



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:04 PM UTC

PDB ID : 4URL / pdb_00004url
Title : Crystal Structure of Staph ParE43kDa in complex with KBD
Authors : Lu, J.; Patel, S.; Sharma, N.; Soisson, S.; Kishii, R.; Takei, M.; Fukuda, Y.;
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Deposited on : 2014-06-30
Resolution : 2.29 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

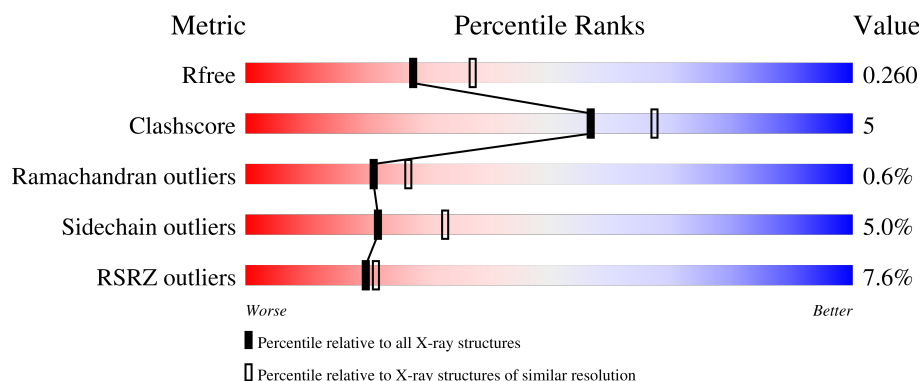
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.29 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (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 $\leq 5\%$. 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	406	5% 77% 12% 10%
1	B	406	8% 71% 17% 11%

2 Entry composition [i](#)

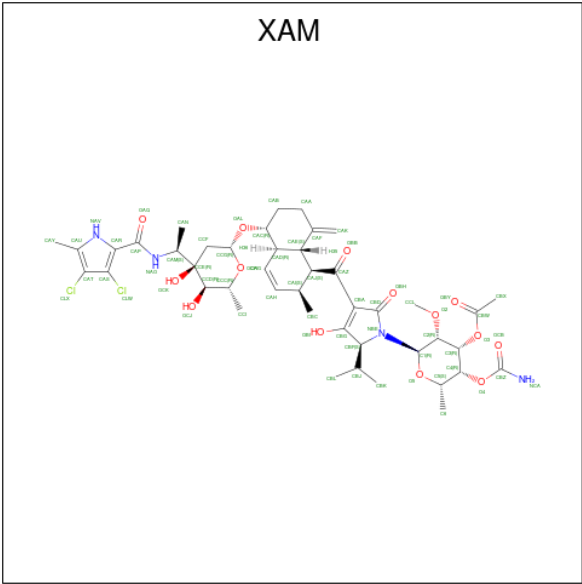
There are 3 unique types of molecules in this entry. The entry contains 5748 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 DNA TOPOISOMERASE IV, B SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	364	Total	C	N	O	S	0	0	0
			2755	1718	485	550	2			
1	B	363	Total	C	N	O	S	0	1	0
			2759	1729	482	545	3			

- Molecule 2 is (1R,4aS,5S,6S,8aR)-5-{[(5S)-1-(3-O-acetyl-4-O-carbamoyl-6-deoxy-2-O-methyl-alpha-L-talopyranosyl)-4-hydroxy-2-oxo-5-(propan-2-yl)-2,5-dihydro-1H-pyrrol-3-yl]carbonyl}-6-methyl-4-methylidene-1,2,3,4,4a,5,6,8a-octahydronaphthalen-1-yl 2,6-dideoxy-3-C-[(1S)-1-{[(3,4-dichloro-5-methyl-1H-pyrrol-2-yl)carbonyl]amino}ethyl]-beta-D-ribo-hexopyranoside (CCD ID: XAM) (formula: C₄₄H₆₀Cl₂N₄O₁₄).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	0	0
			64	44	2	4	14		
2	B	1	Total	C	Cl	N	O	0	0
			64	44	2	4	14		

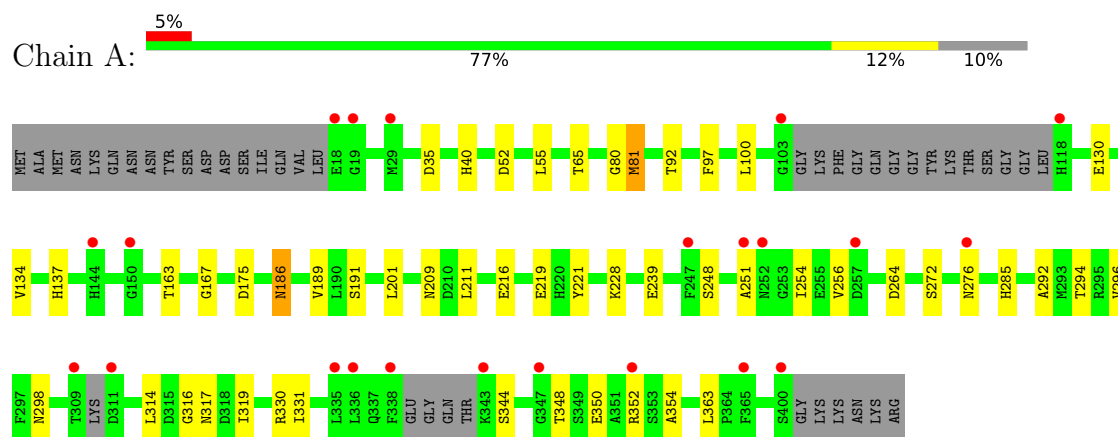
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	52	Total 52	O 52	0	0
3	B	54	Total 54	O 54	0	0

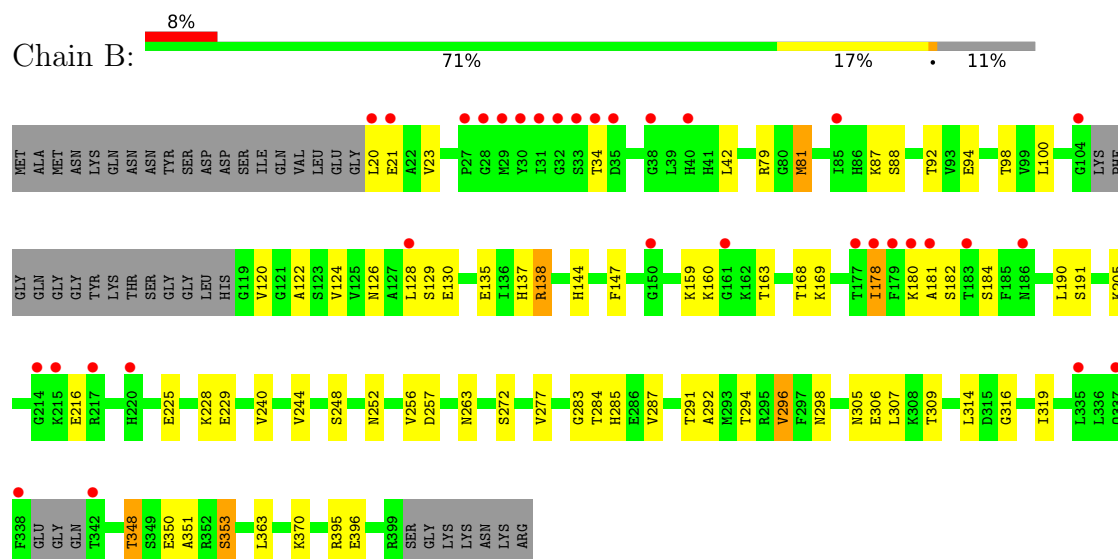
3 Residue-property plots [i](#)

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: DNA TOPOISOMERASE IV, B SUBUNIT



• Molecule 1: DNA TOPOISOMERASE IV, B SUBUNIT



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	54.45Å 136.81Å 69.19Å 90.00° 111.92° 90.00°	Depositor
Resolution (Å)	49.73 – 2.29 49.73 – 2.29	Depositor EDS
% Data completeness (in resolution range)	98.8 (49.73-2.29) 99.2 (49.73-2.29)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.22 (at 2.29Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, R_{free}	0.217 , 0.252 (Not available) , 0.260	Depositor DCC
R_{free} test set	1311 reflections (3.14%)	wwPDB-VP
Wilson B-factor (Å ²)	44.1	Xtriage
Anisotropy	0.140	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 42.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.027 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5748	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.54% 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: XAM

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	0.88	1/2796 (0.0%)	1.40	12/3778 (0.3%)
1	B	0.90	1/2804 (0.0%)	1.42	25/3785 (0.7%)
All	All	0.89	2/5600 (0.0%)	1.41	37/7563 (0.5%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	81	MET	SD-CE	-5.98	1.64	1.79
1	B	81	MET	SD-CE	-5.12	1.66	1.79

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	316	GLY	CA-C-N	7.20	130.27	120.54
1	A	316	GLY	C-N-CA	7.20	130.27	120.54
1	B	190	LEU	CA-C-N	6.82	129.75	120.54
1	B	190	LEU	C-N-CA	6.82	129.75	120.54
1	A	317	ASN	CA-CB-CG	6.64	119.25	112.60
1	B	88	SER	N-CA-C	-6.40	101.48	110.50
1	B	306	GLU	N-CA-C	-6.17	104.82	112.90
1	B	130	GLU	N-CA-C	-6.01	104.64	111.07
1	B	283	GLY	CA-C-N	5.99	128.30	120.28
1	B	283	GLY	C-N-CA	5.99	128.30	120.28
1	B	277	VAL	CA-C-N	5.90	129.14	120.82
1	B	277	VAL	C-N-CA	5.90	129.14	120.82
1	B	178	ILE	N-CA-C	-5.89	107.17	112.12
1	A	228	LYS	N-CA-C	-5.88	104.78	111.07
1	B	87	LYS	N-CA-C	-5.83	104.83	111.07
1	A	35	ASP	CA-CB-CG	5.78	118.38	112.60
1	A	175	ASP	CA-C-N	5.75	127.98	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	175	ASP	C-N-CA	5.75	127.98	120.28
1	B	191	SER	CA-C-N	5.65	127.78	120.44
1	B	191	SER	C-N-CA	5.65	127.78	120.44
1	A	130	GLU	N-CA-C	-5.65	105.20	111.36
1	B	42	LEU	CA-C-N	5.50	128.00	120.46
1	B	42	LEU	C-N-CA	5.50	128.00	120.46
1	A	80	GLY	N-CA-C	-5.49	105.84	112.48
1	B	122	ALA	CA-C-N	5.48	127.62	120.28
1	B	122	ALA	C-N-CA	5.48	127.62	120.28
1	B	129	SER	CA-C-N	5.38	127.43	120.44
1	B	129	SER	C-N-CA	5.38	127.43	120.44
1	B	180	LYS	CA-C-N	5.37	131.80	121.54
1	B	180	LYS	C-N-CA	5.37	131.80	121.54
1	B	309	THR	CA-C-N	5.03	127.95	120.31
1	B	309	THR	C-N-CA	5.03	127.95	120.31
1	A	352	ARG	CA-C-N	5.01	127.40	120.29
1	A	352	ARG	C-N-CA	5.01	127.40	120.29
1	B	395	ARG	CA-C-N	5.01	126.99	120.28
1	B	395	ARG	C-N-CA	5.01	126.99	120.28
1	A	167	GLY	N-CA-C	5.00	117.48	110.38

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2755	0	2626	23	0
1	B	2759	0	2671	28	0
2	A	64	0	59	4	0
2	B	64	0	59	2	0
3	A	52	0	0	0	0
3	B	54	0	0	0	0
All	All	5748	0	5415	51	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 5.

All (51) 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:B:94:GLU:O	1:B:98:THR:HB	1.62	0.99
1:A:298:ASN:HD21	1:A:314:LEU:H	1.15	0.93
1:A:296:VAL:HG11	1:A:363:LEU:HD23	1.64	0.79
1:A:292:ALA:O	1:A:296:VAL:HG12	1.86	0.76
1:B:298:ASN:HD21	1:B:314:LEU:H	1.34	0.73
1:A:40:HIS:CE1	1:A:186:ASN:H	2.10	0.69
1:B:284:THR:HG21	1:B:348:THR:O	1.95	0.67
1:B:252:ASN:HD21	1:B:353:SER:HB2	1.60	0.66
1:A:186:ASN:HD22	1:A:189:VAL:H	1.44	0.65
1:B:81:MET:HE3	1:B:168:THR:HG21	1.77	0.65
1:A:251:ALA:HB3	1:A:354:ALA:HA	1.80	0.64
1:B:128:LEU:HD22	1:B:178:ILE:HG21	1.80	0.63
1:A:92:THR:HG23	2:A:2000:XAM:H30	1.81	0.62
1:A:40:HIS:HE1	1:A:186:ASN:H	1.48	0.59
1:B:296:VAL:HG22	1:B:363:LEU:HD23	1.85	0.59
1:A:65:THR:HG23	1:A:211:LEU:HD23	1.86	0.58
1:B:92:THR:HG23	2:B:2000:XAM:H30	1.85	0.57
1:B:292:ALA:O	1:B:296:VAL:HG13	2.06	0.56
1:A:52:ASP:HA	1:A:55:LEU:HD12	1.88	0.55
1:A:81:MET:HE2	2:A:2000:XAM:CLW	2.45	0.53
1:A:296:VAL:CG1	1:A:363:LEU:HD23	2.38	0.52
1:B:294:THR:HA	1:B:319:ILE:HD13	1.93	0.51
1:A:272:SER:HB2	1:A:285:HIS:NE2	2.27	0.50
1:A:254:ILE:HG12	1:A:331:ILE:HG12	1.93	0.50
1:A:186:ASN:ND2	1:A:189:VAL:H	2.10	0.49
1:A:92:THR:CG2	2:A:2000:XAM:H30	2.43	0.49
1:B:228:LYS:HG3	1:B:244:VAL:HB	1.93	0.49
1:B:144[B]:HIS:CD2	1:B:160:LYS:HG3	2.49	0.48
1:A:294:THR:HA	1:A:319:ILE:HD13	1.97	0.47
1:A:137:HIS:HD2	1:A:163:THR:OG1	1.98	0.46
1:B:137:HIS:HD2	1:B:163:THR:OG1	1.98	0.46
1:B:120:VAL:HB	1:B:124:VAL:HG21	1.97	0.46
1:B:135:GLU:HB2	1:B:169:LYS:HB3	1.98	0.46
1:B:20:LEU:HB2	1:B:21:GLU:H	1.53	0.45
1:A:81:MET:CE	2:A:2000:XAM:CLW	3.03	0.44
1:B:294:THR:HG21	1:B:316:GLY:HA2	1.99	0.44
1:B:23:VAL:HG21	1:B:124:VAL:HG22	2.00	0.43
1:B:298:ASN:HD21	1:B:314:LEU:N	2.10	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:126:ASN:HD21	1:B:147:PHE:HB2	1.83	0.43
1:B:240:VAL:HA	1:B:263:ASN:HA	2.01	0.43
1:B:20:LEU:HG	1:B:100:LEU:HB2	2.00	0.42
1:A:191:SER:HB2	1:A:221:TYR:OH	2.19	0.42
1:B:79:ARG:O	1:B:138:ARG:HD2	2.20	0.42
1:B:284:THR:HG23	1:B:351:ALA:HB3	2.00	0.42
1:B:81:MET:HE2	2:B:2000:XAM:CLW	2.57	0.42
1:B:287:VAL:O	1:B:291:THR:HG23	2.20	0.42
1:B:225:GLU:HB2	1:B:229:GLU:HG3	2.02	0.42
1:A:239:GLU:HB2	1:A:264:ASP:CG	2.45	0.41
1:B:272:SER:HB2	1:B:285:HIS:NE2	2.35	0.41
1:A:52:ASP:O	1:A:55:LEU:HB2	2.21	0.40
1:A:81:MET:HE1	1:A:97:PHE:CE2	2.56	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	356/406 (88%)	341 (96%)	13 (4%)	2 (1%)	21	27
1	B	358/406 (88%)	343 (96%)	13 (4%)	2 (1%)	21	27
All	All	714/812 (88%)	684 (96%)	26 (4%)	4 (1%)	21	27

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	181	ALA
1	A	348	THR
1	A	344	SER
1	B	348	THR

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	287/343 (84%)	275 (96%)	12 (4%)	26	40
1	B	289/343 (84%)	272 (94%)	17 (6%)	18	26
All	All	576/686 (84%)	547 (95%)	29 (5%)	22	33

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	100	LEU
1	A	134	VAL
1	A	186	ASN
1	A	201	LEU
1	A	209	ASN
1	A	216	GLU
1	A	219	GLU
1	A	248	SER
1	A	256	VAL
1	A	276	ASN
1	A	330	ARG
1	A	350	GLU
1	B	34	THR
1	B	138	ARG
1	B	159	LYS
1	B	182	SER
1	B	184	SER
1	B	205	LYS
1	B	216	GLU
1	B	248	SER
1	B	256	VAL
1	B	257	ASP
1	B	296	VAL
1	B	305	ASN
1	B	307	LEU
1	B	350	GLU
1	B	353	SER

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Mol	Chain	Res	Type
1	B	370	LYS
1	B	396	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	40	HIS
1	A	101	HIS
1	A	137	HIS
1	A	144	HIS
1	A	186	ASN
1	A	195	GLN
1	A	263	ASN
1	A	298	ASN
1	A	317	ASN
1	B	126	ASN
1	B	137	HIS
1	B	195	GLN
1	B	252	ASN
1	B	298	ASN
1	B	386	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](#)

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	XAM	A	2000	-	68,69,69	1.35	7 (10%)	81,106,106	1.38	9 (11%)
2	XAM	B	2000	-	68,69,69	1.44	9 (13%)	81,106,106	1.27	5 (6%)

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	XAM	A	2000	-	-	6/43/133/133	0/6/6/6
2	XAM	B	2000	-	-	2/43/133/133	0/6/6/6

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2000	XAM	OBB-CAZ	7.68	1.35	1.22
2	A	2000	XAM	OBB-CAZ	7.42	1.35	1.22
2	B	2000	XAM	C1-NBE	3.77	1.52	1.44
2	A	2000	XAM	CCE-CCD	3.39	1.62	1.53
2	A	2000	XAM	C1-NBE	3.27	1.51	1.44
2	B	2000	XAM	O4-CBZ	3.25	1.41	1.35
2	B	2000	XAM	CBA-CAZ	-3.20	1.37	1.47
2	B	2000	XAM	OBI-CBG	-3.06	1.22	1.32
2	A	2000	XAM	OBI-CBG	-3.04	1.22	1.32
2	A	2000	XAM	CBA-CAZ	-2.86	1.38	1.47
2	B	2000	XAM	CBF-CBG	2.74	1.57	1.50
2	A	2000	XAM	O4-CBZ	2.26	1.40	1.35
2	B	2000	XAM	CCE-CCD	2.17	1.59	1.53
2	B	2000	XAM	CAT-CAU	2.17	1.40	1.36
2	B	2000	XAM	CBD-NBE	2.10	1.43	1.37
2	A	2000	XAM	CBD-NBE	2.08	1.43	1.37

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2000	XAM	CAJ-CAE-CAF	7.24	123.42	115.61
2	A	2000	XAM	CAJ-CAE-CAF	5.28	121.31	115.61
2	A	2000	XAM	C4-O4-CBZ	5.22	124.60	117.03
2	A	2000	XAM	C2-C1-NBE	3.54	117.70	113.50
2	B	2000	XAM	C4-O4-CBZ	3.44	122.01	117.03
2	A	2000	XAM	OBB-CAZ-CBA	-2.56	116.41	119.67
2	A	2000	XAM	CAE-CAD-CAG	2.37	112.08	108.17
2	A	2000	XAM	O4-CBZ-NCA	2.33	114.53	110.92
2	B	2000	XAM	OBB-CAZ-CBA	-2.20	116.86	119.67
2	A	2000	XAM	CAE-CAJ-CAI	2.18	115.28	111.36
2	A	2000	XAM	CAS-CAT-CAU	-2.17	105.58	109.06
2	A	2000	XAM	O4-CBZ-OCB	-2.13	119.80	123.06
2	B	2000	XAM	CAE-CAJ-CAI	2.07	115.08	111.36
2	B	2000	XAM	CAE-CAD-CAG	2.04	111.53	108.17

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	2000	XAM	NBE-CBF-CBJ-CBL
2	A	2000	XAM	NBE-CBF-CBJ-CBK
2	A	2000	XAM	OCB-CBZ-O4-C4
2	A	2000	XAM	NCA-CBZ-O4-C4
2	A	2000	XAM	CBG-CBF-CBJ-CBK
2	B	2000	XAM	O5-C1-NBE-CBF
2	A	2000	XAM	CBG-CBF-CBJ-CBL
2	B	2000	XAM	C2-C1-NBE-CBF

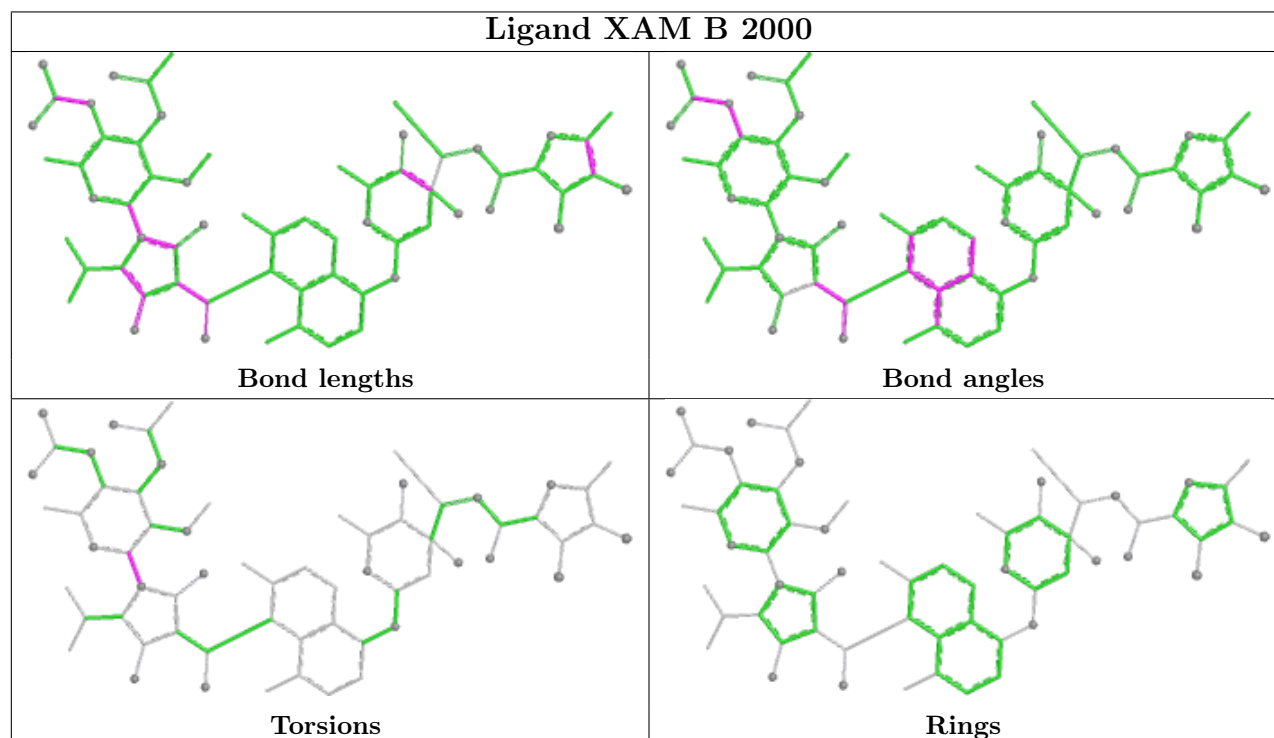
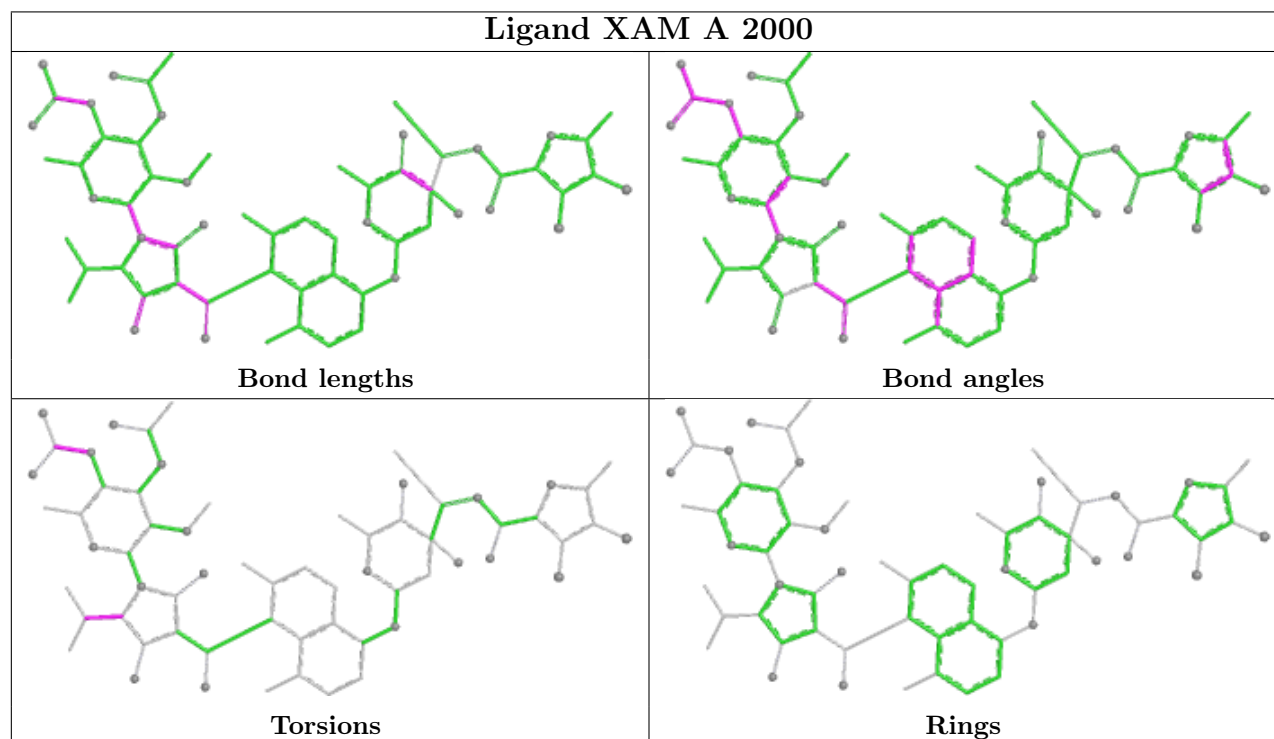
There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	2000	XAM	4	0
2	B	2000	XAM	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the

average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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	364/406 (89%)	0.55	22 (6%) 27 29	36, 52, 77, 94	0
1	B	363/406 (89%)	0.48	33 (9%) 15 16	26, 50, 78, 96	1 (0%)
All	All	727/812 (89%)	0.52	55 (7%) 20 21	26, 51, 78, 96	1 (0%)

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	20	LEU	4.7
1	B	29	MET	4.0
1	A	103	GLY	3.8
1	B	35	ASP	3.8
1	B	342	THR	3.5
1	A	118	HIS	3.5
1	A	247	PHE	3.5
1	B	179	PHE	3.5
1	B	180	LYS	3.4
1	A	336	LEU	3.4
1	B	338	PHE	3.2
1	B	214	GLY	3.2
1	A	29	MET	3.0
1	B	183	THR	3.0
1	B	33	SER	3.0
1	B	337	GLN	3.0
1	A	335	LEU	2.9
1	B	32	GLY	2.8
1	B	178	ILE	2.7
1	A	144	HIS	2.7
1	B	181	ALA	2.7
1	A	343	LYS	2.6
1	A	311	ASP	2.6
1	B	150	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	31	ILE	2.5
1	A	252	ASN	2.4
1	A	276	ASN	2.4
1	A	150	GLY	2.4
1	A	18	GLU	2.4
1	B	85	ILE	2.4
1	B	128	LEU	2.4
1	A	19	GLY	2.3
1	B	177	THR	2.3
1	A	338	PHE	2.3
1	B	161	GLY	2.3
1	A	309	THR	2.3
1	A	257	ASP	2.3
1	B	104	GLY	2.3
1	A	251	ALA	2.3
1	A	400	SER	2.3
1	A	347	GLY	2.2
1	B	335	LEU	2.2
1	A	365	PHE	2.2
1	A	352	ARG	2.2
1	B	28	GLY	2.2
1	B	220	HIS	2.1
1	B	34	THR	2.1
1	B	186	ASN	2.1
1	B	215	LYS	2.1
1	B	30	TYR	2.1
1	B	27	PRO	2.1
1	B	217	ARG	2.1
1	B	21	GLU	2.1
1	B	38	GLY	2.1
1	B	40	HIS	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](#)

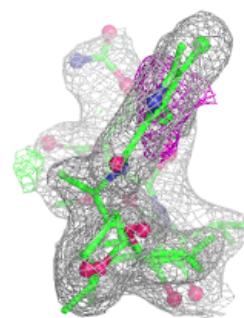
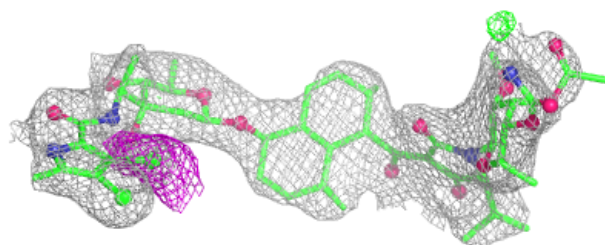
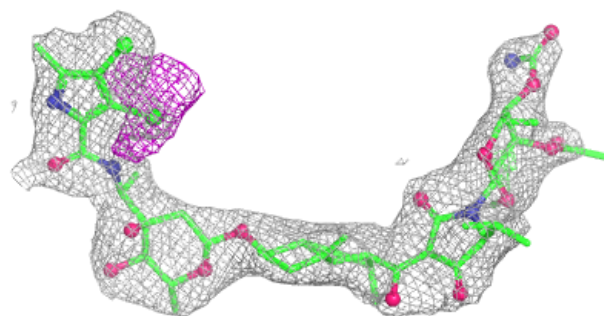
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists 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	XAM	A	2000	64/64	0.89	0.12	48,68,83,88	0
2	XAM	B	2000	64/64	0.90	0.12	40,61,85,90	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.

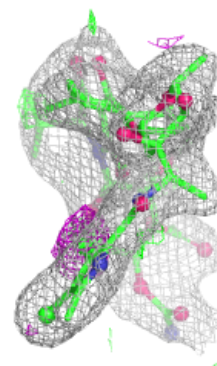
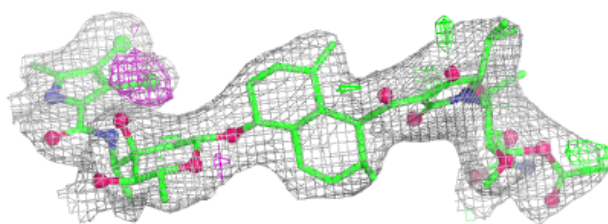
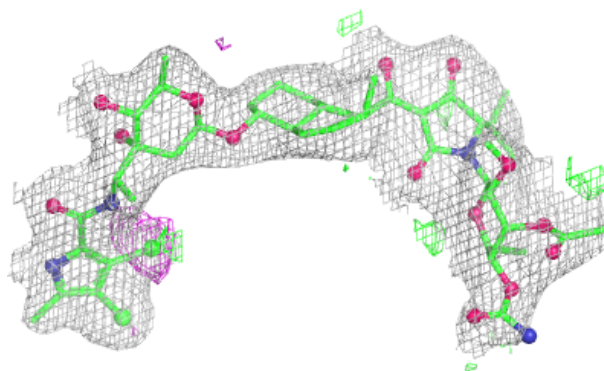
Electron density around XAM A 2000:

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 XAM B 2000:

$2mF_o-DF_c$ (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.