Full wwPDB X-ray Structure Validation Report (i)

Oct 18, 2023 – 03:27 PM EDT

PDB ID	:	2DW5
Title	:	Crystal structure of human peptidylarginine deiminase 4 in complex with N-alpha-benzoyl-N5-(2-fluoro-1-iminoethyl)-L-ornithine amide
Authors	:	Luo, Y.; Arita, K.; Sato, M.; Thompson, P.R.
Deposited on	:	2006-08-04
Resolution	:	2.30 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:

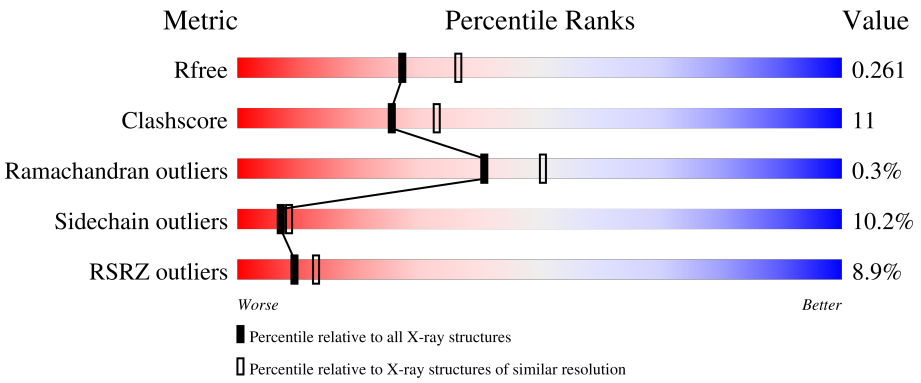
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber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

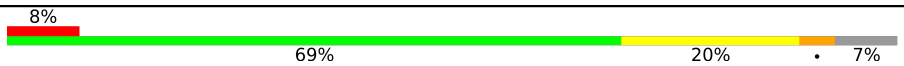
The reported resolution of this entry is 2.30 Å.

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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 5118 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	626	4928	3143	827	923	35	26	0	0

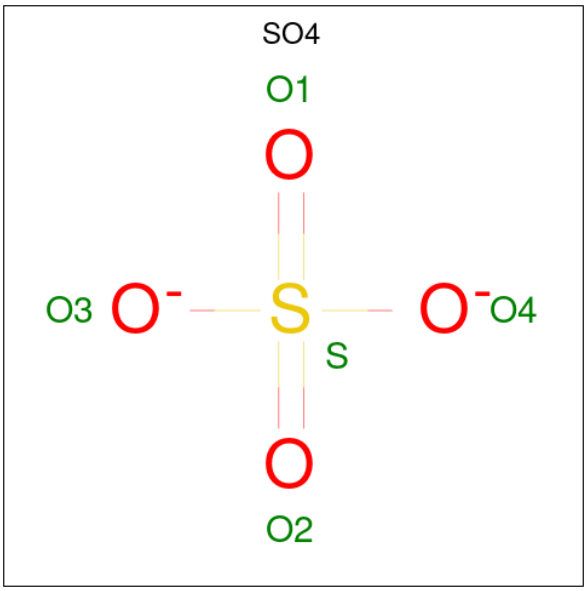
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	GLY	-	cloning artifact	UNP Q9UM07
A	-6	PRO	-	cloning artifact	UNP Q9UM07
A	-5	LEU	-	cloning artifact	UNP Q9UM07
A	-4	GLY	-	cloning artifact	UNP Q9UM07
A	-3	SER	-	cloning artifact	UNP Q9UM07
A	-2	PRO	-	cloning artifact	UNP Q9UM07
A	-1	GLU	-	cloning artifact	UNP Q9UM07
A	0	PHE	-	cloning artifact	UNP Q9UM07

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

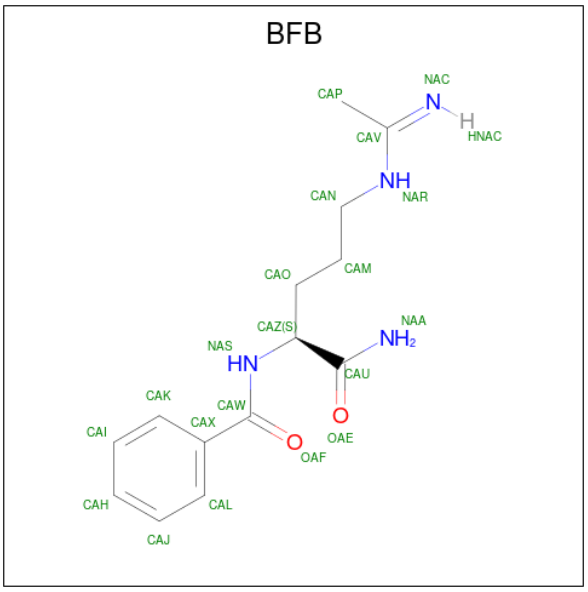
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
2	A	5	5	5	0	0

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



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

- Molecule 4 is N-[(1S)-1-(AMINOCARBONYL)-4-(ETHANIMIDOYLAMINO)BUTYL]BENZAMIDE (three-letter code: BFB) (formula: $C_{14}H_{20}N_4O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	20	14	4	2	0	0

- Molecule 5 is water.

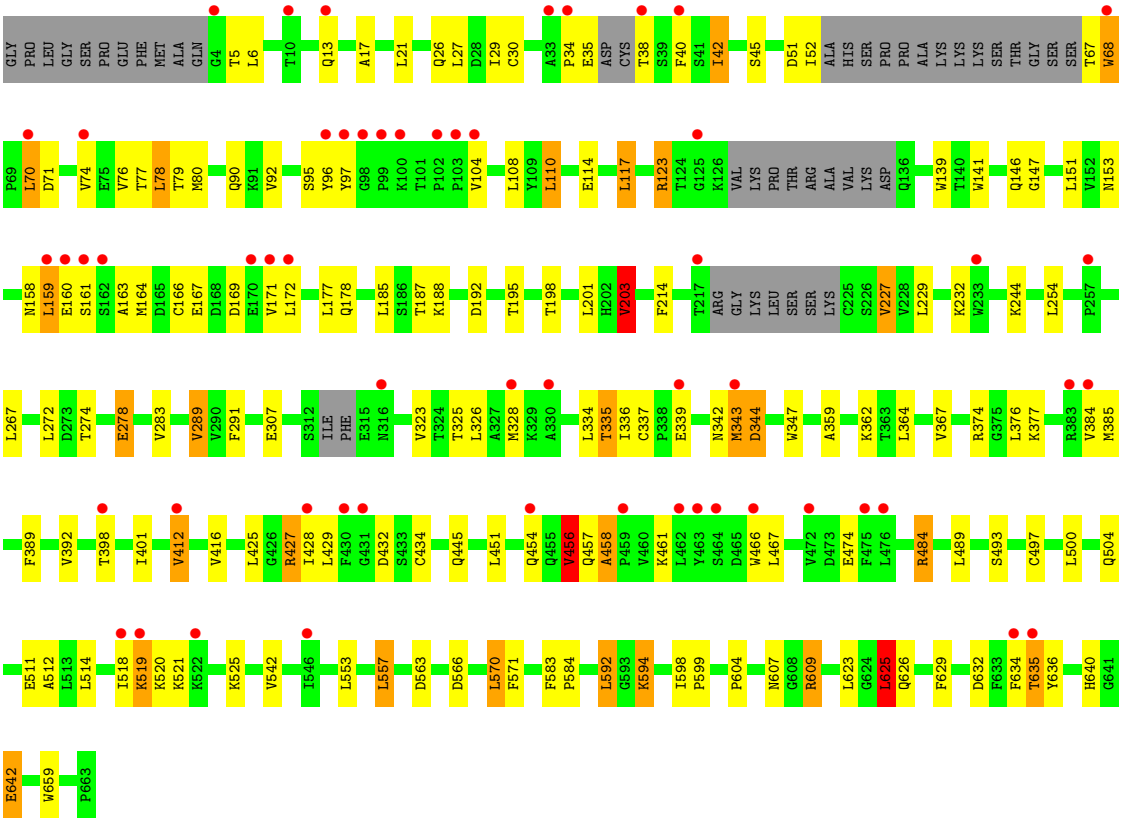
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	150	150	150	0	0

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	146.26Å 60.52Å 114.91Å 90.00° 124.19° 90.00°	Depositor
Resolution (Å)	42.70 – 2.30 42.65 – 2.20	Depositor EDS
% Data completeness (in resolution range)	91.3 (42.70-2.30) 86.5 (42.65-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.16 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.198 , 0.252 0.205 , 0.261	Depositor DCC
R_{free} test set	1842 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	44.2	Xtriage
Anisotropy	0.695	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 60.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	5118	wwPDB-VP
Average B, all atoms (Å^2)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.14% 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: SO4, CA, BFB

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	0.78	3/5045 (0.1%)	0.92	13/6844 (0.2%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	520	LYS	CB-CG	-9.63	1.26	1.52
1	A	519	LYS	CB-CG	-5.40	1.38	1.52
1	A	141	TRP	CB-CG	-5.01	1.41	1.50

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	520	LYS	CB-CG-CD	17.68	157.57	111.60
1	A	519	LYS	CA-CB-CG	16.84	150.44	113.40
1	A	520	LYS	CA-CB-CG	16.69	150.12	113.40
1	A	519	LYS	CB-CG-CD	10.59	139.13	111.60
1	A	412	VAL	CB-CA-C	-8.84	94.60	111.40
1	A	377	LYS	CA-CB-CG	8.66	132.46	113.40
1	A	427	ARG	NE-CZ-NH2	-7.41	116.59	120.30
1	A	123	ARG	NE-CZ-NH2	-7.16	116.72	120.30
1	A	203	VAL	CB-CA-C	-6.44	99.16	111.40
1	A	456	VAL	CG1-CB-CG2	5.61	119.88	110.90
1	A	427	ARG	NE-CZ-NH1	5.49	123.04	120.30
1	A	625	LEU	CA-CB-CG	5.12	127.08	115.30
1	A	392	VAL	CB-CA-C	-5.09	101.72	111.40

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	4928	0	4884	104	0
2	A	5	0	0	0	0
3	A	15	0	0	0	0
4	A	20	0	16	1	0
5	A	150	0	0	6	0
All	All	5118	0	4900	104	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 11.

All (104) 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:416:VAL:HG21	1:A:557:LEU:O	1.55	1.06
1:A:635:THR:HG22	1:A:636:TYR:CD1	1.99	0.96
1:A:367:VAL:HG21	1:A:384:VAL:CG1	1.99	0.93
1:A:367:VAL:HG21	1:A:384:VAL:HG12	1.55	0.86
1:A:203:VAL:HG22	1:A:229:LEU:HD13	1.61	0.82
1:A:203:VAL:HG13	1:A:267:LEU:HD23	1.62	0.81
1:A:454:GLN:O	5:A:908:HOH:O	2.00	0.80
1:A:484:ARG:NH1	1:A:563:ASP:OD1	2.15	0.79
1:A:67:THR:N	1:A:97:TYR:HH	1.81	0.79
1:A:425:LEU:HD12	1:A:456:VAL:HG13	1.67	0.77
1:A:178:GLN:HE21	1:A:362:LYS:NZ	1.88	0.71
1:A:367:VAL:CG2	1:A:384:VAL:CG1	2.68	0.71
1:A:198:THR:HG23	1:A:272:LEU:HD12	1.72	0.71
1:A:367:VAL:HG21	1:A:384:VAL:HG11	1.73	0.70
1:A:164:MET:CG	1:A:385:MET:HE1	2.21	0.70
1:A:416:VAL:CG2	1:A:557:LEU:O	2.38	0.70
1:A:367:VAL:CG2	1:A:384:VAL:HG12	2.22	0.69
1:A:427:ARG:HD2	1:A:458:ALA:O	1.93	0.67
1:A:30:CYS:SG	1:A:70:LEU:HD23	2.35	0.66
1:A:635:THR:HG22	1:A:636:TYR:CE1	2.32	0.65
1:A:164:MET:HG2	1:A:385:MET:HE1	1.80	0.64
1:A:434:CYS:HB2	5:A:1033:HOH:O	1.97	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:609:ARG:HD3	5:A:1029:HOH:O	1.98	0.64
1:A:518:ILE:HD11	1:A:634:PHE:CE1	2.34	0.63
1:A:518:ILE:HD11	1:A:634:PHE:CD1	2.34	0.62
1:A:117:LEU:HD13	1:A:289:VAL:HG13	1.81	0.62
1:A:445:GLN:NE2	5:A:998:HOH:O	2.18	0.62
1:A:51:ASP:HB2	1:A:77:THR:HG23	1.80	0.62
1:A:153:ASN:HB3	1:A:166:CYS:HB3	1.80	0.62
1:A:337:CYS:SG	1:A:342:ASN:ND2	2.73	0.60
1:A:42:ILE:O	1:A:42:ILE:HG23	2.02	0.58
1:A:52:ILE:HG23	1:A:68:TRP:CH2	2.39	0.58
1:A:635:THR:CG2	1:A:636:TYR:CE1	2.87	0.58
1:A:178:GLN:HE21	1:A:362:LYS:HZ1	1.51	0.58
1:A:114:GLU:O	1:A:187:THR:HA	2.04	0.58
1:A:307:GLU:OE2	1:A:335:THR:HG21	2.04	0.58
1:A:343:MET:O	1:A:344:ASP:HB2	2.04	0.58
1:A:71:ASP:O	1:A:74:VAL:HG12	2.05	0.57
1:A:367:VAL:CG2	1:A:384:VAL:HG11	2.33	0.57
1:A:278:GLU:N	1:A:278:GLU:OE1	2.37	0.57
1:A:553:LEU:HD23	1:A:557:LEU:HD22	1.88	0.56
1:A:307:GLU:OE2	1:A:335:THR:CG2	2.54	0.56
1:A:623:LEU:HB2	1:A:625:LEU:HD22	1.88	0.55
1:A:632:ASP:OD1	1:A:642:GLU:OE2	2.27	0.53
1:A:518:ILE:HG21	1:A:521:LYS:HB2	1.90	0.53
1:A:123:ARG:HD3	1:A:659:TRP:CD1	2.44	0.52
1:A:139:TRP:CD1	1:A:147:GLY:HA3	2.44	0.52
1:A:27:LEU:HD13	1:A:78:LEU:HD22	1.91	0.51
1:A:553:LEU:CD2	1:A:557:LEU:HD22	2.40	0.51
1:A:166:CYS:HB2	1:A:254:LEU:HD22	1.92	0.51
1:A:467:LEU:HD13	1:A:474:GLU:HB2	1.93	0.50
1:A:92:VAL:HB	1:A:108:LEU:HB3	1.94	0.50
1:A:17:ALA:HB3	1:A:110:LEU:CD1	2.41	0.50
1:A:334:LEU:HD11	1:A:336:ILE:CD1	2.41	0.50
1:A:511:GLU:HG3	1:A:525:LYS:NZ	2.27	0.50
1:A:51:ASP:HB2	1:A:77:THR:CG2	2.42	0.49
1:A:42:ILE:O	1:A:42:ILE:CG2	2.61	0.49
1:A:27:LEU:CD1	1:A:78:LEU:HD22	2.43	0.49
1:A:67:THR:N	1:A:97:TYR:OH	2.44	0.48
1:A:96:TYR:HB2	1:A:104:VAL:HG23	1.96	0.47
1:A:278:GLU:CD	1:A:278:GLU:H	2.17	0.47
1:A:425:LEU:CD1	1:A:456:VAL:HG13	2.39	0.47
1:A:159:LEU:HD23	1:A:159:LEU:O	2.15	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:45:SER:OG	1:A:90:GLN:NE2	2.48	0.47
1:A:34:PRO:HG2	1:A:104:VAL:HG21	1.96	0.47
1:A:623:LEU:HB2	1:A:625:LEU:CD2	2.45	0.47
1:A:598:ILE:O	1:A:629:PHE:HA	2.16	0.46
1:A:74:VAL:HG13	1:A:74:VAL:O	2.16	0.46
1:A:512:ALA:HB1	1:A:604:PRO:HB3	1.98	0.46
1:A:466:TRP:CZ3	1:A:542:VAL:HG13	2.51	0.45
1:A:542:VAL:HG11	1:A:571:PHE:CD1	2.52	0.45
1:A:518:ILE:O	1:A:518:ILE:HG23	2.15	0.45
1:A:272:LEU:HD23	1:A:283:VAL:HG22	1.99	0.45
1:A:635:THR:CG2	1:A:636:TYR:CD1	2.85	0.45
1:A:151:LEU:HD21	1:A:359:ALA:HB2	1.98	0.44
1:A:163:ALA:HB1	1:A:167:GLU:OE1	2.17	0.44
1:A:518:ILE:CG2	1:A:521:LYS:HB2	2.47	0.44
1:A:192:ASP:O	1:A:195:THR:HB	2.17	0.44
1:A:5:THR:O	1:A:26:GLN:HG2	2.18	0.44
1:A:626:GLN:HB2	5:A:961:HOH:O	2.18	0.44
1:A:432:ASP:OD1	1:A:461:LYS:HD3	2.17	0.43
1:A:493:SER:CB	1:A:566:ASP:HB3	2.48	0.43
1:A:289:VAL:CG2	1:A:291:PHE:CE1	3.02	0.43
1:A:40:PHE:HA	1:A:95:SER:O	2.19	0.43
1:A:171:VAL:HG11	1:A:177:LEU:CD2	2.49	0.43
1:A:428:ILE:HD13	1:A:451:LEU:HD22	2.02	0.42
1:A:497:CYS:HB3	1:A:570:LEU:HD13	2.01	0.42
1:A:198:THR:HG22	1:A:274:THR:CG2	2.50	0.42
1:A:158:ASN:ND2	1:A:172:LEU:HD13	2.35	0.42
1:A:599:PRO:CG	1:A:642:GLU:HG3	2.50	0.42
1:A:114:GLU:HB2	1:A:188:LYS:HB3	2.01	0.41
1:A:553:LEU:O	1:A:557:LEU:HB2	2.20	0.41
1:A:214:PHE:CE2	1:A:227:VAL:HG13	2.55	0.41
1:A:347:TRP:CE2	4:A:800:BFB:HAO2	2.55	0.41
1:A:164:MET:HG3	1:A:385:MET:HE1	1.99	0.41
1:A:326:LEU:HD23	1:A:592:LEU:HD22	2.02	0.41
1:A:29:ILE:HD12	1:A:76:VAL:HG21	2.03	0.41
1:A:117:LEU:HD23	1:A:117:LEU:HA	1.90	0.41
1:A:484:ARG:HD2	5:A:1057:HOH:O	2.21	0.40
1:A:272:LEU:CD2	1:A:283:VAL:HG22	2.51	0.40
1:A:334:LEU:HD11	1:A:336:ILE:HD11	2.02	0.40
1:A:457:GLN:O	1:A:458:ALA:C	2.59	0.40
1:A:583:PHE:O	1:A:584:PRO:C	2.59	0.40
1:A:594:LYS:HA	1:A:625:LEU:HD12	2.04	0.40

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	614/671 (92%)	586 (95%)	26 (4%)	2 (0%)	41 50

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	484	ARG
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	557/594 (94%)	500 (90%)	57 (10%)	7 8

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LEU
1	A	13	GLN
1	A	21	LEU
1	A	35	GLU
1	A	38	THR
1	A	42	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	68	TRP
1	A	70	LEU
1	A	78	LEU
1	A	79	THR
1	A	80	MET
1	A	110	LEU
1	A	117	LEU
1	A	146	GLN
1	A	159	LEU
1	A	160	GLU
1	A	161	SER
1	A	169	ASP
1	A	185	LEU
1	A	201	LEU
1	A	203	VAL
1	A	227	VAL
1	A	232	LYS
1	A	244	LYS
1	A	278	GLU
1	A	289	VAL
1	A	323	VAL
1	A	325	THR
1	A	328	MET
1	A	335	THR
1	A	339	GLU
1	A	343	MET
1	A	344	ASP
1	A	364	LEU
1	A	374	ARG
1	A	376	LEU
1	A	389	PHE
1	A	398	THR
1	A	401	ILE
1	A	412	VAL
1	A	429	LEU
1	A	456	VAL
1	A	489	LEU
1	A	500	LEU
1	A	504	GLN
1	A	514	LEU
1	A	519	LYS
1	A	557	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	570	LEU
1	A	592	LEU
1	A	594	LYS
1	A	607	ASN
1	A	609	ARG
1	A	625	LEU
1	A	635	THR
1	A	640	HIS
1	A	642	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	GLN
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	346	GLN
1	A	445	GLN
1	A	448	GLN
1	A	502	GLN
1	A	504	GLN
1	A	505	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	906	-	4,4,4	0.14	0	6,6,6	0.12	0
4	BFB	A	800	1	20,20,20	0.84	0	22,25,25	2.24	4 (18%)
3	SO4	A	907	-	4,4,4	0.23	0	6,6,6	0.15	0
3	SO4	A	905	-	4,4,4	0.20	0	6,6,6	0.26	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
4	BFB	A	800	1	-	5/18/19/19	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	800	BFB	CAP-CAV-NAR	-8.30	103.60	114.24
4	A	800	BFB	CAM-CAN-NAR	-3.90	101.07	112.21
4	A	800	BFB	OAE-CAU-CAZ	-2.31	116.88	120.27
4	A	800	BFB	CAO-CAZ-NAS	-2.27	106.28	110.88

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	800	BFB	CAO-CAM-CAN-NAR
4	A	800	BFB	CAM-CAO-CAZ-CAU
4	A	800	BFB	OAE-CAU-CAZ-NAS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
4	A	800	BFB	NAA-CAU-CAZ-NAS
4	A	800	BFB	CAM-CAO-CAZ-NAS

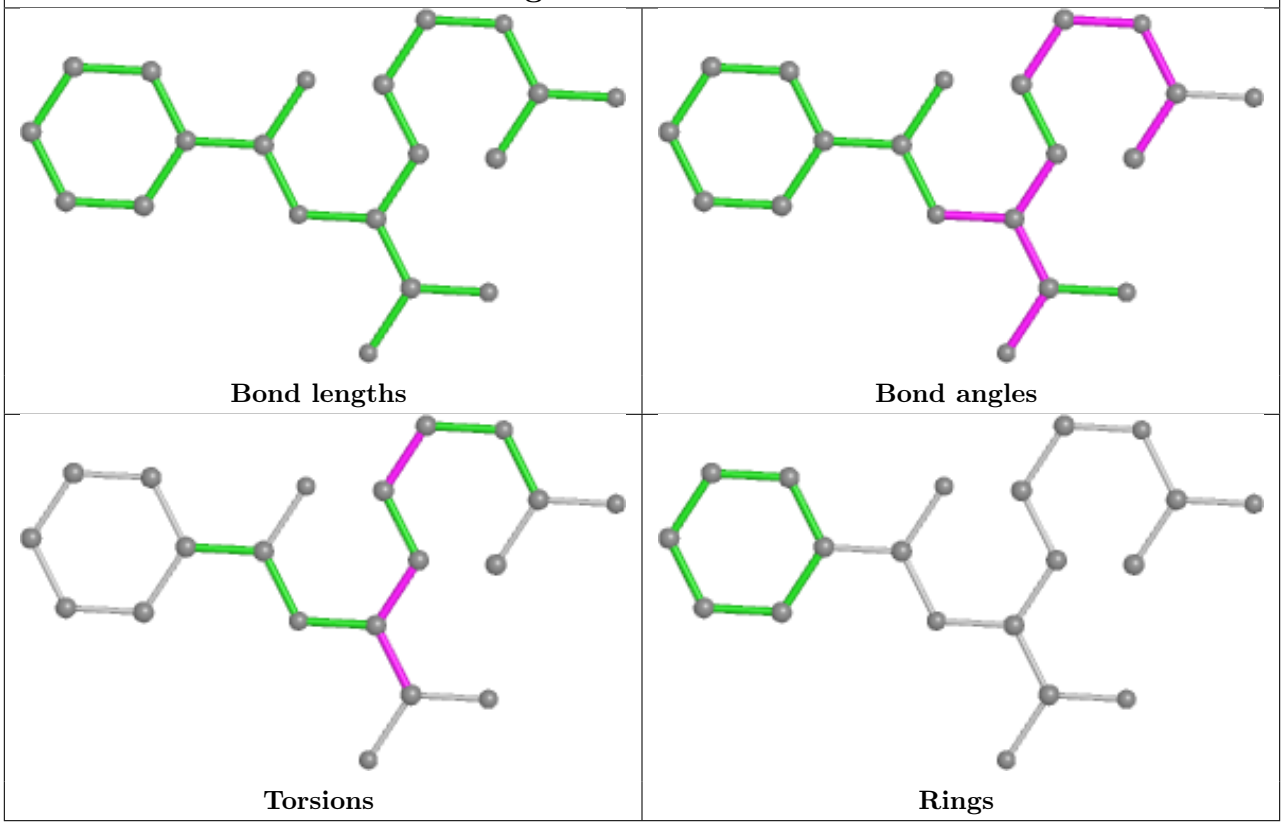
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	800	BFB	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.

Ligand BFB 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	626/671 (93%)	0.49	56 (8%) 9 13	47, 60, 78, 92	6 (0%)

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	159	LEU	5.5
1	A	104	VAL	4.7
1	A	98	GLY	4.5
1	A	217	THR	4.3
1	A	103	PRO	4.2
1	A	100	LYS	3.7
1	A	462	LEU	3.7
1	A	518	ILE	3.6
1	A	96	TYR	3.4
1	A	99	PRO	3.3
1	A	330	ALA	3.3
1	A	328	MET	3.3
1	A	522	LYS	3.3
1	A	634	PHE	3.2
1	A	398	THR	3.1
1	A	74	VAL	3.1
1	A	343	MET	3.0
1	A	233	TRP	3.0
1	A	68	TRP	2.9
1	A	38	THR	2.9
1	A	412	VAL	2.9
1	A	172	LEU	2.8
1	A	171	VAL	2.8
1	A	34	PRO	2.8
1	A	40	PHE	2.7
1	A	476	LEU	2.7
1	A	160	GLU	2.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	519	LYS	2.7
1	A	430	PHE	2.7
1	A	97	TYR	2.6
1	A	102	PRO	2.6
1	A	339	GLU	2.6
1	A	70	LEU	2.6
1	A	125	GLY	2.6
1	A	161	SER	2.5
1	A	10	THR	2.5
1	A	383	ARG	2.4
1	A	546	ILE	2.4
1	A	162	SER	2.4
1	A	13	GLN	2.3
1	A	33	ALA	2.3
1	A	464	SER	2.3
1	A	428	ILE	2.3
1	A	459	PRO	2.2
1	A	463	TYR	2.2
1	A	170	GLU	2.2
1	A	431	GLY	2.1
1	A	466	TRP	2.1
1	A	635	THR	2.1
1	A	472	VAL	2.1
1	A	4	GLY	2.1
1	A	257	PRO	2.1
1	A	384	VAL	2.1
1	A	454	GLN	2.0
1	A	316	ASN	2.0
1	A	475	PHE	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)

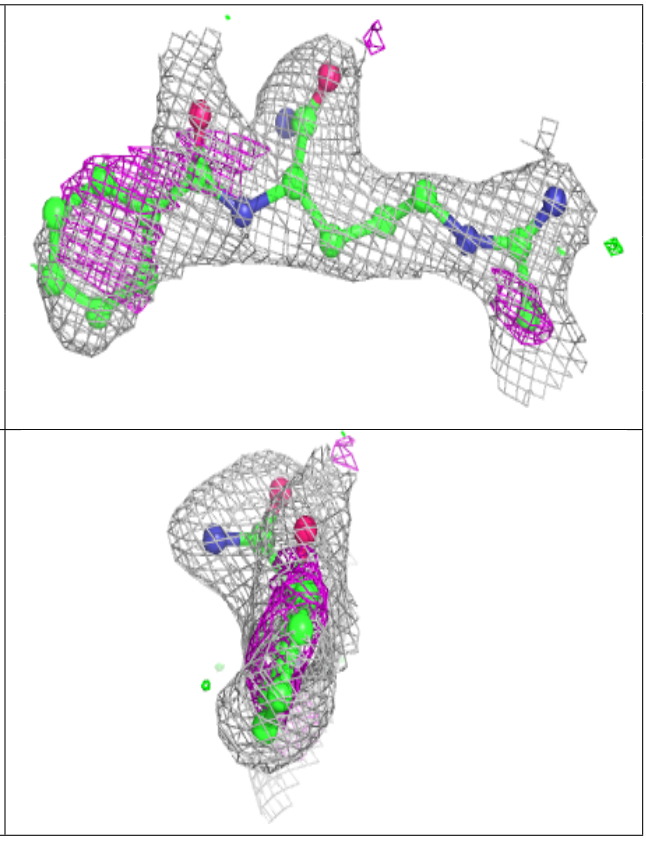
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	BFB	A	800	20/20	0.80	0.24	64,67,71,71	0
3	SO4	A	906	5/5	0.93	0.27	94,95,95,96	0
2	CA	A	902	1/1	0.95	0.10	72,72,72,72	0
3	SO4	A	907	5/5	0.95	0.18	94,94,94,95	0
3	SO4	A	905	5/5	0.95	0.20	94,95,95,96	0
2	CA	A	904	1/1	0.97	0.15	67,67,67,67	0
2	CA	A	903	1/1	0.98	0.17	65,65,65,65	0
2	CA	A	901	1/1	0.98	0.18	61,61,61,61	0
2	CA	A	900	1/1	0.99	0.03	55,55,55,55	0

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

Electron density around BFB 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.