



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:47 PM UTC

PDB ID : 3QGD / pdb_00003qgd
Title : Crystal structure of the hepatitis C virus NS5B RNA-dependent RNA polymerase complex with (2E)-3-(4-{{[(1-{{[(13-cyclohexyl-6-oxo-6,7-dihydro-5H-indolo[1,2-d][1,4]benzodiazepin-10-yl)carbonyl]amino}cyclopentyl)carbonyl]amino}phenyl)prop-2-enoic acid and (2R)-4-(2,6-dimethoxypyrimidin-4-yl)-1-[(4-ethylphenyl)sulfonyl]-N-(4-methoxybenzyl)piperazine-2-carboxamide
Authors : Sheriff, S.
Deposited on : 2011-01-24
Resolution : 2.60 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)

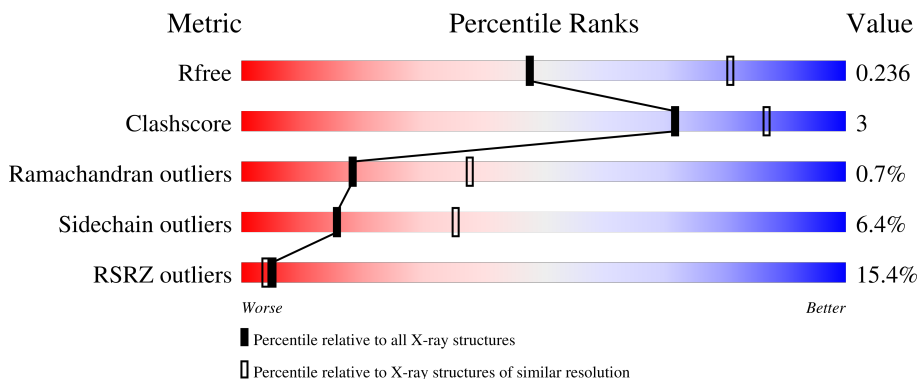
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	574	10% 81% 11% 6%
1	B	574	18% 78% 10% 10%

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 8421 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.

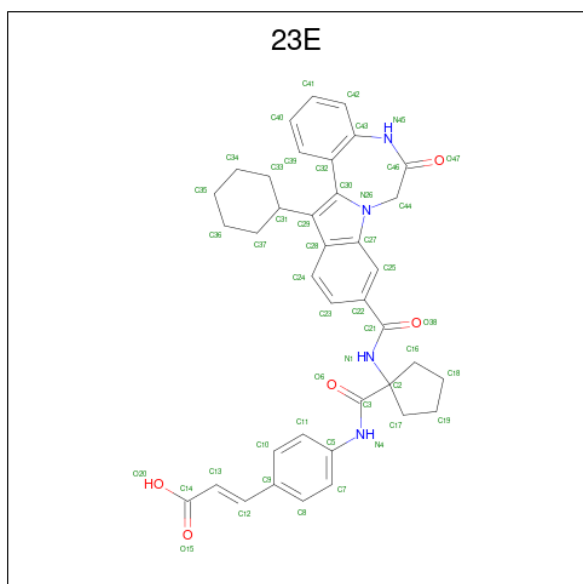
- Molecule 1 is a protein called RNA-directed RNA polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	538	Total	C	N	O	S	0	0	0
			4162	2625	736	769	32			
1	B	515	Total	C	N	O	S	0	0	0
			3999	2518	712	737	32			

There are 2 discrepancies between the modelled and reference sequences:

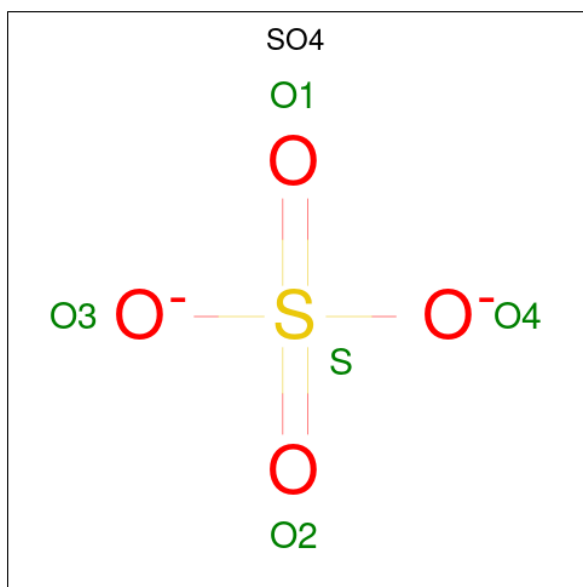
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP Q9WMX2
B	0	MET	-	initiating methionine	UNP Q9WMX2

- Molecule 2 is (2E)-3-(4-((1-((13-cyclohexyl-6-oxo-6,7-dihydro-5H-indolo[1,2-d][1,4]benzodiazepin-10-yl)carbonyl]amino)cyclopentyl)carbonyl]amino)phenyl)prop-2-enoic acid (CCD ID: 23E) (formula: C₃₈H₃₈N₄O₅).



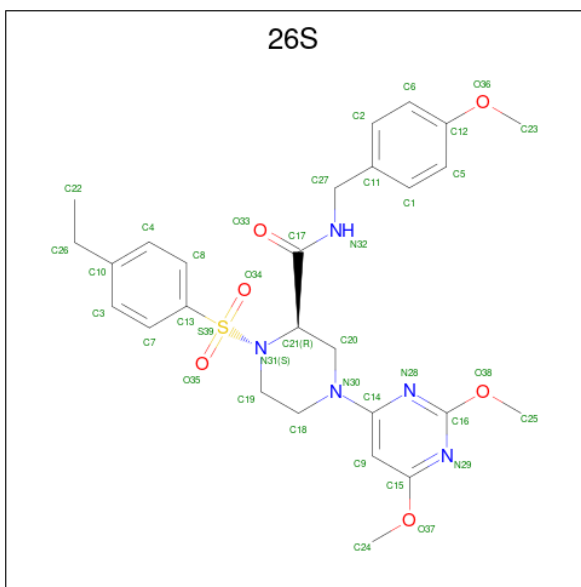
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			47	38	4	5		
2	B	1	Total	C	N	O	0	0
			47	38	4	5		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 4 is (2R)-4-(2,6-dimethoxypyrimidin-4-yl)-1-[(4-ethylphenyl)sulfonyl]-N-(4-methoxybenzyl)piperazine-2-carboxamide (CCD ID: 26S) (formula: C₂₇H₃₃N₅O₆S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	S	0	0
			39	27	5	6	1		

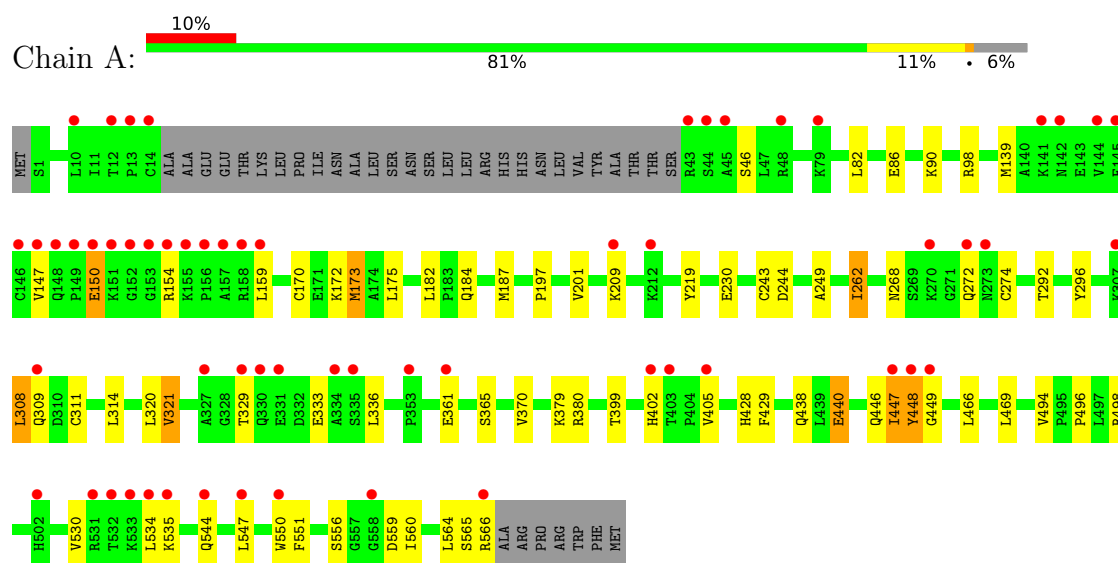
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	61	Total O 61 61	0	0
5	B	36	Total O 36 36	0	0

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: RNA-directed RNA polymerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	66.00Å 91.60Å 231.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.56 – 2.60 43.56 – 2.60	Depositor EDS
% Data completeness (in resolution range)	97.3 (43.56-2.60) 97.2 (43.56-2.60)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.46 (at 2.61Å)	Xtriage
Refinement program	BUSTER-TNT BUSTER 2.9.7, BUSTER 2.9.7	Depositor
R, R_{free}	0.233 , 0.262 (Not available) , 0.236	Depositor DCC
R_{free} test set	639 reflections (1.49%)	wwPDB-VP
Wilson B-factor (Å ²)	37.1	Xtriage
Anisotropy	0.555	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 46.6	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	0.91	EDS
Total number of atoms	8421	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.46% 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: 23E, SO4, 26S

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	0.77	1/4252 (0.0%)	1.30	13/5769 (0.2%)
1	B	0.78	1/4083 (0.0%)	1.28	10/5537 (0.2%)
All	All	0.77	2/8335 (0.0%)	1.29	23/11306 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	173	MET	SD-CE	-6.77	1.62	1.79
1	A	173	MET	SD-CE	-6.38	1.63	1.79

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	447	ILE	CA-C-N	9.13	138.98	121.54
1	A	447	ILE	C-N-CA	9.13	138.98	121.54
1	A	534	LEU	CA-C-N	6.39	129.67	120.79
1	A	534	LEU	C-N-CA	6.39	129.67	120.79
1	A	244	ASP	N-CA-C	-6.20	99.76	109.25
1	B	530	VAL	N-CA-C	6.19	118.09	109.55
1	A	447	ILE	CB-CA-C	5.95	118.52	111.32
1	B	244	ASP	N-CA-C	-5.89	100.23	109.25
1	A	565	SER	CA-C-N	5.78	132.10	121.70
1	A	565	SER	C-N-CA	5.78	132.10	121.70
1	B	359	ASP	CA-CB-CG	5.71	118.31	112.60
1	A	530	VAL	N-CA-C	5.50	117.14	109.55
1	A	175	LEU	N-CA-C	5.38	121.68	113.61
1	A	530	VAL	CA-C-N	5.28	127.31	120.44
1	A	530	VAL	C-N-CA	5.28	127.31	120.44
1	A	559	ASP	CA-CB-CG	5.26	117.86	112.60
1	B	175	LEU	N-CA-C	5.24	121.47	113.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	534	LEU	CA-C-N	5.17	127.97	120.79
1	B	534	LEU	C-N-CA	5.17	127.97	120.79
1	B	261	TYR	N-CA-C	5.16	116.91	111.28
1	B	530	VAL	CA-C-N	5.05	127.00	120.44
1	B	530	VAL	C-N-CA	5.05	127.00	120.44
1	B	201	VAL	N-CA-CB	5.03	116.43	110.55

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	4162	0	4156	27	0
1	B	3999	0	4019	27	0
2	A	47	0	37	3	0
2	B	47	0	37	0	0
3	A	10	0	0	0	0
3	B	20	0	0	0	0
4	B	39	0	33	1	0
5	A	61	0	0	0	0
5	B	36	0	0	0	0
All	All	8421	0	8282	55	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 3.

All (55) 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:170:CYS:HA	1:A:173:MET:HE3	1.53	0.90
1:B:170:CYS:HA	1:B:173:MET:HE3	1.52	0.90
1:B:321:VAL:HG21	1:B:365:SER:HB3	1.56	0.85
1:B:321:VAL:HG21	1:B:365:SER:CB	2.14	0.77
1:A:187:MET:HE1	1:A:292:THR:HG22	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:187:MET:HE1	1:B:292:THR:HG22	1.68	0.74
1:A:172:LYS:HE3	1:A:560:ILE:HD13	1.74	0.68
1:B:321:VAL:CG2	1:B:365:SER:HB3	2.23	0.67
1:A:405:VAL:HG11	1:A:446:GLN:HG2	1.77	0.66
1:A:308:LEU:HB3	1:A:311:CYS:SG	2.38	0.64
1:B:197:PRO:O	1:B:201:VAL:HG23	1.99	0.63
1:B:308:LEU:HB3	1:B:311:CYS:SG	2.38	0.63
1:A:197:PRO:O	1:A:201:VAL:HG23	1.99	0.61
1:A:399:THR:HG21	1:A:428:HIS:NE2	2.15	0.61
1:B:399:THR:HG21	1:B:428:HIS:NE2	2.17	0.59
1:B:219:TYR:HB3	1:B:320:LEU:HD23	1.86	0.57
1:A:361:GLU:HG2	1:A:370:VAL:O	2.03	0.57
1:A:314:LEU:HB3	1:A:321:VAL:HG23	1.87	0.56
1:B:458:ASP:O	1:B:461:GLN:HG2	2.06	0.56
1:A:219:TYR:HB3	1:A:320:LEU:HD23	1.86	0.56
1:B:321:VAL:CG2	1:B:365:SER:CB	2.82	0.54
1:B:361:GLU:HG2	1:B:370:VAL:O	2.09	0.52
1:A:268:ASN:HB3	1:A:274:CYS:SG	2.49	0.51
2:A:601:23E:O6	2:A:601:23E:H7	2.12	0.50
1:A:82:LEU:HD13	1:A:249:ALA:HB2	1.94	0.49
1:B:234:ARG:CG	1:B:262:ILE:HD11	2.44	0.48
1:B:257:THR:HG22	1:B:262:ILE:HD12	1.96	0.48
1:A:230:GLU:HG2	1:A:262:ILE:HG23	1.96	0.48
1:B:82:LEU:HD13	1:B:249:ALA:HB2	1.96	0.48
1:A:544:GLN:HG3	1:A:566:ARG:C	2.39	0.47
1:A:321:VAL:HG11	1:A:365:SER:HB3	1.96	0.47
1:B:414:MET:HG2	1:B:447:ILE:HD12	1.97	0.47
1:A:446:GLN:O	1:A:447:ILE:HD13	2.15	0.46
1:B:268:ASN:ND2	1:B:272:GLN:HG2	2.32	0.45
1:B:359:ASP:HB3	1:B:362:LEU:HD12	1.98	0.45
1:A:496:PRO:HD2	2:A:601:23E:H13	1.98	0.45
1:A:268:ASN:ND2	1:A:272:GLN:HG2	2.31	0.45
1:B:197:PRO:HA	4:B:602:26S:H6	1.99	0.45
1:B:446:GLN:HE21	1:B:446:GLN:HB3	1.64	0.44
1:A:150:GLU:H	1:A:150:GLU:HG3	1.67	0.44
1:A:321:VAL:CG1	1:A:365:SER:HB3	2.47	0.44
1:B:440:GLU:H	1:B:440:GLU:CD	2.27	0.43
1:B:399:THR:HG23	1:B:429:PHE:CZ	2.54	0.43
1:A:182:LEU:HD12	1:A:243:CYS:SG	2.58	0.43
1:A:399:THR:HG23	1:A:429:PHE:CZ	2.54	0.43
1:A:440:GLU:H	1:A:440:GLU:CD	2.28	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:234:ARG:HG3	1:B:262:ILE:HD11	2.01	0.42
1:B:405:VAL:HG13	1:B:445:CYS:HA	2.02	0.42
1:B:150:GLU:H	1:B:150:GLU:HG3	1.67	0.41
1:A:466:LEU:HD22	1:A:551:PHE:HE2	1.85	0.41
1:A:187:MET:HE1	1:A:292:THR:CG2	2.46	0.41
1:A:494:VAL:HG22	2:A:601:23E:C30	2.51	0.41
1:B:187:MET:HE3	1:B:296:TYR:CD2	2.54	0.41
1:A:187:MET:HE3	1:A:296:TYR:CD2	2.55	0.40
1:B:169:VAL:HG12	1:B:173:MET:HE2	2.03	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	534/574 (93%)	523 (98%)	7 (1%)	4 (1%)	18	38
1	B	511/574 (89%)	500 (98%)	8 (2%)	3 (1%)	21	42
All	All	1045/1148 (91%)	1023 (98%)	15 (1%)	7 (1%)	18	38

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	449	GLY
1	B	541	ALA
1	A	550	TRP
1	A	147	VAL
1	A	448	TYR
1	B	147	VAL
1	B	449	GLY

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	447/486 (92%)	418 (94%)	29 (6%)	15	35
1	B	432/486 (89%)	405 (94%)	27 (6%)	16	36
All	All	879/972 (90%)	823 (94%)	56 (6%)	16	35

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	SER
1	A	86	GLU
1	A	90	LYS
1	A	98	ARG
1	A	139	MET
1	A	150	GLU
1	A	154	ARG
1	A	159	LEU
1	A	184	GLN
1	A	209	LYS
1	A	262	ILE
1	A	308	LEU
1	A	309	GLN
1	A	321	VAL
1	A	329	THR
1	A	333	GLU
1	A	336	LEU
1	A	379	LYS
1	A	380	ARG
1	A	402	HIS
1	A	438	GLN
1	A	440	GLU
1	A	448	TYR
1	A	469	LEU
1	A	498	ARG
1	A	535	LYS
1	A	547	LEU

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Mol	Chain	Res	Type
1	A	556	SER
1	A	564	LEU
1	B	46	SER
1	B	86	GLU
1	B	98	ARG
1	B	100	LYS
1	B	139	MET
1	B	141	LYS
1	B	150	GLU
1	B	154	ARG
1	B	159	LEU
1	B	160	ILE
1	B	184	GLN
1	B	209	LYS
1	B	262	ILE
1	B	308	LEU
1	B	309	GLN
1	B	321	VAL
1	B	329	THR
1	B	333	GLU
1	B	336	LEU
1	B	379	LYS
1	B	402	HIS
1	B	438	GLN
1	B	440	GLU
1	B	446	GLN
1	B	461	GLN
1	B	469	LEU
1	B	535	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	438	GLN
1	A	446	GLN
1	B	438	GLN
1	B	446	GLN
1	B	461	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

9 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$
3	SO4	A	652	-	4,4,4	0.32	0	6,6,6	0.29	0
3	SO4	B	653	-	4,4,4	0.46	0	6,6,6	0.16	0
3	SO4	B	657	-	4,4,4	0.50	0	6,6,6	0.25	0
3	SO4	B	656	-	4,4,4	0.47	0	6,6,6	0.27	0
3	SO4	B	658	-	4,4,4	0.35	0	6,6,6	0.19	0
2	23E	B	601	-	52,53,53	1.70	8 (15%)	68,77,77	1.75	14 (20%)
4	26S	B	602	-	42,42,42	1.55	6 (14%)	55,59,59	0.99	1 (1%)
2	23E	A	601	-	52,53,53	1.67	6 (11%)	68,77,77	1.50	11 (16%)
3	SO4	A	653	-	4,4,4	0.79	0	6,6,6	0.23	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
4	26S	B	602	-	-	0/33/46/46	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	23E	B	601	-	-	1/28/57/57	0/6/7/7
2	23E	A	601	-	-	4/28/57/57	0/6/7/7

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	602	26S	S39-N31	6.70	1.73	1.63
2	B	601	23E	C32-C30	5.35	1.52	1.47
2	A	601	23E	O15-C14	4.97	1.35	1.23
2	A	601	23E	C30-N26	-4.88	1.31	1.39
2	B	601	23E	C30-N26	-4.69	1.32	1.39
2	B	601	23E	O15-C14	4.68	1.34	1.23
2	A	601	23E	C32-C30	4.49	1.51	1.47
2	B	601	23E	C28-C29	3.87	1.50	1.44
2	A	601	23E	C28-C29	3.64	1.50	1.44
2	B	601	23E	O20-C14	-3.06	1.22	1.30
2	B	601	23E	C8-C7	2.78	1.43	1.38
2	A	601	23E	C27-N26	-2.50	1.35	1.39
2	A	601	23E	O20-C14	-2.43	1.24	1.30
2	B	601	23E	C27-N26	-2.42	1.35	1.39
4	B	602	26S	O35-S39	2.42	1.46	1.43
4	B	602	26S	O34-S39	2.18	1.45	1.43
4	B	602	26S	C15-N29	2.14	1.36	1.33
2	B	601	23E	C9-C12	2.07	1.53	1.47
4	B	602	26S	O38-C16	2.06	1.38	1.33
4	B	602	26S	C17-N32	2.03	1.38	1.33

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	23E	C9-C12-C13	7.30	142.87	126.92
2	B	601	23E	C12-C13-C14	4.55	134.13	122.32
2	A	601	23E	C17-C2-C16	-4.42	97.83	103.39
2	A	601	23E	C16-C2-C3	4.15	120.45	110.75
2	B	601	23E	C27-N26-C30	3.86	111.46	108.37
2	A	601	23E	C27-C28-C29	-3.73	103.88	107.02
2	A	601	23E	C27-N26-C30	3.57	111.23	108.37
2	B	601	23E	C17-C2-C16	-3.51	98.98	103.39
2	A	601	23E	C24-C28-C27	3.18	122.91	119.24
2	A	601	23E	C9-C12-C13	2.97	133.41	126.92
2	B	601	23E	C27-C28-C29	-2.94	104.54	107.02
4	B	602	26S	C11-C27-N32	-2.89	106.99	113.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	23E	C23-C24-C28	-2.72	116.38	120.86
2	A	601	23E	C23-C24-C28	-2.58	116.61	120.86
2	A	601	23E	C3-C2-N1	-2.50	107.27	110.76
2	B	601	23E	C16-C2-C3	2.49	116.57	110.75
2	B	601	23E	C28-C29-C30	-2.38	104.98	107.28
2	A	601	23E	C28-C29-C31	-2.36	121.00	126.87
2	B	601	23E	C7-C5-N4	2.34	128.26	120.41
2	A	601	23E	C36-C37-C31	-2.29	107.06	111.24
2	B	601	23E	C24-C28-C27	2.15	121.72	119.24
2	B	601	23E	C5-N4-C3	2.13	130.64	126.86
2	B	601	23E	C28-C29-C31	-2.13	121.58	126.87
2	A	601	23E	C33-C31-C29	2.12	117.32	113.00
2	B	601	23E	O47-C46-C44	-2.12	117.54	121.40
2	B	601	23E	C11-C5-N4	-2.04	113.55	120.41

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	23E	C13-C12-C9-C8
2	A	601	23E	C13-C12-C9-C10
2	A	601	23E	C12-C13-C14-O15
2	A	601	23E	C12-C13-C14-O20
2	B	601	23E	C9-C12-C13-C14

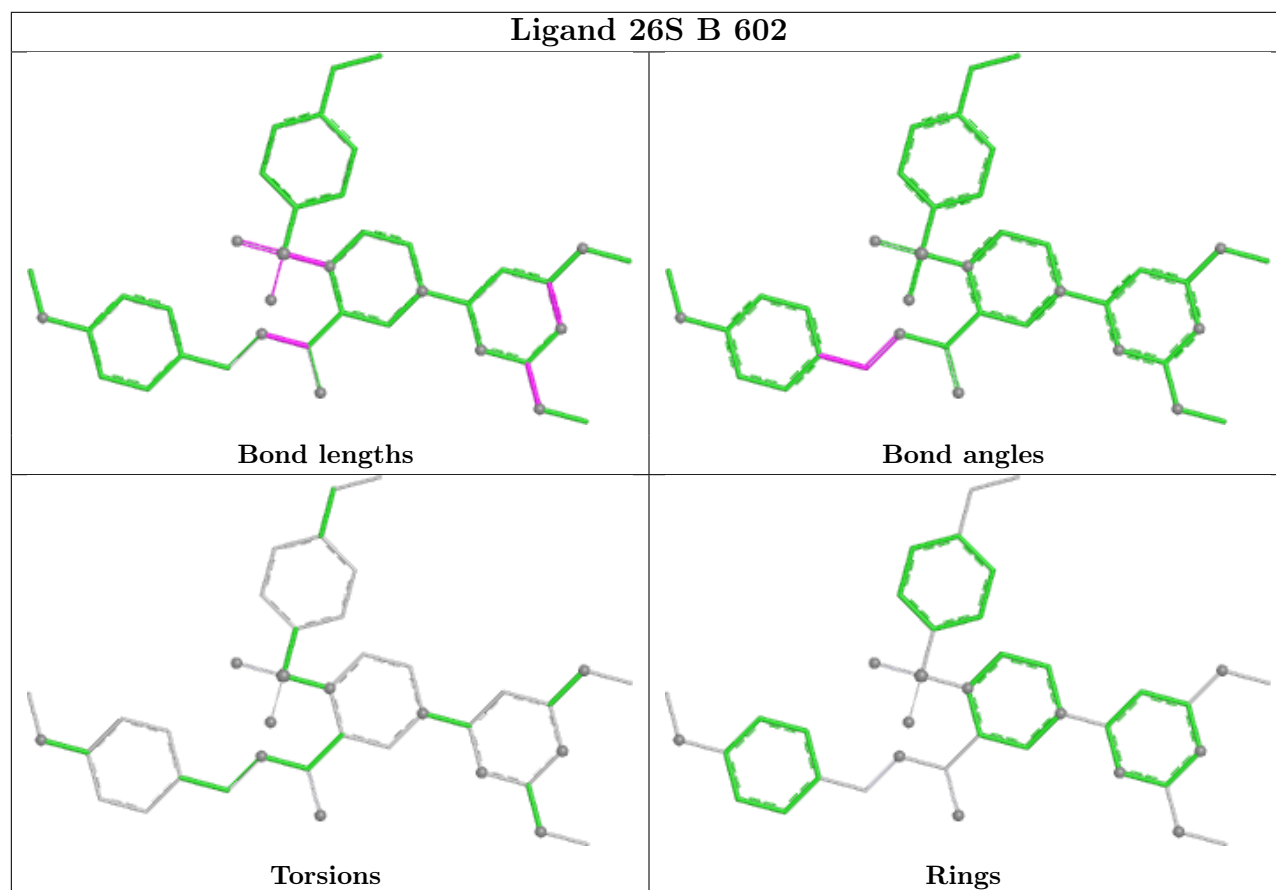
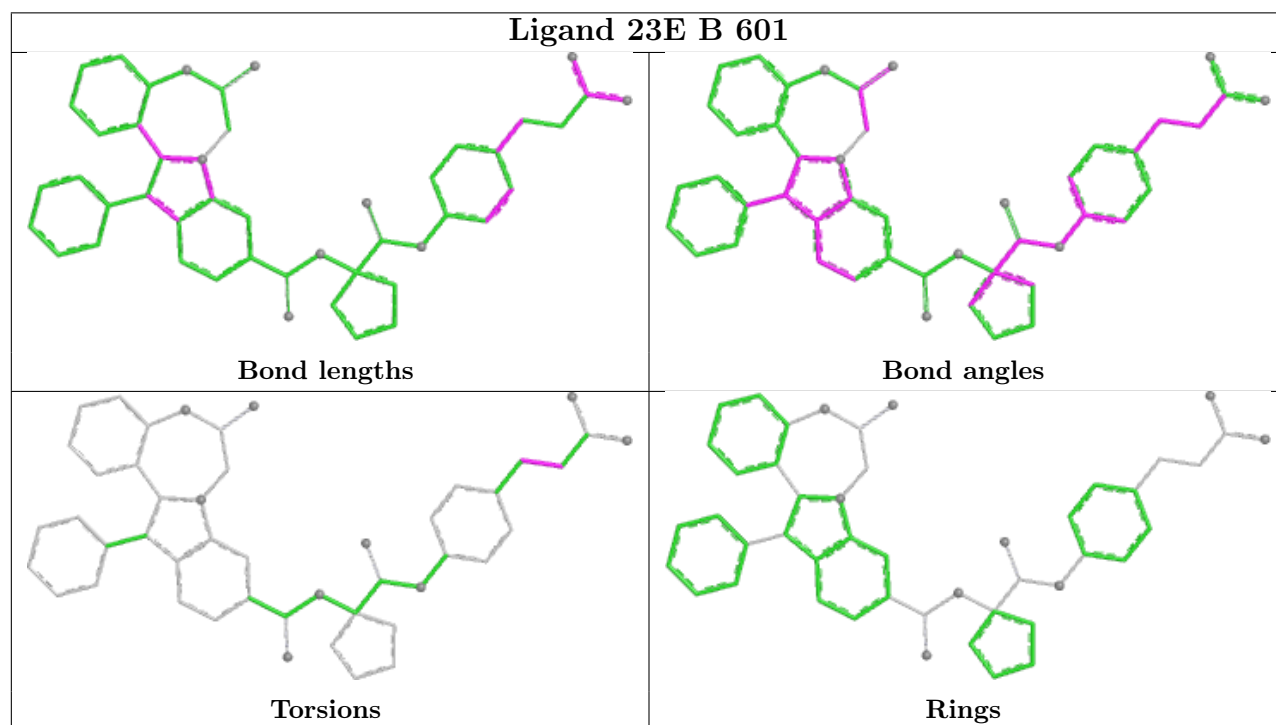
There are no ring outliers.

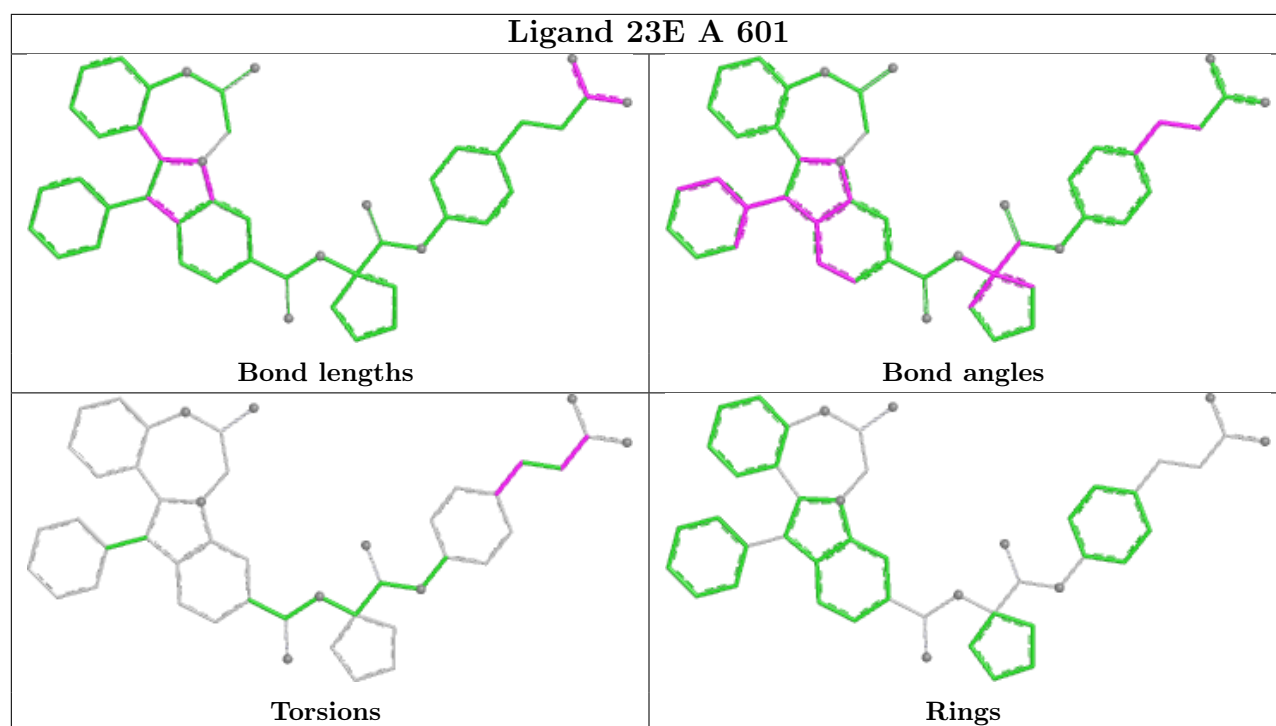
2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	602	26S	1	0
2	A	601	23E	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	538/574 (93%)	0.67	59 (10%)	10 8	22, 38, 78, 134	0
1	B	515/574 (89%)	0.99	103 (20%)	3 2	23, 42, 93, 142	0
All	All	1053/1148 (91%)	0.83	162 (15%)	5 4	22, 40, 84, 142	0

All (162) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	147	VAL	7.2
1	A	149	PRO	7.0
1	B	147	VAL	6.8
1	A	448	TYR	6.3
1	B	149	PRO	6.2
1	B	542	ALA	6.1
1	A	535	LYS	5.8
1	B	151	LYS	5.4
1	B	42	SER	5.3
1	A	151	LYS	5.2
1	A	402	HIS	5.2
1	B	405	VAL	5.1
1	B	150	GLU	5.1
1	B	402	HIS	4.8
1	B	404	PRO	4.7
1	B	146	CYS	4.6
1	A	154	ARG	4.5
1	A	13	PRO	4.5
1	B	148	GLN	4.5
1	B	403	THR	4.4
1	B	535	LYS	4.4
1	A	531	ARG	4.4
1	A	155	LYS	4.3
1	A	532	THR	4.3

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Mol	Chain	Res	Type	RSRZ
1	B	94	PRO	4.1
1	A	150	GLU	4.0
1	A	148	GLN	4.0
1	A	12	THR	4.0
1	B	401	ARG	3.9
1	A	152	GLY	3.9
1	B	14	CYS	3.9
1	B	153	GLY	3.8
1	B	93	PRO	3.8
1	A	146	CYS	3.8
1	B	97	ALA	3.8
1	B	157	ALA	3.7
1	A	144	VAL	3.7
1	B	272	GLN	3.7
1	B	399	THR	3.7
1	A	212	LYS	3.7
1	B	144	VAL	3.7
1	B	449	GLY	3.6
1	A	14	CYS	3.6
1	B	400	ALA	3.5
1	A	533	LYS	3.5
1	B	448	TYR	3.4
1	A	327	ALA	3.4
1	B	155	LYS	3.4
1	B	152	GLY	3.4
1	B	110	ASN	3.4
1	B	95	HIS	3.4
1	B	438	GLN	3.4
1	A	566	ARG	3.4
1	A	447	ILE	3.3
1	B	111	LEU	3.3
1	B	451	CYS	3.3
1	B	531	ARG	3.2
1	B	534	LEU	3.2
1	B	159	LEU	3.2
1	B	156	PRO	3.2
1	A	48	ARG	3.2
1	A	153	GLY	3.2
1	B	44	SER	3.2
1	B	47	LEU	3.2
1	B	540	PRO	3.1
1	A	44	SER	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	10	LEU	3.1
1	B	397	TRP	3.1
1	B	139	MET	3.1
1	B	154	ARG	3.1
1	A	141	LYS	3.0
1	A	156	PRO	3.0
1	B	90	LYS	3.0
1	B	270	LYS	3.0
1	B	447	ILE	3.0
1	B	45	ALA	3.0
1	A	335	SER	3.0
1	A	449	GLY	2.9
1	A	145	PHE	2.9
1	A	309	GLN	2.9
1	B	13	PRO	2.9
1	B	46	SER	2.9
1	B	50	LYS	2.9
1	B	145	PHE	2.9
1	B	108	VAL	2.8
1	A	209	LYS	2.8
1	B	441	LYS	2.8
1	B	352	ASP	2.8
1	A	403	THR	2.8
1	B	11	ILE	2.8
1	B	106	LYS	2.7
1	B	212	LYS	2.7
1	B	539	ILE	2.7
1	A	331	GLU	2.7
1	B	43	ARG	2.7
1	A	550	TRP	2.7
1	A	272	GLN	2.7
1	A	329	THR	2.7
1	A	270	LYS	2.7
1	A	330	GLN	2.7
1	B	351	GLY	2.6
1	A	273	ASN	2.6
1	A	157	ALA	2.6
1	A	142	ASN	2.6
1	A	558	GLY	2.6
1	B	7	THR	2.6
1	B	269	SER	2.6
1	A	43	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	8	GLY	2.6
1	B	105	ALA	2.6
1	B	158	ARG	2.5
1	B	307	LYS	2.5
1	B	102	GLY	2.5
1	B	96	SER	2.5
1	B	143	GLU	2.5
1	A	534	LEU	2.5
1	B	86	GLU	2.5
1	B	135	ASP	2.4
1	B	452	TYR	2.4
1	B	450	ALA	2.4
1	B	84	SER	2.4
1	B	487	SER	2.4
1	B	213	CYS	2.4
1	B	435	ALA	2.4
1	B	532	THR	2.4
1	A	307	LYS	2.4
1	B	536	LEU	2.4
1	B	48	ARG	2.4
1	B	140	ALA	2.4
1	B	541	ALA	2.4
1	B	160	ILE	2.3
1	B	406	ASN	2.3
1	A	79	LYS	2.3
1	B	436	GLN	2.3
1	A	334	ALA	2.3
1	B	337	ARG	2.3
1	B	101	PHE	2.3
1	A	502	HIS	2.2
1	B	141	LYS	2.2
1	B	142	ASN	2.2
1	B	220	ASP	2.2
1	A	159	LEU	2.2
1	A	45	ALA	2.2
1	A	361	GLU	2.2
1	B	91	LEU	2.2
1	B	1	SER	2.2
1	A	544	GLN	2.1
1	A	10	LEU	2.1
1	A	547	LEU	2.1
1	B	384	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	117	ASN	2.1
1	B	118	HIS	2.1
1	B	222	ARG	2.1
1	B	6	TRP	2.1
1	A	405	VAL	2.1
1	B	85	VAL	2.1
1	A	158	ARG	2.0
1	B	98	ARG	2.0
1	B	209	LYS	2.0
1	B	395	ALA	2.0
1	A	353	PRO	2.0
1	B	514	GLN	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.

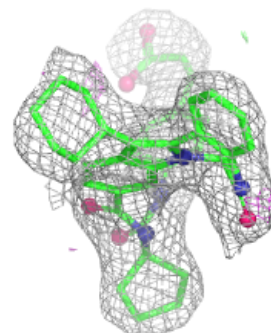
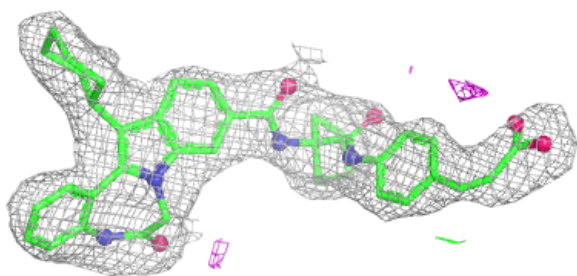
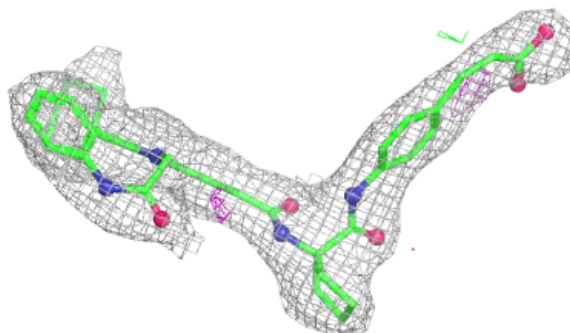
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	SO4	B	658	5/5	0.73	0.21	123,128,128,129	0
3	SO4	B	657	5/5	0.74	0.16	96,100,101,102	0
3	SO4	A	652	5/5	0.76	0.21	85,89,90,91	0
3	SO4	B	653	5/5	0.76	0.14	83,87,89,89	0
3	SO4	B	656	5/5	0.88	0.16	71,75,76,76	0
3	SO4	A	653	5/5	0.90	0.11	53,57,57,58	0
2	23E	B	601	47/47	0.91	0.11	25,37,47,59	0
4	26S	B	602	39/39	0.91	0.11	33,40,50,52	0
2	23E	A	601	47/47	0.93	0.09	21,31,54,67	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.

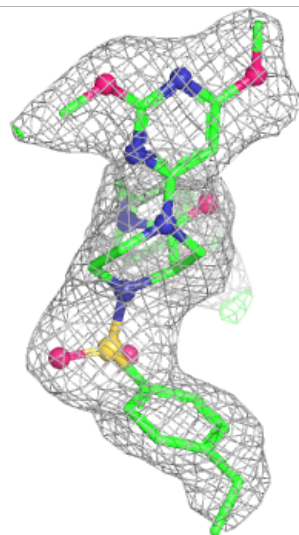
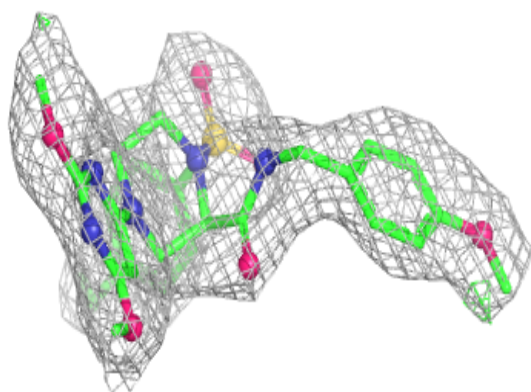
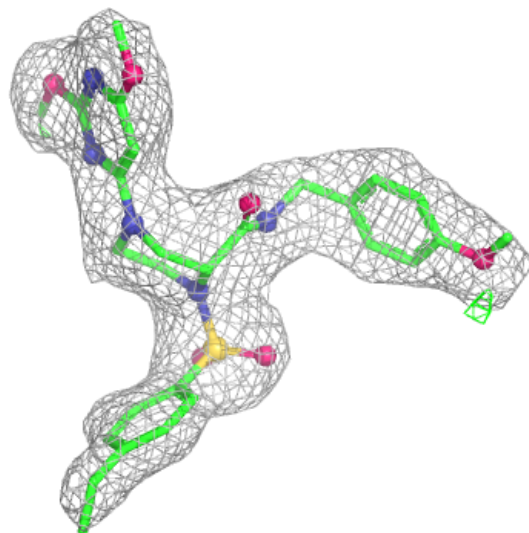
Electron density around 23E B 601:

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



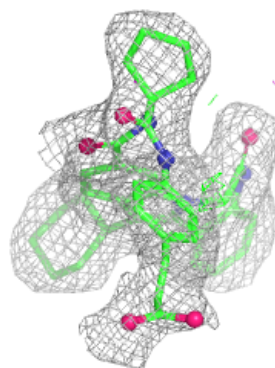
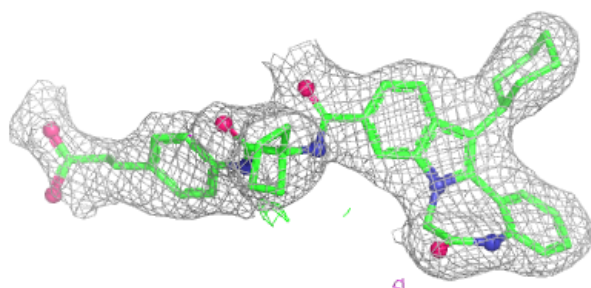
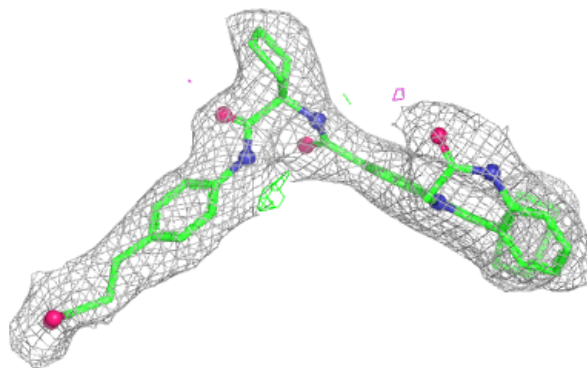
Electron density around 26S B 602:

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



Electron density around 23E A 601:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.