



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:50 PM UTC

PDB ID : 4FK3 / pdb_00004fk3
Title : B-Raf Kinase V600E Oncogenic Mutant in Complex with PLX3203
Authors : Zhang, Y.; Wang, W.; Zhang, K.Y.J.
Deposited on : 2012-06-12
Resolution : 2.65 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

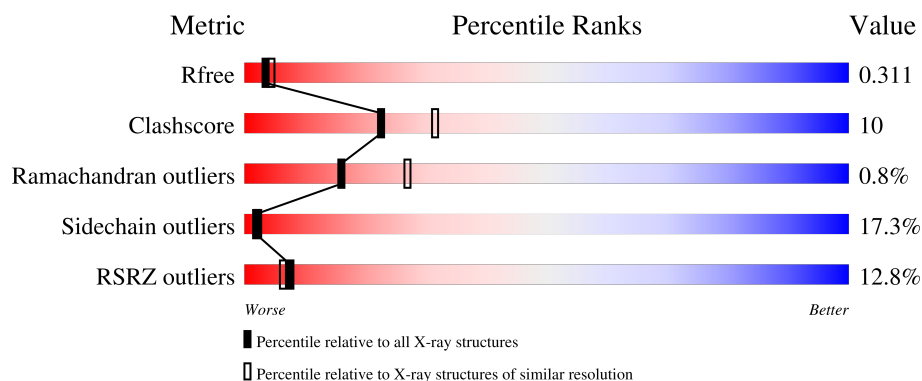
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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}	180053	1110 (2.66-2.66)
Clashscore	190562	1141 (2.66-2.66)
Ramachandran outliers	187476	1126 (2.66-2.66)
Sidechain outliers	187428	1126 (2.66-2.66)
RSRZ outliers	180081	1110 (2.66-2.66)

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 $\leq 5\%$. 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	292	7% 61% 19% 5% 14%
1	B	292	16% 53% 30% 5% 12%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4119 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	251	Total	C	N	O	S	0	0	0
			2005	1272	356	364	13			
1	B	257	Total	C	N	O	S	0	0	0
			2054	1302	365	375	12			

There are 58 discrepancies between the modelled and reference sequences:

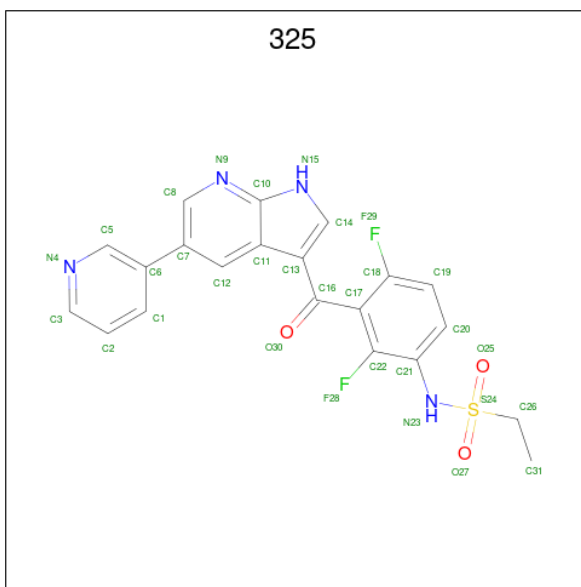
Chain	Residue	Modelled	Actual	Comment	Reference
A	432	MET	-	expression tag	UNP P15056
A	433	LYS	-	expression tag	UNP P15056
A	434	LYS	-	expression tag	UNP P15056
A	435	GLY	-	expression tag	UNP P15056
A	436	HIS	-	expression tag	UNP P15056
A	437	HIS	-	expression tag	UNP P15056
A	438	HIS	-	expression tag	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	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	600	GLU	VAL	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	432	MET	-	expression tag	UNP P15056
B	433	LYS	-	expression tag	UNP P15056
B	434	LYS	-	expression tag	UNP P15056
B	435	GLY	-	expression tag	UNP P15056
B	436	HIS	-	expression tag	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	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	600	GLU	VAL	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 N-{2,4-difluoro-3-[(5-pyridin-3-yl-1H-pyrrolo[2,3-b]pyridin-3-yl)carbonyl]phenyl}ethanesulfonamide (CCD ID: 325) (formula: C₂₁H₁₆F₂N₄O₃S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	S	0	0
			31	21	2	4	3	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	21	Total O 21 21	0	0
3	B	8	Total O 8 8	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	51.20Å 105.41Å 110.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	55.24 – 2.65 55.24 – 2.65	Depositor EDS
% Data completeness (in resolution range)	99.4 (55.24-2.65) 99.4 (55.24-2.65)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.51 (at 2.65Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.259 , 0.315 0.255 , 0.311	Depositor DCC
R_{free} test set	912 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	41.5	Xtriage
Anisotropy	0.663	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 60.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	0.085 for -h,l,k	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	4119	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.00% of the height of the origin peak. No significant pseudotranslation is detected.*

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:
325

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	0.32	0/2046	0.78	0/2755
1	B	0.32	0/2095	0.78	3/2822 (0.1%)
All	All	0.32	0/4141	0.78	3/5577 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	493	GLN	N-CA-C	-6.98	105.29	113.88
1	B	491	THR	CA-C-N	5.53	126.75	119.84
1	B	491	THR	C-N-CA	5.53	126.75	119.84

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	2005	0	2019	34	0
1	B	2054	0	2069	53	0
2	A	31	0	16	1	0
3	A	21	0	0	1	0
3	B	8	0	0	1	0
All	All	4119	0	4104	86	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 10.

All (86) 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:687:LYS:HA	1:A:690:LYS:HB3	1.71	0.72
1:A:550:MET:HE3	1:A:684:ASN:HB2	1.73	0.69
1:A:646:LEU:HD22	1:A:689:MET:HE1	1.76	0.66
1:B:688:ARG:HB2	1:B:717:LEU:HD21	1.77	0.66
1:B:539:HIS:ND1	1:B:544:SER:OG	2.29	0.66
1:B:496:GLN:O	1:B:500:ASN:ND2	2.30	0.65
1:A:710:ILE:O	1:A:714:ILE:HG13	1.97	0.65
1:B:698:LYS:O	1:B:704:ARG:NH1	2.31	0.64
1:A:620:MET:HE2	1:A:625:ILE:HG12	1.81	0.63
1:B:623:GLU:OE2	1:B:704:ARG:NH2	2.32	0.62
1:B:678:LEU:HD22	1:B:693:MET:HE3	1.82	0.61
1:B:499:LYS:NZ	3:B:801:HOH:O	2.34	0.61
1:A:496:GLN:NE2	3:A:908:HOH:O	2.34	0.60
1:B:688:ARG:HG2	1:B:691:ARG:HH12	1.66	0.60
1:B:668:MET:HB3	1:B:674:LEU:HB2	1.83	0.60
1:A:523:PRO:O	1:A:524:GLN:HB2	2.02	0.60
1:A:684:ASN:OD1	1:A:684:ASN:N	2.35	0.58
1:B:539:HIS:HA	1:B:543:ALA:HB3	1.85	0.58
1:B:492:PRO:HG3	1:B:495:LEU:HD22	1.85	0.58
1:B:491:THR:O	1:B:493:GLN:N	2.36	0.57
1:B:681:VAL:HG21	1:B:690:LYS:HE2	1.85	0.57
1:B:698:LYS:HB2	1:B:704:ARG:HG2	1.86	0.57
1:B:688:ARG:NH2	1:B:716:GLU:OE2	2.37	0.57
1:A:617:ILE:HD12	1:A:662:ARG:HD2	1.87	0.56
1:B:707:PHE:HA	1:B:710:ILE:HB	1.88	0.56
1:B:462:ARG:HA	1:B:472:TYR:HA	1.88	0.56
1:A:594:ASP:H	2:A:801:325:HN23	1.51	0.56
1:B:684:ASN:OD1	1:B:684:ASN:N	2.30	0.56
1:A:477:HIS:ND1	1:B:565:ASP:OD2	2.25	0.54
1:B:555:ASP:OD2	1:B:559:GLN:NE2	2.38	0.54
1:B:492:PRO:HA	1:B:495:LEU:HB2	1.89	0.54
1:B:495:LEU:HD12	1:B:525:LEU:HD11	1.90	0.53
1:A:647:TYR:O	1:A:651:THR:OG1	2.20	0.53
1:B:515:LEU:HB3	1:B:530:GLN:HB3	1.90	0.53
1:B:539:HIS:O	1:B:544:SER:N	2.41	0.53
1:B:573:ILE:HG22	1:B:575:ARG:HG3	1.92	0.51
1:B:688:ARG:NH2	1:B:713:GLU:OE1	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:707:PHE:HA	1:A:710:ILE:HB	1.93	0.50
1:B:595:PHE:O	1:B:597:LEU:N	2.44	0.50
1:A:661:ASN:HB3	1:A:664:GLN:HB2	1.94	0.50
1:A:695:GLU:HB3	1:A:705:PRO:HD3	1.93	0.50
1:A:681:VAL:HG21	1:A:690:LYS:HE2	1.94	0.49
1:A:710:ILE:HG23	1:A:714:ILE:HD11	1.94	0.49
1:B:501:GLU:HA	1:B:504:VAL:HG12	1.95	0.49
1:B:541:LEU:HD21	1:B:649:LEU:HD23	1.95	0.48
1:A:458:THR:HB	1:A:475:LYS:HB2	1.96	0.48
1:A:507:LYS:O	1:A:570:LYS:NZ	2.44	0.48
1:A:454:ASP:HB2	1:A:522:LYS:HB2	1.95	0.48
1:A:653:GLN:OE1	1:A:680:LYS:HG2	2.13	0.47
1:A:688:ARG:HG3	1:A:688:ARG:HH11	1.79	0.47
1:B:698:LYS:HA	1:B:698:LYS:HE2	1.97	0.47
1:B:624:VAL:HA	1:B:632:PRO:HB2	1.95	0.47
1:A:688:ARG:HG3	1:A:688:ARG:NH1	2.31	0.46
1:B:688:ARG:HD3	1:B:717:LEU:HD21	1.98	0.45
1:A:503:GLY:O	1:A:507:LYS:HG3	2.17	0.45
1:A:541:LEU:HD23	1:A:648:GLU:HB3	1.99	0.45
1:B:617:ILE:HA	1:B:620:MET:HE3	1.98	0.45
1:A:668:MET:HB3	1:A:674:LEU:HB2	1.98	0.45
1:A:644:ILE:O	1:A:648:GLU:HG3	2.17	0.44
1:B:452:ILE:HD12	1:B:528:VAL:HG21	1.98	0.44
1:B:640:TYR:HA	1:B:696:CYS:O	2.18	0.44
1:B:682:ARG:HB3	1:B:684:ASN:OD1	2.18	0.44
1:B:486:ASN:O	1:B:486:ASN:ND2	2.47	0.44
1:A:539:HIS:HA	1:A:543:ALA:HB3	2.00	0.43
1:B:499:LYS:HD2	1:B:499:LYS:HA	1.73	0.43
1:A:709:ARG:O	1:A:713:GLU:HG2	2.18	0.43
1:B:491:THR:HA	1:B:492:PRO:HD3	1.83	0.43
1:B:687:LYS:HB2	1:B:687:LYS:HE3	1.78	0.43
1:B:620:MET:HB3	1:B:625:ILE:HG13	2.00	0.43
1:B:716:GLU:O	1:B:720:GLU:N	2.42	0.43
1:B:503:GLY:O	1:B:507:LYS:HG3	2.18	0.43
1:B:481:ALA:HB2	1:B:531:TRP:HE3	1.84	0.42
1:B:473:LYS:HB2	1:B:531:TRP:CH2	2.54	0.42
1:B:522:LYS:HD3	1:B:522:LYS:HA	1.81	0.42
1:B:667:GLU:O	1:B:671:ARG:HB2	2.19	0.42
1:A:558:ARG:HH11	1:A:562:ARG:NH2	2.17	0.42
1:A:700:LYS:HD2	1:A:700:LYS:H	1.84	0.41
1:A:717:LEU:HD12	1:A:717:LEU:HA	1.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:585:HIS:NE2	1:B:586:GLU:OE2	2.53	0.41
1:B:523:PRO:HB2	1:B:524:GLN:H	1.58	0.41
1:B:620:MET:HE3	1:B:620:MET:HB2	1.99	0.41
1:A:507:LYS:HB2	1:A:507:LYS:HE2	1.64	0.40
1:A:582:ILE:HG23	1:A:590:VAL:HG13	2.03	0.40
1:B:623:GLU:HG3	1:B:701:ARG:HD2	2.03	0.40
1:B:522:LYS:HB2	1:B:523:PRO:HD3	2.03	0.40
1:B:538:TYR:CD1	1:B:542:HIS:HD2	2.40	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	245/292 (84%)	234 (96%)	10 (4%)	1 (0%)	30	45
1	B	251/292 (86%)	239 (95%)	9 (4%)	3 (1%)	10	17
All	All	496/584 (85%)	473 (95%)	19 (4%)	4 (1%)	16	27

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	524	GLN
1	B	523	PRO
1	B	596	GLY
1	B	492	PRO

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	220/256 (86%)	183 (83%)	37 (17%)	2	2
1	B	225/256 (88%)	185 (82%)	40 (18%)	2	2
All	All	445/512 (87%)	368 (83%)	77 (17%)	2	2

All (77) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	449	ASP
1	A	467	SER
1	A	475	LYS
1	A	484	MET
1	A	485	LEU
1	A	487	VAL
1	A	488	THR
1	A	491	THR
1	A	493	GLN
1	A	494	GLN
1	A	499	LYS
1	A	507	LYS
1	A	511	VAL
1	A	520	SER
1	A	541	LEU
1	A	547	LYS
1	A	551	LYS
1	A	553	LEU
1	A	589	THR
1	A	614	SER
1	A	616	SER
1	A	617	ILE
1	A	620	MET
1	A	637	SER
1	A	653	GLN
1	A	664	GLN
1	A	674	LEU
1	A	680	LYS
1	A	681	VAL
1	A	682	ARG
1	A	684	ASN
1	A	688	ARG
1	A	690	LYS

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Mol	Chain	Res	Type
1	A	701	ARG
1	A	702	ASP
1	A	710	ILE
1	A	717	LEU
1	B	449	ASP
1	B	457	ILE
1	B	459	VAL
1	B	461	GLN
1	B	462	ARG
1	B	463	ILE
1	B	467	SER
1	B	470	THR
1	B	482	VAL
1	B	484	MET
1	B	485	LEU
1	B	488	THR
1	B	495	LEU
1	B	508	THR
1	B	520	SER
1	B	521	THR
1	B	527	ILE
1	B	532	CYS
1	B	533	GLU
1	B	541	LEU
1	B	550	MET
1	B	551	LYS
1	B	583	PHE
1	B	586	GLU
1	B	587	ASP
1	B	594	ASP
1	B	600	GLU
1	B	625	ILE
1	B	636	GLN
1	B	660	ASN
1	B	662	ARG
1	B	667	GLU
1	B	668	MET
1	B	674	LEU
1	B	675	SER
1	B	679	SER
1	B	684	ASN
1	B	703	GLU

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Mol	Chain	Res	Type
1	B	719	ARG
1	B	720	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	664	GLN
1	B	530	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	325	A	801	-	34,34,34	1.89	9 (26%)	46,50,50	2.23	18 (39%)

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	325	A	801	-	-	3/20/20/20	0/4/4/4

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	325	C10-N15	-4.42	1.30	1.36
2	A	801	325	C21-N23	-4.06	1.36	1.42
2	A	801	325	C11-C10	3.69	1.45	1.41
2	A	801	325	C14-N15	-3.59	1.31	1.37
2	A	801	325	C26-S24	3.15	1.79	1.76
2	A	801	325	C11-C13	-3.08	1.40	1.45
2	A	801	325	C8-N9	2.81	1.40	1.34
2	A	801	325	O27-S24	2.13	1.46	1.43
2	A	801	325	O25-S24	2.11	1.46	1.43

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	325	C11-C10-N9	-5.10	120.12	126.31
2	A	801	325	C11-C10-N15	4.98	110.24	108.42
2	A	801	325	C26-S24-N23	-4.36	100.41	106.68
2	A	801	325	O27-S24-C26	-4.10	102.67	108.70
2	A	801	325	C18-C17-C22	3.78	119.37	115.66
2	A	801	325	O25-S24-N23	3.51	115.73	107.23
2	A	801	325	C14-C13-C16	-3.45	122.83	127.28
2	A	801	325	O27-S24-N23	3.26	115.13	107.23
2	A	801	325	C13-C14-N15	3.13	112.34	110.22
2	A	801	325	O25-S24-O27	-2.98	115.18	119.34
2	A	801	325	C11-C13-C16	2.92	131.43	126.45
2	A	801	325	C20-C21-N23	2.89	126.50	120.92
2	A	801	325	O25-S24-C26	-2.61	104.86	108.70
2	A	801	325	C12-C11-C13	2.59	137.99	133.77
2	A	801	325	C22-C21-N23	-2.56	117.77	120.73
2	A	801	325	C8-N9-C10	2.47	121.04	116.19
2	A	801	325	C7-C8-N9	-2.29	120.65	124.28
2	A	801	325	C12-C7-C8	2.23	119.49	117.10

There are no chirality outliers.

All (3) torsion outliers are listed below:

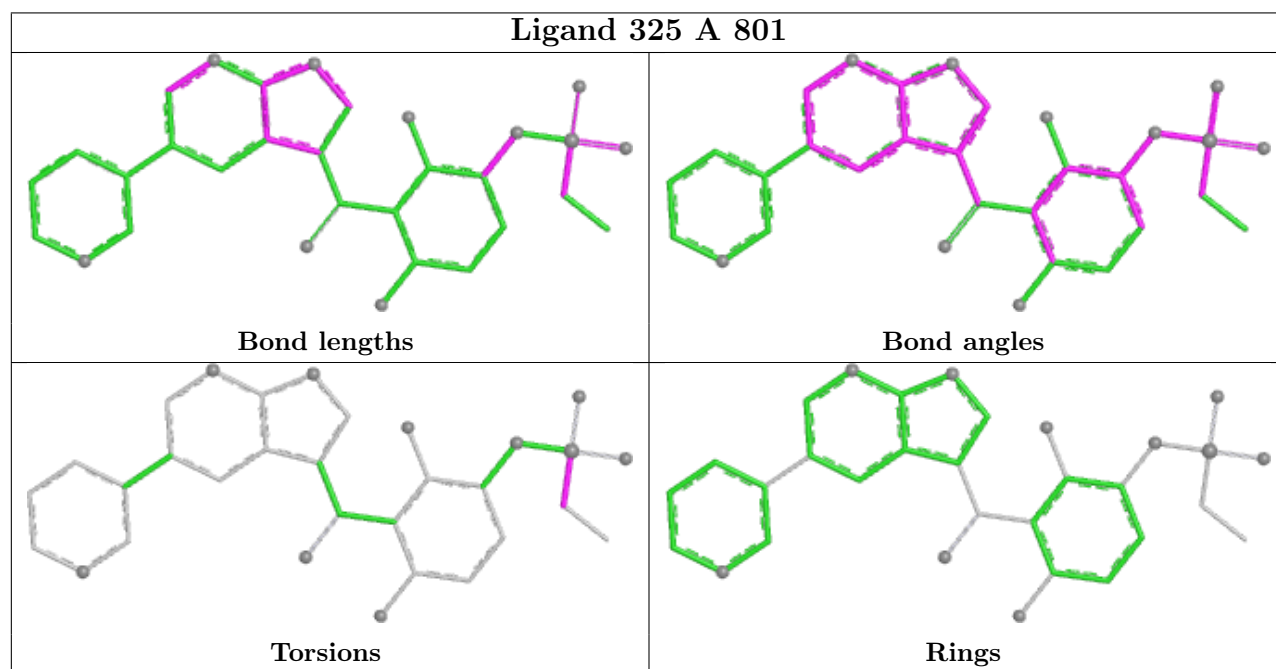
Mol	Chain	Res	Type	Atoms
2	A	801	325	C31-C26-S24-N23
2	A	801	325	C31-C26-S24-O25
2	A	801	325	C31-C26-S24-O27

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	325	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	251/292 (85%)	0.52	19 (7%) 20 15	22, 47, 85, 105	0
1	B	257/292 (88%)	0.98	46 (17%) 3 2	21, 58, 115, 161	0
All	All	508/584 (86%)	0.75	65 (12%) 7 6	21, 51, 100, 161	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	466	GLY	5.4
1	B	491	THR	4.6
1	A	718	ALA	4.4
1	B	467	SER	4.4
1	B	459	VAL	4.2
1	B	465	SER	4.1
1	B	493	GLN	3.9
1	B	597	LEU	3.9
1	B	596	GLY	3.8
1	B	488	THR	3.5
1	A	627	MET	3.4
1	A	687	LYS	3.4
1	A	467	SER	3.3
1	B	468	PHE	3.2
1	B	523	PRO	3.1
1	B	595	PHE	3.1
1	B	470	THR	3.1
1	B	495	LEU	3.0
1	A	468	PHE	3.0
1	B	469	GLY	3.0
1	B	462	ARG	3.0
1	B	463	ILE	3.0
1	B	486	ASN	2.9
1	B	492	PRO	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	490	PRO	2.8
1	A	492	PRO	2.8
1	A	466	GLY	2.7
1	B	454	ASP	2.7
1	B	458	THR	2.7
1	A	714	ILE	2.6
1	B	457	ILE	2.6
1	A	543	ALA	2.6
1	B	487	VAL	2.6
1	A	716	GLU	2.5
1	B	489	ALA	2.5
1	A	554	ILE	2.5
1	B	461	GLN	2.5
1	B	721	LEU	2.5
1	A	461	GLN	2.4
1	B	662	ARG	2.4
1	A	717	LEU	2.4
1	B	475	LYS	2.4
1	A	523	PRO	2.4
1	A	696	CYS	2.3
1	B	472	TYR	2.3
1	B	464	GLY	2.3
1	A	709	ARG	2.3
1	B	659	ILE	2.2
1	A	486	ASN	2.2
1	B	455	GLY	2.2
1	B	534	GLY	2.2
1	B	580	ASN	2.2
1	B	473	LYS	2.2
1	B	717	LEU	2.2
1	A	493	GLN	2.2
1	B	485	LEU	2.2
1	B	546	THR	2.1
1	B	719	ARG	2.1
1	B	599	THR	2.1
1	A	490	PRO	2.1
1	B	672	GLY	2.1
1	B	522	LYS	2.1
1	B	657	SER	2.0
1	B	543	ALA	2.0
1	B	525	LEU	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](#)

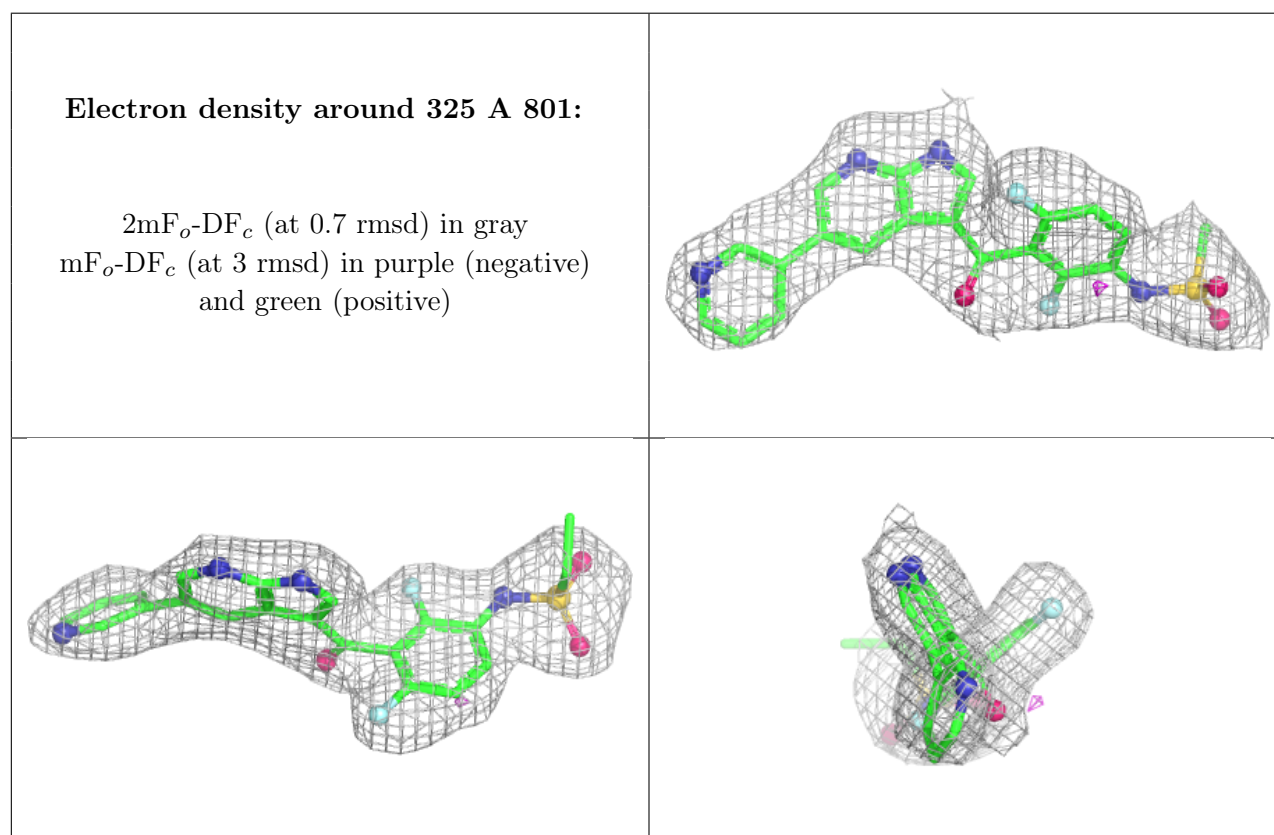
There are no oligosaccharides in this entry.

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($\text{\AA}^2$)	Q<0.9
2	325	A	801	31/31	0.96	0.09	38,45,63,77	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 ⓘ

There are no such residues in this entry.