

Full wwPDB X-ray Structure Validation Report (i)

Aug 28, 2023 - 04:59 AM EDT

PDB ID	:	3L5S
Title	:	Crystal structure of macrophage migration inhibitory factor (MIF) with imid
		azopyrimidinylphenyl inhibitor at 1.86A resolution
Authors	:	McLean, L.; Zhang, Y.
Deposited on	:	2009-12-22
Resolution	:	1.86 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:

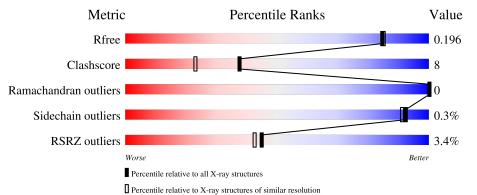
MolProbity	:	4.02b-467 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)		
EDS	:	2.35
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal 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 1.86 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	2469 (1.86-1.86)
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)
RSRZ outliers	127900	2436 (1.86-1.86)

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	122	4% 79%	14% •	7%
1	В	122	2% 8 4%	12%	·
1	С	122	4% 86%	10%	•



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2985 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	114	Total	С	Ν	Ο	\mathbf{S}	0	2	0
1	11	114	873	554	151	162	6	0	2	0
1	В	117	Total	С	Ν	Ο	\mathbf{S}	0	0	0
	D	117	893	565	156	166	6	0	0	U
1	С	117	Total	С	Ν	0	S	0	1	0
	U	111	896	567	156	167	6			0

• Molecule 1 is a protein called Macrophage migration inhibitory factor.

A115LEU-expression tagUNP P14174A116GLU-expression tagUNP P14174A117HIS-expression tagUNP P14174A118HIS-expression tagUNP P14174A119HIS-expression tagUNP P14174A120HIS-expression tagUNP P14174A121HIS-expression tagUNP P14174A122HIS-expression tagUNP P14174B115LEU-expression tagUNP P14174B116GLU-expression tagUNP P14174B117HIS-expression tagUNP P14174B118HIS-expression tagUNP P14174B119HIS-expression tagUNP P14174B120HIS-expression tagUNP P14174B120HIS-expression tagUNP P14174B121HIS-expression tagUNP P14174C115LEU-expression tagUNP P14174C116GLU-expression tagUNP P14174C116GLU-expression tagUNP P14174C118HIS-expression tagUNP P14174C119HIS-expression tagUNP P14174C120HIS	Chain	Residue	Modelled	Actual	Comment	Reference
A117HIS-expression tagUNP P14174A118HIS-expression tagUNP P14174A119HIS-expression tagUNP P14174A120HIS-expression tagUNP P14174A121HIS-expression tagUNP P14174A122HIS-expression tagUNP P14174B115LEU-expression tagUNP P14174B116GLU-expression tagUNP P14174B117HIS-expression tagUNP P14174B118HIS-expression tagUNP P14174B119HIS-expression tagUNP P14174B120HIS-expression tagUNP P14174B121HIS-expression tagUNP P14174B121HIS-expression tagUNP P14174B121HIS-expression tagUNP P14174C115LEU-expression tagUNP P14174C116GLU-expression tagUNP P14174C118HIS-expression tagUNP P14174C119HIS-expression tagUNP P14174C120HIS-expression tagUNP P14174C120HIS-expression tagUNP P14174C120HIS	А	115	LEU	-	expression tag	UNP P14174
A118HIS-expression tagUNP P14174A119HIS-expression tagUNP P14174A120HIS-expression tagUNP P14174A121HIS-expression tagUNP P14174A122HIS-expression tagUNP P14174B115LEU-expression tagUNP P14174B116GLU-expression tagUNP P14174B116GLU-expression tagUNP P14174B117HIS-expression tagUNP P14174B119HIS-expression tagUNP P14174B120HIS-expression tagUNP P14174B121HIS-expression tagUNP P14174B122HIS-expression tagUNP P14174C115LEU-expression tagUNP P14174C116GLU-expression tagUNP P14174C117HIS-expression tagUNP P14174C118HIS-expression tagUNP P14174C120HIS-expression tagUNP P14174C118HIS-expression tagUNP P14174C120HIS-expression tagUNP P14174C120HIS-expression tagUNP P14174C119HIS	А	116	GLU	-	expression tag	UNP P14174
A119HIS-expression tagUNP P14174A120HIS-expression tagUNP P14174A121HIS-expression tagUNP P14174A122HIS-expression tagUNP P14174B115LEU-expression tagUNP P14174B116GLU-expression tagUNP P14174B117HIS-expression tagUNP P14174B118HIS-expression tagUNP P14174B119HIS-expression tagUNP P14174B120HIS-expression tagUNP P14174B121HIS-expression tagUNP P14174B122HIS-expression tagUNP P14174C115LEU-expression tagUNP P14174C116GLU-expression tagUNP P14174C118HIS-expression tagUNP P14174C118HIS-expression tagUNP P14174C120HIS-expression tagUNP P14174C121HIS-expression tagUNP P14174	А	117	HIS	-	expression tag	UNP P14174
A120HIS-expression tagUNP P14174A121HIS-expression tagUNP P14174A122HIS-expression tagUNP P14174B115LEU-expression tagUNP P14174B116GLU-expression tagUNP P14174B117HIS-expression tagUNP P14174B118HIS-expression tagUNP P14174B119HIS-expression tagUNP P14174B120HIS-expression tagUNP P14174B121HIS-expression tagUNP P14174B122HIS-expression tagUNP P14174C115LEU-expression tagUNP P14174C116GLU-expression tagUNP P14174C118HIS-expression tagUNP P14174C119HIS-expression tagUNP P14174C120HIS-expression tagUNP P14174C121HIS-expression tagUNP P14174	А	118	HIS	-	expression tag	UNP P14174
A121HIS-expression tagUNP P14174A122HIS-expression tagUNP P14174B115LEU-expression tagUNP P14174B116GLU-expression tagUNP P14174B117HIS-expression tagUNP P14174B118HIS-expression tagUNP P14174B119HIS-expression tagUNP P14174B120HIS-expression tagUNP P14174B121HIS-expression tagUNP P14174B122HIS-expression tagUNP P14174C115LEU-expression tagUNP P14174C116GLU-expression tagUNP P14174C118HIS-expression tagUNP P14174C120HIS-expression tagUNP P14174C120HIS-expression tagUNP P14174C120HIS-expression tagUNP P14174C121HIS-expression tagUNP P14174	А	119	HIS	-	expression tag	UNP P14174
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B115LEU-expression tagUNP P14174B116GLU-expression tagUNP P14174B117HIS-expression tagUNP P14174B118HIS-expression tagUNP P14174B119HIS-expression tagUNP P14174B120HIS-expression tagUNP P14174B121HIS-expression tagUNP P14174B122HIS-expression tagUNP P14174C115LEU-expression tagUNP P14174C116GLU-expression tagUNP P14174C117HIS-expression tagUNP P14174C118HIS-expression tagUNP P14174C120HIS-expression tagUNP P14174C120HIS-expression tagUNP P14174C121HIS-expression tagUNP P14174C120HIS-expression tagUNP P14174C121HIS-expression tagUNP P14174	А		HIS	-	expression tag	UNP P14174
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B117HIS-expression tagUNP P14174B118HIS-expression tagUNP P14174B119HIS-expression tagUNP P14174B120HIS-expression tagUNP P14174B121HIS-expression tagUNP P14174B122HIS-expression tagUNP P14174C115LEU-expression tagUNP P14174C116GLU-expression tagUNP P14174C117HIS-expression tagUNP P14174C118HIS-expression tagUNP P14174C120HIS-expression tagUNP P14174C121HIS-expression tagUNP P14174	В	115	LEU	-	expression tag	UNP P14174
B118HIS-expression tagUNP P14174B119HIS-expression tagUNP P14174B120HIS-expression tagUNP P14174B121HIS-expression tagUNP P14174B122HIS-expression tagUNP P14174C115LEU-expression tagUNP P14174C116GLU-expression tagUNP P14174C117HIS-expression tagUNP P14174C118HIS-expression tagUNP P14174C120HIS-expression tagUNP P14174C120HIS-expression tagUNP P14174C121HIS-expression tagUNP P14174	В	116	GLU	-	expression tag	UNP P14174
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B121HIS-expression tagUNP P14174B122HIS-expression tagUNP P14174C115LEU-expression tagUNP P14174C116GLU-expression tagUNP P14174C117HIS-expression tagUNP P14174C118HIS-expression tagUNP P14174C119HIS-expression tagUNP P14174C120HIS-expression tagUNP P14174C121HIS-expression tagUNP P14174	В	119	HIS	-	expression tag	UNP P14174
B122HIS-expression tagUNP P14174C115LEU-expression tagUNP P14174C116GLU-expression tagUNP P14174C117HIS-expression tagUNP P14174C118HIS-expression tagUNP P14174C119HIS-expression tagUNP P14174C120HIS-expression tagUNP P14174C121HIS-expression tagUNP P14174	В	120	HIS	-	expression tag	UNP P14174
C115LEU-expression tagUNP P14174C116GLU-expression tagUNP P14174C117HIS-expression tagUNP P14174C118HIS-expression tagUNP P14174C119HIS-expression tagUNP P14174C120HIS-expression tagUNP P14174C121HIS-expression tagUNP P14174	В	121	HIS	-	expression tag	UNP P14174
C116GLU-expression tagUNP P14174C117HIS-expression tagUNP P14174C118HIS-expression tagUNP P14174C119HIS-expression tagUNP P14174C120HIS-expression tagUNP P14174C121HIS-expression tagUNP P14174	В	122	HIS	-	expression tag	UNP P14174
C117HIS-expression tagUNP P14174C118HIS-expression tagUNP P14174C119HIS-expression tagUNP P14174C120HIS-expression tagUNP P14174C121HIS-expression tagUNP P14174		115	LEU	-	expression tag	UNP P14174
C118HIS-expression tagUNP P14174C119HIS-expression tagUNP P14174C120HIS-expression tagUNP P14174C121HIS-expression tagUNP P14174	С	116	GLU	-	expression tag	UNP P14174
C119HIS-expression tagUNP P14174C120HIS-expression tagUNP P14174C121HIS-expression tagUNP P14174		117	HIS	-	expression tag	UNP P14174
C120HIS-expression tagUNP P14174C121HIS-expression tagUNP P14174	С	118	HIS	-	expression tag	UNP P14174
C 121 HIS - expression tag UNP P14174		119	HIS	-	- 0	UNP P14174
		120	HIS	-		
	С	121	HIS	-	expression tag	UNP P14174

There are 24 discrepancies between the modelled and reference sequences:

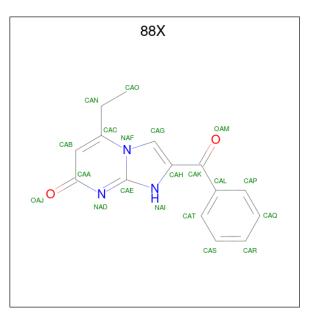
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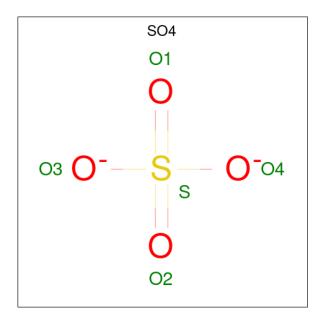
Chain	Residue	Modelled	Actual	Comment	Reference
С	122	HIS	-	expression tag	UNP P14174

• Molecule 2 is 5-ethyl-2-(phenylcarbonyl)imidazo[1,2-a]pyrimidin-7(1H)-one (three-letter code: 88X) (formula: $C_{15}H_{13}N_3O_2$).



]	Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
	2	А	1	Total 20	C 15	N 3	O 2	0	0

• Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).





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

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	96	Total O 96 96	0	0
4	В	115	Total O 115 115	0	0
4	С	82	TotalO8282	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.

- Chain A:
 79%
 14%
 7%

 Image: State S
- Molecule 1: Macrophage migration inhibitory factor



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	67.66Å 67.41Å 88.45Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.70 - 1.86	Depositor
	33.70 - 1.86	EDS
% Data completeness	97.9(33.70-1.86)	Depositor
(in resolution range)	98.1 (33.70-1.86)	EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$0.50 (at 1.85 \text{\AA})$	Xtriage
Refinement program	CNS, CNX 2005	Depositor
R, R_{free}	0.185 , 0.201	Depositor
It, Itfree	0.179 , 0.196	DCC
R_{free} test set	1716 reflections $(4.96%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	23.2	Xtriage
Anisotropy	0.244	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.38, 45.9	EDS
L-test for $twinning^2$	$< L > = 0.48, < L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.024 for k,h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2985	wwPDB-VP
Average B, all atoms $(Å^2)$	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.41% 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: SO4, $88\mathrm{X}$

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		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.27	0/899	0.47	0/1223	
1	В	0.26	0/914	0.46	0/1243	
1	С	0.24	0/920	0.46	0/1251	
All	All	0.26	0/2733	0.47	0/3717	

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	873	0	872	19	0
1	В	893	0	882	10	0
1	С	896	0	887	10	0
2	А	20	0	13	4	0
3	В	5	0	0	0	0
3	С	5	0	0	0	0
4	А	96	0	0	2	0
4	В	115	0	0	2	0
4	С	82	0	0	0	0
All	All	2985	0	2654	41	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 8.

All (41) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:102:ASN:HD22	1:A:104:ALA:H	1.23	0.86
2:A:123:88X:H2AO	2:A:123:88X:HAG	1.62	0.81
1:A:5[B]:VAL:HG12	1:A:59:CYS:SG	2.28	0.74
1:B:47:MET:HE3	1:B:58:LEU:HG	1.74	0.69
1:A:102:ASN:ND2	1:A:104:ALA:H	1.91	0.68
1:A:47:MET:HE3	1:A:58:LEU:HG	1.76	0.67
1:A:3:PHE:CE2	1:A:5[B]:VAL:HG13	2.30	0.66
2:A:123:88X:HAG	2:A:123:88X:CAO	2.25	0.66
4:B:196:HOH:O	1:C:2:MET:HE1	1.95	0.66
1:B:19:LEU:HD22	1:B:39:VAL:HG23	1.77	0.65
1:C:1:PRO:HD2	1:C:37:ILE:HD13	1.81	0.62
2:A:123:88X:H2AO	2:A:123:88X:CAG	2.33	0.57
2:A:123:88X:CAO	2:A:123:88X:CAG	2.82	0.56
1:B:102:ASN:ND2	1:B:104:ALA:H	2.04	0.56
1:C:4:ILE:CD1	1:C:40:HIS:HB3	2.36	0.56
1:A:105:ASN:HD22	1:C:72:ASN:ND2	2.07	0.53
1:A:4:ILE:HD12	1:A:40:HIS:HB3	1.92	0.52
1:A:4:ILE:CD1	1:A:40:HIS:HB3	2.39	0.52
1:A:3:PHE:CE2	1:A:5[A]:VAL:HG22	2.45	0.51
1:B:102:ASN:HD22	1:B:104:ALA:H	1.58	0.51
1:A:4:ILE:HG12	4:A:220:HOH:O	2.11	0.49
1:A:5[B]:VAL:CG2	1:A:41:VAL:HG22	2.42	0.49
1:A:3:PHE:CE2	1:A:5[A]:VAL:CG2	2.95	0.49
1:B:11:ARG:HD2	4:B:215:HOH:O	2.12	0.49
1:A:1:PRO:HD2	1:A:37:ILE:HD13	1.96	0.48
1:C:4:ILE:HD13	1:C:40:HIS:HB3	1.95	0.47
1:A:5[B]:VAL:HG23	1:A:41:VAL:HA	1.97	0.47
4:A:124:HOH:O	1:B:2:MET:HE3	2.15	0.46
1:A:102:ASN:HD22	1:A:104:ALA:N	2.02	0.46
1:C:33:PRO:HA	1:C:34:PRO:HD3	1.87	0.45
1:B:33:PRO:HA	1:B:34:PRO:HD3	1.87	0.45
1:A:2:MET:HE3	1:C:58:LEU:HD13	1.99	0.44
1:B:1:PRO:HD2	1:B:37:ILE:HD13	2.00	0.44
1:C:33:PRO:HG2	1:C:36:TYR:HD2	1.83	0.44
1:B:109:ASN:O	1:B:110:ASN:HB2	2.18	0.43
1:C:4:ILE:HD12	1:C:40:HIS:HB3	1.99	0.43
1:A:19:LEU:HD22	1:A:39:VAL:HG23	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4:ILE:HD12	1:B:4:ILE:N	2.35	0.42
1:A:33:PRO:HA	1:A:34:PRO:HD3	1.95	0.41
1:A:47:MET:CE	1:A:58:LEU:HG	2.49	0.41
1:C:90:SER:HA	1:C:91:PRO:HD3	1.94	0.40

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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	А	114/122~(93%)	112 (98%)	2(2%)	0	100 100
1	В	$115/122 \ (94\%)$	112 (97%)	3(3%)	0	100 100
1	С	116/122~(95%)	115 (99%)	1 (1%)	0	100 100
All	All	345/366~(94%)	339~(98%)	6 (2%)	0	100 100

There are no Ramachandran outliers to report.

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	96/102~(94%)	95~(99%)	1 (1%)	76 69
1	В	97/102~(95%)	97~(100%)	0	100 100
1	С	98/102~(96%)	98 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	291/306~(95%)	290 (100%)	1 (0%)	92 91

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	102	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	102	ASN
1	А	105	ASN
1	А	109	ASN
1	В	62	HIS
1	В	102	ASN
1	В	105	ASN
1	В	109	ASN
1	С	24	GLN
1	С	105	ASN
1	С	109	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)

3 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



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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		n Res	Link	Bond lengths			Bond angles				
	IVI0I	туре	Unam		nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
	3	SO4	С	123	-	4,4,4	0.27	0	6,6,6	0.07	0	
Ī	3	SO4	В	123	-	4,4,4	0.29	0	6,6,6	0.06	0	
	2	88X	А	123	-	20,22,22	1.65	6 (30%)	22,31,31	0.95	1 (4%)	

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.

Mo	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	88X	А	123	-	-	2/10/10/10	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	А	123	88X	CAE-NAD	3.31	1.40	1.32
2	А	123	88X	CAN-CAC	3.09	1.53	1.50
2	А	123	88X	CAH-NAI	-2.63	1.33	1.37
2	А	123	88X	CAG-NAF	-2.40	1.33	1.38
2	А	123	88X	CAH-CAK	2.18	1.53	1.46
2	А	123	88X	CAL-CAK	2.13	1.53	1.49

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	А	123	88X	CAN-CAC-CAB	-2.39	117.96	124.50

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	А	123	88X	CAB-CAC-CAN-CAO
2	А	123	88X	NAF-CAC-CAN-CAO

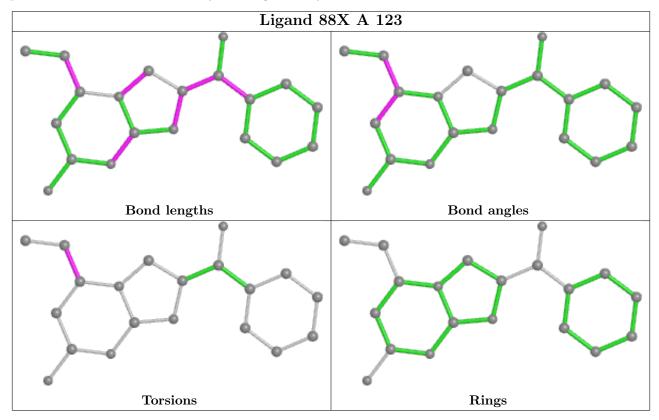
There are no ring outliers.



1 monom	er is inv	olved in	4 short	contacts:
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	А	123	88X	4	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 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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q < 0.9
1	А	114/122~(93%)	0.10	5 (4%) 34 33	16, 21, 33, 39	0
1	В	117/122~(95%)	-0.09	2 (1%) 70 70	15, 20, 32, 45	0
1	С	117/122~(95%)	0.25	5 (4%) 35 33	17, 25, 36, 44	0
All	All	348/366~(95%)	0.08	12 (3%) 45 42	15, 22, 34, 45	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	4	ILE	3.4
1	С	16	ASP	3.0
1	С	88	ARG	2.9
1	С	4	ILE	2.6
1	С	70	ALA	2.3
1	А	88	ARG	2.3
1	А	5[A]	VAL	2.2
1	А	60[A]	SER	2.2
1	В	117	HIS	2.2
1	С	85	GLU	2.1
1	А	35	GLN	2.1
1	В	88	ARG	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 monosaccharides in this entry.

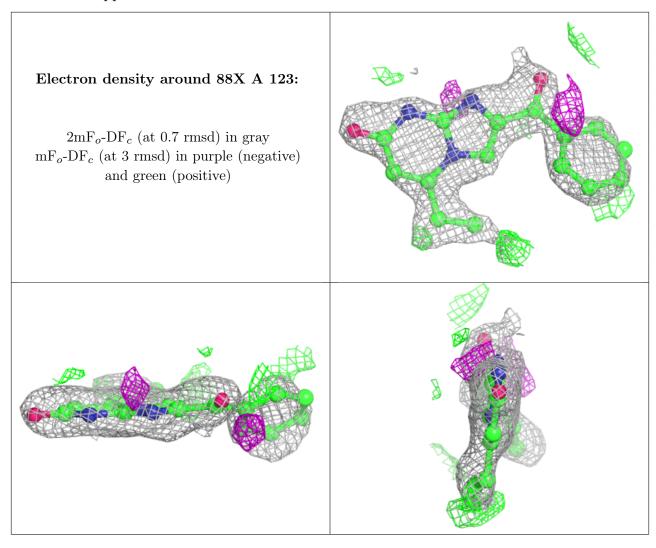


6.4 Ligands (i)

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	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	Q<0.9
2	88X	А	123	20/20	0.82	0.23	$51,\!52,\!53,\!53$	0
3	SO4	В	123	5/5	0.90	0.26	68,68,69,69	0
3	SO4	С	123	5/5	0.92	0.35	61,61,62,63	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.

