

Full wwPDB X-ray Structure Validation Report (i)

Nov 6, 2023 – 02:47 AM EST

PDB ID	:	8EYB
Title	:	Crystal structure of PTP1B D181A/Q262A/C215A phosphatase domain with
		JAK2 activation loop phosphopeptide
Authors	:	Morris, R.; Kershaw, N.J.; Babon, J.J.
Deposited on	:	2022-10-26
Resolution	:	2.35 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org A user guide is available at https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

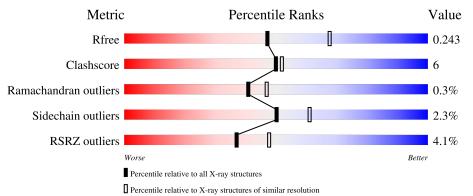
MolProbity Mogul Xtriage (Phenix) EDS	:	4.02b-467 1.8.5 (274361), CSD as541be (2020) 1.13 2.36
buster-report Percentile statistics Refmac	: : :	1.1.7 (2018) 20191225.v01 (using entries in the PDB archive December 25th 2019) 5.8.0158 7.0.044 (Gargrove)
Ideal geometry (DNA, RNA) Validation Pipeline (wwPDB-VP)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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 2.35 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	2096 (2.36-2.32)
Clashscore	141614	2193 (2.36-2.32)
Ramachandran outliers	138981	2159 (2.36-2.32)
Sidechain outliers	138945	2160 (2.36-2.32)
RSRZ outliers	127900	2067 (2.36-2.32)

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

Mol	Chain	Length	Quality of chain				
1	А	296	3%	83%		11% • 5%	
1	В	296	5%	83%		15% ••	
2	D	16	6% 19% 6% 6%		69%		
2	Е	16	38%	6%	56%		



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4800 atoms, of which 24 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Δ	281	Total	С	Ν	0	\mathbf{S}	0	0	0
	A	201	2199	1403	382	401	13	0	0	0
1	р	294	Total	С	Ν	0	S	0	1	0
	D	294	2328	1481	400	432	15	0		U

• Molecule 1 is a protein called Tyrosine-protein phosphatase non-receptor type 1.

Residue	Modelled	Actual	Comment	Reference
181	ALA	ASP	engineered mutation	UNP P18031
215	ALA	CYS	engineered mutation	UNP P18031
262	ALA	GLN	engineered mutation	UNP P18031
283	ALA	GLY	conflict	UNP P18031
286	ALA	SER	conflict	UNP P18031
287	ALA	VAL	conflict	UNP P18031
181	ALA	ASP	engineered mutation	UNP P18031
215	ALA	CYS	engineered mutation	UNP P18031
262	ALA	GLN	engineered mutation	UNP P18031
283	ALA	GLY	conflict	UNP P18031
286	ALA	SER	conflict	UNP P18031
287	ALA	VAL	conflict	UNP P18031
	$ \begin{array}{r} 181 \\ 215 \\ 262 \\ 283 \\ 286 \\ 287 \\ 181 \\ 215 \\ 262 \\ 283 \\ 286 \\ \end{array} $	181 ALA 215 ALA 262 ALA 283 ALA 286 ALA 287 ALA 181 ALA 215 ALA 286 ALA 287 ALA 288 ALA 287 ALA 283 ALA 284 ALA 285 ALA 283 ALA 286 ALA	181 ALA ASP 215 ALA CYS 262 ALA GLN 283 ALA GLY 286 ALA SER 287 ALA VAL 181 ALA CYS 215 ALA SER 287 ALA VAL 181 ALA CYS 262 ALA GLN 283 ALA SER 283 ALA SER 286 ALA SER	181ALAASPengineered mutation215ALACYSengineered mutation262ALAGLNengineered mutation283ALAGLYconflict286ALASERconflict287ALAVALconflict181ALAASPengineered mutation215ALACYSengineered mutation215ALAGLNengineered mutation262ALAGLNengineered mutation283ALAGLYconflict286ALASERconflict

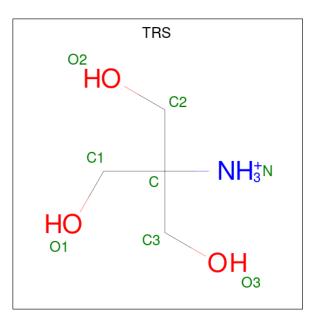
There are 12 discrepancies between the modelled and reference sequences:

• Molecule 2 is a protein called Tyrosine-protein kinase JAK2 activation loop phosphopeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
0	л	Б	Total	С	Ν	0	Р	0	0	0
	D	5	51	32	6	12	1	0	0	0
0	F	7	Total	С	Ν	0	Р	0	0	0
	Ľ	1	64	39	8	16	1	0	0	0

• Molecule 3 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: $C_4H_{12}NO_3$) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
2	Λ	1	Total	С	Η	Ν	Ο	0	0	
5	A	1	20	4	12	1	3	0	0	
2	Р	1	Total	С	Η	Ν	Ο	0	0	
5	D	1	20	4	12	1	3	0	0	

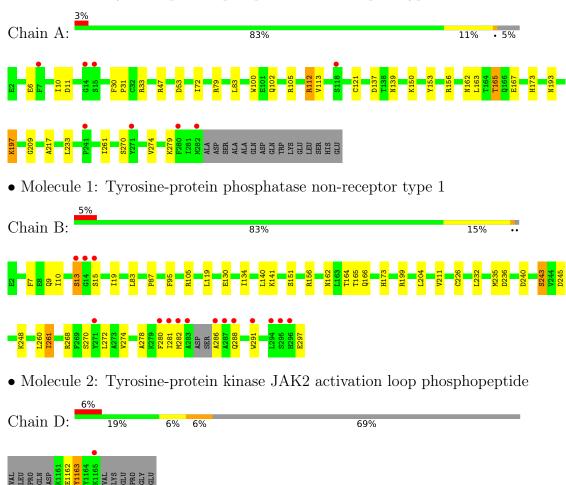
• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	60	Total O 60 60	0	0
4	В	53	Total O 53 53	0	0
4	Е	5	Total O 5 5	0	0



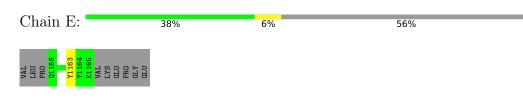
3 Residue-property plots (i)

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: Tyrosine-protein phosphatase non-receptor type 1

• Molecule 2: Tyrosine-protein kinase JAK2 activation loop phosphopeptide





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants	88.38Å 88.38Å 190.34Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.85 - 2.35	Depositor
Resolution (A)	48.85 - 2.35	EDS
% Data completeness	99.7(48.85 - 2.35)	Depositor
(in resolution range)	95.7(48.85 - 2.35)	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$0.96 (at 2.34 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
D D.	0.207 , 0.243	Depositor
R, R_{free}	0.207 , 0.243	DCC
R_{free} test set	2005 reflections $(5.48%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	51.3	Xtriage
Anisotropy	0.154	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.32 , 47.9	EDS
L-test for twinning ²	$< L > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.026 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4800	wwPDB-VP
Average B, all atoms $(Å^2)$	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.07% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: TRS, PTR

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	Mol Chain		lengths	Bond angles		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.38	0/2251	0.53	0/3051	
1	В	0.38	0/2380	0.53	0/3220	
2	D	0.42	0/34	0.42	0/42	
2	Е	0.36	0/47	0.61	0/60	
All	All	0.38	0/4712	0.53	0/6373	

There are no bond length outliers.

There are no bond angle outliers.

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	А	2199	0	2109	20	0
1	В	2328	0	2230	33	0
2	D	51	0	36	2	0
2	Е	64	0	42	0	0
3	А	8	12	12	0	0
3	В	8	12	12	0	0
4	А	60	0	0	1	0
4	В	53	0	0	1	0
4	Ε	5	0	0	0	0
All	All	4776	24	4441	53	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 6.

All (53) 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:236:ASP:HB2	1:B:281:ILE:HD11	1.27	1.15
1:A:162:ASN:OD1	1:A:165:THR:HG22	1.85	0.76
1:B:280:PHE:HE2	1:B:286:ALA:HB1	1.52	0.74
1:B:280:PHE:CE2	1:B:286:ALA:HB1	2.31	0.66
1:B:278:ALA:HA	1:B:281:ILE:HG22	1.78	0.65
1:B:278:ALA:O	1:B:281:ILE:HG22	2.00	0.62
1:B:232:LEU:HD23	1:B:235:MET:CE	2.30	0.61
1:B:270:SER:O	1:B:274:VAL:HG23	2.00	0.60
1:B:240:ASP:O	1:B:243:SER:HB3	2.03	0.59
1:A:162:ASN:HB3	1:A:165:THR:HG23	1.86	0.57
1:A:113:VAL:HG13	1:A:121:CYS:O	2.05	0.57
1:B:151:SER:OG	1:B:297:GLU:HA	2.05	0.57
1:B:236:ASP:CB	1:B:281:ILE:HD11	2.18	0.56
1:B:134:ILE:HG13	1:B:141:LYS:HG3	1.87	0.56
1:B:280:PHE:HE2	1:B:286:ALA:CB	2.20	0.55
1:A:79:ARG:CZ	1:A:233:LEU:HD11	2.36	0.54
1:A:47:ARG:HG2	2:D:1162:GLU:HG2	1.91	0.52
1:A:137:ASP:OD1	1:A:137:ASP:N	2.43	0.52
1:B:83:LEU:HD11	1:B:226:CYS:SG	2.50	0.52
1:B:162:ASN:OD1	1:B:164:THR:HB	2.10	0.51
1:A:270:SER:O	1:A:274:VAL:HG23	2.10	0.51
1:B:10:ILE:HG23	1:B:15:SER:HB2	1.93	0.51
1:B:156:ARG:HB2	1:B:173:HIS:HB3	1.94	0.50
1:A:72:ILE:HD12	1:A:83:LEU:HD13	1.94	0.49
1:A:100:TRP:HH2	1:A:167:GLU:HB3	1.76	0.49
1:A:162:ASN:HB3	1:A:165:THR:CG2	2.42	0.49
1:B:140:LEU:HD23	1:B:162:ASN:HA	1.95	0.48
1:B:9:GLN:O	1:B:13:SER:OG	2.29	0.48
1:B:165:THR:O	1:B:166:GLN:HB2	2.14	0.48
1:A:112:ARG:HG3	4:A:448:HOH:O	2.14	0.47
1:A:217:ALA:HB2	2:D:1163:PTR:CD2	2.44	0.47
1:B:204:LEU:CD2	1:B:211:VAL:HG11	2.45	0.47
1:B:7:PHE:HZ	1:B:268:ARG:HH11	1.61	0.47
1:B:119:LEU:HD23	1:B:119:LEU:HA	1.75	0.47
1:A:150:LYS:HD2	1:A:153:TYR:CZ	2.50	0.47
1:B:288:GLN:HA	1:B:291:TRP:CE3	2.50	0.46
1:B:232:LEU:HA	1:B:235:MET:HE2	1.97	0.45

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Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:102:GLN:O	1:A:209:GLY:HA3	2.16	0.45
1:A:6:GLU:O	1:A:10:ILE:HG13	2.16	0.45
1:B:130:GLU:OE1	1:B:130:GLU:N	2.47	0.45
1:B:232:LEU:HD23	1:B:235:MET:HE1	1.98	0.44
1:B:260:LEU:O	1:B:261:ILE:HB	2.17	0.44
1:A:156:ARG:HB2	1:A:173:HIS:HB3	1.99	0.44
1:B:278:ALA:O	1:B:282:MET:HG2	2.18	0.43
1:B:245:ASP:OD2	1:B:248:LYS:HG3	2.19	0.42
1:B:199:ARG:HD3	4:B:443:HOH:O	2.20	0.42
1:A:139:ASN:OD1	1:A:163:LEU:HB2	2.19	0.42
1:A:33:ARG:N	1:A:53:ASP:OD2	2.48	0.41
1:B:278:ALA:CA	1:B:281:ILE:HG22	2.47	0.41
1:A:193:ASN:OD1	1:A:197:LYS:HE3	2.20	0.41
1:B:7:PHE:HZ	1:B:268:ARG:NH1	2.19	0.41
1:B:87:PRO:HG3	1:B:95:PHE:CD1	2.56	0.41
1:A:30:PHE:HB3	1:A:31:PRO:HD2	2.02	0.41

Continued from previous page...

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	Perce	ntiles
1	А	279/296~(94%)	270~(97%)	8(3%)	1 (0%)	34	38
1	В	291/296~(98%)	282~(97%)	8(3%)	1 (0%)	41	47
2	D	2/16~(12%)	2 (100%)	0	0	100	100
2	Е	4/16~(25%)	3~(75%)	1 (25%)	0	100	100
All	All	576/624~(92%)	557~(97%)	17 (3%)	2 (0%)	41	47

All (2) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	А	261	ILE
1	В	261	ILE

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	А	228/264~(86%)	222~(97%)	6 (3%)	46 56
1	В	242/264~(92%)	237~(98%)	5(2%)	53 65
2	D	3/14~(21%)	3~(100%)	0	100 100
2	Ε	4/14~(29%)	4 (100%)	0	100 100
All	All	477/556~(86%)	466~(98%)	11 (2%)	50 61

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	11	ASP
1	А	105	ARG
1	А	112	ARG
1	А	165	THR
1	А	197	LYS
1	А	279	LYS
1	В	13	SER
1	В	19	ILE
1	В	105	ARG
1	В	243	SER
1	В	272	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.



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

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	Turne	Chain	Res	Link	Bo	ond leng	\mathbf{ths}	В	ond ang	les
IVIOI	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
2	PTR	D	1163	2	$15,\!16,\!17$	1.33	1 (6%)	19,22,24	0.64	0
2	PTR	Е	1163	2	15,16,17	1.35	2 (13%)	19,22,24	0.74	1 (5%)

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	PTR	D	1163	2	-	0/10/11/13	0/1/1/1
2	PTR	Е	1163	2	-	1/10/11/13	0/1/1/1

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1163	PTR	OH-CZ	-4.32	1.30	1.40
2	Е	1163	PTR	OH-CZ	-3.70	1.32	1.40
2	Ε	1163	PTR	P-OH	2.35	1.62	1.59

All (3) bond length outliers are listed below:

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
2	Е	1163	PTR	O3P-P-OH	2.06	111.69	105.24

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	Ε	1163	PTR	CA-CB-CG-CD1



There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1163	PTR	1	0

5.5 Carbohydrates (i)

There are no monosaccharides 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 Typ	Type	pe Chain	Chain	Chain	Chain	Chain	Chain	Chain	Res	Link	B	ond leng	gths	В	ond ang	gles
	Type	Unain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2						
3	TRS	А	301	-	7,7,7	0.55	0	$9,\!9,\!9$	0.70	0						
3	TRS	В	301	-	7,7,7	0.63	0	$9,\!9,\!9$	0.69	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
3	TRS	А	301	-	-	2/9/9/9	-
3	TRS	В	301	-	-	3/9/9/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:



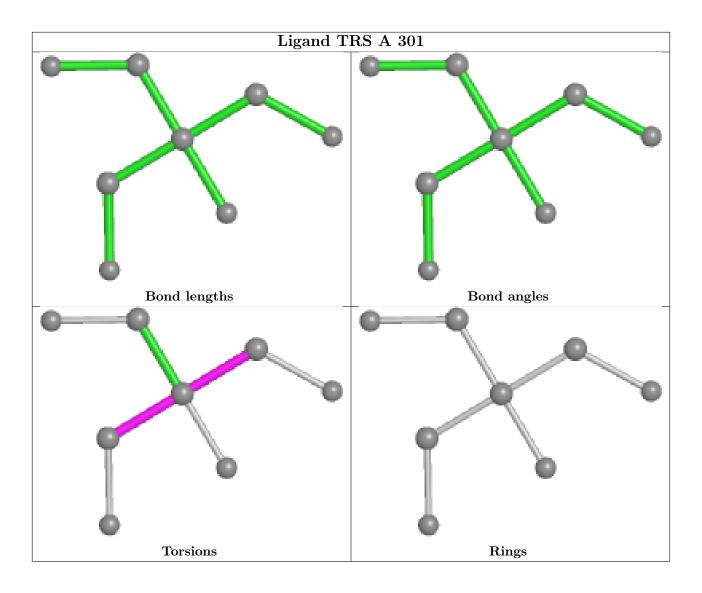
Mol	Chain	Res	Type	Atoms
3	В	301	TRS	N-C-C1-O1
3	В	301	TRS	C2-C-C1-O1
3	А	301	TRS	N-C-C1-O1
3	А	301	TRS	C1-C-C3-O3
3	В	301	TRS	C1-C-C3-O3

There are no ring outliers.

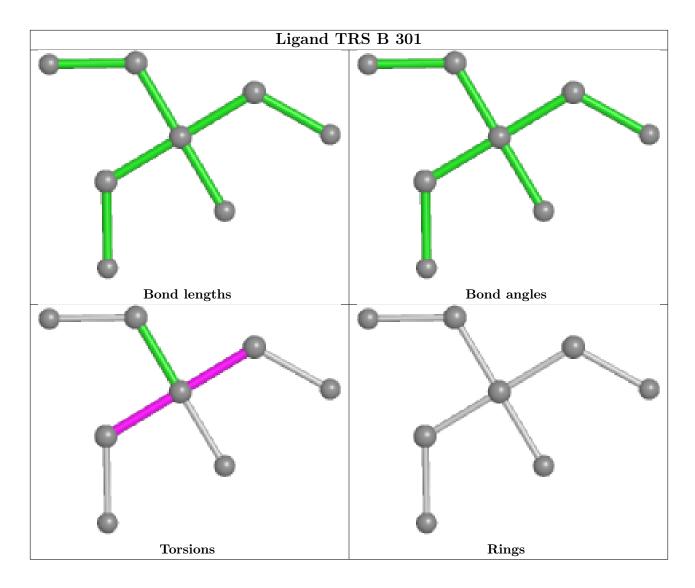
No monomer is involved in short contacts.

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 then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and sufficient 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 (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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 $>$	$\# RSRZ {>}2$	$OWAB(Å^2)$	$\mathbf{Q}{<}0.9$
1	А	281/296~(94%)	0.03	8 (2%) 53 63	38, 55, 94, 107	0
1	В	294/296~(99%)	0.20	15 (5%) 28 39	38, 56, 93, 112	0
2	D	4/16~(25%)	1.00	1 (25%) 0 1	71, 73, 76, 86	0
2	Е	6/16~(37%)	-0.36	0 100 100	52, 61, 63, 71	0
All	All	585/624~(93%)	0.12	24 (4%) 37 48	38, 56, 94, 112	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	282	MET	4.7
1	В	282	MET	4.5
1	А	280	PHE	4.1
1	В	294	LEU	3.9
1	В	283	ALA	3.8
1	В	15	SER	3.5
1	В	296	HIS	3.3
1	В	288	GLN	3.2
1	В	281	ILE	3.1
1	В	291	TRP	3.1
1	В	287	ALA	3.0
1	А	7	PHE	3.0
1	А	14	GLY	2.9
1	А	271	TYR	2.9
1	А	15	SER	2.8
1	А	241	PRO	2.6
1	В	271	TYR	2.4
1	В	13	SER	2.3
1	В	286	ALA	2.3
1	В	14	GLY	2.2
1	A	118	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	В	280	PHE	2.2
2	D	1165	LYS	2.1
1	В	295	SER	2.1

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, 95^{th} 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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
2	PTR	D	1163	16/17	0.98	0.12	42,54,65,66	0
2	PTR	Е	1163	16/17	0.99	0.12	45,50,56,61	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

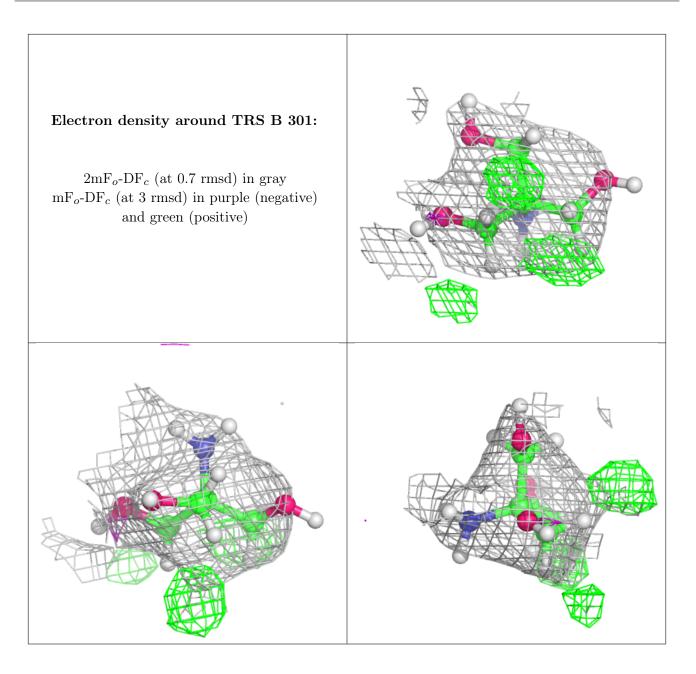
6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} 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.

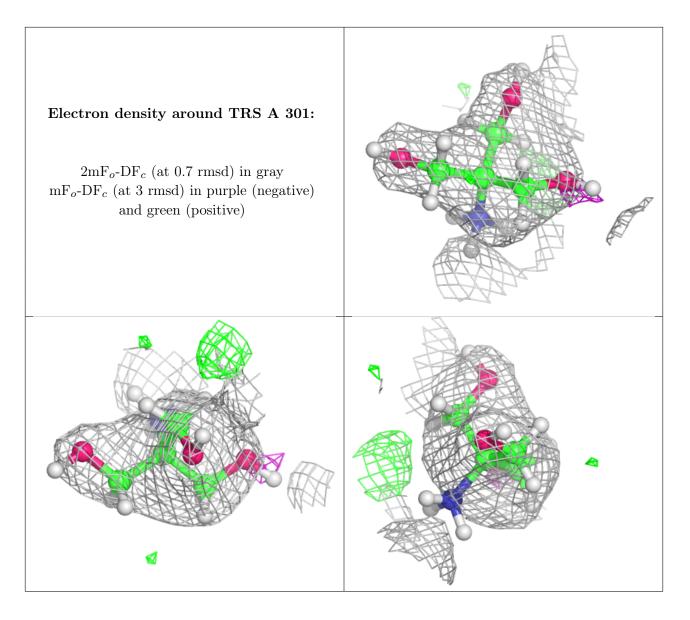
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$B-factors(Å^2)$	Q<0.9
3	TRS	В	301	8/8	0.86	0.15	59,74,86,91	0
3	TRS	А	301	8/8	0.89	0.14	$61,\!75,\!85,\!85$	0

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.









6.5 Other polymers (i)

There are no such residues in this entry.

