



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:56 AM UTC

PDB ID : 8A5J / pdb_00008a5j
Title : Crystal structure of Human STE20-like kinase 1, MST1 in complex with compound XMU-MP-1
Authors : Nawrotek, A.; Vuillard, L.; Miallau, L.
Deposited on : 2022-06-15
Resolution : 2.12 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

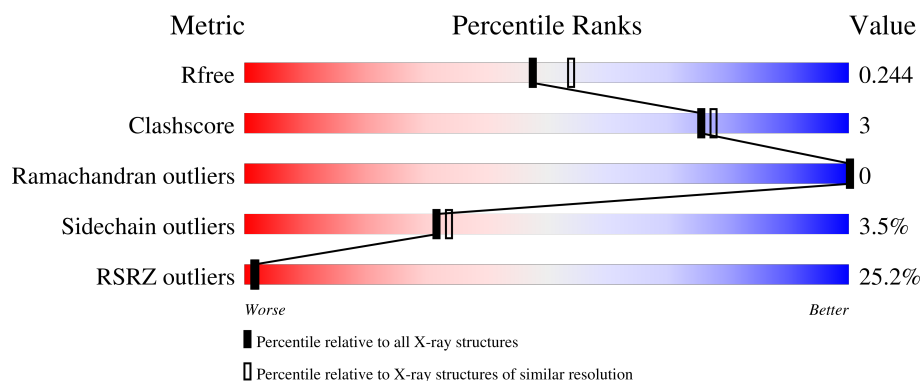
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.12 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	8290 (2.14-2.10)
Clashscore	190562	8817 (2.14-2.10)
Ramachandran outliers	187476	8738 (2.14-2.10)
Sidechain outliers	187428	8739 (2.14-2.10)
RSRZ outliers	180081	8294 (2.14-2.10)

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	282	12% 88% 10% ..
1	B	282	35% 80% 9% 12%

2 Entry composition [i](#)

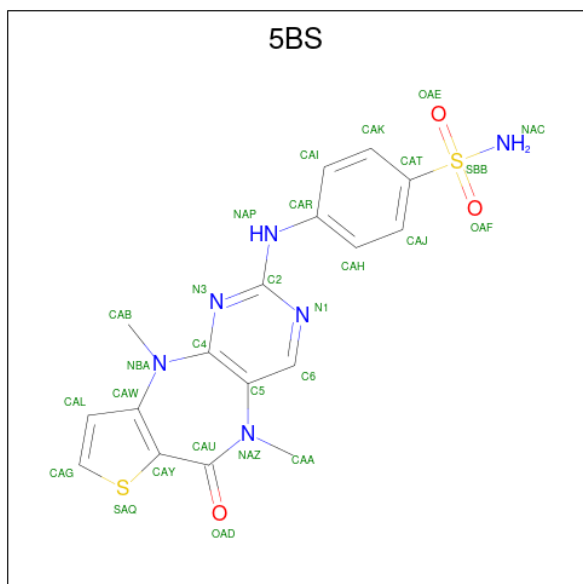
There are 3 unique types of molecules in this entry. The entry contains 4369 atoms, of which 0 are hydrogens and 0 are deuteriums.

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/threonine-protein kinase 4 37kDa subunit.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	279	Total	C	N	O	P	S	0	6	0
			2252	1440	377	419	2	14			
1	B	249	Total	C	N	O	P	S	0	2	0
			1980	1262	335	367	2	14			

- Molecule 2 is 4-[(5,10-dimethyl-6-oxo-6,10-dihydro-5H-pyrimido[5,4-b]thieno[3,2-e][1,4]diazepin-2-yl)amino]benzenesulfonamide (CCD ID: 5BS) (formula: C₁₇H₁₆N₆O₃S₂) (labeled as "Ligand of Interest" by depositor).

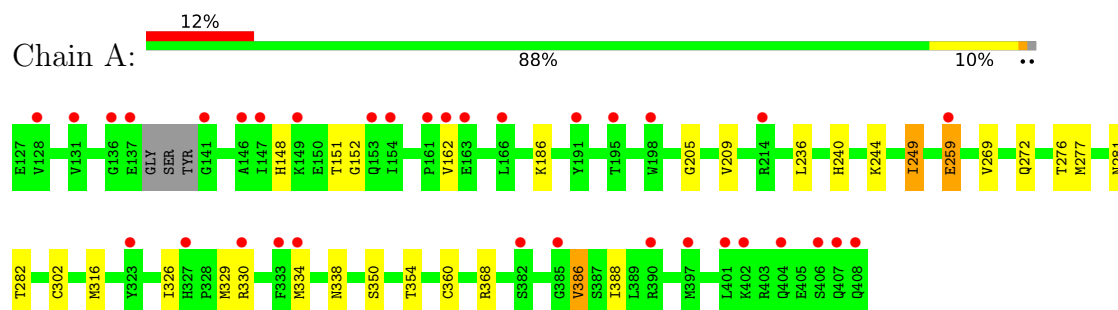


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	63	Total 63	O 63	0	0
3	B	18	Total 18	O 18	0	0

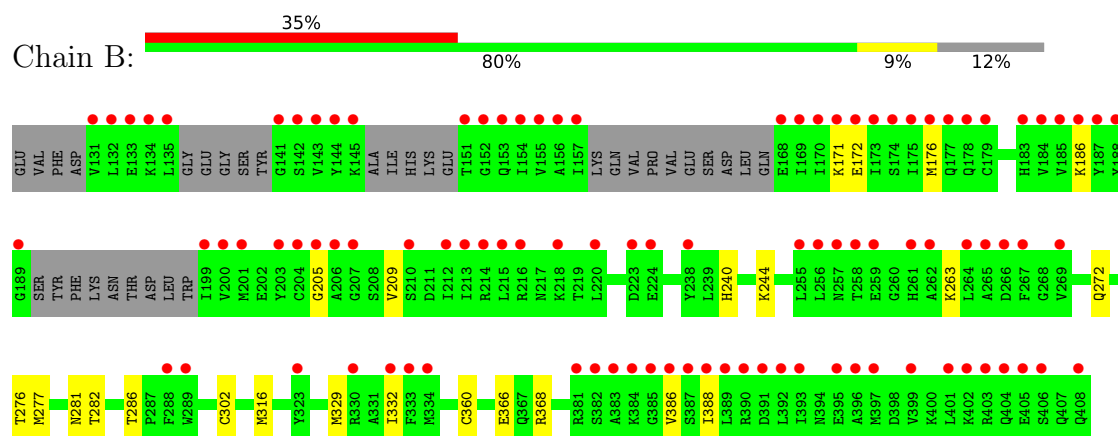
3 Residue-property plots [i](#)

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/threonine-protein kinase 4 37kDa subunit



- Molecule 1: Serine/threonine-protein kinase 4 37kDa subunit



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	111.41Å 111.41Å 170.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	93.29 – 2.12 93.29 – 2.12	Depositor EDS
% Data completeness (in resolution range)	85.8 (93.29-2.12) 85.8 (93.29-2.12)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.54 (at 2.12Å)	Xtriage
Refinement program	BUSTER 2.11.8	Depositor
R, R_{free}	0.243 , 0.248 0.232 , 0.244	Depositor DCC
R_{free} test set	2753 reflections (5.23%)	wwPDB-VP
Wilson B-factor (Å ²)	50.6	Xtriage
Anisotropy	0.023	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 46.0	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	4369	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.24% 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: 5BS, TPO

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	0.79	0/2291	1.05	3/3097 (0.1%)
1	B	0.72	0/1997	1.06	2/2692 (0.1%)
All	All	0.76	0/4288	1.05	5/5789 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	205	GLY	N-CA-C	6.45	120.70	112.83
1	A	205	GLY	N-CA-C	6.24	120.44	112.83
1	A	152	GLY	CA-C-N	5.56	128.65	120.82
1	A	152	GLY	C-N-CA	5.56	128.65	120.82
1	B	286	THR	CB-CA-C	5.34	116.29	110.15

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	2252	0	2294	17	0
1	B	1980	0	2018	11	0
2	A	28	0	0	0	0
2	B	28	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	63	0	0	0	0
3	B	18	0	0	0	0
All	All	4369	0	4312	26	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 (26) 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:329:MET:HE1	1:B:329:MET:HE1	1.61	0.81
1:A:244:LYS:NZ	1:A:272:GLN:HE22	1.83	0.77
1:A:244:LYS:HZ1	1:A:272:GLN:HE22	1.31	0.77
1:B:244:LYS:NZ	1:B:272:GLN:HE22	1.85	0.74
1:B:244:LYS:HZ1	1:B:272:GLN:HE22	1.38	0.72
1:B:209:VAL:HG11	1:B:316:MET:HE2	1.78	0.65
1:A:209:VAL:HG11	1:A:316:MET:HE2	1.83	0.60
1:A:244:LYS:HZ1	1:A:272:GLN:NE2	2.01	0.58
1:A:326:ILE:HD12	1:A:330[A]:ARG:HG2	1.86	0.58
1:A:360:CYS:O	1:A:368:ARG:HD2	2.05	0.56
1:B:360:CYS:O	1:B:368:ARG:HD2	2.05	0.56
1:B:244:LYS:HZ1	1:B:272:GLN:NE2	2.06	0.52
1:A:329:MET:CE	1:B:329:MET:HE1	2.36	0.52
1:A:350:SER:O	1:A:354:THR:HG23	2.10	0.50
1:A:148:HIS:HD2	1:A:151:THR:H	1.59	0.50
1:A:236:LEU:HD21	1:A:249[A]:ILE:HD11	1.94	0.49
1:B:172:GLU:O	1:B:176:MET:HG3	2.14	0.48
1:A:334:MET:HE2	1:A:338:ASN:HD21	1.77	0.47
1:A:277:MET:HA	1:A:277:MET:HE2	1.95	0.47
1:A:329:MET:HE1	1:B:329:MET:CE	2.40	0.47
1:B:277:MET:HE2	1:B:277:MET:HA	1.95	0.47
1:A:259:GLU:O	1:A:386:VAL:HG13	2.19	0.43
1:A:240:HIS:CG	1:A:302:CYS:HB3	2.55	0.42
1:A:236:LEU:HD21	1:A:249[A]:ILE:CD1	2.50	0.41
1:B:240:HIS:CG	1:B:302:CYS:HB3	2.55	0.41
2:B:501:5BS:N3	2:B:501:5BS:CAH	2.85	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	279/282 (99%)	268 (96%)	11 (4%)	0	100	100
1	B	239/282 (85%)	231 (97%)	8 (3%)	0	100	100
All	All	518/564 (92%)	499 (96%)	19 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	248/244 (102%)	238 (96%)	10 (4%)	28	28
1	B	216/244 (88%)	208 (96%)	8 (4%)	30	31
All	All	464/488 (95%)	446 (96%)	18 (4%)	32	29

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	162	VAL
1	A	186	LYS
1	A	249[A]	ILE
1	A	249[B]	ILE
1	A	259	GLU
1	A	269[A]	VAL
1	A	269[B]	VAL
1	A	281	ASN

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Mol	Chain	Res	Type
1	A	386	VAL
1	A	388	ILE
1	B	171	LYS
1	B	186	LYS
1	B	263	LYS
1	B	281	ASN
1	B	332	ILE
1	B	366	GLU
1	B	386	VAL
1	B	388	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	148	HIS
1	A	153	GLN
1	A	167	GLN
1	A	177	GLN
1	A	194	ASN
1	A	272	GLN
1	A	296	GLN
1	A	327	HIS
1	A	338	ASN
1	A	404	GLN
1	B	272	GLN
1	B	296	GLN
1	B	327	HIS
1	B	404	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	TPO	A	276	1	8,10,11	1.00	0	10,14,16	1.60	3 (30%)
1	TPO	B	282	1	8,10,11	1.10	1 (12%)	10,14,16	1.71	3 (30%)
1	TPO	A	282	1	8,10,11	1.41	1 (12%)	10,14,16	1.70	3 (30%)
1	TPO	B	276	1	8,10,11	0.87	0	10,14,16	1.77	4 (40%)

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
1	TPO	A	276	1	-	1/9/11/13	-
1	TPO	B	282	1	-	0/9/11/13	-
1	TPO	A	282	1	-	0/9/11/13	-
1	TPO	B	276	1	-	3/9/11/13	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	282	TPO	P-OG1	-3.40	1.53	1.59
1	B	282	TPO	P-OG1	-2.67	1.54	1.59

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	282	TPO	CG2-CB-CA	-3.31	106.81	113.26
1	A	282	TPO	CG2-CB-CA	-3.19	107.04	113.26
1	B	282	TPO	O2P-P-OG1	3.07	117.80	105.85
1	B	276	TPO	P-OG1-CB	-2.87	115.53	123.33
1	A	282	TPO	O3P-P-OG1	2.86	117.00	105.85
1	B	276	TPO	CG2-CB-CA	-2.82	107.77	113.26
1	B	276	TPO	O3P-P-OG1	2.74	116.53	105.85
1	A	276	TPO	P-OG1-CB	-2.64	116.16	123.33
1	A	276	TPO	CG2-CB-CA	-2.55	108.29	113.26
1	A	282	TPO	P-OG1-CB	-2.41	116.77	123.33
1	A	276	TPO	O-C-CA	-2.29	118.89	124.77
1	B	276	TPO	O-C-CA	-2.11	119.34	124.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	282	TPO	P-OG1-CB	-2.10	117.62	123.33

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	276	TPO	O-C-CA-CB
1	B	276	TPO	O-C-CA-CB
1	B	276	TPO	N-CA-CB-CG2
1	B	276	TPO	CB-OG1-P-O1P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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	5BS	A	501	-	28,31,31	0.35	0	35,47,47	2.28	2 (5%)
2	5BS	B	501	-	28,31,31	0.36	0	35,47,47	2.24	3 (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	5BS	A	501	-	-	0/10/10/10	0/3/4/4
2	5BS	B	501	-	-	0/10/10/10	0/3/4/4

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	5BS	C5-C4-NBA	12.85	128.41	120.14
2	B	501	5BS	C5-C4-NBA	12.60	128.25	120.14
2	B	501	5BS	C5-C4-N3	-2.58	119.23	123.32
2	A	501	5BS	C5-C4-N3	-2.58	119.23	123.32
2	B	501	5BS	C6-C5-NAZ	-2.02	115.70	118.99

There are no chirality outliers.

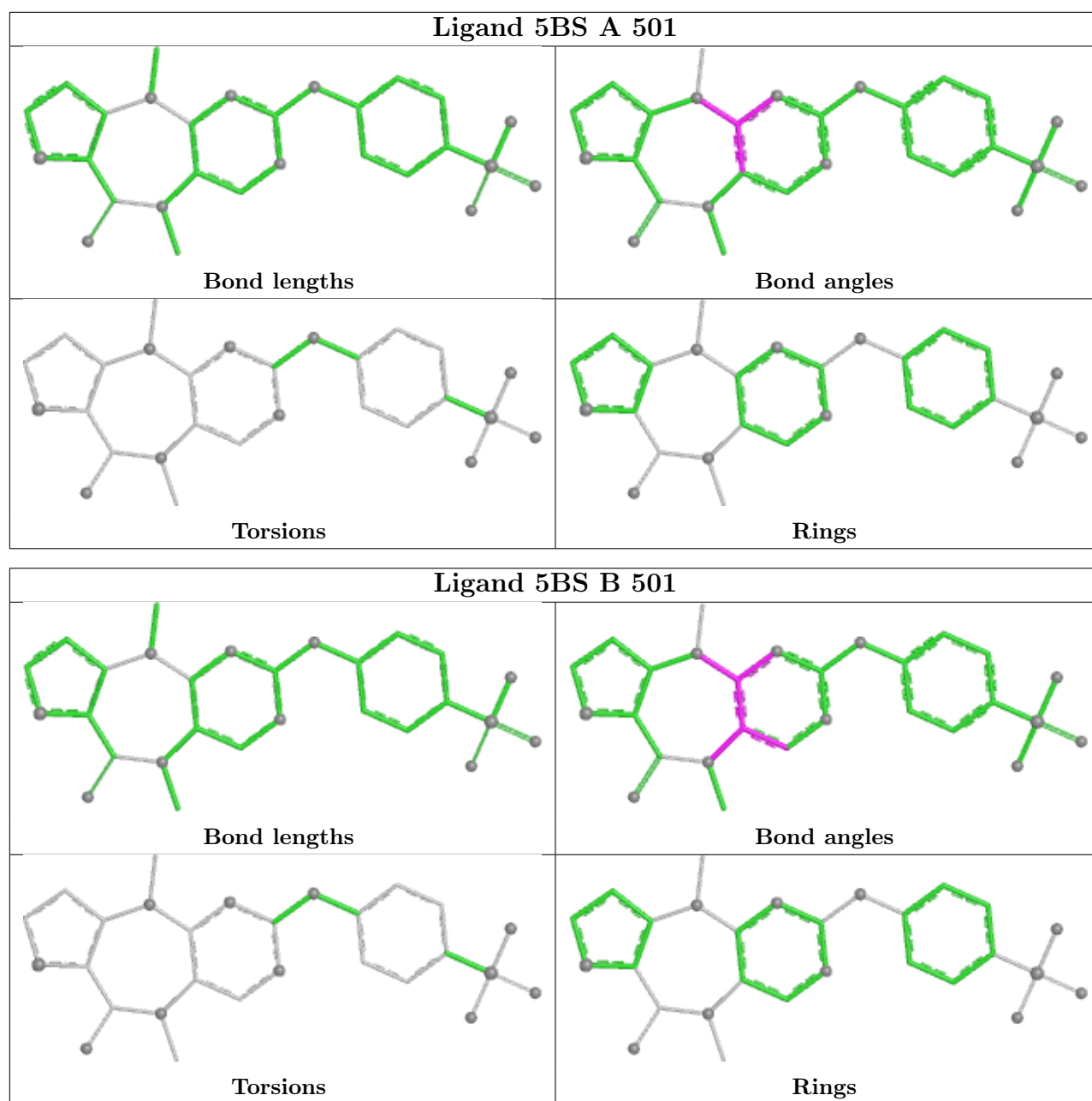
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	5BS	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	277/282 (98%)	0.75	34 (12%) 8 9	22, 48, 75, 104	7 (2%)
1	B	247/282 (87%)	2.09	98 (39%) 1 1	42, 63, 129, 144	3 (1%)
All	All	524/564 (92%)	1.38	132 (25%) 1 2	22, 54, 117, 144	10 (1%)

All (132) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	169	ILE	9.6
1	B	157	ILE	9.2
1	B	131	VAL	8.6
1	B	170	ILE	8.6
1	B	132	LEU	8.5
1	B	145	LYS	7.7
1	B	135	LEU	7.6
1	A	162	VAL	7.3
1	B	155	VAL	7.3
1	B	142	SER	5.4
1	B	156	ALA	5.3
1	B	392	LEU	5.3
1	B	189	GLY	5.3
1	B	200	VAL	5.2
1	B	154	ILE	5.1
1	B	144	TYR	5.1
1	B	168	GLU	5.0
1	B	223	ASP	4.8
1	B	399	VAL	4.7
1	B	141	GLY	4.7
1	B	199	ILE	4.6
1	B	397[A]	MET	4.6
1	A	141	GLY	4.6
1	B	215	LEU	4.6

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Mol	Chain	Res	Type	RSRZ
1	B	214	ARG	4.5
1	B	401	LEU	4.5
1	B	382	SER	4.4
1	B	396	ALA	4.2
1	B	151	THR	4.2
1	B	143	VAL	4.2
1	B	152	GLY	4.2
1	B	185	VAL	4.1
1	B	187	TYR	4.0
1	B	334	MET	4.0
1	B	203	TYR	4.0
1	B	134	LYS	3.9
1	B	402	LYS	3.9
1	B	388	ILE	3.8
1	B	390	ARG	3.8
1	B	385	GLY	3.8
1	B	188	TYR	3.6
1	B	387	SER	3.6
1	B	332	ILE	3.5
1	B	172	GLU	3.5
1	A	161	PRO	3.5
1	B	171	LYS	3.5
1	A	408	GLN	3.5
1	B	173	ILE	3.4
1	B	175	ILE	3.4
1	B	408	GLN	3.4
1	A	214	ARG	3.3
1	B	204	CYS	3.3
1	B	258	THR	3.3
1	B	205	GLY	3.3
1	B	406	SER	3.3
1	B	174	SER	3.2
1	B	179	CYS	3.2
1	B	255[A]	LEU	3.2
1	A	334	MET	3.2
1	A	146	ALA	3.2
1	B	206	ALA	3.1
1	B	395	GLU	3.1
1	B	333	PHE	3.1
1	B	259	GLU	3.1
1	B	261	HIS	3.1
1	B	393	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	264	LEU	3.0
1	A	137	GLU	2.9
1	B	133	GLU	2.9
1	A	333	PHE	2.8
1	B	186	LYS	2.8
1	A	136	GLY	2.8
1	B	218	LYS	2.8
1	A	147	ILE	2.8
1	B	257	ASN	2.7
1	B	389	LEU	2.7
1	A	382	SER	2.7
1	B	391	ASP	2.7
1	A	385	GLY	2.7
1	A	128	VAL	2.7
1	A	131	VAL	2.6
1	B	238	TYR	2.6
1	B	403	ARG	2.6
1	B	288	PHE	2.6
1	A	397[A]	MET	2.6
1	A	330[A]	ARG	2.6
1	A	401	LEU	2.6
1	B	256	LEU	2.6
1	B	207	GLY	2.5
1	B	289	TRP	2.5
1	A	195	THR	2.5
1	A	198	TRP	2.5
1	A	407	GLN	2.5
1	A	406	SER	2.5
1	B	176	MET	2.5
1	A	327	HIS	2.4
1	B	330	ARG	2.4
1	B	381	ARG	2.4
1	B	213	ILE	2.4
1	B	220	LEU	2.4
1	B	178	GLN	2.4
1	B	384	LYS	2.3
1	B	405	GLU	2.3
1	B	383	ALA	2.3
1	A	259	GLU	2.3
1	B	262	ALA	2.3
1	B	265	ALA	2.3
1	B	183	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	390	ARG	2.2
1	B	216	ARG	2.2
1	A	149	LYS	2.2
1	B	184	VAL	2.2
1	A	153	GLN	2.2
1	B	323	TYR	2.2
1	B	201	MET	2.2
1	B	153	GLN	2.2
1	B	404	GLN	2.2
1	A	166	LEU	2.2
1	A	154	ILE	2.1
1	A	402	LYS	2.1
1	B	266	ASP	2.1
1	B	269	VAL	2.1
1	A	163	GLU	2.1
1	A	323	TYR	2.1
1	B	212	ILE	2.1
1	B	267	PHE	2.1
1	A	404	GLN	2.1
1	B	177	GLN	2.1
1	B	386	VAL	2.1
1	A	191	TYR	2.0
1	B	224	GLU	2.0
1	B	210	SER	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	TPO	B	276	11/12	0.75	0.15	61,68,102,105	0
1	TPO	A	276	11/12	0.88	0.11	56,60,89,96	0
1	TPO	B	282	11/12	0.95	0.09	56,57,66,67	0
1	TPO	A	282	11/12	0.97	0.07	39,45,48,50	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

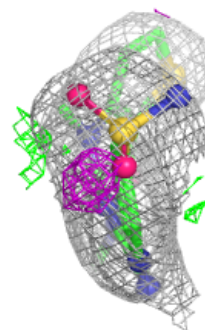
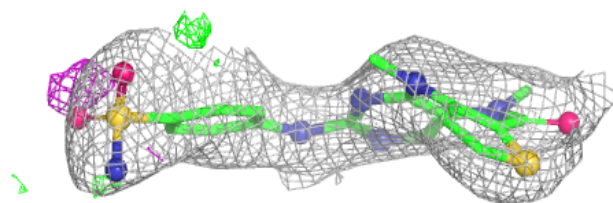
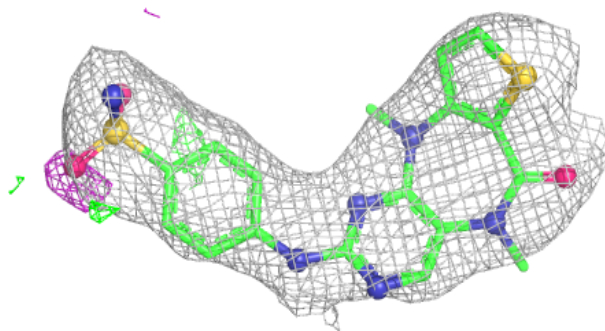
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	5BS	B	501	28/28	0.87	0.17	108,109,113,113	0
2	5BS	A	501	28/28	0.97	0.08	43,46,58,58	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.

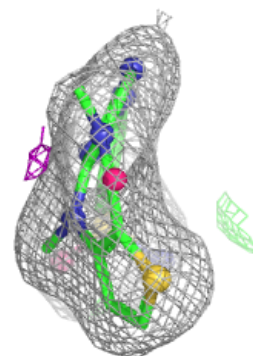
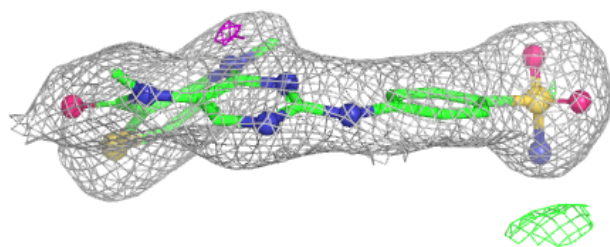
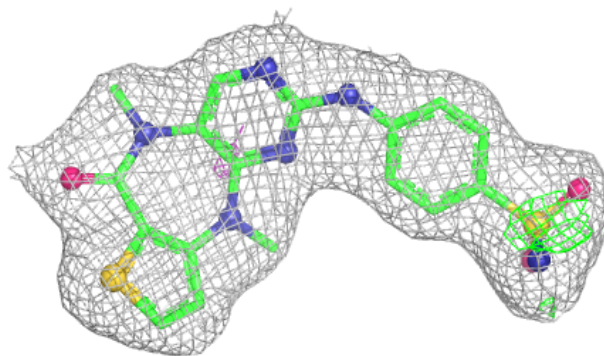
Electron density around 5BS B 501:

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 5BS A 501:

$2mF_o-DF_c$ (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.