



Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 02:26 am BST

PDB ID : 5HID
Title : BRAF Kinase domain b3aC loop deletion mutant in complex with AZ628
Authors : Whalen, D.M.; Foster, S.A.; Ozen, A.; Wongchenko, M.; Yin, J.; Schaefer, G.; Mayfield, J.; Chmielecki, J.; Stephens, P.; Albacker, L.; Yan, Y.; Song, K.; Hatzivassiliou, G.; Eigenbrot, C.; Yu, C.; Shaw, A.S.; Manning, G.; Skelton, N.J.; Hymowitz, S.G.; Malek, S.
Deposited on : 2016-01-11
Resolution : 2.50 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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 : 2.11
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) : 2.11

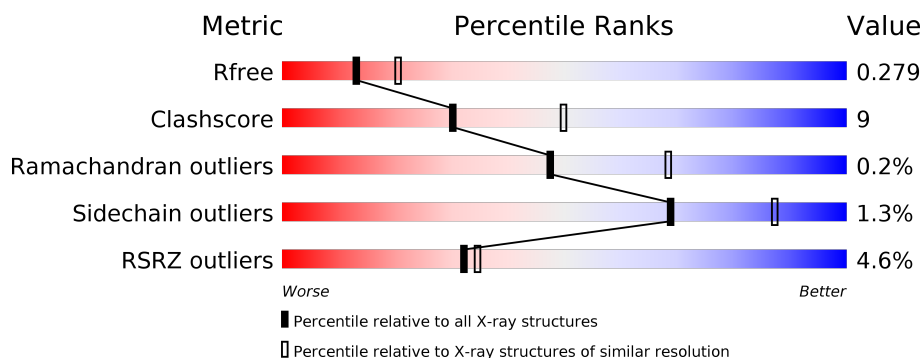
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 on 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 $\leq 5\%$. 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	283	<div> <div style="width: 100%; height: 10px; background-color: red; position: relative;"> % </div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 83% 7% 9% </div> </div>
1	B	283	<div> <div style="width: 100%; height: 10px; background-color: red; position: relative;"> 7% </div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 81% 12% • 5% </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4430 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 Serine/threonine-protein kinase B-raf.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	257	Total	C	N	O	S	0	3	0
			2080	1316	371	380	13			
1	B	269	Total	C	N	O	S	0	0	0
			2155	1364	385	393	13			

There are 58 discrepancies between the modelled and reference sequences:

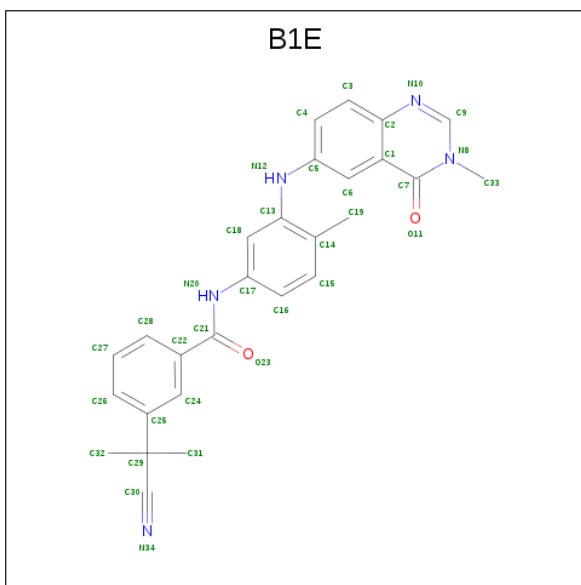
Chain	Residue	Modelled	Actual	Comment	Reference
A	436	MET	-	initiating methionine	UNP P15056
A	437	HIS	-	expression tag	UNP P15056
A	438	HIS	-	expression tag	UNP P15056
A	439	HIS	-	expression tag	UNP P15056
A	440	HIS	-	expression tag	UNP P15056
A	441	HIS	-	expression tag	UNP P15056
A	442	GLY	-	expression tag	UNP P15056
A	443	SER	-	expression tag	UNP P15056
A	?	-	ASN	deletion	UNP P15056
A	?	-	VAL	deletion	UNP P15056
A	?	-	THR	deletion	UNP P15056
A	?	-	ALA	deletion	UNP P15056
A	?	-	PRO	deletion	UNP P15056
A	543	ALA	ILE	engineered mutation	UNP P15056
A	544	SER	ILE	engineered mutation	UNP P15056
A	551	LYS	ILE	engineered mutation	UNP P15056
A	562	ARG	GLN	engineered mutation	UNP P15056
A	588	ASN	LEU	engineered mutation	UNP P15056
A	630	SER	LYS	engineered mutation	UNP P15056
A	667	GLU	PHE	engineered mutation	UNP P15056
A	673	SER	TYR	engineered mutation	UNP P15056
A	688	ARG	ALA	engineered mutation	UNP P15056
A	706	SER	LEU	engineered mutation	UNP P15056
A	709	ARG	GLN	engineered mutation	UNP P15056
A	713	GLU	SER	engineered mutation	UNP P15056

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Chain	Residue	Modelled	Actual	Comment	Reference
A	716	GLU	LEU	engineered mutation	UNP P15056
A	720	GLU	SER	engineered mutation	UNP P15056
A	722	SER	PRO	engineered mutation	UNP P15056
A	723	GLY	LYS	engineered mutation	UNP P15056
B	436	MET	-	initiating methionine	UNP P15056
B	437	HIS	-	expression tag	UNP P15056
B	438	HIS	-	expression tag	UNP P15056
B	439	HIS	-	expression tag	UNP P15056
B	440	HIS	-	expression tag	UNP P15056
B	441	HIS	-	expression tag	UNP P15056
B	442	GLY	-	expression tag	UNP P15056
B	443	SER	-	expression tag	UNP P15056
B	?	-	ASN	deletion	UNP P15056
B	?	-	VAL	deletion	UNP P15056
B	?	-	THR	deletion	UNP P15056
B	?	-	ALA	deletion	UNP P15056
B	?	-	PRO	deletion	UNP P15056
B	543	ALA	ILE	engineered mutation	UNP P15056
B	544	SER	ILE	engineered mutation	UNP P15056
B	551	LYS	ILE	engineered mutation	UNP P15056
B	562	ARG	GLN	engineered mutation	UNP P15056
B	588	ASN	LEU	engineered mutation	UNP P15056
B	630	SER	LYS	engineered mutation	UNP P15056
B	667	GLU	PHE	engineered mutation	UNP P15056
B	673	SER	TYR	engineered mutation	UNP P15056
B	688	ARG	ALA	engineered mutation	UNP P15056
B	706	SER	LEU	engineered mutation	UNP P15056
B	709	ARG	GLN	engineered mutation	UNP P15056
B	713	GLU	SER	engineered mutation	UNP P15056
B	716	GLU	LEU	engineered mutation	UNP P15056
B	720	GLU	SER	engineered mutation	UNP P15056
B	722	SER	PRO	engineered mutation	UNP P15056
B	723	GLY	LYS	engineered mutation	UNP P15056

- Molecule 2 is 3-(2-cyanopropan-2-yl)-N-{4-methyl-3-[(3-methyl-4-oxo-3,4-dihydroquinazolin-6-yl)amino]phenyl}benzamide (three-letter code: B1E) (formula: C₂₇H₂₅N₅O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			34	27	5	2		
2	B	1	Total	C	N	O	0	0
			34	27	5	2		

- Molecule 3 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	4	3		
3	B	1	Total	C	O	0	0
			7	4	3		

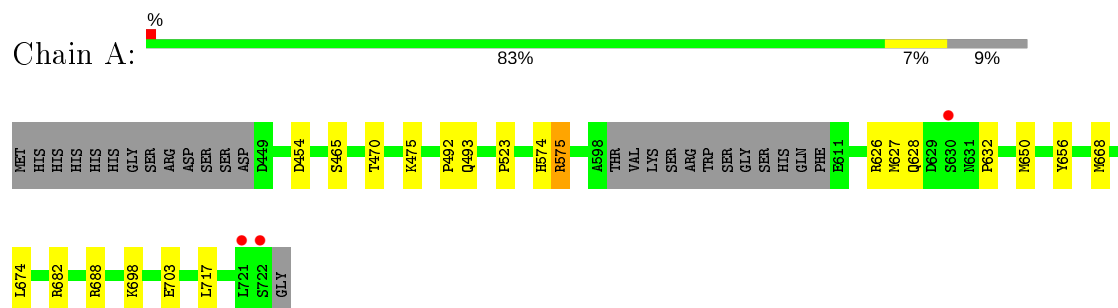
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	59	Total 59	O 59	0	0
4	B	54	Total 54	O 54	0	0

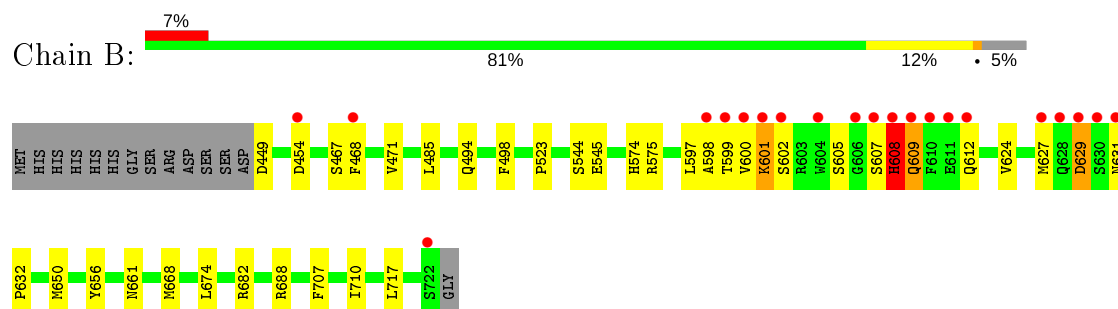
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Serine/threonine-protein kinase B-raf



- Molecule 1: Serine/threonine-protein kinase B-raf



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	49.71Å 100.40Å 108.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.86 – 2.50 47.86 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.2 (47.86-2.50) 98.5 (47.86-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 2.51Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, R_{free}	0.234 , 0.279 0.230 , 0.279	Depositor DCC
R_{free} test set	979 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	34.1	Xtriage
Anisotropy	0.585	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 52.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4430	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 55.81 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.9954e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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.

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: PEG, B1E

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	0.53	0/2127	0.69	0/2862
1	B	0.57	0/2201	0.74	1/2965 (0.0%)
All	All	0.55	0/4328	0.72	1/5827 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	608	HIS	C-N-CA	8.03	141.78	121.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	608	HIS	Peptide
1	B	609	GLN	Mainchain

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	2080	0	2096	14	0
1	B	2155	0	2159	66	0
2	A	34	0	25	0	0
2	B	34	0	25	0	0
3	A	7	0	10	1	0
3	B	7	0	10	0	0
4	A	59	0	0	0	0
4	B	54	0	0	0	0
All	All	4430	0	4325	80	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 9.

All (80) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:602:SER:CB	1:B:605:SER:CB	1.97	1.42
1:B:602:SER:CB	1:B:605:SER:HB3	1.55	1.36
1:B:602:SER:HB3	1:B:605:SER:HB2	1.15	1.13
1:B:602:SER:CB	1:B:605:SER:HB2	1.67	1.10
1:B:602:SER:HB2	1:B:605:SER:CB	1.70	1.09
1:B:602:SER:HB2	1:B:605:SER:HB3	1.09	1.09
1:B:609:GLN:NE2	1:B:612:GLN:HG3	1.69	1.08
1:B:468:PHE:HD2	1:B:494:GLN:CG	1.66	1.06
1:A:493:GLN:N	1:A:493:GLN:OE1	1.90	1.04
1:B:600:VAL:HG12	1:B:612:GLN:CB	1.88	1.03
1:B:602:SER:H	1:B:608:HIS:CE1	1.79	1.01
1:B:468:PHE:HD2	1:B:494:GLN:CD	1.63	1.00
1:B:468:PHE:CD2	1:B:494:GLN:CD	2.41	0.94
1:B:600:VAL:HG12	1:B:612:GLN:CG	1.99	0.91
1:B:600:VAL:HG12	1:B:612:GLN:HB3	1.53	0.90
1:B:600:VAL:CG1	1:B:612:GLN:HB3	2.02	0.90
1:B:600:VAL:CG1	1:B:612:GLN:CG	2.54	0.86
1:B:468:PHE:CD2	1:B:494:GLN:CG	2.57	0.85
1:B:602:SER:OG	1:B:605:SER:HB3	1.76	0.84
1:B:609:GLN:NE2	1:B:612:GLN:CG	2.40	0.84
1:B:602:SER:OG	1:B:605:SER:CB	2.25	0.84
1:B:600:VAL:HG12	1:B:612:GLN:HG3	1.59	0.83
1:B:602:SER:N	1:B:608:HIS:ND1	2.31	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:600:VAL:CG1	1:B:612:GLN:HG3	2.13	0.75
1:B:609:GLN:HE22	1:B:612:GLN:HG3	1.51	0.74
1:B:605:SER:OG	1:B:608:HIS:HB3	1.93	0.69
1:B:602:SER:HB3	1:B:605:SER:CB	1.86	0.69
1:B:605:SER:O	1:B:608:HIS:CD2	2.46	0.69
1:B:544:SER:OG	1:B:545:GLU:N	2.24	0.68
1:B:600:VAL:CG1	1:B:612:GLN:CB	2.60	0.67
1:B:544:SER:C	1:B:545:GLU:HG3	2.16	0.65
1:B:602:SER:OG	1:B:608:HIS:CB	2.45	0.65
1:B:600:VAL:HG11	1:B:612:GLN:CD	2.18	0.64
1:A:668:MET:HB3	1:A:674:LEU:HB2	1.80	0.63
1:A:475:LYS:HB3	3:A:802:PEG:H41	1.78	0.63
1:B:471:VAL:HG23	1:B:597:LEU:HD21	1.79	0.62
1:B:602:SER:OG	1:B:608:HIS:HB2	2.01	0.61
1:B:668:MET:HB3	1:B:674:LEU:HB2	1.81	0.60
1:B:485:LEU:HD12	1:B:498:PHE:HB2	1.84	0.59
1:A:574:HIS:O	1:A:575:ARG:HB2	2.03	0.59
1:B:467:SER:OG	1:B:599:THR:OG1	2.21	0.58
1:B:574:HIS:O	1:B:575:ARG:HB2	2.03	0.58
1:B:602:SER:N	1:B:608:HIS:CE1	2.63	0.58
1:B:600:VAL:HG11	1:B:612:GLN:CG	2.33	0.57
1:B:600:VAL:HG11	1:B:612:GLN:OE1	2.05	0.56
1:B:468:PHE:CD2	1:B:494:GLN:HG2	2.38	0.55
1:A:698:LYS:HD2	1:A:703:GLU:HB3	1.88	0.54
1:B:601:LYS:CB	1:B:608:HIS:HE1	2.21	0.53
1:B:602:SER:HB2	1:B:605:SER:CA	2.35	0.51
1:B:607:SER:O	1:B:608:HIS:HB3	2.09	0.51
1:B:602:SER:OG	1:B:608:HIS:CG	2.65	0.50
1:A:627:MET:HA	1:A:632:PRO:HG3	1.94	0.49
1:B:605:SER:HB3	1:B:608:HIS:CG	2.47	0.48
1:B:602:SER:HG	1:B:608:HIS:CG	2.31	0.48
1:B:601:LYS:CB	1:B:608:HIS:CE1	2.97	0.47
1:B:600:VAL:CB	1:B:612:GLN:HB3	2.45	0.47
1:B:609:GLN:HE21	1:B:612:GLN:HG3	1.68	0.47
1:A:492:PRO:HD2	1:A:493:GLN:OE1	2.15	0.46
1:B:468:PHE:HD2	1:B:494:GLN:HG3	1.70	0.46
1:A:688:ARG:HD3	1:A:717:LEU:HD13	1.97	0.46
1:B:471:VAL:CG2	1:B:597:LEU:HD21	2.46	0.46
1:A:465:SER:HB2	1:A:470:THR:HG23	1.97	0.45
1:B:602:SER:HG	1:B:608:HIS:HB2	1.81	0.45
1:A:492:PRO:N	1:A:493:GLN:OE1	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:468:PHE:CD2	1:B:494:GLN:NE2	2.84	0.45
1:B:707:PHE:HA	1:B:710:ILE:HB	1.98	0.45
1:B:598:ALA:O	1:B:600:VAL:HG23	2.17	0.45
1:B:605:SER:CB	1:B:608:HIS:HB3	2.47	0.44
1:A:626:ARG:HE	1:A:628:GLN:NE2	2.16	0.44
1:B:624:VAL:HA	1:B:632:PRO:HB2	2.00	0.44
1:A:650:MET:O	1:A:682:ARG:HG2	2.18	0.44
1:B:650:MET:O	1:B:682:ARG:HG2	2.18	0.43
1:B:544:SER:O	1:B:545:GLU:HG3	2.18	0.43
1:B:627:MET:HA	1:B:632:PRO:HG3	2.00	0.42
1:B:605:SER:OG	1:B:607:SER:O	2.36	0.42
1:A:492:PRO:CD	1:A:493:GLN:OE1	2.68	0.41
1:A:454:ASP:OD1	1:A:523:PRO:HD3	2.20	0.41
1:B:454:ASP:OD1	1:B:523:PRO:HD3	2.21	0.41
1:B:629:ASP:C	1:B:631:ASN:H	2.24	0.41
1:B:688:ARG:HD3	1:B:717:LEU:HD13	2.03	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	255/283 (90%)	247 (97%)	8 (3%)	0	100	100
1	B	267/283 (94%)	256 (96%)	10 (4%)	1 (0%)	34	54
All	All	522/566 (92%)	503 (96%)	18 (3%)	1 (0%)	47	68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	601	LYS

5.3.2 Protein sidechains ⓘ

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	229/249 (92%)	227 (99%)	2 (1%)	78	92
1	B	236/249 (95%)	232 (98%)	4 (2%)	60	82
All	All	465/498 (93%)	459 (99%)	6 (1%)	69	87

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	575	ARG
1	A	656	TYR
1	B	449	ASP
1	B	629	ASP
1	B	656	TYR
1	B	661	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	496	GLN
1	A	500	ASN
1	A	628	GLN
1	B	493	GLN
1	B	494	GLN
1	B	496	GLN
1	B	500	ASN
1	B	609	GLN
1	B	661	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	B1E	A	801	-	35,37,37	0.96	1 (2%)	45,54,54	1.35	4 (8%)
3	PEG	A	802	-	6,6,6	0.12	0	5,5,5	0.11	0
2	B1E	B	801	-	35,37,37	0.97	1 (2%)	45,54,54	1.57	9 (20%)
3	PEG	B	802	-	6,6,6	0.35	0	5,5,5	0.18	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
2	B1E	A	801	-	-	4/18/21/21	0/4/4/4
3	PEG	A	802	-	-	0/4/4/4	-
2	B1E	B	801	-	-	4/18/21/21	0/4/4/4
3	PEG	B	802	-	-	4/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	B1E	C7-C1	3.93	1.48	1.41
2	A	801	B1E	C7-C1	3.84	1.48	1.41

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	801	B1E	C9-N10-C2	5.79	121.68	116.69
2	A	801	B1E	C9-N10-C2	5.03	121.03	116.69
2	B	801	B1E	C15-C14-C13	3.80	121.02	117.44
2	B	801	B1E	C14-C13-N12	3.32	124.99	118.70
2	A	801	B1E	C15-C14-C13	3.04	120.31	117.44
2	B	801	B1E	C19-C14-C15	-2.57	115.30	120.31
2	B	801	B1E	C1-C2-N10	-2.49	118.69	122.44
2	B	801	B1E	C18-C13-N12	-2.25	116.38	121.05
2	B	801	B1E	C19-C14-C13	2.11	123.64	121.25
2	A	801	B1E	C14-C13-N12	2.10	122.67	118.70
2	A	801	B1E	C1-C2-N10	-2.08	119.31	122.44
2	B	801	B1E	C1-C7-N8	2.05	117.55	116.15
2	B	801	B1E	C3-C2-N10	2.04	121.86	118.52

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	802	PEG	O1-C1-C2-O2
3	B	802	PEG	O2-C3-C4-O4
3	B	802	PEG	C1-C2-O2-C3
2	A	801	B1E	C18-C13-N12-C5
2	B	801	B1E	C18-C13-N12-C5
3	B	802	PEG	C4-C3-O2-C2
2	B	801	B1E	C14-C13-N12-C5
2	A	801	B1E	C24-C25-C29-C32
2	A	801	B1E	C26-C25-C29-C32
2	B	801	B1E	C24-C25-C29-C31
2	B	801	B1E	C26-C25-C29-C31
2	A	801	B1E	C14-C13-N12-C5

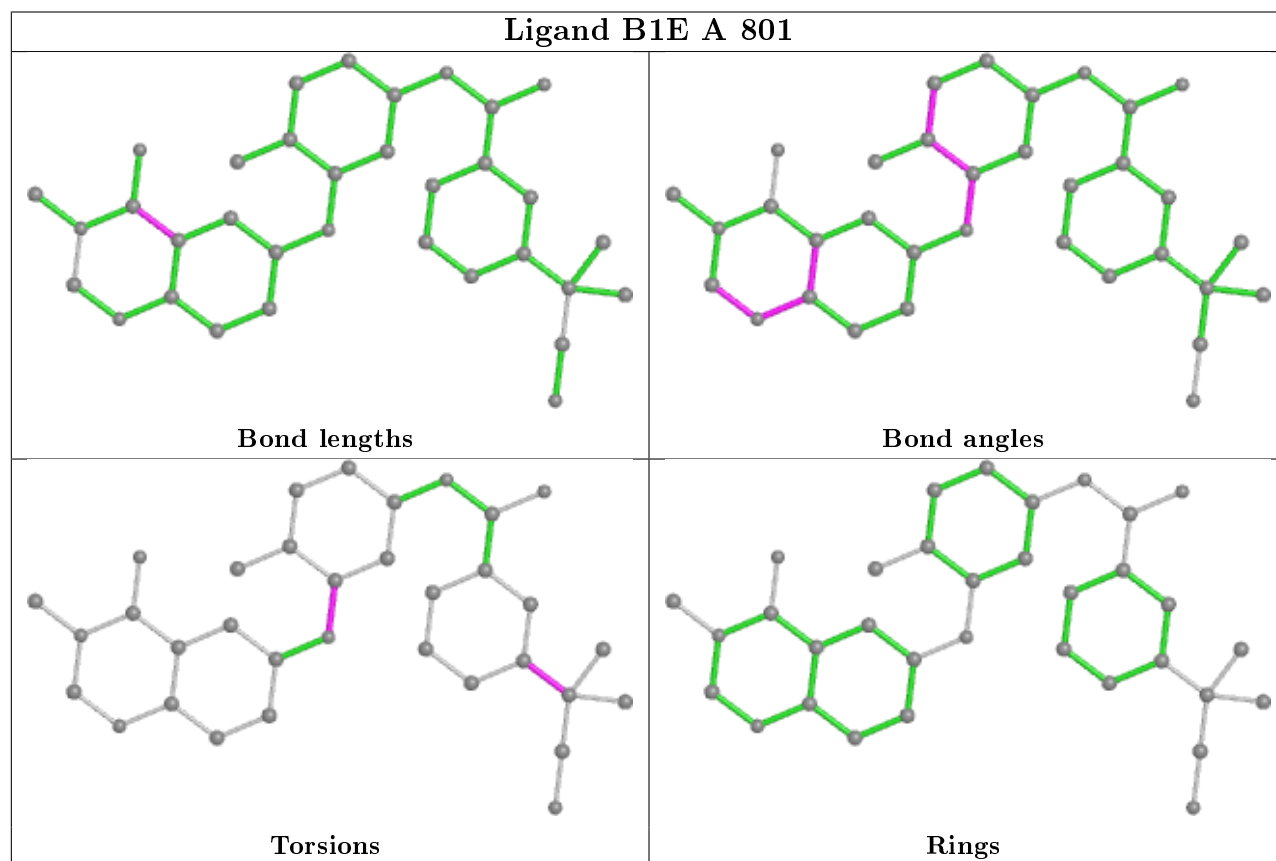
There are no ring outliers.

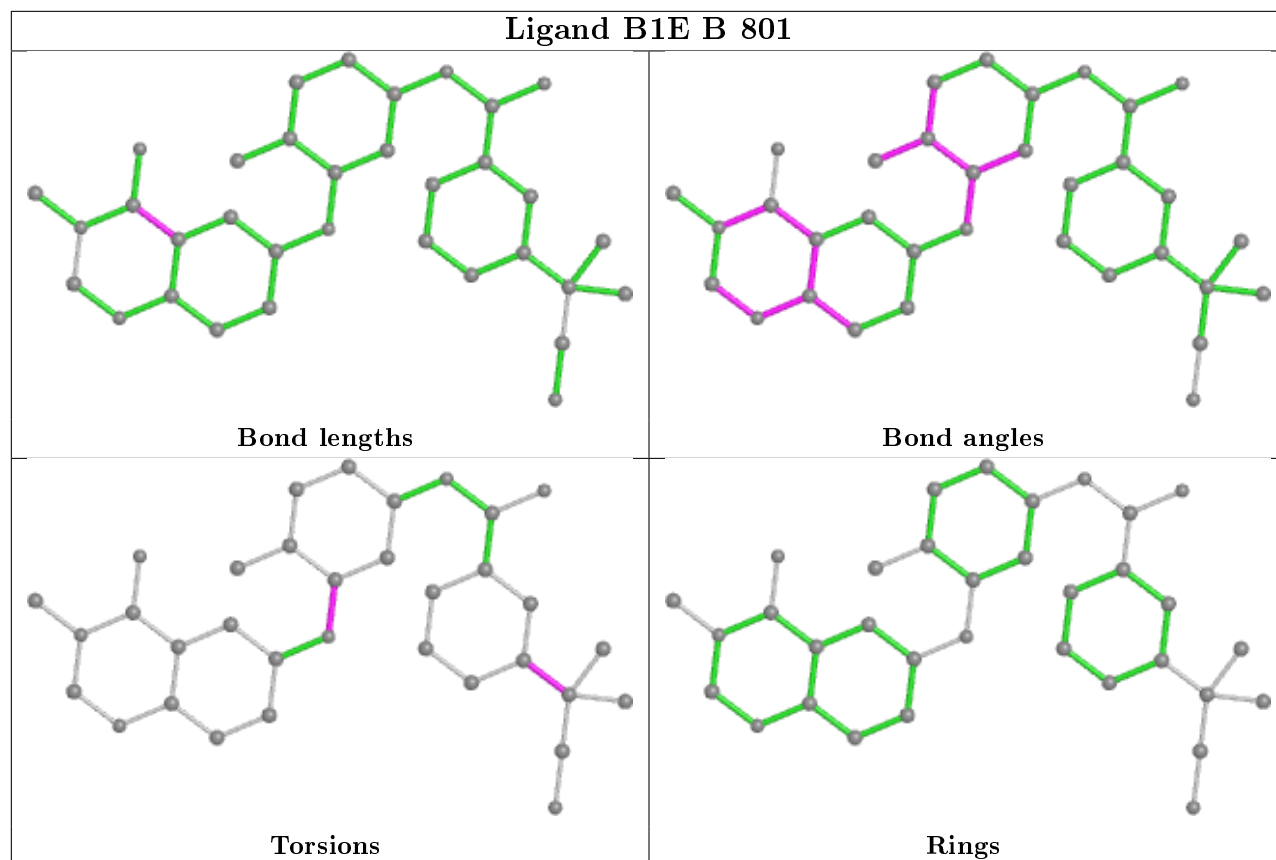
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	802	PEG	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 than 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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	257/283 (90%)	0.07	3 (1%) 79 80	22, 37, 66, 93	0
1	B	269/283 (95%)	0.29	21 (7%) 13 13	20, 39, 79, 97	0
All	All	526/566 (92%)	0.18	24 (4%) 32 34	20, 37, 73, 97	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	468	PHE	8.2
1	B	606	GLY	6.2
1	B	610	PHE	6.1
1	B	601	LYS	5.7
1	B	631	ASN	5.5
1	B	608	HIS	5.2
1	B	630	SER	5.1
1	B	602	SER	5.1
1	B	629	ASP	4.6
1	B	600	VAL	4.5
1	A	721	LEU	4.5
1	B	599	THR	4.3
1	B	607	SER	4.1
1	A	630	SER	4.0
1	B	609	GLN	3.7
1	B	611	GLU	3.5
1	B	604	TRP	3.1
1	B	598	ALA	2.8
1	B	627	MET	2.6
1	A	722	SER	2.5
1	B	628	GLN	2.4
1	B	612	GLN	2.3
1	B	722	SER	2.2
1	B	454	ASP	2.1

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 carbohydrates in this entry.

6.4 Ligands [i](#)

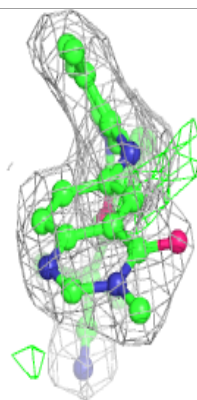
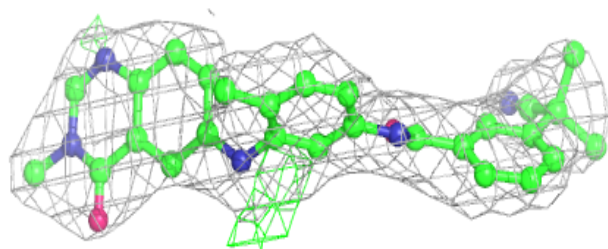
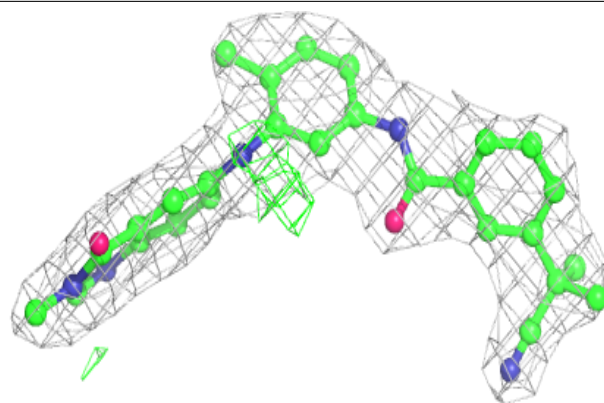
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	PEG	B	802	7/7	0.80	0.39	36,39,43,44	0
3	PEG	A	802	7/7	0.88	0.36	52,52,54,55	0
2	B1E	B	801	34/34	0.94	0.15	19,24,30,33	0
2	B1E	A	801	34/34	0.94	0.15	20,22,26,28	0

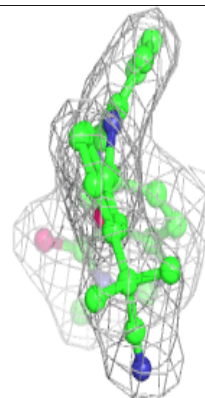
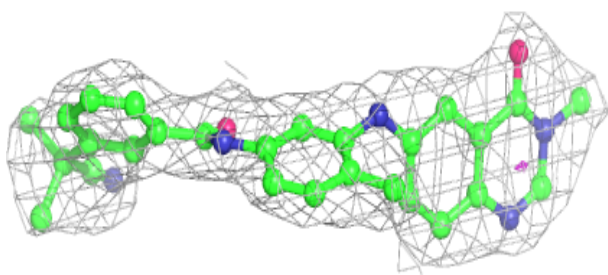
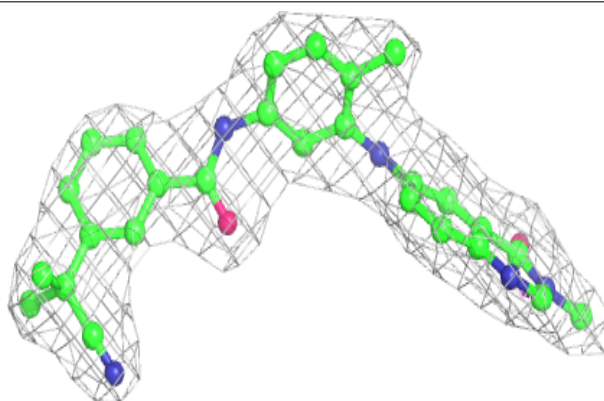
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around B1E B 801:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around B1E A 801:**

$2mF_o-DF_c$ (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.