



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 06:02 PM UTC

PDB ID : 7T4U / pdb_00007t4u
Title : Crystal Structure of cGMP-dependent Protein Kinase
Authors : Zebisch, M.; Silvestre, L.; Fischmann, T.O.
Deposited on : 2021-12-10
Resolution : 1.99 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

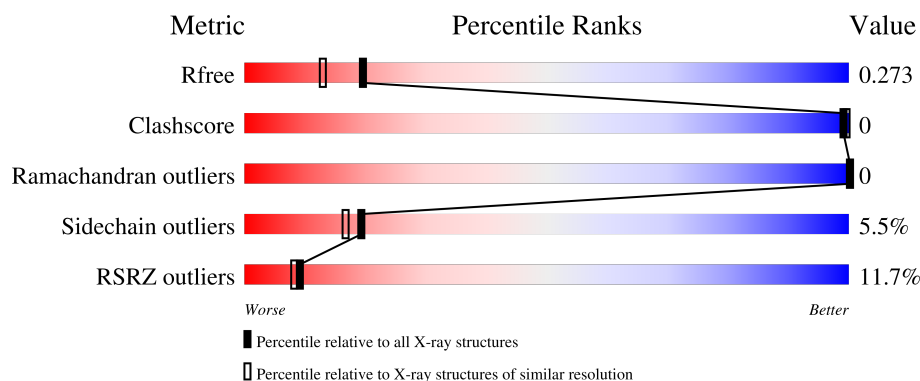
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.99 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	469	16% 93% 6%
1	B	469	7% 90% 8% .

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 7807 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.

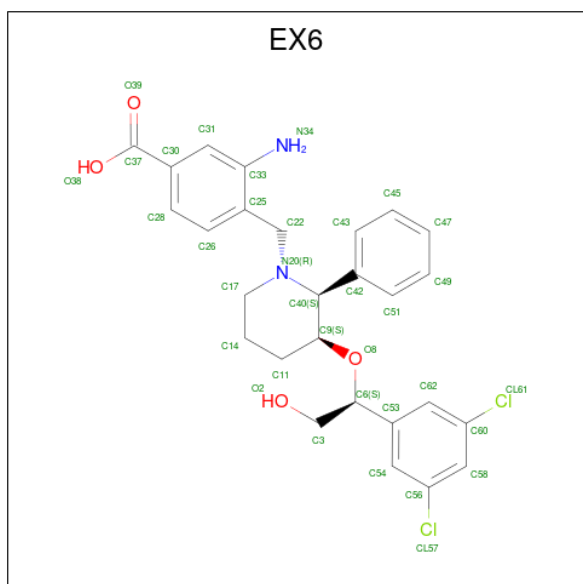
- Molecule 1 is a protein called cGMP-dependent protein kinase 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	467	Total	C	N	O	P	S	0	1	0
			3740	2392	623	710	1	14			
1	B	461	Total	C	N	O	P	S	0	0	0
			3690	2365	616	695	1	13			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	218	SER	-	expression tag	UNP Q13976
B	218	SER	-	expression tag	UNP Q13976

- Molecule 2 is 3-amino-4-((2S,3S)-3-[(1S)-1-(3,5-dichlorophenyl)-2-hydroxyethoxy]-2-phenylpiperidin-1-yl)methyl)benzoic acid (CCD ID: EX6) (formula: C₂₇H₂₈Cl₂N₂O₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 35	C 27	Cl 2	N 2	O 4	0	0
2	B	1	Total 35	C 27	Cl 2	N 2	O 4	0	0

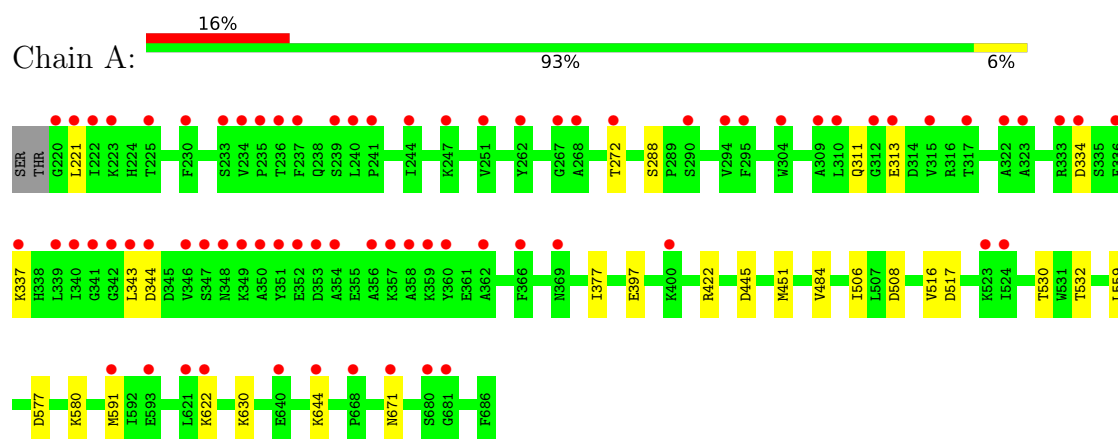
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	132	Total 132	O 132	0	0
3	B	175	Total 175	O 175	0	0

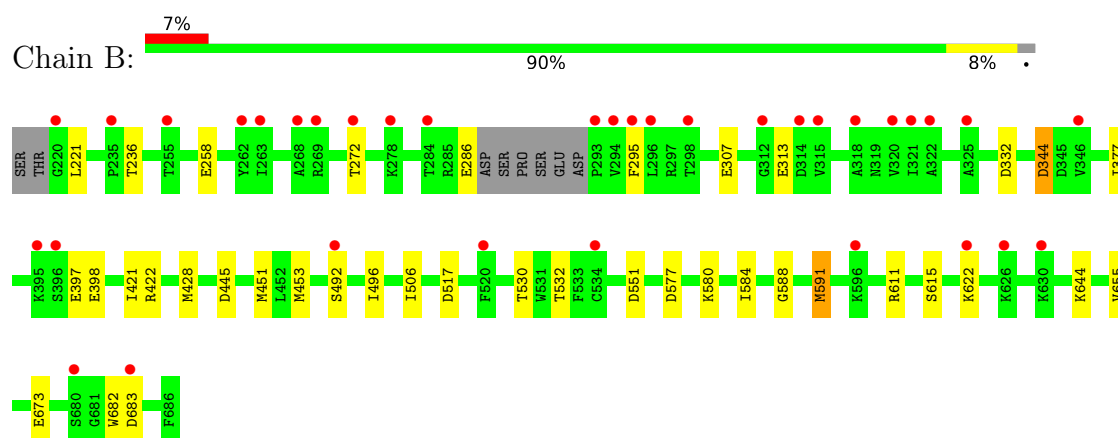
3 Residue-property plots

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: cGMP-dependent protein kinase 1



- Molecule 1: cGMP-dependent protein kinase 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	93.46Å 102.71Å 103.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.36 – 1.99 39.36 – 1.99	Depositor EDS
% Data completeness (in resolution range)	66.4 (39.36-1.99) 66.4 (39.36-1.99)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.76 (at 2.00Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.214 , 0.260 0.226 , 0.273	Depositor DCC
R_{free} test set	2244 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	32.6	Xtriage
Anisotropy	0.071	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 41.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.000 for -h,l,k	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7807	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.57% 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: TPO, EX6

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	0.91	1/3816 (0.0%)	1.12	5/5151 (0.1%)
1	B	0.89	1/3764 (0.0%)	1.15	11/5077 (0.2%)
All	All	0.90	2/7580 (0.0%)	1.13	16/10228 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	377	ILE	CG1-CD1	-6.97	1.24	1.51
1	A	377	ILE	CG1-CD1	-6.29	1.27	1.51

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	682	TRP	CA-C-N	7.79	133.17	120.63
1	B	682	TRP	C-N-CA	7.79	133.17	120.63
1	B	673	GLU	N-CA-C	-6.36	102.05	109.93
1	B	332	ASP	CA-CB-CG	6.28	118.88	112.60
1	B	344	ASP	CA-CB-CG	6.19	118.79	112.60
1	A	517	ASP	CA-CB-CG	5.76	118.36	112.60
1	A	577	ASP	CA-CB-CG	5.76	118.36	112.60
1	B	588	GLY	N-CA-C	5.66	121.19	112.81
1	A	445	ASP	CA-CB-CG	5.59	118.19	112.60
1	B	295	PHE	CA-CB-CG	5.51	119.31	113.80
1	B	445	ASP	CA-CB-CG	5.37	117.97	112.60
1	B	517	ASP	CA-CB-CG	5.19	117.79	112.60
1	B	398	GLU	N-CA-C	5.12	117.53	111.33
1	A	508	ASP	CA-CB-CG	5.12	117.72	112.60
1	A	516	VAL	N-CA-C	5.10	116.03	111.90
1	B	577	ASP	CA-CB-CG	5.09	117.69	112.60

There are no chirality outliers.

There are no planarity outliers.

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	3740	0	3680	1	0
1	B	3690	0	3645	3	0
2	A	35	0	0	0	0
2	B	35	0	0	0	0
3	A	132	0	0	0	0
3	B	175	0	0	0	0
All	All	7807	0	7325	4	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 0.

All (4) 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:428:MET:HE1	1:B:453:MET:HE2	1.85	0.59
1:B:496:ILE:HD12	1:B:551:ASP:O	2.17	0.44
1:A:484:VAL:HG22	1:A:559:LEU:HD21	2.00	0.43
1:B:591:MET:HE3	1:B:591:MET:HA	2.03	0.41

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	465/469 (99%)	455 (98%)	10 (2%)	0	100	100
1	B	456/469 (97%)	445 (98%)	11 (2%)	0	100	100
All	All	921/938 (98%)	900 (98%)	21 (2%)	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	402/403 (100%)	382 (95%)	20 (5%)	22	20
1	B	395/403 (98%)	371 (94%)	24 (6%)	17	14
All	All	797/806 (99%)	753 (94%)	44 (6%)	19	17

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	221	LEU
1	A	272	THR
1	A	288	SER
1	A	311	GLN
1	A	313	GLU
1	A	334	ASP
1	A	337	LYS
1	A	343	LEU
1	A	344	ASP
1	A	397	GLU
1	A	422	ARG
1	A	451	MET
1	A	506	ILE
1	A	530	THR
1	A	580	LYS
1	A	591	MET
1	A	622	LYS
1	A	630	LYS

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Mol	Chain	Res	Type
1	A	644	LYS
1	A	671	ASN
1	B	221	LEU
1	B	236	THR
1	B	258	GLU
1	B	272	THR
1	B	286	GLU
1	B	307	GLU
1	B	313	GLU
1	B	344	ASP
1	B	397	GLU
1	B	421	ILE
1	B	422	ARG
1	B	451	MET
1	B	492	SER
1	B	506	ILE
1	B	530	THR
1	B	580	LYS
1	B	584	ILE
1	B	591	MET
1	B	611	ARG
1	B	615	SER
1	B	622	LYS
1	B	644	LYS
1	B	655	VAL
1	B	683	ASP

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	432	HIS
1	A	679	ASN
1	B	311	GLN
1	B	432	HIS
1	B	679	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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	532	1	8,10,11	1.30	1 (12%)	10,14,16	1.29	3 (30%)
1	TPO	B	532	1	8,10,11	1.04	0	10,14,16	1.21	2 (20%)

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	532	1	-	0/9/11/13	-
1	TPO	B	532	1	-	1/9/11/13	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	532	TPO	P-OG1	-2.42	1.55	1.59

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	532	TPO	P-OG1-CB	-2.39	116.83	123.33
1	B	532	TPO	O-C-CA	-2.33	118.78	124.77
1	A	532	TPO	O-C-CA	-2.22	119.07	124.77
1	B	532	TPO	P-OG1-CB	-2.02	117.84	123.33
1	A	532	TPO	O3P-P-OG1	2.00	113.66	105.85

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	532	TPO	CB-OG1-P-O3P

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	EX6	B	9901	-	38,38,38	1.04	2 (5%)	45,53,53	1.07	3 (6%)
2	EX6	A	9901	-	38,38,38	0.95	1 (2%)	45,53,53	1.18	3 (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	EX6	B	9901	-	-	1/22/36/36	0/4/4/4
2	EX6	A	9901	-	-	2/22/36/36	0/4/4/4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	9901	EX6	C40-N20	4.06	1.51	1.47
2	A	9901	EX6	C40-N20	3.83	1.51	1.47
2	B	9901	EX6	C22-N20	2.28	1.51	1.47

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	9901	EX6	C22-C25-C33	3.49	124.73	120.78
2	A	9901	EX6	C42-C40-N20	3.13	118.11	112.50
2	B	9901	EX6	C42-C40-N20	2.92	117.73	112.50
2	B	9901	EX6	C22-C25-C33	2.69	123.83	120.78
2	A	9901	EX6	C25-C33-N34	2.40	124.18	120.73
2	B	9901	EX6	C25-C33-N34	2.35	124.11	120.73

There are no chirality outliers.

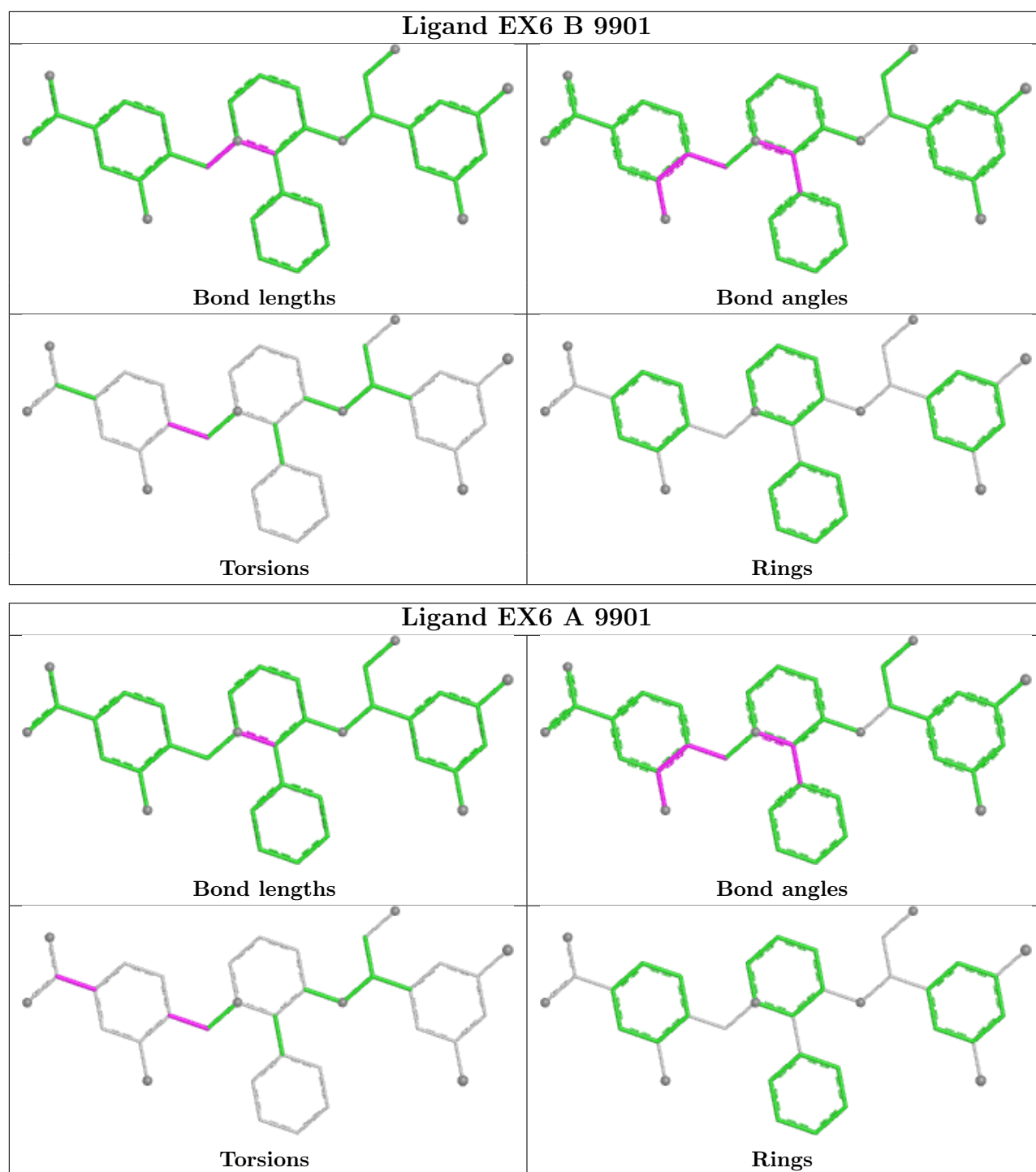
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	9901	EX6	N20-C22-C25-C33
2	A	9901	EX6	N20-C22-C25-C33
2	A	9901	EX6	C28-C30-C37-O38

There are no ring outliers.

No monomer is involved in short contacts.

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	466/469 (99%)	0.89	73 (15%) 5 4	19, 39, 83, 98	1 (0%)
1	B	460/469 (98%)	0.60	35 (7%) 20 18	24, 38, 71, 114	0
All	All	926/938 (98%)	0.74	108 (11%) 9 8	19, 38, 79, 114	1 (0%)

All (108) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	340	ILE	5.2
1	A	221	LEU	5.1
1	A	343	LEU	5.0
1	A	346	VAL	4.8
1	B	294	VAL	4.6
1	A	240	LEU	4.5
1	B	295	PHE	4.4
1	B	315	VAL	4.4
1	A	237	PHE	4.4
1	A	267	GLY	4.3
1	A	339	LEU	4.2
1	A	523	LYS	4.2
1	A	290	SER	4.2
1	A	244	ILE	4.1
1	A	351	TYR	4.1
1	B	314	ASP	4.0
1	A	360	TYR	3.8
1	A	225	THR	3.8
1	A	347	SER	3.8
1	A	235	PRO	3.6
1	A	350	ALA	3.5
1	A	236	THR	3.5
1	A	268	ALA	3.5
1	B	395	LYS	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	296	LEU	3.4
1	A	681	GLY	3.3
1	A	310	LEU	3.3
1	B	293	PRO	3.3
1	A	241	PRO	3.2
1	A	622	LYS	3.2
1	A	336	PHE	3.1
1	B	235	PRO	3.1
1	A	356	ALA	3.0
1	A	315	VAL	3.0
1	A	312	GLY	3.0
1	A	323	ALA	3.0
1	B	269	ARG	3.0
1	A	354	ALA	3.0
1	B	318	ALA	3.0
1	A	222	ILE	2.9
1	A	348	ASN	2.9
1	A	668	PRO	2.9
1	A	272	THR	2.8
1	A	362	ALA	2.8
1	A	352	GLU	2.8
1	A	680	SER	2.8
1	A	358	ALA	2.8
1	B	262	TYR	2.7
1	B	321	ILE	2.7
1	A	621	LEU	2.7
1	A	671	ASN	2.7
1	B	278	LYS	2.7
1	A	262	TYR	2.7
1	A	220	GLY	2.6
1	A	344	ASP	2.6
1	A	223	LYS	2.6
1	B	492	SER	2.6
1	A	353	ASP	2.6
1	B	255	THR	2.6
1	A	309	ALA	2.5
1	B	325	ALA	2.5
1	A	359	LYS	2.5
1	A	317	THR	2.4
1	A	337	LYS	2.4
1	B	622	LYS	2.4
1	A	366	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	626	LYS	2.4
1	A	334	ASP	2.4
1	A	251	VAL	2.4
1	A	294	VAL	2.4
1	A	233	SER	2.4
1	B	396	SER	2.4
1	B	220	GLY	2.3
1	B	298	THR	2.3
1	B	683	ASP	2.3
1	A	369	ASN	2.3
1	A	247	LYS	2.3
1	B	320	VAL	2.3
1	A	304	TRP	2.2
1	A	349	LYS	2.2
1	A	333	ARG	2.2
1	A	341	GLY	2.2
1	B	346	VAL	2.2
1	A	342	GLY	2.2
1	A	230	PHE	2.1
1	A	644	LYS	2.1
1	A	313	GLU	2.1
1	A	295	PHE	2.1
1	A	234	VAL	2.1
1	A	400	LYS	2.1
1	B	534	CYS	2.1
1	B	322	ALA	2.1
1	A	640	GLU	2.1
1	B	312	GLY	2.1
1	A	322	ALA	2.1
1	A	357	LYS	2.0
1	A	524	ILE	2.0
1	B	596	LYS	2.0
1	B	680	SER	2.0
1	A	591	MET	2.0
1	B	272	THR	2.0
1	B	284	THR	2.0
1	B	268	ALA	2.0
1	A	593	GLU	2.0
1	B	630	LYS	2.0
1	A	239	SER	2.0
1	B	263	ILE	2.0
1	B	520	PHE	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($\text{\AA}^2$)	Q<0.9
1	TPO	B	532	11/12	0.91	0.09	38,39,43,43	0
1	TPO	A	532	11/12	0.96	0.08	36,38,46,47	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

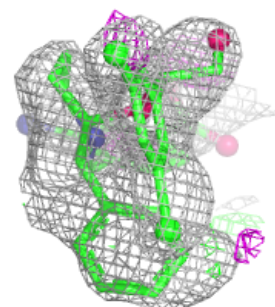
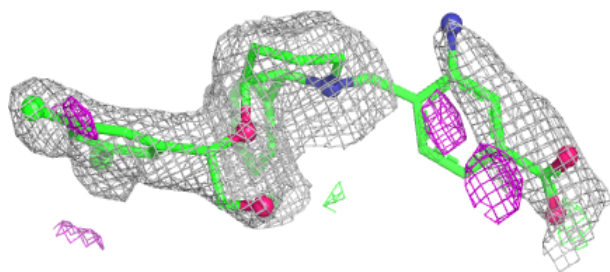
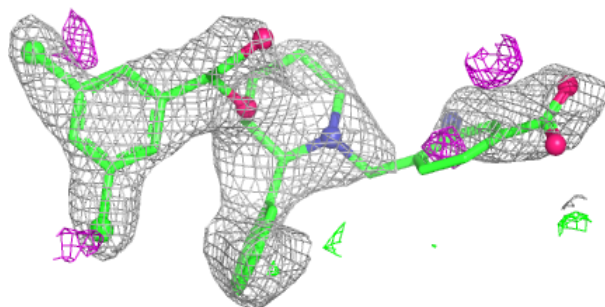
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	EX6	A	9901	35/35	0.71	0.18	73,77,86,88	0
2	EX6	B	9901	35/35	0.89	0.10	28,44,50,55	0

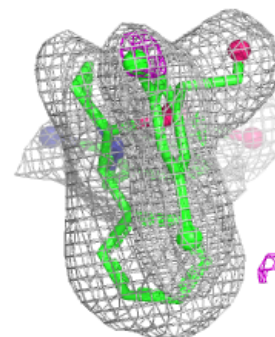
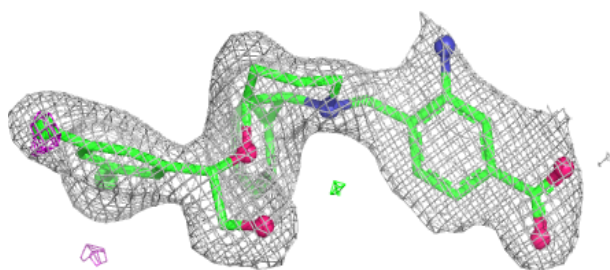
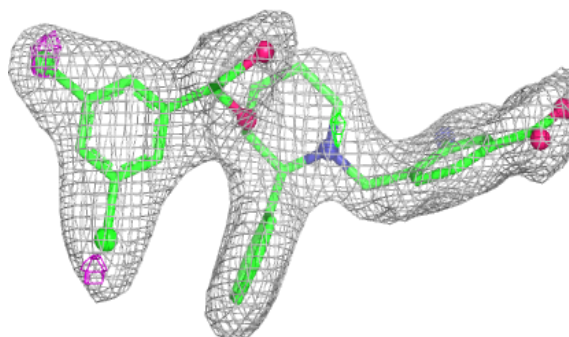
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around EX6 A 9901:

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

**Electron density around EX6 B 9901:**

$2mF_o-DF_c$ (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.