Full wwPDB X-ray Structure Validation Report (i)

Oct 25, 2023 – 06:02 AM EDT

PDB ID	:	3B1U
Title	:	Crystal structure of human peptidylarginine deiminase 4 in complex with o-F-amidine
Authors	:	Causey, C.P.; Jones, J.E.; Slack, J.L.; Kamei, D.; Jones Jr, L.E.; Subramanian, V.; Knuckley, B.; Ebrahimi, P.; Chumanevich, A.A.; Luo, Y.; Hashimoto, H.; Shimizu, T.; Sato, M.; Hofseth, L.J.; Thompson, P.R.
Deposited on	:	2011-07-13
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 (i)) were used in the production of this report:

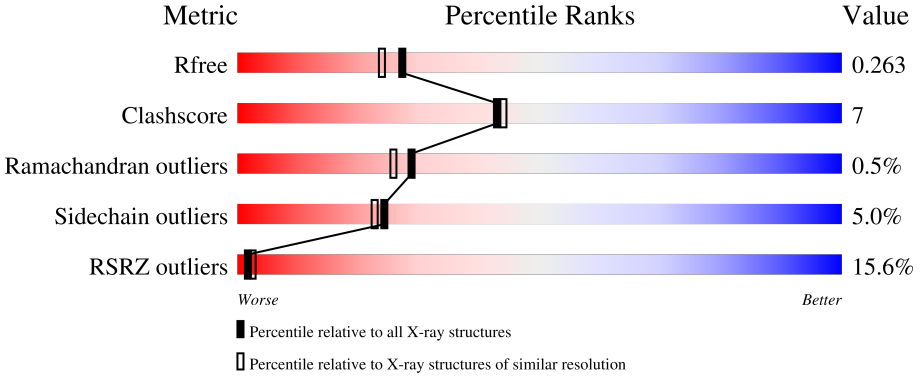
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
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	A	671	15% 80% 12% • 6%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 5164 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.

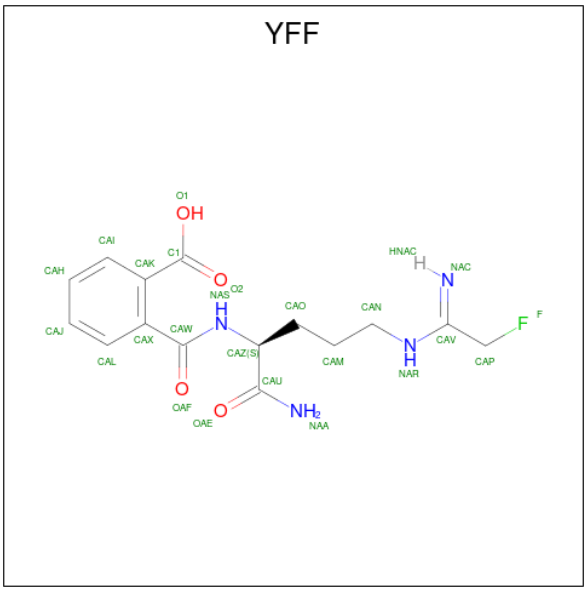
- Molecule 1 is a protein called Protein-arginine deiminase type-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	628	4947	3158	829	925	35	0	0	0

There are 11 discrepancies between the modelled and reference sequences:

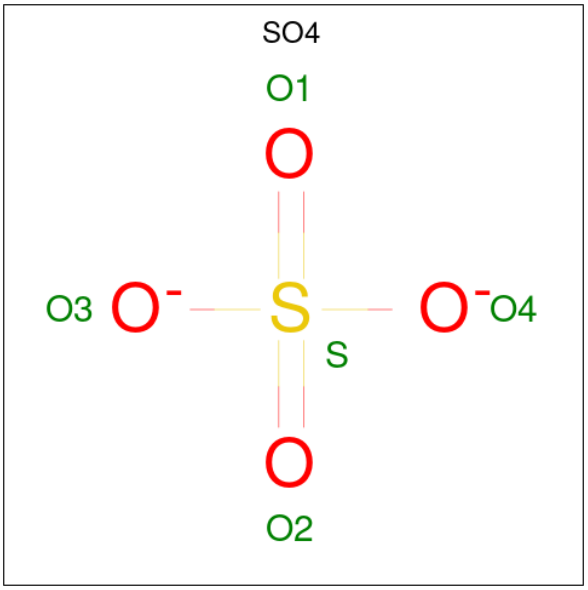
Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	GLY	-	expression tag	UNP Q9UM07
A	-6	PRO	-	expression tag	UNP Q9UM07
A	-5	LEU	-	expression tag	UNP Q9UM07
A	-4	GLY	-	expression tag	UNP Q9UM07
A	-3	SER	-	expression tag	UNP Q9UM07
A	-2	PRO	-	expression tag	UNP Q9UM07
A	-1	GLU	-	expression tag	UNP Q9UM07
A	0	PHE	-	expression tag	UNP Q9UM07
A	55	SER	GLY	SEE REMARK 999	UNP Q9UM07
A	82	ALA	VAL	SEE REMARK 999	UNP Q9UM07
A	112	ALA	GLY	SEE REMARK 999	UNP Q9UM07

- Molecule 2 is 2-{[(2S)-1-amino-5-{[(1Z)-2-fluoroethanimidoyl]amino}-1-oxopentan-2-yl]carbamoyl}benzoic acid (three-letter code: YFF) (formula: $C_{15}H_{19}FN_4O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	23	15	4	4	0	0

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
3	A	1	5	4	1	0	0
			Total	O	S		
3	A	1	5	4	1	0	0
			Total	O	S		
3	A	1	5	4	1	0	0

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
4	A	5	5	5	0	0

- Molecule 5 is water.

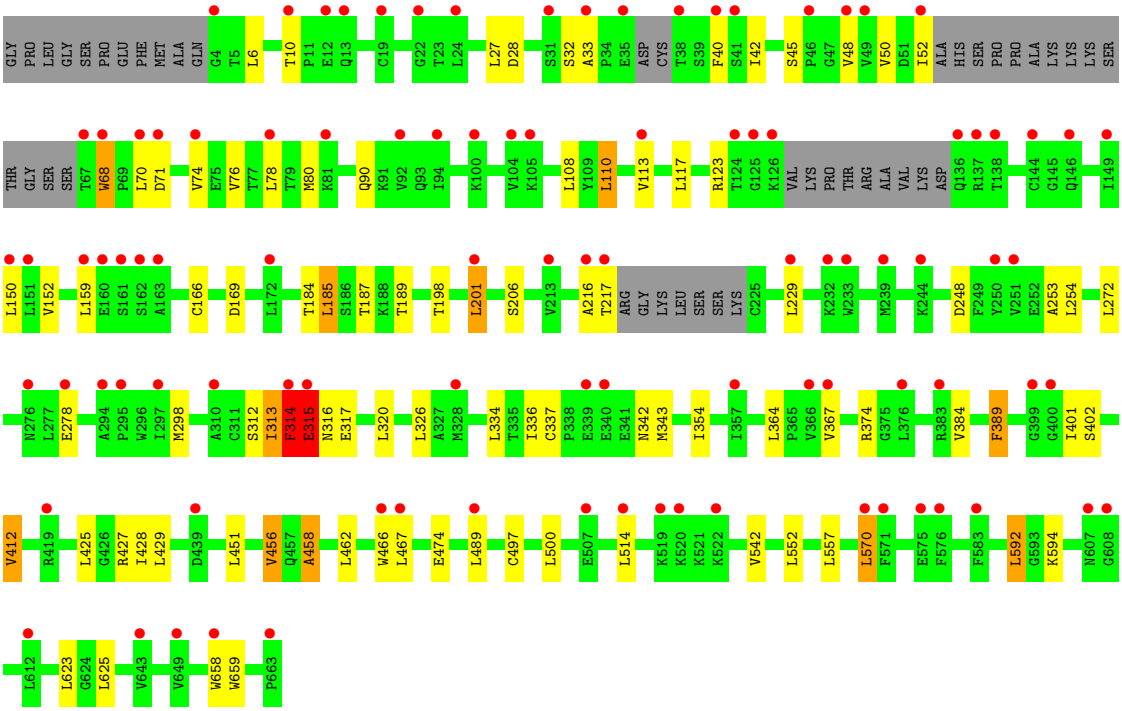
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	174	174	174	0	0

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: Protein-arginine deiminase type-4

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	146.42Å 60.47Å 115.51Å 90.00° 124.43° 90.00°	Depositor
Resolution (Å)	20.00 – 2.10 19.88 – 2.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-2.10) 91.5 (19.88-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.47 (at 2.09Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.219 , 0.250 0.230 , 0.263	Depositor DCC
R_{free} test set	2254 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	51.7	Xtriage
Anisotropy	0.222	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 55.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	5164	wwPDB-VP
Average B, all atoms (Å^2)	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.08% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: YFF, CA, SO4

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	0.30	0/5066	0.49	0/6874

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	A	4947	0	4905	67	0
2	A	23	0	15	0	0
3	A	15	0	0	0	0
4	A	5	0	0	0	0
5	A	174	0	0	0	0
All	All	5164	0	4920	67	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 7.

All (67) 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:313:ILE:HG12	1:A:314:PHE:N	1.58	1.14
1:A:313:ILE:CG1	1:A:314:PHE:H	1.71	1.04
1:A:313:ILE:HG12	1:A:314:PHE:HD2	1.31	0.95
1:A:313:ILE:HG12	1:A:314:PHE:H	0.79	0.90
1:A:313:ILE:CG1	1:A:314:PHE:HD2	1.87	0.88
1:A:425:LEU:HD12	1:A:456:VAL:HG13	1.58	0.86
1:A:367:VAL:HG21	1:A:384:VAL:CG1	2.12	0.80
1:A:367:VAL:HG21	1:A:384:VAL:HG12	1.67	0.77
1:A:42:ILE:HG21	1:A:50:VAL:HG11	1.66	0.76
1:A:6:LEU:HD21	1:A:28:ASP:HB2	1.68	0.73
1:A:298:MET:HE1	1:A:412:VAL:HG22	1.71	0.72
1:A:313:ILE:HG12	1:A:314:PHE:CD2	2.21	0.72
1:A:27:LEU:HD13	1:A:78:LEU:HD13	1.71	0.71
1:A:623:LEU:HB2	1:A:625:LEU:HD23	1.73	0.70
1:A:201:LEU:HD13	1:A:229:LEU:HD11	1.73	0.69
1:A:314:PHE:O	1:A:316:ASN:N	2.28	0.67
1:A:354:ILE:HD12	1:A:367:VAL:HG22	1.79	0.65
1:A:425:LEU:HD12	1:A:456:VAL:CG1	2.26	0.64
1:A:6:LEU:HD21	1:A:28:ASP:CB	2.28	0.63
1:A:52:ILE:HD12	1:A:76:VAL:HG22	1.81	0.62
1:A:313:ILE:CG1	1:A:314:PHE:CD2	2.78	0.60
1:A:185:LEU:HD22	1:A:187:THR:HG23	1.84	0.59
1:A:313:ILE:HD11	1:A:314:PHE:CD2	2.37	0.59
1:A:314:PHE:H	1:A:314:PHE:HD2	1.52	0.57
1:A:108:LEU:HG	1:A:110:LEU:HD13	1.86	0.57
1:A:201:LEU:HD13	1:A:229:LEU:CD1	2.34	0.57
1:A:367:VAL:HG21	1:A:384:VAL:HG11	1.84	0.56
1:A:71:ASP:O	1:A:74:VAL:HG12	2.06	0.56
1:A:462:LEU:CD2	1:A:552:LEU:HD22	2.38	0.54
1:A:123:ARG:HD3	1:A:659:TRP:CD1	2.43	0.54
1:A:367:VAL:HG23	1:A:389:PHE:CE2	2.44	0.53
1:A:10:THR:HG22	1:A:32:SER:CB	2.39	0.52
1:A:74:VAL:HG13	1:A:74:VAL:O	2.10	0.52
1:A:497:CYS:SG	1:A:570:LEU:HD13	2.50	0.51
1:A:313:ILE:CD1	1:A:314:PHE:CD2	2.93	0.51
1:A:216:ALA:O	1:A:217:THR:HG22	2.11	0.51
1:A:462:LEU:HD23	1:A:552:LEU:HD22	1.93	0.51
1:A:33:ALA:CB	1:A:70:LEU:HD11	2.41	0.50
1:A:428:ILE:HD13	1:A:451:LEU:HD22	1.93	0.50
1:A:166:CYS:HB2	1:A:254:LEU:HD22	1.95	0.49
1:A:27:LEU:HD11	1:A:78:LEU:HD22	1.96	0.48
1:A:326:LEU:HD23	1:A:592:LEU:HD22	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:354:ILE:CD1	1:A:367:VAL:HG22	2.45	0.47
1:A:456:VAL:HG21	1:A:658:TRP:HB2	1.97	0.47
1:A:198:THR:HG23	1:A:272:LEU:HB2	1.96	0.46
1:A:594:LYS:HA	1:A:625:LEU:HD13	1.96	0.46
1:A:10:THR:HG22	1:A:32:SER:HB3	1.97	0.46
1:A:314:PHE:O	1:A:315:GLU:C	2.55	0.46
1:A:48:VAL:HG23	1:A:90:GLN:HE21	1.81	0.45
1:A:337:CYS:SG	1:A:342:ASN:ND2	2.90	0.45
1:A:401:ILE:HG23	1:A:402:SER:N	2.32	0.44
1:A:466:TRP:CZ3	1:A:542:VAL:HG13	2.52	0.44
1:A:313:ILE:O	1:A:314:PHE:O	2.35	0.44
1:A:427:ARG:HD2	1:A:458:ALA:O	2.18	0.44
1:A:313:ILE:C	1:A:314:PHE:O	2.56	0.44
1:A:334:LEU:HD11	1:A:336:ILE:HG13	1.99	0.44
1:A:467:LEU:HD13	1:A:474:GLU:HB2	1.99	0.43
1:A:33:ALA:HB1	1:A:70:LEU:HD11	2.00	0.43
1:A:40:PHE:CE1	1:A:42:ILE:HD13	2.53	0.43
1:A:52:ILE:HG23	1:A:68:TRP:CZ2	2.53	0.43
1:A:45:SER:OG	1:A:90:GLN:NE2	2.52	0.43
1:A:312:SER:HA	1:A:320:LEU:HD11	2.01	0.43
1:A:298:MET:CE	1:A:412:VAL:HG22	2.43	0.42
1:A:298:MET:HB3	1:A:412:VAL:HG21	1.99	0.42
1:A:113:VAL:HB	1:A:189:THR:HG22	2.01	0.42
1:A:152:VAL:HA	1:A:253:ALA:HB3	2.02	0.41
1:A:184:THR:HG22	1:A:248:ASP:OD2	2.21	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	618/671 (92%)	598 (97%)	17 (3%)	3 (0%)	29 26

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	314	PHE
1	A	315	GLU
1	A	458	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	Outliers	Percentiles
1	A	559/594 (94%)	531 (95%)	28 (5%)	24 23

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	68	TRP
1	A	80	MET
1	A	110	LEU
1	A	117	LEU
1	A	150	LEU
1	A	159	LEU
1	A	169	ASP
1	A	185	LEU
1	A	201	LEU
1	A	206	SER
1	A	278	GLU
1	A	313	ILE
1	A	314	PHE
1	A	315	GLU
1	A	317	GLU
1	A	343	MET
1	A	364	LEU
1	A	374	ARG
1	A	389	PHE
1	A	412	VAL
1	A	429	LEU
1	A	456	VAL

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Mol	Chain	Res	Type
1	A	489	LEU
1	A	500	LEU
1	A	514	LEU
1	A	557	LEU
1	A	570	LEU
1	A	592	LEU

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

Mol	Chain	Res	Type
1	A	43	ASN
1	A	90	GLN
1	A	136	GLN
1	A	178	GLN
1	A	303	GLN
1	A	342	ASN
1	A	448	GLN
1	A	504	GLN
1	A	505	GLN
1	A	524	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 9 ligands modelled in this entry, 5 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	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	SO4	A	905	-	4,4,4	0.14	0	6,6,6	0.05	0
3	SO4	A	906	-	4,4,4	0.15	0	6,6,6	0.05	0
3	SO4	A	907	-	4,4,4	0.14	0	6,6,6	0.05	0
2	YFF	A	800	1	23,23,24	0.70	0	27,30,31	1.18	3 (11%)

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	YFF	A	800	1	-	10/22/23/25	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	800	YFF	CAO-CAZ-NAS	-3.38	104.05	110.88
2	A	800	YFF	CAP-CAV-NAR	2.83	117.87	114.24
2	A	800	YFF	CAM-CAN-NAR	-2.63	104.70	112.21

There are no chirality outliers.

All (10) torsion outliers are listed below:

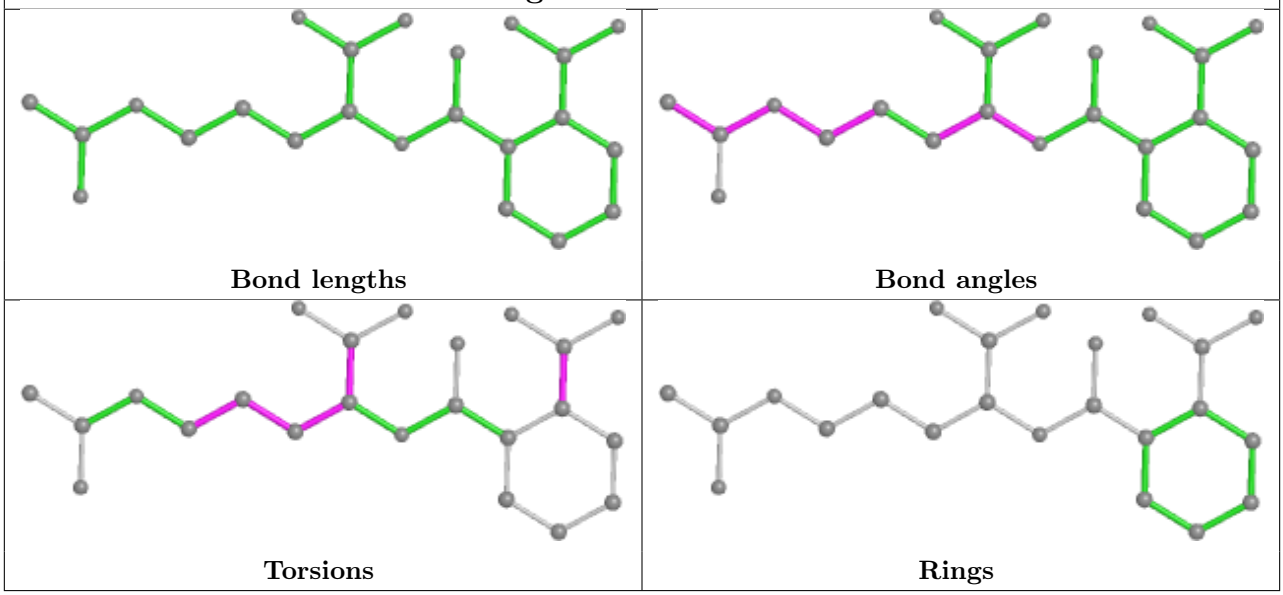
Mol	Chain	Res	Type	Atoms
2	A	800	YFF	CAO-CAM-CAN-NAR
2	A	800	YFF	CAN-CAM-CAO-CAZ
2	A	800	YFF	CAM-CAO-CAZ-CAU
2	A	800	YFF	OAE-CAU-CAZ-NAS
2	A	800	YFF	O1-C1-CAK-CAI
2	A	800	YFF	NAA-CAU-CAZ-NAS
2	A	800	YFF	O2-C1-CAK-CAI
2	A	800	YFF	CAM-CAO-CAZ-NAS
2	A	800	YFF	O2-C1-CAK-CAX
2	A	800	YFF	O1-C1-CAK-CAX

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 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.

Ligand YFF A 800



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, 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	628/671 (93%)	0.86	98 (15%) 2 2	56, 78, 110, 137	0

All (98) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	217	THR	11.7
1	A	159	LEU	7.6
1	A	314	PHE	7.1
1	A	74	VAL	6.0
1	A	137	ARG	5.4
1	A	522	LYS	5.2
1	A	136	GLN	4.8
1	A	576	PHE	4.6
1	A	519	LYS	4.6
1	A	160	GLU	4.5
1	A	125	GLY	4.3
1	A	213	VAL	4.2
1	A	419	ARG	4.1
1	A	520	LYS	4.1
1	A	100	LYS	4.0
1	A	70	LEU	3.9
1	A	328	MET	3.9
1	A	315	GLU	3.9
1	A	67	THR	3.8
1	A	12	GLU	3.8
1	A	94	ILE	3.7
1	A	251	VAL	3.7
1	A	162	SER	3.7
1	A	104	VAL	3.6
1	A	658	TRP	3.6
1	A	4	GLY	3.6
1	A	81	LYS	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	68	TRP	3.5
1	A	78	LEU	3.5
1	A	383	ARG	3.5
1	A	13	GLN	3.5
1	A	161	SER	3.5
1	A	163	ALA	3.4
1	A	612	LEU	3.4
1	A	232	LYS	3.3
1	A	663	PRO	3.3
1	A	570	LEU	3.3
1	A	10	THR	3.2
1	A	24	LEU	3.2
1	A	340	GLU	3.1
1	A	31	SER	3.1
1	A	276	ASN	3.0
1	A	172	LEU	3.0
1	A	92	VAL	3.0
1	A	583	PHE	2.9
1	A	151	LEU	2.9
1	A	575	GLU	2.9
1	A	38	THR	2.8
1	A	138	THR	2.8
1	A	339	GLU	2.8
1	A	49	VAL	2.8
1	A	35	GLU	2.7
1	A	144	CYS	2.7
1	A	146	GLN	2.7
1	A	514	LEU	2.7
1	A	149	ILE	2.7
1	A	105	LYS	2.7
1	A	233	TRP	2.6
1	A	244	LYS	2.6
1	A	41	SER	2.6
1	A	466	TRP	2.6
1	A	126	LYS	2.6
1	A	229	LEU	2.6
1	A	439	ASP	2.5
1	A	489	LEU	2.5
1	A	310	ALA	2.5
1	A	22	GLY	2.5
1	A	33	ALA	2.5
1	A	52	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	400	GLY	2.4
1	A	399	GLY	2.4
1	A	507	GLU	2.4
1	A	294	ALA	2.4
1	A	376	LEU	2.4
1	A	46	PRO	2.3
1	A	71	ASP	2.3
1	A	357	ILE	2.3
1	A	150	LEU	2.3
1	A	201	LEU	2.3
1	A	216	ALA	2.3
1	A	649	VAL	2.3
1	A	607	ASN	2.2
1	A	295	PRO	2.2
1	A	643	VAL	2.2
1	A	297	ILE	2.1
1	A	571	PHE	2.1
1	A	467	LEU	2.1
1	A	48	VAL	2.1
1	A	113	VAL	2.1
1	A	124	THR	2.1
1	A	278	GLU	2.1
1	A	608	GLY	2.1
1	A	250	TYR	2.1
1	A	366	VAL	2.0
1	A	367	VAL	2.0
1	A	19	CYS	2.0
1	A	40	PHE	2.0
1	A	239	MET	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)

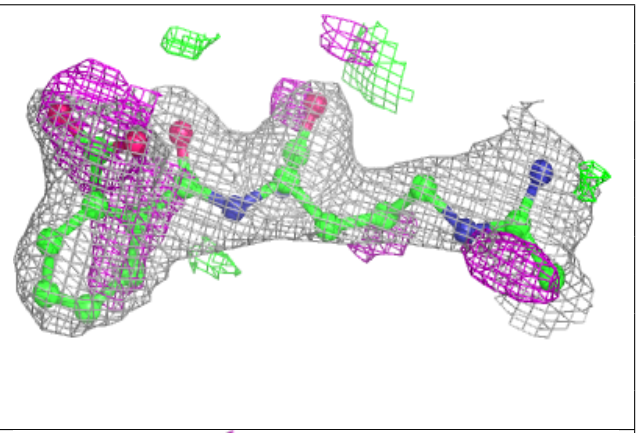
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

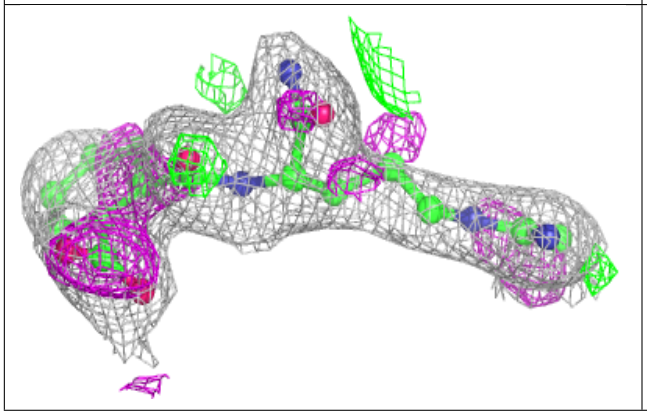
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	YFF	A	800	23/24	0.79	0.27	61,63,64,64	0
3	SO4	A	907	5/5	0.88	0.32	87,87,87,87	0
3	SO4	A	905	5/5	0.94	0.22	92,92,92,92	0
3	SO4	A	906	5/5	0.96	0.29	94,94,94,94	0
4	CA	A	901	1/1	0.97	0.10	54,54,54,54	0
4	CA	A	903	1/1	0.97	0.13	59,59,59,59	0
4	CA	A	904	1/1	0.97	0.15	54,54,54,54	0
4	CA	A	902	1/1	0.98	0.10	54,54,54,54	0
4	CA	A	900	1/1	0.99	0.03	49,49,49,49	0

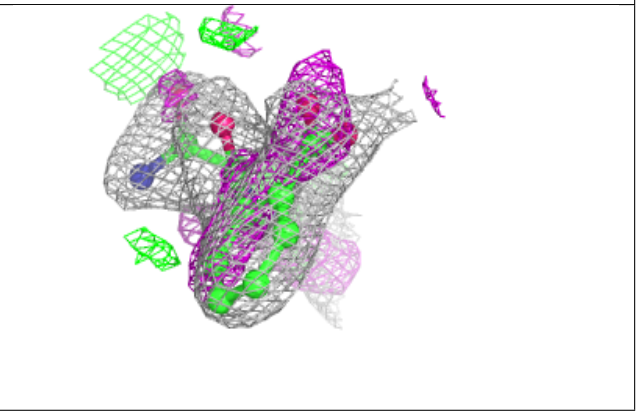
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around YFF A 800:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)







6.5 Other polymers (i)

There are no such residues in this entry.