Full wwPDB X-ray Structure Validation Report (i)

Jun 18, 2024 – 08:51 PM EDT

PDB ID	:	3ZC6
Title	:	Crystal structure of JAK3 kinase domain in complex with an indazole substituted pyrrolopyrazine inhibitor
Authors	:	Kuglstatter, A.; Jestel, A.; Nagel, S.; Boettcher, J.; Blaesse, M.
Deposited on	:	2012-11-16
Resolution	:	2.42 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:

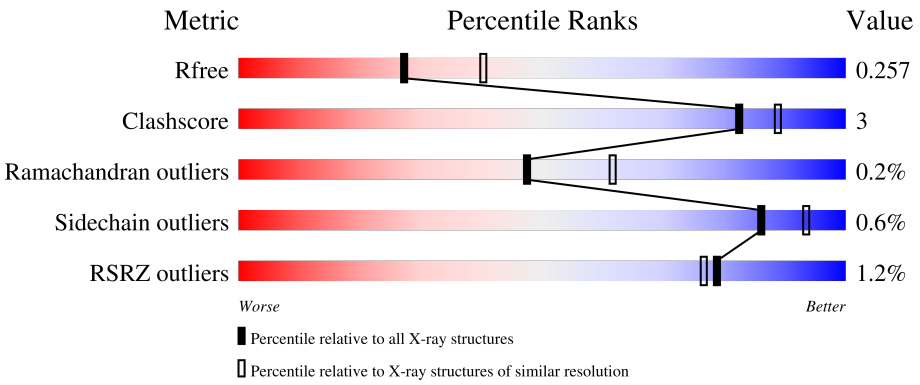
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (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 2.42 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	4647 (2.44-2.40)
Clashscore	141614	5161 (2.44-2.40)
Ramachandran outliers	138981	5073 (2.44-2.40)
Sidechain outliers	138945	5074 (2.44-2.40)
RSRZ outliers	127900	4543 (2.44-2.40)

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	288	2%, 92%, 5% •
1	B	288	88%, 9% •
1	C	288	%, 91%, 5% •
1	D	288	%, 86%, 6% • 7%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 9695 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.

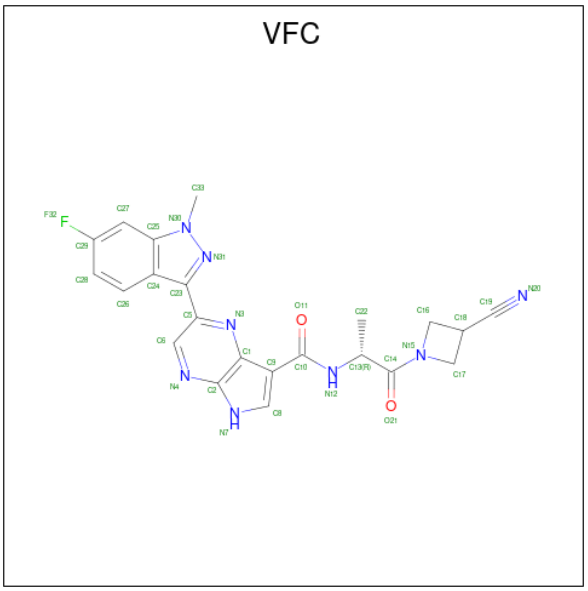
- Molecule 1 is a protein called TYROSINE-PROTEIN KINASE JAK3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	279	2304	1460	408	420	2	14	39	6	0
1	B	278	2304	1458	406	423	2	15	38	7	0
1	C	277	2305	1460	409	419	2	15	53	7	0
1	D	269	2221	1411	392	402	2	14	26	4	0

There are 8 discrepancies between the modelled and reference sequences:

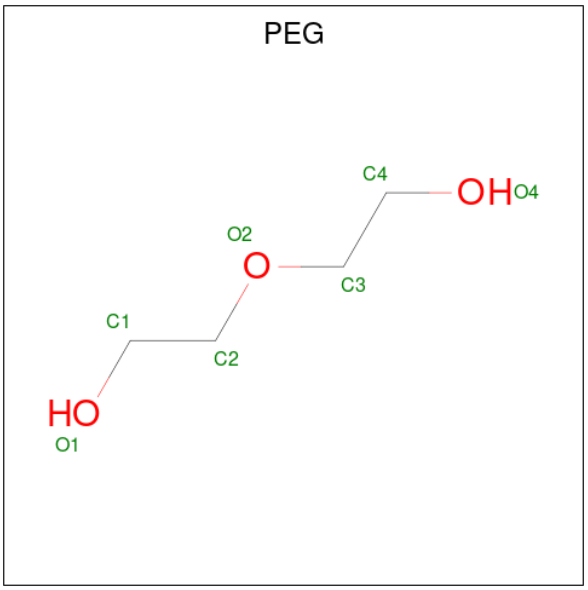
Chain	Residue	Modelled	Actual	Comment	Reference
A	1040	SER	CYS	engineered mutation	UNP P52333
A	1048	SER	CYS	engineered mutation	UNP P52333
B	1040	SER	CYS	engineered mutation	UNP P52333
B	1048	SER	CYS	engineered mutation	UNP P52333
C	1040	SER	CYS	engineered mutation	UNP P52333
C	1048	SER	CYS	engineered mutation	UNP P52333
D	1040	SER	CYS	engineered mutation	UNP P52333
D	1048	SER	CYS	engineered mutation	UNP P52333

- Molecule 2 is N-[(2R)-1-(3-cyanoazetidin-1-yl)-1-oxidanylidene-propan-2-yl]-2-(6-fluoranyl -1-methyl-indazol-3-yl)-5H-pyrrolo[2,3-b]pyrazine-7-carboxamide (three-letter code: VFC) (formula: $C_{22}H_{19}FN_8O_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	F	N	O		
2	A	1	33	22	1	8	2	0	0
			Total	C	F	N	O		
2	B	1	33	22	1	8	2	0	0
			Total	C	F	N	O		
2	C	1	33	22	1	8	2	0	0
			Total	C	F	N	O		
2	D	1	33	22	1	8	2	0	0

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

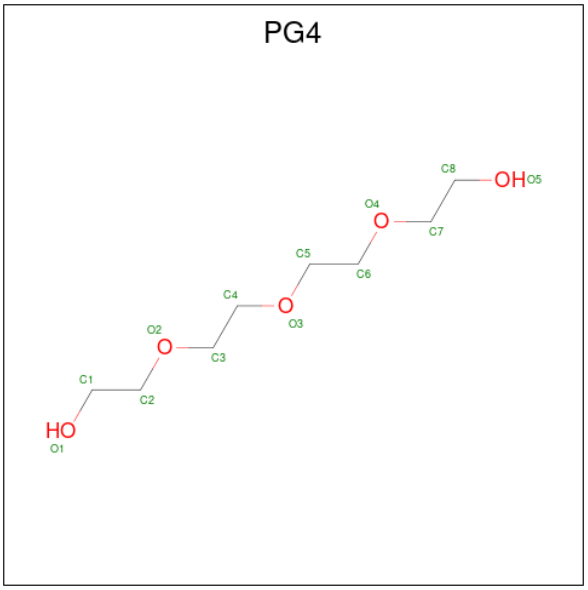


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	7	4	3	0	0
			Total	C	O		
3	B	1	7	4	3	0	0

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
4	A	3	3	3	0	0
			Total	Cl		
4	D	1	1	1	0	0

- Molecule 5 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	B	1	13	8	5	0	0
			Total	C	O		
5	C	1	13	8	5	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	116	116	116	0	0

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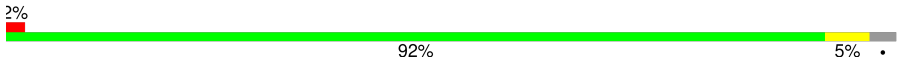
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	B	101	101	101	0	0
			Total	O		
6	C	84	84	84	0	0
			Total	O		
6	D	83	84	84	0	1

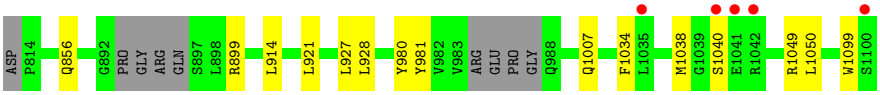
3 Residue-property plots (i)

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 JAK3

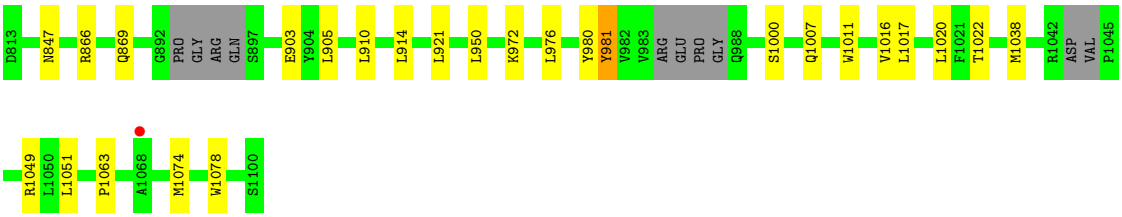
Chain A:





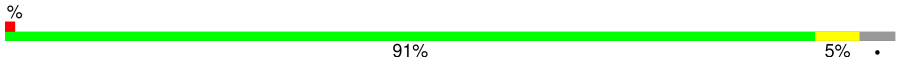
• Molecule 1: TYROSINE-PROTEIN KINASE JAK3

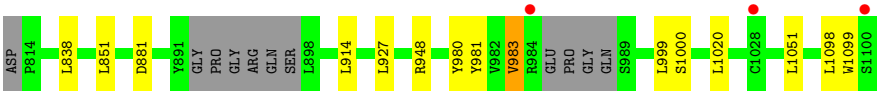
Chain B:



• Molecule 1: TYROSINE-PROTEIN KINASE JAK3

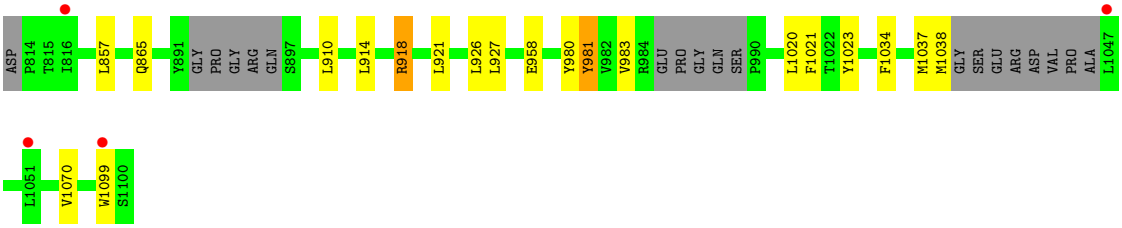
Chain C:





• Molecule 1: TYROSINE-PROTEIN KINASE JAK3

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	57.17Å 117.72Å 105.83Å 90.00° 97.66° 90.00°	Depositor
Resolution (Å)	104.89 – 2.42 48.24 – 2.42	Depositor EDS
% Data completeness (in resolution range)	99.8 (104.89-2.42) 99.8 (48.24-2.42)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.31 (at 2.42Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.191 , 0.254 0.204 , 0.257	Depositor DCC
R_{free} test set	1128 reflections (2.13%)	wwPDB-VP
Wilson B-factor (Å^2)	31.7	Xtriage
Anisotropy	0.483	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 47.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	9695	wwPDB-VP
Average B, all atoms (Å^2)	48.0	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 37.86 % 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 4.0244e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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: PEG, PG4, PTR, VFC, CL

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	0.50	0/2322	0.65	0/3132
1	B	0.51	0/2321	0.64	0/3128
1	C	0.49	0/2323	0.61	0/3132
1	D	0.49	0/2237	0.64	0/3013
All	All	0.50	0/9203	0.64	0/12405

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2304	0	2276	9	0
1	B	2304	0	2264	15	0
1	C	2305	0	2276	8	0
1	D	2221	0	2201	15	0
2	A	33	0	19	0	0
2	B	33	0	19	0	0
2	C	33	0	18	0	0
2	D	33	0	19	0	0
3	A	7	0	10	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	7	0	10	0	0
4	A	3	0	0	0	0
4	D	1	0	0	0	0
5	B	13	0	18	0	0
5	C	13	0	18	0	0
6	A	116	0	0	1	0
6	B	101	0	0	2	0
6	C	84	0	0	0	0
6	D	84	0	0	0	0
All	All	9695	0	9148	46	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 3.

All (46) 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:D:918[A]:ARG:HH11	1:D:918[A]:ARG:HG3	0.98	1.11
1:D:981:PTR:HE1	1:D:983:VAL:HG22	1.52	0.88
1:D:918[A]:ARG:HG3	1:D:918[A]:ARG:NH1	1.77	0.88
1:D:910:LEU:HD21	1:D:1020:LEU:HD21	1.59	0.84
1:D:918[A]:ARG:HH11	1:D:918[A]:ARG:CG	1.87	0.79
1:C:927:LEU:HD22	1:C:1099:TRP:CZ3	2.25	0.71
1:D:914:LEU:HD11	1:D:1020:LEU:HD23	1.74	0.68
1:D:918[A]:ARG:NH1	1:D:918[A]:ARG:CG	2.54	0.66
1:C:838:LEU:HD21	1:C:851:LEU:HD22	1.78	0.66
1:D:927:LEU:HD22	1:D:1099:TRP:CZ3	2.37	0.60
1:B:910:LEU:HD21	1:B:1020:LEU:HD21	1.88	0.56
1:C:999:LEU:HB2	1:C:1051:LEU:HD13	1.90	0.54
1:C:948:ARG:NH1	1:C:983:VAL:HG21	2.25	0.52
6:A:3073:HOH:O	1:B:866[A]:ARG:NH1	2.43	0.51
1:A:928:LEU:HD13	1:B:976:LEU:HB2	1.94	0.50
1:A:1038:MET:HE1	1:A:1050:LEU:HD13	1.94	0.49
1:A:1038:MET:HB2	1:A:1049:ARG:HG3	1.94	0.49
1:D:1034:PHE:HA	1:D:1037:MET:HE3	1.95	0.49
1:A:1007[B]:GLN:NE2	1:A:1007[B]:GLN:H	2.11	0.48
1:B:905:LEU:HD12	1:B:905:LEU:N	2.29	0.47
1:D:914:LEU:HD23	1:D:921:LEU:HD13	1.96	0.47
1:D:981:PTR:CE1	1:D:983:VAL:HG22	2.34	0.47
1:A:927:LEU:HD22	1:A:1099:TRP:CZ3	2.51	0.46
1:A:1038:MET:HB2	1:A:1049:ARG:CG	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:926:LEU:HD11	1:D:1023:TYR:CZ	2.51	0.46
1:B:1007[B]:GLN:NE2	6:B:3077:HOH:O	2.49	0.44
1:B:950:LEU:HG	1:B:1016:VAL:HG21	1.99	0.44
1:B:1000:SER:HB3	1:B:1051:LEU:HD11	2.00	0.44
1:B:866[B]:ARG:NH2	6:B:3020:HOH:O	0.67	0.44
1:C:927:LEU:HD22	1:C:1099:TRP:CE3	2.52	0.43
1:B:903:GLU:HG3	1:B:905:LEU:HD11	2.00	0.43
1:D:1021:PHE:CE2	1:D:1070:VAL:HG11	2.53	0.43
1:B:914:LEU:HD23	1:B:921:LEU:HD13	2.01	0.43
1:B:1017:LEU:HB3	1:B:1074:MET:HE2	2.01	0.42
1:C:1000:SER:HB3	1:C:1051:LEU:HD21	2.01	0.42
1:D:857:LEU:HD11	1:D:865:GLN:HA	2.01	0.42
1:B:972:LYS:HE3	1:B:981:PTR:HE1	2.02	0.42
1:A:1034:PHE:HB3	1:A:1038:MET:HE3	2.02	0.41
1:B:1011:TRP:CE3	1:B:1078:TRP:HA	2.55	0.41
1:C:914:LEU:HD11	1:C:1020:LEU:HD23	2.01	0.41
1:D:927:LEU:HD22	1:D:1099:TRP:CE3	2.55	0.41
1:A:914:LEU:HD23	1:A:921:LEU:HD13	2.02	0.41
1:B:1038:MET:HB2	1:B:1049:ARG:CG	2.50	0.41
1:A:856:GLN:HB3	1:A:899:ARG:HD3	2.03	0.41
1:B:1022:THR:HG23	1:B:1063:PRO:HB3	2.03	0.41
1:C:927:LEU:HD21	1:C:1098:LEU:HB2	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	277/288 (96%)	268 (97%)	8 (3%)	1 (0%)	34 47
1	B	275/288 (96%)	266 (97%)	9 (3%)	0	100 100
1	C	276/288 (96%)	269 (98%)	6 (2%)	1 (0%)	34 47

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	263/288 (91%)	259 (98%)	4 (2%)	0	100	100
All	All	1091/1152 (95%)	1062 (97%)	27 (2%)	2 (0%)	47	61

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1040	SER
1	C	983	VAL

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	249/250 (100%)	249 (100%)	0	100	100
1	B	249/250 (100%)	247 (99%)	2 (1%)	81	91
1	C	249/250 (100%)	248 (100%)	1 (0%)	91	96
1	D	240/250 (96%)	236 (98%)	4 (2%)	60	77
All	All	987/1000 (99%)	980 (99%)	7 (1%)	86	92

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	847	ASN
1	B	869	GLN
1	C	881	ASP
1	D	918[A]	ARG
1	D	918[B]	ARG
1	D	958	GLU
1	D	1038	MET

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	858	GLN
1	C	1002	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

8 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
1	PTR	B	981	1	15,16,17	2.02	1 (6%)	17,22,24	0.54	0
1	PTR	B	980	1	15,16,17	1.97	1 (6%)	17,22,24	0.57	0
1	PTR	D	980	1	15,16,17	2.08	1 (6%)	17,22,24	0.63	1 (5%)
1	PTR	D	981	1	15,16,17	2.03	1 (6%)	17,22,24	0.63	0
1	PTR	C	980	1	15,16,17	2.10	1 (6%)	17,22,24	0.53	0
1	PTR	C	981	1	15,16,17	2.06	1 (6%)	17,22,24	0.49	0
1	PTR	A	981	1	15,16,17	1.95	1 (6%)	17,22,24	0.56	0
1	PTR	A	980	1	15,16,17	2.05	1 (6%)	17,22,24	0.60	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
1	PTR	B	981	1	-	0/10/11/13	0/1/1/1
1	PTR	B	980	1	-	0/10/11/13	0/1/1/1
1	PTR	D	980	1	-	0/10/11/13	0/1/1/1
1	PTR	D	981	1	-	0/10/11/13	0/1/1/1
1	PTR	C	980	1	-	0/10/11/13	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PTR	C	981	1	-	2/10/11/13	0/1/1/1
1	PTR	A	981	1	-	0/10/11/13	0/1/1/1
1	PTR	A	980	1	-	0/10/11/13	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	980	PTR	OH-CZ	-7.70	1.23	1.40
1	A	980	PTR	OH-CZ	-7.44	1.23	1.40
1	D	980	PTR	OH-CZ	-7.42	1.24	1.40
1	D	981	PTR	OH-CZ	-7.34	1.24	1.40
1	C	981	PTR	OH-CZ	-7.33	1.24	1.40
1	B	980	PTR	OH-CZ	-7.04	1.24	1.40
1	B	981	PTR	OH-CZ	-7.01	1.24	1.40
1	A	981	PTR	OH-CZ	-6.85	1.25	1.40

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	980	PTR	O2P-P-OH	2.21	111.86	105.32

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C	981	PTR	CA-CB-CG-CD2
1	C	981	PTR	CA-CB-CG-CD1

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	981	PTR	1	0
1	D	981	PTR	2	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 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	$\#\|Z\| > 2$
5	PG4	C	2104	-	12,12,12	0.56	0	11,11,11	0.33	0
2	VFC	C	2103	-	30,37,37	2.49	9 (30%)	30,55,55	1.92	9 (30%)
3	PEG	A	2104	-	6,6,6	0.62	0	5,5,5	0.56	0
2	VFC	A	2103	-	30,37,37	2.37	8 (26%)	30,55,55	1.73	7 (23%)
3	PEG	B	2105	-	6,6,6	0.51	0	5,5,5	0.10	0
2	VFC	D	2103	-	30,37,37	2.13	7 (23%)	30,55,55	1.83	8 (26%)
2	VFC	B	2103	-	30,37,37	2.21	7 (23%)	30,55,55	1.88	6 (20%)
5	PG4	B	2104	-	12,12,12	0.63	0	11,11,11	0.56	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
5	PG4	C	2104	-	-	6/10/10/10	-
2	VFC	C	2103	-	-	0/14/30/30	0/5/5/5
3	PEG	A	2104	-	-	4/4/4/4	-
2	VFC	A	2103	-	-	0/14/30/30	0/5/5/5
3	PEG	B	2105	-	-	1/4/4/4	-
2	VFC	D	2103	-	-	0/14/30/30	0/5/5/5
2	VFC	B	2103	-	-	1/14/30/30	0/5/5/5
5	PG4	B	2104	-	-	4/10/10/10	-

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2103	VFC	C17-C18	-6.21	1.51	1.55
2	C	2103	VFC	C17-C18	-5.85	1.51	1.55
2	D	2103	VFC	C17-C18	-5.83	1.51	1.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2103	VFC	C17-C18	-5.57	1.51	1.55
2	C	2103	VFC	C19-N20	5.52	1.24	1.14
2	A	2103	VFC	C6-N4	5.41	1.40	1.31
2	A	2103	VFC	C16-C18	-5.41	1.51	1.55
2	A	2103	VFC	C5-N3	5.18	1.40	1.33
2	B	2103	VFC	C5-N3	5.18	1.40	1.33
2	C	2103	VFC	C5-N3	5.13	1.40	1.33
2	D	2103	VFC	C6-N4	4.89	1.40	1.31
2	B	2103	VFC	C6-N4	4.85	1.40	1.31
2	C	2103	VFC	C6-N4	4.84	1.39	1.31
2	D	2103	VFC	C5-N3	4.68	1.40	1.33
2	B	2103	VFC	C16-C18	-4.28	1.52	1.55
2	D	2103	VFC	C16-C18	-4.11	1.52	1.55
2	C	2103	VFC	C16-C18	-4.03	1.52	1.55
2	C	2103	VFC	C18-C19	-3.51	1.38	1.48
2	B	2103	VFC	C27-C29	2.80	1.40	1.36
2	D	2103	VFC	C23-C5	-2.74	1.48	1.50
2	C	2103	VFC	C23-C5	-2.69	1.48	1.50
2	A	2103	VFC	C14-N15	2.69	1.38	1.35
2	C	2103	VFC	C27-C29	2.39	1.39	1.36
2	D	2103	VFC	C14-N15	2.32	1.38	1.35
2	A	2103	VFC	C27-C29	2.29	1.39	1.36
2	B	2103	VFC	C9-C10	-2.23	1.47	1.50
2	A	2103	VFC	C23-C5	-2.19	1.48	1.50
2	D	2103	VFC	C27-C29	2.17	1.39	1.36
2	B	2103	VFC	F32-C29	-2.12	1.31	1.36
2	A	2103	VFC	C13-C14	-2.04	1.49	1.53
2	C	2103	VFC	C14-N15	2.04	1.37	1.35

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	2103	VFC	C23-C5-N3	5.54	123.28	116.49
2	B	2103	VFC	C23-C5-N3	5.50	123.24	116.49
2	B	2103	VFC	C16-N15-C17	-5.34	90.95	94.69
2	D	2103	VFC	C16-N15-C17	-4.87	91.28	94.69
2	A	2103	VFC	C23-C5-N3	4.84	122.43	116.49
2	C	2103	VFC	C16-N15-C17	-4.76	91.36	94.69
2	D	2103	VFC	C23-C5-N3	4.33	121.80	116.49
2	A	2103	VFC	C16-N15-C17	-3.75	92.06	94.69
2	C	2103	VFC	C22-C13-C14	-3.01	104.07	109.87
2	D	2103	VFC	C5-C6-N4	-2.94	121.42	123.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	2103	VFC	C6-C5-C23	-2.87	117.57	121.53
2	B	2103	VFC	C6-C5-N3	-2.85	118.56	120.78
2	A	2103	VFC	C6-C5-N3	-2.75	118.64	120.78
2	D	2103	VFC	C22-C13-C14	-2.75	104.58	109.87
2	A	2103	VFC	C22-C13-C14	-2.72	104.63	109.87
2	C	2103	VFC	C13-N12-C10	2.54	127.23	121.31
2	B	2103	VFC	C13-N12-C10	2.53	127.19	121.31
2	B	2103	VFC	C6-C5-C23	-2.41	118.20	121.53
2	D	2103	VFC	C13-N12-C10	2.40	126.88	121.31
2	B	2103	VFC	C22-C13-C14	-2.39	105.28	109.87
2	D	2103	VFC	C28-C29-C27	-2.34	120.59	123.32
2	C	2103	VFC	C28-C29-C27	-2.21	120.74	123.32
2	D	2103	VFC	C22-C13-N12	-2.13	106.47	110.38
2	A	2103	VFC	O21-C14-N15	2.11	124.13	121.61
2	A	2103	VFC	C5-C6-N4	-2.11	122.04	123.62
2	A	2103	VFC	C28-C29-C27	-2.11	120.86	123.32
2	C	2103	VFC	C6-C5-N3	-2.10	119.14	120.78
2	C	2103	VFC	C28-C26-C24	-2.06	118.27	121.15
2	D	2103	VFC	C6-C5-C23	-2.01	118.75	121.53
2	C	2103	VFC	C5-C6-N4	-2.01	122.11	123.62

There are no chirality outliers.

All (16) torsion outliers are listed below:

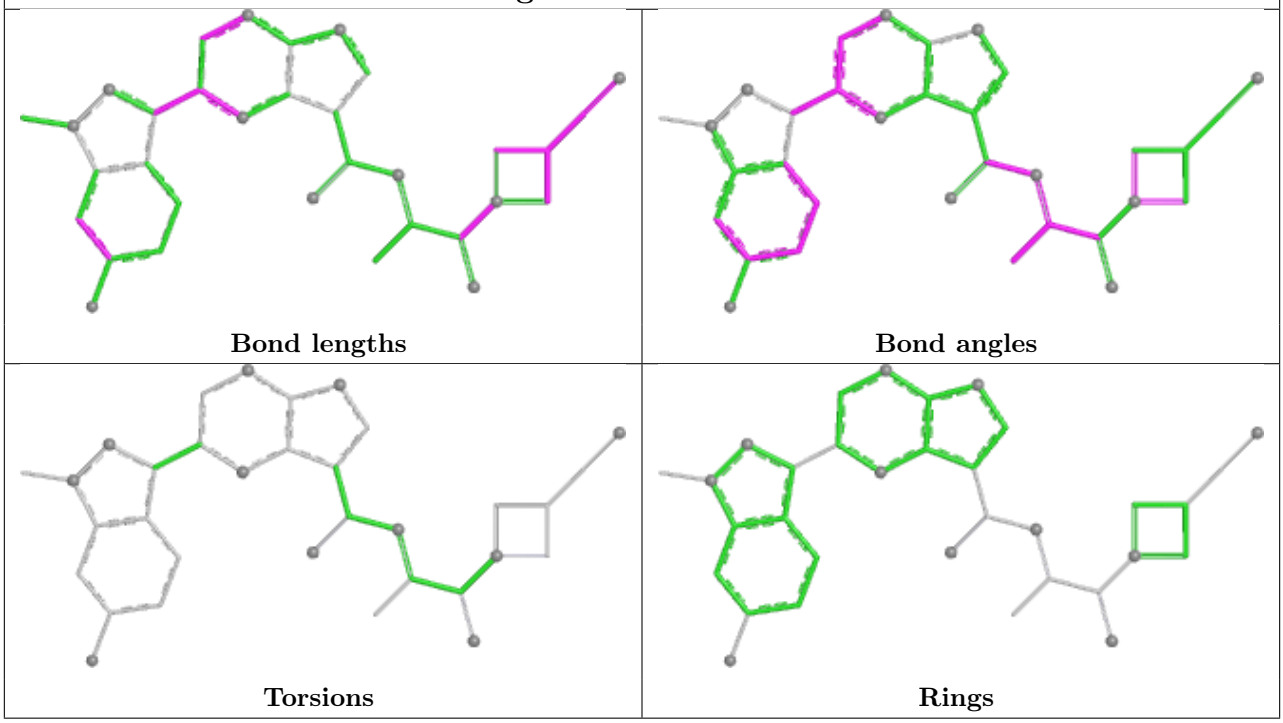
Mol	Chain	Res	Type	Atoms
5	B	2104	PG4	O2-C3-C4-O3
5	C	2104	PG4	O2-C3-C4-O3
5	C	2104	PG4	O1-C1-C2-O2
3	A	2104	PEG	O1-C1-C2-O2
3	B	2105	PEG	O2-C3-C4-O4
5	B	2104	PG4	O3-C5-C6-O4
5	C	2104	PG4	O4-C7-C8-O5
3	A	2104	PEG	O2-C3-C4-O4
5	B	2104	PG4	C8-C7-O4-C6
5	C	2104	PG4	C4-C3-O2-C2
3	A	2104	PEG	C4-C3-O2-C2
5	B	2104	PG4	C6-C5-O3-C4
2	B	2103	VFC	C14-C13-N12-C10
5	C	2104	PG4	C6-C5-O3-C4
5	C	2104	PG4	C3-C4-O3-C5
3	A	2104	PEG	C1-C2-O2-C3

There are no ring outliers.

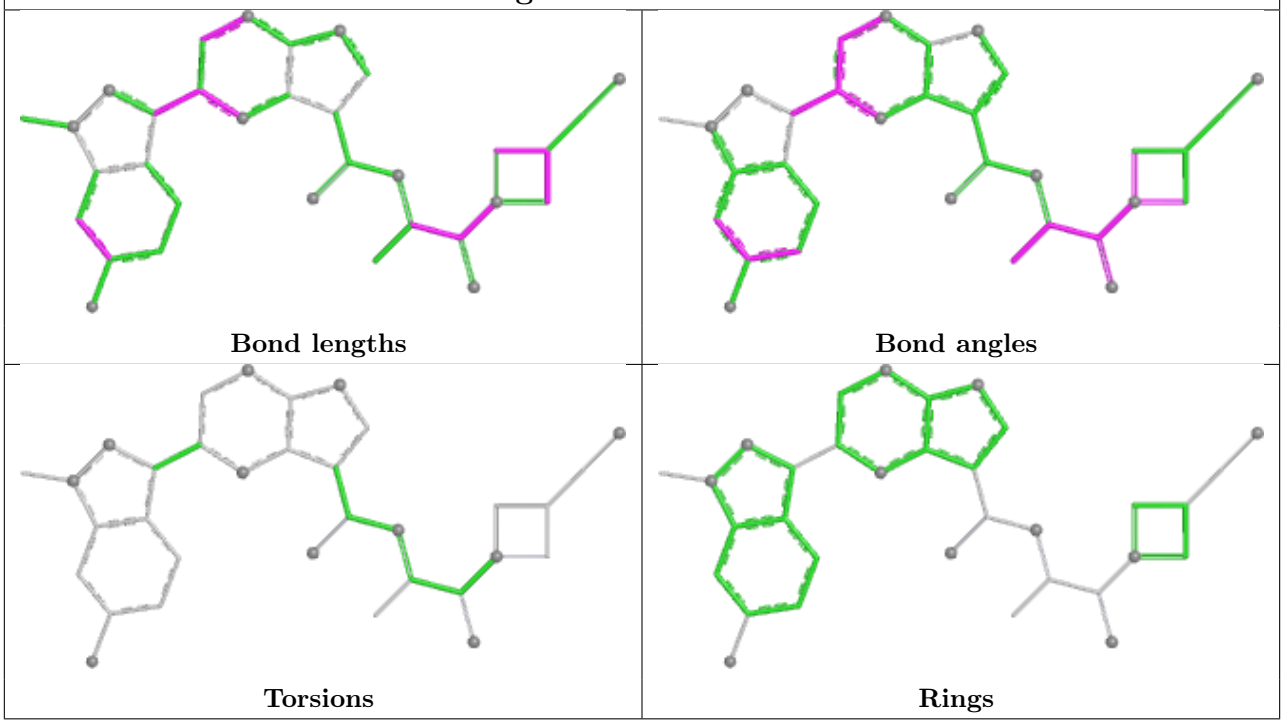
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand VFC C 2103



Ligand VFC A 2103



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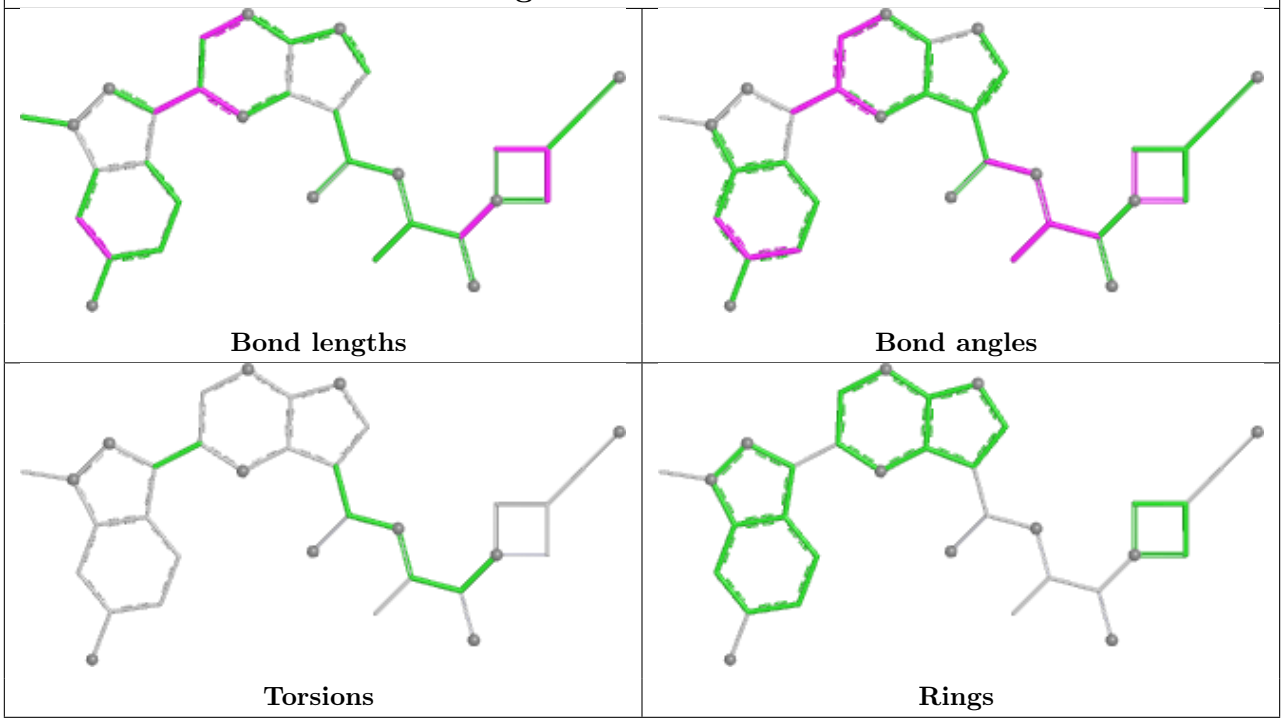
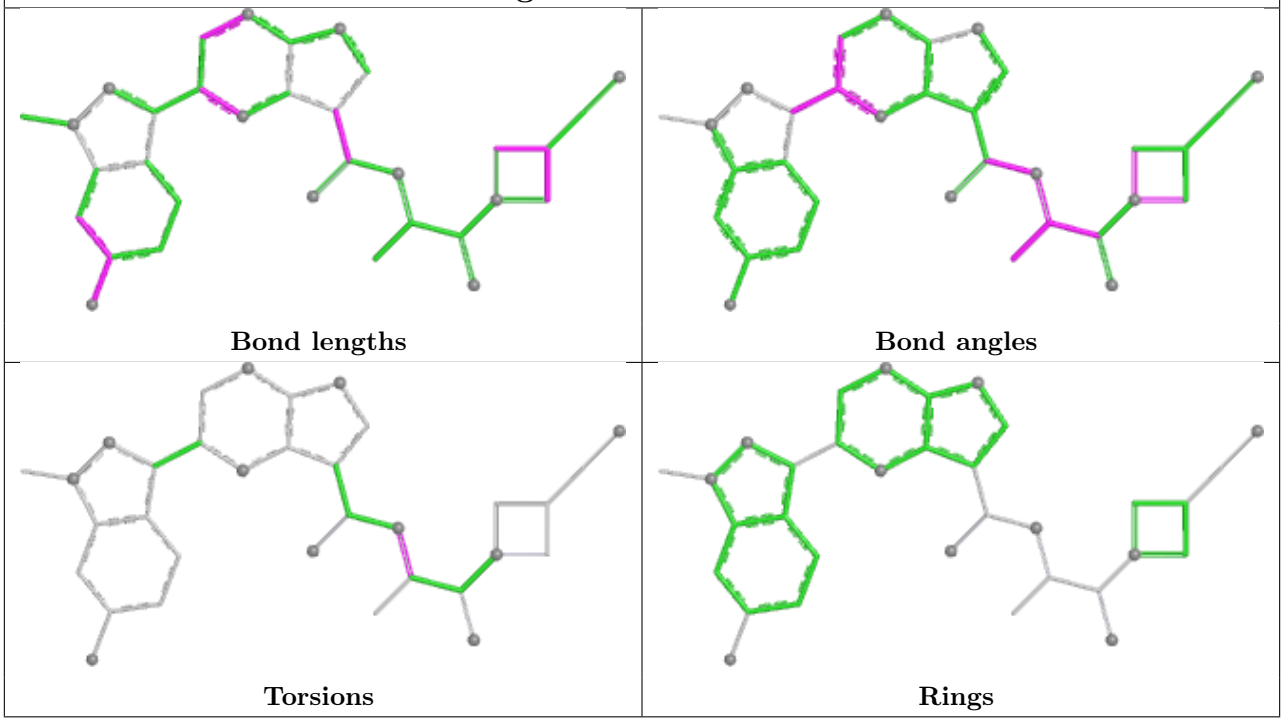


Ligand VFC B 2103



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	277/288 (96%)	-0.14	5 (1%)	68	65	25, 43, 77, 122	11 (3%)
1	B	276/288 (95%)	-0.07	1 (0%)	92	91	25, 44, 79, 132	12 (4%)
1	C	275/288 (95%)	-0.07	3 (1%)	80	78	29, 49, 80, 109	15 (5%)
1	D	267/288 (92%)	-0.10	4 (1%)	73	71	28, 46, 75, 88	8 (2%)
All	All	1095/1152 (95%)	-0.09	13 (1%)	79	76	25, 45, 79, 132	46 (4%)

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1040	SER	4.4
1	B	1068	ALA	3.0
1	D	1047	LEU	2.9
1	A	1041	GLU	2.9
1	A	1042	ARG	2.8
1	C	1100	SER	2.8
1	C	984	ARG	2.4
1	C	1028	CYS	2.4
1	D	1099	TRP	2.3
1	D	816	ILE	2.3
1	A	1100	SER	2.2
1	D	1051	LEU	2.2
1	A	1035	LEU	2.1

6.2 Non-standard residues in protein, DNA, RNA chains (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
1	PTR	B	981	16/17	0.82	0.22	53,84,93,94	0
1	PTR	A	980	16/17	0.85	0.14	48,65,82,83	0
1	PTR	D	981	16/17	0.85	0.22	50,79,92,92	0
1	PTR	D	980	16/17	0.89	0.17	45,64,85,89	0
1	PTR	A	981	16/17	0.89	0.16	52,76,85,85	0
1	PTR	C	980	16/17	0.91	0.16	49,63,84,87	0
1	PTR	B	980	16/17	0.92	0.16	50,59,79,85	0
1	PTR	C	981	16/17	0.92	0.15	52,78,89,92	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

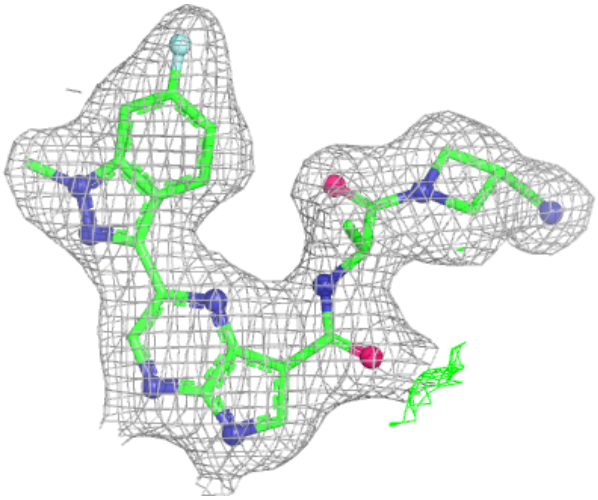
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

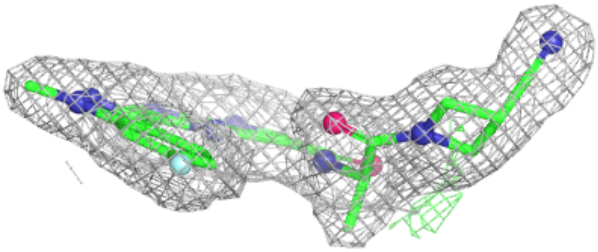
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	PEG	A	2104	7/7	0.78	0.19	67,69,73,76	0
5	PG4	C	2104	13/13	0.85	0.23	57,79,87,88	0
3	PEG	B	2105	7/7	0.89	0.24	72,76,84,86	0
5	PG4	B	2104	13/13	0.91	0.14	53,61,73,73	0
2	VFC	A	2103	33/33	0.96	0.12	25,33,41,49	0
4	CL	A	2105	1/1	0.97	0.10	51,51,51,51	0
2	VFC	C	2103	33/33	0.97	0.12	29,40,47,49	0
2	VFC	D	2103	33/33	0.97	0.13	26,36,44,48	0
4	CL	D	2104	1/1	0.98	0.07	45,45,45,45	0
2	VFC	B	2103	33/33	0.98	0.13	19,32,41,46	0
4	CL	A	2107	1/1	0.98	0.12	50,50,50,50	0
4	CL	A	2106	1/1	0.99	0.11	32,32,32,32	0

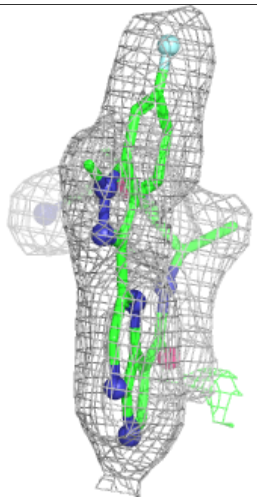
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around VFC A 2103:

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







Electron density around VFC C 2103:

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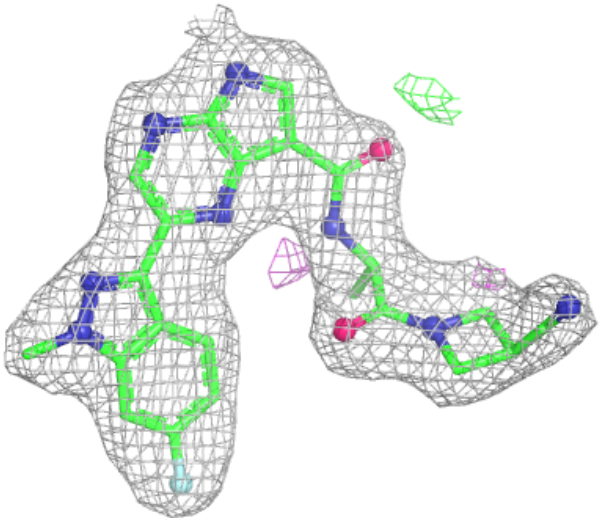
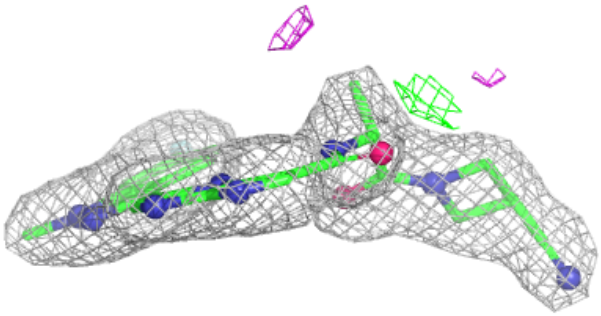
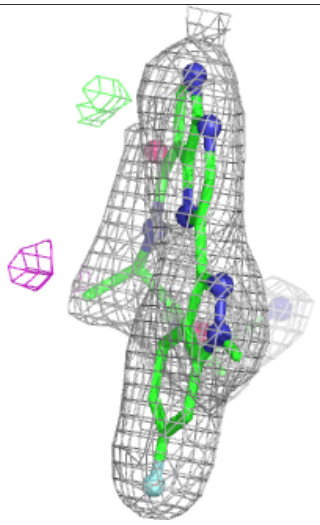
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

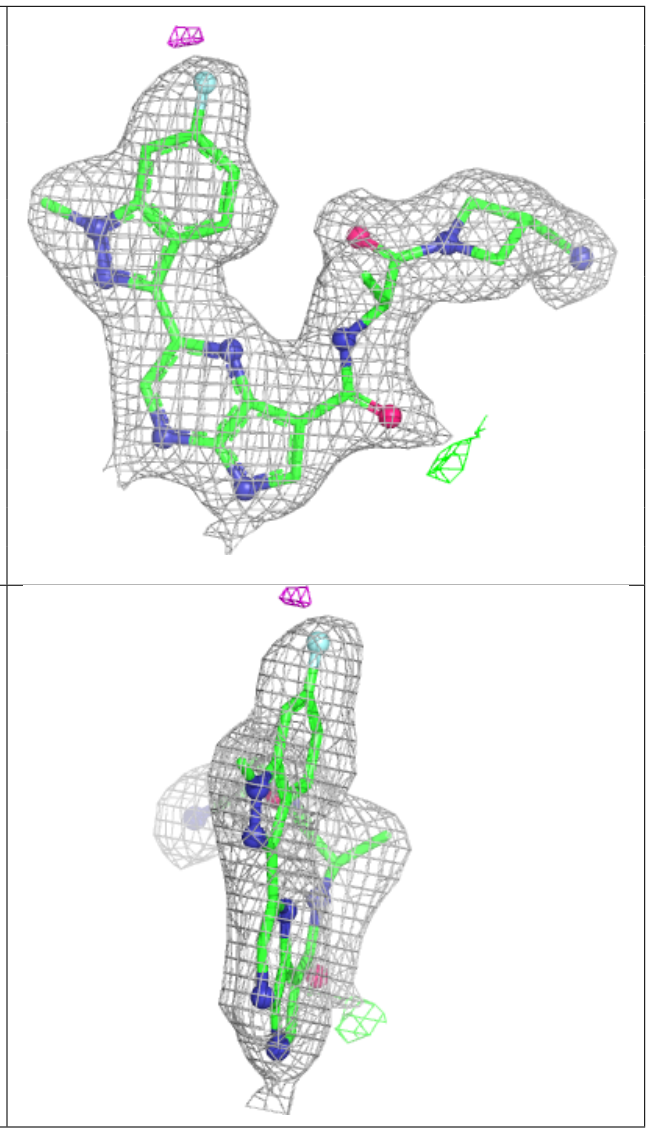






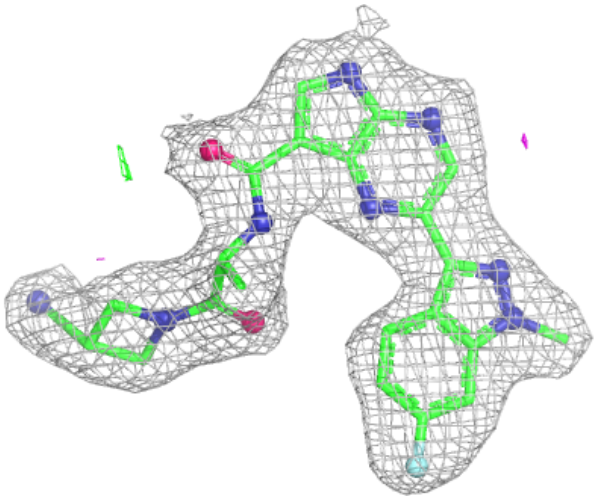
Electron density around VFC D 2103:

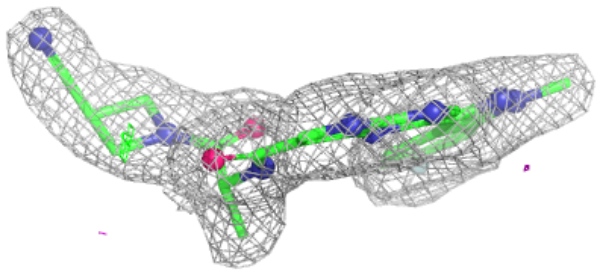
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

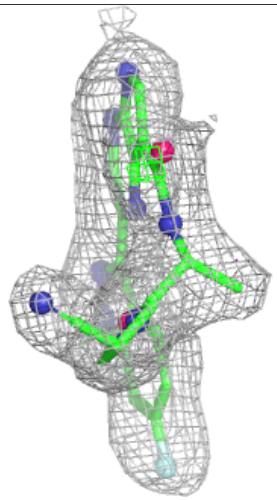


Electron density around VFC B 2103:

$2mF_o$-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.