

Full wwPDB X-ray Structure Validation Report (i)

Aug 19, 2023 – 07:15 PM EDT

PDB ID	:	2G09
Title	:	X-ray structure of mouse pyrimidine 5'-nucleotidase type 1, product complex
Authors	:	Bitto, E.; Bingman, C.A.; Wesenberg, G.E.; Phillips Jr., G.N.; Center for
		Eukaryotic Structural Genomics (CESG)
Deposited on	:	2006-02-11
Resolution	:	2.10 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:

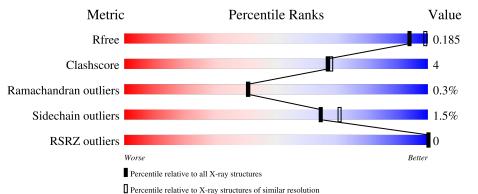
MolProbity	:	4.02b-467 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)		
EDS	:	2.35
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 2.10 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	5197(2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 <=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	297	89%	9%	·
1	В	297	88%	10%	•••



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 5556 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
1	А	291	Total 2334	C 1491	N 389	0 441			0	1	0
1	В	291	Total 2326	C 1487	N 387	0 439	$\frac{S}{5}$	Se 8	0	1	0

• Molecule 1 is a protein called Cytosolic 5'-nucleotidase III.

Chain	Residue	Modelled	Actual	Comment	Reference
А	1	SER	-	cloning artifact	UNP Q9D020
А	12	MSE	MET	modified residue	UNP Q9D020
А	13	MSE	MET	modified residue	UNP Q9D020
А	52	MSE	MET	modified residue	UNP Q9D020
А	110	MSE	MET	modified residue	UNP Q9D020
А	141	MSE	MET	modified residue	UNP Q9D020
А	192	MSE	MET	modified residue	UNP Q9D020
А	245	MSE	MET	modified residue	UNP Q9D020
А	273	MSE	MET	modified residue	UNP Q9D020
В	1	SER	-	cloning artifact	UNP Q9D020
В	12	MSE	MET	modified residue	UNP Q9D020
В	13	MSE	MET	modified residue	UNP Q9D020
В	52	MSE	MET	modified residue	UNP Q9D020
В	110	MSE	MET	modified residue	UNP Q9D020
В	141	MSE	MET	modified residue	UNP Q9D020
В	192	MSE	MET	modified residue	UNP Q9D020
В	245	MSE	MET	modified residue	UNP Q9D020
В	273	MSE	MET	modified residue	UNP Q9D020

There are 18 discrepancies between the modelled and reference sequences:

• Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

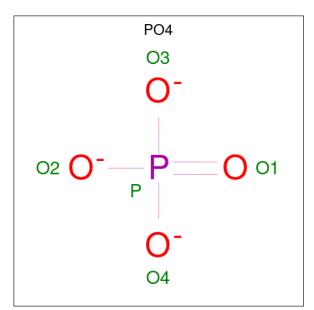
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	Total Mg 1 1	0	0



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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	В	1	Total Mg 1 1	0	0

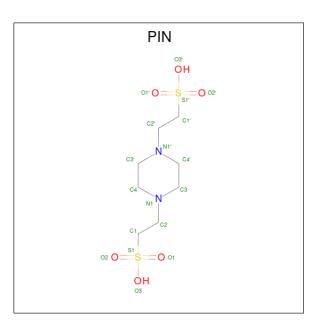
• Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{P} \\ 5 & 4 & 1 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{P} \\ 5 & 4 & 1 \end{array}$	0	0

• Molecule 4 is PIPERAZINE-N, N'-BIS(2-ETHANESULFONIC ACID) (three-letter code: PIN) (formula: $\rm C_8H_{18}N_2O_6S_2).$





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf		
4	Λ	1	Total	С	Ν	0	S	0	0	
4	4 A	1	18	8	2	6	2	0	0	
4	D	D	1	Total	С	Ν	0	S	0	0
4	D	1	18	8	2	6	2	0	U	

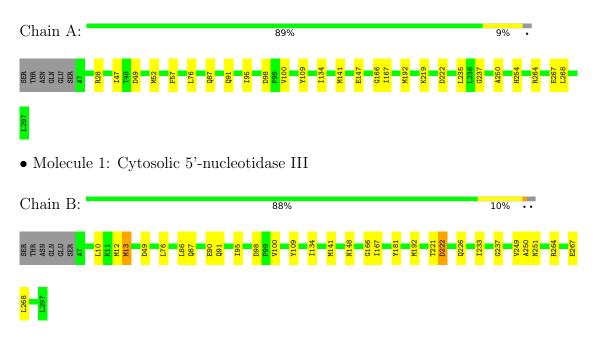
• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	426	Total O 426 426	0	0
5	В	422	Total O 422 422	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: Cytosolic 5'-nucleotidase III



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32	Depositor
Cell constants	134.01Å 134.01Å 39.09Å	Deneiten
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	32.19 - 2.10	Depositor
Resolution (A)	32.19 - 2.10	EDS
% Data completeness	98.9 (32.19-2.10)	Depositor
(in resolution range)	98.9 (32.19-2.10)	EDS
R _{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$3.02 (at 2.10 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
D D	0.150 , 0.198	Depositor
R, R_{free}	0.165 , 0.185	DCC
R_{free} test set	2257 reflections $(4.97%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	32.9	Xtriage
Anisotropy	0.091	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.30, 38.3	EDS
L-test for twinning ²	$< L > = 0.49, < L^2 > = 0.32$	Xtriage
	0.488 for -h,-k,l	
Estimated twinning fraction	0.038 for h,-h-k,-l	Xtriage
	0.037 for -k,-h,-l	
F_o, F_c correlation	0.96	EDS
Total number of atoms	5556	wwPDB-VP
Average B, all atoms $(Å^2)$	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.32% 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: PIN, MG, PO4

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		Bo	nd lengths	Bond angles		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.63	0/2366	0.63	0/3172	
1	В	0.64	1/2358~(0.0%)	0.63	0/3161	
All	All	0.63	1/4724~(0.0%)	0.63	0/6333	

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	В	13	MSE	SE-CE	-5.14	1.65	1.95

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	2334	0	2353	15	0
1	В	2326	0	2346	21	1
2	А	1	0	0	0	0
2	В	1	0	0	0	0
3	А	5	0	0	0	0
3	В	5	0	0	0	0
4	А	18	0	18	0	0
4	В	18	0	18	1	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 4.

All (37) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:B:233:ILE:HD11	1:B:249:VAL:HG11	1.63	0.80
1:B:10:LEU:HA	1:B:13:MSE:HE3	1.64	0.79
1:B:98:ASP:OD1	1:B:100:VAL:HG22	1.95	0.66
1:B:222:ASP:HB3	5:B:1016:HOH:O	1.95	0.66
1:A:98:ASP:OD1	1:A:100:VAL:HG12	1.98	0.63
1:B:222:ASP:OD1	1:B:222:ASP:N	2.25	0.62
1:B:10:LEU:HA	1:B:13:MSE:CE	2.32	0.59
1:B:87:GLN:O	1:B:91:GLN:HG3	2.03	0.58
1:B:10:LEU:HD23	1:B:13:MSE:HE1	1.86	0.57
1:B:10:LEU:HD23	1:B:13:MSE:CE	2.34	0.57
1:A:76:LEU:HD12	1:A:134:ILE:HD11	1.89	0.53
1:A:91:GLN:HB3	5:A:1260:HOH:O	2.08	0.53
1:A:167:ILE:HG21	1:A:192:MSE:HE3	1.91	0.52
1:B:49:ASP:OD2	1:B:237:GLY:HA2	2.12	0.49
1:B:264:ARG:HD2	1:B:267:GLU:OE1	2.12	0.49
1:A:254:HIS:HD2	5:A:1039:HOH:O	1.94	0.49
1:A:264:ARG:HD2	1:A:267:GLU:OE1	2.14	0.47
1:A:147:GLU:HG2	5:A:909:HOH:O	2.13	0.47
1:B:86:LEU:O	1:B:90:GLU:HG3	2.15	0.46
1:B:95:ILE:HG21	1:B:109:TYR:CG	2.50	0.46
1:B:166:GLY:HA3	5:B:1083:HOH:O	2.15	0.46
1:A:95:ILE:HG21	1:A:109:TYR:CG	2.50	0.46
1:A:87:GLN:O	1:A:91:GLN:HG3	2.18	0.43
1:A:49:ASP:OD2	1:A:237:GLY:HA2	2.19	0.43
1:A:166:GLY:HA3	5:A:1136:HOH:O	2.17	0.43
1:B:167:ILE:HG21	1:B:192:MSE:HE3	2.01	0.42
4:B:906:PIN:H11	4:B:906:PIN:H41	1.77	0.42
1:B:264:ARG:CZ	1:B:268:LEU:HD11	2.50	0.42
1:B:98:ASP:OD1	1:B:100:VAL:CG2	2.65	0.42
1:A:264:ARG:CZ	1:A:268:LEU:HD11	2.50	0.41
1:A:47:ILE:O	1:A:235:LEU:HA	2.20	0.41



Chain Non-H H(added) Clashes Symm-Clashes Mol H(model) 426 5А 0 50 1 5 В 422 0 0 4 0 All All 0 1 5556473537

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:MSE:SE	1:A:57:PHE:HA	2.70	0.41
1:B:10:LEU:CD2	1:B:13:MSE:HE1	2.51	0.41
1:B:251[A]:ASN:HB3	5:B:1270:HOH:O	2.20	0.41
1:B:226:GLN:HG2	5:B:1182:HOH:O	2.21	0.41
1:B:76:LEU:HD12	1:B:134:ILE:HD11	2.02	0.40
1:A:219:LYS:NZ	5:A:1017:HOH:O	2.53	0.40

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All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:12:MSE:SE	5:A:1260:HOH:O[3_564]	1.98	0.22

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	290/297~(98%)	285~(98%)	4 (1%)	1 (0%)	41	41
1	В	289/297~(97%)	283 (98%)	5 (2%)	1 (0%)	41	41
All	All	579/594~(98%)	568 (98%)	9(2%)	2 (0%)	41	41

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	250	ALA
1	В	250	ALA

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	Rotameric Outliers	
1	А	261/258~(101%)	258~(99%)	3(1%)	73 79
1	В	260/258~(101%)	255~(98%)	5(2%)	57 63
All	All	521/516~(101%)	513~(98%)	8 (2%)	65 71

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	\mathbf{Res}	Type
1	А	28	ARG
1	А	141	MSE
1	А	222	ASP
1	В	141	MSE
1	В	148	ASN
1	В	181	TYR
1	В	221	THR
1	В	222	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	В	148	ASN

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 monosaccharides in this entry.



5.6 Ligand geometry (i)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 for Mogul analysis.

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 I		Link	Bond lengths			В	ond ang	les	
10101	Type	Unam	nes	LIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
4	PIN	А	905	-	18,18,18	1.67	2 (11%)	22,26,26	2.00	9 (40%)
3	PO4	В	904	2	4,4,4	1.41	1 (25%)	6,6,6	1.73	2 (33%)
3	PO4	А	903	2	4,4,4	1.46	1 (25%)	6,6,6	1.06	1 (16%)
4	PIN	В	906	-	18,18,18	1.73	2 (11%)	22,26,26	1.67	7 (31%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PIN	А	905	-	-	6/12/22/22	0/1/1/1
4	PIN	В	906	-	-	6/12/22/22	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	В	906	PIN	C1'-S1'	4.31	1.83	1.77
4	А	905	PIN	C1-S1	4.13	1.83	1.77
4	В	906	PIN	C1-S1	4.08	1.83	1.77
4	А	905	PIN	C1'-S1'	3.87	1.83	1.77
3	А	903	PO4	P-O2	-2.75	1.46	1.54
3	В	904	PO4	P-01	-2.09	1.45	1.50

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^{o})$	$Ideal(^{o})$
4	А	905	PIN	C4'-N1'-C3'	5.43	121.06	108.83
4	В	906	PIN	C4-N1-C3	3.66	117.07	108.83



Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	В	904	PO4	O2-P-O1	-2.86	100.42	110.89
4	В	906	PIN	O2'-S1'-C1'	2.85	110.34	106.92
3	В	904	PO4	O4-P-O3	2.72	116.70	107.97
4	А	905	PIN	O3'-S1'-C1'	2.70	110.13	105.77
4	А	905	PIN	C2'-N1'-C4'	-2.61	104.56	111.23
4	А	905	PIN	O1-S1-C1	2.58	110.02	106.92
4	А	905	PIN	O1'-S1'-C1'	2.42	109.83	106.92
4	А	905	PIN	O3-S1-C1	2.40	109.65	105.77
4	А	905	PIN	C4-C3'-N1'	2.26	115.28	110.64
4	В	906	PIN	C4'-C3-N1	2.26	115.27	110.64
4	В	906	PIN	O3'-S1'-C1'	2.20	109.32	105.77
4	В	906	PIN	O2-S1-C1	2.17	109.53	106.92
4	В	906	PIN	O1-S1-C1	2.16	109.52	106.92
4	А	905	PIN	C3-C4'-N1'	2.14	115.03	110.64
4	А	905	PIN	O2-S1-C1	2.04	109.37	106.92
4	В	906	PIN	O1'-S1'-C1'	2.04	109.37	106.92
3	А	903	PO4	O3-P-O2	-2.02	101.47	107.97

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There are no chirality outliers.

Mol	Chain	Res	Type	Atoms
4	А	905	PIN	S1-C1-C2-N1
4	А	905	PIN	S1'-C1'-C2'-N1'
4	А	905	PIN	C2'-C1'-S1'-O1'
4	А	905	PIN	C2'-C1'-S1'-O3'
4	В	906	PIN	C2-C1-S1-O3
4	В	906	PIN	C2'-C1'-S1'-O3'
4	А	905	PIN	C1-C2-N1-C4
4	А	905	PIN	C2'-C1'-S1'-O2'
4	В	906	PIN	C2-C1-S1-O1
4	В	906	PIN	C2-C1-S1-O2
4	В	906	PIN	C2'-C1'-S1'-O1'
4	В	906	PIN	C2'-C1'-S1'-O2'

All (12) torsion outliers are listed below:

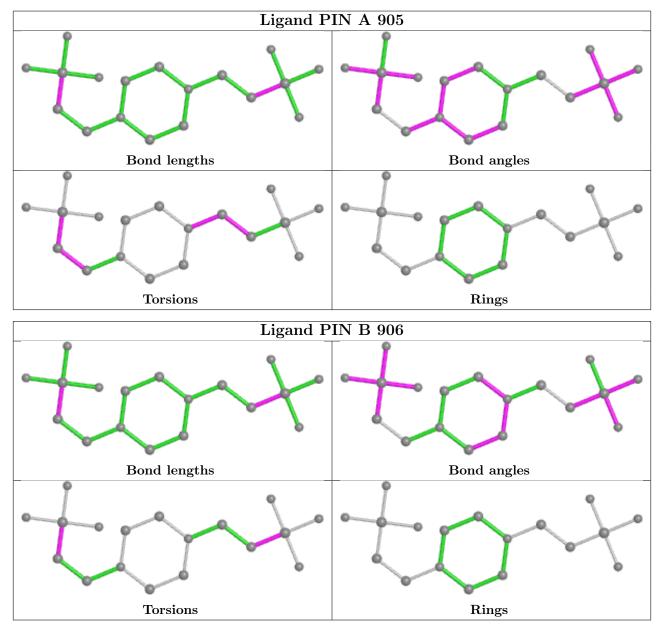
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	906	PIN	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 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 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 (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	$\langle RSRZ \rangle$	#	₽RSR	Z>2	$OWAB(Å^2)$	Q < 0.9
1	А	283/297~(95%)	-0.62	0	100	100	27, 35, 45, 55	1 (0%)
1	В	283/297~(95%)	-0.61	0	100	100	27, 35, 45, 56	1 (0%)
All	All	566/594~(95%)	-0.62	0	100	100	27, 35, 45, 56	2(0%)

There are no RSRZ outliers to report.

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 monosaccharides in this entry.

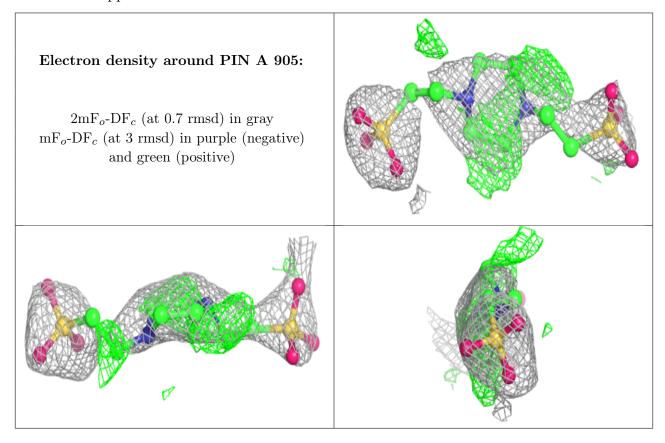
6.4 Ligands (i)

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.

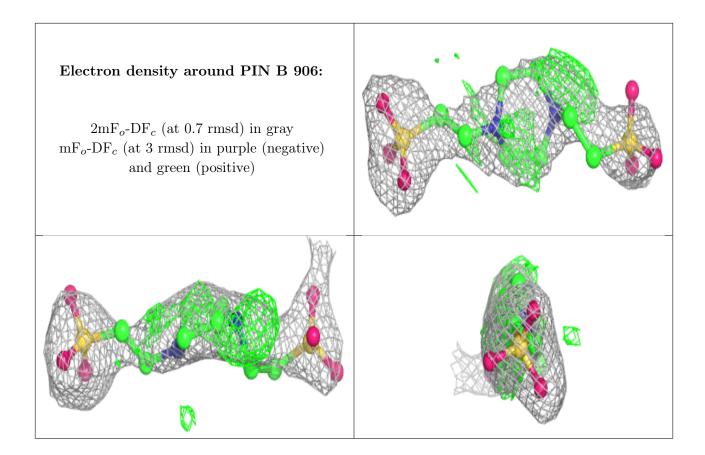
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$B-factors(Å^2)$	Q<0.9
4	PIN	А	905	18/18	0.76	0.23	$50,\!57,\!65,\!65$	18
4	PIN	В	906	18/18	0.83	0.22	52,56,71,71	18
2	MG	А	901	1/1	0.99	0.04	24,24,24,24	0
2	MG	В	902	1/1	0.99	0.03	$25,\!25,\!25,\!25$	0
3	PO4	А	903	5/5	1.00	0.03	21,22,22,25	0
3	PO4	В	904	5/5	1.00	0.04	21,22,23,23	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.

