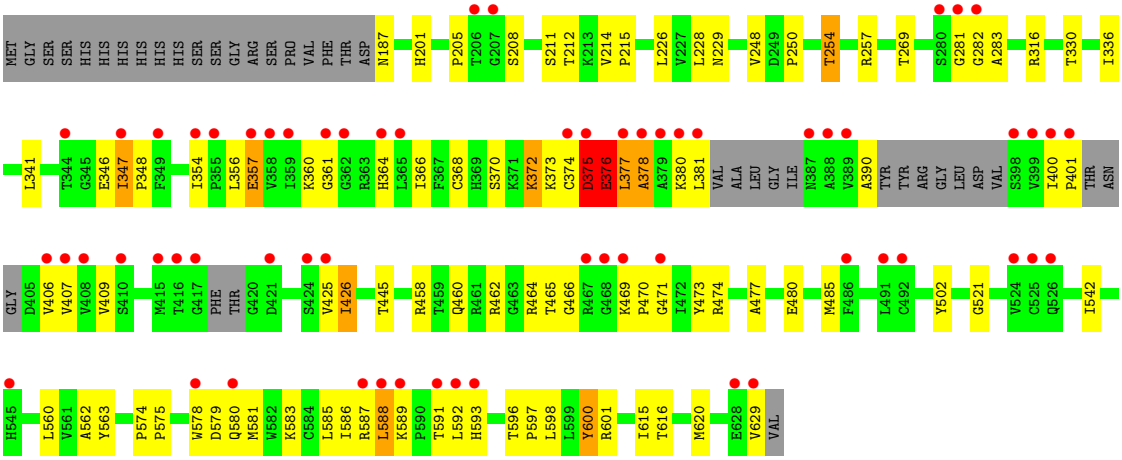
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	46	46	46	0	0
			Total	O		
4	B	58	58	58	0	0

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.

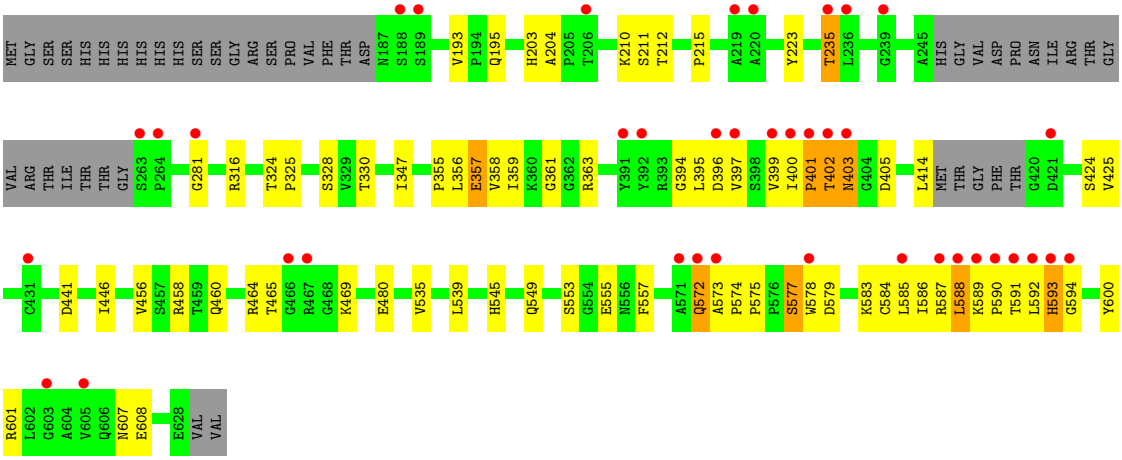
- Molecule 1: Serine protease NS3

Chain A:



- Molecule 1: Serine protease NS3

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	81.39Å 104.23Å 117.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.09 – 2.30 47.67 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (36.09-2.30) 93.2 (47.67-2.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.36 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.232 , 0.292 0.236 , 0.291	Depositor DCC
R_{free} test set	2282 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	50.2	Xtriage
Anisotropy	0.130	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 45.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.53$, $< L^2 > = 0.37$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	6495	wwPDB-VP
Average B, all atoms (Å^2)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.93% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: CA, 2SY

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	0.50	0/3277	0.68	1/4471 (0.0%)
1	B	0.48	0/3241	0.67	2/4425 (0.0%)
All	All	0.49	0/6518	0.67	3/8896 (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	3
1	B	0	4
All	All	0	7

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	588	LEU	CA-CB-CG	6.28	129.75	115.30
1	A	375	ASP	CB-CG-OD1	-6.00	112.90	118.30
1	B	460	GLN	CA-CB-CG	5.92	126.42	113.40

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	375	ASP	Peptide
1	A	376	GLU	Peptide
1	A	377	LEU	Peptide

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Mol	Chain	Res	Type	Group
1	B	401	PRO	Peptide
1	B	402	THR	Peptide
1	B	579	ASP	Peptide
1	B	589	LYS	Peptide

5.2 Too-close contacts (i)

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	3203	0	3162	75	0
1	B	3165	0	3122	52	0
2	A	21	0	13	1	0
3	A	2	0	0	0	0
4	A	46	0	0	0	0
4	B	58	0	0	2	0
All	All	6495	0	6297	127	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 10.

All (127) 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:400:ILE:HD12	1:A:401:PRO:HD2	1.60	0.81
1:A:378:ALA:C	1:A:380:LYS:H	1.87	0.76
1:A:460:GLN:HE21	1:A:464:ARG:HH21	1.33	0.76
1:B:441:ASP:O	1:B:601:ARG:NH1	2.21	0.73
1:A:376:GLU:HA	1:A:378:ALA:HA	1.73	0.70
1:A:370:SER:O	1:A:374:CYS:HB2	1.92	0.69
1:A:589:LYS:HD2	1:A:589:LYS:O	1.95	0.67
1:B:592:LEU:O	1:B:594:GLY:N	2.26	0.67
1:A:377:LEU:O	1:A:380:LYS:HB3	1.96	0.65
1:B:575:PRO:HG3	1:B:585:LEU:HD12	1.78	0.65
1:A:347:ILE:HG12	1:A:354:ILE:H	1.63	0.63
1:B:607:ASN:OD1	1:B:608:GLU:N	2.31	0.63
1:B:195:GLN:HA	1:B:316:ARG:HH21	1.63	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:195:GLN:HA	1:B:316:ARG:NH2	2.14	0.62
1:A:575:PRO:HG3	1:A:585:LEU:HD12	1.81	0.62
1:B:591:THR:HG23	1:B:593:HIS:H	1.64	0.62
1:A:375:ASP:OD1	1:A:380:LYS:HE3	2.00	0.61
1:A:187:ASN:HB3	1:A:201:HIS:O	2.01	0.60
1:A:368:CYS:HB2	1:A:374:CYS:HA	1.83	0.60
1:B:363:ARG:CZ	1:B:403:ASN:ND2	2.65	0.60
1:B:553:SER:OG	1:B:555:GLU:OE1	2.19	0.60
1:B:347:ILE:HD11	1:B:356:LEU:HD12	1.84	0.60
1:B:578:TRP:CZ2	1:B:588:LEU:HG	2.37	0.60
1:A:400:ILE:HG12	1:A:406:VAL:HG21	1.84	0.58
1:A:400:ILE:HD12	1:A:401:PRO:CD	2.32	0.56
1:A:373:LYS:HD3	1:A:376:GLU:HG2	1.88	0.56
1:A:458:ARG:NH2	1:A:477:ALA:O	2.39	0.56
1:B:363:ARG:NH2	1:B:400:ILE:O	2.37	0.56
1:B:574:PRO:HG2	1:B:607:ASN:ND2	2.20	0.56
1:A:377:LEU:HD23	1:A:409:VAL:HG11	1.88	0.55
1:A:426:ILE:HD13	1:A:474:ARG:HB2	1.88	0.55
1:B:396:ASP:OD2	1:B:397:VAL:HG22	2.06	0.55
1:B:330:THR:HG21	1:B:458:ARG:HB3	1.87	0.55
1:B:587:ARG:O	1:B:590:PRO:HD2	2.07	0.55
1:B:363:ARG:CZ	1:B:403:ASN:HD22	2.20	0.54
1:A:248:VAL:O	1:A:250:PRO:HD3	2.07	0.54
1:B:577:SER:OG	1:B:578:TRP:N	2.41	0.54
1:A:574:PRO:O	1:A:596:THR:OG1	2.19	0.53
1:B:361:GLY:HA2	1:B:405:ASP:OD2	2.09	0.53
1:A:281:GLY:O	1:A:283:ALA:N	2.39	0.53
1:A:341:LEU:CD1	1:A:474:ARG:HB3	2.40	0.52
1:A:445:THR:HG23	1:A:601:ARG:HB2	1.91	0.52
1:A:205:PRO:O	1:A:208:SER:HB3	2.10	0.52
1:B:572:GLN:O	1:B:591:THR:HG21	2.10	0.52
1:A:578:TRP:CH2	1:A:588:LEU:HD22	2.45	0.51
1:A:378:ALA:C	1:A:380:LYS:N	2.62	0.51
1:B:572:GLN:HB2	1:B:591:THR:OG1	2.10	0.51
1:A:425:VAL:HG23	1:A:465:THR:HB	1.93	0.51
1:B:212:THR:C	1:B:215:PRO:HD2	2.31	0.51
1:A:589:LYS:HA	1:A:592:LEU:HD23	1.93	0.50
1:A:616:THR:HG22	1:A:620:MET:HE3	1.93	0.50
1:B:572:GLN:C	1:B:591:THR:HG21	2.31	0.50
1:A:376:GLU:CA	1:A:378:ALA:HA	2.42	0.50
1:B:402:THR:HG22	1:B:403:ASN:H	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:364:HIS:HB2	1:A:407:VAL:HG22	1.94	0.49
1:A:591:THR:O	1:A:593:HIS:N	2.45	0.49
1:A:616:THR:HG22	1:A:620:MET:CE	2.42	0.49
1:A:502:TYR:OH	2:A:701:2SY:H1	2.12	0.49
1:A:378:ALA:O	1:A:380:LYS:HG2	2.13	0.49
1:A:380:LYS:HG3	1:A:381:LEU:N	2.27	0.49
1:A:346:GLU:OE1	1:A:346:GLU:N	2.45	0.48
1:B:330:THR:HG23	1:B:480:GLU:OE1	2.13	0.48
1:B:399:VAL:O	1:B:401:PRO:HD3	2.13	0.48
1:B:193:VAL:HG11	1:B:223:TYR:CE2	2.48	0.48
1:B:587:ARG:O	1:B:587:ARG:HG3	2.14	0.48
1:A:629:VAL:HA	4:B:702:HOH:O	2.12	0.48
1:A:563:TYR:HE2	1:A:615:ILE:HD13	1.78	0.48
1:A:560:LEU:O	1:A:600:TYR:OH	2.25	0.48
1:B:574:PRO:HG2	1:B:607:ASN:HD21	1.79	0.47
1:B:545:HIS:O	1:B:549:GLN:HG3	2.14	0.47
1:A:380:LYS:HG3	1:A:381:LEU:H	1.78	0.47
1:A:560:LEU:HD22	1:A:600:TYR:CE2	2.49	0.47
1:B:324:THR:HG21	1:B:456:VAL:HG12	1.97	0.47
1:A:354:ILE:CD1	1:A:426:ILE:HG21	2.45	0.47
1:A:372:LYS:O	1:A:376:GLU:N	2.47	0.47
1:A:254:THR:HG22	1:A:257:ARG:O	2.15	0.47
1:A:591:THR:C	1:A:593:HIS:H	2.19	0.46
1:A:346:GLU:HG3	1:A:356:LEU:HD23	1.97	0.46
1:A:354:ILE:HD11	1:A:426:ILE:HG21	1.96	0.46
1:A:330:THR:HG23	1:A:480:GLU:OE1	2.16	0.46
1:B:583:LYS:O	1:B:585:LEU:N	2.48	0.46
1:A:390:ALA:HA	1:A:409:VAL:O	2.15	0.46
1:A:229:ASN:O	1:A:269:THR:HA	2.16	0.45
1:B:210:LYS:H	1:B:235:THR:HG21	1.81	0.45
1:B:355:PRO:HG2	1:B:358:VAL:HG13	1.98	0.45
1:A:341:LEU:HD11	1:A:474:ARG:HB3	1.99	0.45
1:A:377:LEU:HD23	1:A:409:VAL:CG1	2.47	0.45
1:A:357:GLU:H	1:A:357:GLU:HG2	1.51	0.45
1:A:376:GLU:O	1:A:376:GLU:HG3	2.18	0.44
1:A:466:GLY:HA2	1:A:469:LYS:O	2.17	0.44
1:B:363:ARG:NH1	1:B:403:ASN:ND2	2.65	0.44
1:B:414:LEU:C	1:B:464:ARG:HH12	2.20	0.44
1:A:360:LYS:HA	1:A:361:GLY:HA2	1.60	0.44
1:B:591:THR:HG23	1:B:593:HIS:CG	2.52	0.44
1:B:535:VAL:O	1:B:539:LEU:HG	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:336:ILE:HA	1:A:471:GLY:O	2.17	0.44
1:B:394:GLY:O	1:B:395:LEU:HD23	2.18	0.43
1:A:214:VAL:HB	1:A:215:PRO:HD3	2.01	0.43
1:A:583:LYS:O	1:A:586:ILE:HG12	2.19	0.43
1:A:460:GLN:NE2	1:A:464:ARG:HH21	2.09	0.43
1:A:542:ILE:HD11	1:A:562:ALA:HB3	2.00	0.43
1:B:400:ILE:HG23	1:B:402:THR:HB	2.01	0.43
1:A:426:ILE:HD13	1:A:474:ARG:HD2	2.01	0.42
1:B:203:HIS:ND1	1:B:204:ALA:O	2.50	0.42
1:B:397:VAL:O	1:B:397:VAL:HG23	2.20	0.42
1:B:601:ARG:HG3	4:B:716:HOH:O	2.20	0.42
1:A:462:ARG:HG3	1:A:473:TYR:CG	2.55	0.42
1:A:360:LYS:HE2	1:A:360:LYS:HB3	1.84	0.41
1:A:226:LEU:HD21	1:A:228:LEU:HD21	2.02	0.41
1:B:591:THR:CG2	1:B:593:HIS:H	2.33	0.41
1:B:358:VAL:HG23	1:B:359:ILE:HG23	2.03	0.41
1:B:469:LYS:H	1:B:469:LYS:HG2	1.57	0.41
1:B:573:ALA:HA	1:B:591:THR:HG21	2.01	0.41
1:A:201:HIS:CE1	1:A:521:GLY:HA3	2.55	0.41
1:A:380:LYS:HG3	1:A:381:LEU:HG	2.01	0.41
1:B:357:GLU:H	1:B:357:GLU:HG3	1.40	0.41
1:B:425:VAL:HG23	1:B:465:THR:HB	2.03	0.41
1:B:446:ILE:HG21	1:B:557:PHE:CE2	2.56	0.41
1:A:575:PRO:HG3	1:A:585:LEU:CD1	2.50	0.41
1:A:579:ASP:OD1	1:A:580:GLN:N	2.54	0.41
1:A:347:ILE:HA	1:A:348:PRO:HD3	1.93	0.41
1:A:212:THR:C	1:A:215:PRO:HD2	2.42	0.40
1:B:325:PRO:HD2	1:B:328:SER:OG	2.22	0.40
1:A:469:LYS:HA	1:A:470:PRO:HD3	1.99	0.40
1:A:591:THR:C	1:A:593:HIS:N	2.75	0.40
1:A:366:ILE:HG12	1:A:426:ILE:HB	2.03	0.40
1:B:585:LEU:C	1:B:587:ARG:H	2.25	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	417/464 (90%)	392 (94%)	21 (5%)	4 (1%)	15	17
1	B	415/464 (89%)	390 (94%)	19 (5%)	6 (1%)	11	11
All	All	832/928 (90%)	782 (94%)	40 (5%)	10 (1%)	13	14

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	378	ALA
1	B	593	HIS
1	B	281	GLY
1	B	572	GLN
1	A	282	GLY
1	B	584	CYS
1	A	372	LYS
1	A	581	MET
1	B	211	SER
1	B	586	ILE

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	351/382 (92%)	338 (96%)	13 (4%)	34	48
1	B	345/382 (90%)	339 (98%)	6 (2%)	60	76
All	All	696/764 (91%)	677 (97%)	19 (3%)	44	61

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	211	SER
1	A	254	THR

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Mol	Chain	Res	Type
1	A	316	ARG
1	A	347	ILE
1	A	357	GLU
1	A	376	GLU
1	A	426	ILE
1	A	485	MET
1	A	587	ARG
1	A	588	LEU
1	A	597	PRO
1	A	598	LEU
1	A	600	TYR
1	B	235	THR
1	B	357	GLU
1	B	403	ASN
1	B	424	SER
1	B	577	SER
1	B	600	TYR

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	201	HIS
1	A	460	GLN
1	B	403	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	2SY	A	701	-	20,23,23	0.69	0	24,32,32	1.21	2 (8%)

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
2	2SY	A	701	-	-	2/8/8/8	0/3/3/3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	701	2SY	C10-C6-N2	3.56	118.53	112.71
2	A	701	2SY	C6-N2-C5	2.46	128.27	124.80

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	701	2SY	C10-C6-N2-C1
2	A	701	2SY	C10-C6-N2-C5

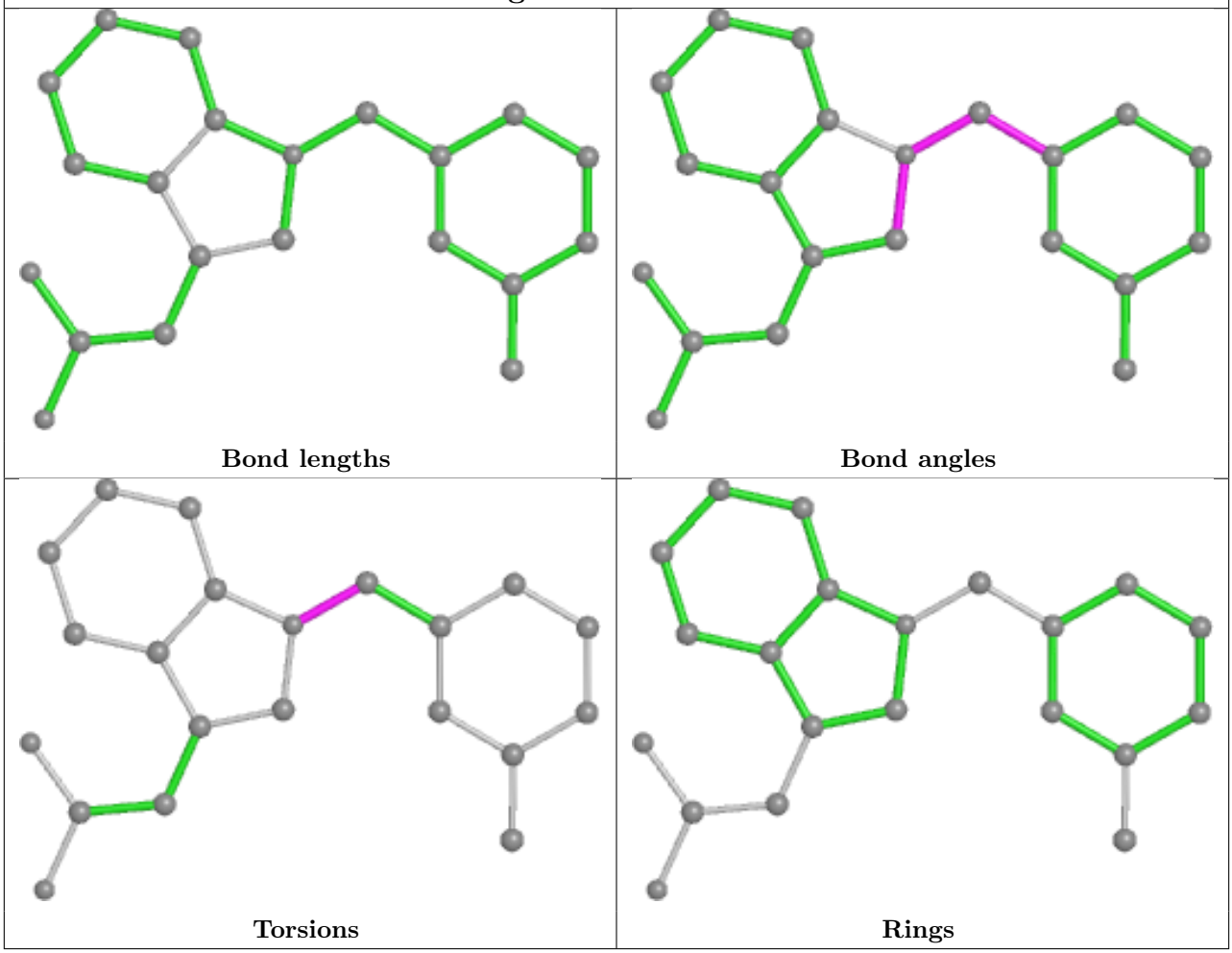
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	701	2SY	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 then 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.

Ligand 2SY A 701



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	426/464 (91%)	0.98	62 (14%) 2 3	43, 59, 96, 171	0
1	B	420/464 (90%)	0.75	39 (9%) 8 11	40, 60, 94, 109	0
All	All	846/928 (91%)	0.86	101 (11%) 4 6	40, 59, 95, 171	0

All (101) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	379	ALA	22.0
1	B	592	LEU	8.7
1	A	525[A]	CYS	8.6
1	B	402	THR	8.2
1	A	378	ALA	7.7
1	A	377	LEU	7.2
1	A	592	LEU	6.8
1	B	403	ASN	6.6
1	A	388	ALA	6.4
1	A	416	THR	6.3
1	A	206	THR	6.2
1	B	591	THR	6.1
1	A	375	ASP	5.8
1	A	524	VAL	5.6
1	B	401	PRO	5.4
1	B	263	SER	5.1
1	A	362	GLY	5.1
1	A	358	VAL	4.9
1	A	588	LEU	4.9
1	A	354	ILE	4.7
1	B	239	GLY	4.7
1	B	572	GLN	4.7
1	A	374	CYS	4.5
1	B	400	ILE	4.5

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Mol	Chain	Res	Type	RSRZ
1	B	588	LEU	4.4
1	A	389	VAL	4.4
1	B	590	PRO	4.3
1	B	578	TRP	4.3
1	B	589	LYS	4.1
1	A	381	LEU	4.1
1	B	220	ALA	3.9
1	A	207	GLY	3.9
1	A	421	ASP	3.8
1	A	281	GLY	3.7
1	A	401	PRO	3.6
1	B	573	ALA	3.5
1	A	471	GLY	3.5
1	A	424	SER	3.5
1	A	357	GLU	3.5
1	A	355	PRO	3.5
1	A	417	GLY	3.5
1	A	589	LYS	3.4
1	A	593	HIS	3.4
1	B	281	GLY	3.4
1	B	264	PRO	3.4
1	A	364	HIS	3.4
1	A	347	ILE	3.3
1	A	398	SER	3.3
1	A	387	ASN	3.3
1	A	467	ARG	3.3
1	B	397	VAL	3.2
1	A	400	ILE	3.1
1	B	189	SER	3.1
1	B	235	THR	3.1
1	A	282	GLY	3.1
1	B	587	ARG	3.1
1	B	392	TYR	3.0
1	A	280	SER	3.0
1	B	236	LEU	3.0
1	A	399	VAL	2.9
1	B	431[A]	CYS	2.9
1	B	399	VAL	2.9
1	B	467	ARG	2.9
1	B	594	GLY	2.8
1	B	466	GLY	2.8
1	B	219	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	603	GLY	2.8
1	A	587	ARG	2.7
1	A	359	ILE	2.7
1	A	629	VAL	2.7
1	A	415	MET	2.7
1	B	593	HIS	2.7
1	A	591	THR	2.7
1	B	421	ASP	2.6
1	A	425	VAL	2.6
1	A	408	VAL	2.5
1	A	365	LEU	2.5
1	A	407	VAL	2.5
1	A	580	GLN	2.5
1	A	486	PHE	2.4
1	A	361	GLY	2.4
1	B	391	TYR	2.4
1	A	628	GLU	2.4
1	A	380	LYS	2.4
1	A	578	TRP	2.3
1	A	410	SER	2.3
1	A	406	VAL	2.3
1	B	605	VAL	2.3
1	A	491	LEU	2.2
1	A	344	THR	2.2
1	A	492	CYS	2.2
1	B	396	ASP	2.2
1	A	469	LYS	2.2
1	B	206	THR	2.1
1	B	585	LEU	2.1
1	B	571	ALA	2.1
1	B	188	SER	2.1
1	A	349	PHE	2.1
1	A	545	HIS	2.0
1	A	526	GLN	2.0
1	A	468	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 monosaccharides in this entry.

6.4 Ligands (i)

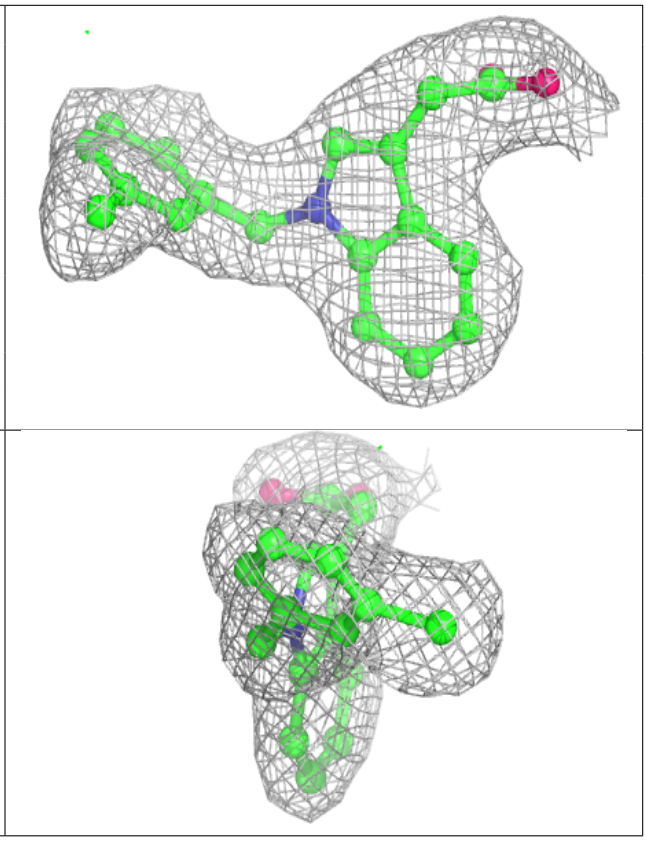
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	CA	A	703	1/1	0.89	0.14	76,76,76,76	0
2	2SY	A	701	21/21	0.95	0.13	42,49,57,59	0
3	CA	A	702	1/1	0.96	0.14	68,68,68,68	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 2SY A 701:

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.