Full wwPDB X-ray Structure Validation Report (i)

Jun 23, 2024 – 03:23 AM EDT

PDB ID	:	6DKW
Title	:	Crystal structure of Trk-A in complex with the Pan-Trk Kinase Inhibitor, compound 3.
Authors	:	Greasley, S.E.; Brown, D.
Deposited on	:	2018-05-31
Resolution	:	2.91 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:

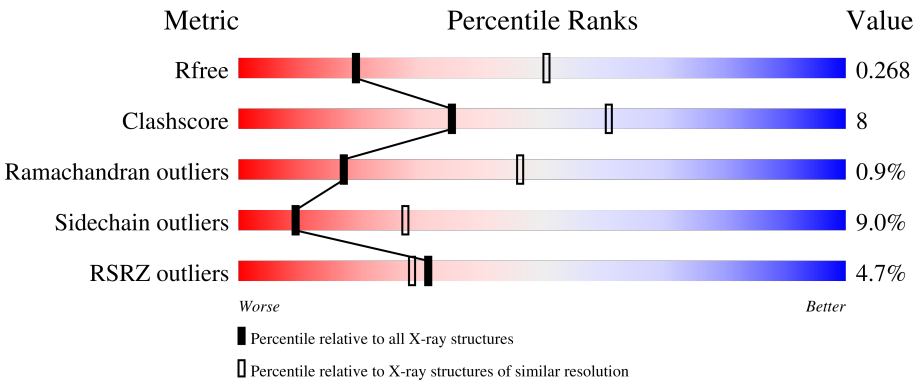
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.91 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	2307 (2.94-2.90)
Clashscore	141614	2531 (2.94-2.90)
Ramachandran outliers	138981	2462 (2.94-2.90)
Sidechain outliers	138945	2464 (2.94-2.90)
RSRZ outliers	127900	2248 (2.94-2.90)

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	308	3% 72% 18% • 8%
1	B	308	6% 70% 13% • 13%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4656 atoms, of which 50 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 Tyrosine-protein kinase receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	284	2290	1463	420	391	16	0	2	0
1	B	269	2171	1388	392	375	16	0	2	0

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	489	MET	-	initiating methionine	UNP J3KP20
A	490	HIS	-	expression tag	UNP J3KP20
A	491	HIS	-	expression tag	UNP J3KP20
A	492	HIS	-	expression tag	UNP J3KP20
A	493	HIS	-	expression tag	UNP J3KP20
A	494	HIS	-	expression tag	UNP J3KP20
A	495	HIS	-	expression tag	UNP J3KP20
A	496	LEU	-	expression tag	UNP J3KP20
A	497	VAL	-	expression tag	UNP J3KP20
A	498	PRO	-	expression tag	UNP J3KP20
A	499	ARG	-	expression tag	UNP J3KP20
A	500	GLY	-	expression tag	UNP J3KP20
A	501	SER	-	expression tag	UNP J3KP20
B	489	MET	-	initiating methionine	UNP J3KP20
B	490	HIS	-	expression tag	UNP J3KP20
B	491	HIS	-	expression tag	UNP J3KP20
B	492	HIS	-	expression tag	UNP J3KP20
B	493	HIS	-	expression tag	UNP J3KP20
B	494	HIS	-	expression tag	UNP J3KP20
B	495	HIS	-	expression tag	UNP J3KP20
B	496	LEU	-	expression tag	UNP J3KP20
B	497	VAL	-	expression tag	UNP J3KP20
B	498	PRO	-	expression tag	UNP J3KP20
B	499	ARG	-	expression tag	UNP J3KP20
B	500	GLY	-	expression tag	UNP J3KP20

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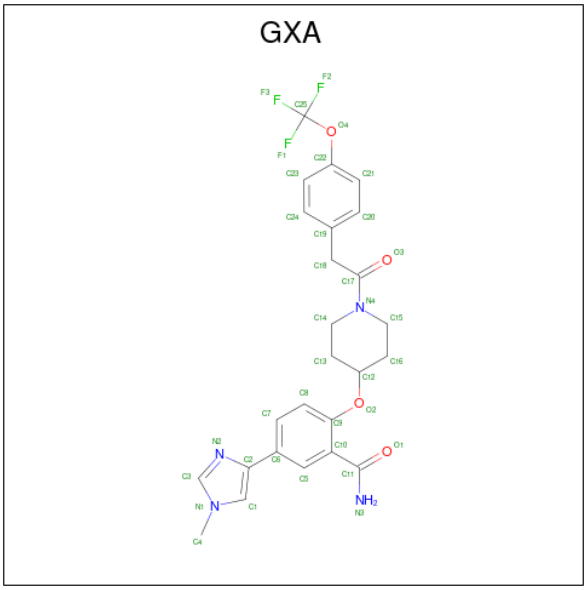
Chain	Residue	Modelled	Actual	Comment	Reference
B	501	SER	-	expression tag	UNP J3KP20

- Molecule 2 is 5-(1-methyl-1H-imidazol-4-yl)-2-[(1-{[4-(trifluoromethoxy)phenyl]acetyl}piperidin-4-yl)oxy]benzamide (three-letter code: GXA) (formula: $C_{25}H_{25}F_3N_4O_4$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	F	H	N	O		
2	A	1	61	25	3	25	4	4	0	0
2	B	1	61	25	3	25	4	4	0	0

- Molecule 3 is water.

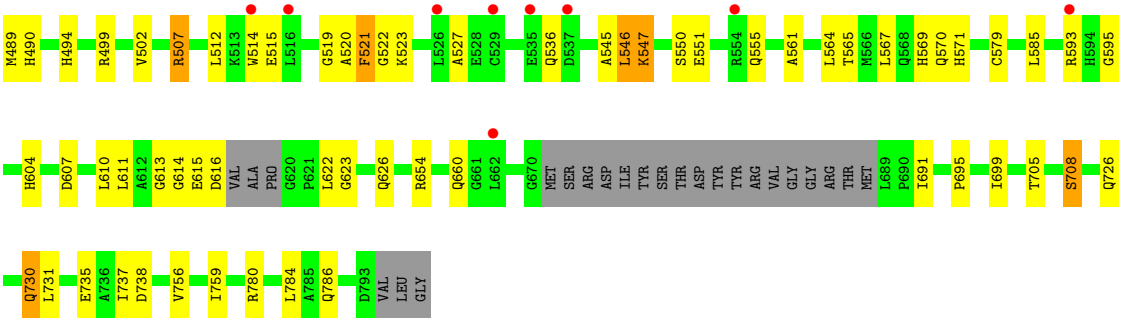
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	35	35	35	0	0
3	B	38	38	38	0	0

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.

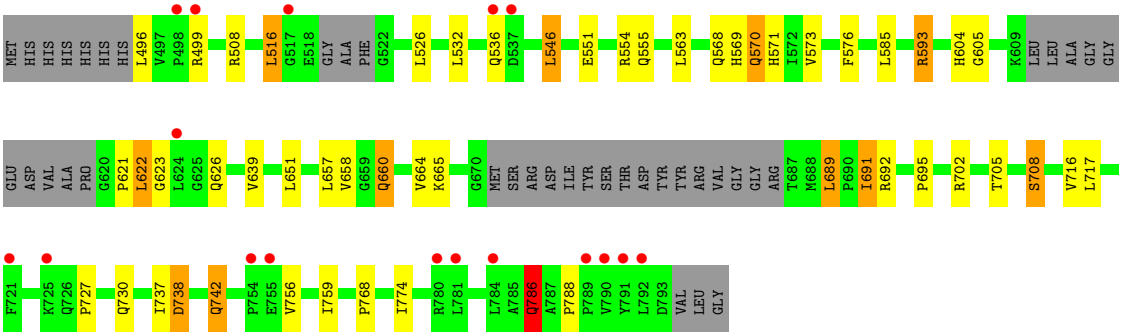
• Molecule 1: Tyrosine-protein kinase receptor

Chain A:



• Molecule 1: Tyrosine-protein kinase receptor

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	93.98Å 93.98Å 159.27Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	81.39 – 2.91 81.39 – 2.91	Depositor EDS
% Data completeness (in resolution range)	99.0 (81.39-2.91) 99.3 (81.39-2.91)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	3.87 (at 2.91Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.231 , 0.262 0.238 , 0.268	Depositor DCC
R_{free} test set	931 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å^2)	81.5	Xtriage
Anisotropy	0.680	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 58.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.035 for -h,-k,l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	4656	wwPDB-VP
Average B, all atoms (Å^2)	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.02% 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: GXA

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	0.51	0/2350	0.75	2/3178 (0.1%)
1	B	0.48	0/2223	0.69	0/3006
All	All	0.50	0/4573	0.72	2/6184 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	613	GLY	N-CA-C	-7.83	93.52	113.10
1	A	615	GLU	C-N-CA	6.59	138.18	121.70

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	2290	0	2270	45	0
1	B	2171	0	2167	31	0
2	A	36	25	0	1	0
2	B	36	25	0	0	0
3	A	35	0	0	1	0
3	B	38	0	0	0	0
All	All	4606	50	4437	74	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (74) 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:522:GLY:HA2	1:A:547:LYS:CE	1.71	1.19
1:A:522:GLY:HA2	1:A:547:LYS:HE2	1.13	1.11
1:A:521:PHE:CD1	1:A:547:LYS:NZ	2.25	1.04
1:A:521:PHE:HD1	1:A:547:LYS:NZ	1.61	0.98
1:A:519:GLY:HA3	1:A:523:LYS:HA	1.51	0.90
1:A:547:LYS:N	1:A:547:LYS:HE3	1.87	0.89
1:A:520:ALA:HB2	3:A:915:HOH:O	1.73	0.87
1:A:607:ASP:O	1:A:611:LEU:HD12	1.77	0.85
1:A:522:GLY:CA	1:A:547:LYS:NZ	2.41	0.83
1:A:521:PHE:HD1	1:A:547:LYS:HZ3	1.18	0.82
1:A:521:PHE:CD1	1:A:547:LYS:HG2	2.15	0.81
1:A:522:GLY:N	1:A:547:LYS:NZ	2.29	0.79
1:A:522:GLY:N	1:A:547:LYS:HZ3	1.79	0.79
1:A:522:GLY:CA	1:A:547:LYS:CE	2.58	0.78
1:A:522:GLY:HA2	1:A:547:LYS:NZ	1.98	0.78
1:A:545:ALA:O	1:A:547:LYS:HE2	1.87	0.75
1:A:522:GLY:CA	1:A:547:LYS:HZ1	2.00	0.71
1:A:551:GLU:O	1:A:555:GLN:HG2	1.94	0.68
1:B:689:LEU:HD13	1:B:691:ILE:HD13	1.77	0.66
1:B:604:HIS:HB3	1:B:622:LEU:HD13	1.78	0.66
1:B:569:HIS:CD2	1:B:571:HIS:H	2.14	0.65
1:B:569:HIS:HD2	1:B:571:HIS:H	1.45	0.65
1:B:593:ARG:HD3	1:B:660:GLN:HB3	1.78	0.64
1:A:521:PHE:HD1	1:A:547:LYS:HG2	1.62	0.63
1:A:569:HIS:CD2	1:A:571:HIS:H	2.20	0.60
1:A:545:ALA:O	1:A:547:LYS:CE	2.49	0.59
1:A:569:HIS:HD2	1:A:571:HIS:H	1.50	0.59
1:B:689:LEU:HD13	1:B:691:ILE:CD1	2.32	0.58
1:B:593:ARG:NH2	1:B:660:GLN:CB	2.68	0.56
1:B:593:ARG:NH2	1:B:660:GLN:HB3	2.20	0.56
1:B:705:THR:H	1:B:708:SER:HB3	1.71	0.55
1:B:692:ARG:HB3	1:B:727:PRO:HG2	1.90	0.53
1:B:695:PRO:HG3	1:B:708:SER:HA	1.90	0.53
1:B:546:LEU:HD22	1:B:585:LEU:HD12	1.91	0.53
1:A:502:VAL:HA	1:A:565:THR:HG21	1.89	0.53
1:A:730:GLN:HB2	1:B:737:ILE:HD13	1.91	0.53
1:B:593:ARG:HH21	1:B:660:GLN:HB3	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:658:VAL:HG22	1:B:664:VAL:HG22	1.91	0.52
1:A:695:PRO:HG3	1:A:708:SER:HA	1.92	0.52
1:B:516:LEU:HD21	1:B:526:LEU:HB2	1.90	0.52
1:B:786:GLN:O	1:B:788:PRO:HD3	2.10	0.51
1:A:705:THR:H	1:A:708:SER:HB3	1.75	0.51
1:A:521:PHE:C	1:A:547:LYS:HD2	2.31	0.51
1:A:607:ASP:O	1:A:611:LEU:CD1	2.55	0.50
1:A:547:LYS:HE3	1:A:547:LYS:H	1.73	0.49
1:A:623:GLY:H	1:A:626:GLN:HE21	1.59	0.48
1:A:521:PHE:O	1:A:547:LYS:HD2	2.12	0.48
1:B:756:VAL:HA	1:B:759:ILE:HD12	1.96	0.47
1:A:699:ILE:HG21	1:A:737:ILE:HG23	1.97	0.47
1:A:607:ASP:HB3	1:A:610:LEU:HD23	1.97	0.46
1:A:546:LEU:C	1:A:547:LYS:HE3	2.36	0.46
1:A:507:ARG:HG2	1:A:579:CYS:SG	2.56	0.46
1:A:595:GLY:HA2	2:A:801:GXA:C1	2.46	0.46
1:B:605:GLY:HA2	1:B:621:PRO:HB3	1.97	0.46
1:A:561:ALA:O	1:A:565:THR:HG23	2.16	0.46
1:A:546:LEU:HD22	1:A:585:LEU:HD12	1.98	0.45
1:B:689:LEU:HD11	1:B:702:ARG:NH1	2.32	0.44
1:B:573:VAL:HG21	1:B:657:LEU:HD13	2.00	0.44
1:A:731:LEU:HD22	1:A:735:GLU:HB3	2.00	0.43
1:B:570:GLN:HA	1:B:665:LYS:HZ1	1.83	0.43
1:B:593:ARG:NH2	1:B:660:GLN:HB2	2.33	0.43
1:B:738:ASP:O	1:B:742:GLN:HB2	2.18	0.43
1:A:604:HIS:HB3	1:A:622:LEU:HG	2.00	0.43
1:A:564:LEU:HD23	1:A:567:LEU:HD12	2.00	0.43
1:B:651:LEU:HG	1:B:716:VAL:HG21	1.99	0.43
1:B:623:GLY:H	1:B:626:GLN:HE21	1.67	0.42
1:B:717:LEU:HD23	1:B:717:LEU:HA	1.92	0.42
1:A:756:VAL:HA	1:A:759:ILE:HD12	2.01	0.42
1:B:532:LEU:HD21	1:B:576:PHE:CG	2.56	0.41
1:B:593:ARG:HH21	1:B:660:GLN:CB	2.32	0.41
1:A:780:ARG:NH2	1:A:784:LEU:HD21	2.35	0.41
1:A:610:LEU:HD12	1:B:768:PRO:HD3	2.02	0.41
1:A:512:LEU:HD23	1:A:527:ALA:HB2	2.03	0.41
1:B:639:VAL:HG23	1:B:774:ILE:HG13	2.02	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	280/308 (91%)	265 (95%)	12 (4%)	3 (1%)	14 41
1	B	263/308 (85%)	248 (94%)	13 (5%)	2 (1%)	19 49
All	All	543/616 (88%)	513 (94%)	25 (5%)	5 (1%)	17 46

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	551	GLU
1	A	614	GLY
1	A	660	GLN
1	B	786	GLN
1	A	550	SER

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	240/259 (93%)	219 (91%)	21 (9%)	10 28
1	B	230/259 (89%)	209 (91%)	21 (9%)	9 27
All	All	470/518 (91%)	428 (91%)	42 (9%)	9 28

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	489	MET

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Mol	Chain	Res	Type
1	A	490	HIS
1	A	494	HIS
1	A	499	ARG
1	A	507	ARG
1	A	514	TRP
1	A	515	GLU
1	A	521	PHE
1	A	536	GLN
1	A	546	LEU
1	A	547	LYS
1	A	570	GLN
1	A	593	ARG
1	A	616	ASP
1	A	654	ARG
1	A	691	ILE
1	A	708	SER
1	A	726	GLN
1	A	730	GLN
1	A	738	ASP
1	A	786	GLN
1	B	496	LEU
1	B	499	ARG
1	B	508	ARG
1	B	516	LEU
1	B	536	GLN
1	B	546	LEU
1	B	554	ARG
1	B	555	GLN
1	B	563	LEU
1	B	568	GLN
1	B	570	GLN
1	B	593	ARG
1	B	622	LEU
1	B	660	GLN
1	B	689	LEU
1	B	691	ILE
1	B	708	SER
1	B	730	GLN
1	B	738	ASP
1	B	742	GLN
1	B	786	GLN

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	569	HIS
1	A	626	GLN
1	A	730	GLN
1	A	742	GLN
1	B	568	GLN
1	B	569	HIS
1	B	626	GLN
1	B	660	GLN
1	B	730	GLN
1	B	742	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)

2 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	GXA	A	801	-	37,39,39	0.37	0	51,56,56	0.59	0
2	GXA	B	801	-	37,39,39	0.41	0	51,56,56	0.59	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	GXA	A	801	-	-	2/25/35/35	0/4/4/4
2	GXA	B	801	-	-	3/25/35/35	0/4/4/4

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	GXA	C9-C10-C11-O1
2	B	801	GXA	C9-C10-C11-O1
2	A	801	GXA	C9-C10-C11-N3
2	B	801	GXA	C9-C10-C11-N3
2	B	801	GXA	C8-C9-O2-C12

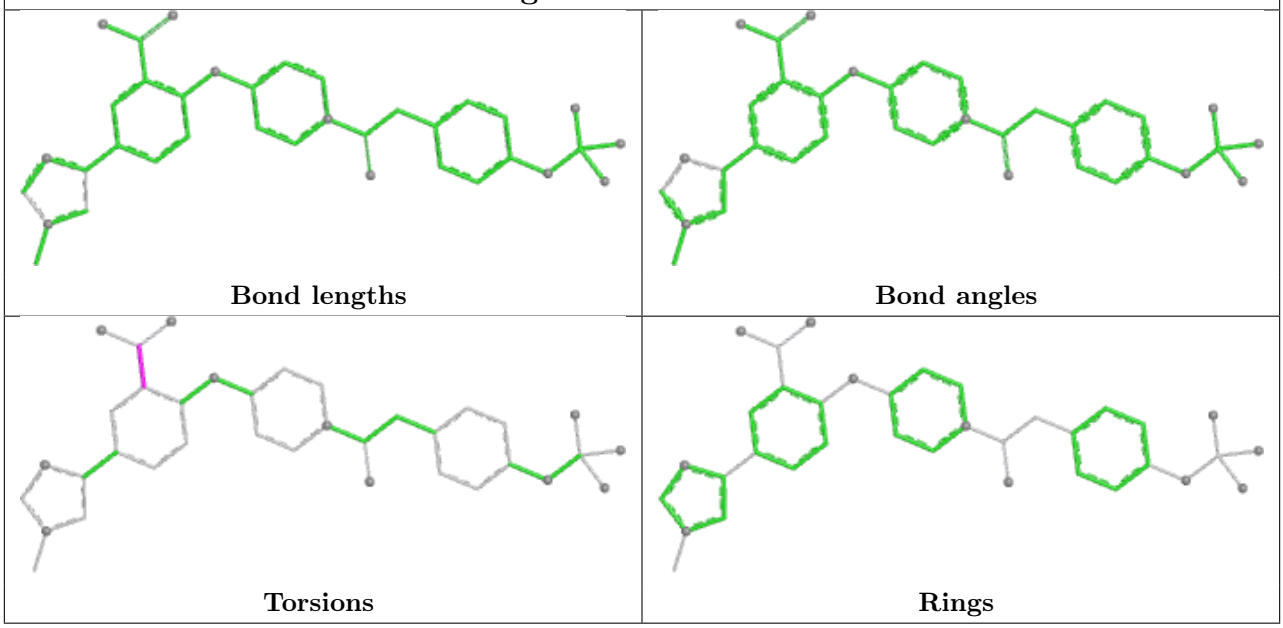
There are no ring outliers.

1 monomer is involved in 1 short contact:

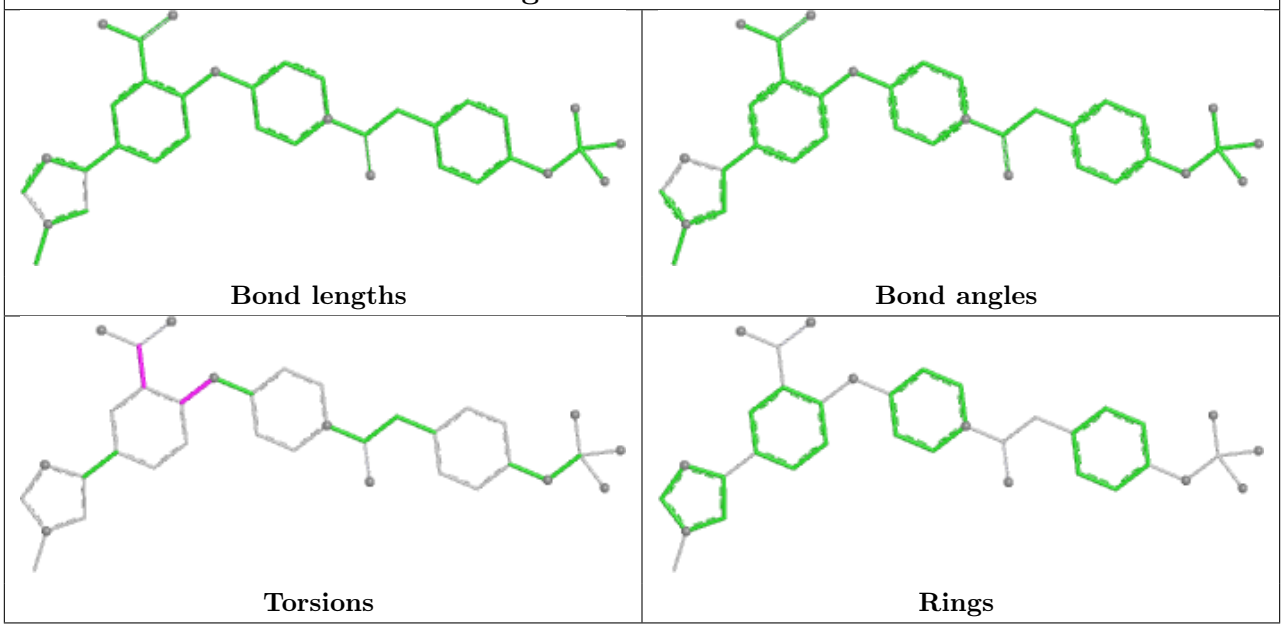
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	GXA	1	0

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 GXA A 801



Ligand GXA B 801



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	284/308 (92%)	0.17	9 (3%)	47	44	60, 87, 131, 161	0
1	B	269/308 (87%)	0.35	17 (6%)	20	17	60, 96, 148, 183	0
All	All	553/616 (89%)	0.26	26 (4%)	31	28	60, 90, 140, 183	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	789	PRO	6.7
1	B	791	TYR	4.7
1	A	516	LEU	4.4
1	B	790	VAL	4.3
1	A	537	ASP	4.2
1	B	517	GLY	4.2
1	B	499	ARG	3.2
1	B	792	LEU	2.9
1	A	526	LEU	2.6
1	A	662	LEU	2.6
1	B	784	LEU	2.6
1	B	755	GLU	2.6
1	B	537	ASP	2.5
1	B	754	PRO	2.5
1	B	536	GLN	2.5
1	B	781	LEU	2.4
1	A	593	ARG	2.4
1	B	624	LEU	2.3
1	A	529	CYS	2.2
1	B	498	PRO	2.2
1	A	535	GLU	2.2
1	B	725	LYS	2.2
1	A	514	TRP	2.1
1	B	721	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	554	ARG	2.1
1	B	780	ARG	2.0

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

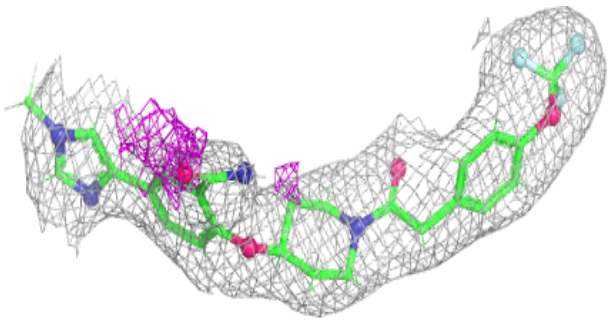
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

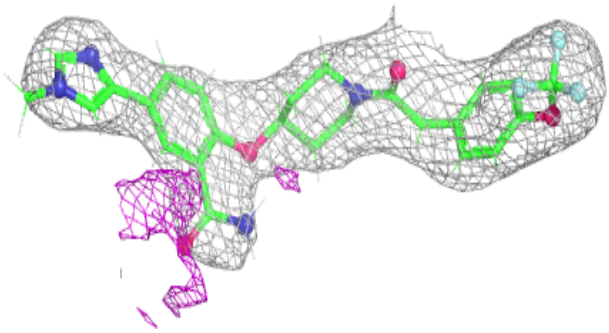
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	GXA	B	801	36/36	0.95	0.24	54,66,90,91	0
2	GXA	A	801	36/36	0.96	0.30	64,76,82,83	0

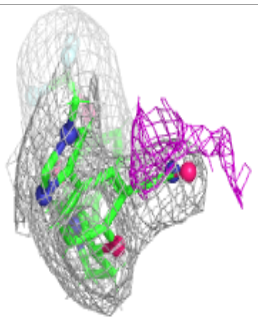
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around GXA 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)

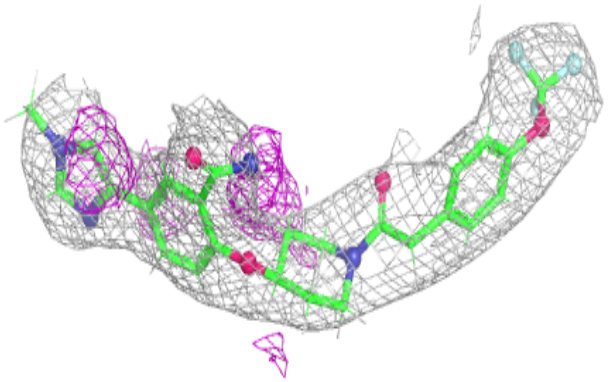


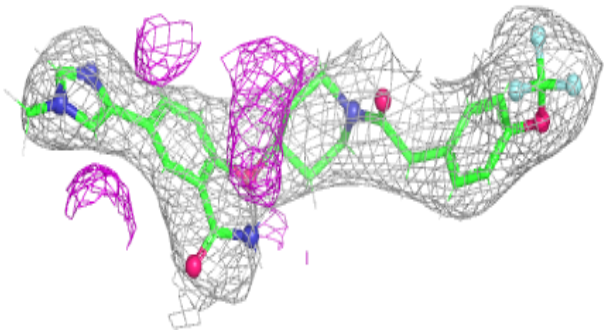


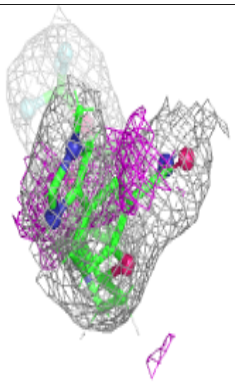


Electron density around GXA A 801:

$2mF_o$-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.